

Supplementary Material

Supplementary Methods

Sample preparation and genomic profiling

All tumor tissues (fresh-frozen, FF; or formalin fixed paraffin-embedded, FFPE) obtained from participants were reviewed by two independent pathologists before sample disposal to confirm the pathologic diagnoses of biliary tract carcinomas (BTCs). Serial sections on tissue slides was performed to evaluate tumor content and percentage. Only samples with estimated tumor purity >20% on histopathologic assessment were further subjected to genomic profiling. Tumor purity assessed in our study is the proportion of cancer cells in the tissues. Tumor tissue section from each patient was hematoxylin-eosin (HE) stained, and the proportion of cancer cells was then estimated by pathologists. For sections with tumor purity over 20%, bulk tumor tissues were subjected to extract DNA and sequencing. For those tumor tissues with purity less than 20%, micro-resected tumor section was performed to remove non-cancerous cells and stroma to improve tumor purity. DNAs were extracted from paired tumor and blood samples using DNA Extraction Kits (Qiagen). DNAs yield and quality were quantified using the Qubit 3.0 (Invitrogen) and NanoDrop 2000 (Thermo Scientific) and the integrity was further visually inspected by agarose gel electrophoresis.

Genomic alterations profiling was performed in 2 major next-generation sequencing (NGS) platform, including whole-exome sequencing (WES) and a custom hybridization capture-based targeted panel sequencing (TPS)[1] provided by Origimed (Cancer Sequencing YS panel, CSYS, Shanghai, China). WES libraries were prepared from DNA extracted from tumor and normal samples using the Agilent's SureSelect Human All Exon V6 Kit (Agilent Technologies Inc.), and the sequencing was conducted using the Illumina HiSeq XTEN platform for paired-end 150bp reads. For CSYS platform, 50–250ng DNA was used to construct libraries, targeted genomic regions were hybrid-captured, and sequence reads were generated using Illumina (San Diego, CA) instruments with the referred procedures followed the steps described in Frampton et al,[2].

WES data analysis

Somatic mutation calling and filtering

Paired-end reads from paired tumor and normal-control samples were aligned to the human reference genome (GRCh37) using the Burrows-Wheeler Aligner (BWA) (version 0.7.10)[3]. Somatic mutation calling was processed using GATK (version 3.7)[4] followed the GATK Best Practices by using its Mutect2 function with duplicate and unmapped reads removed. A stringent downstream filter comprised of the following criteria was used to obtained high quality somatic variants: Variant Allele Fraction (VAF) $\geq 5\%$ with >5 variant supporting reads in the tumor sample, and VAF $< 1\%$ in the normal-control samples; a minimum of 5X coverage; strand bias ≤ 0.95 . Variants with PASS tag was retained and annotated by ANNOVAR (version: 2018-04-16)[5] using multiple specific databases (e.g. ExAC03, dbNSFP33a, ClinVar-20170130, avsnp150, Cosmic70). To make a possible comparison with target sequencing, non-coding variants in the introns, upstream or downstream of coding regions in 3'- and 5'-UTRs, and in intergenic regions were discarded.

Tumor mutation burden (TMB)

TMB analysis of WES data was performed followed with Chalmers et al,[6]. Briefly, all base substitutions and indels identified by WES in the coding region of genes as non-synonymous alterations, were all counted, except alterations listed as known somatic alterations in COSMIC or truncations in tumor suppressor genes were not counted. Known germline alterations in dbSNP or occurring with two or more counts in the ExAC database were not counted. TMB was calculated as the total number of mutation counts divided by the size of the coding region of the whole-exome territory.

Analysis of significantly mutated genes

MutSigCV (version 1.41)[7] was performed on the somatic variations of WES data to identify the significantly mutated genes that were mutated more often than expected by chance. MutsigCV's q-value < 0.1 was taken as threshold to detect significantly mutated genes. Populational frequencies of mutated genes was calculated by integrating WES and TPS samples together. In addition, mutual co-occurrence and exclusive event analysis on top 20 significantly mutated genes was performed by "somaticInteractions" function from Maftools (version 2.2.10)[8], using pair-wise Fisher's Exact test to detect such significant pair of genes. Then "oncostrip" function was used to visualize mutually exclusive set of genes for *TP53* and *KRAS*.

Somatic copy-number alterations (SCNAs) calling

According to the Agilent Target BED file, copy number for each segment was first analyzed by Control-FREEC (version 11.4)[9] and segments with same copy number were merged together to

generate a unique segment file. GISTIC2 (version 2.0.23)[10] was then used to calculate significant copy number gains and losses at a confidence level 0.99. Focal amplifications and deletions were selected using a threshold of GISTIC's q-value ≤ 0.01 .

Identifications and annotations of germline variants

Germline variants were identified using GATK (version 3.7) and its HaplotypeCaller function in single-sample mode with duplicate and unmapped reads removed. Variants were then filtered using VariantFiltration function of GATK with parameters "DP <4 || QD <2.0 || FS >60.0 || MQ <40.0 || MQRankSum <-12.5 || ReadPosRankSum <-8.0" and "DP <4 || QD <2.0 || FS >200.0 || ReadPosRankSum <-20.0" for SNVs and indels, respectively. Furthermore, to exclude potential tumor-in-normal contamination, germline mutations with VAF in normal-control sample <30%, and co-localizing with any known somatic mutation, which germline variants located at the same protein residue as recurrent ($n \geq 3$) somatic mutations in TCGA MC3 MAF[11] were further filtered. After the filtration, variants annotations were firstly obtained by ANNOVAR (version: 2018-04-16), and the evidence for pathogenic variations mainly derived from the public databases, including the Human Gene Mutation Database, Clinvar, Sorting Intolerant From Tolerant (SIFT), and the standard from American College of Medical Genetics (ACMG). A further manual review was performed to reduce the false positive variants.

Determination of MSI status

Microsatellites in the human reference genome (GRCh37) was identified using RepeatFinder (version 1.0)[12] with default parameters. To detect the microsatellite instability status, MANTIS (version 1.0.4)[13] was used with modified parameters "-mrq 20.0 -mlq 25.0 -mlc 20 -mrr 1" to fit for the whole-exome data, taken both tumor and non-tumor bam files as inputs. Any Step-Wise Difference (DIF) value calculated by MANTIS greater than or equal to 0.4 is treated as unstable. For 160 BTCs samples, only one patient was classified as MSI-H tumor, and MSI-PCR testing as the gold standard method was also performed to confirm the MSI-H status in tumor tissues.

TPS analysis for detecting somatic alterations

The raw sequencing data underwent stringent quality control of read depth and ratio of target capture. Data quality was inspected and controlled by examining sequencing coverage and uniformity, and a suite of customized bioinformatics pipelines was applied for discovery of SNVs,

short and long indels, SCNAs and gene rearrangements. The bioinformatics pipelines of CSTS have been described in our previous reports[1].

TMB was calculated from TPS data for each sample by counting the number of somatic mutations, including coding SNVs and indels, per megabase (Mb) of the sequence examined. Known somatic mutations in the Catalog of Somatic Mutations in Cancer (COSMIC) and known germline polymorphisms in the U.S. National Center for Biotechnology Information's Single Nucleotide Polymorphism Database (dbSNP) were not counted[6].

TPS panel designed 572 microsatellite loci (MSLs) targeted region as candidate MSI markers, which were done as previously described[13,14]. Using custom predictive model analyzed by a random forest algorithm combined with an orthogonal validation of PCR testing or IHC method as the gold standard, MSI status for each tumor sample could be judged. PCR products were analyzed by Sanger sequencing using an ABI 3730 Genetic Analyzer (Thermo Fisher Scientific, Waltham, MA).

Finally, all the detected mutations were compared with our in-house database of genomic changes specific to clinical annotation. A manual review process was performed to ensure no false positives or mistakes in clinical annotations, including complex variant curation and clinical relevance inference based on our in-house database. Based on the annotated mutations, a succinct report with relevant references to literature and clinical trials was generated.

Identification of hypermutated tumors

To determine a threshold of hypermutation in BTCs, a segmented linear regression analysis or "broken-stick analysis" was performed on the mutation burdens from WES cohort and TPS cohort, which refers to method from Campbell's colleagues[15]. Briefly, using the R package "Segmented", an iterative process was used to determine segment breakpoints at which a statistically significant change in the slope of adjacent regression lines occurred[16]. Consequently, the threshold was determined to 9.36 Mut/Mb in WES and 16.1 Mut/Mb in TPS, respectively.

Mutational landscape construction

A mutational case was defined as sample with no less than one non-silent mutation in coding region or SCNAs detected in individual genes. We determine 68 potential driver mutation genes of BTCs (Supplementary Table S4) as following: (1) genes that simultaneously captured by both WES and

CSYS platform; (2) significantly mutated genes identified by MutSigSV from our WES data; (3) recurrent mutations summarized from three previous studies which investigated the genomic landscape of BTCs, including Nakamura et al[17], Jusakul et al[18], and Montal et al[19]; (4) Tier1 cancer-related genes presented in COSMIC Cancer Gene Census database (version 91, <https://cancer.sanger.ac.uk/census>). The mutational landscape was constructed according to the populational frequencies (>5%) with a slight modification and integrated the mutations of *IDH2* and *MUC4* which showed significantly different rate as comparing with previous cohorts. The mutational spectrum was visualized by Maftools (version 2.2.10).

Mutations enriched for oncogenic pathways

Recurrent alterations of BTCs presented in Figure 1C could be roughly classified into four major functional families, that are cell cycle/cyclins genes, receptor tyrosine kinases genes, chromatin-modifying genes and others. Furthermore, ten curated pathways with oncogene and tumor suppressor gene information were retrieved from a study of TCGA program[20]. The mutational map of these 10 pathways was constructed according to the paper with a slight modification by integrating the description of percentage of mutational cases for each subtype of BTCs (Supplementary Figure S5).

Determining the scope of DNA damage response (DDR) genes

The scope and definition of DDR genes were collected from Human DNA Repair Genes (<https://www.mdanderson.org/documents/Labs/Wood-Laboratory/human-dna-repair-genes.html>). As most DDR genes have not yet been determined to have oncogenic or pathogenic effects in BTCs, we narrowed the scope of DDR genes into 47 coding genes that could be captured by both WES and CSYS platform (Supplementary Table S6), listing as: *TP53*, *MUTYH*, *APEX1*, *PARP1*, *PARP2*, *PARP3*, *MGMT*, *MSH2*, *MSH6*, *MLH1*, *PMS2*, *ERCC1*, *RAD51*, *RAD51B*, *RAD51D*, *XRCC2*, *XRCC3*, *RAD52*, *RAD54L*, *RAD54B*, *BRCA1*, *RAD50*, *MRE11A*, *NBN*, *FANCA*, *FANCC*, *BRCA2*, *FANCD2*, *FANCE*, *FANCF*, *FANCG*, *BRIP1*, *FANCL*, *FANCM*, *PALB2*, *RAD51C*, *PRKDC*, *POLB*, *POLD1*, *POLE*, *FEN1*, *BLM*, *ATM*, *RECQL*, *ATR*, *CHEK1* and *CHEK2*.

Mutational signature analysis and identification of aristolochic acid (AA) signature

Mutational signatures were inferred for ICC samples performed WES from our cohort. Firstly, we excluded 4 hypermutated ICCs as considering hypermutated tumors has been demonstrated to have significantly different substitution patterns. Next, the 96 mutational subtypes generated from somatic SNVs based on 6 single-base substitutions (SBSs, C>A, C>G, C>T, T>A, T>C and T>G) in 16 possible combinations of neighboring bases for each SBS were used as input data to infer their contributions to observed mutations. We implemented a non-negative matrix factorization (NMF) approach[21] to decipher the mutational signatures (Signature A, B, and C) of all samples with the number based on the signature stability and Frobenius reconstruction errors. Finally, three mutational signatures (A, B, and C) were linked to the known COSMIC cancer signatures (<https://cancer.sanger.ac.uk/cosmic/signatures>) with comparing cosine similarities to infer their exposure contributions.

Mutational signature activity (mSigAct, v2.0.0-branch) was applied to assess presence of the AA signature in all ICC samples. The mSigAct software[22] provided a signature presence test to infer whether the observed mutation spectrum could be better explained with a contribution from the AA mutational signature (COSMIC signature 22) than without it and compared them with a likelihood ratio test. The null hypothesis was that the mutational counts were generated without the AA signature and the alternative hypothesis was that they were from the AA signature. The test was then carried out by a standard likelihood ratio test on these two hypotheses. The mSigAct revealed strong evidence of AA exposure with FDR < 0.05.

Immunohistochemistry for expressions of MMR genes

Whole sections from available FFPE of BTCs tissues were prepared into to 4 or 5 µm-thick on glass slides. For samples identified as MSI-H tumors, the primary antibodies used were anti-MSH2 (Invitrogen, clone 25D12), anti-MSH6 (Ventana, clone 44), anti-MLH1 (Ventana, clone M1) and anti-PMS2 (Agilent Dako, Clone EP51). The secondary antibodies were added to all sections, including the negative control slides. During interpretation, loss of nuclear staining in the tumor cells with positively stained internal control was counted as an abnormal result for 4 MMR genes.

References

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Supplementary Figures

Figure S1. Correlation analysis of alterations in cocaptured genes between whole-exome sequencing (WES) and targeted panel sequencing (TPS). (A) Linear correlation between the variant allele fractions of cocaptured somatic single-nucleotide variants (SNVs, blue line) and indels (dark line) derived from WES and those derived from the TPS panel. (B) Identification of copy-number variants (CNVs) in individual genes from WES and TPS. The dashed line indicates the diploid copy-number (normal), and the vertical axis represents the number of copy-number gains (red) or copy-number losses (blue).

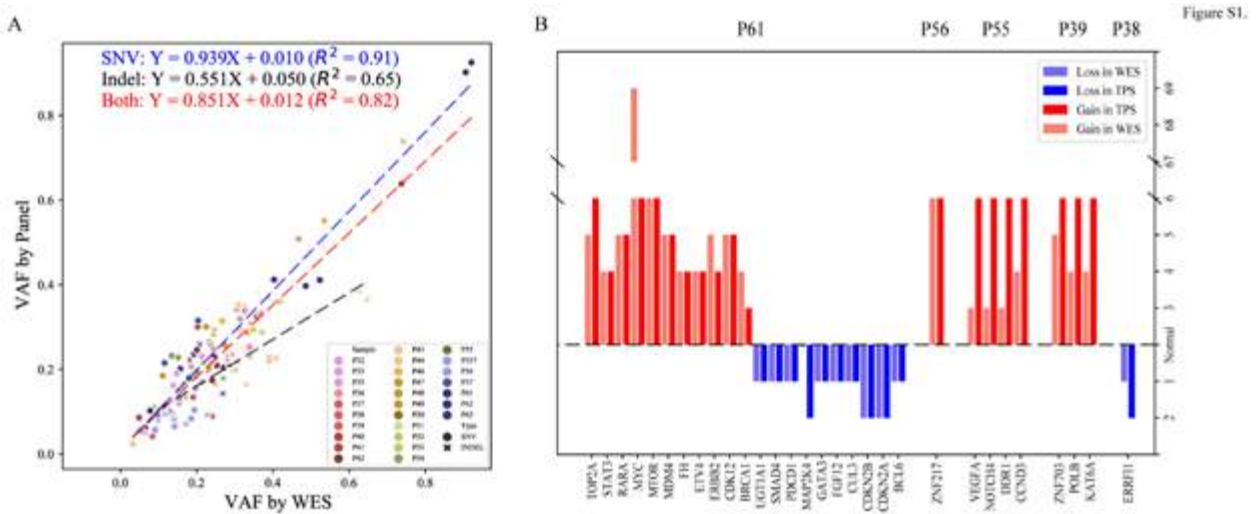


Figure S2. Distribution of somatic tumor mutation burden (TMB) and differences among the three subtypes of biliary tract cancer. (A) Distribution of TMB assessed by WES (top) or TPS (bottom) for each patient highlights the hypermutated group. Hypermutated cases are separated on the left, and the most drastic change point in the mutation rate (vertical dashed line) was chosen as the cutoff to discriminate hypermutated cases from non-hypermutated cases. (B) Linear correlation between TMB evaluated from WES and that evaluated from TPS. (C-D) Landscape of TMB across the major tumor types in WES data (C) or TPS data (D). The median level of TMB for each tumor type and in our cohort is highlighted.

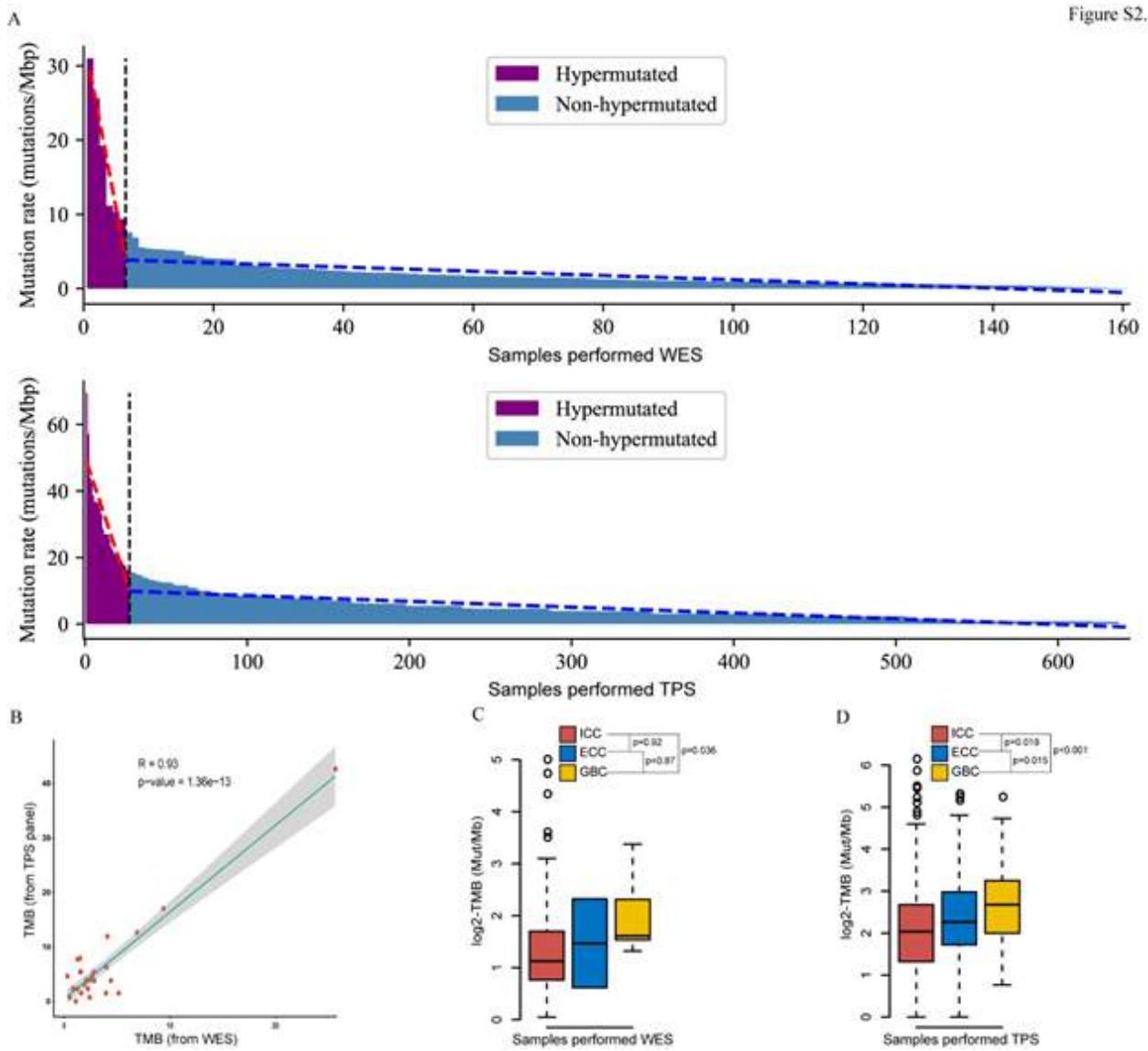


Figure S3. Somatic interactions of cooccurring or exclusively occurring mutations among the top 20 significantly mutated genes in 803 BTC patients. (A) Pairwise Fisher's exact tests were performed to detect significant pairs of genes. The cooccurring relationships are colored by a green box, while the exclusively occurring mutations are colored by a pink box. (B) *TP53* mutations are exclusive to alterations in *ARID1A*, *MUC4*, *IDH1* and *EPHA2*. (C) *KRAS* mutations are exclusively associated with alterations in *LRP1B*, *TERT*, *PIK3CA*, *IDH1* and *EPHA2*.

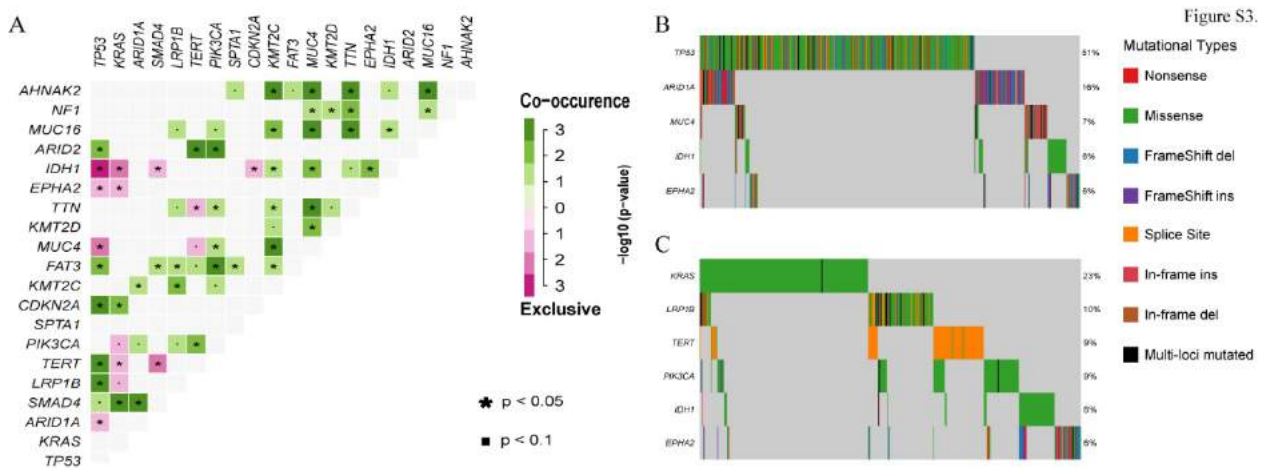
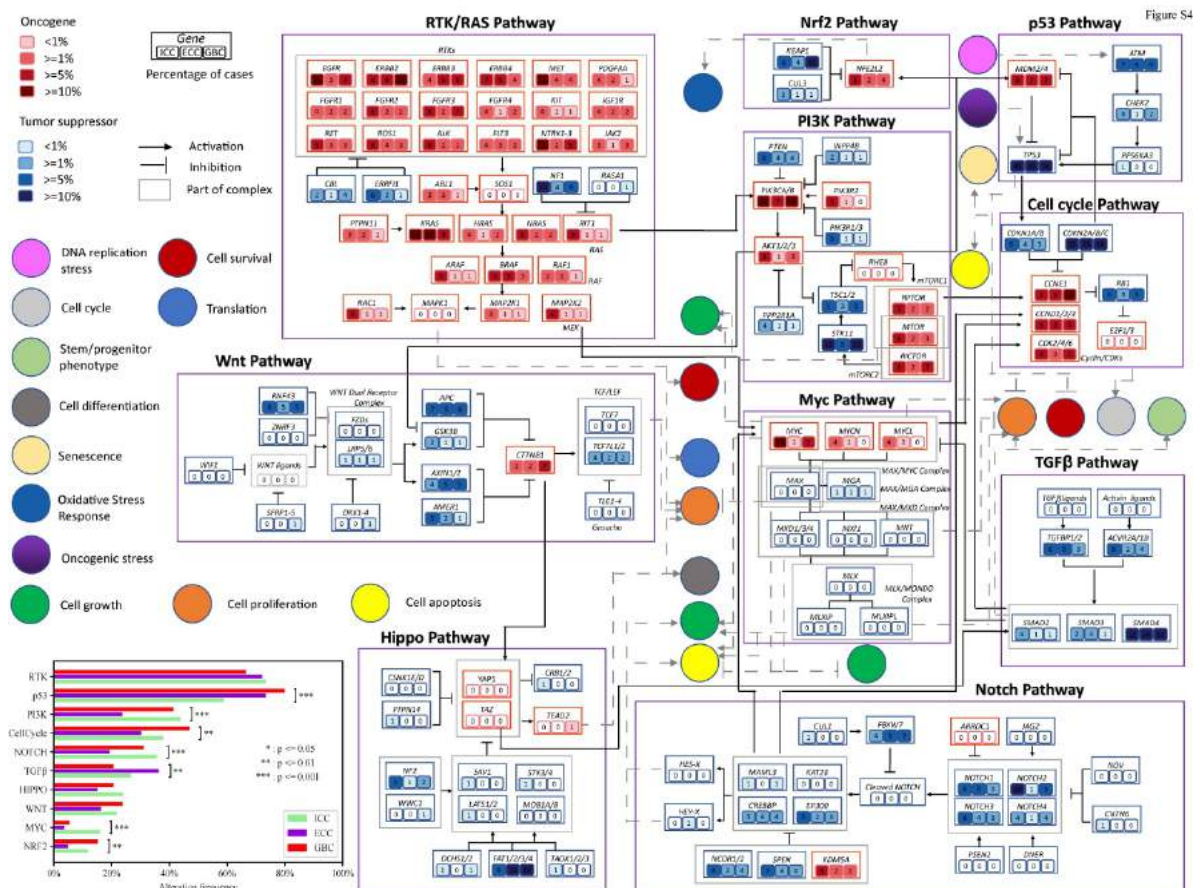


Figure S4. Integration of somatic mutations and SCNAs to decipher the mutational landscape of BTC patients. Pathway components and interactions in the ten selected oncogenic pathways are plotted. Somatic alteration (mutation and CNV) spectra of components in these pathways among the three subtypes (ICC, ECC, and GBC). The numbers of altered samples in each subtype are labeled in the boxes, and the color intensity indicates the average frequency of the alteration in each subtype. The numbers of patients harboring altered pathways are compiled in the top left corner of the plot.



Supplementary Tables

Table S1. Detailed clinicopathological features of 803 BTC patients. (*status: 1-relapse/death; 0-censored)

Sample_ID	Tumor_Type	Age	Sex	Seq_Method	AJCC_Stage	Tissue_Source	Pathology_Differentiation	HBV/HCV_Infection	N_Stage	M_Stage	Vascular_Invasion	CA19-9>200	RFS_status	RFS	OS_Status	OS
SH_01	ICC	61	Male	WES	II	primary tumor	moderate	Negative	N0	M0	negative	negative	1	13	0	51
SH_02	ICC	44	Female	WES	II	primary tumor	moderate	Negative	N0	M0	positive	negative	1	1	1	11
SH_03	ICC	59	Female	WES	III+IV	primary tumor	moderate	Negative	N0	M0	positive	negative	1	5	1	11
SH_05	ICC	43	Female	WES	II	primary tumor	moderate	Positive	N0	M0	negative	negative	0	51	0	51
SH_06	ICC	48	Male	WES	I	primary tumor	moderate	Positive	N0	M0	negative	negative	0	51	0	51
SH_07	ICC	61	Female	WES	I	primary tumor	moderate	Negative	N0	M0	negative	positive	1	1	1	23
SH_08	ICC	45	Male	WES	III+IV	primary tumor	moderate	Positive	N0	M0	negative	NA	0	49	0	49
SH_09	ICC	62	Male	WES	II	primary tumor	moderate	Positive	N0	M0	negative	negative	1	2	1	18
SH_10	ICC	46	Male	WES	III+IV	primary tumor	moderate	Positive	N1	M0	negative	negative	1	0	1	38
SH_100	ICC	38	Female	WES	II	primary tumor	moderate	Positive	N0	M0	negative	negative	1	3	0	34
SH_101	ICC	54	Male	WES	I	primary tumor	moderate	Negative	N0	M0	negative	negative	1	9	0	34
SH_107	ICC	65	Male	WES	II	primary tumor	moderate	Negative	N0	M0	negative	negative	1	5	1	21
SH_108	ICC	57	Female	WES	II	primary tumor	moderate	Negative	N0	M0	negative	positive	1	2	1	8
SH_110	ICC	51	Male	WES	II	primary tumor	moderate	Positive	N0	M0	positive	negative	1	NA	1	4
SH_111	ICC	85	Male	WES	I	primary tumor	moderate	Negative	N0	M0	negative	positive	1	6	1	10
SH_113	ICC	40	Male	WES	I	primary tumor	moderate	Positive	N0	M0	negative	negative	1	12	1	31
SH_115	ICC	51	Female	WES	II	primary tumor	moderate	Negative	N0	M0	negative	positive	1	2	1	5
SH_118	ICC	43	Male	WES	I	primary tumor	moderate	Positive	N0	M0	negative	negative	1	6	1	16
SH_119	ICC	44	Male	WES	I	primary tumor	moderate	Positive	N0	M0	negative	negative	0	32	0	32
SH_120	ICC	51	Male	WES	III+IV	primary tumor	moderate	Positive	N0	M1	negative	positive	1	8	1	22
SH_121	ICC	48	Male	WES	II	primary tumor	moderate	Positive	N0	M0	positive	negative	1	9	1	15
SH_122	ICC	49	Male	WES	I	primary tumor	moderate	Negative	N0	M0	negative	negative	0	32	0	32
SH_123	ICC	64	Female	WES	III+IV	primary tumor	moderate	Negative	N0	M0	negative	negative	1	3	1	9
SH_125	ICC	35	Female	WES	II	primary tumor	moderate	Positive	N0	M0	positive	negative	1	6	1	14
SH_127	ICC	40	Male	WES	I	primary tumor	moderate	Positive	N0	M0	negative	negative	NA	NA	1	2
SH_128	ICC	63	Male	WES	I	primary tumor	poor	Positive	N0	M0	negative	negative	1	4	1	7
SH_129	ICC	68	Female	WES	I	primary tumor	moderate	Negative	N0	M0	negative	positive	1	1	0	42
SH_13	ICC	47	Male	WES	I	primary tumor	moderate	Positive	N0	M0	negative	negative	NA	NA	0	50
SH_130	ICC	54	Male	WES	III+IV	primary tumor	poor	Positive	N1	M0	negative	negative	NA	NA	1	7
SH_131	ICC	48	Male	WES	II	primary tumor	moderate	Positive	N0	M0	positive	negative	1	1	1	3
SH_132	ICC	70	Female	WES	I	primary tumor	moderate	Positive	N0	M0	negative	negative	NA	NA	1	1
SH_133	ICC	66	Male	WES	III+IV	primary tumor	moderate	Negative	N1	M0	negative	negative	1	0	1	26
SH_134	ICC	59	Female	WES	I	primary tumor	moderate	Negative	N0	M0	negative	positive	1	10	1	12
SH_135	ICC	68	Male	WES	I	primary tumor	moderate	Negative	N0	M0	negative	negative	NA	NA	1	3
SH_137	ICC	58	Female	WES	II	primary tumor	poor	Negative	N0	M0	negative	positive	NA	NA	1	4
SH_139	ICC	65	Male	WES	II	primary tumor	moderate	Negative	N0	M0	negative	negative	1	3	1	9
SH_140	ICC	59	Female	WES	III+IV	primary tumor	moderate	Positive	N1	M0	negative	negative	1	9	1	11
SH_141	ICC	62	Male	WES	III+IV	primary tumor	moderate	Negative	N1	M0	positive	negative	1	2	1	9
SH_142	ICC	52	Male	WES	I	primary tumor	moderate	Positive	N0	M0	negative	negative	NA	NA	1	8
SH_143	ICC	54	Male	WES	II	primary tumor	moderate	Positive	N0	M0	positive	negative	1	2	1	5
SH_144	ICC	62	Male	WES	I	primary tumor	moderate	Negative	N0	M0	negative	negative	NA	NA	1	18
SH_146	ICC	60	Male	WES	I	primary tumor	moderate	Negative	N0	M0	negative	positive	1	1	1	6
SH_147	ICC	48	Male	WES	II	primary tumor	poor	Positive	N0	M0	positive	negative	1	1	0	28
SH_16	ICC	63	Female	WES	II	primary tumor	moderate	Positive	N0	M0	negative	negative	NA	NA	1	5
SH_17	ICC	55	Male	WES	III+IV	primary tumor	moderate	Negative	N1	M1	negative	positive	1	3	1	6
SH_18	ICC	50	Male	WES	I	primary tumor	moderate	Positive	N0	M0	negative	negative	1	1	1	4
SH_19	ICC	56	Female	WES	I	primary tumor	well	Positive	N0	M0	negative	NA	NA	NA	0	49
SH_20	ICC	44	Male	WES	I	primary tumor	moderate	Positive	N0	M0	negative	negative	NA	NA	1	16
SH_24	ICC	55	Female	WES	II	primary tumor	moderate	Negative	N0	M0	positive	positive	1	3	1	6
SH_25	ICC	52	Male	WES	I	primary tumor	moderate	Positive	N0	M0	negative	negative	0	51	0	51
SH_26	ICC	49	Male	WES	II	primary tumor	moderate	Positive	N0	M0	positive	negative	1	27	1	33
SH_28	ICC	48	Male	WES	III+IV	primary tumor	moderate	Positive	N0	M1	positive	negative	NA	NA	1	1
SH_29	ICC	74	Female	WES	III+IV	primary tumor	moderate	Negative	N1	M0	negative	positive	1	2	1	4
SH_33	ICC	38	Female	WES	I	primary tumor	moderate	Negative	N0	M0	negative	positive	1	3	1	5
SH_34	ICC	52	Male	WES	I	primary tumor	moderate	Negative	N0	M0	negative	positive	1	5	1	6
SH_35	ICC	72	Male	WES	I	primary tumor	moderate	Positive	N0	M0	negative	negative	1	5	1	28
SH_41	ICC	36	Male	WES	I	primary tumor	moderate	Positive	N0	M0	negative	negative	1	15	1	18
SH_42	ICC	43	Female	WES	II	primary tumor	moderate	Positive	N0	M0	positive	negative	1	32	0	48
SH_44	ICC	73	Female	WES	II	primary tumor	moderate	Negative	N0	M0	positive	negative	1	NA	1	0
SH_46	ICC	52	Female	WES	III+IV	primary tumor	moderate	Negative	N1	M0	negative	negative	1	4	1	21
SH_48	ICC	56	Male	WES	I	primary tumor	moderate	Positive	N0	M0	negative	negative	0	49	0	49
SH_50	ICC	65	Female	WES	I	primary tumor	moderate	Positive	N0	M0	negative	negative	1	31	0	47
SH_51	ICC	52	Male	WES	II	primary tumor	moderate	Negative	N0	M0	positive	negative	1	1	1	22
SH_52	ICC	49	Male	WES	II	primary tumor	moderate	Positive	N0	M0	positive	positive	1	4	1	7
SH_53	ICC	69	Male	WES	I	primary tumor	moderate	Negative	N0	M0	negative	negative	1	10	0	48
SH_56	ICC	38	Male	WES	III+IV	primary tumor	moderate	Positive	N0	M1	negative	negative	1	1	1	4
SH_58	ICC	41	Male	WES	II	primary tumor	moderate	Positive	N0	M0	positive	negative	1	3	1	6
SH_59	ICC	60	Female	WES	III+IV	primary tumor	moderate	Positive	N0	M1	negative	positive	1	NA	1	4
SH_61	ICC	39	Female	WES	III+IV	primary tumor	moderate	Negative	N1	M0	negative	positive	1	1	1	8
SH_63	ICC	52	Female	WES	III+IV	primary tumor	moderate	Negative	N1	M0	negative	positive	1	5	1	12
SH_64	ICC	51	Male	WES	III+IV	primary tumor	moderate	Positive	N1	M0	positive	positive	NA	NA	1	2
SH_66	ICC	63	Female	WES	I	primary tumor	moderate	Negative	N0	M0	negative	positive	NA	NA	1	11
SH_67	ICC	66	Male	WES	I	primary tumor	moderate	Negative	N0	M0	negative	negative	NA	NA	0	46
SH_69	ICC	50	Male	WES	III+IV	primary tumor	moderate	Positive	N1	M0	negative	positive	1	21	1	23
SH_70	ICC	54	Female	WES	II	primary tumor	moderate	Negative	N0	M0	negative	negative	1	3	1	9
SH_71	ICC	59	Male	WES	I	primary tumor	moderate	Positive	N0	M0	negative	negative	0	46	0	46
SH_74	ICC	38	Male	WES	I	primary tumor	moderate	Negative	N0	M0	negative	negative	0	41	0	41
SH_79	ICC	43	Female	WES	II	primary tumor	moderate	Positive	N0	M0	negative	negative	0	35	0	35
SH_80	ICC	59	Female	WES	I	primary tumor	moderate	Negative	N0	M0	negative	negative	1	3	1	20
SH_81	ICC	38	Male	WES	III+IV	primary tumor	moderate	Negative	N1	M0	negative	positive	1	2	1	22
SH_82	ICC	43	Female	WES	I	primary tumor	moderate	Negative	N0	M0	negative	negative	1	13	1	34
SH_85	ICC	57	Female	WES	II	primary tumor	moderate	Positive	N0	M0	negative	negative	1	3	1	5
SH_86	ICC	66	Male	WES	I	primary tumor	moderate	Negative	N0	M0	negative	positive	0	35	0	35
SH_87	ICC	53	Male	WES	II	primary tumor	moderate	Positive	N0	M0	positive	negative	1	4	1	12
SH_88	ICC	56	Male	WES	I	primary tumor	moderate	Positive	N0	M0	negative	positive	1	21	0	35
SH_89	ICC	64	Female	WES	I	primary tumor	moderate	Negative	N0	M0	negative	negative	1	9	1	31
SH_90	ICC	56	Male	WES	III+IV	primary tumor	moderate	Negative	N1	M0	negative	negative	1	2	1	7
SH_91	ICC	65	Female	WES	I	primary tumor	moderate	Negative	N0	M0	negative	negative	0	39	0	39
SH_94	ICC	51	Male	WES	II	primary tumor	moderate	Positive	N0	M0	negative	negative	0	34	0	34
SH_95	ICC	48	Male	WES	II	primary tumor	moderate	Positive	N0	M0	negative	positive	1	0	1	9
SH_98	ICC	63	Male	WES	III+IV	primary tumor	moderate	Negative	N1	M0	negative	negative	NA	NA	1	5
SH_99	ICC	65	Male	WES	II	primary tumor	moderate	Negative	N0	M0	negative	negative	NA	NA	0	35
XH_P01	ICC	43	Male	WES	III+IV	primary tumor	poor	Negative	N1	M0	negative	negative	1	3	1	10
XH_P02	ICC	25	Female	WES	III+IV	primary tumor	moderate	Negative	N0	M1	negative	positive	1	2	1	13
XH_P03	ICC	60	Female	WES	III+IV	primary tumor	moderate	Negative	N1	M0	negative	positive	1	16	1	20
XH_P04	ICC	45	Female	WES	II	primary tumor	poor	Positive	NX	M0	positive	negative	1	5	0	41
XH_P05	ICC	43	Female	WES	III+IV	primary tumor	poor	Positive	N1	M1	negative	negative	1	2	1	11
XH_P06	ICC	62	Male	WES	I	primary tumor	poor	Negative	NX	M0	negative	negative	1	46	0	48
XH_P07	ICC	59	Female	WES	III+IV	primary tumor	moderate	Negative	N1	M0	negative	negative	1	14	1	18
XH_P08	ICC	63	Female	WES	III+IV	primary tumor	poor	Negative	N1	M0	negative	negative	1	2	1	16
XH_P09	ICC	63	Male	WES	II	primary tumor	moderate	Negative	N0	M0	negative	negative	1	16	1	22
XH_P10	ICC	44	Male	WES	III+IV	primary tumor	poor	Positive	N1	M1	negative	negative	1	2	1	9
XH_P11	ICC	45	Male	WES	I	primary tumor	poor	Positive	N0	M0	negative	negative	1	3	1	14
XH_P12	ICC	57	Female	WES	II	primary tumor	poor	Positive	N0	M0	negative	negative	1	32	1	50
XH_P13	ICC	65	Female	WES	III+IV	primary tumor	moderate	Negative	N1	M0	negative	negative	1	14	1	17
XH_P15																

XH_P25	ICC	56	Male	WES	II	primary tumor	poor	Positive	NX	M0	negative	positive	1	13	1	18
XH_P27	ICC	34	Male	WES	II	primary tumor	poor	Negative	N0	M0	negative	negative	1	3	1	10
XH_P28	ICC	52	Male	WES	II	primary tumor	poor	Negative	N0	M0	negative	negative	1	20	0	60
XH_P29	ICC	49	Male	WES	II	primary tumor	moderate	Negative	N0	M0	negative	negative	1	4	1	7
XH_P30	ICC	48	Male	WES	I	primary tumor	poor	Negative	N0	M0	negative	negative	1	13	1	31
XH_P31	ICC	62	Female	WES	II	primary tumor	moderate	Positive	N0	M0	positive	negative	1	6	1	17
XH_P32	ICC	51	Female	WES	III+IV	primary tumor	poor	Negative	N1	M1	positive	positive	1	1	1	12
XH_P33	ICC	62	Male	WES	III+IV	primary tumor	moderate	Positive	N1	M0	negative	positive	1	18	1	35
XH_P34	ICC	51	Female	WES	II	primary tumor	moderate	Negative	N0	M0	positive	negative	1	9	1	14
XH_P35	ICC	68	Male	WES	III+IV	primary tumor	moderate	Negative	NX	M0	positive	negative	1	3	1	19
XH_P36	ICC	40	Female	WES	III+IV	primary tumor	moderate	Negative	N0	M0	negative	positive	1	5	0	34
XH_P37	ICC	61	Female	WES	III+IV	primary tumor	poor	Negative	N1	M0	negative	positive	1	5	1	16
XH_P38	ICC	53	Female	WES	II	primary tumor	poor	Negative	N0	M0	negative	negative	1	10	1	44
XH_P39	ICC	69	Female	WES	III+IV	primary tumor	moderate	Negative	N1	M0	negative	positive	1	3	1	10
XH_P40	ECC	47	Male	WES	I	primary tumor	poor	Negative	N0	M0	negative	negative	1	32	1	40
XH_P41	ICC	61	Male	WES	III+IV	primary tumor	moderate	Negative	N1	M0	negative	negative	1	6	1	12
XH_P42	ICC	51	Male	WES	I	primary tumor	poor	Negative	N0	M0	negative	negative	1	2	0	54
XH_P43	ICC	42	Male	WES	III+IV	primary tumor	moderate	Negative	N1	M0	positive	positive	1	16	1	48
XH_P44	ICC	52	Male	WES	III+IV	primary tumor	moderate	Negative	N1	M0	negative	positive	1	3	1	7
XH_P45	ICC	38	Female	WES	I	primary tumor	moderate	Negative	N0	M0	negative	negative	1	19	1	42
XH_P46	ICC	65	Male	WES	I	primary tumor	poor	Negative	N0	M0	negative	positive	1	4	1	16
XH_P47	ICC	67	Male	WES	I	primary tumor	poor	Negative	N0	M0	negative	positive	1	6	0	18
XH_P48	ICC	52	Male	WES	III+IV	primary tumor	poor	Negative	N1	M0	negative	negative	1	6	0	30
XH_P49	ICC	65	Female	WES	III+IV	primary tumor	poor	Positive	N1	M1	negative	positive	1	6	0	20
XH_P50	ICC	51	Male	WES	III+IV	metastatic tumor	moderate	Negative	N1	M1	negative	negative	1	3	1	15
XH_P51	ICC	53	Female	WES	I	primary tumor	poor	Positive	N0	M0	negative	negative	1	12	0	30
XH_P52	GBC	52	Male	WES	II	metastatic tumor	moderate	Negative	N0	M0	negative	positive	1	3	1	22
XH_P53	GBC	58	Female	WES	III+IV	primary tumor	poor	Negative	N0	M0	negative	negative	1	2	0	22
XH_P54	ICC	57	Female	WES	III+IV	primary tumor	moderate	Negative	N1	M1	negative	negative	1	3	1	12
XH_P55	GBC	56	Female	WES	III+IV	primary tumor	moderate	Negative	N0	M0	negative	negative	1	2	1	24
XH_P57	ECC	72	Male	WES	III+IV	primary tumor	moderate	Negative	N1	M0	negative	positive	1	2	0	17
XH_P56	ICC	77	Male	WES	I	primary tumor	moderate	Positive	N0	M0	negative	positive	1	3	0	14
XH_P57	GBC	69	Female	WES	III+IV	primary tumor	moderate	Negative	N1	M0	negative	positive	1	2	0	15
XH_P61	GBC	58	Male	WES	III+IV	primary tumor	poor	Negative	N1	M0	positive	negative	1	1	0	5
XH_P62	ICC	36	Male	WES	III+IV	primary tumor	moderate	Negative	N0	M1	negative	negative	1	1	0	13
XH_P63	ICC	63	Female	WES	III+IV	primary tumor	poor	Negative	N0	M1	negative	positive	1	2	0	12
XH_P87	ICC	54	Male	WES	I	primary tumor	moderate	Negative	N0	M0	negative	negative	0	18	0	21
XH_P88	ICC	62	Male	WES	I	primary tumor	poor	Negative	N0	M0	negative	negative	1	18	0	21
XH_P89	ICC	77	Female	WES	I	primary tumor	moderate	Negative	N0	M0	negative	positive	1	7	1	11
XH_P90	ICC	68	Female	WES	III+IV	primary tumor	poor	Negative	N1	M1	negative	negative	1	2	1	5
XH_P91	ICC	70	Female	WES	III+IV	primary tumor	poor	Negative	N1	M0	negative	negative	1	4	0	17
XH_P92	ICC	57	Male	WES	II	primary tumor	poor	Negative	N0	M0	negative	positive	1	7	0	18
XH_P93	ICC	57	Male	WES	II	primary tumor	poor	Negative	N0	M0	negative	negative	1	1	1	4
XH_P94	ICC	32	Male	WES	III+IV	primary tumor	poor	Negative	N1	M1	positive	positive	1	1	0	16
XH_P95	ICC	38	Female	WES	I	primary tumor	poor	Negative	N0	M0	negative	negative	0	8	0	8
XH_P96	ICC	67	Female	WES	I	primary tumor	moderate	Negative	N0	M0	negative	negative	0	6	0	16
XH_P97	GBC	55	Male	WES	II	primary tumor	poor	Negative	N0	M0	negative	negative	1	4	0	19
XH_P99	ICC	49	Male	WES	II	primary tumor	poor	Negative	N0	M0	negative	positive	1	4	0	11
116K0135A1	ICC	44	Male	CSYS	NA	primary tumor	poor	Negative	NX	MX	NA	NA	NA	NA	NA	NA
116L0197A1	ECC	44	Female	CSYS	NA	primary tumor	poor	Negative	N1	M0	NA	NA	NA	NA	NA	NA
116L0221A1	ICC	67	Male	CSYS	III+IV	metastatic tumor	NA	Negative	NX	M1	NA	NA	NA	NA	NA	NA
116L0254A1	ECC	48	Male	CSYS	I	primary tumor	moderate	Negative	N0	M0	NA	NA	NA	NA	NA	NA
116L0263A1	GBC	58	Female	CSYS	NA	metastatic tumor	NA	Negative	NX	MX	NA	NA	NA	NA	NA	NA
116L0279A1	ECC	64	Female	CSYS	NA	primary tumor	poor	Negative	N0	M0	NA	NA	NA	NA	NA	NA
116L0287A1	ICC	52	Male	CSYS	NA	primary tumor	moderate	Negative	NX	MX	NA	NA	NA	NA	NA	NA
117B0454A1	GBC	74	Female	CSYS	NA	metastatic tumor	moderate	Negative	NX	MX	NA	NA	NA	NA	NA	NA
117B0488A1	ECC	69	Female	CSYS	I	primary tumor	moderate	Negative	N0	M0	NA	NA	NA	NA	NA	NA
117B0545A1	GBC	54	Female	CSYS	III+IV	primary tumor	poor	Negative	N1	MX	NA	NA	NA	NA	NA	NA
117C0618A1	GBC	67	Female	CSYS	III+IV	primary tumor	poor	Negative	N1	MX	NA	NA	NA	NA	NA	NA
117C0646A1	ICC	62	Male	CSYS	NA	primary tumor	moderate	Negative	NX	MX	NA	NA	NA	NA	NA	NA
117C0651A1	ECC	63	Male	CSYS	I	primary tumor	moderate	Negative	N0	M0	NA	NA	NA	NA	NA	NA
117C0664A1	ICC	47	Male	CSYS	I	primary tumor	moderate	Positive	N0	M0	NA	NA	NA	NA	NA	NA
117C0733A1	ECC	50	Male	CSYS	NA	primary tumor	poor	Negative	N0	M0	NA	NA	NA	NA	NA	NA
117C0866A1	GBC	58	Male	CSYS	NA	primary tumor	well	Negative	NX	MX	NA	NA	NA	NA	NA	NA
117D0978A1	ICC	38	Male	CSYS	NA	primary tumor	poor	Negative	NX	MX	NA	NA	NA	NA	NA	NA
117D0997A1	ECC	66	Male	CSYS	III+IV	primary tumor	poor	Negative	N1	M0	NA	NA	NA	NA	NA	NA
117D1007A1	ECC	64	Male	CSYS	III+IV	primary tumor	moderate	Negative	N1	M0	NA	NA	NA	NA	NA	NA
117D1030A1	ICC	82	Male	CSYS	III+IV	metastatic tumor	poor	Negative	NX	M1	NA	NA	NA	NA	NA	NA
117D1074R1	ICC	60	Male	CSYS	NA	primary tumor	NA	Negative	NX	MX	NA	NA	NA	NA	NA	NA
117D1101A1	ICC	54	Male	CSYS	III+IV	primary tumor	poor	Negative	N1	M0	NA	NA	NA	NA	NA	NA
117D1130A1	ECC	44	Female	CSYS	III+IV	metastatic tumor	NA	Negative	N1	M1	NA	NA	NA	NA	NA	NA
117D1192A1	ICC	79	Male	CSYS	III+IV	primary tumor	moderate	Negative	N1	M0	NA	NA	NA	NA	NA	NA
117E1223A1	ECC	83	Male	CSYS	NA	primary tumor	moderate	Negative	N1	M0	NA	NA	NA	NA	NA	NA
117E1250R1	GBC	62	Male	CSYS	III+IV	metastatic tumor	moderate	NA	N1	M0	NA	NA	NA	NA	NA	NA
117E1259R1	ICC	49	Male	CSYS	III+IV	metastatic tumor	poor	Positive	NX	M1	NA	NA	NA	NA	NA	NA
117E1261R1	ICC	40	Male	CSYS	I	primary tumor	poor	Negative	N0	M0	NA	NA	NA	NA	NA	NA
117E1396A1	ICC	69	Male	CSYS	NA	primary tumor	NA	Negative	NX	MX	NA	NA	NA	NA	NA	NA
117E1425A1	ICC	60	Male	CSYS	III+IV	primary tumor	moderate	Positive	N1	M1	NA	NA	NA	NA	NA	NA
117E1443A1	ECC	68	Male	CSYS	I	primary tumor	moderate	Negative	N0	M0	NA	NA	NA	NA	NA	NA
117E1534A1	GBC	52	Female	CSYS	III+IV	primary tumor	moderate	Negative	N0	M1	NA	NA	NA	NA	NA	NA
117F1556A1	ICC	66	Female	CSYS	NA	primary tumor	NA	Negative	NX	MX	NA	NA	NA	NA	NA	NA
117F1640A1	ICC	63	Male	CSYS	I	primary tumor	moderate	Negative	N0	M0	NA	NA	NA	NA	NA	NA
117F1648A2	ICC	62	Male	CSYS	III+IV	primary tumor	poor	Negative	NX	M1	NA	NA	NA	NA	NA	NA
117F1689A1	ICC	69	Male	CSYS	NA	primary tumor	poor	Negative	NX	MX	NA	NA	NA	NA	NA	NA
117F1759A1	ECC	57	Female	CSYS	III+IV	metastatic tumor	poor	Negative	NX	M1	NA	NA	NA	NA	NA	NA
117F1767A1	ICC	54	Male	CSYS	NA	primary tumor	poor	Negative	NX	MX	NA	NA	NA	NA	NA	NA
117F1770A1	GBC	72	Male	CSYS	III+IV	primary tumor	moderate	Negative	N0	M0	NA	NA	NA	NA	NA	NA
117F1811A1	GBC	66	Male	CSYS	III+IV	primary tumor	poor	Negative	N1	M0	NA	NA	NA	NA	NA	NA
117G2016A1	ECC	54	Female	CSYS	I	primary tumor	poor	Negative	N0	M0	NA	NA	NA	NA	NA	NA
117G2026A1	GBC	66	Male	CSYS	III+IV	metastatic tumor	poor	Negative	NX	M1	NA	NA	NA	NA	NA	NA
117G2087A1	ECC	60	Male	CSYS	III+IV	metastatic tumor	poor	Negative	NX	M1	NA	NA	NA	NA	NA	NA
117H2198A1	ICC	43	Male	CSYS	NA	primary tumor	NA	Negative	NX	MX	NA	NA	NA	NA	NA	NA
117H2255A1	GBC	58	Female	CSYS	III+IV	primary tumor	poor	Negative	N1	M0	NA	NA	NA	NA	NA	NA
117H2289A1	ICC	50	Male	CSYS	III+IV	primary tumor	poor	Positive	NX	M1	NA	NA	NA	NA	NA	NA
117H2404A1	ECC	39	Male	CSYS	III+IV	primary tumor	poor	Negative	N1	M0	NA	NA	NA	NA	NA	NA
117H2427A1	GBC	60	Male	CSYS	III+IV	primary tumor	moderate	Negative	N0	M1	NA	NA	NA	NA	NA	NA
117H2467A1	ICC	46	Male	CSYS	III+IV	recurrent tumor	moderate	NA	NX	MX	NA	NA	NA	NA	NA	NA
117H2489A1	ICC	62	Female	CSYS	III+IV	primary tumor	moderate	Negative	NX	M1	NA	NA	NA	NA	NA	NA
117H2552A1	ECC	70	Female	CSYS	II	primary tumor	moderate	Negative	N0	M0	NA	NA	NA	NA	NA	NA
117I2596A1	ECC	48	Male	CSYS	I	primary tumor	moderate	Negative	N0	M0	NA	NA	NA	NA	NA	NA
117I2661A1	ICC	46	Male	CSYS	III+IV	primary tumor	poor	Negative	NX	MX	NA	NA	NA	NA	NA	NA
117I2687A1	ICC	66	Female	CSYS	III+IV	primary tumor	poor	Positive	N1	M0	NA	NA	NA	NA	NA	NA
117I2735A1	ECC	54	Male	CSYS	II	primary tumor	moderate	Negative	N0	M0	NA	NA	NA	NA	NA	NA
117I2766A1	ECC	60	Female	CSYS	II	primary tumor	well	Negative	N0	M0	NA	NA	NA	NA	NA	NA
117I2799A1																

117J3045A1	ICC	37	Male	CYS5	NA	primary tumor	poor	Positive	NX	MX	NA	NA	NA	NA	NA	NA
117J3086A1	ICC	86	Male	CYS5	III+IV	primary tumor	poor	Negative	N1	M1	NA	NA	NA	NA	NA	NA
117J3117A1	GBC	55	Male	CYS5	III+IV	primary tumor	NA	Negative	N0	M0	NA	NA	NA	NA	NA	NA
117J3131A1	ICC	53	Male	CYS5	I	primary tumor	moderate	Positive	N0	M0	NA	NA	NA	NA	NA	NA
117J3133A1	ECC	58	Female	CYS5	I	primary tumor	moderate	Negative	N0	M0	NA	NA	NA	NA	NA	NA
117J3136A1	GBC	57	Female	CYS5	III+IV	metastatic tumor	NA	NA	NX	M1	NA	NA	NA	NA	NA	NA
117J3193A1	ECC	50	Female	CYS5	III+IV	primary tumor	moderate	Negative	NX	M1	NA	NA	NA	NA	NA	NA
117J3213A1	ICC	49	Male	CYS5	NA	primary tumor	moderate	Positive	NX	MX	NA	NA	NA	NA	NA	NA
117J3223A1	GBC	31	Female	CYS5	III+IV	metastatic tumor	moderate	Negative	N0	M0	NA	NA	NA	NA	NA	NA
117J3239A1	GBC	61	Female	CYS5	III+IV	primary tumor	poor	Negative	N1	M0	NA	NA	NA	NA	NA	NA
117J3282A1	GBC	72	Male	CYS5	III+IV	primary tumor	poor	Negative	N1	M0	NA	NA	NA	NA	NA	NA
117J3295A1	ECC	56	Female	CYS5	III+IV	primary tumor	moderate	Negative	N1	M0	NA	NA	NA	NA	NA	NA
117J3306A1	ICC	58	Male	CYS5	II	primary tumor	moderate	Positive	N0	M0	NA	NA	NA	NA	NA	NA
117J3318A1	GBC	73	Male	CYS5	III+IV	primary tumor	moderate	Negative	N1	M0	NA	NA	NA	NA	NA	NA
117K3377A1	ICC	74	Male	CYS5	NA	primary tumor	NA	Negative	N0	M0	NA	NA	NA	NA	NA	NA
117K3386A1	ICC	65	Male	CYS5	III+IV	primary tumor	moderate	Positive	NX	M1	NA	NA	NA	NA	NA	NA
117K3403A1	ECC	53	Male	CYS5	I	primary tumor	poor	Negative	N0	M0	NA	NA	NA	NA	NA	NA
117K3508A1	GBC	51	Female	CYS5	III+IV	metastatic tumor	poor	Negative	N1	M1	NA	NA	NA	NA	NA	NA
117K3520A1	ICC	53	Female	CYS5	III+IV	primary tumor	well	Negative	N1	M0	NA	NA	NA	NA	NA	NA
117K3527A1	ICC	67	Female	CYS5	I	primary tumor	poor	Positive	N0	M0	NA	NA	NA	NA	NA	NA
117K3556A1	ICC	60	Male	CYS5	III+IV	primary tumor	poor	Positive	NX	MX	NA	NA	NA	NA	NA	NA
117K3576A1	ICC	54	Male	CYS5	III+IV	primary tumor	moderate	Negative	N1	M0	NA	NA	NA	NA	NA	NA
117K3596A1	ECC	75	Female	CYS5	II	primary tumor	poor	Negative	N0	M0	NA	NA	NA	NA	NA	NA
117K3609A1	ICC	48	Male	CYS5	III+IV	primary tumor	poor	Positive	N1	M1	NA	NA	NA	NA	NA	NA
117K3620A1	ICC	52	Male	CYS5	III+IV	primary tumor	moderate	NA	NX	M1	NA	NA	NA	NA	NA	NA
117K3660A1	GBC	73	Female	CYS5	NA	primary tumor	moderate	Negative	NX	MX	NA	NA	NA	NA	NA	NA
117K3669A1	ICC	54	Female	CYS5	III+IV	primary tumor	poor	Negative	N1	M1	NA	NA	NA	NA	NA	NA
117K3688A1	GBC	49	Female	CYS5	III+IV	primary tumor	poor	Negative	N0	M0	NA	NA	NA	NA	NA	NA
117K3699A1	ICC	67	Female	CYS5	III+IV	metastatic tumor	moderate	Negative	NX	M1	NA	NA	NA	NA	NA	NA
117K3728A1	ECC	61	Female	CYS5	II	primary tumor	poor	Negative	N1	M0	NA	NA	NA	NA	NA	NA
117K3750A1	ICC	52	Male	CYS5	III+IV	primary tumor	poor	NA	N1	M0	NA	NA	NA	NA	NA	NA
117L3780A1	ECC	60	Male	CYS5	I	primary tumor	moderate	Negative	N0	M0	NA	NA	NA	NA	NA	NA
117L3815A1	GBC	57	Female	CYS5	III+IV	primary tumor	well	Negative	NX	M1	NA	NA	NA	NA	NA	NA
117L3816A1	ICC	58	Female	CYS5	III+IV	primary tumor	poor	Positive	N1	M0	NA	NA	NA	NA	NA	NA
117L3817A1	ICC	65	Male	CYS5	II	primary tumor	poor	Negative	N0	M0	NA	NA	NA	NA	NA	NA
117L3842A1	ICC	40	Male	CYS5	II	primary tumor	poor	Positive	N0	M0	NA	NA	NA	NA	NA	NA
117L3851A1	ECC	60	Female	CYS5	III+IV	metastatic tumor	NA	Negative	NX	M1	NA	NA	NA	NA	NA	NA
117L3938A1	GBC	49	Female	CYS5	III+IV	primary tumor	poor	Negative	N0	M0	NA	NA	NA	NA	NA	NA
117L3940A1	ICC	65	Male	CYS5	III+IV	primary tumor	well	Negative	N0	M1	NA	NA	NA	NA	NA	NA
117L3952A1	ICC	51	Female	CYS5	III+IV	primary tumor	moderate	NA	N1	M0	NA	NA	NA	NA	NA	NA
117L3964A1	ICC	52	Female	CYS5	I	primary tumor	moderate	Negative	N0	M0	NA	NA	NA	NA	NA	NA
117L3965A1	ICC	64	Male	CYS5	II	primary tumor	poor	Negative	N0	M0	NA	NA	NA	NA	NA	NA
117L4005A1	ICC	51	Male	CYS5	III+IV	primary tumor	poor	Positive	N0	M1	NA	NA	NA	NA	NA	NA
117L4040A1	GBC	54	Female	CYS5	III+IV	primary tumor	poor	Negative	N1	M0	NA	NA	NA	NA	NA	NA
117L4049A1	ICC	63	Male	CYS5	I	primary tumor	moderate	Negative	N0	M0	NA	NA	NA	NA	NA	NA
117L4084A1	ICC	66	Male	CYS5	I	primary tumor	moderate	Negative	N0	M0	NA	NA	NA	NA	NA	NA
117L4087A1	ECC	59	Female	CYS5	II	primary tumor	NA	Negative	N1	M0	NA	NA	NA	NA	NA	NA
117L4089A1	ECC	46	Female	CYS5	II	primary tumor	poor	Negative	N1	M0	NA	NA	NA	NA	NA	NA
117L4100A1	ICC	54	Male	CYS5	III+IV	primary tumor	moderate	Positive	N1	M0	NA	NA	NA	NA	NA	NA
117L4103A1	GBC	50	Female	CYS5	III+IV	metastatic tumor	poor	Negative	NX	M1	NA	NA	NA	NA	NA	NA
117L4125A1	ICC	65	Female	CYS5	III+IV	metastatic tumor	moderate	Negative	NX	M1	NA	NA	NA	NA	NA	NA
117L4126A1	ICC	62	Male	CYS5	III+IV	recurrent tumor	poor	Positive	NX	M1	NA	NA	NA	NA	NA	NA
117L4133A1	GBC	52	Female	CYS5	II	primary tumor	poor	Negative	N0	M0	NA	NA	NA	NA	NA	NA
117L4139A1	ECC	63	Male	CYS5	I	primary tumor	moderate	NA	N0	M0	NA	NA	NA	NA	NA	NA
118A4239A1	ECC	73	Female	CYS5	II	primary tumor	poor	Negative	N1	M0	NA	NA	NA	NA	NA	NA
118A4277A1	ICC	68	Female	CYS5	III+IV	primary tumor	poor	Negative	N1	M0	NA	NA	NA	NA	NA	NA
118A4280A1	GBC	79	Male	CYS5	III+IV	primary tumor	poor	Negative	N0	M0	NA	NA	NA	NA	NA	NA
118A4284A1	ICC	52	Male	CYS5	II	primary tumor	moderate	Positive	N0	M0	NA	NA	NA	NA	NA	NA
118A4298A1	ICC	57	Male	CYS5	III+IV	primary tumor	poor	Negative	NX	M1	NA	NA	NA	NA	NA	NA
118A4330A1	ECC	74	Male	CYS5	II	primary tumor	moderate	Negative	N0	M0	NA	NA	NA	NA	NA	NA
118A4336A1	GBC	73	Male	CYS5	III+IV	primary tumor	moderate	Negative	N1	M0	NA	NA	NA	NA	NA	NA
118A4375A1	ICC	67	Male	CYS5	III+IV	primary tumor	moderate	Positive	NX	M1	NA	NA	NA	NA	NA	NA
118A4386A1	ICC	57	Female	CYS5	III+IV	primary tumor	poor	Negative	N1	M0	NA	NA	NA	NA	NA	NA
118A4387A1	GBC	74	Male	CYS5	III+IV	metastatic tumor	NA	Negative	NX	M1	NA	NA	NA	NA	NA	NA
118A4434A1	ICC	43	Female	CYS5	II	primary tumor	well	Positive	N0	M0	NA	NA	NA	NA	NA	NA
118A4438A1	ICC	67	Female	CYS5	II	primary tumor	poor	Negative	N0	M0	NA	NA	NA	NA	NA	NA
118A4486A1	GBC	66	Male	CYS5	III+IV	primary tumor	well	Negative	N0	M0	NA	NA	NA	NA	NA	NA
118A4544A1	GBC	70	Male	CYS5	II	primary tumor	poor	Negative	N0	M0	NA	NA	NA	NA	NA	NA
118A4682A2	ICC	57	Male	CYS5	II	primary tumor	moderate	Positive	N0	M0	NA	NA	NA	NA	NA	NA
118A4689A1	ECC	34	Female	CYS5	II	primary tumor	NA	Negative	N0	M0	NA	NA	NA	NA	NA	NA
118A4698A1	ECC	56	Female	CYS5	NA	primary tumor	poor	Negative	NX	MX	NA	NA	NA	NA	NA	NA
118A4765A2	ICC	59	Female	CYS5	I	primary tumor	moderate	Negative	N0	M0	NA	NA	NA	NA	NA	NA
118B4778A1	ICC	52	Male	CYS5	III+IV	metastatic tumor	moderate	Negative	NX	M1	NA	NA	NA	NA	NA	NA
118B4782A1	ICC	80	Female	CYS5	III+IV	primary tumor	moderate	Negative	N0	M1	NA	NA	NA	NA	NA	NA
118B4789A1	ECC	80	Female	CYS5	III+IV	metastatic tumor	NA	Negative	NX	M1	NA	NA	NA	NA	NA	NA
118B4791A2	ECC	76	Male	CYS5	II	primary tumor	moderate	Positive	N1	M0	NA	NA	NA	NA	NA	NA
118B4864A2	ICC	59	Female	CYS5	NA	primary tumor	poor	Negative	NX	MX	NA	NA	NA	NA	NA	NA
118B4888A1	ICC	62	Female	CYS5	NA	primary tumor	moderate	Negative	N0	MX	NA	NA	NA	NA	NA	NA
118B4909A1	GBC	67	Female	CYS5	III+IV	metastatic tumor	NA	Negative	NX	M1	NA	NA	NA	NA	NA	NA
118B4937A1	ICC	61	Female	CYS5	III+IV	primary tumor	NA	Negative	NX	M1	NA	NA	NA	NA	NA	NA
118B5017A1	ECC	60	Male	CYS5	II	primary tumor	poor	Negative	N1	M0	NA	NA	NA	NA	NA	NA
118B5044A1	ECC	68	Male	CYS5	II	primary tumor	moderate	NA	N1	M0	NA	NA	NA	NA	NA	NA
118B5053A1	ECC	60	Female	CYS5	II	primary tumor	poor	Negative	N0	M0	NA	NA	NA	NA	NA	NA
118B5073A1	GBC	62	Female	CYS5	III+IV	metastatic tumor	NA	Negative	N1	M1	NA	NA	NA	NA	NA	NA
118B5110A1	ICC	74	Male	CYS5	NA	primary tumor	poor	Negative	NX	MX	NA	NA	NA	NA	NA	NA
118B5118A1	ICC	65	Male	CYS5	NA	primary tumor	moderate	Negative	NX	MX	NA	NA	NA	NA	NA	NA
118B5121A1	ECC	62	Male	CYS5	II	primary tumor	poor	Negative	N0	M0	NA	NA	NA	NA	NA	NA
118B5127A1	ECC	63	Female	CYS5	II	primary tumor	moderate	Negative	N0	M0	NA	NA	NA	NA	NA	NA
118C5128A1	ICC	65	Male	CYS5	I	primary tumor	moderate	Negative	N0	M0	NA	NA	NA	NA	NA	NA
118C5132A1	ICC	55	Male	CYS5	III+IV	primary tumor	moderate	Negative	N1	M1	NA	NA	NA	NA	NA	NA
118C5169A1	ICC	60	Female	CYS5	III+IV	primary tumor	moderate	Negative	N1	M0	NA	NA	NA	NA	NA	NA
118C5218A1	ICC	63	Male	CYS5	III+IV	primary tumor	poor	Negative	NX	M1	NA	NA	NA	NA	NA	NA
118C5252A1	ICC	57	Male	CYS5	NA	primary tumor	NA	Positive	NX	MX	NA	NA	NA	NA	NA	NA
118C5275A1	ICC	61	Female	CYS5	III+IV	primary tumor	poor	Negative	N1	M0	NA	NA	NA	NA	NA	NA
118C5293A1	ICC	71	Male	CYS5	NA	primary tumor	moderate	Negative	NX	MX	NA	NA	NA	NA	NA	NA
118C5350A2	ECC	66	Male	CYS5	NA	primary tumor	poor	Negative	NX	MX	NA	NA	NA	NA	NA	NA
118C5506A1	ICC	64	Male	CYS5	III+IV	primary tumor	poor	NA	N1	M0	NA	NA	NA	NA	NA	NA
118C5592A1	ICC	76	Female	CYS5	NA	primary tumor	NA	Positive	NX	MX	NA	NA	NA	NA	NA	NA
118C5597A1	ECC	67	Male	CYS5	II	primary tumor	moderate	Negative	N0	M0	NA	NA	NA	NA	NA	NA
118C5599A1	ICC	59	Female	CYS5	III+IV	primary tumor	poor	Negative	N1	M0	NA	NA	NA	NA	NA	NA
118C5623A1	GBC	53	Female	CYS5	NA	primary tumor	poor	Negative	NX	MX	NA	NA	NA	NA	NA	NA
118C5635A1	ICC	59	Male	CYS5	III+IV	primary tumor	poor	Negative	N1	M0	NA	NA	NA	NA	NA	NA
118C5668A1	ICC	65	Female	CYS5	III+IV	primary tumor	poor	Positive	N1	M0	NA	NA	NA	NA	NA	NA
118C5749A1	GBC</															

118D6094D1	GBC	74	Male	CSYS	II	primary tumor	poor	Negative	N0	M0	NA	NA	NA	NA	NA	NA
118D6120A1	GBC	54	Female	CSYS	II	primary tumor	moderate	Negative	N0	M0	NA	NA	NA	NA	NA	NA
118D6166A1	ICC	72	Female	CSYS	III+IV	primary tumor	poor	Negative	N0	M0	NA	NA	NA	NA	NA	NA
118D6220A1	ICC	46	Female	CSYS	III+IV	primary tumor	well	Negative	NX	M1	NA	NA	NA	NA	NA	NA
118D6255A1	ICC	56	Female	CSYS	III+IV	primary tumor	poor	Positive	NX	M1	NA	NA	NA	NA	NA	NA
118D6295A1	ECC	38	Female	CSYS	III+IV	primary tumor	poor	Negative	NX	M1	NA	NA	NA	NA	NA	NA
118D6350A1	ICC	69	Male	CSYS	III+IV	primary tumor	moderate	Positive	N0	M0	NA	NA	NA	NA	NA	NA
118D6360A1	ICC	61	Female	CSYS	III	primary tumor	moderate	Positive	N0	M0	NA	NA	NA	NA	NA	NA
118D6403A1	ICC	73	Male	CSYS	NA	primary tumor	poor	Negative	NX	MX	NA	NA	NA	NA	NA	NA
118D6420A1	GBC	81	Male	CSYS	I	primary tumor	well	Negative	N0	M0	NA	NA	NA	NA	NA	NA
118D6519A1	ECC	47	Male	CSYS	III+IV	primary tumor	poor	NA	NX	M1	NA	NA	NA	NA	NA	NA
118D6546A1	GBC	57	Female	CSYS	III+IV	metastatic tumor	NA	Negative	NX	M1	NA	NA	NA	NA	NA	NA
118D6605A1	ECC	71	Female	CSYS	I	primary tumor	poor	Negative	N0	M0	NA	NA	NA	NA	NA	NA
118D6683A1	ICC	66	Male	CSYS	III+IV	primary tumor	poor	Negative	NX	M1	NA	NA	NA	NA	NA	NA
118D6684A1	ICC	60	Male	CSYS	III+IV	primary tumor	poor	Negative	NX	MX	NA	NA	NA	NA	NA	NA
118D6719A1	ICC	69	Male	CSYS	III+IV	primary tumor	moderate	Negative	N1	M0	NA	NA	NA	NA	NA	NA
118D6898A1	ECC	65	Male	CSYS	III+IV	primary tumor	well	Negative	N1	M0	NA	NA	NA	NA	NA	NA
118D6984A1	ECC	73	Male	CSYS	II	primary tumor	poor	Negative	N1	M0	NA	NA	NA	NA	NA	NA
118D6985A1	ICC	56	Male	CSYS	III+IV	primary tumor	poor	Negative	N1	M0	NA	NA	NA	NA	NA	NA
118E7021A1	GBC	82	Male	CSYS	II	primary tumor	poor	Negative	N0	M0	NA	NA	NA	NA	NA	NA
118E7059A1	ICC	62	Male	CSYS	NA	primary tumor	poor	Negative	NX	MX	NA	NA	NA	NA	NA	NA
118E7103A1	ECC	42	Female	CSYS	II	primary tumor	well	Negative	N0	M0	NA	NA	NA	NA	NA	NA
118E7142A1	ECC	51	Male	CSYS	II	primary tumor	moderate	Negative	N1	M0	NA	NA	NA	NA	NA	NA
118E7171A1	GBC	66	Female	CSYS	II	primary tumor	moderate	Negative	N0	M0	NA	NA	NA	NA	NA	NA
118E7187A1	ICC	83	Female	CSYS	I	primary tumor	moderate	Negative	N0	M0	NA	NA	NA	NA	NA	NA
118E7191A1	ICC	65	Female	CSYS	I	primary tumor	moderate	Negative	N0	M0	NA	NA	NA	NA	NA	NA
118E7218A1	ECC	66	Male	CSYS	III+IV	metastatic tumor	moderate	Negative	NX	M1	NA	NA	NA	NA	NA	NA
118E7249A1	GBC	45	Female	CSYS	II	primary tumor	moderate	Negative	N0	M0	NA	NA	NA	NA	NA	NA
118E7270A1	ECC	55	Male	CSYS	II	primary tumor	moderate	Negative	N0	M0	NA	NA	NA	NA	NA	NA
118E7290A1	ECC	31	Male	CSYS	III+IV	metastatic tumor	NA	Negative	N1	M1	NA	NA	NA	NA	NA	NA
118E7304A1	ECC	59	Male	CSYS	II	metastatic tumor	poor	Negative	N0	M0	NA	NA	NA	NA	NA	NA
118E7306A1	ICC	63	Male	CSYS	NA	primary tumor	poor	NA	NX	MX	NA	NA	NA	NA	NA	NA
118E7325A1	GBC	53	Female	CSYS	II	primary tumor	poor	Negative	N0	M0	NA	NA	NA	NA	NA	NA
118E7344A1	ICC	60	Male	CSYS	III+IV	primary tumor	poor	Negative	N0	M0	NA	NA	NA	NA	NA	NA
118E7407A1	ECC	72	Male	CSYS	III+IV	primary tumor	moderate	Negative	N1	M1	NA	NA	NA	NA	NA	NA
118E7446A1	ICC	65	Female	CSYS	III+IV	primary tumor	moderate	Negative	N0	M0	NA	NA	NA	NA	NA	NA
118E7470A1	ICC	54	Female	CSYS	I	primary tumor	moderate	Negative	N0	M0	NA	NA	NA	NA	NA	NA
118E7477A1	ICC	62	Male	CSYS	III+IV	primary tumor	poor	Negative	N0	M0	NA	NA	NA	NA	NA	NA
118E7484A1	ICC	59	Male	CSYS	III+IV	metastatic tumor	poor	Positive	NX	M1	NA	NA	NA	NA	NA	NA
118E7554A2	GBC	54	Female	CSYS	III+IV	metastatic tumor	NA	Negative	N0	M1	NA	NA	NA	NA	NA	NA
118E7614A1	ICC	45	Male	CSYS	II	primary tumor	moderate	Negative	N0	M0	NA	NA	NA	NA	NA	NA
118E7632A1	ICC	49	Female	CSYS	NA	primary tumor	poor	Negative	NX	MX	NA	NA	NA	NA	NA	NA
118E7633A1	ICC	71	Male	CSYS	I	primary tumor	poor	Positive	N0	M0	NA	NA	NA	NA	NA	NA
118E7744A1	ECC	61	Male	CSYS	I	primary tumor	moderate	NA	N0	M0	NA	NA	NA	NA	NA	NA
118E7805A1	ICC	64	Female	CSYS	II	primary tumor	poor	Positive	N0	M0	NA	NA	NA	NA	NA	NA
118E7868A1	ECC	63	Female	CSYS	I	primary tumor	moderate	Negative	N0	M0	NA	NA	NA	NA	NA	NA
118E7888A1	GBC	64	Female	CSYS	III+IV	primary tumor	poor	Negative	N0	M1	NA	NA	NA	NA	NA	NA
118E7901A1	ICC	48	Male	CSYS	III+IV	primary tumor	moderate	NA	N0	M1	NA	NA	NA	NA	NA	NA
118E7926A1	ICC	43	Female	CSYS	III+IV	primary tumor	poor	Positive	NX	M1	NA	NA	NA	NA	NA	NA
118E7940A1	ECC	77	Male	CSYS	II	primary tumor	poor	NA	N1	M0	NA	NA	NA	NA	NA	NA
118E7964A1	ICC	67	Male	CSYS	III+IV	metastatic tumor	poor	Negative	NX	MX	NA	NA	NA	NA	NA	NA
118E7982A2	ECC	58	Male	CSYS	II	primary tumor	moderate	NA	N1	M0	NA	NA	NA	NA	NA	NA
118F7997A1	ICC	48	Female	CSYS	III+IV	primary tumor	moderate	Negative	N0	M0	NA	NA	NA	NA	NA	NA
118F8082A1	ICC	68	Male	CSYS	III+IV	metastatic tumor	moderate	Negative	NX	M1	NA	NA	NA	NA	NA	NA
118F8090A1	ICC	54	Female	CSYS	NA	primary tumor	poor	Negative	NX	MX	NA	NA	NA	NA	NA	NA
118F8094A1	ECC	47	Male	CSYS	II	primary tumor	moderate	Negative	N1	M0	NA	NA	NA	NA	NA	NA
118F8096A1	ECC	59	Male	CSYS	II	primary tumor	poor	Negative	N1	M0	NA	NA	NA	NA	NA	NA
118F8114A1	GBC	52	Male	CSYS	III+IV	metastatic tumor	poor	Negative	N1	M0	NA	NA	NA	NA	NA	NA
118F8152A1	ICC	59	Male	CSYS	III+IV	primary tumor	poor	Positive	N1	M0	NA	NA	NA	NA	NA	NA
118F8157A1	ICC	58	Female	CSYS	III+IV	metastatic tumor	NA	Negative	NX	M1	NA	NA	NA	NA	NA	NA
118F8167A1	ECC	44	Male	CSYS	III+IV	metastatic tumor	NA	Negative	NX	M1	NA	NA	NA	NA	NA	NA
118F8170A1	GBC	55	Female	CSYS	III+IV	metastatic tumor	NA	NA	NX	M1	NA	NA	NA	NA	NA	NA
118F8189A1	ICC	61	Female	CSYS	III+IV	primary tumor	poor	Negative	N0	M1	NA	NA	NA	NA	NA	NA
118F8201A1	ICC	75	Female	CSYS	III+IV	primary tumor	poor	Negative	N0	M0	NA	NA	NA	NA	NA	NA
118F8208A1	ECC	35	Female	CSYS	NA	primary tumor	moderate	Negative	NX	MX	NA	NA	NA	NA	NA	NA
118F8237A1	ICC	61	Male	CSYS	II	primary tumor	poor	Negative	N0	M0	NA	NA	NA	NA	NA	NA
118F8276A1	ICC	57	Female	CSYS	III+IV	primary tumor	moderate	NA	N0	M0	NA	NA	NA	NA	NA	NA
118F8372A1	GBC	67	Female	CSYS	II	primary tumor	poor	NA	N0	M0	NA	NA	NA	NA	NA	NA
118F8377A1	GBC	72	Female	CSYS	III+IV	primary tumor	poor	Negative	N1	M0	NA	NA	NA	NA	NA	NA
118F8392A1	ECC	64	Male	CSYS	II	primary tumor	moderate	Negative	N1	M0	NA	NA	NA	NA	NA	NA
118F8415A1	ECC	55	Female	CSYS	III+IV	metastatic tumor	moderate	Negative	NX	M1	NA	NA	NA	NA	NA	NA
118F8458A1	ICC	42	Male	CSYS	III+IV	primary tumor	poor	Negative	N1	M0	NA	NA	NA	NA	NA	NA
118F8489A1	ICC	47	Male	CSYS	III+IV	metastatic tumor	NA	Negative	NX	M1	NA	NA	NA	NA	NA	NA
118F8522A1	ICC	68	Female	CSYS	I	primary tumor	poor	Negative	N0	M0	NA	NA	NA	NA	NA	NA
118F8546A1	ICC	46	Male	CSYS	NA	primary tumor	poor	Negative	NX	MX	NA	NA	NA	NA	NA	NA
118F8558A1	ICC	67	Male	CSYS	III+IV	primary tumor	moderate	Negative	N0	M0	NA	NA	NA	NA	NA	NA
118F8601A1	ICC	50	Male	CSYS	III+IV	primary tumor	moderate	Negative	N0	M0	NA	NA	NA	NA	NA	NA
118F8632A1	GBC	66	Female	CSYS	III+IV	primary tumor	poor	Negative	N0	M0	NA	NA	NA	NA	NA	NA
118F8646A1	ECC	82	Female	CSYS	III+IV	primary tumor	poor	Negative	N1	M1	NA	NA	NA	NA	NA	NA
118F8770A1	ICC	55	Female	CSYS	III+IV	primary tumor	moderate	Negative	N1	M0	NA	NA	NA	NA	NA	NA
118F8792A1	ICC	64	Male	CSYS	III+IV	primary tumor	poor	Positive	N0	M0	NA	NA	NA	NA	NA	NA
118F8797A1	ICC	55	Male	CSYS	III+IV	primary tumor	poor	Negative	N1	M0	NA	NA	NA	NA	NA	NA
118F8813A2	ECC	72	Male	CSYS	I	primary tumor	well	Positive	N0	M0	NA	NA	NA	NA	NA	NA
118F8844A1	GBC	62	Male	CSYS	III+IV	metastatic tumor	moderate	Negative	N1	M0	NA	NA	NA	NA	NA	NA
118F8850A1	ICC	60	Female	CSYS	III+IV	primary tumor	poor	Negative	N1	M0	NA	NA	NA	NA	NA	NA
118F8903A1	GBC	59	Male	CSYS	III+IV	primary tumor	moderate	Negative	N1	M0	NA	NA	NA	NA	NA	NA
118G1224A1	ICC	39	Male	CSYS	III+IV	primary tumor	moderate	Negative	N1	M1	NA	NA	NA	NA	NA	NA
118G1344A1	ICC	57	Male	CSYS	III+IV	primary tumor	poor	Negative	N0	M0	NA	NA	NA	NA	NA	NA
118G1348A1	GBC	48	Female	CSYS	II	primary tumor	poor	Negative	N0	M0	NA	NA	NA	NA	NA	NA
118G8977A1	ICC	44	Male	CSYS	NA	primary tumor	poor	Positive	NX	MX	NA	NA	NA	NA	NA	NA
118G9081A1	ICC	59	Male	CSYS	III+IV	primary tumor	moderate	Positive	N1	M1	NA	NA	NA	NA	NA	NA
118G9119A1	ICC	46	Female	CSYS	I	primary tumor	poor	Negative	N0	M0	NA	NA	NA	NA	NA	NA
118G9120A1	ECC	52	Female	CSYS	NA	primary tumor	poor	Negative	NX	MX	NA	NA	NA	NA	NA	NA
118G9233A1	ICC	71	Male	CSYS	III+IV	primary tumor	poor	Negative	N0	M0	NA	NA	NA	NA	NA	NA
118G9262A1	ICC	51	Female	CSYS	I	primary tumor	poor	Negative	N0	M0	NA	NA	NA	NA	NA	NA
118G9348A1	GBC	55	Male	CSYS	II	primary tumor	moderate	Negative	N0	M0	NA	NA	NA	NA	NA	NA
118G9364A1	ICC	65	Male	CSYS	III+IV	primary tumor	poor	Negative	NX	M1	NA	NA	NA	NA	NA	NA
118G9391A1	ICC	65	Male	CSYS	III+IV	primary tumor	poor	NA	N0	M0	NA	NA	NA	NA	NA	NA
118G9397A1	GBC	47	Male	CSYS	II	primary tumor	moderate	Negative	N0	M0	NA	NA	NA	NA	NA	NA
118G9417A2	ECC	67	Male	CSYS	II	primary tumor	moderate	NA	N0	M0	NA	NA	NA	NA	NA	NA
118G9421A1	ICC	71	Male	CSYS	III+IV	primary tumor	poor	Negative	N1	M0	NA	NA	NA	NA	NA	NA
118G9423A1	GBC	75	Female	CSYS	III+IV	primary tumor	poor	Negative	N0	M0	NA	NA	NA	NA	NA	NA
118G9448A1	GBC	78	Male	CSYS	III+IV	metastatic tumor	poor	NA	NX	M1	NA	NA	NA			

118G9797A1	GBC	47	Female	CSYS	II	primary tumor	poor	Negative	N0	M0	NA	NA	NA	NA	NA	NA
118G9912A1	GBC	64	Male	CSYS	III+IV	primary tumor	poor	Negative	N0	M0	NA	NA	NA	NA	NA	NA
118G9955A1	GBC	50	Male	CSYS	I	primary tumor	poor	Negative	N0	M0	NA	NA	NA	NA	NA	NA
118G9970A1	ECC	49	Female	CSYS	NA	primary tumor	moderate	Negative	NX	MX	NA	NA	NA	NA	NA	NA
118H1438M1	ICC	56	Female	CSYS	I	primary tumor	moderate	Negative	N0	M0	NA	NA	NA	NA	NA	NA
118H1479A1	ICC	69	Female	CSYS	III+IV	primary tumor	poor	Negative	N1	M0	NA	NA	NA	NA	NA	NA
118H1515A1	GBC	67	Male	CSYS	III+IV	primary tumor	moderate	Negative	N1	M0	NA	NA	NA	NA	NA	NA
118H1577A1	ICC	74	Male	CSYS	III+IV	primary tumor	NA	Negative	NX	M1	NA	NA	NA	NA	NA	NA
118H1607A1	ICC	35	Male	CSYS	III+IV	primary tumor	poor	Negative	N0	M0	NA	NA	NA	NA	NA	NA
118H1642A1	ECC	65	Male	CSYS	III+IV	primary tumor	poor	Negative	N1	M0	NA	NA	NA	NA	NA	NA
118H1685A1	ICC	55	Male	CSYS	II	primary tumor	poor	Negative	N0	M0	NA	NA	NA	NA	NA	NA
118H1689A1	ICC	69	Male	CSYS	III+IV	metastatic tumor	NA	Negative	NX	M1	NA	NA	NA	NA	NA	NA
118H1733A1	ECC	43	Male	CSYS	NA	primary tumor	poor	Negative	NX	MX	NA	NA	NA	NA	NA	NA
118H1787A1	GBC	59	Female	CSYS	III+IV	metastatic tumor	NA	Negative	NX	M1	NA	NA	NA	NA	NA	NA
118H1840A1	ICC	65	Male	CSYS	NA	primary tumor	poor	Negative	NX	MX	NA	NA	NA	NA	NA	NA
118H2136A1	ECC	63	Female	CSYS	III+IV	metastatic tumor	moderate	Negative	NX	M1	NA	NA	NA	NA	NA	NA
118H2149S1	ICC	73	Male	CSYS	III+IV	primary tumor	moderate	NA	N1	M1	NA	NA	NA	NA	NA	NA
118H2157A1	ICC	53	Male	CSYS	NA	primary tumor	poor	Positive	NX	MX	NA	NA	NA	NA	NA	NA
118H2438A1	ECC	73	Female	CSYS	II	primary tumor	moderate	Negative	N0	M0	NA	NA	NA	NA	NA	NA
118H2472A1	ICC	66	Male	CSYS	NA	primary tumor	moderate	Negative	NX	MX	NA	NA	NA	NA	NA	NA
118H2473A1	ECC	78	Male	CSYS	I	primary tumor	moderate	Negative	N0	M0	NA	NA	NA	NA	NA	NA
118H2475M1	ECC	55	Male	CSYS	III+IV	primary tumor	moderate	Negative	N1	M0	NA	NA	NA	NA	NA	NA
118H2476A1	ICC	55	Male	CSYS	III+IV	primary tumor	moderate	Positive	NX	M1	NA	NA	NA	NA	NA	NA
118H2503A1	GBC	60	Male	CSYS	III+IV	primary tumor	moderate	Negative	N1	M1	NA	NA	NA	NA	NA	NA
118H2531A3	GBC	27	Female	CSYS	NA	metastatic tumor	NA	NA	NX	MX	NA	NA	NA	NA	NA	NA
118H2540A1	ECC	58	Male	CSYS	III+IV	primary tumor	poor	Positive	N1	M0	NA	NA	NA	NA	NA	NA
118H2588A1	ECC	78	Male	CSYS	NA	primary tumor	poor	Negative	NX	MX	NA	NA	NA	NA	NA	NA
118H2593A1	ICC	74	Female	CSYS	I	primary tumor	moderate	Positive	N0	M0	NA	NA	NA	NA	NA	NA
118H2626A1	ICC	65	Male	CSYS	III+IV	recurrent tumor	NA	Positive	NX	MX	NA	NA	NA	NA	NA	NA
118H2716A1	ICC	58	Male	CSYS	III+IV	primary tumor	poor	Negative	N1	M0	NA	NA	NA	NA	NA	NA
118H2758A1	ECC	54	Female	CSYS	I	primary tumor	moderate	Negative	N0	M0	NA	NA	NA	NA	NA	NA
118I2919A1	ICC	56	Male	CSYS	III+IV	metastatic tumor	NA	Positive	NX	M1	NA	NA	NA	NA	NA	NA
118I2978M1	ICC	69	Male	CSYS	III+IV	metastatic tumor	moderate	Negative	N0	M0	NA	NA	NA	NA	NA	NA
118I3162A1	ICC	63	Male	CSYS	III+IV	primary tumor	moderate	Positive	N1	M0	NA	NA	NA	NA	NA	NA
118I3202A1	ICC	55	Female	CSYS	III+IV	recurrent tumor	moderate	Negative	NX	MX	NA	NA	NA	NA	NA	NA
118I3402A1	ICC	53	Male	CSYS	II	primary tumor	poor	Positive	N0	M0	NA	NA	NA	NA	NA	NA
118I3426A1	ECC	67	Female	CSYS	I	primary tumor	moderate	NA	N0	M0	NA	NA	NA	NA	NA	NA
118I3457A2	ICC	57	Female	CSYS	NA	primary tumor	moderate	Positive	NX	MX	NA	NA	NA	NA	NA	NA
118I3472M1	GBC	47	Female	CSYS	III+IV	primary tumor	moderate	Negative	N1	M0	NA	NA	NA	NA	NA	NA
118I3488A1	ICC	67	Female	CSYS	III+IV	primary tumor	poor	Positive	N1	M0	NA	NA	NA	NA	NA	NA
118I3510A1	ICC	55	Female	CSYS	III+IV	primary tumor	poor	NA	N1	M0	NA	NA	NA	NA	NA	NA
118I3529A1	ECC	73	Male	CSYS	II	primary tumor	poor	Positive	N0	M0	NA	NA	NA	NA	NA	NA
118I3532A1	ICC	59	Male	CSYS	III+IV	primary tumor	poor	Positive	N1	M0	NA	NA	NA	NA	NA	NA
118I3573A1	GBC	61	Female	CSYS	III+IV	metastatic tumor	moderate	Negative	NX	M1	NA	NA	NA	NA	NA	NA
118I3576A1	ICC	65	Male	CSYS	II	primary tumor	poor	Positive	N0	M0	NA	NA	NA	NA	NA	NA
118I3592A2	ECC	63	Male	CSYS	NA	primary tumor	poor	NA	N1	MX	NA	NA	NA	NA	NA	NA
118I3607A2	ICC	60	Female	CSYS	III+IV	primary tumor	poor	Positive	N0	M0	NA	NA	NA	NA	NA	NA
118I3629A1	ECC	59	Female	CSYS	III+IV	primary tumor	moderate	Negative	N1	M0	NA	NA	NA	NA	NA	NA
118I3652A1	ICC	75	Male	CSYS	III+IV	primary tumor	NA	Positive	N1	M1	NA	NA	NA	NA	NA	NA
118I3743M1	GBC	64	Female	CSYS	III+IV	metastatic tumor	NA	Negative	NX	M1	NA	NA	NA	NA	NA	NA
118I3752D1	ICC	53	Male	CSYS	NA	primary tumor	poor	Positive	NX	MX	NA	NA	NA	NA	NA	NA
118I3763A1	GBC	65	Male	CSYS	II	primary tumor	poor	Negative	N0	M0	NA	NA	NA	NA	NA	NA
118I3817A1	ICC	43	Male	CSYS	III+IV	primary tumor	poor	Positive	N0	M0	NA	NA	NA	NA	NA	NA
118I3847A1	ICC	63	Male	CSYS	III+IV	primary tumor	poor	Negative	N0	M0	NA	NA	NA	NA	NA	NA
118I3850D1	ECC	69	Female	CSYS	I	primary tumor	moderate	Positive	N0	M0	NA	NA	NA	NA	NA	NA
118I3860A1	ICC	62	Male	CSYS	III+IV	primary tumor	poor	Negative	N1	M0	NA	NA	NA	NA	NA	NA
118I3960A1	GBC	72	Male	CSYS	III+IV	primary tumor	poor	NA	N0	M0	NA	NA	NA	NA	NA	NA
118I3967M1	ICC	75	Male	CSYS	NA	primary tumor	poor	Negative	NX	MX	NA	NA	NA	NA	NA	NA
118I4062A1	ICC	69	Male	CSYS	III+IV	recurrent tumor	moderate	Negative	NX	MX	NA	NA	NA	NA	NA	NA
118I4224A1	ICC	57	Male	CSYS	III+IV	recurrent tumor	poor	Positive	NX	MX	NA	NA	NA	NA	NA	NA
118I4228A1	ICC	62	Female	CSYS	III+IV	primary tumor	moderate	Negative	N1	M0	NA	NA	NA	NA	NA	NA
118I4287M1	ICC	55	Male	CSYS	I	primary tumor	moderate	Positive	N0	M0	NA	NA	NA	NA	NA	NA
118I4299M1	GBC	68	Female	CSYS	NA	metastatic tumor	poor	NA	NX	MX	NA	NA	NA	NA	NA	NA
118I4384A1	ICC	69	Female	CSYS	NA	primary tumor	NA	Positive	NX	MX	NA	NA	NA	NA	NA	NA
118I4450M1	ICC	54	Male	CSYS	III+IV	primary tumor	moderate	Negative	NX	M1	NA	NA	NA	NA	NA	NA
118I4625A1	ICC	60	Male	CSYS	III+IV	primary tumor	poor	Negative	N1	M0	NA	NA	NA	NA	NA	NA
118I4646M1	ICC	60	Male	CSYS	III+IV	primary tumor	poor	Negative	N0	M0	NA	NA	NA	NA	NA	NA
118I4748M1	ICC	63	Male	CSYS	III+IV	primary tumor	poor	Positive	N0	M0	NA	NA	NA	NA	NA	NA
118I4750A1	ICC	55	Male	CSYS	III+IV	metastatic tumor	poor	Negative	N1	M0	NA	NA	NA	NA	NA	NA
118I4755M1	ICC	45	Male	CSYS	II	primary tumor	poor	Positive	N0	M0	NA	NA	NA	NA	NA	NA
118I4761A1	ICC	69	Male	CSYS	III+IV	primary tumor	poor	Positive	N1	M0	NA	NA	NA	NA	NA	NA
118I4779J1	ECC	51	Male	CSYS	II	primary tumor	poor	NA	N0	M0	NA	NA	NA	NA	NA	NA
118I4845A1	ICC	66	Male	CSYS	II	primary tumor	moderate	Positive	N0	M0	NA	NA	NA	NA	NA	NA
118I4887A1	GBC	58	Female	CSYS	III+IV	primary tumor	poor	Negative	N0	M0	NA	NA	NA	NA	NA	NA
118I4963M1	GBC	56	Female	CSYS	NA	primary tumor	NA	Positive	N1	MX	NA	NA	NA	NA	NA	NA
118I5065A1	ICC	63	Male	CSYS	III+IV	primary tumor	poor	Positive	NX	MX	NA	NA	NA	NA	NA	NA
118I5083M1	ICC	42	Female	CSYS	III+IV	primary tumor	moderate	NA	N1	M1	NA	NA	NA	NA	NA	NA
118I5085M1	ICC	51	Female	CSYS	NA	primary tumor	poor	Positive	NX	MX	NA	NA	NA	NA	NA	NA
118I5119A1	ECC	58	Male	CSYS	III+IV	metastatic tumor	moderate	Negative	NX	M1	NA	NA	NA	NA	NA	NA
118I5135A1	ICC	74	Male	CSYS	III+IV	primary tumor	poor	Negative	N0	M0	NA	NA	NA	NA	NA	NA
118I5144A1	GBC	38	Female	CSYS	III+IV	primary tumor	moderate	Negative	N0	M0	NA	NA	NA	NA	NA	NA
118I5169M1	ICC	75	Female	CSYS	III+IV	primary tumor	moderate	Negative	NX	M1	NA	NA	NA	NA	NA	NA
118I5206M1	ECC	39	Female	CSYS	III+IV	metastatic tumor	poor	Positive	NX	M1	NA	NA	NA	NA	NA	NA
118I5249M1	ECC	59	Female	CSYS	II	primary tumor	poor	Positive	N1	M0	NA	NA	NA	NA	NA	NA
118I5276A1	ECC	55	Female	CSYS	I	primary tumor	poor	Positive	N0	M0	NA	NA	NA	NA	NA	NA
118I5402A1	ICC	50	Male	CSYS	III+IV	metastatic tumor	poor	Positive	N1	M0	NA	NA	NA	NA	NA	NA
118I5518M1	ICC	34	Male	CSYS	III+IV	primary tumor	poor	Positive	NX	M1	NA	NA	NA	NA	NA	NA
118I5583A1	ICC	67	Male	CSYS	NA	primary tumor	poor	Positive	NX	MX	NA	NA	NA	NA	NA	NA
118K5630A1	ICC	65	Male	CSYS	III+IV	primary tumor	moderate	Positive	N1	M0	NA	NA	NA	NA	NA	NA
118K5635M1	ECC	54	Male	CSYS	II	primary tumor	moderate	Negative	N0	M0	NA	NA	NA	NA	NA	NA
118K5684M1	GBC	74	Male	CSYS	III+IV	metastatic tumor	moderate	Positive	NX	M1	NA	NA	NA	NA	NA	NA
118K5718A1	ICC	66	Male	CSYS	II	primary tumor	poor	Positive	N0	M0	NA	NA	NA	NA	NA	NA
118K5909A1	GBC	67	Female	CSYS	NA	primary tumor	moderate	Positive	NX	MX	NA	NA	NA	NA	NA	NA
118K5971J1	ICC	42	Male	CSYS	I	primary tumor	moderate	Positive	N0	M0	NA	NA	NA	NA	NA	NA
118K5984A1	ICC	56	Female	CSYS	III+IV	primary tumor	moderate	Positive	NX	M1	NA	NA	NA	NA	NA	NA
118K5992M1	ICC	60	Male	CSYS	NA	primary tumor	NA	Positive	NX	MX	NA	NA	NA	NA	NA	NA
118K5993A1	GBC	52	Female	CSYS	III+IV	recurrent tumor	NA	Positive	NX	MX	NA	NA	NA	NA	NA	NA
118K6072M1	ICC	56	Male	CSYS	III+IV	primary tumor	moderate	Positive	N1	M0	NA	NA	NA	NA	NA	NA
118K6080A1	GBC	68	Female	CSYS	III+IV	primary tumor	moderate	Positive	N1	M0	NA	NA	NA	NA	NA	NA
118K6130M1	ICC	52	Female	CSYS	I	primary tumor	poor	Negative	N0	M0	NA	NA	NA	NA	NA	NA
118K6186A1	ICC	63	Male	CSYS	III+IV	primary tumor	moderate	NA	N0	M0	NA	NA	NA	NA	NA	NA
118K6209A1	ICC	69	Female	CSYS	NA	primary tumor	moderate	Negative	NX	MX	NA	NA	NA	NA	NA	NA
118K6272A1	GBC	52	Female	CSYS	II	primary tumor	moderate	Positive	N0	M0	NA	NA				

118K6595M2	GBC	56	Female	CSYS	III+IV	primary tumor	NA	Positive	NX	M1	NA	NA	NA	NA	NA	NA
118K6631A1	ICC	46	Male	CSYS	III+IV	primary tumor	moderate	Positive	N1	M0	NA	NA	NA	NA	NA	NA
118K6637M1	ECC	74	Female	CSYS	NA	primary tumor	NA	Negative	NX	MX	NA	NA	NA	NA	NA	NA
118K6653A1	GBC	68	Male	CSYS	III+IV	metastatic tumor	NA	Negative	NX	M1	NA	NA	NA	NA	NA	NA
118K6674A1	ECC	71	Male	CSYS	III+IV	metastatic tumor	poor	Negative	N1	M0	NA	NA	NA	NA	NA	NA
118K6703A1	ICC	61	Male	CSYS	II	primary tumor	moderate	Negative	N0	M0	NA	NA	NA	NA	NA	NA
118K6789A1	ICC	65	Female	CSYS	III+IV	primary tumor	moderate	Positive	N1	M1	NA	NA	NA	NA	NA	NA
118K6855M1	ECC	53	Male	CSYS	I	primary tumor	poor	Negative	N0	M0	NA	NA	NA	NA	NA	NA
118K6924A1	ICC	62	Female	CSYS	I	primary tumor	poor	Negative	N0	M0	NA	NA	NA	NA	NA	NA
118K6958A1	GBC	66	Male	CSYS	III+IV	metastatic tumor	NA	Negative	NX	M1	NA	NA	NA	NA	NA	NA
118K6975A1	ECC	65	Female	CSYS	II	primary tumor	moderate	Positive	N0	M0	NA	NA	NA	NA	NA	NA
118K6977A1	GBC	64	Female	CSYS	III+IV	metastatic tumor	poor	Negative	NX	M1	NA	NA	NA	NA	NA	NA
118K6986A1	ICC	53	Male	CSYS	III+IV	primary tumor	poor	Positive	NX	MX	NA	NA	NA	NA	NA	NA
118K7052M1	ICC	46	Female	CSYS	III+IV	primary tumor	moderate	Positive	N0	M1	NA	NA	NA	NA	NA	NA
118K7082A1	ICC	62	Female	CSYS	III+IV	primary tumor	poor	Negative	N1	M0	NA	NA	NA	NA	NA	NA
118K7083M1	ICC	65	Female	CSYS	III+IV	primary tumor	moderate	Positive	N0	M0	NA	NA	NA	NA	NA	NA
118L7106A1	GBC	59	Male	CSYS	I	primary tumor	moderate	Negative	N0	M0	NA	NA	NA	NA	NA	NA
118L7131A1	ECC	72	Male	CSYS	III+IV	metastatic tumor	moderate	Negative	NX	M1	NA	NA	NA	NA	NA	NA
118L7133A1	ICC	40	Male	CSYS	NA	primary tumor	poor	Positive	NX	MX	NA	NA	NA	NA	NA	NA
118L7161A1	GBC	62	Female	CSYS	I	primary tumor	moderate	Negative	N0	M0	NA	NA	NA	NA	NA	NA
118L7198A1	ICC	56	Male	CSYS	III+IV	primary tumor	poor	Negative	N0	M0	NA	NA	NA	NA	NA	NA
118L7202A1	GBC	45	Female	CSYS	III+IV	metastatic tumor	moderate	Negative	NX	M1	NA	NA	NA	NA	NA	NA
118L7212A1	ICC	69	Female	CSYS	I	primary tumor	poor	Negative	N0	M0	NA	NA	NA	NA	NA	NA
118L7229A1	GBC	71	Female	CSYS	I	primary tumor	moderate	Negative	N0	M0	NA	NA	NA	NA	NA	NA
118L7236A1	ICC	47	Female	CSYS	III+IV	primary tumor	NA	Positive	NX	M1	NA	NA	NA	NA	NA	NA
118L7265A2	ECC	49	Male	CSYS	II	primary tumor	moderate	Negative	N0	MX	NA	NA	NA	NA	NA	NA
118L7275A1	ECC	63	Female	CSYS	III+IV	primary tumor	poor	Positive	NX	M1	NA	NA	NA	NA	NA	NA
118L7370A1	ICC	65	Female	CSYS	III+IV	primary tumor	moderate	Positive	N1	M0	NA	NA	NA	NA	NA	NA
118L7386A1	ICC	56	Male	CSYS	III+IV	primary tumor	moderate	Negative	N1	M0	NA	NA	NA	NA	NA	NA
118L7404M1	GBC	61	Female	CSYS	III+IV	metastatic tumor	poor	Negative	NX	M1	NA	NA	NA	NA	NA	NA
118L7413A1	ECC	60	Female	CSYS	III+IV	metastatic tumor	poor	Positive	NX	M1	NA	NA	NA	NA	NA	NA
118L7497M1	ICC	70	Male	CSYS	III+IV	primary tumor	NA	Positive	NX	M1	NA	NA	NA	NA	NA	NA
118L7516M1	ICC	71	Female	CSYS	II	primary tumor	moderate	Positive	N0	M0	NA	NA	NA	NA	NA	NA
118L7537A1	ECC	51	Male	CSYS	II	primary tumor	poor	Positive	N1	M0	NA	NA	NA	NA	NA	NA
118L7560M1	ICC	56	Male	CSYS	I	primary tumor	moderate	Negative	N0	M0	NA	NA	NA	NA	NA	NA
118L7574A1	ICC	56	Female	CSYS	III+IV	primary tumor	poor	Negative	N1	M0	NA	NA	NA	NA	NA	NA
118L7607A1	ICC	63	Male	CSYS	NA	primary tumor	poor	Negative	NX	MX	NA	NA	NA	NA	NA	NA
118L7654M1	ICC	68	Male	CSYS	NA	primary tumor	moderate	Positive	NX	MX	NA	NA	NA	NA	NA	NA
118L7656M1	ICC	62	Male	CSYS	I	primary tumor	moderate	Negative	N0	M0	NA	NA	NA	NA	NA	NA
118L7756A1	ICC	47	Male	CSYS	I	primary tumor	moderate	Negative	N0	M0	NA	NA	NA	NA	NA	NA
118L7757A1	ICC	39	Male	CSYS	I	primary tumor	poor	Positive	N0	M0	NA	NA	NA	NA	NA	NA
118L7820I1	ICC	31	Male	CSYS	NA	primary tumor	poor	Negative	NX	MX	NA	NA	NA	NA	NA	NA
118L7848M1	ICC	69	Female	CSYS	III+IV	primary tumor	moderate	Positive	N1	M0	NA	NA	NA	NA	NA	NA
118L7853A1	ECC	53	Male	CSYS	II	primary tumor	poor	Negative	N0	M0	NA	NA	NA	NA	NA	NA
118L7860A1	GBC	82	Male	CSYS	III+IV	primary tumor	poor	Negative	N1	M1	NA	NA	NA	NA	NA	NA
118L7867A1	ICC	43	Female	CSYS	III+IV	primary tumor	moderate	Positive	NX	M1	NA	NA	NA	NA	NA	NA
118L7895A1	ECC	30	Male	CSYS	III+IV	metastatic tumor	poor	Positive	NX	M1	NA	NA	NA	NA	NA	NA
118L8016M1	ECC	33	Male	CSYS	I	primary tumor	moderate	Negative	N0	M0	NA	NA	NA	NA	NA	NA
118L8023M2	ICC	74	Male	CSYS	III+IV	metastatic tumor	poor	Negative	NX	M1	NA	NA	NA	NA	NA	NA
118L8029M1	ICC	55	Male	CSYS	III+IV	primary tumor	moderate	Negative	N0	M0	NA	NA	NA	NA	NA	NA
118L8044A1	ECC	64	Female	CSYS	III+IV	primary tumor	poor	Positive	NX	M1	NA	NA	NA	NA	NA	NA
118L8083A1	ICC	59	Male	CSYS	I	primary tumor	poor	Positive	N0	M0	NA	NA	NA	NA	NA	NA
118L8213A1	ICC	66	Female	CSYS	I	recurrent tumor	poor	Negative	N0	M0	NA	NA	NA	NA	NA	NA
118L8367M1	GBC	49	Female	CSYS	III+IV	primary tumor	poor	Negative	N0	M0	NA	NA	NA	NA	NA	NA
118L8370M1	ECC	64	Male	CSYS	I	primary tumor	moderate	Negative	N0	M0	NA	NA	NA	NA	NA	NA
118L8457A1	ICC	32	Male	CSYS	III+IV	primary tumor	poor	Positive	N0	M0	NA	NA	NA	NA	NA	NA
118L8475A1	ICC	52	Female	CSYS	III+IV	primary tumor	poor	Positive	N0	M0	NA	NA	NA	NA	NA	NA
118L8606A1	GBC	60	Male	CSYS	III+IV	primary tumor	poor	Negative	N1	MX	NA	NA	NA	NA	NA	NA
118L8638M2	ICC	51	Female	CSYS	I	primary tumor	moderate	Negative	N0	M0	NA	NA	NA	NA	NA	NA
118L8642M1	GBC	64	Female	CSYS	III+IV	metastatic tumor	poor	Negative	N0	M1	NA	NA	NA	NA	NA	NA
118L8875M1	ICC	63	Female	CSYS	III+IV	primary tumor	moderate	Positive	N0	M0	NA	NA	NA	NA	NA	NA
118L8884A1	ECC	54	Male	CSYS	II	primary tumor	poor	NA	N0	M0	NA	NA	NA	NA	NA	NA
118L8913A1	ECC	73	Male	CSYS	II	primary tumor	moderate	Positive	N0	M0	NA	NA	NA	NA	NA	NA
118L8983A1	ECC	73	Male	CSYS	II	primary tumor	poor	Negative	N0	M0	NA	NA	NA	NA	NA	NA
118L8989A1	ECC	67	Male	CSYS	II	primary tumor	poor	Positive	N0	M0	NA	NA	NA	NA	NA	NA
118L9109A2	ICC	54	Female	CSYS	III+IV	primary tumor	poor	Negative	N1	M0	NA	NA	NA	NA	NA	NA
118L9110M1	ICC	51	Male	CSYS	II	primary tumor	moderate	Positive	N0	M0	NA	NA	NA	NA	NA	NA
119A1499I1	ICC	60	Male	CSYS	NA	primary tumor	poor	Positive	NX	MX	NA	NA	NA	NA	NA	NA
119A1568M1	ECC	61	Male	CSYS	III+IV	metastatic tumor	moderate	Positive	NX	M1	NA	NA	NA	NA	NA	NA
119A1621M1	GBC	65	Female	CSYS	III+IV	primary tumor	moderate	Negative	N0	M0	NA	NA	NA	NA	NA	NA
119A1715M1	ICC	73	Female	CSYS	III+IV	primary tumor	poor	Negative	NX	MX	NA	NA	NA	NA	NA	NA
119A1725M1	ICC	71	Female	CSYS	III+IV	primary tumor	poor	Negative	NX	M1	NA	NA	NA	NA	NA	NA
119A1933A1	ICC	66	Female	CSYS	NA	primary tumor	poor	Negative	NX	MX	NA	NA	NA	NA	NA	NA
119A1949A1	ICC	65	Female	CSYS	III+IV	primary tumor	poor	Negative	N1	MX	NA	NA	NA	NA	NA	NA
119A9209D1	ECC	62	Male	CSYS	II	primary tumor	moderate	Negative	N1	M0	NA	NA	NA	NA	NA	NA
119A9336A1	ECC	58	Male	CSYS	III+IV	primary tumor	moderate	Negative	NX	M0	NA	NA	NA	NA	NA	NA
119A9340A1	ECC	46	Male	CSYS	NA	metastatic tumor	poor	Positive	NX	MX	NA	NA	NA	NA	NA	NA
119A9694A1	ICC	67	Male	CSYS	I	primary tumor	moderate	Positive	N0	M0	NA	NA	NA	NA	NA	NA
119A9698A1	GBC	79	Female	CSYS	II	primary tumor	poor	Negative	N0	M0	NA	NA	NA	NA	NA	NA
119A9702A1	ICC	43	Male	CSYS	NA	primary tumor	moderate	Negative	NX	MX	NA	NA	NA	NA	NA	NA
119A9806A1	ECC	72	Male	CSYS	III+IV	primary tumor	moderate	Negative	N1	MX	NA	NA	NA	NA	NA	NA
119A9889A1	ICC	65	Male	CSYS	III+IV	primary tumor	poor	NA	N1	M0	NA	NA	NA	NA	NA	NA
216L0152A1	ICC	72	Male	CSYS	III+IV	primary tumor	NA	Negative	NX	M1	NA	NA	NA	NA	NA	NA
216L0276A1	ICC	61	Female	CSYS	NA	primary tumor	NA	Negative	NX	MX	NA	NA	NA	NA	NA	NA
217A0361A1	ICC	50	Female	CSYS	NA	primary tumor	NA	Negative	N1	M0	NA	NA	NA	NA	NA	NA
217B0420A1	ECC	63	Male	CSYS	III+IV	metastatic tumor	poor	Negative	N0	M0	NA	NA	NA	NA	NA	NA
217B0528A1	ICC	44	Female	CSYS	NA	primary tumor	NA	Negative	NX	MX	NA	NA	NA	NA	NA	NA
217C0588A1	ICC	55	Female	CSYS	III+IV	primary tumor	poor	Positive	N1	M0	NA	NA	NA	NA	NA	NA
217C0745A1	ICC	48	Female	CSYS	III+IV	primary tumor	moderate	Negative	N1	M0	NA	NA	NA	NA	NA	NA
217D0937A1	ICC	56	Male	CSYS	II	primary tumor	moderate	Negative	N0	M0	NA	NA	NA	NA	NA	NA
217E1258A1	ICC	53	Female	CSYS	III+IV	metastatic tumor	poor	Positive	N1	M0	NA	NA	NA	NA	NA	NA
217E1387A1	ICC	65	Female	CSYS	III+IV	recurrent tumor	NA	Positive	NX	MX	NA	NA	NA	NA	NA	NA
217F1558A1	ICC	67	Male	CSYS	NA	primary tumor	NA	Negative	NX	MX	NA	NA	NA	NA	NA	NA
217F1599A1	ECC	54	Female	CSYS	II	primary tumor	poor	Negative	N0	M0	NA	NA	NA	NA	NA	NA
217F1625A1	ICC	88	Female	CSYS	NA	primary tumor	NA	Negative	NX	MX	NA	NA	NA	NA	NA	NA
217F1660A1	GBC	53	Female	CSYS	III+IV	metastatic tumor	NA	Negative	NX	M1	NA	NA	NA	NA	NA	NA
217F1870A1	ICC	83	Male	CSYS	II	metastatic tumor	NA	Negative	N0	M0	NA	NA	NA	NA	NA	NA
217G1915A1	GBC	73	Male	CSYS	III+IV	metastatic tumor	poor	Negative	NX	M1	NA	NA	NA	NA	NA	NA
217G2113A1	ICC	59	Male	CSYS	III+IV	primary tumor	moderate	Negative	N1	M0	NA	NA	NA	NA	NA	NA
217H2225A1	GBC	51	Female	CSYS	NA	primary tumor	poor	Negative	NX	MX	NA	NA	NA	NA	NA	NA
217H2254A1	ICC	57	Male	CSYS	III+IV	primary tumor	poor	NA	N1	M0	NA	NA	NA	NA	NA	NA
217H2400A1	ICC	28	Male	CSYS	NA	primary tumor	NA	Negative	NX	MX	NA	NA	NA	NA	NA	NA

218C5441A1	ICC	56	Female	CSYS	NA	primary tumor	NA	Negative	NX	MX	NA	NA	NA	NA	NA	NA
218C5575A1	ICC	58	Male	CSYS	III+IV	metastatic tumor	poor	Positive	NX	M1	NA	NA	NA	NA	NA	NA
218C5588A2	GBC	44	Female	CSYS	III+IV	metastatic tumor	NA	Negative	NX	M1	NA	NA	NA	NA	NA	NA
218C5780A1	ICC	32	Female	CSYS	NA	primary tumor	NA	Positive	NX	MX	NA	NA	NA	NA	NA	NA
218D5915A1	GBC	58	Male	CSYS	II	primary tumor	moderate	Negative	N0	M0	NA	NA	NA	NA	NA	NA
218D6413A1	ICC	50	Male	CSYS	NA	primary tumor	NA	Positive	NX	MX	NA	NA	NA	NA	NA	NA
218D6471A1	ICC	66	Male	CSYS	III+IV	primary tumor	poor	Positive	NX	MX	NA	NA	NA	NA	NA	NA
218D6874A1	ICC	62	Female	CSYS	III+IV	primary tumor	poor	Negative	NX	M1	NA	NA	NA	NA	NA	NA
218E7563A1	ICC	60	Female	CSYS	NA	primary tumor	NA	Negative	NX	MX	NA	NA	NA	NA	NA	NA
218E7564A1	ICC	71	Male	CSYS	I	primary tumor	NA	Negative	N0	M0	NA	NA	NA	NA	NA	NA
218E7890A1	ICC	53	Female	CSYS	III+IV	primary tumor	poor	NA	N0	M0	NA	NA	NA	NA	NA	NA
218F8298A1	ICC	42	Female	CSYS	NA	primary tumor	NA	NA	NX	MX	NA	NA	NA	NA	NA	NA
218F8400A1	ICC	52	Male	CSYS	NA	primary tumor	poor	NA	N1	MX	NA	NA	NA	NA	NA	NA
218F8651A1	ECC	55	Female	CSYS	II	primary tumor	moderate	Negative	N1	M0	NA	NA	NA	NA	NA	NA
218G8980A1	ECC	79	Female	CSYS	I	primary tumor	moderate	Negative	N0	M0	NA	NA	NA	NA	NA	NA
218G9808A1	ICC	49	Female	CSYS	NA	primary tumor	NA	Negative	N1	M0	NA	NA	NA	NA	NA	NA
218G9947A1	ECC	53	Male	CSYS	III+IV	metastatic tumor	moderate	Negative	NX	M1	NA	NA	NA	NA	NA	NA
218G9952A1	ICC	60	Female	CSYS	III+IV	primary tumor	poor	Negative	N1	M1	NA	NA	NA	NA	NA	NA
218H1383A1	ICC	55	Male	CSYS	II	primary tumor	poor	Positive	N0	M0	NA	NA	NA	NA	NA	NA
218H1627A1	ECC	78	Male	CSYS	I	primary tumor	poor	Negative	N0	M0	NA	NA	NA	NA	NA	NA
218H1955A1	ICC	53	Male	CSYS	III+IV	primary tumor	poor	Positive	N0	M0	NA	NA	NA	NA	NA	NA
218H2052A1	ICC	45	Female	CSYS	III+IV	primary tumor	poor	Negative	N1	M0	NA	NA	NA	NA	NA	NA
218H2159A1	ECC	62	Male	CSYS	II	primary tumor	moderate	NA	N0	M0	NA	NA	NA	NA	NA	NA
218I2875A1	ICC	46	Female	CSYS	NA	primary tumor	NA	Negative	NX	MX	NA	NA	NA	NA	NA	NA
218I3043A1	GBC	62	Female	CSYS	II	primary tumor	poor	Negative	N0	M0	NA	NA	NA	NA	NA	NA
218I3048A1	ECC	60	Male	CSYS	III+IV	primary tumor	poor	NA	N0	M1	NA	NA	NA	NA	NA	NA
218J4306A1	ICC	49	Male	CSYS	III+IV	recurrent tumor	moderate	Positive	NX	MX	NA	NA	NA	NA	NA	NA
218J4308A1	ICC	37	Male	CSYS	NA	primary tumor	moderate	Positive	N1	MX	NA	NA	NA	NA	NA	NA
218J4341A1	ICC	40	Male	CSYS	NA	primary tumor	poor	Positive	NX	MX	NA	NA	NA	NA	NA	NA
218J4343A1	ICC	76	Female	CSYS	III+IV	metastatic tumor	moderate	Negative	NX	M1	NA	NA	NA	NA	NA	NA
218J4612A1	ICC	36	Female	CSYS	III+IV	primary tumor	moderate	Negative	N1	M0	NA	NA	NA	NA	NA	NA
218J5499A1	ICC	44	Male	CSYS	III+IV	primary tumor	poor	Negative	N1	M0	NA	NA	NA	NA	NA	NA
218K6790A1	ICC	68	Male	CSYS	III+IV	recurrent tumor	poor	Positive	NX	MX	NA	NA	NA	NA	NA	NA
218K6907A1	ICC	54	Female	CSYS	NA	primary tumor	poor	Positive	NX	MX	NA	NA	NA	NA	NA	NA
218L7136A1	ECC	34	Female	CSYS	III+IV	primary tumor	moderate	Positive	N1	M0	NA	NA	NA	NA	NA	NA
218L7137A1	ICC	56	Male	CSYS	III+IV	primary tumor	moderate	Positive	N0	M1	NA	NA	NA	NA	NA	NA
218L7990A1	ICC	49	Male	CSYS	III+IV	primary tumor	poor	Positive	N1	M0	NA	NA	NA	NA	NA	NA
218L9107A1	GBC	55	Female	CSYS	III+IV	metastatic tumor	NA	Negative	NX	M1	NA	NA	NA	NA	NA	NA
219A1770D1	ECC	61	Female	CSYS	II	primary tumor	poor	Negative	N1	M0	NA	NA	NA	NA	NA	NA
219A9920A1	ICC	55	Female	CSYS	III+IV	metastatic tumor	poor	Positive	NX	MX	NA	NA	NA	NA	NA	NA
240S9085A1	ICC	63	Male	CSYS	III+IV	primary tumor	moderate	Negative	NX	MX	NA	NA	NA	NA	NA	NA
618F8157A2	ICC	58	Female	CSYS	III+IV	metastatic tumor	NA	Negative	NX	M1	NA	NA	NA	NA	NA	NA
618F8167A2	ECC	44	Male	CSYS	III+IV	metastatic tumor	NA	Negative	NX	M1	NA	NA	NA	NA	NA	NA
ASCO795410	ICC	54	Male	CSYS	NA	primary tumor	NA	Negative	NX	MX	NA	NA	NA	NA	NA	NA
CASE111111	GBC	69	Female	CSYS	II	primary tumor	poor	Negative	N0	M0	NA	NA	NA	NA	NA	NA
CASE222222	GBC	74	Male	CSYS	III+IV	primary tumor	moderate	Negative	N0	M0	NA	NA	NA	NA	NA	NA
CASE333333	GBC	54	Female	CSYS	II	primary tumor	poor	Negative	N0	M0	NA	NA	NA	NA	NA	NA
CASE444444	GBC	64	Female	CSYS	II	primary tumor	poor	Negative	N0	M0	NA	NA	NA	NA	NA	NA
CASE555555	GBC	40	Female	CSYS	III+IV	primary tumor	poor	Negative	N0	MX	NA	NA	NA	NA	NA	NA
R18C5410R2	ECC	68	Male	CSYS	I	primary tumor	moderate	Negative	N0	M0	NA	NA	NA	NA	NA	NA
R18C5411R2	ECC	53	Female	CSYS	I	primary tumor	poor	Negative	N0	M0	NA	NA	NA	NA	NA	NA
R18D6313R1	GBC	45	Female	CSYS	NA	primary tumor	NA	Negative	NX	MX	NA	NA	NA	NA	NA	NA
R18D6314R1	GBC	37	Female	CSYS	NA	primary tumor	moderate	Negative	N0	MX	NA	NA	NA	NA	NA	NA
R18D6315R1	GBC	73	Male	CSYS	NA	primary tumor	poor	Negative	NX	MX	NA	NA	NA	NA	NA	NA
R18D6316R1	GBC	63	Male	CSYS	II	primary tumor	moderate	Negative	N0	M0	NA	NA	NA	NA	NA	NA
R18D6317R1	GBC	60	Female	CSYS	NA	primary tumor	poor	Negative	NX	MX	NA	NA	NA	NA	NA	NA
R18D6417R1	GBC	55	Female	CSYS	III+IV	primary tumor	poor	Negative	N1	M0	NA	NA	NA	NA	NA	NA
R18D6463R1	GBC	69	Female	CSYS	II	primary tumor	poor	Negative	N0	M0	NA	NA	NA	NA	NA	NA
R18D6470R1	GBC	58	Male	CSYS	II	primary tumor	poor	Negative	N0	M0	NA	NA	NA	NA	NA	NA
R18D6483R1	GBC	54	Female	CSYS	III+IV	primary tumor	poor	Negative	NX	M1	NA	NA	NA	NA	NA	NA
R18D6488R1	GBC	37	Female	CSYS	III+IV	primary tumor	poor	Negative	N1	M0	NA	NA	NA	NA	NA	NA
R18D6489R1	GBC	51	Female	CSYS	III+IV	primary tumor	moderate	Negative	N0	M1	NA	NA	NA	NA	NA	NA
R18D6500R1	GBC	65	Female	CSYS	II	primary tumor	poor	Negative	N0	M0	NA	NA	NA	NA	NA	NA
R18D6508R1	GBC	67	Male	CSYS	III+IV	primary tumor	poor	Negative	N0	M0	NA	NA	NA	NA	NA	NA
R18D6510R1	GBC	64	Female	CSYS	II	primary tumor	poor	Negative	N0	M0	NA	NA	NA	NA	NA	NA
R18D6521R1	GBC	79	Female	CSYS	II	primary tumor	poor	Negative	N0	M0	NA	NA	NA	NA	NA	NA
R18D6523R1	GBC	74	Female	CSYS	III+IV	primary tumor	poor	NA	N1	M0	NA	NA	NA	NA	NA	NA
R18D6529R1	GBC	52	Female	CSYS	III+IV	primary tumor	poor	Negative	N1	M0	NA	NA	NA	NA	NA	NA
R18D6531R1	GBC	56	Male	CSYS	III+IV	primary tumor	poor	Positive	N0	M0	NA	NA	NA	NA	NA	NA
R18D6542R1	GBC	50	Female	CSYS	II	primary tumor	poor	Negative	N0	M0	NA	NA	NA	NA	NA	NA
R18D6543R1	GBC	45	Male	CSYS	II	primary tumor	poor	Negative	N0	M0	NA	NA	NA	NA	NA	NA
R18D6640R1	GBC	65	Male	CSYS	III+IV	primary tumor	poor	Negative	N0	M0	NA	NA	NA	NA	NA	NA
R18D6641R1	GBC	69	Female	CSYS	II	primary tumor	poor	Negative	N0	M0	NA	NA	NA	NA	NA	NA
R18D6643R1	GBC	85	Female	CSYS	II	primary tumor	poor	Negative	N0	M0	NA	NA	NA	NA	NA	NA
R18D6713R1	GBC	82	Female	CSYS	II	primary tumor	moderate	Negative	N0	M0	NA	NA	NA	NA	NA	NA
R18D6714R1	GBC	55	Male	CSYS	III+IV	primary tumor	poor	Positive	N0	M0	NA	NA	NA	NA	NA	NA
R18D6831R1	ICC	67	Male	CSYS	NA	primary tumor	poor	Negative	NX	MX	NA	NA	NA	NA	NA	NA
R18D6917S2	GBC	68	Female	CSYS	III+IV	primary tumor	moderate	Negative	N1	M0	NA	NA	NA	NA	NA	NA
R18E7186R1	ECC	60	Male	CSYS	NA	primary tumor	NA	Negative	N0	M0	NA	NA	NA	NA	NA	NA
R18F8364R1	GBC	71	Female	CSYS	II	primary tumor	moderate	NA	N0	M0	NA	NA	NA	NA	NA	NA
R18F8368R1	GBC	68	Male	CSYS	I	primary tumor	moderate	Negative	N0	M0	NA	NA	NA	NA	NA	NA
R18F8384R1	GBC	63	Female	CSYS	II	primary tumor	moderate	Negative	N0	M0	NA	NA	NA	NA	NA	NA
R18F8385R1	GBC	70	Female	CSYS	NA	primary tumor	poor	NA	NX	MX	NA	NA	NA	NA	NA	NA
R18F8390R1	GBC	61	Female	CSYS	III+IV	primary tumor	poor	Negative	N1	M0	NA	NA	NA	NA	NA	NA
R18F8410R1	GBC	59	Female	CSYS	III+IV	primary tumor	poor	Negative	N0	M1	NA	NA	NA	NA	NA	NA
R18F8428R1	GBC	71	Female	CSYS	III+IV	primary tumor	moderate	Negative	N0	M0	NA	NA	NA	NA	NA	NA
R18F8429R1	GBC	52	Female	CSYS	II	primary tumor	poor	Negative	N0	M0	NA	NA	NA	NA	NA	NA
R18F8432R1	GBC	58	Female	CSYS	III+IV	primary tumor	poor	Positive	NX	M1	NA	NA	NA	NA	NA	NA
R18F8433R1	GBC	68	Female	CSYS	II	primary tumor	moderate	Negative	N0	M0	NA	NA	NA	NA	NA	NA
R18F8442R1	GBC	73	Male	CSYS	III+IV	primary tumor	moderate	Negative	N0	M0	NA	NA	NA	NA	NA	NA
R18F8445R1	GBC	62	Female	CSYS	II	primary tumor	poor	Negative	N0	M0	NA	NA	NA	NA	NA	NA
R18F8636M2	ICC	68	Female	CSYS	NA	primary tumor	NA	Negative	NX	MX	NA	NA	NA	NA	NA	NA
R18G9202R1	ECC	53	Female	CSYS	I	primary tumor	moderate	Negative	N0	M0	NA	NA	NA	NA	NA	NA
R18G9203R1	ECC	59	Male	CSYS	II	primary tumor	moderate	Negative	N0	M0	NA	NA	NA	NA	NA	NA
R18G9211R1	ECC	49	Female	CSYS	III+IV	primary tumor	moderate	Negative	N0	M0	NA	NA	NA	NA	NA	NA
R18G9220R1	ICC	38	Female	CSYS	III+IV	primary tumor	moderate	NA	N1	M0	NA	NA	NA	NA	NA	NA
R18G9241R1	ECC	54	Male	CSYS	II	primary tumor	moderate	Negative	N0	M0	NA	NA	NA	NA	NA	NA
R18G9243R1	ECC	62	Male	CSYS	II	primary tumor	moderate	Negative	N0	M0	NA	NA	NA	NA	NA	NA
R18G9244R1	ECC	77	Male	CSYS	I	primary tumor	moderate	NA	N0	M0	NA	NA	NA	NA	NA	NA
R18G9245R1	ICC	56	Male	CSYS	III+IV	primary tumor	moderate	Negative	N0	M0	NA	NA	NA	NA	NA	NA
R18G9249R1	ECC	52	Male	CSYS	II	primary tumor	moderate	Negative	N0	M0	NA	NA	NA	NA	NA	NA
R18G9250R1	ECC	58	Male	CSYS	III+IV	primary tumor	moderate	NA	N0	M0	NA	NA	NA	NA	NA	NA
R18G9251R1	ECC	73	Male	CSYS	III+IV	primary tumor	moderate	Negative	N0	M1	NA	NA	NA	NA	NA	NA
R18G9255R1	ECC	67	Male	CSYS	I	primary tumor	moderate	NA	N0	M0	NA					

R18H2220M1	ECC	71	Female	CSYS	II	primary tumor	moderate	Negative	N0	M0	NA	NA	NA	NA	NA	NA

1 **Table S2.** Gene list of the capture-based NGS platform (Cancer Sequencing YS panel, CSYS).

Exons of 450 cancer-related genes									
ABL1	ABL2	ACVR1B	ACVR2A	ADAM29	ADGRA2	AKT1	AKT2	AKT3	ALK
AMER1	APC	APEX1	AR	ARAF	ARFRP1	ARID1A	ARID1B	ARID2	ASXL1
ATF1	ATM	ATR	ATRX	AURKA	AURKB	AXIN1	AXIN2	AXL	BAP1
BARD1	BCL2	BCL2L1	BCL2L11	BCL2L2	BCL6	BCOR	BCORL1	BCR	BIRC5
BLK	BLM	BMPR1A	BMX	BRAF	BRCA1	BRCA2	BRD4	BRIP1	BTG1
BTK	CAMTA1	CARD11	CBFB	CBL	CCND1	CCND2	CCND3	CCNE1	CD274
CD79A	CD79B	CDC73	CDH1	CDK12	CDK4	CDK6	CDK8	CDKN1A	CDKN1B
CDKN2A	CDKN2B	CDKN2C	CEBPA	CFTR	CHD2	CHD4	CHEK1	CHEK2	CIC
COL1A1	CRBN	CREB3L1	CREB3L2	CREBBP	CRKL	CRLF2	CSF1	CSF1R	CSK
CSNK1A1	CTCF	CTNNA1	CTNNB1	CUL3	CXCR4	CYLD	CYP17A1	CYP2D6	DAXX
DDR1	DDR2	DICER1	DNMT3A	DOT1L	DPYD	EGF	EGFR	EMSY	EP300
EPCAM	EPHA2	EPHA3	EPHA5	EPHA7	EPHB1	ERBB2	ERBB3	ERBB4	ERCC1
ERG	ERRFI1	ESR1	ETV1	ETV4	ETV5	ETV6	EWSR1	EZH2	FAM135B
FAM46C	FANCA	FANCC	FANCD2	FANCE	FANCF	FANCG	FANCL	FANCM	FAS
FAT1	FAT3	FAT4	FBXW7	FEN1	FEV	FGF10	FGF12	FGF14	FGF19
FGF23	FGF3	FGF4	FGF6	FGF7	FGFR1	FGFR2	FGFR3	FGFR4	FGR
FH	FLCN	FLI1	FLT1	FLT3	FLT4	FOS	FOXL2	FOXO1	FOXP1
FRS2	FUBP1	FUS	FYN	GABRA6	GATA1	GATA2	GATA3	GATA4	GATA6
GID4	GLI1	GLI2	GLI3	GNA11	GNA13	GNAQ	GNAS	GRIN2A	GRM3
GSK3B	H3F3A	HCK	HDAC9	HGF	HNFB1A	HRAS	HSD3B1	HSP90AA1	HTATIP2
IDH1	IDH2	IGF1R	IGF2	IKBKE	IKZF1	IL7R	INHBA	INPP4B	IRF2
IRF4	IRS2	ITK	JAK1	JAK2	JAK3	JUN	KAT6A	KDM5A	KDM5B
KDM5C	KDM6A	KDR	KEAP1	KEL	KIT	KLHL6	KMT2A	KMT2C	KMT2D
KRAS	LCK	LIMK1	LMO1	LRP1	LRP1B	LRP2	LYN	LZTR1	MACC1
MAGI2	MAP2K1	MAP2K2	MAP2K4	MAP3K1	MAP3K13	MAP4K5	MCL1	MDM2	MDM4
MED12	MEF2B	MEN1	MERTK	MET	MGMT	MITF	MLH1	MPL	MRE11A
MS4A1	MSH2	MSH6	MST1R	MTOR	MUTYH	MYB	MYC	MYCL	MYCN
MYD88	NBN	NCOA2	NCOR1	NEK11	NF1	NF2	NFE2L2	NFIB	NFKBIA
NKX2-1	NOTCH1	NOTCH2	NOTCH3	NOTCH4	NPM1	NR4A3	NRAS	NRG1	NRG3
NSD1	NTRK1	NTRK2	NTRK3	NUP93	PAK3	PALB2	PARK2	PARP1	PARP2
PARP3	PARP4	PAX5	PBRM1	PCA3	PDCD1	PDCD1LG2	PDGFB	PDGFRA	PDGFRB
PDK1	PIK3C2B	PIK3CA	PIK3CB	PIK3CD	PIK3CG	PIK3R1	PIK3R2	PKD2	PLA2G1B
PLCG2	PMS2	POLB	POLD1	POLE	PPP2R1A	PRDM1	PREX2	PRKACA	PRKAR1A
PRKCI	PRKDC	PRSS1	PRSS8	PTCH1	PTEN	PTK2	PTK6	PTPN11	QKI
RAC1	RAD50	RAD51	RAD51B	RAD51C	RAD51D	RAD52	RAD54B	RAD54L	RAF1
RANBP2	RARA	RB1	RBM10	RECQL	REL	RELA	RELB	RET	RHBDF2
RHOA	RICTOR	RNF43	ROCK1	ROCK2	ROS1	RPTOR	RUNX1	RUNX1T1	RXRA
SDHA	SDHB	SDHC	SDHD	SETD2	SF3B1	SIK1	SLIT2	SMAD2	SMAD3
SMAD4	SMARCA4	SMARCB1	SMARCD1	SMO	SNCAIP	SOC31	SOX10	SOX2	SOX9
SPEN	SPINK1	SPOP	SPTA1	SRC	SRMS	SS18	SSX1	STAG2	STAT3
STAT4	STK11	STK24	SUFU	SYK	TAF1	TBX3	TCF7L2	TEK	TERT
TET1	TET2	TET3	TFE3	TGFBR1	TGFBR2	TIE1	TIPARP	TMPPSS2	TNFAIP3
TNFRSF14	TNFSF11	TNFSF13B	TNK2	TOP1	TOP2A	TP53	TPMT	TSC1	TSC2
TSHR	TYK2	U2AF1	UGT1A1	VEGFA	VHL	WEE1	WEE2	WHSC1	WISP3

WT1	XIAP	XPO1	XRCC2	XRCC3	YES1	ZBTB2	ZNF217	ZNF703	ZNF750
Selected introns of 38 genes frequently rearranged in cancer									
ALK	BCR	BRAF	BRCA1	BRCA2	DDR2	EGFR	FGFR1	FGFR2	FGFR3
KIT	MET	MSH2	NTRK1	NTRK2	PDGFRA	RAF1	RARA	RET	ROS1
AKT3	ERBB2	ERBB4	NTRK3	BCL2	BRD4	ETV1	ETV4	ETV5	ETV6
EWSR1	MYB	NOTCH2	SS18	TMPRSS2	NOTCH1	NRG1	PDGFB	JAK2	

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1 **Table S3.** Potentially actionable targets (PATs) in BTC patients.

Targets	Mutation Types	Drugs	OncoKB level	ESCAT tier
ABL1	E255K, E255V, F317C, F317L, F317L, F317V, F359C, F359I, F359V, T315A, Y253H, BCR-ABL1 Fusion	Bosutinib	2B	III-A
ALK	Fusions	Crizotinib	2B	III-A
BRAF	V600E	Encorafenib; Cetuximab; Binimetinib; Dabrafenib; Panitumumab; Trametinib	2B	III-A
BRCA1	Oncogenic Mutations	Olaparib	2B	III-A
BRCA2	Oncogenic Mutations	Olaparib	2B	III-A
CDK4	Amplification	Abemaciclib; Palbociclib	2B	III-A
EGFR	A763_Y764insFQEA	Afatinib; Erlotinib; Gefitinib	2B	III-A
ERBB2	Amplification, Oncogenic Mutations	Ado-Trastuzumab Emtansine; Trastuzumab; Carboplatin-Taxol Regimen	2B	III-A
KIT	C809G, D816A, D816E, D816F, D816G, D816H, D816N, D816V, D816Y, D820A, D820E, D820G, D820Y, N822H, N822I, N822K, N822Y, R796G, Y823D, T670I, V654A, D816, Oncogenic Mutations	Sorafenib; Imatinib	2B	III-A
MET	Amplification, D1010mut, Exon 14 Deletion, Exon 14 splice mutation, Y1003mut	Cabozantinib; Crizotinib	2B	III-A
PDGFR A	Oncogenic Mutations, D842V	Imatinib, Dasatinib	2B	III-A
RET	Fusions, Oncogenic Mutations	Cabozantinib; Vandetanib; LOXO-292	2B	III-A
TSC1	Oncogenic Mutations	Everolimus	2B	III-A
TSC2	Oncogenic Mutations	Everolimus	2B	III-A
FGFR2	Fusions	BGJ398; Debio1347; AZD4547; Erdafitinib	3A	I-B
IDH1	Oncogenic Mutations	BGJ398; Debio1347; AZD4547; Erdafitinib	3A	I-B
AKT1	E17K	AZD5363	3B	II-B
NTRK	Fusions	larotrectinib	3B	I-C
MSI-H	dMMR	pembrolizumab	3B	I-C

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Table S4. The somatic variants from coding regions of 803 patients with biliary tract carcinoma.

Sample.ID	Chr.	Start_Pos	End_Pos	Variant_Class	Variant_Type	Ref_Allele	Tumor_Allele1	Tumor_Allele2	Gene Symbol	DNA_CHANGE	AA_CHANGE
116K0135A1	12	25398284	25398284	Missense_Mutation	SNP	C	T	T	KRAS	c.35G>A	p.G12D
116K0135A1	17	7577142	7577142	Nonsense_Mutation	SNP	C	A	A	TP53	c.796G>T	p.G266*
116K0135A1	2	47698190	47698190	Missense_Mutation	SNP	A	G	G	MSH2	c.1748A>G	p.N583S
116K0135A1	1	158606546	158606546	Missense_Mutation	SNP	T	G	G	SPTA1	c.5195A>C	p.K1732T
116K0135A1	1	158609707	158609707	Missense_Mutation	SNP	G	T	T	SPTA1	c.4828C>A	p.Q1610K
116L0197A1	-	-	-	Missense_Mutation	SNP	-	-	-	TP53	c.654_655insGT	p.V218dup
116L0197A1	17	7578212	7578212	Nonsense_Mutation	SNP	G	A	A	TP53	c.637C>T	p.R213*
116L0197A1	11	92534643	92534643	Missense_Mutation	SNP	A	G	G	FAT3	c.8464A>G	p.I2822V
116L0197A1	2	48025777	48025777	Missense_Mutation	SNP	A	G	G	MSH6	c.655A>G	p.S219G
116L0197A1	1	40366499	40366499	Missense_Mutation	SNP	G	T	T	MYCL	c.698C>A	p.P233H
116L0197A1	8	69002826	69002826	Missense_Mutation	SNP	C	A	A	PREX2	c.2126C>A	p.A709E
116L0197A1	1	158615147	158615147	Missense_Mutation	SNP	G	A	A	SPTA1	c.4025C>T	p.A1342V
116L0197A1	X	123181290	123181290	Missense_Mutation	SNP	C	T	T	STAG2	c.754C>T	p.R252W
116L0221A1	3	52439128	52439128	Nonsense_Mutation	SNP	G	A	A	BAP1	c.1114C>T	p.Q372*
116L0221A1	-	-	-	Frame_Shift_Ins	INS	-	-	-	PBRM1	c.3550dupA	p.M184Nfs*11
116L0254A1	-	-	-	In_Frame_Del	INS	-	-	-	BRAF	c.1457_1471delP	N486_P490del
116L0254A1	16	2112992	2112992	Missense_Mutation	SNP	G	A	A	TSC2	c.1381G>A	p.V461M
116L0254A1	17	7577575	7577575	Missense_Mutation	SNP	A	C	C	TP53	c.706T>G	p.Y236D
116L0254A1	7	2976787	2976787	Missense_Mutation	SNP	C	T	T	CARD11	c.1225G>A	p.E409K
116L0254A1	17	11984782	11984782	Nonsense_Mutation	SNP	C	T	T	MAP2K4	c.328C>T	p.R110*
116L0254A1	18	48603023	48603023	Nonsense_Mutation	SNP	C	T	T	SMAD4	c.1324C>T	p.Q442*
116L0254A1	19	11138553	11138553	Missense_Mutation	SNP	C	G	G	SMARCA4	c.3309C>G	p.C1103W
116L0263A1	17	37881426	37881426	Missense_Mutation	SNP	A	G	G	ERBB3	c.2528A>G	p.R843G
116L0263A1	17	37868208	37868208	Missense_Mutation	SNP	C	T	T	ERBB2	c.839C>T	p.S280F
116L0263A1	1	156845889	156845889	Missense_Mutation	SNP	C	T	T	NTRK1	c.1501C>T	p.R501C
116L0263A1	17	7577557	7577557	Missense_Mutation	SNP	A	T	T	TP53	c.724T>A	p.C242S
116L0263A1	9	21971000	21971000	Nonsense_Mutation	SNP	C	A	A	CDKN2A	c.358G>T	p.E120*
116L0263A1	9	21994137	21994137	Splice_Site	SNP	C	A	A	CDKN2A	c.193+1G>T	-
116L0263A1	3	41266137	41266137	Missense_Mutation	SNP	C	T	T	CTNNB1	c.134C>T	p.S45F
116L0263A1	-	-	-	Frame_Shift_Del	INS	-	-	-	SMAD4	c.854del	p.N2851fs*51
116L0263A1	3	170015084	170015084	Splice_Site	SNP	C	G	G	PRKCI	c.1498-8C>G	-
116L0279A1	12	25398284	25398284	Missense_Mutation	SNP	C	A	A	KRAS	c.35G>T	p.G12V
116L0279A1	6	93955072	93955072	Missense_Mutation	SNP	A	T	T	EPHA7	c.282T>A	p.D942E
116L0279A1	20	57429454	57429454	Missense_Mutation	SNP	C	T	T	GNAS	c.947C>T	p.T316M
116L0279A1	12	49435757	49435757	Nonsense_Mutation	SNP	G	T	T	KMT2D	c.6126C>A	p.C2042*
116L0287A1	8	38283676	38283676	Missense_Mutation	SNP	C	T	T	GFGR1	c.709G>A	p.G237S
116L0287A1	5	149513266	149513266	Missense_Mutation	SNP	G	A	A	PDGFRB	c.817C>T	p.R273C
116L0287A1	4	88989068	88989068	Missense_Mutation	SNP	C	A	A	PKD2	c.2377C>A	p.H793N
116L0287A1	2	198267484	198267484	Missense_Mutation	SNP	G	A	A	SF3B1	c.1873C>T	p.R625C
117B0454A1	-	-	-	Frame_Shift_Del	INS	-	-	-	BAP1	c.1746delC	p.S583Rfs*34
117B0454A1	-	-	-	Frame_Shift_Del	INS	-	-	-	PBRM1	c.1704_1705del	p.K569Nfs*3
117B0454A1	17	7577138	7577138	Missense_Mutation	SNP	C	G	G	TP53	c.800G>C	p.R267P
117B0454A1	1	16475389	16475389	Missense_Mutation	SNP	G	C	C	EPHA2	c.307C>G	p.R103G
117B0488A1	12	25398284	25398284	Missense_Mutation	SNP	C	T	T	KRAS	c.35G>A	p.G12D
117B0488A1	17	7577539	7577539	Missense_Mutation	SNP	G	A	A	TP53	c.742C>T	p.R248W
117B0488A1	X	63411777	63411777	Missense_Mutation	SNP	C	T	T	AMER1	c.1390G>A	p.A464T
117B0545A1	1	16261091	16261091	Missense_Mutation	SNP	C	T	T	SPEN	c.8356C>T	p.H2786Y
117B0545A1	12	56478854	56478854	Missense_Mutation	SNP	G	C	C	ERBB3	c.310G>C	p.V104L
117B0545A1	2	142012219	142012219	Splice_Site	SNP	A	G	G	LRP1B	c.344-9T>C	-
117B0545A1	-	-	-	Frame_Shift_Del	INS	-	-	-	LRP1B	c.3794del	p.S1265Lfs*23
117C0618A1	12	52374945	52374945	Missense_Mutation	SNP	A	G	G	ACVR1B	c.773A>G	p.H258R
117C0618A1	1	27094336	27094336	Missense_Mutation	SNP	G	T	T	ARID1A	c.3044G>T	p.G1015V
117C0618A1	21	39774503	39774503	Missense_Mutation	SNP	G	A	A	ERG	c.670C>T	p.R224W
117C0618A1	20	57430298	57430298	Missense_Mutation	SNP	C	T	T	GNAS	c.1978C>T	p.R660C
117C0618A1	1	202736067	202736067	Missense_Mutation	SNP	C	T	T	KDM5B	c.698G>A	p.R233H
117C0618A1	12	49420606	49420606	Missense_Mutation	SNP	C	T	T	KMT2D	c.15143G>A	p.R5048H
117C0618A1	-	-	-	Frame_Shift_Ins	INS	-	-	-	PBRM1	c.4535_4536dup	p.E1513Rfs*35
117C0618A1	-	-	-	Splice_Site	SNP	-	-	-	RECQL	c.868-3delT	-
117C0618A1	1	11169753	11169753	Missense_Mutation	SNP	G	A	A	MTOR	c.7400C>T	p.A2467V
117C0618A1	17	29557904	29557904	Nonsense_Mutation	SNP	C	G	G	NF1	c.3158C>G	p.S1053*
117C0618A1	-	-	-	In_Frame_Del	INS	-	-	-	NF2	c.380del	p.L127*
117C0618A1	1	179198519	179198519	Missense_Mutation	SNP	A	G	G	ABL2	c.14T>C	p.V5A
117C0618A1	10	89717778	89717778	Splice_Site	SNP	T	C	C	PTEN	c.801+2T>C	-
117C0618A1	17	7574003	7574003	Nonsense_Mutation	SNP	G	A	A	TP53	c.1024C>T	p.R342*
117C0618A1	-	-	-	Frame_Shift_Del	INS	-	-	-	TP53	c.902del	p.P301Qfs*44
117C0618A1	-	-	-	Missense_Mutation	SNP	-	-	-	CTNNB1	c.133_135del	p.S45del
117C0618A1	15	99250981	99250981	Missense_Mutation	SNP	C	A	A	IGF1R	c.285C>A	p.S95R
117C0618A1	5	156679629	156679629	Missense_Mutation	SNP	C	T	T	ITK	c.1804C>T	p.R602W
117C0618A1	9	98240363	98240363	Missense_Mutation	SNP	G	A	A	PTCH1	c.1321C>T	p.R441C
117C0618A1	3	187443373	187443373	Missense_Mutation	SNP	G	A	A	BCL6	c.1753C>T	p.R585W
117C0618A1	X	129148573	129148573	Nonsense_Mutation	SNP	C	T	T	BCORL1	c.1825C>T	p.R609*
117C0618A1	1	51436158	51436158	Missense_Mutation	SNP	A	G	G	CDKN2C	c.118A>G	p.T40A
117C0618A1	X	48652558	48652558	Missense_Mutation	SNP	C	T	T	GATA1	c.1229C>T	p.P410L
117C0618A1	11	64572285	64572285	Missense_Mutation	SNP	G	A	A	MEN1	c.1354C>T	p.R452W
117C0618A1	2	47672796	47672796	Missense_Mutation	SNP	G	T	T	MSH2	c.1386G>T	p.Q462H
117C0618A1	-	-	-	Frame_Shift_Ins	INS	-	-	-	PIK3CB	c.1810dup	p.R604Pfs*29
117C0618A1	-	-	-	Frame_Shift_Del	INS	-	-	-	RNF43	c.1976del	p.G659Vfs*41
117C0618A1	14	81609778	81609778	Missense_Mutation	SNP	C	T	T	TSHR	c.1376C>T	p.A459V
117C0646A1	11	118374777	118374777	Missense_Mutation	SNP	G	A	A	KMT2A	c.8170G>A	p.D2724N
117C0646A1	8	93074800	93074800	Splice_Site	SNP	C	A	A	RUNX1T1	c.-20G>T	-
117C0646A1	12	56478932	56478932	Missense_Mutation	SNP	G	T	T	ERBB3	c.388G>T	p.A130S
117C0646A1	9	135798734	135798734	Splice_Site	SNP	C	T	T	TSC1	c.508+1G>A	-
117C0646A1	13	32914817	32914817	Missense_Mutation	SNP	G	A	A	BRCA2	c.6325G>A	p.V2109I
117C0646A1	17	7577534	7577534	Missense_Mutation	SNP	C	G	G	TP53	c.747G>C	p.R249S
117C0646A1	20	30659499	30659499	Missense_Mutation	SNP	G	A	A	HCK	c.34G>A	p.G12R
117C0646A1	4	55973998	55973998	Missense_Mutation	SNP	T	G	G	KDR	c.1318A>C	p.T440P
117C0646A1	1	204426884	204426884	Missense_Mutation	SNP	G	A	A	PIK3C2B	c.1685C>T	p.P562L
117C0646A1	16	10274172	10274172	Missense_Mutation	SNP	C	T	T	GRIN2A	c.97G>A	p.A33T
117C0646A1	8	48690301	48690301	Missense_Mutation	SNP	-	-	-	PRKDC	c.11987T>A	p.L3996Q
117C0651A1	-	-	-	Frame_Shift_Ins	INS	-	-	-	ARID1A	c.635_2636insCA	p.V879Afs*58
117C0651A1	11	108199955	108199955	Nonsense_Mutation	SNP	C	T	T	ATM	c.7297C>T	p.Q2433*
117C0651A1	-	-	-	Frame_Shift_Ins	INS	-	-	-	EPHA2	c.279dup	p.I94Vfs*4
117C0651A1	2	141660539	141660539	Missense_Mutation	SNP	C	A	A	LRP1B	c.3716G>T	p.C1239F
117C0651A1	15	67482870	67482870	Missense_Mutation	SNP	C	T	T	SMAD3	c.1274C>T	p.S425F
117C0664A1	12	115112364	115112364	Missense_Mutation	SNP	C	T	T	TBX3	c.1376G>A	p.R459H
117C0664A1	10	114905771	114905771	Nonsense_Mutation	SNP	C	T	T	TCF7L2	c.721C>T	p.Q241*

117C0664A1	X	48651642	48651642	Missense_Mutation	SNP	C	T	T	GATA1	c.808C>T	p.R270W
117C0733A1	21	44524456	44524456	Missense_Mutation	SNP	G	T	T	U2AF1	c.101C>A	p.S34Y
117C0733A1	12	25398284	25398284	Missense_Mutation	SNP	C	A	A	KRAS	c.35G>T	p.G12V
117C0733A1	9	101908873	101908873	Nonsense_Mutation	SNP	C	T	T	TGFBR1	c.1237C>T	p.R413*
117C0733A1	6	32170055	32170055	Missense_Mutation	SNP	C	T	T	NOTCH4	c.3553G>A	p.G1185R
117C0866A1	-	-	-	Frame_Shift_Ins	INS	-	-	-	STK11	c.400dup	p.C134Lfs*29
117C0866A1	13	32912691	32912691	Missense_Mutation	SNP	A	T	T	BRCA2	c.4199A>T	p.H1400L
117C0866A1	3	30691929	30691929	Missense_Mutation	SNP	A	G	G	TGFBR2	c.431A>G	p.N1445
117D0978A1	3	178936082	178936082	Missense_Mutation	SNP	G	A	A	PIK3CA	c.1624G>A	p.E542K
117D0978A1	17	7578406	7578406	Missense_Mutation	SNP	C	T	T	TP53	c.524G>A	p.R175H
117D0978A1	12	25398284	25398284	Missense_Mutation	SNP	C	G	G	KRAS	c.35G>C	p.G12A
117D0978A1	9	21971017	21971017	Missense_Mutation	SNP	G	C	C	CDKN2A	c.341C>G	p.P114R
117D0978A1	17	7578268	7578268	Missense_Mutation	SNP	A	G	G	TP53	c.581T>C	p.L194P
117D1007A1	12	25398284	25398284	Missense_Mutation	SNP	C	A	A	KRAS	c.35G>T	p.G12V
117D1007A1	18	48604760	48604760	Missense_Mutation	SNP	C	T	T	SMAD4	c.1582C>T	p.H528Y
117D1007A1	17	7577018	7577018	Splice_Site	SNP	C	G	G	TP53	c.919+1G>C	-
117D1007A1	9	21971101	21971101	Missense_Mutation	SNP	G	T	T	CDKN2A	c.257C>A	p.A86D
117D1030A1	1	7151437	7151437	Splice_Site	SNP	G	A	A	CAMTA1	c.302+6G>A	-
117D1030A1	12	12038903	12038903	Missense_Mutation	SNP	G	T	T	ETV6	c.1196G>T	p.R399L
117D1030A1	12	25380275	25380275	Missense_Mutation	SNP	T	G	G	KRAS	c.183A>C	p.Q61H
117D1030A1	19	1220717	1220717	Splice_Site	SNP	G	C	C	STK11	c.734+1G>C	-
117D1030A1	X	66765161	66765161	Missense_Mutation	SNP	A	T	T	AR	c.173A>T	p.Q58L
117D1030A1	6	32163723	32163723	Missense_Mutation	SNP	G	T	T	NOTCH4	c.5503C>A	p.R1835S
117D1030A1	17	56774083	56774083	Missense_Mutation	SNP	C	T	T	RAD51C	c.434C>T	p.P145L
117D1074R1	1	120612014	120612014	Missense_Mutation	SNP	C	A	A	NOTCH2	c.7G>T	p.A35
117D1074R1	6	157528292	157528292	Missense_Mutation	SNP	C	T	T	ARID1B	c.6017C>T	p.A2006V
117D1074R1	17	63554344	63554344	Missense_Mutation	SNP	T	C	C	AXIN2	c.395A>G	p.K132R
117D1074R1	-	-	-	Frame_Shift_Del	INS	-	-	-	BAP1	c.586del	p.W196Gfs*35
117D1074R1	17	59878736	59878736	Missense_Mutation	SNP	G	A	A	BRIP1	c.1018C>T	p.L340F
117D1074R1	3	89528647	89528647	Missense_Mutation	SNP	G	C	C	EPHA3	c.2947G>C	p.V983L
117D1074R1	16	9857127	9857127	Missense_Mutation	SNP	G	A	A	GRIN2A	c.4274C>T	p.S1425L
117D1074R1	16	9857217	9857217	Missense_Mutation	SNP	G	A	A	GRIN2A	c.4184C>T	p.A1395V
117D1074R1	1	120612013	120612013	Missense_Mutation	SNP	G	A	A	NOTCH2	c.8C>T	p.A3V
117D1074R1	1	17349159	17349159	Missense_Mutation	SNP	G	A	A	SDHB	c.709C>T	p.P237S
117D1074R1	19	17950435	17950435	Missense_Mutation	SNP	C	T	T	JAK3	c.1292G>A	p.R431Q
117D1101A1	17	7577142	7577142	Missense_Mutation	SNP	C	T	T	TP53	c.796G>A	p.G266R
117D1101A1	-	-	-	Frame_Shift_Ins	INS	-	-	-	CFTR	c.50dup	p.S180fs*27
117D1130A1	6	117717432	117717432	Splice_Site	SNP	T	C	C	ROS1	c.780-5A>G	-
117D1130A1	17	7578212	7578212	Nonsense_Mutation	SNP	G	A	A	TP53	c.637C>T	p.R213*
117D1130A1	X	66765455	66765455	Missense_Mutation	SNP	A	G	G	AR	c.467A>G	p.D156G
117D1130A1	11	92534643	92534643	Missense_Mutation	SNP	A	G	G	FAT3	c.8464A>G	p.I2822V
117D1130A1	2	48025777	48025777	Missense_Mutation	SNP	A	G	G	MSH6	c.655A>G	p.S219G
117D1130A1	1	40366499	40366499	Missense_Mutation	SNP	G	T	T	MYCL	c.698C>A	p.P233H
117D1130A1	8	69002826	69002826	Missense_Mutation	SNP	C	A	A	PREX2	c.2126C>A	p.A709E
117D1130A1	X	123181290	123181290	Missense_Mutation	SNP	C	T	T	STAG2	c.754C>T	p.R252W
117D1192A1	13	32915174	32915174	Missense_Mutation	SNP	G	C	C	BRCA2	c.6682G>C	p.V2228L
117D1192A1	-	-	-	Frame_Shift_Del	INS	-	-	-	TGFBR2	c.677del	p.D226fs*38
117E1223A1	12	25398284	25398284	Missense_Mutation	SNP	C	T	T	KRAS	c.35G>A	p.G12D
117E1223A1	13	32914817	32914817	Missense_Mutation	SNP	G	A	A	BRCA2	c.6325G>A	p.V2109I
117E1223A1	17	7578492	7578492	Nonsense_Mutation	SNP	C	T	T	TP53	c.438G>A	p.W146*
117E1223A1	X	66764995	66764995	Missense_Mutation	SNP	G	A	A	AR	c.7G>A	p.V3M
117E1223A1	9	21970899	21970899	Splice_Site	SNP	A	G	G	CDKN2A	c.457+2T>C	-
117E1223A1	3	51980306	51980306	Missense_Mutation	SNP	G	A	A	PARP3	c.1223G>A	p.R408H
117E1223A1	11	128638021	128638021	Missense_Mutation	SNP	C	T	T	FLI1	c.239C>T	p.P80L
117E1223A1	7	142655047	142655047	Missense_Mutation	SNP	C	T	T	KEL	c.539G>A	p.R180H
117E1223A1	6	161969931	161969931	Missense_Mutation	SNP	G	T	T	PRKN	c.1038C>A	p.R346E
117E1223A1	1	16261134	16261134	Missense_Mutation	SNP	C	T	T	SPEN	c.8399C>T	p.A2800V
117E1250R1	-	-	-	Splice_Site	SNP	-	-	-	TP53	c.77_96+8del	-
117E1250R1	17	74475297	74475297	Missense_Mutation	SNP	C	T	T	RHBDF2	c.422G>A	p.R141H
117E1250R1	-	-	-	Missense_Mutation	SNP	-	-	-	ARID1B	c.121_123dup	p.S41dup
117E1250R1	15	90628339	90628339	Splice_Site	SNP	G	A	A	IDH2	c.1081-9C>T	-
117E1250R1	12	49420858	49420858	Missense_Mutation	SNP	C	T	T	KMT2D	c.14891G>A	p.R4964H
117E1250R1	19	42777428	42777428	Missense_Mutation	SNP	A	G	G	CIC	c.1493A>G	p.N498S
117E1250R1	14	45665454	45665454	Missense_Mutation	SNP	C	T	T	FANCM	c.5420C>T	p.T1807I
117E1250R1	4	187540652	187540652	Missense_Mutation	SNP	A	C	C	FAT1	c.7088T>G	p.V2363G
117E1250R1	11	92087587	92087587	Missense_Mutation	SNP	C	T	T	FAT3	c.2309C>T	p.T770M
117E1259R1	10	123243238	123243238	Nonsense_Mutation	SNP	G	A	A	FGFR2	c.2275C>T	p.R759*
117E1259R1	17	7577534	7577534	Missense_Mutation	SNP	C	A	A	TP53	c.747G>T	p.R249S
117E1259R1	3	130992408	130992408	Missense_Mutation	SNP	C	T	T	NEK11	c.1708C>T	p.R570C
117E1259R1	9	98239029	98239029	Splice_Site	SNP	T	C	C	PTCH1	c.1602+12A>G	-
117E1259R1	1	27105700	27105700	Missense_Mutation	SNP	C	T	T	ARID1A	c.5311C>T	p.P1771S
117E1259R1	3	142217611	142217611	Missense_Mutation	SNP	T	G	G	ATR	c.5386A>C	p.K1796Q
117E1259R1	4	66230894	66230894	Missense_Mutation	SNP	G	A	A	EPHA5	c.2077C>T	p.R693C
117E1259R1	6	93979351	93979351	Missense_Mutation	SNP	C	G	G	EPHA7	c.1477G>C	p.V493L
117E1259R1	3	134898755	134898755	Missense_Mutation	SNP	G	A	A	EPHB1	c.1813G>A	p.E605K
117E1259R1	16	89877407	89877407	Missense_Mutation	SNP	G	C	C	FANCA	c.356C>G	p.S119C
117E1259R1	9	97879592	97879592	Splice_Site	SNP	C	G	G	FANCC	c.1072+5G>C	-
117E1259R1	16	56839548	56839548	Splice_Site	SNP	G	A	A	NUP93	c.489+4G>A	-
117E1259R1	8	48872522	48872522	Splice_Site	SNP	C	T	T	PRKDC	c.154+11G>A	-
117E1259R1	12	1034604	1034604	Splice_Site	SNP	T	C	C	RAD52	c.543+12A>G	-
117E1259R1	-	-	-	Splice_Site	SNP	-	-	-	RELA	c.1033+6delG	-
117E1259R1	-	-	-	Frame_Shift_Del	INS	-	-	-	SDHA	c.1945_1946del	p.L649Efs*4
117E1259R1	1	16260531	16260531	Missense_Mutation	SNP	C	T	T	SPEN	c.7796C>T	p.S2599L
117E1259R1	14	81609751	81609751	Missense_Mutation	SNP	G	A	A	TSHR	c.1349G>A	p.R450H
117E1261R1	10	43601830	43601830	Missense_Mutation	SNP	G	A	A	RET	c.874G>A	p.V292M
117E1261R1	8	38271189	38271189	Missense_Mutation	SNP	C	A	A	FGFR1	c.2426G>T	p.R809L
117E1261R1	17	7574035	7574035	Splice_Site	SNP	T	C	C	TP53	c.994-2A>G	-
117E1261R1	1	16459821	16459821	Missense_Mutation	SNP	G	A	A	EPHA2	c.1907C>T	p.S636L
117E1261R1	9	98218566	98218566	Missense_Mutation	SNP	C	T	T	PTCH1	c.3298G>A	p.V1100I
117E1261R1	-	-	-	In_Frame_Del	INS	-	-	-	RB1	c.1641_1658del	p.K548_C553del
117E1261R1	16	396430	396430	Missense_Mutation	SNP	G	C	C	AXIN1	c.596C>G	p.P199R
117E1261R1	-	-	-	Frame_Shift_Del	INS	-	-	-	CYP17A1	985_987delinsA	p.Y329Kfs*90
117E1261R1	3	185783775	185783775	Missense_Mutation	SNP	T	C	C	ETV5	c.737A>G	p.Q246R
117E1261R1	16	89871721	89871721	Missense_Mutation	SNP	G	C	C	FANCA	c.676C>G	p.Q226E
117E1261R1	4	187541859	187541859	Missense_Mutation	SNP	C	T	T	FAT1	c.5881G>A	p.G1961S
117E1261R1	4	187509906	187509906	Missense_Mutation	SNP	G	C	C	FAT1	c.13607C>G	p.P4536R
117E1261R1	20	57429772	57429772	Missense_Mutation	SNP	A	T	T	GNAS	c.1265A>T	p.Q422L
117E1261R1	7	151970833	151970833	Missense_Mutation	SNP	G	C	C	KMT2C	c.969C>G	p.I323M

117E1261R1	2	141004742	141004742	Splice_Site	SNP	C	T	T	LRP1B	c.13248-11G>A	-
117E1261R1	2	170030506	170030506	Missense_Mutation	SNP	C	T	T	LRP2	c.10937G>A	p.R3646H
117E1261R1	2	170097611	170097611	Missense_Mutation	SNP	C	T	T	LRP2	c.3932G>A	p.R1311H
117E1261R1	2	170135979	170135979	Missense_Mutation	SNP	G	A	A	LRP2	c.1468C>T	p.R490C
117E1261R1	12	133236099	133236099	Splice_Site	SNP	G	C	C	POLE	c.3061-4C>G	-
117E1261R1	2	74273621	74273621	Missense_Mutation	SNP	C	T	T	TET3	c.577C>T	p.R193C
117E1261R1	17	38548848	38548848	Missense_Mutation	SNP	C	A	A	TOP2A	c.3953G>T	p.R1318L
117E1261R1	19	10478867	10478867	Missense_Mutation	SNP	C	T	T	TYK2	c.329G>A	p.R110Q
117E1396A1	1	162740252	162740252	Missense_Mutation	SNP	C	T	T	DDR2	c.1454C>T	p.S485F
117E1396A1	12	25398285	25398285	Missense_Mutation	SNP	C	A	A	KRAS	c.34G>T	p.G12C
117E1396A1	17	7578469	7578469	Missense_Mutation	SNP	C	A	A	TP53	c.461G>T	p.G154V
117E1396A1	9	21971186	21971186	Nonsense_Mutation	SNP	G	A	A	CDKN2A	c.172C>T	p.R58*
117E1396A1	1	9783284	9783284	Missense_Mutation	SNP	A	G	G	PIK3CD	c.2528A>G	p.N843S
117E1396A1	X	76814235	76814235	Missense_Mutation	SNP	C	A	A	ATRX	c.6409G>T	p.A2137S
117E1396A1	1	97847966	97847966	Missense_Mutation	SNP	G	A	A	DPYD	c.1957C>T	p.L653F
117E1396A1	11	92534624	92534624	Missense_Mutation	SNP	A	C	C	FAT3	c.8445A>C	p.E2815D
117E1396A1	13	102379019	102379019	Missense_Mutation	SNP	C	A	A	FGF14	c.565G>T	p.G189W
117E1396A1	20	57415798	57415798	Nonsense_Mutation	SNP	G	T	T	GNAS	c.637G>T	p.E213*
117E1396A1	4	142949972	142949972	Missense_Mutation	SNP	C	A	A	INPP4B	c.2738G>T	p.R913I
117E1396A1	7	142641494	142641494	Splice_Site	SNP	A	G	G	KEL	c.1414-7T>C	-
117E1396A1	2	141122329	141122329	Nonsense_Mutation	SNP	C	A	A	LRP1B	c.11032G>T	p.E3678*
117E1396A1	1	40363571	40363571	Missense_Mutation	SNP	T	C	C	MYCL	c.568A>G	p.T190A
117E1396A1	1	120483388	120483388	Splice_Site	SNP	C	A	A	NOTCH2	c.2982-9G>T	-
117E1396A1	10	83635580	83635580	Missense_Mutation	SNP	A	T	T	NRG3	c.484A>T	p.T162S
117E1396A1	10	83635460	83635460	Missense_Mutation	SNP	C	A	A	NRG3	c.364C>A	p.P122T
117E1396A1	8	48872717	48872717	Splice_Site	SNP	C	A	A	PRKDC	c.-31G>T	-
117E1396A1	1	158592947	158592947	Missense_Mutation	SNP	T	A	A	SPTA1	c.5946A>T	p.Q1928H
117E1425A1	5	161116687	161116687	Missense_Mutation	SNP	C	A	A	GABRA6	c.575C>A	p.P192Q
117E1443A1	9	133760796	133760796	Missense_Mutation	SNP	G	A	A	ABL1	c.3176G>A	p.C1059Y
117E1443A1	3	178916646	178916646	Missense_Mutation	SNP	G	C	C	PIK3CA	c.33G>C	p.W111C
117E1443A1	17	7578442	7578442	Missense_Mutation	SNP	T	C	C	TP53	c.488A>G	p.Y163C
117E1443A1	9	21971116	21971116	Missense_Mutation	SNP	G	A	A	CDKN2A	c.242C>T	p.P81L
117E1443A1	-	-	-	In_Frame_Del	INS	-	-	-	ARID1B	c.369-392del	Q124-Q131del
117E1443A1	-	-	-	Frame_Shift_Del	INS	-	-	-	ATR	c.4670del	p.K1557fs*8
117E1443A1	11	92533398	92533398	Missense_Mutation	SNP	G	A	A	FAT3	c.7219G>A	p.A2407T
117E1443A1	1	206653375	206653375	Missense_Mutation	SNP	G	C	C	IKBKE	c.1259G>C	p.G420A
117E1443A1	2	141473639	141473639	Missense_Mutation	SNP	A	T	T	LRP1B	c.5926T>A	p.L1976I
117E1443A1	-	-	-	In_Frame_Del	INS	-	-	-	SMAD4	c.998-1009del	b.V333-G336del
117E1534A1	5	38982019	38982019	Missense_Mutation	SNP	G	A	A	RICTOR	c.703C>T	p.L235F
117E1534A1	5	156672790	156672790	Missense_Mutation	SNP	G	A	A	ITK	c.1504G>A	p.G502R
117E1534A1	15	41021015	41021015	Missense_Mutation	SNP	G	C	C	RAD51	c.637G>C	p.E213Q
117E1534A1	5	121736682	121736682	Missense_Mutation	SNP	A	G	G	SNCAIP	c.59A>G	p.D20G
117E1534A1	X	123020156	123020156	Missense_Mutation	SNP	G	A	A	XIAP	c.644G>A	p.R215H
117F1556A1	15	90631838	90631838	Missense_Mutation	SNP	C	T	T	IDH2	c.515G>A	p.R172K
117F1556A1	-	-	-	Frame_Shift_Ins	INS	-	-	-	ARID1A	c.1113dup	p.Q372Afs*28
117F1640A1	15	90631628	90631628	Missense_Mutation	SNP	G	T	T	IDH2	c.641C>A	p.A214E
117F1640A1	17	7579406	7579406	Nonsense_Mutation	SNP	G	T	T	TP53	c.281C>A	p.S94*
117F1640A1	17	48262951	48262951	Missense_Mutation	SNP	C	T	T	COL1A1	c.4307G>A	p.R1436H
117F1640A1	-	-	-	Splice_Site	SNP	-	-	-	CDK8	c.204+2dupT	-
117F1640A1	11	92532310	92532310	Missense_Mutation	SNP	G	A	A	FAT3	c.6131G>A	p.R2044H
117F1640A1	8	11606603	11606603	Splice_Site	SNP	G	A	A	GATA4	c.783+9G>A	-
117F1640A1	17	74470540	74470540	Missense_Mutation	SNP	C	G	G	RHBDF2	c.1466G>C	p.R489P
117F1640A1	2	198266713	198266713	Missense_Mutation	SNP	C	T	T	SF3B1	c.2219G>A	p.G740E
117F1648A2	2	141215115	141215115	Nonsense_Mutation	SNP	G	T	T	LRP1B	c.9731C>A	p.S3244*
117F1648A2	2	209113113	209113113	Missense_Mutation	SNP	G	A	A	IDH1	c.394C>T	p.R132C
117F1648A2	7	42012189	42012189	Missense_Mutation	SNP	C	T	T	GLI3	c.1850G>A	p.G617H
117F1689A1	2	209113113	209113113	Missense_Mutation	SNP	G	A	A	IDH1	c.394C>T	p.R132C
117F1689A1	-	-	-	Frame_Shift_Del	INS	-	-	-	EPHA2	c.351-357del	P.F1195fs*41
117F1689A1	7	151962169	151962169	Missense_Mutation	SNP	G	T	T	KMT2C	c.1138C>A	p.R380S
117F1759A1	11	108213974	108213974	Missense_Mutation	SNP	G	T	T	ATM	c.8294G>T	p.G2765V
117F1759A1	8	38273409	38273409	Missense_Mutation	SNP	C	T	T	FGFR1	c.1833G>A	p.M611I
117F1759A1	19	1220649	1220649	Missense_Mutation	SNP	G	A	A	STK11	c.667G>A	p.E223K
117F1759A1	-	-	-	Frame_Shift_Del	INS	-	-	-	ARID1A	c.264-270del	p.G89Afs*10
117F1759A1	19	10599915	10599915	Missense_Mutation	SNP	C	A	A	KEAP1	c.1661G>T	p.R554L
117F1759A1	12	133263850	133263850	Nonsense_Mutation	SNP	C	A	A	POLE	c.52G>T	p.E18*
117F1759A1	19	45504848	45504848	Missense_Mutation	SNP	C	G	G	RELB	c.11C>G	p.S4C
117F1759A1	19	11144147	11144147	Missense_Mutation	SNP	G	A	A	SMARCA4	c.3728G>A	p.R1243Q
117F1767A1	12	25398285	25398285	Missense_Mutation	SNP	C	G	G	KRAS	c.34G>C	p.G12R
117F1767A1	-	-	-	Frame_Shift_Ins	INS	-	-	-	TP53	c.243-244dup	P.P82Hfs*42
117F1767A1	1	27102076	27102076	Nonsense_Mutation	SNP	G	T	T	ARID1A	c.5002G>T	p.E1668*
117F1767A1	6	157521932	157521932	Nonsense_Mutation	SNP	G	T	T	ARID1B	c.4204G>A	p.E1402*
117F1767A1	16	3808012	3808012	Missense_Mutation	SNP	G	A	A	CREBBP	3407C>T;3414C	[S1136F;I1138M]
117F1767A1	7	151875055	151875055	Missense_Mutation	SNP	G	C	C	KMT2C	c.7483C>G	p.Q2495S
117F1770A1	-	-	-	Frame_Shift_Ins	INS	-	-	-	ATM	c.5712dup	p.S1905ifs*25
117F1770A1	-	-	-	Frame_Shift_Del	INS	-	-	-	STK11	c.785del	p.K262Sfs*25
117F1770A1	2	121726437	121726437	Missense_Mutation	SNP	G	A	A	GLI2	c.791G>A	p.R264Q
117F1770A1	12	57589078	57589078	Missense_Mutation	SNP	C	G	G	LRP1	c.8333C>G	p.S2778C
117F1770A1	18	18548826	18548826	Splice_Site	SNP	C	T	T	ROCK1	c.2915-5G>A	-
117F1770A1	17	70120232	70120232	Nonsense_Mutation	SNP	C	T	T	SOX9	c.1234C>T	p.Q412*
117F1770A1	13	108922284	108922284	Missense_Mutation	SNP	C	T	T	TNFSF13B	c.41C>T	p.S14F
117F1811A1	19	1221989	1221989	Nonsense_Mutation	SNP	C	T	T	STK11	c.904C>T	p.Q302*
117F1811A1	14	75745705	75745705	Missense_Mutation	SNP	A	G	G	FOS	c.20A>G	p.N75
117G2016A1	2	209113113	209113113	Missense_Mutation	SNP	G	A	A	IDH1	c.394C>T	p.R132C
117G2016A1	7	151891600	151891600	Nonsense_Mutation	SNP	G	A	A	KMT2C	c.4432C>T	p.Q1478*
117G2016A1	1	11172979	11172979	Splice_Site	SNP	G	T	T	MTOR	c.7301-5C>A	-
117G2026A1	-	-	-	Frame_Shift_Del	INS	-	-	-	ARID1A	c.4982-4985del	p.M1661Kfs*11
117G2026A1	17	7577559	7577559	Missense_Mutation	SNP	G	A	A	TP53	c.722C>T	p.S241F
117G2026A1	19	10610285	10610285	Missense_Mutation	SNP	G	A	A	KEAP1	c.425C>T	p.T142M
117G2087A1	7	140481402	140481402	Missense_Mutation	SNP	C	G	G	BRAF	c.1406G>C	p.G469A
117G2087A1	17	7574034	7574034	Splice_Site	SNP	C	T	T	TP53	c.994-1G>A	-
117G2087A1	-	-	-	Frame_Shift_Ins	INS	-	-	-	ARID1A	c.4518-4519dup	p.N1507ifs*21
117G2087A1	1	27102132	27102132	Nonsense_Mutation	SNP	G	A	A	ARID1A	c.5058G>A	p.W1686*
117G2087A1	22	41572870	41572870	Nonsense_Mutation	SNP	C	T	T	EP300	c.5155C>T	p.Q1719*
117G2087A1	3	134670774	134670774	Missense_Mutation	SNP	G	A	A	EPHB1	c.685G>A	p.A229T
117G2087A1	4	143191848	143191848	Missense_Mutation	SNP	C	G	G	INPP4B	c.583G>C	p.D195H
117G2087A1	7	142638388	142638388	Missense_Mutation	SNP	C	T	T	KEL	c.2150G>A	p.C717Y
117G2087A1	19	15280950	15280950	Missense_Mutation	SNP	C	G	G	NOTCH3	c.5146G>C	p.E1716Q
117G2087A1	8	68965472	68965472	Missense_Mutation	SNP	C	T	T	PREX2	c.1084C>T	p.R362W

117G2087A1		-	-	Frame_Shift_Del	INS	-	-	-	SMAD4	c.1586del	p.L529Yfs*8
117H2198A1		-	-	Frame_Shift_Del	INS	-	-	-	TP53	c.902del	p.P301Qfs*44
117H2198A1	2	141200100	141200100	Missense_Mutation	SNP	C	G	G	LRP1B	c.10387G>C	p.A3463P
117H2255A1	11	69633620	69633620	Missense_Mutation	SNP	C	A	A	FGF3	c.82G>T	p.D28Y
117H2255A1		-	-	Frame_Shift_Ins	INS	-	-	-	ARID2	C.282dup	P.R95Afs*16
117H2255A1		-	-	Frame_Shift_Del	INS	-	-	-	ARID2	C.1261del	P.V421Cfs*19
117H2255A1	15	88472463	88472463	Missense_Mutation	SNP	A	T	T	NTRK3	c.2092T>A	p.F698I
117H2255A1	2	178098953	178098953	Missense_Mutation	SNP	C	T	T	NFE2L2	c.92G>A	p.G31E
117H2255A1	20	54945564	54945564	Missense_Mutation	SNP	C	G	G	AURKA	c.1006G>C	p.E336Q
117H2255A1	3	178936082	178936082	Missense_Mutation	SNP	G	A	A	PIK3CA	c.1624G>A	p.E542K
117H2255A1	6	157099560	157099560	Missense_Mutation	SNP	C	T	T	ARID1B	c.497C>T	p.A166V
117H2255A1	7	117232211	117232211	Missense_Mutation	SNP	G	A	A	CFTR	c.1990G>A	p.E664K
117H2255A1	X	39923194	39923194	Missense_Mutation	SNP	C	G	G	BCOR	c.3514G>C	p.E1172Q
117H2255A1	X	39923194	39923194	Missense_Mutation	SNP	C	T	T	BCOR	c.3514G>A	p.E1172K
117H2289A1	1	27102066	27102066	Splice_Site	SNP	A	T	T	ARID1A	c.4994-2A>T	-
117H2289A1	11	92533302	92533302	Missense_Mutation	SNP	A	T	T	FAT3	c.7123A>T	p.S2375C
117H2289A1		-	-	Frame_Shift_Del	INS	-	-	-	TP53	c.153del	p.E510fs*72
117H2289A1	19	15285084	15285084	Missense_Mutation	SNP	C	T	T	NOTCH3	c.4531G>A	p.G1511S
117H2289A1	19	15302470	15302470	Splice_Site	SNP	T	A	A	NOTCH3	c.803-2A>T	-
117H2289A1	2	11351887	11351887	Missense_Mutation	SNP	T	A	A	ROCK2	c.2123A>T	p.H708L
117H2289A1	7	6027263	6027263	Splice_Site	SNP	T	A	A	PM52	c.1145-12A>T	-
117H2289A1	X	53244031	53244031	Splice_Site	SNP	T	A	A	KDM5C	c.964-2A>T	-
117H2404A1		-	-	Splice_Site	SNP	-	-	-	PIK3CD	c.1690-3delC	-
117H2404A1	1	16477434	16477434	Missense_Mutation	SNP	G	A	A	EPHA2	c.110C>T	p.A37V
117H2404A1		-	-	Frame_Shift_Del	INS	-	-	-	ARID1A	c.4555del	p.Q1519Rfs*8
117H2404A1		-	-	Frame_Shift_Del	INS	-	-	-	ARID1A	c.5548del	p.D1850Tfs*33
117H2404A1	12	416672	416672	Missense_Mutation	SNP	T	C	C	KDM5A	c.3878A>G	p.E1293G
117H2404A1	12	25398279	25398279	Missense_Mutation	SNP	C	T	T	KRAS	c.40G>A	p.V14I
117H2404A1		-	-	Frame_Shift_Del	INS	-	-	-	KMT2D	c.7061del	p.P2354Lfs*30
117H2404A1		-	-	Frame_Shift_Del	INS	-	-	-	KMT2D	c.1940del	p.P647Hfs*283
117H2404A1	13	25060405	25060405	Missense_Mutation	SNP	C	T	T	PARP4	c.1253G>A	p.G418D
117H2404A1	14	68758655	68758655	Missense_Mutation	SNP	G	A	A	RAD51B	c.811G>A	p.A271T
117H2404A1	15	67482825	67482825	Missense_Mutation	SNP	T	A	A	SMAD3	c.1229T>A	p.V410D
117H2404A1		-	-	Frame_Shift_Del	INS	-	-	-	BLM	c.3651del	p.K1217Nfs*62
117H2404A1		-	-	Frame_Shift_Del	INS	-	-	-	AXIN1	c.978del	p.S327Pfs*87
117H2404A1		-	-	In_Frame_Del	INS	-	-	-	CDH1	c.2064_2065del	p.C688*
117H2404A1	19	11132462	11132462	Missense_Mutation	SNP	T	C	C	SMARCA4	c.2678T>C	p.L893P
117H2404A1	19	42795540	42795540	Missense_Mutation	SNP	G	A	A	CIC	c.2620G>A	p.G874S
117H2404A1		-	-	Frame_Shift_Ins	INS	-	-	-	POLD1	c.3231dup	p.I1078Hfs*28
117H2404A1	2	74273951	74273951	Missense_Mutation	SNP	A	G	G	TET3	c.907A>G	p.R303G
117H2404A1		-	-	Frame_Shift_Del	INS	-	-	-	ACVR2A	c.677_680del	p.K226Sfs*15
117H2404A1		-	-	Frame_Shift_Del	INS	-	-	-	ACVR2A	c.1310del	p.K437Rfs*5
117H2404A1	2	170092549	170092549	Missense_Mutation	SNP	C	T	T	LRP2	c.4721G>A	p.I1574D
117H2404A1		-	-	Splice_Site	SNP	-	-	-	SRC	c.-4-9_-4-8delTC	-
117H2404A1		-	-	Missense_Mutation	SNP	-	-	-	CTNNB1	c.133_135del	p.S45del
117H2404A1		-	-	Frame_Shift_Del	INS	-	-	-	GATA2	c.599del	p.G200Vfs*18
117H2404A1	4	20258283	20258283	Splice_Site	SNP	T	G	G	SLIT2	c.180-12T>G	-
117H2404A1	4	55151582	55151582	Missense_Mutation	SNP	C	A	A	PDGFRA	c.2368C>A	p.L790I
117H2404A1	4	66361144	66361144	Missense_Mutation	SNP	A	G	G	EPHA5	c.1028T>C	p.F343S
117H2404A1	4	187527264	187527264	Missense_Mutation	SNP	G	A	A	FAT1	c.10310C>T	p.A3437V
117H2404A1	4	187557310	187557310	Missense_Mutation	SNP	G	A	A	FAT1	c.4052C>T	p.P1351L
117H2404A1	6	41905071	41905071	Missense_Mutation	SNP	T	A	A	CCND3	c.476A>T	p.D159V
117H2404A1	6	157256712	157256712	Splice_Site	SNP	T	C	C	ARID1B	c.2037+2T>C	-
117H2404A1	6	157517367	157517367	Missense_Mutation	SNP	A	G	G	ARID1B	c.3931A>G	p.N1311D
117H2404A1	6	162683710	162683710	Missense_Mutation	SNP	C	T	T	PRKN	c.259G>A	p.D87N
117H2404A1	6	163984691	163984691	Missense_Mutation	SNP	T	C	C	QKI	c.874T>C	p.Y292H
117H2404A1		-	-	Frame_Shift_Del	INS	-	-	-	MAGI2	c.277del	p.L935fs*81
117H2404A1		-	-	Frame_Shift_Del	INS	-	-	-	ABL1	c.2409del	p.R804Gfs*3
117H2404A1		-	-	Frame_Shift_Del	INS	-	-	-	KDM6A	c.1237del	p.T413Lfs*26
117H2404A1	X	66765161	66765161	Missense_Mutation	SNP	A	T	T	AR	c.173A>T	p.Q58L
117H2427A1	11	92573800	92573800	Missense_Mutation	SNP	C	T	T	FAT3	c.10441C>T	p.P3481S
117H2427A1	11	119146732	119146732	Missense_Mutation	SNP	C	T	T	CBL	c.895C>T	p.R299C
117H2427A1	12	49443583	49443583	Nonsense_Mutation	SNP	G	C	C	KMT2D	c.3788C>G	p.S1263*
117H2427A1	16	56782202	56782202	Nonsense_Mutation	SNP	C	T	T	NUP93	c.43C>T	p.Q15*
117H2427A1	17	7578275	7578275	Nonsense_Mutation	SNP	G	A	A	TP53	c.574C>T	p.Q192*
117H2427A1	17	11998985	11998985	Nonsense_Mutation	SNP	C	T	T	MAP2K4	c.487C>T	p.Q163*
117H2427A1	17	70119789	70119789	Missense_Mutation	SNP	G	A	A	SOX9	c.791G>A	p.R264K
117H2427A1	19	2210734	2210734	Missense_Mutation	SNP	C	T	T	DOT1L	c.1231C>T	p.R411C
117H2427A1	2	178098953	178098953	Missense_Mutation	SNP	C	G	G	NFE2L2	c.92G>C	p.G31A
117H2427A1	20	36031708	36031708	Missense_Mutation	SNP	G	C	C	SRC	c.1537G>C	p.E513Q
117H2427A1	3	178936082	178936082	Missense_Mutation	SNP	G	A	A	PIK3CA	c.1624G>A	p.E542K
117H2427A1	3	183273347	183273347	Missense_Mutation	SNP	G	C	C	KLHL6	c.95C>G	p.S32C
117H2427A1		-	-	In_Frame_Del	INS	-	-	-	CDKN2A	c.132del	p.Y44*
117H2427A1	X	53239895	53239895	Nonsense_Mutation	SNP	C	A	A	KDM5C	c.1546G>T	p.E516*
117H2427A1	X	76855262	76855262	Missense_Mutation	SNP	C	T	T	ATRX	c.5725G>A	p.E1909K
117H2427A1		-	-	Frame_Shift_Del	INS	-	-	-	STAG2	c.2848_2849del	p.E950Tfs*12
117H2467A1	11	46337914	46337914	Missense_Mutation	SNP	C	T	T	CREB3L1	c.1109C>T	p.T370I
117H2467A1	2	209113113	209113113	Missense_Mutation	SNP	G	A	A	IDH1	c.394C>T	p.R132C
117H2467A1	3	178952085	178952085	Missense_Mutation	SNP	A	T	T	PIK3CA	c.3140A>T	p.H1047L
117H2489A1	1	158590091	158590091	Missense_Mutation	SNP	G	T	T	SPTA1	c.6286C>A	p.Q2096K
117H2489A1	1	226567659	226567659	Missense_Mutation	SNP	G	A	A	PARP1	c.1507C>T	p.L503F
117H2489A1	11	92532310	92532310	Missense_Mutation	SNP	C	A	A	FAT3	c.6131G>A	p.R204AH
117H2489A1	12	25398284	25398284	Missense_Mutation	SNP	C	T	T	KRAS	c.35G>A	p.G12D
117H2489A1		-	-	Splice_Site	SNP	-	-	-	TP53	93+1_993+3del	-
117H2489A1		-	-	Frame_Shift_Ins	INS	-	-	-	SMAD4	c.1399_1414dup	p.P472Rfs*27
117H2489A1	22	41574752	41574752	Missense_Mutation	SNP	C	T	T	EP300	c.7037C>T	p.S2346F
117H2489A1		-	-	In_Frame_Del	INS	-	-	-	CDKN2A	c.90_96delinsT	p.L31_L32del
117H2552A1	1	158614075	158614075	Missense_Mutation	SNP	G	A	A	SPTA1	c.4306C>T	p.R1436W
117H2552A1	12	25380275	25380275	Missense_Mutation	SNP	T	G	G	KRAS	c.183A>C	p.Q61H
117H2552A1	12	115118688	115118688	Missense_Mutation	SNP	C	T	T	TBX3	c.653G>A	p.G218E
117H2552A1	15	67473760	67473760	Missense_Mutation	SNP	T	A	A	SMAD3	c.840T>A	p.N280K
117H2552A1	17	7577084	7577084	Missense_Mutation	SNP	T	A	A	TP53	c.854A>T	p.E285V
117H2552A1	19	11132468	11132468	Missense_Mutation	SNP	A	T	T	SMARCA4	c.2684A>T	p.Q895L
117H2552A1	3	41266137	41266137	Missense_Mutation	SNP	C	T	T	CTNNB1	c.134C>T	p.S45F
117H2552A1	3	47164663	47164663	Missense_Mutation	SNP	T	A	A	SETD2	c.1463A>T	p.Y488F
117H2552A1	5	1293461	1293461	Missense_Mutation	SNP	C	T	T	TERT	c.1540G>A	p.V514M
117H2552A1	7	6026741	6026741	Missense_Mutation	SNP	T	C	C	PM52	c.1655A>G	p.H552R
117H2552A1		-	-	Frame_Shift_Ins	INS	-	-	-	RBM10	c.1620_1627dup	p.T543Rfs*164

11712596A1	1	158582613	158582613	Missense_Mutation	SNP	C	T	T	SPTA1	c.7128G>A	p.M2376I
11712596A1	11	8251907	8251907	Missense_Mutation	SNP	C	T	T	LMO1	c.170G>A	p.R57H
11712596A1	13	102521064	102521064	Splice_Site	SNP	G	A	A	FGF14	c.423+11C>T	-
11712596A1	16	9857380	9857380	Missense_Mutation	SNP	T	C	C	GRIN2A	c.4021A>G	p.S1341G
11712596A1	-	-	-	In_Frame_Ins	INS	-	-	-	TP53	66_467insCCGT	T155_R156insPV
11712596A1	18	48575102	48575102	Nonsense_Mutation	SNP	G	A	A	SMAD4	c.296G>A	p.W99*
11712596A1	2	140990778	140990778	Missense_Mutation	SNP	C	T	T	LRP1B	c.13777G>A	p.G4593S
11712596A1	7	140453127	140453127	Missense_Mutation	SNP	C	T	T	BRAF	c.1808G>A	p.R603Q
11712596A1	7	151845726	151845726	Missense_Mutation	SNP	T	A	A	KMT2C	c.13286A>T	p.H4429L
11712661A1	12	49434040	49434040	Nonsense_Mutation	SNP	C	A	A	KMT2D	c.7513G>T	p.E2505*
11712661A1	-	-	-	Splice_Site	SNP	-	-	-	CHD2	907-12_4907-9	-
11712661A1	17	29657313	29657313	Splice_Site	SNP	G	A	A	NF1	c.5610-1G>A	-
11712661A1	2	198263263	198263263	Missense_Mutation	SNP	C	G	G	SF3B1	c.3056G>C	p.R1019T
11712661A1	4	126371893	126371893	Missense_Mutation	SNP	T	A	A	FAT4	c.9722T>A	p.F3241Y
11712661A1	9	137300846	137300846	Missense_Mutation	SNP	G	A	A	RXRA	c.491G>A	p.R164H
11712687A1	1	16255661	16255661	Missense_Mutation	SNP	G	T	T	SPEN	c.2926G>T	p.V976L
11712687A1	6	394867	394867	Missense_Mutation	SNP	C	T	T	IRF4	c.263C>T	p.P88L
11712735A1	1	158615041	158615041	Missense_Mutation	SNP	T	A	A	SPTA1	c.4131A>T	p.R1377S
11712735A1	11	108151875	108151875	Missense_Mutation	SNP	G	A	A	ATM	c.3556G>A	p.E1186K
11712735A1	12	46233261	46233261	Missense_Mutation	SNP	C	T	T	ARID2	c.1480C>T	p.H494Y
11712735A1	15	88428973	88428973	Splice_Site	SNP	A	T	T	NTRK3	c.2134-7T>A	-
11712735A1	17	7578190	7578190	Missense_Mutation	SNP	T	C	C	TP53	c.659A>G	p.Y220C
11712735A1	18	48591888	48591888	Missense_Mutation	SNP	G	C	C	SMAD4	c.1051G>C	p.D351H
11712735A1	4	153249504	153249504	Missense_Mutation	SNP	C	G	G	FBXW7	c.1274G>C	p.W425S
11712735A1	-	-	-	Frame_Shift_Del	INS	-	-	-	APC	c.4612_4613del	p.E1538fs*5
11712735A1	-	-	-	Frame_Shift_Del	INS	-	-	-	ARID1B	c.502_550del	p.G168Tfs*82
11712735A1	7	140481411	140481411	Missense_Mutation	SNP	C	G	G	BRAF	c.1397G>C	p.G466A
11712735A1	9	98211585	98211585	Missense_Mutation	SNP	C	G	G	PTCH1	c.3570G>C	p.L1190F
11712735A1	X	44929487	44929487	Nonsense_Mutation	SNP	C	T	T	KDM6A	c.2743C>T	p.Q915*
11712735A1	X	70641188	70641188	Missense_Mutation	SNP	C	G	G	TAF1	c.4474C>G	p.Q1492E
11712766A1	1	8075447	8075447	Splice_Site	SNP	G	C	C	ERRF1	c.126-3C>G	-
11712766A1	1	43770579	43770579	Missense_Mutation	SNP	T	G	G	TIE1	c.116T>G	p.F39C
11712766A1	10	89624310	89624310	Splice_Site	SNP	C	G	G	PTEN	c.79+5C>G	-
11712766A1	2	141609279	141609279	Missense_Mutation	SNP	A	C	C	LRP1B	c.4653T>G	p.S1551R
11712766A1	7	73535316	73535316	Missense_Mutation	SNP	C	T	T	UMK1	c.1718C>T	p.P573L
11712799A1	12	6702686	6702686	Missense_Mutation	SNP	C	T	T	CHD4	c.2410G>A	p.V804I
11712799A1	17	7577556	7577556	Missense_Mutation	SNP	C	G	G	TP53	c.725G>C	p.C242S
11712805A1	1	27106747	27106747	Nonsense_Mutation	SNP	G	T	T	ARID1A	c.6358G>T	p.E2120*
11712805A1	17	7578496	7578496	Missense_Mutation	SNP	A	G	G	TP53	c.434T>C	p.L145P
11712805A1	17	12016658	12016658	Missense_Mutation	SNP	G	A	A	MAP2K4	c.794G>A	p.G265D
11712805A1	18	48575671	48575671	Nonsense_Mutation	SNP	C	G	G	SMAD4	c.431C>G	p.S144*
11712805A1	-	-	-	Frame_Shift_Ins	INS	-	-	-	RBM10	c.1268dup	p.T424Yfs*19
11712844A1	-	-	-	Frame_Shift_Del	INS	-	-	-	FGF6	c.328del	p.H101Tfs*19
11712844A1	-	-	-	Frame_Shift_Del	INS	-	-	-	NF1	c.3720_3726del	p.R1241Wfs*23
11712844A1	17	29684098	29684098	Missense_Mutation	SNP	T	G	G	NF1	c.7859T>G	p.L2620R
11712844A1	3	30691911	30691911	Missense_Mutation	SNP	G	T	T	TGFBR2	c.413G>T	p.C138F
11712844A1	7	140453193	140453193	Missense_Mutation	SNP	T	A	A	BRAF	c.1742A>T	p.N581I
11712845A1	1	16235953	16235953	Missense_Mutation	SNP	A	G	G	SPEN	c.1019A>G	p.Q340R
11712845A1	1	27087961	27087961	Nonsense_Mutation	SNP	C	T	T	ARID1A	c.2248C>T	p.R750*
11712845A1	1	156846188	156846188	Splice_Site	SNP	C	A	A	NTRK1	c.1615-4C>A	-
11712845A1	10	43614982	43614982	Missense_Mutation	SNP	C	T	T	RET	c.2396C>T	p.P799L
11712845A1	10	70333117	70333117	Missense_Mutation	SNP	C	T	T	TET1	c.1022C>T	p.A341V
11712845A1	11	108114722	108114722	Missense_Mutation	SNP	A	G	G	ATM	c.539A>G	p.Q180R
11712845A1	17	7577120	7577120	Missense_Mutation	SNP	C	A	A	TP53	c.818G>T	p.R273L
11712845A1	17	70120193	70120193	Missense_Mutation	SNP	A	T	T	SOX9	c.1195A>T	p.T399S
11712845A1	17	80789374	80789374	Nonsense_Mutation	SNP	G	T	T	ZNF750	c.957C>A	p.Y319*
11712845A1	19	17955124	17955124	Missense_Mutation	SNP	G	T	T	JAK3	c.103C>A	p.P35T
11712845A1	2	225342966	225342966	Missense_Mutation	SNP	C	T	T	CUL3	c.2126G>A	p.R709Q
11712845A1	3	178936091	178936091	Missense_Mutation	SNP	G	A	A	PIK3CA	c.1633G>A	p.E545K
11712845A1	6	43738502	43738502	Missense_Mutation	SNP	G	A	A	VEGFA	c.59G>A	p.R20Q
11712845A1	8	69058436	69058436	Splice_Site	SNP	C	G	G	PREX2	c.4088-8C>G	-
11712845A1	-	-	-	Frame_Shift_Del	INS	-	-	-	CDKN2A	c.253del	p.A85Lfs*61
11712858A1	1	11526529	11526529	Missense_Mutation	SNP	T	C	C	NRAS	c.182A>G	p.Q61R
11712858A1	1	158615326	158615326	Missense_Mutation	SNP	C	T	T	SPTA1	c.3955G>A	p.I3139K
11712858A1	2	209113113	209113113	Missense_Mutation	SNP	G	A	A	IDH1	c.394C>T	p.R132C
11712888A1	-	-	-	Frame_Shift_Del	INS	-	-	-	ARID1A	559_2561delins	p.P854ifs*5
11712888A1	12	25398284	25398284	Missense_Mutation	SNP	C	A	A	KRAS	c.35G>T	p.G12V
11712888A1	12	56495760	56495760	Missense_Mutation	SNP	A	T	T	ERBB3	c.3950A>T	p.F1317V
11712888A1	18	48604667	48604667	Missense_Mutation	SNP	C	T	T	SMAD4	c.1489C>T	p.R497C
11712888A1	21	44524472	44524472	Missense_Mutation	SNP	G	T	T	U2AF1	c.85C>A	p.H29N
11712888A1	X	44945149	44945149	Missense_Mutation	SNP	A	T	T	KDM6A	c.3629A>T	p.N1210I
11712888A1	X	47039620	47039620	Nonsense_Mutation	SNP	C	T	T	RBM10	c.1072C>T	p.Q358*
11712908A1	1	2492165	2492165	Splice_Site	SNP	C	T	T	TNFRSF14	c.551+12C>T	-
11712908A1	17	7578450	7578450	Missense_Mutation	SNP	C	T	T	TP53	480G>A;481G>A	[M160];A161S
11712908A1	-	-	-	In_Frame_Del	INS	-	-	-	GATA6	c.531_548del	b.A178_A183del
11712908A1	19	10600527	10600527	Missense_Mutation	SNP	T	C	C	KEAP1	c.1328A>G	p.Y443C
11712908A1	3	30713733	30713733	Missense_Mutation	SNP	C	A	A	TGFBR2	c.1058C>A	p.S353Y
11712908A1	6	93982034	93982034	Missense_Mutation	SNP	T	A	A	EPHA7	c.1431A>T	p.E477D
11712919A1	1	156838381	156838381	Missense_Mutation	SNP	G	A	A	NTRK1	c.659G>A	p.R220Q
11712919A1	-	-	-	Frame_Shift_Ins	INS	-	-	-	ARID2	c.5249dup	P.N1750Kfs*10
11712919A1	17	7578518	7578518	Missense_Mutation	SNP	C	G	G	TP53	c.412G>C	p.A138P
11712919A1	17	37868208	37868208	Missense_Mutation	SNP	C	A	A	ERBB2	c.929C>A	p.S310Y
11712919A1	19	15271796	15271796	Missense_Mutation	SNP	G	C	C	NOTCH3	c.6643C>G	p.P2215A
11712919A1	2	141598583	141598583	Missense_Mutation	SNP	G	A	A	LRP1B	c.5018C>T	p.T1673M
11712919A1	3	89456470	89456470	Missense_Mutation	SNP	C	T	T	EPHA3	c.1646C>T	p.A549V
11712919A1	3	134898755	134898755	Missense_Mutation	SNP	G	A	A	EPHB1	c.1813G>A	p.E605K
11712919A1	-	-	-	In_Frame_Del	INS	-	-	-	APC	C.2853_2858del	P.Y951*
11712919A1	-	-	-	Frame_Shift_Ins	INS	-	-	-	APC	c.4666dup	P.T1556Nfs*3
11712931A1	1	204402554	204402554	Splice_Site	SNP	C	T	T	PIK3C2B	c.3844-1G>A	-
11712931A1	11	125499172	125499172	Missense_Mutation	SNP	A	G	G	CHEK1	c.335A>G	p.H112R
11712931A1	17	7578265	7578265	Missense_Mutation	SNP	A	T	T	TP53	c.584T>A	p.I195N
11712931A1	17	66511703	66511703	Missense_Mutation	SNP	G	C	C	PRKAR1A	c.163G>C	p.E55Q
11712931A1	18	19761540	19761540	Splice_Site	SNP	G	A	A	GATA6	c.1428+1G>A	-
11712931A1	18	48584552	48584552	Nonsense_Mutation	SNP	C	G	G	SMAD4	c.725C>G	p.S242*
11712931A1	3	130889693	130889693	Missense_Mutation	SNP	C	T	T	NEK11	c.1361C>T	p.S454L
11712931A1	3	178936091	178936091	Missense_Mutation	SNP	G	A	A	PIK3CA	c.1633G>A	p.E545K
11712931A1	4	110864995	110864995	Splice_Site	SNP	C	G	G	EGF	c.510-3C>G	-
11712931A1	5	112175897	112175897	Nonsense_Mutation	SNP	G	T	T	APC	c.4606G>T	p.E1536*

117J2931A1	6	152129279	152129279	Missense_Mutation	SNP	C	G	G	ESR1	c.232C>G	p.L78V
117J2931A1	7	14027714	14027714	Missense_Mutation	SNP	C	T	T	ETV1	c.130G>A	p.E44K
117J2931A1	8	93003987	93003987	Missense_Mutation	SNP	G	A	A	RUNX1T1	c.760C>T	p.H254Y
117J2978A1	11	108141854	108141854	Nonsense_Mutation	SNP	G	T	T	ATM	c.2902G>T	p.E968*
117J2978A1	12	25398284	25398284	Missense_Mutation	SNP	C	T	T	KRAS	c.35G>A	p.G12D
117J3004A1		-	-	Frame_Shift_Del	INS	-	-	-	ARID1A	c.267_295del	p.S90Pfs*11
117J3004A1		-	-	Frame_Shift_Ins	INS	-	-	-	TP53	c.437_462dup	p.T155Gfs*24
117J3004A1	3	52610556	52610556	Splice_Site	SNP	C	T	T	PBRM1	c.3616+1G>A	-
117J3004A1	3	178916725	178916725	Missense_Mutation	SNP	C	T	T	PIK3CA	c.112C>T	p.R38C
117J3004A1	5	131972837	131972837	Missense_Mutation	SNP	G	A	A	RAD50	c.3420G>A	p.M1140I
117J3045A1	13	110437380	110437380	Missense_Mutation	SNP	G	A	A	IRS2	c.1021C>T	p.R341C
117J3045A1	17	63010902	63010902	Missense_Mutation	SNP	T	A	A	GNAI3	c.607A>T	p.T203S
117J3086A1		-	-	In_Frame_Del	INS	-	-	-	SPEN	c.1711_1728del	p.E571_K576del
117J3086A1	13	48919262	48919262	Nonsense_Mutation	SNP	A	T	T	RB1	c.427A>T	p.K143*
117J3086A1	14	95572475	95572475	Nonsense_Mutation	SNP	C	A	A	DICER1	c.2890G>T	p.E964*
117J3086A1	17	7577539	7577539	Missense_Mutation	SNP	G	A	A	TP53	c.742C>T	p.R248W
117J3086A1	17	37876038	37876038	Splice_Site	SNP	A	T	T	ERBB2	c.1899-2A>T	-
117J3086A1	2	29416137	29416137	Missense_Mutation	SNP	C	T	T	ALK	c.4816G>A	p.D1606N
117J3086A1		-	-	Frame_Shift_Del	INS	-	-	-	ACVR2A	c.834del	p.K280Rfs*31
117J3086A1		-	-	Missense_Mutation	SNP	-	-	-	KIT	c.972_1974delins	p.G658W
117J3086A1	5	138163231	138163231	Missense_Mutation	SNP	T	G	G	CTNNA1	c.886T>G	p.F296V
117J3086A1	7	77756727	77756727	Missense_Mutation	SNP	C	A	A	MAGI2	c.3210G>T	p.R1070S
117J3117A1		-	-	Splice_Site	SNP	-	-	-	RB1	c.520+1_2520+4	-
117J3117A1	17	7577548	7577548	Missense_Mutation	SNP	C	T	T	TP53	c.733G>A	p.G245S
117J3117A1	7	55238870	55238870	Missense_Mutation	SNP	G	A	A	EGFR	c.1883G>A	p.C628Y
117J3117A1	7	151970960	151970960	Splice_Site	SNP	G	A	A	KMT2C	c.850-8C>T	-
117J3131A1	11	92495113	92495113	Missense_Mutation	SNP	T	G	G	FAT3	c.3761T>G	p.F1254C
117J3131A1	16	2138234	2138234	Missense_Mutation	SNP	T	C	C	TSC2	c.5167T>C	p.S1723P
117J3131A1	16	89877212	89877212	Splice_Site	SNP	T	A	A	FANCA	c.427-2A>T	-
117J3131A1	17	7577550	7577550	Missense_Mutation	SNP	C	T	T	TP53	c.731G>A	p.G244D
117J3131A1	18	19751966	19751966	Missense_Mutation	SNP	T	A	A	GATA6	c.861T>A	p.S287R
117J3131A1	2	48028142	48028142	Nonsense_Mutation	SNP	G	A	A	MSH6	c.3020G>A	p.W1007*
117J3131A1	7	20199458	20199458	Missense_Mutation	SNP	C	T	T	MACC1	c.526G>A	p.E176K
117J3131A1	8	37691530	37691530	Missense_Mutation	SNP	G	T	T	ADGRA2	c.1492G>T	p.D498Y
117J3131A1	8	41791594	41791594	Missense_Mutation	SNP	T	C	C	KAT6A	c.4144A>G	p.T1382A
117J3133A1	1	16258497	16258497	Missense_Mutation	SNP	A	T	T	SPEN	c.5762A>T	p.K1921I
117J3133A1	11	2161474	2161474	Missense_Mutation	SNP	G	A	A	IGF2	c.53C>T	p.A18V
117J3133A1	11	128651900	128651900	Nonsense_Mutation	SNP	C	T	T	FLI1	c.637C>T	p.R213*
117J3133A1	17	7578526	7578526	Missense_Mutation	SNP	C	A	A	TP53	c.404G>T	p.C135F
117J3133A1	19	11141552	11141552	Missense_Mutation	SNP	G	A	A	SMARCA4	c.3529G>A	p.D1177N
117J3133A1	19	41743892	41743892	Missense_Mutation	SNP	C	G	G	AXL	c.827C>G	p.P276R
117J3133A1	20	57415595	57415595	Missense_Mutation	SNP	G	A	A	GNAS	c.434G>A	p.R145H
117J3133A1	20	57415892	57415892	Missense_Mutation	SNP	G	A	A	GNAS	c.731G>A	p.R244H
117J3133A1	3	71050193	71050193	Missense_Mutation	SNP	T	G	G	FOXP1	c.992A>C	p.H331P
117J3133A1		-	-	Frame_Shift_Del	INS	-	-	-	FOXL2	c.892_893delins	p.H298Ffs*58
117J3133A1	3	178916617	178916617	Missense_Mutation	SNP	C	T	T	PIK3CA	c.4C>T	p.P2S
117J3133A1	4	187540509	187540509	Missense_Mutation	SNP	A	G	G	FAT1	c.7231T>C	p.C2411R
117J3133A1	7	151900051	151900051	Nonsense_Mutation	SNP	T	A	A	KMT2C	c.4060A>T	p.K1354*
117J3133A1	9	139404312	139404312	Missense_Mutation	SNP	C	T	T	NOTCH1	c.2842G>A	p.E948K
117J3136A1	12	46242663	46242663	Missense_Mutation	SNP	G	A	A	ARID2	c.1625G>A	p.R542Q
117J3136A1	12	51207840	51207840	Missense_Mutation	SNP	G	A	A	ATF1	c.376G>A	p.D126N
117J3136A1	17	7577538	7577538	Missense_Mutation	SNP	C	T	T	TP53	c.743G>A	p.R248Q
117J3136A1	17	37868208	37868208	Missense_Mutation	SNP	C	A	A	ERBB2	c.929C>A	p.S310Y
117J3136A1	2	25505279	25505279	Missense_Mutation	SNP	G	A	A	DNMT3A	c.479C>T	p.S160F
117J3136A1	3	47164273	47164273	Nonsense_Mutation	SNP	G	C	C	SETD2	c.1853C>G	p.S618*
117J3136A1	3	142272239	142272239	Missense_Mutation	SNP	C	T	T	ATR	c.2635G>A	p.A879T
117J3136A1	X	44936044	44936044	Missense_Mutation	SNP	G	T	T	KDM6A	c.2961G>T	p.K987N
117J3193A1	10	43609948	43609948	Missense_Mutation	SNP	T	G	G	RET	c.1900T>G	p.C634G
117J3193A1	12	25380276	25380276	Missense_Mutation	SNP	T	C	C	KRAS	c.182A>G	p.Q61R
117J3193A1	17	7578406	7578406	Missense_Mutation	SNP	C	T	T	TP53	c.524G>A	p.R175H
117J3193A1	3	52651369	52651369	Missense_Mutation	SNP	C	G	G	PBRM1	c.1727G>C	p.R576P
117J3193A1	5	176721790	176721790	Missense_Mutation	SNP	A	C	C	NSD1	c.7421A>C	p.Q2474P
117J3193A1	7	42011956	42011956	Missense_Mutation	SNP	C	T	T	GLI3	c.2083G>A	p.V695I
117J3193A1	7	42018223	42018223	Missense_Mutation	SNP	G	A	A	GLI3	c.1622C>T	p.T541M
117J3213A1	11	108202605	108202605	Splice_Site	SNP	G	C	C	ATM	c.7630-1G>C	-
117J3213A1	12	25398284	25398284	Missense_Mutation	SNP	C	A	A	KRAS	c.35G>T	p.G12V
117J3213A1	9	80537112	80537112	Missense_Mutation	SNP	T	A	A	GNAQ	c.286A>T	p.T96S
117J3237A1	1	27094280	27094280	Splice_Site	SNP	G	A	A	ARID1A	c.2989-1G>A	-
117J3237A1	17	7577517	7577517	Missense_Mutation	SNP	A	G	G	TP53	c.764T>C	p.I255T
117J3237A1		-	-	Frame_Shift_Ins	INS	-	-	-	SMAD4	c.807dup	p.G270Wfs*73
117J3237A1	2	109381151	109381151	Missense_Mutation	SNP	G	A	A	RANBP2	c.4156G>A	p.V1386I
117J3237A1	5	112173704	112173704	Nonsense_Mutation	SNP	C	T	T	APC	c.2413C>T	p.R805*
117J3237A1	7	42005672	42005672	Missense_Mutation	SNP	T	A	A	GLI3	c.2999A>T	p.H1000L
117J3239A1	1	9783248	9783248	Missense_Mutation	SNP	C	T	T	PIK3CD	c.2492C>T	p.S831L
117J3239A1	1	244006417	244006417	Splice_Site	SNP	G	C	C	AKT3	c.46+10C>G	-
117J3239A1	11	76174909	76174909	Nonsense_Mutation	SNP	C	T	T	EMSY	c.616C>T	p.R206*
117J3239A1	11	108206593	108206593	Missense_Mutation	SNP	G	C	C	ATM	c.8173G>C	p.D2725H
117J3239A1	11	108213982	108213982	Nonsense_Mutation	SNP	G	T	T	ATM	c.8302G>T	p.E2768*
117J3239A1	11	118366470	118366470	Missense_Mutation	SNP	C	G	G	KMT2A	c.5419C>G	p.Q1807E
117J3239A1	12	133202857	133202857	Missense_Mutation	SNP	T	C	C	POLE	c.6377A>G	p.N2126S
117J3239A1	13	32913221	32913221	Missense_Mutation	SNP	G	C	C	BRCA2	c.4729G>C	p.E1577Q
117J3239A1	13	32913587	32913587	Missense_Mutation	SNP	G	A	A	BRCA2	c.5095G>A	p.D1699N
117J3239A1	15	91354500	91354500	Missense_Mutation	SNP	G	A	A	BLM	c.3940G>A	p.E1314K
117J3239A1	16	3790535	3790535	Missense_Mutation	SNP	C	G	G	CREBBP	c.3998G>C	p.R1333T
117J3239A1	17	7573991	7573991	Missense_Mutation	SNP	C	T	T	TP53	c.1036G>A	p.E346K
117J3239A1	17	37868177	37868177	Splice_Site	SNP	T	G	G	ERBB2	c.902-4T>G	-
117J3239A1	17	40481778	40481778	Missense_Mutation	SNP	C	T	T	STAT3	c.1126G>A	p.A376T
117J3239A1	17	59761343	59761343	Missense_Mutation	SNP	C	T	T	BRIP1	c.3064G>A	p.E1022K
117J3239A1	17	63554530	63554530	Missense_Mutation	SNP	G	A	A	AXIN2	c.209C>T	p.S70F
117J3239A1	17	76219630	76219630	Missense_Mutation	SNP	G	A	A	BIRC5	c.424G>A	p.D142N
117J3239A1		-	-	Frame_Shift_Del	INS	-	-	-	GATA6	c.1182del	p.S395Pfs*26
117J3239A1	18	60985744	60985744	Missense_Mutation	SNP	C	G	G	BCL2	c.156G>C	p.Q52H
117J3239A1	19	50910347	50910347	Missense_Mutation	SNP	G	C	C	POLD1	c.1602G>C	p.E534D
117J3239A1	2	141625284	141625284	Missense_Mutation	SNP	G	T	T	LRP1B	c.4454C>A	p.T1485K
117J3239A1	2	141747173	141747173	Missense_Mutation	SNP	G	T	T	LRP1B	c.2698C>A	p.P900T
117J3239A1	2	141771315	141771315	Splice_Site	SNP	C	A	A	LRP1B	c.2191-1G>T	-
117J3239A1	2	142004929	142004929	Splice_Site	SNP	A	G	G	LRP1B	c.464-6T>C	-
117J3239A1	2	170077050	170077050	Missense_Mutation	SNP	G	C	C	LRP2	c.5562C>G	p.I1854M

117J3239A1	2	178098945	178098945	Missense_Mutation	SNP	G	C	C	NFE2L2	c.100C>G	p.R34G
117J3239A1	22	29115403	29115403	Missense_Mutation	SNP	G	C	C	CHEK2	c.663C>G	p.I221M
117J3239A1	3	138665213	138665213	Missense_Mutation	SNP	C	T	T	FOXL2	c.352G>A	p.E118K
117J3239A1	3	142274791	142274791	Missense_Mutation	SNP	G	C	C	ATR	c.2269C>G	p.Q757E
117J3239A1	3	142277502	142277502	Missense_Mutation	SNP	G	T	T	ATR	c.1849C>A	p.L617I
117J3239A1	3	178941890	178941890	Missense_Mutation	SNP	G	A	A	PIK3CA	c.2209G>A	p.E737K
117J3239A1	3	185155396	185155396	Missense_Mutation	SNP	C	A	A	MAP3K13	c.637C>A	p.H213N
117J3239A1	3	185190815	185190815	Missense_Mutation	SNP	G	T	T	MAP3K13	c.1696G>T	p.A566S
117J3239A1	4	1977011	1977011	Splice_Site	SNP	C	T	T	NSD2	c.3515-10C>T	-
117J3239A1	4	126238326	126238326	Missense_Mutation	SNP	C	T	T	FAT4	c.760C>T	p.H254Y
117J3239A1	4	126370128	126370128	Missense_Mutation	SNP	G	A	A	FAT4	c.7957G>A	p.E2653K
117J3239A1	5	149437141	149437141	Missense_Mutation	SNP	G	A	A	CSF1R	c.2147C>T	p.S716F
117J3239A1	6	93967194	93967194	Missense_Mutation	SNP	C	G	G	EPHA7	c.2158G>C	p.D720H
117J3239A1	8	38314954	38314954	Missense_Mutation	SNP	C	G	G	FGFR1	c.11G>C	p.W4S
117J3239A1	8	48691327	48691327	Missense_Mutation	SNP	C	G	G	PRKDC	c.11612G>C	p.R3871T
117J3239A1	9	101900314	101900314	Missense_Mutation	SNP	C	G	G	TGFB1R	c.748C>G	p.Q250E
117J3282A1	11	108201043	108201043	Nonsense_Mutation	SNP	T	A	A	ATM	c.7410T>A	p.Y2470*
117J3282A1	19	1220434	1220434	Missense_Mutation	SNP	A	C	C	STK11	c.527A>C	p.D176A
117J3282A1	19	42777250	42777250	Missense_Mutation	SNP	G	A	A	CIC	c.1315G>A	p.E439K
117J3282A1	3	142272717	142272717	Missense_Mutation	SNP	T	C	C	ATR	c.2482A>G	p.I828V
117J3295A1	1	156834205	156834205	Missense_Mutation	SNP	G	T	T	NTRK1	c.272G>T	p.G91V
117J3295A1	-	-	-	Frame_Shift_Del	INS	-	-	-	PTEN	C.243del	P.F81Lfs*18
117J3306A1	1	27057874	27057874	Nonsense_Mutation	SNP	C	T	T	ARID1A	c.1582C>T	p.Q528*
117J3306A1	1	162729667	162729667	Nonsense_Mutation	SNP	G	A	A	DDR2	c.753G>A	p.W251*
117J3306A1	10	123263446	123263446	Missense_Mutation	SNP	C	T	T	FGFR2	c.1297G>A	p.E433K
117J3306A1	-	-	-	In_Frame_Ins	INS	-	-	-	FGFR2	168insAACTTCT389	C390insNFLIA
117J3306A1	17	7579373	7579373	Missense_Mutation	SNP	C	T	T	TP53	c.314G>A	p.G105D
117J3306A1	2	48033372	48033372	Missense_Mutation	SNP	G	A	A	MSH6	c.3676G>A	p.A1226T
117J3306A1	20	57429649	57429649	Missense_Mutation	SNP	C	T	T	GNAS	c.1142C>T	p.P381L
117J3306A1	20	57429659	57429659	Missense_Mutation	SNP	C	T	T	GNAS	c.1339C>T	p.A447S
117J3306A1	3	52442055	52442055	Missense_Mutation	SNP	G	C	C	BAP1	c.294C>G	p.S98R
117J3306A1	-	-	-	Frame_Shift_Ins	INS	-	-	-	FOXP1	-1629_1630ins	p.R544Sfs*9
117J3318A1	12	46125084	46125084	Nonsense_Mutation	SNP	C	T	T	ARID2	c.271C>T	p.Q91*
117J3318A1	12	56492633	56492633	Missense_Mutation	SNP	A	G	G	ERBB3	c.2783A>G	p.E928G
117J3318A1	17	7578392	7578392	Missense_Mutation	SNP	C	T	T	TP53	c.538G>A	p.E180K
117J3318A1	-	-	-	Frame_Shift_Del	INS	-	-	-	SIK1	C.351del	P.N118Tfs*4
117J3318A1	3	41268766	41268766	Missense_Mutation	SNP	A	T	T	CTNNB1	c.1004A>T	p.K335I
117J3318A1	12	25398284	25398284	Missense_Mutation	SNP	C	A	A	KRAS	c.35G>T	p.G121V
117K3377A1	1	16258484	16258484	Missense_Mutation	SNP	C	T	T	SPEN	c.5749C>T	p.R1917C
117K3377A1	-	-	-	Frame_Shift_Del	INS	-	-	-	STK11	c.298del	p.Q100Nfs*3
117K3377A1	6	157517297	157517297	Splice_Site	SNP	A	G	G	ARID1B	c.3863-2A>G	-
117K3386A1	-	-	-	Frame_Shift_Ins	INS	-	-	-	EPHA2	c.1320dup	p.K441Ofs*13
117K3386A1	1	51436176	51436176	Splice_Site	SNP	A	G	G	CDKN2C	c.129+7A>G	-
117K3386A1	10	43597793	43597793	Missense_Mutation	SNP	G	A	A	RET	c.341G>A	p.R114H
117K3386A1	-	-	-	In_Frame_Del	INS	-	-	-	FGFR2	c.772_813del	p.L258_G271del
117K3386A1	19	33792353	33792353	Missense_Mutation	SNP	C	A	A	CEBPA	c.968G>T	p.R323L
117K3386A1	3	10183830	10183830	Missense_Mutation	SNP	C	T	T	VHL	c.299C>T	p.T100M
117K3386A1	4	55946257	55946257	Missense_Mutation	SNP	C	T	T	KDR	c.3922G>A	p.G1308R
117K3403A1	1	43805738	43805738	Missense_Mutation	SNP	T	A	A	MPL	c.794T>A	p.L265H
117K3403A1	1	65303679	65303679	Missense_Mutation	SNP	T	C	C	JAK1	c.3076A>G	p.K1026E
117K3403A1	1	98015244	98015244	Missense_Mutation	SNP	G	T	T	DPYD	c.1396C>A	p.P466T
117K3403A1	1	98205939	98205939	Splice_Site	SNP	T	A	A	DPYD	c.321+9A>T	-
117K3403A1	-	-	-	Frame_Shift_Ins	INS	-	-	-	ABL2	c.2518dup	p.S840Kfs*52
117K3403A1	1	193117007	193117007	Missense_Mutation	SNP	A	G	G	CDC73	c.740A>G	p.K247R
117K3403A1	1	193181580	193181580	Missense_Mutation	SNP	A	T	T	CDC73	c.1127A>T	p.N376I
117K3403A1	11	46321682	46321682	Missense_Mutation	SNP	T	A	A	CREB3L1	c.299T>A	p.L100H
117K3403A1	11	92495345	92495345	Splice_Site	SNP	T	A	A	FAT3	c.3984+9T>A	-
117K3403A1	-	-	-	Frame_Shift_Del	INS	-	-	-	KMT2D	c.6594del	p.Y2199Ifs*65
117K3403A1	14	50929435	50929435	Missense_Mutation	SNP	T	C	C	MAP4K5	c.884A>G	p.P295S
117K3403A1	17	7578291	7578291	Splice_Site	SNP	T	A	A	TP53	c.560-2A>T	-
117K3403A1	17	40485698	40485698	Missense_Mutation	SNP	T	C	C	STAT3	c.1042A>G	p.K348E
117K3403A1	19	15355518	15355518	Splice_Site	SNP	T	A	A	BRD4	c.2211+3A>T	-
117K3403A1	2	141474278	141474278	Missense_Mutation	SNP	C	G	G	LRP1B	c.5866G>C	p.F1956Q
117K3403A1	2	212248591	212248591	Missense_Mutation	SNP	T	A	A	ERBB4	c.3676A>T	p.I1226L
117K3403A1	2	212488781	212488781	Splice_Site	SNP	A	T	T	ERBB4	c.2080-12T>A	-
117K3403A1	20	31024668	31024668	Missense_Mutation	SNP	A	T	T	ASXL1	c.4153A>T	p.R1385W
117K3403A1	21	39817423	39817423	Missense_Mutation	SNP	A	T	T	ERG	c.161T>A	p.M54K
117K3403A1	3	10123082	10123082	Missense_Mutation	SNP	A	T	T	FANCD2	c.3158A>T	p.Q1053L
117K3403A1	3	195596414	195596414	Splice_Site	SNP	T	A	A	TNKG	c.1733-2A>T	-
117K3403A1	4	126371728	126371728	Missense_Mutation	SNP	A	T	T	FAT4	c.9557A>T	p.D3186V
117K3403A1	5	251451	251451	Splice_Site	SNP	A	T	T	SDHA	c.1664-2A>T	-
117K3403A1	6	157522010	157522010	Missense_Mutation	SNP	A	T	T	ARID1B	c.4282A>T	p.S1428C
117K3403A1	8	69046362	69046362	Missense_Mutation	SNP	T	A	A	PREX2	c.3835T>A	p.S1279T
117K3403A1	8	92972637	92972637	Missense_Mutation	SNP	T	A	A	RUNX1T1	c.1537A>T	p.I513F
117K3403A1	8	93115083	93115083	Splice_Site	SNP	A	T	T	RUNX1T1	c.28+2T>A	-
117K3403A1	X	48650475	48650475	Nonsense_Mutation	SNP	G	T	T	GATA1	c.445G>T	p.G149*
117K3508A1	17	7577534	7577534	Missense_Mutation	SNP	C	A	A	TP53	c.747G>T	p.R249S
117K3508A1	22	21348029	21348029	Missense_Mutation	SNP	T	C	C	LZTR1	c.1339T>C	p.F447L
117K3508A1	3	181430615	181430615	Missense_Mutation	SNP	G	A	A	SOX2	c.467G>A	p.R156H
117K3508A1	7	41729517	41729517	Missense_Mutation	SNP	A	T	T	INHBA	c.1012T>A	p.W338R
117K3508A1	9	21971145	21971145	Missense_Mutation	SNP	G	T	T	CDKN2A	c.213C>A	p.N71K
117K3520A1	12	25398284	25398284	Missense_Mutation	SNP	C	A	A	KRAS	c.35G>T	p.G12V
117K3520A1	18	19752072	19752072	Missense_Mutation	SNP	T	C	C	GATA6	c.967T>C	p.Y323H
117K3520A1	18	48591892	48591892	Missense_Mutation	SNP	G	A	A	SMAD4	c.1055G>A	p.G352E
117K3520A1	18	48593406	48593406	Missense_Mutation	SNP	G	A	A	SMAD4	c.1157G>A	p.G386D
117K3527A1	12	25398284	25398284	Missense_Mutation	SNP	C	T	T	KRAS	c.35G>A	p.G12D
117K3527A1	12	46233111	46233111	Splice_Site	SNP	G	A	A	ARID2	c.1331-1G>A	-
117K3527A1	13	28578283	28578283	Missense_Mutation	SNP	G	A	A	FLT3	c.2888C>T	p.S963L
117K3527A1	17	7577108	7577108	Missense_Mutation	SNP	C	T	T	TP53	c.830G>A	p.C277Y
117K3527A1	19	45918127	45918127	Missense_Mutation	SNP	C	T	T	ERCC1	c.694G>A	p.V232I
117K3527A1	22	41489103	41489103	Splice_Site	SNP	G	A	A	EP300	c.94+1G>A	-
117K3527A1	3	138664879	138664879	Missense_Mutation	SNP	G	A	A	FOXL2	c.686C>T	p.A229V
117K3527A1	7	106508826	106508826	Missense_Mutation	SNP	G	A	A	PIK3CG	c.820G>A	p.V274I
117K3556A1	10	131506271	131506271	Missense_Mutation	SNP	C	A	A	MGMT	c.331C>A	p.P111T
117K3556A1	11	108117798	108117798	Missense_Mutation	SNP	C	T	T	ATM	c.1009C>T	p.R337C
117K3556A1	2	121726436	121726436	Nonsense_Mutation	SNP	C	T	T	GLI2	c.790C>T	p.R264*
117K3556A1	3	178916725	178916725	Missense_Mutation	SNP	C	T	T	PIK3CA	c.112C>T	p.R38C
117K3556A1	5	138266623	138266623	Missense_Mutation	SNP	A	G	G	CTNNA1	c.2297A>G	p.H766R

117K3556A1	5	156668740	156668740	Splice_Site	SNP	A	G	G	ITK	c.1060+10A>G	-
117K3556A1	7	42004287	42004287	Missense_Mutation	SNP	T	G	G	GLI3	c.4384A>C	p.I1462L
117K3576A1	1	158619676	158619676	Missense_Mutation	SNP	C	T	T	SPTA1	c.3539G>A	p.G1180D
117K3576A1	17	29548950	29548950	Splice_Site	SNP	A	G	G	NF1	c.1721+3A>G	-
117K3576A1	3	49936071	49936071	Nonsense_Mutation	SNP	A	T	T	MST1R	c.1599T>A	p.C533*
117K3576A1	7	55087043	55087043	Missense_Mutation	SNP	C	G	G	EGFR	c.73C>G	p.L25V
117K3596A1	10	114919749	114919749	Missense_Mutation	SNP	C	G	G	TCF7L2	c.1371C>G	p.C457W
117K3596A1	12	25398285	25398285	Missense_Mutation	SNP	C	A	A	KRAS	c.34G>T	p.G12C
117K3596A1	-	-	-	Frame_Shift_Ins	INS	-	-	-	TP53	C.756dup	P.T253Hfs*11
117K3596A1	5	149515139	149515139	Missense_Mutation	SNP	G	A	A	PDGFRB	c.343C>T	p.R115W
117K3609A1	19	15378374	15378374	Splice_Site	SNP	G	A	A	BRD4	c.424-12C>T	-
117K3609A1	2	178098800	178098800	Missense_Mutation	SNP	T	C	C	NFE2L2	c.245A>G	p.E82G
117K3609A1	3	30691943	30691943	Missense_Mutation	SNP	T	A	A	TGFBR2	c.445T>A	p.F149I
117K3609A1	3	30732948	30732948	Missense_Mutation	SNP	T	C	C	TGFBR2	c.1561T>C	p.W521R
117K3609A1	3	52443761	52443761	Splice_Site	SNP	T	C	C	BAP1	c.38-2A>G	-
117K3620A1	1	27056352	27056352	Nonsense_Mutation	SNP	C	T	T	ARID1A	c.1348C>T	p.Q450*
117K3620A1	-	-	-	Frame_Shift_Ins	INS	-	-	-	ARID1A	c.6747dup	p.E2250Rfs*28
117K3620A1	16	68845758	68845758	Missense_Mutation	SNP	G	A	A	CDH1	c.1004G>A	p.R335Q
117K3620A1	2	178095644	178095644	Missense_Mutation	SNP	C	G	G	NFE2L2	c.1687G>C	p.E563Q
117K3620A1	22	38370170	38370170	Missense_Mutation	SNP	G	A	A	SOX10	c.733C>T	p.T245S
117K3620A1	7	41729816	41729816	Missense_Mutation	SNP	A	G	G	INHBA	c.713T>C	p.L238P
117K3620A1	8	139165017	139165017	Missense_Mutation	SNP	T	G	G	FAM135B	c.1701A>C	p.E567D
117K3660A1	12	56481922	56481922	Missense_Mutation	SNP	G	A	A	ERBB3	c.850G>A	p.G284R
117K3660A1	17	7578271	7578271	Missense_Mutation	SNP	T	C	C	TP53	c.578A>G	p.H193R
117K3660A1	18	48604690	48604690	Missense_Mutation	SNP	T	G	G	SMAD4	c.1512T>G	p.S504R
117K3669A1	1	27101099	27101099	Nonsense_Mutation	SNP	C	T	T	ARID1A	c.4381C>T	p.I461*
117K3669A1	-	-	-	Frame_Shift_Del	INS	-	-	-	SPTA1	C.1349del	P.K450Rfs*43
117K3669A1	12	56495328	56495328	Missense_Mutation	SNP	G	A	A	ERBB3	c.3518G>A	p.R1173Q
117K3669A1	17	70118937	70118937	Missense_Mutation	SNP	C	T	T	SOX9	c.509C>T	p.P170L
117K3669A1	19	2216398	2216398	Missense_Mutation	SNP	G	A	A	DOT1L	c.2042G>A	p.R681H
117K3669A1	2	209113112	209113112	Missense_Mutation	SNP	C	A	A	IDH1	c.395G>T	p.R132L
117K3669A1	20	57429158	57429158	Missense_Mutation	SNP	G	A	A	GNAS	c.838G>A	p.A280T
117K3669A1	22	21350115	21350115	Missense_Mutation	SNP	G	A	A	LZTR1	c.2023G>A	p.G675R
117K3669A1	3	52439278	52439278	Nonsense_Mutation	SNP	G	A	A	BAP1	c.964C>T	p.Q322*
117K3669A1	-	-	-	Frame_Shift_Del	INS	-	-	-	PBRM1	C.3833del	P.P1278Lfs*10
117K3669A1	4	1806600	1806600	Missense_Mutation	SNP	G	A	A	FGFR3	c.1316G>A	p.R439H
117K3669A1	4	126412679	126412679	Missense_Mutation	SNP	G	C	C	FAT4	c.14702G>C	p.G4901A
117K3669A1	-	-	-	Frame_Shift_Del	INS	-	-	-	APC	C.4056_4072del	P.F1354Ifs*15
117K3669A1	5	131972883	131972883	Missense_Mutation	SNP	C	T	T	RAD50	c.3466C>T	p.R1156C
117K3669A1	5	147207669	147207669	Missense_Mutation	SNP	T	C	C	SPINK1	c.110A>G	p.N37S
117K3669A1	6	117683996	117683996	Missense_Mutation	SNP	T	C	C	ROS1	c.3151A>G	p.I051V
117K3669A1	7	152346028	152346028	Missense_Mutation	SNP	T	C	C	XRCC2	c.542A>G	p.E181G
117K3669A1	X	48891040	48891040	Missense_Mutation	SNP	C	T	T	TFE3	c.1076G>A	p.R359Q
117K3688A1	10	123325192	123325192	Nonsense_Mutation	SNP	G	A	A	FGFR2	c.136C>T	p.Q46*
117K3688A1	12	25398284	25398284	Missense_Mutation	SNP	C	G	G	KRAS	c.35G>C	p.G12A
117K3688A1	12	46245033	46245033	Nonsense_Mutation	SNP	C	T	T	ARID2	c.3127C>T	p.Q1043*
117K3688A1	12	46245376	46245376	Nonsense_Mutation	SNP	C	G	G	ARID2	c.3470C>G	p.S1157*
117K3688A1	12	115112364	115112364	Missense_Mutation	SNP	C	T	T	TBX3	c.1376G>A	p.R459H
117K3688A1	-	-	-	Frame_Shift_Del	INS	-	-	-	FOS	c.894_895del	p.F298Lfs*51
117K3688A1	16	31191485	31191485	Splice_Site	SNP	C	G	G	FUS	c.-51C>G	-
117K3688A1	-	-	-	In_Frame_Del	INS	-	-	-	TP53	c.469_486del	p.V157_1162del
117K3688A1	17	56432344	56432344	Missense_Mutation	SNP	G	A	A	RNF43	c.2312C>T	p.S771L
117K3688A1	2	47656970	47656970	Missense_Mutation	SNP	G	A	A	MSH2	c.1166G>A	p.R389Q
117K3688A1	2	121745999	121745999	Missense_Mutation	SNP	G	A	A	GLI2	c.2509G>A	p.E837K
117K3688A1	3	41274855	41274855	Missense_Mutation	SNP	C	T	T	CTNNB1	c.1105C>T	p.H369Y
117K3688A1	3	178936082	178936082	Missense_Mutation	SNP	G	A	A	PIK3CA	c.1624G>A	p.E542K
117K3688A1	5	176618955	176618955	Missense_Mutation	SNP	G	C	C	NSD1	c.998G>C	p.R333T
117K3688A1	5	176638333	176638333	Missense_Mutation	SNP	C	T	T	NSD1	c.2933C>T	p.P978L
117K3688A1	7	92462399	92462399	Splice_Site	SNP	G	A	A	CDK6	c.233+6C>T	-
117K3688A1	7	106508682	106508682	Missense_Mutation	SNP	C	T	T	PIK3CG	c.676C>T	p.R226C
117K3688A1	8	48766767	48766767	Missense_Mutation	SNP	-	-	-	PRKDC	c.6769G>C	p.E2257Q
117K3699A1	12	25398285	25398285	Missense_Mutation	SNP	C	A	A	KRAS	c.34G>T	p.G12C
117K3699A1	-	-	-	Frame_Shift_Ins	INS	-	-	-	SOX9	C.1074_1075dup	P.P359Rfs*25
117K3699A1	20	57484420	57484420	Missense_Mutation	SNP	C	T	T	GNAS	c.601C>T	p.R201C
117K3699A1	3	49397742	49397742	Missense_Mutation	SNP	G	A	A	RHOA	c.482C>T	p.A161V
117K3699A1	-	-	-	Frame_Shift_Ins	INS	-	-	-	APC	C.4666dup	P.T1556Nfs*73
117K3699A1	9	101907038	101907038	Missense_Mutation	SNP	A	T	T	TGFBR1	c.998A>T	p.Q333V
117K3728A1	1	27059236	27059236	Nonsense_Mutation	SNP	C	T	T	ARID1A	c.1873C>T	p.Q625*
117K3728A1	12	25398284	25398284	Missense_Mutation	SNP	C	T	T	KRAS	c.35G>A	p.G12D
117K3728A1	-	-	-	Frame_Shift_Del	INS	-	-	-	TP53	c.1179_1180del	p.D393Efs*77
117K3728A1	19	11170486	11170486	Missense_Mutation	SNP	G	A	A	SMARCA4	c.4789G>A	p.E1597K
117K3728A1	7	78150951	78150951	Missense_Mutation	SNP	C	T	T	MAGI2	c.550G>A	p.G184S
117K3750A1	1	2491310	2491310	Missense_Mutation	SNP	T	C	C	TNFRSF14	c.353T>C	p.V118A
117K3750A1	1	9782576	9782576	Splice_Site	SNP	G	A	A	PIK3CD	c.2348-10G>A	-
117K3750A1	1	16257510	16257510	Missense_Mutation	SNP	G	A	A	SPEN	c.4775G>A	p.R1592Q
117K3750A1	1	65301152	65301152	Missense_Mutation	SNP	A	G	G	JAK1	c.3296T>C	p.M1099T
117K3750A1	1	65309758	65309758	Missense_Mutation	SNP	T	C	C	JAK1	c.2392A>G	p.T798A
117K3750A1	1	162740216	162740216	Missense_Mutation	SNP	G	A	A	DDR2	c.1418G>A	p.R473H
117K3750A1	1	179095717	179095717	Missense_Mutation	SNP	T	A	A	ABL2	c.482A>T	p.Y161F
117K3750A1	1	204438447	204438447	Nonsense_Mutation	SNP	G	A	A	PIK3C2B	c.484C>T	p.R162*
117K3750A1	1	226590082	226590082	Splice_Site	SNP	T	C	C	PARP1	c.121-2A>G	-
117K3750A1	-	-	-	In_Frame_Del	INS	-	-	-	TCF7L2	c.80_82del	p.Z28del
117K3750A1	10	123298201	123298201	Missense_Mutation	SNP	A	T	T	FGFR2	c.653T>A	p.M218K
117K3750A1	-	-	-	Missense_Mutation	SNP	-	-	-	NUP98	C.1585_1587del	P.K529del
117K3750A1	11	118390416	118390416	Nonsense_Mutation	SNP	C	T	T	KMT2A	c.11230C>T	p.R3744*
117K3750A1	-	-	-	Splice_Site	SNP	-	-	-	ARID2	c.419-10dupT	-
117K3750A1	12	49433223	49433223	Missense_Mutation	SNP	T	C	C	KMT2D	c.8224A>G	p.T2742A
117K3750A1	-	-	-	Frame_Shift_Del	INS	-	-	-	KMT2D	C.7061del	P.P2354Lfs*30
117K3750A1	12	50483664	50483664	Splice_Site	SNP	T	C	C	SMARCD1	c.772-3T>C	-
117K3750A1	12	50484355	50484355	Missense_Mutation	SNP	T	A	A	SMARCD1	c.1115T>A	p.I372N
117K3750A1	12	57560824	57560824	Missense_Mutation	SNP	C	T	T	LRP1	c.2909C>T	p.S970L
117K3750A1	12	57595294	57595294	Missense_Mutation	SNP	G	A	A	LRP1	c.10360G>A	p.A3454T
117K3750A1	12	115109887	115109887	Missense_Mutation	SNP	G	A	A	TBX3	c.1991C>T	p.A664V
117K3750A1	13	102568842	102568842	Missense_Mutation	SNP	G	A	A	FGF14	c.154C>T	p.R52C
117K3750A1	14	45620619	45620619	Missense_Mutation	SNP	G	A	A	FANCM	c.938G>A	p.R313H
117K3750A1	16	3790400	3790400	Missense_Mutation	SNP	C	T	T	CREBBP	c.4133G>A	p.R1378Q
117K3750A1	16	9862740	9862740	Missense_Mutation	SNP	C	T	T	GRIN2A	c.2563G>A	p.D855N
117K3750A1	-	-	-	In_Frame_Del	INS	-	-	-	THAP11	C.330_338del	P.Q130_Q132del

117K3750A1	16	81969962	81969962	Missense_Mutation	SNP	G	A	A	PLCG2	c.3031G>A	p.A1011T
117K3750A1	17	7578406	7578406	Missense_Mutation	SNP	C	T	T	TP53	c.524G>A	p.R175H
117K3750A1	17	11984788	11984788	Missense_Mutation	SNP	G	T	T	MAP2K4	c.334G>T	p.A112S
117K3750A1	17	11998928	11998928	Nonsense_Mutation	SNP	C	T	T	MAP2K4	c.430C>T	p.Q144*
117K3750A1		-	-	Frame_Shift_Del	INS	-	-	-	RNF43	C.1976del	P.G659Vfs*41
117K3750A1		-	-	Frame_Shift_Del	INS	-	-	-	BRIP1	C.2990_2993del	P.T997Rfs*61
117K3750A1		-	-	Frame_Shift_Del	INS	-	-	-	ROCK1	C.3921del	P.K1307Nfs*73
117K3750A1	19	42383667	42383667	Missense_Mutation	SNP	G	A	A	CD79A	c.442G>A	p.E148K
117K3750A1	19	45525373	45525373	Missense_Mutation	SNP	G	A	A	RELB	c.563C>A	p.P188H
117K3750A1		-	-	Splice_Site	SNP	-	-	-	RGPD4	c.73-3delT	-
117K3750A1		-	-	Missense_Mutation	SNP	-	-	-	RANBP2	C.6090_6092del	P.E2030del
117K3750A1	2	121747898	121747898	Missense_Mutation	SNP	C	T	T	GLI2	c.4408C>T	p.R1470W
117K3750A1	2	141274532	141274532	Missense_Mutation	SNP	C	A	A	LRP1B	c.8075G>T	p.G2692V
117K3750A1		-	-	Frame_Shift_Del	INS	-	-	-	ACVR2A	C.1310del	P.K437Rfs*5
117K3750A1		-	-	Frame_Shift_Del	INS	-	-	-	CASP8	C.1326_1327del	P.C443Pfs*12
117K3750A1	2	215633992	215633992	Missense_Mutation	SNP	A	T	T	BAR1D1	c.1359T>A	p.D453E
117K3750A1	20	30661518	30661518	Splice_Site	SNP	G	A	A	HCK	c.164-1G>A	-
117K3750A1	20	57429088	57429088	Missense_Mutation	SNP	G	A	A	GNAS	c.581G>A	p.R194Q
117K3750A1	21	39755530	39755530	Missense_Mutation	SNP	G	A	A	ERG	c.1184C>T	p.P395L
117K3750A1		-	-	Frame_Shift_Del	INS	-	-	-	EWSR1	C.1616_1617del	P.E539Vfs*5
117K3750A1	22	41566575	41566575	Missense_Mutation	SNP	G	T	T	EP300	c.4452G>T	p.K1484N
117K3750A1		-	-	Frame_Shift_Del	INS	-	-	-	TGFBR2	C.382_383del	P.K128Afs*3
117K3750A1	3	71021235	71021235	Missense_Mutation	SNP	G	A	A	FOXP1	c.1627C>T	p.R543C
117K3750A1		-	-	Frame_Shift_Ins	INS	-	-	-	PRKCI	C.79dup	P.R27Pfs*16
117K3750A1		-	-	Missense_Mutation	SNP	-	-	-	TNK2	C.920_922del	P.F307del
117K3750A1	4	1807638	1807638	Missense_Mutation	SNP	C	T	T	FGFR3	c.1807C>T	p.R603W
117K3750A1	4	106155916	106155916	Nonsense_Mutation	SNP	C	T	T	TET2	c.817C>T	p.Q273*
117K3750A1		-	-	Frame_Shift_Ins	INS	-	-	-	FAT4	C.2738dup	P.Q914Pfs*8
117K3750A1		-	-	Frame_Shift_Del	INS	-	-	-	FAT1	C.1607_1608del	P.L536Qfs*25
117K3750A1		-	-	Missense_Mutation	SNP	-	-	-	MAP3K1	C.3767_3769del	P.S1256del
117K3750A1	5	149503808	149503808	Splice_Site	SNP	G	A	A	PDGFRB	c.2023+5C>T	-
117K3750A1	5	149512334	149512334	Missense_Mutation	SNP	G	A	A	PDGFRB	c.1106C>T	p.T369M
117K3750A1	6	30863256	30863256	Missense_Mutation	SNP	C	A	A	DDR1	c.1589C>A	p.P530H
117K3750A1	6	32166736	32166736	Missense_Mutation	SNP	C	T	T	NOTCH4	c.4502G>A	p.R1501Q
117K3750A1	6	36651948	36651948	Missense_Mutation	SNP	C	A	A	CDKN1A	c.70C>A	p.P24T
117K3750A1	6	138192644	138192644	Missense_Mutation	SNP	G	A	A	TNFAIP3	c.280G>A	p.A94T
117K3750A1	7	86415839	86415839	Missense_Mutation	SNP	C	T	T	GRM3	c.731C>T	p.A244V
117K3750A1		-	-	Splice_Site	SNP	-	-	-	BRAF	c.1993-11delT	-
117K3750A1	7	151845112	151845112	Splice_Site	SNP	C	T	T	KMT2C	c.13894+6G>A	-
117K3750A1	8	11400849	11400849	Missense_Mutation	SNP	C	T	T	BLK	c.116C>T	p.P39L
117K3750A1	8	48843298	48843298	Missense_Mutation	SNP	G	A	A	PRKDC	c.1826C>T	p.A609V
117K3750A1	9	98231242	98231242	Missense_Mutation	SNP	G	A	A	PTCH1	c.2041C>T	p.P681S
117K3750A1		-	-	Splice_Site	SNP	-	-	-	TGFBR1	c.1131-3delT	-
117K3750A1		-	-	Frame_Shift_Ins	INS	-	-	-	NR4A3	C.449dup	P.Q151Afs*89
117K3750A1		-	-	Splice_Site	SNP	-	-	-	KDM6A	737-7_3737-6del	-
117K3750A1	X	47038783	47038783	Nonsense_Mutation	SNP	G	T	T	RBM10	c.790G>T	p.E264*
117K3750A1		-	-	Frame_Shift_Del	INS	-	-	-	BCORL1	C.4451del	P.P1484Qfs*7
117L3780A1		-	-	Frame_Shift_Del	INS	-	-	-	ARID1A	c.6744_6747del	p.H2248Qfs*18
117L3780A1	12	25398284	25398284	Missense_Mutation	SNP	C	A	A	KRAS	c.35G>T	p.G12V
117L3780A1	18	48593387	48593387	Splice_Site	SNP	A	T	T	SMAD4	c.1140-2A>T	-
117L3815A1	1	156843595	156843595	Missense_Mutation	SNP	G	A	A	NTRK1	c.1021G>A	p.V341M
117L3815A1	13	41134628	41134628	Missense_Mutation	SNP	C	T	T	FOXO1	c.1000G>A	p.E334K
117L3815A1	17	7576855	7576855	Nonsense_Mutation	SNP	G	A	A	TP53	c.991C>T	p.Q331*
117L3815A1	17	41203134	41203134	Missense_Mutation	SNP	T	C	C	BRCA1	c.5278A>G	p.L1760V
117L3815A1	18	19751791	19751791	Missense_Mutation	SNP	C	G	G	GATA6	c.686C>G	p.S229W
117L3815A1	2	141200065	141200065	Splice_Site	SNP	A	G	G	LRP1B	c.10414+8T>C	-
117L3815A1	3	3215926	3215926	Missense_Mutation	SNP	T	C	C	CRBN	c.194A>G	p.E65G
117L3815A1	4	1906094	1906094	Missense_Mutation	SNP	C	A	A	NSD2	c.749C>A	p.T250N
117L3815A1	7	13975403	13975403	Missense_Mutation	SNP	C	T	T	ETV1	c.484G>A	p.D162N
117L3815A1	7	106522569	106522569	Missense_Mutation	SNP	G	A	A	PIK3CG	c.2546G>A	p.R849Q
117L3816A1	11	108200961	108200961	Missense_Mutation	SNP	G	A	A	ATM	c.7328G>A	p.R2443Q
117L3816A1	12	46231410	46231410	Nonsense_Mutation	SNP	C	G	G	ARID2	c.1250C>G	p.S417*
117L3816A1		-	-	Frame_Shift_Del	INS	-	-	-	TP53	c.383_387delins	P.P128Lfs*41
117L3816A1	18	19752152	19752152	Missense_Mutation	SNP	G	T	T	GATA6	c.1047G>T	p.W349C
117L3816A1	19	11169494	11169494	Missense_Mutation	SNP	C	A	A	SMARCA4	c.4660C>A	p.L1554I
117L3816A1	20	36030892	36030892	Missense_Mutation	SNP	C	T	T	SRC	c.1171C>T	p.R391C
117L3816A1	4	187584566	187584566	Missense_Mutation	SNP	A	G	G	FAT1	c.3467T>C	p.V1156A
117L3816A1	8	93004079	93004079	Missense_Mutation	SNP	G	A	A	RUNX1T1	c.668C>T	p.S223L
117L3816A1	X	47429308	47429308	Missense_Mutation	SNP	G	A	A	ARAF	c.1436G>A	p.R479H
117L3817A1	11	108224492	108224492	Splice_Site	SNP	G	C	C	ATM	c.8672-1G>C	-
117L3817A1	13	43155275	43155275	Missense_Mutation	SNP	G	A	A	TNFSF11	c.14G>A	p.R5K
117L3817A1	16	2130195	2130195	Missense_Mutation	SNP	G	C	C	TSC2	c.3427G>C	p.D1143H
117L3817A1	19	11144798	11144798	Splice_Site	SNP	G	T	T	SMARCA4	c.3874-1G>T	-
117L3817A1	2	212576772	212576772	Splice_Site	SNP	G	A	A	ERBB4	c.1124+3C>T	-
117L3817A1	3	41266113	41266113	Missense_Mutation	SNP	C	T	T	CTNBN1	c.110C>T	p.S37F
117L3817A1	3	89391031	89391031	Missense_Mutation	SNP	G	T	T	EPHA3	c.1097G>A	p.C366F
117L3817A1	4	187541076	187541076	Missense_Mutation	SNP	C	T	T	FAT1	c.6664G>A	p.D2222N
117L3817A1	7	77764356	77764356	Missense_Mutation	SNP	G	A	A	MAGI2	c.3013C>T	p.R1005C
117L3842A1	11	119149250	119149250	Nonsense_Mutation	SNP	C	T	T	CBL	c.1258C>T	p.R420*
117L3842A1		-	-	In_Frame_Del	INS	-	-	-	TP53	c.512_520del	171_R174delinsG
117L3842A1	4	187557957	187557957	Missense_Mutation	SNP	T	C	C	FAT1	c.3754A>G	p.L1252V
117L3851A1	1	27105892	27105892	Missense_Mutation	SNP	C	A	A	ARID1A	c.5503C>A	p.Q1835K
117L3851A1	1	120459238	120459238	Missense_Mutation	SNP	C	T	T	NOTCH2	c.6107G>A	p.R2036Q
117L3851A1	12	25398284	25398284	Missense_Mutation	SNP	C	A	A	KRAS	c.35G>T	p.G12V
117L3851A1	16	3778618	3778618	Missense_Mutation	SNP	C	A	A	CREBBP	c.6430G>T	p.A2144S
117L3851A1	17	41245489	41245489	Missense_Mutation	SNP	G	T	T	BRCA1	c.2059C>A	p.Q687K
117L3851A1	17	78921158	78921158	Splice_Site	SNP	G	A	A	RPTOR	c.3265+7G>A	-
117L3851A1	19	10610154	10610154	Missense_Mutation	SNP	C	A	A	KEAP1	c.556G>T	p.G186C
117L3851A1	2	198266834	198266834	Missense_Mutation	SNP	T	C	C	SF3B1	c.2098A>G	p.R700E
117L3851A1	8	71053502	71053502	Missense_Mutation	SNP	C	T	T	NCOA2	c.2945G>A	p.R982Q
117L3938A1	10	43606743	43606743	Missense_Mutation	SNP	C	T	T	RET	c.1352C>T	p.T451M
117L3938A1		-	-	Frame_Shift_Del	INS	-	-	-	TP53	c.626_627del	p.R209Kfs*6
117L3938A1	7	117282657	117282657	Splice_Site	SNP	A	G	G	CFTR	c.3873+10A>G	-
117L3940A1	12	25398284	25398284	Missense_Mutation	SNP	C	A	A	KRAS	c.35G>T	p.G12V
117L3940A1	12	50479995	50479995	Nonsense_Mutation	SNP	G	T	T	SMARCD1	c.229G>T	p.G77*
117L3940A1	17	62009553	62009553	Splice_Site	SNP	A	G	G	CD79B	c.67+2T>C	-
117L3940A1	3	178936082	178936082	Missense_Mutation	SNP	G	A	A	PIK3CA	c.1624G>A	p.E542K
117L3940A1	4	126367653	126367653	Nonsense_Mutation	SNP	C	T	T	FAT4	c.7399C>T	p.Q2467*

117L3952A1	1	65303760	65303760	Missense_Mutation	SNP	A	G	G	JAK1	c.2995T>C	p.Y999H
117L3952A1	1	156843554	156843554	Missense_Mutation	SNP	T	C	C	NTRK1	c.980T>C	p.F327S
117L3952A1	10	70405595	70405595	Missense_Mutation	SNP	C	A	A	TE11	c.3109C>A	p.Q1037K
117L3952A1		-	-	In_Frame_Del	INS	-	-	-	PARP4	333delinsGAAT	40_I445delinsNLVF
117L3952A1		-	-	Frame_Shift_Ins	INS	-	-	-	BRCA2	C.4169dup	P.L1390Ffs*13
117L3952A1	19	42778531	42778531	Missense_Mutation	SNP	C	A	A	CIC	c.2596C>A	p.P866T
117L3952A1		-	-	In_Frame_Del	INS	-	-	-	ROS1	C.5341_5362de	P.I1781*
117L3952A1	6	117710734	117710734	Missense_Mutation	SNP	T	C	C	ROS1	c.1538A>G	p.D513G
117L3964A1	12	25398284	25398284	Missense_Mutation	SNP	C	A	A	KRAS	c.35G>T	p.G12V
117L3964A1	12	49420739	49420739	Missense_Mutation	SNP	C	T	T	KMT2D	c.15010G>A	p.E5004K
117L3965A1		-	-	Frame_Shift_Del	INS	-	-	-	ARID1A	C.5038_5042de	P.L1680Gfs*16
117L3965A1	12	46244247	46244247	Nonsense_Mutation	SNP	G	T	T	ARID2	c.2341G>T	p.G781*
117L3965A1	13	32930610	32930610	Missense_Mutation	SNP	G	A	A	BRCA2	c.7481G>A	p.R2494Q
117L3965A1		-	-	Frame_Shift_Ins	INS	-	-	-	PBRM1	C.4198dup	M.1400Nfs*109
117L3965A1	5	176518789	176518789	Missense_Mutation	SNP	A	T	T	FGFR4	c.707A>T	p.N236I
117L3965A1	6	162206852	162206852	Missense_Mutation	SNP	G	A	A	PRKN	c.823C>T	p.R275W
117L4005A1		-	-	Frame_Shift_Ins	INS	-	-	-	ARID1A	c.4933dup	p.S1645Ffs*3
117L4005A1		-	-	Frame_Shift_Del	INS	-	-	-	CHD4	c.4376_4377de	p.Y1459Cfs*10
117L4005A1	17	48275831	48275831	Missense_Mutation	SNP	T	G	G	COL1A1	c.506A>C	p.E169A
117L4040A1	13	41134892	41134892	Missense_Mutation	SNP	T	C	C	FOXO1	c.736A>G	p.FO246G
117L4040A1	15	88680700	88680700	Missense_Mutation	SNP	T	G	G	NTRK3	c.557A>C	p.N186T
117L4040A1	17	7577507	7577507	Missense_Mutation	SNP	T	G	G	TP53	c.774A>C	p.E258D
117L4040A1		-	-	In_Frame_Del	INS	-	-	-	NF1	C.5300_5314de	A1767_K1771del
117L4040A1		-	-	Frame_Shift_Del	INS	-	-	-	BRCA1	C.4485del	P.R1495Sfs*10
117L4040A1	6	32187569	32187569	Splice_Site	SNP	A	G	G	NOTCH4	c.1316-6T>C	-
117L4040A1	8	37688272	37688272	Missense_Mutation	SNP	C	T	T	ADGRA2	c.763C>T	p.R255C
117L4049A1	1	16458871	16458871	Splice_Site	SNP	A	G	G	EPHA2	c.2115+2T>C	-
117L4049A1		-	-	Frame_Shift_Ins	INS	-	-	-	PBRM1	810_1811insAA	p.G604Efs*7
117L4049A1	7	42188023	42188023	Missense_Mutation	SNP	C	T	T	GLI3	c.169G>A	p.A57T
117L4084A1	12	25398284	25398284	Missense_Mutation	SNP	C	T	T	KRAS	c.35G>A	p.G12D
117L4084A1		-	-	Frame_Shift_Del	INS	-	-	-	PBRM1	c.1284_1285de	p.S429Tfs*14
117L4084A1	6	30862458	30862458	Splice_Site	SNP	G	A	A	DDR1	c.1513+10G>A	-
117L4084A1	7	13975478	13975478	Missense_Mutation	SNP	G	T	T	ETV1	c.409C>A	p.P137T
117L4084A1	8	93017416	93017416	Missense_Mutation	SNP	G	T	T	RUNX1T1	c.557C>A	p.T186N
117L4084A1		-	-	Frame_Shift_Del	INS	-	-	-	AMER1	353_1362delins	p.E452Hfs*5
117L4087A1		-	-	Frame_Shift_Del	INS	-	-	-	MEN1	c.249_252del	p.I855fs*33
117L4087A1	17	7576857	7576857	Missense_Mutation	SNP	A	G	G	TP53	c.989T>C	p.L330P
117L4087A1	3	49927438	49927438	Missense_Mutation	SNP	C	T	T	MST1R	c.3866G>A	p.R1289H
117L4087A1	4	126239421	126239421	Missense_Mutation	SNP	C	T	T	FAT4	c.1855C>T	p.R619C
117L4087A1	7	18767243	18767243	Missense_Mutation	SNP	G	C	C	HDAC9	c.1763G>C	p.R588P
117L4089A1		-	-	Frame_Shift_Ins	INS	-	-	-	ARID1A	C.6341dup	P.Q2115Afs*35
117L4089A1	10	114925329	114925329	Missense_Mutation	SNP	C	T	T	TCF7L2	c.1163C>T	p.A388V
117L4089A1	12	56478786	56478786	Missense_Mutation	SNP	G	A	A	ERBB3	c.242G>A	p.R811Q
117L4089A1	13	28588663	28588663	Missense_Mutation	SNP	C	G	G	FLT3	c.2785G>C	p.D929H
117L4089A1	13	102568833	102568833	Missense_Mutation	SNP	C	T	T	FGF14	c.163G>A	p.G55S
117L4089A1		-	-	Frame_Shift_Del	INS	-	-	-	AXIN1	C.1523del	P.G508Vfs*197
117L4089A1	16	3788627	3788627	Missense_Mutation	SNP	G	A	A	CREBBP	c.4327C>T	p.R1443C
117L4089A1	17	7577548	7577548	Missense_Mutation	SNP	C	A	A	TP53	c.733G>T	p.G245C
117L4089A1	17	12011119	12011119	Missense_Mutation	SNP	A	T	T	MAP2K4	c.526A>T	p.I176F
117L4089A1		-	-	Splice_Site	SNP	-	-	-	COL1A1	c.1300-7delC	-
117L4089A1	17	48272920	48272920	Splice_Site	SNP	A	G	G	COL1A1	c.1155+8T>C	-
117L4089A1		-	-	Frame_Shift_Del	INS	-	-	-	AXIN2	C.1994del	P.G665Afs*24
117L4089A1		-	-	In_Frame_Del	INS	-	-	-	SMAD4	C.94_95del	P.S32*
117L4089A1		-	-	Frame_Shift_Del	INS	-	-	-	SMAD4	C.158_162del	P.E53Gfs*15
117L4089A1		-	-	In_Frame_Del	INS	-	-	-	SMAD4	C.1313_1314de	P.F438*
117L4089A1	19	15285059	15285059	Missense_Mutation	SNP	A	G	G	NOTCH3	c.4556T>C	p.L1519P
117L4089A1	19	17945927	17945927	Missense_Mutation	SNP	T	G	G	JAK3	c.2012A>C	p.D671A
117L4089A1	2	47637413	47637413	Nonsense_Mutation	SNP	C	T	T	MSH2	c.547C>T	p.Q183*
117L4089A1	2	191895741	191895741	Missense_Mutation	SNP	G	A	A	STAT4	c.2177C>T	p.A726V
117L4089A1	2	212426705	212426705	Missense_Mutation	SNP	G	T	T	ERBB4	c.2410C>A	p.L804M
117L4089A1	3	52437639	52437639	Missense_Mutation	SNP	G	A	A	BAP1	c.1522C>T	p.R508C
117L4089A1	3	181430166	181430166	Missense_Mutation	SNP	G	T	T	SOX2	c.18G>T	p.E6D
117L4089A1	3	183211878	183211878	Missense_Mutation	SNP	A	G	G	KLHL6	c.1339T>C	p.C447R
117L4089A1	5	180046110	180046110	Splice_Site	SNP	C	A	A	FLT4	c.2762-1G>T	-
117L4089A1	7	41730086	41730086	Missense_Mutation	SNP	G	A	A	INHBA	c.443C>T	p.S148L
117L4089A1	7	81358991	81358991	Missense_Mutation	SNP	T	C	C	HGF	c.970A>G	p.I324V
117L4089A1	7	151873888	151873888	Nonsense_Mutation	SNP	G	A	A	KMT2C	c.8650C>T	p.R2884*
117L4089A1	8	139323164	139323164	Splice_Site	SNP	C	A	A	FAM135B	c.78-1G>T	-
117L4089A1	9	21971120	21971120	Nonsense_Mutation	SNP	G	A	A	CDKN2A	c.238C>T	p.R80*
117L4089A1	9	133760147	133760147	Missense_Mutation	SNP	G	A	A	ABL1	c.2527G>A	p.V843M
117L4089A1	9	135776154	135776154	Missense_Mutation	SNP	A	G	G	TSC1	c.2573T>C	p.V588A
117L4089A1		-	-	Frame_Shift_Ins	INS	-	-	-	KDM6A	C.1271dup	P.L425Tfs*7
117L4089A1	X	44966679	44966679	Missense_Mutation	SNP	G	T	T	KDM6A	c.3903G>T	p.K1301N
117L4089A1	X	53224583	53224583	Missense_Mutation	SNP	G	A	A	KDM5C	c.3130C>T	p.H1044Y
117L4089A1	X	53245002	53245002	Missense_Mutation	SNP	C	T	T	KDM5C	c.938G>A	p.R313Q
117L4100A1	3	52441213	52441213	Missense_Mutation	SNP	A	C	C	BAP1	c.557T>G	p.L186R
117L4100A1	5	180057710	180057710	Missense_Mutation	SNP	C	T	T	FLT4	c.245G>A	p.R82Q
117L4103A1		-	-	Frame_Shift_Ins	INS	-	-	-	EPHA2	C.1000dup	P.Y334Lfs*47
117L4103A1	1	27105553	27105553	Nonsense_Mutation	SNP	C	T	T	ARID1A	c.5164C>T	p.R1722*
117L4103A1	12	25398284	25398284	Missense_Mutation	SNP	C	T	T	KRAS	c.35G>A	p.G12D
117L4103A1	3	52598207	52598207	Missense_Mutation	SNP	C	T	T	PBRM1	c.3659G>A	p.R1220K
117L4103A1	3	178936091	178936091	Missense_Mutation	SNP	G	A	A	PIK3CA	c.1633G>A	p.E545K
117L4103A1	5	156649874	156649874	Missense_Mutation	SNP	G	A	A	ITK	c.497G>A	p.R166Q
117L4103A1	7	151960190	151960190	Missense_Mutation	SNP	G	C	C	KMT2C	c.1210C>G	p.L404V
117L4103A1	8	11400840	11400840	Missense_Mutation	SNP	C	T	T	BLK	c.107C>T	p.P36L
117L4125A1		-	-	Frame_Shift_Del	INS	-	-	-	EPHA2	c.921del	p.C307Wfs*86
117L4125A1	12	69229720	69229720	Missense_Mutation	SNP	A	T	T	MDM2	c.796A>T	p.S266C
117L4125A1	2	209113112	209113112	Missense_Mutation	SNP	C	A	A	IDH1	c.395G>T	p.R132L
117L4126A1	1	204515977	204515977	Missense_Mutation	SNP	A	T	T	MDM4	c.875A>T	p.D292V
117L4126A1	1	226253379	226253379	Missense_Mutation	SNP	G	C	C	H3F3A	c.151G>C	p.E51Q
117L4126A1	11	69631202	69631202	Splice_Site	SNP	T	A	A	FGF3	c.221-11A>T	-
117L4126A1	11	76261137	76261137	Missense_Mutation	SNP	A	C	C	EMSY	c.3916A>C	p.T1306P
117L4126A1		-	-	Frame_Shift_Del	INS	-	-	-	POLE	C.4090del	P.R1364Vfs*5
117L4126A1		-	-	Splice_Site	SNP	-	-	-	TP53	c.373_375+9de	-
117L4126A1	19	15281220	15281220	Missense_Mutation	SNP	C	A	A	NOTCH3	c.5036G>T	p.G1679V
117L4126A1	2	121745934	121745934	Missense_Mutation	SNP	C	T	T	GLI2	c.2444C>T	p.S815L
117L4126A1	4	153249384	153249384	Missense_Mutation	SNP	C	A	A	FBXW7	c.1394G>T	p.R465L
117L4126A1	7	117232062	117232062	Missense_Mutation	SNP	A	T	T	CFTR	c.1841A>T	p.D614V

117L4126A1	9	87636352	87636352	Nonsense_Mutation	SNP	G	T	T	NTRK2	c.2517G>T	p.*839Y
117L4133A1	11	94800480	94800480	Missense_Mutation	SNP	G	C	C	SRSF8	c.90G>C	p.L30F
117L4133A1	17	7577082	7577082	Missense_Mutation	SNP	C	T	T	TP53	c.856G>A	p.E286K
117L4133A1	18	48604655	48604655	Missense_Mutation	SNP	G	A	A	SMAD4	c.1477G>A	p.D493N
117L4133A1	6	36651918	36651918	Missense_Mutation	SNP	G	A	A	CDKN1A	c.40G>A	p.G14S
117L4133A1	7	142649593	142649593	Splice_Site	SNP	C	T	T	KEL	c.1203+3G>A	-
117L4139A1	10	8100573	8100573	Missense_Mutation	SNP	T	A	A	GATA3	c.547T>A	p.C183S
117L4139A1	10	43595967	43595967	Missense_Mutation	SNP	C	T	T	RET	c.134C>T	p.A45V
117L4139A1	11	108115753	108115753	Missense_Mutation	SNP	G	C	C	ATM	c.901G>C	p.G301R
117L4139A1	11	108163495	108163495	Missense_Mutation	SNP	A	T	T	ATM	c.4586A>T	p.Y1529F
117L4139A1		-	-	Splice_Site	SNP	-	-	-	RB1	1390-38_1396d	-
117L4139A1	17	7576927	7576927	Splice_Site	SNP	C	A	A	TP53	c.920-1G>T	-
117L4139A1		-	-	Frame_Shift_Del	INS	-	-	-	LZTR1	c.2312del	p.Q771Rfs*18
117L4139A1	3	185797820	185797820	Missense_Mutation	SNP	G	C	C	ETV5	c.436C>G	p.Q146E
117L4139A1	7	18767372	18767372	Missense_Mutation	SNP	C	A	A	HDAC9	c.1892C>A	p.S631Y
118A4239A1	16	3900929	3900929	Missense_Mutation	SNP	C	G	G	CREBBP	c.167G>C	p.S56T
118A4239A1	17	7577538	7577538	Missense_Mutation	SNP	C	T	T	TP53	c.743G>A	p.R248Q
118A4239A1	17	56435317	56435317	Missense_Mutation	SNP	G	A	A	RNF43	c.1820C>T	p.S607L
118A4239A1	18	48603147	48603147	Splice_Site	SNP	G	A	A	SMAD4	c.1447+1G>A	-
118A4239A1	4	1962801	1962801	Missense_Mutation	SNP	G	A	A	NSD2	c.3295G>A	p.E1099K
118A4239A1	5	176563022	176563022	Missense_Mutation	SNP	A	T	T	NSD1	c.918A>T	p.E306D
118A4277A1	11	118376686	118376686	Nonsense_Mutation	SNP	C	A	A	KMT2A	c.10079C>A	p.S3360*
118A4277A1	12	25398284	25398284	Missense_Mutation	SNP	C	T	T	KRAS	c.35G>A	p.G12D
118A4277A1		-	-	Frame_Shift_Del	INS	-	-	-	ARID2	C.2032_2038del	P.A678Lfs*21
118A4277A1	12	121426784	121426784	Missense_Mutation	SNP	C	T	T	HNF1A	c.475C>T	p.R159W
118A4277A1	17	7577548	7577548	Missense_Mutation	SNP	C	T	T	TP53	c.733G>A	p.G245S
118A4277A1	19	14208444	14208444	Missense_Mutation	SNP	A	G	G	PRKACA	c.589T>C	p.W197R
118A4280A1	1	17349155	17349155	Missense_Mutation	SNP	A	T	T	SDHB	c.713T>A	p.F238Y
118A4280A1		-	-	Missense_Mutation	SNP	-	-	-	FAM46C	857_858delins	p.R286I
118A4280A1	1	158647473	158647473	Splice_Site	SNP	G	A	A	SPTA1	c.957+7C>T	-
118A4280A1		-	-	Frame_Shift_Del	INS	-	-	-	ARID2	C.2560_2561del	P.V854Nfs*96
118A4280A1		-	-	Frame_Shift_Del	INS	-	-	-	RB1	2058delinsCC	p.F684Pfs*7
118A4280A1	17	7578190	7578190	Missense_Mutation	SNP	T	C	C	TP53	c.659A>G	p.Y220C
118A4280A1	19	10610252	10610252	Missense_Mutation	SNP	A	T	T	KEAP1	c.458T>A	p.L153H
118A4280A1	19	42777783	42777783	Missense_Mutation	SNP	C	G	G	CIC	c.1848C>G	p.F616L
118A4280A1		-	-	Missense_Mutation	SNP	-	-	-	LRP1B	740_5741delins	p.G1914L
118A4280A1	22	23523338	23523338	Missense_Mutation	SNP	C	T	T	BCR	c.191C>T	p.A64V
118A4280A1	3	178922328	178922328	Missense_Mutation	SNP	C	G	G	PIK3CA	c.1097C>G	p.P366R
118A4280A1	3	187443373	187443373	Missense_Mutation	SNP	G	A	A	BCL6	c.1753C>T	p.R585W
118A4280A1	X	47045541	47045541	Missense_Mutation	SNP	G	T	T	RBM10	c.2508G>T	p.R836S
118A4284A1	16	10031854	10031854	Missense_Mutation	SNP	C	A	A	GRIN2A	c.969G>T	p.Q323H
118A4284A1	19	11143993	11143993	Missense_Mutation	SNP	C	T	T	SMARCA4	c.3574C>T	p.R1192C
118A4298A1	13	48939100	48939100	Missense_Mutation	SNP	T	C	C	RB1	c.932T>C	p.L311P
118A4298A1	17	78914407	78914407	Splice_Site	SNP	G	T	T	RPTOR	c.3025+6G>T	-
118A4298A1	19	4110622	4110622	Missense_Mutation	SNP	C	A	A	MAP2K2	c.335G>T	p.R112L
118A4298A1	2	209113112	209113112	Missense_Mutation	SNP	C	A	A	IDH1	c.395G>T	p.R132L
118A4298A1	6	138198224	138198224	Missense_Mutation	SNP	G	A	A	TNFAIP3	c.817G>A	p.V273I
118A4298A1	9	80336361	80336361	Missense_Mutation	SNP	T	A	A	GNAQ	c.958A>T	p.S320C
118A4330A1	1	27105529	27105529	Nonsense_Mutation	SNP	G	T	T	ARID1A	c.5140G>T	p.E1714*
118A4330A1	7	117149095	117149095	Missense_Mutation	SNP	G	T	T	CFTR	c.172G>T	p.D58Y
118A4330A1	9	21971120	21971120	Nonsense_Mutation	SNP	G	A	A	CDKN2A	c.238C>T	p.R80*
118A4336A1		-	-	Missense_Mutation	SNP	-	-	-	STK11	c.190_192dup	p.K64dup
118A4336A1	2	212615432	212615432	Splice_Site	SNP	G	A	A	ERBB4	c.557-3C>T	-
118A4336A1	7	151917611	151917611	Nonsense_Mutation	SNP	G	A	A	KMT2C	c.3709C>T	p.R1237*
118A4375A1	12	57579467	57579467	Missense_Mutation	SNP	G	A	A	LRP1	c.6617G>A	p.R2206H
118A4375A1	18	48604773	48604773	Missense_Mutation	SNP	C	A	A	SMAD4	c.1595C>A	p.A532D
118A4375A1	21	44524456	44524456	Missense_Mutation	SNP	G	A	A	U2AF1	c.101C>T	p.S34F
118A4375A1	8	32505505	32505505	Missense_Mutation	SNP	T	C	C	NRG1	c.269T>C	p.L90P
118A4375A1		-	-	Frame_Shift_Del	INS	-	-	-	AR	C.1484del	P.5495Tfs*15
118A4386A1		-	-	Frame_Shift_Del	INS	-	-	-	ARID1A	C.1015del	P.A339Lfs*24
118A4386A1	12	25398284	25398284	Missense_Mutation	SNP	C	T	T	KRAS	c.35G>A	p.G12D
118A4386A1	13	32912573	32912573	Missense_Mutation	SNP	C	G	G	BRCA2	c.4081C>G	p.Q1361E
118A4386A1	16	3900377	3900377	Missense_Mutation	SNP	G	A	A	CREBBP	c.719C>T	p.A240V
118A4386A1	18	48604643	48604643	Nonsense_Mutation	SNP	G	T	T	SMAD4	c.1465G>T	p.G489*
118A4386A1	20	36031747	36031747	Missense_Mutation	SNP	A	C	C	SRC	c.1576A>C	p.T526P
118A4386A1	5	67591097	67591097	Missense_Mutation	SNP	A	G	G	PIK3R1	c.1690A>G	p.N564D
118A4387A1	12	56491645	56491645	Missense_Mutation	SNP	G	T	T	ERBB3	c.2537G>T	p.S846I
118A4387A1	12	57858503	57858503	Missense_Mutation	SNP	C	T	T	GLI1	c.118C>T	p.R40W
118A4387A1	17	7577509	7577509	Missense_Mutation	SNP	C	T	T	TP53	c.772G>A	p.E258K
118A4387A1	2	191903933	191903933	Missense_Mutation	SNP	C	T	T	STAT4	c.1426G>A	p.D476N
118A4387A1		-	-	Missense_Mutation	SNP	-	-	-	PDGFRA	904_1905delins	p.S635S
118A4387A1	5	131924401	131924401	Missense_Mutation	SNP	T	A	A	RAD50	c.1074T>A	p.D358E
118A4387A1	9	21971120	21971120	Nonsense_Mutation	SNP	G	A	A	CDKN2A	c.238C>T	p.R80*
118A4434A1	3	178916944	178916944	Missense_Mutation	SNP	A	G	G	PIK3CA	c.331A>G	p.K111E
118A4438A1	12	115118843	115118843	Missense_Mutation	SNP	G	T	T	TBX3	c.498C>A	p.H166Q
118A4438A1	15	66727441	66727441	Missense_Mutation	SNP	T	G	G	MAP2K1	c.157T>G	p.F53V
118A4438A1		-	-	Frame_Shift_Ins	INS	-	-	-	FUS	c.621_624dup	p.G209Lfs*33
118A4438A1	17	70120517	70120517	Missense_Mutation	SNP	A	G	G	SOX9	c.1519A>G	p.T507A
118A4438A1		-	-	In_Frame_Del	INS	-	-	-	BAP1	c.1255delinsTG	p.K419*
118A4486A1	1	179090819	179090819	Nonsense_Mutation	SNP	T	A	A	ABL2	c.871A>T	p.K291*
118A4486A1	19	15288780	15288780	Missense_Mutation	SNP	G	A	A	NOTCH3	c.3959C>T	p.S1320L
118A4486A1	3	41266137	41266137	Missense_Mutation	SNP	C	T	T	CTNNB1	c.134C>T	p.S45F
118A4486A1	3	142178079	142178079	Missense_Mutation	SNP	G	C	C	ATR	c.7339C>G	p.P2447A
118A4554A1	10	89720789	89720789	Nonsense_Mutation	SNP	G	T	T	PTEN	c.940G>T	p.E314*
118A4554A1	11	92088480	92088480	Missense_Mutation	SNP	C	G	G	FAT3	c.3202C>G	p.R1068G
118A4554A1		-	-	Frame_Shift_Del	INS	-	-	-	TP53	547_553delins	P.S183Mfs*24
118A4682A2	2	58468446	58468446	Missense_Mutation	SNP	C	T	T	FANCL	c.3G>A	p.M1I
118A4689A1	12	12022535	12022535	Missense_Mutation	SNP	C	T	T	ETV6	c.641C>T	p.P214L
118A4689A1	12	49423015	49423015	Nonsense_Mutation	SNP	C	A	A	KMT2D	c.14080G>T	p.E4694*
118A4689A1	17	7578406	7578406	Missense_Mutation	SNP	C	T	T	TP53	c.524G>A	p.R175H
118A4689A1	17	7579489	7579489	Missense_Mutation	SNP	C	T	T	TP53	c.198G>A	p.M66I
118A4689A1		-	-	Frame_Shift_Del	INS	-	-	-	SMAD2	C.503_506del	P.H168Pfs*39
118A4689A1	5	1268675	1268675	Missense_Mutation	SNP	C	T	T	TERT	c.2542G>A	p.D848N
118A4689A1	7	81339472	81339472	Missense_Mutation	SNP	A	G	G	HGF	c.1532T>C	p.L511S
118A4689A1	9	21968728	21968728	Missense_Mutation	SNP	G	A	A	CDKN2A	c.500C>T	p.A167V
118A4698A1	12	57598259	57598259	Missense_Mutation	SNP	G	A	A	LRP1	c.11018G>A	p.C3673Y
118A4698A1	2	209113113	209113113	Missense_Mutation	SNP	G	A	A	IDH1	c.394C>T	p.R132C
118A4698A1	3	71021168	71021168	Missense_Mutation	SNP	A	G	G	FOX P1	c.1694T>C	p.V565A

118A4698A1	5	149449595	149449595	Missense_Mutation	SNP	C	G	G	CSF1R	c.1351G>C	p.D451H
118A4698A1	7	140453136	140453136	Missense_Mutation	SNP	A	T	T	BRAF	c.1799T>A	p.V600E
118A4765A2	1	11190635	11190635	Missense_Mutation	SNP	C	T	T	MTOR	c.5564G>A	p.S1855N
118A4765A2	1	16456803	16456803	Nonsense_Mutation	SNP	T	A	A	EPHA2	c.2587A>T	p.K863*
118A4765A2	14	35871868	35871868	Missense_Mutation	SNP	T	C	C	NFKBIA	c.638A>G	p.E213G
118A4765A2	4	153244237	153244237	Missense_Mutation	SNP	G	T	T	FBXW7	c.1920C>A	p.S640R
118B4778A1	12	25398281	25398281	Missense_Mutation	SNP	C	T	T	KRAS	c.38G>A	p.G13D
118B4778A1	14	50971556	50971556	Missense_Mutation	SNP	C	G	G	MAP4K5	c.128G>C	p.G43A
118B4778A1		-	-	Frame_Shift_Del	INS	-	-	-	TP53	C.1045del	P.E349Nfs*21
118B4778A1	3	30715688	30715688	Missense_Mutation	SNP	C	A	A	TGFB2	c.1346C>A	p.S449Y
118B4778A1	3	52436390	52436390	Nonsense_Mutation	SNP	G	A	A	BAP1	c.2104C>T	p.Q702*
118B4778A1	3	195611671	195611671	Splice_Site	SNP	C	A	A	TNK2	c.456+12G>T	-
118B4778A1	5	149510154	149510154	Missense_Mutation	SNP	G	C	C	PDGFRB	c.1315C>G	p.R439G
118B4778A1	9	87549162	87549162	Missense_Mutation	SNP	C	G	G	NTRK2	c.1719C>G	p.C573W
118B4778A1		-	-	Frame_Shift_Del	INS	-	-	-	AMER1	C.275_306del	P.K925fs*5
118B4782A1	15	66729181	66729181	Missense_Mutation	SNP	A	G	G	MAP2K1	c.389A>G	p.Y130C
118B4782A1	3	37067240	37067240	Missense_Mutation	SNP	T	A	A	MLH1	c.1151T>A	p.V384D
118B4782A1		-	-	Frame_Shift_Del	INS	-	-	-	CDKN2A	C.47_50del	P.L16Pfs*9
118B4789A1	19	1207162	1207162	Nonsense_Mutation	SNP	A	T	T	STK11	c.250A>T	p.K84*
118B4789A1	7	151873336	151873336	Nonsense_Mutation	SNP	G	A	A	KMT2C	c.9202C>T	p.Q3068*
118B4791A2	1	158614085	158614085	Missense_Mutation	SNP	C	G	G	SPTA1	c.4296G>C	p.L1432F
118B4791A2	11	92495145	92495145	Missense_Mutation	SNP	G	A	A	FAT3	c.3793G>A	p.L1265K
118B4791A2	11	92616277	92616277	Missense_Mutation	SNP	C	T	T	FAT3	c.12655C>T	p.R4219C
118B4791A2	11	92616454	92616454	Missense_Mutation	SNP	C	T	T	FAT3	c.12832C>T	p.R4278W
118B4791A2	11	94153350	94153350	Splice_Site	SNP	G	C	C	MRE11	c.2071_3C>G	-
118B4791A2	17	1303394	1303394	Missense_Mutation	SNP	C	T	T	YWHAE	c.11G>A	p.R4Q
118B4791A2		-	-	Frame_Shift_Del	INS	-	-	-	SMAD4	C.1245_1248de	P.D415Efs*20
118B4791A2	18	48603032	48603032	Nonsense_Mutation	SNP	C	T	T	SMAD4	c.1333C>T	p.R445*
118B4791A2	19	15288622	15288622	Missense_Mutation	SNP	C	T	T	NOTCH3	c.4117G>A	p.E1373K
118B4791A2		-	-	Frame_Shift_Ins	INS	-	-	-	NFE2L2	C.304dup	P.Y102Lfs*16
118B4791A2	3	37035147	37035147	Missense_Mutation	SNP	G	C	C	MLH1	c.109G>C	p.E37Q
118B4791A2	4	126238851	126238851	Missense_Mutation	SNP	G	A	A	FAT4	c.1285G>A	p.E429K
118B4791A2	7	42088134	42088134	Missense_Mutation	SNP	G	A	A	GLI3	c.635C>T	p.S212L
118B4791A2	7	140453155	140453155	Missense_Mutation	SNP	C	T	T	BRAF	c.1780G>A	p.D594N
118B4791A2	X	129147104	129147104	Missense_Mutation	SNP	G	A	A	BCORL1	c.356G>A	p.G119E
118B4864A2	19	18266930	18266930	Missense_Mutation	SNP	G	A	A	PIK3R2	c.241G>A	p.V81M
118B4864A2	2	209113113	209113113	Missense_Mutation	SNP	G	A	A	IDH1	c.394C>T	p.R132C
118B4864A2	3	138375035	138375035	Missense_Mutation	SNP	C	A	A	PIK3CB	c.3024G>T	p.L1008F
118B4864A2	8	69002809	69002809	Splice_Site	SNP	T	C	C	PREX2	c.2114-5T>C	-
118B4888A1	12	25398284	25398284	Missense_Mutation	SNP	C	T	T	KRAS	c.35G>A	p.G12D
118B4888A1	15	66727517	66727517	Missense_Mutation	SNP	A	T	G	MAP2K1	c.233A>G	p.N78S
118B4888A1	17	7576852	7576852	Splice_Site	SNP	C	T	T	TP53	c.993+1G>A	-
118B4888A1	18	48591919	48591919	Missense_Mutation	SNP	G	A	A	SMAD4	c.1082G>A	p.R361H
118B4888A1	X	76874372	76874372	Missense_Mutation	SNP	T	A	A	ATRX	c.5350A>T	p.I1784F
118B4909A1	12	50479178	50479178	Missense_Mutation	SNP	C	T	T	SMARCD1	c.26C>T	p.S9F
118B4909A1	13	48919331	48919331	Nonsense_Mutation	SNP	G	T	T	RB1	c.496G>T	p.E166*
118B4909A1	16	348049	348049	Nonsense_Mutation	SNP	G	T	T	AXIN1	c.1457C>A	p.S486*
118B4909A1		-	-	Frame_Shift_Ins	INS	-	-	-	PRSS8	c.882_903dup	p.D302Pfs*71
118B4909A1	17	7572986	7572986	Nonsense_Mutation	SNP	G	A	A	TP53	c.1123C>T	p.Q375*
118B4909A1	4	153249457	153249457	Missense_Mutation	SNP	G	A	A	FBXW7	c.1321C>T	p.R441W
118B4909A1	7	86394636	86394636	Nonsense_Mutation	SNP	C	T	T	GRM3	c.175C>T	p.R59*
118B4909A1	8	69033161	69033161	Nonsense_Mutation	SNP	C	T	T	PREX2	c.3601C>T	p.Q1201*
118B4937A1	1	27107195	27107195	Nonsense_Mutation	SNP	C	A	A	ARID1A	c.6806C>A	p.S2269*
118B4937A1	2	209113113	209113113	Missense_Mutation	SNP	G	A	A	IDH1	c.394C>T	p.R132C
118B4937A1	3	52643328	52643328	Splice_Site	SNP	C	A	A	PBRM1	c.2567+1G>T	-
118B4937A1	3	178916930	178916930	Missense_Mutation	SNP	G	T	T	PIK3CA	c.317G>T	p.G106V
118B5017A1	12	25398284	25398284	Missense_Mutation	SNP	C	T	T	KRAS	c.35G>A	p.G12D
118B5017A1	X	110439168	110439168	Missense_Mutation	SNP	G	T	T	PAK3	c.1209G>T	p.L403F
118B5044A1	12	25398284	25398284	Missense_Mutation	SNP	C	T	T	KRAS	c.35G>A	p.G12D
118B5044A1	16	31202119	31202119	Missense_Mutation	SNP	C	G	G	FUS	c.1349C>G	p.P450R
118B5044A1	17	7577538	7577538	Missense_Mutation	SNP	C	T	T	TP53	c.743G>A	p.R248Q
118B5044A1	17	56492700	56492700	Missense_Mutation	SNP	C	T	T	RNF43	c.239G>A	p.G80E
118B5044A1	6	138199731	138199731	Missense_Mutation	SNP	G	A	A	TNFAIP3	c.1149G>A	p.M383I
118B5053A1	12	25398284	25398284	Missense_Mutation	SNP	C	T	T	KRAS	c.35G>A	p.G12D
118B5053A1	17	7578539	7578539	Missense_Mutation	SNP	T	A	A	TP53	c.391A>T	p.N131Y
118B5053A1	8	93017450	93017450	Missense_Mutation	SNP	C	T	T	RUNX1T1	c.523G>A	p.A175T
118B5053A1	9	21971186	21971186	Nonsense_Mutation	SNP	G	A	A	CDKN2A	c.172C>T	p.R58*
118B5073A1	12	6692265	6692265	Missense_Mutation	SNP	G	C	C	CHD4	c.4075C>G	p.Q1359E
118B5073A1	17	17118505	17118505	Missense_Mutation	SNP	C	T	T	FLCN	c.1426G>A	p.D476N
118B5073A1	19	1220640	1220640	Nonsense_Mutation	SNP	C	T	T	STK11	c.658C>T	p.Q220*
118B5073A1	19	10600447	10600447	Missense_Mutation	SNP	G	A	A	KEAP1	c.1408C>T	p.R470C
118B5073A1	20	31022862	31022862	Missense_Mutation	SNP	C	A	A	ASXL1	c.2347C>A	p.P783T
118B5110A1	1	115258745	115258745	Missense_Mutation	SNP	C	G	G	NRAS	c.37G>C	p.G13R
118B5110A1	15	90631839	90631839	Missense_Mutation	SNP	T	A	A	IDH2	c.514A>T	p.R172W
118B5110A1	17	7578263	7578263	Nonsense_Mutation	SNP	G	A	A	TP53	c.586C>T	p.R196*
118B5110A1	17	7578454	7578454	Missense_Mutation	SNP	G	A	A	TP53	c.476C>T	p.A159V
118B5110A1		-	-	Frame_Shift_Ins	INS	-	-	-	BCL2L1	c.172_173dup	p.S59Afs*26
118B5110A1	3	52621446	52621446	Nonsense_Mutation	SNP	C	A	A	PBRM1	c.2971G>T	p.E991*
118B5110A1	5	121758671	121758671	Missense_Mutation	SNP	C	T	T	SNCAIP	c.239C>T	p.S80L
118B5118A1		-	-	Frame_Shift_Del	INS	-	-	-	ACVR1B	C.1009del	P.R337Gfs*4
118B5118A1		-	-	In_Frame_Del	INS	-	-	-	PARP2	C.1236_1241de	P.K413_E414del
118B5118A1	17	37666010	37666010	Missense_Mutation	SNP	G	A	A	CDK12	c.2662G>A	p.E888K
118B5118A1		-	-	Splice_Site	SNP	-	-	-	ETV4	C.-12_1del	-
118B5118A1	4	55597558	55597558	Missense_Mutation	SNP	G	A	A	KIT	c.2206G>A	p.A736T
118B5118A1	4	55599291	55599291	Missense_Mutation	SNP	C	A	A	KIT	c.2417C>A	p.R806K
118B5121A1	11	94200987	94200987	Nonsense_Mutation	SNP	G	A	A	MRE11	c.1090C>T	p.R364*
118B5121A1	12	25398282	25398282	Missense_Mutation	SNP	C	A	A	KRAS	c.37G>T	p.G13C
118B5121A1		-	-	In_Frame_Ins	INS	-	-	-	KMT2D	c.4484dup	p.Y1495*
118B5121A1	12	112926890	112926890	Missense_Mutation	SNP	A	G	G	PTPN11	c.1510A>G	p.M504V
118B5121A1	17	7578534	7578534	Missense_Mutation	SNP	C	G	G	TP53	c.396G>C	p.K132N
118B5121A1	17	63010545	63010545	Missense_Mutation	SNP	C	T	T	GNA13	c.964G>A	p.V322I
118B5121A1	18	48591891	48591891	Missense_Mutation	SNP	G	A	A	SMAD4	c.1054G>A	p.G352R
118B5121A1	7	140481402	140481402	Missense_Mutation	SNP	C	T	T	BRAF	c.1406G>A	p.G469E
118B5121A1	8	139164639	139164639	Missense_Mutation	SNP	G	C	C	FAM135B	c.2079C>G	p.S693R
118B5121A1	9	139391547	139391547	Missense_Mutation	SNP	G	A	A	NOTCH1	c.6644C>T	p.S2215L
118B5127A1		-	-	Frame_Shift_Del	INS	-	-	-	AXIN1	C.1632_1668de	P.R545Gfs*148
118C5128A1		-	-	Missense_Mutation	SNP	-	-	-	TET1	c.1035_1037de	p.H345del
118C5128A1	12	25398284	25398284	Missense_Mutation	SNP	C	A	A	KRAS	c.35G>T	p.G12V

118C5132A1	1	27097721	27097721	Nonsense_Mutation	SNP	G	T	T	ARID1A	c.3310G>T	p.E1104*
118C5132A1	2	48027494	48027494	Missense_Mutation	SNP	G	A	A	MSH6	c.2372G>A	p.R791H
118C5132A1		-	-	Frame_Shift_Del	INS	-	-	-	PBRM1	C.310del	P.E104Kfs*9
118C5132A1	4	153247367	153247367	Nonsense_Mutation	SNP	G	A	A	FBXW7	c.1435C>T	p.R479*
118C5169A1	5	131973805	131973805	Missense_Mutation	SNP	G	A	A	RAD50	c.3508G>A	p.D1170N
118C5169A1	X	48887754	48887754	Missense_Mutation	SNP	G	A	A	TFEB	c.1643C>T	p.S548F
118C5218A1	1	120497687	120497687	Missense_Mutation	SNP	C	T	T	NOTCH2	c.2195G>A	p.G732E
118C5218A1	17	29422382	29422382	Nonsense_Mutation	SNP	G	T	T	NF1	c.55G>T	p.E19*
118C5218A1	17	29527461	29527461	Nonsense_Mutation	SNP	C	T	T	NF1	c.910C>T	p.R304*
118C5218A1	9	87342561	87342561	Splice_Site	SNP	C	A	A	NTRK2	c.854-8C>A	-
118C5252A1		-	-	Frame_Shift_Ins	INS	-	-	-	TP53	C.216dup	P.V73Rfs*76
118C5252A1	2	209113113	209113113	Missense_Mutation	SNP	G	A	A	IDH1	c.394C>T	p.R132C
118C5252A1	22	21348283	21348283	Missense_Mutation	SNP	C	T	T	LZTR1	c.1424C>T	p.T475M
118C5252A1	4	106164897	106164897	Nonsense_Mutation	SNP	C	A	A	TET2	c.3765C>A	p.Y1255*
118C5275A1	10	123279564	123279564	Missense_Mutation	SNP	A	G	G	FGFR2	c.868T>C	p.W290R
118C5275A1	12	52377935	52377935	Missense_Mutation	SNP	A	G	G	ACVR1B	c.1087A>G	p.I363V
118C5275A1	19	1221211	1221211	Splice_Site	SNP	G	C	C	STK11	c.735-1G>C	-
118C5275A1	2	209113113	209113113	Missense_Mutation	SNP	G	A	A	IDH1	c.394C>T	p.R132C
118C5275A1	4	153247173	153247173	Missense_Mutation	SNP	T	G	G	FBXW7	c.1629A>C	p.R543S
118C5293A1	1	27056307	27056307	Nonsense_Mutation	SNP	C	T	T	ARID1A	c.1303C>T	p.Q435*
118C5293A1	1	158644142	158644142	Missense_Mutation	SNP	C	A	A	SPTA1	c.1327G>T	p.A443S
118C5293A1		-	-	Frame_Shift_Ins	INS	-	-	-	LRP1B	4477_4478insT	p.S1493Lfs*14
118C5293A1		-	-	Missense_Mutation	SNP	-	-	-	FEV	c.465_467del	p.Q156del
118C5350A2	11	9607076	9607076	Splice_Site	SNP	T	A	A	WEE1	c.1470+2T>A	-
118C5350A2	12	25398284	25398284	Missense_Mutation	SNP	C	T	T	KRAS	c.35G>A	p.G12D
118C5350A2	12	46230571	46230571	Nonsense_Mutation	SNP	C	T	T	ARID2	c.820C>T	p.R274*
118C5350A2	17	7578460	7578460	Missense_Mutation	SNP	A	T	T	TP53	c.470T>A	p.V157D
118C5350A2	2	141709457	141709457	Nonsense_Mutation	SNP	G	T	T	LRP1B	c.2940C>A	p.C980*
118C5506A1	11	76257063	76257063	Missense_Mutation	SNP	A	G	G	EMSY	c.3496A>G	p.M1166V
118C5506A1	17	11998898	11998898	Missense_Mutation	SNP	C	T	T	MAP2K4	c.400C>T	p.R134W
118C5506A1	17	15968937	15968937	Missense_Mutation	SNP	C	T	T	NCOR1	c.4813G>A	p.A1605T
118C5506A1		-	-	Missense_Mutation	SNP	-	-	-	IDH1	393_394delinsC	p.R132C
118C5592A1	1	16464453	16464453	Nonsense_Mutation	SNP	C	A	A	EPHA2	c.1207G>T	p.E403*
118C5592A1	2	29917717	29917717	Missense_Mutation	SNP	T	A	A	ALK	c.951A>T	p.R317S
118C5592A1		-	-	Frame_Shift_Ins	INS	-	-	-	BAP1	c.758dup	p.T254Dfs*30
118C5592A1	3	89468367	89468367	Missense_Mutation	SNP	A	T	T	EPHA3	c.1901A>T	p.E634V
118C5592A1	7	127569277	127569277	Nonsense_Mutation	SNP	C	T	T	SDN1	c.1564C>T	p.Q522*
118C5592A1	7	151878482	151878482	Missense_Mutation	SNP	T	C	C	KMT2C	c.6463A>G	p.N2155D
118C5592A1	8	92983052	92983052	Missense_Mutation	SNP	C	T	T	RUNX1T1	c.1262G>A	p.R421H
118C5597A1	12	25398284	25398284	Missense_Mutation	SNP	C	A	A	KRAS	c.35G>T	p.G12V
118C5597A1	17	7578190	7578190	Missense_Mutation	SNP	T	C	C	TP53	c.659A>G	p.Y220C
118C5597A1		-	-	Frame_Shift_Ins	INS	-	-	-	SMAD4	c.1242dup	p.D415Rfs*14
118C5597A1		-	-	Frame_Shift_Del	INS	-	-	-	CDKN2A	c.135_150del	p.R465fs*2
118C5599A1	12	25398285	25398285	Missense_Mutation	SNP	C	G	G	KRAS	c.34G>C	p.G12R
118C5599A1	17	7577124	7577124	Missense_Mutation	SNP	C	T	T	TP53	c.814G>A	p.V272M
118C5599A1		-	-	Frame_Shift_Del	INS	-	-	-	SMAD4	c.1286_1295del	p.I429Mfs*4
118C5599A1	8	128751001	128751001	Missense_Mutation	SNP	G	A	A	MYC	c.538G>A	p.A180T
118C5599A1		-	-	Frame_Shift_Ins	INS	-	-	-	CDKN2A	c.277dup	p.T93Nfs*27
118C5623A1	1	202729652	202729652	Missense_Mutation	SNP	C	T	T	KDM5B	c.1076G>A	p.R359Q
118C5623A1	12	6702590	6702590	Missense_Mutation	SNP	G	A	A	CHD4	c.2506C>T	p.R836C
118C5623A1	12	49438276	49438276	Nonsense_Mutation	SNP	T	A	A	KMT2D	c.4993A>T	p.K1665*
118C5623A1		-	-	Missense_Mutation	SNP	-	-	-	TP53	c.456_458del	p.P153del
118C5623A1	17	76210392	76210392	Splice_Site	SNP	G	T	T	BIRC5	c.-6G>T	-
118C5623A1	19	15376218	15376218	Missense_Mutation	SNP	G	T	T	BRD4	c.796C>A	p.Q266K
118C5623A1	19	17948832	17948832	Missense_Mutation	SNP	C	T	T	JAK3	c.1610G>A	p.R537Q
118C5623A1	2	141283813	141283813	Missense_Mutation	SNP	C	A	A	LRP1B	c.7869G>T	p.K2623N
118C5623A1	4	1902652	1902652	Missense_Mutation	SNP	C	T	T	NSD2	c.271C>T	p.P91S
118C5623A1	7	148523608	148523608	Missense_Mutation	SNP	T	C	C	EZH2	c.845A>G	p.H282R
118C5635A1	1	27097802	27097802	Nonsense_Mutation	SNP	C	T	T	ARID1A	c.3391C>T	p.Q1131*
118C5635A1	12	25398285	25398285	Missense_Mutation	SNP	C	T	T	KRAS	c.34G>A	p.G12S
118C5635A1		-	-	In Frame Ins	INS	-	-	-	FOS	c.735dup	p.D246*
118C5635A1	17	7574003	7574003	Nonsense_Mutation	SNP	G	A	A	TP53	c.1024C>T	p.R342*
118C5635A1	17	11998898	11998898	Missense_Mutation	SNP	C	T	T	MAP2K4	c.400C>T	p.R134W
118C5635A1	2	198267471	198267471	Missense_Mutation	SNP	G	T	T	SF3B1	c.1886C>A	p.A629D
118C5635A1	8	68930080	68930080	Splice_Site	SNP	G	C	C	PREX2	c.142-1G>C	-
118C5635A1	9	21971116	21971116	Missense_Mutation	SNP	G	C	C	CDKN2A	c.242C>G	p.P81R
118C5668A1	1	78428586	78428586	Missense_Mutation	SNP	G	T	T	FUBP1	c.1213C>A	p.Q405K
118C5668A1	12	25398284	25398284	Missense_Mutation	SNP	C	T	T	KRAS	c.35G>A	p.G12D
118C5668A1	X	123224544	123224544	Missense_Mutation	SNP	C	T	T	STAG2	c.3397C>T	p.R1133W
118C5749A1	4	126241857	126241857	Missense_Mutation	SNP	G	A	A	FAT4	c.4291G>A	p.E1431K
118C5749A1	7	140453136	140453136	Missense_Mutation	SNP	A	T	T	BRAF	c.1799T>A	p.V600E
118C5765A1	7	140453136	140453136	Missense_Mutation	SNP	A	T	T	BRAF	c.1799T>A	p.V600E
118C5765A1		-	-	In Frame Ins	INS	-	-	-	RBM10	c.310_324dup	D104_R108dup
118C5766A1	10	123279669	123279669	Missense_Mutation	SNP	G	A	A	FGFR2	c.763C>T	p.R255W
118C5766A1	12	4387995	4387995	Missense_Mutation	SNP	G	A	A	CCND2	c.481G>A	p.E161K
118C5766A1	12	46245246	46245246	Nonsense_Mutation	SNP	C	T	T	ARID2	c.3340C>T	p.Q1114*
118C5766A1	12	52380684	52380684	Missense_Mutation	SNP	G	A	A	ACVR1B	c.1342G>A	p.G448R
118C5766A1	17	7577085	7577085	Missense_Mutation	SNP	C	T	T	TP53	c.853G>A	p.E285K
118C5766A1		-	-	Frame_Shift_Del	INS	-	-	-	NF1	56delinsCTCTCT	p.L1253Sfs*17
118C5766A1	2	141130697	141130697	Missense_Mutation	SNP	C	T	T	LRP1B	c.10648G>A	p.E3550K
118C5766A1	2	170082929	170082929	Splice_Site	SNP	T	C	C	LRP2	c.5394+3A>G	-
118C5766A1	X	70602520	70602520	Splice_Site	SNP	G	A	A	TAF1	c.1725+7G>A	-
118C5792A1	16	396356	396356	Nonsense_Mutation	SNP	G	A	A	AXIN1	c.670C>T	p.Q224*
118C5833A1	1	65323437	65323437	Missense_Mutation	SNP	G	A	A	JAK1	c.1360C>T	p.R454W
118C5833A1	1	158582669	158582669	Nonsense_Mutation	SNP	C	A	A	SPTA1	c.7072G>T	p.E2358*
118C5833A1	13	32931974	32931974	Nonsense_Mutation	SNP	A	C	C	BRCA2	7713A>C;7742T	[E2571D;L2581*]
118C5833A1	16	3828151	3828151	Missense_Mutation	SNP	G	C	C	CREBBP	c.1974C>G	p.I658M
118C5833A1	2	169999288	169999288	Missense_Mutation	SNP	T	G	G	LRP2	c.13004A>C	p.K4335T
118C5833A1	5	121759251	121759251	Missense_Mutation	SNP	G	C	C	SNCAIP	c.819G>C	p.K273N
118C5833A1	5	176523183	176523183	Splice_Site	SNP	G	A	A	FGFR4	c.1944+3G>A	-
118C5910A1	12	25398284	25398284	Missense_Mutation	SNP	C	T	T	KRAS	c.35G>A	p.G12D
118C5910A1	17	7578454	7578454	Missense_Mutation	SNP	G	A	A	TP53	c.476C>T	p.A159V
118D5912A3	1	158581097	158581097	Missense_Mutation	SNP	C	A	A	SPTA1	c.7217G>T	p.G2406V
118D5912A3	12	25380275	25380275	Missense_Mutation	SNP	T	G	G	KRAS	c.183A>C	p.Q61H
118D5912A3		-	-	Splice_Site	SNP	-	-	-	STK11	290+3_290+4del	-
118D5912A3	3	89528621	89528621	Missense_Mutation	SNP	C	T	T	EPHA3	c.2921C>T	p.T974M
118D5912A3	4	126369874	126369874	Missense_Mutation	SNP	G	T	T	FAT4	c.7703G>T	p.R2568I
118D5912A3	5	180055906	180055906	Missense_Mutation	SNP	G	A	A	FLT4	c.1079C>T	p.A360V

118D5925A1	12	25398284	25398284	Missense_Mutation	SNP	C	A	A	KRAS	c.35G>T	p.G12V
118D5925A1	7	55259515	55259515	Missense_Mutation	SNP	T	G	G	EGFR	c.2573T>G	p.L858R
118D5925A1	9	21971111	21971111	Missense_Mutation	SNP	G	C	C	CDKN2A	c.247C>G	p.H83D
118D5949A1	12	25398284	25398284	Missense_Mutation	SNP	C	A	A	KRAS	c.35G>T	p.G12V
118D5949A1	17	7577559	7577559	Missense_Mutation	SNP	G	A	A	TP53	c.722C>T	p.S241F
118D5949A1	5	38967303	38967303	Missense_Mutation	SNP	G	A	A	RICTOR	c.1178C>T	p.A393V
118D5949A1	7	41729394	41729394	Missense_Mutation	SNP	G	A	A	INHBA	c.1135C>T	p.R379W
118D5960A1	12	56493528	56493528	Missense_Mutation	SNP	A	T	T	ERBB3	c.2936A>T	p.K979M
118D5960A1		-	-	Splice_Site	SNP	-	-	-	RB1	98_1498+1del	-
118D5960A1	2	141747096	141747096	Splice_Site	SNP	T	C	C	LRP1B	c.2770+5A>G	-
118D5960A1	22	41521980	41521980	Nonsense_Mutation	SNP	C	G	G	EP300	c.842C>G	p.S281*
118D5960A1	3	37053586	37053586	Missense_Mutation	SNP	A	G	G	MLH1	c.673A>G	p.S225G
118D5960A1	7	81372666	81372666	Splice_Site	SNP	T	C	C	HGF	c.865+3A>G	-
118D5960A1	8	92972730	92972730	Missense_Mutation	SNP	C	A	A	RUNX1T1	c.1444G>T	p.G482C
118D5960A1	9	21994276	21994276	Nonsense_Mutation	SNP	G	A	A	CDKN2A	c.55C>T	p.R19*
118D5965A1		-	-	Frame_Shift_Del	INS	-	-	-	ARID1A	c.3238_3251del	p.L1080Ffs*20
118D5965A1		-	-	Frame_Shift_Ins	INS	-	-	-	NRG3	c.423_424insT	p.A142Cfs*14
118D5965A1	11	92577865	92577865	Missense_Mutation	SNP	C	T	T	FAT3	c.11332C>T	p.R3778C
118D5965A1		-	-	Splice_Site	SNP	-	-	-	ATM	35_1235+1del	-
118D5965A1	11	108216637	108216637	Splice_Site	SNP	T	C	C	ATM	c.8584+2T>C	-
118D5965A1	12	25398285	25398285	Missense_Mutation	SNP	C	A	A	KRAS	c.34G>T	p.G12C
118D5965A1		-	-	Frame_Shift_Ins	INS	-	-	-	SMAD3	c.177_178dup	p.V60Afs*57
118D5965A1	18	48575197	48575197	Missense_Mutation	SNP	T	G	G	SMAD4	c.391T>G	p.Y131D
118D5965A1	19	4090604	4090604	Missense_Mutation	SNP	C	T	T	MAP2K2	c.1195G>A	p.A399T
118D5965A1	2	141253197	141253197	Missense_Mutation	SNP	A	T	T	LRP1B	c.8971T>A	p.C2991S
118D5965A1	2	170090092	170090092	Missense_Mutation	SNP	G	A	A	LRP2	c.4927C>T	p.R1643W
118D5965A1	7	106509436	106509436	Missense_Mutation	SNP	G	A	A	PIK3CG	c.1430G>A	p.R477H
118D6010J1	3	51979191	51979191	Missense_Mutation	SNP	C	T	T	PARP3	c.812C>T	p.P271L
118D6010J1	3	52441973	52441973	Splice_Site	SNP	C	T	T	BAP1	c.375+1G>A	-
118D6094D1	1	27058078	27058078	Missense_Mutation	SNP	C	A	A	ARID1A	c.1786C>A	p.S596S
118D6094D1	11	60235910	60235910	Missense_Mutation	SNP	C	T	T	MS4A1	c.863C>T	p.S288F
118D6094D1	17	7578550	7578550	Missense_Mutation	SNP	G	A	A	TP53	c.380C>T	p.S127F
118D6094D1		-	-	Frame_Shift_Del	INS	-	-	-	STK11	c.866_878del	p.M289Nfs*43
118D6094D1	3	51978529	51978529	Missense_Mutation	SNP	C	G	G	PARP3	c.436C>G	p.H146D
118D6094D1	3	134880937	134880937	Missense_Mutation	SNP	G	C	C	EPH1	c.1500G>C	p.M500I
118D6094D1		-	-	Frame_Shift_Del	INS	-	-	-	JAK2	3142_3147del	p.F1048Lfs*3
118D6094D1	9	21970901	21970901	Missense_Mutation	SNP	C	G	G	CDKN2A	c.457G>C	p.D153H
118D6094D1		-	-	In_Frame_Del	INS	-	-	-	KDM6A	c.491_494del	p.C164*
118D6120A1	12	52385664	52385664	Nonsense_Mutation	SNP	C	T	T	ACVR1B	c.1402C>T	p.Q468*
118D6120A1	12	57598196	57598196	Missense_Mutation	SNP	G	A	A	LRP1	c.10955G>A	p.R3652Q
118D6166A1	12	25398285	25398285	Missense_Mutation	SNP	C	A	A	KRAS	c.34G>T	p.G12C
118D6166A1	17	56492739	56492739	Missense_Mutation	SNP	C	T	T	RNF43	c.200G>A	p.G67D
118D6166A1		-	-	Frame_Shift_Del	INS	-	-	-	EP300	c.3954_3955del	p.G1319Rfs*5
118D6166A1	8	90967754	90967754	Missense_Mutation	SNP	T	C	C	NBN	c.1154A>G	p.K385R
118D6166A1	X	47040707	47040707	Nonsense_Mutation	SNP	C	T	T	RBM10	c.1342C>T	p.Q448*
118D6220A1		-	-	Frame_Shift_Del	INS	-	-	-	ARID1A	c.6001del	p.M2001Cfs*14
118D6220A1	1	115256529	115256529	Missense_Mutation	SNP	T	C	C	NRAS	c.182A>G	p.Q61R
118D6220A1	16	68863701	68863701	Splice_Site	SNP	G	A	A	CDH1	c.2439+1G>A	-
118D6220A1	17	7577539	7577539	Missense_Mutation	SNP	G	A	A	TP53	c.742C>T	p.R248W
118D6220A1	18	48604785	48604785	Missense_Mutation	SNP	T	G	G	SMAD4	c.1607T>G	p.L536R
118D6220A1	22	29687545	29687545	Splice_Site	SNP	C	T	T	EWSR1	c.975-6C>T	-
118D6220A1		-	-	In_Frame_Del	INS	-	-	-	CDKN2A	c.58_63del	p.A20_A21del
118D6255A1		-	-	Frame_Shift_Del	INS	-	-	-	BAP1	c.354del	p.F118Lfs*69
118D6295A1	1	43777390	43777390	Missense_Mutation	SNP	G	A	A	TIE1	c.1382G>A	p.R461H
118D6350A1		-	-	Frame_Shift_Del	INS	-	-	-	ARID1A	95_2000delinsA	p.I666Ffs*76
118D6350A1		-	-	In_Frame_Del	INS	-	-	-	ARID2	c.423_439del	p.Y141*
118D6350A1	3	178936082	178936082	Missense_Mutation	SNP	G	A	A	PIK3CA	c.1624G>A	p.E542K
118D6350A1	7	151879625	151879625	Nonsense_Mutation	SNP	C	A	A	KMT2C	c.5320G>T	p.E1774*
118D6350A1	X	63410813	63410813	Missense_Mutation	SNP	C	T	T	AMER1	c.2354G>A	p.S785N
118D6360A1	1	27101714	27101714	Splice_Site	SNP	A	T	T	ARID1A	c.4993+3A>T	-
118D6360A1	1	158583611	158583611	Missense_Mutation	SNP	G	A	A	SPTA1	c.6889C>T	p.R2297W
118D6360A1	12	25398284	25398284	Missense_Mutation	SNP	C	T	T	KRAS	c.35G>A	p.G12D
118D6360A1	14	95560464	95560464	Missense_Mutation	SNP	C	T	T	DICER1	c.5125G>A	p.T1709N
118D6360A1	14	95562619	95562619	Nonsense_Mutation	SNP	G	T	T	DICER1	c.4638C>A	p.Y1546*
118D6360A1		-	-	Frame_Shift_Del	INS	-	-	-	PALB2	c.1037_1041del	p.K346Tfs*13
118D6360A1	16	56865774	56865774	Missense_Mutation	SNP	A	G	G	NUP93	c.1106A>G	p.N369S
118D6360A1	22	30051652	30051652	Nonsense_Mutation	SNP	C	T	T	NF2	c.586C>T	p.R196*
118D6360A1	22	41566555	41566555	Missense_Mutation	SNP	C	T	T	EP300	c.4432C>T	p.R1478C
118D6360A1	5	131915116	131915116	Missense_Mutation	SNP	A	G	G	RAD50	c.473A>G	p.H158R
118D6360A1	7	106508703	106508703	Missense_Mutation	SNP	A	G	G	PIK3CG	c.697A>G	p.I233V
118D6403A1		-	-	In_Frame_Ins	INS	-	-	-	ARID1A	c.2445dup	p.N816*
118D6403A1	12	25398284	25398284	Missense_Mutation	SNP	C	T	T	KRAS	c.35G>A	p.G12D
118D6403A1	12	49433354	49433354	Missense_Mutation	SNP	T	C	C	KMT2D	c.8093A>G	p.N2698S
118D6403A1	16	9943687	9943687	Missense_Mutation	SNP	G	C	C	GRIN2A	c.1254C>G	p.I418M
118D6403A1	17	7578268	7578268	Missense_Mutation	SNP	A	C	C	TP53	c.581T>G	p.L194R
118D6403A1		-	-	Frame_Shift_Ins	INS	-	-	-	NCOR1	c.1573dup	p.T525Nfs*11
118D6403A1	18	48591890	48591890	Missense_Mutation	SNP	T	A	A	SMAD4	c.1053T>A	p.D351E
118D6403A1		-	-	Frame_Shift_Ins	INS	-	-	-	RANBP2	534_535insTTT	p.K179Ffs*2
118D6403A1	3	178952085	178952085	Missense_Mutation	SNP	A	T	T	PIK3CA	c.3140A>T	p.H1047L
118D6420A1		-	-	Frame_Shift_Ins	INS	-	-	-	CDKN1B	c.204_205insCC	p.L70Pfs*2
118D6420A1		-	-	Frame_Shift_Ins	INS	-	-	-	CDKN1B	c.224_225dup	p.W765fs*44
118D6420A1	12	49434810	49434810	Missense_Mutation	SNP	C	T	T	KMT2D	c.6743G>A	p.R2248H
118D6420A1	12	115118961	115118961	Splice_Site	SNP	G	T	T	TBX3	c.390-10C>A	-
118D6420A1	22	21351626	21351626	Missense_Mutation	SNP	G	A	A	LZTR1	c.2512G>A	p.A838T
118D6420A1	3	41266104	41266104	Missense_Mutation	SNP	G	A	A	CTNNB1	c.101G>A	p.G34E
118D6420A1		-	-	Frame_Shift_Del	INS	-	-	-	FBXW7	C.798del	P.K266Nfs*3
118D6420A1	8	69039666	69039666	Splice_Site	SNP	C	T	T	PREX2	c.3766+12C>T	-
118D6420A1	8	139207558	139207558	Splice_Site	SNP	G	A	A	FAM135B	c.824-8C>T	-
118D6519A1	12	25398285	25398285	Missense_Mutation	SNP	C	A	A	KRAS	c.34G>T	p.G12C
118D6519A1	17	7578554	7578554	Missense_Mutation	SNP	A	T	T	TP53	c.376T>A	p.Y126N
118D6519A1	20	57430164	57430164	Missense_Mutation	SNP	C	T	T	GNAS	c.1657C>T	p.P553S
118D6519A1		-	-	In_Frame_Del	INS	-	-	-	CDKN2A	c.34_69del	p.S12_G23del
118D6546A1	1	27023855	27023855	Nonsense_Mutation	SNP	C	T	T	ARID1A	c.961C>T	p.Q321*
118D6546A1	11	92088462	92088462	Missense_Mutation	SNP	G	A	A	FAT3	c.3184G>A	p.V1062M
118D6546A1	15	49716719	49716719	Nonsense_Mutation	SNP	G	A	A	FGF7	c.225G>A	p.W75*
118D6546A1	15	67477203	67477203	Splice_Site	SNP	G	A	A	SMAD3	c.1009+1G>A	-
118D6546A1	18	48591918	48591918	Missense_Mutation	SNP	C	T	T	SMAD4	c.1081C>T	p.R361C
118D6546A1	2	198266834	198266834	Missense_Mutation	SNP	T	C	C	SF3B1	c.2098A>G	p.K700E

118D6546A1	7	42065982	42065982	Missense_Mutation	SNP	G	A	A	GLI3	c.1058C>T	p.A353V
118D6546A1	7	140453154	140453154	Missense_Mutation	SNP	T	C	C	BRAF	c.1781A>G	p.D594G
118D6605A1	1	27100207	27100207	Nonsense_Mutation	SNP	C	T	T	ARID1A	c.4003C>T	p.R1335*
118D6605A1	12	115111972	115111972	Nonsense_Mutation	SNP	G	A	A	TBX3	c.1768C>T	p.Q590*
118D6605A1	17	7577520	7577520	Missense_Mutation	SNP	A	T	T	TP53	c.761T>A	p.I254N
118D6605A1	-	-	-	Missense_Mutation	SNP	-	-	-	ERBB2	C.2090_2092de	P.V697del
118D6605A1	2	170050322	170050322	Missense_Mutation	SNP	C	T	T	LRP2	c.8779G>A	p.G2927S
118D6605A1	3	47103828	47103828	Nonsense_Mutation	SNP	G	A	A	SETD2	c.6118C>T	p.R2040*
118D6605A1	7	2976766	2976766	Missense_Mutation	SNP	C	T	T	CARD11	c.1246G>A	p.E416K
118D6605A1	7	50450283	50450283	Missense_Mutation	SNP	A	G	G	IKZF1	c.467A>G	p.Q156R
118D6605A1	7	140453193	140453193	Missense_Mutation	SNP	T	C	C	BRAF	c.1742A>G	p.N581S
118D6683A1	17	7577551	7577551	Missense_Mutation	SNP	C	T	T	TP53	c.730G>A	p.G244S
118D6683A1	-	-	-	Frame_Shift_Del	INS	-	-	-	PBRM1	c.1106del	p.G369Efs*35
118D6684A1	17	7577141	7577141	Missense_Mutation	SNP	C	T	T	TP53	c.797G>A	p.G266E
118D6684A1	-	-	-	Frame_Shift_Del	INS	-	-	-	TP53	c.452delinsAA	p.P151Qfs*30
118D6684A1	2	209113112	209113112	Missense_Mutation	SNP	C	A	A	IDH1	c.395G>T	p.R132L
118D6719A1	1	226252030	226252030	Splice_Site	SNP	G	A	A	H3F3A	c.-23-4G>A	-
118D6719A1	12	4488690	4488690	Missense_Mutation	SNP	C	T	T	FGF23	c.59G>A	p.S20N
118D6719A1	12	25398281	25398281	Missense_Mutation	SNP	C	T	T	KRAS	c.38G>A	p.G13D
118D6719A1	12	49447386	49447386	Missense_Mutation	SNP	A	C	C	KMT2D	c.712T>G	p.L238V
118D6719A1	14	45633742	45633742	Missense_Mutation	SNP	A	G	G	FANCM	c.1762A>G	p.I588V
118D6719A1	15	67473704	67473704	Missense_Mutation	SNP	G	A	A	SMAD3	c.784G>A	p.D262N
118D6719A1	15	93444499	93444499	Missense_Mutation	SNP	A	G	G	CHD2	c.32A>G	p.E11G
118D6719A1	16	89862323	89862323	Missense_Mutation	SNP	C	T	T	FANCA	c.997G>A	p.V333M
118D6719A1	17	7576852	7576852	Splice_Site	SNP	C	T	T	TP53	c.993+1G>A	-
118D6719A1	19	10602580	10602580	Missense_Mutation	SNP	C	T	T	KEAP1	c.998G>A	p.G333D
118D6719A1	2	141215125	141215125	Missense_Mutation	SNP	G	A	A	LRP1B	c.9721C>T	p.H3241Y
118D6719A1	2	198266611	198266611	Missense_Mutation	SNP	C	T	T	SF3B1	c.2225G>A	p.G742D
118D6719A1	3	41266137	41266137	Missense_Mutation	SNP	C	T	T	CTNBN1	c.134C>T	p.S45F
118D6719A1	6	30863250	30863250	Missense_Mutation	SNP	G	C	C	DDR1	c.1583G>C	p.G528A
118D6719A1	7	151846063	151846063	Nonsense_Mutation	SNP	G	A	A	KMT2C	c.12949C>T	p.Q4317*
118D6719A1	8	139160859	139160859	Missense_Mutation	SNP	C	T	T	FAM135B	c.3352G>A	p.V1118I
118D6719A1	9	21971029	21971029	Nonsense_Mutation	SNP	C	T	T	CDKN2A	c.329G>A	p.W110*
118D6719A1	9	137300951	137300951	Missense_Mutation	SNP	G	T	T	RXRA	c.596G>T	p.G199V
118D6719A1	X	47040904	47040904	Splice_Site	SNP	A	T	T	RBM10	c.1436-2A>T	-
118D6898A1	7	151845915	151845915	Missense_Mutation	SNP	A	T	T	KMT2C	c.13097T>A	p.I4366N
118D6898A1	-	-	-	Splice_Site	SNP	-	-	-	PRKDC	3465-5_3465-4c	-
118D6898A1	9	139391932	139391932	Missense_Mutation	SNP	G	A	A	NOTCH1	c.6259C>T	p.R2087W
118D6984A1	12	25398281	25398281	Missense_Mutation	SNP	C	T	T	KRAS	c.38G>A	p.G13D
118D6984A1	17	7578508	7578508	Missense_Mutation	SNP	C	T	T	TP53	c.422G>A	p.C141Y
118D6984A1	3	178938934	178938934	Missense_Mutation	SNP	G	A	A	PIK3CA	c.2176G>A	p.E726K
118D6984A1	9	21971036	21971036	Missense_Mutation	SNP	C	A	A	CDKN2A	c.322G>T	p.D108Y
118D6984A1	-	-	-	In_Frame_Del	INS	-	-	-	RXRA	c.84_92del	M28_P31delins
118D6984A1	-	-	-	Frame_Shift_Del	INS	-	-	-	RBM10	c.705del	p.K235Nfs*31
118D6985A1	1	97771837	97771837	Missense_Mutation	SNP	C	A	A	DPYD	c.2075G>T	p.R692L
118D6985A1	12	57603962	57603962	Splice_Site	SNP	T	C	C	LRP1	c.12580+10T>C	-
118D6985A1	17	7577534	7577534	Missense_Mutation	SNP	C	A	A	TP53	c.747G>T	p.R249S
118D6985A1	19	4123888	4123888	Splice_Site	SNP	C	A	A	MAP2K2	c.-16G>T	-
118E7021A1	12	49441824	49441824	Missense_Mutation	SNP	C	A	A	KMT2D	c.4160G>T	p.G1387V
118E7021A1	-	-	-	Frame_Shift_Del	INS	-	-	-	TP53	769_771delinsA	P.L257Mfs*88
118E7021A1	17	7578457	7578457	Missense_Mutation	SNP	C	A	A	TP53	c.473G>T	p.R158L
118E7021A1	19	30308420	30308420	Missense_Mutation	SNP	G	A	A	CCNE1	c.434G>A	p.R145Q
118E7021A1	2	141272296	141272296	Missense_Mutation	SNP	C	A	A	LRP1B	c.8195G>T	p.C2732F
118E7021A1	2	141812805	141812805	Missense_Mutation	SNP	C	G	G	LRP1B	c.1432G>C	p.D478H
118E7021A1	22	21348031	21348031	Missense_Mutation	SNP	C	G	G	LZTR1	c.1341C>G	p.F447L
118E7021A1	6	32551999	32551999	Missense_Mutation	SNP	SNP	SNP	SNP	HLA-DRB1	c.231C>G	p.D77E
118E7021A1	7	50455067	50455067	Missense_Mutation	SNP	A	G	G	IKZF1	c.614A>G	p.Y205C
118E7059A1	17	7577559	7577559	Missense_Mutation	SNP	G	T	T	TP53	c.722C>A	p.S241Y
118E7059A1	17	29546098	29546098	Nonsense_Mutation	SNP	C	T	T	NF1	c.1603C>T	p.Q535*
118E7059A1	17	29661945	29661945	Nonsense_Mutation	SNP	C	T	T	NF1	c.5902C>T	p.R1968*
118E7059A1	19	2213593	2213593	Missense_Mutation	SNP	C	G	G	DOT1L	c.1613C>G	p.A538G
118E7059A1	19	10602369	10602369	Nonsense_Mutation	SNP	C	T	T	KEAP1	c.1209G>A	p.W403*
118E7059A1	-	-	-	Frame_Shift_Del	INS	-	-	-	KEAP1	C.1006del	P.R336dfs*64
118E7059A1	19	18267022	18267022	Splice_Site	SNP	A	G	G	PIK3R2	c.322+11A>G	-
118E7059A1	4	20490443	20490443	Nonsense_Mutation	SNP	C	T	T	SLIT2	c.613C>T	p.R205*
118E7059A1	4	153249384	153249384	Missense_Mutation	SNP	C	T	T	FBXW7	c.1394G>A	p.R465H
118E7059A1	-	-	-	Frame_Shift_Ins	INS	-	-	-	MAGI2	C.4262dup	P.A1422Rfs*19
118E7103A1	13	28622541	28622541	Missense_Mutation	SNP	T	G	G	FLT3	c.1076A>C	p.Y359S
118E7103A1	16	89818613	89818613	Missense_Mutation	SNP	T	C	C	FANCA	c.2999A>G	p.H1000R
118E7103A1	18	42531133	42531133	Missense_Mutation	SNP	G	A	A	SETBP1	c.1828G>A	p.V610I
118E7103A1	5	112173549	112173549	Missense_Mutation	SNP	A	G	G	APC	c.2258A>G	p.H753R
118E7103A1	X	48125796	48125796	Missense_Mutation	SNP	A	G	G	SSX1	c.541A>G	p.S181G
118E7142A1	12	25398284	25398284	Missense_Mutation	SNP	C	A	A	KRAS	c.35G>T	p.G12V
118E7142A1	17	7578406	7578406	Missense_Mutation	SNP	C	T	T	TP53	c.524G>A	p.R175H
118E7142A1	-	-	-	Splice_Site	SNP	-	-	-	MAP2K4	c.633+2dup	-
118E7142A1	2	212286784	212286784	Missense_Mutation	SNP	G	T	T	ERBB4	c.2912C>A	p.A971D
118E7142A1	-	-	-	Missense_Mutation	SNP	-	-	-	CDKN2A	C.130_132del	P.Y44del
118E7171A1	1	158637645	158637645	Splice_Site	SNP	T	C	C	SPTA1	c.2038+3A>G	-
118E7171A1	15	88669526	88669526	Nonsense_Mutation	SNP	G	A	A	NTRK3	c.1372C>T	p.R458*
118E7171A1	17	7577509	7577509	Nonsense_Mutation	SNP	C	A	A	TP53	c.772G>T	p.E258*
118E7171A1	17	12011106	12011106	Splice_Site	SNP	G	C	C	MAP2K4	c.514-1G>C	-
118E7171A1	3	70008488	70008488	Nonsense_Mutation	SNP	C	T	T	MITF	c.775C>T	p.R259*
118E7171A1	3	169998173	169998173	Missense_Mutation	SNP	G	C	C	PRKCI	c.864G>C	p.E288D
118E7171A1	5	180057057	180057057	Missense_Mutation	SNP	G	A	A	FLT4	c.562C>T	p.R188W
118E7171A1	9	98247979	98247979	Missense_Mutation	SNP	T	A	A	PTCH1	c.572A>T	p.Y191F
118E7187A1	10	123274822	123274822	Missense_Mutation	SNP	C	T	T	FGFR2	c.1096G>A	p.E366K
118E7187A1	12	25398284	25398284	Missense_Mutation	SNP	C	T	T	KRAS	c.35G>A	p.G12D
118E7187A1	13	28919596	28919596	Nonsense_Mutation	SNP	G	A	A	FLT1	c.2341C>T	p.R781*
118E7187A1	17	7577538	7577538	Missense_Mutation	SNP	C	T	T	TP53	c.743G>A	p.R248Q
118E7187A1	18	48591904	48591904	Missense_Mutation	SNP	C	G	G	SMAD4	c.1067C>G	p.P356R
118E7191A1	1	27023696	27023696	Nonsense_Mutation	SNP	C	T	T	ARID1A	c.802C>T	p.Q268*
118E7191A1	1	158651439	158651439	Missense_Mutation	SNP	G	A	A	SPTA1	c.409C>T	p.R137C
118E7191A1	12	25398284	25398284	Missense_Mutation	SNP	C	T	T	KRAS	c.35G>A	p.G12D
118E7191A1	18	48603080	48603080	Nonsense_Mutation	SNP	C	T	T	SMAD4	c.1381C>T	p.Q461*
118E7191A1	2	178098800	178098800	Missense_Mutation	SNP	T	A	A	NFE2L2	c.245A>T	p.E82V
118E7191A1	20	57484421	57484421	Missense_Mutation	SNP	G	A	A	GNAS	c.602G>A	p.R201H
118E7191A1	-	-	-	Frame_Shift_Del	INS	-	-	-	RBM10	c.495del	p.K165Nfs*101
118E7218A1	1	115256529	115256529	Missense_Mutation	SNP	T	A	A	NRAS	c.182A>T	p.Q61L

118E7218A1	11	64577316	64577316	Missense_Mutation	SNP	A	C	C	MEN1	c.266T>G	p.L89R
118E7218A1	17	7578212	7578212	Nonsense_Mutation	SNP	G	A	A	TP53	c.637C>T	p.R213*
118E7249A1	1	158624504	158624504	Missense_Mutation	SNP	C	A	A	SPTA1	c.2933G>T	p.G978V
118E7249A1	12	46287201	46287201	Splice_Site	SNP	A	G	G	ARID2	c.5148-2A>G	-
118E7249A1	17	757570	757570	Missense_Mutation	SNP	C	A	A	TP53	c.711G>T	p.M237I
118E7270A1	17	7578265	7578265	Missense_Mutation	SNP	A	G	G	TP53	c.584T>C	p.I195T
118E7270A1	2	141459401	141459401	Missense_Mutation	SNP	C	A	A	LRP1B	c.6316G>T	p.G2106W
118E7270A1	2	141771296	141771296	Nonsense_Mutation	SNP	C	A	A	LRP1B	c.2209G>T	p.E737*
118E7270A1	21	44524456	44524456	Missense_Mutation	SNP	G	A	A	U2AF1	c.101C>T	p.S34F
118E7270A1	4	20568947	20568947	Missense_Mutation	SNP	G	A	A	SLIT2	c.2788G>A	p.D930N
118E7270A1	4	153247289	153247289	Missense_Mutation	SNP	G	A	A	FBXW7	c.1513C>T	p.R505C
118E7290A1		-	-	Frame_Shift_Del	INS	-	-	-	TP53	.761_772delins	p.I254Kfs*6
118E7290A1	17	7579312	7579312	Splice_Site	SNP	C	T	T	TP53	c.375G>A	-
118E7290A1	6	117679130	117679130	Missense_Mutation	SNP	T	C	C	ROS1	c.3691A>G	p.I1231V
118E7290A1	6	151687723	151687723	Missense_Mutation	SNP	G	A	A	ZBTB2	c.478C>T	p.R160W
118E7304A1		-	-	In_Frame_Ins	INS	-	-	-	ARID2	c.1268dup	p.Y423*
118E7304A1	12	69964192	69964192	Nonsense_Mutation	SNP	C	T	T	FRS2	c.148C>T	p.R50C
118E7304A1	17	7579377	7579377	Nonsense_Mutation	SNP	G	A	A	TP53	c.310C>T	p.Q104*
118E7304A1	19	41726703	41726703	Missense_Mutation	SNP	A	T	T	AXL	c.248A>T	p.Q83L
118E7306A1	1	8073757	8073757	Nonsense_Mutation	SNP	C	T	T	ERRFI1	c.902G>A	p.W301*
118E7306A1	11	46332655	46332655	Missense_Mutation	SNP	G	A	A	CREB3L1	c.668G>A	p.R223H
118E7306A1	12	46245663	46245663	Missense_Mutation	SNP	G	T	T	ARID2	c.3757G>T	p.A1253S
118E7306A1	17	38563832	38563832	Missense_Mutation	SNP	C	T	T	TOP2A	c.1595G>A	p.R532H
118E7306A1	17	78727989	78727989	Splice_Site	SNP	A	T	T	RPTOR	c.830+4A>T	-
118E7306A1	2	109384745	109384745	Missense_Mutation	SNP	G	A	A	RANBP2	c.7750G>A	p.D2584N
118E7306A1	2	141055406	141055406	Missense_Mutation	SNP	G	A	A	LRP1B	c.12938C>T	p.P4313L
118E7306A1	20	52192647	52192647	Missense_Mutation	SNP	C	T	T	ZNF217	c.2656G>A	p.A886T
118E7306A1	4	187527243	187527243	Missense_Mutation	SNP	T	C	C	FAT1	c.10331A>G	p.N3444S
118E7306A1	7	2977554	2977554	Missense_Mutation	SNP	C	T	T	CARD11	c.1130G>A	p.P377Q
118E7306A1	7	80292448	80292448	Missense_Mutation	SNP	C	T	T	CD36	c.572C>T	p.R191L
118E7306A1	X	66766174	66766174	Missense_Mutation	SNP	G	C	C	AR	c.1186G>C	p.G396R
118E7325A1	1	158605703	158605703	Missense_Mutation	SNP	C	T	T	SPTA1	c.5432G>A	p.R1811Q
118E7325A1	15	93527621	93527621	Nonsense_Mutation	SNP	G	A	A	CHD2	c.3128G>A	p.W1043*
118E7325A1	17	7577099	7577099	Missense_Mutation	SNP	C	G	G	TP53	c.839G>C	p.R280T
118E7325A1	6	157527680	157527680	Missense_Mutation	SNP	G	A	A	ARID1B	c.5405G>A	p.R1802Q
118E7325A1	7	42004863	42004863	Missense_Mutation	SNP	C	T	T	GLI3	c.3808G>A	p.G1270S
118E7325A1	7	142641481	142641481	Nonsense_Mutation	SNP	G	A	A	KEL	c.1420C>T	p.Q474*
118E7344A1		-	-	Frame_Shift_Del	INS	-	-	-	TP53	C.347del	P.S116Lfs*7
118E7344A1	4	153271242	153271242	Missense_Mutation	SNP	C	T	T	FBXW7	c.536G>A	p.R179H
118E7344A1	7	81358997	81358997	Missense_Mutation	SNP	T	C	C	HGF	c.964A>G	p.N322D
118E7407A1	1	32741546	32741546	Missense_Mutation	SNP	C	A	A	LCK	c.513C>A	p.D171E
118E7407A1		-	-	Frame_Shift_Ins	INS	-	-	-	BRCA2	C.1759dup	P.T587Nfs*3
118E7407A1	17	7577108	7577108	Missense_Mutation	SNP	C	A	A	TP53	c.830G>T	p.C2077F
118E7407A1		-	-	Frame_Shift_Del	INS	-	-	-	DOT1L	C.4330_4340del	P.L1444Gfs*90
118E7407A1	2	29497991	29497991	Missense_Mutation	SNP	C	G	G	ALK	c.2015G>C	p.G672T
118E7407A1		-	-	In_Frame_Del	INS	-	-	-	PRKCI	C.54_59del	P.S19_G20del
118E7407A1	4	110916047	110916047	Splice_Site	SNP	C	T	T	EGF	c.3005+11C>T	-
118E7407A1	5	176562150	176562150	Missense_Mutation	SNP	T	C	C	NSD1	c.46T>C	p.F16L
118E7446A1	12	112926910	112926910	Missense_Mutation	SNP	G	C	C	PTPN11	c.1530G>C	p.Q510H
118E7446A1	16	396533	396533	Nonsense_Mutation	SNP	T	A	A	AXIN1	c.493A>T	p.K165*
118E7446A1	17	7578394	7578394	Missense_Mutation	SNP	T	A	A	TP53	c.536A>T	p.H179L
118E7446A1	17	29483155	29483155	Splice_Site	SNP	G	A	A	NF1	c.204+11G>A	-
118E7446A1	18	23618578	23618578	Missense_Mutation	SNP	T	C	C	SS18	c.821A>G	p.Q274R
118E7446A1		-	-	Frame_Shift_Del	INS	-	-	-	GNAS	C.736del	P.R246Vfs*25
118E7446A1	22	30077445	30077445	Missense_Mutation	SNP	A	T	T	NF2	c.1592A>T	p.K531M
118E7446A1	8	48771477	48771477	Missense_Mutation	SNP				PRKDC	c.6277A>G	p.N2093V
118E7470A1	1	158612676	158612676	Missense_Mutation	SNP	C	A	A	SPTA1	c.4533G>T	p.E1511D
118E7470A1	11	108224531	108224531	Missense_Mutation	SNP	G	A	A	ATM	c.8710G>A	p.E2904K
118E7470A1	2	141473542	141473542	Missense_Mutation	SNP	C	T	T	LRP1B	c.6023G>A	p.G2008D
118E7470A1	3	52649463	52649463	Missense_Mutation	SNP	C	T	T	PBRM1	.828G>A;1870G;[D610N];E624Q]	
118E7477A1	12	25398284	25398284	Missense_Mutation	SNP	C	T	T	KRAS	c.35G>A	p.G12D
118E7477A1		-	-	Frame_Shift_Del	INS	-	-	-	RNF43	C.69_72del	P.G24Lfs*26
118E7477A1	2	191895815	191895815	Splice_Site	SNP	G	A	A	STAT4	c.2112-9C>T	-
118E7477A1	3	10076158	10076158	Missense_Mutation	SNP	G	A	A	FANCD2	c.211G>A	p.D71N
118E7477A1	X	70617240	70617240	Missense_Mutation	SNP	C	T	T	TAF1	c.3604C>T	p.R1202C
118E7484A1	1	155880444	155880444	Splice_Site	SNP	T	A	A	RII1	c.106+3A>T	-
118E7484A1	1	158582656	158582656	Missense_Mutation	SNP	T	A	A	SPTA1	c.7085A>T	p.Q2362L
118E7484A1	13	32912396	32912396	Missense_Mutation	SNP	A	G	G	BRCA2	c.3904A>G	p.T1302A
118E7484A1	13	48923156	48923156	Nonsense_Mutation	SNP	A	T	T	RB1	c.604A>T	p.K202*
118E7484A1	14	45628487	45628487	Splice_Site	SNP	A	T	T	FANCM	c.1581+4A>T	-
118E7484A1	14	45644605	45644605	Missense_Mutation	SNP	A	T	T	FANCM	c.2648A>T	p.N883I
118E7484A1		-	-	In_Frame_Del	INS	-	-	-	TP53	c.598_609del	p.N200_V203del
118E7484A1	19	2202777	2202777	Missense_Mutation	SNP	A	T	T	DOT1L	c.786A>T	p.E262D
118E7484A1	2	74328674	74328674	Nonsense_Mutation	SNP	G	T	T	TET3	c.4759G>T	p.G1587*
118E7484A1	21	39755484	39755484	Missense_Mutation	SNP	C	G	G	ERG	c.1230G>C	p.K410N
118E7484A1	3	47162071	47162071	Missense_Mutation	SNP	T	A	A	SETD2	c.4055A>T	p.Q1352L
118E7484A1		-	-	Frame_Shift_Del	INS	-	-	-	EPHA3	c.1547del	p.G516Dfs*29
118E7484A1	5	35857107	35857107	Missense_Mutation	SNP	A	T	T	IL7R	c.28A>T	p.M10L
118E7484A1	5	131972826	131972826	Missense_Mutation	SNP	A	T	T	RAD50	c.3409A>T	p.S1137C
118E7484A1	5	176523136	176523136	Missense_Mutation	SNP	G	T	T	FGFR4	c.1900G>T	p.A634S
118E7484A1	6	93967207	93967207	Missense_Mutation	SNP	T	A	A	EPHA7	c.2145A>T	p.E715D
118E7484A1	8	48766731	48766731	Missense_Mutation	SNP	T	A	A	PRKDC	c.6805A>T	p.N2269Y
118E7554A2		-	-	In_Frame_Del	INS	-	-	-	TP53	.723_735delins	p.C242_G245del
118E7554A2	17	29665110	29665110	Nonsense_Mutation	SNP	C	T	T	NF1	c.6772C>T	p.R2258*
118E7554A2	22	42525787	42525787	Missense_Mutation	SNP	G	A	A	CYP2D6	c.305C>T	p.P102L
118E7554A2	3	134911420	134911420	Missense_Mutation	SNP	G	A	A	EPHB1	c.1885G>A	p.E629K
118E7554A2	3	142242884	142242884	Missense_Mutation	SNP	C	T	T	ATR	c.4103G>A	p.R1368Q
118E7554A2	3	181430278	181430278	Missense_Mutation	SNP	C	A	A	SOX2	c.130C>A	p.P44T
118E7554A2	8	139180187	139180187	Missense_Mutation	SNP	G	T	T	FAM135B	c.1209C>A	p.N403K
118E7554A2	X	70597003	70597003	Missense_Mutation	SNP	A	T	T	TAF1	c.736A>T	p.S246C
118E7554A2	X	129148828	129148828	Missense_Mutation	SNP	G	A	A	BCORL1	c.2080G>A	p.V694M
118E7614A1		-	-	Frame_Shift_Ins	INS	-	-	-	ARID1A	c.3027dup	p.K1010Qfs*74
118E7614A1	16	3778882	3778882	Missense_Mutation	SNP	C	T	T	CREBBP	c.6166G>A	p.V2056M
118E7614A1	3	30732969	30732969	Missense_Mutation	SNP	C	T	T	TGFB2	c.1582C>T	p.R528C
118E7614A1		-	-	Frame_Shift_Del	INS	-	-	-	PBRM1	c.1335del	p.D446ifs*7
118E7614A1		-	-	Frame_Shift_Del	INS	-	-	-	MAP3K1	c.1053_1063del	p.G352Yfs*29
118E7614A1		-	-	Frame_Shift_Ins	INS	-	-	-	ARID1B	c.3438dup	p.Q1147Sfs*7
118E7614A1	X	47044967	47044967	Nonsense_Mutation	SNP	C	T	T	RBM10	c.2293C>T	p.R765*

118E7632A1	1	7798423	7798423	Missense_Mutation	SNP	C	T	T	CAMTA1	c.4063C>T	p.P1355S
118E7632A1	1	16259091	16259091	Missense_Mutation	SNP	T	C	C	SPEN	c.6356T>C	p.V2119A
118E7632A1	1	156844702	156844702	Missense_Mutation	SNP	C	T	T	NTRK1	c.1238C>T	p.S413L
118E7632A1	10	70446106	70446106	Splice_Site	SNP	C	G	G	TET1	c.5053-7C>G	-
118E7632A1	12	25398285	25398285	Missense_Mutation	SNP	C	T	T	KRAS	c.34G>A	p.G12S
118E7632A1	12	49428067	49428067	Missense_Mutation	SNP	C	T	T	KMT2D	c.10523G>A	p.R3508Q
118E7632A1	15	99456264	99456264	Splice_Site	SNP	G	A	A	IGF1R	c.1590-9G>A	-
118E7632A1	17	29587401	29587401	Missense_Mutation	SNP	T	C	C	NF1	c.4445T>C	p.I1482T
118E7632A1	2	170063706	170063706	Missense_Mutation	SNP	C	T	T	LRP2	c.6524G>A	p.R1215Q
118E7632A1	2	198257053	198257053	Missense_Mutation	SNP	G	A	A	SF3B1	c.3889C>T	p.R1297C
118E7632A1	3	52677328	52677328	Missense_Mutation	SNP	T	C	C	PBRM1	c.931A>G	p.T311A
118E7632A1	4	55131089	55131089	Missense_Mutation	SNP	C	T	T	PDGFRA	c.632C>T	p.T211I
118E7632A1	-	-	-	In_Frame_Ins	INS	-	-	-	KIT	c.1712_1741dup	p.I571_H580dup
118E7632A1	4	153249385	153249385	Missense_Mutation	SNP	G	A	A	FBXW7	c.1393C>T	p.R465C
118E7632A1	5	112174282	112174282	Nonsense_Mutation	SNP	T	G	G	APC	c.2991T>G	p.Y997*
118E7632A1	6	117681126	117681126	Missense_Mutation	SNP	A	T	T	ROS1	c.3494T>A	p.V1165D
118E7632A1	X	47039404	47039404	Missense_Mutation	SNP	C	T	T	RBM10	c.1027C>T	p.R343C
118E7633A1	1	46740370	46740370	Missense_Mutation	SNP	A	G	G	RAD54L	c.1850A>G	p.Y617C
118E7633A1	1	59247890	59247890	Missense_Mutation	SNP	T	G	G	JUN	c.853A>C	p.K285Q
118E7633A1	11	60233587	60233587	Missense_Mutation	SNP	C	T	T	MS4A1	c.530C>T	p.S177F
118E7633A1	13	48881502	48881502	Nonsense_Mutation	SNP	G	A	A	RB1	c.224G>A	p.W75*
118E7633A1	-	-	-	Frame_Shift_Ins	INS	-	-	-	JAK3	c.2362dup	p.L788Pfs*13
118E7633A1	19	52715937	52715937	Splice_Site	SNP	A	G	G	PPP2R1A	c.504-2A>G	-
118E7633A1	4	55152030	55152030	Missense_Mutation	SNP	C	T	T	PDGFRA	c.2462C>T	p.A821V
118E7633A1	4	187557957	187557957	Missense_Mutation	SNP	T	C	C	FAT1	c.3754A>G	p.I1252V
118E7633A1	6	112035608	112035608	Missense_Mutation	SNP	G	A	A	FYN	c.286C>T	p.R96W
118E7633A1	X	48650564	48650564	Missense_Mutation	SNP	C	G	G	GATA1	c.534C>G	p.S178R
118E7744A1	12	25398284	25398284	Missense_Mutation	SNP	C	A	A	KRAS	c.35G>T	p.G12V
118E7744A1	17	7578457	7578457	Missense_Mutation	SNP	C	G	G	TP53	c.473G>C	p.R158P
118E7744A1	18	18622670	18622670	Missense_Mutation	SNP	C	T	T	ROCK1	c.676G>A	p.E226K
118E7805A1	16	9857071	9857071	Missense_Mutation	SNP	C	A	A	GRIN2A	c.4330G>T	p.V1444F
118E7805A1	17	7577121	7577121	Missense_Mutation	SNP	G	T	T	TP53	c.817C>A	p.R273S
118E7805A1	17	29677251	29677251	Nonsense_Mutation	SNP	A	T	T	NF1	c.7372A>T	p.R2458*
118E7805A1	17	38555286	38555286	Splice_Site	SNP	G	T	T	TOP2A	c.3288+6C>A	-
118E7805A1	17	74733439	74733439	Splice_Site	SNP	G	A	A	SRSF2	c.-197C>T	-
118E7805A1	6	32170300	32170300	Missense_Mutation	SNP	A	T	T	NOTCH4	c.3308T>A	p.L1103Q
118E7805A1	8	90983389	90983389	Splice_Site	SNP	T	A	A	NBN	c.702+12A>T	-
118E7868A1	12	25398281	25398281	Missense_Mutation	SNP	C	T	T	KRAS	c.38G>A	p.G13D
118E7868A1	17	7574003	7574003	Nonsense_Mutation	SNP	G	A	A	TP53	c.1024C>T	p.R342*
118E7868A1	-	-	-	Frame_Shift_Ins	INS	-	-	-	RBM10	c.931dup	p.S311Kfs*70
118E7888A1	11	22646687	22646687	Missense_Mutation	SNP	G	C	C	FANCF	c.670C>G	p.P224A
118E7888A1	11	76165796	76165796	Missense_Mutation	SNP	G	A	A	EMSY	c.249G>A	p.M83I
118E7888A1	11	92533642	92533642	Missense_Mutation	SNP	G	A	A	FAT3	c.7463G>A	p.G2488E
118E7888A1	12	57605284	57605284	Missense_Mutation	SNP	G	A	A	LRP1	c.13106G>A	p.R4369Q
118E7888A1	12	112926270	112926270	Missense_Mutation	SNP	C	T	T	PTPN11	c.1403C>T	p.T468M
118E7888A1	17	1268292	1268292	Missense_Mutation	SNP	C	G	G	YWHAE	c.125G>C	p.R42T
118E7888A1	17	7577156	7577156	Splice_Site	SNP	C	A	A	TP53	c.783-1G>T	-
118E7888A1	2	141283830	141283830	Missense_Mutation	SNP	C	G	G	LRP1B	c.7852G>C	p.D2618H
118E7888A1	3	178916836	178916836	Missense_Mutation	SNP	C	G	G	PIK3CA	c.223C>G	p.Q75E
118E7888A1	8	93003925	93003925	Nonsense_Mutation	SNP	G	T	T	RUNX1T1	c.822C>A	p.Y274*
118E7901A1	12	25398284	25398284	Missense_Mutation	SNP	C	A	A	KRAS	c.35G>T	p.G12V
118E7926A1	1	6947759	6947759	Missense_Mutation	SNP	C	A	A	CAMTA1	c.280C>A	p.P94T
118E7926A1	-	-	-	Frame_Shift_Del	INS	-	-	-	EPHA2	C.1379del	p.P460Rfs*33
118E7926A1	1	158612617	158612617	Missense_Mutation	SNP	G	A	A	SPTA1	c.4592C>T	p.A1531V
118E7926A1	-	-	-	Frame_Shift_Ins	INS	-	-	-	ABL2	c.1500dup	p.G501Rfs*8
118E7926A1	1	202710606	202710606	Missense_Mutation	SNP	C	A	A	KDM5B	c.2942G>T	p.G981V
118E7926A1	-	-	-	Splice_Site	SNP	-	-	-	ARID2	c.5364-5del	-
118E7926A1	12	49428423	49428423	Missense_Mutation	SNP	C	A	A	KMT2D	c.10382G>T	p.R3461M
118E7926A1	-	-	-	Frame_Shift_Del	INS	-	-	-	LRP1	C.12750del	p.S4251Lfs*91
118E7926A1	13	28623626	28623626	Missense_Mutation	SNP	G	A	A	FLT3	c.931C>T	p.R311W
118E7926A1	15	99467241	99467241	Missense_Mutation	SNP	G	T	T	IGF1R	c.2622G>T	p.E874D
118E7926A1	16	3778512	3778512	Missense_Mutation	SNP	T	C	C	CREBBP	c.6536A>G	p.N2179S
118E7926A1	16	50783930	50783930	Missense_Mutation	SNP	G	T	T	CYLD	c.321G>C	p.E107D
118E7926A1	17	7578406	7578406	Missense_Mutation	SNP	C	T	T	TP53	c.524G>A	p.R175H
118E7926A1	-	-	-	Frame_Shift_Del	INS	-	-	-	TP53	C.102del	p.L35Cfs*9
118E7926A1	-	-	-	Frame_Shift_Del	INS	-	-	-	NF1	C.2033del	p.P678Rfs*10
118E7926A1	17	78936362	78936362	Missense_Mutation	SNP	C	T	T	RPTOR	c.3794C>T	p.A1265V
118E7926A1	18	48575185	48575185	Missense_Mutation	SNP	T	C	C	SMAD4	c.379T>C	p.C127R
118E7926A1	19	30308407	30308407	Nonsense_Mutation	SNP	C	T	T	CCNE1	c.421C>T	p.Q141*
118E7926A1	-	-	-	Splice_Site	SNP	-	-	-	RANBP2	c.141-4dup	-
118E7926A1	2	121743882	121743882	Missense_Mutation	SNP	C	T	T	GLI2	c.1985C>T	p.S662L
118E7926A1	2	209113113	209113113	Missense_Mutation	SNP	G	A	A	IDH1	c.394C>T	p.R132C
118E7926A1	20	31023957	31023957	Missense_Mutation	SNP	C	T	T	ASXL1	c.3442C>T	p.R1148C
118E7926A1	20	57484420	57484420	Missense_Mutation	SNP	C	A	A	GNAS	c.601C>A	p.R201S
118E7926A1	-	-	-	Frame_Shift_Ins	INS	-	-	-	PBRM1	C.773dup	p.N258Kfs*6
118E7926A1	3	142269129	142269129	Missense_Mutation	SNP	G	T	T	ATR	c.2821C>A	p.L941I
118E7926A1	-	-	-	Frame_Shift_Del	INS	-	-	-	PRKCI	C.826del	p.T276Qfs*7
118E7926A1	-	-	-	Frame_Shift_Ins	INS	-	-	-	MAP3K13	c.1603dup	p.R535Kfs*45
118E7926A1	-	-	-	Splice_Site	SNP	-	-	-	SLIT2	c.1439-7del	-
118E7926A1	5	149513557	149513557	Missense_Mutation	SNP	C	T	T	PDGFRB	c.646G>A	p.V216I
118E7926A1	7	18684405	18684405	Missense_Mutation	SNP	T	A	A	HDAC9	c.1015T>A	p.S339T
118E7926A1	8	68864646	68864646	Missense_Mutation	SNP	G	A	A	PREX2	c.17G>A	p.R6H
118E7940A1	16	89851304	89851304	Missense_Mutation	SNP	G	C	C	FANCA	c.1428C>G	p.F476L
118E7940A1	17	15995380	15995380	Splice_Site	SNP	A	G	G	NCOR1	c.2821-8T>C	-
118E7940A1	19	41727824	41727824	Missense_Mutation	SNP	T	C	C	AXL	c.449T>C	p.V150A
118E7940A1	9	133760532	133760532	Missense_Mutation	SNP	G	A	A	ABL1	c.2912G>A	p.G971E
118E7964A1	10	89725215	89725215	Missense_Mutation	SNP	A	C	C	PTEN	c.1198A>C	p.I400L
118E7964A1	-	-	-	Frame_Shift_Del	INS	-	-	-	KMT2A	c.2641_2642del	p.E881Kfs*4
118E7964A1	12	133218777	133218777	Missense_Mutation	SNP	C	A	A	POLE	c.5159G>T	p.G1720V
118E7964A1	-	-	-	Splice_Site	SNP	-	-	-	NUP93	2349_2349+1d	-
118E7964A1	17	7577581	7577581	Missense_Mutation	SNP	A	G	G	TP53	c.700T>C	p.Y234H
118E7964A1	-	-	-	Frame_Shift_Del	INS	-	-	-	GNAI3	c.134_135del	p.V45Efs*56
118E7964A1	-	-	-	Frame_Shift_Del	INS	-	-	-	SMAD4	c.1558_1561del	p.E520Hfs*16
118E7964A1	19	10610224	10610224	Nonsense_Mutation	SNP	G	C	C	KEAP1	c.486C>G	p.Y162*
118E7964A1	2	198266713	198266713	Missense_Mutation	SNP	C	A	A	SF3B1	c.2219G>T	p.G740V
118E7964A1	-	-	-	Missense_Mutation	SNP	-	-	-	EP300	c.4357_4359del	p.P1453del
118E7964A1	3	134967244	134967244	Missense_Mutation	SNP	G	C	C	EPHB1	2583G>C;2590G	[W861C;D864H]
118E7964A1	3	185774956	185774956	Missense_Mutation	SNP	A	G	G	ETV5	c.1117T>C	p.F373L

118E7964A1		-	-	Frame_Shift_Del	INS	-	-	-	SDHA	c.1583_1584de	p.V528Gfs*74
118E7964A1		-	-	Frame_Shift_Del	INS	-	-	-	APC	c.7724_7725de	p.S2575Cfs*7
118E7964A1		-	-	Frame_Shift_Del	INS	-	-	-	NSD1	c.3539_3540de	p.K1180Rfs*4
118E7964A1	6	41904310	41904310	Missense_Mutation	SNP	G	A	A	CCND3	c.698C>T	p.T231I
118E7964A1		-	-	Frame_Shift_Del	INS	-	-	-	KMT2C	c.3176_3177de	p.H1059Lfs*11
118E7964A1		-	-	Frame_Shift_Del	INS	-	-	-	CDKN2A	C.47_50del	p.L16Pfs*9
118E7982A2	1	8074337	8074337	Missense_Mutation	SNP	C	T	T	ERRFI1	c.322G>A	p.E108K
118E7982A2	1	110466159	110466159	Missense_Mutation	SNP	G	A	A	CSF1	c.916G>A	p.E306K
118E7982A2	11	118348894	118348894	Missense_Mutation	SNP	A	C	C	KMT2A	3547A>C;3554A	N1183H;K1185M
118E7982A2		-	-	Frame_Shift_Del	INS	-	-	-	RB1	c.1252del	p.R418Efs*2
118E7982A2	14	45639831	45639831	Missense_Mutation	SNP	C	T	T	FANCM	c.2042C>T	p.S681L
118E7982A2	17	29664885	29664885	Missense_Mutation	SNP	G	A	A	NF1	c.6691G>A	p.E2231K
118E7982A2		-	-	Frame_Shift_Ins	INS	-	-	-	MSH6	c.3261dup	p.F1088Lfs*5
118E7982A2		-	-	Frame_Shift_Del	INS	-	-	-	ACVR2A	c.338del	p.K113Sfs*37
118E7982A2	4	126242661	126242661	Missense_Mutation	SNP	G	C	C	FAT4	c.5095G>C	p.E1699Q
118E7982A2	4	153245404	153245404	Missense_Mutation	SNP	G	A	A	FBXW7	c.1787C>T	p.S596F
118E7982A2		-	-	Missense_Mutation	SNP	-	-	-	FBXW7	c.1423_1425de	p.V475del
118E7982A2	6	36652071	36652071	Missense_Mutation	SNP	T	C	C	CDKN1A	c.193T>C	p.W65R
118E7982A2	8	141727804	141727804	Missense_Mutation	SNP	T	C	C	PTK2	c.2101A>G	p.I701V
118F7997A1	1	120471692	120471692	Missense_Mutation	SNP	C	T	T	NOTCH2	c.3799G>A	p.E1267K
118F7997A1	11	108235809	108235809	Missense_Mutation	SNP	G	C	C	ATM	c.8851G>C	p.V2951L
118F7997A1	12	25398284	25398284	Missense_Mutation	SNP	C	G	G	KRAS	c.35G>C	p.G12A
118F7997A1	2	141264356	141264356	Splice_Site	SNP	T	G	G	LRP1B	c.8521+9A>C	-
118F7997A1	3	142261571	142261571	Missense_Mutation	SNP	C	G	G	ATR	c.3386G>C	p.G1129A
118F8082A1	12	25398281	25398281	Missense_Mutation	SNP	C	T	T	KRAS	c.38G>A	p.G13D
118F8082A1	17	7577058	7577058	Nonsense_Mutation	SNP	C	A	A	TP53	c.880G>T	p.E294*
118F8082A1		-	-	Frame_Shift_Ins	INS	-	-	-	SMAD4	c.221dup	p.Q75Tfs*29
118F8090A1	1	9784994	9784994	Missense_Mutation	SNP	G	A	A	PIK3CD	c.2997G>A	p.K999K
118F8090A1	12	4409117	4409117	Missense_Mutation	SNP	C	T	T	CCND2	c.812C>T	p.S271L
118F8090A1	12	25398284	25398284	Missense_Mutation	SNP	C	T	T	KRAS	c.35G>A	p.G12D
118F8090A1	17	7577551	7577551	Missense_Mutation	SNP	C	A	A	TP53	c.730G>T	p.G244C
118F8090A1	18	48593558	48593558	Splice_Site	SNP	G	T	T	SMAD4	c.1308+1G>T	-
118F8094A1	12	25398285	25398285	Missense_Mutation	SNP	C	G	G	KRAS	c.34G>C	p.G12R
118F8094A1	13	29005422	29005422	Missense_Mutation	SNP	C	T	T	FLT1	c.839G>A	p.R280Q
118F8094A1	17	7578406	7578406	Missense_Mutation	SNP	C	T	T	TP53	c.524G>A	p.R175H
118F8094A1	7	151949114	151949114	Nonsense_Mutation	SNP	C	A	A	KMT2C	c.1531G>T	p.E511*
118F8094A1	9	21971077	21971077	Missense_Mutation	SNP	A	T	T	CDKN2A	c.281T>A	p.L94Q
118F8096A1		-	-	Frame_Shift_Ins	INS	-	-	-	TP53	C.750dup	P.1251Hfs*13
118F8096A1		-	-	Frame_Shift_Del	INS	-	-	-	TGFBFR1	c.1347_1350de	p.L450Gfs*14
118F8114A1		-	-	Missense_Mutation	SNP	-	-	-	TP53	c.321_323del	p.G108del
118F8114A1		-	-	Missense_Mutation	SNP	-	-	-	EPHA5	948_2949delins	p.T983N
118F8114A1		-	-	Frame_Shift_Ins	INS	-	-	-	FBXW7	c.1463_1466dup	p.E489Dfs*2
118F8114A1	6	32188062	32188062	Splice_Site	SNP	C	T	T	NOTCH4	c.1160-1G>A	-
118F8114A1	8	128751112	128751112	Missense_Mutation	SNP	A	G	G	MYC	c.649A>G	p.S217G
118F8152A1	12	52374741	52374741	Splice_Site	SNP	T	C	C	ACVR1B	c.581-12T>C	-
118F8152A1	3	37067240	37067240	Missense_Mutation	SNP	T	A	A	MLH1	c.1151T>A	p.V384D
118F8152A1	3	89390226	89390226	Splice_Site	SNP	G	A	A	EPHA3	c.970+5G>A	-
118F8152A1		-	-	Frame_Shift_Del	INS	-	-	-	CDKN2A	C.47_50del	p.L16Pfs*9
118F8157A1	11	108128226	108128226	Nonsense_Mutation	SNP	G	T	T	ATM	c.2269G>T	p.G757*
118F8157A1	17	16004563	16004563	Splice_Site	SNP	C	A	A	NCOR1	c.2690+1G>T	-
118F8167A1	3	30713760	30713760	Missense_Mutation	SNP	A	G	G	TGFBFR2	c.1085A>G	p.H362R
118F8167A1		-	-	Frame_Shift_Del	INS	-	-	-	BAP1	c.421del	p.H141Lfs*46
118F8167A1	7	77789586	77789586	Missense_Mutation	SNP	C	A	A	MAGI2	c.2601G>T	p.E867D
118F8170A1		-	-	Frame_Shift_Ins	INS	-	-	-	TP53	c.131_132insA	p.M44Lfs*8
118F8170A1	17	56435317	56435317	Missense_Mutation	SNP	G	A	A	RNF43	c.1820C>T	p.S607L
118F8170A1	19	10610618	10610618	Missense_Mutation	SNP	A	G	G	KEAP1	c.92T>C	p.V31A
118F8170A1	2	170068570	170068570	Missense_Mutation	SNP	G	T	T	LRP2	c.6188C>A	p.S2063Y
118F8170A1		-	-	Frame_Shift_Del	INS	-	-	-	BAP1	c.2129_2142de	p.H710Pfs*2
118F8170A1		-	-	In_Frame_Del	INS	-	-	-	PRKDC	c.11736del	p.C3912*
118F8189A1	17	7578557	7578557	Splice_Site	SNP	G	C	C	TP53	c.376-3C>G	-
118F8201A1	20	57485805	57485805	Missense_Mutation	SNP	C	T	T	GNAS	c.1106C>T	p.T369I
118F8201A1		-	-	Frame_Shift_Del	INS	-	-	-	BAP1	c.97_106del	p.Y33Rfs*36
118F8208A1	11	92086588	92086588	Missense_Mutation	SNP	C	A	A	FAT3	c.1310C>A	p.T437N
118F8208A1	11	108196235	108196235	Missense_Mutation	SNP	A	C	C	ATM	c.6771A>C	p.E2257D
118F8208A1	12	25398284	25398284	Missense_Mutation	SNP	C	T	T	KRAS	c.35G>A	p.G12D
118F8208A1	17	7577094	7577094	Missense_Mutation	SNP	G	A	A	TP53	c.844C>T	p.R282W
118F8208A1		-	-	In_Frame_Ins	INS	-	-	-	ZNF703	c.58_69dup	p.S20_G23dup
118F8237A1	1	158584994	158584994	Splice_Site	SNP	C	T	T	SPTA1	c.6788+12G>A	-
118F8237A1	12	25398281	25398281	Missense_Mutation	SNP	C	T	T	KRAS	c.38G>A	p.G13D
118F8237A1	17	7578406	7578406	Missense_Mutation	SNP	C	T	T	TP53	c.524G>A	p.R175H
118F8237A1	18	48593505	48593505	Missense_Mutation	SNP	G	C	C	SMAD4	c.1256G>C	p.G419A
118F8237A1	19	1220649	1220649	Missense_Mutation	SNP	G	A	A	STK11	c.667G>A	p.E223K
118F8237A1	2	61706035	61706035	Missense_Mutation	SNP	C	T	T	XP01	c.3136G>A	p.D1046N
118F8237A1	22	29092948	29092948	Missense_Mutation	SNP	G	A	A	CHEK2	c.1036C>T	p.R346C
118F8237A1	3	187446190	187446190	Nonsense_Mutation	SNP	C	A	A	BCL6	c.1498G>T	p.E500*
118F8237A1	5	112162891	112162891	Nonsense_Mutation	SNP	C	T	T	APC	c.1495C>T	p.R499*
118F8276A1	12	25378562	25378562	Missense_Mutation	SNP	C	G	G	KRAS	c.436G>C	p.A146P
118F8276A1	17	7576852	7576852	Splice_Site	SNP	C	T	T	TP53	c.993+1G>A	-
118F8276A1	19	4117549	4117549	Missense_Mutation	SNP	A	C	C	MAP2K2	c.171T>G	p.F57L
118F8276A1	19	15296082	15296082	Missense_Mutation	SNP	G	A	A	NOTCH3	c.2282C>T	p.P761L
118F8276A1	3	30664717	30664717	Missense_Mutation	SNP	G	A	A	TGFBFR2	c.121G>A	p.E41K
118F8372A1	1	158606546	158606546	Missense_Mutation	SNP	T	G	G	SPTA1	c.5195A>C	p.K1732T
118F8372A1		-	-	In_Frame_Del	INS	-	-	-	TP53	c.471_518del	p.A159_R174del
118F8372A1	19	11135028	11135028	Missense_Mutation	SNP	G	A	A	SMARCA4	c.2995G>A	p.D999N
118F8372A1		-	-	Splice_Site	SNP	-	-	-	RUNX1	59-12_59-11de	-
118F8372A1	3	138665289	138665289	Missense_Mutation	SNP	C	G	G	FOXL2	c.276G>C	p.E92D
118F8377A1	12	46287315	46287315	Nonsense_Mutation	SNP	C	T	T	ARID2	c.5260C>T	p.R1754*
118F8377A1	17	7577099	7577099	Missense_Mutation	SNP	C	T	T	TP53	c.839G>A	p.R280K
118F8377A1	18	739820	739820	Splice_Site	SNP	G	A	A	YES1	c.1061-9C>T	-
118F8377A1		-	-	Frame_Shift_Del	INS	-	-	-	KEAP1	c.1626_1627de	p.E542Dfs*31
118F8377A1	19	42796446	42796446	Splice_Site	SNP	C	T	T	CIC	c.3009-6C>T	-
118F8377A1	2	142004783	142004783	Splice_Site	SNP	G	A	A	LRP1B	c.592+12C>T	-
118F8377A1	4	153273928	153273928	Splice_Site	SNP	G	C	C	FBXW7	c.46C>G	-
118F8377A1	8	71068319	71068319	Missense_Mutation	SNP	C	T	T	NCOA2	c.2281G>A	p.E761K
118F8377A1	9	5126352	5126352	Missense_Mutation	SNP	G	A	A	JAK2	c.3197G>A	p.G1066D
118F8392A1	11	118355614	118355614	Missense_Mutation	SNP	G	T	T	KMT2A	c.4256G>T	p.G1419V
118F8392A1	12	25380275	25380275	Missense_Mutation	SNP	T	G	G	KRAS	c.183A>C	p.Q61H
118F8392A1		-	-	Frame_Shift_Ins	INS	-	-	-	STK11	c.157_158insT	p.D53Vfs*110

118F8415A1	1	27094361	27094361	Nonsense_Mutation	SNP	G	A	A	ARID1A	c.3069G>A	p.W1023*
118F8415A1	12	49444878	49444878	Missense_Mutation	SNP	C	A	A	KMT2D	c.2588G>T	p.R863L
118F8415A1	13	41134822	41134822	Missense_Mutation	SNP	C	T	T	FOXO1	c.806G>A	p.R269Q
118F8415A1	17	7577548	7577548	Missense_Mutation	SNP	C	T	T	TP53	c.733G>A	p.G245S
118F8415A1		-	-	Frame_Shift_Del	INS	-	-	-	SMAD4	c.793del	p.T265Lfs*71
118F8415A1	2	198299719	198299719	Missense_Mutation	SNP	G	A	A	SF3B1	c.5C>T	p.A2V
118F8415A1		-	-	Frame_Shift_Del	INS	-	-	-	PBRM1	c.2581del	p.I861Yfs*6
118F8415A1	7	2987341	2987341	Missense_Mutation	SNP	G	A	A	CARD11	c.88C>T	p.R30W
118F8415A1	7	151845790	151845790	Missense_Mutation	SNP	C	G	G	KMT2C	c.13222G>C	p.E4408Q
118F8458A1	1	158613185	158613185	Missense_Mutation	SNP	C	T	T	SPTA1	c.4369G>A	p.A1457T
118F8458A1	12	465645	465645	Missense_Mutation	SNP	G	A	A	KDM5A	c.731C>T	p.A244V
118F8458A1	12	49422858	49422858	Missense_Mutation	SNP	C	T	T	KMT2D	c.14237G>A	p.R4746Q
118F8458A1		-	-	Frame_Shift_Del	INS	-	-	-	KMT2D	c.5956del	p.T1986Pfs*61
118F8458A1	12	57863295	57863295	Missense_Mutation	SNP	G	T	T	GLI1	c.1267G>T	p.G423C
118F8458A1		-	-	Frame_Shift_Ins	INS	-	-	-	POLE	c.382dup	p.I128Nfs*76
118F8458A1	13	32953610	32953610	Missense_Mutation	SNP	A	G	G	BRCA2	c.8911A>G	p.K2971E
118F8458A1	13	110435825	110435825	Missense_Mutation	SNP	G	A	A	IRS2	c.2576C>T	p.T859M
118F8458A1	15	75093027	75093027	Missense_Mutation	SNP	T	C	C	CSK	c.562T>C	p.W188R
118F8458A1		-	-	Missense_Mutation	SNP	-	-	-	TP53	c.572_574del	p.P191del
118F8458A1		-	-	Frame_Shift_Ins	INS	-	-	-	MAP2K4	c.69dup	p.V24Rfs*17
118F8458A1		-	-	Missense_Mutation	SNP	-	-	-	GATA6	c.134_136del	p.S45del
118F8458A1	19	10610256	10610256	Missense_Mutation	SNP	C	T	T	KEAP1	c.454G>A	p.V152I
118F8458A1	19	15298722	15298722	Missense_Mutation	SNP	G	A	A	NOTCH3	c.1576C>T	p.P526S
118F8458A1		-	-	Splice_Site	SNP	-	-	-	CIC	176-14_3176-12	-
118F8458A1	2	16086115	16086115	Missense_Mutation	SNP	C	T	T	MYCN	c.1291C>T	p.H431Y
118F8458A1		-	-	Frame_Shift_Del	INS	-	-	-	ACVR2A	C.36_39del	p.F12Lfs*61
118F8458A1	2	170060692	170060692	Missense_Mutation	SNP	C	T	T	LRP2	c.7805G>A	p.G2602D
118F8458A1	22	41556665	41556665	Missense_Mutation	SNP	T	C	C	EP300	c.3610T>C	p.C1204R
118F8458A1	3	38182308	38182308	Missense_Mutation	SNP	C	T	T	MYD88	c.428C>T	p.S143F
118F8458A1	3	191888366	191888366	Missense_Mutation	SNP	C	T	T	FGF12	c.308G>A	p.R103H
118F8458A1	5	112176515	112176515	Missense_Mutation	SNP	C	A	A	APC	c.5224C>A	p.R1742S
118F8458A1	5	138269729	138269729	Missense_Mutation	SNP	T	C	C	CTNNA1	c.2672T>C	p.V891A
118F8458A1	6	106536126	106536126	Missense_Mutation	SNP	G	T	T	PRDM1	c.93G>T	p.E31D
118F8458A1	7	41729607	41729607	Missense_Mutation	SNP	G	A	A	INHBA	c.922C>T	p.R308C
118F8458A1		-	-	Frame_Shift_Del	INS	-	-	-	NRG1	c.472del	p.A158Rfs*5
118F8458A1	8	71068513	71068513	Missense_Mutation	SNP	T	C	C	NCOA2	c.2087A>G	p.D696G
118F8458A1	9	93624559	93624559	Missense_Mutation	SNP	G	A	A	SYK	c.650G>A	p.R217H
118F8458A1	9	93639919	93639919	Missense_Mutation	SNP	G	T	T	SYK	c.1179G>T	p.E393D
118F8458A1	9	137300076	137300076	Missense_Mutation	SNP	G	A	A	RXRA	c.361G>A	p.A121T
118F8458A1	X	66943638	66943638	Missense_Mutation	SNP	G	T	T	AR	c.2718G>T	p.K906N
118F8489A1	17	29541460	29541460	Splice_Site	SNP	T	A	A	NF1	c.1393-9T>A	-
118F8522A1		-	-	Frame_Shift_Del	INS	-	-	-	PTEN	c.219_222del	p.E730fs*25
118F8522A1		-	-	Splice_Site	SNP	-	-	-	PBRM1	1302-29_1313d	-
118F8522A1	6	41909260	41909260	Missense_Mutation	SNP	G	A	A	CCND3	c.128C>T	p.S43F
118F8522A1	7	151864290	151864290	Missense_Mutation	SNP	C	A	A	KMT2C	c.9691G>T	p.A3231S
118F8546A1	17	7577121	7577121	Missense_Mutation	SNP	G	A	A	TP53	c.817C>T	p.R273C
118F8546A1		-	-	Missense_Mutation	SNP	-	-	-	TP53	c.787_789del	p.N263del
118F8546A1	4	187629400	187629400	Missense_Mutation	SNP	C	T	T	FAT1	c.1582G>A	p.E528K
118F8546A1	7	116412023	116412023	Missense_Mutation	SNP	A	T	T	MET	c.3008A>T	p.Y1003F
118F8558A1	15	88679244	88679244	Missense_Mutation	SNP	C	T	T	NTRK3	c.793G>A	p.A265T
118F8558A1	17	7577518	7577518	Missense_Mutation	SNP	T	A	A	TP53	c.763A>T	p.I255F
118F8558A1	17	56437614	56437614	Splice_Site	SNP	T	C	C	RNF43	c.850-2A>G	-
118F8558A1	5	67591128	67591128	Missense_Mutation	SNP	G	C	C	PIK3R1	1721G>C;1730Gp.[R574T];R577K	-
118F8558A1	7	42004379	42004379	Missense_Mutation	SNP	G	A	A	GLI3	c.4292C>T	p.P1431L
118F8558A1	7	140453154	140453154	Missense_Mutation	SNP	T	C	C	BRAF	c.1781A>G	p.D594G
118F8601A1	4	55946274	55946274	Missense_Mutation	SNP	G	A	A	KDR	c.3905C>T	p.T1302I
118F8601A1	9	101904982	101904982	Nonsense_Mutation	SNP	C	T	T	TGFB1	c.970C>T	p.Q324*
118F8601A1		-	-	Frame_Shift_Del	INS	-	-	-	RBM10	c.1998del	p.E667Kfs*37
118F8632A1	12	49421846	49421846	Nonsense_Mutation	SNP	C	A	A	KMT2D	c.14461G>T	p.E4821*
118F8632A1	12	133250284	133250284	Missense_Mutation	SNP	C	G	G	POLE	c.1236G>C	p.K412N
118F8632A1	17	7578550	7578550	Missense_Mutation	SNP	G	A	A	TP53	c.380C>T	p.S127F
118F8632A1	19	11144113	11144113	Missense_Mutation	SNP	G	T	T	SMARCA4	3694G>T;3695G	p.G1232F
118F8632A1	6	112015871	112015871	Missense_Mutation	SNP	C	G	G	FYN	c.1079G>C	p.R360T
118F8632A1	7	18788726	18788726	Nonsense_Mutation	SNP	C	T	T	HDAC9	c.1999C>T	p.R667*
118F8646A1	12	25398284	25398284	Missense_Mutation	SNP	C	T	T	KRAS	c.35G>A	p.G12D
118F8646A1	13	110435910	110435910	Missense_Mutation	SNP	C	T	T	IRS2	c.2491G>A	p.G831R
118F8646A1		-	-	In_Frame_Ins	INS	-	-	-	SOX9	c.1089_1109dup	p.A371_P377dup
118F8646A1		-	-	Frame_Shift_Del	INS	-	-	-	STK11	c.787_790del	p.F264Rfs*22
118F8646A1	19	15288644	15288644	Missense_Mutation	SNP	C	G	G	NOTCH3	c.4095G>C	p.Q1365H
118F8646A1	5	112178000	112178000	Nonsense_Mutation	SNP	C	T	T	APC	c.6709C>T	p.R2237*
118F8770A1	11	118361941	118361941	Missense_Mutation	SNP	A	G	G	KMT2A	c.4727A>G	p.Y1576C
118F8770A1	12	25398284	25398284	Missense_Mutation	SNP	C	A	A	KRAS	c.35G>T	p.G12V
118F8770A1	12	57598946	57598946	Missense_Mutation	SNP	G	A	A	LRP1	c.11249G>A	p.R3750Q
118F8792A1		-	-	Missense_Mutation	SNP	-	-	-	FGFR2	c.1635_1637del	p.K545del
118F8792A1	3	10114944	10114944	Missense_Mutation	SNP	A	C	C	FANCD2	c.2613A>C	p.K871N
118F8792A1	3	52441430	52441430	Missense_Mutation	SNP	T	C	C	BAP1	c.422A>G	p.H141R
118F8797A1	10	89720649	89720649	Splice_Site	SNP	A	G	G	PTEN	c.802-2A>G	-
118F8797A1	13	48934234	48934234	Nonsense_Mutation	SNP	C	A	A	RB1	c.689C>A	p.S230*
118F8797A1	14	45645216	45645216	Nonsense_Mutation	SNP	A	T	T	FANCM	c.3259A>T	p.K1087*
118F8797A1	17	7577120	7577120	Missense_Mutation	SNP	C	T	T	TP53	c.818G>A	p.R273H
118F8797A1	17	29562760	29562760	Missense_Mutation	SNP	G	T	T	NF1	c.3840G>T	p.I1280F
118F8797A1	2	25523034	25523034	Missense_Mutation	SNP	G	A	A	DNMT3A	c.151C>T	p.P51S
118F8797A1	4	1953960	1953960	Splice_Site	SNP	C	T	T	NSD2	c.2137+2C>T	-
118F8797A1		-	-	Frame_Shift_Del	INS	-	-	-	RICTOR	c.3655del	p.S1219Vfs*11
118F8797A1	6	93974325	93974325	Missense_Mutation	SNP	T	A	A	EPHA7	c.1729A>T	p.I577F
118F8797A1	8	48767810	48767810	Nonsense_Mutation	SNP	-	-	-	PRKDC	c.6733A>T	p.K2245*
118F8797A1	X	129150082	129150082	Nonsense_Mutation	SNP	G	T	T	BCORL1	c.3334G>T	p.E1112*
118F8813A2		-	-	Frame_Shift_Del	INS	-	-	-	ARID1A	c.229del	p.A77Pfs*24
118F8813A2	11	92534248	92534248	Missense_Mutation	SNP	C	T	T	FAT3	c.8069C>T	p.S2690F
118F8813A2	12	46123909	46123909	Nonsense_Mutation	SNP	G	T	T	ARID2	c.175G>T	p.G59*
118F8813A2	17	7578440	7578440	Nonsense_Mutation	SNP	T	A	A	TP53	c.490A>T	p.K164*
118F8813A2	18	48575209	48575209	Nonsense_Mutation	SNP	C	T	T	SMAD4	c.403C>T	p.R135*
118F8813A2	3	49397721	49397721	Missense_Mutation	SNP	C	G	G	RHOA	c.503G>C	p.R168T
118F8813A2	3	49412969	49412969	Missense_Mutation	SNP	C	A	A	RHOA	c.54G>T	p.K18N
118F8813A2	3	191888403	191888403	Nonsense_Mutation	SNP	C	A	A	FGF12	c.271G>T	p.E91*
118F8813A2	5	161116166	161116166	Missense_Mutation	SNP	A	T	T	GABRA6	c.437A>T	p.Y146F
118F8813A2	8	32472087	32472087	Splice_Site	SNP	G	T	T	NRG1	c.451+5G>T	-
118F8844A1	1	16475389	16475389	Missense_Mutation	SNP	G	A	A	EPHA2	c.307C>T	p.R103C

118F8844A1	12	46246290	46246290	Nonsense_Mutation	SNP	C	T	T	ARID2	c.4384C>T	p.Q1462*
118F8844A1	12	57559938	57559938	Missense_Mutation	SNP	G	A	A	LRP1	c.2743G>A	p.D915N
118F8844A1	16	9943686	9943686	Missense_Mutation	SNP	C	T	T	GRIN2A	c.1255G>A	p.V419M
118F8844A1	17	38556655	38556655	Missense_Mutation	SNP	T	-	C	TOP2A	c.2806A>G	p.T936E
118F8844A1	3	178952074	178952074	Missense_Mutation	SNP	G	A	A	PIK3CA	c.3129G>A	p.M1043I
118F8844A1	5	225600	225600	Missense_Mutation	SNP	G	A	A	SDHA	c.379G>A	p.V127M
118F8844A1	5	176707786	176707786	Missense_Mutation	SNP	G	A	A	NSD1	c.5843G>A	p.R1948H
118F8850A1	1	16256981	16256981	Missense_Mutation	SNP	C	T	T	SPEN	c.4246C>T	p.R1416C
118F8850A1	-	-	-	Frame_Shift_Del	INS	-	-	-	ARID1A	C.827del	P.G276Efs*87
118F8850A1	1	43777462	43777462	Missense_Mutation	SNP	G	A	A	TIE1	c.1454G>A	p.R485Q
118F8850A1	1	162722894	162722894	Missense_Mutation	SNP	G	A	A	DDR2	c.92G>A	p.R31H
118F8850A1	1	202718170	202718170	Missense_Mutation	SNP	G	A	A	KDM5B	c.2027C>T	p.A676V
118F8850A1	10	8100645	8100645	Missense_Mutation	SNP	G	A	A	GATA3	c.619G>A	p.A207T
118F8850A1	11	92532114	92532114	Missense_Mutation	SNP	G	A	A	FAT3	c.5935G>A	p.G1979S
118F8850A1	11	108115753	108115753	Missense_Mutation	SNP	G	A	A	ATM	c.901G>A	p.G301S
118F8850A1	11	118365088	118365088	Missense_Mutation	SNP	G	A	A	KMT2A	c.5264G>A	p.S1755N
118F8850A1	-	-	-	Frame_Shift_Del	INS	-	-	-	KMT2D	C.7548del	P.N2517fs*26
118F8850A1	-	-	-	Frame_Shift_Ins	INS	-	-	-	LRP1	C.12575dup	P.D4193Rfs*9
118F8850A1	12	133245212	133245212	Splice_Site	SNP	G	A	A	POLE	c.2026+9C>T	-
118F8850A1	13	110436318	110436318	Missense_Mutation	SNP	C	T	T	IRS2	c.2083G>A	p.A695T
118F8850A1	15	88576153	88576153	Missense_Mutation	SNP	C	T	T	NTRK3	c.1520G>A	p.R507H
118F8850A1	-	-	-	Frame_Shift_Del	INS	-	-	-	CHD2	C.4173del	P.K1391Nfs*15
118F8850A1	16	9858165	9858165	Missense_Mutation	SNP	T	C	C	GRIN2A	c.3236A>G	p.N1079S
118F8850A1	-	-	-	Frame_Shift_Ins	INS	-	-	-	NF1	C.2033dup	P.I679Dfs*21
118F8850A1	-	-	-	Frame_Shift_Del	INS	-	-	-	NF1	C.7626_7627de	P.S2543Ffs*2
118F8850A1	17	37864598	37864598	Missense_Mutation	SNP	G	A	A	ERBB2	c.250G>A	p.V84M
118F8850A1	17	41267752	41267752	Missense_Mutation	SNP	A	T	T	BRCA1	[125T>A;127T>A]	p.[I42K;F43I]
118F8850A1	17	80789063	80789063	Missense_Mutation	SNP	G	A	A	ZNF750	c.1268C>T	p.T423M
118F8850A1	18	42643239	42643239	Missense_Mutation	SNP	G	A	A	SETBP1	c.4367G>A	p.R1456H
118F8850A1	19	15375253	15375253	Missense_Mutation	SNP	C	T	T	BRD4	c.1174G>A	p.D392N
118F8850A1	19	40746008	40746008	Missense_Mutation	SNP	C	T	T	AKT2	c.583G>A	p.A195T
118F8850A1	19	50905635	50905635	Splice_Site	SNP	G	A	A	POLD1	c.758+5G>A	-
118F8850A1	-	-	-	Frame_Shift_Del	INS	-	-	-	MSH2	c.473_474del	p.R159Tfs*18
118F8850A1	-	-	-	Frame_Shift_Ins	INS	-	-	-	TET3	C.5243dup	P.T1749Hfs*5
118F8850A1	2	121746027	121746027	Missense_Mutation	SNP	C	T	T	GLI2	c.2537C>T	p.P846L
118F8850A1	2	202150030	202150030	Nonsense_Mutation	SNP	C	T	T	CASP8	c.1345C>T	p.R449*
118F8850A1	-	-	-	Frame_Shift_Ins	INS	-	-	-	CASP8	C.1470dup	P.L491Tfs*6
118F8850A1	-	-	-	Frame_Shift_Ins	INS	-	-	-	ASXL1	C.1934dup	P.G646Wfs*12
118F8850A1	-	-	-	Frame_Shift_Del	INS	-	-	-	TGFBF2	c.717_718del	p.E240Afs*5
118F8850A1	-	-	-	Frame_Shift_Del	INS	-	-	-	PBRM1	C.2727del	P.K909Nfs*6
118F8850A1	3	170015091	170015091	Splice_Site	SNP	G	T	T	PRKCI	c.1498-1G>T	-
118F8850A1	5	1279521	1279521	Missense_Mutation	SNP	C	T	T	TERT	c.2015G>A	p.R672H
118F8850A1	-	-	-	Frame_Shift_Del	INS	-	-	-	APC	C.1742del	P.K581Rfs*9
118F8850A1	7	18975437	18975437	Missense_Mutation	SNP	G	A	A	HDAC9	c.2800G>A	p.G934S
118F8850A1	7	117250697	117250697	Missense_Mutation	SNP	A	G	G	CFTR	c.3113A>G	p.Q1038R
118F8850A1	7	151873322	151873322	Missense_Mutation	SNP	C	T	T	KMT2C	c.9216G>A	p.KM307I
118F8850A1	8	11607696	11607696	Missense_Mutation	SNP	A	G	G	GATA4	c.860A>G	p.E287G
118F8850A1	8	31498051	31498051	Missense_Mutation	SNP	G	A	A	NRG1	c.551G>A	p.R184H
118F8850A1	8	32505822	32505822	Missense_Mutation	SNP	C	T	T	NRG1	c.586C>T	p.R196W
118F8850A1	8	41790777	41790777	Missense_Mutation	SNP	G	A	A	KAT6A	c.4961C>T	p.P1654L
118F8850A1	8	42220198	42220198	Missense_Mutation	SNP	G	T	T	POLB	c.690G>T	p.K230N
118F8850A1	8	95419766	95419766	Missense_Mutation	SNP	A	G	G	RAD54B	c.682T>C	p.F228L
118F8850A1	9	21971120	21971120	Nonsense_Mutation	SNP	G	A	A	CDKN2A	c.238C>T	p.R80*
118F8850A1	-	-	-	Frame_Shift_Del	INS	-	-	-	TSC1	C.1808del	P.P603Rfs*26
118F8850A1	9	139404203	139404203	Missense_Mutation	SNP	G	A	A	NOTCH1	c.2951C>T	p.T984M
118F8850A1	X	47426763	47426763	Missense_Mutation	SNP	G	T	T	ARAF	c.1008G>T	p.K336N
118F8903A1	1	27101510	27101510	Missense_Mutation	SNP	C	T	T	ARID1A	c.4792C>T	p.R1598C
118F8903A1	12	56489567	56489567	Missense_Mutation	SNP	A	T	T	ERBB3	c.2032A>T	p.R678W
118F8903A1	15	88576199	88576199	Missense_Mutation	SNP	A	G	G	NTRK3	c.1474T>C	p.S492P
118F8903A1	17	7577121	7577121	Missense_Mutation	SNP	G	A	A	TP53	c.817C>T	p.R273C
118F8903A1	19	1207162	1207162	Nonsense_Mutation	SNP	A	T	T	STK11	c.250A>T	p.K84*
118F8903A1	19	10610285	10610285	Missense_Mutation	SNP	G	A	A	KEAP1	c.425C>T	p.T142M
118F8903A1	3	134851763	134851763	Missense_Mutation	SNP	G	A	A	EPHB1	c.1169G>A	p.R390H
118F8903A1	5	112177911	112177911	Nonsense_Mutation	SNP	C	G	G	APC	c.6620C>G	p.S2207*
118F8903A1	5	176517950	176517950	Missense_Mutation	SNP	A	G	G	FGFR4	c.448A>G	p.T150A
118F8903A1	8	48701588	48701588	Nonsense_Mutation	SNP	-	-	-	PRKDC	c.10780G>T	p.E3594*
118G1224A1	-	-	-	Frame_Shift_Del	INS	-	-	-	ARID1A	c.4750del	p.Q1584Rfs*28
118G1224A1	1	202743853	202743853	Missense_Mutation	SNP	C	T	T	KDM5B	c.293G>A	p.R98H
118G1224A1	12	25398284	25398284	Missense_Mutation	SNP	C	T	T	KRAS	c.35G>A	p.G12D
118G1224A1	17	7578442	7578442	Missense_Mutation	SNP	T	C	C	TP53	c.488A>G	p.Y163C
118G1224A1	22	23634808	23634808	Missense_Mutation	SNP	G	A	A	BCR	c.2863G>A	p.E955K
118G1224A1	5	121761117	121761117	Missense_Mutation	SNP	C	T	T	SNCAIP	c.1073C>T	p.A358V
118G1344A1	1	27101468	27101468	Nonsense_Mutation	SNP	C	T	T	ARID1A	c.4750C>T	p.Q1584*
118G1344A1	12	25398284	25398284	Missense_Mutation	SNP	C	A	A	KRAS	c.35G>T	p.G12V
118G1344A1	15	75093221	75093221	Missense_Mutation	SNP	A	G	G	CSK	c.680A>G	p.D227G
118G1344A1	17	7577538	7577538	Missense_Mutation	SNP	C	T	T	TP53	c.743G>A	p.R248Q
118G1344A1	X	44913082	44913082	Missense_Mutation	SNP	C	T	T	KDM6A	c.757C>T	p.H253Y
118G1348A1	10	89717708	89717708	Nonsense_Mutation	SNP	C	T	T	PTEN	c.733C>T	p.Q245*
118G1348A1	-	-	-	Frame_Shift_Del	INS	-	-	-	TP53	C.626_627del	P.R209Kfs*6
118G1348A1	4	187539330	187539330	Missense_Mutation	SNP	C	T	T	FAT1	c.8410G>A	p.D2804N
118G8977A1	12	49425544	49425544	Missense_Mutation	SNP	T	C	C	KMT2D	c.12944A>G	p.Q4315R
118G8977A1	17	7577609	7577609	Splice_Site	SNP	C	T	T	TP53	c.673-1G>A	-
118G9081A1	1	11190804	11190804	Missense_Mutation	SNP	C	T	T	MTOR	c.5395G>A	p.E1799K
118G9081A1	-	-	-	Frame_Shift_Del	INS	-	-	-	EPHA2	c.2459del	p.E820Gfs*7
118G9081A1	-	-	-	Frame_Shift_Del	INS	-	-	-	ARID1A	4_733delinsAAC	p.G242Lfs*120
118G9081A1	12	25380275	25380275	Missense_Mutation	SNP	T	A	A	KRAS	c.183A>T	p.Q61H
118G9081A1	15	67477103	67477103	Missense_Mutation	SNP	T	C	C	SMAD3	c.910T>C	p.F304L
118G9081A1	19	15271517	15271517	Missense_Mutation	SNP	C	A	A	NOTCH3	c.6922G>T	p.G2308W
118G9081A1	3	52595851	52595851	Missense_Mutation	SNP	C	A	A	PBRM1	4064G>T;4076G	G1355V;R1359L
118G9081A1	4	175898265	175898265	Missense_Mutation	SNP	G	A	A	ADAM29	c.1589G>A	p.R530H
118G9081A1	-	-	-	In_Frame_Del	INS	-	-	-	ARID1B	c.3447_3454del	p.F1150*
118G9119A1	1	120510085	120510085	Missense_Mutation	SNP	A	C	C	NOTCH2	c.1424T>G	p.I475S
118G9119A1	-	-	-	Frame_Shift_Del	INS	-	-	-	BIRC3	603delinsGTC	p.Y195Vfs*21
118G9119A1	15	40998493	40998493	Splice_Site	SNP	G	T	T	RAD51	c.343+1G>T	-
118G9119A1	15	90631839	90631839	Missense_Mutation	SNP	T	A	A	IDH2	c.514A>T	p.R172W
118G9119A1	-	-	-	In_Frame_Ins	INS	-	-	-	BAP1	c.1847_1854dup	p.G619*
118G9120A1	17	7577099	7577099	Missense_Mutation	SNP	C	T	T	TP53	c.839G>A	p.R280K
118G9233A1	1	158596763	158596763	Missense_Mutation	SNP	G	A	A	SPTA1	c.5699C>T	p.S1900F

118G9233A1	11	92543090	92543090	Missense_Mutation	SNP	G	A	A	FAT3	c.9329G>A	p.G3110D
118G9233A1		-	-	Frame_Shift_Del	INS	-	-	-	TP53	c.922_928del	p.L308Tfs*35
118G9233A1	2	170009390	170009390	Missense_Mutation	SNP	C	T	T	LRP2	c.12380G>A	p.R4127H
118G9233A1	6	94120602	94120602	Missense_Mutation	SNP	G	A	A	EPHA7	c.449C>T	p.A150V
118G9262A1	18	48591889	48591889	Missense_Mutation	SNP	A	G	G	SMAD4	c.1052A>G	p.D351G
118G9262A1	20	57484421	57484421	Missense_Mutation	SNP	G	A	A	GNAS	c.602G>A	p.R201H
118G9348A1	1	179086473	179086473	Missense_Mutation	SNP	C	T	T	ABL2	c.1402G>A	p.V468I
118G9348A1		-	-	Frame_Shift_Del	INS	-	-	-	TP53	c.184_211del	p.E62Pfs*52
118G9348A1	19	11134267	11134267	Missense_Mutation	SNP	G	T	T	SMARCA4	c.2933G>T	p.R978L
118G9348A1	6	152163886	152163886	Nonsense_Mutation	SNP	G	T	T	ESR1	c.607G>T	p.E203*
118G9364A1		-	-	Frame_Shift_Del	INS	-	-	-	ARID1A	c.245del	p.G82Vfs*19
118G9364A1	12	25380275	25380275	Missense_Mutation	SNP	T	G	G	KRAS	c.183A>C	p.Q61H
118G9364A1	17	7577539	7577539	Missense_Mutation	SNP	G	A	A	TP53	c.742C>T	p.R248W
118G9364A1		-	-	Frame_Shift_Ins	INS	-	-	-	TGFBR2	1452_1453insA	p.E485Kfs*4
118G9364A1	9	21974679	21974679	Nonsense_Mutation	SNP	G	A	A	CDKN2A	c.148C>T	p.Q50*
118G9391A1		-	-	Frame_Shift_Del	INS	-	-	-	ARID1A	c.1273del	p.Q425Rfs*8
118G9391A1	12	25398284	25398284	Missense_Mutation	SNP	C	T	T	KRAS	c.35G>A	p.G12D
118G9391A1		-	-	Frame_Shift_Del	INS	-	-	-	TP53	c.642_643del	p.H214Qfs*7
118G9391A1	7	140477815	140477815	Missense_Mutation	SNP	A	T	T	BRAF	c.1493T>A	p.F498Y
118G9391A1	9	21971111	21971111	Missense_Mutation	SNP	G	A	A	CDKN2A	c.247C>T	p.H83Y
118G9397A1	12	57590958	57590958	Splice_Site	SNP	G	A	A	LRP1	c.9076+10G>A	-
118G9397A1		-	-	Missense_Mutation	SNP	-	-	-	TP53	c.764_766del	p.L255del
118G9397A1		-	-	Frame_Shift_Ins	INS	-	-	-	STK11	c.842dup	p.L282Afs*3
118G9397A1	8	41790808	41790808	Missense_Mutation	SNP	G	A	A	KAT6A	c.4930C>T	p.P1644S
118G9397A1	8	41806794	41806794	Missense_Mutation	SNP	C	G	G	KAT6A	c.1686G>C	p.W562C
118G9417A2	12	25398284	25398284	Missense_Mutation	SNP	C	T	T	KRAS	c.35G>A	p.G12D
118G9417A2	12	49428435	49428435	Missense_Mutation	SNP	A	G	G	KMT2D	c.10370T>C	p.L3457P
118G9417A2	14	95574391	95574391	Missense_Mutation	SNP	T	C	C	DICER1	c.2476A>G	p.T826A
118G9417A2	17	7577106	7577106	Missense_Mutation	SNP	G	T	T	TP53	c.832C>A	p.P278T
118G9417A2	17	7577144	7577144	Missense_Mutation	SNP	A	G	G	TP53	c.794T>C	p.L265P
118G9417A2	17	41222990	41222990	Missense_Mutation	SNP	G	C	C	BRCA1	c.4941C>G	p.N1647K
118G9417A2	18	48604722	48604722	Missense_Mutation	SNP	G	C	C	SMAD4	c.1544G>C	p.R515T
118G9417A2	3	71026870	71026870	Missense_Mutation	SNP	T	C	C	FOXP1	c.1352A>G	p.Q451G
118G9417A2	3	156421477	156421477	Missense_Mutation	SNP	G	T	T	TIPARP	c.1512G>T	p.W504C
118G9417A2	4	1980613	1980613	Missense_Mutation	SNP	C	T	T	NSD2	c.4075C>T	p.R1359W
118G9417A2	9	139401365	139401365	Missense_Mutation	SNP	C	A	A	NOTCH1	3704G>T;3709A	[S1235I;K1237Q]
118G9417A2	X	100617204	100617204	Missense_Mutation	SNP	C	T	T	BTX	c.545G>A	p.R182Q
118G9421A1	16	2135300	2135300	Missense_Mutation	SNP	G	A	A	TSC2	c.4639G>A	p.V1547I
118G9421A1		-	-	Frame_Shift_Del	INS	-	-	-	CDKN2A	C.152_156del	P.V51Dfs*67
118G9423A1	1	193104711	193104711	Nonsense_Mutation	SNP	C	T	T	CDC73	c.415C>T	p.R139*
118G9423A1		-	-	Missense_Mutation	SNP	-	-	-	KMT2D	597_7599delins	p.T2533S
118G9423A1	17	7577538	7577538	Missense_Mutation	SNP	C	T	T	TP53	c.743G>A	p.R248Q
118G9423A1	19	10610223	10610223	Missense_Mutation	SNP	G	T	T	KEAP1	c.487C>A	p.Q163K
118G9423A1	20	30661134	30661134	Missense_Mutation	SNP	C	A	A	HCK	c.133C>A	p.H45N
118G9423A1		-	-	Frame_Shift_Del	INS	-	-	-	SETD2	C.5214del	P.L1738Ffs*4
118G9423A1	3	130748692	130748692	Missense_Mutation	SNP	C	T	T	NEK11	c.140C>T	p.S47L
118G9423A1	4	66217130	66217130	Missense_Mutation	SNP	G	T	T	EPHA5	c.2485C>A	p.P829T
118G9448A1	1	27102193	27102193	Missense_Mutation	SNP	A	T	T	ARID1A	c.5119A>T	p.S1707C
118G9448A1	10	84738788	84738788	Nonsense_Mutation	SNP	C	T	T	NRG3	c.1495C>T	p.R499*
118G9448A1	10	89711975	89711975	Missense_Mutation	SNP	T	G	G	PTEN	c.593T>G	p.M198R
118G9448A1	12	46244139	46244139	Nonsense_Mutation	SNP	C	T	T	ARID2	c.2233C>T	p.Q745*
118G9448A1	12	46244959	46244959	Nonsense_Mutation	SNP	C	A	A	ARID2	c.3053C>A	p.S1018*
118G9448A1	12	56491597	56491597	Missense_Mutation	SNP	T	C	C	ERBB3	c.2489T>C	p.M830T
118G9448A1	16	9934597	9934597	Missense_Mutation	SNP	C	T	T	GRIN2A	c.1558G>A	p.E520K
118G9448A1	17	7574003	7574003	Nonsense_Mutation	SNP	G	A	A	TP53	c.1024C>T	p.R342*
118G9448A1		-	-	Frame_Shift_Ins	INS	-	-	-	TP53	c.162_163insT	p.T55Yfs*2
118G9448A1	19	14213709	14213709	Missense_Mutation	SNP	C	G	G	PRKACA	c.255G>C	p.Q85H
118G9448A1	2	11337440	11337440	Missense_Mutation	SNP	A	G	G	ROCK2	c.3314T>C	p.L1105P
118G9448A1	2	225362475	225362475	Nonsense_Mutation	SNP	T	A	A	CUL3	c.1702A>T	p.K568*
118G9448A1	3	89390914	89390914	Missense_Mutation	SNP	C	G	G	EPHA3	c.980C>G	p.S327C
118G9448A1	3	195594327	195594327	Missense_Mutation	SNP	G	A	A	TNK2	c.2797C>T	p.R933W
118G9448A1		-	-	Frame_Shift_Ins	INS	-	-	-	ETV1	c.414dup	p.T139Hfs*24
118G9448A1	8	69129904	69129904	Missense_Mutation	SNP	G	A	A	PREX2	c.4658G>A	p.G1553E
118G9512A1	1	11205035	11205035	Missense_Mutation	SNP	C	T	T	MTOR	c.4754G>A	p.R1585Q
118G9512A1	16	2124214	2124214	Missense_Mutation	SNP	A	G	G	TSC2	c.2369A>G	p.Y790C
118G9512A1	17	7578406	7578406	Missense_Mutation	SNP	C	T	T	TP53	c.524G>A	p.R175H
118G9512A1	22	42524339	42524339	Missense_Mutation	SNP	A	G	G	CYP2D6	c.680T>C	p.V227A
118G9512A1	3	30729980	30729980	Missense_Mutation	SNP	C	G	G	TGFBR2	c.1501C>G	p.P501A
118G9512A1	7	151845579	151845579	Missense_Mutation	SNP	C	T	T	KMT2C	c.13433G>A	p.R4478Q
118G9512A1	8	92983007	92983007	Missense_Mutation	SNP	C	T	T	RUNX1T1	c.1307G>A	p.R436Q
118G9512A1	X	47034459	47034459	Nonsense_Mutation	SNP	C	T	T	RBM10	c.544C>T	p.Q182*
118G9558J1	17	7578535	7578535	Missense_Mutation	SNP	T	C	C	TP53	c.395A>G	p.K132R
118G9558J1	18	45368223	45368223	Nonsense_Mutation	SNP	G	T	T	SMAD2	c.1289C>A	p.S430*
118G9558J1		-	-	Frame_Shift_Del	INS	-	-	-	STK11	c.482_483del	p.I161Rfs*8
118G9558J1	5	112128185	112128185	Missense_Mutation	SNP	C	T	T	APC	c.688C>T	p.R230C
118G9558J1	X	66941797	66941797	Missense_Mutation	SNP	T	G	G	AR	c.2441T>G	p.F814C
118G9559A1	12	25398284	25398284	Missense_Mutation	SNP	C	T	T	KRAS	c.35G>A	p.G12D
118G9559A1	17	7578442	7578442	Missense_Mutation	SNP	T	C	C	TP53	c.488A>G	p.Y163C
118G9559A1	18	48603032	48603032	Nonsense_Mutation	SNP	C	T	T	SMAD4	c.1333C>T	p.R445*
118G9559A1	7	151856061	151856061	Missense_Mutation	SNP	G	A	A	KMT2C	c.11557C>T	p.R3853W
118G9559A1		-	-	Frame_Shift_Ins	INS	-	-	-	CDKN2A	C.243dup	P.V82Rfs*38
118G9581A1		-	-	Frame_Shift_Ins	INS	-	-	-	APC	C.4666dup	P.T1555Nfs*3
118G9603A1	1	158624424	158624424	Missense_Mutation	SNP	T	G	G	SPTA1	c.3013A>C	p.T1005P
118G9603A1	13	28601290	28601290	Missense_Mutation	SNP	C	G	G	FLT3	c.2142G>C	p.W714C
118G9603A1	15	88423632	88423632	Missense_Mutation	SNP	G	A	A	NTRK3	c.2161C>T	p.R721C
118G9603A1		-	-	Frame_Shift_Del	INS	-	-	-	TP53	c.879_880del	p.E294Afs*11
118G9603A1		-	-	Frame_Shift_Del	INS	-	-	-	SMAD4	c.889del	p.H297ifs*39
118G9603A1		-	-	Missense_Mutation	SNP	-	-	-	SMAD4	c.1137_1139de	p.R380del
118G9603A1	2	141607761	141607761	Missense_Mutation	SNP	C	T	T	LRP1B	c.4849G>A	p.E1617K
118G9603A1	3	41266124	41266124	Missense_Mutation	SNP	A	G	G	CTNNB1	c.121A>G	p.T41A
118G9603A1	3	87027819	87027819	Missense_Mutation	SNP	C	T	T	VGLL3	c.260G>A	p.R87H
118G9603A1	3	170011214	170011214	Missense_Mutation	SNP	G	C	C	PRKCI	c.1335G>C	p.E445D
118G9603A1	4	20525790	20525790	Missense_Mutation	SNP	C	A	A	SLIT2	c.1428C>A	p.F476L
118G9603A1	4	153249456	153249456	Missense_Mutation	SNP	C	T	T	FBXW7	c.1322G>A	p.R441Q
118G9603A1	7	2951868	2951868	Missense_Mutation	SNP	C	T	T	CARD11	c.3082G>A	p.E1028K
118G9603A1	7	41729606	41729606	Missense_Mutation	SNP	C	T	T	INHBA	c.923G>A	p.R308H
118G9603A1	7	151853002	151853002	Nonsense_Mutation	SNP	C	A	A	KMT2C	c.11953G>T	p.E3985*
118G9617A1	17	7577534	7577534	Missense_Mutation	SNP	C	A	A	TP53	c.747G>T	p.R249S

118G9617A1	19	10602300	10602300	Nonsense_Mutation	SNP	A	C	C	KEAP1	c.1278T>G	p.Y426*
118G9617A1	X	39934298	39934298	Missense_Mutation	SNP	C	G	G	BCOR	c.301G>C	p.G101R
118G9617A1	X	70345909	70345909	Nonsense_Mutation	SNP	C	T	T	MED12	c.2446C>T	p.R816*
118G9617A1	17	7577534	7577534	Missense_Mutation	SNP	C	A	A	TP53	c.747G>T	p.R249S
118G9617A1	X	39934298	39934298	Missense_Mutation	SNP	C	G	G	BCOR	c.301G>C	p.G101R
118G9676A1		-	-	Frame_Shift_Del	INS	-	-	-	ARID1A	c.609del	p.H203Qfs*29
118G9676A1	12	25398284	25398284	Missense_Mutation	SNP	C	T	T	KRAS	c.35G>A	p.G12D
118G9676A1	17	7578268	7578268	Missense_Mutation	SNP	A	G	G	TP53	c.581T>C	p.L194P
118G9676A1		-	-	In_Frame_Ins	INS	-	-	-	CDKN2A	c.131dup	p.Y44*
118G9722A1		-	-	Splice_Site	SNP	-	-	-	CYLD	c.1-16_2351-2del	-
118G9722A1	17	7577114	7577114	Missense_Mutation	SNP	C	T	T	TP53	c.824G>A	p.C275Y
118G9722A1	4	66213918	66213918	Nonsense_Mutation	SNP	C	A	A	EPHA5	c.2512G>T	p.G838*
118G9722A1	8	141810631	141810631	Missense_Mutation	SNP	C	T	T	PTK2	c.1086G>A	p.M362I
118G9724A1	17	29665743	29665743	Nonsense_Mutation	SNP	G	T	T	NF1	c.6841G>T	p.G2281*
118G9729A1		-	-	Frame_Shift_Del	INS	-	-	-	TP53	c.876del	p.E294Sfs*51
118G9729A1	4	143235911	143235911	Missense_Mutation	SNP	C	T	T	INPP4B	c.377G>A	p.R126Q
118G9729A1	8	69046362	69046362	Missense_Mutation	SNP	T	A	A	PREX2	c.3835T>A	p.S1279T
118G9729A1	9	21971117	21971117	Missense_Mutation	SNP	G	T	T	CDKN2A	c.241C>A	p.P81T
118G9742A1	11	92533107	92533107	Missense_Mutation	SNP	G	A	A	FAT3	c.6928G>A	p.V2310I
118G9742A1	12	25398284	25398284	Missense_Mutation	SNP	C	T	T	KRAS	c.35G>A	p.G12D
118G9742A1	17	48269373	48269373	Missense_Mutation	SNP	C	A	A	COL1A1	c.1996G>T	p.D666Y
118G9742A1	17	66518996	66518996	Missense_Mutation	SNP	G	T	T	PRKAR1A	c.277G>T	p.G93C
118G9742A1	2	48033780	48033780	Nonsense_Mutation	SNP	C	T	T	MSH6	c.3991C>T	p.R1331*
118G9742A1	2	198266834	198266834	Missense_Mutation	SNP	T	C	C	SF3B1	c.2098A>G	p.K700E
118G9742A1	8	139163791	139163791	Missense_Mutation	SNP	G	T	T	FAM135B	c.2927C>A	p.P976Q
118G9742A1	X	76907651	76907651	Nonsense_Mutation	SNP	G	A	A	ATRX	c.4510C>T	p.R1504*
118G9781A1	1	27942071	27942071	Missense_Mutation	SNP	T	C	C	FGR	c.892A>G	p.M298V
118G9781A1	1	158609403	158609403	Missense_Mutation	SNP	T	A	A	SPTA1	c.4949A>T	p.Q1650L
118G9781A1	12	69218398	69218398	Missense_Mutation	SNP	A	T	T	MDM2	c.490A>T	p.T164S
118G9781A1		-	-	Frame_Shift_Ins	INS	-	-	-	TP53	c.494_495dup	p.Q167Hfs*4
118G9781A1	20	31022763	31022763	Missense_Mutation	SNP	C	A	A	ASXL1	c.2248C>A	p.P750T
118G9781A1	3	47164685	47164685	Nonsense_Mutation	SNP	T	A	A	SETD2	c.1441A>T	p.R481*
118G9781A1	4	187538357	187538357	Splice_Site	SNP	T	A	A	FAT1	c.8879-2A>T	-
118G9781A1	5	176519743	176519743	Missense_Mutation	SNP	A	T	T	FGFR4	c.1015A>T	p.I339F
118G9781A1	8	69129852	69129852	Missense_Mutation	SNP	T	A	A	PREX2	c.4606T>A	p.C1536S
118G9797A1	1	120478095	120478095	Missense_Mutation	SNP	C	G	G	NOTCH2	c.3655G>C	p.G1219R
118G9797A1	15	45003751	45003751	Missense_Mutation	SNP	C	T	T	B2M	c.7C>T	p.R3C
118G9797A1	17	7577082	7577082	Missense_Mutation	SNP	C	T	T	TP53	c.856G>A	p.E286K
118G9797A1	2	11337395	11337395	Missense_Mutation	SNP	C	T	T	ROCK2	c.3359G>A;3364C>A	p.R1120Q;Q1122E
118G9797A1	2	141777614	141777614	Missense_Mutation	SNP	G	T	T	LRP1B	c.1847C>A	p.T616N
118G9912A1	1	158641935	158641935	Missense_Mutation	SNP	G	A	A	SPTA1	c.1402C>T	p.A688C
118G9912A1	2	212248377	212248377	Missense_Mutation	SNP	G	A	A	ERBB4	c.3890C>T	p.P1297L
118G9912A1	5	38950829	38950829	Splice_Site	SNP	T	C	C	RICTOR	c.3128-7A>G	-
118G9955A1	17	16024432	16024432	Missense_Mutation	SNP	C	A	A	NCOR1	c.1786G>T	p.A596S
118G9955A1	3	41266100	41266100	Missense_Mutation	SNP	T	C	C	CTNNB1	c.97T>C	p.S33P
118G9955A1		-	-	Splice_Site	SNP	-	-	-	IRF4	c.4-12_404-9delC	-
118G9955A1		-	-	In_Frame_Ins	INS	-	-	-	KAT6A	c.1536dup	p.E513*
118G9970A1	19	18266993	18266993	Missense_Mutation	SNP	G	A	A	PIK3R2	c.304G>A	p.D102N
118G9970A1	4	20525654	20525654	Missense_Mutation	SNP	C	T	T	SLIT2	c.1292C>T	p.P431L
118H1438M1	3	52442078	52442078	Missense_Mutation	SNP	A	G	G	BAP1	c.271T>C	p.C91R
118H1479A1		-	-	Frame_Shift_Del	INS	-	-	-	EPHA2	c.1436_1449del	p.S479Cfs*112
118H1479A1		-	-	Frame_Shift_Ins	INS	-	-	-	ARID2	c.2364dup	p.V789Cfs*52
118H1479A1		-	-	Splice_Site	SNP	-	-	-	POLE	c.5812-7_5812-6del	-
118H1479A1	15	90631839	90631839	Missense_Mutation	SNP	T	C	C	IDH2	c.514A>G	p.R172G
118H1479A1		-	-	Frame_Shift_Del	INS	-	-	-	TP53	c.810_825del	p.F270Lfs*70
118H1479A1	7	73530217	73530217	Missense_Mutation	SNP	A	G	G	LIMK1	c.1496A>G	p.K499R
118H1515A1	11	60231782	60231782	Missense_Mutation	SNP	C	A	A	MS4A1	c.301C>A	p.L101M
118H1515A1	17	7578239	7578239	Nonsense_Mutation	SNP	C	A	A	TP53	c.610G>T	p.E204*
118H1515A1	17	15983971	15983971	Missense_Mutation	SNP	A	G	G	NCOR1	c.3248T>C	p.V1083A
118H1515A1		-	-	Frame_Shift_Del	INS	-	-	-	STK11	c.610_613del	p.F204Rfs*82
118H1577A1		-	-	Splice_Site	SNP	-	-	-	MRE11	c.9+6_659+7del	-
118H1577A1	17	7577124	7577124	Missense_Mutation	SNP	C	A	A	TP53	c.814G>T	p.V272L
118H1577A1	2	47601141	47601141	Missense_Mutation	SNP	A	G	G	EPCAM	c.379A>G	p.T127A
118H1577A1	2	141027805	141027805	Splice_Site	SNP	A	T	T	LRP1B	c.1324T>+6T>A	-
118H1577A1	2	170063350	170063350	Missense_Mutation	SNP	C	G	G	LRP2	c.6880G>C	p.D2294H
118H1577A1	6	135514976	135514976	Missense_Mutation	SNP	G	T	T	MYB	c.763G>T	p.V255F
118H1577A1	X	66765409	66765409	Missense_Mutation	SNP	G	T	T	AR	c.421G>T	p.A141S
118H1607A1	11	92085831	92085831	Missense_Mutation	SNP	G	A	A	FAT3	c.553G>A	p.A185T
118H1607A1		-	-	Frame_Shift_Del	INS	-	-	-	TP53	c.365_366del	p.V122Dfs*26
118H1607A1		-	-	Frame_Shift_Del	INS	-	-	-	NF1	c.3936del	p.D1313Ifs*14
118H1607A1	19	11141507	11141507	Missense_Mutation	SNP	G	A	A	SMARCA4	c.3484G>A	p.G1162S
118H1607A1	22	30051652	30051652	Nonsense_Mutation	SNP	C	T	T	NF2	c.586C>T	p.R196*
118H1642A1	12	56478817	56478817	Missense_Mutation	SNP	G	A	A	ERBB3	c.273G>A	p.M91I
118H1642A1	14	36986773	36986773	Missense_Mutation	SNP	C	A	A	NKX2-1	c.916G>T	p.A306S
118H1642A1	17	7577120	7577120	Missense_Mutation	SNP	C	T	T	TP53	c.818G>A	p.R273H
118H1642A1	22	23656785	23656785	Missense_Mutation	SNP	G	A	A	BCR	c.3610G>A	p.A1204T
118H1642A1	7	151856085	151856085	Nonsense_Mutation	SNP	C	A	A	KMT2C	c.11533G>T	p.E3845*
118H1685A1	1	27088759	27088759	Nonsense_Mutation	SNP	C	T	T	ARID1A	c.2368C>T	p.Q790*
118H1685A1	19	42797228	42797228	Missense_Mutation	SNP	C	T	T	CIC	c.3590C>T	p.S1197F
118H1689A1	18	48604778	48604778	Nonsense_Mutation	SNP	C	T	T	SMAD4	c.1600C>T	p.Q534*
118H1689A1	19	1220579	1220579	Splice_Site	SNP	G	C	C	STK11	c.598-1G>C	-
118H1733A1	12	25398284	25398284	Missense_Mutation	SNP	C	A	A	KRAS	c.35G>T	p.G12V
118H1733A1	17	7577539	7577539	Missense_Mutation	SNP	G	A	A	TP53	c.742C>T	p.R248W
118H1787A1	12	46230571	46230571	Nonsense_Mutation	SNP	C	T	T	ARID2	c.820C>T	p.R274*
118H1787A1	14	45623912	45623912	Missense_Mutation	SNP	C	T	T	FANCM	c.1196C>T	p.S399L
118H1787A1	17	7577082	7577082	Missense_Mutation	SNP	C	T	T	TP53	c.856G>A	p.E286K
118H1787A1	6	36653561	36653561	Missense_Mutation	SNP	C	T	T	CDKN1A	c.479C>T	p.S160F
118H1787A1	8	41905993	41905993	Missense_Mutation	SNP	C	T	T	KAT6A	c.503G>A	p.R168Q
118H1840A1	12	57567022	57567022	Missense_Mutation	SNP	C	T	T	LRP1	c.3235C>T	p.R1079W
118H1840A1	13	28626712	28626712	Missense_Mutation	SNP	T	C	C	FLT3	c.584A>G	p.E195G
118H1840A1	2	209113113	209113113	Missense_Mutation	SNP	G	A	A	IDH1	c.394C>T	p.R132C
118H1840A1	3	52643328	52643328	Splice_Site	SNP	C	T	T	PBRM1	c.2567+1G>A	-
118H1840A1	X	66942707	66942707	Nonsense_Mutation	SNP	G	T	T	AR	c.2488G>T	p.E830*
118H1840A1	X	76939715	76939715	Missense_Mutation	SNP	C	T	T	ATRX	c.1033G>A	p.A345T
118H2136A1	1	27106354	27106354	Nonsense_Mutation	SNP	C	T	T	ARID1A	c.5965C>T	p.R1989*
118H2136A1	10	43610033	43610033	Missense_Mutation	SNP	A	G	G	RET	c.1985A>G	p.G632R
118H2136A1	13	49030487	49030487	Splice_Site	SNP	T	A	A	RB1	c.1960+2T>A	-
118H2136A1	15	91358353	91358353	Missense_Mutation	SNP	G	C	C	BLM	c.4098G>C	p.R1366N

118H2136A1		-	-	Frame_Shift_Ins	INS	-	-	-	TP53	C.342dup	P.H115Afs*34
118H2136A1	17	63531744	63531744	Missense_Mutation	SNP	T	C	C	AXIN2	c.2237A>G	p.D746G
118H2136A1	17	78599496	78599496	Missense_Mutation	SNP	G	C	C	RPTOR	c.168G>C	p.K56N
118H2136A1		-	-	Frame_Shift_Del	INS	-	-	-	SMAD4	C.953del	P.P3181fs*18
118H2136A1	2	170059470	170059470	Splice_Site	SNP	C	A	A	LRP2	c.8006-1G>T	-
118H2136A1	20	57429628	57429628	Missense_Mutation	SNP	C	T	T	GNAS	c.1121C>T	p.P374L
118H2136A1	3	12660112	12660112	Missense_Mutation	SNP	C	G	G	RAF1	c.109G>C	p.G37R
118H2136A1	3	138409835	138409835	Splice_Site	SNP	G	C	C	PIK3CB	c.2036+7C>G	-
118H2136A1	3	185191256	185191256	Missense_Mutation	SNP	C	G	G	MAP3K13	c.2137C>G	p.P713A
118H2136A1	7	106508522	106508522	Missense_Mutation	SNP	G	C	C	PIK3CG	c.516G>C	p.E172D
118H2136A1	7	140481402	140481402	Missense_Mutation	SNP	C	G	G	BRAF	c.1406G>C	p.G469A
118H2136A1	8	48715963	48715963	Nonsense_Mutation	SNP	-	-	-	PRKDC	c.9825G>A	p.W3275*
118H2136A1	8	48765245	48765245	Missense_Mutation	SNP	C	A	A	PRKDC	c.6993G>T	p.E2331D
118H2136A1	9	139393361	139393361	Missense_Mutation	SNP	T	C	C	NOTCH1	c.6170A>G	p.Q2057R
118H2136A1	X	76814163	76814163	Missense_Mutation	SNP	A	G	G	ATRX	c.6481T>C	p.Y2161H
118H2149S1	1	9777149	9777149	Missense_Mutation	SNP	C	T	T	PIK3CD	c.913C>T	p.P305S
118H2149S1	1	27940979	27940979	Missense_Mutation	SNP	G	A	A	FGR	c.1211C>T	p.A404V
118H2149S1	1	43770729	43770729	Missense_Mutation	SNP	C	T	T	TIE1	c.266C>T	p.T89M
118H2149S1	1	179100530	179100530	Missense_Mutation	SNP	C	T	T	ABL2	c.307G>A	p.G103R
118H2149S1	10	131265562	131265562	Splice_Site	SNP	T	C	C	MGMT	c.81+2T>C	-
118H2149S1	11	92534025	92534025	Missense_Mutation	SNP	G	A	A	FAT3	c.7846G>A	p.G2616S
118H2149S1	11	108204681	108204681	Missense_Mutation	SNP	A	G	G	ATM	c.7996A>G	p.T2666A
118H2149S1	11	119145633	119145633	Missense_Mutation	SNP	G	A	A	CBL	c.839G>A	p.R280Q
118H2149S1	11	128680615	128680615	Missense_Mutation	SNP	G	A	A	FLI1	c.1091G>A	p.G364D
118H2149S1	12	57563000	57563000	Missense_Mutation	SNP	G	A	A	LRP1	c.3073G>A	p.G1025R
118H2149S1	12	112915797	112915797	Missense_Mutation	SNP	C	T	T	PTPN11	c.1070C>T	p.T357M
118H2149S1	12	122492869	122492869	Missense_Mutation	SNP	G	A	A	BCL7A	c.598G>A	p.G200S
118H2149S1		-	-	Frame_Shift_Del	INS	-	-	-	FLT3	c.2955_2956del	p.P986Afs*27
118H2149S1	14	95599700	95599700	Nonsense_Mutation	SNP	C	T	T	DICER1	c.96G>A	p.W32*
118H2149S1	16	2131685	2131685	Missense_Mutation	SNP	G	A	A	TSC2	c.3700G>A	p.A1234T
118H2149S1	16	68867356	68867356	Missense_Mutation	SNP	G	A	A	CDH1	c.2603G>A	p.R868H
118H2149S1	17	37871746	37871746	Missense_Mutation	SNP	G	A	A	ERBB2	c.1270G>A	p.V424I
118H2149S1		-	-	Frame_Shift_Del	INS	-	-	-	RNF43	c.1976del	p.G659Vfs*41
118H2149S1	19	3114953	3114953	Missense_Mutation	SNP	A	C	C	GNAA1	c.488A>C	p.D163A
118H2149S1	19	18273784	18273784	Missense_Mutation	SNP	G	A	A	PIK3R2	c.1117G>A	p.G373R
118H2149S1	19	50906837	50906837	Missense_Mutation	SNP	C	T	T	POLD1	c.1225C>T	p.R409W
118H2149S1	2	16085728	16085728	Missense_Mutation	SNP	C	T	T	MYCN	c.904C>T	p.R302C
118H2149S1	2	47637357	47637357	Missense_Mutation	SNP	G	A	A	MSH2	c.491G>A	p.G164E
118H2149S1	2	141272257	141272257	Missense_Mutation	SNP	C	T	T	LRP1B	c.8234G>A	p.C2745Y
118H2149S1	2	141747101	141747101	Missense_Mutation	SNP	C	A	A	LRP1B	c.2770G>T	p.A924S
118H2149S1	2	148680563	148680563	Missense_Mutation	SNP	G	A	A	ACVR2A	c.1099G>A	p.A367T
118H2149S1		-	-	Frame_Shift_Del	INS	-	-	-	ACVR2A	c.1310del	p.K437Rfs*5
118H2149S1	20	30689231	30689231	Missense_Mutation	SNP	G	A	A	HCK	c.1427G>A	p.R476H
118H2149S1	20	36031750	36031750	Missense_Mutation	SNP	G	A	A	SRC	c.1579G>A	p.E527K
118H2149S1	20	57430079	57430079	Missense_Mutation	SNP	G	A	A	GNAS	c.1759G>A	p.G587R
118H2149S1	20	57484421	57484421	Missense_Mutation	SNP	G	A	A	GNAS	c.602G>A	p.R201H
118H2149S1	22	21343116	21343116	Missense_Mutation	SNP	A	G	G	LZTR1	c.548A>G	p.Y183C
118H2149S1	22	24159067	24159067	Missense_Mutation	SNP	T	C	C	SMARCB1	c.739T>C	p.S247P
118H2149S1	22	42525829	42525829	Missense_Mutation	SNP	C	T	T	CYP2D6	c.263G>A	p.R88H
118H2149S1		-	-	Frame_Shift_Del	INS	-	-	-	XPC	c.2782_2785del	p.K928Qfs*18
118H2149S1	3	52651532	52651532	Nonsense_Mutation	SNP	G	A	A	PBRM1	c.1564C>T	p.R522*
118H2149S1	3	128205829	128205829	Missense_Mutation	SNP	C	T	T	GATA2	c.46G>A	p.V16M
118H2149S1	4	88986961	88986961	Missense_Mutation	SNP	A	G	G	PKD2	c.2288A>G	p.D763G
118H2149S1	4	106164898	106164898	Missense_Mutation	SNP	G	A	A	TEF2	c.3766G>A	p.G1256S
118H2149S1	4	126329910	126329910	Missense_Mutation	SNP	T	A	A	FAT4	c.5881T>A	p.S1961T
118H2149S1	4	126369876	126369876	Missense_Mutation	SNP	G	A	A	FAT4	c.7705G>A	p.A2569T
118H2149S1	4	153244065	153244065	Missense_Mutation	SNP	G	T	T	FBXW7	c.2092C>A	p.L698M
118H2149S1	5	149456996	149456996	Missense_Mutation	SNP	G	A	A	CSF1R	c.732C>T	p.L244L
118H2149S1	5	156667179	156667179	Missense_Mutation	SNP	T	A	A	ITK	c.959T>A	p.I320N
118H2149S1	6	394941	394941	Missense_Mutation	SNP	C	T	T	IRF4	c.337C>T	p.R113W
118H2149S1	6	93965625	93965625	Missense_Mutation	SNP	C	T	T	EPHA7	c.2303G>A	p.S768N
118H2149S1	6	138202412	138202412	Missense_Mutation	SNP	G	A	A	TNFAIP3	c.2329G>A	p.G777S
118H2149S1	7	50450329	50450329	Missense_Mutation	SNP	G	T	T	IKZF1	c.513G>T	p.K171N
118H2149S1		-	-	Frame_Shift_Del	INS	-	-	-	CFTR	c.2835_2836del	p.K946Nfs*28
118H2149S1	8	139164544	139164544	Missense_Mutation	SNP	C	T	T	FAM135B	c.2174G>A	p.R725Q
118H2149S1	9	133760442	133760442	Missense_Mutation	SNP	C	T	T	ABL1	c.2822C>T	p.A941V
118H2157A1	11	92531778	92531778	Missense_Mutation	SNP	G	A	A	FAT3	c.5599G>A	p.V1867I
118H2157A1	15	99486181	99486181	Missense_Mutation	SNP	A	G	G	IGF1R	c.3487A>G	p.T1163A
118H2157A1		-	-	In_Frame_Del	INS	-	-	-	CYLD	c.1421_1434del	p.S474*
118H2157A1	17	7578190	7578190	Missense_Mutation	SNP	T	C	C	TP53	c.659A>G	p.Y220C
118H2157A1	17	29684041	29684041	Nonsense_Mutation	SNP	C	A	A	NF1	c.7802C>A	p.S2601*
118H2157A1	19	1226453	1226453	Missense_Mutation	SNP	G	T	T	STK11	c.1109G>T	p.G370V
118H2157A1	3	89456434	89456434	Missense_Mutation	SNP	G	A	A	EPHA3	c.1610G>A	p.G537D
118H2157A1	6	157511321	157511321	Missense_Mutation	SNP	A	G	G	ARID1B	c.3839A>G	p.D1280G
118H2157A1	9	36846891	36846891	Missense_Mutation	SNP	G	T	T	PAX5	c.1048C>A	p.Q350K
118H2438A1	1	16464509	16464509	Missense_Mutation	SNP	C	T	T	EPHA2	c.1151G>A	p.R384H
118H2438A1		-	-	Frame_Shift_Ins	INS	-	-	-	ARID1A	c.4303_4340dup	p.A1448Rfs*46
118H2438A1	17	7577559	7577559	Missense_Mutation	SNP	G	T	T	TP53	c.722C>A	p.S241Y
118H2438A1	18	48593397	48593397	Missense_Mutation	SNP	T	G	G	SMAD4	c.1148T>G	p.I383R
118H2438A1	2	170115694	170115694	Missense_Mutation	SNP	T	C	C	LRP2	c.2354A>G	p.N785S
118H2438A1	8	68864735	68864735	Missense_Mutation	SNP	C	T	T	PREX2	c.106C>T	p.R36W
118H2472A1	1	158622390	158622390	Missense_Mutation	SNP	C	T	T	SPTA1	c.3242G>A	p.R1081H
118H2472A1		-	-	Missense_Mutation	SNP	-	-	-	KRAS	c.35_36delinsTC	p.G12V
118H2472A1	2	198267483	198267483	Missense_Mutation	SNP	C	T	T	SF3B1	c.1874G>A	p.R625H
118H2472A1	3	52637554	52637554	Missense_Mutation	SNP	C	T	T	PBRM1	c.2762G>A	p.R921Q
118H2472A1	7	142458528	142458528	Missense_Mutation	SNP	G	A	A	PRSS1	c.163G>A	p.E55K
118H2472A1	9	21971120	21971120	Nonsense_Mutation	SNP	G	A	A	CDKN2A	c.238C>T	p.R80*
118H2473A1	10	84733640	84733640	Missense_Mutation	SNP	G	A	A	NRG3	c.1381G>A	p.D461N
118H2473A1	15	67482861	67482861	Missense_Mutation	SNP	C	T	T	SMAD3	c.1265C>T	p.S422F
118H2473A1	15	93515167	93515167	Splice_Site	SNP	T	C	C	CHD2	c.2352+10T>C	-
118H2473A1		-	-	Frame_Shift_Del	INS	-	-	-	TP53	c.994_1012del	p.I332Sfs*7
118H2473A1	17	29528441	29528441	Nonsense_Mutation	SNP	C	T	T	NF1	c.1198C>T;1205C>G	p.Q400*;S402L
118H2473A1	17	29528489	29528489	Nonsense_Mutation	SNP	C	T	T	NF1	c.1246C>T	p.R416*
118H2473A1	17	29667602	29667602	Missense_Mutation	SNP	G	A	A	NF1	c.7001G>A	p.G2334D
118H2473A1	19	2199922	2199922	Nonsense_Mutation	SNP	C	T	T	DOT1L	c.691C>T	p.R231*
118H2473A1	19	11136147	11136147	Missense_Mutation	SNP	A	C	C	SMARCA4	c.3131A>C	p.K1044T
118H2473A1	22	42525827	42525827	Missense_Mutation	SNP	C	T	T	CYP2D6	c.265G>A	p.E89K
118H2473A1	3	178952090	178952090	Missense_Mutation	SNP	G	C	C	PIK3CA	c.3145G>C	p.G1049R

118H2473A1	5	112137007	112137007	Missense_Mutation	SNP	C	T	T	APC	c.761C>T	p.S254L
118H2473A1	5	176662911	176662911	Missense_Mutation	SNP	A	C	C	NSD1	c.3886A>C	p.K1296Q
118H2473A1	9	139390602	139390602	Missense_Mutation	SNP	G	A	A	NOTCH1	c.7589C>T	p.S2530F
118H2475M1	12	25398284	25398284	Missense_Mutation	SNP	C	A	A	KRAS	c.35G>T	p.G12V
118H2475M1	2	198266834	198266834	Missense_Mutation	SNP	T	C	C	SF3B1	c.2098A>G	p.K700E
118H2475M1	7	117232475	117232475	Missense_Mutation	SNP	A	G	G	CFTR	c.2254A>G	p.V752V
118H2475M1	9	101900221	101900221	Missense_Mutation	SNP	G	T	T	TGFBR1	c.655G>T	p.V219F
118H2476A1	-	-	-	Frame_Shift_Del	INS	-	-	-	LRP1	11695_11696del	p.S3899Cfs*4
118H2476A1	-	-	-	Missense_Mutation	SNP	-	-	-	CREBBP	c.5039_5041del	p.S1680del
118H2476A1	-	-	-	In_Frame_Ins	INS	-	-	-	MSH6	c.1608dup	p.K537*
118H2476A1	3	52442512	52442512	Missense_Mutation	SNP	T	C	C	BAP1	c.233A>G	p.N78S
118H2476A1	-	-	-	Frame_Shift_Ins	INS	-	-	-	TNFAIP3	c.655dup	p.E219Gfs*35
118H2476A1	7	140453136	140453136	Missense_Mutation	SNP	A	T	T	BRAF	c.1799T>A	p.V600E
118H2503A1	12	49433655	49433655	Nonsense_Mutation	SNP	G	C	C	KMT2D	c.7898C>G	p.S2633*
118H2503A1	16	23646503	23646503	Missense_Mutation	SNP	T	C	C	PALB2	c.1364A>G	p.N455S
118H2503A1	16	68867235	68867235	Missense_Mutation	SNP	G	A	A	CDH1	c.2482G>A	p.D28N
118H2503A1	17	7577505	7577505	Missense_Mutation	SNP	T	A	A	TP53	c.776A>T	p.D259V
118H2503A1	20	52193685	52193685	Nonsense_Mutation	SNP	G	A	A	ZNF217	c.1618C>T	p.Q540*
118H2503A1	3	47158212	47158212	Missense_Mutation	SNP	C	A	A	SETD2	c.4487G>T	p.R1496L
118H2503A1	3	52440271	52440271	Nonsense_Mutation	SNP	G	A	A	BAP1	c.781C>T	p.G216*
118H2503A1	3	52598140	52598140	Missense_Mutation	SNP	C	A	A	PBRM1	c.3726G>T	p.Q1242H
118H2503A1	9	139401405	139401405	Missense_Mutation	SNP	C	T	T	NOTCH1	c.3664G>A	p.V1222M
118H2503A1	X	123197056	123197056	Splice_Site	SNP	G	C	C	STAG2	c.1821+1G>C	-
118H2531A3	11	128680614	128680614	Missense_Mutation	SNP	G	A	A	FLI1	c.1090G>A	p.G364S
118H2531A3	12	12870900	12870900	Missense_Mutation	SNP	C	G	G	CDKN1B	c.127C>G	p.R43G
118H2531A3	12	133254193	133254193	Missense_Mutation	SNP	G	A	A	POLE	c.691C>T	p.R231C
118H2531A3	17	7577094	7577094	Missense_Mutation	SNP	G	A	A	TP53	c.844C>T	p.R282W
118H2531A3	19	17940997	17940997	Missense_Mutation	SNP	C	G	G	JAK3	c.3127G>C	p.D1043H
118H2540A1	-	-	-	Frame_Shift_Ins	INS	-	-	-	ARID1A	c.4689dup	p.M1564Hfs*8
118H2540A1	10	104353749	104353749	Splice_Site	SNP	G	A	A	SUFU	c.684-1G>A	-
118H2540A1	17	7578505	7578505	Missense_Mutation	SNP	G	A	A	TP53	c.425C>T	p.P142L
118H2588A1	16	343642	343642	Nonsense_Mutation	SNP	G	A	A	AXIN1	c.2032C>T	p.Q678*
118H2588A1	17	7578433	7578433	Nonsense_Mutation	SNP	G	C	C	TP53	c.497C>G	p.S166*
118H2588A1	18	48604778	48604778	Nonsense_Mutation	SNP	C	T	T	SMAD4	c.1600C>T	p.Q534*
118H2588A1	19	15288868	15288868	Missense_Mutation	SNP	G	A	A	NOTCH3	c.3871C>T	p.R1291C
118H2588A1	2	141665655	141665655	Splice_Site	SNP	A	T	T	LRP1B	c.3320-9T>A	-
118H2588A1	22	41545883	41545883	Missense_Mutation	SNP	C	T	T	EP300	c.2498C>T	p.S833L
118H2588A1	3	178921553	178921553	Missense_Mutation	SNP	T	A	A	PIK3CA	c.1035T>A	p.N345K
118H2588A1	7	151853289	151853289	Splice_Site	SNP	C	G	G	KMT2C	c.11812+1G>C	-
118H2588A1	9	97869493	97869493	Nonsense_Mutation	SNP	G	C	C	FANCC	c.1388C>G	p.S463*
118H2593A1	1	120462972	120462972	Missense_Mutation	SNP	G	A	A	NOTCH2	c.5359C>T	p.R1787W
118H2593A1	12	25398284	25398284	Missense_Mutation	SNP	C	T	T	KRAS	c.35G>A	p.G12D
118H2593A1	20	36024580	36024580	Missense_Mutation	SNP	C	T	T	SRC	c.569C>T	p.S190L
118H2593A1	-	-	-	Frame_Shift_Del	INS	-	-	-	CDKN1A	C.251_288del	P.R84Hfs*32
118H2593A1	9	101904862	101904862	Nonsense_Mutation	SNP	G	T	T	TGFBR1	c.850G>T	p.E284*
118H2626A1	11	92257952	92257952	Missense_Mutation	SNP	T	A	A	FAT3	c.3445T>A	p.S1149T
118H2626A1	11	108216606	108216606	Missense_Mutation	SNP	A	G	G	ATM	c.8555A>G	p.Y2852C
118H2626A1	12	25398284	25398284	Missense_Mutation	SNP	C	A	A	KRAS	c.35G>T	p.G12V
118H2626A1	19	10463722	10463722	Missense_Mutation	SNP	C	T	T	TYK2	c.3080G>A	p.R1027H
118H2626A1	2	74317026	74317026	Missense_Mutation	SNP	G	A	A	TEF3	c.2891G>A	p.R964Q
118H2626A1	4	55946257	55946257	Missense_Mutation	SNP	C	T	T	KDR	c.3922G>A	p.G1308R
118H2626A1	7	138252244	138252244	Missense_Mutation	SNP	A	G	G	TRIM24	c.1447A>G	p.I483V
118H2626A1	8	41800520	41800520	Splice_Site	SNP	T	A	A	KAT6A	c.2229-2A>T	-
118H2716A1	12	25398285	25398285	Missense_Mutation	SNP	C	T	T	KRAS	c.34G>A	p.G12S
118H2716A1	17	7578406	7578406	Missense_Mutation	SNP	C	T	T	TP53	c.524G>A	p.R175H
118H2716A1	9	101908834	101908834	Missense_Mutation	SNP	G	A	A	TGFBR1	c.1198G>A	p.D400N
118H2758A1	-	-	-	Splice_Site	SNP	-	-	-	PTEN	209+4_209+7del	-
118H2758A1	-	-	-	Frame_Shift_Ins	INS	-	-	-	PTEN	c.920dup	p.R308Afs*4
118H2758A1	12	56482552	56482552	Missense_Mutation	SNP	G	A	A	ERBB3	c.1009G>A	p.G337R
118H2758A1	17	7578403	7578403	Missense_Mutation	SNP	C	T	T	TP53	c.527G>A	p.C176V
118H2758A1	-	-	-	Frame_Shift_Del	INS	-	-	-	SMAD4	c.579_580del	p.E193Dfs*12
118H2758A1	19	10600330	10600330	Missense_Mutation	SNP	C	G	G	KEAP1	c.1525G>C	p.G509R
118H2758A1	2	141283484	141283484	Missense_Mutation	SNP	C	A	A	LRP1B	c.7955G>T	p.C2652F
118H2758A1	-	-	-	Frame_Shift_Del	INS	-	-	-	PIK3R1	c.622del	p.S208Lfs*2
118H2758A1	-	-	-	Frame_Shift_Del	INS	-	-	-	APC	c.5455_5458del	p.N1819Pfs*43
118I2919A1	-	-	-	Frame_Shift_Del	INS	-	-	-	EPHA2	c.1429_1432del	p.G477Tfs*15
118I2919A1	12	133202852	133202852	Missense_Mutation	SNP	C	T	T	POLE	c.6382G>A	p.D2128N
118I2919A1	17	7577534	7577534	Missense_Mutation	SNP	C	A	A	TP53	c.747G>T	p.R249S
118I2919A1	2	61753601	61753601	Missense_Mutation	SNP	G	A	A	XP01	c.182C>T	p.T61I
118I2919A1	2	141643827	141643827	Missense_Mutation	SNP	G	T	T	LRP1B	c.3844C>A	p.L1282I
118I2919A1	6	41909240	41909240	Missense_Mutation	SNP	G	C	C	CNN3	c.148C>G	p.R50G
118I2919A1	X	123022478	123022478	Missense_Mutation	SNP	A	G	G	XIAP	c.887A>G	p.D296G
118I2978M1	15	67473693	67473693	Missense_Mutation	SNP	A	G	G	SMAD3	c.773A>G	p.D258G
118I2978M1	18	48575192	48575192	Missense_Mutation	SNP	A	G	G	SMAD4	c.386A>G	p.N129S
118I2978M1	-	-	-	Frame_Shift_Del	INS	-	-	-	PBRM1	C.3507del	P.I1170Sfs*23
118I2978M1	-	-	-	Frame_Shift_Ins	INS	-	-	-	ARID1B	C.1400_1410dup	P.A471Sfs*35
118I2978M1	X	44921964	44921964	Missense_Mutation	SNP	A	G	G	KDM6A	c.1498A>G	p.S500G
118I3162A1	1	120050217	120050217	Missense_Mutation	SNP	G	A	A	HSD3B1	c.118G>A	p.G40R
118I3162A1	12	25398284	25398284	Missense_Mutation	SNP	C	T	T	KRAS	c.35G>A	p.G12D
118I3162A1	17	7576928	7576928	Splice_Site	SNP	T	A	A	TP53	c.920-2A>T	-
118I3162A1	19	11143991	11143991	Missense_Mutation	SNP	A	G	G	SMARCA4	c.3572A>G	p.H1191R
118I3162A1	20	57484420	57484420	Missense_Mutation	SNP	C	T	T	GNAS	c.601C>T	p.R201C
118I3162A1	22	41574029	41574029	Missense_Mutation	SNP	G	T	T	EP300	c.6314G>T	p.G2105V
118I3162A1	4	20525511	20525511	Missense_Mutation	SNP	G	A	A	SLIT2	c.1259G>A	p.R420Q
118I3162A1	6	93979390	93979390	Splice_Site	SNP	A	G	G	EPHA7	c.1450-12T>C	-
118I3162A1	6	117718076	117718076	Splice_Site	SNP	A	T	T	ROS1	c.779+2T>A	-
118I3162A1	-	-	-	Frame_Shift_Del	INS	-	-	-	BCORL1	C.2495del	P.G832Afs*21
118I3202A1	12	49448150	49448150	Nonsense_Mutation	SNP	C	T	T	KMT2D	c.450G>A	p.W150*
118I3202A1	15	91312768	91312768	Missense_Mutation	SNP	G	T	T	BLM	c.2507G>T	p.R836M
118I3202A1	7	140453136	140453136	Missense_Mutation	SNP	A	T	T	BRAF	c.1799T>A	p.V600E
118I3202A1	9	98211397	98211397	Missense_Mutation	SNP	T	G	G	PTCH1	c.3758A>C	p.Q1253P
118I3202A1	X	129159159	129159159	Missense_Mutation	SNP	C	A	A	BCORL1	c.3883C>A	p.L1295M
118I3202A1	19	11135115	11135115	Splice_Site	SNP	G	A	A	SMARCA4	c.3081+1G>A	-
118I3426A1	1	7724489	7724489	Missense_Mutation	SNP	G	A	A	CAMTA1	c.1882G>A	p.E628K
118I3426A1	1	204394048	204394048	Nonsense_Mutation	SNP	C	A	A	PIK3C2B	c.4837G>T	p.E1613*
118I3426A1	12	56488302	56488302	Missense_Mutation	SNP	G	C	C	ERBB3	c.1821G>C	p.Q607H
118I3426A1	14	95592940	95592940	Missense_Mutation	SNP	C	G	G	DICER1	c.880G>C	p.D294H
118I3426A1	17	7578275	7578275	Nonsense_Mutation	SNP	G	A	A	TP53	c.574C>T	p.Q192*

11813426A1	2	16082426	16082426	Missense_Mutation	SNP	G	C	C	MYCN	c.240G>C	p.E80D
11813426A1	2	74275364	74275364	Missense_Mutation	SNP	C	T	T	TET3	c.2320C>T	p.H774Y
11813426A1	2	141215176	141215176	Missense_Mutation	SNP	C	T	T	LRP1B	c.9670G>A	p.E3224K
11813426A1	20	31023588	31023588	Missense_Mutation	SNP	A	G	G	ASXL1	c.3073A>G	p.K1025E
11813426A1	22	21345973	21345973	Missense_Mutation	SNP	G	A	A	LZTR1	c.848G>A	p.R283Q
11813426A1	3	49939840	49939840	Missense_Mutation	SNP	G	T	T	MTST1R	c.1203C>A	p.F401L
11813426A1	3	71050211	71050211	Splice_Site	SNP	C	G	G	FOXP1	c.975-1G>C	-
11813426A1	5	112176873	112176873	Missense_Mutation	SNP	C	T	T	APC	c.5582C>T	p.S1861F
11813426A1	6	152332800	152332800	Missense_Mutation	SNP	A	T	T	ESR1	c.1106A>T	p.D369V
11813426A1	6	163983083	163983083	Missense_Mutation	SNP	G	A	A	QKI	c.616G>A	p.D206N
11813426A1	7	18630059	18630059	Missense_Mutation	SNP	G	A	A	HDAC9	c.356G>A	p.R119H
11813426A1	7	41730075	41730075	Missense_Mutation	SNP	G	A	A	INHBA	c.454C>T	p.R152C
11813426A1	7	86468307	86468307	Missense_Mutation	SNP	G	C	C	GRM3	c.1477G>C	p.D493H
11813426A1	7	117243617	117243617	Missense_Mutation	SNP	C	A	A	CFTR	c.2689C>A	p.H897N
11813426A1	7	141430086	141430086	Splice_Site	SNP	G	C	C	WEE2	c.1679-9G>C	-
11813426A1	9	21971036	21971036	Missense_Mutation	SNP	C	T	T	CDKN2A	c.322G>A	p.D108N
11813426A1	X	66905906	66905906	Missense_Mutation	SNP	G	A	A	AR	c.1823G>A	p.R608Q
11813426A1	X	76855029	76855029	Missense_Mutation	SNP	T	C	C	ATRX	c.5807A>G	p.K1936R
11813457A2	-	-	-	Frame_Shift_Ins	INS	-	-	-	ROCK1	c.3921dup	p.W1308Mfs*11
11813457A2	-	-	-	In_Frame_Del	INS	-	-	-	BAP1	c.149_150del	p.F50*
11813472M1	4	20598129	20598129	Missense_Mutation	SNP	G	A	A	SLIT2	c.3412G>A	p.V1138I
11813472M1	6	152265322	152265322	Nonsense_Mutation	SNP	C	T	T	ESR1	c.775C>T	p.R259*
11813488A1	12	25398284	25398284	Missense_Mutation	SNP	C	A	A	KRAS	c.35G>T	p.G12V
11813488A1	2	198266835	198266835	Missense_Mutation	SNP	C	A	A	SF3B1	c.2097G>T;2098A	p.Q699H;K700E
11813488A1	3	30715615	30715615	Missense_Mutation	SNP	A	G	G	TGFB2	c.1273A>G	p.M425V
11813488A1	-	-	-	Frame_Shift_Del	INS	-	-	-	RBM10	c.2581del	p.I861Lfs*25
11813510A1	1	11187848	11187848	Missense_Mutation	SNP	T	C	C	MTOR	c.6049A>G	p.I2017V
11813510A1	-	-	-	Frame_Shift_Del	INS	-	-	-	EPHA2	c.1379del	p.P460Rfs*33
11813510A1	10	89692800	89692800	Missense_Mutation	SNP	C	A	A	PTEN	c.284C>A	p.P95Q
11813510A1	11	118374156	118374156	Missense_Mutation	SNP	G	A	A	KMT2A	c.7549G>A	p.A2517T
11813510A1	12	416835	416835	Missense_Mutation	SNP	G	A	A	KDM5A	c.3715C>T	p.R1239W
11813510A1	-	-	-	Frame_Shift_Del	INS	-	-	-	ARID2	c.951_954del	p.L317Ffs*10
11813510A1	-	-	-	Frame_Shift_Del	INS	-	-	-	KMT2D	c.7061del	p.P2354Lfs*30
11813510A1	-	-	-	Frame_Shift_Del	INS	-	-	-	BRCA2	c.5351del	p.N1784Tfs*7
11813510A1	17	7579312	7579312	Missense_Mutation	SNP	C	T	T	TP53	c.375G>A	p.T125T
11813510A1	17	8110622	8110622	Missense_Mutation	SNP	G	A	A	AURKB	c.270C>T	p.N90N
11813510A1	17	12044500	12044500	Missense_Mutation	SNP	G	A	A	MAP2K4	c.1123G>A	p.V375I
11813510A1	17	37881332	37881332	Missense_Mutation	SNP	G	A	A	ERBB2	c.2524G>A	p.V842I
11813510A1	17	63533790	63533790	Missense_Mutation	SNP	G	A	A	AXIN2	c.1364C>T	p.P455L
11813510A1	17	70120496	70120496	Nonsense_Mutation	SNP	C	T	T	SOX9	c.1498C>T	p.Q500*
11813510A1	-	-	-	Frame_Shift_Del	INS	-	-	-	ACVR2A	c.1310del	p.K437Rfs*5
11813510A1	-	-	-	Frame_Shift_Del	INS	-	-	-	TGFB2	c.383del	p.K1285fs*35
11813510A1	4	55964878	55964878	Missense_Mutation	SNP	G	A	A	KDR	c.2359C>T	p.R787W
11813510A1	4	66356202	66356202	Missense_Mutation	SNP	A	C	C	EPHA5	c.1295T>G	p.L432R
11813510A1	-	-	-	Frame_Shift_Del	INS	-	-	-	PIK3R1	c.607del	p.Y203Tfs*4
11813510A1	-	-	-	Frame_Shift_Del	INS	-	-	-	CTNNA1	c.2213del	p.N738Ifs*53
11813510A1	6	135518403	135518403	Missense_Mutation	SNP	T	C	C	MYB	c.1508T>C	p.V503A
11813510A1	-	-	-	In_Frame_Del	INS	-	-	-	MAGI2	c.3207_3208del	p.Y1069*
11813510A1	7	151836767	151836767	Missense_Mutation	SNP	T	C	C	KMT2C	c.14453A>G	p.E4818G
11813510A1	7	151878034	151878034	Missense_Mutation	SNP	A	G	G	KMT2C	c.6911T>C	p.M2304T
11813510A1	7	152007121	152007121	Missense_Mutation	SNP	A	G	G	KMT2C	c.779T>C	p.L260P
11813510A1	8	71078959	71078959	Missense_Mutation	SNP	G	A	A	NCOA2	c.572C>T	p.P191L
11813510A1	8	139164508	139164508	Missense_Mutation	SNP	G	C	C	FAM135B	c.2210C>G	p.T737R
11813510A1	9	5126729	5126729	Missense_Mutation	SNP	C	T	T	JAK2	c.3337C>T	p.R1113C
11813510A1	9	87570290	87570290	Missense_Mutation	SNP	C	T	T	NTRK2	c.2030C>T	p.A677V
11813529A1	1	16482332	16482332	Splice_Site	SNP	C	T	T	EPHA2	c.85+11G>A	-
11813529A1	11	92616148	92616148	Missense_Mutation	SNP	C	T	T	FAT3	c.12526C>T	p.R4176C
11813529A1	17	7578460	7578460	Missense_Mutation	SNP	A	C	C	TP53	c.470T>G	p.V157G
11813529A1	-	-	-	Frame_Shift_Del	INS	-	-	-	SMAD4	c.681del	p.S227Rfs*14
11813529A1	4	55152038	55152038	Missense_Mutation	SNP	G	A	A	PDGFR	c.2470G>A	p.V824I
11813529A1	9	21971203	21971203	Missense_Mutation	SNP	A	T	T	CDKN2A	c.155T>A	p.M52K
11813529A1	-	-	-	Frame_Shift_Del	INS	-	-	-	RBM10	c.2118_2121del	p.R706Sfs*95
11813532A1	12	92538065	92538065	Missense_Mutation	SNP	T	A	A	BTG1	c.307A>T	p.T103S
11813532A1	17	7577548	7577548	Missense_Mutation	SNP	C	T	T	TP53	c.733G>A	p.G245S
11813532A1	18	48604665	48604665	Missense_Mutation	SNP	G	A	A	SMAD4	c.1487G>A	p.R496H
11813532A1	-	-	-	Frame_Shift_Ins	INS	-	-	-	TGFB2	c.229_232dup	p.E78Vfs*2
11813532A1	9	5126342	5126342	Missense_Mutation	SNP	C	T	T	JAK2	c.3187C>T	p.R1063C
11813573A1	-	-	-	Missense_Mutation	SNP	-	-	-	TET1	c.5877_5879del	p.E1959del
11813573A1	12	493228	493228	Missense_Mutation	SNP	C	G	G	KDM5A	c.335G>C	p.R112T
11813573A1	17	7577575	7577575	Missense_Mutation	SNP	A	G	G	TP53	c.706T>C	p.Y236H
11813573A1	-	-	-	Frame_Shift_Ins	INS	-	-	-	STK11	c.842dup	p.L282Afs*3
11813573A1	3	178936082	178936082	Missense_Mutation	SNP	G	A	A	PIK3CA	c.1624G>A	p.E542K
11813573A1	3	178936980	178936980	Splice_Site	SNP	A	G	G	PIK3CA	c.1665-4A>G	-
11813573A1	8	37555773	37555773	Missense_Mutation	SNP	G	A	A	ZNF703	c.1354G>A	p.E452K
11813576A1	12	25398284	25398284	Missense_Mutation	SNP	C	G	G	KRAS	c.35G>C	p.G12A
11813576A1	17	7577142	7577142	Missense_Mutation	SNP	C	T	T	TP53	c.796G>A	p.G266R
11813592A2	-	-	-	Frame_Shift_Del	INS	-	-	-	ARID1A	c.3893del	p.G1298Efs*3
11813592A2	1	156845877	156845877	Missense_Mutation	SNP	C	T	T	NTRK1	c.1489C>T	p.H497Y
11813592A2	1	241682991	241682991	Missense_Mutation	SNP	G	C	C	FH	c.32C>G	p.S111W
11813592A2	10	89624289	89624289	Missense_Mutation	SNP	C	G	G	PTEN	c.63C>G	p.F21L
11813592A2	11	92526050	92526050	Missense_Mutation	SNP	G	C	C	FAT3	c.4729G>C	p.E1577Q
11813592A2	12	56474020	56474020	Splice_Site	SNP	C	G	G	ERBB3	c.-65C>G	-
11813592A2	12	56481922	56481922	Missense_Mutation	SNP	G	A	A	ERBB3	c.850G>A	p.G284R
11813592A2	15	91312441	91312441	Missense_Mutation	SNP	G	A	A	BLM	c.2386G>A	p.E796K
11813592A2	18	48603023	48603023	Nonsense_Mutation	SNP	C	T	T	SMAD4	c.1324C>T	p.Q442*
11813592A2	19	11144536	11144536	Missense_Mutation	SNP	C	G	G	SMARCA4	c.3868C>G	p.L1290V
11813592A2	20	62338444	62338444	Splice_Site	SNP	-	-	-	ARFRP1	c.-1-3C>A	-
11813592A2	3	178936091	178936091	Missense_Mutation	SNP	G	A	A	PIK3CA	c.1633G>A	p.E545K
11813592A2	4	126412807	126412807	Missense_Mutation	SNP	G	A	A	FAT4	c.14830G>A	p.V494I
11813592A2	7	55218984	55218984	Splice_Site	SNP	C	T	T	EGFR	c.560-3C>T	-
11813592A2	8	71068334	71068334	Missense_Mutation	SNP	C	G	G	NCOA2	c.2266G>C	p.D756H
11813592A2	9	101894916	101894916	Nonsense_Mutation	SNP	C	T	T	TGFB1	c.469C>T	p.R157*
11813592A2	X	44936067	44936067	Missense_Mutation	SNP	T	G	G	KDM6A	c.2828T>G	p.I943S
11813592A2	X	47430749	47430749	Missense_Mutation	SNP	C	T	T	ARAF	c.1714C>T	p.R572W
11813607A2	1	158589112	158589112	Missense_Mutation	SNP	C	G	G	SPTA1	c.6430G>C	p.E2144Q
11813607A2	1	158613109	158613109	Splice_Site	SNP	G	C	C	SPTA1	c.4442+3C>G	-
11813607A2	-	-	-	Frame_Shift_Ins	INS	-	-	-	TP53	c.902dup	p.G302Rfs*4
11813607A2	17	37646932	37646932	Missense_Mutation	SNP	C	G	G	CDK12	c.2054C>G	p.S685C

11813607A2	18	45372090	45372090	Missense_Mutation	SNP	G	T	T	SMAD2	c.989C>A	p.P330H
11813607A2	19	41727883	41727883	Missense_Mutation	SNP	G	C	C	AXL	c.508G>C	p.D170H
11813607A2	2	121746932	121746932	Missense_Mutation	SNP	G	A	A	GLI2	c.3442G>A	p.E1148K
11813607A2	20	57429319	57429319	Missense_Mutation	SNP	C	T	T	GNAS	c.812C>T	p.T271M
11813607A2	3	52692343	52692343	Splice_Site	SNP	G	T	T	PBRM1	c.529-12C>A	-
11813607A2	3	178919314	178919314	Missense_Mutation	SNP	C	A	A	PIK3CA	c.799C>A	p.L267M
11813607A2	4	185311889	185311889	Missense_Mutation	SNP	C	T	T	IRF2	c.709G>A	p.D237N
11813607A2	-	-	-	Frame_Shift_Del	INS	-	-	-	MAGI2	c.3111del	P.L1039Wfs*35
11813607A2	7	151945106	151945106	Missense_Mutation	SNP	T	C	C	KMT2C	c.2413A>G	p.S805G
11813607A2	9	21971036	21971036	Missense_Mutation	SNP	C	T	T	CDKN2A	c.322G>A	p.D108N
11813607A2	X	47045464	47045464	Nonsense_Mutation	SNP	C	T	T	RBM10	c.2431C>T	p.Q811*
11813629A1	-	-	-	Frame_Shift_Del	INS	-	-	-	STK11	C.153_157del	P.M511fs*110
11813652A1	10	70451566	70451566	Missense_Mutation	SNP	G	T	T	TET1	c.6406G>T	p.V2136F
11813652A1	12	25398284	25398284	Missense_Mutation	SNP	C	T	T	KRAS	c.35G>A	p.G12D
11813652A1	-	-	-	Frame_Shift_Del	INS	-	-	-	STK11	C.64_92del	P.M22Hfs*131
11813652A1	2	141641582	141641582	Missense_Mutation	SNP	C	A	A	LRP1B	c.3973G>T	p.A1325S
11813652A1	2	141751692	141751692	Missense_Mutation	SNP	T	G	G	LRP1B	c.2516A>C	p.E839A
11813743M1	-	-	-	Frame_Shift_Ins	INS	-	-	-	EPHA2	c.1199_1203dup	p.L402Afs*7
11813743M1	1	27100292	27100292	Splice_Site	SNP	G	A	A	ARID1A	c.4005-1G>A	-
11813743M1	14	45623981	45623981	Missense_Mutation	SNP	G	A	A	FANCM	c.1265G>A	p.R422H
11813743M1	17	7578457	7578457	Missense_Mutation	SNP	C	T	T	TP53	c.473G>A	p.R158H
11813743M1	-	-	-	Frame_Shift_Ins	INS	-	-	-	SMAD4	c.692dup	p.S232Qfs*3
11813743M1	20	57485014	57485014	Missense_Mutation	SNP	G	A	A	GNAS	c.848G>A	p.R283H
11813743M1	-	-	-	Frame_Shift_Del	INS	-	-	-	KMT2C	c.4937del	p.G1646Vfs*19
11813752D1	11	64573752	64573752	Missense_Mutation	SNP	A	C	C	MEN1	c.1001T>G	p.V334G
11813752D1	12	69203080	69203080	Splice_Site	SNP	T	C	C	MDM2	c.99+8T>C	-
11813752D1	13	43175020	43175020	Missense_Mutation	SNP	G	A	A	TNFSF11	c.216G>A	p.A72A
11813752D1	17	17116985	17116985	Missense_Mutation	SNP	G	A	A	FLCN	c.1724C>T	p.S575L
11813752D1	17	41244192	41244192	Missense_Mutation	SNP	G	C	C	BRCA1	c.3356C>G	p.T1119S
11813752D1	19	10602748	10602748	Missense_Mutation	SNP	G	T	T	KEAP1	c.830C>A	p.T277K
11813752D1	2	112751824	112751824	Splice_Site	SNP	C	A	A	MERTK	c.1297-4C>A	-
11813752D1	3	69987112	69987112	Missense_Mutation	SNP	G	T	T	MITF	c.173G>T	p.G58V
11813752D1	4	106197291	106197291	Missense_Mutation	SNP	G	A	A	TET2	c.5624G>A	p.C1875Y
11813752D1	9	21971179	21971179	Missense_Mutation	SNP	G	A	A	CDKN2A	c.179C>T	p.A60V
11813763A1	-	-	-	Frame_Shift_Del	INS	-	-	-	KMT2D	C.11684del	P.G3895Afs*84
11813763A1	12	133257726	133257726	Missense_Mutation	SNP	G	A	A	POLE	c.202C>T	p.P68S
11813763A1	16	3788629	3788629	Missense_Mutation	SNP	G	A	A	CREBBP	c.4325C>T	p.P1442L
11813763A1	17	7577609	7577609	Splice_Site	SNP	C	A	A	TP53	c.673-1G>T	-
11813763A1	2	141299380	141299380	Missense_Mutation	SNP	C	T	T	LRP1B	c.7355G>A	p.G2452E
11813763A1	4	55991418	55991418	Missense_Mutation	SNP	C	T	T	KDR	c.43G>A	p.V15M
11813763A1	X	39921616	39921616	Nonsense_Mutation	SNP	C	A	A	BCOR	c.4102G>T	p.E1368*
11813817A1	-	-	-	In_Frame_Del	INS	-	-	-	TP53	C.789_803del	P.L264_N268del
11813817A1	X	44918604	44918604	Missense_Mutation	SNP	G	A	A	KDM6A	c.1087G>A	p.E363K
11813847A1	12	25398284	25398284	Missense_Mutation	SNP	C	A	A	KRAS	c.35G>T	p.G12V
11813847A1	13	26956990	26956990	Nonsense_Mutation	SNP	C	T	T	CDK8	c.496C>T	p.R166*
11813847A1	17	7577570	7577570	Missense_Mutation	SNP	C	T	T	TP53	c.711G>A	p.M237I
11813847A1	22	29664332	29664332	Missense_Mutation	SNP	T	C	C	EWSR1	c.7T>C	p.S3P
11813847A1	6	117681042	117681042	Missense_Mutation	SNP	T	A	A	ROS1	c.3578A>T	p.N1193I
11813847A1	7	2959024	2959024	Missense_Mutation	SNP	G	A	A	CARD11	c.2492C>T	p.T831I
11813850D1	16	23646483	23646483	Missense_Mutation	SNP	C	G	G	PALB2	c.1384G>C	p.E462Q
11813850D1	-	-	-	Frame_Shift_Del	INS	-	-	-	PALB2	054_1056delins	p.E352Kfs*4
11813850D1	-	-	-	Frame_Shift_Del	INS	-	-	-	BAP1	C.714del	P.I2395fs*10
11813860A1	1	27023685	27023685	Nonsense_Mutation	SNP	C	A	A	ARID1A	c.791C>A	p.S264*
11813860A1	11	92534203	92534203	Missense_Mutation	SNP	C	T	T	FAT3	c.8024C>T	p.S2675L
11813860A1	12	25398282	25398282	Missense_Mutation	SNP	C	A	A	KRAS	c.37G>T	p.G13C
11813860A1	19	1220485	1220485	Missense_Mutation	SNP	C	G	G	STK11	c.578C>G	p.S193C
11813860A1	19	1220629	1220629	Missense_Mutation	SNP	C	T	T	STK11	c.647C>T	p.S216F
11813860A1	20	57429128	57429128	Missense_Mutation	SNP	G	A	A	GNAS	c.808G>A	p.A270T
11813860A1	4	55980357	55980357	Missense_Mutation	SNP	T	A	A	KDR	c.734A>T	p.N245I
11813860A1	7	151945622	151945622	Nonsense_Mutation	SNP	C	A	A	KMT2C	c.1897G>T	p.E633*
11813960A1	1	32741508	32741508	Splice_Site	SNP	C	G	G	LCK	c.482-7C>G	-
11813960A1	1	120471846	120471846	Splice_Site	SNP	G	C	C	NOTCH2	c.3656-11C>G	-
11813960A1	1	150551604	150551604	Missense_Mutation	SNP	C	G	G	MCL1	c.403G>C	p.G135R
11813960A1	12	133209059	133209059	Missense_Mutation	SNP	C	G	G	POLE	c.6172G>C	p.E2058Q
11813960A1	14	95570075	95570075	Missense_Mutation	SNP	G	C	C	DICER1	c.3658C>G	p.Q1220E
11813960A1	16	2129377	2129377	Missense_Mutation	SNP	C	T	T	TSC2	c.3232C>T	p.R1078W
11813960A1	16	9858439	9858439	Missense_Mutation	SNP	G	C	C	GRIN2A	c.2962C>G	p.L988W
11813960A1	16	89871757	89871757	Missense_Mutation	SNP	G	C	C	FANCA	c.640C>G	p.L214V
11813960A1	17	7577099	7577099	Missense_Mutation	SNP	C	T	T	TP53	c.839G>A	p.R280K
11813960A1	17	29556139	29556139	Missense_Mutation	SNP	G	A	A	NF1	c.2506G>A	p.E836K
11813960A1	17	29557890	29557890	Nonsense_Mutation	SNP	G	A	A	NF1	c.3144G>A	p.V1048*
11813960A1	17	33443866	33443866	Splice_Site	SNP	G	A	A	RAD51D	c.323+12C>T	-
11813960A1	17	40489460	40489460	Nonsense_Mutation	SNP	C	A	A	STAT3	c.790G>T	p.E264*
11813960A1	19	10599973	10599973	Missense_Mutation	SNP	C	G	G	KEAP1	c.1603G>C	p.E535Q
11813960A1	19	10600378	10600378	Missense_Mutation	SNP	C	G	G	KEAP1	c.1477G>C	p.E493Q
11813960A1	2	170060716	170060716	Missense_Mutation	SNP	T	C	C	LRP2	c.7781A>G	p.H2594R
11813960A1	6	117641019	117641019	Splice_Site	SNP	G	A	A	ROS1	c.5940+12C>T	-
11813960A1	8	68995502	68995502	Missense_Mutation	SNP	A	T	T	PREX2	c.1906A>T	p.I636F
11813960A1	9	5044518	5044518	Nonsense_Mutation	SNP	C	T	T	JAK2	c.466C>T	p.Q156*
11813967M1	1	27087440	27087440	Nonsense_Mutation	SNP	G	T	T	ARID1A	c.2014G>T	p.E672*
11813967M1	1	46726267	46726267	Missense_Mutation	SNP	G	A	A	RAD54L	c.461G>A	p.R154Q
11813967M1	1	158612287	158612287	Missense_Mutation	SNP	G	C	C	SPTA1	c.4651C>G	p.R1551G
11813967M1	12	25398284	25398284	Missense_Mutation	SNP	C	T	T	KRAS	c.35G>A	p.G12D
11813967M1	16	81888057	81888057	Missense_Mutation	SNP	A	T	T	PLCG2	c.202A>T	p.M68L
11813967M1	19	10599916	10599916	Nonsense_Mutation	SNP	G	A	A	KEAP1	c.1660C>T	p.R554*
11813967M1	19	17952448	17952448	Splice_Site	SNP	C	A	A	JAK3	c.984+1G>T	-
11813967M1	4	126328026	126328026	Splice_Site	SNP	T	C	C	FAT4	c.5308-9T>C	-
11813967M1	5	35873749	35873749	Missense_Mutation	SNP	A	C	C	IL7R	c.705A>C	p.S235S
11813967M1	5	112128185	112128185	Missense_Mutation	SNP	C	T	T	APC	c.688C>T	p.R230C
11813967M1	-	-	-	In_Frame_Ins	INS	-	-	-	ARID1B	c.363_368dup	Q130_Q131dup
11813967M1	6	157505488	157505488	Nonsense_Mutation	SNP	G	T	T	ARID1B	c.3469G>T	p.E1157*
11813967M1	8	71041103	71041103	Missense_Mutation	SNP	C	G	G	NCOA2	c.3437G>C	p.G1146A
11813967M1	9	133760285	133760285	Missense_Mutation	SNP	G	A	A	ABL1	c.2665G>A	p.A889T
11813967M1	9	139391265	139391265	Missense_Mutation	SNP	T	A	A	NOTCH1	c.6926A>T	p.E2309V
11813967M1	9	139409801	139409801	Missense_Mutation	SNP	G	A	A	NOTCH1	c.1955C>T	p.S652L
11813967M1	-	-	-	Frame_Shift_Ins	INS	-	-	-	RBM10	c.627dup	p.K210Qfs*6
11814062A1	-	-	-	Frame_Shift_Ins	INS	-	-	-	ARID1A	C.3216dup	P.W1073Mfs*32
11814062A1	1	206658350	206658350	Nonsense_Mutation	SNP	G	T	T	IKBKE	c.1444G>T	p.G482*

118I4062A1	12	12871086	12871086	Nonsense_Mutation	SNP	G	T	T	CDKN1B	c.313G>T	p.E105*
118I4062A1	12	25398284	25398284	Missense_Mutation	SNP	C	T	T	KRAS	c.35G>A	p.G12D
118I4062A1	17	7578394	7578394	Missense_Mutation	SNP	T	A	A	TP53	c.536A>T	p.H179L
118I4224A1		-	-	Splice_Site	SNP	-	-	-	KMT2A	c.3569+1del	-
118I4224A1		-	-	Frame_Shift_Ins	INS	-	-	-	TP53	c.120_121dup	p.D41Gfs*4
118I4224A1	2	140995831	140995831	Missense_Mutation	SNP	C	T	T	LRP1B	c.13450G>A	p.G4484R
118I4224A1		-	-	Splice_Site	SNP	-	-	-	EGFR	2185-9_2185-8c	-
118I4224A1	9	98215869	98215869	Missense_Mutation	SNP	T	A	A	PTCH1	c.3340A>T	p.R1114W
118I4228A1	1	8074231	8074231	Missense_Mutation	SNP	G	A	A	ERRF1	c.428C>T	p.A143V
118I4228A1	1	11259456	11259456	Missense_Mutation	SNP	G	C	C	MTOR	c.4112C>G	p.P1371R
118I4228A1	1	27106354	27106354	Nonsense_Mutation	SNP	C	T	T	ARID1A	c.5965C>T	p.R1989*
118I4228A1	12	6692520	6692520	Missense_Mutation	SNP	T	C	C	CHD4	c.3904A>G	p.I1302V
118I4228A1	17	7577538	7577538	Missense_Mutation	SNP	C	T	T	TP53	c.743G>A	p.R248Q
118I4228A1	18	48593406	48593406	Missense_Mutation	SNP	G	T	T	SMAD4	c.1157G>T	p.G386V
118I4228A1	2	47643508	47643508	Missense_Mutation	SNP	A	C	C	MSH2	c.1016A>C	p.Q339P
118I4228A1	7	81339562	81339562	Splice_Site	SNP	G	A	A	HGF	c.1445-3C>T	-
118I4228A1	X	39932447	39932447	Missense_Mutation	SNP	C	T	T	BCOR	c.2152G>A	p.D718N
118I4287M1	1	16262141	16262141	Missense_Mutation	SNP	C	T	T	SPEN	c.9406C>T	p.R3136C
118I4287M1	10	84738818	84738818	Missense_Mutation	SNP	G	A	A	NRG3	c.1525G>A	p.A509T
118I4287M1	10	123274774	123274774	Missense_Mutation	SNP	A	G	G	FGFR2	c.1144T>C	p.C328R
118I4287M1	14	105239435	105239435	Splice_Site	SNP	C	T	T	AKT1	c.958-6G>A	-
118I4287M1	16	9923507	9923507	Missense_Mutation	SNP	G	A	A	GRIN2A	c.1780C>T	p.P594S
118I4287M1	17	7579358	7579358	Missense_Mutation	SNP	C	T	T	TP53	c.329G>A	p.R110H
118I4287M1	17	56440640	56440640	Missense_Mutation	SNP	G	A	A	RNF43	c.578C>T	p.A193V
118I4287M1	2	48030630	48030630	Missense_Mutation	SNP	C	T	T	MSH6	c.3244C>T	p.P1082S
118I4287M1	2	61753549	61753549	Splice_Site	SNP	G	A	A	XPO1	c.228+6C>T	-
118I4287M1	2	109368337	109368337	Missense_Mutation	SNP	G	T	T	RANBP2	c.1642G>T	p.V548L
118I4287M1	2	141641379	141641379	Splice_Site	SNP	T	G	G	LRP1B	c.4169+7A>C	-
118I4287M1	3	52441235	52441235	Missense_Mutation	SNP	G	A	A	BAP1	c.535C>T	p.R179W
118I4287M1	3	142275266	142275266	Missense_Mutation	SNP	C	G	G	ATR	c.2037G>C	p.L679F
118I4287M1	3	178916930	178916930	Missense_Mutation	SNP	G	T	T	PIK3CA	c.317G>T	p.G106V
118I4287M1	3	185775016	185775016	Missense_Mutation	SNP	G	C	C	ETV5	c.1057C>G	p.P353A
118I4287M1	4	126372111	126372111	Missense_Mutation	SNP	G	T	T	FAT4	c.9940G>T	p.G3314C
118I4287M1	7	117243698	117243698	Missense_Mutation	SNP	G	A	A	CFTR	c.2770G>A	p.D924N
118I4287M1	8	48811106	48811106	Missense_Mutation	SNP	C	A	A	PRKDC	c.3388G>T	p.A1130S
118I4299M1		-	-	Frame_Shift_Del	INS	-	-	-	ARID1A	c.5198_5204del	p.E1733Gfs*35
118I4299M1		-	-	Frame_Shift_Del	INS	-	-	-	TP53	c.956del	p.K319Rfs*26
118I4299M1		-	-	Splice_Site	SNP	-	-	-	EGFR	c.1881-6dup	-
118I4384A1		-	-	Splice_Site	SNP	-	-	-	BAP1	c.67+2_67+4del	-
118I4450M1		-	-	Frame_Shift_Ins	INS	-	-	-	ERRF1	c.336_339dup	p.G114Mfs*4
118I4450M1		-	-	Frame_Shift_Del	INS	-	-	-	ARID1A	c.2186_2196del	p.P729Lfs*84
118I4450M1	11	108213974	108213974	Missense_Mutation	SNP	G	T	T	ATM	c.8294G>T	p.G2765S
118I4450M1	8	32505402	32505402	Missense_Mutation	SNP	G	A	A	NRG1	c.166G>A	p.V56M
118I4450M1	X	47041442	47041442	Splice_Site	SNP	G	A	A	RBM10	c.1785+1G>A	-
118I4625A1	12	25398285	25398285	Missense_Mutation	SNP	C	A	A	KRAS	c.34G>T	p.G12C
118I4625A1		-	-	Frame_Shift_Ins	INS	-	-	-	KMT2D	c.15539dup	p.L5183Pfs*16
118I4625A1	2	170066064	170066064	Missense_Mutation	SNP	G	A	A	LRP2	c.6368C>T	p.A2123V
118I4625A1	2	198266713	198266713	Missense_Mutation	SNP	C	T	T	SF3B1	c.2219G>A	p.G740E
118I4646M1	1	158614125	158614125	Missense_Mutation	SNP	C	G	G	SPTA1	c.4256G>C	p.R1419T
118I4646M1	11	125514167	125514167	Splice_Site	SNP	A	T	T	CHEK1	c.1101+4A>T	-
118I4646M1	12	115112332	115112332	Missense_Mutation	SNP	C	T	T	TBX3	c.1408G>A	p.A470T
118I4646M1		-	-	In_Frame_Ins	INS	-	-	-	FLT1	c.2178_2180dup	p.*734Sext*1
118I4646M1		-	-	Frame_Shift_Del	INS	-	-	-	TP53	c.365_366del	p.V122Dfs*26
118I4646M1	17	48263861	48263861	Nonsense_Mutation	SNP	G	C	C	COL1A1	c.3822C>G	p.Y1274*
118I4646M1	19	40744823	40744823	Missense_Mutation	SNP	T	C	C	AKT2	c.697A>G	p.N233D
118I4646M1	2	25467502	25467502	Missense_Mutation	SNP	G	A	A	DNMT3A	c.1574C>T	p.A525V
118I4646M1	2	47690161	47690161	Splice_Site	SNP	T	G	G	MSH2	c.1387-9T>G	-
118I4646M1		-	-	Frame_Shift_Del	INS	-	-	-	BAP1	c.145del	p.L49Cfs*23
118I4646M1	7	117243635	117243635	Missense_Mutation	SNP	T	G	G	CFTR	c.2707T>G	p.Y903D
118I4748M1	19	11123691	11123691	Missense_Mutation	SNP	A	G	G	SMARCA4	c.2341A>G	p.M781V
118I4748M1	7	140453136	140453136	Missense_Mutation	SNP	A	T	T	BRAF	c.1799T>A	p.V600E
118I4748M1	8	139163664	139163664	Missense_Mutation	SNP	C	A	A	FAM135B	c.3054G>T	p.E1018D
118I4750A1	10	89692853	89692853	Missense_Mutation	SNP	A	C	C	PTEN	c.337A>C	p.S113R
118I4750A1	4	55593651	55593651	Missense_Mutation	SNP	C	T	T	KIT	c.1717C>T	p.P573S
118I4755M1	1	158618388	158618388	Missense_Mutation	SNP	C	T	T	SPTA1	c.3625G>A	p.A1209T
118I4755M1	17	7577568	7577568	Missense_Mutation	SNP	C	A	A	TP53	c.713G>T	p.C238F
118I4755M1	8	69030814	69030814	Missense_Mutation	SNP	C	G	G	PREX2	c.3356C>G	p.A1119G
118I4761A1	12	25398284	25398284	Missense_Mutation	SNP	C	T	T	KRAS	c.35G>A	p.G12D
118I4761A1		-	-	Frame_Shift_Del	INS	-	-	-	TP53	c.486del	p.Y163Tfs*7
118I4761A1		-	-	Frame_Shift_Ins	INS	-	-	-	FBXW7	c.1627dup	p.R543Kfs*8
118I4761A1	6	152265353	152265353	Missense_Mutation	SNP	G	A	A	ESR1	c.806G>A	p.R269H
118I4779J1		-	-	Splice_Site	SNP	-	-	-	ARID2	715+2_1715+5	-
118I4779J1	15	66727442	66727442	Missense_Mutation	SNP	T	G	G	MAP2K1	c.158T>G	p.F53C
118I4779J1		-	-	Frame_Shift_Ins	INS	-	-	-	TP53	c.915dup	p.R306Afs*31
118I4779J1	19	10602367	10602367	Missense_Mutation	SNP	G	A	A	KEAP1	c.1211C>T	p.S404L
118I4779J1	5	112175897	112175897	Nonsense_Mutation	SNP	G	T	T	APC	c.4606G>T	p.E1536*
118I4845A1		-	-	Frame_Shift_Del	INS	-	-	-	ARID1A	c.5624del	P.P1875Hfs*8
118I4845A1	10	104592349	104592349	Missense_Mutation	SNP	A	T	T	CYP17A1	c.1058T>A	p.L353Q
118I4845A1	16	10032132	10032132	Missense_Mutation	SNP	A	T	T	GRIN2A	c.691T>A	p.C231S
118I4845A1	19	41745061	41745061	Splice_Site	SNP	C	G	G	AXL	c.1135-8C>G	-
118I4845A1	2	170089935	170089935	Missense_Mutation	SNP	G	A	A	LRP2	c.5084C>T	p.S1695L
118I4845A1	2	209113113	209113113	Missense_Mutation	SNP	G	A	A	IDH1	c.394C>T	p.R132C
118I4845A1	X	63411267	63411267	Missense_Mutation	SNP	G	A	A	AMER1	c.1900C>T	p.R634C
118I4887A1	1	7724066	7724066	Missense_Mutation	SNP	T	C	C	CAMTA1	c.1459T>C	p.C487R
118I4887A1	14	20823952	20823952	Missense_Mutation	SNP	C	T	T	PARP2	c.983C>T	p.S328L
118I4887A1	16	67116197	67116197	Missense_Mutation	SNP	C	T	T	CBFB	c.481C>T	p.R161W
118I4887A1	17	29533378	29533378	Nonsense_Mutation	SNP	C	T	T	NF1	c.1381C>T	p.R461*
118I4887A1	17	29576091	29576091	Nonsense_Mutation	SNP	C	G	G	NF1	c.4064C>G	p.S1355*
118I4887A1	18	48584552	48584552	Nonsense_Mutation	SNP	C	G	G	SMAD4	c.725C>G	p.S242*
118I4887A1		-	-	Splice_Site	SNP	-	-	-	ACVR2A	c.817-9_857del	-
118I4887A1	2	202149890	202149890	Nonsense_Mutation	SNP	T	A	A	CASP8	c.1205T>A	p.L402*
118I4887A1	3	178936091	178936091	Missense_Mutation	SNP	G	A	A	PIK3CA	c.1633G>A	p.E545K
118I4887A1	4	55956164	55956164	Missense_Mutation	SNP	G	A	A	KDR	c.3151C>T	p.R1051W
118I4887A1	7	148515112	148515112	Missense_Mutation	SNP	T	G	G	EZH2	c.1097A>C	p.N366T
118I4963M1	12	49421833	49421833	Missense_Mutation	SNP	C	T	T	KMT2D	c.14474G>A	p.R4825Q
118I4963M1	15	88476400	88476400	Missense_Mutation	SNP	T	C	C	NTRK3	c.1732A>G	p.S758A
118I4963M1		-	-	Frame_Shift_Del	INS	-	-	-	TP53	c.626_627del	P.R209Kfs*6
118I4963M1	17	29654575	29654575	Missense_Mutation	SNP	C	T	T	NF1	c.5327C>T	p.S1776L

118J4963M1	2	141356367	141356367	Missense_Mutation	SNP	T	G	G	LRP1B	c.7027A>C	p.S2343R
118J4963M1		-	-	In_Frame_Del	INS	-	-	-	ARID1B	C.363_380del	Q126_Q131del
118J5065A1	11	76162890	76162890	Splice_Site	SNP	T	A	A	EMSY	c.71-12T>A	-
118J5065A1	12	49446348	49446348	Missense_Mutation	SNP	T	C	C	KMT2D	c.1257A>G	p.L419L
118J5065A1	12	69968689	69968689	Missense_Mutation	SNP	G	T	T	FRS2	c.1481G>T	p.G494V
118J5065A1	13	49050868	49050868	Missense_Mutation	SNP	T	C	C	RB1	c.2552T>C	p.M851T
118J5065A1	17	7579494	7579494	Nonsense_Mutation	SNP	T	A	A	TP53	c.193A>T	p.R65*
118J5065A1	2	141986863	141986863	Missense_Mutation	SNP	T	C	C	LRP1B	c.739A>G	p.I247V
118J5065A1	20	57429815	57429815	Missense_Mutation	SNP	G	T	T	GNAS	c.1495G>T	p.A499S
118J5065A1		-	-	Frame_Shift_Del	INS	-	-	-	NOTCH4	C.989del	P.G330Afs*15
118J5083M1		-	-	Frame_Shift_Del	INS	-	-	-	ARID1A	delinsAGGTAGG	p.G314Rfs*48
118J5083M1	11	69458744	69458744	Missense_Mutation	SNP	G	A	A	CCND1	c.559G>A	p.A187T
118J5083M1	12	25398284	25398284	Missense_Mutation	SNP	C	T	T	KRAS	c.35G>A	p.G12D
118J5083M1	16	23646321	23646321	Nonsense_Mutation	SNP	T	A	A	PALB2	c.1546A>T	p.R516*
118J5083M1		-	-	Frame_Shift_Del	INS	-	-	-	SMAD4	C.321_330del	P.E108Mfs*11
118J5083M1	18	48581157	48581157	Nonsense_Mutation	SNP	C	G	G	SMAD4	c.461C>G	p.S154*
118J5083M1	19	42797344	42797344	Missense_Mutation	SNP	C	T	T	CIC	c.3706C>T	p.P1236S
118J5083M1	4	88979247	88979247	Missense_Mutation	SNP	A	T	T	PKD2	c.2011A>T	p.I671F
118J5083M1		-	-	In_Frame_Del	INS	-	-	-	TET2	C.3463_3479del	P.P1155*
118J5083M1		-	-	In_Frame_Del	INS	-	-	-	PIK3R1	C.1392_1403del	P.D464_4467del
118J5083M1	7	148529748	148529748	Missense_Mutation	SNP	G	C	C	EZH2	c.341C>G	p.S114C
118J5085M1	1	98348861	98348861	Missense_Mutation	SNP	C	T	T	DPYD	c.109G>A	p.D37N
118J5085M1	12	56489534	56489534	Missense_Mutation	SNP	C	T	T	ERBB3	c.1999C>T	p.R667C
118J5085M1	15	93552474	93552474	Missense_Mutation	SNP	T	A	A	CHD2	c.4513T>A	p.C1505S
118J5085M1	2	209113113	209113113	Missense_Mutation	SNP	G	A	A	IDH1	c.394C>T	p.R132C
118J5119A1	10	43601922	43601922	Missense_Mutation	SNP	C	A	A	RET	c.966C>A	p.D322E
118J5119A1	17	7577539	7577539	Missense_Mutation	SNP	G	A	A	TP53	c.742C>T	p.R248W
118J5119A1	17	41607296	41607296	Missense_Mutation	SNP	C	T	T	ETV4	c.911G>A	p.R304Q
118J5119A1	2	140995765	140995765	Missense_Mutation	SNP	C	G	G	LRP1B	c.13516G>C	p.D4506H
118J5119A1	22	30074230	30074230	Missense_Mutation	SNP	T	A	A	NF2	c.1492T>A	p.F498I
118J5119A1	3	37081683	37081683	Missense_Mutation	SNP	G	A	A	MLH1	c.1565G>A	p.R522Q
118J5119A1	3	178921551	178921551	Missense_Mutation	SNP	A	G	G	PIK3CA	c.1033A>G	p.N345D
118J5119A1	5	38953598	38953598	Missense_Mutation	SNP	C	G	G	RICTOR	c.2755G>C	p.E919Q
118J5135A1	11	65427594	65427594	Splice_Site	SNP	C	A	A	RELA	c.427+1G>T	-
118J5135A1	11	92086687	92086687	Missense_Mutation	SNP	C	T	T	FAT3	c.1409C>T	p.P470L
118J5135A1	17	41219675	41219675	Missense_Mutation	SNP	G	A	A	BRCA1	c.5024C>T	p.T1675I
118J5135A1	3	52643347	52643347	Missense_Mutation	SNP	C	T	T	PBRM1	c.2549G>A	p.R850Q
118J5135A1		-	-	Splice_Site	SNP	-	-	-	PIK3R1	746-28_1746-7	-
118J5135A1	6	112015644	112015644	Missense_Mutation	SNP	T	C	C	FYN	c.1207A>G	p.I403V
118J5135A1	8	92998483	92998483	Missense_Mutation	SNP	T	C	C	RUNX1T1	c.1037A>G	p.E346G
118J5144A1	17	37868208	37868208	Missense_Mutation	SNP	C	T	T	ERBB2	c.929C>T	p.S310F
118J5144A1	20	39751885	39751885	Missense_Mutation	SNP	G	A	A	TOP1	c.2246G>A	p.R749Q
118J5144A1	21	44524456	44524456	Missense_Mutation	SNP	G	A	A	U2AF1	c.101C>T	p.S34F
118J5144A1	5	112177203	112177203	Missense_Mutation	SNP	C	T	T	APC	c.5912C>T	p.S1971F
118J5169M1	1	202710848	202710848	Missense_Mutation	SNP	A	T	T	KDM5B	c.2700T>A	p.D900E
118J5169M1	12	1039246	1039246	Nonsense_Mutation	SNP	C	T	T	RAD52	c.251G>A	p.W84*
118J5169M1	12	4554445	4554445	Missense_Mutation	SNP	G	T	T	FGF6	c.292C>A	p.L98I
118J5169M1		-	-	Frame_Shift_Del	INS	-	-	-	CDKN1B	c.410del	p.P137Rfs*8
118J5169M1	12	25398285	25398285	Missense_Mutation	SNP	C	A	A	KRAS	c.34G>T	p.G12C
118J5169M1		-	-	Splice_Site	SNP	-	-	-	ARID2	c.4774-1del	-
118J5169M1	17	7577570	7577570	Missense_Mutation	SNP	C	T	T	TP53	c.711G>A	p.M237I
118J5169M1		-	-	Frame_Shift_Del	INS	-	-	-	SMAD4	c.814_818del	p.R272Cfs*6
118J5169M1	19	42788891	42788891	Missense_Mutation	SNP	C	T	T	CIC	c.35C>T	p.S12F
118J5169M1	3	10140458	10140458	Missense_Mutation	SNP	G	A	A	FANCD2	c.4240G>A	p.D1414N
118J5169M1		-	-	Frame_Shift_Ins	INS	-	-	-	KMT2C	12476_12477dup	p.S4160Afs*5
118J5169M1	9	21994135	21994135	Splice_Site	SNP	T	C	C	CDKN2A	c.193+3A>G	-
118J5169M1	X	47039817	47039817	Splice_Site	SNP	G	A	A	RBM10	c.1161-1G>A	-
118J5206M1	12	25398284	25398284	Missense_Mutation	SNP	C	T	T	KRAS	c.35G>A	p.G12D
118J5206M1	12	46233257	46233257	Missense_Mutation	SNP	G	T	T	ARID2	c.1476G>T	p.Q492H
118J5206M1	17	7578461	7578461	Missense_Mutation	SNP	C	A	A	TP53	c.469G>T	p.V157F
118J5206M1		-	-	Frame_Shift_Del	INS	-	-	-	KDM6A	C.695del	P.L1232Cfs*10
118J5249M1	12	46245027	46245027	Nonsense_Mutation	SNP	C	T	T	ARID2	c.3121C>T	p.Q1041*
118J5249M1	14	105237170	105237170	Missense_Mutation	SNP	G	C	C	AKT1	c.1275C>G	p.F425L
118J5249M1	17	7578382	7578382	Nonsense_Mutation	SNP	G	C	C	TP53	c.548C>G	p.S183*
118J5249M1	20	39704825	39704825	Missense_Mutation	SNP	C	G	G	TOP1	c.170C>G	p.S57C
118J5249M1	3	178936094	178936094	Missense_Mutation	SNP	C	G	G	PIK3CA	c.1636C>G	p.Q546E
118J5249M1	6	94120359	94120359	Missense_Mutation	SNP	C	T	T	EPHA7	c.692G>A	p.R231Q
118J5249M1	6	112029201	112029201	Missense_Mutation	SNP	G	C	C	FYN	c.367C>G	p.R123G
118J5249M1		-	-	Frame_Shift_Ins	INS	-	-	-	RBM10	c.819_820insTG	p.Q274Cfs*35
118J5249M1	X	53226131	53226131	Missense_Mutation	SNP	C	G	G	KDM5C	c.2718G>C	p.E906D
118J5276A1		-	-	Frame_Shift_Del	INS	-	-	-	SPEN	c.6948del	p.S2318Lfs*35
118J5276A1	1	16263745	16263745	Missense_Mutation	SNP	T	A	A	SPEN	c.10114T>A	p.S3372T
118J5276A1	1	120057209	120057209	Missense_Mutation	SNP	G	A	A	HSD3B1	c.1063G>A	p.E355K
118J5276A1	1	226252059	226252059	Missense_Mutation	SNP	C	G	G	H3F3A	c.7C>G	p.R3G
118J5276A1	12	427483	427483	Missense_Mutation	SNP	G	T	T	KDM5A	c.2686C>A	p.Q896K
118J5276A1	17	7578290	7578290	Splice_Site	SNP	C	A	A	TP53	c.560-1G>T	-
118J5276A1	19	11169566	11169566	Splice_Site	SNP	G	A	A	SMARCA4	c.4731+1G>A	-
118J5276A1	2	212566814	212566814	Missense_Mutation	SNP	C	T	T	ERBB4	c.1367G>A	p.G456E
118J5276A1	2	212589881	212589881	Missense_Mutation	SNP	A	T	T	ERBB4	c.661T>A	p.C221S
118J5276A1	X	39932902	39932902	Missense_Mutation	SNP	C	T	T	BCOR	c.1697G>A	p.R566H
118J5402A1	1	115256530	115256530	Missense_Mutation	SNP	G	T	T	NRAS	c.181C>A	p.Q61K
118J5402A1	15	88472464	88472464	Missense_Mutation	SNP	G	C	C	NTRK3	c.2091C>G	p.D697E
118J5402A1	17	7577551	7577551	Missense_Mutation	SNP	C	G	G	TP53	c.730G>C	p.G244R
118J5402A1	2	109357112	109357112	Missense_Mutation	SNP	C	T	T	RANBP2	c.950C>T	p.A317V
118J5402A1	2	141526925	141526925	Splice_Site	SNP	G	A	A	LRP1B	c.5627-12C>T	-
118J5402A1	4	143067101	143067101	Missense_Mutation	SNP	T	C	C	INPP4B	c.1612A>G	p.M538V
118J5402A1	4	153332838	153332838	Nonsense_Mutation	SNP	C	A	A	FBXW7	c.118G>T	p.E40*
118J5402A1	8	32505516	32505516	Missense_Mutation	SNP	G	A	A	NRG1	c.280G>A	p.G94S
118J5402A1	X	44733158	44733158	Splice_Site	SNP	C	T	T	KDM6A	c.162-12C>T	-
118J5518M1	3	41266097	41266097	Missense_Mutation	SNP	G	A	A	CTNNB1	c.94G>A	p.D32N
118J5518M1	3	47162341	47162341	Missense_Mutation	SNP	A	C	C	SETD2	c.3785T>G	p.F1262C
118J5583A1		-	-	Frame_Shift_Del	INS	-	-	-	ARID1A	c.5756_5787del	p.S1919Rfs*15
118J5583A1	1	115258747	115258747	Missense_Mutation	SNP	C	A	A	NRAS	c.35G>T	p.G12V
118J5583A1	1	158614191	158614191	Splice_Site	SNP	G	T	T	SPTA1	c.4195-5C>A	-
118J5583A1		-	-	Frame_Shift_Del	INS	-	-	-	TP53	c.109_134del	p.S37Vfs*6
118J5583A1	18	18550317	18550317	Missense_Mutation	SNP	C	T	T	ROCK1	c.2812G>A	p.V938I
118J5583A1	2	61708325	61708325	Missense_Mutation	SNP	T	C	C	XP01	c.3064A>G	p.I1022V
118J5583A1	3	178951947	178951947	Missense_Mutation	SNP	T	G	G	PIK3CA	c.3002T>G	p.L1001R

118J5583A1	4	110890182	110890182	Missense_Mutation	SNP	C	T	T	EGF	c.1631C>T	p.S544F
118J5583A1	6	157100380	157100380	Missense_Mutation	SNP	G	T	T	ARID1B	c.1317G>T	p.E439D
118J5583A1	6	157517322	157517322	Missense_Mutation	SNP	A	G	G	ARID1B	c.3886A>G	p.M1296V
118J5583A1	X	129148987	129148987	Nonsense_Mutation	SNP	A	T	T	BCORL1	c.2239A>T	p.K747*
118K5630A1	1	120512184	120512184	Missense_Mutation	SNP	C	T	T	NOTCH2	c.1058G>A	p.C353Y
118K5630A1	17	7577538	7577538	Missense_Mutation	SNP	C	T	T	TP53	c.743G>A	p.R248Q
118K5630A1	4	153249385	153249385	Missense_Mutation	SNP	G	A	A	FBXW7	c.1393C>T	p.R465C
118K5630A1	7	140494154	140494154	Missense_Mutation	SNP	G	A	A	BRAF	c.1094C>T	p.S365L
118K5630A1	-	-	-	Frame_Shift_Del	INS	-	-	-	BCOR	c.3913_3917del	p.E1305Lfs*68
118K5635M1	1	27092809	27092809	Nonsense_Mutation	SNP	C	T	T	ARID1A	c.2830C>T	p.Q944*
118K5635M1	16	10274090	10274090	Missense_Mutation	SNP	G	A	A	GRIN2A	c.179C>T	p.A60V
118K5635M1	16	50811844	50811844	Missense_Mutation	SNP	T	A	A	CYLD	c.1130T>A	p.I377N
118K5635M1	17	7577016	7577016	Splice_Site	SNP	T	C	C	TP53	c.919+3A>G	-
118K5635M1	17	7577117	7577117	Missense_Mutation	SNP	A	T	T	TP53	c.821T>A	p.V274D
118K5635M1	2	141143491	141143491	Missense_Mutation	SNP	C	T	T	LRP1B	c.10502G>A	p.C3501Y
118K5635M1	2	170092375	170092375	Missense_Mutation	SNP	C	T	T	LRP2	c.4895G>A	p.R1632Q
118K5635M1	5	176522396	176522396	Nonsense_Mutation	SNP	C	T	T	FGFR4	c.1585C>T	p.R529*
118K5635M1	-	-	-	Frame_Shift_Del	INS	-	-	-	DDR1	c.1356_1375del	p.R453Dfs*20
118K5635M1	8	41792377	41792377	Missense_Mutation	SNP	T	C	C	KAT6A	c.3361A>G	p.I1121V
118K5635M1	X	44966786	44966786	Splice_Site	SNP	G	A	A	KDM6A	c.4005+5G>A	-
118K5684M1	12	25398284	25398284	Missense_Mutation	SNP	C	T	T	KRAS	c.35G>A	p.G12D
118K5684M1	5	1280264	1280264	Splice_Site	SNP	C	T	T	TERT	c.1950+9G>A	-
118K5684M1	5	56111590	56111590	Nonsense_Mutation	SNP	A	T	T	MAP3K1	c.190A>T	p.K64*
118K5684M1	6	94066572	94066572	Missense_Mutation	SNP	T	C	C	EPHA7	c.1187A>G	p.E396G
118K5718A1	12	46244022	46244022	Nonsense_Mutation	SNP	A	T	T	ARID2	c.2116A>T	p.K706*
118K5718A1	16	3781441	3781441	Missense_Mutation	SNP	C	A	A	CREBBP	c.4924G>T	p.V1642F
118K5718A1	17	7577534	7577534	Missense_Mutation	SNP	C	A	A	TP53	c.747G>T	p.R249S
118K5718A1	20	57429115	57429115	Missense_Mutation	SNP	C	T	T	GNAS	c.608C>T	p.A203V
118K5718A1	22	30032748	30032748	Nonsense_Mutation	SNP	G	A	A	NF2	c.123G>A	p.W41*
118K5718A1	5	1268630	1268630	Splice_Site	SNP	C	T	T	TERT	c.2582+5G>A	-
118K5718A1	-	-	-	Splice_Site	SNP	-	-	-	ITK	515-12_1515-2	-
118K5718A1	7	140453987	140453987	Missense_Mutation	SNP	T	C	C	BRAF	c.1741A>G	p.N581D
118K5909A1	1	243858901	243858901	Missense_Mutation	SNP	G	A	A	AKT3	c.164C>T	p.S55L
118K5909A1	17	7577094	7577094	Missense_Mutation	SNP	G	A	A	TP53	c.844C>T	p.R282W
118K5909A1	17	59926534	59926534	Nonsense_Mutation	SNP	G	A	A	BRIP1	c.463C>T	p.Q155*
118K5909A1	-	-	-	Frame_Shift_Del	INS	-	-	-	DNMT3A	c.421_433del	p.E141Pfs*17
118K5909A1	2	212812256	212812256	Missense_Mutation	SNP	C	T	T	ERBB4	c.320G>A	p.G107E
118K5909A1	-	-	-	Frame_Shift_Del	INS	-	-	-	FBXW7	c.870del	p.Y291Mfs*51
118K5909A1	8	68864619	68864619	Splice_Site	SNP	C	T	T	PREX2	c.-11C>T	-
118K5909A1	9	21971186	21971186	Nonsense_Mutation	SNP	G	A	A	CDKN2A	c.172C>T	p.R58*
118K5909A1	X	70612764	70612764	Missense_Mutation	SNP	G	A	A	TAF1	c.3031G>A	p.G1011R
118K5971J1	12	25398284	25398284	Missense_Mutation	SNP	C	T	T	KRAS	c.35G>A	p.G12D
118K5984A1	12	25398284	25398284	Missense_Mutation	SNP	C	T	T	KRAS	c.35G>A	p.G12D
118K5984A1	17	7577105	7577105	Missense_Mutation	SNP	G	A	A	TP53	c.833C>T	p.P278L
118K5984A1	4	126373264	126373264	Missense_Mutation	SNP	G	A	A	FAT4	c.11093G>A	p.R3698Q
118K5984A1	-	-	-	Splice_Site	SNP	-	-	-	ATRX	c.3737-9del	-
118K5992M1	1	226567661	226567661	Missense_Mutation	SNP	G	C	C	PARP1	c.1505C>G	p.A502G
118K5992M1	10	89711894	89711894	Missense_Mutation	SNP	A	G	G	PTEN	c.512A>G	p.Q171R
118K5992M1	11	108235879	108235879	Missense_Mutation	SNP	C	T	T	ATM	c.8921C>T	p.P2974L
118K5992M1	12	25398284	25398284	Missense_Mutation	SNP	C	T	T	KRAS	c.35G>A	p.G12D
118K5992M1	12	49434990	49434990	Missense_Mutation	SNP	C	T	T	KMT2D	c.6563G>A	p.R2188H
118K5992M1	16	23641346	23641346	Missense_Mutation	SNP	G	A	A	PALB2	c.2129C>T	p.T710M
118K5992M1	17	7578217	7578217	Missense_Mutation	SNP	G	A	A	TP53	c.632C>T	p.T211I
118K5992M1	17	37676315	37676315	Missense_Mutation	SNP	G	A	A	CDK12	c.3070G>A	p.E1024K
118K5992M1	2	29416667	29416667	Missense_Mutation	SNP	T	C	C	ALK	c.4286A>G	p.Q1429R
118K5992M1	2	112751824	112751824	Splice_Site	SNP	C	A	A	MERTK	c.1297-4C>A	-
118K5992M1	2	173429747	173429747	Nonsense_Mutation	SNP	C	T	T	PKD1	c.637C>T	p.R213*
118K5992M1	20	31023931	31023931	Missense_Mutation	SNP	C	A	A	ASXL1	c.3416C>A	p.T1139K
118K5992M1	3	185783608	185783608	Missense_Mutation	SNP	C	T	T	ETV5	c.904G>A	p.D302N
118K5992M1	7	80276070	80276070	Missense_Mutation	SNP	G	T	T	CD36	c.14G>T	p.R5L
118K5992M1	7	127714549	127714549	Splice_Site	SNP	C	T	T	SND1	c.1780-5C>T	p.R1389*
118K5992M1	8	141756950	141756950	Missense_Mutation	SNP	C	T	T	PTK2	c.1493G>A	p.R498H
118K5992M1	9	5557694	5557694	Missense_Mutation	SNP	C	A	A	PDCD1LG2	c.708C>G	p.F236L
118K5993A1	17	7578257	7578257	Nonsense_Mutation	SNP	C	A	A	TP53	c.592G>T	p.E198*
118K6072M1	-	-	-	In_Frame_Del	INS	-	-	-	ARID1A	7_4217delinsG	p.Y1389*
118K6072M1	12	25398285	25398285	Missense_Mutation	SNP	C	G	G	KRAS	c.34G>C	p.G12R
118K6072M1	3	30691910	30691910	Missense_Mutation	SNP	T	G	G	TGFBR2	c.412T>G	p.C138G
118K6072M1	4	185339864	185339864	Splice_Site	SNP	T	G	G	IRF2	c.188-2A>C	-
118K6072M1	9	21971111	21971111	Missense_Mutation	SNP	G	A	A	CDKN2A	c.247C>T	p.H83Y
118K6080A1	-	-	-	In_Frame_Ins	INS	-	-	-	EPHA2	C.719dup	p.E241*
118K6080A1	17	7577022	7577022	Nonsense_Mutation	SNP	G	A	A	TP53	c.916C>T	p.R306*
118K6130M1	-	-	-	Frame_Shift_Ins	INS	-	-	-	ARID1A	c.1113dup	p.Q372Afs*28
118K6130M1	10	89653846	89653846	Missense_Mutation	SNP	C	A	A	PTEN	c.144C>A	p.N48K
118K6130M1	19	11143985	11143985	Missense_Mutation	SNP	G	A	A	SMARCA4	c.3566G>A	p.R1189Q
118K6186A1	1	46739143	46739143	Splice_Site	SNP	C	A	A	RAD54L	c.1486+6C>A	-
118K6186A1	1	78430841	78430841	Missense_Mutation	SNP	G	A	A	FUBP1	c.548C>T	p.P183L
118K6186A1	12	25398284	25398284	Missense_Mutation	SNP	C	T	T	KRAS	c.35G>A	p.G12D
118K6186A1	12	57593115	57593115	Missense_Mutation	SNP	C	T	T	LRP1	c.9797C>T	p.T3266M
118K6186A1	13	26978111	26978111	Missense_Mutation	SNP	G	A	A	CDK8	c.1288G>A	p.A430T
118K6186A1	16	67650786	67650786	Splice_Site	SNP	G	A	A	CTCF	c.1086+5G>A	-
118K6186A1	17	7578212	7578212	Nonsense_Mutation	SNP	G	A	A	TP53	c.637C>T	p.R213*
118K6186A1	18	48593443	48593443	Nonsense_Mutation	SNP	G	A	A	SMAD4	c.1194G>A	p.W398*
118K6186A1	19	10464891	10464891	Missense_Mutation	SNP	C	A	A	TYK2	c.2735G>T	p.S912I
118K6186A1	19	41744411	41744411	Missense_Mutation	SNP	G	A	A	AXL	c.1031G>A	p.R344Q
118K6186A1	19	50905864	50905864	Splice_Site	SNP	C	T	T	POLD1	c.841-5C>T	-
118K6186A1	2	141110639	141110639	Missense_Mutation	SNP	G	A	A	LRP1B	c.11533C>T	p.L3845F
118K6186A1	-	-	-	In_Frame_Del	INS	-	-	-	SRMS	c.1464_1465del	p.*489Sext*59
118K6186A1	5	131973900	131973900	Missense_Mutation	SNP	C	G	G	RAD50	c.3603C>G	p.C1201W
118K6186A1	5	161116252	161116252	Splice_Site	SNP	G	A	A	GABRA6	c.447-8G>A	-
118K6186A1	7	41730102	41730102	Missense_Mutation	SNP	C	T	T	INHBA	c.427G>A	p.E143K
118K6186A1	8	41791906	41791906	Missense_Mutation	SNP	G	A	A	KAT6A	c.3832C>T	p.R1278C
118K6186A1	9	21994140	21994140	Missense_Mutation	SNP	G	A	A	CDKN2A	c.191C>T	p.P64L
118K6186A1	9	35078227	35078227	Missense_Mutation	SNP	G	A	A	FANCG	c.421C>T	p.R141C
118K6209A1	-	-	-	Frame_Shift_Ins	INS	-	-	-	ARID1A	c.2172_2175dup	p.P726Afs*92
118K6209A1	19	18273784	18273784	Missense_Mutation	SNP	G	A	A	PIK3R2	c.1117G>A	p.G373R
118K6209A1	2	209113113	209113113	Missense_Mutation	SNP	G	A	A	IDH1	c.394C>T	p.R132C
118K6209A1	3	52651426	52651426	Missense_Mutation	SNP	T	A	A	PBRM1	c.1670A>T	p.D557V
118K6272A1	1	11204742	11204742	Missense_Mutation	SNP	C	T	T	MTOR	c.4835G>A	p.R1612Q

118K6272A1	11	92532669	92532669	Missense_Mutation	SNP	G	A	A	FAT3	c.6490G>A	p.G2164R
118K6272A1	11	92533086	92533086	Missense_Mutation	SNP	G	T	T	FAT3	c.6907G>T	p.G2303W
118K6272A1	11	92616250	92616250	Missense_Mutation	SNP	C	T	T	FAT3	c.12628C>T	p.R4210W
118K6272A1	11	108138018	108138018	Missense_Mutation	SNP	G	C	C	ATM	c.2587G>C	p.D863H
118K6272A1		-	-	Frame_Shift_Del	INS	-	-	-	TP53	c.561_564del	p.L188Pfs*58
118K6272A1	17	48265353	48265353	Splice_Site	SNP	G	C	C	COL1A1	c.3262-9C>G	-
118K6272A1	19	10610205	10610205	Missense_Mutation	SNP	G	A	A	KEAP1	c.505C>T	p.R169C
118K6272A1	2	215645433	215645433	Missense_Mutation	SNP	T	A	A	BAR1	c.1165A>T	p.S389C
118K6272A1	22	21304119	21304119	Missense_Mutation	SNP	G	C	C	CRKL	c.898G>C	p.D300H
118K6272A1	3	156421343	156421343	Nonsense_Mutation	SNP	C	T	T	TIPARP	c.1378C>T	p.Q460*
118K6272A1	3	178922301	178922301	Missense_Mutation	SNP	G	A	A	PIK3CA	c.1070G>A	p.R357Q
118K6272A1	7	151845790	151845790	Missense_Mutation	SNP	C	G	G	KMT2C	c.13222G>C	p.E4408Q
118K6272A1	8	31497666	31497666	Missense_Mutation	SNP	C	G	G	NRG1	c.166C>G	p.P56A
118K6285M1	1	43817931	43817931	Missense_Mutation	SNP	G	T	T	MPL	c.1610G>T	p.R537L
118K6285M1		-	-	Frame_Shift_Del	INS	-	-	-	KMT2D	c.14312del	p.V4771Afs*26
118K6285M1	12	49434495	49434495	Missense_Mutation	SNP	G	A	A	KMT2D	c.7058C>T	p.P2353L
118K6285M1	16	56782164	56782164	Missense_Mutation	SNP	A	G	G	NUP93	c.5A>G	p.D2G
118K6285M1	16	56865836	56865836	Missense_Mutation	SNP	G	A	A	NUP93	c.1168G>A	p.V390M
118K6285M1	16	68842741	68842741	Missense_Mutation	SNP	C	A	A	CDH1	c.677C>A	p.A226D
118K6285M1	17	7578253	7578253	Missense_Mutation	SNP	C	A	A	TP53	c.596G>T	p.G199V
118K6285M1	17	59870987	59870987	Missense_Mutation	SNP	T	C	C	BRIP1	c.1444A>G	p.I482V
118K6285M1	18	19751656	19751656	Missense_Mutation	SNP	G	A	A	GATA6	c.551G>A	p.S184N
118K6285M1	19	10472988	10472988	Missense_Mutation	SNP	C	T	T	TYK2	c.1621G>A	p.G541R
118K6285M1		-	-	Splice_Site	SNP	-	-	-	EP300	c.1623-5dup	-
118K6285M1	3	119720881	119720881	Splice_Site	SNP	T	A	A	GSK3B	c.282+12A>T	-
118K6285M1	4	187532570	187532570	Missense_Mutation	SNP	G	T	T	FAT1	c.9823C>A	p.H3275N
118K6285M1	4	187541786	187541786	Missense_Mutation	SNP	G	T	T	FAT1	c.5954C>A	p.S1985Y
118K6285M1	5	251216	251216	Missense_Mutation	SNP	G	A	A	SDHA	c.1661G>A	p.R554Q
118K6285M1	5	156671429	156671429	Missense_Mutation	SNP	C	A	A	ITK	c.1390C>A	p.L464M
118K6285M1	6	33288998	33288998	Missense_Mutation	SNP	C	T	T	DAXX	c.554G>A	p.R185Q
118K6285M1	9	102590768	102590768	Missense_Mutation	SNP	C	A	A	NR4A3	c.444C>A	p.F148L
118K612M1	17	7578503	7578503	Missense_Mutation	SNP	C	T	T	TP53	c.427G>A	p.V143M
118K612M1		-	-	In_Frame_Del	INS	-	-	-	CDKN2A	c.83_100del	p.V28_E33del
118K612M1		-	-	Frame_Shift_Del	INS	-	-	-	KDM6A	c.3388_3395del	p.N1305fs*18
118K6336A1	11	125499349	125499349	Missense_Mutation	SNP	G	A	A	CHEK1	c.418G>A	p.E140K
118K6336A1	16	2130267	2130267	Missense_Mutation	SNP	G	C	C	TSC2	c.3499G>C	p.E1167Q
118K6336A1		-	-	Frame_Shift_Del	INS	-	-	-	TP53	c.626_627del	p.R209Kfs*6
118K6336A1	18	42532639	42532639	Nonsense_Mutation	SNP	A	T	T	SETBP1	c.3334A>T	p.K1112*
118K6336A1	2	141283547	141283547	Missense_Mutation	SNP	G	C	C	LRP1B	c.7892C>G	p.T2631R
118K6336A1	2	212543774	212543774	Splice_Site	SNP	T	A	A	ERBB4	c.1622+3A>T	-
118K6336A1	3	41266101	41266101	Missense_Mutation	SNP	C	T	T	CTNNB1	c.98C>T	p.S33F
118K6336A1	4	153249478	153249478	Missense_Mutation	SNP	T	A	A	FBXW7	c.1300A>T	p.I434F
118K6336A1	7	20198075	20198075	Missense_Mutation	SNP	C	T	T	MACC1	c.1909G>A	p.E637K
118K6336A1	7	151921590	151921590	Missense_Mutation	SNP	T	C	C	KMT2C	c.3088A>G	p.I1030V
118K6349A1	11	92616149	92616149	Missense_Mutation	SNP	G	A	A	FAT3	c.12527G>A	p.R4176H
118K6349A1	17	37868208	37868208	Missense_Mutation	SNP	C	T	T	ERBB2	c.929C>T	p.S310F
118K6349A1	17	80789199	80789199	Missense_Mutation	SNP	C	T	T	ZNF750	c.1132G>A	p.E378K
118K6349A1	18	48575671	48575671	Nonsense_Mutation	SNP	C	G	G	SMAD4	c.431C>G	p.S144*
118K6349A1	3	189526226	189526226	Missense_Mutation	SNP	G	A	A	TP63	c.490G>A	p.A164T
118K6349A1	7	41729593	41729593	Missense_Mutation	SNP	C	G	G	INHBA	c.936G>C	p.L132F
118K6372A3		-	-	Frame_Shift_Del	INS	-	-	-	ARID1A	c.817del	p.A273Pfs*90
118K6372A3		-	-	Frame_Shift_Ins	INS	-	-	-	ARID1A	c.3216dup	p.W1073Mfs*32
118K6372A3		-	-	Splice_Site	SNP	-	-	-	FUBP1	c.1781-6dup	-
118K6372A3	1	158623086	158623086	Missense_Mutation	SNP	G	A	A	SPTA1	c.3166C>T	p.R1056C
118K6372A3	1	162729663	162729663	Missense_Mutation	SNP	T	C	C	DDR2	c.749T>C	p.V250A
118K6372A3	11	22646455	22646455	Missense_Mutation	SNP	T	C	C	FANCF	c.902A>G	p.D301G
118K6372A3	11	118376407	118376407	Missense_Mutation	SNP	A	C	C	KMT2A	c.9800A>C	p.N3267T
118K6372A3		-	-	Missense_Mutation	SNP	-	-	-	CHD4	c.4586_4588del	p.K1529del
118K6372A3	12	21628745	21628745	Missense_Mutation	SNP	A	C	C	RECQL	c.963T>G	p.C321W
118K6372A3		-	-	Splice_Site	SNP	-	-	-	KMT2D	c.13840-10del	-
118K6372A3	12	49445244	49445244	Missense_Mutation	SNP	G	A	A	KMT2D	c.2222C>T	p.P741L
118K6372A3	12	52385715	52385715	Nonsense_Mutation	SNP	C	T	T	ACVR1B	c.1453C>T	p.R485*
118K6372A3	12	56478854	56478854	Missense_Mutation	SNP	G	T	T	ERBB3	c.310G>T	p.V104L
118K6372A3		-	-	Frame_Shift_Ins	INS	-	-	-	APEX1	c.146dup	p.D50Rfs*28
118K6372A3		-	-	Frame_Shift_Ins	INS	-	-	-	FANCM	c.2604dup	p.E869Rfs*3
118K6372A3	16	67662352	67662352	Missense_Mutation	SNP	G	A	A	CTCF	c.1598G>A	p.R533H
118K6372A3		-	-	Frame_Shift_Ins	INS	-	-	-	CDH1	c.377dup	p.P127Afs*41
118K6372A3		-	-	Frame_Shift_Del	INS	-	-	-	USP6	c.3752del	p.G1251Afs*14
118K6372A3		-	-	Frame_Shift_Del	INS	-	-	-	TP53	c.532del	p.H178Tfs*69
118K6372A3	17	29541518	29541518	Missense_Mutation	SNP	C	A	A	NF1	c.1442C>A	p.P481H
118K6372A3	17	29661899	29661899	Nonsense_Mutation	SNP	G	A	A	NF1	c.5856G>A	p.V1952*
118K6372A3		-	-	Splice_Site	SNP	-	-	-	SPOP	c.353-12del	-
118K6372A3		-	-	Frame_Shift_Del	INS	-	-	-	RNF43	c.1976del	p.G659Vfs*41
118K6372A3	17	78897476	78897476	Splice_Site	SNP	A	G	G	RPTOR	c.2808+3A>G	-
118K6372A3	18	23632782	23632782	Missense_Mutation	SNP	G	T	T	SS18	c.413C>A	p.P138H
118K6372A3		-	-	Frame_Shift_Del	INS	-	-	-	ROCK2	c.412del	p.W138Gfs*31
118K6372A3		-	-	Missense_Mutation	SNP	-	-	-	XPO1	c.116_118del	p.E39del
118K6372A3	2	121746006	121746006	Missense_Mutation	SNP	C	T	T	GLI2	c.2516C>T	p.S839L
118K6372A3	2	170042491	170042491	Missense_Mutation	SNP	C	T	T	LRP2	c.9367G>A	p.D3123N
118K6372A3		-	-	Splice_Site	SNP	-	-	-	LRP2	c.770-5del	-
118K6372A3	22	21344765	21344765	Missense_Mutation	SNP	G	A	A	LZTR1	c.742G>A	p.G248R
118K6372A3		-	-	Missense_Mutation	SNP	-	-	-	SMARCB1	c.1091_1093del	p.K364del
118K6372A3	22	30057302	30057302	Nonsense_Mutation	SNP	C	T	T	NF2	c.784C>T	p.R262*
118K6372A3	22	41556717	41556717	Missense_Mutation	SNP	A	C	C	EP300	c.3662A>C	p.Q1221P
118K6372A3	3	49927438	49927438	Missense_Mutation	SNP	C	T	T	MST1R	c.3866G>A	p.R1289H
118K6372A3		-	-	Frame_Shift_Del	INS	-	-	-	PBRM1	c.773del	p.N258Mfs*25
118K6372A3	3	142268966	142268966	Splice_Site	SNP	C	T	T	ATR	c.2976+8G>A	-
118K6372A3	3	185191097	185191097	Missense_Mutation	SNP	G	A	A	MAP3K13	c.1978G>A	p.G660R
118K6372A3	4	126369973	126369973	Missense_Mutation	SNP	A	G	G	FAT4	c.7802A>G	p.V2601C
118K6372A3	4	187539894	187539894	Missense_Mutation	SNP	C	T	T	FAT1	c.7846G>A	p.V2616I
118K6372A3		-	-	Splice_Site	SNP	-	-	-	ITK	061-7_1061-6d	-
118K6372A3		-	-	Splice_Site	SNP	-	-	-	ARID1B	c.1927-3del	-
118K6372A3	6	157488293	157488293	Missense_Mutation	SNP	C	T	T	ARID1B	c.2999C>T	p.A1000V
118K6372A3	6	157522130	157522130	Missense_Mutation	SNP	C	T	T	ARID1B	c.4402C>T	p.R1468C
118K6372A3	6	157528657	157528657	Nonsense_Mutation	SNP	C	T	T	ARID1B	c.6382C>T	p.R2128*
118K6372A3	7	55221830	55221830	Missense_Mutation	SNP	G	A	A	EGFR	c.874G>A	p.V292M
118K6372A3	7	140481411	140481411	Missense_Mutation	SNP	C	A	A	BRAF	c.1397G>T	p.G466V
118K6372A3	7	140507836	140507836	Missense_Mutation	SNP	G	A	A	BRAF	c.635C>T	p.T212I

118K6372A3	9	102609909	102609909	Splice_Site	SNP	C	A	A	NR4A3	c.1633+12C>A	-
118K6377A1	1	27106308	27106308	Nonsense_Mutation	SNP	G	A	A	ARID1A	c.5919G>A	p.W1973*
118K6377A1		-	-	Frame_Shift_Del	INS	-	-	-	ARID2	c.1010_1020del	p.N337Rfs*8
118K6377A1	17	7577547	7577547	Missense_Mutation	SNP	C	T	T	TP53	c.734G>A	p.G245D
118K6377A1	18	48591891	48591891	Missense_Mutation	SNP	G	A	A	SMAD4	c.1054G>A	p.G352R
118K6377A1	6	163876338	163876338	Missense_Mutation	SNP	A	G	G	QKI	c.170A>G	p.Y57C
118K6454A1		-	-	Frame_Shift_Del	INS	-	-	-	EPHA2	c.1244delinsCT	p.R415Pfs*39
118K6454A1	1	115256529	115256529	Missense_Mutation	SNP	T	C	C	NRAS	c.182A>G	p.Q61R
118K6454A1	3	52439883	52439883	Nonsense_Mutation	SNP	G	A	A	BAP1	c.829C>T	p.Q277*
118K6479M1	11	60231786	60231786	Missense_Mutation	SNP	C	A	A	MS4A1	c.305C>A	p.A102E
118K6479M1	17	7578406	7578406	Missense_Mutation	SNP	C	T	T	TP53	c.524G>A	p.R175H
118K6479M1	3	41267364	41267364	Splice_Site	SNP	A	C	C	CTNNB1	c.936+12A>C	-
118K6479M1	4	88967920	88967920	Missense_Mutation	SNP	C	G	G	PKD2	c.1446C>G	p.F482L
118K6509A1	12	46230571	46230571	Nonsense_Mutation	SNP	C	T	T	ARID2	c.820C>T	p.R274*
118K6509A1	12	49426907	49426907	Nonsense_Mutation	SNP	G	A	A	KMT2D	c.11581C>T	p.Q3861*
118K6509A1	15	66729154	66729154	Missense_Mutation	SNP	G	C	C	MAP2K1	c.362G>C	p.C121S
118K6509A1	16	2103385	2103385	Nonsense_Mutation	SNP	C	T	T	TSC2	c.268C>T	p.Q90*
118K6509A1	16	2130180	2130180	Nonsense_Mutation	SNP	C	T	T	TSC2	c.3412C>T	p.R1138*
118K6509A1	17	7577511	7577511	Missense_Mutation	SNP	A	G	G	TP53	c.770T>C	p.L257P
118K6509A1	18	48575209	48575209	Nonsense_Mutation	SNP	C	T	T	SMAD4	c.403C>T	p.R135*
118K6509A1	18	48591918	48591918	Missense_Mutation	SNP	C	T	T	SMAD4	c.1081C>T	p.R361C
118K6509A1	2	148677797	148677797	Splice_Site	SNP	A	C	C	ACVR2A	c.963-2A>C	-
118K6509A1	5	231091	231091	Missense_Mutation	SNP	G	C	C	SDHA	c.871G>C	p.E291Q
118K6509A1	5	149502735	149502735	Missense_Mutation	SNP	G	A	A	PDGFRB	c.2053C>T	p.R685C
118K6509A1	X	129190052	129190052	Missense_Mutation	SNP	G	A	A	BCORL1	c.5077G>A	p.L1693K
118K6518A1	12	25398284	25398284	Missense_Mutation	SNP	C	A	A	KRAS	c.35G>T	p.G12V
118K6518A1	17	7577526	7577526	Missense_Mutation	SNP	A	G	G	TP53	c.755T>C	p.L252P
118K6518A1	20	31022853	31022853	Nonsense_Mutation	SNP	C	T	T	ASXL1	c.2338C>T	p.Q780*
118K6518A1		-	-	Frame_Shift_Del	INS	-	-	-	PBRM1	c.559del	p.E187Sfs*7
118K6518A1	5	112102032	112102032	Nonsense_Mutation	SNP	A	T	T	APC	c.145A>T	p.K49*
118K6557A1	1	43775149	43775149	Missense_Mutation	SNP	C	T	T	TIE1	c.1279C>T	p.R427C
118K6557A1	10	8115751	8115751	Missense_Mutation	SNP	G	A	A	GATA3	c.1100G>A	p.R367Q
118K6557A1	12	25398282	25398282	Missense_Mutation	SNP	C	A	A	KRAS	c.37G>T	p.G13C
118K6557A1	12	57859588	57859588	Missense_Mutation	SNP	G	A	A	GLI1	c.519G>A	p.M173I
118K6557A1		-	-	Missense_Mutation	SNP	-	-	-	TP53	c.764_766del	p.L255del
118K6557A1	17	29679367	29679367	Missense_Mutation	SNP	G	A	A	NF1	c.7550G>A	p.R2517Q
118K6557A1		-	-	Frame_Shift_Del	INS	-	-	-	IRF2	c.642del	p.S215Afs*2
118K6557A1	9	21971209	21971209	Splice_Site	SNP	T	A	A	CDKN2A	c.151-2A>T	-
118K6580A1	16	2124337	2124337	Missense_Mutation	SNP	C	T	T	TSC2	c.2492C>T	p.T831M
118K6580A1	17	7577509	7577509	Nonsense_Mutation	SNP	C	A	A	TP53	c.772G>T	p.E258*
118K6580A1	2	141665451	141665451	Missense_Mutation	SNP	A	G	G	LRP1B	c.3515T>C	p.L1172P
118K6580A1	7	20199837	20199837	Nonsense_Mutation	SNP	C	T	T	MACC1	c.147G>A	p.W49*
118K6595M2		-	-	Frame_Shift_Del	INS	-	-	-	MTOR	c.5274_5290del	p.Q1758Hfs*3
118K6595M2	12	57597207	57597207	Missense_Mutation	SNP	C	A	A	LRP1	c.10854C>A	p.F3618L
118K6595M2	17	7578406	7578406	Missense_Mutation	SNP	C	T	T	TP53	c.524G>A	p.R175H
118K6595M2	17	29509525	29509525	Splice_Site	SNP	G	C	C	NF1	c.731-1G>C	-
118K6595M2	17	48263830	48263830	Missense_Mutation	SNP	C	T	T	COL1A1	c.3853G>A	p.D1285N
118K6595M2	7	92462405	92462405	Missense_Mutation	SNP	C	T	T	CDK6	c.233G>A	p.R78K
118K6595M2	7	127724808	127724808	Missense_Mutation	SNP	C	G	G	SND1	c.2143C>G	p.R715G
118K6595M2	9	87635254	87635254	Missense_Mutation	SNP	C	G	G	NTRK2	c.2306C>G	p.P769R
118K6631A1	12	25398284	25398284	Missense_Mutation	SNP	C	A	A	KRAS	c.35G>T	p.G12V
118K6631A1	4	20620399	20620399	Missense_Mutation	SNP	T	C	C	SLIT2	c.4357T>C	p.C1453R
118K6637M1	12	25398285	25398285	Missense_Mutation	SNP	C	A	A	KRAS	c.34G>T	p.G12C
118K6637M1		-	-	Frame_Shift_Del	INS	-	-	-	TP53	c.626_627del	p.R209Kfs*6
118K6637M1	17	12013738	12013738	Missense_Mutation	SNP	A	T	T	MAP2K4	c.680A>T	p.H227L
118K6637M1	18	48575671	48575671	Nonsense_Mutation	SNP	C	G	G	SMAD4	c.431C>G	p.S144*
118K6637M1		-	-	Frame_Shift_Del	INS	-	-	-	AMER1	84_988delinsGC	p.C328Wfs*4
118K6653A1	17	7577114	7577114	Missense_Mutation	SNP	C	T	T	TP53	c.824G>A	p.C275Y
118K6653A1	22	21341825	21341825	Missense_Mutation	SNP	G	A	A	LZTR1	c.353G>A	p.R118H
118K6653A1	4	110882136	110882136	Nonsense_Mutation	SNP	C	T	T	EGF	c.1180C>T	p.R394*
118K6674A1	12	25380275	25380275	Missense_Mutation	SNP	T	G	G	KRAS	c.183A>C	p.Q61H
118K6674A1	17	7578534	7578534	Missense_Mutation	SNP	C	G	G	TP53	c.396G>C	p.K132N
118K6674A1	2	112765986	112765986	Missense_Mutation	SNP	G	A	A	MERTK	c.1894G>A	p.E632K
118K6674A1	2	212426807	212426807	Missense_Mutation	SNP	G	T	T	ERBB4	c.2308C>A	p.L770M
118K6674A1	3	52441219	52441219	Missense_Mutation	SNP	T	G	G	BAP1	c.551A>C	p.D184A
118K6674A1	7	80299287	80299287	Missense_Mutation	SNP	C	A	A	CD36	c.767C>A	p.P256H
118K6703A1		-	-	In_Frame_Del	INS	-	-	-	LZTR1	c.2248_2253del	p.G750_F751del
118K6703A1		-	-	In_Frame_Del	INS	-	-	-	BAP1	c.1063_1081del	p.Q355*
118K6703A1	3	183212058	183212058	Missense_Mutation	SNP	T	A	A	KLHL6	c.1159A>T	p.T387S
118K6703A1	7	140453193	140453193	Missense_Mutation	SNP	T	C	C	BRAF	c.1742A>G	p.N581S
118K6789A1	2	209113113	209113113	Missense_Mutation	SNP	G	A	A	IDH1	c.394C>T	p.R132C
118K6789A1	20	57428356	57428356	Missense_Mutation	SNP	G	T	T	GNAS	c.36G>T	p.M12I
118K6789A1	3	185146700	185146700	Missense_Mutation	SNP	A	G	G	MAP3K13	c.331A>G	p.S111G
118K6855M1	10	84738731	84738731	Missense_Mutation	SNP	G	T	T	NRG3	c.1438G>T	p.G480W
118K6855M1	11	92086957	92086957	Missense_Mutation	SNP	G	T	T	FAT3	c.1679G>T	p.S560I
118K6855M1	17	7578463	7578463	Missense_Mutation	SNP	C	G	G	TP53	c.467G>C	p.R156P
118K6855M1	18	48604790	48604790	Nonsense_Mutation	SNP	G	T	T	SMAD4	c.1612G>T	p.E538*
118K6924A1	12	25398284	25398284	Missense_Mutation	SNP	C	T	T	KRAS	c.35G>A	p.G12D
118K6924A1	3	30732996	30732996	Missense_Mutation	SNP	C	T	T	TGFBR2	c.1609C>T	p.R537C
118K6924A1		-	-	Frame_Shift_Del	INS	-	-	-	RBM10	c.1630del	p.H544Ifs*160
118K6958A1	1	27105586	27105586	Nonsense_Mutation	SNP	G	T	T	ARID1A	c.5197G>T	p.E1733*
118K6958A1	1	158626386	158626386	Missense_Mutation	SNP	T	C	C	SPTA1	c.2866A>G	p.K956E
118K6958A1	12	25398284	25398284	Missense_Mutation	SNP	C	T	T	KRAS	c.35G>A	p.G12D
118K6958A1	17	7577094	7577094	Missense_Mutation	SNP	G	A	A	TP53	c.844C>T	p.R828W
118K6958A1		-	-	Frame_Shift_Del	INS	-	-	-	SMAD4	C.563_564del	P.N188Tfs*17
118K6958A1	3	142241669	142241669	Missense_Mutation	SNP	A	C	C	ATR	c.4167T>G	p.D1389E
118K6958A1	8	11412317	11412317	Missense_Mutation	SNP	C	T	T	BLK	c.538C>T	p.R180C
118K6975A1	13	32931985	32931985	Missense_Mutation	SNP	C	A	A	BRCA2	c.7724C>A	p.T2575N
118K6975A1	17	7577121	7577121	Missense_Mutation	SNP	G	A	A	TP53	c.817C>T	p.R273C
118K6975A1	17	37868208	37868208	Missense_Mutation	SNP	C	T	T	ERBB2	c.929C>T	p.S310F
118K6975A1	2	170028581	170028581	Missense_Mutation	SNP	C	T	T	LRP2	c.11207G>A	p.R3736H
118K6975A1	7	140481402	140481402	Missense_Mutation	SNP	C	A	A	BRAF	c.1406G>T	p.G469V
118K6975A1	8	48710791	48710791	Splice_Site	SNP	-	-	-	PRKDC	c.10455+9C>T	-
118K6975A1	9	21971186	21971186	Nonsense_Mutation	SNP	G	A	A	CDKN2A	c.172C>T	p.R58*
118K6975A1	X	15540551	15540551	Nonsense_Mutation	SNP	C	G	G	BMX	c.593C>G	p.S198*
118K6977A1	1	43787162	43787162	Missense_Mutation	SNP	G	T	T	TIE1	c.3244G>T	p.V1082L
118K6977A1	11	65425793	65425793	Missense_Mutation	SNP	C	T	T	RELA	c.842G>A	p.S281N
118K6977A1	11	92616427	92616427	Missense_Mutation	SNP	G	C	C	FAT3	c.12805G>C	p.E4269Q

118K6977A1		-	-	Frame_Shift_Del	INS	-	-	-	TP53	C.254del	P.P85Lfs*38
118K6977A1	19	4090615	4090615	Missense_Mutation	SNP	G	T	T	MAP2K2	c.1184C>A	p.P395H
118K6977A1	3	30729864	30729864	Splice_Site	SNP	C	G	G	TGFBF2	c.1397-12C>G	-
118K6977A1	4	1808030	1808030	Missense_Mutation	SNP	G	C	C	FGFR3	c.2006G>C	p.G69P
118K6977A1	4	55968099	55968099	Missense_Mutation	SNP	C	G	G	KDR	c.2231G>C	p.G744A
118K6977A1		-	-	Frame_Shift_Del	INS	-	-	-	CSNK1A1	C.626_635del	P.Y209Cfs*13
118K6986A1	12	50480122	50480122	Missense_Mutation	SNP	G	A	A	SMARCD1	c.356G>A	p.R119Q
118K6986A1	16	50783661	50783661	Missense_Mutation	SNP	G	A	A	CYLD	c.52G>A	p.E18K
118K6986A1		-	-	Frame_Shift_Del	INS	-	-	-	TP53	c.923del	p.L308Rfs*37
118K6986A1	17	78854209	78854209	Splice_Site	SNP	G	C	C	RPTOR	c.1510-6G>C	-
118K6986A1	18	23632790	23632790	Missense_Mutation	SNP	C	A	A	SS18	c.405G>T	p.M135I
118K6986A1	2	25497848	25497848	Missense_Mutation	SNP	G	A	A	DNMT3A	c.601C>T	p.R201C
118K6986A1	2	29917793	29917793	Missense_Mutation	SNP	C	T	T	ALK	c.875G>A	p.R292H
118K6986A1	2	109383574	109383574	Missense_Mutation	SNP	G	T	T	RANBP2	c.6579G>T	p.E2193D
118K6986A1	22	21344757	21344757	Missense_Mutation	SNP	G	A	A	LZTR1	c.734G>A	p.G245E
118K6986A1	6	30858775	30858775	Missense_Mutation	SNP	A	C	C	DDR1	c.443A>C	p.E148A
118K6986A1	7	6017398	6017398	Splice_Site	SNP	T	A	A	PMS2	c.2276-10A>T	-
118K6986A1	7	42088124	42088124	Missense_Mutation	SNP	C	A	A	GLI3	c.645G>T	p.M215I
118K6986A1	7	80302163	80302163	Splice_Site	SNP	A	T	T	CD36	c.1199+4A>T	-
118K6986A1	X	53223818	53223818	Missense_Mutation	SNP	C	T	T	KDM5C	c.3541G>A	p.A1181T
118K7052M1	1	115256529	115256529	Missense_Mutation	SNP	T	C	C	NRAS	c.182A>G	p.Q61R
118K7052M1	13	103053877	103053877	Missense_Mutation	SNP	G	A	A	FGF14	c.152C>T	p.T51M
118K7052M1		-	-	Frame_Shift_Ins	INS	-	-	-	BAP1	c.476_510dup	p.V171Lfs*28
118K7052M1		-	-	Frame_Shift_Ins	INS	-	-	-	PBRM1	c.1248dup	p.Y417Lfs*3
118K7052M1	4	66231757	66231757	Missense_Mutation	SNP	C	A	A	EPHA5	c.1943G>T	p.R648I
118K7052M1	6	117674224	117674224	Missense_Mutation	SNP	A	G	G	ROS1	c.4250T>C	p.I1417T
118K7082A1	12	25398284	25398284	Missense_Mutation	SNP	C	T	T	KRAS	c.35G>A	p.G12D
118K7082A1	15	93522483	93522483	Missense_Mutation	SNP	C	G	G	CHD2	c.2846C>G	p.T949R
118K7082A1	17	7578271	7578271	Missense_Mutation	SNP	T	A	A	TP53	c.578A>T	p.H193L
118K7082A1	18	48581281	48581281	Nonsense_Mutation	SNP	C	G	G	SMAD4	c.585C>G	p.Y195*
118K7082A1		-	-	Frame_Shift_Del	INS	-	-	-	SMARCA4	426_432delinsT	p.Q144Cfs*158
118K7082A1	2	121708868	121708868	Missense_Mutation	SNP	C	T	T	GLI2	c.304C>T	p.R102W
118K7082A1	20	57484421	57484421	Missense_Mutation	SNP	G	A	A	GNAS	c.602G>A	p.R201H
118K7082A1		-	-	Frame_Shift_Del	INS	-	-	-	KMT2C	c.11228del	p.K3743Rfs*2
118K7082A1	8	41834792	41834792	Missense_Mutation	SNP	C	T	T	KAT6A	c.1097G>A	p.R366Q
118K7083M1	1	16459975	16459975	Splice_Site	SNP	C	T	T	EPHA2	c.1864+1G>A	-
118K7083M1		-	-	Frame_Shift_Ins	INS	-	-	-	TP53	C.93dup	p.L325fs*11
118K7083M1		-	-	Frame_Shift_Del	INS	-	-	-	NF1	C.1584del	P.L529Sfs*27
118K7083M1	3	178936082	178936082	Missense_Mutation	SNP	G	A	A	PIK3CA	c.1624G>A	p.E542K
118L7106A1		-	-	Frame_Shift_Del	INS	-	-	-	TP53	c.1002del	p.R335Vfs*10
118L7106A1		-	-	Frame_Shift_Del	INS	-	-	-	MSH2	c.1171_1202del	p.A391Lfs*15
118L7106A1	20	57485733	57485733	Splice_Site	SNP	C	T	T	GNAS	c.1039-5C>T	-
118L7106A1		-	-	Frame_Shift_Del	INS	-	-	-	MST1R	c.722_770del	p.H241Pfs*6
118L7106A1	4	1920319	1920319	Missense_Mutation	SNP	T	C	C	NSD2	c.1379T>C	p.F460S
118L7131A1		-	-	In_Frame_Del	INS	-	-	-	ARID2	c.2495_2503del	p.S832*
118L7131A1	17	5036249	5036249	Missense_Mutation	SNP	G	T	T	USP6	c.240G>T	p.M80I
118L7131A1	17	7578493	7578493	Nonsense_Mutation	SNP	C	T	T	TP53	c.437G>A	p.W146*
118L7131A1	4	153258986	153258986	Nonsense_Mutation	SNP	G	A	A	FBXW7	c.829C>T	p.Q277*
118L7133A1	17	7579414	7579414	Nonsense_Mutation	SNP	C	T	T	TP53	c.273G>A	p.W91*
118L7161A1	15	67457641	67457641	Missense_Mutation	SNP	C	A	A	SMAD3	c.451C>A	p.P151T
118L7161A1	17	7577108	7577108	Missense_Mutation	SNP	C	A	A	TP53	c.830G>T	p.C277F
118L7161A1		-	-	Frame_Shift_Del	INS	-	-	-	PIK3R1	C.98del	P.N33Lfs*5
118L7161A1		-	-	Frame_Shift_Ins	INS	-	-	-	APC	C.4666dup	P.T1556Nfs*3
118L7198A1	1	16475389	16475389	Missense_Mutation	SNP	G	A	A	EPHA2	c.307C>T	p.R103C
118L7198A1	10	123239508	123239508	Nonsense_Mutation	SNP	C	A	A	FGFR2	c.2329G>T	p.E77*
118L7198A1	17	7578475	7578475	Missense_Mutation	SNP	G	A	A	TP53	c.455C>T	p.P152L
118L7198A1	17	37868208	37868208	Missense_Mutation	SNP	C	T	T	ERBB2	c.929C>T	p.S310F
118L7198A1	3	52443729	52443729	Splice_Site	SNP	C	T	T	BAP1	c.67+1G>A	-
118L7198A1	7	128852243	128852243	Missense_Mutation	SNP	G	A	A	SMO	c.2315G>A	p.R772H
118L7198A1	7	140453193	140453193	Missense_Mutation	SNP	T	A	A	BRAF	c.1742A>T	p.N581I
118L7202A1	1	158624504	158624504	Missense_Mutation	SNP	C	A	A	SPTA1	c.2933G>T	p.G978V
118L7202A1	12	46287201	46287201	Splice_Site	SNP	A	G	G	ARID2	c.5148-2A>G	-
118L7202A1		-	-	Frame_Shift_Del	INS	-	-	-	CTCF	C.1331_1332del	P.T444Sfs*7
118L7202A1	17	7577570	7577570	Missense_Mutation	SNP	C	A	A	TP53	c.711G>T	p.M237I
118L7202A1	X	110463640	110463640	Missense_Mutation	SNP	G	A	A	PAK3	c.1600G>A	p.A534T
118L7212A1	1	51439730	51439730	Nonsense_Mutation	SNP	G	T	T	CDKN2C	c.295G>T	p.E99*
118L7212A1	11	118375313	118375313	Missense_Mutation	SNP	G	T	T	KMT2A	c.8706G>T	p.Q2902H
118L7212A1	12	46240644	46240644	Nonsense_Mutation	SNP	A	T	T	ARID2	c.1504A>T	p.R502*
118L7212A1		-	-	Frame_Shift_Del	INS	-	-	-	ARID2	c.1611_1626del	p.D537Efs*15
118L7212A1		-	-	Frame_Shift_Del	INS	-	-	-	KMT2D	192_193delins	p.R65Vfs*65
118L7212A1	17	7577534	7577534	Missense_Mutation	SNP	C	A	A	TP53	c.747G>T	p.R249S
118L7212A1		-	-	In_Frame_Del	INS	-	-	-	PIK3CA	c.1342_1353del	P.V448_445del
118L7212A1	5	180047312	180047312	Splice_Site	SNP	C	A	A	FLT4	c.2407-4G>T	-
118L7212A1	7	2962378	2962378	Missense_Mutation	SNP	C	T	T	CARD11	c.2159G>A	p.R720Q
118L7229A1	1	16475388	16475388	Missense_Mutation	SNP	C	G	G	EPHA2	c.308G>C	p.R103P
118L7229A1		-	-	Frame_Shift_Del	INS	-	-	-	ARID1A	c.487_508del	p.A163Tfs*62
118L7229A1	2	141108580	141108580	Missense_Mutation	SNP	G	C	C	LRP1B	c.11678C>G	p.A3893G
118L7229A1	8	93107283	93107283	Missense_Mutation	SNP	G	C	C	RUNX1T1	c.238C>G	p.L80V
118L7236A1	1	27094328	27094328	Nonsense_Mutation	SNP	T	A	A	ARID1A	c.3036T>A	p.Y1012*
118L7236A1		-	-	Frame_Shift_Ins	INS	-	-	-	ACVR1B	c.1335_1338dup	p.L447Cfs*20
118L7236A1	19	1207085	1207085	Missense_Mutation	SNP	G	T	T	STK11	c.173G>T	p.G58V
118L7236A1	2	148680663	148680663	Missense_Mutation	SNP	G	A	A	ACVR2A	c.1199G>A	p.R400H
118L7236A1	X	129159276	129159276	Missense_Mutation	SNP	C	T	T	BCORL1	c.4000C>T	p.R1334W
118L7265A2	12	25398284	25398284	Missense_Mutation	SNP	C	T	T	KRAS	c.35G>A	p.G12D
118L7265A2	13	110434682	110434682	Missense_Mutation	SNP	C	T	T	IRS2	c.3719G>A	p.R1240H
118L7265A2	17	7578265	7578265	Missense_Mutation	SNP	A	G	G	TP53	c.584T>C	p.I195T
118L7265A2	2	141641467	141641467	Missense_Mutation	SNP	T	C	C	LRP1B	c.4088A>G	p.K1363R
118L7265A2	2	202136270	202136270	Missense_Mutation	SNP	A	G	G	CASP8	c.433A>G	p.S145G
118L7275A1	12	25398284	25398284	Missense_Mutation	SNP	C	T	T	KRAS	c.35G>A	p.G12D
118L7275A1	17	7578382	7578382	Nonsense_Mutation	SNP	G	T	T	TP53	c.548C>A	p.S183*
118L7275A1	9	135787732	135787732	Missense_Mutation	SNP	G	A	A	TSC1	c.850C>T	p.R284C
118L7370A1		-	-	Frame_Shift_Del	INS	-	-	-	KRAS	c.498_499del	p.H166Qfs*9
118L7370A1	12	25398285	25398285	Missense_Mutation	SNP	C	A	A	KRAS	c.34G>T	p.G12C
118L7370A1	22	24145600	24145600	Missense_Mutation	SNP	A	T	T	SMARCB1	c.619A>T	p.N207Y
118L7386A1	1	27099947	27099947	Nonsense_Mutation	SNP	C	T	T	ARID1A	c.3826C>T	p.R1276*
118L7386A1	14	75748096	75748096	Nonsense_Mutation	SNP	C	A	A	FOS	c.1112C>A	p.S371*
118L7386A1	17	59793342	59793342	Missense_Mutation	SNP	G	A	A	BRIP1	c.2462C>T	p.A821V
118L7386A1	22	21343161	21343161	Missense_Mutation	SNP	G	A	A	LZTR1	c.593G>A	p.R198K

118L7386A1		-	-	Missense_Mutation	SNP	-	-	-	PIK3CA	C.328_330del	P.E110del
118L7386A1		-	-	In_Frame_Del	INS	-	-	-	PDGFRB	C.181_204del	P.V61_E68del
118L7386A1	7	6426900	6426900	Missense_Mutation	SNP	A	C	C	RAC1	c.93A>C	p.E31D
118L7386A1	7	81336624	81336624	Missense_Mutation	SNP	C	T	T	HGF	c.1598G>A	p.R533Q
118L7386A1	8	48711869	48711869	Missense_Mutation	SNP				PRKDC	c.10198T>G	p.V3400G
118L7404M1	1	120466361	120466361	Missense_Mutation	SNP	T		G	NOTCH2	c.4758A>C	p.E1586D
118L7404M1	1	158609445	158609445	Missense_Mutation	SNP	G	C	C	SPTA1	c.4907C>G	p.A1636G
118L7404M1	12	49432299	49432299	Missense_Mutation	SNP	T	G	G	KMT2D	c.8840A>C	p.H2947P
118L7404M1	12	57560824	57560824	Missense_Mutation	SNP	C	T	T	LRP1	c.2909C>T	p.S970L
118L7404M1	13	25026701	25026701	Missense_Mutation	SNP	A	G	G	PARP4	c.2857T>C	p.F953L
118L7404M1	16	3786029	3786029	Splice_Site	SNP	G	A	A	CREBBP	c.4728+8C>T	-
118L7404M1	17	7578263	7578263	Nonsense_Mutation	SNP	G	A	A	TP53	c.586C>T	p.R196*
118L7404M1	19	15353845	15353845	Missense_Mutation	SNP	G	A	A	BRD4	c.3035C>T	p.P1012L
118L7404M1	2	170002327	170002327	Missense_Mutation	SNP	C	G	G	LRP2	c.12918G>C	p.E4306D
118L7404M1	22	24176339	24176339	Missense_Mutation	SNP	G	A	A	SMARCB1	c.1130G>A	p.R377H
118L7404M1	4	66356209	66356209	Missense_Mutation	SNP	C	T	T	EPHA5	c.1288G>A	p.D430N
118L7404M1	5	176636872	176636872	Missense_Mutation	SNP	A	G	G	NSD1	c.1472A>G	p.E491G
118L7404M1	6	157405841	157405841	Missense_Mutation	SNP	A	G	G	ARID1B	c.2083A>G	p.T695A
118L7404M1	7	18833040	18833040	Missense_Mutation	SNP	G	A	A	HDAC9	c.2278G>A	p.E760K
118L7404M1	9	97933432	97933432	Splice_Site	SNP	A	G	G	FANCC	c.457-7T>C	-
118L7413A1		-	-	In_Frame_Ins	INS	-	-	-	PTEN	c.439_456dup	p.K147_1152dup
118L7413A1	7	142640096	142640096	Missense_Mutation	SNP	C	T	T	KEL	c.1807G>A	p.A603T
118L7497M1		-	-	Frame_Shift_Ins	INS	-	-	-	ARID1A	c.961_986dup	p.A330Rfs*42
118L7497M1	1	204499861	204499861	Missense_Mutation	SNP	A	G	G	MDM4	c.203A>G	p.Q68R
118L7497M1	10	88659835	88659835	Missense_Mutation	SNP	C	A	A	BMPRI1A	c.482C>A	p.A161D
118L7497M1	11	92616320	92616320	Missense_Mutation	SNP	G	A	A	FAT3	c.12698G>A	p.R4233H
118L7497M1	13	28897002	28897002	Missense_Mutation	SNP	C	T	T	FLT1	c.2878G>A	p.V960I
118L7497M1	16	67644855	67644855	Missense_Mutation	SNP	A	T	T	CTCF	c.120A>T	p.L40F
118L7497M1	17	80789046	80789046	Missense_Mutation	SNP	C	T	T	ZNF750	c.1285G>A	p.G429S
118L7497M1	18	48593533	48593533	Missense_Mutation	SNP	G	T	T	SMAD4	c.1284G>T	p.K428N
118L7497M1	2	121746077	121746077	Missense_Mutation	SNP	T	G	G	GLI2	c.2587T>G	p.S863A
118L7497M1	X	44969471	44969471	Nonsense_Mutation	SNP	C	T	T	KDM6A	c.4153C>T	p.Q1385*
118L7516M1	12	121438953	121438953	Missense_Mutation	SNP	C	G	G	HNFI1A	c.1854C>G	p.L618M
118L7516M1	13	49039470	49039470	Missense_Mutation	SNP	C	G	G	RB1	c.2455C>G	p.L819V
118L7516M1		-	-	In_Frame_Del	INS	-	-	-	IRS2	c.2096_2104del	P.A699_A701del
118L7516M1	14	95562437	95562437	Missense_Mutation	SNP	C	T	T	DICER1	c.4820G>A	p.R1607Q
118L7516M1	16	2124198	2124198	Splice_Site	SNP	C	T	T	TSC2	c.2356-3C>T	-
118L7516M1	16	56871605	56871605	Missense_Mutation	SNP	G	A	A	NUP93	c.1985G>A	p.R662K
118L7516M1	2	170034537	170034537	Splice_Site	SNP	C	A	A	LRP2	c.10170-1G>T	-
118L7516M1	2	209113113	209113113	Missense_Mutation	SNP	G	A	A	IDH1	c.394C>T	p.R132C
118L7516M1	3	47165993	47165993	Missense_Mutation	SNP	T	C	C	SETD2	c.133A>G	p.M45V
118L7516M1	3	195609000	195609000	Missense_Mutation	SNP	T	C	C	TNK2	c.809A>G	p.D270G
118L7516M1	4	1806153	1806153	Missense_Mutation	SNP	C	T	T	FGFR3	c.1172C>T	p.A391V
118L7516M1	4	187584755	187584755	Missense_Mutation	SNP	G	A	A	FAT1	c.3278C>T	p.T1093M
118L7537A1	1	27057961	27057961	Nonsense_Mutation	SNP	C	T	T	ARID1A	c.1669C>T	p.Q557*
118L7537A1		-	-	Splice_Site	SNP	-	-	-	SPTA1	376-30_3376-1	-
118L7537A1	17	7577539	7577539	Missense_Mutation	SNP	G	A	A	TP53	c.742C>T	p.R248W
118L7537A1	18	48575152	48575152	Missense_Mutation	SNP	C	A	A	SMAD4	c.346C>A	p.Q116K
118L7537A1		-	-	Frame_Shift_Del	INS	-	-	-	ARID1B	C.1160_1200del	P.A387Gfs*134
118L7537A1	7	140453155	140453155	Missense_Mutation	SNP	C	T	T	BRAF	c.1780G>A	p.D594N
118L7537A1	X	44929085	44929085	Nonsense_Mutation	SNP	G	T	T	KDM6A	c.2185G>T	p.E729*
118L7537A1	X	47032526	47032526	Splice_Site	SNP	G	T	T	RBM10	c.433-1G>T	-
118L7560M1	2	209113113	209113113	Missense_Mutation	SNP	G	A	A	IDH1	c.394C>T	p.R132C
118L7560M1		-	-	Frame_Shift_Del	INS	-	-	-	PBRM1	c.818_860del	p.A273Vfs*13
118L7574A1	17	7577609	7577609	Splice_Site	SNP	C	T	T	TP53	c.673-1G>A	-
118L7574A1	19	11123735	11123735	Nonsense_Mutation	SNP	C	A	A	SMARCA4	c.2385C>A	p.Y795*
118L7574A1	9	21971111	21971111	Missense_Mutation	SNP	G	A	A	CDKN2A	c.247C>T	p.H83Y
118L7574A1	X	76814140	76814140	Missense_Mutation	SNP	C	A	A	ATRX	c.6504G>T	p.Q2168H
118L7607A1	17	7577538	7577538	Missense_Mutation	SNP	C	T	T	TP53	c.743G>A	p.R248Q
118L7607A1	9	93641101	93641101	Missense_Mutation	SNP	A	G	G	SYK	c.1378A>G	p.K460E
118L7654M1		-	-	Frame_Shift_Ins	INS	-	-	-	ARID1A	C.748_758dup	P.S255Rfs*112
118L7654M1	12	49444501	49444501	Nonsense_Mutation	SNP	A	T	T	KMT2D	c.2870T>A	p.L957*
118L7654M1	14	102548726	102548726	Missense_Mutation	SNP	T	C	C	HSP90AA1	c.2177A>G	p.Y726C
118L7654M1	2	209113113	209113113	Missense_Mutation	SNP	G	A	A	IDH1	c.394C>T	p.R132C
118L7654M1	7	151846234	151846234	Missense_Mutation	SNP	A	C	C	KMT2C	c.12778T>G	p.S4260A
118L7654M1		-	-	Splice_Site	SNP	-	-	-	KMT2C	775-26_12775-	-
118L7654M1	7	151893098	151893098	Splice_Site	SNP	T	A	A	KMT2C	c.4274-2A>T	-
118L7654M1		-	-	Frame_Shift_Del	INS	-	-	-	PTCH1	C.2144del	P.F715Sfs*31
118L7656M1		-	-	Frame_Shift_Del	INS	-	-	-	TNFRSF14	c.218_219del	p.T73Sfs*3
118L7656M1		-	-	Frame_Shift_Del	INS	-	-	-	EPHA2	c.987del	p.S330Pfs*63
118L7656M1		-	-	Frame_Shift_Ins	INS	-	-	-	ARID1A	c.676_679dup	p.P227Rfs*174
118L7656M1		-	-	Missense_Mutation	SNP	-	-	-	RARA	c.499_501del	p.K167del
118L7656M1		-	-	Frame_Shift_Del	INS	-	-	-	BCOR	c.524_527del	p.K175Rfs*40
118L7756A1		-	-	Frame_Shift_Ins	INS	-	-	-	ARID1A	C.3121dup	P.L1041Pfs*6
118L7756A1	10	89690802	89690802	Splice_Site	SNP	G	C	C	PTEN	c.210-1G>C	-
118L7756A1		-	-	Frame_Shift_Ins	INS	-	-	-	SMAD4	C.421dup	P.I141Nfs*2
118L7756A1	20	57484421	57484421	Missense_Mutation	SNP	G	A	A	GNAS	c.602G>A	p.R201H
118L7756A1	7	140481412	140481412	Missense_Mutation	SNP	C	G	G	BRAF	c.1396G>C	p.G466R
118L7757A1		-	-	Frame_Shift_Ins	INS	-	-	-	EPHA2	c.1153dup	p.Y385Lfs*69
118L7757A1	1	158612266	158612266	Missense_Mutation	SNP	C	T	T	SPTA1	c.4672G>A	p.V1558I
118L7757A1		-	-	Splice_Site	SNP	-	-	-	PARP1	c.2848+11del	-
118L7757A1	12	25380276	25380276	Missense_Mutation	SNP	T	A	A	KRAS	c.182A>T	p.Q61L
118L7757A1		-	-	Frame_Shift_Ins	INS	-	-	-	TP53	c.267dup	p.S90Lfs*59
118L7757A1	17	56440631	56440631	Splice_Site	SNP	C	G	G	RNF43	c.582+5G>C	-
118L7757A1	2	141643893	141643893	Missense_Mutation	SNP	C	T	T	LRP1B	c.3778G>A	p.A1260T
118L7757A1	2	170101208	170101208	Missense_Mutation	SNP	T	C	C	LRP2	c.3425A>G	p.N1142S
118L7757A1	2	212295774	212295774	Missense_Mutation	SNP	G	A	A	ERBB4	c.2539C>T	p.R847C
118L7757A1		-	-	Frame_Shift_Del	INS	-	-	-	CDKN2A	c.118_142del	p.A40Rfs*5
118L7820J1	1	158641959	158641959	Missense_Mutation	SNP	C	T	T	SPTA1	c.1378G>A	p.A460T
118L7820J1		-	-	Frame_Shift_Del	INS	-	-	-	ATM	C.3272_3273del	P.E1091Vfs*4
118L7820J1		-	-	Frame_Shift_Del	INS	-	-	-	PARP4	C.3032_3071del	P.H1011Lfs*16
118L7820J1	13	102375233	102375233	Missense_Mutation	SNP	G	A	A	FGF14	c.707C>T	p.A236V
118L7820J1	17	7574021	7574021	Nonsense_Mutation	SNP	C	A	A	TP53	c.1006G>T	p.E336*
118L7820J1		-	-	Missense_Mutation	SNP	-	-	-	ASXL1	478_3479delins	p.G1160F
118L7820J1	3	52439898	52439898	Missense_Mutation	SNP	G	C	C	BAP1	c.814C>G	p.Q272E
118L7820J1	8	68999961	68999961	Missense_Mutation	SNP	C	A	A	PREX2	c.2030C>A	p.T677K
118L7848M1		-	-	Splice_Site	SNP	-	-	-	EPHA2	865-10_1865-1	-
118L7848M1	12	25398284	25398284	Missense_Mutation	SNP	C	A	A	KRAS	c.35G>T	p.G12V

118L7848M1	12	133225654	133225654	Missense_Mutation	SNP	C	T	T	POLE	c.4010G>A	p.S1337N
118L7848M1	20	30662502	30662502	Missense_Mutation	SNP	G	A	A	HCK	c.343G>A	p.V115I
118L7848M1	4	20620585	20620585	Nonsense_Mutation	SNP	G	T	T	SLIT2	c.4543G>T	p.E151S*
118L7848M1		-	-	Frame_Shift_Del	INS	-	-	-	BCORL1	C.2228del	P.R743Pfs*40
118L7853A1		-	-	Frame_Shift_Del	INS	-	-	-	ARID1A	c.4912del	p.D1638Ifs*16
118L7853A1	12	46285669	46285669	Nonsense_Mutation	SNP	C	T	T	ARID2	c.5029C>T	p.R1777*
118L7853A1	15	88423551	88423551	Missense_Mutation	SNP	C	T	T	NTRK3	c.2242G>A	p.E748K
118L7853A1		-	-	Missense_Mutation	SNP	-	-	-	TP53	000_1001delins	p.G334L
118L7860A1	1	78430001	78430001	Missense_Mutation	SNP	C	T	T	FUBP1	c.878G>A	p.R293K
118L7860A1	11	92577541	92577541	Missense_Mutation	SNP	C	T	T	FAT3	c.11008C>T	p.R3670W
118L7860A1	12	46243472	46243472	Nonsense_Mutation	SNP	C	T	T	ARID2	c.1825C>T	p.Q609*
118L7860A1	12	46243484	46243484	Nonsense_Mutation	SNP	C	T	T	ARID2	c.1837C>T	p.Q613*
118L7860A1	12	46244709	46244709	Nonsense_Mutation	SNP	C	T	T	ARID2	c.2803C>T	p.Q935*
118L7860A1	12	46254641	46254641	Nonsense_Mutation	SNP	C	T	T	ARID2	c.4831C>T	p.Q1611*
118L7860A1	17	7577085	7577085	Nonsense_Mutation	SNP	C	A	A	TP53	c.853G>T	p.E285*
118L7860A1	17	7577538	7577538	Missense_Mutation	SNP	C	T	T	TP53	c.743G>A	p.R248Q
118L7860A1	17	48263773	48263773	Missense_Mutation	SNP	G	C	C	COL1A1	c.3910C>G	p.Q1304E
118L7860A1	2	170013946	170013946	Missense_Mutation	SNP	C	G	G	LRP2	c.11954G>C	p.G3985A
118L7860A1	3	178936037	178936037	Missense_Mutation	SNP	G	A	A	PIK3CA	c.1579G>A	p.D527N
118L7860A1	3	178936091	178936091	Missense_Mutation	SNP	G	A	A	PIK3CA	c.1633G>A	p.E545K
118L7860A1	3	183226037	183226037	Missense_Mutation	SNP	A	T	T	KLHL6	c.719T>A	p.M240K
118L7860A1	4	110901298	110901298	Splice_Site	SNP	A	G	G	EGF	c.2221+3A>G	-
118L7860A1	5	176665478	176665478	Missense_Mutation	SNP	G	C	C	NSD1	c.4162G>C	p.E1388Q
118L7860A1	6	117714466	117714466	Missense_Mutation	SNP	C	G	G	ROS1	c.1183G>C	p.E395Q
118L7860A1	8	11566174	11566174	Missense_Mutation	SNP	C	T	T	GATA4	c.353C>T	p.A118V
118L7860A1	9	21971036	21971036	Missense_Mutation	SNP	C	T	T	CDKN2A	c.322G>A	p.D108N
118L7867A1		-	-	Frame_Shift_Del	INS	-	-	-	ARID1A	c.3300del	p.Y1101Mfs*60
118L7867A1	12	56478983	56478983	Missense_Mutation	SNP	C	T	T	ERBB3	c.439C>T	p.P147S
118L7867A1	15	93486100	93486100	Missense_Mutation	SNP	C	T	T	CHD2	c.854C>T	p.A285V
118L7867A1		-	-	Frame_Shift_Del	INS	-	-	-	TP53	c.46del	p.Q168Ifs*28
118L7867A1	19	10602745	10602745	Missense_Mutation	SNP	G	A	A	KEAP1	c.833C>T	p.P278L
118L7867A1	19	15299917	15299917	Missense_Mutation	SNP	G	A	A	NOTCH3	c.1261C>T	p.R421C
118L7867A1	2	212286794	212286794	Nonsense_Mutation	SNP	T	A	A	ERBB4	c.2902A>T	p.K968*
118L7867A1	3	142278223	142278223	Nonsense_Mutation	SNP	C	T	T	ATR	c.1602G>A	p.W534*
118L7867A1	6	157505389	157505389	Nonsense_Mutation	SNP	G	T	T	ARID1B	c.3370G>T	p.E1124*
118L7895A1	1	16460082	16460082	Missense_Mutation	SNP	C	A	A	EPHA2	c.1758G>T	p.K586N
118L7895A1		-	-	In_Frame_Del	INS	-	-	-	TP53	c.794_817del	p.L265_V272del
118L7895A1	9	21971194	21971194	Missense_Mutation	SNP	C	T	T	CDKN2A	c.164G>A	p.G55D
118L7895A1	X	123019820	123019820	Missense_Mutation	SNP	C	T	T	XIAP	c.308C>T	p.T103M
118L8016M1	12	25398284	25398284	Missense_Mutation	SNP	C	A	A	KRAS	c.35G>T	p.G12V
118L8016M1	16	354440	354440	Missense_Mutation	SNP	C	T	T	AXIN1	c.1118G>A	p.R373H
118L8016M1	17	7578508	7578508	Missense_Mutation	SNP	C	T	T	TP53	c.422G>A	p.C141Y
118L8016M1	17	37880257	37880257	Missense_Mutation	SNP	C	G	G	ERBB2	c.2301C>G	p.I767M
118L8016M1	2	198267360	198267360	Missense_Mutation	SNP	T	G	G	SF3B1	c.1997A>C	p.K666T
118L8016M1	4	88996022	88996022	Missense_Mutation	SNP	G	A	A	PKD2	c.2581G>A	p.D861N
118L8016M1	7	116412023	116412023	Missense_Mutation	SNP	A	G	G	MET	c.3008A>G	p.Y1003C
118L8016M1	8	69017412	69017412	Missense_Mutation	SNP	C	T	T	PREX2	c.2755C>T	p.H919Y
118L8023M2		-	-	In_Frame_Ins	INS	-	-	-	EPHA2	c.719dup	p.E241*
118L8023M2	13	32912432	32912432	Nonsense_Mutation	SNP	A	T	T	BRCA2	c.3940A>T	p.K1314*
118L8023M2	20	31023598	31023598	Missense_Mutation	SNP	C	G	G	ASXL1	c.3083C>G	p.S1028W
118L8023M2	3	52443864	52443864	Missense_Mutation	SNP	C	T	T	BAP1	c.31G>A	p.D11N
118L8029M1		-	-	Frame_Shift_Del	INS	-	-	-	SPEN	C.3154del	P.110525fs*40
118L8029M1		-	-	Frame_Shift_Del	INS	-	-	-	SPEN	C.7484del	P.P2495Lfs*4
118L8029M1		-	-	Frame_Shift_Del	INS	-	-	-	EPHA2	C.843del	P.F281Lfs*112
118L8029M1	1	27056238	27056238	Nonsense_Mutation	SNP	C	T	T	ARID1A	c.1234C>T	p.Q412*
118L8029M1		-	-	Frame_Shift_Del	INS	-	-	-	JAK1	C.2580del	P.K860Nfs*16
118L8029M1		-	-	Missense_Mutation	SNP	-	-	-	JAK1	C.2118_2120de	P.E706del
118L8029M1	1	241665738	241665738	Splice_Site	SNP	C	A	A	FH	c.1236+5G>T	-
118L8029M1		-	-	Frame_Shift_Del	INS	-	-	-	CHD4	C.218del	P.K738fs*129
118L8029M1		-	-	Frame_Shift_Del	INS	-	-	-	HNF1A	C.872del	P.P291Ofs*51
118L8029M1		-	-	Frame_Shift_Del	INS	-	-	-	BRCA2	C.1813del	P.I605Yfs*9
118L8029M1	14	36987159	36987159	Missense_Mutation	SNP	C	T	T	NKX2-1	c.530G>A	p.G177E
118L8029M1		-	-	Frame_Shift_Del	INS	-	-	-	B2M	C.43_44del	P.L15fs*41
118L8029M1	15	67477113	67477113	Missense_Mutation	SNP	G	A	A	SMAD3	c.920G>A	p.C307Y
118L8029M1	16	10274135	10274135	Missense_Mutation	SNP	T	C	C	GRIN2A	c.134A>G	p.D45G
118L8029M1	17	7578388	7578388	Missense_Mutation	SNP	C	T	T	TP53	c.542G>A	p.R181H
118L8029M1		-	-	Frame_Shift_Del	INS	-	-	-	RNF43	C.1943_1944de	P.S648Cfs*98
118L8029M1	19	15299971	15299971	Missense_Mutation	SNP	C	T	T	NOTCH3	c.1207G>A	p.E403K
118L8029M1	2	141122273	141122273	Missense_Mutation	SNP	C	A	A	LRP1B	c.11088G>T	p.E3696D
118L8029M1		-	-	Frame_Shift_Del	INS	-	-	-	ACVR2A	C.1310del	P.K437Rfs*5
118L8029M1		-	-	Splice_Site	SNP	-	-	-	CASP8	23-6_-123-3del	-
118L8029M1		-	-	Frame_Shift_Ins	INS	-	-	-	ERBB4	C.1798dup	P.A600Gfs*10
118L8029M1		-	-	Frame_Shift_Del	INS	-	-	-	TGFBFR2	C.383del	P.K1285fs*35
118L8029M1		-	-	Frame_Shift_Del	INS	-	-	-	TGFBFR2	C.1229_1230de	P.V410Gfs*2
118L8029M1	3	37090440	37090440	Nonsense_Mutation	SNP	G	T	T	MLH1	c.2035G>T	p.E679*
118L8029M1		-	-	In_Frame_Del	INS	-	-	-	PBRM1	C.159_160del	P.Y54*
118L8029M1	3	89456470	89456470	Missense_Mutation	SNP	C	T	T	EPHA3	c.1646C>T	p.A549V
118L8029M1	3	178936082	178936082	Missense_Mutation	SNP	G	A	A	PIK3CA	c.1624G>A	p.E542K
118L8029M1		-	-	Frame_Shift_Del	INS	-	-	-	SLIT2	C.2712del	P.K904Nfs*13
118L8029M1	4	126336687	126336687	Missense_Mutation	SNP	G	A	A	FAT4	c.6569G>A	p.R2190H
118L8029M1	4	153250856	153250856	Missense_Mutation	SNP	T	C	C	FBXW7	c.1204A>G	p.T402A
118L8029M1		-	-	Frame_Shift_Del	INS	-	-	-	RAD50	C.2165del	P.K722Rfs*14
118L8029M1	5	149497260	149497260	Missense_Mutation	SNP	C	T	T	PDGFRB	c.3058G>A	p.D1020N
118L8029M1	5	156671313	156671313	Missense_Mutation	SNP	G	A	A	ITK	c.1274G>A	p.C425Y
118L8029M1	5	176666797	176666797	Missense_Mutation	SNP	A	T	T	NSD1	c.4233A>T	p.K1411N
118L8029M1	5	180058718	180058718	Missense_Mutation	SNP	A	G	G	FLT4	c.119T>C	p.V40A
118L8029M1		-	-	Splice_Site	SNP	-	-	-	FYN	c.345-9delT	-
118L8029M1	8	32621591	32621591	Missense_Mutation	SNP	G	A	A	NRG1	c.1123G>A	p.E375K
118L8029M1		-	-	Splice_Site	SNP	-	-	-	NBN	c.1398-10delT	-
118L8029M1	X	76909699	76909699	Splice_Site	SNP	A	C	C	ATRX	c.4215-9T>G	-
118L8044A1	1	16258127	16258127	Nonsense_Mutation	SNP	C	T	T	SPEN	c.5392C>T	p.Q1798*
118L8044A1	1	32741204	32741204	Missense_Mutation	SNP	G	A	A	LCK	c.412G>A	p.E138K
118L8044A1	1	204506578	204506578	Missense_Mutation	SNP	C	G	G	MDM4	c.364C>G	p.I122V
118L8044A1	1	206648248	206648248	Missense_Mutation	SNP	C	G	G	IKBKE	c.269C>G	p.S90C
118L8044A1	11	22646489	22646489	Nonsense_Mutation	SNP	G	A	A	FANCF	c.868C>T	p.Q290*
118L8044A1	11	92564779	92564779	Splice_Site	SNP	C	T	T	FAT3	c.9482-9C>T	-
118L8044A1	12	46254583	46254583	Splice_Site	SNP	G	C	C	ARID2	c.4774-1G>C	-
118L8044A1	12	133233991	133233991	Missense_Mutation	SNP	C	G	G	POLE	c.3403G>C	p.E1135Q

118L8044A1	12	133244079	133244079	Splice_Site	SNP	C	T	T	POLE	c.2319+10G>A	-
118L8044A1	13	25072298	25072298	Missense_Mutation	SNP	G	T	T	PARP4	c.547C>A	p.P183T
118L8044A1	13	48934254	48934254	Missense_Mutation	SNP	G	C	C	RB1	c.709G>C	p.E237Q
118L8044A1	14	81574987	81574987	Missense_Mutation	SNP	G	A	A	TSHR	c.724G>A	p.E242K
118L8044A1	15	75092849	75092849	Splice_Site	SNP	G	C	C	CSK	c.556+3G>C	-
118L8044A1	15	88690645	88690645	Splice_Site	SNP	G	C	C	NTRK3	c.396-11C>G	-
118L8044A1	15	99465606	99465606	Missense_Mutation	SNP	G	A	A	IGF1R	c.2431G>A	p.E811K
118L8044A1	17	7578406	7578406	Missense_Mutation	SNP	C	T	T	TP53	c.524G>A	p.R175H
118L8044A1	18	739737	739737	Nonsense_Mutation	SNP	G	A	A	YES1	c.1135C>T	p.Q379*
118L8044A1	19	11097056	11097056	Nonsense_Mutation	SNP	C	T	T	SMARCA4	c.547C>T	p.Q183*
118L8044A1	2	11337318	11337318	Missense_Mutation	SNP	C	A	A	ROCK2	c.3436G>T	p.D1146Y
118L8044A1	2	47606929	47606929	Missense_Mutation	SNP	C	T	T	EPCAM	c.679C>T	p.H227Y
118L8044A1	3	47061326	47061326	Missense_Mutation	SNP	G	A	A	SETD2	c.7355C>T	p.S2452L
118L8044A1	4	55565800	55565800	Missense_Mutation	SNP	C	G	G	KIT	c.624C>G	p.F208L
118L8044A1	5	176638948	176638948	Missense_Mutation	SNP	C	T	T	NSD1	c.3548C>T	p.S1183F
118L8044A1	7	20199233	20199233	Missense_Mutation	SNP	G	C	C	MACC1	c.751C>G	p.L251V
118L8044A1	7	127544837	127544837	Nonsense_Mutation	SNP	G	T	T	SND1	c.1492G>T	p.E498*
118L8044A1	8	93107578	93107578	Missense_Mutation	SNP	C	T	T	RUNX1T1	c.118G>A	p.E40K
118L8044A1	9	27228199	27228199	Splice_Site	SNP	C	T	T	TEK	c.3201-5C>T	-
118L8044A1	X	15552336	15552336	Missense_Mutation	SNP	G	A	A	BMX	c.1021G>A	p.D341N
118L8044A1	X	70339981	70339981	Missense_Mutation	SNP	G	A	A	MED12	c.514G>A	p.E172K
118L8044A1	X	70643021	70643021	Missense_Mutation	SNP	G	T	T	TAF1	c.4567G>T	p.D1523Y
118L8044A1	1	16258127	16258127	Nonsense_Mutation	SNP	C	T	T	SPEN	c.5392C>T	p.Q1798*
118L8044A1	-	-	-	In_Frame_Del	INS	-	-	-	SPEN	c.5997_6004del	p.G2000*
118L8044A1	1	204506578	204506578	Missense_Mutation	SNP	C	G	G	MDM4	c.364C>G	p.L122V
118L8044A1	1	206648248	206648248	Missense_Mutation	SNP	C	G	G	IKBKE	c.269C>G	p.S90C
118L8044A1	10	114925435	114925435	Missense_Mutation	SNP	C	G	G	TCF7L2	c.1495C>G	p.R499G
118L8044A1	11	22646489	22646489	Nonsense_Mutation	SNP	G	A	A	FANCF	c.868C>T	p.Q290*
118L8044A1	-	-	-	Frame_Shift_Del	INS	-	-	-	MS4A1	c.478_487del	p.P107fTs*34
118L8044A1	11	92564779	92564779	Splice_Site	SNP	C	T	T	FAT3	c.9482-9C>T	-
118L8044A1	12	46254583	46254583	Splice_Site	SNP	G	C	C	ARID2	c.4774-1G>C	-
118L8044A1	12	133244079	133244079	Splice_Site	SNP	C	T	T	POLE	c.2319+10G>A	-
118L8044A1	13	25072298	25072298	Missense_Mutation	SNP	G	T	T	PARP4	c.547C>A	p.P183T
118L8044A1	13	48934254	48934254	Missense_Mutation	SNP	G	C	C	RB1	c.709G>C	p.E237Q
118L8044A1	14	81574987	81574987	Missense_Mutation	SNP	G	A	A	TSHR	c.724G>A	p.E242K
118L8044A1	15	75092849	75092849	Splice_Site	SNP	G	C	C	CSK	c.556+3G>C	-
118L8044A1	15	88690645	88690645	Splice_Site	SNP	G	C	C	NTRK3	c.396-11C>G	-
118L8044A1	15	99465606	99465606	Missense_Mutation	SNP	G	A	A	IGF1R	c.2431G>A	p.E811K
118L8044A1	18	739737	739737	Nonsense_Mutation	SNP	G	A	A	YES1	c.1135C>T	p.Q379*
118L8044A1	19	11097056	11097056	Nonsense_Mutation	SNP	C	T	T	SMARCA4	c.547C>T	p.Q183*
118L8044A1	2	11337318	11337318	Missense_Mutation	SNP	C	A	A	ROCK2	c.3436G>T	p.D1146Y
118L8044A1	3	47061326	47061326	Missense_Mutation	SNP	G	A	A	SETD2	c.7355C>T	p.S2452L
118L8044A1	3	178936091	178936091	Missense_Mutation	SNP	G	A	A	PIK3CA	c.1633G>A	p.E545K
118L8044A1	4	55565800	55565800	Missense_Mutation	SNP	C	G	G	KIT	c.624C>G	p.F208L
118L8044A1	4	153268144	153268144	Nonsense_Mutation	SNP	G	A	A	FBXW7	c.664C>T	p.R222*
118L8044A1	5	176638948	176638948	Missense_Mutation	SNP	C	T	T	NSD1	c.3548C>T	p.S1183F
118L8044A1	7	20199233	20199233	Missense_Mutation	SNP	G	C	C	MACC1	c.751C>G	p.L251V
118L8044A1	7	127544837	127544837	Nonsense_Mutation	SNP	G	T	T	SND1	c.1492G>T	p.E498*
118L8044A1	9	5126756	5126756	Nonsense_Mutation	SNP	C	T	T	JAK2	c.3364C>T	p.R1122*
118L8044A1	X	15552336	15552336	Missense_Mutation	SNP	G	A	A	BMX	c.1021G>A	p.D341N
118L8044A1	X	63410021	63410021	Missense_Mutation	SNP	C	T	T	AMER1	c.3146G>A	p.R1049Q
118L8044A1	X	70339981	70339981	Missense_Mutation	SNP	G	A	A	MED12	c.514G>A	p.E172K
118L8044A1	X	70346933	70346933	Missense_Mutation	SNP	C	T	T	MED12	c.2800C>T	p.H934Y
118L8044A1	X	70643021	70643021	Missense_Mutation	SNP	G	T	T	TAF1	c.4567G>T	p.D1523Y
118L8083A1	-	-	-	Frame_Shift_Del	INS	-	-	-	KMT2D	C.5921del	P.T1974Rfs*73
118L8083A1	17	7577117	7577117	Missense_Mutation	SNP	A	C	C	TP53	c.821T>G	p.V274G
118L8083A1	3	119585439	119585439	Missense_Mutation	SNP	G	A	A	GSK3B	c.946C>T	p.R316W
118L8083A1	X	39914756	39914756	Missense_Mutation	SNP	C	T	T	BCOR	c.4504G>A	p.D1502N
118L8213A1	-	-	-	Frame_Shift_Del	INS	-	-	-	ARID1A	c.291_301del	p.P98Efs*9
118L8213A1	12	25398285	25398285	Missense_Mutation	SNP	C	A	A	KRAS	c.34G>T	p.G12C
118L8213A1	-	-	-	Frame_Shift_Ins	INS	-	-	-	LRP1	c.9496_9497ins	p.D3166Vfs*36
118L8213A1	13	32910944	32910944	Missense_Mutation	SNP	A	T	T	BRCA2	c.2452A>T	p.N818Y
118L8213A1	16	341199	341199	Missense_Mutation	SNP	G	C	C	AXIN1	c.2285C>G	p.S762C
118L8213A1	17	7578413	7578413	Missense_Mutation	SNP	C	T	T	TP53	c.517G>A	p.V173M
118L8213A1	-	-	-	Frame_Shift_Ins	INS	-	-	-	RNF43	c.190dup	p.T64Nfs*11
118L8213A1	19	42796456	42796456	Missense_Mutation	SNP	A	T	T	CIC	c.3013A>T	p.T1005S
118L8213A1	5	1282656	1282656	Missense_Mutation	SNP	C	T	T	TERT	c.1657G>A	p.V553I
118L8213A1	5	38963091	38963091	Nonsense_Mutation	SNP	G	A	A	RICTOR	c.1453C>T	p.R485*
118L8213A1	6	32190870	32190870	Splice_Site	SNP	G	T	T	NOTCH4	c.74-7C>A	-
118L8213A1	X	47045475	47045475	Nonsense_Mutation	SNP	C	G	G	RBM10	c.2442C>G	p.Y814*
118L8367M1	-	-	-	Frame_Shift_Del	INS	-	-	-	ARID1A	2G>A;c.5944_5945del	1981Y/V;1982Kfs*9]
118L8367M1	16	2126493	2126493	Missense_Mutation	SNP	G	T	T	TSC2	c.2744G>T	p.G915V
118L8367M1	-	-	-	In_Frame_Ins	INS	-	-	-	TP53	c.681dup	p.D228*
118L8367M1	17	11998897	11998897	Missense_Mutation	SNP	T	G	G	MAP2K4	c.399T>G	p.I133M
118L8367M1	19	1220698	1220698	Missense_Mutation	SNP	G	C	C	STK11	c.716G>C	p.W239S
118L8367M1	2	109368371	109368371	Missense_Mutation	SNP	T	A	A	RANBP2	c.1676T>A	p.I559K
118L8367M1	2	191898347	191898347	Missense_Mutation	SNP	A	C	C	STAT4	c.1721T>G	p.V574G
118L8367M1	3	41266097	41266097	Missense_Mutation	SNP	G	T	T	CTNBN1	c.94G>T	p.D32Y
118L8367M1	3	52437790	52437790	Missense_Mutation	SNP	C	G	G	BAP1	c.1371G>C	p.K457N
118L8367M1	3	130992335	130992335	Missense_Mutation	SNP	C	G	G	NEK11	c.1635C>G	p.I545M
118L8367M1	7	42005889	42005889	Missense_Mutation	SNP	G	A	A	GLI3	c.2782C>T	p.R928C
118L8367M1	-	-	-	In_Frame_Del	INS	-	-	-	CFTR	4230_4236del	Q1411_Q1412del
118L8367M1	9	135786877	135786877	Missense_Mutation	SNP	C	A	A	TSC1	c.992G>T	p.S331I
118L8370M1	15	49716538	49716538	Missense_Mutation	SNP	A	G	G	FGF7	c.44A>G	p.Y15C
118L8370M1	17	56437605	56437605	Missense_Mutation	SNP	C	T	T	RNF43	c.857G>A	p.D286Q
118L8370M1	17	59878736	59878736	Missense_Mutation	SNP	G	A	A	BRIP1	c.1018C>T	p.L340F
118L8370M1	19	11152182	11152182	Missense_Mutation	SNP	A	G	G	SMARCA4	c.4466A>G	p.N1489S
118L8370M1	19	41759543	41759543	Missense_Mutation	SNP	A	G	G	AXL	c.1939A>G	p.I647V
118L8370M1	4	55136826	55136826	Missense_Mutation	SNP	G	A	A	PDGFRA	c.1148G>A	p.R383H
118L8370M1	4	66197706	66197706	Missense_Mutation	SNP	G	T	T	EPHA5	c.2993C>A	p.A998D
118L8370M1	5	121736798	121736798	Missense_Mutation	SNP	G	T	T	SNCAIP	c.175G>T	p.A595S
118L8370M1	6	117677785	117677785	Splice_Site	SNP	A	T	T	ROS1	c.4141+7T>A	-
118L8370M1	8	71036972	71036972	Missense_Mutation	SNP	C	T	T	NCOA2	c.4045G>A	p.A1349T
118L8457A1	14	105239924	105239924	Splice_Site	SNP	G	A	A	AKT1	c.703-7C>T	-
118L8457A1	17	7577120	7577120	Missense_Mutation	SNP	C	A	A	TP53	c.818G>T	p.R273L
118L8457A1	17	47677762	47677762	Missense_Mutation	SNP	C	T	T	SPOP	c.1103G>A	p.R368H
118L8457A1	2	29519851	29519851	Missense_Mutation	SNP	C	T	T	ALK	c.1720G>A	p.G574R
118L8457A1	2	141130655	141130655	Nonsense_Mutation	SNP	G	A	A	LRP1B	c.10690C>T	p.Q3564*

118L8457A1	2	141609252	141609252	Missense_Mutation	SNP	C	A	A	LRP1B	c.4680G>T	p.M1560I
118L8457A1	2	212289029	212289029	Splice_Site	SNP	A	G	G	ERBB4	c.2720-3T>C	-
118L8457A1	5	176619009	176619009	Nonsense_Mutation	SNP	C	G	G	NSD1	c.1052C>G	p.S351*
118L8457A1	7	141408647	141408647	Missense_Mutation	SNP	T	C	C	WEE2	c.89T>C	p.V30A
118L8475A1	-	-	-	Frame_Shift_Del	INS	-	-	-	ARID1A	c.3530del	p.P117Qfs*3
118L8475A1	10	123325014	123325014	Missense_Mutation	SNP	T	C	C	FGFR2	c.314A>G	p.Y105C
118L8475A1	16	396149	396149	Missense_Mutation	SNP	T	G	G	AXIN1	c.877A>C	p.R293R
118L8475A1	17	29562641	29562641	Nonsense_Mutation	SNP	C	T	T	NF1	c.3721C>T	p.R1241*
118L8475A1	3	52620644	52620644	Missense_Mutation	SNP	G	C	C	PBRM1	c.3109C>G	p.R1037G
118L8475A1	-	-	-	Frame_Shift_Del	INS	-	-	-	IRF2	c.175del	p.A590fs*11
118L8475A1	9	139396719	139396719	Splice_Site	SNP	C	T	T	NOTCH1	c.5384+5G>A	-
118L8475A1	9	139413166	139413166	Missense_Mutation	SNP	C	T	T	NOTCH1	c.976G>A	p.G326S
118L8475A1	X	70344083	70344083	Missense_Mutation	SNP	G	A	A	MED12	c.1819G>A	p.D607N
118L8606A1	-	-	-	Frame_Shift_Del	INS	-	-	-	ARID1A	c.867del	p.T290Pfs*73
118L8606A1	17	7577094	7577094	Missense_Mutation	SNP	G	A	A	TP53	c.844C>T	p.R282W
118L8606A1	17	29553452	29553452	Splice_Site	SNP	G	T	T	NF1	c.2002-1G>T	-
118L8606A1	17	37619371	37619371	Splice_Site	SNP	G	A	A	CDK12	c.1046+1G>A	-
118L8606A1	-	-	-	Frame_Shift_Del	INS	-	-	-	RAD51C	c.896del	p.P299Lfs*3
118L8606A1	19	33792773	33792773	Missense_Mutation	SNP	G	C	C	CEBPA	c.548C>G	p.P183R
118L8606A1	2	25467120	25467120	Missense_Mutation	SNP	C	A	A	DNMT3A	c.1755G>T	p.M585I
118L8606A1	2	142004825	142004825	Missense_Mutation	SNP	G	C	C	LRP1B	c.562C>G	p.P188A
118L8606A1	2	191929601	191929601	Missense_Mutation	SNP	C	A	A	STAT4	c.714G>T	p.W238C
118L8606A1	20	39751925	39751925	Missense_Mutation	SNP	C	G	G	TOP1	c.2286C>G	p.D762E
118L8606A1	20	52194888	52194888	Missense_Mutation	SNP	G	T	T	ZNF217	c.1468C>A	p.L490I
118L8606A1	3	47162860	47162860	Missense_Mutation	SNP	C	T	T	SETD2	c.3266G>A	p.R1089Q
118L8606A1	3	70014398	70014398	Nonsense_Mutation	SNP	A	C	C	MITF	c.1259A>C	p.*420S
118L8606A1	3	169988318	169988318	Missense_Mutation	SNP	C	G	G	PRKCI	c.560C>G	p.T187R
118L8606A1	4	55980368	55980368	Missense_Mutation	SNP	C	A	A	KDR	c.723G>T	p.K241N
118L8606A1	5	112164551	112164551	Splice_Site	SNP	A	C	C	APC	c.1627-2A>C	-
118L8606A1	6	43749782	43749782	Missense_Mutation	SNP	G	T	T	VEGFA	c.1175G>T	p.R392L
118L8606A1	7	55249180	55249180	Splice_Site	SNP	G	T	T	EGFR	c.2469+9G>T	-
118L8606A1	8	48711936	48711936	Nonsense_Mutation	SNP	-	-	-	PRKDC	c.10131C>A	p.Y3377*
118L8606A1	9	139405215	139405215	Missense_Mutation	SNP	G	A	A	NOTCH1	c.2630C>T	p.R877L
118L8638M2	-	-	-	Splice_Site	SNP	-	-	-	FUBP1	120+1_120+5d	-
118L8638M2	11	118362545	118362545	Nonsense_Mutation	SNP	C	T	T	KMT2A	c.4906C>T	p.R1636*
118L8638M2	-	-	-	Frame_Shift_Ins	INS	-	-	-	GATA6	C.581_582dup	P.G195Wfs*100
118L8638M2	3	178947852	178947852	Missense_Mutation	SNP	C	A	A	PIK3CA	c.2727C>A	p.F909L
118L8638M2	9	135786956	135786956	Splice_Site	SNP	C	T	T	TSC1	c.914-1G>A	-
118L8638M2	9	139399486	139399486	Missense_Mutation	SNP	C	T	T	NOTCH1	c.4657G>A	p.E1553K
118L8642M1	-	-	-	Frame_Shift_Ins	INS	-	-	-	ARID1A	c.3154dup	p.Y1052Lfs*53
118L8642M1	-	-	-	In_Frame_Del	INS	-	-	-	PBX3	C.1821del	P.V607*
118L8642M1	-	-	-	Frame_Shift_Del	INS	-	-	-	IGF1R	c.1314_1323del	p.N438Kfs*25
118L8642M1	-	-	-	Frame_Shift_Del	INS	-	-	-	TP53	c.340_343del	p.L114Ifs*8
118L8642M1	2	11355098	11355098	Missense_Mutation	SNP	G	C	C	ROCK2	c.1804C>G	p.L602V
118L8642M1	2	141081457	141081457	Splice_Site	SNP	C	A	A	LRP1B	c.12514+5G>T	-
118L8642M1	-	-	-	Frame_Shift_Del	INS	-	-	-	APC	c.7929_7932del	p.Y2645Kfs*14
118L8642M1	5	147209156	147209156	Splice_Site	SNP	C	G	G	SPINK1	c.87+6G>C	-
118L8642M1	6	35423622	35423622	Missense_Mutation	SNP	C	G	G	FANCE	c.347C>G	p.S116C
118L8642M1	7	42116457	42116457	Splice_Site	SNP	C	T	T	GLI3	c.368-1G>A	-
118L8875M1	-	-	-	Frame_Shift_Del	INS	-	-	-	ARID1A	c.6711del	p.L2238Cfs*29
118L8875M1	11	532682	532682	Missense_Mutation	SNP	T	G	G	HRAS	c.524A>C	p.D175A
118L8875M1	-	-	-	Frame_Shift_Del	INS	-	-	-	FOXP1	c.1668del	p.N558Tfs*41
118L8884A1	12	25398284	25398284	Missense_Mutation	SNP	C	T	T	KRAS	c.35G>A	p.G12D
118L8884A1	14	45653093	45653093	Missense_Mutation	SNP	G	T	T	FANCM	c.4503G>T	p.Q1501H
118L8884A1	17	7576852	7576852	Splice_Site	SNP	C	T	T	TP53	c.993+1G>A	-
118L8884A1	3	37070324	37070324	Nonsense_Mutation	SNP	C	T	T	MLH1	c.1459C>T	p.R487*
118L8884A1	-	-	-	Frame_Shift_Ins	INS	-	-	-	PBRM1	c.310dup	p.E104Gfs*4
118L8884A1	7	117235045	117235045	Missense_Mutation	SNP	G	A	A	CFTR	c.2552G>A	p.R851Q
118L8913A1	1	27087868	27087868	Splice_Site	SNP	G	A	A	ARID1A	c.2162-7G>A	-
118L8913A1	1	243809206	243809206	Missense_Mutation	SNP	G	T	T	AKT3	c.418C>A	p.H140N
118L8913A1	11	92087187	92087187	Missense_Mutation	SNP	A	G	G	FAT3	c.1909A>G	p.K637E
118L8913A1	12	25398284	25398284	Missense_Mutation	SNP	C	A	A	KRAS	c.35G>T	p.G12V
118L8913A1	13	102521110	102521110	Missense_Mutation	SNP	T	G	G	FGF14	c.388A>C	p.I130L
118L8913A1	18	48604750	48604750	Missense_Mutation	SNP	G	T	T	SMAD4	c.1572G>T	p.W524C
118L8913A1	19	45532237	45532237	Splice_Site	SNP	-	-	-	RELB	c.986-12G>A	-
118L8913A1	3	187449633	187449633	Missense_Mutation	SNP	A	G	G	BCL6	c.247T>C	p.F83L
118L8913A1	-	-	-	In_Frame_Ins	INS	-	-	-	ARID1B	c.369_392dup	Q124_Q131dup
118L8913A1	7	116415025	116415025	Missense_Mutation	SNP	C	G	G	MET	c.3119C>G	p.S1040Q
118L8913A1	X	70348534	70348534	Missense_Mutation	SNP	T	C	C	MED12	3441T>C;3443C	p.R1148P
118L8983A1	1	27058093	27058093	Nonsense_Mutation	SNP	C	T	T	ARID1A	c.1801C>T	p.Q601*
118L8983A1	1	27100919	27100919	Nonsense_Mutation	SNP	C	T	T	ARID1A	c.4201C>T	p.Q1401*
118L8983A1	12	6687306	6687306	Splice_Site	SNP	G	C	C	CHD4	c.5120-3C>G	-
118L8983A1	12	112888210	112888210	Missense_Mutation	SNP	G	A	A	PTPN11	c.226G>A	p.E76K
118L8983A1	16	68855957	68855957	Missense_Mutation	SNP	A	T	T	CDH1	c.1765A>T	p.N589Y
118L8983A1	16	81990330	81990330	Missense_Mutation	SNP	C	A	A	PLCG2	c.3601C>A	p.R1201S
118L8983A1	-	-	-	Missense_Mutation	SNP	-	-	-	TP53	c.526_528del	p.C176del
118L8983A1	17	37868208	37868208	Missense_Mutation	SNP	C	T	T	ERBB2	c.929C>G	p.S310F
118L8983A1	18	48575132	48575132	Missense_Mutation	SNP	T	G	G	SMAD4	c.326T>G	p.L109R
118L8983A1	18	48603041	48603041	Nonsense_Mutation	SNP	C	T	T	SMAD4	c.1342C>T	p.Q448*
118L8983A1	21	44524456	44524456	Missense_Mutation	SNP	G	A	A	U2AF1	c.101C>T	p.S34F
118L8983A1	5	149459731	149459731	Missense_Mutation	SNP	C	G	G	CSF1R	c.476G>C	p.W159S
118L8983A1	7	13935508	13935508	Missense_Mutation	SNP	C	T	T	ETV1	c.1417G>A	p.E473K
118L8983A1	-	-	-	Frame_Shift_Del	INS	-	-	-	CD36	c.483del	p.I162Lfs*14
118L8983A1	7	152009018	152009018	Nonsense_Mutation	SNP	G	A	A	KMT2C	c.604C>T	p.Q202*
118L8989A1	14	68963831	68963831	Splice_Site	SNP	C	T	T	RAD51B	c.1037-10C>T	-
118L8989A1	17	7577121	7577121	Missense_Mutation	SNP	G	A	A	TP53	c.817C>T	p.R273C
118L8989A1	2	170131604	170131604	Nonsense_Mutation	SNP	G	T	T	LRP2	c.1917C>A	p.Y639*
118L8989A1	3	52441192	52441192	Missense_Mutation	SNP	T	C	C	BAP1	c.578A>G	p.H193R
118L8989A1	4	153245515	153245515	Missense_Mutation	SNP	A	G	G	FBXW7	c.1676T>C	p.L559P
118L9109A2	12	25398284	25398284	Missense_Mutation	SNP	C	T	T	KRAS	c.35G>A	p.G12D
118L9109A2	14	69077785	69077785	Missense_Mutation	SNP	C	A	A	RAD51B	c.1099C>A	p.P367T
118L9109A2	-	-	-	Frame_Shift_Del	INS	-	-	-	TP53	194_197delinsA	p.R65Nfs*58
118L9109A2	-	-	-	In_Frame_Del	INS	-	-	-	FOXL2	c.672_696delinsb	A.227_A234del
118L9110M1	17	7578461	7578461	Missense_Mutation	SNP	C	A	A	TP53	c.469G>T	p.V157F
118L9110M1	17	15995258	15995258	Nonsense_Mutation	SNP	T	A	A	NCOR1	c.2935A>T	p.R979*
118L9110M1	7	18687547	18687547	Missense_Mutation	SNP	A	G	G	HDAC9	c.1166A>G	p.N389S
119A1499J1	1	158582758	158582758	Splice_Site	SNP	G	A	A	SPTA1	c.6990-7C>T	-
119A1499J1	-	-	-	Frame_Shift_Ins	INS	-	-	-	PTEN	C.1028dup	P.K344Efs*17

119A1499J1	12	49445723	49445723	Missense_Mutation	SNP	C	A	A	KMT2D	c.1743G>T	p.M581I
119A1499J1	7	128846109	128846109	Missense_Mutation	SNP	G	C	C	SMO	c.1039G>C	p.G347R
119A1568M1	12	25398284	25398284	Missense_Mutation	SNP	C	T	T	KRAS	c.35G>A	p.G12D
119A1568M1	17	7578268	7578268	Missense_Mutation	SNP	A	C	C	TP53	c.581T>G	p.L194R
119A1568M1		-	-	Frame_Shift_Ins	INS	-	-	-	NF1	c.2596_2599dup	p.M867Tfs*7
119A1568M1	2	25463181	25463181	Missense_Mutation	SNP	C	T	T	DNMT3A	c.2312G>A	p.R771Q
119A1568M1	2	170012811	170012811	Missense_Mutation	SNP	G	A	A	LRP2	c.12124C>T	p.R4042C
119A1568M1	20	36028607	36028607	Missense_Mutation	SNP	A	T	T	SRC	c.949A>T	p.M317L
119A1621M1		-	-	Frame_Shift_Del	INS	-	-	-	EPHA2	c.1825del	p.H6091fs*10
119A1621M1		-	-	Frame_Shift_Ins	INS	-	-	-	ARID1A	c.2343dup	p.H782Tfs*35
119A1621M1	2	141709477	141709477	Missense_Mutation	SNP	C	T	T	LRP1B	c.2920G>A	p.V974I
119A1621M1	22	23596126	23596126	Missense_Mutation	SNP	C	T	T	BCR	c.1420C>T	p.R474W
119A1621M1	4	126370060	126370060	Missense_Mutation	SNP	A	G	G	FAT4	c.7889A>G	p.E2630G
119A1621M1		-	-	Frame_Shift_Ins	INS	-	-	-	KDM6A	c.1918_1919dup	p.Q641fs*51
119A1621M1	X	70614053	70614053	Missense_Mutation	SNP	C	T	T	TAF1	c.3424C>T	p.R1142W
119A1715M1	10	89717720	89717720	Missense_Mutation	SNP	G	A	A	PTEN	c.745G>A	p.V249M
119A1715M1		-	-	Frame_Shift_Del	INS	-	-	-	ATM	c.8283_8284del	p.Q2762Afs*6
119A1715M1	12	25398284	25398284	Missense_Mutation	SNP	C	T	T	KRAS	c.35G>A	p.G12D
119A1715M1	17	74732555	74732555	Splice_Site	SNP	G	A	A	SRSF2	c.363-9C>T	-
119A1715M1	19	1220721	1220721	Splice_Site	SNP	G	A	A	STK11	c.734+5G>A	-
119A1715M1	4	66361184	66361184	Missense_Mutation	SNP	C	T	T	EPHA5	c.988G>A	p.E330K
119A1715M1	4	187549788	187549788	Nonsense_Mutation	SNP	C	A	A	FAT1	c.4453G>T	p.E1485*
119A1715M1		-	-	Frame_Shift_Del	INS	-	-	-	RBM10	c.2467_2504del	p.E823Rfs*12
119A1725M1	12	25398281	25398281	Missense_Mutation	SNP	C	T	T	KRAS	c.38G>A	p.G13D
119A1725M1	12	56487277	56487277	Missense_Mutation	SNP	C	T	T	ERBB3	c.1423C>T	p.R475W
119A1725M1	17	7577565	7577565	Missense_Mutation	SNP	T	C	C	TP53	c.716A>G	p.N239S
119A1725M1	2	170112747	170112747	Splice_Site	SNP	C	A	A	LRP2	c.2640-1G>T	-
119A1725M1		-	-	Frame_Shift_Del	INS	-	-	-	CDKN2A	c.52_83del	p.T18Afs*15
119A1933A1	1	11316237	11316237	Missense_Mutation	SNP	G	A	A	MTOR	c.517C>T	p.R173C
119A1933A1	1	27099988	27099988	Splice_Site	SNP	G	A	A	ARID1A	c.3866+1G>A	-
119A1933A1	10	89692905	89692905	Missense_Mutation	SNP	G	A	A	PTEN	c.389G>A	p.R130Q
119A1933A1	12	49438646	49438646	Missense_Mutation	SNP	C	T	T	KMT2D	c.4844G>A	p.R1615Q
119A1933A1	19	11097280	11097280	Splice_Site	SNP	C	A	A	SMARCA4	c.760+11C>A	-
119A1933A1	2	61121627	61121627	Missense_Mutation	SNP	C	G	G	REL	c.249C>G	p.D83E
119A1933A1	3	41266097	41266097	Missense_Mutation	SNP	G	T	T	CTNNB1	c.94G>T	p.D32Y
119A1933A1	3	89259511	89259511	Missense_Mutation	SNP	G	T	T	EPHA3	c.655G>T	p.D219Y
119A1933A1	3	178936091	178936091	Missense_Mutation	SNP	G	A	A	PIK3CA	c.1633G>A	p.E545K
119A1933A1	3	195594719	195594719	Missense_Mutation	SNP	G	A	A	TNK2	c.2405C>T	p.R802L
119A1933A1	4	66535454	66535454	Missense_Mutation	SNP	C	T	T	EPHA5	c.7G>A	p.G3S
119A1933A1		-	-	In_Frame_Ins	INS	-	-	-	ARID1B	c.363_380dup	Q126_Q131dup
119A1933A1	9	139401157	139401157	Splice_Site	SNP	G	A	A	NOTCH1	c.3901+11C>T	-
119A1949A1	12	25398284	25398284	Missense_Mutation	SNP	C	A	A	KRAS	c.35G>T	p.G12V
119A1949A1	18	48584708	48584708	Splice_Site	SNP	A	G	G	SMAD4	c.788-2A>G	-
119A1949A1	22	24129456	24129456	Splice_Site	SNP	C	T	T	SMARCB1	c.93+7C>T	-
119A1949A1	7	13946149	13946149	Missense_Mutation	SNP	T	C	C	ETV1	c.1016A>G	p.Q339R
119A9209D1	12	121434449	121434449	Missense_Mutation	SNP	A	G	G	HNFA1	c.1213A>G	p.M405V
119A9209D1	17	7578263	7578263	Nonsense_Mutation	SNP	G	A	A	TP53	c.586C>T	p.R196*
119A9336A1	17	7577105	7577105	Missense_Mutation	SNP	G	C	C	TP53	c.833C>G	p.P278R
119A9336A1	2	121746593	121746593	Missense_Mutation	SNP	G	A	A	GLI2	c.3103G>A	p.V1035M
119A9336A1	21	44524456	44524456	Missense_Mutation	SNP	G	A	A	UZAF1	c.101C>T	p.S34F
119A9336A1	3	130871239	130871239	Missense_Mutation	SNP	G	A	A	NEK11	c.655G>A	p.A219T
119A9336A1	6	43746274	43746274	Splice_Site	SNP	G	T	T	VEGFA	c.932+1G>T	-
119A9340A1	1	206665040	206665040	Missense_Mutation	SNP	A	G	G	IKBKE	c.1793A>G	p.Q598R
119A9340A1		-	-	Frame_Shift_Del	INS	-	-	-	BAP1	c.2034del	p.F6781fs*14
119A9694A1	11	22646462	22646462	Missense_Mutation	SNP	A	G	G	FANCF	c.895T>C	p.S299P
119A9694A1	12	4488639	4488639	Missense_Mutation	SNP	C	G	G	FGF23	c.110G>C	p.G37A
119A9694A1		-	-	Frame_Shift_Ins	INS	-	-	-	DICER1	c.536_539dup	p.I181Cfs*15
119A9694A1	17	7578524	7578524	Nonsense_Mutation	SNP	G	A	A	TP53	c.406C>T	p.Q136*
119A9694A1	2	121742123	121742123	Missense_Mutation	SNP	C	T	T	GLI2	c.1760C>T	p.T587M
119A9694A1		-	-	Frame_Shift_Ins	INS	-	-	-	IRF2	c.102dup	p.Q35fs*9
119A9698A1	1	16462185	16462185	Nonsense_Mutation	SNP	G	A	A	EPHA2	c.1393C>T	p.R465*
119A9698A1		-	-	In_Frame_Del	INS	-	-	-	ARID1A	c.2667del	p.M890*
119A9698A1	1	27105581	27105581	Nonsense_Mutation	SNP	T	G	G	ARID1A	c.5192T>G	p.L1731*
119A9698A1	1	27105679	27105679	Nonsense_Mutation	SNP	G	T	T	ARID1A	c.5290G>C	p.E1764*
119A9698A1	11	92531644	92531644	Missense_Mutation	SNP	A	T	T	FAT3	c.5465A>T	p.K1822M
119A9698A1	11	108196806	108196806	Nonsense_Mutation	SNP	C	T	T	ATM	c.6829C>T	p.Q2277*
119A9698A1	11	108218086	108218086	Missense_Mutation	SNP	G	A	A	ATM	c.8665G>A	p.D2889N
119A9698A1	12	51213429	51213429	Missense_Mutation	SNP	G	C	C	ATF1	c.683G>C	p.R228P
119A9698A1	13	28623777	28623777	Missense_Mutation	SNP	C	G	G	FLT3	c.877G>C	p.E293Q
119A9698A1	15	66774131	66774131	Missense_Mutation	SNP	G	A	A	MAP2K1	c.607G>A	p.E203K
119A9698A1	17	7577141	7577141	Missense_Mutation	SNP	C	T	T	TP53	c.797G>A	p.G266E
119A9698A1	17	56436149	56436149	Nonsense_Mutation	SNP	G	A	A	RNF43	c.988C>T	p.R330*
119A9698A1	18	48581229	48581229	Nonsense_Mutation	SNP	C	G	G	SMAD4	c.533C>G	p.S178*
119A9698A1	19	11132522	11132522	Missense_Mutation	SNP	C	T	T	SMARCA4	c.2738C>T	p.P913L
119A9698A1	20	57415513	57415513	Missense_Mutation	SNP	G	A	A	GNAS	c.352G>A	p.E118K
119A9698A1	21	42870101	42870101	Missense_Mutation	SNP	G	T	T	TMPRSS2	c.71C>A	p.S24Y
119A9698A1	3	178936082	178936082	Missense_Mutation	SNP	G	A	A	PIK3CA	c.1624G>A	p.E542K
119A9698A1	4	55564449	55564449	Splice_Site	SNP	G	C	C	KIT	c.338-1G>C	-
119A9698A1	7	116412040	116412040	Missense_Mutation	SNP	G	A	A	MET	c.3025G>A	p.E1009K
119A9698A1	7	140453155	140453155	Missense_Mutation	SNP	C	T	T	BRAF	c.1780G>A	p.D594N
119A9698A1	8	69000039	69000039	Missense_Mutation	SNP	G	A	A	PREX2	c.2108G>A	p.G703E
119A9698A1	8	139164406	139164406	Missense_Mutation	SNP	A	G	G	FAM135B	c.2312T>C	p.V771A
119A9698A1		-	-	Frame_Shift_Del	INS	-	-	-	CDKN2A	c.324_346del	p.A109Mfs*16
119A9698A1	X	47044700	47044700	Splice_Site	SNP	G	A	A	RBM10	c.2101-1G>A	-
119A9698A1	X	66765547	66765547	Nonsense_Mutation	SNP	G	T	T	AR	c.559G>C	p.E187*
119A9702A1	12	25398284	25398284	Missense_Mutation	SNP	C	T	T	KRAS	c.35G>A	p.G12D
119A9702A1		-	-	Frame_Shift_Ins	INS	-	-	-	STK11	c.516dup	p.V173Cfs*93
119A9702A1	19	11107018	11107018	Nonsense_Mutation	SNP	C	T	T	SMARCA4	c.1723C>T	p.Q575*
119A9702A1	7	18688280	18688280	Missense_Mutation	SNP	T	C	C	HDAC9	c.1432T>C	p.Y478H
119A9806A1		-	-	Splice_Site	SNP	-	-	-	HTATIP2	c.82_101+25de	-
119A9806A1		-	-	Frame_Shift_Ins	INS	-	-	-	ARID2	c.341dup	p.P115Tfs*39
119A9806A1	17	38560458	38560458	Missense_Mutation	SNP	C	A	A	TOP2A	c.2229G>T	p.T743N
119A9806A1		-	-	Frame_Shift_Ins	INS	-	-	-	PBRM1	c.757_758dup	p.D253Efs*31
119A9806A1		-	-	Splice_Site	SNP	-	-	-	CD36	c.701+5_701+8del	-
119A9806A1		-	-	Frame_Shift_Ins	INS	-	-	-	TGFBFR1	c.1284_1285ins	p.Y429Lfs*2
119A9806A1		-	-	Frame_Shift_Del	INS	-	-	-	TFE3	c.669_672del	p.S224Pfs*118
119A9889A1	10	123310911	123310911	Missense_Mutation	SNP	T	A	A	FGFR2	c.517A>T	p.N173Y
119A9889A1	17	5076250	5076250	Missense_Mutation	SNP	G	A	A	USP6	c.4198G>A	p.E1400K

119A9889A1	17	7578442	7578442	Missense_Mutation	SNP	T	G	G	TP53	c.488A>C	p.Y163S
119A9889A1	3	130992328	130992328	Missense_Mutation	SNP	A	G	G	NEK11	c.1628A>G	p.K543R
119A9889A1	7	117232434	117232434	Nonsense_Mutation	SNP	T	A	A	CFTR	c.2213T>A	p.L738*
119A9889A1	8	93026977	93026977	Missense_Mutation	SNP	C	T	T	RUNX1T1	c.187G>A	p.G63R
119A9889A1	X	123220554	123220554	Missense_Mutation	SNP	C	G	G	STAG2	c.3211C>G	p.R1071G
216L0152A1		-	-	Frame_Shift_Ins	INS	-	-	-	EPHA2	c.1141_1151dup	p.Y385Pfs*12
216L0152A1		-	-	Frame_Shift_Del	INS	-	-	-	TGFBF1	c.528_532del	p.L177Rfs*5
216L0152A1		-	-	Frame_Shift_Ins	INS	-	-	-	CDKN1B	c.356dup	p.G120Wfs*5
216L0152A1		-	-	Frame_Shift_Ins	INS	-	-	-	KEAP1	c.1637dup	p.V547Rfs*27
216L0152A1		-	-	Frame_Shift_Ins	INS	-	-	-	ARID1A	c.5888_5889dup	p.E1964Mfs*52
216L0152A1	11	118344506	118344506	Missense_Mutation	SNP	C	T	T	KMT2A	c.2632C>T	p.R878W
216L0276A1	17	7578554	7578554	Missense_Mutation	SNP	A	T	T	TP53	c.376T>A	p.Y126N
216L0276A1	9	98239918	98239918	Missense_Mutation	SNP	C	T	T	PTCH1	c.1414G>A	p.A472T
216L0276A1	6	93956606	93956606	Missense_Mutation	SNP	C	T	T	EPHA7	c.2630G>A	p.R877H
216L0276A1	4	126372666	126372666	Missense_Mutation	SNP	A	C	C	FAT4	c.10495A>C	p.T3499P
217A0361A1	2	29474097	29474097	Missense_Mutation	SNP	G	A	A	ALK	c.2078C>T	p.P693L
217A0361A1	2	209113113	209113113	Missense_Mutation	SNP	G	C	C	IDH1	c.394C>G	p.R132G
217A0361A1		-	-	Frame_Shift_Ins	INS	-	-	-	EPHA2	c.1723dupT	p.Y575Lfs*21
217A0361A1		-	-	In_Frame_Del	INS	-	-	-	PBRM1	c.2994delC	p.Y998*
217B0420A1	21	44514790	44514790	Missense_Mutation	SNP	C	T	T	U2AF1	c.457G>A	p.A153T
217B0420A1	12	25398284	25398284	Missense_Mutation	SNP	C	T	T	KRAS	c.35G>A	p.G12D
217B0420A1	6	117708169	117708169	Splice_Site	SNP	A	G	G	ROS1	c.2015-7T>C	-
217B0420A1	17	7577539	7577539	Missense_Mutation	SNP	G	A	A	TP53	c.742C>T	p.R248W
217B0420A1	11	69514229	69514229	Missense_Mutation	SNP	C	G	G	FGF19	c.452G>C	p.R151P
217B0420A1	12	57574940	57574940	Missense_Mutation	SNP	A	G	G	LRP1	c.5528A>G	p.D1843G
217B0528A1	16	2137891	2137891	Missense_Mutation	SNP	G	C	C	TSC2	c.5017G>C	p.V1673L
217B0528A1		-	-	Frame_Shift_Ins	INS	-	-	-	STK11	c.361_362insTT	p.E121Vfs*9
217B0528A1	2	209108226	209108226	Missense_Mutation	SNP	T	C	C	IDH1	c.623A>G	p.Y208C
217B0528A1	7	151877980	151877980	Missense_Mutation	SNP	A	G	G	KMT2C	c.6965T>C	p.V2322A
217B0528A1	17	15952304	15952304	Splice_Site	SNP	T	C	C	NCOR1	c.6393-2A>G	-
217B0528A1	13	25052393	25052393	Missense_Mutation	SNP	G	T	T	PARP4	c.1470C>A	p.H490Q
217C0588A1	1	162746131	162746131	Missense_Mutation	SNP	C	T	T	DDR2	c.2254C>T	p.R752C
217C0588A1	7	140453136	140453136	Missense_Mutation	SNP	A	T	T	BRAF	c.1799T>A	p.V600E
217C0588A1	2	209113112	209113112	Missense_Mutation	SNP	C	A	A	IDH1	c.395G>T	p.R132L
217C0745A1	19	52715982	52715982	Missense_Mutation	SNP	C	T	T	PPP2R1A	c.547C>T	p.R183W
217C0745A1	3	178916930	178916930	Missense_Mutation	SNP	G	T	T	PIK3CA	c.317G>T	p.G106V
217D0937A1		-	-	Frame_Shift_Ins	INS	-	-	-	ARID1A	c.2624dup	p.M875Ifs*61
217D0937A1	20	57430394	57430394	Splice_Site	SNP	G	A	A	GNAS	c.2068+6G>A	-
217E1258A1	8	38272358	38272358	Missense_Mutation	SNP	A	G	G	FGFR1	c.1916T>C	p.L639T
217E1258A1	19	17955175	17955175	Missense_Mutation	SNP	G	A	A	JAK3	c.52C>T	p.L18F
217E1258A1	17	7577534	7577534	Missense_Mutation	SNP	C	A	A	TP53	c.747G>T	p.R249S
217E1258A1	1	204415111	204415111	Missense_Mutation	SNP	T	A	A	PIK3C2B	c.2651A>T	p.Q884L
217E1258A1	13	48881516	48881516	Nonsense_Mutation	SNP	A	T	T	RB1	c.238A>T	p.K80*
217E1258A1	20	31022879	31022879	Missense_Mutation	SNP	A	T	T	ASXL1	c.2364A>T	p.E788D
217E1258A1	X	76937219	76937219	Nonsense_Mutation	SNP	T	A	A	ATRX	c.3529A>T	p.K1177*
217E1258A1	2	25463271	25463271	Missense_Mutation	SNP	G	A	A	DNMT3A	c.2222C>T	p.A741V
217E1258A1	14	45644490	45644490	Missense_Mutation	SNP	A	G	G	FANCM	c.2533A>G	p.I845V
217E1258A1	6	394881	394881	Missense_Mutation	SNP	T	A	A	IRF4	c.277T>A	p.W93R
217E1258A1	7	151970849	151970849	Missense_Mutation	SNP	T	A	A	KMT2C	c.953A>T	p.Q318L
217E1258A1	12	49439944	49439944	Missense_Mutation	SNP	C	A	A	KMT2D	c.4597G>T	p.G1533C
217E1258A1	2	47709916	47709916	Splice_Site	SNP	A	T	T	MSH2	c.2635-2A>T	-
217E1258A1	X	110388152	110388152	Splice_Site	SNP	T	A	A	PAK3	c.339+2T>A	-
217E1258A1	19	14204552	14204552	Missense_Mutation	SNP	A	G	G	PRKACA	c.818T>C	p.L273P
217E1258A1	8	92999196	92999196	Missense_Mutation	SNP	C	G	G	RUNX1T1	c.885G>C	p.L295F
217E1258A1	22	38373903	38373903	Missense_Mutation	SNP	A	T	T	SOX10	c.668T>A	p.M223K
217E1258A1	1	16262741	16262741	Missense_Mutation	SNP	C	T	T	SPEN	c.10006C>T	p.R3336W
217E1258A1	10	104268931	104268931	Missense_Mutation	SNP	G	T	T	SUFU	c.188G>T	p.G63V
217E1387A1	17	37883956	37883956	Missense_Mutation	SNP	C	A	A	ERBB2	c.3427C>A	p.P1143T
217F1558A1	16	2138141	2138141	Splice_Site	SNP	G	C	C	TSC2	c.5160+1G>C	-
217F1558A1	15	90631839	90631839	Missense_Mutation	SNP	T	A	A	IDH2	c.514A>T	p.R172W
217F1558A1	17	7577514	7577514	Missense_Mutation	SNP	G	T	T	TP53	c.767C>A	p.T256K
217F1558A1		-	-	Frame_Shift_Ins	INS	-	-	-	ARID1A	c.5548dup	p.D1850Gfs*4
217F1558A1	7	151927097	151927097	Missense_Mutation	SNP	A	C	C	KMT2C	c.2887T>G	p.C963G
217F1599A1	12	25398284	25398284	Missense_Mutation	SNP	C	T	T	KRAS	c.35G>A	p.G12D
217F1599A1	18	48591888	48591888	Missense_Mutation	SNP	G	T	T	SMAD4	c.1051G>T	p.D351Y
217F1625A1		-	-	Frame_Shift_Ins	INS	-	-	-	ARID1A	c.5423dup	p.F1809Vfs*2
217F1625A1	3	52436390	52436390	Nonsense_Mutation	SNP	G	A	A	BAP1	c.2104C>T	p.Q702*
217F1625A1		-	-	In_Frame_Ins	INS	-	-	-	CFTR	c.3492dup	p.K1165*
217F1625A1	7	18687615	18687615	Missense_Mutation	SNP	G	T	T	HDAC9	c.1234G>T	p.V412L
217F1660A1	17	7577548	7577548	Missense_Mutation	SNP	C	T	T	TP53	c.733G>A	p.G245S
217F1660A1	5	149499084	149499084	Missense_Mutation	SNP	T	C	C	PDGFRB	c.2744A>G	p.N915S
217F1660A1	5	138266629	138266629	Splice_Site	SNP	G	A	A	CTNNA1	c.2298+5G>A	-
217F1870A1	X	63411227	63411227	Missense_Mutation	SNP	T	C	C	AMER1	c.1940A>G	p.Q647R
217F1870A1	12	46243818	46243818	Splice_Site	SNP	G	A	A	ARID2	c.1913-1G>A	-
217F1870A1	8	139155364	139155364	Splice_Site	SNP	G	C	C	FAM135B	c.3541-12C>G	-
217F1870A1	9	35078227	35078227	Missense_Mutation	SNP	G	A	A	FANCG	c.421C>T	p.R141C
217F1870A1		-	-	In_Frame_Del	INS	-	-	-	FAT1	c.3386_3391del	V1129_E1130del
217F1870A1	8	69002843	69002843	Missense_Mutation	SNP	C	A	A	PREX2	c.2143C>A	p.P715T
217F1870A1	X	47045667	47045667	Nonsense_Mutation	SNP	C	T	T	RBM10	c.2548C>T	p.Q850*
217F1870A1	11	65429463	65429463	Missense_Mutation	SNP	C	A	A	RELA	c.131G>T	p.G44V
217G1915A1	11	76169271	76169271	Missense_Mutation	SNP	G	T	T	EMSY	c.290G>T	p.R97L
217G2113A1	7	140453136	140453136	Missense_Mutation	SNP	A	T	T	BRAF	c.1799T>A	p.V600E
217G2113A1	17	7577497	7577497	Splice_Site	SNP	A	T	T	TP53	c.782+2T>A	-
217G2113A1		-	-	Frame_Shift_Del	INS	-	-	-	SMAD4	c.1607del	p.L536Qfs*16
217H2225A1		-	-	Frame_Shift_Ins	INS	-	-	-	ATM	1_7922insAGAG	p.K2643Sfs*6
217H2225A1	4	55603449	55603449	Splice_Site	SNP	G	A	A	KIT	c.2802+3G>A	-
217H2225A1	8	32585527	32585527	Missense_Mutation	SNP	C	A	A	NRG1	c.1106C>A	p.T369N
217H2225A1		-	-	Frame_Shift_Ins	INS	-	-	-	ARID1A	c.3732dup	p.F1245Lfs*14
217H2254A1	12	25398285	25398285	Missense_Mutation	SNP	C	T	T	KRAS	c.34G>A	p.G12S
217H2254A1	17	7578217	7578217	Missense_Mutation	SNP	G	A	A	TP53	c.632C>T	p.T211I
217H2400A1		-	-	Frame_Shift_Del	INS	-	-	-	ARID1A	c.3524del	p.P1175Hfs*5
217H2400A1		-	-	Frame_Shift_Del	INS	-	-	-	GATA3	c.708del	p.S237Afs*29
217H2400A1		-	-	Frame_Shift_Del	INS	-	-	-	KMT2D	c.7061del	p.P2354Lfs*30
217H2400A1		-	-	Frame_Shift_Del	INS	-	-	-	KMT2D	c.1940del	p.P647Hfs*283
217H2400A1	13	25029208	25029208	Missense_Mutation	SNP	G	A	A	PARP4	c.2705C>T	p.A902V
217H2400A1	13	25030478	25030478	Splice_Site	SNP	C	T	T	PARP4	c.2562+1G>A	-
217H2400A1	17	7578262	7578262	Missense_Mutation	SNP	C	T	T	TP53	c.587G>A	p.R196Q
217H2400A1	17	7578406	7578406	Missense_Mutation	SNP	C	T	T	TP53	c.524G>A	p.R175H

217H2400A1		-	-	Frame_Shift_Del	INS	-	-	-	NCOR1	C.1584del	P.E529Kfs*26
217H2400A1	18	18533624	18533624	Missense_Mutation	SNP	G	A	A	ROCK1	c.3976C>T	p.R1326C
217H2400A1		-	-	Frame_Shift_Del	INS	-	-	-	TGFBFR2	C.1226_1229del	P.S409Wfs*21
217H2400A1	3	37053589	37053589	Nonsense_Mutation	SNP	C	T	T	MLH1	c.676C>T	p.R26*
217H2400A1		-	-	Frame_Shift_Del	INS	-	-	-	FAT1	C.7381del	P.Y2461Tfs*20
217H2400A1	6	35423676	35423676	Missense_Mutation	SNP	G	A	A	FANCE	c.401G>A	p.R134H
217H2400A1		-	-	Frame_Shift_Del	INS	-	-	-	ARID1B	C.3851del	P.G1284Efs*2
217H2400A1		-	-	Frame_Shift_Ins	INS	-	-	-	ARID1B	C.5870dup	P.V1958Rfs*5
217H2400A1		-	-	Frame_Shift_Del	INS	-	-	-	ARID1B	C.6216del	P.N2073Tfs*26
217H2400A1		-	-	Frame_Shift_Del	INS	-	-	-	QKI	C.401del	P.K134Rfs*14
217H2400A1	7	106508082	106508082	Missense_Mutation	SNP	C	T	T	PIK3CG	c.76C>T	p.R26C
217H2400A1		-	-	Frame_Shift_Del	INS	-	-	-	KMT2C	C.8390del	P.K2797Rfs*26
217H2400A1		-	-	Frame_Shift_Del	INS	-	-	-	AMER1	C.780del	P.K260Nfs*22
217H2423A1	19	1221336	1221336	Nonsense_Mutation	SNP	A	T	T	STK11	c.859A>T	p.K287*
217H2423A1	20	30659499	30659499	Missense_Mutation	SNP	G	A	A	HCK	c.34G>A	p.G12R
217H2487A1	12	56481622	56481622	Missense_Mutation	SNP	T	G	G	ERBB3	c.657T>G	p.F219L
217H2487A1	15	91303853	91303853	Missense_Mutation	SNP	A	G	G	BLM	c.1250A>G	p.N417S
217H2487A1	17	29528086	29528086	Nonsense_Mutation	SNP	C	G	G	NF1	c.1094C>G	p.S365*
217H2487A1	17	29553492	29553492	Nonsense_Mutation	SNP	C	T	T	NF1	c.2041C>T	p.R681*
217H2487A1	17	37868208	37868208	Missense_Mutation	SNP	C	T	T	ERBB2	c.929C>T	p.S310F
217H2487A1		-	-	Frame_Shift_Del	INS	-	-	-	SMAD4	c.767del	p.Q256Rfs*80
217H2487A1	X	44945115	44945115	Nonsense_Mutation	SNP	C	T	T	KDM6A	c.3595C>T	p.Q1199*
217I2570A1	1	158623223	158623223	Splice_Site	SNP	G	C	C	SPTA1	c.3037-8C>G	-
217I2570A1	16	396812	396812	Missense_Mutation	SNP	G	A	A	AXIN1	c.214C>T	p.P72S
217I2570A1		-	-	Frame_Shift_Del	INS	-	-	-	TSC2	c.729_730del	p.C244Sfs*93
217I2570A1	17	7577534	7577534	Missense_Mutation	SNP	C	A	A	TP53	c.747G>T	p.R249S
217I2570A1	2	121746789	121746789	Missense_Mutation	SNP	C	T	T	GLI2	c.3299C>T	p.P1100L
217I2570A1	4	55972925	55972925	Missense_Mutation	SNP	C	G	G	KDR	c.1465G>C	p.E489Q
217I2570A1		-	-	Frame_Shift_Del	INS	-	-	-	FAT4	c.4187_4190del	p.G1396Dfs*14
217I2570A1	5	180048866	180048866	Missense_Mutation	SNP	C	T	T	FLT4	c.1696G>A	p.E566K
217I2570A1		-	-	In_Frame_Del	INS	-	-	-	KMT2C	c.2448del	p.Y816*
217I2570A1	8	141716207	141716207	Splice_Site	SNP	G	A	A	PTK2	c.2295+11C>T	-
217I2570A1	X	70613164	70613164	Missense_Mutation	SNP	C	G	G	TAF1	c.3125C>G	p.S1042C
217I2920A1	1	27023663	27023663	Missense_Mutation	SNP	G	T	T	ARID1A	c.769G>T	p.A257S
217I2920A1	17	7577547	7577547	Missense_Mutation	SNP	C	T	T	TP53	c.734G>A	p.G245D
217I2920A1	2	212426722	212426722	Missense_Mutation	SNP	A	C	C	ERBB4	c.2393T>G	p.L798R
217I2920A1	7	151945112	151945112	Missense_Mutation	SNP	C	A	A	KMT2C	c.2407G>T	p.A803S
217I2921A1	1	158650531	158650531	Splice_Site	SNP	G	A	A	SPTA1	c.532-12C>T	-
217I2921A1	12	56482369	56482369	Missense_Mutation	SNP	C	G	G	ERBB3	c.917C>G	p.P306R
217I2921A1	17	7577538	7577538	Missense_Mutation	SNP	C	T	T	TP53	c.743G>A	p.R248Q
217I2921A1	17	37863344	37863344	Missense_Mutation	SNP	A	C	C	ERBB2	c.175A>C	p.N59H
217I2921A1		-	-	Frame_Shift_Del	INS	-	-	-	DNMT3A	708_1719delins	p.G570Qfs*78
217I2921A1	2	58390085	58390085	Splice_Site	SNP	G	A	A	FANCL	c.822-3C>T	-
217I2921A1	2	170063141	170063141	Missense_Mutation	SNP	C	A	A	LRP2	c.7089G>T	p.L2363F
217I2921A1	4	153247174	153247174	Missense_Mutation	SNP	C	G	G	FBXW7	c.1628G>C	p.R543T
217I2921A1	7	77648765	77648765	Missense_Mutation	SNP	G	A	A	MAGI2	c.4235C>T	p.P1412L
217I3201A1	1	27101242	27101242	Nonsense_Mutation	SNP	T	A	A	ARID1A	c.4524T>A	p.Y1508*
217I3201A1	2	209113112	209113112	Missense_Mutation	SNP	C	A	A	IDH1	c.395G>T	p.R132L
217I3201A1	3	12626437	12626437	Missense_Mutation	SNP	C	T	T	RAF1	c.1712G>A	p.S571N
217I3201A1		-	-	Frame_Shift_Ins	INS	-	-	-	PBRM1	c.773dup	p.N258Kfs*6
217I3201A1	4	110897341	110897341	Missense_Mutation	SNP	T	A	A	EGF	c.2003T>A	p.M668K
217K3355A1	12	25398284	25398284	Missense_Mutation	SNP	C	T	T	KRAS	c.35G>A	p.G12D
217K3355A1	17	7578271	7578271	Missense_Mutation	SNP	T	C	C	TP53	c.578A>G	p.H193R
217K3355A1	18	48604788	48604788	Missense_Mutation	SNP	A	G	G	SMAD4	c.1610A>G	p.D537G
217K3355A1	2	198266611	198266611	Missense_Mutation	SNP	C	T	T	SF3B1	c.2225G>A	p.G742D
217K3355A1		-	-	In_Frame_Del	INS	-	-	-	CDKN2A	c.349_353del	p.L117*
217K3692A1	1	158651311	158651311	Splice_Site	SNP	C	T	T	SPTA1	c.531+6G>A	-
217K3692A1	1	162724518	162724518	Missense_Mutation	SNP	T	C	C	DDR2	c.290T>C	p.I97T
217K3692A1	15	88727493	88727493	Missense_Mutation	SNP	C	T	T	NTRK3	c.286G>A	p.A96T
217K3692A1		-	-	In_Frame_Del	INS	-	-	-	TP53	c.852_884del	p.E285_P295del
217K3692A1	3	134880980	134880980	Missense_Mutation	SNP	G	A	A	EPHB1	c.1543G>A	p.G515S
217K3692A1	3	185181346	185181346	Nonsense_Mutation	SNP	G	A	A	MAP3K13	c.1287G>A	p.W429*
217K3692A1	7	73535232	73535232	Missense_Mutation	SNP	G	A	A	LIMK1	c.1634G>A	p.R545Q
217K3692A1	X	66937323	66937323	Missense_Mutation	SNP	T	C	C	AR	c.2177T>C	p.F726S
217K3729A1		-	-	Frame_Shift_Del	INS	-	-	-	ARID1A	5391_5392delins	p.S1798Qfs*8
217K3729A1	12	25398284	25398284	Missense_Mutation	SNP	C	A	A	KRAS	c.35G>T	p.G12V
217K3729A1	17	38560458	38560458	Missense_Mutation	SNP	C	A	A	TOP2A	c.2229G>T	p.T0743N
217K3729A1		-	-	Frame_Shift_Ins	INS	-	-	-	RNF43	c.1371_1372dup	p.L458Pfs*45
217K3729A1		-	-	Splice_Site	SNP	-	-	-	LRP1B	2767_2770+10del	-
217K3729A1		-	-	Frame_Shift_Ins	INS	-	-	-	MACC1	c.1946_1949dup	p.S651Lfs*14
217K3729A1	7	42004656	42004656	Missense_Mutation	SNP	G	A	A	GLI3	c.4015C>T	p.R1339C
217K3730A1	12	49427693	49427693	Nonsense_Mutation	SNP	G	A	A	KMT2D	c.10795C>T	p.Q3599*
217K3730A1	4	20598069	20598069	Missense_Mutation	SNP	G	T	T	SLIT2	c.3352G>T	p.V1118F
217K3730A1	9	135777994	135777994	Nonsense_Mutation	SNP	G	A	A	TSC1	c.2389C>T	p.Q797*
217L3903A1	1	115256529	115256529	Missense_Mutation	SNP	T	A	A	NRAS	c.182A>T	p.Q61L
217L3903A1		-	-	Frame_Shift_Del	INS	-	-	-	TP53	c.64del	p.L22Yfs*22
217L3903A1	3	178952030	178952030	Missense_Mutation	SNP	G	C	C	PIK3CA	c.3085G>C	p.D1029H
217L3903A1	X	76940011	76940011	Missense_Mutation	SNP	C	T	T	ATRX	c.737G>A	p.R246H
218A4699A1	1	158605803	158605803	Missense_Mutation	SNP	T	C	C	SPTA1	c.5332A>G	p.K1778E
218A4699A1	1	179112155	179112155	Missense_Mutation	SNP	G	A	A	ABL2	c.25C>T	p.P9S
218A4699A1	12	25398284	25398284	Missense_Mutation	SNP	C	A	A	KRAS	c.35G>T	p.G12V
218A4699A1	14	45645043	45645043	Missense_Mutation	SNP	T	C	C	FANCM	c.3086T>C	p.L1029S
218A4699A1	17	7577570	7577570	Missense_Mutation	SNP	C	T	T	TP53	c.711G>A	p.M237I
218A4699A1	5	112043565	112043565	Missense_Mutation	SNP	G	A	A	APC	c.151G>A	p.A51T
218A4699A1	8	37696517	37696517	Missense_Mutation	SNP	G	A	A	ADGRA2	c.2303G>A	p.G768E
218A4699A1	X	47028867	47028867	Nonsense_Mutation	SNP	T	A	A	RBM10	c.171T>A	p.Y57*
218B4967A1	1	46738363	46738363	Missense_Mutation	SNP	G	C	C	RAD54L	c.1264G>C	p.E422Q
218B4967A1	10	89685313	89685313	Missense_Mutation	SNP	C	G	G	PTEN	c.208C>G	p.L70V
218B4967A1	11	92086395	92086395	Missense_Mutation	SNP	C	G	G	FAT3	c.1117C>G	p.P373A
218B4967A1	17	7578206	7578206	Missense_Mutation	SNP	T	C	C	TP53	c.643A>G	p.S215G
218B4967A1	3	49412973	49412973	Missense_Mutation	SNP	C	T	T	RHOA	c.50G>A	p.G17E
218B4967A1	7	18975551	18975551	Missense_Mutation	SNP	C	T	T	HDAC9	c.2914C>T	p.L972F
218B4967A1	8	69017409	69017409	Missense_Mutation	SNP	C	T	T	PREX2	c.2752C>T	p.R918W
218C5441A1	17	7577141	7577141	Missense_Mutation	SNP	C	T	T	TP53	c.797G>A	p.G266E
218C5441A1	17	37881440	37881440	Missense_Mutation	SNP	C	T	T	ERBB2	c.2632C>T	p.H878Y
218C5441A1	8	93003911	93003911	Missense_Mutation	SNP	C	T	T	RUNX1T1	c.836G>A	p.R279Q
218C5575A1	11	118359366	118359366	Missense_Mutation	SNP	A	T	T	KMT2A	c.4370A>T	p.K1457M
218C5575A1	14	20813099	20813099	Missense_Mutation	SNP	G	C	C	PARP2	c.55G>C	p.E19Q

218C5575A1	16	68867257	68867257	Missense_Mutation	SNP	A	G	G	CDH1	c.2504A>G	p.Y835C
218C5575A1	16	89836259	89836259	Missense_Mutation	SNP	C	A	A	FANCA	c.2490G>T	p.L830F
218C5575A1	17	7577559	7577559	Missense_Mutation	SNP	G	C	C	TP53	c.722C>G	p.S241C
218C5575A1	2	141460104	141460104	Missense_Mutation	SNP	T	A	A	LRP1B	c.6042A>T	p.E2014D
218C5575A1	3	52663008	52663008	Nonsense_Mutation	SNP	C	A	A	PBRM1	c.1345G>T	p.E449*
218C5588A2	1	158592947	158592947	Missense_Mutation	SNP	T	A	A	SPTA1	c.5946A>T	p.Q1982H
218C5588A2	12	57538862	57538862	Missense_Mutation	SNP	C	T	T	LRP1	c.556C>T	p.R186C
218C5588A2	17	7577507	7577507	Missense_Mutation	SNP	T	G	G	TP53	c.774A>C	p.E258D
218C5588A2	2	198267484	198267484	Missense_Mutation	SNP	G	A	A	SF3B1	c.1873C>T	p.R625C
218C5780A1	17	7578406	7578406	Missense_Mutation	SNP	C	T	T	TP53	c.524G>A	p.R175H
218C5780A1	17	29533379	29533379	Missense_Mutation	SNP	G	A	A	NF1	c.1382G>A	p.R461Q
218C5780A1	6	32166817	32166817	Missense_Mutation	SNP	C	T	T	NOTCH4	c.4421G>A	p.R1474Q
218D5915A1	17	7578431	7578431	Nonsense_Mutation	SNP	G	A	A	TP53	c.499C>T	p.Q167*
218D5915A1		-	-	Frame_Shift_Ins	INS	-	-	-	COL1A1	c.2069_2109dup	p.G704Pfs*76
218D5915A1	5	38950441	38950441	Missense_Mutation	SNP	T	C	C	RICTOR	c.3509A>G	p.E1170G
218D5915A1	6	93969182	93969182	Missense_Mutation	SNP	G	T	T	EPHA7	c.1814C>A	p.T605N
218D6413A1	1	158597523	158597523	Splice_Site	SNP	T	C	C	SPTA1	c.5566-10A>G	-
218D6413A1	10	70405010	70405010	Missense_Mutation	SNP	A	G	G	TET1	c.2524A>G	p.I842V
218D6413A1	12	1022603	1022603	Missense_Mutation	SNP	T	A	A	RAD52	c.1211A>T	p.H404L
218D6413A1	12	25398285	25398285	Missense_Mutation	SNP	C	A	A	KRAS	c.34G>T	p.G121C
218D6413A1	13	28896915	28896915	Splice_Site	SNP	A	G	G	FLT1	c.2953+12T>C	-
218D6413A1	16	2100429	2100429	Missense_Mutation	SNP	A	G	G	TSC2	c.167A>G	p.N56S
218D6413A1	17	7579722	7579722	Splice_Site	SNP	C	G	G	TP53	c.75-1G>C	-
218D6413A1	17	48270360	48270360	Missense_Mutation	SNP	C	T	T	COL1A1	c.1816G>A	p.A606T
218D6413A1	2	212812269	212812269	Missense_Mutation	SNP	G	A	A	ERBB4	c.307C>T	p.R103C
218D6413A1	7	20199671	20199671	Missense_Mutation	SNP	T	C	C	MACC1	c.313A>G	p.R105G
218D6413A1	7	41739882	41739882	Missense_Mutation	SNP	C	T	T	INHBA	c.91G>A	p.A31T
218D6413A1		-	-	Splice_Site	SNP	-	-	-	CFTR	c.210-7_1210-6del	-
218D6413A1	8	139149456	139149456	Missense_Mutation	SNP	G	A	A	FAM135B	c.3949C>T	p.R1317C
218D6413A1		-	-	Frame_Shift_Del	INS	-	-	-	CDKN2A	c.332del	p.G111Afs*35
218D6471A1		-	-	Frame_Shift_Ins	INS	-	-	-	ARID1A	c.5548dup	p.D1850Gfs*4
218D6471A1		-	-	Frame_Shift_Del	INS	-	-	-	TGFB2	c.1483del	p.R495Efs*23
218D6471A1	3	71064802	71064802	Nonsense_Mutation	SNP	A	T	T	FOXP1	c.872T>A	p.L291*
218D6471A1		-	-	Splice_Site	SNP	-	-	-	RICTOR	c.1152-5dup	-
218D6874A1	10	104356918	104356918	Missense_Mutation	SNP	G	A	A	SUFU	c.778G>A	p.E260K
218E7563A1	2	29443591	29443591	Missense_Mutation	SNP	C	T	T	ALK	c.3626G>A	p.R1209Q
218E7564A1	11	69625249	69625249	Missense_Mutation	SNP	C	T	T	FGF3	c.544G>C	p.V182M
218E7564A1		-	-	Frame_Shift_Ins	INS	-	-	-	ATM	c.2547_2592dup	p.S865Gfs*10
218E7564A1	12	25398284	25398284	Missense_Mutation	SNP	C	T	T	KRAS	c.35G>A	p.G12D
218E7564A1	19	1221340	1221340	Splice_Site	SNP	G	T	T	STK11	c.862+1G>T	-
218E7564A1		-	-	Frame_Shift_Del	INS	-	-	-	BARD1	c.631_632del	p.L211Sfs*2
218E7564A1	3	47144879	47144879	Missense_Mutation	SNP	C	T	T	SETD2	c.4874G>A	p.R1625H
218E7890A1	1	97547948	97547948	Missense_Mutation	SNP	C	T	T	DPYD	c.2845G>A	p.D949N
218E7890A1	11	92534419	92534419	Missense_Mutation	SNP	G	A	A	FAT3	c.8240G>A	p.R2747Q
218E7890A1	12	50481161	50481161	Nonsense_Mutation	SNP	C	T	T	SMARCD1	c.547C>T	p.R183*
218E7890A1	13	28597543	28597543	Missense_Mutation	SNP	G	C	C	FLT3	c.2362C>G	p.L788V
218F8298A1	12	25398284	25398284	Missense_Mutation	SNP	C	T	T	KRAS	c.35G>A	p.G12D
218F8400A1	4	55140693	55140693	Splice_Site	SNP	C	T	T	PDGFRA	c.1559-5C>T	-
218F8400A1	9	139412297	139412297	Nonsense_Mutation	SNP	C	A	A	NOTCH1	c.1348G>T	p.E450*
218F8651A1		-	-	In_Frame_Del	INS	-	-	-	TP53	c.754_759del	p.L252_7253del
218F8651A1	17	12028645	12028645	Missense_Mutation	SNP	G	A	A	MAP2K4	c.848G>A	p.G283E
218F8651A1	4	126239844	126239844	Nonsense_Mutation	SNP	C	T	T	FAT4	c.2278C>T	p.Q760*
218G8980A1	1	16261701	16261701	Missense_Mutation	SNP	C	A	A	SPEN	c.8966C>A	p.A2989D
218G8980A1	1	158612193	158612193	Splice_Site	SNP	A	C	C	SPTA1	c.4737+8T>G	-
218G8980A1	1	193117054	193117054	Missense_Mutation	SNP	C	T	T	CDC73	c.787C>T	p.R263C
218G8980A1	10	104592424	104592424	Missense_Mutation	SNP	A	C	C	CYP17A1	c.983T>G	p.L328R
218G8980A1	11	92565001	92565001	Missense_Mutation	SNP	A	C	C	FAT3	c.9695A>C	p.N3232T
218G8980A1	12	6690202	6690202	Splice_Site	SNP	A	G	G	CHD4	c.4909+8T>C	-
218G8980A1	12	25398284	25398284	Missense_Mutation	SNP	C	T	T	KRAS	c.35G>A	p.G12D
218G8980A1	12	57548458	57548458	Missense_Mutation	SNP	C	T	T	LRP1	c.1201C>T	p.R401C
218G8980A1	13	28609708	28609708	Missense_Mutation	SNP	T	C	C	FLT3	c.1521A>G	p.I507M
218G8980A1	13	110437616	110437616	Missense_Mutation	SNP	G	A	A	IRS2	c.785C>T	p.S262L
218G8980A1	15	75093390	75093390	Missense_Mutation	SNP	G	A	A	CSK	c.760G>A	p.V254M
218G8980A1	16	2105412	2105412	Missense_Mutation	SNP	T	A	A	TSC2	c.491T>A	p.V164D
218G8980A1	16	9916145	9916145	Missense_Mutation	SNP	T	C	C	GRIN2A	c.2144A>G	p.D715G
218G8980A1	17	41605981	41605981	Missense_Mutation	SNP	A	G	G	ETV4	c.1361T>C	p.V454A
218G8980A1		-	-	Frame_Shift_Ins	INS	-	-	-	RNF43	c.2094dup	p.I7000fs*47
218G8980A1	17	63052458	63052458	Missense_Mutation	SNP	C	T	T	GNA13	c.254G>A	p.R85H
218G8980A1	17	78867626	78867626	Missense_Mutation	SNP	C	T	T	RPTOR	c.2362C>T	p.R788C
218G8980A1	19	14213683	14213683	Missense_Mutation	SNP	C	T	T	PRKACA	c.281G>A	p.R94H
218G8980A1	19	15298710	15298710	Nonsense_Mutation	SNP	C	A	A	NOTCH3	c.1588G>T	p.E530*
218G8980A1	2	25467502	25467502	Missense_Mutation	SNP	G	A	A	DNMT3A	c.1574C>T	p.A525V
218G8980A1	2	47630542	47630542	Splice_Site	SNP	G	T	T	MSH2	c.211+1G>T	-
218G8980A1		-	-	Frame_Shift_Del	INS	-	-	-	ACVR2A	c.1310del	p.K437Rfs*5
218G8980A1	2	198257804	198257804	Nonsense_Mutation	SNP	C	T	T	SF3B1	c.3648G>A	p.W1216*
218G8980A1	2	198267373	198267373	Missense_Mutation	SNP	G	C	C	SF3B1	c.1984C>G	p.H662D
218G8980A1	20	31020720	31020720	Missense_Mutation	SNP	G	T	T	ASXL1	c.1017G>T	p.Q339H
218G8980A1	4	126240490	126240490	Missense_Mutation	SNP	A	C	C	FAT4	c.2924A>C	p.Q975P
218G8980A1	4	126411235	126411235	Missense_Mutation	SNP	T	C	C	FAT4	c.13258T>C	p.V4420H
218G8980A1	5	38962976	38962976	Splice_Site	SNP	A	G	G	RICTOR	c.1566+2T>C	-
218G8980A1	7	41729394	41729394	Missense_Mutation	SNP	G	A	A	INHBA	c.1135C>T	p.R379W
218G8980A1	8	37691318	37691318	Missense_Mutation	SNP	T	A	A	ADGRA2	c.1409T>A	p.I470N
218G8980A1	8	71041004	71041004	Missense_Mutation	SNP	G	A	A	NCOA2	c.3536C>T	p.T1179M
218G8980A1	9	5522590	5522590	Missense_Mutation	SNP	A	C	C	PDCD1LG2	c.44A>C	p.H15P
218G8980A1	9	27204927	27204927	Missense_Mutation	SNP	G	C	C	TEK	c.2228G>C	p.G743A
218G8980A1	X	76855026	76855026	Missense_Mutation	SNP	C	T	T	ATRX	c.5810G>A	p.G1937E
218G8980A1	X	100611203	100611203	Missense_Mutation	SNP	C	T	T	BTX	c.1403G>A	p.R468H
218G8980A1	X	123034349	123034349	Missense_Mutation	SNP	C	G	G	XIAP	c.1106C>G	p.Q369S
218G8980A1	X	123205175	123205175	Splice_Site	SNP	T	C	C	STAG2	c.2533+2T>C	-
218G9808A1	10	89717661	89717661	Nonsense_Mutation	SNP	C	G	G	PTEN	c.686C>G	p.S229*
218G9808A1	2	111907671	111907671	Missense_Mutation	SNP	G	A	A	BCL2L11	c.265G>A	p.A89T
218G9808A1	2	198267491	198267491	Missense_Mutation	SNP	C	A	A	SF3B1	c.1866G>T	p.E622D
218G9808A1	3	52437267	52437267	Nonsense_Mutation	SNP	G	A	A	BAP1	c.1777C>T	p.Q593*
218G9808A1	3	142257358	142257358	Missense_Mutation	SNP	C	A	A	ATR	c.3691G>T	p.A1231S
218G9947A1	12	25380275	25380275	Missense_Mutation	SNP	T	G	G	KRAS	c.183A>C	p.Q61H
218G9952A1	12	25398284	25398284	Missense_Mutation	SNP	C	T	T	KRAS	c.35G>A	p.G12D
218G9952A1	17	29670025	29670025	Splice_Site	SNP	A	G	G	NF1	c.7063-2A>G	-
218G9952A1	21	44524456	44524456	Missense_Mutation	SNP	G	A	A	U2AF1	c.101C>T	p.S34F

218G9952A1	3	189604320	189604320	Missense_Mutation	SNP	C	T	T	TP63	c.1487C>T	p.P496L
218G9952A1		-	-	Frame_Shift_Del	INS	-	-	-	KMT2C	C.10545del	P.F3515Lfs*18
218G9952A1	9	21971028	21971028	Nonsense_Mutation	SNP	C	T	T	CDKN2A	c.330G>A	p.W110*
218H1383A1	1	43773507	43773507	Missense_Mutation	SNP	G	T	T	TIE1	c.954G>T	p.Q318H
218H1383A1	1	158617446	158617446	Missense_Mutation	SNP	A	G	G	SPTA1	c.3779T>C	p.L1260P
218H1383A1	11	69589800	69589800	Missense_Mutation	SNP	G	A	A	FGF4	c.53C>T	p.A18V
218H1383A1	11	108173611	108173611	Missense_Mutation	SNP	A	C	C	ATM	c.5351A>C	p.N1784T
218H1383A1	12	51189780	51189780	Missense_Mutation	SNP	G	A	A	ATF1	c.182G>A	p.R61H
218H1383A1	13	32972432	32972432	Missense_Mutation	SNP	A	G	G	BRCA2	c.9782A>G	p.D3261G
218H1383A1		-	-	Frame_Shift_Del	INS	-	-	-	B2M	c.43_44del	p.L15Ffs*41
218H1383A1	15	90631877	90631877	Missense_Mutation	SNP	C	T	T	IDH2	c.476G>A	p.R159H
218H1383A1	16	9858133	9858133	Missense_Mutation	SNP	C	T	T	GRIN2A	c.3268G>A	p.V1090M
218H1383A1	17	37687478	37687478	Missense_Mutation	SNP	G	C	C	CDK12	c.4355G>C	p.G1452A
218H1383A1	17	48271816	48271816	Splice_Site	SNP	G	T	T	COL1A1	c.1516-8C>A	-
218H1383A1	17	78811739	78811739	Missense_Mutation	SNP	C	T	T	RPTOR	c.1154C>T	p.A385V
218H1383A1	19	2226439	2226439	Missense_Mutation	SNP	A	G	G	DOT1L	c.3919A>G	p.S1307G
218H1383A1		-	-	Missense_Mutation	SNP	-	-	-	SMARCA4	c.3634_3636del	p.E1212del
218H1383A1	20	57415601	57415601	Missense_Mutation	SNP	C	T	T	GNAS	c.440C>T	p.P147L
218H1383A1	3	12641190	12641190	Missense_Mutation	SNP	C	T	T	RAF1	c.1108G>A	p.G370R
218H1383A1	3	37038192	37038192	Missense_Mutation	SNP	G	A	A	MLH1	c.199G>A	p.G67R
218H1383A1	3	70014295	70014295	Missense_Mutation	SNP	G	A	A	MITF	c.1156G>A	p.V386I
218H1383A1	3	128200008	128200008	Missense_Mutation	SNP	G	T	T	GATA2	c.1297C>A	p.G433M
218H1383A1		-	-	Frame_Shift_Del	INS	-	-	-	TET2	c.1243del	p.V415Ffs*12
218H1383A1	5	112116536	112116536	Missense_Mutation	SNP	G	T	T	APC	c.581G>T	p.R194M
218H1383A1	5	121776414	121776414	Missense_Mutation	SNP	G	A	A	SNCAIP	c.1387G>A	p.V463I
218H1383A1	6	117677874	117677874	Nonsense_Mutation	SNP	G	T	T	ROS1	c.4059C>A	p.Y1353*
218H1383A1	7	142459867	142459867	Missense_Mutation	SNP	C	T	T	PRSS1	c.443C>T	p.A148V
218H1383A1	8	48872556	48872556	Missense_Mutation	SNP	A	G	G	PRKDC	c.131T>C	p.L44P
218H1383A1	8	95470504	95470504	Missense_Mutation	SNP	G	T	T	RAD54B	c.296C>A	p.P99H
218H1383A1	X	53225149	53225149	Missense_Mutation	SNP	C	A	A	KDM5C	c.3069G>T	p.K1023N
218H1383A1		-	-	Frame_Shift_Ins	INS	-	-	-	ATRX	c.477dup	p.R160Tfs*29
218H1627A1		-	-	Frame_Shift_Ins	INS	-	-	-	ARID2	c.5309dup	p.T1771Nfs*11
218H1627A1	16	347779	347779	Missense_Mutation	SNP	C	T	T	AXIN1	c.1727G>A	p.R576Q
218H1627A1	17	7577105	7577105	Missense_Mutation	SNP	G	A	A	TP53	c.833C>T	p.P278L
218H1627A1	17	37868208	37868208	Missense_Mutation	SNP	C	T	T	ERBB2	c.929C>T	p.S310F
218H1627A1	17	37881440	37881440	Missense_Mutation	SNP	C	T	T	ERBB2	c.2632C>T	p.H878Y
218H1627A1		-	-	In_Frame_Del	INS	-	-	-	ERBB4	c.3579_3590del	N1193_P1196del
218H1627A1	3	142184013	142184013	Missense_Mutation	SNP	T	C	C	ATR	c.6967A>G	p.T2323V
218H1627A1		-	-	In_Frame_Del	INS	-	-	-	KMT2C	c.5427del	p.L1810*
218H1627A1	8	37555941	37555941	Missense_Mutation	SNP	G	T	T	ZNF703	c.1522G>T	p.A508S
218H1627A1	9	21971186	21971186	Nonsense_Mutation	SNP	G	A	A	CDKN2A	c.172C>T	p.R58*
218H1627A1	X	110439716	110439716	Nonsense_Mutation	SNP	C	T	T	PAK3	c.1255C>T	p.R419*
218H1955A1	17	7578449	7578449	Missense_Mutation	SNP	C	T	T	TP53	c.481G>A	p.A161T
218H1955A1		-	-	Frame_Shift_Del	INS	-	-	-	PBRM1	c.3197_3213del	p.P1066Rfs*10
218H1955A1	4	20569192	20569192	Missense_Mutation	SNP	C	T	T	SLIT2	c.2902C>T	p.H968Y
218H1955A1	7	42005901	42005901	Missense_Mutation	SNP	C	T	T	GLI3	c.2770G>A	p.A924T
218H2052A1	1	16462185	16462185	Nonsense_Mutation	SNP	G	A	A	EPHA2	c.1393C>T	p.R465*
218H2052A1		-	-	Frame_Shift_Ins	INS	-	-	-	TP53	c.902dup	p.G302Rfs*4
218H2052A1	17	37880998	37880998	Missense_Mutation	SNP	G	T	T	ERBB2	c.2327G>T	p.G776V
218H2052A1	17	41245075	41245075	Missense_Mutation	SNP	C	T	T	BRCA1	c.2473G>A	p.D825N
218H2159A1	12	25398284	25398284	Missense_Mutation	SNP	C	A	A	KRAS	c.35G>T	p.G12V
218H2159A1	17	7577108	7577108	Missense_Mutation	SNP	C	A	A	TP53	c.830G>T	p.C277F
218I2875A1	1	16256442	16256442	Missense_Mutation	SNP	A	T	T	SPEN	c.3707A>T	p.D1236V
218I2875A1	12	133218820	133218820	Missense_Mutation	SNP	T	C	C	POLE	c.5116A>G	p.M1706V
218I2875A1		-	-	Frame_Shift_Del	INS	-	-	-	CTCF	c.615_624del	p.K206Rfs*13
218I2875A1	17	7578203	7578203	Missense_Mutation	SNP	C	A	A	TP53	c.646G>T	p.V216L
218I2875A1	2	209113113	209113113	Missense_Mutation	SNP	G	A	A	IDH1	c.394C>T	p.R132C
218I2875A1	20	36012626	36012626	Missense_Mutation	SNP	G	A	A	SRC	c.70G>A	p.V24M
218I3043A1		-	-	Frame_Shift_Del	INS	-	-	-	TP53	c.626_627del	p.R209Kfs*6
218I3043A1	19	42796753	42796753	Missense_Mutation	SNP	G	A	A	CIC	c.3211G>A	p.G1071S
218I3043A1	2	140997050	140997050	Missense_Mutation	SNP	G	T	T	LRP1B	c.13376C>A	p.T4459N
218I3043A1	2	141598571	141598571	Missense_Mutation	SNP	A	G	G	LRP1B	c.5030T>C	p.P1767A
218I3043A1	8	90958514	90958514	Missense_Mutation	SNP	T	C	C	NBN	c.1924A>G	p.K642E
218I3048A1	1	32751309	32751309	Nonsense_Mutation	SNP	C	T	T	LCK	c.1522C>T	p.Q508*
218I3048A1	10	70426835	70426835	Missense_Mutation	SNP	C	G	G	TET1	c.4495C>G	p.L1499V
218I3048A1	17	7577099	7577099	Missense_Mutation	SNP	C	T	T	TP53	c.839G>A	p.R280K
218I3048A1	17	7577543	7577543	Missense_Mutation	SNP	C	T	T	TP53	c.738G>A	p.M246I
218I3048A1	3	142168452	142168452	Splice_Site	SNP	G	C	C	ATR	c.7762-8C>G	-
218I3048A1	3	142176554	142176554	Missense_Mutation	SNP	G	C	C	ATR	c.7547C>G	p.T2516S
218I3048A1	X	70612782	70612782	Missense_Mutation	SNP	C	T	T	TAF1	c.3049C>T	p.R1017C
218I3048A1		-	-	In_Frame_Ins	INS	-	-	-	STAG2	c.2133dup	p.N712*
218I4306A1		-	-	Frame_Shift_Ins	INS	-	-	-	EPHA2	c.1589_1590ins	p.E530Dfs*66
218J4306A1	1	158606472	158606472	Missense_Mutation	SNP	G	A	A	SPTA1	c.5269C>T	p.R1757C
218J4306A1	2	209113113	209113113	Missense_Mutation	SNP	G	A	A	IDH1	c.394C>T	p.R132C
218J4306A1		-	-	Frame_Shift_Ins	INS	-	-	-	NF2	c.186dup	p.G63Wfs*23
218J4306A1	8	68864674	68864674	Missense_Mutation	SNP	G	C	C	PREX2	c.45G>C	p.K15N
218J4308A1	13	32911410	32911410	Nonsense_Mutation	SNP	C	A	A	BRCA2	c.2918C>A	p.S973*
218J4308A1	16	89845208	89845208	Splice_Site	SNP	C	G	G	FANCA	c.1826+1G>C	-
218J4308A1		-	-	Frame_Shift_Ins	INS	-	-	-	STK11	c.1012dup	p.V338Gfs*22
218J4308A1	19	45916954	45916954	Missense_Mutation	SNP	G	C	C	ERCC1	c.824C>G	p.P275R
218J4308A1	2	121746495	121746495	Missense_Mutation	SNP	C	A	A	GLI2	c.3005C>A	p.A1002D
218J4308A1	20	57484464	57484464	Missense_Mutation	SNP	C	G	G	GNAS	c.645C>G	p.D215E
218J4308A1	3	195605917	195605917	Splice_Site	SNP	C	T	T	TNK2	c.1014+3G>A	-
218J4341A1	1	11187212	11187212	Splice_Site	SNP	A	C	C	MTOR	c.6217-11T>G	-
218J4341A1	12	46231201	46231201	Splice_Site	SNP	G	T	T	ARID2	c.1120+1G>T	-
218J4341A1		-	-	Frame_Shift_Del	INS	-	-	-	ARID2	c.1616_1632del	p.S539Yfs*4
218J4341A1	17	7573976	7573976	Nonsense_Mutation	SNP	T	A	A	TP53	c.1051A>T	p.K351*
218J4341A1	3	178952085	178952085	Missense_Mutation	SNP	A	G	G	PIK3CA	c.3140A>G	p.H1047R
218J4341A1	7	55211089	55211089	Missense_Mutation	SNP	T	A	A	EGFR	c.332T>A	p.M111K
218J4341A1	8	32613989	32613989	Missense_Mutation	SNP	A	G	G	NRG1	c.410A>G	p.N137S
218J4341A1	8	48792158	48792158	Nonsense_Mutation	SNP				PRKDC	c.5128A>T	p.R1710*
218J4343A1	12	25398284	25398284	Missense_Mutation	SNP	C	T	T	KRAS	c.35G>A	p.G12D
218J4343A1	18	48591895	48591895	Missense_Mutation	SNP	A	G	G	SMAD4	c.1058A>G	p.Y353C
218J4343A1	22	29669841	29669841	Nonsense_Mutation	SNP	C	T	T	EWRS1	c.214C>T	p.Q72*
218J4343A1	9	22008876	22008876	Missense_Mutation	SNP	A	G	G	CDKN2B	c.77T>C	p.L26P
218J4343A1		-	-	Splice_Site	SNP	-	-	-	RBM10	c.543_576+4de	-
218J4612A1	3	178952085	178952085	Missense_Mutation	SNP	A	G	G	PIK3CA	c.3140A>G	p.H1047R
218J4612A1	3	189584549	189584549	Missense_Mutation	SNP	G	A	A	TP63	c.845G>A	p.G282E

218J4612A1	6	30866999	30866999	Missense_Mutation	SNP	C	T	T	DDR1	c.2557C>T	p.R853W
218J4612A1	X	44949176	44949176	Splice_Site	SNP	G	C	C	KDM6A	c.3736+1G>C	-
218J4612A1	X	47426725	47426725	Missense_Mutation	SNP	G	A	A	ARAF	c.970G>A	p.V324M
218J5499A1	12	4554699	4554699	Missense_Mutation	SNP	C	T	T	FGF6	c.38G>A	p.R13Q
218J5499A1	-	-	-	Frame_Shift_Del	INS	-	-	-	NF1	c.4354_4358del	p.H14525fs*13
218J5499A1	19	52719151	52719151	Splice_Site	SNP	G	C	C	PPP2R1A	c.922+5G>C	-
218J5499A1	22	41513644	41513644	Missense_Mutation	SNP	G	T	T	EP300	c.548G>T	p.G183V
218J5499A1	7	2984069	2984069	Missense_Mutation	SNP	G	C	C	CARD11	c.461C>G	p.A154G
218K6790A1	11	118373323	118373323	Missense_Mutation	SNP	T	C	C	KMT2A	c.6716T>C	p.L2239P
218K6790A1	12	12870782	12870782	Missense_Mutation	SNP	C	A	A	CDKN1B	c.9C>A	p.N3K
218K6790A1	14	36986493	36986493	Missense_Mutation	SNP	C	G	G	NKX2-1	c.1196G>C	p.R399P
218K6790A1	15	75090959	75090959	Missense_Mutation	SNP	G	T	T	CSK	c.19G>T	p.A7S
218K6790A1	-	-	-	Splice_Site	SNP	-	-	-	TP53	3-1delinsACCAC	-
218K6790A1	17	7577565	7577565	Missense_Mutation	SNP	T	C	C	TP53	c.716A>G	p.N239S
218K6790A1	17	37671991	37671991	Missense_Mutation	SNP	C	A	A	CDK12	c.2776C>A	p.L926I
218K6790A1	2	198266609	198266609	Missense_Mutation	SNP	A	C	C	SF3B1	c.2227T>G	p.L743V
218K6790A1	6	138192350	138192350	Splice_Site	SNP	-	-	-	TNFAIP3	c.-15-5T>C	-
218K6790A1	7	81359066	81359066	Missense_Mutation	SNP	G	C	C	HGF	c.895C>G	p.P299A
218K6907A1	17	7578406	7578406	Missense_Mutation	SNP	C	T	T	TP53	c.524G>A	p.R175H
218K6907A1	2	141259449	141259449	Splice_Site	SNP	A	T	T	LRP1B	c.8663-6T>A	-
218K6907A1	6	32187467	32187467	Missense_Mutation	SNP	C	T	T	NOTCH4	c.1412G>A	p.R471H
218K6907A1	8	68968203	68968203	Missense_Mutation	SNP	T	C	C	PREX2	c.1232T>C	p.L411P
218K6907A1	X	70338696	70338696	Missense_Mutation	SNP	A	G	G	MED12	c.92A>G	p.Q31R
218L7136A1	12	58145430	58145430	Missense_Mutation	SNP	C	T	T	CDK4	c.71G>A	p.R24H
218L7136A1	16	81957117	81957117	Missense_Mutation	SNP	G	T	T	PLCG2	c.2335G>T	p.D779Y
218L7137A1	12	25398284	25398284	Missense_Mutation	SNP	C	A	A	KRAS	c.35G>T	p.G12V
218L7137A1	20	57484420	57484420	Missense_Mutation	SNP	C	G	G	GNAS	c.601C>G	p.R201G
218L7990A1	1	206649713	206649713	Splice_Site	SNP	A	T	T	IKBKE	c.540+8A>T	-
218L7990A1	17	7577114	7577114	Missense_Mutation	SNP	C	A	A	TP53	c.824G>T	p.C275F
218L7990A1	3	189607225	189607225	Missense_Mutation	SNP	C	G	G	TP63	c.1604C>G	p.S535C
218L7990A1	7	117144312	117144312	Missense_Mutation	SNP	C	G	G	CFTR	c.59C>G	p.T20S
218L9107A1	16	67654728	67654728	Splice_Site	SNP	T	G	G	CTCF	c.1207+8T>G	-
218L9107A1	17	7578370	7578370	Splice_Site	SNP	C	T	T	TP53	c.559+1G>A	-
218L9107A1	5	180047888	180047888	Missense_Mutation	SNP	C	T	T	FLT4	c.2287G>A	p.V763M
218L9107A1	-	-	-	In_Frame_Del	INS	-	-	-	WISP3	c.623_625del	(208_C209del)insS
219A1770D1	17	7578413	7578413	Missense_Mutation	SNP	C	T	T	TP53	c.517G>A	p.V173M
219A1770D1	-	-	-	Frame_Shift_Del	INS	-	-	-	SMAD4	C.1596_1603del	P.L533Pfs*41
219A1770D1	2	141819768	141819768	Missense_Mutation	SNP	C	T	T	LRP1B	c.1088G>A	p.R363K
219A1770D1	4	66230893	66230893	Missense_Mutation	SNP	C	T	T	EPHA5	c.2078G>A	p.R693H
219A1770D1	4	126239215	126239215	Missense_Mutation	SNP	T	G	G	FAT4	c.1649T>G	p.L550R
219A1770D1	X	100611040	100611040	Missense_Mutation	SNP	C	A	A	BTB	c.1566G>T	p.L522L
219A1770D1	X	123019573	123019573	Missense_Mutation	SNP	G	C	C	XIAP	c.61G>C	p.E21Q
219A9920A1	1	120484314	120484314	Missense_Mutation	SNP	G	A	A	NOTCH2	c.2816C>T	p.P939L
219A9920A1	17	7578392	7578392	Nonsense_Mutation	SNP	C	A	A	TP53	c.538G>T	p.E180*
219A9920A1	2	142004878	142004878	Missense_Mutation	SNP	C	G	G	LRP1B	c.509G>C	p.R170T
219A9920A1	7	106508720	106508720	Missense_Mutation	SNP	C	A	A	PIK3CG	c.714C>A	p.D238E
219A9920A1	9	133759526	133759526	Missense_Mutation	SNP	C	T	T	ABL1	c.1906C>T	p.R636C
219A9920A1	X	44921969	44921969	Missense_Mutation	SNP	G	T	T	KDM6A	c.1503G>T	p.Q501H
24059085A1	9	87570318	87570318	Missense_Mutation	SNP	G	C	C	NTRK2	c.2058G>C	p.Q686H
24059085A1	17	7577559	7577559	Missense_Mutation	SNP	G	C	C	TP53	c.722C>G	p.S241C
24059085A1	2	141108425	141108425	Missense_Mutation	SNP	C	T	T	LRP1B	c.11833G>A	p.G3945R
24059085A1	3	52441226	52441226	Nonsense_Mutation	SNP	C	A	A	BAP1	c.544G>T	p.E182*
618F8157A2	11	108128226	108128226	Nonsense_Mutation	SNP	G	T	T	ATM	c.2269G>T	p.G757*
618F8157A2	17	16004563	16004563	Splice_Site	SNP	C	A	A	NCOR1	c.2690+1G>T	-
618F8167A2	3	30713760	30713760	Missense_Mutation	SNP	A	G	G	TGFBR2	c.1085A>G	p.H362R
618F8167A2	-	-	-	Frame_Shift_Del	INS	-	-	-	BAP1	c.421del	p.H1411fs*46
618F8167A2	7	77789586	77789586	Missense_Mutation	SNP	C	A	A	MAGI2	c.2601G>T	p.E867D
ASCO795410	3	142272103	142272103	Missense_Mutation	SNP	C	T	T	ATR	2771G>A;2777T>C	(5924N;F926C)
ASCO795410	-	-	-	Frame_Shift_Del	INS	-	-	-	SETD2	C.5481del	P.W1827Cfs*11
ASCO795410	12	25398281	25398281	Missense_Mutation	SNP	C	T	T	KRAS	c.38G>A	p.G13D
CASE111111	1	27088755	27088755	Nonsense_Mutation	SNP	C	A	A	ARID1A	c.2364C>A	p.Y788*
CASE111111	1	202710591	202710591	Missense_Mutation	SNP	G	A	A	KDM5B	c.2957C>T	p.P986L
CASE111111	1	204437999	204437999	Missense_Mutation	SNP	G	A	A	PIK3C2B	c.932C>T	p.P311L
CASE111111	10	43601830	43601830	Missense_Mutation	SNP	G	A	A	RET	c.874G>A	p.V292M
CASE111111	11	9597523	9597523	Missense_Mutation	SNP	A	G	G	WEE1	c.665A>G	p.K222R
CASE111111	11	92088570	92088570	Missense_Mutation	SNP	G	A	A	FAT3	c.3292G>A	p.G1098R
CASE111111	12	25398284	25398284	Missense_Mutation	SNP	C	T	T	KRAS	c.35G>A	p.G12D
CASE111111	-	-	-	Splice_Site	SNP	-	-	-	RB1	c.1128-5delT	-
CASE111111	13	48947631	48947631	Splice_Site	SNP	A	G	G	RB1	c.1215+3A>G	-
CASE111111	16	81968061	81968061	Missense_Mutation	SNP	A	T	T	PLCG2	c.2767A>T	p.N923Y
CASE111111	16	81969933	81969933	Missense_Mutation	SNP	G	A	A	PLCG2	c.3002G>A	p.R1001H
CASE111111	17	7577085	7577085	Nonsense_Mutation	SNP	C	A	A	TP53	c.853G>T	p.E285*
CASE111111	17	7577609	7577609	Splice_Site	SNP	C	T	T	TP53	c.673-1G>A	-
CASE111111	17	15961283	15961283	Missense_Mutation	SNP	C	A	A	NCOR1	c.6106G>T	p.A2036S
CASE111111	17	15983379	15983379	Splice_Site	SNP	C	G	G	NCOR1	c.3401-1G>C	-
CASE111111	17	29527462	29527462	Missense_Mutation	SNP	G	A	A	NF1	c.911G>A	p.R304Q
CASE111111	17	37627362	37627362	Missense_Mutation	SNP	T	A	A	CDK12	c.1277T>A	p.F426Y
CASE111111	17	38510560	38510560	Missense_Mutation	SNP	C	T	T	RARA	c.814C>T	p.R272W
CASE111111	19	30314572	30314572	Missense_Mutation	SNP	G	A	A	CCNE1	c.1121G>A	p.R374Q
CASE111111	2	121708880	121708880	Missense_Mutation	SNP	C	T	T	GLI2	c.316C>T	p.H106Y
CASE111111	20	62173546	62173546	Missense_Mutation	SNP	G	T	T	SRMS	c.916C>A	p.R306S
CASE111111	22	41574907	41574907	Missense_Mutation	SNP	G	A	A	EP300	c.7192G>A	p.D2398N
CASE111111	3	38182748	38182748	Missense_Mutation	SNP	C	T	T	MYD88	c.925C>T	p.R309C
CASE111111	3	142268985	142268985	Missense_Mutation	SNP	G	A	A	ATR	c.2965C>T	p.R989C
CASE111111	4	55946257	55946257	Missense_Mutation	SNP	C	T	T	KDR	c.3922G>A	p.G1308R
CASE111111	4	187541228	187541228	Missense_Mutation	SNP	G	A	A	FAT1	c.6512C>T	p.P2171L
CASE111111	5	38975689	38975689	Missense_Mutation	SNP	C	T	T	RICTOR	c.839G>A	p.R280Q
CASE111111	5	176523067	176523067	Missense_Mutation	SNP	C	T	T	FGFR4	c.1831C>T	p.R611W
CASE111111	6	138201337	138201337	Missense_Mutation	SNP	T	C	C	TNFAIP3	c.2036T>C	p.L679T
CASE111111	7	2976817	2976817	Missense_Mutation	SNP	C	T	T	CARD11	c.1195G>A	p.E399K
CASE111111	7	116340214	116340214	Missense_Mutation	SNP	G	A	A	MET	c.1076G>A	p.R359Q
CASE111111	7	151874767	151874767	Missense_Mutation	SNP	C	T	T	KMT2C	c.7771G>A	p.G2591R
CASE111111	8	41836193	41836193	Missense_Mutation	SNP	C	T	T	KAT6A	c.1010G>A	p.R337H
CASE111111	9	98220390	98220390	Missense_Mutation	SNP	G	A	A	PTCH1	c.3073C>T	p.R1025C
CASE111111	X	129159352	129159352	Missense_Mutation	SNP	C	A	A	BCORL1	c.4076C>A	p.A1359E
CASE222222	1	45805988	45805988	Splice_Site	SNP	C	A	A	MUTYH	c.-62G>T	-
CASE222222	11	108117784	108117784	Missense_Mutation	SNP	A	G	G	ATM	c.995A>G	p.Y332C
CASE222222	11	118344839	118344839	Missense_Mutation	SNP	C	G	G	KMT2A	c.2965C>G	p.L989V

CASE222222	14	95566106	95566106	Splice_Site	SNP	C	A	A	DICER1	c.4206+11G>T	-
CASE222222	14	102549644	102549644	Splice_Site	SNP	G	T	T	HSP90AA1	c.1853-5C>A	-
CASE222222	16	3807850	3807850	Missense_Mutation	SNP	T	C	C	CREBBP	c.3569A>G	p.D1190G
CASE222222	16	23646324	23646324	Nonsense_Mutation	SNP	T	A	A	PALB2	c.1543A>T	p.K515*
CASE222222	17	7577509	7577509	Missense_Mutation	SNP	C	T	T	TP53	c.772G>A	p.E258K
CASE222222	2	121744143	121744143	Missense_Mutation	SNP	C	T	T	GLI2	c.2246C>T	p.P749L
CASE222222	21	44840885	44840885	Splice_Site	SNP	C	T	T	SIK1	c.748+5G>A	-
CASE222222	-	-	-	Frame_Shift_Del	INS	-	-	-	SETD2	c.5533del	P.S1845Vfs*20
CASE222222	3	49940126	49940126	Missense_Mutation	SNP	C	T	T	MST1R	c.917G>A	p.R306H
CASE222222	3	195593777	195593777	Nonsense_Mutation	SNP	C	T	T	TNK2	c.3093G>A	p.W1031*
CASE222222	4	1952795	1952795	Splice_Site	SNP	C	G	G	NSD2	c.1882-4C>G	-
CASE222222	4	126336878	126336878	Missense_Mutation	SNP	G	A	A	FAT4	c.6760G>A	p.D2254N
CASE222222	5	131927598	131927598	Missense_Mutation	SNP	A	G	G	RAD50	c.1665A>G	p.I555M
CASE222222	6	32165209	32165209	Missense_Mutation	SNP	A	T	T	NOTCH4	c.4919T>A	p.L1640Q
CASE222222	9	21971209	21971209	Splice_Site	SNP	T	C	C	CDKN2A	c.151-2A>G	-
CASE222222	X	76874314	76874314	Missense_Mutation	SNP	C	T	T	ATRX	c.5408G>A	p.R1803H
CASE222222	X	123185061	123185061	Missense_Mutation	SNP	C	T	T	STAG2	c.1108C>T	p.R370W
CASE333333	1	158632689	158632689	Missense_Mutation	SNP	A	G	G	SPTA1	c.2267T>C	p.I756T
CASE333333	10	70404467	70404467	Missense_Mutation	SNP	A	C	C	TET1	c.1981A>C	p.N661H
CASE333333	10	104595035	104595035	Missense_Mutation	SNP	C	T	T	CYP17A1	c.412G>A	p.G138S
CASE333333	10	123239457	123239457	Missense_Mutation	SNP	C	G	G	FGFR2	c.2380G>C	p.D794H
CASE333333	12	112939990	112939990	Missense_Mutation	SNP	T	C	C	PTPN11	c.1642T>C	p.S548P
CASE333333	17	38555017	38555017	Splice_Site	SNP	C	T	T	TOP2A	c.3453+8G>A	-
CASE333333	19	2216771	2216771	Splice_Site	SNP	G	A	A	DOT1L	c.2408+7G>A	-
CASE333333	19	10475580	10475580	Missense_Mutation	SNP	C	T	T	TYK2	c.1156G>A	p.V386M
CASE333333	19	15272347	15272347	Missense_Mutation	SNP	C	T	T	NOTCH3	c.6092G>A	p.R2031H
CASE333333	19	15303304	15303304	Missense_Mutation	SNP	C	T	T	NOTCH3	c.224G>A	p.R755Q
CASE333333	19	42776140	42776140	Missense_Mutation	SNP	C	T	T	CIC	c.205C>T	p.R69V
CASE333333	2	29416667	29416667	Missense_Mutation	SNP	T	C	C	ALK	c.4286A>G	p.Q1429R
CASE333333	2	29462691	29462691	Missense_Mutation	SNP	G	A	A	ALK	c.2210C>T	p.S737L
CASE333333	2	29543716	29543716	Missense_Mutation	SNP	C	T	T	ALK	c.1447G>A	p.E483K
CASE333333	4	175896743	175896743	Missense_Mutation	SNP	G	A	A	ADAM29	c.67G>A	p.E23K
CASE333333	5	131915115	131915115	Missense_Mutation	SNP	C	T	T	RAD50	c.472C>T	p.H158Y
CASE333333	-	-	-	Frame_Shift_Ins	INS	-	-	-	RAD50	C.2165dup	P.E723Gfs*5
CASE333333	8	48689409	48689409	Splice_Site	SNP	-	-	-	PRKDC	c.12180-3C>T	-
CASE333333	9	93626890	93626890	Missense_Mutation	SNP	A	G	G	SYK	c.737A>G	p.Y246C
CASE444444	1	16262537	16262537	Missense_Mutation	SNP	C	T	T	SPEN	c.9802C>T	p.R3268C
CASE444444	1	97981368	97981368	Missense_Mutation	SNP	T	G	G	DPYD	c.1654A>C	p.T552P
CASE444444	1	120491753	120491753	Splice_Site	SNP	G	C	C	NOTCH2	c.2480-4C>G	-
CASE444444	11	111965567	111965567	Missense_Mutation	SNP	A	G	G	SDHD	c.353A>G	p.D118G
CASE444444	12	1034604	1034604	Splice_Site	SNP	T	C	C	RAD52	c.543+12A>G	-
CASE444444	17	7578212	7578212	Nonsense_Mutation	SNP	G	A	A	TP53	c.637C>T	p.R213*
CASE444444	17	29654521	29654521	Missense_Mutation	SNP	G	T	T	NF1	c.5273G>T	p.G1758V
CASE444444	17	56448400	56448400	Splice_Site	SNP	G	A	A	RNF43	c.253-6C>T	-
CASE444444	18	60795959	60795959	Missense_Mutation	SNP	G	A	A	BCL2	c.619C>T	p.R207W
CASE444444	19	42794884	42794884	Missense_Mutation	SNP	T	C	C	CIC	c.1964T>C	p.L655P
CASE444444	4	20618743	20618743	Missense_Mutation	SNP	G	T	T	SLIT2	c.4058G>T	p.G1353V
CASE444444	X	48123213	48123213	Splice_Site	SNP	A	G	G	SSX1	c.331-4A>G	-
CASE555555	1	16262429	16262429	Missense_Mutation	SNP	G	A	A	SPEN	c.9694G>A	p.E3232K
CASE555555	1	204438084	204438084	Missense_Mutation	SNP	G	C	C	PIK3C2B	c.847C>G	p.Q283E
CASE555555	10	43606814	43606814	Missense_Mutation	SNP	C	T	T	RET	c.1423C>T	p.R475W
CASE555555	11	92085554	92085554	Missense_Mutation	SNP	C	G	G	FAT3	c.276C>G	p.F92L
CASE555555	11	92531376	92531376	Missense_Mutation	SNP	C	T	T	FAT3	c.5197C>T	p.R1733C
CASE555555	12	92538031	92538031	Missense_Mutation	SNP	C	A	A	BTG1	c.341G>T	p.R114I
CASE555555	-	-	-	Frame_Shift_Ins	INS	-	-	-	BRCA2	C.1813dup	P.I605Nfs*11
CASE555555	13	48936983	48936983	Nonsense_Mutation	SNP	C	T	T	RB1	c.751C>T	p.R251*
CASE555555	17	7577099	7577099	Missense_Mutation	SNP	C	G	G	TP53	c.839G>C	p.R280T
CASE555555	17	56448354	56448354	Missense_Mutation	SNP	T	C	C	RNF43	c.293A>G	p.N98S
CASE555555	2	112758843	112758843	Missense_Mutation	SNP	G	A	A	MERTK	c.1670G>A	p.R557Q
CASE555555	2	141283818	141283818	Nonsense_Mutation	SNP	C	A	A	LRP1B	c.7864G>T	p.E2622*
CASE555555	3	130799295	130799295	Missense_Mutation	SNP	G	A	A	NEK11	c.199G>A	p.E67K
CASE555555	3	142281429	142281429	Missense_Mutation	SNP	G	A	A	ATR	c.815C>T	p.S272L
CASE555555	4	126370901	126370901	Missense_Mutation	SNP	C	A	A	FAT4	c.8730C>A	p.F2910L
CASE555555	5	35876391	35876391	Missense_Mutation	SNP	A	C	C	IL7R	c.1183A>C	p.R395Q
CASE555555	6	162206948	162206948	Splice_Site	SNP	G	A	A	PRKN	c.735-8C>T	-
R18C5410R2	17	7577538	7577538	Missense_Mutation	SNP	C	T	T	TP53	c.743G>A	p.R248Q
R18C5410R2	20	31021211	31021211	Nonsense_Mutation	SNP	C	T	T	ASXL1	c.1210C>T	p.R404*
R18C5410R2	5	121758851	121758851	Missense_Mutation	SNP	T	A	A	SNAIP1	c.419T>A	p.L140Q
R18C5410R2	5	149497300	149497300	Missense_Mutation	SNP	G	A	A	PDGFRB	c.3018C>T	p.S1006S
R18C5410R2	8	71068858	71068858	Missense_Mutation	SNP	T	G	G	NCOA2	c.1742A>C	p.D581A
R18C5411R2	1	27056207	27056207	Nonsense_Mutation	SNP	C	G	G	ARID1A	c.1203C>G	p.Y401*
R18C5411R2	1	115256530	115256530	Missense_Mutation	SNP	G	T	T	NRAS	c.181C>A	p.Q61K
R18C5411R2	-	-	-	Frame_Shift_Ins	INS	-	-	-	SMAD4	C.153dup	P.D52Rfs*2
R18C5411R2	2	61726995	61726995	Missense_Mutation	SNP	G	T	T	XPO1	c.443C>A	p.T148N
R18C5411R2	X	44949082	44949082	Missense_Mutation	SNP	G	A	A	KDM6A	c.3643G>A	p.G1215R
R18D6313R1	9	135772702	135772702	Nonsense_Mutation	SNP	A	C	C	TSC1	c.2844T>G	p.Y948*
R18D6314R1	-	-	-	Frame_Shift_Del	INS	-	-	-	ARID1A	c.5327delinsTT	p.E1776Gfs*3
R18D6314R1	-	-	-	Frame_Shift_Del	INS	-	-	-	ARID2	c.4632-4651del	p.A1547Gfs*14
R18D6314R1	7	2974086	2974086	Splice_Site	SNP	C	A	A	CARD11	c.1518+1G>T	-
R18D6315R1	1	27106354	27106354	Nonsense_Mutation	SNP	C	T	T	ARID1A	c.5965C>T	p.R1989*
R18D6316R1	-	-	-	Frame_Shift_Del	INS	-	-	-	JAK1	c.472del	p.L158Cfs*10
R18D6316R1	15	93557954	93557954	Missense_Mutation	SNP	G	T	T	CHD2	c.4721G>T	p.G1574V
R18D6316R1	16	360008	360008	Nonsense_Mutation	SNP	G	A	A	AXIN1	c.1081C>T	p.Q361*
R18D6316R1	17	37868208	37868208	Missense_Mutation	SNP	C	T	T	ERBB2	c.929C>T	p.S310F
R18D6316R1	2	29419665	29419665	Missense_Mutation	SNP	T	C	C	ALK	c.4135A>G	p.I1379V
R18D6316R1	7	116371867	116371867	Missense_Mutation	SNP	A	G	G	MET	c.1346A>G	p.D449G
R18D6317R1	-	-	-	In_Frame_Ins	INS	-	-	-	EPHA2	c.713dup	p.E241*
R18D6317R1	17	7577120	7577120	Missense_Mutation	SNP	C	T	T	TP53	c.818G>A	p.R273H
R18D6317R1	X	47044850	47044850	Nonsense_Mutation	SNP	C	T	T	RBM10	c.2176C>T	p.R726*
R18D6417R1	1	9780797	9780797	Splice_Site	SNP	C	T	T	PIK3CD	c.1522-3C>T	-
R18D6417R1	11	108201099	108201099	Missense_Mutation	SNP	C	T	T	ATM	c.7466C>T	p.S2489F
R18D6417R1	12	6687638	6687638	Missense_Mutation	SNP	C	T	T	CHD4	c.5056G>A	p.E1686K
R18D6417R1	12	49425896	49425896	Nonsense_Mutation	SNP	G	A	A	KMT2D	c.12592C>T	p.R4198*
R18D6417R1	15	93543766	93543766	Missense_Mutation	SNP	C	T	T	CHD2	c.4033C>T	p.R1345W
R18D6417R1	17	16040727	16040727	Splice_Site	SNP	C	T	T	NCOR1	c.1408-1G>A	-
R18D6417R1	2	121745873	121745873	Missense_Mutation	SNP	G	A	A	GLI2	c.2383G>A	p.E795K
R18D6417R1	2	212488655	212488655	Missense_Mutation	SNP	C	A	A	ERBB4	c.2194G>T	p.V732F
R18D6417R1	3	178936082	178936082	Missense_Mutation	SNP	G	A	A	PIK3CA	c.1624G>A	p.E542K

R18D6417R1	3	178936091	178936091	Missense_Mutation	SNP	G	A	A	PIK3CA	c.1633G>A	p.E545K
R18D6417R1	6	32184839	32184839	Missense_Mutation	SNP	C	G	G	NOTCH4	c.1744G>C	p.E582Q
R18D6417R1	6	33286968	33286968	Missense_Mutation	SNP	C	G	G	DAXX	c.1969G>C	p.E657Q
R18D6417R1	6	33287293	33287293	Missense_Mutation	SNP	C	G	G	DAXX	c.1804G>C	p.E602Q
R18D6417R1	X	70608704	70608704	Missense_Mutation	SNP	G	C	C	TAF1	c.2746G>C	p.E196Q
R18D6463R1	1	16477446	16477446	Missense_Mutation	SNP	T	A	A	EPHA2	c.98A>T	p.D33V
R18D6463R1	13	48951052	48951052	Splice_Site	SNP	A	G	G	RB1	c.1216-2A>G	-
R18D6463R1	2	19192525	19192525	Splice_Site	SNP	C	G	G	STAT4	c.782+8G>C	-
R18D6463R1	3	178936082	178936082	Missense_Mutation	SNP	G	A	A	PIK3CA	c.1624G>A	p.E542K
R18D6470R1	-	-	-	Frame_Shift_Del	INS	-	-	-	RAD54L	c.488del	p.F1635fs*25
R18D6470R1	10	90768757	90768757	Splice_Site	SNP	A	G	G	FAS	c.443+3A>G	-
R18D6470R1	11	108117783	108117783	Missense_Mutation	SNP	T	C	C	ATM	c.994T>C	p.Y332H
R18D6470R1	11	108178659	108178659	Nonsense_Mutation	SNP	A	T	T	ATM	c.5710A>T	p.K1904*
R18D6470R1	11	119169120	119169120	Missense_Mutation	SNP	A	T	T	CBL	c.2304A>T	p.E768D
R18D6470R1	-	-	-	Frame_Shift_Del	INS	-	-	-	ARID2	c.130del	p.E445fs*14
R18D6470R1	13	48934148	48934148	Splice_Site	SNP	T	C	C	RB1	c.608-5T>C	-
R18D6470R1	14	45620637	45620637	Missense_Mutation	SNP	A	G	G	FANCM	c.956A>G	p.N319S
R18D6470R1	14	95599677	95599677	Missense_Mutation	SNP	T	A	A	DICER1	c.119A>T	p.N40I
R18D6470R1	-	-	-	Frame_Shift_Del	INS	-	-	-	NUP93	c.880_892del	p.R294Tfs*24
R18D6470R1	16	67645024	67645024	Missense_Mutation	SNP	A	G	G	CTCF	c.289A>G	p.T97A
R18D6470R1	17	7579494	7579494	Nonsense_Mutation	SNP	T	A	A	TP53	c.193A>T	p.R65*
R18D6470R1	17	16012219	16012219	Missense_Mutation	SNP	C	T	T	NCOR1	c.2063G>A	p.R688Q
R18D6470R1	17	38555391	38555391	Splice_Site	SNP	T	A	A	TOP2A	c.3197-8A>T	-
R18D6470R1	17	59878832	59878832	Nonsense_Mutation	SNP	T	A	A	BRIP1	c.922A>T	p.K308*
R18D6470R1	18	45395607	45395607	Splice_Site	SNP	T	C	C	SMAD2	c.430+7A>G	-
R18D6470R1	2	61719504	61719504	Missense_Mutation	SNP	T	G	G	XPO1	c.1679A>C	p.K560T
R18D6470R1	4	143066982	143066982	Splice_Site	SNP	T	C	C	INPP4B	c.1720+11A>G	-
R18D6470R1	4	175898741	175898741	Missense_Mutation	SNP	A	G	G	ADAM29	c.2065A>G	p.I689V
R18D6470R1	5	38955718	38955718	Missense_Mutation	SNP	T	C	C	RICTOR	c.2588A>G	p.Y863C
R18D6470R1	8	31497909	31497909	Missense_Mutation	SNP	A	C	C	NRG1	c.409A>C	p.N137H
R18D6483R1	1	16262648	16262648	Missense_Mutation	SNP	G	C	C	SPEN	c.9913G>C	p.E330SQ
R18D6483R1	1	158650489	158650489	Missense_Mutation	SNP	C	T	T	SPTA1	c.562G>A	p.E188K
R18D6483R1	11	92532543	92532543	Missense_Mutation	SNP	G	T	T	FAT3	c.6364G>T	p.V2122F
R18D6483R1	11	119146713	119146713	Missense_Mutation	SNP	C	G	G	CBL	c.876C>G	p.I292M
R18D6483R1	-	-	-	Frame_Shift_Ins	INS	-	-	-	ARID2	c.4903_4904dup	p.W1636Cfs*66
R18D6483R1	-	-	-	Frame_Shift_Del	INS	-	-	-	ACVR1B	c.559_560del	p.S187Hfs*43
R18D6483R1	13	43155412	43155412	Missense_Mutation	SNP	C	G	G	TNFSF11	c.151C>G	p.Q51E
R18D6483R1	14	81422193	81422193	Missense_Mutation	SNP	C	G	G	TSHR	c.169C>G	p.L57V
R18D6483R1	17	7577099	7577099	Missense_Mutation	SNP	C	T	T	TP53	c.839G>A	p.R280K
R18D6483R1	17	12011144	12011144	Missense_Mutation	SNP	C	T	T	MAP2K4	c.551C>T	p.S184L
R18D6483R1	17	29663744	29663744	Missense_Mutation	SNP	T	A	A	NF1	c.6239T>A	p.I2080N
R18D6483R1	19	17945815	17945815	Splice_Site	SNP	G	A	A	JAK3	c.2048-3C>T	-
R18D6483R1	3	178936091	178936091	Missense_Mutation	SNP	G	A	A	PIK3CA	c.1633G>A	p.E545K
R18D6483R1	4	187539252	187539252	Nonsense_Mutation	SNP	G	A	A	FAT1	c.8488C>T	p.Q2830*
R18D6483R1	6	30865360	30865360	Missense_Mutation	SNP	G	C	C	DDR1	c.2091G>C	p.Q697H
R18D6483R1	7	127727059	127727059	Nonsense_Mutation	SNP	C	T	T	SND1	c.2374C>T	p.Q792*
R18D6483R1	7	148513873	148513873	Splice_Site	SNP	G	A	A	EZH2	c.1411-3C>T	-
R18D6483R1	8	68965459	68965459	Missense_Mutation	SNP	G	C	C	PREX2	c.1071G>C	p.L357F
R18D6483R1	9	135787737	135787737	Nonsense_Mutation	SNP	G	T	T	TSC1	c.845C>A	p.S282*
R18D6488R1	12	115109962	115109962	Missense_Mutation	SNP	C	T	T	TBX3	c.1916G>A	p.R639H
R18D6488R1	13	110437691	110437691	Missense_Mutation	SNP	G	A	A	IRS2	c.710C>T	p.S237L
R18D6488R1	17	7574021	7574021	Nonsense_Mutation	SNP	C	A	A	TP53	c.1006G>T	p.E336*
R18D6488R1	22	30069414	30069414	Nonsense_Mutation	SNP	G	T	T	NF2	c.1279G>T	p.E427*
R18D6489R1	16	50816345	50816345	Nonsense_Mutation	SNP	C	A	A	CYLD	c.1794C>A	p.Y598*
R18D6489R1	17	7578263	7578263	Nonsense_Mutation	SNP	G	A	A	TP53	c.586C>T	p.R196*
R18D6489R1	2	141004672	141004672	Missense_Mutation	SNP	G	A	A	LRP1B	c.13307C>T	p.S4436F
R18D6489R1	2	170070170	170070170	Missense_Mutation	SNP	G	A	A	LRP2	c.6037C>T	p.R2013C
R18D6489R1	3	134851591	134851591	Missense_Mutation	SNP	G	A	A	EPHB1	c.997G>A	p.V333I
R18D6489R1	-	-	-	Frame_Shift_Del	INS	-	-	-	PRKDC	c.12342del	p.N4115Tfs*48
R18D6500R1	1	204416690	204416690	Missense_Mutation	SNP	G	A	A	PIK3C2B	c.2363C>T	p.S788L
R18D6500R1	13	32893318	32893318	Missense_Mutation	SNP	G	A	A	BRCA2	c.172G>A	p.E58K
R18D6500R1	17	7578528	7578528	Missense_Mutation	SNP	A	T	T	TP53	c.402T>A	p.F134L
R18D6500R1	7	42005843	42005843	Missense_Mutation	SNP	G	A	A	GLI3	c.2828C>T	p.T943M
R18D6500R1	8	48826630	48826630	Splice_Site	SNP	A	G	G	PRKDC	c.2618-6T>C	-
R18D6500R1	X	63412907	63412907	Missense_Mutation	SNP	T	C	C	AMER1	c.260A>G	p.K87R
R18D6500R1	X	76938635	76938635	Missense_Mutation	SNP	C	T	T	ATRX	c.2113G>A	p.D705N
R18D6508R1	11	111957566	111957566	Splice_Site	SNP	C	T	T	SDHD	c.-66C>T	-
R18D6508R1	12	25398284	25398284	Missense_Mutation	SNP	C	G	G	KRAS	c.35G>C	p.G12A
R18D6508R1	16	23619201	23619201	Missense_Mutation	SNP	G	A	A	PALB2	c.3334C>T	p.P1112S
R18D6508R1	17	37868208	37868208	Missense_Mutation	SNP	C	A	A	ERBB2	c.929C>A	p.S310Y
R18D6508R1	18	48591918	48591918	Missense_Mutation	SNP	C	T	T	SMAD4	c.1081C>T	p.R361C
R18D6508R1	19	42776461	42776461	Nonsense_Mutation	SNP	G	T	T	CIC	c.526G>T	p.E176*
R18D6508R1	2	109388204	109388204	Missense_Mutation	SNP	C	A	A	RANBP2	c.7897C>A	p.L2633I
R18D6508R1	5	112176329	112176329	Nonsense_Mutation	SNP	C	T	T	APC	c.5038C>T	p.Q1680*
R18D6508R1	7	6026649	6026649	Missense_Mutation	SNP	C	T	T	PMS2	c.1747G>A	p.E583K
R18D6510R1	1	115256529	115256529	Missense_Mutation	SNP	T	A	A	NRAS	c.182A>T	p.Q61L
R18D6510R1	11	69514104	69514104	Missense_Mutation	SNP	C	T	T	FGF19	c.577G>A	p.E193K
R18D6510R1	12	46211585	46211585	Nonsense_Mutation	SNP	C	G	G	ARID2	c.551C>G	p.S184*
R18D6510R1	17	17124746	17124746	Missense_Mutation	SNP	G	C	C	FLCN	c.976C>G	p.L326V
R18D6510R1	17	56780658	56780658	Missense_Mutation	SNP	C	G	G	RAD51C	c.673C>G	p.L225V
R18D6510R1	19	15302774	15302774	Missense_Mutation	SNP	G	A	A	NOTCH3	c.676C>T	p.P226S
R18D6510R1	21	36164509	36164509	Missense_Mutation	SNP	C	T	T	RUNX1	c.1366G>A	p.E456K
R18D6510R1	22	41523488	41523488	Splice_Site	SNP	C	G	G	EP300	c.907-3C>G	-
R18D6510R1	3	178936091	178936091	Missense_Mutation	SNP	G	A	A	PIK3CA	c.1633G>A	p.E545K
R18D6510R1	3	178938934	178938934	Missense_Mutation	SNP	G	A	A	PIK3CA	c.2176G>A	p.E726K
R18D6510R1	3	185200173	185200173	Missense_Mutation	SNP	G	A	A	MAP3K13	c.2830G>A	p.D944N
R18D6510R1	4	187524726	187524726	Missense_Mutation	SNP	G	A	A	FAT1	c.10954C>T	p.P3652S
R18D6510R1	6	135521246	135521246	Missense_Mutation	SNP	G	A	A	MYB	c.1370G>A	p.R457K
R18D6510R1	7	81346668	81346668	Missense_Mutation	SNP	C	T	T	HGF	c.1285G>A	p.E429K
R18D6510R1	7	106513354	106513354	Missense_Mutation	SNP	C	T	T	PIK3CG	c.2258C>T	p.S753F
R18D6510R1	7	116339297	116339297	Missense_Mutation	SNP	G	C	C	MET	c.159G>C	p.Q53H
R18D6510R1	8	11615824	11615824	Missense_Mutation	SNP	C	G	G	GATA4	c.1169C>G	p.S390C
R18D6510R1	8	32620804	32620804	Nonsense_Mutation	SNP	C	G	G	NRG1	c.875C>G	p.S292*
R18D6510R1	8	48842522	48842522	Missense_Mutation	SNP	G	A	A	PRKDC	c.1943C>T	p.S648L
R18D6510R1	8	48847559	48847559	Splice_Site	SNP	C	G	G	PRKDC	c.1497+10G>C	-
R18D6510R1	9	80430659	80430659	Missense_Mutation	SNP	C	T	T	GNAAQ	c.349G>A	p.D117N
R18D6510R1	X	70339981	70339981	Missense_Mutation	SNP	G	A	A	MED12	c.514G>A	p.E172K
R18D6510R1	X	70347799	70347799	Nonsense_Mutation	SNP	C	G	G	MED12	c.3038C>G	p.S1013*

R18D6521R1		-	-	Frame_Shift_Del	INS	-	-	-	ARID1A	c.6384_6406del	p.Q2128Hfs*14
R18D6521R1	13	26923240	26923240	Missense_Mutation	SNP	T	C	C	CDK8	c.236T>C	p.I79T
R18D6521R1	14	95578516	95578516	Missense_Mutation	SNP	G	T	T	DICER1	c.2109C>A	p.H703Q
R18D6521R1	16	9857538	9857538	Missense_Mutation	SNP	C	T	T	GRIN2A	c.3863G>A	p.R1288H
R18D6521R1		-	-	Frame_Shift_Del	INS	-	-	-	TP53	C.868del	P.R290Afs*55
R18D6521R1	19	10599915	10599915	Missense_Mutation	SNP	C	T	T	KEAP1	c.1661G>A	p.R554Q
R18D6521R1	19	17953875	17953875	Missense_Mutation	SNP	T	A	A	JAK3	c.527A>T	p.E176V
R18D6521R1	2	47693793	47693793	Splice_Site	SNP	C	G	G	MSH2	c.1511-4C>G	-
R18D6521R1	2	141079628	141079628	Missense_Mutation	SNP	C	T	T	LRP1B	c.12544G>A	p.E4182K
R18D6521R1	2	141260649	141260649	Nonsense_Mutation	SNP	C	A	A	LRP1B	c.8545G>T	p.E2849*
R18D6521R1	3	41266137	41266137	Missense_Mutation	SNP	C	T	T	CTNNB1	c.134C>T	p.S45F
R18D6521R1	4	187524422	187524422	Missense_Mutation	SNP	G	T	T	FAT1	c.11258C>A	p.S3753Y
R18D6521R1	6	157256633	157256633	Missense_Mutation	SNP	C	A	A	ARID1B	c.1960C>A	p.Q654K
R18D6521R1	7	81388068	81388068	Missense_Mutation	SNP	T	G	G	HGF	c.307A>C	p.S103R
R18D6523R1	17	7578403	7578403	Missense_Mutation	SNP	C	T	T	TP53	c.527G>A	p.C176Y
R18D6523R1	17	37868208	37868208	Missense_Mutation	SNP	C	T	T	ERBB2	c.929C>T	p.S310F
R18D6523R1	17	56492790	56492790	Missense_Mutation	SNP	A	C	C	RNF43	c.149T>G	p.V50G
R18D6523R1		-	-	Frame_Shift_Ins	INS	-	-	-	TET2	c.2520dup	p.V841Sfs*5
R18D6523R1	9	21971035	21971035	Missense_Mutation	SNP	T	C	C	CDKN2A	c.323A>G	p.D108G
R18D6529R1	10	89717607	89717607	Splice_Site	SNP	C	G	G	PTEN	c.635-3C>G	-
R18D6529R1	11	119167693	119167693	Missense_Mutation	SNP	T	G	G	CBL	c.2102T>G	p.M701R
R18D6529R1	12	4383376	4383376	Missense_Mutation	SNP	G	C	C	CCND2	c.170G>C	p.R57T
R18D6529R1	12	46245858	46245858	Nonsense_Mutation	SNP	C	T	T	ARID2	3952C>T;3959C	[Q1318*;S1320L]
R18D6529R1	12	133238115	133238115	Missense_Mutation	SNP	C	G	G	POLE	c.2862G>C	p.K954N
R18D6529R1	13	32914890	32914890	Nonsense_Mutation	SNP	C	G	G	BRCA2	5398C>G;6425C	[S2133*;S2142C]
R18D6529R1	14	81422193	81422193	Missense_Mutation	SNP	C	T	T	TSNR	c.169C>T	p.L57L
R18D6529R1	16	89839697	89839697	Missense_Mutation	SNP	C	G	G	FANCA	c.1996G>C	p.D666H
R18D6529R1	17	7577082	7577082	Missense_Mutation	SNP	C	T	T	TP53	c.856G>A	p.E286K
R18D6529R1		-	-	Frame_Shift_Del	INS	-	-	-	ROCK2	c.2855_2874del	p.E952Afs*14
R18D6529R1	3	30715684	30715684	Missense_Mutation	SNP	T	G	G	TGFB2	c.1342T>G	p.Y448D
R18D6529R1	4	1805458	1805458	Missense_Mutation	SNP	C	G	G	FGFR3	c.970C>G	p.L324V
R18D6529R1	4	126373483	126373483	Missense_Mutation	SNP	A	T	T	FAT4	c.11312A>T	p.N3771I
R18D6529R1	4	153244293	153244293	Nonsense_Mutation	SNP	T	A	A	FBXW7	c.1864A>T	p.B622*
R18D6529R1	7	117199602	117199602	Missense_Mutation	SNP	C	G	G	CFTR	c.1477C>G	p.Q493E
R18D6529R1	7	141414215	141414215	Splice_Site	SNP	C	T	T	WEE2	c.539+10C>T	-
R18D6529R1	7	142651602	142651602	Missense_Mutation	SNP	C	G	G	KEL	c.685G>C	p.E229Q
R18D6531R1	14	45606403	45606403	Missense_Mutation	SNP	G	C	C	FANCM	c.640G>C	p.D214H
R18D6531R1	7	18688315	18688315	Splice_Site	SNP	C	T	T	HDAC9	c.1458+9C>T	-
R18D6531R1	7	42065851	42065851	Missense_Mutation	SNP	G	T	T	GLI3	c.1189C>A	p.P397T
R18D6531R1	X	66931262	66931262	Missense_Mutation	SNP	T	G	G	AR	c.1904T>G	p.L635R
R18D6542R1	1	16255703	16255703	Missense_Mutation	SNP	G	C	C	SPEN	c.2968G>C	p.D990H
R18D6542R1	1	16255796	16255796	Missense_Mutation	SNP	G	C	C	SPEN	c.3061G>C	p.D1021H
R18D6542R1	1	16255841	16255841	Missense_Mutation	SNP	G	C	C	SPEN	c.3106G>C	p.E1036Q
R18D6542R1	1	16458218	16458218	Missense_Mutation	SNP	C	T	T	EPHA2	c.2473G>A	p.E825K
R18D6542R1	11	108175420	108175420	Nonsense_Mutation	SNP	C	T	T	ATM	c.5515C>T	p.Q1839*
R18D6542R1	11	119170447	119170447	Missense_Mutation	SNP	C	T	T	CBL	c.2677C>T	p.R893W
R18D6542R1	17	7578191	7578191	Missense_Mutation	SNP	A	T	T	TP53	c.658T>A	p.Y220N
R18D6542R1	19	1220629	1220629	Missense_Mutation	SNP	C	T	T	STK11	c.647C>T	p.S216F
R18D6542R1	19	1220701	1220701	Missense_Mutation	SNP	C	T	T	STK11	c.719C>T	p.S240L
R18D6542R1	19	42795328	42795328	Missense_Mutation	SNP	A	G	G	CIC	c.2408A>G	p.N803S
R18D6542R1	2	178098960	178098960	Missense_Mutation	SNP	C	G	G	NFE2L2	c.85G>C	p.D29H
R18D6542R1	4	88957483	88957483	Missense_Mutation	SNP	C	T	T	PKD2	c.821C>T	p.S274F
R18D6542R1	4	187524189	187524189	Splice_Site	SNP	C	G	G	FAT1	c.11351-1G>C	-
R18D6542R1	7	140477831	140477831	Nonsense_Mutation	SNP	G	A	A	BRAF	c.1477C>T	p.Q493*
R18D6542R1	8	48856408	48856408	Splice_Site	SNP	C	G	G	PRKDC	c.808+5G>C	-
R18D6543R1	17	7574018	7574018	Missense_Mutation	SNP	G	A	A	TP53	c.1009C>T	p.R337C
R18D6543R1		-	-	Frame_Shift_Del	INS	-	-	-	KDM6A	c.2512_2515del	p.N839Vfs*27
R18D6543R1	X	66766006	66766006	Missense_Mutation	SNP	G	A	A	AR	c.1018G>A	p.E340K
R18D6640R1		-	-	Frame_Shift_Del	INS	-	-	-	TP53	c.870_876del	p.K291Gfs*52
R18D6640R1	18	48593391	48593391	Nonsense_Mutation	SNP	T	A	A	SMAD4	c.1142T>A	p.L381*
R18D6641R1	1	65312335	65312335	Missense_Mutation	SNP	C	G	G	JAK1	c.1984G>C	p.E662Q
R18D6641R1	10	114912095	114912095	Missense_Mutation	SNP	C	T	T	TCF7L2	c.1096C>T	p.H366Y
R18D6641R1	12	56491645	56491645	Missense_Mutation	SNP	G	T	T	ERBB3	c.2537G>T	p.S846I
R18D6641R1	17	7577085	7577085	Missense_Mutation	SNP	C	T	T	TP53	c.853G>A	p.E285K
R18D6641R1	17	41244447	41244447	Missense_Mutation	SNP	T	C	C	BRCA1	c.3101A>G	p.N1034S
R18D6641R1	18	48584497	48584497	Nonsense_Mutation	SNP	C	T	T	SMAD4	c.670C>T	p.Q224*
R18D6641R1	2	141143543	141143543	Missense_Mutation	SNP	T	C	C	LRP1B	c.10450A>G	p.K3484E
R18D6641R1	3	185183588	185183588	Missense_Mutation	SNP	A	G	G	MAP3K13	c.1442A>G	p.N481S
R18D6641R1	7	77764470	77764470	Missense_Mutation	SNP	C	T	T	MAGI2	c.2899G>A	p.A967T
R18D6641R1	7	142643377	142643377	Missense_Mutation	SNP	C	T	T	KEL	c.1231G>A	p.V411M
R18D6641R1	8	139153458	139153458	Missense_Mutation	SNP	C	A	A	FAM135B	c.3773G>T	p.S1258I
R18D6641R1	9	21971108	21971108	Missense_Mutation	SNP	C	T	T	CDKN2A	c.250G>A	p.D84N
R18D6641R1	X	66905905	66905905	Nonsense_Mutation	SNP	C	T	T	AR	c.1822C>T	p.R608*
R18D6641R1	X	70602478	70602478	Missense_Mutation	SNP	G	T	T	TAF1	c.1690G>T	p.G564W
R18D6643R1	11	108143267	108143267	Missense_Mutation	SNP	C	G	G	ATM	c.3086C>G	p.T1029R
R18D6643R1	12	25398281	25398281	Missense_Mutation	SNP	C	T	T	KRAS	c.38G>A	p.G13D
R18D6643R1	16	396649	396649	Missense_Mutation	SNP	T	G	G	AXIN1	c.377A>C	p.K126T
R18D6643R1	16	89837054	89837054	Splice_Site	SNP	C	G	G	FANCA	c.2152-12G>C	-
R18D6643R1	17	7578190	7578190	Missense_Mutation	SNP	T	C	C	TP53	c.659A>G	p.Y220C
R18D6643R1	18	48604821	48604821	Missense_Mutation	SNP	C	T	T	SMAD4	c.1643C>T	p.P548L
R18D6643R1	3	47164342	47164342	Nonsense_Mutation	SNP	G	C	C	SETD2	c.1784C>G	p.S595*
R18D6643R1	7	2984130	2984130	Missense_Mutation	SNP	C	T	T	CARD11	c.400G>A	p.E134K
R18D6643R1	7	86415650	86415650	Missense_Mutation	SNP	A	C	C	GRM3	c.542A>C	p.K181T
R18D6643R1	7	127714563	127714563	Missense_Mutation	SNP	G	A	A	SDN1	c.1789G>A	p.E597K
R18D6643R1	9	21971111	21971111	Missense_Mutation	SNP	G	A	A	CDKN2A	c.247C>T	p.H83Y
R18D6713R1		-	-	In_Frame_Del	INS	-	-	-	ACVR1B	c.323_331del	p.108_111del
R18D6713R1	12	57578943	57578943	Missense_Mutation	SNP	G	A	A	LRP1	c.6418G>A	p.V2140I
R18D6713R1	17	7578266	7578266	Missense_Mutation	SNP	T	A	A	TP53	c.583A>T	p.I195F
R18D6713R1		-	-	Frame_Shift_Del	INS	-	-	-	TP53	C.277del	P.L93Cfs*30
R18D6713R1	2	141115559	141115559	Missense_Mutation	SNP	C	T	T	LRP1B	c.11384G>A	p.G3795E
R18D6713R1	20	57429235	57429235	Missense_Mutation	SNP	C	T	T	GNAS	c.728C>T	p.P243L
R18D6713R1	3	134670657	134670657	Missense_Mutation	SNP	C	T	T	EPHB1	c.568C>T	p.R190C
R18D6713R1	4	126370607	126370607	Missense_Mutation	SNP	G	A	A	FAT4	c.8436G>A	p.M2812I
R18D6713R1	4	187549458	187549458	Missense_Mutation	SNP	C	A	A	FAT1	c.4660G>T	p.D1554Y
R18D6713R1	6	36651988	36651988	Missense_Mutation	SNP	T	C	C	CDKN1A	c.110T>C	p.L37P
R18D6713R1	7	92354942	92354942	Missense_Mutation	SNP	C	A	A	CDK6	c.535G>T	p.V179L
R18D6713R1	7	141427152	141427152	Missense_Mutation	SNP	G	A	A	WEE2	c.1441G>A	p.A481T
R18D6713R1		-	-	Missense_Mutation	SNP	-	-	-	EZH2	024_1025delins	p.A342I

R18D6713R1	8	139380195	139380195	Missense_Mutation	SNP	G	A	A	FAM135B	c.32C>T	p.S11L
R18D6714R1	2	209113112	209113112	Missense_Mutation	SNP	C	A	A	IDH1	c.395G>T	p.R132L
R18D6714R1	3	52442594	52442594	Nonsense_Mutation	SNP	T	A	A	BAP1	c.151A>T	p.K51*
R18D6831R1	1	65330568	65330568	Missense_Mutation	SNP	G	A	A	JAK1	c.1078C>T	p.R360W
R18D6831R1	12	25398284	25398284	Missense_Mutation	SNP	C	T	T	KRAS	c.35G>A	p.G12D
R18D6831R1	-	-	-	In_Frame_Del	INS	-	-	-	TP53	c.844_849del	p.R282_R283del
R18D6831R1	3	185198046	185198046	Missense_Mutation	SNP	A	G	G	MAP3K13	c.2528A>G	p.Q843R
R18D6831R1	4	126372500	126372500	Missense_Mutation	SNP	C	A	A	FAT4	c.10329C>A	p.F3443L
R18D6831R1	-	-	-	Frame_Shift_Ins	INS	-	-	-	CDKN2A	c.225_243dup	p.V82Rfs*44
R18D6917S2	1	16202810	16202810	Missense_Mutation	SNP	C	T	T	SPEN	c.518C>T	p.P173L
R18D6917S2	10	43597849	43597849	Missense_Mutation	SNP	C	T	T	RET	c.397C>T	p.R133C
R18D6917S2	12	56482369	56482369	Missense_Mutation	SNP	C	G	G	ERBB3	c.917C>G	p.P306R
R18D6917S2	17	7577156	7577156	Splice_Site	SNP	C	A	A	TP53	c.783-1G>T	-
R18D6917S2	4	153247288	153247288	Missense_Mutation	SNP	C	T	T	FBXW7	c.1514G>A	p.R505H
R18D6917S2	8	68950401	68950401	Missense_Mutation	SNP	A	C	C	PREX2	c.713A>C	p.N238T
R18E7186R1	11	61562846	61562846	Missense_Mutation	SNP	G	A	A	FEN1	c.13G>A	p.G55
R18E7186R1	17	7578542	7578542	Missense_Mutation	SNP	G	C	C	TP53	c.388C>G	p.L130V
R18E7186R1	2	141128790	141128790	Missense_Mutation	SNP	C	G	G	LRP1B	c.10833G>C	p.L3611F
R18E7186R1	3	89390090	89390090	Missense_Mutation	SNP	C	T	T	EPHA3	c.839C>T	p.A280V
R18E7186R1	4	153249385	153249385	Missense_Mutation	SNP	G	A	A	FBXW7	c.1393C>T	p.R465C
R18E7186R1	7	41739911	41739911	Missense_Mutation	SNP	G	T	T	INHBA	c.62C>A	p.S21Y
R18E7186R1	7	151873435	151873435	Nonsense_Mutation	SNP	G	A	A	KMT2C	c.9103C>T	p.Q3035*
R18F8364R1	13	28611311	28611311	Splice_Site	SNP	A	T	T	FLT3	c.1309+11T>A	-
R18F8364R1	16	68844245	68844245	Splice_Site	SNP	G	A	A	CDH1	c.832+1G>A	-
R18F8364R1	19	10602494	10602494	Missense_Mutation	SNP	G	A	A	KEAP1	c.1084C>T	p.R362W
R18F8364R1	3	178916890	178916890	Missense_Mutation	SNP	C	T	T	PIK3CA	c.277C>T	p.R93W
R18F8364R1	8	11615801	11615801	Splice_Site	SNP	G	T	T	GATA4	c.1147-1G>T	-
R18F8364R1	X	15574239	15574239	Missense_Mutation	SNP	T	C	C	BMX	c.1997T>C	p.I666T
R18F8364R1	X	47428427	47428427	Missense_Mutation	SNP	C	G	G	ARAF	c.1295C>G	p.S432C
R18F8368R1	1	8073694	8073694	Missense_Mutation	SNP	C	T	T	ERRF1	c.965G>A	p.R322K
R18F8368R1	11	92531664	92531664	Missense_Mutation	SNP	A	T	T	FAT3	c.5485A>T	p.S1829C
R18F8368R1	15	93536086	93536086	Splice_Site	SNP	C	T	T	CHD2	c.3456-3C>T	-
R18F8368R1	16	3820729	3820729	Missense_Mutation	SNP	T	A	A	CREBBP	c.2722A>T	p.S908C
R18F8368R1	17	7577081	7577081	Missense_Mutation	SNP	T	A	A	TP53	c.857A>T	p.E286V
R18F8368R1	3	156396271	156396271	Missense_Mutation	SNP	C	G	G	TIPARP	c.785C>G	p.T262S
R18F8368R1	4	110897215	110897215	Missense_Mutation	SNP	C	G	G	EGF	c.1877C>G	p.S626C
R18F8368R1	4	143114256	143114256	Missense_Mutation	SNP	C	G	G	INPP4B	c.1165G>C	p.F389Q
R18F8368R1	6	117709028	117709028	Missense_Mutation	SNP	C	T	T	ROS1	c.1929G>A	p.M643I
R18F8368R1	7	127528043	127528043	Missense_Mutation	SNP	G	C	C	SND1	c.1432G>C	p.E478Q
R18F8368R1	7	128845240	128845240	Missense_Mutation	SNP	C	T	T	SMO	c.734C>T	p.T245M
R18F8368R1	7	151919153	151919153	Splice_Site	SNP	T	A	A	KMT2C	c.3434-2A>T	-
R18F8368R1	7	151960145	151960145	Nonsense_Mutation	SNP	G	A	A	KMT2C	c.1255C>T	p.Q419*
R18F8368R1	X	66943532	66943532	Missense_Mutation	SNP	C	T	T	AR	c.2612C>T	p.A871V
R18F8368R1	X	70602466	70602466	Missense_Mutation	SNP	C	G	G	TAF1	c.1678C>G	p.R560G
R18F8384R1	1	97564154	97564154	Missense_Mutation	SNP	C	T	T	DPYD	c.2657G>A	p.R886H
R18F8384R1	-	-	-	Frame_Shift_Del	INS	-	-	-	HRAS	C.169_188del	P.S57Mfs*2
R18F8384R1	12	52385761	52385761	Nonsense_Mutation	SNP	G	A	A	ACVR1B	c.1499G>A	p.W500*
R18F8384R1	17	7577523	7577523	Missense_Mutation	SNP	G	T	T	TP53	c.758C>A	p.T253N
R18F8384R1	-	-	-	Frame_Shift_Del	INS	-	-	-	TP53	.726_730delins	p.M243Afs*3
R18F8384R1	2	109384335	109384335	Missense_Mutation	SNP	C	A	A	RANBP2	c.7340C>A	p.S2447Y
R18F8384R1	4	153259070	153259070	Missense_Mutation	SNP	T	C	C	FBXW7	c.745A>G	p.K249E
R18F8384R1	9	21971138	21971138	Missense_Mutation	SNP	C	T	T	CDKN2A	c.220G>A	p.D74N
R18F8385R1	7	151877808	151877808	Missense_Mutation	SNP	C	G	G	KMT2C	c.7137G>C	p.E2379D
R18F8390R1	1	11194405	11194405	Splice_Site	SNP	C	T	T	MTOR	c.5246+3G>A	-
R18F8390R1	1	158613182	158613182	Missense_Mutation	SNP	C	T	T	SPTA1	c.4372G>A	p.E1458K
R18F8390R1	12	46230533	46230533	Nonsense_Mutation	SNP	C	G	G	ARID2	c.782C>G	p.S261*
R18F8390R1	12	49420253	49420253	Missense_Mutation	SNP	C	A	A	KMT2D	c.15496G>T	p.A5166S
R18F8390R1	12	49422953	49422953	Missense_Mutation	SNP	G	C	C	KMT2D	c.14142C>G	p.I4714M
R18F8390R1	12	133252721	133252721	Missense_Mutation	SNP	C	T	T	POLE	c.979G>A	p.E327K
R18F8390R1	17	7577085	7577085	Missense_Mutation	SNP	C	T	T	TP53	c.853G>A	p.E285K
R18F8390R1	2	109347797	109347797	Missense_Mutation	SNP	C	G	G	RANBP2	c.272C>G	p.P91R
R18F8390R1	5	56111522	56111522	Missense_Mutation	SNP	C	T	T	MAP3K1	c.122C>T	p.A41V
R18F8390R1	7	142658153	142658153	Missense_Mutation	SNP	G	A	A	KEL	c.262C>T	p.H88Y
R18F8390R1	7	151919152	151919152	Splice_Site	SNP	C	G	G	KMT2C	c.3434-1G>C	-
R18F8390R1	8	37698769	37698769	Missense_Mutation	SNP	G	T	T	ADGRA2	c.2913G>T	p.E971D
R18F8390R1	9	133710845	133710845	Missense_Mutation	SNP	C	G	G	ABL1	c.12C>G	p.I4M
R18F8410R1	1	27092775	27092775	Missense_Mutation	SNP	A	T	T	ARID1A	c.2796A>T	p.Q932H
R18F8410R1	1	158647604	158647604	Missense_Mutation	SNP	T	A	A	SPTA1	c.833A>T	p.Q278L
R18F8410R1	10	84118611	84118611	Missense_Mutation	SNP	C	T	T	NRG3	c.940C>T	p.H314Y
R18F8410R1	16	56878455	56878455	Missense_Mutation	SNP	G	T	T	NUP93	c.2394G>T	p.M798I
R18F8410R1	17	7578416	7578416	Missense_Mutation	SNP	C	A	A	TP53	c.514G>T	p.V172F
R18F8410R1	3	195594503	195594503	Missense_Mutation	SNP	C	T	T	TNK2	c.2621G>A	p.R874H
R18F8410R1	7	81346572	81346572	Missense_Mutation	SNP	A	T	T	HGF	c.1381T>A	p.W461R
R18F8410R1	9	5066798	5066798	Splice_Site	SNP	G	A	A	JAK2	c.1326+9G>A	-
R18F8428R1	17	7577094	7577094	Missense_Mutation	SNP	G	A	A	TP53	c.844C>T	p.R282W
R18F8428R1	3	178921552	178921552	Missense_Mutation	SNP	A	C	C	PIK3CA	c.1034A>C	p.N345T
R18F8428R1	8	139323096	139323096	Missense_Mutation	SNP	C	T	T	FAM135B	c.145G>A	p.A49T
R18F8428R1	X	76778767	76778767	Missense_Mutation	SNP	C	G	G	ATRX	c.6812G>C	p.R2271T
R18F8429R1	1	27094291	27094291	Missense_Mutation	SNP	C	A	A	ARID1A	c.2999C>A	p.S1000Y
R18F8429R1	15	88727469	88727469	Missense_Mutation	SNP	C	T	T	NTRK3	c.310G>A	p.G104R
R18F8429R1	22	41566521	41566521	Missense_Mutation	SNP	G	C	C	EP300	c.4398G>C	p.W1466C
R18F8429R1	3	178952085	178952085	Missense_Mutation	SNP	A	G	G	PIK3CA	c.3140A>G	p.H1047R
R18F8432R1	-	-	-	Frame_Shift_Del	INS	-	-	-	PTEN	c.416_419del	p.L139Yfs*7
R18F8432R1	13	110437226	110437226	Missense_Mutation	SNP	G	C	C	IRS2	c.1175C>G	p.P392R
R18F8432R1	17	7578437	7578437	Nonsense_Mutation	SNP	G	A	A	TP53	c.493C>T	p.Q165*
R18F8432R1	-	-	-	In_Frame_Ins	INS	-	-	-	PREX2	c.2731dup	p.R911Kfs*17
R18F8432R1	9	98209213	98209213	Missense_Mutation	SNP	C	A	A	PTCH1	c.4325G>T	p.R1442L
R18F8433R1	1	27106720	27106720	Missense_Mutation	SNP	G	A	A	ARID1A	c.6331G>A	p.V211I
R18F8433R1	1	110459981	110459981	Missense_Mutation	SNP	C	T	T	CSF1	c.292C>T	p.R98C
R18F8433R1	14	105246551	105246551	Missense_Mutation	SNP	C	T	T	AKT1	c.49G>A	p.E17K
R18F8433R1	16	81969884	81969884	Missense_Mutation	SNP	G	A	A	PLCG2	c.2953G>A	p.V985I
R18F8433R1	16	89862356	89862356	Missense_Mutation	SNP	G	A	A	FANCA	c.964C>T	p.H322Y
R18F8433R1	17	7578443	7578443	Missense_Mutation	SNP	A	C	C	TP53	c.487T>G	p.Y163D
R18F8433R1	2	141093274	141093274	Missense_Mutation	SNP	T	G	G	LRP1B	c.12026A>C	p.N4009T
R18F8433R1	2	198265062	198265062	Missense_Mutation	SNP	G	A	A	SF3B1	c.2815C>T	p.R939C
R18F8433R1	3	70014337	70014337	Missense_Mutation	SNP	G	A	A	MITF	c.1198G>A	p.A400T
R18F8433R1	6	93979375	93979375	Nonsense_Mutation	SNP	G	A	A	EPHA7	c.1453C>T	p.Q485*
R18F8442R1	11	92616460	92616460	Missense_Mutation	SNP	G	A	A	FAT3	c.12838G>A	p.V4280M

R18F8442R1		-	-	Frame_Shift_Del	INS	-	-	-	TP53	C.267del	P.S90Pfs*33
R18F8442R1	2	178098957	178098957	Missense_Mutation	SNP	G	A	A	NFE2L2	c.88C>T	p.L30F
R18F8442R1	3	178927458	178927458	Missense_Mutation	SNP	C	G	G	PIK3CA	c.1221C>G	p.C407W
R18F8442R1	3	178951979	178951979	Missense_Mutation	SNP	G	C	C	PIK3CA	c.3034G>C	p.E1012Q
R18F8442R1	4	126241650	126241650	Missense_Mutation	SNP	A	G	G	FAT4	c.4084A>G	p.T1362A
R18F8442R1		-	-	Frame_Shift_Del	INS	-	-	-	RBM10	c.485del	p.M162Sfs*104
R18F8445R1	12	46243401	46243401	Missense_Mutation	SNP	A	G	G	ARID2	c.1754A>G	p.D585G
R18F8445R1	17	7578461	7578461	Missense_Mutation	SNP	C	A	A	TP53	c.469G>T	p.V157F
R18F8445R1	22	29696116	29696116	Nonsense_Mutation	SNP	G	T	T	EWSR1	c.1936G>T	p.E646*
R18F8636M2		-	-	In_Frame_Del	INS	-	-	-	EPHA2	c.1715_1738del	p.D573_E580del
R18F8636M2	1	16462239	16462239	Missense_Mutation	SNP	G	A	A	EPHA2	c.1339C>T	p.R447C
R18F8636M2		-	-	In_Frame_Del	INS	-	-	-	ARID1A	c.6177_6182del	p.E2059_L2061delinsK
R18F8636M2		-	-	Frame_Shift_Ins	INS	-	-	-	KMT2D	c.4168dup	p.A1390Gfs*42
R18F8636M2	13	32914082	32914082	Missense_Mutation	SNP	G	A	A	BRCA2	c.5590G>A	p.D1864N
R18F8636M2	2	212812269	212812269	Missense_Mutation	SNP	G	A	A	ERBB4	c.307C>T	p.R103C
R18F8636M2	3	37067240	37067240	Missense_Mutation	SNP	T	A	A	MLH1	c.1151T>A	p.V384D
R18F8636M2	3	38182641	38182641	Missense_Mutation	SNP	T	C	C	MYD88	c.818T>C	p.L273P
R18F8636M2	4	187629096	187629096	Missense_Mutation	SNP	G	C	C	FAT1	c.1886C>G	p.S629W
R18F8636M2	7	18629980	18629980	Missense_Mutation	SNP	A	G	G	HDAC9	c.277A>G	p.I93V
R18F8636M2	7	140453154	140453154	Missense_Mutation	SNP	T	C	C	BRAF	c.1781A>G	p.D594G
R18F8636M2	7	141408627	141408627	Missense_Mutation	SNP	G	C	C	WEE2	c.69G>C	p.E23D
R18F8636M2	8	92982876	92982876	Splice_Site	SNP	G	C	C	RUNX1T1	c.1428+10C>G	-
R18F8636M2	9	5029776	5029776	Splice_Site	SNP	T	C	C	JAK2	c.227-7T>C	-
R18G9202R1	13	28602354	28602354	Missense_Mutation	SNP	C	T	T	FLT3	c.2014G>A	p.E672K
R18G9202R1	17	7577538	7577538	Missense_Mutation	SNP	C	T	T	TP53	c.743G>A	p.R248Q
R18G9202R1	17	41622708	41622708	Missense_Mutation	SNP	C	T	T	ETV4	c.88G>A	p.E30K
R18G9202R1	20	57484421	57484421	Missense_Mutation	SNP	G	A	A	GNAS	c.602G>A	p.R201H
R18G9202R1		-	-	Frame_Shift_Del	INS	-	-	-	CDKN2A	c.52_83del	p.T18Afs*15
R18G9202R1	X	47040995	47040995	Nonsense_Mutation	SNP	C	T	T	RBM10	c.1525C>T	p.Q509*
R18G9203R1	10	70406465	70406465	Nonsense_Mutation	SNP	G	T	T	TET1	c.3979G>T	p.T1327*
R18G9203R1	22	38379425	38379425	Missense_Mutation	SNP	C	T	T	SOX10	c.367G>A	p.A123T
R18G9203R1	4	187516839	187516839	Splice_Site	SNP	T	A	A	FAT1	c.13138+4A>T	-
R18G9203R1	9	139390917	139390917	Missense_Mutation	SNP	G	T	T	NOTCH1	c.7274C>A	p.A2425D
R18G9211R1	1	27106354	27106354	Nonsense_Mutation	SNP	C	T	T	ARID1A	c.5965C>T	p.R1989*
R18G9211R1	1	156844729	156844729	Missense_Mutation	SNP	C	T	T	NTRK1	c.1265C>T	p.A422V
R18G9211R1	10	123239466	123239466	Missense_Mutation	SNP	A	T	T	FGFR2	c.2371T>A	p.S791T
R18G9211R1	12	25398281	25398281	Missense_Mutation	SNP	C	T	T	KRAS	c.38G>A	p.G13D
R18G9211R1	17	7577124	7577124	Missense_Mutation	SNP	C	T	T	TP53	c.814G>A	p.V272M
R18G9211R1	17	41245859	41245859	Missense_Mutation	SNP	C	T	T	BRCA1	c.1689G>A	p.Q563Q
R18G9211R1		-	-	Frame_Shift_Ins	INS	-	-	-	SMAD4	c.692dup	p.S232Qfs*3
R18G9211R1	18	48593520	48593520	Missense_Mutation	SNP	A	T	T	SMAD4	c.1271A>T	p.D424V
R18G9211R1	19	33793251	33793251	Missense_Mutation	SNP	G	C	C	CEBPA	c.70C>G	p.H24D
R18G9211R1	7	151859696	151859696	Missense_Mutation	SNP	C	T	T	KMT2C	c.10966G>A	p.A3656T
R18G9211R1	X	123229283	123229283	Missense_Mutation	SNP	C	T	T	STAG2	c.3656C>T	p.S1219L
R18G9220R1	1	16475487	16475487	Missense_Mutation	SNP	C	T	T	EPHA2	c.209G>A	p.C70Y
R18G9220R1		-	-	Frame_Shift_Del	INS	-	-	-	ARID1A	c.836_873del	p.P279Hfs*108
R18G9220R1		-	-	Frame_Shift_Ins	INS	-	-	-	BRCA2	c.8021dup	p.I2675Dfs*6
R18G9220R1	17	78831689	78831689	Missense_Mutation	SNP	G	T	T	RPTOR	c.1498G>T	p.A500S
R18G9220R1	18	48591856	48591856	Missense_Mutation	SNP	A	C	C	SMAD4	c.1019A>C	p.K340T
R18G9220R1	3	191888367	191888367	Missense_Mutation	SNP	G	T	T	FGF12	c.307C>A	p.R103S
R18G9220R1	4	55972050	55972050	Missense_Mutation	SNP	C	T	T	KDR	c.1594G>A	p.A532T
R18G9220R1	X	47044604	47044604	Splice_Site	SNP	G	T	T	RBM10	c.2100+1G>T	-
R18G9241R1		-	-	In_Frame_Del	INS	-	-	-	ARID2	c.3437_3445del	p.S1146*
R18G9241R1	2	112722842	112722842	Missense_Mutation	SNP	A	T	T	MERTK	c.832A>T	p.I278F
R18G9241R1		-	-	Frame_Shift_Del	INS	-	-	-	ASXL1	c.1797del	p.T600Pfs*103
R18G9243R1		-	-	Frame_Shift_Ins	INS	-	-	-	SMARCD1	c.207_210dup	p.P71Dfs*61
R18G9243R1		-	-	In_Frame_Ins	INS	-	-	-	TP53	c.155_158dup	p.W53*
R18G9243R1	17	38559194	38559194	Missense_Mutation	SNP	T	C	C	TOP2A	c.2396A>G	p.D799G
R18G9244R1	12	115114110	115114110	Splice_Site	SNP	T	C	C	TBX3	c.1099+8A>G	-
R18G9244R1	2	74320789	74320789	Missense_Mutation	SNP	C	T	T	TET3	c.3263C>T	p.T1088I
R18G9244R1	2	170062706	170062706	Splice_Site	SNP	C	G	G	LRP2	c.7391-8G>C	p.C7391-8G>C
R18G9244R1	7	77756686	77756686	Missense_Mutation	SNP	C	T	T	MAGI2	c.3251G>A	p.R1084Q
R18G9244R1	7	117254762	117254762	Missense_Mutation	SNP	A	T	T	CFTR	c.3463A>T	p.S1155C
R18G9244R1	8	37691533	37691533	Nonsense_Mutation	SNP	G	T	T	ADGRA2	c.1495G>T	p.E499*
R18G9244R1		-	-	Missense_Mutation	SNP	-	-	-	RUNX1T1	c.183_185del	p.V62del
R18G9244R1	9	5534820	5534820	Missense_Mutation	SNP	T	C	C	PDCD1LG2	c.131T>C	p.F44S
R18G9245R1	1	158605742	158605742	Missense_Mutation	SNP	A	G	G	SPTA1	c.5393T>C	p.V1798A
R18G9245R1	11	92534385	92534385	Nonsense_Mutation	SNP	C	T	T	FAT3	c.8206C>A	p.Q2736*
R18G9245R1	12	56481922	56481922	Missense_Mutation	SNP	G	A	A	ERBB3	c.850G>A	p.G284R
R18G9245R1	17	7577538	7577538	Missense_Mutation	SNP	C	T	T	TP53	c.743G>A	p.R248Q
R18G9245R1		-	-	Frame_Shift_Del	INS	-	-	-	MAD2K2A	c.70_86del	p.V24Rfs*11
R18G9245R1	19	2226538	2226538	Missense_Mutation	SNP	A	C	C	DOT1L	c.4018A>C	p.K1340Q
R18G9245R1	9	5069196	5069196	Missense_Mutation	SNP	C	A	A	JAK2	c.1501C>A	p.P501T
R18G9245R1	X	44733234	44733234	Splice_Site	SNP	G	T	T	KDM6A	c.225+1G>T	-
R18G9249R1	1	32741220	32741220	Missense_Mutation	SNP	C	A	A	LCK	c.428C>A	p.A143E
R18G9249R1	13	28891687	28891687	Missense_Mutation	SNP	G	A	A	FLT1	c.3334C>T	p.R1112C
R18G9249R1	16	9862896	9862896	Nonsense_Mutation	SNP	C	A	A	GRIN2A	c.2407G>T	p.E803*
R18G9249R1		-	-	Frame_Shift_Del	INS	-	-	-	TP53	c.997del	p.R333Vfs*12
R18G9249R1	2	48030799	48030799	Missense_Mutation	SNP	G	A	A	MSH6	c.3413G>A	p.G1138E
R18G9249R1	7	127714681	127714681	Missense_Mutation	SNP	G	A	A	SND1	c.1907G>A	p.R636H
R18G9249R1	7	151880109	151880109	Missense_Mutation	SNP	G	T	T	KMT2C	c.5215C>A	p.P1739T
R18G9249R1	8	32463111	32463111	Missense_Mutation	SNP	C	T	T	NRG1	c.955C>T	p.L319L
R18G9250R1	1	51436086	51436086	Missense_Mutation	SNP	G	T	T	CDKN2C	c.46G>T	p.G16W
R18G9250R1	12	1039231	1039231	Missense_Mutation	SNP	G	A	A	RAD52	c.266C>T	p.T89M
R18G9250R1	12	56478854	56478854	Missense_Mutation	SNP	G	T	T	ERBB3	c.310G>T	p.V104L
R18G9250R1	17	7577121	7577121	Missense_Mutation	SNP	G	A	A	TP53	c.817C>T	p.R273C
R18G9250R1	17	37879658	37879658	Missense_Mutation	SNP	G	A	A	ERBB2	c.2033G>A	p.R678Q
R18G9250R1		-	-	Frame_Shift_Ins	INS	-	-	-	MSH6	c.2548dup	p.Y850Lfs*8
R18G9250R1	2	234668955	234668955	Missense_Mutation	SNP	G	A	A	UGT1A1	c.22G>A	p.G8R
R18G9250R1	3	52668619	52668619	Nonsense_Mutation	SNP	G	A	A	PBRM1	c.1300C>T	p.R434*
R18G9250R1	6	30866038	30866038	Missense_Mutation	SNP	G	A	A	DDR1	c.2294G>A	p.R765Q
R18G9250R1		-	-	Frame_Shift_Del	INS	-	-	-	MAGI2	c.1243del	p.R415Gfs*6
R18G9250R1		-	-	Frame_Shift_Del	INS	-	-	-	PRKDC	c.3179del	p.F1060Sfs*46
R18G9250R1	X	47044541	47044541	Nonsense_Mutation	SNP	C	T	T	RBM10	c.2038C>T	p.R680*
R18G9251R1		-	-	Frame_Shift_Del	INS	-	-	-	SRC	c.1560_1573del	p.E520Dfs*51
R18G9251R1		-	-	Frame_Shift_Del	INS	-	-	-	LZTR1	c.2412del	p.K805Sfs*8
R18G9255R1	11	92600168	92600168	Missense_Mutation	SNP	C	T	T	FAT3	c.11920C>T	p.R3974W
R18G9255R1	17	7578190	7578190	Missense_Mutation	SNP	T	C	C	TP53	c.659A>G	p.Y220C

R18G9255R1	17	7579359	7579359	Missense_Mutation	SNP	G	A	A	TP53	c.328C>T	p.R110C
R18G9255R1	17	37619346	37619346	Missense_Mutation	SNP	C	G	G	CDK12	c.1022C>G	p.S341C
R18G9255R1	18	42530035	42530035	Missense_Mutation	SNP	C	A	A	SETBP1	c.730G>A	p.E244K
R18G9255R1	20	31016158	31016158	Missense_Mutation	SNP	C	A	A	ASXL1	c.404C>A	p.S135Y
R18G9255R1	3	89259506	89259506	Missense_Mutation	SNP	C	G	G	EPHA3	c.650C>G	p.P217R
R18G9255R1	8	48748975	48748975	Nonsense_Mutation	SNP	G	C	C	PRKDC	c.7874C>G	p.S2625*
R18G9255R1	8	48749017	48749017	Missense_Mutation	SNP	G	A	A	PRKDC	c.7832C>T	p.S2611F
R18G9257R1	11	108153578	108153578	Missense_Mutation	SNP	A	C	C	ATM	c.3718A>C	p.N1240H
R18G9257R1	13	32968898	32968898	Missense_Mutation	SNP	A	T	T	BRCA2	c.9329A>T	p.N3110I
R18G9257R1	17	47699369	47699369	Missense_Mutation	SNP	C	T	T	SPOP	c.139G>A	p.E47K
R18G9257R1	19	1218486	1218486	Nonsense_Mutation	SNP	G	T	T	STK11	c.361G>T	p.E121*
R18G9257R1	22	21347167	21347167	Missense_Mutation	SNP	C	T	T	LZTR1	c.1234C>T	p.R412C
R18G9258R1	13	108922466	108922466	Missense_Mutation	SNP	G	A	A	TNFSF13B	c.223G>A	p.D75N
R18G9258R1		-	-	Frame_Shift_Del	INS	-	-	-	TP53	c.420_428delins	p.C141AFs*5
R18G9258R1	6	157528883	157528883	Missense_Mutation	SNP	T	C	C	ARID1B	c.6608T>C	p.L2203P
R18G9258R1	9	101908864	101908864	Nonsense_Mutation	SNP	G	T	T	TGFB1	c.1228G>T	p.E410*
R18G9465R1	11	108200967	108200967	Missense_Mutation	SNP	T	C	C	ATM	c.7334T>C	p.L2445P
R18G9465R1	12	56478854	56478854	Missense_Mutation	SNP	G	T	T	ERBB3	c.310G>T	p.V104L
R18G9465R1	12	56487218	56487218	Missense_Mutation	SNP	A	G	G	ERBB3	c.1364A>G	p.Y455C
R18G9465R1		-	-	In_Frame_Ins	INS	-	-	-	AXIN1	c.345_350dup	p.L115_D116dup
R18G9465R1		-	-	Frame_Shift_Ins	INS	-	-	-	SMAD4	c.332dup	p.H111Qfs*3
R18G9465R1	19	11135058	11135058	Missense_Mutation	SNP	C	T	T	SMARCA4	c.3025C>T	p.R1009C
R18G9465R1	7	140453134	140453134	Missense_Mutation	SNP	T	C	C	BRAF	c.1801A>G	p.K601E
R18G9465R1	9	36846874	36846874	Missense_Mutation	SNP	G	A	A	PAX5	c.833C>T	p.T278M
R18G9465R1	9	87570217	87570217	Missense_Mutation	SNP	G	A	A	NTRK2	c.1957G>A	p.V653M
R18G9477R1	15	99192881	99192881	Missense_Mutation	SNP	C	T	T	IGF1R	c.71C>T	p.S24L
R18G9477R1	17	7579312	7579312	Missense_Mutation	SNP	C	A	A	TP53	c.375G>T	p.T125T
R18G9477R1	3	89521695	89521695	Missense_Mutation	SNP	G	T	T	EPHA3	c.2772G>T	p.W924C
R18G9477R1	3	178922324	178922324	Missense_Mutation	SNP	G	A	A	PIK3CA	c.1093G>C	p.E365K
R18G9477R1	6	33286547	33286547	Missense_Mutation	SNP	C	G	G	DAXX	c.2196G>C	p.E732D
R18G9477R1	X	53222304	53222304	Missense_Mutation	SNP	G	C	C	KDM5C	c.4528C>G	p.P1510A
R18G9484R1	17	7577153	7577153	Missense_Mutation	SNP	C	A	A	TP53	c.785G>T	p.G262V
R18G9499R1	11	118343871	118343871	Missense_Mutation	SNP	G	C	C	KMT2A	c.1997G>C	p.G666A
R18G9499R1	19	17954626	17954626	Missense_Mutation	SNP	C	T	T	JAK3	c.268G>A	p.V90M
R18G9499R1	3	142217458	142217458	Missense_Mutation	SNP	C	T	T	ATR	c.5539G>A	p.G1847R
R18G9499R1	5	156671391	156671391	Missense_Mutation	SNP	G	A	A	ITK	c.1352G>A	p.R451Q
R18G9499R1	6	36652246	36652246	Missense_Mutation	SNP	C	T	T	CDKN1A	c.368C>T	p.S123L
R18G9499R1	7	19035653	19035653	Missense_Mutation	SNP	G	T	T	HDAC9	c.3178G>T	p.G1060C
R18G9501R1		-	-	Frame_Shift_Ins	INS	-	-	-	ARID1A	c.6706dup	p.R2236Pfs*42
R18G9501R1	1	158637816	158637816	Missense_Mutation	SNP	G	C	C	SPTA1	c.1870C>G	p.Q624E
R18G9501R1		-	-	Missense_Mutation	SNP	-	-	-	CCND1	c.683_685del	p.R228del
R18G9501R1		-	-	Frame_Shift_Del	INS	-	-	-	CREBBP	c.3317_3329del	p.P106Lfs*6
R18G9501R1		-	-	Splice_Site	SNP	-	-	-	NCOR1	c.42+5_242+6del	-
R18G9501R1	17	38560458	38560458	Missense_Mutation	SNP	C	A	A	TOP2A	c.2229G>T	p.K743N
R18G9501R1		-	-	Frame_Shift_Ins	INS	-	-	-	TOP2A	c.214dup	p.Y72Lfs*2
R18G9501R1	2	11389904	11389904	Missense_Mutation	SNP	C	G	G	ROCK2	c.345G>C	p.Q115H
R18G9501R1		-	-	Missense_Mutation	SNP	-	-	-	BCL2L1	c.351_353del	p.T118del
R18G9501R1		-	-	Frame_Shift_Ins	INS	-	-	-	ROS1	c.1720_1721dup	P.V575Lfs*11
R18G9501R1	7	151947971	151947971	Missense_Mutation	SNP	C	T	T	KMT2C	c.1702G>A	p.G568S
R18G9503R1	12	25398284	25398284	Missense_Mutation	SNP	C	G	G	KRAS	c.35G>C	p.G12A
R18G9503R1	17	7574017	7574017	Missense_Mutation	SNP	C	G	G	TP53	c.1010G>C	p.R337P
R18G9503R1		-	-	Frame_Shift_Del	INS	-	-	-	SOX9	c.724_740del	p.K242Gfs*4
R18G9503R1	9	101900191	101900191	Nonsense_Mutation	SNP	G	T	T	TGFB1	c.625G>T	p.E209*
R18G9504R1		-	-	Frame_Shift_Ins	INS	-	-	-	JAK1	c.1289dup	P.L431Vfs*22
R18G9504R1	1	193119422	193119422	Splice_Site	SNP	A	T	T	CDC73	c.829-12A>T	-
R18G9504R1	10	70446225	70446225	Missense_Mutation	SNP	A	C	C	TET1	c.5165A>C	p.K1722T
R18G9504R1	12	52387796	52387796	Nonsense_Mutation	SNP	C	T	T	ACVR1B	c.1543C>T	p.R515*
R18G9504R1	14	23778068	23778068	Missense_Mutation	SNP	C	T	T	BCL2L2	c.476C>T	p.A159V
R18G9504R1	16	3777750	3777750	Missense_Mutation	SNP	T	C	C	CREBBP	c.7298A>G	p.D2433G
R18G9504R1	17	7577121	7577121	Missense_Mutation	SNP	G	A	A	TP53	c.817C>T	p.R273C
R18G9504R1	17	29670031	29670031	Missense_Mutation	SNP	C	A	A	NF1	c.7067C>A	p.P2356Q
R18G9504R1	19	10473296	10473296	Missense_Mutation	SNP	C	T	T	TYK2	c.1405G>A	p.G469S
R18G9504R1	19	40761125	40761125	Missense_Mutation	SNP	C	T	T	AKT2	c.227G>A	p.R76H
R18G9504R1	2	29473967	29473967	Splice_Site	SNP	G	A	A	ALK	c.2204+4C>T	-
R18G9504R1	2	141122224	141122224	Splice_Site	SNP	C	T	T	LRP1B	c.11131+6G>A	-
R18G9504R1		-	-	Splice_Site	SNP	-	-	-	LRP1B	c.9964-4dup	-
R18G9504R1	3	12650322	12650322	Missense_Mutation	SNP	T	C	C	RAF1	c.524A>G	p.H175R
R18G9504R1	3	37035145	37035145	Missense_Mutation	SNP	T	G	G	MLH1	c.107T>G	p.I36S
R18G9504R1	3	134644703	134644703	Missense_Mutation	SNP	C	T	T	EPHB1	c.104C>T	p.T35M
R18G9504R1		-	-	Splice_Site	SNP	-	-	-	SLIT2	c.1833-9dup	-
R18G9504R1	4	66280156	66280156	Missense_Mutation	SNP	T	G	G	EPHA5	c.1533A>C	p.Q511H
R18G9504R1	7	117307044	117307044	Missense_Mutation	SNP	G	T	T	CFTR	c.4325G>T	p.S1442I
R18G9504R1		-	-	Missense_Mutation	SNP	-	-	-	CDKN2A	c.192_194del	P.L65del
R18G9508R1	12	25398284	25398284	Missense_Mutation	SNP	C	G	G	KRAS	c.35G>C	p.G12A
R18G9509R1	1	27089676	27089676	Nonsense_Mutation	SNP	C	T	T	ARID1A	c.2632C>T	p.Q878*
R18G9509R1	17	7577099	7577099	Missense_Mutation	SNP	C	T	T	TP53	c.839G>A	p.R280K
R18G9509R1	9	87342612	87342612	Missense_Mutation	SNP	C	A	A	NTRK2	c.897C>A	p.H299Q
R18H2220M1	1	11186709	11186709	Nonsense_Mutation	SNP	T	A	A	MTOR	c.6496A>T	p.K2166*
R18H2220M1	17	7578202	7578202	Missense_Mutation	SNP	A	C	C	TP53	c.647T>G	p.V216G
R18H2220M1	18	48603032	48603032	Nonsense_Mutation	SNP	C	T	T	SMAD4	c.1333C>T	p.R445*
R18H2220M1	6	138196907	138196907	Missense_Mutation	SNP	C	T	T	TNFAIP3	c.569C>T	p.S190L
R18H2220M1	7	148514980	148514980	Missense_Mutation	SNP	G	A	A	EZH2	c.1229C>T	p.S410L
R18H2220M1	X	129149695	129149695	Nonsense_Mutation	SNP	A	T	T	BCORL1	c.2947A>T	p.K983*
SH_O1	1	162725527	162725527	Silent	SNV	T	C	C	DDR2	c.639T>C	P.N213N
SH_O1	1	186099838	186099838	Splice_Site	SNV	C	T	T	HMCN1	c.13230+9C>T	-
SH_O1	1	186862271	186862271	Missense_Mutation	SNV	A	T	T	PLA2G4A	c.244A>T	P.N82Y
SH_O1	1	201060930	201060930	Splice_Site	SNV	C	A	A	CACNA1S	c.542-10G>T	-
SH_O1	1	248343682	248343682	Missense_Mutation	SNV	A	G	G	OR2M2	c.395A>G	P.Y132C
SH_O1	1	27277241	27277241	Frame_Shift_Del	INDEL	G	-	-	KDF1	c.1046delC	P.T349fs
SH_O1	11	621598	621598	Silent	SNV	G	A	A	CDHR5	c.471C>T	P.D157D
SH_O1	12	58113926	58113926	Missense_Mutation	SNV	C	G	G	OS9	c.1645C>G	P.R549G
SH_O1	13	100207882	100207882	Missense_Mutation	SNV	A	G	G	TM9SF2	c.1733A>G	P.Y578C
SH_O1	14	90767602	90767602	Missense_Mutation	SNV	T	A	A	NRDE2	c.1526A>T	P.D509V
SH_O1	15	85406805	85406805	Missense_Mutation	SNV	G	A	A	ALPK3	c.5039G>A	P.S1680N
SH_O1	19	17085966	17085966	Missense_Mutation	SNV	G	A	A	CPAMD8	c.2152C>T	P.R718C
SH_O1	19	55241136	55241136	Missense_Mutation	SNV	C	A	A	KIR3DL3	c.833C>A	P.A278D
SH_O1	2	61441650	61441650	Missense_Mutation	SNV	C	G	G	USP34	c.8227G>C	P.D2743H
SH_O1	3	143185925	143185925	Missense_Mutation	SNV	C	T	T	SLC9A9	c.1423G>A	P.V475I

SH_01	5	41067320	41067320	Missense_Mutation	SNV	C	G	G	MROH2B	c.91G>C	P.E31Q
SH_01	6	33288240	33288240	Missense_Mutation	SNV	C	T	T	DAXX	c.1168G>A	P.E390K
SH_01	7	38803062	38803062	Missense_Mutation	SNV	T	A	A	VPS41	c.1415A>T	P.D472V
SH_01	8	141262967	141262967	Frame_Shift_Ins	INDEL	-	A	A	TRAPPC9	c.2339dupT	P.L780fs
SH_02	19	10433378	10433378	Silent	SNV	A	G	G	RAVER1	c.1167T>C	P.N389N
SH_02	19	9069847	9069847	Missense_Mutation	SNV	G	A	A	MUC16	c.17599C>T	P.P5867S
SH_02	2	216286937	216286937	Missense_Mutation	SNV	C	A	A	FN1	c.1423G>T	P.G475W
SH_03	1	10471591	10471591	Silent	SNV	G	A	A	PGD	c.570G>A	P.A190A
SH_03	1	29344901	29344901	Silent	SNV	G	A	A	EPB41	c.1071G>A	P.P357P
SH_03	10	11527879	11527879	Silent	SNV	C	T	T	USP6NL	c.747G>A	P.L249L
SH_03	10	117093839	117093839	Missense_Mutation	SNV	G	A	A	ATRN1	c.3085G>A	P.E1029K
SH_03	10	93252175	93252175	Missense_Mutation	SNV	G	A	A	HECTD2	c.1378G>A	P.D460N
SH_03	11	58275454	58275454	Missense_Mutation	SNV	C	T	T	OR5B21	c.125G>A	P.G42E
SH_03	12	21377711	21377711	Missense_Mutation	SNV	G	T	T	SLC01B1	c.1803G>T	P.K601N
SH_03	12	25398284	25398284	Missense_Mutation	SNV	C	T	T	KRAS	c.35G>A	P.G12D
SH_03	13	103385224	103385224	Silent	SNV	G	A	A	CCDC168	c.17823C>T	P.D5941D
SH_03	18	48591930	48591930	Missense_Mutation	SNV	G	A	A	SMAD4	c.1093G>A	P.G365S
SH_03	4	8477600	8477600	Missense_Mutation	SNV	A	C	C	TRMT44	c.2146A>C	P.T716P
SH_03	5	13792115	13792115	Missense_Mutation	SNV	G	C	C	DNAH5	c.8436C>G	P.I2812M
SH_05	1	15970017	15970017	Missense_Mutation	SNV	G	T	T	DDI2	c.761G>T	P.G254V
SH_05	12	4870167	4870167	Missense_Mutation	SNV	G	A	A	GALNT8	c.1217G>A	P.R406Q
SH_05	12	7973877	7973877	Missense_Mutation	SNV	T	A	A	SLC2A14	c.978A>T	P.Q326H
SH_05	14	88654388	88654388	Missense_Mutation	SNV	C	T	T	KCNK10	c.919G>A	P.G307S
SH_05	15	24923954	24923954	Silent	SNV	T	A	A	NPAP1	c.2940T>A	P.S980S
SH_05	16	14947821	14947821	Missense_Mutation	SNV	A	G	G	NOMO1	c.901A>G	P.T301A
SH_05	17	39240887	39240887	Silent	SNV	C	G	G	KRTAP4-7	c.429C>G	P.T143T
SH_05	17	41907409	41907409	Missense_Mutation	SNV	T	G	G	MPP3	c.289A>C	P.T97P
SH_05	17	7577568	7577568	Missense_Mutation	SNV	C	A	A	TP53	c.713G>T	P.C238F
SH_05	19	51334742	51334742	Missense_Mutation	SNV	G	T	T	KLK15	c.7C>A	P.L3I
SH_05	7	20420460	20420460	Splice_Site	SNV	A	G	G	ITGB8	c.801+6A>G	
SH_05	7	57188582	57188582	Silent	SNV	A	T	T	ZNF479	c.540T>A	P.T180T
SH_05	7	80447713	80447713	Missense_Mutation	SNV	G	T	T	SEMA3C	c.349C>A	P.R117S
SH_05	8	26627987	26627987	Silent	SNV	C	A	A	ADRA1A	c.1080G>T	P.L360L
SH_05	8	59409434	59409434	Missense_Mutation	SNV	C	T	T	CYP7A1	c.637G>A	P.D213N
SH_05	X	129499646	129499646	Nonsense_Mutation	SNV	T	A	A	SLC25A14	c.851T>A	P.L284*
SH_05	X	74649819	74649819	Splice_Site	SNV	C	T	T	ZDHH15	c.423-4G>A	
SH_05	X	91131848	91131848	Silent	SNV	T	A	A	PCDH11X	c.609T>A	P.V203V
SH_05	X	9866272	9866272	Nonsense_Mutation	SNV	G	T	T	SHROOM2	c.2833G>T	P.E945*
SH_06	1	5925295	5925295	Missense_Mutation	SNV	A	C	C	NPHP4	c.2144T>G	P.V715G
SH_06	18	12463443	12463443	Silent	SNV	C	T	T	SPIRE1	c.1545G>A	P.R515R
SH_06	19	43967775	43967775	Missense_Mutation	SNV	T	G	G	LYPD3	c.358A>C	P.T120P
SH_06	2	179517003	179517003	Missense_Mutation	SNV	G	A	A	TTN	c.34678C>T	P.P11560S
SH_07	12	25398284	25398284	Missense_Mutation	SNV	C	TRUE	TRUE	KRAS	c.35G>A	P.G12D
SH_08	1	248129634	248129634	Missense_Mutation	SNV	T	A	A	OR2AK2	c.1001T>A	P.L334Q
SH_08	1	26152814	26152814	Frame_Shift_Ins	INDEL	-	TG	TG	MTFR1L	c.155-156dupG	P.L53fs
SH_08	1	34667819	34667819	Missense_Mutation	SNV	C	G	G	C1orf94	c.1405C>G	P.P469A
SH_08	1	68947861	68947861	Missense_Mutation	SNV	T	A	A	DEPDC1	c.1630A>T	P.S544C
SH_08	1	94940756	94940756	Nonsense_Mutation	SNV	C	T	T	ABCD3	c.463C>T	P.R155*
SH_08	11	26558957	26558957	Silent	SNV	C	T	T	ANO3	c.1164C>T	P.I388I
SH_08	11	4144502	4144502	Missense_Mutation	SNV	C	T	T	RRM1	c.1208C>T	P.P403L
SH_08	11	4790634	4790634	Missense_Mutation	SNV	T	C	C	OR51F1	c.514A>G	P.R172G
SH_08	11	49974335	49974335	Missense_Mutation	SNV	T	A	A	OR4C13	c.361T>A	P.Y121N
SH_08	11	5510223	5510223	Missense_Mutation	SNV	C	T	T	OR52D1	c.287C>T	P.S96F
SH_08	12	124358269	124358269	Splice_Site	SNV	C	A	A	DNAH10	c.7584+12C>A	
SH_08	12	62785633	62785633	Frame_Shift_Ins	INDEL	-	A	A	USP15	c.2278dupA	P.R760fs
SH_08	13	103395589	103395589	Silent	SNV	T	G	G	CCDC168	c.7458A>C	P.L2486I
SH_08	15	55929382	55929382	Missense_Mutation	SNV	A	C	C	PRTG	c.2609T>G	P.V870G
SH_08	18	2599075	2599075	Nonsense_Mutation	SNV	A	T	T	NDC80	c.1279A>T	P.X427*
SH_08	18	63476982	63476982	Missense_Mutation	SNV	A	T	T	CDH7	c.253A>T	P.I85F
SH_08	19	53086139	53086139	Missense_Mutation	SNV	G	T	T	ZNF701	c.1025G>T	P.G342V
SH_08	19	54760159	54760159	Silent	SNV	C	A	A	LILRB5	c.402G>T	P.V134V
SH_08	19	58198693	58198693	Silent	SNV	C	A	A	ZNF551	c.966C>A	P.L322L
SH_08	19	9068836	9068836	Missense_Mutation	SNV	G	A	A	MUC16	c.18610C>T	P.L6204F
SH_08	19	9091198	9091198	Missense_Mutation	SNV	G	A	A	MUC16	c.617C>T	P.A206V
SH_08	2	152426737	152426737	Missense_Mutation	SNV	T	A	A	NEB	c.17288A>T	P.D5763V
SH_08	2	182347092	182347092	Silent	SNV	T	C	C	ITGA4	c.846T>C	P.Y282Y
SH_08	2	207452041	207452041	Splice_Site	SNV	T	G	G	ADAM23	c.1738-8T>G	
SH_08	2	55812299	55812299	Missense_Mutation	SNV	A	G	G	PPP4R3B	c.1121T>C	P.M374T
SH_08	21	14983010	14983010	Missense_Mutation	SNV	G	C	C	POTED	c.461G>C	P.R154T
SH_08	21	17135205	17135205	Splice_Site	SNV	T	C	C	USP25	c.46-5T>C	
SH_08	3	121438521	121438521	Missense_Mutation	SNV	T	A	A	GOLGB1	c.743A>T	P.Q248L
SH_08	3	193130046	193130046	Missense_Mutation	SNV	G	C	C	ATP13A4	c.3129C>G	P.F1043L
SH_08	4	144618702	144618702	Missense_Mutation	SNV	A	T	T	FREM3	c.3127T>A	P.S1043T
SH_08	4	15826591	15826591	Missense_Mutation	SNV	G	T	T	CD38	c.451G>T	P.G151C
SH_08	4	165118501	165118501	Silent	SNV	T	G	G	ANP32C	c.363A>C	P.V121V
SH_08	5	180657785	180657785	Silent	SNV	G	T	T	TRIM41	c.855G>T	P.L285L
SH_08	6	147106755	147106755	Missense_Mutation	SNV	G	C	C	ADGB	c.4222G>C	P.A1408P
SH_08	7	102743935	102743935	Missense_Mutation	SNV	A	G	G	NAPEPLD	c.1123T>C	P.F375L
SH_08	7	117876942	117876942	Nonsense_Mutation	SNV	C	A	A	ANKRD7	c.674C>A	P.S225*
SH_08	7	143632711	143632711	Missense_Mutation	SNV	G	A	A	OR2F2	c.386G>A	P.R129H
SH_08	7	84628984	84628984	Silent	SNV	G	T	T	SEMA3D	c.2106C>A	P.V702V
SH_08	8	67067878	67067878	Silent	SNV	G	C	C	TRIM55	c.1545G>C	P.A515A
SH_08	8	71075095	71075095	Splice_Site	SNV	A	C	C	NCOA2	c.833-6T>G	
SH_08	X	101821163	101821163	Splice_Site	SNV	A	T	T	NXF4	n.1363A>T	
SH_08	X	105125700	105125700	Splice_Site	SNV	G	T	T	NRK	c.181-1G>T	
SH_09	1	120930078	120930078	Missense_Mutation	SNV	G	A	A	FCGR1B	c.247C>T	P.R83C
SH_09	1	24301546	24301546	Splice_Site	SNV	A	G	G	SRSF10	n.802-5T>C	
SH_09	1	33330385	33330385	Silent	SNV	G	C	C	FNDC5	c.513C>G	P.L171L
SH_09	1	75218038	75218038	Silent	SNV	A	G	G	TYW3	c.390A>G	P.T130T
SH_09	10	25861694	25861694	Nonsense_Mutation	SNV	G	A	A	GPR158	c.1631G>A	P.W544*
SH_09	11	4976165	4976165	Missense_Mutation	SNV	G	A	A	OR51A2	c.779C>T	P.A260V
SH_09	13	111077183	111077183	Frame_Shift_Del	INDEL	G	-	-	COL4A2	c.283delG	P.A95fs
SH_09	13	42877460	42877460	Silent	SNV	T	C	C	AKAP11	c.4578T>C	P.S1526S
SH_09	2	141250202	141250202	Missense_Mutation	SNV	C	A	A	LRP1B	c.9095G>T	P.G3032V
SH_09	20	34430626	34430626	Missense_Mutation	SNV	A	T	T	PHF20	c.215A>T	P.Q72L
SH_09	4	95191958	95191958	Missense_Mutation	SNV	G	A	A	SMARCAD1	c.1561G>A	P.A521T
SH_09	7	50444466	50444466	Silent	SNV	C	A	A	IKZF1	c.396C>A	P.L132L
SH_09	8	110980831	110980831	Splice_Site	SNV	G	T	T	KCNV1	c.992-3C>A	

SH_09	8	59515912	59515912	Missense_Mutation	SNV	T	C	C	NSMAF	c.995A>G	P.Y332C
SH_10	1	111216638	111216638	Missense_Mutation	SNV	T	G	G	KCNA3	c.794A>C	P.Y265S
SH_10	1	160106787	160106787	Missense_Mutation	SNV	A	C	C	ATP1A2	c.2806A>C	P.T936P
SH_10	1	197397096	197397096	Missense_Mutation	SNV	G	A	A	CRB1	c.2305G>A	P.V769I
SH_10	1	27057766	27057766	Nonsense_Mutation	SNV	C	T	T	ARID1A	c.1474C>T	P.Q492*
SH_10	1	50317156	50317156	Silent	SNV	C	T	T	AGBL4	c.69G>A	P.G232G
SH_10	15	54916034	54916034	Frame_Shift_Del	INDEL	T	-	-	UNC13C	c.6242delT	P.F2081fs
SH_10	15	65553304	65553304	Missense_Mutation	SNV	G	A	A	PARP16	c.752C>T	P.P251L
SH_10	15	93595630	93595630	Missense_Mutation	SNV	G	A	A	RGMA	c.262C>T	P.R88C
SH_10	15	94883491	94883491	Missense_Mutation	SNV	C	G	G	MCTP2	c.844C>G	P.L282V
SH_10	17	18188822	18188822	Missense_Mutation	SNV	G	A	A	TOP3A	c.1325C>T	P.T442I
SH_10	17	35548072	35548072	Missense_Mutation	SNV	C	T	T	ACACA	c.4561G>A	P.D1521N
SH_10	17	73239608	73239608	Missense_Mutation	SNV	A	C	C	GGA3	c.128T>G	P.I43S
SH_10	17	73887396	73887396	Missense_Mutation	SNV	C	T	T	TRIM65	c.952G>A	P.A318T
SH_10	19	50138891	50138891	Missense_Mutation	SNV	G	A	A	RRAS	c.599C>T	P.P200L
SH_10	19	54403899	54403899	Missense_Mutation	SNV	G	A	A	PRKCG	c.1471G>A	P.E491K
SH_10	2	183731159	183731159	Missense_Mutation	SNV	G	A	A	FRZB	c.122C>T	P.P41L
SH_10	2	242026810	242026810	Silent	SNV	T	C	C	SNED1	c.4125T>C	P.Y1375Y
SH_10	20	57485829	57485829	Missense_Mutation	SNV	A	G	G	GNAS	c.1130A>G	P.N377S
SH_10	21	31973533	31973533	Missense_Mutation	SNV	G	T	T	KRTAP22-1	c.94G>T	P.A32S
SH_10	3	12586867	12586867	Missense_Mutation	SNV	G	T	T	MKRN20S	c.97C>A	P.Q33K
SH_10	3	186969515	186969521	Frame_Shift_Del	INDEL	AGGCTGT	-	-	MASP1	c.918delACAG	P.Q305fs
SH_10	3	42742237	42742237	Missense_Mutation	SNV	G	A	A	HHATL	c.82C>T	P.R28W
SH_10	7	150269953	150269953	Missense_Mutation	SNV	G	T	T	GIMAP4	c.795G>T	P.K265N
SH_10	7	158540897	158540897	Missense_Mutation	SNV	G	T	T	ESYT2	c.1713C>A	P.D571E
SH_10	7	96650088	96650088	Missense_Mutation	SNV	A	G	G	DLX5	c.830T>C	P.L277S
SH_10	8	59059801	59059801	Missense_Mutation	SNV	G	A	A	FAM110B	c.1012G>A	P.V338M
SH_10	9	37441440	37441440	Missense_Mutation	SNV	A	C	C	ZBTB5	c.1109T>G	P.L370R
SH_100	10	76781010	76781010	Silent	SNV	A	T	T	KAT6B	c.2439A>T	P.A813A
SH_100	14	42356383	42356383	Missense_Mutation	SNV	C	A	A	LRFN5	c.555C>A	P.N185K
SH_100	16	17211774	17211774	Silent	SNV	G	A	A	XYLT1	c.2286C>T	P.P762P
SH_100	16	568941	568941	Splice_Site	SNV	A	G	G	RAB11FIP3	c.753-2A>G	
SH_100	17	72366769	72366769	Silent	SNV	C	T	T	GPR142	c.468C>T	P.G156G
SH_100	2	118735598	118735598	Missense_Mutation	SNV	C	A	A	CCDC93	c.629G>T	P.G210V
SH_100	2	169791787	169791787	Missense_Mutation	SNV	G	A	A	ABC811	c.2963C>T	P.A988V
SH_100	2	179426577	179426577	Silent	SNV	C	T	T	TTN	c.79359G>A	P.K26453K
SH_100	22	16266960	16266960	Missense_Mutation	SNV	A	G	G	POTEH	c.1489T>C	P.F497L
SH_100	4	145580881	145580881	Missense_Mutation	SNV	G	A	A	HHIP	c.722G>A	P.R241H
SH_100	4	2097630	2097630	Silent	SNV	G	A	A	POLN	c.2013C>T	P.H671H
SH_100	5	37153998	37153998	Silent	SNV	T	C	C	C5orf42	c.8055A>G	P.A2685A
SH_100	5	96315225	96315225	Missense_Mutation	SNV	A	T	T	LNPEP	c.403A>T	P.T135S
SH_100	6	138583961	138583961	Missense_Mutation	SNV	C	A	A	ARFGF3	c.1341C>A	P.S447R
SH_100	6	24528252	24528252	Missense_Mutation	SNV	T	A	A	ALDH5A1	c.1201T>A	P.S401T
SH_100	7	26680305	26680305	Splice_Site	SNV	G	C	C	C7orf71	c.201-10G>C	
SH_100	7	99621357	99621357	Silent	SNV	G	T	T	ZKSCAN1	c.120G>T	P.R40R
SH_100	8	67831323	67831323	Silent	SNV	T	C	C	MCMDC2	c.1965T>C	P.Y655Y
SH_100	9	139357484	139357484	Missense_Mutation	SNV	G	A	A	SEC16A	c.4748C>T	P.T1583M
SH_100	X	123480532	123480532	Missense_Mutation	SNV	G	A	A	SH2D1A	c.40G>A	P.E14K
SH_101	1	173446546	173446546	Missense_Mutation	SNV	G	A	A	PRDX6	c.10G>A	P.G4S
SH_101	1	228362441	228362441	Missense_Mutation	SNV	C	A	A	IBA57	c.390C>A	P.S130R
SH_101	10	51579175	51579175	Missense_Mutation	SNV	A	C	C	NCOA4	c.82A>C	P.S28R
SH_101	13	99087969	99087969	Splice_Site	SNV	C	A	A	FARP1	c.2274+9C>A	
SH_101	14	75420612	75420612	Missense_Mutation	SNV	A	C	C	PGF	c.113T>G	P.V38G
SH_101	15	43571977	43571977	Silent	SNV	C	A	A	TGM7	c.1524G>T	P.L508L
SH_101	16	57945763	57945763	Missense_Mutation	SNV	C	A	A	CNGB1	c.2386G>T	P.A796S
SH_101	18	42532845	42532845	Silent	SNV	C	A	A	SETBP1	c.3540C>A	P.G1180G
SH_101	19	41119074	41119074	Silent	SNV	G	T	T	LTBP4	c.2604G>T	P.A868A
SH_101	19	4513287	4513287	Missense_Mutation	SNV	C	T	T	PLIN4	c.643G>A	P.A215T
SH_101	19	6396450	6396450	Silent	SNV	C	G	G	LOC390877	c.60C>G	P.G20G
SH_101	2	202252434	202252434	Missense_Mutation	SNV	G	T	T	TRAK2	c.1688C>A	P.P563H
SH_101	2	37152334	37152334	Silent	SNV	C	T	T	STRN	c.252G>A	P.L84L
SH_101	2	55825578	55825578	Missense_Mutation	SNV	T	C	C	PPP4R3B	c.895A>G	P.K299E
SH_101	21	45528860	45528860	Splice_Site	SNV	C	T	T	PWP2	c.19-5C>T	
SH_101	5	170323065	170323065	Silent	SNV	A	G	G	RANBP17	c.435A>G	P.E145E
SH_101	5	5464725	5464725	Missense_Mutation	SNV	T	C	C	ICE1	c.5278T>C	P.S1760P
SH_101	6	7558461	7558461	Missense_Mutation	SNV	G	A	A	DSP	c.386G>A	P.R129Q
SH_101	7	50455052	50455052	Missense_Mutation	SNV	C	A	A	IKZF1	c.599C>A	P.P200H
SH_101	7	55240762	55240762	Missense_Mutation	SNV	G	A	A	EGFR	c.2006G>A	P.R669Q
SH_107	1	205895738	205895738	Silent	SNV	G	A	A	SLC26A9	c.1314C>T	P.I438I
SH_107	10	135053221	135053221	Missense_Mutation	SNV	C	T	T	VENTX	c.283C>T	P.R95C
SH_107	10	71968993	71968993	Silent	SNV	C	A	A	PPA1	c.693G>T	P.V231V
SH_107	10	90497497	90497497	Silent	SNV	C	T	T	LIPK	c.775C>T	P.L259L
SH_107	10	98144423	98144423	Silent	SNV	C	T	T	TLI2	c.2115G>A	P.S705S
SH_107	11	22398184	22398184	Missense_Mutation	SNV	G	T	T	SLC17A6	c.1379G>T	P.C460F
SH_107	12	25398284	25398284	Missense_Mutation	SNV	C	A	A	KRAS	c.35G>T	P.G12V
SH_107	13	61141657	61141657	Splice_Site	SNV	A	G	G	TDRD3	c.2119-2A>G	
SH_107	15	24922841	24922841	Silent	SNV	A	C	C	NPAP1	c.1827A>C	P.A609A
SH_107	15	25223587	25223587	Missense_Mutation	SNV	C	G	G	SNRPN	c.719C>G	P.P240R
SH_107	16	81969881	81969881	Missense_Mutation	SNV	C	T	T	PLCG2	c.2950C>T	P.R984C
SH_107	17	12901792	12901792	Missense_Mutation	SNV	A	C	C	ELAC2	c.1337T>G	P.L446R
SH_107	17	79496251	79496251	Missense_Mutation	SNV	G	A	A	FSCN2	c.694G>A	P.V232M
SH_107	2	209113113	209113113	Missense_Mutation	SNV	G	A	A	IDH1	c.394C>T	P.R132C
SH_107	2	60995638	60995638	Missense_Mutation	SNV	G	T	T	PAPOLG	c.280G>T	P.G94C
SH_107	4	174253396	174253396	Splice_Site	SNV	T	C	C	HMG82	c.472-7A>G	
SH_107	4	54424083	54424083	Frame_Shift_Del	INDEL	T	-	-	LNK1	c.50delA	P.Y17fs
SH_107	7	63720585	63720587	Splice_Site	INDEL	TTA	-	-	ZNF679	0-12 40-10delATT	
SH_107	8	106573623	106573623	Nonsense_Mutation	SNV	C	T	T	ZFPM2	c.334C>T	P.R112*
SH_107	X	114541292	114541292	Missense_Mutation	SNV	A	C	C	LUZP4	c.619A>C	P.N207H
SH_108	1	109369841	109369841	Nonsense_Mutation	SNV	G	T	T	AKNAD1	c.1922C>A	P.S641*
SH_108	1	152052228	152052228	Silent	SNV	C	T	T	LOC100131107	c.1056G>A	P.P352P
SH_108	1	153735305	153735305	Missense_Mutation	SNV	G	A	A	INTS3	c.1618G>A	P.E540K
SH_108	1	2700312	2700312	Missense_Mutation	SNV	C	T	T	TTC34	c.529G>A	P.A177T
SH_108	1	27100292	27100292	Splice_Site	SNV	G	C	C	ARID1A	c.4005-1G>C	
SH_108	1	3679830	3679830	Missense_Mutation	SNV	G	T	T	CCDC27	c.1113G>T	P.E371D
SH_108	1	67559216	67559216	Frame_Shift_Ins	INDEL	-	T	T	C1orf141	c.674dupA	P.N225fs
SH_108	11	111904162	111904162	Missense_Mutation	SNV	T	C	C	DLAT	c.695T>C	P.M232T
SH_108	11	118942532	118942532	Missense_Mutation	SNV	G	A	A	VP511	c.830G>A	P.R277H
SH_108	11	494979	494979	Missense_Mutation	SNV	C	T	T	RNH1	c.1202G>A	P.R401H

SH_108	11	51412298	51412298	Missense_Mutation	SNV	T	C	C	OR4A5	c.98A>G	P.Y33C
SH_108	12	123103017	123103017	Splice_Site	INDEL	-	G	G	KNTC1	86-12_6086-11nsG	
SH_108	12	20885887	20885887	Missense_Mutation	SNV	G	A	A	SLC01C1	c.877G>A	P.G293R
SH_108	12	25398284	25398284	Missense_Mutation	SNV	C	A	A	KRAS	c.35G>T	P.G12V
SH_108	12	41967137	41967137	Missense_Mutation	SNV	C	G	G	PDZRN4	c.2556C>G	P.S852R
SH_108	12	48596381	48596381	Missense_Mutation	SNV	G	A	A	OR10AD1	c.695C>T	P.S232F
SH_108	12	52864372	52864372	Missense_Mutation	SNV	G	C	C	KRT6C	c.1120C>G	P.L374V
SH_108	12	58131354	58131354	Missense_Mutation	SNV	T	A	A	AGAP2	c.676A>T	P.S226C
SH_108	12	6707550	6707550	Nonsense_Mutation	SNV	C	T	T	CHD4	c.1524G>A	P.W508*
SH_108	12	88589318	88589318	Silent	SNV	C	T	T	TMTC3	c.2637C>T	P.D879D
SH_108	13	110438120	110438120	Missense_Mutation	SNV	G	C	C	IRS2	c.281C>G	P.A94G
SH_108	14	21961267	21961267	Missense_Mutation	SNV	C	G	G	TOX4	c.1423C>G	P.L475V
SH_108	14	93412799	93412799	Missense_Mutation	SNV	C	T	T	ITPK1	c.778G>A	P.E260K
SH_108	15	29415586	29415586	Missense_Mutation	SNV	C	G	G	FAM189A1	c.1576G>C	P.E526Q
SH_108	15	34147045	34147045	Silent	SNV	T	C	C	RYR3	c.13939T>C	P.L4647L
SH_108	15	89391214	89391214	Silent	SNV	C	T	T	ACAN	c.1677C>T	P.G559G
SH_108	16	16313478	16313478	Missense_Mutation	SNV	A	G	G	ABCC6	c.407T>C	P.L136P
SH_108	16	23360010	23360010	Silent	SNV	C	T	T	SCNN1B	c.90C>T	P.C30C
SH_108	16	88951511	88951511	Nonsense_Mutation	SNV	G	A	A	CBFA2T3	c.1060C>T	P.R354*
SH_108	17	10222426	10222426	Missense_Mutation	SNV	C	T	T	MYH13	c.3419G>A	P.R1140H
SH_108	17	42152809	42152809	Missense_Mutation	SNV	G	C	C	G6PC3	c.548G>C	P.G183A
SH_108	17	7577559	7577559	Missense_Mutation	SNV	G	A	A	TP53	c.722C>T	P.S241F
SH_108	17	76122990	76122990	Splice_Site	SNV	G	A	A	TMC6	c.-74-3C>T	
SH_108	18	67614066	67614066	Missense_Mutation	SNV	G	A	A	CD226	c.286C>T	P.R96W
SH_108	19	45648183	45648183	Silent	SNV	C	G	G	PPP1R37	c.1059C>G	P.L353L
SH_108	19	52869634	52869634	Nonsense_Mutation	SNV	C	T	T	ZNFG10	c.1003C>T	P.Q335*
SH_108	19	56274176	56274176	Missense_Mutation	SNV	G	A	A	RFPL4A	c.499G>A	P.V167M
SH_108	19	9057855	9057855	Missense_Mutation	SNV	G	T	T	MUC16	c.29591C>A	P.T9864N
SH_108	2	141625299	141625299	Missense_Mutation	SNV	C	T	T	LRP1B	c.4439G>A	P.S1480N
SH_108	2	174230331	174230331	Splice_Site	SNV	C	G	G	CDC47	c.1035+11C>G	
SH_108	20	3146827	3146827	Silent	SNV	C	T	T	LZTS3	c.639G>A	P.G213G
SH_108	22	26176157	26176157	Nonsense_Mutation	SNV	C	T	T	MYO18B	c.2203C>T	P.Q735*
SH_108	22	39710716	39710716	Missense_Mutation	SNV	T	C	C	RPL3	c.824A>G	P.H275R
SH_108	3	178952085	178952085	Missense_Mutation	SNV	A	G	G	PIK3CA	c.3140A>G	P.H1047R
SH_108	3	182941958	182941958	Nonsense_Mutation	SNV	A	C	C	MCF2L2	c.2136T>G	P.Y121*
SH_108	3	52545756	52545756	Missense_Mutation	SNV	G	A	A	STAB1	c.2878G>A	P.G960S
SH_108	3	61548051	61548051	Splice_Site	SNV	G	T	T	PTPRG	c.85+5G>T	
SH_108	3	77607107	77607107	Missense_Mutation	SNV	G	T	T	ROBO2	c.1184G>T	P.R395I
SH_108	4	145038018	145038018	Nonsense_Mutation	SNV	G	A	A	GYP4	c.307C>T	P.R103*
SH_108	5	132160905	132160905	Missense_Mutation	SNV	C	T	T	SHROOM1	c.928G>A	P.E310K
SH_108	5	149431584	149431584	Silent	SNV	C	T	T	HMGXB3	c.3708C>T	P.D1236D
SH_108	5	43174972	43174972	Missense_Mutation	SNV	G	A	A	ZNFI13	c.1609G>A	P.E537K
SH_108	6	152265535	152265535	Missense_Mutation	SNV	G	A	A	ESR1	c.988G>A	P.E330K
SH_108	6	26452100	26452100	Missense_Mutation	SNV	G	C	C	BTN3A3	c.586G>C	P.E196Q
SH_108	7	127954977	127954977	Missense_Mutation	SNV	C	T	T	RBM28	c.1462G>A	P.E488K
SH_108	7	158424395	158424395	Missense_Mutation	SNV	G	A	A	NCAPG2	c.3395C>T	P.S1132L
SH_108	7	29186261	29186261	Missense_Mutation	SNV	C	T	T	CHN2	c.62C>T	P.T21I
SH_108	7	30721577	30721577	Missense_Mutation	SNV	C	G	G	CRHR2	c.264G>C	P.E88D
SH_108	8	100654571	100654571	Missense_Mutation	SNV	G	A	A	VPS13B	c.5828G>A	P.R1943Q
SH_108	8	110416854	110416854	Missense_Mutation	SNV	G	A	A	PKHD1L1	c.1445G>A	P.R482Q
SH_108	8	145168736	145168736	Silent	SNV	G	A	A	WDR97	c.3360G>A	P.L1120L
SH_108	8	145692708	145692708	Silent	SNV	G	C	C	KIFC2	c.453G>C	P.R151R
SH_108	8	55542151	55542151	Missense_Mutation	SNV	A	T	T	RP1	c.5709A>T	P.E1903D
SH_108	8	93004034	93004034	Missense_Mutation	SNV	C	T	T	RUNX1T1	c.824G>A	P.R275Q
SH_108	9	125424476	125424476	Missense_Mutation	SNV	T	A	A	OR1L1	c.482T>A	P.L161H
SH_108	9	33030547	33030547	Silent	SNV	T	A	A	DNAJA1	c.54T>A	P.S18S
SH_108	9	87342596	87342596	Missense_Mutation	SNV	C	G	G	NTRK2	c.881C>G	P.S294C
SH_108	X	24844692	24844692	Missense_Mutation	SNV	A	T	T	POLA1	c.3692A>T	P.D1231V
SH_108	X	69263794	69263794	Silent	SNV	G	A	A	AWAT2	c.249C>T	P.S83S
SH_110	1	153642663	153642663	Missense_Mutation	SNV	C	T	T	ILF2	c.49G>A	P.G17R
SH_110	1	158913594	158913594	Missense_Mutation	SNV	G	T	T	PYHIN1	c.1017G>T	P.R339S
SH_110	1	160209613	160209613	Silent	SNV	C	A	A	DCAF8	c.597G>T	P.L199L
SH_110	1	175323551	175323551	Missense_Mutation	SNV	T	C	C	TNR	c.2359A>G	P.I787V
SH_110	1	39878310	39878310	Silent	SNV	A	T	T	KIAA0754	c.2373A>T	P.S791S
SH_110	10	5248281	5248281	Missense_Mutation	SNV	G	T	T	AKR1C4	c.491G>T	P.G164V
SH_110	10	5967365	5967365	Silent	SNV	C	T	T	FBXO18	c.2461C>T	P.L821L
SH_110	10	79616501	79616501	Missense_Mutation	SNV	C	A	A	DLG5	c.523G>T	P.A175S
SH_110	11	17596262	17596262	Splice_Site	SNV	T	A	A	OTOG	c.2330-5T>A	
SH_110	15	44093333	44093333	Missense_Mutation	SNV	A	G	G	HYPK	c.190A>G	P.M64V
SH_110	17	1704227	1704231	Frame_Shift_Del	INDEL	ACCAG	-	-	SMYD4	457_461delCTG	P.L153fs
SH_110	17	7577535	7577535	Missense_Mutation	SNV	C	A	A	TP53	c.746G>C	P.R249M
SH_110	18	24917153	24917153	Splice_Site	SNV	T	C	C	LOC105372038	n.251-2A>G	
SH_110	19	42312940	42312940	Missense_Mutation	SNV	T	A	A	CEACAM3	c.514T>A	P.C172S
SH_110	19	58145986	58145986	Splice_Site	SNV	T	C	C	ZNFX11	c.130-11T>C	
SH_110	2	216248111	216248112	Frame_Shift_Del	INDEL	TG	-	-	FN1	4989_4990delC	P.Y1663fs
SH_110	2	219330857	219330857	Missense_Mutation	SNV	T	C	C	USP37	c.2342A>G	P.N781S
SH_110	20	23065896	23065896	Missense_Mutation	SNV	G	A	A	CD93	c.934C>T	P.R312C
SH_110	20	33077647	33077647	Silent	SNV	A	G	G	ITCH	c.2358A>G	P.Q786Q
SH_110	3	125701106	125701106	Splice_Site	SNV	T	A	A	ROPN1B	c.397-7T>A	
SH_110	5	161576158	161576158	Silent	SNV	C	A	A	GABRG2	c.967C>A	P.R323R
SH_110	6	43269002	43269002	Splice_Site	SNV	G	A	A	SLC22A7	c.945+6G>A	
SH_110	6	43603619	43603619	Missense_Mutation	SNV	G	C	C	MAD2L1BP	c.7G>C	P.A3P
SH_110	7	44097465	44097465	Splice_Site	SNV	G	T	T	DBNL	c.552+7G>T	
SH_110	8	13965710	13965710	Missense_Mutation	SNV	C	A	A	SGCZ	c.480G>T	P.E160D
SH_111	1	110581320	110581320	Missense_Mutation	SNV	C	T	T	STRIP1	c.266C>T	P.T89M
SH_111	1	121116750	121116750	Missense_Mutation	SNV	G	T	T	SRGAP2C	c.343G>T	P.A115S
SH_111	1	156449559	156449559	Missense_Mutation	SNV	C	A	A	MEF2D	c.426G>T	P.M142I
SH_111	1	17657625	17657625	Missense_Mutation	SNV	G	T	T	PADI4	c.254G>T	P.G85V
SH_111	1	236212233	236212233	Silent	SNV	G	A	A	NID1	c.282C>T	P.P94P
SH_111	1	27106504	27106504	Nonsense_Mutation	SNV	C	T	T	ARID1A	c.6115C>T	P.Q2039*
SH_111	1	68942629	68942629	Missense_Mutation	SNV	G	A	A	DEPDC1	c.2422C>T	P.R808C
SH_111	1	74507219	74507219	Frame_Shift_Ins	INDEL	-	T	T	LRRICQ	c.1395dupA	P.Y466fs
SH_111	10	102275937	102275937	Missense_Mutation	SNV	T	C	C	SEC31B	c.119A>G	P.N40S
SH_111	10	108357142	108357142	Nonsense_Mutation	SNV	G	A	A	SORCS1	c.3232C>T	P.R1078*
SH_111	10	59959035	59959035	Silent	SNV	G	A	A	IPMK	c.594C>T	P.Y198Y
SH_111	10	71255367	71255367	Silent	SNV	C	T	T	TSPAN15	c.375C>T	P.N125N
SH_111	11	111848524	111848524	Splice_Site	SNV	G	T	T	DIXDC1	c.23+5G>T	
SH_111	11	119291030	119291030	Missense_Mutation	SNV	C	T	T	THY1	c.104G>A	P.R35H

SH_111	11	92715229	92715229	Missense_Mutation	SNV	A	T	T	MTNR1B	c.840A>T	P.E280D
SH_111	12	25398284	25398284	Missense_Mutation	SNV	C	T	T	KRAS	c.35G>A	P.G12D
SH_111	12	58013409	58013409	Splice_Site	SNV	C	A	A	LOC101927583	n.2120+5G>T	
SH_111	12	8375111	8375111	Silent	SNV	C	T	T	FAM90A1	c.702G>A	P.A234A
SH_111	14	93412735	93412735	Missense_Mutation	SNV	T	A	A	ITPK1	c.842A>T	P.D281V
SH_111	14	94088174	94088174	Missense_Mutation	SNV	C	T	T	UNC79	c.4064C>T	P.P1355L
SH_111	15	22383359	22383359	Missense_Mutation	SNV	C	G	G	OR4N4	c.887C>G	P.T296S
SH_111	15	99671001	99671001	Silent	SNV	G	A	A	SYNM	c.2433G>A	P.T811T
SH_111	16	19620328	19620328	Missense_Mutation	SNV	A	G	G	C16orf62	c.1181A>G	P.K394R
SH_111	16	20435280	20435280	Silent	SNV	G	A	A	ACSM5	c.810G>A	P.T270T
SH_111	17	7324624	7324624	Silent	SNV	A	C	C	SPEM1	c.630A>C	P.P210P
SH_111	2	113539278	113539278	Silent	SNV	T	C	C	IL1A	c.222A>G	P.V74V
SH_111	2	159033054	159033054	Frame_Shift_Ins	INDEL	-	A	A	CCDC148	c.1169dupT	P.L390fs
SH_111	2	27857793	27857793	Splice_Site	SNV	T	G	G	GNP1	c.393+2T>G	
SH_111	2	68882553	68882553	Missense_Mutation	SNV	G	A	A	PROKR1	c.1027G>A	P.V343M
SH_111	20	55777539	55777539	Missense_Mutation	SNV	G	A	A	BMP7	c.752C>T	P.T251M
SH_111	21	30699470	30699470	Frame_Shift_Del	INDEL	T	-	-	BACH1	c.1326delT	P.S443fs
SH_111	3	148896286	148896286	Missense_Mutation	SNV	C	G	G	CP	c.2794G>C	P.D932H
SH_111	3	30713853	30713853	Missense_Mutation	SNV	G	A	A	TGFBR2	c.1253G>A	P.C418Y
SH_111	3	54933813	54933813	Splice_Site	SNV	A	T	T	CACNA2D3	c.2369-2A>T	
SH_111	5	147051334	147051334	Silent	SNV	G	A	A	JAKMIP2	c.36C>T	P.P12P
SH_111	6	160174638	160174638	Missense_Mutation	SNV	G	A	A	WTAP	c.599G>A	P.S200N
SH_111	6	24875951	24875951	Silent	SNV	C	T	T	FAM65B	c.156G>A	P.A52A
SH_111	7	121965521	121965521	Splice_Site	SNV	T	C	C	CADPS2	c.3594+10A>G	
SH_111	7	144345911	144345911	Missense_Mutation	SNV	A	T	T	TPK1	c.247T>A	P.Y83N
SH_111	8	25199252	25199252	Splice_Site	SNV	C	T	T	DOCK5	c.2440-3C>T	
SH_111	8	89209488	89209488	Missense_Mutation	SNV	C	T	T	MMP16	c.180G>A	P.M60I
SH_111	9	125424800	125424800	Missense_Mutation	SNV	A	G	G	OR1L1	c.806A>G	P.K269R
SH_111	9	125424802	125424802	Missense_Mutation	SNV	G	A	A	OR1L1	c.808G>A	P.D270N
SH_111	9	130982480	130982480	Missense_Mutation	SNV	C	T	T	DNM1	c.709C>T	P.R237W
SH_111	9	86468653	86468653	Missense_Mutation	SNV	A	C	C	KIF27	c.3050T>G	P.L1017R
SH_111	X	37587545	37587545	Nonsense_Mutation	SNV	C	T	T	XK	c.1165C>T	P.Q389*
SH_111	X	47032597	47032597	Splice_Site	SNV	G	A	A	RBM10	c.502+1G>A	
SH_113	1	13183781	13183781	Missense_Mutation	SNV	G	T	T	HNRNPCL2	c.92C>A	P.S31Y
SH_113	1	39775375	39775375	Splice_Site	SNV	A	G	G	MACF1	c.2931+7A>G	
SH_113	1	43773103	43773103	Missense_Mutation	SNV	C	A	A	TIE1	c.773C>A	P.A258D
SH_113	10	119003551	119003551	Missense_Mutation	SNV	G	A	A	SLC18A2	c.191G>A	P.R64K
SH_113	10	132891516	132891516	Missense_Mutation	SNV	C	A	A	TCERG1L	c.1670G>T	P.R557I
SH_113	10	29769544	29769544	Missense_Mutation	SNV	G	T	T	SVIL	c.4369C>A	P.L1457I
SH_113	11	124180558	124180558	Silent	SNV	A	G	G	OR8D1	c.105T>C	P.Y35Y
SH_113	11	126080806	126080806	Missense_Mutation	SNV	G	A	A	RPUSD4	c.334C>T	P.P112S
SH_113	11	126391275	126391275	Missense_Mutation	SNV	G	A	A	KIRREL3	c.368C>T	P.A123V
SH_113	11	55872934	55872934	Missense_Mutation	SNV	G	T	T	OR8H2	c.416G>T	P.R139M
SH_113	11	62327300	62327300	Missense_Mutation	SNV	C	A	A	EEF1G	c.1165G>T	P.D389Y
SH_113	11	986887	986887	Silent	SNV	G	T	T	AP2A2	c.1068G>T	P.L1356L
SH_113	12	129293321	129293321	Splice_Site	SNV	A	T	T	SLC15A4	c.1258+12T>A	
SH_113	12	9254111	9254111	Frame_Shift_Del	INDEL	CTGT	-	-	A2M	423_1426delAC	P.T475fs
SH_113	13	80911668	80911668	Missense_Mutation	SNV	C	G	G	SPRY2	c.173G>C	P.G58A
SH_113	14	21991956	21991956	Missense_Mutation	SNV	A	T	T	SALL2	c.1501T>A	P.C501S
SH_113	2	107002879	107002879	Splice_Site	SNV	C	A	A	PLGLA	n.244+8C>A	
SH_113	2	179605000	179605000	Silent	SNV	G	T	T	TTN	c.12009C>A	P.V4003V
SH_113	3	35835429	35835429	Silent	SNV	T	C	C	ARPP21	c.2418T>C	P.A806A
SH_113	3	56651150	56651150	Silent	SNV	T	C	C	CCDC66	c.1752T>C	P.N584N
SH_113	4	55973998	55973998	Missense_Mutation	SNV	T	C	C	KDR	c.1318A>G	P.T440A
SH_113	4	68380089	68380089	Missense_Mutation	SNV	T	C	C	CENPC	c.1147A>G	P.T383A
SH_113	4	956312	956312	Missense_Mutation	SNV	C	A	A	DGKQ	c.2125G>T	P.A709S
SH_113	5	37048753	37048753	Missense_Mutation	SNV	C	T	T	NIPBL	c.6739C>T	P.R2247C
SH_113	5	41149466	41149466	Missense_Mutation	SNV	T	C	C	C6	c.2500A>G	P.I834V
SH_113	6	33263862	33263862	Silent	SNV	C	A	A	RGL2	c.465G>T	P.T155T
SH_113	7	73462526	73462526	Missense_Mutation	SNV	G	T	T	ELN	c.740G>T	P.G247V
SH_113	7	82580151	82580151	Silent	SNV	G	A	A	PCLO	c.9753C>T	P.I3251I
SH_113	8	107773510	107773510	Missense_Mutation	SNV	G	A	A	ABRA	c.901C>T	P.R301C
SH_113	8	145947384	145947384	Missense_Mutation	SNV	A	G	G	ZNF251	c.1661T>C	P.I554T
SH_113	9	35802548	35802548	Missense_Mutation	SNV	A	G	G	NPR2	c.1759A>G	P.I587V
SH_115	1	152284210	152284210	Missense_Mutation	SNV	C	T	T	FLG	c.3152G>A	P.R1051H
SH_115	1	247062817	247062817	Splice_Site	SNV	A	C	C	AHCTF1	c.1433-3T>G	
SH_115	11	73022494	73022494	Missense_Mutation	SNV	C	A	A	ARHGEF17	c.2811C>A	P.D937E
SH_115	11	76371887	76371887	Silent	SNV	C	A	A	LRRC32	c.750G>T	P.L250L
SH_115	14	77751890	77751890	Missense_Mutation	SNV	C	T	T	POMT3	c.1418G>A	P.R473Q
SH_115	16	684601	684601	Missense_Mutation	SNV	T	C	C	METTL26	c.380A>G	P.N127S
SH_115	17	29622596	29622596	Missense_Mutation	SNV	T	C	C	OMG	c.754A>G	P.T252A
SH_115	17	30986316	30986316	Missense_Mutation	SNV	G	T	T	MYO1D	c.2162C>A	P.T721N
SH_115	17	48667880	48667880	Missense_Mutation	SNV	A	C	C	CACNA1G	c.2350A>C	P.S784R
SH_115	19	43259170	43259170	Missense_Mutation	SNV	G	A	A	PSG8	c.958C>T	P.R320C
SH_115	2	113785536	113785536	Missense_Mutation	SNV	T	A	A	IL36B	c.418A>T	P.T140S
SH_115	2	152289674	152289674	Missense_Mutation	SNV	A	G	G	RIF1	c.1009A>G	P.T337A
SH_115	2	203378462	203378462	Nonsense_Mutation	SNV	C	T	T	BMPR2	c.439C>T	P.R147*
SH_115	20	44036884	44036884	Missense_Mutation	SNV	G	A	A	DBNDD2	c.83G>A	P.S28N
SH_115	22	16287550	16287550	Silent	SNV	G	A	A	POTEH	c.336C>T	P.S112S
SH_115	3	178952085	178952085	Missense_Mutation	SNV	A	G	G	PIK3CA	c.3140A>G	P.H1047R
SH_115	4	56502258	56502258	Silent	SNV	G	T	T	NMU	c.102C>A	P.G34G
SH_115	5	37006698	37006698	Splice_Site	SNV	C	T	T	NIPBL	c.4087+8C>T	
SH_115	5	67591077	67591077	Missense_Mutation	SNV	G	A	A	PIK3R1	c.1670G>A	P.R557Q
SH_115	7	140453136	140453136	Missense_Mutation	SNV	A	T	T	BRAF	c.1799T>A	P.V600E
SH_115	7	148771598	148771598	Missense_Mutation	SNV	A	C	C	ZNF786	c.178T>G	P.W60G
SH_115	8	133882025	133882025	Silent	SNV	C	T	T	TG	c.228C>T	P.N76N
SH_115	8	42694370	42694370	Frame_Shift_Ins	INDEL	-	A	A	THAP1	c.225dupT	P.A76fs
SH_115	8	57026165	57026165	Missense_Mutation	SNV	C	T	T	MOS	c.377G>A	P.R126H
SH_115	8	92972548	92972548	Silent	SNV	C	T	T	RUNX1T1	c.1737G>A	P.P579P
SH_115	9	386353	386353	Missense_Mutation	SNV	G	A	A	DOCK4	c.2801G>A	P.R934Q
SH_118	1	176863905	176863905	Silent	SNV	T	A	A	ASTN1	c.2733A>T	P.P911P
SH_118	1	89732172	89732172	Missense_Mutation	SNV	T	C	C	GBP5	c.725A>G	P.Q242R
SH_118	10	112839054	112839054	Missense_Mutation	SNV	A	T	T	ADRA2A	c.1300A>T	P.S434C
SH_118	10	13164469	13164469	Missense_Mutation	SNV	A	T	T	OPTN	c.864A>T	P.E288D
SH_118	10	22675791	22675791	Missense_Mutation	SNV	T	C	C	SPAG6	c.506T>C	P.I169T
SH_118	11	122756913	122756913	Splice_Site	SNV	G	T	T	C11orf63	c.344+12G>T	
SH_118	11	6245708	6245708	Silent	SNV	C	T	T	FAM160A2	c.39G>A	P.R13R
SH_118	13	78235572	78235572	Missense_Mutation	SNV	C	G	G	LOC100129307	c.1190G>C	P.R397T

SH_118	17	48917669	48917669	Missense_Mutation	SNV	G	C	C	WFIKKN2	c.1020G>C	P.E340D
SH_118	19	19680276	19680276	Silent	SNV	G	A	A	PBX4	c.750C>T	P.G250G
SH_118	19	40834359	40834359	Missense_Mutation	SNV	C	T	T	C19orf47	c.511G>A	P.V171M
SH_118	19	4306232	4306234	Missense_Mutation	INDEL	AGT	-	-	FSD1	c.149_151delAG	P.E50_F51delinsV
SH_118	2	132021093	132021093	Missense_Mutation	SNV	A	G	G	POTEE	c.2065A>G	P.N689D
SH_118	2	166850884	166850884	Missense_Mutation	SNV	C	A	A	SCN1A	c.4624G>T	P.V1542F
SH_118	21	46687568	46687568	Missense_Mutation	SNV	T	A	A	POFUT2	c.1073A>T	P.E358V
SH_118	3	169497224	169497224	Missense_Mutation	SNV	C	T	T	MYNN	c.935C>T	P.S312L
SH_118	3	31725287	31725287	Missense_Mutation	SNV	T	A	A	OSBPL10	c.1373A>T	P.K458I
SH_118	3	97887561	97887561	Silent	SNV	A	T	T	OR5H15	c.18A>T	P.A6A
SH_118	5	140167794	140167794	Missense_Mutation	SNV	C	A	A	PCDHA1	c.1919C>A	P.A640D
SH_118	7	82531991	82531991	Missense_Mutation	SNV	C	T	T	PCLO	c.13504G>A	P.D4502N
SH_118	8	94767159	94767159	Missense_Mutation	SNV	G	C	C	TMEM67	c.17G>C	P.G6A
SH_118	9	133932471	133932471	Missense_Mutation	SNV	G	T	T	LAMC3	c.2095G>T	P.G699C
SH_118	X	50377499	50377499	Missense_Mutation	SNV	T	A	A	SHROOM4	c.1574A>T	P.Q525L
SH_119	1	103387119	103387119	Silent	SNV	A	T	T	COL11A1	c.3546T>A	P.P1182P
SH_119	1	109007883	109007883	Silent	SNV	T	A	A	NBPF6	c.1584T>A	P.I528I
SH_119	1	109803859	109803859	Missense_Mutation	SNV	A	T	T	CELSR2	c.4154A>T	P.Q1385L
SH_119	1	109823787	109823787	Missense_Mutation	SNV	T	A	A	PSRC1	c.606A>T	P.R202S
SH_119	1	110134771	110134771	Silent	SNV	A	T	T	GNAI3	c.981A>T	P.T327T
SH_119	1	112042988	112042988	Missense_Mutation	SNV	T	A	A	ADORA3	c.541A>T	P.S181C
SH_119	1	11827056	11827056	Missense_Mutation	SNV	G	A	A	C1orf167	c.1213G>A	P.G405R
SH_119	1	118514487	118514487	Missense_Mutation	SNV	T	A	A	SPAG17	c.6325A>T	P.R2109W
SH_119	1	12776220	12776220	Missense_Mutation	SNV	T	A	A	AADACL3	c.41T>A	P.V14E
SH_119	1	13330623	13330623	Nonsense_Mutation	SNV	A	T	T	PRAMEF22	c.663T>A	P.C221*
SH_119	1	144867918	144867918	Splice_Site	SNV	T	C	C	PDE4DIP	c.5518+3A>G	
SH_119	1	145558247	145558247	Missense_Mutation	SNV	A	T	T	ANKRD35	c.94A>T	P.S32C
SH_119	1	145597578	145597578	Splice_Site	SNV	T	C	C	POLR3C	c.1049-4A>G	
SH_119	1	149898602	149898602	Silent	SNV	C	A	A	SF3B4	c.372G>T	P.G124G
SH_119	1	151090447	151090447	Missense_Mutation	SNV	A	T	T	GABPB2	c.1062A>T	P.R354S
SH_119	1	151774931	151774931	Missense_Mutation	SNV	T	A	A	LINGO4	c.250A>T	P.S84C
SH_119	1	151787148	151787148	Nonsense_Mutation	SNV	T	A	A	RORC	c.772A>T	P.K258*
SH_119	1	152382333	152382333	Missense_Mutation	SNV	T	A	A	CRNN	c.1225A>T	P.S409C
SH_119	1	152882585	152882585	Silent	SNV	A	G	G	IVL	c.312A>G	P.P104P
SH_119	1	153043107	153043107	Missense_Mutation	SNV	T	A	A	SPRR2B	c.209A>T	P.K70M
SH_119	1	153580528	153580528	Missense_Mutation	SNV	T	A	A	S100A16	c.100A>T	P.S34C
SH_119	1	154234163	154234163	Silent	SNV	A	T	T	UBAP2L	c.2892A>T	P.G964G
SH_119	1	154295520	154295520	Nonsense_Mutation	SNV	A	T	T	AQP10	c.295A>T	P.K99*
SH_119	1	15429900	15429900	Missense_Mutation	SNV	C	T	T	KAZN	c.1825C>T	P.P609S
SH_119	1	154574588	154574588	Missense_Mutation	SNV	T	A	A	ADAR	c.530A>T	P.Y177F
SH_119	1	155230223	155230223	Missense_Mutation	SNV	T	A	A	SCAMP3	c.286A>T	P.T96S
SH_119	1	155448365	155448365	Missense_Mutation	SNV	T	A	A	ASH1L	c.4296A>T	P.L1432F
SH_119	1	155874533	155874533	Missense_Mutation	SNV	T	A	A	RIT1	c.226A>T	P.T76S
SH_119	1	156376964	156376964	Missense_Mutation	SNV	A	T	T	C1orf61	c.331T>A	P.C111S
SH_119	1	15684631	15684631	Missense_Mutation	SNV	A	T	T	FHAD1	c.2522A>T	P.E841V
SH_119	1	156882027	156882027	Splice_Site	SNV	T	A	A	PEAR1	c.1952-12T>A	
SH_119	1	157067737	157067737	Missense_Mutation	SNV	T	A	A	ETV3L	c.530A>T	P.Q177L
SH_119	1	157488251	157488251	Missense_Mutation	SNV	A	T	T	FCRL5	c.2770T>A	P.Y924N
SH_119	1	158389916	158389916	Silent	SNV	A	T	T	OR10K2	c.741T>A	P.I247I
SH_119	1	158576331	158576331	Missense_Mutation	SNV	T	C	C	OR10Z1	c.103T>C	P.Y35H
SH_119	1	159015243	159015243	Missense_Mutation	SNV	T	A	A	IFI16	c.1318T>A	P.F440I
SH_119	1	159842349	159842349	Missense_Mutation	SNV	T	A	A	CFAP45	c.1582A>T	P.T528S
SH_119	1	159856340	159856340	Missense_Mutation	SNV	T	A	A	CFAP45	c.728A>T	P.Q243L
SH_119	1	160523799	160523799	Missense_Mutation	SNV	T	A	A	CD84	c.526A>T	P.N176Y
SH_119	1	161024252	161024252	Missense_Mutation	SNV	A	T	T	ARHGAP30	c.440T>A	P.F147Y
SH_119	1	161165954	161165954	Splice_Site	SNV	A	T	T	ADAMTS4	c.1090+7T>A	
SH_119	1	161968022	161968022	Missense_Mutation	SNV	T	A	A	OLFML2B	c.1070A>T	P.H357L
SH_119	1	167096999	167096999	Missense_Mutation	SNV	T	A	A	DUSP27	c.2631T>A	P.D877E
SH_119	1	167487657	167487657	Missense_Mutation	SNV	A	T	T	CD247	c.46T>A	P.L16M
SH_119	1	168513158	168513158	Silent	SNV	A	T	T	XCL2	c.45T>A	P.T15T
SH_119	1	169519870	169519870	Splice_Site	SNV	A	G	G	F5	c.1396+8T>C	
SH_119	1	169564086	169564086	Nonsense_Mutation	SNV	T	A	A	SELP	c.2131A>T	P.K711*
SH_119	1	171504565	171504565	Splice_Site	SNV	A	T	T	PRRC2C	c.1868-2A>T	
SH_119	1	172417594	172417594	Missense_Mutation	SNV	T	A	A	C1orf105	c.121T>A	P.S41T
SH_119	1	175130037	175130037	Nonsense_Mutation	SNV	A	T	T	KIAA0040	c.113T>A	P.L38*
SH_119	1	175375420	175375420	Missense_Mutation	SNV	A	T	T	TNR	c.431T>A	P.L144Q
SH_119	1	176564581	176564581	Missense_Mutation	SNV	T	A	A	PAPPA2	c.1841T>A	P.L614Q
SH_119	1	179452349	179452349	Missense_Mutation	SNV	A	T	T	AXNDN1	c.2084A>T	P.Q695L
SH_119	1	179815404	179815404	Missense_Mutation	SNV	T	A	A	TOR1AIP2	c.1215A>T	P.L405F
SH_119	1	181546907	181546907	Missense_Mutation	SNV	T	A	A	CACNA1E	c.518T>A	P.L173Q
SH_119	1	183201909	183201909	Nonsense_Mutation	SNV	C	T	T	LAMC2	c.2137C>T	P.Q713Q
SH_119	1	183208627	183208627	Missense_Mutation	SNV	G	A	A	LAMC2	c.2998G>A	P.A1000T
SH_119	1	183885704	183885704	Nonsense_Mutation	SNV	A	T	T	RG1L	c.1867A>T	P.K623*
SH_119	1	185932990	185932990	Silent	SNV	T	A	A	HMCN1	c.2061T>A	P.A687A
SH_119	1	185951443	185951443	Silent	SNV	A	T	T	HMCN1	c.2712A>T	P.G904G
SH_119	1	185953438	185953438	Silent	SNV	T	A	A	HMCN1	c.2928T>A	P.V976V
SH_119	1	185964041	185964041	Silent	SNV	T	A	A	HMCN1	c.3600T>A	P.P1200P
SH_119	1	185966618	185966618	Missense_Mutation	SNV	T	A	A	HMCN1	c.3836T>A	P.V1279E
SH_119	1	186287674	186287674	Silent	SNV	T	A	A	TPR	c.6726A>T	P.P2242P
SH_119	1	186646003	186646003	Nonsense_Mutation	SNV	T	A	A	PTGS2	c.685A>T	P.K229*
SH_119	1	19018446	19018446	Missense_Mutation	SNV	A	T	T	PAX7	c.785A>T	P.Q262L
SH_119	1	192985494	192985494	Missense_Mutation	SNV	T	A	A	UCHL5	c.974A>T	P.Q325L
SH_119	1	197094228	197094228	Silent	SNV	G	A	A	ASPM	c.3030C>T	P.D1010D
SH_119	1	197890658	197890658	Missense_Mutation	SNV	A	T	T	LHX9	c.575A>T	P.Y192F
SH_119	1	200529913	200529913	Silent	SNV	T	A	A	KIF14	c.2694A>T	P.A898A
SH_119	1	201038314	201038314	Missense_Mutation	SNV	T	A	A	CACNA1S	c.2501A>T	P.H834L
SH_119	1	201181196	201181196	Missense_Mutation	SNV	A	G	G	IGFN1	c.7175A>G	P.Y2392C
SH_119	1	203466094	203466094	Splice_Site	SNV	T	A	A	OPTC	c.232-11T>A	
SH_119	1	203689873	203689873	Splice_Site	SNV	A	T	T	ATP2B4	c.2598+5A>T	
SH_119	1	204197873	204197873	Silent	SNV	T	A	A	PLEKHA6	c.2868A>T	P.T956T
SH_119	1	205899115	205899115	Missense_Mutation	SNV	T	A	A	SLC26A9	c.622A>T	P.M208L
SH_119	1	207252304	207252304	Silent	SNV	A	T	T	PKFB2	c.1356A>T	P.A452A
SH_119	1	213139656	213139656	Missense_Mutation	SNV	A	T	T	VASH2	c.271A>T	P.I91F
SH_119	1	223176096	223176096	Missense_Mutation	SNV	A	T	T	DISP1	c.1357A>T	P.M453L
SH_119	1	223178411	223178411	Silent	SNV	A	T	T	DISP1	c.3672A>T	P.A1224A
SH_119	1	224495722	224495722	Missense_Mutation	SNV	T	A	A	NVL	c.268A>T	P.N90Y
SH_119	1	226420236	226420236	Missense_Mutation	SNV	T	A	A	LIN9	c.1538A>T	P.H513L
SH_119	1	228525739	228525739	Missense_Mutation	SNV	T	A	A	OBSCN	c.16895T>A	P.L5632Q

SH_119	1	22902927	22902927	Missense_Mutation	SNV	A	T	T	EPHA8	c.377A>T	P.Y126F
SH_119	1	22919920	22919920	Missense_Mutation	SNV	T	A	A	EPHA8	c.1417T>A	P.Y473N
SH_119	1	229763428	229763428	Silent	SNV	A	T	T	URB2	c.48A>T	P.T16T
SH_119	1	229768107	229768107	Missense_Mutation	SNV	A	T	T	URB2	c.218A>T	P.Y73F
SH_119	1	231344750	231344750	Missense_Mutation	SNV	A	T	T	TRIM67	c.1877A>T	P.D626V
SH_119	1	232650879	232650879	Silent	SNV	T	A	A	SIPA1L2	c.207A>T	P.P69P
SH_119	1	235409824	235409824	Splice_Site	SNV	T	C	C	ARID4B	c.357A>G	P.T119T
SH_119	1	236746148	236746148	Missense_Mutation	SNV	T	A	A	HEATR1	c.2450A>T	P.Q817L
SH_119	1	236760210	236760210	Missense_Mutation	SNV	T	A	A	HEATR1	c.670A>T	P.I224L
SH_119	1	236899908	236899908	Silent	SNV	A	T	T	ACTN2	c.99A>T	P.P33P
SH_119	1	238048720	238048720	Missense_Mutation	SNV	A	T	T	ZP4	c.1131T>A	P.S377R
SH_119	1	243328876	243328876	Missense_Mutation	SNV	T	A	A	CEP170	c.2092A>T	P.T698S
SH_119	1	243778465	243778465	Splice_Site	SNV	T	C	C	AKT3	c.562-2A>G	
SH_119	1	247264327	247264327	Silent	SNV	T	A	A	ZNF669	c.486A>T	P.P162P
SH_119	1	247875399	247875399	Missense_Mutation	SNV	T	C	C	OR6F1	c.659A>G	P.Y220C
SH_119	1	248903065	248903065	Silent	SNV	A	T	T	LYPD8	c.87T>A	P.T29T
SH_119	1	24981391	24981391	Silent	SNV	C	A	A	SRRM1	c.1086C>A	P.S362S
SH_119	1	26392813	26392813	Missense_Mutation	SNV	T	G	G	TRIM63	c.278A>C	P.Q93P
SH_119	1	26515998	26515998	Missense_Mutation	SNV	C	T	T	CNKSR1	c.2122C>T	P.P708S
SH_119	1	26694142	26694142	Silent	SNV	T	A	A	ZNF683	c.261A>T	P.P87P
SH_119	1	29070398	29070398	Missense_Mutation	SNV	A	T	T	YTHDF2	c.1466A>T	P.Q489L
SH_119	1	31230577	31230577	Missense_Mutation	SNV	A	T	T	LAPTM5	c.16T>A	P.S6T
SH_119	1	34673816	34673816	Missense_Mutation	SNV	T	A	A	C1orf94	c.1505T>A	P.L502Q
SH_119	1	35447612	35447612	Missense_Mutation	SNV	T	A	A	TMEM35B	c.398A>T	P.Q133L
SH_119	1	46472002	46472002	Silent	SNV	A	T	T	MAST2	c.837A>T	P.T279T
SH_119	1	47548087	47548087	Missense_Mutation	SNV	T	G	G	CYP4Z1	c.446T>G	P.L149R
SH_119	1	55119552	55119552	Missense_Mutation	SNV	A	T	T	MROH7	c.953A>T	P.N318I
SH_119	1	55152062	55152062	Silent	SNV	C	T	T	MROH7	c.2652C>T	P.C884C
SH_119	1	57349294	57349294	Silent	SNV	A	T	T	C8A	c.795A>T	P.V265V
SH_119	1	59922760	59922760	Splice_Site	SNV	A	T	T	FGGY	c.670+12A>T	
SH_119	1	6214762	6214762	Missense_Mutation	SNV	G	T	T	CHD5	c.703C>A	P.Q235K
SH_119	1	64643545	64643545	Silent	SNV	T	A	A	ROR1	c.1821T>A	P.S607S
SH_119	1	6522970	6522970	Missense_Mutation	SNV	A	T	T	TNFRSF25	c.659T>A	P.L220Q
SH_119	1	79383640	79383640	Silent	SNV	A	C	C	ADGRL4	c.1557T>G	P.V519V
SH_119	1	85570272	85570272	Silent	SNV	A	T	T	WDR63	c.1428A>T	P.S476S
SH_119	1	89659026	89659026	Missense_Mutation	SNV	T	A	A	GBP4	c.433A>T	P.S145C
SH_119	1	95294069	95294069	Missense_Mutation	SNV	A	T	T	SLC44A3	c.436A>T	P.S146C
SH_119	1	9992936	9992936	Silent	SNV	T	A	A	LZIC	c.357A>T	P.V119V
SH_119	10	100242464	100242464	Silent	SNV	A	T	T	HPSE2	c.1368T>A	P.A456A
SH_119	10	102088970	102088970	Missense_Mutation	SNV	A	T	T	PKD2L1	c.206T>A	P.L69Q
SH_119	10	102510522	102510522	Missense_Mutation	SNV	T	A	A	PAX2	c.284T>A	P.V95E
SH_119	10	105838347	105838347	Splice_Site	SNV	A	T	T	COL17A1	c.53-3T>A	
SH_119	10	112838295	112838295	Missense_Mutation	SNV	T	A	A	ADRA2A	c.541T>A	P.F181I
SH_119	10	120809466	120809466	Silent	SNV	T	A	A	EIF3A	c.2505A>T	P.A835A
SH_119	10	124399886	124399886	Missense_Mutation	SNV	A	T	T	DMBT1	c.6883A>T	P.T2295S
SH_119	10	126507985	126507985	Missense_Mutation	SNV	A	G	G	FAM175B	c.233A>G	P.E78G
SH_119	10	135027563	135027563	Silent	SNV	A	G	G	KNDC1	c.4614A>G	P.L1538L
SH_119	10	15014579	15014579	Missense_Mutation	SNV	A	T	T	MEIG1	c.206A>T	P.Y69F
SH_119	10	21962788	21962788	Missense_Mutation	SNV	A	T	T	MLLT10	c.1561A>T	P.T521S
SH_119	10	23326397	23326397	Nonsense_Mutation	SNV	A	T	T	ARMC3	c.2587A>T	P.R863*
SH_119	10	25885621	25885621	Missense_Mutation	SNV	A	G	G	GPR158	c.2048A>G	P.Y683C
SH_119	10	29812662	29812662	Missense_Mutation	SNV	T	A	A	SVIL	c.1951A>T	P.S651C
SH_119	10	43291974	43291974	Missense_Mutation	SNV	C	T	T	BMS1	c.1282C>T	P.R428C
SH_119	10	43656042	43656042	Missense_Mutation	SNV	A	T	T	CSGALNACT2	c.979A>T	P.S327C
SH_119	10	46272760	46272760	Missense_Mutation	SNV	A	T	T	FAM21C	c.2182A>T	P.S728C
SH_119	10	46968575	46968575	Splice_Site	SNV	A	T	T	SYT15	c.355+6T>A	
SH_119	10	51769531	51769531	Missense_Mutation	SNV	A	T	T	AGAP6	c.1646A>T	P.Q549L
SH_119	10	55626482	55626482	Missense_Mutation	SNV	T	A	A	PCDH15	c.3652A>T	P.M1218L
SH_119	10	74994592	74994592	Missense_Mutation	SNV	C	T	T	FAM149B1	c.1370C>T	P.S457L
SH_119	10	75407400	75407400	Silent	SNV	A	T	T	SYNPQ2L	c.2010T>A	P.S670S
SH_119	10	7682717	7682717	Missense_Mutation	SNV	C	A	A	ITIH5	c.401G>T	P.G134V
SH_119	10	7763739	7763739	Missense_Mutation	SNV	A	T	T	ITIH2	c.866A>T	P.E289V
SH_119	10	90568136	90568136	Missense_Mutation	SNV	A	T	T	LIPM	c.229A>T	P.R77W
SH_119	11	100819186	100819186	Splice_Site	SNV	A	T	T	ARHGAP42	c.1044-2A>T	
SH_119	11	100836393	100836393	Splice_Site	SNV	A	T	T	ARHGAP42	c.1445-9A>T	
SH_119	11	100999800	100999800	Nonsense_Mutation	SNV	A	T	T	PGR	c.2T>A	P.M1?
SH_119	11	102593382	102593382	Missense_Mutation	SNV	T	A	A	MMP8	c.56A>T	P.Q19L
SH_119	11	103070122	103070122	Missense_Mutation	SNV	A	T	T	DYNC2H1	c.8005A>T	P.S2669C
SH_119	11	107965721	107965721	Splice_Site	SNV	A	T	T	CUL5	c.1743+7A>T	
SH_119	11	108536020	108536020	Missense_Mutation	SNV	A	T	T	DDX10	c.140A>T	P.Q47L
SH_119	11	108593923	108593923	Missense_Mutation	SNV	G	A	A	DDX10	c.1699G>A	P.E567K
SH_119	11	111368725	111368725	Nonsense_Mutation	SNV	A	T	T	BTG4	c.309T>A	P.C103*
SH_119	11	111915958	111915958	Splice_Site	SNV	A	T	T	DLAT	c.1290+4A>T	
SH_119	11	113628549	113628549	Missense_Mutation	SNV	T	A	A	ZW10	c.760A>T	P.R254W
SH_119	11	1151627	1151627	Missense_Mutation	SNV	A	T	T	MUC5AC	c.1A>T	P.M1?
SH_119	11	116633571	116633571	Missense_Mutation	SNV	T	A	A	BUD13	c.734A>T	P.H245L
SH_119	11	117329461	117329461	Splice_Site	SNV	T	A	A	DSCAML1	c.3748+9A>T	
SH_119	11	117866339	117866339	Missense_Mutation	SNV	T	A	A	IL10RA	c.724T>A	P.F242I
SH_119	11	119043108	119043108	Missense_Mutation	SNV	A	T	T	NLRX1	c.114A>T	P.Q38H
SH_119	11	124761432	124761432	Missense_Mutation	SNV	C	T	T	ROBO4	c.1276G>A	P.G426S
SH_119	11	128933805	128933805	Missense_Mutation	SNV	T	A	A	ARHGAP32	c.835A>T	P.T279S
SH_119	11	130777872	130777872	Missense_Mutation	SNV	T	A	A	SNX19	c.281A>T	P.Q94L
SH_119	11	134238601	134238601	Missense_Mutation	SNV	A	T	T	GLB1L2	c.953A>T	P.H318L
SH_119	11	18743106	18743106	Silent	SNV	G	A	A	IGSF22	c.354C>T	P.S118S
SH_119	11	1908759	1908759	Missense_Mutation	SNV	A	T	T	LSP1	c.800A>T	P.E267V
SH_119	11	20005673	20005673	Missense_Mutation	SNV	A	T	T	NAV2	c.2456A>T	P.Y819F
SH_119	11	2444225	2444225	Missense_Mutation	SNV	A	T	T	TRPM5	c.42T>A	P.D14E
SH_119	11	2593278	2593278	Missense_Mutation	SNV	A	T	T	KCNQ1	c.719A>T	P.H240L
SH_119	11	35453944	35453944	Missense_Mutation	SNV	A	T	T	PAMR1	c.2123T>A	P.V708E
SH_119	11	35453945	35453945	Missense_Mutation	SNV	C	T	T	PAMR1	c.2122G>A	P.V708M
SH_119	11	36397717	36397717	Splice_Site	SNV	A	T	T	PRR5L	c.2+9A>T	
SH_119	11	3714478	3714478	Missense_Mutation	SNV	T	A	A	NUP98	c.4295A>T	P.Y1432F
SH_119	11	43427103	43427103	Missense_Mutation	SNV	A	T	T	TTC17	c.1519A>T	P.S507S
SH_119	11	44939571	44939571	Missense_Mutation	SNV	A	T	T	TSPAN18	c.307A>T	P.I103F
SH_119	11	46392894	46392894	Missense_Mutation	SNV	A	T	T	DGKZ	c.1166A>T	P.K389M
SH_119	11	47609903	47609903	Missense_Mutation	SNV	T	A	A	FAM180B	c.469T>A	P.W157R
SH_119	11	5067880	5067880	Missense_Mutation	SNV	T	A	A	OR52J3	c.125T>A	P.L42Q
SH_119	11	51515748	51515748	Missense_Mutation	SNV	T	A	A	OR4C46	c.467T>A	P.I156K

SH_119	11	51515749	51515749	Silent	SNV	A	C	C	OR4C46	c.468A>C	P.I156I
SH_119	11	55659015	55659015	Missense_Mutation	SNV	T	A	A	TRIM51	c.1266T>A	P.F422L
SH_119	11	56000335	56000335	Missense_Mutation	SNV	A	C	C	OR5T2	c.327T>G	P.D109E
SH_119	11	61026245	61026245	Missense_Mutation	SNV	T	A	A	VWCE	c.2770A>T	P.T924S
SH_119	11	6261397	6261397	Missense_Mutation	SNV	A	T	T	CNGA4	c.373A>T	P.T125S
SH_119	11	64022882	64022882	Missense_Mutation	SNV	A	T	T	PLCB3	c.482A>T	P.K161M
SH_119	11	6477326	6477326	Silent	SNV	T	A	A	TRIM3	c.1509A>T	P.A503A
SH_119	11	66358745	66358745	Missense_Mutation	SNV	T	A	A	CCDC87	c.1742A>T	P.K581M
SH_119	11	68030220	68030220	Silent	SNV	T	A	A	C11orf24	c.243A>T	P.T81T
SH_119	11	68171171	68171171	Splice_Site	SNV	A	T	T	LRP5	c.-137+4A>T	
SH_119	11	73941339	73941339	Missense_Mutation	SNV	A	T	T	PPME1	c.448A>T	P.I150F
SH_119	11	76922906	76922906	Missense_Mutation	SNV	A	T	T	MYO7A	c.6278A>T	P.K2093M
SH_119	11	77702289	77702289	Silent	SNV	T	A	A	INTS4	c.111A>T	P.A37A
SH_119	11	8462246	8462246	Missense_Mutation	SNV	A	T	T	STK33	c.803T>A	P.I268K
SH_119	11	88045643	88045643	Missense_Mutation	SNV	T	A	A	CTSC	c.398A>T	P.N133I
SH_119	11	88911873	88911873	Missense_Mutation	SNV	A	T	T	TYR	c.752A>T	P.Y251F
SH_119	11	89911120	89911120	Missense_Mutation	SNV	T	A	A	NAALAD2	c.1594T>A	P.S532T
SH_119	11	92533570	92533570	Missense_Mutation	SNV	T	A	A	FAT3	c.7391T>A	P.L2464Q
SH_119	11	93528081	93528081	Silent	SNV	A	T	T	MED17	c.867A>T	P.P289P
SH_119	11	93819280	93819280	Nonsense_Mutation	SNV	C	T	T	HEPHL1	c.2005C>T	P.R669*
SH_119	11	94126683	94126683	Silent	SNV	A	T	T	GNR83	c.615T>A	P.A205A
SH_119	12	100904910	100904910	Missense_Mutation	SNV	A	T	T	NR1H4	c.434A>T	P.E145V
SH_119	12	104118860	104118860	Silent	SNV	C	A	A	STAB2	c.4791C>A	P.G1597G
SH_119	12	104118861	104118861	Missense_Mutation	SNV	A	G	G	STAB2	c.4792A>G	P.S1598G
SH_119	12	105322003	105322003	Silent	SNV	T	A	A	SLC41A2	c.303A>T	P.A101A
SH_119	12	10586504	10586504	Silent	SNV	T	C	C	KLRC2	c.369A>G	P.T123T
SH_119	12	10774505	10774505	Missense_Mutation	SNV	A	T	T	STYK1	c.1034T>A	P.M345K
SH_119	12	109046121	109046121	Missense_Mutation	SNV	T	A	A	CORO1C	c.1087A>T	P.S363C
SH_119	12	109870803	109870803	Missense_Mutation	SNV	A	T	T	MYO1H	c.2003A>T	P.Y668F
SH_119	12	109968357	109968357	Missense_Mutation	SNV	A	T	T	UBE3B	c.2816A>T	P.H939L
SH_119	12	112182565	112182565	Silent	SNV	A	T	T	ACAD10	c.1926A>T	P.T642T
SH_119	12	116408484	116408484	Silent	SNV	T	A	A	MED13L	c.5982A>T	P.T1994T
SH_119	12	120613934	120613934	Splice_Site	SNV	T	A	A	GCN1	c.913+12A>T	
SH_119	12	120613935	120613935	Splice_Site	SNV	G	T	T	GCN1	c.913+11C>A	
SH_119	12	122818637	122818637	Nonsense_Mutation	SNV	G	A	A	CLIP1	c.2647C>T	P.Q883*
SH_119	12	123472453	123472453	Splice_Site	SNV	G	A	A	PITPNM2	c.2980-5C>T	
SH_119	12	123651251	123651251	Missense_Mutation	SNV	T	A	A	MPHOSPH9	c.2542A>T	P.T848S
SH_119	12	124840022	124840022	Nonsense_Mutation	SNV	T	A	A	NCOR2	c.3307A>T	P.K1103*
SH_119	12	125441289	125441289	Missense_Mutation	SNV	T	A	A	DHX37	c.2401A>T	P.I801F
SH_119	12	133424751	133424751	Splice_Site	SNV	T	A	A	CHFR	c.1613-10A>T	
SH_119	12	14976470	14976470	Missense_Mutation	SNV	A	G	G	C12orf60	c.601A>G	P.K201E
SH_119	12	2027580	2027580	Silent	SNV	T	A	A	CACNA2D4	c.60A>T	P.A20A
SH_119	12	22627686	22627686	Missense_Mutation	SNV	T	A	A	C2CD5	c.2048A>T	P.E683V
SH_119	12	25157405	25157405	Missense_Mutation	SNV	A	T	T	LOC645177	c.130A>T	P.S44C
SH_119	12	25243079	25243079	Nonsense_Mutation	SNV	T	A	A	LRMP	c.554T>A	P.L185*
SH_119	12	2760876	2760876	Missense_Mutation	SNV	T	A	A	CACNA1C	c.4016T>A	P.L1339Q
SH_119	12	32134470	32134470	Missense_Mutation	SNV	A	T	T	KIAA1551	c.581A>T	P.Q194L
SH_119	12	3726177	3726177	Missense_Mutation	SNV	T	A	A	CRACR2A	c.2054A>T	P.Y685F
SH_119	12	40441900	40441900	Silent	SNV	T	A	A	SLC2A13	c.669A>T	P.A223A
SH_119	12	416623	416623	Missense_Mutation	SNV	T	A	A	KDM5A	c.3927A>T	P.L1309F
SH_119	12	45168561	45168561	Nonsense_Mutation	SNV	A	T	T	NELL2	c.1113T>A	P.Y371*
SH_119	12	46592528	46592528	Splice_Site	SNV	T	A	A	SLC38A1	c.1004-2A>T	
SH_119	12	4835747	4835747	Silent	SNV	A	T	T	GALNT8	c.261A>T	P.T87T
SH_119	12	48888578	48888578	Splice_Site	SNV	C	T	T	C12orf54	c.243-3C>T	
SH_119	12	49217252	49217252	Splice_Site	SNV	A	C	C	CACNB3	c.168+3A>C	
SH_119	12	49521873	49521873	Silent	SNV	G	A	A	TUBA1B	c.1224C>T	P.Y408Y
SH_119	12	49959442	49959442	Missense_Mutation	SNV	T	A	A	MCRS1	c.197A>T	P.K66M
SH_119	12	50757002	50757002	Missense_Mutation	SNV	A	G	G	FAM186A	c.338T>C	P.M113T
SH_119	12	52758778	52758779	Frame_Shift_Del	INDEL	AT	-	-	KRT85	c.596_597delAT	P.H199fs
SH_119	12	53007614	53007614	Missense_Mutation	SNV	T	A	A	KRT73	c.842A>T	P.H281L
SH_119	12	53412590	53412590	Missense_Mutation	SNV	A	T	T	EIF4B	c.160A>T	P.T54S
SH_119	12	53686114	53686114	Missense_Mutation	SNV	A	G	G	ESPL1	c.5849A>G	P.Y1950C
SH_119	12	53722674	53722674	Silent	SNV	T	A	A	SP7	c.552A>T	P.T184T
SH_119	12	53946413	53946413	Silent	SNV	T	A	A	ATF7	c.57A>T	P.T19T
SH_119	12	54905728	54905728	Splice_Site	SNV	T	A	A	NCKAP1L	c.635-5T>A	
SH_119	12	55846616	55846616	Missense_Mutation	SNV	A	T	T	OR6C2	c.619A>T	P.I207F
SH_119	12	57009268	57009268	Missense_Mutation	SNV	T	A	A	BAZ2A	c.260A>T	P.Y87F
SH_119	12	57397765	57397765	Missense_Mutation	SNV	T	A	A	ZBTB39	c.937A>T	P.I313L
SH_119	12	57600268	57600268	Missense_Mutation	SNV	A	T	T	LRP1	c.11603A>T	P.Q3868L
SH_119	12	57677748	57677748	Missense_Mutation	SNV	T	A	A	R3HDM2	c.988A>T	P.S330C
SH_119	12	57882876	57882876	Missense_Mutation	SNV	A	T	T	MARS	c.184A>T	P.T62S
SH_119	12	58024298	58024298	Missense_Mutation	SNV	A	T	T	B4GALNT1	c.329T>A	P.L110Q
SH_119	12	5841688	5841688	Nonsense_Mutation	SNV	C	A	A	ANO2	c.1558G>T	P.E520*
SH_119	12	66345189	66345189	Silent	SNV	T	A	A	HMG2A	c.276T>A	P.P92P
SH_119	12	6666280	6666280	Missense_Mutation	SNV	T	A	A	NOP2	c.2306A>T	P.Q769L
SH_119	12	66715758	66715758	Missense_Mutation	SNV	A	T	T	HELB	c.2186A>T	P.Q729L
SH_119	12	70048843	70048843	Silent	SNV	A	T	T	BEST3	c.1533T>A	P.L511L
SH_119	12	7047640	7047640	Splice_Site	SNV	A	T	T	ATN1	c.2518-4A>T	
SH_119	12	70928618	70928618	Missense_Mutation	SNV	A	T	T	PTPRB	c.6199T>A	P.C2067S
SH_119	12	7970499	7970499	Silent	SNV	A	T	T	SLC2A14	c.1272T>A	P.A424A
SH_119	12	85446008	85446008	Missense_Mutation	SNV	A	T	T	LRRIQ1	c.732A>T	P.K244N
SH_119	12	85466830	85466830	Silent	SNV	A	T	T	LRRIQ1	c.2841A>T	P.T947T
SH_119	12	85547816	85547816	Missense_Mutation	SNV	A	C	C	LRRIQ1	c.4664A>C	P.Q1555P
SH_119	12	89917772	89917772	Missense_Mutation	SNV	T	A	A	POC1B-GALNT4	c.546A>T	P.Q182H
SH_119	12	91348357	91348357	Missense_Mutation	SNV	T	A	A	CCER1	c.163A>T	P.S55C
SH_119	12	95443013	95443013	Splice_Site	SNV	T	A	A	NR2C1	c.966-4A>T	
SH_119	12	95926982	95926982	Missense_Mutation	SNV	T	A	A	USP44	c.1051A>T	P.S351C
SH_119	12	96974418	96974418	Missense_Mutation	SNV	A	T	T	CFAP54	c.2840A>T	P.Y947F
SH_119	12	970386	970386	Missense_Mutation	SNV	A	T	T	WNK1	c.1828A>T	P.S610C
SH_119	12	99638169	99638169	Missense_Mutation	SNV	T	C	C	ANKS1B	c.2370A>G	P.I790M
SH_119	13	103389773	103389773	Missense_Mutation	SNV	T	A	A	CCDC168	c.13274A>T	P.K4425I
SH_119	13	107209408	107209408	Silent	SNV	T	A	A	ARGLU1	c.645A>T	P.A215A
SH_119	13	107822921	107822921	Nonsense_Mutation	SNV	G	T	T	FAM155A	c.1301C>A	P.S434*
SH_119	13	108861215	108861215	Missense_Mutation	SNV	T	C	C	LIG4	c.2402A>G	P.Y801C
SH_119	13	111102119	111102119	Missense_Mutation	SNV	T	A	A	COL4A2	c.1172T>A	P.L391H
SH_119	13	21417069	21417069	Missense_Mutation	SNV	T	A	A	XPO4	c.692A>T	P.N231I
SH_119	13	23929590	23929590	Silent	SNV	T	A	A	SACS	c.720A>T	P.A240A
SH_119	13	25008540	25008540	Missense_Mutation	SNV	T	A	A	PARP4	c.4739A>T	P.Q1580L

SH_119	13	25281243	25281243	Missense_Mutation	SNV	T	A	A	ATP12A	c.2270T>A	P.I757K
SH_119	13	25399879	25399879	Missense_Mutation	SNV	A	T	T	RNF17	c.2214A>T	P.E738D
SH_119	13	25671186	25671186	Missense_Mutation	SNV	A	C	C	PABPC3	c.850A>C	P.K284Q
SH_119	13	25671389	25671389	Silent	SNV	A	T	T	PABPC3	c.1053A>T	P.T351T
SH_119	13	28623522	28623522	Splice_Site	SNV	T	A	A	FLT3	c.1035A>T	P.V345V
SH_119	13	30346253	30346253	Missense_Mutation	SNV	T	A	A	UBL3	c.219A>T	P.L73F
SH_119	13	33347443	33347443	Missense_Mutation	SNV	A	T	T	PDS5B	c.4289A>T	P.E1430V
SH_119	13	39262527	39262527	Missense_Mutation	SNV	A	G	G	FREM2	c.1046A>G	P.E349G
SH_119	13	39265875	39265875	Missense_Mutation	SNV	T	A	A	FREM2	c.4394T>A	P.M1465K
SH_119	13	46170688	46170688	Nonsense_Mutation	SNV	A	T	T	ERIC6B	c.453T>A	P.Y151*
SH_119	13	52293340	52293340	Missense_Mutation	SNV	A	T	T	WDFY2	c.341A>T	P.Q114L
SH_119	13	95899894	95899894	Splice_Site	SNV	T	A	A	ABCC4	c.185+3A>T	
SH_119	14	100002353	100002353	Missense_Mutation	SNV	T	A	A	CCDC85C	c.866A>T	P.Q289L
SH_119	14	100317234	100317234	Missense_Mutation	SNV	A	G	G	EML1	c.112A>G	P.I38V
SH_119	14	100808791	100808791	Missense_Mutation	SNV	T	A	A	WARS	c.1057A>T	P.S353C
SH_119	14	100950389	100950389	Silent	SNV	A	G	G	WDR25	c.1029A>G	P.P343P
SH_119	14	102568340	102568340	Missense_Mutation	SNV	A	T	T	HSP90AA1	c.238T>A	P.C805
SH_119	14	104470604	104470604	Missense_Mutation	SNV	T	A	A	TDRD9	c.1513T>A	P.C505S
SH_119	14	19571376	19571376	Missense_Mutation	SNV	A	T	T	POTEG	c.1155A>T	P.E385D
SH_119	14	19574260	19574260	Silent	SNV	T	A	A	POTEG	c.1317T>A	P.A439A
SH_119	14	20837522	20837522	Missense_Mutation	SNV	T	A	A	TEP1	c.7313A>T	P.K2438M
SH_119	14	21215769	21215769	Silent	SNV	A	T	T	EDDM3A	c.30A>T	P.I10I
SH_119	14	21547147	21547147	Missense_Mutation	SNV	A	T	T	ARHGEF40	c.209A>T	P.Q70L
SH_119	14	23898291	23898291	Missense_Mutation	SNV	A	T	T	MYH7	c.1280T>A	P.L427Q
SH_119	14	24614592	24614592	Missense_Mutation	SNV	T	A	A	PSME2	c.227A>T	P.D76V
SH_119	14	24884675	24884675	Silent	SNV	G	A	A	NYNRIN	c.3720G>A	P.A1240A
SH_119	14	31388185	31388185	Silent	SNV	T	A	A	STRN3	c.1227A>T	P.A409A
SH_119	14	36337141	36337141	Missense_Mutation	SNV	A	T	T	BRMS1L	c.757A>T	P.S253C
SH_119	14	52520946	52520946	Silent	SNV	A	T	T	NID2	c.861T>A	P.L287V
SH_119	14	58605793	58605793	Missense_Mutation	SNV	T	A	A	C14orf37	c.284A>T	P.E95V
SH_119	14	64542703	64542703	Missense_Mutation	SNV	A	T	T	SYNE2	c.10907A>T	P.E3636V
SH_119	14	64634290	64634290	Missense_Mutation	SNV	A	T	T	SYNE2	c.16838A>T	P.E5613V
SH_119	14	64898591	64898591	Splice_Site	SNV	T	G	G	MTHFD1	c.1494+12T>G	
SH_119	14	65208994	65208994	Missense_Mutation	SNV	A	T	T	PLEKHG3	c.2759A>T	P.E920V
SH_119	14	74824304	74824304	Missense_Mutation	SNV	T	A	A	VRTN	c.818T>A	P.L173Q
SH_119	14	76644365	76644365	Missense_Mutation	SNV	A	T	T	GPATCH2L	c.1183A>T	P.I395F
SH_119	14	79181183	79181183	Missense_Mutation	SNV	T	A	A	NRXN3	c.626T>A	P.L209Q
SH_119	14	81965866	81965866	Splice_Site	SNV	T	A	A	SEL1L	c.832-4A>T	
SH_119	14	86089332	86089332	Missense_Mutation	SNV	T	A	A	FLRT2	c.1474T>A	P.C492S
SH_119	14	88693819	88693819	Missense_Mutation	SNV	A	T	T	KCNK10	c.566T>A	P.I189N
SH_119	14	89154632	89154632	Missense_Mutation	SNV	T	A	A	EML5	c.2725A>T	P.M909L
SH_119	14	90429693	90429693	Missense_Mutation	SNV	A	T	T	TDP1	c.235A>T	P.S79C
SH_119	14	91633583	91633583	Missense_Mutation	SNV	A	T	T	C14orf159	c.118A>T	P.S40C
SH_119	14	95669729	95669729	Nonsense_Mutation	SNV	T	A	A	CLMN	c.1957A>T	P.K653*
SH_119	15	23283157	23283157	Splice_Site	SNV	T	A	A	HERC2P2	n.5187-4A>T	
SH_119	15	33443550	33443550	Missense_Mutation	SNV	T	A	A	FMN1	c.1898A>T	P.Q633L
SH_119	15	33835859	33835859	Missense_Mutation	SNV	A	T	T	RVR3	c.683A>T	P.H228L
SH_119	15	33905481	33905481	Silent	SNV	A	T	T	RVR3	c.2262A>T	P.S754S
SH_119	15	35084333	35084333	Missense_Mutation	SNV	G	T	T	ACTC1	c.766C>A	P.R256S
SH_119	15	42162648	42162648	Missense_Mutation	SNV	A	T	T	SPTBN5	c.5558T>A	P.V1853D
SH_119	15	42167176	42167176	Missense_Mutation	SNV	T	A	A	SPTBN5	c.4366A>T	P.R1456W
SH_119	15	43307939	43307940	Frame_Shift_Del	INDEL	AT	-	-	UBR1	3155_3156delA	P.Y1052fs
SH_119	15	43446997	43446997	Missense_Mutation	SNV	A	T	T	TMEM62	c.1150A>T	P.S384C
SH_119	15	43724410	43724410	Silent	SNV	T	A	A	TP53BP1	c.3657A>T	P.T1219T
SH_119	15	43827419	43827419	Missense_Mutation	SNV	T	A	A	PPIP5K1	c.3755A>T	P.E1252V
SH_119	15	44913948	44913948	Splice_Site	SNV	C	A	A	SPG11	c.2620+9G>T	
SH_119	15	44943729	44943729	Silent	SNV	T	A	A	SPG11	c.1416A>T	P.V472V
SH_119	15	45399031	45399031	Missense_Mutation	SNV	T	A	A	DUOX2	c.1830A>T	P.L610F
SH_119	15	49301469	49301469	Silent	SNV	T	A	A	SECISBP2L	c.1971A>T	P.I657I
SH_119	15	50154546	50154546	Nonsense_Mutation	SNV	T	A	A	ATP8B4	c.3193A>T	P.K1065*
SH_119	15	52529710	52529710	Missense_Mutation	SNV	T	A	A	MYO5C	c.2837A>T	P.K946M
SH_119	15	52849387	52849387	Missense_Mutation	SNV	T	A	A	ARPP19	c.135A>T	P.K45N
SH_119	15	54307454	54307454	Missense_Mutation	SNV	T	A	A	UNC13C	c.2354T>A	P.I785N
SH_119	15	54527312	54527312	Splice_Site	SNV	T	A	A	UNC13C	c.3154+2T>A	
SH_119	15	56388429	56388429	Silent	SNV	T	A	A	RFX7	c.1497A>T	P.T499T
SH_119	15	59528811	59528811	Missense_Mutation	SNV	T	A	A	MYO1E	c.393A>T	P.R131S
SH_119	15	62147130	62147130	Missense_Mutation	SNV	T	A	A	VP513C	c.11100A>T	P.K3700N
SH_119	15	63954122	63954122	Silent	SNV	T	A	A	HERC1	c.9000A>T	P.P3000P
SH_119	15	64592676	64592676	Missense_Mutation	SNV	T	A	A	CSNK1G1	c.23A>T	P.K8M
SH_119	15	65553347	65553347	Missense_Mutation	SNV	G	A	A	PARP16	c.709C>T	P.R237C
SH_119	15	65799697	65799697	Splice_Site	SNV	T	A	A	DPP8	c.308-4A>T	
SH_119	15	72292276	72292276	Missense_Mutation	SNV	T	A	A	MYO9A	c.1386A>T	P.K462N
SH_119	15	74474721	74474721	Missense_Mutation	SNV	T	A	A	STRA6	c.1381A>T	P.R461W
SH_119	15	78841176	78841176	Nonsense_Mutation	SNV	A	T	T	PSMA4	c.676A>T	P.R226*
SH_119	15	78921777	78921777	Silent	SNV	G	T	T	CHRN84	c.870C>A	P.L290L
SH_119	15	79183829	79183829	Missense_Mutation	SNV	C	A	A	MORF4L1	c.89C>A	P.P30H
SH_119	15	79288145	79288145	Splice_Site	SNV	A	T	T	RASGRF1	c.2967-3T>A	
SH_119	15	83725173	83725173	Missense_Mutation	SNV	T	A	A	BTBD1	c.526A>T	P.R176W
SH_119	15	83935660	83935660	Missense_Mutation	SNV	T	A	A	BNC1	c.342A>T	P.Q114H
SH_119	15	86686984	86686984	Missense_Mutation	SNV	T	A	A	AGBL1	c.170T>A	P.L57Q
SH_119	15	89381952	89381952	Silent	SNV	G	A	A	ACAN	c.129G>A	P.L43L
SH_119	15	89424819	89424819	Missense_Mutation	SNV	A	G	G	HAPLN3	c.448T>C	P.V150R
SH_119	15	92987891	92987891	Missense_Mutation	SNV	T	A	A	ST8SIA2	c.574T>A	P.Y192N
SH_119	15	99478246	99478246	Missense_Mutation	SNV	A	T	T	IGF1R	c.3150A>T	P.E1050D
SH_119	16	1262530	1262530	Splice_Site	SNV	T	A	A	CACNA1H	c.4777+2T>A	
SH_119	16	1485086	1485086	Splice_Site	SNV	T	A	A	CCDC154	c.1692+4A>T	
SH_119	16	21123137	21123137	Splice_Site	SNV	A	G	G	DNAH3	c.1921-12T>C	
SH_119	16	21262133	21262133	Missense_Mutation	SNV	A	T	T	ANKS4B	c.1246A>T	P.S416C
SH_119	16	22926576	22926576	Missense_Mutation	SNV	T	A	A	HS3S2T	c.797T>A	P.L266Q
SH_119	16	24135213	24135213	Missense_Mutation	SNV	T	A	A	PRKCB	c.976T>A	P.S326T
SH_119	16	27483142	27483142	Missense_Mutation	SNV	T	A	A	GTF3C1	c.4453A>T	P.T1485S
SH_119	16	29909302	29909302	Missense_Mutation	SNV	A	T	T	SEZ6L2	c.83T>A	P.L28Q
SH_119	16	32182377	32182377	Splice_Site	SNV	T	A	A	HERC2P4	n.1890+4A>T	
SH_119	16	396776	396776	Nonsense_Mutation	SNV	T	A	A	AXIN1	c.250A>T	P.K84*
SH_119	16	46508243	46508243	Splice_Site	SNV	T	A	A	ANKRD26P1	n.3451-2A>T	
SH_119	16	46771662	46771662	Missense_Mutation	SNV	T	A	A	MYLK3	c.962A>T	P.Q321L
SH_119	16	48167719	48167719	Missense_Mutation	SNV	A	T	T	ABCC12	c.1007T>A	P.L336Q
SH_119	16	48304150	48304150	Silent	SNV	A	T	T	LONP2	c.1074A>T	P.G358G

SH_119	16	50745688	50745688	Silent	SNV	A	T	T	NOD2	c.1785A>T	P.P595P
SH_119	16	52473506	52473506	Missense_Mutation	SNV	T	A	A	TOX3	c.1362A>T	P.Q454H
SH_119	16	55725927	55725927	Missense_Mutation	SNV	A	T	T	SLC6A2	c.881A>T	P.Y294F
SH_119	16	56443361	56443361	Missense_Mutation	SNV	T	A	A	AMFR	c.488A>T	P.Q163L
SH_119	16	56531746	56531746	Missense_Mutation	SNV	T	A	A	BB52	c.1706A>T	P.Q599L
SH_119	16	56704477	56704477	Nonsense_Mutation	SNV	A	T	T	MT1H	c.88A>T	P.K30*
SH_119	16	56938317	56938317	Missense_Mutation	SNV	A	T	T	SLC12A3	c.2894A>T	P.Q965L
SH_119	16	57685157	57685157	Missense_Mutation	SNV	A	T	T	ADGRG1	c.110A>T	P.Q37L
SH_119	16	57758742	57758742	Missense_Mutation	SNV	A	T	T	DRC7	c.1753A>T	P.I585F
SH_119	16	67229816	67229816	Missense_Mutation	SNV	A	T	T	E2F4	c.940A>T	P.S314C
SH_119	16	67267986	67267986	Silent	SNV	A	T	T	FHOD1	c.1698T>A	P.S566S
SH_119	16	67404918	67404918	Missense_Mutation	SNV	A	T	T	LRRC36	c.904A>T	P.S302C
SH_119	16	69602396	69602396	Splice_Site	SNV	A	T	T	NFAT5	c.74-2A>T	
SH_119	16	69680984	69680984	Missense_Mutation	SNV	A	T	T	NFAT5	c.307A>T	P.T103S
SH_119	16	70998672	70998672	Missense_Mutation	SNV	T	A	A	HYDIN	c.5747A>T	P.Q1916L
SH_119	16	71009073	71009073	Missense_Mutation	SNV	A	T	T	HYDIN	c.4738T>A	P.C1580S
SH_119	16	71054141	71054141	Missense_Mutation	SNV	A	T	T	HYDIN	c.3266T>A	P.L1089Q
SH_119	16	71509706	71509706	Silent	SNV	T	A	A	ZNF19	c.744A>T	P.T248T
SH_119	16	72159863	72159863	Splice_Site	SNV	T	A	A	PMFBP1	c.1818+4A>T	
SH_119	16	72984390	72984390	Missense_Mutation	SNV	T	A	A	ZFH3	c.3194A>T	P.E1065V
SH_119	16	72992423	72992423	Missense_Mutation	SNV	T	A	A	ZFH3	c.1622A>T	P.Q541L
SH_119	16	75276951	75276951	Missense_Mutation	SNV	T	A	A	BCAR1	c.188A>T	P.E63V
SH_119	16	7759084	7759084	Missense_Mutation	SNV	C	A	A	RBFOX1	c.941C>A	P.P314H
SH_119	16	84516298	84516298	Missense_Mutation	SNV	A	T	T	TLDC1	c.977T>A	P.L326Q
SH_119	16	86566057	86566057	Missense_Mutation	SNV	T	A	A	MTHFSD	c.712A>T	P.I238L
SH_119	16	88502420	88502420	Missense_Mutation	SNV	G	T	T	ZNF469	c.8458G>T	P.D2820Y
SH_119	16	89713675	89713675	Missense_Mutation	SNV	T	A	A	CHMP1A	c.317A>T	P.Q106L
SH_119	16	89849452	89849452	Missense_Mutation	SNV	T	A	A	FANCA	c.1529A>T	P.Y510F
SH_119	17	10544603	10544603	Splice_Site	SNV	T	A	A	MYH3	c.2046A>T	P.P682P
SH_119	17	11786894	11786894	Splice_Site	SNV	T	A	A	DNAH9	c.10807-9T>A	
SH_119	17	16068419	16068419	Silent	SNV	T	A	A	NCOR1	c.492A>T	P.P164P
SH_119	17	17699107	17699107	Missense_Mutation	SNV	A	T	T	RAI1	c.2845A>T	P.M949L
SH_119	17	18007965	18007965	Silent	SNV	T	A	A	DRG2	c.924T>A	P.I308I
SH_119	17	20135564	20135564	Missense_Mutation	SNV	G	T	T	SPEC1	c.2197G>T	P.V733L
SH_119	17	26085914	26085914	Missense_Mutation	SNV	T	A	A	NOS2	c.3347A>T	P.Q1116L
SH_119	17	26109071	26109071	Missense_Mutation	SNV	A	G	G	NOS2	c.692T>C	P.V231A
SH_119	17	26668457	26668457	Missense_Mutation	SNV	A	T	T	TNFAIP1	c.493A>T	P.S165C
SH_119	17	26887125	26887125	Missense_Mutation	SNV	T	A	A	PIGS	c.761A>T	P.Y254F
SH_119	17	29281490	29281490	Splice_Site	SNV	T	A	A	ADAP2	c.805-6T>A	
SH_119	17	33259383	33259383	Splice_Site	SNV	T	A	A	CCT6B	c.1236+3A>T	
SH_119	17	33806597	33806597	Missense_Mutation	SNV	T	A	A	SLFN12L	c.632A>T	P.K211I
SH_119	17	33806598	33806598	Nonsense_Mutation	SNV	T	A	A	SLFN12L	c.631A>T	P.K211*
SH_119	17	34067491	34067491	Missense_Mutation	SNV	A	T	T	RASL10B	c.280A>T	P.I94F
SH_119	17	37356606	37356606	Splice_Site	SNV	A	T	T	RPL19	c.5+4A>T	
SH_119	17	39086223	39086223	Missense_Mutation	SNV	T	A	A	KRT23	c.194A>T	P.E65V
SH_119	17	39137384	39137384	Missense_Mutation	SNV	T	A	A	KRT40	c.707A>T	P.E236V
SH_119	17	39412055	39412055	Missense_Mutation	SNV	T	A	A	KRTAP9-9	c.433T>A	P.C145S
SH_119	17	39619260	39619260	Missense_Mutation	SNV	A	G	G	KRT32	c.1039T>C	P.Y347H
SH_119	17	39661506	39661506	Silent	SNV	G	A	A	KRT13	c.297C>T	P.L99L
SH_119	17	39778605	39778605	Splice_Site	SNV	A	T	T	KRT17	c.672+2T>A	
SH_119	17	39888954	39888954	Missense_Mutation	SNV	A	T	T	HAP1	c.566T>A	P.L189Q
SH_119	17	40054028	40054028	Missense_Mutation	SNV	T	A	A	ACLY	c.1403A>T	P.K468M
SH_119	17	40142271	40142271	Splice_Site	SNV	T	A	A	DNAJC7	c.431+11A>T	
SH_119	17	40344300	40344300	Missense_Mutation	SNV	T	A	A	GHDC	c.848A>T	P.Q283L
SH_119	17	42338101	42338101	Missense_Mutation	SNV	A	T	T	SLC4A1	c.251T>A	P.L84Q
SH_119	17	42739769	42739769	Missense_Mutation	SNV	T	A	A	MEIOC	c.289T>A	P.C97S
SH_119	17	43247046	43247046	Missense_Mutation	SNV	A	T	T	HEXIM2	c.797A>T	P.Q266L
SH_119	17	48243426	48243426	Missense_Mutation	SNV	C	T	T	SGCA	c.25C>T	P.P9S
SH_119	17	48646546	48646546	Missense_Mutation	SNV	T	A	A	CACNA1G	c.375T>A	P.F125L
SH_119	17	48694820	48694820	Silent	SNV	C	T	T	CACNA1G	c.4989C>T	P.A1663A
SH_119	17	49067881	49067881	Silent	SNV	T	A	A	SPAG9	c.2517A>T	P.A839A
SH_119	17	54933869	54933869	Splice_Site	SNV	A	T	T	DGKE	c.1099-4A>T	
SH_119	17	55028025	55028025	Missense_Mutation	SNV	T	A	A	COIL	c.578A>T	P.Y193F
SH_119	17	57290403	57290403	Missense_Mutation	SNV	A	T	T	SMG8	c.2219A>T	P.Q740L
SH_119	17	60768066	60768066	Missense_Mutation	SNV	A	T	T	MRC2	c.3956A>T	P.Q1319L
SH_119	17	61558959	61558959	Silent	SNV	A	T	T	ACE	c.978A>T	P.A326A
SH_119	17	61950652	61950652	Missense_Mutation	SNV	A	T	T	CSH2	c.58T>A	P.W20R
SH_119	17	62291499	62291499	Missense_Mutation	SNV	T	A	A	TEX2	c.79A>T	P.R27W
SH_119	17	63898403	63898403	Missense_Mutation	SNV	T	A	A	CEP112	c.2030A>T	P.Q677L
SH_119	17	6493836	6493836	Missense_Mutation	SNV	T	A	A	KIAA0753	c.2555A>T	P.N852I
SH_119	17	6661443	6661443	Missense_Mutation	SNV	A	T	T	XAF1	c.68A>T	P.H23L
SH_119	17	6663876	6663876	Missense_Mutation	SNV	A	T	T	XAF1	c.377A>T	P.Q126L
SH_119	17	67305544	67305544	Missense_Mutation	SNV	T	A	A	ABCA5	c.328A>T	P.T110S
SH_119	17	72356294	72356294	Missense_Mutation	SNV	T	A	A	BTBD17	c.176A>T	P.Q59L
SH_119	17	72443011	72443011	Silent	SNV	C	T	T	GPRC5C	c.1206C>T	P.I402I
SH_119	17	7246865	7246865	Missense_Mutation	SNV	T	A	A	ACAP1	c.512T>A	P.L171Q
SH_119	17	74289407	74289407	Silent	SNV	T	A	A	QRICH2	c.903A>T	P.S301S
SH_119	17	7578455	7578455	Missense_Mutation	SNV	C	G	G	TP53	c.475G>C	P.A159P
SH_119	17	76118840	76118840	Splice_Site	SNV	A	T	T	TMC6	c.1083-10T>A	
SH_119	17	76446414	76446414	Silent	SNV	A	T	T	DNAH17	c.10962T>A	P.A3654A
SH_119	17	76449447	76449447	Missense_Mutation	SNV	T	A	A	DNAH17	c.10507A>T	P.R3503W
SH_119	17	76526588	76526588	Missense_Mutation	SNV	A	T	T	DNAH17	c.3121T>A	P.S1041T
SH_119	17	77102803	77102803	Missense_Mutation	SNV	T	A	A	RBFOX3	c.290A>T	P.Q97L
SH_119	17	77984068	77984068	Missense_Mutation	SNV	T	A	A	TBC1D16	c.670A>T	P.S224C
SH_119	17	78168994	78168994	Missense_Mutation	SNV	A	T	T	CARD14	c.1361A>T	P.Q454L
SH_119	17	78178881	78178881	Missense_Mutation	SNV	T	A	A	CARD14	c.2446T>A	P.Y816N
SH_119	17	79655738	79655738	Missense_Mutation	SNV	A	C	C	HGS	c.296A>C	P.Q99P
SH_119	17	80038319	80038319	Missense_Mutation	SNV	T	A	A	FASN	c.6974A>T	P.Q2325L
SH_119	17	80048258	80048258	Silent	SNV	T	A	A	FASN	c.1863A>T	P.A621A
SH_119	17	8015465	8015465	Nonsense_Mutation	SNV	T	A	A	ALOXE3	c.1126A>T	P.K376*
SH_119	17	80521337	80521337	Missense_Mutation	SNV	A	T	T	FOXK2	c.527A>T	P.Q176L
SH_119	17	9570027	9570027	Silent	SNV	A	T	T	USP43	c.699A>T	P.L233L
SH_119	18	12122314	12122314	Missense_Mutation	SNV	T	A	A	ANKRD62	c.1253T>A	P.L418Q
SH_119	18	12351196	12351196	Silent	SNV	T	A	A	AFG3L2	c.1440A>T	P.I480I
SH_119	18	14537923	14537923	Frame_Shift_Del	INDEL	G	-	-	POTEC	c.687delC	P.A230fs
SH_119	18	20572948	20572948	Silent	SNV	A	C	C	RBBP8	c.1158A>C	P.T386T
SH_119	18	20596798	20596798	Missense_Mutation	SNV	A	T	T	RBBP8	c.2365A>T	P.S789C
SH_119	18	29432410	29432410	Missense_Mutation	SNV	T	A	A	TRAPP8	c.3560A>T	P.Q1187L

SH_119	18	2951094	2951094	Silent	SNV	T	A	A	LPIN2	c.549A>T	P.V183V
SH_119	18	51731502	51731502	Nonsense_Mutation	SNV	T	A	A	MBD2	c.568A>T	P.K190*
SH_119	18	59895685	59895685	Silent	SNV	A	T	T	KIAA1468	c.1302A>T	P.T434T
SH_119	18	60241696	60241696	Silent	SNV	T	G	G	ZCHC2	c.2382T>G	P.P794P
SH_119	18	6948522	6948522	Missense_Mutation	SNV	C	A	A	LAMA1	c.8590G>T	P.V2864L
SH_119	18	6985374	6985374	Missense_Mutation	SNV	A	T	T	LAMA1	c.5522T>A	P.L1841Q
SH_119	18	7009239	7009239	Nonsense_Mutation	SNV	T	A	A	LAMA1	c.4000A>T	P.R1334*
SH_119	18	9954125	9954125	Missense_Mutation	SNV	A	T	T	VAPA	c.802A>T	P.N268Y
SH_119	19	10262205	10262205	Missense_Mutation	SNV	T	A	A	DNMT1	c.2134A>T	P.M712L
SH_119	19	10798253	10798253	Missense_Mutation	SNV	A	T	T	ILF3	c.2303A>T	P.Y768F
SH_119	19	11892571	11892571	Missense_Mutation	SNV	A	T	T	ZNF441	c.1932A>T	P.K644N
SH_119	19	12830084	12830084	Nonsense_Mutation	SNV	T	A	A	TNPO2	c.166A>T	P.K56*
SH_119	19	14028916	14028916	Missense_Mutation	SNV	A	T	T	CC2D1A	c.782A>T	P.Q261L
SH_119	19	14703169	14703169	Splice_Site	SNV	A	T	T	CLEC17A	c.276A>T	P.P92P
SH_119	19	14910228	14910228	Missense_Mutation	SNV	A	T	T	OR7C1	c.721T>A	P.C241S
SH_119	19	14938140	14938140	Nonsense_Mutation	SNV	A	T	T	OR7A5	c.914T>A	P.L305*
SH_119	19	14952199	14952199	Nonsense_Mutation	SNV	A	T	T	OR7A10	c.491T>A	P.L164*
SH_119	19	15350788	15350788	Missense_Mutation	SNV	T	A	A	BRD4	c.3215A>T	P.Q1072L
SH_119	19	16855259	16855259	Missense_Mutation	SNV	T	A	A	NWD1	c.226T>A	P.C76S
SH_119	19	17487911	17487911	Missense_Mutation	SNV	T	A	A	PLVAP	c.187A>T	P.T63S
SH_119	19	19825167	19825167	Splice_Site	SNV	T	A	A	ZNF14	c.130+3A>T	
SH_119	19	23328191	23328191	Missense_Mutation	SNV	A	T	T	ZNF730	c.345A>T	P.K115N
SH_119	19	30017525	30017525	Missense_Mutation	SNV	A	T	T	VSTM2B	c.35A>T	P.Y12F
SH_119	19	33092917	33092917	Splice_Site	SNV	T	G	G	ANKRD27	c.2767+4A>C	
SH_119	19	33355184	33355184	Missense_Mutation	SNV	T	A	A	SLC7A9	c.296A>T	P.Y99F
SH_119	19	35420778	35420778	Splice_Site	SNV	G	T	T	ZNF30	c.-64-10G>T	
SH_119	19	35719225	35719225	Missense_Mutation	SNV	T	A	A	FAM187B	c.359A>T	P.H120L
SH_119	19	35940991	35940991	Frame_Shift_Del	INDEL	T	-	-	FFAR2	c.375delT	P.Y125fs
SH_119	19	35940992	35940992	Missense_Mutation	SNV	G	A	A	FFAR2	c.376G>A	P.G126R
SH_119	19	37488058	37488058	Missense_Mutation	SNV	A	T	T	ZNF568	c.1273A>T	P.S425C
SH_119	19	37677174	37677174	Missense_Mutation	SNV	T	A	A	ZNF585B	c.1265A>T	P.K422M
SH_119	19	3831810	3831810	Missense_Mutation	SNV	T	A	A	ZFR2	c.446A>T	P.Q149L
SH_119	19	3852539	3852539	Missense_Mutation	SNV	T	A	A	ZFR2	c.127A>T	P.S43C
SH_119	19	38689034	38689034	Missense_Mutation	SNV	A	T	T	SIPA1L3	c.4846A>T	P.I1616F
SH_119	19	38946293	38946293	Missense_Mutation	SNV	T	A	A	RYR1	c.1693T>A	P.C565S
SH_119	19	38989769	38989769	Missense_Mutation	SNV	T	A	A	RYR1	c.6913T>A	P.C2305S
SH_119	19	38996483	38996483	Missense_Mutation	SNV	T	A	A	RYR1	c.8438T>A	P.L2813Q
SH_119	19	3908286	3908286	Missense_Mutation	SNV	A	T	T	ATCAY	c.565A>T	P.N189Y
SH_119	19	39734311	39734311	Silent	SNV	T	A	A	IFNL3	c.552A>T	P.R184R
SH_119	19	39735447	39735447	Missense_Mutation	SNV	T	A	A	IFNL3	c.161A>T	P.K54M
SH_119	19	39976413	39976413	Missense_Mutation	SNV	A	T	T	TIMM50	c.767A>T	P.E256V
SH_119	19	40408377	40408377	Missense_Mutation	SNV	T	C	C	FCGBP	c.4462A>G	P.I1488V
SH_119	19	40761086	40761086	Missense_Mutation	SNV	T	A	A	AKT2	c.266A>T	P.H89L
SH_119	19	42125779	42125779	Splice_Site	SNV	A	T	T	CEACAM4	c.670-11T>A	
SH_119	19	43243004	43243004	Missense_Mutation	SNV	A	T	T	PSG3	c.302T>A	P.V101E
SH_119	19	43382400	43382400	Missense_Mutation	SNV	G	A	A	PSG1	c.95C>T	P.T32I
SH_119	19	44580556	44580556	Missense_Mutation	SNV	A	T	T	ZNF284	c.14A>T	P.K5M
SH_119	19	45296740	45296740	Missense_Mutation	SNV	A	T	T	CBLC	c.1009A>T	P.S337C
SH_119	19	45315801	45315801	Missense_Mutation	SNV	A	T	T	BCAM	c.500A>T	P.Q167L
SH_119	19	46321288	46321288	Nonsense_Mutation	SNV	G	A	A	SYMPK	c.3010C>T	P.Q1004*
SH_119	19	46664070	46664070	Silent	SNV	T	A	A	IGFL2	c.306T>A	P.V102V
SH_119	19	46974046	46974046	Missense_Mutation	SNV	G	T	T	PNMAL1	c.247C>A	P.P83T
SH_119	19	49692314	49692314	Missense_Mutation	SNV	A	T	T	TRPM4	c.1985A>T	P.D662V
SH_119	19	50154500	50154500	Missense_Mutation	SNV	A	C	C	SCAF1	c.854A>C	P.E285A
SH_119	19	50195571	50195571	Missense_Mutation	SNV	T	A	A	CPT1C	c.62T>A	P.V21E
SH_119	19	50461894	50461894	Splice_Site	SNV	A	T	T	SIGLEC11	c.1363+6T>A	
SH_119	19	51362778	51362778	Splice_Site	SNV	A	T	T	KLK3	c.631-8A>T	
SH_119	19	51470515	51470515	Missense_Mutation	SNV	T	A	A	KLK6	c.107A>T	P.Q36L
SH_119	19	51526433	51526433	Missense_Mutation	SNV	T	A	A	KLK11	c.515A>T	P.Q172L
SH_119	19	52034690	52034690	Missense_Mutation	SNV	A	T	T	SIGLEC6	c.151T>A	P.C51S
SH_119	19	52942137	52942137	Missense_Mutation	SNV	T	A	A	ZNF534	c.1424T>A	P.F475Y
SH_119	19	53007923	53007923	Missense_Mutation	SNV	A	T	T	ZNF578	c.79A>T	P.R27VW
SH_119	19	53208806	53208806	Missense_Mutation	SNV	T	A	A	ZNF611	c.1502A>T	P.K501M
SH_119	19	53282109	53282109	Missense_Mutation	SNV	T	A	A	ZNF600	c.33A>T	P.K111N
SH_119	19	53453502	53453502	Missense_Mutation	SNV	T	A	A	ZNF816	c.1526A>T	P.Y509F
SH_119	19	53667895	53667895	Missense_Mutation	SNV	A	T	T	ZNF665	c.1848T>A	P.H616Q
SH_119	19	53747053	53747053	Nonsense_Mutation	SNV	A	T	T	ZNF677	c.113T>A	P.L38*
SH_119	19	55175453	55175453	Silent	SNV	A	T	T	LILRB4	c.312A>T	P.V104V
SH_119	19	55363541	55363541	Silent	SNV	T	A	A	KIR3DL2	c.159T>A	P.R53R
SH_119	19	55832369	55832369	Silent	SNV	T	A	A	TMEM150B	c.36A>T	P.L12L
SH_119	19	56283365	56283365	Frame_Shift_Ins	INDEL	-	A	A	RFPL4A11	c.197dupA	P.L67fs
SH_119	19	56329362	56329362	Missense_Mutation	SNV	T	A	A	NLRP11	c.179A>T	P.Y60F
SH_119	19	56413491	56413491	Missense_Mutation	SNV	A	T	T	NLRP13	c.2699T>A	P.L900Q
SH_119	19	56423919	56423919	Missense_Mutation	SNV	A	G	G	NLRP13	c.1264T>C	P.C422R
SH_119	19	56569698	56569698	Missense_Mutation	SNV	A	T	T	NLRP5	c.3392A>T	P.Q1131L
SH_119	19	57840540	57840540	Missense_Mutation	SNV	A	T	T	ZNF543	c.1710A>T	P.S750S
SH_119	19	58118585	58118585	Missense_Mutation	SNV	A	T	T	ZNF530	c.1593A>T	P.Q531H
SH_119	19	58420718	58420718	Missense_Mutation	SNV	T	A	A	ZNF417	c.925A>T	P.S309C
SH_119	19	59068063	59068063	Missense_Mutation	SNV	T	A	A	UBE2M	c.338A>T	P.N113I
SH_119	19	6714059	6714059	Silent	SNV	T	A	A	C3	c.717A>T	P.T239T
SH_119	19	6916299	6916299	Missense_Mutation	SNV	A	T	T	ADGRE1	c.1184A>T	P.E395V
SH_119	19	9048696	9048696	Missense_Mutation	SNV	T	A	A	MUC16	c.32935A>T	P.T10979S
SH_119	19	9049462	9049462	Silent	SNV	A	T	T	MUC16	c.32169T>A	P.A10723A
SH_119	19	9064052	9064052	Nonsense_Mutation	SNV	A	T	T	MUC16	c.23394T>A	P.C7798*
SH_119	19	9071660	9071660	Silent	SNV	T	A	A	MUC16	c.15786A>T	P.T5262T
SH_119	19	9075153	9075153	Missense_Mutation	SNV	C	A	A	MUC16	c.12293G>T	P.S4098I
SH_119	19	9075971	9075971	Silent	SNV	T	A	A	MUC16	c.11475A>T	P.P3825P
SH_119	19	9577862	9577862	Silent	SNV	A	G	G	ZNF560	c.1761T>C	P.L587L
SH_119	19	9721235	9721235	Nonsense_Mutation	SNV	T	A	A	ZNF561	c.1102A>T	P.K368*
SH_119	2	100623906	100623906	Missense_Mutation	SNV	T	A	A	AFF3	c.191A>T	P.E64V
SH_119	2	101182980	101182980	Missense_Mutation	SNV	A	T	T	PDCL3	c.22A>T	P.T8S
SH_119	2	102781563	102781563	Splice_Site	SNV	A	T	T	IL1R1	c.297-12A>T	
SH_119	2	103136421	103136421	Splice_Site	SNV	A	G	G	SLC9A4	c.1818+7A>G	
SH_119	2	105961828	105961828	Nonstop_Mutation	SNV	A	C	C	C2orf49	c.573A>C	P.Ter191Cext*?
SH_119	2	108477368	108477368	Missense_Mutation	SNV	T	A	A	RGPD4	c.1905T>A	P.H635Q
SH_119	2	112786192	112786192	Silent	SNV	A	T	T	MERTK	c.2751A>T	P.A917A
SH_119	2	113780356	113780356	Splice_Site	SNV	T	A	A	IL36B	c.392-2A>T	
SH_119	2	11767202	11767202	Missense_Mutation	SNV	A	T	T	GREB1	c.4421A>T	P.Q1474L

SH_119	2	120640187	120640187	Missense_Mutation	SNV	A	T	T	PTPN4	c.575A>T	P.H192L
SH_119	2	128855116	128855116	Missense_Mutation	SNV	A	T	T	UGGT1	c.172A>T	P.T58S
SH_119	2	131103934	131103934	Missense_Mutation	SNV	A	C	C	IMP4	c.763A>C	P.M255L
SH_119	2	136569919	136569919	Missense_Mutation	SNV	A	T	T	LCT	c.2315T>A	P.V772E
SH_119	2	141143540	141143540	Missense_Mutation	SNV	T	A	A	LRP1B	c.10453A>T	P.N3485Y
SH_119	2	159537134	159537134	Missense_Mutation	SNV	A	T	T	PKP4	c.3395A>T	P.K1132I
SH_119	2	159537135	159537135	Missense_Mutation	SNV	A	T	T	PKP4	c.3396A>T	P.K1132N
SH_119	2	163072416	163072416	Silent	SNV	T	A	A	FAP	c.783A>T	P.I261I
SH_119	2	165552311	165552311	Missense_Mutation	SNV	T	A	A	COBLL1	c.1906A>T	P.T636S
SH_119	2	166183470	166183470	Missense_Mutation	SNV	A	T	T	SCN2A	c.2125A>T	P.S709C
SH_119	2	166764192	166764192	Missense_Mutation	SNV	T	A	A	TTC21B	c.2564A>T	P.Q855L
SH_119	2	168103327	168103327	Missense_Mutation	SNV	A	T	T	XIRP2	c.5425A>T	P.I1809F
SH_119	2	170063206	170063206	Missense_Mutation	SNV	T	A	A	LRP2	c.7024A>T	P.N2342Y
SH_119	2	171070912	171070912	Silent	SNV	T	A	A	MYO3B	c.345T>A	P.T115T
SH_119	2	175326222	175326222	Splice_Site	SNV	T	C	C	GPR155	c.1470-2A>G	
SH_119	2	175619008	175619008	Missense_Mutation	SNV	T	A	A	CHRNA1	c.479A>T	P.Q160L
SH_119	2	179413835	179413835	Missense_Mutation	SNV	A	T	T	TTN	c.87595T>A	P.L29199I
SH_119	2	179417635	179417635	Missense_Mutation	SNV	A	T	T	TTN	c.85069T>A	P.S28357T
SH_119	2	179417927	179417927	Silent	SNV	A	T	T	TTN	c.84777T>A	P.P28259P
SH_119	2	179437100	179437100	Missense_Mutation	SNV	A	T	T	TTN	c.68836T>A	P.C22946S
SH_119	2	18113513	18113513	Missense_Mutation	SNV	A	T	T	KCN53	c.1238A>T	P.Y413F
SH_119	2	186654677	186654677	Silent	SNV	T	A	A	FSIP2	c.2814T>A	P.L938L
SH_119	2	189599392	189599392	Missense_Mutation	SNV	G	T	T	DIRC1	c.256C>A	P.L86I
SH_119	2	189867050	189867050	Silent	SNV	A	T	T	COL3A1	c.2418A>T	P.P806P
SH_119	2	202358262	202358262	Silent	SNV	A	T	T	ALS2CR11	c.2802T>A	P.P934P
SH_119	2	206659775	206659775	Missense_Mutation	SNV	A	T	T	NRP2	c.2774A>T	P.E925V
SH_119	2	208425086	208425086	Missense_Mutation	SNV	A	T	T	CREB1	c.251A>T	P.Q84L
SH_119	2	209201588	209201588	Missense_Mutation	SNV	A	T	T	PIKFYVE	c.4547A>T	P.K1516M
SH_119	2	209357998	209357998	Nonsense_Mutation	SNV	G	T	T	PTH2R	c.934G>T	P.E312*
SH_119	2	214878801	214878801	Splice_Site	SNV	A	T	T	SPAG16	n.1807A>T	
SH_119	2	220348946	220348946	Missense_Mutation	SNV	T	A	A	SPEG	c.6761T>A	P.L2254Q
SH_119	2	220353787	220353787	Missense_Mutation	SNV	T	A	A	SPEG	c.8161T>A	P.W2721R
SH_119	2	220478470	220478470	Splice_Site	SNV	A	T	T	STK11IP	c.2538-4A>T	
SH_119	2	220493244	220493244	Missense_Mutation	SNV	T	A	A	SLC4A3	c.169T>A	P.W57R
SH_119	2	226447431	226447431	Missense_Mutation	SNV	A	T	T	NYAP2	c.1298A>T	P.H433L
SH_119	2	230312255	230312255	Splice_Site	SNV	T	C	C	DNER	c.1263A>G	P.G421G
SH_119	2	234627755	234627755	Missense_Mutation	SNV	A	T	T	UGT1A4	c.289A>T	P.T97S
SH_119	2	235951376	235951376	Missense_Mutation	SNV	A	T	T	SH3BP4	c.1963A>T	P.S655C
SH_119	2	237395519	237395519	Nonsense_Mutation	SNV	T	A	A	IQCA1	c.673A>T	P.K225*
SH_119	2	238257010	238257010	Silent	SNV	A	T	T	COL6A3	c.6948T>A	P.P2316P
SH_119	2	241700261	241700261	Splice_Site	SNV	C	T	T	KIF1A	c.2266-1G>A	
SH_119	2	242066314	242066314	Silent	SNV	T	A	A	PASK	c.2016A>T	P.A672A
SH_119	2	25754369	25754369	Missense_Mutation	SNV	T	A	A	DTNB	c.974A>T	P.E325V
SH_119	2	26667182	26667182	Missense_Mutation	SNV	A	T	T	DRC1	c.1121A>T	P.K374I
SH_119	2	29356607	29356607	Missense_Mutation	SNV	A	T	T	CLIP4	c.454A>T	P.N152Y
SH_119	2	31410672	31410672	Missense_Mutation	SNV	T	A	A	CAPN14	c.1539A>T	P.E513D
SH_119	2	31600003	31600003	Missense_Mutation	SNV	T	A	A	XDH	c.1343A>T	P.E48V
SH_119	2	32474989	32474989	Silent	SNV	A	T	T	NLR4	c.1944T>A	P.A648A
SH_119	2	32668631	32668631	Silent	SNV	A	G	G	BIRC6	c.4311A>G	P.S1437S
SH_119	2	32730271	32730271	Splice_Site	SNV	A	T	T	BIRC6	c.9699A>T	P.A3233A
SH_119	2	33572536	33572536	Missense_Mutation	SNV	A	T	T	LTBP1	c.2981A>T	P.Y994F
SH_119	2	42720536	42720536	Missense_Mutation	SNV	T	A	A	KCN33	c.106A>T	P.S36C
SH_119	2	46605841	46605841	Nonsense_Mutation	SNV	A	T	T	EPAS1	c.1489A>T	P.K497*
SH_119	2	55791498	55791498	Silent	SNV	T	A	A	PPP4R3B	c.2211A>T	P.P737P
SH_119	2	61483549	61483549	Missense_Mutation	SNV	T	A	A	USP34	c.6191A>T	P.H2064L
SH_119	2	64685489	64685489	Missense_Mutation	SNV	A	G	G	LGA1L	c.446A>G	P.H149R
SH_119	2	66667702	66667702	Silent	SNV	A	T	T	MEIS1	c.390A>T	P.A130A
SH_119	2	69204616	69204616	Splice_Site	SNV	T	A	A	GKN1	c.55-11T>A	
SH_119	2	71816758	71816758	Missense_Mutation	SNV	G	A	A	DYSF	c.3387G>A	P.M1129I
SH_119	2	73996404	73996404	Missense_Mutation	SNV	T	A	A	DUSP11	c.623A>T	P.Y208F
SH_119	2	74135834	74135834	Missense_Mutation	SNV	T	A	A	ACTG2	c.161T>A	P.V54E
SH_119	2	74808801	74808801	Missense_Mutation	SNV	T	A	A	M1AP	c.769A>T	P.M257L
SH_119	2	80529404	80529404	Missense_Mutation	SNV	T	A	A	LRR11	c.1541A>T	P.Q514L
SH_119	2	9048826	9048826	Missense_Mutation	SNV	A	T	T	MBOAT2	c.53T>A	P.L18Q
SH_119	2	96076652	96076652	Missense_Mutation	SNV	C	T	T	FAHD2A	c.563C>T	P.A188V
SH_119	2	9668039	9668039	Missense_Mutation	SNV	T	A	A	ADAM17	c.495A>T	P.L165F
SH_119	2	97026404	97026404	Missense_Mutation	SNV	A	T	T	NCAPH	c.1510A>T	P.N504Y
SH_119	2	97530828	97530828	Missense_Mutation	SNV	T	A	A	SEMA4C	c.659A>T	P.Y220F
SH_119	20	1616954	1616954	Missense_Mutation	SNV	T	A	A	SIRPG	c.628A>T	P.T210S
SH_119	20	19665861	19665861	Missense_Mutation	SNV	G	A	A	SLC24A3	c.1180G>A	P.G394S
SH_119	20	20033147	20033147	Missense_Mutation	SNV	A	G	G	CRNKL1	c.287T>C	P.V96A
SH_119	20	21687214	21687214	Missense_Mutation	SNV	T	A	A	PAX1	c.425T>A	P.V142E
SH_119	20	23028754	23028754	Missense_Mutation	SNV	T	A	A	THBD	c.1388A>T	P.E463V
SH_119	20	23966809	23966809	Missense_Mutation	SNV	C	T	T	GGTLC1	c.208G>A	P.G70R
SH_119	20	25261031	25261031	Missense_Mutation	SNV	A	T	T	PYGB	c.1222A>T	P.N408Y
SH_119	20	30527026	30527026	Silent	SNV	T	A	A	TTL9	c.1200T>A	P.P400P
SH_119	20	30556175	30556175	Missense_Mutation	SNV	T	A	A	XKR7	c.197T>A	P.V66E
SH_119	20	31692643	31692643	Nonsense_Mutation	SNV	A	T	T	BPIFB4	c.1708A>T	P.K570*
SH_119	20	33703495	33703495	Missense_Mutation	SNV	T	A	A	EDEM2	c.1367A>T	P.E456V
SH_119	20	34022535	34022535	Silent	SNV	A	G	G	GDF5	c.678T>C	P.I226I
SH_119	20	35668692	35668692	Splice_Site	SNV	T	A	A	RLB1	c.490-4A>T	
SH_119	20	36406054	36406054	Splice_Site	SNV	A	T	T	CTNBL1	c.743-2A>T	
SH_119	20	36641090	36641090	Missense_Mutation	SNV	T	A	A	TTI1	c.1129A>T	P.S377C
SH_119	20	37174977	37174977	Missense_Mutation	SNV	A	T	T	RALGAPB	c.2806A>T	P.R936W
SH_119	20	37581107	37581107	Missense_Mutation	SNV	A	T	T	FAM83D	c.1702A>T	P.S568C
SH_119	20	3765945	3765945	Missense_Mutation	SNV	T	A	A	CENPB	c.1186A>T	P.T396S
SH_119	20	42694395	42694395	Missense_Mutation	SNV	C	T	T	TOX2	c.878C>T	P.P293L
SH_119	20	47258735	47258735	Missense_Mutation	SNV	T	A	A	PREX1	c.3746A>T	P.K1249M
SH_119	20	47695092	47695092	Splice_Site	INDEL	A	-	-	CSE1L	c.1253-6delA	
SH_119	20	47733764	47733764	Nonsense_Mutation	SNV	T	A	A	STAU1	c.1306A>T	P.K436*
SH_119	20	50407599	50407599	Nonsense_Mutation	SNV	T	A	A	SALL4	c.1423A>T	P.K475*
SH_119	20	57480539	57480539	Splice_Site	SNV	A	T	T	GNAS	c.530+4A>T	
SH_119	20	58453085	58453085	Missense_Mutation	SNV	T	A	A	SYCP2	c.2957A>T	P.K986M
SH_119	20	62737376	62737376	Missense_Mutation	SNV	A	T	T	NPBWR2	c.809T>A	P.L270H
SH_119	21	16338771	16338771	Frame_Shift_Del	INDEL	T	-	-	NRIP1	c.1743delA	P.Y582fs
SH_119	21	16338772	16338772	Missense_Mutation	SNV	G	A	A	NRIP1	c.1742C>T	P.P581L
SH_119	21	19629064	19629064	Silent	SNV	T	C	C	CHODL	c.261T>C	P.N87N
SH_119	21	27348267	27348267	Missense_Mutation	SNV	C	A	A	APP	c.1299G>T	P.Q433H

SH_119	21	41446962	41446962	Splice_Site	SNV	A	T	T	DSCAM	c.4888+2T>A	
SH_119	21	43321802	43321802	Missense_Mutation	SNV	T	A	A	C2CD2	c.1489A>T	P.S497C
SH_119	21	43413159	43413159	Missense_Mutation	SNV	T	A	A	ZBTB21	c.1046A>T	P.Q349L
SH_119	21	44841919	44841919	Splice_Site	SNV	T	A	A	SIK1	c.274-2A>T	
SH_119	21	45774583	45774583	Missense_Mutation	SNV	T	A	A	TRPM2	c.218T>A	P.V73E
SH_119	21	46066653	46066653	Frame_Shift_Del	INDEL	C	-	-	KRTAP10-11	c.282delC	P.C95fs
SH_119	21	46086493	46086493	Missense_Mutation	SNV	A	T	T	KRTAP12-2	c.311T>A	P.L104Q
SH_119	22	16277843	16277843	Silent	SNV	T	A	A	POTEH	c.1071A>T	P.I357I
SH_119	22	17976530	17976530	Missense_Mutation	SNV	A	T	T	CECR2	c.191A>T	P.Q64L
SH_119	22	19223255	19223255	Silent	SNV	T	A	A	CLTCL1	c.933A>T	P.P311P
SH_119	22	20024365	20024365	Missense_Mutation	SNV	A	T	T	TANGO2	c.44A>T	P.K15I
SH_119	22	21065029	21065029	Missense_Mutation	SNV	T	A	A	PI4KA	c.6041A>T	P.K2014M
SH_119	22	21385366	21385366	Missense_Mutation	SNV	A	G	G	SLC7A4	c.736T>C	P.Y246H
SH_119	22	22892611	22892611	Missense_Mutation	SNV	A	T	T	PRAME	c.490T>A	P.L164M
SH_119	22	24086414	24086414	Missense_Mutation	SNV	T	A	A	ZNF70	c.914A>T	P.K305M
SH_119	22	26860783	26860783	Silent	SNV	T	A	A	HP54	c.813A>T	P.A271A
SH_119	22	28492398	28492398	Splice_Site	SNV	T	A	A	TTC28	c.3548-2A>T	
SH_119	22	29669815	29669815	Missense_Mutation	SNV	A	T	T	EWSR1	c.188A>T	P.Q63L
SH_119	22	31013440	31013440	Missense_Mutation	SNV	T	A	A	TCN2	c.1064T>A	P.V355E
SH_119	22	32269261	32269261	Missense_Mutation	SNV	G	A	A	DEPDC5	c.3479G>A	P.S1160N
SH_119	22	32754173	32754173	Missense_Mutation	SNV	A	T	T	RFPL3	c.115A>T	P.S39C
SH_119	22	35811931	35811931	Missense_Mutation	SNV	A	T	T	MCMS	c.1313A>T	P.D438V
SH_119	22	38273931	38273931	Missense_Mutation	SNV	A	T	T	EIF3L	c.1184A>T	P.Q395L
SH_119	22	38882323	38882323	Missense_Mutation	SNV	G	A	A	DDX17	c.1813C>T	P.R605W
SH_119	22	40055777	40055777	Missense_Mutation	SNV	T	A	A	CACNA1I	c.2419T>A	P.F807I
SH_119	22	40365493	40365493	Missense_Mutation	SNV	A	T	T	GRAP2	c.769A>T	P.M257L
SH_119	22	44589713	44589713	Splice_Site	SNV	T	A	A	PARVG	c.583+10T>A	
SH_119	22	45958887	45958887	Missense_Mutation	SNV	A	C	C	FBLN1	c.1793A>C	P.Q598P
SH_119	3	10413649	10413649	Silent	SNV	T	A	A	ATP2B2	c.1503A>T	P.T501T
SH_119	3	11198887	11198887	Silent	SNV	T	A	A	SLC9C1	c.651A>T	P.I217I
SH_119	3	124103755	124103755	Missense_Mutation	SNV	T	A	A	KALRN	c.1828T>A	P.C610S
SH_119	3	126229580	126229580	Missense_Mutation	SNV	G	A	A	UROCI	c.184C>T	P.P625
SH_119	3	127390284	127390284	Missense_Mutation	SNV	T	A	A	PODXL2	c.1433T>A	P.I478N
SH_119	3	128077070	128077070	Missense_Mutation	SNV	A	T	T	EEFSEC	c.1454A>T	P.D485V
SH_119	3	128623244	128623244	Missense_Mutation	SNV	A	T	T	ACAD9	c.1045A>T	P.M349L
SH_119	3	12976961	12976961	Missense_Mutation	SNV	T	A	A	IQSEC1	c.1555A>T	P.N519Y
SH_119	3	131268871	131268871	Missense_Mutation	SNV	A	T	T	CPNE4	c.1276T>A	P.Y426N
SH_119	3	132075694	132075694	Missense_Mutation	SNV	A	T	T	ACPP	c.1133A>T	P.H378L
SH_119	3	132337466	132337466	Splice_Site	SNV	T	A	A	ACAD11	c.1414+12A>T	
SH_119	3	132360859	132360859	Missense_Mutation	SNV	T	A	A	ACAD11	c.494A>T	P.Q165L
SH_119	3	138121086	138121086	Missense_Mutation	SNV	A	T	T	MRAS	c.602A>T	P.H201L
SH_119	3	13916487	13916487	Silent	SNV	A	T	T	WNT7A	c.255T>A	P.S85S
SH_119	3	1414093	1414093	Missense_Mutation	SNV	T	A	A	CNTN6	c.1603T>A	P.W535R
SH_119	3	148458820	148458820	Nonsense_Mutation	SNV	A	T	T	AGTR1	c.85A>T	P.K29*
SH_119	3	150911419	150911419	Missense_Mutation	SNV	A	T	T	MED12L	c.2111A>T	P.H704L
SH_119	3	150916900	150916900	Missense_Mutation	SNV	A	T	T	GPR171	c.274T>A	P.C92S
SH_119	3	15119651	15119651	Missense_Mutation	SNV	T	C	C	RBSN	c.929A>G	P.Y310C
SH_119	3	155210644	155210644	Splice_Site	SNV	T	A	A	PLCH1	c.2147-2A>T	
SH_119	3	155286055	155286055	Missense_Mutation	SNV	T	A	A	PLCH1	c.794A>T	P.E265V
SH_119	3	158384162	158384162	Missense_Mutation	SNV	A	T	T	GFM1	c.1645A>T	P.T549S
SH_119	3	158523163	158523163	Missense_Mutation	SNV	A	G	G	MFS1	c.10A>G	P.N4D
SH_119	3	168845708	168845708	Missense_Mutation	SNV	T	A	A	MECOM	c.382A>T	P.S128C
SH_119	3	17052911	17052911	Silent	SNV	T	C	C	PLCL2	c.2061T>C	P.D687D
SH_119	3	172766763	172766763	Missense_Mutation	SNV	T	A	A	SPATA16	c.734A>T	P.D245V
SH_119	3	178745227	178745227	Silent	SNV	T	A	A	ZMAT3	c.642A>T	P.T214T
SH_119	3	179076760	179076760	Silent	SNV	A	T	T	MFN1	c.381A>T	P.T127T
SH_119	3	183823640	183823640	Missense_Mutation	SNV	T	A	A	HTR3E	c.808T>A	P.Y270N
SH_119	3	183954141	183954141	Missense_Mutation	SNV	A	T	T	VWASB2	c.566A>T	P.Q189L
SH_119	3	183976257	183976257	Missense_Mutation	SNV	A	T	T	ECE2	c.662A>T	P.Q221L
SH_119	3	185304301	185304301	Missense_Mutation	SNV	A	T	T	SEN2	c.100A>T	P.S34C
SH_119	3	185542560	185542560	Splice_Site	SNV	T	A	A	IGF2BP2	c.178+11A>T	
SH_119	3	185990076	185990076	Nonsense_Mutation	SNV	T	A	A	DGKG	c.967A>T	P.K323*
SH_119	3	187388070	187388070	Missense_Mutation	SNV	A	T	T	SST	c.10T>A	P.C4S
SH_119	3	189706687	189706687	Splice_Site	SNV	A	T	T	P3H2	c.955+9T>A	
SH_119	3	193029642	193029642	Missense_Mutation	SNV	T	A	A	ATP13A5	c.2408A>T	P.Q803L
SH_119	3	195518151	195518151	Silent	SNV	A	T	T	MUC4	c.300T>A	P.T100T
SH_119	3	21552416	21552416	Missense_Mutation	SNV	T	A	A	ZNF385D	c.376A>T	P.S126C
SH_119	3	31621525	31621525	Silent	SNV	A	T	T	TRTB3	c.648A>T	P.V216V
SH_119	3	32932313	32932313	Silent	SNV	G	A	A	TRIM71	c.1617G>A	P.E539E
SH_119	3	37535989	37535989	Splice_Site	SNV	T	A	A	ITGA9	c.545-3T>A	
SH_119	3	38622494	38622494	Silent	SNV	G	C	C	SCN5A	c.3156C>G	P.A1052A
SH_119	3	44328923	44328923	Missense_Mutation	SNV	T	A	A	TOPAZ1	c.3479T>A	P.V1160E
SH_119	3	44867945	44867945	Missense_Mutation	SNV	A	T	T	KIF15	c.2779A>T	P.S927C
SH_119	3	45965182	45965182	Missense_Mutation	SNV	T	A	A	FYCO1	c.4327A>T	P.I1443F
SH_119	3	48607617	48607617	Splice_Site	SNV	T	A	A	COL7A1	c.7441-6A>T	
SH_119	3	48629432	48629432	Missense_Mutation	SNV	T	A	A	COL7A1	c.1256A>T	P.Q419L
SH_119	3	49055043	49055043	Splice_Site	SNV	T	A	A	DALRD3	c.718+3A>T	
SH_119	3	49570051	49570051	Missense_Mutation	SNV	A	T	T	DAG1	c.2107A>T	P.T703S
SH_119	3	51929251	51929251	Silent	SNV	T	A	A	IQCF1	c.273A>T	P.A91A
SH_119	3	52027799	52027799	Missense_Mutation	SNV	T	A	A	RPL29	c.446A>T	P.K149I
SH_119	3	52485850	52485850	Missense_Mutation	SNV	T	A	A	TNNC1	c.227A>T	P.E76V
SH_119	3	53217135	53217135	Splice_Site	SNV	A	T	T	PRKCD	c.572-2A>T	
SH_119	3	54661900	54661900	Missense_Mutation	SNV	T	A	A	CACNA2D3	c.1050T>A	P.S350R
SH_119	3	62543149	62543149	Missense_Mutation	SNV	T	C	C	CADPS	c.1684A>G	P.K562E
SH_119	3	87039772	87039772	Missense_Mutation	SNV	T	A	A	VGLL3	c.122A>T	P.Q41L
SH_119	3	97595483	97595483	Silent	SNV	A	G	G	CRYBG3	c.5445A>G	P.A1815A
SH_119	3	97686259	97686259	Missense_Mutation	SNV	T	A	A	MINA	c.179A>T	P.E60V
SH_119	3	98073430	98073430	Missense_Mutation	SNV	T	A	A	OR5K4	c.733T>A	P.F245I
SH_119	4	10083026	10083026	Silent	SNV	T	A	A	WDR1	c.819A>T	P.V273V
SH_119	4	106576777	106576777	Silent	SNV	T	A	A	ARHGEF38	c.1131T>A	P.A377A
SH_119	4	108940731	108940731	Missense_Mutation	SNV	A	T	T	HADH	c.455A>T	P.Q152L
SH_119	4	114199612	114199612	Splice_Site	INDEL	A	-	-	ANK2	c.1720-4delA	
SH_119	4	123132087	123132087	Missense_Mutation	SNV	A	T	T	KIAA1109	c.2084A>T	P.Q695L
SH_119	4	123246471	123246471	Missense_Mutation	SNV	A	T	T	KIAA1109	c.10991A>T	P.D3664V
SH_119	4	129121747	129121747	Nonsense_Mutation	SNV	A	T	T	LARP1B	c.2236A>T	P.R746*
SH_119	4	134084217	134084217	Silent	SNV	T	C	C	PCDH10	c.2883T>C	P.S961S
SH_119	4	13589365	13589365	Missense_Mutation	SNV	T	C	C	BOD1L1	c.8311A>G	P.R2771G
SH_119	4	141868808	141868808	Missense_Mutation	SNV	C	T	T	RNF150	c.890G>A	P.R297Q

SH_119	4	145640104	145640104	Nonsense_Mutation	SNV	A	T	T	HHIP	c.1756A>T	P.K586*
SH_119	4	148984337	148984337	Missense_Mutation	SNV	A	T	T	ARHGAP10	c.2066A>T	P.N689I
SH_119	4	152498952	152498952	Silent	SNV	A	C	C	FAM160A1	c.456A>C	P.G152G
SH_119	4	153883988	153883988	Silent	SNV	A	G	G	FHDC1	c.873A>G	P.L291L
SH_119	4	154702659	154702659	Nonsense_Mutation	SNV	T	A	A	SFRP2	c.832A>T	P.K278*
SH_119	4	159076755	159076755	Splice_Site	SNV	A	T	T	FAM198B	c.1149+8T>A	
SH_119	4	15937806	15937806	Silent	SNV	T	A	A	FGFBP1	c.450A>T	P.L150L
SH_119	4	164394412	164394412	Missense_Mutation	SNV	A	C	C	TKTL2	c.475T>G	P.S159A
SH_119	4	164394868	164394868	Nonsense_Mutation	SNV	T	A	A	TKTL2	c.19A>T	P.K7*
SH_119	4	174169288	174169288	Missense_Mutation	SNV	A	T	T	GALNT7	c.284A>T	P.Q95L
SH_119	4	175898417	175898417	Missense_Mutation	SNV	T	A	A	ADAM29	c.1741T>A	P.C581S
SH_119	4	186209239	186209239	Splice_Site	SNV	A	T	T	SNX25	c.670+3A>T	
SH_119	4	187510324	187510324	Missense_Mutation	SNV	T	A	A	FAT1	c.13189A>T	P.I4397L
SH_119	4	25253938	25253938	Splice_Site	SNV	T	C	C	PI4K2B	c.269-5T>C	
SH_119	4	25675937	25675937	Silent	SNV	A	G	G	SLC34A2	c.1236A>G	P.A412A
SH_119	4	25677761	25677761	Missense_Mutation	SNV	C	T	T	SLC34A2	c.1463C>T	P.A488V
SH_119	4	2835429	2835429	Silent	SNV	T	A	A	SH3BP2	c.1554T>A	P.S518S
SH_119	4	30723300	30723300	Missense_Mutation	SNV	A	G	G	PCDH7	c.256A>G	P.T86A
SH_119	4	30725916	30725916	Nonsense_Mutation	SNV	A	T	T	PCDH7	c.2872A>T	P.K958*
SH_119	4	36286088	36286088	Silent	SNV	A	T	T	DTHD1	c.387A>T	P.S129S
SH_119	4	38126728	38126728	Splice_Site	SNV	A	T	T	TBC1D1	c.3085-4A>T	
SH_119	4	39255564	39255564	Missense_Mutation	SNV	A	T	T	WDR19	c.2435A>T	P.Q812L
SH_119	4	40351163	40351163	Silent	SNV	T	A	A	CHRNA9	c.630T>A	P.A210A
SH_119	4	42122136	42122136	Missense_Mutation	SNV	A	T	T	BEND4	c.1322T>A	P.V441E
SH_119	4	42592867	42592867	Missense_Mutation	SNV	C	T	T	ATP8A1	c.485G>A	P.G162E
SH_119	4	46966983	46966983	Splice_Site	SNV	A	T	T	GABRA4	c.1134+4T>A	
SH_119	4	47597807	47597807	Silent	SNV	A	G	G	CORIN	c.2748T>C	P.Y916Y
SH_119	4	56448298	56448298	Missense_Mutation	SNV	T	A	A	PDCL2	c.113A>T	P.Q38L
SH_119	4	57215634	57215634	Silent	SNV	T	A	A	AASDH	c.1983A>T	P.S661S
SH_119	4	6382725	6382725	Missense_Mutation	SNV	T	A	A	PPP2R2C	c.146A>T	P.E49V
SH_119	4	66189875	66189875	Missense_Mutation	SNV	T	A	A	EPHA5	c.3071A>T	P.Q1024L
SH_119	4	72313400	72313400	Nonsense_Mutation	SNV	A	T	T	SLC4A4	c.1003A>T	P.K335*
SH_119	4	76530824	76530824	Splice_Site	SNV	A	T	T	CDKL2	c.543-6T>A	
SH_119	4	84191035	84191035	Missense_Mutation	SNV	T	A	A	COQ2	c.890A>T	P.Y297F
SH_119	5	100147637	100147637	Silent	SNV	T	G	G	STRSIA4	c.994A>C	P.R332R
SH_119	5	112116599	112116599	Missense_Mutation	SNV	A	T	T	APC	c.644A>T	P.Q215L
SH_119	5	121409725	121409725	Missense_Mutation	SNV	A	G	G	LOX	c.328T>C	P.C110R
SH_119	5	126738327	126738327	Missense_Mutation	SNV	T	A	A	MEGF10	c.870T>A	P.D290E
SH_119	5	126771071	126771071	Missense_Mutation	SNV	T	A	A	MEGF10	c.1994T>A	P.F665Y
SH_119	5	128326089	128326089	Nonsense_Mutation	SNV	A	T	T	SLC27A6	c.901A>T	P.K301*
SH_119	5	137243561	137243561	Missense_Mutation	SNV	A	G	G	PKD2L2	c.1040A>G	P.N347S
SH_119	5	138163242	138163242	Missense_Mutation	SNV	G	T	T	CTNNA1	c.897G>T	P.E299D
SH_119	5	140167186	140167186	Silent	SNV	C	T	T	PCDHA1	c.1311C>T	P.A437A
SH_119	5	140215249	140215249	Silent	SNV	G	A	A	PCDHA7	c.1281G>A	P.A427A
SH_119	5	140255343	140255343	Missense_Mutation	SNV	T	A	A	PCDHA12	c.286T>A	P.C96S
SH_119	5	140474424	140474424	Missense_Mutation	SNV	T	C	C	PCDHB2	c.50T>C	P.L17P
SH_119	5	140482146	140482146	Missense_Mutation	SNV	A	T	T	PCDHB3	c.1913A>T	P.H638L
SH_119	5	140567770	140567770	Missense_Mutation	SNV	A	T	T	PCDHB9	c.878A>T	P.Q293L
SH_119	5	140594491	140594491	Missense_Mutation	SNV	T	C	C	PCDHB13	c.796T>C	P.S266P
SH_119	5	140778452	140778452	Missense_Mutation	SNV	A	T	T	PCDHGB5	c.758A>T	P.E253V
SH_119	5	141041681	141041681	Missense_Mutation	SNV	T	A	A	ARAP3	c.2942A>T	P.R981I
SH_119	5	141244731	141244731	Missense_Mutation	SNV	T	A	A	PCDH1	c.1213A>T	P.I405F
SH_119	5	149581924	149581924	Silent	SNV	T	A	A	SLC6A7	c.873T>A	P.A291A
SH_119	5	151043792	151043792	Missense_Mutation	SNV	G	A	A	SPARC	c.736C>T	P.L246F
SH_119	5	154315430	154315430	Silent	SNV	T	A	A	GEMIN5	c.480A>T	P.S160S
SH_119	5	156753269	156753269	Missense_Mutation	SNV	A	T	T	CYFIP2	c.2073A>T	P.E691D
SH_119	5	16764414	16764414	Missense_Mutation	SNV	T	A	A	MYO10	c.1271A>T	P.N424I
SH_119	5	178139478	178139478	Missense_Mutation	SNV	T	A	A	ZNF354A	c.1275A>T	P.K425N
SH_119	5	178563024	178563024	Silent	SNV	C	T	T	ADAMTS2	c.1971G>A	P.L657L
SH_119	5	21975294	21975294	Silent	SNV	T	A	A	CDH12	c.432A>T	P.S144S
SH_119	5	225645	225645	Missense_Mutation	SNV	A	T	T	SDHA	c.424A>T	P.M142L
SH_119	5	26902708	26902708	Missense_Mutation	SNV	A	T	T	CDH9	c.1130T>A	P.I377K
SH_119	5	26906171	26906171	Silent	SNV	T	A	A	CDH9	c.708A>T	P.I236I
SH_119	5	32037363	32037363	Missense_Mutation	SNV	T	A	A	PDZD2	c.1434T>A	P.D478E
SH_119	5	32783020	32783020	Nonsense_Mutation	SNV	A	T	T	NPR3	c.1312A>T	P.K438*
SH_119	5	35010157	35010157	Missense_Mutation	SNV	C	G	G	AGXT2	c.1061G>C	P.G354A
SH_119	5	37000636	37000636	Missense_Mutation	SNV	A	G	G	NIPBL	c.3466A>G	P.M1156V
SH_119	5	37815958	37815958	Missense_Mutation	SNV	T	A	A	GDNF	c.431A>T	P.Y144F
SH_119	5	39130690	39130690	Splice_Site	SNV	A	T	T	FYB	c.1870+2T>A	
SH_119	5	66449352	66449352	Missense_Mutation	SNV	A	T	T	MAST4	c.3592A>T	P.N1198Y
SH_119	5	72853467	72853467	Splice_Site	SNV	T	A	A	ANKRA2	c.449-2A>T	
SH_119	5	81608541	81608541	Silent	SNV	A	T	T	ATP6AP1L	c.243A>T	P.V81V
SH_119	5	82837882	82837882	Missense_Mutation	SNV	A	T	T	VCAN	c.9060A>T	P.R3020S
SH_119	5	93989002	93989002	Missense_Mutation	SNV	A	T	T	SLF1	c.908A>T	P.D303V
SH_119	6	108499292	108499292	Splice_Site	SNV	T	A	A	NR2E1	c.607-7T>A	
SH_119	6	109935621	109935621	Missense_Mutation	SNV	T	A	A	AK9	c.1462A>T	P.M488L
SH_119	6	110763638	110763638	Missense_Mutation	SNV	T	A	A	SLC22A16	c.992A>T	P.Q331L
SH_119	6	117662737	117662737	Missense_Mutation	SNV	T	C	C	ROS1	c.4728A>G	P.I1576M
SH_119	6	125569430	125569430	Missense_Mutation	SNV	A	C	C	TPD52L1	c.200A>C	P.Y67S
SH_119	6	136599326	136599326	Silent	SNV	A	T	T	BCLAF1	c.687T>A	P.P229P
SH_119	6	137519389	137519389	Missense_Mutation	SNV	T	A	A	IFNGR1	c.1249A>T	P.S417C
SH_119	6	138576598	138576598	Missense_Mutation	SNV	G	C	C	ARFGEF3	c.796G>C	P.V266C
SH_119	6	138628511	138628511	Missense_Mutation	SNV	A	T	T	ARFGEF3	c.3950A>T	P.Y1317F
SH_119	6	13977775	13977775	Missense_Mutation	SNV	C	T	T	RNF182	c.425C>T	P.P142L
SH_119	6	144814510	144814510	Missense_Mutation	SNV	A	T	T	UTRN	c.4511A>T	P.Q1504L
SH_119	6	149833385	149833385	Missense_Mutation	SNV	T	A	A	PPIL4	c.1133A>T	P.H378L
SH_119	6	152554911	152554911	Splice_Site	SNV	T	A	A	SYNE1	c.20499+5A>T	
SH_119	6	160479077	160479077	Missense_Mutation	SNV	A	T	T	IGF2R	c.2819A>T	P.N940I
SH_119	6	165712993	165712993	Splice_Site	SNV	T	A	A	C6orf118	c.877-2A>T	
SH_119	6	24777537	24777537	Splice_Site	SNV	A	G	G	GMNN	c.51+12A>G	
SH_119	6	26446013	26446013	Missense_Mutation	SNV	A	T	T	BTN3A3	c.515A>T	P.Y172F
SH_119	6	27101157	27101157	Missense_Mutation	SNV	A	T	T	HIST1H2AG	c.307A>T	P.I103F
SH_119	6	28239825	28239825	Missense_Mutation	SNV	A	T	T	ZSCAN26	c.128A>T	P.K43I
SH_119	6	28402285	28402285	Missense_Mutation	SNV	A	T	T	ZSCAN23	c.1127T>A	P.L376Q
SH_119	6	28500177	28500177	Nonsense_Mutation	SNV	A	T	T	GPX5	c.439A>T	P.K147*
SH_119	6	30546166	30546166	Splice_Site	SNV	A	T	T	ABCF1	c.381+4A>T	
SH_119	6	30671957	30671957	Missense_Mutation	SNV	T	A	A	MDC1	c.5003A>T	P.Q1668L
SH_119	6	32008187	32008187	Missense_Mutation	SNV	A	T	T	CYP21A2	c.944A>T	P.Q315L

SH_119	6	33406350	33406350	Splice_Site	SNV	A	T	T	SYNGAP1	c.1531+10A>T	
SH_119	6	33543695	33543695	Silent	SNV	T	A	A	BAK1	c.81A>T	P.V27V
SH_119	6	35096967	35096967	Splice_Site	SNV	A	T	T	TCP11	c.276-8T>A	
SH_119	6	36672184	36672184	Nonsense_Mutation	SNV	A	T	T	RAB44	c.172A>T	P.K58*
SH_119	6	38994446	38994446	Splice_Site	SNV	A	T	T	DNAH8	c.13836+3A>T	
SH_119	6	42034075	42034075	Missense_Mutation	SNV	A	T	T	TAf8	c.515A>T	P.Y172F
SH_119	6	42619808	42619808	Splice_Site	SNV	A	T	T	UBR2	c.2613A>T	P.T871T
SH_119	6	42830284	42830284	Missense_Mutation	SNV	A	G	G	GLTSCR1L	c.2386A>G	P.R796G
SH_119	6	49574885	49574885	Silent	SNV	T	C	C	RHAG	c.1116A>G	P.A372A
SH_119	6	4996215	4996215	Missense_Mutation	SNV	T	A	A	RPP40	c.794A>T	P.E265V
SH_119	6	49976862	49976862	Missense_Mutation	SNV	A	G	G	DEFB110	c.178T>C	P.C60R
SH_119	6	51712640	51712640	Silent	SNV	T	A	A	PKHD1	c.8040A>T	P.P2680P
SH_119	6	52761649	52761649	Silent	SNV	T	A	A	GSTA3	c.624A>T	P.A208A
SH_119	6	55216285	55216285	Missense_Mutation	SNV	A	G	G	GFRAL	c.605A>G	P.K1202R
SH_119	6	55264003	55264003	Missense_Mutation	SNV	A	T	T	GFRAL	c.978A>T	P.K326N
SH_119	6	57467155	57467155	Missense_Mutation	SNV	A	T	T	PRIM2	c.1096A>T	P.S366C
SH_119	6	82935195	82935195	Missense_Mutation	SNV	T	A	A	IBTK	c.824A>T	P.Q275L
SH_119	6	84859375	84859375	Missense_Mutation	SNV	T	A	A	CEP162	c.3449A>T	P.H1150L
SH_119	6	85447044	85447044	Missense_Mutation	SNV	A	T	T	TBX18	c.1183T>A	P.C395S
SH_119	6	89816936	89816936	Missense_Mutation	SNV	A	G	G	SRSF12	c.107T>C	P.I36T
SH_119	7	100636024	100636024	Missense_Mutation	SNV	C	T	T	MUC12	c.2180C>T	P.S727L
SH_119	7	100646531	100646531	Silent	SNV	A	T	T	MUC12	c.12687A>T	P.T4229T
SH_119	7	100675016	100675016	Missense_Mutation	SNV	A	T	T	MUC17	c.319A>T	P.S107C
SH_119	7	100687033	100687033	Silent	SNV	T	A	A	MUC17	c.12336T>A	P.A4112A
SH_119	7	102108744	102108744	Missense_Mutation	SNV	A	T	T	LRWD1	c.383A>T	P.Q128L
SH_119	7	103131192	103131192	Silent	SNV	T	C	C	RELN	c.9528A>G	P.E3176E
SH_119	7	105909612	105909612	Silent	SNV	G	C	C	NAMPT	c.594C>G	P.V198V
SH_119	7	107431656	107431656	Missense_Mutation	SNV	A	G	G	SLC26A3	c.407T>C	P.M136T
SH_119	7	120979077	120979077	Missense_Mutation	SNV	T	A	A	WNT16	c.746T>A	P.I249K
SH_119	7	123150025	123150025	Silent	SNV	A	T	T	IQUB	c.462T>A	P.L154L
SH_119	7	123455084	123455084	Splice_Site	SNV	A	T	T	HYALP1	n.892A>T	
SH_119	7	126544162	126544162	Silent	SNV	T	A	A	GRM8	c.882A>T	P.A294A
SH_119	7	127014164	127014164	Missense_Mutation	SNV	T	A	A	ZNF800	c.1226A>T	P.K409I
SH_119	7	127235515	127235515	Missense_Mutation	SNV	A	T	T	FSCN3	c.299A>T	P.H100L
SH_119	7	127544860	127544860	Frame_Shift_Del	INDEL	A	-	-	SND1	c.1515delA	P.D506fs
SH_119	7	130368449	130368449	Frame_Shift_Del	INDEL	C	-	-	TSGA13	c.85delG	P.V29fs
SH_119	7	131864596	131864596	Missense_Mutation	SNV	T	A	A	PLXNA4	c.3724A>T	P.I1242F
SH_119	7	136699651	136699651	Silent	SNV	T	A	A	CHRM2	c.39T>A	P.A13A
SH_119	7	138732341	138732341	Nonstop_Mutation	SNV	T	C	C	ZC3HAV1	c.2708A>G	P.Ter903Wext*?
SH_119	7	139741562	139741562	Missense_Mutation	SNV	T	A	A	PARP12	c.1064A>T	P.Q355L
SH_119	7	141450153	141450153	Nonstop_Mutation	SNV	A	T	T	SSBP1	c.446A>T	P.Ter149Lext**?
SH_119	7	141643769	141643769	Splice_Site	SNV	A	T	T	CLEC5A	c.140-5T>A	
SH_119	7	141705384	141705384	Silent	SNV	T	C	C	MGAM	c.54T>C	P.V18V
SH_119	7	141705385	141705385	Missense_Mutation	SNV	C	A	A	MGAM	c.55C>A	P.L19I
SH_119	7	142568157	142568157	Missense_Mutation	SNV	A	G	G	EPHB6	c.1922A>G	P.E641G
SH_119	7	149522043	149522043	Splice_Site	SNV	A	T	T	SSPO	c.13841-11A>T	
SH_119	7	150691046	150691046	Missense_Mutation	SNV	A	T	T	NOS3	c.155A>T	P.H52L
SH_119	7	150716334	150716334	Missense_Mutation	SNV	T	A	A	ATG9B	c.1091A>T	P.Y364F
SH_119	7	150767992	150767992	Silent	SNV	A	T	T	SLC4A2	c.1743A>T	P.S581S
SH_119	7	150884051	150884051	Missense_Mutation	SNV	A	T	T	ASB10	c.167T>A	P.L56H
SH_119	7	150901674	150901674	Missense_Mutation	SNV	A	T	T	IQCA1L	c.260T>A	P.L87H
SH_119	7	157903543	157903543	Missense_Mutation	SNV	T	A	A	PTPRN2	c.1507A>T	P.S503C
SH_119	7	158715200	158715200	Missense_Mutation	SNV	A	T	T	WDR60	c.2054A>T	P.Q685L
SH_119	7	18066597	18066597	Missense_Mutation	SNV	A	T	T	PRPS1L1	c.809T>A	P.V270E
SH_119	7	19738071	19738071	Missense_Mutation	SNV	T	A	A	TWISTN8	c.885A>T	P.Q295H
SH_119	7	20418782	20418782	Nonsense_Mutation	SNV	T	A	A	ITGB8	c.497T>A	P.L166*
SH_119	7	2974137	2974137	Missense_Mutation	SNV	A	T	T	CARD11	c.1468T>A	P.F490I
SH_119	7	31126076	31126076	Missense_Mutation	SNV	T	A	A	ADCYAP1R1	c.748T>A	P.Y250N
SH_119	7	35733830	35733830	Silent	SNV	T	C	C	HERPUD2	c.111A>G	P.L37L
SH_119	7	38305149	38305149	Missense_Mutation	SNV	T	A	A	TARP	c.119A>T	P.Y40F
SH_119	7	4198152	4198152	Silent	SNV	A	G	G	SDK1	c.159A>G	P.S53S
SH_119	7	42006128	42006128	Missense_Mutation	SNV	T	C	C	GLI3	c.2543A>G	P.D848G
SH_119	7	45123806	45123806	Missense_Mutation	SNV	T	A	A	NACAD	c.1973A>T	P.K658M
SH_119	7	45701681	45701681	Silent	SNV	A	T	T	ADCY1	c.798A>T	P.S266S
SH_119	7	47925305	47925305	Missense_Mutation	SNV	T	A	A	PKD1L1	c.3184A>T	P.S1062C
SH_119	7	4796793	4796793	Missense_Mutation	SNV	A	T	T	FOXK1	c.1219A>T	P.T407S
SH_119	7	48431656	48431656	Silent	SNV	C	G	G	ABCA13	c.11793C>G	P.T3931T
SH_119	7	50057825	50057825	Splice_Site	SNV	A	G	G	ZPBp	c.780+11T>C	
SH_119	7	5529802	5529802	Missense_Mutation	SNV	T	A	A	FBXL18	c.2042A>T	P.E681V
SH_119	7	5568230	5568230	Missense_Mutation	SNV	T	A	A	ACTB	c.484A>T	P.T162S
SH_119	7	56142414	56142414	Nonsense_Mutation	SNV	C	T	T	SUMF2	c.532C>T	P.R178*
SH_119	7	63680478	63680478	Missense_Mutation	SNV	A	T	T	ZNF735	c.1049A>T	P.E350V
SH_119	7	72159711	72159711	Missense_Mutation	SNV	T	A	A	TYW1B	c.1472A>T	P.Q491L
SH_119	7	7622860	7622860	Missense_Mutation	SNV	A	G	G	MIOS	c.1505A>G	P.K502R
SH_119	7	8099799	8099799	Missense_Mutation	SNV	C	T	T	GLCC1	c.887C>T	P.P296L
SH_119	7	81642783	81642783	Silent	SNV	A	G	G	CACNA2D1	c.1266T>C	P.N422N
SH_119	7	82545753	82545753	Missense_Mutation	SNV	T	A	A	PCLO	c.11549A>T	P.Q3850L
SH_119	7	82583237	82583237	Silent	SNV	A	T	T	PCLO	c.7032T>A	P.P2344P
SH_119	7	82595339	82595339	Silent	SNV	T	A	A	PCLO	c.3765A>T	P.S1255S
SH_119	7	83689823	83689823	Missense_Mutation	SNV	T	A	A	SEMA3A	c.505A>T	P.S169C
SH_119	7	90528627	90528627	Missense_Mutation	SNV	A	T	T	CDK14	c.661A>T	P.M221L
SH_119	7	94539923	94539923	Silent	SNV	T	A	A	PPP1R9A	c.498T>A	P.A166A
SH_119	7	97493810	97493810	Splice_Site	SNV	T	A	A	ASNS	c.187-2A>T	
SH_119	7	98507696	98507696	Frame_Shift_Del	INDEL	C	-	-	TRRAP	c.1369delC	P.H457fs
SH_119	7	99631564	99631564	Missense_Mutation	SNV	A	T	T	ZKSCAN1	c.1328A>T	P.H443L
SH_119	8	100729472	100729472	Silent	SNV	C	T	T	VPS13B	c.6603C>T	P.S2201S
SH_119	8	100836129	100836129	Missense_Mutation	SNV	A	T	T	VPS13B	c.9328A>T	P.T3110S
SH_119	8	101075705	101075705	Missense_Mutation	SNV	A	T	T	RGS22	c.1255T>A	P.W419R
SH_119	8	101721781	101721781	Missense_Mutation	SNV	T	A	A	PABPC1	c.1151A>T	P.Q384L
SH_119	8	104394777	104394777	Silent	SNV	T	A	A	CTHRC1	c.639T>A	P.S213S
SH_119	8	10464617	10464617	Missense_Mutation	SNV	T	A	A	RP1L1	c.6991A>T	P.T2331S
SH_119	8	108509638	108509638	Missense_Mutation	SNV	T	A	A	ANGPT1	c.149A>T	P.H50L
SH_119	8	110287574	110287574	Splice_Site	SNV	T	A	A	NUDCD1	c.1086+7A>T	
SH_119	8	110302071	110302071	Silent	SNV	T	A	A	NUDCD1	c.645A>T	P.L215L
SH_119	8	110980551	110980551	Silent	SNV	A	T	T	KCNV1	c.1269T>A	P.P423P
SH_119	8	11687801	11687801	Missense_Mutation	SNV	A	T	T	FDT1	c.751A>T	P.N251Y
SH_119	8	12250795	12250795	Splice_Site	SNV	A	T	T	DEFB109P1	n.187T>A	
SH_119	8	125082827	125082827	Silent	SNV	A	T	T	FER1L6	c.3954A>T	P.I1318I

SH_119	8	131896862	131896862	Missense_Mutation	SNV	T	A	A	ADCY8	c.2057A>T	P.E686V
SH_119	8	139164223	139164223	Missense_Mutation	SNV	A	G	G	FAM135B	c.2495T>C	P.I832T
SH_119	8	139715588	139715588	Splice_Site	SNV	A	T	T	COL22A1	c.2520T>A	P.G840G
SH_119	8	143846567	143846567	Splice_Site	SNV	A	T	T	LYNX1	c.155-9T>A	
SH_119	8	145278066	145278066	Missense_Mutation	SNV	A	T	T	MROH1	c.1271A>T	P.E424V
SH_119	8	1513975	1513975	Missense_Mutation	SNV	A	T	T	DLGAP2	c.1117A>T	P.S373C
SH_119	8	19315934	19315934	Splice_Site	SNV	A	T	T	CSGALNACT1	c.851+3T>A	
SH_119	8	20107310	20107310	Missense_Mutation	SNV	T	A	A	LZTS1	c.1714A>T	P.S572C
SH_119	8	23712004	23712004	Silent	SNV	C	T	T	STC1	c.33G>A	P.L11L
SH_119	8	27287675	27287675	Splice_Site	SNV	A	T	T	PTK2B	c.614+3A>T	
SH_119	8	30704323	30704323	Silent	SNV	T	A	A	TEX15	c.2211A>T	P.T737T
SH_119	8	31004626	31004626	Silent	SNV	A	G	G	WRN	c.3441A>G	P.A1147A
SH_119	8	35624472	35624472	Missense_Mutation	SNV	C	T	T	UNC5D	c.2351C>T	P.A784V
SH_119	8	37696501	37696501	Missense_Mutation	SNV	G	A	A	ADGRA2	c.2287G>A	P.G763R
SH_119	8	37792013	37792013	Splice_Site	SNV	A	T	T	GOT1L1	c.1073-9T>A	
SH_119	8	38008322	38008322	Silent	SNV	T	C	C	STAR	c.15A>G	P.T5T
SH_119	8	49832965	49832965	Missense_Mutation	SNV	T	A	A	SNAI2	c.115A>T	P.M39L
SH_119	8	55541716	55541716	Silent	SNV	T	A	A	RP1	c.5274T>A	P.S1758S
SH_119	8	66605875	66605875	Splice_Site	SNV	A	T	T	MTFR1	c.67-4A>T	
SH_119	8	68934262	68934262	Splice_Site	SNV	A	T	T	PREX2	c.337-9A>T	
SH_119	8	69688676	69688676	Missense_Mutation	SNV	A	G	G	C8orf34	c.1447A>G	P.M483V
SH_119	8	7190825	7190825	Missense_Mutation	SNV	A	T	T	USP17L1	c.917A>T	P.Y306F
SH_119	8	72959392	72959392	Silent	SNV	T	A	A	TRPA1	c.1956A>T	P.R652R
SH_119	8	75233195	75233195	Missense_Mutation	SNV	A	T	T	JPH1	c.328T>A	P.W110R
SH_119	8	75263618	75263618	Missense_Mutation	SNV	A	T	T	GDAP1	c.23A>T	P.E8V
SH_119	8	77745615	77745615	Missense_Mutation	SNV	A	T	T	ZFH4	c.3367A>T	P.T1123S
SH_119	8	79601546	79601546	Missense_Mutation	SNV	A	G	G	ZC2HC1A	c.442A>G	P.L148V
SH_119	8	80950452	80950452	Nonsense_Mutation	SNV	T	A	A	TPD52	c.574A>T	P.K192*
SH_119	8	90965555	90965555	Missense_Mutation	SNV	T	A	A	NBN	c.1762A>T	P.N588Y
SH_119	8	90995053	90995053	Missense_Mutation	SNV	T	A	A	NBN	c.68A>T	P.E23V
SH_119	8	9592454	9592454	Missense_Mutation	SNV	A	T	T	TNKS	c.2393A>T	P.Q798L
SH_119	9	100692896	100692896	Missense_Mutation	SNV	A	T	T	HEMGN	c.781T>A	P.Y261N
SH_119	9	101784386	101784386	Missense_Mutation	SNV	A	T	T	COL15A1	c.1715A>T	P.E572V
SH_119	9	101814676	101814676	Missense_Mutation	SNV	A	T	T	COL15A1	c.2911A>T	P.T971S
SH_119	9	107367401	107367401	Missense_Mutation	SNV	T	A	A	OR13C2	c.508A>T	P.R170W
SH_119	9	111903647	111903647	Missense_Mutation	SNV	A	G	G	FRR5L1	c.838T>C	P.F280L
SH_119	9	113189902	113189902	Missense_Mutation	SNV	T	A	A	SVEP1	c.5944A>T	P.R1982W
SH_119	9	113538138	113538138	Nonsense_Mutation	SNV	A	T	T	MUSK	c.1021A>T	P.R341*
SH_119	9	114486151	114486151	Silent	SNV	A	T	T	C9orf84	c.1566T>A	P.P522P
SH_119	9	115945043	115945043	Splice_Site	SNV	T	C	C	FKBP15	c.1914+3A>G	
SH_119	9	116060057	116060057	Silent	SNV	A	T	T	RNF183	c.408T>A	P.S136S
SH_119	9	125748501	125748501	Missense_Mutation	SNV	A	T	T	RABGAP1	c.393A>T	P.E131D
SH_119	9	12704631	12704631	Missense_Mutation	SNV	A	T	T	TYRP1	c.1187A>T	P.N396I
SH_119	9	129453183	129453183	Missense_Mutation	SNV	T	A	A	LMX1B	c.395T>A	P.L132Q
SH_119	9	131186439	131186439	Missense_Mutation	SNV	T	A	A	CERCAM	c.215T>A	P.L72Q
SH_119	9	131347058	131347058	Missense_Mutation	SNV	A	T	T	SPTAN1	c.2496A>T	P.E832D
SH_119	9	131398640	131398640	Missense_Mutation	SNV	T	A	A	WDR34	c.623A>T	P.Q208L
SH_119	9	132593216	132593216	Missense_Mutation	SNV	T	A	A	C9orf78	c.476A>T	P.K159M
SH_119	9	133258883	133258883	Splice_Site	SNV	A	G	G	HMCN2	c.7060-8A>G	
SH_119	9	133951258	133951258	Missense_Mutation	SNV	A	T	T	LAMC3	c.3535A>T	P.R1179W
SH_119	9	135772727	135772727	Missense_Mutation	SNV	T	A	A	TSC1	c.2819A>T	P.Q940L
SH_119	9	135864542	135864542	Missense_Mutation	SNV	G	A	A	GFI1B	c.605G>A	P.G202D
SH_119	9	137645753	137645753	Splice_Site	SNV	T	A	A	COL5A1	c.1773+4T>A	
SH_119	9	138516290	138516290	Missense_Mutation	SNV	T	A	A	GLT6D1	c.484A>T	P.I162F
SH_119	9	21187053	21187053	Missense_Mutation	SNV	T	A	A	IFNA4	c.478A>T	P.S160C
SH_119	9	26996313	26996313	Missense_Mutation	SNV	A	T	T	LRR19	c.780T>A	P.N260K
SH_119	9	32630687	32630687	Missense_Mutation	SNV	T	A	A	TAF1L	c.4891A>T	P.T1631S
SH_119	9	33364085	33364085	Missense_Mutation	SNV	A	T	T	NFX1	c.2954A>T	P.D985V
SH_119	9	33548561	33548561	Missense_Mutation	SNV	T	A	A	ANKRD18B	c.1586T>A	P.M529K
SH_119	9	35060790	35060790	Splice_Site	SNV	T	A	A	VCP	c.1482+8A>T	
SH_119	9	36356404	36356404	Missense_Mutation	SNV	T	A	A	RNF38	c.805A>T	P.S269C
SH_119	9	36665353	36665353	Nonsense_Mutation	SNV	A	T	T	MELK	c.1060A>T	P.K354*
SH_119	9	36665561	36665561	Missense_Mutation	SNV	A	G	G	MELK	c.1268A>G	P.Y423C
SH_119	9	38596345	38596345	Missense_Mutation	SNV	T	A	A	ANKRD18A	c.992A>T	P.K331M
SH_119	9	38620267	38620267	Missense_Mutation	SNV	T	A	A	ANKRD18A	c.16A>T	P.S6C
SH_119	9	43920246	43920246	Splice_Site	SNV	T	A	A	CNTNAP3P2	n.3845-3T>A	
SH_119	9	72520864	72520864	Splice_Site	SNV	C	A	A	C9orf135	c.508-6C>A	
SH_119	9	74675410	74675410	Splice_Site	SNV	T	A	A	C9orf57	c.13+3A>T	
SH_119	9	95012487	95012487	Silent	SNV	T	A	A	IARS	c.2514A>T	P.R838R
SH_119	9	96416737	96416737	Missense_Mutation	SNV	A	T	T	PHF2	c.832A>T	P.I278F
SH_119	9	98669432	98669432	Nonsense_Mutation	SNV	A	T	T	ERCC6L2	c.700A>T	P.R234*
SH_119	X	100809225	100809225	Missense_Mutation	SNV	A	C	C	ARMCX1	c.1312A>C	P.N438H
SH_119	X	101096635	101096635	Splice_Site	SNV	T	A	A	NXF5	c.240+11A>T	
SH_119	X	10180534	10180534	Frame_Shift_Ins	INDEL	-	T	T	CLCN4	c.1136dupT	P.M379fs
SH_119	X	107920727	107920727	Splice_Site	SNV	A	T	T	COL4A5	c.3791-3A>T	
SH_119	X	108906543	108906543	Missense_Mutation	SNV	T	A	A	ACSL4	c.1602A>T	P.E534D
SH_119	X	118219478	118219478	Silent	SNV	A	T	T	KIAA1210	c.4716T>A	P.A1572A
SH_119	X	118223259	118223259	Missense_Mutation	SNV	A	T	T	KIAA1210	c.1934T>A	P.M645K
SH_119	X	12720135	12720135	Splice_Site	SNV	T	A	A	FRMPD4	c.1070+6T>A	
SH_119	X	129354456	129354456	Splice_Site	SNV	T	A	A	ZNF280C	c.1396-2A>T	
SH_119	X	12938956	12938956	Silent	SNV	A	G	G	TLR8	c.1851A>G	P.L617L
SH_119	X	133119345	133119345	Missense_Mutation	SNV	T	A	A	GPC3	c.132A>T	P.R44S
SH_119	X	133919983	133919983	Splice_Site	SNV	T	A	A	FAM122B	c.441-6A>T	
SH_119	X	135126797	135126797	Missense_Mutation	SNV	A	T	T	SLC9A6	c.2020A>T	P.I674F
SH_119	X	135430026	135430026	Silent	SNV	A	T	T	ADGRG4	c.4161A>T	P.P1387P
SH_119	X	135431670	135431670	Frame_Shift_Del	INDEL	G	-	-	ADGRG4	c.5806delG	P.A1936fs
SH_119	X	13621529	13621529	Missense_Mutation	SNV	T	A	A	EGFL6	c.494T>A	P.L165Q
SH_119	X	138667339	138667339	Splice_Site	SNV	T	A	A	MCF2	c.2813-2A>T	
SH_119	X	140969477	140969477	Silent	SNV	G	A	A	MAGEC3	c.804G>A	P.Q268Q
SH_119	X	148062323	148062323	Splice_Site	SNV	A	T	T	AFF2	c.3518+3A>T	
SH_119	X	41003771	41003771	Splice_Site	SNV	A	G	G	USP9X	c.1315-4A>G	
SH_119	X	47060933	47060933	Silent	SNV	G	C	C	UBA1	c.735G>C	P.G245G
SH_119	X	47272277	47272277	Missense_Mutation	SNV	A	T	T	ZNF157	c.805A>T	P.T269S
SH_119	X	47426129	47426129	Missense_Mutation	SNV	A	T	T	ARAF	c.649A>T	P.N217Y
SH_119	X	54048758	54048758	Missense_Mutation	SNV	T	A	A	PHF8	c.335A>T	P.K112M
SH_119	X	65409598	65409598	Nonsense_Mutation	SNV	T	A	A	HEPH	c.890T>A	P.L297*
SH_119	X	65413410	65413410	Nonsense_Mutation	SNV	T	A	A	HEPH	c.1308T>A	P.Y436*
SH_119	X	70331299	70331299	Missense_Mutation	SNV	T	A	A	IL2RG	c.91A>T	P.N31Y

SH_119	X	70361081	70361081	Missense_Mutation	SNV	A	T	T	MED12	c.6269A>T	P.Q2090L
SH_119	X	78010453	78010453	Silent	SNV	T	C	C	LPAR4	c.87T>C	P.N29N
SH_119	X	99848912	99848912	Silent	SNV	T	A	A	TNMD	c.201T>A	P.T67T
SH_119	Y	14952176	14952176	Silent	SNV	A	T	T	USP9Y	c.5724A>T	P.T1908T
SH_119	Y	21883052	21883052	Missense_Mutation	SNV	T	A	A	KDM5D	c.1610A>T	P.E537V
SH_120	1	200377084	200377084	Missense_Mutation	SNV	T	G	G	ZNF281	c.1750A>C	P.J584L
SH_120	1	215807811	215807811	Frame_Shift_Ins	INDEL	-	C	C	USH2A	c.15286dupG	P.E5096fs
SH_120	12	25398285	25398285	Missense_Mutation	SNV	C	A	A	KRAS	c.34G>T	P.G12C
SH_120	12	6566581	6566581	Missense_Mutation	SNV	A	G	G	TAPBPL	c.575A>G	P.Q192R
SH_120	13	33629207	33629207	Missense_Mutation	SNV	G	T	T	KL	c.1354G>T	P.V452F
SH_120	16	58287944	58287944	Missense_Mutation	SNV	C	T	T	CCDC113	c.271C>T	P.R91C
SH_120	2	137928486	137928486	Missense_Mutation	SNV	G	T	T	THSD7B	c.1701G>T	P.K567N
SH_120	3	105400433	105400433	Missense_Mutation	SNV	G	C	C	CBLB	c.2402C>G	P.S801C
SH_120	4	23816104	23816104	Missense_Mutation	SNV	A	C	C	PPARGC1A	c.1002T>G	P.S334R
SH_120	8	143993984	143993984	Missense_Mutation	SNV	G	A	A	CYP11B2	c.1360C>T	P.R454C
SH_120	8	2038013	2038013	Splice_Site	SNV	C	T	T	MYOM2	c.1827C>T	P.T609T
SH_120	9	114820772	114820772	Missense_Mutation	SNV	T	A	A	SUSD1	c.2045A>T	P.N682I
SH_120	9	128347883	128347883	Missense_Mutation	SNV	C	A	A	MAPKAP1	c.622G>T	P.G208W
SH_121	1	156177730	156177730	Missense_Mutation	SNV	G	C	C	SLC25A44	c.703G>C	P.V235L
SH_121	1	156202181	156202181	Missense_Mutation	SNV	G	A	A	PMF1-BGLAP	c.232G>A	P.D78N
SH_121	1	161059016	161059016	Nonsense_Mutation	SNV	G	T	T	NECTIN4	c.71C>A	P.S24*
SH_121	1	204588236	204588236	Missense_Mutation	SNV	C	T	T	LRRN2	c.885G>A	P.M295I
SH_121	1	99753679	99753679	Silent	SNV	C	T	T	PLPPR4	c.381C>T	P.S127S
SH_121	10	37508335	37508335	Missense_Mutation	SNV	A	G	G	ANKRD30A	c.3527A>G	P.Q1176R
SH_121	11	17582329	17582329	Silent	SNV	A	T	T	OTOG	c.1452A>T	P.P484P
SH_121	11	4790976	4790976	Missense_Mutation	SNV	G	T	T	OR51F1	c.172C>A	P.H58N
SH_121	11	60073583	60073583	Missense_Mutation	SNV	G	C	C	MS4A4A	c.398G>C	P.G133A
SH_121	12	112227632	112227632	Missense_Mutation	SNV	A	G	G	ALDH2	c.446A>G	P.Y149C
SH_121	12	53186577	53186577	Missense_Mutation	SNV	G	T	T	KRT3	c.941C>A	P.A314D
SH_121	12	60169172	60169172	Missense_Mutation	SNV	G	A	A	SLC16A7	c.1096G>A	P.V366M
SH_121	12	63989812	63989812	Silent	SNV	C	A	A	DPY19L2	c.1467G>T	P.P489P
SH_121	12	65232608	65232608	Silent	SNV	G	T	T	TBC1D30	c.909G>T	P.L1303L
SH_121	12	65232609	65232609	Missense_Mutation	SNV	G	T	T	TBC1D30	c.910G>T	P.A304S
SH_121	13	48953730	48953730	Nonsense_Mutation	SNV	C	T	T	RB1	c.1333C>T	P.R445*
SH_121	14	31626160	31626160	Silent	SNV	T	C	C	HECTD1	c.1818A>G	P.K606K
SH_121	16	19722744	19722744	Missense_Mutation	SNV	C	G	G	KNOP1	c.937G>C	P.E313Q
SH_121	16	70590870	70590870	Missense_Mutation	SNV	A	G	G	SF3B3	c.1948A>G	P.K650E
SH_121	2	188228181	188228181	Silent	SNV	T	C	C	CALCRL	c.549A>G	P.S183S
SH_121	2	189434045	189434045	Missense_Mutation	SNV	T	C	C	GULP1	c.479T>C	P.V160A
SH_121	3	186395235	186395249	Missense_Mutation	INDEL	CATGGACAC	-	-	HRG	69delCCCCCATC	P.386_H390del
SH_121	3	45988342	45988342	Silent	SNV	C	T	T	CXCR6	c.369C>T	P.I123I
SH_121	3	57131806	57131806	Missense_Mutation	SNV	G	T	T	IL17RD	c.1493C>A	P.A498D
SH_121	3	9828890	9828890	Silent	SNV	G	A	A	TADA3	c.699C>T	P.D233D
SH_121	4	37831635	37831635	Missense_Mutation	SNV	A	C	C	PGM2	c.131A>C	P.K44T
SH_121	5	127637068	127637068	Splice_Site	SNV	A	G	G	FBN2	c.6046+6T>C	
SH_121	5	136964010	136964010	Missense_Mutation	SNV	T	C	C	KLHL3	c.1471A>G	P.M491V
SH_121	5	162910182	162910182	Splice_Site	SNV	A	G	G	HMMR	c.1685+4A>G	
SH_121	6	129621954	129621954	Silent	SNV	T	C	C	LAMA2	c.3111T>C	P.I1037I
SH_121	6	24843737	24843737	Nonsense_Mutation	SNV	C	A	A	FAM65B	c.1210G>T	P.E404*
SH_121	6	46135309	46135309	Missense_Mutation	SNV	G	T	T	ENPP5	c.691C>A	P.L231M
SH_121	7	16745698	16745698	Missense_Mutation	SNV	A	C	C	BZW2	c.1245A>C	P.E415D
SH_121	8	130789776	130789776	Missense_Mutation	SNV	C	A	A	GSDMC	c.58G>T	P.D20Y
SH_121	8	75925113	75925113	Splice_Site	SNV	T	C	C	CRISPLD1	c.-65-12T>C	
SH_121	9	113166647	113166647	Missense_Mutation	SNV	T	C	C	SVEP1	c.9626A>G	P.E3209G
SH_122	1	115217380	115217380	Missense_Mutation	SNV	A	G	G	AMPD1	c.1892T>C	P.L631S
SH_122	1	151142989	151142992	Splice_Site	INDEL	ACTC	-	-	TMOD4	5+3_1015+6delGAGT	
SH_122	1	167088659	167088659	Missense_Mutation	SNV	G	A	A	DUSP27	c.611G>A	P.R204Q
SH_122	1	214542866	214542866	Missense_Mutation	SNV	C	A	A	PTPN14	c.3205G>T	P.V1069L
SH_122	11	118065080	118065080	Missense_Mutation	SNV	T	G	G	JAML	c.1145A>C	P.K382T
SH_122	11	56000281	56000281	Missense_Mutation	SNV	C	A	A	OR5T2	c.381G>T	P.K127N
SH_122	11	57296320	57296320	Missense_Mutation	SNV	G	A	A	TIMM10	c.143C>T	P.S48F
SH_122	11	67191096	67191096	Missense_Mutation	SNV	A	G	G	CARNS1	c.1877A>G	P.Q626R
SH_122	11	82705139	82705139	Missense_Mutation	SNV	G	T	T	RAB30	c.119C>A	P.A40D
SH_122	11	9770684	9770684	Silent	SNV	G	A	A	SWAP70	c.1431G>A	P.K477K
SH_122	12	113728805	113728805	Splice_Site	SNV	T	C	C	TPCN1	c.2175+2T>C	
SH_122	12	89819052	89819052	Silent	SNV	C	T	T	POC1B	c.1092G>A	P.T364T
SH_122	15	33928584	33928584	Missense_Mutation	SNV	G	A	A	RYR3	c.3389G>A	P.R1130H
SH_122	15	91025246	91025246	Silent	SNV	G	A	A	IQGAP1	c.3384G>A	P.K1128K
SH_122	17	17380384	17380384	Missense_Mutation	SNV	G	A	A	MED9	c.29G>A	P.R10Q
SH_122	17	29685499	29685499	Missense_Mutation	SNV	C	T	T	NF1	c.7972C>T	P.H2658Y
SH_122	17	37903122	37903122	Missense_Mutation	SNV	G	A	A	GRB7	c.1571G>A	P.R524H
SH_122	19	36293942	36293942	Missense_Mutation	SNV	G	A	A	PRODH2	c.1268C>T	P.A423V
SH_122	19	38382377	38382377	Missense_Mutation	SNV	T	G	G	WDR87	c.3209A>C	P.E1070A
SH_122	19	55435147	55435147	Silent	SNV	G	A	A	NLRP7	c.3075C>T	P.S1025S
SH_122	19	55857643	55857643	Silent	SNV	C	T	T	KMT5C	c.633C>T	P.D211D
SH_122	2	209113112	209113112	Missense_Mutation	SNV	C	A	A	IDH1	c.395G>T	P.R132L
SH_122	3	108780897	108780897	Missense_Mutation	SNV	T	A	A	MORC1	c.904A>T	P.I302L
SH_122	4	70346634	70346634	Splice_Site	SNV	C	G	G	UGT2B4	c.1091-6G>C	
SH_122	5	121356358	121356358	Missense_Mutation	SNV	C	G	G	SRFBP1	c.928C>G	P.L1310V
SH_122	5	140167440	140167440	Missense_Mutation	SNV	C	A	A	PCDHA1	c.1565C>A	P.P522H
SH_122	5	64748604	64748604	Missense_Mutation	SNV	G	A	A	ADAMT56	c.773C>T	P.A258V
SH_122	6	51720720	51720720	Missense_Mutation	SNV	C	T	T	PKHD1	c.7882G>A	P.E2628K
SH_122	7	100606261	100606261	Missense_Mutation	SNV	G	A	A	MUC3A	c.3607G>A	P.D1203N
SH_122	7	47842947	47842947	Splice_Site	SNV	G	C	C	PKD1L1	c.7828-5C>G	
SH_122	7	6062981	6062981	Missense_Mutation	SNV	G	A	A	AIMP2	c.502G>A	P.E168K
SH_122	8	1719266	1719266	Silent	SNV	C	T	T	CLN8	c.46C>T	P.L16L
SH_122	X	12736297	12736297	Missense_Mutation	SNV	G	T	T	FRMPD4	c.3352G>T	P.A1118S
SH_122	X	138633418	138633418	Missense_Mutation	SNV	T	C	C	F9	c.718T>C	P.W240R
SH_122	X	149678287	149678287	Missense_Mutation	SNV	A	G	G	MAML1	c.1898A>G	P.V633C
SH_123	1	100155038	100155041	Frame_Shift_Del	INDEL	AATG	-	-	PALMD1	223_1226delAT	P.N408fs
SH_123	1	110022069	110022069	Missense_Mutation	SNV	C	T	T	SYPL2	c.718C>T	P.H240Y
SH_123	1	160326909	160326909	Missense_Mutation	SNV	G	T	T	NCSTN	c.1813G>T	P.A605S
SH_123	1	196274360	196274360	Splice_Site	SNV	T	C	C	KCNT2	c.2523+4A>G	
SH_123	1	19981627	19981627	Missense_Mutation	SNV	G	A	A	NBL1	c.104G>A	P.C35Y
SH_123	1	6314094	6314094	Missense_Mutation	SNV	T	C	C	GPR153	c.470A>G	P.Y157C
SH_123	1	78433858	78433858	Missense_Mutation	SNV	G	C	C	FUBP1	c.241C>G	P.Q81E
SH_123	10	115981204	115981204	Missense_Mutation	SNV	C	G	G	TDRD1	c.2859C>G	P.N953K
SH_123	10	82331298	82331298	Silent	SNV	C	T	T	SH2D4B	c.312C>T	P.A104A

SH_123	11	1016371	1016373	Missense_Mutation	INDEL	AAG	-	-	MUC6	6428_6430delC	P.S2143del
SH_123	11	32118719	32118719	Missense_Mutation	SNV	G	C	C	RCN1	c.284G>C	P.G95A
SH_123	11	4608632	4608632	Missense_Mutation	SNV	C	A	A	OR52I2	c.590C>A	P.P197H
SH_123	11	5799345	5799345	Missense_Mutation	SNV	G	A	A	OR52N5	c.520C>T	P.R174C
SH_123	11	60496979	60496979	Missense_Mutation	SNV	T	A	A	MS4A18	c.191T>A	P.V64E
SH_123	11	687999	687999	Nonsense_Mutation	SNV	G	C	C	DEAF1	c.576C>G	P.Y192*
SH_123	11	77594962	77594962	Missense_Mutation	SNV	G	A	A	INTS4	c.2629C>T	P.P877S
SH_123	12	109182506	109182506	Missense_Mutation	SNV	T	C	C	SSH1	c.2408A>G	P.N803S
SH_123	12	15262150	15262150	Missense_Mutation	SNV	C	T	T	RERG	c.437G>A	P.R146Q
SH_123	12	52627311	52627311	Silent	SNV	G	A	A	KRT7	c.231G>A	P.R77R
SH_123	12	56568456	56568456	Missense_Mutation	SNV	C	T	T	SMARCC2	c.1475G>A	P.G492D
SH_123	12	62929421	62929421	Missense_Mutation	SNV	G	A	A	MON2	c.1832G>A	P.G611D
SH_123	12	69085850	69085850	Missense_Mutation	SNV	A	G	G	NUP107	c.319A>G	P.I107V
SH_123	13	101936280	101936280	Splice_Site	SNV	G	T	T	NALCN	c.1134+4C>A	
SH_123	13	46099156	46099156	Missense_Mutation	SNV	A	G	G	COG3	c.2200A>G	P.T734A
SH_123	14	95669906	95669906	Missense_Mutation	SNV	C	T	T	CLMN	c.1780G>A	P.D594N
SH_123	14	96768405	96768405	Missense_Mutation	SNV	C	T	T	ATG2B	c.5078G>A	P.R1693K
SH_123	15	45386807	45386807	Missense_Mutation	SNV	G	C	C	DUOX2	c.4478C>G	P.P1493R
SH_123	16	28913639	28913639	Frame_Shift_Ins	INDEL	-	C	C	ATP2A1	c.2089dupC	P.R697fs
SH_123	16	31435158	31435158	Splice_Site	INDEL	-	C	C	ITGAD	c.3049-3dupC	P.G611D
SH_123	16	70996011	70996011	Missense_Mutation	SNV	C	T	T	HYDIN	c.5819G>A	P.G1940E
SH_123	16	86601102	86601102	Missense_Mutation	SNV	G	A	A	FOXC2	c.161G>A	P.R54H
SH_123	17	29483057	29483071	Missense_Mutation	INDEL	GGAATGTCT	-	-	NF1	4delGGAATGTCT	P.K40_14del
SH_123	17	38079462	38079462	Missense_Mutation	SNV	G	C	C	ORMDL3	c.229C>G	P.Q77E
SH_123	17	39777943	39777943	Missense_Mutation	SNV	C	T	T	KRT17	c.736G>A	P.G246S
SH_123	17	61621609	61621609	Splice_Site	SNV	G	A	A	KCNH6	c.2234-1G>A	
SH_123	17	7573976	7573976	Missense_Mutation	SNV	T	C	C	TP53	c.1051A>G	P.K351E
SH_123	17	79654108	79654108	Silent	SNV	C	T	T	HGS	c.274C>T	P.L92L
SH_123	18	76757181	76757181	Silent	SNV	C	A	A	SALL3	c.3762C>A	P.G1254G
SH_123	19	10624875	10624875	Silent	SNV	C	T	T	S1PR5	c.813G>A	P.L271L
SH_123	19	19762593	19762593	Missense_Mutation	SNV	G	A	A	ATP13A1	c.2240C>T	P.T747M
SH_123	19	22586244	22586244	Missense_Mutation	SNV	T	C	C	ZNF98	c.101A>G	P.Q34R
SH_123	19	33089162	33089162	Silent	SNV	T	C	C	ANKRD27	c.3042A>G	P.G1014G
SH_123	19	35800921	35800921	Missense_Mutation	SNV	A	G	G	MAG	c.1301A>G	P.E434G
SH_123	19	36564435	36564435	Splice_Site	SNV	T	G	G	WDR62	c.1233+2T>G	
SH_123	19	41269577	41269577	Missense_Mutation	SNV	A	G	G	SNRPA	c.686A>G	P.N229S
SH_123	19	41509955	41509955	Missense_Mutation	SNV	C	A	A	CYP2B6	c.221C>A	P.P74H
SH_123	19	44513074	44513074	Splice_Site	SNV	C	T	T	ZNF230	c.142+6C>T	
SH_123	19	46375654	46375654	Nonsense_Mutation	SNV	C	T	T	FOXA3	c.391C>T	P.Q131*
SH_123	19	46388166	46388166	Silent	SNV	G	A	A	IRF2BP1	c.867C>T	P.V289V
SH_123	19	47126919	47126919	Silent	SNV	G	A	A	PTGIR	c.564C>T	P.Y188Y
SH_123	19	48832748	48832748	Splice_Site	SNV	C	G	G	EMP3	c.321C>G	P.T107T
SH_123	19	49392831	49392831	Missense_Mutation	SNV	G	A	A	TULP2	c.572C>T	P.P191L
SH_123	19	50826910	50826910	Missense_Mutation	SNV	G	T	T	KCNC3	c.1300C>A	P.L434M
SH_123	19	52471891	52471891	Silent	SNV	A	G	G	ZNF350	c.178T>C	P.L60L
SH_123	19	59027759	59027759	Splice_Site	SNV	C	T	T	ZBTB45	c.1279+3G>A	
SH_123	2	135884178	135884178	Missense_Mutation	SNV	C	G	G	RAB3GAP1	c.925C>G	P.H309D
SH_123	2	234681191	234681191	Frame_Shift_Del	INDEL	T	-	-	UGT1A6	c.1585delT	P.S529fs
SH_123	2	58311207	58311207	Splice_Site	INDEL	-	T	T	VRK2	c.137-9dupT	
SH_123	20	40733366	40733366	Splice_Site	SNV	G	T	T	PTPRT	c.3448-8C>A	
SH_123	20	56234706	56234706	Frame_Shift_Ins	INDEL	-	CATCATCAA	CATCATCAA	PMEPA1	2_73insTTGATG	M24_V25insLMM
SH_123	21	10910352	10910352	Silent	SNV	G	A	A	TPTE	c.990C>T	P.D330D
SH_123	21	35468920	35468920	Missense_Mutation	SNV	A	G	G	SLC5A3	c.1423A>G	P.M475V
SH_123	22	18371802	18371802	Missense_Mutation	SNV	C	G	G	MICAL3	c.1889G>C	P.S630T
SH_123	22	40760365	40760365	Missense_Mutation	SNV	G	A	A	ADSL	c.1187G>A	P.R396H
SH_123	22	46611071	46611071	Missense_Mutation	SNV	C	A	A	PPARA	c.210C>A	P.D70E
SH_123	3	183209922	183209922	Silent	SNV	G	A	A	KLHL6	c.1659C>T	P.I553I
SH_123	3	38156521	38156521	Missense_Mutation	SNV	G	A	A	DLEC1	c.3842G>A	P.R1281H
SH_123	4	100273815	100273815	Frame_Shift_Del	INDEL	T	-	-	ADH1C	c.18delA	P.V7fS
SH_123	4	52895026	52895026	Missense_Mutation	SNV	C	T	T	SGCB	c.491G>A	P.S164N
SH_123	4	5418608	5418608	Missense_Mutation	SNV	T	C	C	STK32B	c.368T>C	P.V123A
SH_123	4	5633750	5633750	Missense_Mutation	SNV	C	G	G	EVC2	c.1240G>C	P.E414Q
SH_123	5	150663622	150663622	Silent	SNV	G	T	T	SLC36A3	c.1080C>A	P.L360L
SH_123	5	26885718	26885718	Splice_Site	SNV	C	T	T	CDH9	c.1882+5G>A	
SH_123	6	128135034	128135034	Missense_Mutation	SNV	T	C	C	THEMIS	c.752A>G	P.E251G
SH_123	6	69666596	69666596	Missense_Mutation	SNV	G	A	A	ADGRB3	c.1420G>A	P.G474S
SH_123	6	90660516	90660516	Missense_Mutation	SNV	C	T	T	BACH2	c.1309G>A	P.A437T
SH_123	7	100490833	100490833	Missense_Mutation	SNV	C	G	G	ACHE	c.1021G>C	P.D341H
SH_123	7	103969292	103969306	Missense_Mutation	INDEL	AGCTGTACC	-	-	LHFPL3	delGCTGTACCA	P.K23_127del
SH_123	7	121943770	121943770	Frame_Shift_Ins	INDEL	-	T	T	FEZF1	c.721dupA	P.I241fs
SH_123	7	138863321	138863321	Missense_Mutation	SNV	G	A	A	TTCC26	c.1219G>A	P.G407S
SH_123	7	141795424	141795424	Silent	SNV	G	A	A	MGAM	c.4830G>A	P.Q1610Q
SH_123	8	57079730	57079730	Missense_Mutation	SNV	C	T	T	PLAG1	c.575G>A	P.R192H
SH_123	9	13176348	13176348	Missense_Mutation	SNV	C	G	G	MPDZ	c.2718G>C	P.Q906H
SH_123	9	86421324	86421324	Nonsense_Mutation	SNV	G	A	A	GKAP1	c.109C>T	P.R37*
SH_123	X	107381045	107381045	Missense_Mutation	SNV	C	T	T	ATG4A	c.328C>T	P.R110C
SH_123	X	3241027	3241027	Missense_Mutation	SNV	G	T	T	MXRA5	c.2699C>A	P.S900Y
SH_123	X	7175381	7175381	Missense_Mutation	SNV	C	T	T	STS	c.251C>T	P.T84I
SH_125	1	205273506	205273506	Missense_Mutation	SNV	C	A	A	NUAK2	c.1091G>T	P.G364V
SH_125	1	233121966	233121966	Missense_Mutation	SNV	A	T	T	PCNX2	c.6112T>A	P.F2038I
SH_125	1	245530375	245530375	Silent	SNV	C	T	T	KIF26B	c.705C>T	P.H235H
SH_125	1	39920706	39920706	Missense_Mutation	SNV	G	T	T	MACF1	c.14835G>T	P.Q4945H
SH_125	10	125516776	125516776	Nonsense_Mutation	SNV	C	A	A	CPXM2	c.1870G>T	P.E624*
SH_125	10	27040647	27040647	Missense_Mutation	SNV	G	A	A	AB1	c.1150C>T	P.P384S
SH_125	10	49203417	49203417	Silent	SNV	T	C	C	FAM25G	c.264A>G	P.G88G
SH_125	10	61552723	61552723	Silent	SNV	C	G	G	CCDC6	c.1377G>C	P.S459S
SH_125	12	122748705	122748705	Silent	SNV	C	A	A	VPS33A	c.144G>T	P.L48L
SH_125	12	56481655	56481655	Silent	SNV	G	A	A	ERBB3	c.690G>A	P.E230E
SH_125	14	21109124	21109124	Missense_Mutation	SNV	T	C	C	OR6S1	c.727A>G	P.T243A
SH_125	15	48052552	48052552	Missense_Mutation	SNV	A	T	T	SEMA6D	c.161A>T	P.Q54L
SH_125	15	81638761	81638761	Frame_Shift_Del	INDEL	T	-	-	TMC3	c.1217delA	P.N406fs
SH_125	15	89836213	89836213	Frame_Shift_Ins	INDEL	-	A	A	FANCI	c.2216dupA	P.N739fs
SH_125	17	20361556	20361556	Missense_Mutation	SNV	C	T	T	LGALS9B	c.273G>A	P.M91I
SH_125	17	7577534	7577534	Missense_Mutation	SNV	C	A	A	TP53	c.747G>T	P.R249S
SH_125	17	77755496	77755496	Nonsense_Mutation	SNV	G	T	T	CBX2	c.184G>T	P.E62*
SH_125	18	678707	678707	Missense_Mutation	SNV	T	G	G	ENOSF1	c.661A>C	P.T221P
SH_125	19	40704404	40704404	Missense_Mutation	SNV	T	A	A	MAP3K10	c.805T>A	P.W269R
SH_125	19	53612744	53612744	Missense_Mutation	SNV	A	G	G	ZNF415	c.554T>C	P.I185T

SH_125	19	55284899	55284899	Missense_Mutation	SNV	G	A	A	KIR2DL1	c.185G>A	P.R62K
SH_125	19	58153221	58153221	Missense_Mutation	SNV	G	T	T	ZNF211	c.1562G>T	P.G521V
SH_125	2	55470681	55470681	Missense_Mutation	SNV	C	G	G	MTIF2	c.1435G>C	P.E479Q
SH_125	20	3759058	3759058	Splice_Site	SNV	G	C	C	SPEF1	c.603+10C>G	
SH_125	20	62597586	62597586	Silent	SNV	G	T	T	ZNF512B	c.942C>A	P.I314I
SH_125	21	32007769	32007769	Missense_Mutation	SNV	G	T	T	KRTAP20-2	c.187G>T	P.G63C
SH_125	21	36259172	36259172	Missense_Mutation	SNV	G	A	A	RUNX1	c.238C>T	P.R80C
SH_125	21	47965164	47965164	Missense_Mutation	SNV	G	T	T	DIP2A	c.2162G>T	P.G721V
SH_125	22	18299497	18299497	Missense_Mutation	SNV	C	T	T	MICAL3	c.5404G>A	P.D1802N
SH_125	22	19209622	19209622	Splice_Site	SNV	G	T	T	CLTCL1	c.2419-6C>A	
SH_125	22	20230163	20230163	Missense_Mutation	SNV	C	T	T	RTN4R	c.493G>A	P.A165T
SH_125	22	50968978	50968978	Silent	SNV	G	T	T	ODF3B	c.693C>A	P.P231P
SH_125	3	142277598	142277598	Missense_Mutation	SNV	G	T	T	ATR	c.1753C>A	P.H585N
SH_125	3	194152498	194152498	Missense_Mutation	SNV	T	G	G	ATP13A3	c.2369A>C	P.H790P
SH_125	3	45077180	45077180	Missense_Mutation	SNV	G	A	A	CLEC3B	c.247G>A	P.V83M
SH_125	4	17634226	17634226	Nonsense_Mutation	SNV	G	A	A	FAM184B	c.3112C>T	P.Q1038*
SH_125	4	75959104	75959104	Missense_Mutation	SNV	G	C	C	PARM1	c.781G>C	P.A261P
SH_125	5	125819209	125819209	Missense_Mutation	SNV	G	T	T	GRAMD3	c.835G>T	P.D279Y
SH_125	5	139661100	139661100	Silent	SNV	C	T	T	PFDN1	c.219G>A	P.K73K
SH_125	5	32059467	32059467	Splice_Site	SNV	G	T	T	PDZD2	c.2318+5G>T	
SH_125	5	37138912	37138912	Missense_Mutation	SNV	T	C	C	C5orf42	c.8540A>G	P.D2847G
SH_125	6	107372386	107372386	Silent	SNV	G	A	A	C6orf203	c.669G>A	P.V223V
SH_125	6	108214859	108214859	Nonsense_Mutation	SNV	G	A	A	SEC63	c.1501C>T	P.Q501*
SH_125	6	138584341	138584341	Missense_Mutation	SNV	T	A	A	ARFGEF3	c.1721T>A	P.I574K
SH_125	6	155571044	155571044	Nonsense_Mutation	SNV	G	T	T	TIAM2	c.667G>T	P.E223*
SH_125	6	168273023	168273023	Missense_Mutation	SNV	G	T	T	AFDN	c.544G>T	P.D182Y
SH_125	6	46847555	46847555	Missense_Mutation	SNV	C	T	T	ADGRF5	c.1036G>A	P.G346S
SH_125	6	65301096	65301096	Missense_Mutation	SNV	G	A	A	EYS	c.4664C>T	P.T1555I
SH_125	6	75844446	75844446	Silent	SNV	C	T	T	COL12A1	c.5520G>A	P.K1840K
SH_125	6	83949327	83949327	Silent	SNV	G	C	C	ME1	c.843C>G	P.L281L
SH_125	7	100549646	100549646	Missense_Mutation	SNV	T	C	C	MUC3A	c.227T>C	P.M76T
SH_125	7	104751254	104751254	Missense_Mutation	SNV	A	C	C	KMT2E	c.4007A>C	P.N1336T
SH_125	7	138719380	138719380	Missense_Mutation	SNV	A	T	T	ZC3HAV1L	c.410T>A	P.M1317K
SH_125	7	143747693	143747693	Missense_Mutation	SNV	A	G	G	OR2A5	c.199A>G	P.I67V
SH_125	8	142450415	142450415	Missense_Mutation	SNV	C	T	T	MROH5	c.3133G>A	P.V1045M
SH_125	9	6498096	6498096	Frame_Shift_Del	INDEL	G	-	-	UHRF2	c.1846delG	P.E616fs
SH_125	9	77362834	77362834	Splice_Site	SNV	T	C	C	TRPM6	c.5043-4A>G	
SH_125	X	100601518	100601518	Missense_Mutation	SNV	T	A	A	TIMM8A	c.263A>T	P.K88M
SH_125	X	11215073	11215073	Silent	SNV	T	C	C	ARHGAP6	c.792A>G	P.S264S
SH_125	X	127185710	127185710	Missense_Mutation	SNV	C	G	G	ACTRT1	c.476G>C	P.G159A
SH_127	1	2421257	2421257	Missense_Mutation	SNV	A	T	T	PLCH2	c.1385A>T	P.L462V
SH_127	10	69700720	69700720	Missense_Mutation	SNV	T	C	C	HERC4	c.2480A>G	P.K827R
SH_127	10	89264720	89264736	Frame_Shift_Del	INDEL	GCCCTGGCT	-	-	MINPP1	delGGCCCTGGCT	P.A20fs
SH_127	10	96269940	96269940	Splice_Site	SNV	A	T	T	TBC1D12	c.1689+4A>T	
SH_127	11	56258310	56258310	Silent	SNV	C	A	A	OR5M8	c.537G>T	P.A179A
SH_127	11	60711227	60711244	Missense_Mutation	INDEL	TTGGCGATG	-	-	SLC15A3	delGAGGACATC	P.E305_F310del
SH_127	11	73471602	73471602	Splice_Site	SNV	C	T	T	RAB6A	c.70+9G>A	
SH_127	12	54394068	54394068	Silent	SNV	G	C	C	HOXC9	c.96G>C	P.G32G
SH_127	12	6554406	6554406	Splice_Site	SNV	G	C	C	CD27	c.136+9G>C	
SH_127	14	52985913	52985913	Missense_Mutation	SNV	T	A	A	TXNDC16	c.476A>T	P.Y159F
SH_127	15	74564066	74564066	Missense_Mutation	SNV	A	T	T	CCDC33	c.569A>T	P.E190V
SH_127	15	76494607	76494609	Splice_Site	INDEL	TAA	-	-	TMEM266	21+2_1021+4delTAA	
SH_127	2	162805701	162805701	Missense_Mutation	SNV	T	G	G	SLC4A10	c.2309T>G	P.L770R
SH_127	3	161214760	161214760	Missense_Mutation	SNV	A	T	T	OTOL1	c.165A>T	P.E55D
SH_127	3	168802733	168802733	Silent	SNV	C	T	T	MECOM	c.3315G>A	P.A1105A
SH_127	3	44948517	44948517	Missense_Mutation	SNV	C	A	A	TGM4	c.1152C>A	P.F384L
SH_127	3	45988819	45988819	Nonsense_Mutation	SNV	C	A	A	CXCR6	c.846C>A	P.C282*
SH_127	4	155411772	155411772	Silent	SNV	G	A	A	DCHS2	c.736C>T	P.L246L
SH_127	5	140744890	140744890	Silent	SNV	T	A	A	PCDHGA5	c.993T>A	P.A331A
SH_127	6	154735543	154735543	Silent	SNV	G	C	C	CNKSR3	c.960C>G	P.P320P
SH_127	6	27277644	27277644	Missense_Mutation	SNV	C	G	G	POM121L2	c.2306G>C	P.G769A
SH_127	6	3140625	3140625	Missense_Mutation	SNV	A	T	T	BPHL	c.619A>T	P.I207F
SH_127	6	7230336	7230336	Missense_Mutation	SNV	C	G	G	RREB1	c.2004C>G	P.I668M
SH_127	7	104782874	104782874	Missense_Mutation	SNV	T	A	A	SRPK2	c.1091A>T	P.D364V
SH_127	7	151699844	151699844	Missense_Mutation	SNV	T	A	A	GALNTL5	c.704T>A	P.V235E
SH_127	7	30893042	30893042	Silent	SNV	C	T	T	FAM188B	c.1644C>T	P.D548D
SH_127	7	34851445	34851445	Missense_Mutation	SNV	A	T	T	NPSR1	c.415A>T	P.I139F
SH_127	7	36446098	36446098	Missense_Mutation	SNV	G	T	T	ANLN	c.796G>T	P.D266Y
SH_128	1	109649750	109649750	Splice_Site	SNV	G	T	T	C1orf194	c.163-6C>A	
SH_128	1	109649751	109649751	Splice_Site	SNV	A	T	T	C1orf194	c.163-7T>A	
SH_128	1	110737263	110737263	Silent	SNV	C	A	A	SLC6A17	c.1362C>A	P.A454A
SH_128	1	151867527	151867527	Silent	SNV	A	C	C	THEM4	c.243T>G	P.R81R
SH_128	1	152081126	152081126	Missense_Mutation	SNV	G	T	T	TCHH	c.4567C>A	P.Q1523K
SH_128	1	158724748	158724748	Missense_Mutation	SNV	C	T	T	OR6K6	c.143C>T	P.A48V
SH_128	1	186008949	186008949	Missense_Mutation	SNV	G	T	T	HMCN1	c.6118G>T	P.A2040S
SH_128	1	1956375	1956375	Splice_Site	SNV	C	T	T	GABRD	c.69-6C>T	
SH_128	1	201061111	201061111	Missense_Mutation	SNV	G	C	C	CACNA1S	c.530C>G	P.S177W
SH_128	1	215813980	215813980	Frame_Shift_Ins	INDEL	-	C	C	USH2A	c.14887dupG	P.E4963fs
SH_128	1	243319677	243319677	Nonsense_Mutation	SNV	T	A	A	CEP170	c.3463A>T	P.K1155*
SH_128	1	2576820	2576820	Silent	SNV	G	T	T	TTC34	c.870C>A	P.G290G
SH_128	1	37948355	37948355	Missense_Mutation	SNV	G	A	A	ZC3H12A	c.943G>A	P.G315R
SH_128	1	40872474	40872474	Missense_Mutation	SNV	A	G	G	SMAP2	c.80A>G	P.N27S
SH_128	1	7798224	7798224	Missense_Mutation	SNV	C	A	A	CAMTA1	c.3864C>A	P.S1288R
SH_128	10	129904172	129904172	Missense_Mutation	SNV	C	T	T	MKI67	c.4852G>A	P.E1618K
SH_128	10	43615037	43615037	Silent	SNV	C	T	T	RET	c.2451C>T	P.R817R
SH_128	10	75830581	75830581	Splice_Site	SNV	A	T	T	VCL	c.390+3A>T	
SH_128	10	89622183	89622183	Missense_Mutation	SNV	C	T	T	KLIN	c.62G>A	P.R21Q
SH_128	11	124487256	124487256	Missense_Mutation	SNV	C	A	A	PANX3	c.411C>A	P.S137R
SH_128	11	13438723	13438723	Silent	SNV	A	G	G	BTBD10	c.525T>C	P.T175T
SH_128	11	17122828	17122828	Silent	SNV	T	A	A	PIK3C2A	c.4005A>T	P.S1335S
SH_128	11	21250965	21250965	Missense_Mutation	SNV	A	T	T	NELL1	c.1598A>T	P.K533I
SH_128	11	34938235	34938235	Silent	SNV	G	A	A	PDHX	c.33G>A	P.P111P
SH_128	11	47333296	47333296	Missense_Mutation	SNV	A	G	G	MADD	c.3863A>G	P.D1288G
SH_128	11	62288510	62288510	Missense_Mutation	SNV	G	C	C	AHNAK	c.13379C>G	P.S4460C
SH_128	11	68700868	68700868	Missense_Mutation	SNV	A	T	T	IGHMBP2	c.1337A>T	P.Q446L
SH_128	11	68854064	68854064	Missense_Mutation	SNV	A	G	G	TPCND3	c.2077A>G	P.I693V
SH_128	11	76825287	76825287	Splice_Site	SNV	G	T	T	CAPN5	c.507-1G>T	
SH_128	12	123678991	123678991	Missense_Mutation	SNV	T	A	A	MPHOSPH9	c.2183A>T	P.Y728F

SH_128	12	124399435	124399435	Silent	SNV	C	T	T	DNAH10	c.10257C>T	P.S3419S
SH_128	12	133502748	133502748	Missense_Mutation	SNV	C	G	G	ZNF605	c.1230G>C	P.Q410H
SH_128	12	51236851	51236851	Missense_Mutation	SNV	C	T	T	TMPRSS12	c.104C>T	P.P35L
SH_128	12	54379492	54379492	Missense_Mutation	SNV	G	T	T	HOXC10	c.449G>T	P.R150L
SH_128	12	661265	661265	Missense_Mutation	SNV	C	A	A	B4GALNT3	c.1144C>A	P.R382S
SH_128	12	9070332	9070332	Missense_Mutation	SNV	G	T	T	PHC1	c.59G>T	P.G20V
SH_128	13	114062306	114062306	Missense_Mutation	SNV	G	T	T	LOC101928841	c.199C>A	P.L67I
SH_128	13	114152743	114152743	Missense_Mutation	SNV	A	T	T	TMC03	c.531A>T	P.L177F
SH_128	13	99947324	99947324	Frame_Shift_Del	INDEL	T	-	-	GPR183	c.1076delA	P.N359fs
SH_128	14	102904496	102904496	Missense_Mutation	SNV	G	T	T	TECPR2	c.2532G>T	P.W844C
SH_128	14	70245218	70245218	Missense_Mutation	SNV	C	T	T	SLC10A1	c.775G>A	P.G259R
SH_128	14	77951074	77951074	Silent	SNV	C	T	T	ISM2	c.330G>A	P.Q110Q
SH_128	14	94039067	94039067	Missense_Mutation	SNV	C	G	G	UNC79	c.1444C>G	P.L482V
SH_128	14	99969294	99969294	Missense_Mutation	SNV	T	A	A	CCNK	c.984T>A	P.S328R
SH_128	15	63882902	63882902	Silent	SNV	C	T	T	USP3	c.1308C>T	P.G436G
SH_128	15	74003483	74003483	Missense_Mutation	SNV	G	T	T	CD276	c.1554G>T	P.Q518H
SH_128	15	74481552	74481552	Frame_Shift_Del	INDEL	C	-	-	STRA6	c.994delG	P.D332fs
SH_128	15	78780991	78780991	Missense_Mutation	SNV	A	T	T	IREB2	c.1204A>T	P.T402S
SH_128	16	28328771	28328771	Missense_Mutation	SNV	G	A	A	SBK1	c.59G>A	P.G20E
SH_128	16	48226422	48226422	Splice_Site	SNV	G	T	T	ABCC11	c.2706+9C>A	
SH_128	17	36622676	36622676	Missense_Mutation	SNV	G	A	A	ARHGAP23	c.752G>A	P.R251H
SH_128	17	55183902	55183902	Silent	SNV	A	G	G	AKAP1	c.1077A>G	P.A359A
SH_128	17	57741313	57741313	Silent	SNV	A	G	G	CLTC	c.1491A>G	P.A497A
SH_128	17	72937869	72937869	Missense_Mutation	SNV	A	G	G	OTOP3	c.401A>G	P.Y134C
SH_128	17	73835918	73835918	Splice_Site	SNV	A	T	T	UNC13D	c.1055+2T>A	
SH_128	17	74774288	74774288	Missense_Mutation	SNV	G	T	T	MFSD11	c.1204G>T	P.A402S
SH_128	17	7573996	7573996	Missense_Mutation	SNV	A	C	C	TP53	c.1031T>G	P.L344R
SH_128	17	77811696	77811696	Frame_Shift_Ins	INDEL	-	TA	TA	CBX4	c.117_118dupT	P.N40fs
SH_128	18	14105152	14105152	Nonsense_Mutation	SNV	C	A	A	ZNF519	c.1387G>T	P.E463*
SH_128	18	44284595	44284595	Missense_Mutation	SNV	T	C	C	ST8SIA5	c.272A>G	P.Y91C
SH_128	18	77037163	77037163	Missense_Mutation	SNV	G	A	A	ATP9B	c.1378G>A	P.G460R
SH_128	19	13910666	13910666	Missense_Mutation	SNV	G	T	T	ZSWIM4	c.286G>T	P.A96S
SH_128	19	13919736	13919736	Missense_Mutation	SNV	C	A	A	ZSWIM4	c.799C>A	P.Q267K
SH_128	19	1826866	1826866	Splice_Site	SNV	G	A	A	REXO1	c.1911+11C>T	
SH_128	19	2988081	2988081	Splice_Site	SNV	G	A	A	TLE6	c.703-8G>A	
SH_128	19	42473645	42473645	Missense_Mutation	SNV	C	T	T	ATP1A3	c.2663G>A	P.R888Q
SH_128	19	42911380	42911380	Silent	SNV	G	A	A	LIPE	c.2083C>T	P.L695L
SH_128	19	49100007	49100007	Silent	SNV	C	A	A	SULT2B1	c.612C>A	P.G204G
SH_128	19	50118217	50118217	Missense_Mutation	SNV	G	T	T	PRR12	c.4975G>T	P.V1659L
SH_128	19	54485526	54485526	Missense_Mutation	SNV	C	T	T	CACNG8	c.701C>T	P.A234V
SH_128	19	55592170	55592170	Missense_Mutation	SNV	G	A	A	EPS8L1	c.79G>A	P.A27T
SH_128	19	56206342	56206342	Silent	SNV	G	T	T	EPN1	c.1773G>T	P.L591L
SH_128	19	57327999	57327999	Missense_Mutation	SNV	C	T	T	PEG3	c.1811G>A	P.R604H
SH_128	2	109384034	109384034	Missense_Mutation	SNV	G	A	A	RANBP2	c.7039G>A	P.G2347S
SH_128	2	152496949	152496949	Missense_Mutation	SNV	T	G	G	NEB	c.8605A>C	P.N2869H
SH_128	2	162251685	162251685	Missense_Mutation	SNV	A	G	G	PSMD14	c.742A>G	P.M248V
SH_128	2	1664682	1664682	Missense_Mutation	SNV	G	T	T	PXDN	c.1808C>A	P.A603D
SH_128	2	17699586	17699586	Missense_Mutation	SNV	T	G	G	RAD51AP2	c.97A>C	P.S33R
SH_128	2	183731007	183731007	Missense_Mutation	SNV	A	G	G	FRZB	c.274T>C	P.Y92H
SH_128	2	202558641	202558641	Missense_Mutation	SNV	T	C	C	MPP4	c.37A>G	P.K13E
SH_128	2	207171802	207171802	Missense_Mutation	SNV	A	T	T	ZDBF2	c.2544A>T	P.E848D
SH_128	2	207636665	207636665	Silent	SNV	A	G	G	FASTKD2	c.1038A>G	P.Q346Q
SH_128	2	215890488	215890488	Missense_Mutation	SNV	A	C	C	ABCA12	c.242T>G	P.L81R
SH_128	2	231775073	231775073	Missense_Mutation	SNV	G	A	A	GPR55	c.605C>T	P.S202F
SH_128	2	241715334	241715334	Missense_Mutation	SNV	T	C	C	KIF1A	c.892A>G	P.K298E
SH_128	2	63272303	63272303	Missense_Mutation	SNV	C	T	T	EHBP1	c.3488C>T	P.A1163V
SH_128	20	20020291	20020291	Nonsense_Mutation	SNV	C	A	A	CRNKL1	c.1954G>T	P.E652*
SH_128	3	101578168	101578168	Missense_Mutation	SNV	C	G	G	NFKBIZ	c.1810C>G	P.R604G
SH_128	3	128758582	128758582	Missense_Mutation	SNV	T	A	A	EFCC1	c.1688T>A	P.L563Q
SH_128	3	129252533	129252533	Missense_Mutation	SNV	C	G	G	RHO	c.1019C>G	P.T340R
SH_128	3	150931202	150931202	Silent	SNV	C	T	T	P2RY14	c.903G>A	P.P301P
SH_128	3	151166575	151166575	Silent	SNV	C	A	A	IGSF10	c.1194G>T	P.P398P
SH_128	3	154145382	154145382	Missense_Mutation	SNV	C	G	G	GPR149	c.1097G>C	P.R366P
SH_128	3	154834261	154834261	Splice_Site	SNV	A	G	G	MME	c.359-7A>G	
SH_128	3	170585827	170585827	Missense_Mutation	SNV	C	A	A	RPL22L1	c.199G>T	P.V67F
SH_128	3	175455171	175455171	Silent	SNV	T	A	A	NAALADL2	c.1974T>A	P.V658V
SH_128	3	196449409	196449409	Silent	SNV	A	T	T	PIGX	c.300A>T	P.R100R
SH_128	3	25665866	25665866	Missense_Mutation	SNV	T	A	A	TOP2B	c.2402A>T	P.Q801L
SH_128	3	47165258	47165258	Nonsense_Mutation	SNV	C	A	A	SETD2	c.868G>T	P.E290*
SH_128	3	87294880	87294880	Missense_Mutation	SNV	A	C	C	CHMP2B	c.20A>C	P.K7T
SH_128	3	89259185	89259185	Missense_Mutation	SNV	C	T	T	EPHA3	c.329C>T	P.P110L
SH_128	4	144618046	144618046	Silent	SNV	C	T	T	FREM3	c.3783G>A	P.Q1261Q
SH_128	4	5731114	5731114	Silent	SNV	C	T	T	EVC	c.381C>T	P.F127F
SH_128	4	667183	667183	Silent	SNV	T	C	C	ATP5I	c.99A>G	P.L33L
SH_128	4	68441149	68441149	Missense_Mutation	SNV	A	T	T	STAP1	c.239A>T	P.Q80L
SH_128	4	79400873	79400873	Splice_Site	SNV	G	T	T	FRAS1	c.8443+1G>T	
SH_128	4	89589096	89589096	Silent	SNV	A	G	G	HERC3	c.1143A>G	P.P381P
SH_128	5	132087754	132087754	Missense_Mutation	SNV	C	A	A	CCN12	c.871C>A	P.Q291K
SH_128	5	13751352	13751352	Missense_Mutation	SNV	C	A	A	DNAH5	c.11046G>T	P.K3682N
SH_128	5	138773156	138773156	Silent	SNV	T	G	G	DNAJC18	c.132A>C	P.A44A
SH_128	5	140230276	140230276	Silent	SNV	C	T	T	PCDHA9	c.2196C>T	P.C732C
SH_128	5	140870391	140870391	Missense_Mutation	SNV	G	C	C	PCDHGC5	c.1584G>C	P.Q528H
SH_128	5	14280489	14280489	Missense_Mutation	SNV	C	G	G	TRIO	c.291C>G	P.D97E
SH_128	5	31267811	31267811	Splice_Site	SNV	A	G	G	CDH6	c.228+3A>G	
SH_128	5	74651259	74651259	Missense_Mutation	SNV	C	T	T	HMGCR	c.1792C>T	P.R598C
SH_128	6	133100511	133100511	Missense_Mutation	SNV	G	C	C	SLC18B1	c.691C>G	P.L231V
SH_128	6	138726283	138726283	Missense_Mutation	SNV	C	G	G	HEBP2	c.137C>G	P.P46R
SH_128	6	17788054	17788054	Missense_Mutation	SNV	C	T	T	KIF13A	c.3314G>A	P.R1105Q
SH_128	6	32798107	32798107	Silent	SNV	C	A	A	TAP2	c.1572G>T	P.G524G
SH_128	6	33400547	33400547	Missense_Mutation	SNV	A	T	T	SYNGAP1	c.473A>T	P.Q158L
SH_128	6	35467937	35467937	Splice_Site	SNV	G	T	T	TULP1	c.1165-8C>A	
SH_128	6	41059275	41059275	Missense_Mutation	SNV	C	A	A	NFYA	c.556C>A	P.P186T
SH_128	6	42713053	42713053	Silent	SNV	C	G	G	TBCC	c.759G>C	P.V253V
SH_128	6	64404493	64404493	Nonsense_Mutation	SNV	C	A	A	PHF3	c.2255C>A	P.S752*
SH_128	6	75912486	75912486	Missense_Mutation	SNV	G	T	T	COL12A1	c.23C>A	P.A8E
SH_128	6	84303452	84303452	Missense_Mutation	SNV	C	A	A	SNAP91	c.1441G>T	P.A481S
SH_128	6	90573128	90573128	Missense_Mutation	SNV	C	T	T	CASP8AP2	c.1700C>T	P.S567F
SH_128	7	106710735	106710735	Missense_Mutation	SNV	T	C	C	PRKAR2B	c.317T>C	P.I106T

SH_128	7	141423844	141423844	Silent	SNV	A	G	G	WEE2	c.1131A>G	P.K377K
SH_128	7	149513059	149513059	Nonsense_Mutation	SNV	G	A	A	SSPO	c.10962G>A	P.W3654*
SH_128	8	48647870	48647870	Missense_Mutation	SNV	G	T	T	SPIDR	c.2606G>T	P.S869I
SH_128	9	101751487	101751487	Missense_Mutation	SNV	G	A	A	COL15A1	c.751G>A	P.E251K
SH_128	9	114804403	114804403	Missense_Mutation	SNV	C	G	G	SUSD1	c.2192G>C	P.R731T
SH_128	9	116224120	116224120	Frame_Shift_Del	INDEL	C	-	-	RGS3	c.216delC	P.W73fs
SH_128	9	123780066	123780066	Missense_Mutation	SNV	T	C	C	C5	c.1589A>G	P.Q530R
SH_128	9	134151534	134151534	Silent	SNV	G	C	C	FAM78A	c.33C>G	P.S11S
SH_128	9	34724376	34724376	Missense_Mutation	SNV	G	A	A	FAM205A	c.2861C>T	P.P954L
SH_128	9	67930495	67930495	Missense_Mutation	SNV	G	C	C	ANKRD20A3	c.312G>C	P.L104F
SH_128	9	99521410	99521410	Nonsense_Mutation	SNV	C	A	A	ZNF510	c.1702G>T	P.G568*
SH_128	X	115588781	115588781	Missense_Mutation	SNV	T	G	G	SLC6A14	c.1621T>G	P.F541V
SH_128	X	129519343	129519343	Missense_Mutation	SNV	C	T	T	GPR119	c.79G>A	P.V27M
SH_128	X	23410817	23410817	Silent	SNV	G	A	A	PTCHD1	c.1182G>A	P.T394T
SH_128	X	24078209	24078209	Missense_Mutation	SNV	G	T	T	EIF2S3	c.388G>T	P.V130F
SH_128	X	47062621	47062621	Splice_Site	INDEL	-	T	T	UBA1	c.1419+9dupT	
SH_129	1	158911819	158911819	Missense_Mutation	SNV	G	A	A	PYHIN1	c.632G>A	P.R211Q
SH_129	1	185931768	185931768	Missense_Mutation	SNV	T	A	A	HMCN1	c.1947T>A	P.D649E
SH_129	1	227834307	227834307	Missense_Mutation	SNV	C	A	A	ZNF678	c.186C>A	P.D62E
SH_129	1	25228934	25228934	Silent	SNV	C	T	T	RUNX3	c.969G>A	P.P232P
SH_129	1	46874779	46874779	Missense_Mutation	SNV	C	T	T	FAAH	c.1084C>T	P.P362S
SH_129	1	53543382	53543382	Frame_Shift_Ins	INDEL	-	G	G	PODN	c.856dupG	P.A286fs
SH_129	10	101961894	101961894	Frame_Shift_Ins	INDEL	-	T	T	CHUK	c.1519dupA	P.M507fs
SH_129	11	116798030	116798030	Missense_Mutation	SNV	G	A	A	SIK3	c.44C>T	P.T15I
SH_129	11	120008562	120008562	Silent	SNV	G	A	A	TRIM29	c.178C>T	P.L60L
SH_129	11	59225149	59225149	Missense_Mutation	SNV	C	T	T	OR4D6	c.716C>T	P.T239M
SH_129	11	62380940	62380940	Missense_Mutation	SNV	C	T	T	ROM1	c.187C>T	P.P63S
SH_129	11	62931321	62931321	Missense_Mutation	SNV	G	A	A	SLC22A25	c.1619C>T	P.A540V
SH_129	11	92523203	92523203	Missense_Mutation	SNV	C	A	A	FAT3	c.4430C>A	P.T1477K
SH_129	12	114841613	114841613	Missense_Mutation	SNV	C	T	T	TBX5	c.91G>A	P.A311T
SH_129	12	123276583	123276583	Missense_Mutation	SNV	G	T	T	CCDC62	c.687G>T	P.K229N
SH_129	12	15130986	15130986	Nonsense_Mutation	SNV	C	T	T	PDE6H	c.40C>T	P.Q14*
SH_129	12	25398284	25398284	Missense_Mutation	SNV	C	T	T	KRAS	c.35G>A	P.G12D
SH_129	12	54394208	54394208	Missense_Mutation	SNV	C	T	T	HOXC9	c.236C>T	P.P79L
SH_129	12	70975011	70975011	Nonsense_Mutation	SNV	G	A	A	PTPRB	c.2383C>T	P.Q795*
SH_129	13	50285084	50285084	Silent	SNV	A	G	G	KPNA3	c.846T>C	P.D282D
SH_129	14	105413795	105413795	Missense_Mutation	SNV	C	T	T	AHNAK2	c.7993G>A	P.E2665K
SH_129	14	23549113	23549113	Missense_Mutation	SNV	T	A	A	ACIN1	c.1605A>T	P.E535D
SH_129	15	64422138	64422138	Missense_Mutation	SNV	G	T	T	SNX1	c.831G>T	P.Q277H
SH_129	15	79227355	79227355	Missense_Mutation	SNV	T	C	C	CTSH	c.370A>G	P.K124E
SH_129	16	24135257	24135257	Silent	SNV	C	T	T	PRKCB	c.1020C>T	P.T340T
SH_129	16	24581635	24581635	Missense_Mutation	SNV	A	C	C	RBBP6	c.3624A>C	P.K1208N
SH_129	17	15532029	15532029	Missense_Mutation	SNV	G	A	A	TRIM16	c.1595C>T	P.A532V
SH_129	17	34171885	34171885	Frame_Shift_Ins	INDEL	-	G	G	TAF15	c.1580dupG	P.Y528fs
SH_129	17	39643395	39643395	Missense_Mutation	SNV	C	T	T	KRT36	c.1015G>A	P.E339K
SH_129	17	66039357	66039357	Missense_Mutation	SNV	G	T	T	KPNA2	c.808G>T	P.D270Y
SH_129	17	7578406	7578406	Missense_Mutation	SNV	C	T	T	TP53	c.524G>A	P.R175H
SH_129	19	11833852	11833852	Missense_Mutation	SNV	C	A	A	ZNF823	c.497G>T	P.C166F
SH_129	19	40411763	40411763	Frame_Shift_Ins	INDEL	-	T	T	FCGBP	c.3864_3865insA	P.H1289fs
SH_129	19	41289949	41289949	Missense_Mutation	SNV	C	G	G	RAB4B	c.399C>G	P.F133L
SH_129	19	50187307	50187307	Missense_Mutation	SNV	A	G	G	PRMT1	c.482A>G	P.Y161C
SH_129	19	54140051	54140051	Missense_Mutation	SNV	T	A	A	DPRX	c.385T>A	P.F129I
SH_129	19	7119591	7119591	Silent	SNV	G	A	A	INSR	c.3663C>T	P.S1221S
SH_129	2	152135364	152135364	Silent	SNV	A	G	G	NMI	c.318T>C	P.L106L
SH_129	2	179534998	179534998	Missense_Mutation	SNV	A	C	C	TTN	c.34211T>G	P.V11404G
SH_129	2	206036979	206036979	Silent	SNV	G	A	A	PARDB3	c.1665G>A	P.G555G
SH_129	2	233899020	233899020	Silent	SNV	C	T	T	NEU2	c.396C>T	P.H132H
SH_129	2	39222277	39222277	Silent	SNV	G	A	A	SOS1	c.3333C>T	P.S1111S
SH_129	2	73679160	73679160	Missense_Mutation	SNV	C	A	A	ALMS1	c.5503C>A	P.P1835T
SH_129	20	3686472	3686472	Missense_Mutation	SNV	G	T	T	SIGLEC1	c.625C>A	P.Q209K
SH_129	20	36868058	36868058	Missense_Mutation	SNV	G	T	T	KIAA1755	c.1619C>A	P.A540D
SH_129	3	121345679	121345679	Missense_Mutation	SNV	G	A	A	FBX040	c.2052G>A	P.M684I
SH_129	3	158254895	158254895	Missense_Mutation	SNV	G	A	A	RSRC1	c.493G>A	P.V165I
SH_129	3	97194294	97194294	Missense_Mutation	SNV	A	T	T	EPHA6	c.169A>T	P.J57F
SH_129	4	154626161	154626161	Missense_Mutation	SNV	T	G	G	TLR2	c.2102T>G	P.F701C
SH_129	4	169315746	169315746	Missense_Mutation	SNV	C	T	T	DDX60L	c.3680G>A	P.R1227Q
SH_129	4	68449286	68449286	Splice_Site	SNV	C	T	T	STAP1	c.531-6C>T	
SH_129	4	94006296	94006296	Missense_Mutation	SNV	G	A	A	GRID2	c.395G>A	P.G132E
SH_129	5	132534816	132534816	Missense_Mutation	SNV	T	C	C	FSTL4	c.2500A>G	P.T834A
SH_129	5	140475961	140475961	Silent	SNV	C	T	T	PCDH82	c.1587C>T	P.F529F
SH_129	5	41058274	41058274	Missense_Mutation	SNV	G	T	T	MROH2B	c.647C>A	P.T216K
SH_129	6	111983103	111983116	Frame_Shift_Del	INDEL	CTGTAGCCTG	-	-	FYN	c.53delGCGAGGG	P.E480fs
SH_129	6	33284572	33284572	Missense_Mutation	SNV	C	T	T	ZBTB22	c.122G>A	P.S41N
SH_129	7	76126759	76126759	Missense_Mutation	SNV	G	A	A	DTX2	c.1115G>A	P.G372D
SH_129	7	77797412	77797412	Missense_Mutation	SNV	G	A	A	MAGI2	c.2417C>T	P.A806V
SH_129	8	24207486	24207486	Splice_Site	SNV	G	A	A	ADAM28	c.2099+1G>A	
SH_129	8	91013798	91013798	Splice_Site	SNV	G	T	T	DEC1	c.69+9G>T	
SH_129	9	118949636	118949636	Missense_Mutation	SNV	T	C	C	PAPPA	c.619T>C	P.F207L
SH_129	9	123152034	123152034	Silent	SNV	G	A	A	CDK5RAP2	c.5373C>T	P.A1791A
SH_129	9	130504196	130504196	Silent	SNV	G	T	T	SH2D3C	c.897C>A	P.G299G
SH_129	9	34658538	34658538	Missense_Mutation	SNV	G	T	T	IL11RA	c.668G>T	P.G223V
SH_129	X	118771070	118771070	Silent	SNV	G	A	A	SEPT6	c.876C>T	P.T292T
SH_129	X	129173244	129173244	Silent	SNV	G	A	A	BCORL1	c.4605G>A	P.K1535K
SH_129	X	132161989	132161989	Missense_Mutation	SNV	G	A	A	USP26	c.260C>T	P.S87F
SH_129	X	41333619	41333619	Missense_Mutation	SNV	C	T	T	NYX	c.913C>T	P.L305F
SH_129	X	70823875	70823875	Missense_Mutation	SNV	G	A	A	ACRC	c.748G>A	P.D250N
SH_13	1	103352460	103352460	Silent	SNV	T	C	C	COL11A1	c.4644A>G	P.K1548K
SH_13	1	108724567	108724567	Missense_Mutation	SNV	G	T	T	SLC25A24	c.394C>A	P.Q132K
SH_13	1	114680475	114680475	Missense_Mutation	SNV	C	A	A	SYT6	c.458G>T	P.R153L
SH_13	1	117146380	117146380	Missense_Mutation	SNV	C	A	A	IGSF3	c.1490G>T	P.G497V
SH_13	1	152193463	152193463	Missense_Mutation	SNV	C	A	A	HRNR	c.642G>T	P.Q214H
SH_13	1	155874285	155874285	Missense_Mutation	SNV	A	T	T	RI1T	c.246T>A	P.F82L
SH_13	1	159802968	159802968	Missense_Mutation	SNV	G	A	A	SLAMF8	c.670G>A	P.A224T
SH_13	1	228407193	228407193	Missense_Mutation	SNV	T	A	A	OBSCN	c.2822T>A	P.Y941E
SH_13	1	34070903	34070903	Missense_Mutation	SNV	G	T	T	CSMD2	c.6511C>A	P.H2171N
SH_13	1	97915674	97915674	Nonsense_Mutation	SNV	T	A	A	DPYD	c.1846A>T	P.K616*
SH_13	10	27405029	27405075	Frame_Shift_Del	INDEL	AATCACTGGG	-	-	YME1L1	c.AGGTGCTTCCAG	P.G583fs
SH_13	10	49917882	49917882	Silent	SNV	G	T	T	WDFY4	c.105G>T	P.G35G

SH_13	10	50533075	50533075	Nonsense_Mutation	SNV	G	T	T	C10orf71	c.2485G>T	P.E829*
SH_13	10	89653867	89653867	Splice_Site	SNV	G	A	A	PTEN	c.164+1G>A	
SH_13	11	111228162	111228162	Splice_Site	SNV	T	A	A	POU2AF1	c.456+8A>T	
SH_13	11	113221975	113221975	Missense_Mutation	SNV	T	G	G	TTC12	c.1280T>G	P.F427C
SH_13	11	114270739	114270739	Silent	SNV	C	A	A	C11orf71	c.315G>T	P.V105V
SH_13	11	4976182	4976182	Silent	SNV	C	A	A	OR51A2	c.762G>T	P.L254L
SH_13	11	5020384	5020384	Missense_Mutation	SNV	C	T	T	OR51L1	c.172C>T	P.H58Y
SH_13	11	59564765	59564765	Missense_Mutation	SNV	A	G	G	STX3	c.796A>G	P.I266V
SH_13	12	112614475	112614475	Missense_Mutation	SNV	C	T	T	HECTD4	c.10993G>A	P.V3665M
SH_13	12	6960098	6960098	Missense_Mutation	SNV	C	T	T	CDC43	c.19G>A	P.V71
SH_13	12	80732888	80732888	Missense_Mutation	SNV	T	G	G	OTOGL	c.4867T>G	P.F1623V
SH_13	14	103969471	103969471	Silent	SNV	G	T	T	MARK3	c.2169G>T	P.L723L
SH_13	14	105420665	105420665	Missense_Mutation	SNV	T	A	A	AHNAK2	c.1123A>T	P.S375C
SH_13	14	23299285	23299285	Missense_Mutation	SNV	G	T	T	MRPL52	c.52G>T	P.V18L
SH_13	14	23826721	23826721	Missense_Mutation	SNV	G	A	A	EF5	c.893C>T	P.P298L
SH_13	14	23946563	23946563	Nonsense_Mutation	SNV	G	T	T	NGDN	c.868G>T	P.E290*
SH_13	16	68057083	68057083	Missense_Mutation	SNV	C	A	A	DDX28	c.23G>T	P.R8L
SH_13	16	68248230	68248230	Splice_Site	SNV	A	C	C	NFATC3	c.3107-2A>C	
SH_13	16	70925750	70925750	Missense_Mutation	SNV	A	G	G	HYDIN	c.9455T>C	P.I3152T
SH_13	16	70969907	70969907	Missense_Mutation	SNV	C	A	A	HYDIN	c.7106G>T	P.G2369V
SH_13	16	85834894	85834894	Splice_Site	SNV	A	T	T	COX4I1	c.73+10A>T	
SH_13	17	3301642	3301642	Silent	SNV	T	A	A	OR1E1	c.63A>T	P.P21P
SH_13	17	34074884	34074884	Nonsense_Mutation	SNV	G	T	T	GAS2L2	c.816C>A	P.C272*
SH_13	17	40966589	40966589	Silent	SNV	C	A	A	BECN1	c.933G>T	P.V311V
SH_13	17	45777066	45777066	Splice_Site	SNV	A	T	T	TBKBP1	c.872+3A>T	
SH_13	17	74625520	74625520	Silent	SNV	G	A	A	ST6GALNAC1	c.9C>T	P.N3N
SH_13	17	7577534	7577534	Missense_Mutation	SNV	C	A	A	TP53	c.747G>T	P.R249S
SH_13	17	76134461	76134461	Missense_Mutation	SNV	C	G	G	TMC8	c.1565C>G	P.S522W
SH_13	18	22806113	22806113	Missense_Mutation	SNV	A	G	G	ZNF521	c.1109T>C	P.L370S
SH_13	18	29171935	29171935	Splice_Site	SNV	G	T	T	TTR	c.69+1G>T	
SH_13	18	33744438	33744438	Missense_Mutation	SNV	G	A	A	ELP2	c.1957G>A	P.A653T
SH_13	18	42532203	42532203	Silent	SNV	G	T	T	SETBP1	c.2898G>T	P.V966V
SH_13	18	52896252	52896252	Silent	SNV	G	T	T	TCF4	c.1705C>A	P.R569R
SH_13	19	40411969	40411969	Missense_Mutation	SNV	C	A	A	FCGBP	c.3659G>T	P.G1220V
SH_13	19	42482130	42482130	Missense_Mutation	SNV	A	T	T	ATP1A3	c.1934T>A	P.I645N
SH_13	19	55317435	55317435	Silent	SNV	C	A	A	KIR2DL4	c.391C>A	P.R131R
SH_13	19	56223303	56223303	Missense_Mutation	SNV	G	C	C	NLRP9	c.2706C>G	P.C902W
SH_13	19	57647140	57647140	Missense_Mutation	SNV	G	A	A	ZIM3	c.565C>T	P.H189Y
SH_13	19	577939	577939	Missense_Mutation	SNV	G	T	T	BSG	c.233G>T	P.R78L
SH_13	2	179443615	179443615	Silent	SNV	A	G	G	TTN	c.63219T>C	P.Y21073Y
SH_13	2	189925466	189925466	Frame_Shift_Del	INDEL	G	-	-	COL5A2	c.2075delC	P.P692fs
SH_13	2	71360152	71360152	Missense_Mutation	SNV	G	A	A	MPHOSPH10	c.214G>A	P.D72N
SH_13	2	72725596	72725596	Missense_Mutation	SNV	C	A	A	EXOC6B	c.1324G>T	P.A442S
SH_13	2	80529586	80529586	Missense_Mutation	SNV	G	T	T	LRRTM1	c.1359C>A	P.F453L
SH_13	20	3211715	3211715	Splice_Site	SNV	G	C	C	SLC4A11	c.1043-11C>G	
SH_13	20	48744532	48744532	Missense_Mutation	SNV	G	T	T	TMEM189	c.662C>A	P.T221N
SH_13	20	61542712	61542712	Missense_Mutation	SNV	C	A	A	DIDO1	c.253G>T	P.G85C
SH_13	20	61982181	61982181	Missense_Mutation	SNV	C	A	A	CHRNA4	c.582G>T	P.M194I
SH_13	20	62124632	62124632	Nonsense_Mutation	SNV	C	T	T	EEF1A2	c.630G>A	P.W210*
SH_13	21	35468082	35468082	Silent	SNV	G	T	T	SLC5A3	c.585G>T	P.G195G
SH_13	21	45502786	45502786	Missense_Mutation	SNV	G	A	A	TRAPP10	c.1841G>A	P.S614N
SH_13	22	20907437	20907437	Missense_Mutation	SNV	A	G	G	MED15	c.214A>G	P.K72E
SH_13	22	37471174	37471174	Splice_Site	SNV	C	T	T	TMPPRS6	c.1342+1G>A	
SH_13	22	40054956	40054956	Missense_Mutation	SNV	A	G	G	CACNA1I	c.2060A>G	P.Q687R
SH_13	3	111793176	111793176	Missense_Mutation	SNV	G	T	T	TMPPRS7	c.1322G>T	P.G441V
SH_13	3	11300845	11300845	Missense_Mutation	SNV	C	A	A	HRH1	c.122C>A	P.T41K
SH_13	3	124732832	124732832	Missense_Mutation	SNV	C	A	A	HEG1	c.1591G>T	P.A531S
SH_13	3	193082072	193082072	Splice_Site	SNV	G	C	C	ATP13A5	c.64-3C>G	
SH_13	3	38797459	38797459	Splice_Site	SNV	G	T	T	SCN10A	c.1291-10C>A	
SH_13	3	50412208	50412208	Nonsense_Mutation	SNV	G	T	T	CACNA2D2	c.1944C>A	P.Y648*
SH_13	3	57817197	57817197	Nonsense_Mutation	SNV	G	T	T	SLMAP	c.286G>T	P.E96*
SH_13	4	135121249	135121249	Missense_Mutation	SNV	A	C	C	PABPC4L	c.1100T>G	P.L367R
SH_13	5	131398462	131398462	Missense_Mutation	SNV	C	A	A	IL3	c.437C>A	P.T146N
SH_13	5	31995683	31995683	Missense_Mutation	SNV	A	T	T	PDZD2	c.980A>T	P.E327V
SH_13	5	35697790	35697790	Splice_Site	SNV	A	G	G	SPEF2	c.2038-2A>G	
SH_13	5	70751716	70751716	Missense_Mutation	SNV	G	T	T	BDP1	c.12G>T	P.R4S
SH_13	6	102266269	102266269	Missense_Mutation	SNV	G	T	T	GRIK2	c.1228G>T	P.G410C
SH_13	6	132892350	132892350	Missense_Mutation	SNV	G	A	A	TAAR6	c.890G>A	P.C297Y
SH_13	6	28473524	28473524	Missense_Mutation	SNV	C	A	A	GPX6	c.415G>T	P.D139Y
SH_13	6	30698749	30698749	Silent	SNV	C	A	A	FLOT1	c.708G>T	P.R236R
SH_13	6	42612073	42612073	Missense_Mutation	SNV	A	C	C	UBR2	c.2219A>C	P.K740T
SH_13	6	46047610	46047610	Missense_Mutation	SNV	G	A	A	CLIC5	c.370C>T	P.L124F
SH_13	6	65301109	65301109	Nonsense_Mutation	SNV	C	A	A	EYS	c.4651G>T	P.E1551*
SH_13	7	107696124	107696124	Missense_Mutation	SNV	G	T	T	LAMB4	c.3708C>A	P.F1236L
SH_13	7	123092932	123092932	Silent	SNV	C	G	G	IQUB	c.2241G>C	P.L747L
SH_13	7	141618961	141618961	Missense_Mutation	SNV	G	T	T	OR9A4	c.286G>T	P.A96S
SH_13	7	31912917	31912917	Silent	SNV	G	T	T	PDE1C	c.597C>A	P.I199I
SH_13	7	81579718	81579718	Missense_Mutation	SNV	C	T	T	CACNA2D1	c.3266G>A	P.R1089H
SH_13	7	99032823	99032823	Missense_Mutation	SNV	G	T	T	ATP5J2-PTCD1	c.190C>A	P.P64T
SH_13	8	2976107	2976107	Missense_Mutation	SNV	A	T	T	CSMD1	c.6244T>A	P.Y2082N
SH_13	8	75156754	75156754	Splice_Site	SNV	C	A	A	JPH1	c.1905+10G>T	
SH_13	8	95508665	95508665	Missense_Mutation	SNV	G	A	A	KIAA1429	c.4274C>T	P.A1425V
SH_13	9	101748165	101748165	Missense_Mutation	SNV	A	G	G	COL15A1	c.419A>G	P.E140G
SH_13	9	139368612	139368612	Silent	SNV	C	A	A	SEC16A	c.3456G>T	P.P1152P
SH_13	9	5919945	5919945	Silent	SNV	T	C	C	KIAA2026	c.6051A>G	P.T2017T
SH_13	9	77436710	77436710	Silent	SNV	G	A	A	TRPM6	c.870C>T	P.G290G
SH_13	9	96030136	96030136	Missense_Mutation	SNV	C	G	G	WNK2	c.3805C>G	P.R1269G
SH_13	X	114418979	114418979	Nonsense_Mutation	SNV	C	A	A	LRCH2	c.616G>T	P.E206*
SH_13	X	49066496	49066496	Missense_Mutation	SNV	A	G	G	CACNA1F	c.4595T>C	P.L1532P
SH_130	1	1421986	1421986	Missense_Mutation	SNV	G	T	T	ATAD3B	c.1014G>T	P.M338I
SH_130	1	1421987	1421987	Missense_Mutation	SNV	G	T	T	ATAD3B	c.1015G>T	P.G339W
SH_130	1	15428051	15428051	Silent	SNV	T	A	A	KAZN	c.1560T>A	P.A520A
SH_130	1	155927566	155927566	Silent	SNV	C	T	T	ARHGEF2	c.1653G>A	P.V551V
SH_130	1	161160769	161160769	Missense_Mutation	SNV	C	A	A	ADAMT54	c.2512G>T	P.A838S
SH_130	1	180044231	180044231	Missense_Mutation	SNV	G	T	T	CEP350	c.5642G>T	P.R1881L
SH_130	1	198682206	198682206	Splice_Site	SNV	T	A	A	PTPRC	c.808+5T>A	
SH_130	1	21191018	21191018	Missense_Mutation	SNV	C	A	A	EIF4G3	c.2897G>T	P.C966F
SH_130	1	237824130	237824130	Missense_Mutation	SNV	G	T	T	RYR2	c.8319G>T	P.W2773C

SH_130	1	247978864	247978864	Silent	SNV	G	A	A	OR14A16	c.168C>T	P.P56P
SH_130	1	248224164	248224164	Missense_Mutation	SNV	C	A	A	OR2L3	c.181C>A	P.L61I
SH_130	1	248224885	248224885	Missense_Mutation	SNV	C	A	A	OR2L3	c.902C>A	P.T301K
SH_130	1	45473170	45473170	Missense_Mutation	SNV	C	A	A	HECTD3	c.1418G>T	P.R473L
SH_130	10	101590191	101590191	Splice_Site	SNV	G	T	T	ABCC2	c.2747+1G>T	
SH_130	10	103789389	103789389	Splice_Site	SNV	C	A	A	C10orf76	c.414+6G>T	
SH_130	10	115357747	115357747	Missense_Mutation	SNV	G	A	A	NRAP	c.4313C>T	P.A1438V
SH_130	10	125805589	125805589	Missense_Mutation	SNV	A	T	T	CHST15	c.140T>A	P.V47E
SH_130	10	135126297	135126297	Missense_Mutation	SNV	C	A	A	ZNF511	c.686C>A	P.P229H
SH_130	10	18266928	18266928	Silent	SNV	C	G	G	SLC39A12	c.849C>G	P.T283T
SH_130	10	226061	226061	Missense_Mutation	SNV	A	G	G	ZMYND11	c.109A>G	P.I37V
SH_130	10	49635192	49635192	Splice_Site	SNV	T	G	G	MAPK8	c.1060+6T>G	
SH_130	10	50666905	50666905	Missense_Mutation	SNV	A	G	G	ERCC6	c.4438T>C	P.S1480P
SH_130	10	52588005	52588005	Nonsense_Mutation	SNV	C	A	A	A1CF	c.655G>T	P.E219*
SH_130	10	52834576	52834576	Silent	SNV	C	A	A	PRKG1	c.226C>A	P.R76R
SH_130	10	70764800	70764800	Splice_Site	SNV	A	G	G	KIAA1279	c.526-2A>G	
SH_130	11	102736636	102736636	Missense_Mutation	SNV	C	G	G	MMP12	c.1073G>C	P.R358T
SH_130	11	123479437	123479437	Silent	SNV	G	T	T	GRAMD1B	c.1176G>T	P.V392V
SH_130	11	123909020	123909020	Missense_Mutation	SNV	G	A	A	OR10G7	c.689C>T	P.S230L
SH_130	11	5776918	5776918	Silent	SNV	C	A	A	OR52N4	c.948C>A	P.T316T
SH_130	11	64323775	64323775	Missense_Mutation	SNV	G	A	A	SLC22A11	c.304G>A	P.A102T
SH_130	11	65618597	65618597	Silent	SNV	C	T	T	SNX3	c.675C>T	P.C225C
SH_130	12	104461804	104461804	Missense_Mutation	SNV	G	T	T	HCFC2	c.392G>T	P.S131I
SH_130	12	3149329	3149329	Silent	SNV	G	T	T	TEAD4	c.1095G>T	P.P365P
SH_130	12	4628057	4628057	Splice_Site	SNV	T	C	C	C12orf4	c.729-11A>G	
SH_130	12	57828687	57828687	Silent	SNV	T	A	A	INHBC	c.18T>A	P.L6L
SH_130	12	7069873	7069873	Missense_Mutation	SNV	G	C	C	PTPN6	c.1721G>C	P.R574P
SH_130	12	88568497	88568497	Missense_Mutation	SNV	C	T	T	TMTC3	c.1313C>T	P.A438V
SH_130	13	114061329	114061329	Missense_Mutation	SNV	C	A	A	LOC101928841	c.1176G>T	P.Q392H
SH_130	13	48947539	48947539	Splice_Site	SNV	A	G	G	RB1	c.1128-2A>G	
SH_130	13	61103226	61103226	Missense_Mutation	SNV	G	T	T	TDRD3	c.1867G>T	P.G623W
SH_130	13	61103227	61103227	Missense_Mutation	SNV	G	T	T	TDRD3	c.1868G>T	P.G623V
SH_130	14	20181623	20181623	Missense_Mutation	SNV	C	G	G	OR11H2	c.453G>C	P.M151I
SH_130	14	24040569	24040569	Silent	SNV	G	T	T	JPH4	c.1371C>A	P.S457S
SH_130	14	53619451	53619451	Missense_Mutation	SNV	C	A	A	DDHD1	c.366G>T	P.Q122H
SH_130	15	40708323	40708323	Missense_Mutation	SNV	G	T	T	IVD	c.926G>T	P.C309F
SH_130	15	50763999	50763999	Splice_Site	SNV	A	G	G	USP8	c.849+7A>G	
SH_130	15	57837794	57837794	Missense_Mutation	SNV	C	G	G	CGNL1	c.3505C>G	P.R1169G
SH_130	15	72454657	72454657	Missense_Mutation	SNV	G	C	C	GRAMD2	c.1018C>G	P.Q340E
SH_130	16	11369763	11369763	Missense_Mutation	SNV	C	A	A	PRM2	c.347G>T	P.G116V
SH_130	16	3781828	3781828	Silent	SNV	C	A	A	CREBBP	c.4839G>T	P.V1613V
SH_130	16	50816304	50816304	Nonsense_Mutation	SNV	G	T	T	CYLD	c.1753G>T	P.E585*
SH_130	16	53501036	53501036	Nonsense_Mutation	SNV	A	T	T	RBL2	c.1930A>T	P.R644*
SH_130	16	89789814	89789814	Missense_Mutation	SNV	G	T	T	ZNF276	c.703G>T	P.D235Y
SH_130	2	220246123	220246123	Silent	SNV	A	G	G	DNPEP	c.1197T>C	P.Y399Y
SH_130	2	49195955	49195955	Missense_Mutation	SNV	C	A	A	FSHR	c.736G>C	P.A246S
SH_130	2	64863208	64863208	Silent	SNV	C	T	T	SERTAD2	c.798G>A	P.G266G
SH_130	2	9000856	9000856	Silent	SNV	G	T	T	MBOAT2	c.957C>A	P.S319S
SH_130	3	133495987	133495987	Missense_Mutation	SNV	G	T	T	TF	c.1967G>T	P.C656F
SH_130	3	133547664	133547664	Missense_Mutation	SNV	G	T	T	RAB6B	c.595C>A	P.P199T
SH_130	3	137717926	137717926	Silent	SNV	G	A	A	CLDN18	c.216G>A	P.L72L
SH_130	3	168833418	168833418	Silent	SNV	G	T	T	MECOM	c.1873C>A	P.R625R
SH_130	3	186331011	186331011	Silent	SNV	T	C	C	AHSG	c.81T>C	P.Y27Y
SH_130	3	49936290	49936290	Splice_Site	SNV	C	A	A	MST1R	c.1548+10G>T	
SH_130	4	13371542	13371542	Silent	SNV	T	C	C	RAB28	c.621A>G	P.Q207Q
SH_130	4	183836170	183836170	Silent	SNV	C	A	A	DCTD	c.183G>T	P.G61G
SH_130	4	30724764	30724764	Silent	SNV	C	T	T	PCDH7	c.1720C>T	P.L574L
SH_130	4	44638032	44638032	Missense_Mutation	SNV	C	T	T	YIPF7	c.259G>A	P.A87T
SH_130	4	87968323	87968323	Silent	SNV	T	A	A	AFF1	c.636T>A	P.P212P
SH_130	4	92520063	92520063	Missense_Mutation	SNV	C	G	G	CCSER1	c.2558C>G	P.A853G
SH_130	5	138758421	138758421	Missense_Mutation	SNV	G	T	T	DNAJC18	c.755C>A	P.P252H
SH_130	5	140263706	140263706	Missense_Mutation	SNV	C	T	T	PCDHA13	c.1853C>T	P.A618V
SH_130	5	140554686	140554686	Missense_Mutation	SNV	C	A	A	PCDH87	c.2270C>A	P.S575Y
SH_130	5	39135107	39135107	Missense_Mutation	SNV	G	T	T	FYB	c.1555C>A	P.P519T
SH_130	5	39382768	39382768	Missense_Mutation	SNV	G	C	C	DAB2	c.1230C>G	P.I410M
SH_130	6	146673473	146673473	Missense_Mutation	SNV	A	G	G	GRM1	c.1274A>G	P.Q425R
SH_130	6	150211941	150211941	Splice_Site	SNV	C	T	T	RAET1E	c.85+12G>A	
SH_130	6	160968906	160968906	Missense_Mutation	SNV	G	T	T	LPA	c.5219C>A	P.P1740Q
SH_130	6	31504460	31504460	Missense_Mutation	SNV	C	A	A	DDX39B	c.433G>T	P.V145F
SH_130	6	42713784	42713784	Missense_Mutation	SNV	C	T	T	TBCC	c.28G>A	P.A10T
SH_130	6	74072590	74072590	Silent	SNV	C	A	A	KHDC3L	c.138C>A	P.R46R
SH_130	6	78172048	78172048	Missense_Mutation	SNV	C	A	A	HTR1B	c.1073G>T	P.G358V
SH_130	6	83075166	83075166	Nonsense_Mutation	SNV	C	A	A	TPBG	c.488C>A	P.S163*
SH_130	6	84765103	84765103	Silent	SNV	C	T	T	MRAP2	c.66C>T	P.T22T
SH_130	7	100635286	100635286	Missense_Mutation	SNV	C	A	A	MUC12	c.1442C>A	P.P481H
SH_130	7	131883300	131883300	Silent	SNV	G	T	T	PLXNA4	c.2682C>A	P.V894V
SH_130	7	150763726	150763726	Missense_Mutation	SNV	A	T	T	SLC4A2	c.701A>T	P.N234I
SH_130	7	156799271	156799271	Nonsense_Mutation	SNV	G	A	A	MXN1	c.118C>T	P.Q40*
SH_130	7	38502670	38502670	Missense_Mutation	SNV	C	T	T	AMPH	c.793G>A	P.E265K
SH_130	7	5347779	5347779	Silent	SNV	C	A	A	TNRC18	c.8865G>T	P.T2955T
SH_130	7	55229263	55229263	Missense_Mutation	SNV	G	T	T	EGFR	c.1570G>T	P.V524F
SH_130	7	99260471	99260471	Missense_Mutation	SNV	G	T	T	CYP3A5	c.833C>A	P.S278Y
SH_130	8	104427611	104427611	Missense_Mutation	SNV	G	T	T	DCAF13	c.393G>T	P.R131S
SH_130	8	105361442	105361442	Nonsense_Mutation	SNV	C	A	A	DCSTAMP	c.662C>A	P.S221*
SH_130	8	24346664	24346664	Splice_Site	SNV	A	G	G	ADAM7	c.1092-8A>G	
SH_130	8	28573681	28573681	Silent	SNV	G	C	C	EXTL3	c.105G>C	P.T35T
SH_130	8	665995	665995	Missense_Mutation	SNV	T	G	G	ERIC1	c.35A>C	P.K12T
SH_130	8	72756027	72756027	Missense_Mutation	SNV	C	A	A	MSC	c.387G>T	P.R129S
SH_130	9	136654384	136654384	Missense_Mutation	SNV	C	T	T	VAV2	c.1270G>A	P.D424N
SH_130	9	140948389	140948389	Missense_Mutation	SNV	C	A	A	CACNA1B	c.3899C>A	P.A1300E
SH_130	9	26842467	26842467	Silent	SNV	T	C	C	CAAP1	c.483A>G	P.L161L
SH_130	9	74344996	74344996	Silent	SNV	T	A	A	TMEM2	c.1758A>T	P.G586G
SH_130	9	90535372	90535372	Missense_Mutation	SNV	G	T	T	SPATA31C1	c.550G>T	P.G184C
SH_131	1	12460335	12460335	Missense_Mutation	SNV	A	T	T	VPS13D	c.11732A>T	P.Q3911L
SH_131	1	148017622	148017622	Missense_Mutation	SNV	A	T	T	NBPF8	c.1681T>A	P.W561R
SH_131	1	155207274	155207274	Missense_Mutation	SNV	T	A	A	GBA	c.857A>T	P.Q286L
SH_131	1	156351299	156351299	Missense_Mutation	SNV	G	C	C	RHBG	c.628G>C	P.D210H
SH_131	1	156554689	156554689	Silent	SNV	C	G	G	TTC24	c.1272C>G	P.L424L

SH_131	1	158590176	158590176	Silent	SNV	T	A	A	SPTA1	c.6201A>T	P.S20675
SH_131	1	159846499	159846499	Frame_Shift_Ins	INDEL	-	T	T	CFAP45	c.1198dupA	P.R400fs
SH_131	1	160604625	160604625	Missense_Mutation	SNV	A	T	T	SLAMF1	c.478T>A	P.L160M
SH_131	1	169673698	169673698	Splice_Site	SNV	A	T	T	SELL	c.805+11T>A	
SH_131	1	179623487	179623487	Missense_Mutation	SNV	A	T	T	TDRD5	c.2312A>T	P.E771V
SH_131	1	196392233	196392233	Missense_Mutation	SNV	C	A	A	KCNT2	c.1132G>T	P.A378S
SH_131	1	203830821	203830821	Nonsense_Mutation	SNV	A	T	T	SNRPE	c.34A>T	P.K12*
SH_131	1	215820908	215820908	Missense_Mutation	SNV	C	T	T	USH2A	c.14747G>A	P.G4916D
SH_131	1	215901593	215901593	Missense_Mutation	SNV	C	T	T	USH2A	c.11845G>A	P.G3949S
SH_131	1	229567738	229567738	Splice_Site	SNV	C	A	A	ACTA1	c.808+3G>T	
SH_131	1	243716053	243716053	Missense_Mutation	SNV	A	T	T	AKT3	c.1141T>A	P.L381M
SH_131	1	247654472	247654472	Missense_Mutation	SNV	G	T	T	OR2W5	c.43G>T	P.V15L
SH_131	1	248524891	248524891	Silent	SNV	C	T	T	OR2T4	c.9C>T	P.N3N
SH_131	1	26515327	26515327	Silent	SNV	A	T	T	CNKSR1	c.1776A>T	P.L592L
SH_131	1	27621003	27621003	Splice_Site	SNV	A	T	T	WDTC1	c.758-2A>T	
SH_131	1	38488401	38488401	Missense_Mutation	SNV	A	T	T	UTP11	c.598A>T	P.N200Y
SH_131	1	67356867	67356867	Missense_Mutation	SNV	A	T	T	WDR78	c.613T>A	P.Y205N
SH_131	10	108466295	108466295	Splice_Site	INDEL	G	-	-	SORCS1	c.1233+8delC	
SH_131	10	1245940	1245940	Silent	SNV	G	A	A	ADARB2	c.1830C>T	P.P610P
SH_131	10	134722047	134722047	Missense_Mutation	SNV	C	A	A	CFAP46	c.2849G>T	P.R950L
SH_131	10	16877003	16877003	Splice_Site	SNV	T	C	C	CUBN	c.10362+10A>G	
SH_131	10	27826809	27826809	Missense_Mutation	SNV	A	T	T	RAB18	c.383A>T	P.Q128L
SH_131	10	51130638	51130638	Silent	SNV	A	T	T	PARG	c.1287T>A	P.V429V
SH_131	11	102487587	102487587	Silent	SNV	G	T	T	MMP20	c.330C>A	P.L110L
SH_131	11	102667820	102667820	Missense_Mutation	SNV	T	A	A	MMP1	c.226A>T	P.S76C
SH_131	11	10821805	10821805	Missense_Mutation	SNV	T	C	C	EIF4G2	c.1837A>G	P.I613V
SH_131	11	132305072	132305072	Missense_Mutation	SNV	G	T	T	OPCML	c.945C>A	P.S315R
SH_131	11	16117579	16117579	Missense_Mutation	SNV	T	C	C	SOX6	c.1064A>G	P.H355R
SH_131	11	45971785	45971785	Silent	SNV	T	A	A	PHF21A	c.1116A>T	P.L372L
SH_131	11	57561528	57561528	Missense_Mutation	SNV	C	T	T	CTNND1	c.242C>T	P.S81L
SH_131	11	6806814	6806814	Silent	SNV	A	T	T	OR2AG1	c.546A>T	P.P182P
SH_131	11	85968550	85968550	Splice_Site	INDEL	A	-	-	EED	c.553-7delA	
SH_131	11	9101037	9101037	Missense_Mutation	SNV	A	T	T	SCUBE2	c.276T>A	P.N92K
SH_131	12	107080718	107080718	Missense_Mutation	SNV	A	T	T	RFK4	c.461A>T	P.Y154F
SH_131	12	11342549	11342549	Frame_Shift_Del	INDEL	C	-	-	CCDC63	c.1385delC	P.P462fs
SH_131	12	112668590	112668615	Frame_Shift_Del	INDEL	ACTGATGA	-	-	HECTD4	5CGTCCCTTCAT	P.V1937fs
SH_131	12	11506787	11506787	Missense_Mutation	SNV	C	T	T	PRB1	c.250G>A	P.G84R
SH_131	12	21788503	21788503	Silent	SNV	G	A	A	LDHB	c.978C>T	P.D326D
SH_131	12	29648281	29648281	Missense_Mutation	SNV	T	A	A	OVCH1	c.391A>T	P.N131Y
SH_131	12	2994567	2994567	Missense_Mutation	SNV	A	T	T	RHNO1	c.35A>T	P.Q12L
SH_131	12	39967595	39967595	Missense_Mutation	SNV	A	T	T	ABCD2	c.1926T>A	P.D642E
SH_131	12	48145291	48145291	Silent	SNV	A	T	T	RAPGEF3	c.393T>A	P.S131S
SH_131	12	50452758	50452758	Missense_Mutation	SNV	A	T	T	ASIC1	c.209A>T	P.H70L
SH_131	12	52845352	52845352	Missense_Mutation	SNV	T	A	A	KRT6B	c.511A>T	P.N171Y
SH_131	12	53237959	53237959	Missense_Mutation	SNV	A	T	T	KRT78	c.635T>A	P.M212K
SH_131	12	59272763	59272763	Silent	SNV	T	A	A	LRIG3	c.1746A>T	P.T582T
SH_131	12	7848149	7848149	Missense_Mutation	SNV	T	A	A	GDF3	c.176A>T	P.E59V
SH_131	12	86377356	86377356	Silent	SNV	T	A	A	MGAT4C	c.240A>T	P.S80S
SH_131	12	95479603	95479603	Missense_Mutation	SNV	A	G	G	FGD6	c.4060T>C	P.W1354R
SH_131	13	108518427	108518427	Missense_Mutation	SNV	G	T	T	FAM155A	c.518C>A	P.P173H
SH_131	13	21562330	21562330	Missense_Mutation	SNV	T	A	A	LATS2	c.1589A>T	P.Q530L
SH_131	13	24797806	24797806	Missense_Mutation	SNV	A	T	T	SPATA13	c.739A>T	P.M247L
SH_131	13	53035553	53035553	Missense_Mutation	SNV	G	C	C	CKAP2	c.595G>C	P.D199H
SH_131	13	98673301	98673301	Missense_Mutation	SNV	A	G	G	IPO5	c.3175A>G	P.I1059V
SH_131	14	21789464	21789464	Missense_Mutation	SNV	T	A	A	RPGRI1	c.1514T>A	P.L505Q
SH_131	14	31420109	31420109	Missense_Mutation	SNV	T	A	A	STRN3	c.502A>T	P.S168C
SH_131	14	69814679	69814679	Missense_Mutation	SNV	C	A	A	GALNT16	c.1499C>A	P.P500Q
SH_131	14	94395463	94395463	Nonsense_Mutation	SNV	A	T	T	FAM181A	c.832A>T	P.K278*
SH_131	15	100801716	100801716	Silent	SNV	C	T	T	ADAMTS17	c.999G>A	P.P333P
SH_131	15	25963545	25963545	Splice_Site	SNV	C	T	T	ATP10A	c.1365G>A	P.A455A
SH_131	15	31339447	31339447	Missense_Mutation	SNV	A	G	G	TRPM1	c.1682T>C	P.L561P
SH_131	15	42129008	42129008	Silent	SNV	G	T	T	JMJD7	c.732G>T	P.A244A
SH_131	15	49776595	49776595	Missense_Mutation	SNV	G	T	T	FGF7	c.479G>T	P.G160V
SH_131	15	55664086	55664086	Missense_Mutation	SNV	T	A	A	CCPG1	c.611A>T	P.K204M
SH_131	15	73635865	73635865	Missense_Mutation	SNV	A	T	T	HCN4	c.1070T>A	P.L357H
SH_131	15	74166078	74166078	Missense_Mutation	SNV	C	G	G	TBC1D21	c.28C>G	P.L10V
SH_131	16	22114849	22114849	Missense_Mutation	SNV	A	T	T	VWA3A	c.482A>T	P.K161M
SH_131	16	23208733	23208733	Silent	SNV	T	A	A	SCNN1G	c.1062T>A	P.S354S
SH_131	17	15609773	15609773	Missense_Mutation	SNV	A	T	T	ZNF286A	c.199A>T	P.R67W
SH_131	17	26861836	26861836	Missense_Mutation	SNV	C	A	A	FOXN1	c.1247C>A	P.P416Q
SH_131	17	38451717	38451717	Splice_Site	SNV	C	T	T	CDC6	c.1184+9C>T	
SH_131	17	39471690	39471690	Nonsense_Mutation	SNV	G	T	T	KRTAP17-1	c.213C>A	P.C71*
SH_131	17	39882134	39882134	Silent	SNV	G	A	A	HAP1	c.1332C>T	P.P444P
SH_131	17	41886396	41886396	Silent	SNV	T	C	C	MPP3	c.1509A>G	P.V503V
SH_131	17	42165866	42165866	Silent	SNV	A	C	C	HDAC5	c.1491T>G	P.T497T
SH_131	17	56060741	56060741	Missense_Mutation	SNV	G	A	A	VEZF1	c.47C>T	P.S16F
SH_131	17	7578239	7578239	Nonsense_Mutation	SNV	C	A	A	TP53	c.610G>T	P.E204*
SH_131	18	28934553	28934553	Silent	SNV	A	T	T	DSG1	c.2394A>T	P.P798P
SH_131	19	12014711	12014711	Splice_Site	SNV	A	G	G	ZNF69	c.191-9A>G	
SH_131	19	2834510	2834510	Missense_Mutation	SNV	A	T	T	ZNF554	c.1277A>T	P.H426L
SH_131	19	36213507	36213507	Missense_Mutation	SNV	A	T	T	KMT2B	c.2609A>T	P.H870L
SH_131	19	37117073	37117073	Nonsense_Mutation	SNV	G	T	T	ZNF382	c.271G>T	P.E91*
SH_131	19	38160851	38160851	Missense_Mutation	SNV	C	T	T	ZNF781	c.199G>A	P.G67R
SH_131	19	45296780	45296780	Missense_Mutation	SNV	G	T	T	CBLC	c.1049G>T	P.W350L
SH_131	19	5456494	5456494	Missense_Mutation	SNV	A	T	T	ZNRF4	c.992A>T	P.Y331F
SH_131	19	56244066	56244066	Missense_Mutation	SNV	T	A	A	NLRP9	c.1131A>T	P.K377N
SH_131	19	57036779	57036779	Missense_Mutation	SNV	A	T	T	ZNF471	c.1121A>T	P.Q374L
SH_131	19	58100036	58100036	Splice_Site	SNV	A	T	T	ZIK1	c.199+3A>T	
SH_131	19	58199438	58199438	Missense_Mutation	SNV	A	T	T	ZNF551	c.1711A>T	P.S571C
SH_131	19	964249	964249	Splice_Site	SNV	G	A	A	ARID3A	c.768G>A	P.G256G
SH_131	2	166165177	166165177	Missense_Mutation	SNV	T	C	C	SCN2A	c.478T>C	P.Y160H
SH_131	2	179247810	179247810	Missense_Mutation	SNV	G	A	A	OSBP16	c.1756G>A	P.A586T
SH_131	2	179400006	179400006	Missense_Mutation	SNV	G	A	A	TTN	c.96413C>T	P.P32138L
SH_131	2	179594929	179594929	Silent	SNV	A	T	T	TTN	c.17247T>A	P.S5749S
SH_131	2	179612601	179612601	Silent	SNV	A	G	G	TTN	c.14526T>C	P.N4842N
SH_131	2	179640512	179640512	Missense_Mutation	SNV	A	T	T	TTN	c.6079T>A	P.Y2027N
SH_131	2	202245857	202245857	Missense_Mutation	SNV	T	A	A	TRAK2	c.2154A>T	P.R718S
SH_131	2	209198037	209198037	Splice_Site	SNV	A	G	G	PIKFYVE	c.3964-2A>G	

SH_131	2	219486194	219486194	Missense_Mutation	SNV	T	A	A	PLCD4	c.412T>A	P.W138R
SH_131	2	236659018	236659018	Missense_Mutation	SNV	C	T	T	AGAP1	c.559C>T	P.P187S
SH_131	2	47273501	47273501	Missense_Mutation	SNV	A	T	T	TTCT7A	c.1850A>T	P.E617V
SH_131	2	74641666	74641666	Silent	SNV	T	A	A	C2orf81	c.1557A>T	P.T519T
SH_131	20	31619555	31619555	Splice_Site	SNV	T	A	A	BP1FB6	c.97+5T>A	
SH_131	20	36789850	36789850	Silent	SNV	T	A	A	TGM2	c.162A>T	P.V54V
SH_131	20	4705585	4705585	Missense_Mutation	SNV	C	A	A	PRND	c.388C>A	P.Q130K
SH_131	20	47297852	47297852	Silent	SNV	T	C	C	PREX1	c.1356A>G	P.L452L
SH_131	22	25282591	25282591	Missense_Mutation	SNV	C	T	T	SGSM1	c.1831C>T	P.R611C
SH_131	22	32482268	32482268	Nonsense_Mutation	SNV	T	A	A	SLCSA1	c.1083T>A	P.C361*
SH_131	22	50502577	50502577	Missense_Mutation	SNV	C	A	A	MLC1	c.945G>T	P.Q315H
SH_131	3	115395178	115395178	Frame_Shift_Del	INDEL	G	-	-	GAP43	c.457delG	P.D153fs
SH_131	3	123010209	123010209	Missense_Mutation	SNV	T	A	A	ADCV5	c.2028A>T	P.K676N
SH_131	3	129023648	129023648	Nonsense_Mutation	SNV	A	T	T	HMCES	c.1045A>T	P.K349*
SH_131	3	139088125	139088125	Missense_Mutation	SNV	C	A	A	COPB2	c.1379G>T	P.R460I
SH_131	3	139088127	139088127	Silent	SNV	T	C	C	COPB2	c.1377A>G	P.R459R
SH_131	3	170625534	170625534	Missense_Mutation	SNV	T	A	A	EIF5A2	c.62A>T	P.Q21L
SH_131	3	176755903	176755903	Missense_Mutation	SNV	C	A	A	TBL1XR1	c.1105G>T	P.D369Y
SH_131	3	182590191	182590191	Silent	SNV	A	G	G	ATP11B	c.1914A>G	P.K638K
SH_131	3	383699	383699	Missense_Mutation	SNV	T	A	A	CHL1	c.613T>A	P.F205I
SH_131	3	38593058	38593058	Splice_Site	SNV	A	T	T	SCNSA	c.4811-9T>A	
SH_131	3	38946723	38946723	Missense_Mutation	SNV	T	A	A	SCN11A	c.1563A>T	P.R521S
SH_131	3	51749744	51749744	Missense_Mutation	SNV	C	A	A	GRM2	c.1955C>A	P.T652N
SH_131	3	51750100	51750100	Missense_Mutation	SNV	A	G	G	GRM2	c.2311A>G	P.I771V
SH_131	4	37447057	37447057	Silent	SNV	T	A	A	NWBD2	c.3447T>A	P.L1149L
SH_131	4	48993572	48993572	Missense_Mutation	SNV	T	A	A	CVH43	c.256T>A	P.S86T
SH_131	5	132535320	132535320	Missense_Mutation	SNV	C	A	A	FSTL4	c.1996G>T	P.A666S
SH_131	5	133643968	133643968	Missense_Mutation	SNV	T	C	C	CDKL3	c.1225A>G	P.I409V
SH_131	5	137420325	137420325	Missense_Mutation	SNV	G	A	A	WNT8A	c.295G>A	P.A99T
SH_131	5	178311177	178311177	Missense_Mutation	SNV	A	T	T	ZNF354B	c.1724A>T	P.E575V
SH_131	5	24487809	24487809	Missense_Mutation	SNV	T	C	C	CDH10	c.548A>G	P.E183G
SH_131	5	70351201	70351201	Missense_Mutation	SNV	T	A	A	GTF2H2	c.448A>T	P.S150C
SH_131	6	109980447	109980447	Missense_Mutation	SNV	T	A	A	AK9	c.614A>T	P.E205V
SH_131	6	118813033	118813033	Splice_Site	SNV	T	A	A	CEP85L	c.1258-5A>T	
SH_131	6	130370426	130370426	Splice_Site	SNV	G	T	T	L3MBTL3	c.103-1G>T	
SH_131	6	131574200	131574200	Missense_Mutation	SNV	G	A	A	AKAP7	c.73G>A	P.A25T
SH_131	6	136709537	136709537	Missense_Mutation	SNV	T	A	A	MAP7	c.586A>T	P.S196C
SH_131	6	152532640	152532640	Missense_Mutation	SNV	T	A	A	SYNE1	c.22365A>T	P.Q7455H
SH_131	6	159657345	159657345	Missense_Mutation	SNV	T	A	A	FNDCl	c.4066T>A	P.W1356R
SH_131	6	161807841	161807841	Silent	SNV	T	A	A	PARK2	c.1152A>T	P.S384S
SH_131	6	30883177	30883177	Missense_Mutation	SNV	A	T	T	VAR52	c.329A>T	P.E110V
SH_131	6	52943682	52943682	Silent	SNV	C	T	T	FBX09	c.423C>T	P.G141G
SH_131	6	74121997	74121997	Silent	SNV	T	A	A	DDX43	c.1350T>A	P.V450V
SH_131	6	85457815	85457815	Splice_Site	SNV	A	T	T	TBX18	c.772-10T>A	
SH_131	6	88120348	88120348	Missense_Mutation	SNV	A	G	G	CFAP206	c.154A>G	P.R52G
SH_131	6	88125402	88125402	Splice_Site	SNV	A	T	T	CFAP206	c.284-2A>T	
SH_131	7	100087151	100087151	Missense_Mutation	SNV	A	T	T	NYAP1	c.1807A>T	P.I603F
SH_131	7	103243800	103243800	Missense_Mutation	SNV	T	A	A	RELN	c.3284A>T	P.E1095V
SH_131	7	127724820	127724820	Missense_Mutation	SNV	G	T	T	SDN1	c.2155G>T	P.A719S
SH_131	7	140374503	140374503	Missense_Mutation	SNV	G	T	T	ADCK2	c.1026G>T	P.K342N
SH_131	7	142571345	142571345	Missense_Mutation	SNV	G	T	T	TRPV6	c.1764C>A	P.N588K
SH_131	7	143979885	143979885	Splice_Site	SNV	T	A	A	ARHGGEF34P	n.2250-2A>T	
SH_131	7	147815235	147815235	Frame_Shift_Del	INDEL	C	-	-	CNTNAP2	c.2411delC	P.P804fs
SH_131	7	150831646	150831654	Frame_Shift_Del	INDEL	GGGGGCACA	-	-	AGAP3	1495+1delGGG	P.G497fs
SH_131	7	2617917	2617917	Silent	SNV	G	T	T	IQCE	c.507G>T	P.P169T
SH_131	7	2629736	2629736	Nonsense_Mutation	SNV	A	T	T	IQCE	c.1240A>T	P.R414*
SH_131	7	27148292	27148292	Nonsense_Mutation	SNV	T	A	A	HOXA3	c.574A>T	P.K192*
SH_131	7	38457432	38457432	Missense_Mutation	SNV	T	A	A	AMPH	c.1391A>T	P.E464V
SH_131	7	42005003	42005003	Missense_Mutation	SNV	T	A	A	GLI3	c.3668A>T	P.Y1223F
SH_131	7	44279206	44279206	Missense_Mutation	SNV	T	A	A	CAMK2B	c.1003A>T	P.M335L
SH_131	7	45115444	45115444	Nonsense_Mutation	SNV	A	T	T	CCM2	c.1186A>T	P.K396*
SH_131	7	6022520	6022520	Silent	SNV	C	A	A	PMS2	c.2109G>T	P.T703T
SH_131	7	6565851	6565851	Splice_Site	SNV	T	A	A	GRID2IP	c.919+4A>T	
SH_131	7	97822611	97822611	Missense_Mutation	SNV	A	T	T	LMTK2	c.2834A>T	P.E945V
SH_131	7	97863051	97863051	Missense_Mutation	SNV	A	A	A	TECPR1	c.1354A>T	P.R452W
SH_131	8	100973434	100973434	Splice_Site	SNV	A	G	G	RG522	c.*46-10T>C	
SH_131	8	116616395	116616395	Nonsense_Mutation	SNV	T	A	A	TRPS1	c.1774A>T	P.R592*
SH_131	8	119936895	119936895	Silent	SNV	T	A	A	TNFRSF11B	c.924A>T	P.G308G
SH_131	8	2832079	2832079	Silent	SNV	G	C	C	CSMD1	c.8634C>G	P.G2878G
SH_131	8	57228583	57228583	Silent	SNV	T	A	A	SDR16C5	c.324A>T	P.V108V
SH_131	9	138660691	138660691	Missense_Mutation	SNV	T	A	A	KCNT1	c.1283T>A	P.L428Q
SH_131	X	110951488	110951488	Missense_Mutation	SNV	A	T	T	ALG13	c.617A>T	P.K206I
SH_131	X	49088392	49088392	Splice_Site	SNV	A	T	T	CACNA1F	c.26-3T>A	
SH_131	X	70341616	70341616	Missense_Mutation	SNV	A	T	T	MED12	c.1051A>T	P.M351L
SH_131	Y	14832516	14832516	Splice_Site	SNV	A	T	T	USP9Y	c.97-6A>T	
SH_132	1	247836117	247836117	Missense_Mutation	SNV	G	A	A	OR13G1	c.227C>T	P.P76L
SH_132	1	248487170	248487170	Missense_Mutation	SNV	C	T	T	OR2M7	c.701G>A	P.R234H
SH_132	1	33960027	33960027	Missense_Mutation	SNV	A	A	A	ZSCAN20	c.2083G>A	P.E695K
SH_132	1	92508402	92508402	Nonsense_Mutation	SNV	A	T	T	EPHX4	c.340A>T	P.R114*
SH_132	10	125804227	125804227	Missense_Mutation	SNV	C	A	A	CHST15	c.755G>T	P.C252F
SH_132	11	3060460	3060460	Silent	SNV	C	T	T	CARS	c.615G>A	P.A205A
SH_132	11	89450816	89450816	Missense_Mutation	SNV	C	G	G	TRIM77	c.1129C>G	P.L377V
SH_132	12	29608179	29608179	Splice_Site	SNV	T	A	A	OVCH1	c.2437+3A>T	
SH_132	12	51127954	51127954	Missense_Mutation	SNV	G	A	A	DJP28	c.4018G>A	P.D1340N
SH_132	16	87637894	87637911	Missense_Mutation	INDEL	TCGTGCTGCTG	-	-	HPH3	delCTGCTGCTGCTG	A152 A157del
SH_132	17	53068211	53068211	Missense_Mutation	SNV	A	G	G	STXBP4	c.73A>G	P.I25V
SH_132	17	76117181	76117181	Missense_Mutation	SNV	T	C	C	TM6C	c.1448A>G	P.N483S
SH_132	19	39125730	39125730	Missense_Mutation	SNV	G	C	C	EIF3K	c.519G>C	P.P173N
SH_132	2	207407998	207407998	Silent	SNV	C	G	G	ADAM23	c.678C>G	P.T226T
SH_132	2	209113113	209113113	Missense_Mutation	SNV	G	A	A	IDH1	c.394C>T	P.R132C
SH_132	3	119222460	119222460	Missense_Mutation	SNV	A	G	G	TIMMDC1	c.442A>G	P.I148V
SH_132	3	124527879	124527879	Missense_Mutation	SNV	A	G	G	ITGB5	c.1253T>C	P.I418T
SH_132	3	183994711	183994711	Missense_Mutation	SNV	T	C	C	ECE2	c.71T>C	P.L24S
SH_132	6	150005276	150005276	Nonsense_Mutation	SNV	G	A	A	LATS1	c.949C>T	P.Q317*
SH_132	7	2565091	2565091	Missense_Mutation	SNV	G	T	T	LFNG	c.625G>T	P.A209S
SH_132	X	148062316	148062316	Missense_Mutation	SNV	G	A	A	AF2	c.3514G>A	P.G1172R
SH_132	X	3238828	3238828	Missense_Mutation	SNV	A	T	T	MXRA5	c.4898T>A	P.F1633Y
SH_133	1	152187174	152187174	Missense_Mutation	SNV	G	T	T	HRNR	c.6931C>A	P.H2311N

SH_133	1	160192555	160192555	Missense_Mutation	SNV	G	C	C	DCAF8	c.1326C>G	P.F442L
SH_133	1	173526502	173526502	Nonsense_Mutation	SNV	G	A	A	SLC9C2	c.1192C>T	P.R398*
SH_133	1	216850804	216850804	Missense_Mutation	SNV	C	G	G	ESRRG	c.17G>C	P.R6P
SH_133	1	248185835	248185835	Missense_Mutation	SNV	T	A	A	OR2L5	c.586T>A	P.Y196N
SH_133	1	248487703	248487703	Missense_Mutation	SNV	G	T	T	OR2M7	c.168C>A	P.H56Q
SH_133	1	26230211	26230211	Missense_Mutation	SNV	G	A	A	STMN1	c.107C>T	P.P36L
SH_133	1	29606044	29606044	Missense_Mutation	SNV	G	A	A	PTPRU	c.1640G>A	P.R547H
SH_133	1	39823347	39823347	Missense_Mutation	SNV	A	G	G	MACF1	c.5539A>G	P.S1847G
SH_133	1	42049239	42049239	Silent	SNV	G	A	A	HIVEP3	c.1230C>T	P.N410N
SH_133	1	49193587	49193587	Nonsense_Mutation	SNV	G	A	A	BEND5	c.730C>T	P.R244*
SH_133	1	55559732	55559732	Missense_Mutation	SNV	G	A	A	USP24	c.6232C>T	P.P2078S
SH_133	1	874822	874822	Missense_Mutation	SNV	C	A	A	SAMD11	c.688C>A	P.H230N
SH_133	1	91182581	91182581	Missense_Mutation	SNV	C	T	T	BARHL2	c.172G>A	P.V58I
SH_133	1	92944306	92944306	Missense_Mutation	SNV	C	T	T	GFI1	c.929G>A	P.R310Q
SH_133	10	129536928	129536928	Missense_Mutation	SNV	C	A	A	FOXI2	c.656C>A	P.A219E
SH_133	10	50594558	50594558	Silent	SNV	G	A	A	DRGX	c.492C>T	P.Y164Y
SH_133	10	64136198	64136198	Silent	SNV	G	A	A	ZNF365	c.246G>A	P.P82P
SH_133	10	72513565	72513565	Silent	SNV	G	A	A	ADAMTS14	c.2739G>A	P.T913T
SH_133	11	124489462	124489462	Missense_Mutation	SNV	G	C	C	PANX3	c.810G>C	P.Q270H
SH_133	11	124495747	124495747	Missense_Mutation	SNV	G	T	T	TBRG1	c.402G>T	P.K134N
SH_133	11	1977498	1977498	Missense_Mutation	SNV	A	G	G	MRPL23	c.310A>G	P.T104A
SH_133	11	33565454	33565454	Missense_Mutation	SNV	G	T	T	KIAA1549L	c.1454G>T	P.S485I
SH_133	11	46800054	46800054	Silent	SNV	G	A	A	CKAP5	c.2529C>T	P.D843D
SH_133	11	755975	755975	Missense_Mutation	SNV	C	T	T	TALDO1	c.194C>T	P.A65V
SH_133	12	109637326	109637326	Missense_Mutation	SNV	T	A	A	ACACB	c.2747T>A	P.V916D
SH_133	12	132837669	132837669	Missense_Mutation	SNV	C	T	T	GALNT9	c.626G>A	P.R209Q
SH_133	12	18234370	18234370	Nonsense_Mutation	SNV	G	A	A	RERGL	c.370C>T	P.R124*
SH_133	12	25398285	25398285	Missense_Mutation	SNV	C	A	A	KRAS	c.34G>T	P.G12C
SH_133	12	27126968	27126968	Missense_Mutation	SNV	C	T	T	TM75F3	c.1643G>A	P.R548Q
SH_133	12	56481627	56481627	Missense_Mutation	SNV	C	A	A	ERBB3	c.662C>A	P.P221H
SH_133	12	81647354	81647354	Nonsense_Mutation	SNV	C	T	T	ACSS3	c.1900C>T	P.R634*
SH_133	12	85460577	85460577	Missense_Mutation	SNV	G	T	T	LRRIQ1	c.2596G>T	P.V866F
SH_133	13	101890116	101890116	Missense_Mutation	SNV	G	A	A	NALCN	c.1424C>T	P.T475M
SH_133	13	103400936	103400936	Missense_Mutation	SNV	G	T	T	CCDC168	c.2111C>A	P.S704Y
SH_133	13	49281758	49281758	Missense_Mutation	SNV	G	A	A	CYSLTR2	c.805G>A	P.V269I
SH_133	13	52523858	52523858	Silent	SNV	C	T	T	ATP7B	c.2805G>A	P.T935T
SH_133	14	19563432	19563432	Nonsense_Mutation	SNV	G	T	T	POTEG	c.946G>T	P.G316*
SH_133	14	65009472	65009472	Silent	SNV	C	T	T	HSPA2	c.1905C>T	P.I635I
SH_133	15	45398328	45398328	Missense_Mutation	SNV	C	T	T	DUOX2	c.2143G>A	P.D715N
SH_133	15	75975220	75975220	Nonsense_Mutation	SNV	G	A	A	CSPG4	c.4612C>T	P.Q1538*
SH_133	15	79265694	79265694	Missense_Mutation	SNV	G	A	A	RASGRF1	c.3563C>T	P.T1188M
SH_133	15	86259119	86259119	Silent	SNV	G	A	A	AKAP13	c.1563G>A	P.S521S
SH_133	15	88576096	88576096	Missense_Mutation	SNV	G	A	A	NTRK3	c.1577C>T	P.P526L
SH_133	16	32264962	32264962	Silent	SNV	T	C	C	TP53TG3D	c.288T>C	P.H96H
SH_133	16	75665747	75665747	Frame_Shift_Del	INDEL	C	-	-	KARS	c.1006delG	P.V336fs
SH_133	17	10543537	10543537	Missense_Mutation	SNV	G	A	A	MYH3	c.2458C>T	P.R820C
SH_133	17	10549104	10549104	Missense_Mutation	SNV	G	A	A	MYH3	c.1061C>T	P.T354M
SH_133	17	33267585	33267585	Missense_Mutation	SNV	C	T	T	CCT6B	c.830G>A	P.R277H
SH_133	17	73723903	73723903	Silent	SNV	C	T	T	ITGB4	c.436C>T	P.L146L
SH_133	18	48591919	48591919	Missense_Mutation	SNV	G	A	A	SMAD4	c.1082G>A	P.R361H
SH_133	18	59166595	59166595	Silent	SNV	G	A	A	CDH20	c.423G>A	P.T141T
SH_133	19	11327936	11327936	Missense_Mutation	SNV	G	A	A	DOCK6	c.3682C>T	P.R1228W
SH_133	19	18707544	18707544	Silent	SNV	G	T	T	CRLF1	c.912C>A	P.G304G
SH_133	19	2339972	2339972	Splice_Site	SNV	G	A	A	SPPL2B	c.742+7G>A	
SH_133	19	31768611	31768611	Silent	SNV	C	T	T	TSH23	c.2088G>A	P.K696K
SH_133	19	37382567	37382567	Missense_Mutation	SNV	C	A	A	ZNF829	c.1126G>T	P.D376Y
SH_133	19	3964908	3964908	Silent	SNV	G	A	A	DAPK3	c.144C>T	P.R48R
SH_133	19	46733629	46733629	Missense_Mutation	SNV	G	A	A	IGFL1	c.178G>A	P.V60I
SH_133	19	47228739	47228739	Missense_Mutation	SNV	G	A	A	STRN4	c.1436C>T	P.T479M
SH_133	19	47844845	47844845	Silent	SNV	C	T	T	CSAR2	c.789C>T	P.S263S
SH_133	19	48305953	48305953	Silent	SNV	G	T	T	TPRX1	c.315C>A	P.G105G
SH_133	19	50243064	50243064	Frame_Shift_Del	INDEL	G	-	-	TSKS	c.1748delC	P.P583fs
SH_133	19	50476388	50476388	Splice_Site	SNV	C	T	T	SIGLEC16	n.1551+9C>T	
SH_133	19	52942411	52942411	Silent	SNV	G	A	A	ZNF534	c.1698G>A	P.A566A
SH_133	19	5455995	5455995	Missense_Mutation	SNV	G	A	A	ZNRF4	c.493G>A	P.D165N
SH_133	19	55753733	55753733	Splice_Site	SNV	C	T	T	PPP6R1	c.731+11G>A	
SH_133	19	57286598	57286598	Missense_Mutation	SNV	G	A	A	ZIM2	c.1042C>T	P.R348W
SH_133	19	9062407	9062407	Missense_Mutation	SNV	G	T	T	MUC16	c.25039C>A	P.P8347T
SH_133	2	136873083	136873083	Missense_Mutation	SNV	C	T	T	CXCR4	c.427G>A	P.V143I
SH_133	2	160043530	160043530	Missense_Mutation	SNV	G	A	A	TANC1	c.2713G>A	P.V905M
SH_133	2	166895977	166895977	Missense_Mutation	SNV	G	T	T	SCN1A	c.2545C>A	P.L849I
SH_133	2	166898844	166898844	Nonsense_Mutation	SNV	G	A	A	SCN1A	c.2134C>T	P.R712*
SH_133	2	179260240	179260240	Missense_Mutation	SNV	G	A	A	OSBP16	c.2834G>A	P.R945Q
SH_133	2	179522883	179522883	Splice_Site	SNV	C	A	A	TTN	c.37713G>T	P.V12571V
SH_133	2	189904068	189904068	Silent	SNV	G	A	A	COL5A2	c.3855C>T	P.P1285P
SH_133	2	200137047	200137047	Missense_Mutation	SNV	C	T	T	SATB2	c.2089G>A	P.E697K
SH_133	2	210642204	210642204	Missense_Mutation	SNV	G	A	A	UNC80	c.521G>A	P.R174Q
SH_133	2	220088899	220088899	Silent	SNV	G	A	A	ATG9A	c.1194C>T	P.D398D
SH_133	2	228769723	228769723	Missense_Mutation	SNV	G	A	A	DAW1	c.682G>A	P.V228I
SH_133	2	27601343	27601343	Nonsense_Mutation	SNV	G	A	A	ZNF513	c.604C>T	P.R202*
SH_133	2	43452831	43452831	Frame_Shift_Ins	INDEL	-	C	C	ZFP36L2	c.111dupG	P.T38fs
SH_133	2	84777081	84777081	Missense_Mutation	SNV	C	T	T	DNAH6	c.1385C>T	P.S462L
SH_133	2	98273619	98273619	Missense_Mutation	SNV	T	A	A	ACTR1B	c.1024A>T	P.I342F
SH_133	22	43603587	43603587	Missense_Mutation	SNV	G	A	A	SCUBE1	c.2767C>T	P.R923C
SH_133	22	43831108	43831108	Missense_Mutation	SNV	G	A	A	MPPED1	c.379G>A	P.E127K
SH_133	22	43933407	43933407	Missense_Mutation	SNV	C	T	T	EFCAB6	c.3898G>A	P.V1300M
SH_133	3	12224924	12224924	Missense_Mutation	SNV	A	C	C	SYN2	c.1418A>C	P.Q473P
SH_133	3	148894115	148894115	Missense_Mutation	SNV	T	G	G	CP	c.3103A>C	P.I1035L
SH_133	3	178921553	178921553	Missense_Mutation	SNV	T	A	A	PIK3CA	c.1035T>A	P.N345K
SH_133	3	36763045	36763045	Missense_Mutation	SNV	C	T	T	DCLK3	c.1558G>A	P.V520I
SH_133	3	49698778	49698778	Missense_Mutation	SNV	C	A	A	BSN	c.9500C>A	P.P3167H
SH_133	3	49831352	49831352	Missense_Mutation	SNV	G	A	A	CDHR4	c.1367C>T	P.A456V
SH_133	3	67411060	67411060	Frame_Shift_Del	INDEL	A	-	-	SCULG2	c.1316delT	P.L439fs
SH_133	4	144545333	144545333	Missense_Mutation	SNV	G	T	T	FREM3	c.5581C>A	P.L1861M
SH_133	4	183267884	183267884	Missense_Mutation	SNV	C	A	A	TENM3	c.313C>A	P.L105I
SH_133	4	187554989	187554989	Splice_Site	SNV	A	G	G	FAT1	c.4184-12T>C	
SH_133	4	40099049	40099049	Missense_Mutation	SNV	G	A	A	N4BP2	c.89G>A	P.R30H
SH_133	4	57522119	57522119	Silent	SNV	G	A	A	HOPX	c.48C>T	P.I16I

SH_133	4	77324344	77324344	Missense_Mutation	SNV	C	A	A	CCDC158	c.17G>T	P.W6L
SH_133	5	112175752	112175752	Frame_Shift_Del	INDEL	T	-	-	APC	c.4463delT	P.L1488fs
SH_133	5	118969858	118969858	Missense_Mutation	SNV	G	A	A	FAM170A	c.274G>A	P.V92M
SH_133	5	140215137	140215137	Missense_Mutation	SNV	C	T	T	PCDHA7	c.1169C>T	P.T390M
SH_133	5	140431404	140431404	Missense_Mutation	SNV	T	C	C	PCDHB1	c.349T>C	P.F117L
SH_133	5	140764210	140764210	Missense_Mutation	SNV	G	A	A	PCDHGA7	c.1744G>A	P.A582T
SH_133	5	140773552	140773552	Missense_Mutation	SNV	C	T	T	PCDHGA8	c.1172C>T	P.P391L
SH_133	5	33577076	33577076	Missense_Mutation	SNV	G	C	C	ADAMTS12	c.3055C>G	P.L1019V
SH_133	5	34796132	34796132	Missense_Mutation	SNV	G	A	A	RAI14	c.256G>C	P.G86R
SH_133	6	152674520	152674520	Nonsense_Mutation	SNV	C	A	A	SYNE1	c.11086G>T	P.E369E*
SH_133	6	26123757	26123757	Frame_Shift_Ins	INDEL	-	G	G	HIST1H2BC	c.375dupC	P.K126fs
SH_133	6	4943906	4943906	Nonsense_Mutation	SNV	G	A	A	CDYL	c.852G>A	P.W284*
SH_133	6	83905381	83905381	Missense_Mutation	SNV	G	A	A	RWDD2A	c.44G>A	P.R15Q
SH_133	6	88853781	88853781	Nonsense_Mutation	SNV	G	A	A	CNR1	c.1213C>T	P.R405*
SH_133	7	126173278	126173278	Missense_Mutation	SNV	G	T	T	GRM8	c.2158C>A	P.H720N
SH_133	7	140048419	140048419	Splice_Site	SNV	G	T	T	SLC37A3	c.1024+7C>A	
SH_133	7	156752835	156752835	Silent	SNV	C	T	T	NOM1	c.1599C>T	P.S533S
SH_133	7	28848874	28848874	Missense_Mutation	SNV	G	A	A	CREB5	c.680G>A	P.R227Q
SH_133	7	30962227	30962227	Missense_Mutation	SNV	G	A	A	AQP1	c.598G>A	P.A200T
SH_133	7	69064885	69064885	Silent	SNV	G	A	A	AUTS2	c.246G>C	P.S82S
SH_133	7	73752935	73752935	Silent	SNV	C	T	T	CLIP2	c.279C>T	P.G93G
SH_133	7	75694258	75694258	Missense_Mutation	SNV	C	T	T	MDH2	c.746C>T	P.P249L
SH_133	7	99802682	99802682	Silent	SNV	G	A	A	STAG3	c.3006G>A	P.Q1002Q
SH_133	8	104928737	104928737	Missense_Mutation	SNV	G	A	A	RIMS2	c.2008G>A	P.V670I
SH_133	8	125080023	125080023	Missense_Mutation	SNV	C	A	A	FER1L6	c.3694C>A	P.P1232T
SH_133	8	134034311	134034311	Missense_Mutation	SNV	G	A	A	TG	c.6952G>A	P.D2318N
SH_133	8	24811765	24811765	Nonsense_Mutation	SNV	G	A	A	NEFL	c.1099C>T	P.R367*
SH_133	8	32614052	32614052	Splice_Site	SNV	G	A	A	NRG1	c.921+5G>A	
SH_133	8	41122786	41122786	Missense_Mutation	SNV	G	A	A	SFRP1	c.845C>T	P.T282M
SH_133	8	66659975	66659975	Missense_Mutation	SNV	C	T	T	PDE7A	c.347G>A	P.R116Q
SH_133	9	108297336	108297336	Splice_Site	SNV	G	C	C	FSD1L	c.1127-12G>C	
SH_133	X	138643671	138643671	Splice_Site	SNV	T	A	A	F9	c.839-12T>A	
SH_133	X	140785800	140785800	Missense_Mutation	SNV	G	T	T	SPANXC	c.116C>A	P.P39Q
SH_134	1	111957781	111957781	Missense_Mutation	SNV	C	T	T	OVGP1	c.1342G>A	P.G448S
SH_134	1	32381586	32381586	Splice_Site	SNV	T	C	C	PTPA42	c.99A>G	P.E33E
SH_134	1	3784569	3784569	Silent	SNV	C	G	G	DFFB	c.534C>G	P.G178G
SH_134	10	102739956	102739958	Missense_Mutation	INDEL	GTT	-	-	SEMA4G	1207_1209delT	P.L403del
SH_134	10	43606853	43606853	Missense_Mutation	SNV	A	T	T	RET	c.1462A>T	P.T488S
SH_134	10	89711966	89711966	Missense_Mutation	SNV	T	C	C	PTEN	c.584T>C	P.F195S
SH_134	11	57886041	57886041	Silent	SNV	T	C	C	OR9I1	c.876A>G	P.L292L
SH_134	11	66033568	66033568	Missense_Mutation	SNV	G	A	A	KLC2	c.1376G>A	P.G459D
SH_134	11	71208554	71208554	Missense_Mutation	SNV	A	G	G	NADSYN1	c.1790A>G	P.E597G
SH_134	11	78177001	78177001	Missense_Mutation	SNV	A	T	T	NARS2	c.404T>A	P.I135K
SH_134	12	108985455	108985455	Silent	SNV	C	T	T	TMEM119	c.705G>A	P.P235P
SH_134	12	25398284	25398284	Missense_Mutation	SNV	C	G	G	KRAS	c.35G>C	P.G12A
SH_134	12	58014749	58014749	Silent	SNV	C	T	T	SLC26A10	c.264C>T	P.G88G
SH_134	12	72022795	72022795	Missense_Mutation	SNV	T	G	G	ZFC3H1	c.3849A>C	P.K1283N
SH_134	12	80770982	80770982	Splice_Site	SNV	T	A	A	OTOGL	c.6834T>A	P.P2278P
SH_134	13	24871809	24871809	Frame_Shift_Ins	INDEL	-	T	T	SPATA13	c.3519_3520ins	P.K1174fs
SH_134	13	96438330	96438330	Splice_Site	SNV	A	T	T	DNAJC3	c.1208+5A>T	
SH_134	14	75330206	75330206	Missense_Mutation	SNV	G	A	A	PROX2	c.332C>T	P.P111L
SH_134	15	32460267	32460267	Missense_Mutation	SNV	G	A	A	CHRNA7	c.1117G>A	P.A373T
SH_134	15	33955053	33955053	Silent	SNV	G	C	C	RYR3	c.5322G>C	P.V1774V
SH_134	15	43512935	43512935	Missense_Mutation	SNV	C	A	A	EPB42	c.89G>T	P.S30I
SH_134	15	52506866	52506866	Missense_Mutation	SNV	T	C	C	MYO5C	c.3976A>G	P.M1326V
SH_134	15	90125922	90125922	Nonsense_Mutation	SNV	G	A	A	TICRR	c.660G>A	P.W220*
SH_134	15	90347207	90347207	Missense_Mutation	SNV	C	A	A	ANPEP	c.1206G>T	P.E402D
SH_134	16	20944736	20944736	Frame_Shift_Del	INDEL	T	-	-	DNAH3	c.12091delA	P.T4031fs
SH_134	16	28499036	28499036	Silent	SNV	G	C	C	CLN3	c.321C>G	P.P107P
SH_134	16	4458241	4458241	Missense_Mutation	SNV	C	T	T	CORO7	c.244G>A	P.D82N
SH_134	16	731334	731334	Silent	SNV	C	T	T	STUB1	c.126C>T	P.I42L
SH_134	17	17928015	17928015	Nonsense_Mutation	SNV	G	C	C	ATPAF2	c.426C>G	P.Y142*
SH_134	17	2604454	2604454	Silent	SNV	G	A	A	CLUH	c.891C>T	P.F297F
SH_134	17	40950129	40950129	Missense_Mutation	SNV	C	T	T	COA3	c.271G>A	P.E91K
SH_134	17	7574017	7574017	Missense_Mutation	SNV	C	A	A	TP53	c.1010G>T	P.R337L
SH_134	17	7577547	7577547	Missense_Mutation	SNV	C	T	T	TP53	c.734G>A	P.G245D
SH_134	19	17756595	17756595	Missense_Mutation	SNV	G	C	C	UNC13A	c.2244C>G	P.D748E
SH_134	19	35758719	35758719	Splice_Site	SNV	C	A	A	LSR	c.1855-8C>A	
SH_134	19	53619609	53619609	Nonsense_Mutation	SNV	G	C	C	ZNF415	c.93C>G	P.Y31*
SH_134	19	54802050	54802050	Missense_Mutation	SNV	C	T	T	LILRA3	c.946G>A	P.A316T
SH_134	19	56009241	56009241	Splice_Site	SNV	C	T	T	SSC5D	c.1388-6C>T	
SH_134	19	984437	984437	Silent	SNV	C	T	T	WDR18	c.84C>T	P.G28G
SH_134	2	118771520	118771520	Splice_Site	SNV	G	A	A	CCDC93	c.42+10C>T	
SH_134	2	131130445	131130445	Splice_Site	SNV	G	A	A	PTPN18	c.920-1G>A	
SH_134	20	40877391	40877391	Missense_Mutation	SNV	C	T	T	PTPRT	c.2305G>A	P.V769M
SH_134	5	140755446	140755446	Missense_Mutation	SNV	G	T	T	PCDHGA6	c.1796G>C	P.G599V
SH_134	5	33576822	33576822	Missense_Mutation	SNV	C	G	G	ADAMTS12	c.3054G>C	P.E1018D
SH_134	6	26205128	26205128	Missense_Mutation	SNV	G	A	A	HIST1H4E	c.256G>A	P.D86N
SH_134	6	30708545	30708545	Missense_Mutation	SNV	C	T	T	FLOT1	c.241G>A	P.E81K
SH_134	6	46659271	46659271	Missense_Mutation	SNV	A	G	G	TDRD6	c.3406A>G	P.T1136A
SH_134	6	73332234	73332234	Missense_Mutation	SNV	T	C	C	KCNQ5	c.317T>C	P.V106A
SH_134	7	131913188	131913188	Missense_Mutation	SNV	G	A	A	PLXNA4	c.1645C>T	P.R549C
SH_134	7	142612744	142612744	Splice_Site	SNV	T	A	A	TRPV5	c.1123-6A>T	
SH_134	7	23293812	23293812	Missense_Mutation	SNV	C	G	G	GNPMB	c.248C>G	P.T83S
SH_134	9	104171708	104171708	Missense_Mutation	SNV	C	T	T	ZNF189	c.1616C>T	P.S539L
SH_134	9	107599377	107599377	Missense_Mutation	SNV	C	T	T	ABCA1	c.1195G>A	P.V399M
SH_134	X	100747980	100747980	Silent	SNV	G	A	A	ARMCX4	c.4404G>A	P.Q1468Q
SH_134	X	114400852	114400852	Missense_Mutation	SNV	C	A	A	LRCH2	c.1052G>T	P.S351I
SH_134	X	129299554	129299554	Missense_Mutation	SNV	C	T	T	AIFM1	c.77G>A	P.R26Q
SH_134	X	51151318	51151318	Missense_Mutation	SNV	C	T	T	Cxorfe7	c.1450C>T	P.P484S
SH_134	X	69366580	69366580	Missense_Mutation	SNV	C	T	T	IGBP1	c.580C>T	P.L194F
SH_135	1	118491040	118491040	Nonsense_Mutation	SNV	C	T	T	WDR3	c.1435C>T	P.Q479*
SH_135	1	11883785	11883785	Missense_Mutation	SNV	A	G	G	CLCN6	c.409A>G	P.L137V
SH_135	1	15264362	15264362	Silent	SNV	G	A	A	PKLR	c.876C>T	P.S292S
SH_135	1	156018394	156018394	Missense_Mutation	SNV	G	T	T	UBQLN4	c.738C>A	P.D246E
SH_135	1	159002369	159002369	Frame_Shift_Del	INDEL	A	-	-	IFI16	c.1049delA	P.Q350fs
SH_135	1	176671803	176671803	Silent	SNV	G	T	T	PAPPA2	c.3297G>T	P.L1099L
SH_135	1	186120313	186120313	Splice_Site	INDEL	T	-	-	HMCN1	c.14609-11delT	

SH_135	1	196303097	196303097	Missense_Mutation	SNV	C	G	G	KCNT2	c.1877G>C	P.R626T
SH_135	1	196759303	196759303	Missense_Mutation	SNV	T	A	A	CFHR3	c.559T>A	P.S187T
SH_135	1	206328960	206328960	Splice_Site	SNV	A	C	C	CTSE	c.561-2A>C	
SH_135	1	21900187	21900187	Missense_Mutation	SNV	G	A	A	ALPL	c.892G>A	P.E298K
SH_135	1	223976872	223976872	Missense_Mutation	SNV	G	C	C	TP53BP2	c.3001C>G	P.P1001A
SH_135	1	231830517	231830517	Missense_Mutation	SNV	G	C	C	DISC1	c.1013G>C	P.R338P
SH_135	1	237774219	237774219	Missense_Mutation	SNV	G	A	A	RYR2	c.4841G>A	P.R1614H
SH_135	1	247492768	247492768	Missense_Mutation	SNV	G	T	T	ZNF496	c.113C>A	P.P38H
SH_135	1	47610279	47610279	Missense_Mutation	SNV	A	G	G	CYP4A22	c.955A>G	P.M319V
SH_135	1	52264057	52264057	Missense_Mutation	SNV	T	C	C	NRDC	c.2468A>G	P.Y823C
SH_135	1	54607096	54607096	Silent	SNV	G	A	A	CDCP2	c.438C>T	P.G146G
SH_135	1	76384798	76384798	Missense_Mutation	SNV	C	G	G	ASB17	c.727G>C	P.D243H
SH_135	1	7731083	7731083	Missense_Mutation	SNV	G	A	A	CAMTA1	c.2765G>A	P.R922H
SH_135	1	7731084	7731084	Silent	SNV	C	A	A	CAMTA1	c.2766C>A	P.R922R
SH_135	1	86622024	86622024	Missense_Mutation	SNV	G	C	C	COL24A1	c.56C>G	P.T19R
SH_135	10	6521061	6521061	Missense_Mutation	SNV	C	G	G	PRKQ	c.1246G>C	P.Y416L
SH_135	11	102733870	102733870	Silent	SNV	G	A	A	MMP12	c.1371C>T	P.I457I
SH_135	11	113264223	113264223	Missense_Mutation	SNV	T	A	A	ANKK1	c.206T>A	P.I69N
SH_135	11	118955769	118955769	Missense_Mutation	SNV	C	T	T	HMB5	c.26C>T	P.A9V
SH_135	11	17653705	17653705	Frame_Shift_Del	INDEL	T	-	-	OTOG	c.7040delIT	P.L2347fs
SH_135	11	20805362	20805362	Silent	SNV	A	T	T	NELL1	c.405A>T	P.R135R
SH_135	11	71698065	71698065	Missense_Mutation	SNV	G	C	C	RNF121	c.318G>C	P.W106C
SH_135	11	96092240	96092240	Missense_Mutation	SNV	T	C	C	CCDC82	c.1483A>G	P.T495A
SH_135	12	16035656	16035656	Silent	SNV	G	A	A	STRAP	c.15G>A	P.Q5Q
SH_135	12	25173843	25173843	Splice_Site	SNV	T	A	A	LOC645177	c.1305+2T>A	
SH_135	12	2742879	2742882	Splice_Site	INDEL	GTGA	-	-	CACNA1C	2+3_3972+6delGAGT	
SH_135	12	6692459	6692459	Missense_Mutation	SNV	T	C	C	CHD4	c.3965A>G	P.Y1322C
SH_135	12	97151272	97151272	Splice_Site	SNV	G	T	T	CFAP54	c.7947-1G>T	
SH_135	12	99640648	99640648	Splice_Site	SNV	A	G	G	ANKS1B	c.1757-6T>C	
SH_135	13	114088137	114088137	Missense_Mutation	SNV	C	T	T	ADPRHL1	c.425G>A	P.R142Q
SH_135	13	114782808	114782808	Nonsense_Mutation	SNV	G	A	A	RASA3	c.1015C>T	P.R339*
SH_135	13	28794407	28794407	Nonsense_Mutation	SNV	G	T	T	PAN3	c.892G>T	P.G298*
SH_135	13	38266351	38266351	Missense_Mutation	SNV	A	T	T	TRPC4	c.1019T>A	P.F340Y
SH_135	13	99948153	99948153	Missense_Mutation	SNV	C	T	T	GPR183	c.247G>A	P.A83T
SH_135	14	20924154	20924154	Frame_Shift_Ins	INDEL	-	C	C	APEX1	c.146dupC	P.D50fs
SH_135	14	21681156	21681156	Silent	SNV	A	C	C	HNRNPC	c.525T>G	P.S175S
SH_135	14	37737996	37737996	Nonsense_Mutation	SNV	A	T	T	MIPOL1	c.385A>T	P.K129*
SH_135	14	74988750	74988750	Splice_Site	SNV	G	A	A	LTBP2	c.2660-8C>T	
SH_135	14	81950704	81950704	Missense_Mutation	SNV	A	C	C	SEL1L	c.1911T>G	P.H637Q
SH_135	15	25220642	25220642	Missense_Mutation	SNV	G	T	T	SNRPN	c.141G>T	P.E47D
SH_135	15	41071483	41071483	Missense_Mutation	SNV	G	A	A	DNAJC17	c.233C>T	P.A78V
SH_135	15	45427385	45427385	Missense_Mutation	SNV	G	A	A	DUOX1	c.391G>A	P.D131N
SH_135	16	11940401	11940401	Missense_Mutation	SNV	T	C	C	RS1L1D1	c.592A>G	P.I198V
SH_135	16	29997924	29997924	Silent	SNV	A	C	C	TAOK2	c.2331A>C	P.S777S
SH_135	16	68011904	68011904	Silent	SNV	C	T	T	DPEP3	c.768G>A	P.E256E
SH_135	16	89764086	89764086	Frame_Shift_Ins	INDEL	-	AG	AG	SPATA2L	c.930_931insCT	P.S311fs
SH_135	16	89764088	89764088	Missense_Mutation	SNV	A	C	C	SPATA2L	c.929T>G	P.L310R
SH_135	17	12917796	12917796	Silent	SNV	T	G	G	ELAC2	c.450A>C	P.A150A
SH_135	17	19286158	19286158	Silent	SNV	C	T	T	MAPK7	c.2196C>T	P.G732G
SH_135	17	19611607	19611607	Splice_Site	SNV	G	A	A	SLC47A2	c.629+8C>T	
SH_135	17	34746986	34746986	Silent	SNV	C	A	A	TBC1D3F	c.1098G>T	P.G366G
SH_135	17	38289323	38289323	Missense_Mutation	SNV	G	A	A	MSL1	c.728G>A	P.R243Q
SH_135	17	65732794	65732794	Missense_Mutation	SNV	T	C	C	NOL11	c.521T>C	P.V174A
SH_135	17	73664598	73664598	Missense_Mutation	SNV	G	C	C	SAP30BP	c.109G>C	P.E37Q
SH_135	17	7577018	7577018	Splice_Site	SNV	C	A	A	TP53	c.919+1G>T	
SH_135	17	76411040	76411040	Missense_Mutation	SNV	C	G	G	PGS1	c.1483C>G	P.H495D
SH_135	17	7912916	7912916	Splice_Site	SNV	G	A	A	GUCY2D	c.1749+12G>A	
SH_135	18	31709893	31709893	Missense_Mutation	SNV	G	A	A	NOL4	c.356C>T	P.T119M
SH_135	18	48591888	48591888	Missense_Mutation	SNV	G	T	T	SMAD4	c.1051G>T	P.D351Y
SH_135	18	61306469	61306469	Missense_Mutation	SNV	C	A	A	SERPINB4	c.718G>T	P.D240Y
SH_135	18	658196	658196	Missense_Mutation	SNV	G	C	C	TYMSO5	c.52C>G	P.P18A
SH_135	18	9337317	9337317	Silent	SNV	C	G	G	TWSG1	c.90C>G	P.L30L
SH_135	19	10463703	10463703	Missense_Mutation	SNV	G	C	C	TYK2	c.3099C>G	P.N1033K
SH_135	19	11979192	11979192	Missense_Mutation	SNV	A	T	T	ZNF439	c.1308A>T	P.K436N
SH_135	19	14717866	14717866	Missense_Mutation	SNV	C	A	A	CLEC17A	c.956C>A	P.A319D
SH_135	19	35613764	35613764	Missense_Mutation	SNV	G	A	A	FXD3	c.193G>A	P.E65K
SH_135	19	44934469	44934469	Missense_Mutation	SNV	C	G	G	ZNF229	c.469G>C	P.D157H
SH_135	19	50399165	50399165	Silent	SNV	G	A	A	IL4I1	c.225C>T	P.L75L
SH_135	19	50399300	50399300	Silent	SNV	G	A	A	IL4I1	c.90C>T	P.L30L
SH_135	19	57641791	57641791	Missense_Mutation	SNV	T	G	G	USP29	c.1748T>G	P.L583R
SH_135	2	101624549	101624549	Missense_Mutation	SNV	G	A	A	TBC1D8	c.3157C>T	P.P1053S
SH_135	2	102984428	102984428	Missense_Mutation	SNV	C	A	A	IL18R1	c.202C>A	P.L68M
SH_135	2	107460197	107460197	Silent	SNV	C	T	T	ST6GAL2	c.237G>A	P.A79A
SH_135	2	179597289	179597289	Missense_Mutation	SNV	T	G	G	TTN	c.15548A>C	P.K5183T
SH_135	2	187533560	187533560	Silent	SNV	T	C	C	ITGAV	c.2367T>C	P.N789N
SH_135	2	198363515	198363515	Missense_Mutation	SNV	G	A	A	HSPD1	c.58C>T	P.P20S
SH_135	2	242373687	242373687	Missense_Mutation	SNV	C	T	T	FARP2	c.982C>T	P.P328S
SH_135	2	37455310	37455310	Silent	SNV	T	C	C	CEBPZ	c.1026A>G	P.L342L
SH_135	2	63058148	63058148	Splice_Site	SNV	A	C	C	EHBP1	c.495-6A>C	
SH_135	2	63223821	63223821	Missense_Mutation	SNV	C	A	A	EHBP1	c.3131C>A	P.A1044E
SH_135	2	69771687	69771687	Splice_Site	SNV	G	C	C	AAK1	c.283-11C>G	
SH_135	20	35414983	35414983	Missense_Mutation	SNV	G	A	A	SOGA1	c.4891C>T	P.R1631C
SH_135	20	62366761	62366761	Silent	SNV	G	A	A	ZGPAT	c.1242G>A	P.A414A
SH_135	21	27326987	27326987	Missense_Mutation	SNV	C	A	A	APP	c.1604G>T	P.R535L
SH_135	21	31802902	31802902	Nonsense_Mutation	SNV	C	G	G	KRTAP13-4	c.309C>G	P.Y103*
SH_135	21	31971156	31971156	Missense_Mutation	SNV	T	G	G	KRTAP6-2	c.38A>C	P.H13P
SH_135	21	34954302	34954302	Missense_Mutation	SNV	C	T	T	DONSON	c.1106G>A	P.G369D
SH_135	21	45821606	45821606	Silent	SNV	C	G	G	TRPM2	c.2364C>G	P.A788A
SH_135	21	46069666	46069666	Silent	SNV	C	T	T	KRTAP10-11	c.591C>T	P.V197V
SH_135	22	38897182	38897182	Frame_Shift_Ins	INDEL	-	A	A	DDX17	c.390dupT	P.E131fs
SH_135	22	40661931	40661931	Missense_Mutation	SNV	G	T	T	TNRC6B	c.1697G>T	P.G566V
SH_135	22	46658521	46658521	Silent	SNV	C	G	G	PKDREJ	c.699G>C	P.L233L
SH_135	3	101284835	101284835	Nonstop_Mutation	SNV	T	G	G	TRMT10C	c.1210T>G	P.Ter40Aext*?
SH_135	3	122646768	122646768	Missense_Mutation	SNV	A	G	G	SEMA5B	c.719T>C	P.V240A
SH_135	3	123456371	123456371	Missense_Mutation	SNV	G	A	A	MYLK	c.80C>T	P.P27L
SH_135	3	157820626	157820626	Missense_Mutation	SNV	G	C	C	SHOX2	c.396C>G	P.D132E
SH_135	3	165548484	165548484	Missense_Mutation	SNV	T	G	G	BCHC	c.338A>C	P.N131T
SH_135	3	173998882	173998882	Missense_Mutation	SNV	T	C	C	NLG1	c.2261T>C	P.L754P

SH_135	3	184119478	184119478	Splice_Site	SNV	G	C	C	LOC105374250	c.-199+5G>C	
SH_135	3	46728593	46728593	Silent	SNV	T	A	A	ALS2CL	c.414A>T	P.S138S
SH_135	3	47307213	47307213	Splice_Site	SNV	C	G	G	KIF9	c.916+7G>C	
SH_135	3	58092555	58092555	Silent	SNV	C	T	T	FLNB	c.1896C>T	P.Y632Y
SH_135	3	63594966	63594966	Missense_Mutation	SNV	G	C	C	SYNPR	c.574G>C	P.V192L
SH_135	3	63824177	63824177	Splice_Site	SNV	T	A	A	THOC7	c.-19-2A>T	
SH_135	3	7456852	7456852	Splice_Site	SNV	T	A	A	GRM7	c.1174+2T>A	
SH_135	3	77638054	77638054	Missense_Mutation	SNV	A	C	C	ROBO2	c.2593A>C	P.K865Q
SH_135	4	118005950	118005950	Silent	SNV	A	T	T	TRAM1L1	c.600T>A	P.I200I
SH_135	4	15539586	15539586	Missense_Mutation	SNV	C	T	T	CC2D2A	c.1829C>T	P.P610L
SH_135	4	26483689	26483689	Silent	SNV	G	A	A	CKAR	c.858C>T	P.S286S
SH_135	4	68527936	68527936	Missense_Mutation	SNV	T	C	C	UBA6	c.1075A>G	P.T359A
SH_135	4	68703995	68703995	Missense_Mutation	SNV	T	C	C	TMPRSS11D	c.370A>G	P.R124G
SH_135	4	86938433	86938433	Missense_Mutation	SNV	T	A	A	MAPK10	c.1343A>T	P.D448V
SH_135	4	94032012	94032012	Missense_Mutation	SNV	A	T	T	GRID2	c.358A>T	P.M120L
SH_135	5	121786780	121786780	Missense_Mutation	SNV	C	A	A	SNCAIP	c.2238C>A	P.H746Q
SH_135	5	137626366	137626366	Missense_Mutation	SNV	C	T	T	CDC25C	c.826G>A	P.D276N
SH_135	5	1394869	1394869	Missense_Mutation	SNV	C	T	T	SLC6A3	c.1844G>A	P.R615H
SH_135	5	140530319	140530319	Missense_Mutation	SNV	A	G	G	PCDHB6	c.73A>G	P.T25A
SH_135	5	159437658	159437658	Silent	SNV	C	T	T	TTC1	c.123C>T	P.S41S
SH_135	5	38962588	38962588	Missense_Mutation	SNV	T	G	G	RICTOR	c.1667A>C	P.K556T
SH_135	5	5303745	5303751	Frame_Shift_Del	INDEL	CCCTCGG	-	-	ADAMTS16	c.3060delCTC	P.S1019fs
SH_135	5	53751807	53751807	Missense_Mutation	SNV	C	T	T	HSPB3	c.188C>T	P.P63L
SH_135	5	80409724	80409724	Nonsense_Mutation	SNV	C	T	T	RASGRF2	c.2455C>T	P.R819*
SH_135	6	109767486	109767486	Missense_Mutation	SNV	C	T	T	MICAL1	c.2176G>A	P.E726K
SH_135	6	13327129	13327129	Frame_Shift_Del	INDEL	A	-	-	TBC1D7	c.2delT	P.M1fs
SH_135	6	158900821	158900821	Silent	SNV	G	A	A	TULP4	c.1065G>A	P.S355S
SH_135	6	161032713	161032713	Silent	SNV	G	A	A	LPA	c.2484C>T	P.H828H
SH_135	6	26033440	26033440	Silent	SNV	C	T	T	HIST1H2AB	c.357G>A	P.K119K
SH_135	6	29911975	29911975	Missense_Mutation	SNV	C	G	G	HLA-A	c.696C>G	P.F232L
SH_135	6	32021156	32021156	Splice_Site	SNV	T	C	C	TNXB	c.8785+9A>G	
SH_135	6	69348639	69348639	Silent	SNV	T	G	G	ADGRB3	c.72T>G	P.A24A
SH_135	6	69646425	69646425	Missense_Mutation	SNV	G	C	C	ADGRB3	c.883G>C	P.E295Q
SH_135	6	71186851	71186851	Splice_Site	INDEL	C	-	-	FAM135A	c.369-10delC	
SH_135	6	75892822	75892822	Missense_Mutation	SNV	A	C	C	COL12A1	c.1835T>G	P.L612R
SH_135	6	7845531	7845531	Missense_Mutation	SNV	A	C	C	BMP6	c.823A>C	P.S275R
SH_135	6	83767734	83767734	Nonsense_Mutation	SNV	T	A	A	UBE3D	c.85A>T	P.K29*
SH_135	6	99374622	99374622	Silent	SNV	T	G	G	FBXL4	c.243A>C	P.V81V
SH_135	7	116937823	116937823	Missense_Mutation	SNV	A	C	C	WNT2	c.696T>G	P.D232E
SH_135	7	150068604	150068604	Missense_Mutation	SNV	C	G	G	REPIN1	c.445C>G	P.R149G
SH_135	7	150878359	150878359	Silent	SNV	G	A	A	ASB10	c.771C>T	P.D257D
SH_135	7	27187159	27187159	Silent	SNV	C	T	T	HOXA6	c.210G>A	P.A70A
SH_135	7	36895324	36895324	Silent	SNV	T	C	C	ELMO1	c.576A>G	P.L192L
SH_135	7	4167123	4167123	Missense_Mutation	SNV	T	G	G	SDK1	c.3934T>G	P.Y1312D
SH_135	7	47342638	47342638	Missense_Mutation	SNV	T	A	A	TNS3	c.3367A>T	P.S1123C
SH_135	7	89790632	89790632	Splice_Site	INDEL	GT	-	-	STEAP1	c.97+1_597+2delGT	
SH_135	7	94039078	94039078	Missense_Mutation	SNV	G	A	A	COL1A2	c.980G>A	P.R327H
SH_135	8	110535458	110535458	Splice_Site	SNV	T	A	A	PKHD1L1	c.12331-4T>A	
SH_135	8	114111149	114111149	Silent	SNV	G	T	T	CSMD3	c.753C>A	P.I251I
SH_135	8	136619211	136619211	Missense_Mutation	SNV	G	A	A	KHDRBS3	c.821G>A	P.G274E
SH_135	8	136619212	136619212	Silent	SNV	A	T	T	KHDRBS3	c.822A>T	P.G274G
SH_135	8	139701164	139701164	Missense_Mutation	SNV	T	G	G	COL22A1	c.2858A>C	P.E953A
SH_135	8	143602256	143602256	Silent	SNV	C	T	T	ADGRB1	c.2994C>T	P.I998I
SH_135	8	88365898	88365898	Missense_Mutation	SNV	T	G	G	CNBD1	c.1187T>G	P.L396R
SH_135	8	92145440	92145440	Silent	SNV	C	T	T	LRRC69	c.486C>T	P.Y162Y
SH_135	9	101824260	101824260	Missense_Mutation	SNV	C	A	A	COL15A1	c.3410C>A	P.A1137E
SH_135	9	113169297	113169297	Silent	SNV	T	C	C	SVEP1	c.8583A>G	P.E2861E
SH_135	9	131255075	131255075	Missense_Mutation	SNV	G	C	C	ODF2	c.1728G>C	P.E576D
SH_135	9	132481528	132481528	Missense_Mutation	SNV	G	A	A	PRRX2	c.278G>A	P.G93E
SH_135	9	136277538	136277538	Missense_Mutation	SNV	C	T	T	REXO4	c.791G>A	P.R264H
SH_135	9	137591754	137591754	Splice_Site	SNV	G	A	A	COL5A1	c.278-1G>A	
SH_135	9	137990304	137990304	Missense_Mutation	SNV	G	C	C	OLFM1	c.629G>C	P.R210T
SH_135	9	140110380	140110380	Missense_Mutation	SNV	C	T	T	NDOR1	c.1465C>T	P.R489W
SH_135	9	140387525	140387525	Missense_Mutation	SNV	G	C	C	PNPLA7	c.2137C>G	P.R713G
SH_135	9	16437085	16437085	Silent	SNV	G	A	A	BNC2	c.981C>T	P.S327S
SH_135	9	17464512	17464512	Missense_Mutation	SNV	G	T	T	CNTLN	c.3422G>T	P.R1141M
SH_135	9	40706066	40706066	Silent	SNV	C	T	T	SPATA31A3	c.3723C>T	P.A1241A
SH_135	9	43625463	43625463	Missense_Mutation	SNV	C	T	T	SPATA31A6	c.3224G>A	P.R1075K
SH_135	9	82333783	82333783	Missense_Mutation	SNV	G	A	A	TLE4	c.1583G>A	P.S528N
SH_135	9	84610048	84610048	Missense_Mutation	SNV	C	G	G	SPATA31D1	c.4663C>G	P.P1555A
SH_135	9	90745831	90745831	Silent	SNV	A	G	G	SPATA31C2	c.2121T>C	P.L707L
SH_135	9	91991854	91991854	Silent	SNV	C	T	T	SEMA4D	c.1776G>A	P.A592A
SH_135	9	93375582	93375582	Silent	SNV	G	A	A	DIRAS2	c.528C>T	P.L176L
SH_135	X	125686088	125686088	Silent	SNV	G	C	C	DCAF12L1	c.504C>G	P.G168G
SH_135	X	140994553	140994553	Silent	SNV	T	C	C	MAGEC1	c.1363T>C	P.L455L
SH_135	X	47044992	47044992	Missense_Mutation	SNV	C	T	T	RBM10	c.2318C>T	P.A773V
SH_135	X	69502174	69502174	Missense_Mutation	SNV	T	G	G	RAB41	c.107T>G	P.F36C
SH_135	X	71495426	71495426	Missense_Mutation	SNV	C	G	G	RPS4X	c.230G>C	P.R77P
SH_137	1	241901790	241901790	Splice_Site	SNV	G	A	A	WDR64	c.1290G>A	P.T430T
SH_137	11	108203492	108203492	Nonsense_Mutation	SNV	C	T	T	ATM	c.7792C>T	P.R2598*
SH_137	11	68029844	68029844	Missense_Mutation	SNV	G	C	C	C11orf24	c.619C>G	P.L207V
SH_137	12	20769211	20769211	Silent	SNV	C	T	T	PDE3A	c.1317C>T	P.S439S
SH_137	12	25398284	25398284	Missense_Mutation	SNV	C	A	A	KRAS	c.35G>T	P.G12V
SH_137	12	5154061	5154061	Missense_Mutation	SNV	C	T	T	KCNA5	c.748C>T	P.R250W
SH_137	13	43500560	43500560	Missense_Mutation	SNV	G	T	T	EPSTI1	c.569C>A	P.T190N
SH_137	15	43571977	43571977	Silent	SNV	C	A	A	TGM7	c.1524G>T	P.L508L
SH_137	16	24166004	24166004	Splice_Site	SNV	G	T	T	PRKCB	c.1066-1G>T	
SH_137	16	66839741	66839741	Splice_Site	SNV	C	T	T	NAE1	c.1428-12G>A	
SH_137	17	38152515	38152515	Missense_Mutation	SNV	A	G	G	PSMD3	c.1400A>G	P.Y467C
SH_137	19	36034295	36034295	Missense_Mutation	SNV	G	T	T	GAPDH5	c.795G>T	P.R265S
SH_137	19	40363914	40363914	Missense_Mutation	SNV	G	A	A	FCGBP	c.14728C>T	P.L4910F
SH_137	20	44048180	44048180	Missense_Mutation	SNV	T	C	C	PIGT	c.463T>C	P.F155L
SH_137	3	170908566	170908575	Frame_Shift_Del	INDEL	TGACTCAGCC	-	-	TNIG	c.428delGGCTGA	P.G140fs
SH_137	5	33576343	33576343	Missense_Mutation	SNV	G	A	A	ADAMTS12	c.3533C>T	P.T1178M
SH_137	5	63991419	63991419	Silent	SNV	C	T	T	FAM159B	c.277C>T	P.L93L
SH_137	6	76731925	76731925	Missense_Mutation	SNV	C	T	T	IMPG1	c.340G>A	P.V114I
SH_137	6	83847259	83847259	Silent	SNV	G	A	A	DOPEY1	c.3471G>A	P.V1157V
SH_137	7	557051	557051	Missense_Mutation	SNV	A	T	T	PDGFA	c.140T>A	P.L47H

SH_137	7	74197350	74197350	Missense_Mutation	SNV	G	A	A	NCF1	c.520G>A	P.E174K
SH_137	8	131149206	131149206	Silent	SNV	G	A	A	ASAP1	c.1138C>T	P.L380L
SH_137	9	34658538	34658538	Missense_Mutation	SNV	G	T	T	IL11RA	c.668G>T	P.G223V
SH_137	X	48558900	48558900	Missense_Mutation	SNV	G	T	T	SUV39H1	c.617G>T	P.C206F
SH_137	X	71424900	71424900	Frame_Shift_Ins	INDEL	-	T	T	ERCC6L	c.3716_3717ins	P.T1240fs
SH_139	1	118461210	118461210	Splice_Site	SNV	T	C	C	GDAP2	c.316+9A>G	
SH_139	1	152282017	152282017	Missense_Mutation	SNV	G	T	T	FLG	c.5345C>A	P.T1782K
SH_139	1	182354621	182354621	Nonsense_Mutation	SNV	A	T	T	GLUL	c.674T>A	P.L225*
SH_139	1	19528290	19528290	Missense_Mutation	SNV	G	A	A	UBR4	c.196C>T	P.H66Y
SH_139	12	106708150	106708150	Silent	SNV	A	C	C	TCP11L2	c.172A>C	P.R58R
SH_139	12	52946471	52946471	Nonsense_Mutation	SNV	G	A	A	KRT71	c.391C>T	P.R131*
SH_139	13	95114363	95114363	Missense_Mutation	SNV	T	C	C	DCIT	c.944A>G	P.N315S
SH_139	15	59064273	59064273	Missense_Mutation	SNV	G	T	T	FAM63B	c.679G>T	P.A227S
SH_139	15	99482579	99482579	Silent	SNV	C	A	A	IGF1R	c.3447C>A	P.V1149V
SH_139	16	86601038	86601038	Missense_Mutation	SNV	G	A	A	FOXC2	c.97G>A	P.G33S
SH_139	19	30020720	30020720	Splice_Site	SNV	T	C	C	VSTM2B	c.298-6T>C	
SH_139	19	42461207	42461207	Nonsense_Mutation	SNV	C	T	T	RABAC1	c.432G>A	P.W144*
SH_139	2	137814268	137814268	Missense_Mutation	SNV	C	A	A	THSD7B	c.418C>A	P.H140N
SH_139	2	207804397	207804397	Splice_Site	SNV	T	C	C	CPO	c.68+6T>C	
SH_139	3	100287677	100287677	Silent	SNV	C	T	T	TMEM45A	c.600C>T	P.V200V
SH_139	5	149669160	149669160	Missense_Mutation	SNV	G	A	A	CAMK2A	c.29C>T	P.T10M
SH_139	5	150506042	150506042	Splice_Site	SNV	C	A	A	ANXA6	c.978-1G>T	
SH_139	6	112015613	112015613	Missense_Mutation	SNV	C	T	T	FYN	c.1238G>A	P.R413Q
SH_139	6	12136101	12136101	Missense_Mutation	SNV	G	C	C	HIVEP1	c.6463G>C	P.D2155H
SH_139	7	129929507	129929507	Missense_Mutation	SNV	C	T	T	CPA2	c.1180C>T	P.R394C
SH_139	7	81593617	81593617	Nonsense_Mutation	SNV	G	T	T	CACNA2D1	c.2633C>A	P.S878*
SH_139	8	114388963	114388963	Splice_Site	SNV	C	A	A	CSMD3	c.58+4G>T	
SH_139	8	17043889	17043889	Silent	SNV	A	G	G	ZDHHC2	c.207A>G	P.S69S
SH_139	9	34724008	34724008	Missense_Mutation	SNV	G	A	A	FAM205A	c.3229C>T	P.R1077C
SH_139	X	47466554	47466554	Missense_Mutation	SNV	T	C	C	SYN1	c.421A>G	P.I141V
SH_139	X	69282394	69282394	Missense_Mutation	SNV	A	G	G	OTUD6A	c.20A>G	P.E7G
SH_140	1	12321179	12321179	Missense_Mutation	SNV	G	A	A	VPS13D	c.1387G>A	P.E463K
SH_140	1	152195670	152195670	Silent	SNV	G	C	C	HRNR	c.60C>G	P.T20T
SH_140	1	172411244	172411244	Silent	SNV	T	C	C	PIGC	c.519A>G	P.V173V
SH_140	1	184679567	184679567	Silent	SNV	G	A	A	EDEM3	c.1806C>T	P.L602L
SH_140	1	202992017	202992017	Missense_Mutation	SNV	A	T	T	TMEM183A	c.980A>T	P.H327L
SH_140	1	203194885	203194885	Missense_Mutation	SNV	C	T	T	CHIT1	c.169G>A	P.A57T
SH_140	1	232002303	232002303	Missense_Mutation	SNV	G	T	T	DISC1	c.2016G>T	P.Q672H
SH_140	1	36212367	36212367	Missense_Mutation	SNV	C	G	G	CLSPN	c.2662G>C	P.D888H
SH_140	1	74929218	74929218	Missense_Mutation	SNV	G	T	T	FPGT-TNNI3K	c.2447G>T	P.W816L
SH_140	1	74929219	74929219	Nonsense_Mutation	SNV	G	A	A	FPGT-TNNI3K	c.2448G>A	P.W816*
SH_140	10	105903325	105903325	Missense_Mutation	SNV	C	A	A	CFAP43	c.4017G>T	P.K1339N
SH_140	10	13702476	13702476	Missense_Mutation	SNV	T	C	C	FRMD4A	c.1786A>G	P.N596D
SH_140	10	25885616	25885616	Missense_Mutation	SNV	A	T	T	GPR158	c.2043A>T	P.F681D
SH_140	10	32580127	32580142	Frame_Shift_Del	INDEL	GTGTTTAAA	-	-	EPC1	9delTCAATTTAA	P.S308fs
SH_140	10	47086937	47086937	Missense_Mutation	SNV	A	G	G	NPY4R	c.154A>G	P.T52A
SH_140	10	51866195	51866195	Silent	SNV	A	G	G	FAM21A	c.1839A>G	P.A613A
SH_140	11	122929771	122929771	Missense_Mutation	SNV	A	G	G	HSPA8	c.1319T>C	P.I440T
SH_140	11	133814242	133814242	Missense_Mutation	SNV	A	T	T	IGSF9B	c.282T>A	P.D94E
SH_140	11	4080616	4080616	Silent	SNV	G	C	C	STIM1	c.603G>C	P.G201G
SH_140	11	56345101	56345101	Missense_Mutation	SNV	C	A	A	OR5M10	c.97G>T	P.A33S
SH_140	11	56345102	56345102	Silent	SNV	C	T	T	OR5M10	c.96G>A	P.L32L
SH_140	11	57995536	57995536	Missense_Mutation	SNV	G	T	T	OR10Q1	c.812C>A	P.T271N
SH_140	11	62290722	62290722	Missense_Mutation	SNV	C	G	G	AHNAK	c.11167G>C	P.G3723R
SH_140	12	132393680	132393680	Splice_Site	SNV	G	T	T	ULK1	c.565-1G>T	
SH_140	12	29502037	29502037	Silent	SNV	A	G	G	ERGIC2	c.702T>C	P.D234D
SH_140	12	30877346	30877346	Missense_Mutation	SNV	G	C	C	CAPRIN2	c.1945C>G	P.P649A
SH_140	12	52567428	52567428	Missense_Mutation	SNV	C	T	T	KRT80	c.787G>A	P.A263T
SH_140	12	58014112	58014112	Missense_Mutation	SNV	A	G	G	SLC26A10	c.109A>G	P.T37A
SH_140	12	6730336	6730336	Missense_Mutation	SNV	C	G	G	LPAR5	c.79G>C	P.V27L
SH_140	13	103390153	103390153	Silent	SNV	A	T	T	CCDC168	c.1289AT>A	P.P4298P
SH_140	13	19751595	19751595	Missense_Mutation	SNV	C	A	A	TUBA3C	c.528G>T	P.Q176H
SH_140	13	32954039	32954039	Nonsense_Mutation	SNV	C	T	T	BRCA2	c.9106C>T	P.Q0306*
SH_140	13	48942667	48942667	Nonsense_Mutation	SNV	G	T	T	RB1	c.1054G>T	P.E352*
SH_140	14	37641547	37641547	Silent	SNV	G	T	T	SLC25A21	c.9C>A	P.A3A
SH_140	15	88690602	88690602	Nonsense_Mutation	SNV	G	T	T	NTRK3	c.428C>A	P.S143*
SH_140	15	94841562	94841562	Nonsense_Mutation	SNV	T	A	A	MCTP2	c.68T>A	P.L23*
SH_140	16	10864187	10864187	Missense_Mutation	SNV	G	T	T	TVP23A	c.584C>A	P.A195D
SH_140	16	4908007	4908007	Missense_Mutation	SNV	A	G	G	UBN1	c.266A>G	P.D89G
SH_140	16	82891983	82891983	Missense_Mutation	SNV	C	T	T	CDH13	c.203C>T	P.S68F
SH_140	16	85699957	85699957	Splice_Site	SNV	A	G	G	GSE1	c.2818+4A>G	
SH_140	16	88691630	88691630	Missense_Mutation	SNV	G	A	A	ZC3H18	c.2135G>A	P.G712D
SH_140	16	90025448	90025448	Silent	SNV	C	A	A	DEF8	c.369C>A	P.I123I
SH_140	17	30376157	30376157	Missense_Mutation	SNV	G	T	T	LRRC37B	c.2174G>T	P.R725L
SH_140	17	41566881	41566881	Frame_Shift_Ins	INDEL	-	A	A	DXH8	c.218dupA	P.N73fs
SH_140	17	55062796	55062796	Missense_Mutation	SNV	G	T	T	SCPEP1	c.283G>T	P.D95Y
SH_140	17	56572598	56572598	Missense_Mutation	SNV	T	G	G	MTMR4	c.2905A>C	P.N969H
SH_140	17	7579311	7579311	Splice_Site	SNV	C	A	A	TP53	c.375+1G>T	
SH_140	19	10107105	10107105	Splice_Site	SNV	T	A	A	COL5A3	c.1422+4A>T	
SH_140	19	11553282	11553282	Missense_Mutation	SNV	G	C	C	PRKCSH	c.550G>C	P.E184Q
SH_140	19	18896845	18896845	Silent	SNV	G	A	A	COMP	c.1419C>T	P.D473D
SH_140	19	41105308	41105308	Missense_Mutation	SNV	T	A	A	LTBP4	c.76T>A	P.S26T
SH_140	19	43268270	43268270	Nonsense_Mutation	SNV	G	T	T	PSG8	c.228C>A	P.Y76*
SH_140	19	46886706	46886706	Missense_Mutation	SNV	C	A	A	PPP5C	c.672C>A	P.S224R
SH_140	19	49657228	49657228	Missense_Mutation	SNV	G	A	A	HRC	c.1267C>T	P.P423S
SH_140	19	51022639	51022639	Missense_Mutation	SNV	G	T	T	LRRC4B	c.331C>A	P.H111N
SH_140	19	54632428	54632428	Splice_Site	SNV	C	G	G	PRPF31	c.1147-4C>G	
SH_140	19	54746415	54746415	Splice_Site	SNV	G	C	C	LILRA6	c.33-7C>G	
SH_140	19	57334150	57334150	Missense_Mutation	SNV	C	T	T	PEG3	c.536G>A	P.R179H
SH_140	19	806448	806448	Silent	SNV	G	A	A	PTBP1	c.1011G>A	P.L337L
SH_140	19	8435960	8435960	Missense_Mutation	SNV	C	G	G	ANGPTL4	c.568C>G	P.Q190E
SH_140	2	10008515	10008515	Missense_Mutation	SNV	C	G	G	TAF1B	c.510C>G	P.I170M
SH_140	2	141762979	141762979	Silent	SNV	A	G	G	LRP1B	c.2428T>C	P.H180L
SH_140	2	153533164	153533164	Silent	SNV	T	C	C	PRPF40A	c.786A>G	P.A262A
SH_140	2	161052067	161052067	Missense_Mutation	SNV	A	G	G	ITGB6	c.406T>C	P.Y136H
SH_140	2	220480797	220480797	Missense_Mutation	SNV	G	T	T	STK11IP	c.3149G>T	P.R1050L
SH_140	20	31954677	31954677	Silent	SNV	C	T	T	CDK5RAP1	c.1527G>A	P.V509V
SH_140	20	43251494	43251494	Silent	SNV	C	T	T	ADA	c.756G>A	P.L252L

SH_140	20	60888859	60888859	Splice_Site	SNV	C	A	A	LAMA5	c.8505-1G>T	
SH_140	20	60888861	60888861	Splice_Site	SNV	G	A	A	LAMA5	c.8505-3C>T	
SH_140	21	15537680	15537680	Missense_Mutation	SNV	T	A	A	LIP1	c.765A>T	P.R255S
SH_140	21	16337081	16337081	Nonsense_Mutation	SNV	C	A	A	NRIP1	c.3433G>T	P.G1145*
SH_140	22	30975186	30975186	Missense_Mutation	SNV	C	A	A	PE51	c.1444G>T	P.G482C
SH_140	22	50967557	50967557	Splice_Site	SNV	T	C	C	TYMP	c.417+8A>G	
SH_140	3	148563264	148563264	Missense_Mutation	SNV	G	A	A	CPB1	c.832G>A	P.E278K
SH_140	3	32030675	32030675	Missense_Mutation	SNV	T	G	G	ZNF860	c.104T>G	P.L35W
SH_140	3	73433915	73433915	Missense_Mutation	SNV	G	T	T	PDZRN3	c.896C>A	P.A299E
SH_140	3	73433916	73433916	Missense_Mutation	SNV	C	T	T	PDZRN3	c.895G>A	P.A299T
SH_140	4	155241686	155241686	Frame_Shift_Del	INDEL	G	-	-	DCHS2	c.3500delC	P.S1167fs
SH_140	4	25146671	25146671	Missense_Mutation	SNV	C	A	A	SEPSEC5	c.889G>T	P.G297C
SH_140	5	150897269	150897269	Missense_Mutation	SNV	C	T	T	FAT2	c.11375G>A	P.R3792Q
SH_140	5	37169448	37169448	Silent	SNV	A	C	C	C5orf42	c.6678T>G	P.P2226P
SH_140	6	155749923	155749923	Splice_Site	SNV	C	T	T	NOX3	c.1145+5G>A	
SH_140	6	31608924	31608924	Missense_Mutation	SNV	C	T	T	BAG6	c.2636G>A	P.G879E
SH_140	6	41303637	41303637	Missense_Mutation	SNV	C	A	A	NCR2	c.23C>A	P.P8Q
SH_140	6	43415495	43415495	Missense_Mutation	SNV	C	T	T	ABCC10	c.3779C>T	P.P1260L
SH_140	6	619531	619531	Silent	SNV	C	A	A	EXOC2	c.435G>T	P.S145S
SH_140	7	112423847	112423847	Missense_Mutation	SNV	G	T	T	TMEM168	c.1034C>A	P.A345E
SH_140	7	131870125	131870125	Missense_Mutation	SNV	C	G	G	PLXNA4	c.3091G>C	P.D1031H
SH_140	7	134223038	134223038	Splice_Site	SNV	C	A	A	AKR1B10	c.825+9C>A	
SH_140	7	134223039	134223039	Splice_Site	SNV	C	T	T	AKR1B10	c.825+10C>T	
SH_140	7	35288451	35288451	Missense_Mutation	SNV	C	A	A	TBX20	c.383G>T	P.R128M
SH_140	7	4249721	4249721	Missense_Mutation	SNV	G	T	T	SDK1	c.927G>T	P.W309C
SH_140	7	48564012	48564012	Silent	SNV	T	A	A	ABCA13	c.14220T>A	P.I4740I
SH_140	8	8176074	8176074	Missense_Mutation	SNV	C	A	A	SGK223	c.3811G>T	P.A1271S
SH_140	8	97614760	97614760	Splice_Site	SNV	C	T	T	SDC2	c.306+4C>T	
SH_140	9	101156534	101156534	Missense_Mutation	SNV	C	T	T	GABBR2	c.1301G>A	P.S434N
SH_140	9	101784396	101784396	Silent	SNV	T	A	A	COL15A1	c.1725T>A	P.P575P
SH_140	9	104312898	104312898	Missense_Mutation	SNV	G	T	T	RNF20	c.1103G>T	P.R368L
SH_140	9	130495572	130495572	Missense_Mutation	SNV	C	G	G	TOR2A	c.685G>C	P.V229L
SH_140	9	35077350	35077350	Missense_Mutation	SNV	G	A	A	FANCG	c.557C>T	P.P186L
SH_140	X	109693883	109693883	Missense_Mutation	SNV	C	A	A	RGAG1	c.38C>A	P.T13K
SH_140	X	135593723	135593827	Missense_Mutation	INDEL	GATTGAGAT	-	-	HTATSF1	c.1824_1928delP	E.608_5642del
SH_140	X	151900607	151900607	Missense_Mutation	SNV	G	T	T	MAGEA12	c.194C>A	P.P65H
SH_140	X	2945349	2945349	Splice_Site	SNV	T	G	G	ARSH	c.1037-5T>G	
SH_140	X	31645909	31645909	Nonsense_Mutation	SNV	T	A	A	DMD	c.8074A>T	P.K2692*
SH_140	X	43655116	43655116	Missense_Mutation	SNV	C	A	A	MAOB	c.638G>T	P.G213V
SH_140	X	48341392	48341392	Missense_Mutation	SNV	A	T	T	FTSJ1	c.565A>T	P.S189C
SH_140	X	83129053	83129053	Missense_Mutation	SNV	C	A	A	CYL1	c.1337C>A	P.A446D
SH_141	1	104120437	104120437	Missense_Mutation	SNV	G	C	C	AMY2B	c.1316G>C	P.R439T
SH_141	1	10431286	10431286	Missense_Mutation	SNV	C	G	G	KIF1B	c.4774C>G	P.V1592V
SH_141	1	114340440	114340440	Missense_Mutation	SNV	A	C	C	RSBN1	c.922T>G	P.S308A
SH_141	1	169828347	169828347	Silent	SNV	G	A	A	SCYL3	c.1147C>T	P.L383L
SH_141	1	169828348	169828348	Missense_Mutation	SNV	C	A	A	SCYL3	c.1146G>T	P.L382F
SH_141	1	17350557	17350557	Nonsense_Mutation	SNV	C	A	A	SDHB	c.553G>T	P.E185*
SH_141	1	202278196	202278196	Missense_Mutation	SNV	A	C	C	LGR6	c.1298A>C	P.Q433P
SH_141	1	2130383	2130383	Silent	SNV	C	T	T	FAAP20	c.45G>A	P.A15A
SH_141	1	26212309	26212309	Nonsense_Mutation	SNV	C	A	A	TMN1	c.430G>T	P.E144*
SH_141	1	26629322	26629322	Missense_Mutation	SNV	G	A	A	UBXN11	c.53C>T	P.S18L
SH_141	1	38034653	38034653	Missense_Mutation	SNV	T	G	G	GNL2	c.1871A>C	P.E624A
SH_141	1	38341323	38341323	Missense_Mutation	SNV	C	G	G	INPP5B	c.1251G>C	P.K417N
SH_141	1	95609561	95609561	Missense_Mutation	SNV	C	T	T	TMEM56	c.104C>T	P.S35F
SH_141	1	981124	981124	Missense_Mutation	SNV	G	T	T	AGRN	c.2548G>T	P.D850Y
SH_141	10	135020810	135020810	Missense_Mutation	SNV	T	A	A	KNDC1	c.3749T>A	P.L1250Q
SH_141	10	16806507	16806507	Missense_Mutation	SNV	C	T	T	RSU1	c.163G>A	P.V55M
SH_141	10	38121463	38121463	Missense_Mutation	SNV	T	C	C	ZNF248	c.820A>G	P.I274V
SH_141	10	73434879	73434879	Missense_Mutation	SNV	A	G	G	CDH23	c.1460A>G	P.N487S
SH_141	10	75673516	75673516	Missense_Mutation	SNV	T	A	A	PLAU	c.629T>A	P.I210N
SH_141	10	79785496	79785496	Missense_Mutation	SNV	G	T	T	POLR3A	c.202C>A	P.P68T
SH_141	11	125542520	125542520	Missense_Mutation	SNV	A	C	C	ACRV1	c.766T>G	P.C256G
SH_141	11	128360402	128360402	Missense_Mutation	SNV	G	A	A	ETS1	c.284C>T	P.A95V
SH_141	11	17333656	17333656	Missense_Mutation	SNV	G	A	A	NUCB2	c.901G>A	P.V301I
SH_141	11	56409209	56409209	Missense_Mutation	SNV	G	A	A	OR5AP2	c.707C>T	P.S236L
SH_141	11	58190258	58190258	Silent	SNV	C	G	G	OR5B2	c.477G>C	P.G159G
SH_141	12	100453202	100453202	Missense_Mutation	SNV	C	A	A	UHRF1BP1L	c.1853G>T	P.C618F
SH_141	12	100691850	100691850	Missense_Mutation	SNV	T	C	C	SCYL2	c.377T>C	P.L126S
SH_141	12	11463289	11463289	Nonsense_Mutation	SNV	G	C	C	PRB4	c.44C>G	P.S15*
SH_141	12	122657079	122657079	Silent	SNV	A	C	C	IL31	c.375T>G	P.S125S
SH_141	12	133635293	133635293	Silent	SNV	C	T	T	ZNF84	c.1992C>T	P.P664F
SH_141	12	51453144	51453144	Missense_Mutation	SNV	A	T	T	LETMD1	c.1052A>T	P.E351V
SH_141	12	56384564	56384564	Silent	SNV	C	T	T	RAB5B	c.414C>T	P.A138A
SH_141	12	70352246	70352246	Missense_Mutation	SNV	G	A	A	MYRFL	c.2668G>A	P.D890N
SH_141	13	23928670	23928670	Missense_Mutation	SNV	G	A	A	SACS	c.1640C>T	P.A547V
SH_141	13	39265120	39265120	Silent	SNV	C	G	G	FREM2	c.3639C>G	P.L1213L
SH_141	14	90450886	90450886	Missense_Mutation	SNV	G	T	T	TDP1	c.911G>T	P.R304L
SH_141	14	95570125	95570125	Missense_Mutation	SNV	T	C	C	DICER1	c.3608A>G	P.N1203S
SH_141	15	65450936	65450936	Nonsense_Mutation	SNV	A	T	T	CLPX	c.869T>A	P.L290*
SH_141	15	74032879	74032879	Silent	SNV	C	A	A	C15orf59	c.261G>T	P.A87A
SH_141	16	11076740	11076740	Silent	SNV	C	T	T	CLEC16A	c.957C>T	P.F319F
SH_141	16	29828302	29828302	Silent	SNV	G	C	C	PAGR1	c.456G>C	P.P152P
SH_141	16	30748790	30748790	Missense_Mutation	SNV	C	G	G	SRCAP	c.7429C>G	P.L2477V
SH_141	16	72110310	72110310	Missense_Mutation	SNV	A	T	T	HPR	c.377A>T	P.N126I
SH_141	16	89293624	89293624	Missense_Mutation	SNV	G	A	A	ZNF778	c.928G>A	P.E310K
SH_141	16	89349639	89349639	Missense_Mutation	SNV	T	C	C	ANKRD11	c.3311A>G	P.D1104G
SH_141	17	37604108	37604108	Silent	SNV	T	C	C	MED1	c.75A>G	P.A25A
SH_141	17	39186251	39186251	Missense_Mutation	SNV	G	T	T	KRTAP1-4	c.80C>A	P.P27Q
SH_141	17	61958860	61958860	Silent	SNV	G	A	A	GH2	c.30C>T	P.L10L
SH_141	17	72939718	72939718	Missense_Mutation	SNV	C	A	A	OTOP3	c.650C>A	P.T217N
SH_141	17	7577534	7577534	Missense_Mutation	SNV	C	A	A	TP53	c.747G>T	P.R249S
SH_141	18	3534337	3534337	Missense_Mutation	SNV	T	G	G	DLGAP1	c.1428A>C	P.E476D
SH_141	18	5406824	5406824	Silent	SNV	G	A	A	EPB41L3	c.1794C>T	P.A598A
SH_141	19	1220391	1220391	Missense_Mutation	SNV	G	T	T	STK11	c.484G>T	P.D162Y
SH_141	19	38989882	38989882	Splice_Site	SNV	C	T	T	RYR1	c.7026C>T	P.N2342N
SH_141	19	4013176	4013176	Missense_Mutation	SNV	G	T	T	PIAS4	c.283G>T	P.A95S
SH_141	19	48945409	48945409	Missense_Mutation	SNV	G	A	A	GRIN2D	c.2443G>A	P.E815K
SH_141	19	54314454	54314454	Silent	SNV	G	A	A	NLRP12	c.459C>T	P.L153L

SH_141	19	9049125	9049125	Missense_Mutation	SNV	G	T	T	MUC16	c.32506C>A	P.P10836T
SH_141	19	9325136	9325136	Silent	SNV	G	A	A	OR7D4	c.378C>T	P.I126I
SH_141	2	178482221	178482221	Silent	SNV	G	A	A	TTIC30A	c.1209C>G	P.N403N
SH_141	2	179396768	179396768	Missense_Mutation	SNV	G	C	C	TTN	c.99651C>G	P.I33217M
SH_141	2	203914526	203914526	Splice_Site	SNV	T	C	C	NBEAL1	c.144-11T>C	
SH_141	2	230875533	230875533	Missense_Mutation	SNV	T	A	A	FBXO36	c.500T>A	P.L167H
SH_141	2	231264962	231264962	Splice_Site	SNV	G	T	T	SP140L	c.1238+5G>T	
SH_141	2	28828736	28828736	Missense_Mutation	SNV	C	T	T	PLB1	c.2945C>T	P.T982M
SH_141	2	74184338	74184338	Missense_Mutation	SNV	C	G	G	DGUOK	c.369C>G	P.H123Q
SH_141	20	1223449	1223449	Missense_Mutation	SNV	C	T	T	RAD21L1	c.1043C>T	P.S348L
SH_141	20	23731467	23731467	Missense_Mutation	SNV	C	T	T	CS11	c.37G>A	P.A13T
SH_141	20	25656194	25656194	Missense_Mutation	SNV	C	T	T	ZNF337	c.1730G>A	P.C577Y
SH_141	20	39794955	39794955	Missense_Mutation	SNV	C	A	A	PLCG1	c.1921C>A	P.Q641K
SH_141	20	44531175	44531175	Silent	SNV	G	A	A	PLTP	c.726C>T	P.I242I
SH_141	21	17246830	17246830	Silent	SNV	A	G	G	USP25	c.2994A>G	P.R998R
SH_141	22	17601380	17601380	Missense_Mutation	SNV	C	A	A	CECR6	c.638G>T	P.G213V
SH_141	22	32545746	32545746	Missense_Mutation	SNV	A	T	T	C22orf42	c.676T>A	P.Y226N
SH_141	3	189612142	189612142	Missense_Mutation	SNV	G	A	A	TP63	c.1894G>A	P.E632K
SH_141	3	53707056	53707056	Missense_Mutation	SNV	G	A	A	CACNA1D	c.1123G>A	P.D375N
SH_141	4	106638858	106638858	Missense_Mutation	SNV	C	T	T	GSTCD	c.88C>T	P.H30Y
SH_141	4	20543217	20543217	Silent	SNV	C	T	T	SLIT2	c.2118C>T	P.A706A
SH_141	5	140730577	140730577	Silent	SNV	A	G	G	PCDHGB1	c.750A>G	P.E250E
SH_141	5	141243441	141243441	Missense_Mutation	SNV	G	A	A	PCDH1	c.2503C>T	P.R835C
SH_141	5	41018003	41018003	Missense_Mutation	SNV	T	A	A	MROH2B	c.2833A>T	P.T945S
SH_141	6	100965917	100965917	Silent	SNV	A	C	C	ASCC3	c.5877T>G	P.S1959S
SH_141	6	165832122	165832122	Splice_Site	SNV	C	T	T	PDE10A	c.998+1G>A	
SH_141	6	36076212	36076212	Missense_Mutation	SNV	G	C	C	MAPK14	c.1071G>C	P.E357D
SH_141	6	90397840	90397840	Missense_Mutation	SNV	G	A	A	MDN1	c.11312C>T	P.S3771L
SH_141	7	102604079	102604079	Missense_Mutation	SNV	C	G	G	FBXL13	c.625G>C	P.D209H
SH_141	7	140082295	140082295	Missense_Mutation	SNV	G	A	A	SLC37A3	c.32C>T	P.S11F
SH_141	7	146825878	146825878	Missense_Mutation	SNV	G	T	T	CNTNAP2	c.1033G>T	P.V345F
SH_141	7	30825394	30825394	Missense_Mutation	SNV	G	A	A	FAM188B	c.449G>A	P.G150D
SH_141	7	32582833	32582833	Silent	SNV	C	T	T	AVL9	c.174C>T	P.P58P
SH_141	8	11189627	11189627	Nonsense_Mutation	SNV	G	T	T	SLC35G5	c.1012G>T	P.E338*
SH_141	8	113323333	113323333	Missense_Mutation	SNV	G	T	T	CSMD3	c.7447C>A	P.Q2483K
SH_141	8	24192998	24192998	Missense_Mutation	SNV	G	A	A	ADAM28	c.1411G>A	P.E471K
SH_141	8	48767815	48767815	Silent	SNV	C	T	T	PRKDC	c.6726G>A	P.E2242E
SH_141	9	33548311	33548311	Nonsense_Mutation	SNV	G	T	T	ANKRD18B	c.1336G>T	P.E446*
SH_141	9	86530464	86530464	Silent	SNV	G	A	A	KIF27	c.43C>T	P.L15L
SH_141	9	96019387	96019387	Missense_Mutation	SNV	C	T	T	WNK2	c.2348C>T	P.A783V
SH_141	X	154009536	154009536	Missense_Mutation	SNV	G	A	A	MPP1	c.1151C>T	P.A384V
SH_142	1	152328545	152328545	Missense_Mutation	SNV	C	T	T	FLG2	c.1717G>A	P.G573S
SH_142	1	160128882	160128882	Nonsense_Mutation	SNV	C	T	T	ATP1A4	c.616C>T	P.R206*
SH_142	1	169521867	169521867	Silent	SNV	T	A	A	F5	c.1224A>T	P.T408T
SH_142	11	1015833	1015833	Missense_Mutation	SNV	A	T	T	MUC6	c.6968T>A	P.L2323H
SH_142	11	60511334	60511334	Missense_Mutation	SNV	A	T	T	MS4A18	c.950A>T	P.N317I
SH_142	13	46549875	46549875	Missense_Mutation	SNV	T	A	A	ZC3H13	c.2011A>T	P.R671W
SH_142	16	88889111	88889111	Missense_Mutation	SNV	T	A	A	GALN5	c.1250A>T	P.D417V
SH_142	17	40066498	40066498	Nonsense_Mutation	SNV	C	A	A	ACLY	c.322G>T	P.E108*
SH_142	17	7577534	7577534	Missense_Mutation	SNV	C	A	A	TP53	c.747G>T	P.R249S
SH_142	18	12840737	12840737	Missense_Mutation	SNV	T	C	C	PTPN2	c.49A>G	P.M17V
SH_142	19	51381807	51381807	Missense_Mutation	SNV	A	G	G	KLK2	c.778A>G	P.N260D
SH_142	19	53855810	53855810	Missense_Mutation	SNV	A	T	T	ZNF845	c.1882A>T	P.T628S
SH_142	19	55495073	55495073	Silent	SNV	T	A	A	NLRP2	c.2007T>A	P.S669S
SH_142	2	152584345	152584345	Missense_Mutation	SNV	G	C	C	NEB	c.154C>G	P.L52V
SH_142	2	95818945	95818945	Silent	SNV	C	T	T	ZNF514	c.273G>A	P.L91L
SH_142	21	47981673	47981673	Silent	SNV	A	T	T	DIP2A	c.4032A>T	P.V1344V
SH_142	22	30064329	30064329	Missense_Mutation	SNV	A	T	T	NF2	c.893A>T	P.Q298L
SH_142	5	160042933	160042933	Missense_Mutation	SNV	G	T	T	ATP10B	c.2565C>A	P.F855L
SH_142	6	30864789	30864789	Splice_Site	SNV	A	T	T	DDR1	c.1759-2A>T	
SH_142	7	98460938	98460938	Missense_Mutation	SNV	G	T	T	TMEM130	c.171C>A	P.D57E
SH_142	7	98581022	98581022	Missense_Mutation	SNV	G	A	A	TRRAP	c.8941G>A	P.V2981M
SH_142	7	99757853	99757853	Missense_Mutation	SNV	C	T	T	GAL3ST4	c.1159G>A	P.G387S
SH_142	9	116050472	116050472	Missense_Mutation	SNV	A	T	T	PRPF4	c.950A>T	P.D317V
SH_143	1	158517848	158517848	Silent	SNV	A	G	G	OR6Y1	c.48T>C	P.R16R
SH_143	1	158906853	158906853	Missense_Mutation	SNV	G	C	C	PYHIN1	c.153G>C	P.L51F
SH_143	1	168054847	168054847	Silent	SNV	G	A	A	GRP161	c.1572C>T	P.G524G
SH_143	11	123676773	123676773	Silent	SNV	G	A	A	ORM6M1	c.285C>T	P.C95C
SH_143	11	64390360	64390377	Missense_Mutation	INDEL	GACGGCCCC	-	-	NRXN2	delGGGGAGGGG	G1341_V1346del
SH_143	11	65810698	65810698	Silent	SNV	G	A	A	GAL3ST3	c.576C>T	P.R192R
SH_143	11	66114676	66114676	Missense_Mutation	SNV	T	A	A	B4GAT1	c.341A>T	P.E114V
SH_143	12	103696114	103696114	Silent	SNV	G	T	T	C12orf42	c.855C>A	P.L285L
SH_143	12	12871186	12871186	Nonsense_Mutation	SNV	C	A	A	CDKN1B	c.413C>A	P.S138*
SH_143	12	77236716	77236716	Silent	SNV	A	G	G	ZDHH17	c.1284A>G	P.A428A
SH_143	13	26620769	26620769	Missense_Mutation	SNV	A	G	G	SHISA2	c.770T>C	P.V257A
SH_143	15	102358648	102358648	Missense_Mutation	SNV	A	G	G	OR4F15	c.259A>G	P.K87E
SH_143	15	22382718	22382718	Silent	SNV	G	A	A	OR4N4	c.246G>A	P.L82L
SH_143	15	23812278	23812278	Missense_Mutation	SNV	G	T	T	MKRN3	c.1349G>T	P.R450L
SH_143	15	41554970	41554970	Missense_Mutation	SNV	T	G	G	CHP1	c.238T>G	P.F80V
SH_143	15	43495413	43495413	Missense_Mutation	SNV	G	A	A	EPB42	c.1769C>T	P.T590I
SH_143	16	1258196	1258196	Missense_Mutation	SNV	C	T	T	CACNA1H	c.3338C>T	P.P1113L
SH_143	16	3339800	3339817	Missense_Mutation	INDEL	CCCCACAGT	-	-	ZNF263	delGGCCACAA	P.A433_E438del
SH_143	17	56247732	56247732	Missense_Mutation	SNV	C	T	T	OR4D2	c.716C>T	P.T239I
SH_143	17	72287244	72287244	Silent	SNV	C	G	G	DNAI2	c.696C>G	P.L232L
SH_143	17	72576200	72576200	Missense_Mutation	SNV	G	C	C	CD300LD	c.526C>G	P.L176V
SH_143	17	7578530	7578530	Missense_Mutation	SNV	A	G	G	TP53	c.400T>C	P.F134L
SH_143	18	47500762	47500762	Missense_Mutation	SNV	G	A	A	MYO5B	c.1280C>T	P.S427F
SH_143	2	131976469	131976469	Missense_Mutation	SNV	A	G	G	POTEE	c.494A>G	P.D165G
SH_143	2	75280721	75280721	Splice_Site	SNV	C	T	T	TACR1	c.735+11G>A	
SH_143	2	86255777	86255777	Missense_Mutation	SNV	C	T	T	POLR1A	c.4837G>A	P.G1613S
SH_143	20	20144789	20144789	Silent	SNV	C	T	T	CFAP61	c.1122C>T	P.P374P
SH_143	21	39817354	39817354	Missense_Mutation	SNV	C	A	A	ERG	c.230G>T	P.C77F
SH_143	21	43959744	43959744	Missense_Mutation	SNV	A	C	C	SLC37A1	c.473A>C	P.Y158S
SH_143	22	18171920	18171920	Splice_Site	SNV	T	A	A	BCL2L13	c.458+12T>A	
SH_143	3	148727077	148727077	Missense_Mutation	SNV	A	G	G	GYG1	c.496A>G	P.I166V
SH_143	3	158520026	158520026	Missense_Mutation	SNV	G	T	T	MFSD1	c.232G>T	P.A78S
SH_143	3	38138125	38138125	Missense_Mutation	SNV	A	C	C	DLEC1	c.2237A>C	P.E746A
SH_143	3	42742268	42742268	Silent	SNV	C	G	G	HHATL	c.51G>C	P.L17L

SH_143	3	89521634	89521634	Missense_Mutation	SNV	A	G	G	EPHA3	c.2711A>G	P.D904G
SH_143	4	5633724	5633724	Silent	SNV	G	A	A	EV2	c.1266C>T	P.L422L
SH_143	5	140720334	140720334	Missense_Mutation	SNV	G	T	T	PCDHGA2	c.1796G>T	P.G599V
SH_143	5	71490897	71490897	Missense_Mutation	SNV	A	G	G	MAP1B	c.1337A>G	P.N446S
SH_143	5	7707830	7707830	Frame_Shift_Del	INDEL	T	-	-	ADCY2	c.1282delT	P.S428fs
SH_143	6	46846033	46846033	Nonsense_Mutation	SNV	G	T	T	ADGRF5	c.1146C>A	P.C382*
SH_143	6	64694495	64694495	Missense_Mutation	SNV	G	T	T	EYS	c.6836C>A	P.A2279E
SH_143	7	27868383	27868383	Missense_Mutation	SNV	G	T	T	TAX1BP1	c.2179G>T	P.D727Y
SH_143	7	43503278	43503278	Missense_Mutation	SNV	A	G	G	HECW1	c.2569A>G	P.T857A
SH_143	8	119122426	119122426	Missense_Mutation	SNV	T	C	C	EXT1	c.860A>G	P.H287R
SH_143	8	144895892	144895892	Missense_Mutation	SNV	G	C	C	SCRIB	c.361C>G	P.P121A
SH_143	8	145657749	145657749	Silent	SNV	G	A	A	TONSL	c.3654C>T	P.L1218L
SH_143	8	146076454	146076454	Missense_Mutation	SNV	G	C	C	COMM5	c.270C>G	P.H90Q
SH_143	8	32616818	32616818	Splice_Site	SNV	A	G	G	NRG1	c.922-6A>G	
SH_143	8	87683256	87683256	Nonsense_Mutation	SNV	T	A	A	CNGB3	c.409A>T	P.K137*
SH_143	9	97321230	97321230	Missense_Mutation	SNV	G	A	A	FBP2	c.1010C>T	P.A337V
SH_143	X	128701285	128701285	Missense_Mutation	SNV	A	G	G	OCRL	c.1411A>G	P.I471V
SH_143	X	151869767	151869767	Missense_Mutation	SNV	A	G	G	MAGEA6	c.457A>G	P.K153E
SH_143	X	69353826	69353826	Missense_Mutation	SNV	C	T	T	IGBP1	c.29C>T	P.P10L
SH_143	X	77224545	77224545	Silent	SNV	C	T	T	PGAM4	c.591G>A	P.V197V
SH_144	1	152883791	152883791	Missense_Mutation	SNV	G	T	T	IVL	c.1518G>T	P.Q506H
SH_144	1	158670122	158670122	Silent	SNV	G	A	A	OR6K2	c.321C>T	P.G107G
SH_144	10	101165535	101165535	Missense_Mutation	SNV	T	A	A	GOT1	c.620A>T	P.K207M
SH_144	11	5632106	5632106	Missense_Mutation	SNV	C	T	T	TRIM6	c.1085C>T	P.S362F
SH_144	12	25398284	25398284	Missense_Mutation	SNV	C	A	A	KRAS	c.35G>T	P.G12V
SH_144	12	2675598	2675598	Missense_Mutation	SNV	C	T	T	CACNA1C	c.1519C>T	P.R507C
SH_144	12	95927629	95927629	Missense_Mutation	SNV	C	T	T	USP44	c.404G>A	P.G135D
SH_144	13	99036977	99036977	Splice_Site	SNV	T	A	A	FARP1	c.497-7T>A	
SH_144	15	29346119	29346119	Missense_Mutation	SNV	G	A	A	APBA2	c.32G>A	P.S11N
SH_144	15	68617541	68617541	Silent	SNV	G	A	A	ITGA11	c.2250C>T	P.V750V
SH_144	15	86076959	86076959	Missense_Mutation	SNV	A	G	G	AKAP13	c.326A>G	P.N109S
SH_144	16	56969335	56969335	Missense_Mutation	SNV	A	G	G	HERPUD1	c.245A>G	P.H82R
SH_144	16	9857975	9857975	Silent	SNV	G	A	A	GRIN2A	c.3426C>T	P.P1142P
SH_144	17	3916801	3916801	Missense_Mutation	SNV	G	A	A	ZZEF1	c.8521C>T	P.H2841Y
SH_144	17	48605584	48605584	Missense_Mutation	SNV	G	A	A	MYCBPAP	c.2489G>A	P.G830D
SH_144	19	40433036	40433036	Silent	SNV	G	A	A	FCGBP	c.1233C>T	P.T411T
SH_144	19	9067768	9067768	Missense_Mutation	SNV	C	G	G	MUC16	c.19678G>C	P.A6560P
SH_144	20	1616925	1616925	Silent	SNV	G	A	A	SIRPG	c.657C>T	P.D219D
SH_144	21	34950679	34950679	Silent	SNV	C	T	T	DONSON	c.1635G>A	P.P545P
SH_144	3	164905979	164905979	Silent	SNV	A	G	G	SLITRK3	c.2640T>C	P.S880S
SH_144	3	5024843	5024843	Silent	SNV	C	T	T	BHLHE40	c.705C>T	P.S235S
SH_144	3	78663961	78663961	Splice_Site	SNV	A	G	G	ROBO1	c.3983-11T>C	
SH_144	4	177058738	177058738	Frame_Shift_Del	INDEL	C	-	-	WDR17	c.1407delC	P.I471fs
SH_144	4	177649010	177649010	Silent	SNV	G	A	A	VEGFC	c.474C>T	P.S158S
SH_144	4	90170826	90170826	Missense_Mutation	SNV	T	C	C	GPRIN3	c.436A>G	P.I146V
SH_144	5	140182649	140182649	Missense_Mutation	SNV	C	T	T	PCDHA3	c.1867C>T	P.R623C
SH_144	6	101173474	101173474	Missense_Mutation	SNV	A	C	C	ASCC3	c.1843T>G	P.L615V
SH_144	6	46977694	46977694	Missense_Mutation	SNV	C	T	T	ADGRF1	c.1477G>A	P.V493I
SH_144	X	27998532	27998532	Missense_Mutation	SNV	T	C	C	DCAF8L1	c.920A>G	P.E307G
SH_144	X	79985517	79985517	Missense_Mutation	SNV	A	G	G	BRWD3	c.1130T>C	P.L377S
SH_146	3	47165534	47165534	Nonsense_Mutation	SNV	G	A	A	SETD2	c.592C>T	P.Q198*
SH_146	5	140774176	140774176	Missense_Mutation	SNV	G	T	T	PCDHGA8	c.1796G>T	P.G599V
SH_147	1	53723145	53723145	Splice_Site	SNV	G	T	T	LRP8	c.2210-9C>A	
SH_147	10	33200967	33200967	Nonsense_Mutation	SNV	C	A	A	ITGB1	c.1555G>T	P.E519*
SH_147	11	55433390	55433390	Missense_Mutation	SNV	G	T	T	OR4C6	c.748G>T	P.V250F
SH_147	11	60105210	60105210	Splice_Site	SNV	T	G	G	MS4A6E	c.148-4T>G	
SH_147	12	100166768	100166768	Missense_Mutation	SNV	C	G	G	ANKS1B	c.1060G>C	P.D354H
SH_147	12	31944829	31944829	Missense_Mutation	SNV	G	T	T	H3F3C	c.272C>A	P.A91E
SH_147	12	94580225	94580225	Missense_Mutation	SNV	G	A	A	PLXNC1	c.1415G>A	P.C472Y
SH_147	16	49671974	49671974	Missense_Mutation	SNV	G	T	T	ZNFA23	c.909C>A	P.S303R
SH_147	17	3438998	3438998	Missense_Mutation	SNV	G	T	T	TRPV3	c.653C>A	P.A218E
SH_147	17	7577046	7577046	Nonsense_Mutation	SNV	C	A	A	TP53	c.892G>T	P.E298*
SH_147	2	128387313	128387313	Missense_Mutation	SNV	A	G	G	MYO7B	c.4640A>G	P.Q1547R
SH_147	3	52637689	52637689	Missense_Mutation	SNV	C	A	A	PBRM1	c.2627G>T	P.R876L
SH_147	5	140768936	140768936	Missense_Mutation	SNV	G	T	T	PCDHGB4	c.1485G>T	P.E495D
SH_147	6	52878499	52878499	Silent	SNV	C	A	A	ICK	c.1113G>T	P.P371P
SH_147	6	7583200	7583200	Missense_Mutation	SNV	T	G	G	DSP	c.3908T>G	P.L1303R
SH_147	8	81430634	81430634	Splice_Site	SNV	C	G	G	ZBTB10	c.1961-4C>G	
SH_147	8	92007983	92007983	Silent	SNV	G	T	T	TMEM55A	c.696C>A	P.L232L
SH_147	8	92007984	92007984	Missense_Mutation	SNV	A	T	T	TMEM55A	c.695T>A	P.L232H
SH_147	9	32634328	32634328	Missense_Mutation	SNV	G	T	T	TAFL1	c.1250C>A	P.A417D
SH_147	X	147919231	147919231	Missense_Mutation	SNV	C	A	A	AFF2	c.1147C>A	P.Q383K
SH_147	X	27766382	27766382	Missense_Mutation	SNV	C	T	T	DCAF8L2	c.1370C>T	P.A457V
SH_16	1	148888233	148888233	Splice_Site	SNV	G	T	T	LOC101927429	n.540+8G>T	
SH_16	1	151681548	151681548	Missense_Mutation	SNV	C	A	A	CELF3	c.271G>T	P.A91S
SH_16	1	201180607	201180607	Missense_Mutation	SNV	T	A	A	IGFN1	c.6586T>A	P.F2196I
SH_16	1	24076378	24076378	Missense_Mutation	SNV	A	G	G	TCEB3	c.257A>G	P.H86R
SH_16	1	39768605	39768605	Missense_Mutation	SNV	T	A	A	MACF1	c.2659T>A	P.C887S
SH_16	10	107005371	107005371	Missense_Mutation	SNV	G	T	T	SORCS3	c.2940G>T	P.Q980H
SH_16	11	95712566	95712566	Missense_Mutation	SNV	C	T	T	MAML2	c.3017G>A	P.S1006N
SH_16	12	46125092	46125092	Frame_Shift_Del	INDEL	C	-	-	ARID2	c.279delC	P.L94fs
SH_16	12	7252302	7252302	Missense_Mutation	SNV	T	C	C	C1RL	c.545A>G	P.E182G
SH_16	14	56104500	56104500	Missense_Mutation	SNV	A	G	G	KTNN1	c.1720A>G	P.I574V
SH_16	15	28451412	28451412	Missense_Mutation	SNV	C	A	A	HERC2	c.7186G>T	P.A2396S
SH_16	16	71509288	71509288	Missense_Mutation	SNV	C	T	T	ZNFR19	c.1162G>A	P.D388N
SH_16	16	74425621	74425621	Silent	SNV	C	G	G	NPIP815	c.975C>G	P.V325V
SH_16	16	79245590	79245590	Missense_Mutation	SNV	G	T	T	WWOX	c.803G>T	P.R268L
SH_16	17	10408714	10408714	Silent	SNV	A	G	G	MYH1	c.2289T>C	P.G763G
SH_16	17	7577534	7577534	Missense_Mutation	SNV	C	A	A	TP53	c.747G>T	P.R249S
SH_16	19	8997470	8997470	Missense_Mutation	SNV	T	C	C	MUC16	c.40952A>G	P.N13651S
SH_16	2	231065609	231065609	Missense_Mutation	SNV	A	G	G	SP110	c.1139T>C	P.V380A
SH_16	2	26437363	26437363	Missense_Mutation	SNV	T	G	G	HADHA	c.867A>C	P.K289N
SH_16	20	9353722	9353722	Missense_Mutation	SNV	G	T	T	PLCB4	c.715G>T	P.V239L
SH_16	3	111870794	111870794	Missense_Mutation	SNV	G	T	T	SLC9C1	c.3290C>A	P.A1097D
SH_16	3	178937402	178937402	Missense_Mutation	SNV	A	C	C	PIK3CA	c.1790A>C	P.Q597P
SH_16	6	112397659	112397659	Missense_Mutation	SNV	G	T	T	TUBE1	c.502C>A	P.P168T
SH_16	6	143605321	143605321	Silent	SNV	A	T	T	AI61	c.444A>T	P.G148G
SH_16	6	28365896	28365896	Missense_Mutation	SNV	G	A	A	ZSCAN12	c.287C>T	P.T96I

SH_16	6	3137682	3137682	Missense_Mutation	SNV	G	A	A	BPHL	c.568G>A	P.E190K
SH_16	6	5613523	5613523	Frame_Shift_Del	INDEL	T	-	-	FARS2	c.1188delT	P.D397fs
SH_16	7	11514106	11514106	Missense_Mutation	SNV	G	A	A	THSD7A	c.2107C>T	P.P703S
SH_16	7	148904439	148904439	Splice_Site	SNV	C	A	A	ZNF282	c.713-4C>A	
SH_16	8	35624493	35624493	Missense_Mutation	SNV	C	A	A	UNC5D	c.2372C>A	P.T791K
SH_16	9	18635934	18635934	Splice_Site	SNV	T	A	A	ADAMTSL1	c.602-7T>A	
SH_16	9	27172744	27172744	Missense_Mutation	SNV	G	C	C	TEK	c.759G>C	P.K253N
SH_16	9	33467459	33467459	Frame_Shift_Del	INDEL	C	-	-	NOL6	c.1658delG	P.G553fs
SH_17	1	160105259	160105259	Silent	SNV	C	T	T	ATP1A2	c.2151C>T	P.N717N
SH_17	1	186084057	186084057	Nonsense_Mutation	SNV	C	T	T	HMCN1	c.11383C>T	P.R379S*
SH_17	11	6291978	6291978	Silent	SNV	C	T	T	CCKBR	c.504C>T	P.D168D
SH_17	11	7110527	7110527	Missense_Mutation	SNV	C	T	T	RBMXL2	c.176C>T	P.P59L
SH_17	12	25398284	25398284	Missense_Mutation	SNV	C	T	T	KRAS	c.35G>A	P.G12D
SH_17	17	7578404	7578404	Missense_Mutation	SNV	A	T	T	TP53	c.526T>A	P.C176S
SH_17	20	39800857	39800857	Missense_Mutation	SNV	C	T	T	PLCG1	c.2833C>T	P.R945W
SH_17	6	152673313	152673313	Missense_Mutation	SNV	G	A	A	SYNE1	c.11384C>T	P.T3795M
SH_17	6	25726439	25726439	Missense_Mutation	SNV	C	T	T	HIST1H2AA	c.317G>A	P.G106D
SH_17	7	129350276	129350276	Silent	SNV	A	G	G	NRF1	c.828A>G	P.E276E
SH_17	X	53619395	53619395	Missense_Mutation	SNV	C	T	T	HUWE1	c.3935G>A	P.R1312H
SH_18	1	158054241	158054241	Missense_Mutation	SNV	G	T	T	KIRREL	c.82G>T	P.G28C
SH_18	1	230468694	230468694	Missense_Mutation	SNV	C	T	T	PGBD5	c.1169G>A	P.R390Q
SH_18	11	12020291	12020291	Silent	SNV	T	C	C	DKK3	c.387A>G	P.S129S
SH_18	11	5254266	5254266	Silent	SNV	G	T	T	HBD	c.372C>A	P.T124T
SH_18	12	26277461	26277461	Silent	SNV	G	A	A	BHLHE41	c.117C>T	P.D39D
SH_18	13	46726927	46726927	Missense_Mutation	SNV	T	G	G	LCP1	c.727A>C	P.S243R
SH_18	15	48533766	48533766	Missense_Mutation	SNV	G	T	T	SLC12A1	c.1270G>T	P.V424F
SH_18	17	48677006	48677006	Missense_Mutation	SNV	G	T	T	CACNA1G	c.3476G>T	P.R1159L
SH_18	19	58153454	58153454	Missense_Mutation	SNV	A	G	G	ZNF211	c.1795A>G	P.K599E
SH_18	19	9076224	9076224	Missense_Mutation	SNV	C	A	A	MUC16	c.11222G>T	P.G3741V
SH_18	2	20405124	20405124	Missense_Mutation	SNV	T	C	C	SDC1	c.128A>G	P.N435
SH_18	3	110912063	110912063	Missense_Mutation	SNV	G	A	A	NECTIN3	c.1301G>A	P.R434K
SH_18	4	26640392	26640392	Splice_Site	SNV	G	T	T	TBC1D19	c.175-1G>T	
SH_18	5	169533358	169533358	Missense_Mutation	SNV	G	A	A	FOXI1	c.397G>A	P.A133T
SH_19	1	160788066	160788066	Missense_Mutation	SNV	C	G	G	LY9	c.1131C>G	P.C377W
SH_19	1	85736473	85736473	Silent	SNV	T	G	G	BCL10	c.174A>C	P.R58R
SH_19	10	127524684	127524684	Frame_Shift_Ins	INDEL	-	T	T	BCCIP	c.786_787insT	P.K263fs
SH_19	10	49447708	49447708	Missense_Mutation	SNV	C	A	A	FRMPD2	c.728G>T	P.S243I
SH_19	10	93601080	93601080	Missense_Mutation	SNV	T	C	C	TNKS2	c.1714T>C	P.Y572H
SH_19	11	8661866	8661866	Nonsense_Mutation	SNV	G	A	A	TRIM66	c.1621C>T	P.Q541*
SH_19	13	101997759	101997759	Nonsense_Mutation	SNV	C	T	T	NALCN	c.657G>A	P.W219*
SH_19	16	1306632	1306632	Silent	SNV	C	T	T	TPSD1	c.198C>T	P.C66C
SH_19	4	110454797	110454797	Missense_Mutation	SNV	G	A	A	SEC24B	c.3439G>A	P.D1147N
SH_19	6	30313242	30313242	Splice_Site	SNV	A	T	T	RPP21	c.159-2A>T	
SH_19	7	48413961	48413961	Silent	SNV	C	T	T	ABCA13	c.11151C>T	P.T3717T
SH_19	7	8198260	8198260	Missense_Mutation	SNV	G	A	A	ICA1	c.602C>T	P.A201V
SH_19	9	101900207	101900207	Missense_Mutation	SNV	G	T	T	TGFB1	c.641G>T	P.G214V
SH_20	1	248343535	248343535	Missense_Mutation	SNV	T	C	C	OR2M2	c.248T>C	P.F83S
SH_20	1	53728185	53728185	Silent	SNV	C	A	A	LRP8	c.1707G>T	P.G569G
SH_20	1	75708631	75708631	Missense_Mutation	SNV	T	A	A	SLC44A5	c.411A>T	P.K137N
SH_20	10	33218859	33218859	Missense_Mutation	SNV	T	C	C	ITGB1	c.267A>G	P.I89M
SH_20	10	6527155	6527155	Missense_Mutation	SNV	T	A	A	PRKCQ	c.977A>T	P.N326I
SH_20	11	61732277	61732277	Silent	SNV	C	T	T	FTH1	c.474G>A	P.K158K
SH_20	12	41337930	41337930	Frame_Shift_Ins	INDEL	-	GA	GA	CNTN1	1642_1643dupC	P.D548fs
SH_20	12	66622112	66622112	Silent	SNV	C	T	T	IRAK3	c.666C>T	P.N222N
SH_20	12	93245003	93245003	Missense_Mutation	SNV	T	C	C	EEA1	c.682A>G	P.K228E
SH_20	13	28964068	28964068	Missense_Mutation	SNV	T	C	C	FLT1	c.1834A>G	P.T612A
SH_20	17	7577534	7577534	Missense_Mutation	SNV	C	A	A	TP53	c.747G>T	P.R249S
SH_20	19	55363450	55363450	Splice_Site	SNV	C	A	A	KIR3DL2	c.71-3C>A	
SH_20	19	56423938	56423938	Missense_Mutation	SNV	G	T	T	NLRP13	c.1245C>A	P.N415K
SH_20	3	111923246	111923246	Missense_Mutation	SNV	G	A	A	SLC9C1	c.1847C>T	P.A616V
SH_20	3	146312817	146312817	Splice_Site	SNV	A	T	T	PLSCR5	c.232+11T>A	
SH_20	3	58084471	58084471	Missense_Mutation	SNV	A	T	T	FLNB	c.1181A>T	P.E394V
SH_20	3	74350606	74350606	Nonsense_Mutation	SNV	T	A	A	CNTN3	c.2038A>T	P.K680*
SH_20	4	107845802	107845802	Missense_Mutation	SNV	A	T	T	DKK2	c.429T>A	P.D143E
SH_20	5	140236939	140236939	Missense_Mutation	SNV	G	A	A	PCDHA10	c.1306G>A	P.A436T
SH_20	6	26091275	26091275	Missense_Mutation	SNV	G	A	A	HFE	c.283G>A	P.D95N
SH_20	7	131829986	131829986	Missense_Mutation	SNV	C	A	A	PLXNA4	c.5117G>T	P.G1706V
SH_20	7	54610501	54610501	Missense_Mutation	SNV	A	T	T	VSTM2A	c.78A>T	P.Q26H
SH_20	8	87423940	87423940	Missense_Mutation	SNV	A	T	T	WWP1	c.898A>T	P.S300C
SH_20	X	147018025	147018025	Missense_Mutation	SNV	A	G	G	FMR1	c.883A>G	P.K295E
SH_24	18	48604743	48604743	Frame_Shift_Del	INDEL	ATTCACTTAC	-	-	SMAD4	TTGAAATTCACT	P.C523fs
SH_24	6	27925499	27925499	Missense_Mutation	SNV	A	C	C	OR2B6	c.481A>G	P.T161P
SH_25	1	151789714	151789714	Missense_Mutation	SNV	G	A	A	RORC	c.50C>T	P.S17L
SH_25	1	155207299	155207299	Missense_Mutation	SNV	C	T	T	GBA	c.832G>A	P.G278R
SH_25	1	158614179	158614179	Missense_Mutation	SNV	T	C	C	SPTA1	c.4202A>G	P.Q1401R
SH_25	1	180155280	180155280	Missense_Mutation	SNV	T	A	A	QSOX1	c.980T>A	P.L327Q
SH_25	1	225510522	225510522	Missense_Mutation	SNV	T	A	A	DNAH14	c.9213T>A	P.D3071E
SH_25	1	24696306	24696306	Missense_Mutation	SNV	G	T	T	STPG1	c.595C>A	P.L199I
SH_25	10	17026108	17026108	Silent	SNV	A	T	T	CUBN	c.4521T>A	P.T1507T
SH_25	10	27323935	27323935	Missense_Mutation	SNV	T	A	A	ANKRD26	c.3441A>T	P.Q1147H
SH_25	10	29822291	29822291	Silent	SNV	C	A	A	SVIL	c.1005G>T	P.A335A
SH_25	11	1099786	1099786	Frame_Shift_Del	INDEL	G	-	-	MUC2	c.7371delG	P.R2459fs
SH_25	11	56258299	56258299	Missense_Mutation	SNV	A	T	T	OR5M8	c.548T>A	P.L183Q
SH_25	11	56756576	56756576	Missense_Mutation	SNV	T	G	G	OR5AK2	c.188T>G	P.L63R
SH_25	12	1702845	1702845	Missense_Mutation	SNV	T	C	C	FBXL14	c.388A>G	P.I130V
SH_25	12	31236909	31236909	Missense_Mutation	SNV	G	A	A	DDX11	c.307G>A	P.G103S
SH_25	12	63974547	63974547	Missense_Mutation	SNV	T	A	A	DPY19L2	c.1795A>T	P.I599L
SH_25	12	78582472	78582472	Silent	SNV	T	A	A	NAV3	c.5970T>A	P.I1990I
SH_25	13	103389927	103389927	Missense_Mutation	SNV	T	C	C	CCDC168	c.13120A>G	P.K4374E
SH_25	13	76374968	76374968	Missense_Mutation	SNV	G	C	C	LMO7	c.611G>C	P.R204T
SH_25	14	64892794	64892794	Missense_Mutation	SNV	A	T	T	MTHFD1	c.1011A>T	P.E337D
SH_25	15	31294159	31294159	Missense_Mutation	SNV	C	A	A	TRPM1	c.4795G>T	P.V1599L
SH_25	16	60392609	60392609	Missense_Mutation	SNV	A	T	T	LOC729159	c.998T>A	P.L333Q
SH_25	17	41852171	41852171	Silent	SNV	G	A	A	DUSP3	c.261C>T	P.G87G
SH_25	19	33953923	33953923	Missense_Mutation	SNV	T	C	C	PEPD	c.649A>G	P.M217V
SH_25	19	58017748	58017748	Missense_Mutation	SNV	T	A	A	ZNF773	c.278T>A	P.I93Q
SH_25	2	108455427	108455427	Splice_Site	SNV	A	G	G	RGPD4	c.405+7A>G	
SH_25	2	109382945	109382945	Missense_Mutation	SNV	G	A	A	RANBP2	c.5950G>A	P.G1984S

SH_25	2	131220756	131220756	Missense_Mutation	SNV	C	A	A	POTEI	c.2861G>T	P.W954L
SH_25	2	179480059	179480059	Missense_Mutation	SNV	A	T	T	TTN	c.43690T>A	P.C14564S
SH_25	2	222428585	222428585	Missense_Mutation	SNV	C	T	T	EPHA4	c.689G>A	P.R230Q
SH_25	3	100489594	100489594	Silent	SNV	A	T	T	AB13BP	c.2601T>A	P.T867T
SH_25	3	56694964	56694964	Missense_Mutation	SNV	T	A	A	FAM208A	c.1242A>T	P.E144D
SH_25	4	187455400	187455400	Missense_Mutation	SNV	C	A	A	MTNR1A	c.496G>T	P.G166W
SH_25	4	38696488	38696488	Missense_Mutation	SNV	A	G	G	KLF3	c.817A>G	P.K273E
SH_25	4	52743962	52743962	Silent	SNV	G	A	A	DCUN1D4	c.285G>A	P.K95K
SH_25	6	102250231	102250231	Missense_Mutation	SNV	G	C	C	GRIK2	c.1121G>C	P.R374T
SH_25	6	150240933	150240933	Silent	SNV	A	G	G	RAET1G	c.105T>C	P.Y35Y
SH_25	6	41711073	41711073	Missense_Mutation	SNV	T	A	A	PGC	c.383A>T	P.Q128L
SH_25	6	43333120	43333120	Frame_Shift_Del	INDEL	C	-	-	ZNF318	c.458delG	P.G153fs
SH_25	6	49754093	49754093	Missense_Mutation	SNV	T	A	A	PGK2	c.808A>T	P.M270L
SH_25	7	100636133	100636133	Silent	SNV	T	C	C	MUC12	c.2289T>C	P.R763R
SH_25	7	80091863	80091863	Silent	SNV	A	T	T	GNAT3	c.675T>A	P.A225A
SH_25	8	142487587	142487587	Splice_Site	SNV	A	G	G	MROH5	c.1366-5T>C	
SH_25	8	61178570	61178570	Missense_Mutation	SNV	C	T	T	CA8	c.331G>A	P.E111K
SH_25	9	113168980	113168980	Missense_Mutation	SNV	T	C	C	SVEP1	c.8900A>G	P.H2967R
SH_25	X	122755252	122755252	Silent	SNV	A	T	T	THOC2	c.3972T>A	P.S1324S
SH_26	1	103491886	103491886	Nonsense_Mutation	SNV	A	T	T	COL11A1	c.783T>A	P.Y261*
SH_26	1	145456723	145456723	Frame_Shift_Del	INDEL	C	-	-	POLR3GL	c.571delG	P.E191fs
SH_26	1	151001429	151001429	Splice_Site	SNV	G	T	T	PRUNE1	c.387+9G>T	
SH_26	1	151789184	151789184	Missense_Mutation	SNV	T	C	C	RORC	c.191A>G	P.H64R
SH_26	1	152383072	152383072	Silent	SNV	C	A	A	CRNN	c.486G>T	P.A162A
SH_26	1	155931448	155931448	Splice_Site	SNV	T	A	A	ARHGEF2	c.1468+4A>T	
SH_26	1	161559531	161559531	Missense_Mutation	SNV	A	T	T	FCGR2C	c.313A>T	P.N105Y
SH_26	1	162335213	162335213	Missense_Mutation	SNV	A	G	G	NOS1AP	c.74A>G	P.Q25R
SH_26	1	171753573	171753573	Missense_Mutation	SNV	A	C	C	METTL13	c.589A>C	P.T197P
SH_26	1	186045576	186045576	Missense_Mutation	SNV	G	T	T	HMCN1	c.8307G>T	P.Q2769H
SH_26	1	201194977	201194977	Missense_Mutation	SNV	C	G	G	IGFN1	c.10512C>G	P.I3504M
SH_26	1	222920395	222920395	Silent	SNV	A	T	T	FAM177B	c.213A>T	P.A71A
SH_26	1	43784956	43784956	Silent	SNV	A	T	T	TIE1	c.2973A>T	P.L991L
SH_26	1	45253107	45253107	Missense_Mutation	SNV	A	T	T	BEST4	c.184T>A	P.Y62N
SH_26	1	47610033	47610033	Missense_Mutation	SNV	A	T	T	CYP4A22	c.795A>T	P.Q265H
SH_26	10	105200499	105200499	Silent	SNV	G	T	T	PDCD11	c.4449G>T	P.V1483V
SH_26	10	134691545	134691545	Missense_Mutation	SNV	A	T	T	CFAP46	c.4052T>A	P.L1351Q
SH_26	10	61443912	61443912	Missense_Mutation	SNV	T	A	A	SLC16A9	c.138A>T	P.E46D
SH_26	10	98303889	98303889	Missense_Mutation	SNV	T	C	C	TM95F3	c.1129A>G	P.I377V
SH_26	11	1020229	1020229	Missense_Mutation	SNV	C	T	T	MUC6	c.3669G>A	P.M1223I
SH_26	11	125448157	125448157	Splice_Site	SNV	G	T	T	EI24	c.399+4G>T	
SH_26	11	16847727	16847727	Missense_Mutation	SNV	C	G	G	PLEKHA7	c.1283G>C	P.R428T
SH_26	11	59604645	59604645	Splice_Site	SNV	A	T	T	GIF	c.871+2T>A	
SH_26	12	104715085	104715085	Silent	SNV	A	T	T	TXNRD1	c.1206A>T	P.V402V
SH_26	12	109964161	109964161	Splice_Site	SNV	A	T	T	UBE3B	c.2569-2A>T	
SH_26	12	118848896	118848896	Silent	SNV	C	G	G	SUDS3	c.822C>G	P.A274A
SH_26	12	54447850	54447850	Silent	SNV	C	T	T	HOXC4	c.144C>T	P.H48H
SH_26	12	7064439	7064439	Splice_Site	SNV	T	G	G	PTPN6	c.633+9T>G	
SH_26	12	70980902	70980902	Silent	SNV	G	A	A	PTPRB	c.2196C>T	P.S732S
SH_26	12	80660340	80660340	Silent	SNV	C	T	T	OTOGL	c.2307C>T	P.G769G
SH_26	12	99065362	99065362	Missense_Mutation	SNV	A	T	T	APAF1	c.1625A>T	P.H542L
SH_26	13	103387815	103387815	Frame_Shift_Ins	INDEL	-	A	A	CCDC168	15231_15232in	P.L5078fs
SH_26	13	103387816	103387816	Missense_Mutation	SNV	T	A	A	CCDC168	c.15231A>T	P.L5077F
SH_26	13	28136914	28136914	Missense_Mutation	SNV	T	A	A	LNK2	c.860A>T	P.N287I
SH_26	13	41706613	41706613	Missense_Mutation	SNV	C	T	T	KBTBD6	c.35G>A	P.R12H
SH_26	13	48934155	48934155	Nonsense_Mutation	SNV	G	T	T	RB1	c.610G>T	P.E204*
SH_26	14	21024751	21024751	Missense_Mutation	SNV	T	A	A	RNASE9	c.478A>T	P.R160W
SH_26	14	34400402	34400402	Missense_Mutation	SNV	G	A	A	EGLN3	c.95C>T	P.P32L
SH_26	15	41961511	41961511	Missense_Mutation	SNV	G	A	A	MGA	c.419G>A	P.R140H
SH_26	15	43352244	43352244	Splice_Site	SNV	A	C	C	UBR1	c.861+6T>G	
SH_26	15	48559862	48559862	Silent	SNV	A	T	T	SLC12A1	c.2259A>T	P.A753A
SH_26	15	52540980	52540980	Missense_Mutation	SNV	C	T	T	MYO5C	c.1663G>A	P.V555I
SH_26	17	27286237	27286237	Missense_Mutation	SNV	A	T	T	SEZ6	c.1913T>A	P.L638Q
SH_26	17	36485747	36485747	Silent	SNV	G	A	A	GPR179	c.3705C>T	P.S1235S
SH_26	17	42744211	42744211	Missense_Mutation	SNV	T	A	A	MEIOC	c.932T>A	P.M311K
SH_26	17	55187384	55187384	Splice_Site	SNV	A	T	T	AKAP1	c.1715-2A>T	
SH_26	17	7578177	7578177	Missense_Mutation	SNV	C	A	A	TP53	c.672G>T	P.E224D
SH_26	18	56008937	56008937	Missense_Mutation	SNV	G	T	T	NEDD4L	c.922G>T	P.A308S
SH_26	18	57103235	57103235	Missense_Mutation	SNV	T	A	A	CCBE1	c.1126A>T	P.S376C
SH_26	18	8114778	8114778	Splice_Site	SNV	A	G	G	PTPRM	c.2131-11A>G	
SH_26	19	18324189	18324189	Missense_Mutation	SNV	C	T	T	PDE4C	c.1597G>A	P.D533N
SH_26	19	22847939	22847939	Missense_Mutation	SNV	T	A	A	ZNF492	c.1468T>A	P.S490T
SH_26	19	34929592	34929592	Nonsense_Mutation	SNV	A	T	T	UBA2	c.502A>T	P.R168*
SH_26	19	41600269	41600269	Missense_Mutation	SNV	A	T	T	CYP2A13	c.1093A>T	P.M365L
SH_26	19	43420615	43420615	Missense_Mutation	SNV	A	C	C	PSG6	c.89T>G	P.L30R
SH_26	19	45397225	45397225	Missense_Mutation	SNV	A	T	T	TOMM40	c.545A>T	P.Q182L
SH_26	19	48305649	48305649	Missense_Mutation	SNV	T	A	A	TPRX1	c.619A>T	P.I207F
SH_26	19	9677401	9677401	Missense_Mutation	SNV	T	C	C	ZNF121	c.388A>G	P.S130G
SH_26	2	107075753	107075753	Nonsense_Mutation	SNV	A	C	C	RGPD3	c.108T>G	P.Y36*
SH_26	2	133075566	133075566	Missense_Mutation	SNV	T	A	A	ZNF806	c.1027T>A	P.Y343N
SH_26	2	197987363	197987363	Splice_Site	SNV	T	A	A	ANKRD44	c.693+11A>T	
SH_26	2	207615711	207615711	Frame_Shift_Del	INDEL	G	-	-	MDH1B	c.999delC	P.I334fs
SH_26	20	44279191	44279191	Missense_Mutation	SNV	A	T	T	WFD11	c.49T>A	P.C17S
SH_26	20	45004377	45004377	Missense_Mutation	SNV	T	C	C	ELMO2	c.596A>G	P.Y199C
SH_26	20	61391368	61391368	Splice_Site	SNV	A	T	T	NTSR1	c.1008-2A>T	
SH_26	22	26343745	26343745	Missense_Mutation	SNV	A	T	T	MYO18B	c.5702A>T	P.Q1901L
SH_26	22	30518101	30518101	Silent	SNV	A	T	T	HORMAD2	c.717A>T	P.T239T
SH_26	22	44583718	44583718	Silent	SNV	G	A	A	PARVG	c.207G>A	P.E69E
SH_26	3	105243336	105243336	Silent	SNV	A	T	T	ALCAM	c.378A>T	P.T126T
SH_26	3	113378388	113378388	Missense_Mutation	SNV	A	G	G	USF3	c.2141T>C	P.L174P
SH_26	3	130311438	130311438	Silent	SNV	T	C	C	COL6A6	c.4326T>C	P.Y1442Y
SH_26	4	108614942	108614942	Missense_Mutation	SNV	T	C	C	PAPSS1	c.396A>G	P.I132M
SH_26	4	126412071	126412071	Silent	SNV	G	A	A	FAT4	c.14094G>A	P.L4698L
SH_26	4	15560785	15560785	Splice_Site	SNV	T	A	A	CC2D2A	c.2830-3T>A	
SH_26	4	165118701	165118701	Missense_Mutation	SNV	T	A	A	ANP32C	c.163A>T	P.T55S
SH_26	4	55976869	55976869	Missense_Mutation	SNV	A	T	T	KDR	c.1043T>A	P.V348D
SH_26	4	80905082	80905082	Missense_Mutation	SNV	C	A	A	ANTXR2	c.1129G>T	P.D377Y
SH_26	4	96199465	96199465	Nonsense_Mutation	SNV	A	T	T	UNC5C	c.539T>A	P.L180*
SH_26	5	132228797	132228797	Missense_Mutation	SNV	T	G	G	AFF4	c.2321A>C	P.N774T

SH_26	5	140788050	140788050	Missense_Mutation	SNV	A	T	T	PCDHGB6	c.281A>T	P.Q94L
SH_26	5	156514136	156514136	Missense_Mutation	SNV	C	A	A	HAVCR2	c.883G>T	P.G295C
SH_26	5	19483540	19483540	Nonsense_Mutation	SNV	G	T	T	CDH18	c.1643C>A	P.S548*
SH_26	5	19839092	19839092	Missense_Mutation	SNV	T	C	C	CDH18	c.4A>G	P.K2E
SH_26	5	89918411	89918411	Splice_Site	SNV	T	C	C	ADGRV1	c.454-3T>C	
SH_26	6	155761094	155761094	Missense_Mutation	SNV	T	A	A	NOX3	c.664A>T	P.T222S
SH_26	6	26107950	26107950	Silent	SNV	A	T	T	HIST1H1T	c.372T>A	P.A124A
SH_26	6	29342352	29342352	Missense_Mutation	SNV	G	T	T	OR12D3	c.713C>A	P.S238Y
SH_26	6	29574706	29574706	Missense_Mutation	SNV	G	T	T	GABBR1	c.1654C>A	P.Q525K
SH_26	6	32797229	32797229	Missense_Mutation	SNV	A	C	C	TAP2	c.1880T>G	P.V627G
SH_26	6	33371764	33371764	Missense_Mutation	SNV	A	T	T	KIFC1	c.614A>T	P.E205V
SH_26	7	138258349	138258349	Missense_Mutation	SNV	A	T	T	TRIM24	c.1874A>T	P.Q625L
SH_26	7	141755491	141755491	Missense_Mutation	SNV	A	T	T	MGAM	c.3448A>T	P.T1150S
SH_26	7	141763320	141763320	Missense_Mutation	SNV	T	A	A	MGAM	c.4279T>A	P.F1427I
SH_26	7	144060399	144060399	Nonsense_Mutation	SNV	G	T	T	ARHGEF5	c.637G>T	P.E213*
SH_26	7	151945241	151945241	Missense_Mutation	SNV	T	A	A	KMT2C	c.2278A>T	P.I760L
SH_26	7	56052539	56052539	Splice_Site	SNV	G	T	T	GBAS	c.469-1G>T	
SH_26	7	99221754	99221754	Silent	SNV	A	T	T	ZSCAN25	c.756A>T	P.I252I
SH_26	8	100733119	100733119	Missense_Mutation	SNV	A	T	T	VPS13B	c.6969A>T	P.E2323D
SH_26	8	105509634	105509634	Silent	SNV	A	G	G	LRP12	c.1089T>C	P.C363C
SH_26	8	113655811	113655811	Splice_Site	SNV	A	C	C	MIR2053	n.90A>C	
SH_26	8	133141758	133141758	Silent	SNV	C	T	T	KCNQ3	c.2010G>A	P.L670L
SH_26	8	16850679	16850679	Missense_Mutation	SNV	T	A	A	FGF20	c.538A>T	P.R180W
SH_26	8	56435975	56435975	Missense_Mutation	SNV	T	C	C	XKR4	c.1142T>C	P.F381S
SH_26	8	56708615	56708615	Silent	SNV	A	T	T	TGS1	c.1167A>T	P.L389L
SH_26	8	86250689	86250689	Splice_Site	SNV	A	G	G	CA1	c.38-11T>C	
SH_26	9	117692411	117692411	Missense_Mutation	SNV	A	T	T	TNFSF8	c.173T>A	P.M58K
SH_26	9	118666932	118666932	Splice_Site	SNV	A	T	T	LINC00474	n.77-11T>A	
SH_26	9	125486740	125486740	Missense_Mutation	SNV	C	A	A	OR1L4	c.472C>A	P.L158M
SH_26	9	39118130	39118130	Missense_Mutation	SNV	T	G	G	CNTNAP3	c.2207A>C	P.Y736S
SH_26	9	40705661	40705663	Missense_Mutation	INDEL	TAT	-	-	SPATA31A3	3319_3321delA	P.I1107del
SH_26	X	104512082	104512082	Silent	SNV	A	T	T	IL1RAPL2	c.555A>T	P.P185P
SH_26	X	36317165	36317165	Missense_Mutation	SNV	G	T	T	CFAP47	c.7760G>T	P.S2587I
SH_26	X	47308003	47308003	Missense_Mutation	SNV	C	A	A	ZNF41	c.908G>T	P.G303V
SH_26	X	50134504	50134504	Nonsense_Mutation	SNV	C	T	T	DGKK	c.1775G>A	P.V592*
SH_28	1	111957125	111957125	Frame_Shift_Del	INDEL	T	-	-	OVGP1	c.1998delA	P.E667fs
SH_28	1	186092174	186092174	Silent	SNV	G	A	A	HMCN1	c.12321G>A	P.P4107P
SH_28	1	207245668	207245668	Missense_Mutation	SNV	G	T	T	PFKFB2	c.1470G>T	P.K490N
SH_28	1	248343439	248343439	Missense_Mutation	SNV	T	C	C	OR2M2	c.152T>C	P.L51P
SH_28	1	52878217	52878217	Missense_Mutation	SNV	T	A	A	PRPF38A	c.530T>A	P.L177Q
SH_28	1	53682484	53682484	Silent	SNV	C	T	T	C1orf123	c.252G>A	P.R84R
SH_28	1	63299696	63299696	Splice_Site	INDEL	T	-	-	ATG4C	c.934-6delT	
SH_28	1	70504220	70504220	Missense_Mutation	SNV	A	G	G	LRRC7	c.2599A>G	P.T867A
SH_28	1	86426921	86426921	Splice_Site	SNV	A	T	T	COL24A1	c.2562-11T>A	
SH_28	10	17032333	17032333	Splice_Site	SNV	C	T	T	CUBN	c.4350G>A	P.E1450E
SH_28	10	6259131	6259131	Missense_Mutation	SNV	A	G	G	PFKFB3	c.415A>G	P.T139A
SH_28	10	78761223	78761223	Missense_Mutation	SNV	C	A	A	KCNMA1	c.2208G>T	P.E736D
SH_28	10	89692847	89692847	Missense_Mutation	SNV	T	C	C	PTEN	c.331T>C	P.W111R
SH_28	11	117303080	117303080	Missense_Mutation	SNV	G	A	A	DSCAML1	c.5347C>T	P.R1783W
SH_28	11	55653610	55653610	Frame_Shift_Del	INDEL	A	-	-	TRIM51	c.430delA	P.M144fs
SH_28	12	110815425	110815425	Splice_Site	INDEL	-	A	A	ANAPC7	c.1235-4dupT	
SH_28	12	123801862	123801862	Silent	SNV	T	C	C	SBN01	c.2841A>G	P.S947S
SH_28	12	48465478	48465478	Missense_Mutation	SNV	C	T	T	SENP1	c.967G>A	P.V323M
SH_28	12	52758834	52758834	Missense_Mutation	SNV	G	A	A	KRT85	c.541C>T	P.R181W
SH_28	12	54063678	54063678	Nonsense_Mutation	SNV	G	A	A	ATP5G2	c.142C>T	P.R48*
SH_28	12	6125705	6125705	Missense_Mutation	SNV	C	A	A	VWF	c.5288G>T	P.R1763L
SH_28	12	8085704	8085704	Missense_Mutation	SNV	C	T	T	SLC2A3	c.148G>A	P.G50R
SH_28	12	90028984	90028984	Frame_Shift_Del	INDEL	T	-	-	ATP2B1	c.451delA	P.T151fs
SH_28	13	114469224	114469224	Silent	SNV	G	T	T	TMEM255B	c.183G>T	P.G61G
SH_28	14	102349849	102349849	Silent	SNV	C	T	T	PPP2R5C	c.672C>T	P.F224F
SH_28	14	23893245	23893245	Silent	SNV	C	T	T	MYH7	c.2793G>A	P.E931E
SH_28	14	88940113	88940113	Frame_Shift_Del	INDEL	T	-	-	PTPN21	c.2545delA	P.I849fs
SH_28	15	30382058	30382058	Silent	SNV	C	A	A	GOLGA8J	c.1030C>A	P.R344R
SH_28	15	55613506	55613506	Missense_Mutation	SNV	T	C	C	PIGB	c.335T>C	P.L112P
SH_28	15	74640322	74640322	Missense_Mutation	SNV	C	G	G	CYP11A1	c.344G>C	P.G115A
SH_28	17	7577534	7577534	Missense_Mutation	SNV	C	A	A	TP53	c.747G>T	P.R249S
SH_28	17	8171937	8171937	Missense_Mutation	SNV	G	A	A	PFAS	c.3469G>A	P.V1157M
SH_28	17	8659736	8659736	Missense_Mutation	SNV	T	A	A	SPDYE4	c.359A>T	P.K120I
SH_28	19	11123688	11123688	Missense_Mutation	SNV	G	A	A	SMARCA4	c.2338G>A	P.E780K
SH_28	19	41307092	41307092	Silent	SNV	C	T	T	EGLN2	c.615C>T	P.R205R
SH_28	19	42914611	42914611	Missense_Mutation	SNV	G	A	A	LIPE	c.1267C>T	P.R423C
SH_28	19	51165297	51165297	Silent	SNV	G	A	A	SHANK1	c.6411C>T	P.Y2137Y
SH_28	19	53385106	53385106	Missense_Mutation	SNV	C	G	G	ZNF320	c.273G>C	P.E91D
SH_28	19	6719407	6719407	Missense_Mutation	SNV	T	C	C	C3	c.82A>G	P.I28V
SH_28	2	125405360	125405360	Silent	SNV	G	A	A	CNTNAP5	c.1899G>A	P.Q633Q
SH_28	2	128467270	128467270	Nonsense_Mutation	SNV	G	A	A	WDR33	c.3469C>T	P.R1157*
SH_28	2	196689003	196689003	Silent	SNV	A	G	G	DNAH7	c.9267T>C	P.H3089H
SH_28	2	210685243	210685243	Missense_Mutation	SNV	G	T	T	UNC80	c.2171G>T	P.S724I
SH_28	20	57009718	57009718	Missense_Mutation	SNV	A	C	C	VAPB	c.272A>C	P.Q91P
SH_28	20	61597917	61597917	Missense_Mutation	SNV	G	T	T	SLC17A9	c.1084G>T	P.A362S
SH_28	21	35154395	35154395	Silent	SNV	A	G	G	ITSN1	c.1782A>G	P.R594R
SH_28	3	119336894	119336894	Missense_Mutation	SNV	G	A	A	PLA1A	c.735G>A	P.M245I
SH_28	3	164785144	164785144	Frame_Shift_Del	INDEL	T	-	-	SI	c.619delA	P.S207fs
SH_28	3	168833263	168833263	Silent	SNV	T	C	C	MECOM	c.2028A>G	P.G676G
SH_28	4	111543439	111543439	Missense_Mutation	SNV	A	T	T	PITX2	c.178T>A	P.S60T
SH_28	5	129243945	129243945	Silent	SNV	G	A	A	CHSY3	c.978G>A	P.V326V
SH_28	5	139231295	139231295	Silent	SNV	G	T	T	NRG2	c.1468C>A	P.R490R
SH_28	5	140625308	140625308	Silent	SNV	G	T	T	PCDH15	c.162G>T	P.L54L
SH_28	5	159840963	159840963	Silent	SNV	G	A	A	SLU7	c.348C>T	P.R116R
SH_28	6	117888071	117888071	Missense_Mutation	SNV	C	T	T	GOPC	c.1180G>A	P.G394S
SH_28	6	165827144	165827144	Silent	SNV	G	T	T	PDE10A	c.1123C>A	P.R375R
SH_28	6	46801209	46801209	Missense_Mutation	SNV	C	A	A	MEP1A	c.1543C>A	P.P515T
SH_28	7	107542817	107542817	Missense_Mutation	SNV	T	A	A	DLD	c.246T>A	P.N82K
SH_28	7	40899911	40899911	Splice_Site	SNV	G	T	T	SUGCT	c.1253-4G>T	
SH_28	7	70881056	70881056	Splice_Site	SNV	C	T	T	WBSR17	c.764-7C>T	
SH_28	X	53603909	53603909	Silent	SNV	C	T	T	HUWE1	c.5835G>A	P.V1945V
SH_29	10	71678036	71678036	Splice_Site	SNV	G	T	T	COL13A1	c.997-5G>T	
SH_29	12	12038893	12038893	Missense_Mutation	SNV	A	G	G	ETV6	c.1186A>G	P.R396G

SH_29	12	25398284	25398284	Missense_Mutation	SNV	C	A	A	KRAS	c.35G>T	P.G12V
SH_29	15	66782901	66782901	Missense_Mutation	SNV	G	T	T	MAP2K1	c.1130C>T	P.S377F
SH_29	17	7578395	7578395	Missense_Mutation	SNV	G	A	A	TP53	c.535C>T	P.H179Y
SH_29	19	14094065	14094065	Silent	SNV	C	T	T	RFK1	c.447G>A	P.T149T
SH_29	22	32754310	32754310	Silent	SNV	C	T	T	RFPL3	c.252C>T	P.V84V
SH_29	3	32398937	32398937	Missense_Mutation	SNV	A	G	G	CMTM8	c.220A>G	P.M74V
SH_29	7	105255059	105255059	Silent	SNV	C	T	T	ATXN7L1	c.1074G>A	P.P358P
SH_29	8	145114792	145114792	Silent	SNV	G	A	A	OPLAH	c.144C>T	P.T48T
SH_29	9	112153424	112153424	Silent	SNV	G	A	A	PTPN3	c.1965C>T	P.Y655Y
SH_33	1	153905343	153905343	Missense_Mutation	SNV	C	T	T	DENND4B	c.3617G>A	P.R1206Q
SH_33	10	112838102	112838102	Missense_Mutation	SNV	C	A	A	ADRA2A	c.348C>A	P.F116L
SH_33	10	68940163	68940163	Missense_Mutation	SNV	G	A	A	CTNNA3	c.959C>T	P.T320M
SH_33	11	121430301	121430301	Missense_Mutation	SNV	A	C	C	SORL1	c.2984A>C	P.E995A
SH_33	12	113726026	113726026	Missense_Mutation	SNV	C	T	T	TPCN1	c.1909C>T	P.P637S
SH_33	12	25398284	25398284	Missense_Mutation	SNV	C	A	A	KRAS	c.35G>T	P.G12V
SH_33	15	23690558	23690558	Missense_Mutation	SNV	C	T	T	GOLGA6L2	c.112G>A	P.A38T
SH_33	16	449461	449461	Missense_Mutation	SNV	C	G	G	NME4	c.308C>G	P.S103C
SH_33	17	7578513	7578525	Frame_Shift_Del	INDEL	TTGCCAGTT	-	-	TP53	17delCCAACCTG	P.C135fs
SH_33	2	125192246	125192246	Missense_Mutation	SNV	G	T	T	CNTNAP5	c.715G>T	P.A239S
SH_33	2	220505520	220505520	Missense_Mutation	SNV	T	C	C	SLC4A3	c.3538T>C	P.W1180R
SH_33	20	62227109	62227109	Missense_Mutation	SNV	T	A	A	GMEB2	c.473A>T	P.D158V
SH_33	3	137787000	137787000	Missense_Mutation	SNV	C	T	T	DZIP1L	c.1825G>A	P.G609R
SH_33	4	187530361	187530361	Silent	SNV	C	A	A	FAT1	c.10182G>T	P.V3394V
SH_33	5	176522365	176522365	Silent	SNV	C	A	A	FGFR4	c.1554C>A	P.V518V
SH_33	6	166873029	166873029	Missense_Mutation	SNV	C	T	T	RP56KA2	c.1007G>A	P.P336Q
SH_33	7	146805424	146805424	Missense_Mutation	SNV	G	T	T	CNTNAP2	c.736G>T	P.V246F
SH_33	7	27238939	27238939	Missense_Mutation	SNV	G	A	A	HOXA13	c.758C>T	P.P253L
SH_33	9	35802213	35802213	Missense_Mutation	SNV	T	C	C	NPR2	c.1643T>C	P.V548A
SH_33	9	38396888	38396888	Silent	SNV	C	T	T	ALDH1B1	c.1143C>T	P.G381G
SH_33	X	100745656	100745656	Frame_Shift_Del	INDEL	G	-	-	ARMCX4	c.2080delG	P.A694fs
SH_33	X	100745657	100745657	Missense_Mutation	SNV	C	A	A	ARMCX4	c.2081C>A	P.A694D
SH_33	X	132161384	132161384	Missense_Mutation	SNV	A	G	G	USP26	c.865T>C	P.F289L
SH_33	X	18602479	18602479	Splice_Site	SNV	T	C	C	CDKL5	c.554+6T>C	P.
SH_33	X	49114840	49114840	Frame_Shift_Del	INDEL	T	-	-	FOXP3	c.123delA	P.G43fs
SH_33	X	76856044	76856044	Splice_Site	SNV	G	T	T	ATRX	c.5567-11C>A	P.
SH_34	1	11014114	11014114	Missense_Mutation	SNV	G	A	A	C1orf127	c.1061C>T	P.P354L
SH_34	1	1153964	1153964	Silent	SNV	G	A	A	SD4	c.786C>T	P.P262P
SH_34	1	1248918	1248918	Missense_Mutation	SNV	G	A	A	CPSF3L	c.1030C>T	P.R344W
SH_34	1	16378220	16378220	Missense_Mutation	SNV	G	A	A	CLCNKB	c.1313G>A	P.FR38H
SH_34	10	65357815	65357815	In Frame Ins	INDEL	-	AAGTTAAATGG	AAGTTAAATGG	REEP3	AGTTAAAGTTA	InsTerFRKLLNGYWCINI
SH_34	11	32118715	32118715	Missense_Mutation	SNV	G	A	A	RCN1	c.280G>C	P.D94N
SH_34	11	5221093	5221093	Missense_Mutation	SNV	C	T	T	OR51V1	c.838G>A	P.V280M
SH_34	11	64004663	64004663	Frame_Shift_Del	INDEL	A	-	-	VEGFB	c.386delA	P.K129fs
SH_34	12	9075393	9075393	Splice_Site	SNV	C	T	T	PHC1	c.612+9C>T	P.
SH_34	13	29001983	29001983	Silent	SNV	G	A	A	FLT1	c.1182C>T	P.D394D
SH_34	16	89777069	89777069	Missense_Mutation	SNV	G	A	A	VPS9D1	c.1183C>T	P.R395W
SH_34	17	7577509	7577509	Missense_Mutation	SNV	C	G	G	TP53	c.772G>C	P.E258Q
SH_34	19	57133360	57133360	Silent	SNV	C	T	T	ZNF71	c.705C>T	P.I235I
SH_34	2	100167958	100167958	Missense_Mutation	SNV	C	T	T	AFF3	c.3659G>A	P.R1220Q
SH_34	20	1552646	1552646	Silent	SNV	C	A	A	SIRPB1	c.471G>T	P.V157V
SH_34	20	61461004	61461004	Missense_Mutation	SNV	G	T	T	COL9A3	c.1078G>T	P.A360S
SH_34	20	62076690	62076690	Missense_Mutation	SNV	C	T	T	KCNQ2	c.415G>A	P.V139M
SH_34	21	27840860	27840860	Missense_Mutation	SNV	C	T	T	CYR1	c.752G>A	P.R251H
SH_34	22	30000101	30000101	Splice_Site	INDEL	-	GGACCTCTTTGA	GGACCTCTTTGA	NF2	GGGAAGGACCTCTTTGATTGGTGTGCCGGACTCT	
SH_34	22	32588955	32588955	Missense_Mutation	SNV	T	C	C	RFPL2	c.490A>G	P.I164V
SH_34	3	134920360	134920360	Silent	SNV	C	A	A	EPHB1	c.2175C>A	P.L725L
SH_34	3	39108051	39108051	Frame_Shift_Ins	INDEL	-	T	T	WDR48	c.37dupT	P.S13fs
SH_34	6	6654824	6654824	Silent	SNV	C	T	T	LY86	c.453C>T	P.T151T
SH_34	7	140453154	140453154	Missense_Mutation	SNV	T	C	C	BRAF	c.1781A>G	P.D594G
SH_34	9	26109943	26109943	Splice_Site	SNV	T	A	A	LOC100506422	c.34-8T>A	P.
SH_35	1	144882622	144882622	Nonsense_Mutation	SNV	T	A	A	PDE4DIP	c.3397A>T	P.K1133*
SH_35	1	158435940	158435940	Silent	SNV	C	T	T	OR10K1	c.589C>T	P.L197L
SH_35	1	228468251	228468251	Missense_Mutation	SNV	A	C	C	OBSCN	c.7951A>C	P.K2651Q
SH_35	10	134464009	134464009	Splice_Site	SNV	G	A	A	INPP5A	c.306G>A	P.T102T
SH_35	12	104378698	104378698	Splice_Site	INDEL	-	AGGATGCAAA	AGGATGCAAA	TDG	964+1insAGGATGCAAA	
SH_35	12	129822359	129822359	Silent	SNV	C	T	T	TMEM132D	c.1119G>A	P.A373A
SH_35	12	57567046	57567046	Missense_Mutation	SNV	G	C	C	LRP1	c.3259G>C	P.D1087H
SH_35	12	58240172	58240172	Missense_Mutation	SNV	A	T	T	CTDSP2	c.47T>A	P.L16Q
SH_35	12	72665953	72665953	Splice_Site	SNV	G	C	C	TRHDE-AS1	n.746-11C>G	P.
SH_35	14	61924300	61924300	Missense_Mutation	SNV	A	T	T	PRKCH	c.1181A>T	P.D394V
SH_35	14	69795268	69795268	Missense_Mutation	SNV	A	C	C	GALNT16	c.670A>C	P.M224L
SH_35	15	49325204	49325204	Nonsense_Mutation	SNV	G	A	A	SECISBP2L	c.622C>T	P.R208*
SH_35	16	17234999	17234999	Splice_Site	SNV	C	T	T	XYLT1	c.1587+11G>A	P.
SH_35	17	48773448	48773448	Missense_Mutation	SNV	T	C	C	ANKRD40	c.1017A>G	P.I339M
SH_35	2	102818104	102818104	Missense_Mutation	SNV	A	G	G	IL1RL2	c.578A>G	P.Y193C
SH_35	2	136873013	136873013	Missense_Mutation	SNV	A	G	G	CXCR4	c.497T>C	P.I166T
SH_35	2	204009852	204009852	Missense_Mutation	SNV	G	A	A	NBEAL1	c.5186G>A	P.R1729Q
SH_35	2	241685218	241685218	Missense_Mutation	SNV	C	G	G	KIF1A	c.3311G>C	P.R1104P
SH_35	20	1961294	1961294	Missense_Mutation	SNV	C	T	T	PDYN	c.440G>A	P.R147K
SH_35	22	30057328	30057328	Splice_Site	INDEL	-	CTGGATAAGAA	CTGGATAAGAA	NF2	AAACCACTGGATAAGAAATTGATGCTCTCAA	
SH_35	22	30064436	30064436	Splice_Site	SNV	G	A	A	NF2	c.999+1G>A	P.
SH_35	22	30064437	30064437	Splice_Site	INDEL	-	TCGCTCGAGAGAT	TCGCTCGAGAGAT	NF2	GCCTCTCGAGAGAGAGAGATGAGGGAGG	
SH_35	3	12616309	12616309	Missense_Mutation	SNV	G	A	A	MKRN2	c.532G>A	P.E178K
SH_35	3	129262117	129262117	Missense_Mutation	SNV	G	T	T	H1FOO	c.56G>T	P.G19V
SH_35	3	183953050	183953050	Missense_Mutation	SNV	C	T	T	VWA5B2	c.398C>T	P.T133I
SH_35	3	38674672	38674672	Nonsense_Mutation	SNV	G	A	A	SCN5A	c.127C>T	P.R43*
SH_35	3	44945459	44945459	Missense_Mutation	SNV	C	T	T	TGM4	c.1055C>T	P.T352M
SH_35	4	170983036	170983036	Splice_Site	SNV	C	A	A	AADAT	c.1248+7G>T	P.
SH_35	4	87696336	87696336	Missense_Mutation	SNV	G	A	A	PTPN13	c.5464G>A	P.D1822N
SH_35	5	110712615	110712615	Missense_Mutation	SNV	G	A	A	CAMK4	c.361G>A	P.P121I
SH_35	5	140573833	140573833	Missense_Mutation	SNV	G	A	A	PCDH810	c.1708G>A	P.A570T
SH_35	5	7784532	7784532	Missense_Mutation	SNV	C	A	A	ADCY2	c.2439C>A	P.F813L
SH_35	6	26205091	26205091	Silent	SNV	C	T	T	HIST1H4E	c.219C>T	P.Y73Y
SH_35	6	74528152	74528152	Missense_Mutation	SNV	T	C	C	CD109	c.3902T>C	P.V1301A
SH_41	1	157660082	157660082	Silent	SNV	C	T	T	FCRL3	c.1653G>A	P.G551G
SH_41	1	208062174	208062174	Silent	SNV	G	A	A	CD34	c.825C>T	P.F275F
SH_41	1	247061569	247061569	Missense_Mutation	SNV	G	T	T	AHCTF1	c.1564C>A	P.L522I
SH_41	10	89717672	89717672	Nonsense_Mutation	SNV	C	T	T	PTEN	c.697C>T	P.R233*

SH_41	11	31312387	31312387	Frame_Shift_Del	INDEL	A	-	-	DCDC1	c.767delT	P.L256fs
SH_41	11	55653674	55653674	Missense_Mutation	SNV	A	C	C	TRIM51	c.487A>C	P.T163P
SH_41	11	55735542	55735542	Missense_Mutation	SNV	A	T	T	OR10AG1	c.398T>A	P.I133N
SH_41	11	60541301	60541301	Splice_Site	SNV	G	T	T	MS4A15	c.499-9G>T	
SH_41	11	8720838	8720838	Silent	SNV	G	A	A	ST5	c.2820C>T	P.I940I
SH_41	12	51584328	51584328	Missense_Mutation	SNV	G	A	A	POU6F1	c.608C>T	P.P203L
SH_41	12	57596242	57596242	Frame_Shift_Del	INDEL	A	-	-	LRP1	c.10634delA	P.N3545fs
SH_41	12	58190116	58190116	Missense_Mutation	SNV	C	A	A	TSFM	c.728C>A	P.S243Y
SH_41	12	6729407	6729407	Silent	SNV	G	A	A	LPAR5	c.1008C>T	P.A336A
SH_41	12	78574763	78574763	Missense_Mutation	SNV	C	T	T	NAV3	c.5630C>T	P.S1877F
SH_41	13	21563060	21563060	Missense_Mutation	SNV	C	A	A	LATS2	c.859G>T	P.A287S
SH_41	13	49050852	49050852	Nonsense_Mutation	SNV	C	T	T	RB1	c.2536C>T	P.Q846*
SH_41	14	105406645	105406645	Missense_Mutation	SNV	G	A	A	AHNAK2	c.15143C>T	P.S5048F
SH_41	14	53130556	53130556	Silent	SNV	T	A	A	ERO1A	c.639A>T	P.T213T
SH_41	15	28483324	28483324	Missense_Mutation	SNV	G	T	T	HERC2	c.3788C>A	P.A1263D
SH_41	15	66727451	66727451	Missense_Mutation	SNV	A	C	C	MAP2K1	c.167A>C	P.Q56P
SH_41	17	48753285	48753285	Silent	SNV	G	T	T	ABCC3	c.2901G>T	P.G967G
SH_41	17	51901132	51901132	Silent	SNV	G	T	T	KIF2B	c.738G>T	P.V246V
SH_41	17	7577534	7577534	Missense_Mutation	SNV	C	A	A	TP53	c.747G>T	P.R249S
SH_41	18	5395656	5395656	Silent	SNV	C	T	T	EPB41L3	c.2517G>A	P.T839T
SH_41	19	17547396	17547396	Missense_Mutation	SNV	G	T	T	TMEM221	c.747C>A	P.S249R
SH_41	2	143742720	143742720	Missense_Mutation	SNV	G	T	T	KYNU	c.797G>T	P.G266V
SH_41	2	150327236	150327236	Missense_Mutation	SNV	C	A	A	LYPD6	c.388C>A	P.P130T
SH_41	2	179553444	179553444	Silent	SNV	G	T	T	TTN	c.31206C>A	P.S10402S
SH_41	2	189867729	189867729	Missense_Mutation	SNV	G	A	A	COL3A1	c.2494G>A	P.E832K
SH_41	2	228881815	228881815	Missense_Mutation	SNV	T	C	C	SPHKAP	c.3755A>G	P.N1252S
SH_41	20	47990211	47990211	Missense_Mutation	SNV	G	A	A	KCNB1	c.1886C>T	P.A629V
SH_41	3	142422812	142422812	Missense_Mutation	SNV	A	T	T	PLS1	c.1474A>T	P.T492S
SH_41	3	167254745	167254745	Missense_Mutation	SNV	T	C	C	WDR49	c.811A>G	P.I271V
SH_41	3	183975398	183975398	Missense_Mutation	SNV	A	G	G	ECE2	c.334A>G	P.M112V
SH_41	5	127610310	127610310	Missense_Mutation	SNV	A	C	C	FBN2	c.7660T>G	P.F2554V
SH_41	5	149927871	149927871	Missense_Mutation	SNV	C	T	T	NDST1	c.2237C>T	P.A746V
SH_41	5	45645361	45645361	Missense_Mutation	SNV	A	T	T	HCN1	c.775T>A	P.F259I
SH_41	6	58287587	58287587	Splice_Site	SNV	C	T	T	LINC00680	n.126+12G>A	
SH_41	7	5553282	5553282	Splice_Site	SNV	C	A	A	FBXL18	c.18+6G>T	
SH_41	7	5643166	5643166	Silent	SNV	G	A	A	FSCN1	c.1029G>A	P.R343R
SH_41	8	145140994	145140994	Missense_Mutation	SNV	G	T	T	GPAA1	c.1832G>T	P.W611L
SH_41	8	22009360	22009360	Silent	SNV	G	A	A	LG13	c.648C>T	P.F216F
SH_41	8	41575200	41575200	Silent	SNV	G	A	A	ANK1	c.1227C>T	P.H409H
SH_41	9	70918720	70918720	Missense_Mutation	SNV	G	T	T	FOXO4L3	c.853G>T	P.A285S
SH_41	X	47429396	47429396	Silent	SNV	T	G	G	ARAF	c.1524T>G	P.P508P
SH_41	X	54955222	54955222	Missense_Mutation	SNV	A	C	C	TRO	c.2065A>C	P.T689P
SH_42	1	9778973	9778973	Splice_Site	SNV	G	A	A	PIK3CD	c.1242G>C	P.A414A
SH_42	12	46246569	46246569	Missense_Mutation	SNV	G	T	T	ARID2	c.4663G>T	P.A1555S
SH_42	12	57397394	57397394	Silent	SNV	C	A	A	ZBTB39	c.1308G>T	P.L436L
SH_42	15	81631832	81631832	Missense_Mutation	SNV	A	T	T	TMC3	c.1858T>A	P.Y620N
SH_42	17	78914348	78914348	Missense_Mutation	SNV	G	A	A	RPTOR	c.2972G>A	P.R991Q
SH_42	19	44470902	44470902	Missense_Mutation	SNV	C	A	A	ZNF221	c.1248C>A	P.H416Q
SH_42	2	209113113	209113113	Missense_Mutation	SNV	G	A	A	IDH1	c.394C>T	P.R132C
SH_42	2	21231975	21231975	Missense_Mutation	SNV	C	T	T	APOB	c.7765G>A	P.E2589K
SH_42	3	127323538	127323538	Missense_Mutation	SNV	T	A	A	MCM2	c.324T>A	P.S108R
SH_42	4	165118559	165118559	Missense_Mutation	SNV	A	T	T	ANP32C	c.305T>A	P.I102K
SH_42	5	176301435	176301435	Missense_Mutation	SNV	A	C	C	UNC5A	c.1246A>C	P.T416P
SH_42	7	100187952	100187967	Frame_Shift_Del	INDEL	TTGGAAGAG	-	-	FBXO24	delCTGGGAAGAG	P.W88fs
SH_42	X	129168470	129168470	Missense_Mutation	SNV	A	G	G	BCORL1	c.4346A>G	P.K1449R
SH_44	1	152785137	152785137	Missense_Mutation	SNV	G	T	T	LCE1B	c.215G>T	P.G72V
SH_44	1	182523777	182523777	Missense_Mutation	SNV	T	G	G	RGSL1	c.3146T>G	P.L1049R
SH_44	1	201709159	201709159	Missense_Mutation	SNV	A	G	G	NAV1	c.8A>G	P.H3R
SH_44	1	201981144	201981144	Missense_Mutation	SNV	T	C	C	ELF3	c.223T>C	P.W75R
SH_44	1	231411243	231411243	Missense_Mutation	SNV	A	G	G	GNPAT	c.1753A>G	P.I585V
SH_44	1	34083096	34083096	Splice_Site	SNV	T	C	C	CSMD2	c.5946+3A>G	
SH_44	1	3599664	3599664	Missense_Mutation	SNV	C	T	T	TP73	c.106C>T	P.R36W
SH_44	1	37282808	37282808	Silent	SNV	G	A	A	GRIK3	c.1944C>T	P.I648I
SH_44	1	45268672	45268672	Silent	SNV	G	A	A	PLK3	c.795G>A	P.L265L
SH_44	1	46509357	46509357	Silent	SNV	C	T	T	PIK3R3	c.1374G>A	P.S458S
SH_44	10	6520975	6520975	Missense_Mutation	SNV	C	A	A	PRKCQ	c.1332G>T	P.M444I
SH_44	10	89690847	89690847	Splice_Site	SNV	G	A	A	PTEN	c.253+1G>A	
SH_44	11	133816111	133816111	Missense_Mutation	SNV	C	G	G	IGSF9B	c.107G>C	P.R36T
SH_44	11	69588259	69588259	Splice_Site	SNV	G	T	T	FGF4	c.445-6C>A	
SH_44	12	56482340	56482340	Silent	SNV	G	T	T	ERBB3	c.888G>T	P.V296V
SH_44	12	56482341	56482341	Missense_Mutation	SNV	G	T	T	ERBB3	c.889G>T	P.D297Y
SH_44	14	102816331	102816331	Missense_Mutation	SNV	C	T	T	CINP	c.361G>A	P.E121K
SH_44	14	39648393	39648393	Silent	SNV	G	A	A	PNN	c.597G>A	P.R199R
SH_44	15	22382597	22382597	Missense_Mutation	SNV	A	G	G	OR4N4	c.125A>G	P.N42S
SH_44	15	45007706	45007728	Frame_Shift_Del	INDEL	GACATTGAA	-	-	B2M	c.ATCCGACATTG	P.P52fs
SH_44	15	83331571	83331571	Missense_Mutation	SNV	C	A	A	APB2	c.2555G>T	P.G852V
SH_44	15	88423670	88423670	Splice_Site	INDEL	T	-	-	NTRK3	c.2134-11delA	
SH_44	16	30776762	30776762	Missense_Mutation	SNV	A	G	G	RNF40	c.935A>G	P.Y312C
SH_44	16	67911571	67911571	Splice_Site	SNV	G	A	A	EDC4	c.789+12G>A	
SH_44	16	70989370	70989370	Missense_Mutation	SNV	A	T	T	HYDIN	c.6224T>A	P.V2075E
SH_44	17	40043958	40043958	Splice_Site	SNV	T	C	C	ACLY	c.1771-2A>G	
SH_44	17	40937447	40937447	Missense_Mutation	SNV	G	A	A	WNK4	c.415G>A	P.E139K
SH_44	17	41180652	41180652	Missense_Mutation	SNV	G	T	T	RND2	c.639G>T	P.E213D
SH_44	17	4907333	4907333	Missense_Mutation	SNV	A	C	C	KIF1C	c.905A>C	P.D302A
SH_44	17	7578177	7578177	Splice_Site	SNV	C	T	T	TP53	c.672G>A	P.E224E
SH_44	19	1220449	1220449	Missense_Mutation	SNV	A	G	G	STK11	c.542A>G	P.N181S
SH_44	19	48052644	48052644	Missense_Mutation	SNV	G	C	C	ZNF541	c.406C>G	P.Q136E
SH_44	19	50910345	50910345	Nonsense_Mutation	SNV	G	T	T	POLD1	c.1600G>T	P.E534*
SH_44	19	55317424	55317424	Missense_Mutation	SNV	C	T	T	KIR2DL4	c.380C>T	P.S127L
SH_44	19	56703300	56703300	Silent	SNV	C	T	T	ZSCAN5B	c.507G>A	P.V169V
SH_44	19	7976372	7976372	Missense_Mutation	SNV	G	A	A	MAP2K7	c.1036G>A	P.E346K
SH_44	2	113007828	113007828	Silent	SNV	T	C	C	ZC3H8	c.96A>G	P.T32T
SH_44	2	179433009	179433009	Silent	SNV	G	T	T	TTN	c.72927C>A	P.L24309L
SH_44	2	207634902	207634902	Missense_Mutation	SNV	C	G	G	FASTKD2	c.865C>G	P.L289V
SH_44	2	61413571	61413571	Splice_Site	SNV	C	T	T	AHSA2	c.193-10C>T	
SH_44	2	69759291	69759291	Missense_Mutation	SNV	C	G	G	AAK1	c.538G>C	P.E180Q
SH_44	20	40877335	40877335	Missense_Mutation	SNV	G	C	C	PTPR	c.2361C>G	P.T787M
SH_44	20	60419757	60419757	Missense_Mutation	SNV	C	T	T	CDH4	c.499C>T	P.R167W

SH_44	22	18064136	18064136	Silent	SNV	G	A	A	SLC25A18	c.156G>A	P.L52L
SH_44	22	36962434	36962434	Silent	SNV	G	A	A	CACNG2	c.402C>T	P.I134I
SH_44	22	41360075	41360075	Missense_Mutation	SNV	C	T	T	RBX1	c.182C>A	P.A61V
SH_44	3	130871234	130871234	Nonsense_Mutation	SNV	C	A	A	NEK11	c.650C>G	P.S217*
SH_44	3	13649565	13649565	Missense_Mutation	SNV	C	T	T	FBLN2	c.1310C>T	P.S437F
SH_44	3	4703915	4703915	Missense_Mutation	SNV	G	C	C	ITPR1	c.1401G>C	P.Q467H
SH_44	3	56597721	56597721	Missense_Mutation	SNV	A	G	G	CCDC66	c.10A>G	P.K4E
SH_44	4	123267913	123267913	Missense_Mutation	SNV	C	T	T	KIAA1109	c.1286G>C	P.P4290L
SH_44	4	169182051	169182051	Silent	SNV	T	C	C	DDX60	c.3363A>G	P.L1121L
SH_44	4	169325132	169325132	Frame_Shift_Ins	INDEL	-	A	A	DDX60L	c.3338dupT	P.L1113fs
SH_44	4	66242784	66242784	Splice_Site	SNV	G	A	A	EPHA5	c.1791-3C>T	
SH_44	5	140567922	140567922	Missense_Mutation	SNV	C	A	A	PCDH89	c.1030C>A	P.P344T
SH_44	5	156770275	156770275	Silent	SNV	G	T	T	FNDC9	c.270C>A	P.T90T
SH_44	5	31294219	31294219	Nonsense_Mutation	SNV	C	T	T	CDH6	c.379C>T	P.R127*
SH_44	5	31532521	31532521	Missense_Mutation	SNV	C	T	T	C5orf22	c.22C>T	P.R8C
SH_44	5	41917285	41917285	Missense_Mutation	SNV	G	A	A	C5orf51	c.769G>A	P.G257R
SH_44	6	13053760	13053760	Frame_Shift_Del	INDEL	A	-	-	PHACTR1	c.414delA	P.A139fs
SH_44	6	28359202	28359202	Missense_Mutation	SNV	G	C	C	ZSCAN12	c.865C>G	P.L289V
SH_44	6	35754907	35754907	Splice_Site	SNV	G	A	A	CLPS1	c.222+10G>A	
SH_44	7	1489909	1489909	Silent	SNV	G	C	C	MICALL2	c.159C>G	P.L53L
SH_44	7	37355563	37355563	Missense_Mutation	SNV	T	G	G	ELMO1	c.80A>C	P.K27T
SH_44	7	3990590	3990590	Missense_Mutation	SNV	A	G	G	SDK1	c.883A>G	P.I295V
SH_44	7	74197947	74197947	Missense_Mutation	SNV	G	T	T	NCF1	c.654G>T	P.E218D
SH_44	8	11991418	11991418	Missense_Mutation	SNV	C	T	T	USP17L7	c.101G>A	P.R34Q
SH_44	8	144940597	144940597	Silent	SNV	G	A	A	EPPK1	c.6825C>T	P.P2275P
SH_44	8	28360629	28360629	Missense_Mutation	SNV	G	C	C	FZD3	c.99G>C	P.L33F
SH_44	8	41792315	41792315	Missense_Mutation	SNV	A	C	C	KAT6A	c.3423T>G	P.D1141E
SH_44	9	112189399	112189399	Missense_Mutation	SNV	C	T	T	PTPN3	c.832G>A	P.E278K
SH_44	9	117092830	117092830	Silent	SNV	G	T	T	ORM2	c.231G>T	P.T77T
SH_44	9	119449033	119449033	Missense_Mutation	SNV	C	T	T	ASTN2	c.52G>A	P.D18N
SH_44	9	71555718	71555718	Splice_Site	SNV	T	C	C	PIP5K1B	c.1502+12T>C	
SH_44	X	153042370	153042370	Missense_Mutation	SNV	T	G	G	PLXNB3	c.4931T>G	P.V1644G
SH_44	X	47429025	47429025	Missense_Mutation	SNV	T	C	C	ARAF	c.1388T>C	P.L463S
SH_44	X	53106662	53106662	Missense_Mutation	SNV	A	G	G	GPR173	c.859A>G	P.M287V
SH_44	X	79698068	79698068	Silent	SNV	T	G	G	FAM46D	c.30T>G	P.T10T
SH_44	X	82764359	82764359	Missense_Mutation	SNV	C	A	A	POU3F4	c.1027C>A	P.Q343K
SH_44	X	9673033	9673033	Missense_Mutation	SNV	C	T	T	TBL1X	c.1115C>T	P.A372V
SH_46	12	11992223	11992223	Missense_Mutation	SNV	C	G	G	ETV6	c.313C>G	P.R105G
SH_46	12	25398284	25398284	Missense_Mutation	SNV	C	T	T	KRAS	c.35G>A	P.G12D
SH_46	14	96807908	96807908	Frame_Shift_Del	INDEL	A	-	-	ATG2B	c.875delT	P.L292fs
SH_46	2	209113113	209113113	Missense_Mutation	SNV	G	A	A	IDH1	c.394C>T	P.R132C
SH_46	22	30057328	30057328	Splice_Site	INDEL	-	ACCACCTGGATAA	ACCACCTGGATAA	NF2	TATTAAACCACTGGATAAGAAAATTGAT	
SH_46	3	52668666	52668666	Frame_Shift_Del	INDEL	G	-	-	PBRM1	c.1253delC	P.P418fs
SH_46	4	62849178	62849178	Silent	SNV	G	T	T	ADGRL3	c.2889G>T	P.V963V
SH_46	5	140564296	140564296	Missense_Mutation	SNV	C	T	T	PCDH816	c.2162C>T	P.S721L
SH_46	6	30075934	30075934	Missense_Mutation	SNV	A	C	C	TRIM31	c.779T>G	P.F260C
SH_46	7	149484874	149484874	Silent	SNV	C	T	T	SSPO	c.3696C>T	P.D1232D
SH_46	X	37431496	37431496	Missense_Mutation	SNV	G	A	A	LANCL3	c.373G>A	P.A125T
SH_48	1	150039960	150039960	Missense_Mutation	SNV	G	A	A	VPS45	c.46G>A	P.E16K
SH_48	1	155448157	155448157	Missense_Mutation	SNV	T	C	C	ASH1L	c.4504A>G	P.M1502V
SH_48	1	156264146	156264146	Splice_Site	SNV	C	G	G	GLMP	c.579+10G>C	
SH_48	1	169509601	169509601	Missense_Mutation	SNV	T	C	C	F5	c.4727A>G	P.N1576S
SH_48	1	224318274	224318274	Missense_Mutation	SNV	A	C	C	FBXO28	c.368A>C	P.Q123P
SH_48	1	225195220	225195220	Missense_Mutation	SNV	T	G	G	DNAH14	c.1081T>G	P.S361A
SH_48	1	228464928	228464928	Missense_Mutation	SNV	C	A	A	OBSCN	c.6668C>A	P.T2223N
SH_48	1	228464929	228464929	Silent	SNV	C	A	A	OBSCN	c.6669C>A	P.T2223T
SH_48	1	231471924	231471924	Missense_Mutation	SNV	T	G	G	EXOC8	c.1568A>C	P.K523T
SH_48	1	247875463	247875463	Missense_Mutation	SNV	C	G	G	OR6F1	c.595G>C	P.A199P
SH_48	1	248128836	248128836	Missense_Mutation	SNV	C	T	T	OR2AK2	c.203C>T	P.T68I
SH_48	10	20106112	20106112	Missense_Mutation	SNV	A	G	G	PLXDC2	c.104A>G	P.Q35R
SH_48	10	267258	267258	Nonsense_Mutation	SNV	A	T	T	ZMYND11	c.400A>T	P.R134*
SH_48	10	27702354	27702354	Missense_Mutation	SNV	T	C	C	PTCHD3	c.826A>G	P.K276E
SH_48	10	28970333	28970333	Missense_Mutation	SNV	A	G	G	BAMBI	c.223A>G	P.S75G
SH_48	10	93619301	93619301	Missense_Mutation	SNV	T	G	G	TNKS2	c.3177T>G	P.I1059M
SH_48	11	1075781	1075781	Silent	SNV	C	A	A	MUC2	c.207C>A	P.G69G
SH_48	11	6636205	6636205	Silent	SNV	A	G	G	TPP1	c.1443T>C	P.F481F
SH_48	11	67401718	67401718	Missense_Mutation	SNV	T	G	G	TBX10	c.491A>C	P.Q164P
SH_48	11	72316235	72316235	Silent	SNV	G	A	A	PDE2A	c.249C>T	P.S83S
SH_48	11	72316236	72316236	Missense_Mutation	SNV	G	C	C	PDE2A	c.248C>G	P.S83C
SH_48	11	85692231	85692231	Missense_Mutation	SNV	C	T	T	PICALM	c.1570G>A	P.G524R
SH_48	11	893426	893426	Splice_Site	SNV	C	T	T	CHID1	c.701+1G>A	
SH_48	12	110940153	110940153	Missense_Mutation	SNV	T	G	G	RAD9B	c.11T>G	P.M4R
SH_48	12	26784800	26784800	Missense_Mutation	SNV	T	C	C	ITPR2	c.2933A>G	P.Q978R
SH_48	13	86369778	86369778	Missense_Mutation	SNV	G	T	T	SLITRK6	c.866C>A	P.S289Y
SH_48	13	99457388	99457388	Missense_Mutation	SNV	C	T	T	DOCK9	c.5626G>A	P.E1876K
SH_48	14	94741772	94741772	Silent	SNV	C	T	T	PPP4R4	c.2511C>T	P.P837P
SH_48	15	40468676	40468676	Splice_Site	SNV	A	C	C	BUB1B	c.385-2A>C	
SH_48	15	45404807	45404807	Silent	SNV	C	A	A	DUOX2	c.270G>T	P.R90R
SH_48	16	30748863	30748863	Missense_Mutation	SNV	C	G	G	SRCAP	c.7502C>G	P.P2501R
SH_48	16	8875190	8875190	Missense_Mutation	SNV	A	G	G	ABAT	c.1406A>G	P.D469G
SH_48	17	2281170	2281170	Missense_Mutation	SNV	T	G	G	SGSM2	c.2687T>G	P.F896C
SH_48	17	73847671	73847671	Missense_Mutation	SNV	G	A	A	WBP2	c.146C>T	P.T49I
SH_48	17	8349126	8349126	Missense_Mutation	SNV	A	C	C	NDEL1	c.184A>C	P.N62H
SH_48	18	14851748	14851748	Missense_Mutation	SNV	G	A	A	ANKRD30B	c.3448G>A	P.V1150I
SH_48	19	21607171	21607171	Missense_Mutation	SNV	C	G	G	ZNFA93	c.1710C>G	P.H570Q
SH_48	19	32968420	32968420	Splice_Site	SNV	T	C	C	DPY19L3	c.1698-8T>C	
SH_48	19	33424486	33424486	Missense_Mutation	SNV	T	C	C	CEP89	c.757A>G	P.M253V
SH_48	19	39908540	39908540	Splice_Site	SNV	G	A	A	PLEKHG2	c.883-5G>A	
SH_48	19	42126042	42126042	Splice_Site	SNV	C	T	T	CEACAM4	c.669+1G>A	
SH_48	19	42911506	42911506	Missense_Mutation	SNV	C	T	T	LIPE	c.1957G>A	P.G653S
SH_48	19	45867689	45867689	Missense_Mutation	SNV	G	C	C	ERCC2	c.711C>G	P.H237Q
SH_48	19	46144940	46144940	Silent	SNV	C	A	A	EML2	c.582G>T	P.R194R
SH_48	19	46144941	46144941	Missense_Mutation	SNV	C	A	A	EML2	c.581G>T	P.R194L
SH_48	19	52569023	52569023	Silent	SNV	A	G	G	ZNFA81	c.2112T>C	P.T704T
SH_48	19	5265071	5265071	Missense_Mutation	SNV	G	C	C	PTPRS	c.516C>G	P.F172L
SH_48	2	128941363	128941363	Splice_Site	SNV	A	G	G	UGGT1	c.4359A>G	P.Q1453Q
SH_48	2	1695711	1695711	Missense_Mutation	SNV	A	C	C	PXDN	c.333T>G	P.N111K
SH_48	20	40162094	40162094	Missense_Mutation	SNV	T	C	C	CHD6	c.149A>G	P.D50G

SH_48	22	20100738	20100738	Silent	SNV	G	A	A	TRMT2A	c.1452C>T	P.F484F
SH_48	3	15731711	15731711	Missense_Mutation	SNV	T	C	C	ANKRD28	c.1226A>G	P.H409R
SH_48	3	41942261	41942261	Missense_Mutation	SNV	T	G	G	ULK4	c.1243A>C	P.T415P
SH_48	5	10748320	10748320	Missense_Mutation	SNV	T	G	G	DAP	c.119A>C	P.K40T
SH_48	5	65455039	65455039	Splice_Site	SNV	C	G	G	SREK1	c.296-8C>G	
SH_48	5	66391445	66391445	Missense_Mutation	SNV	C	G	G	MAST4	c.854C>G	P.S285W
SH_48	5	68840897	68840897	Missense_Mutation	SNV	T	C	C	OCLN	c.1204T>C	P.Y402H
SH_48	6	18207631	18207631	Splice_Site	SNV	A	C	C	KDM1B	c.966A>C	P.V322V
SH_48	7	129098559	129098559	Missense_Mutation	SNV	G	T	T	STRIP2	c.1281G>T	P.K427N
SH_48	7	51150927	51150927	Splice_Site	SNV	T	C	C	COBL	c.1097-2A>G	
SH_48	7	75610920	75610920	Missense_Mutation	SNV	T	C	C	POR	c.727T>C	P.S243P
SH_48	7	896012	896012	Silent	SNV	A	G	G	SUN1	c.1368A>G	P.L456L
SH_48	8	142185524	142185524	Missense_Mutation	SNV	G	T	T	DENND3	c.2261G>T	P.G754V
SH_48	8	145678610	145678610	Silent	SNV	C	T	T	CYHR1	c.480G>A	P.Q160Q
SH_48	8	2823298	2823298	Missense_Mutation	SNV	T	A	A	CSMD1	c.9279A>T	P.K3093N
SH_48	8	2823300	2823300	Missense_Mutation	SNV	T	G	G	CSMD1	c.9277A>C	P.K3093Q
SH_48	8	48879955	48879955	Missense_Mutation	SNV	C	T	T	MCM4	c.1084C>T	P.P362S
SH_48	9	4849475	4849475	Missense_Mutation	SNV	G	A	A	RCL1	c.422G>A	P.S141N
SH_48	X	70443741	70443741	Missense_Mutation	SNV	A	T	T	GJB1	c.184A>T	P.S62C
SH_48	X	7889816	7889816	Missense_Mutation	SNV	T	A	A	PNPLA4	c.349A>T	P.N117Y
SH_50	1	100345543	100345543	Missense_Mutation	SNV	G	T	T	AGL	c.1676G>T	P.G559V
SH_50	1	164761941	164761941	Missense_Mutation	SNV	A	G	G	PBX1	c.476A>G	P.Q159R
SH_50	1	236433273	236433273	Missense_Mutation	SNV	A	G	G	ERO1B	c.124T>C	P.C42R
SH_50	1	2408030	2408030	Nonsense_Mutation	SNV	G	T	T	PLCH2	c.3G>T	P.M17
SH_50	10	71142485	71142485	Missense_Mutation	SNV	C	T	T	HK1	c.1508C>T	P.T503M
SH_50	12	58121327	58121327	Missense_Mutation	SNV	A	G	G	AGAP2	c.289G>C	P.C966R
SH_50	13	107220055	107220055	Silent	SNV	G	A	A	ARGLU1	c.213C>T	P.D71D
SH_50	13	99555311	99555311	Missense_Mutation	SNV	C	T	T	DOCK9	c.1091G>A	P.G364E
SH_50	17	10442778	10442778	Missense_Mutation	SNV	C	T	T	MYH2	c.1249G>A	P.G417S
SH_50	17	41959644	41959644	Splice_Site	SNV	G	A	A	MPP2	c.816+8C>T	
SH_50	17	62525490	62525490	Missense_Mutation	SNV	A	C	C	CEP95	c.899A>C	P.E300A
SH_50	17	7577498	7577498	Splice_Site	SNV	C	A	A	TP53	c.782+1G>T	
SH_50	2	10059883	10059883	Missense_Mutation	SNV	A	G	G	TAF1B	c.734A>G	P.E245G
SH_50	2	177036509	177036509	Missense_Mutation	SNV	G	T	T	HOXD3	c.806G>T	P.R269L
SH_50	20	61527574	61527574	Splice_Site	SNV	C	T	T	DIDO1	c.2214+11G>A	
SH_50	21	15599454	15599454	Frame_Shift_Del	INDEL	A	-	-	RBM11	c.707delA	P.Y236fs
SH_50	22	21133604	21133604	Nonsense_Mutation	SNV	A	T	T	SERPIND1	c.4A>T	P.K2*
SH_50	3	120123719	120123719	Missense_Mutation	SNV	C	G	G	FSTL1	c.562G>C	P.L188Q
SH_50	3	56026112	56026112	Missense_Mutation	SNV	T	C	C	ERC2	c.2228A>G	P.K743R
SH_50	5	1294023	1294023	Silent	SNV	G	T	T	TERT	c.978C>A	P.A326A
SH_50	8	113323360	113323360	Nonsense_Mutation	SNV	C	A	A	CSMD3	c.7420G>T	P.G2474*
SH_50	8	120598546	120598546	Missense_Mutation	SNV	T	A	A	ENPP2	c.1247A>T	P.K416I
SH_50	8	141745351	141745351	Missense_Mutation	SNV	T	A	A	PTK2	c.2029A>T	P.S677C
SH_50	9	140777321	140777321	Silent	SNV	G	T	T	CACNA1B	c.516G>T	P.V172V
SH_50	X	100748157	100748157	Silent	SNV	T	C	C	ARMCX4	c.4581T>C	P.S1527S
SH_50	X	17819198	17819198	Silent	SNV	T	A	A	RAI2	c.783A>T	P.G261G
SH_50	X	3228746	3228746	Missense_Mutation	SNV	T	G	G	MXRA5	c.7498A>C	P.N2500H
SH_50	X	70361781	70361781	Missense_Mutation	SNV	G	A	A	MED12	c.6457G>A	P.A2153T
SH_51	1	157509008	157509008	Missense_Mutation	SNV	T	A	A	FCRL5	c.1270A>T	P.R424W
SH_51	1	171688329	171688329	Missense_Mutation	SNV	C	G	G	VAMP4	c.143G>C	P.R48T
SH_51	1	186008081	186008081	Missense_Mutation	SNV	G	T	T	HMCN1	c.5972G>T	P.C1991F
SH_51	1	186141211	186141211	Silent	SNV	C	T	T	HMCN1	c.15762C>T	P.C5254C
SH_51	1	241667429	241667429	Missense_Mutation	SNV	C	A	A	FH	c.1021G>T	P.D341Y
SH_51	1	3643789	3643789	Splice_Site	SNV	G	T	T	TP73	c.695+1G>T	
SH_51	1	47075713	47075713	Silent	SNV	G	A	A	MOB3C	c.738C>T	P.R246R
SH_51	1	55509596	55509596	Silent	SNV	C	T	T	PCSK9	c.288C>T	P.R96R
SH_51	1	77510056	77510056	Silent	SNV	C	A	A	ST6GALNAC5	c.429C>A	P.V143V
SH_51	10	114057904	114057904	Missense_Mutation	SNV	G	A	A	TECTB	c.749G>A	P.R250Q
SH_51	11	122944224	122944224	Silent	SNV	G	T	T	CLMP	c.1080C>A	P.P360P
SH_51	11	5841654	5841654	Missense_Mutation	SNV	C	A	A	OR52N2	c.89C>A	P.S30Y
SH_51	11	61917614	61917614	Missense_Mutation	SNV	T	G	G	INCENP	c.2477T>G	P.L826R
SH_51	11	67352618	67352618	Missense_Mutation	SNV	G	A	A	GSTP1	c.242G>A	P.G81E
SH_51	12	105557961	105557961	Missense_Mutation	SNV	G	C	C	KIAA1033	c.3233G>C	P.R1078T
SH_51	12	21997857	21997857	Splice_Site	SNV	G	A	A	ABCC9	c.3097-8C>T	
SH_51	13	36158140	36158140	Missense_Mutation	SNV	A	G	G	NBEA	c.520A>G	P.T174A
SH_51	14	75590874	75590874	Missense_Mutation	SNV	T	C	C	NEK9	c.272A>G	P.K91R
SH_51	15	56736697	56736697	Missense_Mutation	SNV	T	C	C	MNS1	c.631A>G	P.K211E
SH_51	15	80452129	80452129	Missense_Mutation	SNV	A	T	T	FAH	c.224A>T	P.Q75L
SH_51	15	85165000	85165000	Missense_Mutation	SNV	C	A	A	ZSCAN2	c.1574C>A	P.T525K
SH_51	16	2263877	2263877	Missense_Mutation	SNV	C	A	A	PGP	c.818G>T	P.G273V
SH_51	16	309997	309997	Missense_Mutation	SNV	G	T	T	FAM234A	c.415G>T	P.A139S
SH_51	17	67252332	67252332	Missense_Mutation	SNV	A	T	T	ABCA5	c.3824T>A	P.V1275D
SH_51	17	74474996	74474996	Silent	SNV	C	T	T	RHBDF2	c.651G>A	P.L217L
SH_51	17	7577534	7577534	Missense_Mutation	SNV	C	A	A	TP53	c.747G>T	P.R249S
SH_51	18	44121743	44121743	Silent	SNV	T	C	C	LOXHD1	c.576A>G	P.T192T
SH_51	18	5419865	5419865	Missense_Mutation	SNV	C	A	A	EPB41L3	c.1405G>T	P.G469C
SH_51	19	13445238	13445238	Missense_Mutation	SNV	C	G	G	CACNA1A	c.1152G>C	P.Q384H
SH_51	19	24115260	24115260	Frame_Shift_Del	INDEL	A	-	-	ZNF726	c.345delA	P.G116fs
SH_51	2	230724031	230724031	Nonsense_Mutation	SNV	G	A	A	TRIP12	c.484C>T	P.Q162*
SH_51	20	39802378	39802378	Missense_Mutation	SNV	G	T	T	PLCG1	c.3481G>T	P.V1161L
SH_51	20	53208187	53208187	Missense_Mutation	SNV	A	C	C	DOK5	c.118A>C	P.N40H
SH_51	20	62323101	62323101	Missense_Mutation	SNV	A	T	T	RTEL1	c.2563A>T	P.S855C
SH_51	22	20780311	20780311	Missense_Mutation	SNV	C	G	G	SCARF2	c.1967G>C	P.R656P
SH_51	3	49845239	49845239	Missense_Mutation	SNV	C	T	T	UBA7	c.2645G>A	P.R882H
SH_51	4	10083071	10083082	Splice_Site	INDEL	TTAGAGAGA	-	-	WDR1	777-3delTTTCTCTCTAAC	
SH_51	4	155489625	155489625	Missense_Mutation	SNV	G	A	A	FGB	c.634G>A	P.D212N
SH_51	4	190947588	190947588	Silent	SNV	G	A	A	FRG2	c.282C>T	P.N94N
SH_51	4	48073630	48073630	Missense_Mutation	SNV	C	A	A	TXK	c.1419G>T	P.L473F
SH_51	6	158873184	158873184	Missense_Mutation	SNV	C	G	G	TULP4	c.743C>G	P.P248R
SH_51	6	33245650	33245655	Missense_Mutation	INDEL	CTAAAG	-	-	B3GALT4	54_459delCTAAP.L152_K153del	
SH_51	7	146825887	146825887	Missense_Mutation	SNV	A	G	G	CNTNAP2	c.1042A>G	P.T348A
SH_51	7	151904477	151904477	Missense_Mutation	SNV	G	C	C	KMT2C	c.3749C>G	P.S1250C
SH_51	7	44797630	44797630	Missense_Mutation	SNV	C	A	A	ZMIZ2	c.640C>A	P.L214M
SH_51	7	69599520	69599520	Splice_Site	SNV	A	G	G	AUTS2	c.625-2A>G	
SH_51	8	101178075	101178075	Silent	SNV	A	G	G	SPAG1	c.174A>G	P.T58T
SH_51	8	121301897	121301897	Missense_Mutation	SNV	G	C	C	COL14A1	c.4128G>C	P.K1376N
SH_51	8	143624772	143624772	Silent	SNV	G	A	A	ADGRB1	c.4422G>A	P.K1474K
SH_51	8	1497807	1497807	Missense_Mutation	SNV	C	A	A	DLGAP2	c.948C>A	P.H316Q

SH_51	8	25220572	25220572	Missense_Mutation	SNV	A	G	G	DOCK5	c.2959A>G	P.M987V
SH_51	8	67488461	67488461	Silent	SNV	C	T	T	MYBL1	c.1251G>A	P.G417G
SH_51	9	138712974	138712974	Missense_Mutation	SNV	C	A	A	CAMSAP1	c.3533G>T	P.R1178L
SH_51	X	19398339	19398339	Missense_Mutation	SNV	C	G	G	MAP3K15	c.2488G>C	P.A830P
SH_52	1	150310780	150310780	Missense_Mutation	SNV	A	G	G	PRPF3	c.1180A>G	P.I394V
SH_52	1	226026499	226026499	Missense_Mutation	SNV	A	G	G	EPHX1	c.509A>G	P.H170R
SH_52	1	248813579	248813579	Missense_Mutation	SNV	A	T	T	OR2T27	c.607T>A	P.C203S
SH_52	10	27964267	27964267	Missense_Mutation	SNV	A	T	T	MKX	c.950T>A	P.L137H
SH_52	11	64398026	64398026	Missense_Mutation	SNV	A	T	T	NRXN2	c.3605T>A	P.V1202E
SH_52	12	22354673	22354673	Missense_Mutation	SNV	A	G	G	STRSIA1	c.455T>C	P.F152S
SH_52	12	96912713	96912713	Missense_Mutation	SNV	A	T	T	CFAP54	c.806A>T	P.E269V
SH_52	14	23896835	23896835	Missense_Mutation	SNV	A	T	T	MYH7	c.1847T>A	P.L616Q
SH_52	14	75329483	75329483	Missense_Mutation	SNV	T	A	A	PROX2	c.1055A>T	P.H352L
SH_52	15	73996270	73996270	Missense_Mutation	SNV	A	T	T	CD276	c.1004A>T	P.E335V
SH_52	15	99874205	99874205	Missense_Mutation	SNV	A	T	T	LRRC28	c.463A>T	P.M155L
SH_52	2	130930883	130930883	Missense_Mutation	SNV	T	C	C	SMPD4	c.431A>G	P.Y144C
SH_52	2	168726411	168726411	Missense_Mutation	SNV	T	A	A	B3GALT1	c.862T>A	P.W288R
SH_52	2	206884550	206884550	Missense_Mutation	SNV	T	A	A	INO80D	c.1318A>T	P.R440W
SH_52	2	212248411	212248411	Missense_Mutation	SNV	A	G	G	ERBB4	c.3856T>C	P.S1286P
SH_52	2	86831392	86831392	Silent	SNV	T	G	G	RNF103	c.1620A>C	P.S140T
SH_52	3	155205805	155205805	Splice_Site	SNV	G	A	A	PLCH1	c.2583+12C>T	
SH_52	3	16635220	16635220	Missense_Mutation	SNV	A	T	T	DAZL	c.737T>A	P.V246E
SH_52	3	167189420	167189420	Missense_Mutation	SNV	T	A	A	SERPINI2	c.233A>T	P.Q78L
SH_52	4	146807071	146807071	Missense_Mutation	SNV	C	T	T	ZNF827	c.1506G>A	P.M502I
SH_52	5	13721242	13721242	Missense_Mutation	SNV	A	T	T	DNAH5	c.12146T>A	P.L4049Q
SH_52	5	140215289	140215289	Missense_Mutation	SNV	G	A	A	PCDHA7	c.1321G>A	P.V441M
SH_52	5	140574441	140574441	Silent	SNV	T	A	A	PCDHB10	c.2316T>A	P.V772V
SH_52	5	140751778	140751778	Missense_Mutation	SNV	A	T	T	PCDHB3	c.1817A>T	P.Y606F
SH_52	5	140774176	140774176	Missense_Mutation	SNV	G	T	T	PCDHGA8	c.1796G>T	P.G599V
SH_52	5	16676268	16676268	Splice_Site	SNV	A	T	T	MYO10	c.4543-5T>A	
SH_52	5	33984538	33984538	Missense_Mutation	SNV	C	A	A	SLC45A2	c.151G>T	P.V511L
SH_52	5	7893003	7893003	Missense_Mutation	SNV	A	T	T	MTRR	c.1534A>T	P.S512C
SH_52	6	34825597	34825597	Missense_Mutation	SNV	A	T	T	UHRF1BP1	c.1670A>T	P.Y557F
SH_52	6	38548105	38548105	Missense_Mutation	SNV	C	A	A	BTBD9	c.923G>T	P.G308V
SH_52	6	38862563	38862563	Silent	SNV	A	T	T	DNAH8	c.8670A>T	P.I2890I
SH_52	6	45882026	45882026	Missense_Mutation	SNV	A	T	T	CLIC5	c.1004T>A	P.L1335Q
SH_52	7	94139506	94139506	Missense_Mutation	SNV	A	C	C	CASD1	c.110A>C	P.H37P
SH_52	7	97873920	97873920	Missense_Mutation	SNV	C	A	A	TECPR1	c.494G>T	P.R165L
SH_52	8	104922697	104922697	Silent	SNV	C	T	T	RIMS2	c.1197C>T	P.D399D
SH_52	8	29195990	29195990	Missense_Mutation	SNV	A	T	T	DUSP4	c.608T>A	P.L203H
SH_52	8	82356823	82356823	Missense_Mutation	SNV	A	T	T	PMP2	c.260T>A	P.L87Q
SH_52	9	133230220	133230220	Silent	SNV	G	T	T	HMCN2	c.3261G>T	P.A1087A
SH_52	9	136405769	136405769	Silent	SNV	C	T	T	ADAMTSL2	c.462C>T	P.T154T
SH_53	1	156498302	156498302	Missense_Mutation	SNV	G	A	A	IQGAP3	c.4672C>T	P.H1558Y
SH_53	1	16464659	16464659	Frame_Shift_Ins	INDEL	-	A	A	EPHA2	c.1000dupT	P.Y334fs
SH_53	1	197111506	197111506	Missense_Mutation	SNV	T	C	C	ASPM	c.1876A>G	P.K626E
SH_53	1	27105550	27105550	Nonsense_Mutation	SNV	C	T	T	ARID1A	c.5161C>T	P.R1721*
SH_53	10	13656040	13656040	Missense_Mutation	SNV	C	T	T	PRPF18	c.746C>T	P.S249L
SH_53	12	112318261	112318261	Missense_Mutation	SNV	C	T	T	MAPKAPK5	c.590C>T	P.A197V
SH_53	12	113533132	113533132	Splice_Site	SNV	C	T	T	DTX1	c.1551C>T	P.G517G
SH_53	12	41967566	41967566	Missense_Mutation	SNV	G	A	A	PDZRN4	c.2985G>A	P.M995I
SH_53	12	71003122	71003122	Splice_Site	SNV	G	A	A	PTPRB	c.709-3C>T	
SH_53	14	21897454	21897454	Missense_Mutation	SNV	T	G	G	CHD8	c.884A>C	P.Q295P
SH_53	16	16291888	16291888	Missense_Mutation	SNV	T	C	C	ABCC6	c.1328A>G	P.Y443C
SH_53	16	67696157	67696157	Silent	SNV	C	A	A	PARD6A	c.645C>A	P.L215L
SH_53	16	71127847	71127847	Splice_Site	SNV	A	G	G	HYDIN	c.1409-9T>C	
SH_53	17	17700957	17700957	Silent	SNV	G	T	T	RAI1	c.4695G>T	P.V1565V
SH_53	17	5436190	5436190	Missense_Mutation	SNV	G	A	A	NLRP1	c.3260C>T	P.T1087M
SH_53	17	54969228	54969228	Missense_Mutation	SNV	G	A	A	TRIM25	c.1726C>T	P.R576W
SH_53	17	57951937	57951937	Missense_Mutation	SNV	C	G	G	TUBD1	c.249G>C	P.L83F
SH_53	19	11258684	11258684	Splice_Site	SNV	C	A	A	SPC24	c.410+5G>T	
SH_53	19	14066781	14066781	Missense_Mutation	SNV	G	T	T	DCAF15	c.424G>T	P.V142L
SH_53	19	36360590	36360590	Missense_Mutation	SNV	G	T	T	APLP1	c.169G>T	P.A57S
SH_53	19	46886660	46886660	Splice_Site	SNV	C	T	T	PP5C	c.634-8C>T	
SH_53	19	57286803	57286803	Silent	SNV	C	T	T	ZIM2	c.837G>A	P.P279P
SH_53	2	226378249	226378249	Missense_Mutation	SNV	C	A	A	NYAP2	c.384C>A	P.D128E
SH_53	2	75118019	75118019	Missense_Mutation	SNV	C	T	T	HK2	c.2705C>T	P.A902V
SH_53	22	38895436	38895436	Silent	SNV	G	A	A	DDX17	c.507C>T	P.P169P
SH_53	3	75788489	75788489	Silent	SNV	C	T	T	ZNF717	c.285G>A	P.Q95Q
SH_53	4	1806099	1806099	Missense_Mutation	SNV	A	G	G	FGFR3	c.1118A>G	P.Y373C
SH_53	5	173426809	173426809	Splice_Site	SNV	T	C	C	C5orf47	c.511+7T>C	
SH_53	5	36679852	36679852	Silent	SNV	C	T	T	SLC1A3	c.984C>T	P.H328H
SH_53	6	10695230	10695230	Silent	SNV	C	G	G	PAK1IP1	c.12C>G	P.V4V
SH_53	6	78632903	78632903	Missense_Mutation	SNV	C	T	T	MEI4	c.998C>T	P.T333I
SH_53	7	149503850	149503850	Missense_Mutation	SNV	G	A	A	SSPO	c.8678G>A	P.R2893H
SH_53	7	57522840	57522840	Silent	SNV	T	C	C	ZNF716	c.228T>C	P.N76N
SH_53	8	65527782	65527782	Silent	SNV	A	G	G	CYP7B1	c.858T>C	P.H286H
SH_53	9	18777780	18777780	Silent	SNV	C	T	T	ADAMTSL1	c.3553C>T	P.L1185L
SH_56	1	175323607	175323607	Missense_Mutation	SNV	T	C	C	TNR	c.2303A>G	P.E768G
SH_56	1	27092812	27092812	Nonsense_Mutation	SNV	G	T	T	ARID1A	c.2833G>T	P.G945*
SH_56	1	64515434	64515434	Missense_Mutation	SNV	T	C	C	ROR1	c.235T>C	P.C79R
SH_56	10	54031200	54031200	Missense_Mutation	SNV	C	T	T	PRKG1	c.1219C>T	P.R407C
SH_56	11	16362672	16362672	Silent	SNV	C	T	T	SOX6	c.123G>A	P.L41L
SH_56	11	26660711	26660711	Missense_Mutation	SNV	G	C	C	ANO3	c.2247G>C	P.L749F
SH_56	12	6972503	6972503	Missense_Mutation	SNV	A	G	G	USP5	c.1916A>G	P.E639G
SH_56	13	24874584	24874584	Missense_Mutation	SNV	C	T	T	SPATA13	c.3629C>T	P.A1210V
SH_56	13	75886884	75886884	Missense_Mutation	SNV	C	A	A	TBC1D4	c.2349G>T	P.M783I
SH_56	13	90883530	90883530	Splice_Site	SNV	C	A	A	MIR622	n.95C>A	
SH_56	16	57778317	57778317	Silent	SNV	C	T	T	KATNB1	c.183C>T	P.G61G
SH_56	17	30202297	30202297	Missense_Mutation	SNV	T	C	C	UTP6	c.1261A>G	P.I421V
SH_56	17	7579485	7579485	Nonsense_Mutation	SNV	C	A	A	TP53	c.202G>T	P.E68*
SH_56	2	162875305	162875305	Nonsense_Mutation	SNV	C	A	A	DDP4	c.1354G>T	P.E452*
SH_56	20	45865227	45865227	Missense_Mutation	SNV	G	C	C	ZMYND8	c.2486C>G	P.S829C
SH_56	22	18609267	18609267	Silent	SNV	C	T	T	TUBA8	c.324C>T	P.A108A
SH_56	22	29138118	29138118	Missense_Mutation	SNV	T	G	G	HSCB	c.35T>G	P.V12G
SH_56	3	122869138	122869138	Missense_Mutation	SNV	G	T	T	PDIA5	c.1200G>T	P.L400F
SH_56	6	29275027	29275027	Silent	SNV	T	C	C	OR14J1	c.561T>C	P.C187C
SH_56	7	129037061	129037061	Splice_Site	SNV	A	T	T	AHCYL2	c.718-2A>T	

SH_56	8	3226842	3226842	Missense_Mutation	SNV	C	A	A	CSMD1	c.2833G>T	P.G945W
SH_56	8	77766065	77766065	Missense_Mutation	SNV	G	A	A	ZFHx4	c.6908G>A	P.R2303Q
SH_56	X	69385729	69385729	Silent	SNV	G	A	A	IGBP1	c.918G>A	P.K306K
SH_58	1	110587495	110587495	Missense_Mutation	SNV	C	A	A	STRIP1	c.1035C>A	P.S345R
SH_58	1	145562056	145562056	Missense_Mutation	SNV	G	A	A	ANKRD35	c.1474G>A	P.E492K
SH_58	1	167409971	167409971	Missense_Mutation	SNV	A	T	T	CD247	c.92T>A	P.L31H
SH_58	1	17698833	17698833	Silent	SNV	A	T	T	PADI6	c.93A>T	P.T31T
SH_58	1	1854415	1854415	Splice_Site	SNV	T	A	A	CFAP74	c.4683+9A>T	
SH_58	1	207072737	207072737	Silent	SNV	C	A	A	IL24	c.120C>A	P.T40T
SH_58	1	22033256	22033256	Missense_Mutation	SNV	T	C	C	USP48	c.2069A>G	P.E690G
SH_58	1	226175617	226175617	Nonsense_Mutation	SNV	C	A	A	SDE2	c.1114G>T	P.E372*
SH_58	1	230907846	230907846	Splice_Site	SNV	G	T	T	CAPN9	c.686+1G>T	
SH_58	1	248343929	248343929	Silent	SNV	C	T	T	OR2M2	c.642C>T	P.I214I
SH_58	1	248436229	248436229	Silent	SNV	C	T	T	OR2T33	c.888G>A	P.K296K
SH_58	1	37271916	37271916	Silent	SNV	G	A	A	GRIK3	c.2103C>T	P.J701I
SH_58	1	41094539	41094539	Silent	SNV	A	G	G	RIMS3	c.657T>C	P.D219D
SH_58	1	52947569	52947569	Missense_Mutation	SNV	A	T	T	ZCCHC11	c.1542T>A	P.D514E
SH_58	1	53544202	53544202	Silent	SNV	G	A	A	PODN	c.1107G>A	P.L369L
SH_58	10	125528200	125528200	Missense_Mutation	SNV	T	C	C	CPXM2	c.1141A>G	P.N381D
SH_58	10	81319120	81319120	Silent	SNV	G	C	C	SFTPA2	c.120C>G	P.G40G
SH_58	11	119206919	119206919	Missense_Mutation	SNV	G	A	A	RNF26	c.1087G>A	P.G363S
SH_58	11	123988417	123988417	Silent	SNV	C	T	T	VWA5A	c.81C>T	P.Y27Y
SH_58	11	28116225	28116225	Nonsense_Mutation	SNV	C	A	A	KIF18A	c.448G>T	P.E150*
SH_58	11	36614684	36614684	Missense_Mutation	SNV	G	C	C	RAG2	c.1035C>G	P.F345L
SH_58	11	56237071	56237071	Silent	SNV	T	C	C	OR5M3	c.903A>G	P.K301K
SH_58	11	66838987	66838987	Missense_Mutation	SNV	T	A	A	RHOD	c.349T>A	P.F117I
SH_58	12	11149831	11149831	Missense_Mutation	SNV	C	T	T	TAS2R20	c.644G>A	P.G215E
SH_58	12	124840118	124840118	Splice_Site	SNV	C	A	A	NCOR2	c.3212-1G>T	
SH_58	12	49745126	49745127	Frame_Shift_Del	INDEL	AA	-	-	DNAJC22	c.868_869delAA	P.N290fs
SH_58	12	52886456	52886456	Nonsense_Mutation	SNV	T	A	A	KRT6A	c.517A>T	P.L371*
SH_58	12	57422907	57422907	Splice_Site	SNV	T	A	A	MYO1A	c.3005+9A>T	
SH_58	12	58089821	58089821	Splice_Site	SNV	G	A	A	OS9	c.480G>A	P.K160K
SH_58	14	105416790	105416790	Frame_Shift_Del	INDEL	T	-	-	AHNK2	c.4998delA	P.S1667fs
SH_58	14	44975880	44975880	Missense_Mutation	SNV	G	A	A	FSCB	c.311C>T	P.A104V
SH_58	15	25953373	25953373	Missense_Mutation	SNV	C	A	A	ATP10A	c.2419G>T	P.G807C
SH_58	15	31229467	31229467	Splice_Site	SNV	G	A	A	FAN1	c.*3+5G>A	
SH_58	15	43308034	43308034	Missense_Mutation	SNV	T	C	C	UBR1	c.3061A>G	P.R1021G
SH_58	15	48527135	48527135	Silent	SNV	C	A	A	SLC12A1	c.1149C>A	P.V383V
SH_58	15	91035806	91035806	Silent	SNV	G	A	A	IQGAP1	c.4491G>A	P.Q1497Q
SH_58	16	28113251	28113251	Missense_Mutation	SNV	A	C	C	XPO6	c.2920T>G	P.F974V
SH_58	16	50744570	50744570	Missense_Mutation	SNV	G	T	T	NOD2	c.667G>T	P.D223Y
SH_58	16	50744571	50744571	Missense_Mutation	SNV	A	T	T	NOD2	c.668A>T	P.D223V
SH_58	16	74425905	74425905	Missense_Mutation	SNV	G	C	C	NPIP15	c.1259G>C	P.R420T
SH_58	17	10363305	10363305	Silent	SNV	G	A	A	MYH4	c.1380C>T	P.I460I
SH_58	17	26938585	26938585	Missense_Mutation	SNV	C	A	A	SGK494	c.811G>T	P.A271S
SH_58	17	27001380	27001380	Missense_Mutation	SNV	T	A	A	SUPT6H	c.189T>A	P.D63E
SH_58	17	27936012	27936012	Missense_Mutation	SNV	G	T	T	ANKRD13B	c.565G>T	P.D189Y
SH_58	17	36622418	36622418	Missense_Mutation	SNV	A	T	T	ARHGAP23	c.494A>T	P.Q165L
SH_58	17	40061912	40061912	Splice_Site	SNV	C	T	T	ACLY	c.867-1G>A	
SH_58	17	61511848	61511848	Nonsense_Mutation	SNV	C	T	T	CYB561	c.671G>A	P.W224*
SH_58	17	7578224	7578224	Nonsense_Mutation	SNV	T	A	A	TP53	c.625A>T	P.R209*
SH_58	17	76456070	76456070	Missense_Mutation	SNV	T	A	A	DNAH17	c.9449A>T	P.E3150V
SH_58	18	55319709	55319709	Splice_Site	SNV	C	A	A	ATP8B1	c.3261+7G>T	
SH_58	18	9887580	9887580	Silent	SNV	G	A	A	TXNDC2	c.1104G>A	P.Q368Q
SH_58	19	19035081	19035081	Missense_Mutation	SNV	C	G	G	DDX49	c.816C>G	P.S272R
SH_58	19	36394686	36394686	Missense_Mutation	SNV	G	T	T	HCST	c.122G>T	P.G41V
SH_58	19	4164504	4164504	Missense_Mutation	SNV	A	T	T	CREB3L3	c.578A>T	P.Q193L
SH_58	19	44981055	44981055	Missense_Mutation	SNV	G	A	A	ZNFI180	c.1568C>T	P.P523L
SH_58	19	7620180	7620180	Frame_Shift_Del	INDEL	A	-	-	PNPLA6	c.2893delA	P.S965fs
SH_58	2	109383358	109383358	Silent	SNV	G	A	A	RANBP2	c.6363G>A	P.Q2121Q
SH_58	2	160139338	160139338	Frame_Shift_Del	INDEL	C	-	-	WDSUB1	c.243delG	P.W81fs
SH_58	2	179427165	179427165	Nonsense_Mutation	SNV	A	T	T	TTN	c.78771T>A	P.Y26257*
SH_58	2	179498064	179498064	Splice_Site	SNV	A	T	T	TTN	c.38024-11T>A	
SH_58	2	179542355	179542355	Silent	SNV	A	T	T	TTN	c.33333T>A	P.P11111P
SH_58	2	179611206	179611206	Silent	SNV	A	T	T	TTN	c.15921T>A	P.P5307P
SH_58	2	179997145	179997145	Missense_Mutation	SNV	G	T	T	SESTD1	c.858C>A	P.N286K
SH_58	2	220333672	220333672	Silent	SNV	G	A	A	SPEG	c.3393G>A	P.E1131E
SH_58	2	228104959	228104959	Splice_Site	SNV	C	T	T	COL4A3	c.234+11C>T	
SH_58	2	95513760	95513760	Splice_Site	SNV	A	G	G	ANKRD20A8P	n.643+2T>C	
SH_58	2	96781498	96781498	Missense_Mutation	SNV	A	T	T	ADRA2B	c.391T>A	P.C131S
SH_58	2	98458319	98458319	Missense_Mutation	SNV	G	T	T	TMEM131	c.682C>A	P.P228T
SH_58	20	3760330	3760330	Missense_Mutation	SNV	T	A	A	SPEF1	c.202A>T	P.N68Y
SH_58	20	60991294	60991294	Splice_Site	SNV	T	A	A	RBBP8NL	c.314-2A>T	
SH_58	20	9624935	9624935	Silent	SNV	C	T	T	PAK5	c.42G>A	P.P14P
SH_58	21	33065634	33065634	Missense_Mutation	SNV	G	C	C	SCAF4	c.1441C>G	P.P481A
SH_58	22	30189610	30189610	Frame_Shift_Del	INDEL	C	-	-	ASCC2	c.1516delG	P.A506fs
SH_58	22	35480473	35480473	Missense_Mutation	SNV	C	A	A	ISX	c.479C>A	P.P160H
SH_58	3	130187749	130187749	Nonsense_Mutation	SNV	A	T	T	COL6A5	c.6901A>T	P.R2301*
SH_58	3	184586829	184586829	Splice_Site	SNV	G	T	T	VP58	c.1597+5G>T	
SH_58	3	184910636	184910636	Missense_Mutation	SNV	C	A	A	EHHADH	c.1262G>T	P.G421V
SH_58	3	185232321	185232321	Splice_Site	SNV	A	T	T	LIPH	c.983-12T>A	
SH_58	3	48680384	48680389	Splice_Site	INDEL	CCCCAT	-	-	CELSR3	11_8406+16delATGGGG	
SH_58	3	50417151	50417151	Splice_Site	SNV	C	T	T	CACNA2D2	c.993+5G>A	
SH_58	3	77651371	77651371	Silent	SNV	A	T	T	ROBO2	c.2805A>T	P.P935P
SH_58	4	108574771	108574771	Silent	SNV	T	C	C	PAPS51	c.1113A>G	P.E371E
SH_58	4	5630395	5630395	Missense_Mutation	SNV	C	T	T	EVG2	c.1537G>A	P.G513S
SH_58	5	127686642	127686642	Silent	SNV	A	G	G	FBN2	c.2730T>C	P.N910N
SH_58	5	149361085	149361085	Silent	SNV	C	T	T	SLC26A2	c.1929C>T	P.P643P
SH_58	5	180477298	180477298	Missense_Mutation	SNV	T	A	A	BTNL9	c.665T>A	P.L222H
SH_58	5	60067866	60067866	Missense_Mutation	SNV	A	T	T	ELOVL7	c.119T>A	P.L40H
SH_58	5	60067867	60067867	Missense_Mutation	SNV	G	T	T	ELOVL7	c.118C>A	P.L40I
SH_58	5	71479618	71479618	Missense_Mutation	SNV	T	A	A	MAP1B	c.335T>A	P.L112Q
SH_58	6	159166544	159166544	Silent	SNV	A	T	T	SYTL3	c.684A>T	P.T228T
SH_58	7	115580744	115580744	Missense_Mutation	SNV	T	A	A	TFEC	c.818A>T	P.Q273L
SH_58	7	20406662	20406662	Nonsense_Mutation	SNV	G	T	T	ITGB8	c.241G>T	P.E81*
SH_58	7	93519584	93519584	Silent	SNV	G	T	T	TFPI2	c.103C>A	P.R35R
SH_58	8	61654710	61654710	Missense_Mutation	SNV	A	T	T	CHD7	c.719A>T	P.Q240L
SH_58	9	19516234	19516234	Missense_Mutation	SNV	T	A	A	SLC24A2	c.1852A>T	P.I618F

SH_58	X	144905208	144905208	Missense_Mutation	SNV	T	A	A	SLITRK2	c.1265T>A	P.L422Q
SH_58	X	99849248	99849248	Splice_Site	SNV	T	A	A	TNMD	c.322-10T>A	
SH_59	1	186303541	186303541	Missense_Mutation	SNV	T	C	C	TPR	c.5098A>G	P.M1700V
SH_59	1	222802659	222802659	Silent	SNV	C	A	A	MTA3	c.2097C>A	P.G699G
SH_59	1	247586609	247586609	Missense_Mutation	SNV	C	A	A	NLRP3	c.361C>A	P.L121M
SH_59	12	25398284	25398284	Missense_Mutation	SNV	C	T	T	KRAS	c.35G>A	P.K21D
SH_59	12	48919813	48919813	Silent	SNV	A	T	T	OR8S1	c.399A>T	P.G133G
SH_59	12	53207801	53207801	Silent	SNV	G	A	A	KRT4	c.42C>T	P.G14G
SH_59	12	6080796	6080796	Missense_Mutation	SNV	G	A	A	VWF	c.7517C>T	P.P2506L
SH_59	13	78335108	78335108	Silent	SNV	G	A	A	SLAIN1	c.1068G>T	P.L356L
SH_59	14	105418360	105418360	Missense_Mutation	SNV	G	A	A	AHNAK2	c.3428C>T	P.A1143V
SH_59	15	33992040	33992040	Splice_Site	SNV	T	G	G	RYR3	c.6379+6T>G	
SH_59	15	68609602	68609602	Splice_Site	SNV	C	T	T	ITGA11	c.2715+1G>A	
SH_59	15	75684622	75684622	Missense_Mutation	SNV	T	C	C	SIN3A	c.2812A>G	P.S938G
SH_59	16	24268113	24268113	Missense_Mutation	SNV	C	A	A	CACNG3	c.38C>A	P.T13N
SH_59	16	70926383	70926383	Missense_Mutation	SNV	T	A	A	HYDIN	c.9298A>T	P.J1310F
SH_59	17	36508652	36508652	Silent	SNV	G	A	A	SOC57	c.525G>A	P.L175L
SH_59	17	7578555	7578555	Splice_Site	SNV	C	T	T	TP53	c.376-1G>A	
SH_59	18	21044196	21044196	Missense_Mutation	SNV	A	G	G	RIOK3	c.352A>G	P.K118E
SH_59	19	36592216	36592216	Missense_Mutation	SNV	G	C	C	WDR62	c.2968G>C	P.E990Q
SH_59	19	45556377	45556377	Silent	SNV	C	T	T	CLASRP	c.135C>T	P.D45D
SH_59	19	4682840	4682840	Missense_Mutation	SNV	G	A	A	DPP9	c.2342C>T	P.A781V
SH_59	2	172950481	172950481	Missense_Mutation	SNV	C	G	G	DLX1	c.76C>G	P.P26A
SH_59	2	220038876	220038876	Silent	SNV	C	T	T	CNPPD1	c.564G>A	P.L188L
SH_59	2	242189388	242189388	Missense_Mutation	SNV	T	A	A	HDLBP	c.1281A>T	P.R427S
SH_59	3	193855521	193855521	Silent	SNV	C	T	T	HE51	c.342C>T	P.F114F
SH_59	3	47035468	47035468	Frame_Shift_Ins	INDEL	-	AA	AA	NBEAL2	1156_1157insA	P.R386fs
SH_59	3	53684912	53684912	Nonsense_Mutation	SNV	G	A	A	CACNA1D	c.590G>A	P.W197*
SH_59	4	39077684	39077684	Frame_Shift_Ins	INDEL	-	A	A	KLHL5	c.490dupA	P.M164fs
SH_59	7	100635176	100635176	Silent	SNV	A	G	G	MUC12	c.1332A>G	P.P444P
SH_59	7	124387076	124387076	Missense_Mutation	SNV	A	T	T	GPR37	c.1345T>A	P.C495S
SH_59	7	42085104	42085104	Silent	SNV	T	A	A	GLI3	c.705A>T	P.A235A
SH_59	8	141669637	141669637	Silent	SNV	C	A	A	PTK2	c.3126G>T	P.V1042V
SH_59	9	116779055	116779055	Missense_Mutation	SNV	G	A	A	ZNF618	c.739G>A	P.A247T
SH_59	9	134323164	134323164	Missense_Mutation	SNV	G	T	T	PRRC2B	c.1093G>T	P.D365Y
SH_59	X	47045027	47045027	Nonsense_Mutation	SNV	A	T	T	RBM10	c.2353A>T	P.K785*
SH_59	X	70349261	70349261	Missense_Mutation	SNV	A	C	C	MED12	c.3673A>C	P.K1225Q
SH_61	11	46894714	46894714	Missense_Mutation	SNV	T	G	G	LRP4	c.4520A>C	P.K1507T
SH_61	8	144992723	144992723	Missense_Mutation	SNV	C	T	T	PLEC	c.11347G>A	P.E3783K
SH_61	X	15262714	15262714	Missense_Mutation	SNV	G	A	A	ASB9	c.799C>T	P.R267W
SH_61	X	47424204	47424204	Missense_Mutation	SNV	C	T	T	ARAF	c.209C>T	P.T70M
SH_63	1	152279994	152279994	Silent	SNV	T	C	C	FLG	c.7368A>G	P.Q2456H
SH_63	1	152280133	152280133	Missense_Mutation	SNV	C	T	T	FLG	c.7229G>A	P.R2410H
SH_63	1	152280540	152280540	Missense_Mutation	SNV	C	G	G	FLG	c.6822G>C	P.Q2274H
SH_63	1	154543934	154543934	Missense_Mutation	SNV	G	A	A	CHRN2	c.635G>A	P.R212H
SH_63	1	67194943	67194943	Splice_Site	SNV	C	T	T	SGIP1	c.1152-4C>T	
SH_63	1	89521775	89521775	Missense_Mutation	SNV	C	T	T	GBP1	c.1292G>A	P.G431E
SH_63	10	104268946	104268946	Missense_Mutation	SNV	T	C	C	SUFU	c.203T>C	P.L68S
SH_63	10	127349670	127349670	Missense_Mutation	SNV	G	T	T	TEX36	c.184C>A	P.Q62K
SH_63	10	73544798	73544798	Missense_Mutation	SNV	C	T	T	CDH23	c.5653C>T	P.R1885C
SH_63	11	118764729	118764729	Missense_Mutation	SNV	G	A	A	CXCR5	c.476G>A	P.R159H
SH_63	11	17653759	17653759	Missense_Mutation	SNV	G	A	A	OTOG	c.7094G>A	P.R2365H
SH_63	11	56043599	56043599	Frame_Shift_Del	INDEL	T	-	-	OR5T1	c.486delT	P.A163fs
SH_63	11	62474578	62474578	Splice_Site	SNV	T	C	C	BSCL2	c.87+3A>G	
SH_63	12	3659248	3659248	Silent	SNV	G	A	A	PRMT8	c.381G>A	P.K127K
SH_63	12	48737167	48737167	Silent	SNV	C	T	T	ZNF641	c.864G>A	P.G288G
SH_63	12	7241272	7241272	Silent	SNV	C	A	A	C1R	c.972G>T	P.L324L
SH_63	13	102568894	102568894	Missense_Mutation	SNV	G	T	T	FGF14	c.102C>A	P.S34R
SH_63	13	20797280	20797280	Missense_Mutation	SNV	C	T	T	GJB6	c.340G>A	P.D114N
SH_63	15	33833073	33833073	Nonsense_Mutation	SNV	G	T	T	RYR3	c.628G>T	P.G210*
SH_63	16	8997165	8997165	Missense_Mutation	SNV	G	C	C	USP7	c.1751C>G	P.S584C
SH_63	17	29314958	29314958	Splice_Site	SNV	A	G	G	RNF135	c.517-4A>G	
SH_63	17	29585521	29585521	Splice_Site	SNV	G	C	C	NF1	c.4332+1G>C	
SH_63	17	31618659	31618659	Missense_Mutation	SNV	C	G	G	ASIC2	c.475G>C	P.G159R
SH_63	17	45291195	45291195	Splice_Site	SNV	G	A	A	MYL4	c.163+3G>A	
SH_63	17	7577538	7577538	Missense_Mutation	SNV	C	T	T	TP53	c.743G>A	P.R248Q
SH_63	18	29340285	29340285	Missense_Mutation	SNV	G	A	A	SLC25A52	c.370C>T	P.R124C
SH_63	18	77227587	77227587	Splice_Site	SNV	C	T	T	NFATC1	c.2092+5C>T	
SH_63	19	38860665	38860665	Missense_Mutation	SNV	T	C	C	CATSPERG	c.3074T>C	P.F1025S
SH_63	2	165986510	165986510	Silent	SNV	G	A	A	SCN3A	c.2715C>T	P.V905V
SH_63	2	167060926	167060926	Missense_Mutation	SNV	T	G	G	SCN9A	c.4414A>C	P.N1472H
SH_63	2	190530907	190530907	Missense_Mutation	SNV	C	G	G	ASNSD1	c.49C>G	P.Q17E
SH_63	2	85262234	85262234	Missense_Mutation	SNV	C	G	G	KCMF1	c.280C>G	P.Q94E
SH_63	20	18461131	18461131	Missense_Mutation	SNV	T	C	C	POLR3F	c.536T>C	P.I197T
SH_63	22	37771192	37771192	Missense_Mutation	SNV	C	T	T	ELFN2	c.383G>A	P.R128H
SH_63	3	164907236	164907236	Silent	SNV	G	A	A	SLITRK3	c.1383C>T	P.L461L
SH_63	3	183957181	183957181	Splice_Site	SNV	G	A	A	VWA5B2	c.1549-1G>A	
SH_63	3	47898936	47898936	Missense_Mutation	SNV	T	A	A	MAP4	c.3133A>T	P.I1045F
SH_63	5	140209476	140209476	Missense_Mutation	SNV	C	A	A	PCDHA6	c.1800C>A	P.D600E
SH_63	5	140720660	140720660	Missense_Mutation	SNV	G	A	A	PCDHGA2	c.2122G>A	P.V708I
SH_63	5	65458332	65458332	Missense_Mutation	SNV	C	T	T	SREK1	c.667C>T	P.R223W
SH_63	5	6737691	6737691	Missense_Mutation	SNV	G	A	A	PAPD7	c.35G>A	P.R123K
SH_63	5	82940474	82940474	Missense_Mutation	SNV	G	T	T	HAPLN1	c.483C>A	P.F161L
SH_63	5	90001230	90001230	Silent	SNV	C	T	T	ADGRV1	c.8400C>T	P.A2800A
SH_63	5	92923847	92923847	Missense_Mutation	SNV	G	A	A	NR2F1	c.688G>A	P.A230T
SH_63	6	112041037	112041037	Missense_Mutation	SNV	G	A	A	FYN	c.218C>T	P.T73M
SH_63	6	33143401	33143401	Missense_Mutation	SNV	G	A	A	COL11A2	c.2068C>T	P.R690C
SH_63	6	46135305	46135305	Missense_Mutation	SNV	T	C	C	ENPP5	c.695A>G	P.N232S
SH_63	6	47681774	47681774	Missense_Mutation	SNV	A	T	T	ADGRF4	c.793A>T	P.T265S
SH_63	6	64472524	64472524	Missense_Mutation	SNV	C	T	T	EYS	c.7901G>A	P.C2634Y
SH_63	7	150901820	150901820	Silent	SNV	G	A	A	IQCA1L	c.114C>T	P.S38S
SH_63	7	34125504	34125504	Missense_Mutation	SNV	C	G	G	BMFER	c.1545C>G	P.F515L
SH_63	7	57187736	57187736	Missense_Mutation	SNV	C	G	G	ZNF479	c.1386G>C	P.E462D
SH_63	8	113599310	113599310	Silent	SNV	T	C	C	CSMD3	c.3558A>G	P.Q1186Q
SH_63	8	121344387	121344387	Missense_Mutation	SNV	C	T	T	COL14A1	c.4667C>T	P.P1556L
SH_63	8	126044542	126044542	Silent	SNV	G	A	A	KIAA0196	c.3276C>T	P.N1092T
SH_63	9	103035322	103035322	Missense_Mutation	SNV	T	A	A	INVS	c.1460T>A	P.M487K
SH_63	9	136379827	136379827	Missense_Mutation	SNV	G	C	C	TMEM8C	c.597C>G	P.N199K

SH_63	9	96021359	96021359	Silent	SNV	C	T	T	WVK2	c.2529C>T	P.L843L
SH_63	X	106888567	106888567	Missense_Mutation	SNV	C	A	A	PRP51	c.79C>A	P.H27N
SH_63	X	11187706	11187706	Silent	SNV	C	T	T	ARHGAP6	c.1728G>A	P.Q576Q
SH_63	X	21875409	21875409	Silent	SNV	C	T	T	YY2	c.807C>T	P.A269A
SH_63	X	35820977	35820977	Nonsense_Mutation	SNV	G	T	T	MAGEB16	c.664G>T	P.E222*
SH_63	X	8763404	8763404	Silent	SNV	G	A	A	FAM9A	c.546C>T	P.I182I
SH_64	1	151679994	151679994	Missense_Mutation	SNV	G	A	A	CELF3	c.620C>T	P.T207I
SH_64	1	152324169	152324169	Missense_Mutation	SNV	A	T	T	FLG2	c.6093T>A	P.S2031R
SH_64	1	156255485	156255485	Silent	SNV	C	T	T	TMEM79	c.468C>T	P.C156C
SH_64	1	156641644	156641644	Missense_Mutation	SNV	G	T	T	NE5	c.2336C>A	P.P779H
SH_64	1	204118896	204118896	Silent	SNV	C	A	A	ETNK2	c.453G>T	P.L151L
SH_64	1	209788657	209788657	Missense_Mutation	SNV	G	A	A	LAMB3	c.3478C>T	P.H1160Y
SH_64	1	39775993	39775993	Missense_Mutation	SNV	A	G	G	MACF1	c.3008A>G	P.D1003G
SH_64	1	48231758	48231758	Missense_Mutation	SNV	G	A	A	TRABD2B	c.1370C>T	P.P457L
SH_64	10	134004294	134004294	Missense_Mutation	SNV	A	G	G	DPYSL4	c.83A>G	P.D28G
SH_64	11	104912392	104912392	Missense_Mutation	SNV	C	G	G	CARD16	c.329G>C	P.G110A
SH_64	11	55587681	55587681	Silent	SNV	T	C	C	OR5D18	c.576T>C	P.D192D
SH_64	11	62296777	62296777	Missense_Mutation	SNV	G	C	C	AHNAK	c.5112C>G	P.H1704Q
SH_64	12	15073918	15073918	Missense_Mutation	SNV	C	A	A	ERP27	c.95G>T	P.S32I
SH_64	12	2702394	2702394	Missense_Mutation	SNV	A	T	T	CACNA1C	c.2546A>T	P.E849V
SH_64	12	65232577	65232577	Missense_Mutation	SNV	A	T	T	TBC1D30	c.878A>T	P.E293V
SH_64	12	7647755	7647755	Missense_Mutation	SNV	A	T	T	CD163	c.1342T>A	P.5448T
SH_64	13	99853802	99853802	Missense_Mutation	SNV	G	T	T	UBAC2	c.137G>T	P.R46L
SH_64	15	41865614	41865614	Missense_Mutation	SNV	G	T	T	TYRO3	c.2094G>T	P.W698C
SH_64	15	45456966	45456966	Splice_Site	SNV	T	A	A	DUOX1	c.4534-11T>A	
SH_64	17	3101040	3101040	Silent	SNV	A	T	T	OR1A2	c.228A>T	P.V76V
SH_64	17	7577534	7577534	Missense_Mutation	SNV	C	A	A	TP53	c.747G>T	P.R249S
SH_64	2	128334281	128334281	Missense_Mutation	SNV	A	T	T	MYO7B	c.847A>T	P.M283L
SH_64	2	200804867	200804867	Splice_Site	SNV	C	A	A	TYW5	c.304-11G>T	
SH_64	2	212576833	212576833	Missense_Mutation	SNV	A	G	G	ERBB4	c.1066T>C	P.F356L
SH_64	2	234627496	234627496	Silent	SNV	G	T	T	UGT1A4	c.30G>T	P.P10P
SH_64	2	88407989	88407989	Missense_Mutation	SNV	G	T	T	SMYD1	c.1245G>T	P.M415I
SH_64	22	46733701	46733701	Missense_Mutation	SNV	G	T	T	TRMU	c.108G>T	P.M36I
SH_64	22	46785261	46785261	Missense_Mutation	SNV	C	A	A	CELSR1	c.6481G>T	P.G2161C
SH_64	4	119659414	119659414	Splice_Site	SNV	A	T	T	SEC24D	c.2499+2T>A	
SH_64	4	121958488	121958488	Missense_Mutation	SNV	A	G	G	NDNF	c.638T>C	P.V213A
SH_64	4	130023842	130023842	Missense_Mutation	SNV	G	T	T	C4orf33	c.77G>T	P.G26V
SH_64	4	183815639	183815639	Splice_Site	SNV	T	C	C	CTD	c.394+3A>G	
SH_64	5	140256509	140256509	Silent	SNV	G	A	A	PCDHA12	c.1452G>A	P.A484A
SH_64	5	161576191	161576191	Missense_Mutation	SNV	G	A	A	GABRG2	c.1000G>A	P.A334T
SH_64	5	60825973	60825973	Missense_Mutation	SNV	G	T	T	ZSWIM6	c.1932G>T	P.M644I
SH_64	6	26598557	26598557	Missense_Mutation	SNV	G	T	T	ABT1	c.503G>T	P.P168M
SH_64	6	31912624	31912624	Missense_Mutation	SNV	T	A	A	C2	c.2023T>A	P.C675S
SH_64	7	103180757	103180757	Missense_Mutation	SNV	C	T	T	RELN	c.6817G>A	P.G2273S
SH_64	7	107738918	107738918	Missense_Mutation	SNV	T	A	A	LAMB4	c.1290A>T	P.E430D
SH_64	7	116423410	116423410	Missense_Mutation	SNV	A	T	T	MET	c.3685A>T	P.M1229L
SH_64	7	141920332	141920332	Missense_Mutation	SNV	T	A	A	MGAM2	c.6021T>A	P.S2007R
SH_64	7	55750530	55750530	Splice_Site	INDEL	G	-	-	FKBP9P1	n.686-12delC	
SH_64	7	82581706	82581706	Missense_Mutation	SNV	A	T	T	PCLO	c.8563T>A	P.L2855I
SH_64	8	113246675	113246675	Missense_Mutation	SNV	C	T	T	CSMD3	c.10152G>A	P.M3384I
SH_64	8	133041356	133041356	Missense_Mutation	SNV	A	T	T	OC90	c.1102T>A	P.W368R
SH_64	8	42045020	42045020	Silent	SNV	G	T	T	PLAT	c.435C>A	P.G145G
SH_64	8	72981427	72981427	Missense_Mutation	SNV	T	A	A	TRPA1	c.275A>T	P.H92L
SH_64	9	125239745	125239745	Missense_Mutation	SNV	G	T	T	OR1J1	c.461C>A	P.A154E
SH_64	9	21217180	21217180	Missense_Mutation	SNV	G	A	A	IFNA16	c.125C>T	P.A42V
SH_66	1	2105415	2105415	Silent	SNV	C	T	T	PRKC2	c.816C>T	P.T727T
SH_66	12	25398284	25398284	Missense_Mutation	SNV	C	G	G	KRAS	c.35G>C	P.G12A
SH_66	16	2283025	2283025	Silent	SNV	A	C	C	E4F1	c.897A>C	P.G299G
SH_66	16	24886938	24886938	Splice_Site	SNV	T	C	C	SLCSA11	c.181-10T>C	
SH_66	22	19124841	19124841	Missense_Mutation	SNV	A	C	C	DGCR14	c.1030T>G	P.F344V
SH_66	22	43986044	43986044	Missense_Mutation	SNV	G	C	C	EFCAB6	c.2942C>G	P.T981S
SH_66	5	153175078	153175078	Silent	SNV	C	T	T	GRIA1	c.2313C>T	P.G771G
SH_66	9	140043509	140043509	Silent	SNV	C	T	T	GRIN1	c.619C>T	P.L207L
SH_66	9	35061070	35061070	Missense_Mutation	SNV	T	C	C	VCP	c.1301A>G	P.D434G
SH_67	1	148341939	148341939	Missense_Mutation	SNV	A	C	C	NBPF9	c.634T>G	P.S212A
SH_67	10	72633267	72633267	Missense_Mutation	SNV	G	T	T	SGPL1	c.1219G>T	P.A407S
SH_67	11	44286426	44286426	Missense_Mutation	SNV	G	A	A	ALX4	c.1214C>T	P.A405V
SH_67	14	21161742	21161742	Missense_Mutation	SNV	G	A	A	ANG	c.19G>A	P.V7I
SH_69	1	145299871	145299871	Missense_Mutation	SNV	G	T	T	NBPF10	c.920G>T	P.R307I
SH_69	1	228459745	228459745	Missense_Mutation	SNV	C	A	A	OBSCN	c.5809C>A	P.Q1937K
SH_69	1	228487233	228487233	Splice_Site	SNV	C	T	T	OBSCN	c.13474+10C>T	
SH_69	1	65309803	65309803	Missense_Mutation	SNV	G	A	A	JAK1	c.2347C>T	P.L783F
SH_69	14	20216204	20216204	Silent	SNV	G	C	C	OR4Q3	c.618G>C	P.L206L
SH_69	16	11362921	11362921	Missense_Mutation	SNV	C	T	T	TNP2	c.199G>A	P.G67S
SH_69	16	50741788	50741788	Missense_Mutation	SNV	C	A	A	NOD2	c.482C>A	P.A161D
SH_69	19	43689246	43689246	Missense_Mutation	SNV	C	T	T	PSG5	c.118G>A	P.A40T
SH_69	2	108487603	108487603	Missense_Mutation	SNV	T	C	C	RGPD4	c.3143T>C	P.V1048A
SH_69	2	96546346	96546346	Missense_Mutation	SNV	C	G	G	ANKRD36C	c.4488G>C	P.L1496F
SH_69	5	159854783	159854783	Silent	SNV	G	T	T	PTTG1	c.432G>T	P.V144V
SH_69	8	73848937	73848937	Silent	SNV	C	A	A	KCNB2	c.1347C>A	P.I449I
SH_70	1	197479681	197479681	Missense_Mutation	SNV	A	G	G	DENND1B	c.2237T>C	P.L746P
SH_70	1	200008926	200008926	Splice_Site	SNV	A	G	G	NR5A2	c.202+3A>G	
SH_70	1	226574083	226574083	Missense_Mutation	SNV	C	T	T	PARP1	c.778G>A	P.D260N
SH_70	1	235345367	235345367	Missense_Mutation	SNV	G	A	A	ARID4B	c.2867C>T	P.P956L
SH_70	11	7642253	7642253	Missense_Mutation	SNV	A	G	G	PPFIBP2	c.370A>G	P.T124A
SH_70	12	104048404	104048404	Silent	SNV	T	A	A	STAB2	c.1479T>A	P.A493A
SH_70	12	79689895	79689895	Missense_Mutation	SNV	T	G	G	SYT1	c.521T>G	P.M174R
SH_70	13	49684548	49684548	Splice_Site	SNV	A	C	C	FNDC3A	c.7+6A>C	
SH_70	14	101349285	101349285	Missense_Mutation	SNV	G	A	A	RTL1	c.1841C>T	P.A614V
SH_70	15	48776091	48776091	Silent	SNV	G	A	A	FBN1	c.3762C>T	P.C1254C
SH_70	15	59500001	59500001	Missense_Mutation	SNV	T	A	A	LDHAL6B	c.862T>A	P.Y288N
SH_70	16	48175175	48175175	Missense_Mutation	SNV	C	T	T	ABCC12	c.365G>A	P.R122H
SH_70	16	69170708	69170708	Missense_Mutation	SNV	C	T	T	UTP4	c.20C>T	P.A7V
SH_70	17	27861114	27861117	Splice_Site	INDEL	TCTC	-	-	TAOK1	2-11_2362-8delCTCT	
SH_70	2	24283674	24283674	Splice_Site	SNV	G	A	A	FKBP1B	c.-2-10G>A	
SH_70	2	71576596	71576596	Missense_Mutation	SNV	C	T	T	ZN6F38	c.512C>T	P.P171L
SH_70	20	47688902	47688903	Frame_Shift_Del	INDEL	AT	-	-	CSE1L	c.848_849delAT	P.D283fs
SH_70	20	5933137	5933137	Silent	SNV	C	T	T	MCM8	c.216C>T	P.F72F

SH_70	20	62168506	62168506	Silent	SNV	A	C	C	PTK6	c.162T>G	P.G54G
SH_70	22	19344435	19344435	Missense_Mutation	SNV	C	A	A	HIRA	c.2374G>T	P.A792S
SH_70	22	38204131	38204131	Missense_Mutation	SNV	C	T	T	GCAT	c.157C>T	P.R53C
SH_70	3	45972616	45972616	Missense_Mutation	SNV	A	T	T	FYCO1	c.4198T>A	P.S1400T
SH_70	4	151849656	151849656	Splice_Site	INDEL	AAG	-	-	LRBA	9+10_549+12delCTT	
SH_70	5	140595018	140595018	Silent	SNV	C	T	T	PCDH13	c.1323C>T	P.I441I
SH_70	5	140712198	140712198	Silent	SNV	C	T	T	PCDHGA1	c.1947C>T	P.H649H
SH_70	5	154396819	154396819	Missense_Mutation	SNV	C	A	A	KIF4B	c.3400C>A	P.Q1134K
SH_70	5	169101307	169101307	Frame_Shift_Del	INDEL	A	-	-	DOCK2	c.332delA	P.K111fs
SH_70	5	176004723	176004723	Missense_Mutation	SNV	C	T	T	CDHR2	c.1436C>T	P.T479M
SH_70	6	25653642	25653642	Missense_Mutation	SNV	G	A	A	SCGN	c.115G>A	P.A39T
SH_70	6	26199965	26199965	Missense_Mutation	SNV	T	G	G	HIST1H2BF	c.179T>G	P.M60R
SH_70	6	27100374	27100374	Missense_Mutation	SNV	G	T	T	HIST1H2BJ	c.156C>A	P.D52E
SH_70	6	31324628	31324628	Missense_Mutation	SNV	G	T	T	HLA-B	c.180C>A	P.F60L
SH_70	7	127014776	127014776	Missense_Mutation	SNV	G	C	C	ZNF800	c.614C>G	P.P205R
SH_70	8	113529433	113529433	Missense_Mutation	SNV	C	T	T	CSMD3	c.4274G>A	P.R1425H
SH_70	X	105011452	105011452	Missense_Mutation	SNV	G	C	C	IL1RAPL2	c.1859G>C	P.G620A
SH_70	X	105970265	105970265	Missense_Mutation	SNV	C	G	G	RNF128	c.122C>G	P.A41G
SH_70	X	53112240	53112240	Missense_Mutation	SNV	G	C	C	TSPYL2	c.560G>C	P.R187T
SH_70	X	70523144	70523144	Missense_Mutation	SNV	A	C	C	ITGB1BP2	c.350A>C	P.N117T
SH_70	X	90690678	90690678	Silent	SNV	C	A	A	PABPC5	c.102C>A	P.L34L
SH_71	1	12726141	12726141	Missense_Mutation	SNV	G	A	A	AADACL4	c.619G>A	P.V207M
SH_71	1	145281968	145281968	Missense_Mutation	SNV	A	T	T	NOTCH2NL	c.648A>T	P.R216S
SH_71	1	152086470	152086470	Silent	SNV	A	T	T	TCHH	c.87T>A	P.T29T
SH_71	1	159828008	159828008	Missense_Mutation	SNV	G	A	A	VSIG8	c.302C>T	P.A101V
SH_71	1	160147404	160147404	Missense_Mutation	SNV	T	A	A	ATP1A4	c.94T>A	P.W32R
SH_71	1	161476312	161476312	Missense_Mutation	SNV	A	T	T	FCGR2A	c.295A>T	P.S99C
SH_71	1	181479644	181479644	Missense_Mutation	SNV	A	T	T	CACNA1E	c.298A>T	P.I100F
SH_71	1	19181133	19181133	Silent	SNV	G	A	A	TAS1R2	c.831C>T	P.P277P
SH_71	1	196309613	196309613	Silent	SNV	T	A	A	KCNT2	c.1641A>T	P.T547T
SH_71	1	201177789	201177789	Silent	SNV	A	T	T	IGFN1	c.3768A>T	P.S1256S
SH_71	1	201195010	201195010	Silent	SNV	G	A	A	IGFN1	c.10545G>A	P.T3515T
SH_71	1	20412610	20412610	Silent	SNV	A	T	T	PLA2G5	c.75A>T	P.LA25L
SH_71	1	20656805	20656805	Missense_Mutation	SNV	A	T	T	VWA5B1	c.1387A>T	P.I463F
SH_71	1	209974729	209974729	Silent	SNV	T	C	C	IRF6	c.30A>G	P.L10L
SH_71	1	21795269	21795269	Silent	SNV	A	T	T	NBPF3	c.222A>T	P.L74L
SH_71	1	223116553	223116553	Missense_Mutation	SNV	A	T	T	DISP1	c.388A>T	P.N130Y
SH_71	1	231401865	231401865	Missense_Mutation	SNV	A	G	G	GNPAT	c.695A>G	P.Y232C
SH_71	1	24022297	24022297	Missense_Mutation	SNV	A	T	T	RPL11	c.406A>T	P.R136W
SH_71	1	247031021	247031021	Missense_Mutation	SNV	T	C	C	AHCTF1	c.3181A>G	P.K1061E
SH_71	1	248031306	248031306	Missense_Mutation	SNV	T	A	A	TRIM58	c.812T>A	P.M271K
SH_71	1	28354311	28354311	Missense_Mutation	SNV	T	A	A	EYA3	c.329A>T	P.Y110F
SH_71	1	3102742	3102742	Missense_Mutation	SNV	A	T	T	PRDM16	c.91A>T	P.S31C
SH_71	1	90484250	90484250	Missense_Mutation	SNV	A	T	T	ZNF326	c.814A>T	P.M272L
SH_71	10	105889993	105889993	Silent	SNV	T	C	C	CFAP43	c.4902A>G	P.T1634T
SH_71	10	18169595	18169595	Missense_Mutation	SNV	A	T	T	MRC1	c.2861A>T	P.N954I
SH_71	10	55943333	55943333	Silent	SNV	T	A	A	PCDH15	c.1476A>T	P.V492V
SH_71	11	121481850	121481850	Missense_Mutation	SNV	A	T	T	SORL1	c.5305A>T	P.M1769L
SH_71	11	1260724	1260724	Missense_Mutation	SNV	T	G	G	MUC5B	c.3511T>G	P.C1171G
SH_71	11	18108760	18108760	Silent	SNV	T	A	A	SAAL1	c.783A>T	P.P261P
SH_71	11	75115772	75115772	Missense_Mutation	SNV	G	T	T	RPS3	c.595G>T	P.G199C
SH_71	12	12870990	12870990	Nonsense_Mutation	SNV	A	T	T	CDKN1B	c.217A>T	P.K73*
SH_71	12	132685736	132685736	Missense_Mutation	SNV	A	T	T	GALNT9	c.1334T>A	P.F445Y
SH_71	12	15654750	15654750	Missense_Mutation	SNV	T	A	A	PTPRO	c.858T>A	P.T286L
SH_71	12	4705744	4705744	Splice_Site	SNV	A	T	T	DYRK4	n.962-11A>T	
SH_71	12	4870133	4870133	Missense_Mutation	SNV	T	A	A	GALNT8	c.1183T>A	P.C395S
SH_71	12	52992743	52992743	Missense_Mutation	SNV	C	T	T	KRT72	c.580G>A	P.G194R
SH_71	12	85255635	85255635	Missense_Mutation	SNV	A	T	T	SLC6A15	c.1648T>A	P.Y550N
SH_71	12	91502374	91502374	Missense_Mutation	SNV	A	T	T	LUM	c.383T>A	P.L128Q
SH_71	12	97084952	97084952	Missense_Mutation	SNV	A	T	T	CFAP54	c.6128A>T	P.Y2043F
SH_71	13	45149121	45149121	Missense_Mutation	SNV	A	T	T	TSC22D1	c.1090T>A	P.L364M
SH_71	13	46065104	46065104	Splice_Site	SNV	A	T	T	COG3	c.968+11A>T	
SH_71	13	76301222	76301222	Silent	SNV	A	T	T	LMO7	c.198A>T	P.P66P
SH_71	14	20404317	20404317	Silent	SNV	G	T	T	OR4K1	c.492G>T	P.V164V
SH_71	15	30900711	30900711	Missense_Mutation	SNV	T	A	A	GOLGA8H	c.438T>A	P.N146K
SH_71	15	33954893	33954893	Missense_Mutation	SNV	A	T	T	RYR3	c.5162A>T	P.Q1721L
SH_71	15	41120653	41120653	Silent	SNV	G	T	T	PPP1R14D	c.187C>A	P.R63R
SH_71	15	42342792	42342792	Missense_Mutation	SNV	T	A	A	PLA2G4E	c.110A>T	P.E37V
SH_71	15	49037129	49037129	Frame_Shift_Del	INDEL	A	-	-	CEP152	c.3695delT	P.L1232fs
SH_71	15	55783366	55783366	Silent	SNV	T	A	A	DYX1C1	c.360A>T	P.A120A
SH_71	15	55972250	55972250	Splice_Site	SNV	A	T	T	PRTG	c.973+2T>A	
SH_71	15	56387737	56387737	Missense_Mutation	SNV	T	A	A	RFX7	c.2189A>T	P.Q730L
SH_71	15	64680075	64680075	Missense_Mutation	SNV	G	T	T	TRIP4	c.13G>T	P.G5W
SH_71	15	64680076	64680076	Missense_Mutation	SNV	G	T	T	TRIP4	c.14G>T	P.G5V
SH_71	15	92705976	92705976	Splice_Site	SNV	C	G	G	SLCO3A1	c.1754-10C>G	
SH_71	16	12093152	12093152	Splice_Site	SNV	A	T	T	SNX29	c.8-2A>T	
SH_71	16	3283657	3283657	Silent	SNV	T	A	A	ZNF200	c.99A>T	P.R33R
SH_71	16	48396197	48396197	Missense_Mutation	SNV	A	T	T	SIAH1	c.236T>A	P.V79E
SH_71	16	67911472	67911472	Missense_Mutation	SNV	G	T	T	EDC4	c.702G>T	P.R234S
SH_71	16	69727852	69727852	Missense_Mutation	SNV	A	T	T	NFAT5	c.4121A>T	P.Q1374L
SH_71	16	71007873	71007873	Silent	SNV	A	T	T	HYDIN	c.5088T>A	P.I1696I
SH_71	17	10362659	10362659	Missense_Mutation	SNV	A	T	T	MYH4	c.1496T>A	P.L499Q
SH_71	17	16021198	16021198	Splice_Site	SNV	T	A	A	NCOR1	c.2055+4A>T	
SH_71	17	39120715	39120715	Silent	SNV	T	G	G	KRT39	c.534A>C	P.A178A
SH_71	17	48191581	48191581	Silent	SNV	G	A	A	SAMD14	c.912C>T	P.P304P
SH_71	17	7577568	7577568	Missense_Mutation	SNV	C	A	A	TP53	c.713G>T	P.C238F
SH_71	18	30913191	30913191	Missense_Mutation	SNV	T	G	G	CCDC178	c.826A>C	P.K276Q
SH_71	18	50866104	50866104	Missense_Mutation	SNV	C	G	G	DCC	c.2186C>G	P.P729R
SH_71	19	31769226	31769226	Silent	SNV	A	T	T	TSHZ3	c.1473T>A	P.P491P
SH_71	19	35836550	35836550	Missense_Mutation	SNV	T	A	A	CD22	c.2254T>A	P.Y752N
SH_71	19	55107274	55107274	Missense_Mutation	SNV	T	A	A	LILRA1	c.832T>A	P.S278T
SH_71	19	57051027	57051027	Missense_Mutation	SNV	A	G	G	ZFP28	c.242A>G	P.E81G
SH_71	19	57327876	57327876	Missense_Mutation	SNV	T	A	A	PEG3	c.1934A>T	P.H645L
SH_71	19	9056879	9056879	Silent	SNV	A	T	T	MUC16	c.30567T>A	P.S10189S
SH_71	2	113081919	113081919	Missense_Mutation	SNV	C	T	T	ZC3H6	c.1531C>T	P.P511S
SH_71	2	113082677	113082677	Silent	SNV	A	T	T	ZC3H6	c.1989A>T	P.A663A
SH_71	2	113537149	113537149	Silent	SNV	G	A	A	IL1A	c.414C>T	P.D138D
SH_71	2	125555776	125555776	Silent	SNV	A	T	T	CNTNAP5	c.3093A>T	P.T1031T

SH_71	2	149679720	149679720	Nonsense_Mutation	SNV	T	A	A	KIF5C	c.141T>A	P.Y47*
SH_71	2	167279707	167279707	Missense_Mutation	SNV	A	T	T	SCN7A	c.2156T>A	P.L719Q
SH_71	2	189850408	189850408	Silent	SNV	T	A	A	COL3A1	c.351T>A	P.P117P
SH_71	2	192194682	192194682	Silent	SNV	A	T	T	MYO1B	c.273A>T	P.A91A
SH_71	2	209113365	209113365	Missense_Mutation	SNV	T	A	A	IDH1	c.142A>T	P.N48Y
SH_71	2	21232828	21232828	Silent	SNV	T	A	A	APOB	c.6912A>T	P.T2304T
SH_71	2	239003074	239003074	Missense_Mutation	SNV	A	T	T	SLCY	c.1043A>T	P.Q348L
SH_71	2	242076617	242076617	Missense_Mutation	SNV	T	A	A	PASK	c.939A>T	P.L313F
SH_71	2	44528130	44528130	Splice_Site	SNV	T	A	A	SLC3A1	c.1012-12T>A	
SH_71	2	47630423	47630423	Silent	SNV	C	A	A	MSH2	c.93C>A	P.T31T
SH_71	2	74074873	74074873	Silent	SNV	A	T	T	STAMPB	c.735A>T	P.S245S
SH_71	20	3102162	3102162	Missense_Mutation	SNV	T	A	A	UBOX5	c.1123A>T	P.S375C
SH_71	20	44669966	44669966	Splice_Site	SNV	A	T	T	SLC12A5	c.924-2A>T	
SH_71	20	45891038	45891038	Missense_Mutation	SNV	T	A	A	ZMYND8	c.1615A>T	P.N539Y
SH_71	20	55748285	55748285	Missense_Mutation	SNV	C	T	T	BMP7	c.1117G>A	P.A373T
SH_71	21	10916449	10916449	Missense_Mutation	SNV	T	A	A	TPTE	c.783A>T	P.Q261H
SH_71	21	10951307	10951307	Missense_Mutation	SNV	T	A	A	TPTE	c.291A>T	P.L97F
SH_71	3	10089723	10089723	Silent	SNV	G	T	T	FANCD2	c.1401G>T	P.T467T
SH_71	3	111317017	111317017	Silent	SNV	A	T	T	CD96	c.858A>T	P.T286T
SH_71	3	125179630	125179630	Missense_Mutation	SNV	T	A	A	SNX4	c.929A>T	P.Y310F
SH_71	3	132036312	132036312	Silent	SNV	A	T	T	ACPP	c.12A>T	P.AAA
SH_71	3	160395290	160395290	Silent	SNV	C	A	A	ARL14	c.156C>A	P.I52I
SH_71	3	18083033	18083033	Missense_Mutation	SNV	G	A	A	LOC339862	c.316G>A	P.G106S
SH_71	3	47651717	47651717	Missense_Mutation	SNV	T	A	A	SMARCC1	c.2882A>T	P.Q961L
SH_71	4	106510453	106510453	Missense_Mutation	SNV	C	T	T	ARHGEF38	c.245C>T	P.P82L
SH_71	4	143181694	143181694	Silent	SNV	T	A	A	INPP4B	c.639A>T	P.T213T
SH_71	4	148834219	148834219	Splice_Site	SNV	T	A	A	ARHGAP10	c.1163-6T>A	
SH_71	4	159756593	159756593	Missense_Mutation	SNV	A	T	T	FNIP2	c.761A>T	P.Q254L
SH_71	4	437355	437355	Nonsense_Mutation	SNV	C	A	A	ZNF721	c.901G>T	P.G301*
SH_71	5	140751633	140751633	Missense_Mutation	SNV	A	T	T	PCDHGB3	c.1672A>T	P.N558Y
SH_71	5	168201298	168201298	Missense_Mutation	SNV	T	A	A	SLIT3	c.1237A>T	P.N413Y
SH_71	5	176318173	176318173	Silent	SNV	C	A	A	HK3	c.279G>T	P.V93V
SH_71	5	52942144	52942144	Missense_Mutation	SNV	A	T	T	NDUFS4	c.259A>T	P.M87L
SH_71	5	90024644	90024644	Missense_Mutation	SNV	T	A	A	ADGRV1	c.10320T>A	P.S3440R
SH_71	6	114264511	114264511	Splice_Site	SNV	T	A	A	HDAC2	c.1378+4A>T	
SH_71	6	137815010	137815010	Missense_Mutation	SNV	T	A	A	OLIG3	c.298A>T	P.N100Y
SH_71	6	152722287	152722287	Missense_Mutation	SNV	A	T	T	SYNE1	c.7036T>A	P.L2346M
SH_71	6	155750005	155750005	Silent	SNV	T	A	A	NOX3	c.1068A>T	P.A356A
SH_71	6	24447101	24447101	Silent	SNV	C	A	A	GPLD1	c.1785G>T	P.L595L
SH_71	6	36104687	36104687	Silent	SNV	A	T	T	MAPK13	c.642A>T	P.A214A
SH_71	6	88769271	88769271	Missense_Mutation	SNV	T	A	A	SPACA1	c.575T>A	P.V192E
SH_71	6	89977435	89977435	Missense_Mutation	SNV	A	T	T	GABRR2	c.699T>A	P.F233L
SH_71	7	100683484	100683484	Silent	SNV	A	T	T	MUC17	c.8787A>T	P.P2929P
SH_71	7	146829371	146829371	Missense_Mutation	SNV	C	T	T	CNTNAP2	c.1118C>T	P.T373M
SH_71	7	36461510	36461510	Missense_Mutation	SNV	A	T	T	ANLN	c.2097A>T	P.Q699H
SH_71	7	45124415	45124439	Frame_Shift_Del	INDEL	FGAGGTCTGA	-	-	NACAD	TGCTCCTCAGAC	P.A447fs
SH_71	7	82580537	82580537	Missense_Mutation	SNV	T	A	A	PCLO	c.9367A>T	P.T3123S
SH_71	8	110587828	110587828	Missense_Mutation	SNV	A	T	T	SYBU	c.1296T>A	P.D432E
SH_71	8	135612685	135612685	Silent	SNV	T	A	A	ZFAT	c.2433A>T	P.T811T
SH_71	8	36766896	36766896	Missense_Mutation	SNV	A	T	T	KCNU1	c.2174A>T	P.H725L
SH_71	8	48827961	48827961	Missense_Mutation	SNV	T	A	A	PRKDC	c.2544A>T	P.L848F
SH_71	8	69552677	69552677	Missense_Mutation	SNV	A	T	T	C8orf34	c.1172A>T	P.Q391L
SH_71	8	70967630	70967630	Missense_Mutation	SNV	T	A	A	PRDM14	c.1393A>T	P.T465S
SH_71	8	91937869	91937869	Missense_Mutation	SNV	A	T	T	NECAB1	c.601A>T	P.N201Y
SH_71	8	94772166	94772166	Silent	SNV	G	A	A	TMEM67	c.108G>A	P.P36P
SH_71	9	101810231	101810231	Silent	SNV	A	T	T	COL15A1	c.2742A>T	P.P914P
SH_71	9	116259668	116259668	Silent	SNV	A	G	G	RG53	c.825A>G	P.R275R
SH_71	9	21333634	21333634	Missense_Mutation	SNV	C	A	A	KLHL9	c.1225G>T	P.A409S
SH_71	9	33338526	33338526	Missense_Mutation	SNV	A	T	T	NFX1	c.2057A>T	P.D686V
SH_71	9	6014278	6014278	Nonsense_Mutation	SNV	T	A	A	RANBP6	c.274A>T	P.K92*
SH_71	9	84605951	84605951	Missense_Mutation	SNV	G	A	A	SPATA31D1	c.566G>A	P.R189Q
SH_71	9	84609680	84609680	Missense_Mutation	SNV	T	A	A	SPATA31D1	c.4295T>A	P.L1432H
SH_71	X	117676887	117676887	Splice_Site	SNV	A	T	T	DOCK11	c.220-2A>T	
SH_71	X	124455317	124455317	Missense_Mutation	SNV	A	T	T	TEX13C	c.1349A>T	P.Q450L
SH_71	X	131219616	131219616	Missense_Mutation	SNV	A	T	T	FRMD7	c.593T>A	P.V198E
SH_71	X	154319075	154319075	Missense_Mutation	SNV	A	T	T	BRCC3	c.509A>T	P.Y170F
SH_71	X	24380967	24380967	Silent	SNV	T	A	A	SUPT20HL1	c.90T>A	P.P30P
SH_71	X	34148324	34148324	Missense_Mutation	SNV	A	T	T	FAM47A	c.2072T>A	P.V691E
SH_71	X	53430585	53430585	Missense_Mutation	SNV	T	A	A	SMC1A	c.2267A>T	P.E756V
SH_74	10	115336953	115336953	Missense_Mutation	SNV	C	T	T	HABP2	c.298C>T	P.L100F
SH_74	10	135233650	135233650	Missense_Mutation	SNV	C	T	T	MTG1	c.986C>T	P.P329L
SH_74	11	113269863	113269863	Missense_Mutation	SNV	A	T	T	ANKK1	c.1172A>T	P.Q391L
SH_74	11	5411452	5411452	Missense_Mutation	SNV	G	A	A	OR51M1	c.824G>A	P.R275H
SH_74	11	55406246	55406246	Missense_Mutation	SNV	A	G	G	OR4P4	c.413A>G	P.K138R
SH_74	12	57556141	57556141	Silent	SNV	G	T	T	LRP1	c.2244G>T	P.L748L
SH_74	12	7459223	7459223	Missense_Mutation	SNV	G	A	A	ACSM4	c.296G>A	P.R99Q
SH_74	14	20611945	20611945	Silent	SNV	G	A	A	OR4N5	c.51G>A	P.L17L
SH_74	14	65252602	65252602	Missense_Mutation	SNV	A	G	G	SPTB	c.3629T>C	P.F1210S
SH_74	17	35836890	35836890	Splice_Site	SNV	C	A	A	TADA2A	c.1147-12C>A	
SH_74	19	13211506	13211506	Missense_Mutation	SNV	C	T	T	LYL1	c.392G>A	P.R131Q
SH_74	19	19576376	19576376	Silent	SNV	C	T	T	GATAD2A	c.222C>T	P.G74G
SH_74	19	50298881	50298881	Splice_Site	SNV	C	T	T	AP2A1	c.706-6C>T	
SH_74	19	50549938	50549938	Silent	SNV	C	T	T	ZNF473	c.2238C>T	P.V746V
SH_74	2	138414474	138414474	Missense_Mutation	SNV	T	A	A	THSD7B	c.4214T>A	P.I1405K
SH_74	2	177017521	177017521	Missense_Mutation	SNV	A	G	G	HOXD4	c.619A>G	P.M207V
SH_74	2	65541233	65541233	Missense_Mutation	SNV	C	T	T	SPRED2	c.650G>A	P.R217Q
SH_74	3	4687363	4687363	Missense_Mutation	SNV	G	A	A	ITPR1	c.806G>A	P.R269Q
SH_74	3	52443565	52443565	Splice_Site	SNV	C	T	T	BAP1	c.122+5G>A	
SH_74	3	97251308	97251308	Missense_Mutation	SNV	A	T	T	EPHA6	c.483A>T	P.R161S
SH_74	4	30724929	30724929	Missense_Mutation	SNV	G	A	A	PCDH7	c.1885G>A	P.V629M
SH_74	5	161520898	161520898	Missense_Mutation	SNV	A	G	G	GABRG2	c.172A>G	P.T58A
SH_74	5	37179516	37179516	Missense_Mutation	SNV	T	C	C	C5orf42	c.5767A>G	P.R1923G
SH_74	5	40955662	40955662	Splice_Site	SNV	C	T	T	C7	c.1260+7C>T	
SH_74	6	25770603	25770603	Splice_Site	SNV	T	C	C	SLC17A4	c.370-9T>C	
SH_74	6	31630061	31630061	Silent	SNV	G	A	A	GPANK1	c.1053C>T	P.Y351Y
SH_74	6	96971097	96971097	Silent	SNV	C	G	G	UFL1	c.153C>G	P.L51L
SH_74	7	151879655	151879655	Nonsense_Mutation	SNV	G	A	A	KMT2C	c.5290C>T	P.Q1764*
SH_74	9	133730260	133730260	Missense_Mutation	SNV	G	T	T	ABL1	c.326G>T	P.G109V

SH_74	9	43627372	43627372	Missense_Mutation	SNV	T	C	C	SPATA31A6	c.1315A>G	P.T439A
SH_74	9	97555152	97555152	Missense_Mutation	SNV	A	G	G	C9orf3	c.1070A>G	P.N357S
SH_74	X	129058934	129058934	Missense_Mutation	SNV	A	T	T	UTP14A	c.1356A>T	P.R452S
SH_79	1	152286108	152286108	Silent	SNV	G	A	A	FLG	c.1254C>T	P.S418S
SH_79	1	230883258	230883258	Missense_Mutation	SNV	C	T	T	CAPN9	c.16C>T	P.R6W
SH_79	1	55181597	55181597	Nonsense_Mutation	SNV	C	T	T	TTC4	c.16C>T	P.Q6*
SH_79	1	86934709	86934709	Missense_Mutation	SNV	G	A	A	CLCA1	c.55G>A	P.A19T
SH_79	12	49361759	49361759	Missense_Mutation	SNV	C	A	A	WNT10B	c.681G>T	P.M227I
SH_79	12	57872896	57872896	Silent	SNV	G	A	A	ARHGAP9	c.294C>T	P.P98P
SH_79	15	55932003	55932003	Missense_Mutation	SNV	G	A	A	PRTG	c.2161C>T	P.P721S
SH_79	18	10789289	10789289	Nonsense_Mutation	SNV	G	A	A	PIEZO2	c.1957C>T	P.Q653*
SH_79	2	113514408	113514408	Silent	SNV	T	C	C	CKAP2L	c.45A>G	P.L15L
SH_79	2	28739716	28739716	Nonsense_Mutation	SNV	G	T	T	PLB1	c.97G>T	P.E33*
SH_79	3	135789393	135789393	Missense_Mutation	SNV	C	T	T	PPP2R3A	c.2543C>T	P.T848M
SH_79	5	176887561	176887561	Splice_Site	SNV	G	A	A	DBN1	c.832-5C>T	
SH_79	8	142151322	142151322	Silent	SNV	T	C	C	DENND3	c.282T>C	P.N94N
SH_79	8	36790435	36790435	Splice_Site	SNV	C	T	T	KCNU1	c.2932-3C>T	
SH_79	9	117849127	117849127	Missense_Mutation	SNV	C	T	T	TNC	c.883G>A	P.V295M
SH_79	9	35609179	35609179	Missense_Mutation	SNV	T	C	C	TESK1	c.841T>C	P.S281P
SH_79	X	9866263	9866263	Missense_Mutation	SNV	G	A	A	SHROOM2	c.2824G>A	P.D942N
SH_80	1	110051093	110051093	Missense_Mutation	SNV	C	T	T	AMIGO1	c.442G>A	P.A148T
SH_80	1	113933701	113933701	Nonsense_Mutation	SNV	C	T	T	MAGI3	c.46C>T	P.Q16*
SH_80	1	115256529	115256529	Missense_Mutation	SNV	T	C	C	NRAS	c.182A>G	P.Q61R
SH_80	1	115256530	115256530	Missense_Mutation	SNV	G	T	T	NRAS	c.181C>A	P.Q61K
SH_80	1	158263012	158263012	Missense_Mutation	SNV	T	A	A	CD1C	c.900T>A	P.F300L
SH_80	1	161495275	161495275	Missense_Mutation	SNV	T	C	C	HSPA6	c.827T>C	P.L276P
SH_80	1	174987615	174987615	Missense_Mutation	SNV	G	C	C	MRPS14	c.143C>G	P.A48G
SH_80	1	186106036	186106036	Missense_Mutation	SNV	T	A	A	HMCN1	c.13549T>A	P.S4517T
SH_80	1	186281392	186281392	Nonsense_Mutation	SNV	T	A	A	PRG4	c.3756T>A	P.Y1252*
SH_80	1	232940856	232940856	Silent	SNV	G	A	A	MAP10	c.87G>A	P.Z29R
SH_80	1	234556514	234556514	Silent	SNV	A	C	C	TARBP1	c.3489T>G	P.S1163S
SH_80	10	105233320	105233320	Missense_Mutation	SNV	C	T	T	CALHM3	c.685G>A	P.E229K
SH_80	10	16893363	16893363	Missense_Mutation	SNV	C	T	T	CUBN	c.9534G>A	P.M3178I
SH_80	10	49986752	49986752	Missense_Mutation	SNV	G	A	A	WDFY4	c.3272G>A	P.R1091H
SH_80	11	106680764	106680764	Silent	SNV	C	A	A	GUCY1A2	c.1647G>T	P.L549L
SH_80	11	1220154	1220154	Missense_Mutation	SNV	G	T	T	MUC5AC	c.4702G>T	P.G1568C
SH_80	11	85397172	85397172	Nonsense_Mutation	SNV	A	G	G	CCDC89	c.2T>C	P.M17
SH_80	12	57389405	57389405	Missense_Mutation	SNV	T	C	C	GPR182	c.412T>C	P.Y138H
SH_80	12	75804410	75804410	Missense_Mutation	SNV	A	G	G	GLIPR1L2	c.431A>G	P.Y144C
SH_80	12	80714376	80714376	Missense_Mutation	SNV	A	T	T	OTOGL	c.3950A>T	P.Y1317F
SH_80	14	93723599	93723599	Missense_Mutation	SNV	A	G	G	BTBD7	c.1550T>C	P.L517S
SH_80	16	30616450	30616450	Missense_Mutation	SNV	C	T	T	ZNF689	c.638G>A	P.R213H
SH_80	16	84516259	84516259	Missense_Mutation	SNV	G	A	A	TLCD1	c.1016C>T	P.R239M
SH_80	19	10421576	10421576	Silent	SNV	C	A	A	FDX1L	c.357G>T	P.V119V
SH_80	19	38673170	38673170	Missense_Mutation	SNV	C	T	T	SIPA1L3	c.4220C>T	P.S1407L
SH_80	19	44531609	44531609	Missense_Mutation	SNV	A	T	T	ZNF222	c.229A>T	P.M77L
SH_80	19	4902616	4902616	Silent	SNV	G	A	A	ARRDC5	c.264C>T	P.Y88Y
SH_80	19	55143558	55143558	Silent	SNV	G	A	A	LILRB1	c.531G>A	P.S177S
SH_80	2	166848129	166848129	Nonsense_Mutation	SNV	G	A	A	SCN1A	c.5656C>T	P.R1886*
SH_80	2	219320415	219320415	Missense_Mutation	SNV	T	C	C	USP37	c.2740A>G	P.I914V
SH_80	2	226447616	226447616	Missense_Mutation	SNV	T	A	A	NYAP2	c.1483T>A	P.Y495N
SH_80	20	53205321	53205321	Missense_Mutation	SNV	A	G	G	DOK5	c.61A>G	P.T21A
SH_80	22	46773045	46773045	Missense_Mutation	SNV	G	C	C	CELSR1	c.7497C>G	P.N2499K
SH_80	3	134670397	134670397	Missense_Mutation	SNV	C	T	T	EPHB1	c.308C>T	P.P103L
SH_80	3	52443757	52443757	Frame_Shift_Del	INDEL	G	-	-	BAP1	c.40delC	P.L14fs
SH_80	3	97983712	97983712	Missense_Mutation	SNV	G	A	A	OR5H6	c.584G>A	P.C195Y
SH_80	4	79500256	79500256	Missense_Mutation	SNV	A	G	G	ANXA3	c.179A>G	P.Y60C
SH_80	5	155756543	155756543	Splice_Site	SNV	G	T	T	SGCD	c.-43-1G>T	
SH_80	5	72383891	72383903	Frame_Shift_Del	INDEL	AGGACGATA	-	-	FCHO2	2321delCAGGA	P.Y773fs
SH_80	6	35773583	35773583	Nonsense_Mutation	SNV	C	T	T	LHFP5L	c.136C>T	P.Q46*
SH_80	6	40399853	40399853	Missense_Mutation	SNV	A	G	G	LRFN2	c.1000T>C	P.S334P
SH_80	7	135421920	135421920	Missense_Mutation	SNV	G	T	T	FAM180A	c.104C>A	P.P35Q
SH_80	7	140159588	140159588	Missense_Mutation	SNV	T	C	C	MKRN1	c.463A>G	P.N155D
SH_80	7	150900168	150900168	Missense_Mutation	SNV	C	A	A	IQCA1L	c.474G>T	P.M158I
SH_80	8	110510963	110510963	Missense_Mutation	SNV	G	T	T	PKHD1L1	c.10791G>T	P.M3597I
SH_80	9	124532835	124532835	Missense_Mutation	SNV	C	A	A	DAB2IP	c.1826C>A	P.S609Y
SH_80	9	140136272	140136272	Nonsense_Mutation	SNV	G	T	T	TUBB4B	c.157G>T	P.E53*
SH_80	X	100645492	100645492	Missense_Mutation	SNV	A	T	T	BTX	c.46T>A	P.C16S
SH_80	X	124454177	124454177	Missense_Mutation	SNV	G	A	A	TEX13C	c.209G>A	P.S70N
SH_80	X	13753378	13753378	Missense_Mutation	SNV	T	G	G	OFD1	c.24T>G	P.F8L
SH_80	X	15403215	15403215	Missense_Mutation	SNV	C	T	T	PIR	c.784G>A	P.E262K
SH_80	X	23019839	23019839	Silent	SNV	A	G	G	DDX53	c.1665A>G	P.V555V
SH_81	1	149785218	149785218	Missense_Mutation	SNV	T	C	C	HIST2H3D	c.19A>G	P.T7A
SH_81	1	233802459	233802459	Silent	SNV	G	A	A	KCNK1	c.474G>A	P.V158V
SH_81	1	241797231	241797231	Missense_Mutation	SNV	G	T	T	CHML	c.1838C>A	P.P613Q
SH_81	11	47193243	47193243	Missense_Mutation	SNV	C	T	T	ARFGAP2	c.697G>A	P.D233N
SH_81	12	51754557	51754557	Missense_Mutation	SNV	T	G	G	GALNT6	c.1115A>C	P.Y372S
SH_81	12	76752543	76752543	Missense_Mutation	SNV	C	A	A	OSBPL8	c.2251G>T	P.V751L
SH_81	14	102805285	102805285	Missense_Mutation	SNV	C	T	T	ZNF839	c.1444C>T	P.R482C
SH_81	14	88983510	88983510	Silent	SNV	T	C	C	PTPN21	c.276A>G	P.A92A
SH_81	16	57508784	57508784	Missense_Mutation	SNV	C	T	T	DOK4	c.520G>A	P.V174M
SH_81	17	74053597	74053597	Nonsense_Mutation	SNV	G	A	A	SRP68	c.751C>T	P.Q251*
SH_81	2	125555700	125555700	Missense_Mutation	SNV	C	T	T	CNTNAP5	c.3017C>T	P.T1006M
SH_81	2	185803163	185803163	Missense_Mutation	SNV	G	T	T	ZNF804A	c.3040G>T	P.G1014C
SH_81	2	198266713	198266713	Missense_Mutation	SNV	C	T	T	SF3B1	c.2219G>A	P.G740E
SH_81	2	80085156	80085156	Missense_Mutation	SNV	G	A	A	CTNNA2	c.316G>A	P.A106T
SH_81	3	52831902	52831902	Missense_Mutation	SNV	G	A	A	ITIH3	c.619G>A	P.D207N
SH_81	5	10397404	10397404	Splice_Site	SNV	G	A	A	MARCH6	c.718-1G>A	
SH_81	5	127493768	127493768	Missense_Mutation	SNV	G	A	A	SLC12A2	c.2387G>A	P.G796D
SH_81	5	156589869	156589869	Silent	SNV	G	A	A	FAM71B	c.1407C>T	P.S469S
SH_81	6	137519730	137519730	Missense_Mutation	SNV	T	G	G	IFNGR1	c.908A>C	P.K303T
SH_81	6	74073373	74073373	Silent	SNV	G	A	A	KHDC3L	c.444G>A	P.S148S
SH_81	7	140453149	140453149	Missense_Mutation	SNV	C	G	G	BRAF	c.1786G>C	P.G596R
SH_81	9	101891223	101891226	Frame_Shift_Del	INDEL	ACAG	-	-	TGFBF1	187_190delGAC	P.D63fs
SH_82	1	161276581	161276581	Missense_Mutation	SNV	T	A	A	MPZ	c.365A>T	P.N122I
SH_82	1	208219299	208219299	Missense_Mutation	SNV	T	C	C	PLXNA2	c.3419A>G	P.Y1140C
SH_82	18	57136753	57136753	Nonsense_Mutation	SNV	G	A	A	CCBE1	c.352C>T	P.R18*
SH_82	7	100680600	100680600	Missense_Mutation	SNV	C	A	A	MUC17	c.5903C>A	P.T1968K

SH_82	8	114111096	114111096	Missense_Mutation	SNV	C	G	G	CSMD3	c.806G>C	P.W269S
SH_82	X	77224504	77224504	Missense_Mutation	SNV	G	T	T	PGAM4	c.632C>A	P.P211Q
SH_85	1	151027510	151027510	Silent	SNV	G	A	A	CDC42SE1	c.147C>T	P.A49A
SH_85	1	158299402	158299402	Missense_Mutation	SNV	G	A	A	CD1B	c.644C>T	P.P215L
SH_85	1	158746718	158746718	Missense_Mutation	SNV	C	A	A	OR6N2	c.708G>T	P.K236N
SH_85	1	75097523	75097523	Missense_Mutation	SNV	C	A	A	ERICH3	c.693G>T	P.M231I
SH_85	10	50819847	50819847	Missense_Mutation	SNV	A	G	G	SLC18A3	c.1061A>G	P.H354R
SH_85	10	99656674	99656674	Missense_Mutation	SNV	C	T	T	CRTAC1	c.1208G>A	P.R403Q
SH_85	12	49165607	49165607	Silent	SNV	A	G	G	ADCY9A	c.2937T>C	P.A979A
SH_85	14	24706305	24706305	Missense_Mutation	SNV	T	C	C	GMPR2	c.494T>C	P.V165A
SH_85	14	47324319	47324322	Frame_Shift_Del	INDEL	TTGT	-	-	MDGA2	581_2584delAC	P.T861fs
SH_85	15	24921631	24921631	Missense_Mutation	SNV	G	C	C	NPAP1	c.617G>C	P.G206A
SH_85	15	41819471	41819471	Missense_Mutation	SNV	C	T	T	RPAP1	c.1640G>A	P.R547Q
SH_85	15	48722919	48722919	Missense_Mutation	SNV	A	G	G	FBN1	c.6820T>C	P.C2274R
SH_85	16	71022312	71022312	Missense_Mutation	SNV	G	A	A	HYDIN	c.3968C>T	P.S1323F
SH_85	17	29667567	29667567	Silent	SNV	G	A	A	NF1	c.6966G>A	P.V2322V
SH_85	17	7577121	7577121	Missense_Mutation	SNV	G	T	T	TP53	c.817C>A	P.R273S
SH_85	18	29340201	29340201	Nonsense_Mutation	SNV	G	A	A	SLC25A52	c.454C>T	P.Q152*
SH_85	19	14071278	14071278	Missense_Mutation	SNV	G	A	A	DCAF15	c.1633G>A	P.G545S
SH_85	19	18700265	18700265	Silent	SNV	C	T	T	C19orf60	c.225C>T	P.G755G
SH_85	19	47572471	47572471	Missense_Mutation	SNV	G	C	C	ZC3H4	c.2276C>G	P.P759R
SH_85	2	181925392	181925392	Missense_Mutation	SNV	G	A	A	UBE2E3	c.379G>A	P.V1127I
SH_85	2	239056572	239056572	Silent	SNV	G	C	C	KLHL30	c.1248G>C	P.S416S
SH_85	22	28397455	28397455	Silent	SNV	G	A	A	TTC28	c.4305C>T	P.A1435A
SH_85	3	188327596	188327596	Silent	SNV	T	C	C	LPP	c.1077T>C	P.P359P
SH_85	4	126239141	126239141	Silent	SNV	C	T	T	FAT4	c.1575C>T	P.I525I
SH_85	5	1221295	1221295	Missense_Mutation	SNV	G	A	A	SLC6A19	c.1568G>A	P.G523D
SH_85	5	433010	433010	Missense_Mutation	SNV	C	A	A	AHRR	c.1072C>A	P.L358M
SH_85	5	76249961	76249961	Missense_Mutation	SNV	A	G	G	CRHBP	c.283A>G	P.I95V
SH_85	6	165752824	165752824	Silent	SNV	T	C	C	PDE10A	c.2121A>G	P.G707G
SH_85	6	18171617	18171617	Silent	SNV	T	C	C	KDM1B	c.441T>C	P.C147C
SH_85	6	24278368	24278368	Silent	SNV	T	C	C	DCDC2	c.831A>G	P.K277K
SH_85	6	41655744	41655744	Missense_Mutation	SNV	A	G	G	TFEB	c.572T>C	P.L191P
SH_85	6	52617677	52617677	Missense_Mutation	SNV	T	C	C	GSTA2	c.389A>G	P.N130S
SH_85	7	73938437	73938437	Missense_Mutation	SNV	T	C	C	GTGF1RD1	c.1139T>C	P.I380T
SH_85	9	93375718	93375718	Missense_Mutation	SNV	A	G	G	DIRAS2	c.392T>C	P.V131A
SH_85	X	102586465	102586465	Frame_Shift_Del	INDEL	T	-	-	TCEAL7	c.134delIT	P.L45fs
SH_86	1	159912834	159912834	Missense_Mutation	SNV	C	T	T	IGSF9	c.166G>A	P.E56K
SH_86	1	16475486	16475486	Missense_Mutation	SNV	G	C	C	EPHA2	c.210C>G	P.C70W
SH_86	1	175334260	175334260	Missense_Mutation	SNV	T	A	A	TNR	c.1474A>T	P.T492S
SH_86	1	27276585	27276585	Frame_Shift_Ins	INDEL	-	C	C	KDF1	c.1171dupG	P.A391fs
SH_86	1	94370099	94370099	Missense_Mutation	SNV	T	C	C	GCLM	c.172A>G	P.I58V
SH_86	10	96602680	96602680	Missense_Mutation	SNV	G	A	A	CYP2C19	c.1048G>A	P.A350T
SH_86	16	29923194	29923194	Splice_Site	SNV	G	A	A	KCTD13	c.505-6C>T	
SH_86	16	88501585	88501585	Silent	SNV	C	T	T	ZNF469	c.7623C>T	P.H2541H
SH_86	2	179421718	179421718	Missense_Mutation	SNV	G	T	T	TTN	c.83240C>A	P.T27747N
SH_86	2	27522156	27522156	Missense_Mutation	SNV	C	T	T	TRIM54	c.385C>A	P.H129Y
SH_86	3	148559623	148559623	Missense_Mutation	SNV	G	A	A	CPB1	c.488G>A	P.G163E
SH_86	5	139244708	139244708	Missense_Mutation	SNV	T	C	C	NRG2	c.1163A>G	P.N388S
SH_86	5	161118994	161118994	Missense_Mutation	SNV	C	A	A	GABRA6	c.874C>A	P.H292N
SH_86	6	146480713	146480713	Silent	SNV	C	T	T	GRM1	c.930C>T	P.G310G
SH_86	6	30858846	30858861	Frame_Shift_Del	INDEL	GTCAATGAGC	-	-	DDR1	delCGGGTCATC	P.R172fs
SH_86	6	7413144	7413144	Missense_Mutation	SNV	G	A	A	RIOK1	c.1412G>A	P.G471E
SH_86	7	146536869	146536869	Missense_Mutation	SNV	G	A	A	CNTNAP2	c.275G>A	P.R92Q
SH_87	1	26671702	26671702	Missense_Mutation	SNV	C	G	G	AIM1L	c.1447G>C	P.G483R
SH_87	10	129868571	129868571	Missense_Mutation	SNV	T	A	A	PTPRE	c.1183T>A	P.V395N
SH_87	11	118392772	118392772	Missense_Mutation	SNV	G	T	T	KMT2A	c.11795G>T	P.R3932L
SH_87	11	1252747	1252747	Missense_Mutation	SNV	G	T	T	MUC5B	c.1635G>T	P.Q545H
SH_87	11	134237144	134237144	Splice_Site	SNV	T	C	C	GLB1L2	c.805-7T>C	
SH_87	11	407887	407887	Silent	SNV	C	T	T	SIGIRR	c.411G>A	P.L137L
SH_87	12	46245900	46245916	Frame_Shift_Del	INDEL	ATGGAGCAT	-	-	ARID2	2delGAATGGAG	P.N1333fs
SH_87	12	52822234	52822234	Silent	SNV	A	T	T	KRT75	c.1188T>A	P.A396A
SH_87	13	109704736	109704736	Missense_Mutation	SNV	C	G	G	MYO16	c.2961C>G	P.F987L
SH_87	15	64017691	64017691	Missense_Mutation	SNV	G	T	T	HERC1	c.3368C>A	P.P1123H
SH_87	15	76183325	76183325	Silent	SNV	C	G	G	UBE2Q2	c.951C>G	P.G317G
SH_87	16	30663177	30663177	Silent	SNV	G	A	A	PRR14	c.84G>A	P.R28R
SH_87	16	70883779	70883779	Silent	SNV	C	T	T	HYDIN	c.12723G>A	P.Q4241Q
SH_87	17	72301531	72301531	Silent	SNV	A	T	T	DNAI2	c.1161A>T	P.T387T
SH_87	17	7578226	7578226	Missense_Mutation	SNV	T	A	A	TP53	c.623A>T	P.D208V
SH_87	2	179419416	179419416	Missense_Mutation	SNV	A	T	T	TTN	c.83735T>A	P.L27912H
SH_87	2	217543719	217543719	Frame_Shift_Ins	INDEL	-	T	T	IGFBP5	c.420dupA	P.H141fs
SH_87	2	32602801	32602801	Missense_Mutation	SNV	G	T	T	BIRC6	c.471G>T	P.Q157H
SH_87	22	19839462	19839462	Missense_Mutation	SNV	T	C	C	C22orf29	c.323A>G	P.D108G
SH_87	3	9146461	9146461	Missense_Mutation	SNV	T	C	C	SRGAP3	c.326A>G	P.E109G
SH_87	4	3449285	3449285	Silent	SNV	G	T	T	HGFAC	c.1443G>T	P.T481T
SH_87	4	4204226	4204226	Missense_Mutation	SNV	T	A	A	OTOP1	c.679A>T	P.N227Y
SH_87	5	163276	163276	Missense_Mutation	SNV	T	A	A	PLEKHG4B	c.2021T>A	P.L674Q
SH_87	6	129835749	129835749	Splice_Site	SNV	T	C	C	LAMA2	c.9211+9T>C	
SH_87	7	138546006	138546006	Missense_Mutation	SNV	C	T	T	KIAA1549	c.5126G>A	P.G1709D
SH_87	7	37956008	37956008	Silent	SNV	G	A	A	SFRP4	c.132C>T	P.N44N
SH_87	8	145745694	145745694	Missense_Mutation	SNV	G	A	A	LRRC14	c.402G>A	P.M134I
SH_87	8	48880035	48880035	Silent	SNV	G	A	A	MCMA4	c.1164G>A	P.V388V
SH_87	9	135798860	135798862	Missense_Mutation	INDEL	ACA	-	-	TSC1	381_383delITG	P.V128del
SH_87	9	33794883	33794883	Splice_Site	SNV	C	G	G	PRSS3	c.82+12C>G	
SH_87	X	122336563	122336563	Missense_Mutation	SNV	A	C	C	GRIA3	c.344A>C	P.K115T
SH_87	X	152959638	152959638	Silent	SNV	C	T	T	SLC6A8	c.1278C>T	P.S426S
SH_88	1	43885836	43885836	Missense_Mutation	SNV	G	A	A	SZT2	c.1103G>A	P.R368H
SH_88	1	94930315	94930315	Splice_Site	INDEL	-	T	T	ABCD3	c.148-8dupT	
SH_88	11	64701305	64701305	Missense_Mutation	SNV	G	A	A	PPP2R5B	c.1483G>A	P.G495S
SH_88	11	82877707	82877707	Missense_Mutation	SNV	A	T	T	PCF11	c.1768A>T	P.S590C
SH_88	13	113770009	113770009	Missense_Mutation	SNV	G	A	A	F7	c.466G>A	P.G156S
SH_88	14	23540747	23540747	Missense_Mutation	SNV	G	A	A	ACIN1	c.5C>T	P.S2F
SH_88	17	45421670	45421670	Splice_Site	SNV	C	T	T	EFCAB13	c.434+12C>T	
SH_88	17	76456275	76456275	Missense_Mutation	SNV	G	T	T	DNAH17	c.9404C>A	P.A3135E
SH_88	18	30913366	30913366	Splice_Site	SNV	T	G	G	CCDC178	c.659-8A>C	
SH_88	19	57327976	57327976	Missense_Mutation	SNV	G	A	A	PEG3	c.1834C>T	P.P612S
SH_88	2	40656342	40656342	Frame_Shift_Ins	INDEL	-	T	T	SLC8A1	c.1078dupA	P.S360fs
SH_88	20	4776504	4776504	Missense_Mutation	SNV	A	G	G	RASSF2	c.244T>C	P.S82P

SH_88	21	31869297	31869297	Silent	SNV	G	A	A	KRTAP19-4	c.132C>T	P.N44N
SH_88	3	14206941	14206941	Missense_Mutation	SNV	T	C	C	XPC	c.766A>G	P.N256D
SH_88	4	74279300	74279300	Frame_Shift_Del	INDEL	G	-	-	ALB	c.1007delG	P.S336fs
SH_88	5	137756620	137756620	Missense_Mutation	SNV	C	T	T	KDM3B	c.3941C>T	P.P1314L
SH_88	6	116441262	116441262	Missense_Mutation	SNV	A	C	C	COL10A1	c.2017T>G	P.S673A
SH_88	6	44988339	44988339	Missense_Mutation	SNV	G	A	A	SUPT3H	c.217C>T	P.R73W
SH_88	6	75865411	75865411	Missense_Mutation	SNV	G	A	A	COL12A1	c.3410C>T	P.P1137L
SH_88	7	141722246	141722246	Splice_Site	INDEL	T	-	-	MGAM	c.882+9delT	
SH_88	8	27296873	27296873	Missense_Mutation	SNV	A	C	C	PTK2B	c.1792A>C	P.N598H
SH_88	9	5713917	5713917	Silent	SNV	G	A	A	RIC1	c.354G>A	P.G118G
SH_88	X	111020157	111020157	Missense_Mutation	SNV	C	T	T	TRPC5	c.2306G>A	P.S769N
SH_88	X	151138721	151138721	Missense_Mutation	SNV	T	G	G	GABRE	c.210A>C	P.E70D
SH_89	10	119805477	119805477	Missense_Mutation	SNV	G	C	C	RAB11FIP2	c.198C>G	P.F66L
SH_89	15	66729175	66729175	Missense_Mutation	SNV	G	A	A	MAP2K1	c.383G>A	P.G128D
SH_89	18	31323712	31323712	Silent	SNV	T	A	A	ASXL3	c.3900T>A	P.I1300I
SH_89	18	5145596	5145596	Missense_Mutation	SNV	C	T	T	AKAIN1	c.175G>A	P.V59I
SH_89	19	15754772	15754772	Missense_Mutation	SNV	C	T	T	CYP4F3	c.254C>T	P.P85L
SH_89	5	121759202	121759202	Missense_Mutation	SNV	A	G	G	SNCAIP	c.770A>G	P.D257G
SH_89	5	140031727	140031727	Silent	SNV	G	A	A	IK	c.231G>A	P.K77K
SH_90	1	109198321	109198321	Splice_Site	SNV	C	A	A	HENMT1	c.151-1G>T	
SH_90	1	109810543	109810543	Missense_Mutation	SNV	G	T	T	CELSR2	c.6179G>T	P.R2060L
SH_90	1	109953700	109953700	Missense_Mutation	SNV	C	T	T	PSMA5	c.320G>A	P.C107Y
SH_90	1	110085864	110085864	Nonsense_Mutation	SNV	C	T	T	GPR61	c.220C>T	P.R74*
SH_90	1	12907955	12907955	Missense_Mutation	SNV	G	T	T	HNRNPCL1	c.188C>A	P.A63D
SH_90	1	13839850	13839850	Missense_Mutation	SNV	C	A	A	LRRC38	c.239G>T	P.G80V
SH_90	1	144868013	144868013	Missense_Mutation	SNV	C	T	T	PDE4DIP	c.5108G>A	P.G1703D
SH_90	1	155796708	155796708	Missense_Mutation	SNV	G	C	C	GON4L	c.617C>G	P.S206C
SH_90	1	157068490	157068490	Splice_Site	SNV	G	T	T	ETV3L	c.486+8C>A	
SH_90	1	161277173	161277173	Missense_Mutation	SNV	C	G	G	MPZ	c.109G>C	P.E37Q
SH_90	1	163138132	163138132	Missense_Mutation	SNV	C	A	A	RG55	c.71G>T	P.G24V
SH_90	1	175046848	175046848	Missense_Mutation	SNV	C	A	A	TNN	c.294C>A	P.D98E
SH_90	1	179035966	179035966	Missense_Mutation	SNV	A	T	T	FAM20B	c.970A>T	P.I324F
SH_90	1	179562594	179562594	Splice_Site	SNV	G	T	T	TDRD5	c.233-1G>T	
SH_90	1	181688996	181688996	Missense_Mutation	SNV	C	T	T	CACNA1E	c.1748C>T	P.T583I
SH_90	1	182617404	182617404	Silent	SNV	C	T	T	RG58	c.228G>A	P.T76T
SH_90	1	190067439	190067439	Silent	SNV	G	A	A	BRINP3	c.1704C>T	P.G568G
SH_90	1	201838826	201838826	Missense_Mutation	SNV	G	T	T	IP09	c.2113G>T	P.D705Y
SH_90	1	22165342	22165342	Missense_Mutation	SNV	C	A	A	HSPG2	c.10129G>T	P.A3377S
SH_90	1	221912939	221912939	Missense_Mutation	SNV	C	A	A	DUSP10	c.148G>T	P.V50F
SH_90	1	228210370	228210370	Missense_Mutation	SNV	C	T	T	WNT3A	c.74C>T	P.S25L
SH_90	1	228482105	228482105	Missense_Mutation	SNV	T	A	A	OBSCN	c.11384T>A	P.L3795H
SH_90	1	231472123	231472123	Missense_Mutation	SNV	G	C	C	EXOC8	c.1369C>G	P.H457D
SH_90	1	232596667	232596667	Missense_Mutation	SNV	T	C	C	SIPA1L2	c.3061A>G	P.J1021V
SH_90	1	232650572	232650572	Nonsense_Mutation	SNV	C	A	A	SIPA1L2	c.514G>T	P.E172*
SH_90	1	237729945	237729945	Missense_Mutation	SNV	C	A	A	RYR2	c.3293C>A	P.A1098D
SH_90	1	240370867	240370867	Missense_Mutation	SNV	G	T	T	FMN2	c.2767G>T	P.G923C
SH_90	1	26316019	26316019	Missense_Mutation	SNV	C	A	A	PAFAH2	c.164G>T	P.R55L
SH_90	1	29639164	29639164	Missense_Mutation	SNV	G	T	T	PTPRU	c.3164G>T	P.R1055L
SH_90	1	40228862	40228862	Missense_Mutation	SNV	C	A	A	BMP8B	c.961G>T	P.A321S
SH_90	1	43022042	43022042	Missense_Mutation	SNV	G	T	T	CCDC30	c.641G>T	P.S214I
SH_90	1	45166656	45166656	Silent	SNV	G	A	A	C1orf228	c.504G>A	P.V168V
SH_90	1	897290	897290	Missense_Mutation	SNV	T	G	G	KLHL17	c.574T>G	P.S192A
SH_90	10	13152488	13152488	Splice_Site	SNV	G	T	T	OPTN	c.369+12G>T	
SH_90	10	32311157	32311160	Frame_Shift_Del	INDEL	TCAG	-	-	KIF5B	940_1943delCT	P.T647fs
SH_90	10	50339858	50339858	Missense_Mutation	SNV	C	A	A	FAM170B	c.652G>T	P.A218S
SH_90	10	61828560	61828560	Missense_Mutation	SNV	C	T	T	ANK3	c.12079G>A	P.D4027N
SH_90	11	102206691	102206691	Splice_Site	SNV	A	G	G	BIRC3	c.1325-6A>G	
SH_90	11	10477956	10477956	Splice_Site	SNV	G	T	T	AMPD3	c.16+7G>T	
SH_90	11	118359339	118359339	Missense_Mutation	SNV	G	T	T	KMT2A	c.4343G>T	P.C1448F
SH_90	11	123477491	123477491	Missense_Mutation	SNV	G	T	T	GRAMD1B	c.1090G>T	P.D364Y
SH_90	11	130275690	130275690	Missense_Mutation	SNV	G	T	T	ADAMT58	c.2433C>A	P.D811E
SH_90	11	16847695	16847695	Missense_Mutation	SNV	C	A	A	PLEKHA7	c.1315G>T	P.A439S
SH_90	11	17633783	17633783	Missense_Mutation	SNV	C	A	A	OTOG	c.6234C>A	P.H2078Q
SH_90	11	20658776	20658776	Missense_Mutation	SNV	G	A	A	SLC6A5	c.1094G>A	P.R365H
SH_90	11	46910976	46910976	Missense_Mutation	SNV	T	C	C	LRP4	c.2201A>G	P.H734R
SH_90	11	4976182	4976182	Silent	SNV	C	T	T	OR51A2	c.762G>A	P.L254L
SH_90	11	551827	551827	Missense_Mutation	SNV	G	T	T	LRRC56	c.973G>T	P.G325C
SH_90	11	55587398	55587398	Missense_Mutation	SNV	G	T	T	OR5D18	c.293G>T	P.C98F
SH_90	11	61563713	61563713	Missense_Mutation	SNV	G	A	A	FEN1	c.880G>A	P.V294M
SH_90	11	63683082	63683082	Missense_Mutation	SNV	G	C	C	RCOR2	c.129C>G	P.D43E
SH_90	11	66278161	66278161	Missense_Mutation	SNV	G	T	T	BBS1	c.31G>T	P.A11S
SH_90	11	71939475	71939475	Silent	SNV	G	C	C	INPPL1	c.330G>C	P.V110V
SH_90	11	7817647	7817647	Missense_Mutation	SNV	C	A	A	OR5P2	c.843G>T	P.L281F
SH_90	11	78602346	78602346	Missense_Mutation	SNV	T	G	G	TENM4	c.785A>C	P.Q262P
SH_90	11	87908378	87908378	Missense_Mutation	SNV	C	A	A	RAB38	c.175G>T	P.V59L
SH_90	12	104054121	104054121	Missense_Mutation	SNV	C	T	T	STAB2	c.1747C>T	P.L583F
SH_90	12	117768772	117768772	Silent	SNV	G	T	T	NOS1	c.103C>A	P.R35R
SH_90	12	118821811	118821811	Splice_Site	SNV	T	A	A	SUDS3	c.213-6T>A	
SH_90	12	2558139	2558139	Splice_Site	SNV	T	A	A	CACNA1C	c.478-3T>A	
SH_90	12	49167362	49167362	Silent	SNV	C	A	A	ADCY6	c.2511G>T	P.G837G
SH_90	12	52579220	52579220	Missense_Mutation	SNV	C	T	T	KRT80	c.452G>A	P.G151E
SH_90	12	52985302	52985302	Nonsense_Mutation	SNV	G	T	T	KRT72	c.909C>A	P.Y303*
SH_90	12	55688438	55688438	Silent	SNV	T	A	A	OR6C6	c.579A>T	P.L193L
SH_90	12	55820602	55820602	Missense_Mutation	SNV	A	T	T	OR6C7	c.565A>T	P.T189S
SH_90	12	66232350	66232350	Splice_Site	SNV	G	A	A	HMG2A	c.249+1G>A	
SH_90	12	6965218	6965218	Missense_Mutation	SNV	T	A	A	USP5	c.342T>A	P.F114L
SH_90	12	70929938	70929938	Missense_Mutation	SNV	C	T	T	PTPRB	c.5948G>A	P.G1983D
SH_90	12	9994993	9994993	Missense_Mutation	SNV	C	A	A	KLRF1	c.401C>A	P.T134K
SH_90	13	103391271	103391271	Missense_Mutation	SNV	C	A	A	CCDC168	c.11776G>T	P.A3926S
SH_90	13	20233359	20233359	Missense_Mutation	SNV	T	C	C	MPHOSPH8	c.1721T>C	P.V574A
SH_90	13	36367616	36367616	Missense_Mutation	SNV	C	A	A	DCLK1	c.1024G>T	P.D342Y
SH_90	13	38320109	38320109	Missense_Mutation	SNV	T	C	C	TRPC4	c.862A>G	P.R288G
SH_90	13	52325468	52325468	Missense_Mutation	SNV	T	G	G	WDFY2	c.748T>G	P.Y250D
SH_90	13	88329796	88329796	Missense_Mutation	SNV	G	A	A	SLITRK5	c.2153G>A	P.G718D
SH_90	14	105405796	105405796	Missense_Mutation	SNV	G	T	T	AHNAK2	c.15992C>A	P.S5331Y
SH_90	14	22102091	22102091	Missense_Mutation	SNV	G	T	T	OR10G2	c.908C>A	P.A303D
SH_90	14	24632636	24632636	Silent	SNV	G	T	T	IRF9	c.414G>T	P.V138V
SH_90	14	24649736	24649736	Missense_Mutation	SNV	T	G	G	IP04	c.3158A>C	P.K1053T

SH_90	14	80669199	80669199	Missense_Mutation	SNV	C	T	T	DIQ2	c.655G>A	P.A219T
SH_90	15	33928648	33928648	Missense_Mutation	SNV	G	T	T	RYR3	c.3453G>T	P.M1151I
SH_90	15	48441237	48441237	Missense_Mutation	SNV	C	G	G	MYEF2	c.1559G>C	P.S520T
SH_90	15	48888545	48888545	Missense_Mutation	SNV	C	A	A	FBN1	c.473G>T	P.G158V
SH_90	15	60639885	60639885	Missense_Mutation	SNV	C	A	A	ANXA2	c.964G>T	P.D322Y
SH_90	15	78836555	78836555	Missense_Mutation	SNV	G	T	T	PSMA4	c.233G>T	P.G78V
SH_90	15	83332351	83332351	Missense_Mutation	SNV	G	T	T	AP3B2	c.2305C>A	P.P769T
SH_90	15	91021124	91021124	Splice_Site	SNV	A	G	G	IQGAP1	c.3329+3A>G	
SH_90	16	1505182	1505182	Missense_Mutation	SNV	C	A	A	CLCN7	c.979G>T	P.D327Y
SH_90	16	3490822	3490822	Missense_Mutation	SNV	C	A	A	ZNF597	c.145G>T	P.D49Y
SH_90	16	4650138	4650138	Silent	SNV	G	T	T	C16orf96	c.3246G>T	P.S1082S
SH_90	16	47533729	47533729	Missense_Mutation	SNV	G	A	A	PHKB	c.229G>A	P.G77S
SH_90	16	70916555	70916555	Splice_Site	SNV	C	A	A	HYDIN	c.10215+8G>T	
SH_90	16	86601020	86601020	Missense_Mutation	SNV	G	T	T	FOXC2	c.79G>T	P.A27S
SH_90	17	39458727	39458727	Missense_Mutation	SNV	C	A	A	KRTAP29-1	c.377G>T	P.C126F
SH_90	17	39553443	39553443	Splice_Site	SNV	C	A	A	KRT31	c.348+1G>T	
SH_90	17	39646022	39646022	Missense_Mutation	SNV	C	A	A	KRT36	c.95G>T	P.R32L
SH_90	17	40257105	40257105	Silent	SNV	C	A	A	DXH58	c.1332G>T	P.G444G
SH_90	17	43923828	43923828	Missense_Mutation	SNV	G	T	T	SPPL2C	c.1556G>T	P.R519L
SH_90	17	46928502	46928502	Missense_Mutation	SNV	A	G	G	CALCO2	c.667A>G	P.K223E
SH_90	17	61498172	61498172	Missense_Mutation	SNV	C	T	T	TANC2	c.4829C>T	P.A1610V
SH_90	17	61557709	61557709	Missense_Mutation	SNV	A	G	G	ACE	c.667A>G	P.T232A
SH_90	17	66914585	66914585	Missense_Mutation	SNV	T	C	C	ABCA8	c.1891A>G	P.I631V
SH_90	17	71238441	71238441	Silent	SNV	T	A	A	C17orf80	c.1572T>A	P.L524L
SH_90	17	72538991	72538991	Splice_Site	SNV	G	T	T	CD300C	c.527+9C>A	
SH_90	17	7577534	7577534	Missense_Mutation	SNV	C	A	A	TP53	c.747G>T	P.R249S
SH_90	17	78268730	78268730	Missense_Mutation	SNV	T	A	A	RNF213	c.1683T>A	P.F561L
SH_90	18	24127375	24127375	Missense_Mutation	SNV	G	C	C	KCTD1	c.1126C>G	P.P376A
SH_90	18	7002376	7002376	Silent	SNV	G	T	T	LAMA1	c.4269C>A	P.G1423G
SH_90	18	72343937	72343937	Missense_Mutation	SNV	G	A	A	ZNF407	c.962G>A	P.R321Q
SH_90	19	12937655	12937655	Nonsense_Mutation	SNV	G	T	T	RTBDN	c.396C>A	P.C132*
SH_90	19	36370299	36370299	Missense_Mutation	SNV	G	T	T	APLP1	c.1912G>T	P.G638C
SH_90	19	5131936	5131936	Missense_Mutation	SNV	G	T	T	KDM4B	c.1824G>T	P.K608N
SH_90	19	57868600	57868600	Missense_Mutation	SNV	G	T	T	ZNF304	c.1504G>T	P.A502S
SH_90	19	9049310	9049310	Missense_Mutation	SNV	G	T	T	MUC16	c.32321C>A	P.A10774E
SH_90	2	120734565	120734565	Silent	SNV	A	G	G	PTPN4	c.2700A>G	P.Q900Q
SH_90	2	128322829	128322829	Missense_Mutation	SNV	G	A	A	MYO7B	c.154G>A	P.D52N
SH_90	2	160843807	160843807	Missense_Mutation	SNV	G	T	T	PLA2R1	c.1897C>A	P.P633N
SH_90	2	166211091	166211091	Silent	SNV	G	C	C	SCN2A	c.3309G>C	P.V1103V
SH_90	2	166848676	166848676	Missense_Mutation	SNV	G	C	C	SCN1A	c.5109C>G	P.D1703E
SH_90	2	170662182	170662240	Frame_Shift_Del	INDEL	TTGTGGAAG	-	-	SSB	TGTAATTGTGGA	P.R60fs
SH_90	2	171092540	171092540	Missense_Mutation	SNV	G	T	T	MYO3B	c.643G>T	P.A215S
SH_90	2	179436743	179436743	Missense_Mutation	SNV	G	A	A	TTN	c.69193C>T	P.P23065S
SH_90	2	18112837	18112837	Missense_Mutation	SNV	G	T	T	KCNS3	c.562G>T	P.A188S
SH_90	2	209308253	209308253	Missense_Mutation	SNV	A	C	C	PTH2R	c.357A>C	P.K119N
SH_90	2	220331955	220331955	Missense_Mutation	SNV	G	T	T	SPEG	c.2941G>T	P.A981S
SH_90	2	220371069	220371069	Missense_Mutation	SNV	A	T	T	GMPPA	c.1087A>T	P.N363Y
SH_90	2	220494354	220494354	Missense_Mutation	SNV	C	T	T	SLCA3	c.548C>T	P.A183V
SH_90	2	222298873	222298874	Frame_Shift_Del	INDEL	AC	-	-	EPHA4	2484_2485del	P.M828fs
SH_90	2	223160365	223160365	Silent	SNV	C	G	G	PAX3	c.333G>C	P.T111T
SH_90	2	232389978	232389978	Missense_Mutation	SNV	G	T	T	NMUR1	c.1057C>A	P.P353T
SH_90	2	234967610	234967610	Splice_Site	SNV	G	C	C	SPP2	c.333+8G>C	
SH_90	2	240036802	240036802	Nonsense_Mutation	SNV	C	A	A	HDAC4	c.1723G>T	P.E575*
SH_90	2	24524114	24524114	Splice_Site	SNV	A	C	C	ITSN2	c.996-6T>G	
SH_90	2	26677581	26677581	Nonsense_Mutation	SNV	G	A	A	DRC1	c.1986G>A	P.W662*
SH_90	2	37516651	37516651	Missense_Mutation	SNV	C	T	T	PRKD3	c.565G>A	P.G189R
SH_90	2	43015711	43015711	Silent	SNV	G	T	T	HAAO	c.117C>A	P.G39G
SH_90	2	55155791	55155791	Missense_Mutation	SNV	G	T	T	EML6	c.3907G>T	P.A1303S
SH_90	2	71304731	71304731	Missense_Mutation	SNV	G	T	T	NAGK	c.947G>T	P.G316V
SH_90	2	71375187	71375187	Frame_Shift_Del	INDEL	C	-	-	MPHOSPH10	c.1619delC	P.P540fs
SH_90	2	74783894	74783894	Missense_Mutation	SNV	G	T	T	DOK1	c.682G>T	P.G228C
SH_90	2	86297387	86297387	Silent	SNV	C	A	A	POLR1A	c.1620G>T	P.R540R
SH_90	2	96795692	96795692	Missense_Mutation	SNV	G	T	T	ASTL	c.745C>A	P.P249T
SH_90	20	30584986	30584986	Missense_Mutation	SNV	C	A	A	XKR7	c.1466C>A	P.A489E
SH_90	20	33501306	33501306	Splice_Site	SNV	G	T	T	ACSS2	c.570+7G>T	
SH_90	20	33711738	33711738	Nonsense_Mutation	SNV	G	A	A	EDEM2	c.958C>T	P.Q320*
SH_90	20	33868547	33868547	Missense_Mutation	SNV	C	A	A	EIF6	c.279G>T	P.Q93H
SH_90	20	35443597	35443597	Missense_Mutation	SNV	G	A	A	SOGA1	c.2248C>T	P.P750S
SH_90	20	40727180	40727180	Missense_Mutation	SNV	G	T	T	PTPRT	c.3784C>A	P.P1262T
SH_90	20	50140058	50140058	Missense_Mutation	SNV	G	A	A	NFATC2	c.662C>T	P.P221L
SH_90	20	57268916	57268916	Missense_Mutation	SNV	G	T	T	NPEPL1	c.190G>T	P.A64S
SH_90	20	57766452	57766452	Silent	SNV	G	T	T	ZNF831	c.378G>T	P.P126P
SH_90	20	61477089	61477089	Missense_Mutation	SNV	C	T	T	DPH3P1	c.74C>T	P.P25L
SH_90	20	62679615	62679615	Silent	SNV	G	T	T	SOX18	c.1059C>A	P.G353G
SH_90	21	31661769	31661769	Missense_Mutation	SNV	G	T	T	KRTAP25-1	c.40C>A	P.H14N
SH_90	21	31869280	31869280	Missense_Mutation	SNV	C	A	A	KRTAP19-4	c.149G>T	P.R50L
SH_90	21	33716979	33716979	Missense_Mutation	SNV	C	T	T	URB1	c.4157G>A	P.C1386Y
SH_90	21	47954002	47954002	Silent	SNV	A	G	G	DIP2A	c.1386A>G	P.T462T
SH_90	22	18379039	18379039	Missense_Mutation	SNV	G	C	C	MICAL3	c.1295C>G	P.T432R
SH_90	22	25425493	25425493	Silent	SNV	G	T	T	KIAA1671	c.1527G>T	P.A509A
SH_90	22	32200902	32200902	Splice_Site	SNV	G	A	A	DEPDC5	c.1217+1G>A	
SH_90	22	44602285	44602285	Silent	SNV	G	T	T	PARVG	c.975G>T	P.T325T
SH_90	3	113380252	113380252	Missense_Mutation	SNV	G	A	A	USF3	c.277C>T	P.R93W
SH_90	3	128853696	128853696	Missense_Mutation	SNV	C	G	G	ISY1	c.586G>C	P.P196Q
SH_90	3	13670711	13670711	Missense_Mutation	SNV	G	A	A	FBLN2	c.2761G>A	P.V921M
SH_90	3	138474692	138474692	Missense_Mutation	SNV	C	A	A	PIK3CB	c.301G>T	P.D101Y
SH_90	3	182615091	182615091	Missense_Mutation	SNV	A	G	G	ATP11B	c.3049A>G	P.M1017V
SH_90	3	184700404	184700404	Silent	SNV	C	T	T	VP58	c.3471C>T	P.S1157S
SH_90	3	194081566	194081566	Missense_Mutation	SNV	A	T	T	LRRC15	c.225T>A	P.N75K
SH_90	3	35750466	35750466	Missense_Mutation	SNV	C	G	G	ARPP21	c.801C>G	P.N267K
SH_90	4	113435851	113435851	Missense_Mutation	SNV	A	T	T	NEUROG2	c.781T>A	P.Y261N
SH_90	4	138452122	138452122	Missense_Mutation	SNV	G	A	A	PCDH18	c.1121C>T	P.P374L
SH_90	4	38022260	38022260	Missense_Mutation	SNV	G	A	A	TBC1D1	c.1021G>A	P.G341R
SH_90	4	78815299	78815299	Missense_Mutation	SNV	G	T	T	MRPL1	c.565G>T	P.D189Y
SH_90	4	78987134	78987134	Splice_Site	SNV	C	A	A	FRAS1	c.77-5C>A	
SH_90	4	8293228	8293228	Silent	SNV	G	A	A	HTRA3	c.840G>A	P.E280E
SH_90	4	8584268	8584268	Missense_Mutation	SNV	C	A	A	GPR78	c.679C>A	P.R227S
SH_90	4	89649749	89649749	Missense_Mutation	SNV	T	G	G	FAM13A	c.2029A>C	P.K677Q

SH_90	5	121758812	121758812	Missense_Mutation	SNV	G	A	A	SNCAIP	c.380G>A	P.G127D
SH_90	5	138456824	138456824	Silent	SNV	G	T	T	SIL1	c.144C>A	P.T48T
SH_90	5	140264201	140264201	Missense_Mutation	SNV	C	A	A	PCDHA13	c.2348C>A	P.A783E
SH_90	5	140625227	140625227	Silent	SNV	C	A	A	PCDHB15	c.81C>A	P.G27G
SH_90	5	140720777	140720777	Missense_Mutation	SNV	C	T	T	PCDHGA2	c.2239C>T	P.R747W
SH_90	5	146798103	146798103	Missense_Mutation	SNV	T	C	C	DPYSL3	c.562A>G	P.T188A
SH_90	5	160071232	160071232	Missense_Mutation	SNV	T	C	C	ATP10B	c.781A>G	P.R261G
SH_90	5	40853925	40853925	Nonsense_Mutation	SNV	G	T	T	CARD6	c.2491G>T	P.E831*
SH_90	5	55081594	55081594	Missense_Mutation	SNV	G	T	T	DDX4	c.657G>T	P.E219D
SH_90	5	64558701	64558701	Missense_Mutation	SNV	C	A	A	ADAMTS6	c.1709G>T	P.C570F
SH_90	6	106555106	106555106	Silent	SNV	G	T	T	PRDM1	c.2223G>T	P.R741R
SH_90	6	144508366	144508366	Missense_Mutation	SNV	G	T	T	STX11	c.602G>T	P.R201L
SH_90	6	149997839	149997839	Missense_Mutation	SNV	A	T	T	LATS1	c.2628T>A	P.S876R
SH_90	6	159618553	159618553	Missense_Mutation	SNV	G	T	T	FND1	c.200G>T	P.S67I
SH_90	6	168352294	168352294	Frame_Shift_Ins	INDEL	-	G	G	AFDN	c.4240dupG	P.E1414fs
SH_90	6	26022174	26022174	Missense_Mutation	SNV	G	T	T	HIST1H4A	c.268G>T	P.A90S
SH_90	6	26217347	26217347	Missense_Mutation	SNV	C	G	G	HIST1H2AE	c.145C>G	P.P49A
SH_90	6	28327532	28327532	Missense_Mutation	SNV	G	T	T	ZKSCAN3	c.169G>T	P.A57S
SH_90	6	29454993	29454993	Silent	SNV	C	A	A	MA51L	c.687G>T	P.G229G
SH_90	6	33635036	33635036	Missense_Mutation	SNV	G	C	C	ITPR3	c.1682G>C	P.R561P
SH_90	6	50683324	50683324	Missense_Mutation	SNV	C	G	G	TFAP2D	c.535C>G	P.Q179E
SH_90	6	71567899	71567899	Silent	SNV	G	T	T	SMAP1	c.1236G>T	P.P412P
SH_90	6	83767661	83767661	Missense_Mutation	SNV	G	A	A	UBE3D	c.62C>T	P.T21I
SH_90	6	86282021	86282031	Frame_Shift_Del	INDEL	TCGTTTACAT	-	-	SNX14	333delAATGTA	P.K108fs
SH_90	6	90581050	90581050	Silent	SNV	G	T	T	CASP8AP2	c.5835G>T	P.G1945G
SH_90	7	111368600	111368600	Silent	SNV	C	A	A	DOCK4	c.5631G>T	P.P1877P
SH_90	7	128454716	128454716	Silent	SNV	C	A	A	CCDC136	c.2788C>A	P.R930R
SH_90	7	138711555	138711555	Missense_Mutation	SNV	T	C	C	ZC3HAV1L	c.785A>G	P.H262R
SH_90	7	142658054	142658054	Missense_Mutation	SNV	G	T	T	KEL	c.361C>A	P.L121I
SH_90	7	149430774	149430774	Missense_Mutation	SNV	G	T	T	KRBA1	c.2830G>T	P.A944S
SH_90	7	149511875	149511875	Nonsense_Mutation	SNV	G	A	A	SSPO	c.10425G>A	P.W3475*
SH_90	7	150269312	150269312	Missense_Mutation	SNV	G	T	T	GIMAP4	c.154G>T	P.G52C
SH_90	7	150648887	150648887	Missense_Mutation	SNV	G	T	T	KCNH2	c.1594C>A	P.L532M
SH_90	7	21599350	21599350	Silent	SNV	T	C	C	DNAH11	c.822T>C	P.P274P
SH_90	7	21789410	21789410	Silent	SNV	C	T	T	DNAH11	c.8788C>T	P.L2930L
SH_90	7	32535362	32535362	Missense_Mutation	SNV	G	T	T	AVL9	c.41G>T	P.G14V
SH_90	7	47920360	47920360	Missense_Mutation	SNV	G	T	T	PKD1L1	c.3486C>A	P.S1162R
SH_90	7	47944053	47944053	Missense_Mutation	SNV	G	T	T	PKD1L1	c.1853C>A	P.618K
SH_90	7	6731631	6731631	Silent	SNV	C	G	G	ZNF12	c.828G>C	P.V276V
SH_90	7	82595337	82595337	Missense_Mutation	SNV	G	T	T	PCLO	c.3767C>A	P.A1256D
SH_90	8	10468264	10468264	Missense_Mutation	SNV	G	A	A	RP11	c.3344C>T	P.A1115V
SH_90	8	119936964	119936964	Silent	SNV	A	G	G	TNFRSF11B	c.855T>C	P.I285I
SH_90	8	135600604	135600604	Silent	SNV	C	A	A	ZFAT	c.2562G>T	P.G854G
SH_90	8	142488730	142488730	Missense_Mutation	SNV	A	G	G	MROH5	c.1231T>C	P.Y411H
SH_90	8	144942421	144942421	Missense_Mutation	SNV	C	T	T	EPPK1	c.5001G>A	P.M1667I
SH_90	8	56015729	56015729	Silent	SNV	C	A	A	XKR4	c.681C>A	P.A227A
SH_90	8	85441565	85441565	Silent	SNV	C	T	T	RALYL	c.48C>T	P.G166G
SH_90	8	87683304	87683304	Missense_Mutation	SNV	C	A	A	CNGB3	c.361G>T	P.A121S
SH_90	8	93029523	93029523	Missense_Mutation	SNV	G	A	A	RUNX1T1	c.157C>T	P.P53S
SH_90	8	97157059	97157059	Missense_Mutation	SNV	C	A	A	GDF6	c.1100G>T	P.G367V
SH_90	9	109701346	109701346	Missense_Mutation	SNV	T	G	G	ZNF462	c.6385T>G	P.S2129A
SH_90	9	109701347	109701347	Missense_Mutation	SNV	C	A	A	ZNF462	c.6386C>A	P.S2129Y
SH_90	9	127765388	127765388	Splice_Site	SNV	C	T	T	SCAI	c.1065+5G>A	
SH_90	9	130272502	130272502	Silent	SNV	G	T	T	FAM129B	c.1045C>A	P.R349R
SH_90	9	138439749	138439749	Missense_Mutation	SNV	C	T	T	OBP2A	c.176C>T	P.A59V
SH_90	9	138651570	138651577	Frame_Shift_Del	INDEL	CCTCCTGA	-	-	KCNT1	1_778delGACCT	P.258fs
SH_90	9	140919585	140919585	Missense_Mutation	SNV	A	G	G	CACNA1B	c.3247A>G	P.M1083V
SH_90	9	36882080	36882080	Silent	SNV	G	T	T	PAX5	c.933C>A	P.T311T
SH_90	9	71628567	71628567	Missense_Mutation	SNV	C	A	A	PRKACG	c.442G>T	P.A148S
SH_90	9	88650301	88650301	Nonsense_Mutation	SNV	G	A	A	GOLM1	c.997C>T	P.Q333*
SH_90	9	92220635	92220635	Missense_Mutation	SNV	G	T	T	GADD45G	c.209G>T	P.G70V
SH_90	X	106844339	106844339	Missense_Mutation	SNV	C	A	A	FRMPD3	c.3169C>A	P.H1057N
SH_90	X	110463640	110463640	Missense_Mutation	SNV	G	A	A	PAK3	c.1600G>A	P.A534T
SH_90	X	130220331	130220331	Missense_Mutation	SNV	C	T	T	ARHGAP36	c.1274C>T	P.A425V
SH_90	X	130408836	130408836	Missense_Mutation	SNV	G	T	T	IGSF1	c.3503C>A	P.P1168H
SH_90	X	24382330	24382330	Missense_Mutation	SNV	G	T	T	SUPT20H1	c.1453G>T	P.A485S
SH_90	X	3241813	3241813	Missense_Mutation	SNV	A	G	G	MXRA5	c.1913T>C	P.I638T
SH_90	X	51150018	51150018	Silent	SNV	C	T	T	Cxorf67	c.150C>T	P.S50S
SH_90	X	73961449	73961449	Silent	SNV	C	T	T	KIAA2022	c.2943G>A	P.G981G
SH_91	1	119466161	119466161	Silent	SNV	A	G	G	TBX15	c.441T>C	P.S147S
SH_91	1	204168364	204168364	Missense_Mutation	SNV	C	T	T	GOLT1A	c.319G>A	P.G107S
SH_91	1	3753967	3753967	Silent	SNV	A	G	G	CEP104	c.1008T>C	P.F336F
SH_91	11	6453208	6453208	Nonsense_Mutation	SNV	C	T	T	HPX	c.875G>A	P.W292*
SH_91	11	71259797	71259797	Missense_Mutation	SNV	G	A	A	KRTAP5-9	c.94G>A	P.G32S
SH_91	12	72388266	72388266	Missense_Mutation	SNV	C	T	T	TPH2	c.989C>T	P.P330L
SH_91	17	63193302	63193302	Missense_Mutation	SNV	A	G	G	RG59	c.910A>G	P.I304V
SH_91	19	54135383	54135383	Missense_Mutation	SNV	G	A	A	DPRX	c.23G>A	P.R8H
SH_91	19	58757694	58757694	Missense_Mutation	SNV	A	G	G	ZNF544	c.61A>G	P.M21V
SH_91	2	153435446	153435446	Missense_Mutation	SNV	G	T	T	FMNL2	c.750G>T	P.E250D
SH_91	2	209113113	209113113	Missense_Mutation	SNV	G	A	A	IDH1	c.394C>T	P.R132C
SH_91	X	106356707	106356707	Splice_Site	SNV	G	A	A	RBM41	n.672-9C>T	
SH_91	X	120182341	120182341	Missense_Mutation	SNV	G	A	A	GLUD2	c.803G>A	P.R268H
SH_94	1	152732155	152732155	Missense_Mutation	SNV	G	A	A	KPRP	c.91G>A	P.A31T
SH_94	1	156909500	156909500	Silent	SNV	C	A	A	ARHGEF11	c.3816G>T	P.G1272G
SH_94	1	158533025	158533025	Silent	SNV	G	A	A	OR6P1	c.370C>T	P.L124L
SH_94	1	20097963	20097963	Silent	SNV	T	A	A	TMCO4	c.192A>T	P.T64T
SH_94	1	222825366	222825366	Silent	SNV	A	C	C	MIA3	c.591A>C	P.S197S
SH_94	1	32936476	32936476	Missense_Mutation	SNV	A	T	T	ZBTB88	c.251A>T	P.Y84F
SH_94	1	39768645	39768645	Missense_Mutation	SNV	G	A	A	MACF1	c.2699G>A	P.R900Q
SH_94	1	72241959	72241959	Missense_Mutation	SNV	A	T	T	NEGR1	c.431T>A	P.L144N
SH_94	1	94654872	94654872	Silent	SNV	T	C	C	ARHGAP29	c.1476A>G	P.S492S
SH_94	10	135345210	135345210	Frame_Shift_Del	INDEL	C	-	-	CYP2E1	c.460delC	P.L154fs
SH_94	10	23319572	23319572	Missense_Mutation	SNV	A	T	T	ARMC3	c.2072A>T	P.E691V
SH_94	10	75434614	75434614	Missense_Mutation	SNV	T	A	A	AGAP5	c.1804A>T	P.T602S
SH_94	10	89690843	89690843	Nonsense_Mutation	SNV	A	T	T	PTEN	c.250A>T	P.R84*
SH_94	11	118959406	118959406	Missense_Mutation	SNV	A	C	C	HMBS	c.149A>C	P.Q50P
SH_94	11	62367715	62367715	Missense_Mutation	SNV	A	G	G	MTA2	c.113T>C	P.V38A
SH_94	11	94353020	94353020	Missense_Mutation	SNV	G	T	T	PIWIL4	c.2263G>T	P.V755F

SH_94	12	72956755	72956755	Silent	SNV	T	A	A	TRHDE	c.1842T>A	P.I614I
SH_94	12	99640197	99640197	Missense_Mutation	SNV	A	T	T	ANKS1B	c.2202T>A	P.S734R
SH_94	13	103392851	103392851	Missense_Mutation	SNV	T	G	G	CCDC168	c.10196A>C	P.Y3399S
SH_94	13	49039389	49039389	Frame_Shift_Del	INDEL	T	-	-	RB1	c.2376delT	P.P793fs
SH_94	15	45814375	45814375	Missense_Mutation	SNV	T	C	C	SLC30A4	c.178A>G	P.R60G
SH_94	15	49254658	49254658	Silent	SNV	C	A	A	SHC4	c.555G>T	P.L185L
SH_94	15	56132699	56132699	Silent	SNV	T	C	C	NEDD4	c.3234A>G	P.P1078P
SH_94	15	70961218	70961218	Missense_Mutation	SNV	C	T	T	UACA	c.1766G>A	P.R589G
SH_94	16	1449434	1449434	Silent	SNV	C	A	A	UNKL	c.675G>T	P.A225A
SH_94	16	2812720	2812720	Frame_Shift_Del	INDEL	A	-	-	SRRM2	c.2195delA	P.N732fs
SH_94	16	89967103	89967103	Silent	SNV	C	T	T	TCF25	c.1282C>T	P.L428L
SH_94	17	20135522	20135522	Missense_Mutation	SNV	G	A	A	SPECC1	c.2155G>A	P.E719K
SH_94	17	27903575	27903575	Missense_Mutation	SNV	T	C	C	GIT1	c.1372A>G	P.S458G
SH_94	17	33520403	33520403	Silent	SNV	A	T	T	SLC35G3	c.924T>C	P.S308S
SH_94	17	68171535	68171535	Missense_Mutation	SNV	G	A	A	KCNJ2	c.355G>A	P.G119S
SH_94	17	7578168	7578190	Frame_Shift_Del	INDEL	ACCTCAGGC	-	-	TP53	ATGAGCGCGCT	P.Y220fs
SH_94	18	19088328	19088328	Splice_Site	INDEL	-	T	T	GREB1L	c.4531-13dupT	
SH_94	19	19136593	19136593	Missense_Mutation	SNV	A	C	C	SUGP2	c.564T>G	P.S188R
SH_94	19	22498378	22498378	Missense_Mutation	SNV	C	G	G	ZNF729	c.2159C>G	P.A720G
SH_94	19	44237030	44237030	Silent	SNV	C	A	A	SMG9	c.1464G>T	P.T488T
SH_94	2	103335600	103335600	Missense_Mutation	SNV	C	T	T	MFS9	c.521G>A	P.R174Q
SH_94	2	15307245	15307247	Missense_Mutation	INDEL	AGA	-	-	NBAS	7041_7043delT	P.L2348del
SH_94	2	179638773	179638773	Missense_Mutation	SNV	C	A	A	TTN	c.7122G>T	P.Q2374H
SH_94	2	18745093	18745093	Missense_Mutation	SNV	G	T	T	NT5C1B	c.1802C>A	P.A601D
SH_94	2	80831222	80831222	Missense_Mutation	SNV	C	A	A	CTNNA2	c.2213C>A	P.T738K
SH_94	20	1532412	1532412	Missense_Mutation	SNV	A	T	T	SIRPD	c.346T>A	P.Y116N
SH_94	20	30418646	30418646	Missense_Mutation	SNV	A	C	C	MYLK2	c.1249A>C	P.T417P
SH_94	20	49552780	49552780	Missense_Mutation	SNV	G	T	T	DPM1	c.688C>A	P.L230I
SH_94	21	30909664	30909664	Missense_Mutation	SNV	G	T	T	GRIK1	c.2233C>A	P.L745M
SH_94	22	17128681	17128681	Splice_Site	SNV	T	A	A	TPTEP1	n.1126+6T>A	
SH_94	22	18185059	18185059	Missense_Mutation	SNV	A	T	T	BCL2L13	c.579A>T	P.R193S
SH_94	22	30682080	30682080	Missense_Mutation	SNV	T	A	A	GATS13	c.751A>T	P.S251C
SH_94	3	137483868	137483868	Missense_Mutation	SNV	G	T	T	SOX14	c.242G>T	P.R81L
SH_94	3	149459450	149459450	Missense_Mutation	SNV	T	A	A	COMMMD2	c.458A>T	P.H153L
SH_94	3	179050845	179050845	Nonsense_Mutation	SNV	A	T	T	ZNF639	c.238A>T	P.R80*
SH_94	3	196730771	196730771	Splice_Site	SNV	C	T	T	MELTF	c.2137+1G>A	
SH_94	3	2787274	2787274	Nonsense_Mutation	SNV	T	A	A	CNTN4	c.251T>A	P.L84*
SH_94	3	38781183	38781183	Splice_Site	SNV	G	A	A	SCN10A	c.2107-4C>T	
SH_94	3	45869950	45869950	Missense_Mutation	SNV	T	A	A	LZTF11	c.707A>T	P.Q236L
SH_94	3	48728864	48728864	Nonsense_Mutation	SNV	G	C	C	IP6K2	c.480C>G	P.Y160*
SH_94	3	54919573	54919573	Silent	SNV	G	T	T	CACNA2D3	c.2016G>T	P.A672A
SH_94	4	122825507	122825507	Silent	SNV	A	T	T	TRPC3	c.2223T>A	P.A741A
SH_94	4	40356119	40356119	Missense_Mutation	SNV	T	A	A	CHRNA9	c.1022T>A	P.I341N
SH_94	4	46930264	46930264	Missense_Mutation	SNV	T	G	G	GABRA4	c.1643A>C	P.E548A
SH_94	4	55964424	55964424	Missense_Mutation	SNV	G	T	T	KDR	c.2389C>A	P.L1797M
SH_94	4	74283828	74283828	Silent	SNV	A	G	G	ALB	c.1452A>G	P.L484L
SH_94	4	81967509	81967509	Missense_Mutation	SNV	G	T	T	BMP3	c.934G>T	P.D312Y
SH_94	5	137496591	137496591	Nonsense_Mutation	SNV	C	A	A	BRD8	c.2425G>T	P.E809*
SH_94	5	140480240	140480240	Missense_Mutation	SNV	G	T	T	PCDH83	c.7G>T	P.A35
SH_94	5	169693807	169693807	Splice_Site	SNV	C	A	A	LCP2	c.772+5G>T	
SH_94	5	169697839	169697839	Missense_Mutation	SNV	T	A	A	LCP2	c.407A>T	P.E136V
SH_94	5	38949465	38949465	Frame_Shift_Del	INDEL	G	-	-	RICTOR	c.4201delC	P.L1401fs
SH_94	5	70806005	70806005	Missense_Mutation	SNV	T	G	G	BDP1	c.3086T>G	P.I1029S
SH_94	5	74101066	74101066	Silent	SNV	G	T	T	FAM169A	c.714C>A	P.L238L
SH_94	6	43488766	43488766	Missense_Mutation	SNV	G	T	T	POLR1C	c.902G>T	P.R301L
SH_94	6	57498995	57498995	Missense_Mutation	SNV	A	T	T	PRIM2	c.1259A>T	P.Y420F
SH_94	7	126173556	126173556	Missense_Mutation	SNV	G	T	T	GRM8	c.1880C>A	P.T627K
SH_94	7	143097027	143097027	Silent	SNV	A	G	G	EPHA1	c.552T>C	P.A184A
SH_94	7	36336642	36336642	Silent	SNV	G	T	T	EEPDI	c.1356G>T	P.G452G
SH_94	7	63796736	63796736	Missense_Mutation	SNV	G	A	A	ZNF736	c.103G>A	P.E35K
SH_94	7	82451998	82451998	Silent	SNV	C	T	T	PCLO	c.14604G>A	P.Q4868Q
SH_94	7	99017783	99017783	Splice_Site	SNV	A	G	G	ATPS12-PTCD1	c.2068-11T>C	
SH_94	8	113516187	113516187	Missense_Mutation	SNV	A	T	T	CSMD3	c.4603T>A	P.Y1535N
SH_94	8	128752857	128752857	Missense_Mutation	SNV	G	C	C	MYC	c.1018G>C	P.V340L
SH_94	8	73993274	73993274	Missense_Mutation	SNV	T	A	A	SBSPPON	c.389A>T	P.Q130L
SH_94	9	107595019	107595019	Frame_Shift_Del	INDEL	A	-	-	ABCA1	c.1345delT	P.W449fs
SH_94	9	135777083	135777083	Nonsense_Mutation	SNV	T	A	A	TSC1	c.2395A>T	P.K799*
SH_94	9	14759790	14759790	Missense_Mutation	SNV	A	T	T	FREM1	c.922T>A	P.S308T
SH_94	9	16436624	16436624	Missense_Mutation	SNV	G	T	T	BNC2	c.1442C>A	P.A481E
SH_94	9	17786417	17786417	Nonsense_Mutation	SNV	A	T	T	SH3GL2	c.226A>T	P.K76*
SH_94	9	96054925	96054925	Missense_Mutation	SNV	G	T	T	WNK2	c.5289G>T	P.L1763F
SH_94	X	77284795	77284795	Missense_Mutation	SNV	T	A	A	ATP7A	c.2965T>A	P.F989I
SH_94	X	77284796	77284796	Missense_Mutation	SNV	T	G	G	ATP7A	c.2966T>G	P.F989C
SH_94	X	78618526	78618526	Silent	SNV	A	T	T	ITM2A	c.222T>A	P.R74R
SH_95	1	149783852	149783852	Silent	SNV	A	G	G	HIST2H2BF	c.27T>C	P.P9P
SH_95	1	159410218	159410218	Missense_Mutation	SNV	G	T	T	OR10J1	c.670G>T	P.V224F
SH_95	1	214814366	214814366	Silent	SNV	C	T	T	CENPF	c.2685C>T	P.H895H
SH_95	1	55224012	55224012	Missense_Mutation	SNV	G	A	A	PARS2	c.823C>T	P.R275C
SH_95	11	67789219	67789219	Splice_Site	SNV	C	T	T	ALDH3B1	c.478-4C>T	
SH_95	12	85264405	85264405	Silent	SNV	C	T	T	SLC6A15	c.1026G>A	P.A342A
SH_95	13	21557710	21557710	Missense_Mutation	SNV	T	A	A	LATS2	c.2135A>T	P.H712L
SH_95	15	58465397	58465397	Missense_Mutation	SNV	T	G	G	AQP9	c.369T>G	P.I123M
SH_95	15	83481947	83481947	Silent	SNV	G	A	A	WHAMM	c.702G>A	P.V234V
SH_95	17	11659887	11659887	Splice_Site	SNV	G	T	T	DNAH9	c.6741G>T	P.V2247V
SH_95	17	18233896	18233896	Missense_Mutation	SNV	T	C	C	SHMT1	c.730A>G	P.I244V
SH_95	17	5072078	5072078	Missense_Mutation	SNV	G	A	A	USP6	c.3245G>A	P.R1082Q
SH_95	17	61902624	61902633	Frame_Shift_Del	INDEL	TGCAGATTC	-	-	FTSJ3	573delTGAATC	P.H188fs
SH_95	17	7576927	7576927	Splice_Site	SNV	C	A	A	TP53	c.920-1G>T	
SH_95	17	7578419	7578419	Nonsense_Mutation	SNV	C	A	A	TP53	c.511G>T	P.E171*
SH_95	19	42854300	42854300	Missense_Mutation	SNV	G	A	A	MEGF8	c.2500G>A	P.E834K
SH_95	19	43373002	43373002	Silent	SNV	G	T	T	PSG1	c.894C>A	P.P298P
SH_95	19	436191	436191	Silent	SNV	C	A	A	SHC2	c.927G>T	P.P309P
SH_95	19	43773563	43773563	Silent	SNV	A	G	G	PSG9	c.21T>C	P.P7P
SH_95	2	20990038	20990038	Missense_Mutation	SNV	T	A	A	LDAH	c.275A>T	P.Q92M
SH_95	2	99232702	99232702	Missense_Mutation	SNV	A	G	G	UNC50	c.434A>G	P.Q145R
SH_95	20	20071526	20071526	Missense_Mutation	SNV	G	T	T	CFAP61	c.605G>T	P.R202L
SH_95	20	23016479	23016479	Missense_Mutation	SNV	G	T	T	SSTR4	c.359G>T	P.R120L
SH_95	20	23584331	23584331	Missense_Mutation	SNV	C	T	T	CST9	c.296G>A	P.R99H

SH_95	3	112648154	112648154	Missense_Mutation	SNV	C	A	A	CD200R1	c.403G>T	P.D135Y
SH_95	3	142119349	142119349	Missense_Mutation	SNV	A	T	T	XRN1	c.2144T>A	P.V715D
SH_95	3	158317966	158317966	Splice_Site	SNV	A	T	T	MLF1	c.493+4A>T	
SH_95	3	36931370	36931370	Missense_Mutation	SNV	C	T	T	TRANK1	c.857G>A	P.C286Y
SH_95	3	39436033	39436033	Missense_Mutation	SNV	A	T	T	SLC25A38	c.758A>T	P.Q253L
SH_95	3	71101704	71101704	Missense_Mutation	SNV	C	A	A	FOXP1	c.494G>T	P.G165V
SH_95	5	140209436	140209436	Missense_Mutation	SNV	C	T	T	PCDHA6	c.1760C>T	P.A587V
SH_95	5	90079728	90079728	Missense_Mutation	SNV	A	G	G	ADGRV1	c.13507A>G	P.S4503G
SH_95	6	159653744	159653744	Missense_Mutation	SNV	C	T	T	FNDC1	c.2200C>T	P.P734S
SH_95	6	53761699	53761699	Splice_Site	SNV	G	T	T	LRRC1	c.567+9G>T	
SH_95	6	78172786	78172786	Missense_Mutation	SNV	G	A	A	HTR1B	c.335C>T	P.T112I
SH_95	7	151945330	151945330	Missense_Mutation	SNV	G	T	T	KMT2C	c.2189C>A	P.S730Y
SH_95	7	91503086	91503086	Missense_Mutation	SNV	C	T	T	MTERF1	c.962G>A	P.S321N
SH_95	8	11189000	11189000	Frame_Shift_Del	INDEL	A	-	-	SLC35G5	c.386delA	P.N129fs
SH_95	8	120431397	120431397	Missense_Mutation	SNV	G	A	A	NOV	c.589G>A	P.V197I
SH_95	8	144896218	144896218	Missense_Mutation	SNV	T	A	A	SCRIB	c.230A>T	P.E77V
SH_95	8	73117533	73117533	Splice_Site	SNV	C	G	G	LOC392232	n.2513+1G>C	
SH_95	9	19276317	19276317	Missense_Mutation	SNV	A	G	G	DENND4C	c.145A>G	P.I49V
SH_95	X	49033526	49033526	Silent	SNV	G	A	A	PRICKLE3	c.777C>T	P.Y259Y
SH_98	1	145650534	145650534	Silent	SNV	T	C	C	RNF115	c.213T>C	P.F71F
SH_98	1	171752872	171752872	Splice_Site	SNV	T	G	G	METTL13	c.154-8T>G	
SH_98	10	105889958	105889958	Missense_Mutation	SNV	A	G	G	CFAP43	c.4937T>C	P.I1646T
SH_98	10	128147638	128147638	Missense_Mutation	SNV	T	C	C	C10orf90	c.1868A>G	P.K623R
SH_98	12	11174371	11174371	Missense_Mutation	SNV	A	G	G	TAS2R19	c.800T>C	P.V267A
SH_98	12	126068387	126068387	Splice_Site	SNV	T	C	C	TMEM132B	c.1279-10T>C	
SH_98	13	20637113	20637113	Splice_Site	SNV	T	C	C	ZMYM2	c.3037+2T>C	
SH_98	15	81221384	81221384	Silent	SNV	C	T	T	CEMIP	c.2481C>T	P.D827D
SH_98	16	19083402	19083402	Silent	SNV	C	A	A	COQ7	c.112C>A	P.R38R
SH_98	16	30745237	30745237	Nonsense_Mutation	SNV	G	T	T	SRCAP	c.6517G>T	P.E2173*
SH_98	17	26686410	26686410	Missense_Mutation	SNV	C	T	T	TMEM199	c.358C>T	P.R120C
SH_98	17	26902473	26902473	Silent	SNV	C	T	T	ALDOC	c.78G>A	P.P26P
SH_98	17	33690347	33690347	Silent	SNV	G	A	A	SLFN11	c.480C>T	P.I160I
SH_98	17	35549227	35549227	Missense_Mutation	SNV	T	C	C	ACACA	c.4220A>G	P.Y1407C
SH_98	17	36625495	36625495	Missense_Mutation	SNV	C	A	A	ARHGAP23	c.1759C>A	P.P587T
SH_98	17	39274122	39274122	Missense_Mutation	SNV	C	G	G	KRTAP4-11	c.446G>C	P.C149S
SH_98	17	66246484	66246484	Silent	SNV	C	T	T	AMZ2	c.156C>T	P.T52T
SH_98	17	79478964	79478964	Frame_Shift_Del	INDEL	G	-	-	ACTG1	c.328delC	P.L110fs
SH_98	3	112648004	112648004	Missense_Mutation	SNV	A	T	T	CD200R1	c.553T>A	P.S185T
SH_98	5	130517915	130517915	Splice_Site	SNV	T	A	A	LYRM7	c.92-7T>A	
SH_98	5	140762685	140762685	Missense_Mutation	SNV	G	T	T	PCDHGA7	c.219G>T	P.Q73H
SH_98	6	32411602	32411602	Missense_Mutation	SNV	G	C	C	HLA-DRA	c.680G>C	P.G227A
SH_98	7	158705673	158705673	Splice_Site	SNV	A	G	G	WDR60	c.1591-3A>G	
SH_98	7	47344561	47344561	Silent	SNV	C	A	A	TNS3	c.2691G>T	P.G897G
SH_98	7	90225967	90225967	Missense_Mutation	SNV	C	A	A	CDK14	c.26C>A	P.P9Q
SH_98	8	101721692	101721692	Missense_Mutation	SNV	G	A	A	PABPC1	c.1240C>T	P.P414S
SH_98	8	17089978	17089978	Silent	SNV	A	C	C	CNOT7	c.687T>G	P.S229S
SH_98	8	95508590	95508590	Missense_Mutation	SNV	T	C	C	KIAA1429	c.4349A>G	P.E1450G
SH_98	9	107367427	107367427	Missense_Mutation	SNV	A	C	C	OR13C2	c.482T>G	P.V161G
SH_98	X	117677486	117677486	Missense_Mutation	SNV	T	C	C	DOCK11	c.322T>C	P.Y108H
SH_98	X	5810898	5810898	Missense_Mutation	SNV	C	G	G	NLGN4X	c.2411G>C	P.S804T
SH_99	1	117509574	117509574	Missense_Mutation	SNV	T	C	C	PTGFRN	c.1681T>C	P.F561L
SH_99	1	149291202	149291202	Splice_Site	SNV	A	T	T	FAM231D	n.1447-2A>T	
SH_99	1	151263518	151263518	Missense_Mutation	SNV	A	T	T	ZNF687	c.3547A>T	P.R1183W
SH_99	1	159828021	159828021	Missense_Mutation	SNV	C	T	T	VSIG8	c.289G>A	P.V97I
SH_99	1	166927098	166927098	Missense_Mutation	SNV	C	T	T	ILDR2	c.287G>A	P.S96N
SH_99	1	183109595	183109595	Silent	SNV	T	A	A	LAMC1	c.4530T>A	P.V1510V
SH_99	1	203466135	203466135	Missense_Mutation	SNV	A	T	T	OPTC	c.262A>T	P.S88C
SH_99	1	206648264	206648264	Silent	SNV	G	T	T	IKBKE	c.285G>T	P.L95L
SH_99	1	22150826	22150826	Missense_Mutation	SNV	C	T	T	HSPG2	c.12791G>A	P.G4264E
SH_99	1	22927164	22927164	Missense_Mutation	SNV	T	A	A	EPHA8	c.2399T>A	P.I800N
SH_99	1	229568405	229568405	Missense_Mutation	SNV	G	T	T	ACTA1	c.352C>A	P.R118S
SH_99	1	245862253	245862253	Missense_Mutation	SNV	T	A	A	KIF26B	c.6092T>A	P.V2031D
SH_99	1	245927411	245927411	Missense_Mutation	SNV	C	T	T	SMYD3	c.1117G>A	P.V373M
SH_99	1	247319994	247319994	Missense_Mutation	SNV	C	G	G	ZNF124	c.744G>C	P.R248S
SH_99	1	248004936	248004936	Missense_Mutation	SNV	C	A	A	OR11L1	c.263G>T	P.W88L
SH_99	1	248309355	248309355	Missense_Mutation	SNV	G	T	T	OR2M5	c.906G>T	P.R302S
SH_99	1	40097227	40097227	Missense_Mutation	SNV	G	A	A	HEYL	c.172C>T	P.S58C
SH_99	1	43649426	43649426	Silent	SNV	T	A	A	CFAP57	c.639T>A	P.V213V
SH_99	1	52924039	52924039	Missense_Mutation	SNV	C	G	G	ZCCHC11	c.3404G>C	P.R1135T
SH_99	1	72241850	72241850	Splice_Site	SNV	T	A	A	NEGR1	c.535+5A>T	
SH_99	10	115973299	115973299	Missense_Mutation	SNV	G	A	A	TDRD1	c.2026G>A	P.E676K
SH_99	10	115987852	115987852	Missense_Mutation	SNV	A	T	T	TDRD1	c.3506A>T	P.N1169I
SH_99	10	119100618	119100618	Splice_Site	SNV	C	A	A	PDZD8	c.873-5G>T	
SH_99	10	12123583	12123583	Silent	SNV	C	T	T	DHTKD1	c.267C>T	P.I89I
SH_99	10	134162503	134162503	Silent	SNV	A	T	T	LRRC27	c.963A>T	P.L321L
SH_99	10	22676827	22676827	Missense_Mutation	SNV	A	C	C	SPAG6	c.679A>C	P.I227L
SH_99	10	29762890	29762890	Silent	SNV	C	G	G	SVIL	c.4476G>C	P.S1492S
SH_99	10	63976895	63976895	Missense_Mutation	SNV	C	A	A	RTKN2	c.1002G>T	P.L1334F
SH_99	10	70723092	70723092	Missense_Mutation	SNV	A	G	G	DDX21	c.449A>G	P.H150R
SH_99	11	105929699	105929699	Silent	SNV	T	C	C	KBTBD3	c.126A>G	P.L42L
SH_99	11	14856619	14856619	Silent	SNV	T	C	C	PDE3B	c.2298T>C	P.G766G
SH_99	11	18723250	18723250	Silent	SNV	C	T	T	TMEM86A	c.417C>T	P.L139L
SH_99	11	20122660	20122660	Missense_Mutation	SNV	G	A	A	NAV2	c.6167G>A	P.G2056E
SH_99	11	27114793	27114793	Missense_Mutation	SNV	A	T	T	BBOX1	c.413A>T	P.Y138F
SH_99	11	27406880	27406880	Silent	SNV	T	A	A	LGR4	c.537A>T	P.L179L
SH_99	11	48327792	48327792	Silent	SNV	T	C	C	OR4S1	c.18T>C	P.N6N
SH_99	11	57102046	57102046	Missense_Mutation	SNV	T	C	C	SSRP1	c.131A>G	P.Q44R
SH_99	11	5799397	5799397	Silent	SNV	G	A	A	OR52N5	c.468C>T	P.A156A
SH_99	11	61630785	61630785	Missense_Mutation	SNV	A	T	T	FADS2	c.946A>T	P.T316S
SH_99	11	62298592	62298592	Silent	SNV	T	G	G	AHNAK	c.3297A>C	P.P1099P
SH_99	11	63665721	63665721	Silent	SNV	A	G	G	MARK2	c.306A>G	P.R102R
SH_99	11	6964436	6964436	Silent	SNV	A	T	T	ZNF215	c.606A>T	P.S202S
SH_99	11	73074427	73074427	Missense_Mutation	SNV	A	T	T	ARHGEF17	c.5173A>T	P.S1725C
SH_99	11	8646530	8646530	Silent	SNV	C	A	A	TRIM66	c.2121G>T	P.V707V
SH_99	11	93435990	93435990	Missense_Mutation	SNV	T	C	C	CEP295	c.5501T>C	P.V1834A
SH_99	12	100441357	100441357	Frame_Shift_Del	INDEL	A	-	-	UHRF1BP1L	c.4032delT	P.I1344fs
SH_99	12	109998867	109998867	Missense_Mutation	SNV	C	A	A	MMAB	c.562G>T	P.V188L
SH_99	12	112888278	112888278	Silent	SNV	T	G	G	PTPN11	c.294T>G	P.L98L

SH_99	12	124298384	124298384	Missense_Mutation	SNV	T	A	A	DNAH10	c.3351T>A	P.S1117R
SH_99	12	124352133	124352133	Silent	SNV	G	A	A	DNAH10	c.6933G>A	P.Q2311Q
SH_99	12	132426326	132426326	Missense_Mutation	SNV	A	T	T	PUS1	c.950A>T	P.Q317L
SH_99	12	15800073	15800073	Missense_Mutation	SNV	C	T	T	EPS8	c.1556G>A	P.R519H
SH_99	12	43821205	43821205	Missense_Mutation	SNV	C	T	T	ADAMTS20	c.4013G>A	P.S1338N
SH_99	12	53073903	53073903	Missense_Mutation	SNV	G	T	T	KRT7	c.230C>A	P.S77Y
SH_99	12	56619414	56619414	Silent	SNV	T	C	C	NABP2	c.225T>C	P.A75A
SH_99	12	64472797	64472797	Silent	SNV	A	T	T	SRGAP1	c.1224A>T	P.T408T
SH_99	12	6710638	6710638	Missense_Mutation	SNV	C	A	A	CHD4	c.616G>T	P.G206C
SH_99	12	72343413	72343413	Missense_Mutation	SNV	G	T	T	TPH2	c.586G>T	P.D196Y
SH_99	12	85449971	85449971	Missense_Mutation	SNV	A	G	G	LRRIQ1	c.1400A>G	P.E467G
SH_99	13	66879141	66879141	Silent	SNV	T	A	A	PCDH9	c.3234A>T	P.R1078R
SH_99	15	29428579	29428579	Missense_Mutation	SNV	G	C	C	FAM189A1	c.917C>G	P.P306R
SH_99	15	45983167	45983167	Splice_Site	SNV	A	T	T	SQRDL	c.1296-4A>T	
SH_99	15	50494759	50494759	Missense_Mutation	SNV	A	T	T	SLC27A2	c.764A>T	P.K255M
SH_99	15	70960775	70960775	Frame_Shift_Del	INDEL	T	-	-	UACA	c.2209delA	P.S737fs
SH_99	15	74240248	74240248	Splice_Site	SNV	G	A	A	LOXL1	c.1602+5G>A	
SH_99	15	92988061	92988061	Silent	SNV	C	A	A	STR5IA2	c.744C>A	P.G248G
SH_99	16	11862261	11862261	Missense_Mutation	SNV	T	A	A	ZC3H7A	c.1270A>T	P.T424S
SH_99	16	23116833	23116833	Frame_Shift_Del	INDEL	C	-	-	USP31	c.1018delG	P.V340fs
SH_99	16	23390074	23390074	Silent	SNV	T	C	C	SCNN1B	c.1452T>C	P.N484N
SH_99	16	23392021	23392021	Nonsense_Mutation	SNV	C	T	T	SCNN1B	c.1822C>T	P.Q608*
SH_99	16	29874177	29874177	Nonsense_Mutation	SNV	A	T	T	CDIPT	c.2T>A	P.M1?
SH_99	16	60392721	60392721	Missense_Mutation	SNV	C	T	T	LOC729159	c.886G>A	P.E296K
SH_99	16	65032724	65032724	Silent	SNV	A	G	G	CDH11	c.264T>C	P.I88I
SH_99	17	35641738	35641738	Splice_Site	INDEL	C	-	-	ACACA	c.471+1delG	
SH_99	17	37234265	37234265	Missense_Mutation	SNV	C	G	G	PLXDC1	c.1087G>C	P.D363H
SH_99	17	42745523	42745523	Missense_Mutation	SNV	T	A	A	MEIOC	c.2244T>A	P.S748R
SH_99	17	43906946	43906946	Missense_Mutation	SNV	G	C	C	CHRR1	c.454G>C	P.G152R
SH_99	17	44109017	44109017	Missense_Mutation	SNV	G	T	T	KANSL1	c.3140C>A	P.A1047E
SH_99	17	56277584	56277584	Splice_Site	SNV	A	G	G	EPX	c.1538-2A>G	
SH_99	17	58136784	58136784	Splice_Site	SNV	T	C	C	HEATR6	c.1722A>G	P.K574K
SH_99	17	7577120	7577120	Missense_Mutation	SNV	C	T	T	TP53	c.818G>A	P.R273H
SH_99	17	7684027	7684027	Missense_Mutation	SNV	T	A	A	DNAH2	c.5930T>A	P.L1977Q
SH_99	17	79916821	79916821	Missense_Mutation	SNV	C	T	T	NOTUM	c.523G>A	P.A175T
SH_99	18	14791470	14791470	Missense_Mutation	SNV	C	G	G	ANKRD30B	c.1805C>G	P.T602S
SH_99	18	18690847	18690847	Missense_Mutation	SNV	T	C	C	ROCK1	c.25A>G	P.T9A
SH_99	18	22806182	22806182	Missense_Mutation	SNV	T	C	C	ZNF521	c.1040A>G	P.N347S
SH_99	18	23658119	23658119	Missense_Mutation	SNV	T	A	A	SS18	c.152A>T	P.Q51L
SH_99	18	2705796	2705796	Silent	SNV	A	G	G	SMCHD1	c.1947A>G	P.Q649Q
SH_99	18	5291250	5291250	Missense_Mutation	SNV	G	C	C	ZBTB14	c.957C>G	P.H319Q
SH_99	18	54362409	54362409	Missense_Mutation	SNV	G	C	C	WDR7	c.1337G>C	P.G446A
SH_99	19	10428248	10428248	Missense_Mutation	SNV	A	T	T	RAVER1	c.2153T>A	P.F718Y
SH_99	19	12163615	12163615	Nonsense_Mutation	SNV	A	T	T	ZNF878	c.2T>A	P.M1?
SH_99	19	15569464	15569464	Missense_Mutation	SNV	G	A	A	RASAL3	c.665C>T	P.P222L
SH_99	19	18901419	18901419	Missense_Mutation	SNV	T	A	A	COMP	c.169A>T	P.R57W
SH_99	19	21991512	21991512	Nonsense_Mutation	SNV	T	A	A	ZNF43	c.1309A>T	P.K437*
SH_99	19	22498424	22498424	Silent	SNV	T	A	A	ZNF729	c.2205T>A	P.T735T
SH_99	19	33321530	33321530	Missense_Mutation	SNV	T	A	A	SLC7A9	c.1460A>T	P.E487V
SH_99	19	37734526	37734526	Missense_Mutation	SNV	C	T	T	ZNF383	c.1388C>T	P.S463L
SH_99	19	38385310	38385310	Missense_Mutation	SNV	T	A	A	WDR87	c.1033A>T	P.S345C
SH_99	19	39056410	39056410	Missense_Mutation	SNV	G	A	A	RYR1	c.13436G>A	P.G4479E
SH_99	19	39409078	39409078	Silent	SNV	C	T	T	SARS2	c.906G>A	P.A302A
SH_99	19	49551638	49551638	Splice_Site	SNV	A	T	T	CGB8	c.16-9T>A	
SH_99	19	49573943	49573943	Missense_Mutation	SNV	T	A	A	KCNA7	c.748A>T	P.I250F
SH_99	19	50949187	50949187	Missense_Mutation	SNV	A	T	T	MYBPC2	c.1184A>T	P.Y395F
SH_99	19	55872239	55872239	Missense_Mutation	SNV	T	A	A	FAM71E2	c.793A>T	P.T265S
SH_99	19	58453032	58453032	Missense_Mutation	SNV	T	A	A	ZNF256	c.1144A>T	P.S382C
SH_99	19	5915128	5915128	Missense_Mutation	SNV	A	C	C	CAPS	c.697A>C	P.N233H
SH_99	19	6586369	6586369	Missense_Mutation	SNV	C	T	T	CD70	c.244G>A	P.G82S
SH_99	19	7755298	7755298	Silent	SNV	C	T	T	FCER2	c.612G>A	P.E204E
SH_99	2	137928508	137928508	Missense_Mutation	SNV	G	A	A	THSD7B	c.1723G>A	P.G575R
SH_99	2	162696317	162696317	Missense_Mutation	SNV	T	C	C	SLC4A10	c.296T>C	P.V99A
SH_99	2	175337958	175337958	Missense_Mutation	SNV	C	A	A	GPR155	c.595G>T	P.A199S
SH_99	2	198367935	198367935	Missense_Mutation	SNV	T	G	G	HSPE1	c.261T>G	P.D87E
SH_99	2	210843267	210843267	Missense_Mutation	SNV	A	G	G	UNC80	c.8755A>G	P.T2919A
SH_99	2	242195596	242195596	Splice_Site	INDEL	-	AG	AG	HDLBP1	c.981+2_981+3insCT	
SH_99	20	23016847	23016847	Missense_Mutation	SNV	C	A	A	SSTR4	c.727C>A	P.L243M
SH_99	20	30436225	30436225	Silent	SNV	G	A	A	DUSP15	c.870C>T	P.S290S
SH_99	20	34241735	34241735	Missense_Mutation	SNV	G	A	A	RBM12	c.1510C>T	P.P504S
SH_99	20	43600795	43600795	Nonsense_Mutation	SNV	G	T	T	STK4	c.112G>T	P.E38*
SH_99	21	28211978	28211978	Silent	SNV	G	T	T	ADAMTS1	c.1956C>A	P.V652V
SH_99	22	19808743	19808743	Splice_Site	SNV	C	A	A	GNB1L	c.128+8G>T	
SH_99	22	29966476	29966476	Frame_Shift_Del	INDEL	A	-	-	NIPSNAP1	c.84delT	P.F28fs
SH_99	22	38039793	38039793	Missense_Mutation	SNV	A	G	G	SH3BP1	c.616A>G	P.R206G
SH_99	22	42180353	42180353	Missense_Mutation	SNV	C	T	T	MEI1	c.3098C>T	P.T1033I
SH_99	22	51048663	51048663	Missense_Mutation	SNV	A	C	C	MAPK8IP2	c.2324A>C	P.H775P
SH_99	3	113179525	113179525	Missense_Mutation	SNV	G	C	C	SPICE1	c.1374C>G	P.N458K
SH_99	3	132180013	132180013	Silent	SNV	A	G	G	DNAJC13	c.1677A>G	P.V559V
SH_99	3	184003327	184003327	Missense_Mutation	SNV	C	T	T	ECE2	c.1123C>T	P.R375C
SH_99	3	190158052	190158052	Silent	SNV	T	A	A	TMEM207	c.285A>T	P.G95G
SH_99	3	3139934	3139934	Silent	SNV	T	G	G	IL5RA	c.408A>C	P.T136T
SH_99	3	48510523	48510523	Missense_Mutation	SNV	G	A	A	SHISA5	c.685C>T	P.P229S
SH_99	3	64607992	64607992	Silent	SNV	C	A	A	ADAMTS9	c.2484G>T	P.V828V
SH_99	4	10567698	10567698	Missense_Mutation	SNV	A	T	T	CLNK	c.227T>A	P.M76K
SH_99	4	1379675	1379675	Missense_Mutation	SNV	G	A	A	UVSSA	c.2056G>A	P.V686M
SH_99	4	140441478	140441478	Missense_Mutation	SNV	T	A	A	SETD7	c.715A>T	P.N239Y
SH_99	4	74275104	74275116	Frame_Shift_Del	INDEL	CTTTTATGCC	-	-	ALB	c.527delACCTTTTA	P.Y172fs
SH_99	4	7726879	7726879	Splice_Site	SNV	A	T	T	SORCS2	c.2612-2A>T	
SH_99	5	111540117	111540117	Missense_Mutation	SNV	G	A	A	EPB41L4A	c.1331C>T	P.P444L
SH_99	5	134782493	134782493	Silent	SNV	T	C	C	DCANP1	c.306A>G	P.A102A
SH_99	5	140073865	140073883	Frame_Shift_Del	INDEL	CCCTTTTGAG	-	-	HARS2	c.8delTGATCCTT	P.V109fs
SH_99	5	145969766	145969766	Missense_Mutation	SNV	T	C	C	PPP2R2B	c.1094A>G	P.N365S
SH_99	5	160761852	160761852	Silent	SNV	G	A	A	GABRB2	c.739C>T	P.L247L
SH_99	5	161580363	161580363	Missense_Mutation	SNV	C	T	T	GABRG2	c.1393C>T	P.L465F
SH_99	5	167929115	167929115	Splice_Site	SNV	G	A	A	RARS	c.1057+5G>A	
SH_99	5	26915890	26915890	Missense_Mutation	SNV	T	A	A	CDH9	c.371A>T	P.Y124F
SH_99	5	32010481	32010481	Missense_Mutation	SNV	C	A	A	PDZD2	c.1300C>A	P.P434T

SH_99	5	38338834	38338834	Missense_Mutation	SNV	T	A	A	EGFLAM	c.242T>A	P.L81Q
SH_99	5	38412726	38412726	Silent	SNV	C	A	A	EGFLAM	c.1470C>A	P.G490G
SH_99	5	38506152	38506152	Silent	SNV	A	G	G	LIFR	c.1146T>C	P.L382L
SH_99	5	488440	488440	Silent	SNV	T	A	A	SLC9A3	c.666A>T	P.A222A
SH_99	5	54404055	54404055	Missense_Mutation	SNV	G	A	A	GZMA	c.460G>A	P.G154S
SH_99	6	109802547	109802547	Missense_Mutation	SNV	T	A	A	ZBTB24	c.683A>T	P.E228V
SH_99	6	111587678	111587678	Missense_Mutation	SNV	A	T	T	MFS04B	c.913A>T	P.S305C
SH_99	6	112462042	112462042	Missense_Mutation	SNV	A	C	C	LAMA4	c.2896T>G	P.F966V
SH_99	6	151672199	151672199	Missense_Mutation	SNV	G	C	C	AKAP12	c.2673G>C	P.M891I
SH_99	6	31712030	31712030	Missense_Mutation	SNV	G	C	C	MSH5	c.601G>C	P.D201H
SH_99	6	33168241	33168241	Missense_Mutation	SNV	C	A	A	RXR8	c.13G>T	P.A5S
SH_99	6	43323428	43323428	Silent	SNV	T	C	C	ZNF318	c.1644A>G	P.A548A
SH_99	7	122261550	122261550	Silent	SNV	C	T	T	CADPS2	c.1089G>A	P.L363L
SH_99	7	134800350	134800350	Nonsense_Mutation	SNV	C	T	T	AGBL3	c.2329C>T	P.Q777*
SH_99	7	142574150	142574150	Splice_Site	SNV	C	A	A	TRPV6	c.882+11G>T	
SH_99	7	143748025	143748025	Missense_Mutation	SNV	C	G	G	OR2A5	c.531C>G	P.F177L
SH_99	7	27195946	27195946	Silent	SNV	G	T	T	HOXA7	c.219C>A	P.G73G
SH_99	7	44747549	44747549	Missense_Mutation	SNV	G	A	A	OGDH	c.3011G>A	P.R1004H
SH_99	7	48311617	48311617	Missense_Mutation	SNV	C	G	G	ABCA13	c.2354C>G	P.P785R
SH_99	7	56945249	56945249	Splice_Site	SNV	A	T	T	LOC100130849	n.195-6T>A	
SH_99	8	133961016	133961016	Splice_Site	SNV	C	A	A	TG	c.5234-5C>A	
SH_99	8	142458115	142458115	Missense_Mutation	SNV	A	G	G	MROH5	c.2711T>C	P.L904P
SH_99	8	143958306	143958306	Splice_Site	INDEL	G	-	-	CYP11B1	c.596-5delC	
SH_99	8	21560317	21560317	Splice_Site	SNV	C	T	T	GFRA2	c.903G>A	P.Q301Q
SH_99	9	111741564	111741564	Missense_Mutation	SNV	T	A	A	CTNNAL1	c.1098A>T	P.Q366H
SH_99	9	130482367	130482367	Missense_Mutation	SNV	T	C	C	TTC16	c.398T>C	P.L133P
SH_99	9	79318286	79318286	Missense_Mutation	SNV	A	G	G	PRUNE2	c.8243T>C	P.L2748P
SH_99	X	100808778	100808778	Missense_Mutation	SNV	A	T	T	ARMCX1	c.865A>T	P.S289C
SH_99	X	129349898	129349898	Missense_Mutation	SNV	T	A	A	ZNF280C	c.1705A>T	P.T569S
SH_99	X	12939574	12939574	Silent	SNV	T	C	C	TLR8	c.2469T>C	P.S823S
SH_99	X	13337934	13337934	Silent	SNV	T	A	A	ATXN3L	c.120A>T	P.L40L
SH_99	X	37664381	37664381	Missense_Mutation	SNV	A	G	G	CYBB	c.1274A>G	P.Y425C
XH_P01	1	149859194	149859194	Missense_Mutation	SNV	G	C	C	HIST2H2AB	c.273C>G	P.D91E
XH_P01	1	222838724	222838724	Silent	SNV	T	C	C	MAI3	c.2121T>C	P.P707P
XH_P01	1	228475953	228475953	Missense_Mutation	SNV	G	T	T	OBSCN	c.10003G>T	P.A3335S
XH_P01	1	229738394	229738394	Missense_Mutation	SNV	A	G	G	TAF5L	c.520T>C	P.Y174H
XH_P01	1	237664085	237664085	Missense_Mutation	SNV	G	A	A	RYR2	c.2278G>A	P.D760N
XH_P01	1	67672667	67672667	Missense_Mutation	SNV	G	A	A	IL23R	c.727G>A	P.D243N
XH_P01	11	118235819	118235819	Missense_Mutation	SNV	C	G	G	UBE4A	c.24C>G	P.N8K
XH_P01	11	26587304	26587304	Silent	SNV	G	A	A	MUC15	c.183C>T	P.N61N
XH_P01	11	71714951	71714951	Silent	SNV	G	C	C	NUMA1	c.6276C>G	P.T2092T
XH_P01	11	93862514	93862514	Silent	SNV	C	T	T	PANX1	c.36C>T	P.F12F
XH_P01	12	10213820	10213820	Silent	SNV	T	C	C	CLEC9A	c.267T>C	P.C89C
XH_P01	12	107371696	107371696	Missense_Mutation	SNV	C	A	A	MTERF2	c.797G>T	P.S266I
XH_P01	12	26648182	26648182	Silent	SNV	T	C	C	ITPR2	c.5085A>G	P.L1695L
XH_P01	12	57573673	57573673	Missense_Mutation	SNV	C	G	G	LRP1	c.5075C>G	P.S1692C
XH_P01	12	8667850	8667850	Missense_Mutation	SNV	C	T	T	CLEC4D	c.47C>T	P.P16L
XH_P01	12	88500811	88500811	Missense_Mutation	SNV	G	C	C	CEP290	c.2548C>G	P.Q850E
XH_P01	13	110959359	110959359	Missense_Mutation	SNV	T	G	G	COL4A1	c.16A>C	P.S6R
XH_P01	13	111955360	111955360	Missense_Mutation	SNV	C	T	T	ARHGEF7	c.2066C>T	P.S689F
XH_P01	13	43566239	43566239	Silent	SNV	G	C	C	EPST11	c.63C>G	P.T21T
XH_P01	15	73660199	73660199	Missense_Mutation	SNV	G	T	T	HCN4	c.413C>A	P.S138Y
XH_P01	16	24583242	24583242	Missense_Mutation	SNV	A	C	C	RBBP6	c.4855A>C	P.S1619R
XH_P01	16	88599909	88599909	Missense_Mutation	SNV	C	T	T	ZFPM1	c.1543C>T	P.P515S
XH_P01	17	18539782	18539782	Missense_Mutation	SNV	G	A	A	TBC1D28	c.626C>T	P.T209I
XH_P01	17	5991412	5991412	Missense_Mutation	SNV	C	T	T	WSCD1	c.530C>T	P.A177V
XH_P01	17	79518111	79518111	Missense_Mutation	SNV	C	A	A	FAAP100	c.409G>T	P.D137Y
XH_P01	18	66506122	66506122	Silent	SNV	G	T	T	CCDC102B	c.786G>T	P.V262V
XH_P01	19	10602341	10602341	Missense_Mutation	SNV	G	A	A	KEAP1	c.1237C>T	P.R413C
XH_P01	19	43093599	43093599	Splice_Site	SNV	A	G	G	CEACAM8	c.703+10T>C	
XH_P01	19	52091424	52091424	Missense_Mutation	SNV	C	T	T	ZNF175	c.1840C>T	P.P614S
XH_P01	19	53014288	53014288	Silent	SNV	C	T	T	ZNF578	c.654C>T	P.L218L
XH_P01	19	54632474	54632474	Missense_Mutation	SNV	G	A	A	PRPF31	c.1189G>A	P.G397S
XH_P01	2	202134249	202134249	Missense_Mutation	SNV	A	G	G	CASP8	c.322A>G	P.M108V
XH_P01	2	210558106	210558106	Missense_Mutation	SNV	G	A	A	MAP2	c.1212G>A	P.M404I
XH_P01	2	215910727	215910727	Missense_Mutation	SNV	G	T	T	ABCA12	c.706C>A	P.P236T
XH_P01	20	36769757	36769757	Missense_Mutation	SNV	C	T	T	TGM2	c.1026G>A	P.M342I
XH_P01	22	38234520	38234520	Silent	SNV	G	T	T	ANKRD54	c.462C>A	P.G154I
XH_P01	22	45750972	45750972	Silent	SNV	G	A	A	SMC1B	c.2985C>T	P.I95I
XH_P01	3	121134796	121134804	Missense_Mutation	INDEL	ATTTGACAG	-	-	STXBPSL	c.3216delTTTGA	F1070_R1072del
XH_P01	3	46775282	46775282	Missense_Mutation	SNV	T	G	G	PRSS46	c.364A>C	P.S122R
XH_P01	4	3449695	3449695	Silent	SNV	C	T	T	HGFAC	c.1590C>T	P.P530P
XH_P01	4	99407920	99407920	Missense_Mutation	SNV	G	A	A	TSPAN5	c.248C>T	P.A83V
XH_P01	5	11346513	11346513	Silent	SNV	C	T	T	CTNND2	c.1326G>A	P.P442P
XH_P01	5	125939460	125939460	Missense_Mutation	SNV	T	G	G	PHAX	c.295T>G	P.F99V
XH_P01	5	140214119	140214119	Missense_Mutation	SNV	G	A	A	PCDHA7	c.151G>A	P.D51N
XH_P01	5	176721441	176721441	Missense_Mutation	SNV	G	A	A	NSD1	c.7072G>A	P.D2358N
XH_P01	5	94764383	94764383	Missense_Mutation	SNV	A	T	T	FAM81B	c.733A>T	P.I245F
XH_P01	7	100684905	100684905	Missense_Mutation	SNV	G	A	A	MUC17	c.10208G>A	P.S3403N
XH_P01	7	105255226	105255226	Missense_Mutation	SNV	G	T	T	ATXN7L1	c.907C>A	P.P303T
XH_P01	7	150696136	150696136	Missense_Mutation	SNV	C	A	A	NOS3	c.919C>A	P.P307T
XH_P01	8	142486189	142486189	Missense_Mutation	SNV	G	A	A	MROH5	c.1504C>T	P.R502C
XH_P01	8	146068297	146068297	Missense_Mutation	SNV	T	C	C	ZNF7	c.1838T>C	P.I613T
XH_P01	8	68423880	68423880	Missense_Mutation	SNV	C	G	G	CPA6	c.328G>C	P.F110Q
XH_P01	8	94738721	94738721	Missense_Mutation	SNV	T	C	C	FAM92A1	c.757T>C	P.C253R
XH_P01	9	113096539	113096539	Missense_Mutation	SNV	G	A	A	TXNDC8	c.86C>T	P.S29L
XH_P01	9	140057773	140057773	Missense_Mutation	SNV	C	A	A	GRIN1	c.2324C>A	P.S757Y
XH_P01	9	86616477	86616477	Silent	SNV	T	A	A	RM1	c.576T>A	P.G192G
XH_P01	X	8553320	8553320	Missense_Mutation	SNV	G	A	A	ANOS1	c.844C>T	P.R282C
XH_P01	Y	16942259	16942259	Silent	SNV	G	A	A	NLGN4Y	c.1461G>A	P.S487S
XH_P02	1	150915032	150915032	Splice_Site	SNV	T	G	G	SETDB1	c.548-7T>G	
XH_P02	1	173493988	173493988	Missense_Mutation	SNV	G	T	T	SLC9C2	c.2444C>A	P.A815D
XH_P02	1	26691694	26691694	Missense_Mutation	SNV	C	A	A	ZNF683	c.343G>T	P.A115S
XH_P02	1	26691695	26691695	Missense_Mutation	SNV	C	A	A	ZNF683	c.342G>T	P.Q114H
XH_P02	1	85656188	85656188	Silent	SNV	G	A	A	SYDE2	c.993C>T	P.L331L
XH_P02	10	105176422	105176422	Missense_Mutation	SNV	G	T	T	PDCD11	c.1693G>T	P.V565L
XH_P02	10	128147615	128147615	Silent	SNV	G	A	A	C10orf90	c.1891C>T	P.L631L
XH_P02	10	49935617	49935617	Missense_Mutation	SNV	T	C	C	WDFY4	c.884T>C	P.V295A

XH_P02	10	97373840	97373840	Missense_Mutation	SNV	G	T	T	ALDH18A1	c.1678C>A	P.Q560K
XH_P02	11	111715447	111715447	Splice_Site	SNV	C	T	T	ALG9	c.896-1G>A	
XH_P02	11	117306527	117306527	Splice_Site	SNV	C	A	A	DSCAML1	c.4901-12G>T	
XH_P02	11	122852165	122852165	Missense_Mutation	SNV	G	T	T	BSX	c.215C>A	P.P72H
XH_P02	11	17575067	17575067	Splice_Site	SNV	G	C	C	OTOG	c.576+1G>C	
XH_P02	11	32954189	32954189	Missense_Mutation	SNV	C	G	G	QSER1	c.998C>G	P.P333R
XH_P02	11	46406842	46406877	Missense_Mutation	INDEL	ACGTTGTAGG	-	-	CHRM4	GGACGCCCTAC	P.L411_V422del
XH_P02	11	55419162	55419162	Silent	SNV	G	A	A	OR452	c.783G>A	P.T261T
XH_P02	11	58190486	58190486	Silent	SNV	G	A	A	OR5B2	c.249C>T	P.F83F
XH_P02	11	63993277	63993277	Missense_Mutation	SNV	G	A	A	TRPT1	c.56C>T	P.A19V
XH_P02	12	114804154	114804154	Missense_Mutation	SNV	T	A	A	TBX5	c.798A>T	P.K266N
XH_P02	12	124319945	124319945	Splice_Site	SNV	A	C	C	DNAH10	c.4426-8A>C	
XH_P02	12	54903516	54903516	Silent	SNV	G	C	C	NCKAP1L	c.420G>C	P.L140L
XH_P02	13	27246022	27246029	Frame_Shift_Del	INDEL	GATGGGCT	-	-	WASF3	c.445delTGGG	P.D146fs
XH_P02	13	42263587	42263624	Frame_Shift_Del	INDEL	TAGTTGATCA	-	-	VWA8	TTTCCAGTGATC	P.H1333fs
XH_P02	13	99036996	99036996	Missense_Mutation	SNV	A	G	G	FARP1	c.509A>G	P.D170G
XH_P02	14	52481797	52481797	Silent	SNV	G	T	T	NID2	c.3225C>A	P.R1075R
XH_P02	14	58714498	58714498	Missense_Mutation	SNV	G	A	A	PSMA3	c.52G>A	P.D18N
XH_P02	14	64407358	64407358	Missense_Mutation	SNV	G	T	T	SYNE2	c.106G>T	P.A36S
XH_P02	14	78709655	78709655	Silent	SNV	C	T	T	NRXN3	c.219C>T	P.C73C
XH_P02	15	35202495	35202495	Missense_Mutation	SNV	C	T	T	AQR	c.1504G>A	P.V502I
XH_P02	15	89060216	89060216	Splice_Site	SNV	G	C	C	DET1	c.1272-12C>G	
XH_P02	15	99434840	99434840	Silent	SNV	G	A	A	IGF1R	c.927G>A	P.S309S
XH_P02	16	1259233	1259233	Missense_Mutation	SNV	C	A	A	CACNA1H	c.3565C>A	P.R189S
XH_P02	16	24573001	24573001	Missense_Mutation	SNV	C	G	G	RBBP6	c.916C>G	P.P306A
XH_P02	16	74415476	74415476	Silent	SNV	C	T	T	NPIP815	c.129C>T	P.D43D
XH_P02	16	75665348	75665348	Missense_Mutation	SNV	C	A	A	KARS	c.1302G>T	P.M434I
XH_P02	17	1401300	1401300	Missense_Mutation	SNV	C	T	T	INPP5K	c.665G>A	P.R222K
XH_P02	17	29548945	29548945	Frame_Shift_Ins	INDEL	-	AG	AG	NF1	c.1720_1721dup	P.P575fs
XH_P02	17	32957157	32957157	Missense_Mutation	SNV	A	T	T	TMEM132E	c.1469A>T	P.E490V
XH_P02	17	46669797	46669797	Missense_Mutation	SNV	T	C	C	HOXB5	c.584A>G	P.K195R
XH_P02	17	54939559	54939559	Missense_Mutation	SNV	A	G	G	DGKE	c.1471A>G	P.I491V
XH_P02	17	58136863	58136863	Nonsense_Mutation	SNV	G	C	C	HEATR6	c.1643C>G	P.S548*
XH_P02	17	60642376	60642376	Missense_Mutation	SNV	G	C	C	TLK2	c.846G>C	P.K282N
XH_P02	17	71427811	71427811	Splice_Site	SNV	G	T	T	SDK2	c.1313-3C>A	
XH_P02	17	78073445	78073445	Silent	SNV	G	C	C	CCDC40	c.3300G>C	P.L1100L
XH_P02	19	19369352	19369352	Missense_Mutation	SNV	C	T	T	HAPLN4	c.797G>A	P.C266Y
XH_P02	19	3600621	3600621	Silent	SNV	G	A	A	TBXA2R	c.12C>T	P.N4N
XH_P02	19	41239209	41239209	Missense_Mutation	SNV	G	A	A	ITPKC	c.1614G>A	P.M538I
XH_P02	19	44082863	44082863	Splice_Site	SNV	G	C	C	PINLYP	c.259+5G>C	
XH_P02	19	44681311	44681311	Silent	SNV	C	T	T	ZNF226	c.1896C>T	P.A632A
XH_P02	19	5221145	5221145	Silent	SNV	G	A	A	PTPRS	c.3321C>T	P.G1107G
XH_P02	19	52876405	52876405	Missense_Mutation	SNV	G	C	C	ZNF880	c.54G>C	P.Q118H
XH_P02	19	53304356	53304356	Missense_Mutation	SNV	A	G	G	ZNF28	c.742T>C	P.Y248H
XH_P02	19	56090932	56090932	Missense_Mutation	SNV	C	T	T	ZNF579	c.74G>A	P.G25D
XH_P02	19	581560	581560	Silent	SNV	G	A	A	BSG	c.690G>A	P.E230E
XH_P02	19	8373094	8373094	Silent	SNV	G	T	T	CD320	c.81C>A	P.L27L
XH_P02	2	100203615	100203615	Splice_Site	SNV	C	A	A	AFF3	c.2591+1G>T	
XH_P02	2	171243770	171243770	Missense_Mutation	SNV	G	A	A	MYO3B	c.1529G>A	P.R510K
XH_P02	2	186670236	186670236	Missense_Mutation	SNV	C	A	A	FSIP2	c.16203C>A	P.D5401E
XH_P02	2	201862262	201862262	Missense_Mutation	SNV	A	G	G	FAM126B	c.532T>C	P.F178L
XH_P02	2	20251182	20251182	Missense_Mutation	SNV	T	A	A	LAPTM4A	c.100A>T	P.T34S
XH_P02	2	55106756	55106756	Missense_Mutation	SNV	G	C	C	EML6	c.2417G>C	P.G806A
XH_P02	21	43846809	43846809	Missense_Mutation	SNV	G	A	A	UBASH3A	c.936G>A	P.M312I
XH_P02	3	27363704	27363704	Missense_Mutation	SNV	G	C	C	NEK10	c.411C>G	P.I137M
XH_P02	3	47618948	47618948	Missense_Mutation	SNV	C	G	G	CSPG5	c.154G>C	P.E52Q
XH_P02	4	13603624	13603624	Frame_Shift_Ins	INDEL	-	CA	CA	BOD1L1	c.4898_4899dup	P.H1634fs
XH_P02	4	157782554	157782569	Splice_Site	INDEL	AATAAAAAAT	-	-	PDGFC	c.0+27delGTATATTTTATTTC	
XH_P02	4	52861722	52861722	Missense_Mutation	SNV	C	A	A	LRRCC6	c.1466G>T	P.G489V
XH_P02	4	95202724	95202724	Missense_Mutation	SNV	G	C	C	SMARCAD1	c.2715G>C	P.K905N
XH_P02	5	140044539	140044539	Missense_Mutation	SNV	C	A	A	WDR55	c.42C>A	P.S14R
XH_P02	5	140784744	140784744	Missense_Mutation	SNV	G	T	T	PCDHGA9	c.2225G>T	P.G742V
XH_P02	6	100055062	100055062	Splice_Site	SNV	C	T	T	PRDM13	c.144+8C>T	
XH_P02	6	136787905	136787905	Missense_Mutation	SNV	G	C	C	MAP7	c.16C>G	P.L6V
XH_P02	6	168927051	168927051	Missense_Mutation	SNV	G	C	C	SMOC2	c.282G>C	P.R94S
XH_P02	6	17601146	17601146	Missense_Mutation	SNV	T	G	G	FAM8A1	c.506T>G	P.L169R
XH_P02	6	99283623	99283623	Missense_Mutation	SNV	G	C	C	POU3F2	c.874G>C	P.G292R
XH_P02	7	120496816	120496816	Nonsense_Mutation	SNV	A	T	T	TSPAN12	c.2T>A	P.M1?
XH_P02	7	121944378	121944378	Silent	SNV	C	T	T	FEZ1	c.114G>A	P.A38A
XH_P02	7	127326763	127326763	Missense_Mutation	SNV	C	T	T	SND1	c.175C>T	P.L59F
XH_P02	7	13946129	13946129	Missense_Mutation	SNV	C	A	A	ETV1	c.1036G>T	P.D346Y
XH_P02	7	42088288	42088288	Missense_Mutation	SNV	C	T	T	GLI3	c.481G>A	P.A161T
XH_P02	7	5270481	5270481	Missense_Mutation	SNV	T	G	G	WIPI2	c.1235T>G	P.L412R
XH_P02	7	65547932	65547932	Splice_Site	SNV	G	T	T	ASL	c.348+9G>T	
XH_P02	7	99914732	99914732	Missense_Mutation	SNV	G	A	A	SPDYE3	c.1300G>A	P.G434S
XH_P02	8	113267550	113267550	Silent	SNV	T	C	C	CSMD3	c.9462A>G	P.L3154L
XH_P02	8	14490529	14490529	Missense_Mutation	SNV	G	C	C	PLEC	c.13541C>G	P.A4514G
XH_P02	8	25136112	25136112	Missense_Mutation	SNV	G	T	T	DOCK5	c.252G>T	P.E84D
XH_P02	9	124544696	124544704	Missense_Mutation	INDEL	CCGTAACGG	-	-	DAB2IP	c.3126delCGTA	P.R1040_G1042del
XH_P02	9	131233655	131233655	Silent	SNV	G	A	A	ODF2	c.474G>A	P.E158E
XH_P02	9	137326016	137326016	Missense_Mutation	SNV	G	A	A	RXRA	c.1204G>A	P.A402T
XH_P02	9	140218174	140218174	Splice_Site	SNV	C	G	G	EXD3	c.2184+3G>C	
XH_P02	9	35650527	35650527	Missense_Mutation	SNV	G	A	A	SIT1	c.208C>T	P.R70W
XH_P02	9	73168099	73168099	Silent	SNV	G	A	A	TRPM3	c.2862C>T	P.V954V
XH_P02	9	95481094	95481094	Silent	SNV	G	T	T	BCID2	c.1833C>A	P.S611S
XH_P02	X	44703479	44703479	Missense_Mutation	SNV	G	C	C	DUSP21	c.101G>C	P.G34A
XH_P02	X	76872153	76872153	Missense_Mutation	SNV	C	T	T	ATRX	c.5494G>A	P.E1832K
XH_P02	X	9622356	9622356	Missense_Mutation	SNV	G	C	C	TBL1X	c.205G>C	P.E69Q
XH_P03	1	15495211	15495211	Missense_Mutation	SNV	A	C	C	C1orf195	c.161T>G	P.L54R
XH_P03	1	155291136	155291136	Silent	SNV	G	A	A	RUSC1-AS1	c.144C>T	P.S48S
XH_P03	1	159907625	159907625	Missense_Mutation	SNV	C	A	A	IGSF9	c.251G>T	P.R84L
XH_P03	1	161967977	161967977	Missense_Mutation	SNV	C	A	A	OLFML2B	c.1115G>T	P.W372L
XH_P03	1	215408203	215408203	Nonsense_Mutation	SNV	G	A	A	KCNK2	c.984G>A	P.W328*
XH_P03	1	53732201	53732201	Silent	SNV	C	T	T	LRP8	c.1371G>A	P.V457V
XH_P03	10	27499836	27499836	Missense_Mutation	SNV	C	T	T	ACBD5	c.1006G>A	P.G336R
XH_P03	11	118362629	118362629	Silent	SNV	C	T	T	KMT2A	c.4981C>T	P.L1661L
XH_P03	11	20065830	20065830	Splice_Site	SNV	G	C	C	NAV2	c.3007+12G>C	
XH_P03	11	77412557	77412557	Missense_Mutation	SNV	T	A	A	RSF1	c.1717A>T	P.T573S

XH_P03	12	10961913	10961913	Silent	SNV	G	A	A	TAS2R9	c.762C>T	P.S254S
XH_P03	12	112471137	112471141	Frame_Shift_Del	INDEL	GTCTG	-	-	NAA25	592_2696delCA	P.Q898fs
XH_P03	12	130926460	130926460	Silent	SNV	C	T	T	RIMBP2	c.1386G>A	P.P462P
XH_P03	12	32137217	32137217	Missense_Mutation	SNV	A	C	C	KIAA1551	c.3328A>C	P.S1110R
XH_P03	12	40882992	40882992	Missense_Mutation	SNV	G	T	T	MUC19	c.16238G>T	P.W5413L
XH_P03	13	73345038	73345038	Splice_Site	SNV	G	A	A	DIS3	c.1755+4C>T	
XH_P03	14	45599894	45599894	Splice_Site	SNV	A	G	G	FKBP3	c.210+8T>C	
XH_P03	15	65622694	65622694	Nonsense_Mutation	SNV	G	A	A	IGDCC3	c.1795C>T	P.Q599*
XH_P03	15	83499668	83499668	Missense_Mutation	INDEL	-	CCCCCA	CCCCCA	WHAMM	65_1970dupAC	P.656_P657dup
XH_P03	16	30018509	30018509	Silent	SNV	G	A	A	DOCA2	c.639C>T	P.L213L
XH_P03	17	11686963	11686963	Nonsense_Mutation	SNV	G	A	A	DNAH9	c.7719G>A	P.W2573*
XH_P03	17	29684099	29684101	Missense_Mutation	INDEL	TAC	-	-	NF1	7861_7863delA	P.T2621del
XH_P03	17	36483753	36483753	Missense_Mutation	SNV	C	T	T	GPR179	c.5699G>A	P.S1900N
XH_P03	17	48941207	48941207	Missense_Mutation	SNV	T	G	G	TOB1	c.172A>C	P.I58L
XH_P03	17	77080716	77080716	Silent	SNV	G	T	T	ENGASE	c.1539G>T	P.L513L
XH_P03	17	79671676	79671676	Missense_Mutation	SNV	T	A	A	MRPL12	c.275T>A	P.I92N
XH_P03	19	44377599	44377599	Missense_Mutation	SNV	C	T	T	ZNF404	c.758G>A	P.R253Q
XH_P03	19	4546298	4546298	Splice_Site	SNV	A	T	T	SEMA6B	c.1680-12T>A	
XH_P03	19	4817728	4817728	Missense_Mutation	SNV	T	G	G	TICAM1	c.662A>C	P.H221P
XH_P03	2	163059643	163059643	Missense_Mutation	SNV	T	C	C	FAP	c.985A>G	P.T329A
XH_P03	2	181848774	181848774	Missense_Mutation	SNV	C	G	G	UBE2E3	c.199C>G	P.Q67E
XH_P03	2	185803076	185803076	Missense_Mutation	SNV	A	T	T	ZNF804A	c.2953A>T	P.N985Y
XH_P03	2	96521150	96521150	Missense_Mutation	SNV	G	A	A	ANKRD36C	c.5957C>T	P.A1986V
XH_P03	20	42789050	42789050	Splice_Site	SNV	G	T	T	JPH2	c.380-3C>A	
XH_P03	20	42789051	42789051	Splice_Site	SNV	C	T	T	JPH2	c.380-4G>A	
XH_P03	3	14964543	14964543	Splice_Site	SNV	G	A	A	FGD5	c.3808-10G>A	
XH_P03	3	178936091	178936091	Missense_Mutation	SNV	G	A	A	PIK3CA	c.1633G>A	P.E545K
XH_P03	3	45134810	45134810	Missense_Mutation	SNV	G	A	A	CDCP1	c.1586C>T	P.S529F
XH_P03	3	50143140	50143140	Missense_Mutation	SNV	A	G	G	RBM5	c.853A>G	P.M285V
XH_P03	4	100824906	100824906	Missense_Mutation	SNV	T	C	C	DNAJB14	c.992A>G	P.N331S
XH_P03	4	17887763	17887763	Missense_Mutation	SNV	G	A	A	LCORL	c.704C>T	P.S235F
XH_P03	5	113740517	113740517	Missense_Mutation	SNV	G	T	T	KCNN2	c.965G>T	P.W322L
XH_P03	5	113740518	113740518	Missense_Mutation	SNV	G	T	T	KCNN2	c.966G>T	P.W322C
XH_P03	5	140202741	140202741	Missense_Mutation	SNV	G	A	A	PCDH45	c.1381G>A	P.V461M
XH_P03	5	92929283	92929283	Missense_Mutation	SNV	C	T	T	NR2F1	c.1007C>T	P.S336L
XH_P03	5	95234171	95234171	Missense_Mutation	SNV	G	T	T	ELL2	c.1298C>A	P.T433N
XH_P03	6	161006150	161006150	Missense_Mutation	SNV	C	G	G	LPA	c.4217G>C	P.G1406A
XH_P03	6	42225920	42225920	Silent	SNV	G	A	A	TRERF1	c.2349C>T	P.N783N
XH_P03	7	135433253	135433253	Missense_Mutation	SNV	C	A	A	FAM180A	c.76G>T	P.A26S
XH_P03	7	143043691	143043691	Silent	SNV	C	T	T	CLCN1	c.2304C>T	P.F768F
XH_P03	7	148506444	148506444	Missense_Mutation	SNV	G	A	A	EZH2	c.2068C>T	P.R690C
XH_P03	8	146032778	146032778	Silent	SNV	C	G	G	ZNF517	c.456C>G	P.S152S
XH_P03	9	125589002	125589002	Missense_Mutation	SNV	T	C	C	PDCL	c.65A>G	P.D22G
XH_P03	X	147003491	147003491	Missense_Mutation	SNV	C	T	T	FMR1	c.92C>T	P.A31V
XH_P03	X	41088615	41088615	Missense_Mutation	SNV	A	G	G	USP9X	c.7171A>G	P.M2391V
XH_P03	X	53563452	53563452	Missense_Mutation	SNV	C	A	A	HUWE1	c.12314G>T	P.S410S1
XH_P03	X	53615355	53615355	Missense_Mutation	SNV	G	T	T	HUWE1	c.4601C>A	P.T1534K
XH_P04	1	1653154	1653155	Splice_Site	INDEL	AG	-	-	CDK11A	112-5_112-4delCT	
XH_P04	1	66075632	66075632	Missense_Mutation	SNV	G	A	A	LEPR	c.1755G>A	P.M58S1
XH_P04	1	68905317	68905320	Frame_Shift_Del	INDEL	CTTC	-	-	RPE65	649_652delGAA	P.E217fs
XH_P04	1	91980363	91980364	Splice_Site	INDEL	TT	-	-	CD7	19-11_919-10delTT	
XH_P04	11	380337	380337	Missense_Mutation	SNV	C	G	G	B4GALNT4	c.2761C>G	P.P921A
XH_P04	11	46717223	46717223	Missense_Mutation	SNV	G	C	C	ARHGAP1	c.216C>G	P.I72M
XH_P04	11	5462320	5462320	Missense_Mutation	SNV	C	T	T	OR5111	c.425G>A	P.R142H
XH_P04	11	6220784	6220784	Missense_Mutation	SNV	G	A	A	OR52W1	c.331G>A	P.A111T
XH_P04	11	797770	797772	Missense_Mutation	INDEL	AAG	-	-	PAN01	.145_147delAA	P.K49del
XH_P04	12	111779848	111779850	Missense_Mutation	INDEL	ACA	-	-	CUX2	3652_3654delA	P.N1218del
XH_P04	12	57485551	57485551	Missense_Mutation	SNV	C	T	T	NAB2	c.727C>T	P.R243C
XH_P04	12	78400963	78400964	Frame_Shift_Del	INDEL	AA	-	-	NAV3	1646_1647delA	P.K549fs
XH_P04	14	39555003	39555003	Frame_Shift_Del	INDEL	G	-	-	SEC23A	c.791delC	P.S264fs
XH_P04	14	51088550	51088550	Splice_Site	INDEL	T	-	-	ATL1	c.991-3delT	
XH_P04	15	53992072	53992073	Frame_Shift_Del	INDEL	TT	-	-	WDR72	1639_1640delA	P.K547fs
XH_P04	15	62266480	62266483	Splice_Site	INDEL	TATT	-	-	VPS13C	8+4_2538+7delAATA	
XH_P04	16	4723530	4723530	Missense_Mutation	SNV	A	G	G	MGRN1	c.827A>G	P.N276S
XH_P04	16	58540824	58540824	Frame_Shift_Del	INDEL	G	-	-	NDRG4	c.682delG	P.V228fs
XH_P04	16	66762968	66762970	Missense_Mutation	INDEL	TCA	-	-	DYNC1L12	.843_845delTG	P.D281del
XH_P04	17	33771703	33771703	Missense_Mutation	SNV	C	T	T	SLFN13	c.997G>A	P.V333M
XH_P04	17	38711735	38711735	Silent	SNV	G	A	A	CCR7	c.207C>T	P.I69I
XH_P04	18	21112253	21112256	Splice_Site	INDEL	GAGA	-	-	NPC1	55-8_3755-5delTCTC	
XH_P04	18	2739508	2739510	Missense_Mutation	INDEL	AGG	-	-	SMCHD1	3506_3508delG	P.G1169del
XH_P04	18	61602442	61602442	Missense_Mutation	SNV	C	G	G	SERPINB10	c.1160C>G	P.T387S
XH_P04	19	22157509	22157509	Missense_Mutation	SNV	C	A	A	ZNF208	c.327G>T	P.E109D
XH_P04	19	52569420	52569420	Missense_Mutation	SNV	T	C	C	ZNF841	c.1715A>G	P.N572S
XH_P04	2	155711682	155711682	Missense_Mutation	SNV	A	G	G	KCNJ3	c.1363A>G	P.T455A
XH_P04	2	1796166	1796166	Missense_Mutation	SNV	G	T	T	MYT1L	c.3347C>A	P.S1116Y
XH_P04	2	55402952	55402955	Frame_Shift_Del	INDEL	TGAC	-	-	CLHC1	366_1369delGT	P.V456fs
XH_P04	2	74688843	74688844	Frame_Shift_Del	INDEL	AT	-	-	MOGS	1754_1755delA	P.V585fs
XH_P04	20	35532493	35532567	Frame_Shift_Del	INDEL	TATTCACCTCA	-	-	SAMHD1	3TAATAAACTGA	P.I499fs
XH_P04	20	60989462	60989462	Silent	SNV	G	A	A	RBBP8NL	c.945C>T	P.S315S
XH_P04	3	52437595	52437596	Frame_Shift_Del	INDEL	AG	-	-	BAP1	1565_1566delC	P.P522fs
XH_P04	4	106180824	106180826	Missense_Mutation	INDEL	CTT	-	-	TET2	3854_3856delT	P.F1285del
XH_P04	4	13604703	13604703	Missense_Mutation	SNV	T	A	A	BOD11L1	c.3821A>T	P.H1274L
XH_P04	4	153259068	153259068	Silent	SNV	T	C	C	FBXW7	c.747A>G	P.K249K
XH_P04	4	187524609	187524609	Missense_Mutation	SNV	G	A	A	FAT1	c.11071C>T	P.H3691Y
XH_P04	5	176518670	176518673	Splice_Site	INDEL	CTCT	-	-	FGFR4	4-12_604-9delCTCT	
XH_P04	6	144869774	144869774	Splice_Site	SNV	A	T	T	UTRN	c.6596-2A>T	
XH_P04	6	152668244	152668244	Missense_Mutation	SNV	G	T	T	SYNE1	c.11815C>A	P.L3939M
XH_P04	6	25435814	25435814	Missense_Mutation	SNV	T	A	A	CARMIL1	c.353T>A	P.F118Y
XH_P04	6	35392280	35392280	Missense_Mutation	SNV	C	T	T	PPARD	c.802C>T	P.P268S
XH_P04	6	46656550	46656550	Nonsense_Mutation	SNV	C	T	T	TDRD6	c.685C>T	P.R229*
XH_P04	7	122338518	122338520	Missense_Mutation	INDEL	ACA	-	-	RNF133	.453_455delTG	P.V152del
XH_P04	7	134891878	134891878	Silent	SNV	A	C	C	WDR91	c.588T>G	P.R196R
XH_P04	7	40535940	40535940	Silent	SNV	G	A	A	SUGCT	c.1065G>A	P.P355P
XH_P04	7	47832299	47832299	Missense_Mutation	SNV	T	C	C	PKD1L1	c.8452A>G	P.T2818A
XH_P04	7	99489911	99489913	Missense_Mutation	INDEL	AGA	-	-	TRIM4	1376_1378delT	P.F459del
XH_P04	8	145170488	145170488	Missense_Mutation	SNV	C	T	T	WDR97	c.4322C>T	P.T1441M
XH_P04	8	37555654	37555654	Missense_Mutation	SNV	G	A	A	ZNF703	c.1235G>A	P.G412E
XH_P04	8	53062362	53062362	Missense_Mutation	SNV	C	T	T	ST18	c.1982G>A	P.C661Y

XH_P04	9	127262988	127262988	Missense_Mutation	SNV	C	T	T	NR5A1	c.251G>A	P.R84H
XH_P04	9	35684796	35684798	Missense_Mutation	INDEL	CCA	-	-	TPM2	.570_572delTG	190_G191delinsW
XH_P04	X	105875919	105875919	Silent	SNV	A	G	G	CXorf57	c.1044A>G	P.K348K
XH_P04	X	37655319	37655322	Frame_Shift_Del	INDEL	CTTA	-	-	CYBB	.602_605delAC	P.Y201fs
XH_P05	1	101196794	101196794	Silent	SNV	C	T	T	VCAM1	c.1245C>T	P.L415L
XH_P05	1	158435621	158435621	Silent	SNV	G	A	A	OR10K1	c.270G>A	P.K90K
XH_P05	1	197147562	197147562	Missense_Mutation	SNV	T	C	C	ZBTB41	c.1757A>G	P.H586R
XH_P05	1	204889759	204889759	Splice_Site	SNV	G	A	A	NFASC	c.-199-1G>A	
XH_P05	1	248112802	248112802	Missense_Mutation	SNV	T	C	C	OR2L8	c.643T>C	P.C215R
XH_P05	1	248185319	248185319	Missense_Mutation	SNV	C	A	A	OR2L5	c.70C>A	P.L24I
XH_P05	10	112764539	112764539	Missense_Mutation	SNV	A	G	G	SHOC2	c.1148A>G	P.K383R
XH_P05	10	61834319	61834319	Missense_Mutation	SNV	G	T	T	ANK3	c.6320C>A	P.T2107N
XH_P05	11	108043227	108043227	Missense_Mutation	SNV	C	G	G	NPAT	c.2484G>C	P.Q828H
XH_P05	11	14380346	14380346	Missense_Mutation	SNV	C	T	T	RRAS2	c.71G>A	P.G24D
XH_P05	11	65824404	65824404	Silent	SNV	G	A	A	SF3B2	c.645G>A	P.V215V
XH_P05	11	68846406	68846406	Missense_Mutation	SNV	T	C	C	TPCN2	c.1457T>C	P.L486P
XH_P05	11	95825221	95825221	Silent	SNV	C	T	T	MAML2	c.1974G>A	P.Q658Q
XH_P05	12	111348909	111348909	Missense_Mutation	SNV	A	T	T	MYL2	c.473T>A	P.I158N
XH_P05	12	133208980	133208980	Nonsense_Mutation	SNV	G	T	T	POLE	c.6251C>A	P.S2084*
XH_P05	13	103390725	103390725	Missense_Mutation	SNV	A	G	G	CCDC168	c.12322T>C	P.Y4108H
XH_P05	13	103391555	103391555	Missense_Mutation	SNV	C	T	T	CCDC168	c.11492G>A	P.R3831Q
XH_P05	14	20404251	20404251	Silent	SNV	A	T	T	OR4K1	c.426A>T	P.V142V
XH_P05	15	41099840	41099840	Missense_Mutation	SNV	G	T	T	ZFYVE19	c.53G>T	P.C18F
XH_P05	15	41857274	41857274	Missense_Mutation	SNV	A	T	T	TYRO3	c.718A>T	P.N240Y
XH_P05	15	42930926	42930926	Missense_Mutation	SNV	C	T	T	STARD9	c.475C>T	P.R159W
XH_P05	15	51397322	51397322	Missense_Mutation	SNV	C	A	A	TNFAIP8L3	c.52G>T	P.A18S
XH_P05	15	72432064	72432064	Missense_Mutation	SNV	T	C	C	SEN8	c.100T>C	P.F34L
XH_P05	16	81295871	81295871	Missense_Mutation	SNV	C	A	A	BCO1	c.454C>A	P.L152M
XH_P05	17	39464717	39464717	Silent	SNV	G	A	A	KRTAP16-1	c.789C>T	P.I263I
XH_P05	17	43195485	43195485	Missense_Mutation	SNV	C	A	A	PLCD3	c.1136G>T	P.R379L
XH_P05	17	7577541	7577541	Missense_Mutation	SNV	T	A	A	TP53	c.740A>T	P.N247I
XH_P05	18	29972863	29972863	Missense_Mutation	SNV	T	C	C	GAREM1	c.257A>G	P.Y86C
XH_P05	18	76757121	76757121	Silent	SNV	G	A	A	SALL3	c.3702G>A	P.Q1234Q
XH_P05	19	10610202	10610202	Missense_Mutation	SNV	C	G	G	KEAP1	c.508G>C	P.A170P
XH_P05	19	41858919	41858921	Missense_Mutation	INDEL	GCG	-	-	TGFB1	c.29_31delCGC	P.P10del
XH_P05	19	42703686	42703686	Silent	SNV	C	T	T	DEDD2	c.885G>A	P.L295L
XH_P05	19	47258831	47258831	Missense_Mutation	SNV	G	A	A	FKRP	c.124G>A	P.A42T
XH_P05	19	49514534	49514534	Missense_Mutation	SNV	T	C	C	RUVBL2	c.866T>C	P.V289A
XH_P05	19	53015366	53015366	Missense_Mutation	SNV	C	A	A	ZNFX8	c.1732C>A	P.H578N
XH_P05	2	133075404	133075404	Frame_Shift_Del	INDEL	T	-	-	ZNFX8	c.866delT	P.F289fs
XH_P05	2	191235749	191235749	Missense_Mutation	SNV	C	T	T	INPP1	c.821C>T	P.A274V
XH_P05	2	232457934	232457934	Missense_Mutation	SNV	G	A	A	C2orf57	c.272G>A	P.S91N
XH_P05	20	55093211	55093211	Missense_Mutation	SNV	G	T	T	RTFDC1	c.901G>T	P.D301Y
XH_P05	20	58440877	58440877	Missense_Mutation	SNV	T	C	C	SYCP2	c.4364A>G	P.K1455R
XH_P05	21	18981391	18981391	Silent	SNV	T	C	C	BTG3	c.72A>G	P.K24K
XH_P05	22	16287712	16287712	Missense_Mutation	SNV	C	A	A	POTEH	c.174G>T	P.S58S
XH_P05	22	16287713	16287713	Missense_Mutation	SNV	C	A	A	POTEH	c.173G>T	P.R58M
XH_P05	3	99513635	99513635	Missense_Mutation	SNV	C	A	A	COL8A1	c.890C>A	P.P297Q
XH_P05	4	6302503	6302503	Silent	SNV	C	T	T	WFS1	c.981C>T	P.L327L
XH_P05	4	72316208	72316208	Missense_Mutation	SNV	G	T	T	SLC4A4	c.1156G>G	P.D386Y
XH_P05	5	1210580	1210580	Missense_Mutation	SNV	C	A	A	SLC6A19	c.365C>A	P.S122Y
XH_P05	5	149375561	149375561	Frame_Shift_Del	INDEL	A	-	-	TIGD6	c.351delIT	P.Q118fs
XH_P05	5	31302318	31302318	Missense_Mutation	SNV	G	T	T	CDH6	c.912G>T	P.E304D
XH_P05	5	73165977	73165977	Missense_Mutation	SNV	C	T	T	ARHGEF28	c.2509C>T	P.P837S
XH_P05	5	82834438	82834438	Silent	SNV	G	A	A	VCAN	c.5616G>A	P.P1872P
XH_P05	6	117046997	117046997	Missense_Mutation	SNV	G	T	T	KPNA5	c.1083G>T	P.W361C
XH_P05	6	117923259	117923259	Missense_Mutation	SNV	C	T	T	GOPC	c.193G>A	P.E65K
XH_P05	6	152651958	152651958	Missense_Mutation	SNV	G	T	T	SYNE1	c.13649C>A	P.T4550K
XH_P05	6	32609940	32609940	Missense_Mutation	SNV	A	T	T	HLA-DQA1	c.523A>T	P.S175C
XH_P05	7	149467533	149467533	Nonsense_Mutation	SNV	G	T	T	ZNFX8	c.147C>A	P.C49*
XH_P05	7	87080969	87080969	Silent	SNV	A	G	G	ABC84	c.678T>C	P.I26I
XH_P05	8	116616447	116616447	Silent	SNV	T	A	A	TRPS1	c.1722A>T	P.G574G
XH_P05	8	19679938	19679938	Splice_Site	SNV	G	A	A	INTS10	c.442-12G>A	
XH_P05	8	9437709	9437709	Missense_Mutation	SNV	G	A	A	TNKS	c.714G>A	P.M238I
XH_P05	9	135073987	135073987	Missense_Mutation	SNV	T	C	C	NTNG2	c.848T>C	P.V283A
XH_P05	9	37126350	37126350	Missense_Mutation	SNV	G	T	T	ZCCHC7	c.21G>T	P.E7D
XH_P05	X	150869486	150869486	Missense_Mutation	SNV	A	G	G	PRRG3	c.677A>G	P.N226S
XH_P05	X	18220019	18220019	Nonsense_Mutation	SNV	C	A	A	BEND2	c.949G>T	P.E317*
XH_P05	X	46917987	46917987	Missense_Mutation	SNV	C	A	A	JADE3	c.1980C>A	P.N600K
XH_P05	X	9673133	9673133	Silent	SNV	C	G	G	TBL1X	c.1215C>G	P.V405V
XH_P06	1	203154322	203154322	Missense_Mutation	SNV	G	A	A	CHI3L1	c.247C>T	P.L83F
XH_P06	1	237774081	237774081	Missense_Mutation	SNV	C	T	T	RVR2	c.4703C>T	P.A1568V
XH_P06	10	123279556	123279556	Missense_Mutation	INDEL	ATGTGGGGCC	-	-	FGFR2	ATGCCAGCCCCC	Y281_K292del
XH_P06	11	103866971	103866971	Missense_Mutation	SNV	T	A	A	PDGFD	c.332A>T	P.Y111F
XH_P06	11	60668333	60668333	Silent	SNV	G	A	A	PRPF19	c.711C>T	P.I237I
XH_P06	11	62489400	62489400	Silent	SNV	C	G	G	HNRNPUL2	c.1374G>C	P.V458V
XH_P06	11	970204	970204	Missense_Mutation	SNV	T	A	A	AP2A	c.172T>A	P.Y58N
XH_P06	13	37393812	37393812	Silent	SNV	T	C	C	RFXAP	c.318T>C	P.A106A
XH_P06	13	50587139	50587139	Missense_Mutation	SNV	A	G	G	TRIM13	c.1072A>G	P.S538G
XH_P06	13	52598520	52598520	Silent	SNV	T	C	C	ALG11	c.654T>C	P.N218N
XH_P06	14	24040526	24040526	Nonsense_Mutation	SNV	G	A	A	JPH4	c.1414C>T	P.R472*
XH_P06	17	7605866	7605866	Missense_Mutation	SNV	G	A	A	WRAP53	c.1160G>A	P.R387H
XH_P06	19	39898700	39898700	Missense_Mutation	SNV	G	T	T	ZFP36	c.360G>T	P.E120D
XH_P06	19	56320517	56320517	Missense_Mutation	SNV	C	A	A	NLRP11	c.1162G>T	P.D388Y
XH_P06	20	34828358	34828358	Missense_Mutation	SNV	G	A	A	AAR2	c.568G>A	P.E190K
XH_P06	3	52441246	52441246	Missense_Mutation	SNV	G	A	A	BAP1	c.524C>T	P.P175L
XH_P06	4	70462079	70462079	Missense_Mutation	SNV	C	G	G	UGT2A1	c.912G>C	P.Q304H
XH_P06	5	140744110	140744110	Missense_Mutation	SNV	G	T	T	PCDHGA5	c.213G>T	P.R71S
XH_P06	5	140779426	140779426	Missense_Mutation	SNV	G	A	A	PCDHGB5	c.1732G>A	P.A578T
XH_P06	6	20124649	20124649	Silent	SNV	T	C	C	MBOAT1	c.897A>G	P.A299A
XH_P06	6	55684654	55684654	Splice_Site	SNV	A	G	G	BMP5	c.491-9T>C	
XH_P06	6	65622479	65622479	Missense_Mutation	SNV	G	C	C	EYS	c.2539C>G	P.H847D
XH_P06	9	135779187	135779187	Nonsense_Mutation	SNV	C	A	A	TSC1	c.2059G>T	P.E687*
XH_P06	9	139744560	139744560	Frame_Shift_Ins	INDEL	-	AG	AG	PHPT1	.258_259dupG	P.K87fs
XH_P06	X	109697368	109697368	Missense_Mutation	SNV	C	A	A	RGAG1	c.3523C>A	P.Q1175K
XH_P06	X	125685479	125685479	Silent	SNV	G	A	A	DCAF12L1	c.1113C>T	P.S371S
XH_P06	X	83389787	83389787	Splice_Site	SNV	T	C	C	RPS6KA6	c.646+3A>G	
XH_P07	1	16474948	16474948	Frame_Shift_Ins	INDEL	-	AGTG	AGTG	EPHA2	.747_748insCAC	P.D250fs

XH_P07	1	24447730	24447730	Silent	SNV	C	T	T	IL22RA1	c.1290G>A	P.Q430Q
XH_P07	1	35580033	35580033	Missense_Mutation	SNV	G	T	T	ZMYM1	c.2602G>T	P.V868L
XH_P07	1	8074115	8074115	Frame_Shift_Del	INDEL	G	-	-	ERRF1	c.544delC	P.L182fs
XH_P07	10	118306822	118306822	Nonsense_Mutation	SNV	C	A	A	PNLP	c.63C>A	P.Y21*
XH_P07	11	32635525	32635525	Missense_Mutation	SNV	T	C	C	CCDC73	c.2339A>G	P.N780S
XH_P07	11	61498848	61498848	Silent	SNV	C	T	T	DAGLA	c.909C>T	P.Y303Y
XH_P07	13	28124466	28124474	Frame_Shift_Del	INDEL	TCACCTTAA	-	-	LNK2	1937+4delTTAA	P.L645fs
XH_P07	16	88706365	88706365	Missense_Mutation	SNV	G	T	T	IL17C	c.479G>T	P.R160L
XH_P07	17	76704300	76704300	Frame_Shift_Del	INDEL	T	-	-	CYTH1	c.149delA	P.N50fs
XH_P07	17	76993313	76993313	Missense_Mutation	SNV	T	C	C	CANT1	c.392A>G	P.K131R
XH_P07	17	78617539	78617539	Missense_Mutation	SNV	A	T	T	RPTOR	c.277A>T	P.M93L
XH_P07	19	54672371	54672371	Silent	SNV	G	A	A	TMC4	c.496C>T	P.L166L
XH_P07	19	8167683	8167683	Missense_Mutation	SNV	T	C	C	FBN3	c.5014A>G	P.K1672E
XH_P07	2	166535267	166535267	Silent	SNV	A	G	G	CSRN3	c.762A>G	P.A254A
XH_P07	2	1926644	1926644	Silent	SNV	G	A	A	MYT1L	c.897C>T	P.Y299Y
XH_P07	2	209113113	209113113	Missense_Mutation	SNV	G	A	A	IDH1	c.394C>T	P.R132C
XH_P07	3	13417789	13417789	Splice_Site	SNV	G	C	C	NUP210	c.1293+2C>G	
XH_P07	3	183962425	183962425	Silent	SNV	C	A	A	ALG3	c.546G>T	P.G182G
XH_P07	3	52588739	52588739	Splice_Site	INDEL	C	-	-	PBRM1	c.4288+1delG	
XH_P07	6	36070442	36070442	Missense_Mutation	SNV	A	C	C	MAPK14	c.857A>C	P.Y286S
XH_P07	6	53387336	53387336	Splice_Site	INDEL	-	A	A	GLCL	c.151-12dupT	
XH_P07	7	45701692	45701692	Missense_Mutation	SNV	C	T	T	ADCY1	c.809C>T	P.P270L
XH_P07	7	73449745	73449745	Splice_Site	SNV	G	T	T	ELN	c.133+1G>T	
XH_P07	7	74105444	74105444	Splice_Site	INDEL	G	-	-	GTF2I	c.238+1delG	
XH_P07	9	32974548	32974548	Missense_Mutation	SNV	A	T	T	APTX	c.824T>A	P.L275H
XH_P07	X	107400378	107400378	Missense_Mutation	SNV	C	A	A	COL4A6	c.4976G>T	P.C1659F
XH_P08	1	10238810	10238810	Nonsense_Mutation	SNV	G	T	T	UBE4B	c.3634G>T	P.E1212*
XH_P08	1	115256529	115256529	Missense_Mutation	SNV	T	C	C	NRAS	c.182A>G	P.Q61R
XH_P08	1	150199097	150199097	Missense_Mutation	SNV	T	A	A	ANP32E	c.401A>T	P.E134V
XH_P08	1	247013661	247013661	Missense_Mutation	SNV	C	T	T	AHCTF1	c.5647G>A	P.E1883K
XH_P08	1	27100927	27100927	Missense_Mutation	SNV	G	T	T	ARID1A	c.4209G>T	P.Q1403H
XH_P08	10	14885378	14885378	Missense_Mutation	SNV	C	T	T	HSPA14	c.230C>T	P.S77L
XH_P08	11	10792125	10792125	Missense_Mutation	SNV	A	G	G	CTR9	c.2318A>G	P.K773R
XH_P08	11	726294	726294	Splice_Site	INDEL	-	C	C	EP8L2	c.1754-5dupC	
XH_P08	12	416963	416963	Missense_Mutation	SNV	G	A	A	KDM5A	c.3587C>T	P.S1196F
XH_P08	14	24601533	24601533	Missense_Mutation	SNV	G	A	A	FITM1	c.380G>A	P.R127Q
XH_P08	16	2162340	2162340	Splice_Site	SNV	C	A	A	PKD1	c.3295+1G>T	
XH_P08	16	30724886	30724886	Missense_Mutation	SNV	A	T	T	SRCAP	c.2347A>T	P.M783L
XH_P08	18	52928759	52928759	Missense_Mutation	SNV	T	C	C	TCF4	c.928A>G	P.R310G
XH_P08	19	15852665	15852665	Missense_Mutation	SNV	G	A	A	OR10H3	c.463G>A	P.V155I
XH_P08	2	158115066	158115066	Missense_Mutation	SNV	G	T	T	GALNT5	c.472G>T	P.G158W
XH_P08	2	1652604	1652604	Missense_Mutation	SNV	C	T	T	PXDN	c.2948G>A	P.G983D
XH_P08	2	29234310	29234310	Splice_Site	SNV	G	A	A	FAM179A	c.831-11G>A	
XH_P08	20	45242138	45242138	Missense_Mutation	SNV	G	A	A	SLC13A3	c.197C>T	P.A66V
XH_P08	3	121207626	121207626	Silent	SNV	C	T	T	POLQ	c.4152G>A	P.A1384A
XH_P08	3	140678331	140678331	Missense_Mutation	SNV	G	T	T	SLC25A36	c.233G>T	P.R78L
XH_P08	4	25418083	25418083	Missense_Mutation	SNV	T	G	G	ANAPC4	c.1941T>G	P.D647E
XH_P08	5	67576346	67576346	Splice_Site	SNV	A	T	T	PIK3R1	c.635-10A>T	
XH_P08	6	143081215	143081215	Silent	SNV	T	C	C	HIVEP2	c.6210A>G	P.L2070L
XH_P08	7	116380114	116380114	Nonsense_Mutation	SNV	C	A	A	MET	c.1503C>A	P.Y501*
XH_P08	8	145739921	145739921	Splice_Site	SNV	G	A	A	RECQL4	c.1621-12C>T	
XH_P08	8	55538282	55538282	Missense_Mutation	SNV	C	A	A	RP1	c.1840C>A	P.H614N
XH_P08	9	2039777	2039777	Missense_Mutation	INDEL	CAGCAG	-	-	SMARCA2	02_707delGCAAGC.Q235_Q236del	
XH_P08	X	75649221	75649221	Missense_Mutation	SNV	G	A	A	MAGEE1	c.898G>A	P.A300T
XH_P08	X	79932611	79932611	Missense_Mutation	SNV	C	T	T	BRWD3	c.4906G>A	P.V1636I
XH_P09	1	115218197	115218197	Missense_Mutation	SNV	C	T	T	AMPD1	c.1732G>A	P.A578T
XH_P09	1	16458604	16458637	Frame_Shift_Del	INDEL	AGACACCTTC	-	-	EPHA2	TGGTCTGCAAGC	P.N750fs
XH_P09	10	95518532	95518532	Silent	SNV	T	C	C	LG1	c.231T>C	P.S77S
XH_P09	11	34680381	34680381	Missense_Mutation	SNV	A	G	G	EHF	c.737A>G	P.Y246C
XH_P09	13	103301837	103301837	Splice_Site	INDEL	G	-	-	TPP2	c.2952+1delG	
XH_P09	13	61985922	61985922	Silent	SNV	G	A	A	PCDH20	c.2310C>T	P.V770V
XH_P09	14	21359882	21359882	Missense_Mutation	SNV	C	T	T	RNASE3	c.37C>T	P.L13F
XH_P09	14	36988440	36988440	Nonsense_Mutation	SNV	G	T	T	NKX2-1	c.123C>A	P.Y41*
XH_P09	14	74407706	74407706	Silent	SNV	G	A	A	FAM161B	c.1512C>T	P.S504S
XH_P09	17	26732433	26732433	Silent	SNV	G	A	A	SLC46A1	c.282C>T	P.F94F
XH_P09	17	42949912	42949912	Missense_Mutation	SNV	A	G	G	EFTUD2	c.791T>C	P.I264T
XH_P09	17	7906389	7906389	Silent	SNV	G	A	A	GUCY2D	c.24G>A	P.A8A
XH_P09	17	80210924	80210924	Missense_Mutation	SNV	C	T	T	CSNK1D	c.533G>A	P.R178Q
XH_P09	18	67614640	67614640	Nonsense_Mutation	SNV	C	A	A	CD226	c.3G>T	P.M17
XH_P09	19	6678196	6678196	Missense_Mutation	SNV	C	A	A	C3	c.4817G>T	P.G1606V
XH_P09	19	7976189	7976189	Missense_Mutation	SNV	G	A	A	MAP2K7	c.958G>A	P.D320N
XH_P09	2	138413101	138413101	Missense_Mutation	SNV	C	T	T	THSD7B	c.3976C>T	P.R1326C
XH_P09	2	15618381	15618381	Missense_Mutation	SNV	C	G	G	NBAS	c.1116G>C	P.R372S
XH_P09	21	19713841	19713841	Missense_Mutation	SNV	T	C	C	TMPPRSS15	c.1453A>G	P.K485E
XH_P09	22	21340177	21340177	Missense_Mutation	SNV	C	A	A	LZTR1	c.311C>A	P.S104Y
XH_P09	3	10357042	10357042	Missense_Mutation	SNV	G	A	A	SEC13	c.265C>T	P.R89C
XH_P09	3	156396253	156396253	Frame_Shift_Del	INDEL	A	-	-	TIPARP	c.767delA	P.D256fs
XH_P09	3	49739838	49739838	Splice_Site	SNV	G	C	C	RNF123	c.1629G>C	P.G543G
XH_P09	3	66436487	66436487	Silent	SNV	G	A	A	LRIG1	c.1707C>T	P.F569F
XH_P09	5	37057308	37057308	Silent	SNV	C	A	A	NIPBL	c.7284C>A	P.L2428L
XH_P09	6	105609626	105609626	Silent	SNV	G	T	T	POPD3C	c.159C>A	P.V53V
XH_P09	6	129465137	129465137	Missense_Mutation	SNV	G	A	A	LAMA2	c.731G>A	P.R244K
XH_P09	6	131211522	131211522	Silent	SNV	C	T	T	EPB41L2	c.1572G>A	P.Q524Q
XH_P09	6	151130273	151130273	Frame_Shift_Ins	INDEL	-	CCAGA	CCAGA	PLEKHG1	48_952dupAGAG	P.L318fs
XH_P09	6	34857302	34857302	Frame_Shift_Ins	INDEL	-	GGCGGC	GGCGGC	ANKS1A	83_138dupGGCG	P.G45_G46dup
XH_P09	6	3751754	3751754	Silent	SNV	C	A	A	PXDC1	c.12G>T	P.A4A
XH_P09	6	47846407	47846407	Missense_Mutation	SNV	C	T	T	PTCHD4	c.2173G>A	P.A725T
XH_P09	6	6152165	6152165	Silent	SNV	T	C	C	F13A1	c.1926A>G	P.V642V
XH_P09	7	117365321	117365321	Splice_Site	SNV	G	A	A	CTTNBP2	c.4056-10C>T	
XH_P09	8	113392682	113392682	Missense_Mutation	SNV	G	T	T	CSMD3	c.5723C>A	P.T1908K
XH_P09	8	133899201	133899201	Silent	SNV	A	G	G	TG	c.1584A>G	P.S528S
XH_P09	8	145154262	145154262	Missense_Mutation	SNV	C	G	G	SHARPIN	c.840G>C	P.E280D
XH_P09	X	38262901	38262901	Missense_Mutation	SNV	C	T	T	OTC	c.571C>T	P.L191F
XH_P10	1	110085668	110085668	Missense_Mutation	SNV	G	C	C	GPR61	c.24G>C	P.Q8H
XH_P10	1	115456674	115456674	Splice_Site	SNV	T	A	A	SYCP1	c.1718+8T>A	
XH_P10	1	120384101	120384101	Missense_Mutation	SNV	T	C	C	NBPF7	c.461A>G	P.D154G
XH_P10	1	152276716	152276716	Nonsense_Mutation	SNV	G	T	T	FLG	c.10646C>A	P.S5349*
XH_P10	1	153614832	153614832	Missense_Mutation	SNV	A	T	T	CHTOP	c.333A>T	P.R111S

XH_P10	1	161693401	161693401	Silent	SNV	T	A	A	FCRLB	c.297T>A	P.S995
XH_P10	1	182636106	182636106	Missense_Mutation	SNV	T	A	A	RG58	c.29A>T	P.N10I
XH_P10	1	184701982	184701982	Missense_Mutation	SNV	G	C	C	EDEM3	c.601C>G	P.P201A
XH_P10	1	201983028	201983028	Missense_Mutation	SNV	A	T	T	ELF3	c.877A>T	P.M293L
XH_P10	1	205132039	205132039	Splice_Site	SNV	A	G	G	DSTYK	c.1641+12T>C	
XH_P10	1	215802332	215802332	Missense_Mutation	SNV	T	C	C	USH2A	c.15343A>G	P.I5115V
XH_P10	1	223284802	223284802	Missense_Mutation	SNV	A	T	T	TLR5	c.1572T>A	P.H524Q
XH_P10	1	227170471	227170471	Splice_Site	SNV	A	G	G	COQ8A	c.939+7A>G	
XH_P10	1	236371346	236371346	Splice_Site	SNV	T	C	C	GPR137B	c.1092-4T>C	
XH_P10	1	236966910	236966910	Missense_Mutation	SNV	A	T	T	MTR	c.217A>T	P.T73S
XH_P10	1	248112618	248112618	Silent	SNV	C	A	A	OR2L8	c.459C>A	P.I153I
XH_P10	1	2529644	2529644	Splice_Site	SNV	A	G	G	MMEL1	c.1272+2T>C	
XH_P10	1	4832433	4832433	Silent	SNV	G	A	A	AJAP1	c.1011G>A	P.S337S
XH_P10	1	89426907	89426907	Missense_Mutation	SNV	T	C	C	KYAT3	c.730A>G	P.I244V
XH_P10	1	9323763	9323763	Missense_Mutation	SNV	A	G	G	H6PD	c.1244A>G	P.H415R
XH_P10	10	103899315	103899315	Silent	SNV	G	T	T	PPRC1	c.1050G>T	P.G350G
XH_P10	10	120445656	120445656	Missense_Mutation	SNV	G	A	A	CACUL1	c.1094C>T	P.S365F
XH_P10	10	15614215	15614215	Missense_Mutation	SNV	T	A	A	ITGA8	c.2587A>T	P.I863L
XH_P10	10	16960680	16960680	Missense_Mutation	SNV	A	G	G	CUBN	c.6941T>C	P.L2314S
XH_P10	10	17087135	17087135	Silent	SNV	G	A	A	CUBN	c.3543C>T	P.Y1181Y
XH_P10	11	113092057	113092057	Splice_Site	SNV	A	G	G	NCAM1	c.1089+10A>G	
XH_P10	11	14515222	14515222	Silent	SNV	T	G	G	COPB1	c.457A>C	P.R153R
XH_P10	11	57995931	57995931	Silent	SNV	G	A	A	OR10Q1	c.417C>T	P.I139I
XH_P10	11	68696655	68696655	Silent	SNV	G	T	T	IGHMBP2	c.1065G>T	P.A355A
XH_P10	11	8476297	8476297	Missense_Mutation	SNV	G	C	C	STK33	c.657C>G	P.N219K
XH_P10	11	94704658	94704658	Splice_Site	SNV	T	C	C	CWC15	c.132-7A>G	
XH_P10	12	119594505	119594505	Missense_Mutation	SNV	C	T	T	SRRM4	c.1738C>T	P.R580C
XH_P10	12	120574327	120574327	Silent	SNV	T	C	C	GCN1	c.6987A>G	P.T2329T
XH_P10	12	124887114	124887114	Splice_Site	SNV	G	C	C	NCOR2	c.1480-7C>G	
XH_P10	12	133254232	133254232	Missense_Mutation	SNV	T	A	A	POLE	c.652A>T	P.I218F
XH_P10	12	14591213	14591213	Splice_Site	SNV	G	A	A	ATF7IP	c.1926+12G>A	
XH_P10	12	20893226	20893226	Missense_Mutation	SNV	T	C	C	SLCO1C1	c.1303T>C	P.Y435H
XH_P10	12	250375	250375	Silent	SNV	C	A	A	IQSEC3	c.2077C>A	P.R693R
XH_P10	12	48737351	48737351	Frame_Shift_Del	INDEL	G	-	-	ZNFX61	c.680delC	P.P227fs
XH_P10	12	54932678	54932678	Missense_Mutation	SNV	T	A	A	NCKAP1L	c.3044T>A	P.Y1015D
XH_P10	12	5674825	5674825	Nonsense_Mutation	SNV	T	A	A	ANO2	c.2641A>T	P.K881*
XH_P10	12	62932235	62932235	Missense_Mutation	SNV	C	T	T	MON2	c.2314C>T	P.L772F
XH_P10	12	6946165	6946165	Missense_Mutation	SNV	G	A	A	P3H3	c.1472G>A	P.G491E
XH_P10	12	69759596	69759596	Missense_Mutation	SNV	A	G	G	YEAT54	c.265A>G	P.T89A
XH_P10	13	33333804	33333804	Missense_Mutation	SNV	G	C	C	PD55B	c.3348G>C	P.M1116I
XH_P10	13	38213401	38213401	Missense_Mutation	SNV	T	A	A	TRPC4	c.2115A>T	P.Q705H
XH_P10	14	105174894	105174894	Silent	SNV	G	T	T	INF2	c.1857G>T	P.V619V
XH_P10	14	105615377	105615377	Silent	SNV	T	A	A	JAG2	c.1803A>T	P.A601A
XH_P10	14	31819042	31819042	Silent	SNV	T	A	A	HEATR5A	c.2661A>T	P.V887V
XH_P10	14	55462343	55462343	Silent	SNV	T	A	A	WDHD1	c.762A>T	P.L254L
XH_P10	14	64194406	64194406	Missense_Mutation	SNV	G	A	A	SGPP1	c.257C>T	P.P86L
XH_P10	14	78365505	78365505	Missense_Mutation	SNV	A	C	C	ADCK1	c.441A>C	P.E147D
XH_P10	14	94756345	94756345	Missense_Mutation	SNV	G	A	A	SERPINA10	c.586C>T	P.R196C
XH_P10	15	31362097	31362097	Missense_Mutation	SNV	T	C	C	TRPM1	c.350A>G	P.Q117R
XH_P10	15	43269043	43269043	Missense_Mutation	SNV	G	A	A	UBR1	c.4241C>T	P.P1414L
XH_P10	15	51687131	51687131	Missense_Mutation	SNV	G	C	C	GLDN	c.641G>C	P.G214A
XH_P10	15	64015465	64015465	Missense_Mutation	SNV	C	G	G	HERC1	c.3658G>C	P.V1220L
XH_P10	15	68599767	68599767	Frame_Shift_Del	INDEL	G	-	-	ITGA11	c.3300delC	P.M1101fs
XH_P10	15	73075906	73075906	Missense_Mutation	SNV	G	A	A	ADPGK	c.127C>T	P.P43S
XH_P10	15	74327873	74327873	Missense_Mutation	SNV	G	A	A	PML	c.2071G>A	P.V691I
XH_P10	15	92459396	92459396	Frame_Shift_Del	INDEL	G	-	-	SLCO3A1	c.356delG	P.G119fs
XH_P10	16	25251928	25251928	Nonsense_Mutation	SNV	T	A	A	ZKSCAN2	c.2113A>T	P.K705*
XH_P10	16	31447482	31447482	Missense_Mutation	SNV	T	A	A	ZNFX843	c.689A>T	P.Q230L
XH_P10	16	47497784	47497784	Splice_Site	SNV	A	G	G	PHKB	c.-57-9A>G	
XH_P10	16	57690174	57690174	Missense_Mutation	SNV	G	T	T	ADGRG1	c.1054G>T	P.D352Y
XH_P10	16	62055223	62055223	Missense_Mutation	SNV	T	A	A	CNDH8	c.85A>T	P.M29L
XH_P10	16	84188387	84188387	Silent	SNV	G	A	A	DNAAF1	c.558G>A	P.K186K
XH_P10	17	10210383	10210383	Splice_Site	SNV	T	A	A	MYH13	c.5170-2A>T	
XH_P10	17	11845672	11845672	Missense_Mutation	SNV	T	A	A	DNAH9	c.12713T>A	P.I4238N
XH_P10	17	29622292	29622292	Missense_Mutation	SNV	A	G	G	OMG	c.1058T>C	P.L353P
XH_P10	17	35736272	35736272	Silent	SNV	C	T	T	C1orf78	c.343C>T	P.L115L
XH_P10	17	42432372	42432372	Missense_Mutation	SNV	T	A	A	FAM171A2	c.1210A>T	P.S404C
XH_P10	17	45043999	45043999	Missense_Mutation	SNV	G	T	T	GOSR2	c.683G>T	P.S228I
XH_P10	17	56296840	56296840	Silent	SNV	G	A	A	MKS1	c.33C>T	P.R11R
XH_P10	17	62499104	62499104	Missense_Mutation	SNV	C	T	T	DDX5	c.923G>A	P.S308N
XH_P10	17	66347754	66347754	Missense_Mutation	SNV	A	T	T	ARSG	c.493A>T	P.M165L
XH_P10	17	7578176	7578176	Splice_Site	SNV	C	T	T	TP53	c.672+1G>A	
XH_P10	17	76498683	76498683	Missense_Mutation	SNV	T	C	C	DNAH17	c.5180A>G	P.N1727S
XH_P10	17	79254487	79254487	Missense_Mutation	SNV	A	C	C	SLC38A10	c.548T>G	P.L183R
XH_P10	17	79254488	79254488	Missense_Mutation	SNV	G	C	C	SLC38A10	c.547C>G	P.L183V
XH_P10	18	10770301	10770301	Missense_Mutation	SNV	T	A	A	PIEZO2	c.2716A>T	P.R906W
XH_P10	18	30257200	30257200	Missense_Mutation	SNV	C	A	A	KLHL14	c.1682G>T	P.S561I
XH_P10	18	47390570	47390570	Missense_Mutation	SNV	G	C	C	MYO5B	c.3784C>G	P.L1262V
XH_P10	18	48255980	48255980	Missense_Mutation	SNV	C	G	G	MAPK4	c.887C>G	P.A296G
XH_P10	18	67741193	67741193	Silent	SNV	A	T	T	RTTN	c.1866T>A	P.S622S
XH_P10	18	77728085	77728085	Splice_Site	SNV	G	T	T	HSBP1L1	c.119-4G>T	
XH_P10	19	10397892	10397892	Silent	SNV	T	C	C	ICAM4	c.204T>C	P.N68N
XH_P10	19	12978664	12978664	Silent	SNV	C	T	T	MAST1	c.2439C>T	P.D813D
XH_P10	19	16003156	16003156	Missense_Mutation	SNV	T	A	A	CYP4F2	c.488A>T	P.Y163F
XH_P10	19	35434352	35434352	Missense_Mutation	SNV	A	G	G	ZNFX30	c.485A>G	P.H162R
XH_P10	19	36505084	36505084	Missense_Mutation	SNV	C	A	A	ALKBH6	c.52G>T	P.G18C
XH_P10	19	36507099	36507099	Nonsense_Mutation	SNV	G	T	T	CLIP3	c.1605C>A	P.C535*
XH_P10	19	3831759	3831759	Missense_Mutation	SNV	T	A	A	ZFR2	c.497A>T	P.Y166F
XH_P10	19	4409468	4409468	Silent	SNV	T	C	C	CHAF1A	c.672T>C	P.S224S
XH_P10	19	45667416	45667416	Splice_Site	SNV	C	A	A	TRAPPC6A	c.354+6G>T	
XH_P10	19	50209346	50209346	Missense_Mutation	SNV	T	G	G	CPT1C	c.1112T>G	P.L371R
XH_P10	19	55340876	55340876	Missense_Mutation	SNV	T	A	A	KIR3DL1	c.1061T>A	P.L354H
XH_P10	19	56203380	56203380	Silent	SNV	A	T	T	EPN1	c.1281A>T	P.A427A
XH_P10	19	58500056	58500056	Missense_Mutation	SNV	A	T	T	ZNFX606	c.211T>A	P.F71I
XH_P10	2	122106163	122106163	Silent	SNV	C	T	T	CLASP1	c.4161G>A	P.Q1387Q
XH_P10	2	128522477	128522477	Missense_Mutation	SNV	T	A	A	WDR33	c.551A>T	P.Y184F
XH_P10	2	157186393	157186393	Silent	SNV	T	C	C	NR4A2	c.306A>G	P.Q102Q
XH_P10	2	175292572	175292572	Missense_Mutation	SNV	A	C	C	SCRN3	c.1203A>C	P.K401N

XH_P10	2	196825613	196825613	Silent	SNV	A	T	T	DNAH7	c.2262T>A	P.P754P
XH_P10	2	20840859	20840859	Missense_Mutation	SNV	G	C	C	HS1BP3	c.280C>G	P.P94A
XH_P10	2	238267714	238267714	Silent	SNV	A	T	T	COL6A3	c.6372T>A	P.P2124P
XH_P10	2	39931321	39931321	Missense_Mutation	SNV	G	C	C	TMEM178A	c.501G>C	P.E167D
XH_P10	2	46739679	46739679	Missense_Mutation	SNV	C	G	G	ATP6V1E2	c.172G>C	P.E58Q
XH_P10	2	61605547	61605547	Missense_Mutation	SNV	T	C	C	USP34	c.1027A>G	P.T343A
XH_P10	2	98906978	98906978	Missense_Mutation	SNV	A	T	T	VWA3B	c.3050A>T	P.Q1017L
XH_P10	20	20505548	20505548	Splice_Site	SNV	T	A	A	RALGAP2	c.3694-6A>T	
XH_P10	20	36784376	36784376	Silent	SNV	C	A	A	TGM2	c.306G>T	P.L102L
XH_P10	20	57599042	57599042	Missense_Mutation	SNV	T	A	A	TUBB1	c.560T>A	P.L187Q
XH_P10	21	11049611	11049611	Missense_Mutation	SNV	A	G	G	BAGE2	c.290T>C	P.M97T
XH_P10	22	18095623	18095623	Silent	SNV	A	G	G	ATP6V1E1	c.165T>C	P.N55N
XH_P10	22	18387485	18387485	Missense_Mutation	SNV	G	C	C	MICAL3	c.385C>G	P.L129V
XH_P10	22	19484972	19484972	Splice_Site	SNV	T	C	C	CDC45	c.749+2T>C	
XH_P10	22	19484974	19484974	Splice_Site	SNV	C	T	T	CDC45	c.749+4C>T	
XH_P10	22	33245528	33245528	Splice_Site	INDEL	A	-	-	TIMP3	c.204+8delA	
XH_P10	22	36902196	36902196	Missense_Mutation	SNV	C	T	T	FOXRED2	c.274G>A	P.E92K
XH_P10	22	45972975	45972975	Missense_Mutation	SNV	C	G	G	FBLN1	c.1959C>G	P.D653E
XH_P10	3	145791075	145791075	Missense_Mutation	SNV	T	A	A	PLOD2	c.1679A>T	P.Q560L
XH_P10	3	14964552	14964552	Splice_Site	SNV	G	A	A	FGD5	c.3808-1G>A	
XH_P10	3	164786622	164786622	Splice_Site	SNV	T	A	A	SI	c.374-3A>T	
XH_P10	3	180324162	180324162	Splice_Site	SNV	T	C	C	TTC14	c.1049+2T>C	
XH_P10	3	189691695	189691695	Splice_Site	SNV	T	A	A	P3H2	c.1548+3A>T	
XH_P10	3	195497151	195497151	Missense_Mutation	SNV	G	A	A	MUC4	c.11117C>T	P.A3706V
XH_P10	3	38833611	38833611	Missense_Mutation	SNV	T	A	A	SCN10A	c.319A>T	P.T107S
XH_P10	3	42261087	42261087	Missense_Mutation	SNV	A	C	C	TRAK1	c.2065A>C	P.S689R
XH_P10	3	44402962	44402962	Missense_Mutation	SNV	G	A	A	TCAIM	c.271G>A	P.E91K
XH_P10	3	44879864	44879864	Missense_Mutation	SNV	A	T	T	KIF15	c.3269A>T	P.Q1090L
XH_P10	3	58398686	58398686	Silent	SNV	A	G	G	PXK	c.1470A>G	P.T490T
XH_P10	3	71823611	71823611	Silent	SNV	G	A	A	PROK2	c.270C>T	P.S90S
XH_P10	4	38830955	38830955	Frame_Shift_Del	INDEL	G	-	-	TLR6	c.140delC	P.P47fs
XH_P10	4	668024	668024	Missense_Mutation	SNV	C	T	T	ATP5I	c.13G>A	P.V5M
XH_P10	4	72994513	72994513	Missense_Mutation	SNV	A	G	G	NPFFR2	c.214A>G	P.I72V
XH_P10	4	80328611	80328611	Silent	SNV	C	A	A	GK2	c.744G>T	P.L248L
XH_P10	5	11199654	11199654	Missense_Mutation	SNV	A	T	T	CTNND2	c.1608T>A	P.D536E
XH_P10	5	113740320	113740320	Silent	SNV	T	C	C	KCNN2	c.768T>C	P.I256I
XH_P10	5	140175455	140175455	Silent	SNV	C	T	T	PCDHA2	c.906C>T	P.I302I
XH_P10	5	140777949	140777949	Silent	SNV	T	A	A	PCDHGB5	c.255T>A	P.L85L
XH_P10	5	156907988	156907988	Missense_Mutation	SNV	C	G	G	ADAM19	c.2726G>C	P.R909T
XH_P10	5	156929868	156929868	Silent	SNV	C	G	G	ADAM19	c.1251G>C	P.R417R
XH_P10	5	23523476	23523476	Splice_Site	SNV	A	G	G	PRDM9	c.950+9A>G	
XH_P10	5	95084136	95084136	Missense_Mutation	SNV	A	T	T	RHOBTB3	c.515A>T	P.Y172F
XH_P10	6	108882753	108882753	Silent	SNV	C	G	G	FOXO3	c.342C>G	P.T114T
XH_P10	6	117700231	117700231	Missense_Mutation	SNV	C	A	A	ROS1	c.2588G>T	P.R863L
XH_P10	6	12125566	12125566	Missense_Mutation	SNV	T	G	G	HIVEP1	c.5538T>G	P.F1846L
XH_P10	6	130497044	130497044	Missense_Mutation	SNV	T	C	C	SAMD3	c.764A>G	P.Q255R
XH_P10	6	132910082	132910082	Missense_Mutation	SNV	T	A	A	TAAR5	c.744A>T	P.R248S
XH_P10	6	161653213	161653213	Silent	SNV	G	A	A	AGPAT4	c.33C>T	P.F111F
XH_P10	6	166720756	166720756	Missense_Mutation	SNV	A	C	C	PRR18	c.875T>G	P.L292R
XH_P10	6	25862217	25862217	Missense_Mutation	SNV	A	G	G	SLC17A3	c.344T>C	P.I115T
XH_P10	6	43030851	43030851	Missense_Mutation	SNV	A	T	T	KLK4	c.455A>T	P.Q152L
XH_P10	6	4999080	4999080	Splice_Site	SNV	A	G	G	RPP40	c.365-5T>C	
XH_P10	6	97001277	97001277	Silent	SNV	A	G	G	UFL1	c.2283A>G	P.Q761Q
XH_P10	6	99365567	99365567	Missense_Mutation	SNV	T	C	C	FBXL4	c.541A>G	P.T181A
XH_P10	7	102016347	102016347	Silent	SNV	A	C	C	LOC100289561	c.93A>C	P.I31I
XH_P10	7	104749493	104749493	Missense_Mutation	SNV	C	G	G	KMT2E	c.3573C>G	P.S1191R
XH_P10	7	107735780	107735780	Missense_Mutation	SNV	A	T	T	LAMB4	c.1363T>A	P.C455S
XH_P10	7	114655782	114655782	Missense_Mutation	SNV	A	T	T	MDFC	c.534A>T	P.E178D
XH_P10	7	129474788	129474788	Missense_Mutation	SNV	T	C	C	UBE2H	c.331A>G	P.M111V
XH_P10	7	143792541	143792541	Nonsense_Mutation	SNV	T	A	A	OR2A12	c.341T>A	P.L114*
XH_P10	7	149506250	149506250	Missense_Mutation	SNV	G	T	T	SSPO	c.9240G>T	P.Q3080H
XH_P10	7	1785003	1785003	Silent	SNV	T	A	A	ELFN1	c.771T>A	P.A257A
XH_P10	7	5372637	5372637	Silent	SNV	C	A	A	TNRC18	c.5763G>T	P.V1921V
XH_P10	7	5983029	5983029	Missense_Mutation	SNV	C	T	T	RSPH10B	c.1684G>A	P.A562T
XH_P10	7	82586052	82586052	Missense_Mutation	SNV	G	C	C	PCLO	c.4217C>G	P.P1406R
XH_P10	7	99688069	99688069	Frame_Shift_Del	INDEL	G	-	-	COPS6	c.387delG	P.P130fs
XH_P10	7	99696202	99696202	Missense_Mutation	SNV	T	C	C	MCMT7	c.191A>G	P.H64R
XH_P10	8	103324475	103324475	Splice_Site	SNV	T	C	C	UBR5	c.2152-2A>G	
XH_P10	8	10465144	10465144	Missense_Mutation	SNV	C	G	G	RP11	c.6464G>C	P.G2155A
XH_P10	8	110452977	110452977	Missense_Mutation	SNV	T	A	A	PKHD1L1	c.3995T>A	P.V1332E
XH_P10	8	110587217	110587217	Missense_Mutation	SNV	T	C	C	SYBU	c.1907A>G	P.Y636C
XH_P10	8	57219372	57219372	Nonsense_Mutation	SNV	A	T	T	SDR16C5	c.573T>A	P.C191*
XH_P10	8	70650421	70650421	Missense_Mutation	SNV	A	G	G	SLC05A1	c.1277T>C	P.V426A
XH_P10	8	9473163	9473163	Missense_Mutation	SNV	C	T	T	TNKS	c.970C>T	P.P324S
XH_P10	9	104432937	104432937	Missense_Mutation	SNV	T	A	A	GRIN3A	c.1757A>T	P.K586M
XH_P10	9	111745457	111745457	Missense_Mutation	SNV	T	C	C	CTNNAL1	c.868A>G	P.I290V
XH_P10	9	111909481	111909481	Splice_Site	SNV	A	T	T	FRRS1L	c.477-12T>A	
XH_P10	9	114820713	114820713	Missense_Mutation	SNV	T	C	C	SUSD1	c.2104A>G	P.N702D
XH_P10	9	131825873	131825873	Missense_Mutation	SNV	G	A	A	MIGA2	c.1133G>A	P.R378Q
XH_P10	9	133235846	133235846	Silent	SNV	C	G	G	HMCN2	c.4131C>G	P.V1377V
XH_P10	9	136131555	136131567	Frame_Shift_Del	INDEL	GCGCATGGA	-	-	ABO	60delTTGTCATG	P.V183fs
XH_P10	9	137694778	137694778	Silent	SNV	T	A	A	COL5A1	c.3051T>A	P.P1017P
XH_P10	9	21971209	21971209	Splice_Site	SNV	T	A	A	CDKN2A	c.151-2A>T	
XH_P10	9	72000810	72000810	Missense_Mutation	SNV	C	A	A	FAM189A2	c.803C>A	P.P268H
XH_P10	9	847135	847135	Missense_Mutation	SNV	C	T	T	DMRT1	c.530C>T	P.A177V
XH_P10	X	117707935	117707935	Missense_Mutation	SNV	C	A	A	DOCK11	c.1343C>A	P.S448Y
XH_P10	X	118679419	118679419	Splice_Site	SNV	T	A	A	Cxorf56	c.137+7A>T	
XH_P10	X	118759344	118759344	Splice_Site	SNV	T	C	C	SEPT6	c.1281-2A>G	
XH_P10	X	14868754	14868754	Missense_Mutation	SNV	C	A	A	FANCB	c.1369G>T	P.V457F
XH_P10	X	152686563	152686563	Missense_Mutation	SNV	A	C	C	ZFP92	c.728A>C	P.K243T
XH_P10	X	153209551	153209551	Missense_Mutation	SNV	A	G	G	RENBP	c.194T>C	P.V65A
XH_P10	X	49075334	49075334	Splice_Site	SNV	T	C	C	CACNA1F	c.2733+7A>G	
XH_P10	X	6452079	6452079	Missense_Mutation	SNV	G	C	C	VCX3A	c.268C>G	P.P90A
XH_P11	1	10327436	10327436	Splice_Site	SNV	A	T	T	KIF1B	c.430-2A>T	
XH_P11	1	103404615	103404615	Silent	SNV	G	C	C	COL11A1	c.3297C>G	P.G1099G
XH_P11	1	108145666	108145666	Splice_Site	SNV	T	A	A	VAV3	c.452+3A>T	
XH_P11	1	11008434	11008434	Silent	SNV	C	T	T	C1orf127	c.1758G>A	P.E586E
XH_P11	1	110466115	110466115	Missense_Mutation	SNV	T	A	A	CSF1	c.872T>A	P.M291K

XH_P11	1	110580561	110580561	Nonsense_Mutation	SNV	A	T	T	STRIP1	c.229A>T	P.K77*
XH_P11	1	110655275	110655275	Missense_Mutation	SNV	A	T	T	UBL4B	c.119A>T	P.Q40L
XH_P11	1	110925532	110925532	Missense_Mutation	SNV	A	T	T	SLC16A4	c.144T>A	P.F48L
XH_P11	1	114184577	114184577	Missense_Mutation	SNV	A	T	T	MAGI3	c.1405A>T	P.T469S
XH_P11	1	118533485	118533485	Missense_Mutation	SNV	T	A	A	SPAG17	c.5520A>T	P.E1840D
XH_P11	1	118596689	118596689	Missense_Mutation	SNV	A	T	T	SPAG17	c.2750T>A	P.I917K
XH_P11	1	120168570	120168570	Missense_Mutation	SNV	G	A	A	ZNFG97	c.154C>T	P.H52Y
XH_P11	1	12032972	12032972	Missense_Mutation	SNV	A	T	T	PLOD1	c.1946A>T	P.P649V
XH_P11	1	12089129	12089129	Missense_Mutation	SNV	A	T	T	MIIP	c.587A>T	P.E196V
XH_P11	1	145304601	145304601	Missense_Mutation	SNV	A	T	T	NBPF10	c.1534A>T	P.I512F
XH_P11	1	147381324	147381324	Missense_Mutation	SNV	A	T	T	GJA8	c.1242A>T	P.R414S
XH_P11	1	152283052	152283052	Missense_Mutation	SNV	C	T	T	FLG	c.4310G>A	P.R1437H
XH_P11	1	153662818	153662818	Missense_Mutation	SNV	T	A	A	NPR1	c.2991T>A	P.D997E
XH_P11	1	158906786	158906786	Missense_Mutation	SNV	T	A	A	PYHIN1	c.86T>A	P.L29Q
XH_P11	1	159023358	159023358	Silent	SNV	A	T	T	IFI16	c.1953A>T	P.I651I
XH_P11	1	161277194	161277194	Missense_Mutation	SNV	T	A	A	MPZ	c.88A>T	P.I30F
XH_P11	1	162731053	162731053	Missense_Mutation	SNV	A	T	T	DDR2	c.908A>T	P.Q303L
XH_P11	1	166987164	166987164	Nonsense_Mutation	SNV	A	T	T	MAEL	c.916A>T	P.K306*
XH_P11	1	167992297	167992297	Splice_Site	SNV	A	T	T	DCAF6	c.1516+12A>T	
XH_P11	1	171763626	171763626	Missense_Mutation	SNV	A	T	T	METTL13	c.1316A>T	P.Q439L
XH_P11	1	176934382	176934382	Splice_Site	SNV	A	C	C	ASTN1	c.1524-9T>G	
XH_P11	1	179815653	179815653	Silent	SNV	G	A	A	TOR1AIP2	c.966C>T	P.S322S
XH_P11	1	179966255	179966255	Silent	SNV	A	C	C	CEP350	c.963A>C	P.S321S
XH_P11	1	186876132	186876132	Splice_Site	SNV	T	A	A	PLA2G4A	c.414T>A	P.V138V
XH_P11	1	192321220	192321220	Missense_Mutation	SNV	T	A	A	RGS21	c.132T>A	P.S44R
XH_P11	1	198713229	198713229	Missense_Mutation	SNV	T	A	A	PTPRC	c.2261T>A	P.F754Y
XH_P11	1	20097951	20097951	Silent	SNV	T	A	A	TMCO4	c.204A>T	P.A68A
XH_P11	1	201054691	201054691	Silent	SNV	C	A	A	CACNA1S	c.1023G>T	P.R341R
XH_P11	1	203144581	203144581	Missense_Mutation	SNV	T	A	A	MYBPH	c.214A>T	P.S72C
XH_P11	1	204985459	204985459	Missense_Mutation	SNV	A	T	T	NFASC	c.3515A>T	P.Q1172L
XH_P11	1	206649519	206649519	Splice_Site	SNV	C	T	T	IKBKE	c.359-5C>T	
XH_P11	1	206772913	206772913	Missense_Mutation	SNV	T	A	A	EIF2D	c.734A>T	P.E245V
XH_P11	1	207134144	207134144	Silent	SNV	T	A	A	FCAMR	c.1077A>T	P.I359I
XH_P11	1	207697162	207697162	Missense_Mutation	SNV	T	G	G	CR1	c.694T>G	P.C232G
XH_P11	1	21903087	21903087	Missense_Mutation	SNV	A	C	C	ALPL	c.1262A>C	P.Y421S
XH_P11	1	223567317	223567317	Missense_Mutation	SNV	A	T	T	CCDC185	c.500A>T	P.Q167L
XH_P11	1	223984215	223984215	Nonsense_Mutation	SNV	T	A	A	TP53BP2	c.2026A>T	P.K676*
XH_P11	1	223986038	223986038	Silent	SNV	G	A	A	TP53BP2	c.1827C>T	P.6709T
XH_P11	1	223991121	223991121	Missense_Mutation	SNV	T	A	A	TP53BP2	c.683A>T	P.Q228L
XH_P11	1	225305581	225305581	Splice_Site	SNV	A	T	T	DNAH14	c.3973-2A>T	
XH_P11	1	225533711	225533711	Nonsense_Mutation	SNV	A	T	T	DNAH14	c.10447A>T	P.K3483*
XH_P11	1	228412198	228412198	Silent	SNV	A	C	C	OBSCN	c.2692A>C	P.R898R
XH_P11	1	228431079	228431079	Missense_Mutation	SNV	A	T	T	OBSCN	c.3125A>T	P.Q1042L
XH_P11	1	228494079	228494079	Missense_Mutation	SNV	A	T	T	OBSCN	c.11666A>T	P.Q3889L
XH_P11	1	22852727	22852727	Silent	SNV	A	T	T	ZBTB40	c.3558A>T	P.T1186T
XH_P11	1	228563859	228563859	Missense_Mutation	SNV	T	A	A	OBSCN	c.22937T>A	P.L7646Q
XH_P11	1	228646135	228646135	Missense_Mutation	SNV	T	A	A	HIST3H2BB	c.305T>A	P.L102Q
XH_P11	1	237550652	237550652	Silent	SNV	A	T	T	RVR2	c.648A>T	P.P216P
XH_P11	1	237789049	237789049	Silent	SNV	A	G	G	RVR2	c.6111A>G	P.T2037T
XH_P11	1	243229377	243229377	Splice_Site	SNV	T	A	A	LINC01347	n.2507A>T	
XH_P11	1	243329015	243329015	Missense_Mutation	SNV	T	A	A	CEP170	c.1953A>T	P.Q651H
XH_P11	1	24448020	24448020	Missense_Mutation	SNV	T	A	A	IL22RA1	c.1000A>T	P.I334F
XH_P11	1	245851517	245851517	Missense_Mutation	SNV	A	T	T	KIF26B	c.5232A>T	P.R1744S
XH_P11	1	246797883	246797883	Missense_Mutation	SNV	A	T	T	CNST	c.812A>T	P.H271L
XH_P11	1	248309085	248309085	Silent	SNV	A	T	T	OR2M5	c.636A>T	P.A212A
XH_P11	1	248343805	248343805	Missense_Mutation	SNV	A	T	T	OR2M2	c.518A>T	P.E173V
XH_P11	1	248636880	248636880	Missense_Mutation	SNV	A	T	T	OR2T3	c.229A>T	P.M77L
XH_P11	1	26526403	26526403	Missense_Mutation	SNV	A	T	T	CATSPER4	c.841A>T	P.I281F
XH_P11	1	26672425	26672425	Missense_Mutation	SNV	C	A	A	AIM1L	c.724G>T	P.V242L
XH_P11	1	26688660	26688660	Missense_Mutation	SNV	A	T	T	ZNFG63	c.1150T>A	P.W384R
XH_P11	1	33060697	33060697	Missense_Mutation	SNV	A	T	T	ZBTB8A	c.866A>T	P.H289L
XH_P11	1	3334551	3334551	Missense_Mutation	SNV	T	A	A	PRDM16	c.2851T>A	P.Y951N
XH_P11	1	3425710	3425710	Missense_Mutation	SNV	T	A	A	MEGF6	c.1457A>T	P.Q486L
XH_P11	1	37325569	37325569	Missense_Mutation	SNV	A	T	T	GRIK3	c.836T>A	P.L279Q
XH_P11	1	40236825	40236825	Missense_Mutation	SNV	T	A	A	OXC2	c.103A>T	P.S35C
XH_P11	1	40756575	40756575	Missense_Mutation	SNV	A	T	T	ZMPSTE24	c.1109A>T	P.K370M
XH_P11	1	44595497	44595497	Missense_Mutation	SNV	T	A	A	KLF17	c.554T>A	P.V185E
XH_P11	1	45469920	45469920	Missense_Mutation	SNV	T	A	A	HECTD3	c.2272A>T	P.T758S
XH_P11	1	4772061	4772061	Missense_Mutation	SNV	T	A	A	AJAP1	c.131T>A	P.L44Q
XH_P11	1	54262715	54262715	Missense_Mutation	SNV	T	A	A	NDC1	c.1205A>T	P.D402V
XH_P11	1	59125755	59125755	Missense_Mutation	SNV	T	C	C	MYSM1	c.2401A>G	P.I801V
XH_P11	1	65858280	65858280	Silent	SNV	A	T	T	DNAJC6	c.1635A>T	P.P545P
XH_P11	1	67313226	67313226	Missense_Mutation	SNV	A	T	T	WDR78	c.1232T>A	P.L411Q
XH_P11	1	67560969	67560969	Silent	SNV	T	A	A	C1orf141	c.552A>T	P.P184P
XH_P11	1	74832999	74832999	Missense_Mutation	SNV	T	A	A	FPGT-TNNI3K	c.1579T>A	P.C527S
XH_P11	1	75108743	75108743	Missense_Mutation	SNV	A	C	C	ERICH3	c.283T>G	P.L95V
XH_P11	1	85583420	85583420	Missense_Mutation	SNV	T	A	A	WDR63	c.1678T>A	P.L560I
XH_P11	1	87045812	87045812	Silent	SNV	A	T	T	CLCA4	c.2544A>T	P.I848I
XH_P11	1	91733321	91733321	Silent	SNV	A	T	T	HFM1	c.3864T>A	P.T1288T
XH_P11	1	92646194	92646194	Missense_Mutation	SNV	A	T	T	KIAA1107	c.1415A>T	P.Q472L
XH_P11	10	100150374	100150374	Missense_Mutation	SNV	C	T	T	PYROXD2	c.1273G>A	P.D425N
XH_P11	10	102056727	102056727	Splice_Site	SNV	T	A	A	PKD2L1	c.1044+10A>T	
XH_P11	10	112581358	112581358	Missense_Mutation	SNV	A	T	T	RBM20	c.2981A>T	P.D994V
XH_P11	10	118364969	118364969	Missense_Mutation	SNV	A	T	T	PNLIPRP1	c.1244A>T	P.K415I
XH_P11	10	121335228	121335228	Silent	SNV	T	A	A	TIAL1	c.1128A>T	P.I376I
XH_P11	10	121411297	121411297	Missense_Mutation	SNV	C	A	A	BAG3	c.110C>A	P.P37H
XH_P11	10	123847226	123847226	Silent	SNV	A	T	T	TACC2	c.5211A>T	P.A1737A
XH_P11	10	129904062	129904062	Silent	SNV	T	A	A	MKI67	c.4962A>T	P.P1654P
XH_P11	10	135015264	135015264	Silent	SNV	A	T	T	KNDCC1	c.3249A>T	P.P1083P
XH_P11	10	24873923	24873923	Silent	SNV	T	A	A	ARHGAP21	c.5295A>T	P.I1765I
XH_P11	10	25284682	25284682	Missense_Mutation	SNV	T	A	A	ENKUR	c.154A>T	P.I52F
XH_P11	10	31810285	31810285	Silent	SNV	A	T	T	ZEB1	c.1974A>T	P.T658T
XH_P11	10	32580144	32580144	Missense_Mutation	SNV	T	A	A	EPC1	c.922A>T	P.S308C
XH_P11	10	34630694	34630694	Missense_Mutation	SNV	T	G	G	PAR3	c.2269A>C	P.I757L
XH_P11	10	43292911	43292911	Missense_Mutation	SNV	G	C	C	BMS1	c.2029G>C	P.E677Q
XH_P11	10	45956744	45956744	Missense_Mutation	SNV	T	A	A	MARCH8	c.358A>T	P.T120S
XH_P11	10	50151412	50151412	Missense_Mutation	SNV	T	A	A	WDFY4	c.7667T>A	P.L2556H
XH_P11	10	51769402	51769402	Missense_Mutation	SNV	A	T	T	AGAP6	c.1517A>T	P.H506L

XH_P11	10	63983070	63983070	Silent	SNV	T	A	A	RTKN2	c.708A>T	P.L236L
XH_P11	10	69750720	69750720	Missense_Mutation	SNV	C	T	T	HERC4	c.1384G>A	P.A462T
XH_P11	10	69991121	69991121	Missense_Mutation	SNV	T	A	A	ATOH7	c.314A>T	P.E105V
XH_P11	10	70141012	70141012	Missense_Mutation	SNV	T	A	A	RUFY2	c.982A>T	P.E328L
XH_P11	10	70863725	70863725	Missense_Mutation	SNV	G	T	T	SRGN	c.326G>T	P.G109V
XH_P11	10	78669774	78669774	Missense_Mutation	SNV	C	T	T	KCNMA1	c.2935G>A	P.A979T
XH_P11	10	78761335	78761335	Missense_Mutation	SNV	T	A	A	KCNMA1	c.2096A>T	P.K699M
XH_P11	10	85992497	85992497	Missense_Mutation	SNV	T	A	A	LRIT1	c.1058A>T	P.E353V
XH_P11	10	88418450	88418450	Splice_Site	SNV	T	A	A	OPN4	c.661+6T>A	
XH_P11	10	90486632	90486632	Silent	SNV	T	C	C	LIPK	c.186T>C	P.Y62Y
XH_P11	10	94230081	94230081	Missense_Mutation	SNV	T	G	G	IDE	c.473A>C	P.K158T
XH_P11	11	102100651	102100651	Missense_Mutation	SNV	A	T	T	YAP1	c.1333A>T	P.S445C
XH_P11	11	1078540	1078540	Missense_Mutation	SNV	T	A	A	MUC2	c.748T>A	P.C250S
XH_P11	11	118038791	118038791	Splice_Site	SNV	A	T	T	SCN2B	c.448+9T>A	
XH_P11	11	118509703	118509703	Nonsense_Mutation	SNV	T	A	A	PHLDB1	c.2630T>A	P.L877*
XH_P11	11	123479435	123479435	Missense_Mutation	SNV	G	T	T	GRAMD1B	c.1174G>T	P.V392L
XH_P11	11	123894400	123894400	Missense_Mutation	SNV	C	G	G	OR10G9	c.681C>G	P.I227M
XH_P11	11	124551301	124551301	Silent	SNV	A	G	G	SPA17	c.171A>G	P.P57P
XH_P11	11	17653625	17653625	Splice_Site	SNV	A	T	T	OTOG	c.6970-10A>T	
XH_P11	11	30358143	30358143	Missense_Mutation	SNV	A	C	C	ARL14EP	c.584A>C	P.Y195S
XH_P11	11	376697	376697	Missense_Mutation	SNV	T	A	A	B4GALNT4	c.1574T>A	P.V525E
XH_P11	11	49974217	49974217	Silent	SNV	A	T	T	OR4C13	c.243A>T	P.T81T
XH_P11	11	55541348	55541348	Silent	SNV	T	A	A	OR5D13	c.435T>A	P.L145L
XH_P11	11	5626603	5626603	Missense_Mutation	SNV	G	C	C	TRIM6	c.640G>C	P.E214Q
XH_P11	11	56467921	56467921	Missense_Mutation	SNV	C	T	T	OR9G9	c.58C>T	P.P20S
XH_P11	11	57099227	57099227	Missense_Mutation	SNV	C	T	T	SSRP1	c.1138G>A	P.A380T
XH_P11	11	5878235	5878235	Missense_Mutation	SNV	A	T	T	OR52E8	c.698T>A	P.L233Q
XH_P11	11	63283171	63283171	Nonsense_Mutation	SNV	C	T	T	LGALS12	c.853C>T	P.Q285*
XH_P11	11	65325201	65325201	Missense_Mutation	SNV	T	A	A	LTBP3	c.230A>T	P.K77M
XH_P11	11	65350003	65350003	Silent	SNV	A	T	T	EHBP1L1	c.1860A>T	P.S620S
XH_P11	11	74952918	74952918	Missense_Mutation	SNV	T	A	A	TPBGL	c.824T>A	P.L275Q
XH_P11	11	75378511	75378511	Missense_Mutation	SNV	T	A	A	MAP6	c.904A>T	P.R302W
XH_P11	11	76371120	76371120	Missense_Mutation	SNV	A	T	T	LRRC32	c.1517T>A	P.L506Q
XH_P11	11	82880256	82880256	Missense_Mutation	SNV	A	T	T	PCF11	c.2879A>T	P.H960L
XH_P11	11	93913103	93913103	Missense_Mutation	SNV	C	T	T	PANX1	c.881C>T	P.T294M
XH_P11	12	101689317	101689317	Silent	SNV	A	T	T	UTP20	c.1311A>T	P.V437V
XH_P11	12	102122917	102122917	Silent	SNV	A	C	C	SYCP3	c.627T>G	P.A209A
XH_P11	12	105519895	105519895	Missense_Mutation	SNV	A	T	T	KIAA1033	c.900A>T	P.E300D
XH_P11	12	108642066	108642066	Silent	SNV	A	T	T	WSCD2	c.1644A>T	P.A548A
XH_P11	12	109858782	109858782	Splice_Site	SNV	A	T	T	MYO1H	c.1550-4A>T	
XH_P11	12	113645809	113645809	Missense_Mutation	SNV	T	A	A	IQCD	c.163A>T	P.I55F
XH_P11	12	117191863	117191863	Nonsense_Mutation	SNV	A	T	T	RNFT2	c.625A>T	P.K209*
XH_P11	12	118610442	118610442	Silent	SNV	T	A	A	TAOK3	c.1719A>T	P.T573T
XH_P11	12	122396931	122396931	Silent	SNV	T	A	A	WDR66	c.2064T>A	P.P688P
XH_P11	12	122409475	122409475	Missense_Mutation	SNV	G	T	T	WDR66	c.2783G>T	P.S928I
XH_P11	12	124332644	124332644	Splice_Site	SNV	T	A	A	DNAH10	c.5595+2T>A	
XH_P11	12	132562031	132562031	Missense_Mutation	SNV	A	T	T	EP400	c.9185A>T	P.Q3062L
XH_P11	12	21196456	21196456	Missense_Mutation	SNV	A	T	T	SLC01B7	c.775A>T	P.N259Y
XH_P11	12	26348644	26348644	Missense_Mutation	SNV	G	T	T	SSPN	c.39G>T	P.Q13H
XH_P11	12	2760891	2760891	Missense_Mutation	SNV	A	T	T	CACNA1C	c.4031A>T	P.E1344V
XH_P11	12	32136405	32136405	Missense_Mutation	SNV	A	T	T	KIAA1551	c.2516A>T	P.K839M
XH_P11	12	40441985	40441985	Missense_Mutation	SNV	T	A	A	SLC2A13	c.584A>T	P.Y195F
XH_P11	12	46322603	46322603	Missense_Mutation	SNV	T	A	A	SCAF11	c.881A>T	P.E294V
XH_P11	12	48962871	48962871	Missense_Mutation	SNV	A	T	T	LALBA	c.286T>A	P.C96S
XH_P11	12	51054047	51054047	Silent	SNV	A	T	T	DIP2B	c.372A>T	P.P124P
XH_P11	12	53201609	53201609	Nonsense_Mutation	SNV	G	A	A	KRT4	c.1165C>T	P.R389*
XH_P11	12	53415595	53415595	Silent	SNV	A	T	T	EIF4B	c.483A>T	P.L161L
XH_P11	12	57593803	57593803	Missense_Mutation	SNV	A	T	T	LRP1	c.10009A>T	P.S337C
XH_P11	12	57602502	57602502	Missense_Mutation	SNV	A	T	T	LRP1	c.12047A>T	P.Y4016F
XH_P11	12	57858966	57858966	Nonsense_Mutation	SNV	T	A	A	GLI1	c.462T>A	P.C154*
XH_P11	12	57873068	57873068	Missense_Mutation	SNV	T	A	A	ARHGAP9	c.122A>T	P.Q41L
XH_P11	12	6554316	6554316	Missense_Mutation	SNV	T	A	A	CD27	c.55T>A	P.S19T
XH_P11	12	69783940	69783940	Missense_Mutation	SNV	A	T	T	YEATS4	c.366A>T	P.E122D
XH_P11	12	70989989	70989989	Missense_Mutation	SNV	A	T	T	PTPRB	c.1098T>A	P.D366E
XH_P11	12	72017923	72017923	Missense_Mutation	SNV	T	C	C	ZFC3H1	c.4467A>G	P.I1489M
XH_P11	12	78570945	78570945	Missense_Mutation	SNV	T	A	A	NAV3	c.5149T>A	P.F1717I
XH_P11	12	80747121	80747121	Frame_Shift_Del	INDEL	G	-	-	OTOGL	c.5400delG	P.K1801fs
XH_P11	12	81063191	81063191	Missense_Mutation	SNV	T	A	A	PTPRQ	c.5885T>A	P.L1962Q
XH_P11	12	81101647	81101647	Missense_Mutation	SNV	C	T	T	MYF6	c.149C>T	P.P50L
XH_P11	12	86229969	86229969	Missense_Mutation	SNV	A	T	T	RASSF9	c.11T>A	P.F4Y
XH_P11	12	8667914	8667914	Silent	SNV	A	T	T	CLEC4D	c.111A>T	P.A37A
XH_P11	13	111090347	111090347	Splice_Site	SNV	A	T	T	COL4A2	c.826-2A>T	
XH_P11	13	25008845	25008845	Silent	SNV	T	A	A	PARP4	c.443A>T	P.P1478P
XH_P11	13	58207642	58207642	Missense_Mutation	SNV	T	A	A	PCDH17	c.962T>A	P.V321E
XH_P11	13	77756024	77756024	Missense_Mutation	SNV	T	A	A	MYCBP2	c.4753A>T	P.S1585C
XH_P11	13	99083293	99083293	Splice_Site	SNV	C	T	T	FARP1	c.1906-4C>T	
XH_P11	14	100792568	100792568	Splice_Site	SNV	A	T	T	SLC25A47	c.144+3A>T	
XH_P11	14	102500476	102500476	Missense_Mutation	SNV	A	T	T	DYNC1H1	c.10577A>T	P.Q3526L
XH_P11	14	102718293	102718293	Missense_Mutation	SNV	T	C	C	MOK	c.233A>G	P.Y78C
XH_P11	14	104492006	104492006	Missense_Mutation	SNV	C	T	T	TDRD9	c.2824C>T	P.P942S
XH_P11	14	20182033	20182033	Missense_Mutation	SNV	A	T	T	OR11H2	c.43T>A	P.S15T
XH_P11	14	20345285	20345285	Missense_Mutation	SNV	T	A	A	OR4K2	c.859T>A	P.Y287N
XH_P11	14	21991690	21991690	Silent	SNV	T	A	A	SALL2	c.1767A>T	P.A589A
XH_P11	14	23871992	23871992	Missense_Mutation	SNV	T	A	A	MYH6	c.916A>T	P.N306Y
XH_P11	14	24613173	24613173	Splice_Site	SNV	T	A	A	PSME2	c.552+11A>T	
XH_P11	14	38222435	38222435	Missense_Mutation	SNV	A	T	T	TTC6	c.3309A>T	P.Q1103H
XH_P11	14	54946533	54946533	Nonsense_Mutation	SNV	T	A	A	GMFB	c.328A>T	P.K110*
XH_P11	14	58605536	58605536	Missense_Mutation	SNV	T	C	C	C14orf37	c.541A>G	P.K181E
XH_P11	14	65041181	65041181	Missense_Mutation	SNV	T	A	A	PPP1R36	c.542T>A	P.V181E
XH_P11	14	68219062	68219062	Missense_Mutation	SNV	T	A	A	ZFYVE26	c.7370A>T	P.Q2457L
XH_P11	14	73720624	73720624	Nonsense_Mutation	SNV	T	A	A	PAPLN	c.1176T>A	P.C392*
XH_P11	14	74823599	74823599	Missense_Mutation	SNV	T	A	A	VRTN	c.113T>A	P.L38Q
XH_P11	14	92136196	92136196	Missense_Mutation	SNV	G	A	A	CATSPERB	c.1249C>T	P.H417Y
XH_P11	14	92441585	92441585	Missense_Mutation	SNV	T	A	A	TRIP11	c.5385A>T	P.K1795N
XH_P11	14	92470389	92470389	Missense_Mutation	SNV	T	C	C	TRIP11	c.3928A>G	P.I1310V
XH_P11	14	94041486	94041486	Missense_Mutation	SNV	T	A	A	UNC79	c.1622T>A	P.L541Q
XH_P11	14	94420755	94420755	Missense_Mutation	SNV	T	A	A	ASB2	c.386A>T	P.K129M
XH_P11	14	99640913	99640913	Missense_Mutation	SNV	T	A	A	BCL11B	c.2257A>T	P.T753S

XH_P11	14	99697763	99697763	Missense_Mutation	SNV	T	A	A	BCL11B	c.556A>T	P.S186C
XH_P11	15	101562114	101562114	Missense_Mutation	SNV	A	T	T	LRRK1	c.1804A>T	P.T602S
XH_P11	15	22369062	22369062	Missense_Mutation	SNV	A	C	C	OR4M2	c.487A>C	P.I163L
XH_P11	15	23811694	23811694	Silent	SNV	G	A	A	MKNR3	c.765G>A	P.G255G
XH_P11	15	33091112	33091112	Silent	SNV	A	T	T	FMN1	c.3354T>A	P.S1118S
XH_P11	15	42054382	42054382	Missense_Mutation	SNV	A	T	T	MGA	c.7566A>T	P.Q2522H
XH_P11	15	51792010	51792010	Silent	SNV	T	A	A	DMXL2	c.3411A>T	P.S1137S
XH_P11	15	52263903	52263903	Missense_Mutation	SNV	T	A	A	LEO1	c.40A>T	P.S14C
XH_P11	15	52338748	52338748	Missense_Mutation	SNV	A	T	T	MAPK6	c.91A>T	P.N31Y
XH_P11	15	57213245	57213245	Missense_Mutation	SNV	A	G	G	TCF12	c.97A>G	P.S33G
XH_P11	15	59179748	59179748	Splice_Site	SNV	T	A	A	SLTM	c.2322-9A>T	
XH_P11	15	66828351	66828351	Missense_Mutation	SNV	A	T	T	ZWILCH	c.1080A>T	P.L360F
XH_P11	15	74427083	74427083	Missense_Mutation	SNV	A	T	T	ISLR2	c.1988A>T	P.E663V
XH_P11	15	75015158	75015158	Missense_Mutation	SNV	T	A	A	CYP1A1	c.281A>T	P.Q94L
XH_P11	15	81199019	81199019	Missense_Mutation	SNV	T	A	A	CEMIP	c.1427T>A	P.L476Q
XH_P11	15	90992870	90992870	Missense_Mutation	SNV	A	T	T	IQGAP1	c.1157A>T	P.Q386L
XH_P11	16	11852279	11852279	Splice_Site	SNV	T	A	A	ZC3H7A	c.2428+8A>T	
XH_P11	16	12142268	12142268	Missense_Mutation	SNV	A	T	T	SNX29	c.539A>T	P.K180M
XH_P11	16	1486441	1486441	Splice_Site	SNV	T	A	A	CCDC154	c.1487+5A>T	
XH_P11	16	1552645	1552645	Splice_Site	SNV	G	T	T	TELO2	c.1654-1G>T	
XH_P11	16	17294396	17294396	Missense_Mutation	SNV	C	A	A	XYLT1	c.1029G>T	P.Q343H
XH_P11	16	1735447	1735447	Nonsense_Mutation	SNV	A	T	T	HN1L	c.52A>T	P.KJ18*
XH_P11	16	19451366	19451366	Silent	SNV	T	A	A	TMC5	c.6T>A	P.S2S
XH_P11	16	23486290	23486290	Missense_Mutation	SNV	G	C	C	GGA2	c.1385C>G	P.P462R
XH_P11	16	2980644	2980644	Missense_Mutation	SNV	A	T	T	FLYWCH1	c.559A>T	P.R187W
XH_P11	16	31046327	31046327	Missense_Mutation	SNV	A	G	G	STX4	c.110A>G	P.Y37C
XH_P11	16	31288067	31288067	Splice_Site	SNV	T	A	A	ITGAM	c.1083+2T>A	
XH_P11	16	31374649	31374649	Missense_Mutation	SNV	T	A	A	ITGAX	c.1664T>A	P.L555Q
XH_P11	16	31393213	31393213	Silent	SNV	G	A	A	ITGAX	c.3477G>A	P.P1159P
XH_P11	16	3254365	3254365	Missense_Mutation	SNV	T	A	A	OR1F1	c.119T>A	P.L40Q
XH_P11	16	32890861	32890861	Splice_Site	SNV	A	T	T	SLC6A10P	n.3029-9T>A	
XH_P11	16	4438057	4438064	Frame_Shift_Del	INDEL	CGCGCTCA	-	-	CORO7	# 661delITGAGC	P.E219fs
XH_P11	16	47117433	47117433	Missense_Mutation	SNV	C	T	T	NETO2	c.1256G>A	P.R419Q
XH_P11	16	49670335	49670335	Missense_Mutation	SNV	T	A	A	ZNF423	c.2548A>T	P.N850Y
XH_P11	16	50188158	50188158	Missense_Mutation	SNV	A	T	T	PAPD5	c.581A>T	P.Q194L
XH_P11	16	50340952	50340952	Splice_Site	SNV	T	A	A	ADCY7	c.1753-9T>A	
XH_P11	16	57110738	57110738	Missense_Mutation	SNV	A	G	G	NLRC5	c.4759A>G	P.R1587G
XH_P11	16	57597029	57597029	Missense_Mutation	SNV	T	A	A	ADGRG5	c.167T>A	P.L56Q
XH_P11	16	57689897	57689897	Missense_Mutation	SNV	T	A	A	ADGRG1	c.1010T>A	P.L337Q
XH_P11	16	57805253	57805253	Nonsense_Mutation	SNV	T	A	A	KIFC3	c.205A>T	P.K69*
XH_P11	16	57994796	57994796	Nonsense_Mutation	SNV	C	T	T	CNGB1	c.482G>A	P.W161*
XH_P11	16	65025681	65025681	Missense_Mutation	SNV	C	G	G	CDH11	c.801G>C	P.K267N
XH_P11	16	67354676	67354676	Missense_Mutation	SNV	A	T	T	KCTD19	c.116T>A	P.L39Q
XH_P11	16	68405275	68405275	Silent	SNV	T	A	A	SMPD3	c.810A>T	P.G270G
XH_P11	16	70843761	70843761	Silent	SNV	A	T	T	HYDIN	c.14808T>A	P.T4936T
XH_P11	16	81157318	81157318	Missense_Mutation	SNV	A	G	G	PKD1L2	c.4364T>C	P.V1455A
XH_P11	16	81946207	81946207	Missense_Mutation	SNV	A	T	T	PLCG2	c.1940A>T	P.Y647F
XH_P11	16	87417139	87417139	Missense_Mutation	SNV	G	A	A	FBXO31	c.212C>T	P.P711L
XH_P11	16	87795598	87795598	Missense_Mutation	SNV	T	A	A	KLHDC4	c.148A>T	P.R50W
XH_P11	16	88501076	88501076	Missense_Mutation	SNV	T	A	A	ZNF469	c.7114T>A	P.S2372T
XH_P11	17	10309651	10309651	Silent	SNV	A	T	T	MYH8	c.2235T>A	P.S745S
XH_P11	17	10419328	10419328	Silent	SNV	C	T	T	MYH1	c.420G>A	P.V140V
XH_P11	17	1173936	1173936	Missense_Mutation	SNV	T	A	A	BHLHA9	c.79T>A	P.C27S
XH_P11	17	12656355	12656355	Missense_Mutation	SNV	C	A	A	MYOCD	c.1750C>A	P.Q584K
XH_P11	17	15406345	15406345	Missense_Mutation	SNV	T	A	A	TVP23C	c.664A>T	P.S222C
XH_P11	17	16456008	16456008	Nonsense_Mutation	SNV	A	T	T	ZNF287	c.1448T>A	P.L483*
XH_P11	17	18671881	18671881	Missense_Mutation	SNV	T	A	A	FBXW10	c.1739T>A	P.L580Q
XH_P11	17	28405286	28405286	Missense_Mutation	SNV	T	C	C	EFCAB5	c.2791T>C	P.S931P
XH_P11	17	36622886	36622886	Missense_Mutation	SNV	A	T	T	ARHGAP23	c.962A>T	P.E321V
XH_P11	17	37374196	37374196	Silent	SNV	T	A	A	STAC2	c.321A>T	P.P107P
XH_P11	17	39724760	39724760	Missense_Mutation	SNV	C	A	A	KRT9	c.1170G>T	P.K390N
XH_P11	17	39741272	39741272	Missense_Mutation	SNV	A	T	T	KRT14	c.563T>A	P.L188Q
XH_P11	17	40332941	40332941	Missense_Mutation	SNV	A	T	T	CNKH4	c.23T>A	P.LBQ
XH_P11	17	48680533	48680533	Missense_Mutation	SNV	G	A	A	CACNA1G	c.4142G>A	P.R1381Q
XH_P11	17	4995277	4995277	Missense_Mutation	SNV	A	T	T	ZFP3	c.478A>T	P.M160L
XH_P11	17	5037241	5037241	Silent	SNV	G	A	A	USP6	c.444G>A	P.V148V
XH_P11	17	59667963	59667963	Silent	SNV	T	A	A	NACA2	c.579A>T	P.A193A
XH_P11	17	61561900	61561900	Missense_Mutation	SNV	T	G	G	ACE	c.1919T>G	P.I640R
XH_P11	17	62265728	62265728	Missense_Mutation	SNV	T	A	A	TEX2	c.2224A>T	P.T742S
XH_P11	17	66268769	66268769	Splice_Site	SNV	A	T	T	SLC16A6	c.505+11T>A	
XH_P11	17	70120481	70120481	Missense_Mutation	SNV	C	A	A	SOX9	c.1483C>A	P.P495T
XH_P11	17	72246161	72246161	Silent	SNV	T	A	A	TTYH2	c.1017T>A	P.T339T
XH_P11	17	72522045	72522045	Missense_Mutation	SNV	T	A	A	CD300LB	c.212A>T	P.E71V
XH_P11	17	72932032	72932032	Missense_Mutation	SNV	T	A	A	OTOP3	c.16T>A	P.S6T
XH_P11	17	72949646	72949646	Silent	SNV	A	T	T	HID1	c.1965T>A	P.A655A
XH_P11	17	7320990	7320990	Missense_Mutation	SNV	G	T	T	NLGN2	c.2380G>T	P.G794C
XH_P11	17	7507153	7507153	Missense_Mutation	SNV	G	A	A	FXR2	c.371C>T	P.P124L
XH_P11	17	7558003	7558004	Splice_Site	INDEL	GT	-	-	ATP1B2	#63+2_363+3delTG	
XH_P11	17	7577587	7577587	Missense_Mutation	SNV	T	A	A	TP53	c.694A>T	P.I232F
XH_P11	17	7578226	7578226	Missense_Mutation	SNV	T	A	A	TP53	c.623A>T	P.D208V
XH_P11	17	76540027	76540027	Missense_Mutation	SNV	A	T	T	DNAH17	c.2444T>A	P.L815Q
XH_P11	17	80543794	80543794	Missense_Mutation	SNV	A	T	T	FOXX2	c.1294A>T	P.S432C
XH_P11	17	9676188	9676188	Missense_Mutation	SNV	T	A	A	DHRS7C	c.623A>T	P.E208V
XH_P11	18	11689607	11689607	Silent	SNV	A	T	T	GNAL	c.45A>T	P.P15P
XH_P11	18	13038575	13038575	Missense_Mutation	SNV	A	T	T	CEP192	c.1806A>T	P.K602N
XH_P11	18	21474994	21474994	Missense_Mutation	SNV	A	T	T	LAMA3	c.758A>T	P.H253L
XH_P11	18	2722522	2722522	Missense_Mutation	SNV	A	C	C	SMCHD1	c.2464A>C	P.K822Q
XH_P11	18	5423365	5423365	Splice_Site	SNV	A	T	T	EPB41L3	c.1339+12T>A	
XH_P11	18	64211317	64211317	Missense_Mutation	SNV	G	C	C	CDH19	c.1105C>G	P.L369V
XH_P11	18	72343308	72343308	Silent	SNV	A	T	T	ZNF407	c.333A>T	P.T111T
XH_P11	18	74672633	74672633	Splice_Site	SNV	A	T	T	ZNF236	c.5243-2A>T	
XH_P11	19	1042135	1042135	Silent	SNV	A	C	C	ABCA7	c.375A>C	P.L125L
XH_P11	19	11728111	11728111	Missense_Mutation	SNV	T	C	C	ZNF627	c.697T>C	P.Y233H
XH_P11	19	13054581	13054581	Nonsense_Mutation	SNV	G	T	T	CALR	c.1108G>T	P.E370*
XH_P11	19	1399572	1399572	Missense_Mutation	SNV	T	A	A	GAMT	c.342A>T	P.K114N
XH_P11	19	14091471	14091471	Missense_Mutation	SNV	T	A	A	RFK1	c.652A>T	P.S218C
XH_P11	19	1418659	1418659	Splice_Site	SNV	C	T	T	DAZAP1	c.238-6C>T	
XH_P11	19	14938527	14938527	Missense_Mutation	SNV	T	A	A	OR7A5	c.527A>T	P.H176L

XH_P11	19	15730539	15730539	Nonstop_Mutation	SNV	A	T	T	CYP4F8	c.491A>T	P.Ter164Lex*?
XH_P11	19	17010292	17010292	Missense_Mutation	SNV	A	T	T	CPAMD8	c.4983T>A	P.F1661L
XH_P11	19	17296790	17296790	Missense_Mutation	SNV	A	T	T	MYO9B	c.2557A>T	P.I853F
XH_P11	19	17471364	17471364	Frame_Shift_Del	INDEL	G	-	-	PLVAP	c.1295delC	P.P432fs
XH_P11	19	17918872	17918872	Missense_Mutation	SNV	T	A	A	B3GNT3	c.256T>A	P.Y86N
XH_P11	19	1800363	1800363	Missense_Mutation	SNV	T	A	A	ATP8B3	c.1097A>T	P.Y366F
XH_P11	19	1827407	1827407	Missense_Mutation	SNV	T	A	A	REXO1	c.1381A>T	P.T461S
XH_P11	19	19136612	19136612	Missense_Mutation	SNV	T	A	A	SUGP2	c.545A>T	P.E182V
XH_P11	19	19349151	19349151	Nonsense_Mutation	SNV	A	T	T	NCAN	c.3340A>T	P.K1114*
XH_P11	19	20727849	20727849	Missense_Mutation	SNV	T	C	C	ZNF737	c.1160A>G	P.H387R
XH_P11	19	22001965	22001965	Missense_Mutation	SNV	A	T	T	ZNF43	c.44T>A	P.L15Q
XH_P11	19	31040399	31040399	Missense_Mutation	SNV	T	G	G	ZNF536	c.3873T>G	P.C1291W
XH_P11	19	31040400	31040400	Missense_Mutation	SNV	A	T	T	ZNF536	c.3874A>T	P.I1292F
XH_P11	19	33095278	33095278	Missense_Mutation	SNV	T	A	A	ANKRD27	c.2546A>T	P.E849V
XH_P11	19	33698025	33698025	Silent	SNV	A	T	T	LRP3	c.1857A>T	P.R619R
XH_P11	19	36049497	36049497	Missense_Mutation	SNV	A	T	T	ATP4A	c.1347T>A	P.D494E
XH_P11	19	36340136	36340136	Splice_Site	SNV	A	T	T	NPHS1	c.840+2T>A	P.P432fs
XH_P11	19	36342421	36342421	Missense_Mutation	SNV	A	T	T	NPHS1	c.212T>A	P.L71Q
XH_P11	19	37853035	37853035	Missense_Mutation	SNV	G	C	C	HKR1	c.284G>C	P.S95T
XH_P11	19	38877661	38877661	Missense_Mutation	SNV	A	T	T	GGN	c.241T>A	P.S81T
XH_P11	19	39026650	39026650	Missense_Mutation	SNV	A	T	T	RYR1	c.11530A>T	P.N3844Y
XH_P11	19	39061251	39061251	Missense_Mutation	SNV	A	T	T	RYR1	c.13664A>T	P.Y4555F
XH_P11	19	39088026	39088026	Splice_Site	SNV	T	A	A	MAP4K1	c.1779-2A>T	
XH_P11	19	39329231	39329231	Missense_Mutation	SNV	T	C	C	HNRNPL	c.964A>G	P.K322E
XH_P11	19	39370142	39370142	Splice_Site	SNV	T	A	A	SIRT2	c.685-2A>T	P.T139S
XH_P11	19	41008183	41008183	Missense_Mutation	SNV	A	T	T	SPTBN4	c.1046A>T	P.Q349L
XH_P11	19	41263279	41263279	Missense_Mutation	SNV	A	T	T	SNRPA	c.116A>T	P.Q39L
XH_P11	19	4216921	4216921	Silent	SNV	A	T	T	ANKRD24	c.1764A>T	P.G588G
XH_P11	19	44352308	44352391	Missense_Mutation	INDEL	TTCAACATGA	-	-	ZNF283	AATCCATACAG	P.N386_F413del
XH_P11	19	45368854	45368854	Missense_Mutation	SNV	A	T	T	NECTIN2	c.415A>T	P.T139S
XH_P11	19	4544319	4544319	Missense_Mutation	SNV	A	T	T	SEMA6B	c.1961T>A	P.L654Q
XH_P11	19	46262753	46262753	Splice_Site	SNV	A	T	T	BHMG1	c.1245+5A>T	
XH_P11	19	47259495	47259495	Missense_Mutation	SNV	C	T	T	FKRP	c.788C>T	P.A263V
XH_P11	19	47424658	47424658	Missense_Mutation	SNV	A	C	C	ARHGAP35	c.2726A>C	P.E909A
XH_P11	19	4816360	4816360	Missense_Mutation	SNV	T	A	A	TICAM1	c.2030A>T	P.Q677L
XH_P11	19	49001914	49001914	Silent	SNV	C	T	T	LMTK3	c.2499G>A	P.E833E
XH_P11	19	49388703	49388703	Splice_Site	SNV	A	T	T	TULP2	c.1061+2T>A	
XH_P11	19	49510613	49510613	Silent	SNV	A	T	T	RUVBL2	c.348A>T	P.P116P
XH_P11	19	50128360	50128360	Splice_Site	SNV	A	T	T	PRR12	c.5869-2A>T	
XH_P11	19	51410215	51410215	Missense_Mutation	SNV	A	T	T	KLK4	c.455T>A	P.I152K
XH_P11	19	51650074	51650074	Missense_Mutation	SNV	T	A	A	SIGLEC7	c.1091T>A	P.L364Q
XH_P11	19	51957571	51957571	Splice_Site	SNV	T	A	A	SIGLEC8	c.1149-2A>T	
XH_P11	19	5212443	5212443	Missense_Mutation	SNV	A	T	T	PTPRS	c.4674T>A	P.H1558Q
XH_P11	19	52619682	52619682	Silent	SNV	T	A	A	ZNF616	c.735A>T	P.V245V
XH_P11	19	53644475	53644475	Missense_Mutation	SNV	T	A	A	ZNF347	c.1609A>T	P.T537S
XH_P11	19	54502990	54502990	Missense_Mutation	SNV	T	A	A	CACNG6	c.509T>A	P.L170Q
XH_P11	19	55423540	55423540	Missense_Mutation	SNV	C	G	G	NCR1	c.684C>G	P.D228E
XH_P11	19	56156320	56156320	Missense_Mutation	SNV	G	A	A	ZNF581	c.383G>A	P.S128N
XH_P11	19	58189659	58189659	Missense_Mutation	SNV	C	A	A	ZSCAN4	c.688C>A	P.P230T
XH_P11	19	7762190	7762190	Splice_Site	SNV	T	A	A	FCER2	c.251-6A>T	
XH_P11	19	7830719	7830719	Missense_Mutation	SNV	A	T	T	CLEC4M	c.410A>T	P.Q137L
XH_P11	19	7927358	7927358	Missense_Mutation	SNV	A	T	T	EVISL	c.1885A>T	P.N629Y
XH_P11	19	902047	902047	Missense_Mutation	SNV	T	A	A	R3HDM4	c.155A>T	P.N52I
XH_P11	19	9028402	9028402	Splice_Site	SNV	T	A	A	MUC16	c.36396-6A>T	
XH_P11	19	9057035	9057035	Silent	SNV	A	T	T	MUC16	c.30411T>A	P.S10137S
XH_P11	19	9065786	9065786	Frame_Shift_Ins	INDEL	-	G	G	MUC16	21659_21660ins	P.T7221fs
XH_P11	19	9204736	9204736	Missense_Mutation	SNV	A	T	T	OR1M1	c.816A>T	P.K272N
XH_P11	2	100623239	100623239	Missense_Mutation	SNV	T	A	A	AFB3	c.728A>T	P.Q243L
XH_P11	2	10192447	10192447	Missense_Mutation	SNV	A	T	T	KLF11	c.1301A>T	P.E434V
XH_P11	2	102440494	102440494	Silent	SNV	A	T	T	MAP4K4	c.285A>T	P.P95P
XH_P11	2	105859191	105859191	Missense_Mutation	SNV	T	A	A	GPR45	c.876T>A	P.T292L
XH_P11	2	107459548	107459548	Missense_Mutation	SNV	A	T	T	ST6GAL2	c.886T>A	P.C296S
XH_P11	2	109383541	109383541	Silent	SNV	A	T	T	RANBP2	c.6546A>T	P.T2182T
XH_P11	2	120438813	120438813	Silent	SNV	A	T	T	TMEM177	c.384A>T	P.T128T
XH_P11	2	121742321	121742321	Splice_Site	SNV	T	A	A	GLI2	c.1956+2T>A	
XH_P11	2	128377990	128377990	Silent	SNV	C	T	T	MYO7B	c.3396C>T	P.I1132I
XH_P11	2	131674965	131674965	Splice_Site	SNV	T	A	A	ARHGEF4	c.-108-5T>A	
XH_P11	2	133076099	133076099	Silent	SNV	A	T	T	ZNF806	c.1560A>T	P.S520S
XH_P11	2	141806736	141806736	Missense_Mutation	SNV	T	A	A	LRP1B	c.1608A>T	P.R536S
XH_P11	2	144765091	144765091	Missense_Mutation	SNV	T	A	A	GTDC1	c.533A>T	P.K178M
XH_P11	2	1481312	1481312	Missense_Mutation	SNV	A	T	T	TPO	c.1274A>T	P.N425I
XH_P11	2	159035463	159035463	Silent	SNV	T	C	C	CCDC148	c.978A>G	P.K326K
XH_P11	2	162760524	162760524	Nonsense_Mutation	SNV	G	T	T	SLC4A10	c.1453G>T	P.G485*
XH_P11	2	165997248	165997248	Missense_Mutation	SNV	C	A	A	SCN3A	c.1932G>T	P.M644I
XH_P11	2	166613679	166613679	Missense_Mutation	SNV	T	G	G	GALNT3	c.1270A>C	P.S424R
XH_P11	2	168101702	168101702	Missense_Mutation	SNV	T	A	A	XIRP2	c.3134T>A	P.I1045K
XH_P11	2	168105365	168105365	Missense_Mutation	SNV	A	T	T	XIRP2	c.7463A>T	P.E2488V
XH_P11	2	168821245	168821245	Splice_Site	SNV	T	C	C	STK39	c.1499-9A>G	
XH_P11	2	169707374	169707374	Missense_Mutation	SNV	T	A	A	NOSTRIN	c.659T>A	P.F220Y
XH_P11	2	170063022	170063022	Nonsense_Mutation	SNV	A	T	T	LRP2	c.7208T>A	P.L2403*
XH_P11	2	175087791	175087791	Missense_Mutation	SNV	T	A	A	OLA1	c.343A>T	P.S115C
XH_P11	2	179412323	179412323	Missense_Mutation	SNV	A	T	T	TTN	c.89107T>A	P.Y29703N
XH_P11	2	179477760	179477760	Missense_Mutation	SNV	A	T	T	TTN	c.44765T>A	P.V14922E
XH_P11	2	179590334	179590334	Missense_Mutation	SNV	A	T	T	TTN	c.19646T>A	P.V6549E
XH_P11	2	179733959	179733959	Missense_Mutation	SNV	T	A	A	CCDC141	c.2279A>T	P.E760V
XH_P11	2	18112546	18112546	Missense_Mutation	SNV	A	T	T	KCNS3	c.271A>T	P.M91L
XH_P11	2	185801729	185801729	Missense_Mutation	SNV	T	A	A	ZNF804A	c.1606T>A	P.C536S
XH_P11	2	198495806	198495806	Missense_Mutation	SNV	T	A	A	RFTN2	c.857A>T	P.E286V
XH_P11	2	201469525	201469525	Missense_Mutation	SNV	A	T	T	AOX1	c.776A>T	P.Y259F
XH_P11	2	202068479	202068479	Silent	SNV	A	T	T	CASP10	c.711A>T	P.A237A
XH_P11	2	204036749	204036749	Splice_Site	SNV	A	T	T	NBEAL1	c.6111+3A>T	
XH_P11	2	207007452	207007452	Missense_Mutation	SNV	T	A	A	NDUFS1	c.983A>T	P.D328V
XH_P11	2	211163253	211163253	Silent	SNV	T	A	A	MYL1	c.195A>T	P.T65T
XH_P11	2	211465293	211465293	Nonsense_Mutation	SNV	A	T	T	CP51	c.1582A>T	P.K528*
XH_P11	2	217559329	217559329	Missense_Mutation	SNV	A	T	T	IGFBP5	c.170T>A	P.M57K
XH_P11	2	219090676	219090676	Splice_Site	SNV	A	T	T	ARPC2	c.108A>T	P.A36A
XH_P11	2	233244233	233244233	Missense_Mutation	SNV	T	A	A	ALPP	c.320T>A	P.V107E
XH_P11	2	242794453	242794453	Silent	SNV	G	T	T	PDCD1	c.489C>A	P.A163A

XH_P11	2	31178842	31178842	Splice_Site	SNV	A	T	T	GALNT14	c.483T>A	P.P161P
XH_P11	2	3750010	3750010	Missense_Mutation	SNV	A	T	T	ALLC	c.1033A>T	P.J345F
XH_P11	2	48602480	48602480	Silent	SNV	A	G	G	FOXN2	c.1194A>G	P.K398K
XH_P11	2	50282144	50282144	Nonsense_Mutation	SNV	G	A	A	NRXN1	c.3877C>T	P.R1293*
XH_P11	2	69046378	69046378	Missense_Mutation	SNV	T	A	A	ARHGAP25	c.1127T>A	P.V376E
XH_P11	2	69372485	69372485	Missense_Mutation	SNV	A	T	T	ANTXR1	c.979A>T	P.T327S
XH_P11	2	73800483	73800483	Missense_Mutation	SNV	A	T	T	ALMS1	c.11476A>T	P.S3826C
XH_P11	2	74752852	74752852	Missense_Mutation	SNV	G	A	A	DQX1	c.5C>T	P.T2I
XH_P11	2	79384810	79384810	Missense_Mutation	SNV	A	T	T	REG3A	c.348T>A	P.N116K
XH_P11	2	85785593	85785593	Missense_Mutation	SNV	T	A	A	GGCX	c.509A>T	P.Q170L
XH_P11	2	88396102	88396102	Splice_Site	SNV	A	T	T	SMYD1	c.699-12A>T	
XH_P11	2	95942340	95942340	Splice_Site	SNV	A	G	G	PROM2	c.619-2A>G	
XH_P11	2	97327961	97327961	Missense_Mutation	SNV	A	T	T	FER1L5	c.1028A>T	P.Q343L
XH_P11	2	97845512	97845512	Splice_Site	SNV	A	T	T	ANKRD36	c.1662+9A>T	
XH_P11	20	13029591	13029591	Splice_Site	SNV	A	T	T	SPTLC3	c.118-2A>T	
XH_P11	20	18122902	18122902	Missense_Mutation	SNV	A	T	T	PET117	c.147A>T	P.K49N
XH_P11	20	23017157	23017157	Missense_Mutation	SNV	A	T	T	SSTR4	c.1037A>T	P.Y346F
XH_P11	20	2636125	2636125	Frame_Shift_Del	INDEL	A	-	-	NOP56	c.725delA	P.K242fs
XH_P11	20	33364210	33364210	Missense_Mutation	SNV	T	A	A	NCOA6	c.277A>T	P.S93C
XH_P11	20	34090273	34090273	Missense_Mutation	SNV	A	T	T	CEP250	c.2180A>T	P.H727L
XH_P11	20	35547789	35547789	Missense_Mutation	SNV	T	A	A	SAMHD1	c.830A>T	P.E277V
XH_P11	20	35579920	35579920	Nonsense_Mutation	SNV	T	A	A	SAMHD1	c.127A>T	P.K43*
XH_P11	20	35882691	35882691	Missense_Mutation	SNV	C	T	T	GHRH	c.230G>A	P.R77H
XH_P11	20	3686576	3686576	Missense_Mutation	SNV	T	A	A	SIGLEC1	c.521A>T	P.Q174L
XH_P11	20	43615891	43615891	Missense_Mutation	SNV	A	T	T	STK4	c.479A>T	P.E160V
XH_P11	20	44674996	44674996	Missense_Mutation	SNV	A	G	G	SLC12A5	c.1777A>G	P.M593V
XH_P11	20	47569272	47569272	Missense_Mutation	SNV	A	T	T	ARFGEF2	c.454A>T	P.I152F
XH_P11	20	47689178	47689178	Missense_Mutation	SNV	A	T	T	CSE1L	c.842A>T	P.Q281L
XH_P11	20	58581847	58581847	Splice_Site	SNV	G	A	A	CDH26	c.294+5G>A	
XH_P11	20	61880250	61880250	Splice_Site	SNV	A	T	T	NKAIN4	c.193-3T>A	
XH_P11	20	62195325	62195325	Missense_Mutation	SNV	T	A	A	HELZ2	c.4850A>T	P.Q1617L
XH_P11	21	33717819	33717819	Missense_Mutation	SNV	T	A	A	URB1	c.3934A>T	P.S1312C
XH_P11	21	37418294	37418294	Silent	SNV	T	A	A	SETD4	c.312A>T	P.P104P
XH_P11	21	38511013	38511013	Missense_Mutation	SNV	A	T	T	TTC3	c.1658A>T	P.E553V
XH_P11	21	45825020	45825020	Splice_Site	SNV	A	T	T	TRPM2	c.2539-5A>T	
XH_P11	21	46020705	46020705	Missense_Mutation	SNV	T	A	A	KRTAP10-7	c.169T>A	P.C57S
XH_P11	21	48022264	48022264	Missense_Mutation	SNV	T	A	A	S100B	c.65A>T	P.E22V
XH_P11	22	17621989	17621989	Missense_Mutation	SNV	T	A	A	CECR5	c.616A>T	P.N206Y
XH_P11	22	26291143	26291143	Missense_Mutation	SNV	T	A	A	MYO18B	c.4567T>A	P.F1523I
XH_P11	22	35719787	35719787	Silent	SNV	A	T	T	TOM1	c.429A>T	P.S143S
XH_P11	22	37584212	37584212	Silent	SNV	T	A	A	C1QTNF6	c.42A>T	P.T14T
XH_P11	22	37769948	37769948	Missense_Mutation	SNV	T	G	G	ELFN2	c.1627A>C	P.K543Q
XH_P11	22	39267556	39267556	Splice_Site	SNV	G	A	A	CBX6	c.180-5C>T	
XH_P11	22	40037046	40037046	Silent	SNV	G	A	A	CACNA1I	c.915G>A	P.A305A
XH_P11	22	40140175	40140175	Missense_Mutation	SNV	A	T	T	ENTHD1	c.1333T>A	P.S445T
XH_P11	22	43218426	43218426	Splice_Site	SNV	T	A	A	ARFGAP3	c.541-11A>T	
XH_P11	22	45182343	45182343	Missense_Mutation	SNV	A	T	T	PRR5-ARHGAP8	c.329A>T	P.Q110L
XH_P11	22	46653706	46653706	Silent	SNV	A	T	T	PKDREJ	c.5514T>A	P.S1838S
XH_P11	3	121441230	121441230	Splice_Site	SNV	T	A	A	GOLGB1	c.532-5A>T	
XH_P11	3	124732556	124732556	Missense_Mutation	SNV	T	A	A	HEG1	c.1867A>T	P.T623S
XH_P11	3	128348790	128348790	Splice_Site	SNV	T	A	A	RPN1	c.1036+4A>T	
XH_P11	3	128749534	128749534	Splice_Site	SNV	C	A	A	EFCC1	c.981-12C>A	
XH_P11	3	130107796	130107796	Missense_Mutation	SNV	A	T	T	COL6A5	c.2235A>T	P.R745S
XH_P11	3	133347527	133347527	Missense_Mutation	SNV	C	A	A	TOPBP1	c.2571G>T	P.R857S
XH_P11	3	13381535	13381535	Splice_Site	SNV	T	A	A	NUP210	c.3292-2A>T	
XH_P11	3	142274729	142274729	Silent	SNV	T	A	A	ATR	c.2331A>T	P.P777P
XH_P11	3	154146959	154146959	Missense_Mutation	SNV	T	A	A	GPR149	c.446A>T	P.Q149L
XH_P11	3	156183448	156183448	Missense_Mutation	SNV	G	T	T	KCNAB1	c.544G>T	P.G182W
XH_P11	3	159605645	159605645	Missense_Mutation	SNV	A	T	T	SCHIP1	c.1106A>T	P.Q369L
XH_P11	3	164725748	164725748	Silent	SNV	A	T	T	SI	c.4218T>A	P.T1406T
XH_P11	3	170732381	170732381	Missense_Mutation	SNV	T	A	A	SLC2A2	c.248A>T	P.E83V
XH_P11	3	184009005	184009005	Missense_Mutation	SNV	A	T	T	ECE2	c.1925A>T	P.K642M
XH_P11	3	184099591	184099591	Missense_Mutation	SNV	T	G	G	CHRD	c.599T>G	P.I200S
XH_P11	3	185867920	185867920	Missense_Mutation	SNV	T	A	A	DGKG	c.2260A>T	P.S754C
XH_P11	3	192517238	192517238	Missense_Mutation	SNV	A	T	T	MB21D2	c.413T>A	P.M138K
XH_P11	3	193220392	193220392	Missense_Mutation	SNV	A	T	T	ATP13A4	c.271T>A	P.W91R
XH_P11	3	196626808	196626808	Missense_Mutation	SNV	A	T	T	SENPS	c.1633A>T	P.N545Y
XH_P11	3	36779838	36779838	Missense_Mutation	SNV	T	A	A	DCLK3	c.313A>T	P.S105C
XH_P11	3	46755854	46755854	Missense_Mutation	SNV	T	A	A	PRSS50	c.608A>T	P.Q203L
XH_P11	3	48501901	48501901	Missense_Mutation	SNV	A	T	T	ATRIP	c.1067A>T	P.Q356L
XH_P11	3	49011252	49011252	Splice_Site	SNV	A	T	T	ARIH2	c.888+3A>T	
XH_P11	3	52536089	52536089	Silent	SNV	T	C	C	STAB1	c.399T>C	P.N133N
XH_P11	3	52840986	52840986	Missense_Mutation	SNV	A	T	T	ITIH3	c.2126A>T	P.Y709F
XH_P11	3	68934324	68934324	Splice_Site	SNV	A	T	T	FAM19A4	c.14+2T>A	
XH_P11	3	72428408	72428408	Missense_Mutation	SNV	T	A	A	RYBP	c.299A>T	P.K100I
XH_P11	3	73432931	73432931	Missense_Mutation	SNV	C	T	T	PDZRN3	c.1880G>A	P.G627E
XH_P11	4	100208008	100208008	Splice_Site	SNV	T	A	A	ADH1A	c.258A>T	P.P86P
XH_P11	4	128554246	128554246	Missense_Mutation	SNV	C	A	A	INTU	c.57C>A	P.D19E
XH_P11	4	151142863	151142863	Silent	SNV	T	A	A	DCLK2	c.1167T>A	P.T389T
XH_P11	4	155411997	155411997	Missense_Mutation	SNV	A	T	T	DCHS2	c.511T>A	P.S171T
XH_P11	4	185694238	185694238	Silent	SNV	T	A	A	ACSL1	c.912A>T	P.T304T
XH_P11	4	26483699	26483699	Missense_Mutation	SNV	C	T	T	CKKAR	c.848G>A	P.R283Q
XH_P11	4	42403143	42403143	Missense_Mutation	SNV	A	T	T	SHISA3	c.392A>T	P.Q131L
XH_P11	4	42454003	42454003	Missense_Mutation	SNV	T	A	A	ATP8A1	c.2846A>T	P.Q949L
XH_P11	4	47655624	47655624	Nonsense_Mutation	SNV	T	A	A	CORIN	c.1477A>T	P.R493*
XH_P11	4	5586546	5586546	Missense_Mutation	SNV	T	A	A	EVG2	c.2621A>T	P.Q874L
XH_P11	4	57180394	57180394	Silent	SNV	A	T	T	KIAA1211	c.726A>T	P.A242A
XH_P11	4	66217260	66217260	Silent	SNV	A	T	T	EPHAs	c.2355T>A	P.S785S
XH_P11	4	70823137	70823137	Missense_Mutation	SNV	A	T	T	CSN2	c.527T>A	P.L176Q
XH_P11	4	71844923	71844923	Missense_Mutation	SNV	A	T	T	MOB1B	c.503A>T	P.Y168F
XH_P11	4	77677974	77677974	Silent	SNV	A	T	T	SHROOM3	c.5082A>T	P.T1694T
XH_P11	4	88536818	88536818	Missense_Mutation	SNV	A	T	T	DSPP	c.3004A>T	P.N1002Y
XH_P11	4	89020494	89020494	Missense_Mutation	SNV	T	C	C	ABCG2	c.1474A>G	P.I492V
XH_P11	5	115346583	115346583	Missense_Mutation	SNV	T	G	G	LVN	c.2239T>G	P.L747V
XH_P11	5	118503451	118503451	Missense_Mutation	SNV	A	T	T	DMXL1	c.5290A>T	P.I1764L
XH_P11	5	121759360	121759360	Missense_Mutation	SNV	G	C	C	SNCAIP	c.928G>C	P.E310Q
XH_P11	5	127681252	127681252	Nonsense_Mutation	SNV	A	T	T	FBN2	c.3014T>A	P.L1005*
XH_P11	5	131994015	131994015	Missense_Mutation	SNV	T	A	A	IL13	c.137T>A	P.L46H

XH_P11	5	136320846	136320846	Missense_Mutation	SNV	T	A	A	SPOCK1	c.974A>T	P.K325M
XH_P11	5	137243545	137243545	Missense_Mutation	SNV	T	A	A	PKD2L2	c.1024T>A	P.W342R
XH_P11	5	13862801	13862801	Missense_Mutation	SNV	A	T	T	DNAH5	c.4652T>A	P.V1551E
XH_P11	5	138661321	138661321	Missense_Mutation	SNV	A	G	G	MATR3	c.2341A>G	P.I781V
XH_P11	5	139227555	139227555	Nonsense_Mutation	SNV	T	A	A	NRG2	c.2302A>T	P.R768*
XH_P11	5	139231183	139231183	Splice_Site	SNV	A	T	T	NRG2	c.1574+6T>A	
XH_P11	5	140255653	140255653	Nonsense_Mutation	SNV	T	A	A	PCDHA12	c.596T>A	P.L199*
XH_P11	5	140263733	140263733	Missense_Mutation	SNV	A	T	T	PCDHA13	c.1880A>T	P.Y627F
XH_P11	5	140347116	140347116	Silent	SNV	T	A	A	PCDHAC2	c.765T>A	P.P255P
XH_P11	5	140865147	140865147	Missense_Mutation	SNV	A	T	T	PCDHGC4	c.407A>T	P.Q136L
XH_P11	5	141036345	141036345	Missense_Mutation	SNV	A	T	T	ARAP3	c.3595T>A	P.C1199S
XH_P11	5	141051138	141051138	Missense_Mutation	SNV	T	A	A	ARAP3	c.1853A>T	P.Q618L
XH_P11	5	145883002	145883002	Missense_Mutation	SNV	A	T	T	TCERG1	c.2384A>T	P.K795I
XH_P11	5	145887511	145887511	Missense_Mutation	SNV	A	T	T	TCERG1	c.2923A>T	P.S975C
XH_P11	5	149677801	149677801	Missense_Mutation	SNV	A	T	T	ARSI	c.686T>A	P.L229H
XH_P11	5	150923958	150923958	Nonsense_Mutation	SNV	T	A	A	FAT2	c.6730A>T	P.R2244*
XH_P11	5	151178857	151178857	Missense_Mutation	SNV	A	G	G	G3BP1	c.826A>G	P.K276E
XH_P11	5	151784182	151784182	Missense_Mutation	SNV	T	A	A	NMUR2	c.493A>T	P.R165W
XH_P11	5	156887267	156887267	Missense_Mutation	SNV	C	G	G	NIPAL4	c.125C>G	P.A42G
XH_P11	5	156899467	156899467	Silent	SNV	T	A	A	NIPAL4	c.900T>A	P.S300S
XH_P11	5	157053510	157053510	Missense_Mutation	SNV	A	T	T	SOX30	c.1185T>A	P.H395Q
XH_P11	5	157053564	157053564	Missense_Mutation	SNV	A	T	T	SOX30	c.1131T>A	P.S377R
XH_P11	5	169472877	169472877	Missense_Mutation	SNV	A	T	T	DOCK2	c.3934A>T	P.I1312F
XH_P11	5	169679439	169679439	Missense_Mutation	SNV	T	A	A	LCP2	c.1322A>T	P.Q441L
XH_P11	5	170323057	170323057	Missense_Mutation	SNV	A	G	G	RANBP17	c.427A>G	P.T143A
XH_P11	5	170669805	170669805	Silent	SNV	A	T	T	RANBP17	c.2757A>T	P.S919S
XH_P11	5	171789808	171789808	Nonsense_Mutation	SNV	T	A	A	SH3PXD2B	c.493A>T	P.K165*
XH_P11	5	180056746	180056746	Missense_Mutation	SNV	C	A	A	FLT4	c.766G>T	P.A256S
XH_P11	5	180056747	180056747	Missense_Mutation	SNV	C	A	A	FLT4	c.765G>T	P.W255C
XH_P11	5	3600293	3600293	Missense_Mutation	SNV	C	A	A	IRX1	c.1231C>A	P.P411T
XH_P11	5	3600294	3600294	Missense_Mutation	SNV	C	A	A	IRX1	c.1232C>A	P.P411Q
XH_P11	5	38489334	38489334	Silent	SNV	T	A	A	LIFR	c.2181A>T	P.A727A
XH_P11	5	38885449	38885449	Splice_Site	SNV	A	T	T	OSMR	c.704-2A>T	
XH_P11	5	39311276	39311276	Silent	SNV	T	A	A	C9	c.1074A>T	P.L358L
XH_P11	5	59284496	59284496	Missense_Mutation	SNV	G	A	A	PDE4D	c.91C>T	P.R31C
XH_P11	5	64521985	64521985	Silent	SNV	A	T	T	ADAMT56	c.1995T>A	P.R665R
XH_P11	5	68661453	68661453	Nonsense_Mutation	SNV	G	A	A	TAF9	c.112C>T	P.Q38*
XH_P11	5	82808022	82808022	Silent	SNV	C	G	G	VCAN	c.849C>G	P.L283L
XH_P11	5	90670801	90670801	Missense_Mutation	SNV	T	C	C	ARRDC3	c.148A>G	P.I50V
XH_P11	5	95751755	95751755	Missense_Mutation	SNV	A	T	T	PCSK1	c.691T>A	P.Y231N
XH_P11	5	98224856	98224856	Missense_Mutation	SNV	T	C	C	CHD1	c.2267A>G	P.K756R
XH_P11	6	109286307	109286307	Missense_Mutation	SNV	A	T	T	ARMC2	c.1915A>T	P.T639S
XH_P11	6	10930657	10930657	Missense_Mutation	SNV	A	T	T	SYCP2L	c.1543A>T	P.S515C
XH_P11	6	109311861	109311861	Missense_Mutation	SNV	T	A	A	SESN1	c.1234A>T	P.M4412L
XH_P11	6	12122866	12122866	Silent	SNV	A	T	T	HIVEP1	c.2838A>T	P.I946I
XH_P11	6	131903778	131903778	Silent	SNV	A	G	G	ARG1	c.483A>G	P.G161G
XH_P11	6	136667043	136667043	Silent	SNV	T	A	A	MAP7	c.2256A>T	P.T752T
XH_P11	6	160328317	160328317	Silent	SNV	G	T	T	MAS1	c.330G>T	P.V110V
XH_P11	6	160494893	160494893	Silent	SNV	C	A	A	IGF2R	c.5052C>A	P.S1684S
XH_P11	6	160668208	160668208	Splice_Site	SNV	T	A	A	SLC22A2	c.957+8A>T	
XH_P11	6	170034587	170034587	Missense_Mutation	SNV	T	A	A	WDR27	c.1657A>T	P.R553W
XH_P11	6	170604533	170604533	Missense_Mutation	SNV	A	T	T	FAM120B	c.40A>T	P.R14W
XH_P11	6	24528345	24528345	Missense_Mutation	SNV	A	T	T	ALDH5A1	c.1294A>T	P.M432L
XH_P11	6	26384085	26384085	Silent	SNV	A	T	T	BTN2A2	c.36A>T	P.P12P
XH_P11	6	26501919	26501919	Missense_Mutation	SNV	T	A	A	BTN1A1	c.181T>A	P.L61M
XH_P11	6	34789692	34789692	Splice_Site	SNV	A	T	T	UHRF1BP1	c.208-2A>T	
XH_P11	6	35810331	35810331	Missense_Mutation	SNV	T	A	A	SRPK1	c.1671A>T	P.E557D
XH_P11	6	37140784	37140784	Missense_Mutation	SNV	A	G	G	PIM1	c.620A>G	P.Y207C
XH_P11	6	42072464	42072464	Silent	SNV	T	A	A	C6orf132	c.3186A>T	P.I1062I
XH_P11	6	42930845	42930845	Missense_Mutation	SNV	A	C	C	CNPY3-GNMT	c.289A>C	P.I97L
XH_P11	6	44241086	44241086	Missense_Mutation	SNV	T	A	A	TMEM151B	c.419T>A	P.L140Q
XH_P11	6	55922643	55922643	Splice_Site	SNV	C	A	A	COL21A1	c.2687-1G>T	
XH_P11	6	56918377	56918377	Frame_Shift_Del	INDEL	G	-	-	KIAA1586	c.999delG	P.E333fs
XH_P11	6	57244790	57244790	Missense_Mutation	SNV	A	G	G	PRIM2	c.551A>G	P.Y184C
XH_P11	6	65531582	65531582	Missense_Mutation	SNV	A	T	T	EYS	c.3199T>A	P.C1067S
XH_P11	6	66115217	66115217	Silent	SNV	A	G	G	EYS	c.906T>C	P.L302L
XH_P11	6	69349336	69349336	Splice_Site	SNV	A	T	T	ADGRB3	c.757+12A>T	
XH_P11	6	71003995	71003995	Missense_Mutation	SNV	T	A	A	COL9A1	c.571A>T	P.S191C
XH_P11	6	7365738	7365738	Missense_Mutation	SNV	T	A	A	CAGE1	c.2156A>T	P.D719V
XH_P11	6	83845497	83845497	Silent	SNV	A	T	T	DOPEY1	c.3003A>T	P.S1001S
XH_P11	6	8413810	8413810	Missense_Mutation	SNV	T	A	A	SLC35B3	c.1178A>T	P.K393M
XH_P11	6	90457105	90457105	Nonsense_Mutation	SNV	T	A	A	MDN1	c.3847A>T	P.R1283*
XH_P11	7	102856898	102856898	Splice_Site	SNV	A	T	T	DPY19L2P2	n.2980+12T>A	
XH_P11	7	103162486	103162486	Missense_Mutation	SNV	C	T	T	RELN	c.7651G>A	P.A2551T
XH_P11	7	106508991	106508991	Missense_Mutation	SNV	T	A	A	PIK3CG	c.985T>A	P.C329S
XH_P11	7	106520073	106520073	Missense_Mutation	SNV	A	T	T	PIK3CG	c.2501A>T	P.H834L
XH_P11	7	117232155	117232155	Missense_Mutation	SNV	T	A	A	CFTR	c.1934T>A	P.M645K
XH_P11	7	120965532	120965532	Splice_Site	SNV	A	T	T	WNT16	c.63A>T	P.L21L
XH_P11	7	121652098	121652098	Missense_Mutation	SNV	T	A	A	PTPRZ1	c.2998T>A	P.S1000T
XH_P11	7	12383835	12383835	Missense_Mutation	SNV	G	T	T	VWDE	c.4064C>A	P.A1355E
XH_P11	7	127013894	127013894	Missense_Mutation	SNV	T	A	A	ZNF800	c.1496A>T	P.Q499L
XH_P11	7	134650060	134650064	Frame_Shift_Del	INDEL	TTGAG	-	-	CALD1	534 1538delTTG	P.L512fs
XH_P11	7	141464013	141464013	Missense_Mutation	SNV	C	G	G	TAS2R3	c.55C>G	P.L19V
XH_P11	7	142574237	142574237	Missense_Mutation	SNV	A	T	T	TRPV6	c.806T>A	P.T269Q
XH_P11	7	143792609	143792609	Missense_Mutation	SNV	T	A	A	OR2A12	c.409T>A	P.W137R
XH_P11	7	146825887	146825887	Missense_Mutation	SNV	A	T	T	CNTNAP2	c.1042A>T	P.T348S
XH_P11	7	1484749	1484749	Silent	SNV	T	A	A	MICALL2	c.957A>T	P.P319P
XH_P11	7	150932468	150932468	Missense_Mutation	SNV	A	T	T	CHPF2	c.574A>T	P.S192C
XH_P11	7	150935660	150935660	Missense_Mutation	SNV	A	T	T	CHPF2	c.2188A>T	P.S730C
XH_P11	7	17869650	17869650	Missense_Mutation	SNV	T	A	A	SNX13	c.1618A>T	P.T540S
XH_P11	7	20441375	20441375	Missense_Mutation	SNV	A	T	T	ITGB8	c.1313A>T	P.K438I
XH_P11	7	23385576	23385576	Silent	SNV	A	T	T	IGF2BP3	c.924T>A	P.T308T
XH_P11	7	24708197	24708197	Silent	SNV	A	T	T	MPP6	c.1032A>T	P.I344I
XH_P11	7	2692550	2692550	Splice_Site	SNV	A	T	T	TTYH3	c.928-2A>T	
XH_P11	7	48559691	48559691	Missense_Mutation	SNV	T	G	G	ABCA13	c.13852T>G	P.F4618V
XH_P11	7	55492962	55492962	Nonsense_Mutation	SNV	A	T	T	LANCL2	c.1024A>T	P.K342*
XH_P11	7	6075189	6075189	Silent	SNV	T	C	C	ANKRD61	c.429T>C	P.N143N
XH_P11	7	6692663	6692663	Missense_Mutation	SNV	A	T	T	ZNF316	c.1436A>T	P.H479L

XH_P11	7	72732888	72732888	Missense_Mutation	SNV	T	A	A	TRIM50	c.659A>T	P.E220V
XH_P11	7	76984861	76984861	Splice_Site	SNV	T	A	A	GSAP	c.1120+11A>T	
XH_P11	7	82583921	82583921	Silent	SNV	A	T	T	PCLO	c.6348T>A	P.L2116L
XH_P11	7	83640552	83640552	Missense_Mutation	SNV	A	T	T	SEMA3A	c.872T>A	P.L291Q
XH_P11	7	87536623	87536623	Silent	SNV	A	T	T	DBF4	c.471A>T	P.T157T
XH_P11	7	91631099	91631099	Missense_Mutation	SNV	A	T	T	AKAP9	c.1868A>T	P.E623V
XH_P11	8	105361105	105361105	Missense_Mutation	SNV	G	A	A	DCSTAMP	c.325G>A	P.G109R
XH_P11	8	124975603	124975603	Silent	SNV	T	A	A	FER1L6	c.162T>A	P.S54S
XH_P11	8	133900474	133900474	Missense_Mutation	SNV	A	T	T	TG	c.2422A>T	P.S808C
XH_P11	8	143866665	143866665	Missense_Mutation	SNV	A	T	T	LY6D	c.359T>A	P.L120Q
XH_P11	8	1626739	1626739	Missense_Mutation	SNV	A	T	T	DLGAP2	c.2366A>T	P.E789V
XH_P11	8	20112463	20112463	Missense_Mutation	SNV	G	C	C	LZTS1	c.230C>G	P.S77C
XH_P11	8	24775411	24775411	Silent	SNV	T	A	A	NEFM	c.915T>A	P.P305P
XH_P11	8	29207762	29207762	Missense_Mutation	SNV	A	T	T	DUSP4	c.34T>A	P.C12S
XH_P11	8	3063060	3063060	Silent	SNV	T	A	A	CSMD1	c.4950A>T	P.I1650I
XH_P11	8	42179909	42179909	Missense_Mutation	SNV	A	T	T	IKBKB	c.1877A>T	P.K626M
XH_P11	8	49644026	49644026	Missense_Mutation	SNV	A	C	C	EFCAB1	c.95T>G	P.F32C
XH_P11	8	52287162	52287162	Silent	SNV	T	A	A	PXDNL	c.3687A>T	P.G1229G
XH_P11	8	72211921	72211921	Silent	SNV	T	A	A	EYA1	c.591A>T	P.T197T
XH_P11	8	77754968	77754968	Nonsense_Mutation	SNV	A	T	T	ZFHx4	c.3472A>T	P.R1158*
XH_P11	8	80677605	80677605	Missense_Mutation	SNV	T	A	A	HEY1	c.745A>T	P.T249S
XH_P11	9	113168934	113168934	Missense_Mutation	SNV	A	T	T	SVEP1	c.8946T>A	P.H2982Q
XH_P11	9	12698449	12698449	Splice_Site	SNV	A	T	T	TYRP1	c.709-2A>T	
XH_P11	9	13206036	13206036	Silent	SNV	T	A	A	MPDZ	c.1353A>T	P.T451T
XH_P11	9	133948110	133948110	Missense_Mutation	SNV	G	A	A	LAMC3	c.3305G>A	P.R1102H
XH_P11	9	133951254	133951254	Silent	SNV	T	A	A	LAMC3	c.3531T>A	P.A1177A
XH_P11	9	139976496	139976496	Missense_Mutation	SNV	T	A	A	UAP1L1	c.1411T>A	P.L171M
XH_P11	9	140082221	140082221	Missense_Mutation	SNV	T	A	A	ANAPC2	c.452A>T	P.E151V
XH_P11	9	140108411	140108411	Splice_Site	SNV	C	T	T	NDOR1	c.411-8C>T	
XH_P11	9	17330679	17330679	Missense_Mutation	SNV	A	T	T	CNTLN	c.1391A>T	P.Q464L
XH_P11	9	21141223	21141223	Missense_Mutation	SNV	A	T	T	IFNW1	c.347T>A	P.L116Q
XH_P11	9	21481239	21481239	Missense_Mutation	SNV	T	A	A	IFNE	c.455A>T	P.H152L
XH_P11	9	33533514	33533514	Silent	SNV	A	T	T	ANKRD18B	c.573A>T	P.A191A
XH_P11	9	38411463	38411463	Silent	SNV	T	A	A	IGFBPL1	c.771A>T	P.T257T
XH_P11	9	79634898	79634898	Nonsense_Mutation	SNV	A	T	T	FOXB2	c.328A>T	P.K110*
XH_P11	9	91159284	91159284	Splice_Site	SNV	T	A	A	NXNL2	c.303-10T>A	
XH_P11	9	93606602	93606602	Splice_Site	SNV	G	A	A	SYK	c.417+5G>A	
XH_P11	9	95778017	95778017	Splice_Site	SNV	A	T	T	FGD3	c.1183-2A>T	
XH_P11	9	990823	990823	Missense_Mutation	SNV	A	T	T	DMRT3	c.1237A>T	P.S413C
XH_P11	X	100613596	100613596	Splice_Site	SNV	A	T	T	BTX	c.974+9T>A	
XH_P11	X	100747535	100747535	Missense_Mutation	SNV	A	T	T	ARMCX4	c.3959A>T	P.E1320V
XH_P11	X	101909212	101909303	Frame_Shift_Del	INDEL	ATAGAGAA	-	-	GPRASP1	TAAGGATAGAG	P.D125FS
XH_P11	X	102632577	102632577	Missense_Mutation	SNV	A	T	T	BEX3	c.398A>T	P.N133I
XH_P11	X	110391038	110391038	Missense_Mutation	SNV	A	T	T	PAK3	c.458A>T	P.Q153L
XH_P11	X	110973782	110973782	Missense_Mutation	SNV	A	T	T	ALG13	c.1945A>T	P.S649C
XH_P11	X	114425982	114425982	Missense_Mutation	SNV	A	T	T	RBMXL3	c.1978A>T	P.S660C
XH_P11	X	117770326	117770326	Missense_Mutation	SNV	T	A	A	DOCK11	c.3904T>A	P.W1302R
XH_P11	X	118223089	118223089	Missense_Mutation	SNV	A	T	T	KIAA1210	c.2104T>A	P.L702I
XH_P11	X	125954989	125954989	Missense_Mutation	SNV	A	T	T	PRR32	c.368A>T	P.Q123L
XH_P11	X	134156367	134156367	Silent	SNV	C	T	T	FAM127C	c.123G>A	P.P41P
XH_P11	X	135106540	135106540	Missense_Mutation	SNV	A	T	T	SLC9A6	c.1514A>T	P.Y505F
XH_P11	X	135572524	135572524	Missense_Mutation	SNV	T	A	A	BR53	c.667T>A	P.L223I
XH_P11	X	141291237	141291237	Silent	SNV	A	T	T	MAGEC2	c.537T>A	P.P179P
XH_P11	X	148037128	148037128	Splice_Site	SNV	T	A	A	AFF2	c.1459-5T>A	
XH_P11	X	151815491	151815491	Missense_Mutation	SNV	T	A	A	GABRQ	c.389T>A	P.L130Q
XH_P11	X	152686475	152686475	Missense_Mutation	SNV	A	T	T	ZFP92	c.640A>T	P.S214C
XH_P11	X	152807125	152807125	Splice_Site	SNV	A	T	T	ATP2B3	c.407-2A>T	
XH_P11	X	153416401	153416401	Missense_Mutation	SNV	A	T	T	OPN1LW	c.386A>T	P.E129V
XH_P11	X	18221726	18221726	Missense_Mutation	SNV	T	A	A	BEND2	c.802A>T	P.S268C
XH_P11	X	23751309	23751309	Silent	SNV	T	A	A	ACOT9	c.144A>T	P.V48V
XH_P11	X	24006594	24006594	Missense_Mutation	SNV	T	A	A	KLHL15	c.1259A>T	P.E420V
XH_P11	X	24006595	24006595	Nonsense_Mutation	SNV	C	A	A	KLHL15	c.1258G>T	P.E420*
XH_P11	X	24521566	24521566	Missense_Mutation	SNV	A	T	T	PKD3	c.443A>T	P.Q148L
XH_P12	1	120341157	120341157	Silent	SNV	A	T	T	REG4	c.372T>A	P.G124G
XH_P12	1	149916917	149916917	Silent	SNV	C	T	T	OTUD7B	c.1371G>A	P.E457E
XH_P12	1	159683396	159683396	Splice_Site	SNV	G	A	A	CRP	c.198-3C>T	
XH_P12	1	174973834	174973834	Missense_Mutation	SNV	T	C	C	CACYBP	c.100T>C	P.S34P
XH_P12	1	176564590	176564590	Missense_Mutation	SNV	G	A	A	PAPPA2	c.1850G>A	P.R617H
XH_P12	1	43317025	43317025	Silent	SNV	G	T	T	ZNF691	c.489G>T	P.R163R
XH_P12	10	105750590	105750590	Missense_Mutation	SNV	A	G	G	SLK	c.308A>G	P.N103S
XH_P12	10	48413992	48413992	Silent	SNV	G	A	A	GDF2	c.876C>T	P.S292S
XH_P12	10	97920441	97920441	Silent	SNV	G	T	T	ZNF518A	c.4362G>T	P.V1454V
XH_P12	11	134028234	134028234	Missense_Mutation	SNV	G	A	A	NCAPD3	c.4024C>T	P.P1342S
XH_P12	12	108919308	108919308	Missense_Mutation	SNV	G	C	C	SART3	c.2449C>G	P.L817V
XH_P12	12	14766195	14766195	Missense_Mutation	SNV	A	T	T	GUCY2C	c.3078T>A	P.F1026L
XH_P12	12	40914221	40914221	Splice_Site	SNV	A	G	G	MUC19	c.20531-8A>G	
XH_P12	12	53189718	53189718	Missense_Mutation	SNV	C	T	T	KRT3	c.109G>A	P.G37R
XH_P12	13	20716365	20716365	Missense_Mutation	SNV	C	T	T	GJA3	c.1063G>A	P.V355I
XH_P12	13	25281315	25281315	Missense_Mutation	SNV	C	T	T	ATP12A	c.2342C>T	P.T781I
XH_P12	13	25745485	25745485	Missense_Mutation	SNV	G	T	T	AMER2	c.273C>A	P.D91E
XH_P12	13	48563108	48563108	Missense_Mutation	SNV	C	A	A	SUCLA2	c.280G>T	P.D94Y
XH_P12	13	97485160	97485160	Missense_Mutation	SNV	C	A	A	HS6S3	c.1124C>A	P.P375H
XH_P12	14	77872347	77872347	Missense_Mutation	SNV	C	G	G	NOXRED1	c.814G>C	P.E272Q
XH_P12	15	42740297	42740297	Missense_Mutation	SNV	A	T	T	ZNF106	c.594T>A	P.S198R
XH_P12	18	24442406	24442406	Nonsense_Mutation	SNV	C	A	A	AQP4	c.187G>T	P.E63*
XH_P12	18	43526704	43526704	Silent	SNV	C	T	T	EPG5	c.1602G>A	P.K534K
XH_P12	19	17435731	17435731	Missense_Mutation	SNV	G	C	C	ANO8	c.3126C>G	P.S1042R
XH_P12	19	20307863	20307863	Missense_Mutation	SNV	G	A	A	ZNF486	c.344G>A	P.C115Y
XH_P12	19	46294273	46294273	Missense_Mutation	SNV	G	T	T	DMWD	c.514C>A	P.Q172K
XH_P12	19	49604664	49604664	Frame_Shift_Ins	INDEL	-	A	A	SNRNP70	c.413dupA	P.R139fs
XH_P12	19	57840518	57840518	Missense_Mutation	SNV	C	T	T	ZNF543	c.1688C>T	P.T563I
XH_P12	19	619773	619773	Splice_Site	SNV	G	A	A	POLRMT	c.2887-8C>T	
XH_P12	2	62100411	62100411	Missense_Mutation	SNV	A	T	T	CC74	c.845T>A	P.L282H
XH_P12	2	79349129	79349129	Missense_Mutation	SNV	A	T	T	REG1A	c.199A>T	P.M67L
XH_P12	20	15210595	15210595	Missense_Mutation	SNV	A	G	G	MACROD2	c.428A>G	P.H143R
XH_P12	22	41077833	41077833	Silent	SNV	C	T	T	MCHR1	c.1170C>T	P.R390R
XH_P12	3	140406700	140406700	Missense_Mutation	SNV	G	T	T	TRIM42	c.1176G>T	P.K392N
XH_P12	3	180369939	180369939	Splice_Site	INDEL	T	-	-	CCDC39	c.1034+12delA	

XH_P12	3	183226120	183226120	Missense_Mutation	SNV	G	T	T	KLHL6	c.636C>A	P.D212E
XH_P12	4	101344506	101344506	Missense_Mutation	SNV	T	C	C	EMCN	c.432A>G	P.I144M
XH_P12	4	1165095	1165095	Missense_Mutation	SNV	C	T	T	SPON2	c.400G>A	P.G134R
XH_P12	4	126372696	126372696	Missense_Mutation	SNV	A	G	G	FAT4	c.10525A>G	P.M3509V
XH_P12	4	177083301	177083301	Silent	SNV	C	T	T	WDR17	c.2898C>T	P.C966C
XH_P12	4	8229831	8229831	Missense_Mutation	SNV	C	T	T	SH3TC1	c.2182C>T	P.P728S
XH_P12	5	11346648	11346648	Missense_Mutation	SNV	C	A	A	CTNND2	c.1191G>T	P.R397S
XH_P12	6	35211400	35211400	Missense_Mutation	SNV	G	A	A	SCUBE3	c.1936G>A	P.G646S
XH_P12	7	150027864	150027864	Missense_Mutation	SNV	A	G	G	ZBED6CL	c.371A>G	P.Q124R
XH_P12	7	45753535	45753535	Missense_Mutation	SNV	C	T	T	ADCY1	c.3301C>T	P.L1101F
XH_P12	7	4839054	4839054	Silent	SNV	G	A	A	RADIL	c.3183C>T	P.D1061D
XH_P12	7	50057879	50057879	Missense_Mutation	SNV	C	T	T	ZPBP	c.737G>A	P.R246Q
XH_P12	7	64168245	64168245	Missense_Mutation	SNV	G	C	C	ZNF107	c.1563G>C	P.E521D
XH_P12	7	64292175	64292175	Frame_Shift_Ins	INDEL	-	A	A	ZNF138	c.466dupA	P.I56fs
XH_P12	7	92848737	92848737	Missense_Mutation	SNV	A	G	G	HEPACAM2	c.107T>C	P.V36A
XH_P12	8	113317056	113317056	Missense_Mutation	SNV	T	A	A	CSMD3	c.8040A>T	P.K2680N
XH_P12	8	69028159	69028159	Silent	SNV	C	T	T	PREX2	c.3318C>T	P.D1106D
XH_P12	X	12904891	12904891	Missense_Mutation	SNV	A	G	G	TLR7	c.1264A>G	P.R422G
XH_P12	X	77224854	77224854	Silent	SNV	A	G	G	PGAM4	c.282T>C	P.G94G
XH_P13	1	152275306	152275306	Missense_Mutation	SNV	G	A	A	FLG	c.12056C>T	P.A4019V
XH_P13	1	152785216	152785216	Silent	SNV	G	A	A	LCE1B	c.294G>A	P.Q98Q
XH_P13	1	158390649	158390649	Missense_Mutation	SNV	C	T	T	OR10K2	c.8G>A	P.R3Q
XH_P13	1	17085998	17085998	Missense_Mutation	SNV	C	A	A	MST1L	c.899G>T	P.G300V
XH_P13	1	93341931	93341931	Silent	SNV	A	G	G	FAM69A	c.111T>C	P.F37F
XH_P13	10	55582706	55582706	Missense_Mutation	SNV	T	C	C	PCDH15	c.4801A>G	P.I1601V
XH_P13	10	70700833	70700833	Silent	SNV	T	C	C	DDX50	c.1773T>C	P.T591T
XH_P13	11	125848197	125848197	Splice_Site	SNV	A	G	G	CDON	c.3356+2T>C	
XH_P13	11	18313169	18313169	Missense_Mutation	SNV	T	C	C	HP55	c.1918A>G	P.I640V
XH_P13	11	46709804	46709804	Missense_Mutation	SNV	T	C	C	ARHGAP1	c.236A>G	P.D79G
XH_P13	11	58379120	58379120	Missense_Mutation	SNV	G	C	C	ZFP91	c.763G>C	P.E255Q
XH_P13	11	92600134	92600150	Frame_Shift_Del	INDEL	GCGGATAAC	-	-	FAT3	95delAGCGGAT	P.A3964fs
XH_P13	12	115110047	115110047	Missense_Mutation	SNV	C	T	T	TBX3	c.1831G>A	P.A611T
XH_P13	12	133367816	133367816	Missense_Mutation	SNV	A	G	G	GOLGA3	c.2533T>C	P.R845L
XH_P13	12	1702388	1702392	Frame_Shift_Del	INDEL	GAGAG	-	-	FBXL14	841_845delCTC	P.L281fs
XH_P13	12	25398284	25398284	Missense_Mutation	SNV	C	T	T	KRAS	c.35G>A	P.G12D
XH_P13	12	57569323	57569334	Missense_Mutation	INDEL	GGGCATGG	-	-	LRP1	644delCATGGA	M1212_G1215del
XH_P13	12	62929428	62929428	Splice_Site	SNV	G	A	A	MON2	c.1831+8G>A	
XH_P13	12	8990075	8990075	Silent	SNV	A	C	C	A2ML1	c.768A>C	P.V256V
XH_P13	13	48939029	48939029	Splice_Site	SNV	G	C	C	RB1	c.862-1G>C	
XH_P13	15	64427018	64427018	Splice_Site	SNV	G	A	A	SNX1	c.1365+12G>A	
XH_P13	16	56901024	56901024	Frame_Shift_Del	INDEL	C	-	-	SLC12A3	c.327delC	P.S110fs
XH_P13	17	7578382	7578382	Nonsense_Mutation	SNV	G	T	T	TP53	c.548C>A	P.S183*
XH_P13	18	32407609	32407609	Missense_Mutation	SNV	C	A	A	DTNA	c.1054C>A	P.P352T
XH_P13	18	44585965	44585965	Silent	SNV	C	T	T	KATNAL2	c.273C>T	P.F91F
XH_P13	19	1507331	1507331	Silent	SNV	C	T	T	ADAMTSL5	c.762G>A	P.A254A
XH_P13	19	30164799	30164799	Missense_Mutation	SNV	T	G	G	PLEKHF1	c.53T>G	P.V18G
XH_P13	19	39522547	39522547	Silent	SNV	G	A	A	FBXO27	c.321C>T	P.R107R
XH_P13	19	4702093	4702093	Missense_Mutation	SNV	G	C	C	DPP9	c.958C>G	P.P320A
XH_P13	2	113588157	113588157	Splice_Site	SNV	C	T	T	IL1B	c.598-7G>A	
XH_P13	2	180348009	180348009	Silent	SNV	A	T	T	ZNF385B	c.432T>A	P.S144S
XH_P13	2	198266834	198266834	Missense_Mutation	SNV	T	C	C	SF3B1	c.2098A>G	P.K700E
XH_P13	2	241684943	241684943	Splice_Site	SNV	C	A	A	KIF1A	c.3375-9G>T	
XH_P13	2	98408917	98408917	Missense_Mutation	SNV	T	A	A	TMEM131	c.4076A>T	P.D1359V
XH_P13	20	31383295	31383295	Missense_Mutation	SNV	T	G	G	DNMT3B	c.1207T>G	P.C403G
XH_P13	20	33337761	33337761	Frame_Shift_Del	INDEL	C	-	-	NCOA6	c.2237delG	P.G746fs
XH_P13	21	45713715	45713715	Missense_Mutation	SNV	C	T	T	AIRE	c.1322C>T	P.T441M
XH_P13	3	124732416	124732416	Missense_Mutation	INDEL	-	AGAGGAGGAGGAGAGGAGGAGG	HEG1	106dupCTCTCC	S.665_669dup	
XH_P13	3	127396614	127396614	Silent	SNV	C	T	T	ABTB1	c.531C>T	P.A177A
XH_P13	3	49753557	49753557	Missense_Mutation	SNV	G	T	T	RNF123	c.3362G>T	P.R1121L
XH_P13	3	7620616	7620616	Missense_Mutation	SNV	A	T	T	GRM7	c.2023A>T	P.T675S
XH_P13	4	119219892	119219892	Silent	SNV	A	G	G	PRSS12	c.1833T>C	P.N611N
XH_P13	4	146059690	146059690	Missense_Mutation	SNV	T	C	C	OTUD4	c.2042A>G	P.N681S
XH_P13	5	150656998	150656998	Missense_Mutation	SNV	G	A	A	SLC36A3	c.1492C>T	P.P498S
XH_P13	6	143784108	143784108	Missense_Mutation	SNV	G	C	C	PEX3	c.261G>C	P.E87D
XH_P13	7	148487454	148487454	Missense_Mutation	SNV	G	A	A	CUL1	c.1727G>A	P.G576D
XH_P13	7	18801895	18801895	Missense_Mutation	SNV	T	C	C	HDAC9	c.2159T>C	P.L720P
XH_P13	7	99129330	99129330	Missense_Mutation	SNV	T	C	C	ZKSCAN5	c.1978T>C	P.S660P
XH_P13	8	125463583	125463583	Missense_Mutation	SNV	A	C	C	TRMT12	c.415A>C	P.N139H
XH_P13	8	135524749	135524749	Silent	SNV	C	T	T	ZFAT	c.3294G>A	P.A1098A
XH_P13	X	149867658	149867658	Splice_Site	INDEL	T	-	-	MTMR1	c.147-3delT	
XH_P13	X	37312611	37312611	Frame_Shift_Del	INDEL	C	-	-	PRRG1	c.401delC	P.P134fs
XH_P13	X	47045136	47045136	Nonsense_Mutation	SNV	C	T	T	RBM10	c.2377C>T	P.R793*
XH_P15	1	110591793	110591793	Frame_Shift_Del	INDEL	T	-	-	STRIP1	c.1437delT	P.I479fs
XH_P15	1	1226722	1226722	Missense_Mutation	INDEL	-	GCA	GCA	SCNN1D	2143_2144insA	L714_L715insC
XH_P15	1	1875802	1875802	Frame_Shift_Ins	INDEL	-	CGGT	CGGT	CFAP74	450_2453dupA	P.L819fs
XH_P15	1	26509741	26509741	Frame_Shift_Del	INDEL	C	-	-	CNKS1R	c.678delC	P.D226fs
XH_P15	1	46685774	46685774	Missense_Mutation	SNV	C	T	T	LURAP1	c.602C>T	P.P201L
XH_P15	1	6647539	6647539	Frame_Shift_Ins	INDEL	-	C	C	ZBTB48	c.1230dupC	P.T411fs
XH_P15	1	877515	877516	Frame_Shift_Del	INDEL	GG	-	-	SAMD11	c.870_871delGG	P.E291fs
XH_P15	1	93299181	93299181	Frame_Shift_Ins	INDEL	-	AT	AT	RPL5	c.155_156dupTA	P.V53fs
XH_P15	10	45939270	45939270	Missense_Mutation	SNV	C	A	A	ALOX5	c.1668C>A	P.F556L
XH_P15	10	89711879	89711882	Frame_Shift_Del	INDEL	TAAC	-	-	PTEN	499_502delACT	P.T167fs
XH_P15	10	97444362	97444362	Frame_Shift_Ins	INDEL	-	TC	TC	TCTN3	c.987_988dupG	P.T330fs
XH_P15	10	99531082	99531108	Missense_Mutation	INDEL	AACTGCACG	-	-	SFRP5	c.ATCGCGGTGCP	C.162_L170del
XH_P15	11	102714170	102714171	Splice_Site	INDEL	TA	-	-	MMP3	c.105+2_105+3delTA	
XH_P15	11	118897733	118897733	Frame_Shift_Ins	INDEL	-	A	A	SLC37A4	c.697dupT	P.Y233fs
XH_P15	11	18723515	18723515	Frame_Shift_Ins	INDEL	-	G	G	TMEM86A	c.685dupG	P.E229fs
XH_P15	11	1905812	1905812	Splice_Site	INDEL	-	TA	TA	LSP1	c.31+3_531+4dupAT	
XH_P15	11	28104442	28104442	Missense_Mutation	SNV	T	A	A	KIF18A	c.1223A>T	P.K408M
XH_P15	11	34654158	34654158	Frame_Shift_Ins	INDEL	-	GATT	GATT	EHF	c.24_27dupATTG	P.V10fs
XH_P15	11	36310918	36310918	Frame_Shift_Ins	INDEL	-	GCCT	GCCT	COMMD9	c.44_45insAGG	P.L16fs
XH_P15	11	63586402	63586402	Missense_Mutation	SNV	G	A	A	C11orf84	c.862G>A	P.D288N
XH_P15	11	64543964	64543964	Splice_Site	INDEL	-	T	T	SF1	c.535+5dupA	
XH_P15	11	67410314	67410314	Frame_Shift_Ins	INDEL	-	GG	GG	ACY3	c.839_840dupCC	P.V281fs
XH_P15	11	71955041	71955041	Frame_Shift_Ins	INDEL	-	GAC	GAC	PHOX2A	c.7_8insGTC	P.Y3delinsCH
XH_P15	11	75153602	75153602	Frame_Shift_Ins	INDEL	-	GCT	GCT	GDPD5	c.970_972dupAG	P.S324dup
XH_P15	11	76922242	76922242	Missense_Mutation	INDEL	-	ACC	ACC	MYO7A	c.6098_6099insCC	E2033delinsDQ
XH_P15	12	11061483	11061483	Frame_Shift_Ins	INDEL	-	CAA	CAA	TAS2R13	c.412_414dupTT	P.L138dup

XH_P15	12	30872054	30872054	Frame_Shift_Ins	INDEL	-	ACT	ACT	CAPRIN2	251_2253dupA	P.S751dup
XH_P15	12	48173947	48173947	Frame_Shift_Ins	INDEL	-	TACT	TACT	SLC48A1	325_328dupTA	P.Y110fs
XH_P15	12	4920326	4920326	Missense_Mutation	SNV	G	C	C	KCNAB	c.1119G>C	P.M373I
XH_P15	12	57039021	57039021	Frame_Shift_Ins	INDEL	-	TGG	TGG	ATP5B	241_243dupCC	P.P81dup
XH_P15	12	92537947	92537947	Frame_Shift_Ins	INDEL	-	T	T	BTG1	c.424dupA	P.M142fs
XH_P15	13	23911365	23911365	Missense_Mutation	SNV	G	A	A	SACS	c.6209C>T	P.P2070L
XH_P15	13	49050843	49050843	Nonsense_Mutation	SNV	G	T	T	RB1	c.2527G>T	P.E843*
XH_P15	13	76055493	76055504	Missense_Mutation	INDEL	5TGAGGTCG	-	-	TBC1D4	411delCACGACG	P.H134_1137del
XH_P15	13	78492216	78492216	Splice_Site	SNV	C	T	T	EDNRB	c.483+10G>A	
XH_P15	14	104387272	104387272	Splice_Site	INDEL	-	T	T	C14orf2	c.51+4dupA	
XH_P15	14	20849516	20849516	Nonsense_Mutation	SNV	G	A	A	TEP1	c.4279C>T	P.R1427*
XH_P15	14	21541273	21541273	Frame_Shift_Ins	INDEL	-	C	C	ARHGEF40	c.78dupC	P.T27fs
XH_P15	14	24528128	24528128	Frame_Shift_Ins	INDEL	-	CT	CT	CARMIL3	1505_1506dupG	P.A503fs
XH_P15	14	24802202	24802202	Splice_Site	INDEL	-	AGGG	AGGG	ADCY4	9-12_160-9dupCCCT	
XH_P15	14	31358824	31358824	Frame_Shift_Ins	INDEL	-	TCAC	TCAC	COCH	482_1485dupCA	P.I496fs
XH_P15	14	31790758	31790758	Frame_Shift_Ins	INDEL	-	AACT	AACT	HEATR5A	915_3916insAG	P.V1306fs
XH_P15	14	50053052	50053053	Frame_Shift_Del	INDEL	GC	-	-	RPS29	c.12_13delGC	P.Q5fs
XH_P15	14	50300137	50300137	Splice_Site	INDEL	-	T	T	NEMF	c.735+3dupA	
XH_P15	14	50555913	50555913	Splice_Site	SNV	A	G	G	LINC01599	n.48T>C	
XH_P15	14	50952325	50952325	Frame_Shift_Ins	INDEL	-	CA	CA	MAP4K5	c.291_292dupTC	P.G98fs
XH_P15	14	55636160	55636162	Missense_Mutation	INDEL	GTA	-	-	DLGAP5	1503_1505delTA	P.T502del
XH_P15	14	92409302	92409303	Frame_Shift_Del	INDEL	TA	-	-	FBLN5	c.20_21delTA	P.I7fs
XH_P15	15	101833228	101833228	Splice_Site	INDEL	-	C	C	SNRPA1	c.230+1dupG	
XH_P15	15	23812308	23812308	Missense_Mutation	SNV	G	T	T	MKRN3	c.1379G>T	P.S460I
XH_P15	15	38235601	38235601	Splice_Site	INDEL	-	A	A	TMC05A	c.627+5dupA	
XH_P15	15	62237949	62237949	Missense_Mutation	SNV	T	C	C	VPS13C	c.5113A>G	P.I1705V
XH_P15	15	62299587	62299587	Silent	SNV	A	G	G	VPS13C	c.1210T>C	P.L404L
XH_P15	15	62299588	62299588	Silent	SNV	C	T	T	VPS13C	c.1209G>A	P.Q403Q
XH_P15	15	63414237	63414237	Missense_Mutation	INDEL	-	GGC	GGC	LACTB	168_170dupGG	P.A57dup
XH_P15	15	68501975	68501975	Frame_Shift_Ins	INDEL	-	A	A	CLN6	c.664dupT	P.W222fs
XH_P15	15	74494557	74494557	Frame_Shift_Del	INDEL	A	-	-	STRA6	c.52delT	P.Y18fs
XH_P15	15	89443007	89443007	Frame_Shift_Del	INDEL	G	-	-	MFGE8	c.774delC	P.I259fs
XH_P15	16	2358443	2358443	Splice_Site	INDEL	-	CACT	CACT	ABCA3	5+4_1285+7dupAGTG	
XH_P15	16	68867322	68867322	Frame_Shift_Ins	INDEL	-	AGGA	AGGA	CDH1	570_2573dupAC	P.D85fs
XH_P15	16	71706204	71706204	Frame_Shift_Ins	INDEL	-	A	A	PHLP2	c.1492dupT	P.Y498fs
XH_P15	17	15848840	15848842	Missense_Mutation	INDEL	TCT	-	-	ADORA2B	c.280_282delTT	P.F94del
XH_P15	17	16075109	16075114	Splice_Site	INDEL	ATATTT	-	-	NCOR1	+3_435+8delAAATAT	
XH_P15	17	38560458	38560458	Missense_Mutation	SNV	C	A	A	TOP2A	c.2229G>T	P.K743N
XH_P15	17	40336409	40336409	Frame_Shift_Ins	INDEL	-	AGCA	AGCA	HCRT	155_158dupTG	P.H54fs
XH_P15	17	43215332	43215332	Frame_Shift_Ins	INDEL	-	C	C	ACBD4	c.630dupC	P.V211fs
XH_P15	17	43552749	43552749	Frame_Shift_Ins	INDEL	-	T	T	PLEKHM1	c.639dupA	P.L214fs
XH_P15	17	5071260	5071260	Missense_Mutation	SNV	C	T	T	USP6	c.3070C>T	P.R1024W
XH_P15	17	5418828	5418828	Missense_Mutation	SNV	A	G	G	NLRP1	c.3845T>C	P.M1282T
XH_P15	17	62045456	62045456	Silent	SNV	G	A	A	SCN4A	c.963C>T	P.N321N
XH_P15	17	72301563	72301563	Missense_Mutation	SNV	C	T	T	DNAI2	c.1193C>T	P.S398L
XH_P15	17	73102118	73102119	Frame_Shift_Del	INDEL	GC	-	-	SLC16A5	1508_1509delC	P.S503fs
XH_P15	17	73235158	73235158	Frame_Shift_Ins	INDEL	-	CACT	CACT	GGA3	567_1570dupAC	P.A524fs
XH_P15	17	79418847	79418847	Missense_Mutation	SNV	G	A	A	BAHCC1	c.4055G>A	P.R1352H
XH_P15	17	80656339	80656339	Frame_Shift_Ins	INDEL	-	GGCC	GGCC	RAB40B	130_133dupGG	P.H45fs
XH_P15	18	12014299	12014301	Missense_Mutation	INDEL	GCG	-	-	IMPA2	c.419_421delGG	P.R140del
XH_P15	18	44559687	44559687	Missense_Mutation	SNV	G	A	A	TCEB3B	c.1949C>T	P.T650M
XH_P15	18	51888540	51888540	Frame_Shift_Ins	INDEL	-	T	T	C18orf54	c.812dupT	P.P272fs
XH_P15	19	10400734	10400734	Frame_Shift_Del	INDEL	TGCGCCGGG	-	-	ICAM5	5CTGCGCCGGG	P.G7fs
XH_P15	19	10935797	10935797	Frame_Shift_Ins	INDEL	-	G	G	DNM2	c.1960dupG	P.E654fs
XH_P15	19	11485584	11485584	Frame_Shift_Ins	INDEL	-	CTA	CTA	SWSAP1	c.166_168dupCT	P.L56dup
XH_P15	19	12958818	12958818	Frame_Shift_Ins	INDEL	-	CC	CC	MAST1	c.722_723dupCC	P.T242fs
XH_P15	19	15536187	15536189	Missense_Mutation	INDEL	AGC	-	-	WIZ	1472_1474delG	P.5491_5492delinsD
XH_P15	19	18643010	18643024	Missense_Mutation	INDEL	TACACCCCC	-	-	FKBP8	108delCTTGGGG	P.L399_4A03del
XH_P15	19	22379432	22379432	Silent	SNV	A	G	G	ZNFE76	c.4T>C	P.L2L
XH_P15	19	30106230	30106230	Silent	SNV	T	G	G	POP4	c.606T>G	P.L202L
XH_P15	19	35715965	35715965	Frame_Shift_Ins	INDEL	-	TCCT	TCCT	FAM187B	869_872dupAG	P.L1292fs
XH_P15	19	36017858	36017867	Frame_Shift_Del	INDEL	ATGAAGTGC	-	-	SBSN	1326delAGCA	P.I439fs
XH_P15	19	36486332	36486332	Frame_Shift_Ins	INDEL	-	CT	CT	SDHAF1	c.157_158dupC	P.Y54fs
XH_P15	19	36501809	36501809	Missense_Mutation	SNV	C	T	T	ALKBH6	c.323G>A	P.G108E
XH_P15	19	39361489	39361489	Missense_Mutation	SNV	C	T	T	RINL	c.745G>A	P.D249N
XH_P15	19	43679507	43679507	Frame_Shift_Ins	INDEL	-	T	T	PSG5	c.823dupA	P.I275fs
XH_P15	19	47192929	47192933	Frame_Shift_Del	INDEL	GTTCAC	-	-	PRKD2	832_1836delTG	P.V611fs
XH_P15	19	48945578	48945578	Frame_Shift_Del	INDEL	G	-	-	GRIN2D	c.2613delG	P.W871fs
XH_P15	19	49951302	49951302	Frame_Shift_Ins	INDEL	-	GGTA	GGTA	PIH1D1	351_354dupTA	P.A119fs
XH_P15	19	50919981	50919982	Splice_Site	INDEL	GT	-	-	POLD1	167+2_3067+3delTG	
XH_P15	19	58420589	58420589	Frame_Shift_Ins	INDEL	-	TT	TT	ZNF417	c.1053_1054insA	P.H352fs
XH_P15	19	59065565	59065572	Frame_Shift_Del	INDEL	GAACAAATA	-	-	CHMP2A	8_15delATTATTGT	P.L3fs
XH_P15	2	101670669	101670670	Frame_Shift_Del	INDEL	AG	-	-	TBC1D8	c.486_487delCT	P.Y162fs
XH_P15	2	113332737	113332737	Frame_Shift_Ins	INDEL	-	CTAC	CTAC	POLR1B	672_2675dupC	P.P893fs
XH_P15	2	145157709	145157709	Nonsense_Mutation	SNV	T	A	A	ZEB2	c.973A>T	P.K325*
XH_P15	2	160879231	160879233	Missense_Mutation	INDEL	TAA	-	-	PLA2R1	1237_1239delGT	P.L413del
XH_P15	2	191845336	191845336	Splice_Site	INDEL	C	-	-	STAT1	c.1632+10delG	
XH_P15	2	197738399	197738399	Splice_Site	INDEL	-	ATTA	ATTA	PGAP1	8+6_978+9dupTAAT	
XH_P15	2	242814426	242814428	Missense_Mutation	INDEL	TCA	-	-	RTPS	c.721_723delAT	P.I241del
XH_P15	2	48698513	48698518	Splice_Site	INDEL	ACCCCC	-	-	PPP1R21	+7_1088+12delACCCCC	
XH_P15	2	73635784	73635784	Frame_Shift_Ins	INDEL	-	A	A	ALMS1	c.360dupA	P.V121fs
XH_P15	2	9637293	9637293	Missense_Mutation	SNV	C	T	T	ADAM17	c.1733G>A	P.C578Y
XH_P15	2	97427091	97427091	Frame_Shift_Ins	INDEL	-	AGCT	AGCT	CNNM4	356_359dupAG	P.V121fs
XH_P15	20	10256220	10256220	Splice_Site	INDEL	-	C	C	SNAP25	c.72+9_72+10insC	
XH_P15	20	10654168	10654169	Frame_Shift_Del	INDEL	GG	-	-	JAG1	c.10_11delCC	P.P4fs
XH_P15	20	21367645	21367645	Splice_Site	INDEL	-	TAAA	TAAA	XRN2	1+3_3021+6dupAAAT	
XH_P15	20	33077677	33077677	Frame_Shift_Ins	INDEL	-	GCC	GCC	ITCH	389_2391dupG	P.A797dup
XH_P15	20	43552884	43552885	Frame_Shift_Del	INDEL	TT	-	-	PABPC1L	c.959_960delTT	P.I320fs
XH_P15	20	44598226	44598226	Frame_Shift_Ins	INDEL	-	C	C	ZNF335	c.305dupG	P.P103fs
XH_P15	20	46262946	46262946	Splice_Site	INDEL	A	-	-	NCOA3	c.1112+7delA	
XH_P15	20	47739677	47739677	Frame_Shift_Ins	INDEL	-	GT	GT	STAU1	c.691_692dupA	P.L232fs
XH_P15	20	60902411	60902411	Frame_Shift_Ins	INDEL	-	CAC	CAC	LAMA5	987_4989dupG	P.V1663dup
XH_P15	20	62520589	62520593	Frame_Shift_Del	INDEL	AAGGT	-	-	TPD52L2	50_450+4delGG	P.K150fs
XH_P15	21	37417936	37417936	Frame_Shift_Ins	INDEL	-	CTGA	CTGA	SETD4	669_670insTCA	P.D224fs
XH_P15	21	38114037	38114038	Frame_Shift_Del	INDEL	CA	-	-	SIM2	c.871_872delAC	P.T291fs
XH_P15	22	20307492	20307524	In_Frame_Del	INDEL	TCGCTCCATG	-	-	DGCR6L	TCGCGCCATGGA	P.M1_A7del
XH_P15	22	26181425	26181425	Frame_Shift_Ins	INDEL	-	AGC	AGC	MYO18B	2347_2349dupA	P.S784dup
XH_P15	22	38083967	38083967	Missense_Mutation	SNV	C	A	A	NOL12	c.134C>A	P.A45D

XH_P15	22	46932215	46932229	Missense_Mutation	INDEL	TGTAATAGC	-	-	CELSR1	3delTGAGCTAT	V.280_M284del
XH_P15	3	101474341	101474341	Missense_Mutation	SNV	C	-	G	CEP97	c.796C>G	P.L266V
XH_P15	3	113594396	113594396	Frame_Shift_Ins	INDEL	-	-	TATG	TATG	GRAMD1C	327_330dupAT
XH_P15	3	179298703	179298708	Missense_Mutation	INDEL	TGTTCA	-	-	ACTL6A	53_85delGTTG	V.285_H286del
XH_P15	3	180320212	180320212	Splice_Site	INDEL	-	AA	AA	TTC14	61+3_161+4dupAA	
XH_P15	3	40352489	40352489	Frame_Shift_Ins	INDEL	-	T	T	EIF1B	c.138dupT	P.V47fs
XH_P15	3	42727133	42727133	Missense_Mutation	SNV	C	T	T	KLHL40	c.23C>T	P.A8V
XH_P15	3	45823712	45823712	Frame_Shift_Ins	INDEL	-	T	T	SLC6A20	c.124dupA	P.S42fs
XH_P15	3	47084059	47084059	Frame_Shift_Del	INDEL	C	-	-	SETD2	c.7230delG	P.J2411fs
XH_P15	3	47374726	47374726	Frame_Shift_Ins	INDEL	-	C	C	KLHL18	c.682dupC	P.R228fs
XH_P15	3	58094969	58094969	Frame_Shift_Del	INDEL	T	-	-	FLNB	c.2119delT	P.S707fs
XH_P15	3	58154312	58154315	Frame_Shift_Del	INDEL	TAAC	-	-	FLNB	439_7442delAC	P.N2480fs
XH_P15	4	106190765	106190765	Splice_Site	SNV	A	G	G	TET2	c.4045-2A>G	
XH_P15	4	138450913	138450913	Missense_Mutation	SNV	G	C	C	PCDH18	c.2330C>G	P.S777W
XH_P15	4	139980616	139980622	Frame_Shift_Del	INDEL	TGACTAC	-	-	ELF2	30_1036delGTGA	P.V344fs
XH_P15	4	184367966	184367981	Frame_Shift_Del	INDEL	TAGACCAGTC	-	-	CDKN2AIP	44delTCCACAGAC	P.S377fs
XH_P15	4	959035	959035	Frame_Shift_Ins	INDEL	-	CC	CC	DGKQ	1661_1662dupC	P.L555fs
XH_P15	5	127710331	127710331	Silent	SNV	A	T	T	FBN2	c.2085T>A	P.R695R
XH_P15	5	33944831	33944831	Silent	SNV	G	A	A	SLC45A2	c.1515C>T	P.V505V
XH_P15	5	53814873	53814880	Frame_Shift_Del	INDEL	CCAGCCAC	-	-	SNX18	5_1102delCCAC	P.H366fs
XH_P15	6	116381223	116381223	Missense_Mutation	SNV	G	C	C	FRK	c.252C>G	P.H84Q
XH_P15	6	121427164	121427164	Splice_Site	INDEL	-	T	T	TBC1D32	c.3465+4dupA	
XH_P15	6	130762171	130762197	Missense_Mutation	INDEL	TTGGCAGCA	-	-	TMEM200A	5ATTGGCAGCAAP	R.204_S212del
XH_P15	6	134493912	134493912	Splice_Site	INDEL	-	CT	CT	SGK1	35-2_835-1dupAG	
XH_P15	6	136476805	136476808	Frame_Shift_Del	INDEL	TGCT	-	-	PDE7B	620_623delITGD	P.L207fs
XH_P15	6	162683710	162683710	Missense_Mutation	SNV	C	T	T	PARK2	c.259G>A	P.D87N
XH_P15	6	17794483	17794483	Frame_Shift_Ins	INDEL	-	TAGT	TAGT	KIF13A	218_3219insAC	P.V1073fs
XH_P15	6	24495516	24495516	Missense_Mutation	SNV	G	A	A	ALDH5A1	c.292G>A	P.A98T
XH_P15	6	26022047	26022047	Frame_Shift_Ins	INDEL	-	TA	TA	HIST1H4A	c.142_143insAT	P.S48fs
XH_P15	6	28333382	28333382	Frame_Shift_Ins	INDEL	-	GGCA	GGCA	ZKSCAN3	938_941dupGG	P.H314fs
XH_P15	6	43400951	43400951	Frame_Shift_Ins	INDEL	-	CT	CT	ABCC10	1236_1237dupC	P.Y413fs
XH_P15	6	44253899	44253899	Silent	SNV	G	A	A	TCTE1	c.648C>T	P.S216S
XH_P15	7	128482269	128482269	Splice_Site	INDEL	-	G	G	FLNC	c.2122-13dupG	
XH_P15	7	138713681	138713681	Frame_Shift_Ins	INDEL	-	C	C	ZC3HAV1L	c.526dupG	P.E176fs
XH_P15	7	13971133	13971133	Missense_Mutation	SNV	C	T	T	ETV1	c.796G>A	P.D266N
XH_P15	7	150164095	150164095	Silent	SNV	C	T	T	GIMAP8	c.309C>T	P.I103I
XH_P15	7	30068407	30068407	Frame_Shift_Ins	INDEL	-	CT	CT	PLEKHA8	c.30_31dupCT	P.Y11fs
XH_P15	7	44104864	44104864	Nonsense_Mutation	SNV	C	A	A	PGAM2	c.265G>C	P.E89*
XH_P15	7	73118738	73118738	Frame_Shift_Ins	INDEL	-	TGAG	TGAG	STX1A	298_299insCTC	P.I100fs
XH_P15	7	89856600	89856600	Frame_Shift_Ins	INDEL	-	TA	TA	STEAP2	1811_812dupTA	P.L272fs
XH_P15	7	92761723	92761723	Nonsense_Mutation	SNV	G	A	A	SAMD9L	c.3562C>T	P.R1188*
XH_P15	8	104312436	104312436	Missense_Mutation	SNV	A	C	C	FZD6	c.101A>C	P.K34T
XH_P15	8	14944735	14944742	Frame_Shift_Del	INDEL	CCGGCCTC	-	-	EPPK1	102687delGAGG	P.E894fs
XH_P15	8	27145644	27145644	Frame_Shift_Del	INDEL	A	-	-	TRIM35	c.786delT	P.C262fs
XH_P15	8	27145645	27145645	Splice_Site	SNV	C	T	T	TRIM35	c.786-1G>A	
XH_P15	8	30585153	30585153	Frame_Shift_Ins	INDEL	-	GA	GA	GSR	c.199_200insTC	P.Y67fs
XH_P15	8	53045681	53045681	Missense_Mutation	SNV	G	A	A	ST18	c.2380C>T	P.R794C
XH_P15	8	72756341	72756341	Missense_Mutation	SNV	C	T	T	MSC	c.73G>A	P.A25T
XH_P15	8	90965619	90965622	Frame_Shift_Del	INDEL	TAAC	-	-	NBN	695_1698delGT	P.Q565fs
XH_P15	9	129376788	129376788	Frame_Shift_Ins	INDEL	-	CG	CG	LMX1B	c.60_61insCG	P.C21fs
XH_P15	9	135979141	135979141	Frame_Shift_Ins	INDEL	-	AGTC	AGTC	RALGDS	582_1585dupG	P.Y529fs
XH_P15	9	139686484	139686484	Splice_Site	INDEL	-	GG	GG	TMEM141	105+4_205+5dupGG	
XH_P15	9	139835501	139835506	Missense_Mutation	INDEL	AGCAGC	-	-	FBXW5	75_1580delGCT	P.L526_L527del
XH_P15	9	140331030	140331032	Missense_Mutation	INDEL	GCT	-	-	ENTPD8	1727_729delAG	P.S243del
XH_P15	9	19126149	19126150	Frame_Shift_Del	INDEL	GG	-	-	PLIN2	c.188_189delCC	P.T63fs
XH_P15	9	37800650	37800650	Splice_Site	INDEL	-	TTG	TTG	DCAF10	20+6_20+7insTTG	
XH_P15	9	37800650	37800650	Splice_Site	INDEL	T	-	-	DCAF10	c.20+6delT	
XH_P15	9	86571117	86571117	Frame_Shift_Ins	INDEL	-	AGT	AGT	C9orf64	296_298dupAC	P.Y99dup
XH_P15	9	97844955	97844955	Frame_Shift_Ins	INDEL	-	GAT	GAT	C9orf3	419_2421dupG	P.D807dup
XH_P15	X	41204684	41204684	Missense_Mutation	INDEL	-	ATA	ATA	DDX3X	199_1201dupAP	V.400_1401insN
XH_P15	X	57021122	57021126	Frame_Shift_Del	INDEL	ATTTG	-	-	SPIN3	255_259delCAA	P.K86fs
XH_P15	X	68058601	68058601	Frame_Shift_Ins	INDEL	-	ACAT	ACAT	EFNB1	273_274insTAC	P.V92fs
XH_P16	1	198697459	198697459	Splice_Site	SNV	T	A	A	PTPRC	c.1721-10T>A	
XH_P16	1	54509117	54509117	Missense_Mutation	SNV	C	T	T	TMEM59	c.472G>A	P.A158T
XH_P16	1	8397927	8397927	Missense_Mutation	SNV	A	G	G	SLC45A1	c.1751A>G	P.E584G
XH_P16	10	103900368	103900368	Silent	SNV	C	A	A	PPRC1	c.2103C>A	P.A701A
XH_P16	10	82267045	82267045	Missense_Mutation	SNV	T	G	G	TSPAN14	c.194T>G	P.V65G
XH_P16	10	88203077	88203077	Silent	SNV	G	C	C	WAPL	c.3348C>G	P.A1116A
XH_P16	10	88768297	88768297	Silent	SNV	G	A	A	AGAP11	c.288G>A	P.E96E
XH_P16	11	50003751	50003751	Missense_Mutation	SNV	A	C	C	OR4C12	c.287T>G	P.M96R
XH_P16	12	8375278	8375278	Missense_Mutation	SNV	C	T	T	FAM90A1	c.535G>A	P.V179I
XH_P16	13	20637066	20637066	Missense_Mutation	SNV	G	A	A	ZMYM2	c.2992G>A	P.V998I
XH_P16	13	53421212	53421212	Missense_Mutation	SNV	A	T	T	PCDH8	c.1360T>A	P.S454T
XH_P16	14	23447665	23447665	Splice_Site	SNV	A	G	G	AJUBA	c.1007-11T>C	
XH_P16	14	25100338	25100338	Missense_Mutation	SNV	C	G	G	GZMB	c.683G>C	P.R228P
XH_P16	15	74468454	74468454	Missense_Mutation	SNV	C	T	T	ISLR	c.1255C>T	P.L149F
XH_P16	16	31382991	31382991	Frame_Shift_Ins	INDEL	-	T	T	ITGAX	2046_2047ins	P.P683fs
XH_P16	16	31382992	31382992	Frame_Shift_Ins	INDEL	-	TG	TG	ITGAX	2047_2048insT	P.P683fs
XH_P16	16	89347823	89347823	Silent	SNV	C	A	A	ANKRD11	c.5127G>T	P.V1709V
XH_P16	17	10297566	10297566	Splice_Site	SNV	C	T	T	MYH8	c.5166G>A	P.Q1722Q
XH_P16	17	18700880	18700880	Splice_Site	SNV	A	T	T	TVP23B	c.49-12A>T	
XH_P16	19	32083744	32083744	Silent	SNV	G	A	A	THEG5	c.246G>A	P.L82L
XH_P16	19	3633460	3633460	Frame_Shift_Del	INDEL	G	-	-	PIP5K1C	c.1979delC	P.P660fs
XH_P16	19	44680888	44680888	Silent	SNV	A	G	G	ZNF226	c.1473A>G	P.Q491Q
XH_P16	19	50213590	50213590	Missense_Mutation	SNV	T	A	A	CPT1C	c.1547T>A	P.I516N
XH_P16	19	6743270	6743270	Splice_Site	SNV	G	T	T	TRIP10	c.408+3G>T	
XH_P16	2	17913067	17913067	Missense_Mutation	SNV	A	G	G	SMC6	c.422T>C	P.L141P
XH_P16	2	231134655	231134655	Silent	SNV	G	A	A	SP140	c.1251G>A	P.A417A
XH_P16	2	242163117	242163117	Missense_Mutation	SNV	T	C	C	ANO7	c.2615T>C	P.V872A
XH_P16	2	28634869	28634869	Frame_Shift_Del	INDEL	A	-	-	FOSL2	c.536delA	P.K179fs
XH_P16	2	97833499	97833499	Missense_Mutation	SNV	G	C	C	ANKRD36	c.1628G>C	P.G543A
XH_P16	20	62195645	62195645	Silent	SNV	C	T	T	HELZ2	c.4530G>A	P.P1510P
XH_P16	20	9510313	9510313	Missense_Mutation	SNV	G	A	A	LAMP5	c.557G>A	P.R186Q
XH_P16	21	47648346	47648346	Splice_Site	SNV	A	G	G	LSS	c.180+2T>C	
XH_P16	22	36177688	36177688	Missense_Mutation	SNV	G	T	T	RBFOX2	c.355C>A	P.P119T
XH_P16	3	168806806	168806806	Missense_Mutation	SNV	G	T	T	MECOM	c.3198C>A	P.H1066Q
XH_P16	3	178917478	178917478	Missense_Mutation	SNV	G	A	A	PIK3CA	c.353G>A	P.G118D
XH_P16	3	52437845	52437848	Frame_Shift_Del	INDEL	ACTG	-	-	BAP1	313_1316delCA	P.S438fs

XH_P16	4	160274909	160274909	Silent	SNV	C	T	T	RAPGEF2	c.3879C>T	P.S1293S
XH_P16	5	136324278	136324278	Missense_Mutation	SNV	T	C	C	SPOCK1	c.761A>G	P.N254S
XH_P16	5	148407689	148407689	Missense_Mutation	SNV	G	A	A	SH3TC2	c.1606C>T	P.R536W
XH_P16	5	38407201	38407201	Missense_Mutation	SNV	C	T	T	EGFLAM	c.1100C>T	P.S367L
XH_P16	5	98221357	98221357	Splice_Site	INDEL	-	A	A	CHD1	c.2497>dupT	
XH_P16	6	136590653	136590653	Missense_Mutation	SNV	G	A	A	BCLAF1	c.2135C>T	P.S712F
XH_P16	6	44392313	44392313	Missense_Mutation	SNV	G	T	T	CDC5L	c.1562G>T	P.R521L
XH_P16	6	56418088	56418088	Frame_Shift_Ins	INDEL	-	T	T	DST	c.9144dupA	P.A3049fs
XH_P16	7	111976201	111976201	Silent	SNV	C	A	A	ZNF277	c.844C>A	P.R282R
XH_P16	7	121616296	121616296	Frame_Shift_Del	INDEL	T	-	-	PTPRZ1	c.527delT	P.L176fs
XH_P16	7	146818146	146818146	Missense_Mutation	SNV	A	G	G	CNTNAP2	c.830A>G	P.H277R
XH_P16	7	18688241	18688241	Missense_Mutation	SNV	C	G	G	HDAC9	c.1402C>G	P.Q468E
XH_P16	8	134062215	134062215	Missense_Mutation	SNV	T	G	G	SLA	c.180A>C	P.K60N
XH_P16	8	145060131	145060131	Missense_Mutation	SNV	A	C	C	PARP10	c.230T>G	P.V77G
XH_P16	9	136599206	136599206	Silent	SNV	G	A	A	SARDH	c.90C>T	P.S30S
XH_P16	X	16887325	16887325	Missense_Mutation	SNV	T	G	G	RBBP7	c.167A>C	P.E56A
XH_P17	1	150116893	150116893	Missense_Mutation	SNV	A	G	G	VPS45	c.1411A>G	P.R471G
XH_P17	1	151681773	151681773	Missense_Mutation	SNV	T	C	C	CELF3	c.188A>G	P.D63G
XH_P17	1	17727720	17727720	Missense_Mutation	SNV	G	A	A	PADI6	c.1871G>A	P.G624D
XH_P17	1	197313501	197313501	Missense_Mutation	SNV	G	A	A	CRB1	c.743G>A	P.C248Y
XH_P17	10	104356900	104356900	Nonsense_Mutation	SNV	A	T	T	SUFU	c.760A>C	P.R254*
XH_P17	10	75560464	75560464	Frame_Shift_Del	INDEL	C	-	-	ZSWIM8	c.5085delC	P.V1696fs
XH_P17	11	34680218	34680218	Nonsense_Mutation	SNV	G	A	A	EHF	c.677G>A	P.W226*
XH_P17	11	64564284	64564284	Silent	SNV	G	T	T	MAP4K2	c.1465C>A	P.R489R
XH_P17	13	111274693	111274693	Silent	SNV	C	T	T	NAXD	c.231C>T	P.G77G
XH_P17	14	105417034	105417034	Missense_Mutation	SNV	T	C	C	AHNAK2	c.4754A>G	P.K1585R
XH_P17	14	91356823	91356823	Splice_Site	SNV	G	A	A	RPS6KA5	c.993+8C>T	
XH_P17	16	15790606	15790606	Missense_Mutation	SNV	A	G	G	NDE1	c.836A>G	P.Y279C
XH_P17	16	31539967	31539967	Silent	SNV	C	T	T	AHP5	c.264C>T	P.F88F
XH_P17	16	53256655	53256655	Silent	SNV	T	C	C	CHD9	c.1884T>C	P.D628D
XH_P17	19	43237120	43237120	Silent	SNV	G	A	A	PSG3	c.525C>T	P.D175D
XH_P17	19	47200450	47200450	Silent	SNV	C	T	T	PRKD2	c.1281G>A	P.T427T
XH_P17	19	8154821	8154821	Silent	SNV	G	A	A	FBN3	c.6207C>T	P.P2069P
XH_P17	2	179981410	179981410	Missense_Mutation	SNV	A	T	T	SESTD1	c.1632T>A	P.F544L
XH_P17	2	234627609	234627609	Missense_Mutation	SNV	T	C	C	UGT1A4	c.143T>C	P.L48S
XH_P17	20	16486474	16486474	Missense_Mutation	SNV	T	C	C	KIF16B	c.893A>G	P.N298S
XH_P17	20	47274740	47274740	Silent	SNV	G	A	A	PREX1	c.1908C>T	P.G636G
XH_P17	21	45844768	45844768	Missense_Mutation	SNV	G	A	A	TRPM2	c.3733G>A	P.V1245M
XH_P17	21	47704502	47704502	Silent	SNV	T	C	C	MCM3AP	c.699A>G	P.E233E
XH_P17	22	21330964	21330964	Missense_Mutation	SNV	C	T	T	ALFM3	c.1055C>T	P.T352M
XH_P17	22	51159965	51159965	Missense_Mutation	SNV	C	T	T	SHANK3	c.3662C>T	P.P1221L
XH_P17	3	52539331	52539331	Splice_Site	SNV	A	T	T	STAB1	c.1519-4A>T	
XH_P17	3	97596432	97596432	Nonsense_Mutation	SNV	G	T	T	CRYBG3	c.6394G>T	P.E2132*
XH_P17	4	88055769	88055769	Missense_Mutation	SNV	A	T	T	AFF1	c.3458A>T	P.Y1153F
XH_P17	5	149512405	149512405	Silent	SNV	C	T	T	PDGFRB	c.1035G>A	P.P345P
XH_P17	6	24839358	24839358	Missense_Mutation	SNV	G	C	C	FAM65B	c.2000C>G	P.A667G
XH_P17	6	44117662	44117662	Missense_Mutation	SNV	A	C	C	TMEM63B	c.1480A>C	P.I494L
XH_P17	7	120704280	120704280	Splice_Site	SNV	C	T	T	CPED1	c.541-12C>T	
XH_P17	7	140481411	140481411	Missense_Mutation	SNV	C	A	A	BRAF	c.1397G>T	P.G466V
XH_P17	8	144789836	144789836	Splice_Site	SNV	C	T	T	CCDC166	c.444G>A	P.K148K
XH_P17	8	25890659	25890659	Missense_Mutation	SNV	C	G	G	EBF2	c.493G>C	P.E165Q
XH_P17	8	57128950	57128950	Splice_Site	SNV	C	T	T	CHCHD7	c.132C>T	P.I44I
XH_P17	9	114986141	114986141	Missense_Mutation	SNV	G	C	C	PTBP3	c.1565C>G	P.S522C
XH_P17	9	134362687	134362687	Splice_Site	SNV	C	T	T	PRRC2B	c.5984+6C>T	
XH_P17	9	38068518	38068518	Frame_Shift_Ins	INDEL	-	G	G	SHB	c.124dupC	P.Q42fs
XH_P17	X	107924981	107924981	Splice_Site	SNV	G	T	T	COL4A5	c.4070-9G>T	
XH_P17	X	32407785	32407785	Frame_Shift_Ins	INDEL	-	T	T	DMD	c.4326dupA	P.L1443fs
XH_P18	1	115251238	115251238	Frame_Shift_Del	INDEL	A	-	-	NRAS	c.488delT	P.1163fs
XH_P18	1	158450049	158450049	Missense_Mutation	SNV	G	A	A	OR10R2	c.382G>A	P.A128T
XH_P18	10	118443293	118443293	Splice_Site	SNV	C	G	G	HSPA12A	c.886+9G>C	
XH_P18	10	50028381	50028381	Missense_Mutation	SNV	G	A	A	WDFY4	c.5608G>A	P.A1870T
XH_P18	11	56058264	56058264	Missense_Mutation	SNV	G	A	A	OR8H1	c.275C>T	P.S92F
XH_P18	11	612757	612757	Missense_Mutation	SNV	C	T	T	IRF7	c.1400G>A	P.R467H
XH_P18	11	64110663	64110663	Missense_Mutation	SNV	C	T	T	CCDC88B	c.1075C>T	P.L359F
XH_P18	11	6554289	6554289	Missense_Mutation	SNV	C	G	G	DNHD1	c.2380C>G	P.L794V
XH_P18	11	67811294	67811294	Missense_Mutation	SNV	G	A	A	TCIRG1	c.727G>A	P.V243I
XH_P18	11	68475782	68475782	Missense_Mutation	SNV	C	A	A	TESMIN	c.1521G>T	P.M507I
XH_P18	11	77590088	77590088	Missense_Mutation	SNV	C	G	G	INTS4	c.2799G>C	P.E933D
XH_P18	12	123200497	123200497	Missense_Mutation	SNV	G	A	A	HCAH3	c.788C>T	P.T263M
XH_P18	12	25398285	25398285	Missense_Mutation	SNV	C	A	A	KRAS	c.34G>T	P.G12C
XH_P18	12	40940944	40940944	Silent	SNV	C	T	T	MUC19	c.23139C>T	P.T7713T
XH_P18	12	52865464	52865464	Missense_Mutation	SNV	G	C	C	KRT6C	c.808C>G	P.L270V
XH_P18	13	113803460	113803460	Missense_Mutation	SNV	C	A	A	F10	c.1096C>A	P.R366S
XH_P18	13	36686200	36686200	Nonsense_Mutation	SNV	G	A	A	DCLK1	c.529C>T	P.R177*
XH_P18	14	20847178	20847178	Silent	SNV	G	A	A	TEP1	c.4890C>T	P.D1630D
XH_P18	14	35592700	35592700	Frame_Shift_Del	INDEL	T	-	-	KIAA0391	c.257delT	P.L86fs
XH_P18	14	77685214	77685214	Missense_Mutation	SNV	G	C	C	TMEM63C	c.58G>C	P.D20H
XH_P18	15	43023935	43023935	Missense_Mutation	SNV	C	T	T	CDAN1	c.1622G>A	P.R541Q
XH_P18	15	48786440	48786440	Missense_Mutation	SNV	C	T	T	FBN1	c.2689G>A	P.G897S
XH_P18	15	65491108	65491108	Missense_Mutation	SNV	G	A	A	CILP	c.1516C>T	P.R506C
XH_P18	15	79603645	79603645	Silent	SNV	G	A	A	TMED3	c.54G>A	P.L18L
XH_P18	16	1709952	1709952	Silent	SNV	G	A	A	CRAMP1	c.2301G>A	P.T767T
XH_P18	16	22926676	22926676	Silent	SNV	G	A	A	HS3ST2	c.897G>A	P.T299T
XH_P18	16	682597	682597	Nonsense_Mutation	SNV	G	T	T	WFIKK1	c.187G>C	P.E63*
XH_P18	16	84179152	84179152	Missense_Mutation	SNV	G	C	C	DNAAF1	c.107G>C	P.R36P
XH_P18	17	40028336	40028336	Silent	SNV	C	T	T	ACLY	c.2742G>A	P.A914A
XH_P18	17	46930276	46930276	Splice_Site	SNV	C	G	G	CALCOCO2	c.898-12C>G	
XH_P18	17	55822346	55822346	Silent	SNV	G	A	A	CCDC182	c.288C>T	P.R96R
XH_P18	18	12699131	12699131	Nonsense_Mutation	SNV	G	A	A	CEP76	c.367C>T	P.Q123*
XH_P18	18	32825531	32825531	Missense_Mutation	SNV	G	A	A	ZNF397	c.862G>A	P.D288N
XH_P18	18	42530447	42530447	Missense_Mutation	SNV	C	T	T	SETBP1	c.1142C>T	P.S381L
XH_P18	18	48591933	48591933	Nonsense_Mutation	SNV	C	T	T	SMAD4	c.1096C>T	P.Q366*
XH_P18	18	7080391	7080391	Missense_Mutation	SNV	C	T	T	LAMA1	c.127G>A	P.E43K
XH_P18	19	17648265	17648265	Missense_Mutation	SNV	C	T	T	FAM129C	c.601C>T	P.R201W
XH_P18	2	114257213	114257213	Missense_Mutation	SNV	G	A	A	FOXO4L1	c.380G>A	P.R127H
XH_P18	2	114355053	114355053	Splice_Site	SNV	C	T	T	WASH2P	n.1307-10C>T	
XH_P18	2	120223398	120223398	Missense_Mutation	SNV	A	T	T	SCTR	c.470T>A	P.L157H
XH_P18	2	165947654	165947654	Missense_Mutation	SNV	G	C	C	SCN3A	c.4862C>G	P.A1621G

XH_P18	20	30436343	30436343	Missense_Mutation	SNV	C	T	T	DUSP15	c.752G>A	P.S251N
XH_P18	20	45021755	45021755	Missense_Mutation	SNV	T	C	C	ELMO2	c.220A>G	P.I74V
XH_P18	20	55033716	55033716	Frame_Shift_Del	INDEL	C	-	-	CASS4	c.2115delC	P.S706fs
XH_P18	20	57766219	57766219	Frame_Shift_Ins	INDEL	-	C	C	ZNF831	c.153dupC	P.T52fs
XH_P18	22	30064391	30064391	Nonsense_Mutation	SNV	C	T	T	NF2	c.955C>T	P.Q319*
XH_P18	3	130095279	130095279	Silent	SNV	C	A	A	COL6A5	c.267C>A	P.G89G
XH_P18	3	134348527	134348527	Silent	SNV	C	T	T	KY	c.273G>A	P.L91L
XH_P18	3	192516769	192516769	Silent	SNV	G	A	A	MB21D2	c.882C>T	P.S294S
XH_P18	4	78079683	78079683	Splice_Site	SNV	C	T	T	CCNG2	c.1-3C>T	
XH_P18	5	128932256	128932256	Missense_Mutation	SNV	A	G	G	ADAMTS19	c.1377A>G	P.I459M
XH_P18	5	150051388	150051388	Silent	SNV	G	A	A	MYO23	c.342G>A	P.G114G
XH_P18	6	167754781	167754781	Missense_Mutation	SNV	T	C	C	TTLL2	c.1393T>C	P.Y465H
XH_P18	6	26598218	26598218	Silent	SNV	C	A	A	ABT1	c.318C>A	P.T106T
XH_P18	7	154876053	154876053	Silent	SNV	C	G	G	HTR5A	c.930C>G	P.L310L
XH_P18	7	31144526	31144526	Splice_Site	SNV	A	G	G	ADCYAP1R1	c.1218+3A>G	
XH_P18	7	4107515	4107515	Missense_Mutation	SNV	C	T	T	SDK1	c.2957C>T	P.T986I
XH_P18	9	113217858	113217858	Splice_Site	SNV	C	T	T	SVEP1	c.3787+12G>A	
XH_P18	9	117749	117749	Missense_Mutation	SNV	C	T	T	FOXD4	c.371G>A	P.R124H
XH_P18	9	117840316	117840316	Silent	SNV	G	A	A	TNC	c.2580C>T	P.I860I
XH_P18	9	123935683	123935683	Missense_Mutation	SNV	G	A	A	CNTRL	c.6580G>A	P.E2194K
XH_P18	9	127549470	127549470	Missense_Mutation	SNV	G	A	A	OLFML2A	c.307G>A	P.E103K
XH_P18	9	32573010	32573010	Missense_Mutation	SNV	C	T	T	NDUFB6	c.49G>A	P.E17K
XH_P18	X	120009158	120009158	Missense_Mutation	SNV	C	G	G	CT47B1	c.367G>C	P.V123L
XH_P18	X	30327273	30327273	Missense_Mutation	SNV	C	T	T	NR0B1	c.208G>A	P.G70S
XH_P18	X	41043854	41043854	Missense_Mutation	SNV	A	T	T	USP9X	c.3484A>T	P.I1162F
XH_P18	X	47028898	47028898	Splice_Site	SNV	G	A	A	RBM10	c.201+1G>A	
XH_P18	X	64738312	64738312	Silent	SNV	G	A	A	LAS1L	c.1431C>T	P.D477D
XH_P18	X	92927194	92927194	Missense_Mutation	SNV	A	C	C	NAP1L3	c.1110T>G	P.N370K
XH_P20	1	104166510	104166510	Missense_Mutation	SNV	C	T	T	AMY2A	c.1124C>T	P.P375L
XH_P20	1	248004654	248004654	Missense_Mutation	SNV	G	A	A	OR11L1	c.545C>T	P.P182I
XH_P20	1	42660569	42660569	Missense_Mutation	SNV	C	G	G	FOXJ3	c.926G>C	P.S309T
XH_P20	1	44128657	44128657	Silent	SNV	A	C	C	KDM4A	c.522A>C	P.P174P
XH_P20	1	86047648	86047648	Silent	SNV	A	G	G	CYR61	c.315A>G	P.T105R
XH_P20	1	87043754	87043754	Splice_Site	SNV	C	T	T	CLCA4	c.2121C>T	P.N707N
XH_P20	10	113913376	113913376	Missense_Mutation	SNV	T	G	G	GPAM	c.2419A>C	P.S807R
XH_P20	11	117309618	117309618	Missense_Mutation	SNV	C	A	A	DSCAML1	c.4406G>T	P.G1469V
XH_P20	11	62287822	62287822	Silent	SNV	G	A	A	AHNAK	c.1406T>C	P.D4689D
XH_P20	11	64029057	64029057	Missense_Mutation	SNV	G	T	T	PLCB3	c.1833G>T	P.R611S
XH_P20	12	46123836	46123836	Frame_Shift_Ins	INDEL	-	A	A	ARID2	c.109dupA	P.I37fs
XH_P20	12	7277231	7277231	Silent	SNV	C	A	A	RBP5	c.201G>T	P.L67L
XH_P20	16	20749214	20749214	Frame_Shift_Del	INDEL	T	-	-	THUMPDP1	c.471delA	P.V158fs
XH_P20	16	3169341	3169341	Missense_Mutation	SNV	G	T	T	ZNF205	c.680G>T	P.R227I
XH_P20	16	3169342	3169342	Missense_Mutation	SNV	A	T	T	ZNF205	c.681A>T	P.R227S
XH_P20	17	19700909	19700909	Nonsense_Mutation	SNV	G	A	A	ULK2	c.1609C>T	P.Q537*
XH_P20	17	32906211	32906211	Missense_Mutation	SNV	T	C	C	C17orf102	c.89A>G	P.Q30R
XH_P20	17	3558527	3558527	Frame_Shift_Ins	INDEL	-	T	T	CTNS	c.345dupT	P.L116fs
XH_P20	17	46675333	46675333	Silent	SNV	C	T	T	HOXB6	c.180G>A	P.P60P
XH_P20	17	47295128	47295128	Missense_Mutation	SNV	G	T	T	AB13	c.295G>T	P.A99S
XH_P20	17	61833623	61833623	Missense_Mutation	SNV	T	A	A	CCDC47	c.925A>T	P.T309S
XH_P20	17	62499430	62499430	Missense_Mutation	SNV	A	C	C	DDX5	c.686T>G	P.I229S
XH_P20	17	67151195	67151195	Missense_Mutation	SNV	A	G	G	ABCA10	c.3659T>C	P.I1220T
XH_P20	19	17448421	17448421	Missense_Mutation	SNV	A	T	T	GTPBP3	c.1A>T	P.M1?
XH_P20	19	287603	287603	Frame_Shift_Ins	INDEL	-	A	A	PLPP2	c.352dupT	P.Y118fs
XH_P20	19	33716448	33716448	Splice_Site	SNV	G	A	A	SLC7A10	c.151+11C>T	
XH_P20	19	40322434	40322434	Splice_Site	SNV	T	G	G	DYRK1B	c.63+11A>C	
XH_P20	19	4525772	4525772	Missense_Mutation	SNV	A	G	G	PLIN5	c.593T>C	P.F198S
XH_P20	19	46915241	46915241	Missense_Mutation	SNV	C	T	T	CCDC8	c.827G>A	P.R276H
XH_P20	19	55812869	55812869	Splice_Site	SNV	C	A	A	BRSK1	c.679-11C>A	
XH_P20	2	170025100	170025100	Missense_Mutation	SNV	C	T	T	LRP2	c.11584G>A	P.D3862N
XH_P20	2	209113113	209113113	Missense_Mutation	SNV	G	A	A	IDH1	c.394C>T	P.R132C
XH_P20	2	219688611	219688611	Splice_Site	SNV	C	T	T	PRKAG3	c.1354-10G>A	
XH_P20	2	241696735	241696735	Splice_Site	SNV	C	T	T	KIF1A	c.2858+1G>A	
XH_P20	2	242590732	242590732	Frame_Shift_Del	INDEL	A	-	-	ATG4B	c.170delA	P.N57fs
XH_P20	2	46231746	46231746	Silent	SNV	C	T	T	PRKCE	c.1032C>T	P.S344S
XH_P20	20	25596768	25596768	Silent	SNV	T	C	C	NANP	c.540A>G	P.Q180Q
XH_P20	20	37464638	37464638	Missense_Mutation	SNV	C	T	T	PPP1R16B	c.70C>T	P.R24W
XH_P20	20	56139592	56139592	Missense_Mutation	SNV	C	T	T	PCK1	c.1241C>T	P.P414L
XH_P20	22	36661955	36661955	Missense_Mutation	SNV	A	C	C	APOL1	c.1073A>C	P.H358P
XH_P20	22	39132380	39132380	Silent	SNV	A	C	C	UON3	c.2109T>G	P.P703P
XH_P20	3	30713759	30713759	Missense_Mutation	SNV	C	T	T	TGFB2	c.1159C>T	P.H387Y
XH_P20	3	46759092	46759092	Missense_Mutation	SNV	A	G	G	PRSS50	c.142T>C	P.S48P
XH_P20	4	99997531	99997531	Missense_Mutation	SNV	A	C	C	ADH5	c.737T>G	P.F246C
XH_P20	5	130775337	130775337	Missense_Mutation	SNV	T	C	C	RAPGEF6	c.3706A>G	P.I1236V
XH_P20	5	140798530	140798530	Silent	SNV	C	T	T	PCDHGB7	c.1104C>T	P.L368L
XH_P20	5	179302035	179302035	Missense_Mutation	SNV	C	T	T	TBC1D9B	c.2053G>A	P.V685M
XH_P20	5	90671344	90671344	Missense_Mutation	SNV	C	A	A	ARRDC3	c.597G>T	P.R199S
XH_P20	6	144783784	144783784	Splice_Site	SNV	T	G	G	UTRN	c.2854-6T>G	
XH_P20	6	52380816	52380816	Silent	SNV	G	A	A	TRAM2	c.399C>T	P.Y133Y
XH_P20	7	126409909	126409909	Splice_Site	SNV	T	C	C	GRM8	c.1357+10A>G	
XH_P20	7	157959907	157959907	Missense_Mutation	SNV	C	T	T	PTPRN2	c.512G>A	P.R171Q
XH_P20	7	158566022	158566022	Splice_Site	SNV	C	T	T	ESYT2	c.947+10G>A	
XH_P20	7	29126126	29126126	Missense_Mutation	SNV	T	C	C	CPVL	c.583A>G	P.N195D
XH_P20	9	107556705	107556727	Frame_Shift_Del	INDEL	TCGATGAGC	-	-	ABCA1	GACGAGGGCTC	P.G1816fs
XH_P20	9	35698173	35698173	Splice_Site	SNV	G	A	A	TLN1	c.7372-4C>T	
XH_P20	X	110494522	110494522	Splice_Site	SNV	T	C	C	CAPN6	c.894-8A>G	
XH_P21	1	16475402	16475418	Frame_Shift_Del	INDEL	TCATGAAG	-	-	EPHA2	delGTATCTTCA	P.R93fs
XH_P21	1	27089779	27089779	Splice_Site	SNV	A	T	T	ARID1A	c.2732+3A>T	
XH_P21	1	48698073	48698073	Missense_Mutation	SNV	T	C	C	SLCSA9	c.932T>C	P.L311P
XH_P21	11	113639609	113639609	Silent	SNV	C	T	T	ZW10	c.186G>A	P.Q62Q
XH_P21	11	117074070	117074070	Silent	SNV	G	A	A	TAGLN	c.228G>A	P.P76P
XH_P21	11	4095774	4095774	Silent	SNV	G	A	A	STIM1	c.834G>A	P.E278E
XH_P21	11	60705508	60705508	Splice_Site	SNV	G	T	T	SLC15A3	c.1436-11C>A	
XH_P21	12	32908789	32908789	Missense_Mutation	SNV	C	T	T	YARS2	c.20G>A	P.R7Q
XH_P21	12	56094189	56094189	Splice_Site	SNV	G	A	A	ITGA7	c.671-12C>T	
XH_P21	14	21831293	21831293	Missense_Mutation	SNV	C	T	T	SUPT16H	c.1411G>A	P.E471K
XH_P21	14	53347983	53347983	Missense_Mutation	SNV	T	G	G	FERMT2	c.731A>C	P.D244A
XH_P21	14	93290937	93290937	Missense_Mutation	SNV	T	C	C	GOLGA5	c.1667T>C	P.L556S
XH_P21	15	40094264	40094264	Missense_Mutation	SNV	A	C	C	GPR176	c.614T>G	P.V205G

XH_P21	16	11785284	11785284	Missense_Mutation	SNV	T	C	C	TXNDC11	c.1843A>G	P.N615D
XH_P21	17	56060555	56060555	Missense_Mutation	SNV	T	A	A	VEZF1	c.233A>T	P.Y78F
XH_P21	18	76752084	76752084	Silent	SNV	G	C	C	SALL3	c.93G>C	P.G31G
XH_P21	19	3110297	3110297	Missense_Mutation	SNV	C	T	T	GNA11	c.287C>T	P.T96M
XH_P21	19	44792033	44792033	Missense_Mutation	SNV	C	T	T	ZNF235	c.1555G>A	P.V519M
XH_P21	19	8551102	8551102	Missense_Mutation	SNV	G	T	T	HNRNPM	c.1385G>T	P.G462V
XH_P21	2	170012809	170012809	Silent	SNV	G	A	A	LRP2	c.12126C>T	P.R4042R
XH_P21	2	171863153	171863153	Splice_Site	SNV	C	T	T	TLK1	c.1455G>A	P.T485T
XH_P21	2	179472377	179472377	Missense_Mutation	SNV	C	G	G	TTN	c.48115G>C	P.G16039R
XH_P21	20	60884451	60884451	Missense_Mutation	SNV	T	C	C	LAMA5	c.11029A>G	P.M3677V
XH_P21	22	17445688	17445688	Missense_Mutation	SNV	A	T	T	GAB4	c.1444T>A	P.S482T
XH_P21	3	52649430	52649430	Nonsense_Mutation	SNV	T	A	A	PBRM1	c.1861A>T	P.K621*
XH_P21	5	122718697	122718697	Missense_Mutation	SNV	T	C	C	CEP120	c.1765A>G	P.I589V
XH_P21	5	149918784	149918784	Splice_Site	SNV	C	T	T	NDST1	c.1438-6C>T	
XH_P21	5	176522651	176522651	Missense_Mutation	SNV	C	T	T	FGFR4	c.1748C>T	P.P583L
XH_P21	5	77334917	77334917	Missense_Mutation	SNV	C	T	T	AP3B1	c.2612G>A	P.G871E
XH_P21	5	7897231	7897231	Missense_Mutation	SNV	C	A	A	MTRR	c.1823C>A	P.S608Y
XH_P21	6	123369766	123369766	Splice_Site	SNV	G	A	A	CLV52	c.565-1G>A	
XH_P21	6	38690689	38690689	Missense_Mutation	SNV	G	A	A	DNAH8	c.104G>A	P.R35H
XH_P21	6	43167899	43167899	Splice_Site	SNV	G	A	A	CUL9	c.3384+5G>A	
XH_P21	7	105305727	105305727	Missense_Mutation	SNV	G	C	C	ATXN7L1	c.364C>G	P.H122D
XH_P21	7	149129166	149129166	Missense_Mutation	SNV	C	G	G	ZNF777	c.2197G>C	P.E733Q
XH_P21	7	35242154	35242154	Missense_Mutation	SNV	G	T	T	TBX20	c.1232C>A	P.P411H
XH_P21	7	70598012	70598012	Missense_Mutation	SNV	A	T	T	WBSCR17	c.224A>T	P.Y75F
XH_P21	X	154493522	154493522	Missense_Mutation	SNV	T	G	G	RAB39B	c.52A>C	P.T18P
XH_P24	1	248814142	248814142	Frame_Shift_Ins	INDEL	-	TGTACTTCCT	TGTACTTCCT	OR2T27	44insAGGAAG	P.L15fs
XH_P24	18	48575131	48575131	Frame_Shift_Ins	INDEL	-	SACCATTATTCA	GACCATTATTCA	SMAD4	326insGACCAAT	P.L109fs
XH_P24	22	30077521	30077521	Frame_Shift_Ins	INDEL	-	CG	CG	NF2	1668-1669insC	P.A557fs
XH_P24	6	28097573	28097573	Missense_Mutation	SNV	G	C	C	ZSCAN16	c.892G>C	P.G298R
XH_P24	7	138732549	138732549	Frame_Shift_Ins	INDEL	-	TTTCAGAAAG	TTTCAGAAAG	ZC3HAV1	2500insCTTTTC	P.D834fs
XH_P25	1	170521361	170521361	Nonsense_Mutation	SNV	G	T	T	GORAB	c.403G>T	P.E135*
XH_P25	1	173930226	173930226	Missense_Mutation	SNV	G	A	A	RC3H1	c.2359C>T	P.H787Y
XH_P25	1	196577385	196577385	Missense_Mutation	SNV	C	T	T	KCNT2	c.55G>A	P.D19N
XH_P25	1	223989973	223989973	Missense_Mutation	SNV	A	C	C	TP53BP2	c.1070T>G	P.I357S
XH_P25	1	240370732	240370732	Missense_Mutation	SNV	G	T	T	FMN2	c.2632G>T	P.G878C
XH_P25	11	124543592	124543592	Missense_Mutation	SNV	C	A	A	SIAE	c.13G>T	P.G5W
XH_P25	11	124543593	124543593	Silent	SNV	C	A	A	SIAE	c.12G>T	P.P4P
XH_P25	11	1578670	1578670	Missense_Mutation	SNV	G	A	A	DUSP8	c.956C>T	P.P319L
XH_P25	11	373469	373469	Silent	SNV	G	T	T	B4GALNT4	c.657G>T	P.A219A
XH_P25	11	78467903	78467903	Silent	SNV	G	A	A	TENM4	c.2703C>T	P.L901L
XH_P25	12	113549986	113549986	Missense_Mutation	SNV	C	A	A	RASAL1	c.1279G>T	P.V427L
XH_P25	12	130833889	130833889	Silent	SNV	G	A	A	PIWIL1	c.840G>A	P.L280L
XH_P25	12	41900447	41900447	Missense_Mutation	SNV	G	A	A	PDZRN4	c.1033G>A	P.A345T
XH_P25	12	50358787	50358787	Missense_Mutation	SNV	G	A	A	AQP5	c.625G>A	P.G209R
XH_P25	12	7355295	7355295	Missense_Mutation	SNV	A	G	G	PEX5	c.841A>G	P.I281V
XH_P25	13	114059226	114059226	Silent	SNV	C	T	T	LOC101928841	c.3279G>A	P.T1093T
XH_P25	13	53313269	53313269	Missense_Mutation	SNV	G	T	T	LECT1	c.110C>A	P.A37E
XH_P25	13	73636749	73636749	Missense_Mutation	SNV	A	G	G	KLF5	c.1012A>G	P.I338V
XH_P25	13	84453670	84453670	Missense_Mutation	SNV	G	A	A	SLITRK1	c.1973C>T	P.A658V
XH_P25	15	25223443	25223443	Frame_Shift_Ins	INDEL	-	C	C	SNRNP	c.668dupC	P.P224fs
XH_P25	15	62948259	62948259	Missense_Mutation	SNV	G	T	T	TLN2	c.634G>T	P.V212L
XH_P25	15	68492004	68492005	Frame_Shift_Del	INDEL	AA	-	-	CALML4	c.178-179delTT	P.F60fs
XH_P25	16	1306884	1306884	Missense_Mutation	SNV	T	A	A	TPSD1	c.341T>A	P.I114N
XH_P25	16	22343426	22343426	Missense_Mutation	SNV	C	T	T	POLR3E	c.1882C>T	P.R628C
XH_P25	17	12852965	12852965	Splice_Site	SNV	G	A	A	ARHGAP44	c.974-1G>A	
XH_P25	17	15539578	15539578	Silent	SNV	C	A	A	TRIM16	c.621G>T	P.S207S
XH_P25	17	30980907	30980907	Missense_Mutation	SNV	C	T	T	MYO1D	c.2549G>A	P.R850Q
XH_P25	17	43923696	43923696	Missense_Mutation	SNV	C	A	A	SPPL2C	c.1424C>A	P.A475D
XH_P25	17	43923697	43923697	Silent	SNV	C	A	A	SPPL2C	c.1425C>A	P.A475A
XH_P25	17	47218678	47218678	Silent	SNV	C	T	T	B4GALNT2	c.84C>T	P.F28F
XH_P25	17	7577070	7577070	Frame_Shift_Del	INDEL	GGAGA	-	-	TP53	864-868delTCT	P.N288fs
XH_P25	17	76100671	76100672	Frame_Shift_Del	INDEL	GT	-	-	TNRC6C	4926-4927delC	P.Q1642fs
XH_P25	17	7906637	7906637	Missense_Mutation	SNV	C	A	A	GUCY2D	c.272C>A	P.A91E
XH_P25	18	13885084	13885084	Missense_Mutation	SNV	C	T	T	MC2R	c.434G>A	P.R145H
XH_P25	18	8783914	8783914	Silent	SNV	G	T	T	MTCL1	c.804G>T	P.L268L
XH_P25	18	8783915	8783915	Nonsense_Mutation	SNV	G	T	T	MTCL1	c.805G>T	P.E269*
XH_P25	19	11559980	11559980	Missense_Mutation	SNV	G	T	T	PRKCSH	c.1421G>T	P.R474L
XH_P25	19	21240796	21240796	Missense_Mutation	SNV	A	G	G	ZNF430	c.1679A>G	P.N560S
XH_P25	19	39018362	39018362	Missense_Mutation	SNV	G	T	T	RYR1	c.10762G>T	P.D3588Y
XH_P25	19	4523635	4523635	Missense_Mutation	SNV	C	A	A	PLIN5	c.1297G>T	P.D433Y
XH_P25	19	4523636	4523636	Silent	SNV	C	A	A	PLIN5	c.1296G>T	P.G432G
XH_P25	19	5957919	5957919	Splice_Site	SNV	G	A	A	RANBP3	c.78+10C>T	
XH_P25	19	7998877	7998877	Silent	SNV	G	A	A	TIMM44	c.555C>T	P.S185S
XH_P25	2	110881564	110881564	Missense_Mutation	SNV	C	A	A	NPHP1	c.2006G>T	P.R669L
XH_P25	2	113817047	113817047	Splice_Site	SNV	G	A	A	IL36RN	c.29+3G>A	
XH_P25	2	160245943	160245943	Missense_Mutation	SNV	C	G	G	BAZ2B	c.3021G>C	P.E1007D
XH_P25	2	228884239	228884239	Missense_Mutation	SNV	C	A	A	SPHKAP	c.1331G>T	P.W444L
XH_P25	2	233986944	233986944	Missense_Mutation	SNV	G	A	A	INPP5D	c.326G>A	P.G109D
XH_P25	2	234463031	234463031	Missense_Mutation	SNV	C	G	G	USP40	c.724G>C	P.A242P
XH_P25	2	25976397	25976397	Splice_Site	SNV	T	C	C	ASXL2	c.1142+6A>G	
XH_P25	2	98354504	98354504	Missense_Mutation	SNV	G	A	A	ZAP70	c.1670G>A	P.R557Q
XH_P25	22	28378504	28378504	Missense_Mutation	SNV	G	A	A	TTC28	c.7151C>T	P.T2384M
XH_P25	22	40140184	40140184	Missense_Mutation	SNV	C	A	A	ENTHD1	c.1324G>T	P.A442S
XH_P25	3	11402185	11402185	Nonsense_Mutation	SNV	C	G	G	ATG7	c.1610C>G	P.S537*
XH_P25	3	129247918	129247918	Silent	SNV	C	T	T	RHO	c.342C>T	P.G114G
XH_P25	3	141305476	141305476	Splice_Site	SNV	T	C	C	RASA2	c.1827-12T>C	
XH_P25	3	155654143	155654143	Silent	SNV	C	T	T	GMPS	c.1824C>T	P.I608I
XH_P25	3	164907582	164907582	Missense_Mutation	SNV	G	A	A	SLITRK3	c.1037C>T	P.S346F
XH_P25	3	190158126	190158126	Missense_Mutation	SNV	G	T	T	TMEM207	c.211C>A	P.L71I
XH_P25	3	190158127	190158127	Silent	SNV	G	T	T	TMEM207	c.210C>A	P.V70V
XH_P25	3	193355029	193355029	Missense_Mutation	SNV	G	T	T	OPA1	c.829G>T	P.D277Y
XH_P25	3	52620655	52620655	Missense_Mutation	SNV	A	T	T	PBRM1	c.3098T>A	P.V1033D
XH_P25	3	58486842	58486842	Missense_Mutation	SNV	G	T	T	KCTD6	c.197G>T	P.S66L
XH_P25	4	121616342	121616342	Missense_Mutation	SNV	A	G	G	PRDM5	c.1724T>C	P.F575S
XH_P25	5	17275669	17275669	Missense_Mutation	SNV	C	T	T	BASP1	c.344C>T	P.A115V
XH_P25	5	70945025	70945025	Frame_Shift_Del	INDEL	A	-	-	MC2C2	c.1318delA	P.I440fs
XH_P25	5	7867230	7867230	Missense_Mutation	SNV	C	A	A	FASTKD3	c.967G>T	P.V323L
XH_P25	5	89938743	89938743	Missense_Mutation	SNV	G	C	C	ADGRV1	c.2438G>C	P.R813P

XH_P25	6	106555213	106555213	Missense_Mutation	SNV	A	T	T	PRDM1	c.2330A>T	P.Q777L
XH_P25	6	152652741	152652741	Frame_Shift_Ins	INDEL	-	C	C	SYNE1	c.12865dupG	P.A4289fs
XH_P25	7	100161551	100161551	Frame_Shift_Del	INDEL	C	-	-	AGFG2	c.1271delC	P.P424fs
XH_P25	7	43918743	43918743	Missense_Mutation	SNV	C	G	G	URGPC	c.319G>C	P.A107P
XH_P25	7	44806172	44806172	Silent	SNV	T	G	G	ZMI22	c.2391T>G	P.P797P
XH_P25	7	81346681	81346681	Splice_Site	SNV	A	G	G	HGF	c.1272T>C	P.R424R
XH_P25	8	133953677	133953677	Missense_Mutation	SNV	T	C	C	TG	c.5123T>C	P.I1708T
XH_P25	9	117536	117536	Missense_Mutation	SNV	C	T	T	FOX4	c.584G>A	P.R195Q
XH_P25	9	32631851	32631851	Silent	SNV	G	T	T	TAF1L	c.3727C>A	P.R1243R
XH_P25	9	36169791	36169791	Missense_Mutation	SNV	G	A	A	CCIN	c.292G>A	P.E98K
XH_P25	X	125299685	125299685	Missense_Mutation	SNV	G	T	T	DCAF12L2	c.223C>A	P.L75M
XH_P27	1	179414125	179414125	Silent	SNV	A	G	G	AXDND1	c.1584A>G	P.E528E
XH_P27	1	18808631	18808631	Missense_Mutation	SNV	G	A	A	KLHDC7A	c.1156G>A	P.A386T
XH_P27	1	34329964	34329964	Missense_Mutation	SNV	G	A	A	HMGB4	c.172G>A	P.A58T
XH_P27	1	35370539	35370539	Missense_Mutation	SNV	C	A	A	DLGAP3	c.446G>T	P.G149V
XH_P27	1	8422759	8422772	Frame_Shift_Del	INDEL	TGTCCTCTGC	-	-	REER	c.86delAAAGCAG	P.K625fs
XH_P27	10	124742302	124742302	Silent	SNV	C	T	T	PSK	c.270C>T	P.F90F
XH_P27	11	103055658	103055658	Missense_Mutation	SNV	A	T	T	DYNC2H1	c.6511A>T	P.T2171S
XH_P27	11	124749086	124749086	Missense_Mutation	SNV	G	C	C	ROBO3	c.3534G>C	P.R1178S
XH_P27	12	121442106	121442106	Silent	SNV	G	C	C	C12orf43	c.732C>G	P.T244T
XH_P27	12	12277603	12277603	Splice_Site	INDEL	-	A	A	LRP6	c.4450-8dupT	
XH_P27	12	40884463	40884463	Silent	SNV	C	G	G	MUC19	c.17709C>G	P.T5903T
XH_P27	13	108882125	108882125	Missense_Mutation	SNV	A	T	T	ABHD13	c.559A>T	P.I187F
XH_P27	15	42285075	42285075	Missense_Mutation	SNV	C	T	T	PLA2G4E	c.1330G>A	P.V444I
XH_P27	16	28116004	28116004	Nonsense_Mutation	SNV	C	A	A	XP06	c.2767G>T	P.E923*
XH_P27	17	10219334	10219334	Missense_Mutation	SNV	T	C	C	MYH13	c.3747A>G	P.I1249M
XH_P27	17	33884249	33884249	Missense_Mutation	SNV	A	G	G	SLFN14	c.833T>C	P.L278S
XH_P27	17	38179531	38179531	Silent	SNV	C	T	T	MED24	c.2064G>A	P.L688L
XH_P27	17	77073866	77073866	Silent	SNV	G	A	A	ENGASE	c.336G>A	P.A112A
XH_P27	18	29110998	29110998	Missense_Mutation	SNV	G	A	A	DSG2	c.1063G>A	P.A355T
XH_P27	19	40316855	40316855	Missense_Mutation	SNV	G	A	A	DYRK1B	c.1483C>T	P.P495S
XH_P27	19	57133313	57133313	Frame_Shift_Del	INDEL	G	-	-	ZNF71	c.659delG	P.G220fs
XH_P27	2	108488685	108488685	Missense_Mutation	SNV	C	A	A	RGPD4	c.4225C>A	P.H1409N
XH_P27	2	165997191	165997191	Silent	SNV	T	C	C	SCN3A	c.1989A>G	P.L663L
XH_P27	2	225706624	225706624	Splice_Site	INDEL	A	-	-	DOCK10	c.2551-11delT	
XH_P27	20	43926873	43926873	Missense_Mutation	SNV	C	G	G	MATN4	c.1363G>C	P.V455L
XH_P27	21	41668064	41668064	Silent	SNV	G	A	A	DSG1	c.2100C>T	P.D700D
XH_P27	3	20212651	20212651	Silent	SNV	A	T	T	SGO1	c.1356T>A	P.V452V
XH_P27	3	52437289	52437289	Frame_Shift_Ins	INDEL	-	A	A	BAP1	c.1754_1755ins	P.I586fs
XH_P27	4	57871762	57871762	Splice_Site	SNV	A	T	T	POLR2B	c.1098-4A>T	
XH_P27	7	133943088	133943088	Missense_Mutation	SNV	C	T	T	LRGUK	c.2278C>T	P.P760S
XH_P27	7	81381436	81381436	Missense_Mutation	SNV	C	G	G	HGF	c.625G>C	P.V209L
XH_P27	8	22995468	22995468	Missense_Mutation	SNV	T	C	C	TNFRSF10D	c.1076A>G	P.K359R
XH_P27	9	37441257	37441257	Missense_Mutation	SNV	A	G	G	ZBTB5	c.1292T>C	P.I431T
XH_P27	9	40704387	40704387	Silent	SNV	C	T	T	SPATA31A3	c.2044C>T	P.L682L
XH_P28	1	1296629	1296629	Silent	SNV	C	T	T	MXR8	c.15G>A	P.A5A
XH_P28	1	145487324	145487324	Missense_Mutation	SNV	C	A	A	LXL1	c.313C>A	P.Q105K
XH_P28	1	154562702	154562702	Silent	SNV	A	G	G	ADAR	c.1569T>C	P.T523T
XH_P28	1	16460396	16460396	Missense_Mutation	SNV	C	T	T	EPHA2	c.1697G>A	P.R566H
XH_P28	1	1904424	1904424	Missense_Mutation	SNV	C	T	T	CFAP74	c.737G>A	P.R246Q
XH_P28	1	19212008	19212008	Missense_Mutation	SNV	G	A	A	ALDH4A1	c.232C>T	P.P78S
XH_P28	1	201282405	201282405	Missense_Mutation	SNV	G	A	A	PKP1	c.418G>A	P.A140T
XH_P28	1	201984399	201984399	Missense_Mutation	SNV	G	A	A	ELF3	c.1064G>A	P.G355D
XH_P28	1	203798691	203798691	Silent	SNV	C	T	T	ZC3H11A	c.411C>T	P.S137S
XH_P28	1	235323959	235323959	Missense_Mutation	SNV	T	C	C	RBM34	c.232A>G	P.T78A
XH_P28	1	248570275	248570275	Missense_Mutation	SNV	T	C	C	OR2T1	c.980T>C	P.F327S
XH_P28	1	3328624	3328624	Silent	SNV	G	A	A	PRDM16	c.1863G>A	P.T621T
XH_P28	1	35334506	35334506	Missense_Mutation	SNV	G	A	A	DLGAP3	c.2185C>T	P.R729C
XH_P28	1	43232368	43232368	Missense_Mutation	SNV	G	A	A	P3H1	c.275C>T	P.S92F
XH_P28	1	63790160	63790160	Silent	SNV	G	A	A	FOX3D	c.1431G>A	P.A477A
XH_P28	1	6533472	6533472	Frame_Shift_Del	INDEL	C	-	-	PLEKHG5	c.802delG	P.E268fs
XH_P28	1	7724165	7724165	Missense_Mutation	SNV	C	T	T	CAMTA1	c.1558C>T	P.R520W
XH_P28	1	94522178	94522178	Silent	SNV	G	A	A	ABCA4	c.2361C>T	P.T787T
XH_P28	1	980820	980820	Frame_Shift_Ins	INDEL	-	G	G	AGRN	c.2459dupG	P.L821fs
XH_P28	10	100177413	100177413	Missense_Mutation	SNV	G	A	A	HP51	c.2011C>T	P.H671Y
XH_P28	10	105238607	105238607	Silent	SNV	G	A	A	CALHM3	c.183C>T	P.L61L
XH_P28	10	105807524	105807524	Nonsense_Mutation	SNV	C	A	A	COL17A1	c.2308G>T	P.G770*
XH_P28	10	135085339	135085339	Silent	SNV	G	A	A	ADAM8	c.1077C>T	P.A359A
XH_P28	10	21806265	21806265	Missense_Mutation	SNV	C	T	T	SKIDA1	c.487G>A	P.A163T
XH_P28	10	76790232	76790232	Silent	SNV	C	T	T	KAT6B	c.5101C>T	P.L1701L
XH_P28	10	85956347	85956347	Missense_Mutation	SNV	G	A	A	CDHR1	c.238G>A	P.V80I
XH_P28	10	94450019	94450019	Silent	SNV	A	G	G	HHEX	c.276A>G	P.G92G
XH_P28	10	94712026	94712026	Splice_Site	SNV	A	G	G	EXOC6	c.1402-4A>G	
XH_P28	11	116717260	116717260	Missense_Mutation	SNV	G	A	A	SIK3	c.3161C>T	P.A1054V
XH_P28	11	121466482	121466482	Splice_Site	SNV	G	A	A	SORL1	c.4519+1G>A	
XH_P28	11	122805215	122805215	Missense_Mutation	SNV	C	G	G	C11orf63	c.1066C>G	P.Q356E
XH_P28	11	123908980	123908980	Silent	SNV	G	A	A	OR10G7	c.729C>T	P.H243H
XH_P28	11	128391866	128391866	Silent	SNV	C	T	T	ETS1	c.24G>A	P.K8K
XH_P28	11	133790624	133790624	Missense_Mutation	SNV	G	A	A	IGSF9B	c.2996C>T	P.P999L
XH_P28	11	44069683	44069683	Missense_Mutation	SNV	A	G	G	ACCSL	c.97A>G	P.T33A
XH_P28	11	6239872	6239872	Missense_Mutation	SNV	C	T	T	FAM160A2	c.1393G>A	P.A465T
XH_P28	11	63999443	63999443	Splice_Site	SNV	G	A	A	DNAIC4	c.180+7G>A	
XH_P28	11	6561152	6561152	Missense_Mutation	SNV	G	A	A	DNHD1	c.3467G>A	P.R1156Q
XH_P28	11	71729269	71729269	Frame_Shift_Ins	INDEL	-	T	T	NUMA1	c.937dupA	P.I313fs
XH_P28	11	73021808	73021808	Nonsense_Mutation	SNV	C	T	T	ARHGEF17	c.2125C>T	P.R709*
XH_P28	11	8118251	8118251	Frame_Shift_Ins	INDEL	-	T	T	TUB	c.753dupT	P.D252fs
XH_P28	11	94800405	94800405	Frame_Shift_Del	INDEL	C	-	-	SRSF8	c.20delC	P.P7fs
XH_P28	11	9754192	9754192	Nonsense_Mutation	SNV	C	T	T	SWAP70	c.841C>T	P.R281*
XH_P28	12	119540104	119540104	Silent	SNV	G	A	A	SRM4	c.195G>A	P.Q65Q
XH_P28	12	120210692	120210692	Missense_Mutation	SNV	G	A	A	CIT	c.1964C>T	P.A655V
XH_P28	12	122674857	122674857	Silent	SNV	C	T	T	LRR43	c.843C>T	P.D281D
XH_P28	12	129566528	129566528	Missense_Mutation	SNV	C	T	T	TMEM132D	c.1699G>A	P.G567S
XH_P28	12	133810910	133810910	Silent	SNV	A	G	G	ANHX	c.33T>C	P.H111H
XH_P28	12	2102299	2102299	Silent	SNV	A	G	G	DCP1B	c.450T>C	P.N150N
XH_P28	12	21615043	21615043	Missense_Mutation	SNV	C	T	T	PYROXD1	c.982C>T	P.H328Y
XH_P28	12	54757554	54757554	Frame_Shift_Del	INDEL	C	-	-	GPR84	c.82delG	P.V28fs
XH_P28	12	57396918	57396918	Missense_Mutation	SNV	G	A	A	ZBTB39	c.1784C>T	P.A595V
XH_P28	12	57858985	57858985	Missense_Mutation	SNV	C	T	T	GLI1	c.481C>T	P.R161W

XH_P28	12	6637841	6637841	Splice_Site	SNV	C	A	A	NCAPD2	c.3300-4C>A	
XH_P28	13	103387482	103387482	Missense_Mutation	SNV	T	C	C	CCDC168	c.15565A>G	P.K5189E
XH_P28	13	110835395	110835395	Silent	SNV	C	T	T	COL4A1	c.2040G>A	P.E680E
XH_P28	13	28959036	28959036	Missense_Mutation	SNV	A	T	T	FLT1	c.2102T>A	P.I701K
XH_P28	13	31232944	31232944	Silent	SNV	G	A	A	USPL1	c.2187G>A	P.P729P
XH_P28	14	100615721	100615721	Missense_Mutation	SNV	C	T	T	DEGS2	c.409G>A	P.G137S
XH_P28	14	103568923	103568923	Missense_Mutation	SNV	G	A	A	EXOC3L4	c.863G>A	P.R288H
XH_P28	14	103931985	103931985	Missense_Mutation	SNV	C	T	T	MARK3	c.632C>T	P.T211M
XH_P28	14	103932414	103932414	Missense_Mutation	SNV	C	T	T	MARK3	c.883C>T	P.R295C
XH_P28	14	104633185	104633185	Splice_Site	SNV	C	T	T	KIF26A	c.924-11C>T	
XH_P28	14	105688102	105688102	Missense_Mutation	SNV	C	T	T	BRF1	c.853G>A	P.E285K
XH_P28	14	23817149	23817149	Missense_Mutation	SNV	G	T	T	SLC22A17	c.241C>A	P.L81I
XH_P28	14	23865570	23865570	Silent	SNV	G	A	A	MYH6	c.2352C>T	P.S784S
XH_P28	14	44975941	44975941	Frame_Shift_Ins	INDEL	-	T	T	FSCB	c.249dupA	P.E84fs
XH_P28	14	55241717	55241717	Missense_Mutation	SNV	G	A	A	SAMD4A	c.1517G>A	P.R506Q
XH_P28	14	55818138	55818138	Missense_Mutation	SNV	G	T	T	FBXO34	c.1030G>T	P.G344W
XH_P28	14	62200939	62200939	Missense_Mutation	SNV	A	T	T	HIF1A	c.1036A>T	P.T346S
XH_P28	14	65209863	65209863	Silent	SNV	C	T	T	PLEKHG3	c.3102C>T	P.S1034S
XH_P28	14	70040029	70040029	Missense_Mutation	SNV	G	A	A	CCDC177	c.311C>T	P.A104V
XH_P28	14	71444720	71444720	Missense_Mutation	SNV	G	A	A	PCNX1	c.1666G>A	P.A556T
XH_P28	14	73614807	73614807	Missense_Mutation	SNV	G	A	A	PSEN1	c.80G>A	P.R27H
XH_P28	14	76147940	76147940	Silent	SNV	C	T	T	TTL5	c.234C>T	P.R78R
XH_P28	14	76241937	76241937	Silent	SNV	C	T	T	TTL5	c.2247C>T	P.A749A
XH_P28	14	86088574	86088574	Missense_Mutation	SNV	G	A	A	FLRT2	c.716G>A	P.R239H
XH_P28	14	90752749	90752749	Silent	SNV	G	A	A	NRDE2	c.3246C>T	P.S1082S
XH_P28	14	99641398	99641398	Missense_Mutation	SNV	G	A	A	BCL11B	c.1772C>T	P.A591V
XH_P28	14	99976715	99976715	Missense_Mutation	SNV	C	A	A	CCNK	c.1339C>A	P.L447M
XH_P28	15	35189856	35189856	Missense_Mutation	SNV	T	C	C	AQR	c.2294A>G	P.D765G
XH_P28	15	42700450	42700450	Missense_Mutation	SNV	G	T	T	CAPN3	c.1842G>T	P.E614D
XH_P28	15	43821376	43821376	Missense_Mutation	SNV	C	T	T	MAP1A	c.7705C>T	P.R2569C
XH_P28	15	44216401	44216401	Splice_Site	SNV	A	G	G	FRMD5	c.-61+2T>C	
XH_P28	15	84611424	84611424	Missense_Mutation	SNV	C	T	T	ADAMTSL3	c.2194C>T	P.H732Y
XH_P28	15	93588329	93588329	Missense_Mutation	SNV	G	A	A	RGMA	c.1276C>T	P.R426W
XH_P28	15	93595343	93595343	Silent	SNV	G	A	A	RGMA	c.549C>T	P.T183T
XH_P28	16	11370114	11370114	Silent	SNV	C	T	T	PRM2	c.114G>A	P.P38P
XH_P28	16	11773145	11773145	Missense_Mutation	SNV	G	A	A	TXNDC11	c.2864C>T	P.S955L
XH_P28	16	1417273	1417273	Silent	SNV	C	T	T	UNKL	c.354G>A	P.A118A
XH_P28	16	1706892	1706892	Missense_Mutation	SNV	C	T	T	CRAMP1	c.2134C>T	P.R712C
XH_P28	16	21726417	21726417	Missense_Mutation	SNV	G	A	A	OTOA	c.1195G>A	P.V399I
XH_P28	16	23544090	23544090	Splice_Site	SNV	C	T	T	EARS2	c.959-4G>A	
XH_P28	16	23598596	23598596	Missense_Mutation	SNV	C	T	T	NDUFAB1	c.213G>A	P.M71I
XH_P28	16	27481536	27481536	Silent	SNV	C	A	A	GTF3C1	c.4707G>T	P.V1569V
XH_P28	16	27709660	27709660	Missense_Mutation	SNV	C	T	T	KIAA0556	c.952C>T	P.R318W
XH_P28	16	2806550	2806550	Missense_Mutation	SNV	G	A	A	SRRM2	c.185G>A	P.R62H
XH_P28	16	2815737	2815737	Silent	SNV	C	T	T	SRRM2	c.5208C>T	P.A1736A
XH_P28	16	3076774	3076774	Missense_Mutation	SNV	G	A	A	THOC6	c.578G>A	P.R193Q
XH_P28	16	30999077	30999077	Splice_Site	SNV	C	T	T	HSDB37	c.532-12C>T	
XH_P28	16	48149326	48149326	Missense_Mutation	SNV	C	A	A	ABCC12	c.1989G>T	P.Q663H
XH_P28	16	53342661	53342661	Missense_Mutation	SNV	G	A	A	CHD9	c.7117G>A	P.E2373K
XH_P28	16	55522566	55522566	Missense_Mutation	SNV	G	A	A	MMP2	c.794G>A	P.R265H
XH_P28	16	67198839	67198839	Splice_Site	SNV	T	C	C	HSF4	c.123+2T>C	
XH_P28	16	70292001	70292001	Silent	SNV	G	A	A	AARS	c.2112C>T	P.S704S
XH_P28	16	8722915	8722915	Silent	SNV	C	T	T	METTL22	c.462C>T	P.D154D
XH_P28	16	88008733	88008733	Silent	SNV	A	G	G	BANP	c.12A>G	P.E4E
XH_P28	16	8941640	8941640	Silent	SNV	G	A	A	PM22	c.699G>A	P.A233A
XH_P28	16	89763967	89763967	Silent	SNV	C	T	T	SPATA2L	c.1050G>A	P.S350S
XH_P28	16	9858581	9858581	Missense_Mutation	SNV	A	T	T	GRIN2A	c.2820T>A	P.N940K
XH_P28	17	1631740	1631740	Missense_Mutation	SNV	G	A	A	WDR81	c.334G>A	P.V112M
XH_P28	17	17398719	17398719	Missense_Mutation	SNV	C	T	T	RASD1	c.566G>A	P.R189H
XH_P28	17	18022900	18022900	Silent	SNV	G	A	A	MYO15A	c.786G>A	P.A262A
XH_P28	17	21087119	21087119	Silent	SNV	G	A	A	DHRS7B	c.477G>A	P.T159T
XH_P28	17	26086032	26086032	Missense_Mutation	SNV	C	T	T	NOS2	c.3229G>A	P.G1077S
XH_P28	17	27068496	27068496	Missense_Mutation	SNV	G	A	A	NEK8	c.1957G>A	P.G653R
XH_P28	17	28544188	28544188	Missense_Mutation	SNV	C	T	T	SLC6A4	c.833G>A	P.G278D
XH_P28	17	32965105	32965105	Missense_Mutation	SNV	G	A	A	TMEM132E	c.3079G>A	P.A1027T
XH_P28	17	33738570	33738570	Silent	SNV	G	A	A	SLFN12	c.1524C>T	P.C508C
XH_P28	17	37879658	37879658	Missense_Mutation	SNV	G	A	A	ERBB2	c.2033G>A	P.R678Q
XH_P28	17	40500444	40500444	Missense_Mutation	SNV	G	A	A	STAT3	c.91C>T	P.R31W
XH_P28	17	4462215	4462215	Missense_Mutation	SNV	A	C	C	GGT6	c.577T>G	P.F193V
XH_P28	17	46655662	46655662	Frame_Shift_Del	INDEL	A	-	-	HOXB4	c.20deIT	P.L7fs
XH_P28	17	5347661	5347661	Missense_Mutation	SNV	G	A	A	DHX33	c.1469C>T	P.P490L
XH_P28	17	61622511	61622511	Silent	SNV	C	T	T	KCNH6	c.2469C>T	P.H823H
XH_P28	17	62290817	62290817	Missense_Mutation	SNV	C	T	T	TEX2	c.761G>A	P.R254Q
XH_P28	17	6703429	6703429	Nonsense_Mutation	SNV	G	A	A	TEKT1	c.1174C>T	P.Q392*
XH_P28	17	7094084	7094084	Silent	SNV	A	G	G	DLG4	c.2109T>C	P.R703R
XH_P28	17	71387631	71387631	Silent	SNV	C	T	T	SDK2	c.3945G>A	P.T1315T
XH_P28	17	72843517	72843517	Missense_Mutation	SNV	G	A	A	GRIN2C	c.1931C>T	P.T644M
XH_P28	17	72956286	72956286	Silent	SNV	C	T	T	HID1	c.786G>A	P.V262V
XH_P28	17	73517808	73517808	Missense_Mutation	SNV	G	A	A	TSEN54	c.646G>A	P.A216T
XH_P28	17	74003351	74003351	Missense_Mutation	SNV	C	T	T	EVPL	c.6001G>A	P.E2001K
XH_P28	17	7401124	7401124	Silent	SNV	C	T	T	POLR2A	c.1137C>T	P.G379G
XH_P28	17	74163791	74163791	Silent	SNV	A	C	C	RNF157	c.384T>G	P.A128A
XH_P28	17	76130996	76130996	Missense_Mutation	SNV	G	A	A	TMC8	c.1033G>A	P.A345T
XH_P28	17	76137108	76137108	Missense_Mutation	SNV	C	T	T	TMC8	c.2096C>T	P.A699V
XH_P28	17	7754477	7754477	Missense_Mutation	SNV	C	G	G	KDM6B	c.3812C>G	P.S1271C
XH_P28	17	77808469	77808469	Silent	SNV	C	T	T	CBX4	c.972G>A	P.P324P
XH_P28	17	78081349	78081349	Splice_Site	SNV	C	T	T	GAA	c.693-7C>T	
XH_P28	17	78172202	78172202	Missense_Mutation	SNV	G	A	A	CARD14	c.1663G>A	P.V555I
XH_P28	17	80159666	80159666	Missense_Mutation	SNV	C	T	T	CCDC57	c.155G>A	P.C52Y
XH_P28	17	8926332	8926332	Silent	SNV	G	A	A	NTN1	c.642G>A	P.S214S
XH_P28	18	24035760	24035760	Missense_Mutation	SNV	G	A	A	KCTD1	c.721C>T	P.R241W
XH_P28	18	3879988	3879988	Silent	SNV	G	A	A	DLGAP1	c.81C>T	P.S27S
XH_P28	18	60241823	60241823	Missense_Mutation	SNV	G	A	A	ZCHC2	c.2509G>A	P.G837R
XH_P28	18	7015799	7015799	Silent	SNV	G	A	A	LAMA1	c.3048C>T	P.C1016C
XH_P28	18	7023335	7023335	Silent	SNV	G	A	A	LAMA1	c.2529C>T	P.G843G
XH_P28	18	74208486	74208486	Frame_Shift_Del	INDEL	GG	-	-	C18orf65	c.336-337delGG	P.A113fs
XH_P28	19	10610139	10610139	Missense_Mutation	SNV	C	T	T	KEAP1	c.571G>A	P.A191T
XH_P28	19	15122052	15122052	Missense_Mutation	SNV	C	T	T	CCDC105	c.415C>T	P.R139C

XH_P28	19	16466591	16466591	Silent	SNV	C	T	T	EPS15L1	c.2658G>A	P.A886A
XH_P28	19	17392616	17392616	Missense_Mutation	SNV	G	A	A	ANKLE1	c.49G>A	P.G175
XH_P28	19	17450246	17450246	Missense_Mutation	SNV	G	A	A	GTBPBP3	c.812G>A	P.R271Q
XH_P28	19	20228702	20228702	Frame_Shift_Del	INDEL	A	-	-	ZNF90	c.345delA	P.G116fs
XH_P28	19	30164847	30164847	Missense_Mutation	SNV	G	A	A	PLEKHF1	c.101G>A	P.R34Q
XH_P28	19	30935520	30935520	Missense_Mutation	SNV	G	A	A	ZNF536	c.1051G>A	P.G351S
XH_P28	19	31770647	31770647	Missense_Mutation	SNV	C	T	T	TSHZ3	c.52G>A	P.E18K
XH_P28	19	35758381	35758381	Missense_Mutation	SNV	A	C	C	LSR	c.1598A>C	P.D533A
XH_P28	19	36221512	36221512	Silent	SNV	C	T	T	KMT2B	c.5271C>T	P.G1757G
XH_P28	19	38055624	38055624	Missense_Mutation	SNV	C	T	T	ZNF571	c.1706G>A	P.R569H
XH_P28	19	38609985	38609985	Frame_Shift_Del	INDEL	C	-	-	SIPA1L3	c.2337delC	P.I780fs
XH_P28	19	39669208	39669208	Missense_Mutation	SNV	C	T	T	PAK4	c.1765C>T	P.R589C
XH_P28	19	3977539	3977539	Missense_Mutation	SNV	C	T	T	EEF2	c.2137G>A	P.A713T
XH_P28	19	39799069	39799069	Missense_Mutation	SNV	G	A	A	LRFN1	c.1520C>T	P.T507M
XH_P28	19	39888220	39888220	Missense_Mutation	SNV	G	T	T	MED29	c.477G>T	P.W159C
XH_P28	19	40587790	40587790	Silent	SNV	C	T	T	ZNF780A	c.168G>A	P.T56T
XH_P28	19	41113263	41113263	Splice_Site	SNV	C	T	T	LTBP4	c.1193-8C>T	
XH_P28	19	41173899	41173907	Missense_Mutation	INDEL	TGCTGTTGC	-	-	NUMBL	c.1181delGCAAA_Q392_Q394del	
XH_P28	19	41351919	41351919	Silent	SNV	G	C	C	CYP2A6	c.915C>G	P.T305T
XH_P28	19	42569497	42569497	Missense_Mutation	SNV	C	T	T	GRIK5	c.122G>A	P.R41H
XH_P28	19	44612194	44612194	Silent	SNV	G	A	A	ZNF224	c.1881G>A	P.E627E
XH_P28	19	45974060	45974060	Silent	SNV	G	A	A	FOSB	c.300G>A	P.P100P
XH_P28	19	47341769	47341769	Missense_Mutation	SNV	C	T	T	AP251	c.412G>A	P.E138K
XH_P28	19	47570024	47570024	Silent	SNV	C	T	T	ZC3H4	c.3501G>A	P.T1167T
XH_P28	19	47935484	47935484	Missense_Mutation	SNV	C	T	T	SLC8A2	c.2329G>A	P.V777I
XH_P28	19	48955975	48955975	Missense_Mutation	SNV	C	T	T	GRWD1	c.1034C>T	P.P345L
XH_P28	19	50100978	50100978	Missense_Mutation	SNV	G	A	A	PRR12	c.3386G>A	P.R1129H
XH_P28	19	50165782	50165782	Silent	SNV	G	A	A	IRF3	c.501C>T	P.C167C
XH_P28	19	50266381	50266381	Missense_Mutation	SNV	G	A	A	TSK5	c.124C>T	P.R42W
XH_P28	19	50334697	50334697	Silent	SNV	C	T	T	MED25	c.1209C>T	P.S403S
XH_P28	19	50338373	50338373	Missense_Mutation	SNV	G	A	A	MED25	c.1613G>A	P.R538Q
XH_P28	19	50917032	50917032	Nonsense_Mutation	SNV	C	T	T	POLD1	c.2284C>T	P.R762*
XH_P28	19	51455893	51455893	Frame_Shift_Del	INDEL	G	-	-	KLK5	c.21delC	P.W8fs
XH_P28	19	55665463	55665463	Missense_Mutation	SNV	G	A	A	TNNI3	c.481C>T	P.R161W
XH_P28	19	55708681	55708681	Nonsense_Mutation	SNV	G	C	C	PTPRH	c.1260C>G	P.Y420*
XH_P28	19	55993414	55993414	Missense_Mutation	SNV	C	T	T	ZNF628	c.854C>T	P.A285V
XH_P28	19	56090637	56090637	Silent	SNV	G	A	A	ZNF579	c.369C>T	P.H123H
XH_P28	19	56156372	56156372	Silent	SNV	C	T	T	ZNF581	c.435C>T	P.H145H
XH_P28	19	58991281	58991281	Splice_Site	INDEL	C	-	-	ZNF446	c.713-11delC	
XH_P28	19	59028908	59028908	Missense_Mutation	SNV	G	A	A	ZBTB45	c.133C>T	P.R45C
XH_P28	19	6185636	6185636	Silent	SNV	T	G	G	ACSBG2	c.1512T>G	P.G504G
XH_P28	19	815231	815231	Missense_Mutation	SNV	C	T	T	PLPPR3	c.358G>A	P.G120S
XH_P28	2	160229572	160229572	Silent	SNV	G	A	A	BAZ2B	c.4089C>T	P.G1363G
XH_P28	2	17692078	17692078	Missense_Mutation	SNV	T	A	A	RAD51AP2	c.3473A>T	P.N1158I
XH_P28	2	179441464	179441464	Silent	SNV	G	A	A	TTN	c.64584C>T	P.S21528S
XH_P28	2	179616465	179616465	Silent	SNV	A	G	G	TTN	c.10662T>C	P.A3554A
XH_P28	2	189873814	189873814	Silent	SNV	C	T	T	COL3A1	c.3690C>T	P.N1230N
XH_P28	2	202614445	202614445	Missense_Mutation	SNV	C	T	T	ALS2	c.1805G>A	P.R602H
XH_P28	2	218675013	218675013	Missense_Mutation	SNV	C	T	T	TNS1	c.4708G>A	P.G1570S
XH_P28	2	222428935	222428935	Silent	SNV	G	A	A	EPHA4	c.339C>T	P.G113G
XH_P28	2	232392908	232392908	Missense_Mutation	SNV	G	A	A	NMUR1	c.824C>T	P.A275V
XH_P28	2	233684582	233684582	Nonsense_Mutation	SNV	C	T	T	GIGYF2	c.2416C>T	P.R806*
XH_P28	2	241405579	241405579	Missense_Mutation	SNV	G	A	A	GPC1	c.1549G>A	P.A517T
XH_P28	2	241689855	241689855	Missense_Mutation	SNV	C	A	A	KIF1A	c.2968G>T	P.A990S
XH_P28	2	32800277	32800277	Missense_Mutation	SNV	G	A	A	BIRC6	c.13199G>A	P.R4400Q
XH_P28	2	48026540	48026540	Missense_Mutation	SNV	T	C	C	MSH6	c.1418T>C	P.L473P
XH_P28	2	69049599	69049599	Missense_Mutation	SNV	C	T	T	ARHGAP25	c.1328C>T	P.T443I
XH_P28	2	85786207	85786207	Splice_Site	SNV	G	C	C	GGCX	c.215-9C>G	
XH_P28	2	9484764	9484764	Missense_Mutation	SNV	G	A	A	ASAP2	c.953G>A	P.G318E
XH_P28	20	21687066	21687066	Splice_Site	SNV	G	A	A	PAX1	c.287-10G>A	
XH_P28	20	259914	259914	Missense_Mutation	SNV	G	T	T	C20orf96	c.361C>A	P.L121I
XH_P28	20	31044128	31044128	Silent	SNV	C	T	T	NOL4L	c.912G>A	P.T304T
XH_P28	20	32666332	32666332	Missense_Mutation	SNV	G	A	A	RALY	c.850G>A	P.A284T
XH_P28	20	33588465	33588465	Silent	SNV	C	T	T	MYH7B	c.5277C>T	P.T1759T
XH_P28	20	35060130	35060130	Missense_Mutation	SNV	C	A	A	DLGAP4	c.10C>A	P.L4I
XH_P28	20	42142604	42142604	Missense_Mutation	SNV	C	T	T	L3MBTL1	c.197C>T	P.P66L
XH_P28	20	42744935	42744935	Silent	SNV	C	T	T	JPH2	c.1380G>A	P.A460A
XH_P28	20	44577619	44577619	Silent	SNV	G	A	A	ZNF335	c.4002C>T	P.Y1334Y
XH_P28	20	44987147	44987147	Missense_Mutation	SNV	C	T	T	SLC35C2	c.86G>A	P.R29Q
XH_P28	20	48522829	48522829	Missense_Mutation	SNV	G	A	A	SPATA2	c.890C>T	P.S297L
XH_P28	20	48760152	48760152	Missense_Mutation	SNV	C	T	T	TMEM189	c.128G>A	P.R43H
XH_P28	20	50406788	50406788	Missense_Mutation	SNV	C	T	T	SALL4	c.2234G>A	P.R745H
XH_P28	20	51870090	51870090	Missense_Mutation	SNV	G	T	T	TSHZ2	c.84G>T	P.E28D
XH_P28	20	51871597	51871597	Missense_Mutation	SNV	G	A	A	TSHZ2	c.1591G>A	P.G531R
XH_P28	20	54972283	54972283	Missense_Mutation	SNV	G	A	A	CSTF1	c.190G>A	P.A64T
XH_P28	20	55758870	55758870	Missense_Mutation	SNV	C	T	T	BMP7	c.866G>A	P.R289H
XH_P28	20	60895821	60895821	Silent	SNV	G	A	A	LAMA5	c.6622C>T	P.L2208L
XH_P28	20	60913389	60913389	Missense_Mutation	SNV	C	T	T	LAMA5	c.1655G>A	P.R552H
XH_P28	20	60966461	60966461	Silent	SNV	G	A	A	CABLES2	c.1140C>T	P.P380P
XH_P28	20	61288203	61288203	Missense_Mutation	SNV	C	T	T	SLCO4A1	c.397C>T	P.R133C
XH_P28	20	62577812	62577812	Missense_Mutation	SNV	C	T	T	UCKL1	c.253G>A	P.A85T
XH_P28	20	62701931	62701931	Silent	SNV	G	A	A	TCEA2	c.762G>A	P.T254T
XH_P28	20	7962997	7962997	Silent	SNV	A	G	G	TMX4	c.951T>C	P.A317A
XH_P28	20	9404515	9404515	Nonsense_Mutation	SNV	C	T	T	PLCB4	c.2404C>T	P.R802*
XH_P28	21	45522737	45522737	Missense_Mutation	SNV	C	A	A	TRAPP10	c.3425C>A	P.T1142N
XH_P28	22	17619172	17619172	Silent	SNV	C	T	T	CECR5	c.921G>A	P.A307A
XH_P28	22	18300666	18300666	Silent	SNV	C	T	T	MICAL3	c.4761G>A	P.A1587A
XH_P28	22	24622121	24622121	Silent	SNV	G	A	A	GGT5	c.1152C>T	P.H384H
XH_P28	22	29445904	29445904	Missense_Mutation	SNV	G	A	A	ZNRF3	c.1735G>A	P.V579M
XH_P28	22	29735018	29735018	Silent	SNV	G	A	A	AP1B1	c.2124C>T	P.G708G
XH_P28	22	40417522	40417522	Silent	SNV	G	A	A	FAM83F	c.1008G>A	P.P336P
XH_P28	22	47057349	47057349	Splice_Site	SNV	G	A	A	GRAMD4	c.466+10G>A	
XH_P28	3	125298752	125298752	Silent	SNV	G	T	T	OSBP11	c.366C>A	P.T122T
XH_P28	3	132280031	132280031	Missense_Mutation	SNV	G	A	A	ACAD11	c.2032C>T	P.R678C
XH_P28	3	138738766	138738766	Silent	SNV	C	T	T	PRR23B	c.738G>A	P.A246A
XH_P28	3	151163149	151163149	Silent	SNV	G	A	A	IGSF10	c.4620C>T	P.H1540H
XH_P28	3	15116352	15116352	Missense_Mutation	SNV	C	T	T	RBSN	c.1292G>A	P.R431H
XH_P28	3	178916936	178916936	Missense_Mutation	SNV	G	A	A	PIK3CA	c.323G>A	P.R108H

XH_P28	3	179437801	179437801	Silent	SNV	T	C	C	USP13	c.879T>C	P.I293I
XH_P28	3	183975265	183975265	Silent	SNV	C	T	T	ECE2	c.201C>T	P.C67C
XH_P28	3	184429232	184429232	Silent	SNV	C	T	T	MAGEF1	c.378G>A	P.R126R
XH_P28	3	26751633	26751633	Missense_Mutation	SNV	T	C	C	LRRC3B	c.470T>C	P.L157P
XH_P28	3	42236377	42236377	Missense_Mutation	SNV	A	C	C	TRAK1	c.1057A>C	P.R353Q
XH_P28	3	52712520	52712520	Nonsense_Mutation	SNV	G	A	A	PBRM1	c.232C>T	P.R78*
XH_P28	4	144616958	144616958	Missense_Mutation	SNV	A	G	G	FREM3	c.4871T>C	P.V1624A
XH_P28	4	153303455	153303455	Silent	SNV	A	G	G	FBXW7	c.33T>C	P.H111H
XH_P28	4	15937774	15937774	Missense_Mutation	SNV	G	A	A	FGFBP1	c.482C>T	P.P161L
XH_P28	4	169196555	169196555	Nonsense_Mutation	SNV	G	A	A	DDX60	c.2245C>T	P.R749*
XH_P28	4	184932524	184932524	Missense_Mutation	SNV	G	A	A	STOX2	c.2533G>A	P.D845N
XH_P28	4	2460957	2460957	Missense_Mutation	SNV	G	A	A	CFAP99	c.1427G>A	P.R476H
XH_P28	4	3240637	3240637	Silent	SNV	C	T	T	HTT	c.9147C>T	P.V3049V
XH_P28	4	47408822	47408822	Missense_Mutation	SNV	C	T	T	GABRB1	c.959C>T	P.A320V
XH_P28	4	52861210	52861210	Missense_Mutation	SNV	C	T	T	LRRC66	c.1978G>A	P.D660N
XH_P28	4	55956164	55956164	Missense_Mutation	SNV	G	A	A	KDR	c.3151C>T	P.R1051W
XH_P28	4	66197723	66197723	Silent	SNV	A	G	G	EPHA5	c.2976T>C	P.S992S
XH_P28	4	83785565	83785565	Frame_Shift_Del	INDEL	T	-	-	SEC31A	c.1384delA	P.I462fs
XH_P28	4	88047293	88047293	Frame_Shift_Del	INDEL	C	-	-	AFF1	c.2621delC	P.P874fs
XH_P28	5	134364584	134364584	Missense_Mutation	SNV	G	A	A	PITX1	c.830C>T	P.T277M
XH_P28	5	134782185	134782185	Missense_Mutation	SNV	G	A	A	DCANP1	c.614C>T	P.S205L
XH_P28	5	138730227	138730227	Missense_Mutation	SNV	C	T	T	PROB1	c.544G>A	P.A182T
XH_P28	5	140222691	140222691	Silent	SNV	C	T	T	PCDH8	c.1785C>T	P.P595R
XH_P28	5	148748030	148748030	Missense_Mutation	SNV	C	T	T	PCYOX1L	c.1247C>T	P.T416M
XH_P28	5	16699587	16699587	Silent	SNV	C	T	T	MYO10	c.3528G>A	P.P1176P
XH_P28	5	16701243	16701243	Silent	SNV	G	A	A	MYO10	c.3261C>T	P.G1087G
XH_P28	5	175957111	175957111	Missense_Mutation	SNV	G	A	A	RNF44	c.673C>T	P.R225C
XH_P28	5	178549673	178549673	Silent	SNV	C	T	T	ADAMTS2	c.3060G>A	P.A1020A
XH_P28	5	178581175	178581175	Silent	SNV	G	A	A	ADAMTS2	c.1257C>T	P.D419D
XH_P28	5	180036991	180036991	Missense_Mutation	SNV	C	T	T	FLT4	c.3721G>A	P.A1241T
XH_P28	5	31294176	31294176	Silent	SNV	C	A	A	CDH6	c.336C>A	P.A112A
XH_P28	5	35667295	35667295	Missense_Mutation	SNV	C	T	T	SPEF2	c.1289C>T	P.A430V
XH_P28	5	40692086	40692086	Missense_Mutation	SNV	G	A	A	PTGER4	c.1073G>A	P.R358H
XH_P28	5	92929447	92929447	Missense_Mutation	SNV	G	A	A	NR2F1	c.1171G>A	P.V391I
XH_P28	6	12120605	12120605	Missense_Mutation	SNV	A	G	G	HIVEP1	c.577A>G	P.N193D
XH_P28	6	143755092	143755092	Silent	SNV	G	T	T	ADAT2	c.87C>A	P.A29A
XH_P28	6	161771192	161771192	Missense_Mutation	SNV	C	T	T	PARK2	c.1337G>A	P.C446Y
XH_P28	6	47522495	47522495	Silent	SNV	C	T	T	CD2AP	c.534C>T	P.T178D
XH_P28	6	7247252	7247252	Silent	SNV	G	A	A	RREB1	c.4404G>A	P.A1468A
XH_P28	7	102962480	102962480	Missense_Mutation	SNV	C	T	T	DNAJC2	c.982G>A	P.E328K
XH_P28	7	107596022	107596022	Missense_Mutation	SNV	C	T	T	LAMB1	c.2744G>A	P.R915H
XH_P28	7	117865007	117865007	Silent	SNV	G	A	A	ANKRD7	c.123G>A	P.L41L
XH_P28	7	121650957	121650957	Silent	SNV	T	C	C	PTPRZ1	c.1857T>C	P.V619Y
XH_P28	7	148463663	148463663	Missense_Mutation	SNV	G	A	A	CUL1	c.800G>A	P.R267H
XH_P28	7	149946093	149946093	Silent	SNV	C	T	T	ACTR3C	c.615G>A	P.L205L
XH_P28	7	150767819	150767819	Missense_Mutation	SNV	G	A	A	SLC4A2	c.1570G>A	P.V524M
XH_P28	7	157333462	157333462	Silent	SNV	C	T	T	PTPRN2	c.2880G>A	P.A960A
XH_P28	7	20687580	20687580	Splice_Site	INDEL	-	T	T	ABCB5	c.1096-6dupT	
XH_P28	7	50450356	50450356	Silent	SNV	C	T	T	IKZF1	c.540C>T	P.Y180Y
XH_P28	7	65551627	65551627	Missense_Mutation	SNV	C	T	T	ASL	c.502C>T	P.R168C
XH_P28	7	73790458	73790458	Missense_Mutation	SNV	C	T	T	CLIP2	c.1727C>T	P.A576V
XH_P28	7	98524852	98524852	Missense_Mutation	SNV	C	T	T	TRRAP	c.3038C>T	P.P1013L
XH_P28	7	98547209	98547209	Splice_Site	SNV	C	T	T	TRRAP	c.4932+5C>T	
XH_P28	7	98552822	98552822	Silent	SNV	C	T	T	TRRAP	c.5811C>T	P.D1937D
XH_P28	8	100654627	100654627	Missense_Mutation	SNV	C	T	T	VPS13B	c.5884C>T	P.P1962S
XH_P28	8	123965564	123965564	Missense_Mutation	SNV	G	A	A	ZHX2	c.1814G>A	P.G605E
XH_P28	8	124658147	124658147	Silent	SNV	C	T	T	KLHL38	c.1578G>A	P.T526T
XH_P28	8	125570011	125570011	Missense_Mutation	SNV	G	A	A	MTSS1	c.1153C>T	P.R385W
XH_P28	8	135621035	135621035	Missense_Mutation	SNV	C	T	T	ZFAT	c.686G>A	P.R229Q
XH_P28	8	14181673	14181673	Missense_Mutation	SNV	C	T	T	SGCZ	c.53G>A	P.R18Q
XH_P28	8	144809687	144809687	Silent	SNV	G	A	A	FAM83H	c.1944C>T	P.G648G
XH_P28	8	145541365	145541365	Missense_Mutation	SNV	G	T	T	DGAT1	c.905C>A	P.P302H
XH_P28	8	22021465	22021465	Missense_Mutation	SNV	G	A	A	SFTPC	c.487G>A	P.A163T
XH_P28	8	22085787	22085787	Silent	SNV	G	A	A	PHYHIP	c.84C>T	P.D28D
XH_P28	8	23106880	23106880	Missense_Mutation	SNV	G	A	A	CHMP7	c.127G>A	P.V43M
XH_P28	8	73848281	73848281	Missense_Mutation	SNV	C	T	T	KCNB2	c.691C>T	P.R231C
XH_P28	8	87076326	87076326	Silent	SNV	G	T	T	PSKH2	c.720C>A	P.T240T
XH_P28	8	98656857	98656857	Silent	SNV	G	A	A	MTDH	c.123G>A	P.G41G
XH_P28	9	108424982	108424982	Missense_Mutation	SNV	G	A	A	TAL2	c.205G>A	P.A69T
XH_P28	9	115652533	115652533	Silent	SNV	G	A	A	SLC46A2	c.429C>T	P.N143N
XH_P28	9	117063343	117063343	Splice_Site	SNV	C	A	A	COL27A1	c.4702-9C>A	
XH_P28	9	117826999	117826999	Silent	SNV	C	T	T	TNC	c.3414G>A	P.T1138T
XH_P28	9	123205916	123205916	Missense_Mutation	SNV	G	T	T	CDK5RAP2	c.3130C>A	P.Q1044K
XH_P28	9	127253433	127253433	Silent	SNV	C	T	T	NR5A1	c.1065G>A	P.V355V
XH_P28	9	130886841	130886841	Splice_Site	SNV	A	G	G	PTGES2	c.-92-12T>C	
XH_P28	9	133257693	133257693	Splice_Site	SNV	C	T	T	HMCN2	c.6871+9C>T	
XH_P28	9	133738371	133738371	Silent	SNV	C	T	T	ABL1	c.771C>T	P.Y257Y
XH_P28	9	136298805	136298805	Missense_Mutation	SNV	C	T	T	ADAMTS13	c.1289C>T	P.A430V
XH_P28	9	136310047	136310047	Silent	SNV	C	T	T	ADAMTS13	c.2484C>T	P.N828N
XH_P28	9	139818433	139818433	Missense_Mutation	SNV	G	A	A	TRAF2	c.1268G>A	P.R423Q
XH_P28	9	139909376	139909376	Missense_Mutation	SNV	G	A	A	ABCA2	c.3871C>T	P.R1291C
XH_P28	9	5044464	5044464	Nonsense_Mutation	SNV	C	T	T	JAK2	c.412C>T	P.R138*
XH_P28	X	100088318	100088318	Missense_Mutation	SNV	C	T	T	CSTF2	c.1417C>T	P.R473C
XH_P28	X	103268037	103268037	Missense_Mutation	SNV	G	A	A	H2BFWT	c.196C>T	P.R66C
XH_P28	X	104465052	104465052	Silent	SNV	G	A	A	TEX13A	c.30C>T	P.S10S
XH_P28	X	141291651	141291651	Silent	SNV	G	A	A	MAGEC2	c.123C>T	P.S41S
XH_P28	X	152612997	152612997	Missense_Mutation	SNV	G	A	A	ZNF275	c.854G>A	P.R285H
XH_P28	X	153039681	153039681	Missense_Mutation	SNV	G	A	A	PLXNB3	c.3629G>A	P.R1210H
XH_P28	X	153041522	153041522	Missense_Mutation	SNV	G	A	A	PLXNB3	c.4651G>A	P.G1551R
XH_P28	X	153132320	153132320	Missense_Mutation	SNV	G	A	A	L1CAM	c.2215C>T	P.R739W
XH_P28	X	153135113	153135113	Missense_Mutation	SNV	C	T	T	L1CAM	c.1129G>A	P.A377T
XH_P28	X	153591108	153591108	Silent	SNV	G	A	A	FLNA	c.2325C>T	P.Y775Y
XH_P28	X	38144935	38144935	Frame_Shift_Del	INDEL	T	-	-	RPGR	c.3317delA	P.K1106fs
XH_P28	X	44918338	44918338	Nonsense_Mutation	SNV	G	A	A	KDM6A	c.963G>A	P.W321*
XH_P28	X	47034427	47034427	Missense_Mutation	SNV	G	A	A	RBM10	c.512G>A	P.R171Q
XH_P28	X	48674984	48674984	Missense_Mutation	SNV	G	A	A	HDAC6	c.1777G>A	P.A593T
XH_P28	X	49032283	49032283	Silent	SNV	A	G	G	PRICKLE3	c.1383T>C	P.R461R
XH_P28	X	50378589	50378589	Missense_Mutation	SNV	G	T	T	SHROOM4	c.484C>A	P.L162M

XH_P28	X	51076108	51076108	Silent	SNV	A	G	G	NUDT10	c.291A>G	P.V97V
XH_P28	X	53240966	53240966	Splice_Site	SNV	T	C	C	KDM5C	c.1242+3A>G	
XH_P28	X	53966652	53966652	Missense_Mutation	SNV	G	A	A	PHF8	c.3055C>T	P.R1019C
XH_P28	X	54783390	54783390	Splice_Site	SNV	G	T	T	ITIH6	c.3109+8C>A	
XH_P28	X	5810919	5810919	Missense_Mutation	SNV	G	T	T	NLGN4X	c.2390C>A	P.T797N
XH_P28	X	67731806	67731806	Missense_Mutation	SNV	T	C	C	YIPF6	c.173T>C	P.V58A
XH_P28	X	69255333	69255333	Silent	SNV	C	T	T	EDA	c.1044C>T	P.G348G
XH_P28	X	70347916	70347916	Missense_Mutation	SNV	G	T	T	MED12	c.3155G>T	P.S1052I
XH_P28	X	9863793	9863793	Silent	SNV	C	T	T	SHROOM2	c.1845C>T	P.H615H
XH_P29	1	201181334	201181334	Missense_Mutation	SNV	A	G	G	IGFN1	c.7313A>G	P.H2438R
XH_P29	1	6523161	6523161	Missense_Mutation	SNV	C	G	G	TNFRSF25	c.589G>C	P.A197P
XH_P29	11	65487511	65487511	Splice_Site	SNV	C	T	T	RNASEH2C	c.468+5G>A	
XH_P29	11	71671823	71671823	Silent	SNV	G	A	A	RNF121	c.33G>A	P.K11K
XH_P29	12	100784828	100784828	Frame_Shift_Ins	INDEL	-	T	T	SLC17A8	c.410dupT	P.W138fs
XH_P29	12	25398284	25398284	Missense_Mutation	SNV	C	T	T	KRAS	c.35G>A	P.G12D
XH_P29	12	94673379	94673379	Frame_Shift_Ins	INDEL	-	A	A	PLXNC1	c.3734dupA	P.N1245fs
XH_P29	17	34958339	34958339	Missense_Mutation	SNV	G	A	A	MRM1	c.100G>A	P.E34K
XH_P29	17	80788076	80788076	Missense_Mutation	SNV	G	A	A	ZNF750	c.2114C>T	P.A705V
XH_P29	18	60230287	60230287	Silent	SNV	A	G	G	ZCCHC2	c.1596A>G	P.Q532Q
XH_P29	19	36205949	36205949	Nonsense_Mutation	SNV	G	T	T	ZBTB32	c.421G>T	P.E141*
XH_P29	19	54632467	54632467	Missense_Mutation	SNV	C	G	G	PRPF31	c.1182C>G	P.F394L
XH_P29	19	5587916	5587916	Silent	SNV	G	A	A	SAFB2	c.2601C>T	P.D867D
XH_P29	19	8807973	8807973	Missense_Mutation	SNV	C	T	T	ACTL9	c.1079G>A	P.R360H
XH_P29	3	112267425	112267425	Missense_Mutation	SNV	C	G	G	ATG3	c.298G>C	P.E100Q
XH_P29	3	178952085	178952085	Missense_Mutation	SNV	A	G	G	PIK3CA	c.3140A>G	P.H1047R
XH_P29	4	68528872	68528872	Missense_Mutation	SNV	C	T	T	UBA6	c.1022G>A	P.R341H
XH_P29	4	83552526	83552526	Missense_Mutation	SNV	G	T	T	SCD5	c.947C>A	P.P316Q
XH_P29	4	982996	982996	Silent	SNV	G	A	A	SLC26A1	c.1731C>T	P.G577G
XH_P29	5	180036033	180036033	Silent	SNV	C	T	T	FLT4	c.3828G>A	P.G1276G
XH_P29	5	23521146	23521146	Silent	SNV	G	A	A	PRDM9	c.366G>A	P.A122A
XH_P29	6	108067995	108067995	Missense_Mutation	SNV	C	T	T	SCML4	c.211G>A	P.A71T
XH_P29	7	154767930	154767930	Missense_Mutation	SNV	G	A	A	PAXIP1	c.550C>T	P.R184C
XH_P29	7	71036298	71036298	Frame_Shift_Ins	INDEL	-	T	T	WBSCR17	c.992dupT	P.V332fs
XH_P29	8	101195601	101195601	Splice_Site	SNV	A	C	C	SPAG1	c.427-2A>C	
XH_P29	8	90921791	90921791	Splice_Site	SNV	A	T	T	OSGIN2	c.45-4A>T	
XH_P29	9	133281519	133281519	Missense_Mutation	SNV	C	T	T	HMCN2	c.1084C>T	P.R3615C
XH_P29	9	34658622	34658622	Frame_Shift_Ins	INDEL	-	G	G	IL11RA	c.752_753insG	P.H251fs
XH_P29	9	34658623	34658623	Frame_Shift_Ins	INDEL	-	CCCAG	CCCAG	IL11RA	753_754insCCC	P.F252fs
XH_P29	X	27839966	27839966	Silent	SNV	C	T	T	MAGEB10	c.543C>T	P.V181V
XH_P30	1	173769667	173769667	Splice_Site	SNV	G	T	T	CENPL	c.1102-10C>A	
XH_P30	1	248570073	248570073	Missense_Mutation	SNV	C	T	T	OR2T1	c.778C>T	P.P260S
XH_P30	11	94331083	94331083	Splice_Site	SNV	T	G	G	PIWIL4	c.1380+2T>G	
XH_P30	12	107486581	107486581	Splice_Site	SNV	C	T	T	CRY1	c.158+1G>A	
XH_P30	12	53410303	53410303	Missense_Mutation	SNV	T	G	G	EIF4B	c.60T>G	P.F20L
XH_P30	15	66727457	66727457	Missense_Mutation	SNV	A	C	C	MAP2K1	c.173A>C	P.Q58P
XH_P30	17	42290196	42290196	Silent	SNV	C	T	T	UBTF	c.651G>A	P.V217V
XH_P30	18	21111668	21111668	Nonstop_Mutation	SNV	A	G	G	C18orf8	c.1974A>G	P.Ter658Wext**
XH_P30	19	18109195	18109195	Missense_Mutation	SNV	G	A	A	CNN1	c.1612G>A	P.A538T
XH_P30	19	58005441	58005441	Missense_Mutation	SNV	A	G	G	ZNF419	c.1519A>G	P.T507A
XH_P30	2	128263138	128263138	Missense_Mutation	SNV	T	C	C	IWS1	c.341A>G	P.N114S
XH_P30	2	86258708	86258708	Silent	SNV	G	A	A	POLR1A	c.4323C>T	P.D1441D
XH_P30	20	10626616	10626616	Splice_Site	INDEL	-	A	A	JAG1	c.1999+2dupT	
XH_P30	20	33875303	33875303	Missense_Mutation	SNV	G	A	A	FAM83C	c.1279C>T	P.P427S
XH_P30	3	142841044	142841044	Silent	SNV	G	A	A	CHST2	c.1386G>A	P.S462S
XH_P30	3	164751200	164751200	Missense_Mutation	SNV	T	A	A	SI	c.2548A>T	P.R750S
XH_P30	3	45817409	45817409	Silent	SNV	C	T	T	SLC6A20	c.426G>A	P.A142A
XH_P30	3	73114721	73114721	Missense_Mutation	SNV	G	A	A	PPP4R2	c.931G>A	P.G311S
XH_P30	4	153247373	153247373	Missense_Mutation	SNV	C	T	T	FBXW7	c.1429G>A	P.G477S
XH_P30	5	153065788	153065788	Nonsense_Mutation	SNV	C	T	T	GRIA1	c.1033C>T	P.R345*
XH_P30	7	43679239	43679239	Missense_Mutation	SNV	T	A	A	COA1	c.383A>T	P.Q128L
XH_P30	9	137593143	137593143	Silent	SNV	G	A	A	COL5A1	c.618G>A	P.V206V
XH_P30	X	101096518	101096518	Missense_Mutation	SNV	C	G	G	NXF5	c.253G>C	P.V85L
XH_P31	1	151773897	151773897	Silent	SNV	G	T	T	LINGOA	c.1284C>A	P.G428G
XH_P31	1	169366603	169366603	Silent	SNV	A	T	T	CCDC181	c.1239T>A	P.A413A
XH_P31	10	95162004	95162004	Silent	SNV	G	A	A	MYOF	c.975C>T	P.T325T
XH_P31	11	46332740	46332740	Missense_Mutation	SNV	C	A	A	CREB3L1	c.753C>A	P.H251Q
XH_P31	11	5411379	5411379	Nonsense_Mutation	SNV	C	T	T	OR51M1	c.751C>T	P.Q251*
XH_P31	11	7111056	7111056	Silent	SNV	C	T	T	RBMXL2	c.705C>T	P.P235P
XH_P31	12	12940193	12940193	Silent	SNV	G	A	A	APOLD1	c.447G>A	P.R149R
XH_P31	12	176434	176434	Missense_Mutation	SNV	G	T	T	IQSEC3	c.386G>T	P.G129V
XH_P31	12	56481922	56481922	Missense_Mutation	SNV	G	A	A	ERBB3	c.850G>A	P.G284R
XH_P31	13	78171660	78171660	Splice_Site	INDEL	-	T	T	SCEL	c.687-13dupT	
XH_P31	14	21541219	21541219	Missense_Mutation	SNV	G	A	A	ARHGEF40	c.19G>A	P.E7K
XH_P31	14	24885799	24885799	Missense_Mutation	SNV	C	T	T	NYNRIN	c.4844C>T	P.S1615L
XH_P31	14	51237115	51237115	Silent	SNV	G	C	C	NIN	c.1425C>G	P.L475L
XH_P31	14	64989660	64989660	Missense_Mutation	SNV	G	A	A	ZBTB1	c.1438G>A	P.G480R
XH_P31	15	78911014	78911014	Splice_Site	SNV	G	A	A	CHRNA3	c.223-11C>T	
XH_P31	16	58031004	58031004	Missense_Mutation	SNV	T	A	A	ZNF319	c.1166A>T	P.H389L
XH_P31	17	11593565	11593565	Missense_Mutation	SNV	C	G	G	DNAH9	c.4426C>G	P.Q1476E
XH_P31	17	2268303	2268303	Silent	SNV	G	A	A	SGSM2	c.1113G>A	P.L371L
XH_P31	17	3417883	3417883	Splice_Site	SNV	G	C	C	TRPV3	c.2278+4C>G	
XH_P31	17	36243573	36243573	Splice_Site	SNV	G	A	A	YWHAEP7	n.108+8C>T	
XH_P31	17	8020082	8020082	Splice_Site	SNV	T	C	C	ALOXE3	c.748+12A>G	
XH_P31	19	19207020	19207020	Splice_Site	SNV	T	C	C	SLC25A42	c.81+6T>C	
XH_P31	19	46196073	46196073	Silent	SNV	C	T	T	QPCTL	c.112C>T	P.L38L
XH_P31	19	50498470	50498470	Missense_Mutation	SNV	C	T	T	VRK3	c.592G>A	P.G198S
XH_P31	19	50763926	50763926	Missense_Mutation	SNV	C	G	G	MYH14	c.2279C>G	P.A760G
XH_P31	19	51633249	51633249	Silent	SNV	C	A	A	SIGLEC9	c.1305C>A	P.S435S
XH_P31	19	56244764	56244764	Nonsense_Mutation	SNV	G	A	A	NLRP9	c.433C>T	P.R145*
XH_P31	19	58083602	58083602	Missense_Mutation	SNV	T	C	C	ZNF416	c.1670A>G	P.K557R
XH_P31	19	58565348	58565348	Missense_Mutation	SNV	G	A	A	ZSCAN1	c.1156G>A	P.G386R
XH_P31	2	175624357	175624357	Silent	SNV	G	A	A	CHRNA1	c.48C>T	P.G16G
XH_P31	2	24949517	24949517	Missense_Mutation	SNV	G	A	A	NCOA1	c.2659G>A	P.D887N
XH_P31	2	74317082	74317082	Missense_Mutation	SNV	G	A	A	TET3	c.2947G>A	P.G983S
XH_P31	21	47704090	47704090	Missense_Mutation	SNV	C	T	T	MCM3AP	c.1111G>A	P.E371K
XH_P31	21	47918732	47918732	Missense_Mutation	SNV	C	T	T	DIP2A	c.641C>T	P.A214V
XH_P31	22	29694815	29694815	Missense_Mutation	SNV	G	T	T	EWSR1	c.1510G>T	P.G504C
XH_P31	3	124174038	124174038	Silent	SNV	G	A	A	KALRN	c.3561G>A	P.K1187K

XH_P31	3	128205017	128205017	Missense_Mutation	SNV	G	A	A	GATA2	c.424C>T	P.P142S
XH_P31	3	52439876	52439876	Nonsense_Mutation	SNV	G	C	C	BAP1	c.836C>G	P.S279*
XH_P31	3	56667888	56667888	Silent	SNV	T	C	C	FAM208A	c.2931A>G	P.P977P
XH_P31	3	98110193	98110193	Silent	SNV	C	A	A	OR5K3	c.684C>A	P.S228S
XH_P31	3	9945092	9945092	Missense_Mutation	SNV	C	G	G	IL17RE	c.144C>G	P.F48L
XH_P31	4	72363373	72363373	Silent	SNV	G	A	A	SLC4A4	c.2130G>A	P.L710L
XH_P31	6	107390590	107390590	Missense_Mutation	SNV	C	A	A	BEND3	c.1805G>T	P.G602V
XH_P31	6	13486970	13486970	Silent	SNV	G	A	A	GFOD1	c.153C>T	P.Y51Y
XH_P31	6	146480500	146480500	Silent	SNV	C	T	T	GRM1	c.717C>T	P.S239S
XH_P31	6	78173104	78173104	Missense_Mutation	SNV	G	A	A	HTR1B	c.17C>T	P.A6V
XH_P31	7	48407455	48407455	Missense_Mutation	SNV	G	A	A	ABCA13	c.10753G>A	P.A3585T
XH_P31	9	136029080	136029080	Missense_Mutation	SNV	G	A	A	GBG1	c.877C>T	P.P293S
XH_P31	9	33973173	33973173	Splice_Site	SNV	T	C	C	UBAP2	c.575+8A>G	
XH_P31	9	87317138	87317138	Silent	SNV	C	T	T	NTRK2	c.277C>T	P.L93L
XH_P31	X	103349764	103349764	Silent	SNV	G	C	C	SLC25A53	c.177C>G	P.A59A
XH_P31	X	134680316	134680316	Frame_Shift_Ins	INDEL	-	T	T	INTS6L	c.359dupT	P.L120fs
XH_P31	X	50653946	50653946	Missense_Mutation	SNV	G	A	A	BMP15	c.163G>A	P.E55K
XH_P32	1	1163875	1163885	Frame_Shift_Del	DEL	GGCTCCGCC	-	CGGCTCCGCCG	SDF4	c.289_299del	p.R97fs
XH_P32	1	59248400	59248411	In_Frame_Del	DEL	5AAGCCCTCC	-	CGAAGCCCTCGG	JUN	c.332_343del	p.111_115del
XH_P32	1	169696611	169696611	Silent	SNP	C	T	C	SELE	c.G1524A	p.G508G
XH_P32	1	228473981	228473981	Silent	SNP	G	T	G	OBSCN	c.G9207T	p.A3069A
XH_P32	2	96691726	96691726	Missense_Mutation	SNP	C	T	C	GPAT2	c.G977A	p.G326D
XH_P32	2	187511467	187511468	Frame_Shift_Del	DEL	TC	-	TC	ITGAV	c.1106_1107del	p.1369fs
XH_P32	2	202356237	202356237	Silent	SNP	C	T	C	C2CD6	c.G4827A	p.K1609K
XH_P32	3	42251577	42251577	Missense_Mutation	SNP	C	A	C	TRAK1	c.C1841A	p.1614K
XH_P32	3	52429416	52429416	Silent	SNP	C	G	C	DNAH1	c.C11061G	p.13687L
XH_P32	3	98001922	98001922	Missense_Mutation	SNP	T	A	T	OR5H2	c.T191A	p.M64K
XH_P32	3	98073305	98073305	Nonsense_Mutation	SNP	C	A	C	OR5K4	c.C608A	p.S203X
XH_P32	3	126915884	126915884	Missense_Mutation	SNP	A	T	A	C3orf56	c.A356T	p.Y19F
XH_P32	3	150421527	150421527	In_Frame_Ins	INS	-	TCCTCCTCCACC	-	ERICH6	sAGAGGTGGAG	E53delinsEEVEEEE
XH_P32	3	178951957	178951957	Missense_Mutation	SNP	G	A	G	PIK3CA	c.G3012A	p.M1004I
XH_P32	3	195507242	195507242	In_Frame_Ins	INS	-	AGATACTGAGGA	-	MUC4	CAGCACTTCCTC	ATPLPVTTSSVS
XH_P32	4	4239589	4239589	Missense_Mutation	SNP	C	T	C	TMEM128	c.G472A	p.V158I
XH_P32	4	25005736	25005736	Silent	SNP	C	T	C	LG12	c.G975A	p.K325K
XH_P32	5	23527389	23527472	In_Frame_Del	DEL	GGGGAGAA	-	AGGGGAGAA	PRDM9	c.2192_2275del	p.731_759del
XH_P32	5	54529084	54529084	Missense_Mutation	SNP	C	G	C	CCNO	c.G268C	p.V90L
XH_P32	5	95730588	95730588	Missense_Mutation	SNP	T	C	T	PCSK1	c.A1864G	p.G622E
XH_P32	5	139781730	139781730	Missense_Mutation	SNP	G	A	A	ANKHD1	c.G178A	p.G60S
XH_P32	5	150512737	150512737	Missense_Mutation	SNP	C	G	C	ANXA6	c.G462C	p.E154D
XH_P32	5	170148829	170148829	Silent	SNP	C	T	C	KCNIP1	c.C324T	p.C108C
XH_P32	6	160525994	160525994	Missense_Mutation	SNP	G	A	G	IGF2R	c.G7354A	p.G2452R
XH_P32	6	170627695	170627695	In_Frame_Ins	INS	-	GCAAGAAGTTC	-	FAM120B	ACCCAGGCAAG	A4insDEPQRQVPMCTG
XH_P32	7	38256827	38256827	Silent	SNP	C	A	C	STARD3NL	c.C474A	p.I158I
XH_P32	7	57522802	57522802	Missense_Mutation	SNP	T	G	T	ZNF716	c.T190G	p.L64V
XH_P32	7	91709094	91709094	Missense_Mutation	SNP	A	C	A	AKAP9	c.A7647C	p.E2549D
XH_P32	7	123302689	123302689	Missense_Mutation	SNP	G	T	G	LMOD2	c.G1049T	p.E518K
XH_P32	7	150783902	150783903	Frame_Shift_Del	DEL	CT	-	CT	AGAP3	c.74_75del	p.A25fs
XH_P32	8	101721812	101721812	Missense_Mutation	SNP	G	C	G	PABPC1	c.C1120G	p.P374G
XH_P32	9	33030613	33030613	Silent	SNP	C	T	C	DNAJA1	c.C120T	p.N40N
XH_P32	9	104499983	104499983	Silent	SNP	C	T	C	GRIN3A	c.G279A	p.P93P
XH_P32	9	131588839	131588839	Silent	SNP	C	T	C	SPOUT1	c.G438A	p.L146L
XH_P32	10	48390752	48390752	Silent	SNP	C	T	C	RBP3	c.G126A	p.P42P
XH_P32	10	95185893	95185893	Missense_Mutation	SNP	C	A	C	MYOF	c.G368T	p.G123V
XH_P32	11	1018419	1018419	Missense_Mutation	SNP	G	A	G	MUC6	c.C4382T	p.T146I
XH_P32	11	6411931	6411948	In_Frame_Del	DEL	FGCTGGCGCT	-	GTGCTGGCGCTG	SMPD1	c.103_120del	p.35_40del
XH_P32	11	30926660	30926660	Missense_Mutation	SNP	G	A	G	DCDC1	c.C1477T	p.R493C
XH_P32	11	30938455	30938455	Silent	SNP	T	C	T	DCDC1	c.A735G	p.K245K
XH_P32	11	55658976	55658976	Silent	SNP	A	G	A	TRIM51	c.A1227G	p.V409V
XH_P32	11	62300443	62300443	Missense_Mutation	SNP	C	A	A	AHNAK	c.G1446T	p.K482N
XH_P32	11	67132692	67132692	Missense_Mutation	SNP	G	A	G	CLCF1	c.C563T	p.S188L
XH_P32	11	67200271	67200271	Silent	SNP	G	A	G	RP5KB2	c.G579A	p.R193R
XH_P32	11	118890121	118890121	Missense_Mutation	SNP	G	A	G	TRAPPC4	c.G22A	p.D8N
XH_P32	12	52284540	52284551	In_Frame_Del	DEL	GCCCCAGGCC	-	GGCCCCAGGCCCA	ANKRD33	c.228_239del	p.76_80del
XH_P32	12	67692735	67692735	Missense_Mutation	SNP	C	T	C	CAND1	c.C860T	p.C287L
XH_P32	13	20025324	20025324	Silent	SNP	A	G	A	TPTE2	c.T552C	p.Y184Y
XH_P32	14	96157138	96157138	Silent	SNP	C	T	C	TCL1B	c.C228T	p.S76S
XH_P32	14	103987608	103987608	Silent	SNP	G	A	G	CKB	c.C645T	p.R215R
XH_P32	14	105211231	105211231	Missense_Mutation	SNP	A	C	A	ADSSL1	c.A541C	p.I181L
XH_P32	15	75650833	75650833	Silent	SNP	A	C	A	MAN2C1	c.T2076G	p.V692V
XH_P32	16	24574971	24574971	Silent	SNP	A	T	A	RBBP6	c.A1506T	p.R502R
XH_P32	16	57546777	57546777	Missense_Mutation	SNP	C	T	C	CCDC102A	c.G1529A	p.R510H
XH_P32	16	70292007	70292007	Silent	SNP	C	T	C	AARS	c.G2106A	p.P702P
XH_P32	17	6929775	6929775	Splice_Site	SNP	G	A	G	BCL6B		
XH_P32	17	18927651	18927651	Silent	SNP	C	A	C	GRAP	c.G345T	p.S115S
XH_P32	17	42982204	42982204	Missense_Mutation	SNP	A	G	A	FAM187A	c.A1007G	p.Q336R
XH_P32	18	33795610	33795610	Silent	SNP	C	A	C	MOCOS	c.C1467A	p.R489R
XH_P32	18	67673641	67673641	Missense_Mutation	SNP	C	G	C	RTTN	c.G3765C	p.W1255C
XH_P32	19	4682879	4682882	Frame_Shift_Del	DEL	AGAG	-	AGAG	DPP9-A51	c.9_12del	p.A3fs
XH_P32	19	10468453	10468453	Missense_Mutation	SNP	C	T	C	TYK2	c.G2453A	p.R818H
XH_P32	19	30500119	30500124	In_Frame_Del	DEL	TGATGA	-	TGATGA	URI1	c.840_845del	p.280_282del
XH_P32	19	32844003	32844003	Silent	SNP	G	A	G	ZNF507	c.G267A	p.P89P
XH_P32	19	40902229	40902229	Missense_Mutation	SNP	T	C	T	PRX	c.A2030G	p.E677G
XH_P32	19	46299167	46299167	In_Frame_Ins	INS	-	CTCCTCCTCCTCG	-	RSPH6A	4insGCGAGGAG	705delinsGEEEEE
XH_P32	19	52888079	52888079	In_Frame_Ins	INS	-	GTGAAA	-	ZNF880	46_1247insGTG	A416delinsGET
XH_P32	19	53911570	53911570	Silent	SNP	G	A	G	ZNF765	c.G603A	p.S201S
XH_P32	19	54744357	54744357	Frame_Shift_Ins	INS	-	CTGCCACC	-	LILRA6	1051insGGTG	p.F351fs
XH_P32	19	58864385	58864385	Silent	SNP	C	A	C	A1BG	c.G249T	p.L83L
XH_P32	20	1294128	1294128	Silent	SNP	G	T	G	SDCBP2	c.C240A	p.G80G
XH_P32	20	1294129	1294129	Missense_Mutation	SNP	C	T	C	SDCBP2	c.G239A	p.G80D
XH_P32	20	3767122	3767184	Frame_Shift_Del	DEL	CGGGGGCCC	-	CCCGGGGGCCCCG	CENPB	NM_001810	wholegene
XH_P32	20	61441003	61441003	Missense_Mutation	SNP	C	T	C	OGFR	c.C386T	p.S129F
XH_P32	21	33641384	33641384	Silent	SNP	G	A	G	MIS18A	c.C666T	p.A222A
XH_P32	22	18300128	18300128	Missense_Mutation	SNP	C	A	C	MICAL3	c.G5299A	p.G1767R
XH_P32	X	40506603	40506603	Missense_Mutation	SNP	C	T	C	Cxorf38	c.G170A	p.R57H
XH_P32	X	106069422	106069422	Silent	SNP	T	A	T	TBC1D8B	c.T990A	p.A330A
XH_P32	X	142718309	142718309	Missense_Mutation	SNP	C	T	C	SLITRK4	c.G616A	p.V206I
XH_P32	1	228473981	228473981	Silent	SNV	G	T	T	OBSCN	c.9207G>T	P.A3069A
XH_P32	10	48390752	48390752	Silent	SNV	C	T	T	RBP3	c.126G>A	P.P42P

XH_P32	10	95185893	95185893	Missense_Mutation	SNV	C	A	A	MYOF	c.368G>T	P.G123V
XH_P32	11	118890121	118890121	Missense_Mutation	SNV	G	A	A	TRAPPC4	c.22G>A	P.D8N
XH_P32	11	30926660	30926660	Missense_Mutation	SNV	G	A	A	DCDC5	c.1477C>T	P.R493C
XH_P32	12	67692735	67692735	Missense_Mutation	SNV	C	T	T	CAND1	c.788C>T	P.P263L
XH_P32	14	103987608	103987608	Silent	SNV	G	A	A	CKB	c.645C>T	P.R215R
XH_P32	14	105211231	105211231	Missense_Mutation	SNV	A	C	C	ADSSL1	c.541A>C	P.I181L
XH_P32	15	75650833	75650833	Silent	SNV	A	C	C	MAN2C1	c.2424T>G	P.V808V
XH_P32	16	24574971	24574971	Silent	SNV	A	T	T	RBBP6	c.1506A>T	P.R502R
XH_P32	17	18927651	18927651	Silent	SNV	C	A	A	GRAP	c.345G>T	P.S115S
XH_P32	17	6929775	6929775	Splice_Site	SNV	G	A	A	BCL6B	c.890-1G>A	
XH_P32	19	58864385	58864385	Silent	SNV	C	A	A	A1BG	c.249G>T	P.L83L
XH_P32	2	187511467	187511468	Frame_Shift_Del	INDEL	TC	-	-	ITGAV	1077_1078delC	P.F360fs
XH_P32	2	202356237	202356237	Silent	SNV	C	T	T	ALS2CR11	c.4827G>A	P.K1609K
XH_P32	20	1294129	1294129	Missense_Mutation	SNV	C	T	T	SDCBP2	c.239G>A	P.G80D
XH_P32	20	61441003	61441003	Missense_Mutation	SNV	C	T	T	OGFR	c.386C>T	P.S129F
XH_P32	3	178951957	178951957	Missense_Mutation	SNV	G	A	A	PIK3CA	c.3012G>A	P.M1004I
XH_P32	3	52429416	52429416	Silent	SNV	C	G	G	DNAH1	c.11061C>G	P.L3687L
XH_P32	3	98073305	98073305	Nonsense_Mutation	SNV	C	A	A	OR5K4	c.608C>A	P.S203*
XH_P32	4	4239589	4239589	Missense_Mutation	SNV	C	T	T	TMEM128	c.472G>A	P.V158I
XH_P32	5	150512737	150512737	Missense_Mutation	SNV	C	G	G	ANXA6	c.558G>C	P.E186D
XH_P32	5	23527389	23527472	Missense_Mutation	INDEL	GGGGAGAA	-	-	PRDM9	GGACACACACAC	P.R758_F785del
XH_P32	5	54529084	54529084	Missense_Mutation	SNV	C	G	G	CNDM	c.268G>C	P.V90L
XH_P32	5	95730588	95730588	Missense_Mutation	SNV	T	C	C	PCSK1	c.1864A>G	P.K622E
XH_P32	7	38256827	38256827	Silent	SNV	C	A	A	STARD3NL	c.474C>A	P.I158I
XH_P32	7	57522802	57522802	Missense_Mutation	SNV	T	G	G	ZNF716	c.190T>G	P.L64V
XH_P32	7	91709094	91709094	Missense_Mutation	SNV	A	C	C	AKAP9	c.7647A>C	P.E2549D
XH_P32	9	104499983	104499983	Silent	SNV	C	T	T	GRIN3A	c.279G>A	P.P93P
XH_P32	9	131588839	131588839	Silent	SNV	C	T	T	SPOUT1	c.438G>A	P.L146L
XH_P32	9	33030613	33030613	Silent	SNV	C	T	T	DNAI1	c.120C>T	P.N40N
XH_P32	X	106069422	106069422	Silent	SNV	T	A	A	TBC1D8B	c.990T>A	P.A330A
XH_P32	X	142718309	142718309	Missense_Mutation	SNV	C	T	T	SLITRK4	c.616G>A	P.V206I
XH_P32	X	40506603	40506603	Missense_Mutation	SNV	C	T	T	Cxorf38	c.170G>A	P.R57H
XH_P33	14	45653104	45653104	Missense_Mutation	SNP	A	T	T	FANCM	c.4514A>T	p.K15505M
XH_P33	1	3649562	3649562	Silent	SNP	G	A	G	TP73	c.G1440A	p.A480A
XH_P33	1	16345867	16345867	Missense_Mutation	SNP	G	A	G	HSPB7	c.C98T	p.S33L
XH_P33	1	18808711	18808711	Silent	SNP	G	C	G	KLHDC7A	c.G1236C	p.G412G
XH_P33	1	19181393	19181393	Missense_Mutation	SNP	T	C	T	TAS1R2	c.A571G	p.I191V
XH_P33	1	19992513	19992513	Silent	SNP	C	T	C	HTR6	c.C267T	p.Y89Y
XH_P33	1	20009737	20009737	Silent	SNP	G	A	G	TMC04	c.C1701T	p.S567S
XH_P33	1	20141528	20141528	Missense_Mutation	SNP	C	T	C	RNF186	c.G67A	p.A23T
XH_P33	1	26487940	26487940	Missense_Mutation	SNP	A	G	A	FAM110D	c.A158G	p.H53R
XH_P33	1	26609259	26609259	Silent	SNP	C	T	C	UBXN11	c.G813A	p.T271T
XH_P33	1	27107135	27107135	Frame_Shift_Ins	INS	-	A	-	ARID1A	c.6747dupA	p.S2249fs
XH_P33	1	33292533	33292533	Splice_Site	INS	-	TTGCTTTC	-	S100BPB	-	-
XH_P33	1	33646950	33646950	Silent	SNP	A	G	A	TRIM62	c.T84C	p.H28H
XH_P33	1	36807481	36807481	Missense_Mutation	SNP	C	T	C	STK40	c.G1198A	p.A400T
XH_P33	1	38023324	38023324	Frame_Shift_Ins	INS	-	T	-	DNALI1	c.269dupT	p.I90fs
XH_P33	1	38023326	38023326	Missense_Mutation	SNP	C	G	C	DNALI1	c.C270G	p.I90M
XH_P33	1	38155914	38155914	Missense_Mutation	SNP	T	C	T	C1orf109	c.A157G	p.K53E
XH_P33	1	43804285	43804285	Frame_Shift_Ins	INS	-	TCTTCTCA	-	MPL	85_286insTCTTC	p.F95fs
XH_P33	1	45476663	45476663	Silent	SNP	G	A	G	HECTD3	c.C267T	p.L89L
XH_P33	1	53600078	53600078	Silent	SNP	A	G	A	SLC1A7	c.T159C	p.P53P
XH_P33	1	66723505	66723505	Missense_Mutation	SNP	C	A	C	PDE4B	c.C498A	p.N166K
XH_P33	1	66723507	66723507	Frame_Shift_Ins	INS	-	AGAAC	-	PDE4B	500_501insAGA	p.N167fs
XH_P33	1	70694110	70694110	Missense_Mutation	SNP	C	T	C	SRSF11	c.C209T	p.S70L
XH_P33	1	75055571	75055571	Missense_Mutation	SNP	T	A	T	ERICH3	c.A1920T	p.L640F
XH_P33	1	78383958	78383958	In_Frame_Ins	INS	-	TTCTAAAA	-	NEXN	5_256insTTCTTA	p.Q85delinsQFLK
XH_P33	1	78383959	78383959	Splice_Site	SNP	G	A	G	NEXN	-	-
XH_P33	1	91182240	91182240	Silent	SNP	C	A	C	BARHL2	c.G513T	p.P171P
XH_P33	1	94342443	94342443	In_Frame_Ins	INS	-	AGTTATAAG	-	DNTTIP2	7_1048insCTTA	p.V350delinsLITV
XH_P33	1	110768764	110768764	Frame_Shift_Ins	INS	-	CTCCCCACCTGT	-	KCNCA	GGGGGCTCCCC	p.G595fs
XH_P33	1	152128110	152128110	In_Frame_Ins	INS	-	AACCTGGCCTTC	-	RPTN	5ACAGACAAGGdelinsQTRDQ	p.G55SHYK
XH_P33	1	152129066	152129101	In_Frame_Del	DEL	TGCTTGTTC	-	TCTGTCTGTTC	RPTN	c.474_509del	p.158_170del
XH_P33	1	152187389	152187427	In_Frame_Del	DEL	GAATGTCTCT	-	AGGAATGTCTCT	HRNR	c.6678_6716del	p.2226_2239del
XH_P33	1	152282032	152282032	Missense_Mutation	SNP	G	C	G	FLG	c.C5330G	p.S1777C
XH_P33	1	152732302	152732340	In_Frame_Del	DEL	GGCTCAATG	-	AGGCTCAATGTC	KPRP	c.238_276del	p.80_92del
XH_P33	1	153317801	153317801	Missense_Mutation	SNP	A	G	A	PGLYRP4	c.T197C	p.V66A
XH_P33	1	159002411	159002411	Frame_Shift_Ins	INS	-	AT	-	IFI16	1091_1092insA	p.T364fs
XH_P33	1	159002413	159002413	Frame_Shift_Ins	INS	-	TTTCA	-	IFI16	993_1094insTT	p.T365fs
XH_P33	1	160302249	160302249	Missense_Mutation	SNP	C	A	C	COPA	c.G485T	p.W162L
XH_P33	1	161483723	161483723	Splice_Site	SNP	G	A	G	FCGR2A	-	-
XH_P33	1	161721745	161721745	Missense_Mutation	SNP	G	A	G	DUSP12	c.G548A	p.R183H
XH_P33	1	176709186	176709186	Silent	SNP	C	T	C	PAPPA2	c.C4005T	p.F1335F
XH_P33	1	176709187	176709187	Missense_Mutation	SNP	C	T	C	PAPPA2	c.C4006T	p.H1336Y
XH_P33	1	185109277	185109277	Frame_Shift_Ins	INS	-	TTTCTAA	-	TRMT1L	58_469insTTAG	p.V157fs
XH_P33	1	186273365	186273365	Frame_Shift_Ins	INS	-	CATCTGTGTTAT	-	PRG4	23insACATCTTG	p.I108fs
XH_P33	1	186280635	186280635	Nonsense_Mutation	SNP	A	T	A	PRG4	c.A3298T	p.K1100X
XH_P33	1	186280637	186280638	Frame_Shift_Del	DEL	AG	-	AG	PRG4	c.3300_3301del	p.K1100fs
XH_P33	1	200539091	200539091	Missense_Mutation	SNP	T	A	T	KIF14	c.A2136T	p.J121F
XH_P33	1	202418191	202418191	Nonsense_Mutation	INS	-	ATT	-	PPP1R12B	1742_1743insA	p.C581delinsX
XH_P33	1	205290794	205290794	Missense_Mutation	SNP	G	A	G	NUAK2	c.C95T	p.T32I
XH_P33	1	207890918	207890918	Frame_Shift_Ins	INS	-	TTCTGTGTGTC	-	CR1L	GGGAGTCTCTG	p.P508fs
XH_P33	1	222876553	222876554	Frame_Shift_Del	DEL	TG	-	TG	AIDA	c.116_117del	p.A39fs
XH_P33	1	228509886	228509886	Missense_Mutation	SNP	C	G	C	OBSCN	c.C15344G	p.P5115R
XH_P33	1	228509888	228509888	Nonsense_Mutation	INS	-	SAGAGGAAGCG	-	OBSCN	GCCTTAGAGAG	p.L5116delinsX
XH_P33	1	228564884	228564884	Missense_Mutation	SNP	G	A	G	OBSCN	c.G23171A	p.R7724H
XH_P33	1	228588680	228588680	Silent	SNP	A	C	A	TRIM11	c.T720G	p.A240A
XH_P33	1	236557771	236557771	Missense_Mutation	SNP	G	A	G	EDARADD	c.G27A	p.M9I
XH_P33	1	243329398	243329398	In_Frame_Ins	INS	-	SACCTTGAGTA	-	CEP170	TCATTTTACTCA	p.SHLHLCFSYRVCQHLLVLSG
XH_P33	2	20205848	20205848	Silent	SNP	G	A	G	MATN3	c.C447T	p.A149A
XH_P33	2	26689660	26689660	Silent	SNP	G	A	G	OTOF	c.C2352T	p.Y784Y
XH_P33	2	27165492	27165492	Silent	SNP	C	A	C	DPYSL5	c.C1314A	p.V438V
XH_P33	2	29150453	29150453	Missense_Mutation	SNP	A	G	A	WDR43	c.A1192G	p.N398D
XH_P33	2	32605282	32605282	Frame_Shift_Ins	INS	-	CAGGTAC	-	BIRC6	59_570insCAGG	p.D190fs
XH_P33	2	33568029	33568029	Frame_Shift_Ins	INS	-	AT	-	LTBP1	2877_2878insA	p.Y959fs
XH_P33	2	33568031	33568031	Splice_Site	SNP	G	A	G	LTBP1	-	-
XH_P33	2	36691676	36691676	Splice_Site	SNP	G	A	G	CRIM1	-	-
XH_P33	2	36691678	36691678	Nonsense_Mutation	INS	-	AACTAAG	-	CRIM1	71_872insAACT	p.C291_E292delinsX

XH_P33	2	55436809	55436809	Nonsense_Mutation	INS	-	TTTTTTATCT	-	CLHC1	292insAGATAA	R98_R99delinsRX
XH_P33	2	64322025	64322025	Silent	SNP	G	A	G	PEL1	c.C1068T	p.D356D
XH_P33	2	65217089	65217089	Silent	SNP	G	C	G	SLC1A4	c.G312C	p.S104S
XH_P33	2	86705748	86705748	Nonsense_Mutation	INS	-	GAATTATCTA	-	KDM3A	2207insGAATT	736_1737delinsGX
XH_P33	2	88125215	88125215	Missense_Mutation	SNP	G	C	G	RGPD2	c.C34G	p.L12V
XH_P33	2	97166296	97166296	Missense_Mutation	SNP	A	G	A	NEURL3	c.T394C	p.C132R
XH_P33	2	97818241	97818241	Missense_Mutation	SNP	T	G	T	ANKRD36	c.T1163G	p.V388G
XH_P33	2	98732147	98732147	Missense_Mutation	SNP	T	C	T	VWA3B	c.T229C	p.S77P
XH_P33	2	99978030	99978030	Frame_Shift_Ins	INS	-	ACTTCTTATTTG	-	E1F5B	67insCACTTCTT	p.S222fs
XH_P33	2	113145814	113145814	Missense_Mutation	SNP	C	T	C	RGPD5	c.G4708A	p.G1570R
XH_P33	2	115822383	115822383	Splice_Site	SNP	G	A	G	DPP10	.	.
XH_P33	2	121736132	121736132	Frame_Shift_Ins	INS	-	CTATT	-	GLI2	491_1492insCT	p.H497fs
XH_P33	2	131802045	131802045	Silent	SNP	C	T	C	ARHGEF4	c.C1773T	p.P591P
XH_P33	2	136396509	136396553	In_Frame_Del	DEL	TTTGAAGTAC	-	AGTTGAAGTACT	R3HDM1	c.868_912del	p.290_304del
XH_P33	2	152487273	152487273	Nonsense_Mutation	INS	-	TTAAATATTACA	-	NEB	914insATGTAA	B72_E2973delinsMX
XH_P33	2	152487275	152487275	Missense_Mutation	SNP	G	T	G	NEB	c.C8912A	p.T2971K
XH_P33	2	153575161	153575161	Nonsense_Mutation	SNP	G	A	G	ARL6IP6	c.G23A	p.W8X
XH_P33	2	163039951	163039951	In_Frame_Ins	INS	-	ATCTTT	-	FAP	66_1767insAAAp	D589delinsEKI
XH_P33	2	165578785	165578785	Frame_Shift_Ins	INS	-	TA	-	COBLL1	c.795_796insTA	p.H266fs
XH_P33	2	165578786	165578786	Frame_Shift_Ins	INS	-	CA	-	COBLL1	c.794_795insTG	p.K265fs
XH_P33	2	170493837	170493837	Frame_Shift_Ins	INS	-	CTCCT	-	PIIG	069_2070insCT	p.S690fs
XH_P33	2	173338810	173338810	Frame_Shift_Ins	INS	-	CACA	-	ITGA6	803_804insCAC	p.L268fs
XH_P33	2	175614857	175614857	Missense_Mutation	SNP	C	A	C	CHRNA1	c.G819T	p.L273F
XH_P33	2	179638614	179638614	Missense_Mutation	SNP	G	T	G	TTN	c.C7143A	p.F2381L
XH_P33	2	216002903	216002903	Frame_Shift_Ins	INS	-	AGTAAGATAT	-	ABCA12	29insATATCTT	p.L10fs
XH_P33	2	223554167	223554167	Nonsense_Mutation	SNP	C	T	C	MOGAT1	c.C457T	p.R153X
XH_P33	2	227915832	227915832	Missense_Mutation	SNP	G	A	G	COL4A4	c.C3011T	p.P1004L
XH_P33	2	231624800	231624877	Frame_Shift_Del	DEL	ATGGATTG	-	TATGGATTGGC	CAB39	c.84_114del	p.K28fs
XH_P33	2	233498669	233498669	Silent	SNP	G	T	G	EFHD1	c.G255T	p.P85P
XH_P33	2	239229372	239229372	Silent	SNP	C	A	C	TRAF3IP1	c.C69A	p.T23T
XH_P33	2	241404499	241404499	Silent	SNP	C	T	C	GPC1	c.C1140T	p.S380S
XH_P33	2	241621869	241621869	Missense_Mutation	SNP	G	A	G	AQP12B	c.C386T	p.T129M
XH_P33	2	241827865	241827865	Silent	SNP	G	A	G	C2orf54	c.C1095T	p.F365F
XH_P33	2	242312576	242312576	Missense_Mutation	SNP	G	T	G	FARP2	c.G54T	p.L18F
XH_P33	2	242312577	242312577	Missense_Mutation	SNP	G	T	G	FARP2	c.G55T	p.G19C
XH_P33	2	242648677	242648677	Silent	SNP	G	A	G	ING5	c.G156A	p.T52T
XH_P33	2	242758179	242758179	Silent	SNP	C	T	C	NEU4	c.C1299T	p.S433S
XH_P33	3	39118670	39118670	Nonsense_Mutation	SNP	G	A	G	WDR48	c.G692A	p.W231X
XH_P33	3	52540773	52540773	Silent	SNP	T	C	T	STAB1	c.T1896C	p.G632G
XH_P33	3	70014263	70014263	Frame_Shift_Ins	INS	-	GAGC	-	M1TF	124_1125insGA	p.E375fs
XH_P33	3	89445074	89445074	Frame_Shift_Ins	INS	-	A	-	EPHA3	1394_1395insp	p.G465fs
XH_P33	3	89445075	89445075	In_Frame_Ins	INS	-	TCT	-	EPHA3	1395_1396insTop	p.G465delinsGS
XH_P33	3	128532244	128532244	Silent	SNP	G	A	G	RAB7A	c.G603A	p.S201S
XH_P33	3	130383927	130383927	Nonsense_Mutation	SNP	C	T	C	COL6A6	c.C6583T	p.R2195X
XH_P33	3	133302808	133302888	Frame_Shift_Del	DEL	SCAGTGA	-	AGCAGTGA	CDV3	c.318_360del	p.S106fs
XH_P33	3	136323310	136323310	Frame_Shift_Ins	INS	-	CACGTATAAA	-	STAG1	138insTTTATA	p.T46fs
XH_P33	3	138724858	138724858	Missense_Mutation	SNP	T	C	T	PRR23A	c.A253G	p.T85A
XH_P33	3	142681657	142681686	In_Frame_Del	DEL	GCCACCGTGG	-	GGCCACCGTGCT	PAQR9	c.493_522del	p.165_174del
XH_P33	3	151451961	151451961	Silent	SNP	G	A	G	AADACL2	c.G138A	p.T46T
XH_P33	3	152018125	152018125	Missense_Mutation	SNP	G	T	G	MBNL1	c.G143T	p.G48V
XH_P33	3	152018126	152018126	Silent	SNP	A	C	A	MBNL1	c.A144C	p.G48G
XH_P33	3	154033019	154033019	Frame_Shift_Ins	INS	-	AAAAT	-	DXH36	418_419insATT	p.L140fs
XH_P33	3	154033020	154033020	Missense_Mutation	SNP	G	A	G	DXH36	c.C418T	p.L140F
XH_P33	3	186358297	186358297	Silent	SNP	C	T	C	FETUB	c.C48T	p.C16C
XH_P33	3	195506023	195506023	Missense_Mutation	SNP	G	A	G	MUC4	c.C12428T	p.T4143M
XH_P33	3	195517242	195517242	Frame_Shift_Ins	INS	-	AATATTTACT	-	MUC4	1209insAGTAA	p.T403fs
XH_P33	3	195517243	195517243	Missense_Mutation	SNP	G	C	G	MUC4	c.C1208G	p.T403S
XH_P33	4	1018271	1018271	Silent	SNP	T	C	T	FGFR1	c.T891C	p.D297D
XH_P33	4	1729765	1729800	In_Frame_Del	DEL	TCCGACGGAG	-	TCCGACGGAGC	TACC3	c.636_671del	p.212_224del
XH_P33	4	3446091	3446091	Missense_Mutation	SNP	G	T	G	HGFAC	c.G652T	p.A218S
XH_P33	4	3446682	3446682	Silent	SNP	C	T	C	HGFAC	c.C978T	p.A326A
XH_P33	4	9270563	9270563	Frame_Shift_Ins	INS	-	A	-	USP17L20	c.1220dupA	p.E407fs
XH_P33	4	9270565	9270565	Missense_Mutation	SNP	G	T	G	USP17L20	c.G1221T	p.E407D
XH_P33	4	24578236	24578236	Frame_Shift_Ins	INS	-	GATACTATGA	-	DXH15	137insTCATAG	p.R46fs
XH_P33	4	37962354	37962354	Nonsense_Mutation	INS	-	TTGAGAT	-	PTTG2	99_300insTTGA	100_K101delinsTX
XH_P33	4	39329290	39329290	Nonsense_Mutation	INS	-	TAATAATTA	-	RF1C	418insTTTAA	140_M141delinsFX
XH_P33	4	39329292	39329292	Missense_Mutation	SNP	G	A	G	RF1C	c.C416T	p.S139L
XH_P33	4	40434705	40434725	In_Frame_Del	DEL	GCGGCGGCT	-	TGCGGCGGCTG	RBM47	c.1278_1298del	p.426_433del
XH_P33	4	55968137	55968137	Silent	SNP	G	A	G	KDR	c.C2193T	p.D731D
XH_P33	4	56744168	56744168	Missense_Mutation	SNP	G	A	G	EXOC1	c.G1160A	p.R387Q
XH_P33	4	73968236	73968236	Nonsense_Mutation	INS	-	TCCCATTTGTTT	-	ANKRD17	677insAAACAA	226_A1227delinsX
XH_P33	4	74270085	74270085	Missense_Mutation	SNP	G	T	G	ALB	c.G41T	p.S14I
XH_P33	4	76928525	76928550	In_Frame_Del	DEL	CCTTACCTTG	-	CCCTTACCTTGC	CXCL9	c.53_64del	p.18_22del
XH_P33	4	77230677	77230677	Missense_Mutation	SNP	G	A	G	STBD1	c.G601A	p.E201K
XH_P33	4	88278465	88278465	Missense_Mutation	SNP	C	T	C	HSD17B11	c.G661A	p.V221I
XH_P33	4	101947064	101947068	Frame_Shift_Del	DEL	GTTAG	-	GTTAG	PPP3CA	c.1364_1368del	p.T455fs
XH_P33	4	107156509	107156509	Frame_Shift_Ins	INS	-	C	-	TBCK	c.1176_1177insp	p.K393fs
XH_P33	4	107156510	107156510	Frame_Shift_Ins	INS	-	AG	-	TBCK	1175_1176insC	p.K392fs
XH_P33	4	129959267	129959267	Missense_Mutation	SNP	A	T	A	SLC11	c.T305A	p.L102H
XH_P33	4	141403540	141403540	Frame_Shift_Ins	INS	-	TATATCAGTACT	-	MGAT4D	insCCAGTACTG	p.K65fs
XH_P33	4	146575269	146575280	In_Frame_Del	DEL	AACGTTTCA	-	AAACGTTTCA	MMAA	c.943_954del	p.315_318del
XH_P33	4	148984372	148984372	Frame_Shift_Ins	INS	-	ATGA	-	ARHGAP10	101_2102insAT	p.A701fs
XH_P33	4	148984374	148984374	Frame_Shift_Ins	INS	-	AG	-	ARHGAP10	2103_2104insA	p.A701fs
XH_P33	4	154502589	154502589	Missense_Mutation	SNP	C	T	C	TMEM131L	c.C769T	p.R257C
XH_P33	4	154502590	154502590	Frame_Shift_Ins	INS	-	TTTTATT	-	TMEM131L	70_771insTTTTA	p.R257fs
XH_P33	4	162841654	162841654	Missense_Mutation	SNP	T	A	T	FSTL5	c.A308T	p.D103V
XH_P33	4	166235300	166235300	Nonsense_Mutation	INS	-	ATTATATCATAT	-	KLHL2	nsAGAGATTAT	M365delinsKRFISYX
XH_P33	4	183652079	183652079	Frame_Shift_Ins	INS	-	ATATTTT	-	TENM3	54_2755insATA	p.E918fs
XH_P33	4	183652080	183652080	Frame_Shift_Ins	INS	-	A	-	TENM3	c.2755_2756insp	p.R919fs
XH_P33	4	186544619	186544619	Missense_Mutation	SNP	C	T	C	SORBS2	c.G1664A	p.R555H
XH_P33	5	878551	878551	Missense_Mutation	SNP	A	G	A	BRD9	c.T1031C	p.V344A
XH_P33	5	7789866	7789869	Frame_Shift_Del	DEL	CCCC	-	CCCC	ADCY2	c.2581_2584del	p.P861fs
XH_P33	5	32403346	32403346	Missense_Mutation	SNP	C	T	C	ZFR	c.G1381A	p.V461I
XH_P33	5	35867486	35867486	Frame_Shift_Ins	INS	-	TGGCTTT	-	IL7R	20_301insTGGC	p.L100fs
XH_P33	5	37148323	37148323	In_Frame_Ins	INS	-	AGATTAGGATTA	-	C5orf42	8259insTAATCC	2753delinsNNPNL
XH_P33	5	40853480	40853480	Missense_Mutation	SNP	G	T	G	CARD6	c.G2046T	p.E682D
XH_P33	5	40853481	40853481	Missense_Mutation	SNP	G	T	G	CARD6	c.G2047T	p.G683C
XH_P33	5	53813830	53813830	Silent	SNP	A	C	A	SNX18	c.A48C	p.P16P

XH_P33	5	58272278	58272278	Frame_Shift_Ins	INS	-	CTTCC	-	PDE4D	056_1057insGG	p.K353fs
XH_P33	5	64273018	64273018	Silent	SNP	G	A	G	CWC27	c.G1209A	p.T403T
XH_P33	5	72858502	72858525	In_Frame_Del	DEL	AGAACACAC	-	GAGAACACACAT	ANKRA2	c.182_205del	p.G1_69del
XH_P33	5	79950724	79950724	In_Frame_Ins	INS	-	CCGCAGCGC	-	MSH3	8_179insCCGCA	p.A60delinsAAAP
XH_P33	5	82817887	82817887	Silent	SNP	A	G	A	VCAN	c.A3762G	p.S1254S
XH_P33	5	90281284	90281284	Nonsense_Mutation	INS	-	TTTTTAAGTTAG	-	ADGRV1	098insTTTTTTTA	p.G6034delinsIFLSX
XH_P33	5	95091218	95091279	Frame_Shift_Del	DEL	CTGTGAAGCC	-	CGTGTGAAGCCA	RHOBTB3	c.801_862del	p.V267fs
XH_P33	5	110836783	110836783	Frame_Shift_Ins	INS	-	TCTGTAAT	-	STARD4	9_20insATTACA	p.G7fs
XH_P33	5	131281106	131281106	Silent	SNP	G	C	G	MEKIN	c.C93G	p.A31A
XH_P33	5	138356939	138356939	Nonsense_Mutation	INS	-	CCCTACCGTTTT	-	SIL1	AAAAAAAACGG	p.V231delinsKKKKRX
XH_P33	5	138730407	138730407	Missense_Mutation	SNP	C	T	C	PROB1	c.G364A	p.G122S
XH_P33	5	140516786	140516786	Silent	SNP	G	A	G	PCDH85	c.G1770A	p.A590A
XH_P33	5	140563579	140563579	Missense_Mutation	SNP	C	T	C	PCDH816	c.C1445T	p.T482I
XH_P33	5	140605030	140605030	Silent	SNP	T	G	T	PCDH814	c.T1953G	p.P651P
XH_P33	5	140731740	140731740	Missense_Mutation	SNP	T	C	T	PCDH81	c.T1913C	p.L638P
XH_P33	5	140763194	140763194	Frame_Shift_Ins	INS	-	TATTTTACATT	-	PCDHGA7	nsCATTATTTTT	p.S243fs
XH_P33	5	141337170	141337171	Frame_Shift_Del	DEL	CC	-	CC	PCDH12	c.246_247del	p.E82fs
XH_P33	5	141337171	141337171	Frame_Shift_Ins	INS	-	GGATG	-	PCDH12	245_246insCAT	p.E82fs
XH_P33	5	145665571	145665571	Frame_Shift_Ins	INS	-	ATTC	-	RBM27	161_3162insAT	p.E1054fs
XH_P33	5	145665572	145665572	Missense_Mutation	SNP	G	T	G	RBM27	c.G3162T	p.E1054D
XH_P33	5	148996328	148996328	Silent	SNP	G	A	G	ARHGEF37	c.G657A	p.V219V
XH_P33	5	176025160	176025231	In_Frame_Del	DEL	CACCGCGAG	-	CCACCGCGAGG	GPRIN1	c.1605_1676del	p.S53_559del
XH_P33	6	10557280	10557280	Missense_Mutation	SNP	T	A	T	GCNT2	c.T624A	p.F208L
XH_P33	6	10587038	10587038	Missense_Mutation	SNP	C	G	C	GCNT2	c.C816G	p.D272E
XH_P33	6	15513482	15513482	Silent	SNP	G	A	G	JARID2	c.G2763A	p.L921L
XH_P33	6	26463739	26463739	Missense_Mutation	SNP	T	C	T	BTN2A1	c.T515C	p.V172A
XH_P33	6	26463741	26463741	Missense_Mutation	SNP	A	T	A	BTN2A1	c.A517T	p.I173F
XH_P33	6	27806601	27806601	Silent	SNP	T	C	T	HIST1H2BN	c.T162C	p.G54G
XH_P33	6	34850732	34850767	In_Frame_Del	DEL	TTTTTCTCTT	-	GCTTTTCTCTTT	TAFF1	c.262_297del	p.88_99del
XH_P33	6	36178202	36178202	Silent	SNP	C	T	C	BRPF3	c.C2076T	p.L962H
XH_P33	6	40360071	40360071	Missense_Mutation	SNP	C	T	C	LRFN2	c.G1981A	p.A661T
XH_P33	6	40360465	40360465	Silent	SNP	A	G	A	LRFN2	c.T1587C	p.I529I
XH_P33	6	43106987	43106987	Silent	SNP	G	A	G	PTK7	c.G1500A	p.A500A
XH_P33	6	44243559	44243559	Silent	SNP	A	G	A	TMEM151B	c.A996G	p.L332L
XH_P33	6	71665986	71665986	Silent	SNP	G	A	G	B3GAT2	c.C147T	p.G49G
XH_P33	6	85473758	85473758	Missense_Mutation	SNP	C	T	C	TBX18	c.G142A	p.G48R
XH_P33	6	111583624	111583624	Frame_Shift_Ins	INS	-	AATCATTAAAT	-	MFSD4B	3insATAATCATT	p.L64fs
XH_P33	6	133078831	133078831	In_Frame_Ins	INS	-	ACACGAGGGGG	-	VNN2	CCCATGCCCTCT	p.4delinsAPMPLVYIM
XH_P33	6	135787437	135787437	Frame_Shift_Ins	INS	-	A	-	AH11	c.263_264insT	p.N88fs
XH_P33	6	135787439	135787439	Frame_Shift_Ins	INS	-	CTAC	-	AH11	261_262insGTA	p.N88fs
XH_P33	6	136582430	136582430	Frame_Shift_Ins	INS	-	AATTTTTTCTCTG	-	BCLAF1	577insGAGAGA	p.E859fs
XH_P33	6	144184370	144184370	Frame_Shift_Ins	INS	-	GTACTAGAGTT	-	LTV1	728insGTACTA	p.E243fs
XH_P33	6	146056499	146056499	Missense_Mutation	SNP	C	G	C	EPM2A	c.G136C	p.A46P
XH_P33	6	146262862	146262862	Missense_Mutation	SNP	C	T	C	SHPRH	c.G2387A	p.R796Q
XH_P33	6	160679400	160679400	Silent	SNP	C	A	C	SLC22A2	c.G390T	p.T130T
XH_P33	6	160769811	160769811	Silent	SNP	C	T	C	SLC22A3	c.C360T	p.T120R
XH_P33	6	165844913	165844913	Nonsense_Mutation	INS	-	CTTAA	-	PDE10A	740_741insTTAA	p.Q248delinsVX
XH_P33	7	1528979	1529005	Frame_Shift_Del	DEL	CACCATCTCT	-	ATCACCATCTCCA	INTS1	c.2293_2318del	p.M765fs
XH_P33	7	1532649	1532649	Missense_Mutation	SNP	G	A	G	INTS1	c.C2162T	p.P721L
XH_P33	7	2578434	2578434	Missense_Mutation	SNP	G	T	G	BRAT1	c.C1915A	p.P639T
XH_P33	7	6043658	6043658	Silent	SNP	A	G	A	PMS2	c.T195C	p.L65L
XH_P33	7	8791095	8791095	Missense_Mutation	SNP	C	G	C	NXP1	c.C512G	p.T171R
XH_P33	7	31887668	31887668	Frame_Shift_Ins	INS	-	GTGTTGCT	-	PDE1C	3_894insAGCA	p.E298fs
XH_P33	7	37934169	37934169	Missense_Mutation	SNP	A	C	A	NME8	c.A1501C	p.T501P
XH_P33	7	42005678	42005678	Missense_Mutation	SNP	G	A	G	GLI3	c.C2993T	p.P998L
XH_P33	7	43496040	43496040	Missense_Mutation	SNP	A	C	A	HECW1	c.A2543C	p.N848T
XH_P33	7	43496043	43496047	Frame_Shift_Del	DEL	GGCGG	-	GGCGG	HECW1	c.2546_2549del	p.R849fs
XH_P33	7	56170560	56170560	Missense_Mutation	SNP	C	T	C	CHCHD2	c.G445A	p.G149S
XH_P33	7	63537941	63537941	Missense_Mutation	SNP	T	C	T	ZNF727	c.T514C	p.C172R
XH_P33	7	63537942	63537942	Missense_Mutation	SNP	G	C	G	ZNF727	c.G515C	p.C172S
XH_P33	7	64168416	64168416	Missense_Mutation	SNP	C	A	C	ZNF107	c.C1845A	p.N615K
XH_P33	7	64168418	64168418	Missense_Mutation	SNP	T	C	T	ZNF107	c.T1847C	p.L616P
XH_P33	7	64169007	64169083	Frame_Shift_Del	DEL	CTACAAGCT	-	CTCTACAAGCTTA	ZNF107	c.2436_2512del	p.P812fs
XH_P33	7	73753250	73753250	Silent	SNP	T	C	T	CLIP2	c.T594C	p.T198T
XH_P33	7	76871086	76871086	Silent	SNP	G	A	G	CCDC146	c.G318A	p.L106L
XH_P33	7	82545635	82545635	Nonsense_Mutation	INS	-	ATTATATT	-	PCLO	6_11667insAAT	p.889_Y3890delinsQIX
XH_P33	7	87079391	87079391	Frame_Shift_Ins	INS	-	GACT	-	ABC84	725_726insAGT	p.S242fs
XH_P33	7	91775459	91775459	Missense_Mutation	SNP	A	C	A	LRRD1	c.T2334G	p.N778K
XH_P33	7	95739378	95739378	Missense_Mutation	SNP	A	G	A	DYNC111	c.A1804G	p.T602A
XH_P33	7	99017680	99017680	Silent	SNP	C	T	C	ATP5J2-PTCD1	c.G2013A	p.P671P
XH_P33	7	100549540	100549540	Missense_Mutation	SNP	A	T	A	MUC3A	c.A121T	p.S41C
XH_P33	7	100642572	100642572	Missense_Mutation	SNP	C	T	A	MUC12	c.C8728T	p.P2910S
XH_P33	7	100679209	100679209	Missense_Mutation	SNP	A	G	A	MUC17	c.A4512G	p.I1504M
XH_P33	7	100679210	100679210	Missense_Mutation	SNP	G	C	G	MUC17	c.G4513C	p.A1505P
XH_P33	7	100683474	100683474	Missense_Mutation	SNP	T	G	T	MUC17	c.T8777G	p.V2926G
XH_P33	7	101272355	101272355	Missense_Mutation	SNP	A	T	A	MYL10	c.T44A	p.L15H
XH_P33	7	102087202	102087202	Silent	SNP	T	C	T	ORA12	c.T237C	p.L79L
XH_P33	7	102584754	102584754	Frame_Shift_Del	DEL	G	-	G	LRRC17	c.1026delG	p.L342fs
XH_P33	7	102584755	102584755	Nonsense_Mutation	SNP	A	T	A	LRRC17	c.A1027T	p.K343X
XH_P33	7	103162576	103162576	Frame_Shift_Ins	INS	-	CCTTCCAATAA	-	RELN	7561insTATTGT	p.N2521fs
XH_P33	7	104787030	104787030	In_Frame_Ins	INS	-	AAG	-	SRPK2	c.663_664insCT	p.M222delinsLM
XH_P33	7	104787031	104787031	Missense_Mutation	SNP	C	G	C	SRPK2	c.G663C	p.L221F
XH_P33	7	105254929	105254929	Missense_Mutation	SNP	G	C	G	ATXN7L1	c.C1480G	p.P494A
XH_P33	7	105254930	105254930	Frame_Shift_Ins	INS	-	AG	-	ATXN7L1	1478_1479insC	p.K493fs
XH_P33	7	105255190	105255190	Frame_Shift_Ins	INS	-	CAAAACCA	-	ATXN7L1	8_1219insTGGT	p.V407fs
XH_P33	7	107580520	107580520	Silent	SNP	C	T	C	LAMB1	c.G3675A	p.R1225R
XH_P33	7	107580521	107580521	Missense_Mutation	SNP	C	T	C	LAMB1	c.G3674A	p.R1225K
XH_P33	7	116339598	116339598	Frame_Shift_Ins	INS	-	T	-	MET	c.461dupT	p.L154fs
XH_P33	7	117250708	117250708	Frame_Shift_Ins	INS	-	TTTTTTTT	-	CFTR	24_3125insTTTT	p.Q1042fs
XH_P33	7	117250709	117250709	Frame_Shift_Ins	INS	-	TTTTTTTATTAT	-	CFTR	3126insTTTTTT	p.Q1042fs
XH_P33	7	129152259	129152259	Nonsense_Mutation	INS	-	ACAAATA	-	SMKR1	75_176insACAA	p.559_K60delinsDKX
XH_P33	7	129152260	129152260	Missense_Mutation	SNP	G	T	G	SMKR1	c.G176T	p.G59V
XH_P33	7	141921566	141921566	In_Frame_Ins	INS	-	TCTTTGGTG	-	MGAM2	5_7256insTCTTT	p.T2419delinsIFGA
XH_P33	7	142723693	142723693	In_Frame_Ins	INS	-	CAGCCATCACTC	-	OR9A2	ACTTGGAGTGAT	p.TMEFALLGVMAVDVRYVAVCN
XH_P33	7	150094853	150094853	Silent	SNP	G	A	G	ZNF775	c.G1284A	p.T428T
XH_P33	7	150878260	150878260	Silent	SNP	C	G	C	ASB10	c.G870C	p.A290A
XH_P33	7	151127240	151127240	In_Frame_Ins	INS	-	TTTTCATT	-	CRYGN	2_443insAAATG	p.A148delinsEMKT
XH_P33	7	158697941	158697941	Missense_Mutation	SNP	T	C	T	WDR60	c.T76C	p.S26P

XH_P33	8	494659	494664	In_Frame_Del	DEL	GGCGGC	-	GGCGGC	TDRP	c.94_99del	p.32_33del
XH_P33	8	8560602	8560602	Missense_Mutation	SNP	C	T	C	CLDN23	c.C694T	p.P232S
XH_P33	8	11995019	11995019	Silent	SNP	T	G	T	USP17L2	c.A1251C	p.A417A
XH_P33	8	12957657	12957657	Missense_Mutation	SNP	C	T	C	DLC1	c.G656A	p.R219Q
XH_P33	8	22273397	22273397	Frame_Shift_Ins	INS	-	TCAGAGTAGCGG	-	SLC39A14	c.GATATCAGAGT	p.H289fs
XH_P33	8	38285486	38285486	Nonsense_Mutation	INS	-	TAAGTAATACTT	-	FGFR1	c.7insGAAAGTAT	p.K103delinsESITX
XH_P33	8	38386106	38386106	Frame_Shift_Ins	INS	-	AAATCAT	-	C8orf86	c.49_50insATGAT	p.S17fs
XH_P33	8	38677932	38677932	Silent	SNP	A	G	A	TACC1	c.A585G	p.E195E
XH_P33	8	53569969	53569969	Nonsense_Mutation	INS	-	TAGTATG	-	RB1CC1	c.19_2420insCAT	p.B807_5808delinsAYX
XH_P33	8	68028309	68028309	Frame_Shift_Ins	INS	-	AAAAAAATCTG	-	CSPP1	c.552insAAAAAA	p.D184fs
XH_P33	8	75233186	75233186	Missense_Mutation	SNP	C	T	C	JPH1	c.G337A	p.G113R
XH_P33	8	94807654	94807654	Silent	SNP	G	A	G	TMEM67	c.G1692A	p.L564L
XH_P33	8	105478933	105478933	Silent	SNP	G	A	G	DPY5	c.C216T	p.F72F
XH_P33	8	122627272	122627272	Frame_Shift_Ins	INS	-	GCATGAG	-	HAS2	c.35_736insCTCA	p.N246fs
XH_P33	8	126163472	126163472	Missense_Mutation	SNP	C	T	C	NSMCE2	c.C217T	p.R73W
XH_P33	8	133984912	133984912	Missense_Mutation	SNP	C	T	C	TG	c.C6125T	p.A2042V
XH_P33	8	133984913	133984913	Nonsense_Mutation	INS	-	TAATAAAA	-	TG	c.26_6127insTAA	p.D42_W2043delinsAX
XH_P33	8	134144102	134144102	Frame_Shift_Ins	INS	-	TTATATC	-	TG	c.99_7910insTTA	p.Y2637fs
XH_P33	8	143763490	143763490	Silent	SNP	T	C	T	PSCA	c.T285C	p.A95A
XH_P33	8	145004639	145004639	Silent	SNP	G	A	G	PLEC	c.C2328T	p.A776A
XH_P33	9	2717905	2717905	Missense_Mutation	SNP	G	A	G	KCNV2	c.C166A	p.E56K
XH_P33	9	5774170	5774170	Missense_Mutation	SNP	G	A	G	RIC1	c.C64085A	p.R1362Q
XH_P33	9	13150667	13150667	Frame_Shift_Ins	INS	-	TTTT	-	MPDZ	c.472_3473insAA	p.P1158fs
XH_P33	9	13150668	13150668	Nonsense_Mutation	INS	-	TTTATTTATTTA	-	MPDZ	c.472insATAAATA	p.S58_1159delinsINXK
XH_P33	9	15474136	15474136	Silent	SNP	C	T	C	PSIP1	c.G729A	p.K243K
XH_P33	9	94172745	94172745	Missense_Mutation	SNP	C	T	C	NFIL3	c.C627A	p.R91H
XH_P33	9	96097747	96097747	Missense_Mutation	SNP	C	T	C	C9orf129	c.C627A	p.G92S
XH_P33	9	104432683	104432683	Missense_Mutation	SNP	A	T	A	GRIN3A	c.T2011A	p.W671R
XH_P33	9	114454175	114454175	Missense_Mutation	SNP	T	A	T	C9orf84	c.A3773T	p.K1258M
XH_P33	9	125512340	125512340	In_Frame_Ins	INS	-	GGG	-	OR1L6	c.214_215insGG	p.I72delinsRV
XH_P33	9	128692068	128692068	Silent	SNP	C	T	C	PBX3	c.C426T	p.L142L
XH_P33	9	130151230	130151304	In_Frame_Del	DEL	ACCCCTAGT	-	TCACCCCTAGTCT	GARNL3	c.c.2575_2649del	p.859_883del
XH_P33	9	131285026	131285026	Missense_Mutation	SNP	G	A	G	GLE1	c.G512A	p.R171Q
XH_P33	9	131804785	131804785	Missense_Mutation	SNP	T	C	T	MIGA2	c.C299C	p.V100A
XH_P33	9	133911706	133911706	Silent	SNP	C	T	C	LAMC3	c.C963T	p.A321A
XH_P33	9	135946599	135946599	Silent	SNP	C	T	C	CEL	c.C1719T	p.P573P
XH_P33	9	138379059	138379059	Silent	SNP	G	T	G	PPP1R26	c.C62703T	p.L901L
XH_P33	9	138903671	138903671	Silent	SNP	A	G	A	NACC2	c.T1455C	p.P485P
XH_P33	9	140173413	140173413	Missense_Mutation	SNP	G	A	G	TOR4A	c.C627A	p.R91H
XH_P33	10	1042083	1042083	Missense_Mutation	SNP	G	A	G	GTPBP4	c.G361A	p.D121N
XH_P33	10	12077162	12077162	Silent	SNP	C	T	C	UPF2	c.G261A	p.K87K
XH_P33	10	22830930	22830930	In_Frame_Ins	INS	-	AGTAAG	-	PIP4K2A	c.661_662insCTTA	p.I221delinsTVF
XH_P33	10	43318594	43318596	In_Frame_Del	DEL	CCA	-	CCA	BMS1	c.c.3161_3163del	p.1054_1055del
XH_P33	10	43883134	43883134	Missense_Mutation	SNP	C	T	C	HNRNPf	c.G199A	p.V67I
XH_P33	10	50678459	50678459	Frame_Shift_Ins	INS	-	AAAG	-	ERCC6	c.3546_3547insCT	p.S1183fs
XH_P33	10	50819182	50819182	Silent	SNP	T	C	T	SLC18A3	c.C396C	p.A132A
XH_P33	10	52601649	52601649	Missense_Mutation	SNP	A	G	A	A1CF	c.C338C	p.I131T
XH_P33	10	55587197	55587197	In_Frame_Ins	INS	-	GGTGCC	-	PCDH15	c.09_4110insGCC	p.P1370delinsPPP
XH_P33	10	61412631	61412631	Missense_Mutation	SNP	T	C	T	SLC16A9	c.A1168G	p.I390V
XH_P33	10	61665886	61665886	Silent	SNP	C	A	C	CCDC6	c.C6297T	p.V99V
XH_P33	10	75155863	75155863	Nonsense_Mutation	INS	-	TATTTTATCTTT	-	ANXA7	c.20insCAAAGATA	p.A07_T108delinsTKIKK
XH_P33	10	75301492	75301492	Missense_Mutation	SNP	G	T	G	USP54	c.C577A	p.Q193K
XH_P33	10	75301494	75301494	In_Frame_Ins	INS	-	ATA	-	USP54	c.c.574_575insTA	p.N192delinsY
XH_P33	10	88702390	88702390	Silent	SNP	G	A	G	MMRN2	c.C2151T	p.A717A
XH_P33	10	89720828	89720828	Frame_Shift_Ins	INS	-	TATTT	-	PTEN	c.979_980insTAT	p.K327fs
XH_P33	10	89720830	89720830	Frame_Shift_Ins	INS	-	TTAATGAT	-	PTEN	c.1_982insTTAAT	p.K327fs
XH_P33	10	91163408	91163408	Missense_Mutation	SNP	A	T	A	IFIT1	c.A1376T	p.Y459F
XH_P33	10	94669344	94669344	Nonsense_Mutation	INS	-	ATCTAAATAATCA	-	EXOC6	c.20insAATCTAAA	p.I207delinsKSKX
XH_P33	10	98079147	98079147	Silent	SNP	G	A	G	DNTT	c.G507A	p.T169T
XH_P33	10	99332379	99332381	In_Frame_Del	DEL	GGC	-	GGC	ANKRD2	c.c.173_175del	p.58_59del
XH_P33	10	99439541	99439541	Missense_Mutation	SNP	G	C	G	AVP1	c.C122G	p.A41G
XH_P33	10	105362335	105362335	Frame_Shift_Ins	INS	-	TCAGGCACTCCA	-	SH3PXD2A	c.ACCGCTGGAGT	p.V852fs
XH_P33	10	124399679	124399679	In_Frame_Del	DEL	CATGTACATT	-	CCATGTACATTG	DMBT1	c.c.4795_4815del	p.1599_1605del
XH_P33	10	124740079	124740079	Silent	SNP	G	A	G	PSK	c.G84A	p.A28A
XH_P33	10	129904590	129904590	Frame_Shift_Ins	INS	-	CTAACACC	-	MKI67	c.3_4434insGGTG	p.L1478fs
XH_P33	10	129921430	129921430	Silent	SNP	A	T	A	MKI67	c.T96A	p.G32G
XH_P33	11	903709	903709	Missense_Mutation	SNP	T	A	T	CHID1	c.A181T	p.T61S
XH_P33	11	993907	993907	Silent	SNP	C	G	C	AP2A2	c.C1707G	p.L569L
XH_P33	11	1858572	1858572	Missense_Mutation	SNP	C	T	C	SVT8	c.C1120T	p.R374W
XH_P33	11	1977552	1977552	Missense_Mutation	SNP	G	A	G	MRPL23	c.G364A	p.A122T
XH_P33	11	5510811	5510825	In_Frame_Del	DEL	CTATTCTCTA	-	TCCTATTCTCTAT	OR52D1	c.c.875_889del	p.292_297del
XH_P33	11	7110363	7110363	Silent	SNP	G	A	G	RBMXL2	c.G12A	p.A4A
XH_P33	11	18111005	18111005	Frame_Shift_Ins	INS	-	SATATAAAAGTC	-	SAAL1	c.542insAGACTTT	p.D214fs
XH_P33	11	18194964	18194964	Missense_Mutation	SNP	A	G	A	MRGPRX4	c.A161G	p.Y54C
XH_P33	11	20623023	20623023	Silent	SNP	C	T	C	SLC6A5	c.C352T	p.L118L
XH_P33	11	31703413	31703413	Silent	SNP	C	T	C	ELP4	c.C1222T	p.L408L
XH_P33	11	31703414	31703414	Missense_Mutation	SNP	T	G	T	ELP4	c.C1223G	p.L408R
XH_P33	11	32456694	32456694	Silent	SNP	C	A	C	WT1	c.G198T	p.P66P
XH_P33	11	46369371	46369371	Splice_Site	INS	-	AAAGCCA	-	DGK2	.	.
XH_P33	11	61914260	61914260	Missense_Mutation	SNP	G	A	G	INCENP	c.C62078A	p.R693Q
XH_P33	11	63403040	63403040	Missense_Mutation	SNP	C	T	C	ATL3	c.C6947A	p.G316E
XH_P33	11	63403041	63403041	Frame_Shift_Ins	INS	-	TTTTTTTTTTTTTT	-	ATL3	c.5insAAAAAAA	p.G316fs
XH_P33	11	64027648	64027648	Frame_Shift_Ins	INS	-	GGTGGTGTCCA	-	PLCB3	c.5AGCTGGGTGG	p.E491fs
XH_P33	11	64029457	64029457	Silent	SNP	C	G	C	PLCB3	c.C1746G	p.P582P
XH_P33	11	64645871	64645871	Silent	SNP	A	G	A	EHD1	c.T66C	p.A22A
XH_P33	11	71948483	71948483	Frame_Shift_Ins	INS	-	C	-	INPPL1	c.c.3196dupC	p.L1065fs
XH_P33	11	73534065	73534065	Missense_Mutation	SNP	T	C	T	MRPL48	c.T8C	p.L3P
XH_P33	11	73534066	73534066	Silent	SNP	G	A	G	MRPL48	c.G9A	p.L3L
XH_P33	11	75277992	75277992	Silent	SNP	C	T	C	SERPINH1	c.C598T	p.L200L
XH_P33	11	82880240	82880317	In_Frame_Del	DEL	GTCTGAGAT	-	GGTCTGAGATT	PCF11	c.c.3256_3333del	p.1086_1111del
XH_P33	11	89177304	89177304	Missense_Mutation	SNP	T	A	T	NOX4	c.A371T	p.E124V
XH_P33	11	107799426	107799426	Silent	SNP	C	A	C	RAB39A	c.C132A	p.T44T
XH_P33	11	117034567	117034567	In_Frame_Ins	INS	-	SATGAAAAATCTTT	-	PAFAH1B2	c.1TTTAGATGAAA	p.6delinsHLDENLFFF
XH_P33	11	117329592	117329592	Missense_Mutation	SNP	C	T	C	DSCAM1	c.C3626A	p.R1209Q
XH_P33	11	128781758	128781758	Missense_Mutation	SNP	C	T	C	KCNJ5	c.C590T	p.A197V
XH_P33	11	132399080	132399080	Missense_Mutation	SNP	A	G	A	OPCML	c.T401C	p.V134A
XH_P33	12	248155	248155	Silent	SNP	C	T	C	IQSEC3	c.C717T	p.A239A
XH_P33	12	319125	319125	Missense_Mutation	SNP	A	G	A	SLC6A12	c.T28C	p.C10R

XH_P33	12	7636167	7636228	Frame_Shift_Del	DEL	ACTGTCCCCC	-	CACTGTCCCCCA	CD163	c.2823_2884del	p.R941fs
XH_P33	12	7923090	7923090	Missense_Mutation	SNP	G	C	G	NANOGB	c.G491C	p.R164T
XH_P33	12	10570989	10570989	Nonsense_Mutation	SNP	G	T	G	KLRC3	c.C440A	p.S147X
XH_P33	12	26275555	26275555	Missense_Mutation	SNP	G	A	G	BHLHE41	c.C893T	p.A298V
XH_P33	12	32481295	32481295	Frame_Shift_Ins	INS	-	AGTCC	-	BICD1	906_1907insAG	p.1636fs
XH_P33	12	49420871	49420871	Nonsense_Mutation	SNP	G	A	G	KMT20	c.C14878T	p.R4960X
XH_P33	12	50571176	50571176	Frame_Shift_Ins	INS	-	GGAAC	-	LIMA1	044_1045insGT	p.T349fs
XH_P33	12	52139801	52139801	In_Frame_Ins	INS	-	AGT	-	SCN8A	2113_2114insAAp.T705delinsKS	
XH_P33	12	52139802	52139802	In_Frame_Ins	INS	-	TATAAAGGT	-	SCN8A	2115insTATAAp.T705delinsTIKV	
XH_P33	12	52284500	52284500	Missense_Mutation	SNP	A	G	A	ANKRD33	c.A188G	p.Q63R
XH_P33	12	53012149	53012149	Missense_Mutation	SNP	C	A	C	KRT73	c.C160T	p.A54S
XH_P33	12	55420611	55420653	Frame_Shift_Del	DEL	ATATTGGGG	-	TATATTGGGCT	NEUROD4	c.388_430del	p.R130fs
XH_P33	12	56194672	56194672	In_Frame_Ins	INS	-	ATAGATATTAT	-	SARNP	149insATAAATp.A50delinsDKYLS	
XH_P33	12	56194673	56194673	Missense_Mutation	SNP	C	T	C	SARNP	c.G148A	p.A50T
XH_P33	12	56814867	56814867	Nonsense_Mutation	INS	-	A	-	TIMELESS	2916_2917insE973_E974delinsX	
XH_P33	12	56814869	56814869	Nonsense_Mutation	INS	-	TCCTTAGG	-	TIMELESS	4_2915insCCTA972_E973delinsSAX	
XH_P33	12	57587453	57587453	Missense_Mutation	SNP	G	A	G	LRP1	c.G7789A	p.E2597K
XH_P33	12	57629558	57629558	Missense_Mutation	SNP	G	A	G	NDUFA4L2	c.C181T	p.R61C
XH_P33	12	57648716	57648716	Missense_Mutation	SNP	G	A	G	R3HDM2	c.C2717T	p.S906L
XH_P33	12	64011087	64011087	Silent	SNP	C	T	C	DPY19L2	c.G1215A	p.T405T
XH_P33	12	81009984	81009984	Silent	SNP	C	T	C	PTPRQ	c.C4653T	p.Y1551Y
XH_P33	12	93772199	93772199	Splice_Site	INS	-	GCTGCTGGTG	-	NUDT4	-	-
XH_P33	12	102589861	102589861	Frame_Shift_Ins	INS	-	ACATGATATTGA	-	PARBPB	90insTTACATGA	p.K430fs
XH_P33	12	118681297	118681297	Missense_Mutation	SNP	C	T	C	TAOK3	c.G217A	p.V73I
XH_P33	12	118681299	118681299	Nonsense_Mutation	INS	-	AGTATTTAACAT	-	TAOK3	AACAAATGGTTAAp.V73delinsVLTNVKYX	
XH_P33	12	121174899	121174899	Silent	SNP	T	C	T	ACADS	c.T321C	p.R107R
XH_P33	12	121605355	121605355	Missense_Mutation	SNP	G	A	G	P2RX7	c.G809A	p.R270H
XH_P33	12	124821696	124821696	Silent	SNP	C	T	C	NCOR2	c.G5688A	p.P1896P
XH_P33	12	124826598	124826598	Silent	SNP	T	C	T	NCOR2	c.A4929G	p.R1643R
XH_P33	12	132688137	132688137	Silent	SNP	A	G	A	GALNT9	c.T78C	p.Y26C
XH_P33	13	23929696	23929696	Frame_Shift_Ins	INS	-	ATCATTG	-	SACS	13_614insCAATp.p.L205fs	
XH_P33	13	24410388	24410388	Frame_Shift_Ins	INS	-	TATTTAA	-	MIPEP	43_1644insTTTAp.p.Q548fs	
XH_P33	13	24410390	24410390	Missense_Mutation	SNP	G	C	G	MIPEP	c.C1642G	p.Q548E
XH_P33	13	49039488	49039488	Nonsense_Mutation	INS	-	AGTAGATTAT	-	RB1	2474insAGTAGA825_7826delinsKX	
XH_P33	13	49039490	49039490	Missense_Mutation	SNP	G	T	G	RB1	c.G2475T	p.M825I
XH_P33	13	53217270	53217270	Missense_Mutation	SNP	A	G	A	HNRNP1A1L2	c.A643G	p.N215D
XH_P33	13	53421432	53421432	Silent	SNP	C	A	C	PCDH8	c.G1140T	p.G380G
XH_P33	13	76447992	76447992	Missense_Mutation	SNP	A	T	A	LMO7DN	c.A200T	p.H67L
XH_P33	13	99907895	99907895	Nonsense_Mutation	SNP	G	A	G	GPR18	c.C232T	p.R78X
XH_P33	13	101277913	101277913	Missense_Mutation	SNP	G	A	G	TMTC4	c.C1322T	p.A441V
XH_P33	13	103399910	103399910	Frame_Shift_Del	DEL	A	-	A	CCDC168	c.3137delIT	p.V1046fs
XH_P33	13	103399911	103399911	Missense_Mutation	SNP	C	T	C	CCDC168	c.G3136A	p.V1046I
XH_P33	13	103483942	103483942	Missense_Mutation	SNP	G	T	G	BIVM	c.G242T	p.R81L
XH_P33	14	24458283	24458283	Missense_Mutation	SNP	G	T	G	DHRS4L2	c.G127T	p.G43W
XH_P33	14	29237757	29237757	Silent	SNP	G	A	G	FOXG1	c.G1272A	p.P424P
XH_P33	14	35483097	35483097	In_Frame_Ins	INS	-	ACAAAGGTA	-	SRP5	729insACAAAp.S243delinsRQRY	
XH_P33	14	45433307	45433308	Frame_Shift_Del	DEL	ATTGGCTAGG	-	GATTGGCTAGGA	TOGARAM1	c.1683_1759del	p.N561fs
XH_P33	14	45716108	45716108	In_Frame_Ins	INS	-	ACTAAGAGG	-	MIS18BP1	1_382insCCTCTp.E128delinsPLSE	
XH_P33	14	70039587	70039587	Silent	SNP	C	T	C	CCDC177	c.G753A	p.S251S
XH_P33	14	75276122	75276122	Missense_Mutation	SNP	C	T	C	YLPM1	c.C4561T	p.P1521S
XH_P33	14	75276123	75276123	Frame_Shift_Ins	INS	-	TTAT	-	YLPM1	562_4563insTTp.P1521fs	
XH_P33	14	77873900	77873900	Silent	SNP	C	T	C	NOXRRED1	c.G438A	p.P146P
XH_P33	14	94545760	94545760	Missense_Mutation	SNP	T	G	T	DDX24	c.A329C	p.E110A
XH_P33	14	94545761	94545761	Nonsense_Mutation	SNP	C	A	C	DDX24	c.G328T	p.E110X
XH_P33	14	100070030	100070030	Silent	SNP	G	A	G	CCDC85C	c.C267T	p.C89C
XH_P33	14	101200780	101200780	Silent	SNP	T	C	T	DLK1	c.T699C	p.C233C
XH_P33	14	103998985	103998985	Missense_Mutation	SNP	C	T	C	TRMT61A	c.C398T	p.T133M
XH_P33	14	105268104	105268104	Silent	SNP	G	A	G	ZBTB42	c.G570A	p.L190L
XH_P33	14	105412827	105412827	Silent	SNP	C	T	C	AHNAK2	c.G8661A	p.S2887S
XH_P33	14	105417614	105417614	Missense_Mutation	SNP	A	C	A	AHNAK2	c.T3874G	p.L1292V
XH_P33	15	22368790	22368790	Frame_Shift_Ins	INS	-	CA	-	OR4M2	c.215_216insCAp.p.W72fs	
XH_P33	15	22369132	22369132	Missense_Mutation	SNP	G	A	G	OR4M2	c.G557A	p.R186Q
XH_P33	15	40903046	40903046	Silent	SNP	T	C	T	KNL1	c.T300C	p.F100F
XH_P33	15	50782542	50782542	In_Frame_Ins	INS	-	AAAGTA	-	USP8	36_1737insAAAp.P579delinsPKY	
XH_P33	15	55710606	55710606	Frame_Shift_Ins	INS	-	GTACT	-	C15orf65	204_205insGTA	p.E68fs
XH_P33	15	56924259	56924259	Frame_Shift_Ins	INS	-	AAAG	-	ZNF280D	2337_2338insCT	p.G780fs
XH_P33	15	59981491	59981491	Missense_Mutation	SNP	T	G	T	BNIP2	c.A149C	p.D50A
XH_P33	15	63433719	63433719	Silent	SNP	T	C	T	LACTB	c.T1359C	p.S453S
XH_P33	15	70959540	70959540	Missense_Mutation	SNP	G	C	G	UACA	c.C3444G	p.N1148K
XH_P33	15	74219546	74219546	Missense_Mutation	SNP	G	T	G	LOXL1	c.G422T	p.R141L
XH_P33	15	101815520	101815520	Frame_Shift_Ins	INS	-	TC	-	SELENOS	c.257_258insGA	p.R86fs
XH_P33	16	334580	334580	Silent	SNP	G	C	G	PDIA2	c.G393C	p.P131P
XH_P33	16	775240	775240	Silent	SNP	G	A	G	CCDC78	c.C489T	p.S163S
XH_P33	16	904551	904551	Missense_Mutation	SNP	G	C	G	LMF1	c.C1685G	p.P562R
XH_P33	16	1268494	1268494	Silent	SNP	C	T	C	CACNA1H	c.C5712T	p.D1904D
XH_P33	16	1270162	1270162	Missense_Mutation	SNP	G	A	G	CACNA1H	c.G6212A	p.R2071H
XH_P33	16	1279623	1279623	Silent	SNP	G	A	G	TPSB2	c.C177T	p.C59C
XH_P33	16	1827836	1827836	Silent	SNP	T	C	T	SPSB3	c.A633G	p.S211S
XH_P33	16	1838037	1838037	Silent	SNP	C	G	C	NUBP2	c.C162G	p.T54T
XH_P33	16	1842209	1842209	Silent	SNP	A	G	A	IGFALS	c.T324C	p.D108D
XH_P33	16	3340524	3340524	Missense_Mutation	SNP	G	A	G	ZNF263	c.G2018A	p.R673H
XH_P33	16	3632477	3632477	Missense_Mutation	SNP	G	A	G	SLX4	c.C5371T	p.R1791C
XH_P33	16	4511849	4511878	In_Frame_Del	DEL	CAGCTCGATC	-	TCAGCTCGATGT	NMRAL1	c.803_832del	p.268_278del
XH_P33	16	8736341	8736341	Frame_Shift_Ins	INS	-	T	-	METT122	c.930dupT	p.T310fs
XH_P33	16	8736343	8736343	Missense_Mutation	SNP	G	C	G	METT122	c.G931C	p.D311H
XH_P33	16	19519072	19519072	Nonsense_Mutation	INS	-	TCITTTTAA	-	GDE1	2_243insTTAAAM81_E82delinsX	
XH_P33	16	19639032	19639032	Nonsense_Mutation	INS	-	AA	-	C16orf62	1354_1355insAA452_V453delinsX	
XH_P33	16	20360359	20360359	Silent	SNP	G	A	G	UMOD	c.C264T	p.G88G
XH_P33	16	22826339	22826339	Silent	SNP	A	G	A	HS3T2	c.A408G	p.V136P
XH_P33	16	30364880	30364880	Missense_Mutation	SNP	G	A	G	CD2BP2	c.C617T	p.A206V
XH_P33	16	30793330	30793332	In_Frame_Del	DEL	GCA	-	GCA	ZNF629	c.2317_2319del	p.773_773del
XH_P33	16	72139936	72139936	Silent	SNP	G	A	G	DXH38	c.G2520A	p.L840L
XH_P33	16	72139937	72139937	Nonsense_Mutation	INS	-	TGTTAAATT	-	DXH38	1_2522insTGTTA841delinsLNX	
XH_P33	16	75563746	75563746	Silent	SNP	T	G	T	CHST5	c.A537C	p.P179P
XH_P33	16	81129759	81129759	Missense_Mutation	SNP	C	A	C	GCSH	c.G125T	p.R42L
XH_P33	17	1637102	1637102	Missense_Mutation	SNP	G	A	G	WDR81	c.G1162A	p.G388R
XH_P33	17	4461748	4461748	Nonsense_Mutation	SNP	G	A	G	GGT6	c.C358T	p.R120X
XH_P33	17	5085389	5085389	Silent	SNP	C	T	C	ZNF594	c.G2163A	p.T721T

XH_P33	17	5087013	5087096	In_Frame_Del	DEL	AACCTTTGATT	-	GAACCTTTGATTA	ZNF594	c.456_539del	p.152_180del
XH_P33	17	8273524	8273524	Missense_Mutation	SNP	A	T	A	KRBA2	c.T161A	p.F54Y
XH_P33	17	8273526	8273526	Nonsense_Mutation	SNP	G	T	G	KRBA2	c.C159A	p.Y53X
XH_P33	17	11513803	11513803	Silent	SNP	G	A	G	DNAH9	c.G705A	p.E235E
XH_P33	17	11513805	11513805	Frame_Shift_Ins	INS	-	CCAAA	-	DNAH9	707_708insCCA	p.S236fs
XH_P33	17	15458614	15458614	In_Frame_Ins	INS	-	TGAATAATT	-	TVP23C	5_77insAATTAT	p.P26delinsQLFT
XH_P33	17	15458616	15458616	Missense_Mutation	SNP	T	G	T	TVP23C	c.A75C	p.R25S
XH_P33	17	17697094	17697108	In_Frame_Del	DEL	CAGCAGCAG	-	GCAGCAGCAGC	RA1	c.832_846del	p.278_282del
XH_P33	17	18023643	18023643	Missense_Mutation	SNP	C	T	C	MYO15A	c.C1529T	p.A510V
XH_P33	17	18167307	18167307	Missense_Mutation	SNP	G	A	G	MIEF2	c.G520A	p.A174T
XH_P33	17	18881381	18881381	Nonsense_Mutation	INS	-	CTGCCAGGCTCG	-	FAM83G	AGACCCGGAGCG	A534delinsGQHVX
XH_P33	17	18881572	18881572	Silent	SNP	C	T	C	FAM83G	c.G1407A	p.R469R
XH_P33	17	27052320	27052320	Splice_Site	INS	-	ATCTCACTAACA	-	TLCD1	.	.
XH_P33	17	28380656	28380656	Nonsense_Mutation	INS	-	GTGTA	-	EFCAB5	516_1517insGT	506_1507delinsCX
XH_P33	17	32908139	32908139	Missense_Mutation	SNP	G	T	G	TMEM132E	c.G44T	p.C15F
XH_P33	17	35733079	35733079	Silent	SNP	T	C	T	C17orf78	c.T45C	p.D15D
XH_P33	17	36508385	36508385	Silent	SNP	T	C	T	SOC5	c.T258C	p.P86P
XH_P33	17	37657596	37657596	Nonsense_Mutation	INS	-	CTAATATA	-	CDK12	3_2514insCTAA	838_F839delinsSX
XH_P33	17	37657597	37657597	Silent	SNP	G	A	G	CDK12	c.G2514A	p.S838S
XH_P33	17	38421318	38421318	Missense_Mutation	SNP	C	A	C	WIPF2	c.C890A	p.P297H
XH_P33	17	39580310	39580310	Missense_Mutation	SNP	G	A	G	KRT37	c.C466T	p.R156C
XH_P33	17	39890876	39890876	Missense_Mutation	SNP	T	C	T	HAP1	c.A11G	p.K4R
XH_P33	17	42475096	42475096	Frame_Shift_Ins	INS	-	ATTAATA	-	GPATCH8	14_4115insTAT	p.G1372fs
XH_P33	17	45235583	45235583	Nonsense_Mutation	SNP	A	C	A	CDC27	c.T281G	p.L94X
XH_P33	17	55028298	55028298	Frame_Shift_Ins	INS	-	AGCAACC	-	COIL	04_305insGGTT	p.1102fs
XH_P33	17	57157227	57157227	In_Frame_Ins	INS	-	TTG	-	TRIM37	1401_402insCA	p.V134delinsVK
XH_P33	17	57157229	57157229	Missense_Mutation	SNP	C	G	C	TRIM37	c.G400C	p.V134L
XH_P33	17	62034818	62034818	Missense_Mutation	SNP	C	A	C	SCN4A	c.G2080T	p.G694C
XH_P33	17	62543873	62543873	Frame_Shift_Ins	INS	-	GAGAT	-	SMURF2	915_1916insAT	p.V639fs
XH_P33	17	62543874	62543874	Missense_Mutation	SNP	C	T	C	SMURF2	c.G1915A	p.V639I
XH_P33	17	62856239	62856239	Missense_Mutation	SNP	A	G	A	LRRC37A3	c.T1379C	p.L460P
XH_P33	17	66985961	66985961	Silent	SNP	A	T	A	ABCA9	c.T3948A	p.V1316V
XH_P33	17	71197860	71197860	Missense_Mutation	SNP	A	G	A	COG1	c.A1894G	p.L632V
XH_P33	17	71232018	71232018	Frame_Shift_Ins	INS	-	5CTTTAATTAAAT	-	C17orf80	CTTTAGCTTTAA	p.Q133fs
XH_P33	17	74733099	74733099	Silent	SNP	G	A	G	SRSF2	c.C144T	p.D48D
XH_P33	17	76968110	76968110	Missense_Mutation	SNP	G	A	G	LGALS3BP	c.C1306T	p.R436W
XH_P33	17	79770740	79770740	Silent	SNP	C	T	C	GCGR	c.C1095T	p.F365F
XH_P33	18	3729175	3729175	Silent	SNP	C	T	C	DLGAP1	c.G645A	p.P215P
XH_P33	18	12454468	12454468	Frame_Shift_Ins	INS	-	AGAGTTA	-	SPIRE1	50_1251insTAA	p.Y417fs
XH_P33	18	18547885	18547885	In_Frame_Ins	INS	-	TATATA	-	ROCK1	19_3020insTAT	A1007delinsVYT
XH_P33	18	50705483	50705483	Nonsense_Mutation	SNP	G	T	G	DCC	c.G1570T	p.E524X
XH_P33	18	55226383	55226383	Silent	SNP	G	C	G	FECH	c.C798G	p.P266P
XH_P33	18	56247180	56247180	Silent	SNP	T	C	T	ALPK2	c.A828G	p.L276L
XH_P33	18	56586657	56586657	In_Frame_Ins	INS	-	ATGGTT	-	ZNF532	38_1139insATG	V380delinsDGL
XH_P33	18	59483514	59483514	Silent	SNP	A	G	A	RNF152	c.T183C	p.P61P
XH_P33	18	77475187	77475187	Missense_Mutation	SNP	T	A	T	CTDP1	c.T1370A	p.M457K
XH_P33	19	1003439	1003439	Missense_Mutation	SNP	G	A	G	GRIN3B	c.G737A	p.R246H
XH_P33	19	1004808	1004808	Silent	SNP	C	T	C	GRIN3B	c.C1308T	p.D436D
XH_P33	19	1049269	1049269	Silent	SNP	G	A	G	ABCA7	c.G2385A	p.L795L
XH_P33	19	1110829	1110829	Silent	SNP	G	A	G	SBNO2	c.C2772T	p.N924N
XH_P33	19	1978978	1978978	Missense_Mutation	SNP	G	A	G	CSNK1G2	c.G568A	p.G190R
XH_P33	19	3611972	3611972	Silent	SNP	G	A	G	CACTIN	c.C226T	p.N742N
XH_P33	19	5110794	5110794	Silent	SNP	A	G	A	KDM4B	c.A1080G	p.A360A
XH_P33	19	5828064	5828064	Silent	SNP	G	C	G	NRTN	c.G474C	p.R158R
XH_P33	19	8196499	8196499	Silent	SNP	G	A	G	FBN3	c.C1929T	p.C643C
XH_P33	19	9072637	9072637	Nonsense_Mutation	INS	-	CA	-	MUC16	4808_14809ins	937_14938delinsX
XH_P33	19	9362031	9362031	Silent	SNP	A	G	A	OR7E24	c.A312G	p.Q104Q
XH_P33	19	9362032	9362032	Missense_Mutation	SNP	A	T	A	OR7E24	c.A313T	p.T105S
XH_P33	19	9452665	9452665	Frame_Shift_Ins	INS	-	GGTTTCTCTT	-	ZNF559	731insGGTTT	p.T244fs
XH_P33	19	11464539	11464539	Missense_Mutation	SNP	C	T	C	CCDC159	c.C761T	p.S254L
XH_P33	19	11917672	11917755	In_Frame_Del	DEL	TCAATATCA	-	TTCAATATCATG	ZNF491	c.904_987del	p.302_329del
XH_P33	19	12791901	12791901	Silent	SNP	T	C	T	DHPS	c.A27G	p.E9E
XH_P33	19	15659002	15659002	Missense_Mutation	SNP	G	T	G	CYP4F22	c.G1220T	p.R407L
XH_P33	19	15659003	15659003	Frame_Shift_Ins	INS	-	TCTCTCTCTCT	-	CYP4F22	1222insTCTCT	p.R407fs
XH_P33	19	17000632	17000632	Missense_Mutation	SNP	G	A	G	F2RL3	c.G358A	p.A120T
XH_P33	19	17283657	17283657	Silent	SNP	C	T	C	MYO9B	c.C2025T	p.I675I
XH_P33	19	17435884	17435884	Silent	SNP	T	C	T	AN08	c.A2973G	p.S991S
XH_P33	19	19791092	19791092	Silent	SNP	C	T	C	ZNF101	c.C934T	p.L312L
XH_P33	19	19905508	19905508	Silent	SNP	C	G	C	ZNF506	c.G1092C	p.P364P
XH_P33	19	20044369	20044369	Missense_Mutation	SNP	T	A	T	ZNF93	c.T605A	p.I202N
XH_P33	19	20044370	20044370	Silent	SNP	T	A	T	ZNF93	c.T606A	p.I202I
XH_P33	19	20229706	20229706	Missense_Mutation	SNP	G	C	G	ZNF90	c.G1343C	p.S448T
XH_P33	19	20727402	20727402	In_Frame_Ins	INS	-	5GGTTGAGGAC	-	ZNF737	ATAAGTGGTCT	EECGKAYKWSSLTTHKVIHTGEKL
XH_P33	19	20727918	20727918	Missense_Mutation	SNP	C	G	C	ZNF737	c.G1091C	p.S364T
XH_P33	19	21477016	21477016	Missense_Mutation	SNP	A	G	A	ZNF708	c.T560C	p.L187P
XH_P33	19	21719097	21719097	Frame_Shift_Ins	INS	-	TTCTGGCTTCTA	-	ZNF429	TTTATTCTGGC	p.F17fs
XH_P33	19	21720463	21720463	Silent	SNP	T	C	T	ZNF429	c.T1416C	p.P472P
XH_P33	19	22154102	22154102	Missense_Mutation	SNP	A	C	A	ZNF208	c.T3734G	p.V1245G
XH_P33	19	22154103	22154103	Missense_Mutation	SNP	C	T	C	ZNF208	c.G3733A	p.V1245I
XH_P33	19	22155615	22155615	Missense_Mutation	SNP	C	T	C	ZNF208	c.G2221A	p.V741I
XH_P33	19	22497267	22497267	Missense_Mutation	SNP	C	T	C	ZNF729	c.C1048T	p.R350C
XH_P33	19	23159061	23159061	Missense_Mutation	SNP	C	T	C	ZNF728	c.G1078A	p.V360I
XH_P33	19	23159522	23159522	Missense_Mutation	SNP	T	C	T	ZNF728	c.A617G	p.H206R
XH_P33	19	23159523	23159523	Missense_Mutation	SNP	G	A	G	ZNF728	c.C616T	p.H206V
XH_P33	19	23542215	23542215	Missense_Mutation	SNP	A	T	A	ZNF91	c.T3470A	p.L1157H
XH_P33	19	23543464	23543464	Missense_Mutation	SNP	T	C	T	ZNF91	c.A2221G	p.K741E
XH_P33	19	31769763	31769763	Silent	SNP	G	A	G	TSB23	c.C936T	p.V312V
XH_P33	19	33424507	33424507	Nonsense_Mutation	SNP	C	A	C	CEP89	c.G736T	p.E246X
XH_P33	19	33424508	33424508	Frame_Shift_Ins	INS	-	5TTGTGATATTC	-	CEP89	735insCAAATAT	p.E245fs
XH_P33	19	33792631	33792631	Silent	SNP	C	A	C	CEBPA	c.G333T	p.T111T
XH_P33	19	34832656	34832656	Nonsense_Mutation	INS	-	3CAGAAGACATT	-	KIAA0355	GGCGTCGAGAA	delinsSAQNSSNTVACRRHSPNX
XH_P33	19	37240878	37240961	In_Frame_Del	DEL	ACATTCCT	-	TCCATATTCCTTA	ZNF850	c.885_968del	p.295_323del
XH_P33	19	38188974	38188988	In_Frame_Del	DEL	ATCTAAGCCT	-	GATCTAAGCCTAA	ZNF607	c.2041_2055del	p.681_685del
XH_P33	19	38893856	38893856	Silent	SNP	G	C	G	FAM98C	c.G63C	p.L21L
XH_P33	19	39915758	39915758	Missense_Mutation	SNP	C	G	C	PLEKHG2	c.C3985G	p.P1329A
XH_P33	19	41307170	41307170	Silent	SNP	G	A	G	EGLN2	c.G693A	p.P231P
XH_P33	19	43234147	43234147	Silent	SNP	G	T	G	PSG3	c.C771A	p.V257V
XH_P33	19	44223113	44223113	Missense_Mutation	SNP	G	A	G	IRGC	c.G403A	p.D135N

XH_P33	19	44351733	44351733	Nonsense_Mutation	INS	-	ACTTAATAATT	-	ZNF283	564insACTTAA	A188delinsALKX
XH_P33	19	45395699	45395699	Silent	SNP	G	A	G	TOMM40	c.G324A	p.G108G
XH_P33	19	45395700	45395700	In_Frame_Ins	INS	-	TCCACC	-	TOMM40	25_326insTCCAA	p.L109delinsFHL
XH_P33	19	46887120	46887120	Silent	SNP	G	A	G	PPP5C	c.G717A	p.S239S
XH_P33	19	48182787	48182787	Silent	SNP	C	T	C	BICRA	c.C360T	p.A120A
XH_P33	19	48183771	48183771	Silent	SNP	C	T	C	BICRA	c.C1344T	p.S448S
XH_P33	19	48685877	48685877	Silent	SNP	G	A	G	C19orf68	c.G441A	p.P147P
XH_P33	19	49218562	49218602	Frame_Shift_Del	DEL	GGCGGGACCC	-	AGGCGGGACCCC	MAMSTR	c.33_73del	p.A11fs
XH_P33	19	49964977	49964977	Missense_Mutation	SNP	C	G	C	ALDH16A1	c.C679G	p.L227V
XH_P33	19	50881840	50881840	Silent	SNP	G	A	G	NR1H2	c.G243A	p.Q81Q
XH_P33	19	51227707	51227707	Silent	SNP	G	C	G	CLEC11A	c.G375C	p.L125L
XH_P33	19	51519346	51519346	Silent	SNP	G	C	G	KLK10	c.C336G	p.T112T
XH_P33	19	53453982	53454065	In_Frame_Del	DEL	AGTATGAAG	-	CAGTATGAAGT	ZNF816	c.963_1046del	p.321_349del
XH_P33	19	53958652	53958652	Silent	SNP	T	C	T	ZNF761	c.T891C	p.P297P
XH_P33	19	55143156	55143156	Silent	SNP	T	C	T	LILRB1	c.T276C	p.H92H
XH_P33	19	55143157	55143157	Missense_Mutation	SNP	G	A	G	LILRB1	c.G277A	p.A93T
XH_P33	19	55351039	55351039	Missense_Mutation	SNP	C	T	C	KIR2DS4	c.C527T	p.P176L
XH_P33	19	55450843	55450843	Missense_Mutation	SNP	G	C	G	NLRP7	c.C1344G	p.F448L
XH_P33	19	56156380	56156380	Missense_Mutation	SNP	C	T	C	ZNF581	c.C443T	p.P148L
XH_P33	19	56443519	56443519	Silent	SNP	C	T	C	NLRP13	c.G159A	p.P53P
XH_P33	19	57743562	57743562	Missense_Mutation	SNP	G	A	G	AURKC	c.G266A	p.R89H
XH_P33	19	58598709	58598709	Missense_Mutation	SNP	C	T	C	ZSCAN18	c.G211A	p.E71K
XH_P33	20	2187943	2187943	Silent	SNP	G	T	G	LOC388780	c.G153T	p.P51P
XH_P33	20	2187944	2187944	Nonsense_Mutation	SNP	C	T	C	LOC388780	c.C154T	p.Q52X
XH_P33	20	5953254	5953254	Missense_Mutation	SNP	A	G	A	MCM8	c.A1256G	p.Y419C
XH_P33	20	21689974	21689974	Missense_Mutation	SNP	C	T	C	PAX1	c.C1174T	p.P392S
XH_P33	20	23016340	23016340	Missense_Mutation	SNP	C	T	C	SSTR4	c.C220T	p.R74C
XH_P33	20	30142623	30142623	Missense_Mutation	SNP	G	A	G	HM13	c.G799A	p.V267I
XH_P33	20	34220149	34220149	Frame_Shift_Ins	INS	-	TCTTGTAA	-	CPN1	1_392insTTACA	p.A131fs
XH_P33	20	35690652	35690652	Nonsense_Mutation	INS	-	TTAAATCTTGAG	-	RBL1	8insAGCTCAAG	p.306_E307delinsX
XH_P33	20	42333925	42333925	Missense_Mutation	SNP	G	A	G	MYBL2	c.G1360A	p.V454M
XH_P33	20	43043159	43043159	Missense_Mutation	SNP	G	A	G	HNFA4	c.G505A	p.V169I
XH_P33	20	44038658	44038658	Missense_Mutation	SNP	G	T	G	DBNDD2	c.G670T	p.D224Y
XH_P33	20	44038659	44038659	Missense_Mutation	SNP	A	C	A	DBNDD2	c.A671C	p.D224A
XH_P33	20	49509359	49509359	Missense_Mutation	SNP	A	T	A	ADNP	c.T1892A	p.L631Q
XH_P33	20	49509360	49509360	Missense_Mutation	SNP	G	T	G	ADNP	c.C1891A	p.L631I
XH_P33	20	57268867	57268867	Silent	SNP	C	A	C	NPEPL1	c.C225A	p.T75T
XH_P33	20	60866809	60866809	Missense_Mutation	SNP	C	T	C	OSBP12	c.C1264T	p.R422W
XH_P33	20	60893912	60893912	Silent	SNP	A	C	A	LAMA5	c.T7029G	p.A243A
XH_P33	20	61162267	61162267	Missense_Mutation	SNP	T	C	T	MIR1-1HG	c.T80C	p.V27A
XH_P33	20	61288038	61288038	Missense_Mutation	SNP	G	A	G	SLCO4A1	c.G232A	p.V78I
XH_P33	20	62221766	62221766	Silent	SNP	C	T	C	GMEB2	c.G1269A	p.P423P
XH_P33	20	62328267	62328267	Silent	SNP	C	T	C	TNFRSF6B	c.C147T	p.C49C
XH_P33	21	34399401	34399401	Silent	SNP	A	G	A	OLIG2	c.A231G	p.S77S
XH_P33	21	43161022	43161022	Silent	SNP	C	T	C	RIPK4	c.G2331A	p.T777T
XH_P33	21	43254638	43254638	Missense_Mutation	SNP	C	T	C	PRDM15	c.G1513A	p.G505S
XH_P33	21	45978090	45978090	Missense_Mutation	SNP	C	T	C	KRTAP10-3	c.G509A	p.C170Y
XH_P33	21	47855876	47855876	Silent	SNP	A	G	A	PCNT	c.A8220G	p.T2740T
XH_P33	22	17589794	17589794	Missense_Mutation	SNP	C	A	C	IL17RA	c.C1583A	p.P528Q
XH_P33	22	18301862	18301862	Frame_Shift_Ins	INS	-	AGGCTGGAAGC	-	MICAL3	13CATACGCTCC	p.Q1189fs
XH_P33	22	22599739	22599739	Missense_Mutation	SNP	G	A	G	VPREB1	c.G425A	p.R142H
XH_P33	22	22599741	22599741	Missense_Mutation	SNP	G	C	G	VPREB1	c.G427C	p.V143L
XH_P33	22	30776095	30776095	Missense_Mutation	SNP	C	T	C	RNF215	c.G964A	p.A322T
XH_P33	22	30951956	30951956	Missense_Mutation	SNP	T	C	T	GAL3ST1	c.A256G	p.T86A
XH_P33	22	36537893	36537893	Silent	SNP	A	G	A	APOL3	c.T564C	p.N188N
XH_P33	22	39883736	39883736	Silent	SNP	G	C	G	MGAT3	c.G384C	p.P128P
XH_P33	22	45792336	45792336	Missense_Mutation	SNP	C	A	C	SMC1B	c.G1144T	p.V382L
XH_P33	22	45792337	45792337	In_Frame_Ins	INS	-	GAAATTTTA	-	SMC1B	2_1143insTAA	p.Q381delinsHKIS
XH_P33	22	46859815	46859815	Silent	SNP	G	A	G	CLSRI1	c.C3972T	p.F1324F
XH_P33	22	50684415	50684415	Missense_Mutation	SNP	T	C	T	HDAC10	c.A1697G	p.Q566R
XH_P33	22	50686830	50686830	Silent	SNP	G	A	G	HDAC10	c.C918T	p.A306A
XH_P33	X	3021841	3021841	Missense_Mutation	SNP	G	A	G	ARF5	c.G1141A	p.P381I
XH_P33	X	13337438	13337438	Frame_Shift_Ins	INS	-	GAAAAGC	-	ATXN3L	15_616insGCTT	p.K206fs
XH_P33	X	15332558	15332558	Silent	SNP	A	G	A	ASB11	c.T51C	p.A171R
XH_P33	X	40495846	40495846	Missense_Mutation	SNP	A	T	A	CXorf38	c.T383A	p.L128Q
XH_P33	X	48690749	48690749	Silent	SNP	C	T	C	PCSK1N	c.G117A	p.E39E
XH_P33	X	69828949	69828949	Missense_Mutation	SNP	C	A	C	TEX11	c.G1871T	p.R624L
XH_P33	X	76778843	76778843	Missense_Mutation	SNP	C	T	C	ATRX	c.G6622A	p.E2208K
XH_P33	X	76778844	76778844	Frame_Shift_Ins	INS	-	TGTTTTTG	-	ATRX	0_6621insCAAA	p.K2207fs
XH_P33	X	135427087	135427087	Frame_Shift_Ins	INS	-	GT	-	ADGRG4	1222_1223insG	p.E408fs
XH_P33	X	148037594	148037594	Frame_Shift_Ins	INS	-	TTTGTTCTGG	-	AFF2	943insTTTGTT	p.A314fs
XH_P33	X	148037596	148037596	Missense_Mutation	SNP	C	A	C	AFF2	c.C944A	p.T315N
XH_P33	X	151337014	151337014	Frame_Shift_Ins	INS	-	CATA	-	GABRA3	164_1165insTA	p.A389fs
XH_P33	X	153706739	153706739	Nonsense_Mutation	INS	-	TGGAGACATGG	-	LAGE3	GTCCCCCATGTG	p.67_P68delinsAPX
XH_P33	1	152282032	152282032	Missense_Mutation	SNV	G	C	C	FLG	c.C530C>G	p.S1777C
XH_P33	1	153317801	153317801	Missense_Mutation	SNV	A	G	G	PGLYRP4	c.197T>C	p.V66A
XH_P33	1	161483723	161483723	Splice_Site	SNV	G	A	A	FCGR2A	c.780+1G>A	
XH_P33	1	75055571	75055571	Missense_Mutation	SNV	T	A	A	ERICH3	c.1920A>T	p.L640F
XH_P33	1	91182240	91182240	Silent	SNV	C	A	A	BARHL2	c.513G>T	p.P171P
XH_P33	10	52601649	52601649	Missense_Mutation	SNV	A	G	G	A1CF	c.338T>C	p.I113T
XH_P33	10	61412631	61412631	Missense_Mutation	SNV	T	C	C	SLC16A9	c.1168A>G	p.I390V
XH_P33	11	128781758	128781758	Missense_Mutation	SNV	C	T	T	KCNJ5	c.590C>T	p.A197V
XH_P33	11	71948483	71948483	Frame_Shift_Ins	INDEL	-	C	C	INPPL1	c.3201dupC	p.S1068fs
XH_P33	12	49420871	49420871	Nonsense_Mutation	SNV	G	A	A	KMT2D	c.14878C>T	p.R4960*
XH_P33	12	53012149	53012149	Missense_Mutation	SNV	C	A	A	KRT73	c.160G>T	p.A54S
XH_P33	12	57648716	57648716	Missense_Mutation	SNV	G	A	A	R3HDM2	c.2873C>T	p.S958L
XH_P33	13	103483942	103483942	Missense_Mutation	SNV	G	T	T	BIVM	c.242G>T	p.R81L
XH_P33	14	29237757	29237757	Silent	SNV	G	A	A	FOXG1	c.1272G>A	p.P424P
XH_P33	14	77873900	77873900	Silent	SNV	C	T	T	NOXRED1	c.438G>A	p.P146P
XH_P33	15	63433719	63433719	Silent	SNV	T	C	C	LACTB	c.1359T>C	p.S453S
XH_P33	17	32908139	32908139	Missense_Mutation	SNV	G	T	T	TMEM132E	c.44G>T	p.C15F
XH_P33	17	62034818	62034818	Missense_Mutation	SNV	C	A	A	SCN4A	c.2080G>T	p.G694C
XH_P33	17	71197860	71197860	Missense_Mutation	SNV	A	G	G	COG1	c.1894A>G	p.I632V
XH_P33	19	21720463	21720463	Silent	SNV	T	C	C	ZNF429	c.1608T>C	p.P536P
XH_P33	19	38188974	38188988	Missense_Mutation	INDEL	ATCTAAGCCT	-	-	ZNF607	55delTTTAGGCC	p.F681_568del
XH_P33	19	57743562	57743562	Missense_Mutation	SNV	G	A	A	AURKC	c.266G>A	p.R89H
XH_P33	2	113942657	113942657	Splice_Site	SNV	C	T	T	PSD4	c.1173+7C>T	
XH_P33	2	153575161	153575161	Nonsense_Mutation	SNV	G	A	A	ARL6IP6	c.23G>A	p.W8*

XH_P33	2	179638614	179638614	Missense_Mutation	SNV	G	T	T	TTN	c.7281C>A	P.F2427L
XH_P33	2	27165492	27165492	Silent	SNV	C	A	A	DPY5L5	c.1314C>A	P.V438V
XH_P33	20	21689974	21689974	Missense_Mutation	SNV	C	T	T	PAX1	c.1174C>T	P.P392S
XH_P33	20	60866809	60866809	Missense_Mutation	SNV	C	T	T	OSBPL2	c.1264C>T	P.R422W
XH_P33	3	151451961	151451961	Splice_Site	SNV	G	A	A	AADACL2	c.138G>A	P.T46T
XH_P33	3	39118670	39118670	Nonsense_Mutation	SNV	G	A	A	WDR48	c.692G>A	P.W231*
XH_P33	3	44816738	44816738	Splice_Site	SNV	G	T	T	KIF15	c.63-8G>T	
XH_P33	4	162841654	162841654	Missense_Mutation	SNV	T	A	A	FSTL5	c.308A>T	P.D103V
XH_P33	4	55968137	55968137	Silent	SNV	G	A	A	KDR	c.2193C>T	P.D731D
XH_P33	5	40853480	40853480	Missense_Mutation	SNV	G	T	T	CARD6	c.2046G>T	P.E682D
XH_P33	5	40853481	40853481	Missense_Mutation	SNV	G	T	T	CARD6	c.2047G>T	P.G683C
XH_P33	5	82817887	82817887	Silent	SNV	A	G	G	VCAN	c.3762A>G	P.S1254S
XH_P33	6	10557280	10557280	Missense_Mutation	SNV	T	A	A	GCNT2	c.624T>A	P.F208L
XH_P33	6	40360071	40360071	Missense_Mutation	SNV	C	T	T	LRFN2	c.1981G>A	P.A661T
XH_P33	7	37934169	37934169	Missense_Mutation	SNV	A	C	C	NME8	c.1501A>C	P.T501P
XH_P33	7	39243828	39243828	Splice_Site	SNV	T	C	C	POU6F2	c.191-6T>C	
XH_P33	7	91775459	91775459	Missense_Mutation	SNV	A	C	C	LRRD1	c.2334T>G	P.N778K
XH_P33	8	75233186	75233186	Missense_Mutation	SNV	C	T	T	JPH1	c.337G>A	P.G113R
XH_P33	8	94807654	94807654	Silent	SNV	G	A	A	TMEM67	c.1449G>A	P.L483L
XH_P33	9	104432683	104432683	Missense_Mutation	SNV	A	T	T	GRIN3A	c.2011T>A	P.W671R
XH_P33	9	114454175	114454175	Missense_Mutation	SNV	T	A	A	C9orf84	c.3773A>T	P.K1258M
XH_P34	1	159847257	159847257	Splice_Site	SNV	C	T	T	CFAP45	c.1045-5G>A	
XH_P34	1	222721291	222721291	Missense_Mutation	SNV	C	A	A	HHIPL2	c.96G>T	P.L32F
XH_P34	1	235335950	235335950	Missense_Mutation	SNV	T	A	A	ARID4B	c.3794A>T	P.K1265M
XH_P34	1	236917388	236917388	Splice_Site	SNV	C	T	T	ACTN2	c.1974+7C>T	
XH_P34	1	35365685	35365685	Missense_Mutation	SNV	C	T	T	DLGAP3	c.1297G>A	P.D433N
XH_P34	1	40033476	40033476	Missense_Mutation	SNV	C	T	T	PABPC4	c.919G>A	P.D307N
XH_P34	10	50340346	50340346	Missense_Mutation	SNV	C	T	T	FAM170B	c.164G>A	P.R55Q
XH_P34	10	54053555	54053555	Splice_Site	SNV	T	A	A	PRKG1	c.1918-7T>A	
XH_P34	10	63760086	63760089	Splice_Site	INDEL	TCTT	-	-	ARID5B	3+7_733+10delCTTT	
XH_P34	11	1087943	1087943	Missense_Mutation	SNV	C	T	T	MUC2	c.3418C>T	P.R1140W
XH_P34	11	113650977	113650977	Missense_Mutation	SNV	C	T	T	CLDN25	c.460C>T	P.P154S
XH_P34	11	130784669	130784669	Missense_Mutation	SNV	G	C	C	SNX19	c.1166C>G	P.T389S
XH_P34	11	55432646	55432646	Missense_Mutation	SNV	G	C	C	OR4C6	c.4G>C	P.E2Q
XH_P34	11	61533447	61533447	Missense_Mutation	SNV	C	G	G	MYRF	c.152C>G	P.S51C
XH_P34	11	62520254	62520254	Missense_Mutation	SNV	C	A	A	ZBTB3	c.1033G>T	P.A345S
XH_P34	12	103352426	103352426	Missense_Mutation	SNV	A	G	G	ASCL1	c.404A>G	P.N135S
XH_P34	12	124832428	124832428	Nonsense_Mutation	SNV	G	A	A	NCOR2	c.3985C>T	P.R1329*
XH_P34	12	3649792	3649792	Missense_Mutation	SNV	G	C	C	PRMT8	c.69G>C	P.Q23H
XH_P34	12	45270449	45270449	Silent	SNV	G	A	A	NELL2	c.60C>T	P.S20S
XH_P34	12	54645964	54645964	Missense_Mutation	SNV	A	G	G	CBX5	c.185T>C	P.L62P
XH_P34	12	54645965	54645965	Frame_Shift_Ins	INDEL	-	CTCTGTGTTACTT	CTCTGTGTTACTT	CBX5	c.120-12delTT	
XH_P34	13	20056699	20056699	Splice_Site	INDEL	A	-	-	TPTE2	c.120-12delTT	
XH_P34	14	34263088	34263088	Splice_Site	INDEL	-	T	T	NPAS3	c.1154-7dupT	
XH_P34	14	76123755	76123755	Missense_Mutation	SNV	T	C	C	C14orf1	c.91A>G	P.T31A
XH_P34	16	67861432	67861457	Frame_Shift_Del	INDEL	ACGAGTACT	-	-	TSNAXIP1	AGAAGGACGAG	P.E617fs
XH_P34	17	19454777	19454777	Missense_Mutation	SNV	A	G	G	SLC47A1	c.539A>G	P.L180S
XH_P34	17	4926940	4926940	Missense_Mutation	SNV	C	T	T	KIF1C	c.2806C>T	P.R936C
XH_P34	17	72999582	72999582	Missense_Mutation	SNV	C	G	G	CDR2L	c.811C>G	P.L271V
XH_P34	18	14542693	14542693	Silent	SNV	C	T	T	POTEC	c.453G>A	P.K151K
XH_P34	19	2276136	2276136	Missense_Mutation	SNV	C	T	T	C19orf35	c.965G>A	P.G322E
XH_P34	19	56284099	56284099	Missense_Mutation	SNV	G	A	A	RFPL4AL1	c.418G>A	P.V140I
XH_P34	19	9071439	9071439	Missense_Mutation	SNV	G	A	A	MUC16	c.16007C>T	P.S5336F
XH_P34	2	160741721	160741721	Nonsense_Mutation	SNV	C	A	A	LY75-CD302	c.997G>T	P.E333*
XH_P34	2	186671135	186671135	Missense_Mutation	SNV	C	T	T	FSIP2	c.17102C>T	P.S5701L
XH_P34	2	203075510	203075510	Missense_Mutation	SNV	A	G	G	SUMO1	c.185T>C	P.L62P
XH_P34	22	20097626	20097626	Missense_Mutation	SNV	G	A	A	DGCR8	c.2218G>A	P.V740M
XH_P34	22	25023406	25023406	Missense_Mutation	SNV	G	A	A	GGT1	c.1028G>A	P.R343H
XH_P34	3	126226930	126226930	Silent	SNV	C	T	T	UROC1	c.420G>A	P.L140L
XH_P34	3	134086356	134086362	Frame_Shift_Del	INDEL	CCTTCTC	-	-	AMOTL2	2_1198delGAG	P.E398fs
XH_P34	3	160141374	160141374	Silent	SNV	A	G	G	SMC4	c.2181A>G	P.V727V
XH_P34	3	194118088	194118088	Silent	SNV	G	A	A	GP5	c.924C>T	P.A308A
XH_P34	3	195936387	195936387	Splice_Site	SNV	C	T	T	ZDHC19	c.269-1G>A	
XH_P34	3	49395261	49395261	Nonstop_Mutation	SNV	A	C	C	GPX1	c.313T>G	P.Ter105Ext*?
XH_P34	3	52441257	52441257	Silent	SNV	G	T	T	BAP1	c.513C>A	P.V171V
XH_P34	3	69168484	69168484	Missense_Mutation	SNV	G	T	T	LMOD3	c.1022C>A	P.T341N
XH_P34	4	110772933	110772933	Silent	SNV	T	G	G	LRIT3	c.390T>G	P.L130L
XH_P34	4	141483539	141483539	Splice_Site	SNV	C	T	T	UCP1	c.629-12G>A	
XH_P34	4	77100735	77100735	Nonsense_Mutation	SNV	C	A	A	SCARB2	c.547G>T	P.E183*
XH_P34	5	127685687	127685687	Silent	SNV	G	A	A	FBN2	c.2823C>T	P.C941C
XH_P34	5	128351733	128351733	Silent	SNV	G	A	A	SLC27A6	c.1125G>A	P.G375G
XH_P34	5	76607816	76607816	Splice_Site	SNV	T	C	C	PDE8B	c.340-3T>C	
XH_P34	6	110112635	110112635	Missense_Mutation	SNV	C	T	T	FIG4	c.2237C>T	P.P746L
XH_P34	6	40360377	40360377	Missense_Mutation	SNV	C	T	T	LRFN2	c.1675G>A	P.V559I
XH_P34	7	100349776	100349776	Missense_Mutation	SNV	G	A	A	ZAN	c.2048G>A	P.S683N
XH_P34	7	149519632	149519632	Nonsense_Mutation	SNV	G	A	A	SSPO	c.13122G>A	P.W4374*
XH_P34	7	151074246	151074246	Nonsense_Mutation	SNV	G	T	T	NUB1	c.1855G>T	P.E619*
XH_P34	8	30701243	30701243	Missense_Mutation	SNV	T	C	C	TEX15	c.5291A>G	P.D1764G
XH_P34	9	131370273	131370273	Missense_Mutation	SNV	T	G	G	SPTAN1	c.4289T>G	P.L1430R
XH_P34	9	134103641	134103641	Silent	SNV	C	T	T	NUP214	c.5967C>T	P.A1989A
XH_P34	X	123034518	123034518	Silent	SNV	G	A	A	XIAP	c.1275G>A	P.E425E
XH_P34	X	138856897	138856897	Missense_Mutation	SNV	C	T	T	ATP11C	c.2177G>A	P.R726H
XH_P34	X	2773183	2773183	Silent	SNV	C	T	T	GYG2	c.474C>T	P.H158H
XH_P34	X	47489199	47489199	Silent	SNV	C	T	T	CFP	c.45G>A	P.P15P
XH_P34	X	74280168	74280168	Splice_Site	SNV	G	T	T	ABCB7	c.1936-3C>A	
XH_P35	1	1670472	1670472	Missense_Mutation	SNP	G	A	G	SLC35E2	c.C347T	p.T116M
XH_P35	1	6188946	6188946	Missense_Mutation	SNP	C	T	C	CHD5	c.G3571A	p.D191N
XH_P35	1	10364110	10364110	Missense_Mutation	SNP	G	A	G	KIF1B	c.G2867A	p.R956Q
XH_P35	1	11199403	11199403	Silent	SNP	C	A	C	MTOR	c.G5088T	p.V1696V
XH_P35	1	17550872	17550872	Silent	SNP	T	G	T	PADI1	c.T357G	p.L119L
XH_P35	1	27105745	27105745	Nonsense_Mutation	SNP	G	T	G	ARID1A	c.G5356T	p.E1786X
XH_P35	1	36025984	36025984	Missense_Mutation	SNP	G	A	G	NCN	c.G181A	p.D61N
XH_P35	1	38305824	38305824	Missense_Mutation	SNP	G	A	G	MTF1	c.C415T	p.R139W
XH_P35	1	40214638	40214638	Missense_Mutation	SNP	G	A	G	PPIE	c.G572A	p.R191H
XH_P35	1	46184960	46184960	Nonsense_Mutation	INS	-	TATTTTAAATTT	-	IPP	AAATGAAATTTdelinsTYYVSTKMKIKNTX	
XH_P35	1	46463416	46463416	Missense_Mutation	SNP	C	T	C	MAST2	c.C130T	p.P44S
XH_P35	1	62910675	62910675	Frame_Shift_Ins	INS	-	TTTACTTCTCT	-	USP1	insATTTTCTACT	p.T275fs
XH_P35	1	100614640	100614640	Silent	SNP	G	A	G	LRRC39	c.C966T	p.N322N

XH_P35	1	109849583	109849583	Missense_Mutation	SNP	C	T	C	MYBPHL	c.G31A	p.A11T
XH_P35	1	110581915	110581915	Frame_Shift_Ins	INS	-	T	-	STRIP1	c.163dupT	p.L54fs
XH_P35	1	117617495	117617495	Missense_Mutation	SNP	C	T	C	TTF2	c.C289T	p.P97S
XH_P35	1	120436630	120436630	Missense_Mutation	SNP	C	T	C	ADAM30	c.G2330A	p.S777N
XH_P35	1	120436632	120436632	Nonsense_Mutation	INS	-	AACCAGCTAA	-	ADAM30	2328insTTAGC776	5777delinsDX
XH_P35	1	120466386	120466386	Missense_Mutation	SNP	C	T	C	NOTCH2	c.G4733A	p.R1578H
XH_P35	1	151204824	151204824	Missense_Mutation	SNP	C	T	C	PIP5K1A	c.C433T	p.R145W
XH_P35	1	152759927	152759950	In_Frame_Del	DEL	CTCCAGCTCT	-	GCTCCAGCTCTG	LCE1E	c.152_175del	p.S1_59del
XH_P35	1	153333264	153333264	Missense_Mutation	SNP	G	A	G	S100A9	c.G295A	p.E99K
XH_P35	1	155011989	155011989	Missense_Mutation	SNP	T	A	T	DCST1	c.T298A	p.L100M
XH_P35	1	156894457	156894457	Silent	SNP	T	A	T	LRRC71	c.T462A	p.I154I
XH_P35	1	160340780	160340780	Missense_Mutation	SNP	C	T	C	NHLH1	c.C259T	p.R87C
XH_P35	1	160811186	160811186	Missense_Mutation	SNP	C	T	C	CD244	c.G484A	p.D162N
XH_P35	1	201181672	201181672	Missense_Mutation	SNP	C	T	C	IGFN1	c.C7651T	p.R2551W
XH_P35	1	201185848	201185848	Missense_Mutation	SNP	C	A	C	IGFN1	c.C9562A	p.L3188M
XH_P35	1	204379981	204379981	Missense_Mutation	SNP	G	A	G	PPP1R15B	c.C559T	p.P187S
XH_P35	1	210010427	210010427	Silent	SNP	C	T	C	DIEXF	c.C933T	p.C311C
XH_P35	1	220191803	220191803	Silent	SNP	C	T	C	EPRS	c.G1482A	p.A494A
XH_P35	1	236306134	236306134	Missense_Mutation	SNP	G	A	G	GPR137B	c.G212A	p.R71H
XH_P35	1	248685312	248685312	Missense_Mutation	SNP	G	A	G	OR2G6	c.G365A	p.R122H
XH_P35	1	248801977	248801977	Missense_Mutation	SNP	A	T	A	OR2T35	c.T583A	p.Y195N
XH_P35	2	17876434	17876434	Missense_Mutation	SNP	C	T	C	SMC6	c.G2663A	p.R888Q
XH_P35	2	17902510	17902510	Missense_Mutation	SNP	G	A	G	SMC6	c.C745T	p.R249C
XH_P35	2	37267597	37267597	Missense_Mutation	SNP	A	G	A	HEATR5B	c.T2921C	p.V974A
XH_P35	2	37267599	37267599	Nonsense_Mutation	SNP	A	C	A	HEATR5B	c.T2919G	p.Y973X
XH_P35	2	54176302	54176302	Missense_Mutation	SNP	G	A	G	PSME4	c.C361T	p.R121C
XH_P35	2	68415816	68415816	Missense_Mutation	SNP	G	A	G	PPP3R1	c.C50T	p.A17V
XH_P35	2	73675421	73675421	Missense_Mutation	SNP	G	T	G	ALMS1	c.G1764T	p.L588F
XH_P35	2	88879049	88879049	Missense_Mutation	SNP	G	A	G	EIF2AK3	c.C1420T	p.R474C
XH_P35	2	97818241	97818241	Missense_Mutation	SNP	T	G	T	ANKRD36	c.T1163G	p.V388G
XH_P35	2	100022844	100022844	Missense_Mutation	SNP	G	A	G	REV1	c.C2554T	p.R852C
XH_P35	2	110849289	110849289	Missense_Mutation	SNP	A	G	A	MALL	c.T164C	p.L55P
XH_P35	2	114713283	114713283	Silent	SNP	G	A	G	ACTR3	c.G1008A	p.T336T
XH_P35	2	133075118	133075118	Missense_Mutation	SNP	G	T	G	ZNF806	c.G579T	p.E193D
XH_P35	2	133075120	133075120	Missense_Mutation	SNP	C	T	C	ZNF806	c.C581T	p.S194F
XH_P35	2	160709792	160709792	Nonsense_Mutation	SNP	C	T	C	LY75	c.G2735A	p.W912X
XH_P35	2	179447755	179447755	Silent	SNP	G	A	G	TTN	c.C38580T	p.S12860S
XH_P35	2	190428890	190428890	Missense_Mutation	SNP	A	C	A	SLC40A1	c.T822G	p.H274Q
XH_P35	2	202207098	202207098	Silent	SNP	C	T	C	ALS2CR12	c.G519A	p.K173K
XH_P35	2	209113113	209113113	Missense_Mutation	SNP	G	C	G	IDH1	c.C394G	p.R132G
XH_P35	2	217498317	217498317	Frame_Shift_Ins	INS	-	GC	-	IGFBP2	c.71_72insGC	p.L24fs
XH_P35	2	217498318	217498318	Frame_Shift_Ins	INS	-	TGCTGCTGCTG	-	IGFBP2	CTCTTGCTGCTG	p.L24fs
XH_P35	2	232262967	232262967	Silent	SNP	G	A	G	B3GN17	c.G537A	p.T179T
XH_P35	2	242009366	242009366	Silent	SNP	C	T	C	SNED1	c.C3339T	p.A1113A
XH_P35	2	242757562	242757562	Missense_Mutation	SNP	G	A	G	NEU4	c.G682A	p.V228M
XH_P35	3	30686325	30686325	Missense_Mutation	SNP	T	C	T	TGFBR2	c.T181C	p.C61R
XH_P35	3	36756856	36756856	Missense_Mutation	SNP	C	T	C	DCLK3	c.G1910A	p.R637Q
XH_P35	3	39453515	39453515	Silent	SNP	A	G	A	RPSA	c.A771G	p.A257V
XH_P35	3	42906774	42906774	Silent	SNP	C	T	C	ACKR2	c.C780T	p.F260F
XH_P35	3	50683187	50683187	Missense_Mutation	SNP	G	T	G	MAPKAPK3	c.G675T	p.M225I
XH_P35	3	52550245	52550245	Missense_Mutation	SNP	T	C	T	STAB1	c.T4135C	p.C1379R
XH_P35	3	69244235	69244235	Missense_Mutation	SNP	G	C	G	FRMD4B	c.C1426G	p.Q476E
XH_P35	3	108776269	108776269	Missense_Mutation	SNP	C	T	C	MORC1	c.G1096A	p.A366T
XH_P35	3	121351315	121351315	In_Frame_Ins	INS	-	GGCTCAGGCTCA	-	HCL51	993insTGAGGCT	P331delinsPEPEP
XH_P35	3	129251554	129251554	Missense_Mutation	SNP	C	T	C	RHO	c.C875T	p.A292V
XH_P35	3	137880741	137880743	In_Frame_Del	DEL	TCG	-	TCG	DBR1	c.1623_1625del	p.541_542del
XH_P35	3	178936083	178936083	Missense_Mutation	SNP	A	T	A	PIK3CA	c.A1625T	p.E542V
XH_P35	3	179046111	179046111	Silent	SNP	G	A	G	ZNF639	c.G30A	p.R10R
XH_P35	3	195507173	195507173	In_Frame_Ins	INS	-	AAGAGAGGTGG	-	MUC4	AGGTCACGCCAC	DTSSVSTGHATSLPVTDTSSVSTGHATP
XH_P35	4	2176479	2176479	Splice_Site	SNP	C	T	C	POLN	-	-
XH_P35	4	9784705	9784705	Missense_Mutation	SNP	A	C	A	DRD5	c.A1052C	p.N351T
XH_P35	4	15689835	15689835	Missense_Mutation	SNP	A	C	A	FAM200B	c.A1235C	p.K412T
XH_P35	4	36317975	36317975	Missense_Mutation	SNP	C	T	C	DTHD1	c.C1337T	p.P446L
XH_P35	4	40434705	40434725	In_Frame_Del	DEL	GCGGCGGCT	-	TGCGGCGGCTG	RBM47	c.1278_1298del	p.426_433del
XH_P35	4	41748011	41748028	In_Frame_Del	DEL	CCGCGCTG	-	GCCGCGGCTGCC	PHOX2B	c.741_758del	p.247_253del
XH_P35	4	56225642	56225642	Silent	SNP	G	A	G	SRD5A3	c.G351A	p.A117A
XH_P35	4	79308695	79308695	Missense_Mutation	SNP	C	T	C	FRAS1	c.C3815T	p.P1272L
XH_P35	4	88359522	88359522	Silent	SNP	G	A	G	NUDT9	c.G441A	p.P147P
XH_P35	4	89950618	89950618	Silent	SNP	C	T	C	FAM13A	c.G210A	p.T70T
XH_P35	4	106196618	106196618	Frame_Shift_Ins	INS	-	TACAGATCCATC	-	TET2	TACCTATACAGA	p.P1651fs
XH_P35	4	166946559	166946559	Frame_Shift_Ins	INS	-	CTACAAGAATC	-	TL11	insAACTCTACA	p.R377fs
XH_P35	5	7866894	7866894	Missense_Mutation	SNP	C	T	C	FASTKD3	c.G1303A	p.V435M
XH_P35	5	32712262	32712262	Missense_Mutation	SNP	A	T	A	NPR3	c.A380T	p.K127M
XH_P35	5	65105431	65105431	Silent	SNP	C	T	C	NLN	c.C1617T	p.V539V
XH_P35	5	76734154	76734154	Silent	SNP	G	A	G	WDR41	c.C915T	p.Y305Y
XH_P35	5	90124829	90124829	Nonsense_Mutation	INS	-	TATCTGTAGATA	-	ADGRV1	TATATTCTATCT	N5479delinsNYYYX
XH_P35	5	122161755	122161755	Missense_Mutation	SNP	A	G	A	SNX2	c.A872G	p.D291G
XH_P35	5	140346712	140346712	Silent	SNP	T	C	T	PCDHAC2	c.T361C	p.L121L
XH_P35	5	149588999	149588999	Missense_Mutation	SNP	G	A	G	SLC6A7	c.G1732A	p.D578N
XH_P35	5	178045557	178045557	Silent	SNP	C	T	C	CLK4	c.G384A	p.S128S
XH_P35	6	7602864	7602864	Nonsense_Mutation	SNP	C	T	C	SNRNP48	c.C604T	p.R202X
XH_P35	6	25495416	25495416	Missense_Mutation	SNP	G	A	G	CARMIL1	c.G1298A	p.G433D
XH_P35	6	40999846	40999846	Missense_Mutation	SNP	T	A	T	UNC5CL	c.A980T	p.Q327L
XH_P35	6	49412434	49412434	Missense_Mutation	SNP	G	A	G	MUT	c.C1594T	p.R532C
XH_P35	6	52850316	52850316	Nonsense_Mutation	SNP	G	A	G	GSTA4	c.C205T	p.R69X
XH_P35	6	63995494	63995494	Frame_Shift_Ins	INS	-	A	-	LGSN	c.327dupT	p.Q110fs
XH_P35	6	74124361	74124361	Missense_Mutation	SNP	G	A	G	DDX43	c.G1697A	p.R566Q
XH_P35	6	90578368	90578368	Nonsense_Mutation	INS	-	AATTATCTTCATC	-	CASP8AP2	CTTCAATTATCT	VCVCHLCLFFITFIYLYHPTSQVVFH5X
XH_P35	6	121768925	121768925	Frame_Shift_Del	DEL	C	-	C	GJA1	c.932delC	p.A311fs
XH_P35	6	135264980	135264980	Missense_Mutation	SNP	G	A	G	ALDH8A1	c.C263T	p.A88V
XH_P35	6	165703524	165703524	Nonsense_Mutation	SNP	G	A	G	C6orf118	c.C1153T	p.R385X
XH_P35	7	14017062	14017062	Frame_Shift_Ins	INS	-	AAGATGATTGTA	-	ETV1	5insAATCAATC	p.Q35fs
XH_P35	7	38304989	38304989	Missense_Mutation	SNP	C	T	C	TARP	c.G106A	p.G36R
XH_P35	7	55496101	55496101	Missense_Mutation	SNP	G	A	G	LANCL2	c.G1219A	p.G407R
XH_P35	7	86813934	86813934	Missense_Mutation	SNP	A	C	A	DMTF1	c.A778C	p.I260L
XH_P35	7	92732231	92732231	Missense_Mutation	SNP	T	A	T	SMAD9	c.A3180T	p.L1060N
XH_P35	7	93065455	93065455	Missense_Mutation	SNP	C	T	C	CALCR	c.G958A	p.V320I
XH_P35	7	103030944	103030944	Missense_Mutation	SNP	A	G	A	SLC26A5	c.T1243C	p.C415R

XH_P35	7	104752364	104752364	Silent	SNP	C	T	C	KMT2E	c.C4161T	p.S1387S	
XH_P35	7	104809669	104809669	Silent	SNP	C	T	C	SRPK2	c.G240A	p.R80R	
XH_P35	7	121653375	121653380	In_Frame_Del	DEL	GTGATGA	-	GTGATGA	PTPRZ1	c.4275_4280del	p.1425_1427del	
XH_P35	7	151164222	151164222	Missense_Mutation	SNP	A	C	A	RHEB	c.T538G	p.S180A	
XH_P35	8	3076776	3076776	Splice_Site	DEL	C	-	C	CSMD1	-	-	
XH_P35	8	27516792	27516792	Missense_Mutation	SNP	A	T	A	SCARA3	c.A1105T	p.N369Y	
XH_P35	8	30643779	30643779	Frame_Shift_Del	DEL	G	-	G	PPP2CB	c.902delC	p.T301fs	
XH_P35	8	69129947	69129947	Silent	SNP	G	A	G	PREX2	c.G4701A	p.R1567R	
XH_P35	8	74464496	74464496	Silent	SNP	G	C	G	STAU2	c.C765G	p.R255R	
XH_P35	8	94747621	94747621	Missense_Mutation	SNP	C	T	C	RBM12B	c.G1018A	p.A340T	
XH_P35	8	103573011	103573037	In_Frame_Del	DEL	TGCAGCCCC	-	CTGCAGCCCCC	ODF1	c.652_678del	p.218_226del	
XH_P35	8	110257638	110257638	Missense_Mutation	SNP	G	A	G	NUDCD1	c.C1285T	p.R429C	
XH_P35	8	124714887	124714887	Missense_Mutation	SNP	C	T	C	ANXA13	c.G181A	p.G61S	
XH_P35	8	142160950	142160950	Silent	SNP	G	A	G	DENND3	c.G513A	p.S171S	
XH_P35	8	144681585	144681585	Silent	SNP	C	T	C	TIGD5	c.C1512T	p.A504A	
XH_P35	8	145948513	145948513	Missense_Mutation	SNP	C	T	C	ZNFX2	c.G532A	p.E178K	
XH_P35	9	14823321	14823321	Missense_Mutation	SNP	G	A	G	FREM1	c.C2174T	p.A725V	
XH_P35	9	26920224	26920224	Splice_Site	SNP	C	T	C	PLAA	-	-	
XH_P35	9	69421983	69421983	Missense_Mutation	SNP	G	C	G	ANKRD20A4	c.G1447C	p.V483L	
XH_P35	9	84199393	84199393	Nonsense_Mutation	SNP	C	T	C	TLF1	c.G2205A	p.W735X	
XH_P35	9	107593319	107593319	Silent	SNP	G	A	G	ABCA1	c.C1779T	p.F593F	
XH_P35	9	120474711	120474711	Missense_Mutation	SNP	G	T	G	TLR4	c.G305T	p.S102I	
XH_P35	9	125486479	125486479	Missense_Mutation	SNP	G	A	G	OR1L4	c.G211A	p.D71N	
XH_P35	9	140120136	140120136	Silent	SNP	C	T	C	CYSRT1	c.C183T	p.H61H	
XH_P35	10	13178833	13178833	Silent	SNP	G	A	G	OPTN	c.G1701A	p.T567T	
XH_P35	10	13213025	13213025	Silent	SNP	C	T	C	MCM10	c.C111T	p.G37G	
XH_P35	10	14976739	14976739	Missense_Mutation	SNP	G	A	G	DCLRE1C	c.C155T	p.T52M	
XH_P35	10	63851876	63851876	Missense_Mutation	SNP	C	T	C	ARID5B	c.C1925T	p.T642M	
XH_P35	10	71129079	71129079	Silent	SNP	C	T	C	HK1	c.C582T	p.V194V	
XH_P35	10	73553306	73553306	Silent	SNP	A	G	A	CDH23	c.A6621G	p.L2207L	
XH_P35	10	75397633	75397633	Missense_Mutation	SNP	G	A	G	MYO21	c.C121T	p.P41S	
XH_P35	10	78647070	78647070	Nonsense_Mutation	INS	-	TTTACACATATT	-	KCNMA1	ATGCAAAATATG14	E1115delins	CKYVX
XH_P35	10	88485912	88485912	Missense_Mutation	SNP	G	A	G	LDB3	c.G1667A	p.S556N	
XH_P35	10	90768673	90768673	Missense_Mutation	SNP	G	A	G	FAS	c.G362A	p.R121Q	
XH_P35	10	105218254	105218254	Silent	SNP	C	T	C	CALHM1	c.G255A	p.P85P	
XH_P35	10	105971864	105971864	Silent	SNP	G	A	G	CFAP43	c.C636T	p.V212V	
XH_P35	10	120488899	120488899	Frame_Shift_Ins	INS	-	CTTGTTAATTG	-	CACUL1	ATAATCAAAATT	p.K169fs	
XH_P35	10	124159904	124159904	Missense_Mutation	SNP	G	A	G	PLEKHA1	c.G244A	p.V82I	
XH_P35	11	320606	320606	Missense_Mutation	SNP	G	T	G	IFITM3	c.C208A	p.P70T	
XH_P35	11	320649	320649	Silent	SNP	G	A	G	IFITM3	c.C165T	p.P55P	
XH_P35	11	824776	824776	Missense_Mutation	SNP	C	T	C	PNPLA2	c.C1429T	p.P477S	
XH_P35	11	1009180	1009180	Missense_Mutation	SNP	C	G	C	AP2A	c.C2504G	p.S835C	
XH_P35	11	1016649	1016649	Missense_Mutation	SNP	G	A	G	MUC6	c.C6152T	p.T2015I	
XH_P35	11	1268481	1268481	Silent	SNP	G	A	G	MUC5B	c.G10371A	p.R3457R	
XH_P35	11	6587042	6587042	In_Frame_Ins	INS	-	GCTCTTCTT	-	DNHD1	4_10875insGCT	E3625delins	ELFL
XH_P35	11	6587044	6587044	Missense_Mutation	SNP	A	A	A	DNHD1	c.A10876G	p.R3626G	
XH_P35	11	10794111	10794111	Missense_Mutation	SNP	G	A	G	CTR9	c.G2417A	p.R806Q	
XH_P35	11	33370147	33370147	Missense_Mutation	SNP	G	A	G	HIPK3	c.G2386A	p.E796K	
XH_P35	11	59982088	59982088	Splice_Site	INS	-	TGATTAATCCTT	-	MS4A4E	-	-	
XH_P35	11	62558120	62558120	Missense_Mutation	SNP	G	A	G	TMEM223	c.C584T	p.T195I	
XH_P35	11	62644260	62644260	Silent	SNP	A	G	A	SLC3A2	c.A210G	p.E70E	
XH_P35	11	63964966	63964966	Silent	SNP	G	A	G	STIP1	c.G942A	p.A314A	
XH_P35	11	66235641	66235641	Silent	SNP	C	T	C	PELI3	c.C42T	p.T14T	
XH_P35	11	66294233	66294233	Missense_Mutation	SNP	C	T	C	BBS1	c.C1294T	p.R432W	
XH_P35	11	66807407	66807407	Silent	SNP	G	A	G	SYT12	c.G9A	p.R3R	
XH_P35	11	69462910	69462910	Silent	SNP	G	A	G	CCND1	c.G723A	p.P241P	
XH_P35	11	102398377	102398377	Missense_Mutation	SNP	G	A	G	MMP7	c.C362T	p.P121L	
XH_P35	11	118827703	118827703	Missense_Mutation	SNP	C	T	C	UPK2	c.C187T	p.R63V	
XH_P35	12	266790	266790	Silent	SNP	C	T	C	IQSEC3	c.C1464T	p.T488T	
XH_P35	12	8374812	8374812	Missense_Mutation	SNP	G	A	G	FAM90A1	c.C1001T	p.P334L	
XH_P35	12	20852524	20852524	Missense_Mutation	SNP	C	T	C	SLCO1C1	c.C14T	p.S5F	
XH_P35	12	40808847	40808847	Splice_Site	SNP	G	A	G	MUC19	-	-	
XH_P35	12	50036051	50036051	Missense_Mutation	SNP	C	T	C	PRPF40B	c.C1813T	p.R605W	
XH_P35	12	54645964	54645964	Missense_Mutation	SNP	A	G	A	CBX5	c.T185C	p.L62P	
XH_P35	12	54645965	54645965	Frame_Shift_Ins	INS	-	CTCTTGTTACTT	-	CBX5	CAGAAAGTAAC	p.L62fs	
XH_P35	12	76424934	76424934	Frame_Shift_Del	DEL	C	-	C	PHLDA1	c.588delG	p.Q196fs	
XH_P35	12	76424936	76424940	Frame_Shift_Del	DEL	GTGTC	-	GTGTC	PHLDA1	c.582_586del	p.Q194fs	
XH_P35	12	77244716	77244716	Nonsense_Mutation	INS	-	CAAATGATT	-	ZDHHC17	1851insCAA	b.Y617delins	YKX
XH_P35	12	77244718	77244718	Nonsense_Mutation	INS	-	ATACATGAATT	-	ZDHHC17	1853insATACA	b.1817delins	NTX
XH_P35	12	99117495	99117495	Missense_Mutation	SNP	C	A	C	APAF1	c.C3121A	p.H1041N	
XH_P35	12	132474616	132474616	Silent	SNP	G	A	G	EP400	c.G2517A	p.R839R	
XH_P35	13	33110750	33110750	Missense_Mutation	SNP	C	G	C	N4BP2L2	c.G415C	p.G139R	
XH_P35	13	39448643	39448643	Missense_Mutation	SNP	G	A	G	FREM2	c.G8201A	p.R2734H	
XH_P35	13	58208588	58208588	Missense_Mutation	SNP	T	G	T	PCDH17	c.T1908G	p.F636L	
XH_P35	13	113201936	113201936	Missense_Mutation	SNP	T	C	T	TUBGCP3	c.A1136G	p.Q379R	
XH_P35	14	19553724	19553724	Missense_Mutation	SNP	G	C	G	POTEG	c.C308C	p.C103S	
XH_P35	14	20019912	20019912	Silent	SNP	G	A	G	POTEM	c.C309T	p.C103C	
XH_P35	14	20019913	20019913	Missense_Mutation	SNP	C	G	C	POTEM	c.G308C	p.C103S	
XH_P35	14	23612372	23612372	Missense_Mutation	SNP	T	G	T	SLC7A8	c.A235C	p.T79P	
XH_P35	14	24774897	24774897	Missense_Mutation	SNP	C	T	C	CIDEB	c.G602A	p.R201H	
XH_P35	14	65415128	65415128	Missense_Mutation	SNP	C	T	C	RAB15	c.G583A	p.E195K	
XH_P35	14	72818827	72818827	Missense_Mutation	SNP	C	A	C	RG56	c.C4A	p.Q2K	
XH_P35	14	88477678	88477678	Missense_Mutation	SNP	G	A	G	GPR65	c.G487A	p.E163K	
XH_P35	15	28951789	28951789	Missense_Mutation	SNP	C	G	C	GOLGA8M	c.G648C	p.E216D	
XH_P35	15	29346574	29346574	Missense_Mutation	SNP	G	A	G	APBA2	c.G487A	p.G163S	
XH_P35	15	37188865	37188865	Missense_Mutation	SNP	T	A	T	MEIS2	c.A961T	p.I321L	
XH_P35	15	40702993	40702993	Silent	SNP	G	A	G	IVD	c.G372A	p.P124P	
XH_P35	15	58936158	58936158	Missense_Mutation	SNP	G	A	G	ADAM10	c.C755T	p.A252V	
XH_P35	15	59963488	59963488	In_Frame_Ins	INS	-	ATCATGTAGTTT	-	BNIP2	GCAGAAACTA	delinsLV	VAENYMIVFCL
XH_P35	15	64388289	64388289	Frame_Shift_Ins	INS	-	G	-	SNX1	c.78dupG	p.E267S	
XH_P35	15	66786812	66786812	Missense_Mutation	SNP	C	T	C	SNAPC5	c.G169A	p.E57K	
XH_P35	15	70979983	70979983	Silent	SNP	G	A	G	UACA	c.C459T	p.D153D	
XH_P35	15	73615878	73615878	Silent	SNP	C	T	C	HCN4	c.G2556A	p.P852P	
XH_P35	15	75809701	75809701	In_Frame_Ins	INS	-	TTGGGATATAT	-	PTPN9	AAATATATATAT	3delins	KKIYISOALKE
XH_P35	15	101109820	101109820	Missense_Mutation	SNP	C	T	C	LINS1	c.G1897A	p.D633N	
XH_P35	16	396485	396485	Missense_Mutation	SNP	T	A	T	AXIN1	c.A541T	p.M181L	
XH_P35	16	2287505	2287505	Missense_Mutation	SNP	G	C	G	DNASE1L2	c.G446C	p.R149P	
XH_P35	16	12061495	12061495	Frame_Shift_Del	DEL	C	-	C	TNFRSF17	c.346delC	p.P116fs	

XH_P35	16	15045759	15045829	Frame_Shift_Del	DEL	CCACCCTCAG	-	TCCACCCTCAGT	NPIPA1	c.930_1000del	p.E310fs
XH_P35	16	31089768	31089768	Missense_Mutation	SNP	C	T	C	ZNF646	c.C2123T	p.P708L
XH_P35	16	56388958	56388958	Frame_Shift_Ins	INS	-	CATAG	-	GNAO1	D58_1059insCA	p.L355fs
XH_P35	16	57468022	57468022	Missense_Mutation	SNP	G	T	G	CIAPIN1	c.C451A	p.P151T
XH_P35	16	67289072	67289072	Silent	SNP	C	T	C	SLC9A5	c.C336T	p.N112N
XH_P35	16	70154480	70154480	Missense_Mutation	SNP	A	G	A	PDPR	c.A85G	p.T29A
XH_P35	16	70154534	70154534	Missense_Mutation	SNP	A	G	A	PDPR	c.A139G	p.I47V
XH_P35	16	72142809	72142809	Silent	SNP	G	A	G	DHX38	c.G3366A	p.L1122L
XH_P35	16	74919684	74919684	Silent	SNP	G	A	G	WDR59	c.C256T	p.D852D
XH_P35	16	84118718	84118718	Missense_Mutation	SNP	G	A	G	MBTPS1	c.C1156T	p.R386C
XH_P35	16	87637894	87637902	In_Frame_Del	DEL	CTGCTGCTG	-	CTGCTGCTG	JPH3	c.431_439del	p.144_147del
XH_P35	17	7578490	7578490	Missense_Mutation	SNP	A	C	A	TP53	c.T44G	p.V15G
XH_P35	17	29664876	29664876	Nonsense_Mutation	SNP	C	T	C	NF1	c.C6619T	p.Q2207X
XH_P35	17	33481662	33481662	Missense_Mutation	SNP	G	A	G	UNC45B	c.G541A	p.V181I
XH_P35	17	34797610	34797610	Frame_Shift_Ins	INS	-	GGGAATTCATG	-	TBC1D38	CGTGGGCATGG	p.P509fs
XH_P35	17	35734873	35734873	Missense_Mutation	SNP	G	A	G	C17orf78	c.G115A	p.V39M
XH_P35	17	40673079	40673079	Missense_Mutation	SNP	G	A	G	ATP6V0A1	c.G2458A	p.G820S
XH_P35	17	40818192	40818192	Missense_Mutation	SNP	C	T	C	TUBG2	c.C931T	p.R311C
XH_P35	17	41959742	41959742	Silent	SNP	G	A	G	MPP2	c.C558T	p.P186P
XH_P35	17	42476377	42476377	Missense_Mutation	SNP	C	T	C	GPATCH8	c.G2834A	p.R945Q
XH_P35	17	48545887	48545887	Silent	SNP	G	A	G	CHAD	c.C288T	p.R96R
XH_P35	17	55918306	55918306	Missense_Mutation	SNP	C	T	C	MRPS23	c.G401A	p.R134Q
XH_P35	17	62018433	62018433	In_Frame_Ins	INS	-	SATGGCGCAC	-	SCN4A	AGGAGGTGTGG	delinsKHEEVCAIKIQRA
XH_P35	17	62892168	62892168	Missense_Mutation	SNP	T	G	T	LRRC37A3	c.A1208C	p.H403P
XH_P35	17	72999576	72999576	Missense_Mutation	SNP	G	A	G	CDR2L	c.G805A	p.D269N
XH_P35	18	13731869	13731869	Frame_Shift_Ins	INS	-	AACTCTTTTCTC	-	RNMT	54insAAACTCT	p.S118fs
XH_P35	18	13731871	13731871	Missense_Mutation	SNP	A	T	A	RNMT	c.A355T	p.T119S
XH_P35	18	19345793	19345793	Missense_Mutation	SNP	G	A	G	MIB1	c.G290A	p.R97Q
XH_P35	18	77703333	77703333	Silent	SNP	A	G	A	PQLC1	c.T333C	p.P111F
XH_P35	19	746301	746301	Silent	SNP	C	T	C	PALM	c.C519T	p.D173D
XH_P35	19	3204593	3204593	Missense_Mutation	SNP	A	T	A	NCLN	c.A1052T	p.E351V
XH_P35	19	4511622	4511622	Missense_Mutation	SNP	C	T	C	PLIN4	c.G2308A	p.G770S
XH_P35	19	8038746	8038746	Missense_Mutation	SNP	G	A	G	ELAVL1	c.C293T	p.P98L
XH_P35	19	9020005	9020005	Missense_Mutation	SNP	C	T	C	MUC16	c.G37490A	p.R12497K
XH_P35	19	9063095	9063095	Silent	SNP	G	A	G	MUC16	c.C24351T	p.S8117S
XH_P35	19	10503997	10503997	Missense_Mutation	SNP	G	A	G	CDC37	c.C847T	p.R283C
XH_P35	19	19243565	19243565	Splice_Site	SNP	T	A	T	TMEM161A	.	.
XH_P35	19	19391098	19391098	Nonsense_Mutation	SNP	G	A	G	SUGP1	c.C1246T	p.Q416X
XH_P35	19	22155423	22155423	Missense_Mutation	SNP	A	T	A	ZNF208	c.T2413A	p.Y805N
XH_P35	19	22836805	22836805	Missense_Mutation	SNP	G	A	G	ZNF492	c.G118A	p.A40T
XH_P35	19	33140695	33140695	Missense_Mutation	SNP	A	C	A	ANKRD27	c.T106G	p.L36V
XH_P35	19	38573264	38573264	Silent	SNP	C	T	C	SIPA1L3	c.C1059T	p.N353N
XH_P35	19	40368493	40368493	Silent	SNP	A	G	A	FCGBP	c.T12855C	p.S4285S
XH_P35	19	42754692	42754692	Silent	SNP	G	A	G	ERF	c.C48T	p.Y16V
XH_P35	19	49878239	49878239	Missense_Mutation	SNP	G	A	G	DKKL1	c.G590A	p.R197Q
XH_P35	19	49926531	49926536	In_Frame_Del	DEL	CAGCAG	-	CAGCAG	PTH2	c.61_66del	p.21_22del
XH_P35	19	55020285	55020285	Silent	SNP	C	A	C	LAIR2	c.C405A	p.G135G
XH_P35	19	55106288	55106288	Missense_Mutation	SNP	A	C	A	LILRA1	c.A229C	p.I77L
XH_P35	19	57868377	57868377	Silent	SNP	G	A	G	ZNF304	c.G1140A	p.Q380Q
XH_P35	20	16730578	16730578	Missense_Mutation	SNP	G	A	G	OTOR	c.G286A	p.V96I
XH_P35	20	25273118	25273118	Silent	SNP	C	T	C	PYGB	c.C2046T	p.F682F
XH_P35	20	49492613	49492613	Missense_Mutation	SNP	A	G	A	BCAS4	c.A569G	p.Q190R
XH_P35	21	43161669	43161669	Missense_Mutation	SNP	C	A	C	RIPK4	c.G1684T	p.D562Y
XH_P35	21	45795846	45795846	Missense_Mutation	SNP	T	C	T	TRPM2	c.T902C	p.L301P
XH_P35	21	45833958	45833958	Splice_Site	SNP	G	A	G	TRPM2	.	.
XH_P35	22	18655973	18655973	Silent	SNP	C	T	C	USP18	c.C948T	p.S316S
XH_P35	22	18655974	18655974	Frame_Shift_Ins	INS	-	GGACTTTA	-	USP18	9_950insGGAC	p.G317fs
XH_P35	22	26829896	26829896	Silent	SNP	C	T	C	ASPHD2	c.C315T	p.Y105Y
XH_P35	22	32628915	32628915	Missense_Mutation	SNP	G	A	G	SLCSA4	c.C992T	p.P331L
XH_P35	22	39267544	39267544	Missense_Mutation	SNP	C	T	C	CBX6	c.G187A	p.E63K
XH_P35	22	40718888	40718888	Silent	SNP	T	G	T	TNRC6B	c.T4815G	p.A1605A
XH_P35	22	50616069	50616069	Missense_Mutation	SNP	A	C	A	PANX2	c.A928C	p.I310L
XH_P35	X	69828947	69828947	Nonsense_Mutation	INS	-	AAAATGGAAAT	-	TEX11	TATAACTATTTCG5	T626delinsYITISILX
XH_P35	X	129299559	129299559	Silent	SNP	G	A	G	AIFM1	c.C72T	p.C24C
XH_P35	X	153296440	153296440	Missense_Mutation	SNP	G	A	G	MECP2	c.C875T	p.A292V
XH_P35	1	155011989	155011989	Missense_Mutation	SNV	T	A	A	DCST1	c.298T>A	P.L100M
XH_P35	1	156894457	156894457	Silent	SNV	T	A	A	LRRC71	c.462T>A	P.I154I
XH_P35	1	17550872	17550872	Silent	SNV	T	G	G	PADI1	c.357T>G	P.L119L
XH_P35	1	201181672	201181672	Missense_Mutation	SNV	C	T	T	IGFN1	c.7651C>T	P.R2551W
XH_P35	1	201185848	201185848	Missense_Mutation	SNV	C	A	A	IGFN1	c.9562C>A	P.L3188M
XH_P35	1	248801977	248801977	Missense_Mutation	SNV	A	T	T	OR2T35	c.583T>A	P.Y195N
XH_P35	1	27105745	27105745	Nonsense_Mutation	SNV	G	T	T	ARID1A	c.5356G>T	P.E1786*
XH_P35	10	124159904	124159904	Missense_Mutation	SNV	G	A	A	PLEKHA1	c.244G>A	P.V82J
XH_P35	10	63851876	63851876	Missense_Mutation	SNV	C	T	T	ARID5B	c.1925C>T	P.T642M
XH_P35	10	73553306	73553306	Silent	SNV	A	G	G	CDH23	c.6621A>G	P.L2207L
XH_P35	11	1009180	1009180	Missense_Mutation	SNV	C	G	G	AP2A2	c.2504C>G	P.S835C
XH_P35	11	10794111	10794111	Missense_Mutation	SNV	G	A	A	CTR9	c.2489G>A	P.R830Q
XH_P35	11	124792272	124792272	Splice_Site	SNV	A	T	T	HEPACAM	c.948+12T>A	
XH_P35	12	124414204	124414204	Splice_Site	SNV	T	C	C	DNAH10	c.12163-7T>C	
XH_P35	12	40808847	40808847	Splice_Site	SNV	G	A	A	MUC19	c.914-1G>A	
XH_P35	12	50036051	50036051	Missense_Mutation	SNV	C	T	T	PRPF40B	c.1918C>T	P.R640W
XH_P35	12	76424936	76424940	Frame_Shift_Del	INDEL	GTTGC	-	-	PHLDA1	582_586delGCA	P.Q195fs
XH_P35	12	9230290	9230290	Splice_Site	SNV	G	A	A	A2M	c.3276+7C>T	
XH_P35	12	99117495	99117495	Missense_Mutation	SNV	C	A	A	APAF1	c.3121C>A	P.H1041N
XH_P35	13	33110750	33110750	Missense_Mutation	SNV	C	G	G	N4BP2L2	c.415G>C	P.G139R
XH_P35	13	39448643	39448643	Missense_Mutation	SNV	G	A	A	FREM2	c.8201G>A	P.R2734H
XH_P35	13	58208588	58208588	Missense_Mutation	SNV	T	G	G	PCDH17	c.1908T>G	P.F636L
XH_P35	14	23612372	23612372	Missense_Mutation	SNV	T	G	G	SLC7A8	c.235A>C	P.T79P
XH_P35	14	24774897	24774897	Missense_Mutation	SNV	C	T	T	CIDEB	c.602G>A	P.R201H
XH_P35	14	65415128	65415128	Missense_Mutation	SNV	C	T	T	RAB15	c.583G>A	P.E195K
XH_P35	14	72818827	72818827	Missense_Mutation	SNV	C	A	A	RG56	c.109C>A	P.Q37K
XH_P35	14	73822324	73822324	Splice_Site	SNV	C	T	T	NUMB	c.126+10G>A	
XH_P35	14	88477678	88477678	Missense_Mutation	SNV	G	A	A	GPR65	c.487G>A	P.E163K
XH_P35	15	101109820	101109820	Missense_Mutation	SNV	C	T	T	LINS1	c.1897G>A	P.D633N
XH_P35	15	28951789	28951789	Missense_Mutation	SNV	C	G	G	GOLGA8M	c.648G>C	P.E216D
XH_P35	15	37188865	37188865	Missense_Mutation	SNV	T	A	A	MEIS2	c.1000A>T	P.I334L
XH_P35	15	64388289	64388289	Frame_Shift_Ins	INDEL	-	G	G	SNX1	c.82dupG	P.A28fs
XH_P35	16	12061495	12061495	Frame_Shift_Del	INDEL	C	-	-	TNFRSF17	c.347delC	P.P116fs

XH_P35	16	396485	396485	Missense_Mutation	SNV	T	A	A	AXIN1	c.541A>T	P.M181L
XH_P35	16	57468022	57468022	Missense_Mutation	SNV	G	T	T	CIAPIN1	c.451C>A	P.P151T
XH_P35	16	72142809	72142809	Silent	SNV	G	A	A	DXH38	c.3366G>A	P.L1122L
XH_P35	16	84118718	84118718	Missense_Mutation	SNV	G	A	A	MBTPS1	c.1156C>T	P.R386C
XH_P35	17	29664876	29664876	Nonsense_Mutation	SNV	C	T	T	NF1	c.6682C>T	P.Q2228*
XH_P35	17	41959742	41959742	Silent	SNV	G	A	A	MPP2	c.726C>T	P.P242P
XH_P35	17	62892168	62892168	Missense_Mutation	SNV	T	G	G	LRRC37A3	c.1208A>C	P.H403P
XH_P35	17	7578490	7578490	Missense_Mutation	SNV	A	C	C	TP53	c.440T>G	P.V147G
XH_P35	18	77703333	77703333	Silent	SNV	A	G	G	PQLC1	c.333T>C	P.F111F
XH_P35	19	1074092	1074092	Splice_Site	SNV	G	A	A	ARHGAP45	c.839-11G>A	
XH_P35	19	19243565	19243565	Splice_Site	SNV	T	A	A	TMEM161A	c.189-2A>T	
XH_P35	19	19391098	19391098	Nonsense_Mutation	SNV	G	A	A	SUGP1	c.1246C>T	P.Q416*
XH_P35	19	3204593	3204593	Missense_Mutation	SNV	A	T	T	NCLN	c.1052A>T	P.E351V
XH_P35	19	55020285	55020285	Silent	SNV	C	A	A	LAIR2	c.405C>A	P.G135G
XH_P35	2	110849289	110849289	Missense_Mutation	SNV	A	G	G	MALL	c.164T>C	P.L55P
XH_P35	2	114713283	114713283	Splice_Site	SNV	G	A	A	ACTR3	c.1008G>A	P.T336T
XH_P35	2	160709792	160709792	Nonsense_Mutation	SNV	C	T	T	LY75-CD302	c.2735G>A	P.W912*
XH_P35	2	178762781	178762781	Splice_Site	SNV	T	A	A	PDE11A	c.1302+4A>T	
XH_P35	2	190428890	190428890	Missense_Mutation	SNV	A	C	C	SLC40A1	c.822T>G	P.H274Q
XH_P35	2	209113113	209113113	Missense_Mutation	SNV	G	C	C	IDH1	c.394C>G	P.H132G
XH_P35	2	242009366	242009366	Silent	SNV	C	T	T	SNED1	c.3339C>T	P.A1113A
XH_P35	2	55214622	55214622	Splice_Site	SNV	C	A	A	RTN4	c.2603+5G>T	
XH_P35	2	73675421	73675421	Missense_Mutation	SNV	G	T	T	ALMS1	c.1764G>T	P.L588F
XH_P35	2	97818241	97818241	Missense_Mutation	SNV	T	G	G	ANKRD36	c.1163T>G	P.V388G
XH_P35	20	5169706	5169706	Splice_Site	SNV	T	G	G	CD52	c.982-7T>G	
XH_P35	21	43161669	43161669	Missense_Mutation	SNV	C	A	A	RIPK4	c.1684G>T	P.D562Y
XH_P35	21	45795846	45795846	Missense_Mutation	SNV	T	C	C	TRPM2	c.902T>C	P.L301P
XH_P35	21	45833958	45833958	Splice_Site	SNV	G	A	A	TRPM2	c.3146+1G>A	
XH_P35	22	39267544	39267544	Missense_Mutation	SNV	C	T	T	CBX6	c.187G>A	P.E63K
XH_P35	22	40718888	40718888	Silent	SNV	T	G	G	TNRC6B	c.2733T>G	P.A911A
XH_P35	22	50616069	50616069	Missense_Mutation	SNV	A	C	C	PANX2	c.928A>C	P.I310L
XH_P35	3	108776269	108776269	Missense_Mutation	SNV	C	T	T	MORC1	c.1096G>A	P.A366T
XH_P35	3	138189876	138189876	Splice_Site	SNV	T	C	C	ESYT3	c.1740+8T>C	
XH_P35	3	172064234	172064234	Splice_Site	SNV	A	C	C	FNDC3B	c.2364+4A>C	
XH_P35	3	178936083	178936083	Missense_Mutation	SNV	A	T	T	PIK3CA	c.1625A>T	P.E542V
XH_P35	3	179046111	179046111	Silent	SNV	G	A	A	ZNF639	c.30G>A	P.R10R
XH_P35	3	30686325	30686325	Missense_Mutation	SNV	T	C	C	TGFBR2	c.256T>C	P.C86R
XH_P35	3	50683187	50683187	Missense_Mutation	SNV	G	T	T	MAPKAPK3	c.675G>T	P.M225I
XH_P35	3	52325942	52325942	Splice_Site	SNV	T	G	G	GLYCTK	n.801+4T>G	
XH_P35	3	69244235	69244235	Missense_Mutation	SNV	G	C	C	FRMD4B	c.1426C>G	P.Q476E
XH_P35	4	154330177	154330177	Splice_Site	SNV	A	T	T	MND1	c.*27+10A>T	
XH_P35	4	15689835	15689835	Missense_Mutation	SNV	A	C	C	FAM200B	c.1235A>C	P.K412T
XH_P35	4	2176479	2176479	Splice_Site	SNV	C	T	T	POLN	c.1249-1G>A	
XH_P35	4	9784705	9784705	Missense_Mutation	SNV	A	C	C	DRD5	c.1052A>C	P.N351T
XH_P35	5	122161755	122161755	Missense_Mutation	SNV	A	G	G	SNX2	c.872A>G	P.D291G
XH_P35	5	149588999	149588999	Missense_Mutation	SNV	G	A	A	SLC6A7	c.1732G>A	P.D578N
XH_P35	5	32712262	32712262	Missense_Mutation	SNV	A	T	T	NPR3	c.380A>T	P.K127M
XH_P35	5	65105431	65105431	Silent	SNV	C	T	T	NLN	c.1617C>T	P.V539V
XH_P35	5	7866894	7866894	Missense_Mutation	SNV	C	T	T	FASTKD3	c.1303G>A	P.V435M
XH_P35	5	78985887	78985887	Splice_Site	SNV	G	A	A	CMYA5	c.149+8G>A	
XH_P35	6	40999846	40999846	Missense_Mutation	SNV	T	A	A	UNC5CL	c.980A>T	P.Q327L
XH_P35	7	103030944	103030944	Missense_Mutation	SNV	A	G	G	SLC26A5	c.1243T>C	P.C415R
XH_P35	7	104752364	104752364	Silent	SNV	C	T	T	KMT2E	c.4161C>T	P.S1387S
XH_P35	7	151164222	151164222	Missense_Mutation	SNV	A	C	C	RHEB	c.538T>G	P.S180A
XH_P35	7	86813934	86813934	Missense_Mutation	SNV	A	C	C	DMTF1	c.778A>C	P.I260L
XH_P35	7	93065455	93065455	Missense_Mutation	SNV	C	T	T	CALCR	c.1060G>A	P.V354I
XH_P35	8	144681585	144681585	Silent	SNV	C	T	T	TIGD5	c.1512C>T	P.A504A
XH_P35	8	144695915	144695915	Splice_Site	SNV	A	G	G	TSTA3	c.748+6T>C	
XH_P35	8	27516792	27516792	Missense_Mutation	SNV	A	T	T	SCARA3	c.1105A>T	P.N369Y
XH_P35	8	3076776	3076776	Splice_Site	INDEL	C	-	-	CSMD1	c.4672+1delG	
XH_P35	8	74464496	74464496	Silent	SNV	G	C	C	STAU2	c.1281C>G	P.R427R
XH_P35	9	120474711	120474711	Missense_Mutation	SNV	G	T	T	TLR4	c.185G>T	P.S62I
XH_P35	9	125486479	125486479	Missense_Mutation	SNV	G	A	A	OR1L4	c.211G>A	P.D71N
XH_P35	9	131767814	131767814	Splice_Site	SNV	T	G	G	NUP188	c.4737+5T>G	
XH_P35	9	140120136	140120136	Silent	SNV	C	T	T	CYSRT1	c.183C>T	P.H61H
XH_P35	9	79234308	79234308	Splice_Site	SNV	G	C	C	PRUNE2	c.936-5C>G	
XH_P35	9	84199393	84199393	Nonsense_Mutation	SNV	C	T	T	TL1	c.2205G>A	P.W735*
XH_P36	1	874456	874456	Missense_Mutation	SNP	G	A	G	SAMD11	c.G467A	p.R156H
XH_P36	1	900461	900461	Missense_Mutation	SNP	G	A	A	KLHL17	c.G1819A	p.A607T
XH_P36	1	1168240	1168240	Frame_Shift_Del	DEL	G	-	G	B3GALT6	c.582delG	p.P194fs
XH_P36	1	1268888	1268888	Missense_Mutation	SNP	G	A	G	TAS1R3	c.G1603A	p.D535N
XH_P36	1	1534720	1534720	Missense_Mutation	SNP	G	A	G	FNDC10	c.C676T	p.P226S
XH_P36	1	1684346	1684346	In_Frame_Ins	INS	-	CCC	-	NADK	1241_1242insGG	p.G414delinsGG
XH_P36	1	2238077	2238077	Missense_Mutation	SNP	A	G	A	SKI	c.A2060G	p.D687G
XH_P36	1	2290124	2290124	Missense_Mutation	SNP	G	A	G	MORN1	c.C776T	p.A259V
XH_P36	1	2572878	2572878	Missense_Mutation	SNP	C	T	C	TTTC34	c.G1630A	p.D544N
XH_P36	1	3541774	3541774	Silent	SNP	C	T	C	TPRG1L	c.C138T	p.L46L
XH_P36	1	3742991	3742991	Nonsense_Mutation	INS	-	TAACCTAAAATA	-	CEP104	AAAGGATATTTT	p.G733delinsAERIFX
XH_P36	1	5937158	5937158	Missense_Mutation	SNP	C	T	C	NPHP4	c.G1276A	p.V426M
XH_P36	1	11082583	11082583	Frame_Shift_Ins	INS	-	CTATTGCTATTG	-	TARDBP	18insGTCTATTG	p.S373fs
XH_P36	1	12919891	12919891	Missense_Mutation	SNP	G	C	G	PRAMEF2	c.G631C	p.E211Q
XH_P36	1	17085996	17085996	Frame_Shift_Del	DEL	C	-	C	MST1L	c.901delG	p.A301fs
XH_P36	1	19180874	19180874	Missense_Mutation	SNP	C	T	C	TAS1R2	c.G1090A	p.D364N
XH_P36	1	19183876	19183876	Silent	SNP	G	T	G	TAS1R2	c.C432A	p.S144S
XH_P36	1	19566360	19566360	Silent	SNP	C	T	C	EMC1	c.G840A	p.L280L
XH_P36	1	20233009	20233009	Frame_Shift_Ins	INS	-	TACCTGGGTCC	-	OTUD3	921insTACCTG	p.I307fs
XH_P36	1	21267982	21267982	Splice_Site	SNP	A	G	A	EIF4G3	.	.
XH_P36	1	21806606	21806606	Missense_Mutation	SNP	T	G	T	NBPF3	c.T1061G	p.F354C
XH_P36	1	22923907	22923907	Missense_Mutation	SNP	G	A	G	EPHA8	c.G1868A	p.G623D
XH_P36	1	23240246	23240246	Frame_Shift_Del	DEL	A	-	A	EPHB2	c.3051delA	p.G1017fs
XH_P36	1	25889626	25889626	Frame_Shift_Ins	INS	-	C	-	LDLRAP1	c.599dupC	p.T200fs
XH_P36	1	27105931	27105931	Frame_Shift_Del	DEL	G	-	G	ARID1A	c.5542delG	p.G1848fs
XH_P36	1	27878528	27878528	Frame_Shift_Del	DEL	G	-	G	AHDC1	c.99delC	p.P33fs
XH_P36	1	28785730	28785730	Frame_Shift_Del	DEL	A	-	A	PHACTR4	c.181delA	p.K61fs
XH_P36	1	32208473	32208473	Silent	SNP	C	T	C	ADGRB2	c.G1218A	p.L406L
XH_P36	1	32800540	32800540	Frame_Shift_Del	DEL	G	-	G	MARCKSL1	c.246delC	p.R82fs
XH_P36	1	33059325	33059325	Frame_Shift_Ins	INS	-	GGTTGTGT	-	ZBTB8A	93_794insGGTT	p.G265fs
XH_P36	1	33059327	33059327	Frame_Shift_Ins	INS	-	GTATTCT	-	ZBTB8A	95_796insGTAT	p.G265fs

XH_P36	1	33060810	33060810	Nonsense_Mutation	INS	-	AATTTTATTAAG	-	ZBTB8A	AAGAAATTTTA	H328delinsRRKKFYX
XH_P36	1	33354802	33354802	Frame_Shift_Ins	INS	-	TG	-	HPCA	c.303_304insTG	p.L101fs
XH_P36	1	33354803	33354803	In_Frame_Ins	INS	-	GAACTC	-	HPCA	04_305insGAA	M102delinsRTL
XH_P36	1	34666397	34666397	Frame_Shift_Ins	INS	-	A	-	C1orf94	c.1035dupA	p.P345fs
XH_P36	1	35226919	35226919	Missense_Mutation	SNP	C	T	C	GJB4	c.C64T	p.R22C
XH_P36	1	35334661	35334661	Missense_Mutation	SNP	A	G	A	DLGAP3	c.T2030C	p.V677A
XH_P36	1	353370730	353370730	Frame_Shift_Ins	INS	-	C	-	DLGAP3	c.254dupG	p.G85fs
XH_P36	1	36030900	36030900	Missense_Mutation	SNP	C	T	C	NCN	c.C1775T	p.A592V
XH_P36	1	36367904	36367904	Missense_Mutation	SNP	G	A	G	AGO1	c.G1138A	p.A380T
XH_P36	1	36380979	36380979	Nonsense_Mutation	SNP	C	T	C	AGO1	c.C1639T	p.R547X
XH_P36	1	36769566	36769566	In_Frame_Ins	INS	-	TTCACTCTGGCA	-	THRAP3	ATCTTGTTCACTG	delinsSSGHILFTLMAIFF
XH_P36	1	38265467	38265467	Missense_Mutation	SNP	G	A	G	MANEAL	c.G300A	p.M100I
XH_P36	1	39893937	39893937	Nonsense_Mutation	INS	-	TGAGTCTATCTT	-	MACF1	0596insATGAGT	H3532delinsQX
XH_P36	1	40775989	40775989	In_Frame_Ins	INS	-	TGGATT	-	COL9A2	84_685insAATC	G229delinsNPG
XH_P36	1	42047087	42047087	Missense_Mutation	SNP	C	T	C	HIVEP3	c.G3382A	p.V1128I
XH_P36	1	43895417	43895417	Missense_Mutation	SNP	C	T	C	SZT2	c.C4039T	p.R1347C
XH_P36	1	44466534	44466534	Missense_Mutation	SNP	G	A	G	SLC6A9	c.C1246T	p.R416W
XH_P36	1	45267397	45267397	Missense_Mutation	SNP	G	A	G	PLK3	c.G539A	p.G180D
XH_P36	1	45407182	45407182	Frame_Shift_Del	DEL	T	-	T	EIF2B3	c.450delA	p.K150fs
XH_P36	1	46812736	46812736	In_Frame_Ins	INS	-	TTATTCACTTAT	-	NSUN4	CTTACTTATTCA	5delinsTHTYLFTYSFYI
XH_P36	1	47748086	47748086	Silent	SNP	G	A	G	STIL	c.C1179T	p.H393H
XH_P36	1	48917261	48917261	Silent	SNP	G	A	G	SPATA6	c.C201T	p.D67D
XH_P36	1	50666631	50666631	Silent	SNP	C	T	C	ELAVL4	c.C858T	p.S286S
XH_P36	1	50941243	50941243	Missense_Mutation	SNP	G	A	G	FAF1	c.C1762T	p.R588W
XH_P36	1	52825774	52825774	Missense_Mutation	SNP	G	C	G	CC2D1B	c.C735G	p.D245E
XH_P36	1	52891139	52891139	Frame_Shift_Ins	INS	-	AAAAACAAAATC	-	ZCCHC11	4752insGATT	p.E1584fs
XH_P36	1	53446142	53446142	Nonsense_Mutation	INS	-	ATATATTAAATT	-	SCP2	insCACATATATT	D256delinsDHIYX
XH_P36	1	55080513	55080513	Frame_Shift_Ins	INS	-	ECTCTTCTCCAA	-	FAM151A	35insTTGGAGG	p.K145fs
XH_P36	1	55614239	55614239	Nonsense_Mutation	INS	-	TTT	-	USP24	1864_1865insA	p.S622delinsX
XH_P36	1	55614240	55614240	Frame_Shift_Ins	INS	-	CACTATCTTTGT	-	USP24	nsATAAACAAAG	p.S622fs
XH_P36	1	57351827	57351827	Frame_Shift_Ins	INS	-	AGAGAGCATATA	-	C8A	AACAAAGAGAG	p.K361fs
XH_P36	1	57378171	57378171	Missense_Mutation	SNP	G	T	G	C8A	c.G1476T	p.M492I
XH_P36	1	57602268	57602268	Frame_Shift_Ins	INS	-	T	-	DAB1	c.253dupA	p.I85fs
XH_P36	1	62675863	62675863	In_Frame_Ins	INS	-	AGCAACTTTTAC	-	L1TD1	nsGCTTAGCAAC	473delinsGLATFTSL
XH_P36	1	62676780	62676780	Frame_Shift_Ins	INS	-	CTCTTGCCTTTC	-	L1TD1	CTATATCTTTTC	p.R778fs
XH_P36	1	63876949	63876949	Frame_Shift_Ins	INS	-	T	-	ALG6	c.628dupT	p.P209fs
XH_P36	1	65147002	65147002	Silent	SNP	C	T	C	CACHD1	c.C2580T	p.H860H
XH_P36	1	66833535	66833535	Splice_Site	SNP	T	C	T	PDE4B	.	.
XH_P36	1	67147843	67147843	Missense_Mutation	SNP	A	G	A	SGIP1	c.A1118G	p.N373S
XH_P36	1	67292634	67292634	Nonsense_Mutation	INS	-	AGAGGGTATTGT	-	WDR78	STAACTACAATA	p.N736delinsKX
XH_P36	1	68624857	68624857	In_Frame_Ins	INS	-	TTTCT	-	WLS	79_180insAGGA	p.M60delinsIGK
XH_P36	1	68624858	68624858	Frame_Shift_Ins	INS	-	ACTTTGCT	-	WLS	8_179insAGCA	p.M60fs
XH_P36	1	68659747	68659747	Silent	SNP	G	A	G	WLS	c.C264T	p.I88I
XH_P36	1	70715677	70715677	Frame_Shift_Ins	INS	-	A	-	SRSF11	c.1066dupA	p.P355fs
XH_P36	1	75065510	75065510	Frame_Shift_Ins	INS	-	STATGTTTCTAA	-	ERIC3	595insTTAGAA	p.D532fs
XH_P36	1	75693468	75693468	Missense_Mutation	SNP	C	A	C	SLC44A5	c.G910T	p.G304W
XH_P36	1	78207315	78207315	Frame_Shift_Ins	INS	-	ATTAAACTTGCT	-	USP33	8insAAGCAAGT	p.I23fs
XH_P36	1	78207317	78207317	Silent	SNP	C	T	C	USP33	c.G66A	p.L122L
XH_P36	1	78309060	78309060	Missense_Mutation	SNP	G	A	G	MIGA1	c.G964A	p.A322T
XH_P36	1	78433883	78433883	Silent	SNP	T	C	T	FUBP1	c.A216G	p.Q72Q
XH_P36	1	79095563	79095563	Missense_Mutation	SNP	C	T	C	IFI44L	c.C686T	p.A229V
XH_P36	1	79116059	79116059	Frame_Shift_Ins	INS	-	ATTTAAATATTAA	-	IFI44	TTTCCATTAAAT	p.I60fs
XH_P36	1	79470864	79470864	In_Frame_Ins	INS	-	TATTTAAAGATTG	-	ADGRL4	insGGAAATCTT	N21delinsKEIFNI
XH_P36	1	86047153	86047153	Missense_Mutation	SNP	G	T	G	CYR61	c.G169T	p.A57S
XH_P36	1	86591275	86591275	Silent	SNP	G	A	G	COL24A1	c.C744T	p.Y248Y
XH_P36	1	90179646	90179646	Frame_Shift_Ins	INS	-	C	-	LRR8C8	c.1518dupC	p.S106fs
XH_P36	1	91967357	91967357	Frame_Shift_Del	DEL	A	-	A	CDC7	c.84delA	p.L28fs
XH_P36	1	91978751	91978751	Nonsense_Mutation	INS	-	ATCAATTAGGA	-	CDC7	TTGGGATCAAT	P237delinsLFGINX
XH_P36	1	92642755	92642755	Frame_Shift_Ins	INS	-	TTTATTTATACTA	-	KIAA1107	nsAGTTTATTATT	p.A156fs
XH_P36	1	92642757	92642757	Silent	SNP	A	T	A	KIAA1107	c.A468T	p.A156A
XH_P36	1	93306137	93306137	Silent	SNP	T	G	T	RPL5	c.T735G	p.A245A
XH_P36	1	93736257	93736257	Silent	SNP	T	C	T	CCDC18	c.T4236C	p.A1412A
XH_P36	1	94140186	94140186	Missense_Mutation	SNP	C	T	C	BCAR3	c.G301A	p.E101K
XH_P36	1	94502756	94502756	Missense_Mutation	SNP	G	A	G	ABCA4	c.C3758T	p.T1253M
XH_P36	1	99772074	99772074	Silent	SNP	G	A	G	PLPPR4	c.G1626A	p.T542T
XH_P36	1	101339807	101339807	Silent	SNP	C	T	C	EXTL2	c.G684A	p.R228R
XH_P36	1	109276077	109276077	Nonsense_Mutation	INS	-	ATATAAGCAAA	-	FNDCT	insAAAAATATAA	888_V689delinsEKIX
XH_P36	1	109735326	109735326	Missense_Mutation	SNP	C	A	C	KIAA1324	c.C763A	p.L255I
XH_P36	1	112269924	112269924	Frame_Shift_Ins	INS	-	C	-	FAM212B	c.559dupG	p.A187fs
XH_P36	1	115258747	115258747	Missense_Mutation	SNP	C	T	C	NRAS	c.G35A	p.G12D
XH_P36	1	117297419	117297419	In_Frame_Ins	INS	-	TTACTGAGAGTC	-	CD2	229insTTACTGA	E76delinsELRV
XH_P36	1	117504106	117504106	Frame_Shift_Ins	INS	-	A	-	PTGFRN	c.1455_1456ins	p.D485fs
XH_P36	1	118596651	118596651	Missense_Mutation	SNP	G	T	G	SPAG17	c.C2788A	p.P930T
XH_P36	1	144922225	144922225	Nonsense_Mutation	SNP	G	A	G	PDE4DIP	c.C1432T	p.R478X
XH_P36	1	145360624	145360624	Silent	SNP	G	A	G	NBPF19	c.G8430A	p.S2810S
XH_P36	1	148341948	148341948	Missense_Mutation	SNP	T	C	T	NBPF14	c.A625G	p.I209V
XH_P36	1	149895835	149895835	Missense_Mutation	SNP	A	T	A	SF3B4	c.T985A	p.S329T
XH_P36	1	151372604	151372604	Frame_Shift_Del	DEL	G	-	G	PSMB4	c.288delG	p.L96fs
XH_P36	1	151681548	151681548	Missense_Mutation	SNP	C	T	C	CELF3	c.G271A	p.A91T
XH_P36	1	151804203	151804203	Missense_Mutation	SNP	C	T	C	RORC	c.G38A	p.R13Q
XH_P36	1	152128948	152128948	Frame_Shift_Del	DEL	T	-	T	RPTN	c.627delA	p.K209fs
XH_P36	1	152129152	152129152	Silent	SNP	G	A	G	RPTN	c.C423T	p.D141D
XH_P36	1	152275289	152275289	Missense_Mutation	SNP	G	A	G	FLG	c.C12073T	p.P4025S
XH_P36	1	152279065	152279065	Missense_Mutation	SNP	C	T	C	FLG	c.G8297A	p.R2766H
XH_P36	1	152280274	152280274	Missense_Mutation	SNP	G	T	G	FLG	c.C7088A	p.S2363Y
XH_P36	1	152283324	152283324	Missense_Mutation	SNP	A	C	A	FLG	c.T4038G	p.H1346Q
XH_P36	1	152285188	152285188	Missense_Mutation	SNP	G	A	G	FLG	c.C2174T	p.T725I
XH_P36	1	152325759	152325759	Silent	SNP	G	A	G	FLG2	c.C4503T	p.H1501H
XH_P36	1	152327942	152327942	Missense_Mutation	SNP	T	C	T	FLG2	c.A2320G	p.S774G
XH_P36	1	152327943	152327943	Silent	SNP	G	A	G	FLG2	c.C2319T	p.H773H
XH_P36	1	152328398	152328398	Missense_Mutation	SNP	T	C	T	FLG2	c.A1864G	p.S622G
XH_P36	1	152328399	152328399	Silent	SNP	G	A	G	FLG2	c.C1863T	p.H621H
XH_P36	1	152770502	152770502	Missense_Mutation	SNP	C	T	C	LCE1D	c.C232T	p.R78C
XH_P36	1	154246391	154246391	Frame_Shift_Del	DEL	C	-	C	HAX1	c.314delC	p.S105fs
XH_P36	1	155148566	155148566	Frame_Shift_Ins	INS	-	C	-	TRIM46	c.151dupC	p.K50fs
XH_P36	1	155580268	155580268	Frame_Shift_Ins	INS	-	C	-	MSTO1	c.138dupC	p.C46fs
XH_P36	1	155638564	155638564	Nonsense_Mutation	INS	-	ACTATATACTAC	-	YY1AP1	TAATCTAGTATAT	34_A235delinsELIX
XH_P36	1	155722346	155722346	Nonsense_Mutation	SNP	G	A	G	GON4L	c.C5878T	p.R1960X

XH_P36	1	156642804	156642804	Frame_Shift_Del	DEL	G	-	G	NES	c.1176delC	p.P392fs
XH_P36	1	157095725	157095725	Nonsense_Mutation	INS	-	CTACCTTCATTC	-	ETV3	7insAGAAATGA	49_F150delinsREX
XH_P36	1	158325766	158325766	Missense_Mutation	SNP	G	A	G	CD1E	c.G208A	p.V70I
XH_P36	1	158533299	158533299	Frame_Shift_Del	DEL	A	-	A	OR6P1	c.96delT	p.F32fs
XH_P36	1	158735706	158735706	Missense_Mutation	SNP	A	G	A	OR6N1	c.T767C	p.L256P
XH_P36	1	158985772	158985772	Missense_Mutation	SNP	G	C	G	IF16	c.G376C	p.A126P
XH_P36	1	159284421	159284421	Nonsense_Mutation	INS	-	CTCTTCTCTATC	-	OR10J3	9insGATAGAAG	T10_E11delinsRX
XH_P36	1	159779252	159779252	Missense_Mutation	SNP	A	G	A	FCRL6	c.A665G	p.D222G
XH_P36	1	161518234	161518234	Missense_Mutation	SNP	G	A	A	FCGR3A	c.C611T	p.P204L
XH_P36	1	161953527	161953527	Missense_Mutation	SNP	G	A	G	OLFML2B	c.C2194T	p.R732C
XH_P36	1	162731166	162731166	Nonsense_Mutation	SNP	C	T	C	DDR2	c.C1021T	p.R341X
XH_P36	1	162766447	162766447	Silent	SNP	T	G	T	HSD17B7	c.T312G	p.L104L
XH_P36	1	164769110	164769110	Nonsense_Mutation	SNP	C	T	C	PBX1	c.C685T	p.R229X
XH_P36	1	166896414	166896414	Missense_Mutation	SNP	C	T	C	ILDR2	c.G884A	p.R295H
XH_P36	1	171553156	171553156	Missense_Mutation	SNP	G	A	G	PRRC2C	c.G7465A	p.A2489T
XH_P36	1	173772575	173772575	Silent	SNP	G	A	G	CENPL	c.C489T	p.C163C
XH_P36	1	173930334	173930334	Frame_Shift_Ins	INS	-	A	-	RC3H1	c.2250dupT	p.L751fs
XH_P36	1	173930336	173930336	In_Frame_Ins	INS	-	TATGTATGTAAT	-	RC3H1	CATTACATTACA	0delinsNALHYHTKIS
XH_P36	1	174200408	174200408	Missense_Mutation	SNP	C	T	C	RABGAP1L	c.C457T	p.R153W
XH_P36	1	175304899	175304899	Frame_Shift_Ins	INS	-	TCATTAATAGTC	-	TNR	80insGAGACTAT	p.R860fs
XH_P36	1	176659361	176659361	Silent	SNP	C	T	C	PAPPA2	c.C2226T	p.Y742Y
XH_P36	1	179887233	179887233	In_Frame_Ins	INS	-	ATTGCTCAGTTC	-	TOR1AI1P1	5insTCCATTGTCT	538delinsKSIAQFL
XH_P36	1	182550367	182550367	Missense_Mutation	SNP	G	A	G	RNASEL	c.C1898T	p.T633M
XH_P36	1	185278146	185278146	Nonsense_Mutation	INS	-	ATAAAATCATTT	-	IVNS1ABP	CTCCATAAATGA	A90_Y91delinsAKX
XH_P36	1	197091723	197091723	Frame_Shift_Ins	INS	-	TTTCTCTCGCAT	-	ASPM	393insATGCAGC	p.V1131fs
XH_P36	1	197128938	197128938	Nonsense_Mutation	INS	-	AAAAATATACTC	-	ZBTB41	1insTAAGAGTAT	p.E761delinsX
XH_P36	1	200569550	200569550	Missense_Mutation	SNP	C	T	C	KIF14	c.G761A	p.R254Q
XH_P36	1	201177935	201177935	Missense_Mutation	SNP	A	G	A	IGFN1	c.A3914G	p.D1305G
XH_P36	1	201178708	201178708	Missense_Mutation	SNP	A	G	A	IGFN1	c.A4687G	p.L1563E
XH_P36	1	202725607	202725607	Missense_Mutation	SNP	C	T	C	KDM5B	c.G1100A	p.R367K
XH_P36	1	202887497	202887497	Nonsense_Mutation	SNP	A	T	A	KLHL12	c.T483A	p.C161X
XH_P36	1	203668744	203668744	Missense_Mutation	SNP	G	A	G	ATP2B4	c.G548A	p.R183H
XH_P36	1	205241128	205241128	Missense_Mutation	SNP	C	T	C	TMCC2	c.C1331T	p.T444M
XH_P36	1	205589712	205589712	In_Frame_Ins	INS	-	ACTGCCTCCCT	-	ELK4	62insAGGGAAAC	5154delinsSGKAV
XH_P36	1	205696901	205696901	Nonsense_Mutation	INS	-	AACCATATACAA	-	NUCKS1	TTATTGTAAATAT	LIST5SHLFENYCNMVLQTFX
XH_P36	1	206758543	206758543	Frame_Shift_Del	DEL	C	-	C	RASSF5	c.561delC	p.R187fs
XH_P36	1	206821938	206821938	Frame_Shift_Del	DEL	G	-	G	DYRK3	c.1395delG	p.Y465fs
XH_P36	1	207198372	207198372	In_Frame_Ins	INS	-	CACCAC	-	C1orf116	42_143insGTGGp	K48delinsSGE
XH_P36	1	209807808	209807808	Missense_Mutation	SNP	C	T	C	LAMB3	c.G548A	p.R183H
XH_P36	1	214820283	214820283	In_Frame_Ins	INS	-	ATTTTTCCTTTT	-	CENPF	1insTCTATTTT	2457delinsLFLLLG
XH_P36	1	214830519	214830519	Missense_Mutation	SNP	C	T	C	CENPF	c.C8729T	p.P2910L
XH_P36	1	220152861	220152861	Nonsense_Mutation	INS	-	GTGTGTATTATT	-	EPRS	sAAATAAAATAT	270_N1271delinsKX
XH_P36	1	222798193	222798193	Frame_Shift_Ins	INS	-	ACTAGTGACACT	-	MI3	2insTCACTAGTC	p.T117fs
XH_P36	1	222903458	222903458	Nonsense_Mutation	INS	-	ACCAATAATAAT	-	BROX	GCAATACCAATA	p.R278delinsTX
XH_P36	1	225490915	225490915	Missense_Mutation	SNP	C	T	C	DNAH14	c.C8410T	p.R2804C
XH_P36	1	226340081	226340081	Missense_Mutation	SNP	T	C	T	CBBD3	c.A1330G	p.A444G
XH_P36	1	226923872	226923872	Frame_Shift_Del	DEL	C	-	C	ITPKB	c.1288delG	p.A430fs
XH_P36	1	227843200	227843200	Nonsense_Mutation	INS	-	TCITTTATGAGC	-	ZNF678	ATGAATTCITTTT	472delinsVEFFYDEX
XH_P36	1	228399732	228399732	Missense_Mutation	SNP	G	A	G	OBSCN	c.G248A	p.R83H
XH_P36	1	228506757	228506757	Silent	SNP	G	A	G	OBSCN	c.G14304A	p.S4768S
XH_P36	1	228522241	228522241	Silent	SNP	A	G	A	OBSCN	c.A16083G	p.A5361A
XH_P36	1	233464042	233464042	Missense_Mutation	SNP	G	T	G	MAP3K21	c.G268T	p.G90C
XH_P36	1	235658047	235658047	Silent	SNP	G	A	G	B3GALNT2	c.C204T	p.N68N
XH_P36	1	235940392	235940392	Missense_Mutation	SNP	T	A	T	LYST	c.A5431T	p.T1811S
XH_P36	1	237948089	237948089	Silent	SNP	C	A	C	RYR2	c.C13077A	p.P4359P
XH_P36	1	242042491	242042491	Missense_Mutation	SNP	C	T	C	EXO1	c.C1955T	p.S652L
XH_P36	1	243333027	243333027	Silent	SNP	A	G	A	CEP170	c.T1452C	p.R484R
XH_P36	1	243507615	243507615	Nonsense_Mutation	INS	-	ATTGATTCTAAC	-	SDCCAG8	162insTATTGAT	D387delinsDYYX
XH_P36	1	245927412	245927412	Silent	SNP	T	C	T	SMYD3	c.A1116G	p.Q372Q
XH_P36	1	247007131	247007131	Frame_Shift_Del	DEL	T	-	T	AHCTF1	c.6491delA	p.N2164fs
XH_P36	1	247013524	247013524	Missense_Mutation	SNP	C	A	C	AHCTF1	c.G5784T	p.R1928N
XH_P36	1	248028086	248028086	Missense_Mutation	SNP	G	A	G	TRIM58	c.G596A	p.R199Q
XH_P36	1	248436586	248436586	Silent	SNP	G	A	G	OR2T33	c.C531T	p.C177C
XH_P36	1	248436712	248436712	Missense_Mutation	SNP	G	T	G	OR2T33	c.C405A	p.S135R
XH_P36	1	248737734	248737734	Missense_Mutation	SNP	G	A	G	OR2T34	c.C325T	p.H109Y
XH_P36	2	3750103	3750103	Missense_Mutation	SNP	C	T	C	ALLC	c.C1126T	p.R376W
XH_P36	2	10269359	10269359	Splice_Site	INS	-	CACCCACTTTAC	-	RRM2	-	-
XH_P36	2	10269360	10269360	Splice_Site	SNP	G	T	G	RRM2	-	-
XH_P36	2	11774324	11774324	Missense_Mutation	SNP	G	A	G	GREB1	c.G5059A	p.D1687N
XH_P36	2	17698432	17698432	Frame_Shift_Ins	INS	-	ATGTGAACAAC	-	RAD51AP2	insAAGGGTTGT	p.K417fs
XH_P36	2	20234799	20234799	Frame_Shift_Ins	INS	-	ATTGAGGATTTC	-	LAPTM4A	457insAAATCC	p.L153fs
XH_P36	2	20478579	20478579	Frame_Shift_Ins	INS	-	TCACITTTATC	-	PUM2	1554insGATGA	p.V518fs
XH_P36	2	20870507	20870507	Frame_Shift_Del	DEL	C	-	C	GDF7	c.675delC	p.R225fs
XH_P36	2	23865497	23865497	Silent	SNP	C	T	C	KLHL29	c.C717T	p.P239P
XH_P36	2	26507756	26507756	Missense_Mutation	SNP	G	T	G	HADHB	c.G1110T	p.Q370H
XH_P36	2	26705384	26705384	Frame_Shift_Del	DEL	G	-	G	OTOF	c.1469delG	p.P490fs
XH_P36	2	26951074	26951074	Frame_Shift_Del	DEL	G	-	G	KCNK3	c.823delG	p.G275fs
XH_P36	2	27248517	27248517	Frame_Shift_Del	DEL	C	-	C	MAPRE3	c.536delC	p.A179fs
XH_P36	2	29016762	29016762	Nonsense_Mutation	SNP	C	T	C	PPP1CB	c.C778T	p.R260X
XH_P36	2	29455174	29455174	Silent	SNP	G	A	G	ALK	c.C2628T	p.A876A
XH_P36	2	31010045	31010045	Missense_Mutation	SNP	C	A	C	CAPN13	c.C147T	p.Q49H
XH_P36	2	36704119	36704119	Frame_Shift_Del	DEL	A	-	A	CRIM1	c.1079delA	p.Q360fs
XH_P36	2	37235963	37235963	Nonsense_Mutation	INS	-	ATGGTGAGTAT	-	HEATR5B	insTGTAATACTC	438_E1439delinsMX
XH_P36	2	37347123	37347123	Frame_Shift_Del	DEL	T	-	T	EIF2AK2	c.1104delA	p.K368fs
XH_P36	2	42720141	42720141	Silent	SNP	C	T	C	KCNG3	c.G501A	p.S167S
XH_P36	2	44190786	44190786	Frame_Shift_Ins	INS	-	CAATTTCTTTTT	-	LRPPRC	429insAAAAAAG	p.Y477fs
XH_P36	2	44190788	44190788	Missense_Mutation	SNP	G	C	G	LRPPRC	c.C1427G	p.T476R
XH_P36	2	46574080	46574080	Missense_Mutation	SNP	A	G	A	EPAS1	c.A95G	p.E32G
XH_P36	2	46842236	46842236	Missense_Mutation	SNP	C	A	C	PIGF	c.G68T	p.S23I
XH_P36	2	48602207	48602207	Silent	SNP	T	C	T	FOXP2	c.T921C	p.S307S
XH_P36	2	50765682	50765682	Frame_Shift_Ins	INS	-	C	-	NRXN1	c.1767dupG	p.L590fs
XH_P36	2	60987361	60987361	Missense_Mutation	SNP	A	G	A	PAPOLG	c.A110G	p.Y37C
XH_P36	2	61753609	61753609	Frame_Shift_Ins	INS	-	TATAATTAAT	-	XP01	174insATTAAT	p.D58fs
XH_P36	2	61753611	61753611	Nonsense_Mutation	INS	-	GCAAATAGTCC	-	XP01	2insTAGGACTA	p.D58delinsX
XH_P36	2	70408460	70408460	Missense_Mutation	SNP	G	A	G	C2orf42	c.C658T	p.R220C
XH_P36	2	71046551	71046551	Silent	SNP	C	T	C	CLEC4F	c.G204A	p.P68P
XH_P36	2	71650264	71650264	Frame_Shift_Ins	INS	-	ACTATCAGTTG	-	ZNF638	nsAGGGACTATC	p.S1207fs
XH_P36	2	73518631	73518631	Missense_Mutation	SNP	T	C	T	EGR4	c.A1724G	p.K575R

XH_P36	2	73799626	73799626	Frame_Shift_Ins	INS	-	ACGGG	-	ALMS1	519_10620insAC	p.D3540fs
XH_P36	2	73799627	73799627	Frame_Shift_Ins	INS	-	AG	-	ALMS1	0620_10621ins	p.D3540fs
XH_P36	2	73828531	73828531	In_Frame_Ins	INS	-	ACAGGG	-	ALMS1	79_12080insAC	L4027delinsHRV
XH_P36	2	74326498	74326498	Silent	SNP	G	T	G	TET3	c.G3363T	p.T1121T
XH_P36	2	74687550	74687550	Frame_Shift_Del	DEL	T	-	T	WBP1	c.C552delT	p.P184fs
XH_P36	2	74742324	74742324	Missense_Mutation	SNP	C	T	C	TLX2	c.C391T	p.R131W
XH_P36	2	74900900	74900900	Missense_Mutation	SNP	G	A	G	SEMA4F	c.G668A	p.R223Q
XH_P36	2	85043102	85043102	Missense_Mutation	SNP	C	T	C	DNAH6	c.C12268T	p.P490Gs
XH_P36	2	96521783	96521783	In_Frame_Ins	INS	-	GGCACAGTAGA	-	ANKRD36C	4insTTTATCTAC	L775delinsYLLCPG
XH_P36	2	97475131	97475131	Silent	SNP	G	A	G	CNNM4	c.G2205A	p.G735G
XH_P36	2	97638040	97638040	Silent	SNP	G	A	G	FAM178B	c.C162T	p.T54T
XH_P36	2	97827852	97827852	Missense_Mutation	SNP	C	T	C	ANKRD36	c.C1406T	p.P469L
XH_P36	2	99182127	99182127	Missense_Mutation	SNP	A	G	A	INPP4A	c.A2027G	p.D676G
XH_P36	2	102482928	102482928	Missense_Mutation	SNP	A	C	A	MAP4K4	c.A1754C	p.K585T
XH_P36	2	110301828	110301828	Frame_Shift_Del	DEL	T	-	T	SEPT10	c.1506delA	p.K502fs
XH_P36	2	112705139	112705139	Missense_Mutation	SNP	T	C	T	MERTK	c.T752C	p.V251A
XH_P36	2	112942828	112942828	Missense_Mutation	SNP	T	C	T	FBLN7	c.T721C	p.C241R
XH_P36	2	120303807	120303807	Frame_Shift_Del	DEL	A	-	A	CFAP221	c.100delA	p.K34fs
XH_P36	2	122205058	122205058	Silent	SNP	C	T	C	CLASP1	c.G1767A	p.V589V
XH_P36	2	128467115	128467115	Missense_Mutation	SNP	G	A	G	WDR33	c.C3514T	p.R1172C
XH_P36	2	128477850	128477850	Silent	SNP	G	A	G	WDR33	c.C1749T	p.L583L
XH_P36	2	128522398	128522398	Frame_Shift_Ins	INS	-	CGTT	-	WDR33	629_630insAAC	p.F210fs
XH_P36	2	128522399	128522399	Nonsense_Mutation	INS	-	CCTTTTATTAT	-	WDR33	insAGATAATAAF	F210_I211delinsX
XH_P36	2	130897920	130897920	Silent	SNP	G	A	G	CCDC74B	c.C510T	p.N170N
XH_P36	2	131803707	131803707	Missense_Mutation	SNP	G	A	G	ARHGEF4	c.G2018A	p.R673H
XH_P36	2	131976173	131976283	In_Frame_Del	DEL	TGGAGACCA	-	CTGGAGACCAC	POTEE	c.198_308del	p.66_103del
XH_P36	2	132290242	132290242	Missense_Mutation	SNP	G	C	G	CCDC74A	c.G566C	p.G189A
XH_P36	2	135745134	135745134	In_Frame_Ins	INS	-	TGACAAGCATA	-	MAP3K19	TCATCTTAGTCT	23delinsEFILCLFSFW
XH_P36	2	135893484	135893484	Frame_Shift_Ins	INS	-	TATCTGTTCTCT	-	RAB3GAP1	TTTTCTTATTCT	p.L635fs
XH_P36	2	141115575	141115575	Missense_Mutation	SNP	C	A	C	LRP1B	c.G11368T	p.G3790C
XH_P36	2	141135790	141135790	Frame_Shift_Del	DEL	A	-	A	LRP1B	c.10597delT	p.V3533fs
XH_P36	2	143798030	143798030	Frame_Shift_Del	DEL	A	-	A	KYNU	c.1075delA	p.K359fs
XH_P36	2	148657041	148657041	Frame_Shift_Del	DEL	A	-	A	ACVR2A	c.278delA	p.E93fs
XH_P36	2	148683686	148683686	Frame_Shift_Del	DEL	A	-	A	ACVR2A	c.979delA	p.K327fs
XH_P36	2	152320446	152320446	In_Frame_Ins	INS	-	TACTACTGGGGG	-	RIF1	3insTATTACTAC	471delinsDITGGV
XH_P36	2	152548835	152548835	Silent	SNP	A	G	A	NEB	c.T1938C	p.S646S
XH_P36	2	160075810	160075810	Missense_Mutation	SNP	C	T	C	TANC1	c.C2837T	p.T946M
XH_P36	2	163291933	163291933	Frame_Shift_Ins	INS	-	TGCTATTAGGA	-	KCNH7	ATTCTATCTAA	p.E570fs
XH_P36	2	166785799	166785799	Missense_Mutation	SNP	C	T	C	TTC21B	c.G1232A	p.R411Q
XH_P36	2	167262863	167262863	Frame_Shift_Ins	INS	-	ACCTTGAGTGAA	-	SCN7A	6insATCTTCAC	p.C1426fs
XH_P36	2	167298238	167298238	Missense_Mutation	SNP	A	C	A	SCN7A	c.T1825G	p.V609D
XH_P36	2	167298240	167298240	Frame_Shift_Ins	INS	-	GGTGATTCC	-	SCN7A	1823insGGAA	p.K608fs
XH_P36	2	168105837	168105837	Nonsense_Mutation	INS	-	TTGATTITGGCT	-	XIRP2	sATGTGTTGATT	23_L2424delinsVMCX
XH_P36	2	168106512	168106512	Frame_Shift_Ins	INS	-	TTTTGGTAAG	-	XIRP2	TATTGTTTTTGG	p.Q2648fs
XH_P36	2	170038761	170038761	Missense_Mutation	SNP	C	T	C	LRP2	c.G9914A	p.R3305H
XH_P36	2	170366973	170366973	Frame_Shift_Ins	INS	-	A	-	KLHL41	c.686dupA	p.E229fs
XH_P36	2	170460581	170460581	Frame_Shift_Del	DEL	T	-	T	PIIG	c.30delT	p.C10fs
XH_P36	2	170606130	170606130	Frame_Shift_Ins	INS	-	T	-	KLHL23	c.1565_1566ins	p.T522fs
XH_P36	2	170606131	170606131	Frame_Shift_Ins	INS	-	AGCACAATCCA	-	KLHL23	1567insAGCAC	p.T522fs
XH_P36	2	172549339	172549339	Frame_Shift_Del	DEL	A	-	A	DYNC1I2	c.161delA	p.E54fs
XH_P36	2	173855617	173855617	Nonsense_Mutation	INS	-	ATGAGGTTTGA	-	RAPGEF4	795insATGAGG	265_A266delinsRX
XH_P36	2	173883474	173883474	Missense_Mutation	SNP	C	T	C	RAPGEF4	c.C1439T	p.A480V
XH_P36	2	175436887	175436887	Missense_Mutation	SNP	C	T	C	WIPF1	c.G646A	p.G216R
XH_P36	2	176995146	176995151	In_Frame_Del	DEL	GCGGCG	-	GCGGCG	HOXD8	c.52_57del	p.18_19del
XH_P36	2	177036404	177036404	Missense_Mutation	SNP	C	T	C	HOXD3	c.C701T	p.T234M
XH_P36	2	179318291	179318291	Nonsense_Mutation	INS	-	AAAATACAAAG	-	DFNB59	TCTTAAAAATACT	52_553delinsTSX
XH_P36	2	179478981	179478981	Silent	SNP	A	G	A	TTN	c.T21948C	p.S7316S
XH_P36	2	179483496	179483496	Missense_Mutation	SNP	T	C	T	TTN	c.A19586G	p.V6529C
XH_P36	2	179536874	179536874	Nonsense_Mutation	INS	-	TAGATGATAGTA	-	TTN	TCAAATATTACT	383_H10384delinsX
XH_P36	2	179549465	179549465	Nonsense_Mutation	INS	-	GTAGAGATTATA	-	TTN	28834insTAAT	3612_K9613delinsX
XH_P36	2	179574422	179574422	In_Frame_Ins	INS	-	TGAGCATTTCTT	-	TTN	ATATCATAAGA	98delinsDIIRNAHGYI
XH_P36	2	179575449	179575449	Missense_Mutation	SNP	C	T	C	TTN	c.G24643A	p.V821S
XH_P36	2	179578885	179578885	Nonsense_Mutation	INS	-	TAATAATGTAGT	-	TTN	ATCAGGAACATA	590_K7591delinsX
XH_P36	2	179587901	179587901	Missense_Mutation	SNP	A	G	A	TTN	c.T18101C	p.L6034T
XH_P36	2	179587903	179587903	Frame_Shift_Ins	INS	-	AGCCTTTC	-	TTN	8_18099insGAA	p.N6033fs
XH_P36	2	179621158	179621158	Missense_Mutation	SNP	A	G	A	TTN	c.T10532C	p.V3511A
XH_P36	2	182763804	182763804	Silent	SNP	C	A	C	SSFA2	c.C9A	p.S3S
XH_P36	2	186662103	186662103	Frame_Shift_Del	DEL	A	-	A	FSIP2	c.10244delA	p.K3414fs
XH_P36	2	187615880	187615880	Silent	SNP	G	A	G	FAM171B	c.G744A	p.L248L
XH_P36	2	189866275	189866275	Frame_Shift_Del	DEL	C	-	C	COL3A1	c.2351delC	p.A784fs
XH_P36	2	189868745	189868745	Missense_Mutation	SNP	G	A	G	COL3A1	c.G2699A	p.G900D
XH_P36	2	191381108	191381108	Nonsense_Mutation	INS	-	AATAATATTTTG	-	NEMP2	5ATAAACAAAT	205_S206delinsX
XH_P36	2	200213696	200213696	In_Frame_Ins	INS	-	TCTTTGCAA	-	SATB2	901insTTGCA	Q301delinsLQRQ
XH_P36	2	202149545	202149545	Missense_Mutation	SNP	T	C	T	CASP8	c.T764C	p.L255S
XH_P36	2	203807528	203807528	Silent	SNP	C	A	C	CARF	c.C108A	p.P36P
XH_P36	2	207169621	207169621	Frame_Shift_Ins	INS	-	TATTCTAATGTC	-	ZDBF2	0insCATATTCTA	p.K123fs
XH_P36	2	207171368	207171368	Frame_Shift_Ins	INS	-	CTTCAGAAGA	-	ZDBF2	2117insCTTCA	p.L706fs
XH_P36	2	207172364	207172364	Missense_Mutation	SNP	G	A	G	ZDBF2	c.G3112A	p.G1038S
XH_P36	2	207174428	207174428	Frame_Shift_Del	DEL	A	-	A	ZDBF2	c.5176delA	p.K1726fs
XH_P36	2	207175098	207175098	Nonsense_Mutation	INS	-	GTAACCTT	-	ZDBF2	6_5847insGTA	949_C1950delinsRX
XH_P36	2	207527743	207527743	Missense_Mutation	SNP	G	T	G	DYTN	c.C1517A	p.A506D
XH_P36	2	210840978	210840978	Missense_Mutation	SNP	G	A	G	UNC80	c.G8525A	p.R2842Q
XH_P36	2	217124353	217124353	Nonsense_Mutation	INS	-	ACATCCTGAGT	-	MARCH4	915insACTCAG	305_Q306delinsX
XH_P36	2	218674638	218674638	Nonsense_Mutation	INS	-	CTACCTTCTCAT	-	TNS1	306insGATGAGA	2_E1603delinsSMRRX
XH_P36	2	218674639	218674639	Missense_Mutation	SNP	G	C	G	TNS1	c.C4805G	p.S1602C
XH_P36	2	219892362	219892362	Missense_Mutation	SNP	G	A	G	CFAP65	c.C2026T	p.R676C
XH_P36	2	219896326	219896326	Missense_Mutation	SNP	C	T	C	CFAP65	c.G505A	p.G169S
XH_P36	2	220083200	220083200	Frame_Shift_Del	DEL	C	-	C	ABCB6	c.196delG	p.A66fs
XH_P36	2	220116337	220116337	Missense_Mutation	SNP	T	C	T	TUBA4A	c.A280G	p.T94A
XH_P36	2	223917773	223917773	Silent	SNP	C	T	C	KCNE4	c.C378T	p.D126D
XH_P36	2	233323757	233323757	Silent	SNP	G	A	G	ALPI	c.G1488A	p.A496A
XH_P36	2	233410400	233410400	Missense_Mutation	SNP	C	T	C	CHRN9	c.C1528T	p.R510C
XH_P36	2	234365952	234365952	Frame_Shift_Del	DEL	G	-	G	DKD	c.2426delG	p.W809fs
XH_P36	2	239057734	239057734	Missense_Mutation	SNP	A	G	A	KLHL30	c.A1426G	p.I476V
XH_P36	2	239258015	239258015	Missense_Mutation	SNP	C	T	C	TRAF3IP1	c.C1219T	p.R407W
XH_P36	2	241885639	241885639	Missense_Mutation	SNP	C	T	C	CROCC2	c.C2332T	p.R778W
XH_P36	2	242179074	242179074	Silent	SNP	G	A	G	HDLBP	c.C2454T	p.G818G
XH_P36	3	367670	367670	Silent	SNP	G	A	G	CHL1	c.G120A	p.Q40Q

XH_P36	3	1371501	1371501	Frame_Shift_Del	DEL	A	-	A	CNTN6	c.934delA	p.K312fs
XH_P36	3	5025215	5025215	In_Frame_Ins	INS	-	CAT	-	BHLHE40	1077_1078insCp.A359delinsAH	
XH_P36	3	5025217	5025217	In_Frame_Ins	INS	-	GAGAAGTGCTG	-	BHLHE40	80insTGGAGAA360delinsAGEVLV	
XH_P36	3	5252820	5252820	Silent	SNP	G	A	G	EDEM1	c.G1599A	p.T533T
XH_P36	3	10382200	10382200	Missense_Mutation	SNP	C	T	C	ATP2B2	c.G2971A	p.V991M
XH_P36	3	12641888	12641888	Frame_Shift_Ins	INS	-	CTGCCAATTAG	-	RAF1	61insCCTAATTG	p.S287fs
XH_P36	3	12942841	12942841	Frame_Shift_Del	DEL	G	-	G	IQSEC1	c.2986delC	p.H996fs
XH_P36	3	25654189	25654189	Silent	SNP	A	G	A	TOP2B	c.T3588C	p.S1196fs
XH_P36	3	25805772	25805772	Frame_Shift_Ins	INS	-	T	-	NGLY1	c.276dupA	p.A93fs
XH_P36	3	27233665	27233665	Frame_Shift_Ins	INS	-	AATAGTTACATG	-	NEK10	TATTGCATGTA	p.M99fs
XH_P36	3	30691872	30691873	Frame_Shift_Del	DEL	AA	-	AA	TGFBR2	c.374_375del	p.E125fs
XH_P36	3	31574563	31574563	Missense_Mutation	SNP	G	A	G	STT3B	c.G73A	p.A25T
XH_P36	3	31663787	31663787	Nonsense_Mutation	INS	-	TGAAGTACATA	-	STT3B	527insCTGAAC	509_L510delinsNX
XH_P36	3	36897022	36897022	Silent	SNP	C	T	C	TRANK1	c.G4059A	p.L1353L
XH_P36	3	38889230	38889230	Nonsense_Mutation	INS	-	CTCTTCTGATTA	-	SCN11A	AAACATAATCAG444_M1445delinsRX	
XH_P36	3	40528589	40528589	Silent	SNP	T	G	T	ZNFB19	c.T456G	p.G152G
XH_P36	3	41275758	41275758	Silent	SNP	G	T	G	CTNNB1	c.G1653T	p.T551T
XH_P36	3	41275760	41275760	Frame_Shift_Ins	INS	-	CTAAGGAATACA	-	CTNNB1	TACTTACTAAGG	p.S552fs
XH_P36	3	42680096	42680096	Frame_Shift_Ins	INS	-	AGATTCTCTTTC	-	NKTR	TCAGAAAGATTG	p.S967fs
XH_P36	3	44636110	44636110	In_Frame_Ins	INS	-	TTTTCCACA	-	ZNFB60	5_426insTTTTCC	A142delinsAFPH
XH_P36	3	44636112	44636112	Frame_Shift_Ins	INS	-	CCTTACAC	-	ZNFB60	7_428insCCTTA	p.F143fs
XH_P36	3	44692631	44692631	Silent	SNP	A	G	A	ZNFB35	c.A72G	p.E24E
XH_P36	3	45943194	45943194	Missense_Mutation	SNP	T	C	T	CCR9	c.T878C	p.I293T
XH_P36	3	46875151	46875151	Frame_Shift_Del	DEL	G	-	G	PRSS42	c.230delC	p.P77fs
XH_P36	3	47891256	47891256	Missense_Mutation	SNP	C	T	C	DHX30	c.C3328T	p.R1110C
XH_P36	3	48461122	48461122	Frame_Shift_Del	DEL	C	-	C	PLXNB1	c.2573delG	p.G585fs
XH_P36	3	48694444	48694444	Silent	SNP	C	T	C	CELSR3	c.G4086A	p.A1362A
XH_P36	3	49210370	49210370	Silent	SNP	G	A	G	KLHDC8B	c.G168A	p.S56S
XH_P36	3	50005145	50005145	Frame_Shift_Del	DEL	G	-	G	RBM6	c.287delG	p.R96fs
XH_P36	3	50155888	50155891	Frame_Shift_Del	DEL	GAGA	-	GAGA	RBMS	c.2447_2450del	p.*816fs
XH_P36	3	50324240	50324240	Missense_Mutation	SNP	C	T	C	LSMEM2	c.C305T	p.A102V
XH_P36	3	50385747	50385747	Splice_Site	SNP	C	T	C	NPRL2	.	.
XH_P36	3	52437315	52437315	Splice_Site	SNP	C	T	C	BAP1	.	.
XH_P36	3	53263342	53263342	Silent	SNP	G	A	G	TKT	c.C1218T	p.S406S
XH_P36	3	77623837	77623837	Frame_Shift_Ins	INS	-	CCTCATAACTAT	-	ROBO2	TTCTGTCTCTCAT	p.Q720fs
XH_P36	3	77657037	77657037	Frame_Shift_Ins	INS	-	C	-	ROBO2	c.3226dupC	p.P1075fs
XH_P36	3	108139971	108139971	Silent	SNP	G	A	G	MYH15	c.C3853T	p.L1285L
XH_P36	3	108229398	108229398	Frame_Shift_Del	DEL	A	-	A	MYH15	c.40delT	p.W14fs
XH_P36	3	111828413	111828413	Silent	SNP	G	A	G	C3orf52	c.G420A	p.S140S
XH_P36	3	112538716	112538716	Silent	SNP	A	G	A	CD200R1L	c.T706C	p.L236L
XH_P36	3	112648129	112648129	Missense_Mutation	SNP	C	T	C	CD200R1	c.G359A	p.R120H
XH_P36	3	112989730	112989730	Silent	SNP	C	A	C	BOC	c.C606A	p.A202A
XH_P36	3	113377483	113377483	Missense_Mutation	SNP	T	G	T	USF3	c.A3046C	p.N1016H
XH_P36	3	113850142	113850142	Missense_Mutation	SNP	T	C	T	DRD3	c.A829G	p.K277E
XH_P36	3	119962621	119962621	Nonsense_Mutation	INS	-	CTAG	-	GPR156	c.98_99insCTAGT33_S34delinsTX	
XH_P36	3	119962623	119962623	Nonsense_Mutation	INS	-	STATTGTGCTAA	-	GPR156	nsTAGTTAGCAC_T33_S34delinsX	
XH_P36	3	121208048	121208048	Frame_Shift_Ins	INS	-	AAGATAGTTTTC	-	POLQ	CAGATAGAAAC	p.T1244fs
XH_P36	3	121208707	121208707	Frame_Shift_Ins	INS	-	CTAAAAATGTAT	-	POLQ	071insGATACAT	p.K1024fs
XH_P36	3	121208709	121208709	In_Frame_Ins	INS	-	TGAGTG	-	POLQ	68_3069insCAC	T1023delinsTTQ
XH_P36	3	122943972	122943972	Missense_Mutation	SNP	G	T	G	SEC22A	c.G369T	p.K123N
XH_P36	3	126707536	126707536	Missense_Mutation	SNP	G	T	G	PLXNA1	c.G100T	p.G34C
XH_P36	3	130361855	130361855	Nonsense_Mutation	SNP	C	T	C	COL6A6	c.C5215T	p.R1739X
XH_P36	3	132051057	132051057	Missense_Mutation	SNP	G	A	G	ACPP	c.G325A	p.V109I
XH_P36	3	132319688	132319688	Frame_Shift_Ins	INS	-	TGTACACATCT	-	ACKR4	448insTGTACA	p.G149fs
XH_P36	3	133666246	133666246	Frame_Shift_Ins	INS	-	CTATTCTTTGCT	-	SLCO2A1	5TGACAGCAAA	p.G383fs
XH_P36	3	136019877	136019877	Missense_Mutation	SNP	G	A	G	PCPB	c.G890A	p.R297H
XH_P36	3	136240241	136240241	Nonsense_Mutation	INS	-	CTTTTCATTTAG	-	STAG1	CAAACTAAATGp.L164delinsKTX	
XH_P36	3	138739338	138739338	Missense_Mutation	SNP	C	T	C	PRR23B	c.G166A	p.A56T
XH_P36	3	142261555	142261555	Frame_Shift_Del	DEL	A	-	A	ATR	c.3402delT	p.F1134fs
XH_P36	3	142269109	142269109	In_Frame_Ins	INS	-	TAAGTTTAAAGT	-	ATR	AAATCCACTTAA47delinsTQIHLNLSFT	
XH_P36	3	143214258	143214258	Frame_Shift_Ins	INS	-	AATGACTTACT	-	SLC9A9	1122insAGTAA	p.N374fs
XH_P36	3	148459721	148459721	Frame_Shift_Del	DEL	T	-	T	AGTR1	c.899delT	p.L300fs
XH_P36	3	149485156	149485156	Frame_Shift_Ins	INS	-	AG	-	ANKUB1	1292_1293insC	p.T431fs
XH_P36	3	153842199	153842199	Frame_Shift_Del	DEL	A	-	A	ARHGEF26	c.1084delA	p.K326fs
XH_P36	3	157816092	157816092	Silent	SNP	C	T	C	SHOX2	c.G720A	p.V240V
XH_P36	3	160231939	160231939	Missense_Mutation	SNP	C	T	C	KPNA4	c.G1063A	p.A355T
XH_P36	3	161221015	161221015	Missense_Mutation	SNP	A	G	A	OTOL1	c.A719G	p.D240G
XH_P36	3	167507164	167507164	Nonsense_Mutation	INS	-	TTACATATTAAAT	-	SERPINI1	ACAATTATACATA	G84delinsNNNLHINYX
XH_P36	3	170856027	170856027	Missense_Mutation	SNP	A	G	A	TNIK	c.T1474C	p.Y492H
XH_P36	3	170856028	170856028	Frame_Shift_Ins	INS	-	TTGTGTTTTGTT	-	TNIK	insAAAAAACAA	p.H491fs
XH_P36	3	175042056	175042056	Frame_Shift_Ins	INS	-	T	-	NAALAD12	c.1033dupT	p.T344fs
XH_P36	3	178952085	178952085	Missense_Mutation	SNP	A	G	A	PIK3CA	c.A3140G	p.L1047R
XH_P36	3	179690970	179690970	Missense_Mutation	SNP	G	A	G	PEX5L	c.C70T	p.R24W
XH_P36	3	183368801	183368801	Frame_Shift_Ins	INS	-	CTTCACCTTTCCA	-	KLHL24	58insCTTCACC	p.D219fs
XH_P36	3	183368803	183368803	Missense_Mutation	SNP	A	T	A	KLHL24	c.A659T	p.E220V
XH_P36	3	183888195	183888195	Missense_Mutation	SNP	C	G	C	DVL3	c.C1803G	p.S601R
XH_P36	3	193854823	193854823	Missense_Mutation	SNP	G	T	G	HE51	c.G278T	p.R93L
XH_P36	3	194081622	194081622	Nonsense_Mutation	INS	-	CAACCTCA	-	LRRC15	0_151insTGAGG_L51_P52delinsX	
XH_P36	3	195295892	195295892	Missense_Mutation	SNP	G	A	G	APOD	c.C449T	p.A150V
XH_P36	3	195508661	195508661	Missense_Mutation	SNP	A	G	A	MUC4	c.T9790C	p.S3264P
XH_P36	4	154798	154798	Nonsense_Mutation	INS	-	ATCTCCAGTATA	-	ZNFT18	GTTTATTCTCCA08_E109delinsHILYIX	
XH_P36	4	437209	437209	Silent	SNP	G	A	G	ZNFT21	c.C1047T	p.Y349Y
XH_P36	4	515806	515806	In_Frame_Ins	INS	-	TGCGCA	-	PIGG	23_1424insTGCp.R475delinsLRS	
XH_P36	4	961739	961739	Missense_Mutation	SNP	G	A	G	DGKQ	c.C740T	p.A247V
XH_P36	4	1719361	1719361	Missense_Mutation	SNP	C	T	C	TMEM129	c.G722A	p.R241Q
XH_P36	4	4304807	4304807	Missense_Mutation	SNP	G	A	G	ZBTB49	c.G1244A	p.R415Q
XH_P36	4	5018651	5018651	Missense_Mutation	SNP	G	A	G	CYT1L	c.C239T	p.S80L
XH_P36	4	8375308	8375308	Missense_Mutation	SNP	C	T	C	ACOX3	c.G1876A	p.V626I
XH_P36	4	20706377	20706377	Frame_Shift_Ins	INS	-	CCCTCTGATT	-	PACRGL	148insCCCTCT	p.E49fs
XH_P36	4	25278714	25278714	Missense_Mutation	SNP	C	T	C	PI4K2B	c.C1351T	p.R451C
XH_P36	4	39458114	39458114	Nonsense_Mutation	INS	-	ACTTAAGGGTTT	-	RPL9	GATATAAACCTT01_N102delinsMIX	
XH_P36	4	39864524	39864524	Missense_Mutation	SNP	C	T	C	PDSSA	c.G2936A	p.R979H
XH_P36	4	41748011	41748028	In_Frame_Del	DEL	CCGCCGCTGG	-	GCCGCCGCTGCC	PHOX2B	c.741_758del	p.247_253del
XH_P36	4	47560133	47560133	Silent	SNP	G	A	G	ATP10D	c.G2277A	p.L759L
XH_P36	4	48622707	48622707	Missense_Mutation	SNP	G	A	G	FRYL	c.C263T	p.T88M
XH_P36	4	57179502	57179502	Frame_Shift_Ins	INS	-	A	-	KIAA1211	c.495dupA	p.P165fs
XH_P36	4	57889645	57889645	Frame_Shift_Ins	INS	-	ACCCCTATTCCA	-	POLR2B	AATCACACCTT	p.K814fs
XH_P36	4	68488908	68488908	Nonsense_Mutation	SNP	C	T	C	UBA6	c.G2873A	p.W958X

XH_P36	4	70146409	70146409	Frame_Shift_Ins	INS	-	CAAG	-	UGT2B28	191_192insCAA	p.F64fs
XH_P36	4	70146410	70146410	Frame_Shift_Ins	INS	-	CTTCTCATACT	-	UGT2B28	TGTTCTTTTCTC	p.F64fs
XH_P36	4	70720027	70720027	Nonsense_Mutation	INS	-	A	-	SULT1E1	c.276_277insT	K93_Q94delinsX
XH_P36	4	70720028	70720028	Frame_Shift_Ins	INS	-	TTTCATTGAATC	-	SULT1E1	TATAGATTCAAT	p.V92fs
XH_P36	4	71232641	71232641	In_Frame_Ins	INS	-	TGG	-	SMR3A	c.335_336insTGP	p.Y112delinsYG
XH_P36	4	71232643	71232643	Frame_Shift_Ins	INS	-	GGAGAATTCAA	-	SMR3A	insCAGGAGAGAA	p.P113fs
XH_P36	4	74021478	74021478	Nonsense_Mutation	INS	-	AAAGTGATGTTT	-	ANKRD17	1insCTAAACATC	177_A178delinsHX
XH_P36	4	77065318	77065318	Silent	SNP	C	T	C	NUP54	c.G279A	p.Q93Q
XH_P36	4	80905990	80905990	Frame_Shift_Del	DEL	C	-	C	ANTXR2	c.1069delG	p.A357fs
XH_P36	4	81791254	81791254	Frame_Shift_Del	DEL	A	-	A	C4orf22	c.441delA	p.G147fs
XH_P36	4	83989669	83989669	Frame_Shift_Ins	INS	-	TAAGTTAACTGG	-	COPS4	nsATTTTAAGTT	p.F361fs
XH_P36	4	88537426	88537426	Silent	SNP	T	C	T	DSPP	c.T3612C	p.S1204S
XH_P36	4	89653284	89653284	Silent	SNP	G	A	G	FAM13A	c.C1650T	p.T550T
XH_P36	4	90857025	90857025	Frame_Shift_Ins	INS	-	ATCATTTAGT	-	MMRN1	2195insATCAT	p.M732fs
XH_P36	4	90857027	90857027	In_Frame_Ins	INS	-	CTC	-	MMRN1	2196_2197insC	b.M732delinsML
XH_P36	4	95173909	95173909	Frame_Shift_Ins	INS	-	A	-	SMARCAD1	c.1033dupA	p.R344fs
XH_P36	4	95191919	95191919	Silent	SNP	C	T	C	SMARCAD1	c.C232T	p.L78L
XH_P36	4	100478535	100478535	Silent	SNP	G	A	G	TRMT10A	c.C387T	p.Y129Y
XH_P36	4	107156505	107156505	Frame_Shift_Del	DEL	T	-	T	TBCK	c.1181delA	p.N394fs
XH_P36	4	110972797	110972797	Nonsense_Mutation	INS	-	CT	-	ELOVL6	c.494_495insAGV	165_F166delinsX
XH_P36	4	110972799	110972799	In_Frame_Ins	INS	-	GCT	-	ELOVL6	c.492_493insAGV	W165delinsSW
XH_P36	4	114275990	114275990	Silent	SNP	C	A	C	ANK2	c.C6216A	p.S2072S
XH_P36	4	114275991	114275991	Frame_Shift_Ins	INS	-	TCCTCTCTGT	-	ANK2	6218insTCCTC	p.12073fs
XH_P36	4	114286281	114286281	Missense_Mutation	SNP	C	T	C	ANK2	c.C4720T	p.R1574C
XH_P36	4	119148049	119148049	Silent	SNP	C	T	C	NDST3	c.C1731T	p.C577C
XH_P36	4	120189503	120189503	Missense_Mutation	SNP	C	A	C	USP53	c.C1216A	p.Q406K
XH_P36	4	134071649	134071649	Frame_Shift_Del	DEL	C	-	C	PCDH10	c.354delC	p.L118fs
XH_P36	4	134072199	134072199	Missense_Mutation	SNP	G	A	G	PCDH10	c.G904A	p.G302R
XH_P36	4	134073341	134073341	Silent	SNP	C	A	C	PCDH10	c.C2046A	p.A682A
XH_P36	4	138442370	138442370	Missense_Mutation	SNP	C	T	C	PCDH18	c.G3218A	p.G1073E
XH_P36	4	138452170	138452170	Missense_Mutation	SNP	A	C	A	PCDH18	c.T1073G	p.L358R
XH_P36	4	145658978	145658978	Frame_Shift_Del	DEL	A	-	A	HHIP	c.1972delA	p.K658fs
XH_P36	4	153268210	153268210	Nonsense_Mutation	INS	-	GAAATGCCTCAC	-	FBXW7	4insAAGTGGAGG	V82_P83delinsKX
XH_P36	4	156643278	156643278	Frame_Shift_Ins	INS	-	TCTTAACCTCTTTT	-	GUCY1A3	6insACTTCTTAA	p.T602fs
XH_P36	4	159573185	159573185	Missense_Mutation	SNP	C	T	C	RXFP1	c.C2108T	p.T703M
XH_P36	4	166946559	166946559	Frame_Shift_Ins	INS	-	CTACAAGAATCC	-	TL11	nsAACTCTACAA	p.R378fs
XH_P36	4	183696222	183696222	Silent	SNP	C	T	C	TENM3	c.C5220T	p.G1740G
XH_P36	4	189022306	189022306	Missense_Mutation	SNP	C	A	C	TRIML2	c.G384T	p.Q128H
XH_P36	5	482774	482774	Silent	SNP	G	A	G	SLC9A3	c.C1245T	p.R415R
XH_P36	5	1212555	1212555	Missense_Mutation	SNP	G	A	G	SLC6A19	c.G619A	p.V207I
XH_P36	5	1882750	1882750	Silent	SNP	C	T	C	IRX4	c.G12A	p.P4P
XH_P36	5	5464054	5464054	Nonsense_Mutation	INS	-	TCTGCACACTGAA	-	ICE1	08insTATCTGAC	536_S1537delinsAIX
XH_P36	5	9190436	9190436	Nonsense_Mutation	SNP	C	T	C	SEMA5A	c.G1216A	p.A406T
XH_P36	5	15928091	15928091	Missense_Mutation	SNP	T	C	T	FBXL7	c.T79C	p.S27P
XH_P36	5	16179661	16179661	Silent	SNP	G	A	G	MARCH11	c.C24T	p.G8G
XH_P36	5	23526788	23526788	Frame_Shift_Ins	INS	-	TTCTTTGATCTCT	-	PRDM9	92insCTTCTTTG	p.Q531fs
XH_P36	5	24492973	24492973	Frame_Shift_Del	DEL	A	-	A	CDH10	c.1577delT	p.F526fs
XH_P36	5	26906213	26906213	In_Frame_Ins	INS	-	ACTTCTCAAATA	-	CDH9	5TAGTGTATTTG	222delinsPSVFEKFL
XH_P36	5	32091037	32091037	Missense_Mutation	SNP	A	G	A	PDZD2	c.A7483G	p.K2495E
XH_P36	5	32780891	32780891	Nonsense_Mutation	INS	-	TCCTAAATCTCT	-	NPR3	60insATTCTCTAA	M421delinsAFLNSX
XH_P36	5	36976160	36976160	In_Frame_Ins	INS	-	ATCTGGTGGAA	-	NIPBL	2insGATATCTGG	384delinsKISGTS
XH_P36	5	36985241	36985241	Frame_Shift_Ins	INS	-	GTGC	-	NIPBL	959_1960insGT	p.Q653fs
XH_P36	5	36985242	36985242	In_Frame_Ins	INS	-	CATTACATTGTTT	-	NIPBL	961insTCATTAC	N654delinsITLFD
XH_P36	5	37438050	37438050	Silent	SNP	G	A	G	WDR70	c.G453A	p.S151S
XH_P36	5	55237462	55237462	In_Frame_Ins	INS	-	CTACAATTAGTA	-	IL6ST	2022insTACTAA	S674delinsSTNCR
XH_P36	5	55237464	55237464	Nonsense_Mutation	INS	-	TCATGTAGATGG	-	IL6ST	2020insCCATCT	S674delinsSPSTX
XH_P36	5	56171053	56171053	Nonsense_Mutation	INS	-	CACACACGATG	-	MAP3K1	2insAAACACAC	7_S628delinsKHTRX
XH_P36	5	61847115	61847115	Frame_Shift_Del	DEL	T	-	T	IP011	c.C2532delT	p.S844fs
XH_P36	5	64867698	64867698	Missense_Mutation	SNP	G	A	G	PPWD1	c.G86A	p.C29Y
XH_P36	5	67589266	67589266	Nonsense_Mutation	INS	-	TACCTTAGTGTA	-	PIK3R1	TGGCTTACCTTA	K56delinsPWLTVX
XH_P36	5	68651571	68651571	In_Frame_Ins	INS	-	GTGTGTGTTTGT	-	AK6	ACAAAAACAAAC	74delinsETKQTTIF
XH_P36	5	68716041	68716041	Frame_Shift_Ins	INS	-	CGAC	-	MARVELD2	829_830insCGA	p.M277fs
XH_P36	5	68716042	68716042	Frame_Shift_Ins	INS	-	TCATGTAGGA	-	MARVELD2	831insTCATGT	p.M277fs
XH_P36	5	70766233	70766233	Frame_Shift_Del	DEL	T	-	T	BDP1	c.931delT	p.P311fs
XH_P36	5	71501039	71501039	Silent	SNP	C	A	C	MAP1B	c.C7002A	p.S2334S
XH_P36	5	71756466	71756466	Silent	SNP	G	A	G	ZNF366	c.C585T	p.C286C
XH_P36	5	74016556	74016556	Nonsense_Mutation	INS	-	TCTTAAATGTTA	-	HEXB	nsTTAATCTTAA	R533delinsLNSX
XH_P36	5	74134851	74134851	Missense_Mutation	SNP	T	C	T	FAM169A	c.A257G	p.Q86R
XH_P36	5	76358967	76358967	Frame_Shift_Del	DEL	A	-	A	AGGF1	c.2035delA	p.K679fs
XH_P36	5	79733694	79733694	Frame_Shift_Ins	INS	-	CATCTCTGAAT	-	ZFYVE16	AATTTTCATCTC	p.F397fs
XH_P36	5	82816284	82816284	Missense_Mutation	SNP	T	A	T	VCAN	c.T2159A	p.V720D
XH_P36	5	82834130	82834130	Frame_Shift_Ins	INS	-	TGGTGAACATT	-	VCAN	2348insTGGTG	p.R783fs
XH_P36	5	89939712	89939712	In_Frame_Ins	INS	-	AGAGGTGGTAT	-	ADGRV1	5ACAAAAGAGG	72delinsKGQKRWYHFF
XH_P36	5	96062499	96062499	Missense_Mutation	SNP	C	T	C	CAST	c.C23T	p.A8V
XH_P36	5	96443159	96443159	Missense_Mutation	SNP	C	T	C	LIX1	c.G292A	p.A98T
XH_P36	5	102895168	102895168	Frame_Shift_Ins	INS	-	TT	-	NUDT12	c.153_154insAA	p.C52fs
XH_P36	5	102895169	102895169	Nonsense_Mutation	INS	-	ATTGGTTAGGAA	-	NUDT12	CTTGGTTCTCTAA	M51delinsISLGSX
XH_P36	5	111504782	111504782	In_Frame_Ins	INS	-	TACAGTTCATCA	-	EPB41L4A	1760insTGATGA	R587delinsLMNCS
XH_P36	5	111504784	111504784	Frame_Shift_Ins	INS	-	TTAGTAATAGT	-	EPB41L4A	1758insACTAT	p.I586fs
XH_P36	5	112769886	112769886	Silent	SNP	G	A	G	TSK1B	c.C651T	p.D217D
XH_P36	5	118324039	118324039	Missense_Mutation	SNP	C	A	C	DTWD2	c.G168T	p.W56C
XH_P36	5	121413097	121413097	Missense_Mutation	SNP	G	T	G	LOX	c.C584A	p.P195H
XH_P36	5	134050742	134050742	Missense_Mutation	SNP	G	A	G	SEC24A	c.G2756A	p.R919H
XH_P36	5	134364858	134364858	Missense_Mutation	SNP	C	T	C	PITX1	c.G556A	p.A186T
XH_P36	5	134367131	134367131	Silent	SNP	G	A	G	PITX1	c.C237T	p.G79G
XH_P36	5	137523102	137523102	Nonstop_Mutation	SNP	A	C	A	KIF20A	c.A2673C	p.X891Y
XH_P36	5	138265000	138265000	Silent	SNP	C	T	C	CTNNA1	c.C516T	p.S172S
XH_P36	5	140047894	140047894	Silent	SNP	T	C	T	WDR55	c.T267C	p.A89A
XH_P36	5	140049102	140049102	Frame_Shift_Del	DEL	A	-	A	WDR55	c.1015delA	p.K339fs
XH_P36	5	140207965	140207965	Missense_Mutation	SNP	G	C	G	PCDHA6	c.G289C	p.G97R
XH_P36	5	140230590	140230590	Frame_Shift_Del	DEL	T	-	T	PCDHA9	c.2510delT	p.I837fs
XH_P36	5	140237134	140237134	Missense_Mutation	SNP	C	T	C	PCDHA10	c.C1501T	p.R501C
XH_P36	5	140475658	140475658	Missense_Mutation	SNP	C	G	C	PCDHB2	c.C1284G	p.F428L
XH_P36	5	140595217	140595217	Missense_Mutation	SNP	G	A	G	PCDHB13	c.G1522A	p.A508T
XH_P36	5	140604336	140604336	Missense_Mutation	SNP	C	T	C	PCDHB14	c.C1259T	p.T420M
XH_P36	5	140683367	140683367	Silent	SNP	C	T	C	SLC25A2	c.G66A	p.A22A
XH_P36	5	140769366	140769366	Missense_Mutation	SNP	C	T	C	PCDHGB4	c.C1915T	p.R639C
XH_P36	5	140778721	140778721	Nonsense_Mutation	INS	-	GCTGACTC	-	PCDHGB5	7_1028insGCTG	343_T344delinsGX

XH_P36	5	140953309	140953309	Frame_Shift_Del	DEL	G	-	G	DIAPH1	c.2081delC	p.P694fs
XH_P36	5	140953564	140953569	In_Frame_Del	DEL	GGAGGA	-	GGAGGA	DIAPH1	c.1821_1826del	p.607_609del
XH_P36	5	143586393	143586393	Missense_Mutation	SNP	G	A	G	KCTD16	c.G116A	p.R39H
XH_P36	5	145547779	145547779	Frame_Shift_Del	DEL	G	-	G	LARS	c.182delC	p.L61fs
XH_P36	5	146754725	146754725	Frame_Shift_Del	DEL	A	-	A	STK32A	c.976delA	p.K326fs
XH_P36	5	147861099	147861099	Frame_Shift_Del	DEL	T	-	T	HTRA	c.1170delA	p.K390fs
XH_P36	5	148407222	148407222	Silent	SNP	G	T	G	SH3TC2	c.C2073A	p.A691A
XH_P36	5	149460507	149460507	Missense_Mutation	SNP	C	A	C	CSF1R	c.G130T	p.G44C
XH_P36	5	149602668	149602668	Silent	SNP	G	A	G	CAMK2A	c.C1317T	p.D439D
XH_P36	5	149901203	149901203	Silent	SNP	C	T	C	NDST1	c.C387T	p.G129G
XH_P36	5	154173390	154173390	Frame_Shift_Del	DEL	C	-	C	LARP1	c.668delC	p.A223fs
XH_P36	5	158139199	158139199	Silent	SNP	G	T	G	EBF1	c.C1419A	p.T473T
XH_P36	5	162917426	162917426	Frame_Shift_Del	DEL	A	-	A	HMMR	c.1732delA	p.K578fs
XH_P36	5	167841357	167841357	Missense_Mutation	SNP	G	A	G	WWC1	c.G946A	p.A316T
XH_P36	5	168098430	168098430	Silent	SNP	G	A	G	SLIT3	c.C3921T	p.G1307G
XH_P36	5	168149299	168149299	Frame_Shift_Del	DEL	G	-	G	SLIT3	c.2445delC	p.P815fs
XH_P36	5	169129368	169129368	Missense_Mutation	SNP	G	T	G	DOCK2	c.G1320T	p.K440N
XH_P36	5	171523524	171523524	Missense_Mutation	SNP	C	T	C	STK10	c.G911A	p.R304Q
XH_P36	5	171638950	171638950	Frame_Shift_Del	DEL	A	-	A	UBTD2	c.589delT	p.S197fs
XH_P36	5	171765667	171765667	Silent	SNP	G	A	G	SH3PXD2B	c.C2442T	p.G814G
XH_P36	5	174868783	174868783	In_Frame_Ins	INS	-	AAATACATTCC	-	DRD1	20insCTGGAAT	440delinsHWNVFG
XH_P36	5	174869195	174869195	In_Frame_Ins	INS	-	ATGTTT	-	DRD1	07_908insAAACb	T303delinsKTS
XH_P36	5	17575279	17575279	Silent	SNP	C	T	C	KIAA1191	c.G297A	p.P99P
XH_P36	5	175843200	175843200	Silent	SNP	C	T	C	CLTB	c.G165A	p.A55A
XH_P36	5	176813456	176813456	Missense_Mutation	SNP	G	A	G	SLC34A1	c.G421A	p.A141T
XH_P36	5	176863433	176863433	Frame_Shift_Del	DEL	G	-	G	GRK6	c.1306delG	p.G436fs
XH_P36	5	176885292	176885292	Missense_Mutation	SNP	C	T	C	DBN1	c.G1543A	p.V515M
XH_P36	5	177548988	177548988	Missense_Mutation	SNP	T	C	T	N4BP3	c.T1621C	p.S541P
XH_P36	5	178309945	178309945	In_Frame_Ins	INS	-	ATTTTAGGTGTG	-	ZNF354B	493insATTTT	G164delinsGILGV
XH_P36	5	178460353	178460353	Frame_Shift_Ins	INS	-	TTCTTTGCATGC	-	ZNF879	405insATTTCTTT	p.H468fs
XH_P36	5	179151749	179151749	Frame_Shift_Ins	INS	-	TACATGTTTCATG	-	CANX	TTTTGTTTACATG	p.K537fs
XH_P36	6	15374448	15374448	Missense_Mutation	SNP	C	T	C	JARID2	c.C146T	p.A49V
XH_P36	6	21594968	21594968	Missense_Mutation	SNP	T	C	T	SOX4	c.T203C	p.V68A
XH_P36	6	22290504	22290504	Missense_Mutation	SNP	G	A	G	PRL	c.C391T	p.R131C
XH_P36	6	24576806	24576806	Nonsense_Mutation	INS	-	SCCTTCAGACTT	-	KIAA0319	89insAAAAGCTC	S463delinsSKVX
XH_P36	6	25606400	25606400	Nonsense_Mutation	INS	-	TAAGAGTATTT	-	CARMIL1	5ATGTTTTAAGA	3_S1244delinsSRMF
XH_P36	6	25606402	25606402	Missense_Mutation	SNP	A	T	A	CARMIL1	c.A3730T	p.S1244C
XH_P36	6	25799032	25799032	Missense_Mutation	SNP	T	C	T	SLC17A1	c.A1385G	p.K462R
XH_P36	6	27861432	27861432	Missense_Mutation	SNP	C	A	C	HIST1H2BO	c.C192A	p.N64K
XH_P36	6	28212908	28212908	Frame_Shift_Del	DEL	T	-	T	ZKSCAN4	c.1159delA	p.T387fs
XH_P36	6	28359148	28359148	Frame_Shift_Ins	INS	-	AAAAATGCTAT	-	ZSCAN12	9insCTGATAGCA	p.C307fs
XH_P36	6	33653236	33653236	Missense_Mutation	SNP	C	T	C	ITPR3	c.C5408T	p.T1803M
XH_P36	6	35426163	35426163	Silent	SNP	T	C	T	FANCE	c.T1059C	p.P353P
XH_P36	6	36931061	36931061	Nonsense_Mutation	INS	-	GAGTCTGATGC	-	PI16	944insGAGTCTC	15_P316delinsRVX
XH_P36	6	41652798	41652798	Nonsense_Mutation	SNP	G	A	G	TFEB	c.C715T	p.R239X
XH_P36	6	42073370	42073372	In_Frame_Del	DEL	AGG	-	AGG	C6orf132	c.2278_2280del	p.760_760del
XH_P36	6	42235991	42235991	Missense_Mutation	SNP	G	C	G	TRERF1	c.C1338G	p.S446R
XH_P36	6	42237313	42237313	Missense_Mutation	SNP	G	T	G	TRERF1	c.C16A	p.L6M
XH_P36	6	43307375	43307375	Frame_Shift_Ins	INS	-	AGTGAGA	-	ZNF318	60_4361insTCTC	p.P1454fs
XH_P36	6	43418816	43418816	Missense_Mutation	SNP	C	T	C	DLK2	c.G502A	p.A168T
XH_P36	6	44223300	44223300	Missense_Mutation	SNP	G	A	G	SLC35B2	c.C43T	p.R15C
XH_P36	6	44269193	44269193	Frame_Shift_Del	DEL	C	-	C	AARS2	c.2607delG	p.K869fs
XH_P36	6	46111312	46111312	Nonsense_Mutation	INS	-	TAGGACAAAATA	-	ENPP4	298insTTAGGAC	3_V434delinsFRTXK
XH_P36	6	46111314	46111314	Frame_Shift_Ins	INS	-	TGCTTCTA	-	ENPP4	9_1300insTGCT	p.S433fs
XH_P36	6	46826739	46826739	Frame_Shift_Del	DEL	C	-	C	ADGRF5	c.2901delG	p.G967fs
XH_P36	6	51947326	51947326	Nonsense_Mutation	INS	-	CGGAGGATGAC	-	PKHD1	insACTCTCATCC	V49delinsTLRX
XH_P36	6	52343894	52343894	Silent	SNP	C	T	C	EFHC1	c.C1338T	p.T446T
XH_P36	6	53363590	53363590	Silent	SNP	T	C	T	GLCL	c.A1764G	p.V588V
XH_P36	6	56480539	56480539	In_Frame_Ins	INS	-	TCTTCCTAA	-	DST	7726insTTAGD	12576delinsLGR1
XH_P36	6	56480541	56480541	In_Frame_Ins	INS	-	GGACATGTTTAA	-	DST	7724insTTAAAC	2575delinsFKHVP
XH_P36	6	62995837	62995837	Missense_Mutation	SNP	T	C	T	KHDRB52	c.A17G	p.Y6C
XH_P36	6	64395565	64395565	Nonsense_Mutation	INS	-	TTTTTCACAGAT	-	PHF3	943insGTTTTTTC	E648delinsGFSQIX
XH_P36	6	66012756	66012756	Missense_Mutation	SNP	G	T	G	LOC441155	c.G342T	p.K141N
XH_P36	6	73952255	73952255	Splice_Site	INS	-	TCATCA	-	KHDC1	-	-
XH_P36	6	76660622	76660622	Nonsense_Mutation	INS	-	CTTTGTTGTTAT	-	IMP1	ATAAAAAACAA	416_G417delinsQX
XH_P36	6	79675743	79675743	Missense_Mutation	SNP	G	A	G	PHIP	c.C2326T	p.A1079V
XH_P36	6	80197020	80197020	Frame_Shift_Ins	INS	-	GTGAAGGAAGA	-	LCA5	795insCTTCTTC	p.E599fs
XH_P36	6	80751910	80751910	Frame_Shift_Del	DEL	A	-	A	TTK	c.2562delA	p.G854fs
XH_P36	6	83847704	83847704	Frame_Shift_Ins	INS	-	TTAATCGTCTCT	-	DOPEY1	17insTTTTTAATC	p.N1306fs
XH_P36	6	85446693	85446693	In_Frame_Ins	INS	-	ACATATTTCTTT	-	TBX18	8AGAAAAAGAA	12delinsRKRYVRQ
XH_P36	6	85446694	85446694	Missense_Mutation	SNP	G	T	G	TBX18	c.C1533A	p.N511K
XH_P36	6	86324630	86324630	Frame_Shift_Ins	INS	-	TTCCCTTATGTG	-	SYNCRIP	ATATATACATA	p.Q537fs
XH_P36	6	88318837	88318837	Frame_Shift_Ins	INS	-	A	-	ORC3	c.175dupA	p.S58fs
XH_P36	6	89793782	89793782	Frame_Shift_Ins	INS	-	A	-	PNRC1	c.851_852insA	p.F284fs
XH_P36	6	89793784	89793784	Frame_Shift_Ins	INS	-	TTCTGTCTGTTT	-	PNRC1	TGCTTTTCTGTC	p.S285fs
XH_P36	6	90459404	90459404	Frame_Shift_Ins	INS	-	ATAGTAAGAATG	-	MDN1	AACATTTTCATTC	p.T1158fs
XH_P36	6	102074256	102074256	Silent	SNP	C	A	C	GRIK2	c.C285A	p.S167fs
XH_P36	6	116263666	116263666	Nonsense_Mutation	SNP	G	A	G	FRK	c.C1429T	p.R477X
XH_P36	6	116720492	116720492	Missense_Mutation	SNP	G	A	G	DSE	c.G79A	p.E27K
XH_P36	6	116938286	116938286	Frame_Shift_Ins	INS	-	GTCTTGT	-	RSPH4A	00_501insGTCT	p.S167fs
XH_P36	6	117609822	117609822	In_Frame_Ins	INS	-	TTGGTTTTCAGT	-	ROS1	77insCAACTGA	2293delinsQLKPN
XH_P36	6	118229019	118229019	Frame_Shift_Ins	INS	-	C	-	SLC35F1	c.131dupC	p.S44fs
XH_P36	6	128403762	128403762	Frame_Shift_Ins	INS	-	TTACAAATAGGA	-	PTPRK	nsATCAATCCTAT	p.S404fs
XH_P36	6	130031231	130031231	Frame_Shift_Del	DEL	G	-	G	ARHGAP18	c.S1delC	p.P17fs
XH_P36	6	134323264	134323264	Missense_Mutation	SNP	A	C	A	SLC2A12	c.T1571G	p.L524R
XH_P36	6	136599393	136599393	Missense_Mutation	SNP	G	A	G	BCLAF1	c.C620T	p.S207f
XH_P36	6	139097330	139097330	Frame_Shift_Del	DEL	A	-	A	CCDC28A	c.343delA	p.K115fs
XH_P36	6	142409404	142409404	Missense_Mutation	SNP	A	G	A	NMBR	c.T392C	p.V131A
XH_P36	6	142711439	142711439	Missense_Mutation	SNP	C	T	C	ADGRG6	c.C1183T	p.R395C
XH_P36	6	146988003	146988003	Silent	SNP	G	A	G	ADGB	c.G804A	p.A268A
XH_P36	6	147136338	147136338	In_Frame_Ins	INS	-	TTCTTTACCTT	-	ADGB	4990insTTCTCTT	K1663delinsKFLYP
XH_P36	6	155153431	155153431	Frame_Shift_Ins	INS	-	G	-	SCAF8	c.2718_2719ins	p.Q096fs
XH_P36	6	155153432	155153432	Frame_Shift_Ins	INS	-	ATTTTCAGAAAT	-	SCAF8	2720insATTTTC	p.N907fs
XH_P36	6	155571012	155571012	Missense_Mutation	SNP	C	T	C	TIAM2	c.C635T	p.A212V
XH_P36	6	158508008	158508008	Frame_Shift_Ins	INS	-	C	-	SYNJ2	c.2620dupC	p.R873fs
XH_P36	6	158900956	158900956	Frame_Shift_Ins	INS	-	C	-	TULP4	c.1201dupC	p.A400fs
XH_P36	6	160679514	160679514	Silent	SNP	G	A	G	SLC22A2	c.C276T	p.Y92Y
XH_P36	6	163149397	163149397	Missense_Mutation	SNP	G	T	G	PACRG	c.G130T	p.V44F

XH_P36	6	170110415	170110415	Missense_Mutation	SNP	G	T	G	PHF10	c.C1030A	p.Q344K	
XH_P36	6	170110416	170110416	Nonsense_Mutation	INS	-	TTTGCTTTATTC	-	PHF10	029insGAAATAA43	Q344delinsRXX	
XH_P36	7	1482030	1482030	Silent	SNP	C	T	C	MICALL2	c.G1509A	p.S503S	
XH_P36	7	4841442	4841442	Frame_Shift_Del	DEL	G	-	G	RADIL	c.2684delC	p.P895fs	
XH_P36	7	4862166	4862166	Missense_Mutation	SNP	C	T	C	RADIL	c.G1474A	p.A492T	
XH_P36	7	5780887	5780887	Missense_Mutation	SNP	C	T	C	RNF216	c.G761A	p.R254Q	
XH_P36	7	5781027	5781027	Frame_Shift_Ins	INS	-	GTAGCAAGTG	-	RNF216	521instCACTTG	p.E207fs	
XH_P36	7	6502731	6502731	Missense_Mutation	SNP	G	A	G	KDEL2	c.C427T	p.R143W	
XH_P36	7	6662266	6662266	Missense_Mutation	SNP	G	T	G	ZNF853	c.G1644T	p.K548N	
XH_P36	7	7612451	7612451	Frame_Shift_Ins	INS	-	TCTATCAACATG	-	MIOS	46insATCATCA	p.Q115fs	
XH_P36	7	12420215	12420215	Frame_Shift_Ins	INS	-	TATTTTCTTTTT	-	VWDE	AAAAAAG	p.R229fs	
XH_P36	7	13975433	13975433	Frame_Shift_Ins	INS	-	GTATTTATAA	-	ETV1	insATGTTTATA	p.S94fs	
XH_P36	7	23728890	23728890	Missense_Mutation	SNP	A	T	A	FAM221A	c.A68T	p.Y23F	
XH_P36	7	24932053	24932053	Frame_Shift_Del	DEL	T	-	T	OSBPL3	c.39delA	p.K13fs	
XH_P36	7	27183075	27183075	Missense_Mutation	SNP	C	T	C	HOXA5	c.G152A	p.G51D	
XH_P36	7	30705147	30705147	Missense_Mutation	SNP	G	A	G	CHRR2	c.C421T	p.R141W	
XH_P36	7	31682378	31682378	Missense_Mutation	SNP	C	T	C	CCDC129	c.C1394T	p.5465F	
XH_P36	7	31793063	31793063	Missense_Mutation	SNP	T	C	T	PDE1C	c.A2065G	p.M689V	
XH_P36	7	37889877	37889877	Frame_Shift_Ins	INS	-	A	-	NME8	c.10dupA	p.S3fs	
XH_P36	7	44560659	44560659	Silent	SNP	C	T	C	NPC1L1	c.G3012A	p.S1004S	
XH_P36	7	45124001	45124001	Missense_Mutation	SNP	T	C	T	NACAD	c.A1778G	p.D593G	
XH_P36	7	45141471	45141471	Missense_Mutation	SNP	G	A	G	TBRG4	c.C1190T	p.A397V	
XH_P36	7	53103788	53103788	Missense_Mutation	SNP	G	A	G	POM121L12	c.G424A	p.A142T	
XH_P36	7	56156631	56156631	Missense_Mutation	SNP	T	C	T	PHKG1	c.A4G	p.T2A	
XH_P36	7	57528754	57528754	In_Frame_Ins	INS	-	ATCTTCTCA	-	ZNF716	7_588insATCTTC	M196delinsSSQ	
XH_P36	7	57528755	57528755	Nonsense_Mutation	INS	-	ACTTTTGGAGT	-	ZNF716	5TATCACTTTTTC	L197delinsMYHFLEX	
XH_P36	7	63674391	63674391	Missense_Mutation	SNP	G	A	G	ZNF735	c.G167A	p.G56D	
XH_P36	7	64451956	64451956	Nonsense_Mutation	SNP	C	T	C	ERV3-1	c.G1449A	p.W483X	
XH_P36	7	70255576	70255576	In_Frame_Ins	INS	-	CCA	-	AUTS2	3302_3303insC	S1101delinsSH	
XH_P36	7	70597900	70597900	Missense_Mutation	SNP	G	A	G	GALNT17	c.G112A	p.A38T	
XH_P36	7	72436399	72436399	Missense_Mutation	SNP	C	T	C	TRIM74	c.G290A	p.S97N	
XH_P36	7	73814818	73814818	Missense_Mutation	SNP	C	T	C	CLIP2	c.C2894T	p.A965V	
XH_P36	7	77379007	77379007	Frame_Shift_Ins	INS	-	TTCTTTTCTCT	-	RSBN1L	instTTTTTCTTTT	p.P324fs	
XH_P36	7	77379009	77379009	Silent	SNP	A	C	A	RSBN1L	c.A972C	p.P324P	
XH_P36	7	77408086	77408086	Silent	SNP	C	T	C	RSBN1L	c.C2142T	p.S714S	
XH_P36	7	86813908	86813908	Nonsense_Mutation	INS	-	ACCCTCTGGT	-	DMTF1	753insACCCTC	V251_T252delinsX	
XH_P36	7	89939531	89939531	Frame_Shift_Del	DEL	A	-	A	CFAP69	c.2805delA	p.P935fs	
XH_P36	7	91631743	91631743	Frame_Shift_Ins	INS	-	A	-	AKAP9	c.2513dupA	p.Q838fs	
XH_P36	7	91631745	91631745	Frame_Shift_Ins	INS	-	GTTTTCTTTTCA	-	AKAP9	515insGGTTTTC	p.Q838fs	
XH_P36	7	94037202	94037202	Missense_Mutation	SNP	C	G	C	COL1A2	c.C638G	p.T213R	
XH_P36	7	94919558	94919558	Nonsense_Mutation	INS	-	AACTAGTTACAT	-	PPP1R9A	8217insAACTAG	072_S1073delinsKNX	
XH_P36	7	94919560	94919560	Missense_Mutation	SNP	C	G	C	PPP1R9A	c.C3218G	p.S1073C	
XH_P36	7	99621198	99621198	Silent	SNP	C	T	C	ZKSCAN1	c.C69T	p.I23I	
XH_P36	7	99758575	99758575	Frame_Shift_Ins	INS	-	TTCCCCAGA	-	GAL3ST4	437insTCTGGG	p.Q146fs	
XH_P36	7	100451920	100451920	Missense_Mutation	SNP	C	T	C	SLC12A9	c.C101T	p.A34V	
XH_P36	7	100552727	100552727	Missense_Mutation	SNP	G	T	G	MUC3A	c.G3308T	p.R1103L	
XH_P36	7	100641373	100641373	Missense_Mutation	SNP	G	A	G	MUC12	c.G7529A	p.S2510N	
XH_P36	7	100676246	100676246	Missense_Mutation	SNP	T	C	T	MUC17	c.T1549C	p.S517P	
XH_P36	7	100677523	100677523	Missense_Mutation	SNP	A	C	A	MUC17	c.A2826C	p.R942S	
XH_P36	7	100677944	100677944	Missense_Mutation	SNP	T	C	T	MUC17	c.T3247C	p.S1083P	
XH_P36	7	100681171	100681171	Missense_Mutation	SNP	C	A	C	MUC17	c.C6474A	p.D2158E	
XH_P36	7	100681172	100681172	Missense_Mutation	SNP	A	G	A	MUC17	c.A6475G	p.R2159G	
XH_P36	7	100681278	100681278	Missense_Mutation	SNP	A	C	A	MUC17	c.A6581C	p.N2194T	
XH_P36	7	100683382	100683382	Silent	SNP	T	C	T	MUC17	c.T8685C	p.D2895D	
XH_P36	7	100683723	100683723	Missense_Mutation	SNP	G	C	G	MUC17	c.G9026C	p.R3009T	
XH_P36	7	100730930	100730930	Frame_Shift_Del	DEL	G	-	G	TRIM56	c.337delG	p.G113fs	
XH_P36	7	100816663	100816663	Missense_Mutation	SNP	G	A	G	NAT16	c.C451T	p.H151Y	
XH_P36	7	102964991	102964991	Frame_Shift_Ins	INS	-	T	-	DNAJC2	c.590dupA	p.N197fs	
XH_P36	7	107234511	107234511	Nonsense_Mutation	INS	-	TCTATAATGGG	-	BCAP29	5GTGCTCATATA	N103delinsSRCSINGHX	
XH_P36	7	112407656	112407656	Missense_Mutation	SNP	T	C	T	TMEM168	c.A1690G	p.I564V	
XH_P36	7	116397525	116397525	Missense_Mutation	SNP	C	T	C	MET	c.C607T	p.H203Y	
XH_P36	7	117397929	117397929	Missense_Mutation	SNP	C	A	C	CTTNBP2	c.G3268T	p.G1090C	
XH_P36	7	122033359	122033359	Nonsense_Mutation	INS	-	TTATTTGAGTTT	-	CADPS2	CTTAAAAACCTCA	A971_S972delinsX	
XH_P36	7	127978355	127978355	Missense_Mutation	SNP	G	T	G	RBM28	c.C490A	p.L164I	
XH_P36	7	128455922	128455922	Silent	SNP	C	T	C	CCDC136	c.C3300T	p.D1100D	
XH_P36	7	128485259	128485259	Missense_Mutation	SNP	C	T	C	FLNC	c.C3740T	p.A1247V	
XH_P36	7	128502976	128502976	Silent	SNP	G	A	G	ATP6V1F	c.G18A	p.K6K	
XH_P36	7	130040097	130040097	Splice_Site	INS	-	GATAATGTTTGG	-	CEP41	.	.	
XH_P36	7	131012702	131012702	Missense_Mutation	SNP	T	G	T	MKLN1	c.T44G	p.L15R	
XH_P36	7	131831415	131831415	Missense_Mutation	SNP	G	A	G	PLXNA4	c.C4909T	p.R1637W	
XH_P36	7	137569816	137569816	Missense_Mutation	SNP	C	T	C	CREB3L2	c.G1006A	p.G336R	
XH_P36	7	138363260	138363260	Silent	SNP	C	T	C	SVOLP	c.G93A	p.T31T	
XH_P36	7	139724377	139724377	Missense_Mutation	SNP	A	T	A	PARP12	c.T2089A	p.F697I	
XH_P36	7	141631618	141631618	Frame_Shift_Ins	INS	-	TTTATAAATG	-	CLECSA	AGAAAACATTTA	p.L95fs	
XH_P36	7	141750074	141750074	In_Frame_Ins	INS	-	CCTATGGATG	-	MGAM	nsCTTTTCTTAT	76delinsFSLWMNN	
XH_P36	7	141795497	141795497	Missense_Mutation	SNP	C	T	C	MGAM	c.C4903T	p.R1635W	
XH_P36	7	141920186	141920186	Missense_Mutation	SNP	G	A	G	MGAM2	c.G5875A	p.D1959N	
XH_P36	7	142565462	142565462	Missense_Mutation	SNP	C	T	C	EPHB6	c.C971T	p.A324V	
XH_P36	7	150325284	150325284	Missense_Mutation	SNP	C	T	C	GIMAP6	c.G178A	p.V60I	
XH_P36	7	150417615	150417615	Missense_Mutation	SNP	C	T	C	GIMAP1	c.C523T	p.R175C	
XH_P36	7	150761288	150761288	Splice_Site	SNP	G	A	G	SLC4A2	.	.	
XH_P36	7	151874148	151874148	Frame_Shift_Del	DEL	T	-	T	KMT2C	c.8390delA	p.K2797fs	
XH_P36	7	151875020	151875020	Frame_Shift_Ins	INS	-	GGCCAGACTT	-	KMT2C	7518insAAGTC	p.Q2506fs	
XH_P36	7	151945313	151945313	Silent	SNP	A	G	A	KMT2C	c.T2206C	p.L736L	
XH_P36	7	152345760	152345760	Frame_Shift_Del	DEL	A	-	A	XRCC2	c.810delT	p.F270fs	
XH_P36	7	158527147	158527147	Missense_Mutation	SNP	C	T	C	ESYT2	c.G2602A	p.A868T	
XH_P36	7	158937413	158937413	Frame_Shift_Del	DEL	G	-	G	VIPR2	c.S1delC	p.P17fs	
XH_P36	8	2813125	2813125	Missense_Mutation	SNP	G	A	G	CSMD1	c.C9980T	p.S3327L	
XH_P36	8	2824227	2824227	Missense_Mutation	SNP	T	A	T	CSMD1	c.A8965T	p.I2989F	
XH_P36	8	3226804	3226804	Silent	SNP	C	G	C	CSMD1	c.G2871C	p.T957T	
XH_P36	8	3265726	3265726	Missense_Mutation	SNP	G	A	G	CSMD1	c.C1766T	p.T589M	
XH_P36	8	6289099	6289099	Frame_Shift_Del	DEL	A	-	A	MCPI1	c.313delA	p.K105fs	
XH_P36	8	7806651	7806651	Missense_Mutation	SNP	G	A	G	ZNF705B	c.G13A	p.E5K	
XH_P36	8	8234868	8234868	In_Frame_Ins	INS	-	GCCACT	-	PRAG1	50_1051insAGT	A351delinsSGA	
XH_P36	8	9953753	9953753	Splice_Site	SNP	G	A	G	MSRA	.	.	
XH_P36	8	10755632	10755632	Missense_Mutation	SNP	T	C	T	XKR6	c.A1756G	p.S586E	
XH_P36	8	15998555	15998555	Splice_Site	INS	-	ATGCTCATACCT	-	MSR1	.	.	
XH_P36	8	17402081	17402081	Frame_Shift_Del	DEL	T	-	T	SLC7A2	c.498delT	p.D166fs	

XH_P36	8	21981180	21981180	Missense_Mutation	SNP	G	A	G	HR	c.C1897T	p.R633W
XH_P36	8	22548022	22548022	Frame_Shift_Del	DEL	G	-	G	EGR3	c.1014delC	p.P338fs
XH_P36	8	23560102	23560102	Silent	SNP	G	A	G	NKX2-6	c.C768T	p.Y256Y
XH_P36	8	36644913	36644913	Frame_Shift_Ins	INS	-	ATATTTCAATAA	-	KCNU1	ATTCAATATTTC	p.195fs
XH_P36	8	37553551	37553551	Silent	SNP	C	T	C	ZNF703	c.C54T	p.S18S
XH_P36	8	37822872	37822872	Silent	SNP	G	A	G	ADR83	c.C1116T	p.C372C
XH_P36	8	38186894	38186894	Splice_Site	SNP	A	G	A	NSD3	.	.
XH_P36	8	38205127	38205127	Nonsense_Mutation	INS	-	TTGATGACCTCG	-	NSD3	insAACCCAGGCT	p.188delinsX
XH_P36	8	38874860	38874860	Missense_Mutation	SNP	C	A	C	ADAM9	c.C533A	p.S178Y
XH_P36	8	42040260	42040260	Silent	SNP	G	A	G	PLAT	c.C513T	p.G171G
XH_P36	8	43037381	43037381	Missense_Mutation	SNP	C	A	C	HGSNAT	c.C1106A	p.P369H
XH_P36	8	61736495	61736495	Missense_Mutation	SNP	C	T	C	CHD7	c.C3298T	p.R1100C
XH_P36	8	67417717	67417717	Silent	SNP	C	T	C	C8orf46	c.C234T	p.T78T
XH_P36	8	67873649	67873649	Missense_Mutation	SNP	C	T	C	TCF24	c.G352A	p.G118S
XH_P36	8	68151020	68151020	Missense_Mutation	SNP	T	C	T	ARFGF1	c.A3088G	p.I1030V
XH_P36	8	72951256	72951256	Nonsense_Mutation	INS	-	ATCAGGACTTTA	-	TRPA1	TTATAATAAAG	p.13delinsAGVLY
XH_P36	8	77619814	77619814	Missense_Mutation	SNP	C	T	C	ZFX4	c.C2624T	p.A875V
XH_P36	8	86019547	86019547	Missense_Mutation	SNP	C	T	C	LRRCC1	c.C17T	p.A6V
XH_P36	8	92030736	92030736	Missense_Mutation	SNP	C	T	C	TMEM55A	c.G368A	p.R123Q
XH_P36	8	95895095	95895095	Nonsense_Mutation	INS	-	TGCTTTAAGAGT	-	CCNE2	AAAGAACTCTTA	p.287delinsKSQRTKLAELX
XH_P36	8	98703408	98703408	Frame_Shift_Ins	INS	-	ATGATTGCTTGA	-	MTDH	ATTTCATGATT	p.S347fs
XH_P36	8	99146236	99146236	Silent	SNP	G	A	G	POP1	c.G795A	p.A265A
XH_P36	8	100789078	100789078	Nonsense_Mutation	INS	-	CCACTGCTCGCT	-	VPS13B	ACTTTGCCACTG	p.246delinsRVDSCTPGX
XH_P36	8	100831011	100831011	Missense_Mutation	SNP	G	T	G	VPS13B	c.G8591T	p.R2864M
XH_P36	8	104897908	104897908	Nonsense_Mutation	SNP	C	T	C	RIMS2	c.C505T	p.R169X
XH_P36	8	105361517	105361517	Nonsense_Mutation	INS	-	GGAGAC	-	DCSTAMP	37_738insGGAG	p.Y246delinsX
XH_P36	8	105361519	105361519	Missense_Mutation	SNP	A	T	A	DCSTAMP	c.A739T	p.I247F
XH_P36	8	105521191	105521191	Missense_Mutation	SNP	T	G	T	LRP12	c.A191C	p.N64T
XH_P36	8	108970494	108970494	Frame_Shift_Ins	INS	-	AAAAA	-	RSPO2	228_229insTTT	p.G77fs
XH_P36	8	108970495	108970495	In_Frame_Ins	INS	-	AAGTATTTA	-	RSPO2	7_228insTAAAT	p.E76delinsDKVYL
XH_P36	8	110457532	110457532	Frame_Shift_Ins	INS	-	AACTT	-	PKHD1L1	434_543insAA	p.V1812fs
XH_P36	8	110464995	110464995	Frame_Shift_Ins	INS	-	G	-	PKHD1L1	c.6557dupG	p.W2186fs
XH_P36	8	110478806	110478806	Splice_Site	SNP	G	T	G	PKHD1L1	.	.
XH_P36	8	110587336	110587336	Silent	SNP	G	A	G	SYBU	c.C1401T	p.G467G
XH_P36	8	110986446	110986446	Missense_Mutation	SNP	A	T	A	KCNV1	c.T172A	p.S58T
XH_P36	8	125326260	125326260	Missense_Mutation	SNP	A	G	A	TMEM65	c.T664C	p.F222L
XH_P36	8	125989809	125989809	In_Frame_Ins	INS	-	TTGATAAGG	-	ZNF572	9_1300insTTGAT	p.1433delinsTLIR
XH_P36	8	125989810	125989810	In_Frame_Ins	INS	-	TTTCTCTGTATC	-	ZNF572	301insTTTCTCTC	p.434delinsLFCMY
XH_P36	8	128750864	128750864	Missense_Mutation	SNP	C	T	C	MYC	c.C401T	p.P134L
XH_P36	8	133764167	133764167	Missense_Mutation	SNP	T	C	T	TMEM71	c.A178G	p.T60A
XH_P36	8	139606411	139606411	Silent	SNP	G	A	G	COL22A1	c.C4464T	p.P1488P
XH_P36	8	139638440	139638440	Missense_Mutation	SNP	C	T	C	COL22A1	c.G3710A	p.G1237E
XH_P36	8	142151365	142151365	Frame_Shift_Ins	INS	-	GTCCGAAGTCTA	-	DENND3	326insGTCCAA	p.A109fs
XH_P36	8	143956491	143956491	Missense_Mutation	SNP	C	T	C	CYP11B1	c.G1280A	p.R427H
XH_P36	8	144732584	144732584	Frame_Shift_Ins	INS	-	GA	-	ZNF623	c.542_543insGA	p.C181fs
XH_P36	8	144732585	144732585	Frame_Shift_Ins	INS	-	CTTCC	-	ZNF623	543_544insCTT	p.C181fs
XH_P36	8	144940503	144940503	Missense_Mutation	SNP	C	T	C	EPPK1	c.G6919A	p.V2307I
XH_P36	8	144998402	144998402	Missense_Mutation	SNP	G	A	G	PLEC	c.C5653T	p.R1885C
XH_P36	8	145109481	145109481	Frame_Shift_Del	DEL	C	-	C	OPLAH	c.2669delG	p.G890fs
XH_P36	8	145154303	145154303	Missense_Mutation	SNP	C	T	C	SHARPIN	c.G799A	p.V267M
XH_P36	8	145650341	145650341	Silent	SNP	G	A	G	VPS28	c.C288T	p.C96C
XH_P36	8	145693999	145693999	Silent	SNP	G	A	G	KIFC2	c.G969A	p.R323R
XH_P36	8	145737394	145737394	Missense_Mutation	SNP	G	A	G	RECQL4	c.C3293T	p.T1098I
XH_P36	9	977357	977357	Missense_Mutation	SNP	A	C	A	DMRT3	c.A356C	p.Q119P
XH_P36	9	1051712	1051712	Frame_Shift_Ins	INS	-	C	-	DMRT2	c.100dupC	p.T33fs
XH_P36	9	2047307	2047307	Missense_Mutation	SNP	C	T	C	SMARCA2	c.C869T	p.A290V
XH_P36	9	5233659	5233659	Missense_Mutation	SNP	G	A	G	INSL4	c.G202A	p.V68M
XH_P36	9	5742994	5742994	Missense_Mutation	SNP	A	G	A	RIC1	c.A1027G	p.T343A
XH_P36	9	5968044	5968044	Frame_Shift_Del	DEL	T	-	T	KIAA2026	c.2187delA	p.K729fs
XH_P36	9	6007719	6007719	Silent	SNP	G	T	G	KIAA2026	c.C69A	p.A23A
XH_P36	9	8524968	8524968	Silent	SNP	G	A	G	PTPRD	c.C627T	p.S209S
XH_P36	9	14841546	14841546	Frame_Shift_Ins	INS	-	TTTGAAGACTT	-	FREM1	80insAAAAGTCT	p.G594fs
XH_P36	9	14841548	14841548	Nonsense_Mutation	INS	-	ATCTATGTATTC	-	FREM1	insCACTGAATAC	p.3G594delinsTLNTX
XH_P36	9	16738425	16738425	Frame_Shift_Ins	INS	-	CACTTCTT	-	BNC2	1_62insAAGAAC	p.L21fs
XH_P36	9	18906821	18906821	Missense_Mutation	SNP	G	A	G	ADAMTSL1	c.G5093A	p.R1698H
XH_P36	9	27220063	27220063	Silent	SNP	C	T	C	TEK	c.C2676T	p.C892C
XH_P36	9	27548256	27548256	Missense_Mutation	SNP	C	T	C	C9orf72	c.G1424A	p.R475Q
XH_P36	9	34623991	34623991	Missense_Mutation	SNP	C	T	C	ARID3C	c.G445A	p.A149T
XH_P36	9	35091693	35091693	Frame_Shift_Del	DEL	G	-	G	PIGO	c.2191delC	p.R731fs
XH_P36	9	35103049	35103049	Silent	SNP	T	G	T	STOML2	c.A43C	p.R15R
XH_P36	9	35105796	35105796	Nonsense_Mutation	INS	-	TTTAAATTTT	-	FAM214B	CATACATAAAAA	p.50delinsYCTYHKNLKNX
XH_P36	9	35404027	35404027	Nonsense_Mutation	INS	-	AAGATAGAAGT	-	UNC13B	74insACAAGAT	p.51591delinsSTRX
XH_P36	9	35607405	35607405	In_Frame_Ins	INS	-	ACCCAAAGCCCT	-	TESK1	620insACCCAA	p.207delinsNPKPW
XH_P36	9	35722212	35722212	Frame_Shift_Ins	INS	-	CTAAGATTTCCC	-	TLN1	52insTGGGAAT	p.K284fs
XH_P36	9	40772354	40772354	Missense_Mutation	SNP	G	A	G	ZNF658	c.C2921T	p.T974M
XH_P36	9	67968558	67968558	Missense_Mutation	SNP	C	T	C	ANKRD20A1	c.C2117T	p.T706I
XH_P36	9	67968560	67968560	Missense_Mutation	SNP	C	A	C	ANKRD20A1	c.C2119A	p.Q707K
XH_P36	9	72965343	72965343	Missense_Mutation	SNP	G	T	G	SMC5	c.G3121T	p.A1041S
XH_P36	9	72965344	72965344	Frame_Shift_Ins	INS	-	TTTCACCTCCA	-	SMC5	3123insTTTCA	p.A1041fs
XH_P36	9	73399023	73399023	Silent	SNP	G	A	G	TRPM3	c.C1146T	p.G382G
XH_P36	9	74332948	74332948	Frame_Shift_Ins	INS	-	CTGAAATTTTGA	-	TMEM2	TATCTGTTCAAA	p.A709fs
XH_P36	9	84606936	84606936	Silent	SNP	T	C	T	SPATA31D1	c.T1551C	p.P517P
XH_P36	9	84607834	84607834	Missense_Mutation	SNP	T	G	T	SPATA31D1	c.T2449G	p.S817A
XH_P36	9	90582462	90582462	Frame_Shift_Ins	INS	-	G	-	CDK20	c.892dupC	p.H298fs
XH_P36	9	91991856	91991856	Missense_Mutation	SNP	C	T	C	SEMA4D	c.G1774A	p.A592T
XH_P36	9	95610784	95610784	Frame_Shift_Ins	INS	-	TTGGAGCCTAT	-	ZNF484	77insGATAGGC	p.V59fs
XH_P36	9	96422612	96422612	Frame_Shift_Del	DEL	A	-	A	PHF2	c.1468delA	p.K490fs
XH_P36	9	99381507	99381507	Missense_Mutation	SNP	T	C	T	CDCL14B	c.A154G	p.I52V
XH_P36	9	100850088	100850088	Silent	SNP	C	T	C	TRIM14	c.G993A	p.A331A
XH_P36	9	105767905	105767905	Missense_Mutation	SNP	C	A	C	CYL2	c.C992A	p.A331C
XH_P36	9	107298869	107298869	In_Frame_Ins	INS	-	GGCATTGTATCG	-	OR13C3	226insCGATCA	p.176delinsRSNAI
XH_P36	9	113192205	113192205	Silent	SNP	T	C	T	SVEP1	c.A5610G	p.T1870T
XH_P36	9	114090063	114090063	Nonsense_Mutation	INS	-	ATGAAGAAATT	-	OR2K2	51insGCAATTTC	p.Y217delinsX
XH_P36	9	114449150	114449150	In_Frame_Ins	INS	-	ATATGGCATGT	-	C9orf84	CAATGTTACATG	p.73delinsAMLHAIFHC
XH_P36	9	115932129	115932129	Nonsense_Mutation	INS	-	GTGTCAGGGAAC	-	FKBP15	2860insCTTCCC	p.R954delinsLPX
XH_P36	9	116276868	116276868	Silent	SNP	G	A	G	RGS5	c.G765A	p.T255T
XH_P36	9	117139586	117139586	Missense_Mutation	SNP	C	A	C	AKNA	c.G144T	p.Q48H
XH_P36	9	117848395	117848395	Nonsense_Mutation	SNP	G	A	G	TNC	c.C1615T	p.Q539X

XH_P36	9	117848781	117848781	Missense_Mutation	SNP	T	C	T	TNC	c.A1229G	p.N410S
XH_P36	9	127920568	127920568	Nonsense_Mutation	SNP	G	A	G	PPP6C	c.C265T	p.R89X
XH_P36	9	130947831	130947831	Nonsense_Mutation	SNP	G	A	G	CI21	c.C511T	p.R171X
XH_P36	9	131483691	131483691	Missense_Mutation	SNP	C	T	C	ZDHC12	c.G601A	p.V201I
XH_P36	9	131709317	131709317	Missense_Mutation	SNP	G	T	G	DOLK	c.C266A	p.P89H
XH_P36	9	135277175	135277175	In_Frame_Ins	INS	-	ACAGTCCCAACC	-	TTF1	insTGAGGTGGG45delinsVRLGLWK	
XH_P36	9	135926232	135926232	Missense_Mutation	SNP	G	A	G	GTFC35	c.G113A	p.R38H
XH_P36	9	137801701	137801701	Silent	SNP	C	T	C	FCN1	c.G924A	p.A308A
XH_P36	9	138395457	138395457	Silent	SNP	G	A	G	MRP52	c.G369A	p.T123T
XH_P36	9	139371084	139371084	Silent	SNP	C	T	C	SEC16A	c.G984A	p.R328R
XH_P36	9	139390736	139390736	Frame_Shift_Del	DEL	G	-	G	NOTCH1	c.7455delC	p.P2485fs
XH_P36	9	139996032	139996032	Missense_Mutation	SNP	C	T	C	MAN1B1	c.C1162T	p.R388W
XH_P36	9	140001244	140001244	Missense_Mutation	SNP	C	A	C	MAN1B1	c.C1549A	p.R517S
XH_P36	9	140081973	140081973	Missense_Mutation	SNP	G	A	G	ANAPC2	c.C700T	p.R234C
XH_P36	9	140140197	140140197	Silent	SNP	C	T	C	FAM166A	c.G165A	p.V55V
XH_P36	10	94773	94773	Missense_Mutation	SNP	C	T	C	TUBB8	c.G137A	p.R46H
XH_P36	10	8019267	8019267	Missense_Mutation	SNP	G	A	G	TAF3	c.G2296A	p.G766S
XH_P36	10	8100708	8100708	Missense_Mutation	SNP	G	A	G	GATA3	c.G682A	p.E228K
XH_P36	10	13481346	13481346	Nonsense_Mutation	INS	-	CTTGCTATTTA	-	BEND7	CACACATAAAAT11	R412delinsHTX
XH_P36	10	14816335	14816335	Missense_Mutation	SNP	C	T	C	FAM1107B	c.G328A	p.G110R
XH_P36	10	19981225	19981225	Missense_Mutation	SNP	G	T	G	MALRD1	c.G6152T	p.W2051L
XH_P36	10	20432247	20432247	Missense_Mutation	SNP	G	A	G	PLXDC2	c.G418A	p.V140I
XH_P36	10	25284588	25284588	Missense_Mutation	SNP	T	C	T	ENKUR	c.A248G	p.Y83C
XH_P36	10	35484127	35484127	Frame_Shift_Ins	INS	-	TAAACCAT	-	CREM	0_11insTAAACC	p.T4fs
XH_P36	10	44788267	44788267	Frame_Shift_Del	DEL	C	-	C	C10orf142	c.G9delC	p.T20fs
XH_P36	10	4699854	4699854	Missense_Mutation	SNP	C	T	C	GPRIN2	c.C974T	p.A325V
XH_P36	10	50732583	50732583	Frame_Shift_Ins	INS	-	GCAGAGGGAGA	-	ERCC6	893insTCTCCC	p.A298fs
XH_P36	10	50953853	50953853	Silent	SNP	G	A	G	OGDHL	c.C840T	p.V280V
XH_P36	10	52005124	52005124	Missense_Mutation	SNP	G	A	G	ASHA2	c.C218T	p.S73F
XH_P36	10	52005126	52005126	In_Frame_Ins	INS	-	CAAGTAATT	-	ASHA2	5_216insAATTAA6.H72delinsQITC	
XH_P36	10	64159513	64159513	Frame_Shift_Del	DEL	A	-	A	ZNF365	c.1189delA	p.K397fs
XH_P36	10	70332889	70332889	Missense_Mutation	SNP	A	G	A	TET1	c.A794G	p.N265S
XH_P36	10	70723214	70723214	Missense_Mutation	SNP	C	T	C	DDX21	c.C571T	p.R191C
XH_P36	10	71142432	71142432	Silent	SNP	G	A	G	HK1	c.G1359A	p.L453L
XH_P36	10	73466731	73466731	Missense_Mutation	SNP	G	A	G	CDH23	c.G3031A	p.E1011K
XH_P36	10	74666426	74666426	Nonsense_Mutation	INS	-	TCAGTATCATC	-	OIT3	18insATCCAGTA	p.C206delinsX
XH_P36	10	75435427	75435427	In_Frame_Ins	INS	-	AAAAAGAAACAC	-	AGAP5	991insGTGTTTTC	I331delinsVFLFI
XH_P36	10	78729786	78729786	Frame_Shift_Del	DEL	T	-	T	KCNMA1	c.2132delA	p.K711fs
XH_P36	10	81317157	81317157	Silent	SNP	G	T	G	SFTPA2	c.C585A	p.A195A
XH_P36	10	91497459	91497459	Frame_Shift_Ins	INS	-	TGCTCTCAGTCC	-	KIF20B	2862insTGCTCTC	p.N954fs
XH_P36	10	92617011	92617011	Missense_Mutation	SNP	C	T	C	HTR7	c.G418A	p.V140I
XH_P36	10	93601946	93601946	Frame_Shift_Del	DEL	A	-	A	TNKS2	c.1857delA	p.T619fs
XH_P36	10	93999314	93999314	Missense_Mutation	SNP	C	T	C	CPEB3	c.G794A	p.G265D
XH_P36	10	95093644	95093644	Nonsense_Mutation	INS	-	CTCATTTTACAG	-	MYOF	51insACCTGTAA7	D1518delinsPPVKX
XH_P36	10	98080475	98080475	Missense_Mutation	SNP	T	C	T	DNTT	c.T608C	p.F203S
XH_P36	10	98741863	98741863	In_Frame_Ins	INS	-	AGCTGCTTGATC	-	LCOR	47insGAGCTGT	P549delinsPSCLDG
XH_P36	10	102242535	102242535	Frame_Shift_Ins	INS	-	G	-	WNT8B	c.1019dupG	p.R340fs
XH_P36	10	102749036	102749036	Missense_Mutation	SNP	C	T	C	TWNK	c.C1069T	p.R357C
XH_P36	10	103530166	103530166	Missense_Mutation	SNP	G	A	G	FGF8	c.C343T	p.R115C
XH_P36	10	103917038	103917038	Missense_Mutation	SNP	G	A	G	NOLC1	c.C269A	p.S90N
XH_P36	10	103990510	103990510	Frame_Shift_Ins	INS	-	G	-	PITX3	c.669dupC	p.G224fs
XH_P36	10	104404668	104404668	Frame_Shift_Del	DEL	C	-	C	TRIM8	c.294delC	p.G98fs
XH_P36	10	104632345	104632345	Frame_Shift_Ins	INS	-	TAAATCTTATAC	-	AS3MT	ACCACTAAATCT	p.T104fs
XH_P36	10	105233174	105233174	In_Frame_Ins	INS	-	GTCTCAGGCAC	-	CALHM3	nsCGCAGTCGCT	277delinsPAVPETP
XH_P36	10	114925317	114925317	Frame_Shift_Del	DEL	A	-	A	TCF7L2	c.1151delA	p.C384fs
XH_P36	10	115601182	115601182	Missense_Mutation	SNP	T	C	T	DCLRE1A	c.A2803G	p.M935V
XH_P36	10	118427804	118427804	Missense_Mutation	SNP	A	G	A	C10orf82	c.T20C	p.F7S
XH_P36	10	120789359	120789359	Frame_Shift_Ins	INS	-	C	-	NANOS1	c.47dupC	p.A16fs
XH_P36	10	121196221	121196221	Missense_Mutation	SNP	T	C	T	GRK5	c.T797C	p.M266T
XH_P36	10	127541779	127541779	Silent	SNP	A	G	A	BCCIP	c.A936G	p.G312G
XH_P36	10	128150079	128150079	Frame_Shift_Ins	INS	-	TCCCCTAA	-	C10orf90	9_1610insTTAG	p.P537fs
XH_P36	10	128150081	128150081	Frame_Shift_Ins	INS	-	TT	-	C10orf90	1607_1608insA	p.E536fs
XH_P36	10	128973731	128973731	Missense_Mutation	SNP	G	A	G	FAM196A	c.C929T	p.P310L
XH_P36	10	129903319	129903319	Missense_Mutation	SNP	A	G	A	MK167	c.T5705C	p.V1902A
XH_P36	10	133955443	133955443	Missense_Mutation	SNP	C	T	C	JAKMIP3	c.C1277T	p.T426M
XH_P36	10	134563094	134563094	Missense_Mutation	SNP	G	A	G	INPP5A	c.G614A	p.R205H
XH_P36	10	134942117	134942117	Missense_Mutation	SNP	C	T	C	ADGRA1	c.C494T	p.T165M
XH_P36	10	135012703	135012703	Silent	SNP	G	A	G	KNDC1	c.G2691A	p.T897T
XH_P36	10	135176380	135176380	Missense_Mutation	SNP	C	A	C	ECHS1	c.G865T	p.D289Y
XH_P36	11	308213	308213	Silent	SNP	C	A	C	IFITM2	c.C21A	p.T77T
XH_P36	11	618713	618713	Missense_Mutation	SNP	C	T	C	CDHR5	c.G1828A	p.G610S
XH_P36	11	1016425	1016425	Frame_Shift_Ins	INS	-	CCTCTACTACC	-	MUC6	6376insGGTAG	p.Q2126fs
XH_P36	11	1016513	1016513	Frame_Shift_Ins	INS	-	ATCGCCTCTCG	-	MUC6	6288insCAGAA	p.Q2096fs
XH_P36	11	2432968	2432968	Missense_Mutation	SNP	C	T	C	TRPM5	c.G2504A	p.R835H
XH_P36	11	3114178	3114178	Missense_Mutation	SNP	C	T	C	OSBPL5	c.G1847A	p.R616Q
XH_P36	11	3848989	3848989	Missense_Mutation	SNP	C	T	C	RHOG	c.G380A	p.R127Q
XH_P36	11	4661623	4661623	Silent	SNP	C	A	C	OR51D1	c.C603A	p.S201S
XH_P36	11	4881339	4881339	Silent	SNP	G	A	G	OR51H1	c.C456T	p.T152T
XH_P36	11	5275557	5275557	Missense_Mutation	SNP	A	G	A	HBG2	c.T280C	p.C94R
XH_P36	11	5364256	5364256	Missense_Mutation	SNP	A	G	A	OR51B5	c.T499C	p.C167R
XH_P36	11	5686526	5686526	Missense_Mutation	SNP	C	T	C	TRIM5	c.G995A	p.R332Q
XH_P36	11	5878544	5878544	Frame_Shift_Ins	INS	-	TATCTCTCTGT	-	OR52E8	insGTAAACAAGA	p.I130fs
XH_P36	11	6472654	6472654	In_Frame_Ins	INS	-	AAGATTCTGCTT	-	TRIM3	1191insAAGCAC	E397delinsESRIL
XH_P36	11	7817937	7817937	Frame_Shift_Ins	INS	-	GTGGTGCTGCTG	-	OR5P2	BinsAACACAGAC	p.C185fs
XH_P36	11	7960556	7960556	Frame_Shift_Ins	INS	-	CTTACAC	-	OR10A3	11_512insGTGT	p.P171fs
XH_P36	11	9861142	9861142	Missense_Mutation	SNP	G	A	G	SBF2	c.C3358T	p.R1120C
XH_P36	11	12316345	12316353	In_Frame_Del	DEL	CTCCTCCTC	-	CTCCTCCTC	MICALCL	c.1367_1375del	p.456_459del
XH_P36	11	14498554	14498554	Nonsense_Mutation	SNP	G	A	G	COPB1	c.C1366T	p.R456X
XH_P36	11	17758073	17758073	Missense_Mutation	SNP	G	A	G	KCN1	c.G524A	p.R175H
XH_P36	11	18428876	18428876	Frame_Shift_Ins	INS	-	ACTTACAGTCTG	-	LDHA	CCAAGACTTACA	p.L260fs
XH_P36	11	20066788	20066788	Silent	SNP	C	T	C	NAV2	c.C732T	p.L244L
XH_P36	11	20181600	20181600	Missense_Mutation	SNP	G	A	G	DBX1	c.C271T	p.R91V
XH_P36	11	20676326	20676326	Missense_Mutation	SNP	G	A	G	SLC6A5	c.G1604A	p.R535H
XH_P36	11	27520343	27520343	Frame_Shift_Ins	INS	-	TG	-	LIN7C	c.446_447insCA	p.E149fs
XH_P36	11	27520345	27520345	Frame_Shift_Ins	INS	-	TATAAATGCCTA	-	LIN7C	sAAAAATAGGCA	p.E149fs
XH_P36	11	30255300	30255300	Nonsense_Mutation	SNP	C	T	C	FSHB	c.C343T	p.R15X
XH_P36	11	32608690	32608690	Frame_Shift_Ins	INS	-	CAATCTCAAATT	-	EIF3M	6insCACAAATCTC	p.D59fs
XH_P36	11	32635937	32635937	Frame_Shift_Ins	INS	-	AAGA	-	CCDC73	926_1927insTC	p.Q643fs

XH_P36	11	32635939	32635939	In_Frame_Ins	INS	-	ATAAAATGTCC	-	CCDC73	nsACTATGGACA42delinsYGFYLS
XH_P36	11	33308862	33308862	Frame_Shift_Ins	INS	-	AAGAAAAT	-	HIPK3	2_903insAAGAA p.P301fs
XH_P36	11	33308864	33308864	Frame_Shift_Ins	INS	-	AGGAC	-	HIPK3	904_905insAGG p.1302fs
XH_P36	11	33596351	33596351	Missense_Mutation	SNP	T	G	T	KIAA1549L	c.T3443G p.11148S
XH_P36	11	34489930	34489930	Silent	SNP	C	T	C	CAT	c.C1422T p.1474I
XH_P36	11	43425610	43425613	Frame_Shift_Del	DEL	GAGT	-	GAGT	TTC17	c.1395_1398del p.Q465fs
XH_P36	11	45671512	45671512	Missense_Mutation	SNP	C	G	C	CHST1	c.G962C p.G321A
XH_P36	11	47261725	47261725	Missense_Mutation	SNP	C	T	C	ACP2	c.G1025A p.R342Q
XH_P36	11	47611863	47611863	Missense_Mutation	SNP	C	T	C	C1QTNF4	c.G500A p.R167H
XH_P36	11	48347449	48347449	Frame_Shift_Del	DEL	A	-	A	OR4C3	c.957delA p.V319fs
XH_P36	11	55798310	55798310	Missense_Mutation	SNP	G	A	G	OR5A51	c.G416A p.R139K
XH_P36	11	55860958	55860958	Frame_Shift_Ins	INS	-	TAATCAAAATT	-	OR8I2	c.176insTAATCA p.M59fs
XH_P36	11	55860960	55860960	In_Frame_Ins	INS	-	ACT	-	OR8I2	c.177_178insAC p.M59delinsMT
XH_P36	11	56237708	56237708	Frame_Shift_Ins	INS	-	T	-	OR5M3	c.265dupA p.T89fs
XH_P36	11	57310811	57310811	Frame_Shift_Ins	INS	-	GTCTCTGTCATT	-	SMTNL1	97insTGTCCTG p.A232fs
XH_P36	11	60506456	60506456	Missense_Mutation	SNP	C	A	C	MS4A18	c.C610A p.L204I
XH_P36	11	61018732	61018732	Silent	SNP	C	T	C	PGA5	c.C1146T p.V382V
XH_P36	11	62289913	62289913	Silent	SNP	T	A	T	AHNAK	c.A11976T p.P3992P
XH_P36	11	62295576	62295576	Missense_Mutation	SNP	G	A	G	AHNAK	c.C6313T p.L2105F
XH_P36	11	63277289	63277289	Missense_Mutation	SNP	C	T	C	LGALS12	c.C295T p.R99W
XH_P36	11	64037690	64037690	Frame_Shift_Del	DEL	G	-	G	BAD	c.498delC p.P166fs
XH_P36	11	64572093	64572093	Frame_Shift_Del	DEL	G	-	G	MEN1	c.1561delC p.R521fs
XH_P36	11	64596977	64596977	Silent	SNP	G	A	G	CDC42BPG	c.C3933T p.H1311H
XH_P36	11	65307555	65307555	Frame_Shift_Del	DEL	C	-	C	LTBP3	c.3314delG p.R1105fs
XH_P36	11	65396411	65396411	Silent	SNP	C	T	C	PCNX3	c.C3933T p.R1311R
XH_P36	11	65733371	65733371	Missense_Mutation	SNP	C	T	C	SART1	c.C752T p.A251V
XH_P36	11	65780794	65780794	Missense_Mutation	SNP	C	T	C	CS76	c.C373T p.R125C
XH_P36	11	66083251	66083251	Silent	SNP	C	T	C	CD248	c.G1248A p.E416E
XH_P36	11	66999319	66999319	Frame_Shift_Ins	INS	-	CTCAAAATCTACC	-	KDM2A	8insAACTCCAA p.F456fs
XH_P36	11	67072394	67072394	Silent	SNP	C	A	C	SSH3	c.C255A p.S85S
XH_P36	11	67187007	67187007	Missense_Mutation	SNP	G	A	G	CARNS1	c.G533A p.R178H
XH_P36	11	67258296	67258296	Missense_Mutation	SNP	C	T	C	AIP	c.C817T p.R273C
XH_P36	11	67261809	67261809	Missense_Mutation	SNP	G	A	G	PITPNM1	c.C2762T p.A921V
XH_P36	11	67264838	67264838	Silent	SNP	G	A	G	PITPNM1	c.C2010T p.P670P
XH_P36	11	67800693	67800693	Silent	SNP	A	G	A	NDUFS8	c.A315G p.P105P
XH_P36	11	68080214	68080214	In_Frame_Ins	INS	-	GCT	-	LRP5	c.32_33insGCT p.P11delinsPL
XH_P36	11	68334537	68334537	Missense_Mutation	SNP	G	A	G	PPP6R3	c.G1031A p.P344Q
XH_P36	11	68517872	68517872	Frame_Shift_Del	DEL	C	-	C	TESMIN	c.257delG p.G86fs
XH_P36	11	70319341	70319341	Frame_Shift_Ins	INS	-	TCACITTA	-	SHANK2	18_3419insTAAC p.A1140fs
XH_P36	11	71195477	71195477	Missense_Mutation	SNP	C	T	C	NADSYN1	c.C1439T p.A480V
XH_P36	11	71712654	71712654	Frame_Shift_Del	DEL	G	-	G	IL18BP	c.563delG p.W118fs
XH_P36	11	71727133	71727133	Missense_Mutation	SNP	C	A	C	NUMA1	c.G1416T p.Q472H
XH_P36	11	75623053	75623053	Missense_Mutation	SNP	G	A	G	UVRAG	c.G563A p.R188H
XH_P36	11	82966931	82966931	Frame_Shift_Del	DEL	A	-	A	ANKRD42	c.1509delA p.V503fs
XH_P36	11	83676491	83676491	In_Frame_Ins	INS	-	ATACTTCAGAGG	-	DLG2	stACTCCCTCTG p.203delinsDTPSEVFP
XH_P36	11	85420388	85420388	Frame_Shift_Del	DEL	T	-	T	SYTL2	c.279delA p.K93V
XH_P36	11	88583231	88583231	Missense_Mutation	SNP	C	T	C	GRM5	c.G754A p.A252T
XH_P36	11	89223652	89223652	Missense_Mutation	SNP	A	G	A	NOX4	c.T127C p.Y43H
XH_P36	11	89447527	89447527	Frame_Shift_Ins	INS	-	TCAGCTATTCTG	-	TRIM77	CCTTATCAGCTA p.L225fs
XH_P36	11	89914834	89914834	Nonsense_Mutation	INS	-	TAGAAAATATAA	-	NAALAD2	AATTAGTAGAA p.502_F603delinsDPX
XH_P36	11	92532469	92532469	Missense_Mutation	SNP	C	T	C	FAT3	c.C6290T p.A2097V
XH_P36	11	94599175	94599175	Missense_Mutation	SNP	G	A	G	AMOTL1	c.G2180A p.R727H
XH_P36	11	95546700	95546700	Nonsense_Mutation	SNP	C	T	C	CEP57	c.C451T p.R151X
XH_P36	11	101323754	101323754	Missense_Mutation	SNP	C	A	C	TRPC6	c.G2728T p.A910S
XH_P36	11	101833918	101833918	In_Frame_Ins	INS	-	TGACTGTITTTCA	-	CEP126	nsTGAATGACTG p.18delinsVNDCFQHC
XH_P36	11	102587116	102587116	Frame_Shift_Ins	INS	-	ATCGGAATTTTT	-	MMP8	nsTATAAAAAAT p.P273fs
XH_P36	11	102661218	102661218	In_Frame_Ins	INS	-	TTAGAATGTAG	-	MMP1	AAAGGGCTACAA p.1delinsYQYKKYLNSKKIC
XH_P36	11	108384793	108384793	Frame_Shift_Del	DEL	A	-	A	EXPH5	c.877delT p.W293fs
XH_P36	11	113694379	113694379	Frame_Shift_Ins	INS	-	CT	-	USP28	c.231_232insAG p.C78fs
XH_P36	11	115109355	115109355	Missense_Mutation	SNP	A	C	A	CADM1	c.T289G p.F97V
XH_P36	11	118526386	118526386	Missense_Mutation	SNP	C	T	C	PHLDB1	c.C3805T p.R1269C
XH_P36	11	119216273	119216273	Frame_Shift_Del	DEL	G	-	G	MFRP	c.498delC p.P166fs
XH_P36	11	121000749	121000749	Missense_Mutation	SNP	C	A	C	TECTA	c.C2770A p.1924M
XH_P36	11	121475863	121475863	Missense_Mutation	SNP	G	T	G	SORL1	c.G4693T p.A1565S
XH_P36	11	123448124	123448124	Missense_Mutation	SNP	C	T	C	GRAMD1B	c.C737T p.R25W
XH_P36	11	123814451	123814451	Frame_Shift_Ins	INS	-	CTGACTTC	-	OR6T1	4_95insGAAGTC p.M32fs
XH_P36	11	124266349	124266349	Missense_Mutation	SNP	A	G	A	OR8B3	c.T899C p.L300P
XH_P36	11	124637789	124637789	Frame_Shift_Ins	INS	-	GGAA	-	MSANTD2	c.272_273insTTC p.N91fs
XH_P36	11	124637790	124637790	In_Frame_Ins	INS	-	GTTGTTCAA	-	MSANTD2	c.1272insTTGAA p.N91delinsIEQH
XH_P36	11	124845049	124845049	Frame_Shift_Del	DEL	A	-	A	CCDC15	c.574delA p.K192fs
XH_P36	11	125221249	125221249	Silent	SNP	G	A	G	PKNOX2	c.G48A p.T16T
XH_P36	12	2907038	2907041	Splice_Site	DEL	GTGA	-	GTGA	FKBP4	.
XH_P36	12	4735969	4735969	Missense_Mutation	SNP	G	A	G	AKAP3	c.C2099T p.S700F
XH_P36	12	4766968	4766968	Missense_Mutation	SNP	G	A	G	NDUFA9	c.G373A p.V125M
XH_P36	12	6131192	6131192	Missense_Mutation	SNP	A	G	A	VWF	c.T3548C p.L1183P
XH_P36	12	9221371	9221371	Missense_Mutation	SNP	G	A	G	A2M	c.C3881T p.P1294L
XH_P36	12	10762506	10762506	In_Frame_Ins	INS	-	TTAATTTTA	-	MAGOHB	9_50insTAAAT p.k17delinsIKLK
XH_P36	12	10762508	10762508	Frame_Shift_Ins	INS	-	TCTT	-	MAGOHB	c.47_48insAAGA p.L16fs
XH_P36	12	11286385	11286385	Nonsense_Mutation	INS	-	TCATATCAGTTT	-	TAS2R30	insTACAACTG p.63_W154delinsVTNX
XH_P36	12	12814973	12814973	Missense_Mutation	SNP	G	A	G	GNP19	c.C410T p.T137M
XH_P36	12	13238177	13238177	Frame_Shift_Ins	INS	-	CA	-	GS61	c.485_486insTG p.Y162fs
XH_P36	12	13238179	13238179	Splice_Site	INS	-	CTGTCTCTG	-	GS61	.
XH_P36	12	18876416	18876416	Missense_Mutation	SNP	T	A	T	PLCZ1	c.A196T p.I66F
XH_P36	12	26752988	26752988	In_Frame_Ins	INS	-	GTG	-	ITPR2	3732_3733insCp.F1245delinsHF
XH_P36	12	26752989	26752989	Frame_Shift_Ins	INS	-	ATATCTTTTTTTT	-	ITPR2	732insAAAAAA p.N1244fs
XH_P36	12	30805220	30805220	Nonsense_Mutation	INS	-	TATTTTTTCATTI	-	JP08	AATACAAATGA p.88_M489delinsKYXK
XH_P36	12	30863059	30863059	Missense_Mutation	SNP	A	G	A	CAPRIN2	c.T2159C p.L720P
XH_P36	12	40672017	40672017	Missense_Mutation	SNP	G	A	G	LRRK2	c.G2195A p.G732E
XH_P36	12	42523647	42523648	Frame_Shift_Del	DEL	TT	-	TT	GXYLT1	c.227_228del p.K76fs
XH_P36	12	43862460	43862460	Nonsense_Mutation	INS	-	TATTAGTGTAAI	-	ADAMTS20	nsGAAAAATTACA p.9_N390delinsRKLHX
XH_P36	12	44149036	44149036	Frame_Shift_Ins	INS	-	TAGAAGATGGA	-	PUS7L	insCTTCCACTCT p.T5fs
XH_P36	12	48141379	48141379	Nonsense_Mutation	SNP	G	A	G	RAPGEF3	c.C1378T p.R460X
XH_P36	12	49521893	49521893	Missense_Mutation	SNP	G	A	G	TUBA1B	c.C1204T p.R402C
XH_P36	12	50747903	50747903	Frame_Shift_Ins	INS	-	AGCAACCTTGT	-	FAM186A	insAAACACAAG p.E904fs
XH_P36	12	50747905	50747905	Nonsense_Mutation	INS	-	ATTT	-	FAM186A	709_2710insAA p.904_E905delinsKX
XH_P36	12	51399180	51399180	Missense_Mutation	SNP	C	T	C	SLC11A2	c.G211A p.G71R
XH_P36	12	52684997	52684997	Missense_Mutation	SNP	C	T	C	KRT81	c.G253A p.E85K
XH_P36	12	53038849	53038849	Missense_Mutation	SNP	C	T	C	KRT2	c.G1874A p.S625N

XH_P36	12	53162773	53162775	In_Frame_Del	DEL	ACT	-	ACT	KRT76	c.1639_1641del	p.547_547del
XH_P36	12	56398615	56398615	Missense_Mutation	SNP	G	A	G	SUOX	c.G1442A	p.R481H
XH_P36	12	56494905	56494905	Missense_Mutation	SNP	C	T	C	ERBB3	c.C3262T	p.P1088S
XH_P36	12	56558476	56558476	Missense_Mutation	SNP	A	T	A	SMARCC2	c.T3179A	p.M1060K
XH_P36	12	56558477	56558477	In_Frame_Ins	INS	-	CCTTGCCCTC	-	SMARCC2	c.3178insGAGG	p.M1060delinsEARM
XH_P36	12	56559113	56559113	Frame_Shift_Del	DEL	G	-	G	SMARCC2	c.3128delC	p.P1043fs
XH_P36	12	56572601	56572601	Missense_Mutation	SNP	G	A	G	SMARCC2	c.C1172T	p.T391M
XH_P36	12	56661723	56661723	Missense_Mutation	SNP	G	T	G	COQ10A	c.G184T	p.G62W
XH_P36	12	56994169	56994169	Nonsense_Mutation	SNP	C	A	C	BAZ2A	c.G4708T	p.G1570X
XH_P36	12	57389231	57389231	Missense_Mutation	SNP	C	T	C	GPR182	c.C238T	p.R80C
XH_P36	12	57906594	57906594	Frame_Shift_Ins	INS	-	GTCCCTTC	-	MARS	c.4_1815insGTCC	p.D605fs
XH_P36	12	57911097	57911097	Silent	SNP	T	C	T	DDIT3	c.A162G	p.S54S
XH_P36	12	58025103	58025103	Frame_Shift_Del	DEL	C	-	C	B4GALNT1	c.263delG	p.G88fs
XH_P36	12	63087738	63087738	Frame_Shift_Ins	INS	-	G	-	PPM1H	c.1114dupC	p.L372fs
XH_P36	12	64055225	64055225	Missense_Mutation	SNP	C	A	C	DPY19L2	c.G487T	p.A163S
XH_P36	12	65226072	65226072	Nonsense_Mutation	INS	-	TTTCAAAAATA	-	TBC1D30	c.CAATATTTTCAA	p.D195delinsGKQYFQKX
XH_P36	12	65226073	65226073	Missense_Mutation	SNP	G	T	G	TBC1D30	c.G583T	p.D195Y
XH_P36	12	71834023	71834023	Missense_Mutation	SNP	C	A	C	LGR5	c.C163A	p.L55M
XH_P36	12	75687029	75687029	Missense_Mutation	SNP	T	A	T	CAPS2	c.A974T	p.K325I
XH_P36	12	75804272	75804272	Missense_Mutation	SNP	C	T	C	GLIPR1L2	c.C293T	p.T98M
XH_P36	12	77244718	77244718	Nonsense_Mutation	INS	-	ATACATGAATT	-	ZDHC17	c.1853insATACA	p.L619delinsNTX
XH_P36	12	78400815	78400815	Frame_Shift_Ins	INS	-	GTAAACCTTC	-	NAV3	c.3insACTGTATAA	p.L7499fs
XH_P36	12	78515938	78515938	In_Frame_Ins	INS	-	AAG	-	NAV3	c.3968_3969insA	p.L1323delinsIR
XH_P36	12	78593137	78593137	Missense_Mutation	SNP	A	G	A	NAV3	c.A6475G	p.T2159A
XH_P36	12	88487681	88487681	Nonsense_Mutation	DEL	T	-	T	CEP290	c.3175delA	p.L1059X
XH_P36	12	88589253	88589253	Frame_Shift_Ins	INS	-	ATTGTGTTTCC	-	TMT3	c.573insGATTGTG	p.L858fs
XH_P36	12	89745700	89745700	Silent	SNP	G	A	G	DUSP6	c.C117T	p.C39C
XH_P36	12	89997947	89997947	Silent	SNP	G	A	G	ATP2B1	c.C2619T	p.G873G
XH_P36	12	91498041	91498041	Silent	SNP	G	T	G	LUM	c.C918A	p.L306I
XH_P36	12	91498042	91498042	Nonsense_Mutation	INS	-	AATTTAGTGT	-	LUM	c.ATAAAAAACAC	p.B06_K307delinsKX
XH_P36	12	93173078	93173078	Splice_Site	INS	-	CTTCCTTTTTCAC	-	EEA1	-	-
XH_P36	12	94543030	94543030	Frame_Shift_Del	DEL	C	-	C	PLXNC1	c.283delC	p.P95fs
XH_P36	12	94797019	94797019	Nonsense_Mutation	INS	-	GTGCGTTTCTT	-	CEP83	c.AAAATAAAGAA	p.L115delinsX
XH_P36	12	97186181	97186181	Silent	SNP	G	A	G	CFAP54	c.G8754A	p.T2918T
XH_P36	12	101473003	101473003	Nonsense_Mutation	SNP	C	T	T	ANO4	c.C1345T	p.R449X
XH_P36	12	104697824	104697824	Missense_Mutation	SNP	C	T	C	EID3	c.C112T	p.R38C
XH_P36	12	107236579	107236579	Frame_Shift_Ins	INS	-	CACCT	-	RIC8B	c.1001_1002insCA	p.E334fs
XH_P36	12	107236581	107236581	Frame_Shift_Ins	INS	-	CACTACTATG	-	RIC8B	c.1004insCACTA	p.K335fs
XH_P36	12	108169390	108169390	Missense_Mutation	SNP	C	T	C	ASCL4	c.C398T	p.A133V
XH_P36	12	108954836	108954836	Missense_Mutation	SNP	G	T	G	SART3	c.C95A	p.A32D
XH_P36	12	109536183	109536183	Missense_Mutation	SNP	C	T	C	UNG	c.C52T	p.P18S
XH_P36	12	113445730	113445730	Missense_Mutation	SNP	G	A	G	OAS2	c.G1877A	p.S626N
XH_P36	12	117217097	117217097	Missense_Mutation	SNP	G	A	G	RNF72	c.G826A	p.A276T
XH_P36	12	118681299	118681299	Nonsense_Mutation	INS	-	TTATCAGTATT	-	TAOK3	c.1insTTAAATACTG	p.V73delinsVKYX
XH_P36	12	118681301	118681301	Missense_Mutation	SNP	C	A	C	TAOK3	c.G213T	p.K71N
XH_P36	12	120760118	120760118	Nonsense_Mutation	INS	-	TATTTATTTTTC	-	PLA2G1B	c.1nsCTAGAGAAAB	p.N110delinsLEKINTX
XH_P36	12	123875311	123875311	Silent	SNP	C	T	C	KMT5A	c.C96T	p.A32A
XH_P36	12	124832387	124832387	Silent	SNP	G	A	G	NCOR2	c.C4026T	p.R1342R
XH_P36	12	124887093	124887093	In_Frame_Ins	INS	-	TGT	-	NCOR2	c.1493_1494insA	p.Q498delinsQQ
XH_P36	12	125396488	125396488	Silent	SNP	T	C	T	UBC	c.A1830G	p.Q610Q
XH_P36	12	125397037	125397037	Silent	SNP	C	T	C	UBC	c.G1281A	p.G427G
XH_P36	12	125397439	125397439	Silent	SNP	A	G	A	UBC	c.T879C	p.S293S
XH_P36	12	130647740	130647740	Missense_Mutation	SNP	T	G	T	FZD10	c.T253G	p.F85V
XH_P36	12	130830392	130830392	Missense_Mutation	SNP	G	T	G	PIWIL1	c.G285T	p.Q95H
XH_P36	12	130830394	130830394	In_Frame_Ins	INS	-	AACAAT	-	PIWIL1	c.187_288insAAC	p.N96delinsKTI
XH_P36	12	130935836	130935836	Silent	SNP	C	T	T	RIMBP2	c.G357A	p.R119R
XH_P36	12	131620642	131620642	Silent	SNP	C	T	C	ADGRD1	c.C2328T	p.G776G
XH_P36	12	133327262	133327262	Frame_Shift_Del	DEL	T	-	T	ANKLE2	c.814delA	p.T272fs
XH_P36	12	133463877	133463877	Missense_Mutation	SNP	G	T	G	CHFR	c.C38A	p.P13Q
XH_P36	12	133696963	133696963	Silent	SNP	T	C	T	ZNFR891	c.A1542G	p.K514K
XH_P36	13	20244471	20244471	In_Frame_Ins	INS	-	CTGGAAAGACT	-	MPHOSPH8	c.2426insCTGGAA	p.L809delinsPGKDL
XH_P36	13	20333558	20333558	Frame_Shift_Ins	INS	-	GTCTACATGGAA	-	PSPC1	c.5insATTTCATG	p.T225fs
XH_P36	13	25670813	25670813	Silent	SNP	C	T	C	PABPC3	c.C477T	p.N159N
XH_P36	13	26542799	26542799	Missense_Mutation	SNP	G	A	G	ATP8A2	c.G3164A	p.L1055Q
XH_P36	13	26789433	26789433	Nonsense_Mutation	SNP	G	A	G	RNF6	c.C586T	p.R196X
XH_P36	13	27216440	27216440	Silent	SNP	G	A	G	WASF3	c.G33A	p.R11R
XH_P36	13	28712860	28712910	In_Frame_Del	DEL	CCCGCCGGG	-	CCCGCCCGGGG	PAN3	c.66_116del	p.22_39del
XH_P36	13	30801573	30801573	Frame_Shift_Del	DEL	T	-	T	KATNAL1	c.1123delA	p.R375fs
XH_P36	13	31714404	31714404	Nonsense_Mutation	INS	-	GAGAACCTATC	-	HSPH1	c.AATATTGTGATAC	p.A55delinsKYLGSFLX
XH_P36	13	32910998	32910998	Frame_Shift_Ins	INS	-	AATGTTGTACTG	-	BRCA2	c.1stTTTGAATGT	p.P836fs
XH_P36	13	33344888	33344888	Frame_Shift_Del	DEL	A	-	A	PD5B8	c.4161delA	p.P1387fs
XH_P36	13	36905543	36905543	Missense_Mutation	SNP	C	T	C	SPG20	c.G1001A	p.R334Q
XH_P36	13	39265390	39265390	Silent	SNP	G	A	G	FREM2	c.G3909A	p.T1303T
XH_P36	13	40175192	40175192	Silent	SNP	C	T	C	LHPF	c.G162A	p.V54V
XH_P36	13	45008838	45008838	Frame_Shift_Del	DEL	G	-	G	TSC22D1	c.185delC	p.P62fs
XH_P36	13	46632361	46632361	Missense_Mutation	SNP	A	G	A	CPB2	c.T841C	p.F281I
XH_P36	13	52604544	52604544	Frame_Shift_Ins	INS	-	C	-	UTP14C	c.1604_1605ins	p.Q535fs
XH_P36	13	52604545	52604545	Missense_Mutation	SNP	G	C	G	UTP14C	c.G1605C	p.Q535H
XH_P36	13	52639565	52639565	Missense_Mutation	SNP	C	T	C	NEK5	c.G2105A	p.S702N
XH_P36	13	53421509	53421509	Missense_Mutation	SNP	C	T	C	PCDH8	c.G1063A	p.A355T
XH_P36	13	77529556	77529556	Missense_Mutation	SNP	C	T	C	ACOD1	c.C355T	p.P119S
XH_P36	13	77641983	77641983	Nonsense_Mutation	INS	-	GATTTTCAATTC	-	MYCBP2	c.8insCTGGGAATT	p.T53_R4064delinsTNWX
XH_P36	13	84454271	84454271	Missense_Mutation	SNP	C	T	C	SLITRK1	c.G1372A	p.A458T
XH_P36	13	92560239	92560239	Frame_Shift_Ins	INS	-	TA	-	GPC5	c.1329_1330insT	p.N443fs
XH_P36	13	92560240	92560240	Nonsense_Mutation	INS	-	GTTTTGTATAC	-	GPC5	c.31insTTGTTTTT	p.44_E445delinsLVFX
XH_P36	13	95121040	95121040	Frame_Shift_Del	DEL	A	-	A	DCT	c.555delT	p.F185fs
XH_P36	13	98828558	98828558	Silent	SNP	C	T	C	RNF113B	c.G933A	p.L311L
XH_P36	13	99091450	99091450	Silent	SNP	G	A	G	FARP1	c.G2433A	p.T811T
XH_P36	13	103390256	103390256	Missense_Mutation	SNP	T	C	T	CCDC168	c.A12791G	p.E4264G
XH_P36	13	103515102	103515102	Frame_Shift_Ins	INS	-	GAGCTCTCTT	-	BIVM-ERCC5	c.1604insGAGC	p.K535fs
XH_P36	13	110434690	110434690	Silent	SNP	C	T	C	IRS2	c.G3711A	p.S1237S
XH_P36	13	111110449	111110449	Missense_Mutation	SNP	C	T	C	COL4A2-AS2	c.G257A	p.R86Q
XH_P36	13	111371669	111371669	Missense_Mutation	SNP	C	T	C	ING1	c.C179T	p.A60V
XH_P36	13	113439523	113439523	Missense_Mutation	SNP	G	T	G	ATP11A	c.G114T	p.E38D
XH_P36	14	19553760	19553760	Missense_Mutation	SNP	G	A	G	POTEG	c.G344A	p.S115N
XH_P36	14	21550439	21550439	Silent	SNP	T	C	T	ARHGEF40	c.T1146C	p.C382C
XH_P36	14	21555623	21555623	Splice_Site	SNP	G	A	G	ARHGEF40	-	-
XH_P36	14	21569511	21569511	Silent	SNP	T	C	T	TMEM253	c.T9C	p.D3D

XH_P36	14	23745293	23745293	In_Frame_Ins	INS	-	GATATACACCC	-	HOMEZ	1144insGGGTG	R382delinsGLYIR
XH_P36	14	31642477	31642477	Silent	SNP	G	A	G	HECTD1	c.C1041T	p.G347G
XH_P36	14	37736246	37736246	Nonsense_Mutation	INS	-	AGCTTTAAACAT	-	MIPOL1	TCCTTTAGCTTTA	S42delinsKHSALNIX
XH_P36	14	39649809	39649809	Missense_Mutation	SNP	G	A	G	PNN	c.G896A	p.R299H
XH_P36	14	39901278	39901278	Missense_Mutation	SNP	A	C	A	FBXO33	c.T89G	p.L30R
XH_P36	14	50626388	50626388	Missense_Mutation	SNP	G	A	G	SOS2	c.C1613T	p.A538V
XH_P36	14	51210171	51210171	Missense_Mutation	SNP	G	A	G	NIN	c.C3125T	p.A1042V
XH_P36	14	57269043	57269043	Missense_Mutation	SNP	G	A	G	OTX2	c.C304T	p.R102C
XH_P36	14	59107555	59107555	In_Frame_Ins	INS	-	TTCACTAAA	-	DACT1	7_448insTTTCACT	E149delinsEFTK
XH_P36	14	59992099	59992099	Frame_Shift_Ins	INS	-	T	-	CCDC175	c.1895dupA	p.N632fs
XH_P36	14	60712698	60712698	Frame_Shift_Ins	INS	-	TCCTGTCTCTGTG	-	PPM1A	34insATCTCTGT	p.R45fs
XH_P36	14	61186779	61186779	Missense_Mutation	SNP	C	A	C	SIX4	c.G1248T	p.Q416H
XH_P36	14	68044071	68044071	Silent	SNP	C	T	C	PLEKHH1	c.C2514T	p.Y838Y
XH_P36	14	68045918	68045918	Missense_Mutation	SNP	C	T	C	PLEKHH1	c.C2917T	p.R973W
XH_P36	14	71199421	71199421	Frame_Shift_Ins	INS	-	TCCTTCCACTTC	-	MAP3K9	4insCCGAAGTG	p.K622fs
XH_P36	14	71206835	71206835	Frame_Shift_Ins	INS	-	GTCTCTCTCCA	-	MAP3K9	696insTGGAGA	p.K232fs
XH_P36	14	72056027	72056027	Missense_Mutation	SNP	T	C	T	SIPA1L1	c.T1438C	p.Y480H
XH_P36	14	74138302	74138302	Splice_Site	INS	-	ATAATTTTCATAA	-	DNAL1	-	-
XH_P36	14	74203800	74203800	Silent	SNP	G	A	G	ELMSAN1	c.C1650T	p.D550D
XH_P36	14	75359617	75359617	Frame_Shift_Del	DEL	C	-	C	DLST	c.S23delIC	p.P175fs
XH_P36	14	75513561	75513561	In_Frame_Ins	INS	-	AGGTGA	-	MLH3	797_2798insTCA	G933delinsVTC
XH_P36	14	75513562	75513562	In_Frame_Ins	INS	-	CAAAATGGA	-	MLH3	6_2797insTCCA	G933delinsSILG
XH_P36	14	75515373	75515376	Frame_Shift_Del	DEL	TCAA	-	TCAA	MLH3	c.983_986del	p.I328fs
XH_P36	14	76429801	76429801	Nonsense_Mutation	SNP	C	A	C	TGFB3	c.G784T	p.G262X
XH_P36	14	86088585	86088585	Missense_Mutation	SNP	T	C	T	FLRT2	c.T727C	p.S243P
XH_P36	14	91444862	91444862	Frame_Shift_Ins	INS	-	TTTGGGT	-	RP56KA5	81_182insAACCT	p.G61fs
XH_P36	14	91444863	91444863	Frame_Shift_Ins	INS	-	TTAAGTT	-	RP56KA5	80_181insAACC	p.G61fs
XH_P36	14	92471769	92471769	In_Frame_Ins	INS	-	SCAAAAGAAGG	-	TRIP11	5TCCATTTCCTTC	B50delinsSISFFCSCK
XH_P36	14	93404844	93404844	Missense_Mutation	SNP	C	T	C	ITPK1	c.G929A	p.G310D
XH_P36	14	93761193	93761193	Frame_Shift_Del	DEL	T	-	T	BTBD7	c.173delA	p.K58fs
XH_P36	14	94107567	94107567	Silent	SNP	C	T	C	UNC79	c.C5463T	p.D1821D
XH_P36	14	94395508	94395508	Nonstop_Mutation	SNP	T	C	T	FAM181A	c.T877C	p.X293Q
XH_P36	14	94417346	94417346	Silent	SNP	G	A	G	ASB2	c.C735T	p.Y245Y
XH_P36	14	95675732	95675732	Silent	SNP	G	A	G	CLMN	c.C885T	p.A295A
XH_P36	14	97022519	97022519	Silent	SNP	G	A	G	PAPOLA	c.G1023A	p.S341S
XH_P36	14	99642353	99642353	Missense_Mutation	SNP	C	T	C	BCL11B	c.G604A	p.V202M
XH_P36	14	100126651	100126651	Silent	SNP	G	T	G	HHIPL1	c.G1410T	p.T470T
XH_P36	14	103336573	103336573	Missense_Mutation	SNP	C	T	C	TRAF3	c.C35T	p.A12V
XH_P36	14	103996592	103996592	Missense_Mutation	SNP	G	A	G	TRMT61A	c.G277A	p.A93T
XH_P36	14	105353222	105353222	Frame_Shift_Ins	INS	-	C	-	CEP170B	c.2437dupC	p.K812fs
XH_P36	14	105408144	105408144	Missense_Mutation	SNP	C	A	C	AHNAK2	c.G13344T	p.K4448N
XH_P36	14	105408615	105408615	Silent	SNP	T	C	T	AHNAK2	c.A12873G	p.V4291V
XH_P36	14	105408617	105408617	Missense_Mutation	SNP	C	T	C	AHNAK2	c.G12871A	p.V4291I
XH_P36	14	105944635	105944635	Missense_Mutation	SNP	C	T	C	CRIP2	c.C298T	p.H100Y
XH_P36	15	22742754	22742754	Missense_Mutation	SNP	G	A	G	GOLGA6L1	c.G1139A	p.R380Q
XH_P36	15	22743174	22743174	Missense_Mutation	SNP	G	A	G	GOLGA6L1	c.G1559A	p.R520K
XH_P36	15	22743191	22743191	Silent	SNP	A	C	A	GOLGA6L1	c.A1576C	p.R526R
XH_P36	15	23021239	23021239	Frame_Shift_Del	DEL	T	-	T	NIPAZ	c.98delA	p.K33fs
XH_P36	15	23889902	23889902	Silent	SNP	G	A	G	MAGEL2	c.C2988T	p.V996V
XH_P36	15	23891598	23891598	Missense_Mutation	SNP	C	T	C	MAGEL2	c.G1292A	p.R431Q
XH_P36	15	24921544	24921544	Missense_Mutation	SNP	G	T	G	NPAP1	c.G530T	p.R177M
XH_P36	15	24924254	24924254	Silent	SNP	A	G	A	NPAP1	c.A3240G	p.G1080G
XH_P36	15	24924255	24924255	Missense_Mutation	SNP	T	C	T	NPAP1	c.T3241C	p.Y1081H
XH_P36	15	26806145	26806145	Silent	SNP	C	T	C	GABRB3	c.G759A	p.R253R
XH_P36	15	27160004	27160004	Silent	SNP	G	A	G	GABRA5	c.G552A	p.A184A
XH_P36	15	27188381	27188381	Silent	SNP	C	A	C	GABRA5	c.C897T	p.T299T
XH_P36	15	28413663	28413663	Missense_Mutation	SNP	C	T	C	HERC2	c.G10303A	p.A3435T
XH_P36	15	28419605	28419605	Silent	SNP	C	T	C	HERC2	c.G9993A	p.T3331T
XH_P36	15	28437288	28437288	Missense_Mutation	SNP	G	A	G	HERC2	c.C8270T	p.A2757V
XH_P36	15	30659672	30659672	Silent	SNP	G	A	G	CHRFAM7A	c.C396T	p.I132I
XH_P36	15	35178833	35178833	Nonsense_Mutation	INS	-	TTTTTGAGTAG	-	AQR	TCCTAATCTACTC	R905delinsPYLIYSKKX
XH_P36	15	39874834	39874834	Missense_Mutation	SNP	G	A	G	THBS1	c.G508A	p.D170N
XH_P36	15	42159792	42159792	Nonsense_Mutation	INS	G	A	G	SPTBN5	c.C6256T	p.Q2086X
XH_P36	15	42300063	42300063	Frame_Shift_Ins	INS	-	TGTTTGCCCT	-	PLA2G4E	257insAGGGGC	p.L86fs
XH_P36	15	43814792	43814792	Frame_Shift_Ins	INS	-	AGGTCCT	-	MAP1A	21_1122insAGG	p.P374fs
XH_P36	15	43896265	43896265	Missense_Mutation	SNP	T	C	T	STRC	c.A4304G	p.E1435G
XH_P36	15	44907750	44907750	Frame_Shift_Del	DEL	A	-	A	SPG11	c.2849delIT	p.L950fs
XH_P36	15	45409422	45409422	Missense_Mutation	SNP	G	A	G	DUOX2	c.G688A	p.V230M
XH_P36	15	49776644	49776644	Frame_Shift_Del	DEL	A	-	A	FGF7	c.528delA	p.G176fs
XH_P36	15	50773790	50773790	Missense_Mutation	SNP	G	A	G	USP8	c.G1100A	p.R367H
XH_P36	15	50925185	50925185	Missense_Mutation	SNP	G	A	G	TRPM7	c.C1012T	p.L338F
XH_P36	15	51857323	51857323	Nonsense_Mutation	DEL	A	-	A	DMXL2	c.326delIT	p.L109X
XH_P36	15	52901069	52901069	Frame_Shift_Del	DEL	T	-	T	FAM214A	c.2063delA	p.N688fs
XH_P36	15	55621922	55621922	Frame_Shift_Del	DEL	T	-	T	PIGB	c.523delIT	p.F175fs
XH_P36	15	55759217	55759217	Nonsense_Mutation	INS	-	GTAAATCTATTCA	-	DNAAF4	4insTGTGAATAG	K184delinsLX
XH_P36	15	55912219	55912219	Frame_Shift_Del	DEL	G	-	G	PRTG	c.3444delIC	p.P1148fs
XH_P36	15	62986516	62986516	Missense_Mutation	SNP	A	G	A	TLN2	c.A1217G	p.K406R
XH_P36	15	63102142	63102142	Missense_Mutation	SNP	G	A	G	TLN2	c.G6682A	p.D2228N
XH_P36	15	64791850	64791850	Frame_Shift_Ins	INS	-	CTTTCCTATT	-	ZNFB609	233insCTTTCC	p.V78fs
XH_P36	15	65499170	65499170	Missense_Mutation	SNP	C	T	C	CILP	c.G374A	p.R125Q
XH_P36	15	66030257	66030257	Nonsense_Mutation	INS	-	TGACAGATCTT	-	DENND4A	ATGGAAAGATC	p.Y276delinsX
XH_P36	15	69331298	69331298	Silent	SNP	C	T	C	NOX5	c.C1389T	p.P463P
XH_P36	15	73660540	73660540	Nonsense_Mutation	SNP	C	T	C	HCN4	c.G72A	p.W24X
XH_P36	15	75498563	75498563	Silent	SNP	C	T	C	C15orf39	c.C174T	p.A58A
XH_P36	15	75969242	75969242	Missense_Mutation	SNP	T	C	T	CSPG4	c.A5618G	p.Q1873R
XH_P36	15	79058543	79058543	Missense_Mutation	SNP	C	T	C	ADAMTS7	c.G3710A	p.S1237N
XH_P36	15	85164712	85164712	Missense_Mutation	SNP	G	A	G	ZSCAN2	c.G1286A	p.R429H
XH_P36	15	85407795	85407795	Missense_Mutation	SNP	C	T	C	ALPK3	c.C5228T	p.P1743L
XH_P36	15	89398826	89398826	Missense_Mutation	SNP	A	G	A	ACAN	c.A3010G	p.T1004A
XH_P36	15	89719201	89719201	Missense_Mutation	SNP	G	A	G	ABHD2	c.G697A	p.V233M
XH_P36	15	100591929	100591929	Missense_Mutation	SNP	A	G	A	ADAMTS17	c.T2303C	p.L768S
XH_P36	15	102242559	102242559	Silent	SNP	C	T	C	TARSL2	c.G1104A	p.P368P
XH_P36	15	102346763	102346763	Missense_Mutation	SNP	G	A	G	OR4F6	c.G841A	p.V281I
XH_P36	16	314836	314836	Missense_Mutation	SNP	G	A	G	FAM234A	c.G1474A	p.A492T
XH_P36	16	842546	842546	Frame_Shift_Del	DEL	G	-	G	CHTF18	c.1434delG	p.E478fs
XH_P36	16	1412305	1412305	Frame_Shift_Del	DEL	C	-	C	GNPTG	c.S10delIC	p.L710fs
XH_P36	16	1709929	1709929	Missense_Mutation	SNP	G	A	G	CRAMP1	c.G2278A	p.A760T
XH_P36	16	1779576	1779600	Frame_Shift_Del	DEL	CGCGGGCGCG	-	CGCGGGGGCGCG	MAPK8IP3	c.599_602del	p.R200fs

XH_P36	16	2762695	2762695	Missense_Mutation	SNP	C	T	C	PRSS27	c.G493A	p.A165T	
XH_P36	16	2903887	2903887	Missense_Mutation	SNP	C	A	C	PRSS22	c.G696T	p.E232D	
XH_P36	16	2983964	2983964	Silent	SNP	G	A	G	FLYWCH1	c.G1497A	p.A499A	
XH_P36	16	3119304	3119304	Frame_Shift_Ins	INS	-	G	-	IL32	c.488_489insG	p.D163fs	
XH_P36	16	3170007	3170007	Missense_Mutation	SNP	C	T	C	ZNF205	c.C1346T	p.P449L	
XH_P36	16	4802553	4802553	Missense_Mutation	SNP	G	A	G	ZNF500	c.C1267T	p.H423Y	
XH_P36	16	5061152	5061152	Frame_Shift_Del	DEL	C	-	C	SEC14L5	c.1857delC	p.S619fs	
XH_P36	16	10867203	10867203	Frame_Shift_Del	DEL	A	-	A	TVP23A	c.420delT	p.P140fs	
XH_P36	16	14970537	14970537	Missense_Mutation	SNP	A	C	A	NOMO1	c.A2533C	p.S845R	
XH_P36	16	15457764	15457764	Missense_Mutation	SNP	G	A	G	NPIPAS	c.C805T	p.R269C	
XH_P36	16	16228273	16228273	Missense_Mutation	SNP	G	A	G	ABCC1	c.G4033A	p.E1345K	
XH_P36	16	19063046	19063046	Silent	SNP	G	A	G	TMC7	c.G753A	p.P251P	
XH_P36	16	19126240	19126240	Missense_Mutation	SNP	C	T	C	ITPRIPL2	c.C457T	p.R153C	
XH_P36	16	19883839	19883839	Missense_Mutation	SNP	G	A	G	GPRC5B	c.C722T	p.T241M	
XH_P36	16	20359850	20359850	Nonsense_Mutation	SNP	C	T	C	UMOD	c.G773A	p.W258X	
XH_P36	16	20948007	20948007	Silent	SNP	G	A	G	DNAH3	c.C11685T	p.V3895Y	
XH_P36	16	22326502	22326502	Nonsense_Mutation	SNP	G	A	G	POLR3E	c.G507A	p.W169X	
XH_P36	16	24582721	24582721	Nonsense_Mutation	INS	-	TTCTCAGGATACT	-	RBBP6	TTTCTTTCTCAG	\$1412delinsHF	LSQDXTX
XH_P36	16	24807240	24807240	Frame_Shift_Del	DEL	A	-	A	TNRC6A	c.3541delA	p.K1181fs	
XH_P36	16	28354502	28354502	Missense_Mutation	SNP	A	C	A	NPIP6B	c.T704G	p.M235R	
XH_P36	16	28354503	28354503	Frame_Shift_Ins	INS	-	CTCC	-	NPIP6B	702_703insGGA	p.M235fs	
XH_P36	16	28898983	28898983	Missense_Mutation	SNP	C	T	C	ATP2A1	c.C493T	p.P165C	
XH_P36	16	28913639	28913639	Frame_Shift_Ins	INS	-	C	-	ATP2A1	c.2082dupC	p.R694fs	
XH_P36	16	29891248	29891248	Frame_Shift_Ins	INS	-	G	-	SEZ6L2	c.1167dupC	p.N390fs	
XH_P36	16	30018105	30018105	Splice_Site	SNP	C	T	C	DOC2A	.	.	
XH_P36	16	30680561	30680561	Silent	SNP	C	A	C	FBR5	c.C2538A	p.A846A	
XH_P36	16	30793666	30793666	Silent	SNP	G	T	G	ZNF629	c.C1983A	p.T661T	
XH_P36	16	30794963	30795046	In_Frame_Del	DEL	AGCTGAAGC	-	CAGCTGAAGCA	ZNF629	c.603_686del	p.201_229del	
XH_P36	16	31121549	31121549	Silent	SNP	C	A	C	BCKDK	c.C447A	p.A149A	
XH_P36	16	31142287	31142287	Nonsense_Mutation	SNP	C	T	C	KAT8	c.C1378T	p.Q460X	
XH_P36	16	46836971	46836971	In_Frame_Ins	INS	-	TTACCAAGGAG	-	C16orf87	5insTACTCTTCTG	59delinsVSLV	NK
XH_P36	16	48595224	48595224	Nonsense_Mutation	INS	-	AACCATTATTGC	-	N4BP1	AAGAGCAATAA	45delinsVF	LESIFFNNFLX
XH_P36	16	49670972	49670972	Silent	SNP	G	A	G	ZNF430C	c.C1740T	p.C580C	
XH_P36	16	53265642	53265642	Frame_Shift_Del	DEL	A	-	A	CHD9	c.2457delA	p.A819fs	
XH_P36	16	53706815	53706815	Missense_Mutation	SNP	A	T	A	RPGRIP1L	c.T996A	p.H332Q	
XH_P36	16	55983808	55983808	Frame_Shift_Ins	INS	-	TCACCTCTGGT	-	CESSA	sCCAACCAGAG	p.R17fs	
XH_P36	16	67006630	67006630	Missense_Mutation	SNP	A	T	A	CE53	c.A418T	p.T140S	
XH_P36	16	67472507	67472507	Missense_Mutation	SNP	C	T	C	ATP6V0D1	c.G980A	p.R327H	
XH_P36	16	67687145	67687145	Frame_Shift_Del	DEL	G	-	G	CARMIL2	c.3108delG	p.P1036fs	
XH_P36	16	67964372	67964372	Silent	SNP	G	A	G	CTRL	c.C438T	p.N146N	
XH_P36	16	68021792	68021792	Missense_Mutation	SNP	C	T	C	DPEP2	c.G695A	p.R232H	
XH_P36	16	70328814	70328814	Frame_Shift_Del	DEL	G	-	G	DDX19B	c.66delG	p.V22fs	
XH_P36	16	72138457	72138457	Frame_Shift_Del	DEL	T	-	T	DXH38	c.2083delT	p.F695fs	
XH_P36	16	72142164	72142164	Silent	SNP	C	T	C	DXH38	c.C3003T	p.F1001F	
XH_P36	16	72153907	72153907	Silent	SNP	G	A	G	PMFBP1	c.C2850T	p.A950A	
XH_P36	16	74660379	74660379	Silent	SNP	G	A	G	RFWD3	c.C2043T	p.I681I	
XH_P36	16	75258768	75258768	Missense_Mutation	SNP	C	T	C	CTRB1	c.C662T	p.P221L	
XH_P36	16	75564074	75564074	Missense_Mutation	SNP	G	A	G	CHTS5	c.C209T	p.S70L	
XH_P36	16	77325354	77325354	Missense_Mutation	SNP	C	T	C	ADAMTS18	c.G2695A	p.G899S	
XH_P36	16	81047739	81047739	Splice_Site	INS	-	ACTTTTAACTTT	-	CENPN	.	.	
XH_P36	16	81047740	81047740	Splice_Site	INS	-	TAAATAATTAAC	-	CENPN	.	.	
XH_P36	16	81095653	81095653	Missense_Mutation	SNP	C	T	C	C16orf46	c.G301A	p.D101N	
XH_P36	16	81301689	81301689	Missense_Mutation	SNP	C	T	C	BCO1	c.C796T	p.R266W	
XH_P36	16	84494362	84494362	Silent	SNP	C	T	C	ATP2C2	c.C1983T	p.S661S	
XH_P36	16	85721176	85721176	Frame_Shift_Ins	INS	-	C	-	GINS2	c.94dupG	p.D32fs	
XH_P36	16	87636771	87636771	Missense_Mutation	SNP	T	C	T	JPH3	c.T19C	p.F7L	
XH_P36	16	88496785	88496785	Silent	SNP	G	A	G	ZNF469	c.G2907A	p.S969S	
XH_P36	16	88870993	88870993	Missense_Mutation	SNP	C	A	C	CDT1	c.C269A	p.A90D	
XH_P36	16	89614422	89614422	Missense_Mutation	SNP	G	A	G	SPG7	c.G1564A	p.A522T	
XH_P36	16	90001937	90001937	Missense_Mutation	SNP	G	A	G	TUBB3	c.G862A	p.G288S	
XH_P36	17	3563601	3563601	Missense_Mutation	SNP	G	A	G	CTNS	c.G1042A	p.V348I	
XH_P36	17	3643130	3643130	Nonsense_Mutation	INS	-	CTTATTATCTCA	-	ITGAE	491insTTAGAGAT	831_E832delinsLRX	
XH_P36	17	3643131	3643131	Silent	SNP	G	T	G	ITGAE	c.C2490A	p.V830V	
XH_P36	17	6531438	6531438	Frame_Shift_Del	DEL	T	-	T	KIAA0753	c.717delA	p.K239fs	
XH_P36	17	7127698	7127698	Missense_Mutation	SNP	C	T	C	ACADVL	c.C1525T	p.R509W	
XH_P36	17	7217630	7217630	Frame_Shift_Del	DEL	T	-	T	GPS2	c.297delA	p.K99fs	
XH_P36	17	15234782	15234782	Nonsense_Mutation	INS	-	TAACCAACTATC	-	TEKT3	21insTGATAGT	N41_L42delinsX	
XH_P36	17	15961041	15961041	In_Frame_Ins	INS	-	GACAAA	-	NCOR1	69_5870insTTT	T1957delinsCP	
XH_P36	17	15961042	15961042	In_Frame_Ins	INS	-	CCAGGG	-	NCOR1	68_5869insCCC	T1957delinsPWT	
XH_P36	17	16097954	16097954	Splice_Site	INS	-	ATCTTTTTTTTT	-	NCOR1	.	.	
XH_P36	17	17696400	17696400	Silent	SNP	C	T	C	RAI1	c.C138T	p.L46L	
XH_P36	17	18651334	18651334	Missense_Mutation	SNP	T	C	T	FBXW10	c.T586C	p.W196R	
XH_P36	17	20163582	20163582	Missense_Mutation	SNP	G	A	G	SPECC1	c.G2672A	p.C891Y	
XH_P36	17	21318768	21318768	Silent	SNP	G	A	G	KCNJ12	c.G114A	p.T38T	
XH_P36	17	25910015	25910015	Frame_Shift_Ins	INS	-	C	-	KSR1	c.454dupC	p.T151fs	
XH_P36	17	26708249	26708249	Silent	SNP	C	T	C	SARM1	c.C495T	p.G165G	
XH_P36	17	26712159	26712159	Missense_Mutation	SNP	C	T	C	SARM1	c.C1492T	p.R498C	
XH_P36	17	27002460	27002460	Frame_Shift_Del	DEL	A	-	A	SUPT6H	c.580delA	p.K194fs	
XH_P36	17	27044426	27044426	Missense_Mutation	SNP	T	A	T	RAB34	c.A301T	p.T101S	
XH_P36	17	27239943	27239943	Missense_Mutation	SNP	C	T	C	PHF12	c.G1646A	p.G549D	
XH_P36	17	27903116	27903116	Missense_Mutation	SNP	C	T	C	GIT1	c.G1645A	p.V549I	
XH_P36	17	28380517	28380517	Nonsense_Mutation	INS	-	AGCTATTAAATT	-	EFCAB5	nsTTAGAGCTAT	9_Q460delinsLELLNX	
XH_P36	17	28380902	28380902	Frame_Shift_Ins	INS	-	TCTACTTGACCC	-	EFCAB5	3insCCTTCTACT	p.I588fs	
XH_P36	17	28706682	28706682	Frame_Shift_Ins	INS	-	C	-	CPD	c.685dupC	p.E228fs	
XH_P36	17	29527509	29527509	Missense_Mutation	SNP	G	A	G	NF1	c.G958A	p.A320T	
XH_P36	17	29632268	29632268	Silent	SNP	G	A	G	EVI2B	c.C360T	p.A120A	
XH_P36	17	33348680	33348680	Frame_Shift_Ins	INS	-	C	-	RFFL	c.300dupG	p.L101fs	
XH_P36	17	33348682	33348682	Missense_Mutation	SNP	T	A	T	RFFL	c.A297T	p.E100V	
XH_P36	17	34062267	34062267	Missense_Mutation	SNP	C	T	C	RASL10B	c.C64T	p.R22C	
XH_P36	17	34893857	34893857	Missense_Mutation	SNP	C	T	C	PIGW	c.C907T	p.R303C	
XH_P36	17	35914047	35914047	Frame_Shift_Ins	INS	-	TTTGCAGATTTT	-	SYNRG	95insATAAAATC	p.P432fs	
XH_P36	17	37650828	37650828	Nonsense_Mutation	INS	-	CTTACACGAGAT	-	CDK12	TTAATGCTTACAC	b.F767delinsLX	
XH_P36	17	38936698	38936698	Missense_Mutation	SNP	C	T	C	KRT27	c.G538A	p.E180K	
XH_P36	17	39340696	39340696	Silent	SNP	G	A	G	KRTAP4-1	c.C354T	p.C118C	
XH_P36	17	40042503	40042503	Missense_Mutation	SNP	T	G	T	ACLY	c.A2066C	p.N689T	
XH_P36	17	40940193	40940193	Frame_Shift_Ins	INS	-	C	-	WNK4	c.902dupC	p.S301fs	
XH_P36	17	41154724	41154724	Missense_Mutation	SNP	G	A	G	RPL27	c.G286A	p.V96I	
XH_P36	17	45234298	45234298	Missense_Mutation	SNP	G	C	G	CDC27	c.C640G	p.L214V	

XH_P36	17	45234343	45234343	Missense_Mutation	SNP	T	G	T	CDC27	c.A595C	p.N199H
XH_P36	17	46154355	46154355	Frame_Shift_Del	DEL	T	-	T	CBX1	c.12delA	p.K4fs
XH_P36	17	46925466	46925466	Missense_Mutation	SNP	G	T	G	CALCO2	c.G5T	p.W2L
XH_P36	17	48470257	48470257	Missense_Mutation	SNP	G	A	G	LRRC59	c.C167T	p.S56L
XH_P36	17	48647125	48647125	Missense_Mutation	SNP	C	T	C	CACNA1G	c.C547T	p.R183C
XH_P36	17	48676979	48676979	Missense_Mutation	SNP	G	A	G	CACNA1G	c.G3380A	p.R1127Q
XH_P36	17	48692826	48692826	Missense_Mutation	SNP	G	A	G	CACNA1G	c.G4762A	p.G1588R
XH_P36	17	53392628	53392628	Silent	SNP	T	C	T	HLF	c.T237C	p.I79I
XH_P36	17	54520274	54520274	Missense_Mutation	SNP	C	T	C	ANKFN1	c.C1088T	p.P363L
XH_P36	17	56329792	56329792	Missense_Mutation	SNP	C	A	C	LPO	c.C781A	p.L261M
XH_P36	17	56385030	56385030	Missense_Mutation	SNP	G	A	G	TSPOAP1	c.C4745T	p.S1582L
XH_P36	17	56388417	56388417	Missense_Mutation	SNP	G	A	G	TSPOAP1	c.C3059T	p.P1020L
XH_P36	17	56400068	56400068	Missense_Mutation	SNP	G	A	G	TSPOAP1	c.C1084T	p.R362C
XH_P36	17	56438293	56438293	Nonsense_Mutation	SNP	G	A	G	RNF43	c.C319T	p.Q107X
XH_P36	17	56676693	56676693	Silent	SNP	C	T	C	TEX14	c.G2031A	p.A677A
XH_P36	17	57746175	57746175	Missense_Mutation	SNP	C	A	C	CLTC	c.C2178A	p.S726R
XH_P36	17	59465981	59465981	Frame_Shift_Del	DEL	A	-	A	BCAS3	c.2662delA	p.K888fs
XH_P36	17	59560599	59560599	Missense_Mutation	SNP	C	G	C	TBX4	c.C1360G	p.R454G
XH_P36	17	59560601	59560601	Frame_Shift_Ins	INS	-	CTGGGGTGGAC	-	TBX4	3insTGTCTGGG	p.R454fs
XH_P36	17	60042378	60042378	Missense_Mutation	SNP	A	C	A	MED13	c.T4833G	p.D1611E
XH_P36	17	61497894	61497894	Frame_Shift_Del	DEL	C	-	C	TANC2	c.4551delC	p.S1517fs
XH_P36	17	65908303	65908303	Nonsense_Mutation	INS	-	TTATTTGATCAC	-	BPTF	TTAGCTTTATT	435_V1436delinsIFX
XH_P36	17	66416494	66416494	Missense_Mutation	SNP	C	A	C	ARSG	c.C1468A	p.L490I
XH_P36	17	73555417	73555417	Silent	SNP	C	T	C	LLGL2	c.C456T	p.N152N
XH_P36	17	73646720	73646720	Nonstop_Mutation	SNP	T	C	T	RECQL5	c.A1308G	p.X436W
XH_P36	17	73759512	73759512	Frame_Shift_Del	DEL	G	-	G	GALK1	c.364delC	p.L122fs
XH_P36	17	73914025	73914025	Silent	SNP	G	A	G	FBF1	c.C2373T	p.D791D
XH_P36	17	74015081	74015081	Missense_Mutation	SNP	G	A	G	EVPL	c.C1198T	p.R400W
XH_P36	17	74072983	74072983	Missense_Mutation	SNP	G	A	G	GALR2	c.G635A	p.R212H
XH_P36	17	77758181	77758181	Silent	SNP	C	T	C	CBX2	c.C939T	p.S313S
XH_P36	17	78090823	78090823	Missense_Mutation	SNP	C	T	C	GAA	c.C2246T	p.A749V
XH_P36	17	79210603	79210603	Splice_Site	SNP	T	C	T	TEPSIN	-	-
XH_P36	17	79249771	79249771	Missense_Mutation	SNP	G	T	G	SLC38A10	c.C910A	p.Q304K
XH_P36	17	79769608	79769608	Missense_Mutation	SNP	C	A	C	GCCR	c.C739A	p.L247M
XH_P36	17	79792754	79792754	Missense_Mutation	SNP	C	T	C	PPP1R27	c.G76A	p.V26M
XH_P36	17	79826463	79826463	Frame_Shift_Del	DEL	G	-	G	ARHGDI	c.792delC	p.P264fs
XH_P36	18	2775745	2775745	Missense_Mutation	SNP	C	T	C	SMCHD1	c.C5189T	p.A1730V
XH_P36	18	3116424	3116424	Frame_Shift_Del	DEL	C	-	C	MYOM1	c.2920delG	p.V974fs
XH_P36	18	8824907	8824907	Silent	SNP	C	T	C	MTCL1	c.C3399T	p.A1133A
XH_P36	18	9221979	9221979	Missense_Mutation	SNP	G	A	G	ANKRD12	c.G856A	p.D286N
XH_P36	18	9221980	9221980	Frame_Shift_Ins	INS	-	CCTCAACTAC	-	ANKRD12	858insCCTCAA	p.D286fs
XH_P36	18	9530853	9530853	Nonsense_Mutation	INS	-	TGTG	-	RALBP1	369_1370insTG	457_E458delinsLX
XH_P36	18	9530855	9530855	In_Frame_Ins	INS	-	ACTCAATTCTGG	-	RALBP1	tsAAATACTCAA	457delinsQKYSILVN
XH_P36	18	10807272	10807272	Frame_Shift_Ins	INS	-	T	-	PIEZO2	c.917_918insA	p.R306fs
XH_P36	18	10807273	10807273	Splice_Site	INS	-	AGTGTCTGGGT	-	PIEZO2	-	-
XH_P36	18	13057634	13057634	Missense_Mutation	SNP	G	A	G	CEP192	c.G4159A	p.G1387R
XH_P36	18	13114225	13114225	Frame_Shift_Ins	INS	-	ACTCTGTC	-	CEP192	4_7265insACTC	p.S2422fs
XH_P36	18	13731800	13731800	Nonsense_Mutation	INS	-	CTGTAAACACT	-	RNMT	TATTACTGTAA	45_G96delinsWYLYX
XH_P36	18	13746253	13746253	Frame_Shift_Del	DEL	A	-	A	RNMT	c.1174delA	p.K392fs
XH_P36	18	14538206	14538206	Silent	SNP	T	C	T	POTEC	c.A564G	p.V188V
XH_P36	18	21921518	21921518	Missense_Mutation	SNP	C	T	C	OSBPL1A	c.G387A	p.M129I
XH_P36	18	22057387	22057387	In_Frame_Ins	INS	-	GAA	-	HRH4	770_771insGA	W257delinsWK
XH_P36	18	22057389	22057389	Frame_Shift_Ins	INS	-	AATTGTATTGCT	-	HRH4	773insAATTGTGA	p.L258fs
XH_P36	18	24127013	24127013	Frame_Shift_Del	DEL	G	-	G	KCTD1	c.1488delC	p.P496fs
XH_P36	18	28710536	28710536	Nonsense_Mutation	INS	-	GTTTGTTAATTC	-	DSCL	AAAAGAGAAATT	876delinsHIKENX
XH_P36	18	32825748	32825748	Missense_Mutation	SNP	G	A	G	ZNF397	c.G1079A	p.R360Q
XH_P36	18	43223957	43223957	Missense_Mutation	SNP	G	A	G	SLC14A2	c.G1183A	p.V395M
XH_P36	18	44102168	44102168	Missense_Mutation	SNP	G	A	G	LOXHD1	c.C1360T	p.R454C
XH_P36	18	47753971	47753971	Frame_Shift_Ins	INS	-	TTCTTTTTCCT	-	CFAP53	5insTCAGGGAA	p.R442fs
XH_P36	18	47753973	47753973	Frame_Shift_Ins	INS	-	TTGTGTAA	-	CFAP53	2_1323insTTAC	p.Q441fs
XH_P36	18	55103822	55103822	Missense_Mutation	SNP	C	A	C	ONECUT2	c.C874A	p.L292M
XH_P36	18	56651438	56651438	Missense_Mutation	SNP	G	A	G	ZNF532	c.G3646A	p.V1216I
XH_P36	18	57013194	57013194	Frame_Shift_Del	DEL	T	-	T	LMAN1	c.912delA	p.K304fs
XH_P36	18	57022886	57022886	In_Frame_Ins	INS	-	CTTTTGACAATC	-	LMAN1	2CATCATTTGCA	8delinsAFPSLSKESKN
XH_P36	18	57022888	57022888	Missense_Mutation	SNP	C	T	C	LMAN1	c.G217A	p.A737T
XH_P36	18	66377374	66377374	Missense_Mutation	SNP	G	A	G	TMX3	c.C149T	p.A50V
XH_P36	18	74091072	74091072	Missense_Mutation	SNP	G	A	G	ZNF516	c.C2988T	p.R1000C
XH_P36	18	76753476	76753476	Silent	SNP	G	A	G	SALL3	c.G1485A	p.S495S
XH_P36	18	77624107	77624107	Missense_Mutation	SNP	C	T	C	KCNQ2	c.C440T	p.A147V
XH_P36	19	436668	436668	Missense_Mutation	SNP	G	T	G	SHC2	c.C736A	p.H246N
XH_P36	19	629605	629605	Missense_Mutation	SNP	G	A	G	POLRMT	c.C575T	p.R253W
XH_P36	19	808433	808433	Silent	SNP	C	T	C	PTBP1	c.C1149T	p.D383D
XH_P36	19	1000483	1000483	Missense_Mutation	SNP	G	A	G	GRIN3B	c.G47A	p.G16E
XH_P36	19	1012099	1012099	Silent	SNP	G	A	G	TMEM259	c.C807T	p.S269S
XH_P36	19	1254317	1254317	Frame_Shift_Del	DEL	G	-	G	MIDN	c.S36delG	p.R179fs
XH_P36	19	1585169	1585169	Missense_Mutation	SNP	T	C	T	MBD3	c.A155G	p.Y52C
XH_P36	19	1611736	1611736	Silent	SNP	G	A	G	TCF3	c.C1926T	p.S642S
XH_P36	19	1816767	1816767	Missense_Mutation	SNP	C	T	C	REXO1	c.G3247A	p.D1083N
XH_P36	19	1819941	1819941	Missense_Mutation	SNP	C	T	C	REXO1	c.G2642A	p.G881D
XH_P36	19	3831790	3831790	Missense_Mutation	SNP	C	T	C	ZFR2	c.G466A	p.G156R
XH_P36	19	3907867	3907867	Missense_Mutation	SNP	G	A	G	ATCAY	c.G494A	p.R165H
XH_P36	19	4207239	4207239	Missense_Mutation	SNP	C	T	C	ANKRD24	c.C467T	p.A156V
XH_P36	19	4322990	4322990	Silent	SNP	G	A	G	FSD1	c.G1047A	p.T349T
XH_P36	19	5245795	5245795	Missense_Mutation	SNP	G	A	G	PTPRS	c.C941T	p.T314M
XH_P36	19	6047495	6047495	Missense_Mutation	SNP	C	T	C	RFK2	c.G13A	p.E5K
XH_P36	19	6213976	6213976	Frame_Shift_Del	DEL	G	-	G	MLT1	c.1381delC	p.Q461fs
XH_P36	19	6477251	6477251	Frame_Shift_Del	DEL	G	-	G	DENND1C	c.359delC	p.P120fs
XH_P36	19	6750380	6750380	Frame_Shift_Del	DEL	C	-	C	TRIP10	c.1305delC	p.D435fs
XH_P36	19	7970711	7970711	Missense_Mutation	SNP	G	T	G	MAP2K7	c.G143T	p.S48I
XH_P36	19	8156455	8156455	Missense_Mutation	SNP	C	A	C	FBN3	c.G5925T	p.E1975D
XH_P36	19	9018533	9018533	Silent	SNP	G	T	G	MUC16	c.C37641A	p.T12547T
XH_P36	19	9046704	9046704	In_Frame_Ins	INS	-	GACAACAATCTC	-	MUC16	34927insGAGAT	11643delinsEIVVS
XH_P36	19	9067934	9067934	In_Frame_Ins	INS	-	ATAGCAGTAACC	-	MUC16	12insATTGGTTA	504delinsSLVTAMF
XH_P36	19	9068827	9068827	Frame_Shift_Ins	INS	-	AG	-	MUC16	18618_18619ins	p.V6207fs
XH_P36	19	9068829	9068829	In_Frame_Ins	INS	-	ACACACACAATG	-	MUC16	18617insCATTTG	6206delinsALCVY
XH_P36	19	9084742	9084742	In_Frame_Ins	INS	-	ACACCTATTCTC	-	MUC16	tsATCAAGAGAA	58delinsHQENRCYW
XH_P36	19	9086879	9086879	Missense_Mutation	SNP	C	A	C	MUC16	c.G4936T	p.G1646C
XH_P36	19	9087185	9087185	In_Frame_Ins	INS	-	ACAAACATT	-	MUC16	9_4630insAATG	V1544delinsMVCW

XH_P36	19	9271744	9271744	Missense_Mutation	SNP	G	A	G	ZNF317	c.G1327A	p.E443K
XH_P36	19	9577251	9577251	Nonstop_Mutation	INS	-	TTTTTTTTTTTC	-	ZNF560	rsCATCAAAAAA	685delinsSSKKKE
XH_P36	19	9767278	9767278	Missense_Mutation	SNP	C	T	C	ZNF562	c.G77A	p.R26Q
XH_P36	19	9965152	9965152	Missense_Mutation	SNP	G	A	G	OLF12	c.C841T	p.R281W
XH_P36	19	10446365	10446365	Frame_Shift_Del	DEL	G	-	G	ICAM3	c.631delC	p.R211fs
XH_P36	19	10577862	10577862	Silent	SNP	C	T	C	PDE4A	c.C1509T	p.V503V
XH_P36	19	10812678	10812678	Missense_Mutation	SNP	C	A	C	QTRT1	c.C296A	p.P99H
XH_P36	19	11141507	11141507	Missense_Mutation	SNP	G	A	G	SMARCA4	c.G3484A	p.G1162S
XH_P36	19	11725438	11725438	Frame_Shift_Ins	INS	-	CAAACTTTATT	-	ZNF627	rsTTTCCAAACAT	p.R34fs
XH_P36	19	11728278	11728278	In_Frame_Ins	INS	-	ATAAGGTTTCCTC	-	ZNF627	insTTCATAAGG	210delinsAFIRLS
XH_P36	19	11891280	11891280	Frame_Shift_Ins	INS	-	SAGGTCITTCATC	-	ZNF441	42insGAGGCTCT	p.L214fs
XH_P36	19	12060335	12060335	Frame_Shift_Ins	INS	-	TGCTTGC	-	ZNF700	DS_1506insTGC	p.I502fs
XH_P36	19	12060336	12060336	Frame_Shift_Ins	INS	-	TTTAT	-	ZNF700	506_1507insTT	p.I502fs
XH_P36	19	12461585	12461585	Frame_Shift_Ins	INS	-	AAGACACATGAT	-	ZNF442	4insTTATCATGT	p.K272fs
XH_P36	19	12502590	12502590	Frame_Shift_Del	DEL	A	-	A	ZNF799	c.622delT	p.W208fs
XH_P36	19	12812581	12812581	Silent	SNP	C	T	C	TNPO2	c.G2496A	p.P832P
XH_P36	19	13246192	13246192	Silent	SNP	C	T	C	NACC1	c.C171T	p.D57D
XH_P36	19	13319692	13319694	In_Frame_Del	DEL	GAT	-	GAT	CACNA1A	c.6659_6661del	2220_2221del
XH_P36	19	14584381	14584381	Missense_Mutation	SNP	C	T	C	PTGER1	c.G752A	p.R251H
XH_P36	19	14938341	14938341	Nonsense_Mutation	INS	-	AACTTGCTCCTTC	-	OR7A5	rsAATAGAGGAC	F238_S239delinsX
XH_P36	19	14939035	14939035	Frame_Shift_Ins	INS	-	TACTTCCACC	-	OR7A5	19insGGTGGAA	p.T7fs
XH_P36	19	14939037	14939037	Missense_Mutation	SNP	T	C	T	OR7A5	c.A17G	p.D6G
XH_P36	19	15291600	15291600	Missense_Mutation	SNP	C	T	C	NOTCH3	c.G3034A	p.G1012R
XH_P36	19	15562864	15562864	Missense_Mutation	SNP	T	C	T	RASAL3	c.A2884G	p.K962E
XH_P36	19	16633994	16633994	Frame_Shift_Del	DEL	G	-	G	CHERP	c.1849delC	p.H617fs
XH_P36	19	17397466	17397501	In_Frame_Del	DEL	GTGTGTGTG	-	TGTGTGTGTGTG	ANKLE1	c.1898_1933del	p.633_645del
XH_P36	19	17449476	17449476	Missense_Mutation	SNP	C	T	C	GTPBP3	c.C517T	p.R173W
XH_P36	19	17611422	17611422	Silent	SNP	C	T	C	SLC27A1	c.C1452T	p.G484G
XH_P36	19	17716896	17716896	Silent	SNP	G	A	G	UNC13A	c.C5079T	p.S1693S
XH_P36	19	18377405	18377405	Frame_Shift_Ins	INS	-	ATGCCACAAA	-	KIAA1683	945insTTGTGG	p.Q315fs
XH_P36	19	19137021	19137021	Nonsense_Mutation	INS	-	CAGGTCA	-	SUGP2	BS_136insTGAC	V46_P47delinsX
XH_P36	19	19368961	19368961	Missense_Mutation	SNP	C	T	C	HAPLN4	c.G874A	p.A292T
XH_P36	19	19646214	19646214	Missense_Mutation	SNP	G	T	G	YJEFN3	c.G348T	p.Q116H
XH_P36	19	19654762	19654762	Frame_Shift_Del	DEL	C	-	C	CILP2	c.1408delC	p.P470fs
XH_P36	19	20116817	20116817	Silent	SNP	C	T	C	ZNF682	c.G1398A	p.T466T
XH_P36	19	21132847	21132847	Silent	SNP	A	C	A	ZNF85	c.A1335C	p.P445P
XH_P36	19	21366317	21366317	Missense_Mutation	SNP	T	A	T	ZNF431	c.T1214A	p.V405E
XH_P36	19	21366318	21366318	Silent	SNP	G	A	G	ZNF431	c.G1215A	p.V405V
XH_P36	19	21476830	21476830	Missense_Mutation	SNP	C	A	C	ZNF708	c.G746T	p.C249F
XH_P36	19	21476831	21476831	Missense_Mutation	SNP	A	G	A	ZNF708	c.T745C	p.C249R
XH_P36	19	21606900	21606900	Missense_Mutation	SNP	G	A	G	ZNF493	c.G1055A	p.R352K
XH_P36	19	21991466	21991466	Missense_Mutation	SNP	A	T	A	ZNF43	c.T1178A	p.V393E
XH_P36	19	22155346	22155346	Silent	SNP	T	C	T	ZNF208	c.A2490G	p.E830E
XH_P36	19	22156714	22156714	Silent	SNP	G	A	G	ZNF208	c.C1122T	p.C374C
XH_P36	19	22363189	22363189	Missense_Mutation	SNP	C	T	C	ZNF676	c.G1330A	p.A444T
XH_P36	19	22375871	22375871	Nonsense_Mutation	INS	-	TTACAGTGATAG	-	ZNF676	TTGGCTATCACT	6_G27delinsLWSLX
XH_P36	19	22497408	22497408	Missense_Mutation	SNP	G	A	G	ZNF729	c.G1189A	p.V397I
XH_P36	19	22499464	22499464	Missense_Mutation	SNP	A	G	A	ZNF729	c.A3245G	p.D1082G
XH_P36	19	22574593	22574593	Missense_Mutation	SNP	C	T	C	ZNF98	c.G1444A	p.V482I
XH_P36	19	22941717	22941717	Missense_Mutation	SNP	G	T	G	ZNF99	c.C994A	p.Q332K
XH_P36	19	23543701	23543701	Missense_Mutation	SNP	T	C	T	ZNF91	c.A1984G	p.T662A
XH_P36	19	23544625	23544625	Missense_Mutation	SNP	C	T	C	ZNF91	c.G1060A	p.A354T
XH_P36	19	23927290	23927290	Silent	SNP	G	A	G	ZNF681	c.C1062T	p.T354T
XH_P36	19	30312660	30312660	Missense_Mutation	SNP	C	T	C	CCNE1	c.C494T	p.A165V
XH_P36	19	30313453	30313453	Silent	SNP	C	T	C	CCNE1	c.C918T	p.G306G
XH_P36	19	30500119	30500124	In_Frame_Del	DEL	TGATGA	-	TGATGA	URI1	c.840_845del	p.280_282del
XH_P36	19	30934880	30934880	Frame_Shift_Del	DEL	G	-	G	ZNF536	c.411delG	p.K137fs
XH_P36	19	30934881	30934881	Missense_Mutation	SNP	C	A	C	ZNF536	c.C412A	p.R138S
XH_P36	19	31768042	31768042	Missense_Mutation	SNP	G	A	G	TSHZ3	c.C2657T	p.T886M
XH_P36	19	31768155	31768155	Silent	SNP	G	A	G	TSHZ3	c.C2544T	p.S848S
XH_P36	19	33167417	33167417	Frame_Shift_Ins	INS	-	G	-	RGS9BP	c.249dupG	p.S83fs
XH_P36	19	33167776	33167776	Frame_Shift_Del	DEL	G	-	G	RGS9BP	c.607delG	p.G203fs
XH_P36	19	35449607	35449607	Silent	SNP	A	G	A	ZNF792	c.T1152C	p.H384H
XH_P36	19	35524868	35524868	Missense_Mutation	SNP	C	T	C	SCN1B	c.C673T	p.R225C
XH_P36	19	36018393	36018393	Missense_Mutation	SNP	A	G	A	SBSN	c.T791C	p.V264A
XH_P36	19	36223175	36223175	Frame_Shift_Del	DEL	C	-	C	KMT2B	c.5725delC	p.P1909fs
XH_P36	19	36303630	36303630	Silent	SNP	G	A	G	PRODH2	c.C306T	p.G102G
XH_P36	19	36362899	36362899	Missense_Mutation	SNP	C	T	C	APLP1	c.C811T	p.P271S
XH_P36	19	36370092	36370092	Silent	SNP	C	T	C	APLP1	c.C1830T	p.V610Y
XH_P36	19	36940815	36940815	Frame_Shift_Del	DEL	T	-	T	ZNF566	c.9delA	p.K3fs
XH_P36	19	37005981	37005981	Missense_Mutation	SNP	A	T	A	ZNF260	c.T160A	p.S54T
XH_P36	19	37039180	37039180	Nonsense_Mutation	INS	-	CATACTGGTGG	-	ZNF529	rsTTTTTCCACCA	D76_177delinsX
XH_P36	19	37240584	37240584	Missense_Mutation	SNP	T	C	T	ZNF850	c.A1262G	p.E421G
XH_P36	19	37368718	37368718	Frame_Shift_Ins	INS	-	CTACCACATTC	-	ZNF345	AGGCCTTACCA	p.L1329fs
XH_P36	19	38028415	38028415	Frame_Shift_Del	DEL	T	-	T	ZNF793	c.855delT	p.C285fs
XH_P36	19	38655461	38655461	Missense_Mutation	SNP	G	A	G	SIPA1L3	c.G4123A	p.G1375fs
XH_P36	19	38885396	38885396	Frame_Shift_Ins	INS	-	C	-	SPRED3	c.538dupC	p.T179fs
XH_P36	19	39200039	39200039	Missense_Mutation	SNP	A	G	A	ACTN4	c.A656G	p.D219G
XH_P36	19	39360822	39360822	Missense_Mutation	SNP	A	G	A	RINL	c.T1103C	p.L368P
XH_P36	19	39379738	39379738	Missense_Mutation	SNP	A	G	A	SIRT2	c.T379C	p.C127R
XH_P36	19	39734782	39734782	Missense_Mutation	SNP	C	T	C	IFNL3	c.G274A	p.V92M
XH_P36	19	41518269	41518269	Missense_Mutation	SNP	C	T	C	CYP2B6	c.C1031T	p.A344V
XH_P36	19	41631436	41631436	Silent	SNP	C	T	C	CYP2F1	c.C1191T	p.Y397Y
XH_P36	19	43528843	43528843	Silent	SNP	G	A	G	PSG11	c.C430T	p.L144L
XH_P36	19	44169554	44169554	Frame_Shift_Ins	INS	-	ATCCCCAACTCA	-	PLAUR	24insATGAGTTG	p.R75fs
XH_P36	19	44660972	44660972	Nonsense_Mutation	INS	-	TGAGATGTAA	-	ZNF234	804insTGAGAT	F58_F269delinsAEMX
XH_P36	19	44660973	44660973	Frame_Shift_Ins	INS	-	AGAAGCTT	-	ZNF234	4_805insAGAA	p.A268fs
XH_P36	19	44933181	44933181	Frame_Shift_Ins	INS	-	GAATAAGAA	-	ZNF229	rsTCGGTTCTTCT	p.R586fs
XH_P36	19	44980744	44980744	Missense_Mutation	SNP	G	T	G	ZNF180	c.C1879A	p.Q627K
XH_P36	19	44980745	44980745	Frame_Shift_Ins	INS	-	TTTTAAGGTAG	-	ZNF180	ACATGTACTACC	p.H626fs
XH_P36	19	45573321	45573321	Missense_Mutation	SNP	G	A	G	CLASRP	c.G1730A	p.R577H
XH_P36	19	46116858	46116858	Missense_Mutation	SNP	C	T	C	EML2	c.G1765A	p.A589T
XH_P36	19	46289347	46289347	Silent	SNP	C	T	C	DMWD	c.G1407A	p.T469T
XH_P36	19	48184060	48184060	Missense_Mutation	SNP	G	A	G	BICRA	c.G1633A	p.A545T
XH_P36	19	49000877	49000877	Missense_Mutation	SNP	A	G	A	LMTK3	c.T3536C	p.L1179P
XH_P36	19	49657889	49657889	In_Frame_Ins	INS	-	TCCTCC	-	HRC	DS_606insGAG	E202delinsEEE
XH_P36	19	49860534	49860534	Nonsense_Mutation	SNP	G	T	G	TEAD2	c.C335A	p.S112X
XH_P36	19	51170969	51170969	Silent	SNP	C	T	C	SHANK1	c.G4248A	p.A1416A

XH_P36	19	51601912	51601912	Frame_Shift_Del	DEL	C	-	C	CTU1	c.993delG	p.G331fs
XH_P36	19	52716080	52716080	Silent	SNP	C	T	C	PPP2R1A	c.C645T	p.D215D
XH_P36	19	53086110	53086110	Silent	SNP	T	A	T	ZNF701	c.T798A	p.G266G
XH_P36	19	53643823	53643823	Missense_Mutation	SNP	G	A	G	ZNF347	c.C2261T	p.A754V
XH_P36	19	53644695	53644695	Silent	SNP	G	A	G	ZNF347	c.C1389T	p.C463C
XH_P36	19	53855284	53855284	Silent	SNP	G	A	G	ZNF845	c.G1356A	p.S452S
XH_P36	19	55481600	55481600	Missense_Mutation	SNP	C	A	C	NLRP2	c.C217A	p.L73I
XH_P36	19	56127331	56127331	Frame_Shift_Del	DEL	G	-	G	ZNF865	c.2347delG	p.G783fs
XH_P36	19	56953857	56953857	Frame_Shift_Ins	INS	-	GATGTCATCCCT	-	ZNF667	GTAAGGAGGAT	p.E169fs
XH_P36	19	57036570	57036570	In_Frame_Ins	INS	-	CTTACATTATAT	-	ZNF471	13insCCTTACAT	1304delinsPIYIM
XH_P36	19	57050528	57050528	Silent	SNP	G	A	G	ZFP28	c.G141A	p.P47P
XH_P36	19	57133248	57133248	Missense_Mutation	SNP	G	A	G	ZNF71	c.G593A	p.R198H
XH_P36	19	57640277	57640277	Nonsense_Mutation	INS	-	CATCCACATATA	-	USP29	5insCTCATCCAC	8_N79delinsNLIHIX
XH_P36	19	57932842	57932842	Frame_Shift_Ins	INS	-	ATTTG	-	ZNF17	982_1983insAT	p.T661fs
XH_P36	19	58049281	58049281	In_Frame_Ins	INS	-	CCCTGCTTC	-	ZNF549	0_871insCCCTG	5290delinsSPCF
XH_P36	19	58050159	58050159	Nonsense_Mutation	INS	-	TTTGTGATGCTT	-	ZNF549	5TGGAATTTTGTG	583_K584delinsX
XH_P36	19	58152336	58152336	Missense_Mutation	SNP	C	T	C	ZNF211	c.C299T	p.A100V
XH_P36	19	58213374	58213374	Missense_Mutation	SNP	T	C	T	ZNF154	c.A943G	p.S315G
XH_P36	19	58485478	58485478	Missense_Mutation	SNP	G	A	G	C19orf18	c.C215T	p.S72L
XH_P36	19	58629726	58629726	Missense_Mutation	SNP	G	A	G	ZSCAN18	c.C38T	p.T13M
XH_P36	20	1460483	1460483	Frame_Shift_Ins	INS	-	AACAATACATAT	-	SIRPB2	TACAAATATGTA	p.P105fs
XH_P36	20	3003413	3003413	Silent	SNP	C	T	C	PTPRA	c.C1380T	p.A460D
XH_P36	20	3003414	3003414	Missense_Mutation	SNP	G	A	G	PTPRA	c.G1381A	p.V461M
XH_P36	20	4228843	4228843	Silent	SNP	G	A	G	ADRA1D	c.C762T	p.Y254Y
XH_P36	20	5903414	5903414	Frame_Shift_Del	DEL	A	-	A	CHGB	c.624delA	p.I208fs
XH_P36	20	14307546	14307546	Missense_Mutation	SNP	G	A	G	FLRT3	c.C607T	p.R203C
XH_P36	20	16347868	16347868	Missense_Mutation	SNP	C	T	C	KIF16B	c.G4102A	p.A1368T
XH_P36	20	18286958	18286958	Missense_Mutation	SNP	A	T	A	ZNF133	c.A180T	p.K60N
XH_P36	20	18296347	18296347	Silent	SNP	G	A	G	ZNF133	c.G795A	p.T265T
XH_P36	20	23345348	23345348	Frame_Shift_Ins	INS	-	AG	-	GZF1	c.328_329insAG	p.L110fs
XH_P36	20	23345349	23345349	Nonsense_Mutation	INS	-	5GTTAAATGGG	-	GZF1	10insAGGTTAAAT	10_E111delinsGX
XH_P36	20	25000780	25000780	Missense_Mutation	SNP	C	T	C	ACSS1	c.G749A	p.R250Q
XH_P36	20	25457670	25457670	Missense_Mutation	SNP	C	T	C	NINL	c.G2257A	p.A753T
XH_P36	20	30606904	30606904	Frame_Shift_Del	DEL	G	-	G	CCM2L	c.625delG	p.G209fs
XH_P36	20	32664877	32664877	Silent	SNP	C	T	C	RALY	c.C654T	p.G218G
XH_P36	20	33328811	33328811	In_Frame_Ins	INS	-	CCC	-	NCOA6	5248_5249insG	51750delinsWA
XH_P36	20	33328812	33328812	Frame_Shift_Ins	INS	-	GTCT	-	NCOA6	247_5248insAG	p.S1750fs
XH_P36	20	33345744	33345744	Silent	SNP	C	T	C	NCOA6	c.G807A	p.Q269Q
XH_P36	20	33589096	33589096	Missense_Mutation	SNP	G	A	G	MYH7B	c.G5650A	p.E1884K
XH_P36	20	34022391	34022391	Missense_Mutation	SNP	C	T	C	GDF5	c.C802T	p.R268W
XH_P36	20	34208670	34208670	Missense_Mutation	SNP	C	T	C	SPAG4	c.C911T	p.S304L
XH_P36	20	36031782	36031782	Nonstop_Mutation	SNP	G	T	G	SRC	c.G1611T	p.X537Y
XH_P36	20	37357196	37357196	Missense_Mutation	SNP	G	A	G	SLC32A1	c.G1492A	p.V498I
XH_P36	20	42788776	42788776	Silent	SNP	G	A	G	JPH2	c.C651T	p.G217G
XH_P36	20	43850774	43850774	Nonsense_Mutation	INS	-	TATGTTGTTGGT	-	SEMG2	TTTAGTATGTTG	W167delinsWIX
XH_P36	20	44530971	44530971	Silent	SNP	G	A	G	PLTP	c.C825T	p.D275D
XH_P36	20	45002133	45002133	Frame_Shift_Del	DEL	G	-	G	ELMO2	c.1321delC	p.H441fs
XH_P36	20	56090848	56090848	Missense_Mutation	SNP	G	A	G	CTCF	c.C316T	p.R106C
XH_P36	20	57768838	57768838	Missense_Mutation	SNP	C	A	C	ZNF831	c.C2764A	p.P922T
XH_P36	20	57768886	57768886	Frame_Shift_Ins	INS	-	C	-	ZNF831	c.2813dupC	p.S938fs
XH_P36	20	60584133	60584133	Missense_Mutation	SNP	A	G	A	TAF4	c.T1859C	p.V620A
XH_P36	20	60705321	60705321	Silent	SNP	C	T	C	LSM14B	c.C642T	p.D214D
XH_P36	20	60776082	60776082	Silent	SNP	C	T	C	MTG2	c.C1170T	p.D390D
XH_P36	20	61982271	61982271	Silent	SNP	G	A	G	CHRNA4	c.C492T	p.D164D
XH_P36	20	62196336	62196336	Missense_Mutation	SNP	A	G	A	HELZ2	c.T2132C	p.L711P
XH_P36	20	62199927	62199927	Missense_Mutation	SNP	C	G	C	HELZ2	c.G1514C	p.R505T
XH_P36	20	62591287	62591287	Frame_Shift_Del	DEL	C	-	C	ZNF512B	c.2633delG	p.G878fs
XH_P36	21	10908835	10908835	Nonsense_Mutation	SNP	C	A	C	TPTE	c.G1096T	p.E366G
XH_P36	21	10908837	10908837	Frame_Shift_Ins	INS	-	TTGTCTTGAGA	-	TPTE	AGTGGGTCTCAA	p.I365fs
XH_P36	21	22664532	22664532	Missense_Mutation	SNP	A	T	A	NCAM2	c.A590T	p.D197V
XH_P36	21	30343059	30343059	Nonsense_Mutation	INS	-	TTCAATAAATAC	-	LTN1	TTAAAGATATT	p.C376delinsX
XH_P36	21	32589885	32589885	Missense_Mutation	SNP	C	T	C	TIAM1	c.G2126A	p.R709Q
XH_P36	21	42866456	42866456	Missense_Mutation	SNP	G	A	G	TMPPRS2	c.C176T	p.P59L
XH_P36	21	43510462	43510462	Missense_Mutation	SNP	G	A	G	UMODL1	c.G845A	p.C282Y
XH_P36	21	45389100	45389100	Missense_Mutation	SNP	G	T	G	AGPAT3	c.G450T	p.E150D
XH_P36	21	45877262	45877262	Silent	SNP	C	T	C	LRRC3	c.C735T	p.S245S
XH_P36	21	47648492	47648492	Silent	SNP	G	C	G	LSS	c.C36G	p.G12G
XH_P36	22	17601702	17601702	Frame_Shift_Ins	INS	-	G	-	CECR6	c.315dupC	p.A106fs
XH_P36	22	18300932	18300932	Frame_Shift_Del	DEL	G	-	G	MICAL3	c.4495delC	p.R1499fs
XH_P36	22	19808804	19808804	Silent	SNP	C	T	C	GNB1L	c.G75A	p.A25A
XH_P36	22	20843349	20843349	Silent	SNP	G	A	G	KLHL22	c.C150T	p.F50F
XH_P36	22	21800025	21800025	Frame_Shift_Del	DEL	C	-	C	HIC2	c.841delC	p.P281fs
XH_P36	22	24124503	24124503	Missense_Mutation	SNP	C	T	C	MMP11	c.C1166T	p.A389V
XH_P36	22	24836696	24836696	Missense_Mutation	SNP	G	A	G	ADORA2A	c.G478A	p.G160R
XH_P36	22	24837032	24837032	Missense_Mutation	SNP	C	A	C	ADORA2A	c.C814A	p.L272M
XH_P36	22	25625546	25625546	Splice_Site	SNP	G	A	G	CRYBB2	.	.
XH_P36	22	26239838	26239838	Silent	SNP	C	A	C	MYO18B	c.C3348A	p.P1116P
XH_P36	22	29446275	29446275	Frame_Shift_Del	DEL	G	-	G	ZNRF3	c.2106delG	p.K702fs
XH_P36	22	29837600	29837600	Missense_Mutation	SNP	G	A	G	RFPL1	c.G443A	p.R148Q
XH_P36	22	30074208	30074208	Silent	SNP	G	A	G	NF2	c.G1221A	p.P407P
XH_P36	22	31998711	31998711	Missense_Mutation	SNP	A	G	A	SF1	c.A1580G	p.H527R
XH_P36	22	32937634	32937634	Silent	SNP	G	A	G	SYN3	c.C840T	p.Y280Y
XH_P36	22	34022242	34022242	Silent	SNP	G	A	G	LARGE1	c.C477T	p.S159S
XH_P36	22	36624038	36624038	Missense_Mutation	SNP	T	G	T	APOL2	c.A426C	p.E142D
XH_P36	22	37770438	37770438	Silent	SNP	C	T	C	ELFN2	c.G1137A	p.T379T
XH_P36	22	38621499	38621499	Missense_Mutation	SNP	A	T	A	TMEM184B	c.T719A	p.L240H
XH_P36	22	38621500	38621500	Missense_Mutation	SNP	G	T	G	TMEM184B	c.C718A	p.L240I
XH_P36	22	39262986	39262986	Missense_Mutation	SNP	G	A	G	CBX6	c.C413T	p.T138M
XH_P36	22	40800400	40800400	Missense_Mutation	SNP	C	T	C	SGSM3	c.C118T	p.R40C
XH_P36	22	40802644	40802644	Missense_Mutation	SNP	G	A	G	SGSM3	c.G974A	p.G325D
XH_P36	22	40815071	40815071	Frame_Shift_Del	DEL	G	-	G	MKL1	c.1371delC	p.P457fs
XH_P36	22	42024155	42024155	Frame_Shift_Del	DEL	T	-	T	XRCC6	c.116delT	p.I39fs
XH_P36	22	44276750	44276750	Silent	SNP	G	A	G	PNPLA5	c.C873T	p.R291R
XH_P36	22	44681360	44681360	Missense_Mutation	SNP	G	A	G	KIAA1644	c.C547T	p.R183W
XH_P36	22	46654519	46654519	Frame_Shift_Ins	INS	-	ACGAGGA	-	PKDREJ	00_4701insTCC	p.K1567fs
XH_P36	22	46932163	46932163	Missense_Mutation	SNP	G	A	G	CELSR1	c.C905T	p.T302M
XH_P36	22	50297990	50297990	Frame_Shift_Ins	INS	-	G	-	ALG12	c.1156dupC	p.Q386fs
XH_P36	22	50591520	50591520	Missense_Mutation	SNP	T	C	T	MOV10L1	c.T320C	p.M107T

XH_P36	22	50658895	50658895	Frame_Shift_Del	DEL	G	-	G	TUBGCP6	c.3893delC	p.P1298fs
XH_P36	22	50728589	50728589	Missense_Mutation	SNP	G	A	G	PLXNB2	c.C425T	p.S142F
XH_P36	22	50987509	50987509	Missense_Mutation	SNP	G	A	G	KLHDC7B	c.G914A	p.G305D
XH_P36	X	2773043	2773043	Missense_Mutation	SNP	A	G	A	GYG2	c.A334G	p.N112D
XH_P36	X	3240378	3240378	Nonsense_Mutation	INS	-	AGCACCTGACAT	-	MXRA5	8insTTAATGTC	116_V1117delinsTX
XH_P36	X	5811016	5811016	Missense_Mutation	SNP	G	A	G	NLGN4X	c.C2293T	p.R765C
XH_P36	X	5821876	5821876	Silent	SNP	G	A	G	NLGN4X	c.C843T	p.G281G
XH_P36	X	11197525	11197525	Frame_Shift_Ins	INS	-	TTTCTGTATAAC	-	ARHGAP6	AAAAAGTTATCA	p.E279fs
XH_P36	X	12904643	12904643	Frame_Shift_Ins	INS	-	C	-	TLR7	c.1017dupC	p.L339fs
XH_P36	X	14599388	14599388	Frame_Shift_Ins	INS	-	T	-	GLRA2	c.355dupT	p.D118fs
XH_P36	X	17750296	17750296	Silent	SNP	C	T	C	NHS	c.C4074T	p.S1358S
XH_P36	X	21444726	21444726	Missense_Mutation	SNP	G	A	G	CNKS2R	c.G176A	p.R59H
XH_P36	X	22056595	22056595	Missense_Mutation	SNP	G	T	G	PHEX	c.G127T	p.G43C
XH_P36	X	22292144	22292144	Frame_Shift_Ins	INS	-	A	-	ZNF645	c.1037dupA	p.C346fs
XH_P36	X	23410920	23410920	Missense_Mutation	SNP	G	T	G	PTCHD1	c.G1285T	p.G429C
XH_P36	X	24734566	24734566	Missense_Mutation	SNP	G	A	G	POLA1	c.G613A	p.A205T
XH_P36	X	24859773	24859773	Silent	SNP	T	C	T	POLA1	c.T3741C	p.L1247L
XH_P36	X	27481249	27481249	Missense_Mutation	SNP	C	A	C	PPP4R3CP	c.G165T	p.Q55H
XH_P36	X	30327013	30327013	Silent	SNP	C	T	C	NR0B1	c.G468A	p.T156T
XH_P36	X	30327352	30327352	Silent	SNP	G	A	G	NR0B1	c.C129T	p.C43C
XH_P36	X	30877624	30877624	Missense_Mutation	SNP	C	T	C	TAB3	c.G82A	p.V28M
XH_P36	X	31986601	31986601	Missense_Mutation	SNP	T	C	T	DMD	c.A2446G	p.T816A
XH_P36	X	32361392	32361392	Frame_Shift_Ins	INS	-	TGATGCATTTC	-	DMD	5insAAGGAAAT	p.S525fs
XH_P36	X	36321999	36321999	Missense_Mutation	SNP	C	T	C	CFAP47	c.C8006T	p.T2669M
XH_P36	X	37028698	37028698	Missense_Mutation	SNP	C	T	C	FAM47C	c.C2215T	p.R739C
XH_P36	X	39923654	39923654	Missense_Mutation	SNP	T	C	T	BCOR	c.A3383G	p.E1128G
XH_P36	X	45023492	45023492	Frame_Shift_Ins	INS	-	GC	-	Cxorf36	c.500_501insGC	p.D167fs
XH_P36	X	45023493	45023493	Frame_Shift_Ins	INS	-	A	-	Cxorf36	c.499_500insT	p.D167fs
XH_P36	X	47271966	47271966	Frame_Shift_Ins	INS	-	GTATAAAATTAA	-	ZNF157	5insCAGTATAAA	p.H165fs
XH_P36	X	47516631	47516631	Silent	SNP	G	A	G	UXT	c.C343T	p.L115L
XH_P36	X	48418176	48418176	Missense_Mutation	SNP	C	T	C	TBC1D25	c.C928T	p.R310C
XH_P36	X	48559092	48559092	Missense_Mutation	SNP	G	A	G	SUV39H1	c.G809A	p.R270H
XH_P36	X	49088214	49088214	Silent	SNP	C	T	C	CACNA1F	c.G201A	p.R67R
XH_P36	X	53106544	53106544	Silent	SNP	C	T	C	GPRI73	c.C741T	p.A247A
XH_P36	X	53115191	53115191	Silent	SNP	C	T	C	TSPYL2	c.C1617T	p.Y539Y
XH_P36	X	53564586	53564586	Missense_Mutation	SNP	C	T	C	HUWE1	c.G12068A	p.R4023H
XH_P36	X	54112348	54112348	In_Frame_Ins	INS	-	AAGAAATGAGGT	-	FAM120C	instAAATACCTCA	80delinsVNTSFFGT
XH_P36	X	66765862	66765862	Missense_Mutation	SNP	G	T	G	AR	c.G874T	p.G292C
XH_P36	X	69510571	69510571	Frame_Shift_Ins	INS	-	CTTCCTTC	-	KIF4A	51_152insCTTC	p.Y51fs
XH_P36	X	69510573	69510573	Silent	SNP	C	T	C	KIF4A	c.C153T	p.Y51Y
XH_P36	X	69669650	69669650	Missense_Mutation	SNP	G	T	G	DLG3	c.G644T	p.R215L
XH_P36	X	70472854	70472854	Frame_Shift_Del	DEL	C	-	C	ZMYM3	c.C252delG	p.G84fs
XH_P36	X	70586340	70586340	Missense_Mutation	SNP	A	T	A	TAF1	c.A176T	p.D59V
XH_P36	X	71426778	71426778	Nonsense_Mutation	INS	-	AGAAAGCTCAA	-	ERCC6L	1839insTTAGAG	613_N614delinsNX
XH_P36	X	74318786	74318786	Silent	SNP	A	G	A	ABC87	c.T366C	p.G122G
XH_P36	X	76938995	76938995	In_Frame_Ins	INS	-	AGATGAAGAATC	-	ATRX	1639insCATTCT	E547delinsHSSSE
XH_P36	X	77224989	77224989	Silent	SNP	G	T	G	PGAM4	c.C147A	p.G49G
XH_P36	X	77268382	77268382	Missense_Mutation	SNP	G	A	A	ATP7A	c.G2179A	p.G727R
XH_P36	X	79699009	79699009	Nonsense_Mutation	INS	-	CAGGTTTCCTGG	-	FAM46D	CTCTTCAGGTT	1324_1325delinsLX
XH_P36	X	79989683	79989683	Frame_Shift_Ins	INS	-	AATTT	-	BRWD3	019_1020insAA	p.H340fs
XH_P36	X	82763673	82763673	Frame_Shift_Del	DEL	G	-	G	POU3F4	c.341delG	p.W114fs
XH_P36	X	91132649	91132649	Silent	SNP	C	T	C	PCDH11X	c.C1410T	p.F470F
XH_P36	X	91133364	91133364	Missense_Mutation	SNP	G	A	G	PCDH11X	c.G2125A	p.A709T
XH_P36	X	95993734	95993734	Missense_Mutation	SNP	A	T	A	DIAPH2	c.A315T	p.E105D
XH_P36	X	99884976	99884976	Nonstop_Mutation	INS	-	CCCTCTGAAACA	-	TSPAN6	sCCAGTGTTTCA	138delinsSVSVEGY
XH_P36	X	100297082	100297082	Frame_Shift_Ins	INS	-	T	-	TRMT2B	c.196dupA	p.S66fs
XH_P36	X	100503224	100503224	Missense_Mutation	SNP	A	G	A	DRP2	c.A1165G	p.N389D
XH_P36	X	100667681	100667681	Frame_Shift_Ins	INS	-	ATTCTTTCCTTG	-	HNRNP2	6insCTATTCTTT	p.A235fs
XH_P36	X	100747417	100747417	Missense_Mutation	SNP	G	A	G	ARMCX4	c.G3841A	p.A1281T
XH_P36	X	101970716	101970716	Missense_Mutation	SNP	A	G	A	RMCX5-SPRASF	c.A919G	p.R307G
XH_P36	X	102864157	102864157	Frame_Shift_Ins	INS	-	CTTCATTTTATT	-	TCEAL3	instTCCTTTCATT	p.G55fs
XH_P36	X	103080247	103080247	Missense_Mutation	SNP	T	G	T	RAB9B	c.A468C	p.K156N
XH_P36	X	105450411	105450411	Missense_Mutation	SNP	A	T	A	MUM1L1	c.A986T	p.D329V
XH_P36	X	105450735	105450735	Missense_Mutation	SNP	G	A	G	MUM1L1	c.G1310A	p.R437K
XH_P36	X	106038848	106038848	Frame_Shift_Ins	INS	-	CTCTAATAATTA	-	RNF128	5insTACCTCTAA	p.V372fs
XH_P36	X	106038850	106038850	In_Frame_Ins	INS	-	ATTAT	-	RNF128	16_1117insATT	b.V372delinsVIY
XH_P36	X	106845186	106845186	Frame_Shift_Del	DEL	G	-	G	FRMPD3	c.4016delG	p.R1339fs
XH_P36	X	107978741	107978741	Missense_Mutation	SNP	C	A	C	IRS4	c.G834T	p.Q278H
XH_P36	X	109693960	109693960	Missense_Mutation	SNP	G	A	G	RTL9	c.G115A	p.V391
XH_P36	X	112065649	112065649	Nonsense_Mutation	SNP	G	A	G	AMOT	c.C706T	p.R236X
XH_P36	X	114082653	114082653	Frame_Shift_Ins	INS	-	AGATTATGCTCG	-	HTR2C	CTTTCAGATTAT	p.C146fs
XH_P36	X	114424574	114424574	Silent	SNP	C	A	C	RBMXL3	c.C570A	p.G190G
XH_P36	X	114426364	114426364	Missense_Mutation	SNP	T	A	T	RBMXL3	c.T2360A	p.L787H
XH_P36	X	117043403	117043403	Nonsense_Mutation	INS	-	GTAGTTAGGGT	-	KLHL13	AAATAAAACCC	p.D403delinsEX
XH_P36	X	118723709	118723709	Frame_Shift_Ins	INS	-	AGATAGGCTCC	-	NKRF	instACGGGAGC	p.R560fs
XH_P36	X	118920652	118920652	Missense_Mutation	SNP	G	T	G	RPL39	c.C151A	p.L51I
XH_P36	X	119602985	119602985	Missense_Mutation	SNP	G	A	G	LAMP2	c.C40T	p.L14F
XH_P36	X	119674393	119674393	In_Frame_Ins	INS	-	GGTTGCTTAGCT	-	CUL4B	TATACCAGCTAA	0delinsDIPAKO
XH_P36	X	119694376	119694376	Nonsense_Mutation	INS	-	AATAAGAGTATA	-	CUL4B	instTAATATACT	0_L41delinsLIYSVFX
XH_P36	X	122387364	122387364	Missense_Mutation	SNP	A	G	A	GRIA3	c.A479G	p.K160R
XH_P36	X	123200251	123200251	Missense_Mutation	SNP	C	A	C	STAG2	c.C2230A	p.Q744K
XH_P36	X	123514660	123514660	Missense_Mutation	SNP	T	C	T	TENM1	c.A7904G	p.V2635C
XH_P36	X	123637491	123637491	Missense_Mutation	SNP	C	T	C	TENM1	c.G3364A	p.V1122I
XH_P36	X	123663816	123663816	Missense_Mutation	SNP	C	T	C	TENM1	c.G2669A	p.R890Q
XH_P36	X	123680932	123680932	In_Frame_Ins	INS	-	ACA	-	TENM1	2442_2443insT	p.T815delinsCT
XH_P36	X	123680934	123680934	Frame_Shift_Ins	INS	-	TTATTTTATTCCT	-	TENM1	CACTAAGGAAT	p.L814fs
XH_P36	X	124454042	124454042	Missense_Mutation	SNP	T	C	T	TEX13C	c.T74C	p.V25A
XH_P36	X	124454575	124454575	Missense_Mutation	SNP	C	T	T	TEX13C	c.C607T	p.P203S
XH_P36	X	125685317	125685317	Missense_Mutation	SNP	T	G	T	DCAF12L1	c.A1275C	p.E425D
XH_P36	X	128621013	128621013	Missense_Mutation	SNP	A	T	A	SMARCA1	c.T2163A	p.D721E
XH_P36	X	129147458	129147458	Missense_Mutation	SNP	T	A	T	BCORL1	c.T710A	p.V237D
XH_P36	X	129147932	129147932	Missense_Mutation	SNP	C	A	C	BCORL1	c.C1184A	p.T395K
XH_P36	X	129270637	129270637	Missense_Mutation	SNP	T	C	T	AIFM1	c.A128G	p.K43R
XH_P36	X	131212863	131212863	Silent	SNP	C	T	C	FRMD7	c.G1137A	p.E379E
XH_P36	X	135313108	135313108	Frame_Shift_Ins	INS	-	AAAAGGGATTI	-	MAP7D3	1326insTAAATC	p.K442fs
XH_P36	X	135630842	135630842	Silent	SNP	C	T	C	VGLL1	c.C309T	p.N103N
XH_P36	X	136649264	136649264	Silent	SNP	G	A	G	ZIC3	c.G414A	p.G138G
XH_P36	X	142718126	142718126	Frame_Shift_Ins	INS	-	AAAAATATACA	-	SLITRK4	ATAGACTGTAT	p.G267fs

XH_P36	X	148037594	148037594	Frame_Shift_Ins	INS	-	TTTCTGGAATTT	-	AFF2	tsTTTGTTCCTGG	p.A314fs
XH_P36	X	148627313	148627313	Missense_Mutation	SNP	G	T	G	CXorf40A	c.G137T	p.R46M
XH_P36	X	148794840	148794840	Frame_Shift_Ins	INS	-	G	-	MAGEA11	c.22dupG	p.R7fs
XH_P36	X	150906974	150906974	Missense_Mutation	SNP	G	T	G	CNGA2	c.G19T	p.G7C
XH_P36	X	152139042	152139042	Missense_Mutation	SNP	G	A	G	ZNF185	c.G941A	p.R314H
XH_P36	X	152686163	152686163	Frame_Shift_Del	DEL	G	-	G	ZFP92	c.328delG	p.G110fs
XH_P36	X	152710513	152710513	Missense_Mutation	SNP	G	T	G	TREX2	c.C376A	p.L126M
XH_P36	X	153048467	153048467	Silent	SNP	G	A	G	SRPK3	c.G642A	p.K214K
XH_P36	X	153050304	153050304	Missense_Mutation	SNP	G	A	G	SRPK3	c.G1345A	p.A49YT
XH_P36	X	153178731	153178731	Missense_Mutation	SNP	C	T	C	ARHGAP4	c.G1352A	p.R451Q
XH_P36	X	153692348	153692348	Missense_Mutation	SNP	G	T	G	PLXNA3	c.G1602T	p.E534D
XH_P36	X	153714260	153714260	Silent	SNP	G	A	G	UBL4A	c.C213T	p.V71V
XH_P36	X	153944567	153944567	Missense_Mutation	SNP	C	T	C	GAB3	c.G110A	p.R37H
XH_P36	X	154754286	154754286	Frame_Shift_Del	DEL	T	-	T	TMLHE	c.189delA	p.K63fs
XH_P36	1	115258747	115258747	Missense_Mutation	SNV	C	T	T	NRAS	c.35G>A	P.G12D
XH_P36	1	1268888	1268888	Missense_Mutation	SNV	G	A	A	TAS1R3	c.1603G>A	P.D535N
XH_P36	1	13635049	13635049	Missense_Mutation	SNV	C	T	T	PRAMEF33P	c.1195C>T	P.R399C
XH_P36	1	144922225	144922225	Nonsense_Mutation	SNV	G	A	A	PDE4DIP	c.1141C>T	P.R381*
XH_P36	1	1461921	1461921	Splice_Site	SNV	C	T	T	ATAD3A	c.1337+10C>T	
XH_P36	1	148341948	148341948	Missense_Mutation	SNV	T	C	C	NBPF9	c.625A>G	P.I209V
XH_P36	1	149895835	149895835	Missense_Mutation	SNV	A	T	T	SF3B4	c.985T>A	P.S329T
XH_P36	1	151804203	151804203	Missense_Mutation	SNV	C	T	T	RORC	c.38G>A	P.R13Q
XH_P36	1	152275289	152275289	Missense_Mutation	SNV	G	A	A	FLG	c.12073C>T	P.P4025S
XH_P36	1	152770502	152770502	Missense_Mutation	SNV	C	T	T	LCE1D	c.232C>T	P.R78C
XH_P36	1	154246391	154246391	Frame_Shift_Del	INDEL	C	-	-	HAX1	c.319delC	P.Q107fs
XH_P36	1	155148566	155148566	Frame_Shift_Ins	INDEL	-	C	C	TRIM46	c.464dupC	P.P156fs
XH_P36	1	155580268	155580268	Frame_Shift_Ins	INDEL	-	C	C	MSTO1	c.141dupC	P.D48fs
XH_P36	1	155722346	155722346	Nonsense_Mutation	SNV	G	A	A	GON4L	c.5878C>T	P.R1960*
XH_P36	1	158325766	158325766	Missense_Mutation	SNV	G	A	A	CD1E	c.775G>A	P.V259I
XH_P36	1	158735706	158735706	Missense_Mutation	SNV	A	G	G	OR6N1	c.767T>C	P.L256P
XH_P36	1	158985772	158985772	Missense_Mutation	SNV	G	C	C	IFI16	c.376G>C	P.A126P
XH_P36	1	159779252	159779252	Missense_Mutation	SNV	A	G	G	FCRL6	c.665A>G	P.D222G
XH_P36	1	161953527	161953527	Missense_Mutation	SNV	G	A	A	OLFML2B	c.2194C>A	P.R732C
XH_P36	1	162731166	162731166	Nonsense_Mutation	SNV	C	T	T	DDR2	c.1021C>T	P.R341*
XH_P36	1	162766447	162766447	Silent	SNV	T	G	G	HSD17B7	c.312T>G	P.L104L
XH_P36	1	164769110	164769110	Nonsense_Mutation	SNV	C	T	T	PBX1	c.685C>T	P.R229*
XH_P36	1	166896414	166896414	Missense_Mutation	SNV	C	T	T	ILDR2	c.884G>A	P.R295H
XH_P36	1	171553156	171553156	Missense_Mutation	SNV	G	A	A	PRRC2C	c.7465G>A	P.A2489T
XH_P36	1	173772575	173772575	Silent	SNV	G	A	A	CENPL	c.627C>T	P.C209C
XH_P36	1	174200408	174200408	Missense_Mutation	SNV	C	T	T	RABGAP1L	c.457C>T	P.R153W
XH_P36	1	175355157	175355157	Splice_Site	SNV	C	T	T	TNR	c.778+11G>A	
XH_P36	1	176659361	176659361	Silent	SNV	C	T	T	PAPPA2	c.2226C>T	P.Y742Y
XH_P36	1	179604781	179604781	Splice_Site	INDEL	T	-	-	TDRD5	c.1300-12delT	
XH_P36	1	182550367	182550367	Missense_Mutation	SNV	G	A	A	RNASL	c.1898C>T	P.T633M
XH_P36	1	19180874	19180874	Missense_Mutation	SNV	C	T	T	TAS1R2	c.1090G>A	P.D364N
XH_P36	1	19183876	19183876	Silent	SNV	G	T	T	TAS1R2	c.432C>A	P.S144S
XH_P36	1	19566360	19566360	Silent	SNV	C	T	T	EMC1	c.906G>A	P.L302L
XH_P36	1	196309709	196309709	Splice_Site	INDEL	A	-	-	KCNT2	c.1554-9delT	
XH_P36	1	197091176	197091176	Splice_Site	INDEL	A	-	-	ASPM	c.3742-3delT	
XH_P36	1	197297540	197297540	Splice_Site	INDEL	A	-	-	CRB1	c.71-12delA	
XH_P36	1	203668744	203668744	Missense_Mutation	SNV	G	A	A	ATP2B4	c.548G>A	P.R183H
XH_P36	1	203821253	203821253	Splice_Site	INDEL	-	T	T	ZC3H11A	c.2175-8dupT	
XH_P36	1	206758543	206758543	Frame_Shift_Del	INDEL	C	-	-	RASSF5	c.1024delC	P.L342fs
XH_P36	1	21267982	21267982	Splice_Site	SNV	A	G	G	E1F4G3	c.1492+2T>C	
XH_P36	1	2238077	2238077	Missense_Mutation	SNV	A	G	G	SKI	c.2060A>G	P.D687G
XH_P36	1	226340081	226340081	Missense_Mutation	SNV	T	C	C	ACBD3	c.1330A>G	P.5444G
XH_P36	1	228399732	228399732	Missense_Mutation	SNV	G	A	A	OBSCN	c.248G>A	P.R83H
XH_P36	1	228494956	228494956	Splice_Site	SNV	G	A	A	OBSCN	c.12194-4G>A	
XH_P36	1	228506757	228506757	Silent	SNV	G	A	A	OBSCN	c.14304G>A	P.54768S
XH_P36	1	233464042	233464042	Missense_Mutation	SNV	G	T	T	MLK4	c.268G>T	P.G90C
XH_P36	1	235275431	235275431	Splice_Site	INDEL	A	-	-	TOMM20	c.394-8delT	
XH_P36	1	235658047	235658047	Silent	SNV	G	A	A	B3GALNT2	c.327C>T	P.N109N
XH_P36	1	235940392	235940392	Missense_Mutation	SNV	T	A	A	LYST	c.5431A>T	P.T1811S
XH_P36	1	242042491	242042491	Missense_Mutation	SNV	C	T	T	EXO1	c.1952C>T	P.S651L
XH_P36	1	245927412	245927412	Silent	SNV	T	C	C	SMYD3	c.1116A>G	P.Q372Q
XH_P36	1	248028086	248028086	Missense_Mutation	SNV	G	A	A	TRIM58	c.596G>A	P.R199Q
XH_P36	1	248436586	248436586	Silent	SNV	G	A	A	OR2T33	c.531C>T	P.C177C
XH_P36	1	248436712	248436712	Missense_Mutation	SNV	G	T	T	OR2T33	c.405C>A	P.S153S
XH_P36	1	2572878	2572878	Missense_Mutation	SNV	C	T	T	TTC34	c.1630G>A	P.5544N
XH_P36	1	25889626	25889626	Frame_Shift_Ins	INDEL	-	C	C	LDLRAP1	c.603dupC	P.S202fs
XH_P36	1	28116067	28116067	Splice_Site	INDEL	C	-	-	STX12	c.119-3delC	
XH_P36	1	28785730	28785730	Frame_Shift_Del	INDEL	A	-	-	PHACTR4	c.160delA	P.S54fs
XH_P36	1	32208473	32208473	Silent	SNV	C	T	T	ADGRB2	c.1218G>A	P.L406L
XH_P36	1	34666397	34666397	Frame_Shift_Ins	INDEL	-	A	A	C1orf94	c.1040dupA	P.Q349fs
XH_P36	1	35226919	35226919	Missense_Mutation	SNV	C	T	T	GJB4	c.64C>T	P.R22C
XH_P36	1	3541774	3541774	Silent	SNV	C	T	T	TPRG1L	c.138C>T	P.L46L
XH_P36	1	36030900	36030900	Missense_Mutation	SNV	C	T	T	NCN	c.1826C>T	P.A609V
XH_P36	1	36367904	36367904	Missense_Mutation	SNV	G	A	A	AGO1	c.1363G>A	P.A455T
XH_P36	1	36380979	36380979	Nonsense_Mutation	SNV	C	T	T	AGO1	c.1864C>T	P.R622*
XH_P36	1	38265467	38265467	Missense_Mutation	SNV	G	A	A	MANEAL	c.300G>A	P.M100I
XH_P36	1	39823033	39823033	Splice_Site	INDEL	T	-	-	MACF1	c.5239-6delT	
XH_P36	1	42047087	42047087	Missense_Mutation	SNV	C	T	T	HIVEP3	c.3382G>A	P.V1128I
XH_P36	1	44466534	44466534	Missense_Mutation	SNV	G	A	A	SLC6A9	c.1441C>T	P.R481W
XH_P36	1	47748086	47748086	Silent	SNV	G	A	A	STIL	c.1179C>T	P.H393H
XH_P36	1	48917261	48917261	Silent	SNV	G	A	A	SPATA6	c.201C>T	P.D67D
XH_P36	1	50941243	50941243	Missense_Mutation	SNV	G	A	A	FAF1	c.1762C>T	P.R588W
XH_P36	1	52825774	52825774	Missense_Mutation	SNV	G	C	C	CC20D18	c.735C>G	P.D245E
XH_P36	1	63876949	63876949	Frame_Shift_Ins	INDEL	-	T	T	ALG6	c.634dupT	P.C212fs
XH_P36	1	67147843	67147843	Missense_Mutation	SNV	A	G	G	SGIP1	c.1106A>G	P.N369S
XH_P36	1	76257129	76257129	Splice_Site	INDEL	T	-	-	RABGGTB	c.469-9delT	
XH_P36	1	78309060	78309060	Missense_Mutation	SNV	G	A	A	MIGA1	c.964G>A	P.A322T
XH_P36	1	78433883	78433883	Silent	SNV	T	C	C	FUBP1	c.216A>G	P.Q72Q
XH_P36	1	86591275	86591275	Silent	SNV	G	A	A	COL24A1	c.744C>T	P.Y248Y
XH_P36	1	874456	874456	Missense_Mutation	SNV	G	A	A	SAMD11	c.467G>A	P.R156H
XH_P36	1	90179646	90179646	Frame_Shift_Ins	INDEL	-	C	C	LRRRC8	c.1524dupC	P.W509fs
XH_P36	1	91967357	91967357	Frame_Shift_Del	INDEL	A	-	-	CD7	c.92delA	P.N31fs
XH_P36	1	93306137	93306137	Silent	SNV	T	G	G	RPL5	c.735T>G	P.A245A
XH_P36	1	94140186	94140186	Missense_Mutation	SNV	C	T	T	BCAR3	c.301G>A	P.E101K

XH_P36	1	94502756	94502756	Missense_Mutation	SNV	G	A	A	ABCA4	c.3758C>T	P.T1253M
XH_P36	1	99772074	99772074	Silent	SNV	G	A	A	PLPPR4	c.1626G>A	P.T542T
XH_P36	10	102242535	102242535	Frame_Shift_Ins	INDEL	-	G	G	WNT8B	c.1025dupG	P.A343fs
XH_P36	10	102250651	102250651	Splice_Site	INDEL	A	-	-	SEC31B	c.2473-11delT	
XH_P36	10	102749036	102749036	Missense_Mutation	SNV	C	T	T	C10orf2	c.1069C>T	P.R357C
XH_P36	10	114154663	114154663	Splice_Site	INDEL	T	-	-	ACSL5	c.140-4delT	
XH_P36	10	114925317	114925317	Frame_Shift_Del	INDEL	A	-	-	TCF7L2	c.1385delA	P.K462fs
XH_P36	10	115601182	115601182	Missense_Mutation	SNV	T	C	C	DCLRE1A	c.2803A>G	P.M935V
XH_P36	10	120789359	120789359	Frame_Shift_Ins	INDEL	-	C	C	NANOS1	c.53dupC	P.P19fs
XH_P36	10	121196221	121196221	Missense_Mutation	SNV	T	C	C	GRK5	c.797T>C	P.M266T
XH_P36	10	124917228	124917228	Splice_Site	INDEL	T	-	-	BUB3	c.266-9delT	
XH_P36	10	12708722	12708722	Splice_Site	INDEL	T	-	-	CAMK1D	c.225-4delT	
XH_P36	10	128780162	128780162	Splice_Site	INDEL	T	-	-	DOCK1	c.172-11delT	
XH_P36	10	133955443	133955443	Missense_Mutation	SNV	C	T	T	JAKMIP3	c.1493C>T	P.T498M
XH_P36	10	134942117	134942117	Missense_Mutation	SNV	C	T	T	ADGRA1	c.785C>T	P.T262M
XH_P36	10	135012703	135012703	Silent	SNV	G	A	A	KND1C	c.2691G>A	P.T897T
XH_P36	10	17363356	17363356	Splice_Site	INDEL	A	-	-	ST8SIA6	c.729-11delT	
XH_P36	10	19981225	19981225	Missense_Mutation	SNV	G	T	T	MALRD1	c.6152G>T	P.W2051L
XH_P36	10	26534838	26534838	Splice_Site	INDEL	T	-	-	GAD2	c.841-5delT	
XH_P36	10	46999854	46999854	Missense_Mutation	SNV	C	T	T	GPRIN2	c.974C>T	P.A325V
XH_P36	10	50953853	50953853	Silent	SNV	G	A	A	OGDHL	c.1296C>T	P.V432V
XH_P36	10	64159513	64159513	Frame_Shift_Del	INDEL	A	-	-	ZNF365	c.1196delA	P.K399fs
XH_P36	10	70332889	70332889	Missense_Mutation	SNV	A	G	G	TET1	c.794A>G	P.N265S
XH_P36	10	70723214	70723214	Missense_Mutation	SNV	C	T	T	DDX21	c.571C>T	P.R191C
XH_P36	10	71142432	71142432	Silent	SNV	G	A	A	HK1	c.1455G>A	P.L485L
XH_P36	10	73466731	73466731	Missense_Mutation	SNV	G	A	A	CDH23	c.3031G>A	P.E1011K
XH_P36	10	78729786	78729786	Frame_Shift_Del	INDEL	T	-	-	KCNMA1	c.2144delA	P.K715fs
XH_P36	10	8019267	8019267	Missense_Mutation	SNV	G	A	A	TAF3	c.2296G>A	P.G766S
XH_P36	10	8100708	8100708	Missense_Mutation	SNV	G	A	A	GATA3	c.682G>A	P.E228K
XH_P36	10	81317157	81317157	Silent	SNV	G	T	T	SFTPA2	c.555C>A	P.A185A
XH_P36	10	89272866	89272866	Splice_Site	INDEL	T	-	-	MINPP1	c.836-9delT	
XH_P36	10	92617011	92617011	Missense_Mutation	SNV	C	T	T	HTR7	c.418G>A	P.V140I
XH_P36	10	93601946	93601946	Frame_Shift_Del	INDEL	A	-	-	TNKS2	c.1865delA	P.N622fs
XH_P36	10	93999314	93999314	Missense_Mutation	SNV	C	T	T	CPEB3	c.794G>A	P.G265D
XH_P36	10	94773	94773	Missense_Mutation	SNV	C	T	T	TUBB8	c.137G>A	P.R46H
XH_P36	10	95995659	95995659	Splice_Site	INDEL	T	-	-	PLCE1	c.1291-5delT	
XH_P36	10	98080475	98080475	Missense_Mutation	SNV	T	C	C	DNTT	c.608T>C	P.F203S
XH_P36	11	101323754	101323754	Missense_Mutation	SNV	C	A	A	TRPC6	c.2728G>T	P.A910S
XH_P36	11	108384793	108384793	Frame_Shift_Del	INDEL	A	-	-	EXPH5	c.1213delT	P.W405fs
XH_P36	11	111366044	111366044	Splice_Site	INDEL	A	-	-	BTG4	c.511-5delT	
XH_P36	11	112020784	112020784	Splice_Site	INDEL	A	-	-	IL18	c.214+11delT	
XH_P36	11	113694379	113694379	Frame_Shift_Ins	INDEL	-	CT	CT	USP28	c.854_855dupA	P.C286fs
XH_P36	11	123448124	123448124	Missense_Mutation	SNV	C	T	T	GRAMD1B	c.73C>T	P.R25W
XH_P36	11	124845049	124845049	Frame_Shift_Del	INDEL	A	-	-	CCDC15	c.581delA	P.K194fs
XH_P36	11	125221249	125221249	Silent	SNV	G	A	A	PKNOX2	c.48G>A	P.T16T
XH_P36	11	130066453	130066453	Splice_Site	INDEL	C	-	-	ST14	c.1224-6delC	
XH_P36	11	14280928	14280928	Missense_Mutation	SNV	C	T	T	SPON1	c.1592C>T	P.P531L
XH_P36	11	14793470	14793470	Splice_Site	INDEL	T	-	-	PDE3B	c.979-5delT	
XH_P36	11	17758073	17758073	Missense_Mutation	SNV	G	A	A	KCNC1	c.524G>A	P.R175H
XH_P36	11	20066788	20066788	Silent	SNV	C	T	T	NAV2	c.3282C>T	P.L1094L
XH_P36	11	2432968	2432968	Missense_Mutation	SNV	C	T	T	TRPM5	c.2504G>A	P.R835H
XH_P36	11	27405964	27405964	Splice_Site	INDEL	A	-	-	LGR4	c.618-10delT	
XH_P36	11	30255300	30255300	Nonsense_Mutation	SNV	C	T	T	FSHB	c.343C>T	P.R115*
XH_P36	11	3114178	3114178	Missense_Mutation	SNV	C	T	T	OSBPL5	c.1847G>A	P.R616Q
XH_P36	11	33596351	33596351	Missense_Mutation	SNV	T	G	G	KIAA1549L	c.3443T>G	P.I1148S
XH_P36	11	34489930	34489930	Silent	SNV	C	T	T	CAT4	c.1422C>T	P.I474I
XH_P36	11	3848989	3848989	Missense_Mutation	SNV	C	T	T	RHOG	c.380G>A	P.R127Q
XH_P36	11	43425610	43425613	Frame_Shift_Del	INDEL	GAGT	-	-	TTC17	397_1400delG	P.5466fs
XH_P36	11	45671512	45671512	Missense_Mutation	SNV	C	G	G	CHST1	c.962G>C	P.G321A
XH_P36	11	4661623	4661623	Silent	SNV	C	A	A	OR51D1	c.603C>A	P.S201S
XH_P36	11	47611863	47611863	Missense_Mutation	SNV	C	T	T	C1QTNF4	c.500G>A	P.R167H
XH_P36	11	48347449	48347449	Frame_Shift_Del	INDEL	A	-	-	OR4C3	c.962delA	P.N321fs
XH_P36	11	5275557	5275557	Missense_Mutation	SNV	A	G	G	HBG2	c.280T>C	P.C94R
XH_P36	11	5364256	5364256	Missense_Mutation	SNV	A	G	G	OR51B5	c.499T>C	P.C167R
XH_P36	11	60506456	60506456	Missense_Mutation	SNV	C	A	A	MS4A18	c.610C>A	P.L204I
XH_P36	11	60666410	60666410	Splice_Site	INDEL	A	-	-	PRPF19	c.985-7delT	
XH_P36	11	63277289	63277289	Missense_Mutation	SNV	C	T	T	LGALS12	c.481C>T	P.R161W
XH_P36	11	63997883	63997885	Splice_Site	INDEL	TTT	-	-	DNAJC4	23-11_423-9delTTT	
XH_P36	11	65396411	65396411	Silent	SNV	C	T	T	PCNX3	c.3933C>T	P.R1311R
XH_P36	11	65733371	65733371	Missense_Mutation	SNV	C	T	T	SART1	c.752C>T	P.A251V
XH_P36	11	65780794	65780794	Missense_Mutation	SNV	C	T	T	CSF6	c.373C>T	P.R125C
XH_P36	11	67072394	67072394	Silent	SNV	C	A	A	SSH3	c.255C>A	P.S85S
XH_P36	11	67187007	67187007	Missense_Mutation	SNV	G	A	A	CARNS1	c.902G>A	P.R301H
XH_P36	11	67258296	67258296	Missense_Mutation	SNV	C	T	T	AIP	c.817C>T	P.R273C
XH_P36	11	67261809	67261809	Missense_Mutation	SNV	G	A	A	PITPNM1	c.2762C>T	P.A921V
XH_P36	11	67263644	67263644	Splice_Site	SNV	C	A	A	PITPNM1	c.2314+5G>T	
XH_P36	11	67264838	67264838	Silent	SNV	G	A	A	PITPNM1	c.2010C>T	P.P670P
XH_P36	11	67800693	67800693	Silent	SNV	A	G	G	NDUF58	c.315A>G	P.P105P
XH_P36	11	69962552	69962552	Splice_Site	INDEL	T	-	-	ANO1	c.856-6delT	
XH_P36	11	7059779	7059779	Splice_Site	INDEL	T	-	-	NLRP14	c.-21-11delT	
XH_P36	11	71195477	71195477	Missense_Mutation	SNV	C	T	T	NADSYN1	c.1439C>T	P.A480V
XH_P36	11	71850756	71850756	Missense_Mutation	SNV	G	A	A	FOLR3	c.616G>A	P.G206S
XH_P36	11	75623053	75623053	Missense_Mutation	SNV	G	A	A	UVRAG	c.563G>A	P.R188H
XH_P36	11	78282493	78282493	Splice_Site	SNV	A	C	C	NARS2	c.-540-4T>G	
XH_P36	11	82536174	82536174	Splice_Site	INDEL	A	-	-	PRCP	c.960-10delT	
XH_P36	11	82966931	82966931	Frame_Shift_Del	INDEL	A	-	-	ANKRD42	c.1517delA	P.K506fs
XH_P36	11	85420388	85420388	Frame_Shift_Del	INDEL	T	-	-	SYTL2	c.1986delA	P.K662fs
XH_P36	11	865495	865495	Splice_Site	INDEL	C	-	-	TSPAN4	c.331-11delC	
XH_P36	11	88068257	88068259	Splice_Site	INDEL	AAA	-	-	CTSC	73-9_173-7delTTT	
XH_P36	11	88583231	88583231	Missense_Mutation	SNV	C	T	T	GRM5	c.754G>A	P.A252T
XH_P36	11	92532469	92532469	Missense_Mutation	SNV	C	T	T	FAT3	c.6290C>T	P.A2097V
XH_P36	11	93439896	93439896	Splice_Site	INDEL	T	-	-	CEP295	c.5597-10delT	
XH_P36	11	94599175	94599175	Missense_Mutation	SNV	G	A	A	AMOTL1	c.2180G>A	P.R727H
XH_P36	11	9861142	9861142	Missense_Mutation	SNV	G	A	A	SBF2	c.3358C>T	P.R1120C
XH_P36	12	100489623	100489623	Splice_Site	INDEL	A	-	-	UHRF1BP1L	c.670-8delT	
XH_P36	12	101473003	101473003	Nonsense_Mutation	SNV	C	T	T	ANO4	c.1345C>T	P.R449*
XH_P36	12	101689237	101689237	Splice_Site	INDEL	T	-	-	UTP20	c.1252-12delT	
XH_P36	12	104697824	104697824	Missense_Mutation	SNV	C	T	T	EID3	c.112C>T	P.R38C

XH_P36	12	109536183	109536183	Missense_Mutation	SNV	C	T	T	UNG	c.52C>T	P.P18S
XH_P36	12	113445730	113445730	Missense_Mutation	SNV	G	A	A	OAS2	c.1877G>A	P.S626N
XH_P36	12	117217097	117217097	Missense_Mutation	SNV	G	A	A	RNFT2	c.826G>A	P.A276T
XH_P36	12	124832387	124832387	Silent	SNV	G	A	A	NCOR2	c.4026C>A	P.R1342R
XH_P36	12	130647740	130647740	Missense_Mutation	SNV	T	G	G	FZD10	c.253T>G	P.F85V
XH_P36	12	130935836	130935836	Silent	SNV	C	T	T	RIMBP2	c.357G>A	P.R119R
XH_P36	12	130941035	130941035	Splice_Site	SNV	G	A	A	RIMBP2	c.307+6C>T	
XH_P36	12	131620642	131620642	Silent	SNV	C	T	T	ADGRD1	c.2328C>T	P.G776G
XH_P36	12	133463877	133463877	Missense_Mutation	SNV	G	T	T	CHFR	c.38C>A	P.P131Q
XH_P36	12	18876416	18876416	Missense_Mutation	SNV	T	A	A	PLCZ1	c.196A>T	P.I66F
XH_P36	12	21727271	21727271	Splice_Site	INDEL	A	-	-	GSY2	c.496-11delT	
XH_P36	12	2907038	2907041	Splice_Site	INDEL	GTGA	-	-	FKBP4	3+4_393+7delAGTG	
XH_P36	12	29614779	29614779	Splice_Site	SNV	C	T	T	OVCH1	c.2280+8G>A	
XH_P36	12	40838232	40838232	Silent	SNV	C	A	A	MUC19	c.4494C>A	P.A1498A
XH_P36	12	4766968	4766968	Missense_Mutation	SNV	G	A	A	NDUFA9	c.373G>A	P.V125M
XH_P36	12	48141379	48141379	Nonsense_Mutation	SNV	G	A	A	RAPGEF3	c.1504C>T	P.R502*
XH_P36	12	49992526	49992526	Splice_Site	SNV	C	T	T	FAM186B	c.2364+12G>A	
XH_P36	12	50026780	50026781	Splice_Site	INDEL	CC	-	-	PRPF40B	349-8_349-7delCC	
XH_P36	12	51399180	51399180	Missense_Mutation	SNV	C	T	T	SLC11A2	c.223G>A	P.G75R
XH_P36	12	52684997	52684997	Missense_Mutation	SNV	C	T	T	KRT81	c.253G>A	P.E85K
XH_P36	12	53038849	53038849	Missense_Mutation	SNV	C	T	T	KRT2	c.1874G>A	P.S625N
XH_P36	12	56398615	56398615	Missense_Mutation	SNV	G	A	A	SUOX	c.1442G>A	P.R481H
XH_P36	12	56494905	56494905	Missense_Mutation	SNV	C	T	T	ERBB3	c.3262C>T	P.P1088S
XH_P36	12	56559113	56559113	Frame_Shift_Del	INDEL	G	-	-	SMARCC2	c.3221delC	P.P1074fs
XH_P36	12	56661723	56661723	Missense_Mutation	SNV	G	T	T	COQ10A	c.184G>T	P.G62W
XH_P36	12	57389231	57389231	Missense_Mutation	SNV	C	T	T	GPR182	c.238C>T	P.R80C
XH_P36	12	57911097	57911097	Silent	SNV	T	C	C	DDIT3	c.162A>G	P.S54S
XH_P36	12	64055225	64055225	Missense_Mutation	SNV	C	A	A	DPY19L2	c.487G>T	P.A163S
XH_P36	12	69085736	69085736	Splice_Site	INDEL	T	-	-	NUPI07	c.217-4delT	
XH_P36	12	71537999	71537999	Splice_Site	INDEL	-	A	A	TSPAN8	c.61-7dupT	
XH_P36	12	72009100	72009100	Splice_Site	INDEL	A	-	-	ZFC3H1	c.5145-4delT	
XH_P36	12	72024509	72024509	Splice_Site	INDEL	A	-	-	ZFC3H1	c.3603-8delT	
XH_P36	12	75687029	75687029	Missense_Mutation	SNV	T	A	A	CAPS2	c.974A>T	P.K325I
XH_P36	12	75804272	75804272	Missense_Mutation	SNV	C	T	T	GLIPR1L2	c.293C>T	P.T98M
XH_P36	12	78593137	78593137	Missense_Mutation	SNV	A	G	G	NAV3	c.6541A>G	P.T2181A
XH_P36	12	89745700	89745700	Silent	SNV	G	A	A	DUSP6	c.117C>T	P.C39C
XH_P36	12	9221371	9221371	Missense_Mutation	SNV	G	A	A	A2M	c.4331C>T	P.P1444L
XH_P36	12	94543030	94543030	Frame_Shift_Del	INDEL	C	-	-	PLXNC1	c.288delC	P.A97fs
XH_P36	12	97186181	97186181	Silent	SNV	G	A	A	CFAP54	c.8754G>A	P.T2918T
XH_P36	13	103390256	103390256	Missense_Mutation	SNV	T	C	C	CCDC168	c.12791A>G	P.E426AG
XH_P36	13	110434690	110434690	Silent	SNV	C	T	T	IRS2	c.3711G>A	P.S1237S
XH_P36	13	111110449	111110449	Missense_Mutation	SNV	C	T	T	COL4A2-AS2	c.257G>A	P.R86Q
XH_P36	13	113439523	113439523	Missense_Mutation	SNV	G	T	T	ATP11A	c.114G>T	P.E38D
XH_P36	13	114538617	114538617	Splice_Site	INDEL	A	-	-	GAS6	c.590-9delT	
XH_P36	13	20656139	20656141	Splice_Site	INDEL	TTT	-	-	ZMYM2	354-7_3454-5delTTT	
XH_P36	13	26542799	26542799	Missense_Mutation	SNV	G	A	A	ATP8A2	c.3164G>A	P.R1055Q
XH_P36	13	26789433	26789433	Nonsense_Mutation	SNV	G	A	A	RNF6	c.586C>T	P.R196*
XH_P36	13	27216440	27216440	Silent	SNV	G	A	A	WASF3	c.33G>A	P.R11R
XH_P36	13	31036852	31036852	Splice_Site	INDEL	A	-	-	HMGB1	c.297-3delT	
XH_P36	13	36905543	36905543	Missense_Mutation	SNV	C	T	T	SPG20	c.1001G>A	P.R334Q
XH_P36	13	39265390	39265390	Silent	SNV	G	A	A	FREM2	c.3909G>A	P.T1303T
XH_P36	13	41897181	41897181	Splice_Site	INDEL	T	-	-	NAA16	c.403-3delT	
XH_P36	13	46632361	46632361	Missense_Mutation	SNV	A	G	G	CPB2	c.841T>C	P.F281L
XH_P36	13	50087175	50087175	Splice_Site	INDEL	T	-	-	PHF11	c.217-12delT	
XH_P36	13	53007887	53007887	Splice_Site	INDEL	A	-	-	VPS36	c.415-4delT	
XH_P36	13	73547716	73547716	Splice_Site	INDEL	T	-	-	PIBF1	c.1965-4delT	
XH_P36	13	77529556	77529556	Missense_Mutation	SNV	C	T	T	ACOD1	c.355C>T	P.P119S
XH_P36	13	79908574	79908574	Splice_Site	INDEL	-	A	A	RBM26	c.2740-10dupT	
XH_P36	13	84454271	84454271	Missense_Mutation	SNV	C	T	T	SLITRK1	c.1372G>A	P.A458T
XH_P36	14	100126651	100126651	Silent	SNV	G	T	T	HHIPL1	c.1410G>T	P.T470T
XH_P36	14	100380645	100380645	Splice_Site	SNV	C	T	T	EML1	c.1677+4C>T	
XH_P36	14	103336573	103336573	Missense_Mutation	SNV	C	T	T	TRAF3	c.35C>T	P.A12V
XH_P36	14	103996592	103996592	Missense_Mutation	SNV	G	A	A	TRMT61A	c.277G>A	P.A93T
XH_P36	14	105353222	105353222	Frame_Shift_Ins	INDEL	-	C	C	CEP170B	c.2653dupC	P.H885fs
XH_P36	14	105408144	105408144	Missense_Mutation	SNV	C	A	A	AHNAK2	c.13644G>T	P.K4548N
XH_P36	14	105944635	105944635	Missense_Mutation	SNV	C	T	T	CRIP2	c.298C>T	P.H100Y
XH_P36	14	20002302	20002302	Splice_Site	INDEL	A	-	-	POTEM	c.1127-7delT	
XH_P36	14	21569511	21569511	Silent	SNV	T	C	C	TMEM253	c.9T>C	P.D3D
XH_P36	14	21957314	21957314	Splice_Site	INDEL	-	T	T	TOX4	c.511-12dupT	
XH_P36	14	31642477	31642477	Silent	SNV	G	A	A	HECTD1	c.1041C>T	P.G347G
XH_P36	14	35497275	35497275	Splice_Site	INDEL	T	-	-	SRP54	c.1181-9delT	
XH_P36	14	39649809	39649809	Missense_Mutation	SNV	G	A	A	PNN	c.896G>A	P.R299H
XH_P36	14	39901278	39901278	Missense_Mutation	SNV	A	C	C	FBXO33	c.89T>G	P.L30R
XH_P36	14	50626388	50626388	Missense_Mutation	SNV	G	A	A	SOS2	c.1613C>T	P.A538V
XH_P36	14	51210171	51210171	Missense_Mutation	SNV	G	A	A	NIN	c.3125C>T	P.A1042V
XH_P36	14	53101641	53101641	Splice_Site	INDEL	T	-	-	GPR137C	c.1113-8delT	
XH_P36	14	55203729	55203729	Splice_Site	INDEL	T	-	-	SAMD4A	c.716-5delT	
XH_P36	14	57103323	57103323	Splice_Site	SNV	T	C	C	TMEM260	c.1869+7T>C	
XH_P36	14	57269043	57269043	Missense_Mutation	SNV	G	A	A	OTX2	c.280C>T	P.R94C
XH_P36	14	60581403	60581403	Splice_Site	INDEL	T	-	-	PCNX4	c.690-7delT	
XH_P36	14	61186779	61186779	Missense_Mutation	SNV	C	A	A	SIX4	c.1248G>T	P.Q416H
XH_P36	14	61278692	61278692	Splice_Site	INDEL	-	T	T	MNAT1	c.421-8dupT	
XH_P36	14	68044071	68044071	Silent	SNV	C	T	T	PLEKHH1	c.2514C>T	P.Y838Y
XH_P36	14	68045918	68045918	Missense_Mutation	SNV	C	T	T	PLEKHH1	c.2917C>T	P.R973W
XH_P36	14	72056027	72056027	Missense_Mutation	SNV	T	C	C	SIPA1L1	c.1438T>C	P.Y480H
XH_P36	14	74203800	74203800	Silent	SNV	G	A	A	ELMSAN1	c.1650C>T	P.D550D
XH_P36	14	74534275	74534275	Splice_Site	INDEL	A	-	-	ALDH6A1	c.814-3delT	
XH_P36	14	75359617	75359617	Frame_Shift_Del	INDEL	C	-	-	DLST	c.527delC	P.P176fs
XH_P36	14	75515373	75515376	Frame_Shift_Del	INDEL	TCAA	-	-	MLH3	983_986delTTG	P.I328fs
XH_P36	14	76429801	76429801	Nonsense_Mutation	SNV	C	A	A	TGFB3	c.784G>T	P.G262*
XH_P36	14	94107567	94107567	Silent	SNV	C	T	T	UNC79	c.5463C>T	P.D1821D
XH_P36	14	94417346	94417346	Splice_Site	SNV	G	A	A	ASB2	c.879C>T	P.Y293Y
XH_P36	14	95675732	95675732	Splice_Site	SNV	G	A	A	CLMN	c.885C>T	P.A295A
XH_P36	14	97022519	97022519	Silent	SNV	G	A	A	PAPOLA	c.1770G>A	P.S590S
XH_P36	15	100591929	100591929	Missense_Mutation	SNV	A	G	G	ADAMTS17	c.2303T>C	P.L768S
XH_P36	15	101865128	101865128	Silent	SNV	G	A	A	PCSK6	c.2079C>T	P.R693R
XH_P36	15	102242559	102242559	Silent	SNV	C	T	T	TARSL2	c.1104G>A	P.P368P
XH_P36	15	102346763	102346763	Missense_Mutation	SNV	G	A	A	OR4F6	c.841G>A	P.V281I

XH_P36	15	22742754	22742754	Missense_Mutation	SNV	G	A	A	GOLGA6L22	c.1103G>A	P.R368Q
XH_P36	15	23891598	23891598	Missense_Mutation	SNV	C	T	T	MAGEL2	c.1292G>A	P.R431Q
XH_P36	15	27160004	27160004	Silent	SNV	G	A	A	GABRA5	c.552G>A	P.A184A
XH_P36	15	27188381	27188381	Silent	SNV	C	T	T	GABRA5	c.897C>T	P.T299T
XH_P36	15	28263537	28263537	Splice_Site	SNV	C	T	T	OCA2	c.807+6G>A	
XH_P36	15	28437288	28437288	Missense_Mutation	SNV	G	A	A	HERC2	c.8270C>T	P.A2757V
XH_P36	15	30659672	30659672	Silent	SNV	G	A	A	CHRFAM7A	c.669C>T	P.I223I
XH_P36	15	40510642	40510642	Splice_Site	INDEL	T	-	-	BUB1B	c.2851-11delT	
XH_P36	15	42159792	42159792	Nonsense_Mutation	SNV	G	A	A	SPTBNS	c.6256C>T	P.Q2086*
XH_P36	15	44964203	44964203	Splice_Site	SNV	C	T	T	PATL2	c.657+10G>A	
XH_P36	15	45409422	45409422	Missense_Mutation	SNV	G	A	A	DUOXA2	c.688G>A	P.V230M
XH_P36	15	50773790	50773790	Missense_Mutation	SNV	G	A	A	USP8	c.1331G>A	P.R444H
XH_P36	15	50925185	50925185	Missense_Mutation	SNV	G	A	A	TRPM7	c.1012C>T	P.L338F
XH_P36	15	55621922	55621922	Frame_Shift_Del	INDEL	T	-	-	PIGB	c.529delT	P.C177fs
XH_P36	15	56720550	56720550	Splice_Site	INDEL	T	-	-	TEX9	c.874-6delT	
XH_P36	15	57545439	57545439	Splice_Site	INDEL	T	-	-	TCF12	c.751-12delT	
XH_P36	15	60747651	60747651	Splice_Site	INDEL	A	-	-	ICE2	c.256-10delT	
XH_P36	15	69331298	69331298	Silent	SNV	C	T	T	NOX5	c.1389C>T	P.P463P
XH_P36	15	69747754	69747755	Splice_Site	INDEL	TT	-	-	RPLP1	266-6 266-5delTT	
XH_P36	15	73660540	73660540	Nonsense_Mutation	SNV	C	T	T	HCN4	c.72G>A	P.W24*
XH_P36	15	75498563	75498563	Silent	SNV	C	T	T	C15orf39	c.174C>T	P.A58A
XH_P36	15	75969242	75969242	Missense_Mutation	SNV	T	C	C	CSPG4	c.5618A>G	P.Q1873R
XH_P36	15	79058543	79058543	Missense_Mutation	SNV	C	T	T	ADAMT57	c.3710G>A	P.S1237N
XH_P36	15	85164712	85164712	Missense_Mutation	SNV	G	A	A	ZSCAN2	c.1286G>A	P.R429H
XH_P36	15	89719201	89719201	Missense_Mutation	SNV	G	A	A	ABHD2	c.697G>A	P.V233M
XH_P36	16	1412305	1412305	Frame_Shift_Del	INDEL	C	-	-	GNPTG	c.514delC	P.H127fs
XH_P36	16	14970537	14970537	Missense_Mutation	SNV	A	C	C	NOMO1	c.2533A>C	P.S845R
XH_P36	16	1709929	1709929	Missense_Mutation	SNV	G	A	A	CRAMP1	c.2278G>A	P.A760T
XH_P36	16	19063046	19063046	Silent	SNV	G	A	A	TMC7	c.1449G>A	P.P483P
XH_P36	16	19126240	19126240	Missense_Mutation	SNV	C	T	T	ITPR1PL2	c.457C>T	P.R153C
XH_P36	16	19883839	19883839	Missense_Mutation	SNV	G	A	A	GPC5B	c.722C>T	P.T241M
XH_P36	16	20948007	20948007	Silent	SNV	G	A	A	DNAH3	c.11823C>T	P.Y3941Y
XH_P36	16	2279560	2279560	Splice_Site	SNV	C	A	A	E4F1	c.310-11C>A	
XH_P36	16	2762695	2762695	Missense_Mutation	SNV	C	T	T	PRSS27	c.493G>A	P.A165T
XH_P36	16	28913639	28913639	Frame_Shift_Ins	INDEL	-	C	C	ATP2A1	c.2089dupC	P.R697fs
XH_P36	16	2903887	2903887	Missense_Mutation	SNV	C	A	A	PRSS22	c.696G>T	P.E232D
XH_P36	16	2983964	2983964	Silent	SNV	G	A	A	FLYWCH1	c.1497G>A	P.A499A
XH_P36	16	29891248	29891248	Frame_Shift_Ins	INDEL	-	G	G	SEZ6L2	c.1299dupC	P.N434fs
XH_P36	16	30018105	30018105	Splice_Site	SNV	C	T	T	DOC2A	c.878+1G>A	
XH_P36	16	30680561	30680561	Silent	SNV	C	A	A	FBR5	c.2538C>A	P.A846A
XH_P36	16	31121549	31121549	Silent	SNV	C	A	A	BCKDK	c.447C>A	P.A149A
XH_P36	16	31142287	31142287	Nonsense_Mutation	SNV	C	T	T	KAT8	c.1378C>T	P.Q460*
XH_P36	16	314836	314836	Missense_Mutation	SNV	G	A	A	FAM234A	c.1474G>A	P.A492T
XH_P36	16	46726279	46726279	Splice_Site	INDEL	T	-	-	ORC6	c.196-11delT	
XH_P36	16	4855316	4855316	Splice_Site	INDEL	A	-	-	GLYR1	c.1570-5delT	
XH_P36	16	49670972	49670972	Silent	SNV	G	A	A	ZNF423	c.1911C>T	P.C637C
XH_P36	16	53265642	53265642	Frame_Shift_Del	INDEL	A	-	-	CHD9	c.2461delA	P.I821fs
XH_P36	16	53706815	53706815	Missense_Mutation	SNV	A	T	T	RPGRIP1L	c.996T>A	P.H332Q
XH_P36	16	67006630	67006630	Missense_Mutation	SNV	A	T	T	CE53	c.418A>T	P.T140S
XH_P36	16	67687145	67687145	Frame_Shift_Del	INDEL	G	-	-	CARMIL2	c.3113delG	P.G1038fs
XH_P36	16	67964372	67964372	Silent	SNV	G	A	A	CTRL	c.438C>T	P.N146N
XH_P36	16	68021792	68021792	Missense_Mutation	SNV	C	T	T	DPEP2	c.695G>A	P.R232H
XH_P36	16	70328814	70328814	Frame_Shift_Del	INDEL	G	-	-	DDX19B	c.68delG	P.G23fs
XH_P36	16	72142164	72142164	Silent	SNV	C	T	T	DXH38	c.3003C>T	P.F1001F
XH_P36	16	72153907	72153907	Silent	SNV	G	A	A	PMFBP1	c.2475C>T	P.A825A
XH_P36	16	74660379	74660379	Silent	SNV	G	A	A	RWD3	c.2043C>T	P.I681I
XH_P36	16	75258768	75258768	Missense_Mutation	SNV	C	T	T	CTR81	c.662C>T	P.P221L
XH_P36	16	75564074	75564074	Missense_Mutation	SNV	G	A	A	CHST5	c.209C>T	P.S70L
XH_P36	16	77325354	77325354	Missense_Mutation	SNV	C	T	T	ADAMTS18	c.2695G>A	P.G899S
XH_P36	16	81058306	81058306	Splice_Site	INDEL	T	-	-	CENPN	c.634-7delT	
XH_P36	16	81095653	81095653	Missense_Mutation	SNV	C	T	T	C16orf46	c.301G>A	P.D101N
XH_P36	16	81173227	81173227	Silent	SNV	C	T	T	PKD1L2	c.3453G>A	P.A1151A
XH_P36	16	81301689	81301689	Missense_Mutation	SNV	C	T	T	BCO1	c.796C>T	P.R266W
XH_P36	16	83214458	83214458	Splice_Site	INDEL	T	-	-	CDH13	c.484-8delT	
XH_P36	16	842546	842546	Frame_Shift_Del	INDEL	G	-	-	CHTF18	c.1440delG	P.L481fs
XH_P36	16	84494362	84494362	Silent	SNV	C	T	T	ATP2C2	c.2523C>T	P.S841S
XH_P36	16	89614422	89614422	Missense_Mutation	SNV	G	A	A	SPG7	c.1564G>A	P.A522T
XH_P36	16	89778933	89778933	Splice_Site	INDEL	G	-	-	VPS9D1	c.544-3delC	
XH_P36	16	90001937	90001937	Missense_Mutation	SNV	G	A	A	TUBB3	c.862G>A	P.G288S
XH_P36	17	16676799	16676799	Splice_Site	INDEL	T	-	-	CCDC144A	c.4252-4delT	
XH_P36	17	17898307	17898307	Splice_Site	SNV	C	A	A	DRC3	c.712-6C>A	
XH_P36	17	20163582	20163582	Missense_Mutation	SNV	G	A	A	SPEC1	c.2915G>A	P.C972Y
XH_P36	17	20859933	20859933	Splice_Site	INDEL	T	-	-	LOC339260	n.641-7delT	
XH_P36	17	25910015	25910015	Frame_Shift_Ins	INDEL	-	C	C	KSR1	c.461dupC	P.P155fs
XH_P36	17	26708249	26708249	Silent	SNV	C	T	T	SARM1	c.492C>T	P.G164G
XH_P36	17	26712159	26712159	Missense_Mutation	SNV	C	T	T	SARM1	c.1489C>T	P.R497C
XH_P36	17	27002460	27002460	Frame_Shift_Del	INDEL	A	-	-	SUPT6H	c.585delA	P.K195fs
XH_P36	17	27044426	27044426	Missense_Mutation	SNV	T	A	A	NARR	c.301A>T	P.T101S
XH_P36	17	27239943	27239943	Missense_Mutation	SNV	C	T	T	PHF12	c.1646G>A	P.G549D
XH_P36	17	27903116	27903116	Missense_Mutation	SNV	C	T	T	GIT1	c.1672G>A	P.V558I
XH_P36	17	28706682	28706682	Frame_Shift_Ins	INDEL	-	C	C	CPD	c.690dupC	P.A231fs
XH_P36	17	29632268	29632268	Silent	SNV	G	A	A	EVI2B	c.360C>T	P.A120A
XH_P36	17	34062267	34062267	Missense_Mutation	SNV	C	T	T	RASL10B	c.64C>T	P.R22C
XH_P36	17	34893857	34893857	Missense_Mutation	SNV	C	T	T	PIGW	c.907C>T	P.R303C
XH_P36	17	3563601	3563601	Missense_Mutation	SNV	G	A	A	CTNS	c.1042G>A	P.V348I
XH_P36	17	39888649	39888649	Splice_Site	INDEL	G	-	-	HAP1	c.574-3delC	
XH_P36	17	40042503	40042503	Missense_Mutation	SNV	T	G	G	ACLY	c.1934A>C	P.N645T
XH_P36	17	40940193	40940193	Frame_Shift_Ins	INDEL	-	C	C	WNK4	c.906dupC	P.G303fs
XH_P36	17	41154724	41154724	Missense_Mutation	SNV	G	A	A	RPL27	c.286G>A	P.V96I
XH_P36	17	48470257	48470257	Missense_Mutation	SNV	G	A	A	LRRCS9	c.167C>T	P.S56L
XH_P36	17	48647125	48647125	Missense_Mutation	SNV	C	T	T	CACNA1G	c.547C>T	P.R183C
XH_P36	17	53392628	53392628	Silent	SNV	T	C	C	HLF	c.492T>C	P.I164I
XH_P36	17	54520274	54520274	Missense_Mutation	SNV	C	T	T	ANKFN1	c.1088C>T	P.P363L
XH_P36	17	56400068	56400068	Missense_Mutation	SNV	G	A	A	TSPOAP1	c.1264C>T	P.R422C
XH_P36	17	56438293	56438293	Nonsense_Mutation	SNV	G	A	A	RNF43	c.700C>T	P.Q234*
XH_P36	17	56676693	56676693	Silent	SNV	C	T	T	TEX14	c.2031G>A	P.A677A
XH_P36	17	57746175	57746175	Missense_Mutation	SNV	C	A	A	CLTC	c.2178C>A	P.S726R
XH_P36	17	59465981	59465981	Frame_Shift_Del	INDEL	A	-	-	BCAS3	c.2670delA	P.G891fs

XH_P36	17	60042378	60042378	Missense_Mutation	SNV	A	C	C	MED13	c.4833T>G	P.D1611E
XH_P36	17	61497894	61497894	Frame_Shift_Del	INDEL	C	-	-	TANC2	c.4556delC	P.P1519fs
XH_P36	17	7127698	7127698	Missense_Mutation	SNV	C	T	T	ACADVL	c.1591C>T	P.R531W
XH_P36	17	73555417	73555417	Silent	SNV	C	T	T	LLGL2	c.456C>T	P.N152N
XH_P36	17	73646720	73646720	Nonstop_Mutation	SNV	T	C	C	RECQL5	c.1308A>G	P.Ter436Wext**
XH_P36	17	73914025	73914025	Silent	SNV	G	A	A	FBF1	c.2373C>T	P.D791D
XH_P36	17	74015081	74015081	Missense_Mutation	SNV	G	A	A	EVPL	c.1198C>T	P.R400W
XH_P36	17	74072983	74072983	Missense_Mutation	SNV	G	A	A	GALR2	c.635G>A	P.R212H
XH_P36	17	7758181	7758181	Silent	SNV	C	T	T	CBX2	c.939C>T	P.S313S
XH_P36	17	79210603	79210603	Splice_Site	SNV	T	C	C	TEPSIN	c.214-2A>G	
XH_P36	17	79249771	79249771	Missense_Mutation	SNV	G	T	T	SLC38A10	c.910C>A	P.Q304K
XH_P36	17	79769608	79769608	Missense_Mutation	SNV	C	A	A	GCCR	c.739C>A	P.L247M
XH_P36	17	79792754	79792754	Missense_Mutation	SNV	C	T	T	PPP1R27	c.76G>A	P.V26M
XH_P36	17	80129734	80129734	Splice_Site	INDEL	-	A	A	CCDC57	c.1730-6dupT	
XH_P36	18	13057634	13057634	Missense_Mutation	SNV	G	A	A	CEP192	c.4159G>A	P.G1387R
XH_P36	18	13746253	13746253	Frame_Shift_Del	INDEL	A	-	-	RNMT	c.1180delA	P.T394fs
XH_P36	18	14523456	14523456	Splice_Site	SNV	G	A	A	POTEC	c.1242+6C>T	
XH_P36	18	14538206	14538206	Silent	SNV	T	C	C	POTEC	c.564A>G	P.V188V
XH_P36	18	21921518	21921518	Missense_Mutation	SNV	C	T	T	OSBPL1A	c.387G>A	P.M129I
XH_P36	18	265533	265533	Splice_Site	INDEL	A	-	-	THOC1	c.55-3delT	
XH_P36	18	2775745	2775745	Missense_Mutation	SNV	C	T	T	SMCHD1	c.5189C>T	P.A1730V
XH_P36	18	30275527	30275528	Splice_Site	INDEL	AA	-	-	KLHL14	70-13_1070-12delTT	
XH_P36	18	3116424	3116424	Frame_Shift_Del	INDEL	C	-	-	MYOM1	c.3208delG	P.V1070fs
XH_P36	18	55103822	55103822	Missense_Mutation	SNV	C	A	A	ONECUT2	c.874C>A	P.L292M
XH_P36	18	56651438	56651438	Missense_Mutation	SNV	G	A	A	ZNF532	c.3646G>A	P.V1216I
XH_P36	18	66377374	66377374	Missense_Mutation	SNV	G	A	A	TMX3	c.149C>T	P.A50V
XH_P36	18	66678157	66678157	Splice_Site	INDEL	T	-	-	CCDC102B	c.1264-11delT	
XH_P36	18	74091072	74091072	Missense_Mutation	SNV	G	A	A	ZNF516	c.2998C>T	P.R1000C
XH_P36	18	76753476	76753476	Silent	SNV	G	A	A	SALL3	c.1485G>A	P.S495S
XH_P36	18	77624107	77624107	Missense_Mutation	SNV	C	T	T	KCNQ2	c.440C>T	P.A147V
XH_P36	18	8824907	8824907	Silent	SNV	C	T	T	MTCL1	c.3399C>T	P.A1133A
XH_P36	19	10577862	10577862	Silent	SNV	C	T	T	PDE4A	c.2226C>T	P.V792V
XH_P36	19	10812678	10812678	Missense_Mutation	SNV	C	A	A	QTRT1	c.296C>A	P.P99H
XH_P36	19	1105178	1105178	Splice_Site	SNV	C	A	A	GPX4	c.85-7C>A	
XH_P36	19	11141507	11141507	Missense_Mutation	SNV	G	A	A	SMARCA4	c.3484G>A	P.G1162S
XH_P36	19	13319692	13319694	Missense_Mutation	INDEL	GAT	-	-	CACNA1A	5668_6670delA	P.H2223del
XH_P36	19	1585169	1585169	Missense_Mutation	SNV	T	C	C	MBD3	c.155A>G	P.Y52C
XH_P36	19	1819941	1819941	Missense_Mutation	SNV	C	T	T	REXO1	c.2642G>A	P.G881D
XH_P36	19	19654762	19654762	Frame_Shift_Del	INDEL	C	-	-	CILP2	c.1412delC	P.P471fs
XH_P36	19	20116817	20116817	Silent	SNV	C	T	T	ZNF682	c.1398G>A	P.T466T
XH_P36	19	23927290	23927290	Silent	SNV	G	A	A	ZNF681	c.1062C>T	P.T354T
XH_P36	19	30312660	30312660	Missense_Mutation	SNV	C	T	T	CCNE1	c.641C>T	P.A214V
XH_P36	19	30313453	30313453	Silent	SNV	C	T	T	CCNE1	c.1053C>T	P.G351G
XH_P36	19	31768042	31768042	Missense_Mutation	SNV	G	A	A	TSHZ3	c.2657C>T	P.T886M
XH_P36	19	31768155	31768155	Silent	SNV	G	A	A	TSHZ3	c.2544C>T	P.S848S
XH_P36	19	33167417	33167417	Frame_Shift_Ins	INDEL	-	G	G	RG59BP	c.251dupG	P.C85fs
XH_P36	19	35524868	35524868	Missense_Mutation	SNV	C	T	T	SCN1B	c.673C>T	P.R225C
XH_P36	19	36223175	36223175	Frame_Shift_Del	INDEL	C	-	-	KMT2B	c.5730delC	P.R1911fs
XH_P36	19	36362899	36362899	Missense_Mutation	SNV	C	T	T	APLP1	c.811C>T	P.P271S
XH_P36	19	36370092	36370092	Silent	SNV	C	T	T	APLP1	c.1830C>T	P.V610Y
XH_P36	19	36940815	36940815	Frame_Shift_Del	INDEL	T	-	-	ZNF566	c.324delA	P.K108fs
XH_P36	19	37005981	37005981	Missense_Mutation	SNV	A	T	T	ZNF260	c.160T>A	P.S54T
XH_P36	19	38028415	38028415	Frame_Shift_Del	INDEL	T	-	-	ZNF793	c.862delT	P.C288fs
XH_P36	19	3831790	3831790	Missense_Mutation	SNV	C	T	T	ZFR2	c.466G>A	P.G156R
XH_P36	19	38655461	38655461	Missense_Mutation	SNV	G	A	A	SIPA1L3	c.4123G>A	P.G1375S
XH_P36	19	38885396	38885396	Frame_Shift_Ins	INDEL	-	C	C	SPRED3	c.544dupC	P.Q182fs
XH_P36	19	39360822	39360822	Missense_Mutation	SNV	A	G	G	RINL	c.1103T>C	P.L368P
XH_P36	19	39379738	39379738	Missense_Mutation	SNV	A	G	G	SIRT2	c.379T>C	P.C127R
XH_P36	19	41518269	41518269	Missense_Mutation	SNV	C	T	T	CYP2B6	c.1031C>T	P.A344V
XH_P36	19	41631436	41631436	Silent	SNV	C	T	T	CYP2F1	c.1191C>T	P.Y397Y
XH_P36	19	4207239	4207239	Missense_Mutation	SNV	C	T	T	ANKRD24	c.467C>T	P.A156V
XH_P36	19	4445624	4445624	Splice_Site	SNV	C	A	A	UBXN6	c.1042-4G>T	
XH_P36	19	45803051	45803051	Splice_Site	INDEL	-	CCCTC	CCCTC	MARK4	8-7_1878-3dupCCCTC	
XH_P36	19	46116858	46116858	Missense_Mutation	SNV	C	T	T	EML2	c.2368G>A	P.A790T
XH_P36	19	46289347	46289347	Silent	SNV	C	T	T	DMWD	c.1407G>A	P.T469T
XH_P36	19	48184060	48184060	Missense_Mutation	SNV	G	A	A	GLTSCR1	c.1633G>A	P.A545T
XH_P36	19	49000877	49000877	Missense_Mutation	SNV	A	G	G	LMTK3	c.3536T>C	P.L1179P
XH_P36	19	49657889	49657889	Missense_Mutation	INDEL	-	TCCTCC	TCCTCC	HRC	90_605dupGGAG	E201_E202dup
XH_P36	19	49860534	49860534	Nonsense_Mutation	SNV	G	T	T	TEAD2	c.335C>A	P.S112*
XH_P36	19	49934716	49934716	Splice_Site	INDEL	G	-	-	SLC17A7	c.1151-11delC	
XH_P36	19	5245795	5245795	Missense_Mutation	SNV	G	A	A	PTPRS	c.980C>T	P.T327M
XH_P36	19	52716080	52716080	Silent	SNV	C	T	T	PPP2R1A	c.645C>T	P.D215D
XH_P36	19	53644695	53644695	Silent	SNV	G	A	A	ZNF347	c.1389C>T	P.C463C
XH_P36	19	55481600	55481600	Missense_Mutation	SNV	C	A	A	NLRP2	c.217C>A	P.L73I
XH_P36	19	55598073	55598073	Splice_Site	SNV	C	T	T	EPS8L1	c.1397-9C>T	
XH_P36	19	56127331	56127331	Frame_Shift_Del	INDEL	G	-	-	ZNF865	c.2351delG	P.G784fs
XH_P36	19	58152336	58152336	Missense_Mutation	SNV	C	T	T	ZNF211	c.677C>T	P.A226V
XH_P36	19	58213374	58213374	Missense_Mutation	SNV	T	C	C	ZNF154	c.943A>G	P.S315G
XH_P36	19	58485478	58485478	Missense_Mutation	SNV	G	A	A	C19orf18	c.215C>T	P.S72L
XH_P36	19	6750380	6750380	Frame_Shift_Del	INDEL	C	-	-	TRIP10	c.1479delC	P.A494fs
XH_P36	19	7512066	7512066	Splice_Site	SNV	T	A	A	ARHGEF18	c.1173+12T>A	
XH_P36	19	8156455	8156455	Missense_Mutation	SNV	C	A	A	FBN3	c.5925G>T	P.E1975D
XH_P36	19	9018533	9018533	Silent	SNV	G	T	T	MUC16	c.37641C>A	P.T12547T
XH_P36	2	102482928	102482928	Missense_Mutation	SNV	A	C	C	MAP4K4	c.2009A>C	P.K670T
XH_P36	2	112705139	112705139	Missense_Mutation	SNV	T	C	C	MERTK	c.752T>C	P.V251A
XH_P36	2	112942828	112942828	Missense_Mutation	SNV	T	C	C	FBLN7	c.721T>C	P.C241R
XH_P36	2	120303807	120303807	Frame_Shift_Del	INDEL	A	-	-	CFAP221	c.106delA	P.R36fs
XH_P36	2	120677822	120677822	Splice_Site	SNV	G	A	A	PTPN4	c.1001+5G>A	
XH_P36	2	122205058	122205058	Silent	SNV	C	T	T	CLASP1	c.1767G>A	P.V589V
XH_P36	2	128467115	128467115	Missense_Mutation	SNV	G	A	A	WDR33	c.3514C>T	P.R1172C
XH_P36	2	128477850	128477850	Silent	SNV	G	A	A	WDR33	c.1749C>T	P.L583L
XH_P36	2	131803707	131803707	Missense_Mutation	SNV	G	A	A	ARHGEF4	c.2018G>A	P.R673H
XH_P36	2	141773495	141773495	Splice_Site	INDEL	A	-	-	LRP1B	c.1971-11delT	
XH_P36	2	143798030	143798030	Frame_Shift_Del	INDEL	A	-	-	KYNU	c.1080delA	P.K360fs
XH_P36	2	148657041	148657041	Frame_Shift_Del	INDEL	A	-	-	ACVR2A	c.285delA	P.D96fs
XH_P36	2	148683686	148683686	Frame_Shift_Del	INDEL	A	-	-	ACVR2A	c.1310delA	P.K437fs
XH_P36	2	160075810	160075810	Missense_Mutation	SNV	C	T	T	TANC1	c.3416C>T	P.T1139M
XH_P36	2	166785799	166785799	Missense_Mutation	SNV	C	T	T	TTC21B	c.1232G>A	P.R411Q

XH_P36	2	170366973	170366973	Frame_Shift_Ins	INDEL	-	A	A	KLHL41	c.690dupA	P.Y231fs
XH_P36	2	170460581	170460581	Frame_Shift_Del	INDEL	T	-	-	PPIG	c.36delT	P.F12fs
XH_P36	2	172549339	172549339	Frame_Shift_Del	INDEL	A	-	-	DYNC112	c.169delA	P.R57fs
XH_P36	2	179478981	179478981	Silent	SNV	A	G	G	TTN	c.44220T>C	P.S14740S
XH_P36	2	179575449	179575449	Missense_Mutation	SNV	C	T	T	TTN	c.27424G>A	P.V9142I
XH_P36	2	182763804	182763804	Silent	SNV	C	A	A	SSFA2	c.468C>A	P.S156S
XH_P36	2	186662103	186662103	Frame_Shift_Del	INDEL	A	-	-	FSIP2	c.10247delA	P.K3416fs
XH_P36	2	187615880	187615880	Silent	SNV	G	A	A	FAM171B	c.744G>A	P.L248L
XH_P36	2	189866275	189866275	Frame_Shift_Del	INDEL	C	-	-	COL3A1	c.2355delC	P.G786fs
XH_P36	2	191941055	191941055	Splice_Site	INDEL	A	-	-	STAT4	c.274-4delT	
XH_P36	2	202149545	202149545	Missense_Mutation	SNV	T	C	C	CASP8	c.860T>C	P.L287S
XH_P36	2	207172364	207172364	Missense_Mutation	SNV	G	A	A	ZDBF2	c.3106G>A	P.G1036S
XH_P36	2	207174428	207174428	Frame_Shift_Del	INDEL	A	-	-	ZDBF2	c.5178delA	P.K1726fs
XH_P36	2	20870507	20870507	Frame_Shift_Del	INDEL	C	-	-	GDF7	c.682delC	P.R228fs
XH_P36	2	210840978	210840978	Missense_Mutation	SNV	G	A	A	UNC80	c.8525G>A	P.R2842Q
XH_P36	2	219892362	219892362	Missense_Mutation	SNV	G	A	A	CFAP65	c.2188C>T	P.R730C
XH_P36	2	219896326	219896326	Missense_Mutation	SNV	C	T	T	CFAP65	c.667G>A	P.G223S
XH_P36	2	233410400	233410400	Missense_Mutation	SNV	C	T	T	CHRN9	c.1528C>T	P.R510C
XH_P36	2	234112838	234112838	Silent	SNV	C	T	T	INPP5D	c.2955C>T	P.P985P
XH_P36	2	234365952	234365952	Frame_Shift_Del	INDEL	G	-	-	DGKD	c.2432delG	P.G811fs
XH_P36	2	23865497	23865497	Silent	SNV	C	T	T	KLHL29	c.717C>T	P.P239P
XH_P36	2	239057734	239057734	Missense_Mutation	SNV	A	G	G	KLHL30	c.1426A>G	P.L476V
XH_P36	2	239258015	239258015	Missense_Mutation	SNV	C	T	T	TRAF3IP1	c.1219C>T	P.R407W
XH_P36	2	242179074	242179074	Silent	SNV	G	A	A	HDLBP	c.2454C>T	P.G818G
XH_P36	2	27248517	27248517	Frame_Shift_Del	INDEL	C	-	-	MAPRE3	c.543delC	P.P182fs
XH_P36	2	29016762	29016762	Nonsense_Mutation	SNV	C	T	T	PPP1CB	c.778C>T	P.R260*
XH_P36	2	29455174	29455174	Silent	SNV	G	A	A	ALK	c.2628C>T	P.A876A
XH_P36	2	31010045	31010045	Missense_Mutation	SNV	C	A	A	CAPN13	c.147G>T	P.Q49H
XH_P36	2	36704119	36704119	Frame_Shift_Del	INDEL	A	-	-	CRIM1	c.1080delA	P.G362fs
XH_P36	2	37347123	37347123	Frame_Shift_Del	INDEL	T	-	-	EIF2AK2	c.1227delA	P.K409fs
XH_P36	2	3750103	3750103	Missense_Mutation	SNV	C	T	T	ALLC	c.1126C>T	P.R376W
XH_P36	2	39559136	39559136	Splice_Site	INDEL	A	-	-	MAP4K3	c.458-6delT	
XH_P36	2	42720141	42720141	Silent	SNV	C	T	T	KCNGB3	c.501G>A	P.S167S
XH_P36	2	42922889	42922891	Splice_Site	INDEL	TTT	-	-	MTA3	24-6 724-4delTTT	
XH_P36	2	50765682	50765682	Frame_Shift_Ins	INDEL	-	C	C	NRXN1	c.1971dupG	P.L658fs
XH_P36	2	54028522	54028522	Splice_Site	INDEL	T	-	-	ERLEC1	c.526-4delT	
XH_P36	2	60987361	60987361	Missense_Mutation	SNV	A	G	G	PAPOLG	c.110A>G	P.Y37C
XH_P36	2	61577527	61577527	Splice_Site	INDEL	A	-	-	USP34	c.1378-3delT	
XH_P36	2	71046551	71046551	Silent	SNV	C	T	T	CLEC4F	c.204G>A	P.P68P
XH_P36	2	73518631	73518631	Missense_Mutation	SNV	T	C	C	EGR4	c.1724A>G	P.K575R
XH_P36	2	74326498	74326498	Silent	SNV	G	T	T	TEI3	c.3363G>T	P.T1121T
XH_P36	2	74900900	74900900	Missense_Mutation	SNV	G	A	A	SEMA4F	c.767G>A	P.R256Q
XH_P36	2	84942754	84942754	Splice_Site	INDEL	A	-	-	DNAH6	c.9611+9delA	
XH_P36	2	85043102	85043102	Missense_Mutation	SNV	C	T	T	DNAH6	c.12268C>T	P.P4090S
XH_P36	2	97475131	97475131	Silent	SNV	G	A	A	CNNM4	c.2205G>A	P.G735G
XH_P36	2	97638040	97638040	Silent	SNV	G	A	A	FAM178B	c.162C>T	P.T54T
XH_P36	20	14307546	14307546	Missense_Mutation	SNV	G	A	A	FLRT3	c.607C>T	P.R203C
XH_P36	20	16347868	16347868	Missense_Mutation	SNV	C	T	T	KIF16B	c.4102G>A	P.A1368T
XH_P36	20	18286958	18286958	Missense_Mutation	SNV	A	T	T	ZNF133	c.138A>T	P.K46N
XH_P36	20	25000780	25000780	Missense_Mutation	SNV	C	T	T	ACSS1	c.1112G>A	P.R371Q
XH_P36	20	25457670	25457670	Missense_Mutation	SNV	C	T	T	NINL	c.2257G>A	P.A753T
XH_P36	20	259074	259074	Splice_Site	SNV	C	T	T	C20orf96	c.463-4G>A	
XH_P36	20	3003414	3003414	Missense_Mutation	SNV	G	A	A	PTPRA	c.1408G>A	P.V470M
XH_P36	20	30606904	30606904	Frame_Shift_Del	INDEL	G	-	-	CCM2L	c.629delG	P.G210fs
XH_P36	20	33345744	33345744	Silent	SNV	C	T	T	NCOA6	c.807G>A	P.Q269Q
XH_P36	20	33589096	33589096	Missense_Mutation	SNV	G	A	A	MYH7B	c.5650G>A	P.E1884K
XH_P36	20	34022391	34022391	Silent	SNV	C	T	T	GDF5	c.822G>A	P.P274P
XH_P36	20	34208670	34208670	Missense_Mutation	SNV	C	T	T	SPAG4	c.911C>T	P.S304L
XH_P36	20	36031782	36031782	Nonstop_Mutation	SNV	G	T	T	SRC	c.1611G>T	P.Ter537Yext*?
XH_P36	20	37357196	37357196	Missense_Mutation	SNV	G	A	A	SLC32A1	c.1492G>A	P.V498I
XH_P36	20	42204858	42204858	Splice_Site	INDEL	C	-	-	SGK2	c.694-3delC	
XH_P36	20	4228843	4228843	Silent	SNV	G	A	A	ADRA1D	c.762C>T	P.Y254Y
XH_P36	20	42788776	42788776	Silent	SNV	G	A	A	JPH2	c.651C>T	P.G217G
XH_P36	20	44530971	44530971	Splice_Site	SNV	G	A	A	PLTP	c.825C>T	P.D275D
XH_P36	20	56090848	56090848	Missense_Mutation	SNV	G	A	A	CTCF	c.1102C>T	P.R368C
XH_P36	20	57768838	57768838	Missense_Mutation	SNV	C	A	A	ZNF831	c.2764C>A	P.P922T
XH_P36	20	57768886	57768886	Frame_Shift_Ins	INDEL	-	C	C	ZNF831	c.2817dupC	P.K940fs
XH_P36	20	5903414	5903414	Frame_Shift_Del	INDEL	A	-	-	CHGB	c.630delA	P.E211fs
XH_P36	20	60705321	60705321	Silent	SNV	C	T	T	LSM14B	c.642C>T	P.D214D
XH_P36	20	60963347	60963348	Splice_Site	INDEL	TT	-	-	RPS21	187-8 187-7delTT	
XH_P36	20	62196336	62196336	Missense_Mutation	SNV	A	G	G	HEL22	c.3839T>C	P.L1280P
XH_P36	20	62199927	62199927	Missense_Mutation	SNV	C	G	G	HEL22	c.1514G>C	P.R505T
XH_P36	21	17203704	17203704	Splice_Site	INDEL	T	-	-	USP25	c.1765-10delT	
XH_P36	21	22664532	22664532	Missense_Mutation	SNV	A	T	T	NCAM2	c.590A>T	P.D197V
XH_P36	21	42866456	42866456	Missense_Mutation	SNV	G	A	A	TMPPRS52	c.176C>T	P.P59L
XH_P36	21	43510462	43510462	Missense_Mutation	SNV	G	A	A	UMODL1	c.845G>A	P.C282Y
XH_P36	21	45877262	45877262	Silent	SNV	C	T	T	LRRC3	c.735C>T	P.S245S
XH_P36	22	16269950	16269950	Splice_Site	INDEL	A	-	-	POTEH	c.1238-7delT	
XH_P36	22	18096096	18096096	Splice_Site	SNV	A	C	C	ATP6V1E1	c.34-10T>G	
XH_P36	22	20843349	20843349	Silent	SNV	G	A	A	KLHL22	c.150C>T	P.F50F
XH_P36	22	25625546	25625546	Splice_Site	SNV	G	A	A	CRYBB2	c.449+1G>A	
XH_P36	22	26239838	26239838	Silent	SNV	C	A	A	MYO18B	c.3348C>A	P.P1116P
XH_P36	22	29446275	29446275	Frame_Shift_Del	INDEL	G	-	-	ZNRF3	c.2111delG	P.G704fs
XH_P36	22	30074208	30074208	Silent	SNV	G	A	A	NF2	c.1470G>A	P.P490P
XH_P36	22	32937634	32937634	Silent	SNV	G	A	A	SYN3	c.837C>T	P.Y279Y
XH_P36	22	34022242	34022242	Silent	SNV	G	A	A	LARGE1	c.477C>T	P.S159S
XH_P36	22	36624038	36624038	Missense_Mutation	SNV	T	G	G	APOL2	c.426A>C	P.E142D
XH_P36	22	39262986	39262986	Missense_Mutation	SNV	G	A	A	CBX6	c.413C>T	P.T138M
XH_P36	22	42024155	42024155	Frame_Shift_Del	INDEL	T	-	-	XRCC6	c.122delT	P.L41fs
XH_P36	22	44583645	44583645	Splice_Site	SNV	G	A	A	PARVG	c.145-11G>A	
XH_P36	22	44681360	44681360	Missense_Mutation	SNV	G	A	A	KIAA1644	c.547C>T	P.R183W
XH_P36	22	46932163	46932163	Missense_Mutation	SNV	G	A	A	CELS1R1	c.905C>T	P.T302M
XH_P36	22	50591520	50591520	Missense_Mutation	SNV	T	C	C	MOV10L1	c.2939T>C	P.M980T
XH_P36	22	50728589	50728589	Missense_Mutation	SNV	G	A	A	PLXNB2	c.425C>T	P.S142F
XH_P36	22	50987509	50987509	Missense_Mutation	SNV	G	A	A	KLHDC7B	c.914G>A	P.G305D
XH_P36	22	51042673	51042673	Silent	SNV	C	T	T	MAPK8IP2	c.945C>T	P.A315A
XH_P36	3	10301806	10301806	Splice_Site	INDEL	T	-	-	TATDN2	c.415-6delT	
XH_P36	3	108139971	108139971	Silent	SNV	G	A	A	MYH15	c.3853C>T	P.L1285L

XH_P36	3	111828413	111828413	Silent	SNV	G	A	A	C3orf52	c.420G>A	P.S140S
XH_P36	3	111940075	111940075	Splice_Site	INDEL	A	-	-	SLC9C1	c.1429-3delT	
XH_P36	3	112538716	112538716	Silent	SNV	A	G	G	CD200R1L	c.706T>C	P.L236L
XH_P36	3	112648129	112648129	Missense_Mutation	SNV	C	T	T	CD200R1	c.428G>A	P.R143H
XH_P36	3	113377483	113377483	Missense_Mutation	SNV	T	G	G	USF3	c.3046A>C	P.N1016H
XH_P36	3	122811188	122811188	Splice_Site	INDEL	T	-	-	PDIA5	c.170-5delT	
XH_P36	3	130107403	130107403	Splice_Site	INDEL	T	-	-	COL6A5	c.1862-12delT	
XH_P36	3	132051057	132051057	Missense_Mutation	SNV	G	A	A	ACPP	c.325G>A	P.V109I
XH_P36	3	136191339	136191339	Splice_Site	INDEL	-	A	A	STAG1	c.1126-6dupT	
XH_P36	3	1371501	1371501	Frame_Shift_Del	INDEL	A	-	-	CNTN6	c.1253delA	P.K418fs
XH_P36	3	138739338	138739338	Missense_Mutation	SNV	C	T	T	PRR23B	c.166G>A	P.A56T
XH_P36	3	148459721	148459721	Frame_Shift_Del	INDEL	T	-	-	AGTR1	c.904delT	P.Y302fs
XH_P36	3	150285470	150285470	Splice_Site	INDEL	T	-	-	EIF2A	c.401-3delT	
XH_P36	3	153842199	153842199	Frame_Shift_Del	INDEL	A	-	-	ARHGEF26	c.1090delA	P.M364fs
XH_P36	3	160231939	160231939	Missense_Mutation	SNV	C	T	T	KPNA4	c.1063G>A	P.A355T
XH_P36	3	161221015	161221015	Missense_Mutation	SNV	A	G	G	OTOL1	c.719A>G	P.D240G
XH_P36	3	175042056	175042056	Frame_Shift_Ins	INDEL	-	T	T	NAALADL2	c.1034dupT	P.M346fs
XH_P36	3	178952085	178952085	Missense_Mutation	SNV	A	G	G	PIK3CA	c.3140A>G	P.H1047R
XH_P36	3	183888195	183888195	Missense_Mutation	SNV	C	G	G	DVL3	c.1803C>G	P.S601R
XH_P36	3	195295892	195295892	Missense_Mutation	SNV	G	A	A	APOD	c.449C>T	P.A150V
XH_P36	3	25654189	25654189	Silent	SNV	A	G	G	TOP2B	c.3588T>C	P.S1196S
XH_P36	3	25657082	25657082	Splice_Site	INDEL	A	-	-	TOP2B	c.3337-5delT	
XH_P36	3	30691872	30691873	Frame_Shift_Del	INDEL	AA	-	-	TGFBFR2	c.457_458delAA	P.K153fs
XH_P36	3	367670	367670	Silent	SNV	G	A	A	CHL1	c.120G>A	P.Q40Q
XH_P36	3	44692631	44692631	Silent	SNV	A	G	G	ZNF35	c.72A>G	P.E24E
XH_P36	3	50005145	50005145	Frame_Shift_Del	INDEL	G	-	-	RBM6	c.293delG	P.G98fs
XH_P36	3	50324240	50324240	Missense_Mutation	SNV	C	T	T	LSMEM2	c.305C>T	P.A102V
XH_P36	3	52437315	52437315	Splice_Site	SNV	C	T	T	BAP1	c.1730-1G>A	
XH_P36	3	53263342	53263342	Silent	SNV	G	A	A	TKT	c.1218C>T	P.S406S
XH_P36	3	55018615	55018615	Splice_Site	INDEL	T	-	-	CACNA2D3	c.2557-11delT	
XH_P36	3	57440505	57440505	Silent	SNV	C	T	T	DNAH12	c.3453G>A	P.T1151T
XH_P36	3	77657037	77657037	Frame_Shift_Ins	INDEL	-	C	C	ROBO2	c.3173dupC	P.V1059fs
XH_P36	3	9970326	9970326	Splice_Site	SNV	G	A	A	IL17RC	c.1110+12G>A	
XH_P36	4	107156505	107156505	Frame_Shift_Del	INDEL	T	-	-	TBCK	c.1370delA	P.N457fs
XH_P36	4	114286281	114286281	Missense_Mutation	SNV	C	T	T	ANK2	c.4693C>T	P.R1565C
XH_P36	4	120189503	120189503	Missense_Mutation	SNV	C	A	A	USP53	c.1216C>A	P.Q406K
XH_P36	4	123270296	123270296	Splice_Site	INDEL	T	-	-	KIAA1109	c.13281-11delT	
XH_P36	4	134071649	134071649	Frame_Shift_Del	INDEL	C	-	-	PCDH10	c.360delC	P.S121fs
XH_P36	4	134073341	134073341	Silent	SNV	C	A	A	PCDH10	c.2046C>A	P.A682A
XH_P36	4	138442370	138442370	Missense_Mutation	SNV	C	T	T	PCDH18	c.3218G>A	P.G1073E
XH_P36	4	155467079	155467079	Splice_Site	SNV	G	T	T	PLRG1	c.378-4C>A	
XH_P36	4	155470090	155470090	Splice_Site	INDEL	A	-	-	PLRG1	c.10-3delT	
XH_P36	4	184431426	184431426	Splice_Site	INDEL	T	-	-	ING2	c.53-3delT	
XH_P36	4	189022306	189022306	Missense_Mutation	SNV	C	A	A	TRIML2	c.384G>T	P.Q128H
XH_P36	4	22820431	22820431	Missense_Mutation	SNV	G	A	A	GBA3	c.374G>A	P.R125Q
XH_P36	4	25278714	25278714	Missense_Mutation	SNV	C	T	T	PI4KB	c.1351C>T	P.R451C
XH_P36	4	2896294	2896294	Splice_Site	INDEL	T	-	-	ADD1	c.592-9delT	
XH_P36	4	38126762	38126762	Splice_Site	SNV	A	G	G	TBC1D1	c.3105+10A>G	
XH_P36	4	39511531	39511532	Splice_Site	INDEL	AA	-	-	UGDH	c.463-5_463-4delTT	
XH_P36	4	39864524	39864524	Missense_Mutation	SNV	C	T	T	PDSSA	c.2936G>A	P.R979H
XH_P36	4	4304807	4304807	Missense_Mutation	SNV	G	A	A	ZBTB49	c.1244G>A	P.R415Q
XH_P36	4	5018651	5018651	Missense_Mutation	SNV	G	A	A	CYT11	c.239C>T	P.S80L
XH_P36	4	57179502	57179502	Frame_Shift_Ins	INDEL	-	A	A	KIAA1211	c.501dupA	P.Q168fs
XH_P36	4	68488908	68488908	Nonsense_Mutation	SNV	C	T	T	UBA6	c.2873G>A	P.W958*
XH_P36	4	70825805	70825805	Splice_Site	INDEL	A	-	-	CSN2	c.52-8delT	
XH_P36	4	81791254	81791254	Frame_Shift_Del	INDEL	A	-	-	C4orf22	c.499delA	P.R167fs
XH_P36	4	89653284	89653284	Silent	SNV	G	A	A	FAM13A	c.1734C>T	P.T578T
XH_P36	4	95173909	95173909	Frame_Shift_Ins	INDEL	-	A	A	SMARCAD1	c.1040dupA	P.N347fs
XH_P36	4	95191919	95191919	Silent	SNV	C	T	T	SMARCAD1	c.1522C>T	P.L508L
XH_P36	4	961739	961739	Missense_Mutation	SNV	G	A	A	DGKQ	c.740C>T	P.A247V
XH_P36	4	99339795	99339795	Splice_Site	INDEL	T	-	-	RAP1GDS1	c.1043-4delT	
XH_P36	5	112346433	112346436	Splice_Site	INDEL	TTTT	-	-	DCP2	c.3-10_943-7delTTTT	
XH_P36	5	112769886	112769886	Silent	SNV	G	A	A	TSK1B	c.651C>T	P.D217D
XH_P36	5	118324039	118324039	Missense_Mutation	SNV	C	A	A	DTWD2	c.168G>T	P.W56C
XH_P36	5	1212555	1212555	Missense_Mutation	SNV	G	A	A	SLC6A19	c.619G>A	P.V207I
XH_P36	5	121413097	121413097	Missense_Mutation	SNV	G	T	T	LOX	c.584C>A	P.P195H
XH_P36	5	134050742	134050742	Missense_Mutation	SNV	G	A	A	SEC24A	c.2756G>A	P.R919H
XH_P36	5	138265000	138265000	Silent	SNV	C	T	T	CTNNA1	c.1965C>T	P.S655S
XH_P36	5	140047894	140047894	Silent	SNV	T	C	C	WDR55	c.267T>C	P.A89A
XH_P36	5	140049102	140049102	Frame_Shift_Del	INDEL	A	-	-	WDR55	c.1022delA	P.K341fs
XH_P36	5	140230590	140230590	Frame_Shift_Del	INDEL	T	-	-	PCDH49	c.2517delT	P.L840fs
XH_P36	5	140237134	140237134	Missense_Mutation	SNV	C	T	T	PCDH10	c.1501C>T	P.R501C
XH_P36	5	140568218	140568218	Silent	SNV	G	A	A	PCDH89	c.1326G>A	P.P442P
XH_P36	5	140604336	140604336	Missense_Mutation	SNV	C	T	T	PCDH814	c.1259C>T	P.T420M
XH_P36	5	140683367	140683367	Silent	SNV	C	T	T	SLC25A2	c.66G>A	P.A22A
XH_P36	5	140769366	140769366	Missense_Mutation	SNV	C	T	T	PCDHGB4	c.1915C>T	P.R639C
XH_P36	5	140953564	140953569	Missense_Mutation	INDEL	GGAGGA	-	-	DIAPH1	c.21_1826delTCG.P608_P609del	
XH_P36	5	143586393	143586393	Missense_Mutation	SNV	G	A	A	KCTD16	c.116G>A	P.R39H
XH_P36	5	145547779	145547779	Frame_Shift_Del	INDEL	G	-	-	LARS	c.344delC	P.P115fs
XH_P36	5	146754725	146754725	Frame_Shift_Del	INDEL	A	-	-	STK32A	c.983delA	P.K328fs
XH_P36	5	148407222	148407222	Silent	SNV	G	T	T	SH3TC2	c.2073C>A	P.A691A
XH_P36	5	149602668	149602668	Silent	SNV	G	A	A	CAMK2A	c.1350C>T	P.D450D
XH_P36	5	149901203	149901203	Silent	SNV	C	T	T	NDST1	c.387C>T	P.G129G
XH_P36	5	154173390	154173390	Frame_Shift_Del	INDEL	C	-	-	LARP1	c.675delC	P.T226fs
XH_P36	5	15928091	15928091	Missense_Mutation	SNV	T	C	C	FBXL7	c.79T>C	P.S27P
XH_P36	5	16179661	16179661	Silent	SNV	G	A	A	MARCH11	c.24C>T	P.G8G
XH_P36	5	162917426	162917426	Frame_Shift_Del	INDEL	A	-	-	HMMR	c.2001delA	P.K667fs
XH_P36	5	167841357	167841357	Missense_Mutation	SNV	G	A	A	WWC1	c.946G>A	P.A316T
XH_P36	5	169129368	169129368	Missense_Mutation	SNV	G	T	T	DOCK2	c.1320G>T	P.K440N
XH_P36	5	171523524	171523524	Missense_Mutation	SNV	C	T	T	STK10	c.911G>A	P.R304Q
XH_P36	5	175775279	175775279	Silent	SNV	C	T	T	KIAA1191	c.483G>A	P.P161P
XH_P36	5	176813456	176813456	Missense_Mutation	SNV	G	A	A	SLC34A1	c.421G>A	P.A141T
XH_P36	5	176863433	176863433	Frame_Shift_Del	INDEL	G	-	-	GRK6	c.1310delG	P.G437fs
XH_P36	5	176916634	176916634	Splice_Site	SNV	G	A	A	PDLIM7	c.635-6C>T	
XH_P36	5	178140631	178140631	Splice_Site	INDEL	A	-	-	ZNF354A	c.131-9delT	
XH_P36	5	1882750	1882750	Silent	SNV	C	T	T	IRX4	c.12G>A	P.P4P
XH_P36	5	32091037	32091037	Missense_Mutation	SNV	A	G	G	PDZD2	c.7483A>G	P.K2495E
XH_P36	5	37438050	37438050	Silent	SNV	G	A	A	WDR70	c.519G>A	P.S173S

XH_P36	5	38903971	38903971	Splice_Site	INDEL	T	-	-	OSMR	c.992-6delT	
XH_P36	5	482774	482774	Silent	SNV	G	A	A	SLC9A3	c.1245C>T	P.R415R
XH_P36	5	5466430	5466430	Splice_Site	INDEL	T	-	-	ICE1	c.5893-9delT	
XH_P36	5	61847115	61847115	Frame_Shift_Del	INDEL	T	-	-	IPO11	c.2539delT	P.S847fs
XH_P36	5	64867698	64867698	Missense_Mutation	SNV	G	A	A	PPWD1	c.464G>A	P.C155Y
XH_P36	5	70766233	70766233	Frame_Shift_Del	INDEL	T	-	-	BDP1	c.938delT	P.L313fs
XH_P36	5	71501039	71501039	Silent	SNV	C	A	A	MAP1B	c.7002C>A	P.S2334S
XH_P36	5	71756466	71756466	Silent	SNV	G	A	A	ZNF366	c.858C>T	P.C286C
XH_P36	5	76358967	76358967	Frame_Shift_Del	INDEL	A	-	-	AGGF1	c.2042delA	P.N681fs
XH_P36	5	82816284	82816284	Missense_Mutation	SNV	T	A	A	VCAN	c.2159T>A	P.V720D
XH_P36	5	86705190	86705190	Splice_Site	INDEL	A	-	-	CCNH	c.82-10delT	
XH_P36	5	87502325	87502328	Splice_Site	INDEL	GAAA	-	-	TMEM161B	9-12_599-9delTTTC	
XH_P36	5	9190436	9190436	Missense_Mutation	SNV	C	T	T	SEMA5A	c.1216G>A	P.A406T
XH_P36	5	96062499	96062499	Missense_Mutation	SNV	C	T	T	CAST	c.23C>T	P.A8V
XH_P36	5	96443159	96443159	Missense_Mutation	SNV	C	T	T	LIX1	c.292G>A	P.A98T
XH_P36	6	102074256	102074256	Splice_Site	SNV	C	A	A	GRIK2	c.285C>A	P.A95A
XH_P36	6	116263666	116263666	Nonsense_Mutation	SNV	G	A	A	FRK	c.1429C>T	P.R477*
XH_P36	6	118229019	118229019	Frame_Shift_Ins	INDEL	-	C	C	SLC35F1	c.133dupC	P.R45fs
XH_P36	6	118635181	118635181	Splice_Site	INDEL	-	T	T	SLC35F1	c.1003-3dupT	
XH_P36	6	132190481	132190481	Splice_Site	INDEL	T	-	-	ENPP1	c.1274-8delT	
XH_P36	6	139097330	139097330	Frame_Shift_Del	INDEL	A	-	-	CCDC28A	c.350delA	P.N117fs
XH_P36	6	142409404	142409404	Missense_Mutation	SNV	A	G	G	NMBR	c.392T>C	P.V131A
XH_P36	6	142711439	142711439	Missense_Mutation	SNV	C	T	T	ADGRG6	c.1183C>T	P.R395C
XH_P36	6	15374448	15374448	Missense_Mutation	SNV	C	T	T	JARID2	c.146C>T	P.A49V
XH_P36	6	160431705	160431705	Splice_Site	INDEL	T	-	-	IGF2R	c.415-6delT	
XH_P36	6	163149397	163149397	Missense_Mutation	SNV	G	T	T	PACRG	c.130G>T	P.V44F
XH_P36	6	21594968	21594968	Missense_Mutation	SNV	T	C	C	SOX4	c.203T>C	P.V68A
XH_P36	6	22290504	22290504	Missense_Mutation	SNV	G	A	A	PRL	c.391C>T	P.R131C
XH_P36	6	25799032	25799032	Missense_Mutation	SNV	T	C	C	SLC17A1	c.1385A>G	P.K462R
XH_P36	6	26598138	26598138	Splice_Site	SNV	G	A	A	ABT1	c.242-4G>A	
XH_P36	6	33653236	33653236	Missense_Mutation	SNV	C	T	T	ITPR3	c.5408C>T	P.T1803M
XH_P36	6	35426163	35426163	Silent	SNV	T	C	C	FANCE	c.1059T>C	P.P353P
XH_P36	6	41652798	41652798	Nonsense_Mutation	SNV	G	A	A	TFEB	c.970C>T	P.R324*
XH_P36	6	42235991	42235991	Missense_Mutation	SNV	G	C	C	TRERF1	c.1338C>G	P.S446R
XH_P36	6	43418816	43418816	Missense_Mutation	SNV	C	T	T	DLK2	c.502G>A	P.A168T
XH_P36	6	43420878	43420878	Splice_Site	SNV	C	T	T	DLK2	c.141-5G>A	
XH_P36	6	43476493	43476493	Splice_Site	SNV	C	T	T	LRRC73	c.433+5G>A	
XH_P36	6	52343894	52343894	Silent	SNV	C	T	T	EFHC1	c.1281C>T	P.T427T
XH_P36	6	52962507	52962507	Splice_Site	INDEL	T	-	-	FBXO9	c.1236-5delT	
XH_P36	6	53363590	53363590	Silent	SNV	T	C	C	GCLC	c.1764A>G	P.V588V
XH_P36	6	56047462	56047462	Splice_Site	INDEL	-	A	A	COL21A1	c.38-9dupT	
XH_P36	6	62995837	62995837	Missense_Mutation	SNV	T	C	C	KHDRBS2	c.17A>G	P.Y6C
XH_P36	6	66012756	66012756	Missense_Mutation	SNV	G	T	T	LOC441155	c.342G>T	P.K114N
XH_P36	6	69785876	69785876	Splice_Site	INDEL	T	-	-	ADGRB3	c.2437-3delT	
XH_P36	6	80751910	80751910	Frame_Shift_Del	INDEL	A	-	-	TTK	c.2568delA	P.K856fs
XH_P36	6	84645930	84645930	Splice_Site	INDEL	T	-	-	CYB5R4	c.956-5delT	
XH_P36	6	86387221	86387222	Splice_Site	INDEL	AA	-	-	SNHG5	54-12_254-11delTT	
XH_P36	6	88221098	88221099	Splice_Site	INDEL	TT	-	-	SLC35A1	10-10_710-9delTT	
XH_P36	6	88318837	88318837	Frame_Shift_Ins	INDEL	-	A	A	ORC3	c.181dupA	P.R61fs
XH_P36	7	100730930	100730930	Frame_Shift_Del	INDEL	G	-	-	TRIM56	c.342delG	P.P115fs
XH_P36	7	103301977	103301977	Splice_Site	INDEL	A	-	-	RELN	c.1290-3delT	
XH_P36	7	112407656	112407656	Missense_Mutation	SNV	T	C	C	TMEM168	c.1690A>G	P.I564V
XH_P36	7	116397525	116397525	Missense_Mutation	SNV	C	T	T	MET	c.1897C>T	P.H633Y
XH_P36	7	127978355	127978355	Missense_Mutation	SNV	G	T	T	RBM28	c.490C>A	P.L164I
XH_P36	7	128485259	128485259	Missense_Mutation	SNV	C	T	T	FLNC	c.3740C>T	P.A1247V
XH_P36	7	128502976	128502976	Silent	SNV	G	A	A	ATP6V1F	c.18G>A	P.K6K
XH_P36	7	131012702	131012702	Missense_Mutation	SNV	T	G	G	MKLN1	c.44T>G	P.L15R
XH_P36	7	131831415	131831415	Missense_Mutation	SNV	G	A	A	PLXNA4	c.4909C>T	P.R1637W
XH_P36	7	134852563	134852563	Splice_Site	INDEL	A	-	-	C7orf49	c.175-4delT	
XH_P36	7	137151696	137151696	Splice_Site	INDEL	A	-	-	DGKI	c.2444-8delT	
XH_P36	7	138363260	138363260	Silent	SNV	C	T	T	SVOPL	c.93G>A	P.T31T
XH_P36	7	139724377	139724377	Missense_Mutation	SNV	A	T	T	PARP12	c.2089T>A	P.F697I
XH_P36	7	142565462	142565462	Missense_Mutation	SNV	C	T	T	EPHB6	c.971C>T	P.A324V
XH_P36	7	150721484	150721484	Frame_Shift_Del	INDEL	C	-	-	EPH9B	c.27delG	P.R10fs
XH_P36	7	150761288	150761288	Splice_Site	SNV	G	A	A	SLC4A2	c.52-1G>A	
XH_P36	7	151945313	151945313	Silent	SNV	A	G	G	KMT2C	c.2206T>C	P.L736L
XH_P36	7	158527147	158527147	Missense_Mutation	SNV	C	T	T	ESYT2	c.2602G>A	P.A868T
XH_P36	7	27183075	27183075	Missense_Mutation	SNV	C	T	T	HOXA5	c.152G>A	P.G51D
XH_P36	7	28858716	28858716	Splice_Site	INDEL	T	-	-	CREB5	c.947-9delT	
XH_P36	7	31682378	31682378	Missense_Mutation	SNV	C	T	T	CCDC129	c.1424C>T	P.S475F
XH_P36	7	31793063	31793063	Missense_Mutation	SNV	T	C	C	PDE1C	c.2245A>G	P.M749V
XH_P36	7	34997686	34997686	Splice_Site	SNV	G	A	A	DPY19L1	c.874-4C>T	
XH_P36	7	37889877	37889877	Frame_Shift_Ins	INDEL	-	A	A	NME8	c.15dupA	P.R6fs
XH_P36	7	44560659	44560659	Silent	SNV	C	T	T	NPC1L1	c.3012G>A	P.S1004S
XH_P36	7	45124001	45124001	Missense_Mutation	SNV	T	C	C	NACAD	c.1778A>G	P.D593G
XH_P36	7	53103788	53103788	Missense_Mutation	SNV	G	A	A	POM121L12	c.424G>A	P.A142T
XH_P36	7	56156631	56156631	Missense_Mutation	SNV	T	C	C	PHKG1	c.4A>G	P.T2A
XH_P36	7	5780887	5780887	Missense_Mutation	SNV	C	T	T	RNF216	c.761G>A	P.R254Q
XH_P36	7	64451956	64451956	Nonsense_Mutation	SNV	C	T	T	ERV3-1	c.1449G>A	P.W483*
XH_P36	7	6485741	6485742	Splice_Site	INDEL	AA	-	-	DAGLB	96-7_96-6delTT	
XH_P36	7	6502731	6502731	Missense_Mutation	SNV	G	A	A	KDEL2R	c.427C>T	P.R143W
XH_P36	7	6565850	6565850	Splice_Site	SNV	C	T	T	GRID2IP	c.919+5G>A	
XH_P36	7	6662266	6662266	Missense_Mutation	SNV	G	T	T	ZNF853	c.1644G>T	P.K548N
XH_P36	7	70597900	70597900	Missense_Mutation	SNV	G	A	A	WBSCR17	c.112G>A	P.A38T
XH_P36	7	73814818	73814818	Missense_Mutation	SNV	C	T	T	CLIP2	c.2999C>T	P.A1000V
XH_P36	7	77408086	77408086	Silent	SNV	C	T	T	RSBN1L	c.2142C>T	P.S714S
XH_P36	7	84671610	84671610	Splice_Site	INDEL	A	-	-	SEMA3D	c.862-9delT	
XH_P36	7	89939531	89939531	Frame_Shift_Del	INDEL	A	-	-	CFAP69	c.2810delA	P.K937fs
XH_P36	7	94037202	94037202	Missense_Mutation	SNV	C	G	G	COL1A2	c.638C>G	P.T213R
XH_P36	7	99312312	99312312	Splice_Site	INDEL	A	-	-	CYP3A7	c.671-7delT	
XH_P36	8	104897908	104897908	Nonsense_Mutation	SNV	C	T	T	RIMS2	c.1081C>T	P.R361*
XH_P36	8	105521191	105521191	Missense_Mutation	SNV	T	G	G	LRP12	c.191A>C	P.N64T
XH_P36	8	10755632	10755632	Missense_Mutation	SNV	T	C	C	XKR6	c.1756A>G	P.K586E
XH_P36	8	110464995	110464995	Frame_Shift_Ins	INDEL	-	G	G	PKHD1L1	c.6563dupG	P.S2190fs
XH_P36	8	110478806	110478806	Splice_Site	SNV	G	T	T	PKHD1L1	c.8414-1G>T	
XH_P36	8	110587336	110587336	Silent	SNV	G	A	A	SYBU	c.1788C>T	P.G596G
XH_P36	8	110986446	110986446	Missense_Mutation	SNV	A	T	T	KCNV1	c.172T>A	P.S58T
XH_P36	8	117862854	117862854	Splice_Site	SNV	T	C	C	RAD21	c.1620+3A>G	

XH_P36	8	121587323	121587323	Splice_Site	SNV	T	A	A	SNTB1	c.1136+3A>T	
XH_P36	8	125326260	125326260	Missense_Mutation	SNV	A	G	G	TMEM65	c.664T>C	P.F222L
XH_P36	8	128750864	128750864	Missense_Mutation	SNV	C	T	T	MYC	c.401C>T	P.P134L
XH_P36	8	133056743	133056743	Splice_Site	SNV	G	A	A	OC90	c.113-7C>T	
XH_P36	8	133764167	133764167	Missense_Mutation	SNV	T	C	C	TMEM71	c.178A>G	P.T60A
XH_P36	8	139638440	139638440	Missense_Mutation	SNV	C	T	T	COL22A1	c.3710G>A	P.G1237E
XH_P36	8	143956491	143956491	Missense_Mutation	SNV	C	T	T	CYP11B1	c.1280G>A	P.R427H
XH_P36	8	144940503	144940503	Missense_Mutation	SNV	C	T	T	EPK1	c.6919G>A	P.V2307I
XH_P36	8	144998402	144998402	Missense_Mutation	SNV	G	A	A	PLEC	c.5776C>T	P.R1926C
XH_P36	8	145650341	145650341	Silent	SNV	G	A	A	VPS28	c.288C>T	P.C96C
XH_P36	8	145693999	145693999	Silent	SNV	G	A	A	KIFC2	c.969G>A	P.R323R
XH_P36	8	145737394	145737394	Missense_Mutation	SNV	G	A	A	RECQL4	c.3293C>T	P.T1098I
XH_P36	8	17402081	17402081	Frame_Shift_Del	INDEL	T	-	-	SLC7A2	c.504delT	P.F168fs
XH_P36	8	21981180	21981180	Missense_Mutation	SNV	G	A	A	HR	c.1897C>T	P.R633W
XH_P36	8	2813125	2813125	Missense_Mutation	SNV	G	A	A	CSMD1	c.9980C>T	P.S3327L
XH_P36	8	2824227	2824227	Missense_Mutation	SNV	T	A	A	CSMD1	c.8965A>T	P.I2989F
XH_P36	8	3226804	3226804	Silent	SNV	C	G	G	CSMD1	c.2871G>C	P.T957T
XH_P36	8	37553551	37553551	Silent	SNV	C	T	T	ZNF703	c.54C>T	P.S18S
XH_P36	8	38186894	38186894	Splice_Site	SNV	A	G	G	WHSC1L1	c.1581+2T>C	
XH_P36	8	38874860	38874860	Missense_Mutation	SNV	C	A	A	ADAM9	c.533C>A	P.S178Y
XH_P36	8	42040260	42040260	Silent	SNV	G	A	A	PLAT	c.780C>T	P.G260G
XH_P36	8	61736495	61736495	Missense_Mutation	SNV	C	T	T	CHD7	c.3298C>T	P.R1100C
XH_P36	8	6289099	6289099	Frame_Shift_Del	INDEL	A	-	-	MCPH1	c.321delA	P.K107fs
XH_P36	8	65517426	65517426	Splice_Site	SNV	A	C	C	CYP7B1	c.1058-12T>G	
XH_P36	8	67417717	67417717	Silent	SNV	C	T	T	C8orf46	c.234C>T	P.T78T
XH_P36	8	68151020	68151020	Missense_Mutation	SNV	T	C	C	ARFGF1	c.3088A>G	P.I1030V
XH_P36	8	77619814	77619814	Missense_Mutation	SNV	C	T	T	ZFXH4	c.2624C>T	P.A875V
XH_P36	8	82588523	82588523	Splice_Site	SNV	A	T	T	IMPA1	c.480-9T>A	
XH_P36	8	92030736	92030736	Missense_Mutation	SNV	C	T	T	TMEM55A	c.368G>A	P.R123Q
XH_P36	8	9609110	9609110	Splice_Site	INDEL	T	-	-	TNKS	c.2833-3delT	
XH_P36	8	99146236	99146236	Silent	SNV	G	A	A	POP1	c.795G>A	P.A265A
XH_P36	8	9953753	9953753	Splice_Site	SNV	G	A	A	MSRA	c.-131-1G>A	
XH_P36	9	105340676	105340676	Splice_Site	SNV	C	T	T	LINC00587	n.196C>T	
XH_P36	9	106885379	106885379	Splice_Site	INDEL	T	-	-	SMC2	c.2133-6delT	
XH_P36	9	113192205	113192205	Silent	SNV	T	C	C	SVEP1	c.5610A>G	P.T1870T
XH_P36	9	116276868	116276868	Silent	SNV	G	A	A	RG53	c.1278G>A	P.T426T
XH_P36	9	117139586	117139586	Missense_Mutation	SNV	C	A	A	AKNA	c.501G>T	P.Q167H
XH_P36	9	117848395	117848395	Nonsense_Mutation	SNV	G	A	A	TNC	c.1615C>T	P.Q539*
XH_P36	9	124089770	124089770	Splice_Site	SNV	G	A	A	GSN	c.1915+10G>A	
XH_P36	9	124545797	124545797	Splice_Site	INDEL	T	-	-	DAB2IP	c.3390-11delT	
XH_P36	9	127920568	127920568	Nonsense_Mutation	SNV	G	A	A	PPP6C	c.442C>T	P.R148*
XH_P36	9	128691915	128691915	Splice_Site	INDEL	T	-	-	PBX3	c.292-11delT	
XH_P36	9	130947831	130947831	Nonsense_Mutation	SNV	G	A	A	CI21	c.583C>T	P.R195*
XH_P36	9	131483691	131483691	Missense_Mutation	SNV	C	T	T	ZDHH12	c.601G>A	P.V201I
XH_P36	9	131709317	131709317	Missense_Mutation	SNV	G	T	T	DOLK	c.266C>A	P.P89H
XH_P36	9	133231492	133231492	Missense_Mutation	SNV	G	A	A	HMCN2	c.3599G>A	P.R1200H
XH_P36	9	133269250	133269250	Frame_Shift_Ins	INDEL	-	G	G	HMCN2	c.8686dupG	P.E2896fs
XH_P36	9	133281350	133281350	Silent	SNV	C	T	T	HMCN2	c.10674C>T	P.D3558D
XH_P36	9	135271808	135271808	Splice_Site	INDEL	-	T	T	TTF1	c.311+11dupA	
XH_P36	9	135534128	135534128	Splice_Site	INDEL	A	-	-	DDX31	c.839-6delT	
XH_P36	9	135926232	135926232	Missense_Mutation	SNV	G	A	A	GTFC35	c.635G>A	P.R212H
XH_P36	9	137801701	137801701	Silent	SNV	C	T	T	FCN1	c.924G>A	P.A308A
XH_P36	9	138395457	138395457	Silent	SNV	G	A	A	MRPS2	c.369G>A	P.T123T
XH_P36	9	139371084	139371084	Silent	SNV	C	T	T	SEC16A	c.984G>A	P.R328R
XH_P36	9	139996032	139996032	Missense_Mutation	SNV	C	T	T	MAN1B1	c.1162C>T	P.R388W
XH_P36	9	140001244	140001244	Missense_Mutation	SNV	C	A	A	MAN1B1	c.1549C>A	P.R517S
XH_P36	9	140081973	140081973	Missense_Mutation	SNV	G	A	A	ANAPC2	c.700C>T	P.R234C
XH_P36	9	140126103	140126103	Splice_Site	INDEL	-	C	C	SLC34A3	c.-39-6dupC	
XH_P36	9	140140197	140140197	Silent	SNV	C	T	T	FAM166A	c.165G>A	P.V55V
XH_P36	9	140732961	140732961	Splice_Site	INDEL	C	-	-	MIR602	n.96delC	
XH_P36	9	18906821	18906821	Missense_Mutation	SNV	G	A	A	ADAMTSL1	c.5093G>A	P.R1698H
XH_P36	9	19300171	19300171	Splice_Site	INDEL	T	-	-	DENND4C	n.1253-7delT	
XH_P36	9	2047307	2047307	Missense_Mutation	SNV	C	T	T	SMARCA2	c.869C>T	P.A290V
XH_P36	9	26906080	26906080	Splice_Site	INDEL	AA	-	-	PLAA	823-7_1823-6delTT	
XH_P36	9	26928300	26928300	Splice_Site	SNV	C	A	A	PLAA	c.444+6G>T	
XH_P36	9	27220063	27220063	Silent	SNV	C	T	T	TEK	c.3120C>T	P.C1040C
XH_P36	9	27548256	27548256	Missense_Mutation	SNV	C	T	T	C9orf72	c.1424G>A	P.R475Q
XH_P36	9	2827162	2827162	Splice_Site	INDEL	A	-	-	PUM3	c.957-11delT	
XH_P36	9	35103049	35103049	Splice_Site	SNV	T	G	G	STOML2	c.43A>C	P.R15R
XH_P36	9	36102078	36102078	Splice_Site	INDEL	T	-	-	RECK	c.915-5delT	
XH_P36	9	37733708	37733708	Splice_Site	INDEL	T	-	-	FRMPD1	c.1123-11delT	
XH_P36	9	40772354	40772354	Missense_Mutation	SNV	G	A	A	ZNF658	c.2921C>T	P.T974M
XH_P36	9	5233659	5233659	Missense_Mutation	SNV	G	A	A	INSL4	c.202G>A	P.V68M
XH_P36	9	5742994	5742994	Missense_Mutation	SNV	A	G	G	RIC1	c.1027A>G	P.T343A
XH_P36	9	73399023	73399023	Splice_Site	SNV	G	A	A	TRPM3	c.687C>T	P.G229G
XH_P36	9	73458046	73458046	Splice_Site	INDEL	A	-	-	TRPM3	c.218-3delT	
XH_P36	9	84606936	84606936	Silent	SNV	T	C	C	SPATA31D1	c.1551T>C	P.P517P
XH_P36	9	8524968	8524968	Silent	SNV	G	A	A	PTPRD	c.636C>T	P.S212S
XH_P36	9	86503511	86503511	Splice_Site	INDEL	A	-	-	KIF27	c.1980-4delT	
XH_P36	9	90582462	90582462	Frame_Shift_Ins	INDEL	-	G	G	CDK20	c.955dupC	P.H319fs
XH_P36	9	96422612	96422612	Frame_Shift_Del	INDEL	A	-	-	PHF2	c.1475delA	P.K492fs
XH_P36	9	977357	977357	Missense_Mutation	SNV	A	C	C	DMRT3	c.356A>C	P.Q119P
XH_P36	9	99381507	99381507	Missense_Mutation	SNV	T	C	C	CDC14B	c.154A>G	P.I52V
XH_P36	X	100503224	100503224	Missense_Mutation	SNV	A	G	G	DRP2	c.1165A>G	P.N389D
XH_P36	X	101970716	101970716	Missense_Mutation	SNV	A	G	G	GPRASP2	c.919A>G	P.R307G
XH_P36	X	105450411	105450411	Missense_Mutation	SNV	A	T	T	MUM1L1	c.986A>T	P.D329V
XH_P36	X	106845186	106845186	Frame_Shift_Del	INDEL	G	-	-	FRMPD3	c.4022delG	P.G1341fs
XH_P36	X	114347904	114347904	Splice_Site	INDEL	-	A	A	LRCH2	c.2128-7dupT	
XH_P36	X	114424574	114424574	Silent	SNV	C	A	A	RBMXL3	c.570C>A	P.G190G
XH_P36	X	117530913	117530914	Splice_Site	INDEL	TT	-	-	WDR44	54-10_1054-9delTT	
XH_P36	X	118920652	118920652	Missense_Mutation	SNV	G	T	T	RPL39	c.151C>A	P.L151I
XH_P36	X	123514660	123514660	Missense_Mutation	SNV	T	C	C	TENM1	c.7925A>G	P.Y2642C
XH_P36	X	123663816	123663816	Missense_Mutation	SNV	C	T	T	TENM1	c.2669G>A	P.R890Q
XH_P36	X	125685317	125685317	Missense_Mutation	SNV	T	G	G	DCAF12L1	c.1275A>C	P.E425D
XH_P36	X	12904643	12904643	Frame_Shift_Ins	INDEL	-	C	C	TLR7	c.1020dupC	P.S341fs
XH_P36	X	129147932	129147932	Missense_Mutation	SNV	C	A	A	BCORL1	c.1184C>A	P.T395K
XH_P36	X	129270637	129270637	Missense_Mutation	SNV	T	C	C	AIFM1	c.128A>G	P.K43R
XH_P36	X	14599388	14599388	Frame_Shift_Ins	INDEL	-	T	T	GLRA2	c.356dupT	P.L119fs

XH_P36	X	147003514	147003514	Splice_Site	SNV	C	T	T	FMR1	c.104+11C>T	
XH_P36	X	148627313	148627313	Missense_Mutation	SNV	G	T	T	CXorf40A	c.137G>T	P.R46M
XH_P36	X	148794840	148794840	Frame_Shift_Ins	INDEL	-	G	G	MAGEA11	c.26dupG	P.L10fs
XH_P36	X	151808938	151808938	Splice_Site	SNV	T	A	A	GABRQ	c.238+11T>A	
XH_P36	X	152686163	152686163	Frame_Shift_Del	INDEL	G	-	-	ZFP92	c.331delG	P.A111fs
XH_P36	X	153178731	153178731	Missense_Mutation	SNV	C	T	T	ARHGAP4	c.1352G>A	P.R451Q
XH_P36	X	153692348	153692348	Missense_Mutation	SNV	G	T	T	PLXNA3	c.1602G>T	P.E534D
XH_P36	X	153944567	153944567	Missense_Mutation	SNV	C	T	T	GAB3	c.110G>A	P.R37H
XH_P36	X	17750296	17750296	Silent	SNV	C	T	T	NHS	c.4137C>T	P.S1379S
XH_P36	X	22056595	22056595	Missense_Mutation	SNV	G	T	T	PHEx	c.127G>T	P.G43C
XH_P36	X	22292144	22292144	Frame_Shift_Ins	INDEL	-	A	A	ZNF645	c.1040dupA	P.N347fs
XH_P36	X	23397692	23397692	Splice_Site	INDEL	T	-	-	PTCHD1	c.352-10delT	
XH_P36	X	23410920	23410920	Missense_Mutation	SNV	G	T	T	PTCHD1	c.1285G>T	P.G429C
XH_P36	X	2773043	2773043	Missense_Mutation	SNV	A	G	G	GYG2	c.334A>G	P.N112D
XH_P36	X	30327013	30327013	Silent	SNV	C	T	T	NR0B1	c.468G>A	P.T156T
XH_P36	X	30877624	30877624	Missense_Mutation	SNV	C	T	T	TAB3	c.82G>A	P.V28M
XH_P36	X	32366648	32366648	Splice_Site	INDEL	A	-	-	DMD	c.5302-3delT	
XH_P36	X	36321999	36321999	Missense_Mutation	SNV	C	T	T	CFAP47	c.8006C>T	P.T2669M
XH_P36	X	37028698	37028698	Missense_Mutation	SNV	C	T	T	FAM47C	c.2215C>T	P.R739C
XH_P36	X	47516631	47516631	Silent	SNV	G	A	A	UXT	c.307C>T	P.L103L
XH_P36	X	53115191	53115191	Silent	SNV	C	T	T	TSPYL2	c.1617C>T	P.Y539Y
XH_P36	X	53564586	53564586	Missense_Mutation	SNV	C	T	T	HUWE1	c.12068G>A	P.R4023H
XH_P36	X	54569370	54569370	Splice_Site	INDEL	T	-	-	GNL3L	c.307-10delT	
XH_P36	X	65822649	65822649	Splice_Site	INDEL	A	-	-	EDA2R	c.353-10delT	
XH_P36	X	7023887	7023887	Splice_Site	INDEL	A	-	-	PUDP	c.131-8delT	
XH_P36	X	70586340	70586340	Missense_Mutation	SNV	A	T	T	TAF1	c.176A>T	P.D59V
XH_P36	X	74318786	74318786	Silent	SNV	A	G	G	ABCB7	c.444T>C	P.G148G
XH_P36	X	76845413	76845413	Splice_Site	INDEL	A	-	-	ATRX	c.6111-3delT	
XH_P36	X	77224989	77224989	Silent	SNV	G	T	T	PGAM4	c.147C>A	P.G49G
XH_P36	X	77268382	77268382	Missense_Mutation	SNV	G	A	A	ATP7A	c.2179G>A	P.T272R
XH_P36	X	79279670	79279670	Splice_Site	SNV	G	T	T	TBX22	c.458+7G>T	
XH_P36	X	82763673	82763673	Frame_Shift_Del	INDEL	G	-	-	POU3F4	c.346delG	P.A116fs
XH_P36	X	95993734	95993734	Missense_Mutation	SNV	A	T	T	DIAPH2	c.315A>T	P.E105D
XH_P37	12	25398284	25398284	Missense_Mutation	SNP	C	T	T	KRAS	c.35G>A	p.G12D
XH_P37	1	78426078	78426078	Missense_Mutation	SNP	G	T	T	FUBP1	c.1447C>A	p.P483T
XH_P37	1	977395	977395	Missense_Mutation	SNP	C	A	C	AGRN	c.C1237A	p.R413S
XH_P37	1	1858140	1858140	Frame_Shift_Ins	INS	-	TCTCCCGAGG	-	CFAP74	3723insCCTCG	p.V1241fs
XH_P37	1	3742991	3742991	Nonsense_Mutation	INS	-	TAACCTAAAATA	-	CEP104	AAAGGATATTTT	5733delinsAERIFX
XH_P37	1	4772675	4772675	In_Frame_Ins	INS	-	ATGAACCTCA	-	AJAP1	746insATGAAG	G249delinsDELR
XH_P37	1	5993378	5993378	Silent	SNP	G	A	G	NPHP4	c.C1131T	p.V377V
XH_P37	1	5993379	5993379	Nonsense_Mutation	INS	-	FAGGTATTCTCTTA	-	NPHP4	ATGCATAAGAA	877_T378delinsDAX
XH_P37	1	6712973	6712973	Frame_Shift_Ins	INS	-	ACAACCTCAGCCA	-	DNAJC11	5TCTATTGGCTG	p.G182fs
XH_P37	1	7798488	7798488	Frame_Shift_Ins	INS	-	AGAGGCT	-	CAMTA1	57_1258insAGAA	p.S419fs
XH_P37	1	9796012	9796012	Silent	SNP	G	A	G	CLSTN1	c.C1608T	p.I536I
XH_P37	1	10357279	10357279	Frame_Shift_Ins	INS	-	AGGAG	-	KIF1B	552_1953insAG	p.D651fs
XH_P37	1	10468171	10468171	Frame_Shift_Ins	INS	-	CTAA	-	PGD	427_428insCTA	p.G143fs
XH_P37	1	10468173	10468173	Frame_Shift_Ins	INS	-	CTACAGGT	-	PGD	9_430insCTACA	p.G143fs
XH_P37	1	12837291	12837291	Missense_Mutation	SNP	T	C	T	PRAMEF12	c.T1001C	p.F334S
XH_P37	1	14108446	14108446	Nonsense_Mutation	INS	-	AAGCTGGGTA	-	PRDM2	554insAAAGCT	185_D1186delinsX
XH_P37	1	15382667	15382667	Silent	SNP	T	C	T	KAZN	c.T525C	p.N175N
XH_P37	1	15495247	15495247	Frame_Shift_Ins	INS	-	ACAGC	-	C1orf195	124_125insGCT	p.V42fs
XH_P37	1	15987798	15987798	Nonsense_Mutation	INS	-	TTCTGATTGACA	-	RSC1A1	nsTGGTTTCTGA	9_T480delinsMVSDX
XH_P37	1	16134066	16134066	Frame_Shift_Ins	INS	-	AACTTGAAATAA	-	UQCRLH	ACATTATTTC	p.V27fs
XH_P37	1	16245978	16245978	Missense_Mutation	SNP	C	T	C	SPEN	c.C1601T	p.T534I
XH_P37	1	16245980	16245980	Missense_Mutation	SNP	C	G	C	SPEN	c.C1603G	p.R535G
XH_P37	1	16641752	16641752	Nonsense_Mutation	INS	-	CTCCCTTAAATG	-	FBXO42	AATACATTTAAG	V54_155delinsVX
XH_P37	1	17084504	17084504	Missense_Mutation	SNP	G	A	G	MST1L	c.C1594T	p.R532W
XH_P37	1	17084505	17084505	Missense_Mutation	SNP	C	G	C	MST1L	c.G1593C	p.Q531H
XH_P37	1	19524505	19524505	Nonsense_Mutation	INS	-	CGGAGAAGCTAA	-	UBR4	687insGTAGCTT	Q229delinsQX
XH_P37	1	19524507	19524507	Frame_Shift_Ins	INS	-	CGTG	-	UBR4	684_685insACA	p.Q229fs
XH_P37	1	20020998	20020998	In_Frame_Ins	INS	-	AAAGAT	-	TMCO4	128_1429insATC	p.L477delinsFL
XH_P37	1	20020999	20020999	Frame_Shift_Ins	INS	-	ATAAGAATTAT	-	TMCO4	1428insAATAAA	p.Q476fs
XH_P37	1	22175460	22175460	Frame_Shift_Ins	INS	-	CATCACT	-	HSPG2	3_7514insAGGT	p.R2505fs
XH_P37	1	22198813	22198813	Nonsense_Mutation	SNP	G	A	G	HSPG2	c.C4090T	p.R1364X
XH_P37	1	23520411	23520411	Nonsense_Mutation	INS	-	GCCTTCTACA	-	HTR1D	302insGTAGAA	01_H102delinsMX
XH_P37	1	23885748	23885748	Frame_Shift_Ins	INS	-	TCCCTCTTTTCC	-	ID3	0insAGGAAAG	p.G57fs
XH_P37	1	24020359	24020359	Frame_Shift_Ins	INS	-	ATTTTCCCAT	-	RPL11	221insATTTC	p.V74fs
XH_P37	1	24997974	24997974	Frame_Shift_Ins	INS	-	5TATTCAAAAGT	-	SRRM1	9insAAGTATTC	p.R833fs
XH_P37	1	26751971	26751971	Frame_Shift_Ins	INS	-	AGGAACCTTAT	-	LIN28A	nsACAAGGAAC	p.R136fs
XH_P37	1	27684800	27684800	Frame_Shift_Ins	INS	-	ACTCTAACTTG	-	MAP3K6	2763insCAAGT	p.S921fs
XH_P37	1	28320072	28320072	Splice_Site	INS	-	TTTTA	-	EYA3	-	
XH_P37	1	28477055	28477055	Nonsense_Mutation	INS	-	CTGTTTCTCTCAC	-	PTAFR	CTTGGTGAGGA	160delinsFLVRKQX
XH_P37	1	29314413	29314413	Frame_Shift_Ins	INS	-	5GAGAATAGTCC	-	EPB41	insGAGGAGAA	p.T155fs
XH_P37	1	31414971	31414971	Splice_Site	INS	-	5AATCTGTGGT	-	PUM1	-	
XH_P37	1	31532354	31532354	In_Frame_Ins	INS	-	CTACTTCTTTTCA	-	PUM1	insTCTGAAAGA	P20delinsPLKEVV
XH_P37	1	32118445	32118445	Frame_Shift_Ins	INS	-	T	-	COL16A1	c.4621_4622ins	p.G1541fs
XH_P37	1	32118446	32118446	In_Frame_Ins	INS	-	AGGTTGTGAAT	-	COL16A1	AAAAAACATTCA	41delinsKKHSPQV7G
XH_P37	1	32154468	32154468	Nonsense_Mutation	INS	-	ACATAATCTCTA	-	COL16A1	761insATAGGA	587_L588delinsGX
XH_P37	1	32790122	32790122	In_Frame_Ins	INS	-	CTGCATCAAGTT	-	HDAC1	324insCTGCATC	E108delinsDCIKL
XH_P37	1	34023424	34023424	Missense_Mutation	SNP	G	A	G	CSMD2	c.C8653T	p.R2885W
XH_P37	1	35480736	35480736	Frame_Shift_Ins	INS	-	GTATGTGTGTGT	-	ZMYM6	insAAACACACA	p.I152fs
XH_P37	1	35579116	35579116	Frame_Shift_Ins	INS	-	ACAACCTGGCAT	-	ZMYM1	5GCAGAGAACAC	p.L487fs
XH_P37	1	36028099	36028099	Frame_Shift_Ins	INS	-	ATAATACAACCTA	-	NCDN	nsAGAAATAATA	p.L400fs
XH_P37	1	36215412	36215412	Frame_Shift_Ins	INS	-	A	-	CLSPN	c.1836_1837ins	p.T613fs
XH_P37	1	36215413	36215413	Splice_Site	INS	-	GGTAAG	-	CLSPN	-	
XH_P37	1	36299771	36299771	Frame_Shift_Ins	INS	-	TTTTTCAATTCAG	-	AGO4	ACGGTTTTTTTTC	p.V520fs
XH_P37	1	38338723	38338723	Nonsense_Mutation	INS	-	ATGCCTACC	-	INPP5B	1574insGGTA	p.K525delinsRX
XH_P37	1	39341321	39341321	Frame_Shift_Ins	INS	-	5CAATCTATAGC	-	GJA9	TAGTGGCTATA	p.R150fs
XH_P37	1	39816687	39816687	Nonsense_Mutation	INS	-	CCTGTAATCCT	-	MACF1	TGTCACTCTGTA	570delinsECPVNPX
XH_P37	1	39877142	39877142	Nonsense_Mutation	INS	-	TCCATCATA	-	KIAA0754	5_1206insTCCA	P402delinsPPSX
XH_P37	1	39877144	39877144	Missense_Mutation	SNP	G	T	G	KIAA0754	c.G1207T	p.A403S
XH_P37	1	40704533	40704533	Frame_Shift_Ins	INS	-	TGCCTATTGGT	-	RLF	TATGGCTGCCTA	p.H1387fs
XH_P37	1	40960979	40960979	In_Frame_Ins	INS	-	GAGACTTTTCTG	-	ZFP69	833insGAGACT	E278delinsECHPDSQ
XH_P37	1	40960981	40960981	Frame_Shift_Ins	INS	-	CGTGGAAAT	-	ZFP69	4_835insCGTGG	p.E278fs
XH_P37	1	41012624	41012624	In_Frame_Ins	INS	-	GGC	-	ZNF684	629_630insGCC	p.N210delinsKR
XH_P37	1	41012625	41012625	Nonsense_Mutation	INS	-	TCTATTATATTTA	-	ZNF684	TAACTTCTATTA	5211delinsNFLQYNFYFYY
XH_P37	1	41514547	41514547	In_Frame_Ins	INS	-	AAGGCA	-	SCMH1	516_617insTGCC	N206delinsMPY
XH_P37	1	42046033	42046033	Frame_Shift_Ins	INS	-	GTCAGAAACG	-	HIVEP3	4436insCGTTT	p.K1479fs

XH_P37	1	43055136	43055136	Frame_Shift_Ins	INS	-	GTATGTGTCTAT	-	CCDC30	sGTAGGGTATG	p.E455fs
XH_P37	1	43896275	43896275	In_Frame_Ins	INS	-	TGAAAATCCAG	-	SZT2	4419insTGAAAA	1473delinsSENSR
XH_P37	1	43903330	43903330	Frame_Shift_Ins	INS	-	TGGTAACCAAG	-	SZT2	185insCTGGTAA	p.L2062fs
XH_P37	1	45292590	45292590	Frame_Shift_Ins	INS	-	TTCTCTCT	-	PTCH2	8_2679insAAGA	p.T893fs
XH_P37	1	45292591	45292591	Missense_Mutation	SNP	G	C	G	PTCH2	c.C2678G	p.T893R
XH_P37	1	45478986	45478986	Frame_Shift_Ins	INS	-	STTTTATCTAGA	-	UROD	237insGTTTATG	p.D79fs
XH_P37	1	45484528	45484528	In_Frame_Ins	INS	-	TCGCCACTATGG	-	ZSWIM5	3156insCCATAG	1052delinsLHSGE
XH_P37	1	46070690	46070690	Splice_Site	INS	-	AAGTACATTAA	-	NASP	-	-
XH_P37	1	46543274	46543274	Nonsense_Mutation	INS	-	TTCCAGTCTGGC	-	110117498-PIK	AATTAGCCAGAC22_D123delinsLNVX	-
XH_P37	1	47110905	47110905	Silent	SNP	C	T	C	ATPAF1	c.G348A	p.R116R
XH_P37	1	47110907	47110907	In_Frame_Ins	INS	-	ACTACTTCTGGT	-	ATPAF1	6insGAACCAGA	116delinsEPEVVR
XH_P37	1	47746544	47746544	Nonsense_Mutation	INS	-	AAGCCCTTCAAA	-	STIL	AATGCTTTTGAA	G529delinsECFX
XH_P37	1	48460195	48460195	Frame_Shift_Ins	INS	-	TATGTCTGACTA	-	TRABD2B	insAGGTAGTCA	p.V59fs
XH_P37	1	52442702	52442702	Frame_Shift_Ins	INS	-	CCAGGAGGTTT	-	RAB3B	ACATAAACTCTC	p.N30fs
XH_P37	1	52891135	52891135	Frame_Shift_Ins	INS	-	ACAAAACTCCAA	-	ZCCHC11	AAGTAATGGAG	p.A1586fs
XH_P37	1	53504718	53504718	Missense_Mutation	SNP	G	A	G	SCP2	c.G256A	p.D86N
XH_P37	1	53504719	53504719	Splice_Site	INS	-	GTTTAAATAGA	-	SCP2	-	-
XH_P37	1	55080512	55080512	Frame_Shift_Ins	INS	-	CC	-	FAM151A	c.435_436insGG	p.N146fs
XH_P37	1	55080514	55080514	Frame_Shift_Ins	INS	-	CTTCTCCAA	-	FAM151A	434insTTGGAG	p.K145fs
XH_P37	1	56977824	56977824	Frame_Shift_Ins	INS	-	TAAGTAGCAT	-	PLPP3	634insATGCTA	p.L212fs
XH_P37	1	57233602	57233602	Frame_Shift_Ins	INS	-	ACCATCTATTAT	-	C1orf168	insAAGAAATAAA	p.N321fs
XH_P37	1	58999933	58999933	Nonsense_Mutation	INS	-	TCACTGGATTTT	-	OMA1	TTTAAAAATCCAA	C268delinsHYLKIQX
XH_P37	1	59148073	59148073	Nonsense_Mutation	INS	-	CACTGTATATTT	-	MYSM1	AGGATAAATATA	p.E215delinsX
XH_P37	1	60499180	60499180	Missense_Mutation	SNP	G	C	G	C1orf87	c.C997G	p.R333G
XH_P37	1	61554336	61554336	In_Frame_Ins	INS	-	GCTTTTCATGTT	-	NFIA	544insGCTTTTTC	Y181delinsYAFHV
XH_P37	1	63097073	63097073	Frame_Shift_Ins	INS	-	TTTTTGGAGATG	-	DOCK7	120insCCATCTC	p.K374fs
XH_P37	1	63999881	63999881	Frame_Shift_Ins	INS	-	TTCTAATAAGAA	-	EFCAB7	TGGGCTTCTAAT	p.L266fs
XH_P37	1	65858477	65858477	Frame_Shift_Ins	INS	-	TGCTTTTGTCTG	-	DNAJC6	1833insTGCTTTT	p.A611fs
XH_P37	1	66102089	66102089	Missense_Mutation	SNP	C	G	C	LEPR	c.C2889G	p.N963K
XH_P37	1	66102091	66102091	Frame_Shift_Ins	INS	-	TAAAGAACATAA	-	LEPR	sAATAATAAAGA	p.F964fs
XH_P37	1	67359077	67359077	Frame_Shift_Ins	INS	-	TTTCTTTCTTCT	-	WDR78	AGAAAGAAAGA	p.T122fs
XH_P37	1	67558986	67558986	In_Frame_Ins	INS	-	GCCTCAATAAAA	-	C1orf141	ATAATATTTTATG	delinsIAAYIFFEAFKISFD
XH_P37	1	68624857	68624857	In_Frame_Ins	INS	-	TTTCTCT	-	WLS	79_180insAGGA	p.M60delinsGK
XH_P37	1	68624858	68624858	Frame_Shift_Ins	INS	-	ACTTTGC	-	WLS	78_179insGCAA	p.M60fs
XH_P37	1	68947873	68947873	Nonsense_Mutation	INS	-	GTGCTTAATTTT	-	DEPDC1	18insAAAAATTA40	G541delinsKNX
XH_P37	1	70226052	70226052	Nonsense_Mutation	INS	-	TTCTGTGAATAT	-	LRRC7	AGGCATTCTTGT	N56delinsALGRHSCNIX
XH_P37	1	70883662	70883662	Frame_Shift_Ins	INS	-	AAAACTC	-	CTH	93_294insAAAA	p.T98fs
XH_P37	1	70883664	70883664	In_Frame_Ins	INS	-	TTTTCT	-	CTH	295_296insTTTT	p.H99delinsLFY
XH_P37	1	71478166	71478166	In_Frame_Ins	INS	-	TAATGAGATAG	-	PTGER3	99insGCCTATCT	1300delinsSLSHYL
XH_P37	1	71536613	71536613	Nonsense_Mutation	INS	-	AAATTTAATTCAA	-	ZRANB2	sTGATTTTGAATT	p.N194delinsX
XH_P37	1	74670532	74670532	In_Frame_Ins	INS	-	AAA	-	PGFT	c.840_841insAA	p.Y280delinsYK
XH_P37	1	74670533	74670533	Frame_Shift_Ins	INS	-	TTCAATATCA	-	PGFT	c.842insTCTCAAT	p.V281fs
XH_P37	1	76878101	76878101	Frame_Shift_Ins	INS	-	CAACTCGAATCA	-	ST6GALNAC3	28insCAACTCG	p.R143fs
XH_P37	1	77620307	77620307	Splice_Site	INS	-	AGAGGCCAAAAG	-	PIGK	-	-
XH_P37	1	77629619	77629619	Nonsense_Mutation	INS	-	STTTTAAAAAGA	-	PIGK	GTTTTCTTTTAA	N167delinsNSQFFFX
XH_P37	1	78958788	78958788	In_Frame_Ins	INS	-	GCAGGTGTGTGT	-	PTGFR	361insGCAGGT	L120delinsLAGCV
XH_P37	1	85589805	85589805	Silent	SNP	A	T	A	WDR63	c.A1866T	p.S622S
XH_P37	1	86123593	86123593	Nonsense_Mutation	INS	-	TCTAAGAGCGTA	-	ZNHI6	AGATTATACGCT87	Y438delinsKIIRSX
XH_P37	1	86437068	86437068	In_Frame_Ins	INS	-	GTT	-	COL24A1	c.272_273insAA	p.L91delinsLT
XH_P37	1	86437069	86437069	Nonsense_Mutation	INS	-	TATATATTATGA	-	COL24A1	CTCTGTCTAAATA1	G92delinsQDSVX
XH_P37	1	87031076	87031076	Frame_Shift_Ins	INS	-	TATGGTACCATC	-	CLCA4	678insCTATGGT	p.F262fs
XH_P37	1	87031078	87031078	Missense_Mutation	SNP	C	A	C	CLCA4	c.C679A	p.P227T
XH_P37	1	89846188	89846188	In_Frame_Ins	INS	-	ATGTTTGAACTC	-	GBP6	ATTGGATGTTTG	60delinsKIGCLNSGI
XH_P37	1	90178875	90178875	Missense_Mutation	SNP	G	T	G	LRRC8C	c.G746T	p.R249M
XH_P37	1	90178876	90178876	In_Frame_Ins	INS	-	TGTTTCTCT	-	LRRC8C	7_748insTTGTT	R249delinsRLLF
XH_P37	1	90493113	90493113	Frame_Shift_Ins	INS	-	TTTTACTTGC	-	ZNF326	985insTTTTACT	p.N328fs
XH_P37	1	91406594	91406594	Frame_Shift_Ins	INS	-	TTGTTATCAGAT	-	ZNF644	sCTACATCTGAT	p.E106fs
XH_P37	1	91978805	91978805	Nonsense_Mutation	INS	-	TAACATCTGTAA	-	CDC7	4insAGTAACAT	p.S255delinsX
XH_P37	1	92446722	92446722	In_Frame_Ins	INS	-	AACTGTGTTTC	-	BRDT	0insATGAACCTG	533delinsPMNCCFL
XH_P37	1	92642493	92642493	In_Frame_Ins	INS	-	ATATTTTATGTTT	-	KIAA1107	ATATAATATTTTAT	delinsSLTYNLLCFQKP
XH_P37	1	92642755	92642755	Frame_Shift_Ins	INS	-	TATACTATTTCT	-	KIAA1107	TTTATTATTACT	p.A156fs
XH_P37	1	92646066	92646066	Nonsense_Mutation	INS	-	SAGACTGAAGA	-	KIAA1107	nsTGAAGAGACT	429_P430delinsPX
XH_P37	1	92944237	92944237	Frame_Shift_Ins	INS	-	TTATTTCTCTGCT	-	GF1	98insGAGCAGAC	p.I333fs
XH_P37	1	93575967	93575967	Frame_Shift_Ins	INS	-	A	-	MTF2	c.186_187insA	p.Y62fs
XH_P37	1	93575968	93575968	Nonsense_Mutation	INS	-	TATTTATATGTT	-	MTF2	GGGATATTTTAT	63delinsPVGYFICK
XH_P37	1	93736231	93736231	Frame_Shift_Ins	INS	-	AAATTTTGGATC	-	CCDC18	1insGCAAAATT	p.K1404fs
XH_P37	1	94645455	94645455	Frame_Shift_Ins	INS	-	AAAG	-	ARHGAP29	2113_2114insCT	p.E705fs
XH_P37	1	94645456	94645456	Frame_Shift_Ins	INS	-	TAGAACATTTAT	-	ARHGAP29	CCATTATAATAAT	p.E705fs
XH_P37	1	95712410	95712410	Frame_Shift_Ins	INS	-	ATTATACCTTTTG	-	RWDD3	insAAATTTATAC	p.L263fs
XH_P37	1	98039406	98039406	In_Frame_Ins	INS	-	AGTTAAGAAGTA	-	DPYD	TGCTTTTACTCT	17delinsCFYFLTRRG
XH_P37	1	98165039	98165039	Nonsense_Mutation	INS	-	CTCACAGATGG	-	DPYD	48insACCATCTCT	83_E184delinsXHLX
XH_P37	1	100214245	100214245	Frame_Shift_Ins	INS	-	AGTAGTCTGTTG	-	FRRS1	0insTACACAGAC	p.K27fs
XH_P37	1	100480954	100480954	In_Frame_Ins	INS	-	CCAAATAATTTT	-	SLC35A3	insATTCCAATA7	286delinsTFQILH
XH_P37	1	100598841	100598841	Missense_Mutation	SNP	A	T	A	TRMT13	c.A117T	p.R39S
XH_P37	1	100598842	100598842	Nonsense_Mutation	INS	-	AGAAGC	-	TRMT13	18_119insAGAA	p.F40delinsX
XH_P37	1	100949886	100949886	Missense_Mutation	SNP	G	A	G	CDC14A	c.G137A	p.R46Q
XH_P37	1	104118078	104118078	Nonsense_Mutation	INS	-	AAATTCTTTCTC	-	AMY2B	AAGATTAAATT09	V340delinsASEDX
XH_P37	1	104118080	104118080	Frame_Shift_Ins	INS	-	TATTC	-	AMY2B	019_1020insTA	p.V340fs
XH_P37	1	109241942	109241942	Nonsense_Mutation	INS	-	AATAAAACATAT	-	PRPF38B	AATGAATAAAAA	R170delinsENFNEX
XH_P37	1	109268510	109268510	Missense_Mutation	SNP	C	A	C	FNDCT	c.C995A	p.T332K
XH_P37	1	109268512	109268512	Nonsense_Mutation	INS	-	TTTAATGAC	-	FNDCT	7_998insTTTAA	p.S333delinsFX
XH_P37	1	109493048	109493048	Frame_Shift_Ins	INS	-	ATGATTTTAGTTT	-	CLCC1	TAAGAAGCTAAA	p.S4fs
XH_P37	1	110022151	110022151	Nonsense_Mutation	INS	-	AAITTTGTGAGAA	-	SYPL2	D1insGAATTTGT	67_A268delinsGNLX
XH_P37	1	110051264	110051264	Nonsense_Mutation	INS	-	AAACTCTACTT	-	AMIGO1	271insAAGTAG	L91_L92delinsKX
XH_P37	1	112042935	112042935	In_Frame_Ins	INS	-	CATCATCTACTTT	-	ADORA3	CATTAAAGTAG	8delinsLTIKVDVAID
XH_P37	1	112308541	112308541	Nonsense_Mutation	INS	-	STAAGACCCATC	-	DDX20	96insTGTAAGAA	N499delinsMX
XH_P37	1	112318853	112318853	Nonsense_Mutation	INS	-	CTATATACAAT	-	KCND3	ATTACCAAGTTG	86delinsYQKPLSCIX
XH_P37	1	11299050	11299050	Frame_Shift_Ins	INS	-	STTGTCTCCCTTC	-	CTTNBP2NL	TCTCAGTTGTTCT	p.C312fs
XH_P37	1	114165602	114165602	Frame_Shift_Ins	INS	-	CTCTTGTGAAGT	-	MAGI3	47insATCTCTTG	p.G449fs
XH_P37	1	114680299	114680299	Missense_Mutation	SNP	T	A	T	SYT6	c.A634T	p.N212Y
XH_P37	1	114680300	114680300	Frame_Shift_Ins	INS	-	AGCCCTGT	-	SYT6	2_633insACAGC	p.E211fs
XH_P37	1	114968344	114968344	Frame_Shift_Ins	INS	-	TAGAAATATTG	-	TRIM33	2insGCTTACATA	p.G474fs
XH_P37	1	120296007	120296007	Nonsense_Mutation	INS	-	TATTATTAATAG	-	HMGCS2	nsTTTGCTATTAA	H355delinsCYX
XH_P37	1	120387075	120387075	Nonsense_Mutation	INS	-	ACTAAATGCTCT	-	NBPF7	84insAGAGCAT	p.W28delinsX
XH_P37	1	120438805	120438805	Missense_Mutation	SNP	C	A	C	ADAM30	c.G155T	p.R52L
XH_P37	1	120438806	120438806	Frame_Shift_Ins	INS	-	TTTTGAACAT	-	ADAM30	154insATGTTC	p.S52fs
XH_P37	1	120468290	120468290	Nonsense_Mutation	INS	-	ATTATATCAACA	-	NOTCH2	49insGTTGTTG	1383delinsWLLIX
XH_P37	1	144881520	144881520	Missense_Mutation	SNP	G	A	G	PDE4DIP	c.C4165T	p.R1389C

XH_P37	1	144892529	144892529	Frame_Shift_Ins	INS	-	ACCCACCTTGT	-	PDE4DIP	3365insCAAAG	p.E1122fs
XH_P37	1	144911948	144911948	In_Frame_Ins	INS	-	CTGAAGAAC	-	PDE4DIP	2650insGTTCC	P884delinsVLOP
XH_P37	1	144911950	144911950	Missense_Mutation	SNP	A	G	A	PDE4DIP	c.T2648C	p.I883T
XH_P37	1	145608291	145608291	Frame_Shift_Ins	INS	-	TTGTGGATTCTT	-	POLR3C	sCAAGAAGAAATC	p.G149fs
XH_P37	1	145608636	145608636	Frame_Shift_Ins	INS	-	GCAAACCTGACA	-	POLR3C	210insTGTCTAG	p.L70fs
XH_P37	1	145608638	145608638	Missense_Mutation	SNP	G	T	G	POLR3C	c.C208A	p.L70I
XH_P37	1	145650529	145650529	In_Frame_Ins	INS	-	CTATTAAAGGAA	-	RNF115	209insCTATTAA	H70delinsPIKGN
XH_P37	1	147092428	147092428	Nonsense_Mutation	INS	-	CTCTCTGAGGT	-	BC19	2468insTCTCTCT	B823_P824delinsIFX
XH_P37	1	149783767	149783767	Frame_Shift_Ins	INS	-	GAGTGTGCAAG	-	HIST2H2BF	112insCTCTGCA	p.Y138fs
XH_P37	1	150936029	150936029	Frame_Shift_Ins	INS	-	TTTTTTTTC AAG	-	SETDB1	82insGTTTTTTT	p.V1161fs
XH_P37	1	152127601	152127601	In_Frame_Ins	INS	-	TCAGCCCTCAC	-	RPTN	74insTGGTGAGG	658delinsHGEGLS
XH_P37	1	152187559	152187559	In_Frame_Ins	INS	-	CTAGGA	-	HRNR	45_6546insTCC	S2182delinsSPS
XH_P37	1	152191626	152191626	In_Frame_Ins	INS	-	CGAGGA	-	HRNR	78_2479insTCC	G827delinsSSG
XH_P37	1	152192114	152192114	Missense_Mutation	SNP	C	T	C	HRNR	c.G1991A	p.R664Q
XH_P37	1	152192683	152192683	Missense_Mutation	SNP	A	C	A	HRNR	c.T1422G	p.H474Q
XH_P37	1	152193659	152193659	Frame_Shift_Ins	INS	-	CAGTCAGCATGC	-	HRNR	46insTCCATGTCT	p.K149fs
XH_P37	1	152280355	152280355	In_Frame_Ins	INS	-	GGA	-	FLG	7006_7007insT	Q2336delinsLQ
XH_P37	1	152281490	152281490	Missense_Mutation	SNP	C	T	C	FLG	c.G5872A	p.G1958R
XH_P37	1	152281491	152281491	Silent	SNP	A	G	A	FLG	c.T5871C	p.P1957P
XH_P37	1	152327966	152327966	Missense_Mutation	SNP	C	G	C	FLG2	c.G2296C	p.G766R
XH_P37	1	152636719	152636719	In_Frame_Del	DEL	5GTCCACGCT	-	TGGTCCACGCTC	LCE2D	c.138_161del	p.46_54del
XH_P37	1	153641033	153641033	Nonsense_Mutation	INS	-	AGGGTTTAATTG	-	ILF2	29insAACCAATTa	b.C37delinsNNX
XH_P37	1	153945498	153945498	Frame_Shift_Ins	INS	-	ACGCT	-	CREB3L4	687_688insACG	p.Q229fs
XH_P37	1	153945929	153945929	Frame_Shift_Ins	INS	-	ATGTACTC	-	CREB3L4	6_887insATGTA	p.T296fs
XH_P37	1	153974459	153974459	Frame_Shift_Ins	INS	-	TCGGGGAGATA	-	NUP210L	sTACTCTTATCTC	p.V1645fs
XH_P37	1	154145660	154145660	Nonsense_Mutation	INS	-	GGCTTCCTTATTC	-	TPM3	nsGAGAAATAGG	29_N30delinsGEX
XH_P37	1	154569676	154569676	Missense_Mutation	SNP	C	T	C	ADAR	c.G1117A	p.A373T
XH_P37	1	154680718	154680718	Nonsense_Mutation	INS	-	CAGTGTGCTAAAT	-	KCNN3	0insTTTATTATG	p.E644delinsFIX
XH_P37	1	155142305	155142305	Missense_Mutation	SNP	A	T	A	KRTCAP2	c.T330A	p.F110L
XH_P37	1	155142306	155142306	Nonsense_Mutation	INS	-	GTGTCTTCCCT	-	KRTCAP2	329insAGGGAA	A110_A111delinsX
XH_P37	1	155160832	155160832	Frame_Shift_Ins	INS	-	CTGTCCACACCC	-	MUC1	insAAGGGTGTG	p.T232fs
XH_P37	1	155174744	155174744	Frame_Shift_Ins	INS	-	CTCCAATACACC	-	THBS3	8insGGGTGTAT	p.F183fs
XH_P37	1	155207975	155207975	Nonsense_Mutation	INS	-	TTTTTATTTTTCT	-	GBA	AAGAAGAAAAA	D_G151delinsKKEEXX
XH_P37	1	155209781	155209781	Missense_Mutation	SNP	G	A	G	GBA	c.C203T	p.P68L
XH_P37	1	155218094	155218094	In_Frame_Ins	INS	-	TTATTGATGATG	-	FAM189B	1292insCATCAT	G431delinsASSIR
XH_P37	1	155218095	155218095	Splice_Site	INS	-	CCTTTCTTG	-	FAM189B	.	.
XH_P37	1	155447927	155447927	In_Frame_Ins	INS	-	GACACT	-	ASH1L	33_4734insAGT	D1578delinsEVS
XH_P37	1	155450723	155450723	Nonsense_Mutation	INS	-	TTAAAAACGTTT	-	ASH1L	938insGAAACG	6_5647delinsMKRFX
XH_P37	1	155646500	155646500	Nonsense_Mutation	INS	-	TTACACTGGGG	-	YY1AP1	TTAAACCCACG	H44_Q45delinsGX
XH_P37	1	155698914	155698914	Splice_Site	INS	-	AGTTCATT	-	DAP3	.	.
XH_P37	1	155912213	155912213	Frame_Shift_Ins	INS	-	CTGTGAT	-	RXFP4	13_714insCTGT	p.R238fs
XH_P37	1	156235714	156235714	Frame_Shift_Ins	INS	-	AATGACCTCTC	-	SMG5	1575insGAGAG	p.S525fs
XH_P37	1	156263355	156263355	Frame_Shift_Ins	INS	-	GCCCTGGC	-	GLMP	2_553insGCCAG	p.L185fs
XH_P37	1	156268868	156268868	Frame_Shift_Ins	INS	-	TTAA	-	VHLL	112_113insTTA	p.A38fs
XH_P37	1	156445012	156445012	Frame_Shift_Ins	INS	-	TACTTATGGTTA	-	MEF2D	3insGTTAACCAT	p.L291fs
XH_P37	1	156928653	156928653	Frame_Shift_Ins	INS	-	TT	-	ARHGEF11	1262_1263insA	p.T421fs
XH_P37	1	156928654	156928654	Frame_Shift_Ins	INS	-	CCTGA	-	ARHGEF11	261_1262insTCA	p.T421fs
XH_P37	1	157665202	157665202	Nonsense_Mutation	INS	-	TCTTCTAGTGA	-	FCRL3	sTGTAACTCACTA	p.A443delinsVX
XH_P37	1	158390303	158390303	Nonsense_Mutation	INS	-	5ATTGTCACTCTG	-	OR10K2	GCATGAAGATG	G119delinsIQSMKMTIX
XH_P37	1	158390535	158390535	Nonsense_Mutation	INS	-	TGCTCTCACTCC	-	OR10K2	2insAGGAGTGA	A41_N42delinsKEX
XH_P37	1	158607956	158607956	Nonsense_Mutation	INS	-	AGCACTACTTCA	-	SPTA1	sCAACATGAAGG	6_K1687delinsANMKX
XH_P37	1	158653270	158653270	Missense_Mutation	SNP	T	G	T	SPTA1	c.A281C	p.H94P
XH_P37	1	158653272	158653272	Frame_Shift_Ins	INS	-	ATGATGGGATA	-	SPTA1	CGAAGATATCC	p.K93fs
XH_P37	1	158908296	158908296	Silent	SNP	C	A	C	PYHIN1	c.C375A	p.L125L
XH_P37	1	158946506	158946506	Nonsense_Mutation	INS	-	AAAGGGAAACT	-	PYHIN1	5insGCTAAAGGG	D459delinsGX
XH_P37	1	159021716	159021716	Missense_Mutation	SNP	G	A	G	IFI1	c.G1745A	p.R582H
XH_P37	1	159505073	159505073	Nonsense_Mutation	INS	-	CTTAATGGATTG	-	OR10J5	ATAATCCAATCC	S242_H243delinsX
XH_P37	1	160000980	160000980	Frame_Shift_Ins	INS	-	CTTTTCTCCGTA	-	PIGM	5insAGTACGGAG	p.V184fs
XH_P37	1	160268972	160268972	Frame_Shift_Ins	INS	-	TTTTTTTTTTCTT	-	COPA	7insAAAAGAAA	p.E593fs
XH_P37	1	160523764	160523764	Frame_Shift_Ins	INS	-	C	-	CD84	c.218_219insG	p.Q73fs
XH_P37	1	160970882	160970882	Frame_Shift_Ins	INS	-	CACCTGGGACAT	-	F11R	169insATGTCC	p.S57fs
XH_P37	1	161173285	161173285	Missense_Mutation	SNP	A	T	A	NDUFS2	c.A154T	p.M52L
XH_P37	1	161173286	161173286	Nonsense_Mutation	INS	-	TTTTGTTTTTTGT	-	NDUFS2	TTTTGTTTTTTGT	Y53delinsILFCVFCCFX
XH_P37	1	161206305	161206305	Nonsense_Mutation	INS	-	GGCATCTACATG	-	NR13	1insGATGTAGG	A17_A18delinsQMX
XH_P37	1	161967854	161967854	Frame_Shift_Ins	INS	-	TGACATCCGGAA	-	OLFML2B	238insATTCCGG	p.P413fs
XH_P37	1	162487951	162487951	Nonsense_Mutation	INS	-	CAACACATAGTA	-	UHMK1	AAGGCAACACA	V288delinsEGNTX
XH_P37	1	162492339	162492339	Frame_Shift_Ins	INS	-	CCACCTTTAATAT	-	UHMK1	1038insCACCT	X346delinsYHLX
XH_P37	1	163318837	163318837	Nonsense_Mutation	INS	-	AACACAAATCTCA	-	NUF2	sAGGCAACACAC	D410delinsKRQTQFX
XH_P37	1	167358984	167358984	Nonsense_Mutation	INS	-	AAAAACACGTGA	-	POU2F1	GAGGAAAAACAA	G262_G263delinsQX
XH_P37	1	169762110	169762110	Missense_Mutation	SNP	C	A	C	METTL18	c.G727T	p.D243Y
XH_P37	1	169822119	169822119	Frame_Shift_Ins	INS	-	ATATAAAGAAGC	-	C1orf112	9insAAATATAAA	p.T716fs
XH_P37	1	169890891	169890891	Nonsense_Mutation	INS	-	TGGGTCTGTGTT	-	KIFAP3	AAAAACAACACAC	I726delinsKIKTNTDPQX
XH_P37	1	171070276	171070276	Frame_Shift_Ins	INS	-	TCTCATCTCTAA	-	FMO3	ATCTCTCCATCT	p.M1fs
XH_P37	1	171080113	171080113	Frame_Shift_Ins	INS	-	TT	-	FMO3	c.613_614insT	p.N205fs
XH_P37	1	171080114	171080114	Nonsense_Mutation	INS	-	CATTTGTAGTGC	-	FMO3	GTGACCAATTGTG	205_Y206delinsKX
XH_P37	1	171605699	171605699	Frame_Shift_Ins	INS	-	TGACTTGG	-	MYOC	0_881insCCAAG	p.D294fs
XH_P37	1	171605701	171605701	Silent	SNP	C	T	C	MYOC	c.G879A	p.T293T
XH_P37	1	172501694	172501694	In_Frame_Ins	INS	-	TTTTCC	-	SUCO	.82_83insTTTTCC	p.G28delinsVFR
XH_P37	1	172501695	172501695	Frame_Shift_Ins	INS	-	CAATCAGATGAT	-	SUCO	CAACCAATCAG	p.G28fs
XH_P37	1	172558670	172558670	Frame_Shift_Ins	INS	-	ACTGAGAAAGA	-	SUCO	41insGACTCAG	p.D247fs
XH_P37	1	172571847	172571847	Nonsense_Mutation	INS	-	5AATTCCACATT	-	SUCO	TCCTTTGAATTCT	Y500delinsSFFEFHIX
XH_P37	1	172579276	172579276	In_Frame_Ins	INS	-	GAAAG	-	SUCO	53_1954insGAAP	K651delinsKEK
XH_P37	1	172579278	172579278	Frame_Shift_Ins	INS	-	AATGATACTTCC	-	SUCO	insAGTAATGAT	p.L652fs
XH_P37	1	173503730	173503730	Missense_Mutation	SNP	G	A	G	SLC9C2	c.C1867T	p.P623S
XH_P37	1	173503732	173503732	Frame_Shift_Ins	INS	-	TTGAATTTTCCA	-	SLC9C2	AAACTTGGAAA	p.Y622fs
XH_P37	1	173545865	173545865	Nonsense_Mutation	INS	-	CAG	-	SLC9C2	-836_837insCT	p.L279delinsFX
XH_P37	1	173545867	173545867	Frame_Shift_Ins	INS	-	ACCAT	-	SLC9C2	834_835insATG	p.L279fs
XH_P37	1	173840118	173840118	Frame_Shift_Ins	INS	-	CTTAGCTCTCT	-	ZBTB37	756insCTTAGC	p.E252fs
XH_P37	1	175375683	175375683	Frame_Shift_Ins	INS	-	CGAGATGCTG	-	TNR	168insCAGCAT	p.T56fs
XH_P37	1	179077263	179077263	Frame_Shift_Ins	INS	-	TAGC	-	ABL2	075_3076insGC	p.P1026fs
XH_P37	1	179084127	179084127	Nonsense_Mutation	INS	-	TTAAAGAGTTTA	-	ABL2	1384insTAAACT	p.M462delinsX
XH_P37	1	179084129	179084129	Nonsense_Mutation	INS	-	TCAGCCAGCTGT	-	ABL2	sATATGACAACCT	M462delinsDMITGX
XH_P37	1	179414304	179414304	Missense_Mutation	SNP	A	T	A	AXDN1	c.A173T	p.Y588F
XH_P37	1	179414305	179414305	Frame_Shift_Ins	INS	-	ATTTCAGGATCT	-	AXDN1	TTTTCTCATTCA	p.Y588fs
XH_P37	1	180044257	180044257	Frame_Shift_Ins	INS	-	ACTACTCTCTCT	-	CEP350	59insATACTACT	p.R1890fs
XH_P37	1	180471302	180471302	Frame_Shift_Ins	INS	-	ATGCCACATCT	-	ACBD6	5GGAGAAAGATG	p.P34fs
XH_P37	1	183498669	183498669	Splice_Site	INS	-	AGGCACTGGC	-	SMG7	.	.
XH_P37	1	186063458	186063458	Frame_Shift_Ins	INS	-	AAATG	-	HMCN1	247_10248insA	p.S3416fs

XH_P37	1	186063460	186063460	In_Frame_Ins	INS	-	ATTATTCT	-	HMCN1	9_10250insATT	N3417delinsNLFY
XH_P37	1	186123113	186123113	Nonsense_Mutation	INS	-	TAATTTTCTCCC	-	HMCN1	TCATACTAATT	K5085delinsWLILFFPX
XH_P37	1	186275835	186275835	Frame_Shift_Ins	INS	-	TTTATTGTGTG	-	PRG4	insACTTTATTGT	p.L194fs
XH_P37	1	186286733	186286733	Splice_Site	INS	-	AACTGTGTGTG	-	TPR	.	.
XH_P37	1	186302419	186302419	Frame_Shift_Ins	INS	-	TATATATCTTGA	-	TPR	GAATACTCAAG	p.L1764fs
XH_P37	1	186355199	186355199	Nonsense_Mutation	INS	-	TAAACTATCTC	-	C1orf27	ATAAATAAAAC	105delinsHLKTLTX
XH_P37	1	193038362	193038362	Frame_Shift_Ins	INS	-	GAAAA	-	TROVE2	178_179insGAA	p.A60fs
XH_P37	1	193038363	193038363	In_Frame_Ins	INS	-	TTTACTGAAATG	-	TROVE2	GTAGGTTTACTG	delinsAKCRFTEMLTL
XH_P37	1	193150487	193150487	Frame_Shift_Ins	INS	-	GGCTTAAGTATT	-	B3GALT2	206insTAATACT	p.S69fs
XH_P37	1	193150489	193150489	Silent	SNP	C	G	C	B3GALT2	c.G204C	p.R68R
XH_P37	1	196227577	196227577	In_Frame_Ins	INS	-	AAAACTACT	-	KCNT2	5_2886insAGTA	S962delinsSVVF
XH_P37	1	196227578	196227578	Frame_Shift_Ins	INS	-	TGATTTCTTGCC	-	KCNT2	ACTAATGGCAAG	p.S962fs
XH_P37	1	196642293	196642293	Frame_Shift_Ins	INS	-	TTCTTCTGGAG	-	CFH	TGTATTCTTCT	p.K82fs
XH_P37	1	196646746	196646746	Nonsense_Mutation	INS	-	TGGAATTTTAAA	-	CFH	TCTAATGGAATT	H191delinsNTCNVFX
XH_P37	1	197072248	197072248	Nonsense_Mutation	INS	-	TTTAAAAATGCAT	-	ASPM	TACTGATGCAT	A2046delinsFLTDAFX
XH_P37	1	197169310	197169310	Frame_Shift_Ins	INS	-	GGAAGACTATC	-	ZBTB41	TTATTGTAGATG	p.E98fs
XH_P37	1	197407801	197407801	Nonsense_Mutation	INS	-	AGCTACAAATGC	-	CRB1	39insGAGCTAC	1180delinsGATNAX
XH_P37	1	197627500	197627500	Splice_Site	INS	-	CATTGTATCATCT	-	DENND1B	.	.
XH_P37	1	198668822	198668822	Nonsense_Mutation	INS	-	ATTGCGATTATA	-	PTPRC	29insATTGCGA	43_A134delinsKRLRX
XH_P37	1	198725307	198725307	Nonsense_Mutation	INS	-	TTTCTTGATGGTT	-	PTPRC	TTTATCTTCTTG	85_X1146delinsSILSSX
XH_P37	1	200376643	200376643	Frame_Shift_Ins	INS	-	ATCACTAACTCT	-	ZNF281	sCCATTAGAGATT	p.S731fs
XH_P37	1	200534609	200534609	Nonsense_Mutation	INS	-	ATTCAGTCACTT	-	KIF14	377insTAAGTGA	793_H794delinsX
XH_P37	1	200539051	200539051	Nonsense_Mutation	INS	-	ATTTCAAAGCCT	-	KIF14	insAAAAAGCCT	S726delinsKRLX
XH_P37	1	200817364	200817364	Frame_Shift_Ins	INS	-	TTTGAATTTACA	-	CAMSAP2	DinsTTATTTGAA	p.E473fs
XH_P37	1	201038658	201038658	Frame_Shift_Ins	INS	-	TACTGTG	-	CACNA1S	81_2432insAAC	p.L811fs
XH_P37	1	201176107	201176107	Frame_Shift_Ins	INS	-	AA	-	IGFN1	2086_2087insA	p.G696fs
XH_P37	1	201176109	201176109	Frame_Shift_Ins	INS	-	CTCTA	-	IGFN1	088_2089insCT	p.G696fs
XH_P37	1	201195059	201195059	Missense_Mutation	SNP	T	G	T	IGFN1	c.T10594G	p.Y3532D
XH_P37	1	202397994	202397994	In_Frame_Ins	INS	-	CCITTTAAATATA	-	PPP1R12B	nsAATCCTTTAA	286delinsPNPLNIE
XH_P37	1	202702982	202702982	Frame_Shift_Ins	INS	-	AGAGAAAA	-	KDM5B	20_3321insTTTT	p.E1107fs
XH_P37	1	202702983	202702983	Frame_Shift_Ins	INS	-	TCTG	-	KDM5B	319_3320insCA	p.E1107fs
XH_P37	1	203036913	203036913	Frame_Shift_Ins	INS	-	ACTCCCTTCTCT	-	PPFIA4	insGTTACTCCC	p.E1038fs
XH_P37	1	203036915	203036915	Missense_Mutation	SNP	T	A	T	PPFIA4	c.T3116A	p.L1039N
XH_P37	1	204091066	204091066	Frame_Shift_Ins	INS	-	A	-	SOX13	c.814_815insA	p.P272fs
XH_P37	1	204091067	204091067	Frame_Shift_Ins	INS	-	TCTAAAT	-	SOX13	15_816insTCTA	p.P272fs
XH_P37	1	204192711	204192711	Nonsense_Mutation	INS	-	AGCCATCTATGC	-	PLEKHA6	3034insGCATAG	Q1012delinsAX
XH_P37	1	205589694	205589694	Frame_Shift_Ins	INS	-	GGAG	-	ELK4	479_480insCTC	p.V160fs
XH_P37	1	207196539	207196539	Frame_Shift_Ins	INS	-	AAACA	-	C1orf116	569_570insGTG	p.A190fs
XH_P37	1	207196540	207196540	Nonsense_Mutation	INS	-	TCTCAAC	-	C1orf116	58_569insGTGGA	190_L191delinsGX
XH_P37	1	212560386	212560386	In_Frame_Ins	INS	-	GTATTTGTGGTA	-	TMEM206	190insTACCACA	N64delinsYHKYN
XH_P37	1	214543029	214543029	Nonsense_Mutation	INS	-	TTTTATGTAAGT	-	PTPN14	sAAAAACACTTA	4_G1015delinsGKTLTX
XH_P37	1	214788329	214788329	Nonsense_Mutation	INS	-	GATACAGCTCG	-	CENPF	nsCTGAGATACA	106_G107delinsSX
XH_P37	1	214815121	214815121	In_Frame_Ins	INS	-	GGGTGTCCTTTG	-	CENPF	AATTCTTGGTGT	7delinsKNSWCFSANA
XH_P37	1	214820283	214820283	In_Frame_Ins	INS	-	ATTTTTCCTTTT	-	CENPF	1insTCTATTTT	2457delinsLFLLLG
XH_P37	1	214820672	214820672	Nonsense_Mutation	INS	-	CACCTCTCATGT	-	CENPF	7760insCACTCT	87_S2588delinsPLSHX
XH_P37	1	214830554	214830554	Nonsense_Mutation	INS	-	AAG	-	CENPF	8764_8765insAp	S2922delinsX
XH_P37	1	214830556	214830556	Frame_Shift_Ins	INS	-	AGGAACAG	-	CENPF	6_8767insAGGA	p.S2922fs
XH_P37	1	215793626	215793626	Nonsense_Mutation	INS	-	CTGCTTCATGG	-	KCTD3	insGTAGCTGCT	703_1704delinsKX
XH_P37	1	215848937	215848937	Frame_Shift_Ins	INS	-	AAAAATAATTCG	-	USH2A	sTTCATAGCGAA	p.G4106fs
XH_P37	1	215953192	215953192	In_Frame_Ins	INS	-	ATCAACAACACACA	-	USH2A	sCAGGGGTGTG	644delinsTRGVCLIVE
XH_P37	1	215953194	215953194	Missense_Mutation	SNP	T	G	T	USH2A	c.A10930C	p.T3644P
XH_P37	1	216166380	216166380	Missense_Mutation	SNP	C	T	C	USH2A	c.G6787A	p.E2263K
XH_P37	1	216172382	216172382	In_Frame_Ins	INS	-	CTCCCC	-	USH2A	03_6504insGGG	K2168delinsKGR
XH_P37	1	220152861	220152861	Nonsense_Mutation	INS	-	CTGTGTGTATTA	-	EPRS	8insAAATAAATAC	Q1270delinsKX
XH_P37	1	220363108	220363108	In_Frame_Ins	INS	-	TGAGAGGCTTA	-	RAB3GAP2	716insCTTCAGCG	0572delinsDFSLSC
XH_P37	1	220363110	220363110	Splice_Site	INS	-	TCITTTCACTTT	-	RAB3GAP2	.	.
XH_P37	1	220835431	220835431	Frame_Shift_Ins	INS	-	CCCT	-	MARK1	2200_2201insCC	p.R734fs
XH_P37	1	220835432	220835432	Frame_Shift_Ins	INS	-	ATGTA	-	MARK1	201_2202insATG	p.R734fs
XH_P37	1	222802636	222802636	Nonsense_Mutation	INS	-	AGAACTAAATCC	-	MIA3	075insAAGAACT	p.F692delinsX
XH_P37	1	225555701	225555701	In_Frame_Ins	INS	-	TAATATTTTTCA	-	DNAH14	2007insGTAAC	T4002delinsNVTIFK
XH_P37	1	225607437	225607437	Nonsense_Mutation	INS	-	TTAATGCAGTAG	-	LBR	TAATGCTACTCG	144_P145delinsHX
XH_P37	1	228475843	228475843	Frame_Shift_Ins	INS	-	A	-	OBSCN	c.9893_9894ins	p.S3298fs
XH_P37	1	228475845	228475845	In_Frame_Ins	INS	-	CTTACC	-	OBSCN	895_9896insCTT	K3299delinsTYQ
XH_P37	1	228646198	228646198	Nonsense_Mutation	INS	-	GTAGATAGAA	-	HIST3H2BB	369insGTAGAT	123_S124delinsTX
XH_P37	1	228646199	228646199	Silent	SNP	C	T	C	HIST3H2BB	c.C369T	p.T123T
XH_P37	1	231401514	231401514	In_Frame_Ins	INS	-	TGAACAACAC	-	GNPAT	sCTTCTCGAACAA	90delinsKLPEQTQL
XH_P37	1	231678354	231678354	Frame_Shift_Ins	INS	-	CT	-	TSNAX	c.364_365insCT	p.T122fs
XH_P37	1	231678356	231678356	Frame_Shift_Ins	INS	-	ACTATTCTATGT	-	TSNAX	7insAAACTATT	p.T122fs
XH_P37	1	232942566	232942566	In_Frame_Ins	INS	-	TGCTGTGCTAGCA	-	MAP10	1798insTCGTGT	C599delinsSCSAA
XH_P37	1	234596085	234596085	Frame_Shift_Ins	INS	-	TAATATTGGGA	-	TARBP1	ATCCCAATCCCA	p.P486fs
XH_P37	1	235973306	235973306	Missense_Mutation	SNP	A	T	A	LYST	c.T812A	p.F271Y
XH_P37	1	235973307	235973307	Frame_Shift_Ins	INS	-	GAGCCCTT	-	LYST	0_811insAAGG	p.F271fs
XH_P37	1	236205459	236205459	Frame_Shift_Ins	INS	-	GATGTGGATTG	-	NID1	886insCATCCA	p.Y296fs
XH_P37	1	236990174	236990174	Nonsense_Mutation	INS	-	TTATACCAITTA	-	MTR	ATCCTTTATACC	5_S326delinsELYTIX
XH_P37	1	237791334	237791334	Frame_Shift_Ins	INS	-	AAAGTCAITATG	-	RYR2	sGCTGCAAAAGTC	p.V2132fs
XH_P37	1	237947363	237947363	Frame_Shift_Ins	INS	-	CGTGTAGTGCTT	-	RYR2	2352insGCGTGT	p.T4117fs
XH_P37	1	241767869	241767869	Frame_Shift_Ins	INS	-	CCTTTGTGCTTT	-	OPN3	TAAGAAAAGCA	p.L129fs
XH_P37	1	242253238	242253238	Missense_Mutation	SNP	C	G	C	PLD5	c.G905C	p.C302S
XH_P37	1	242253240	242253240	Frame_Shift_Ins	INS	-	AACACTTTAAAT	-	PLD5	GAGACATATTA	p.N301fs
XH_P37	1	243388519	243388519	Frame_Shift_Ins	INS	-	AAGTCTAAAGTC	-	CEP170	TCAAGACTTAGA	p.M22fs
XH_P37	1	244724247	244724247	Frame_Shift_Ins	INS	-	AGAATGGATCAT	-	CATSPERE	sAAGAAGAAGTG	p.F285fs
XH_P37	1	246755170	246755170	Frame_Shift_Ins	INS	-	CTATTTGCGATT	-	CNST	TGGTTCTATTGT	p.L1102fs
XH_P37	1	247013112	247013112	Nonsense_Mutation	INS	-	TGGTTATTGTCT	-	AHCTF1	TTTTAGGACAA	66_E2067delinsNHFX
XH_P37	1	247695765	247695772	Frame_Shift_Del	DEL	CCAGGAGG	-	CCAGGAGG	OR2C3	c.42_49del	p.V14fs
XH_P37	1	247751935	247751935	Frame_Shift_Ins	INS	-	TGCCGATGATT	-	OR2G2	TCATATGCCGAT	p.M92fs
XH_P37	1	248020603	248020603	Missense_Mutation	SNP	T	C	T	TRIM58	c.T55C	p.C19R
XH_P37	1	248185868	248185868	Missense_Mutation	SNP	G	T	G	OR2L5	c.G619T	p.V207L
XH_P37	1	248185870	248185870	In_Frame_Ins	INS	-	CATACGGATGG	-	OR2L5	2insCTCATACGG	207delinsVLIRMG
XH_P37	1	248458482	248458482	In_Frame_Ins	INS	-	CGCTCT	-	OR2T12	98_399insAGAG	p.L133delinsLER
XH_P37	1	248487387	248487387	Frame_Shift_Ins	INS	-	AAAGCTTT	-	OR2M7	3_484insAAAG	p.A162fs
XH_P37	1	248487389	248487389	Frame_Shift_Ins	INS	-	CTACTGTGTC	-	OR2M7	482insGAACAA	p.V161fs
XH_P37	1	248652023	248652023	Frame_Shift_Ins	INS	-	GATTTGAGATAT	-	OR2T5	35insGGAATTTG	p.G45fs
XH_P37	1	248790372	248790372	Missense_Mutation	SNP	C	A	C	OR2T11	c.G58T	p.A20S
XH_P37	1	248790373	248790373	Frame_Shift_Ins	INS	-	ATGGT	-	OR2T11	c.56_57insACCA	p.E19fs
XH_P37	1	248844806	248844806	In_Frame_Ins	INS	-	AAAAAAAACCTG	-	OR141	800insCAGGTT	I267delinsTGFFF
XH_P37	1	248845216	248845216	Nonsense_Mutation	INS	-	TTATTCTCATGA	-	OR141	GATCATCATGA	p.Y130delinsX
XH_P37	2	1653285	1653285	Frame_Shift_Ins	INS	-	CTGCTTCTCTG	-	PXDN	2267insCAGAG	p.W756fs
XH_P37	2	1653286	1653286	Missense_Mutation	SNP	A	T	A	PXDN	c.T2266A	p.W756R

XH_P37	2	1926932	1926932	Nonsense_Mutation	INS	-	ATTATGCAGACA	-	MYT1L	sCATGCTGCTCTG	203delinsNMLSAX
XH_P37	2	3653819	3653819	Nonsense_Mutation	INS	-	ATAATTAACAA	-	COLEC11	rsAACATAATTA	p.P13delinsPTX
XH_P37	2	7030374	7030374	In_Frame_Ins	INS	-	ACTTTCAAAAAC	-	RSAD2	TATAAACTTTCA	delinsLLKYKSLCTLDY
XH_P37	2	9595879	9595879	Frame_Shift_Ins	INS	-	GCACC	-	CP5F3	c.485_1486insGC	p.K495fs
XH_P37	2	9770460	9770460	Missense_Mutation	SNP	C	T	C	YWHAQ	c.G122A	p.R41H
XH_P37	2	11341261	11341261	Nonsense_Mutation	INS	-	TTTGATCTCCAG	-	ROCK2	AAGAGCTGGAG	825_826delinsX
XH_P37	2	11341263	11341263	Silent	SNP	A	T	A	ROCK2	c.T2472A	p.S824S
XH_P37	2	11341436	11341436	Missense_Mutation	SNP	C	G	C	ROCK2	c.G2465C	p.R822P
XH_P37	2	11341437	11341437	Frame_Shift_Ins	INS	-	AAGATGCTACAA	-	ROCK2	insGCAATTGTA	p.R822fs
XH_P37	2	11761106	11761106	In_Frame_Ins	INS	-	CAAAGA	-	GREB1	20_4121insCAA	V1374delinsAKI
XH_P37	2	11780490	11780490	Silent	SNP	C	T	C	GREB1	c.C5760T	p.D1920D
XH_P37	2	15417060	15417060	Nonsense_Mutation	INS	-	CTAATCGACTTT	-	NBAS	ATAACATAAAGTC	C1769delinsKIITKVDX
XH_P37	2	15427299	15427299	Nonsense_Mutation	INS	-	TATA	-	NBAS	c.5035_5036insTA	679_E1680delinsVX
XH_P37	2	15427300	15427300	Nonsense_Mutation	INS	-	ACACCTTTACCA	-	NBAS	AATGAATGGTA	A79_E1680delinsHQX
XH_P37	2	15760478	15760478	Nonsense_Mutation	INS	-	SAACTTTTATAA	-	DDX1	GAGATGAACCT	K451delinsKLRX
XH_P37	2	17890014	17890014	Frame_Shift_Ins	INS	-	GAAGAACTGGTTG	-	SMC6	insAAATCAACC	p.A579fs
XH_P37	2	21250721	21250721	In_Frame_Ins	INS	-	TGACTTCTTAAC	-	APOB	2046insGTTAAG	F682delinsLRSX
XH_P37	2	21255429	21255429	Silent	SNP	A	T	A	APOB	c.T1149A	p.V383V
XH_P37	2	21255430	21255430	Frame_Shift_Ins	INS	-	TTTCT	-	APOB	147_1148insAG	p.V383fs
XH_P37	2	21361270	21361270	Nonsense_Mutation	INS	-	CATTTCACAA	-	TDRD15	insTAACATTTC	Q311delinsLTPQX
XH_P37	2	24261327	24261327	In_Frame_Ins	INS	-	AAA	-	WDCP	1037_1038insT	p.A346delinsAL
XH_P37	2	24261328	24261328	Frame_Shift_Ins	INS	-	AAAAAAGTTAA	-	WDCP	ACTTTCAATTAA	p.A346fs
XH_P37	2	25469121	25469121	Frame_Shift_Ins	INS	-	AA	-	DNMT3A	c.880_881insTT	p.A294fs
XH_P37	2	25469122	25469122	Missense_Mutation	SNP	C	G	C	DNMT3A	c.G880C	p.A294P
XH_P37	2	26676298	26676298	In_Frame_Ins	INS	-	GAAAAGTTTACA	-	DRC1	AAACCAGAAAAG	delinsEKEPKFTESD
XH_P37	2	27606331	27606331	Nonsense_Mutation	INS	-	ATTCTGTGAAA	-	PPM1G	AGTTATTTCAC	E369delinsLSVFTGIX
XH_P37	2	27668197	27668197	Missense_Mutation	SNP	G	T	G	IFT172	c.C5034A	p.S1678R
XH_P37	2	27668198	27668198	Nonsense_Mutation	INS	-	ATCATTITT	-	IFT172	2_5033insAAAA	S1678delinsKKX
XH_P37	2	27801022	27801022	In_Frame_Ins	INS	-	TGTTAGCCCCA	-	C2orf16	584insTTGTTAA	G528delinsTLLAPL
XH_P37	2	27801632	27801632	Missense_Mutation	SNP	C	G	C	C2orf16	c.C2193G	p.F731L
XH_P37	2	27878435	27878435	Frame_Shift_Ins	INS	-	TT	-	SUPT7L	c.373_374insAA	p.I125fs
XH_P37	2	27878437	27878437	Frame_Shift_Ins	INS	-	AGTACTTTTGT	-	SUPT7L	372insCAAAAA	p.R124fs
XH_P37	2	27884020	27884020	Nonsense_Mutation	INS	-	AATTTTTTTGAG	-	SUPT7L	AAGCACTCAAA	84delinsSKHKNX
XH_P37	2	29039033	29039033	Frame_Shift_Ins	INS	-	TC	-	SPDYA	c.153_154insTC	p.H51fs
XH_P37	2	29039034	29039034	Frame_Shift_Ins	INS	-	TTTCATAT	-	SPDYA	54_155insTTTCA	p.N52fs
XH_P37	2	30748605	30748605	Nonsense_Mutation	INS	-	ATATAAAAAAG	-	LCLAT1	GAAAGATATAA	W50_L51delinsX
XH_P37	2	37121145	37121145	Missense_Mutation	SNP	C	T	C	STRN	c.G827A	p.G276D
XH_P37	2	37255237	37255237	Nonsense_Mutation	INS	-	AATCAGTACTTT	-	HEATR5B	sGGGAAAAAGT	A8_T1229delinsGKKYX
XH_P37	2	37455137	37455137	Frame_Shift_Ins	INS	-	CTTTTTTGGAC	-	CEBP2	199insAGTCCG	p.T400fs
XH_P37	2	37518081	37518081	Frame_Shift_Ins	INS	-	G	-	PRKD3	c.488_489insC	p.K163fs
XH_P37	2	37518082	37518082	In_Frame_Ins	INS	-	TGACTAGGG	-	PRKD3	7_488insCCCTAG	K163delinsTLVK
XH_P37	2	37543600	37543600	In_Frame_Ins	INS	-	CTGTCTTTATCT	-	PRKD3	58insAGATAAAG	L23delinsQIKTV
XH_P37	2	39213128	39213128	Frame_Shift_Ins	INS	-	AGTTCTCTGTGA	-	SOS1	nsCCAGTACAGA	p.Q1280fs
XH_P37	2	45645665	45645665	In_Frame_Ins	INS	-	ATACAACAGTGA	-	SRBD1	2insTGCTCACTG	724delinsLAHCCIP
XH_P37	2	47184037	47184037	In_Frame_Ins	INS	-	AAATTCCTCAT	-	TTC7A	insATAAAATTCT	S136delinsSIKFSYE
XH_P37	2	48033493	48033493	Frame_Shift_Ins	INS	-	AAAGCAACATCC	-	MSH6	8insGAAAAAGCA	p.H1136fs
XH_P37	2	48848396	48848396	Missense_Mutation	SNP	C	A	C	GTF2A1L	c.C112A	p.H38N
XH_P37	2	48915547	48915547	Frame_Shift_Ins	INS	-	ATTTGTGCTTGC	-	LHCGR	nsTGTAGCAAGG	p.E463fs
XH_P37	2	54001615	54001615	Nonsense_Mutation	INS	-	TTGTGTTCTGTG	-	CHAC2	sGACTGTTGTGG	p.L170delinsX
XH_P37	2	54080474	54080474	Missense_Mutation	SNP	G	A	G	GRP75	c.C1420T	p.P474S
XH_P37	2	54080476	54080476	Nonsense_Mutation	INS	-	GATCTTATGTAA	-	GRP75	AACTGTTTACAT	T473delinsKLFTX
XH_P37	2	54080632	54080632	In_Frame_Ins	INS	-	CCTTACTACAGG	-	GRP75	2insGATGCTGTA	A421delinsRCCSVQP
XH_P37	2	54859817	54859817	In_Frame_Ins	INS	-	AGGATCTCATTT	-	SPTBN1	541insAAGGATC	G1214delinsEGSHVF
XH_P37	2	55253970	55253970	Nonsense_Mutation	INS	-	TTTGTAGGAGA	-	RTN4	insGGATCTCTTA	G16_K217delinsRISX
XH_P37	2	55523564	55523564	Frame_Shift_Ins	INS	-	TCAGA	-	CCDC88A	836_4837insTC	p.S1613fs
XH_P37	2	55523566	55523566	Frame_Shift_Ins	INS	-	TTTTTTTTTTT	-	CCDC88A	4835insAAAAA	p.S1612fs
XH_P37	2	55615993	55615993	Frame_Shift_Ins	INS	-	GAATG	-	CCDC88A	193_194insCAT	p.N65fs
XH_P37	2	55615995	55615995	Frame_Shift_Ins	INS	-	TATTTAATAATT	-	CCDC88A	TTAGAAAAATTAT	p.V64fs
XH_P37	2	55785925	55785925	Nonsense_Mutation	INS	-	TAGAAATTTTAT	-	PPP4R3B	AAATAAAATAA	A29_T730delinsNKIKX
XH_P37	2	58373584	58373584	Nonsense_Mutation	INS	-	ATAATATAATA	-	VRK2	AAGTAATAATA	A68_L26delinsGIEIX
XH_P37	2	58386822	58386822	In_Frame_Ins	INS	-	GGGAAACGTGT	-	VRK2	68insGTGGGAA	389delinsFVGNCL
XH_P37	2	61546454	61546454	Frame_Shift_Ins	INS	-	GTTGTTTACACT	-	USP34	nsAAACAGTGA	p.L1008fs
XH_P37	2	61575319	61575319	Nonsense_Mutation	INS	-	GGGAATGAATT	-	USP34	sTTAAATAATTC	A657_S658delinsDX
XH_P37	2	62066865	62066865	Frame_Shift_Ins	INS	-	AAGATGTGCAG	-	FAM161A	74insCACCTGCA	p.R425fs
XH_P37	2	62450075	62450075	Frame_Shift_Ins	INS	-	G	-	B3GNT2	c.721dupG	p.F240fs
XH_P37	2	62450077	62450077	In_Frame_Ins	INS	-	TCCCTGCGTTGC	-	B3GNT2	723insTCCCTGCG	U241delinsVPCVA
XH_P37	2	64323729	64323729	Nonsense_Mutation	INS	-	TACTAGCTTTCA	-	PEL1	TTGGAATGAAAGG	T7_S108delinsWNESX
XH_P37	2	67631307	67631307	Nonsense_Mutation	INS	-	CTTGACGTATT	-	ETAA1	nsTTGCTCTTGAC	A98_V499delinsCSX
XH_P37	2	67631641	67631641	Nonsense_Mutation	INS	-	XCAGCTGTTTTAT	-	ETAA1	TACTACAACGTG	09_L610delinsLGYX
XH_P37	2	68692191	68692191	Frame_Shift_Ins	INS	-	GAAATGAGTTA	-	FBXO48	nsCTTTAACTCA	p.E29fs
XH_P37	2	68692193	68692193	Missense_Mutation	SNP	C	T	C	FBXO48	c.G85A	p.E29K
XH_P37	2	69741837	69741837	In_Frame_Ins	INS	-	CAGCGG	-	AAK1	41_1542insCCG	Q514delinsHRW
XH_P37	2	69741838	69741838	Frame_Shift_Ins	INS	-	AA	-	AAK1	1540_1541insT	p.Q514fs
XH_P37	2	70052627	70052627	Nonsense_Mutation	INS	-	ATATAGCCTAT	-	ANXA4	TAACAAATATAG	A16_C317delinsHLTX
XH_P37	2	70070394	70070394	Splice_Site	INS	-	AAAAAGAAAGAA	-	GMCL1	.	.
XH_P37	2	70106073	70106073	Frame_Shift_Ins	INS	-	C	-	GMCL1	c.1486dupC	p.L495fs
XH_P37	2	70106075	70106075	Frame_Shift_Ins	INS	-	ACTGTAAGATGG	-	GMCL1	488insCACTGTA	p.L496fs
XH_P37	2	70408629	70408629	In_Frame_Ins	INS	-	CGGTAGGTGGT	-	C2orf42	39insATACCACC	P163delinsPYHLPL
XH_P37	2	71351640	71351640	Frame_Shift_Ins	INS	-	TGGAGATCTCTG	-	MCEE	AAACAACAGATA	p.T25fs
XH_P37	2	71592759	71592759	Frame_Shift_Ins	INS	-	CT	-	ZN6F38	1918_1919insC	p.K640fs
XH_P37	2	71592760	71592760	Nonsense_Mutation	INS	-	TCTAATGCTTTT	-	ZN6F38	nsCATCTTCTAAT	A40_S641delinsNIFX
XH_P37	2	71645759	71645759	Nonsense_Mutation	INS	-	ACACACAATAAC	-	ZN6F38	insGTCAACACAG	7_K1098delinsGHTQX
XH_P37	2	71650361	71650361	Frame_Shift_Ins	INS	-	TCTCTTTTGAC	-	ZN6F38	3718insTCTTC	p.I1239fs
XH_P37	2	72692440	72692440	Frame_Shift_Ins	INS	-	TTTCTTTATAATT	-	EXOC68	sAACTAAATTAAT	p.I565fs
XH_P37	2	73437917	73437917	Frame_Shift_Ins	INS	-	ATTCAATCATCT	-	NOTO	sACCACTTCAAT	p.N206fs
XH_P37	2	73679956	73679956	Frame_Shift_Ins	INS	-	GGGCTTCTCTAT	-	ALMS1	00insTTGGGCT	p.S2100fs
XH_P37	2	73989984	73989984	Nonsense_Mutation	INS	-	TGACTTTTAATT	-	DUSP11	GAACTAATTAAT	p.K313delinsTX
XH_P37	2	74043031	74043031	Nonsense_Mutation	INS	-	TGATTTTACCTTG	-	C2orf78	82insCCTGATT	T561_1562delinsTX
XH_P37	2	74044025	74044025	Frame_Shift_Ins	INS	-	ACAAGATGATG	-	C2orf78	76insGAACAAGA	p.N892fs
XH_P37	2	80101217	80101217	Frame_Shift_Ins	INS	-	CCTCTTCA	-	CTNNA2	11_602insCCTCT	p.H201fs
XH_P37	2	80101219	80101219	Frame_Shift_Ins	INS	-	CTCT	-	CTNNA2	603_604insCTC	p.H201fs
XH_P37	2	84838942	84838942	Frame_Shift_Ins	INS	-	CTTTTCTTGTGA	-	DNAH6	CTGATCTTTTTT	p.R1147fs
XH_P37	2	84940357	84940357	Nonsense_Mutation	INS	-	TTAAAGTGATA	-	DNAH6	AAGCAATTAATA	P3174delinsKQLKWIAIX
XH_P37	2	85768421	85768421	Frame_Shift_Ins	INS	-	TCAGTTTCTTTA	-	MAT2A	CTGGCTCAGTTT	p.I71fs
XH_P37	2	86371519	86371519	Nonsense_Mutation	INS	-	SCAGGTTTACAA	-	IMMT	sCAGTACTTGTAT	A16_R1717delinsQYLYX
XH_P37	2	96259924	96259924	Missense_Mutation	SNP	C	G	C	TRIM43	c.C153G	p.N51K
XH_P37	2	96259925	96259925	In_Frame_Ins	INS	-	TTGAATCAGATC	-	TRIM43	155insTTGAATC	C52delinsFESDR
XH_P37	2	96521901	96521901	In_Frame_Ins	INS	-	AAACGATAGCCT	-	ANKRD36C	5206insAGGCTA	L1736delinsRLSLF

XH_P37	2	96952204	96952204	Frame_Shift_Ins	INS	-	ATGTGCTCTGT	-	SNRNP200	3848insACAGA	p.P1283fs
XH_P37	2	96993664	96993664	In_Frame_Ins	INS	-	TGAAGCTGGTG	-	ITPRIPL1	TGTTCTCTGAAGC	40delinsHLFLKLVGRF
XH_P37	2	96993852	96993852	Frame_Shift_Ins	INS	-	TTAAAAACAGCTC	-	ITPRIPL1	ACCATTTTAAAA	p.1503fs
XH_P37	2	97637754	97637754	Missense_Mutation	SNP	G	C	G	FAM178B	c.C448G	p.L150V
XH_P37	2	97637755	97637755	Silent	SNP	C	T	C	FAM178B	c.G447A	p.E149E
XH_P37	2	97847519	97847519	Frame_Shift_Ins	INS	-	ATCACTCACATG	-	ANKRD36	7insTAATCACTC	p.Q609fs
XH_P37	2	98173423	98173423	Missense_Mutation	SNP	A	G	A	ANKRD36B	c.T1046C	p.M349T
XH_P37	2	98377355	98377355	Frame_Shift_Ins	INS	-	TTGAAGCTCCAT	-	TMEM131	12insCAATGGAC	p.N1638fs
XH_P37	2	98428976	98428976	Nonsense_Mutation	INS	-	TTTAAATTATCTTT	-	TMEM131	TACAAAAAGAT	E592delinsVLQKDNX
XH_P37	2	98866899	98866899	Nonsense_Mutation	INS	-	TACATAGTTGTA	-	VWA3B	TACATCTACATAC	K588delinsNTSTX
XH_P37	2	99013119	99013134	Frame_Shift_Del	DEL	AAGCTGCGCA	-	GAAGCTGCGACC	CNGA3	c.1432_1447del	p.L478fs
XH_P37	2	100019486	100019486	Nonsense_Mutation	SNP	T	A	T	REV1	c.A3247T	p.K1083X
XH_P37	2	100019488	100019488	Nonsense_Mutation	INS	-	AATATACCTGG	-	REV1	ACATTATCCAGG	2_K1083delinsHIIQVYX
XH_P37	2	100910699	100910699	Nonsense_Mutation	INS	-	TTTCTTTATCCC	-	LONRF2	insATGGGGAT	E583delinsEWGX
XH_P37	2	102460702	102460702	Nonsense_Mutation	INS	-	ATATCTTCTTTA	-	MAP4K4	AGTCCCATATCT	3delinsYNSIVPYLLLIX
XH_P37	2	103068372	103068372	Nonsense_Mutation	INS	-	TTTGCAATGGA	-	IL18RAP	nsGATTATTTTGCA	p.L511delinsX
XH_P37	2	108487451	108487451	Frame_Shift_Ins	INS	-	CTTTCCTTTTCTT	-	RGPD4	2992insCTTTCC	p.5997fs
XH_P37	2	108487453	108487453	Missense_Mutation	SNP	G	A	G	RGPD4	c.G2993A	p.G998D
XH_P37	2	108487693	108487693	In_Frame_Ins	INS	-	TTTGCTTTATTG	-	RGPD4	4insGTGTTTGCT	078delinsKCLLYVWP
XH_P37	2	108626789	108626789	Nonsense_Mutation	INS	-	AAAGAATGAGA	-	SLCSA7	TAGGCCAAAGAA	p.L300delinsLIX
XH_P37	2	109116167	109116167	Frame_Shift_Ins	INS	-	AACCTCATGATT	-	GCC2	nsACTGAACAT	p.Q1647fs
XH_P37	2	109347339	109347339	In_Frame_Ins	INS	-	CCAAATTTTCTC	-	RANBP2	sTTTACCAATT	84delinsYQIFLQW
XH_P37	2	109380677	109380677	Nonsense_Mutation	INS	-	ATGATTCTGT	-	RANBP2	insTCTCATGATT	228_K1229delinsVSX
XH_P37	2	109382444	109382444	Nonsense_Mutation	INS	-	TTTGATTTTGT	-	RANBP2	50insTAGTTTGA	817_P1818delinsVXX
XH_P37	2	109382958	109382958	In_Frame_Ins	INS	-	TGAATCCTTGCT	-	RANBP2	4insATTGTAATC	1988delinsKFESLLC
XH_P37	2	112767580	112767580	Frame_Shift_Ins	INS	-	CTTTCAGA	-	MERTK	6_2017insCTTT	p.P672fs
XH_P37	2	113174876	113174876	Frame_Shift_Ins	INS	-	CATTATTCTAT	-	RGPD5	sCATTATAGAA	p.S226fs
XH_P37	2	113260636	113260636	In_Frame_Ins	INS	-	TGCATATTATAT	-	TTL	sTTTCTGCATAT	251delinsKFLHIYI
XH_P37	2	113332919	113332919	Frame_Shift_Ins	INS	-	TTAACATCCCAA	-	POLR1B	389insATTAAAC	p.5796fs
XH_P37	2	114202593	114202593	Missense_Mutation	SNP	G	A	G	CBWD2	c.G391A	p.D131N
XH_P37	2	114202594	114202594	Frame_Shift_Ins	INS	-	CTCACTTCTAAC	-	CBWD2	393insCTCACTT	p.D131fs
XH_P37	2	118854223	118854223	Frame_Shift_Ins	INS	-	CGGTACACACAT	-	INSIG2	insAACGGTACCA	p.R31fs
XH_P37	2	120414028	120414028	Frame_Shift_Ins	INS	-	TTAGTGATAGT	-	CFAP221	506insGTTAGT	p.T835fs
XH_P37	2	120620219	120620219	In_Frame_Ins	INS	-	TTTATGCCAGAG	-	PTPN4	247insTTTATGCG	P82delinsPFMPPE
XH_P37	2	120925501	120925501	In_Frame_Ins	INS	-	TTTGTGTTTGT	-	EPB41L5	1TGACTGTTTGT	delinsIIIMTVCFVFLNYS
XH_P37	2	122106266	122106266	Frame_Shift_Ins	INS	-	GCCTAACTTGA	-	CLASP1	insTACTTCAAG	p.S1345fs
XH_P37	2	122144748	122144748	Frame_Shift_Ins	INS	-	AATGTTCTCTC	-	CLASP1	3240insGAGAG	p.T1080fs
XH_P37	2	128707517	128707517	Frame_Shift_Ins	INS	-	TGTGTGATTAT	-	SAP130	insCCAAATAAAT	p.L872fs
XH_P37	2	129025797	129025797	Missense_Mutation	SNP	G	A	G	HS65T1	c.C1175T	p.A392V
XH_P37	2	130934202	130934202	Frame_Shift_Ins	INS	-	CTACAGGACCT	-	SMPD4	nsCCAAGGTCCTC	p.A27fs
XH_P37	2	130952659	130952659	Missense_Mutation	SNP	C	T	C	TUBA3E	c.G368A	p.R123H
XH_P37	2	132235907	132235907	Nonsense_Mutation	INS	-	ATGTGATTTTCC	-	TUBA3A	TCACAATCGATA	G59delinsAFTIDISX
XH_P37	2	133070479	133070479	Frame_Shift_Ins	INS	-	TGTGCTCTTA	-	ZNF806	54insTGTGTC	p.T18fs
XH_P37	2	135711691	135711691	Frame_Shift_Ins	INS	-	ACTCTTTTCTTT	-	CCNT2	567insCACTCTT	p.H556fs
XH_P37	2	135711884	135711884	Frame_Shift_Ins	INS	-	CT	-	CCNT2	1859_1860insC	p.R620fs
XH_P37	2	135711885	135711885	Frame_Shift_Ins	INS	-	TGCTTT	-	CCNT2	60_1861insTGT	p.R620fs
XH_P37	2	135745134	135745134	Frame_Shift_Ins	INS	-	ATGACAAGCATA	-	MAP3K19	CATCTTATGCTT	p.E323fs
XH_P37	2	135908069	135908069	In_Frame_Ins	INS	-	ACAAGATGAGTA	-	RAB3GAP1	2055insACAAGA	S685delinsSODEY
XH_P37	2	135988261	135988261	Frame_Shift_Ins	INS	-	T	-	ZRANB3	c.1775dupA	p.E592fs
XH_P37	2	135988263	135988263	In_Frame_Ins	INS	-	BATAACCTGTGC	-	ZRANB3	74insAAGCACAC	E592delinsKHLRLE
XH_P37	2	136615557	136615557	Nonsense_Mutation	INS	-	TCAGTGTGTAAT	-	MCM6	sACAGCATTACA	E461delinsEQHYTLXK
XH_P37	2	138722089	138722089	Nonsense_Mutation	INS	-	GAATTTTAA	-	HNMT	8_29insGAATT	S10_D11delinsX
XH_P37	2	138722090	138722090	Frame_Shift_Ins	INS	-	A	-	HNMT	c.29_30insA	p.S10fs
XH_P37	2	139322517	139322517	Nonsense_Mutation	INS	-	ATGAAAACATA	-	SPOPL	CCAAAAAGTAA	10_L331delinsAYYPXK
XH_P37	2	141115676	141115676	Frame_Shift_Ins	INS	-	ACTAAAATGT	-	LRP1B	11267insACAT	p.T3756fs
XH_P37	2	141253294	141253294	Frame_Shift_Ins	INS	-	TATACATA	-	LRP1B	3_8874insTATG	p.Q2958fs
XH_P37	2	141253296	141253296	Frame_Shift_Ins	INS	-	ATTTTATAGCCC	-	LRP1B	TAAGAACCGCTA	p.Q2958fs
XH_P37	2	141598610	141598610	Nonsense_Mutation	INS	-	C	-	LRP1B	4990_4991ins	664_W1665delinsX
XH_P37	2	141598611	141598611	Frame_Shift_Ins	INS	-	AAAGTATGATTA	-	LRP1B	AAAAAATAATC	p.V1664fs
XH_P37	2	148701091	148701091	Nonsense_Mutation	INS	-	TTTATGGGAATT	-	ORC4	TAATCAATTCCC	171_172delinsVX
XH_P37	2	152267851	152267851	Nonsense_Mutation	INS	-	CTAACTCTTGCA	-	RIF1	TACTTTCTAACTC	61_T62delinsKITFX
XH_P37	2	152512936	152512936	Frame_Shift_Ins	INS	-	A	-	NEB	c.6225_6226ins	p.V2076fs
XH_P37	2	152512937	152512937	Nonsense_Mutation	INS	-	ACTACAAGCAC	-	NEB	25insCAGGTGCT	75_V2076delinsIRCLX
XH_P37	2	153000509	153000509	Nonsense_Mutation	INS	-	AGTGATTTAAAC	-	STAM2	TATGATTAAAT	179_E180delinsLLX
XH_P37	2	153000511	153000511	Silent	SNP	C	A	C	STAM2	c.G534T	p.L178L
XH_P37	2	153006702	153006702	In_Frame_Ins	INS	-	ACAGCAAGACCA	-	STAM2	82insTGGTCTTG	L28delinsWSCCL
XH_P37	2	157182444	157182444	Frame_Shift_Ins	INS	-	AGAGATAGCCG	-	NR4A2	1609insCGGCT	p.D537fs
XH_P37	2	160086784	160086784	Missense_Mutation	SNP	C	T	C	TANC1	c.C424AT	p.P1415L
XH_P37	2	160086786	160086791	In_Frame_Del	DEL	GCACAC	-	GCACAC	TANC1	c.4246_4251del	p.1416_1417del
XH_P37	2	160721429	160721429	Frame_Shift_Ins	INS	-	ATAAAAAACAGA	-	LY75	2120insTCTGT	p.G707fs
XH_P37	2	160737723	160737723	Frame_Shift_Ins	INS	-	CTGT	-	LY75	74_1275insAA	p.L425fs
XH_P37	2	160737724	160737724	Frame_Shift_Ins	INS	-	AATATTAAGACT	-	LY75	CAAAGAAGCTC	p.L425fs
XH_P37	2	162087932	162087932	Frame_Shift_Ins	INS	-	GTAAGAAAGTT	-	TANK	GCTATGTAAAGA	p.D324fs
XH_P37	2	163055376	163055376	Nonsense_Mutation	INS	-	AAGGTATTATTA	-	FAP	218insATAATA	406_Y407delinsRX
XH_P37	2	163228584	163228584	Nonsense_Mutation	INS	-	TATT	-	KCNH7	345_3346insAA	116_K1117delinsKX
XH_P37	2	163228586	163228586	Frame_Shift_Ins	INS	-	ATCCTCTCTACT	-	KCNH7	344insAAGTAG	p.L1115fs
XH_P37	2	163291887	163291887	Frame_Shift_Ins	INS	-	ATGTGTATTGG	-	KCNH7	1754insCCAAT	p.G585fs
XH_P37	2	163291888	163291888	Frame_Shift_Ins	INS	-	TG	-	KCNH7	1752_1753insC	p.G585fs
XH_P37	2	164466660	164466660	Nonsense_Mutation	INS	-	ACAGACAACATA	-	FIGN	1649insTAATTG	G550delinsVIVLX
XH_P37	2	164467727	164467727	Nonsense_Mutation	INS	-	TCTCTCAAAG	-	FIGN	582insCTTTTGA	194_L195delinsAFX
XH_P37	2	164467729	164467729	Missense_Mutation	SNP	C	A	C	FIGN	c.G580T	p.A194S
XH_P37	2	165578792	165578792	In_Frame_Ins	INS	-	TCCTCTTACCTAA	-	COBLL1	9insGTTAGGTA	A263delinsVIGKRK
XH_P37	2	165584645	165584645	Frame_Shift_Ins	INS	-	CAACAGA	-	COBLL1	94_495insTCGT	p.P165fs
XH_P37	2	165584647	165584647	Nonsense_Mutation	INS	-	TATTTATTTATG	-	COBLL1	ATCCCACTAAAT	H166delinsTNIHPLNXX
XH_P37	2	166020190	166020190	Nonsense_Mutation	INS	-	TCAAAAAATGCT	-	SCN3A	2insTTAGCATTT	11_V212delinsSIFX
XH_P37	2	166532964	166532964	Frame_Shift_Ins	INS	-	AATAAGAGACTC	-	CSNRP3	52insAAATAAGA	p.A184fs
XH_P37	2	166848796	166848796	Frame_Shift_Ins	INS	-	AATTTTCTTTTT	-	SCN1A	ACTGACAAAAA	p.L1663fs
XH_P37	2	167056294	167056294	In_Frame_Ins	INS	-	CCT	-	SCN9A	4821_4822insA	R1608delinsRR
XH_P37	2	167056295	167056295	Frame_Shift_Ins	INS	-	TT	-	SCN9A	4820_4821insA	p.G1607fs
XH_P37	2	167168170	167168170	Frame_Shift_Ins	INS	-	C	-	SCN9A	c.96_97insG	p.K33fs
XH_P37	2	167168172	167168172	Nonsense_Mutation	INS	-	TATAAAATTT	-	SCN9A	95insAATTTTT	S32_K33delinsX
XH_P37	2	167289045	167289045	Frame_Shift_Ins	INS	-	GATGGAGG	-	SCN7A	4_2375insCCTC	p.D792fs
XH_P37	2	167298238	167298238	Missense_Mutation	SNP	A	C	A	SCN7A	c.T1825G	p.V609D
XH_P37	2	167298240	167298240	In_Frame_Ins	INS	-	GGTGTA	-	SCN7A	22_1823insTAC	K608delinsHQ
XH_P37	2	168101119	168101119	In_Frame_Ins	INS	-	CAAAATTAATTA	-	XIRP2	2insCATCAAAT	7851delinsASNLKL
XH_P37	2	168104370	168104370	In_Frame_Ins	INS	-	TGGAAGTTAATT	-	XIRP2	403insGTTGAAG	1934delinsTVEVNC
XH_P37	2	168115692	168115692	Nonsense_Mutation	INS	-	AGATGATTGAA	-	XIRP2	971insGAGATG	S57_V658delinsERX
XH_P37	2	168920070	168920070	Nonsense_Mutation	INS	-	SAATCGTTAGCT	-	STK39	CAAAATAAGCTA	439_A440delinsSIX

XH_P37	2	170060777	170060777	In_Frame_Ins	INS	-	TGTGAA	-	LRP2	19_7720insTTC	R2574delinsFTR
XH_P37	2	170060778	170060778	Nonsense_Mutation	INS	-	AGTTTAA	-	LRP2	18_7719insTTAA	573_R2574delinsHX
XH_P37	2	170063328	170063328	Frame_Shift_Ins	INS	-	CCCTGAAACCA	-	LRP2	902insATGGTT	p.F2301fs
XH_P37	2	170667793	170667793	In_Frame_Ins	INS	-	ACTTCCAA	-	SS8	8_1099insACTTC	S366delinsSTSQ
XH_P37	2	170667794	170667794	In_Frame_Ins	INS	-	CTCTCTTTGTTC	-	SS8	0insTCACCTCTT	367delinsVTSFLN
XH_P37	2	171917623	171917623	Frame_Shift_Ins	INS	-	ATGTGTCCTTA	-	TLK1	5insATAAGGCC	p.R29fs
XH_P37	2	171917625	171917625	Missense_Mutation	SNP	C	G	C	TLK1	c.G84C	p.K28N
XH_P37	2	172582767	172582767	Frame_Shift_Ins	INS	-	ACTTAAAAATTC	-	DYNC12	1insAAACTCTAA	p.K270fs
XH_P37	2	172582769	172582769	Frame_Shift_Ins	INS	-	GAGTGCAAGAT	-	DYNC12	813insGAGTGC	p.H271fs
XH_P37	2	174228148	174228148	Nonsense_Mutation	INS	-	AACTGAACA	-	CDC47	2_343insAACTGC	p.F114delinsFNX
XH_P37	2	174228150	174228150	Frame_Shift_Ins	INS	-	GATACCTCTG	-	CDC47	345insGATACC	p.L115fs
XH_P37	2	175268943	175268943	Frame_Shift_Ins	INS	-	AGAAAAGTCAT	-	SCRN3	34insAAGAAAA	p.E211fs
XH_P37	2	175268945	175268945	In_Frame_Ins	INS	-	CATAAAGCATGT	-	SCRN3	nsTAACATAAAAC	212delinsFNKHVS
XH_P37	2	175436470	175436470	In_Frame_Ins	INS	-	ATTTCCTGTGGT	-	WIPF1	3insAACCAACAC	355delinsNTNRNIG
XH_P37	2	175439961	175439961	Nonsense_Mutation	INS	-	ACAGAACTATGA	-	WIPF1	9insTTTCATAGT	110_L111delinsISX
XH_P37	2	175666522	175666522	Missense_Mutation	SNP	T	A	T	CHN1	c.A746T	p.E249V
XH_P37	2	175666523	175666523	In_Frame_Ins	INS	-	AGAAGGAATGCT	-	CHN1	TTTTTAGCATTC	249delinsFSIPSQLE
XH_P37	2	176959316	176959316	Frame_Shift_Ins	INS	-	TTTGCTCTTTAT	-	HOXD13	5GCTGTTTGGTC	p.I297fs
XH_P37	2	178080604	178080604	Frame_Shift_Ins	INS	-	TCTTAAGTTACC	-	HNRNPA3	nsTACTCTTAAG	p.K86fs
XH_P37	2	178081619	178081619	Frame_Shift_Ins	INS	-	CTGCATCTCTT	-	HNRNPA3	706insCTGCAT	p.R235fs
XH_P37	2	178416535	178416535	Frame_Shift_Ins	INS	-	TGAAAATTATTC	-	PTC30B	nsATTGGATAAT	p.P319fs
XH_P37	2	178592818	178592818	Frame_Shift_Ins	INS	-	ACCAGAAGAGA	-	PDE11A	9insACATCTCTT	p.I180fs
XH_P37	2	178705102	178705102	Nonsense_Mutation	INS	-	GCAGATGGTT	-	PDE11A	nsGATAACCATC	E15_S16delinsGX
XH_P37	2	179253856	179253856	Frame_Shift_Ins	INS	-	T	-	OSBPL6	c.2184_2185ins	p.C728fs
XH_P37	2	179253857	179253857	In_Frame_Ins	INS	-	ATGAGAAATATTC	-	OSBPL6	2186insATGAGA	I729delinsNENIL
XH_P37	2	179341938	179341938	In_Frame_Ins	INS	-	GGAAAGGAA	-	FKBP7	3_224insTTCTCT	p.R75delinsLPFR
XH_P37	2	179398216	179398216	Missense_Mutation	SNP	C	T	C	TTN	c.G75931A	p.E25311K
XH_P37	2	179399194	179399194	Frame_Shift_Ins	INS	-	ATGGGTGCTGGA	-	TTN	4953insCTCCAG	p.V24985fs
XH_P37	2	179413138	179413138	In_Frame_Ins	INS	-	TTCTGGGTGGA	-	TTN	66020insTTCAA	22007delinsLQPRS
XH_P37	2	179418086	179418086	Frame_Shift_Ins	INS	-	TACAGGTATAAC	-	TTN	346insATGTTTA	p.T20782fs
XH_P37	2	179424482	179424482	In_Frame_Ins	INS	-	AGAAGAGCATG	-	TTN	59182insCCATG	19728delinsPCFLT
XH_P37	2	179435839	179435839	Frame_Shift_Ins	INS	-	AG	-	TTN	7824_47825ins	p.C15942fs
XH_P37	2	179435841	179435841	In_Frame_Ins	INS	-	ATGAGTTCC	-	TTN	2_47823insGGA	P15941delinsPELI
XH_P37	2	179437942	179437942	Frame_Shift_Ins	INS	-	CCTGAGACTT	-	TTN	45722insAAGT	p.S15241fs
XH_P37	2	179449625	179449625	Nonsense_Mutation	INS	-	AGTT	-	TTN	547_37548insA	2516_H12517delinsX
XH_P37	2	179449626	179449626	In_Frame_Ins	INS	-	CCATTTGGT	-	TTN	3_37547insACCA	12516delinsYQMG
XH_P37	2	179449903	179449903	Nonsense_Mutation	INS	-	ACGTATCAAAAT	-	TTN	AACAAAGGATTTC	12458delinsRTRIX
XH_P37	2	179452445	179452445	In_Frame_Ins	INS	-	AAAATGAATTTC	-	TTN	96insTAACAAAT	2132delinsINKFIFE
XH_P37	2	179522491	179522491	Nonsense_Mutation	INS	-	GATCTATCTCTT	-	TTN	377insACAAGAG	26_E12627delinsHKRX
XH_P37	2	179537423	179537423	Frame_Shift_Ins	INS	-	FTGTGCATGCA	-	TTN	TAAAGGATTGC	p.K10297fs
XH_P37	2	179574422	179574422	Frame_Shift_Ins	INS	-	TGAGGACTTTCT	-	TTN	TATCATAAGAA	p.I8298fs
XH_P37	2	179584475	179584475	Nonsense_Mutation	INS	-	AGATTTTATGAT	-	TTN	TTGTATATTCAAT	1_P6672delinsNIVYSX
XH_P37	2	179589227	179589227	Frame_Shift_Ins	INS	-	AAAGACTGAAAA	-	TTN	143insTATTTTTC	p.V5715fs
XH_P37	2	179604496	179604496	Frame_Shift_Ins	INS	-	TCTGACGAAAA	-	TTN	75insTGTTTTTTC	p.L4125fs
XH_P37	2	179616165	179616165	Missense_Mutation	SNP	C	A	C	TTN	c.G10962T	p.M3654I
XH_P37	2	180348051	180348051	Frame_Shift_Ins	INS	-	CTTCACGGGAA	-	ZNF358B	AATCCTCTCCGT	p.A130fs
XH_P37	2	182543288	182543288	Frame_Shift_Ins	INS	-	CCTCGGAC	-	NEUROD1	9_300insGTCCG	p.K100fs
XH_P37	2	182766892	182766892	Nonsense_Mutation	INS	-	TCGAGTTAAAGG	-	SSFA2	54insTTCGAGTT	18_E219delinsTSSX
XH_P37	2	183053773	183053773	Nonsense_Mutation	INS	-	ATTTTAAATGG	-	PDE1A	ATAGATCCATT	2_E363delinsAPHSIX
XH_P37	2	186657903	186657903	Nonsense_Mutation	INS	-	AAATTGTTTAAT	-	FSIP2	5TTTCTAAATTTC	4_K2015delinsSKSFX
XH_P37	2	186668085	186668085	Nonsense_Mutation	INS	-	ATAACTGCCTTC	-	FSIP2	5TATAAAATAAC	N4684delinsLVX
XH_P37	2	186668420	186668420	In_Frame_Ins	INS	-	ATTGGGCACGA	-	FSIP2	insTCTTTATTGG	96delinsNLYWARLP
XH_P37	2	186668422	186668422	Missense_Mutation	SNP	A	T	A	FSIP2	c.A14389T	p.I4797L
XH_P37	2	189867759	189867759	Nonsense_Mutation	INS	-	FAAAAAACAAGG	-	COL3A1	AAATTTTAAAAA	G843delinsEIKFNKAFX
XH_P37	2	190339505	190339505	Frame_Shift_Ins	INS	-	GCCAAGAG	-	WDR75	9_2260insGCCA	p.N735fs
XH_P37	2	190339506	190339506	Nonsense_Mutation	INS	-	GAAA	-	WDR75	260_2261insGA	5754_L755delinsX
XH_P37	2	190531114	190531114	Frame_Shift_Ins	INS	-	CTTGATTTTGGT	-	ASN5D1	TATTTCTTGATT	p.E86fs
XH_P37	2	191302177	191302177	In_Frame_Ins	INS	-	CTGGTAATTCCT	-	MFSD6	3insGATCTGGT	474delinsDDLVPV
XH_P37	2	192550490	192550490	Frame_Shift_Ins	INS	-	A	-	NABP1	c.612dupA	p.R204fs
XH_P37	2	192550492	192550492	Nonstop_Mutation	INS	-	TATTTTCAGAGG	-	NABP1	ATCACTATTTTC	delinsYKNLSFSEVYVRSR
XH_P37	2	192700824	192700824	Frame_Shift_Ins	INS	-	TAATCATTGACC	-	CAVIN2	CTATATGGTCA	p.M368fs
XH_P37	2	196593033	196593033	Missense_Mutation	SNP	T	G	T	SLC39A10	c.T2297G	p.V766G
XH_P37	2	196593035	196593035	Frame_Shift_Ins	INS	-	AGCAAGCAATT	-	SLC39A10	CTGTAAGACAA	p.T767fs
XH_P37	2	196619155	196619155	Frame_Shift_Ins	INS	-	AG	-	DNAH7	1669_11670ins	p.Q3890fs
XH_P37	2	196619157	196619157	Frame_Shift_Ins	INS	-	ATATGAGCCGAT	-	DNAH7	nsAATGAGTCGG	p.Q3890fs
XH_P37	2	196737189	196737189	Nonsense_Mutation	INS	-	TGAAATGGGAT	-	DNAH7	CACATAATCCCA	140_F2141delinsLTX
XH_P37	2	196866581	196866581	Nonsense_Mutation	INS	-	ATTTTAAATTAT	-	DNAH7	CTGAAATAATTA	1_F332delinsRCYPLX
XH_P37	2	197565845	197565845	Nonsense_Mutation	INS	-	ATATTAACCTTTT	-	CCDC150	5TTTGTATATTAT	delinsSLLVLYNFVYVXS
XH_P37	2	197656112	197656112	Nonsense_Mutation	SNP	G	A	G	GTF3C3	c.C484T	p.R162X
XH_P37	2	198413128	198413128	Frame_Shift_Ins	INS	-	GTAAGGTTTATT	-	HSPE1-MOB4	AATAAGTAAGG	p.Y120fs
XH_P37	2	200213653	200213653	In_Frame_Ins	INS	-	ATCTACCAAGCA	-	SATB2	944insTTGCTGG	H315delinsLAGRY
XH_P37	2	200826615	200826615	Frame_Shift_Ins	INS	-	GCAGCAGTATA	-	MAIP1	sATTGGCAGCAG	p.N254fs
XH_P37	2	201437494	201437494	Nonsense_Mutation	INS	-	CTCTTATTAACT	-	SGO2	6insAGCTTCTTA	809delinsKLLINFX
XH_P37	2	201437529	201437529	Frame_Shift_Ins	INS	-	GTCTTCC	-	SGO2	60_2461insGTC	p.P820fs
XH_P37	2	201437531	201437531	Nonsense_Mutation	INS	-	TCTGCCTAAGCT	-	SGO2	TTACTTTCTGCC	1_T822delinsDLLSAX
XH_P37	2	201438146	201438146	Frame_Shift_Ins	INS	-	TATTGATAATGT	-	SGO2	AGTTGTTTATGAT	p.I1026fs
XH_P37	2	201857695	201857695	Frame_Shift_Ins	INS	-	TTTCTTTTATGT	-	FAM126B	AAAGTACTAAAA	p.E220fs
XH_P37	2	201862252	201862252	Frame_Shift_Ins	INS	-	GAGCTGCATTG	-	FAM126B	2insAGGAATGCA	p.L181fs
XH_P37	2	202357813	202357813	Nonsense_Mutation	INS	-	AGCATATCACC	-	C2CD6	1insCTTGGTGA	84_S1085delinsPWX
XH_P37	2	202598158	202598158	Nonsense_Mutation	INS	-	CAAGGATCATA	-	ALS2	21insACTATGA	b.D807delinsELX
XH_P37	2	202938407	202938407	Missense_Mutation	SNP	G	C	G	KIAA2012	c.G57C	p.Q19H
XH_P37	2	202938408	202938408	Nonsense_Mutation	INS	-	GCCTTTTATTA	-	KIAA2012	insGGGCTCTTTT	20_L21delinsRAFYX
XH_P37	2	203160559	203160559	Frame_Shift_Ins	INS	-	5AATGCACCTCC	-	NOP58	ACAAAGAAATGC	p.K357fs
XH_P37	2	204231691	204231691	In_Frame_Ins	INS	-	ACTGAACCTACT	-	AB12	TATTGACTGAAC	0delinsKLLTELNVF
XH_P37	2	204305261	204305261	Frame_Shift_Ins	INS	-	AAAAAGACCAG	-	RAPH1	2652insCTGCT	p.K884fs
XH_P37	2	205551005	205551005	In_Frame_Ins	INS	-	AATGACCTAATC	-	PARD3B	insTTTAATGACC	74delinsKFNLDIY
XH_P37	2	205551007	205551007	Splice_Site	INS	-	TAACACATTTTA	-	PARD3B	.	.
XH_P37	2	206921096	206921096	Frame_Shift_Ins	INS	-	AAAGATTCTGTA	-	INO80D	insAAATACAGA	p.L264fs
XH_P37	2	207174503	207174503	Nonsense_Mutation	INS	-	TCCACAGCTCTT	-	ZDBF2	ATTATATCCACA	delinsPLEPLYQLLSSESIX
XH_P37	2	207639093	207639093	Frame_Shift_Ins	INS	-	TCTATTAATCTT	-	FASTKD2	ATCTGTTCTATT	p.N467fs
XH_P37	2	207655364	207655364	Missense_Mutation	SNP	C	A	C	FASTKD2	c.C1967A	p.A656D
XH_P37	2	207655366	207655366	Frame_Shift_Ins	INS	-	CTTAGTCCTTCA	-	FASTKD2	TCCTGCTTAACT	p.M657fs
XH_P37	2	207804365	207804365	Frame_Shift_Ins	INS	-	TACCATT	-	CPO	2_43insTACCAAT	p.L14fs
XH_P37	2	207804366	207804366	In_Frame_Ins	INS	-	ATATTTCAATTC	-	CPO	44insATATTTCAT	V15delinsDISFL
XH_P37	2	210558164	210558164	Nonsense_Mutation	INS	-	ATTCTCTGAATC	-	MAP2	nsCGATGTTTCT	Q424delinsAMFLX
XH_P37	2	210559797	210559797	In_Frame_Ins	INS	-	ATGGGAGCTGTG	-	MAP2	nsTGGCAATGGG	68delinsDGNGTVYL
XH_P37	2	210685201	210685201	Frame_Shift_Ins	INS	-	ATCT	-	UNC80	129_2130insAT	p.R710fs
XH_P37	2	210685202	210685202	In_Frame_Ins	INS	-	TTATTCGTTTAA	-	UNC80	131insATTATTC	R710delinsRIILFN

XH_P37	2	210787017	210787017	Nonsense_Mutation	INS	-	GTAGTTAATGA	-	UNC80	TTGAAAGTAGTT	1792delinsKVESX
XH_P37	2	211512680	211512680	Nonsense_Mutation	INS	-	ACTTCTGGCA	-	CP51	AATTTTCTCTT	P629delinsKFLSLGTGX
XH_P37	2	215645853	215645853	Frame_Shift_Ins	INS	-	TTTGTTAAGCA	-	BARD1	688insTGCCTA	p.1230fs
XH_P37	2	215807703	215807703	Nonsense_Mutation	INS	-	TTAAATTATTTT	-	ABCA12	28insATAAAAT	M2144delinsNKIIX
XH_P37	2	215807705	215807705	Nonsense_Mutation	INS	-	TGAATTTTCTACT	-	ABCA12	ATATTTAAGTA	12143delinsAKIFKX
XH_P37	2	215868957	215868957	Silent	SNP	G	A	G	ABCA12	c.C1705T	p.L569L
XH_P37	2	215868959	215868959	Frame_Shift_Ins	INS	-	ATAATGTAGGC	-	ABCA12	1703insGCCTA	p.E568fs
XH_P37	2	217364707	217364707	Frame_Shift_Ins	INS	-	AGACATCT	-	RPL37A	8_169insAGACA	p.H56fs
XH_P37	2	217364709	217364709	Frame_Shift_Ins	INS	-	GGAGT	-	RPL37A	170_171insGGA	p.C57fs
XH_P37	2	218674638	218674638	Frame_Shift_Ins	INS	-	TCTACCTTCT	-	TNS1	4806insAGGAAG	p.S1602fs
XH_P37	2	218674639	218674639	Missense_Mutation	SNP	G	C	G	TNS1	c.C4805G	p.S1602C
XH_P37	2	219496954	219496954	Frame_Shift_Ins	INS	-	AGCTGCTTGAT	-	PLCD4	9insATTAGCTG	p.E456fs
XH_P37	2	219562294	219562294	Nonsense_Mutation	INS	-	AAAAAAATAAAC	-	STK36	808insAAAAAA	36_L937delinsQKKX
XH_P37	2	219870919	219870919	Frame_Shift_Ins	INS	-	CCAACCCA	-	CFAP65	5_4746insTGGG	p.Q1582fs
XH_P37	2	220037818	220037818	Frame_Shift_Ins	INS	-	ACTC	-	CNPPD1	722_723insGAC	p.S241fs
XH_P37	2	220045811	220045811	In_Frame_Ins	INS	-	CCACAGTTACTA	-	RETREG2	TCTTCCACAGTT	16delinsVSLPQLLIK
XH_P37	2	220103443	220103443	In_Frame_Ins	INS	-	CTCTTTTATTTCT	-	GLB1L	AAACAGAAATA	284delinsQTEIKEDT
XH_P37	2	223773815	223773815	Nonsense_Mutation	INS	-	TTCATAAAGTACT	-	ACSL3	sGTTATTACATAA	9_V110delinsGYSX
XH_P37	2	225360650	225360650	Frame_Shift_Ins	INS	-	AGTCTTCTTACT	-	CUL3	543insAATAAG	p.Q151fs
XH_P37	2	225360652	225360652	Frame_Shift_Ins	INS	-	AACCTTTAGAG	-	CUL3	11insACTCTCTA	p.A514fs
XH_P37	2	227662984	227662984	In_Frame_Ins	INS	-	GGATGA	-	IRS1	170_471insTCAT	G157delinsGHP
XH_P37	2	227662985	227662985	Frame_Shift_Ins	INS	-	T	-	IRS1	c.469_470insA	p.G157fs
XH_P37	2	227886767	227886767	Nonsense_Mutation	INS	-	ACATCCCTCTCTA	-	COL4A4	AATAATAGAG	P1405delinsKX
XH_P37	2	228860402	228860402	Nonsense_Mutation	INS	-	TCTAAAAATGCA	-	SPHKAP	TTAAAAATGCATT	486_D1487delinsHX
XH_P37	2	228884708	228884708	Nonsense_Mutation	INS	-	GCCTCTGAATGA	-	SPHKAP	ATTATCATCTCA	N289delinsSHTLLSFRSFX
XH_P37	2	230662505	230662505	Nonsense_Mutation	INS	-	GACTTTTACCTT	-	TRIP12	90insATAAGGTA	830_V831delinsLX
XH_P37	2	231256899	231256899	Frame_Shift_Ins	INS	-	GTCTGCGCTTC	-	SP140L	883insGCTCTGG	p.R294fs
XH_P37	2	231338147	231338147	Frame_Shift_Ins	INS	-	TTTTTCTTTTGTG	-	SP100	AATCTCTTTTCT	p.D513fs
XH_P37	2	231338149	231338149	In_Frame_Ins	INS	-	CTGTAT	-	SP100	40_1541insCTG	M514delinsTVL
XH_P37	2	231927370	231927370	Nonsense_Mutation	INS	-	AGGAAGTACAG	-	PSMD1	AAATTAGGAAG	95_Y96delinsERNX
XH_P37	2	232458083	232458083	Frame_Shift_Ins	INS	-	TGGAA	-	TEX44	421_422insTGG	p.P141fs
XH_P37	2	232458084	232458084	Frame_Shift_Ins	INS	-	AACTGCACCTCT	-	TEX44	423insAACTGC	p.P141fs
XH_P37	2	233431616	233431616	Frame_Shift_Ins	INS	-	TCATATCACTTT	-	EIF4E2	AGAAGTCATATC	p.L106fs
XH_P37	2	233636012	233636012	Frame_Shift_Ins	INS	-	A	-	KCNJ13	c.60_61insT	p.V21fs
XH_P37	2	233636013	233636013	In_Frame_Ins	INS	-	ACTCACAAATTGG	-	KCNJ13	insAACCAATTG	M20delinsITNCEL
XH_P37	2	234186258	234186258	Frame_Shift_Ins	INS	-	TTATCATTTTAT	-	ATG16L1	ATTCTATTATCA	p.G170fs
XH_P37	2	234474132	234474132	In_Frame_Ins	INS	-	TGGGTGATGACA	-	USP40	ATTATTGTGCATC	35delinsNIIVITQDI
XH_P37	2	234526800	234526800	Frame_Shift_Ins	INS	-	GTATGAGGTTGA	-	UGT1A8	GAGGTGATGAG	p.P149fs
XH_P37	2	234602146	234602146	Frame_Shift_Ins	INS	-	GG	-	UGT1A6	c.496_497insGG	p.P166fs
XH_P37	2	234602147	234602147	Frame_Shift_Ins	INS	-	TAGATTTTCTCTG	-	UGT1A6	TGGATAGATT	p.P166fs
XH_P37	2	234681087	234681087	Frame_Shift_Ins	INS	-	TGTAA	-	UGT1A1	484_1485insTG	p.L495fs
XH_P37	2	234681088	234681088	Nonsense_Mutation	INS	-	AACACAAAGACA	-	UGT1A1	86insTAACACCA	495_L496delinsLX
XH_P37	2	234698270	234698270	In_Frame_Ins	INS	-	ATTCTCCATTTG	-	MROH2A	D5insCATTCCTC	P135delinsPIPPFL
XH_P37	2	234746295	234746295	Frame_Shift_Ins	INS	-	GC	-	HUJRP	1919_1920insG	p.G640fs
XH_P37	2	238257003	238257003	Frame_Shift_Ins	INS	-	T	-	COL6A3	c.5133_5134ins	p.P1712fs
XH_P37	2	238257004	238257004	Nonsense_Mutation	INS	-	TGAGATTTAAAT	-	COL6A3	insTTTTATTAA	11_P1712delinsYF1X
XH_P37	2	238662004	238662004	Frame_Shift_Ins	INS	-	TGGAATCCCCC	-	LRRFIP1	69insATGGAAAT	p.A123fs
XH_P37	2	238729809	238729809	In_Frame_Ins	INS	-	TGT	-	RBM44	2012_2013insT	p.K671delinsNV
XH_P37	2	238729810	238729810	Nonsense_Mutation	INS	-	AGAGACGGGGG	-	RBM44	insTTGTAGAGA	671_1672delinsKLX
XH_P37	2	240957991	240957991	Frame_Shift_Ins	INS	-	T	-	NDUFA10	c.525_526insA	p.Q176fs
XH_P37	2	240957992	240957992	Frame_Shift_Ins	INS	-	AAAGCAGA	-	NDUFA10	4_525insTCTCG	p.N175fs
XH_P37	2	242026822	242026822	Nonsense_Mutation	SNP	C	A	C	SNED1	c.C4137A	p.Y1379X
XH_P37	2	242026823	242026823	Frame_Shift_Ins	INS	-	GTGATTTGTAAT	-	SNED1	GTGATGTGATT	p.R1380fs
XH_P37	2	242373658	242373658	Frame_Shift_Ins	INS	-	GATAGGGGAATT	-	FARP2	954insGATAGG	p.T318fs
XH_P37	2	242373659	242373659	Nonsense_Mutation	INS	-	TTAAAAATCAG	-	FARP2	CAAAATAAAAA	T318delinsTQNX
XH_P37	2	242501866	242501866	Frame_Shift_Ins	INS	-	T	-	BOK	c.324_325insT	p.A108fs
XH_P37	2	242501867	242501867	In_Frame_Ins	INS	-	TTCTCACT	-	BOK	5_326insTCTCT	V109delinsVPHL
XH_P37	3	9489446	9489446	Nonsense_Mutation	INS	-	ATTCACCTTAAAG	-	SETD5	60insCTATTACAC	20_R621delinsSYSYLX
XH_P37	3	10084834	10084834	Nonsense_Mutation	INS	-	ATGTTGGACATT	-	FANCD2	TTTAAATGTGGG	0delinsRKFKCWTFX
XH_P37	3	12641888	12641888	Nonsense_Mutation	INS	-	CCTGCCAATTAG	-	RAF1	861insCTAAATTG	p.S287delinsSX
XH_P37	3	12641890	12641890	Missense_Mutation	SNP	A	G	A	RAF1	c.T859C	p.S287P
XH_P37	3	16310760	16310760	In_Frame_Ins	INS	-	ATTTTCTTTTCTT	-	OXNAD1	TCCATTTTCTTT	3delinsPCFHFSFLIY
XH_P37	3	16312474	16312474	In_Frame_Ins	INS	-	TTG	-	OXNAD1	c.69_70insTTG	p.A23delinsAL
XH_P37	3	16312476	16312476	Nonsense_Mutation	INS	-	TAATAGCACCA	-	OXNAD1	ACTCATAATAGCA	V24delinsSVTX
XH_P37	3	17052979	17052979	Frame_Shift_Ins	INS	-	ACGACACC	-	PLCL2	3_1764insACGA	p.N588fs
XH_P37	3	17052980	17052980	In_Frame_Ins	INS	-	GAA	-	PLCL2	1764_1765insGA	p.N588delinsNE
XH_P37	3	20216412	20216412	Nonsense_Mutation	INS	-	AAGTAAGCAAA	-	SGO1	11insTCTTTGCT	D204delinsLFAVFX
XH_P37	3	25778885	25778885	Frame_Shift_Ins	INS	-	GT	-	NGLY1	c.942_943insAC	p.C315fs
XH_P37	3	25778886	25778886	Frame_Shift_Ins	INS	-	TACCAACCTTCC	-	NGLY1	sACCTGGGAAGG	p.N314fs
XH_P37	3	25820121	25820121	In_Frame_Ins	INS	-	CTTTAAATAAG	-	NGLY1	sGACCCTTAATTT	164delinsDPYFKELR
XH_P37	3	25833425	25833425	Nonsense_Mutation	INS	-	ATACAAGAATC	-	OXSM	915insATACAA	305_G306delinsX
XH_P37	3	28295256	28295256	In_Frame_Ins	INS	-	ATTGGATCCCT	-	CMC1	TCTATATTGGGA	delinsVSIKFCWTFV
XH_P37	3	29628622	29628622	Nonsense_Mutation	INS	-	GTGGTCCTTAAT	-	RBM53	3insAGTGGTCC	p.F108delinsSX
XH_P37	3	32576104	32576104	Frame_Shift_Ins	INS	-	A	-	DYNC1L1	c.518_519insT	p.E173fs
XH_P37	3	32576105	32576105	Nonsense_Mutation	INS	-	CTTGATTATCTA	-	DYNC1L1	ATAAATAGATAA	E173delinsGNNRX
XH_P37	3	33135360	33135360	Frame_Shift_Ins	INS	-	CTCTCAGACA	-	TMPEE	328insTGCTCTG	p.E110fs
XH_P37	3	37034060	37034060	Frame_Shift_Ins	INS	-	TGGAATGTCAT	-	EPM2AIP1	AATGAATGACA	p.R170fs
XH_P37	3	37365907	37365907	In_Frame_Ins	INS	-	TATGATTTTCTG	-	GOLGA4	1insGTGATGAT	844delinsGDDFSVQ
XH_P37	3	37367511	37367511	In_Frame_Ins	INS	-	GAG	-	GOLGA4	4134_4135insGA	D1378delinsDE
XH_P37	3	37367512	37367512	Nonsense_Mutation	INS	-	AGCC	-	GOLGA4	135_4136insAG	379_N1380delinsX
XH_P37	3	38037304	38037304	Missense_Mutation	SNP	A	G	A	VILL	c.A416G	p.H139R
XH_P37	3	38224579	38224579	Frame_Shift_Ins	INS	-	ATGCTCTAAAGA	-	OXSR1	57insAATGCTCT	p.K52fs
XH_P37	3	38438616	38438616	Frame_Shift_Ins	INS	-	CCCTAAGAGGA	-	XYLB	insACTGCCTTAAC	p.S331fs
XH_P37	3	39111231	39111231	Frame_Shift_Ins	INS	-	A	-	WDR48	c.422_423insA	p.T141fs
XH_P37	3	39111232	39111232	Frame_Shift_Ins	INS	-	CTCTTTATCTTG	-	WDR48	24insCCTCTTTA	p.T141fs
XH_P37	3	40557737	40557737	In_Frame_Ins	INS	-	TCCTCTTTG	-	ZNF620	9_311insTCTCT	H104delinsLLFD
XH_P37	3	40557738	40557738	Frame_Shift_Ins	INS	-	TTGTCTTAATTA	-	ZNF620	2insCTTTGCTCT	p.H104fs
XH_P37	3	42661181	42661181	Frame_Shift_Ins	INS	-	GTAAAAATATAG	-	NKTR	CATCTGTAAAAAT	p.189fs
XH_P37	3	42674292	42674292	In_Frame_Ins	INS	-	TTTCTCTCTTTT	-	NKTR	GTGGTTTCTCT	0delinsNELVSSFFSQ
XH_P37	3	42676851	42676851	Nonsense_Mutation	INS	-	TTTATGTTTTAA	-	NKTR	TTTTTTTTTATG	D387delinsVLLLLFFSFX
XH_P37	3	42678521	42678521	Frame_Shift_Ins	INS	-	CATGCGGTGAT	-	NKTR	AATATTATCATGC	p.G442fs
XH_P37	3	42681052	42681052	Frame_Shift_Ins	INS	-	TAGCCAAGCTA	-	NKTR	3857insTAGCC	p.R1286fs
XH_P37	3	43074841	43074841	Missense_Mutation	SNP	C	A	C	FAM198A	c.C1086A	p.3702fs
XH_P37	3	43344817	43344817	Nonsense_Mutation	INS	-	AAAAATAGATCTT	-	SNRK	GTTTAAAAATAG	delinsKIFRLKIDLLIX
XH_P37	3	44285337	44285337	Frame_Shift_Ins	INS	-	TGCTCTTTACCA	-	TOPAZ1	sGTCTCTGCTCT	p.K447fs
XH_P37	3	44763426	44763426	Nonsense_Mutation	INS	-	TGCTGAATAAGG	-	ZNF502	sTCTGATATGA	373_T374delinsLX
XH_P37	3	44763727	44763727	Frame_Shift_Ins	INS	-	TTATATGGTTT	-	ZNF502	TTACACTTATAT	p.A473fs
XH_P37	3	45436140	45436140	Frame_Shift_Ins	INS	-	AACCAATCTCT	-	LARS2	96insAACCCAA	p.Q65fs

XH_P37	3	45988901	45988901	Nonsense_Mutation	INS	-	AGCAGTGTITTC	-	CXCR6	CATGAAGCAGT	Y311delinsQHEAVFX
XH_P37	3	46063154	46063154	Frame_Shift_Ins	INS	-	AACCTCTTCTT	-	XCR1	286insAAGAAG	p.V96fs
XH_P37	3	47125629	47125629	Frame_Shift_Ins	INS	-	GGAGTAGCTGT	-	SETD2	GTCACAACAGC	p.L1837fs
XH_P37	3	47165686	47165686	Frame_Shift_Ins	INS	-	CAGGACACTATA	-	TTAGATATAGT	p.H103fs	
XH_P37	3	47318793	47318793	Frame_Shift_Ins	INS	-	ACACAGAAGA	-	KIF9	72insTCTTCTG	p.I24fs
XH_P37	3	47318795	47318795	Nonsense_Mutation	INS	-	TGACATTGTTC	-	KIF9	0insTGAACAAA	124_R25delinsX
XH_P37	3	47969822	47969822	In_Frame_Ins	INS	-	TATTTTAAATAC	-	MAP4	5ATAATGTATTTA	04delinsHNVKIGF
XH_P37	3	48466010	48466010	Missense_Mutation	SNP	A	T	A	PLXNB1	c.T11A	p.L4Q
XH_P37	3	48466012	48466012	Silent	SNP	A	G	A	PLXNB1	c.T9C	p.A3A
XH_P37	3	48607914	48607914	Frame_Shift_Ins	INS	-	TGAACCTAATGT	-	COL7A1	64insTGACATT	p.G2455fs
XH_P37	3	48618052	48618052	Missense_Mutation	SNP	T	C	T	COL7A1	c.A5014G	p.K1672E
XH_P37	3	48697796	48697796	Nonsense_Mutation	INS	-	GATCACTGCTA	-	CELSR3	2272insTAGCA	1758_K759delinsX
XH_P37	3	49049990	49049990	Frame_Shift_Ins	INS	-	CTGATAAGGTA	-	WDR6	46insACTGATA	p.C315fs
XH_P37	3	49064039	49064039	Missense_Mutation	SNP	A	T	A	IMPDH2	c.T823A	p.S275T
XH_P37	3	49064040	49064040	In_Frame_Ins	INS	-	GCTCCATCTGCA	-	IMPDH2	322insTGCAGAT	D274delinsDADGA
XH_P37	3	49095207	49095207	In_Frame_Ins	INS	-	CTT	-	QRICH1	425_426insAAB	p.Q142delinsQR
XH_P37	3	49095209	49095210	Frame_Shift_Del	DEL	GG	-	GG	QRICH1	c.423_424del	p.G141fs
XH_P37	3	49308675	49308675	Frame_Shift_Ins	INS	-	TTTGAATTCAT	-	C3orf62	2insCAATGGAA	p.T248fs
XH_P37	3	49841923	49841923	In_Frame_Ins	INS	-	AGACTGAGTCTC	-	FAM212A	368insAGACTGA	P123delinsQTESS
XH_P37	3	50005731	50005731	In_Frame_Ins	INS	-	CTG	-	RBM6	873_874insCTG	p.N291delinsNL
XH_P37	3	50005733	50005733	Frame_Shift_Ins	INS	-	AAATCCC	-	RBM6	75_876insAAAT	p.I292fs
XH_P37	3	50597133	50597133	Nonsense_Mutation	INS	-	CTTTAGACTCTA	-	C3orf18	44insTTAGAGTCT	148_5149delinsPX
XH_P37	3	51265475	51265475	Frame_Shift_Ins	INS	-	A	-	DOCK3	1603_1604ins	p.G535fs
XH_P37	3	51265476	51265476	Nonsense_Mutation	INS	-	5CTGAAATGAGT	-	DOCK3	AAATGTGCTGAA	5_T536delinsGNVLKX
XH_P37	3	52783733	52783733	Missense_Mutation	SNP	A	G	A	NEK4	c.T1214C	p.I405T
XH_P37	3	53326507	53326507	Frame_Shift_Ins	INS	-	TCTCCAGAAAC	-	DCP1A	498insGTTTCTG	p.E166fs
XH_P37	3	53326812	53326812	In_Frame_Ins	INS	-	CCCCAGCTT	-	DCP1A	193insAAGCTG	G65delinsKLGG
XH_P37	3	56647774	56647774	Frame_Shift_Ins	INS	-	TCTAAGCAGGA	-	CCDC66	461insATCTAAG	p.K487fs
XH_P37	3	56651516	56651516	Frame_Shift_Ins	INS	-	TTGTTTGTCTCT	-	CCDC66	sGTGTTTGTCTT	p.H706fs
XH_P37	3	57303683	57303683	Frame_Shift_Ins	INS	-	TCTGTCATAAAT	-	APPL1	ACTTCTCTGTC	p.E700fs
XH_P37	3	58090920	58090920	Nonsense_Mutation	INS	-	TATGTCAACAAT	-	FLNB	TACTGTTATGTC	75delinsIATVMSTIX
XH_P37	3	58853662	58853662	Nonsense_Mutation	INS	-	TTAAATAGACAG	-	C3orf67	1insTACTGTCTA	84_A285delinsVLSIX
XH_P37	3	58853664	58853664	Splice_Site	SNP	T	C	T	C3orf67	-	-
XH_P37	3	63649762	63649762	In_Frame_Ins	INS	-	5GCTTACAATTC	-	STN7	86insTGGCTTAC	145delinsIWLTL
XH_P37	3	63973833	63973833	Silent	SNP	G	A	G	ATXN1	c.G759A	p.L253L
XH_P37	3	65369274	65369274	Frame_Shift_Ins	INS	-	TTTCTAAAAAGT	-	MAG1	ATACAACTTTT	p.I814fs
XH_P37	3	69153769	69153769	Frame_Shift_Ins	INS	-	ACTCCCTCTCTT	-	ARL6IP5	ATTACACTCCCT	p.I183fs
XH_P37	3	69273839	69273839	In_Frame_Ins	INS	-	5CCTCCATTCAG	-	FRMD4B	4insTTCTGAATG	195delinsVLNGGY
XH_P37	3	77623837	77623837	Frame_Shift_Ins	INS	-	TCTCATAACTAT	-	ROBO2	TTCTGTCTCTAT	p.Q720fs
XH_P37	3	77651424	77651424	Missense_Mutation	SNP	T	C	T	ROBO2	c.T2918C	p.I973T
XH_P37	3	78685062	78685062	Frame_Shift_Ins	INS	-	AACTTGTCTGCG	-	ROBO1	insAGTCGCAGA	p.L978fs
XH_P37	3	78706363	78706363	Nonsense_Mutation	INS	-	AGCTTTACTTAA	-	ROBO1	1insATATTAA	797_T798delinsSYX
XH_P37	3	78717697	78717697	Frame_Shift_Ins	INS	-	ATGTTATCTGCA	-	ROBO1	sATAAATGCAGA	p.Y487fs
XH_P37	3	78719447	78719447	Frame_Shift_Ins	INS	-	GATCCGAT	-	ROBO1	8_1239insATCG	p.I413fs
XH_P37	3	78766995	78766995	Nonsense_Mutation	INS	-	AGACAGTCAGC	-	ROBO1	GCCGAGCTGAC	K193delinsKPSX
XH_P37	3	93733357	93733357	Nonsense_Mutation	INS	-	AGTTGTAAATTTT	-	STX19	insGGGAAAAAT	3_V254delinsKITTX
XH_P37	3	97655736	97655736	Frame_Shift_Ins	INS	-	AAAGTATCTGCA	-	CRYBG3	sCATCAAAAGTA	p.L2830fs
XH_P37	3	98110040	98110040	Frame_Shift_Ins	INS	-	G	-	OR5K3	c.S31_532insG	p.P177fs
XH_P37	3	98110041	98110041	In_Frame_Ins	INS	-	AAAAGAAGTTCT	-	OR5K3	CTCAGAAAAGA	78delinsSSEKFSNI
XH_P37	3	98518535	98518535	In_Frame_Ins	INS	-	AGCCAG	-	DCBLD2	08_2009insCTG	p.L670delinsPGF
XH_P37	3	100536328	100536328	Nonsense_Mutation	INS	-	TATCT	-	ABI3BP	597_2698insAG	900_L901delinsRX
XH_P37	3	100536330	100536330	Nonsense_Mutation	INS	-	TCATCTTCTGC	-	ABI3BP	2696insGCAGA	99_V900delinsSRRX
XH_P37	3	100551174	100551174	Frame_Shift_Ins	INS	-	TGTACATATAAT	-	ABI3BP	993insGATTATA	p.R665fs
XH_P37	3	100551176	100551176	Missense_Mutation	SNP	T	A	T	ABI3BP	c.A1991T	p.K664I
XH_P37	3	101476792	101476792	Nonsense_Mutation	INS	-	CAATTTCGAGAA	-	CEP97	insAGATCAITTC	389_D390delinsX
XH_P37	3	105271357	105271357	Nonsense_Mutation	INS	-	AAATTACTTAT	-	ALCAM	CTAAGAAAAAT	518_L519delinsGSX
XH_P37	3	105423000	105423000	In_Frame_Ins	INS	-	CCCACATTCATA	-	CBLB	1278insTATGAA	426delinsNMNVG
XH_P37	3	107097035	107097035	In_Frame_Ins	INS	-	TCACTTCTTCTT	-	CCDC54	insCTGTCACTCT	201delinsSVTFFFN
XH_P37	3	107097037	107097037	Frame_Shift_Ins	INS	-	G	-	CCDC54	c.603_604insG	p.Y201fs
XH_P37	3	107492134	107492134	Frame_Shift_Ins	INS	-	CTTCTTTTCTT	-	BBX	nsCTTTTCTTCT	p.L522fs
XH_P37	3	107492136	107492136	Missense_Mutation	SNP	A	C	A	BBX	c.A1568C	p.D523A
XH_P37	3	108281996	108281996	Frame_Shift_Ins	INS	-	TAAATGTTCTTC	-	KIAA1524	611insTGAAGA	p.P537fs
XH_P37	3	110837698	110837698	Nonsense_Mutation	INS	-	5ACAACTGCATA	-	NECTIN3	TAAGGACAACT	233delinsKDNCTX
XH_P37	3	111764725	111764725	Frame_Shift_Ins	INS	-	5TTATATGTATT	-	TMPR57	288insGTTATAT	p.I96fs
XH_P37	3	111764727	111764727	Missense_Mutation	SNP	A	G	A	TMPR57	c.A289G	p.N97D
XH_P37	3	112299933	112299933	Nonsense_Mutation	INS	-	AGCCATTGAAGA	-	SLC35A5	ATATTAGCCATT	205delinsIDISHX
XH_P37	3	113120579	113120579	Nonsense_Mutation	INS	-	5TTTTTATTAAT	-	CFAP44	ATTGAAATTATA	393_F394delinsVX
XH_P37	3	113169309	113169309	Nonsense_Mutation	INS	-	5AAATATGAAGG	-	SPICE1	CTGAAACCTTC	34delinsSRKLKTFILVFKSX
XH_P37	3	113187735	113187735	Nonsense_Mutation	INS	-	ATGTCCTCTACC	-	SPICE1	CATGTGTAGAG	5_T256delinsYMMWX
XH_P37	3	118865982	118865982	Frame_Shift_Ins	INS	-	TC	-	C3orf30	c.946_947insTC	p.E316fs
XH_P37	3	118865984	118865984	Frame_Shift_Ins	INS	-	T	-	C3orf30	c.948_949insT	p.E316fs
XH_P37	3	119156952	119156952	Splice_Site	INS	-	ATTTCGCAATGA	-	TMEM39A	-	-
XH_P37	3	120050121	120050121	Frame_Shift_Ins	INS	-	TG	-	LRRCS8	1041_1042insC	p.S348fs
XH_P37	3	120050122	120050122	In_Frame_Ins	INS	-	ATAAACATTTTC	-	LRRCS8	341insACAAAAT	347delinsTQNVLY
XH_P37	3	120424944	120424944	Nonsense_Mutation	INS	-	TTTTCTTCTATG	-	RABL3	TAATCCATAGAA	5delinsKSTIHRKKEEX
XH_P37	3	121151774	121151774	Frame_Shift_Ins	INS	-	AGAAGAGTATG	-	POLQ	insCATCTCATAC	p.D2550fs
XH_P37	3	121151776	121151776	Nonsense_Mutation	INS	-	TTTTTATTTA	-	POLQ	7648insTAAAT	2550_V2551delinsX
XH_P37	3	121200540	121200540	Nonsense_Mutation	INS	-	TATCAAAAA	-	POLQ	9_6090insTTTTT	Q2030delinsHFX
XH_P37	3	121200542	121200542	Frame_Shift_Ins	INS	-	GGTA	-	POLQ	6087_6088insTA	p.Q2030fs
XH_P37	3	121208048	121208048	Frame_Shift_Ins	INS	-	5AAGATAGTTTC	-	POLQ	CAGATAGAAAC	p.T1244fs
XH_P37	3	121208707	121208707	Frame_Shift_Ins	INS	-	CTAAAAATGTAT	-	POLQ	071insGATACAT	p.K1024fs
XH_P37	3	121208709	121208709	In_Frame_Ins	INS	-	TGAGTG	-	POLQ	68_3069insCAC	T1023delinsTTQ
XH_P37	3	121256034	121256034	Nonsense_Mutation	INS	-	GTAATATTTTTC	-	POLQ	CAATAAGAAAAA	18_H219delinsYYTX
XH_P37	3	121340958	121340958	Missense_Mutation	SNP	G	T	G	FBXO40	c.G682T	p.A228S
XH_P37	3	121341223	121341223	Missense_Mutation	SNP	G	A	G	FBXO40	c.G947A	p.R316Q
XH_P37	3	121412681	121412681	In_Frame_Ins	INS	-	TGG	-	GOLGB1	6448_6449insCG	E2150delinsAK
XH_P37	3	121412682	121412682	Nonsense_Mutation	INS	-	TGTCCATGGAAG	-	GOLGB1	5TATATCTTCCA	I2151delinsYIFHGLX
XH_P37	3	121508920	121508920	Nonsense_Mutation	INS	-	TTTCTATCTCTC	-	IQCB1	ATCTGAAGGAT	p.G244delinsIX
XH_P37	3	122496735	122496735	Nonsense_Mutation	INS	-	TGTTTTTGTCTG	-	HSPBAP1	TATACAGACAA	F28_K29delinsX
XH_P37	3	124457079	124457079	In_Frame_Ins	INS	-	ATAGACACAGAT	-	UMPS	976insATAGACA	325delinsQJDTD
XH_P37	3	124536550	124536550	Frame_Shift_Ins	INS	-	CTCTTCT	-	ITGB5	5_1046insAGA	p.T349fs
XH_P37	3	124629344	124629344	Missense_Mutation	SNP	A	C	A	MUC13	c.T1252G	p.F418V
XH_P37	3	124646578	124646578	Frame_Shift_Ins	INS	-	GCACCGCTTTA	-	MUC13	312insTAAAGC	p.D104fs
XH_P37	3	124731653	124731653	Nonsense_Mutation	INS	-	CTAAAAATGCTTC	-	HEG1	insTAGGAGAGC	p.A924delinsX
XH_P37	3	124896777	124896777	Frame_Shift_Ins	INS	-	TGTAGGTGTG	-	SLC12A8	332insTCACACC	p.S144fs
XH_P37	3	124951520	124951520	Frame_Shift_Ins	INS	-	ATTTCCCTTGGT	-	ZNF148	CATTCCCAAGG	p.Q684fs
XH_P37	3	126190998	126190998	Nonsense_Mutation	INS	-	5TTTTTCTGTGT	-	ZXDC	AAATATACACAG	G354delinsKSIHRKNX
XH_P37	3	128627939	128627939	Silent	SNP	T	G	T	ACAD9	c.T1482G	p.L494L

XH_P37	3	129156119	129156119	Nonsense_Mutation	INS	-	AAAAGGATGTG	-	MBD4	8insAAACACATG	5123_L124delinsX
XH_P37	3	129218800	129218800	Missense_Mutation	SNP	C	A	C	IFT122	c.C1931A	p.A644D
XH_P37	3	129289773	129289773	Frame_Shift_Ins	INS	-	AGCAGAGCTTTA	-	PLXND1	06insTGTAAAGC	p.E1202fs
XH_P37	3	129290596	129290596	Frame_Shift_Ins	INS	-	CACATTG	-	PLXND1	58_3169insCAAT	p.V1057fs
XH_P37	3	130188306	130188306	Frame_Shift_Ins	INS	-	TTACAAAGATA	-	COL6A5	CAGATATTACAA	p.P2486fs
XH_P37	3	130300705	130300705	Frame_Shift_Ins	INS	-	NAGGAAAAAGCA	-	COL6A6	49insAAAGGAA	p.S1283fs
XH_P37	3	130405224	130405224	Nonsense_Mutation	INS	-	AGITTTTTCTCT	-	PIK3R4	sACAAAGAGGA	102delinsQQRGKNX
XH_P37	3	130447527	130447527	Frame_Shift_Ins	INS	-	TAGTATGATGTT	-	PIK3R4	ACATACCAACT	p.E529fs
XH_P37	3	130673854	130673854	Splice_Site	INS	-	TGATTTAAACTC	-	ATP2C1	.	.
XH_P37	3	130686063	130686063	Frame_Shift_Ins	INS	-	AAAACATAAT	-	ATP2C1	1183insAAAAAC	p.P394fs
XH_P37	3	130686064	130686064	Frame_Shift_Ins	INS	-	AGTT	-	ATP2C1	183_1184insAG	p.A395fs
XH_P37	3	132166265	132166265	In_Frame_Ins	INS	-	CAATATGTATTC	-	DNAJC13	insATCCAATATG	82delinsTSNNMSY
XH_P37	3	132400801	132400801	Nonsense_Mutation	INS	-	AAAAAGATTTTC	-	NPHP3	TAATAGGAAAAA	T1317delinsYNRKILLNNX
XH_P37	3	133379918	133379918	Nonsense_Mutation	INS	-	AGTACATCATT	-	TOPBP1	ACATAATGATG	p.D18delinsDTX
XH_P37	3	134911560	134911560	Frame_Shift_Ins	INS	-	AT	-	EPHB1	2025_2026insA	p.F675fs
XH_P37	3	134911561	134911561	In_Frame_Ins	INS	-	AAAGAGATTAC	-	EPHB1	AAACACAAAAG	76delinsGKHKRITKVH
XH_P37	3	135721304	135721304	Nonsense_Mutation	INS	-	TTTATGCTATTG	-	PPP2R3A	TTTTCTTTATGCG	p.F322delinsX
XH_P37	3	138256168	138256168	Nonsense_Mutation	INS	-	TTTTTGTCTTAC	-	CEP70	CTCTAGAACAA	p.K11delinsDLX
XH_P37	3	138762838	138762838	Frame_Shift_Ins	INS	-	TAGATGCTTTTT	-	PRR23C	insTCAAAAAG	p.R209fs
XH_P37	3	140675488	140675488	In_Frame_Ins	INS	-	TTTGCCAAACATA	-	SLC25A36	162insTTTGCCA	A54delinsALPTY
XH_P37	3	140692776	140692776	Nonsense_Mutation	INS	-	TTACTGAT	-	SLC25A36	1_672insTTACT	R24_D225delinsSYX
XH_P37	3	140692778	140692778	Nonsense_Mutation	INS	-	TTAAAGTAAAGT	-	SLC25A36	sGTTTTTTTAAAG	D225delinsGFLKX
XH_P37	3	141164711	141164711	Frame_Shift_Ins	INS	-	CTCCAGTATGGA	-	ZBTB38	nsCTTTTCTCCAG	p.V1161fs
XH_P37	3	142272215	142272215	Nonsense_Mutation	INS	-	AATATTTATACAT	-	ATR	ATAAAACATGTA	887_A888delinsKX
XH_P37	3	142522994	142522994	Nonsense_Mutation	INS	-	GTAAAGACAAT	-	TRPC1	insACCTGTAAAG	11_H612delinsHLX
XH_P37	3	142746017	142746017	Nonsense_Mutation	INS	-	TAATACCAAAAA	-	U2SURP	5insTTAATACCA	M25_I26delinsIX
XH_P37	3	142746018	142746018	Nonsense_Mutation	INS	-	AACCTGGAGCA	-	U2SURP	6insTAACCTGG	M25_I26delinsMX
XH_P37	3	143412145	143412145	Frame_Shift_Ins	INS	-	AA	-	SLC9A9	c.537_538insTT	p.I180fs
XH_P37	3	143412147	143412147	Nonsense_Mutation	INS	-	TTTCTATTTTCT	-	SLC9A9	insGAAAGAAAA	179_1180delinsX
XH_P37	3	143691687	143691687	Silent	SNP	C	T	C	C3orf58	c.C513T	p.P171P
XH_P37	3	147113798	147113798	Frame_Shift_Ins	INS	-	TGGGGGAA	-	ZIC4	8_679insCTTCC	p.E227fs
XH_P37	3	148459207	148459207	Frame_Shift_Ins	INS	-	GAATTGTGTGC	-	AGTR1	insGTCGAATT	p.A129fs
XH_P37	3	148714156	148714156	In_Frame_Ins	INS	-	TGATGCTTT	-	GYG1	1_212insTGATG	H71delinsLMLY
XH_P37	3	148930338	148930338	Frame_Shift_Ins	INS	-	AACTATTTTTTT	-	CP	nsTAAAAAAAAA	p.K98fs
XH_P37	3	149042680	149042680	Nonsense_Mutation	INS	-	CATTCAATGCTCT	-	TM4SF18	CTCTCAAGACATT	3_T134delinsPDQIE
XH_P37	3	149238759	149238759	In_Frame_Ins	INS	-	CACTACCATTGT	-	WWTR1	5insGTTACAATG	346delinsVTMVI
XH_P37	3	149485171	149485171	Frame_Shift_Ins	INS	-	TCCTCTCTCTCA	-	ANKUB1	8insGATGAGAA	p.N426fs
XH_P37	3	149684339	149684339	In_Frame_Ins	INS	-	ATTCTGTTCACCT	-	PNF2	AACAAAAGTAA	20delinsQNKSEQNYF
XH_P37	3	150908686	150908686	Frame_Shift_Ins	INS	-	GTGCTGCTCTCT	-	MED12L	insCTGCTGCTG	p.H646fs
XH_P37	3	150908687	150908687	In_Frame_Ins	INS	-	CATCCGCCATGA	-	MED12L	8insGTTTCATCCG	646delinsQFIRHVD
XH_P37	3	151163319	151163319	Nonsense_Mutation	INS	-	TTACATTCTACTG	-	IGSF10	CATGGGAGTAGB	84_A1485delinsAWEX
XH_P37	3	154002700	154002700	Nonsense_Mutation	INS	-	STTTTATAGAA	-	DHX36	ATGACATTCTAA	689_K690delinsEX
XH_P37	3	156745908	156745908	Nonsense_Mutation	INS	-	TGGAAATATAT	-	LEKR1	sCACTTTTGGAA	2delinsTWALLEIYKFLX
XH_P37	3	156983447	156983447	Frame_Shift_Ins	INS	-	AGTTG	-	VEPH1	997_1998insCA	p.V666fs
XH_P37	3	156983449	156983449	Frame_Shift_Ins	INS	-	TTTTTAGTTG	-	VEPH1	1996insCAACT	p.V666fs
XH_P37	3	158262051	158262051	Frame_Shift_Ins	INS	-	TCACCTTTGTAG	-	RSRC1	insAACTCACT	p.S273fs
XH_P37	3	158402343	158402343	Nonsense_Mutation	INS	-	AAAATGTTTAA	-	GFM1	TTTTTTAAAAATG	L599delinsQXX
XH_P37	3	160679649	160679649	In_Frame_Ins	INS	-	TCATTTTTAGTA	-	PPM1L	insTCGTCATTTT	548delinsSSFLVS
XH_P37	3	165504041	165504041	Frame_Shift_Ins	INS	-	AACTCTACTATA	-	BCHE	576insTATAGTA	p.Q526fs
XH_P37	3	167006728	167006728	Nonsense_Mutation	INS	-	TAGGAAATAAT	-	ZBBX	sCAAAATATTATT	delinsAISLTFCKYFLIHCYRKX
XH_P37	3	167034877	167034877	Nonsense_Mutation	INS	-	AATTTTTTTGGAT	-	ZBBX	10insCATCCAA	370delinsVIOKXN
XH_P37	3	167034879	167034879	Missense_Mutation	SNP	C	A	C	ZBBX	c.G1108T	p.V370L
XH_P37	3	167189551	167189551	Nonsense_Mutation	INS	-	GTTCCAGGATAA	-	SERPINI2	ATTTCTTTATCCT	Q24_K25delinsHX
XH_P37	3	167189553	167189553	Nonsense_Mutation	SNP	G	A	G	SERPINI2	c.C70T	p.Q24X
XH_P37	3	167728064	167728064	Frame_Shift_Ins	INS	-	GAATATATTTTG	-	GOLIM4	insTTATCAAAAT	p.E667fs
XH_P37	3	167728065	167728065	Frame_Shift_Ins	INS	-	GT	-	GOLIM4	1998_1999insA	p.E667fs
XH_P37	3	168833508	168833508	Frame_Shift_Ins	INS	-	G	-	MECOM	1587_1588ins	p.L530fs
XH_P37	3	168833509	168833509	Frame_Shift_Ins	INS	-	GTGATATGGAA	-	MECOM	1587insTTCCA	p.S529fs
XH_P37	3	173996814	173996814	Nonsense_Mutation	INS	-	TTTTAGATGAT	-	NLGN1	1024insTTTTAG	41_L342delinsEFX
XH_P37	3	173996816	173996816	Frame_Shift_Ins	INS	-	TTGGGTAA	-	NLGN1	5_1026insTTGG	p.L342fs
XH_P37	3	178919265	178919265	Frame_Shift_Ins	INS	-	ATTACTTTATCCA	-	PIK3CA	CTATCATTAATT	p.Y250fs
XH_P37	3	179051684	179051684	Frame_Shift_Ins	INS	-	GGTAGAGAGAAAC	-	ZNF639	nsTATTGGTAGA	p.H311fs
XH_P37	3	182538122	182538122	Nonsense_Mutation	INS	-	TTAGCTGGTCAAC	-	ATP11B	TTTTATTAGCTG	p.Y34delinsYCX
XH_P37	3	182871823	182871823	Frame_Shift_Ins	INS	-	AGGACTATAAC	-	LAMP3	GATAGTGTATA	p.P136fs
XH_P37	3	183245744	183245744	Frame_Shift_Ins	INS	-	AGCTGGGC	-	KLHL6	7_348insGCCCA	p.K116fs
XH_P37	3	183707163	183707163	Nonsense_Mutation	INS	-	GTT	-	ABCC5	137_138insAA	p.C46delinsX
XH_P37	3	183707164	183707164	Frame_Shift_Ins	INS	-	AAGTG	-	ABCC5	136_137insCAC	p.C46fs
XH_P37	3	184020536	184020536	In_Frame_Ins	INS	-	ACCAACTCCATG	-	PSMD2	sTTCTACCAACT	81delinsVFYQLHVI
XH_P37	3	184093778	184093778	Frame_Shift_Ins	INS	-	ACCATAGCTCTC	-	THPO	sAGAGAGAGCT	p.L13fs
XH_P37	3	185993440	185993440	Frame_Shift_Ins	INS	-	ATTGTCCCAA	-	DGKG	806insTTGGGA	p.D269fs
XH_P37	3	185997718	185997718	Frame_Shift_Ins	INS	-	T	-	DGKG	c.713_714insA	p.G238fs
XH_P37	3	185997720	185997720	Nonsense_Mutation	INS	-	TACATTATTTGT	-	DGKG	GGATACAAAT	G238_F239delinsX
XH_P37	3	186272407	186272407	Frame_Shift_Ins	INS	-	T	-	TBCCD1	c.891dupA	p.G298fs
XH_P37	3	186272409	186272409	Nonsense_Mutation	INS	-	TTCTATGTATT	-	TBCCD1	sTAATAAAATACA	97_G298delinsINTX
XH_P37	3	193365903	193365903	Nonsense_Mutation	INS	-	AACTGAATTTCT	-	OPA1	TGTATTAACTGAB	R548delinsLYX
XH_P37	3	194061852	194061852	Missense_Mutation	SNP	G	A	G	CPN2	c.C1580T	p.S527L
XH_P37	3	194158105	194158105	Frame_Shift_Ins	INS	-	CAGTCATCATCA	-	ATP13A3	934insATGATG	p.R645fs
XH_P37	3	195515902	195515902	Frame_Shift_Ins	INS	-	ACAAGAAC	-	MUC4	8_2549insGTTC	p.A850fs
XH_P37	3	195515904	195515904	Silent	SNP	G	A	G	MUC4	c.C2547T	p.S849fs
XH_P37	3	196230026	196230026	Nonsense_Mutation	INS	-	AGAATCAGAGG	-	RNF168	9insTTCTCTGTA	p.A7delinsFLX
XH_P37	3	196386792	196386792	Missense_Mutation	SNP	T	C	T	NRROS	c.T278C	p.L93P
XH_P37	3	196675428	196675428	Missense_Mutation	SNP	C	T	C	PIGZ	c.G340A	p.G114R
XH_P37	3	196743242	196743242	Splice_Site	INS	-	CACCAGGGA	-	MELTF	.	.
XH_P37	3	196812573	196812573	Nonsense_Mutation	INS	-	TTAATTTGTGAC	-	DLG1	ATGTTGTACAA	9delinsLHPCCHKLKIX
XH_P37	3	196888573	196888573	Nonsense_Mutation	INS	-	TATAAAATTTCT	-	DLG1	AAATGAAATTT	p.P174delinsKX
XH_P37	3	197423867	197423867	In_Frame_Ins	INS	-	CTGCCATTCTC	-	RUBCN	315insGAGAAA	439delinsEKWQS
XH_P37	4	154943	154943	Frame_Shift_Ins	INS	-	TTTCTCATGTCC	-	ZNF718	CCAGTGTTCCTCA	p.S156fs
XH_P37	4	366608	366608	Nonsense_Mutation	INS	-	TTACAAATATTAT	-	ZNF141	AAAAATTACAAA	G53delinsEIKITNYPTX
XH_P37	4	1389361	1389457	Frame_Shift_Del	DEL	ATGTGGAGT	-	CATGTGGAGTG	CRIPAK	c.1062_1158del	p.L354fs
XH_P37	4	2083462	2083462	Nonsense_Mutation	INS	-	GTCACTCTTTGTA	-	POLN	206insCTACAAA	36_S737delinsLQRX
XH_P37	4	2955304	2955304	In_Frame_Ins	INS	-	CTGCTGTGTGT	-	NOP14	1insTTACACAC	227delinsDYTQVQ
XH_P37	4	3134640	3134640	Splice_Site	INS	-	TCTAATG	-	HTT	.	.
XH_P37	4	3205873	3205873	Nonsense_Mutation	INS	-	TTTAAT	-	HTT	716_5717insTTT	p.V1906delinsVX
XH_P37	4	3205875	3205875	Nonsense_Mutation	INS	-	CTAAACACAGAC	-	HTT	nsTAGTTCTCTAAA	p.V1906delinsVX
XH_P37	4	4242118	4242118	Nonsense_Mutation	INS	-	CTAGTTATTATA	-	TMEM128	TGCTTTAAATA	110delinsHLLCFKX
XH_P37	4	4304019	4304022	Frame_Shift_Del	DEL	CCCC	-	CCCC	ZBTB49	c.456_459del	p.Y152fs
XH_P37	4	7000864	7000864	Nonsense_Mutation	INS	-	TAACATCTA	-	TBC1D14	8_259insTAACA	p.V86delinsVX
XH_P37	4	7000865	7000865	Frame_Shift_Ins	INS	-	AC	-	TBC1D14	c.259_260insAC	p.E87fs

XH_P37	4	7056211	7056211	Frame_Shift_Ins	INS	-	ACAGAGA	-	TADA2B	93_694insACAG	p.A231fs
XH_P37	4	7056212	7056212	Frame_Shift_Ins	INS	-	G	-	TADA2B	c.694_695insG	p.F232fs
XH_P37	4	9213868	9213868	Missense_Mutation	SNP	G	C	G	USP17L10	c.G1486C	p.D496H
XH_P37	4	9251647	9251647	Frame_Shift_Ins	INS	-	AGAAGTGATGC	-	USP17L11	293insCAGAA	p.E431fs
XH_P37	4	10447574	10447574	Missense_Mutation	SNP	C	T	C	ZN518B	c.G379A	p.V127I
XH_P37	4	10447575	10447575	Nonsense_Mutation	INS	-	GTACTATGGTG	-	ZN518B	AATAGCACCAT	26_V127delinsNHFX
XH_P37	4	10567701	10567701	Frame_Shift_Ins	INS	-	TCCTTTCTGAA	-	CLNK	GTGTTTTCAGAA	p.R75fs
XH_P37	4	13370268	13370268	Missense_Mutation	SNP	C	T	C	RAB28	c.G580A	p.V194M
XH_P37	4	13370270	13370270	In_Frame_Ins	INS	-	TTGCTATTG	-	RAB28	7_578insCAATA	V193delinsAIAM
XH_P37	4	13605245	13605245	In_Frame_Ins	INS	-	ATGAATTGAGA	-	BOD1L1	9insAAGTTCTCA	1093delinsTSSQFIL
XH_P37	4	13612692	13612692	In_Frame_Ins	INS	-	AGA	-	BOD1L1	1356_1357insT	p.T453delinsST
XH_P37	4	13612693	13612693	Frame_Shift_Ins	INS	-	ACATGTGACAGA	-	BOD1L1	insCATCTCTGTC	p.K452fs
XH_P37	4	13616325	13616325	Frame_Shift_Ins	INS	-	ACAGGAAAGCA	-	BOD1L1	69insCTGCTTTC	p.E223fs
XH_P37	4	15518365	15518365	Frame_Shift_Ins	INS	-	ACATATATATT	-	CC2D2A	GTGTCAACATAT	p.T379fs
XH_P37	4	15688732	15688732	Frame_Shift_Ins	INS	-	TTGAATCGAAT	-	FAM200B	133insTTGAAT	p.Q44fs
XH_P37	4	15688734	15688734	Missense_Mutation	SNP	C	T	C	FAM200B	c.C134T	p.T45I
XH_P37	4	15689956	15689956	Nonsense_Mutation	INS	-	CACCATTATTAG	-	FAM200B	ACACAGCACCAT	52delinsDSTQHHYX
XH_P37	4	16026917	16026917	Frame_Shift_Ins	INS	-	G	-	PROM1	c.500_501insC	p.G167fs
XH_P37	4	16026919	16026919	In_Frame_Ins	INS	-	AGAATTGGTGT	-	PROM1	ATAAAAAACACC	67delinsKIKTPIKFG
XH_P37	4	17885899	17885899	Frame_Shift_Ins	INS	-	AA	-	LCORL	.1252_1253insT	p.R418fs
XH_P37	4	17885900	17885900	Frame_Shift_Ins	INS	-	TGTTGACTCT	-	LCORL	1252insAGAGT	p.R418fs
XH_P37	4	20706377	20706377	Frame_Shift_Ins	INS	-	CCCTCTGATT	-	PACRGL	148insCCCTCT	p.E49fs
XH_P37	4	24531358	24531358	Frame_Shift_Ins	INS	-	CCCTTCCTTT	-	DHX15	2136insAAAGG	p.T712fs
XH_P37	4	25256870	25256870	In_Frame_Ins	INS	-	TAATAATCTTA	-	PI4K2B	AAAAGTAAAAA	03delinsKKVKILLDF
XH_P37	4	36230629	36230629	In_Frame_Ins	INS	-	AAATGGAACAA	-	ARAP2	480insTTTGTTC	H160delinsHLFFH
XH_P37	4	37447439	37447439	Frame_Shift_Ins	INS	-	AACAGAAAGAC	-	NWD2	3830insAACAG	p.I1277fs
XH_P37	4	37448332	37448332	Frame_Shift_Ins	INS	-	CC	-	NWD2	.4722_4723insC	p.R1574fs
XH_P37	4	37848718	37848718	Frame_Shift_Ins	INS	-	ACTCTAAAGT	-	PGM2	1175insACTCT	p.G392fs
XH_P37	4	38798825	38798825	Frame_Shift_Ins	INS	-	ATCTGCGCTGG	-	TLR1	628insACCAGG	p.S543fs
XH_P37	4	38990576	38990576	Nonsense_Mutation	INS	-	ATCTTCTCTGAC	-	TMEM156	nsGAGTAGAAG	212_K213delinsEX
XH_P37	4	39274644	39274644	Frame_Shift_Ins	INS	-	T	-	WDR19	-3048_3049ins	p.L1016fs
XH_P37	4	39274646	39274646	Frame_Shift_Ins	INS	-	CTCTGCTTTTCA	-	WDR19	051insGCTCTG	p.I1017fs
XH_P37	4	39310386	39310386	Frame_Shift_Ins	INS	-	GTGCAGTACT	-	RFC1	1755insAGTAC	p.L585fs
XH_P37	4	39344065	39344065	Nonsense_Mutation	INS	-	TGCTTTGTGAG	-	RF1	ATAACTCAACA	p.L77delinsLX
XH_P37	4	39408870	39408870	Frame_Shift_Ins	INS	-	TTCTATAGCGT	-	KL10	TTGTATTCTCTAT	p.K101fs
XH_P37	4	40099007	40099007	Nonsense_Mutation	INS	-	GCAATAAAAA	-	N4BP2	3AAAGCAATTA	p.T16delinsTX
XH_P37	4	40103933	40103933	Frame_Shift_Ins	INS	-	CTTGATATCAGT	-	N4BP2	9insATCTTGGA	p.S156fs
XH_P37	4	40104353	40104353	Missense_Mutation	SNP	C	A	C	N4BP2	c.C888A	p.N296K
XH_P37	4	40104355	40104355	In_Frame_Ins	INS	-	GTGAAGGTAAT	-	N4BP2	nsGAATGTGAAG	97delinsLNVKVMG
XH_P37	4	41635675	41635675	In_Frame_Ins	INS	-	AATCTCCCT	-	LIMCH1	0_1941insAATC	D647delinsEISL
XH_P37	4	42457378	42457378	Frame_Shift_Ins	INS	-	GATA	-	ATP8A1	2707_2708insTA	p.E903fs
XH_P37	4	42457379	42457379	Nonsense_Mutation	INS	-	GGCAGAGAAGG	-	ATP8A1	2707insACCTTC	03_N904delinsTFSAX
XH_P37	4	47427734	47427734	Missense_Mutation	SNP	G	A	G	GABRB1	c.G1124A	p.R375Q
XH_P37	4	47559835	47559835	Nonsense_Mutation	INS	-	ATTAGATATAAA	-	ATP10D	AAATAAAATAG	60_P661delinsLEINX
XH_P37	4	47850332	47850332	Nonsense_Mutation	INS	-	GGACAGAATGT	-	NFXL1	AAAGTTTAAACAT	p.N862delinsX
XH_P37	4	48581108	48581108	In_Frame_Ins	INS	-	TCAGCTTTCAT	-	FRYL	10insCATATGAA	804delinsHMKADS
XH_P37	4	52883425	52883425	Frame_Shift_Ins	INS	-	GGAA	-	LRR66	354_355insTTC	p.N119fs
XH_P37	4	52883427	52883427	In_Frame_Ins	INS	-	TATAGTGTG	-	LRR66	2_353insCACAC	N118delinsTHYN
XH_P37	4	55156615	55156615	Nonsense_Mutation	INS	-	ATAACATTCAT	-	PDGFR4	AACTCTATAAAC	11007delinsEFFHNSINIHX
XH_P37	4	57265517	57265517	Nonsense_Mutation	INS	-	ATAAATTAACCT	-	PPAT	TAATAAAAGGT	55delinsIKVNLVLYX
XH_P37	4	57397076	57397076	Silent	SNP	G	A	G	THEGL	c.G234A	p.E78E
XH_P37	4	57397077	57397077	Frame_Shift_Ins	INS	-	AGAAACTCTTGG	-	THEGL	6insTTAGAACT	p.P79fs
XH_P37	4	57796663	57796663	In_Frame_Ins	INS	-	CTCTTTTGAGAC	-	REST	CTCTTTTCTCTTT	47delinsAFSLRLHLL
XH_P37	4	66217285	66217285	Nonsense_Mutation	INS	-	GAAAGAGAGAC	-	EPHA5	CTCTATTCTCTCT	V757delinsLILSLFSX
XH_P37	4	68472071	68472071	Frame_Shift_Ins	INS	-	GGTGTGTTTAA	-	STAP1	85insTGGTGTG	p.A295fs
XH_P37	4	68497606	68497606	Nonsense_Mutation	INS	-	TTTAATGTAA	-	UBA6	AAATAATTTAA	C1_F722delinsWDEIIX
XH_P37	4	69962362	69962362	Nonsense_Mutation	INS	-	ATCTGTTCACAC	-	UGT2B7	AAATGATCTGT	12_L43delinsNEGKX
XH_P37	4	69964374	69964374	Frame_Shift_Ins	INS	-	CAAGATAATTAC	-	UGT2B7	39insACAAGATA	p.L280fs
XH_P37	4	70066372	70066372	Missense_Mutation	SNP	C	A	C	UGT2B11	c.G1376T	p.R459L
XH_P37	4	70066374	70066374	Frame_Shift_Ins	INS	-	SAAGGGAAAAA	-	UGT2B11	CTAATCTCTTTT	p.D458fs
XH_P37	4	70146411	70146411	Missense_Mutation	SNP	G	A	G	UGT2B28	c.G193A	p.D65N
XH_P37	4	70146412	70146412	Frame_Shift_Ins	INS	-	STCACTGTTTCT	-	UGT2B28	195insGTCACTG	p.D65fs
XH_P37	4	70599137	70599137	Frame_Shift_Ins	INS	-	CTGCAATATTTC	-	SULT1B1	insAGGAAATAA	p.M197fs
XH_P37	4	71472097	71472097	Nonsense_Mutation	INS	-	CACATGCTATT	-	AMBN	CTCATCACATG	N332delinsITCYX
XH_P37	4	71507937	71507937	Frame_Shift_Ins	INS	-	AAATCAATAAT	-	ENAM	AATGGAAATCA	p.N265fs
XH_P37	4	71509605	71509605	Frame_Shift_Ins	INS	-	CTTGTTTGTGAT	-	ENAM	3insTCCCTTGG	p.P821fs
XH_P37	4	71509607	71509607	Missense_Mutation	SNP	A	T	A	ENAM	c.A2464T	p.I822L
XH_P37	4	71555610	71555610	In_Frame_Ins	INS	-	TAGGTAAACAAG	-	UTP3	TTTCGTGAGTGA	06delinsISVGNKPPY
XH_P37	4	71698131	71698131	Frame_Shift_Ins	INS	-	AAATTTTATAGA	-	GRSF1	CAAAATCTATA	p.M74fs
XH_P37	4	72306492	72306492	Splice_Site	INS	-	TCCTGTGG	-	SLC4A4	.	.
XH_P37	4	73013492	73013492	Missense_Mutation	SNP	A	G	A	NPFFR2	c.A1532G	p.E511G
XH_P37	4	73013493	73013493	Frame_Shift_Ins	INS	-	TTGACACGTCT	-	NPFFR2	1534insTTGAC	p.E511fs
XH_P37	4	73185128	73185128	Frame_Shift_Ins	INS	-	AA	-	ADAMT53	.1272_1273insT	p.M425fs
XH_P37	4	73185129	73185129	Nonsense_Mutation	INS	-	ATATAAGTAAA	-	ADAMT53	5TAAAGTTTAC	M425delinsVSKLLIFX
XH_P37	4	73186550	73186550	Frame_Shift_Ins	INS	-	ATACATT	-	ADAMT53	82_983insAATG	p.S328fs
XH_P37	4	73959942	73959942	Nonsense_Mutation	INS	-	TAGCTTAATGA	-	ANKRD17	CTGATTTTCATT	K1477delinsSHMAVFXH
XH_P37	4	74008083	74008083	Frame_Shift_Ins	INS	-	AGTCTGTTTGT	-	ANKRD17	ATATTTACAAAC	p.I589fs
XH_P37	4	76452388	76452388	Frame_Shift_Ins	INS	-	TTACACTGTAG	-	THAP6	insCCATTACAC	p.C169fs
XH_P37	4	76956486	76956486	Nonsense_Mutation	INS	-	STGGACCACTAG	-	CXCL11	TTCTGTAGTTTG	24_F25delinsRIFLX
XH_P37	4	77033573	77033573	In_Frame_Ins	INS	-	AATTTT	-	ART3	005_1006insAAT	V5335delinsSNF
XH_P37	4	77278640	77278640	Frame_Shift_Ins	INS	-	GAGAAATATAC	-	CCDC158	TACTATTGTATA	p.S687fs
XH_P37	4	78641711	78641711	In_Frame_Ins	INS	-	GTCTCTTTCAT	-	CNOT6L	42insTAATGAA	514delinsDNERNL
XH_P37	4	79359737	79359737	Frame_Shift_Ins	INS	-	TCCTTTGATAACA	-	FRAS1	AATTCCTCTTTG	p.P1744fs
XH_P37	4	79847859	79847859	Frame_Shift_Ins	INS	-	GAGTGTAGTTA	-	PAQR3	AAATATTAACT	p.V173fs
XH_P37	4	81207609	81207609	Frame_Shift_Ins	INS	-	GTTGTGGCGATC	-	FGF5	TTTAAAGTTGGC	p.K54fs
XH_P37	4	81866074	81866074	Nonsense_Mutation	INS	-	TATAATGCATTA	-	C4orf22	AGATGTATAATG	.1196delinsNIYX
XH_P37	4	81866076	81866076	Missense_Mutation	SNP	C	A	C	C4orf22	c.C589A	p.L197I
XH_P37	4	82366778	82366778	Frame_Shift_Ins	INS	-	GTATG	-	RASGEF1B	703_704insCAT	p.V235fs
XH_P37	4	82366779	82366779	Nonsense_Mutation	INS	-	ATTGTTGGAATG	-	RASGEF1B	5TAAACATTC	p.V235delinsX
XH_P37	4	83763552	83763552	In_Frame_Ins	INS	-	AGGGATTG	-	SEC31A	1_2592insCAAA	T864delinsTKSL
XH_P37	4	83772756	83772756	In_Frame_Ins	INS	-	AATTAGAATTGA	-	SEC31A	2039insTCAATT	D680delinsVNSNY
XH_P37	4	83772758	83772758	Splice_Site	INS	-	A	-	SEC31A	.	.
XH_P37	4	83788085	83788085	Nonsense_Mutation	INS	-	ATACCAAGATG	-	SEC31A	ATAATAACACTT	353_F354delinsLX
XH_P37	4	84511383	84511383	Frame_Shift_Ins	INS	-	CAATC	-	GPAT3	676_677insCAA	p.V226fs
XH_P37	4	85724601	85724601	Frame_Shift_Ins	INS	-	GG	-	WDFY3	2448_2449insC	p.S817fs
XH_P37	4	85724602	85724602	Frame_Shift_Ins	INS	-	GAAAGTTAATA	-	WDFY3	448insAATATTA	p.V816fs
XH_P37	4	85750297	85750297	Nonsense_Mutation	INS	-	AGAATGTATTIT	-	WDFY3	CATTTAAATAAC	272_D273delinsDIX
XH_P37	4	87662971	87662971	Splice_Site	INS	-	TTTGGCAGACCT	-	PTPN13	.	.

XH_P37	4	87671831	87671831	Missense_Mutation	SNP	G	T	G	PTPN13	c.G2859T	p.K953N
XH_P37	4	87671833	87671833	Nonsense_Mutation	INS	-	AAGCAGCATGC	-	PTPN13	ATAAATAAGCA	954delinsNVVNX
XH_P37	4	88766967	88766967	Frame_Shift_Ins	INS	-	ATGGGTGCTTTT	-	MEPE	48insGATGGGTG	p.T316fs
XH_P37	4	88766969	88766969	Missense_Mutation	SNP	A	T	A	MEPE	c.A949T	p.I317F
XH_P37	4	90169810	90169810	Frame_Shift_Ins	INS	-	AAGAACCAGGAC	-	GPRIN3	insTGCTCTCCTG	p.G484fs
XH_P37	4	90856248	90856248	Frame_Shift_Ins	INS	-	T	-	MMRN1	c.1417_1418ins	p.T473fs
XH_P37	4	90856250	90856250	Nonsense_Mutation	INS	-	GTACATTAATGC	-	MMRN1	1420insGTACAT	73_C474delinsTVHX
XH_P37	4	94411822	94411822	Nonsense_Mutation	INS	-	TTACCTTTTATTA	-	GRID2	AATTAATTACCT	536_M537delinsLX
XH_P37	4	94411824	94411824	Silent	SNP	A	T	A	GRID2	c.A1608T	p.R536R
XH_P37	4	99812397	99812397	Nonsense_Mutation	INS	-	AATTGGTGATT	-	EIF4E	insCATAATCACD	D91_F92delinsAX
XH_P37	4	99812398	99812398	Nonsense_Mutation	INS	-	TTTA	-	EIF4E	270_271insTAA	D91_F92delinsX
XH_P37	4	100512921	100512921	Frame_Shift_Ins	INS	-	TGAAATGGGTCT	-	MTTP	sCAATTGAAATG	p.Q271fs
XH_P37	4	100522869	100522869	In_Frame_Ins	INS	-	TTTTTGTCTTTGA	-	MTTP	4insGAATTTTGG	475delinsRILLRQ
XH_P37	4	100851764	100851764	In_Frame_Ins	INS	-	TGG	-	DNAJB14	c.147_148insCC	p.I50delinsPI
XH_P37	4	100851766	100851766	Frame_Shift_Ins	INS	-	TTAATGTACT	-	DNAJB14	146insAGTACA	p.I49fs
XH_P37	4	102984291	102984291	In_Frame_Ins	INS	-	ATTCCATGTTGT	-	BANK1	DinsGTCATTCCA	603delinsVVIPICCR
XH_P37	4	103987655	103987655	Frame_Shift_Ins	INS	-	ATGGTAAGGATC	-	SLC9B2	DinsTTTCATCCTT	p.V34fs
XH_P37	4	103988642	103988642	Frame_Shift_Ins	INS	-	TATGAAACGCTT	-	SLC9B2	5insAAAGCGCTT	p.T22fs
XH_P37	4	104016396	104016396	In_Frame_Ins	INS	-	GATAAAAAATAAT	-	BDH2	insGTTATTATT	N39delinsVIIIFIIN
XH_P37	4	105412195	105412195	Frame_Shift_Ins	INS	-	AGAAAAAAACCT	-	CXXC4	65insCAGGTTT	p.T25fs
XH_P37	4	106158017	106158017	Frame_Shift_Ins	INS	-	TGTGACTTCTGC	-	TET2	919insTTGTGAC	p.C973fs
XH_P37	4	106158192	106158192	Frame_Shift_Ins	INS	-	CTTTTGTGATTTG	-	TET2	904insGCTTTTGT	p.H1031fs
XH_P37	4	106164912	106164912	Silent	SNP	T	C	T	TET2	c.T3780C	p.N1260N
XH_P37	4	106164913	106164913	Frame_Shift_Ins	INS	-	AAACAAAAACAAG	-	TET2	782insAAAAACA	p.R1261fs
XH_P37	4	106193719	106193719	Splice_Site	INS	-	GAAAAATAGCAAC	-	TET2	.	.
XH_P37	4	106197656	106197656	Frame_Shift_Ins	INS	-	TTTTT	-	TET2	989_5990insTT	p.P1997fs
XH_P37	4	106197657	106197657	In_Frame_Ins	INS	-	AGCCAT	-	TET2	90_5991insAGG	P1997delinsPAI
XH_P37	4	106604317	106604317	Frame_Shift_Ins	INS	-	AACTAAGTGGGA	-	INTS12	2insATCCCACT	p.P321fs
XH_P37	4	108866284	108866284	Frame_Shift_Ins	INS	-	TA	-	CYP2U1	c.649_650insTA	p.P217fs
XH_P37	4	108866286	108866286	Frame_Shift_Ins	INS	-	ATGGAGTGCA	-	CYP2U1	652insATGGGAC	p.P217fs
XH_P37	4	110864539	110864539	In_Frame_Ins	INS	-	ACAACAAAAATTA	-	EGF	458insACAACA	L153delinsHNKII
XH_P37	4	111471041	111471041	Frame_Shift_Ins	INS	-	AT	-	ENPEP	2500_2501insA	p.R834fs
XH_P37	4	111471042	111471042	Nonsense_Mutation	INS	-	TTCTAAGCATAA	-	ENPEP	insTGCTCTCTAA	34_Y835delinsSVFX
XH_P37	4	113187838	113187838	Nonsense_Mutation	INS	-	AATATCTGCTCTC	-	AP1AR	TAACAATTATCT	F0_T171delinsSRFLIX
XH_P37	4	113189527	113189527	Frame_Shift_Ins	INS	-	TTTT	-	AP1AR	772_773insTTT	p.G258fs
XH_P37	4	113189528	113189528	Frame_Shift_Ins	INS	-	GAACGTCTCT	-	AP1AR	774insGAACGT	p.G258fs
XH_P37	4	113481933	113481933	Nonsense_Mutation	INS	-	TGTATGGCTAAG	-	ZGRF1	TCATAAECTTAG	V1581delinsDEX
XH_P37	4	113508855	113508855	Frame_Shift_Ins	INS	-	AGAAAGTACTTT	-	ZGRF1	sTCAGAGAAAGT	p.E1062fs
XH_P37	4	113510998	113510998	Nonsense_Mutation	INS	-	SATGAAGTTTTT	-	ZGRF1	AAATATAAAAAAC	6delinsFSVSIQKNFILNEX
XH_P37	4	114275990	114275990	Silent	SNP	C	A	C	ANK2	c.C6216A	p.S2072S
XH_P37	4	114275991	114275991	In_Frame_Ins	INS	-	TCCTCTCTGT	-	ANK2	6218insTCCTCT	I2073delinsLSVL
XH_P37	4	114277101	114277101	Frame_Shift_Ins	INS	-	AATCATCTGTCT	-	ANK2	7328insAATCAT	p.L2443fs
XH_P37	4	114277991	114277991	Frame_Shift_Ins	INS	-	TTTGGTTCTTTT	-	ANK2	sTCTTGTTTGGG	p.S2739fs
XH_P37	4	114280072	114280072	Frame_Shift_Ins	INS	-	TGTCTCTGGG	-	ANK2	10299insTGTC	p.T3433fs
XH_P37	4	115544459	115544459	Nonsense_Mutation	INS	-	TAGATGGGGCG	-	UGT8	424insTAGATG	G141_M142delinsDX
XH_P37	4	115769457	115769457	Frame_Shift_Ins	INS	-	AAAAAAACATTAT	-	NDST4	854insCATAATC	p.P618fs
XH_P37	4	118005966	118005966	Nonsense_Mutation	INS	-	TGTTCCGTACTC	-	TRAM11L	CAGTGAGTACG	95_Q196delinsQXQ
XH_P37	4	119644806	119644806	Nonsense_Mutation	INS	-	CTCTGCTATTGA	-	SEC24D	GCAACATCAATG	9_1990delinsMQHQX
XH_P37	4	119736768	119736768	Nonsense_Mutation	INS	-	CTTTGTGTATCC	-	SEC24D	11insGGGTAAAC	A171_P172delinsGX
XH_P37	4	122254154	122254154	Nonsense_Mutation	INS	-	CTCA	-	QRFRP	618_619insTGA	G207_P208delinsX
XH_P37	4	122254155	122254155	Frame_Shift_Ins	INS	-	CTCTAGGTAAT	-	QRFRP	insTAAATTACCT	p.T206fs
XH_P37	4	122740015	122740015	Silent	SNP	T	G	T	CCNA2	c.A1056C	p.P352P
XH_P37	4	122740017	122740017	Nonsense_Mutation	INS	-	TGCCTAGATGT	-	CCNA2	054insAACATC	B52_S353delinsNIX
XH_P37	4	123267880	123267880	Missense_Mutation	SNP	G	A	G	KIAA109	c.G12836A	p.R4279H
XH_P37	4	123305067	123305067	In_Frame_Ins	INS	-	ACCAACTTTTACA	-	ADAD1	TAAACACCAACT	59delinsHKHQLYKSF
XH_P37	4	123663361	123663361	Frame_Shift_Ins	INS	-	A	-	BBS12	c.314_315insA	p.L105fs
XH_P37	4	123663362	123663362	Nonsense_Mutation	INS	-	GGATGATTTTAC	-	BBS12	AATTGGATGA	G5_G106delinsLNKFGX
XH_P37	4	123664018	123664018	Frame_Shift_Ins	INS	-	AGTATTATCTGT	-	BBS12	cCTTCAGTATTA	p.P324fs
XH_P37	4	125590492	125590492	Frame_Shift_Ins	INS	-	AAACAATGCAAG	-	ANKRD50	93insTATCTTGC	p.G1135fs
XH_P37	4	126239555	126239555	Frame_Shift_Ins	INS	-	ACATCATACC	-	FAT4	1990insACATC	p.D663fs
XH_P37	4	128732702	128732702	Frame_Shift_Ins	INS	-	A	-	HSPA4L	c.1366_1367ins	p.V456fs
XH_P37	4	128732703	128732703	Frame_Shift_Ins	INS	-	TAACCTTATTC	-	HSPA4L	1368insTAAC	p.V456fs
XH_P37	4	129043100	129043100	Frame_Shift_Ins	INS	-	AGAAAGAAATTAC	-	LARP1B	ATAAAGAAAGG	p.T186fs
XH_P37	4	140811436	140811436	Missense_Mutation	SNP	A	C	A	MAML3	c.T1154G	p.F385C
XH_P37	4	140811438	140811438	Nonsense_Mutation	INS	-	CTCAACA	-	MAML3	1_1152insTGTT	B84_F385delinsPVX
XH_P37	4	141320150	141320150	Nonsense_Mutation	INS	-	ATTTTITTTAAAC	-	CLGN	CTGATGTTTAA	A7_V248delinsSSSDVX
XH_P37	4	141847194	141847194	Nonsense_Mutation	INS	-	ATTCTTCCCTC	-	RNF150	924insAGGGGA	V308_L309delinsX
XH_P37	4	144449139	144449139	Nonsense_Mutation	INS	-	AGGTGGGAATA	-	SMARCA5	AAAAGAGGTGG	G307_D308delinsIX
XH_P37	4	145628399	145628399	Frame_Shift_Ins	INS	-	CAATGACTTTTA	-	HHIP	CAATACCATGA	p.M382fs
XH_P37	4	149075973	149075973	Frame_Shift_Ins	INS	-	AAAGGTACTTCC	-	NR3C2	D94insTGGAGT	p.P698fs
XH_P37	4	154523693	154523693	Splice_Site	INS	-	AGACGAAAAA	-	TMEM131L	.	.
XH_P37	4	154523695	154523695	Nonsense_Mutation	INS	-	TATAGGAAGAGG	-	TMEM131L	2456insTATAGG	p.F819delinsLX
XH_P37	4	154525255	154525255	Frame_Shift_Ins	INS	-	AGCGAGTTCT	-	TMEM131L	3092insAGGCA	p.I1031fs
XH_P37	4	155156087	155156087	Frame_Shift_Ins	INS	-	TTTTTCTCCATCT	-	DCHS2	352insAGATGG	p.S2784fs
XH_P37	4	155506813	155506813	In_Frame_Ins	INS	-	ATTGAAACTACA	-	FGA	AAAAAGGTGTAG	0delinsQKSVSMTCN
XH_P37	4	156294391	156294391	Nonsense_Mutation	INS	-	TATATTTAAGA	-	MAP9	TTTTTTTCTTAA	K127delinsKSVFVSFX
XH_P37	4	156775253	156775253	In_Frame_Ins	INS	-	TTTAAACAAGA	-	ASIC5	TATCTCTCTGTG	7delinsKJPLVLNCF
XH_P37	4	158257727	158257727	Frame_Shift_Ins	INS	-	GAAAAAGGAAT	-	GRIA2	nsTGGTGAAAA	p.S558fs
XH_P37	4	158257846	158257846	Nonsense_Mutation	INS	-	AGCAATTGCAAC	-	GRIA2	TAATGGAGCAAA	597_L598delinsSX
XH_P37	4	159627447	159627447	In_Frame_Ins	INS	-	AAATACGCTAAC	-	ETFHD	1210insAAATAC	V403delinsVKYAK
XH_P37	4	159782777	159782777	Frame_Shift_Ins	INS	-	ATTATCTGTCTT	-	FNIP2	TTTTTATTATCT	p.L84fs
XH_P37	4	159782779	159782779	Missense_Mutation	SNP	C	G	C	FNIP2	c.C254G	p.T85S
XH_P37	4	164247261	164247261	Nonsense_Mutation	INS	-	TTGTTTTATATT	-	NPY1R	sAATAAATAATA	149_P150delinsKX
XH_P37	4	164247263	164247263	Missense_Mutation	SNP	C	G	C	NPY1R	c.G444C	p.W148C
XH_P37	4	169173752	169173752	Frame_Shift_Ins	INS	-	TGCTTAATAAGA	-	DDX60	CATATATCTTAT	p.A1205fs
XH_P37	4	170028106	170028106	Frame_Shift_Ins	INS	-	GTTCCTTAATGG	-	SH3RF1	90insACCACTTA	p.R797fs
XH_P37	4	170506627	170506627	Nonsense_Mutation	INS	-	GTGTGCTTTTTT	-	NEK1	80insGAAAAAGG	G227_S228delinsX
XH_P37	4	170506629	170506629	Nonsense_Mutation	INS	-	ACTACATTAG	-	NEK1	678insCTAATG	G226_Y227delinsHX
XH_P37	4	170613443	170613443	Nonsense_Mutation	INS	-	GAATCCACTTAA	-	CLCN3	ATGATGAATCAAC	G276_S277delinsX
XH_P37	4	170618693	170618693	Frame_Shift_Ins	INS	-	SGTACCATTGTT	-	CLCN3	1insAAGGTACC	p.LK30fs
XH_P37	4	175897678	175897678	Nonsense_Mutation	INS	-	CAATGAGGTTTT	-	ADAM29	insCTACAATGA	B4_G335delinsLLQX
XH_P37	4	177032740	177032740	Nonsense_Mutation	INS	-	SACAGGAAGTCT	-	WDR17	insTGACAGGAA	Q3_V4delinsQX
XH_P37	4	177632805	177632805	Splice_Site	INS	-	GTGAAATTTACT	-	VEGFC	.	.
XH_P37	4	186085300	186085300	Nonsense_Mutation	INS	-	CA	-	CFAP97	1353_1354insT	F452_V453delinsX
XH_P37	4	186283777	186283777	Missense_Mutation	SNP	G	C	G	SNX25	c.G2354C	p.S785T
XH_P37	4	187517755	187517755	In_Frame_Ins	INS	-	ACTTTTTTGGAT	-	FAT1	12939insATTCCA	G4313delinsPSKKV
XH_P37	4	187524621	187524621	Nonsense_Mutation	INS	-	GAAATGCTGCT	-	FAT1	059insTAACAG	p.E3687delinsX
XH_P37	4	187524845	187524845	Frame_Shift_Ins	INS	-	G	-	FAT1	c.10834dupC	p.L3612fs

XH_P37	4	187524847	187524847	Nonsense_Mutation	INS	-	AATCATTGG	-	FAT1	2_10833insCCAA	L3611delinsLOX
XH_P37	4	187539653	187539653	Missense_Mutation	SNP	G	A	G	FAT1	c.C8087T	p.P2696L
XH_P37	4	187541497	187541497	Frame_Shift_Ins	INS	-	CCTT	-	FAT1	242_6243insAA	p.F2081fs
XH_P37	4	187541498	187541498	Nonsense_Mutation	INS	-	AAAGAATATCTT	-	FAT1	2insAACAAAGAT	p.F2081delinsX
XH_P37	4	187542585	187542585	Frame_Shift_Ins	INS	-	AA	-	FAT1	.5154_5155insT	p.I1719fs
XH_P37	4	187542587	187542587	Frame_Shift_Ins	INS	-	ACTCAATGCT	-	FAT1	5153insAGCAT	p.T1718fs
XH_P37	4	187557349	187557349	In_Frame_Ins	INS	-	TGCTTTCAACTA	-	FAT1	ATATTATAGTTG	338delinsNIIVESKFS
XH_P37	4	187628850	187628850	Frame_Shift_Ins	INS	-	AAGACAAGGAG	-	FAT1	32insTACCTCCT	p.A711fs
XH_P37	4	189012829	189012829	Frame_Shift_Ins	INS	-	AAGAATTTTAT	-	TRIML2	12insTTTATAAA	p.K338fs
XH_P37	4	189022359	189022359	Frame_Shift_Ins	INS	-	ATATGAGGATG	-	TRIML2	AAACAACATCCT	p.M111fs
XH_P37	4	189022361	189022361	Missense_Mutation	SNP	C	A	C	TRIML2	c.G329T	p.S110I
XH_P37	5	1064042	1064042	Missense_Mutation	SNP	C	T	C	SLC12A7	c.G2656A	p.D886N
XH_P37	5	1081819	1081819	In_Frame_Ins	INS	-	CTCTCTTTTTTG	-	SLC12A7	170insCAAAAAA	V390delinsVKKER
XH_P37	5	1088434	1088434	Silent	SNP	G	A	G	SLC12A7	c.C531T	p.N177N
XH_P37	5	1321918	1321918	Silent	SNP	A	T	A	CLPTM1L	c.T1332A	p.G444G
XH_P37	5	1321919	1321919	Frame_Shift_Ins	INS	-	CCTT	-	CLPTM1L	330_1331insAA	p.G444fs
XH_P37	5	5461609	5461609	Frame_Shift_Ins	INS	-	TTAAAGTTTATG	-	ICE1	ATGTGTTTAAAC	p.S721fs
XH_P37	5	5462595	5462595	Frame_Shift_Ins	INS	-	TG	-	ICE1	3148_3149insT	p.K1050fs
XH_P37	5	5462596	5462596	Frame_Shift_Ins	INS	-	GGAT	-	ICE1	149_3150insGG	p.K1050fs
XH_P37	5	5463633	5463633	Frame_Shift_Ins	INS	-	G	-	ICE1	c.4187dupG	p.C1396fs
XH_P37	5	5463635	5463635	Frame_Shift_Ins	INS	-	ATGTTGTTTATT	-	ICE1	189insCATGTTG	p.C1396fs
XH_P37	5	5464054	5464054	Nonsense_Mutation	INS	-	TGCACTGAAA	-	ICE1	insTATCTGACAG	536_5153delinsAIX
XH_P37	5	5464384	5464384	In_Frame_Ins	INS	-	AAGTTTTACTG	-	ICE1	nsGCTGAAGTTT	646delinsTKFLVLC
XH_P37	5	7878349	7878349	In_Frame_Ins	INS	-	ATACAAAAATA	-	MTRR	5insAATACAAA	v232delinsEYKKYL
XH_P37	5	9202083	9202083	Nonsense_Mutation	INS	-	TTGTGAGACTG	-	SEMA5A	AATACCACTCTC	p.I306delinsX
XH_P37	5	10426619	10426619	Missense_Mutation	SNP	G	A	G	MARCH6	c.G2176A	p.V726I
XH_P37	5	10426620	10426620	Nonsense_Mutation	INS	-	CAACATAAGCAT	-	MARCH6	78insATCAACAT	26_V727delinsVSTX
XH_P37	5	11199753	11199753	Nonsense_Mutation	INS	-	AAATCATATTAA	-	CTNND2	ATAATTTAATAA	257_Q258delinsLIX
XH_P37	5	13911505	13911505	In_Frame_Ins	INS	-	AAA	-	DNAH5	1633_1634insT	p.N545delinsIY
XH_P37	5	13911507	13911507	Frame_Shift_Ins	INS	-	CTTTGGCTAATG	-	DNAH5	2insATCATTAGC	p.T544fs
XH_P37	5	14508475	14508475	In_Frame_Ins	INS	-	AGGCAG	-	TRIO	38_9239insAGG	R3080delinsQAG
XH_P37	5	14508477	14508477	Silent	SNP	A	T	A	TRIO	c.A9240T	p.R3080R
XH_P37	5	16682120	16682120	Frame_Shift_Ins	INS	-	ATTTTTAAATTTG	-	MYO10	ATATCACAAATT	p.P1350fs
XH_P37	5	23526662	23526662	In_Frame_Ins	INS	-	SATTGCGTTCTA	-	PRDM9	nsGAGTGATTGCG	89delinsGVIAFYML
XH_P37	5	32780891	32780891	Nonsense_Mutation	INS	-	TCCTAAATCTCT	-	NPR3	60insATTCTCTAA	Q421delinsAFLNSX
XH_P37	5	33448805	33448805	Nonsense_Mutation	INS	-	AGTAAATATTGC	-	TARS	TGATCAGTAAAT	K99_T100delinsKX
XH_P37	5	33998923	33998923	Nonsense_Mutation	INS	-	TGTTCTTTGGTT	-	AMACR	nsTAGAACCAAA	p.T188delinsX
XH_P37	5	34813735	34813735	Nonsense_Mutation	INS	-	CTTACTTATCA	-	RAI14	CATTCTTCTACT	A267delinsKSSYSYFIKIX
XH_P37	5	35065430	35065430	Frame_Shift_Ins	INS	-	TAGCTTGACTAA	-	PRLR	ATTCCATTAGTC	p.K443fs
XH_P37	5	36985621	36985621	Frame_Shift_Ins	INS	-	GTCTATTTTCAT	-	NIPBL	sAGACAGCTCAT	p.S780fs
XH_P37	5	37014856	37014856	Missense_Mutation	SNP	C	G	C	NIPBL	c.C4632G	p.I1544M
XH_P37	5	37173943	37173943	Frame_Shift_Ins	INS	-	CTTT	-	C5orf42	084_6085insAA	p.Q2029fs
XH_P37	5	37173944	37173944	Nonsense_Mutation	INS	-	ACTTTTCAITCA	-	C5orf42	insATTTGAAATG	T2028delinsTFEX
XH_P37	5	38445796	38445796	In_Frame_Ins	INS	-	GAAATCTCT	-	EGFLAM	2_2481insGAAA	C827delinsWKSL
XH_P37	5	38463096	38463096	In_Frame_Ins	INS	-	CAAAAAAGCAAA	-	EGFLAM	8insAGCAAAAA	N96delinsKAKSK
XH_P37	5	38949930	38949930	Nonsense_Mutation	INS	-	TACAAAAATGTT	-	RICTOR	CTGGCTTAACAT	1340delinsSVKPGX
XH_P37	5	39153623	39153623	In_Frame_Ins	INS	-	GTTCATGGGA	-	FYB	49insTTTCCCAAT	417delinsFPMELP
XH_P37	5	39377063	39377063	Frame_Shift_Ins	INS	-	AAAGAAATGTTT	-	DAB2	63insTTAAACAT	p.P588fs
XH_P37	5	40767741	40767741	Nonsense_Mutation	INS	-	AAGTTATCAGAT	-	PRKAA1	ATCAGATCTGA	A6_A217delinsYQYIX
XH_P37	5	41917392	41917392	Frame_Shift_Ins	INS	-	CAGCAGATGAA	-	C5orf51	877insCAGCAG	p.R292fs
XH_P37	5	43298814	43298814	Frame_Shift_Ins	INS	-	A	-	HMGCS1	c.253_254insT	p.D85fs
XH_P37	5	43298815	43298815	Frame_Shift_Ins	INS	-	SCAAACTTTTGT	-	HMGCS1	53insTACAAAAA	p.D85fs
XH_P37	5	45262689	45262689	Frame_Shift_Ins	INS	-	C	-	HCN1	.2006_2007insT	p.T669fs
XH_P37	5	52204839	52204839	In_Frame_Ins	INS	-	TAGTTGGCA	-	ITGA1	7_1568insTAGT	Q523delinsLVGK
XH_P37	5	55201951	55201951	Nonsense_Mutation	INS	-	AGTAAGGTGGCT	-	IL31RA	1031insAGTAAQ	B44_M345delinsEX
XH_P37	5	55201953	55201953	In_Frame_Ins	INS	-	TTA	-	IL31RA	1032_1033insT	p.V344delinsVL
XH_P37	5	56219835	56219835	Frame_Shift_Ins	INS	-	CAGAAGCTTTGG	-	MIER3	CCCCCCCCAAG	p.F325fs
XH_P37	5	56527135	56527135	Nonsense_Mutation	INS	-	ATTCTTTAAAAA	-	GPBP1	AAACATCTTTTA	40delinsESHQNILX
XH_P37	5	58284371	58284371	Nonsense_Mutation	INS	-	TTTAGTGATAG	-	PDE4D	ATGAACATATCA	77_H278delinsLTX
XH_P37	5	60455957	60455957	Nonsense_Mutation	INS	-	AGAGGAAAAAT	-	SMIM15	.42insATTTTCCW	14_A15delinsX
XH_P37	5	61689861	61689861	Frame_Shift_Ins	INS	-	AAATAATTTGAT	-	DIMT1	CTTGCACTCAAA	p.N195fs
XH_P37	5	64756155	64756155	Frame_Shift_Ins	INS	-	GTATAGTAAGG	-	ADAMT56	.473insCCTTAC	p.1158fs
XH_P37	5	65349539	65349539	Frame_Shift_Ins	INS	-	CTTTGAACTTTT	-	ERBIN	insGAGCTTTGA	p.1798fs
XH_P37	5	66461413	66461413	Frame_Shift_Del	DEL	C	-	C	MST4	c.5623delC	p.P1875fs
XH_P37	5	66481845	66481845	In_Frame_Ins	INS	-	AAGTTAAAAATA	-	CD180	ACTGTATTTTAA	1delinsHILYFNLNKKI
XH_P37	5	68581252	68581252	Frame_Shift_Ins	INS	-	CAAAATTC	-	CCDC125	53_964insGAAT	p.C322fs
XH_P37	5	68581253	68581253	Frame_Shift_Ins	INS	-	TAAACTT	-	CCDC125	52_963insAAGT	p.D321fs
XH_P37	5	70805913	70805913	Nonsense_Mutation	INS	-	TTCCAGTTCTTTT	-	BDP1	sCTCTTCTCAG	P999delinsGSSSSFFX
XH_P37	5	70819894	70819894	Frame_Shift_Ins	INS	-	C	-	BDP1	.5516_5517insT	p.N1839fs
XH_P37	5	70819895	70819895	Frame_Shift_Ins	INS	-	AGTGAAATCCAA	-	BDP1	TTTAGAGTGAA	p.N1839fs
XH_P37	5	71493956	71493956	In_Frame_Ins	INS	-	AAATGGACATCT	-	MAP1B	4397insAAATGG	1466delinsEMDIL
XH_P37	5	72873829	72873829	Missense_Mutation	SNP	G	A	G	UTP15	c.G473A	p.R158Q
XH_P37	5	72874956	72874956	Nonsense_Mutation	INS	-	CAGGGTAAGTA	-	UTP15	ATATGCAGGGTA	L232delinsGNMQGKX
XH_P37	5	73932272	73932272	Silent	SNP	G	T	G	ENC1	c.C39A	p.A13A
XH_P37	5	73932273	73932273	Frame_Shift_Ins	INS	-	ACTATGCGTA	-	ENC1	.38insTACGCA	p.A13fs
XH_P37	5	74016556	74016556	Nonsense_Mutation	INS	-	TTCTTAAATGTT	-	HEXB	nsTTAATTTCTTA	R533delinsLSNX
XH_P37	5	74109838	74109838	In_Frame_Ins	INS	-	GGAACTTAGG	-	FAM169A	GAGAGCCTAAG	66delinsREPVPNL
XH_P37	5	74137492	74137492	Frame_Shift_Ins	INS	-	ACTTTATGGCTT	-	FAM169A	TTAAAGCCATA	p.P4fs
XH_P37	5	74651001	74651001	Nonsense_Mutation	INS	-	AAACCTTAATCCT	-	HMGCR	ATCTTCAAACTT	62delinsQYNYLQTX
XH_P37	5	74955197	74955197	In_Frame_Ins	INS	-	ATTTGTCTTTTC	-	ANKDD1B	CTTTCCATTGTG	52delinsALISLCLFTVQ
XH_P37	5	75896661	75896661	Frame_Shift_Ins	INS	-	CATTAGA	-	IQGAP2	46_947insCATT	p.L316fs
XH_P37	5	75896663	75896663	In_Frame_Ins	INS	-	ATC	-	IQGAP2	.948_949insAT	p.L316delinsLI
XH_P37	5	75914348	75914348	Frame_Shift_Ins	INS	-	ATTTTCCTTTTT	-	F2RL2	ACACAAAAAAG	p.A40fs
XH_P37	5	75927829	75927829	Frame_Shift_Ins	INS	-	TTCAACATTTTA	-	IQGAP2	TATAATTCAACA	p.A139fs
XH_P37	5	76989045	76989045	Frame_Shift_Ins	INS	-	CCAGCAATGTCT	-	TBCA	22insAAGACATT	p.Q98fs
XH_P37	5	78422006	78422006	Frame_Shift_Ins	INS	-	TGGTTTCTGGTG	-	BHMT	64insCTGGTTTC	p.D255fs
XH_P37	5	78422007	78422007	Nonsense_Mutation	INS	-	TAAGTCTATCA	-	BHMT	nsTCCCTAAGTC	P55_C256delinsDPX
XH_P37	5	79026386	79026386	Frame_Shift_Ins	INS	-	TCAGGGGTAATA	-	CMYA5	9insGTTCAGGG	p.V600fs
XH_P37	5	79026962	79026962	In_Frame_Ins	INS	-	AACGGGGACTT	-	CMYA5	nsATTATAACGGG	92delinsNINGDLRS
XH_P37	5	79028784	79028784	In_Frame_Ins	INS	-	CAATTTCTTTTT	-	CMYA5	7insGTTCAATT	1399delinsGFNF
XH_P37	5	79031434	79031434	In_Frame_Ins	INS	-	TCCTTTTCTCTCA	-	CMYA5	347insTTCCTT	12282delinsSFPFPQ
XH_P37	5	79033190	79033190	Missense_Mutation	SNP	G	T	G	CMYA5	c.G8602T	p.V2868F
XH_P37	5	79033192	79033192	Frame_Shift_Ins	INS	-	CTGTGATCTGGG	-	CMYA5	sCTTCACTGTGA	p.V2868fs
XH_P37	5	79033774	79033774	Frame_Shift_Ins	INS	-	CTGCTCTTTA	-	CMYA5	.9187insCTGCT	p.N3062fs
XH_P37	5	79033776	79033776	In_Frame_Ins	INS	-	TGACAAACCACT	-	CMYA5	STTTTATGACAA	53delinsMFYDKQLFH
XH_P37	5	79732898	79732898	Nonsense_Mutation	INS	-	AATCATATGCA	-	ZFYVE16	GTTAGAATCAT	A132_M133delinsSGX
XH_P37	5	79732900	79732900	In_Frame_Ins	INS	-	ATCTTGAGG	-	ZFYVE16	.5_397insATCTTG	D132delinsDILE
XH_P37	5	79733694	79733694	Frame_Shift_Ins	INS	-	ATTTTCATCTCT	-	ZFYVE16	insGAAATTTTC	p.F397fs

XH_P37	5	79797738	79797738	Splice_Site	INS	-	TTTTATAGGGTA	-	FAM151B	-	-	-
XH_P37	5	82816272	82816272	Missense_Mutation	SNP	C	G	C	VCAN	c.C2147G	p.T716R	
XH_P37	5	82834886	82834886	In_Frame_Ins	INS	-	AATCACTATTTC	-	VCAN	104insAAATCAC	p.1035delinsEITISL	
XH_P37	5	86670701	86670701	In_Frame_Ins	INS	-	TTTTGTATTGTG	-	RASA1	6insATGTTTGTG	p.660delinsKCFVFGV	
XH_P37	5	86674314	86674314	Frame_Shift_Ins	INS	-	ATTACAATTGACA	-	RASA1	6TACTAATTACAA	p.D816fs	
XH_P37	5	88018662	88018662	Missense_Mutation	SNP	G	T	G	MEF2C	c.C1013A	p.p338H	
XH_P37	5	88018663	88018663	Nonsense_Mutation	INS	-	ATTATTACTTACT	-	MEF2C	AAACTAGTAAG	p.338delinsKTSKX	
XH_P37	5	88100560	88100560	In_Frame_Ins	INS	-	GTCTTTTCTTTC	-	MEF2C	ATCTTAAGAAA	p.8delinsHLKKNNMM	
XH_P37	5	94050589	94050589	Frame_Shift_Ins	INS	-	GAAAGACTTTG	-	MCTP1	1692insACAAAG	p.D564fs	
XH_P37	5	95757639	95757639	In_Frame_Ins	INS	-	CTTCTT	-	PCSK1	64_565insAAGAp	p.F189delinsKKF	
XH_P37	5	95757640	95757640	Frame_Shift_Ins	INS	-	TTATGAAATCT	-	PCSK1	4insGGAGAAATT	p.D188fs	
XH_P37	5	96314943	96314943	Nonsense_Mutation	INS	-	ATTAATAAAGAT	-	LNPEP	CTGAATTAAAT	p.41_D42delinsLNXX	
XH_P37	5	96364235	96364235	Nonstop_Mutation	INS	-	CTGCTACTCTGA	-	LNPEP	077insGCTGCTA	p.1026delinsCCYLE	
XH_P37	5	98129002	98129002	Frame_Shift_Ins	INS	-	ATCTGTCA	-	RGM	983insATCTGT	p.R328fs	
XH_P37	5	98236951	98236951	Frame_Shift_Ins	INS	-	ATGATGAAGAAG	-	CHD1	CATAATCTTCT	p.D176fs	
XH_P37	5	98236953	98236953	Missense_Mutation	SNP	C	T	C	CHD1	c.G524A	p.C175Y	
XH_P37	5	101627275	101627275	Frame_Shift_Ins	INS	-	G	-	SLCO4C1	c.390_391insC	p.S131fs	
XH_P37	5	101627277	101627277	In_Frame_Ins	INS	-	GGGTCTCTTTTT	-	SLCO4C1	CCTTCAAAAAGAA	p.0delinsTYLQKETPIYI	
XH_P37	5	102432481	102432481	Frame_Shift_Ins	INS	-	CCCTCTTCA	-	GIN1	617insTGAAGA	p.K206fs	
XH_P37	5	102895000	102895000	In_Frame_Ins	INS	-	AGAAGATCACT	-	NUDT12	AAATCAAGGTGA	p.08delinsNQDGLRL	
XH_P37	5	102895168	102895168	Frame_Shift_Ins	INS	-	TT	-	NUDT12	c.153_154insAA	p.C52fs	
XH_P37	5	102895169	102895169	Nonsense_Mutation	INS	-	CATTCTGTAGGA	-	NUDT12	TGGTCTCTAACG	p.M51delinsLGSX	
XH_P37	5	106717027	106717027	Frame_Shift_Ins	INS	-	TGTGAGATTTT	-	EFNA5	AAACAAAAAT	p.Q206fs	
XH_P37	5	108714446	108714446	In_Frame_Ins	INS	-	AAAACGTATAAG	-	PIA2	TTGAACCTATCA	p.248delinsLELISLTF	
XH_P37	5	111504782	111504782	In_Frame_Ins	INS	-	ATCAGGTTAGT	-	EPB41L4A	ACTATTACTAAC	p.7delinsLTITNLMNCS	
XH_P37	5	112769991	112769991	Nonsense_Mutation	INS	-	CAACAAGGAGG	-	TSK1B	46insCCCTCCTT	p.A183delinsAPPCX	
XH_P37	5	112769993	112769993	Missense_Mutation	SNP	C	G	C	TSK1B	c.G544C	p.A183fs	
XH_P37	5	112860804	112860804	Silent	SNP	T	C	T	YTHDC2	c.T405C	p.P135P	
XH_P37	5	112878160	112878160	Frame_Shift_Ins	INS	-	ACATTATCACTC	-	YTHDC2	CACAAACATTAT	p.F185fs	
XH_P37	5	112878161	112878161	In_Frame_Ins	INS	-	TAT	-	YTHDC2	c.556_557insTA	p.A186delinsVS	
XH_P37	5	112917273	112917273	Missense_Mutation	SNP	C	A	C	YTHDC2	c.C2614A	p.P872T	
XH_P37	5	112917274	112917274	Nonsense_Mutation	INS	-	CATATAATTTAC	-	YTHDC2	ACATTTTCATATA	p.5873delinsPYFTFHIIYYX	
XH_P37	5	114860347	114860347	Nonsense_Mutation	INS	-	AATCCAGCCTAT	-	FEM1C	ATGATTTATAGG	p.D4_F505delinsNVVX	
XH_P37	5	114861034	114861034	Frame_Shift_Ins	INS	-	TAGATATAGAG	-	FEM1C	CAGCGCCTCTAT	p.M275fs	
XH_P37	5	121488320	121488320	Frame_Shift_Ins	INS	-	GCAACTGCTGT	-	ZNF474	36insGGCAACT	p.C212fs	
XH_P37	5	121759035	121759035	In_Frame_Ins	INS	-	CTTTCATTGTTC	-	SNCAIP	604insCTTTCAT	p.S201delinsSLSLF	
XH_P37	5	122515880	122515880	In_Frame_Ins	INS	-	AAATGTATAGGG	-	PRDM6	37insGCAAAAT	p.512delinsQANVRV	
XH_P37	5	122515882	122515882	Missense_Mutation	SNP	C	T	C	PRDM6	c.C1538T	p.P513L	
XH_P37	5	125896792	125896792	In_Frame_Ins	INS	-	TTGTTTTTCTT	-	ALDH7A1	396insAAGAAA	p.G299delinsEEKTR	
XH_P37	5	125939361	125939361	Frame_Shift_Ins	INS	-	TGCCATCCAA	-	PHAX	7insCTTTGCCAT	p.S66fs	
XH_P37	5	126154742	126154742	In_Frame_Ins	INS	-	CTATTTTAAATC	-	LMNB1	5GCGAGCTATTTT	p.146delinsQAAILNHF	
XH_P37	5	127624162	127624162	Nonsense_Mutation	INS	-	GTTAAACTAAA	-	FBN2	AAGATGTTTTAG	p.242_F243delinsEX	
XH_P37	5	130766630	130766630	Frame_Shift_Ins	INS	-	ACAAACAAGTTA	-	RAPGEF6	387insATAACTT	p.S1463fs	
XH_P37	5	132018259	132018259	Frame_Shift_Ins	INS	-	GTTACTGTATAC	-	IL4	95insGGTTACTG	p.Y132fs	
XH_P37	5	132097316	132097316	Frame_Shift_Ins	INS	-	TGGCT	-	SEPT8	795_796insAGC	p.E266fs	
XH_P37	5	134086612	134086612	Frame_Shift_Ins	INS	-	TTTTTAAACGAA	-	CAMLG	64insGTTTTTAA	p.L288fs	
XH_P37	5	134223506	134223506	Frame_Shift_Ins	INS	-	TCAGAGTCATA	-	TXND15	nsCATTCAAGAGT	p.A7fs	
XH_P37	5	135700940	135700940	Splice_Site	SNP	C	G	C	TRPC7	-	-	
XH_P37	5	135700941	135700941	Nonsense_Mutation	INS	-	GATCTGAGATC	-	TRPC7	GAAAGATCTCAC	p.L2delinsTNKKDLRSIX	
XH_P37	5	138651795	138651795	Frame_Shift_Ins	INS	-	TT	-	MATR3	c.183_184insTT	p.T61fs	
XH_P37	5	138651796	138651796	Nonsense_Mutation	INS	-	ATACAAATTAAT	-	MATR3	AAAGAAATACAA	p.63delinsNNKRQITTX	
XH_P37	5	138658597	138658597	Frame_Shift_Ins	INS	-	TTTGGATTCTT	-	MATR3	1226insTTTTGG	p.DA09fs	
XH_P37	5	140048341	140048341	In_Frame_Ins	INS	-	GCTCTC	-	WDR55	25_526insGCTC	p.A175delinsAAL	
XH_P37	5	140053882	140053882	In_Frame_Ins	INS	-	SGTATTTTTATTC	-	HARS	ATAATCAATAAA	p.883delinsVVIKTIK	
XH_P37	5	140073250	140073250	Frame_Shift_Ins	INS	-	TTGTATTACAA	-	HARS2	CTATGTTGTATT	p.K61fs	
XH_P37	5	140076941	140076941	Frame_Shift_Ins	INS	-	AAGATTACAG	-	HARS2	716insAAGATT	p.L239fs	
XH_P37	5	140166126	140166126	Frame_Shift_Ins	INS	-	TCCAATCATTTA	-	PCDHA1	ATATTTCCAATC	p.L84fs	
XH_P37	5	140201420	140201420	Silent	SNP	T	C	T	PCDHA5	c.T60C	p.L20L	
XH_P37	5	140214444	140214444	Frame_Shift_Ins	INS	-	CACAAACAAAAT	-	PCDHA7	GAATTCACAAAC	p.D159fs	
XH_P37	5	140220935	140220935	Frame_Shift_Ins	INS	-	CTATTCTTTATG	-	PCDHA8	CTTTCTATTCT	p.G10fs	
XH_P37	5	140256137	140256137	In_Frame_Ins	INS	-	AATCATTTT	-	PCDHA12	0_1081insAATC	p.Q360delinsQNHf	
XH_P37	5	140256138	140256138	Frame_Shift_Ins	INS	-	ATCCCAT	-	PCDHA12	81_1082insATC	p.E361fs	
XH_P37	5	140262403	140262403	In_Frame_Ins	INS	-	CAAAATGCC	-	PCDHA13	0_551insCAAAA	p.N184delinsTKCH	
XH_P37	5	140530021	140530021	Frame_Shift_Ins	INS	-	CACATCTATCTC	-	PCDHB6	84insACACATCT	p.R61fs	
XH_P37	5	140574045	140574045	Silent	SNP	C	G	C	PCDHB10	c.C1920G	p.L640L	
XH_P37	5	140626468	140626468	Frame_Shift_Ins	INS	-	BTGATGAAATAC	-	PCDHB15	3insAAGTGATG	p.V441fs	
XH_P37	5	140740501	140740501	Nonsense_Mutation	INS	-	TATCTTATGCTCT	-	PCDHB2	TAAATTAATCTT	p.467_D268delinsNFX	
XH_P37	5	140746162	140746162	In_Frame_Ins	INS	-	AAGATAGAGTG	-	PCDHA5	2266insAAGATA	p.H755delinsHKIEC	
XH_P37	5	140856315	140856315	In_Frame_Ins	INS	-	ATTTCATTCTCT	-	PCDHG3	633insATTTCAT	p.Q211delinsQFHFL	
XH_P37	5	141694670	141694670	Frame_Shift_Ins	INS	-	TTAGACCA	-	SPRY4	3_4insTGGTCTA	p.E2fs	
XH_P37	5	142780008	142780008	Frame_Shift_Ins	INS	-	AAAGAGA	-	NR3C1	96_397insTCTC	p.T133fs	
XH_P37	5	142780009	142780009	Frame_Shift_Ins	INS	-	AGAGTCCTTGG	-	NR3C1	TGATCTCCAAGG	p.V132fs	
XH_P37	5	147661734	147661734	Frame_Shift_Ins	INS	-	CTATCATCTCTT	-	SPINK13	nsCATCTCTATCAT	p.P59fs	
XH_P37	5	147781661	147781661	Frame_Shift_Ins	INS	-	SACTTTTGGTGT	-	FBXO38	TTATTGACTTTT	p.S127fs	
XH_P37	5	147863916	147863916	In_Frame_Ins	INS	-	TTAAGGTCTAG	-	HTRA	03insAACTAGA	p.368delinsKLDLKF	
XH_P37	5	149357391	149357391	In_Frame_Ins	INS	-	TTTGCTCTGGTT	-	SLC26A2	177insTTTGCTC	p.Q59delinsHLSWL	
XH_P37	5	149677948	149677948	Nonsense_Mutation	INS	-	C	-	ARSI	c.538_539insG	p.180_D181delinsX	
XH_P37	5	149677949	149677949	Frame_Shift_Ins	INS	-	TCTCCAGTGACA	-	ARSI	insATTGTCACTG	p.Y180fs	
XH_P37	5	150050199	150050199	Missense_Mutation	SNP	C	T	C	MYO23	c.C215T	p.A72V	
XH_P37	5	150050200	150050200	Nonsense_Mutation	INS	-	TCATGATTGTIT	-	MYO23	217insTCATGAT	p.A72delinsASX	
XH_P37	5	150606041	150606041	Nonsense_Mutation	INS	-	TTCTTTGTGACC	-	SLC36A3	8insTAGGTCACT	p.Q360_V361delinsX	
XH_P37	5	154281037	154281037	Nonsense_Mutation	INS	-	CAACTAATTTTT	-	GEMIN5	73insTAAAAAA	p.H958delinsLKNX	
XH_P37	5	154281039	154281039	Nonsense_Mutation	SNP	G	T	G	GEMIN5	c.C2871A	p.Y957X	
XH_P37	5	154395684	154395684	Frame_Shift_Ins	INS	-	GTCTTTTCAACT	-	KIF4B	66insTCGTTCTT	p.V755fs	
XH_P37	5	154395686	154395686	Missense_Mutation	SNP	G	T	G	KIF4B	c.G2267T	p.S756I	
XH_P37	5	156522370	156522370	In_Frame_Ins	INS	-	TAA	-	HAVCR2	c.622_623insTT	p.G208delinsSVR	
XH_P37	5	156522371	156522371	Nonsense_Mutation	INS	-	AATTTTATTTAA	-	HAVCR2	AAATATTAATAA	p.D209delinsHNNKYX	
XH_P37	5	156675883	156675883	Frame_Shift_Ins	INS	-	AGATGGACCCCT	-	ITK	1658insAGATGG	p.S553fs	
XH_P37	5	157221945	157221945	Frame_Shift_Ins	INS	-	T	-	CLINT1	c.1047_1048ins	p.F350fs	
XH_P37	5	157221946	157221946	Nonsense_Mutation	INS	-	TTTTGGTTACAG	-	CLINT1	sGTAGTCTGTAA	p.349_F350delinsEX	
XH_P37	5	158621791	158621791	Nonsense_Mutation	INS	-	TGACATTTTAT	-	RNF145	16insAAATAAAA	p.L107delinsSX	
XH_P37	5	159521058	159521058	Frame_Shift_Ins	INS	-	ATAACCAATCAA	-	PWWP2A	9insTATTGATTG	p.G200fs	
XH_P37	5	159996621	159996621	Frame_Shift_Ins	INS	-	AA	-	ATP10B	3819_3820insT	p.A1274fs	
XH_P37	5	159996623	159996623	In_Frame_Ins	INS	-	AACATGGAC	-	ATP10B	7_3818insGTCC	p.N1273delinsSPCY	
XH_P37	5	160886695	160886695	Silent	SNP	G	A	G	GABRB2	c.C393T	p.H131H	
XH_P37	5	161113998	161113998	Frame_Shift_Ins	INS	-	TTTAGAATTTAT	-	GABRA6	CCCTATTATAGA	p.D72fs	
XH_P37	5	162939148	162939148	In_Frame_Ins	INS	-	TCTCTCAATAT	-	MAT2B	ACAGTTCCTCTCA	p.8delinsENSSLYIR	
XH_P37	5	168189559	168189559	Frame_Shift_Ins	INS	-	TCTGAACACCT	-	SLIT3	595insTAGTGT	p.E532fs	

XH_P37	5	169685144	169685144	In_Frame_Ins	INS	-	CAGGCAGAT	-	LCP2	5_997insATCTG	A333delins	CLA
XH_P37	5	172396471	172396471	Nonsense_Mutation	INS	-	AATAGGAACAC	-	RPL26L1	TACAAAAATAGG	K122delins	NTKX
XH_P37	5	173376594	173376594	Frame_Shift_Ins	INS	-	TTTCTCCCTCTCA	-	CPEB4	1466insTTTCTC	p.P489fs	
XH_P37	5	174868783	174868783	In_Frame_Ins	INS	-	AAATACATCTCA	-	DRD1	20insCTGGAA	440delins	HWNVFG
XH_P37	5	176562785	176562785	Frame_Shift_Ins	INS	-	GTCCTTGTTACT	-	NSD1	nsATAGTCTTTG	p.L227fs	
XH_P37	5	176637253	176637253	In_Frame_Ins	INS	-	GTGGCCCTTTTT	-	NSD1	TTGTATGTGGC	8delins	NCMWPFLL
XH_P37	5	176734136	176734136	Nonsense_Mutation	INS	-	AAAGTATTTATTG	-	MXD3	AACTCAATAAA	S190delins	RHSINTCX
XH_P37	5	176895901	176895901	Splice_Site	SNP	C	T	C	DBN1	-	-	
XH_P37	5	178541069	178541069	Frame_Shift_Ins	INS	-	TCCTGATTCCAA	-	ADAMTS2	nsCCTTTTGGAA	p.N1145fs	
XH_P37	5	178541188	178541188	Frame_Shift_Ins	INS	-	AAAAGACCAGAA	-	ADAMTS2	316insTTTCTCG	p.L1106fs	
XH_P37	5	179136924	179136924	Frame_Shift_Ins	INS	-	AAAGCTAACTAC	-	CANX	5GGAAAAGCTA	p.K193fs	
XH_P37	5	179151749	179151749	Nonsense_Mutation	INS	-	ATGTATTATGTT	-	CANX	ATGTTTCATGTA	538delins	NFVYMFMYVIX
XH_P37	5	179300202	179300202	Frame_Shift_Ins	INS	-	AACAGAGGCTGA	-	TBC1D9B	insACTTTACGCC	p.P745fs	
XH_P37	5	180335794	180335794	Frame_Shift_Ins	INS	-	GATAAAT	-	BTNL8	58_259insGATA	p.K86fs	
XH_P37	5	180335795	180335795	In_Frame_Ins	INS	-	ATCAAAACCCTT	-	BTNL8	260insATCAAA	L87delins	HQNPL
XH_P37	6	572585	572585	Frame_Shift_Ins	INS	-	AGGTGGTTGTA	-	EXOC2	1378insTACAA	p.L460fs	
XH_P37	6	2779651	2779651	Frame_Shift_Ins	INS	-	A	-	WRNIP1	c.1411_1412ins	p.P471fs	
XH_P37	6	2779653	2779653	Frame_Shift_Ins	INS	-	TGTCAATGTGCT	-	WRNIP1	14insTTTGTCAA	p.P471fs	
XH_P37	6	5216916	5216916	Frame_Shift_Ins	INS	-	ATGAAACT	-	LYRM4	1_142insAGTT	p.D48fs	
XH_P37	6	7386031	7386031	Frame_Shift_Ins	INS	-	GGGCTGTTTTTA	-	CAGE1	TGAAGATAAAA	p.D90fs	
XH_P37	6	7579754	7579754	Frame_Shift_Ins	INS	-	AGAAGCAGCTAG	-	DSP	832insAAGAAGC	p.L1111fs	
XH_P37	6	7580957	7580957	In_Frame_Ins	INS	-	GGCCTTTTGCTG	-	DSP	4535insGGCCTT	1512delins	WPFAD
XH_P37	6	7584273	7584273	Nonsense_Mutation	INS	-	CGTAACTGACCT	-	DSP	4982insCGTAA	p.L1661delins	TX
XH_P37	6	7584886	7584886	Frame_Shift_Ins	INS	-	A	-	DSP	c.5594_5595ins	p.R1865fs	
XH_P37	6	7584887	7584887	Nonsense_Mutation	INS	-	TGTGCTCTAAT	-	DSP	596insCTGTCCT	p5_11866delins	RLCFX
XH_P37	6	7606393	7606393	Frame_Shift_Ins	INS	-	AATGTATACTA	-	SNRNP48	937insAATGTT	p.K312fs	
XH_P37	6	7606395	7606395	Missense_Mutation	SNP	A	T	A	SNRNP48	c.A938T	p.D313V	
XH_P37	6	10586649	10586649	Nonsense_Mutation	INS	-	ATTCTGGGTGAG	-	GCNT2	28insGATTCTGG	143_1144delins	X
XH_P37	6	10586651	10586651	In_Frame_Ins	INS	-	ATC	-	GCNT2	c.429_430insAT	p.L143delins	LI
XH_P37	6	12125990	12125990	Frame_Shift_Ins	INS	-	TTGGATGT	-	HIVEP1	2_5963insTTGG	p.L1988fs	
XH_P37	6	12125992	12125992	Frame_Shift_Ins	INS	-	A	-	HIVEP1	c.5964_5965ins	p.L1988fs	
XH_P37	6	12136121	12136121	Frame_Shift_Ins	INS	-	TTGGTATCTATA	-	HIVEP1	4insAATTGGT	p.E2161fs	
XH_P37	6	16307040	16307040	Frame_Shift_Ins	INS	-	ATGCT	-	ATXN1	967_1968insAG	p.G656fs	
XH_P37	6	16307042	16307042	Missense_Mutation	SNP	C	T	C	ATXN1	c.G1966A	p.G656S	
XH_P37	6	17637647	17637647	Frame_Shift_Ins	INS	-	G	-	NUP153	c.2074dupC	p.Q692fs	
XH_P37	6	17637649	17637649	Nonsense_Mutation	INS	-	5GAGTAATTTTG	-	NUP153	AATAAGCAAAA	Q692delins	VSKITPX
XH_P37	6	17646367	17646367	Nonsense_Mutation	INS	-	ACCTTTTGGACG	-	NUP153	AAGCACCGCTCA	51delins	KKHRQKX
XH_P37	6	20102617	20102617	Frame_Shift_Ins	INS	-	TTACATGCATCT	-	MBOAT1	AAAATAAAGATC	p.L463fs	
XH_P37	6	24533902	24533902	Frame_Shift_Ins	INS	-	CATTAAAGAC	-	ALDH5A1	1571insCATTAA	p.Y524fs	
XH_P37	6	25913674	25913674	Nonsense_Mutation	INS	-	GCAGTCTCT	-	SLC17A2	1160insAAGA	p.L387delins	X
XH_P37	6	25914888	25914888	In_Frame_Ins	INS	-	AAAAATAAAGC	-	SLC17A2	074insAAGCTCA	358delins	SVLYFS
XH_P37	6	25914890	25914890	Missense_Mutation	SNP	C	T	C	SLC17A2	c.G1072A	p.V358I	
XH_P37	6	26056277	26056277	Frame_Shift_Ins	INS	-	CGTATGGGAGT	-	HIST1H1C	insGTAACCTCCC	p.K127fs	
XH_P37	6	26197293	26197293	Silent	SNP	C	G	C	HIST1H3D	c.G186C	p.L62L	
XH_P37	6	26273494	26273494	Frame_Shift_Ins	INS	-	CCCTCATATTAT	-	HIST1H2BI	292insCCCTCAT	p.T97fs	
XH_P37	6	26273495	26273495	Missense_Mutation	SNP	G	C	G	HIST1H2BI	c.G292C	p.A98P	
XH_P37	6	26637707	26637707	Frame_Shift_Ins	INS	-	G	-	ZNF322	c.1074_1075ins	p.S539fs	
XH_P37	6	26637708	26637708	Nonsense_Mutation	INS	-	ACCAATATAAA	-	ZNF322	74insTTTTTAAT	58_535delins	NFX
XH_P37	6	27100406	27100406	Frame_Shift_Ins	INS	-	IGCTAAGTAAAC	-	HIST1H2BJ	nsCACTGTTTAC	p.V42fs	
XH_P37	6	27278647	27278647	In_Frame_Ins	INS	-	CCCTCTC	-	POM121L2	02_1303insGAG	A435delins	ERL
XH_P37	6	27368429	27368429	Frame_Shift_Ins	INS	-	GG	-	ZNF391	c.280_281insGG	p.S94fs	
XH_P37	6	27368430	27368430	In_Frame_Ins	INS	-	CTTCGTTTTTAT	-	ZNF391	282insCTTCGTT	S94delins	SVFI
XH_P37	6	28056993	28056993	In_Frame_Ins	INS	-	TTTTTCTCCAGCA	-	ZNF165	nsGATTTTTTCT	01delins	GDFFLQHK
XH_P37	6	28227664	28227664	Frame_Shift_Ins	INS	-	ACTCCAA	-	NKAPL	15_516insACTC	p.S172fs	
XH_P37	6	28268784	28268784	Frame_Shift_Ins	INS	-	AAAATCCCTCAAT	-	PGBD1	insATAAAATC	p.P385fs	
XH_P37	6	35199593	35199593	Frame_Shift_Ins	INS	-	CCCTGTGACGTA	-	SCUBE3	sACACCCCTGTCT	p.F142fs	
XH_P37	6	35201038	35201038	Frame_Shift_Ins	INS	-	CCAATTATCTCA	-	SCUBE3	70insCCCAATTA	p.H223fs	
XH_P37	6	35280317	35280317	Splice_Site	INS	-	ATTCCA	-	DEF6	-	-	
XH_P37	6	36297945	36297946	Frame_Shift_Del	DEL	GG	-	GG	C6orf222	c.522_523del	p.D174fs	
XH_P37	6	36297946	36297946	Frame_Shift_Ins	INS	-	TCCTCTTTCTC	-	C6orf222	522insGAGAAA	p.D174fs	
XH_P37	6	38813525	38813525	In_Frame_Ins	INS	-	5ATATGCCAAATA	-	DNAH8	22insAGATATG	1674delins	VDMQIS
XH_P37	6	38831780	38831780	In_Frame_Ins	INS	-	GTAAG	-	DNAH8	42_6443insGTA	F2148delins	CKV
XH_P37	6	38831782	38831782	Nonsense_Mutation	INS	-	AAATATACCTTCT	-	DNAH8	CTCTAATAATATA	148delins	FLVYNIPX
XH_P37	6	38877467	38877467	Frame_Shift_Ins	INS	-	CAGAGGGGTT	-	DNAH8	9688insCAGAG	p.T3229fs	
XH_P37	6	38994426	38994426	In_Frame_Ins	INS	-	GTCTCAGTGT	-	DNAH8	insCATTTGTCTC	607delins	TVSVFRF
XH_P37	6	41001906	41001906	Frame_Shift_Ins	INS	-	TTATCTTCAT	-	UNC5CL	400insATGAAG	p.G134fs	
XH_P37	6	41884595	41884595	Frame_Shift_Ins	INS	-	AAAGGTGGTAT	-	MED20	97insAATACAC	p.A33fs	
XH_P37	6	42986652	42986652	Missense_Mutation	SNP	G	A	G	KLHDC3	c.G872A	p.R291H	
XH_P37	6	43014274	43014274	Nonsense_Mutation	INS	-	CCCCAAGACCTA	-	CUL7	715insATAGGTC	905_V906delins	EX
XH_P37	6	43034245	43034245	In_Frame_Ins	INS	-	AAA	-	KLC4	c.542_543insAA	p.I181delins	IN
XH_P37	6	43034246	43034246	In_Frame_Ins	INS	-	AAAGGA	-	KLC4	43_544insAAAG	p.I181delins	IKG
XH_P37	6	43153831	43153831	Nonsense_Mutation	SNP	C	T	C	CUL9	c.C889T	p.Q297X	
XH_P37	6	43416877	43416877	Nonsense_Mutation	INS	-	AATGACAT	-	ABCC10	4_4055insAATG	352_51353delins	QX
XH_P37	6	43477337	43477337	Missense_Mutation	SNP	G	C	G	LRR373	c.C187G	p.L63V	
XH_P37	6	43488950	43488950	In_Frame_Ins	INS	-	TTTTTACCT	-	POLR1C	3_954insTTTTTA	p318delins	PFYL
XH_P37	6	43491668	43491668	Missense_Mutation	SNP	T	C	T	XPO5	c.A3553G	p.M1185V	
XH_P37	6	43491670	43491670	In_Frame_Ins	INS	-	TCA	-	XPO5	3550_3551insTG	p.1184delins	LT
XH_P37	6	43519132	43519132	In_Frame_Ins	INS	-	CACACC	-	XPO5	30_1631insGGT	p.K544delins	RCE
XH_P37	6	43555218	43555218	Nonsense_Mutation	INS	-	AACAGAGACTA	-	POLH	GGCTTAACAGAA	V161delins	VAX
XH_P37	6	43582076	43582076	In_Frame_Ins	INS	-	CTGTTGGTAAAA	-	POLH	nsATACTCTGTTG	518delins	DTLVKSL
XH_P37	6	43623389	43623389	In_Frame_Ins	INS	-	TTTTTCTCCTTT	-	RSPH9	440insTTTTCTT	T147delins	IFLS
XH_P37	6	44218099	44218099	In_Frame_Ins	INS	-	TCCTGCAGCTTA	-	HSP90AB1	nsACATCCTGCA	240delins	ETSETCLS
XH_P37	6	44982601	44982601	Frame_Shift_Ins	INS	-	ATTATACC	-	SUPT3H	2_43insGGTATA	p.M15fs	
XH_P37	6	44982602	44982602	Nonsense_Mutation	INS	-	TGTTACC	-	SUPT3H	11_42insGGTAA	Y14_M15delins	X
XH_P37	6	46657444	46657444	Frame_Shift_Ins	INS	-	TTGCGTGGCT	-	TDRD6	c.1580insTTGCC	p.A527fs	
XH_P37	6	46660990	46660990	Nonsense_Mutation	INS	-	SAACATAATCCT	-	TDRD6	c.TTGAGAACAT	709_E171delins	SX
XH_P37	6	47522500	47522500	In_Frame_Ins	INS	-	AAA	-	CD2AP	c.539_540insAA	p.S180delins	SK
XH_P37	6	47522502	47522502	Frame_Shift_Ins	INS	-	AAAAACAACCTC	-	CD2AP	42insCAAAAAC	p.E181fs	
XH_P37	6	50682942	50682942	Silent	SNP	C	T	C	TFAP2D	c.C153T	p.T51T	
XH_P37	6	50807890	50807890	Frame_Shift_Ins	INS	-	CATCCCTGGAAT	-	TFAP2B	63insACATACCC	p.R321fs	
XH_P37	6	50811103	50811103	Nonstop_Mutation	INS	-	CACCTCAGTGT	-	TFAP2B	1382insCACCTC	X461delins	SPSVS
XH_P37	6	52147651	52147651	Nonsense_Mutation	INS	-	ACTAATTTGTAAT	-	MCM3	230insCTTACAT	T77_N78delins	TVIX
XH_P37	6	52993184	52993184	Frame_Shift_Ins	INS	-	CTTTTTCTGTTA	-	GCM1	AAAAAGAAAAA	p.Q377fs	
XH_P37	6	56437777	56437777	Frame_Shift_Ins	INS	-	T	-	DST	c.5452_5453ins	p.P1818fs	
XH_P37	6	56437778	56437778	Frame_Shift_Ins	INS	-	SAAGATGTTA	-	DST	insTCAGTAACAT	p.P1818fs	
XH_P37	6	56481925	56481925	In_Frame_Ins	INS	-	TGGGATATT	-	DST	9_6340insAATA	Q2114delins	NIPQ
XH_P37	6	56484076	56484076	In_Frame_Ins	INS	-	AAATTTAAGCAA	-	DST	nsCACTTTTGCT	586delins	HFLCNLSLT
XH_P37	6	56484331	56484331	In_Frame_Ins	INS	-	AAGAAA	-	DST	500_4501insTTT	p.11501delins	FLI

XH_P37	6	56484333	56484333	Frame_Shift_Ins	INS	-	AATGATAAAA	-	DST	8_4499insTTTTA	p.N1500fs
XH_P37	6	57012343	57012343	Nonsense_Mutation	INS	-	5ATTCTTCCACTG	-	ZNF451	AGACTGATTCT	487_4488delinsEX
XH_P37	6	57012557	57012557	Frame_Shift_Ins	INS	-	CATTTTATAACCC	-	ZNF451	CCACACATTTA	p.R58fs
XH_P37	6	64395565	64395565	Nonsense_Mutation	INS	-	TTTTTTCACAGAT	-	PHF3	943insGTTTTTC	648delinsGFSQIX
XH_P37	6	64422419	64422419	Frame_Shift_Ins	INS	-	TTTTTGACTGAA	-	PHF3	CTCTTGTTTGA	p.F1645fs
XH_P37	6	69349192	69349192	Nonsense_Mutation	INS	-	TGAATAAAAAT	-	ADGRB3	insTATTTGAATA	D209delinsVFEX
XH_P37	6	69349194	69349194	Silent	SNP	C	T	C	ADGRB3	c.C627T	p.D209D
XH_P37	6	70410746	70410746	Frame_Shift_Ins	INS	-	TAGCTGTATCTT	-	LMBRD1	099insAAAGATA	p.Y367fs
XH_P37	6	70890357	70890357	Frame_Shift_Ins	INS	-	TGCTCTCCAGT	-	COL19A1	2718insTGCTC	p.E906fs
XH_P37	6	71234357	71234357	Frame_Shift_Ins	INS	-	G	-	FAM135A	1471_1472ins	p.K491fs
XH_P37	6	71234358	71234358	In_Frame_Ins	INS	-	TCCTCAGTCTCA	-	FAM135A	nsGCTTTCTTCA	491delinsKLSSVSYL
XH_P37	6	71234882	71234882	In_Frame_Ins	INS	-	GGGAGA	-	FAM135A	08_1409insGGG	L470delinsWEI
XH_P37	6	71234883	71234883	Frame_Shift_Ins	INS	-	ATCA	-	FAM135A	409_1410insAT	p.L470fs
XH_P37	6	71236325	71236325	Frame_Shift_Ins	INS	-	ATAACTGTGTTCT	-	FAM135A	insTGAATAATCT	p.Q951fs
XH_P37	6	71483069	71483069	Frame_Shift_Ins	INS	-	CAACTACATTCTG	-	SMAP1	TTCTGCAACTAC	p.I119fs
XH_P37	6	71566718	71566718	Missense_Mutation	SNP	C	G	C	SMAP1	c.C865G	p.Q289E
XH_P37	6	71566720	71566720	In_Frame_Ins	INS	-	GATCACCATA	-	SMAP1	7_868insGATCA	Q289delinsQDHL
XH_P37	6	73935100	73935100	Frame_Shift_Ins	INS	-	AA	-	KHDC1L	c.31_32insTT	p.E11fs
XH_P37	6	73935101	73935101	Nonsense_Mutation	INS	-	TAGTTTTTGTGA	-	KHDC1L	31insTACAAAAA	11_P12delinsYKNX
XH_P37	6	73952211	73952211	Nonsense_Mutation	INS	-	ATCAGTCACATA	-	KHDC1	30insTATGTGAC	K10delinsNMX
XH_P37	6	74119061	74119065	Frame_Shift_Del	DEL	GTAT	-	GTAT	DDX1	c.1270_1274de	p.V424fs
XH_P37	6	74183368	74183368	Frame_Shift_Ins	INS	-	CAGAATCACACT	-	MT01	insGTACAGAACT	p.V272fs
XH_P37	6	74304867	74304867	Nonsense_Mutation	INS	-	CTTTTTTTAATT	-	SLC17A5	AGTACAAATAA	F474_T475delinsX
XH_P37	6	75836089	75836089	Nonsense_Mutation	INS	-	ATCTAAAGTACG	-	COL12A1	AACAATGGTACT	F982_K983delinsX
XH_P37	6	75841788	75841788	Frame_Shift_Ins	INS	-	GTATAATA	-	COL12A1	2_2313insTATT	p.G771fs
XH_P37	6	75841789	75841789	In_Frame_Ins	INS	-	ATTATTGTGTTT	-	COL12A1	nsTCATCAAAAAA	71delinsVKNKNNLR
XH_P37	6	76576737	76576737	Nonsense_Mutation	INS	-	CTGTGAATTTTA	-	MYO6	insGAACTGTGA	20_F621delinsNLX
XH_P37	6	79688361	79688361	Nonsense_Mutation	INS	-	AATTTTGTAGT	-	PHIP	TAAACACTAA	946delinsKTYISFX
XH_P37	6	80878735	80878735	Frame_Shift_Ins	INS	-	ACAATAAGTCTT	-	BCKDHB	622insACAATAA	p.C207fs
XH_P37	6	84799078	84799078	Frame_Shift_Ins	INS	-	AAAGCTGTCTA	-	MRAP2	239insCAAGACT	p.I80fs
XH_P37	6	87969428	87969428	Nonsense_Mutation	INS	-	CTTCTTAATTTC	-	ZNF292	TTGATTCTTCTT	7_E202delinsANFNX
XH_P37	6	88066206	88066206	Frame_Shift_Ins	INS	-	AAAACAGGTT	-	C6orf163	insGGCAAAACT	p.I180fs
XH_P37	6	88074993	88074993	In_Frame_Ins	INS	-	GTCTTTTTTCCCT	-	C6orf163	70insTGTTCTT	T290delinsHVLFP5
XH_P37	6	88367705	88367705	Frame_Shift_Ins	INS	-	G	-	ORC3	c.1231_1232ins	p.N411fs
XH_P37	6	88367707	88367707	Frame_Shift_Ins	INS	-	TTGTTTATCTCT	-	ORC3	TGGGTTTTGTTT	p.N411fs
XH_P37	6	90422330	90422330	Nonsense_Mutation	INS	-	ATGTTTTAACTT	-	MDN1	5GAAGAAAGTTA	6_N2466delinsPTEESX
XH_P37	6	90457159	90457159	Nonsense_Mutation	INS	-	5TTCTAACAGCT	-	MDN1	TACAAAAGCTG	65_K126delinsYKSCX
XH_P37	6	90572153	90572153	Nonsense_Mutation	INS	-	TTTAAGATCTT	-	CASP8AP2	CTAGATTTAAGA	242_S243delinsEIX
XH_P37	6	90572319	90572319	Missense_Mutation	SNP	G	C	G	CASP8AP2	c.G891C	p.K297N
XH_P37	6	90572321	90572321	Frame_Shift_Ins	INS	-	CATTAGTGCAG	-	CASP8AP2	894insCATTAG	p.T298fs
XH_P37	6	90573349	90573349	In_Frame_Ins	INS	-	AGTTAAGTTCAA	-	CASP8AP2	AGAAAGAGTTAA	1delinsGERVKFNFFM
XH_P37	6	90573351	90573351	Silent	SNP	G	A	G	CASP8AP2	c.G1923A	p.V641V
XH_P37	6	97339198	97339198	In_Frame_Ins	INS	-	TGAGCTCCCTGA	-	NDUFA4	310insTCAGGGA	1104delinsGSSSI
XH_P37	6	97634561	97634561	In_Frame_Ins	INS	-	CAGCATTAAAT	-	MMS22L	AATTAATAATTA	99delinsSKLIINADLQL
XH_P37	6	99347335	99347335	In_Frame_Ins	INS	-	TAATTTTCATCAT	-	FBXL4	26insAATGATG	376delinsNDENYE
XH_P37	6	99347336	99347336	Nonsense_Mutation	INS	-	CTATTAT	-	FBXL4	24_1125insATAA	375_E376delinsSX
XH_P37	6	101110357	101110357	Frame_Shift_Ins	INS	-	TTAGTTAAAGTA	-	ASCC3	insAGTGACTT	p.I781fs
XH_P37	6	106967295	106967295	Nonsense_Mutation	INS	-	AGGGGTTTTTAA	-	CRYBG1	ATTCTTAGGGGT	80_Q331delinsQDSX
XH_P37	6	106967297	106967297	Frame_Shift_Ins	INS	-	A	-	CRYBG1	c.990_991insA	p.P330fs
XH_P37	6	109796687	109796687	Splice_Site	INS	-	GCTAAGCC	-	ZBTB24	.	.
XH_P37	6	110423117	110423117	Frame_Shift_Ins	INS	-	CCCAGGCCCCA	-	WASF1	96insATGGGGA	p.P399fs
XH_P37	6	110501811	110501811	Frame_Shift_Ins	INS	-	ACATCATTAAC	-	CDC40	5insACACATCAT	p.D55fs
XH_P37	6	110522828	110522828	Missense_Mutation	SNP	C	T	C	CDC40	c.C344T	p.A115V
XH_P37	6	110530411	110530411	Frame_Shift_Ins	INS	-	TGAACATATGT	-	CDC40	AAATATGAACA	p.V205fs
XH_P37	6	110777928	110777928	Frame_Shift_Ins	INS	-	TTTATTGTTCTAT	-	SLC22A16	scCAGATAGGAA	p.Y16fs
XH_P37	6	110953275	110953275	Nonsense_Mutation	INS	-	TAGATGTTTAA	-	CDK19	ATACAGTTAACAA	2_E143delinsQLQITX
XH_P37	6	111587906	111587906	Nonsense_Mutation	INS	-	TAAAGATGAAG	-	MFS04B	sAGAAATAAAG	A.P381delinsQKX
XH_P37	6	112390695	112390695	Nonsense_Mutation	INS	-	TACAAATAGTTT	-	WISP3	TTTTATTACAAT	2delinsKSFKFYNSFENMX
XH_P37	6	112397691	112397691	Nonsense_Mutation	INS	-	ACCTATGAATA	-	TUBE1	AACATTATTATCA	157_F158delinsIX
XH_P37	6	112462571	112462571	Frame_Shift_Ins	INS	-	TCCGTTTTCTTC	-	LAMA4	02insGGAAGAA	p.V934fs
XH_P37	6	112506457	112506457	In_Frame_Ins	INS	-	TTGATTGTTTTG	-	LAMA4	sTCAAGAAAAA	53delinsVQEKOSKR
XH_P37	6	116289815	116289815	In_Frame_Ins	INS	-	AGTATT	-	FRK	53_554insAATA	p.T185delinsKYS
XH_P37	6	116574423	116574423	In_Frame_Ins	INS	-	AGGGAACAC	-	TSPYL4	8_749insGTGTT	p.I250delinsVVPF
XH_P37	6	116574425	116574425	Frame_Shift_Ins	INS	-	TCCCTAGTTTC	-	TSPYL4	747insGAAACT	p.N249fs
XH_P37	6	116758453	116758453	Frame_Shift_Ins	INS	-	AACTGTGCGAA	-	DSE	GACTTCAATCT	p.I941fs
XH_P37	6	116836981	116836981	Nonsense_Mutation	INS	-	AGAAAGAAATAT	-	FAM26E	AAGAAGAAAG	53delinsSPRLRRKKYX
XH_P37	6	116911561	116911561	Nonsense_Mutation	INS	-	TATCTTTTAAAC	-	RWDD1	AACAGTATCTTT	181_S182delinsSX
XH_P37	6	116914227	116914227	Frame_Shift_Ins	INS	-	CAGT	-	RWDD1	695_696insCAG	p.Y232fs
XH_P37	6	116914229	116914229	In_Frame_Ins	INS	-	TCAACAGTG	-	RWDD1	7_698insTCAACA	N233delinsINSO
XH_P37	6	117113542	117113542	Nonsense_Mutation	INS	-	AGTATATGAATA	-	GPCR6A	AAGGCTTATTCA	F778delinsAKAYSITX
XH_P37	6	117199091	117199091	Nonsense_Mutation	INS	-	ATATAAATACAA	-	RFK6	ATAGAATATAAA	9_Q120delinsKNR1X
XH_P37	6	117199093	117199093	Frame_Shift_Ins	INS	-	CTTTAAGTGT	-	RFK6	359insCTTTAA	p.Q120fs
XH_P37	6	117724426	117724426	Nonsense_Mutation	INS	-	CAAAGCTTGAT	-	ROS1	ACTAAATCAAAAG	51_S152delinsPNX
XH_P37	6	117724428	117724428	Missense_Mutation	SNP	G	T	G	ROS1	c.C451A	p.P151T
XH_P37	6	117860539	117860539	Nonsense_Mutation	INS	-	TCTAATCCATAT	-	DCBLD1	TTATCTCTCTAA	66_K367delinsELSLX
XH_P37	6	117896498	117896498	In_Frame_Ins	INS	-	TTTTGAGATGGA	-	GOPC	468insTCCATCT	A156delinsAPSQK
XH_P37	6	117896500	117896500	Missense_Mutation	SNP	C	T	C	GOPC	c.G466A	p.A156T
XH_P37	6	119252689	119252689	Nonsense_Mutation	INS	-	ATACTTAAATA	-	MCM9	ATATATATTTTA	T.67delinsRYIFX
XH_P37	6	121768594	121768594	Frame_Shift_Ins	INS	-	TGTTTCAGTTTCT	-	GJA1	nsTTCTTGTTCA	p.S201fs
XH_P37	6	123892265	123892265	Frame_Shift_Ins	INS	-	TGGGATTACAAA	-	TRDN	AAGTTTTGTGTA	p.T12fs
XH_P37	6	124979478	124979478	In_Frame_Ins	INS	-	TTTTTTTTTCTA	-	NKAIN2	15insTTTTTTTT	L38delinsLFFFSY
XH_P37	6	125541312	125541312	In_Frame_Ins	INS	-	AAAATCTCCTA	-	TPD52L1	nsACAAAAATCC	K7delinsKTKILLN
XH_P37	6	125597391	125597391	Splice_Site	INS	-	A	-	HDDC2	.	.
XH_P37	6	126249866	126249866	In_Frame_Ins	INS	-	TTTATACTACTG	-	NCOA7	610insTTTATAC	S203delinsSFILL
XH_P37	6	127771265	127771265	Frame_Shift_Ins	INS	-	TAAAGGCTCTTC	-	KIAA0408	TTCTTCAAGAGC	p.K123fs
XH_P37	6	128643204	128643204	Frame_Shift_Ins	INS	-	TTGTTGGTGGTT	-	PTPRK	75insAAACCACC	p.F159fs
XH_P37	6	132030115	132030115	Frame_Shift_Ins	INS	-	ACATCTATCCAC	-	CTAGE9	043insSGTGGA	p.S681fs
XH_P37	6	132030117	132030117	Frame_Shift_Ins	INS	-	GGGGT	-	CTAGE9	040_2041insAC	p.S681fs
XH_P37	6	132938650	132938650	Frame_Shift_Ins	INS	-	AAAGTGAGTAGG	-	TAAR2	60insGCCACTAC	p.I187fs
XH_P37	6	132966974	132966974	In_Frame_Ins	INS	-	AGTGCCCT	-	TAAR1	169insAGGGAG	P57delinsRDTP
XH_P37	6	132966976	132966976	Missense_Mutation	SNP	G	C	G	TAAR1	c.C167G	p.T565
XH_P37	6	133136115	133136115	Frame_Shift_Ins	INS	-	TTAAAGAACACC	-	RPS12	CTTGTTAAAGAA	p.A7fs
XH_P37	6	133783592	133783592	In_Frame_Ins	INS	-	AAT	-	EYAA	c.395_396insAA	Q132delinsQM
XH_P37	6	133783593	133783593	Nonsense_Mutation	INS	-	ATTTAAACT	-	EYAA	6_397insATTTA	p.Q132delinsQIX
XH_P37	6	134350121	134350121	Frame_Shift_Ins	INS	-	TGAG	-	SLC2A12	841_842insCTC	p.I281fs
XH_P37	6	134350123	134350123	Frame_Shift_Ins	INS	-	TGTG	-	SLC2A12	839_840insCAC	p.M280fs
XH_P37	6	135518401	135518401	Missense_Mutation	SNP	C	A	C	MYB	c.C1506A	p.D502E
XH_P37	6	135518402	135518402	Frame_Shift_Ins	INS	-	CTGTAGGGCTT	-	MYB	1508insCTGTAG	p.V503fs

XH_P37	6	139581564	139581564	Nonsense_Mutation	INS	-	TTTATTTGAGAC	-	TXLNB	sCTCTGTCTCAA	298delins	TLNQINXK
XH_P37	6	143780346	143780346	Nonsense_Mutation	INS	-	TATATTAGTGG	-	PEX3	AGTTTTATATTA	M67delins	NVKFYISGX
XH_P37	6	143806292	143806292	Nonsense_Mutation	INS	-	AAGTGTITTTGTC	-	PEX3	TTCTCAAAGTGT	S316delins	LKSKSVFVX
XH_P37	6	143825331	143825331	Nonsense_Mutation	INS	-	TTGATTTTAAAGT	-	FUCA2	CAATGACTTAA	7_K158delins	PKPMTX
XH_P37	6	144184388	144184388	Frame_Shift_Ins	INS	-	AGTTATTGTGC	-	LTV1	746insAGTTAT	p.R249fs	
XH_P37	6	144184390	144184390	In_Frame_Ins	INS	-	AAATGT	-	LTV1	47_748insAAAT	p.R249delins	RKC
XH_P37	6	144262893	144262893	Frame_Shift_Ins	INS	-	AT	-	PLAGL1	.1059_1060insA	p.G354fs	
XH_P37	6	144262894	144262894	In_Frame_Ins	INS	-	CATTGAGATAAT	-	PLAGL1	9insTCAATTATCT	B53delins	NQLSECM
XH_P37	6	144263226	144263226	In_Frame_Ins	INS	-	TTGCAATATCAG	-	PLAGL1	nsAACTGATAT	243delins	KLILQKCP
XH_P37	6	144858852	144858852	Frame_Shift_Ins	INS	-	CAGAACCTTACA	-	UTRN	3369insCAGAAC	p.R2123fs	
XH_P37	6	145069645	145069645	Nonsense_Mutation	INS	-	AATTTGGAGTGC	-	UTRN	AGAATAATTTG	35delins	KKKNNLDVX
XH_P37	6	146216092	146216093	Frame_Shift_Del	DEL	CC	-	CC	SHPRH	c.4536_4537de	p.V1512fs	
XH_P37	6	147012373	147012373	Missense_Mutation	SNP	C	T	C	ADGB	c.C1433T	p.P478L	
XH_P37	6	147012374	147012374	Nonsense_Mutation	INS	-	ATATAAGCATT	-	ADGB	5insTTAATATAA	p.P478delins	PLIX
XH_P37	6	149699424	149699424	Nonsense_Mutation	INS	-	CAGGTATTATT	-	TAB2	sCATCCAGGTAT	125delins	ASRLLFX
XH_P37	6	149718822	149718822	Frame_Shift_Ins	INS	-	GCAG	-	TAB2	686_1687insGC	p.K562fs	
XH_P37	6	149718823	149718823	Missense_Mutation	SNP	T	A	T	TAB2	c.T1687A	p.S563T	
XH_P37	6	150001198	150001198	In_Frame_Ins	INS	-	GATTGTTTAGAC	-	LATS1	1566insGTCTAA	E522delins	ESKQS
XH_P37	6	150004403	150004403	Frame_Shift_Ins	INS	-	G	-	LATS1	c.981_982insC	p.K328fs	
XH_P37	6	150004404	150004404	Frame_Shift_Ins	INS	-	TTGGTGTTTA	-	LATS1	981insTAAACA	p.K327fs	
XH_P37	6	150267603	150267603	In_Frame_Ins	INS	-	STATTTTTTTTT	-	ULBP2	CATTGTGATTTT	49delins	PFVFFFFF
XH_P37	6	151152381	151152381	In_Frame_Ins	INS	-	GTTCGTCAGTTC	-	PLEKHG1	2018insGTTCTG	S673delins	CSAVP
XH_P37	6	151670563	151670563	Frame_Shift_Ins	INS	-	GTTCCTTTCTTC	-	AKAP12	nsTAGGTTCTTT	p.A248fs	
XH_P37	6	151674691	151674691	Missense_Mutation	SNP	G	T	G	AKAP12	c.G4871T	p.G1624V	
XH_P37	6	151790036	151790036	In_Frame_Ins	INS	-	CTAATATTAAAT	-	ARMT1	nsCGGTAAATAT	254delins	SANIKSV
XH_P37	6	152570388	152570388	In_Frame_Ins	INS	-	AGTATTTTGTGT	-	SYNE1	ACTCAAAAACAA	23delins	YSKTKILQTK
XH_P37	6	152570390	152570390	Missense_Mutation	SNP	A	T	A	SYNE1	c.T19265A	p.L6422Q	
XH_P37	6	152737665	152737665	Nonsense_Mutation	INS	-	AAAGAAATTA	-	SYNE1	sCTCAGCTTAAT	76_Q1977delins	NSAX
XH_P37	6	155131308	155131308	Nonsense_Mutation	INS	-	TATATTTAGTGA	-	SCAF8	TTGCTCTTATAT	K462delins	KLVSIX
XH_P37	6	155761235	155761235	Nonsense_Mutation	INS	-	AGGACTCGTAT	-	NOX3	insATTATACGA	75_T176delins	ILRLVX
XH_P37	6	157525047	157525047	In_Frame_Ins	INS	-	CTTTCATGCATA	-	ARID1B	TTTCGTTCTTTCA	delins	SLTVLSCIESTFM
XH_P37	6	159618468	159618468	Missense_Mutation	SNP	C	A	C	FNDC1	c.C115A	p.H39N	
XH_P37	6	159618470	159618470	Frame_Shift_Ins	INS	-	AACAAATATACC	-	FNDC1	insAAAAACAAAT	p.H39fs	
XH_P37	6	160200950	160200950	Nonsense_Mutation	INS	-	ATCATTCTCT	-	TCP1	802insAAGAAAC	E68_E269delins	KKX
XH_P37	6	160200952	160200952	Nonsense_Mutation	INS	-	TCCCAATACACT	-	TCP1	nsGCTAGTGTAT	p.V267delins	CX
XH_P37	6	160218488	160218488	Nonsense_Mutation	INS	-	GAGTCCTTA	-	MRPL18	3_410insGAGTC	p.L137delins	XS
XH_P37	6	161026093	161026093	Missense_Mutation	SNP	G	T	G	LPA	c.C2930A	p.A977E	
XH_P37	6	161071438	161071438	Silent	SNP	C	T	C	LPA	c.G141A	p.L47R	
XH_P37	6	166574443	166574443	Frame_Shift_Ins	INS	-	CCTGTTTGCA	-	T	742insTGCAAA	p.N248fs	
XH_P37	6	170876062	170876062	Silent	SNP	C	T	C	TBP	c.C582T	p.F194F	
XH_P37	7	5239240	5239240	Frame_Shift_Ins	INS	-	CAGACAATATTA	-	WPI2	nsATACAGACAA	p.K36fs	
XH_P37	7	6180585	6180585	Nonsense_Mutation	INS	-	ATCAAACTGGT	-	USP42	sTAGAATCAAAA	255_P256delins	DX
XH_P37	7	7398360	7398360	Nonsense_Mutation	INS	-	ACTGAGTATTA	-	COL28A1	AAGTTGTAAAT	p.V1094delins	VX
XH_P37	7	7612451	7612451	Frame_Shift_Ins	INS	-	CTATCAACATGG	-	MIOS	3insATCTATCAA	p.Q115fs	
XH_P37	7	7623002	7623002	Frame_Shift_Ins	INS	-	AAAAACATTTT	-	MIOS	3insCAGAAAACA	p.K549fs	
XH_P37	7	7623004	7623004	Splice_Site	SNP	G	T	G	MIOS			
XH_P37	7	11068426	11068426	Frame_Shift_Ins	INS	-	CAAAGTGCCAC	-	PHF14	sTCATACAAAGT	p.S479fs	
XH_P37	7	11076278	11076278	In_Frame_Ins	INS	-	ATAGGTATGAAT	-	PHF14	7insATTATAGGT	G12delins	QIIGMND
XH_P37	7	11514032	11514032	Silent	SNP	G	A	G	THSD7A	c.C2181T	p.S727S	
XH_P37	7	11514033	11514033	Nonsense_Mutation	INS	-	GTTTGTTTGAAG	-	THSD7A	nsGACITTCACAA	727_C728delins	XS
XH_P37	7	12409716	12409716	Frame_Shift_Ins	INS	-	TAGACAGTGT	-	VWDE	TTCTCTATAACAC	p.S624fs	
XH_P37	7	12644260	12644260	Frame_Shift_Ins	INS	-	CAGCCTCAGTG	-	SCIN	nsCATTGAGCTC	p.E213fs	
XH_P37	7	15433785	15433785	Frame_Shift_Ins	INS	-	TGAAGTGGTGG	-	AGMO	9insACCCACCA	p.P210fs	
XH_P37	7	16714129	16714129	Nonsense_Mutation	INS	-	AGAGTATAACAA	-	BZW2	7ACTGAGAGTAT	p.F51delins	XS
XH_P37	7	17865701	17865701	Frame_Shift_Ins	INS	-	AT	-	SNX13	.1648_1649insA	p.L550fs	
XH_P37	7	17865702	17865702	In_Frame_Ins	INS	-	CTTATATTCTAA	-	SNX13	1648insTTAGAA	L550delins	LEYKL
XH_P37	7	17879568	17879568	Frame_Shift_Ins	INS	-	TAAGTGAAGAT	-	SNX13	nsTCAGATCTT	p.E407fs	
XH_P37	7	20193994	20193994	Nonsense_Mutation	INS	-	AGTCGTACTCAA	-	MACC1	7GAAAGTTAGT	23_M724delins	TSX
XH_P37	7	20406762	20406762	Frame_Shift_Ins	INS	-	CC	-	ITGB8	c.341_342insCC	p.L114fs	
XH_P37	7	20406763	20406763	Nonsense_Mutation	INS	-	AAATCACTGATG	-	ITGB8	AAAGAAAATCAC	14_N115delins	IVX
XH_P37	7	21470100	21470100	In_Frame_Ins	INS	-	GTGTTTGAGATT	-	SP4	1267insGTGTT	Q422delins	OVFEI
XH_P37	7	21470391	21470391	Frame_Shift_Ins	INS	-	GTGGAAT	-	SP4	57_1558insGTG	p.V519fs	
XH_P37	7	23313755	23313755	Nonsense_Mutation	INS	-	AAAGTACATTTA	-	GNPMB	nsATGAAAGTAA	544_L545delins	LX
XH_P37	7	23724274	23724274	In_Frame_Ins	INS	-	AAATATTAAAT	-	FAM221A	3insCAAATATT	L74delins	QILNK
XH_P37	7	24663371	24663371	Nonsense_Mutation	INS	-	GATAGATTTT	-	MPP6	5CAGGATAGATT	29delins	NSRIDFVMX
XH_P37	7	24718816	24718816	Frame_Shift_Ins	INS	-	TTTTTGAATAA	-	MPP6	TTCTTATTTTGG	p.E394fs	
XH_P37	7	24874321	24874321	Frame_Shift_Ins	INS	-	TTTCAATTTTGA	-	OSBPL3	329insAATCAAA	p.S443fs	
XH_P37	7	25266472	25266472	Frame_Shift_Ins	INS	-	ATATA	-	NPVF	311_312insTAT	p.A104fs	
XH_P37	7	25266473	25266473	Frame_Shift_Ins	INS	-	SGTGGTCTAGAA	-	NPVF	11insTTTCTAGA	p.A104fs	
XH_P37	7	27832764	27832764	In_Frame_Ins	INS	-	ACACCTGGGTA	-	TAX1BP1	3insCCACACCTG	291delins	HHTWVI
XH_P37	7	27835809	27835809	Nonsense_Mutation	INS	-	GATATACAAAG	-	TAX1BP1	ATCCTAGATATA	delins	SIHLIDIRRIYKLX
XH_P37	7	29928952	29928952	Frame_Shift_Ins	INS	-	CTCAAGTTTAC	-	WIPF3	nsACCTCTCAAG	p.S427fs	
XH_P37	7	30118217	30118217	Frame_Shift_Ins	INS	-	GAGAAACAAG	-	PLEKHA8	5insCTAGAAA	p.R458fs	
XH_P37	7	36450774	36450774	Nonsense_Mutation	INS	-	ACTAAAAATTTCC	-	ANLN	35insCTACTAAA	E465_E466delins	HYX
XH_P37	7	36450775	36450775	In_Frame_Ins	INS	-	TTTGCA	-	ANLN	35_1396insTTT	Q465delins	QFA
XH_P37	7	36660416	36660416	Frame_Shift_Ins	INS	-	TGCATGAAGAG	-	AOAH	577insACTCTTC	p.H193fs	
XH_P37	7	37947177	37947177	In_Frame_Ins	INS	-	ACAGAAGGTGAA	-	SFRP4	945insCTCACCT	K315delins	NSPSV
XH_P37	7	39504113	39504113	Nonsense_Mutation	INS	-	CTTTTAGG	-	POU6F2	6_1797insCTTT	599_E600delins	HFX
XH_P37	7	39606107	39606107	Silent	SNP	G	A	G	YAE1D1	c.G90A	p.A30A	
XH_P37	7	39612258	39612258	Frame_Shift_Ins	INS	-	TTTCCACAGAGT	-	YAE1D1	ATTATTTTCCAC	p.Q212fs	
XH_P37	7	40027842	40027842	Frame_Shift_Ins	INS	-	TGGCTTTGTTTT	-	CDK13	7insGTGGTGCTT	p.D619fs	
XH_P37	7	40234660	40234660	Splice_Site	INS	-	AAATTAGATAAA	-	SUGCT			
XH_P37	7	42079784	42079784	Nonsense_Mutation	INS	-	CTGCAAGTGCA	-	GLI3	CTGATTGCACT	294delins	PDCTCRX
XH_P37	7	44524788	44524788	Frame_Shift_Ins	INS	-	GTGAACATCTGG	-	NUDCD3	388insACCAAGAT	p.A96fs	
XH_P37	7	44611308	44611308	Silent	SNP	G	A	G	DDX56	c.C673T	p.L25L	
XH_P37	7	44611309	44611309	Frame_Shift_Ins	INS	-	ATCTGGTTTGAA	-	DDX56	572insTTTCAAC	p.Q224fs	
XH_P37	7	44721404	44721404	Frame_Shift_Ins	INS	-	ATCATCTGTT	-	OGDH	1281insATCAT	p.S427fs	
XH_P37	7	45123127	45123127	Frame_Shift_Ins	INS	-	A	-	NACAD	c.2651_2652ins	p.P884fs	
XH_P37	7	45123128	45123128	In_Frame_Ins	INS	-	GCT	-	NACAD	2650_2651insA	p.P884delins	QOP
XH_P37	7	47921648	47921648	Frame_Shift_Ins	INS	-	TTTCTCT	-	PKD1L1	0_3301insAGAA	p.L1101fs	
XH_P37	7	47921649	47921649	Frame_Shift_Ins	INS	-	ACTTTTCGTTTT	-	PKD1L1	300insTAAACG	p.S1100fs	
XH_P37	7	48278936	48278936	Frame_Shift_Ins	INS	-	AGTAAAGT	-	ABCA13	997insAGTAA	p.H332fs	
XH_P37	7	48278937	48278937	In_Frame_Ins	INS	-	TTACATTG	-	ABCA13	7_998insTTACA	P333delins	LTF
XH_P37	7	48352760	48352760	Frame_Shift_Ins	INS	-	SGTACTATATGA	-	ABCA13	514insCGGTA	p.E320fs	
XH_P37	7	48352762	48352762	Frame_Shift_Ins	INS	-	T	-	ABCA13	c.9616dupT	p.E320fs	
XH_P37	7	48428775	48428775	Missense_Mutation	SNP	C	A	C	ABCA13	c.C11612A	p.T3871N	
XH_P37	7	48428776	48428776	Frame_Shift_Ins	INS	-	AAAAATCTTTCT	-	ABCA13	514insTCAAAA	p.T3871fs	
XH_P37	7	48450249	48450249	Nonsense_Mutation	INS	-	CACAAATTTAAA	-	ABCA13	12204insCACAA	68_L4069delins	GTIX

XH_P37	7	48450251	48450251	Missense_Mutation	SNP	C	A	C	ABCA13	c.C12205A	p.L4069I
XH_P37	7	48685096	48685096	Nonsense_Mutation	INS	-	AAATATATAAAT	-	ABCA13	66insATAAATA	55_L5056delinsHINIX
XH_P37	7	51204016	51204016	Frame_Shift_Ins	INS	-	AAGTATTTTAAG	-	COBL	796insCTTAAA	p.T266fs
XH_P37	7	51204017	51204017	Nonsense_Mutation	INS	-	ATTTAAAAGTAA	-	COBL	5insCTTTACTTTT	5_T266delinsFTFFKX
XH_P37	7	56045959	56045959	Splice_Site	INS	-	AGCAGCTAT	-	NIPSNAP2	-	-
XH_P37	7	56149680	56149680	Frame_Shift_Ins	INS	-	AGCAGTACTT	-	PHKG1	671insAAGTAA	p.R224fs
XH_P37	7	57188164	57188164	Missense_Mutation	SNP	T	A	T	ZNF479	c.A958T	p.T320S
XH_P37	7	57528521	57528521	Frame_Shift_Ins	INS	-	TAGTGTACAAA	-	ZNF716	AATAGTAGTGA	p.C118fs
XH_P37	7	63680300	63680300	In_Frame_Ins	INS	-	ATCCGCTTGAGG	-	ZNF735	GTAGTACCGCT	delinsLLCVPLEELLKD
XH_P37	7	64004798	64004798	Frame_Shift_Ins	INS	-	TTTTTTTGTCATA	-	ZNF680	AGTTATGCAAA	p.F15fs
XH_P37	7	70252419	70252419	Splice_Site	INS	-	ATTATATAATCT	-	AUTS2	-	-
XH_P37	7	72397475	72397475	Nonsense_Mutation	INS	-	GTGAAGATATTT	-	POM121	sTAGCTGTAAAG	p.F67delinsFX
XH_P37	7	73254867	73254867	Frame_Shift_Ins	INS	-	CTTTCCT	-	METTL27	4_265insAGGGA	p.G89fs
XH_P37	7	74211682	74211682	In_Frame_Ins	INS	-	GCG	-	GTFF2IRD2	2168_2169insCp	F723delinsFA
XH_P37	7	74211684	74211684	Frame_Shift_Ins	INS	-	CTGAC	-	GTFF2IRD2	166_2167insGT	p.F723fs
XH_P37	7	75052351	75052351	In_Frame_Ins	INS	-	CTTCTGTT	-	POM121C	1184insAACAC	T395delinsKQEA
XH_P37	7	76825981	76825981	Nonsense_Mutation	INS	-	CACCAAAAATAC	-	FGL2	sCTCTGTATTTT	2_Y313delinsPLYFWX
XH_P37	7	76825983	76825983	Frame_Shift_Ins	INS	-	TCGGAATGGG	-	FGL2	933insTCCCAATTA	p.E311fs
XH_P37	7	82545567	82545567	Frame_Shift_Ins	INS	-	SACTTGAGAATA	-	PCLO	1735insCTATT	p.Q3912fs
XH_P37	7	82784376	82784376	Frame_Shift_Ins	INS	-	AATCCCTCATTTA	-	PCLO	TCCGTAAATGA	p.T527fs
XH_P37	7	82784378	82784378	Missense_Mutation	SNP	T	G	T	PCLO	c.A1579C	p.T527P
XH_P37	7	87737493	87737493	Nonsense_Mutation	INS	-	TTGACTTGACCT	-	ADAM22	AAAAAGTTGACTT	10_G131delinsGNKSX
XH_P37	7	88965095	88965095	Frame_Shift_Ins	INS	-	TCTGTCGTCT	-	ZNF804B	2800insTCTGT	p.Q93fs
XH_P37	7	91503354	91503354	Frame_Shift_Ins	INS	-	AATAATCGAAAC	-	MTERF1	94insATTTTCGA	p.V232fs
XH_P37	7	91630965	91630965	Frame_Shift_Ins	INS	-	TTTCATTATTGC	-	AKAP9	ATTTCAGTTTCT	p.A578fs
XH_P37	7	91632396	91632396	Frame_Shift_Ins	INS	-	ACATCTCAATGA	-	AKAP9	CTCTCTACATCT	p.S1055fs
XH_P37	7	91714959	91714959	Frame_Shift_Ins	INS	-	TCCTCTCTTTTG	-	AKAP9	84insGTTCTCT	p.K2995fs
XH_P37	7	91729058	91729058	Missense_Mutation	SNP	C	A	C	AKAP9	c.C10771A	p.Q3591K
XH_P37	7	91753165	91753165	Missense_Mutation	SNP	C	T	C	CYP51A1	c.G773A	p.R258H
XH_P37	7	91793057	91793057	In_Frame_Ins	INS	-	TGTGTA	-	LRRD1	59_1460insTAC	D487delinsVHN
XH_P37	7	91793058	91793058	Frame_Shift_Ins	INS	-	AGAAAAATTGCA	-	LRRD1	59insCTTGCAAA	p.D487fs
XH_P37	7	91793514	91793514	Frame_Shift_Ins	INS	-	C	-	LRRD1	1002_1003insT	p.H335fs
XH_P37	7	91793515	91793515	Nonsense_Mutation	INS	-	TTTGGAATGCCT	-	LRRD1	2insCTAAGGCA	334_H335delinsDX
XH_P37	7	92129121	92129121	Frame_Shift_Ins	INS	-	TCAT	-	PEX1	443_2444insATA	p.R815fs
XH_P37	7	92129122	92129122	Frame_Shift_Ins	INS	-	TTTGCCTTTCTG	-	PEX1	3insTACAGAAA	p.R815fs
XH_P37	7	92826707	92826707	Nonsense_Mutation	INS	-	TAGTGTGTAA	-	HEPACAM2	ATAATATTAAC	69_K370delinsNIX
XH_P37	7	94052388	94052388	Frame_Shift_Ins	INS	-	GGGGGAAATAT	-	COL1A2	sCATTTGGGGGA	p.G841fs
XH_P37	7	95221896	95221896	In_Frame_Ins	INS	-	TAGTATAAACAT	-	PKD4	3insGAATGTTT	2181delinsRNVYTT
XH_P37	7	95761185	95761185	In_Frame_Ins	INS	-	GAAATTTTTTTG	-	SLC25A13	ATCAGCAAAAAA	8delinsNYQQKNFNVV
XH_P37	7	95814325	95814325	Nonsense_Mutation	INS	-	ACAGGTACTAA	-	SLC25A13	nsCTCATTAGTAA	812_K313delinsPHX
XH_P37	7	98460935	98460935	Silent	SNP	G	A	G	TMEM130	c.C174T	p.N58N
XH_P37	7	98602942	98602942	Frame_Shift_Ins	INS	-	AT	-	TRRAP	10595_10596ins	p.E3532fs
XH_P37	7	98602943	98602943	Frame_Shift_Ins	INS	-	TCCGAACGTGC	-	TRRAP	10597insTCCG	p.E3532fs
XH_P37	7	99129871	99129871	Nonstop_Mutation	INS	-	AGTTCTGTAATG	-	ZKSCAN5	01insTGAGTTCT	767delinsYEFCNA
XH_P37	7	99247819	99247819	Frame_Shift_Ins	INS	-	TTAAAAGAATA	-	CYP3A5	90insGCATATTC	p.I430fs
XH_P37	7	99303142	99303142	Nonsense_Mutation	INS	-	ATAGAGTGTTA	-	CYP3A7	93insTATAACA	p.E498delinsVX
XH_P37	7	99910804	99910804	Frame_Shift_Ins	INS	-	CTCTGAG	-	SPDYE3	05_806insCTCT	p.C269fs
XH_P37	7	100635351	100635351	In_Frame_Ins	INS	-	SAAGTGTGTGT	-	MUC12	08insGGAAGTG	503delinsRKCVCV
XH_P37	7	100679214	100679214	Missense_Mutation	SNP	T	C	T	MUC17	c.T4517C	p.I1506T
XH_P37	7	100680010	100680010	In_Frame_Ins	INS	-	GTAGGAGATGA	-	MUC17	insGGTGTAGGA	771delinsAGVGDDEL
XH_P37	7	100680226	100680226	Silent	SNP	A	T	A	MUC17	c.A5529T	p.T1843T
XH_P37	7	100680228	100680228	Missense_Mutation	SNP	C	A	C	MUC17	c.C5531A	p.A1844E
XH_P37	7	100682792	100682792	Frame_Shift_Ins	INS	-	ATGAAGTACTT	-	MUC17	6insTTAATGAA	p.V2699fs
XH_P37	7	100683565	100683565	Missense_Mutation	SNP	G	C	G	MUC17	c.G8868C	p.R2956S
XH_P37	7	100685009	100685009	Nonsense_Mutation	INS	-	GTAGGAGATAA	-	MUC17	10313insGTAGG	S3438delinsCRRX
XH_P37	7	100685453	100685453	Nonsense_Mutation	INS	-	GTGTGTTGG	-	MUC17	10757insGTTGA	586_Y3587delinsSX
XH_P37	7	100685936	100685936	Frame_Shift_Ins	INS	-	CAGGAAGTGT	-	MUC17	11240insCAGG	p.M3747fs
XH_P37	7	100732051	100732051	Frame_Shift_Ins	INS	-	T	-	TRIM56	1458_1459ins	p.G486fs
XH_P37	7	103202374	103202374	Frame_Shift_Ins	INS	-	GTGTATGG	-	RELN	6_5237insCCAT	p.I1746fs
XH_P37	7	103270521	103270521	Nonsense_Mutation	INS	-	CAATTTCGCATA	-	RELN	ATTCTAGTGCAT	56_D857delinsMFX
XH_P37	7	105132028	105132028	In_Frame_Ins	INS	-	GAAACGTGTAT	-	PUS7	97insTAATACAC	K299delinsNNTRFI
XH_P37	7	105255102	105255102	Frame_Shift_Ins	INS	-	GCACAACCTCAA	-	ATXN7L1	307insGTTTGAG	p.S436fs
XH_P37	7	106888919	106888919	Nonsense_Mutation	INS	-	ATTAAAAATTTT	-	COG5	1805insAAAAAT	A602delinsEKFX
XH_P37	7	106888921	106888921	Nonsense_Mutation	INS	-	CGTTTTTCATCAC	-	COG5	AGAGAAGTATGAT	001_A602delinsKEKX
XH_P37	7	107214202	107214202	Nonsense_Mutation	INS	-	CAAAATAATATA	-	DUS4L	93insTCCAAATA	D98delinsVQIX
XH_P37	7	107427934	107427934	Nonsense_Mutation	INS	-	CAGGAAGTTT	-	SLC26A3	nsCACTAAAACT	2_Q253delinsSTKTSX
XH_P37	7	107599914	107599914	Frame_Shift_Ins	INS	-	AAAGTAAAGGAG	-	LAMB1	70insATTCTCT	p.H824fs
XH_P37	7	107599916	107599916	Missense_Mutation	SNP	C	T	C	LAMB1	c.G2468A	p.C823Y
XH_P37	7	107749682	107749682	In_Frame_Ins	INS	-	AAAAAAAACAA	-	LAMB4	insAAAGTGTTT	112delinsEKCCFFL
XH_P37	7	107752371	107752371	Nonsense_Mutation	INS	-	CAAAGTATTAT	-	LAMB4	213insATAATA	A171_C72delinsIX
XH_P37	7	108205353	108205353	Frame_Shift_Ins	INS	-	GATTTCATCATC	-	THAP5	CAAAGATTGATC	p.G157fs
XH_P37	7	110763375	110763375	Nonsense_Mutation	INS	-	CCCTTAGGTACA	-	LRRN3	GTTTCTCTAG83	F184delinsFVLVX
XH_P37	7	110764638	110764638	Nonsense_Mutation	INS	-	GCCTGAATATCT	-	LRRN3	1insTTGGCCTGA	604delinsGLNLSX
XH_P37	7	110764858	110764858	In_Frame_Ins	INS	-	CATTTTTTCTGT	-	LRRN3	1insCACATTTT	677delinsYTFFSVF
XH_P37	7	112407557	112407557	Frame_Shift_Ins	INS	-	AAACTTGTTTTAG	-	TMEM168	1789insCTAAAA	p.C597fs
XH_P37	7	112424161	112424161	In_Frame_Ins	INS	-	GCCATAAAGTAT	-	TMEM168	insAATATACCTT	240delinsEYIFMAV
XH_P37	7	112462403	112462403	Frame_Shift_Ins	INS	-	AATGGTTTATTA	-	BMT2	sTTAGTAATAAA	p.N205fs
XH_P37	7	113518113	113518113	In_Frame_Ins	INS	-	ATA	-	PPP1R3A	3033_3034insT	p.11012delinsYI
XH_P37	7	113518114	113518114	Nonsense_Mutation	INS	-	TACCTTATTCTCT	-	PPP1R3A	AAAAAAGGAA	11delinsSETGKNKVF
XH_P37	7	114269983	114269983	Missense_Mutation	SNP	C	A	C	FOX2	c.C520A	p.Q174K
XH_P37	7	114269985	114269985	Frame_Shift_Ins	INS	-	TATACATTGGAT	-	FOX2	23insATATACAT	p.Q174fs
XH_P37	7	114655971	114655971	Frame_Shift_Ins	INS	-	CAACAACAATCTT	-	MDFC	724insCAACACA	p.G241fs
XH_P37	7	116436030	116436030	Frame_Shift_Ins	INS	-	CAACAAGTAAAC	-	MET	sCCTTGCAACAA	p.S912fs
XH_P37	7	117254726	117254726	Frame_Shift_Ins	INS	-	AAATTTTACATT	-	CFR	CACTTTAAATT	p.L1143fs
XH_P37	7	117400751	117400751	In_Frame_Ins	INS	-	TATGTTTGCGG	-	CTTNBP2	nsGAAACCCACA	70delinsMKPTNINK
XH_P37	7	121755250	121755250	Nonsense_Mutation	INS	-	GGATCAAAATAT	-	AASS	sATGTGATATT	11307delinsCDIX
XH_P37	7	121758634	121758634	Nonsense_Mutation	INS	-	GGCTATGAAAT	-	AASS	3insGATATTTC	A75_H176delinsDISX
XH_P37	7	122076422	122076422	Frame_Shift_Ins	INS	-	GCCCTCTTTATTA	-	CADPS2	nsTAATAATAAA	p.K830fs
XH_P37	7	122081615	122081615	Nonsense_Mutation	INS	-	ATTTGTCTTCTC	-	CADPS2	GCAACTGAGAA	765_G766delinsX
XH_P37	7	122635249	122635249	In_Frame_Ins	INS	-	ACTTCACTGATG	-	TAS2R16	440insCACTAGT	5147delinsASVKW
XH_P37	7	123332717	123332717	Nonsense_Mutation	INS	-	GCACGTGTAGAC	-	WASL	31insTGGTCTAA	844_P345delinsLVX
XH_P37	7	124422106	124422106	In_Frame_Ins	INS	-	CTGACAGTCTC	-	C7orf77	3insCAGAGACT	G55delinsQRISDG
XH_P37	7	126086406	126086406	Frame_Shift_Ins	INS	-	CATCTGTAGA	-	GRM8	2451insTCTAC	p.T817fs
XH_P37	7	127014689	127014689	In_Frame_Ins	INS	-	CGAATGTAAGG	-	ZNF800	01insCTCTTAC	A234delinsPPYIRF
XH_P37	7	127977184	127977184	Splice_Site	INS	-	A	-	RBM28	-	-
XH_P37	7	127977186	127977186	In_Frame_Ins	INS	-	GAACACAGGAG	-	RBM28	AAACAACCTCTG	3delinsIETTPVFMK
XH_P37	7	129841914	129841914	Nonsense_Mutation	INS	-	GTAATGACTCTC	-	TMEM209	GAGAAAGAGAG	7delinsRQEKRVITLX
XH_P37	7	132192899	132192899	Nonsense_Mutation	INS	-	TTTGCTACTTTT	-	PLXNA4	54insAAAAGTGA	85_A186delinsKKX

XH_P37	7	133868553	133868553	Nonsense_Mutation	INS	-	GTCAAAAATAA	-	LRGUK	ATTATATGTCAA	429delinsQIDYM	KIIFKAX
XH_P37	7	134346379	134346379	Frame_Shift_Ins	INS	-	TAAGTTATATTC	-	BPGM	AGCTCAAGTTA	p.N40fs	
XH_P37	7	134730567	134730567	Nonsense_Mutation	INS	-	GAGTGCCCTGTT	-	AGBL3	50insTGAGTGC	K83_E84delinsKX	
XH_P37	7	135421943	135421943	In_Frame_Ins	INS	-	CTAATTTGT	-	FAM180A	81insACAAAT	p.V27delinsVQIR	
XH_P37	7	135421945	135421945	Missense_Mutation	SNP	C	G	C	FAM180A	c.G79C	p.V27L	
XH_P37	7	137374746	137374746	Frame_Shift_Ins	INS	-	AA	-	DGKI	c.403_404insTT	p.K135fs	
XH_P37	7	137374747	137374747	Nonsense_Mutation	INS	-	ATTTTCACATT	-	DGKI	03insCAATGTTG	35_A136delinsQCX	
XH_P37	7	138579263	138579263	Frame_Shift_Ins	INS	-	GTTCCTATAAG	-	KIAA1549	7insCTGCTTATA	p.R1286fs	
XH_P37	7	138602237	138602237	Frame_Shift_Ins	INS	-	CATTT	-	KIAA1549	134_2135insAA	p.S712fs	
XH_P37	7	138602239	138602239	Frame_Shift_Ins	INS	-	CTGAGTCTTCTT	-	KIAA1549	133insAAAGAA	p.P711fs	
XH_P37	7	138764529	138764529	Nonsense_Mutation	INS	-	TATCATCACCATA	-	ZC3HAV1	158insCTAGGTG	386_5387delinsSX	
XH_P37	7	140394550	140394550	In_Frame_Ins	INS	-	CTAAGGAAAAA	-	ADCK2	29insCACTAAGG	610delinsILRKNL	
XH_P37	7	141478746	141478746	In_Frame_Ins	INS	-	TTTCTCCTGCTG	-	TAS2R4	CAGTGTTCCTCC	3delinsALSVPAEAE	
XH_P37	7	141643714	141643714	Frame_Shift_Ins	INS	-	TTATTTTTTAAT	-	CLEC5A	AGAAAATTAAAA	p.T64fs	
XH_P37	7	141673352	141673352	Frame_Shift_Ins	INS	-	AGCCTGCT	-	TAS2R38	7_138insAGCAG	p.K46fs	
XH_P37	7	141920382	141920382	Missense_Mutation	SNP	T	C	T	MGAM2	c.T6071C	p.L2024P	
XH_P37	7	141921381	141921381	Missense_Mutation	SNP	C	G	C	MGAM2	c.C7070G	p.T2357R	
XH_P37	7	141921382	141921382	Frame_Shift_Ins	INS	-	AGAAGTAAGAG	-	MGAM2	2insAATAGAAG	p.T2357fs	
XH_P37	7	141954985	141954985	Missense_Mutation	SNP	G	T	G	PRSS58	c.C326A	p.T109K	
XH_P37	7	141954986	141954986	In_Frame_Ins	INS	-	CCCCC	-	PRSS58	24_325insGGGG	T109delinsGGT	
XH_P37	7	142658943	142658943	Frame_Shift_Ins	INS	-	ACAGTTGACATT	-	KEL	AAGGAATGTCA	p.S7fs	
XH_P37	7	143657198	143657198	Nonsense_Mutation	INS	-	GGATTATTAATG	-	OR2F1	TTCAAGGATTA	45delinsIKIFDYX	
XH_P37	7	143807135	143807135	In_Frame_Ins	INS	-	TATCTGGGAAC	-	OR2A2	1insACATCTTGG	154delinsHILGTL	
XH_P37	7	143929691	143929691	Nonsense_Mutation	INS	-	TCATCCTAAGAC	-	OR2A1	46insAGTCTTA	2_N83delinsAVLGX	
XH_P37	7	148485768	148485768	Splice_Site	INS	-	ACAAAAATACA	-	CUL1	.	.	
XH_P37	7	148486902	148486902	Nonsense_Mutation	INS	-	TAATTAATGTA	-	CUL1	ATAAACTAATT	53_A554delinsLSLX	
XH_P37	7	149476021	149476021	In_Frame_Ins	INS	-	GCTCAGCTA	-	SSPO	7_988insGCTCAW	329delinsWAQL	
XH_P37	7	150267044	150267044	Frame_Shift_Ins	INS	-	AGATTGTTCTCT	-	GIMAP4	TTTCAGATTGTT	p.Y19fs	
XH_P37	7	151814331	151814331	Frame_Shift_Ins	INS	-	TTCATTTTATCA	-	GALNT11	5GTCTGTCATA	p.C360fs	
XH_P37	7	151875020	151875020	Frame_Shift_Ins	INS	-	GGCCAGACTT	-	KMT2C	7518insAAGTC	p.Q2506fs	
XH_P37	7	151878454	151878454	Frame_Shift_Ins	INS	-	AGAGGGTTTITA	-	KMT2C	6491insTAAAA	p.G2164fs	
XH_P37	7	151879064	151879064	Frame_Shift_Ins	INS	-	CTGG	-	KMT2C	880_5881insCC	p.D1961fs	
XH_P37	7	151879065	151879065	In_Frame_Ins	INS	-	CCT	-	KMT2C	5879_5880insAG	N1960delinsKG	
XH_P37	7	156556491	156556491	Splice_Site	INS	-	TGTTTTAACCA	-	LMBR1	.	.	
XH_P37	7	157208758	157208758	Frame_Shift_Ins	INS	-	CTATCTTGGCCA	-	DNAJB6	8insATCTATCTT	p.S316fs	
XH_P37	7	158282450	158282450	Missense_Mutation	SNP	C	A	C	PTPRN2	c.G140T	p.G47V	
XH_P37	8	195659	195659	Frame_Shift_Ins	INS	-	TA	-	ZNFS96	c.812_813insTA	p.M271fs	
XH_P37	8	195661	195661	Nonsense_Mutation	INS	-	TTTTTGCTAAAG	-	ZNFS96	15insATTTTGTG	72_H273delinsNFCX	
XH_P37	8	2048761	2048761	Frame_Shift_Ins	INS	-	TTCCC	-	MYOM2	536_2537insTTG	p.G846fs	
XH_P37	8	2048762	2048762	Missense_Mutation	SNP	G	C	G	MYOM2	c.G2537C	p.G846A	
XH_P37	8	2823447	2823447	Nonsense_Mutation	INS	-	GTCACCTTATTT	-	CSMD1	ATTATAAAAAATA	44_N3045delinsSIKIKX	
XH_P37	8	2824238	2824238	Nonsense_Mutation	INS	-	AAGGTGTTATC	-	CSMD1	AAAAACAGTATA	985delinsIKNKTTXV	
XH_P37	8	6588332	6588332	Nonsense_Mutation	INS	-	CAAAATGAGCTT	-	AGPAT5	91insACAAAATG	30_C131delinsGTGX	
XH_P37	8	11995399	11995399	Missense_Mutation	SNP	G	T	G	USP17L2	c.C871A	p.L291I	
XH_P37	8	11995400	11995400	Silent	SNP	T	C	T	USP17L2	c.A870G	p.K290K	
XH_P37	8	12958158	12958158	Frame_Shift_Ins	INS	-	ACTGT	-	DLCL	154_155insACA	p.V52fs	
XH_P37	8	16944485	16944485	Nonsense_Mutation	INS	-	GTAAACCATATC	-	MICU3	TATTGGTAACCC	259delinsYPLVTHNX	
XH_P37	8	17613291	17613291	Nonsense_Mutation	INS	-	TCAGTGCCTGCT	-	MTUS1	insGTGCAGGAC	K9delinsSAGHX	
XH_P37	8	17814871	17814871	Nonsense_Mutation	INS	-	AATAATCGACTC	-	PCM1	1746insAATAAT	C582_E583delinsX	
XH_P37	8	18258370	18258370	Frame_Shift_Ins	INS	-	AGAAATCTTTTG	-	NAT2	AATTAAAGAAAT	p.G286fs	
XH_P37	8	18656818	18656818	Frame_Shift_Ins	INS	-	CAGACAGAGCTT	-	PSD3	7insTAAAGAGCTC	p.D156fs	
XH_P37	8	21955795	21955795	In_Frame_Ins	INS	-	ACAATCTTTTAA	-	FAM160B2	743insACAATCT	S248delinsYNLFT	
XH_P37	8	24254894	24254894	Nonsense_Mutation	INS	-	STAATGTAAGTT	-	ADAMDEC1	TTCTGGTAATGT	D5_H106delinsNFWX	
XH_P37	8	24775771	24775771	Frame_Shift_Ins	INS	-	CCTCCTTTACAG	-	NEFM	276insTCTCCTCT	p.A425fs	
XH_P37	8	25364951	25364951	In_Frame_Ins	INS	-	ATGGAACGTCTT	-	CDCA2	25insCATGGAA	908delinsTHGTSS	
XH_P37	8	26221301	26221301	Silent	SNP	G	A	G	PPP2R2A	c.G897A	p.S299S	
XH_P37	8	27516838	27516838	In_Frame_Ins	INS	-	TGAGTT	-	SCARA3	51_1152insTGA	p.S384delinsSEF	
XH_P37	8	27634030	27634030	Nonsense_Mutation	INS	-	AAGCTCTACTTG	-	ESCO2	TAAGTAAGCTCT	9_S70delinsLSKLYLX	
XH_P37	8	27634032	27634032	In_Frame_Ins	INS	-	TAT	-	ESCO2	c.207_208insTA	p.P69delinsPY	
XH_P37	8	28956660	28956660	In_Frame_Ins	INS	-	ATGTGTG	-	KIF13B	13_4314insCAA	S1438delinsSNI	
XH_P37	8	28956662	28956662	Frame_Shift_Ins	INS	-	TTGATCTTGC	-	KIF13B	4312insGCAAG	p.S1438fs	
XH_P37	8	29003927	29003927	Frame_Shift_Ins	INS	-	TGACTTCCTTTG	-	KIF13B	155insGAAAG	p.I719fs	
XH_P37	8	30702137	30702137	Frame_Shift_Ins	INS	-	AAGAGAGAAG	-	TEX15	insCCCTCTCTCT	p.Q1849fs	
XH_P37	8	30703100	30703100	Missense_Mutation	SNP	G	A	G	TEX15	c.C4583T	p.T1528I	
XH_P37	8	30703102	30703102	Nonsense_Mutation	INS	-	TCAGTCTTAGAT	-	TEX15	581insAATCTAA	527_T1528delinsRIX	
XH_P37	8	32621851	32621851	Frame_Shift_Ins	INS	-	AATCTGTTAGCA	-	NRG1	384insCAATCTG	p.F461fs	
XH_P37	8	35579774	35579774	Nonsense_Mutation	INS	-	ATATCTTAACTG	-	UNC5D	GGCAAAATATCT	3_A384delinsARQISX	
XH_P37	8	37624030	37624030	Frame_Shift_Ins	INS	-	CTAAGGCTTCTG	-	PLBP	6insATCTAAGG	p.N152fs	
XH_P37	8	37729139	37729139	Frame_Shift_Ins	INS	-	CTGCACATCT	-	RAB11FIP1	3181insGAATG	p.S1061fs	
XH_P37	8	38095711	38095711	Frame_Shift_Ins	INS	-	ATACAATGCA	-	DDHD2	607insATACAA	p.S202fs	
XH_P37	8	38095713	38095713	Frame_Shift_Ins	INS	-	FAAGTGTAGAA	-	DDHD2	9insTTTAAGTGT	p.V203fs	
XH_P37	8	38271482	38271482	Frame_Shift_Ins	INS	-	TTCCC	-	FGFR1	978_1979insGG	p.Q660fs	
XH_P37	8	38684832	38684832	In_Frame_Ins	INS	-	AGCAAGGAGGA	-	TACC1	1insAAAGCAAG	123delinsYKARRK	
XH_P37	8	39506044	39506044	In_Frame_Ins	INS	-	AACAACACTCCA	-	ADAM18	CATCTAAACCA	6delinsTTSKQHSIHNH	
XH_P37	8	41566310	41566310	Missense_Mutation	SNP	T	G	T	ANK1	c.A1984C	p.N662H	
XH_P37	8	41566312	41566312	Frame_Shift_Ins	INS	-	AGGATTCTGAG	-	ANK1	1982insCTCAG	p.G661fs	
XH_P37	8	41845072	41845072	Frame_Shift_Ins	INS	-	TG	-	KAT6A	c.609_610insCA	p.E204fs	
XH_P37	8	41845074	41845074	Nonsense_Mutation	INS	-	ATGCTCTTAGAA	-	KAT6A	5AAACCTTCTAA	A203delinsETFX	
XH_P37	8	42232365	42232365	Nonsense_Mutation	INS	-	TGTTTGTATCTG	-	DKK4	9insAGAGATAAA	p.T110delinsKRX	
XH_P37	8	42706121	42706121	Frame_Shift_Ins	INS	-	CATCATATTGAC	-	RNF170	6insATGTCAATA	p.S139fs	
XH_P37	8	48882505	48882505	In_Frame_Ins	INS	-	ACC	-	MCMA4	1322_1323insA	p.F441delinsLP	
XH_P37	8	48882506	48882506	Frame_Shift_Ins	INS	-	TCCCATATCTCC	-	MCMA4	1324insTCCCAT	p.F441fs	
XH_P37	8	49986636	49986636	Missense_Mutation	SNP	T	A	T	C8orf22	c.T74A	p.V25D	
XH_P37	8	53555020	53555020	Frame_Shift_Ins	INS	-	ATCATGCTTGTG	-	RB1CC1	AATGGAGACAA	p.V1410fs	
XH_P37	8	53569061	53569061	In_Frame_Ins	INS	-	AAAGACAGACA	-	RB1CC1	8insTTTTTGTCT	110delinsFLVFLK	
XH_P37	8	53586809	53586809	Frame_Shift_Ins	INS	-	AAAGTACTGTT	-	RB1CC1	598insAACAGT	p.A200fs	
XH_P37	8	59405059	59405059	Nonsense_Mutation	INS	-	ATATATTTTGGA	-	CYP7A1	AAATTTTCCAAA	insLKNSDHYLNP	PKYMNIX
XH_P37	8	61750383	61750383	In_Frame_Ins	INS	-	TACTGCAATGA	-	CHD7	AATAGTACTG	8delinsEINSYCN	PEPNVS
XH_P37	8	61757949	61757949	Frame_Shift_Ins	INS	-	A	-	CHD7	c.5191_5192ins	p.L1731fs	
XH_P37	8	61757950	61757950	Frame_Shift_Ins	INS	-	CATAATAATAAT	-	CHD7	c.5193insCATAAT	p.L1731fs	
XH_P37	8	61764785	61764785	Frame_Shift_Ins	INS	-	TTGCAATACAGA	-	CHD7	374insCTTGCAA	p.I1958fs	
XH_P37	8	62577933	62577933	Frame_Shift_Ins	INS	-	ACAAAAA	-	ASPH	99_510insTTTTT	p.S170fs	
XH_P37	8	62577934	62577934	Frame_Shift_Ins	INS	-	ATGGAAATATGT	-	ASPH	509insTACATTT	p.S170fs	
XH_P37	8	67342376	67342376	Nonsense_Mutation	INS	-	TTGAACTCTC	-	RRS1	1011insTTGAA	337_L338delinsSGX	
XH_P37	8	67547069	67547069	Missense_Mutation	SNP	C	A	C	VCPIP1	c.G3336T	p.M112I	
XH_P37	8	67547070	67547070	Frame_Shift_Ins	INS	-	CTGATGGC	-	VCPIP1	4_3335insGCCA	p.M1112fs	
XH_P37	8	67808569	67808569	Frame_Shift_Ins	INS	-	GACATTATCCAT	-	MCMDC2	445insAGACATT	p.M482fs	
XH_P37	8	67808571	67808571	Frame_Shift_Ins	INS	-	TTATTTAA	-	MCMDC2	6_1447insTTAT	p.M482fs	

XH_P37	8	69009402	69009402	Nonsense_Mutation	INS	-	TATTCTTGTTAA	-	PREX2	AGCATCTATTCT	40_E841delinsMCX
XH_P37	8	70744040	70744040	Nonsense_Mutation	INS	-	AAAGTTCACCTTT	-	SLC05A1	AAAAATAAAGTG	290_D291delinsGX
XH_P37	8	71646207	71646207	In_Frame_Ins	INS	-	AAAAAAAATAAA	-	XKR9	AAAACAAAAAA	224delinsSNKKIKNI
XH_P37	8	72951256	72951256	Nonsense_Mutation	INS	-	SACTTTATTATA	-	TRPA1	SGCTATTTATAA	714delinsANSYRLFIKXS
XH_P37	8	73849746	73849746	Missense_Mutation	SNP	T	C	T	KCNB2	c.T2156C	p.F719S
XH_P37	8	74207549	74207549	Missense_Mutation	SNP	G	T	G	RDH10	c.G25T	p.V9L
XH_P37	8	77762561	77762561	Frame_Shift_Ins	INS	-	TGCCACTTTA	-	ZFHx4	3928insTGCCA	p.P1309fs
XH_P37	8	77764584	77764584	Frame_Shift_Ins	INS	-	AAAAATGGAAAG	-	ZFHx4	GTATATAAAAT	p.Q1809fs
XH_P37	8	82606479	82606479	Frame_Shift_Ins	INS	-	TA	-	SLC10A5	c.728_729insTA	p.T243fs
XH_P37	8	82606480	82606480	Nonsense_Mutation	INS	-	TATTTTAATGTTT	-	SLC10A5	TACGAACATTA	243delinsINSYEHX
XH_P37	8	82615184	82615184	Frame_Shift_Ins	INS	-	AATCTTGGAA	-	ZFAND1	656insTTCCAA	p.N219fs
XH_P37	8	82615186	82615186	Frame_Shift_Ins	INS	-	TC	-	ZFAND1	c.653_654insGA	p.N218fs
XH_P37	8	82627265	82627265	Frame_Shift_Ins	INS	-	CAGAAACTTGT	-	ZFAND1	23insAACCAAGT	p.V75fs
XH_P37	8	87235276	87235276	Nonsense_Mutation	INS	-	TGTTTACTGTTG	-	SLC7A13	ATAATGAACAGT	248_V249delinsIEX
XH_P37	8	87549843	87549843	Nonsense_Mutation	INS	-	CTAACTCTATAG	-	CPNE3	insAGTCTAACTC	D171delinsEVX
XH_P37	8	87549845	87549845	In_Frame_Ins	INS	-	ATA	-	CPNE3	514_515insAT	p.G172delinsDR
XH_P37	8	90801558	90801558	Nonsense_Mutation	INS	-	AAAGGTGTTTCA	-	RIPK2	ACTTACAAGGT	insQDCYFMKLHLHQLGVSQX
XH_P37	8	91094923	91094923	Nonsense_Mutation	INS	-	AATCTTATCTCT	-	CALB1	insAAGAAGATAA	p.M1delinsIRRX
XH_P37	8	92032486	92032486	Frame_Shift_Ins	INS	-	TTTT	-	TMEM55A	260_261insGAA	p.I87fs
XH_P37	8	92032487	92032487	Nonsense_Mutation	INS	-	CCAGAATCTAG	-	TMEM55A	AATAATCTAGAT	187_K88delinsKXX
XH_P37	8	94748282	94748282	In_Frame_Ins	INS	-	ACAGTGGATTG	-	RBM12B	67insCTCAATCC	N119delinsNSIHCC
XH_P37	8	94809634	94809634	Frame_Shift_Ins	INS	-	CATAT	-	TMEM67	36_2037insCA	p.E679fs
XH_P37	8	94809636	94809636	Frame_Shift_Ins	INS	-	CCTGAAAAAGT	-	TMEM67	AAACACCTGAA	p.1680fs
XH_P37	8	95448864	95448864	Nonsense_Mutation	INS	-	AGAAAGAGTGAG	-	FSBP	ATAGCCTCACTT	A79delinsFLIASLFSFX
XH_P37	8	95538543	95538543	Nonsense_Mutation	INS	-	TATGTGTAAGG	-	VIRMA	AAGTATCCTTAG	delinsQYQVSLHINKLP
XH_P37	8	95738597	95738597	Frame_Shift_Ins	INS	-	A	-	DPY19L4	c.55_56insA	p.S19fs
XH_P37	8	95738598	95738598	Nonsense_Mutation	INS	-	STATCAAAGATA	-	DPY19L4	ATTAGTATCAAA	9_S20delinsSTKTYX
XH_P37	8	99142344	99142344	Missense_Mutation	SNP	G	A	G	POP1	c.G625A	p.A209T
XH_P37	8	99217456	99217456	In_Frame_Ins	INS	-	GCTTCAGATGAT	-	NIPAL2	674insATCATCT	S225delinsYHLKP
XH_P37	8	99217458	99217458	Nonsense_Mutation	INS	-	TATAAATGAG	-	NIPAL2	672insCTCATT	24_S225delinsISFX
XH_P37	8	100712028	100712028	Nonsense_Mutation	INS	-	GGCTTTG	-	VPS13B	97_6398insGGC	I33_I2134delinsRLX
XH_P37	8	100712030	100712030	Missense_Mutation	SNP	A	T	A	VPS13B	c.A6399T	p.K2133N
XH_P37	8	101163615	101163615	Frame_Shift_Ins	INS	-	CT	-	POLR2K	c.32_33insCT	p.K11fs
XH_P37	8	101163616	101163616	Frame_Shift_Ins	INS	-	CATAATAACTAG	-	POLR2K	insGACATAATA	p.K11fs
XH_P37	8	101541950	101541950	Nonsense_Mutation	INS	-	TTCTGTGTGTTT	-	ANKRD46	TCTTAAACAACAC	P38_N39delinsFX
XH_P37	8	103238253	103238253	In_Frame_Ins	INS	-	CCAGCAAACTAT	-	RRM2B	58insATAGTTTG	S20delinsIVCWS
XH_P37	8	104078644	104078644	Frame_Shift_Ins	INS	-	AAACGCAAACTC	-	ATP6V1C1	D23insGAAACG	p.H341fs
XH_P37	8	104898201	104898201	Frame_Shift_Ins	INS	-	TATGCCT	-	RIMS2	8_799insTATGC	p.H266fs
XH_P37	8	104898203	104898203	Missense_Mutation	SNP	A	T	A	RIMS2	c.A800T	p.H267L
XH_P37	8	108509742	108509742	In_Frame_Ins	INS	-	AAAATTATACTC	-	ANGPT1	insACTGAGTATA	T15delinsTLSIIFH
XH_P37	8	110302105	110302105	Frame_Shift_Ins	INS	-	CATGTATTTTCC	-	NUDCD1	TTCTGGAAAAATA	p.H204fs
XH_P37	8	113332209	113332209	In_Frame_Ins	INS	-	AATTTTAAAGAA	-	CSMD3	TCTCCCTCTTTAA	5delinsAPSPFLKILNGL
XH_P37	8	116631844	116631844	Frame_Shift_Ins	INS	-	CTTCAGGACTTT	-	TRPS1	insTTTAAAGTC	p.L152fs
XH_P37	8	116631846	116631846	Frame_Shift_Ins	INS	-	CAAT	-	TRPS1	451_452insATT	p.S151fs
XH_P37	8	117738327	117738327	Nonsense_Mutation	INS	-	ACTTGATGTCTG	-	EIF3H	17insTCAGACA	P73_D74delinsSDIKX
XH_P37	8	117869004	117869004	Frame_Shift_Ins	INS	-	GATGTTTTTAG	-	RAD21	695insCTAAAA	p.K232fs
XH_P37	8	117869006	117869006	Frame_Shift_Ins	INS	-	AATTATAAATA	-	RAD21	693insTATTITA	p.D231fs
XH_P37	8	120594791	120594791	Frame_Shift_Ins	INS	-	AGCCAAAGGTA	-	ENPP2	TTATTTCTACCTT	p.N532fs
XH_P37	8	120594793	120594793	In_Frame_Ins	INS	-	TTTATGTTTATT	-	ENPP2	1593insAATAAA	L531delinsLINIK
XH_P37	8	120810082	120810082	In_Frame_Ins	INS	-	GGTTGGTATCTC	-	TAF2	TGAAGAGATAC	6delinsNLKRYQPKNA
XH_P37	8	121528268	121528268	Frame_Shift_Ins	INS	-	ACATTTACTTTA	-	MTBP	GCAGGACATTT	p.5695fs
XH_P37	8	123965286	123965286	In_Frame_Ins	INS	-	TTGAGATGTGCT	-	ZHX2	1537insTTGAGAA	A512delinsALRCA
XH_P37	8	124250048	124250048	In_Frame_Ins	INS	-	TTCTCTGTTTAG	-	C8orf76	TACTCTAACCAA	16delinsVTPNKRKTS
XH_P37	8	124267550	124267550	Nonsense_Mutation	INS	-	CAAGCTCTTA	-	ZHX1	637insTAAGAC	E213_I214delinsSX
XH_P37	8	124359569	124359569	In_Frame_Ins	INS	-	AAACTT	-	ATAD2	74_1975insAAAG	Y659delinsKFY
XH_P37	8	124359570	124359570	In_Frame_Ins	INS	-	CATTTAAAGTTA	-	ATAD2	AAAAACTAACTT	58delinsIKTNFKWSI
XH_P37	8	125499027	125499027	Nonsense_Mutation	INS	-	GATCCAATAAAA	-	RNF139	138insTGATCC	379_A380delinsSX
XH_P37	8	130867964	130867964	Nonsense_Mutation	INS	-	TGTAITTTAAATG	-	FAM49B	1insATCATTTTAA	111_I112delinsIIX
XH_P37	8	130867966	130867966	Missense_Mutation	SNP	G	T	G	FAM49B	c.C329A	p.A110D
XH_P37	8	131073058	131073058	In_Frame_Ins	INS	-	GGAAACCTTATCT	-	ASAP1	59insCGGAATA	987delinsRNRVPK
XH_P37	8	131130481	131130481	Nonsense_Mutation	INS	-	TATAAAAAATAT	-	ASAP1	CCAAAAATAAT	T603delinsEAKNNFYIX
XH_P37	8	133014015	133014015	Frame_Shift_Ins	INS	-	ATGG	-	EFR3A	059_2060insAT	p.T687fs
XH_P37	8	133014017	133014017	Frame_Shift_Ins	INS	-	TACTGTCAGTG	-	EFR3A	2062insTACTGT	p.T687fs
XH_P37	8	133650348	133650348	In_Frame_Ins	INS	-	TAAAGGTATGG	-	LRRc6	AAGAACCATAC	6delinsKRTIPLIVE
XH_P37	8	136554966	136554966	In_Frame_Ins	INS	-	TTTCTTTATATT	-	KHDRB53	insTATATTCTTT	T93delinsYVFFIIS
XH_P37	8	136554968	136554968	In_Frame_Ins	INS	-	GTG	-	KHDRB53	279_280insGT	p.T93delinsTV
XH_P37	8	139601616	139601616	In_Frame_Ins	INS	-	TTTTTCTTTCTTT	-	COL22A1	SGATAAAAGAA	587delinsTICKERKKK
XH_P37	8	139601617	139601617	Frame_Shift_Ins	INS	-	GCTTTTGTGTTTA	-	COL22A1	insAAATAAAAC	p.T1587fs
XH_P37	8	139648997	139648997	Frame_Shift_Ins	INS	-	CTTTCTTTCTCT	-	COL22A1	AGGAAAGGAAA	p.Q1181fs
XH_P37	8	139648999	139648999	Missense_Mutation	SNP	G	T	G	COL22A1	c.C3541A	p.Q1181K
XH_P37	8	141034174	141034174	Frame_Shift_Ins	INS	-	TAAAT	-	TRAPPC9	531_2532insAT	p.T844fs
XH_P37	8	141461325	141461325	Missense_Mutation	SNP	G	C	G	TRAPPC9	c.C148G	p.Q50E
XH_P37	8	145583291	145583291	Frame_Shift_Ins	INS	-	CA	-	SLC52A2	c.139_140insCA	p.L47fs
XH_P37	8	145583293	145583293	Silent	SNP	C	G	C	SLC52A2	c.C141G	p.L47L
XH_P37	8	146067356	146067356	In_Frame_Ins	INS	-	ACTCTCTCT	-	ZNF7	6_577insACTCTC	R192delinsRTL5
XH_P37	8	146108089	146108089	In_Frame_Ins	INS	-	CAGTCCTTAGTA	-	ZNF250	insGTTTACTAAG	160delinsCLLRTTEL
XH_P37	9	712427	712427	Missense_Mutation	SNP	A	C	A	KANK1	c.A1187C	p.E396A
XH_P37	9	712428	712428	Frame_Shift_Ins	INS	-	GCTCT	-	KANK1	188_1189insGC	p.E396fs
XH_P37	9	2646449	2646449	Nonsense_Mutation	INS	-	ACTGATC	-	VLDLR	77_1478insACTG	493_K494delinsYX
XH_P37	9	4125919	4125919	Frame_Shift_Ins	INS	-	AAGCAACTCTCT	-	GLIS3	6ATTGAGAGAG	p.Q137fs
XH_P37	9	4826887	4826887	Frame_Shift_Ins	INS	-	CAACAGCACA	-	RCL1	239insCAACAG	p.L80fs
XH_P37	9	5054805	5054805	Nonsense_Mutation	INS	-	TTGGTAAAGAA	-	JAK2	ACATTTTGTGTA	7delinsARIHFGKNVLX
XH_P37	9	5457283	5457283	Missense_Mutation	SNP	G	A	G	CD274	c.G257A	p.R86Q
XH_P37	9	5534873	5534873	Frame_Shift_Ins	INS	-	CACTGTCTTATT	-	PDCD1L62	185insCACCTGT	p.V62fs
XH_P37	9	5831010	5831010	Nonsense_Mutation	INS	-	CAAGCTATTATG	-	ERMP1	insGTCAATAATA	19_I120delinsMSX
XH_P37	9	6420988	6420988	In_Frame_Ins	INS	-	CATTCTCTCTCTG	-	UHRF2	CAATACATTCTCT	77delinsPNTFSLSLF
XH_P37	9	6986655	6986655	Frame_Shift_Ins	INS	-	5AAGGTACACTT	-	KDM4C	ATATAGAAGGT	p.K556fs
XH_P37	9	7798595	7798595	Missense_Mutation	SNP	C	A	C	TMEM261	c.G329T	p.G110W
XH_P37	9	7798596	7798596	In_Frame_Ins	INS	-	AGA	-	TMEM261	c.327_328insTC	p.G110delinsSG
XH_P37	9	8518275	8518275	In_Frame_Ins	INS	-	SGTACAGTGGAA	-	PTPRD	nsTTCTCTCCACT	62delinsGSGFCHTKM
XH_P37	9	8518391	8518391	In_Frame_Ins	INS	-	AACACAAAC	-	PTPRD	9_970insGTTTG	S324delinsVCVS
XH_P37	9	14841546	14841546	Nonsense_Mutation	INS	-	GACTTTTATAGA	-	FREM1	TAGATATCTAT	p.G594delinsTX
XH_P37	9	14859286	14859286	Nonsense_Mutation	INS	-	AGTTAGTGGTT	-	FREM1	526insAACAC	T76_T177delinsNHX
XH_P37	9	14859287	14859287	Silent	SNP	C	A	C	FREM1	c.G525T	p.L175L
XH_P37	9	15571725	15571725	Frame_Shift_Ins	INS	-	G	-	CCDC171	c.145_146insG	p.K49fs
XH_P37	9	15571727	15571727	Frame_Shift_Ins	INS	-	TGACATGGTCTC	-	CCDC171	sAACATGACATG	p.K49fs
XH_P37	9	16738415	16738415	Nonsense_Mutation	INS	-	TTTAC	-	BNC2	71_72insGTAA	D24_D25delinsQX
XH_P37	9	16738417	16738417	In_Frame_Ins	INS	-	CTTTCATACITAT	-	BNC2	insGATAAGTAT	Q24delinsDKYERQ

XH_P37	9	19446365	19446365	Nonsense Mutation	INS	-	TAATATGGATC	-	ACER2	rsACCTCAATATG	97_F198delinsAPX
XH_P37	9	20770236	20770236	Nonsense Mutation	INS	-	ACAAGTGCACCT	-	FOCAD	ACTATACAAGTCT	302_D303delinsDX
XH_P37	9	21305074	21305074	Nonsense Mutation	INS	-	TGTGGACTCT	-	IFNA5	182insAGAGTCT	F61_P62delinsX
XH_P37	9	21409197	21409197	Frame Shift Ins	INS	-	TCTCTACA	-	IFNA5	2_23insTCTCTA	p.L8fs
XH_P37	9	21409199	21409199	Frame Shift Ins	INS	-	GGCTTAGGAAA	-	IFNA8	25insGGCTTAG	p.L8fs
XH_P37	9	23701477	23701477	Nonsense Mutation	INS	-	GGTTTATTACT	-	ELAVL2	rsTAATAGTAAT	A205_P206delinsX
XH_P37	9	24543719	24543719	Nonsense Mutation	INS	-	5AAGTCATTTTA	-	IZUMO3	5insATTTAAAT	69_A170delinsNLKX
XH_P37	9	27044746	27044746	Nonsense Mutation	INS	-	GACTTATAGAGA	-	IFT74	TACAATGACCTTA	54_N355delinsLLQX
XH_P37	9	27168491	27168491	Splice Site	INS	-	GATGAAAGGG	-	TEK	.	.
XH_P37	9	27548409	27548409	In_Frame_Ins	INS	-	TGTAACCTTAATA	-	C9orf72	TAGGCTTATTAA	24delinsILSLVTFK
XH_P37	9	27950114	27950114	Frame Shift Ins	INS	-	AACACCTGGTAT	-	LINGO2	56insTATACCAG	p.K186fs
XH_P37	9	32631334	32631334	Frame Shift Ins	INS	-	TCCATGCTGGAT	-	TAF1L	244insGATCCAG	p.M1415fs
XH_P37	9	33548082	33548082	In_Frame_Ins	INS	-	TGCTGTAAGTGG	-	ANKRD18B	1108insTGCCTG	5369delinsSCCKW
XH_P37	9	33548826	33548826	Missense Mutation	SNP	G	T	G	ANKRD18B	c.G1851T	p.Q617H
XH_P37	9	33548827	33548827	Frame Shift Ins	INS	-	TCCTTTATTCG	-	ANKRD18B	1853insTCCTT	p.Y618fs
XH_P37	9	34343136	34343136	Nonsense Mutation	SNP	G	T	G	NUDT2	c.G142T	p.G48X
XH_P37	9	34343137	34343137	In_Frame_Ins	INS	-	CCAGCTATTTAT	-	NUDT2	44insCCAGCTTA	G48delinsGPIAYL
XH_P37	9	34725246	34725246	Frame Shift Ins	INS	-	ATGCCAAC	-	FAM205A	0_1991insGTTG	p.P664fs
XH_P37	9	35044595	35044595	Missense Mutation	SNP	G	A	G	C9orf131	c.G1864A	p.V622I
XH_P37	9	35044596	35044596	Nonsense Mutation	INS	-	AGCTTCAGAATC	-	C9orf131	56insCTAGCTTC	622_5623delinsSVX
XH_P37	9	35910675	35910675	Nonsense Mutation	INS	-	A	-	SPAAR	c.260_261insA	W87_T88delinsX
XH_P37	9	35910676	35910676	Frame Shift Ins	INS	-	CA	-	SPAAR	c.261_262insCA	p.W87fs
XH_P37	9	35957885	35957885	Frame Shift Ins	INS	-	AT	-	OR252	c.210_211insAT	p.D71fs
XH_P37	9	35957887	35957887	In_Frame_Ins	INS	-	ACCACCTCACCT	-	OR252	209insAGGTGA	L70delinsQVKWL
XH_P37	9	35958042	35958042	Silent	SNP	G	T	G	OR252	c.C54A	p.L18L
XH_P37	9	35958043	35958043	Missense Mutation	SNP	A	G	A	OR252	c.T53C	p.L18P
XH_P37	9	37541248	37541248	Nonsense Mutation	INS	-	AATCTGCTTTAT	-	FBXO10	2AAGAAATAAGG	Q3_C174delinsLYQEX
XH_P37	9	43624874	43624874	In_Frame_Ins	INS	-	5AAAAACAAGTC	-	SPATA31A6	13insGGGACTT	1271delinsRGLVFL
XH_P37	9	43625258	43625258	Silent	SNP	G	A	G	SPATA31A6	c.C3429T	p.G1143G
XH_P37	9	43625429	43625429	In_Frame_Ins	INS	-	AAACATCAAGC	-	SPATA31A6	258insTTGCTTGG	1086delinsNCLMFS
XH_P37	9	43627394	43627394	Frame Shift Ins	INS	-	TCCTATCTCCT	-	SPATA31A6	1293insAGGAG	p.A431fs
XH_P37	9	43627533	43627533	Nonsense Mutation	INS	-	GTCCTATCTCC	-	SPATA31A6	1154insGGAGA	B85_G386delinsRRX
XH_P37	9	43627535	43627535	In_Frame_Ins	INS	-	CTT	-	SPATA31A6	1151_1152insAA	p.N384delinsKSX
XH_P37	9	43853575	43853575	In_Frame_Ins	INS	-	GACATTTAAAA	-	CNTNAP3B	AAAAATGACATT	12delinsRKMFTKKLN
XH_P37	9	74817612	74817612	Nonsense Mutation	INS	-	AATGCAATCAG	-	GDA	TAGGTAATGCA	F114delinsRFGNAIRQLX
XH_P37	9	77455016	77455016	In_Frame_Ins	INS	-	TTTTTCTTTCT	-	TRPM6	AAGAGAAAGG	delinsKKRKRKRKEG
XH_P37	9	78686760	78686760	In_Frame_Ins	INS	-	AGAACAGAGCTC	-	PCSK5	rsCAAAGAACAG	280delinsTQRTELQ
XH_P37	9	78773972	78773972	Frame Shift Ins	INS	-	CC	-	PCSK5	.1504_1505insC	p.V502fs
XH_P37	9	78773974	78773974	In_Frame_Ins	INS	-	TGAGCTCTGTG	-	PCSK5	ACTCACCTGAGC	delinsVQVHSPCLCDVCS
XH_P37	9	79117775	79117775	Nonsense Mutation	INS	-	GGCCTTTTTAA	-	GCNT1	479insGGCGTT	60_S161delinsGAFX
XH_P37	9	79834939	79834939	Frame Shift Ins	INS	-	ACAGTTCCAGAG	-	VP513A	rsTTCTACAGTTC	p.P275fs
XH_P37	9	84606824	84606824	Nonsense Mutation	INS	-	CTGAGAAATGA	-	SPATA31D1	0insTGGCTGAG	80_H481delinsHGX
XH_P37	9	86495281	86495281	Frame Shift Ins	INS	-	AACCTACTTATG	-	KIF27	4insTTCAATAA	p.K858fs
XH_P37	9	86616559	86616559	Frame Shift Ins	INS	-	AGATCATTGTI	-	RM1	TAAGTAGATCA	p.V220fs
XH_P37	9	86617158	86617158	Frame Shift Ins	INS	-	TT	-	RM1	.1257_1258insT	p.K419fs
XH_P37	9	86617159	86617159	Nonsense Mutation	INS	-	AGGATTATGTGA	-	RM1	GTATTAGGATT	L421delinsRSIRIMX
XH_P37	9	86617382	86617382	Frame Shift Ins	INS	-	TATTTTATTTT	-	RM1	2insAATATTTT	p.L494fs
XH_P37	9	86617383	86617383	In_Frame_Ins	INS	-	GAGTGCTTA	-	RM1	2_1483insGAAT	L494delinsLEWL
XH_P37	9	88204558	88204558	In_Frame_Ins	INS	-	CGTATTTTATAA	-	AGTPBP1	TTTCCATTATAA	21delinsHFHYKRLK
XH_P37	9	90343256	90343256	Nonsense Mutation	INS	-	AAACATGTAA	-	CTSL	342insAAACAT	L4_P115delinsANMX
XH_P37	9	91083495	91083495	Nonsense Mutation	INS	-	CTGGAATTTTG	-	SPIN1	5TACACCTGAAA	G188delinsGYTX
XH_P37	9	94487188	94487188	Frame Shift Ins	INS	-	A	-	ROR2	-1587_1588ins	p.R530fs
XH_P37	9	94487189	94487189	Frame Shift Ins	INS	-	TACTACAA	-	ROR2	6_1587insTTGT	p.A529fs
XH_P37	9	94991313	94991313	Frame Shift Ins	INS	-	TGTG	-	IARS	378_3379insCA	p.T1127fs
XH_P37	9	94991314	94991314	Frame Shift Ins	INS	-	GGTTGTTTTTG	-	IARS	3378insCAAAA	p.N1126fs
XH_P37	9	95030514	95030514	Nonsense Mutation	INS	-	AACTTTTTTCC	-	IARS	ATTCAGGAAGAA	458_R459delinsX
XH_P37	9	95155479	95155479	Frame Shift Ins	INS	-	GTCCATTCATTT	-	OGN	rsCAACAAATGA	p.C106fs
XH_P37	9	95610537	95610537	Frame Shift Ins	INS	-	T	-	ZNF484	c.423_424insA	p.C142fs
XH_P37	9	95610538	95610538	In_Frame_Ins	INS	-	TTGCACATGAGA	-	ZNF484	nsTACTCTCATG	141delinsNTLMCKG
XH_P37	9	96025926	96025926	In_Frame_Ins	INS	-	TTCTCA	-	WNK2	89_3490insTCT	E1163delinsESP
XH_P37	9	97346915	97346915	In_Frame_Ins	INS	-	GGATGGCGAT	-	FBP2	nsAAGAATCGCC	124delinsKNRQSSS
XH_P37	9	97897778	97897778	Nonsense Mutation	INS	-	GGAGATGCTTGG	-	FANCC	TGATTCGAAGC	p.K231delinsKX
XH_P37	9	99284852	99284852	Frame Shift Ins	INS	-	TCCTCATGAGCC	-	CDC14B	168insAGGCTCA	p.Q390fs
XH_P37	9	99607277	99607277	Frame Shift Ins	INS	-	TTTTATTGAG	-	ZNF782	.37insCTCAATA	p.L13fs
XH_P37	9	99607279	99607279	In_Frame_Ins	INS	-	ATA	-	ZNF782	c.34_35insTAT	p.D12delinsVY
XH_P37	9	100672756	100672756	Nonsense Mutation	INS	-	ATCAAGACGTGA	-	TRMO	TCTGATCACGTC	84_P185delinsLITSX
XH_P37	9	100692725	100692725	Frame Shift Ins	INS	-	CCAAAGAAACAT	-	HEMGN	5CTGGGATGTTT	p.S318fs
XH_P37	9	100767423	100767423	Nonsense Mutation	INS	-	AATCTAGGCTC	-	ANP32B	insTAAAAATCTA	E169delinsVKFX
XH_P37	9	100823193	100823193	In_Frame_Ins	INS	-	ATCTTTTATTTT	-	NANS	insACCATCTCTT	88delinsSHLYLFM
XH_P37	9	100849752	100849752	In_Frame_Ins	INS	-	ATCACTTACACT	-	TRIM14	insAGTAGTGTA	p.X443delinsX
XH_P37	9	101824324	101824324	Nonsense Mutation	SNP	C	A	C	COL15A1	c.C3474A	p.Y1158X
XH_P37	9	101824325	101824325	Nonsense Mutation	INS	-	ATTAAACAAAA	-	COL15A1	AAATGAATTAAT	R1160delinsLIINELKQKX
XH_P37	9	101894869	101894869	In_Frame_Ins	INS	-	5TATCTCTCAGCC	-	TGFBR1	CTCTGTATTCT	5delinsLTPVFESHY
XH_P37	9	104170383	104170383	Nonsense Mutation	INS	-	AAATAAAGTCAA	-	ZNF189	nsAACAAATAAA	R97delinsRNKX
XH_P37	9	104171321	104171321	In_Frame_Ins	INS	-	TCCTCTGATGTG	-	ZNF189	TATGGATCCCTCT	0delinsSMDPLMFNK
XH_P37	9	106862462	106862462	Nonsense Mutation	INS	-	ACCATATAGGTT	-	SMC2	AATGAACCATAT	K191delinsAQMNHIGX
XH_P37	9	107289135	107289135	Frame Shift Ins	INS	-	TTTTCTAGTCTT	-	OR13C4	6insAAGAACTA	p.A119fs
XH_P37	9	107289258	107289258	Nonsense Mutation	INS	-	TCATTTCCTATG	-	OR13C4	TCTCGCATAAAG	p.I78delinsSX
XH_P37	9	107289413	107289413	In_Frame_Ins	INS	-	AGAAAC	-	OR13C4	.77_78insGTTTC	p.I26delinsMFL
XH_P37	9	107289415	107289415	Frame Shift Ins	INS	-	TTCTTCTCTG	-	OR13C4	76insCAGAGAA	p.I26fs
XH_P37	9	107298679	107298679	In_Frame_Ins	INS	-	ATCAATCATTCTG	-	OR13C3	CATGCGAAATG	9delinsYFTCEMIDNIIP
XH_P37	9	107298788	107298788	Missense Mutation	SNP	A	T	A	OR13C3	c.T307A	p.Y103N
XH_P37	9	107298789	107298789	Nonsense Mutation	INS	-	ATGGCTTCTGTG	-	OR13C3	06insACACAGA	C102_Y103delinsX
XH_P37	9	107513349	107513349	Frame Shift Ins	INS	-	GATTTCATTAT	-	NIPSNAP3A	5ACAGGATTCAT	p.K58fs
XH_P37	9	107521565	107521565	Silent	SNP	A	T	A	NIPSNAP3A	c.A540T	p.L180L
XH_P37	9	108118628	108118628	Frame Shift Ins	INS	-	CACAAATGAAAG	-	SLC44A1	7insCACACAAAT	p.K212fs
XH_P37	9	108125232	108125232	Nonsense Mutation	INS	-	AAATCCTTATCA	-	SLC44A1	TTCAATAATAC	A344delinsAFQX
XH_P37	9	113013101	113013101	Frame Shift Ins	INS	-	TTCTTAAACCC	-	TXN	188insGGGGTTT	p.Q63fs
XH_P37	9	113013102	113013102	Missense Mutation	SNP	G	T	G	TXN	c.C187A	p.Q63K
XH_P37	9	113065977	113065977	In_Frame_Ins	INS	-	TGTAGTGTTC	-	TXNDC8	CCAGTGGAAACA	1delinsDQWNTTVF
XH_P37	9	113197639	113197639	Nonsense Mutation	INS	-	CTACTTTTGTAA	-	SVEP1	ACTAGTTACAAA	K1590delinsNYX
XH_P37	9	114841005	114841005	Splice Site	INS	-	5CTTTTATCATI	-	SUSD1	.	.
XH_P37	9	114990731	114990731	Nonsense Mutation	INS	-	CTGAAGTTCATT	-	PTBP3	AGACAAATGAA	2_V293delinsHVDKX
XH_P37	9	116153083	116153083	Missense Mutation	SNP	T	G	T	ALAD	c.A368C	p.H123P
XH_P37	9	116153085	116153087	In_Frame_Del	DEL	ACC	-	ACC	ALAD	c.364_366del	p.I22_122del
XH_P37	9	119413993	119413993	In_Frame_Ins	INS	-	ATATCATCATCA	-	ASTN2	42insTGATGATC	Q14delinsHDDDM
XH_P37	9	123234094	123234094	In_Frame_Ins	INS	-	5AATAAAGTGTG	-	CDK5RAP2	790insTACACAC	597delinsVHTLFY
XH_P37	9	123937398	123937398	Nonsense Mutation	INS	-	ATAAACCTTACT	-	CNTRL	TGTGCATAAACA	732_G1733delinsX

XH_P37	9	125330751	125330751	Frame_Shift_Ins	INS	-	TTCTGTCTCTCA	-	OR1L8	CAGTGAGAGAC	p.E2fs
XH_P37	9	125391308	125391308	Nonsense_Mutation	INS	-	AACCTCTCAGTAT	-	OR1B1	507insATACTGA	p.C169delinsX
XH_P37	9	125552028	125552028	Frame_Shift_Ins	INS	-	CAGTGACACCA	-	OR5C1	TCGTGCAGCTGA	p.D273fs
XH_P37	9	127119163	127119163	In_Frame_Ins	INS	-	AGTTTT	-	PSMB7	01_602insAAAA	A201delinsENS
XH_P37	9	127119164	127119164	Frame_Shift_Ins	INS	-	CTGGTTCT	-	PSMB7	0_601insAGAAC	p.A201fs
XH_P37	9	127765465	127765465	Frame_Shift_Ins	INS	-	AAATGAAAAAC	-	SCAI	AAGCGACGTTTT	p.E331fs
XH_P37	9	127781460	127781460	In_Frame_Ins	INS	-	AAGGAATAGCTT	-	SCAI	TAGAGTAAGCTA	2delinsINRVSYSFLLTY
XH_P37	9	128420000	128420000	Frame_Shift_Ins	INS	-	AA	-	MAPKAP1	c.427_428insTT	p.S143fs
XH_P37	9	128420002	128420002	In_Frame_Ins	INS	-	GCTTTGTAG	-	MAPKAP1	5_426insCTACAA	L142delinsFYKA
XH_P37	9	129596138	129596138	Nonsense_Mutation	INS	-	GAGTGAA	-	ZBTB43	50_1351insGAG	150_1451delinsCEX
XH_P37	9	131285955	131285955	Missense_Mutation	SNP	A	G	A	GLE1	c.A272G	p.I243V
XH_P37	9	131684606	131684606	In_Frame_Ins	INS	-	CTGCTTCTCTG	-	PHYHD1	TATCTGCTTCTCT	2delinsDFICFLCVSS
XH_P37	9	131745263	131745263	Nonsense_Mutation	INS	-	GGTTCTAAATTT	-	NUP188	CTTGATGGTCTC	4_C585delinsDKSQSX
XH_P37	9	134049597	134049597	Frame_Shift_Ins	INS	-	AGCTAAGTAATT	-	NUP214	insAAAAAGCTAA	p.P1007fs
XH_P37	9	134136574	134136574	Frame_Shift_Ins	INS	-	GACTCAC	-	FAM78A	36_487insGTGA	p.Y163fs
XH_P37	9	134136576	134136576	Frame_Shift_Ins	INS	-	ATAATAAT	-	FAM78A	34_485insATTAT	p.P162fs
XH_P37	9	136029570	136029570	Nonsense_Mutation	INS	-	GGGACTTCTATT	-	GBGT1	419insAATAGAA	p.S140delinsX
XH_P37	9	136256529	136256529	Silent	SNP	G	A	G	STKLD1	c.G540A	p.V180V
XH_P37	9	136256530	136256530	Frame_Shift_Ins	INS	-	ATATACTCAAT	-	STKLD1	5AGAAATATAC	p.L181fs
XH_P37	9	140611253	140611253	Frame_Shift_Ins	INS	-	ACTTC	-	EHMT1	261_262insACT	p.T87fs
XH_P37	10	4872904	4872904	Frame_Shift_Ins	INS	-	ATGAAGGAATT	-	AKR1E2	AGTTATGAAGG	p.A26fs
XH_P37	10	5781842	5781842	Frame_Shift_Ins	INS	-	GTCATAGAAATT	-	FAM208B	467insTGTGATA	p.L489fs
XH_P37	10	5784441	5784441	Frame_Shift_Ins	INS	-	TTGTCTGATTG	-	FAM208B	2467insTTTGTG	p.D822fs
XH_P37	10	5827976	5827976	Nonsense_Mutation	INS	-	GTCTAGTTGAA	-	GD12	ACTAATTCAAC	7_F98delinsNTNFX
XH_P37	10	6506310	6506310	Frame_Shift_Ins	INS	-	TTTC	-	PRKCQ	034_1035insGA	p.I345fs
XH_P37	10	6506312	6506312	Nonsense_Mutation	INS	-	GATTTAAACCTA	-	PRKCQ	AGTAGTTAGTTT	345_Q346delinsX
XH_P37	10	7842022	7842022	Frame_Shift_Ins	INS	-	AGAG	-	ATP5C1	464_465insAGA	p.P155fs
XH_P37	10	7842023	7842023	Nonsense_Mutation	INS	-	TAGCTAGTTTA	-	ATP5C1	5TCACATAGCTAA	P155delinsPSHSX
XH_P37	10	12200065	12200065	In_Frame_Ins	INS	-	AGTCGGCCCGT	-	SEC61A2	CTATTAAAGTCGG	insFRVLDPIKSARYRQYS
XH_P37	10	13481346	13481346	Nonsense_Mutation	INS	-	CTTGCTTATTTA	-	BEND7	CACACATAAAATA	11_R412delinsTHTX
XH_P37	10	16553246	16553246	Nonsense_Mutation	INS	-	TAGATGTCATTT	-	PTER	insCATTAGATG	b.T198delinsTHX
XH_P37	10	16911769	16911769	Nonsense_Mutation	INS	-	AACTTACGATG	-	CUBN	ATATGTCATACC	107_L1308delinsHX
XH_P37	10	16958009	16958009	Frame_Shift_Ins	INS	-	T	-	CUBN	c.7020dupA	p.P2341fs
XH_P37	10	16958011	16958011	Frame_Shift_Ins	INS	-	AAAATATATCTG	-	CUBN	19insAGCAGAT	p.V2340fs
XH_P37	10	17113559	17113559	Frame_Shift_Ins	INS	-	TTTGGTTGATA	-	CUBN	TATAATATACA	p.F831fs
XH_P37	10	21157666	21157666	In_Frame_Ins	INS	-	ACAGGAGAATA	-	NEBL	ATGCAATATTCTC	insKILSKMQYSVPLLETKYL
XH_P37	10	22607770	22607770	In_Frame_Ins	INS	-	AAAGATGCAATT	-	COMMD3	ACTGAAAAGATG	49delinsYTERCNDN
XH_P37	10	23287217	23287217	In_Frame_Ins	INS	-	TTAGAAAATAAA	-	ARMC3	28insTTTTAGAA	176delinsDFRNKF
XH_P37	10	23287218	23287218	Missense_Mutation	SNP	C	A	C	ARMC3	c.C528A	p.D176E
XH_P37	10	24762227	24762227	In_Frame_Ins	INS	-	CTGTGAATATG	-	KIAA1217	GAATCTGTGAA	24delinsPGICEYVSL
XH_P37	10	24873482	24873482	In_Frame_Ins	INS	-	TCCACTCTA	-	ARHGAP21	5736insTAGAAG	S1912delinsSRVD
XH_P37	10	26462870	26462870	Missense_Mutation	SNP	A	T	A	MYO3A	c.A3677T	p.N1261G
XH_P37	10	26462871	26462871	In_Frame_Ins	INS	-	GGTGGTTTC	-	MYO3A	3_3679insGGTG	1122delinsNGGF
XH_P37	10	26463062	26463062	Frame_Shift_Ins	INS	-	TTGCTGTTCTCT	-	MYO3A	870insATTGCTC	p.S1290fs
XH_P37	10	26463473	26463473	Nonsense_Mutation	INS	-	ITGCTAAAAGAA	-	MYO3A	CTCTGATGCTTA	427_F1428delinsILX
XH_P37	10	27409462	27409462	Frame_Shift_Ins	INS	-	TCITTTTTTTTT	-	YME1L1	AATGGGAAAAAA	p.P405fs
XH_P37	10	27459423	27459423	Frame_Shift_Ins	INS	-	ACACAAAGTTTT	-	MASTL	TACTCTACACA	p.S512fs
XH_P37	10	28260052	28260052	Nonsense_Mutation	INS	-	TATTTTGTGTTG	-	ARMC4	AAACAAACAAAC	68_V69delinsNKK
XH_P37	10	28276461	28276461	Nonsense_Mutation	INS	-	TTTITAGAAACA	-	ARMC4	36insATTGTTTC	b.V79delinsDCFx
XH_P37	10	30611527	30611527	Nonsense_Mutation	INS	-	TTTCTTTGTATCA	-	MTPAP	insAACTGATACA	338_L339delinsNX
XH_P37	10	30915118	30915118	Missense_Mutation	SNP	A	G	A	LYZL2	c.T352C	p.Y118H
XH_P37	10	31791412	31791412	Frame_Shift_Ins	INS	-	GTTTTCTAAATA	-	ZE81	CAAAGGTTTTCT	p.P132fs
XH_P37	10	31809689	31809689	Missense_Mutation	SNP	A	T	A	ZE81	c.A1204T	p.N402Y
XH_P37	10	31809691	31809691	Frame_Shift_Ins	INS	-	CGCCACTT	-	ZE81	6_1207insCGCC	p.N402fs
XH_P37	10	31810646	31810646	Nonsense_Mutation	INS	-	AAACTGGGGAG	-	ZE81	sTGGTAAAACCTG	721delinsVKLGXS
XH_P37	10	32098203	32098203	In_Frame_Ins	INS	-	AGA	-	ARHGAP12	1926_1927insTp	G643delinsSG
XH_P37	10	32098205	32098205	Nonsense_Mutation	INS	-	KATTTAATCATI	-	ARHGAP12	ATTAAAAATGAT	42_G643delinsNHX
XH_P37	10	33196070	33196070	Nonsense_Mutation	INS	-	TGTATGTTAACT	-	ITGB1	83insGAAGTTAA	778_E779delinsRSX
XH_P37	10	33196072	33196072	Splice_Site	INS	-	GT	-	ITGB1	.	.
XH_P37	10	37508366	37508366	Silent	SNP	G	C	G	ANKRD30A	c.G3558C	p.T1186T
XH_P37	10	38343519	38343519	In_Frame_Ins	INS	-	TTTCTTGGCTCC	-	ZNF33A	486insTTTCTTG	V162delinsVFAP
XH_P37	10	38343521	38343521	Missense_Mutation	SNP	A	C	A	ZNF33A	c.A487C	p.I163L
XH_P37	10	38344327	38344327	Nonsense_Mutation	INS	-	CATTCTATACAT	-	ZNF33A	TTTTACATCTCA	31delinsKAFSHSLHX
XH_P37	10	38407598	38407598	Nonsense_Mutation	INS	-	GTCTCT	-	ZNF37A	19_1520insGTT	p.K507delinsSSX
XH_P37	10	38407599	38407599	Frame_Shift_Ins	INS	-	ATGTTTAGTAGA	-	ZNF37A	521insGATGTTT	p.K507fs
XH_P37	10	43088989	43088989	Frame_Shift_Ins	INS	-	ATAGAACACA	-	ZNF33B	1_1430insTGTGT	p.E477fs
XH_P37	10	43089048	43089048	In_Frame_Ins	INS	-	5AAACCTTATGA	-	ZNF33B	nsAACATTCTATA	457delinsLTFIRFPQ
XH_P37	10	43292142	43292142	Frame_Shift_Ins	INS	-	TT	-	BMS1	1450_1451insT	p.K484fs
XH_P37	10	43292143	43292143	In_Frame_Ins	INS	-	GCCTGTATT	-	BMS1	1_1452insGCCTC	K484delinsKPVLL
XH_P37	10	43312100	43312100	Frame_Shift_Ins	INS	-	TGCTTTGT	-	BMS1	3_2384insTGCT	p.K795fs
XH_P37	10	43312101	43312101	Nonsense_Mutation	INS	-	CAGCTAGTATTT	-	BMS1	insAAACAGTTA	95_S796delinsKNXS
XH_P37	10	43651090	43651090	Nonsense_Mutation	INS	-	5TAATTCTTGTTT	-	CSGALNACT2	TTCTTGTAATTC	R165delinsHFLX
XH_P37	10	44111850	44111850	Nonsense_Mutation	INS	-	TTAAAAATTCAA	-	ZNF485	AATTTTAAAAAT	p.W29delinsX
XH_P37	10	44112553	44112553	In_Frame_Ins	INS	-	TTCTGTAGTTC	-	ZNF485	sGGATTTTCTGA	163delinsYGFSDVPT
XH_P37	10	45799843	45799843	In_Frame_Ins	INS	-	ACTTTTCTTACT	-	OR13A1	5TTGAGTAAGAA	110delinsLKKHYI
XH_P37	10	45953843	45953843	Nonsense_Mutation	INS	-	TATTTATAGTAG	-	MARCH8	AGAAGCCACTA	p.C241delinsKRSHYX
XH_P37	10	46122437	46122437	Nonsense_Mutation	INS	-	AACATTTTTTAG	-	ZFAND4	834insCTAAAAA	p.S278delinsSX
XH_P37	10	46122439	46122439	Frame_Shift_Ins	INS	-	ACTTGCCATCTA	-	ZFAND4	32insCTAGATGC	p.S278fs
XH_P37	10	49687682	49687682	Nonsense_Mutation	INS	-	TGAAAACTGTG	-	ARHGAP22	5TAATACACAGT	p.G60delinsX
XH_P37	10	49687684	49687684	Missense_Mutation	SNP	C	A	C	ARHGAP22	c.G176T	p.G59V
XH_P37	10	49951067	49951067	Frame_Shift_Ins	INS	-	TTCTCTTACGG	-	WDFY4	5sTATTGTTCTCT	p.S645fs
XH_P37	10	50004483	50004483	Frame_Shift_Ins	INS	-	AGCCTCATTCTC	-	WDFY4	399insAAGCCTC	p.L1466fs
XH_P37	10	50682101	50682101	Frame_Shift_Ins	INS	-	TTTTAACA	-	ERCC6	9_2570insTGTI	p.R857fs
XH_P37	10	50682102	50682102	Frame_Shift_Ins	INS	-	TTCTGTTTAT	-	ERCC6	2569insATAAA	p.R857fs
XH_P37	10	50723453	50723453	Frame_Shift_Ins	INS	-	C	-	ERCC6	c.1707dupG	p.N570fs
XH_P37	10	50723455	50723455	In_Frame_Ins	INS	-	TTTTTCTAGGTA	-	ERCC6	nsTATGTTACCTA	569delinsCYLEKFK
XH_P37	10	51050097	51050097	Nonsense_Mutation	INS	-	TGCTGAAATTA	-	PARG	AAAGCATTAAAT	100_Q401delinsRKHX
XH_P37	10	54040655	54040655	In_Frame_Ins	INS	-	TGG	-	PRKG1	1465_1466insTG	N489delinsMD
XH_P37	10	54040656	54040656	Nonsense_Mutation	INS	-	ATTAATTTCTGTA	-	PRKG1	AAAAAATTAATT	p.N489delinsKX
XH_P37	10	54076563	54076563	Frame_Shift_Ins	INS	-	AACAGAACCTT	-	DKK1	798insAACAGA	p.H266fs
XH_P37	10	55582096	55582096	Nonsense_Mutation	INS	-	AAACAGACCCT	-	PCDH15	insTCTGAGGGT	757_L1758delinsLX
XH_P37	10	60998428	60998428	Nonsense_Mutation	INS	-	GAA	-	PHYHIPL	481_482insGA	p.Y161delinsX
XH_P37	10	60998430	60998430	Nonsense_Mutation	INS	-	AGAGATACTGAA	-	PHYHIPL	84insTAGAGATA	161_R162delinsYX
XH_P37	10	61552752	61552752	Missense_Mutation	SNP	G	T	G	CCDC6	c.C1348A	p.Q450K
XH_P37	10	61552753	61552753	Frame_Shift_Ins	INS	-	ATCCATTGTGTTG	-	CCDC6	insTTACAACACA	p.M449fs
XH_P37	10	61802489	61802489	Nonsense_Mutation	INS	-	ACAAAATTAGGCA	-	ANK3	nsTTGCTGCCTTA	89_K990delinsIAAX
XH_P37	10	61828823	61828823	In_Frame_Ins	INS	-	AGAAAGAAAAA	-	ANK3	1816insCTTTTT	3939delinsAFFLLQ
XH_P37	10	61828824	61828824	Nonsense_Mutation	SNP	C	A	C	ANK3	c.G11815T	p.E3939X

XH_P37	10	61835161	61835161	Frame_Shift_Ins	INS	-	ATCTTCTTTATCT	-	ANK3	5insGAAGATAAA	p.S1826fs
XH_P37	10	61835162	61835162	Missense_Mutation	SNP	G	C	G	ANK3	c.C5477G	p.S1826C
XH_P37	10	64382956	64382956	Nonsense_Mutation	INS	-	5AAACCATTTG	-	ZNF365	76insAGAAAAC	A359delinsEKTIX
XH_P37	10	64573917	64573917	In_Frame_Ins	INS	-	ACC	-	EGR2	c.480_481insGG	p.L161delinsGL
XH_P37	10	69933964	69933964	In_Frame_Ins	INS	-	GCT	-	MYPN	2115_2116insGG	p.T705delinsTA
XH_P37	10	69933966	69933966	Nonsense_Mutation	INS	-	ACTGGAACAAC	-	MYPN	AGTCTTACTGGA	706_5707delinsSX
XH_P37	10	69935216	69935216	Nonsense_Mutation	INS	-	5TCATTAGGCAC	-	MYPN	02insGGTCATT	A901delinsRSLGTX
XH_P37	10	70051995	70051995	Frame_Shift_Ins	INS	-	TAATTTTGTITTT	-	PBLD	5AAAAAAAAC	p.K95fs
XH_P37	10	70520931	70520931	Nonsense_Mutation	INS	-	TTAACAAATATA	-	CCAR1	CTACAAATTAACA	S682delinsKQTSYNSX
XH_P37	10	70644642	70644642	Frame_Shift_Ins	INS	-	TTTTCTTTATCTC	-	STOX1	TTGCCCTTTTCT	p.R364fs
XH_P37	10	70892710	70892710	Frame_Shift_Ins	INS	-	ATATCAAATGCT	-	VPS26A	ACATATATCAAA	p.D20fs
XH_P37	10	73973027	73973027	Frame_Shift_Ins	INS	-	GTITTTTITTAAT	-	ASCC1	cACATTAAAAAC	p.R10fs
XH_P37	10	73973028	73973028	Missense_Mutation	SNP	C	T	C	ASCC1	c.G29A	p.R10K
XH_P37	10	75184941	75184941	In_Frame_Ins	INS	-	5TCTTTTCCGCG	-	MSS51	78insATGCGGA	A360delinsMRKRTS
XH_P37	10	75258652	75258652	Frame_Shift_Ins	INS	-	A	-	USP54	c.4603_4604ins	p.P1535fs
XH_P37	10	75258654	75258654	Frame_Shift_Ins	INS	-	GGTTTCTGTT	-	USP54	c.4602insAACAG	p.H1534fs
XH_P37	10	75413366	75413366	Frame_Shift_Ins	INS	-	TG	-	SYNP02L	c.302_303insCA	p.L101fs
XH_P37	10	75413368	75413368	In_Frame_Ins	INS	-	GTCTAC	-	SYNP02L	00_301insGTAG	p.L101delinsVDL
XH_P37	10	75526555	75526555	Frame_Shift_Ins	INS	-	CTGGCTCTTACC	-	SEC24C	838insTCTGGC	p.R613fs
XH_P37	10	75566525	75566525	Nonsense_Mutation	INS	-	TTTCTTTATTGTG	-	NDST2	88insTCCAAATA	B80_K381delinsSKX
XH_P37	10	76602689	76602689	In_Frame_Ins	INS	-	GAC	-	KAT6B	c.74_75insGAC	p.Q25delinsQT
XH_P37	10	76602691	76602691	Nonsense_Mutation	INS	-	AGGCAATGTTG	-	KAT6B	insACAGGCAAT	R26delinsNRQCX
XH_P37	10	82045268	82045268	Frame_Shift_Ins	INS	-	ATGAA	-	MAT1A	168_169insTTG	p.E57fs
XH_P37	10	82045270	82045270	Nonsense_Mutation	INS	-	AATAGATATTTT	-	MAT1A	67insAAAAATA	C56_E57delinsX
XH_P37	10	86131504	86131504	Frame_Shift_Ins	INS	-	AA	-	CCSER2	c.696_697insAA	p.F232fs
XH_P37	10	86131505	86131505	Nonsense_Mutation	INS	-	TGATTTTGGAG	-	CCSER2	8insTGTGATTT	p.L233delinsQT
XH_P37	10	88232514	88232514	In_Frame_Ins	INS	-	TAAGCAGCCAT	-	WAPL	ACTGTATATGG	77delinsHCWILLTSL
XH_P37	10	91066953	91066953	In_Frame_Ins	INS	-	CGG	-	IFIT2	1240_1241insCG	p.K414delinsTE
XH_P37	10	91066955	91066955	Frame_Shift_Ins	INS	-	GAGATTAT	-	IFIT2	2_1243insGAGA	p.K414fs
XH_P37	10	91067106	91067106	Nonsense_Mutation	INS	-	TTCTGTTTATT	-	IFIT2	4insGATTTCGG	A465_A466delinsX
XH_P37	10	91098703	91098703	Nonsense_Mutation	SNP	G	A	G	IFIT3	c.G291A	p.W97X
XH_P37	10	91098704	91098704	Frame_Shift_Ins	INS	-	CACTGTCTTCTCT	-	IFIT3	93insACACTGT	p.G98fs
XH_P37	10	93786971	93786971	Frame_Shift_Ins	INS	-	TCCAGGTTTTC	-	BTAf1	nsGTGATCCAGG	p.L1774fs
XH_P37	10	95093619	95093619	Frame_Shift_Ins	INS	-	TCTGTATTCTCA	-	MYOF	6insAGTGAGAT	p.P1562fs
XH_P37	10	96110035	96110035	In_Frame_Ins	INS	-	5AAAAATATACA	-	NOC3L	cATGTGTGTATA	21delinsHMYVNFRLR
XH_P37	10	96480233	96480233	In_Frame_Ins	INS	-	TGCAGTATT	-	CYP2C18	3_724insTGCAG	E241delinsECSI
XH_P37	10	96480235	96480235	Missense_Mutation	SNP	C	A	C	CYP2C18	c.C725A	p.T242K
XH_P37	10	97715241	97715241	Nonsense_Mutation	INS	-	CTTCCACAATAT	-	CCD2D8	nsTTATCTCTCCAG	A368delinsLIFHNIFX
XH_P37	10	98741408	98741408	Frame_Shift_Ins	INS	-	ATGTTCAACATTG	-	LCOR	2insATATGTTC	p.H397fs
XH_P37	10	98917627	98917627	Frame_Shift_Ins	INS	-	GGTATT	-	SLIT1	50_361insAAAT	p.L121fs
XH_P37	10	98917628	98917628	Frame_Shift_Ins	INS	-	TCCA	-	SLIT1	359_360insTGG	p.Q120fs
XH_P37	10	99023362	99023362	Frame_Shift_Ins	INS	-	A	-	ARHGAP19	c.427_428insT	p.R143fs
XH_P37	10	99023364	99023364	Nonsense_Mutation	INS	-	TAGTTAAGTTTA	-	ARHGAP19	AAAATTAACCT	A42_R143delinsFNX
XH_P37	10	99344648	99344648	Frame_Shift_Ins	INS	-	CTATGTCGCCAGA	-	HOGA1	TGGTCTATGTG	p.K63fs
XH_P37	10	102050229	102050229	Frame_Shift_Ins	INS	-	GGTCTCCC	-	PKD2L1	3_1914insGGAA	p.S638fs
XH_P37	10	102052707	102052707	Frame_Shift_Ins	INS	-	CACAAAA	-	PKD2L1	36_1737insTTT	p.R579fs
XH_P37	10	102052709	102052709	Frame_Shift_Ins	INS	-	CTGATTTTGTTC	-	PKD2L1	735insGAACAA	p.R579fs
XH_P37	10	102250639	102250639	Frame_Shift_Ins	INS	-	AG	-	SEC31B	2473_2474insC	p.V825fs
XH_P37	10	102250640	102250640	Frame_Shift_Ins	INS	-	TGTATGTCTGT	-	SEC31B	2473insACAGA	p.V825fs
XH_P37	10	102746727	102746727	Frame_Shift_Ins	INS	-	A	-	MRPL43	c.243_244insT	p.G82fs
XH_P37	10	102746728	102746728	In_Frame_Ins	INS	-	GCT	-	MRPL43	c.242_243insAG	p.N81delinsKA
XH_P37	10	102987517	102987517	Frame_Shift_Ins	INS	-	AAGAACTGGG	-	LBX1	c.356insCCAGT	p.R119fs
XH_P37	10	103826842	103826842	Frame_Shift_Ins	INS	-	TCAACATGGT	-	HP56	1612insTCAAC	p.S537fs
XH_P37	10	103899857	103899857	Frame_Shift_Ins	INS	-	TCTTGCTCTT	-	PPRC1	1593insTCTCT	p.A531fs
XH_P37	10	104129628	104129628	Nonsense_Mutation	INS	-	AATAATTTCTTTG	-	GBF1	3227insAATAAT	A076_V1077delinsKX
XH_P37	10	104129630	104129630	Frame_Shift_Ins	INS	-	T	-	GBF1	c.3228_3229ins	p.T1076fs
XH_P37	10	104414489	104414489	Nonsense_Mutation	INS	-	CCCATGCATAT	-	TRIM8	AGCTTCCCATG	C217_K218delinsEX
XH_P37	10	105108703	105108703	Nonsense_Mutation	INS	-	TATATAAGTTAC	-	PCGF6	ACAATTGTAAC	T8_G139delinsKKKYYIX
XH_P37	10	105193784	105193785	Frame_Shift_Del	DEL	TG	-	TG	PDCD11	c.3554_3555del	p.L1185fs
XH_P37	10	105193785	105193785	In_Frame_Ins	INS	-	ACC	-	PDCD11	3555_3556insA	p.L1185delinsLT
XH_P37	10	105330806	105330806	In_Frame_Ins	INS	-	AGTCCC	-	NEURL1	63_264insAGT	p.S58delinsRVP
XH_P37	10	105762741	105762741	Frame_Shift_Ins	INS	-	TCACCTGTATTG	-	SLK	nsCACATCACTT	p.1602fs
XH_P37	10	105957798	105957798	Splice_Site	INS	-	5TTATTGGGTAA	-	CFAP43	.	.
XH_P37	10	105963554	105963554	Nonsense_Mutation	INS	-	AGGCTTAAATT	-	CFAP43	CTTTGTAAATTTAG	B24_V325delinsSLX
XH_P37	10	108389126	108389126	Frame_Shift_Ins	INS	-	TT	-	SORCS1	2495_2496insA	p.L832fs
XH_P37	10	108389127	108389127	Nonsense_Mutation	INS	-	5GTTTATGACCT	-	SORCS1	TAAGATAGGTC	B2_1833delinsQYLRX
XH_P37	10	111630634	111630634	Frame_Shift_Ins	INS	-	ATTC	-	XPNEP1	208_1209insGA	p.S403fs
XH_P37	10	111630635	111630635	Nonsense_Mutation	INS	-	ATTTTTTAATTAG	-	XPNEP1	TTAAACTTAATT	A03_A404delinsLLX
XH_P37	10	112262592	112262592	Frame_Shift_Ins	INS	-	CAACACAGATT	-	DUSP5	c.494insCAACAA	p.V165fs
XH_P37	10	112262594	112262594	Silent	SNP	G	A	G	DUSP5	c.G495A	p.V165V
XH_P37	10	114889731	114889731	Frame_Shift_Ins	INS	-	T	-	TCF7L2	c.108_109insT	p.L36fs
XH_P37	10	114889733	114889733	Frame_Shift_Ins	INS	-	AAAAACTTTC	-	TCF7L2	c.111insAAAAAA	p.N37fs
XH_P37	10	115609647	115609647	Frame_Shift_Ins	INS	-	A	-	DCLRE1A	c.1216_1217ins	p.D406fs
XH_P37	10	115609648	115609648	Nonsense_Mutation	INS	-	AGTGAGAACTT	-	DCLRE1A	AGCATTCAGATT	F407delinsILSLQVLTIX
XH_P37	10	115884951	115884951	In_Frame_Ins	INS	-	TGTATGAAATTTG	-	CCDC186	CAAAAAACAAAT	A3delinsHTKTNFIKAFS
XH_P37	10	115904359	115904359	Missense_Mutation	SNP	C	T	C	CCDC186	c.G1118A	p.R373K
XH_P37	10	115904360	115904360	Frame_Shift_Ins	INS	-	AGCAAAATGCAA	-	CCDC186	7insGTATTATGCA	p.R373fs
XH_P37	10	115986920	115986920	Missense_Mutation	SNP	A	G	A	TDRD1	c.A3265G	p.K1089E
XH_P37	10	116032653	116032653	Nonsense_Mutation	INS	-	AGAAAAAGTGAA	-	VWA2	AAGAAAGAAAA	A6_G177delinsKRKKSEX
XH_P37	10	116931009	116931009	Nonsense_Mutation	INS	-	GTTTTCCTGTAA	-	ATRN1	AAGATGTCTTTC	B6delinsASIHKDVFLX
XH_P37	10	118351356	118351356	Frame_Shift_Ins	INS	-	ATTGAA	-	PNLIPRP1	23_124insATTG	p.P41fs
XH_P37	10	119799892	119799892	Missense_Mutation	SNP	A	G	A	RAB11FIP2	c.T538C	p.F180L
XH_P37	10	119799894	119799894	Nonsense_Mutation	INS	-	GTAAGTGTACAC	-	RAB11FIP2	536insTGTGAC	p.T179delinsMX
XH_P37	10	120801654	120801654	Nonsense_Mutation	INS	-	TATCAGGGCTG	-	EIF3A	AAACAATACAGC	A1126delinsEITIQPX
XH_P37	10	120817553	120817553	Frame_Shift_Ins	INS	-	GACGGAG	-	EIF3A	91_1892insCTCC	p.613fs
XH_P37	10	120817554	120817554	In_Frame_Ins	INS	-	ATTATC	-	EIF3A	90_1891insGAT	p.L631delinsDNI
XH_P37	10	121335250	121335250	Frame_Shift_Ins	INS	-	TT	-	TIAL1	c.1105_1106insA	p.G369fs
XH_P37	10	121335251	121335251	In_Frame_Ins	INS	-	TTCTGCCTTTTAA	-	TIAL1	cAAACTTTAAAA	A69delinsKLKKAELG
XH_P37	10	121337203	121337203	In_Frame_Ins	INS	-	TTATGGAAATAA	-	TIAL1	insCTCTTATTTCT	S218delinsTLUSIC
XH_P37	10	122273487	122273487	Nonsense_Mutation	INS	-	AGGATGATGTA	-	PLPP4	AAAAAAGGATG	K77delinsKKKGX
XH_P37	10	123845303	123845318	Frame_Shift_Del	DEL	5CAGAAAACT	-	AGCAGAAAAATGC	TACC2	c.3288_3303del	p.P1096fs
XH_P37	10	124593223	124593223	Missense_Mutation	SNP	C	A	C	CUZD1	c.G161G	p.R539L
XH_P37	10	124593357	124593357	Nonsense_Mutation	INS	-	TTTATAGAGATT	-	CUZD1	82insTATAAATC	A94_Y495delinsVINLX
XH_P37	10	124593359	124593359	Missense_Mutation	SNP	C	T	C	CUZD1	c.G1480A	p.V494M
XH_P37	10	124692096	124692096	Nonsense_Mutation	INS	-	GTACTGCAGAT	-	C10orf88	cATAAATATCTG	395_Y396delinsEX
XH_P37	10	124692098	124692098	Missense_Mutation	SNP	C	A	C	C10orf88	c.G1183T	p.P395Y
XH_P37	10	124753627	124753627	Frame_Shift_Ins	INS	-	AATGTAAAAACA	-	IKZF5	cATACTGTTTTT	p.P310fs
XH_P37	10	126520011	126520011	In_Frame_Ins	INS	-	AGATGGTTATT	-	ABRAXAS2	cGTCCAGATGGT	A53delinsSPDGLSLY

XH_P37	10	126681876	126681876	Nonsense_Mutation	INS	-	ATGAGTTGGGC	-	CTBP2	AACAGGGCCCA	p.D852delinsX
XH_P37	10	129903188	129903188	Frame_Shift_Ins	INS	-	AA	-	MKI67	5835_5836insT	p.P1946fs
XH_P37	10	129903190	129903190	Frame_Shift_Ins	INS	-	ACGTAGAGGAA	-	MKI67	34insTCTTCTCTC	p.T1945fs
XH_P37	10	129914165	129914165	Frame_Shift_Ins	INS	-	TGAAGAAAGAG	-	MKI69	507insACTCTTTCT	p.D169fs
XH_P37	10	131639244	131639244	In_Frame_Ins	INS	-	TGATGTGAGCTA	-	EBF3	1398insTAGCTCT	S466delinsSSSHH
XH_P37	10	134219589	134219589	Missense_Mutation	SNP	T	A	T	PWWP2B	c.T1585A	p.S529T
XH_P37	10	134219590	134219590	Frame_Shift_Ins	INS	-	CCGT	-	PWWP2B	586_1587insCC	p.S529fs
XH_P37	10	134628206	134628206	Frame_Shift_Ins	INS	-	TTTTCTCTCTGG	-	CFAP46	23insGCGACAG	p.D2411fs
XH_P37	11	320675	320675	Frame_Shift_Ins	INS	-	ATCTGTGTGTGT	-	IFITM3	9insACACACACA	p.H47fs
XH_P37	11	804358	804358	Frame_Shift_Ins	INS	-	IGCTGCATGTTCT	-	PIDD1	1insAGAACATG	p.E11fs
XH_P37	11	1009341	1009341	Frame_Shift_Ins	INS	-	ACAGTCAGCTAC	-	AP2A2	5insAGACAGTC	p.V852fs
XH_P37	11	1025072	1025072	Silent	SNP	G	A	G	MUC6	c.C2997T	p.C999C
XH_P37	11	1026069	1026069	Missense_Mutation	SNP	C	A	C	MUC6	c.G2619T	p.E873D
XH_P37	11	1026071	1026071	Frame_Shift_Ins	INS	-	AAGAT	-	MUC6	616_2617insAT	p.E873fs
XH_P37	11	3800267	3800267	Frame_Shift_Ins	INS	-	AT	-	NUP98	c.190_191insAT	p.G64fs
XH_P37	11	3800268	3800268	Nonsense_Mutation	INS	-	CCTTCTTTTCTA	-	NUP98	nsAGTAGGAAA	T65delinsSRKRRX
XH_P37	11	4661911	4661911	Frame_Shift_Ins	INS	-	CTTCTATGTACCC	-	OR51D1	CTGGTCTTCTATC	p.P297fs
XH_P37	11	4703881	4703881	In_Frame_Ins	INS	-	ATTTCATGCC	-	OR51E2	61insGGCATG	K21delinsGMNK
XH_P37	11	4936668	4936668	In_Frame_Ins	INS	-	TCTCACATTCTT	-	OR51G2	nsAATAAGAAATG	76delinsNKNVREL
XH_P37	11	4945019	4945019	Frame_Shift_Ins	INS	-	TGATT	-	OR51G1	550_551insAAT	p.L184fs
XH_P37	11	4945021	4945021	Frame_Shift_Ins	INS	-	CTTGCTC	-	OR51G1	8_549insGAGAC	p.H183fs
XH_P37	11	5173163	5173163	In_Frame_Ins	INS	-	GATATTTATCAC	-	OR52A1	AAACTGTGATAA	6delinsKNCDEKYLVDV
XH_P37	11	5345266	5345266	Frame_Shift_Ins	INS	-	TGTTGTGGAATC	-	OR51B2	insCTGATTCCA	p.R88fs
XH_P37	11	5536721	5536721	In_Frame_Ins	INS	-	AGACAGACA	-	UBQLNL	D_951insTGTC	Q317delinsHVCCL
XH_P37	11	5536722	5536722	In_Frame_Ins	INS	-	TAAAGG	-	UBQLNL	949_950insCCTT	p.9317delinsPFK
XH_P37	11	5626794	5626794	In_Frame_Ins	INS	-	ATTAACACTCTGT	-	TRIM6	223insATTAAAC	L74delinsSLKLC
XH_P37	11	5626796	5626796	Missense_Mutation	SNP	A	T	A	TRIM6	c.A224T	p.Q75L
XH_P37	11	5686217	5686217	Frame_Shift_Ins	INS	-	CCCCTTCTGTACA	-	TRIM5	304insTGTACAG	p.P435fs
XH_P37	11	5717667	5717667	Nonsense_Mutation	INS	-	CTATGCTACCTC	-	TRIM22	sTTCTCTATGTC	69delinsLLVLYLYX
XH_P37	11	5799298	5799298	Nonsense_Mutation	INS	-	CTAATCTTTATCT	-	OR52N5	67insAGATAAAA	89_H190delinsEDKDX
XH_P37	11	5842185	5842185	In_Frame_Ins	INS	-	CACCAA	-	OR52N2	20_621insCACCP	L207delinsLTK
XH_P37	11	5842186	5842186	In_Frame_Ins	INS	-	CTATTGCGGGG	-	OR52N2	CTGCCCTATTGG	7delinsLRLPYCRGNF
XH_P37	11	5989547	5989547	Frame_Shift_Ins	INS	-	CCATCTTT	-	OR56A5	7_178insAAAGA	p.Q60fs
XH_P37	11	6024345	6024345	In_Frame_Ins	INS	-	AATTCC	-	OR56A4	33_34insGGAA	p.Q12delinsGIQ
XH_P37	11	6292294	6292294	In_Frame_Ins	INS	-	CCCTAAGT	-	CCKBR	3_614insCCCTA	p.D205fs
XH_P37	11	6292296	6292296	Missense_Mutation	SNP	C	G	C	CCKBR	c.C615G	p.D205E
XH_P37	11	6472654	6472654	Frame_Shift_Ins	INS	-	AAGATTCTGCT	-	TRIM3	1191insAGCAG	p.E397fs
XH_P37	11	7022641	7022641	Nonsense_Mutation	INS	-	AAAACCACTCAA	-	ZN2F214	insGTCTTGAGTC	p.D91delinsESX
XH_P37	11	7064869	7064869	Missense_Mutation	SNP	G	A	G	NLRP14	c.G1612A	p.E538K
XH_P37	11	7064870	7064870	In_Frame_Ins	INS	-	CTGTGCCATAAA	-	NLRP14	nsTATTGCTGTCC	38delinsDIAVHKTR
XH_P37	11	8132665	8132665	Nonsense_Mutation	INS	-	CAACCCCAATG	-	RIC3	CAGATCATTTGG	Y48_P49delinsX
XH_P37	11	8483388	8483388	In_Frame_Ins	INS	-	TTGATGCTCTCA	-	STK33	ATTACTGAAGAC	74delinsHITEDINLI
XH_P37	11	8662452	8662452	Nonsense_Mutation	INS	-	AAGCTCAGTCAC	-	TRIM66	1035insGTGACTC	p.H345delinsQX
XH_P37	11	8752589	8752589	Frame_Shift_Ins	INS	-	TCGCCGA	-	ST5	17_248insTCGG	p.P83fs
XH_P37	11	9495530	9495530	Frame_Shift_Ins	INS	-	AAGACAGACAG	-	ZN143	56insGAAGACA	p.G52fs
XH_P37	11	9495531	9495531	Frame_Shift_Ins	INS	-	TATG	-	ZN143	156_157insTAT	p.G52fs
XH_P37	11	9864304	9864304	Nonsense_Mutation	INS	-	CAGTAAATATTG	-	SBF2	5GCGGCAATATT	1042_11043delinsX
XH_P37	11	9875260	9875260	Splice_Site	INS	-	GTCTCCATTAT	-	SBF2	-	
XH_P37	11	10582213	10582213	In_Frame_Ins	INS	-	GATAATTCATAG	-	LYVE1	sGGATTCTATGA	78delinsGFYELSVI
XH_P37	11	10582215	10582215	Frame_Shift_Ins	INS	-	CCTGCTCT	-	LYVE1	9_530insAAGAC	p.T177fs
XH_P37	11	14479425	14479425	Frame_Shift_Ins	INS	-	TAATTTATAGCC	-	COPB1	807insAGGCTAT	p.M936fs
XH_P37	11	14899768	14899768	Frame_Shift_Ins	INS	-	IGATGTGTCTTA	-	CYP2R1	insATTTTAAAGA	p.F469fs
XH_P37	11	14902264	14902264	Frame_Shift_Ins	INS	-	ATGATTGAGTTA	-	CYP2R1	8insAATAACTCA	p.A140fs
XH_P37	11	17115863	17115863	Missense_Mutation	SNP	A	C	A	PIK3C2A	c.T3256G	p.F1086V
XH_P37	11	17153581	17153581	Nonsense_Mutation	INS	-	GCATCTAGCTC	-	PIK3C2A	AATTAAAGCTAG	25_K326delinsKNX
XH_P37	11	17569526	17569526	In_Frame_Ins	INS	-	TCTCCCTGTTTA	-	OTOG	48insATCTCCCTC	G49delinsSLFET
XH_P37	11	18318487	18318487	Frame_Shift_Ins	INS	-	GGTTTATGTTTA	-	HP55	AAATACTAAAC	p.S342fs
XH_P37	11	18727406	18727406	Missense_Mutation	SNP	C	T	C	IGSF22	c.G3868A	p.E1290K
XH_P37	11	19970370	19970370	Missense_Mutation	SNP	G	A	G	NAV2	c.G2197A	p.A733T
XH_P37	11	20411318	20411318	Frame_Shift_Ins	INS	-	CTAAACCAAT	-	PRMT3	sATACCTAAAC	p.F19fs
XH_P37	11	21594954	21594954	Frame_Shift_Ins	INS	-	AAAA	-	NELL1	210_2211insAA	p.K737fs
XH_P37	11	26563586	26563586	Nonsense_Mutation	SNP	G	A	G	ANO3	c.G687A	p.W229X
XH_P37	11	26563587	26563587	In_Frame_Ins	INS	-	GCCTTTACATAT	-	ANO3	sGGATGCCTTTA	30delinsWMPLHFHF
XH_P37	11	26669363	26669363	Frame_Shift_Ins	INS	-	CTTTTTC	-	ANO3	98_2099insCTTT	p.K700fs
XH_P37	11	26669364	26669364	Frame_Shift_Ins	INS	-	CAAAGAGAAG	-	ANO3	2100insCAAAG	p.K700fs
XH_P37	11	31703477	31703477	Missense_Mutation	SNP	T	C	T	ELP4	c.T1286C	p.M429T
XH_P37	11	32858354	32858354	Nonsense_Mutation	INS	-	AAGTGAATAGTT	-	PRRG4	nsAAAAAGTGA	85_E86delinsKSEX
XH_P37	11	32953579	32953579	Missense_Mutation	SNP	C	G	C	QSER1	c.C388G	p.Q130E
XH_P37	11	33308862	33308862	Frame_Shift_Ins	INS	-	AAGAAAAT	-	HIPK3	2_903insAAGAA	p.P301fs
XH_P37	11	33308863	33308863	In_Frame_Ins	INS	-	GGACTTCGTAA	-	HIPK3	4insAAGGACTT	p.301delinsPKDFVS
XH_P37	11	35453970	35453970	Frame_Shift_Ins	INS	-	AAGTGTGATT	-	PAMR1	1_1764insAATCA	p.H588fs
XH_P37	11	35685015	35685015	In_Frame_Ins	INS	-	ACTTCGTGCC	-	TRIM44	6_357insACTCTC	D119delinsELLP
XH_P37	11	44151593	44151593	Splice_Site	INS	-	CTCCACTAGTGT	-	EXT2	-	
XH_P37	11	45948028	45948028	Frame_Shift_Ins	INS	-	CTCCTTGATC	-	LARGE2	1045insCTCCT	p.V348fs
XH_P37	11	46818488	46818488	In_Frame_Ins	INS	-	AGTTTCTTGATT	-	CKAP5	1insAAAAAATCA	447delinsQKNQELL
XH_P37	11	48285506	48285506	Nonsense_Mutation	INS	-	CATTAGAAACAT	-	OR4X1	nsATCATTAGAA	132_Y33delinsNHX
XH_P37	11	49075658	49075658	Frame_Shift_Ins	INS	-	TGTGAGTTTTTT	-	TRIM64C	61insAAAAAAA	p.D321fs
XH_P37	11	49075659	49075659	Missense_Mutation	SNP	C	G	C	TRIM64C	c.G960C	p.M320I
XH_P37	11	55110727	55110727	Nonsense_Mutation	INS	-	TAAAC	-	OR4A16	51_52insTAA	Q17_D18delinsQX
XH_P37	11	55110728	55110728	Nonsense_Mutation	INS	-	TTACTAAGTCTC	-	OR4A16	3insTTTACTAAG	C18_P19delinsVYX
XH_P37	11	55406419	55406419	Frame_Shift_Ins	INS	-	CTCCAAAAAA	-	OR4P4	nsATGCCTCCAA	p.L196fs
XH_P37	11	55406421	55406421	Silent	SNP	A	G	A	OR4P4	c.A588G	p.L196L
XH_P37	11	55419312	55419312	Nonsense_Mutation	INS	-	ATGATGCTGTAG	-	OR4S2	TAGGATGATGC	11_X312delinsKLGX
XH_P37	11	56020046	56020046	In_Frame_Ins	INS	-	TACTGTGCAAGT	-	OR5T3	72insTTTACTTG	F124delinsFLAGY
XH_P37	11	56128570	56128570	Missense_Mutation	SNP	T	G	T	OR8J1	c.T848G	p.I283S
XH_P37	11	56128571	56128571	Frame_Shift_Ins	INS	-	AGAGCAAGATA	-	OR8J1	GTATCAGAGCA	p.I283fs
XH_P37	11	56185173	56185173	Nonsense_Mutation	INS	-	CTCT	-	OR5R1	535_536insAGG	C179_D180delinsX
XH_P37	11	56185174	56185174	Frame_Shift_Ins	INS	-	CATCTT	-	OR5R1	84_535insAAAG	p.C179fs
XH_P37	11	56185465	56185465	Frame_Shift_Ins	INS	-	ATTGTGATGAC	-	OR5R1	sGGAGGTCATC	p.M82fs
XH_P37	11	56344676	56344676	Frame_Shift_Ins	INS	-	C	-	OR5M10	c.521_522insG	p.I174fs
XH_P37	11	56344677	56344677	In_Frame_Ins	INS	-	GTCTTTTACT	-	OR5M10	521insAGTATA	A1174delinsKYKRL
XH_P37	11	56380619	56380619	Frame_Shift_Ins	INS	-	TCCTCTT	-	OR5M1	9_360insAAGA	p.L120fs
XH_P37	11	56380620	56380620	Nonsense_Mutation	INS	-	TC	-	OR5M1	c.358_359insGA	120_D121delinsX
XH_P37	11	56409485	56409485	Frame_Shift_Ins	INS	-	CCTGTGCCTCTT	-	OR5AP2	81insTAAGAGG	p.G144fs
XH_P37	11	57575899	57575899	Nonsense_Mutation	INS	-	AGAAGCAGAG	-	CTNND1	99insATAGAAG	p.K603delinsKX
XH_P37	11	57971005	57971005	In_Frame_Ins	INS	-	ATTGTGCTGTGC	-	OR1S2	9insAGGCAGCG	C217delinsRTAPIL
XH_P37	11	57971509	57971509	Missense_Mutation	SNP	C	A	C	OR1S2	c.G145T	p.V49L
XH_P37	11	57971510	57971510	Nonsense_Mutation	INS	-	TGCTGGTGAAT	-	OR1S2	44insATTTCAC	Y48_V49delinsX

XH_P37	11	58190685	58190685	Frame_Shift_Ins	INS	-	GG	-	OR5B2	c.49_50insCC	p.S17fs
XH_P37	11	58190687	58190687	Frame_Shift_Ins	INS	-	GAAAATTACTT	-	OR5B2	48insAAGTAAT	p.T16fs
XH_P37	11	58206924	58206924	Nonsense_Mutation	INS	-	TCATATTTTAAT	-	OR5B12	TTATAATTAAAA	K234delinsLYNX
XH_P37	11	58274969	58274969	In_Frame_Ins	INS	-	AAAAATAGCCTCT	-	OR5B21	610insAGAGGC	V204delinsRGYFV
XH_P37	11	58602106	58602106	Nonsense_Mutation	INS	-	CAAACACAAGC	-	GLYATL2	CAACAATGCTTGT	p.Y227delinsX
XH_P37	11	58979297	58979297	Frame_Shift_Ins	INS	-	TGGCAAAAGCT	-	MPEG1	1042insAGGCTT	p.P348fs
XH_P37	11	58979299	58979299	Missense_Mutation	SNP	T	A	T	MPEG1	c.A1040T	p.Y347F
XH_P37	11	59189909	59189909	Frame_Shift_Ins	INS	-	CTATGCCTTGGT	-	OR5A2	18insCACCAAGG	p.Y173fs
XH_P37	11	59190095	59190095	Frame_Shift_Ins	INS	-	CACCTTGTGCC	-	OR5A2	332insGGCACA	p.T111fs
XH_P37	11	59480600	59480600	Nonsense_Mutation	INS	-	TCCTATGATTTA	-	OR10V1	TTAAGTAATATCA240_T241delinsFKX	
XH_P37	11	59480602	59480602	Nonsense_Mutation	SNP	G	T	G	OR10V1	c.C171A	p.Y239X
XH_P37	11	59982088	59982088	Splice_Site	INS	-	TGATTAATCCTTT	-	MS4A4E	.	.
XH_P37	11	60107438	60107438	Splice_Site	SNP	G	A	G	MS4A6E	.	.
XH_P37	11	61081925	61081925	In_Frame_Ins	INS	-	CTCTGCCATATT	-	DDB1	sAGAAGAATATG82delinsRRIWQRKE	
XH_P37	11	61551854	61551854	Nonsense_Mutation	INS	-	GCATAATAA	-	MYRF	7_3178insGCAT	T1059delinsTAX
XH_P37	11	62295434	62295434	Missense_Mutation	SNP	T	C	T	AHNK	c.A6455G	p.D2152G
XH_P37	11	63426642	63426642	Frame_Shift_Ins	INS	-	AT	-	ATL3	c.74_75insAT	p.E25fs
XH_P37	11	63426644	63426644	Nonsense_Mutation	INS	-	CTTATTATTCTCA	-	ATL3	ACCTGAGAATA	K26delinsKILLSYLRX
XH_P37	11	63487075	63487075	Missense_Mutation	SNP	G	T	G	RTN3	c.G765T	p.M255I
XH_P37	11	63487077	63487077	Nonsense_Mutation	INS	-	TGAAATGTCTCT	-	RTN3	nsTCTCTGAAATG256_E257delinsSLX	
XH_P37	11	64693315	64693315	In_Frame_Ins	INS	-	CCCGGGCTGTCC	-	PPP2R5B	nsTCCCCGGGGG37delinsLPRVAC	
XH_P37	11	66249840	66249840	Frame_Shift_Ins	INS	-	AAAGGAATACT	-	DPP3	TGTGGAAGGGA	p.P57fs
XH_P37	11	66372879	66372879	In_Frame_Ins	INS	-	TCCCCA	-	CCS	59_560insTCCCQ	Q187delinsLPK
XH_P37	11	66436534	66436534	Frame_Shift_Ins	INS	-	A	-	RBM4B	c.640_641insT	p.A214fs
XH_P37	11	66436535	66436535	Frame_Shift_Ins	INS	-	AGACACCT	-	RBM4B	9_640insAGGTG	p.A214fs
XH_P37	11	66813340	66813340	In_Frame_Ins	INS	-	TTTATTATTTTTC	-	SYT12	sGTCCTTTATTA247delinsGPLLFFPL	
XH_P37	11	67379397	67379397	Frame_Shift_Ins	INS	-	TCCACCTTGCTT	-	NDUFV1	084insTTCCACC	p.L361fs
XH_P37	11	68029953	68029953	In_Frame_Ins	INS	-	CAGCCT	-	C11orf24	09_510insAGGG	T170delinsTGW
XH_P37	11	68363644	68363644	In_Frame_Ins	INS	-	ACAAAAGTGCTT	-	PPP6R3	1910insACAAA	S637delinsNKRSC
XH_P37	11	73007780	73007780	In_Frame_Ins	INS	-	AGG	-	P2RY6	_520_521insAGp	L174delinsQV
XH_P37	11	73007782	73007782	In_Frame_Ins	INS	-	GGTTTC	-	P2RY6	22_523insGGT	p.L174delinsLGF
XH_P37	11	73021217	73021217	Missense_Mutation	SNP	G	A	G	ARHGEF17	c.G1534A	p.G512S
XH_P37	11	74528707	74528707	Nonsense_Mutation	INS	-	CTAAATGCCAT	-	RNF169	GAAAACCTAAATG64_S265delinsLENX	
XH_P37	11	74547728	74547728	In_Frame_Ins	INS	-	GCTCTTCAC	-	RNF169	0_2081insGCTC	V694delinsGSSL
XH_P37	11	74800096	74800096	In_Frame_Ins	INS	-	TTGACCTTTAAA	-	OR2AT4	nsGCATTATAAAG221delinsHLVKKC	
XH_P37	11	76255507	76255507	In_Frame_Ins	INS	-	ACATTTTCC	-	EMSY	7_2918insACAT	p.F973delinsYIFL
XH_P37	11	77413142	77413142	Nonsense_Mutation	INS	-	AAGCAGTGATTG	-	RSF1	TCTCTACAATCA378_Q379delinsLX	
XH_P37	11	77451915	77451915	Frame_Shift_Ins	INS	-	GCCTAATACCCA	-	RSF1	9insTATGGGTAT	p.D147fs
XH_P37	11	77784131	77784131	Frame_Shift_Ins	INS	-	CCTAAATATTTC	-	NDUF2C	3insAAGAAATAT	p.V75fs
XH_P37	11	77825438	77825438	Frame_Shift_Ins	INS	-	ACCCATTCTCG	-	ALG8	547insCGAGAA	p.K183fs
XH_P37	11	82643103	82643103	In_Frame_Ins	INS	-	GTGCTTTGGCTT	-	DDIAS	insCTAGTGTCTT241delinsPLVLWLF	
XH_P37	11	83676491	83676491	Frame_Shift_Ins	INS	-	GGA	-	DLG2	608_609insTTTG	p.E203fs
XH_P37	11	83676492	83676492	Nonsense_Mutation	INS	-	TCAGAGGGAGT	-	DLG2	insGATACCTCCC33_E204delinsGYSYLX	
XH_P37	11	85626513	85626513	Frame_Shift_Ins	INS	-	ATTCTACCCCTG	-	CCDC83	ACATAATTTCTA	p.M282fs
XH_P37	11	88911940	88911940	Frame_Shift_Ins	INS	-	TTCTGGATTCTT	-	TYR	20insCTTCTGG	p.Q273fs
XH_P37	11	89604003	89604003	In_Frame_Ins	INS	-	TCTTTTGCTTTGG	-	TRIM64B	sACAACCAAGG79delinsYNOQSKRKA	
XH_P37	11	92495298	92495298	Frame_Shift_Ins	INS	-	ATGCACG	-	FAT3	46_3947insATG	p.R1316fs
XH_P37	11	92526125	92526125	Frame_Shift_Ins	INS	-	GGCTATGTTTGG	-	FAT3	5insCATGGCTAT	p.L1602fs
XH_P37	11	92532346	92532346	Frame_Shift_Ins	INS	-	TTGTGTAAAGT	-	FAT3	168insTTGTGT	p.A2056fs
XH_P37	11	92532347	92532347	Silent	SNP	C	G	C	FAT3	c.C6168G	p.A2056A
XH_P37	11	92616407	92616407	Frame_Shift_Ins	INS	-	TG	-	FAT3	2785_12786ins	p.E4262fs
XH_P37	11	92616408	92616408	Frame_Shift_Ins	INS	-	AG	-	FAT3	2786_12787ins	p.E4262fs
XH_P37	11	94194127	94194127	Nonsense_Mutation	INS	-	GTGTATGTTGT	-	MRE11	GAGAATAACAA	434delinsRYKEREX
XH_P37	11	94532839	94532839	Frame_Shift_Ins	INS	-	TTGTCTCT	-	AMOTL1	33_334insTTGT	p.Q111fs
XH_P37	11	94532841	94532841	Frame_Shift_Ins	INS	-	A	-	AMOTL1	c.335_336insA	p.G112fs
XH_P37	11	95712595	95712595	Nonsense_Mutation	INS	-	TTCTTTATTGAA	-	MAML2	TCTGTCTCAAT	96delinsPLSSIKNQX
XH_P37	11	101375129	101375144	Frame_Shift_Del	DEL	TCGCTTCAGC	TTGCTTCAGCA	TRPC6	c.556_571del	p.F186fs	
XH_P37	11	101375264	101375264	Frame_Shift_Ins	INS	-	AAAGATGATTTT	-	TRPC6	36insAAAAATC	p.L146fs
XH_P37	11	102195950	102195950	Frame_Shift_Ins	INS	-	G	-	BIRC3	c.710_711insG	p.N237fs
XH_P37	11	102195952	102195952	Frame_Shift_Ins	INS	-	ATGGCCATGTCT	-	BIRC3	13insAATGGCCA	p.Q238fs
XH_P37	11	102201876	102201876	Frame_Shift_Ins	INS	-	ACACATATTATG	-	BIRC3	229insTAACACA	p.Y410fs
XH_P37	11	102206876	102206876	Nonsense_Mutation	INS	-	ATTGATGTTGAT	-	BIRC3	insGGCATTGAT02_G503delinsRHX	
XH_P37	11	102220810	102220810	In_Frame_Ins	INS	-	ATGTGTTTGATA	-	BIRC2	insCTTAATGTTT	75delinsTLNLVLR
XH_P37	11	102587116	102587116	Frame_Shift_Ins	INS	-	ATCGGAATTTT	-	MMP8	nsTATAAAAAAT	p.P273fs
XH_P37	11	102662185	102662185	Frame_Shift_Ins	INS	-	CCTTCAGATGG	-	MMP1	insCAGCATCTG	p.G293fs
XH_P37	11	102826080	102826080	Nonsense_Mutation	INS	-	CATTAACCTCAGC	-	MMP13	ATAATGCTGAG	L88_D89delinsX
XH_P37	11	103058310	103058310	Frame_Shift_Ins	INS	-	G	-	DYNC2H1	c.7135_7136ins	p.Q2379fs
XH_P37	11	103058311	103058311	Frame_Shift_Ins	INS	-	AAAATGCATG	-	DYNC2H1	7137insAAAAAT	p.Q2379fs
XH_P37	11	103086543	103086543	Frame_Shift_Ins	INS	-	AGGTTTTTCTT	-	DYNC2H1	AGACTTAGGTT	p.D2930fs
XH_P37	11	105009699	105009699	In_Frame_Ins	INS	-	ACG	-	CARD18	c.113_114insCG	p.E38delinsDV
XH_P37	11	105009700	105009700	Frame_Shift_Ins	INS	-	TTGTGTCCCTTG	-	CARD18	insTACAAGGGA	p.E38fs
XH_P37	11	106579340	106579340	Frame_Shift_Ins	INS	-	TCCAAGATATTA	-	GUCY1A2	1889insATAATA	p.R630fs
XH_P37	11	108031841	108031841	Frame_Shift_Ins	INS	-	ACATAACCATG	-	NPAT	CTGTGATCATGG	p.S1331fs
XH_P37	11	108236132	108236132	Nonsense_Mutation	INS	-	GAGAACATATG	-	ATM	ACACAGAGAGAA	3delinsGPKQREHMYX
XH_P37	11	108277865	108277865	Frame_Shift_Ins	INS	-	AAAATGATCATC	-	C11orf65	TGAAGATGATC	p.L31fs
XH_P37	11	108352823	108352823	Nonsense_Mutation	INS	-	GATTAAGAAGATT	-	KDEL2C	sCCACAAATCTT	271delinsPQIFNPX
XH_P37	11	111914238	111914238	Nonsense_Mutation	INS	-	TTAATTTTAATC	-	DLAT	CAACTATTAAAT	V393delinsVNYX
XH_P37	11	112119687	112119687	Nonsense_Mutation	INS	-	CAGACCAAAAC	-	PLET1	59insTGTTTTGG	A154delinsFVLVX
XH_P37	11	113670092	113670092	Frame_Shift_Ins	INS	-	GAATAAAATTT	-	USP28	105insCAATTTT	p.D702fs
XH_P37	11	113670093	113670093	In_Frame_Ins	INS	-	ACTTTT	-	USP28	03_2104insAAA	D702delinsKSD
XH_P37	11	114569240	114569240	Frame_Shift_Ins	INS	-	GATC	-	NXPE2	606_607insGAT	p.A202fs
XH_P37	11	117023199	117023199	Silent	SNP	G	A	G	PAFAH1B2	c.G36A	p.P12P
XH_P37	11	117278729	117278729	In_Frame_Ins	INS	-	ACAGAGAACTAT	-	CEP164	3600insACAGAG	1200delinsEQRTM
XH_P37	11	117278731	117278731	Missense_Mutation	SNP	T	A	T	CEP164	c.T3601A	p.S1201T
XH_P37	11	117776424	117776424	In_Frame_Ins	INS	-	ATACACACAACC	-	TMPSR513	ATGCTTGTTGTG12delinsKDAWLVCVHV	
XH_P37	11	118015910	118015910	Frame_Shift_Ins	INS	-	TTCTCCCAGTAT	-	SCN4B	sAGAACTACTGG	p.E32fs
XH_P37	11	118352664	118352664	In_Frame_Ins	INS	-	TTCCCACAGCTAG	-	KMT2A	70insAATCCCAC	1290delinsAIPQLG
XH_P37	11	118365088	118365088	Frame_Shift_Ins	INS	-	AAAA	-	KMT2A	264_526insAA	p.S175fs
XH_P37	11	118365089	118365089	In_Frame_Ins	INS	-	CACACCCATTTT	-	KMT2A	266insTCACACC	1755delinsSSHPL
XH_P37	11	118374226	118374226	In_Frame_Ins	INS	-	SAATGCTTTTCT	-	KMT2A	TTACTGGAATGG0delinsKDILLECFSLKVS	
XH_P37	11	118374778	118374778	In_Frame_Ins	INS	-	STCTTCTTCA	-	KMT2A	GGAATGTCTTCT	24delinsEWNVFTTIGS
XH_P37	11	118376151	118376151	Frame_Shift_Ins	INS	-	AAGG	-	KMT2A	544_9545insAA	p.N3182fs
XH_P37	11	118376153	118376153	Frame_Shift_Ins	INS	-	TGCTA	-	KMT2A	546_9547insTG	p.N3182fs
XH_P37	11	118376691	118376691	In_Frame_Ins	INS	-	AAATA	-	KMT2A	84_10085insAA	P3362delinsQNT
XH_P37	11	118376693	118376693	Nonsense_Mutation	INS	-	GATTTAGATCTT	-	KMT2A	GATGCTAGATT	362_G3363delinsPX
XH_P37	11	118416565	118416565	Nonsense_Mutation	INS	-	TATGTGAC	-	IFT46	5_676insGTCA	26_L227delinsVTX
XH_P37	11	119169197	119169197	Frame_Shift_Ins	INS	-	ATTCACACAGT	-	CBL	2382insATTCA	p.S794fs
XH_P37	11	119169199	119169199	In_Frame_Ins	INS	-	CTG	-	CBL	2383_2384insCB	N795delinsTD

XH_P37	11	119216258	119216258	Frame_Shift_Ins	INS	-	CGTGTCTGA	-	MFRP	513insTCAGGA	p.V171fs
XH_P37	11	119216260	119216260	Nonsense_Mutation	INS	-	CACATCTCTAAA	-	MFRP	511insTTTAGA	71_W172delinsFRX
XH_P37	11	120200860	120200860	Missense_Mutation	SNP	A	G	A	TMEM136	c.A71G	p.E24G
XH_P37	11	120200861	120200861	Frame_Shift_Ins	INS	-	ATCCTATGTT	-	TMEM136	c.73insATCCCTAT	p.E24fs
XH_P37	11	121429332	121429332	Frame_Shift_Ins	INS	-	ACTACTTAAT	-	SORL1	2697insACTAC	p.K899fs
XH_P37	11	121429333	121429333	Missense_Mutation	SNP	G	T	G	SORL1	c.G2697T	p.K899N
XH_P37	11	122671960	122671960	Frame_Shift_Ins	INS	-	ATGTGGATTGG	-	UBASH3B	nsAAGCATGTGG	p.W505fs
XH_P37	11	122805369	122805369	In_Frame_Ins	INS	-	TGATTTTTGACT	-	C11orf63	ATTGCTTTGATT	070delinsTLDLFLVSY
XH_P37	11	122929858	122929858	Frame_Shift_Ins	INS	-	T	-	HSPA8	c.1231dupA	p.T411fs
XH_P37	11	122929860	122929860	In_Frame_Ins	INS	-	CTTCCTTGG	-	HSPA8	c.1230insCCAAC	M410delinsIQGR
XH_P37	11	123476138	123476138	In_Frame_Ins	INS	-	CATATCTATGAG	-	GRAMD1B	727insCATATCT	1242delinsHIYE
XH_P37	11	123909280	123909280	In_Frame_Ins	INS	-	TGGTCTTTTCAT	-	OR10G7	9insAAATGAAA	1433delinsLNEKTR
XH_P37	11	124252806	124252806	Nonsense_Mutation	INS	-	CTTTCAGTACT	-	OR8B2	434insAGTACT	Q45_F146delinsKYYX
XH_P37	11	124266461	124266461	Nonsense_Mutation	INS	-	TTTGTTGTTCTA	-	OR8B3	nsCTGTAGAAAC	263_S264delinsLX
XH_P37	11	124412781	124412781	Frame_Shift_Ins	INS	-	TTGCTTATTAGT	-	OR8B12	CACACACTAATA	p.M257fs
XH_P37	11	124507050	124507050	Frame_Shift_Ins	INS	-	G	-	SIAE	c.1368_1369ins	p.N457fs
XH_P37	11	124507051	124507051	Frame_Shift_Ins	INS	-	AATGACTGTTTC	-	SIAE	8insACTGAAAC	p.M456fs
XH_P37	11	124524648	124524648	Nonsense_Mutation	INS	-	TGTCTATTATT	-	SIAE	AGTAATAATAAA	149_Q150delinsX
XH_P37	11	128332388	128332388	Frame_Shift_Ins	INS	-	TTATTCTATTT	-	ETS1	AATAAAAAATAC	p.D182fs
XH_P37	11	130109749	130109749	Frame_Shift_Ins	INS	-	AAATC	-	ZBTB44	060_1061insGA	p.Q354fs
XH_P37	11	130109750	130109750	Frame_Shift_Ins	INS	-	TATCTGTACC	-	ZBTB44	1060insGGTAC	p.Q354fs
XH_P37	11	130286852	130286852	Frame_Shift_Ins	INS	-	ACTGTCA	-	ADAMTS5	78_1079insTGA	p.T360fs
XH_P37	11	130339171	130339171	In_Frame_Ins	INS	-	ATGAAATTAATG	-	ADAMTS15	58insAATGAAA	519delinsWNEINV
XH_P37	11	130784580	130784580	Missense_Mutation	SNP	A	C	A	SNX19	c.T1255G	p.S419A
XH_P37	11	130784581	130784581	In_Frame_Ins	INS	-	TTGA	-	SNX19	253_1254insTC	p.A418fs
XH_P37	12	995203	995203	Frame_Shift_Ins	INS	-	CTTTGGGT	-	WNK1	2_4493insCTTT	p.V1498fs
XH_P37	12	2970528	2970528	Silent	SNP	G	A	G	FOXN1	c.C1317T	p.G439G
XH_P37	12	4735914	4735914	Frame_Shift_Ins	INS	-	GATGATG	-	AKAP3	53_2154insCAT	p.L178fs
XH_P37	12	4735916	4735916	Frame_Shift_Ins	INS	-	GG	-	AKAP3	c.2151_2152insC	p.L178fs
XH_P37	12	6103325	6103325	Frame_Shift_Ins	INS	-	CCAGATTCTTT	-	VWF	6301insAAAGA	p.G2101fs
XH_P37	12	6879358	6879358	Frame_Shift_Ins	INS	-	TTCTCTCCT	-	PTMS	c.310insTTCTCC	p.P103fs
XH_P37	12	7361628	7361628	In_Frame_Ins	INS	-	CAACTTGATCCT	-	PEX5	9insCTTCAACTT	466delinsLLQLDPR
XH_P37	12	7559292	7559292	Frame_Shift_Ins	INS	-	AATTGTGAAGAA	-	CD163L1	nsTAACCTTTCTCA	p.A318fs
XH_P37	12	8074110	8074110	Nonsense_Mutation	INS	-	TTTAAATTTTAT	-	SLC2A3	90insAAATAAAA	464_F465delinsKX
XH_P37	12	8212465	8212465	Frame_Shift_Ins	INS	-	TTCTTTGAAAC	-	C3AR1	7insATGTTTTCA	p.M106fs
XH_P37	12	8327032	8327032	Frame_Shift_Ins	INS	-	TTTTTGGGTTC	-	ZNF705A	124insGTTTTG	p.S41fs
XH_P37	12	8691902	8691902	In_Frame_Ins	INS	-	AAT	-	CLEC4E	c.130_131insAT	p.V44delinsDL
XH_P37	12	8691903	8691903	Splice_Site	INS	-	AGAAATTTGGT	-	CLEC4E	-	-
XH_P37	12	9083494	9083494	In_Frame_Ins	INS	-	ACCCAT	-	PHC1	76_1077insACCG	P359delinsPPI
XH_P37	12	9356548	9356548	Splice_Site	SNP	C	T	C	PZP	-	-
XH_P37	12	10048418	10048418	In_Frame_Ins	INS	-	TCATTGCTAATG	-	KLRF2	insTTTTCTATTGC	204delinsIFIANAA
XH_P37	12	10959047	10959047	Nonsense_Mutation	INS	-	CTTTTCTTTCCT	-	TAS2R8	GTATAGGAAAA	78_Y179delinsQEIX
XH_P37	12	10959048	10959048	Missense_Mutation	SNP	G	C	G	TAS2R8	c.C532G	p.T178A
XH_P37	12	10999675	10999675	Frame_Shift_Ins	INS	-	CAAA	-	PRR4	159_160insTTT	p.N54fs
XH_P37	12	10999676	10999676	Nonsense_Mutation	INS	-	AATTCTTAT	-	PRR4	8_159insATAAG	p.S53delinsRX
XH_P37	12	11150441	11150441	Frame_Shift_Ins	INS	-	CCTC	-	TAS2R20	c.33_34insGAGC	p.L12fs
XH_P37	12	11150442	11150442	In_Frame_Ins	INS	-	GCATATTTT	-	TAS2R20	2_33insAAATA	p.111delinsKYA
XH_P37	12	11214488	11214488	Frame_Shift_Ins	INS	-	ATCTCAAGT	-	TAS2R46	406insATCTTG	p.P136fs
XH_P37	12	11339296	11339296	Nonsense_Mutation	INS	-	ATCTCACTCAAT	-	TAS2R42	ATTATATTGAG	3delinsSQITFIYVIEY
XH_P37	12	12311996	12311996	Frame_Shift_Ins	INS	-	ACAGGACTTGTA	-	LRP6	58insACTACAAG	p.R853fs
XH_P37	12	12653610	12653610	In_Frame_Ins	INS	-	GGGTGCTTTGAA	-	DUSP16	insATTTTCAAAAG	125delinsYFQSTHL
XH_P37	12	12967078	12967078	Frame_Shift_Ins	INS	-	CATCTCATTTAA	-	DDX47	2insATCATCTCA	p.V34fs
XH_P37	12	12967080	12967080	Frame_Shift_Ins	INS	-	CACAACAA	-	DDX47	3_104insCACAA	p.L35fs
XH_P37	12	15807122	15807122	Missense_Mutation	SNP	G	C	G	EP58	c.C1207G	p.R403G
XH_P37	12	18876378	18876378	Frame_Shift_Ins	INS	-	AGTATTTTTCTT	-	PLCZ1	4insAAAAAGAAA	p.N78fs
XH_P37	12	21015781	21015781	Frame_Shift_Ins	INS	-	ATCAT	-	SLCO1B3	636_637insATC	p.V212fs
XH_P37	12	21015782	21015782	Nonsense_Mutation	INS	-	AAATTTAATAT	-	SLCO1B3	638insAAATT	213_L214delinsEIX
XH_P37	12	21644580	21644580	In_Frame_Ins	INS	-	TAGGCTTAGAG	-	RECQL	7insACCTCTAAG	T29delinsTPLSL
XH_P37	12	21995322	21995322	Frame_Shift_Ins	INS	-	CTTGAATTTGTC	-	ABCC9	insACATGACAA	p.P1133fs
XH_P37	12	22208226	22208226	Splice_Site	INS	-	AGC	-	CMAS	-	-
XH_P37	12	22208227	22208227	Splice_Site	INS	-	CATAAAATACAG	-	CMAS	-	-
XH_P37	12	26639247	26639247	Frame_Shift_Ins	INS	-	STGTGAAAGCTG	-	ITPR2	01insCTCAGCTT	p.L1867fs
XH_P37	12	26731765	26731765	Nonsense_Mutation	INS	-	TTTGAGCTTTTAC	-	ITPR2	AAATAAGTAAA	H1505delinsCKKNX
XH_P37	12	26809467	26809467	Nonsense_Mutation	INS	-	TCACAAATTCAT	-	ITPR2	2207insATGAA	36_F73delinsHLY
XH_P37	12	26809468	26809468	Frame_Shift_Ins	INS	-	AGTAT	-	ITPR2	205_2206insAT	p.L736fs
XH_P37	12	26877613	26877613	In_Frame_Ins	INS	-	AGTGATCTTAT	-	ITPR2	ATCCAGATAAGA	14delinsIHPDKITSLC
XH_P37	12	27234323	27234323	In_Frame_Ins	INS	-	CATATAGACAGA	-	C12orf71	594insTCTGCTCT	K198delinsNLSIW
XH_P37	12	27648716	27648716	Nonsense_Mutation	INS	-	AAACTAAAT	-	SMCO2	1_762insAAACTA	E254delinsENX
XH_P37	12	27648717	27648717	Frame_Shift_Ins	INS	-	AAACCACATGCT	-	SMCO2	63insAAACCCAC	p.E254fs
XH_P37	12	28702099	28702099	Frame_Shift_Ins	INS	-	CTTCAACTCAGT	-	CCDC91	CTTTATCTCTCA	p.1404fs
XH_P37	12	29523156	29523156	Splice_Site	INS	-	AGAATCATTTTA	-	ERGIC2	-	-
XH_P37	12	30815340	30815340	Frame_Shift_Ins	INS	-	GTATAGGTTTG	-	IP08	1insCCACAAC	p.V354fs
XH_P37	12	32136063	32136063	In_Frame_Ins	INS	-	TGTTTACCAGTC	-	KIAA1551	5insAGTTGGTTA	725delinsSVGYQSF
XH_P37	12	32136487	32136487	Nonsense_Mutation	INS	-	TGAAGTT	-	KIAA1551	98_2599insTGA	866_H867delinsIX
XH_P37	12	32136488	32136488	In_Frame_Ins	INS	-	STTCCCTTTGTTA	-	KIAA1551	600insTGTTCCT	H867delinsLPULLY
XH_P37	12	32458865	32458865	In_Frame_Ins	INS	-	CGC	-	BICD1	c.814_815insCG	p.F272delinsSL
XH_P37	12	32458866	32458866	Frame_Shift_Ins	INS	-	TAATCTCA	-	BICD1	5_816insTAATC	p.B272fs
XH_P37	12	32490628	32490628	Frame_Shift_Ins	INS	-	GTGAAACTGAA	-	BICD1	9insTTGGTGAA	p.I816fs
XH_P37	12	42866292	42866292	Nonsense_Mutation	INS	-	TGTGAGTTT CAGA	-	PRICKLE1	AAAGTCTGAACT	p.M9delinsIMFX
XH_P37	12	44148326	44148326	Nonsense_Mutation	INS	-	GGAAAGTTAT	-	PUS7L	GTATATATAACT	H1_R242delinsHYLYIX
XH_P37	12	44605168	44605168	Nonsense_Mutation	INS	-	ATTAAAAACTTTT	-	TMEM117	95insAATTAATA	p.F98delinsFNN
XH_P37	12	44605170	44605170	Nonsense_Mutation	SNP	G	A	G	TMEM117	c.G296A	p.W99X
XH_P37	12	44782151	44782151	Frame_Shift_Ins	INS	-	CCACATATTAAG	-	TMEM117	930insCCACATA	p.F310fs
XH_P37	12	45171088	45171088	Frame_Shift_Ins	INS	-	A	-	NELL2	c.615_616insT	p.Q206fs
XH_P37	12	45171090	45171090	In_Frame_Ins	INS	-	GACTTCCATGG	-	NELL2	4insGTCCATGG	M205delinsSPWKS
XH_P37	12	46322579	46322579	Nonsense_Mutation	INS	-	ACAGTAATCCAT	-	SCAF11	nsAAGATGGAT	302_G303delinsX
XH_P37	12	48095325	48095325	In_Frame_Ins	INS	-	TAAACATTTAAT	-	RPAP3	216insATTAAAT	S72delinsSLNVY
XH_P37	12	48095327	48095327	Frame_Shift_Ins	INS	-	CATAG	-	RPAP3	213_214insCTA	p.S72fs
XH_P37	12	48144843	48144843	Missense_Mutation	SNP	G	A	G	RAPGEF3	c.C537T	p.A178V
XH_P37	12	49333545	49333545	Nonsense_Mutation	INS	-	TGTTAGAAGCGT	-	ARF3	7insCCACGCTCT	93_S94delinsPRFX
XH_P37	12	49426540	49426540	Nonsense_Mutation	INS	-	CCCTCACTCTC	-	KMT2D	11948insGAGAC	B83_L3984delinsREX
XH_P37	12	49434799	49434799	Frame_Shift_Ins	INS	-	ACATCTTT	-	KMT2D	3_6754insAAAG	p.L2252fs
XH_P37	12	49460041	49460041	Nonsense_Mutation	INS	-	TTTACCTATATT	-	RHEBL1	6AGAAAAATAG	A16_N117delinsEKIX
XH_P37	12	50189362	50189362	Nonsense_Mutation	INS	-	ACCCTAGTA	-	NCKAP5L	2281insTACTA	T761_D762delinsYX
XH_P37	12	50747903	50747903	Frame_Shift_Ins	INS	-	AGCAACCCTTGT	-	FAM186A	insAACACAAG	p.E904fs
XH_P37	12	50747905	50747905	Frame_Shift_Ins	INS	-	ATTTT	-	FAM186A	709_2710insAA	p.E904fs
XH_P37	12	51100411	51100411	Frame_Shift_Ins	INS	-	AGGGAATTAC	-	DIP2B	CTAAGAAAGGGA	p.L833fs
XH_P37	12	51138476	51138476	Missense_Mutation	SNP	G	A	G	DIP2B	c.G4585A	p.E1529K

XH_P37	12	52699453	52699453	Frame_Shift_Ins	INS	-	AAGCCTATTTAA	-	KRT86	908insAAGCCTA	p.E303fs
XH_P37	12	53700533	53700533	In_Frame_Ins	INS	-	CTACCTAAACCC	-	C12orf10	CCAGCCTACCTC	delinsHAOPTLNLLAM
XH_P37	12	54676196	54676196	Frame_Shift_Ins	INS	-	AAATAATCTCTT	-	HNRNP1A	insTCAAAATAA	p.V170fs
XH_P37	12	54756849	54756849	Frame_Shift_Ins	INS	-	CCACA	-	GRP84	786_787insTGTG	p.T263fs
XH_P37	12	54756850	54756850	Silent	SNP	G	T	G	GRP84	c.C786A	p.A262A
XH_P37	12	54757616	54757616	In_Frame_Ins	INS	-	CTCCTCTTTTTC	-	GRP84	nsGCAAAAAGG	A7delinsGKKEEP
XH_P37	12	55820944	55820944	In_Frame_Ins	INS	-	GGG	-	OR6C76	.907_908insGG	p.R303delinsRG
XH_P37	12	55820946	55820946	Nonsense_Mutation	INS	-	SAATAGTTCTGA	-	OR6C76	TCTCAGAAATAGT	R303delinsRFSEX
XH_P37	12	56230844	56230844	Frame_Shift_Ins	INS	-	CATTTCACAT	-	MMP19	.1503insAGTGA	p.A501fs
XH_P37	12	56230845	56230845	Missense_Mutation	SNP	G	C	G	MMP19	c.C1502G	p.A501G
XH_P37	12	56492662	56492662	Nonsense_Mutation	INS	-	AACTCGAAGTG	-	ERBB3	.813insAAATCTG	B38_D939delinsKIX
XH_P37	12	56514617	56514617	In_Frame_Ins	INS	-	CTC	-	ZC3H10	c.271_272insCT	p.N91delinsTH
XH_P37	12	56514618	56514618	Frame_Shift_Ins	INS	-	GGTTTTCTTTTAT	-	ZC3H10	73insGGGTTTTCT	p.N91fs
XH_P37	12	56532594	56532594	Frame_Shift_Ins	INS	-	AGGGGCCATTTC	-	ESYT1	AAAGAGAGGGG	p.T836fs
XH_P37	12	56629065	56629065	Silent	SNP	G	A	G	SLC39A5	c.G759A	p.A253A
XH_P37	12	56629066	56629066	Frame_Shift_Ins	INS	-	GTGTGCTCAGCC	-	SLC39A5	nsTCTGTGTGCTG	p.V254fs
XH_P37	12	56720652	56720652	In_Frame_Ins	INS	-	CTTCTCTCTGAT	-	PAN2	.1011insATCAGA	D337delinsESERS
XH_P37	12	56814431	56814431	Missense_Mutation	SNP	T	G	T	TIMELESS	c.A3147C	p.E1049D
XH_P37	12	56814433	56814433	Frame_Shift_Ins	INS	-	TTGTCAT	-	TIMELESS	.44_3145insATG	p.E1049fs
XH_P37	12	56995739	56995739	Missense_Mutation	SNP	G	A	G	BAZ2A	c.C3662T	p.P1221L
XH_P37	12	56995741	56995741	Frame_Shift_Ins	INS	-	ACTCTGG	-	BAZ2A	.59_3660insCCAC	p.Q1220fs
XH_P37	12	57114643	57114643	In_Frame_Ins	INS	-	TCCATTCTCTCTG	-	NACA	.1insCCAGAGAA	A224delinsPREMGK
XH_P37	12	57167943	57167943	Frame_Shift_Ins	INS	-	CTTCTTCTCTTT	-	HSD17B6	.8insTGCTTCTCTT	p.D103fs
XH_P37	12	57396618	57396618	Frame_Shift_Ins	INS	-	SCCATACCAATG	-	ZBTB39	.ACACCTTACATTG	p.Q695fs
XH_P37	12	57397690	57397690	Frame_Shift_Ins	INS	-	CGAC	-	ZBTB39	.011_1012insGT	p.R338fs
XH_P37	12	57397692	57397692	Nonsense_Mutation	INS	-	TGTGAAACATAA	-	ZBTB39	.1010insCTTAGT	B37_R338delinsTX
XH_P37	12	57549899	57549899	Missense_Mutation	SNP	C	T	C	LRP1	c.C1250T	p.T417I
XH_P37	12	57630863	57630863	Frame_Shift_Ins	INS	-	ATTCTTC	-	NDUFA4L2	.5_6insGAAGAA	p.A2fs
XH_P37	12	57630864	57630864	Missense_Mutation	SNP	G	C	G	NDUFA4L2	c.C5G	p.A2G
XH_P37	12	57691140	57691140	Nonsense_Mutation	INS	-	TAAAT	-	R3HDM2	.530_531insATTTC	Q177delinsQFX
XH_P37	12	57691142	57691142	Frame_Shift_Ins	INS	-	TACCTAAATTTAT	-	R3HDM2	.29insATAAATT	p.Q177fs
XH_P37	12	57872954	57872954	Frame_Shift_Ins	INS	-	AACCATCTTCTC	-	ARHGAP9	.insAAGAGAAGA	p.P79fs
XH_P37	12	58018652	58018652	Frame_Shift_Ins	INS	-	ACTCATCTCTA	-	SLC26A10	.1232insACTCA	p.L411fs
XH_P37	12	59274453	59274453	In_Frame_Ins	INS	-	AGATTCTTGGTT	-	LRIG3	.7ACAAATAACCA	A1delinsQITKNLNFV
XH_P37	12	59308052	59308052	Frame_Shift_Ins	INS	-	STAAGTGAATAT	-	LRIG3	.TGCTGATATTCA	p.LR1Gfs
XH_P37	12	64038266	64038266	In_Frame_Ins	INS	-	TTGTGGATTAC	-	DPY19L2	.5ATCAAGTAAAT	A40delinsESSKSTNF
XH_P37	12	64712644	64712644	In_Frame_Ins	INS	-	CTTTACCTCCCA	-	C12orf56	.nsAAATGGGAGG	G02delinsKMGKGKG
XH_P37	12	65226073	65226073	Missense_Mutation	SNP	G	A	G	TBC1D30	c.G583A	p.C1210fs
XH_P37	12	65226074	65226074	Nonsense_Mutation	INS	-	CAAAAATAACTG	-	TBC1D30	.ATTTTCAAAAAT	A196delinsEQYFQX
XH_P37	12	65632524	65632524	Nonsense_Mutation	INS	-	GTGTTAAATATG	-	LEMD3	.AATGAAGTGTGA	A16_M617delinsLQX
XH_P37	12	67692835	67692835	Nonsense_Mutation	INS	-	TCCCCTAATCCC	-	CAND1	.61insCTCCCCCTA	A20_N321delinsELPX
XH_P37	12	67700316	67700316	Nonsense_Mutation	INS	-	SGTGATTTGACT	-	CAND1	.nsTGACGTGAT	G956delinsGCSX
XH_P37	12	68595698	68595698	Frame_Shift_Ins	INS	-	AGAAATAGA	-	IL26	.12_443insTCTAT	p.LR1Gfs
XH_P37	12	68595699	68595699	Nonsense_Mutation	INS	-	GATTTAGTAAAT	-	IL26	.ACGTTAATTTACT	G148delinsTLVX
XH_P37	12	69991479	69991479	Frame_Shift_Ins	INS	-	GGTAAATATGA	-	CC2	.4insCACGGTAA	p.R341fs
XH_P37	12	72025902	72025902	Frame_Shift_Ins	INS	-	BATTTCGTGATA	-	ZFC3H1	.5TCCACATCTACA	p.N1070fs
XH_P37	12	72070757	72070757	Frame_Shift_Ins	INS	-	TAGCTGTGTT	-	THAP2	.557insTAGCTG	p.T186fs
XH_P37	12	72070759	72070759	Frame_Shift_Ins	INS	-	AGTAG	-	THAP2	.558_559insAGT	p.T186fs
XH_P37	12	75692559	75692559	In_Frame_Ins	INS	-	GGCTAATGGTTG	-	CAPS2	.insCATCAACCAT	A255delinsHQPLAHT
XH_P37	12	75824866	75824866	Frame_Shift_Ins	INS	-	AATGTGCACA	-	GLIPR1L2	.961insAATGTG	p.M320fs
XH_P37	12	75824868	75824868	Missense_Mutation	SNP	A	T	A	GLIPR1L2	c.A962T	p.E321V
XH_P37	12	76740337	76740337	Frame_Shift_Ins	INS	-	AAACAGGCTAAC	-	BBS10	.5TAATCAGTTAG	p.N476fs
XH_P37	12	79689947	79689947	Frame_Shift_Ins	INS	-	GC	-	SYT1	.c.573_574insGC	p.K191fs
XH_P37	12	79689948	79689948	Nonsense_Mutation	INS	-	GAACTGAGCTA	-	SYT1	.insAATGAACATG	A192_K193delinsKX
XH_P37	12	80626848	80626848	Frame_Shift_Ins	INS	-	A	-	OTOGL	c.761_762insA	p.I254fs
XH_P37	12	80626849	80626849	Nonsense_Mutation	INS	-	TAAGTGACTGAG	-	OTOGL	.nsTTTTAAGTGA	p.I254delinsLFX
XH_P37	12	80672934	80672934	Frame_Shift_Ins	INS	-	AACATTGGAATG	-	OTOGL	.ACAGCAACATTG	p.V963fs
XH_P37	12	85450416	85450416	Frame_Shift_Ins	INS	-	ATTTCCTTGTTA	-	LRRIQ1	.insCTGATTCTCT	p.S615fs
XH_P37	12	85518207	85518207	Frame_Shift_Ins	INS	-	AGTGCTGTCCAC	-	LRRIQ1	.3918insAGTGC	p.S1306fs
XH_P37	12	85518209	85518209	Missense_Mutation	SNP	A	G	A	LRRIQ1	c.A3919G	p.I1307V
XH_P37	12	88380123	88380123	Silent	SNP	T	C	T	C12orf50	c.A888G	p.E296E
XH_P37	12	88589399	88589399	Frame_Shift_Ins	INS	-	NTCTATCCCTGA	-	TMTIC3	.insGAAATCTTAT	p.E906fs
XH_P37	12	91502739	91502739	Nonsense_Mutation	INS	-	CTTTTACCTTAGC	-	LUM	.8insCCTAAGGTG	A16_T7delinsFLRX
XH_P37	12	91502741	91502741	In_Frame_Ins	INS	-	TAACCAGAT	-	LUM	.5_16insATCTGG	p.F6delinsWLF
XH_P37	12	91552169	91552169	Missense_Mutation	SNP	T	A	T	DCN	c.A442T	p.M148L
XH_P37	12	93226409	93226409	Frame_Shift_Ins	INS	-	CG	-	EEA1	.1132_1133insC	p.K378fs
XH_P37	12	93226411	93226411	Nonsense_Mutation	INS	-	ATGGTTATTGTA	-	EEA1	.ATTATGATCAAA	B77_K378delinsLLX
XH_P37	12	94772625	94772625	In_Frame_Ins	INS	-	AGT	-	CEP83	.c.742_743insAC	p.A248delinsDS
XH_P37	12	94772626	94772626	Nonsense_Mutation	INS	-	GTCACCTATCTG	-	CEP83	.2insTTACAGATA	A48_Q249delinsFRX
XH_P37	12	94796978	94796978	In_Frame_Ins	INS	-	CCT	-	CEP83	.384_385insAG	p.P129delinsRP
XH_P37	12	94796979	94796979	Frame_Shift_Ins	INS	-	CTGAT	-	CEP83	.383_384insATC	p.T128fs
XH_P37	12	95456403	95456403	Nonsense_Mutation	INS	-	ATCATGTATAT	-	NR2C1	.insTGAATATAC	A.K56_V57delinsX
XH_P37	12	95604126	95604126	Nonsense_Mutation	INS	-	TCAGTGTTCTGT	-	FGD6	.TGATGCAGAAC	P313delinsHSDAEHX
XH_P37	12	95663891	95663891	Nonsense_Mutation	INS	-	AAAATGATTATA	-	VEZT	.ACTAGAAAAATG	A259_K260delinsHX
XH_P37	12	95927075	95927075	Nonsense_Mutation	INS	-	CGCTCAGGAAT	-	USP44	.958insAATTCCT	B.S320delinsNSX
XH_P37	12	95927168	95927175	Frame_Shift_Del	DEL	GAAGAAACA	-	GAAGAAACA	USP44	c.858_865del	p.S286fs
XH_P37	12	95927978	95927978	Frame_Shift_Ins	INS	-	TTTTTGTACCTTT	-	USP44	.CACAAAGGTAA	p.H19fs
XH_P37	12	99028179	99028179	Nonsense_Mutation	INS	-	TAGACCATCAC	-	IKBIP	.nsAATAGTGTATG	A.Q65delinsQIVMVX
XH_P37	12	99028181	99028181	Missense_Mutation	SNP	G	T	G	IKBIP	c.C190A	p.Q64K
XH_P37	12	100452367	100452367	Frame_Shift_Ins	INS	-	GATGAAAGTAG	-	UHRF1BP1L	.nsAGTCCACTACT	p.D896fs
XH_P37	12	101316108	101316108	In_Frame_Ins	INS	-	AGGAACATATA	-	ANO4	.AAAAAAGGAAC	A4delinsKKKKEHQIAL
XH_P37	12	101316110	101316110	Splice_Site	SNP	T	C	T	ANO4		
XH_P37	12	101336311	101336311	Frame_Shift_Ins	INS	-	GGACC	-	ANO4	.454_455insGGA	p.E152fs
XH_P37	12	101336313	101336313	Frame_Shift_Ins	INS	-	TTTAA	-	ANO4	.456_457insTTTA	p.E152fs
XH_P37	12	102041901	102041901	In_Frame_Ins	INS	-	TTTGTTTCTGTTT	-	MYBP1	.TTTGTTTCTGTTCT	9delinsVVFVVLVLRQ
XH_P37	12	102140999	102140999	Frame_Shift_Ins	INS	-	AGTACCATGCTG	-	GNPTAB	.714insACAGCAT	p.K1238fs
XH_P37	12	102153861	102153861	In_Frame_Ins	INS	-	AATTTG	-	GNPTAB	.95_3196insCAA	A.T1066delinsQIT
XH_P37	12	102153863	102153863	In_Frame_Ins	INS	-	TTTGTGCT	-	GNPTAB	.3_3194insAGCA	A.1065delinsKQQL
XH_P37	12	102153899	102153899	Nonsense_Mutation	INS	-	CTATGGTTTAT	-	GNPTAB	.AGACATATAAAA	A.D53_L1054delinsKDIX
XH_P37	12	102505971	102505971	Frame_Shift_Ins	INS	-	TC	-	NUP37	c.195_196insGA	p.L66fs
XH_P37	12	102517803	102517803	Frame_Shift_Ins	INS	-	A	-	PARBP	c.137_138insA	p.A46fs
XH_P37	12	102545579	102545579	Splice_Site	INS	-	CTTCCTCTTTC	-	PARBP		
XH_P37	12	104089391	104089391	Nonsense_Mutation	INS	-	GATGTTAGTCA	-	STAB2	.GTTGGAGATGT	A.1147delinsSWRCX
XH_P37	12	104171846	104171846	Frame_Shift_Ins	INS	-	GTAACGTCCC	-	NT5DC3	.1408insGGGCA	p.S470fs
XH_P37	12	104373691	104373691	Frame_Shift_Ins	INS	-	TT	-	TDG	.c.249_250insTT	p.K83fs
XH_P37	12	104373693	104373693	Frame_Shift_Ins	INS	-	TCTTACAGTCCC	-	TDG	.insGCTCTTACAG	p.K84fs
XH_P37	12	105527633	105527633	Frame_Shift_Ins	INS	-	ACATAGACATAT	-	WASHC4	.insATTACATAG	p.F429fs
XH_P37	12	105760434	105760434	Frame_Shift_Ins	INS	-	AAAAAAAGAAAA	-	C12orf75	.TTTAAAAAAATA	p.A49fs

XH_P37	12	107109313	107109313	Frame_Shift_Ins	INS	-	GACGCAGACAC	-	RFX4	insGAAGACGCA	p.I283fs
XH_P37	12	108686305	108686305	Frame_Shift_Ins	INS	-	TCCTCATCATC	-	CMKLR1	435insGATGATC	p.V145fs
XH_P37	12	109017386	109017386	In_Frame_Ins	INS	-	CCACTATCT	-	SELPLG	746insAGATAA	T249delinsKIVA
XH_P37	12	109072161	109072161	Frame_Shift_Ins	INS	-	ACTACGTTTAAG	-	CORO1C	TTAAACTTAAAC	p.I122fs
XH_P37	12	109539785	109539785	Frame_Shift_Ins	INS	-	TAAG	-	UNG	487_488insTAA	p.P163fs
XH_P37	12	109539786	109539786	Frame_Shift_Ins	INS	-	TTAACTTGTAA	-	UNG	GTATTTTAAACT	p.P163fs
XH_P37	12	110457066	110457066	Frame_Shift_Ins	INS	-	ATGTTAAATGT	-	ANKRD13A	TCGTATGTTAA	p.V223fs
XH_P37	12	111894025	111894025	Frame_Shift_Ins	INS	-	CTAAGGGA	-	ATXN2	0_2631insTCCC	p.L877fs
XH_P37	12	111923636	111923636	Frame_Shift_Ins	INS	-	GTGTGATGGTT	-	PTXN2	1951insAACCA	p.P651fs
XH_P37	12	111923637	111923637	Silent	SNP	C	A	C	ATXN2	c.G1950T	p.R650R
XH_P37	12	111963063	111963063	In_Frame_Ins	INS	-	TTGTATAACTAG	-	ATXN2	instCTCTAGTTA	p81delinsVSSYTTN
XH_P37	12	112654155	112654155	Missense_Mutation	SNP	T	G	T	HECTD4	c.A7004C	p.Y2335S
XH_P37	12	112654157	112654157	In_Frame_Ins	INS	-	TCCTATTGGTAA	-	HECTD4	02insGTTACCA	p2334delinsQLPNGG
XH_P37	12	113399019	113399019	In_Frame_Ins	INS	-	TAACAT	-	OAS3	01_1802insTAAp	L601delinsLTL
XH_P37	12	113399021	113399021	In_Frame_Ins	INS	-	CAATAATACACT	-	OAS3	rsCAATCAATAA	p501delinsLQSIHYN
XH_P37	12	116401278	116401278	Frame_Shift_Ins	INS	-	GT	-	MED13L	.6433_6434insA	p.L2145fs
XH_P37	12	116401280	116401280	Nonsense_Mutation	INS	-	TAGGCATTAT	-	MED13L	6432insATAAA	L144_L2145delinsLX
XH_P37	12	116421315	116421315	In_Frame_Ins	INS	-	CTCTGCTCTGG	-	MED13L	562insCAGGA	p1521delinsTRSRG
XH_P37	12	116457180	116457180	Frame_Shift_Ins	INS	-	CAGACAATTGTA	-	MED13L	58insATACAATT	p.L286fs
XH_P37	12	117423111	117423111	Nonsense_Mutation	INS	-	TACTTAATATGT	-	FBXW8	AAATTTCATTAA	T247delinsAGNNFKFTX
XH_P37	12	117907566	117907566	Frame_Shift_Ins	INS	-	CC	-	KSR2	2659_2660insG	p.E887fs
XH_P37	12	117907568	117907568	Frame_Shift_Ins	INS	-	ACTAGGTTTC	-	KSR2	2658insGAAAC	p.Q886fs
XH_P37	12	118473033	118473033	Silent	SNP	C	A	C	WSB2	c.G300T	p.T100T
XH_P37	12	118473034	118473034	In_Frame_Ins	INS	-	GGTATGTAT	-	WSB2	8_299insATACA	T100delinsNTYP
XH_P37	12	120510361	120510361	In_Frame_Ins	INS	-	TTTTTTTTTAA	-	BICDL1	1137insTTTTTT	C379delinsCFFFN
XH_P37	12	120575848	120575848	Frame_Shift_Ins	INS	-	GCTGTGAT	-	GCN1	9_6250insATCA	p.L2084fs
XH_P37	12	120750381	120750381	In_Frame_Ins	INS	-	CCTAACACACAA	-	SIRT4	instTCCCTAACCA	p207delinsLSTHNP
XH_P37	12	122243822	122243822	Nonsense_Mutation	INS	-	TAAACGTTCTTC	-	SETD1B	AGGTTTAAACGT	p119_R120delinsPX
XH_P37	12	122359558	122359558	In_Frame_Ins	INS	-	CTCTCCATGCTAT	-	WDR66	sGACTCTCTCCA	p116delinsETSLMLLC
XH_P37	12	122657270	122657270	Frame_Shift_Ins	INS	-	TAAATCATT	-	IL31	.184insAATGA	p.V62fs
XH_P37	12	122657272	122657272	Missense_Mutation	SNP	C	A	C	IL31	c.G182T	p.G61V
XH_P37	12	122825543	122825543	Frame_Shift_Ins	INS	-	AAAT	-	CLIP1	069_2070insAT	p.Q690fs
XH_P37	12	122825545	122825545	In_Frame_Ins	INS	-	CTGATT	-	CLIP1	67_2068insAAT	p.Q690delinsNQ
XH_P37	12	123014639	123014639	In_Frame_Ins	INS	-	TAACATTAACT	-	KNTC1	AGTCTAACATT	p1elinsKQKXNINIYRHL
XH_P37	12	123072422	123072422	Splice_Site	INS	-	ATTTTAAACA	-	KNTC1	-	-
XH_P37	12	123810856	123810856	Frame_Shift_Ins	INS	-	CAAGATGGAA	-	SBNO1	CTTACTTTTCCA	p.Q573fs
XH_P37	12	124104153	124104153	Frame_Shift_Ins	INS	-	GGTTT	-	DDX55	508_1509insGG	p.R503fs
XH_P37	12	124104154	124104154	Nonsense_Mutation	INS	-	GCATTCATTTTAC	-	DDX55	10insATGCATTC	p.R504delinsRMHSFX
XH_P37	12	124330651	124330651	Frame_Shift_Ins	INS	-	AGAAAGGT	-	DNAH10	0_5411insAGAA	p.R1804fs
XH_P37	12	125570975	125570975	Frame_Shift_Ins	INS	-	CTGCAAGAGTC	-	AACS	459insCTGCAA	p.G153fs
XH_P37	12	125834655	125834655	Frame_Shift_Ins	INS	-	CATCTTGACACA	-	TMEM132B	11insACATCTTG	p.K237fs
XH_P37	12	132522555	132522555	In_Frame_Ins	INS	-	TAGTTCCATTTT	-	EP400	GATCTTTAGTTC	p1delinsQFSSIFQFQL
XH_P37	13	20244447	20244447	Frame_Shift_Ins	INS	-	CCTGGAAAAGA	-	MPHOSPH8	insAGTTCTCGG	p.P801fs
XH_P37	13	21562109	21562109	Frame_Shift_Ins	INS	-	TCAGAGATAG	-	LATS2	1810insCTATC	p.F604fs
XH_P37	13	21562111	21562111	Frame_Shift_Ins	INS	-	GTGCA	-	LATS2	807_1808insTG	p.K603fs
XH_P37	13	25436888	25436888	Frame_Shift_Ins	INS	-	ATAGGTACATGA	-	RNF17	AATATCATAGGT	p.L1307fs
XH_P37	13	25671286	25671286	Frame_Shift_Ins	INS	-	CTCATCTACAGC	-	PABPC3	nsCATCTCATCT	p.F317fs
XH_P37	13	27241792	27241792	Missense_Mutation	SNP	T	A	T	WASF3	c.T407A	p.L316N
XH_P37	13	27241794	27241794	In_Frame_Ins	INS	-	AAATAATATTTT	-	WASF3	410insAAATAA	p.L137delinsQIIFL
XH_P37	13	27679935	27679935	Frame_Shift_Del	DEL	G	-	G	USP12	c.276delC	p.A92fs
XH_P37	13	27679936	27679936	Missense_Mutation	SNP	G	A	G	USP12	c.C275T	p.A92V
XH_P37	13	28588655	28588655	Frame_Shift_Ins	INS	-	TTGTGTGGGGT	-	FLT3	3insTCTTACCCCA	p.R931fs
XH_P37	13	28588656	28588656	Nonsense_Mutation	INS	-	TTTATTT	-	FLT3	1_2792insATAAA	p.R931delinsNKX
XH_P37	13	28712860	28712910	In_Frame_Del	DEL	CCCCGCCGGG	-	CCCCGCCGGGG	PAN3	c.66_116del	p.22_39del
XH_P37	13	32808822	32808822	Frame_Shift_Ins	INS	-	ATTTTTTTTT	-	FRY	9_5640insATTTT	p.P1880fs
XH_P37	13	32808824	32808824	In_Frame_Ins	INS	-	TCTTTT	-	FRY	641_5642insTCT	p.L1881delinsLFL
XH_P37	13	32929292	32929292	Frame_Shift_Ins	INS	-	ATTTAGACAGAA	-	BRCA2	3insAGATTAG	p.K2434fs
XH_P37	13	32929352	32929352	Nonsense_Mutation	INS	-	SACAGAAATCT	-	BRCA2	3insTAGACAGA	p.454_H245delinsIX
XH_P37	13	32954173	32954173	Nonsense_Mutation	INS	-	AGTTGCAAGAT	-	BRCA2	TTTGAAGTTCG	p.49_Q3050delinsYFX
XH_P37	13	33110793	33110793	Nonsense_Mutation	INS	-	CATTATACCAT	-	N4BP2L2	CTAAATGGTAT	p.24_G12delinsMFX
XH_P37	13	36801484	36801484	Frame_Shift_Ins	INS	-	TT	-	CCDC169	c.279_280insAA	p.V94fs
XH_P37	13	36801485	36801485	Nonsense_Mutation	INS	-	GTCTTTTATTTT	-	CCDC169	AGTAAAAATAA	p.93_V94delinsKXX
XH_P37	13	38320583	38320583	Frame_Shift_Ins	INS	-	GAAAGAGCTGC	-	TRPC4	388insGACAGC	p.I130fs
XH_P37	13	39265542	39265542	In_Frame_Ins	INS	-	GCTTCCCATCTG	-	FREM2	062insGTCTTCC	p.1354delinsSASHLL
XH_P37	13	39430388	39430388	In_Frame_Ins	INS	-	TCATTTTTTTTT	-	FREM2	sAGTTTCTTATT	p.2351delinsKSFIFFFL
XH_P37	13	40301667	40301667	Nonsense_Mutation	INS	-	AAACTGCAAAAT	-	COG6	TCCCTAAAACGT	p.603delinsLTKTPX
XH_P37	13	41134000	41134000	Frame_Shift_Ins	INS	-	CTGTGACATGA	-	FOXO1	28insATTCCATG	p.V543fs
XH_P37	13	41341125	41341125	Frame_Shift_Ins	INS	-	AAGAAGAGGTA	-	MRP531	TAATTTTACCTC	p.I66fs
XH_P37	13	42390895	42390895	Nonsense_Mutation	INS	-	GCTGATGTTAT	-	VWA8	886insTATAACA	p.629_E630delinsLX
XH_P37	13	45556286	45556286	Nonsense_Mutation	INS	-	AACATGTTTAT	-	NUFIP1	AAAAACATAAAA	p.K139delinsTX
XH_P37	13	46543546	46543546	Nonsense_Mutation	INS	-	CTGCCATCACTA	-	ZC3H13	8133insTAGTGA	p.M1045delinsX
XH_P37	13	46544565	46544565	Nonsense_Mutation	INS	-	ATTTTCTACTATT	-	ZC3H13	504insAATAGT	p.835_Q836delinsKX
XH_P37	13	47297448	47297448	Nonsense_Mutation	INS	-	TTAAAAGAGAC	-	LRCH1	AGTATTTTAAAA	p.83_E584delinsAQVFX
XH_P37	13	47297450	47297450	Silent	SNP	G	T	G	LRCH1	c.G1749T	p.V583V
XH_P37	13	49841849	49841849	Nonsense_Mutation	INS	-	AATTATGAGATA	-	CDADC1	AGGTAATTATGA	p.18_T219delinsKYERX
XH_P37	13	50296696	50296696	In_Frame_Ins	INS	-	TTAAGATGATG	-	KPNA3	3insAGCATCAT	p.158delinsEHLKS
XH_P37	13	50296698	50296698	Missense_Mutation	SNP	A	T	A	KPNA3	c.T471A	p.L157K
XH_P37	13	50502089	50502089	Frame_Shift_Ins	INS	-	AA	-	SPRYD7	c.238_239insTT	p.P80fs
XH_P37	13	50502091	50502091	Nonsense_Mutation	INS	-	TTATATTAGA	-	SPRYD7	1_237insTCTAAT	p.79_P80delinsLXIX
XH_P37	13	50587285	50587285	In_Frame_Ins	INS	-	CCACATCGACTA	-	TRIM13	GTTTATCCACAT	p.8delinsKESLSTSTFSMS
XH_P37	13	50589872	50589872	Frame_Shift_Ins	INS	-	AAAT	-	KCNRG	243_244insAA	p.R81fs
XH_P37	13	50589873	50589873	In_Frame_Ins	INS	-	CTATAACCATAA	-	KCNRG	nsAACCTATAAC	p.82delinsOPTINV
XH_P37	13	53049243	53049243	Frame_Shift_Ins	INS	-	AAITAAAACAA	-	CKAP2	20insAAAAATTA	p.L673fs
XH_P37	13	61986244	61986244	Frame_Shift_Ins	INS	-	GTACTGCCTT	-	PCDH20	1988insAAGGC	p.V663fs
XH_P37	13	67205362	67205362	In_Frame_Ins	INS	-	TGTATT	-	PCDH9	91_3092insAAT	p.G1031delinsEYS
XH_P37	13	67205363	67205363	In_Frame_Ins	INS	-	AATATGTTTGATA	-	PCDH9	AAATCATATCAA	p1delinsLTKIISNIIINVYLGK
XH_P37	13	74420480	74420480	Frame_Shift_Ins	INS	-	CCCATGAATTTA	-	KLF12	sACTGTAATTC	p.E52fs
XH_P37	13	77641983	77641983	Nonsense_Mutation	INS	-	GATTTTCAATT	-	MYCBP2	3insCCTGGAATT	p.53_R4064delinsTWNX
XH_P37	13	77672052	77672052	Nonsense_Mutation	INS	-	TTACAAACATTTA	-	MYCBP2	AGCCACTAAATG	p.79_E3080delinsSEHX
XH_P37	13	77695627	77695627	Frame_Shift_Ins	INS	-	AA	-	MYCBP2	.8020_8021insT	p.Q2674fs
XH_P37	13	77695628	77695628	Nonsense_Mutation	INS	-	AGAGTGCTTGCT	-	MYCBP2	AAAATAAGCAA	p.A2675delinsKKNQKQXLSX
XH_P37	13	79189802	79189802	Nonsense_Mutation	INS	-	TATACAAAATG	-	RNF219	TCAAATTCCAATT	p.R699delinsNYQFQVFX
XH_P37	13	79190756	79190756	In_Frame_Ins	INS	-	AGTGAAATGAA	-	RNF219	ATTCTTTTTCATT	p1delinsKHXSDFFSLLISSS
XH_P37	13	96536885	96536885	Nonsense_Mutation	INS	-	ATCAGCTATTAC	-	UGGT2	ACAATTGTAATA	p.S1031delinsTCYCNMSX
XH_P37	13	98669104	98669104	Nonsense_Mutation	INS	-	TATTTTCTATT	-	IPO5	AAAGTATATTTT	p.891delinsWIKKIFYFYQX
XH_P37	13	99554691	99554691	Nonsense_Mutation	INS	-	STCTAAATTAGA	-	DOCK9	1234insGTCTAA	p.412_S413delinsVX
XH_P37	13	99966465	99966465	Nonsense_Mutation	INS	-	ATGATTCACTGC	-	UBAC2	AAATATGATTCA	p3delinsLIFKYDSCPKX
XH_P37	13	99966467	99966467	Missense_Mutation	SNP	G	T	G	UBAC2	c.G401T	p.G134V

XH_P37	13	100637715	100637717	In_Frame_Del	DEL	GCG	-	GCG	ZIC2	c.1378_1380del	p.460_460del
XH_P37	13	103393253	103393253	Frame_Shift_Ins	INS	-	AAGAAAAATAT	-	CCDC168	9794insTATATT	p.A3265fs
XH_P37	13	103393254	103393254	Frame_Shift_Ins	INS	-	ATACAAGG	-	CCDC168	2_9793insCCTT	p.A3265fs
XH_P37	13	103400631	103400631	Frame_Shift_Ins	INS	-	AA	-	CCDC168	.2415_2416insT	p.L806fs
XH_P37	13	103400633	103400633	Nonsense_Mutation	INS	-	AAGGCTCAGTC	-	CCDC168	14insATGACTG	p.1805delinsNDX
XH_P37	13	103514771	103514771	Frame_Shift_Ins	INS	-	CTTCTGAGCT	-	BIVM-ERCC5	1273insTCTTCT	p.s424fs
XH_P37	13	103518257	103518257	In_Frame_Ins	INS	-	CCTGCAATCATC	-	BIVM-ERCC5	AATGATCCTGCA	32delinsKMILQSSRA
XH_P37	13	103518259	103518259	Frame_Shift_Ins	INS	-	TC	-	BIVM-ERCC5	.2197_2198insT	p.L733fs
XH_P37	13	108882073	108882073	Silent	SNP	T	A	T	ABHD13	c.T507A	p.S169fs
XH_P37	13	108955691	108955691	Missense_Mutation	SNP	G	T	G	TNFSF13B	c.G515T	p.G172V
XH_P37	13	114152820	114152820	Frame_Shift_Ins	INS	-	AATGTCCCTGT	-	TMCO3	sGTCAAAATGTCC	p.F203fs
XH_P37	13	114294501	114294501	Frame_Shift_Ins	INS	-	TGGAACCAT	-	TFDP1	.1153insTGGAA	p.S384fs
XH_P37	13	115052051	115052051	Frame_Shift_Ins	INS	-	AGGATATT	-	UPF3A	9_480insAGGA	p.A160fs
XH_P37	13	115052052	115052052	Nonsense_Mutation	INS	-	GGCCTTTTAAACA	-	UPF3A	1insTAGGCCTTT	160_1161delinsAX
XH_P37	13	115091571	115091571	Nonsense_Mutation	INS	-	AGAGATAAAAGC	-	CHAMP1	.TCTTCAGAGAT	62_1753delinsPLQRX
XH_P37	14	20215589	20215589	Frame_Shift_Ins	INS	-	A	-	OR4Q3	c.4dupA	p.M1fs
XH_P37	14	20296052	20296052	Nonsense_Mutation	INS	-	A	-	OR4N2	c.445_446insA	V149_L150delinsX
XH_P37	14	20876082	20876082	Frame_Shift_Ins	INS	-	CTTCTCTCCTC	-	TEP1	517insGAGGAG	p.1173fs
XH_P37	14	20978669	20978669	Frame_Shift_Ins	INS	-	TGTA	-	RNA5E10	c.39_40insTGTA	p.L13fs
XH_P37	14	20978671	20978671	Frame_Shift_Ins	INS	-	AAAATGTGGAA	-	RNA5E10	42insAAAATGT	p.M14fs
XH_P37	14	21796726	21796726	Frame_Shift_Ins	INS	-	sACTCTATTCTC	-	RPGRIP1	40insAGACTTCA	p.V1013fs
XH_P37	14	21802846	21802846	In_Frame_Ins	INS	-	ATTTTGCCITTCAC	-	RPGRIP1	2insAGATTITG	107delinsSRFLHL
XH_P37	14	21956790	21956790	Nonsense_Mutation	INS	-	TAAATACAAA	-	TOX4	.TCATTTAAAT	7_P98delinsPNCIIX
XH_P37	14	21990884	21990884	In_Frame_Ins	INS	-	ATTTTGCT	-	SALL2	7_2978insAGAC	T.993delinsKTKS
XH_P37	14	21991982	21991982	Frame_Shift_Ins	INS	-	A	-	SALL2	c.1879dupT	p.S627fs
XH_P37	14	21991984	21991984	In_Frame_Ins	INS	-	TTACCAAT	-	SALL2	7_1878insATTG	A626delinsALVN
XH_P37	14	22102632	22102632	In_Frame_Ins	INS	-	GCCATC	-	OR10G2	66_367insGATG	M123delinsDGM
XH_P37	14	22102995	22102995	Frame_Shift_Ins	INS	-	AT	-	OR10G2	c.3_4insAT	p.G2fs
XH_P37	14	22102997	22102997	Nonsense_Mutation	INS	-	AGGCTATCCCG	-	OR10G2	2insCGGGATAG	M1_G2delinsTGX
XH_P37	14	22133648	22133648	Frame_Shift_Ins	INS	-	TCITTTACTCCAA	-	OR4E2	sACAGTCTTTAC	p.V118fs
XH_P37	14	23103582	23103582	In_Frame_Ins	INS	-	TTCTCT	-	OR6U1	34_135insGAGG	p.I45delinsMRN
XH_P37	14	23103583	23103583	Missense_Mutation	SNP	A	C	A	OR6U1	c.C134G	p.I45S
XH_P37	14	23456765	23456765	In_Frame_Ins	INS	-	AAC	-	C14orf93	1275_1276insG	p.L426delinsVL
XH_P37	14	23456766	23456766	In_Frame_Ins	INS	-	TTACAA	-	C14orf93	74_1275insTTG	E425delinsDCK
XH_P37	14	23512212	23512212	Frame_Shift_Ins	INS	-	TC	-	PSMB11	c.778_779insTC	p.A260fs
XH_P37	14	23512215	23512215	Frame_Shift_Del	DEL	AG	-	AG	PSMB11	c.781_782del	p.S261fs
XH_P37	14	23532716	23532716	Nonsense_Mutation	INS	-	GCCTAGCACAGT	-	ACIN1	59insTACTGTGC	20_P221delinsVLXC
XH_P37	14	23727820	23727820	Frame_Shift_Ins	INS	-	CTTT	-	RNF212B	.291_292insCTT	p.T97fs
XH_P37	14	23727821	23727821	Nonsense_Mutation	INS	-	ACTGTCTATTTC	-	RNF212B	sTTTACTGCTCT	K98delinsILLIFFX
XH_P37	14	23745125	23745125	Missense_Mutation	SNP	G	A	G	HOMEZ	c.C1312T	p.P438S
XH_P37	14	24656772	24656772	In_Frame_Ins	INS	-	AAGATGTGGTGA	-	IP04	insATCTCACCAC	141delinsHLTTSV
XH_P37	14	24766008	24766008	Nonsense_Mutation	INS	-	AGCCAATCTGAC	-	DHR51	230insGTCCGAGT	Q77delinsRRVGX
XH_P37	14	24787704	24787704	In_Frame_Ins	INS	-	GTGGGAATT	-	ADCY4	1_3152insAATT	V1051delinsEFPL
XH_P37	14	24787705	24787705	Frame_Shift_Ins	INS	-	TT	-	ADCY4	3150_3151insA	p.V1051fs
XH_P37	14	24886223	24886223	Frame_Shift_Ins	INS	-	ATAAGTACATG	-	NYNRIN	5269insATAAG	p.T1756fs
XH_P37	14	24974782	24974782	Frame_Shift_Ins	INS	-	TTCTAGTCGTGA	-	CMA1	sACACTCACGAC	p.A117fs
XH_P37	14	31576860	31576860	In_Frame_Ins	INS	-	GCC	-	HECTD1	6530_6531insGG	F2177delinsLA
XH_P37	14	31576861	31576861	Frame_Shift_Ins	INS	-	GGTTTCTG	-	HECTD1	9_6530insCAGA	p.F2177fs
XH_P37	14	32030754	32030754	Splice_Site	INS	-	AACCAATCTGCG	-	NUBPL	.	p.F2177fs
XH_P37	14	32560187	32560187	Frame_Shift_Ins	INS	-	CCACAGTTACCT	-	ARHGAP5	sCACTCCACAGT	p.F104fs
XH_P37	14	33292935	33292935	Frame_Shift_Ins	INS	-	CTTATTTTACCG	-	AKAP6	AGTTTTCTTATT	p.N1972fs
XH_P37	14	35037172	35037172	Nonsense_Mutation	INS	-	CTATTAT	-	SNX6	20_621insATAA	207_N208delinsAX
XH_P37	14	35231099	35231099	In_Frame_Ins	INS	-	TAAATATATTA	-	BAZ1A	.TATTAGTAATA	337delinsDISNIYSL
XH_P37	14	36768381	36768381	Frame_Shift_Ins	INS	-	TGCAGCAAGTA	-	MBP1	45insATTACTTG	p.G282fs
XH_P37	14	37736207	37736207	Nonsense_Mutation	INS	-	TGTAGATAAATG	-	MIPO1	sAAGTTGTAGAT	Q29delinsEHWDXLX
XH_P37	14	39543686	39543686	In_Frame_Ins	INS	-	TTG	-	SEC23A	1035_1036insCp	D346delinsQD
XH_P37	14	39543687	39543687	Frame_Shift_Ins	INS	-	AGTCATTATTTTC	-	SEC23A	.035insCAAAAT	p.I345fs
XH_P37	14	39648988	39648988	In_Frame_Ins	INS	-	TTCTTCATTGA	-	PNN	.TCTTTTCTCTTC	829delinsALFPLVL
XH_P37	14	39650971	39650971	Nonsense_Mutation	INS	-	TTCACTACTA	-	PNN	CTCACTCACTA	R687delinsDFSHYXX
XH_P37	14	45618149	45618149	Frame_Shift_Ins	INS	-	AAAGTACATCA	-	FANCM	sAAAAAAAGTA	p.I264fs
XH_P37	14	45658220	45658220	In_Frame_Ins	INS	-	TCT	-	FANCM	4917_4918insTp	S1639delinsSS
XH_P37	14	45658221	45658221	Nonsense_Mutation	INS	-	GGTTTCACTCTG	-	FANCM	nsAATAGGTTTCp	R1640delinsKX
XH_P37	14	45700488	45700488	Frame_Shift_Ins	INS	-	GGTA	-	MIS18BP1	.449_1450insTA	p.N484fs
XH_P37	14	45700489	45700489	Frame_Shift_Ins	INS	-	AGTGG	-	MIS18BP1	448_1449insCC	p.K483fs
XH_P37	14	45716108	45716108	Nonsense_Mutation	INS	-	AAGAGGTTAGT	-	MIS18BP1	insTAAAACTAA	p.E128delinsX
XH_P37	14	51058322	51058322	Nonsense_Mutation	INS	-	AAATATTAACAG	-	ATL1	.ATAAAAAATATT	A63delinsENKNINSX
XH_P37	14	52937318	52937318	Frame_Shift_Ins	INS	-	TT	-	TXND016	.1377_1378insA	p.P460fs
XH_P37	14	52937319	52937319	Nonsense_Mutation	INS	-	GGGAAGATACTA	-	TXND016	1377insCTAGTA	459_P460delinsFX
XH_P37	14	55423905	55423905	Frame_Shift_Ins	INS	-	AGGATAGGAGG	-	WDHD1	sTCAGAACCTCC	p.K798fs
XH_P37	14	55453990	55453990	Nonsense_Mutation	INS	-	ATGAAAATGTT	-	WDHD1	.ATTAAGAAACA	425_T426delinsYX
XH_P37	14	56078986	56078986	Frame_Shift_Ins	INS	-	GT	-	KTN1	c.220_221insGT	p.E74fs
XH_P37	14	56078987	56078987	Frame_Shift_Ins	INS	-	TTTTGTCAATGT	-	KTN1	22insCTTTTGTG	p.E74fs
XH_P37	14	56757127	56757127	In_Frame_Ins	INS	-	ATGGAAAGGAT	-	PEL12	TTGAAATGGAA	17delinsDVEMERILEL
XH_P37	14	57863585	57863585	In_Frame_Ins	INS	-	CAACAACCAAC	-	NAA30	8insACAACAAC	K296delinsKQQPTI
XH_P37	14	58604857	58604857	Nonsense_Mutation	INS	-	AATGGCAATTTC	-	C14orf37	ATTCTCTAAATTG	K408delinsNLFNLCHX
XH_P37	14	58790329	58790329	Frame_Shift_Ins	INS	-	CACAATATTTTG	-	ARID4A	sCAACAACAATT	p.P192fs
XH_P37	14	58831242	58831242	In_Frame_Ins	INS	-	TCATTTTCTCTA	-	ARID4A	.AAATTTTCTCTA	12delinsKFFSFSSSS
XH_P37	14	58975415	58975415	Frame_Shift_Ins	INS	-	TAGAAGTACGAC	-	KIAA0586	892insTTAGAAC	p.E1297fs
XH_P37	14	62207632	62207632	Nonsense_Mutation	INS	-	CAAAATAAGTTCA	-	HIF1A	.ATAAAACAAAT	A631_Q632delinsNX
XH_P37	14	62207739	62207739	Frame_Shift_Ins	INS	-	AG	-	HIF1A	.1998_1999insA	p.P666fs
XH_P37	14	62207741	62207741	Frame_Shift_Ins	INS	-	TAAATCTGTG	-	HIF1A	.2001insTAAAT	p.S667fs
XH_P37	14	64408656	64408656	Nonsense_Mutation	INS	-	TAATGTCTGTGA	-	SYNE2	.CTTTTAAATGTC	97_L98delinsAPFX
XH_P37	14	64491861	64491861	Frame_Shift_Ins	INS	-	A	-	SYNE2	.5974_5975ins	p.S1992fs
XH_P37	14	64491862	64491862	Nonsense_Mutation	INS	-	AATAAGCAAAA	-	SYNE2	76insAAAAATAAC	S1992delinsSKX
XH_P37	14	64519676	64519676	Frame_Shift_Ins	INS	-	ATCTTCAGAAAA	-	SYNE2	nsACTGATCTTC	p.S3015fs
XH_P37	14	64520249	64520249	Frame_Shift_Ins	INS	-	ATGAGTCATCAA	-	SYNE2	.CCTTGAATGAGT	p.I3206fs
XH_P37	14	64655376	64655376	Frame_Shift_Ins	INS	-	CACCTGTGATA	-	SYNE2	2insCTTACACCT	p.L5941fs
XH_P37	14	65390801	65390801	Frame_Shift_Ins	INS	-	AAAAATGGCCA	-	CHURC1	nsACTAAAAAAT	p.K71fs
XH_P37	14	66082795	66082795	Nonsense_Mutation	INS	-	TCTAAACATTT	-	FUT8	CACCTTCTAAAA	D1_K102delinsKLTFX
XH_P37	14	66096299	66096299	Frame_Shift_Ins	INS	-	AC	-	FUT8	c.B3_84insAC	p.V28fs
XH_P37	14	66096301	66096301	Frame_Shift_Ins	INS	-	ATCTTTTATTTTC	-	FUT8	86insATCTTTTAT	p.Q29fs
XH_P37	14	68250013	68250013	Frame_Shift_Ins	INS	-	GGAACAA	-	ZFYVE26	55_3856insTTG	p.R1286fs
XH_P37	14	69521050	69521050	In_Frame_Ins	INS	-	ACACTGACC	-	DCAF5	9_2350insGTC	L784delinsGQCL
XH_P37	14	69521712	69521712	Missense_Mutation	SNP	C	A	C	DCAF5	c.G1688T	p.S563I
XH_P37	14	69521713	69521713	Frame_Shift_Ins	INS	-	TCAACCA	-	DCAF5	6_1687insTTGG	p.S563fs
XH_P37	14	70839839	70839839	Frame_Shift_Ins	INS	-	C	-	SYNJ2BP	c.306dupG	p.Q120fs
XH_P37	14	70839841	70839841	Frame_Shift_Ins	INS	-	TGTCCTTC	-	SYNJ2BP	4_305insGAAAC	p.V102fs
XH_P37	14	71206838	71206838	Nonsense_Mutation	INS	-	ATATCAGCAAA	-	MAP3K9	sATCCCTTTGCTC	D231delinsESLXC

XH_P37	14	71275774	71275779	In_Frame_Del	DEL	CCTCCT	-	CCTCCT	MAP3K9	c.110_115del	p.37_39del
XH_P37	14	71543046	71543046	Frame_Shift_Ins	INS	-	ATTCAGATTAAA	-	PCNX1	AAAGAAATTCAG	p.D1638fs
XH_P37	14	73578348	73578348	Missense_Mutation	SNP	G	C	G	RBM25	c.G2130C	p.R710S
XH_P37	14	73578350	73578350	Frame_Shift_Ins	INS	-	TGCAAAATAT	-	RBM25	_2133insTGCAA	p.K711fs
XH_P37	14	73711453	73711453	Frame_Shift_Ins	INS	-	AAAACATATTCC	-	PAPLN	57insAAAACAT	p.P52fs
XH_P37	14	73989384	73989384	In_Frame_Ins	INS	-	CCAACAAGT	-	HEATR4	2_473insACCTTG	R158delinsHLLG
XH_P37	14	75538072	75538072	Frame_Shift_Ins	INS	-	GTTGCCCTGG	-	ZC2HC1C	797insGTTGCC	p.I266fs
XH_P37	14	77844378	77844378	Frame_Shift_Ins	INS	-	CTCTTTATGCGT	-	SAMD15	8insGACTCTTTA	p.I206fs
XH_P37	14	77872447	77872447	Nonsense_Mutation	INS	-	TCTTATTAATG	-	NOXRED1	AAAAGCATTAAB	G239delinsEEKKH
XH_P37	14	78183883	78183883	Frame_Shift_Ins	INS	-	GTTTGAATGTTT	-	SLRP	TTTCAGTTTGAA	p.D101fs
XH_P37	14	88477336	88477336	Frame_Shift_Ins	INS	-	AAAGTCTTGCTC	-	GPR65	sAGAGAAAGTCT	p.L49fs
XH_P37	14	88904489	88904489	Frame_Shift_Ins	INS	-	TCATTTT	-	SPATA7	27_1428insTCA	p.Q476fs
XH_P37	14	88904490	88904490	In_Frame_Ins	INS	-	CTTTACCGA	-	SPATA7	8_1429insCTTTA	Q476delinsQLYR
XH_P37	14	89181500	89181500	Nonsense_Mutation	INS	-	AATTCTAGCAA	-	EML5	TATAATTGTCTA	E409delinsDLX
XH_P37	14	89192998	89192998	Frame_Shift_Ins	INS	-	ATATTTC	-	EML5	3_1074insTGAA	p.A358fs
XH_P37	14	89192999	89192999	Frame_Shift_Ins	INS	-	ATGTTAATT	-	EML5	_1073insAAATT	p.A358fs
XH_P37	14	91386592	91386592	Nonsense_Mutation	INS	-	GTGGTAAATTTT	-	RPS6KA5	AAATGAAATTT	F36_137delinsX
XH_P37	14	92470616	92470616	In_Frame_Ins	INS	-	GGATCTCTTTTA	-	TRIP11	TTTCTCTAAAAG	234delinsSFPKRRSLVL
XH_P37	14	92472434	92472434	In_Frame_Ins	INS	-	TGGAAAAAGGA	-	TRIP11	5TATCTCTCTCTT	528delinsLSLFFPLE
XH_P37	14	95590860	95590860	In_Frame_Ins	INS	-	AGATACACAGCA	-	DICER1	1049insACTGTGCT	350delinsNCCVSS
XH_P37	14	96993858	96993858	Frame_Shift_Ins	INS	-	TTTTGCATCCTA	-	PAPOLA	AATTATTTTGCA	p.E141fs
XH_P37	14	100728706	100728706	Frame_Shift_Ins	INS	-	TTTTTTTTTTTGG	-	YY1	TCCCTTTTTTTTT	p.P249fs
XH_P37	14	102664125	102664125	In_Frame_Ins	INS	-	TGTTCTTTC	-	WDR20	6_467insTGTTCT	N156delinsMFFH
XH_P37	14	102664126	102664126	Frame_Shift_Ins	INS	-	CATGCGTAGT	-	WDR20	_468insCATGCC	p.N156fs
XH_P37	14	103932131	103932131	Splice_Site	INS	-	AAATAGAATTAG	-	MARK3	.	.
XH_P37	14	103958256	103958256	Nonsense_Mutation	INS	-	G	-	MARK3	1_1492_1493ins	498_1499delinsX
XH_P37	14	104407851	104407851	Frame_Shift_Ins	INS	-	TAAATTACATT	-	RD3L	2insTTAAATGTA	p.Y61fs
XH_P37	14	105411010	105411010	Missense_Mutation	SNP	C	G	C	AHNAK2	c.G10478C	p.R3493T
XH_P37	14	105411260	105411260	Missense_Mutation	SNP	A	G	A	AHNAK2	c.T10228C	p.S3410P
XH_P37	14	105415352	105415352	Missense_Mutation	SNP	G	C	G	AHNAK2	c.C6136G	p.L2046V
XH_P37	14	105452813	105452813	Silent	SNP	C	A	C	C14orf79	c.C45A	p.L15L
XH_P37	15	23890738	23890738	Frame_Shift_Ins	INS	-	ATGCC	-	MAGEL2	151_2152insGG	p.S718fs
XH_P37	15	27725975	27725975	Nonsense_Mutation	INS	-	ACATTAGCACT	-	GABRG3	insCAAACTAAT	2_A253delinsANISTX
XH_P37	15	30003205	30003205	Splice_Site	SNP	C	A	C	TJP1	.	.
XH_P37	15	30010728	30010728	In_Frame_Ins	INS	-	ATGTCTTTAGTG	-	TJP1	3378insCACTAA	51126delinsGTDI
XH_P37	15	30058507	30058507	Frame_Shift_Ins	INS	-	ATGGAGAGAAA	-	TJP1	CCAAGATTCTC	p.P184fs
XH_P37	15	30919078	30919078	Frame_Shift_Ins	INS	-	TCTGGTCAACC	-	ARHGAP11B	66insTTCTGTGTC	p.Y19fs
XH_P37	15	31251321	31251321	Nonsense_Mutation	INS	-	ATAAAATCCAAC	-	MTMR10	TTTCTGTGGAT	P255delinsLSDFCWLX
XH_P37	15	31947353	31947353	Nonsense_Mutation	INS	-	ATTTATCACTA	-	OTUD7A	5TAATTAGTGAT	D33_F34delinsX
XH_P37	15	31947355	31947355	Nonsense_Mutation	SNP	G	T	G	OTUD7A	c.C95A	p.S32X
XH_P37	15	32928652	32928652	Frame_Shift_Ins	INS	-	TAAG	-	ARHGAP11A	111_1112insTA	p.P371fs
XH_P37	15	32928653	32928653	Frame_Shift_Ins	INS	-	ATTTAATAAAG	-	ARHGAP11A	5ATTTAATTCTAA	p.P371fs
XH_P37	15	32929275	32929275	Nonsense_Mutation	INS	-	TGAATA	-	ARHGAP11A	34_1735insTGA	p.S578delinsSX
XH_P37	15	32929277	32929277	In_Frame_Ins	INS	-	TAGTGTCTTCTC	-	ARHGAP11A	5ATTTTATAGTTG	79delinsTFYCSFSIK
XH_P37	15	32929369	32929369	In_Frame_Ins	INS	-	TCITTTAATTAT	-	ARHGAP11A	1TCACTTCTCTTTA	insYLPYSHSLIIVYVPLGT
XH_P37	15	33873831	33873831	Silent	SNP	C	G	C	RYR3	c.C1560G	p.L520L
XH_P37	15	33873832	33873832	Frame_Shift_Ins	INS	-	ATCATTC	-	RYR3	61_1562insATC	p.Y521fs
XH_P37	15	34078161	34078161	In_Frame_Ins	INS	-	AGGTGCTGTATT	-	RYR3	9568insAGGTGCA	3189delinsARSLI
XH_P37	15	34651412	34651412	Nonsense_Mutation	INS	-	TTGTTTTTTTAA	-	LPCAT4	1insAACTTAAAA	p.S497delinsSTX
XH_P37	15	35084695	35084695	Frame_Shift_Ins	INS	-	TGATACTCTTTA	-	ACTC1	5GAAATAAAGA	p.I177fs
XH_P37	15	35149163	35149163	Frame_Shift_Ins	INS	-	TGTTTTTTGTAT	-	AQR	5TATAAAATACAA	p.T1430fs
XH_P37	15	35274670	35274670	Frame_Shift_Ins	INS	-	AC	-	ZNF770	c.965_966insGT	p.I322fs
XH_P37	15	35274672	35274672	Frame_Shift_Ins	INS	-	CAATAGAAAGA	-	ZNF770	TTTCTCTCTTCTC	p.I322fs
XH_P37	15	37385932	37385932	Splice_Site	INS	-	CCCTCCTAT	-	MEIS2	.	.
XH_P37	15	38591746	38591746	Frame_Shift_Ins	INS	-	GCCAAGCCATCA	-	SPRED1	5AACAGCCAAG	p.M69fs
XH_P37	15	38811550	38811550	In_Frame_Ins	INS	-	TCGTGTGTACTT	-	RASGRP1	nsCTCAAGTACAA	117delinsKYTRFN
XH_P37	15	40057900	40057900	In_Frame_Ins	INS	-	CTTCTT	-	FSIP1	57_358insAAGA	Q120delinsKKQ
XH_P37	15	40917126	40917126	Frame_Shift_Ins	INS	-	GGTGCAGAGGA	-	KNL1	CATATGGGTGC	p.H1555fs
XH_P37	15	41989081	41989081	Frame_Shift_Ins	INS	-	SATATTTTTGTAA	-	MGA	1874insGATATT	p.A625fs
XH_P37	15	41989083	41989083	Nonsense_Mutation	INS	-	CTCTGAGATCT	-	MGA	1876insCTCTGA	625_662delinsALX
XH_P37	15	41991309	41991309	Frame_Shift_Ins	INS	-	TGTTGTCCCATC	-	MGA	1insCTTCTGTTG	p.L174fs
XH_P37	15	42447774	42447774	In_Frame_Ins	INS	-	TGAGTGCAAGT	-	PLA2G4F	25insACACTTGC	P42delinsHTCHT
XH_P37	15	42743063	42743063	Frame_Shift_Ins	INS	-	GCAAAATCCAC	-	ZNF106	1338insGTGGA	p.K446fs
XH_P37	15	42976680	42976680	Nonsense_Mutation	INS	-	ATGATGTTTTCTC	-	STARD9	25insTGATGATG	968_1969delinsFX
XH_P37	15	43019912	43019912	In_Frame_Ins	INS	-	TTATGTAGAAGC	-	CDAN1	3insACAGCTTCT	001delinsGOLLHKN
XH_P37	15	43258484	43258484	Nonsense_Mutation	INS	-	GGAGAGTTTCT	-	UBR1	AGAACAAAGAA	p.G1486delinsGX
XH_P37	15	43814792	43814792	Frame_Shift_Ins	INS	-	AGGTCCT	-	MAP1A	21_1122insAGG	p.P374fs
XH_P37	15	43816603	43816603	Frame_Shift_Ins	INS	-	TCTTCTCCA	-	MAP1A	2_2933insTCTC	p.G978fs
XH_P37	15	43817807	43817807	Frame_Shift_Ins	INS	-	ATCA	-	MAP1A	136_4137insAT	p.V1379fs
XH_P37	15	43817808	43817808	In_Frame_Ins	INS	-	GTGTGCAATGT	-	MAP1A	4138insGTGTCA	1379delinsVVSEC
XH_P37	15	45249155	45249155	In_Frame_Ins	INS	-	CTTGAAACA	-	TERB2	5_127insCTTGA	A42delinsALET
XH_P37	15	45460244	45460244	Frame_Shift_Ins	INS	-	TGATCTTT	-	SHF	6_1227insAAAG	p.S409fs
XH_P37	15	45702712	45702712	Frame_Shift_Ins	INS	-	TTATTTTGTTAT	-	SPATA5L1	419insGTTATT	p.K473fs
XH_P37	15	45702714	45702714	Silent	SNP	C	T	C	SPATA5L1	c.C1420T	p.L474L
XH_P37	15	49048229	49048229	Frame_Shift_Ins	INS	-	TTTTTTCCTTTTT	-	CEP152	AAGGAAAAAAG	p.E1072fs
XH_P37	15	50773951	50773951	Nonsense_Mutation	SNP	G	T	G	USP8	c.G1261T	p.E421X
XH_P37	15	50773953	50773953	Frame_Shift_Ins	INS	-	CTTTTCCACT	-	USP8	3_1264insCTTTT	p.E421fs
XH_P37	15	50904954	50904954	In_Frame_Ins	INS	-	TTCAGAAAGACT	-	TRPM7	TGTTTATAGTTCT	5delinsYCFSSSEVSST
XH_P37	15	51242316	51242316	Missense_Mutation	SNP	G	A	G	AP4E1	c.G1273A	p.D425N
XH_P37	15	51242317	51242317	Frame_Shift_Ins	INS	-	ACACAGCATTC	-	AP4E1	275insAACACAG	p.D425fs
XH_P37	15	51787320	51787320	Frame_Shift_Ins	INS	-	C	-	DMXL2	1_2775_2776ins	p.I926fs
XH_P37	15	51787321	51787321	Nonsense_Mutation	INS	-	ACTAGAGTAGT	-	DMXL2	TAAGCTACTACT	5_L926delinsTFTFPX
XH_P37	15	52689527	52689527	Frame_Shift_Ins	INS	-	TTCTGTTTCTTA	-	MYO5A	190insGTAGGA	p.T397fs
XH_P37	15	52901533	52901533	Nonsense_Mutation	INS	-	CACAAAGAAAA	-	FAM214A	9insGTTATTTTC	533delinsELFSLCX
XH_P37	15	54529834	54529834	Frame_Shift_Ins	INS	-	GCAAGATGCCA	-	UNC13C	175insGGCAAGA	p.K1058fs
XH_P37	15	54630647	54630647	Frame_Shift_Ins	INS	-	AAATACTTTCAG	-	UNC13C	nsCAATAAAATAC	p.F1558fs
XH_P37	15	55484958	55484958	Frame_Shift_Ins	INS	-	TGAAGTTGGGA	-	RSL24D1	55insATTCCCA	p.T52fs
XH_P37	15	55484960	55484960	Missense_Mutation	SNP	C	G	C	RSL24D1	c.G153C	p.W51C
XH_P37	15	56386929	56386929	Nonsense_Mutation	INS	-	GGTTGGTAATTC	-	RFK7	nsCTGATGAATT	p.H999delinsHX
XH_P37	15	56985410	56985410	Frame_Shift_Ins	INS	-	GGAACGTCACTA	-	ZNF280D	AGTACTAGTGA	p.Y116fs
XH_P37	15	62266576	62266576	In_Frame_Ins	INS	-	SAAAGTAAATG	-	VPS13C	2320insCATTTT	1774delinsHFTFI
XH_P37	15	62283910	62283910	Nonsense_Mutation	INS	-	AAAAATAAA	-	VPS13C	5_1316insTTTTT	E439delinsVLFX
XH_P37	15	62283911	62283911	In_Frame_Ins	INS	-	TTTTTGTTTGTGA	-	VPS13C	TTATTTCCACAA	89delinsYYFTNKNINE
XH_P37	15	62945482	62945482	Frame_Shift_Ins	INS	-	AGCTAGTTAAGT	-	TLN2	sCTTCAGCTAGT	p.K162fs
XH_P37	15	63029254	63029254	In_Frame_Ins	INS	-	GGAAAAAGTCCA	-	TLN2	37insGGGAAAA	1179delinsGGKSP5
XH_P37	15	63433703	63433703	Frame_Shift_Ins	INS	-	TTTATAGGAGTT	-	LACTB	344insATTTATA	p.P448fs
XH_P37	15	63908805	63908805	Frame_Shift_Ins	INS	-	AACAATGCCATA	-	HERC1	65insAGATATG	p.A4589fs
XH_P37	15	63930683	63930683	Nonsense_Mutation	INS	-	GGAATCATTA	-	HERC1	GACTTCTCTTAA	4008delinsLYIMTFFNDSSX

XH_P37	15	63955278	63955278	Frame_Shift_Ins	INS	-	GGTTTGGGGAT	-	HERC1	insTTAAATCCCC	p.D2936fs
XH_P37	15	63972968	63972968	In_Frame_Ins	INS	-	CATTACATTTTC	-	HERC1	33insAGAAAAA	078delinsKKNVML
XH_P37	15	64231561	64231561	Splice_Site	INS	-	TCAAAGGTAGGG	-	DAPK2	.	.
XH_P37	15	64973062	64973062	Splice_Site	INS	-	GTGCCACCT	-	ZNF609	.	.
XH_P37	15	65445940	65445940	In_Frame_Ins	INS	-	ATTTTTAGTGGAA	-	CLPX	CCATCTCCACT	50delinsTPSPKIQKL
XH_P37	15	65489569	65489569	Missense_Mutation	SNP	G	A	G	CILP	c.C3055T	p.R1019C
XH_P37	15	65957758	65957758	Nonsense_Mutation	INS	-	CTTTATTTTACT	-	DENND4A	TAGTACAGTAA	8_Q1719delinsVVQX
XH_P37	15	66031209	66031209	In_Frame_Ins	INS	-	CTTGATCATTTTC	-	DENND4A	6insTGAAATG	212delinsLNVQ
XH_P37	15	66031211	66031211	Frame_Shift_Ins	INS	-	TTTCTATAAT	-	DENND4A	634insATTATAC	p.L212fs
XH_P37	15	66618630	66618630	Nonsense_Mutation	INS	-	CTTTGAATTCGT	-	DIS3L	insAAGTCTTTG	84_P585delinsPSLX
XH_P37	15	67687776	67687776	Frame_Shift_Ins	INS	-	A	-	IQCH	1780_1781ins	p.P594fs
XH_P37	15	67687778	67687778	Nonsense_Mutation	INS	-	TTGCACATAATA	-	IQCH	ATAATGTTGCAC	p.P594delinsPX
XH_P37	15	68583449	68583449	In_Frame_Ins	INS	-	TGGAGTTGA	-	FEM1B	1754insTGGAA	p.S585delinsLELT
XH_P37	15	68583451	68583451	Silent	SNP	T	A	T	FEM1B	c.T1755A	p.S585S
XH_P37	15	69553581	69553581	Nonsense_Mutation	INS	-	AATACCATTCT	-	GLCE	TTCTCTAATACCA	p.D249delinsIPNTIPHX
XH_P37	15	70349983	70349983	Frame_Shift_Ins	INS	-	AGACCTTTTG	-	TLF3	871insCAAAAG	p.T291fs
XH_P37	15	71300944	71300944	Nonsense_Mutation	INS	-	AATAGA	-	LRRCA9	11_1412insAAT	p.P471delinsQX
XH_P37	15	73614941	73614941	In_Frame_Ins	INS	-	CAGAAATAACG	-	HCN4	3493insGGTTA	1165delinsGYLL
XH_P37	15	73617435	73617435	Silent	SNP	G	A	G	HCN4	c.C1839T	p.F613F
XH_P37	15	74703199	74703199	Frame_Shift_Ins	INS	-	CACCTCACTCTT	-	SEMA7A	1725insAAGAG	p.P575fs
XH_P37	15	75015469	75015469	Splice_Site	SNP	T	A	T	CYP1A1	.	.
XH_P37	15	81591950	81591950	In_Frame_Ins	INS	-	ATTACATCATAC	-	IL16	insTGCAATACAT	L60delinsLCITSYS
XH_P37	15	84566757	84566757	Nonsense_Mutation	INS	-	TTAGACAAATA	-	ADAMTSL3	insACTTTTAGA	639_K540delinsDFX
XH_P37	15	85147425	85147425	In_Frame_Ins	INS	-	AAAAGAGAACCC	-	ZSCAN2	AACAAAAAAGA	89delinsRNKKENHN
XH_P37	15	85400065	85400065	In_Frame_Ins	INS	-	TCTTGCTCCAG	-	ALPK3	sCATCTCTTCG	901delinsHILLASSSL
XH_P37	15	85666358	85666358	Nonsense_Mutation	INS	-	AAGACATGGAA	-	PDE8A	TTTAAAAAGACA	27delinsHLKRRHGSX
XH_P37	15	86118476	86118476	Nonsense_Mutation	INS	-	TCTAACTGAT	-	AKAP13	GTATTTCTAACG	259delinsYFVFLTX
XH_P37	15	89836232	89836232	Frame_Shift_Ins	INS	-	G	-	FANCI	2229_2230ins	p.A743fs
XH_P37	15	89836233	89836233	Nonsense_Mutation	INS	-	GGGTATGACTG	-	FANCI	31insAAGGGTA	p.F744delinsX
XH_P37	15	90897986	90897986	Missense_Mutation	SNP	G	T	G	ZNF774	c.G94T	p.A32S
XH_P37	15	90897987	90897987	Nonsense_Mutation	INS	-	CTGAGGTAAAT	-	ZNF774	96insCTGAGGT	A32_L133delinsAX
XH_P37	15	91035857	91035857	Missense_Mutation	SNP	C	A	C	IQGAP1	c.C4542A	p.N1514K
XH_P37	15	91479513	91479513	Splice_Site	INS	-	CCTTTTCTGAG	-	UNC45A	.	.
XH_P37	15	91479515	91479515	Frame_Shift_Ins	INS	-	AGCACCGAGCC	-	UNC45A	insTGAAGCACCC	p.A69fs
XH_P37	15	93515585	93515585	In_Frame_Ins	INS	-	TTTAAAGCTTCG	-	CHD2	nsCATTTTTTAA	815delinsPHFKASFE
XH_P37	15	93540313	93540313	In_Frame_Ins	INS	-	CCTCTT	-	CHD2	722_3723insCCT	E1241delinsDLL
XH_P37	15	101013203	101013203	Frame_Shift_Ins	INS	-	GAAACCTCTTA	-	CERS3	TAAAACTAAGAG	p.S222fs
XH_P37	15	101562156	101562156	Frame_Shift_Ins	INS	-	SCCTTTCTCTCG	-	LRRK1	1847insGCCCTTC	p.K616fs
XH_P37	15	101562158	101562158	Silent	SNP	A	G	A	LRRK1	c.A1848G	p.K616K
XH_P37	15	101827205	101827205	In_Frame_Ins	INS	-	ATTGTCTAAATG	-	SNRPA1	TTACTCATTTAG	23delinsFTHLDNFNN
XH_P37	15	102346730	102346730	In_Frame_Ins	INS	-	AGATCACAAAAA	-	OR4F6	sAGGAAGATCAC	70delinsSRKTKETI
XH_P37	16	1544301	1544301	Missense_Mutation	SNP	G	C	G	TELO2	c.G19C	p.E7Q
XH_P37	16	1544302	1544302	Missense_Mutation	SNP	A	G	A	TELO2	c.A20G	p.E7G
XH_P37	16	1652463	1652463	In_Frame_Ins	INS	-	AAATGAACCTTG	-	IFT140	insCAGCAAAGT	93delinsQQSSFIK
XH_P37	16	1915837	1915837	Splice_Site	INS	-	TATATATACACA	-	MEIOB	.	.
XH_P37	16	2580830	2580830	In_Frame_Ins	INS	-	CCT	-	CEMP1	244_245insAG	p.L82delinsQV
XH_P37	16	2580831	2580831	In_Frame_Ins	INS	-	TAA	-	CEMP1	243_244insTT	p.L82delinsLL
XH_P37	16	3255121	3255121	Missense_Mutation	SNP	T	C	T	OR1F1	c.T875C	p.L292P
XH_P37	16	3283687	3283687	Nonsense_Mutation	INS	-	TCTGTGTTAGT	-	ZNF200	TTATAACTAACA	P23_D24delinsPX
XH_P37	16	4432440	4432440	Missense_Mutation	SNP	C	T	C	VASN	c.C1562T	p.T521M
XH_P37	16	8992438	8992438	Nonsense_Mutation	INS	-	CAATTTAGGGAA	-	USP7	TACCTCTTCCTC	848_L849delinsSX
XH_P37	16	11363108	11363108	Nonsense_Mutation	INS	-	CCAACACTAG	-	TNP2	12insCTAGTGT	Q4_T5delinsHX
XH_P37	16	11785246	11785246	Nonsense_Mutation	INS	-	ATTTTAA	-	TXNDC11	43_444insTAA	148_S149delinsPX
XH_P37	16	11785247	11785247	In_Frame_Ins	INS	-	TCTTTA	-	TXNDC11	42_443insTAA	p.P148delinsLTK
XH_P37	16	11850198	11850198	In_Frame_Ins	INS	-	TGATGG	-	ZC3H7A	56_2457insCCA	L819delinsLHQ
XH_P37	16	11850200	11850200	Frame_Shift_Ins	INS	-	CCTTCT	-	ZC3H7A	4_2455insAGA	p.L819fs
XH_P37	16	11868354	11868354	Frame_Shift_Ins	INS	-	TTCTGCACCTGA	-	ZC3H7A	1insTTTCAGGTG	p.E214fs
XH_P37	16	14355266	14355266	Missense_Mutation	SNP	C	G	C	MKL2	c.C3265G	p.L1089V
XH_P37	16	14355268	14355268	Frame_Shift_Ins	INS	-	sGAGGAATTTCA	-	MKL2	8insGTGGAGGA	p.L1089fs
XH_P37	16	14576561	14576561	Frame_Shift_Ins	INS	-	ATTTTAGAGA	-	PARN	1466insTCTCT	p.D489fs
XH_P37	16	14576562	14576562	Frame_Shift_Ins	INS	-	TGCTTTAT	-	PARN	4_1465insATAA	p.D489fs
XH_P37	16	14969083	14969083	Nonsense_Mutation	INS	-	GACATAGTTGCA	-	NOMO1	6insAGGACATA	749_S750delinsX
XH_P37	16	15100439	15100439	Frame_Shift_Ins	INS	-	T	-	PDXDC1	c.497_498insT	p.Q166fs
XH_P37	16	15100441	15100441	Splice_Site	INS	-	AAATCTTTTCTC	-	PDXDC1	.	.
XH_P37	16	16101732	16101732	Frame_Shift_Ins	INS	-	AACTAAAGAT	-	ABCC1	9insCAAACATAA	p.T36fs
XH_P37	16	18888540	18888540	Frame_Shift_Ins	INS	-	GAGAAATCATAC	-	SMG1	3insTCAGTATG	p.I511fs
XH_P37	16	19236066	19236066	Frame_Shift_Ins	INS	-	ATTACATCCACTC	-	SYT17	1123insATTATC	p.SY374fs
XH_P37	16	19620325	19620325	Frame_Shift_Ins	INS	-	CTGGGTTTGA	-	C16orf62	179insACTGGG	p.N393fs
XH_P37	16	19620327	19620327	Frame_Shift_Ins	INS	-	TTTCT	-	C16orf62	180_1181insTT	p.K394fs
XH_P37	16	23632791	23632791	In_Frame_Ins	INS	-	GTGTTG	-	PALB2	04_3005insCAA	E1002delinsATQ
XH_P37	16	23641415	23641415	Frame_Shift_Ins	INS	-	AAAGACTCAGTC	-	PALB2	060insAGACTG	p.P687fs
XH_P37	16	23641417	23641417	Silent	SNP	C	T	C	PALB2	c.G2058A	p.R686R
XH_P37	16	23647022	23647022	Nonsense_Mutation	INS	-	ACAGAGAAATC	-	PALB2	45insAAGATTCTC	282delinsKDFSVX
XH_P37	16	23647024	23647024	In_Frame_Ins	INS	-	AAATCTCCC	-	PALB2	843insGGGAG	I281delinsMGDF
XH_P37	16	24578532	24578532	Nonsense_Mutation	INS	-	TTGTAAAAATAA	-	RBBP6	ATTATTATTGTAA	delinsTLVQICKNNSTTX
XH_P37	16	24581242	24581242	In_Frame_Ins	INS	-	TGTTTATACAC	-	RBBP6	0insGTTTGGTTT	043delinsSVVWFYHP
XH_P37	16	24582815	24582815	Missense_Mutation	SNP	C	A	C	RBBP6	c.C4326A	p.D1442E
XH_P37	16	24582817	24582817	Nonsense_Mutation	INS	-	CTCGATCTTTGG	-	RBBP6	29insATCTCGAT	443_D1444delinsX
XH_P37	16	24806005	24806005	Frame_Shift_Ins	INS	-	TCCTTCTGGAGA	-	TNRC6A	AGAATTCCTTCT	p.N1165fs
XH_P37	16	24918072	24918072	Frame_Shift_Ins	INS	-	ATTCAGCTATTG	-	SLC5A11	nsAAAATTCAGC	p.E297fs
XH_P37	16	27373670	27373670	Nonsense_Mutation	INS	-	ATACGAATTTG	-	IL4R	5TTATAATCAGT	A33delinsNVNIISXN
XH_P37	16	29848143	29848143	Frame_Shift_Ins	INS	-	AATTTCTACCAA	-	MVP	774insAATTTCTA	p.A258fs
XH_P37	16	30007883	30007883	Nonsense_Mutation	INS	-	TTTCAGATTCCG	-	INO80E	insGCTTCAGAT	Q33delinsRFRFRX
XH_P37	16	30106758	30106758	Nonsense_Mutation	SNP	G	A	G	YPEL3	c.C46T	p.Q16X
XH_P37	16	30106760	30106760	Nonsense_Mutation	INS	-	TCTCAACTCAG	-	YPEL3	4insACTGAGTTT	R15_Q16delinsHX
XH_P37	16	30732182	30732182	Frame_Shift_Ins	INS	-	AG	-	SRCAP	3136_3137insA	p.P1046fs
XH_P37	16	30732183	30732183	Nonsense_Mutation	INS	-	CAGTACCTA	-	SRCAP	7_3138insCAGT	P1046delinsPSTX
XH_P37	16	31049483	31049483	Nonsense_Mutation	INS	-	CCCCATGCTAAA	-	STX4	8insGACCCCTAG	G1_102delinsRTPCX
XH_P37	16	31195649	31195649	In_Frame_Ins	INS	-	ATTTCCTTTCACT	-	FUS	53insAATTTCTCT	P151delinsPISFHF
XH_P37	16	31213095	31213095	Nonsense_Mutation	INS	-	ATCTGATCTTTT	-	PYCARD	nsATAAAAAAGAT	p.L114delinsLX
XH_P37	16	31230796	31230796	Nonsense_Mutation	INS	-	GATAAAGAC	-	TRIM72	674insGATAA	p.V225delinsGX
XH_P37	16	31342516	31342516	In_Frame_Ins	INS	-	TCTATCTCT	-	ITGAM	7_3308insTCTA	P1103delinsLYLS
XH_P37	16	31927531	31927531	Nonsense_Mutation	INS	-	CTACATGCTTTA	-	ZNF267	5ATTGTTCTACAT	654_7655delinsHX
XH_P37	16	47163243	47163243	Missense_Mutation	SNP	C	G	C	NETO2	c.G124C	p.A42P
XH_P37	16	48221325	48221325	Nonsense_Mutation	INS	-	TATTATATGTGA	-	ABCC11	ACCTACTCACAT	907delinsSQKEPTHX
XH_P37	16	48595446	48595446	In_Frame_Ins	INS	-	ATATGGTGAAA	-	N4BP1	AAAAATTTTCTA	70delinsKIFLPYFAV
XH_P37	16	50136341	50136341	Frame_Shift_Ins	INS	-	CAAGTACCAAC	-	HEATR3	1223insCAAGT	p.M408fs
XH_P37	16	51174598	51174598	Missense_Mutation	SNP	G	A	G	SALL1	c.C1244T	p.P415L

XH_P37	16	51174600	51174600	Nonsense_Mutation	INS	-	AACC	-	SALL1	241_1242insGG414_P415delinsX
XH_P37	16	53276765	53276765	Missense_Mutation	SNP	G	A	G	CHD9	c.G2891A p.R964Q
XH_P37	16	53283882	53283882	Nonsense_Mutation	INS	-	AGCAATATCATC	-	CHD9	TTAAGAAAGCAA255_1256delinsLX
XH_P37	16	53644906	53644906	In_Frame_Ins	INS	-	TGTAAACAGGTT	-	RPGRIP1L	nsCTTCAACCTC145delinsPFNLLQSL
XH_P37	16	57504261	57504261	Frame_Shift_Ins	INS	-	CACCTCTAAGG	-	POLR2C	79insTCACTCCTC p.P226fs
XH_P37	16	58579281	58579281	Nonsense_Mutation	INS	-	ATGTATATCATC	-	CNOT1	AAAAAGCTATGA369_11370delinsKX
XH_P37	16	58750065	58750065	In_Frame_Ins	INS	-	GTACCCCATAGA	-	GOT2	TGGAATCTATGG48delinsYGIYGVLYI
XH_P37	16	67132649	67132649	Nonsense_Mutation	INS	-	AAATTATGTCTGA	-	CBFB	BinsAAAAATTATC178_1179delinsX
XH_P37	16	67282959	67282959	Silent	SNP	G	T	G	SLC9A5	c.G42T p.A14A
XH_P37	16	67942824	67942824	Nonsense_Mutation	INS	-	TCATTAAAAACC	-	PSKH1	173insCTCATTA758_A59delinsSHX
XH_P37	16	68325159	68325159	Nonsense_Mutation	INS	-	CAATATTTAATC	-	SLC7A6	nsGATCAATATT1_Y282delinsMINIX
XH_P37	16	69373963	69373963	Frame_Shift_Ins	INS	-	GCTAT	-	NIP7	111_112insGCTC p.F37fs
XH_P37	16	69373965	69373965	Missense_Mutation	SNP	G	T	G	NIP7	c.G113T p.R38L
XH_P37	16	70162871	70162871	Nonsense_Mutation	INS	-	AAGACCTGTGA	-	PDP1	insTAGAAGACC651_152delinsGX
XH_P37	16	70868068	70868068	Splice_Site	INS	-	AGGAACATAT	-	HYDIN	.
XH_P37	16	70884465	70884465	Silent	SNP	T	A	T	HYDIN	c.A12537T p.T4197T
XH_P37	16	71683654	71683654	Silent	SNP	C	T	C	PHLP2	c.G2910A p.E970E
XH_P37	16	71683656	71683656	Frame_Shift_Ins	INS	-	TGCT	-	PHLP2	907_2908insAG p.E970fs
XH_P37	16	72110351	72110351	Nonsense_Mutation	INS	-	TTTAAATAAT	-	HPR	insAGTTTTTAAAp.L140delinsQFX
XH_P37	16	72110353	72110353	Silent	SNP	G	T	G	HPR	c.G420T p.L140L
XH_P37	16	72822656	72822656	Frame_Shift_Ins	INS	-	AAAGACA	-	ZFH3	76_6777insTGT p.P2259fs
XH_P37	16	72831315	72831315	In_Frame_Ins	INS	-	ACCAACTCTCTA	-	ZFH3	24insTATAGAG4842delinsYRELVL
XH_P37	16	74443505	74443505	Missense_Mutation	SNP	C	G	C	CLEC18B	c.G1273C p.A425P
XH_P37	16	74670455	74670455	In_Frame_Ins	INS	-	TCITTATTA	-	RFW3	1_1215insTAATA5405delinsSNKE
XH_P37	16	74670457	74670457	Nonsense_Mutation	INS	-	TATATTTATTTTC	-	RFW3	6GCAAGGAAAT7A05_H406delinsARXK
XH_P37	16	74919651	74919651	In_Frame_Ins	INS	-	ACAGGATGAAT	-	WDR59	9insAAAAATTCA863delinsKKIHPVT
XH_P37	16	75203225	75203225	In_Frame_Ins	INS	-	CCAGTGCAAAATG	-	ZFP1	119insCCAGTGC140delinsPSANV
XH_P37	16	75448489	75448489	Frame_Shift_Ins	INS	-	TTAAA	-	CFDP1	168_169insTTTA p.S57fs
XH_P37	16	75448490	75448490	Nonsense_Mutation	INS	-	TGTAAGGAAAT	-	CFDP1	TTAATATTTTCT56_557delinsHITYX
XH_P37	16	75634231	75634231	Nonsense_Mutation	INS	-	ATCAGGGAACAT	-	ADAT1	85insGAATGTTCTD295delinsENVXP
XH_P37	16	75730810	75730810	Missense_Mutation	SNP	C	G	C	DUXB	c.G212C p.R71T
XH_P37	16	75730812	75730812	Silent	SNP	C	T	C	DUXB	c.G210A p.Q70Q
XH_P37	16	77355099	77355099	Nonsense_Mutation	INS	-	TGGTGGCATTTT	-	ADAMTS18	8insTGAAAAATG p.L550delinsLX
XH_P37	16	81060230	81060230	Nonsense_Mutation	INS	-	TTTAAATAATA	-	CENPN	ATAATTTTAAAA46_A247delinsFVX
XH_P37	16	81078215	81078215	Frame_Shift_Ins	INS	-	CTCATGATGCC	-	ATMIN	sAAAGACTACGA p.T548fs
XH_P37	16	83214545	83214545	Nonsense_Mutation	INS	-	CTAATAATTACG	-	CDH13	nsAGTCTAATAA85_1186delinsIVX
XH_P37	16	84115434	84115434	In_Frame_Ins	INS	-	AGCACAGAATT	-	MBTPS1	66insAGAAATTCV456delinsRIILCLV
XH_P37	16	84209761	84209761	Frame_Shift_Ins	INS	-	TGCC	-	DNAAF1	213_1214insTG p.K405fs
XH_P37	16	84209763	84209763	Frame_Shift_Ins	INS	-	TTCTGCTTTT	-	DNAAF1	1216insTTCTG p.K405fs
XH_P37	16	84227743	84227743	Frame_Shift_Ins	INS	-	ACACTTTTCTCTA	-	ADAD2	551insACACTTT p.G184fs
XH_P37	16	88501741	88501741	In_Frame_Ins	INS	-	AGT	-	ZNF469	7779_7780insAp.V2593delinsVS
XH_P37	16	88501743	88501743	In_Frame_Ins	INS	-	TTTGGT	-	ZNF469	781_7782insTTT D2594delinsDLV
XH_P37	17	559142	559142	Frame_Shift_Ins	INS	-	ACCTAACAAC	-	VP53	837insTGTGTG p.L113fs
XH_P37	17	559143	559143	Missense_Mutation	SNP	G	C	G	VP53	c.C336G p.H112Q
XH_P37	17	1703766	1703766	Missense_Mutation	SNP	G	A	G	SMYD4	c.C922T p.P308S
XH_P37	17	2966409	2966409	Nonsense_Mutation	INS	-	CTTTATGGGAC	-	OR1D5	493insGTCCCATR165delinsVPX
XH_P37	17	2995890	2995890	In_Frame_Ins	INS	-	TTCTCTTCTCTC	-	OR1D2	1insATGAGGAA134delinsNEDEA
XH_P37	17	2996067	2996067	Frame_Shift_Ins	INS	-	GTCTATCCGTC	-	OR1D2	24insGGACGGGA p.T75fs
XH_P37	17	3301543	3301543	Frame_Shift_Ins	INS	-	GTGAGAGCTTCC	-	OR1E1	nsGGAGGAAGC p.H54fs
XH_P37	17	3981267	3981267	Nonsense_Mutation	INS	-	AAATAGAAATTC	-	ZZF1	TGCTGTGAATTT7_Q968delinsKKTCCX
XH_P37	17	4053300	4053300	Frame_Shift_Ins	INS	-	TTTTCTTTTTTTT	-	CYB5D2	31insTTTTTTCTT p.F10fs
XH_P37	17	4053302	4053302	Missense_Mutation	SNP	A	T	A	CYB5D2	c.A32T p.Y11F
XH_P37	17	4534980	4534980	Frame_Shift_Ins	INS	-	CTTCCTTCCTCTC	-	ALOX15	1insGAGAGAGG p.K635fs
XH_P37	17	4883134	4883134	Frame_Shift_Ins	INS	-	TTCTTAGGCTT	-	CAMTA2	1489insAAGCC p.A497fs
XH_P37	17	4906118	4906118	Frame_Shift_Ins	INS	-	TAGATCTCCATA	-	KIF1C	2insAGTAGATC p.T234fs
XH_P37	17	5013013	5013013	In_Frame_Ins	INS	-	GCTGGAGGA	-	ZNF232	3_174insTCCTCC6_E58delinsDPPA
XH_P37	17	5298226	5298226	Nonsense_Mutation	INS	-	CCTACCTCTCTT	-	NUP88	sTCAGAAAGAA456delinsIRKKGRSX
XH_P37	17	6590950	6590950	In_Frame_Ins	INS	-	TTCTCTTTTTCTC	-	SLC13A5	1insCTCAGAAAAA448delinsISEKEE
XH_P37	17	7294053	7294053	Missense_Mutation	SNP	A	G	A	PLSCR3	c.T731C p.V244A
XH_P37	17	7646833	7646833	Silent	SNP	G	A	G	DNAH2	c.G2523A p.K841K
XH_P37	17	7678641	7678641	In_Frame_Ins	INS	-	CAATTCTAAGA	-	DNAH2	403insACCAATTC1601delinsLPILRS
XH_P37	17	7690324	7690324	Frame_Shift_Ins	INS	-	TT	-	DNAH2	6576_6577insT p.N2192fs
XH_P37	17	7690326	7690326	Frame_Shift_Ins	INS	-	CTTCCTATCCCCA	-	DNAH2	79insAACTTCTCTA p.G2193fs
XH_P37	17	10215296	10215296	Frame_Shift_Ins	INS	-	CATTGAC	-	MYH13	62_4463insGTC p.M1488fs
XH_P37	17	10247288	10247288	Frame_Shift_Ins	INS	-	GAGTATGATGT	-	MYH13	723insAAACATC p.A575fs
XH_P37	17	10265693	10265693	In_Frame_Ins	INS	-	TGGTGAGTAAT	-	MYH13	82insAAATTACTA111delinsEITHQS
XH_P37	17	10265695	10265695	Nonsense_Mutation	SNP	A	T	A	MYH13	c.T330A p.Y110X
XH_P37	17	10443929	10443929	Nonsense_Mutation	INS	-	TTTTTTTTTTTTTT	-	MYH2	GCAAAAAAAA4delinsDASOLOKKKXIVX
XH_P37	17	11584153	11584153	In_Frame_Ins	INS	-	TGCTCTCAACTC	-	DNAH9	691insTTGCTCT1230delinsFLSTS
XH_P37	17	15234782	15234782	Nonsense_Mutation	INS	-	TACCAACTATCA	-	TEKT3	21insTGATAGT_N41_142delinsX
XH_P37	17	15234783	15234783	Silent	SNP	G	A	G	TEKT3	c.C120T p.S40S
XH_P37	17	15642112	15642112	In_Frame_Ins	INS	-	GCTCCTTTTATC	-	TBC1D26	466insGCTCCTTK155delinsKAPFY
XH_P37	17	15974916	15974916	Nonsense_Mutation	INS	-	AGGTAACCTAAG	-	NCOR1	4007insCTTAGT336_E1337delinsTX
XH_P37	17	15984024	15984024	Nonsense_Mutation	INS	-	ACTCACAAACC	-	NCOR1	3243insGGTTG1081_11082delinsX
XH_P37	17	15984026	15984026	Missense_Mutation	SNP	A	G	A	NCOR1	c.T3241C p.Y1081H
XH_P37	17	16455578	16455578	Frame_Shift_Ins	INS	-	ATTATAT	-	ZNF287	83_1734insAAT p.G578fs
XH_P37	17	16455580	16455580	Nonsense_Mutation	INS	-	CATCACTTAATC	-	ZNF287	732insTGATTAA6578_K579delinsX
XH_P37	17	16525679	16525679	Nonsense_Mutation	INS	-	ACTATATTTTAT	-	ZNF624	ATATTCAATAAA41delinsDFPIFKYSLX
XH_P37	17	16612410	16612410	Nonsense_Mutation	INS	-	TACTGGATATAT	-	CCDC144A	1040insTACTGGGE347delinsVLIDIX
XH_P37	17	16612412	16612412	Silent	SNP	A	G	A	CCDC144A	c.A1041G p.E347E
XH_P37	17	17751062	17751062	In_Frame_Ins	INS	-	ACTTCTTTTCTCT	-	TOM1L2	57insCAGAGAA353delinsQRKEVA
XH_P37	17	18430104	18430104	Frame_Shift_Ins	INS	-	ACTGTCTGATG	-	FAM106A	tsTGACATCAGA p.T5fs
XH_P37	17	18638483	18638483	Frame_Shift_Ins	INS	-	AGAGATACTTGT	-	TRIM16L	58insGGAGATA p.L253fs
XH_P37	17	18682329	18682329	In_Frame_Ins	INS	-	TGCAGTTTCTCG	-	FBXW10	2719insTGCAGT5906delinsGCSFW
XH_P37	17	19705144	19705144	In_Frame_Ins	INS	-	CTTTTCTTTTCTT	-	ULK2	GGAAGAAAGAAA63delinsRKKRKEGV
XH_P37	17	19705146	19705146	Missense_Mutation	SNP	G	T	G	ULK2	c.C1385A p.T462K
XH_P37	17	20108224	20108224	In_Frame_Ins	INS	-	GTAAATTTCACTA	-	SPECC1	20insTGTTAATT P207delinsLJLJLS
XH_P37	17	26684697	26684697	Missense_Mutation	SNP	G	C	G	TMEM199	c.G4C p.A2P
XH_P37	17	26731939	26731939	Frame_Shift_Ins	INS	-	ATGGTGGT	-	SLC46A1	5_776insACCA p.A259fs
XH_P37	17	27620958	27620958	Frame_Shift_Ins	INS	-	GGACAGGAGAG	-	NUFIP2	120insTCTCTCC p.N40fs
XH_P37	17	28296292	28296292	Frame_Shift_Ins	INS	-	TCCC	-	EFCAB5	506_507insTCC p.Y169fs
XH_P37	17	28296294	28296294	In_Frame_Ins	INS	-	TTTTTTTTTTCAGC	-	EFCAB5	6GGAGTTTTTTTT70delinsREFFFSLFF
XH_P37	17	28382976	28382976	In_Frame_Ins	INS	-	GAATAAATCTGA	-	EFCAB5	98insCTGAATA699delinsSLNNLN
XH_P37	17	28419936	28419936	Nonsense_Mutation	INS	-	ATTCCATTTATAT	-	EFCAB5	nsCATAATTTCCA p.I1435delinsITX
XH_P37	17	28512144	28512144	Nonsense_Mutation	INS	-	STGGTTTTTGACT	-	NSRP1	8insAGTGGTTT V323delinsEWFx
XH_P37	17	28512146	28512146	Silent	SNP	A	G	A	NSRP1	c.A969G p.V323V
XH_P37	17	29161225	29161225	Nonsense_Mutation	INS	-	GGATCTAATAGT	-	ATAD5	AACATGGATCTTA42_L43delinsYKFX
XH_P37	17	29182340	29182340	Nonsense_Mutation	INS	-	TATCTGGAAAT	-	ATAD5	ATAAACTATCTG p.D877delinsEX

XH_P37	17	29220586	29220586	In_Frame_Ins	INS	-	GGTAGA	-	ATAD5	15_471insGGT	11572delinsMVE
XH_P37	17	29220588	29220588	Nonsense_Mutation	INS	-	AACCTCAAGATTA	-	ATAD5	718insAACTCA	573_D1574delinsX
XH_P37	17	29533337	29533337	In_Frame_Ins	INS	-	AAC	-	NF1	1340_1341insA	p.L447delinsLT
XH_P37	17	29533339	29533339	Frame_Shift_Ins	INS	-	ATACATATTATAT	-	NF1	343insATACATA	p.H448fs
XH_P37	17	29631621	29631621	Missense_Mutation	SNP	G	T	G	EV12B	c.C1007A	p.A336E
XH_P37	17	29631622	29631622	Frame_Shift_Ins	INS	-	AATGACTCTTTT	-	EV12B	AAGAAAAAAGA	p.A336E
XH_P37	17	30376377	30376377	Frame_Shift_Ins	INS	-	TTCTCACATCCT	-	LRRC37B	insAACTTTCTCA	p.M880fs
XH_P37	17	32483504	32483504	Nonsense_Mutation	INS	-	TCAA	-	ASIC2	c.47_48insTTGA	p.117delinsSX
XH_P37	17	32906217	32906217	Nonsense_Mutation	INS	-	ACCTATTATTCT	-	C17orf102	3insAGAAATAAT	p.28p.29delinsQNXK
XH_P37	17	32906219	32906219	Missense_Mutation	SNP	G	T	G	C17orf102	c.C81A	p.H27Q
XH_P37	17	33289448	33289448	In_Frame_Ins	INS	-	TGTATTTCTGCT	-	ZNFR830	54insATGTATT	p.528delinsSCISAF
XH_P37	17	33521100	33521100	Nonsense_Mutation	INS	-	5ACTAATCATCA	-	SLC35G3	c.CACAATGATGA	p.R76delinsPOX
XH_P37	17	34869471	34869471	Splice_Site	INS	-	CCAGAACAA	-	MYO19	.	.
XH_P37	17	34869473	34869473	Missense_Mutation	SNP	T	A	T	MYO19	c.A816T	p.E272D
XH_P37	17	34942565	34942565	Frame_Shift_Ins	INS	-	TTTCACTCCCTT	-	GGN8P2	3insCTGTTTCAC	p.N526fs
XH_P37	17	35837045	35837045	Silent	SNP	C	T	C	TADA2A	c.C1290T	p.I430I
XH_P37	17	35837047	35837047	Nonsense_Mutation	INS	-	TAACATTAAACA	-	TADA2A	293insATAAACA	p.Y431delinsX
XH_P37	17	35837049	35837049	Frame_Shift_Ins	INS	-	TCATTTTGTGA	-	TADA2A	1295insTCATT	p.D432fs
XH_P37	17	36715915	36715929	In_Frame_Del	DEL	GTAGGCTGA	-	CGTAGGCTGAC	SRCIN1	c.1917_1931del	p.639_G644del
XH_P37	17	37358655	37358655	Frame_Shift_Ins	INS	-	CCAAAA	-	RPL19	98_199insCCAA	p.N66fs
XH_P37	17	37358657	37358657	In_Frame_Ins	INS	-	CTCTAT	-	RPL19	200_201insCTCT	p.T67delinsTSI
XH_P37	17	37584020	37584020	Frame_Shift_Ins	INS	-	T	-	MED1	c.672_673insA	p.Y225fs
XH_P37	17	37584021	37584021	Nonsense_Mutation	INS	-	ATATACACACAT	-	MED1	TATGTATGTGTG	224_Y225delinsYX
XH_P37	17	37604119	37604119	Frame_Shift_Ins	INS	-	TTTTAGATTTTG	-	MED1	CAATCCAAAATC	p.R22fs
XH_P37	17	37922530	37922530	Frame_Shift_Ins	INS	-	AAGAGACTCT	-	IKZF3	c.302insAGAGT	p.R101fs
XH_P37	17	38282571	38282571	Nonsense_Mutation	INS	-	TAGCCCCATTTA	-	MSL1	5TACTTCTAGCCC	p.L39delinsHTDTX
XH_P37	17	38346732	38346732	Frame_Shift_Ins	INS	-	ACATTCTAGACT	-	RAPGEF1	insACACATTTCTA	p.L236fs
XH_P37	17	38556248	38556248	Nonsense_Mutation	INS	-	5AAGAGGCAAA	-	TOP2A	AATGGATTTTGCG	024_11025delinsDX
XH_P37	17	38933305	38933305	Frame_Shift_Ins	INS	-	AATGAATTAAG	-	KRT27	c.1326insCTTAA	p.V442fs
XH_P37	17	38933307	38933307	Frame_Shift_Ins	INS	-	GTATTTTTAGA	-	KRT27	24insATTCTAA	p.V442fs
XH_P37	17	39041136	39041136	Nonsense_Mutation	INS	-	AAACACAGAGT	-	KRT20	TTTCTACTCTG	1delinsLVFPTLCLASRX
XH_P37	17	39150150	39150150	Nonsense_Mutation	INS	-	TCTCAGTACCTA	-	KRTAP3-3	GTGTGAGGTAC	L67_L68delinsHX
XH_P37	17	39464382	39464382	In_Frame_Ins	INS	-	TCCAGCCAACCTG	-	KRTAP16-1	insATCCAGTCT	75delinsNPVGWKKW
XH_P37	17	39725840	39725840	Splice_Site	INS	-	ATCTA	-	KRT9	.	.
XH_P37	17	39767404	39767404	Missense_Mutation	SNP	G	A	G	KRT16	c.C850T	p.R284C
XH_P37	17	40328094	40328094	Silent	SNP	G	A	G	KCNH4	c.C807T	p.A269A
XH_P37	17	41008391	41008391	Nonsense_Mutation	SNP	C	T	C	AOC3	c.C487T	p.R163X
XH_P37	17	41245268	41245268	In_Frame_Ins	INS	-	AAT	-	BRCA1	2138_2139insA	p.T713delinsTF
XH_P37	17	41245269	41245269	Nonsense_Mutation	INS	-	CTCACACATTTA	-	BRCA1	ACCAAATAAATC	E714delinsKQNIQINXV
XH_P37	17	41245706	41245706	Frame_Shift_Ins	INS	-	ATGCACGTGA	-	BRCA1	1701insTCACT	p.K567fs
XH_P37	17	41245708	41245708	Nonsense_Mutation	SNP	T	A	T	BRCA1	c.A1699T	p.K567X
XH_P37	17	41346467	41346467	Nonsense_Mutation	INS	-	AAAAAAACAATG	-	NBR1	TATTTTAAAAAA	522delinsAVPPYFKKQCFX
XH_P37	17	42335045	42335045	Frame_Shift_Ins	INS	-	TTTCCCTC	-	SLCA1	2_1413insGAGG	p.F471fs
XH_P37	17	42335046	42335046	Nonsense_Mutation	INS	-	CTTCATCTATGA	-	SLCA1	412insCTCATAG	71_E472delinsSHRX
XH_P37	17	42398855	42398855	Frame_Shift_Ins	INS	-	AGCATGT	-	SLC25A39	94_395insACAT	p.R132fs
XH_P37	17	42475817	42475817	Frame_Shift_Ins	INS	-	GCATTTTC	-	GPATCH8	93_3394insGAA	p.S1132fs
XH_P37	17	42960502	42960502	Frame_Shift_Ins	INS	-	TTCTCTGTATAG	-	EFTUD2	46insACTATAAC	p.E116fs
XH_P37	17	43310634	43310634	Nonsense_Mutation	INS	-	CCATACATAGA	-	FMN1	insCCCCCATAC	24_E125delinsLPHTX
XH_P37	17	44590703	44590703	Missense_Mutation	SNP	C	G	C	LRRC37A2	c.C625G	p.P209A
XH_P37	17	44590704	44590704	Frame_Shift_Ins	INS	-	TG	-	LRRC37A2	c.626_627insTG	p.P209fs
XH_P37	17	45752065	45752065	Frame_Shift_Ins	INS	-	T	-	KPNB1	c.1394_1395ins	p.S465fs
XH_P37	17	45752066	45752066	Frame_Shift_Ins	INS	-	ATTTCAITTTGCT	-	KPNB1	96insAATTTTCAT	p.S465fs
XH_P37	17	45904472	45904472	In_Frame_Ins	INS	-	CCGATAAGCCAT	-	MRPL10	321insATGGCTT	E107delinsEWLIG
XH_P37	17	46670725	46670725	Frame_Shift_Ins	INS	-	TCTCTCTTTTTT	-	HOBX5	20insAAAAAAGA	p.S107fs
XH_P37	17	47376202	47376202	Frame_Shift_Ins	INS	-	ACCTGCACATCC	-	ZNFR52	394insTGAGATG	p.G465fs
XH_P37	17	47587866	47587866	Nonsense_Mutation	INS	-	TGATTTTCTTAT	-	NGFR	2insCTTGATTTC	221_D222delinsPX
XH_P37	17	48539608	48539608	Frame_Shift_Ins	INS	-	GACACATATGC	-	ACSF2	92insGACACAT	p.K31fs
XH_P37	17	48539610	48539610	Missense_Mutation	SNP	G	T	G	ACSF2	c.G93T	p.K31N
XH_P37	17	48606155	48606155	Frame_Shift_Ins	INS	-	GCTGCAGGTA	-	MYCBPAP	2637insGCTGCG	p.B879fs
XH_P37	17	49269625	49269625	Nonsense_Mutation	INS	-	TTGTGTCATTATG	-	MBTD1	07insTACATAAT	p.69_5570delinsHTX
XH_P37	17	56342311	56342311	Frame_Shift_Ins	INS	-	CGCCTCCGCTT	-	LPO	7insCCTTCGCTT	p.N416fs
XH_P37	17	56342312	56342312	Missense_Mutation	SNP	A	C	A	LPO	c.A1247C	p.N416T
XH_P37	17	57743932	57743932	Missense_Mutation	SNP	G	A	G	CLTC	c.G1886A	p.R629H
XH_P37	17	58147181	58147181	Frame_Shift_Ins	INS	-	GGCTTATTTTAA	-	HEATR6	TCTATTTAAAAAT	p.L277fs
XH_P37	17	58525195	58525195	In_Frame_Ins	INS	-	TGATTT	-	APBP2	91_1292insAA	p.G431delinsEIR
XH_P37	17	58525196	58525196	Splice_Site	INS	-	TCAGAA	-	APBP2	.	.
XH_P37	17	58531834	58531834	Frame_Shift_Ins	INS	-	AATTGAGAAGAT	-	APBP2	CTCACTATTCTTC	p.I318fs
XH_P37	17	60088124	60088124	Nonsense_Mutation	INS	-	GTATGTATTTTTT	-	MED13	ATTAAAAAAA	585_F586delinsLX
XH_P37	17	61482536	61482536	Missense_Mutation	SNP	G	C	G	TANC5	c.G3163C	p.E105SQ
XH_P37	17	61498183	61498183	Frame_Shift_Ins	INS	-	GGCCTCTCCC	-	TANC2	4841insGGGCG	p.R1614fs
XH_P37	17	61498185	61498185	Silent	SNP	A	G	A	TANC2	c.A4842G	p.R1614AR
XH_P37	17	61655971	61655971	Frame_Shift_Ins	INS	-	AGGTTTTTTTTG	-	DCAF7	0insAGAGGTTT	p.D93fs
XH_P37	17	61949552	61949552	Nonsense_Mutation	INS	-	ATTTCATCTGAC	-	CSH2	CACCTAGTCAGAA	101_D102delinsILX
XH_P37	17	61972448	61972448	Nonsense_Mutation	INS	-	ATTTCATCTGAC	-	CSH1	CACCTAGTCAGAA	196_D197delinsILX
XH_P37	17	62855875	62855875	In_Frame_Ins	INS	-	ACTGAGAACTA	-	LRRC37A3	743insTGATGTT	Y581delinsYVVL
XH_P37	17	65105671	65105671	Frame_Shift_Ins	INS	-	CCCAACAATGCT	-	HELZ	insAAAAAGCAT	p.H1351fs
XH_P37	17	65124965	65124965	In_Frame_Ins	INS	-	5TAAAGCCTCTG	-	HELZ	92insAACAGAG	1064delinsLLEALP
XH_P37	17	65909163	65909163	Nonsense_Mutation	INS	-	TACCTTGATCAC	-	BPTF	164insTACCTT	21_V1722delinsFLPX
XH_P37	17	66041912	66041912	Frame_Shift_Ins	INS	-	AAAGATCTTACA	-	KPNA2	GAGCCAAAGAT	p.E458fs
XH_P37	17	66253030	66253030	Frame_Shift_Ins	INS	-	AT	-	AMZ2	c.829_830insAT	p.G277fs
XH_P37	17	66253031	66253031	In_Frame_Ins	INS	-	TGAATATGAAAT	-	AMZ2	nsGTGTGAATAT	277delinsGCEYEIM
XH_P37	17	66381262	66381262	Frame_Shift_Ins	INS	-	TTCAAATATGTG	-	ARSG	GTATCTTCTCAA	p.A347fs
XH_P37	17	66426205	66426205	In_Frame_Ins	INS	-	5AAAAAAGAA	-	WIPI1	insAGTTTTCTT	217delinsQVFFFSF
XH_P37	17	66521946	66521946	Frame_Shift_Ins	INS	-	AAAAACAAGATA	-	PRKAR1A	TTTAAAAAACA	p.G201fs
XH_P37	17	66925302	66925302	Frame_Shift_Ins	INS	-	TAAAGCTTGG	-	ABCA8	5TAATTTTCCAAG	p.T338fs
XH_P37	17	66937094	66937094	Frame_Shift_Ins	INS	-	GGAATGTGTCT	-	ABCA8	06insGAAGACA	p.N36fs
XH_P37	17	67124926	67124926	In_Frame_Ins	INS	-	TTATTTCTAAACA	-	ABCA6	AAAATTGTTT	8delinsTLEKLFRIKALS
XH_P37	17	67282118	67282118	Frame_Shift_Ins	INS	-	GGCCAGAGTTA	-	ABCA5	2193insTAACT	p.I731fs
XH_P37	17	71027773	71027773	In_Frame_Ins	INS	-	ACTGATTGGTGA	-	SLC39A11	AAGAAATCACC	6delinsRKSPSSSN
XH_P37	17	71231951	71231951	Nonsense_Mutation	INS	-	TGATCATGATGG	-	C17orf80	5CTTTTTGATCA	0_D111delinsKLFDQX
XH_P37	17	73177251	73177251	Frame_Shift_Ins	INS	-	T	-	SUMO2	c.53_54insA	p.I18fs
XH_P37	17	73177253	73177253	Nonsense_Mutation	INS	-	AATTTTTTTTTTAC	-	SUMO2	TTGGTAAAAAA	8delinsFLGKKLLX
XH_P37	17	73235616	73235616	Frame_Shift_Del	DEL	G	-	G	GGA3	c.1254delC	p.L418fs
XH_P37	17	73235617	73235617	Missense_Mutation	SNP	A	T	A	GGA3	c.T1253A	p.L418H
XH_P37	17	73328815	73328815	Nonsense_Mutation	INS	-	TAACAAAG	-	GRB2	1_142insCTTTG	48_P49delinsLCX
XH_P37	17	73328817	73328817	Nonsense_Mutation	INS	-	ATTGTGCATGTTA	-	GRB2	ACTATTAAACATG	F47_I48delinsYYX
XH_P37	17	73759186	73759186	In_Frame_Ins	INS	-	TCACCAACTCTA	-	GALK1	0insATTAGAGT	174delinsIRVGDE
XH_P37	17	73945808	73945808	Frame_Shift_Ins	INS	-	AAACCTTCAAAA	-	ACOX1	355insTTTTTGA	p.R452fs

XH_P37	17	73945809	73945809	Frame_Shift_Ins	INS	-	AAGT	-	ACOX1	353_1354insAC	p.R452fs
XH_P37	17	76128573	76128573	Silent	SNP	C	A	C	TMC8	c.C432A	p.G144G
XH_P37	17	76498674	76498674	In_Frame_Ins	INS	-	TCA	-	DNAH17	5188_5189insTC	Q1730delinsLK
XH_P37	17	76498675	76498675	In_Frame_Ins	INS	-	AAATATGTA	-	DNAH17	7_5188insTACA	Q1730delinsYIFQ
XH_P37	17	78280939	78280939	Frame_Shift_Ins	INS	-	TAAACTTATACC	-	RNF213	2440insTTAAAC	p.D813fs
XH_P37	17	78280940	78280940	Missense_Mutation	SNP	G	A	G	RNF214	c.G2400A	p.V814I
XH_P37	17	78321148	78321148	Missense_Mutation	SNP	G	A	G	RNF213	c.G9013A	p.E3005K
XH_P37	17	79202948	79202948	Missense_Mutation	SNP	G	A	G	TEPSIN	c.C1358T	p.T453M
XH_P37	17	79847182	79847182	Frame_Shift_Ins	INS	-	CCGGAAGATTCA	-	ALYREF	GAAGTGAATCT	p.T138fs
XH_P37	18	346644	346644	In_Frame_Ins	INS	-	GAGGTTAGACA	-	COLEC12	5TTCAGTGTCTA	826delinsASVSNL
XH_P37	18	619263	619263	Nonsense_Mutation	INS	-	TGTTCTCTTATA	-	CLUL1	insAATTGTTCTC	p.L53delinsX
XH_P37	18	2732454	2732454	Frame_Shift_Ins	INS	-	ACACAAACACTG	-	SMCHD1	nsGAAAAACACAA	p.E1080fs
XH_P37	18	3129347	3129347	Nonsense_Mutation	INS	-	GTGTCCATTCTT	-	MYOM1	ACAATAAGAAAT	93delinsTYNKNHGX
XH_P37	18	5292059	5292059	Nonsense_Mutation	INS	-	AGAAGATGTTA	-	ZBTB14	5TTAAGTTAACA	H50_R51delinsLSX
XH_P37	18	5416297	5416297	Frame_Shift_Ins	INS	-	GATGATGGATA	-	EPB41L3	7insAGGTATCC	p.R529fs
XH_P37	18	8718634	8718634	Nonsense_Mutation	INS	-	TCATCTAACTCAT	-	MTCL1	87insTTCACTTA	p.E62delinsEFIX
XH_P37	18	10680343	10680343	Frame_Shift_Ins	INS	-	GG	-	PIEZO2	.7465_7466insC	p.Y2489fs
XH_P37	18	10680344	10680344	In_Frame_Ins	INS	-	CAGAGGTAGTT	-	PIEZO2	nsACAGTAACATA	489delinsTVTTSSEY
XH_P37	18	10736650	10736650	Frame_Shift_Ins	INS	-	TTAAATGTGTAAT	-	PIEZO2	92insTCATTACA	p.E1564fs
XH_P37	18	10736652	10736652	Missense_Mutation	SNP	C	G	C	PIEZO2	c.G4690C	p.E1564Q
XH_P37	18	12264445	12264445	Nonsense_Mutation	INS	-	SAATGTTCTTTT	-	CIDEA	insAAGAAATGTT	/108_M109delinsX
XH_P37	18	12449766	12449766	In_Frame_Ins	INS	-	TTTGCACTTAGAT	-	SPIRE1	1740insATCTAA	580delinsRSNAN
XH_P37	18	12449768	12449768	Missense_Mutation	SNP	T	A	T	SPIRE1	c.A1738T	p.S580C
XH_P37	18	12674752	12674752	In_Frame_Ins	INS	-	AGT	-	CEP76	1398_1399insA	p.D467delinsTD
XH_P37	18	12674753	12674753	Splice_Site	INS	-	GCAGGGGGTTTT	-	CEP76	.	.
XH_P37	18	12678426	12678426	Nonsense_Mutation	INS	-	ATTCCACAT	-	CEP76	9_1080insAGTG	p.P360delinsPVX
XH_P37	18	12678427	12678427	Frame_Shift_Ins	INS	-	AAATAGTTGTA	-	CEP76	1079insTACAA	p.P360fs
XH_P37	18	13059288	13059288	In_Frame_Ins	INS	-	AAAACATTATTAT	-	CEP192	nsAATTAATAAACA	489delinsKLKLHLSL
XH_P37	18	14105074	14105074	Nonsense_Mutation	SNP	T	A	T	ZNF519	c.A1465T	p.K489X
XH_P37	18	14105076	14105076	In_Frame_Ins	INS	-	AATCAACTACTGG	-	ZNF519	163insATCCAGT	F488delinsYPLUJF
XH_P37	18	14848876	14848876	Nonsense_Mutation	INS	-	CTTTGGGGATAT	-	ANKRD30B	TAGTACTTTTGG	996delinsVISTFGIX
XH_P37	18	18548799	18548799	In_Frame_Ins	INS	-	TAACATAAAAAA	-	ROCK1	nsTAAGTTTTTTA	879delinsDKFFIVSG
XH_P37	18	18586530	18586530	Frame_Shift_Ins	INS	-	AGACCTTCAAG	-	ROCK1	ATATTACTTTGA	p.T556fs
XH_P37	18	18964292	18964292	Nonsense_Mutation	INS	-	CTAGCACTTTCTT	-	GREB1L	AAGGTCTAGCA	M95delinsKRSISFX
XH_P37	18	19029774	19029774	Frame_Shift_Ins	INS	-	TTCT	-	GREB1L	.697_1698insTT	p.N566fs
XH_P37	18	19029776	19029776	Nonsense_Mutation	INS	-	ATAGCTTTTCAGC	-	GREB1L	700insCATAGCT	p.E567delinsAX
XH_P37	18	19153755	19153755	Nonsense_Mutation	INS	-	AAATTAATGATAT	-	ESCO1	0insGTAATATCA	p.I350delinsMX
XH_P37	18	21736503	21736503	Frame_Shift_Ins	INS	-	TGGACAGATGT	-	CABYR	insACATGGACA	p.S248fs
XH_P37	18	28576950	28576950	Missense_Mutation	SNP	A	T	A	DSC3	c.T2300A	p.M767K
XH_P37	18	28584200	28584200	Frame_Shift_Ins	INS	-	TTTGAATATTTT	-	DSC3	21insAGAAAATA	p.P674fs
XH_P37	18	28602426	28602426	Missense_Mutation	SNP	G	A	G	DSC3	c.C818T	p.P273L
XH_P37	18	28736073	28736073	Missense_Mutation	SNP	C	A	C	DSC1	c.G404T	p.R135L
XH_P37	18	28736074	28736074	Nonsense_Mutation	INS	-	TATATCTTATTA	-	DSC1	GAAAGTAATAAA	5_WJ136delinsSVRXX
XH_P37	18	28911736	28911736	In_Frame_Ins	INS	-	CATATG	-	DSG1	90_591insCATA	K197delinsNIW
XH_P37	18	28911738	28911738	Nonsense_Mutation	INS	-	TATCTTAGCTC	-	DSG1	.593insTATCTTA	198_1199delinsISX
XH_P37	18	28980950	28980951	Frame_Shift_Del	DEL	GG	-	GG	DSG4	c.1384_1385de	p.G462fs
XH_P37	18	28980951	28980951	Frame_Shift_Ins	INS	-	AAAAATTCAAT	-	DSG4	1386insAAAAA	p.G462fs
XH_P37	18	29101100	29101100	In_Frame_Ins	INS	-	ACAGGAATGT	-	DSG2	AAATAACAGGA	delinsVSNIKITGMFQVELS
XH_P37	18	29126302	29126302	Frame_Shift_Ins	INS	-	A	-	DSG2	.2953_2954ins	p.V985fs
XH_P37	18	29126303	29126303	Nonsense_Mutation	INS	-	TCAGTGACTATT	-	DSG2	5insCTTTTCAGTG	V985delinsVFQX
XH_P37	18	29178541	29178541	Frame_Shift_Ins	INS	-	CCGAAAGTCAG	-	TTR	48insGCCGAA	p.T116fs
XH_P37	18	30977148	30977148	Missense_Mutation	SNP	G	C	G	CCDC178	c.C83G	p.A28G
XH_P37	18	34192043	34192043	In_Frame_Ins	INS	-	AAGCCT	-	FHOD3	42_943insAAGC	Q314delinsQKP
XH_P37	18	34233353	34233353	Nonsense_Mutation	INS	-	AAACCCATTACT	-	FHOD3	ATTTAAAAACCC	p.Y565delinsYIX
XH_P37	18	34289352	34289352	Frame_Shift_Ins	INS	-	ATGGAGATTATA	-	FHOD3	956insAATGGAC	p.T652fs
XH_P37	18	34335249	34335249	In_Frame_Ins	INS	-	AAATTACTT	-	FHOD3	4_3825insAAAT	K1275delinsKNVL
XH_P37	18	34335250	34335250	Nonsense_Mutation	INS	-	AACTCTCAGTA	-	FHOD3	nsTCTAAAAATCT	1275delinsSKSISQX
XH_P37	18	42532548	42532548	In_Frame_Ins	INS	-	ACGGGTCATACI	-	SETBP1	3244insACGGG	1081delinsATGHTH
XH_P37	18	42643371	42643371	Nonsense_Mutation	INS	-	TTGAACCT	-	SETBP1	9_4500insTTGA	500_51501delinsAX
XH_P37	18	43843041	43843041	Nonsense_Mutation	INS	-	TTATCAACATTTT	-	C18orf25	TGTACTTATCAA	0delinsSLCTCYHFXY
XH_P37	18	44392511	44392511	Nonsense_Mutation	INS	-	TTTTTTTTTTTTTA	-	PIAS2	ATTATTAATAAAA	T584delinsIPNVX
XH_P37	18	44656695	44656695	In_Frame_Ins	INS	-	GTG	-	HDHD2	c.44_45insCAC	p.L15delinsIT
XH_P37	18	44656696	44656696	Frame_Shift_Ins	INS	-	AGTATGTTTTTT	-	HDHD2	nsACAAAAACCA	p.I15fs
XH_P37	18	47107855	47107855	Silent	SNP	G	A	G	LIPG	c.G642A	p.Q214Q
XH_P37	18	47107857	47107857	In_Frame_Ins	INS	-	ATCTGCGATGCT	-	LIPG	GGCTCATCTCGT	15delinsEGLILHAFYL
XH_P37	18	47363257	47363257	Splice_Site	INS	-	TGTCAACATGGT	-	MYO5B	.	.
XH_P37	18	47500952	47500952	Frame_Shift_Ins	INS	-	CACCTCT	-	MYO5B	9_1090insAGG	p.L364fs
XH_P37	18	48573569	48573569	In_Frame_Ins	INS	-	ACACATCAGAA	-	SMAD4	AAGACACACATG	delinsKKDTHQNTFY
XH_P37	18	48575159	48575159	Frame_Shift_Ins	INS	-	ACACTTTATATA	-	SMAD4	nsAAGACACTTT	p.A118fs
XH_P37	18	48575161	48575161	Missense_Mutation	SNP	T	A	T	SMAD4	c.T355A	p.F119I
XH_P37	18	48581260	48581260	Frame_Shift_Ins	INS	-	ATAATAA	-	SMAD4	54_565insATAA	p.N188fs
XH_P37	18	48581261	48581261	Frame_Shift_Ins	INS	-	CTAAATCAATTA	-	SMAD4	insACCTAAAT	p.R189fs
XH_P37	18	54398786	54398786	Nonsense_Mutation	INS	-	GTTTAAAGTAAAC	-	WDR7	TGAATAGTTTAA	Q649delinsQHFEX
XH_P37	18	55217972	55217972	Frame_Shift_Ins	INS	-	TC	-	FECH	1243_1244insG	p.K415fs
XH_P37	18	55217974	55217974	Nonsense_Mutation	INS	-	AGTAAGCATTTT	-	FECH	AAAAATCAAAATG	p.T414delinsTX
XH_P37	18	55319888	55319888	Frame_Shift_Ins	INS	-	ACCA	-	ATP8B1	088_3089insTG	p.Y1030fs
XH_P37	18	55319890	55319890	Nonsense_Mutation	INS	-	ACATTTTCTATT	-	ATP8B1	87insGAAATAG	A.N1029delinsKKX
XH_P37	18	55321287	55321287	Frame_Shift_Ins	INS	-	GTGCTTCTTGTT	-	ATP8B1	nsACAAAAACAA	p.F984fs
XH_P37	18	56246359	56246359	Nonsense_Mutation	INS	-	AAGTTAATACTG	-	ALPK2	49insTAGAGTAT	150_A551delinsIEYX
XH_P37	18	59483574	59483574	Frame_Shift_Ins	INS	-	AACTTCCCAGCA	-	RNF152	23insTTGCTGGG	p.Q41fs
XH_P37	18	59824989	59824989	Nonsense_Mutation	INS	-	TTGAAAGAATT	-	PIGN	nsCCCAATTCTT	2_E93delinsPKFFQX
XH_P37	18	60241466	60241466	Frame_Shift_Ins	INS	-	GC	-	ZCHCH2	2152_2153insG	p.F718fs
XH_P37	18	60241467	60241467	Frame_Shift_Ins	INS	-	AAATAAACATTG	-	ZCHCH2	54insAGAAATAA	p.F718fs
XH_P37	18	65181242	65181242	Frame_Shift_Ins	INS	-	AAAGATGCACCT	-	DSEL	ACCAAAAGTGC	p.V212fs
XH_P37	18	65181244	65181244	Nonsense_Mutation	SNP	C	T	C	DSEL	c.G632A	p.W211X
XH_P37	18	65181416	65181416	Frame_Shift_Ins	INS	-	AATATGGGGTAT	-	DSEL	CAGTAATAACCC	p.F154fs
XH_P37	18	67688017	67688017	Frame_Shift_Ins	INS	-	ACTCA	-	RTTN	250_3251insTG	p.H1084fs
XH_P37	18	67688018	67688018	Frame_Shift_Ins	INS	-	TGAAATATAATC	-	RTTN	.3250insGATTA	p.H1084fs
XH_P37	18	67697282	67697282	Nonsense_Mutation	INS	-	ATTAGCAGATTG	-	RTTN	AGGCCAACAAAT	delinsFLRPGKAALKKPTICX
XH_P37	18	71793317	71793317	Frame_Shift_Ins	INS	-	CCATTTTACCAT	-	FBXO15	05insGATGGTAA	p.L269fs
XH_P37	18	72020687	72020687	Nonsense_Mutation	INS	-	ATTTAAAAATGT	-	C18orf63	AAAAAAATTTAA	R395delinsRDX
XH_P37	18	72021287	72021287	Missense_Mutation	SNP	C	A	C	C18orf63	c.C1785A	p.H595Q
XH_P37	18	72021289	72021289	Nonsense_Mutation	INS	-	CTATTAGATAGT	-	C18orf63	ACTGCACATTA	T.1596delinsLHXY
XH_P37	18	72234652	72234652	Missense_Mutation	SNP	G	A	G	CNDP1	c.G740A	p.S247N
XH_P37	18	72234653	72234653	Frame_Shift_Ins	INS	-	GAAGAAAAAAA	-	CNDP1	42insAGAAGAA	p.S247fs
XH_P37	18	72347635	72347635	Nonsense_Mutation	INS	-	ATATGTAATAAT	-	ZNF407	1insTTAATATGT	F1554delinsFNMX
XH_P37	18	72347637	72347637	Silent	SNP	C	T	C	ZNF407	c.C4662T	p.F1554F
XH_P37	18	74587580	74587580	Frame_Shift_Ins	INS	-	TGCATATATACA	-	ZNF236	CTAGATGCATAT	p.K267fs

XH_P37	19	111363	111363	Frame_Shift_Ins	INS	-	TGAAGGAGAAA	-	OR4F17	nsAAGTGAAGG	p.A229fs
XH_P37	19	1085966	1085966	Silent	SNP	A	G	A	ARHGAP45	c.A2277G	p.T759T
XH_P37	19	2876193	2876193	Nonsense_Mutation	INS	-	TCATGACTTCAT	-	ZNF556	TTGTTTCATGAC	p.N78delinsKX
XH_P37	19	2915642	2915642	In_Frame_Ins	INS	-	AAATTCAAACAA	-	ZNF57	TCATAAATTCAA	0delinsSIHKFKQDS
XH_P37	19	3611972	3611972	Silent	SNP	G	A	G	CACTIN	c.C226T	p.N742N
XH_P37	19	4217273	4217273	In_Frame_Ins	INS	-	TGT	-	ANKRD24	2116_2117insT	p.A706delinsVS
XH_P37	19	5693622	5693622	Frame_Shift_Ins	INS	-	TCCCTGGC	-	LONP1	D_1891insGCCA	p.Q631fs
XH_P37	19	7083359	7083359	Frame_Shift_Ins	INS	-	ATCT	-	ZNF557	.897_898insATC	p.K299fs
XH_P37	19	7083361	7083361	Frame_Shift_Ins	INS	-	TGCTGAAGGT	-	ZNF557	.900insTGCCTGA	p.A300fs
XH_P37	19	8176051	8176051	Silent	SNP	G	A	G	FBN3	c.C4101T	p.A1367A
XH_P37	19	8976744	8976744	Frame_Shift_Ins	INS	-	AGACCACTTC	-	MUC16	.42322insGAAG	p.H14108fs
XH_P37	19	9015691	9015691	Nonsense_Mutation	INS	-	CACCTCTCTC	-	MUC16	.38132insGAGA	11_Y12712delinsRERX
XH_P37	19	9021134	9021134	Frame_Shift_Ins	INS	-	CCCATATTCAA	-	MUC16	.37189insTTGA	p.T12397fs
XH_P37	19	9046124	9046124	Frame_Shift_Ins	INS	-	CCCCAGAA	-	MUC16	.6_35507insTTC	p.S11836fs
XH_P37	19	9047447	9047447	In_Frame_Ins	INS	-	CACTACAAC	-	MUC16	.3_34184insGTTT	113950delinsSCSA
XH_P37	19	9049256	9049256	Nonsense_Mutation	INS	-	GTTC	-	MUC16	.874_32375insAC	792_V10793delinsX
XH_P37	19	9049257	9049257	In_Frame_Ins	INS	-	GGG	-	MUC16	.2373_32374ins	L10792delinsPL
XH_P37	19	9049690	9049690	Frame_Shift_Ins	INS	-	G	-	MUC16	.31940_31941in	p.S10647fs
XH_P37	19	9049691	9049691	In_Frame_Ins	INS	-	TATTTCCAAT	-	MUC16	.3_31940insATT	10647delinsNWN
XH_P37	19	9057855	9057855	Frame_Shift_Ins	INS	-	ATTTTTAC	-	MUC16	.29591insGTGT	p.T9864fs
XH_P37	19	9064277	9064277	Frame_Shift_Ins	INS	-	AGAGGGGGGG	-	MUC16	.AGCACACATCC	p.S7723fs
XH_P37	19	9066151	9066151	Frame_Shift_Ins	INS	-	CGTCCAATGT	-	MUC16	.21295insACAT	p.L7099fs
XH_P37	19	9067232	9067232	Nonsense_Mutation	INS	-	CAACATTACCA	-	MUC16	.4insTCTTTGGTA	98_T6739delinsRLWX
XH_P37	19	9069596	9069596	In_Frame_Ins	INS	-	CAATTCTATGC	-	MUC16	.insTTTTATGCAT	950delinsSLCIELVV
XH_P37	19	9075104	9075104	In_Frame_Ins	INS	-	ACCTCA	-	MUC16	.41_12342insTG	A4114delinsAEV
XH_P37	19	9075105	9075105	In_Frame_Ins	INS	-	TTTTCTGT	-	MUC16	.1_12341insACAA	A4114delinsDKT
XH_P37	19	9076904	9076904	Nonsense_Mutation	INS	-	TCAGATTCTGG	-	MUC16	.0542insTCCAGG	4_H3515delinsPGIX
XH_P37	19	9082456	9082456	Nonsense_Mutation	INS	-	CTACATCTTTT	-	MUC16	.AAAAATAAAAA	p.T3120delinsIX
XH_P37	19	9084742	9084742	Missense_Mutation	SNP	C	A	C	MUC16	.c.G0703T	p.R2358L
XH_P37	19	9084743	9084743	Frame_Shift_Ins	INS	-	AACACCTATTCT	-	MUC16	.072insGAGAATA	p.R2358fs
XH_P37	19	9225863	9225863	In_Frame_Ins	INS	-	CTTCCCGAATT	-	OR7G1	.7insAGTAATTCT	193delinsSNSGRL
XH_P37	19	9226096	9226096	Frame_Shift_Ins	INS	-	AAACGTT	-	OR7G1	.43_344insAACG	p.L115fs
XH_P37	19	9407497	9407497	In_Frame_Ins	INS	-	AAAGCAAACTA	-	ZNF699	.sATTTCATAGTTT	195delinsHLSLFR
XH_P37	19	9577251	9577251	Nonstop_Mutation	INS	-	TTTTTTTTTTT	-	ZNF560	.nsCATCAAAAAA	685delinsSKKKKX
XH_P37	19	9676879	9676879	Nonsense_Mutation	INS	-	A	-	ZNF121	.c.909_910insT	K304_I305delinsX
XH_P37	19	9676880	9676880	Nonsense_Mutation	INS	-	CTAAACATTAA	-	ZNF121	.TGTTTTAAATG	03_K304delinsVCFX
XH_P37	19	9730116	9730116	Frame_Shift_Ins	INS	-	G	-	ZNF561	.c.16_17insC	p.L6fs
XH_P37	19	9730117	9730117	Nonsense_Mutation	INS	-	TTATTATTATT	-	ZNF561	.AATAAAATAAAT	p.L6_57delinsXX
XH_P37	19	11319384	11319384	Frame_Shift_Ins	INS	-	AGGAAGCA	-	DOCK6	.5_5066insTGCT	p.Q1689fs
XH_P37	19	11411986	11411986	Splice_Site	INS	-	TGAGGATAGAG	-	TSPAN16	.	.
XH_P37	19	11890916	11890916	Frame_Shift_Ins	INS	-	TCITTTCTTCTT	-	ZNF441	.ACATTCTTTTCT	p.V93fs
XH_P37	19	11892457	11892457	Nonsense_Mutation	INS	-	CCACATGTTTA	-	ZNF441	.sCTTTCCACACAT	.6_R607delinsEAFPTX
XH_P37	19	11917373	11917373	In_Frame_Ins	INS	-	ATCAAAAGGTTT	-	ZNF491	.nsACAATCAAAA	202delinsQSKGFS
XH_P37	19	11979184	11979184	Frame_Shift_Ins	INS	-	GTTTTTTCATGT	-	ZNF439	.nsTGAGTTTTTT	p.G298fs
XH_P37	19	12383951	12383951	Frame_Shift_Ins	INS	-	TGGAGAGCAAC	-	ZNF44	.TATAGGGTTGC	p.L373fs
XH_P37	19	12384835	12384835	Frame_Shift_Ins	INS	-	CTATGATTGTAA	-	ZNF44	.ATTCTTCACAAT	p.Q79fs
XH_P37	19	12501902	12501902	Frame_Shift_Ins	INS	-	A	-	ZNF799	.-1309_1310ins	p.R437fs
XH_P37	19	12501903	12501903	Frame_Shift_Ins	INS	-	ATTTTGGTAAC	-	ZNF799	.9insTTAAGTTAC	p.R437fs
XH_P37	19	12504210	12504210	Missense_Mutation	SNP	C	A	C	ZNF799	.c.G31T	p.V11L
XH_P37	19	12504211	12504211	In_Frame_Ins	INS	-	TGGAATATGGA	-	ZNF799	.nsCTTTCCATATT	.10delinsAFPPYS
XH_P37	19	12739198	12739198	Frame_Shift_Ins	INS	-	GTGAATCC	-	ZNF791	.5_856insGTGA	p.S285fs
XH_P37	19	13428073	13428073	Frame_Shift_Ins	INS	-	ACTTCTCTTCTG	-	CACNA1A	.insCAGAGAAA	p.K471fs
XH_P37	19	14141653	14141653	Nonsense_Mutation	INS	-	CTGATTTTGTGA	-	RLN3	.sCTGGCTGATTT	.Q108delinsPGX
XH_P37	19	14269334	14269334	Frame_Shift_Ins	INS	-	GTACC	-	ADGRL1	.179_2180insGG	p.N272fs
XH_P37	19	14677049	14677049	Missense_Mutation	SNP	G	A	G	NDUF87	.c.C310T	p.R104W
XH_P37	19	15067457	15067457	Frame_Shift_Ins	INS	-	CATTCTCGTTT	-	SLC1A6	.1000insAACCA	p.V334fs
XH_P37	19	15083605	15083605	Missense_Mutation	SNP	G	A	G	SLC1A6	.c.C118T	p.R40C
XH_P37	19	15365012	15365012	Frame_Shift_Ins	INS	-	CTGCCAGG	-	BRD4	.8_2109insCCTG	p.S703fs
XH_P37	19	15365014	15365014	Missense_Mutation	SNP	A	T	A	BRD4	.c.T2107A	p.S703T
XH_P37	19	16612186	16612186	Frame_Shift_Ins	INS	-	TCTGTCAAGCTC	-	C19orf44	.584insTTCTGTCA	p.T195fs
XH_P37	19	16872812	16872812	In_Frame_Ins	INS	-	ACATCAATTTAC	-	NWD1	.TTCTCTACATCA	delinsVFFFLTSTVFPYIQ
XH_P37	19	17212978	17212978	Frame_Shift_Del	DEL	CT	-	CT	MYO9B	.c.451_452del	p.L151fs
XH_P37	19	18376973	18376973	Nonsense_Mutation	INS	-	TCCTCAAGACTC	-	KIAA1683	.877insAGAGTCT	59_V460delinsPESX
XH_P37	19	18377664	18377664	In_Frame_Ins	INS	-	TACGAGACT	-	KIAA1683	.5_686insGTCTCC	A229delinsGLVT
XH_P37	19	19136351	19136351	Nonsense_Mutation	INS	-	ATAATCAATGG	-	SUGP2	.CCTGCCCATTTG	N269delinsLPIJ
XH_P37	19	19790925	19790925	In_Frame_Ins	INS	-	TTTTTGACATTC	-	ZNF101	.sCACATTTTGA	256delinsGTFLTVE
XH_P37	19	20045551	20045551	Nonsense_Mutation	INS	-	TTAATAAGGGT	-	ZNF93	.TTATGTTTAAAT	.6_K597delinsEFVSXV
XH_P37	19	21131702	21131702	Nonsense_Mutation	INS	-	GCAAAATACCAT	-	ZNF85	.191insGCAAAA	p.K64delinsSKIPX
XH_P37	19	21239924	21239924	Frame_Shift_Ins	INS	-	ATATTGGATTTC	-	ZNF430	.insGTATATTTC	p.F269fs
XH_P37	19	21301037	21301037	Missense_Mutation	SNP	G	A	G	ZNF714	.c.G1567A	p.A523T
XH_P37	19	21301038	21301038	Frame_Shift_Ins	INS	-	CT	-	ZNF714	.1568_1569insC	p.A523fs
XH_P37	19	21606048	21606048	Frame_Shift_Ins	INS	-	T	-	ZNF493	.c.203_204insT	p.H68fs
XH_P37	19	21606050	21606050	Frame_Shift_Ins	INS	-	CTTAACTGTAAA	-	ZNF493	.nsTTTTCTTAAC	p.L69fs
XH_P37	19	21719234	21719234	Frame_Shift_Ins	INS	-	GCAAAATACCA	-	ZNF429	.SCATAGCAAAA	p.K63fs
XH_P37	19	21719575	21719575	In_Frame_Ins	INS	-	ATTTT	-	ZNF429	.528_529insATT	p.H176delinsHIF
XH_P37	19	21990953	21990953	In_Frame_Ins	INS	-	TTAAAC	-	ZNF43	.90_1691insGTT	p.K564delinsSLK
XH_P37	19	21990955	21990955	Frame_Shift_Ins	INS	-	TCCTCAAC	-	ZNF43	.8_1689insGTTG	p.G563fs
XH_P37	19	21991894	21991894	Nonsense_Mutation	INS	-	ATACTGCAGAGA	-	ZNF43	.GAATTCTCTG	p.K250delinsNLX
XH_P37	19	21992215	21992215	Nonsense_Mutation	INS	-	GTCTCTCAATCT	-	ZNF43	.TAGTAAGGATTC	B3_K144delinsGSKDX
XH_P37	19	22497215	22497215	Nonsense_Mutation	INS	-	TATTTGTAAAGT	-	ZNF729	.insTTATATTGT	F332delinsFLYLX
XH_P37	19	22497217	22497217	Nonsense_Mutation	INS	-	GAATTATCTTAT	-	ZNF729	.AGTATGAATTAT	B3_A334delinsSSVX
XH_P37	19	22940344	22940344	Silent	SNP	A	G	A	ZNF99	.c.T2367C	p.Y789Y
XH_P37	19	22941531	22941531	Missense_Mutation	SNP	G	C	G	ZNF99	.c.C1180G	p.Q394E
XH_P37	19	23329023	23329023	In_Frame_Ins	INS	-	TTATGAATTC	-	ZNF730	.TCTCCATTATGA	delinsGFFSIMNSFMFK
XH_P37	19	23329241	23329241	Nonsense_Mutation	INS	-	TTTGTAATTTCT	-	ZNF730	.6insCATTGTGTA	A.S465delinsSHLX
XH_P37	19	23329243	23329243	Nonsense_Mutation	INS	-	AGTATGAATTAT	-	ZNF730	.1398insAGTATG	p.T466delinsTVX
XH_P37	19	23542290	23542290	Missense_Mutation	SNP	A	G	A	ZNF91	.c.T3395C	p.L1132P
XH_P37	19	23542291	23542291	Missense_Mutation	SNP	G	C	G	ZNF91	.c.C3394G	p.L1132V
XH_P37	19	23543548	23543548	Nonsense_Mutation	INS	-	CTTACTAAGCA	-	ZNF91	.insCTTATGCTTA	E714delinsLMLSKGX
XH_P37	19	23543701	23543701	Missense_Mutation	SNP	T	C	T	ZNF91	.c.A1984G	p.T662A
XH_P37	19	24115997	24115997	Missense_Mutation	SNP	G	A	G	ZNF726	.c.G1079A	p.R360K
XH_P37	19	24310111	24310111	Frame_Shift_Ins	INS	-	C	-	ZNF254	.-1054_1055ins	p.E352fs
XH_P37	19	24310112	24310112	Frame_Shift_Ins	INS	-	CTCTTATGTCTAG	-	ZNF254	.56insTCCTCTTA	p.E352fs
XH_P37	19	24310638	24310638	In_Frame_Ins	INS	-	CAGTATGAATT	-	ZNF254	.TTCTCTCAGTA	nsFTFVGFLFSMMNYLMFSK
XH_P37	19	31768501	31768501	In_Frame_Ins	INS	-	GACTTGACAAA	-	TSZH2	.198insCTTTGTG	T733delinsPFVKM
XH_P37	19	31769765	31769765	Nonsense_Mutation	INS	-	CTGCTATGAAA	-	TSZH2	.934insTTTCAT	B12_A313delinsFSX
XH_P37	19	32843864	32843864	In_Frame_Ins	INS	-	TAGATTAAATT	-	ZNF507	.CAGTATAGATT	T3delinsPQYRFKLV
XH_P37	19	32844204	32844204	Frame_Shift_Ins	INS	-	A	-	ZNF507	.c.468_469insA	p.M156fs

XH_P37	19	32844205	32844205	Nonsense Mutation	INS	-	TCAGCAGTCAG	-	ZNF507	nsACTTTCAGCA	S158delinsVFQSSVX
XH_P37	19	32844704	32844704	In Frame Ins	INS	-	GACAGTATGAG	-	ZNF507	gTTTGGACAGT	23delinsOFQGVESV
XH_P37	19	33090914	33090914	Nonsense Mutation	INS	-	ATATTATTTCG	-	ANKRD27	sATAACGAAAA	7_Q938delinsNKRKX
XH_P37	19	35435054	35435054	Frame_Shift_Ins	INS	-	ACTCCTTACA	-	ZNF307	1188insACTCC	p.T396fs
XH_P37	19	36037879	36037879	Frame_Shift_Ins	INS	-	AAGGTTTAGAC	-	TMEM147	insGACAAGGTT	p.I77fs
XH_P37	19	36237657	36237657	Frame_Shift_Ins	INS	-	GCCTTTGATTG	-	PSENEN	16insAGCCTTTG	p.T72fs
XH_P37	19	36509906	36509906	Frame_Shift_Ins	INS	-	CTGCTTTTGTCA	-	CLIP3	077insTGACAA	p.K359fs
XH_P37	19	36727404	36727404	Missense Mutation	SNP	G	T	G	ZNF146	c.G62T	p.C21F
XH_P37	19	36727405	36727405	Nonsense Mutation	INS	-	ATCTCTTACATT	-	ZNF146	CCACATCTCTTA	21delinsCPHLLHLX
XH_P37	19	37037894	37037894	Nonsense Mutation	INS	-	TGCTCTTTTGAC	-	ZNF529	GAATAGTCAAA	p.T504delinsTEX
XH_P37	19	37382524	37382524	Frame_Shift_Ins	INS	-	AA	-	ZNF829	.1168_1169insT	p.N390fs
XH_P37	19	37382526	37382526	Nonsense Mutation	INS	-	AAGGAGAACAA	-	ZNF829	ATCCTAATTGT	1390delinsLIILICSPVLFX
XH_P37	19	37676623	37676623	Frame_Shift_Ins	INS	-	AGAAACCTTAT	-	ZNF585B	sGCACTCATAAG	p.V606fs
XH_P37	19	37680619	37680619	Nonsense Mutation	INS	-	TTATAAGTCATG	-	ZNF585B	6insCACATGACT	9_Q80delinsAHDLX
XH_P37	19	37733607	37733607	Nonsense Mutation	INS	-	AAAATAAAATG	-	ZNF383	5AAAGAAAAAT	A57_T158delinsQJX
XH_P37	19	37870126	37870126	Frame_Shift_Ins	INS	-	TACATGCTGAG	-	ZNF527	insAATTACATG	p.N46fs
XH_P37	19	37975516	37975516	Frame_Shift_Ins	INS	-	TTGAACAAGATT	-	ZNF570	7insTGTTGAACA	p.E289fs
XH_P37	19	37975859	37975859	Nonsense Mutation	INS	-	TGATGTACAGT	-	ZNF570	0insCTCTGATG	A03_E404delinsILX
XH_P37	19	38028116	38028116	Frame_Shift_Ins	INS	-	AATCATCCTTAT	-	ZNF793	CAGTGAATCAT	p.K186fs
XH_P37	19	38028526	38028526	Nonsense Mutation	INS	-	GGTTGACTT	-	ZNF793	5_967insGGTTG	p.E322delinsEGX
XH_P37	19	38028528	38028528	Missense Mutation	SNP	A	T	A	ZNF793	c.A968T	p.K232M
XH_P37	19	38376859	38376859	Nonsense Mutation	INS	-	CTCAGATGTAG	-	WDR87	2insACTCTACT	84_I2485delinsPLYIX
XH_P37	19	39016054	39016054	Frame_Shift_Ins	INS	-	CCCAG	-	RVR1	523_10524insC	p.T3508fs
XH_P37	19	39299482	39299482	In Frame Ins	INS	-	TCCTTTCTTCT	-	LGALS4	AGAAAGAAAGA	81delinsKERKKRKEG
XH_P37	19	40318278	40318278	Frame_Shift_Ins	INS	-	GC	-	DYRK18	c.825_826insGC	p.S276fs
XH_P37	19	41351373	41351373	Frame_Shift_Ins	INS	-	TGAG	-	CYP2A6	.986_987insCTC	p.E329fs
XH_P37	19	41515259	41515259	In Frame Ins	INS	-	CTCTCTCCTTCT	-	CYP2B6	insTGCCCTCTCT	261delinsLPLSFLS
XH_P37	19	41711887	41711887	Nonsense Mutation	INS	-	GTGGTGAAGAA	-	CYP2S1	GGATGGTGGTG	G7_S398delinsVGWWX
XH_P37	19	42314886	42314886	Missense Mutation	SNP	C	T	C	CEACAM3	c.C644T	p.T21S1
XH_P37	19	42462938	42462938	Nonsense Mutation	INS	-	ACTACC	-	RABAC1	18_219insGGTA	p.Y73delinsX
XH_P37	19	42874964	42874964	Frame_Shift_Ins	INS	-	TCAACCCAAGG	-	MEGF8	917insCTCAAC	p.L2306fs
XH_P37	19	42912387	42912387	Frame_Shift_Ins	INS	-	TGGAAGTGCTA	-	LIPE	507insGATAGCA	p.L503fs
XH_P37	19	43031381	43031381	Frame_Shift_Ins	INS	-	CATAAGTCAGA	-	CEACAM1	6insGATCTGACT	p.I79fs
XH_P37	19	43259334	43259334	Frame_Shift_Ins	INS	-	C	-	PSG8	c.427_428insG	p.K143fs
XH_P37	19	43259335	43259335	Frame_Shift_Ins	INS	-	CTCTGGTCCA	-	PSG8	427insTGGACC	p.K143fs
XH_P37	19	43411278	43411278	In Frame Ins	INS	-	ATAGTCAAAGTC	-	PSG6	ACCAGAGACTT	6delinsLTRDFDVGHFG
XH_P37	19	43430783	43430783	Frame_Shift_Ins	INS	-	TCCAAGTATAGA	-	PSG7	nsTATGCTATA	p.K143fs
XH_P37	19	44056349	44056349	Nonsense Mutation	INS	-	TCTCTCACTGCT	-	XRCC1	nsAAAGCAAGTG	01_E302delinsESKX
XH_P37	19	44470318	44470318	Nonsense Mutation	INS	-	AGTTTGAGAGCC	-	ZNF221	65insAGTTTGA	222_E223delinsEFX
XH_P37	19	44471384	44471384	In Frame Ins	INS	-	GGGAATGAAGT	-	ZNF221	insGATGGGAAT	77delinsLMGMKLC
XH_P37	19	44494249	44494249	Frame_Shift_Ins	INS	-	TTTGATTITGAA	-	ZNF155	AGGTTTITGATT	p.C11fs
XH_P37	19	44501503	44501503	Frame_Shift_Ins	INS	-	TTATAAGGTCTC	-	ZNF155	9insAATTATAA	p.Y498fs
XH_P37	19	44570996	44570996	Frame_Shift_Ins	INS	-	CACAATTATAAT	-	ZNF223	5TGCCCTCACAAT	p.T339fs
XH_P37	19	44611870	44611870	Frame_Shift_Ins	INS	-	GATCCAACCTCC	-	ZNF224	insTCAAGATCCA	p.K519fs
XH_P37	19	44653010	44653010	Frame_Shift_Ins	INS	-	T	-	ZNF234	c.102_103insT	p.Q34fs
XH_P37	19	44653011	44653011	Nonsense Mutation	INS	-	ACTTTTGATTTC	-	ZNF234	nsCCACACTTTGA	35_V36delinsATLX
XH_P37	19	44739502	44739502	Frame_Shift_Ins	INS	-	CTTCATGATTTC	-	ZNF227	5AAGTCTCTAATG	p.N228fs
XH_P37	19	44771155	44771155	Frame_Shift_Ins	INS	-	AGAAATGGCAT	-	ZNF233	5AAAAAGAAAT	p.P93fs
XH_P37	19	44981054	44981054	Frame_Shift_Ins	INS	-	AACCATTTGAAT	-	ZNF180	TGATTACATTCA	p.P523fs
XH_P37	19	45259554	45259554	Frame_Shift_Ins	INS	-	CTATGCTCTAC	-	BCL3	477insSCCTATGC	p.Q159fs
XH_P37	19	45395699	45395699	Silent	SNP	G	A	G	TOMM40	c.G324A	p.G108G
XH_P37	19	45395701	45395701	Nonsense Mutation	INS	-	CCACCTGTAAA	-	TOMM40	327insCACCTG	09_S110delinsFLX
XH_P37	19	46308203	46308203	Silent	SNP	C	T	C	RSPH6A	c.G960A	p.S320S
XH_P37	19	47585552	47585552	Nonsense Mutation	INS	-	ATCTCATTTAA	-	ZC3H4	219insTGTAA	407_D408delinsCX
XH_P37	19	48789961	48789961	In Frame Ins	INS	-	TTTGACAATCCT	-	ZNF114	1insCAGTTTGA	80delinsPQFDNPS
XH_P37	19	49253840	49253840	Missense Mutation	SNP	A	C	C	FUT1	c.G699T	p.K233N
XH_P37	19	49253842	49253842	Nonsense Mutation	INS	-	ATGA	-	FUT1	.696_697insTCA	233_G234delinsSX
XH_P37	19	49377973	49377973	In Frame Ins	INS	-	CTCAGCTTCTCT	-	PPP1R15A	484insTCTCAGC	A495delinsVSASLS
XH_P37	19	49490529	49490529	Nonsense Mutation	INS	-	CCAACCTTCAT	-	GSY1	414insATGAAG	138_1139delinsKX
XH_P37	19	49841233	49841233	Missense Mutation	SNP	A	T	A	CD37	c.A190T	p.T64S
XH_P37	19	49841234	49841234	Nonsense Mutation	INS	-	ATAAGTCTCTGT	-	CD37	192insATAAGTC	p.T64delinsTX
XH_P37	19	49993778	49993778	Frame_Shift_Ins	INS	-	GG	-	RPL13A	c.18_19insGG	p.S6fs
XH_P37	19	49993779	49993779	In Frame Ins	INS	-	CTA	-	RPL13A	c.19_20insCTA	p.R7delinsPR
XH_P37	19	50155362	50155362	In Frame Del	DEL	CGCTCCCGCT	-	CCGCTCCCGCTC	SCAF1	c.1716_1727del	p.572_576del
XH_P37	19	50298990	50298990	In Frame Del	DEL	TAATGAACG	-	GTAATGAACGC	AP2A1	c.809_814del	p.270_272del
XH_P37	19	50549489	50549489	Frame_Shift_Ins	INS	-	CATTITCT	-	ZNF473	53_1754insCAT	p.G585fs
XH_P37	19	50549491	50549491	In Frame Ins	INS	-	TGTTGC	-	ZNF473	55_1756insTGT	G585delinsGCC
XH_P37	19	50905151	50905151	In Frame Ins	INS	-	AAATAC	-	POLD1	33_434insAAAT	p.A145delinsEIP
XH_P37	19	50945503	50945503	Frame_Shift_Ins	INS	-	A	-	MYBP2C	c.836dupA	p.E279fs
XH_P37	19	50945505	50945505	In Frame Ins	INS	-	TTTATTTTATTT	-	MYBP2C	ACAGCTTTATTT	79delinsEKTALFLFIYF
XH_P37	19	51769129	51769129	Frame_Shift_Ins	INS	-	A	-	SIGLECL1	c.121_122insA	p.P41fs
XH_P37	19	52496939	52496939	Frame_Shift_Ins	INS	-	ATGTATGCAGTG	-	ZNF615	05insTTCACTGC	p.G469fs
XH_P37	19	52498031	52498031	In Frame Ins	INS	-	GGAGAAAAA	-	ZNF615	2_313insTTTTTG	S105delinsFFSS
XH_P37	19	52498033	52498033	Missense Mutation	SNP	T	C	T	ZNF615	c.A311G	p.K104R
XH_P37	19	52538619	52538619	Frame_Shift_Ins	INS	-	TAGAAAAAAAC	-	ZNF432	3insGTGGTTT	p.H105fs
XH_P37	19	52826090	52826090	Nonsense Mutation	INS	-	AGGGCTTCTCTC	-	ZNF480	nsTTGTAAGGCT	p.H486delinsHLX
XH_P37	19	52869552	52869552	Frame_Shift_Ins	INS	-	ACATTTCATATC	-	ZNF610	nsCACTACATTCA	p.L264fs
XH_P37	19	52869553	52869553	In Frame Ins	INS	-	ATTTTCCTC	-	ZNF610	3_794insATTTT	V265delinsDFPL
XH_P37	19	52888373	52888373	In Frame Ins	INS	-	GTTTCTCTCCAG	-	ZNF880	TGTAAGGTTTCT	delinsLYICKVSLQCELV
XH_P37	19	52941714	52941714	Nonsense Mutation	INS	-	AATTCTGATTGA	-	ZNF534	nsGTGAATTCTG	p.V306delinsVX
XH_P37	19	53208438	53208438	Frame_Shift_Ins	INS	-	C	-	ZNF611	c.1869dupG	p.C624fs
XH_P37	19	53208440	53208440	Nonsense Mutation	INS	-	TCATCATAGAA	-	ZNF611	5TATGAATTCTA	23delinsMNSMMTX
XH_P37	19	53210021	53210021	Frame_Shift_Ins	INS	-	AA	-	ZNF611	c.286_287insTT	p.H96fs
XH_P37	19	53210023	53210023	Frame_Shift_Ins	INS	-	GTGGCAAAGC	-	ZNF611	.285insGCTTCT	p.S95fs
XH_P37	19	53385138	53385138	Frame_Shift_Ins	INS	-	AAGA	-	ZNF320	.240_241insTCT	p.H81fs
XH_P37	19	53385140	53385140	Nonsense Mutation	INS	-	GAAAGTTTTCAG	-	ZNF320	sGCAACTGAAA	80_H81delinsCNX
XH_P37	19	53855919	53855919	Missense Mutation	SNP	G	A	G	ZNF845	c.G1991A	p.R664K
XH_P37	19	53856266	53856266	Nonsense Mutation	INS	-	5AATTGCCTTGT	-	ZNF845	AGTATGAATTG	D781delinsSLQVLPCELX
XH_P37	19	53884277	53884277	Frame_Shift_Ins	INS	-	ATTGC	-	ZNF525	445_446insATTG	p.S149fs
XH_P37	19	53884279	53884279	Frame_Shift_Ins	INS	-	GTGCTGTGATG	-	ZNF525	48insTGTGCTGT	p.S149fs
XH_P37	19	53885191	53885191	Frame_Shift_Ins	INS	-	TATGA	-	ZNF525	359_1360insTA	p.S453fs
XH_P37	19	53885192	53885192	Frame_Shift_Ins	INS	-	TTCAAGGTTTGT	-	ZNF525	1361insTTTCA	p.L454fs
XH_P37	19	53912149	53912149	Frame_Shift_Ins	INS	-	GATGGCATGTA	-	ZNF765	1183insGATGG	p.Y394fs
XH_P37	19	53993842	53993842	Nonsense Mutation	INS	-	SCGTAAAGATTCT	-	ZNF813	AAAAGCGTAA	19delinsFRNTKAX
XH_P37	19	54969574	54969574	Nonsense Mutation	INS	-	GACTTGTAG	-	LENG8	4_2115insGACT	05_W706delinsATX
XH_P37	19	55174495	55174495	Frame_Shift_Ins	INS	-	G	-	LILRB4	c.10_11insG	p.T4fs
XH_P37	19	55451718	55451718	In Frame Ins	INS	-	GCAGGATGACA	-	NLRP7	9insAATGTCA	T157delinsNVILQF
XH_P37	19	55539129	55539129	Nonsense Mutation	INS	-	TTTCTTCTCTAG	-	GP6	insGGCTGAGGA	143_A144delinsSGX

XH_P37	19	55670544	55670544	Nonsense_Mutation	INS	-	TTATTCTAATCAT	-	DNAAF3	insGGAATGATT	71	E572delins	WEX
XH_P37	19	56009510	56009510	Frame_Shift_Ins	INS	-	TTCATCCACCTTT	-	SSC5D	1652insTTCATC	p.P551fs		
XH_P37	19	56189056	56189056	Nonsense_Mutation	INS	-	GAGCCCAGCTCT	-	EPN1	TCCAGGAGCCCA	p.G63delins	GX	
XH_P37	19	56538482	56538482	Frame_Shift_Ins	INS	-	ATAAATACAAA	-	NLRP5	4insTAATAAATA	p.L295fs		
XH_P37	19	56733059	56733059	Frame_Shift_Ins	INS	-	AAATTGCCAGGA	-	ZSCAN5A	CAAAACATCCTG	p.Q342fs		
XH_P37	19	57036597	57036597	Nonsense_Mutation	INS	-	ATTGGAAGCCTT	-	ZNF471	nsTTTGTTTGAA	13	I314delins	HVFX
XH_P37	19	57066145	57066145	Frame_Shift_Ins	INS	-	TATGGTTTTCTG	-	ZFP28	CATTATATGGT	p.Q664fs		
XH_P37	19	57867553	57867560	Frame_Shift_Del	DEL	GAACACCA	-	GAACACCA	ZNF304	c.316_323del	p.E106fs		
XH_P37	19	57910039	57910039	Frame_Shift_Ins	INS	-	GTGCATGTGTG	-	ZNF548	385insGTGCAT	p.E128fs		
XH_P37	19	57910041	57910041	Missense_Mutation	SNP	A	C	A	ZNF548	c.A386C	p.N129T		
XH_P37	19	57955666	57955666	Missense_Mutation	SNP	T	A	T	ZNF749	c.T889A	p.C297S		
XH_P37	19	57955667	57955667	Nonsense_Mutation	INS	-	AAAGC	-	ZNF749	890_891insAAA	C297_S298delins	X	
XH_P37	19	57956369	57956369	Frame_Shift_Ins	INS	-	TCTCATGCTGAA	-	ZNF749	insATTTTCTCAT	p.G531fs		
XH_P37	19	57985368	57985368	Frame_Shift_Ins	INS	-	GTITTTTAATCAT	-	ZNF772	AGAGCTATGATT	p.K136fs		
XH_P37	19	58049281	58049281	In_Frame_Ins	INS	-	CCCTGCTTC	-	ZNF549	D_871insCCCTG	S290delins	SPCF	
XH_P37	19	58132060	58132060	In_Frame_Ins	INS	-	TATCCCTCTCTAA	-	ZNF134	74insTTATCCCT	L191delins	LSLLK	
XH_P37	19	58189550	58189550	Nonsense_Mutation	INS	-	SACATCTCTTAA	-	ZSCAN4	0insTGACATCTC	Q193delins	QX	
XH_P37	19	58216349	58216349	Splice_Site	INS	-	CTCTTTTCTCTA	-	ZNF154	-	-		
XH_P37	19	58232476	58232476	Nonsense_Mutation	INS	-	SGAAACACACAC	-	ZNF671	nsACAAGTGTGT	228_D229delins	X	
XH_P37	19	58370353	58370353	Frame_Shift_Ins	INS	-	TGGTGTGTGATGA	-	ZNF587	insTCTGTGTGCT	p.A193fs		
XH_P37	19	58421124	58421124	Frame_Shift_Ins	INS	-	TGTAATTAGTT	-	ZNF417	519insAACTAA	p.E173fs		
XH_P37	19	58563951	58563951	In_Frame_Ins	INS	-	TACAAAAAATAA	-	ZSCAN1	nsTTATACAAAA	187delins	LQIKINN	
XH_P37	19	58578567	58578567	Nonsense_Mutation	INS	-	SGTTGATGTGGG	-	ZNF135	TATTGGTTGAT	51_R252delins	VIGX	
XH_P37	19	58945011	58945011	Frame_Shift_Ins	INS	-	AGATTCTATACC	-	ZNF132	insCTCAGGTAT	p.K600fs		
XH_P37	20	168713	168713	Nonsense_Mutation	SNP	G	T	G	DEFB128	c.C96A	p.C32X		
XH_P37	20	168714	168714	Frame_Shift_Ins	INS	-	TGTGAACCTTG	-	DEFB128	95insCAAGTTC	p.C32fs		
XH_P37	20	744602	744602	Missense_Mutation	SNP	G	T	G	SLC52A3	c.C613A	p.P205T		
XH_P37	20	1552540	1552540	Nonsense_Mutation	INS	-	AATTCCTAACTG	-	SIRPB1	nsAACACAGTTAG	Q194delins	NTVRNX	
XH_P37	20	2097743	2097743	Frame_Shift_Ins	INS	-	CAATATGGTT	-	STK35	1325insCAATA	p.L442fs		
XH_P37	20	2820442	2820442	In_Frame_Ins	INS	-	ACAGGTGTAAT	-	PCED1A	17insTTATTACAG	G39delins	GYTCQ	
XH_P37	20	3274887	3274887	Silent	SNP	G	A	G	C20orf194	c.C2136T	p.F712F		
XH_P37	20	3627469	3627469	Frame_Shift_Ins	INS	-	AAAAAGG	-	ATRN	55_4266insAAA	p.P1422fs		
XH_P37	20	3627471	3627471	Missense_Mutation	SNP	G	A	G	ATRN	c.G426T	p.A1423T		
XH_P37	20	3686595	3686595	Frame_Shift_Ins	INS	-	ACAGAAAC	-	SIGLEC1	1_502insGTTC	p.Q168fs		
XH_P37	20	5157373	5157373	Nonsense_Mutation	INS	-	AT	-	CD52	c.371_372insAT	124_F125delins	X	
XH_P37	20	5157374	5157374	Frame_Shift_Ins	INS	-	TCAATTAACCTTT	-	CD52	3insTTCAATTA	p.W124fs		
XH_P37	20	5904228	5904228	In_Frame_Ins	INS	-	TGTATT	-	CHGB	138_1439insTGT	P480delins	VS	
XH_P37	20	7894965	7894965	Silent	SNP	G	A	G	HAO1	c.C391T	p.L131L		
XH_P37	20	7894966	7894966	Frame_Shift_Ins	INS	-	AAACAGAAATG	-	HAO1	0insGGCCATTTC	p.Q130fs		
XH_P37	20	7963266	7963266	Missense_Mutation	SNP	G	T	G	TMX4	c.C682A	p.Q228K		
XH_P37	20	7963267	7963267	Frame_Shift_Ins	INS	-	ATTTGAATCATC	-	TMX4	nsAAAAAGATGAT	p.E227fs		
XH_P37	20	8698448	8698448	Frame_Shift_Ins	INS	-	TG	-	PLCB1	1466_1467insT	p.T489fs		
XH_P37	20	8698449	8698449	Nonsense_Mutation	INS	-	AAACTCTTAGTG	-	PLCB1	nsTCATTAAACTC	9_Y490delins	TSLSNX	
XH_P37	20	9546971	9546971	Frame_Shift_Ins	INS	-	AATACTT	-	PAK5	50_1051insAAG	p.P351fs		
XH_P37	20	9546972	9546972	Nonsense_Mutation	INS	-	GCCCAACTT	-	PAK5	9_1050insAAGT	P350_P351delins	X	
XH_P37	20	10639121	10639121	Missense_Mutation	SNP	T	C	T	JAG1	c.A689G	p.N230S		
XH_P37	20	13071794	13071794	Frame_Shift_Ins	INS	-	CCAAA	-	SPTLC3	671_672insCCA	p.A224fs		
XH_P37	20	13071795	13071795	Nonsense_Mutation	INS	-	ATTGTAGAATGG	-	SPTLC3	CAACTATTGTAG	4_M225delins	AQLLX	
XH_P37	20	13767978	13767978	Nonsense_Mutation	INS	-	TATTCTTAAAAA	-	NDUFAF5	nsTAAATATTCTT	D81_R82delins	DX	
XH_P37	20	13767980	13767980	Missense_Mutation	SNP	G	A	G	NDUFAF5	c.G245A	p.R82H		
XH_P37	20	13850227	13850227	Frame_Shift_Ins	INS	-	ATAACAAACATC	-	SEL1L2	7insTTTGATGTT	p.E393fs		
XH_P37	20	13899716	13899716	In_Frame_Ins	INS	-	AAA	-	SEL1L2	c.336_337insTT	M113delins	FM	
XH_P37	20	13899717	13899717	Frame_Shift_Ins	INS	-	TATTGTGTT	-	SEL1L2	5_336insAAACA	p.K112fs		
XH_P37	20	18296814	18296814	Missense_Mutation	SNP	G	A	G	ZNF133	c.G1262A	p.C421Y		
XH_P37	20	20171995	20171995	Nonsense_Mutation	INS	-	TGAGATATTATT	-	CFAP61	ACCCTATGAGA	108_L509delins	PTLX	
XH_P37	20	20180491	20180491	Missense_Mutation	SNP	A	T	A	CFAP61	c.A1877T	p.Y626F		
XH_P37	20	20180493	20180493	Frame_Shift_Ins	INS	-	CAGAACCCCTAC	-	CFAP61	sAGTTCAGCAAC	p.P627fs		
XH_P37	20	23064587	23064587	Frame_Shift_Ins	INS	-	AAATCCCAATGT	-	CD93	59insTCACATTG	K653delins	CHIGIX	
XH_P37	20	23666542	23666542	Frame_Shift_Ins	INS	-	CTCTAAT	-	CS4	4_415insATTAG	p.Q139fs		
XH_P37	20	23666544	23666544	Missense_Mutation	SNP	C	G	C	CS4	c.G413C	p.C138S		
XH_P37	20	29965236	29965236	In_Frame_Ins	INS	-	CAA	-	DEFB119	c.67_68insTTG	p.R23delins	LG	
XH_P37	20	29965237	29965237	In_Frame_Ins	INS	-	ACTACC	-	DEFB119	66_67insGGTAC	P.R23delins	GSR	
XH_P37	20	31017233	31017233	Frame_Shift_Ins	INS	-	AGCTACAAAAT	-	ASXL1	TTCCAAGCTACA	p.L188fs		
XH_P37	20	31017235	31017235	Splice_Site	SNP	G	T	G	ASXL1	-	-		
XH_P37	20	31023461	31023461	Frame_Shift_Ins	INS	-	AA	-	ASXL1	2946_2947insA	p.K982fs		
XH_P37	20	31814762	31814762	Nonsense_Mutation	INS	-	ATCATATAA	-	BPIFA3	D_541insATCAT	p.L180delins	LIX	
XH_P37	20	32005661	32005661	Frame_Shift_Ins	INS	-	TGGTGTGCTTT	-	SNTA1	565insAAAGCA	p.S189fs		
XH_P37	20	32194829	32194829	Frame_Shift_Ins	INS	-	CAACA	-	CBFA2T2	102_103insCAA	p.S34fs		
XH_P37	20	32194831	32194831	Frame_Shift_Ins	INS	-	TGGAACCTGTG	-	CBFA2T2	105insTGGAA	p.S35fs		
XH_P37	20	32664866	32664866	Missense_Mutation	SNP	G	A	G	RALY	c.G643A	p.G215S		
XH_P37	20	33330414	33330414	Frame_Shift_Ins	INS	-	TGATCAACAA	-	NCOA6	3646insTTGTT	p.S1216fs		
XH_P37	20	33331045	33331045	Frame_Shift_Ins	INS	-	CATGGTCA	-	NCOA6	4_3015insTGAC	p.P1005fs		
XH_P37	20	34292634	34292634	Missense_Mutation	SNP	G	A	G	RBM39	c.C1382T	p.A461V		
XH_P37	20	34292635	34292635	Frame_Shift_Ins	INS	-	TGGTTCCA	-	RBM39	0_1381insTGG	p.A461fs		
XH_P37	20	35060845	35060845	Frame_Shift_Ins	INS	-	GCTGC	-	DLGAP4	725_726insGCT	p.F242fs		
XH_P37	20	39795473	39795473	Frame_Shift_Ins	INS	-	GACGCGC	-	PLCG1	75_2276insGAC	p.E759fs		
XH_P37	20	43530427	43530427	In_Frame_Ins	INS	-	TCACCTTTTATCC	-	YWHAB	insAGCTCACTTT	R85delins	QLTFHC	
XH_P37	20	43727197	43727197	Silent	SNP	C	A	C	KCN51	c.G216T	p.P72P		
XH_P37	20	43836290	43836290	In_Frame_Ins	INS	-	TGTTGATTG	-	SEMG1	2_353insTGTGT	K.118delins	MCIE	
XH_P37	20	43836292	43836292	Nonsense_Mutation	INS	-	AAAATCGCCTTT	-	SEMG1	sTAGAAAAAACTG	118_S119delins	KX	
XH_P37	20	43836540	43836540	Nonsense_Mutation	INS	-	CTCTTTATGGTG	-	SEMG1	sTTGCTCTCTTT	A201delins	CLLYGVX	
XH_P37	20	47569340	47569340	Nonsense_Mutation	INS	-	AACATGGTGATT	-	ARFGEF2	nsTTAAACTAGG	K174delins	KLNX	
XH_P37	20	47587811	47587811	Frame_Shift_Ins	INS	-	AAAATGTCAAAC	-	ARFGEF2	AAGAAAAAATG	p.P449fs		
XH_P37	20	47706129	47706129	Frame_Shift_Ins	INS	-	CAAAGCTCCC	-	CSE1L	1860insCAAG	p.N620fs		
XH_P37	20	47706131	47706131	Missense_Mutation	SNP	G	C	G	CSE1L	c.G1861C	p.D621H		
XH_P37	20	47887996	47887996	Nonsense_Mutation	INS	-	AATCTAACTCCC	-	ZNFX1	3insAAGGAAGT	P118delins	QGSGX	
XH_P37	20	49366531	49366531	Frame_Shift_Ins	INS	-	TGTGGCTTTTTT	-	PARD6B	26insATGTGGC	p.L209fs		
XH_P37	20	49366533	49366533	Frame_Shift_Ins	INS	-	TG	-	PARD6B	c.627_628insTG	p.L209fs		
XH_P37	20	50052291	50052291	Nonsense_Mutation	INS	-	TGACACCTTATT	-	NFATC2	sAATATAATAAG	S99_Q600delins	QIX	
XH_P37	20	50782537	50782537	Frame_Shift_Ins	INS	-	AGGCCCTTGAA	-	ZFP64	314insTTCAAA	p.H105fs		
XH_P37	20	52835582	52835582	Missense_Mutation	SNP	G	A	G	PFND4	c.G298A	p.A100T		
XH_P37	20	56191330	56191330	Missense_Mutation	SNP	C	A	C	ZBP1	c.G229T	p.G77C		
XH_P37	20	56191331	56191331	Nonsense_Mutation	INS	-	TAACAATTATAA	-	ZBP1	228insTTATAAT	E76delins	DYNCX	
XH_P37	20	57767948	57767948	Frame_Shift_Ins	INS	-	CACAT	-	ZNF831	874_1875insCA	p.D625fs		
XH_P37	20	60770997	60770997	In_Frame_Ins	INS	-	CAACACTCCAA	-	MTG2	5insCTCAACAC	115delins	ISTLQG	
XH_P37	20	60864350	60864350	In_Frame_Ins	INS	-	AAATTCAAT	-	OSBPL2	7_1178insAAAT	R393delins	QIQ	
XH_P37	20	62229177	62229177	Missense_Mutation	SNP	G	A	G	GMEB2	c.C394T	p.H132Y		
XH_P37	20	62626447	62626447	Splice_Site	INS	-	CTTTTGTGTTTGA	-	PRPF6	-	-		

XH_P37	20	62648197	62648197	Frame_Shift_Ins	INS	-	CATCAGCACAA	-	PRPF6	547insACATCAG	p.549fs
XH_P37	21	10916450	10916450	Nonsense_Mutation	INS	-	TTTCCATCCACA	-	TPTE	AAATGTGGTGA	51_V262delinsPNWX
XH_P37	21	15988317	15988317	Frame_Shift_Ins	INS	-	ACAAATCTAGAA	-	LOC388813	CCACATCTAGAT	p.N31fs
XH_P37	21	30331831	30331831	Frame_Shift_Ins	INS	-	GGATGTTATTCT	-	LTN1	ATCTTTAGAAAT	p.L880fs
XH_P37	21	31692273	31692273	Frame_Shift_Ins	INS	-	CTGCCTCA	-	KRTAP26-1	80_81insTGAGC	p.I27fs
XH_P37	21	31768435	31768435	Nonsense_Mutation	INS	-	ATTGCAGTTAA	-	KRTAP13-1	TGTCATTGCAGT	512delinsFVIAVNX
XH_P37	21	31798176	31798176	In_Frame_Ins	INS	-	CTTGCCTGACT	-	KRTAP13-3	insATAGTCAGG	L19delinsIVRQEL
XH_P37	21	32537277	32537277	Splice_Site	INS	-	ATGAAATAAAAT	-	TIAM1	.	.
XH_P37	21	33064733	33064733	Nonsense_Mutation	INS	-	TTTATAGATGTG	-	SCAF4	498insTCACATC	D00_D501delinsSHLX
XH_P37	21	33064734	33064734	Frame_Shift_Ins	INS	-	TAGAATTTAGG	-	SCAF4	1497insCCTAA	p.Q499fs
XH_P37	21	33069022	33069022	Frame_Shift_Ins	INS	-	G	-	SCAF4	c.773dupC	p.A258fs
XH_P37	21	33069024	33069024	Nonsense_Mutation	INS	-	TGTTAGTTTTTT	-	SCAF4	AAAAAAAAAAAA	258_V259delinsX
XH_P37	21	33747751	33747751	Nonsense_Mutation	INS	-	ACTAGAAGGTTA	-	URB1	nsTCTTTAACCT	36_I237delinsSLTFX
XH_P37	21	33747753	33747753	Frame_Shift_Ins	INS	-	AG	-	URB1	c.703_704insCT	p.D235fs
XH_P37	21	34056348	34056348	In_Frame_Ins	INS	-	TGA	-	SYNJ1	1199_1200insTp	E400delinsDQ
XH_P37	21	34056350	34056350	Frame_Shift_Ins	INS	-	CATATCTCTTTA	-	SYNJ1	8insCCTAAAGAA	p.E400fs
XH_P37	21	34166584	34166584	In_Frame_Ins	INS	-	CACCTGAATACCT	-	C21orf62	149insAGGTATT	R50delinsQVFSG
XH_P37	21	34804524	34804524	Nonsense_Mutation	INS	-	CTCCTTTAACAT	-	IFNGR2	CTTTTCTCCTTT	P1_L202delinsNFLXL
XH_P37	21	34926657	34926657	In_Frame_Ins	INS	-	TCATATTTATTA	-	SON	CAACATCATAT	7delinsDKSTSYLLTKLR
XH_P37	21	34927415	34927415	Missense_Mutation	SNP	C	G	C	SON	c.C5878G	p.P1960A
XH_P37	21	34958436	34958436	Nonsense_Mutation	INS	-	VTGTGTTAAAGT	-	DONSON	TTTGTACTTTTA	L153delinsSHLCYFNFX
XH_P37	21	35469580	35469580	Nonsense_Mutation	INS	-	BATTAAACATCTT	-	SLCSA3	CAACAGATTAA	V69delinsTNRLTSSGX
XH_P37	21	37742058	37742058	In_Frame_Ins	INS	-	TGCAGATTATC	-	MORC3	nsTCATCTGCAG	727delinsICRIFGG
XH_P37	21	38877705	38877705	Nonsense_Mutation	INS	-	TTTAAATATATA	-	DYRK1A	insTATGTTTAA	15_D416delinsKYVX
XH_P37	21	38877707	38877707	Frame_Shift_Ins	INS	-	GG	-	DYRK1A	1247_1248insG	p.D416fs
XH_P37	21	38877709	38877709	Frame_Shift_Ins	INS	-	T	-	DYRK1A	c.1250dupT	p.L417fs
XH_P37	21	40636904	40636904	Nonsense_Mutation	INS	-	TTTCATTTTTCTA	-	BRWD1	572insCTAGAAA	524_5525delinsFX
XH_P37	21	43282118	43282118	Splice_Site	INS	-	ACTCACTCTCCT	-	PRDM15	.	.
XH_P37	21	43413723	43413723	Frame_Shift_Ins	INS	-	AAAAAGAAATGC	-	ZBTB21	nsCACTGCATT	p.T161fs
XH_P37	21	43704749	43704749	Frame_Shift_Ins	INS	-	GTTCGATTTTAT	-	ABCG1	15insTGTGTGCA	p.T272fs
XH_P37	21	44514767	44514767	Frame_Shift_Ins	INS	-	TTCCAAAAAATA	-	U2AF1	80insTTTTTTTT	p.M160fs
XH_P37	21	45472239	45472239	Frame_Shift_Ins	INS	-	GTCTC	-	TRAPPC10	364_365insGTC	p.D122fs
XH_P37	21	45472241	45472241	Missense_Mutation	SNP	C	G	C	TRAPPC10	c.C366G	p.D122E
XH_P37	21	45548025	45548025	Frame_Shift_Ins	INS	-	AAATTAAGCA	-	PWP2	2354insAAATT	p.G785fs
XH_P37	21	46229000	46229000	Frame_Shift_Ins	INS	-	CTCACTGTAAAG	-	SUMO3	298insCTTACAC	p.D100fs
XH_P37	21	46271526	46271526	Frame_Shift_Ins	INS	-	GGCTTTTTTATA	-	PTTG1IP	35insGTATAAAA	p.K62fs
XH_P37	21	47737264	47737264	Splice_Site	INS	-	TTACATTTCA	-	C21orf58	.	.
XH_P37	22	17445751	17445751	In_Frame_Ins	INS	-	TTTGGTCTCCTA	-	GAB4	81insAATAGGA	461delinsNRRPNH
XH_P37	22	18020327	18020327	In_Frame_Ins	INS	-	TTG	-	CECR2	1233_1234insT	p.G411delinsGL
XH_P37	22	18020328	18020328	Frame_Shift_Ins	INS	-	CTTCTAGGTAT	-	CECR2	1235insCTTTCA	p.K412fs
XH_P37	22	18364038	18364038	Frame_Shift_Ins	INS	-	CCCTCAGGAT	-	MICAL3	2273insATCCTC	p.P758fs
XH_P37	22	19223350	19223350	Missense_Mutation	SNP	C	T	C	CLTC1	c.G383A	p.G280S
XH_P37	22	19223352	19223352	Nonsense_Mutation	INS	-	TAGTTCCTGTTA	-	CLTC1	nsTTAATAACAG	G280delinsFNNRNVX
XH_P37	22	19423320	19423320	In_Frame_Ins	INS	-	ACACAA	-	MRPL40	24_325insACAA	L108delinsLTQ
XH_P37	22	19423322	19423322	Missense_Mutation	SNP	A	T	A	MRPL40	c.A326T	p.E109V
XH_P37	22	19808873	19808873	Frame_Shift_Ins	INS	-	CAGCGCTT	-	GNB1L	5_6insAAGCGC	p.T2fs
XH_P37	22	20073496	20073496	Frame_Shift_Ins	INS	-	GAACCACTGCC	-	DGCR8	TTTAGAACACAC	p.D4fs
XH_P37	22	20109827	20109827	Frame_Shift_Ins	INS	-	AGGT	-	RANBP1	424_425insAG	p.P142fs
XH_P37	22	20109829	20109829	Nonsense_Mutation	INS	-	TCTGAATTCC	-	RANBP1	427insTCTTGA	442_E143delinsPSX
XH_P37	22	20761238	20761238	Nonsense_Mutation	INS	-	ATTTTCTGATGT	-	ZNF74	sAGTGGATTTTC	558_569delinsEWIFX
XH_P37	22	22843355	22843355	Frame_Shift_Ins	INS	-	SACCTGTGGGCC	-	ZNF280B	TGGTGGGGCCA	p.K123fs
XH_P37	22	22843642	22843642	Frame_Shift_Ins	INS	-	AG	-	ZNF280B	c.81_82insCT	p.A28fs
XH_P37	22	22843644	22843644	Frame_Shift_Ins	INS	-	CTATTATTATG	-	ZNF280B	GGCTCAATAATA	p.D27fs
XH_P37	22	24038845	24038845	Frame_Shift_Ins	INS	-	CT	-	RLG4	.1131_1132insC	p.R377fs
XH_P37	22	24038846	24038846	Frame_Shift_Ins	INS	-	TT	-	RLG4	.1132_1133insT	p.V378fs
XH_P37	22	24226079	24226079	Frame_Shift_Ins	INS	-	GTAGTTTTATT	-	SLC2A11	.1025insGTAG	p.G342fs
XH_P37	22	24468371	24468371	Frame_Shift_Ins	INS	-	CTGT	-	CABIN1	393_2394insCT	p.W798fs
XH_P37	22	24468373	24468373	In_Frame_Ins	INS	-	CACCTCTGCG	-	CABIN1	5_2396insCACT	p.I799delinsTLL
XH_P37	22	24717350	24717350	Frame_Shift_Ins	INS	-	A	-	SPECC1L	c.403dupA	p.Q134fs
XH_P37	22	24717352	24717352	Nonsense_Mutation	INS	-	AATTATCAAGGA	-	SPECC1L	CTTTTAATTATC	T135delinsRSFFX
XH_P37	22	25603123	25603123	Frame_Shift_Ins	INS	-	TGCTCAATCTCC	-	CRYBB3	1insCCTGCCTAC	p.V194fs
XH_P37	22	26902819	26902819	Frame_Shift_Ins	INS	-	TTCTGTACACTG	-	TFIP11	92insAACGTGTG	p.L64fs
XH_P37	22	29176959	29176959	Missense_Mutation	SNP	T	C	T	CCDC17	c.T209C	p.I70T
XH_P37	22	29754771	29754771	In_Frame_Ins	INS	-	ACCCTCTGA	-	AP1B1	5_469insTCAGAG	E157delinsSEGE
XH_P37	22	29885211	29885211	Missense_Mutation	SNP	G	C	G	NEFH	c.G1582C	p.A528P
XH_P37	22	30074221	30074221	Frame_Shift_Ins	INS	-	GG	-	NF2	1234_1235insG	p.I412fs
XH_P37	22	30074222	30074222	Frame_Shift_Ins	INS	-	AACAATATCAAA	-	NF2	236insAAACAAT	p.I412fs
XH_P37	22	30221716	30221716	In_Frame_Ins	INS	-	TCTTTCACTGGA	-	ASCC2	nsGGATCCAAGT	G45delinsKDPVKEV
XH_P37	22	30403260	30403260	Frame_Shift_Ins	INS	-	AAACAACAAAC	-	MTMR3	830insAAACAAC	p.T277fs
XH_P37	22	32109168	32109168	Frame_Shift_Ins	INS	-	CAAAAGATCAG	-	PRR14L	insAAGGCTGAT	p.S1553fs
XH_P37	22	32110141	32110141	Frame_Shift_Ins	INS	-	ACAGCGTATGTA	-	PRR14L	684insGTACAT	p.S1228fs
XH_P37	22	32134814	32134814	Frame_Shift_Ins	INS	-	GTGTGTGAAGA	-	PRR14L	AGGTTTCTTCAC	p.V11fs
XH_P37	22	32239107	32239107	Nonsense_Mutation	INS	-	GCAGATTTTCT	-	DEPDC5	9insTTGGCAGAT	770delinsVGRFCX
XH_P37	22	32352372	32352372	Missense_Mutation	SNP	T	G	T	YWHAH	c.T334G	p.C112G
XH_P37	22	32352373	32352373	Nonsense_Mutation	INS	-	ATTACGAACAG	-	YWHAH	86insAATTACGA	112_N113delinsX
XH_P37	22	32756799	32756799	Frame_Shift_Ins	INS	-	A	-	RFPL3	c.934_935insA	p.R312fs
XH_P37	22	32756800	32756800	In_Frame_Ins	INS	-	AATCCAAGC	-	RFPL3	5_936insAATCCA	R312delinsRIOA
XH_P37	22	35942994	35942994	Frame_Shift_Ins	INS	-	T	-	RASD2	c.138_139insT	p.D46fs
XH_P37	22	35942996	35942996	Frame_Shift_Ins	INS	-	GTTTTCTGTCT	-	RASD2	141insGTTTTTC	p.Q47fs
XH_P37	22	37469658	37469658	In_Frame_Ins	INS	-	CAACATCAATC	-	TMPRSS6	insGGAGATTGAG	90delinsGRLMVAQ
XH_P37	22	37770540	37770540	Missense_Mutation	SNP	G	C	G	ELFN2	c.C1035G	p.I345M
XH_P37	22	37904577	37904577	Missense_Mutation	SNP	G	A	G	CARD10	c.C1022T	p.A341V
XH_P37	22	37966343	37966343	Frame_Shift_Ins	INS	-	GG	-	LGALS2	c.325_326insCC	p.L109fs
XH_P37	22	37966345	37966345	Frame_Shift_Ins	INS	-	AGCAAAACAAA	-	LGALS2	nsATTATTTTGT	p.R108fs
XH_P37	22	38021845	38021845	Missense_Mutation	SNP	C	T	C	GGA1	c.C982T	p.P328S
XH_P37	22	38021846	38021846	Frame_Shift_Ins	INS	-	TTGGCATATGAT	-	GGA1	84insTTTGGCAT	p.P328fs
XH_P37	22	38130788	38130788	Frame_Shift_Ins	INS	-	AGGTCCTCTGT	-	TRIOBP	4446insAGGTC	p.R1482fs
XH_P37	22	38134648	38134648	Splice_Site	SNP	G	T	G	TRIOBP	.	.
XH_P37	22	38134649	38134649	Nonsense_Mutation	INS	-	SATCCATCACAT	-	TRIOBP	5108insGATCCA	703_Q1704delinsX
XH_P37	22	40660979	40660979	Frame_Shift_Ins	INS	-	ACCTTGTCCAG	-	TNRC6B	6insTCACCTTGT	p.S249fs
XH_P37	22	40661168	40661168	Frame_Shift_Ins	INS	-	AGAGTGCTCTT	-	TNRC6B	935insAGAGTG	p.P312fs
XH_P37	22	40661374	40661374	Frame_Shift_Ins	INS	-	TCCTAGTCCATT	-	TNRC6B	insAATTTCCTAG	p.S380fs
XH_P37	22	41257741	41257741	Silent	SNP	G	A	G	DNAJB7	c.C258T	p.Y86Y
XH_P37	22	42606518	42606518	Frame_Shift_Ins	INS	-	CAATCATCAATG	-	TCF20	94insAGCATTTGA	p.T1598fs
XH_P37	22	43471550	43471550	In_Frame_Ins	INS	-	TTTTCTTAAGG	-	TTL1	AAAACCTTAAG	15delinsKNLKEKCV
XH_P37	22	46657960	46657960	Frame_Shift_Ins	INS	-	GTCAATTTTGTG	-	PKDREJ	5AAGAGAGACAA	p.P420fs
XH_P37	22	46704403	46704403	In_Frame_Ins	INS	-	TTTAAAGGAAA	-	GTSE1	6insCATTTAAG	109delinsAFKGKT
XH_P37	22	46704486	46704486	Nonsense_Mutation	INS	-	TTACTGAATGTG	-	GTSE1	9insCTTTACTGAG	R136delinsRLYX

XH_P37	22	50181432	50181432	Frame_Shift_Ins	INS	-	ACCAAAACCTT	-	BRD1	2448insAAGGT	p.N816fs
XH_P37	22	50682362	50682362	Frame_Shift_Ins	INS	-	TTTCATCTCTCTC	-	TUBGCP6	insCCGAGAGAG	p.Q176fs
XH_P37	X	3238869	3238869	In_Frame_Ins	INS	-	TCCAAGAAATTC	-	MXRA5	sAATGAGGAAT	19delinsVMRNSWTG
XH_P37	X	3240206	3240206	Frame_Shift_Ins	INS	-	AAACATCGATA	-	MXRA5	s520insATATCG	p.F1174fs
XH_P37	X	5811441	5811441	In_Frame_Ins	INS	-	GAGACTCAC	-	NLGN4X	7_1868insGTGA	Y623delinsCESH
XH_P37	X	11206955	11206955	Nonsense_Mutation	INS	-	CA	-	ARHGAP6	c.429_430insTG	144_K145delinsX
XH_P37	X	11779666	11779666	Nonsense_Mutation	INS	-	AAATCCATGTAT	-	MSL3	ACTGCAATTC	E133delinsINCNSMYFX
XH_P37	X	12938177	12938177	Missense_Mutation	SNP	G	A	G	TLR8	c.G1018A	p.E340K
XH_P37	X	12938178	12938178	In_Frame_Ins	INS	-	ATAATGTAAAT	-	TLR8	nsTCTAGTAATG	40delinsDLVMLNLS
XH_P37	X	12939855	12939855	Frame_Shift_Ins	INS	-	GAACG	-	TLR8	s96_2697insGA	p.N899fs
XH_P37	X	13636104	13636104	Frame_Shift_Ins	INS	-	TCCTTCACAGAA	-	EGFL6	s5insCTTCTTCA	p.D345fs
XH_P37	X	14929488	14929488	Nonsense_Mutation	INS	-	AGACTTAATTAG	-	MOSPD2	4insACAGACTTA	5_L216delinsNRLNX
XH_P37	X	15827376	15827376	Nonsense_Mutation	INS	-	ATAAACATTGT	-	ZRSR2	CAAAGATAAAC	64_M165delinsVYX
XH_P37	X	16887709	16887709	Frame_Shift_Ins	INS	-	GGAAAAAATAG	-	RBBP7	nsAGCCTATTTT	p.R19fs
XH_P37	X	17705872	17705872	Frame_Shift_Ins	INS	-	TTACTCTGTCC	-	NHS	6insTTTACTCT	p.N15fs
XH_P37	X	17744883	17744883	Missense_Mutation	SNP	G	T	G	NHS	c.G2063T	p.R688M
XH_P37	X	17745550	17745550	Frame_Shift_Ins	INS	-	AGTAAAGA	-	NHS	0_2731insAGTA	p.L910fs
XH_P37	X	17745551	17745551	Nonsense_Mutation	INS	-	TGAACCTCCAA	-	NHS	732insCTTGAAC	p.H911delinsPX
XH_P37	X	17746889	17746889	Nonsense_Mutation	INS	-	AAATGAGAGAG	-	NHS	TTTTAAAAATGA	50_H1251delinsIFX
XH_P37	X	18221732	18221732	Nonsense_Mutation	INS	-	A	-	BEND2	c.795_796insT	E266_S267delinsX
XH_P37	X	18221733	18221733	In_Frame_Ins	INS	-	AGAAATAATAC	-	BEND2	CTCTCTGATTAT	5delinsRVSLCIISYNYI
XH_P37	X	18956867	18956867	Frame_Shift_Ins	INS	-	TCGGTTATCTG	-	PHKA2	GGGAACAGATA	p.D307fs
XH_P37	X	20069036	20069036	Frame_Shift_Ins	INS	-	TTGTGAAAAG	-	MAP7D2	624insCTTTTC	p.E208fs
XH_P37	X	20069038	20069038	Frame_Shift_Ins	INS	-	TT	-	MAP7D2	c.621_622insAA	p.E208fs
XH_P37	X	20213200	20213200	Nonsense_Mutation	INS	-	AAGCTTTTATTG	-	RPS6KA3	CTAAACAATAAA	V131delinsLKNKSF
XH_P37	X	21550092	21550092	Frame_Shift_Ins	INS	-	CAATTGTGAAT	-	CNKSR2	sCAGGCAAAAT	p.N355fs
XH_P37	X	21581569	21581569	In_Frame_Ins	INS	-	TTCTTTCTCAAT	-	CNKSR2	1371insTCTCTT	H457delinsHSFSI
XH_P37	X	21581571	21581571	Splice_Site	INS	-	TGC	-	CNKSR2	.	.
XH_P37	X	21675796	21675796	In_Frame_Del	DEL	CAGTGTCACT	-	CCAGTGTCACTG	KLHL34	c.79_111del	p.27_37del
XH_P37	X	21863337	21863337	Nonsense_Mutation	INS	-	TTTGATCTTGTG	-	MBTPS2	ATTGTTTGTGCT	p.F91delinsFTX
XH_P37	X	22291465	22291465	In_Frame_Ins	INS	-	CAGGCATCT	-	ZNF645	7_358insCAGGC	Q119delinsQQAS
XH_P37	X	22291467	22291467	In_Frame_Ins	INS	-	TTCATATTC	-	ZNF645	9_360insTTCAT	C120delinsCSYS
XH_P37	X	23019726	23019726	Frame_Shift_Ins	INS	-	ATTTTGTCTCACT	-	DDX53	sATTATATTTTG	p.I518fs
XH_P37	X	24228695	24228695	Frame_Shift_Ins	INS	-	SGTGTTCGGGAT	-	ZFX	4insAGGTTGTC	p.A311fs
XH_P37	X	24229461	24229461	Frame_Shift_Ins	INS	-	SGAAGATCCTTT	-	ZFX	0insATGGAAGA	p.M567fs
XH_P37	X	24330133	24330133	Frame_Shift_Ins	INS	-	CTCCT	-	SUPT20HL2	99_1300insAG	p.Q434fs
XH_P37	X	24330134	24330134	Silent	SNP	A	G	A	SUPT20HL2	c.T1299C	p.S433S
XH_P37	X	24732779	24732779	Missense_Mutation	SNP	C	A	C	POLA1	c.C455A	p.T152N
XH_P37	X	24742515	24742515	Frame_Shift_Ins	INS	-	C	-	POLA1	c.1264_1265ins	p.E422fs
XH_P37	X	24742516	24742516	Frame_Shift_Ins	INS	-	AAAGAAAATATG	-	POLA1	ATACACAAAGAA	p.E422fs
XH_P37	X	24757629	24757629	Silent	SNP	G	A	G	POLA1	c.G2178A	p.R726R
XH_P37	X	24757630	24757630	In_Frame_Ins	INS	-	GACACTGAGAA	-	POLA1	80insCAGACAG	727delinsADTNI
XH_P37	X	26212634	26212634	In_Frame_Ins	INS	-	CTTGGAATTTTC	-	MAGEB6	672insCTTGGAC	C224delinsS
XH_P37	X	27999010	27999010	Frame_Shift_Ins	INS	-	GCCAGTACTGAA	-	DCAF8L1	42insGTTTCAGTA	p.S148fs
XH_P37	X	29414501	29414501	Nonsense_Mutation	INS	-	AACTAATTTTAT	-	IL1RAPL1	TGTTTAACTAAT	S163delinsSLFNX
XH_P37	X	29973346	29973346	Frame_Shift_Ins	INS	-	GAGTGATCAAA	-	IL1RAPL1	nsAAAAGAGTGC	p.L500fs
XH_P37	X	30327151	30327151	In_Frame_Del	DEL	ATGCTGCCCC	-	GATGCTGCCTCG	NR0B1	c.133_330del	p.45_110del
XH_P37	X	32361392	32361392	Frame_Shift_Ins	INS	-	TGATGCATTTCC	-	DMD	7insAAGGAAT	p.S525fs
XH_P37	X	34962268	34962268	Frame_Shift_Ins	INS	-	CACCT	-	FAM47B	320_1321insCA	p.Q440fs
XH_P37	X	34962270	34962270	Missense_Mutation	SNP	A	T	A	FAM47B	c.A1322T	p.E441V
XH_P37	X	44091917	44091917	Frame_Shift_Ins	INS	-	GTACATTGTGCA	-	EFHC2	30insAATGCACA	p.A477fs
XH_P37	X	44919364	44919364	Nonsense_Mutation	INS	-	AGAAAATAGATT	-	KDM6A	TTAAAAGAAAA	T432delinsLVFKRX
XH_P37	X	44942025	44942025	Nonsense_Mutation	INS	-	CTTTATGATGAC	-	KDM6A	sGTGGTCTTTAT	3_D1014delinsEWSLX
XH_P37	X	46887444	46887444	In_Frame_Ins	INS	-	ATCTCTATATTT	-	JADE3	CTTTAAATCTCT	09delinsPKLSLVFL
XH_P37	X	46951534	46951534	Frame_Shift_Ins	INS	-	GCATTTAATATT	-	RGN	54insTGCAATTA	p.L185fs
XH_P37	X	47039424	47039424	In_Frame_Ins	INS	-	GATCAA	-	RBM10	16_817insGATC	Q272delinsODQ
XH_P37	X	48117290	48117290	Nonsense_Mutation	INS	-	CTGAGAG	-	SSX1	79_180insCTGA	K60_L61delinsNX
XH_P37	X	48418504	48418504	Frame_Shift_Ins	INS	-	GGCAGTAGGA	-	TBC1D25	1257insGGGAG	p.L419fs
XH_P37	X	48458875	48458875	Missense_Mutation	SNP	T	A	T	WDR13	c.T416A	p.L139N
XH_P37	X	48681883	48681883	Frame_Shift_Ins	INS	-	GAAATGGTCTG	-	HDAC6	075insAGAAAT	p.S1025fs
XH_P37	X	49071898	49071898	Nonsense_Mutation	INS	-	GCATCAGTATC	-	CACNA1F	42insACGATAC	A1114delinsARYX
XH_P37	X	49645359	49645359	In_Frame_Ins	INS	-	GGTGTGTTCCCA	-	USP27X	s0insTTGGTTGT	150delinsVWLFPR
XH_P37	X	50053379	50053379	Frame_Shift_Ins	INS	-	GGTATGCTCTCC	-	CNNB3	sAAGTGCGTATG	p.A737fs
XH_P37	X	50053502	50053502	In_Frame_Ins	INS	-	GAATTCCTCCTC	-	CNNB3	sGAGAGAATTC	78delinsREFLLSG
XH_P37	X	50053692	50053692	Frame_Shift_Ins	INS	-	TAAAGATAATTG	-	CNNB3	CTTCTTTAAAGA	p.K841fs
XH_P37	X	50376557	50376557	Frame_Shift_Ins	INS	-	AAATCTGC	-	SHROOM4	5_2516insGCAG	p.A839fs
XH_P37	X	53106728	53106728	Frame_Shift_Ins	INS	-	TTTACTCTGGC	-	GPR173	926insTTCATC	p.R309fs
XH_P37	X	53151534	53151534	In_Frame_Ins	INS	-	ATGAATGTCTCT	-	TSPYL2	s81insCATGAAT	527delinsDMNCLI
XH_P37	X	53584360	53584360	Frame_Shift_Ins	INS	-	TTTCTGGTTATTA	-	HUWE1	GTAGATAATAAA	p.T2730fs
XH_P37	X	54275917	54275917	Nonsense_Mutation	INS	-	ATGGATGCAGAG	-	WNK3	2864insCTCTGCG	K955delinsTLHPX
XH_P37	X	54282286	54282286	Nonsense_Mutation	INS	-	ACGGTAAGCTG	-	WNK3	7AATTTTCAGCT	713_S714delinsX
XH_P37	X	54334497	54334497	Nonsense_Mutation	INS	-	TCATGTTGAAAT	-	WNK3	sACTAATTTCAAA	316_A317delinsNX
XH_P37	X	54957160	54957160	Frame_Shift_Ins	INS	-	AAGCCAGAAC	-	TRO	2597insAAGCC	p.L866fs
XH_P37	X	57405140	57405140	Frame_Shift_Ins	INS	-	ACAA	-	FAAH2	799_800insACA	p.L267fs
XH_P37	X	57405141	57405141	Frame_Shift_Ins	INS	-	TAGCTCTCTTAA	-	FAAH2	TTTACTAGCTCT	p.L267fs
XH_P37	X	57620461	57620461	Frame_Shift_Ins	INS	-	TTGGATGTGAAC	-	ZXDB	981insCTTGGAT	p.V660fs
XH_P37	X	57934884	57934884	Frame_Shift_Ins	INS	-	AAACCCAGTTTG	-	ZXDA	71insTCCAAACT	p.D657fs
XH_P37	X	63412333	63412333	Nonsense_Mutation	INS	-	TTATGTCACCAC	-	AMER1	GGTTGTGGTGA	78_S279delinsALIHX
XH_P37	X	66765778	66765778	Frame_Shift_Ins	INS	-	CTGCTGCTGTT	-	AR	791insCTGCTG	p.R264fs
XH_P37	X	66863139	66863139	Frame_Shift_Ins	INS	-	TTCAATTG	-	AR	58_1659insTTCA	p.Y53fs
XH_P37	X	66863141	66863141	Nonsense_Mutation	INS	-	CAAGTTAG	-	AR	0_1661insCAAG	S54_P555delinsSSX
XH_P37	X	67454353	67454353	Frame_Shift_Ins	INS	-	GGCTATTCCA	-	OPHN1	462insTGGAAAT	p.K154fs
XH_P37	X	67937231	67937231	In_Frame_Ins	INS	-	AAACTCTTGGG	-	STARD8	nsTTCCAAACTC	79delinsLPNSWGT
XH_P37	X	68381584	68381584	Frame_Shift_Ins	INS	-	TCTCGCAGTGG	-	PIA1	1333insCCAATC	p.D445fs
XH_P37	X	69713281	69713281	Nonsense_Mutation	INS	-	TTAAAAATCAAT	-	DLG3	ATGCTTTAAATA	p.Y127delinsX
XH_P37	X	70072985	70072985	Nonsense_Mutation	INS	-	TCTCTGTATAT	-	TEX11	TCAGATATAACA	2_K4143delinsQIX
XH_P37	X	70514190	70514190	Nonsense_Mutation	INS	-	AGTGAAGAAAC	-	NONO	nsAGAAGTGAA	65delinsNRSERTX
XH_P37	X	70597658	70597658	In_Frame_Ins	INS	-	GGCTGAAAAC	-	TAF1	1insGGGCTGGA	327delinsGLKTP
XH_P37	X	70602698	70602698	Frame_Shift_Ins	INS	-	CTGTGGTTCTCT	-	TAF1	814insGCTGTGG	p.F605fs
XH_P37	X	71358444	71358444	Missense_Mutation	SNP	C	G	C	NHSL2	c.C1046G	p.S349C
XH_P37	X	71360264	71360264	Nonsense_Mutation	INS	-	SCACTAACTTCA	-	NHSL2	sAGTATGCACTA	956_D957delinsX
XH_P37	X	71363334	71363334	Nonsense_Mutation	INS	-	TTGGACCTAGAT	-	NHSL2	nsTCTTTTGGAG	1196delinsASFVWX
XH_P37	X	71425693	71425693	Frame_Shift_Ins	INS	-	CAGTAGTGAA	-	ERCC6L	sACTTATTTACA	p.V975fs
XH_P37	X	71846899	71846899	Frame_Shift_Ins	INS	-	GAGTGTATAGA	-	PHKA1	GTGACCTCTAT	p.D572fs
XH_P37	X	71886145	71886145	Frame_Shift_Ins	INS	-	TTGTGCCTTTGG	-	PHKA1	DinsCCCCAAAGG	p.S240fs
XH_P37	X	71904404	71904404	Missense_Mutation	SNP	C	T	C	PHKA1	c.G481A	p.E161K
XH_P37	X	71904405	71904405	Nonsense_Mutation	INS	-	SCCTCTTCTTTA	-	PHKA1	80insATAAGAA	160_E161delinsEX
XH_P37	X	73811450	73811450	Frame_Shift_Ins	INS	-	TGTCC	-	RLIM	99_1700insGG	p.L567fs

XH_P37	X	73811451	73811451	In_Frame_Ins	INS	-	CTTTTGGAG	-	RLIM	3_1699insCTCAA	L567delinsLKKL
XH_P37	X	76855954	76855954	Nonsense_Mutation	INS	-	AACTTTTATTT	-	ATRX	ATTTCAAAATAA	4_W1845delinsISKX
XH_P37	X	77264700	77264700	Nonsense_Mutation	INS	-	TTAACAGGTGAG	-	ATP7A	TTGCTTTTAACA	A604delinsKCFVFNRX
XH_P37	X	77378784	77378784	Nonsense_Mutation	INS	-	TAAAAATGGGA	-	PGK1	ATAAATAAAAAAT	B3_V284delinsPKX
XH_P37	X	77381311	77381311	Frame_Shift_Ins	INS	-	CAGGAGCTTTA	-	PGK1	1239insCAGGA	p.A413fs
XH_P37	X	79932211	79932211	Nonsense_Mutation	INS	-	TTTCAAGACTTT	-	BRWD3	nsATCAAAAGTC	9_S1770delinsDQKXSX
XH_P37	X	83371228	83371247	Frame_Shift_Del	DEL	TTACATCCCA	-	CTTACATCCCAG	RPS6KA6	c.998_1008del	p.I333fs
XH_P37	X	84363543	84363543	Missense_Mutation	SNP	G	T	G	SATL1	c.C432A	p.S144R
XH_P37	X	84363544	84363544	In_Frame_Ins	INS	-	TCA	-	SATL1	c.430_431insTG	p.S144delinsMS
XH_P37	X	84363759	84363759	Silent	SNP	G	A	G	SATL1	c.C216T	p.P72P
XH_P37	X	91132809	91132809	Frame_Shift_Ins	INS	-	TTCAAAGGAGG	-	PCDH11X	571insATTCAA	p.V524fs
XH_P37	X	91133143	91133143	Frame_Shift_Ins	INS	-	GGCTATTGTCAT	-	PCDH11X	insCTGGGCTAT	p.K635fs
XH_P37	X	99662614	99662631	In_Frame_Del	DEL	SATGGGAATTG	-	GGATGGGAATTGG	PCDH19	c.965_982del	p.322_328del
XH_P37	X	100169529	100169529	In_Frame_Ins	INS	-	AGTGTGTGTC	-	XKRX	7_1148insGACA	I383delinsRQHF
XH_P37	X	100169592	100169592	In_Frame_Ins	INS	-	AACGAAAGGAT	-	XKRX	nsACCTCATCTC	B62delinsNLISFNF
XH_P37	X	100356281	100356281	Frame_Shift_Ins	INS	-	GTGACATTACTG	-	CENPI	23insGTGACAT	p.E74fs
XH_P37	X	100356283	100356283	Missense_Mutation	SNP	A	T	A	CENPI	c.A224T	p.K75I
XH_P37	X	100493976	100493976	Missense_Mutation	SNP	A	T	A	DRP2	c.A211T	p.M71L
XH_P37	X	100667186	100667186	Frame_Shift_Ins	INS	-	AATGCAATTTTG	-	HNRNPH2	11insCAATGCA	p.A70fs
XH_P37	X	100668323	100668323	Frame_Shift_Ins	INS	-	AATTCAAAAAA	-	HNRNPH2	nsGTAGAAATTC	p.A449fs
XH_P37	X	101911697	101911697	In_Frame_Ins	INS	-	CCC	-	GPRASP1	2856_2857insC	p.G952delinsGP
XH_P37	X	101911698	101911698	Frame_Shift_Ins	INS	-	AATGACTTCTTC	-	GPRASP1	58insATAATGA	p.T953fs
XH_P37	X	102317920	102317920	Frame_Shift_Ins	INS	-	CTAA	-	BEX1	282_283insTTA	p.K95fs
XH_P37	X	102317922	102317922	In_Frame_Ins	INS	-	TATTGTGTTTTT	-	BEX1	insTTCAAAAACA	94delinsVQKHNIQ
XH_P37	X	102339805	102339805	In_Frame_Ins	INS	-	AGAGAGGAA	-	NXF3	4_35insTTCTCT	p.T12delinsPLS
XH_P37	X	102612735	102612735	Frame_Shift_Ins	INS	-	TTTTTTATCAGA	-	TCEAL9	AAATTTTTTTTAT	p.A41fs
XH_P37	X	102931275	102931275	Missense_Mutation	SNP	G	T	G	MORF4L2	c.C681A	p.H227Q
XH_P37	X	102979512	102979512	Frame_Shift_Ins	INS	-	TTCCCAACATTC	-	GLRA4	27insGGAATGT	p.N76fs
XH_P37	X	103041637	103041637	Nonsense_Mutation	INS	-	ATCTGCACTATA	-	PLP1	436insATCTCG	V145delinsWILHX
XH_P37	X	103359714	103359715	Frame_Shift_Del	DEL	GG	-	GG	ZCCHC18	c.912_913del	p.L304fs
XH_P37	X	103359715	103359715	In_Frame_Ins	INS	-	TCCTCCCTTATC	-	ZCCHC18	914insTCCTCCC	D305delinsVLPHY
XH_P37	X	103360011	103360011	Frame_Shift_Ins	INS	-	AA	-	ZCCHC18	1209_1210insA	p.Q403fs
XH_P37	X	103360012	103360012	Nonstop_Mutation	INS	-	TGTTGGGGGG	-	ZCCHC18	1211insTGTTG	X404delinsLLGE
XH_P37	X	105153712	105153712	Frame_Shift_Ins	INS	-	TTGCCTGTGG	-	NRK	2080insTTGCC	p.Q693fs
XH_P37	X	107414141	107414141	Frame_Shift_Ins	INS	-	TTTCACATTTAG	-	COL4A6	84insTCCTAAAT	p.K1095fs
XH_P37	X	107464598	107464598	Frame_Shift_Ins	INS	-	CTGCATT	-	COL4A6	50_151insAATG	p.P51fs
XH_P37	X	109695074	109695074	Frame_Shift_Ins	INS	-	TGGCTTTGGT	-	RTL9	1230insTGGCT	p.A410fs
XH_P37	X	109695360	109695360	Frame_Shift_Ins	INS	-	G	-	RTL9	c.1515_1516ins	p.P505fs
XH_P37	X	109695361	109695361	Frame_Shift_Ins	INS	-	ATCTAAAGCT	-	RTL9	1517insATTCTA	p.T506fs
XH_P37	X	109695687	109695687	In_Frame_Ins	INS	-	GAGACAGGGGC	-	RTL9	nsCTTCAGAGACA	14delinsLLQROGLS
XH_P37	X	109695913	109695914	Frame_Shift_Del	DEL	GG	-	GG	RTL9	c.2068_2069del	p.G690fs
XH_P37	X	110954911	110954911	Frame_Shift_Ins	INS	-	AAAAAGCT	-	ALG13	43_844insAAAA	p.E281fs
XH_P37	X	110954913	110954913	Nonsense_Mutation	INS	-	AGTATAAAAGT	-	ALG13	846insAGTATA	B82_S283delinsGVX
XH_P37	X	114141710	114141710	Frame_Shift_Ins	INS	-	GCAGCACTTCA	-	HTR2C	110insTGCAGC	p.L370fs
XH_P37	X	114249016	114249016	In_Frame_Ins	INS	-	TGTTATGTGAT	-	IL13RA2	TGCAATCAACA	nsYDLSILFCNQHNRIKSGSSW
XH_P37	X	117742253	117742253	Frame_Shift_Ins	INS	-	AGCAGACTTACA	-	DOCK11	2insAAACGACA	p.L937fs
XH_P37	X	118221220	118221220	Frame_Shift_Ins	INS	-	G	-	KIAA1210	c.3972_3973ins	p.K1325fs
XH_P37	X	118221222	118221222	In_Frame_Ins	INS	-	AGCAATTCTGAC	-	KIAA1210	3971insGTCA	A1324delinsCQNC
XH_P37	X	118257544	118257544	Splice_Site	INS	-	AAGGCTTTTCT	-	KIAA1210	.	.
XH_P37	X	118257546	118257546	Silent	SNP	C	T	C	KIAA1210	c.G480A	p.E160E
XH_P37	X	118723709	118723709	Frame_Shift_Ins	INS	-	AGATAGGGCTCC	-	NKRF	insTACGGGAGC	p.R560fs
XH_P37	X	119293141	119293141	In_Frame_Ins	INS	-	ACCATTA	-	RHOXF2	400_301insACCA	p.S100delinsSTI
XH_P37	X	119293142	119293142	Frame_Shift_Ins	INS	-	CATTC	-	RHOXF2	301_302insCAT	p.D101fs
XH_P37	X	119293332	119293332	Missense_Mutation	SNP	G	C	G	RHOXF2	c.G491C	p.R164P
XH_P37	X	119293333	119293333	Splice_Site	INS	-	ACTTTAAC	-	RHOXF2	.	.
XH_P37	X	119500492	119500492	Nonsense_Mutation	INS	-	TTTCTCCTAGTT	-	ATP1B4	TTTTCTTTCTCCC	E59delinsDFLSPX
XH_P37	X	119581877	119581877	Nonsense_Mutation	INS	-	AGGTGTCTATC	-	LAMP2	GATAAAGATAG	187_L188delinsYX
XH_P37	X	119739402	119739402	In_Frame_Ins	INS	-	GTATACAGC	-	MCT51	5_156insGTATA	p.K52delinsKYTA
XH_P37	X	119739404	119739404	Frame_Shift_Ins	INS	-	T	-	MCT51	c.158dupT	p.I53fs
XH_P37	X	120182711	120182711	In_Frame_Ins	INS	-	CTG	-	GLUD2	1173_1174insC	p.S391delinsSL
XH_P37	X	120182713	120182713	In_Frame_Ins	INS	-	AACAATGTTTT	-	GLUD2	176insCAACAAA	A392delinsNNKCFI
XH_P37	X	123839103	123839103	Splice_Site	INS	-	TTTAAACAAACCT	-	TENM1	.	.
XH_P37	X	125685480	125685480	Frame_Shift_Ins	INS	-	A	-	DCAF12L1	c.1111dupT	p.S371fs
XH_P37	X	125685482	125685482	Frame_Shift_Ins	INS	-	TGTTT	-	DCAF12L1	109_1110insAA	p.G370fs
XH_P37	X	128650425	128650425	Frame_Shift_Ins	INS	-	TTGCCATTATAA	-	SMARCA1	nsATAATTATAA	p.L1104fs
XH_P37	X	129150176	129150176	Frame_Shift_Ins	INS	-	AGCTTGG	-	BCORL1	28_3429insAGC	p.S1143fs
XH_P37	X	129205062	129205062	In_Frame_Ins	INS	-	CCTTTCTTTTCTT	-	ELF4	AGAAAGAAAGA	A54delinsQERKKKEK
XH_P37	X	129205064	129205064	Missense_Mutation	SNP	G	T	G	ELF4	c.C760A	p.Q254K
XH_P37	X	129370583	129370583	Frame_Shift_Ins	INS	-	TTGA	-	ZNF280C	523_524insTCA	p.H175fs
XH_P37	X	129370585	129370585	Nonsense_Mutation	INS	-	CTTAAAG	-	ZNF280C	1_522insCTTTT	A74_H175delinsNFX
XH_P37	X	131526342	131526342	In_Frame_Ins	INS	-	AACCTTACACAT	-	MBNL3	nsTTTATGTGTA	P71delinsPLCVRLI
XH_P37	X	131526344	131526344	Missense_Mutation	SNP	G	C	G	MBNL3	c.C211G	p.P71A
XH_P37	X	131762305	131762305	In_Frame_Ins	INS	-	GTGAGGTAAAT	-	HS6S72	GATTTGTTTAC	B88delinsELCFTTYQY
XH_P37	X	133379417	133379417	Frame_Shift_Ins	INS	-	GAATTTGTGTCT	-	CCDC160	88insAGAAATTG	p.A196fs
XH_P37	X	134185856	134185856	Missense_Mutation	SNP	G	A	G	RTL8A	c.C283T	p.R95W
XH_P37	X	134425455	134425455	Frame_Shift_Ins	INS	-	CACCTTTTTCCTC	-	ZNF75D	TTAGGGGAAAAA	p.E213fs
XH_P37	X	135405194	135405194	Frame_Shift_Ins	INS	-	AAAAATCCAGCT	-	ADGRG4	29insAAAAAATC	p.I110fs
XH_P37	X	135428612	135428612	Nonsense_Mutation	INS	-	ATGCAAGCAAG	-	ADGRG4	insTGAATGCA	A916delinsVECKQEX
XH_P37	X	135431391	135431391	In_Frame_Ins	INS	-	CCCACAAAAAT	-	ADGRG4	CTGGACCCACA	A2delinsSASGPTKNVKT
XH_P37	X	142596761	142596761	Silent	SNP	G	A	G	SPANXN3	c.C309T	p.G103G
XH_P37	X	147106508	147106508	Frame_Shift_Ins	INS	-	AAAAA	-	FMR1NB	756_757insAAA	p.H252fs
XH_P37	X	147106509	147106509	Frame_Shift_Ins	INS	-	GAAACCTTATTI	-	FMR1NB	CAAGTGAACCC	p.G253fs
XH_P37	X	147733581	147733581	Nonsense_Mutation	INS	-	ACTTGCTTATTG	-	AFF2	CAAAAACCTGCT	Q38delinsENKNLLIX
XH_P37	X	148037594	148037594	Frame_Shift_Ins	INS	-	TTTCTGGAATTT	-	AFF2	nsTTTGTTCTCGG	p.A314fs
XH_P37	X	148037596	148037596	Missense_Mutation	SNP	C	G	C	AFF2	c.C946G	p.T315S
XH_P37	X	148037904	148037904	Nonsense_Mutation	INS	-	GGGATGTTAGG	-	AFF2	253insAGGGAT	A18_F419delinsKGXC
XH_P37	X	148037906	148037906	Silent	SNP	A	T	A	AFF2	c.A1254T	p.T418T
XH_P37	X	148693140	148693140	Frame_Shift_Ins	INS	-	GAGC	-	TMEM185A	c.44_45insGCTC	p.F15fs
XH_P37	X	148693142	148693142	In_Frame_Ins	INS	-	TATCTTGAC	-	TMEM185A	2_43insGTCAAG	p.F15delinsVKIF
XH_P37	X	149639324	149639324	In_Frame_Ins	INS	-	CAACAGCAG	-	MAML1D1	1_1405insCAAC	AQ468delinsQQQQ
XH_P37	X	149814270	149814270	Nonsense_Mutation	INS	-	AAGTGAATCTGA	-	MTM1	insAGAAAGTGA	A265_E266delinsKKX
XH_P37	X	150349558	150349558	In_Frame_Del	DEL	ACCACCTGGCC	-	CACCACTGGCCA	GPR50	c.1503_1514del	p.S501_S505del
XH_P37	X	151514145	151514145	Frame_Shift_Ins	INS	-	AA	-	GABRA3	c.169_170insTT	p.P57fs
XH_P37	X	151514146	151514146	Frame_Shift_Ins	INS	-	TTTGCTAGGTGTG	-	GABRA3	ATATGCACCTAC	p.P57fs
XH_P37	X	151815565	151815565	In_Frame_Ins	INS	-	CACCTGTGTG	-	GABRQ	3_464insCACTTC	D155delinsALVY
XH_P37	X	151996388	151996388	Nonsense_Mutation	INS	-	TTGAGCAGCTTG	-	CETN2	nsAATGGCAGGTG	A172_X173delinsX
XH_P37	X	152612427	152612427	In_Frame_Ins	INS	-	TTTTCTTCTGA	-	ZNF275	285insTTTTCTT	p.L95delinsLFSE
XH_P37	X	153136379	153136379	Frame_Shift_Ins	INS	-	GACCCCT	-	L1CAM	4_545insAGGG	p.M182fs

XH_P37	X	153215976	153215976	Frame_Shift_Ins	INS	-	TGTCCTTC	-	HCFC1	1_5722insGAAG	p.L1908fs
XH_P37	X	153649039	153649039	Frame_Shift_Ins	INS	-	TTCTCTGCTCT	-	TAZ	1insACTTCTCTCT	p.V204fs
XH_P37	X	154197683	154197683	Missense_Mutation	SNP	G	C	G	F8	c.C932G	p.T311S
XH_P37	X	154743862	154743862	Frame_Shift_Ins	INS	-	CCACAGTATTAT	-	TMLHE	TAATTATAATAC	p.Q141fs
XH_P37	1	12837291	12837291	Missense_Mutation	SNV	T	C	C	PRAMEF12	c.1001T>C	P.F334s
XH_P37	1	155218094	155218094	Splice_Site	INDEL	-	TTATTGATGATG	TTATTGATGATG	FAM189B	1526insCATCATCAATAA	
XH_P37	1	155698914	155698914	Splice_Site	INDEL	-	AGTTCATTT	AGTTCATTT	DAP3	1_684+2insAGTTCATTT	
XH_P37	1	155698916	155698916	Splice_Site	INDEL	-	ATTGTTTCAGGTT	ATTGTTTCAGGTT	DAP3	4insATCTATTGTTTCAGGTTCTG	
XH_P37	1	156203525	156203525	Splice_Site	INDEL	-	ATTTCCTGTTCTA	ATTTCCTGTTCTA	PMF1-BGLAP	TTGGCTAAATTTCTGTTCTAGGCTCTTAT	
XH_P37	1	159021716	159021716	Missense_Mutation	SNV	G	A	A	IFI16	c.1745G>A	P.R582H
XH_P37	1	161173285	161173285	Missense_Mutation	SNV	A	T	T	NDUF52	c.154A>T	P.M52L
XH_P37	1	201195059	201195059	Missense_Mutation	SNV	T	G	G	IGFN1	c.10594T>G	P.Y3532D
XH_P37	1	248020603	248020603	Missense_Mutation	SNV	T	C	C	TRIM58	c.55T>C	P.C19R
XH_P37	1	46543274	46543274	Frame_Shift_Ins	INDEL	-	TTCCAGCTCTGGC	TTCCAGCTCTGGC	PIK3R3	AATTAGCCAGAC	P.N76fs
XH_P37	1	86437068	86437068	Missense_Mutation	INDEL	-	GTT	GTT	COL24A1	2372_2373insA	L791_G792insT
XH_P37	1	86437069	86437069	Frame_Shift_Ins	INDEL	-	TATATATTTAGA	TATATATTTAGA	COL24A1	ACTCTGTCTAAA	P.L791fs
XH_P37	10	5815797	5815797	Splice_Site	INDEL	-	AGTTGTTGATT	AGTTGTTGATT	GD12	TTAAAAATATCAACAACTGACAAACAAAAAGAT	
XH_P37	11	1025072	1025072	Silent	SNV	G	A	A	MUC6	c.2997C>T	P.C99C
XH_P37	12	102041901	102041901	Missense_Mutation	INDEL	-	TTGTCTCTGTTT	TTGTCTCTGTTT	MY8PC1	TTGTCTCTGTTCTC	S366insFVFLVLRQ
XH_P37	12	91552169	91552169	Missense_Mutation	SNV	T	A	A	DCN	c.442A>T	P.M148L
XH_P37	12	95927168	95927175	Frame_Shift_Del	INDEL	GAAGAACA	-	-	USP44	8_865delTTGTC	P.V287fs
XH_P37	14	103958256	103958256	Frame_Shift_Ins	INDEL	-	G	G	MARK3	c.1729_1730ins	P.V577fs
XH_P37	14	20215589	20215589	Frame_Shift_Ins	INDEL	-	A	A	OR4Q3	c.9dupA	P.E4fs
XH_P37	17	41245268	41245268	Missense_Mutation	INDEL	-	AAT	AAT	BRCA1	2279_2280insA	P.T760_E761insF
XH_P37	17	41245269	41245269	Frame_Shift_Ins	INDEL	-	CTCACACATTTA	CTCACACATTTA	BRCA1	ACCAAAATAAATC	P.T760fs
XH_P37	17	41245706	41245706	Frame_Shift_Ins	INDEL	-	ATGACAGTGA	ATGACAGTGA	BRCA1	1842insTCACT	P.K614fs
XH_P37	17	7294053	7294053	Missense_Mutation	SNV	A	G	G	PLSCR3	c.731T>C	P.V244A
XH_P37	17	78321148	78321148	Missense_Mutation	SNV	G	A	A	RNF213	c.9013G>A	P.E3005K
XH_P37	17	78914290	78914290	Splice_Site	INDEL	-	TATTTTGTGTTAT	TATTTTGTGTTAT	RPTOR	TTTAAATTATTTTGTGTTATTCATTTGTTTTTTT	
XH_P37	19	15083605	15083605	Missense_Mutation	SNV	G	A	A	SLC1A6	c.118C>T	P.R40C
XH_P37	19	24310638	24310638	Frame_Shift_Ins	INDEL	-	CAGTATGAATTA	CAGTATGAATTA	ZNF254	TTCTCTTCAGTA	2insTFVGFSLFMYNLMFSKS
XH_P37	19	42266136	42266136	Splice_Site	SNV	G	C	C	CEACAM6	c.958+5G>C	
XH_P37	2	11780490	11780490	Silent	SNV	C	T	T	GREB1	c.5760C>T	P.D1920D
XH_P37	2	135890564	135890564	Splice_Site	INDEL	-	ATAGACATTATT	ATAGACATTATT	RAB3GAP1	ATAACTCATATAGACATTATTAACTTTTAAATG	
XH_P37	2	179398216	179398216	Missense_Mutation	SNV	C	T	T	TTN	c.98203G>A	P.E32735K
XH_P37	2	179399194	179399194	Frame_Shift_Ins	INDEL	-	ATGGGTGCTGGA	ATGGGTGCTGGA	TTN	7225insCTCCAG	P.V32409fs
XH_P37	2	179616165	179616165	Missense_Mutation	SNV	C	A	A	TTN	c.10962G>T	P.M3654I
XH_P37	2	234186258	234186258	Frame_Shift_Ins	INDEL	-	ATTATCATTTTAT	ATTATCATTTTAT	ATG16L1	ATTCTATTATCA	P.S250fs
XH_P37	2	96993664	96993664	Missense_Mutation	INDEL	-	TGAAGCTGGTG	TGAAGCTGGTG	ITPR1P1	TGTTCTCTGAAGC	Q433insLFLKLVGRF
XH_P37	20	18296814	18296814	Missense_Mutation	SNV	G	A	A	ZNF133	c.1316G>A	P.C439Y
XH_P37	3	121340958	121340958	Missense_Mutation	SNV	G	T	T	FBXO40	c.682G>T	P.A228S
XH_P37	3	129218800	129218800	Missense_Mutation	SNV	C	A	A	IFT122	c.2240C>A	P.A747D
XH_P37	3	143691687	143691687	Silent	SNV	C	T	T	C3orf58	c.513C>T	P.P171P
XH_P37	3	38037304	38037304	Missense_Mutation	SNV	A	G	G	VILL	c.416A>G	P.H139R
XH_P37	4	187539653	187539653	Missense_Mutation	SNV	G	A	A	FAT1	c.8087C>T	P.P2696L
XH_P37	5	140574045	140574045	Silent	SNV	C	G	G	PCDH10	c.1920C>G	P.L640L
XH_P37	5	37014856	37014856	Missense_Mutation	SNV	C	G	G	NIPBL	c.4632C>G	P.J1544M
XH_P37	6	26197293	26197293	Silent	SNV	C	G	G	HIST1H3D	c.186G>C	P.L62L
XH_P37	6	38831782	38831782	In_Frame_Ins	INDEL	-	AATATACCTTCT	AATATACCTTCT	DNAH8	TCTATAATATAC	S2149insLLYNIPSTerTerQ
XH_P37	6	64422419	64422419	Frame_Shift_Ins	INDEL	-	TTTGTGACTGAAT	TTTGTGACTGAAT	PHF3	CTCTTTGTTTGA	P.J1558fs
XH_P37	6	64940723	64940723	Splice_Site	INDEL	-	AATCTTCATTAC	AATCTTCATTAC	EYS	ACAAAAGGGTAATGAAGATTGATACCTTTT	
XH_P37	6	74119061	74119065	Frame_Shift_Del	INDEL	GTTAT	-	-	DDX43	271_1275delTTA	P.V424fs
XH_P37	7	128597275	128597275	Splice_Site	SNV	C	T	T	TNPO3	c.*31+3G>A	
XH_P37	8	99142344	99142344	Missense_Mutation	SNV	G	A	A	POP1	c.625G>A	P.A209T
XH_P37	9	5054805	5054805	In_Frame_Ins	INDEL	-	TTGGTAAGAATG	TTGGTAAGAATG	JAK2	TACATTTTGGTAA	T287insRHFKNVLTerL
XH_P37	X	100493976	100493976	Missense_Mutation	SNV	A	T	T	DRP2	c.211A>T	P.M71L
XH_P37	X	148037594	148037594	Frame_Shift_Ins	INDEL	-	TTTCTGGAATTT	TTTCTGGAATTT	AFF2	instTTGTTTCTG	P.T641fs
XH_P37	X	154197683	154197683	Missense_Mutation	SNV	G	C	C	F8	c.932C>G	P.T311S
XH_P37	X	17744883	17744883	Missense_Mutation	SNV	G	T	T	NHS	c.2126G>T	P.R709M
XH_P37	X	17745550	17745550	Frame_Shift_Ins	INDEL	-	AGTAAAGA	AGTAAAGA	NHS	3_2794insAGTA	P.H932fs
XH_P37	X	21675796	21675828	Missense_Mutation	INDEL	CAGTGTCA	-	-	KLHL34	GCGACGTGACCA	P.F27_G37del
XH_P38	2	209113113	209113113	Missense_Mutation	SNP	G	C	C	IDH1	c.394C>G	p.R132G
XH_P38	17	7577538	7577538	Missense_Mutation	SNP	C	T	T	TP53	c.743G>A	p.R248Q
XH_P38	-	-	-	Frame_Shift_Del	INS	-	-	-	EPHA2	c.1880delT	p.V627Gfs*6
XH_P38	17	16068463	16068463	Missense_Mutation	SNP	C	T	T	NCOR1	c.448G>A	p.G150R
XH_P38	-	-	-	Frame_Shift_Del	INS	-	-	-	ARID1A	c.4977_4978del	p.T1660Nfs*37
XH_P38	17	63010698	63010698	Missense_Mutation	SNP	T	C	C	GNA13	c.811A>G	p.I271V
XH_P38	1	881627	881627	Silent	SNP	G	A	G	NOC2L	c.1843T	p.L615L
XH_P38	1	889238	889238	Missense_Mutation	SNP	G	A	G	GOC2L	c.C812T	p.A271V
XH_P38	1	897738	897738	Silent	SNP	C	T	C	KLHL17	c.C715T	p.L239L
XH_P38	1	909419	909419	Silent	SNP	C	T	C	PLEKHN1	c.C1536T	p.D512D
XH_P38	1	949608	949608	Missense_Mutation	SNP	G	A	G	ISG15	c.G248A	p.S83N
XH_P38	1	1119410	1119410	Missense_Mutation	SNP	G	A	G	TTL10	c.G980A	p.R327H
XH_P38	1	1226757	1226757	Missense_Mutation	SNP	G	A	G	SCNN1D	c.G2176A	p.G726S
XH_P38	1	1226889	1226889	Missense_Mutation	SNP	G	A	G	SCNN1D	c.G2308A	p.G770R
XH_P38	1	1231656	1231656	Silent	SNP	G	A	G	ACAP3	c.C1342T	p.L448L
XH_P38	1	1271799	1271799	Missense_Mutation	SNP	G	A	G	DVL1	c.C1811T	p.S604L
XH_P38	1	1334053	1334057	Splice_Site	DEL	TAGAG	-	TAGAG	CCNL2	.	.
XH_P38	1	1354515	1354515	Missense_Mutation	SNP	C	G	C	ANKRD65	c.G1165C	p.E389Q
XH_P38	1	1354594	1354594	Silent	SNP	A	G	A	ANKRD65	c.T1086C	p.T362T
XH_P38	1	1354800	1354800	Missense_Mutation	SNP	C	T	C	ANKRD65	c.G880A	p.E294K
XH_P38	1	1361555	1361555	Silent	SNP	T	C	T	TMEM88B	c.T48C	p.G16G
XH_P38	1	1421991	1421991	Missense_Mutation	SNP	G	A	G	ATAD3B	c.G1019A	p.R340Q
XH_P38	1	1423267	1423267	Silent	SNP	A	G	A	ATAD3B	c.A1101G	p.A367A
XH_P38	1	1425700	1425700	Silent	SNP	T	C	T	ATAD3B	c.T1263C	p.I421I
XH_P38	1	1562536	1562536	Silent	SNP	G	A	G	MIB2	c.G1473A	p.A491A
XH_P38	1	1573181	1573181	Silent	SNP	C	A	C	CDK11B	c.G639T	p.S213S
XH_P38	1	1689870	1689870	Missense_Mutation	SNP	G	A	G	NADK	c.C101T	p.P34L
XH_P38	1	1847979	1847979	Missense_Mutation	SNP	T	C	T	CALML6	c.T127C	p.W43R
XH_P38	1	1849530	1849530	Missense_Mutation	SNP	T	C	T	TMEM52	c.A421G	p.M141V
XH_P38	1	1849744	1849744	Silent	SNP	G	A	G	TMEM52	c.C297T	p.D99D
XH_P38	1	1854546	1854546	Missense_Mutation	SNP	C	T	C	CFAP74	c.G4561A	p.E1521K
XH_P38	1	1855319	1855319	Silent	SNP	C	T	C	CFAP74	c.G4284A	p.K1428K
XH_P38	1	1855896	1855896	Missense_Mutation	SNP	G	A	G	CFAP74	c.C4168T	p.R1390W
XH_P38	1	1858161	1858161	Silent	SNP	C	T	C	CFAP74	c.G3702A	p.T1234T
XH_P38	1	1859176	1859176	Missense_Mutation	SNP	T	C	T	CFAP74	c.A3397G	p.N1133D
XH_P38	1	1918384	1918384	Silent	SNP	C	T	C	CFAP74	c.G387A	p.A129A
XH_P38	1	1960674	1960674	Silent	SNP	C	T	C	GABRD	c.C816T	p.S272S

XH_P38	1	2433773	2433773	Missense_Mutation	SNP	G	A	G	PLCH2	c.G2803A	p.D935N
XH_P38	1	2434022	2434022	Missense_Mutation	SNP	C	A	C	PLCH2	c.C3052A	p.P1018T
XH_P38	1	2938697	2938697	Silent	SNP	T	G	T	ACTR12	c.T447G	p.S149S
XH_P38	1	3379757	3379757	Missense_Mutation	SNP	A	G	A	ARHGEF16	c.A109G	p.M37V
XH_P38	1	3409208	3409208	Missense_Mutation	SNP	C	T	C	MEGF6	c.G4511A	p.R1504Q
XH_P38	1	3428608	3428608	Missense_Mutation	SNP	G	A	G	MEGF6	c.C938T	p.A313V
XH_P38	1	3511934	3511934	Missense_Mutation	SNP	A	G	A	MEGF6	c.T344C	p.M115T
XH_P38	1	3697733	3697733	Silent	SNP	A	G	A	LRRC47	c.T1671C	p.D557D
XH_P38	1	4772717	4772717	Missense_Mutation	SNP	G	A	G	AJAP1	c.G787A	p.G263R
XH_P38	1	6529443	6529443	Silent	SNP	A	G	A	PLEKHG5	c.T2001C	p.S667S
XH_P38	1	6533393	6533393	Missense_Mutation	SNP	G	C	G	PLEKHG5	c.C713G	p.T238S
XH_P38	1	6614230	6614230	Silent	SNP	G	A	G	NOL9	c.C333T	p.L111L
XH_P38	1	7723534	7723534	Silent	SNP	G	A	G	CAMTA1	c.G837A	p.S279S
XH_P38	1	7844944	7844944	Missense_Mutation	SNP	C	T	C	PER3	c.C7T	p.R3C
XH_P38	1	7887248	7887248	Silent	SNP	G	A	G	PER3	c.G2259A	p.P753P
XH_P38	1	7887605	7887605	Silent	SNP	G	A	G	PER3	c.G2616A	p.S872S
XH_P38	1	7909737	7909737	Missense_Mutation	SNP	C	T	C	UTS2	c.G221A	p.S74N
XH_P38	1	9322159	9322159	Missense_Mutation	SNP	G	A	G	H6PD	c.G820A	p.V274Y
XH_P38	1	9324571	9324571	Silent	SNP	T	C	T	H6PD	c.T2052C	p.Y684Y
XH_P38	1	9324670	9324670	Silent	SNP	A	G	A	H6PD	c.A2151G	p.S717S
XH_P38	1	10689924	10689924	Silent	SNP	C	T	C	PEX14	c.C1014T	p.D338D
XH_P38	1	10699188	10699188	In_Frame_Ins	INS	-	TCGTCC	-	CASZ1	90_5091insGGAA	D1697delinsEDD
XH_P38	1	10708142	10708142	Silent	SNP	A	G	A	CASZ1	c.T3213C	p.F1071F
XH_P38	1	10713765	10713765	Silent	SNP	T	C	T	CASZ1	c.A2349G	p.S783S
XH_P38	1	10725498	10725498	Silent	SNP	G	A	G	CASZ1	c.C147T	p.D49D
XH_P38	1	11008497	11008497	Silent	SNP	G	C	G	C1orf127	c.C1695G	p.G565G
XH_P38	1	11008695	11008695	Silent	SNP	T	C	T	C1orf127	c.A1497G	p.P499P
XH_P38	1	11014118	11014118	Missense_Mutation	SNP	C	T	C	C1orf127	c.G1057A	p.A353T
XH_P38	1	11561593	11561593	Missense_Mutation	SNP	G	A	G	DISP3	c.G544A	p.G182S
XH_P38	1	11579470	11579470	Missense_Mutation	SNP	G	A	G	DISP3	c.G1948A	p.A650T
XH_P38	1	11710779	11710779	In_Frame_Ins	INS	-	GCG	-	FBXO2	134_135insCG	p.A45delinsAA
XH_P38	1	11766424	11766424	Missense_Mutation	SNP	C	T	C	DRAXIN	c.C109T	p.L37F
XH_P38	1	11832289	11832289	Missense_Mutation	SNP	C	A	C	C1orf167	c.C1961A	p.P654H
XH_P38	1	11863566	11863566	Missense_Mutation	SNP	G	T	G	MTFHR	c.C6A	p.D2E
XH_P38	1	12186058	12186058	Missense_Mutation	SNP	A	G	A	TNFRSF8	c.A871G	p.S291G
XH_P38	1	12252955	12252955	Missense_Mutation	SNP	T	G	T	TNFRSF1B	c.T587G	p.M196R
XH_P38	1	16342237	16342237	Silent	SNP	A	G	A	HSPB7	c.T363C	p.T121T
XH_P38	1	16344360	16344360	Silent	SNP	A	G	A	HSPB7	c.T99C	p.A33A
XH_P38	1	16351275	16351275	Missense_Mutation	SNP	A	G	A	CLCNKA	c.A247G	p.R83G
XH_P38	1	16731510	16731510	Missense_Mutation	SNP	C	G	C	SPATA21	c.G763C	p.V255L
XH_P38	1	16736132	16736132	Missense_Mutation	SNP	T	C	T	SPATA21	c.A551G	p.Q184R
XH_P38	1	17282573	17282573	Silent	SNP	G	A	G	CROCC	c.G3786A	p.G1262G
XH_P38	1	17764969	17764969	Silent	SNP	C	T	C	RC2	c.G42A	p.P14P
XH_P38	1	18807953	18807953	Missense_Mutation	SNP	C	A	C	KLHDC7A	c.C478A	p.R160S
XH_P38	1	18809653	18809653	Silent	SNP	C	T	C	KLHDC7A	c.C2178T	p.Y726Y
XH_P38	1	19166243	19166243	Silent	SNP	G	A	G	TAS1R2	c.C2370T	p.I790I
XH_P38	1	19166893	19166893	Missense_Mutation	SNP	C	T	C	TAS1R2	c.G1720A	p.A574T
XH_P38	1	19634721	19634721	Silent	SNP	A	G	A	AKR7A2	c.T522C	p.A174A
XH_P38	1	19992513	19992513	Silent	SNP	C	T	C	HTR6	c.C267T	p.Y89Y
XH_P38	1	20009737	20009737	Silent	SNP	G	A	G	TMC04	c.C1701T	p.S567S
XH_P38	1	20020993	20020993	Silent	SNP	A	G	A	TMC04	c.T1434C	p.R478R
XH_P38	1	20141283	20141283	Silent	SNP	C	T	C	RNF186	c.G312A	p.A104A
XH_P38	1	20656824	20656824	Missense_Mutation	SNP	A	G	A	VWA5B1	c.A1406G	p.N469S
XH_P38	1	21011346	21011346	Silent	SNP	A	G	A	KIF17	c.T2187C	p.T729T
XH_P38	1	21024901	21024901	Missense_Mutation	SNP	C	T	C	KIF17	c.G1204A	p.V402M
XH_P38	1	21031046	21031046	Silent	SNP	C	T	C	KIF17	c.G1017A	p.P339P
XH_P38	1	22141206	22141206	Missense_Mutation	SNP	A	C	A	LDLRAD2	c.A401C	p.N134T
XH_P38	1	22214127	22214127	Silent	SNP	A	G	A	HSPG2	c.T744C	p.L248L
XH_P38	1	22310190	22310190	Silent	SNP	T	C	T	CELA3B	c.T366C	p.N122N
XH_P38	1	22970642	22970642	Silent	SNP	C	T	C	C10C	c.C126T	p.P42P
XH_P38	1	23688933	23688933	Silent	SNP	A	G	A	ZNF436	c.T942C	p.N314N
XH_P38	1	23885493	23885493	Silent	SNP	C	T	C	ID3	c.G318A	p.P106P
XH_P38	1	24201448	24201448	Silent	SNP	C	T	C	CNR2	c.G660A	p.V220V
XH_P38	1	24201643	24201643	Silent	SNP	G	A	G	CNR2	c.C465T	p.G155G
XH_P38	1	24201919	24201919	Silent	SNP	T	C	T	CNR2	c.A189G	p.Q63Q
XH_P38	1	24201920	24201920	Missense_Mutation	SNP	T	C	T	CNR2	c.A188G	p.Q63R
XH_P38	1	24409165	24409165	Silent	SNP	C	T	C	MYOM3	c.G2010A	p.E670E
XH_P38	1	24432539	24432539	Missense_Mutation	SNP	T	A	T	MYOM3	c.A431T	p.E144V
XH_P38	1	24432540	24432540	Nonsense_Mutation	SNP	C	A	C	MYOM3	c.G430T	p.E144X
XH_P38	1	24668667	24668667	Silent	SNP	C	G	C	GRHL3	c.C972G	p.V324V
XH_P38	1	24746100	24746100	Silent	SNP	C	T	C	NIPAL3	c.C63T	p.S21S
XH_P38	1	24782710	24782710	Silent	SNP	C	T	C	NIPAL3	c.C237T	p.P79P
XH_P38	1	26357667	26357667	Silent	SNP	G	A	G	EXTL1	c.G1146A	p.L382L
XH_P38	1	26385003	26385003	Missense_Mutation	SNP	T	C	T	TRIM63	c.A709G	p.K237E
XH_P38	1	26393974	26393974	Silent	SNP	C	T	C	TRIM63	c.G12A	p.K4K
XH_P38	1	26663362	26663362	Missense_Mutation	SNP	C	T	C	CRYBG2	c.G3881A	p.S1294N
XH_P38	1	26671084	26671084	Missense_Mutation	SNP	G	T	G	CRYBG2	c.C2065A	p.P689T
XH_P38	1	26671248	26671248	Missense_Mutation	SNP	A	G	A	CRYBG2	c.T1901C	p.V634A
XH_P38	1	26883511	26883511	Missense_Mutation	SNP	A	C	A	RPS6KA1	c.A1031C	p.K344T
XH_P38	1	27278810	27278810	Missense_Mutation	SNP	C	T	C	KDF1	c.G62A	p.R21Q
XH_P38	1	28476862	28476862	Missense_Mutation	SNP	G	T	G	PTAFR	c.C671A	p.A224D
XH_P38	1	33236285	33236285	Missense_Mutation	SNP	G	A	G	KIAA1522	c.G1328A	p.R443H
XH_P38	1	33832933	33832933	Missense_Mutation	SNP	G	A	G	PHC2	c.C673T	p.P225S
XH_P38	1	33957130	33957130	Silent	SNP	C	A	C	ZSCAN20	c.C1272A	p.A424A
XH_P38	1	35250720	35250720	Silent	SNP	C	T	C	GJB3	c.C357T	p.N119N
XH_P38	1	35250943	35250943	Missense_Mutation	SNP	G	A	G	GJB3	c.G580A	p.A194T
XH_P38	1	35259961	35259961	Silent	SNP	A	G	A	GJA4	c.A147G	p.Q49Q
XH_P38	1	36643701	36643703	In_Frame_Del	DEL	AGA	-	AGA	MAP7D1	c.1496_1498del	p.499_500del
XH_P38	1	36937065	36937065	Silent	SNP	A	G	A	CSF3R	c.T1254C	p.R418R
XH_P38	1	38184055	38184055	Missense_Mutation	SNP	C	T	C	EPHA10	c.G3016A	p.V1006M
XH_P38	1	39847730	39847730	Missense_Mutation	SNP	G	A	G	MACF1	c.G7568A	p.R2523Q
XH_P38	1	40150156	40150156	Silent	SNP	G	A	G	HPCAL4	c.C120T	p.S40S
XH_P38	1	40668255	40668255	Missense_Mutation	SNP	C	G	G	RLF	c.C779G	p.S260C
XH_P38	1	40923019	40923019	Missense_Mutation	SNP	G	A	G	ZFP69B	c.G344A	p.C115Y
XH_P38	1	40981230	40981230	Silent	SNP	G	A	G	EXO5	c.G1014A	p.E338E
XH_P38	1	41848060	41848060	Missense_Mutation	SNP	C	T	C	FOXO6	c.C1187T	p.A396V
XH_P38	1	41848296	41848296	Missense_Mutation	SNP	G	A	G	FOXO6	c.G1423A	p.A475T
XH_P38	1	42047300	42047300	Missense_Mutation	SNP	A	T	A	HIVEP3	c.T3169A	p.S1057T

XH_P38	1	42619152	42619152	Missense_Mutation	SNP	C	A	C	GUCA2B	c.C31A	p.P11T
XH_P38	1	43232316	43232316	Silent	SNP	G	A	G	P3H1	c.C327T	p.F109F
XH_P38	1	43719778	43719778	Silent	SNP	G	A	G	CFAP57	c.G3768A	p.Q1256Q
XH_P38	1	43851797	43851797	Silent	SNP	G	A	G	MED8	c.C327T	p.G109G
XH_P38	1	43886494	43886494	Missense_Mutation	SNP	C	T	C	SZT2	c.C1336T	p.P446S
XH_P38	1	44595047	44595047	Missense_Mutation	SNP	T	A	T	KLF17	c.T104A	p.V35N
XH_P38	1	45250007	45250007	Missense_Mutation	SNP	C	G	C	BEST4	c.G1297C	p.V433L
XH_P38	1	45268754	45268754	Missense_Mutation	SNP	G	A	G	PLK3	c.G877A	p.A293T
XH_P38	1	45292866	45292866	Silent	SNP	G	A	G	PTCH2	c.C2487T	p.D829D
XH_P38	1	45469176	45469176	Silent	SNP	A	T	A	HECTD3	c.T2574A	p.P858P
XH_P38	1	45469555	45469555	Missense_Mutation	SNP	G	A	G	HECTD3	c.C2401T	p.R801W
XH_P38	1	45671966	45671966	Silent	SNP	A	G	A	ZSWIM5	c.T57C	p.A19A
XH_P38	1	46086766	46086766	Missense_Mutation	SNP	C	T	C	CCDC17	c.G1408A	p.V470I
XH_P38	1	46094027	46094027	Silent	SNP	A	G	A	GPBP1L1	c.T1326C	p.S442S
XH_P38	1	46095272	46095272	Silent	SNP	T	C	T	GPBP1L1	c.A1248G	p.K416K
XH_P38	1	46685443	46685443	Missense_Mutation	SNP	C	T	C	LURAP1	c.C271T	p.R91C
XH_P38	1	46870761	46870761	Missense_Mutation	SNP	C	A	C	FAAH	c.C385A	p.P129T
XH_P38	1	46976717	46976717	Silent	SNP	C	T	C	DMBX1	c.C459T	p.A153A
XH_P38	1	47280747	47280748	Frame_Shift_Del	DEL	AT	-	AT	CYP4B1	c.395_396del	p.D132fs
XH_P38	1	47282772	47282772	Missense_Mutation	SNP	C	T	C	CYP4B1	c.C637T	p.R213C
XH_P38	1	48694594	48694594	Missense_Mutation	SNP	G	A	G	SLC5A9	c.G307A	p.G103R
XH_P38	1	48713100	48713100	Missense_Mutation	SNP	C	A	C	SLC5A9	c.C1931A	p.A644E
XH_P38	1	50887065	50887065	Silent	SNP	G	A	G	DMRTA2	c.C144T	p.G48G
XH_P38	1	53527917	53527917	Missense_Mutation	SNP	C	G	C	PODN	c.C26G	p.A9G
XH_P38	1	53535478	53535478	Missense_Mutation	SNP	G	A	G	PODN	c.G95A	p.R32H
XH_P38	1	53537266	53537266	Silent	SNP	G	A	G	PODN	c.G516A	p.T172T
XH_P38	1	53544289	53544289	Silent	SNP	C	T	C	PODN	c.C1251T	p.N417N
XH_P38	1	53553754	53553754	Missense_Mutation	SNP	T	C	T	SLC1A7	c.A1787G	p.Q596R
XH_P38	1	54060016	54060016	Missense_Mutation	SNP	G	C	G	GLI51	c.C560G	p.A187G
XH_P38	1	54060248	54060248	Missense_Mutation	SNP	T	C	T	GLI51	c.A328G	p.T110A
XH_P38	1	54690954	54690954	Missense_Mutation	SNP	T	C	T	MRPL37	c.T1351C	p.F451L
XH_P38	1	55060251	55060251	Missense_Mutation	SNP	C	T	C	ACOT11	c.C494T	p.P165L
XH_P38	1	55073681	55073681	Silent	SNP	A	G	A	ACOT11	c.A1569G	p.R523R
XH_P38	1	55119515	55119515	Missense_Mutation	SNP	T	G	T	MROH7	c.T916G	p.V306D
XH_P38	1	55136529	55136529	Missense_Mutation	SNP	T	C	T	MROH7	c.T80C	p.V27A
XH_P38	1	55224131	55224131	Missense_Mutation	SNP	T	C	T	PARS2	c.A704G	p.N235S
XH_P38	1	55224751	55224751	Missense_Mutation	SNP	C	A	C	PARS2	c.G84T	p.R28S
XH_P38	1	55319902	55319902	Silent	SNP	A	G	A	DHCR24	c.T1026C	p.I342I
XH_P38	1	55457710	55457710	Silent	SNP	G	A	G	TMEM61	c.G567A	p.A189A
XH_P38	1	57257817	57257817	Silent	SNP	T	C	T	C1orf168	c.A669G	p.K223K
XH_P38	1	62456014	62456014	Missense_Mutation	SNP	G	A	G	PATJ	c.G3845A	p.R1282H
XH_P38	1	67109335	67109335	Missense_Mutation	SNP	A	G	A	SGIP1	c.A320G	p.K107R
XH_P38	1	68624878	68624878	Silent	SNP	C	T	C	WLS	c.G159A	p.A53A
XH_P38	1	70493890	70493890	Missense_Mutation	SNP	C	G	C	LRRC7	c.C1717G	p.P573A
XH_P38	1	75055419	75055419	Missense_Mutation	SNP	T	C	T	ERICH3	c.A2072G	p.H691R
XH_P38	1	75622616	75622616	Silent	SNP	C	T	C	LHX8	c.C819T	p.H273H
XH_P38	1	78511960	78511960	Missense_Mutation	SNP	C	T	C	GIPC2	c.C182T	p.S61F
XH_P38	1	79095526	79095526	Missense_Mutation	SNP	G	A	G	IFI44L	c.G649A	p.V217I
XH_P38	1	85016177	85016177	Silent	SNP	A	G	A	SPATA1	c.A1254G	p.L418L
XH_P38	1	85031630	85031630	Silent	SNP	G	A	G	CTB5	c.C591T	p.I197I
XH_P38	1	85040069	85040069	Silent	SNP	G	A	G	CTB5	c.C30T	p.R10R
XH_P38	1	87045897	87045902	In_Frame_Del	DEL	CCTACA	-	CCTACA	CLCA4	c.2629_2634del	p.877_878del
XH_P38	1	89732237	89732237	Silent	SNP	G	A	G	GBP5	c.C660T	p.P220P
XH_P38	1	92200382	92200382	Silent	SNP	T	C	T	TGFBR3	c.A519G	p.S173S
XH_P38	1	94342564	94342564	Missense_Mutation	SNP	C	A	C	DNTTIP2	c.G927T	p.E309D
XH_P38	1	94467447	94467447	Silent	SNP	G	A	G	ABCA4	c.C6249T	p.I2083I
XH_P38	1	99225627	99225627	Silent	SNP	G	A	G	SNX7	c.G1131A	p.E377E
XH_P38	1	107867390	107867390	Missense_Mutation	SNP	G	A	G	NTNG1	c.G733A	p.G245R
XH_P38	1	109261509	109261509	Missense_Mutation	SNP	A	G	A	FNDC7	c.A436G	p.I146V
XH_P38	1	109793851	109793851	Missense_Mutation	SNP	G	T	G	CELSR2	c.G1150T	p.A384S
XH_P38	1	109810544	109810544	Silent	SNP	C	A	C	CELSR2	c.C6180A	p.R2060R
XH_P38	1	110086451	110086451	Silent	SNP	G	A	G	GPR61	c.G807A	p.S269S
XH_P38	1	110151395	110151395	Missense_Mutation	SNP	G	T	G	GNAT2	c.C319A	p.L107I
XH_P38	1	110163879	110163879	Missense_Mutation	SNP	G	A	G	AMPD2	c.G244A	p.A82T
XH_P38	1	110466466	110466466	Missense_Mutation	SNP	T	C	T	CSF1	c.T1223C	p.L408P
XH_P38	1	110466555	110466555	Missense_Mutation	SNP	G	A	G	CSF1	c.G1312A	p.G438R
XH_P38	1	110466810	110466810	Silent	SNP	C	A	C	CSF1	c.C1567A	p.R523R
XH_P38	1	110738296	110738296	Silent	SNP	G	A	G	SLC6A17	c.G1581A	p.S527S
XH_P38	1	112524974	112524974	Silent	SNP	C	T	C	KCND3	c.G375A	p.P125P
XH_P38	1	114354942	114354942	Silent	SNP	T	G	T	RSBN1	c.A93C	p.R31R
XH_P38	1	116206423	116206423	Missense_Mutation	SNP	G	A	G	VANGL1	c.G340A	p.A114T
XH_P38	1	116534852	116534852	Silent	SNP	C	T	C	SLC22A15	c.C288T	p.S96S
XH_P38	1	116609185	116609185	Silent	SNP	G	A	G	SLC22A15	c.G1410A	p.T470T
XH_P38	1	117122291	117122291	Missense_Mutation	SNP	C	G	C	IGSF3	c.G3057C	p.E1019D
XH_P38	1	117603156	117603156	Silent	SNP	G	T	G	TTF2	c.G108T	p.T36T
XH_P38	1	118165973	118165973	Silent	SNP	C	T	C	FAM46C	c.C483T	p.N161N
XH_P38	1	119575818	119575818	Missense_Mutation	SNP	C	G	C	WAR52	c.G799C	p.A267P
XH_P38	1	120384205	120384205	Silent	SNP	A	G	A	NBPF7	c.T357C	p.V119V
XH_P38	1	145562293	145562293	Missense_Mutation	SNP	G	C	G	ANKRD35	c.G1711C	p.E571Q
XH_P38	1	145588905	145588905	Silent	SNP	G	A	G	NUDT17	c.C343T	p.L115L
XH_P38	1	146420082	146420082	Missense_Mutation	SNP	T	G	T	NBPF12	c.T2730G	p.C910W
XH_P38	1	147231249	147231249	Missense_Mutation	SNP	C	T	C	GJA5	c.G98A	p.R33H
XH_P38	1	150526406	150526406	Silent	SNP	C	T	C	ADAMTSL4	c.C939T	p.G313G
XH_P38	1	150529523	150529523	Missense_Mutation	SNP	C	T	C	ADAMTSL4	c.C1858T	p.P620S
XH_P38	1	151260611	151260611	Missense_Mutation	SNP	C	T	C	ZNF687	c.C1844T	p.P615L
XH_P38	1	152081108	152081108	Missense_Mutation	SNP	G	A	G	TCHH	c.C4585T	p.R1529W
XH_P38	1	152084175	152084175	In_Frame_Ins	INS	-	TGCTCGCGCCTG	-	TCHH	insGGAGAGGCGG	insG06delinsQERRREQQ
XH_P38	1	152129066	152129101	In_Frame_Del	DEL	TGCTCTTGTTT	-	CTGCTCTTGTTTC	RPTN	c.474_509del	p.158_170del
XH_P38	1	152187799	152187799	Silent	SNP	G	A	G	HRNR	c.C6306T	p.G2102G
XH_P38	1	152188365	152188365	Missense_Mutation	SNP	C	T	C	HRNR	c.G5740A	p.G1914R
XH_P38	1	152191944	152191944	Missense_Mutation	SNP	T	C	T	HRNR	c.A2161G	p.S721G
XH_P38	1	152324952	152324952	Silent	SNP	T	A	T	FLG2	c.A5310T	p.I1770I
XH_P38	1	152324953	152324953	Missense_Mutation	SNP	A	G	A	FLG2	c.T5309C	p.I1770T
XH_P38	1	152328169	152328169	Missense_Mutation	SNP	A	G	A	FLG2	c.T2093C	p.F698S
XH_P38	1	152488146	152488146	Missense_Mutation	SNP	G	A	G	CRCT1	c.G287A	p.C96Y
XH_P38	1	152552285	152552285	Missense_Mutation	SNP	C	A	C	LCE3D	c.G128T	p.G43V
XH_P38	1	152659471	152659471	Missense_Mutation	SNP	T	G	T	LCE2B	c.T152G	p.I51S
XH_P38	1	152681689	152681689	In_Frame_Ins	INS	-	TGCTGTAGTCTCT	-	LCE4A	insGGCTGCTGTAT	insG46delinsGCCSSG

XH_P38	1	152681835	152681835	Missense_Mutation	SNP	G	T	G	LCE4A	c.G284T	p.G95V
XH_P38	1	152692074	152692074	Missense_Mutation	SNP	G	C	G	C1orf68	c.G77C	p.S26T
XH_P38	1	152733301	152733301	Missense_Mutation	SNP	T	A	T	KPRP	c.T1237A	p.C413S
XH_P38	1	152749008	152749008	In_Frame_Ins	INS	-	CTCTGGGGGCTC	-	LCE1F	nsCAGCTCTGGGGY54delinsSSSGGC	
XH_P38	1	152777908	152777908	Missense_Mutation	SNP	C	T	C	LCE1C	c.G47A	p.C16Y
XH_P38	1	152944499	152944499	Missense_Mutation	SNP	C	T	C	SPRR4	c.C133T	p.P45S
XH_P38	1	153233578	153233578	Silent	SNP	C	T	C	LOR	c.C153T	p.C51C
XH_P38	1	153233701	153233701	Silent	SNP	A	C	A	LOR	c.A276C	p.G92G
XH_P38	1	153233991	153233991	In_Frame_Ins	INS	-	CTCTGGGGCGG	-	LOR	567insCTCTGGGGY189delinsYSGGG	
XH_P38	1	153320372	153320372	Missense_Mutation	SNP	T	G	T	PGLYRP4	c.A37C	p.I13L
XH_P38	1	153333264	153333264	Missense_Mutation	SNP	G	A	G	S100A9	c.G295A	p.E99K
XH_P38	1	153750682	153750682	Missense_Mutation	SNP	G	A	G	SLC27A3	c.G1591A	p.G531R
XH_P38	1	154548306	154548306	Silent	SNP	C	G	C	CHRN2	c.C1407G	p.V469V
XH_P38	1	154744807	154744807	Silent	SNP	C	G	C	KCNN3	c.G1092C	p.L364L
XH_P38	1	154918939	154918939	Missense_Mutation	SNP	A	T	A	PBXIP1	c.T746A	p.L249Q
XH_P38	1	155007165	155007165	Missense_Mutation	SNP	A	G	A	DCST1	c.A224G	p.Y75C
XH_P38	1	155028450	155028450	Missense_Mutation	SNP	C	A	C	ADAM15	c.C748A	p.L250M
XH_P38	1	155239438	155239438	Silent	SNP	G	A	G	CLK2	c.C240T	p.N80N
XH_P38	1	156144971	156144971	Missense_Mutation	SNP	G	A	G	SEMA4A	c.G1133A	p.R378Q
XH_P38	1	156206121	156206121	Missense_Mutation	SNP	G	A	G	PMF1	c.G204A	p.M68I
XH_P38	1	156214533	156214533	Missense_Mutation	SNP	G	A	G	PAQR6	c.C257T	p.P86L
XH_P38	1	156233189	156233189	Silent	SNP	C	T	C	SMG5	c.G1890A	p.A630A
XH_P38	1	156255456	156255456	Missense_Mutation	SNP	G	A	G	TMEM79	c.G439A	p.V147M
XH_P38	1	156526387	156526387	Missense_Mutation	SNP	C	G	C	IQGAP3	c.G1228C	p.V410L
XH_P38	1	156846233	156846233	Silent	SNP	G	A	G	NTRK1	c.G1656A	p.Q552Q
XH_P38	1	157069154	157069154	Silent	SNP	A	G	A	ETV3L	c.T75C	p.D25D
XH_P38	1	157771880	157771880	Silent	SNP	C	T	C	FCRL1	c.G711A	p.P237P
XH_P38	1	158435927	158435927	Silent	SNP	C	A	C	OR10K1	c.C576A	p.S192S
XH_P38	1	158725080	158725080	Missense_Mutation	SNP	C	T	C	OR6K6	c.C475T	p.R159C
XH_P38	1	159175428	159175428	Missense_Mutation	SNP	C	T	C	ACKR1	c.C205T	p.L69F
XH_P38	1	159409857	159409857	Missense_Mutation	SNP	A	G	A	OR10J1	c.A309G	p.I103M
XH_P38	1	159505297	159505297	Silent	SNP	C	T	C	OR10J5	c.G501A	p.P167P
XH_P38	1	159912899	159912899	Missense_Mutation	SNP	C	T	C	IGSF9	c.G101A	p.G34E
XH_P38	1	160062340	160062340	Silent	SNP	G	A	G	IGSF8	c.C1458T	p.D486D
XH_P38	1	160098543	160098543	Silent	SNP	G	A	G	ATP1A2	c.G1119A	p.S373S
XH_P38	1	160105002	160105002	Missense_Mutation	SNP	A	G	A	ATP1A2	c.A2032G	p.I678V
XH_P38	1	160322763	160322763	Silent	SNP	A	G	A	NCSTN	c.A669G	p.S223S
XH_P38	1	161021261	161021261	Silent	SNP	C	T	C	ARHGAP30	c.G732A	p.P244P
XH_P38	1	161088583	161088583	Missense_Mutation	SNP	T	G	T	NIT1	c.T10G	p.F4V
XH_P38	1	161139738	161139738	Missense_Mutation	SNP	G	A	G	PPOX	c.G812A	p.R271H
XH_P38	1	161145005	161145005	Silent	SNP	C	T	C	B4GALT3	c.G267A	p.S89S
XH_P38	1	161161284	161161284	Missense_Mutation	SNP	G	C	G	ADAMTS4	c.C2158G	p.P720A
XH_P38	1	161167854	161167854	Silent	SNP	G	A	G	ADAMTS4	c.C564T	p.S188S
XH_P38	1	161172233	161172233	Missense_Mutation	SNP	C	A	C	NDUFS2	c.C58A	p.P20T
XH_P38	1	161643798	161643798	Missense_Mutation	SNP	T	C	T	FCGR2B	c.T674C	p.I225T
XH_P38	1	161697072	161697072	Missense_Mutation	SNP	G	C	G	FCRLB	c.G735C	p.Q245H
XH_P38	1	161697149	161697149	Missense_Mutation	SNP	G	T	G	FCRLB	c.G812T	p.R271L
XH_P38	1	161970046	161970046	Missense_Mutation	SNP	A	G	A	OLFML2B	c.T809C	p.L270P
XH_P38	1	166039898	166039898	Silent	SNP	C	G	C	FAM78B	c.G366C	p.V122V
XH_P38	1	169510118	169510118	Missense_Mutation	SNP	G	A	G	F5	c.C4210T	p.P1404S
XH_P38	1	169510380	169510380	Silent	SNP	G	A	G	F5	c.C3948T	p.L1316L
XH_P38	1	170928671	170928671	Missense_Mutation	SNP	T	C	T	MROH9	c.T221C	p.V74A
XH_P38	1	171083242	171083242	Missense_Mutation	SNP	A	G	A	FMO3	c.A734G	p.E245G
XH_P38	1	171292269	171292269	Missense_Mutation	SNP	T	G	T	FMO4	c.T259G	p.F87V
XH_P38	1	171486912	171486912	Missense_Mutation	SNP	G	A	G	PRRC2C	c.G703A	p.A235T
XH_P38	1	175375469	175375469	Missense_Mutation	SNP	C	A	C	TNR	c.G382T	p.A128S
XH_P38	1	176175910	176175910	Silent	SNP	A	G	A	RFWD2	c.T205C	p.L69L
XH_P38	1	176564219	176564219	Silent	SNP	T	C	T	PAPPA2	c.T1479C	p.P493P
XH_P38	1	177902753	177902753	Missense_Mutation	SNP	G	C	G	SEC16B	c.C2590G	p.P864A
XH_P38	1	178489978	178489978	Missense_Mutation	SNP	T	G	T	TEX35	c.T536G	p.L179R
XH_P38	1	179312752	179312752	Silent	SNP	C	T	C	SOAT1	c.C795T	p.V265V
XH_P38	1	180064742	180064742	Missense_Mutation	SNP	G	A	G	CEP350	c.G8596A	p.A2866T
XH_P38	1	180897569	180897569	Silent	SNP	C	T	C	KIAA1614	c.C1065T	p.T355T
XH_P38	1	180905448	180905448	Missense_Mutation	SNP	G	T	G	KIAA1614	c.G2403T	p.L801F
XH_P38	1	182353547	182353547	Missense_Mutation	SNP	T	G	T	GLUL	c.A1115C	p.K372T
XH_P38	1	182496829	182496829	Missense_Mutation	SNP	A	G	A	RGSL1	c.A2047G	p.I683V
XH_P38	1	184723721	184723721	Missense_Mutation	SNP	T	G	T	EDEM3	c.A60C	p.R20S
XH_P38	1	184765072	184765072	Missense_Mutation	SNP	A	G	A	FAM129A	c.T1826C	p.L609P
XH_P38	1	185984517	185984517	Silent	SNP	T	C	T	HMCN1	c.T4857C	p.H1619H
XH_P38	1	193074651	193074651	Missense_Mutation	SNP	T	A	T	GLRX2	c.A118T	p.R40W
XH_P38	1	196695742	196695742	Silent	SNP	A	G	A	CFH	c.A2016G	p.Q672Q
XH_P38	1	196709774	196709774	Missense_Mutation	SNP	G	T	G	CFH	c.G2808T	p.E936D
XH_P38	1	196799691	196799691	Silent	SNP	G	A	G	CFHR1	c.G669A	p.P223P
XH_P38	1	197898321	197898321	Missense_Mutation	SNP	G	A	G	LHX9	c.G1126A	p.V376M
XH_P38	1	200089966	200089966	Missense_Mutation	SNP	G	A	G	NR5A2	c.G1045A	p.G349R
XH_P38	1	200534248	200534248	Silent	SNP	C	T	C	KIF14	c.G2547A	p.E849E
XH_P38	1	200558363	200558363	Silent	SNP	T	C	T	KIF14	c.A1623G	p.E541E
XH_P38	1	201022376	201022376	Silent	SNP	G	A	G	CACNA1S	c.C3822T	p.I1274I
XH_P38	1	201035071	201035071	Silent	SNP	G	A	G	CACNA1S	c.C2748T	p.H916H
XH_P38	1	201061138	201061138	Missense_Mutation	SNP	C	T	C	CACNA1S	c.G503A	p.R168Q
XH_P38	1	201184939	201184939	Missense_Mutation	SNP	C	A	C	IGFN1	c.C9268A	p.Q3090K
XH_P38	1	201286771	201286771	Silent	SNP	C	T	C	PKP1	c.C918T	p.A306A
XH_P38	1	201355522	201355522	Missense_Mutation	SNP	T	C	T	LAD1	c.A967G	p.K323E
XH_P38	1	201358304	201358304	Missense_Mutation	SNP	C	A	C	LAD1	c.G166T	p.A56S
XH_P38	1	202183308	202183308	Missense_Mutation	SNP	C	T	C	LGR6	c.C26T	p.S9L
XH_P38	1	202304868	202304868	Silent	SNP	T	C	T	UBE2T	c.A15G	p.S5S
XH_P38	1	202565948	202565948	Silent	SNP	G	A	G	SYT2	c.C1197T	p.I399I
XH_P38	1	203024722	203024722	Silent	SNP	A	T	A	PPFIA4	c.A1992T	p.P664P
XH_P38	1	203276546	203276546	Missense_Mutation	SNP	G	A	G	BTG2	c.G457A	p.V153M
XH_P38	1	204159612	204159612	Nonstop_Mutation	DEL	T	-	T	KISS1	c.417delA	p.X139W
XH_P38	1	204159787	204159787	Missense_Mutation	SNP	G	C	G	KISS1	c.C242G	p.P81R
XH_P38	1	204197356	204197356	Silent	SNP	A	G	A	PLEKHA6	c.T2886C	p.S962S
XH_P38	1	204380483	204380483	Silent	SNP	C	G	G	PPP1R15B	c.G57C	p.R19R
XH_P38	1	204396830	204396830	Silent	SNP	G	A	G	PIK3C2B	c.C4533T	p.S1511S
XH_P38	1	205273346	205273346	Silent	SNP	C	T	C	NUAK2	c.G1251A	p.S417S
XH_P38	1	205290794	205290794	Missense_Mutation	SNP	G	A	G	NUAK2	c.C95T	p.T32I
XH_P38	1	205306692	205306692	Silent	SNP	C	T	C	KLHDC8A	c.G888A	p.A296A
XH_P38	1	205561372	205561372	Silent	SNP	C	T	C	MFSD4A	c.C1254T	p.F418F

XH_P38	1	206651107	206651107	Silent	SNP	G	A	G	IKBKE	c.G462A	p.T154T
XH_P38	1	206665052	206665052	Missense_Mutation	SNP	C	T	C	IKBKE	c.C1550T	p.A517V
XH_P38	1	208207839	208207839	Silent	SNP	G	A	G	PLXNA2	c.C4863T	p.Y1621Y
XH_P38	1	208391098	208391098	Missense_Mutation	SNP	T	C	T	PLXNA2	c.A170G	p.Q57R
XH_P38	1	209785206	209785206	Missense_Mutation	SNP	G	A	G	CAMK1G	c.G985A	p.V329I
XH_P38	1	209788703	209788703	Silent	SNP	T	C	T	LAMB3	c.A3432G	p.S1144S
XH_P38	1	209791929	209791929	Missense_Mutation	SNP	G	T	G	LAMB3	c.C2777A	p.A926D
XH_P38	1	209799205	209799205	Silent	SNP	A	G	A	LAMB3	c.T1764C	p.Y588Y
XH_P38	1	210004199	210004199	Missense_Mutation	SNP	C	G	C	DIEXF	c.C199G	p.Q67E
XH_P38	1	212798336	212798336	Missense_Mutation	SNP	A	G	A	FAM71A	c.A117G	p.I39M
XH_P38	1	213031948	213031948	Missense_Mutation	SNP	G	C	G	FLVCR1	c.G154C	p.A52P
XH_P38	1	214813782	214813782	Missense_Mutation	SNP	A	G	A	CENPF	c.A2101G	p.M701V
XH_P38	1	214814733	214814733	Missense_Mutation	SNP	T	G	T	CENPF	c.T3052G	p.Y1018D
XH_P38	1	214814778	214814778	Missense_Mutation	SNP	G	A	G	CENPF	c.G3097A	p.G1033R
XH_P38	1	214818846	214818846	Missense_Mutation	SNP	A	G	A	CENPF	c.A5933G	p.D1978G
XH_P38	1	214819587	214819587	Missense_Mutation	SNP	A	G	A	CENPF	c.A6674G	p.Q2225R
XH_P38	1	214826196	214826196	Missense_Mutation	SNP	G	A	G	CENPF	c.G8186A	p.R2729Q
XH_P38	1	214830617	214830617	Missense_Mutation	SNP	A	G	A	CENPF	c.A8827G	p.R2943G
XH_P38	1	222802783	222802783	Missense_Mutation	SNP	C	T	C	MIA3	c.C2221T	p.R741W
XH_P38	1	223116472	223116472	Missense_Mutation	SNP	G	A	G	DISP1	c.G307A	p.E103K
XH_P38	1	223116474	223116474	Missense_Mutation	SNP	G	T	G	DISP1	c.G309T	p.E103D
XH_P38	1	223905532	223905532	Silent	SNP	G	A	G	CAPN2	c.G72A	p.L24L
XH_P38	1	223934720	223934720	Silent	SNP	G	A	G	CAPN2	c.G348A	p.A116A
XH_P38	1	226075608	226075608	Silent	SNP	G	A	G	LEFTY1	c.C375T	p.V125V
XH_P38	1	226352498	226352498	Missense_Mutation	SNP	T	G	T	ACBD3	c.A561C	p.E187D
XH_P38	1	226924569	226924569	Missense_Mutation	SNP	G	T	G	ITPKB	c.C591A	p.S197R
XH_P38	1	228113046	228113046	Silent	SNP	C	T	C	WNT9A	c.G270A	p.A90A
XH_P38	1	228335125	228335125	Silent	SNP	C	T	C	GUK1	c.C333T	p.A111A
XH_P38	1	228346425	228346425	Silent	SNP	G	C	G	GJC2	c.G966C	p.A322A
XH_P38	1	228404198	228404198	Silent	SNP	G	A	A	OBSCN	c.G2172A	p.A724A
XH_P38	1	228433346	228433346	Silent	SNP	C	T	C	OBSCN	c.C3714T	p.C1238C
XH_P38	1	228437772	228437772	Silent	SNP	G	A	G	OBSCN	c.G4140A	p.E1380E
XH_P38	1	228451826	228451826	Missense_Mutation	SNP	C	T	C	OBSCN	c.C4595T	p.A1532V
XH_P38	1	228468244	228468244	Silent	SNP	G	A	G	OBSCN	c.G7944A	p.V2648V
XH_P38	1	228526665	228526665	Silent	SNP	T	C	T	OBSCN	c.T17196C	p.A5732A
XH_P38	1	228528563	228528563	Missense_Mutation	SNP	C	G	C	OBSCN	c.C17671G	p.Q5891E
XH_P38	1	228550426	228550426	Missense_Mutation	SNP	C	T	C	OBSCN	c.C18811T	p.P6271S
XH_P38	1	228564884	228564884	Missense_Mutation	SNP	G	A	G	OBSCN	c.G23171A	p.R7724H
XH_P38	1	228588680	228588680	Silent	SNP	A	C	A	TRIM11	c.T720G	p.A240A
XH_P38	1	228602660	228602660	Silent	SNP	G	C	G	TRIM17	c.C114G	p.A38A
XH_P38	1	229730452	229730452	Silent	SNP	G	A	G	TAF5L	c.C1362T	p.S454S
XH_P38	1	229738170	229738170	Silent	SNP	T	G	T	TAF5L	c.G474C	p.R248R
XH_P38	1	229772693	229772693	Missense_Mutation	SNP	T	G	T	URB2	c.T2333G	p.V778G
XH_P38	1	230845977	230845977	Missense_Mutation	SNP	G	A	G	AGT	c.C620T	p.T207M
XH_P38	1	230846449	230846449	Missense_Mutation	SNP	T	A	T	AGT	c.A148T	p.T50S
XH_P38	1	230898397	230898397	Splice_Site	SNP	A	G	A	CAPN9	.	.
XH_P38	1	231298898	231298898	Silent	SNP	C	A	C	TRIM67	c.C183A	p.A61A
XH_P38	1	231488524	231488524	Missense_Mutation	SNP	C	T	C	SPRTN	c.C887T	p.P296L
XH_P38	1	232649870	232649870	Missense_Mutation	SNP	C	T	C	SIPA1L2	c.G1216A	p.V406I
XH_P38	1	232650867	232650867	Silent	SNP	C	T	C	SIPA1L2	c.G219A	p.K73K
XH_P38	1	233121951	233121951	Missense_Mutation	SNP	C	T	C	PCNX2	c.G6127A	p.V2043I
XH_P38	1	234744250	234744250	Silent	SNP	G	A	G	IRF2BP2	c.C991T	p.L331L
XH_P38	1	234744413	234744413	Silent	SNP	C	A	C	IRF2BP2	c.G828T	p.A276A
XH_P38	1	234745009	234745009	Missense_Mutation	SNP	A	G	A	IRF2BP2	c.T232C	p.S78P
XH_P38	1	236925844	236925844	Silent	SNP	G	A	G	ACTN2	c.G2610A	p.S870S
XH_P38	1	237058748	237058748	Silent	SNP	C	T	C	MTR	c.C3343T	p.L1115L
XH_P38	1	240256822	240256822	Silent	SNP	C	A	C	FMN2	c.C1413A	p.A471A
XH_P38	1	241712134	241712134	Silent	SNP	C	T	C	KMO	c.C60T	p.G20G
XH_P38	1	242045275	242045275	Missense_Mutation	SNP	C	T	C	EXO1	c.C2167T	p.R723C
XH_P38	1	246021941	246021941	Silent	SNP	T	C	T	SMYD3	c.A933G	p.A311A
XH_P38	1	247752367	247752367	Missense_Mutation	SNP	A	G	A	OR2G2	c.A706G	p.R236G
XH_P38	1	248028219	248028219	Silent	SNP	G	A	G	TRIM58	c.G729A	p.P243P
XH_P38	1	248039451	248039451	Missense_Mutation	SNP	C	T	C	TRIM58	c.C1121T	p.T374M
XH_P38	1	248059252	248059252	Missense_Mutation	SNP	C	T	C	OR2W3	c.C364T	p.R122W
XH_P38	1	248059612	248059612	Missense_Mutation	SNP	G	A	G	OR2W3	c.G724A	p.G242S
XH_P38	1	248085149	248085149	Missense_Mutation	SNP	C	G	C	OR2T8	c.C830G	p.T277S
XH_P38	1	248202344	248202344	Missense_Mutation	SNP	G	C	G	OR2L2	c.G775C	p.V259L
XH_P38	1	248224099	248224099	Missense_Mutation	SNP	T	C	T	OR2L3	c.T116C	p.I39T
XH_P38	1	248224754	248224754	Silent	SNP	T	C	T	OR2L3	c.T771C	p.T257T
XH_P38	1	248366702	248366702	Silent	SNP	G	A	G	OR2M3	c.G333A	p.E111E
XH_P38	1	248487783	248487783	Missense_Mutation	SNP	G	T	G	OR2M7	c.C88A	p.L30M
XH_P38	1	249108778	249108778	Missense_Mutation	SNP	C	T	C	SH3BP5L	c.G50A	p.R17Q
XH_P38	1	249142018	249142018	Missense_Mutation	SNP	C	T	C	ZNF672	c.C545T	p.A182V
XH_P38	2	1418192	1418192	Silent	SNP	C	G	C	TPO	c.C12G	p.L4L
XH_P38	2	1481231	1481231	Missense_Mutation	SNP	G	C	G	TPO	c.G1193C	p.S398T
XH_P38	2	1652912	1652912	Silent	SNP	G	C	G	PXDN	c.C2640G	p.R880R
XH_P38	2	1795716	1795716	Missense_Mutation	SNP	G	T	G	MYT1L	c.C3484A	p.Q1162K
XH_P38	2	1795717	1795717	Silent	SNP	A	G	A	MYT1L	c.T3483C	p.N1161N
XH_P38	2	1946968	1946968	Silent	SNP	C	T	C	MYT1L	c.G291A	p.E97E
XH_P38	2	3691548	3691548	Missense_Mutation	SNP	A	G	A	COLEC11	c.A434G	p.H145R
XH_P38	2	6990020	6990020	Silent	SNP	C	T	C	CMKP2	c.G1311A	p.T437T
XH_P38	2	9983686	9983686	Missense_Mutation	SNP	G	T	G	TAF1B	c.G16T	p.A6S
XH_P38	2	11053416	11053416	Silent	SNP	C	T	C	KCNF1	c.C864T	p.A288A
XH_P38	2	11053740	11053740	Silent	SNP	C	T	C	KCNF1	c.C1188T	p.I396I
XH_P38	2	11702661	11702661	Missense_Mutation	SNP	A	C	A	GREB1	c.A230C	p.N77T
XH_P38	2	11733134	11733134	Silent	SNP	C	G	C	GREB1	c.C1578G	p.A526A
XH_P38	2	11817812	11817812	Missense_Mutation	SNP	G	C	G	LPIN1	c.C39C	p.E13D
XH_P38	2	17962994	17962998	Frame_Shift_Del	DEL	AAGTT	-	AAGTT	GEN1	c.2515_2519de	p.K839fs
XH_P38	2	18768850	18768850	Silent	SNP	A	G	A	NT5C1B	c.T39C	p.P13P
XH_P38	2	21232478	21232478	Missense_Mutation	SNP	T	C	T	APOB	c.A7262G	p.D2421G
XH_P38	2	24929851	24929851	Silent	SNP	A	T	A	NCOA1	c.A1512T	p.P504P
XH_P38	2	26204640	26204640	Silent	SNP	G	A	G	KIF3C	c.C147T	p.A49A
XH_P38	2	26455127	26455127	Silent	SNP	G	A	G	HADHA	c.C474T	p.Y158Y
XH_P38	2	26534322	26534322	Silent	SNP	G	A	G	ADGRF3	c.C1677T	p.L559L
XH_P38	2	26699855	26699855	Silent	SNP	G	C	G	OTOF	c.C510G	p.V170V
XH_P38	2	26739423	26739423	Silent	SNP	T	C	T	OTOF	c.A372G	p.T124T
XH_P38	2	26760593	26760593	Silent	SNP	G	A	G	OTOF	c.C129T	p.D43D
XH_P38	2	26800422	26800422	Missense_Mutation	SNP	G	A	G	C2orf70	c.G349A	p.G117R

XH_P38	2	28854958	28854958	Missense_Mutation	SNP	C	T	C	PLB1	c.C3920T	p.A1307V
XH_P38	2	33774761	33774761	Silent	SNP	T	C	T	RASGRP3	c.T1482C	p.H494H
XH_P38	2	36739435	36739435	Frame_Shift_Ins	INS	-	A	-	CRIM1	c.1679dupA	p.D560fs
XH_P38	2	38604351	38604351	Missense_Mutation	SNP	A	G	A	ATL2	c.T52C	p.W18R
XH_P38	2	38916970	38916970	Missense_Mutation	SNP	A	T	A	GALM	c.A568T	p.N190Y
XH_P38	2	42275664	42275664	Missense_Mutation	SNP	T	C	T	PKDCC	c.T325C	p.S109P
XH_P38	2	42275819	42275819	Silent	SNP	T	C	T	PKDCC	c.T480C	p.G160G
XH_P38	2	43452183	43452183	Silent	SNP	A	G	A	ZFP36L2	c.T760C	p.L254L
XH_P38	2	43804229	43804229	Silent	SNP	T	C	T	THADA	c.A969G	p.G323G
XH_P38	2	44099433	44099433	Missense_Mutation	SNP	C	A	C	ABCG8	c.C1199A	p.T400K
XH_P38	2	46609572	46609572	Missense_Mutation	SNP	A	C	A	EPAS1	c.A2296C	p.T766P
XH_P38	2	55186394	55186394	Silent	SNP	A	C	A	EML6	c.A4849C	p.R1617R
XH_P38	2	65217089	65217089	Silent	SNP	G	C	G	SLC1A4	c.G312C	p.S104S
XH_P38	2	65296657	65296657	Missense_Mutation	SNP	A	G	A	CEP68	c.A79G	p.R27G
XH_P38	2	65298839	65298839	Silent	SNP	A	G	A	CEP68	c.A609G	p.T203T
XH_P38	2	65299766	65299766	Silent	SNP	T	C	T	CEP68	c.T1536C	p.D512D
XH_P38	2	69040500	69040500	Silent	SNP	G	A	G	ARHGAP25	c.G735A	p.Q245Q
XH_P38	2	70315174	70315174	Missense_Mutation	SNP	T	A	T	PCBP1	c.T299A	p.L100Q
XH_P38	2	70408526	70408526	Missense_Mutation	SNP	T	C	T	C2orf42	c.A592G	p.K198E
XH_P38	2	70933460	70933460	Silent	SNP	G	A	G	ADD2	c.C129T	p.D43D
XH_P38	2	71170807	71170807	Silent	SNP	C	T	C	ATP6V1B1	c.C138T	p.S46S
XH_P38	2	71190384	71190384	Silent	SNP	C	T	C	ATP6V1B1	c.C1002T	p.R334R
XH_P38	2	71211259	71211259	Nonsense_Mutation	SNP	G	T	G	ANKRD53	c.G910T	p.G304X
XH_P38	2	71211815	71211815	Silent	SNP	G	A	G	ANKRD53	c.G978A	p.L326L
XH_P38	2	71221822	71221822	Silent	SNP	A	G	A	TEX261	c.T66C	p.A22A
XH_P38	2	71658541	71658541	Missense_Mutation	SNP	C	T	C	ZNFX638	c.C5735T	p.A1912V
XH_P38	2	71791211	71791211	Silent	SNP	C	T	C	DYSF	c.C2337T	p.I779I
XH_P38	2	71827854	71827854	Missense_Mutation	SNP	G	A	G	DYSF	c.G3683A	p.R1228H
XH_P38	2	71838597	71838597	Silent	SNP	C	A	C	DYSF	c.C3966A	p.I1322I
XH_P38	2	73339708	73339708	Silent	SNP	G	A	G	RAB11FIP5	c.C198T	p.C66C
XH_P38	2	74489318	74489318	Missense_Mutation	SNP	G	A	G	SLC4A5	c.C757T	p.H253Y
XH_P38	2	74642265	74642265	In_Frame_Ins	INS	-	GGGGCGGGTGG	-	C2orf81	GGGGCGGGTGG	delinsGGGATPSPAS
XH_P38	2	74726590	74726590	Silent	SNP	G	A	G	LBX2	c.C75T	p.V25V
XH_P38	2	74761539	74761539	Missense_Mutation	SNP	T	A	T	LOXL3	c.A760T	p.I254F
XH_P38	2	74763258	74763258	Silent	SNP	C	G	C	LOXL3	c.G30C	p.L10L
XH_P38	2	80529738	80529738	Missense_Mutation	SNP	C	A	C	LRRTM1	c.G1207T	p.D403Y
XH_P38	2	80529956	80529956	Missense_Mutation	SNP	T	C	T	LRRTM1	c.A989G	p.N330S
XH_P38	2	86272758	86272758	Silent	SNP	G	A	G	POLR1A	c.C2868T	p.L956L
XH_P38	2	87042751	87042751	Missense_Mutation	SNP	G	A	G	CD8B	c.C584T	p.T195I
XH_P38	2	96780716	96780716	Silent	SNP	T	G	T	ADRA2B	c.A1173C	p.G391G
XH_P38	2	96780986	96780986	In_Frame_Ins	INS	-	TCCTCCTCT	-	ADRA2B	903insAGAGG	delinsEEEE
XH_P38	2	96795600	96795600	Silent	SNP	G	A	G	ASTL	c.C837T	p.Y279Y
XH_P38	2	97508140	97508140	Missense_Mutation	SNP	G	A	G	ANKRD23	c.C136T	p.R46W
XH_P38	2	99779131	99779131	Silent	SNP	T	C	T	LIPT1	c.T711C	p.A237A
XH_P38	2	101587455	101587455	Silent	SNP	C	T	C	NPAS2	c.C1059T	p.Y353Y
XH_P38	2	101925026	101925026	Missense_Mutation	SNP	T	C	T	RNF149	c.A25G	p.S9G
XH_P38	2	102793187	102793187	Missense_Mutation	SNP	C	G	C	IL1R1	c.C1246G	p.L416V
XH_P38	2	105858982	105858982	Missense_Mutation	SNP	C	T	T	GPR45	c.C667T	p.R223C
XH_P38	2	107049593	107049593	Missense_Mutation	SNP	T	C	T	RGPD3	c.A2354G	p.K785R
XH_P38	2	108487330	108487330	Missense_Mutation	SNP	A	G	A	RGPD4	c.A2870G	p.N957S
XH_P38	2	110373197	110373197	Silent	SNP	G	A	G	SOWAHC	c.G1131A	p.K377K
XH_P38	2	112994154	112994154	Silent	SNP	G	A	G	ZC3H8	c.C489T	p.S163S
XH_P38	2	113147159	113147159	Silent	SNP	G	A	G	RGPD5	c.C3363T	p.P1121P
XH_P38	2	114220055	114220055	Silent	SNP	T	C	T	CBWD2	c.T646C	p.L216L
XH_P38	2	119915509	119915509	Silent	SNP	G	T	G	C1QL2	c.C337A	p.R133R
XH_P38	2	120223366	120223366	Missense_Mutation	SNP	G	A	G	SCTR	c.C502T	p.R168W
XH_P38	2	121103903	121103903	Missense_Mutation	SNP	T	G	T	INHBB	c.T139G	p.S47A
XH_P38	2	127656857	127656857	Silent	SNP	G	A	G	TEX51	c.G210A	p.T70T
XH_P38	2	127816632	127816632	Silent	SNP	G	A	G	BIN1	c.C792T	p.A264A
XH_P38	2	128180872	128180872	Silent	SNP	G	T	G	PROC	c.G423T	p.S141S
XH_P38	2	128186063	128186063	Silent	SNP	C	T	C	PROC	c.C927T	p.A309A
XH_P38	2	128393800	128393800	Silent	SNP	T	C	T	MYO7B	c.T5946C	p.Y1982Y
XH_P38	2	128394955	128394955	Missense_Mutation	SNP	A	G	A	MYO7B	c.A6314G	p.Q2105R
XH_P38	2	130737899	130737899	Missense_Mutation	SNP	G	T	G	RAB6C	c.G211T	p.G71C
XH_P38	2	133489401	133489401	Silent	SNP	A	G	A	NCKAP5	c.T1395C	p.D465D
XH_P38	2	135781035	135781035	Missense_Mutation	SNP	C	T	C	MAP3K19	c.G65A	p.R22Q
XH_P38	2	141274576	141274576	Silent	SNP	T	C	T	LRP1B	c.A8031G	p.Q2677Q
XH_P38	2	152410418	152410418	Missense_Mutation	SNP	C	T	C	NEB	c.G14411A	p.R4804H
XH_P38	2	159481643	159481643	Missense_Mutation	SNP	G	A	G	PKP4	c.G857A	p.R286Q
XH_P38	2	160994362	160994362	Missense_Mutation	SNP	C	A	C	ITGB6	c.G958T	p.A320S
XH_P38	2	161029218	161029218	Silent	SNP	G	A	G	ITGB6	c.C498T	p.D166D
XH_P38	2	163005674	163005674	Silent	SNP	G	A	G	GCG	c.C15T	p.Y5Y
XH_P38	2	163291981	163291981	Silent	SNP	G	A	G	KCNH7	c.C1660T	p.L554L
XH_P38	2	166245230	166245230	Silent	SNP	T	A	T	SCN2A	c.T4914A	p.R1638R
XH_P38	2	169103796	169103796	In_Frame_Ins	INS	-	GCCGGG	-	STK39	49_150insCCCCG	delinsAPA
XH_P38	2	171678625	171678625	Silent	SNP	T	C	T	GAD1	c.T111C	p.H37H
XH_P38	2	172966250	172966250	Silent	SNP	T	C	T	DLX2	c.A525G	p.Q175Q
XH_P38	2	172967128	172967128	In_Frame_Ins	INS	-	GCT	-	DLX2	138_139insAG	delinsSL
XH_P38	2	176964652	176964652	Frame_Shift_Del	DEL	T	-	T	HOXD12	c.123delT	p.P41fs
XH_P38	2	178482596	178482596	Silent	SNP	T	G	T	ITC30A	c.A834C	p.P278P
XH_P38	2	178482974	178482974	Silent	SNP	A	G	A	ITC30A	c.T456C	p.N152N
XH_P38	2	179474668	179474668	Missense_Mutation	SNP	G	A	G	TTN	c.C24287T	p.A8096V
XH_P38	2	179497025	179497025	Silent	SNP	A	G	A	TTN	c.T16401C	p.N5467N
XH_P38	2	179605497	179605497	Missense_Mutation	SNP	C	T	C	TTN	c.G11374A	p.V3792I
XH_P38	2	179644855	179644855	Missense_Mutation	SNP	T	C	T	TTN	c.A3463G	p.K1155E
XH_P38	2	179650701	179650701	Silent	SNP	C	T	C	TTN	c.G2106A	p.E702E
XH_P38	2	179698945	179698945	Silent	SNP	G	A	G	CCDC141	c.C4548T	p.V1516V
XH_P38	2	182403891	182403891	Missense_Mutation	SNP	G	C	G	CERKL	c.C1127G	p.T376S
XH_P38	2	191064753	191064753	Missense_Mutation	SNP	C	T	C	C2orf88	c.C167T	p.T56I
XH_P38	2	191231503	191231503	Silent	SNP	G	A	G	INPP1	c.G348A	p.V116V
XH_P38	2	197021276	197021276	Silent	SNP	T	C	T	STK17B	c.A222G	p.R74R
XH_P38	2	201342616	201342616	Silent	SNP	C	T	C	SPATS2L	c.C1332T	p.H444H
XH_P38	2	201354935	201354935	Missense_Mutation	SNP	C	G	C	KCTD18	c.G1169C	p.C390S
XH_P38	2	202358592	202358592	In_Frame_Ins	INS	-	AGA	-	C2CD6	2471_2472insT	delinsHL
XH_P38	2	202358593	202358593	Missense_Mutation	SNP	T	A	T	C2CD6	c.A2471T	p.H824L
XH_P38	2	202508115	202508115	Silent	SNP	A	C	A	TMEM237	c.T9G	p.T3T
XH_P38	2	203500326	203500326	In_Frame_Ins	INS	-	GCC	-	FAM117B	416_417insG	delinsRP
XH_P38	2	204305093	204305093	Silent	SNP	T	C	T	RAPH1	c.A2820G	p.P940P

XH_P38	2	207041441	207041441	Silent	SNP	G	A	G	GPR1	c.C531T	p.D177D
XH_P38	2	207824384	207824384	Missense_Mutation	SNP	T	G	T	CPO	c.T402G	p.S134R
XH_P38	2	210860289	210860289	Silent	SNP	G	A	G	UNC80	c.G9675A	p.T3225T
XH_P38	2	215865575	215865575	Silent	SNP	T	C	T	ABCA12	c.A2079G	p.P693P
XH_P38	2	217148417	217148417	Silent	SNP	C	A	C	MARCH4	c.G552T	p.S184S
XH_P38	2	218682474	218682474	Silent	SNP	A	G	A	TNS1	c.T4206C	p.S1402S
XH_P38	2	218682771	218682771	Silent	SNP	A	G	A	TNS1	c.T3909C	p.G1303G
XH_P38	2	219257795	219257795	Missense_Mutation	SNP	G	A	G	SLC11A1	c.G1256A	p.R419Q
XH_P38	2	219503113	219503113	Silent	SNP	C	T	C	ZNFI42	c.G5013A	p.E1671E
XH_P38	2	219507302	219507302	Missense_Mutation	SNP	C	T	C	ZNFI42	c.G3937A	p.A1313T
XH_P38	2	219527712	219527712	Silent	SNP	C	T	C	BCS1L	c.C636T	p.N212N
XH_P38	2	219527866	219527866	Silent	SNP	T	C	T	BCS1L	c.T657C	p.P219P
XH_P38	2	219528995	219528995	Silent	SNP	T	C	T	RNF25	c.A1065G	p.P355P
XH_P38	2	219529247	219529247	Silent	SNP	A	C	A	RNF25	c.T813G	p.P271P
XH_P38	2	219563504	219563504	Silent	SNP	C	T	C	STK36	c.C3174T	p.S1058S
XH_P38	2	219903258	219903258	Missense_Mutation	SNP	T	G	T	CFAP65	c.A1C	p.M1L
XH_P38	2	220037608	220037608	Missense_Mutation	SNP	A	C	A	CNPPD1	c.T933G	p.S311R
XH_P38	2	220045902	220045902	Silent	SNP	C	T	C	RETREG2	c.C138T	p.A46A
XH_P38	2	220285309	220285309	Silent	SNP	C	T	C	DES	c.C828T	p.D276D
XH_P38	2	220286142	220286142	Silent	SNP	G	A	G	DES	c.G1104A	p.A368A
XH_P38	2	220353013	220353013	Silent	SNP	G	A	G	SPEG	c.G7839A	p.P2613P
XH_P38	2	220354365	220354365	Silent	SNP	C	T	C	SPEG	c.C8625T	p.F2875F
XH_P38	2	220356520	220356520	Silent	SNP	G	T	G	SPEG	c.G9390T	p.P3130P
XH_P38	2	220405230	220405230	Silent	SNP	G	A	G	CHPF	c.C717T	p.H239H
XH_P38	2	220422774	220422774	Silent	SNP	A	G	A	OBSL1	c.T3561C	p.P1187P
XH_P38	2	222308299	222308299	Missense_Mutation	SNP	G	A	G	EPHA4	c.C1649T	p.T550M
XH_P38	2	223917629	223917629	Silent	SNP	C	T	C	KCNE4	c.C234T	p.G78G
XH_P38	2	225362478	225362478	Missense_Mutation	SNP	C	T	C	CUL3	c.G1501A	p.V501I
XH_P38	2	227663185	227663185	Silent	SNP	G	A	G	IRS1	c.C270T	p.D90D
XH_P38	2	228855866	228855866	Missense_Mutation	SNP	G	C	G	SPHKAP	c.C4722G	p.S1574R
XH_P38	2	231256812	231256812	Silent	SNP	A	G	A	SP140L	c.A795G	p.A265A
XH_P38	2	231774844	231774844	Silent	SNP	G	A	G	GPR55	c.C834T	p.N278N
XH_P38	2	231865144	231865144	Missense_Mutation	SNP	G	C	G	SPATA3	c.G365C	p.C122S
XH_P38	2	232263127	232263127	Missense_Mutation	SNP	G	A	G	B3GNT7	c.G697A	p.V233I
XH_P38	2	233345474	233345474	Missense_Mutation	SNP	C	T	C	ECEL1	c.G2099A	p.R700Q
XH_P38	2	233386752	233386752	Missense_Mutation	SNP	G	A	G	PRSS56	c.G328A	p.A110T
XH_P38	2	233391303	233391303	Missense_Mutation	SNP	C	G	C	CHRD	c.C117G	p.N39K
XH_P38	2	234638249	234638249	Silent	SNP	A	G	A	UGT1A3	c.A477G	p.A159A
XH_P38	2	234652347	234652347	Silent	SNP	C	G	C	DNAJB3	c.G216C	p.G72G
XH_P38	2	234727986	234727986	Silent	SNP	C	T	C	MROH2A	c.C3237T	p.C1079C
XH_P38	2	234730807	234730807	Missense_Mutation	SNP	G	A	G	MROH2A	c.G3559A	p.V1187M
XH_P38	2	234732317	234732317	Missense_Mutation	SNP	A	G	A	MROH2A	c.A4144G	p.M1382V
XH_P38	2	234761225	234761225	Missense_Mutation	SNP	C	T	C	HJURP	c.G226A	p.F76K
XH_P38	2	238283605	238283605	Silent	SNP	G	A	G	COL6A3	c.C1308T	p.G436G
XH_P38	2	238990388	238990388	Missense_Mutation	SNP	G	A	G	SCLY	c.G547A	p.A183T
XH_P38	2	239006879	239006879	Silent	SNP	C	T	C	SCLY	c.C1245T	p.F415F
XH_P38	2	239036270	239036270	Silent	SNP	C	T	C	ESPNL	c.C6T	p.S2S
XH_P38	2	239038912	239038912	Silent	SNP	T	C	T	ESPNL	c.T453C	p.L151L
XH_P38	2	239165663	239165663	Silent	SNP	T	C	T	PER2	c.A1965G	p.A655A
XH_P38	2	241404317	241404317	Silent	SNP	C	T	C	GPC1	c.C1059T	p.P353P
XH_P38	2	241451351	241451351	Missense_Mutation	SNP	G	A	G	ANKMY1	c.C1523T	p.T508M
XH_P38	2	241511974	241511974	Silent	SNP	C	T	C	RNPEPL1	c.C663T	p.V221V
XH_P38	2	241513695	241513695	Silent	SNP	G	A	G	RNPEPL1	c.G1104A	p.T368T
XH_P38	2	241531479	241531479	Silent	SNP	A	G	A	CAPN10	c.A600G	p.P200P
XH_P38	2	241536126	241536126	Missense_Mutation	SNP	A	G	A	CAPN10	c.A1510G	p.T504A
XH_P38	2	241622187	241622187	Missense_Mutation	SNP	C	T	C	AQP12B	c.G68A	p.R23Q
XH_P38	2	241664801	241664801	Silent	SNP	C	T	C	KIF1A	c.G3840A	p.P1280P
XH_P38	2	241826517	241826517	Silent	SNP	C	T	C	C2orf54	c.G1314A	p.K438K
XH_P38	2	241831005	241831005	Silent	SNP	C	T	C	C2orf54	c.G690A	p.R230R
XH_P38	2	241870534	241870534	Silent	SNP	G	A	G	CROCC2	c.G936A	p.A312A
XH_P38	2	241873180	241873180	Silent	SNP	A	G	A	CROCC2	c.A1557G	p.A519A
XH_P38	2	241874844	241874844	Missense_Mutation	SNP	G	A	G	CROCC2	c.G2008A	p.E670K
XH_P38	2	241874893	241874893	Missense_Mutation	SNP	G	A	G	CROCC2	c.G2057A	p.R686H
XH_P38	2	242002306	242002306	Missense_Mutation	SNP	G	A	G	SNED1	c.G2356A	p.A786T
XH_P38	2	242003487	242003487	Silent	SNP	C	T	C	SNED1	c.C2544T	p.G848G
XH_P38	2	242004866	242004866	Silent	SNP	A	G	A	SNED1	c.A2865G	p.T955T
XH_P38	2	242793433	242793433	Missense_Mutation	SNP	G	A	G	PDCD1	c.C644T	p.A215V
XH_P38	2	242795029	242795029	Silent	SNP	C	T	C	PDCD1	c.G180A	p.S60S
XH_P38	2	242814639	242814639	Missense_Mutation	SNP	T	C	T	RTP5	c.T932C	p.L311P
XH_P38	2	242815059	242815059	Missense_Mutation	SNP	C	T	C	RTP5	c.C1352T	p.A451V
XH_P38	3	3078900	3078900	Silent	SNP	C	T	C	CNTN4	c.C993T	p.T331T
XH_P38	3	8675539	8675539	Missense_Mutation	SNP	G	A	G	SSUH2	c.C86T	p.P29L
XH_P38	3	8775661	8775661	Silent	SNP	C	T	C	CAV3	c.C99T	p.N33N
XH_P38	3	9851818	9851818	Missense_Mutation	SNP	T	C	T	TTL3	c.T128C	p.L43P
XH_P38	3	10420087	10420087	Silent	SNP	T	C	T	ATP2B2	c.A915G	p.Q305Q
XH_P38	3	10967712	10967712	Silent	SNP	G	A	G	SLC6A11	c.G1143A	p.A381A
XH_P38	3	11059035	11059035	Silent	SNP	G	A	G	SLC6A1	c.G138A	p.T46T
XH_P38	3	11596302	11596302	Silent	SNP	T	C	T	ATG7	c.T1857C	p.D619D
XH_P38	3	12560560	12560560	Silent	SNP	G	A	G	TSEN2	c.G885A	p.E295E
XH_P38	3	13376973	13376973	Missense_Mutation	SNP	G	C	G	NUP210	c.C3824G	p.S1275W
XH_P38	3	13612020	13612020	Silent	SNP	T	C	T	FBLN2	c.T165C	p.C55C
XH_P38	3	13612296	13612296	Silent	SNP	C	T	C	FBLN2	c.C441T	p.A147A
XH_P38	3	13612936	13612936	Missense_Mutation	SNP	A	G	A	FBLN2	c.A1081G	p.S361G
XH_P38	3	13677946	13677946	Silent	SNP	C	T	C	FBLN2	c.C3075T	p.D1025D
XH_P38	3	13679335	13679335	Silent	SNP	C	T	C	FBLN2	c.C3471T	p.D1157D
XH_P38	3	13896140	13896140	Silent	SNP	A	G	A	WNT7A	c.T459C	p.S153S
XH_P38	3	13896284	13896284	Silent	SNP	C	T	C	WNT7A	c.G315A	p.A105A
XH_P38	3	14798976	14798976	Missense_Mutation	SNP	G	A	G	C3orf20	c.G1673A	p.R558H
XH_P38	3	15115478	15115478	Missense_Mutation	SNP	C	T	C	RBSN	c.G2166A	p.M722I
XH_P38	3	15115723	15115723	Missense_Mutation	SNP	T	C	T	RBSN	c.A1921G	p.T641A
XH_P38	3	15115872	15115872	Missense_Mutation	SNP	A	G	A	RBSN	c.T1772C	p.L591P
XH_P38	3	30713842	30713842	Silent	SNP	C	T	C	TGFBF2	c.C1167T	p.N389N
XH_P38	3	31725316	31725316	Silent	SNP	G	A	G	OSBP10	c.C1344T	p.H448H
XH_P38	3	33155782	33155782	Silent	SNP	G	A	G	CRTAP	c.G213A	p.L71L
XH_P38	3	33161898	33161898	Silent	SNP	C	T	C	CRTAP	c.C534T	p.D178D
XH_P38	3	37323642	37323642	Missense_Mutation	SNP	A	G	A	GOLGA4	c.A356G	p.D119G
XH_P38	3	38052725	38052725	Missense_Mutation	SNP	C	T	C	PLCD1	c.G833A	p.R278H
XH_P38	3	38170810	38170810	Missense_Mutation	SNP	C	G	C	ACAA1	c.G516C	p.E172D

XH_P38	3	39184959	39184959	Missense_Mutation	SNP	C	T	C	CSNP1	c.G1417A	p.V473I
XH_P38	3	39185077	39185077	Silent	SNP	G	A	G	CSNP1	c.C1299T	p.S433S
XH_P38	3	39186728	39186728	Silent	SNP	C	T	C	CSNP1	c.G285A	p.R95R
XH_P38	3	40231883	40231883	Silent	SNP	C	T	C	MYRIP	c.C1033T	p.L345L
XH_P38	3	41266914	41266914	Frame_Shift_Ins	INS	-	CAACGAGCTGT	-	CTNNB1	CGGTACACAG	p.V195fs
XH_P38	3	42568895	42568895	Missense_Mutation	SNP	T	C	T	VIPR1	c.T266C	p.M89T
XH_P38	3	42735150	42735150	Missense_Mutation	SNP	T	C	T	HHATL	c.A1207G	p.M403V
XH_P38	3	43074620	43074620	Missense_Mutation	SNP	G	T	G	FAM198A	c.G865T	p.V289L
XH_P38	3	44541028	44541028	Missense_Mutation	SNP	T	C	T	ZNFR52	c.A1241G	p.N414S
XH_P38	3	45267058	45267058	Silent	SNP	G	A	G	TMEM158	c.C462T	p.T154T
XH_P38	3	45557707	45557707	Silent	SNP	G	A	G	LARS2	c.G1983A	p.T661T
XH_P38	3	46399208	46399208	Missense_Mutation	SNP	G	A	G	CCR2	c.G190A	p.V64I
XH_P38	3	46586622	46586622	Missense_Mutation	SNP	T	C	T	LRRC2	c.A247G	p.T83A
XH_P38	3	46592987	46592987	Missense_Mutation	SNP	A	G	A	LRRC2	c.T95C	p.V32A
XH_P38	3	46729757	46729757	Missense_Mutation	SNP	C	G	C	ALS2CL	c.G133C	p.E45Q
XH_P38	3	46945060	46945060	Missense_Mutation	SNP	G	A	G	PTH1R	c.G1696A	p.G566S
XH_P38	3	47036756	47036756	Missense_Mutation	SNP	C	G	G	NBEAL2	c.C1531G	p.R511G
XH_P38	3	47043622	47043622	Silent	SNP	G	A	G	NBEAL2	c.G4995A	p.V1665V
XH_P38	3	47888286	47888286	Missense_Mutation	SNP	T	C	T	DHX30	c.T1724C	p.L575P
XH_P38	3	48461313	48461313	Silent	SNP	C	G	C	PLXNB1	c.G2382C	p.P794P
XH_P38	3	48625266	48625266	Silent	SNP	T	C	T	COL7A1	c.A2817G	p.P939P
XH_P38	3	48658419	48658419	Silent	SNP	C	T	C	TMEM89	c.G336A	p.R112R
XH_P38	3	48677316	48677316	Silent	SNP	G	A	G	CELSR3	c.C9702T	p.P3234P
XH_P38	3	48680252	48680252	Silent	SNP	G	A	G	CELSR3	c.C8472T	p.G2824G
XH_P38	3	49680121	49680121	Missense_Mutation	SNP	G	A	G	BSN	c.G1054A	p.G352S
XH_P38	3	49738945	49738945	Silent	SNP	C	T	C	RNF123	c.C1299T	p.V433V
XH_P38	3	49751585	49751585	Silent	SNP	C	T	C	RNF123	c.C2988T	p.D996D
XH_P38	3	49898273	49898273	Silent	SNP	A	G	A	CAMKV	c.T651C	p.N217N
XH_P38	3	49899795	49899795	Silent	SNP	G	A	G	CAMKV	c.C27T	p.G9G
XH_P38	3	49924940	49924940	Missense_Mutation	SNP	T	C	T	MST1R	c.A3685G	p.R1229G
XH_P38	3	49936102	49936102	Missense_Mutation	SNP	T	C	T	MST1R	c.A1250G	p.Q417R
XH_P38	3	49949071	49949071	Silent	SNP	A	G	A	MON1A	c.T792C	p.P264P
XH_P38	3	50224060	50224060	Missense_Mutation	SNP	G	C	G	SEMA3F	c.G1531C	p.V511L
XH_P38	3	50264608	50264608	Missense_Mutation	SNP	A	C	A	GNAI2	c.A53C	p.H18P
XH_P38	3	50312822	50312822	Silent	SNP	T	C	T	SEMA3B	c.T552C	p.C184C
XH_P38	3	50327429	50327429	Silent	SNP	A	G	A	IFRD2	c.T669C	p.F223F
XH_P38	3	50334231	50334231	Missense_Mutation	SNP	T	A	T	NAT6	c.A664T	p.R222W
XH_P38	3	50355730	50355730	Missense_Mutation	SNP	T	G	T	HYAL2	c.A1252C	p.I418L
XH_P38	3	50378176	50378176	Missense_Mutation	SNP	T	G	T	RASSF1	c.A61C	p.K21Q
XH_P38	3	50645158	50645158	Silent	SNP	A	G	A	CISH	c.T657C	p.S219S
XH_P38	3	50645413	50645413	Silent	SNP	G	A	G	CISH	c.C402T	p.A134A
XH_P38	3	51737965	51737965	Missense_Mutation	SNP	G	A	G	TEX264	c.G653A	p.G218E
XH_P38	3	51928928	51928928	Missense_Mutation	SNP	A	G	A	IQCF1	c.T596C	p.I199T
XH_P38	3	52378506	52378506	Silent	SNP	G	A	G	DNAH1	c.G1287A	p.S429S
XH_P38	3	52398983	52398983	Silent	SNP	G	A	G	DNAH1	c.G5466A	p.L1822L
XH_P38	3	52407041	52407041	Silent	SNP	C	T	C	DNAH1	c.C6957T	p.H2319H
XH_P38	3	52522297	52522297	Missense_Mutation	SNP	G	A	G	NISCH	c.G2789A	p.R930H
XH_P38	3	52540773	52540773	Silent	SNP	T	C	T	STAB1	c.T1896C	p.G632G
XH_P38	3	52548818	52548818	Silent	SNP	C	T	C	STAB1	c.C3780T	p.C1260C
XH_P38	3	52859902	52859902	Missense_Mutation	SNP	C	A	C	ITIH4	c.G759T	p.Q253H
XH_P38	3	53222761	53222761	Silent	SNP	C	T	C	PRKCD	c.C1441T	p.L481L
XH_P38	3	53856653	53856653	Silent	SNP	C	T	C	CHDH	c.G720A	p.A240A
XH_P38	3	54798258	54798258	Silent	SNP	G	A	G	CACNA2D3	c.G1260A	p.Q420Q
XH_P38	3	57131759	57131759	Missense_Mutation	SNP	T	C	T	IL17RD	c.A1972G	p.M658V
XH_P38	3	57542173	57542173	Missense_Mutation	SNP	C	T	C	PDE12	c.C67T	p.R23W
XH_P38	3	62189189	62189189	Missense_Mutation	SNP	G	A	G	PTPRG	c.G1720A	p.G574S
XH_P38	3	63973881	63973881	Silent	SNP	G	A	G	ATXN7	c.G807A	p.P269P
XH_P38	3	64009508	64009508	Missense_Mutation	SNP	T	C	T	PSMD6	c.A4G	p.N2D
XH_P38	3	66430870	66430870	Silent	SNP	G	A	G	LRIG1	c.C3099T	p.S1033S
XH_P38	3	69151152	69151152	Silent	SNP	C	A	C	ARL6IP5	c.C339A	p.I113I
XH_P38	3	75786440	75786440	Silent	SNP	C	T	C	ZNFX17	c.G2334A	p.G778G
XH_P38	3	77614161	77614161	Missense_Mutation	SNP	A	G	A	ROBO2	c.A1739G	p.Y580C
XH_P38	3	87276699	87276699	Silent	SNP	C	T	C	CHMP2B	c.C27T	p.T9T
XH_P38	3	97868419	97868419	Missense_Mutation	SNP	G	A	G	OR5H14	c.G190A	p.G64R
XH_P38	3	97868616	97868616	Silent	SNP	C	T	C	OR5H14	c.C387T	p.P129P
XH_P38	3	97887865	97887865	Missense_Mutation	SNP	G	A	G	OR5H15	c.G322A	p.V108I
XH_P38	3	98250986	98250986	Missense_Mutation	SNP	C	T	C	GPR15	c.C109T	p.P37S
XH_P38	3	98307630	98307630	Missense_Mutation	SNP	C	T	C	CPOX	c.G880A	p.V294I
XH_P38	3	99513875	99513875	Missense_Mutation	SNP	A	G	A	COL8A1	c.A1130G	p.K377R
XH_P38	3	101395629	101395629	Missense_Mutation	SNP	C	T	C	ZBTB11	c.G130A	p.G44S
XH_P38	3	105421034	105421034	Silent	SNP	C	T	C	CBLB	c.G1716A	p.A572A
XH_P38	3	112546473	112546473	Silent	SNP	G	A	G	CD200R1L	c.C171T	p.I57I
XH_P38	3	112993367	112993367	Silent	SNP	G	A	G	BOC	c.G1380A	p.P460P
XH_P38	3	113377505	113377505	Silent	SNP	T	G	T	USF3	c.A3024C	p.L1008L
XH_P38	3	113594377	113594377	Silent	SNP	A	G	A	GRAMD1C	c.A306G	p.L102L
XH_P38	3	113720517	113720517	Missense_Mutation	SNP	T	A	T	CCDC191	c.A2088T	p.E696D
XH_P38	3	113955820	113955820	Silent	SNP	G	C	G	ZNFR80	c.C102G	p.S34S
XH_P38	3	114069526	114069526	Missense_Mutation	SNP	C	T	C	ZBTB20	c.G1399A	p.G467R
XH_P38	3	115395336	115395336	Silent	SNP	T	C	T	GAP43	c.T507C	p.D169D
XH_P38	3	118865332	118865332	Missense_Mutation	SNP	A	G	A	C3orf30	c.A296G	p.D99G
XH_P38	3	118865609	118865609	Silent	SNP	C	T	C	C3orf30	c.C573T	p.S191S
XH_P38	3	118945796	118945796	Missense_Mutation	SNP	G	C	G	B4GALT4	c.C346G	p.Q116E
XH_P38	3	119305379	119305379	Silent	SNP	T	A	T	ADPRH	c.T225A	p.A75A
XH_P38	3	120068022	120068022	Silent	SNP	C	G	C	LRRC58	c.G69C	p.V23V
XH_P38	3	120389335	120389335	Missense_Mutation	SNP	T	A	T	HGD	c.A221T	p.E74V
XH_P38	3	121351315	121351315	In_Frame_Ins	INS	-	GGCTCAGGCTCA	-	HLCS1	P93insTGAGCCT	P331delinsPEPEP
XH_P38	3	121414061	121414061	Missense_Mutation	SNP	C	T	C	GOLGB1	c.G5069A	p.G1690D
XH_P38	3	122003711	122003711	Silent	SNP	C	T	C	CASR	c.C2910T	p.S970S
XH_P38	3	122103120	122103120	Missense_Mutation	SNP	G	A	G	FAM162A	c.G8A	p.S3N
XH_P38	3	122632436	122632436	Missense_Mutation	SNP	A	G	A	SEMA5B	c.T2051C	p.M684T
XH_P38	3	123420352	123420352	Missense_Mutation	SNP	G	A	G	MYLK	c.C1867T	p.R623W
XH_P38	3	124515308	124515308	Silent	SNP	A	G	A	ITGB5	c.T1620C	p.F540F
XH_P38	3	124515509	124515509	Silent	SNP	G	A	G	ITGB5	c.C1419T	p.S473S
XH_P38	3	126071681	126071681	Missense_Mutation	SNP	G	A	G	KLF15	c.C85T	p.R29W
XH_P38	3	126260608	126260608	Silent	SNP	G	T	G	CHST13	c.G213T	p.R71R
XH_P38	3	126268918	126268918	Silent	SNP	G	A	G	C3orf22	c.C219T	p.L73L
XH_P38	3	126451937	126451937	Missense_Mutation	SNP	G	T	G	CHCHD6	c.G283T	p.A95S
XH_P38	3	126723549	126723549	Silent	SNP	C	T	C	PLXNA1	c.C1614T	p.H538H

XH_P38	3	126735453	126735453	Silent	SNP	C	T	C	PLXNA1	c.C3108T	p.T1036T
XH_P38	3	126737268	126737268	Silent	SNP	C	A	C	PLXNA1	c.C3792A	p.L1264L
XH_P38	3	126741011	126741011	Silent	SNP	G	A	G	PLXNA1	c.G4122A	p.T1374T
XH_P38	3	128181777	128181777	Silent	SNP	A	G	A	DNAJB8	c.T312C	p.F104F
XH_P38	3	128200073	128200073	Missense_Mutation	SNP	G	A	G	GATA2	c.C1190T	p.A397V
XH_P38	3	128840321	128840321	Silent	SNP	C	T	C	RAB43	c.G12A	p.P4P
XH_P38	3	129275206	129275206	Silent	SNP	C	T	C	PLXND1	c.G5727A	p.Q1909Q
XH_P38	3	129281718	129281718	Silent	SNP	C	T	C	PLXND1	c.G4737A	p.T1579T
XH_P38	3	129290087	129290087	Silent	SNP	G	A	G	PLXND1	c.C3396T	p.N1132N
XH_P38	3	129308209	129308209	Silent	SNP	G	A	G	PLXND1	c.C1473T	p.N491N
XH_P38	3	130098349	130098349	Silent	SNP	G	A	G	COL6A5	c.G756A	p.R252R
XH_P38	3	130104062	130104062	Silent	SNP	T	C	T	COL6A5	c.T1716C	p.T572T
XH_P38	3	137843106	137843106	Silent	SNP	T	C	T	A4GNT	c.A1023G	p.X341X
XH_P38	3	137843476	137843476	Missense_Mutation	SNP	G	T	G	A4GNT	c.C653A	p.A218D
XH_P38	3	138762707	138762707	Silent	SNP	C	G	C	PRR23C	c.G756C	p.P252P
XH_P38	3	138763343	138763343	Silent	SNP	T	G	T	PRR23C	c.A120C	p.R40R
XH_P38	3	142681090	142681090	Silent	SNP	T	G	T	PAQR9	c.A1089C	p.V363V
XH_P38	3	142681642	142681642	Silent	SNP	G	A	G	PAQR9	c.C537T	p.G179G
XH_P38	3	146177815	146177815	Silent	SNP	C	T	C	PLSCR2	c.G84A	p.Q28Q
XH_P38	3	147114054	147114054	Silent	SNP	A	G	A	ZIC4	c.T423C	p.A141A
XH_P38	3	148847668	148847668	Missense_Mutation	SNP	A	G	A	HP53	c.A158G	p.Q53R
XH_P38	3	149238595	149238595	Nonsense_Mutation	INS	-	TTAA	-	WWTR1	199_1200insTT	400_X401delinsLX
XH_P38	3	150128392	150128392	Missense_Mutation	SNP	G	A	G	TSC22D2	c.G1255A	p.A419T
XH_P38	3	150690439	150690439	Silent	SNP	T	A	T	CLRN1	c.A57T	p.A19A
XH_P38	3	150917000	150917000	Silent	SNP	T	G	T	GPR171	c.A174C	p.T58T
XH_P38	3	151082923	151082923	Silent	SNP	T	C	T	MED12L	c.T3009C	p.N1003N
XH_P38	3	151164174	151164174	Missense_Mutation	SNP	A	C	A	IGSF10	c.T3595G	p.S1199A
XH_P38	3	153839959	153839959	Missense_Mutation	SNP	C	T	C	ARHGEF26	c.C178T	p.L60F
XH_P38	3	171404478	171404478	Missense_Mutation	SNP	C	A	C	PLD1	c.G1864T	p.A622S
XH_P38	3	172165727	172165727	Silent	SNP	C	T	C	GHSR	c.G477A	p.R159R
XH_P38	3	172166033	172166033	Silent	SNP	G	A	G	GHSR	c.C171T	p.G57G
XH_P38	3	179046131	179046131	Missense_Mutation	SNP	G	A	G	ZNF639	c.G50A	p.R17H
XH_P38	3	180321110	180321110	Frame_Shift_Ins	INS	-	TAACGAT	-	TTC14	85_486insTAAC	p.T162fs
XH_P38	3	183226072	183226072	Silent	SNP	G	A	G	KLHL6	c.C684T	p.Y282Y
XH_P38	3	183368216	183368216	Silent	SNP	A	T	A	KLHL24	c.A72T	p.R24R
XH_P38	3	183756637	183756637	Silent	SNP	C	T	C	HTR3D	c.C714T	p.A238A
XH_P38	3	183904049	183904049	Silent	SNP	A	G	A	ABCF3	c.A54G	p.Q18Q
XH_P38	3	183951135	183951135	Silent	SNP	C	T	C	VWA5B2	c.C480T	p.A160A
XH_P38	3	183951431	183951431	Missense_Mutation	SNP	C	T	C	VWA5B2	c.C598T	p.P200S
XH_P38	3	183953972	183953972	Silent	SNP	G	A	G	VWA5B2	c.G477A	p.P159P
XH_P38	3	183955109	183955109	Silent	SNP	C	T	C	VWA5B2	c.C972T	p.P324P
XH_P38	3	183976108	183976108	Silent	SNP	T	C	T	ECE2	c.T513C	p.F171F
XH_P38	3	184039666	184039666	Missense_Mutation	SNP	A	G	A	EIF4G1	c.A706G	p.M236V
XH_P38	3	184073551	184073551	Silent	SNP	C	T	C	CLCN2	c.G969A	p.P323P
XH_P38	3	184082931	184082931	Silent	SNP	T	C	T	POLR2H	c.T168C	p.F56F
XH_P38	3	184099342	184099342	Silent	SNP	G	C	G	CHRD	c.G441C	p.P147P
XH_P38	3	184106493	184106493	Silent	SNP	T	G	T	CHRD	c.T2673G	p.P891P
XH_P38	3	186006618	186006618	Missense_Mutation	SNP	G	C	G	DGKG	c.C425G	p.T142S
XH_P38	3	186395436	186395436	Missense_Mutation	SNP	C	T	C	HRG	c.C1342T	p.R448C
XH_P38	3	186570892	186570892	Silent	SNP	T	G	T	ADIPQO	c.T45G	p.G15G
XH_P38	3	186954324	186954324	Silent	SNP	G	A	G	MASP1	c.C1335T	p.S445S
XH_P38	3	193372726	193372726	Silent	SNP	G	A	G	OPA1	c.G1815A	p.A605A
XH_P38	3	195453249	195453249	Missense_Mutation	SNP	T	C	T	MUC20	c.T1775C	p.M592T
XH_P38	3	195477791	195477791	Silent	SNP	G	A	G	MUC4	c.C2979T	p.I93I
XH_P38	3	195489009	195489009	Missense_Mutation	SNP	C	A	C	MUC4	c.G1600T	p.A534S
XH_P38	3	195489067	195489067	Silent	SNP	C	G	C	MUC4	c.G1542C	p.S514S
XH_P38	3	195497174	195497174	Missense_Mutation	SNP	C	G	C	MUC4	c.G450C	p.M150I
XH_P38	3	195606019	195606019	Silent	SNP	G	A	G	TNK2	c.C1104T	p.R368R
XH_P38	3	195615376	195615376	Silent	SNP	A	G	A	TNK2	c.T273C	p.D91D
XH_P38	3	195936382	195936382	Silent	SNP	G	A	G	ZDHHC19	c.C273T	p.S91S
XH_P38	3	195938177	195938177	Silent	SNP	A	G	A	ZDHHC19	c.T10C	p.L4L
XH_P38	3	196613075	196613075	Silent	SNP	C	T	C	SENP5	c.C1023T	p.D341D
XH_P38	4	517376	517376	Silent	SNP	T	C	T	PIGG	c.T1344C	p.L448L
XH_P38	4	682882	682882	Missense_Mutation	SNP	G	A	G	MFSD7	c.C35T	p.A12V
XH_P38	4	1646017	1646017	Missense_Mutation	SNP	C	G	C	FAM53A	c.G935C	p.S312T
XH_P38	4	1657281	1657281	Silent	SNP	G	A	G	FAM53A	c.C306T	p.T102T
XH_P38	4	1823989	1823989	Silent	SNP	G	A	G	LETM1	c.C1527T	p.T509T
XH_P38	4	2175733	2175733	Silent	SNP	A	G	A	POLN	c.T1323C	p.H441H
XH_P38	4	2306045	2306045	Silent	SNP	G	A	G	ZFYVE28	c.C1932T	p.H644H
XH_P38	4	3039150	3039150	Missense_Mutation	SNP	T	C	T	GRK4	c.T875C	p.V292A
XH_P38	4	3124653	3124653	Silent	SNP	A	G	A	HTT	c.A1311G	p.R437R
XH_P38	4	3231661	3231661	Silent	SNP	G	A	G	HTT	c.G8157A	p.L2719L
XH_P38	4	3318726	3318726	Missense_Mutation	SNP	A	T	A	RGS12	c.A829T	p.M277L
XH_P38	4	3425299	3425299	Silent	SNP	C	T	C	RGS12	c.C1221T	p.P407P
XH_P38	4	3446682	3446682	Silent	SNP	C	T	C	HGFAC	c.C978T	p.A326A
XH_P38	4	3769329	3769329	Silent	SNP	G	A	G	ADRA2C	c.G996A	p.A332A
XH_P38	4	4304522	4304522	Missense_Mutation	SNP	A	C	A	ZBTB49	c.A959C	p.Y320S
XH_P38	4	4861745	4861745	Missense_Mutation	SNP	C	G	C	MSX1	c.C119G	p.A40G
XH_P38	4	5624670	5624670	Missense_Mutation	SNP	T	C	T	EVC2	c.A1855G	p.T619A
XH_P38	4	6303479	6303479	Missense_Mutation	SNP	C	T	C	WFS1	c.C1957T	p.R653C
XH_P38	4	7056450	7056450	Missense_Mutation	SNP	C	T	C	TADA2B	c.C932T	p.A311V
XH_P38	4	7436073	7436073	Silent	SNP	C	T	C	PSAPL1	c.G534A	p.A178A
XH_P38	4	7436239	7436239	Missense_Mutation	SNP	C	T	C	PSAPL1	c.G368A	p.R123H
XH_P38	4	7716061	7716061	Missense_Mutation	SNP	C	T	C	SORCS2	c.C2084T	p.T695M
XH_P38	4	8375342	8375342	Silent	SNP	G	A	G	ACOX3	c.C1842T	p.S614S
XH_P38	4	8594616	8594616	Missense_Mutation	SNP	G	C	G	CPZ	c.G56C	p.R19P
XH_P38	4	11401012	11401012	Silent	SNP	A	G	A	HS3ST1	c.T618C	p.F206F
XH_P38	4	11401087	11401087	Silent	SNP	A	G	A	HS3ST1	c.T543C	p.D181D
XH_P38	4	15964501	15964501	Silent	SNP	G	A	G	FGFBP2	c.C252T	p.F84F
XH_P38	4	16188159	16188159	Silent	SNP	G	A	G	TAPT1	c.C915T	p.S305S
XH_P38	4	17706665	17706665	Silent	SNP	G	T	G	FAM184B	c.C1335A	p.S445S
XH_P38	4	17710905	17710905	Missense_Mutation	SNP	G	C	G	FAM184B	c.C504G	p.H168Q
XH_P38	4	25032135	25032135	Missense_Mutation	SNP	C	T	C	LG12	c.G181A	p.G615S
XH_P38	4	25235801	25235801	Missense_Mutation	SNP	G	A	G	PI4K2B	c.G16A	p.E6K
XH_P38	4	37591815	37591815	Missense_Mutation	SNP	C	G	C	C4orf19	c.C138G	p.S46R
XH_P38	4	38776725	38776725	Missense_Mutation	SNP	C	A	G	TLR10	c.G487T	p.A163S
XH_P38	4	38829163	38829163	Silent	SNP	A	C	A	TLR6	c.T1932G	p.A644A
XH_P38	4	40351207	40351207	Missense_Mutation	SNP	C	T	C	CHRNA9	c.C674T	p.P225L

XH_P38	4	41747990	41748004	In_Frame_Del	DEL	GCCGCCGCT	-	TCGCCGCCGCTG	PHOX2B	c.765_779del	p.255_260del
XH_P38	4	53494241	53494241	Silent	SNP	C	T	C	USP46	c.G186A	p.Q62Q
XH_P38	4	53728701	53728701	Silent	SNP	C	A	C	RASL11B	c.C27A	p.T9T
XH_P38	4	54011603	54011603	Silent	SNP	C	T	C	SCFD2	c.G1458A	p.T486T
XH_P38	4	55133726	55133726	Silent	SNP	T	G	T	PDGFRA	c.T939G	p.G313G
XH_P38	4	55143577	55143577	Silent	SNP	G	A	G	PDGFRA	c.G1809A	p.A603A
XH_P38	4	55152040	55152040	Silent	SNP	C	T	C	PDGFRA	c.C2472T	p.V824V
XH_P38	4	57180626	57180626	Nonsense_Mutation	SNP	C	T	C	KIAA1211	c.C958T	p.R320X
XH_P38	4	57182647	57182647	Silent	SNP	G	A	G	KIAA1211	c.G2979A	p.A993A
XH_P38	4	57221348	57221348	Missense_Mutation	SNP	T	C	T	AASDH	c.A803G	p.K268R
XH_P38	4	57250285	57250285	Missense_Mutation	SNP	T	C	T	AASDH	c.A181G	p.I61V
XH_P38	4	57397157	57397157	Silent	SNP	G	C	G	THEGL	c.G315C	p.G105G
XH_P38	4	70921241	70921241	Missense_Mutation	SNP	T	G	T	HTN1	c.T129G	p.F43L
XH_P38	4	72433545	72433545	Missense_Mutation	SNP	A	C	A	SLCAA4	c.A3220C	p.I1074L
XH_P38	4	72618323	72618323	Missense_Mutation	SNP	G	T	G	GC	c.C1307A	p.T436K
XH_P38	4	74735244	74735244	Silent	SNP	A	G	A	CXCL1	c.A57G	p.A19A
XH_P38	4	75937971	75937971	Missense_Mutation	SNP	C	T	C	PARM1	c.C380T	p.S127L
XH_P38	4	77662248	77662248	Silent	SNP	G	A	G	SHROOM3	c.G2922A	p.S974S
XH_P38	4	77818548	77818548	Missense_Mutation	SNP	T	C	T	SOWAHB	c.A455G	p.D152G
XH_P38	4	79238649	79238649	Silent	SNP	T	C	T	FRAS1	c.T1947C	p.H649H
XH_P38	4	79240063	79240063	Missense_Mutation	SNP	A	G	A	FRAS1	c.A2060G	p.D687G
XH_P38	4	79385719	79385719	Silent	SNP	G	A	G	FRAS1	c.G7011A	p.A2337A
XH_P38	4	83748617	83748617	Missense_Mutation	SNP	C	T	C	SEC31A	c.G2737A	p.V913I
XH_P38	4	85762385	85762385	Silent	SNP	T	C	T	WDFY3	c.A336G	p.L112L
XH_P38	4	87706506	87706506	Missense_Mutation	SNP	T	G	T	PTPN13	c.T5668G	p.Y1890D
XH_P38	4	89671591	89671591	Missense_Mutation	SNP	A	C	A	FAM13A	c.T862G	p.S288A
XH_P38	4	10322513	10322513	Silent	SNP	T	C	T	SLC39A8	c.A600G	p.G200G
XH_P38	4	103228734	103228734	Silent	SNP	C	T	C	SLC39A8	c.G210A	p.T70T
XH_P38	4	104062223	104062223	Silent	SNP	C	T	C	CENPE	c.G5427A	p.T1809T
XH_P38	4	106196951	106196951	Missense_Mutation	SNP	A	G	A	TET2	c.A5284G	p.L1762V
XH_P38	4	110581363	110581363	Missense_Mutation	SNP	T	A	T	MCUB	c.T188A	p.I63N
XH_P38	4	110883121	110883121	Missense_Mutation	SNP	G	A	G	EGF	c.G1166A	p.R389K
XH_P38	4	113199075	113199075	Silent	SNP	A	G	A	TIFA	c.T498C	p.Y166Y
XH_P38	4	119161795	119161795	Silent	SNP	G	A	G	NDST3	c.G2235A	p.P745P
XH_P38	4	119216188	119216188	Missense_Mutation	SNP	G	A	G	PRSS12	c.C1945T	p.R649W
XH_P38	4	119273712	119273712	Missense_Mutation	SNP	C	G	C	PRSS12	c.G164C	p.R55T
XH_P38	4	125590478	125590478	Silent	SNP	T	C	T	ANKRD50	c.A3417G	p.P1139P
XH_P38	4	125591687	125591687	Silent	SNP	A	G	A	ANKRD50	c.T2208C	p.N736N
XH_P38	4	128584580	128584580	Silent	SNP	G	A	G	INTU	c.G813A	p.T271T
XH_P38	4	128723042	128723042	Missense_Mutation	SNP	T	C	T	HSPA4L	c.T509C	p.L170S
XH_P38	4	128814964	128814964	Missense_Mutation	SNP	G	T	G	PLK4	c.G2394T	p.E798D
XH_P38	4	129012181	129012181	Silent	SNP	G	A	G	LARP1B	c.G384A	p.R128R
XH_P38	4	129043286	129043286	Silent	SNP	C	T	C	LARP1B	c.C744T	p.Y248Y
XH_P38	4	140640703	140640703	Missense_Mutation	SNP	G	T	G	MAML3	c.C3179A	p.P1060H
XH_P38	4	140811135	140811135	Silent	SNP	T	C	T	MAML3	c.A1455G	p.K485K
XH_P38	4	141543997	141543997	Silent	SNP	G	A	G	TBC1D9	c.C3153T	p.H1051H
XH_P38	4	143033778	143033778	Silent	SNP	T	C	T	INPP4B	c.A2193G	p.L731L
XH_P38	4	151000419	151000419	Silent	SNP	G	A	G	DCLK2	c.G240A	p.G80G
XH_P38	4	154624656	154624656	Silent	SNP	T	C	T	TLR2	c.T597C	p.N199N
XH_P38	4	154625409	154625409	Silent	SNP	T	C	T	TLR2	c.T1350C	p.S450S
XH_P38	4	155411939	155411939	Missense_Mutation	SNP	A	C	A	DCHS2	c.T569G	p.V190G
XH_P38	4	156787340	156787340	Silent	SNP	G	A	G	ASIC5	c.C39T	p.N13N
XH_P38	4	159631991	159631991	Missense_Mutation	SNP	G	T	G	PPID	c.C904A	p.L302I
XH_P38	4	159642576	159642576	Missense_Mutation	SNP	G	A	G	PPID	c.C145T	p.R49C
XH_P38	4	162307433	162307433	Silent	SNP	G	A	G	FSTL5	c.C1980T	p.T660T
XH_P38	4	164466824	164466824	Silent	SNP	C	T	C	MARCH1	c.G444A	p.A148A
XH_P38	4	169799163	169799163	Missense_Mutation	SNP	C	G	C	PALLD	c.C121G	p.P41A
XH_P38	4	170037572	170037572	Missense_Mutation	SNP	G	A	G	SH3RF1	c.C1987T	p.P663S
XH_P38	4	184203886	184203886	Missense_Mutation	SNP	G	C	G	WWC2	c.G2710C	p.D904H
XH_P38	4	184366145	184366145	Silent	SNP	C	T	C	CDKN2AIP	c.C195T	p.S65S
XH_P38	4	184629569	184629569	Missense_Mutation	SNP	C	T	C	TRAPPC11	c.C3199T	p.R1067C
XH_P38	4	186097045	186097045	Silent	SNP	C	T	C	CFAP97	c.G1215A	p.P405P
XH_P38	4	186299260	186299260	Silent	SNP	A	G	A	LRP2BP	c.T81C	p.Y27F
XH_P38	4	186598483	186598483	Missense_Mutation	SNP	A	G	A	SORBS2	c.T160C	p.Y54H
XH_P38	4	187078819	187078819	Silent	SNP	C	G	C	FAM149A	c.C675G	p.S225S
XH_P38	4	187510280	187510280	Silent	SNP	G	A	G	FAT1	c.C13233T	p.P4411P
XH_P38	4	187517758	187517758	Silent	SNP	G	A	G	FAT1	c.C12936T	p.P4312P
XH_P38	4	187522528	187522528	Silent	SNP	C	T	C	FAT1	c.G11535A	p.T3845T
XH_P38	4	187534375	187534375	Silent	SNP	A	G	A	FAT1	c.T9351C	p.D3117D
XH_P38	4	187629497	187629497	Silent	SNP	G	A	G	FAT1	c.C1485T	p.N495N
XH_P38	4	189061106	189061106	Missense_Mutation	SNP	G	A	G	TRIML1	c.G394A	p.E132K
XH_P38	5	640705	640705	Missense_Mutation	SNP	A	G	A	CEP72	c.A1525G	p.T509A
XH_P38	5	1033594	1033594	Missense_Mutation	SNP	G	A	G	NKD2	c.G310A	p.G104R
XH_P38	5	1201806	1201806	Missense_Mutation	SNP	G	A	G	SLC6A19	c.G41A	p.R14Q
XH_P38	5	1878212	1878212	Silent	SNP	G	A	G	IRX4	c.C1431T	p.G477G
XH_P38	5	7868030	7868030	Missense_Mutation	SNP	T	C	T	FASTKD3	c.A167G	p.K56R
XH_P38	5	10973727	10973727	Silent	SNP	G	A	G	CTNND2	c.C2505T	p.F835F
XH_P38	5	16766269	16766269	Missense_Mutation	SNP	T	C	T	MYO10	c.A1099G	p.T367A
XH_P38	5	31409252	31409252	Silent	SNP	A	G	A	DROSHA	c.T3654C	p.N1218N
XH_P38	5	32074173	32074173	Silent	SNP	G	A	G	PDZ2	c.G2961A	p.G987G
XH_P38	5	32074392	32074392	Silent	SNP	G	A	G	PDZ2	c.G3180A	p.T1060T
XH_P38	5	32087326	32087326	Missense_Mutation	SNP	C	A	C	PDZ2	c.C3772A	p.Q1258K
XH_P38	5	32087430	32087430	Silent	SNP	G	A	G	PDZ2	c.G3876A	p.P1292P
XH_P38	5	32088213	32088213	Silent	SNP	C	T	C	PDZ2	c.C4659T	p.G1553G
XH_P38	5	32088500	32088500	Missense_Mutation	SNP	C	T	C	PDZ2	c.C4946T	p.A1649V
XH_P38	5	34004707	34004707	Missense_Mutation	SNP	C	T	C	AMACR	c.G524A	p.G175D
XH_P38	5	34008100	34008100	Missense_Mutation	SNP	C	T	C	AMACR	c.G25A	p.V9M
XH_P38	5	35692775	35692775	Missense_Mutation	SNP	T	A	T	SPEF2	c.T1848A	p.N616K
XH_P38	5	35861068	35861068	Missense_Mutation	SNP	T	C	T	IL7R	c.T197C	p.I66T
XH_P38	5	35991342	35991342	Missense_Mutation	SNP	T	C	T	UGT3A1	c.A1G	p.M1V
XH_P38	5	38921788	38921788	Missense_Mutation	SNP	G	A	G	OSMR	c.G1657A	p.D553N
XH_P38	5	41000886	41000886	Missense_Mutation	SNP	G	T	G	MROH2B	c.C4244A	p.A1415E
XH_P38	5	43609376	43609376	Missense_Mutation	SNP	C	T	C	NNT	c.C79T	p.R27C
XH_P38	5	44809408	44809408	Missense_Mutation	SNP	T	A	T	MRPS30	c.T344A	p.L115Q
XH_P38	5	52193287	52193287	Silent	SNP	C	T	C	ITGA1	c.C1092T	p.A364A
XH_P38	5	53815066	53815066	Silent	SNP	C	A	C	SNX18	c.C1284A	p.I428I
XH_P38	5	53815240	53815240	Silent	SNP	G	C	G	SNX18	c.G1458C	p.S486S
XH_P38	5	55407542	55407542	Missense_Mutation	SNP	C	T	C	ANKRD55	c.G1033A	p.V345M

XH_P38	5	56111751	56111751	Silent	SNP	G	C	G	MAP3K1	c.G351C	p.A117A
XH_P38	5	56161787	56161787	Silent	SNP	G	A	G	MAP3K1	c.G1284A	p.T428T
XH_P38	5	56177743	56177743	Missense_Mutation	SNP	G	A	G	MAP3K1	c.G2716A	p.V906I
XH_P38	5	56178217	56178217	Silent	SNP	A	C	A	MAP3K1	c.A3190C	p.R1064R
XH_P38	5	60628774	60628774	Silent	SNP	C	T	C	ZSWIM6	c.C675T	p.V225V
XH_P38	5	63257500	63257500	Missense_Mutation	SNP	G	A	G	HTR1A	c.C47T	p.P16L
XH_P38	5	64081367	64081367	Silent	SNP	C	T	C	CWC27	c.C456T	p.D152D
XH_P38	5	66462372	66462372	Silent	SNP	G	A	G	MAST4	c.G6582A	p.P2194P
XH_P38	5	74907503	74907503	Missense_Mutation	SNP	G	A	G	ANKDD1B	c.G44A	p.G15E
XH_P38	5	75923285	75923285	Silent	SNP	C	T	C	IQGAP2	c.C231T	p.A77A
XH_P38	5	78421959	78421959	Missense_Mutation	SNP	G	A	G	BHMT	c.G716A	p.R239Q
XH_P38	5	79950724	79950724	In_Frame_Ins	INS	-	CCGCAGCGC	-	MSH3	8_179insCCGCAAG	A60delinsAAAP
XH_P38	5	80604430	80604430	Silent	SNP	C	T	C	ZCCHC9	c.C435T	p.A145A
XH_P38	5	80736444	80736444	Silent	SNP	A	G	A	SSBP2	c.T801C	p.G267G
XH_P38	5	87493525	87493525	Missense_Mutation	SNP	C	T	C	TMEM161B	c.G601A	p.V201I
XH_P38	5	96031575	96031575	Silent	SNP	C	T	C	CAST	c.C174T	p.S58S
XH_P38	5	96249115	96249115	Silent	SNP	C	T	C	ERAP2	c.C2476T	p.L826L
XH_P38	5	96350710	96350710	Missense_Mutation	SNP	G	A	G	LNPEP	c.G2287A	p.A763T
XH_P38	5	102494181	102494181	Silent	SNP	T	C	T	PPIPSK2	c.T1641C	p.C547C
XH_P38	5	112849608	112849608	Missense_Mutation	SNP	A	T	A	YTHDC2	c.A16T	p.S6C
XH_P38	5	115394626	115394626	Silent	SNP	G	A	G	ARL14EPL	c.G441A	p.P147P
XH_P38	5	115469773	115469773	Silent	SNP	C	T	C	COMMD10	c.C366T	p.T122T
XH_P38	5	128797315	128797315	In_Frame_Ins	INS	-	CCCCGCC	-	ADAMTS19	12_613insCCCCG	N204delinsNPG
XH_P38	5	129520679	129520679	Missense_Mutation	SNP	G	A	G	CHSY3	c.G1844A	p.G615E
XH_P38	5	132083458	132083458	Missense_Mutation	SNP	G	C	G	ACN12	c.G271C	p.A91P
XH_P38	5	132099999	132099999	Silent	SNP	A	G	A	SEPT8	c.T264C	p.Y88Y
XH_P38	5	134076812	134076812	Missense_Mutation	SNP	G	A	G	CAMLG	c.G232A	p.V78I
XH_P38	5	134223593	134223593	Silent	SNP	A	G	A	TXNDC15	c.A108G	p.K36K
XH_P38	5	134782576	134782576	Missense_Mutation	SNP	T	G	T	DCANP1	c.A223C	p.T75P
XH_P38	5	135388663	135388663	Silent	SNP	A	G	A	TGFB1	c.A981G	p.V327V
XH_P38	5	137681261	137681261	Missense_Mutation	SNP	G	A	G	FAM53C	c.G884A	p.R295H
XH_P38	5	138717709	138717709	Silent	SNP	G	A	G	SLC23A1	c.C180T	p.I60I
XH_P38	5	138728533	138728533	Silent	SNP	C	T	C	PROB1	c.G2238A	p.E746E
XH_P38	5	138730037	138730037	Missense_Mutation	SNP	T	C	T	PROB1	c.A734G	p.Q245R
XH_P38	5	138730407	138730407	Missense_Mutation	SNP	C	T	C	PROB1	c.G364A	p.G122S
XH_P38	5	138861078	138861078	Missense_Mutation	SNP	C	T	C	TMEM173	c.G212A	p.R71H
XH_P38	5	139217320	139217320	Silent	SNP	G	C	G	PSD2	c.G1776C	p.V592V
XH_P38	5	140021482	140021482	Silent	SNP	C	T	C	TMC06	c.C342T	p.V114V
XH_P38	5	140168138	140168138	Missense_Mutation	SNP	C	T	C	PCDH1A	c.C2263T	p.R755W
XH_P38	5	140307284	140307284	Silent	SNP	G	A	G	PCDHAC1	c.G807A	p.Q269Q
XH_P38	5	140307746	140307746	Silent	SNP	C	G	C	PCDHAC1	c.C1269G	p.P423P
XH_P38	5	140307969	140307969	Missense_Mutation	SNP	C	G	C	PCDHAC1	c.C1492G	p.L498V
XH_P38	5	140346468	140346468	Silent	SNP	T	A	T	PCDHAC2	c.T117A	p.P39P
XH_P38	5	140346712	140346712	Silent	SNP	T	C	T	PCDHAC2	c.T361C	p.L121L
XH_P38	5	140481475	140481475	Missense_Mutation	SNP	A	T	A	PCDHB3	c.A1242T	p.R414S
XH_P38	5	140481477	140481477	Missense_Mutation	SNP	C	G	C	PCDHB3	c.C1244G	p.S415C
XH_P38	5	140553917	140553917	Missense_Mutation	SNP	G	A	G	PCDHB7	c.G1501A	p.A501T
XH_P38	5	140553919	140553919	Silent	SNP	C	A	A	PCDHB7	c.C1503A	p.A501A
XH_P38	5	140563173	140563173	Missense_Mutation	SNP	G	T	G	PCDHB16	c.G1039T	p.V347L
XH_P38	5	140595106	140595106	Missense_Mutation	SNP	C	G	C	PCDHB13	c.C1411G	p.R471G
XH_P38	5	140604721	140604721	Silent	SNP	C	A	C	PCDHB14	c.C1644A	p.R548R
XH_P38	5	140605131	140605131	Missense_Mutation	SNP	C	T	C	PCDHB14	c.C2054T	p.S685F
XH_P38	5	140605132	140605132	Silent	SNP	C	G	C	PCDHB14	c.C2055G	p.S685S
XH_P38	5	140699057	140699057	Silent	SNP	G	C	G	TAF7	c.C555G	p.A185A
XH_P38	5	140720543	140720543	Missense_Mutation	SNP	C	T	C	PCDHGA2	c.C2005T	p.P669S
XH_P38	5	140751128	140751128	Missense_Mutation	SNP	C	G	C	PCDHGB3	c.C1167G	p.N389K
XH_P38	5	140763029	140763029	Missense_Mutation	SNP	A	G	A	PCDHGA7	c.A563G	p.E188G
XH_P38	5	140772427	140772427	Missense_Mutation	SNP	T	G	T	PCDHGA8	c.T47G	p.L16R
XH_P38	5	140783596	140783596	Silent	SNP	C	T	C	PCDHGA9	c.C1077T	p.D359D
XH_P38	5	140794962	140794962	Silent	SNP	C	T	C	PCDHGA10	c.C2220T	p.S740S
XH_P38	5	140797630	140797630	Silent	SNP	G	T	G	PCDHGB7	c.G204T	p.V68V
XH_P38	5	140810773	140810773	Silent	SNP	G	A	G	PCDHGA12	c.G447A	p.E149E
XH_P38	5	141019110	141019110	Missense_Mutation	SNP	C	A	C	RELL2	c.C397A	p.L133I
XH_P38	5	141019569	141019569	Missense_Mutation	SNP	G	C	G	RELL2	c.G586C	p.G196R
XH_P38	5	141019830	141019830	Missense_Mutation	SNP	C	G	C	RELL2	c.C847G	p.Q283E
XH_P38	5	141052416	141052416	Silent	SNP	G	T	G	ARAP3	c.C1170A	p.P390P
XH_P38	5	141233796	141233796	Silent	SNP	C	T	C	PCDH1	c.G3525A	p.P1175P
XH_P38	5	141242878	141242878	Silent	SNP	G	A	G	PCDH1	c.C1881T	p.T627T
XH_P38	5	141243646	141243646	Silent	SNP	A	G	A	PCDH1	c.T1113C	p.A371A
XH_P38	5	141334921	141334921	Silent	SNP	C	T	C	PCDH12	c.G2496A	p.Q832Q
XH_P38	5	142661490	142661490	Silent	SNP	A	G	A	NR3C1	c.T2298C	p.N766N
XH_P38	5	142678361	142678361	Silent	SNP	G	A	G	NR3C1	c.C1764T	p.H588H
XH_P38	5	146258290	146258290	In_Frame_Ins	INS	-	GCTGCTGCTGCT	-	PPP2R2B	58insAGCAGCAGC	C20delinsSSSSC
XH_P38	5	148206917	148206917	Silent	SNP	C	A	C	ADR82	c.C523A	p.R175R
XH_P38	5	148386525	148386525	Silent	SNP	T	G	T	SH3TC2	c.A3594C	p.P1198P
XH_P38	5	148737644	148737644	Missense_Mutation	SNP	G	C	G	PCYOX1L	c.G13C	p.A5P
XH_P38	5	149361221	149361221	Missense_Mutation	SNP	A	T	A	SLC26A2	c.A2065T	p.T689S
XH_P38	5	149421502	149421502	Silent	SNP	A	G	A	HMGXB3	c.A2700G	p.E900E
XH_P38	5	149431476	149431476	Silent	SNP	C	T	C	HMGXB3	c.C3600T	p.Y1200Y
XH_P38	5	149460343	149460343	Silent	SNP	G	A	G	CSF1R	c.C294T	p.H98H
XH_P38	5	149677593	149677593	Silent	SNP	A	G	A	ARSI	c.T894C	p.N298N
XH_P38	5	149826526	149826526	Silent	SNP	C	T	C	RP514	c.G150A	p.K50K
XH_P38	5	149915402	149915402	Silent	SNP	G	A	G	NDST1	c.G1392A	p.L464L
XH_P38	5	150029415	150029415	Silent	SNP	C	T	C	SYNPO	c.C1578T	p.P526P
XH_P38	5	150227998	150227998	Silent	SNP	C	T	C	IRGM	c.C313T	p.L105L
XH_P38	5	150512740	150512740	Silent	SNP	G	A	G	ANXA6	c.C459T	p.Y153Y
XH_P38	5	150948016	150948016	Silent	SNP	C	T	C	FAT2	c.G477A	p.E159E
XH_P38	5	151784183	151784183	Silent	SNP	G	A	G	NMUR2	c.C492T	p.L164L
XH_P38	5	154395158	154395158	Missense_Mutation	SNP	G	T	G	KIF4B	c.G1739T	p.R580L
XH_P38	5	159992655	159992655	Silent	SNP	T	C	T	ATP10B	c.A4191G	p.V1397V
XH_P38	5	159992754	159992754	Silent	SNP	T	G	T	ATP10B	c.A4092C	p.P1364P
XH_P38	5	161522556	161522556	Silent	SNP	C	T	C	GABRG2	c.C315T	p.N105N
XH_P38	5	167379679	167379679	Missense_Mutation	SNP	G	A	G	TENM2	c.G226A	p.A76T
XH_P38	5	169504743	169504743	Silent	SNP	T	C	T	DOCK2	c.T4896C	p.R1632R
XH_P38	5	169695446	169695446	Silent	SNP	C	T	C	LCP2	c.G564A	p.V188V
XH_P38	5	170883734	170883734	Silent	SNP	G	A	G	PGF18	c.G549A	p.P183P
XH_P38	5	174937193	174937193	Silent	SNP	C	T	C	SFXN1	c.C417T	p.D139D
XH_P38	5	175665522	175665522	Missense_Mutation	SNP	T	A	T	SIMC1	c.T11A	p.F4Y

XH_P38	5	176314639	176314639	Silent	SNP	G	A	G	HK3	c.C1413T	p.A471A
XH_P38	5	176637576	176637576	Missense_Mutation	SNP	T	C	T	NSD1	c.T2176C	p.S726P
XH_P38	5	177031348	177031348	Silent	SNP	T	C	T	B4GALT7	c.T219C	p.R73R
XH_P38	5	177547336	177547336	Missense_Mutation	SNP	G	A	G	N4BP3	c.G488A	p.R163Q
XH_P38	5	177657001	177657001	Missense_Mutation	SNP	G	A	G	PHYKPL	c.C155T	p.A52V
XH_P38	5	177675217	177675217	Silent	SNP	C	T	C	COL23A1	c.G1188A	p.A396A
XH_P38	5	179734200	179734200	Silent	SNP	A	G	A	GFPT2	c.T1650C	p.Y550Y
XH_P38	5	180659796	180659796	Silent	SNP	G	A	G	TRIM41	c.G1047A	p.A349A
XH_P38	6	564145	564145	Silent	SNP	A	G	A	EXOC2	c.T1677C	p.H559H
XH_P38	6	1313258	1313258	Missense_Mutation	SNP	G	C	G	FOXQ1	c.G319C	p.E107Q
XH_P38	6	3273457	3273457	Silent	SNP	A	G	A	SLC22A23	c.T1050C	p.S350S
XH_P38	6	3850463	3850463	Missense_Mutation	SNP	G	A	G	FAM50B	c.G418A	p.G140R
XH_P38	6	6174866	6174866	Missense_Mutation	SNP	G	A	G	F13A1	c.C1694T	p.P565L
XH_P38	6	7229619	7229619	Silent	SNP	G	A	G	RREB1	c.G1287A	p.A429A
XH_P38	6	7247344	7247344	Missense_Mutation	SNP	C	A	C	RREB1	c.C4496A	p.S1499Y
XH_P38	6	10894381	10894381	Missense_Mutation	SNP	G	A	G	SYCP2L	c.G280A	p.V94I
XH_P38	6	11185533	11185533	Silent	SNP	G	A	G	NEDD9	c.C1920T	p.T640T
XH_P38	6	12122174	12122174	Missense_Mutation	SNP	A	G	A	HIVEP1	c.A2146G	p.T716A
XH_P38	6	12124855	12124855	Missense_Mutation	SNP	G	A	G	HIVEP1	c.G4827A	p.M1609I
XH_P38	6	13206282	13206282	Silent	SNP	C	T	C	PHACTR1	c.C624T	p.T208T
XH_P38	6	15496662	15496662	Silent	SNP	C	T	C	JARID2	c.C690T	p.P230P
XH_P38	6	16145325	16145325	Missense_Mutation	SNP	A	G	A	MYLIP	c.A1025G	p.N342S
XH_P38	6	16327330	16327330	Silent	SNP	T	C	T	ATXN1	c.A1212G	p.E404E
XH_P38	6	16328245	16328245	Silent	SNP	G	A	G	ATXN1	c.C297T	p.A99A
XH_P38	6	21065449	21065449	Missense_Mutation	SNP	C	T	C	CDKAL1	c.C1226T	p.P409L
XH_P38	6	21065450	21065450	Silent	SNP	A	G	A	CDKAL1	c.A1227G	p.P409P
XH_P38	6	25776949	25776949	Missense_Mutation	SNP	G	A	G	SLC17A4	c.G1114A	p.A372T
XH_P38	6	26020783	26020783	Silent	SNP	C	T	C	HIST1H3A	c.C66T	p.A22A
XH_P38	6	26020981	26020981	Silent	SNP	C	A	C	HIST1H3A	c.C264A	p.S88S
XH_P38	6	26021945	26021945	Silent	SNP	G	A	G	HIST1H4A	c.G39A	p.K13K
XH_P38	6	26056417	26056417	Silent	SNP	G	A	G	HIST1H1C	c.C240T	p.I80I
XH_P38	6	26184041	26184041	Silent	SNP	A	G	A	HIST1H2BE	c.A18G	p.K6K
XH_P38	6	26199222	26199222	Silent	SNP	G	A	G	HIST1H2AD	c.C250T	p.L84L
XH_P38	6	26216656	26216656	Silent	SNP	T	C	T	HIST1H2BG	c.A216G	p.E72E
XH_P38	6	26285503	26285503	Silent	SNP	C	T	C	HIST1HAH	c.G225A	p.E75E
XH_P38	6	27833174	27833174	Silent	SNP	A	G	A	HIST1H2AL	c.A42G	p.K14K
XH_P38	6	27835272	27835272	Silent	SNP	T	C	T	HIST1H1B	c.A36G	p.P12P
XH_P38	6	27858421	27858421	Silent	SNP	A	G	A	HIST1H3J	c.T150C	p.R50R
XH_P38	6	28227436	28227436	Missense_Mutation	SNP	A	G	A	NKAPL	c.A287G	p.Y96C
XH_P38	6	28227604	28227604	Missense_Mutation	SNP	C	A	C	NKAPL	c.C455A	p.T152N
XH_P38	6	28269663	28269663	Missense_Mutation	SNP	A	G	A	PGBD1	c.A2032G	p.I678V
XH_P38	6	31106516	31106516	Missense_Mutation	SNP	C	T	C	PSORS1C1	c.C127T	p.P43S
XH_P38	6	33636907	33636907	Silent	SNP	C	T	C	ITPR3	c.C2163T	p.H721H
XH_P38	6	33638453	33638453	Missense_Mutation	SNP	A	G	A	ITPR3	c.A2447G	p.D816G
XH_P38	6	33641379	33641379	Silent	SNP	T	C	T	ITPR3	c.T2940C	p.N980N
XH_P38	6	33653486	33653486	Missense_Mutation	SNP	G	A	G	ITPR3	c.G5549A	p.R1850Q
XH_P38	6	34003685	34003685	Silent	SNP	T	C	T	GRM4	c.A1854G	p.T618T
XH_P38	6	34008006	34008006	Silent	SNP	A	G	A	GRM4	c.T1107C	p.D369D
XH_P38	6	34214348	34214348	Missense_Mutation	SNP	C	T	C	SMIM29	c.G363A	p.M121I
XH_P38	6	34857302	34857302	In_Frame_Ins	INS	-	GGCGGC	-	ANKS1A	23_124insGGCG	G41delinsGGG
XH_P38	6	35705892	35705892	Silent	SNP	T	C	T	ARMC12	c.T252C	p.Y84Y
XH_P38	6	36269725	36269725	Missense_Mutation	SNP	A	G	A	PNPLA1	c.A605G	p.E202G
XH_P38	6	36672070	36672070	Missense_Mutation	SNP	C	T	C	RAB44	c.C58T	p.R20W
XH_P38	6	36689630	36689630	Silent	SNP	C	T	C	RAB44	c.C1719T	p.A573A
XH_P38	6	36690455	36690455	Silent	SNP	C	A	C	RAB44	c.C2544A	p.S848S
XH_P38	6	36882353	36882353	Silent	SNP	A	G	A	C6orf89	c.A600G	p.E200E
XH_P38	6	38650588	38650588	Silent	SNP	T	A	T	GL01	c.A372T	p.G124G
XH_P38	6	38840492	38840492	Missense_Mutation	SNP	G	T	G	DNAH8	c.G7171T	p.A2391S
XH_P38	6	38841083	38841083	Silent	SNP	T	C	T	DNAH8	c.T7551C	p.D2517D
XH_P38	6	39033593	39033593	Silent	SNP	G	A	G	GLP1R	c.G390A	p.K130K
XH_P38	6	39041502	39041502	Missense_Mutation	SNP	A	C	A	GLP1R	c.A780C	p.L260F
XH_P38	6	39282036	39282036	Missense_Mutation	SNP	T	C	T	KCNK17	c.A61G	p.S21G
XH_P38	6	39284184	39284184	Silent	SNP	A	G	A	KCNK16	c.T696C	p.Y232Y
XH_P38	6	41303995	41303995	Missense_Mutation	SNP	A	G	A	NCR2	c.A223G	p.M75V
XH_P38	6	41658889	41658889	Silent	SNP	C	T	C	TFEB	c.G105A	p.Q35Q
XH_P38	6	41754576	41754576	Silent	SNP	C	T	C	PRICKLE4	c.C864T	p.L288L
XH_P38	6	41903782	41903782	Missense_Mutation	SNP	A	C	A	CND3	c.T559G	p.S187A
XH_P38	6	42072692	42072692	Silent	SNP	G	T	G	C6orf132	c.C2958A	p.I986I
XH_P38	6	42532102	42532102	Silent	SNP	C	T	C	UBR2	c.C45T	p.S15S
XH_P38	6	43030791	43030791	Missense_Mutation	SNP	G	A	G	KLC4	c.G395A	p.R132H
XH_P38	6	43738977	43738977	Silent	SNP	C	T	C	VEGFA	c.C534T	p.S178S
XH_P38	6	43970827	43970827	Silent	SNP	G	A	G	C6orf223	c.G357A	p.A119A
XH_P38	6	44223010	44223010	Silent	SNP	G	T	G	SLC35B2	c.C333A	p.T111T
XH_P38	6	44250165	44250165	Silent	SNP	A	G	A	TCTE1	c.T978C	p.G326G
XH_P38	6	44255459	44255459	Missense_Mutation	SNP	G	A	G	TCTE1	c.C104T	p.P35L
XH_P38	6	44269193	44269193	Silent	SNP	C	T	C	AARS2	c.G2607A	p.K869K
XH_P38	6	44982593	44982593	Silent	SNP	G	A	G	SUPT3H	c.C51T	p.I17I
XH_P38	6	46620252	46620252	Missense_Mutation	SNP	C	G	C	CYP39A1	c.G68C	p.R23P
XH_P38	6	46801071	46801071	Missense_Mutation	SNP	G	T	G	MEP1A	c.G1405T	p.V469L
XH_P38	6	49485266	49485266	Missense_Mutation	SNP	C	A	C	GLYATL3	c.C310A	p.Q104K
XH_P38	6	50683193	50683193	Missense_Mutation	SNP	G	A	G	TFAP2D	c.G404A	p.G135D
XH_P38	6	52101844	52101844	Missense_Mutation	SNP	T	C	T	IL17F	c.A377G	p.E126G
XH_P38	6	53517035	53517035	Silent	SNP	G	A	G	KLHL31	c.C1266T	p.Y422Y
XH_P38	6	56438601	56438601	In_Frame_Ins	INS	-	GTGAAC	-	DST	42_5243insGTTT	L1748delinsRSL
XH_P38	6	56917538	56917538	Missense_Mutation	SNP	G	A	G	KIAA1586	c.G160A	p.V54M
XH_P38	6	56919443	56919443	Missense_Mutation	SNP	A	G	A	KIAA1586	c.A2065G	p.I689V
XH_P38	6	57055354	57055354	Missense_Mutation	SNP	C	T	C	RAB23	c.G619A	p.G207S
XH_P38	6	64694354	64694354	Missense_Mutation	SNP	C	T	C	EYS	c.G6977A	p.R2326Q
XH_P38	6	65300143	65300143	Missense_Mutation	SNP	G	C	G	EYS	c.C5617G	p.L1873V
XH_P38	6	65301408	65301408	Missense_Mutation	SNP	A	G	A	EYS	c.T4352C	p.I1451T
XH_P38	6	71569090	71569090	Missense_Mutation	SNP	T	C	T	SMAP1	c.T1247C	p.M416T
XH_P38	6	71998778	71998778	Missense_Mutation	SNP	T	C	T	OGFRL1	c.T139C	p.S47P
XH_P38	6	72892383	72892383	Silent	SNP	G	A	G	RIMS1	c.G1209A	p.A403A
XH_P38	6	74019376	74019376	Missense_Mutation	SNP	T	C	T	KHDC1	c.A62G	p.Y21C
XH_P38	6	74161762	74161762	Missense_Mutation	SNP	G	T	G	MB21D1	c.C143A	p.A48E
XH_P38	6	75797302	75797302	Missense_Mutation	SNP	C	T	C	COL12A1	c.G5680A	p.G1894S
XH_P38	6	88224164	88224164	Silent	SNP	T	C	T	RARS2	c.A1179G	p.K393K
XH_P38	6	90039670	90039670	Missense_Mutation	SNP	G	C	G	UBE2J1	c.C685G	p.L229V

XH_P38	6	90497589	90497589	Missense_Mutation	SNP	A	C	A	MDN1	c.T1318G	p.F440V
XH_P38	6	90660754	90660754	Silent	SNP	G	A	G	BACH2	c.C1071T	p.P357P
XH_P38	6	99848777	99848777	Missense_Mutation	SNP	C	G	C	PNISR	c.G2003C	p.R668P
XH_P38	6	106960447	106960447	Silent	SNP	G	A	G	CRYBG1	c.G231A	p.E77E
XH_P38	6	107076696	107076696	Silent	SNP	G	A	G	RTN4IP1	c.C201T	p.I67I
XH_P38	6	107391213	107391213	Silent	SNP	C	T	C	BEND3	c.G1182A	p.T394T
XH_P38	6	108067915	108067915	Silent	SNP	G	A	G	SCML4	c.C291T	p.G97G
XH_P38	6	109591433	109591433	Silent	SNP	T	C	T	C6orf183	c.T1638C	p.N546N
XH_P38	6	109767931	109767931	Missense_Mutation	SNP	C	T	C	MICAL1	c.G2014A	p.A672T
XH_P38	6	109775021	109775021	Missense_Mutation	SNP	C	T	C	MICAL1	c.G286A	p.G96R
XH_P38	6	110777962	110777962	Silent	SNP	A	G	A	SLC22A16	c.T312C	p.N104N
XH_P38	6	111689082	111689082	Missense_Mutation	SNP	C	T	C	REV3L	c.G5909A	p.R1970H
XH_P38	6	114378970	114378970	Silent	SNP	C	T	C	HS3TS5	c.G492A	p.E164E
XH_P38	6	116574994	116574994	Missense_Mutation	SNP	C	G	C	TSPYL4	c.G178C	p.G60R
XH_P38	6	116747769	116747769	Missense_Mutation	SNP	C	T	C	DSE	c.C449T	p.P150L
XH_P38	6	117113653	117113653	Silent	SNP	T	C	T	GPCRC6A	c.A2220G	p.P740P
XH_P38	6	117114025	117114025	Silent	SNP	G	A	G	GPCRC6A	c.C1848T	p.A616A
XH_P38	6	117114223	117114223	Silent	SNP	T	A	T	GPCRC6A	c.A1650T	p.T550T
XH_P38	6	117725578	117725578	Silent	SNP	T	A	T	ROS1	c.A303T	p.L101L
XH_P38	6	121629167	121629167	Silent	SNP	G	A	G	TBC1D32	c.C645T	p.C215C
XH_P38	6	127476516	127476516	Silent	SNP	G	A	G	RSPO3	c.C567A	p.L189L
XH_P38	6	127797179	127797179	Silent	SNP	G	A	G	SOGA3	c.C1992T	p.A664A
XH_P38	6	127797374	127797374	Silent	SNP	G	A	G	SOGA3	c.C1797T	p.N599N
XH_P38	6	128388799	128388799	Silent	SNP	G	T	G	PTPRK	c.C1635A	p.L545L
XH_P38	6	129612808	129612808	Silent	SNP	A	G	A	LAMA2	c.A2799G	p.Q933Q
XH_P38	6	132030037	132030037	Silent	SNP	T	C	T	CTAGE9	c.A2121G	p.P707P
XH_P38	6	132031548	132031548	Nonsense_Mutation	SNP	G	A	G	CTAGE9	c.C610T	p.R204X
XH_P38	6	133045902	133045902	Missense_Mutation	SNP	A	G	A	VNN3	c.T272C	p.F91S
XH_P38	6	139487836	139487836	Silent	SNP	T	C	T	HECA	c.T687C	p.N292N
XH_P38	6	143090734	143090734	Silent	SNP	T	C	T	HIVEP2	c.A5142G	p.G1714G
XH_P38	6	145103215	145103215	Silent	SNP	C	T	C	UTRN	c.C8790T	p.L2930L
XH_P38	6	146056476	146056476	Silent	SNP	G	C	G	EPM2A	c.C159G	p.A53A
XH_P38	6	146234644	146234644	Silent	SNP	G	A	G	SHPRH	c.C4296T	p.C1432C
XH_P38	6	146755140	146755140	Silent	SNP	G	A	G	GRM1	c.G2793A	p.K931K
XH_P38	6	146755324	146755324	Missense_Mutation	SNP	T	C	T	GRM1	c.T2977C	p.S993P
XH_P38	6	146755515	146755515	Silent	SNP	T	G	T	GRM1	c.T3168G	p.G1056G
XH_P38	6	146755842	146755842	Silent	SNP	C	A	C	GRM1	c.C3495A	p.P1165P
XH_P38	6	148664242	148664242	In_Frame_Ins	INS	-	GAGCCC	-	SASH1	39_40insGAGCC	p.P13delinsPEP
XH_P38	6	149795522	149795522	Missense_Mutation	SNP	G	A	G	ZC3H12D	c.C158T	p.P53L
XH_P38	6	150266578	150266578	Silent	SNP	T	C	T	ULBP2	c.T219C	p.P73P
XH_P38	6	150342232	150342232	Missense_Mutation	SNP	G	A	G	RAET1L	c.C440T	p.T147I
XH_P38	6	150346532	150346532	Missense_Mutation	SNP	T	C	T	RAET1L	c.A76G	p.R26G
XH_P38	6	150464356	150464356	Missense_Mutation	SNP	A	G	A	PPP1R14C	c.A28G	p.T10A
XH_P38	6	151670172	151670172	Missense_Mutation	SNP	A	C	A	AKAP12	c.A352C	p.L118Q
XH_P38	6	152129077	152129077	Silent	SNP	T	C	T	ESR1	c.T30C	p.S10S
XH_P38	6	152694184	152694184	Silent	SNP	T	C	T	SYNE1	c.A9516G	p.E3172E
XH_P38	6	157405930	157405930	Silent	SNP	G	A	G	ARID1B	c.G2133A	p.A711A
XH_P38	6	158014097	158014097	Missense_Mutation	SNP	G	A	G	ZDHHC14	c.G484A	p.V162M
XH_P38	6	158492691	158492691	Silent	SNP	C	T	C	SYNJ2	c.C1287T	p.G429G
XH_P38	6	159420574	159420574	Silent	SNP	T	C	T	RSPH3	c.A435G	p.S145S
XH_P38	6	159653094	159653094	Missense_Mutation	SNP	G	T	G	FNDC1	c.G1550T	p.G517V
XH_P38	6	159653635	159653635	Silent	SNP	C	G	C	FNDC1	c.C2091G	p.A697A
XH_P38	6	159672455	159672455	Silent	SNP	C	T	C	FNDC1	c.C4956T	p.D1652D
XH_P38	6	160448324	160448324	Missense_Mutation	SNP	C	G	C	IGF2R	c.C754G	p.L252V
XH_P38	6	160468278	160468278	Silent	SNP	A	G	A	IGF2R	c.A2139G	p.T713T
XH_P38	6	160557643	160557643	Missense_Mutation	SNP	C	T	C	SLC22A1	c.C1022T	p.P341L
XH_P38	6	160679666	160679666	Missense_Mutation	SNP	A	G	A	SLC22A2	c.T124C	p.F42L
XH_P38	6	160969629	160969629	Missense_Mutation	SNP	A	G	A	LPA	c.T5036C	p.M1679T
XH_P38	6	161137779	161137779	Silent	SNP	T	C	T	PLG	c.T771C	p.C257C
XH_P38	6	165715587	165715587	Missense_Mutation	SNP	G	A	G	C6orf118	c.C224T	p.T75M
XH_P38	6	166572045	166572045	Missense_Mutation	SNP	C	T	C	T	c.G892A	p.G298S
XH_P38	6	168343838	168343838	Silent	SNP	T	C	T	AFDN	c.T3060C	p.Y1020Y
XH_P38	6	168366580	168366580	Silent	SNP	G	A	G	AFDN	c.G4962A	p.P1654P
XH_P38	6	168377309	168377309	Silent	SNP	G	A	G	HGC6.3	c.C24T	p.S8S
XH_P38	6	168442687	168442687	Missense_Mutation	SNP	A	C	A	KIF25	c.A685C	p.T229P
XH_P38	6	168479562	168479562	Silent	SNP	C	T	C	FRMD1	c.G213A	p.G71G
XH_P38	6	168708793	168708793	Silent	SNP	C	G	C	DACT2	c.G1134C	p.R378R
XH_P38	6	168711070	168711070	Missense_Mutation	SNP	C	T	C	DACT2	c.G436A	p.V146I
XH_P38	6	170176467	170176467	Missense_Mutation	SNP	A	G	A	ERMARD	c.A1558G	p.K520E
XH_P38	7	297023	297023	Silent	SNP	G	A	G	FAM20C	c.G1416A	p.T472T
XH_P38	7	995003	995003	Missense_Mutation	SNP	G	C	G	ADAP1	c.C41G	p.P14R
XH_P38	7	1097952	1097952	Silent	SNP	C	T	C	GPR146	c.C801T	p.D267D
XH_P38	7	1131411	1131411	Missense_Mutation	SNP	C	T	C	GPFR1	c.C47T	p.P16L
XH_P38	7	1192797	1192797	Missense_Mutation	SNP	C	A	C	ZFAND2A	c.G346T	p.A116S
XH_P38	7	1195215	1195215	Silent	SNP	A	C	A	ZFAND2A	c.T156G	p.V52V
XH_P38	7	1976457	1976457	Missense_Mutation	SNP	C	T	C	MAD1L1	c.G41A	p.R14H
XH_P38	7	2552881	2552881	Frame_Shift_Ins	INS	-	GATG	-	LFNG	138_139insGAT	p.T46fs
XH_P38	7	2582907	2582907	Missense_Mutation	SNP	C	T	C	BRAT1	c.G329A	p.R110Q
XH_P38	7	4304937	4304937	Missense_Mutation	SNP	C	A	C	SDK1	c.C6563A	p.T2188K
XH_P38	7	4823396	4823396	Silent	SNP	C	T	C	AP521	c.C588T	p.S196S
XH_P38	7	4901191	4901191	Missense_Mutation	SNP	T	C	T	PAPOLB	c.A251G	p.K84R
XH_P38	7	5330436	5330436	Silent	SNP	C	T	C	SLC29A4	c.C243T	p.F81F
XH_P38	7	5336667	5336667	Silent	SNP	G	A	G	SLC29A4	c.G720A	p.A240A
XH_P38	7	5352659	5352659	Silent	SNP	G	T	G	TNRC18	c.C7863A	p.S6262S
XH_P38	7	5427517	5427517	Silent	SNP	G	A	G	TNRC18	c.C1938T	p.G646G
XH_P38	7	5428477	5428477	Silent	SNP	A	T	A	TNRC18	c.T978A	p.P326P
XH_P38	7	6063283	6063283	Silent	SNP	C	T	C	AIMP2	c.C717T	p.N239N
XH_P38	7	6189780	6189780	Silent	SNP	T	C	T	USP42	c.T1953C	p.L651L
XH_P38	7	6193464	6193464	Missense_Mutation	SNP	T	G	T	USP42	c.T2279G	p.L760R
XH_P38	7	6537821	6537821	Silent	SNP	G	C	G	GRID2IP	c.C3438G	p.L1146L
XH_P38	7	6547902	6547902	Missense_Mutation	SNP	G	A	G	GRID2IP	c.C2258T	p.P753L
XH_P38	7	6693079	6693079	Silent	SNP	C	T	C	ZNF316	c.C1852T	p.L618L
XH_P38	7	11581121	11581121	Missense_Mutation	SNP	T	C	T	THSD7A	c.A1747G	p.N583D
XH_P38	7	11675855	11675855	Silent	SNP	C	T	C	THSD7A	c.G924A	p.R308R
XH_P38	7	11676551	11676551	Silent	SNP	G	T	G	THSD7A	c.C228A	p.P76P
XH_P38	7	14188806	14188806	Missense_Mutation	SNP	C	T	C	DGKB	c.G2308A	p.G770S
XH_P38	7	16734506	16734506	Nonsense_Mutation	SNP	C	G	C	BZW2	c.C699G	p.Y233X
XH_P38	7	16816718	16816718	Missense_Mutation	SNP	G	T	G	TSPAN13	c.G283T	p.A95S

XH_P38	7	19156668	19156668	In_Frame_Ins	INS	-	CGCCGCCGCC	-	TWIST1	5GCGCGGCGG	3delinsGAGGGGS
XH_P38	7	19184732	19184732	Missense_Mutation	SNP	C	A	C	FERD3L	c.G254T	p.G85V
XH_P38	7	20201458	20201458	Missense_Mutation	SNP	G	A	G	MACC1	c.C28T	p.R10W
XH_P38	7	21956405	21956405	Silent	SNP	G	A	G	CDC47L	c.C132T	p.C44C
XH_P38	7	23226747	23226747	Nonsense_Mutation	INS	-	TTTAAATTCT	-	NUPL2	7_428instTTTAA	143_K144delinsIX
XH_P38	7	27150028	27150028	Missense_Mutation	SNP	G	A	G	HOXA3	c.C232T	p.P78S
XH_P38	7	27204732	27204732	Silent	SNP	C	A	C	HOXA9	c.G345T	p.T115T
XH_P38	7	30113706	30113706	Silent	SNP	A	G	A	PLEKHA8	c.A1320G	p.T440T
XH_P38	7	30174773	30174773	Silent	SNP	C	G	C	MTURN	c.C21G	p.A7A
XH_P38	7	30491311	30491311	Silent	SNP	C	T	C	NOD1	c.G1722A	p.A574A
XH_P38	7	30492237	30492237	Missense_Mutation	SNP	C	T	C	NOD1	c.G796A	p.E266K
XH_P38	7	31855569	31855569	Silent	SNP	G	A	G	PDE1C	c.C1782T	p.A594A
XH_P38	7	34009946	34009946	Silent	SNP	C	T	C	BMPER	c.C408T	p.G136G
XH_P38	7	34917740	34917740	Nonsense_Mutation	SNP	C	T	C	NPSR1	c.C1045T	p.R349X
XH_P38	7	35293193	35293193	Silent	SNP	A	G	A	TBX20	c.T39C	p.S13S
XH_P38	7	36656035	36656035	Missense_Mutation	SNP	G	C	G	AOAH	c.C701G	p.A234G
XH_P38	7	36763672	36763672	Missense_Mutation	SNP	C	T	C	AOAH	c.G82A	p.D28N
XH_P38	7	37960715	37960715	Silent	SNP	T	C	T	EPDR1	c.T174C	p.S58S
XH_P38	7	37961001	37961001	Silent	SNP	C	A	C	EPDR1	c.C34A	p.R12R
XH_P38	7	38305142	38305142	Silent	SNP	G	C	G	TARP	c.C126G	p.G42G
XH_P38	7	43484310	43484310	Silent	SNP	T	C	T	HECW1	c.T1539C	p.S513S
XH_P38	7	44259706	44259706	Silent	SNP	G	A	G	CAMK2B	c.C1305T	p.N435N
XH_P38	7	44747514	44747514	Silent	SNP	C	T	C	OGDH	c.C2976T	p.T992T
XH_P38	7	44802545	44802545	Silent	SNP	C	G	C	ZMI22	c.C1584G	p.L528L
XH_P38	7	45113170	45113170	Silent	SNP	G	A	G	CCM2	c.G642A	p.T214T
XH_P38	7	45122464	45122464	Missense_Mutation	SNP	A	C	A	NACAD	c.T3315G	p.D1105E
XH_P38	7	45123090	45123090	Missense_Mutation	SNP	G	A	G	NACAD	c.C2689T	p.P897S
XH_P38	7	45124008	45124008	Missense_Mutation	SNP	T	C	T	NACAD	c.A1771G	p.K591E
XH_P38	7	45124286	45124286	Missense_Mutation	SNP	A	G	A	NACAD	c.T1493C	p.V498A
XH_P38	7	45124465	45124465	Missense_Mutation	SNP	A	T	A	NACAD	c.T1314A	p.D438E
XH_P38	7	45753324	45753324	Silent	SNP	G	A	G	ADCY1	c.G3090A	p.R1030R
XH_P38	7	47408443	47408443	Missense_Mutation	SNP	C	G	C	TNS3	c.G1800C	p.Q600H
XH_P38	7	47913560	47913560	Missense_Mutation	SNP	G	T	G	PKD1L1	c.C3833A	p.P1278Q
XH_P38	7	47971626	47971626	Silent	SNP	G	A	G	PKD1L1	c.C426T	p.I142I
XH_P38	7	48081095	48081095	Missense_Mutation	SNP	G	T	G	C7orf57	c.G220T	p.A74S
XH_P38	7	50467941	50467941	Silent	SNP	C	T	C	IKZF1	c.C486T	p.N162N
XH_P38	7	55249063	55249063	Silent	SNP	G	A	G	EGFR	c.G1560A	p.Q520Q
XH_P38	7	57528997	57528997	Missense_Mutation	SNP	T	C	T	ZNF716	c.T830C	p.V277A
XH_P38	7	63538449	63538449	Missense_Mutation	SNP	T	A	T	ZNF727	c.T1022A	p.I341N
XH_P38	7	63538450	63538450	Silent	SNP	T	A	T	ZNF727	c.T1023A	p.I341I
XH_P38	7	63796744	63796744	Silent	SNP	T	C	T	ZNF736	c.T111C	p.Y37Y
XH_P38	7	65579838	65579838	Missense_Mutation	SNP	A	G	A	CRCP	c.A23G	p.E8G
XH_P38	7	66460358	66460358	Missense_Mutation	SNP	G	A	G	SBD5	c.C47T	p.A16V
XH_P38	7	70597884	70597884	Silent	SNP	G	A	G	GALNT17	c.G96A	p.A32A
XH_P38	7	72418992	72418992	Missense_Mutation	SNP	C	T	C	POM121	c.C2983T	p.P995S
XH_P38	7	72436307	72436307	Missense_Mutation	SNP	C	T	C	TRIM74	c.G382A	p.V128I
XH_P38	7	72732993	72732993	Missense_Mutation	SNP	A	G	A	TRIM50	c.T554C	p.L185P
XH_P38	7	73012042	73012042	Missense_Mutation	SNP	G	A	G	MLXIPL	c.C1073T	p.A358V
XH_P38	7	73013901	73013901	Silent	SNP	C	T	C	MLXIPL	c.G1026A	p.P342P
XH_P38	7	73020337	73020337	Missense_Mutation	SNP	C	G	C	MLXIPL	c.G723C	p.Q241H
XH_P38	7	73097654	73097654	Missense_Mutation	SNP	C	T	C	DNAJC30	c.G100A	p.G34R
XH_P38	7	73731906	73731906	Silent	SNP	C	T	C	CLIP2	c.C30T	p.P10P
XH_P38	7	73935578	73935578	Silent	SNP	C	T	C	GTFF2IRD1	c.C1053T	p.N351N
XH_P38	7	73969541	73969541	Missense_Mutation	SNP	A	G	A	GTFF2IRD1	c.A2050G	p.M684V
XH_P38	7	74193668	74193668	Missense_Mutation	SNP	G	A	G	NCF1	c.G295A	p.G99S
XH_P38	7	75034350	75034350	Missense_Mutation	SNP	T	C	T	TRIM73	c.T724C	p.W242R
XH_P38	7	75915093	75915093	Missense_Mutation	SNP	G	A	G	SRRM3	c.G1973A	p.R658H
XH_P38	7	75932101	75932101	Silent	SNP	G	A	G	HSPB1	c.G72A	p.P24P
XH_P38	7	76030355	76030355	Missense_Mutation	SNP	C	T	C	SSCAD	c.G139A	p.A47T
XH_P38	7	76054372	76054372	Missense_Mutation	SNP	G	A	G	ZIP3	c.G91A	p.G31R
XH_P38	7	76069629	76069629	Silent	SNP	G	A	G	ZIP3	c.G894A	p.K298K
XH_P38	7	76132898	76132898	Silent	SNP	T	C	T	DTX2	c.T1404C	p.G468G
XH_P38	7	76140186	76140186	Missense_Mutation	SNP	T	C	T	UPK3B	c.T217C	p.S73P
XH_P38	7	76916819	76916819	Silent	SNP	G	A	G	CCDC146	c.G2340A	p.Q780Q
XH_P38	7	76950686	76950686	Missense_Mutation	SNP	C	A	C	GSAP	c.G1217T	p.W406L
XH_P38	7	86468516	86468516	Silent	SNP	C	T	C	GRM3	c.C1686T	p.C562C
XH_P38	7	90233544	90233544	Missense_Mutation	SNP	A	T	A	CDK14	c.A104T	p.C35V
XH_P38	7	90894459	90894459	In_Frame_Ins	INS	-	CCG	-	FZD1	264_265insCCG	p.Q88delinsQP
XH_P38	7	91641928	91641928	Silent	SNP	A	G	A	AKAP9	c.A3504G	p.E1168E
XH_P38	7	91691601	91691601	Silent	SNP	C	T	C	AKAP9	c.C5778T	p.G1926G
XH_P38	7	91712698	91712698	Missense_Mutation	SNP	A	G	A	AKAP9	c.A8375G	p.N2792S
XH_P38	7	91726927	91726927	Silent	SNP	A	C	A	AKAP9	c.A10426C	p.R3476R
XH_P38	7	91779971	91779971	Missense_Mutation	SNP	T	G	T	LRRD1	c.A2155C	p.I719L
XH_P38	7	92734451	92734451	Silent	SNP	A	G	A	SAMD9	c.T960C	p.Y320Y
XH_P38	7	92762681	92762681	Silent	SNP	A	G	A	SAMD9L	c.T2604C	p.A868A
XH_P38	7	92970847	92970847	Silent	SNP	C	T	C	VP550	c.C2167T	p.L723L
XH_P38	7	92985252	92985252	Silent	SNP	T	C	T	VP550	c.T2635C	p.L879L
XH_P38	7	95001555	95001555	Silent	SNP	C	T	C	PON3	c.G297A	p.A99A
XH_P38	7	97823435	97823435	Missense_Mutation	SNP	G	A	G	LMTK2	c.G3658A	p.D1220N
XH_P38	7	97854393	97854393	Silent	SNP	G	A	G	TECPR1	c.C2535T	p.Y845Y
XH_P38	7	97863145	97863145	Silent	SNP	G	A	G	TECPR1	c.C1260T	p.V420V
XH_P38	7	98990419	98990419	Silent	SNP	G	A	G	ARPC1B	c.G909A	p.Q303Q
XH_P38	7	99217424	99217424	Silent	SNP	G	A	G	ZSCAN25	c.G195A	p.E65E
XH_P38	7	99227172	99227172	Silent	SNP	A	G	A	ZSCAN25	c.A1164G	p.E388E
XH_P38	7	99474427	99474427	Missense_Mutation	SNP	A	G	A	OR2AE1	c.T230C	p.I77T
XH_P38	7	100238335	100238335	Silent	SNP	C	T	C	TFR2	c.G447A	p.G149G
XH_P38	7	100459443	100459443	Missense_Mutation	SNP	C	A	C	SLC12A9	c.C1354A	p.P452T
XH_P38	7	100609631	100609631	Missense_Mutation	SNP	C	T	C	MUC3A	c.C4193T	p.A1398V
XH_P38	7	100634964	100634964	Missense_Mutation	SNP	C	A	C	MUC12	c.C1120A	p.P374T
XH_P38	7	100635375	100635375	Missense_Mutation	SNP	A	C	A	MUC12	c.A1531C	p.S511R
XH_P38	7	100635591	100635591	Missense_Mutation	SNP	C	A	C	MUC12	c.C1747A	p.R583S
XH_P38	7	100635679	100635679	Missense_Mutation	SNP	C	G	C	MUC12	c.C1835G	p.T612S
XH_P38	7	100639054	100639054	Missense_Mutation	SNP	G	A	G	MUC12	c.G5210A	p.R1737H
XH_P38	7	100641872	100641872	Silent	SNP	T	C	T	MUC12	c.T8028C	p.S2676S
XH_P38	7	100648117	100648117	Missense_Mutation	SNP	C	G	C	MUC12	c.C14273G	p.T4758R
XH_P38	7	100875772	100875772	Silent	SNP	T	G	T	CLDN15	c.A606C	p.P202P
XH_P38	7	101844851	101844851	Silent	SNP	A	G	A	CUX1	c.A2307G	p.P769P
XH_P38	7	102108532	102108532	Silent	SNP	G	A	G	LRWD1	c.G246A	p.R82R

XH_P38	7	102462538	102462538	Missense_Mutation	SNP	C	A	C	FBXL13	c.G1832T	p.G611V
XH_P38	7	102950891	102950891	Missense_Mutation	SNP	G	A	G	PMPCB	c.G1123A	p.A375T
XH_P38	7	103474041	103474041	Missense_Mutation	SNP	G	C	G	RELN	c.C416G	p.T139S
XH_P38	7	105621512	105621512	Silent	SNP	G	T	G	CDHR3	c.G84T	p.L28L
XH_P38	7	105671267	105671267	Silent	SNP	T	C	T	CDHR3	c.T270TC	p.D690D
XH_P38	7	106513011	106513011	Silent	SNP	C	T	C	PIK3CG	c.C2025T	p.S675S
XH_P38	7	107167769	107167769	Missense_Mutation	SNP	T	C	T	COG5	c.A544G	p.I182V
XH_P38	7	107743664	107743664	Silent	SNP	A	G	A	LAMB4	c.T1005C	p.N335N
XH_P38	7	117306991	117306991	Silent	SNP	C	T	C	CFTR	c.C4272T	p.Y1424Y
XH_P38	7	120969769	120969769	Missense_Mutation	SNP	G	A	G	WNT16	c.G214A	p.G72R
XH_P38	7	120979089	120979089	Missense_Mutation	SNP	C	T	C	WNT16	c.C758T	p.T253I
XH_P38	7	123594206	123594206	Silent	SNP	G	A	G	SPAM1	c.G582A	p.K194K
XH_P38	7	123599845	123599845	Missense_Mutation	SNP	A	T	A	SPAM1	c.A1352T	p.D451V
XH_P38	7	127721507	127721507	Silent	SNP	T	C	T	SND1	c.T2064C	p.T688T
XH_P38	7	127991133	127991133	Missense_Mutation	SNP	G	A	G	PRRT4	c.C2477T	p.P826L
XH_P38	7	127999645	127999645	Missense_Mutation	SNP	C	T	C	PRRT4	c.G401A	p.R134Q
XH_P38	7	128000004	128000004	Silent	SNP	G	A	G	PRRT4	c.C42T	p.C14C
XH_P38	7	128317658	128317658	Missense_Mutation	SNP	C	T	C	FAM71F2	c.C406T	p.R136W
XH_P38	7	128486363	128486363	Silent	SNP	C	T	C	FLNC	c.C3973T	p.L1325L
XH_P38	7	128488734	128488734	Missense_Mutation	SNP	G	A	G	FLNC	c.G4700A	p.R1567Q
XH_P38	7	128587352	128587381	In_Frame_Del	DEL	CGCCCACTCT	-	CGCCCACTCTG	IRF5	c.S02_531del	p.168_177del
XH_P38	7	128641226	128641226	Silent	SNP	G	C	G	TNPO3	c.C759G	p.L253L
XH_P38	7	128843396	128843396	Missense_Mutation	SNP	G	A	G	SMO	c.G503A	p.R168H
XH_P38	7	129938598	129938598	Missense_Mutation	SNP	G	T	G	CPA4	c.G81T	p.L27F
XH_P38	7	129950740	129950740	Missense_Mutation	SNP	G	T	G	CPA4	c.G808T	p.G270C
XH_P38	7	130022041	130022041	Silent	SNP	C	T	C	CPA1	c.C474T	p.Y158Y
XH_P38	7	131190696	131190696	Silent	SNP	T	C	T	PODXL	c.A1314G	p.A438A
XH_P38	7	132192949	132192949	Silent	SNP	T	C	T	PLXNA4	c.A504G	p.S168S
XH_P38	7	133979711	133979711	Silent	SNP	G	A	G	SLC35B4	c.C870T	p.N290N
XH_P38	7	134849577	134849577	Silent	SNP	A	C	A	TMEM140	c.A384C	p.A128A
XH_P38	7	134925411	134925411	Silent	SNP	G	A	G	STRA8	c.G201A	p.A67A
XH_P38	7	135406176	135406176	Silent	SNP	A	G	A	SLC13A4	c.T195C	p.L65L
XH_P38	7	139138950	139138950	Missense_Mutation	SNP	C	G	C	KLRG2	c.G1016C	p.G339A
XH_P38	7	141429371	141429371	Missense_Mutation	SNP	T	G	T	WEE2	c.T1576G	p.Y526D
XH_P38	7	141920378	141920378	Missense_Mutation	SNP	A	A	A	MGAM2	c.A6067T	p.T2023S
XH_P38	7	143657801	143657801	Silent	SNP	A	G	A	OR2F1	c.A738G	p.T246T
XH_P38	7	143771408	143771408	Silent	SNP	G	C	G	OR2A25	c.G96C	p.L32L
XH_P38	7	143771536	143771536	Missense_Mutation	SNP	G	A	G	OR2A25	c.G224A	p.S75N
XH_P38	7	143771937	143771937	Missense_Mutation	SNP	G	C	G	OR2A25	c.G625C	p.A209P
XH_P38	7	143884103	143884103	Silent	SNP	G	A	G	ARHGEF35	c.C1374T	p.C458C
XH_P38	7	144060802	144060802	Missense_Mutation	SNP	C	T	C	ARHGEF5	c.C1040T	p.T347I
XH_P38	7	144077106	144077106	Missense_Mutation	SNP	G	A	G	ARHGEF5	c.G4751A	p.R1584Q
XH_P38	7	148311213	148311213	Missense_Mutation	SNP	C	T	C	C7orf33	c.C284T	p.P95L
XH_P38	7	148802229	148802229	Missense_Mutation	SNP	C	T	C	ZNF425	c.G734A	p.R245Q
XH_P38	7	149129098	149129098	Silent	SNP	G	A	G	ZNF777	c.C2265T	p.C755C
XH_P38	7	149511902	149511902	Silent	SNP	C	T	C	SSPO	c.C10452T	p.C3484C
XH_P38	7	149513077	149513077	Silent	SNP	G	C	G	SSPO	c.G10980C	p.S3660S
XH_P38	7	149513560	149513560	Silent	SNP	T	C	T	SSPO	c.T11181C	p.S3727S
XH_P38	7	149515189	149515189	Splice_Site	DEL	A	-	A	SSPO	.	.
XH_P38	7	149517978	149517978	Missense_Mutation	SNP	G	T	G	SSPO	c.G12321T	p.Q4107H
XH_P38	7	149518148	149518148	Missense_Mutation	SNP	A	G	A	SSPO	c.A12491G	p.H4164R
XH_P38	7	149518961	149518961	Silent	SNP	T	C	T	SSPO	c.T12765C	p.A4255A
XH_P38	7	149543269	149543269	Missense_Mutation	SNP	C	T	C	ZNF862	c.C166T	p.R56C
XH_P38	7	149558409	149558409	Silent	SNP	G	C	G	ZNF862	c.G2160C	p.L720L
XH_P38	7	149559273	149559273	Silent	SNP	C	T	C	ZNF862	c.C3024T	p.L1008L
XH_P38	7	149559465	149559465	Silent	SNP	C	T	C	ZNF862	c.C3216T	p.G1072G
XH_P38	7	150034456	150034456	Missense_Mutation	SNP	G	A	G	LRRC61	c.G506A	p.G169D
XH_P38	7	150066900	150066900	Missense_Mutation	SNP	A	G	A	REPIN1	c.A100G	p.R34G
XH_P38	7	150094683	150094683	Missense_Mutation	SNP	G	A	G	ZNF775	c.G1114A	p.G372S
XH_P38	7	150217309	150217309	Missense_Mutation	SNP	C	T	C	GIMAP7	c.C247T	p.R83C
XH_P38	7	150325175	150325175	Missense_Mutation	SNP	C	T	C	GIMAP6	c.G721A	p.G241S
XH_P38	7	150439374	150439374	Silent	SNP	C	A	C	GIMAP1-GIMAP	c.C147A	p.G49G
XH_P38	7	150491084	150491084	Missense_Mutation	SNP	T	G	T	TMEM176B	c.A280C	p.S94R
XH_P38	7	150704250	150704250	Silent	SNP	C	G	G	NOS3	c.C1998G	p.A666A
XH_P38	7	150768786	150768786	Silent	SNP	G	A	G	SLCA2	c.G2175A	p.T725T
XH_P38	7	150884602	150884602	Missense_Mutation	SNP	T	C	T	ASB10	c.A208G	p.S70G
XH_P38	7	151859288	151859288	Missense_Mutation	SNP	G	T	G	KMT2C	c.C11374A	p.Q3792K
XH_P38	7	154667694	154667694	Silent	SNP	C	T	C	DPP6	c.C1641T	p.G547G
XH_P38	7	155251433	155251433	Missense_Mutation	SNP	C	T	C	EN2	c.C361T	p.L121F
XH_P38	7	155255214	155255214	Silent	SNP	G	A	G	EN2	c.G834A	p.A278A
XH_P38	7	155255332	155255332	Silent	SNP	T	C	T	EN2	c.T952C	p.L318L
XH_P38	7	155503920	155503920	Silent	SNP	A	T	A	RBM33	c.A972T	p.P324P
XH_P38	7	156742779	156742779	Silent	SNP	C	A	C	NOM1	c.C348A	p.A116A
XH_P38	7	157931091	157931091	Missense_Mutation	SNP	C	T	C	PTPRN2	c.G913A	p.V305M
XH_P38	7	157985149	157985149	Missense_Mutation	SNP	C	G	C	PTPRN2	c.G305C	p.S102T
XH_P38	8	1808256	1808256	Silent	SNP	A	G	A	ARHGEF10	c.A387G	p.V129V
XH_P38	8	1900911	1900911	Silent	SNP	C	T	C	ARHGEF10	c.C3324T	p.H1108H
XH_P38	8	2021421	2021421	Missense_Mutation	SNP	G	T	G	MYOM2	c.G961T	p.V321L
XH_P38	8	2820745	2820745	Silent	SNP	G	C	G	CSMD1	c.C9453G	p.L3151L
XH_P38	8	3351195	3351195	Silent	SNP	C	A	C	CSMD1	c.G1398T	p.L466L
XH_P38	8	6371291	6371291	Silent	SNP	A	G	A	ANGPT2	c.T951C	p.Y317Y
XH_P38	8	6389889	6389889	Silent	SNP	C	A	C	ANGPT2	c.G408T	p.A136A
XH_P38	8	7215807	7215807	Missense_Mutation	SNP	C	A	C	ZNF705G	c.G594T	p.R198S
XH_P38	8	9414049	9414049	Silent	SNP	G	A	G	TNKS	c.G600A	p.R200R
XH_P38	8	9564485	9564485	Silent	SNP	G	A	G	TNKS	c.G1434A	p.P478P
XH_P38	8	10383138	10383138	Missense_Mutation	SNP	G	A	G	PRSS55	c.G43A	p.G15R
XH_P38	8	10464755	10464755	Missense_Mutation	SNP	C	T	C	RP11	c.G6853A	p.G2285R
XH_P38	8	10465942	10465942	Missense_Mutation	SNP	T	A	T	RP11	c.A5666T	p.D1889V
XH_P38	8	10468172	10468172	Missense_Mutation	SNP	G	A	G	RP11	c.C3436T	p.R1146W
XH_P38	8	10469030	10469030	Missense_Mutation	SNP	G	A	G	RP11	c.C2578T	p.R860W
XH_P38	8	10469340	10469340	Silent	SNP	G	A	G	RP11	c.C2268T	p.N756N
XH_P38	8	10469817	10469817	Silent	SNP	G	A	G	RP11	c.C1791T	p.G597G
XH_P38	8	10480211	10480211	Silent	SNP	T	C	T	RP11	c.A501G	p.T167T
XH_P38	8	10555301	10555301	Missense_Mutation	SNP	G	T	G	C8orf74	c.G434T	p.C145F
XH_P38	8	10557760	10557760	Missense_Mutation	SNP	A	G	A	C8orf74	c.A664G	p.I222V
XH_P38	8	10583909	10583909	Missense_Mutation	SNP	G	C	G	SOX7	c.C506G	p.T169S
XH_P38	8	10584067	10584067	Silent	SNP	C	T	C	SOX7	c.G348A	p.P116P
XH_P38	8	12957475	12957475	Missense_Mutation	SNP	C	T	C	DLC1	c.G6838A	p.V280M

XH_P38	8	13424866	13424866	Silent	SNP	G	C	G	C8orf48	c.G366C	p.L122L
XH_P38	8	16012648	16012648	Missense_Mutation	SNP	G	C	G	MSR1	c.C823G	p.P275A
XH_P38	8	17500223	17500223	Silent	SNP	T	C	T	PDGFRL	c.T1041C	p.F347F
XH_P38	8	19190491	19190491	Silent	SNP	A	G	A	SH2D4A	c.A72G	p.A24K
XH_P38	8	19316086	19316086	Silent	SNP	G	A	G	CSGALNACT1	c.C702T	p.H234H
XH_P38	8	19363123	19363123	Silent	SNP	G	A	G	CSGALNACT1	c.C223T	p.L75L
XH_P38	8	20107601	20107601	Missense_Mutation	SNP	G	C	G	LZTS1	c.C1423G	p.L475V
XH_P38	8	20110641	20110641	Silent	SNP	C	T	C	LZTS1	c.G801A	p.E267E
XH_P38	8	21978469	21978469	Silent	SNP	A	G	A	HR	c.T2370C	p.D790D
XH_P38	8	21978578	21978578	Silent	SNP	A	G	A	HR	c.T2367C	p.S789S
XH_P38	8	21986657	21986657	Silent	SNP	C	T	C	HR	c.G27A	p.K9K
XH_P38	8	23190941	23190941	Silent	SNP	T	C	T	LOXL2	c.A939G	p.S313S
XH_P38	8	23423697	23423697	Missense_Mutation	SNP	G	A	G	SLC25A37	c.G287A	p.R96Q
XH_P38	8	23429329	23429329	Silent	SNP	T	C	T	SLC25A37	c.T525C	p.F175F
XH_P38	8	24171051	24171051	Silent	SNP	C	T	C	ADAM28	c.C534T	p.H178H
XH_P38	8	24356818	24356818	Missense_Mutation	SNP	A	C	A	ADAM7	c.A1912C	p.N638H
XH_P38	8	26481697	26481697	Missense_Mutation	SNP	G	A	G	DPYSL2	c.G667A	p.A223T
XH_P38	8	26510792	26510792	Silent	SNP	T	C	T	DPYSL2	c.T1821C	p.P607P
XH_P38	8	27328511	27328511	Missense_Mutation	SNP	G	A	G	CHRNA2	c.C65T	p.T22I
XH_P38	8	27824045	27824045	Missense_Mutation	SNP	G	A	G	SCARA5	c.C127T	p.R43W
XH_P38	8	28206275	28206275	Silent	SNP	G	C	G	ZNF395	c.C1503G	p.A501A
XH_P38	8	28932797	28932797	Splice_Site	SNP	C	A	C	KIF13B		
XH_P38	8	36788479	36788479	Missense_Mutation	SNP	A	G	A	KCNU1	c.A2747G	p.N916S
XH_P38	8	37699716	37699718	In_Frame_Del	DEL	AGA	-	AGA	ADGRA2	c.3860_3862del	p.1287_1288del
XH_P38	8	37963239	37963239	Silent	SNP	C	T	C	ASH2L	c.C171T	p.S57S
XH_P38	8	41166638	41166640	In_Frame_Del	DEL	GCT	-	GCT	SFRP1	c.39_41del	p.13_14del
XH_P38	8	54163562	54163562	Silent	SNP	C	A	C	OPRK1	c.G36T	p.P12P
XH_P38	8	59508134	59508134	Missense_Mutation	SNP	T	C	T	NSMAF	c.A1970G	p.Y657C
XH_P38	8	67341378	67341378	Silent	SNP	G	A	G	RRS1	c.G12A	p.Q4Q
XH_P38	8	67341938	67341938	Missense_Mutation	SNP	G	T	G	RRS1	c.G572T	p.R191L
XH_P38	8	67342077	67342077	Silent	SNP	G	A	G	RRS1	c.G711A	p.E237E
XH_P38	8	71593425	71593425	Silent	SNP	G	A	G	XKR9	c.G132A	p.A44A
XH_P38	8	75233158	75233158	Missense_Mutation	SNP	G	T	G	JPH1	c.C365A	p.T122N
XH_P38	8	76465360	76465360	Silent	SNP	A	G	A	HNFG4	c.A543G	p.K181K
XH_P38	8	77618751	77618751	Missense_Mutation	SNP	C	A	C	ZFH4	c.C2428A	p.H810N
XH_P38	8	87076520	87076520	Missense_Mutation	SNP	C	A	C	PSKH2	c.G526T	p.A176S
XH_P38	8	90770315	90770315	Silent	SNP	C	T	C	RIPK2	c.C27T	p.A9A
XH_P38	8	95521985	95521985	Silent	SNP	A	G	A	VIRMA	c.T3810C	p.P1270P
XH_P38	8	98787994	98787994	Silent	SNP	A	G	A	LAPTM4B	c.A30G	p.P10P
XH_P38	8	98788033	98788033	Silent	SNP	G	C	G	LAPTM4B	c.G69C	p.A23A
XH_P38	8	104948947	104948947	Silent	SNP	C	G	C	RIMS2	c.C2061G	p.G687G
XH_P38	8	105478933	105478933	Silent	SNP	G	A	G	DPY5	c.C216T	p.F72F
XH_P38	8	110100245	110100245	Missense_Mutation	SNP	T	G	T	TRHR	c.T504G	p.L168M
XH_P38	8	114186003	114186003	Missense_Mutation	SNP	T	C	T	CSMD3	c.A657G	p.I219M
XH_P38	8	119391791	119391791	Silent	SNP	T	C	T	SAMD12	c.A471G	p.L157L
XH_P38	8	123964953	123964953	Silent	SNP	C	T	C	ZHX2	c.C1203T	p.T401T
XH_P38	8	124658210	124658210	Silent	SNP	C	T	C	KLHL38	c.G1515A	p.A505A
XH_P38	8	125463250	125463250	Missense_Mutation	SNP	T	C	T	TRMT12	c.T82C	p.W28R
XH_P38	8	125463435	125463435	Silent	SNP	C	G	C	TRMT12	c.C267G	p.L89L
XH_P38	8	125499363	125499363	Silent	SNP	G	A	G	RNF139	c.G1473A	p.S491S
XH_P38	8	139164192	139164192	Silent	SNP	G	A	G	FAM135B	c.C2526T	p.P842P
XH_P38	8	139164570	139164570	Silent	SNP	C	T	C	FAM135B	c.G2148A	p.P716P
XH_P38	8	141461062	141461062	Silent	SNP	G	A	G	TRAPPC9	c.C411T	p.N137N
XH_P38	8	142199229	142199229	Missense_Mutation	SNP	G	A	G	DENND3	c.G2989A	p.G997R
XH_P38	8	142200467	142200467	Silent	SNP	G	A	G	DENND3	c.G3090A	p.P1030P
XH_P38	8	142204326	142204326	Silent	SNP	C	G	C	DENND3	c.C3591G	p.G1197G
XH_P38	8	142228149	142228149	Silent	SNP	G	A	G	SLC45A4	c.C1437T	p.T479T
XH_P38	8	142228686	142228686	Silent	SNP	G	A	G	SLC45A4	c.C900T	p.L300L
XH_P38	8	142228909	142228909	Missense_Mutation	SNP	G	A	G	SLC45A4	c.C677T	p.P226L
XH_P38	8	142229834	142229834	Silent	SNP	G	A	G	SLC45A4	c.C372T	p.T124T
XH_P38	8	143782044	143782044	Silent	SNP	A	G	A	LY6K	c.A99G	p.R33R
XH_P38	8	143808951	143808951	Silent	SNP	C	T	C	THEM6	c.C187T	p.L63L
XH_P38	8	143809193	143809193	Silent	SNP	C	T	C	THEM6	c.C429T	p.G143G
XH_P38	8	143956693	143956693	Missense_Mutation	SNP	G	A	G	CYP11B1	c.C1157T	p.A386V
XH_P38	8	143957163	143957163	Silent	SNP	C	G	C	CYP11B1	c.G1086C	p.L362L
XH_P38	8	143960597	143960597	Silent	SNP	G	A	G	CYP11B1	c.C246T	p.D82D
XH_P38	8	143961102	143961102	Missense_Mutation	SNP	C	T	C	CYP11B1	c.G128A	p.R43Q
XH_P38	8	143994041	143994041	Missense_Mutation	SNP	C	T	C	CYP11B2	c.G1303A	p.G435S
XH_P38	8	144102747	144102747	Silent	SNP	C	T	C	LY6E	c.C69T	p.C23C
XH_P38	8	144130643	144130643	Missense_Mutation	SNP	G	A	G	C8orf31	c.G373A	p.G125R
XH_P38	8	144239859	144239859	Silent	SNP	A	G	A	LY6H	c.T294C	p.C98C
XH_P38	8	144623574	144623574	Missense_Mutation	SNP	T	C	T	ZC3H3	c.A18G	p.I6M
XH_P38	8	144654594	144654594	Missense_Mutation	SNP	G	T	G	MROH6	c.C291A	p.H97Q
XH_P38	8	144654693	144654693	Silent	SNP	G	C	G	MROH6	c.C192G	p.P64P
XH_P38	8	144671244	144671244	Silent	SNP	C	G	C	EEF1D	c.G1008C	p.R336R
XH_P38	8	144681714	144681714	Silent	SNP	G	A	G	TIGD5	c.G1641A	p.E547E
XH_P38	8	144688736	144688736	Missense_Mutation	SNP	C	G	C	PYCR3	c.G426C	p.K142N
XH_P38	8	144697070	144697070	Missense_Mutation	SNP	T	C	T	TSTA3	c.A295G	p.M99V
XH_P38	8	144801243	144801243	Silent	SNP	C	T	C	MAPK15	c.C498T	p.P166P
XH_P38	8	144808747	144808747	Silent	SNP	G	A	G	FAM83H	c.C2884T	p.L962L
XH_P38	8	144941419	144941419	Silent	SNP	C	T	C	EPPK1	c.G6003A	p.A2001A
XH_P38	8	144997783	144997783	Missense_Mutation	SNP	G	A	G	PLEC	c.C6272T	p.A2091V
XH_P38	8	144998514	144998514	Silent	SNP	C	T	C	PLEC	c.G5541A	p.A1847A
XH_P38	8	145009203	145009203	Silent	SNP	G	A	G	PLEC	c.C759T	p.D253D
XH_P38	8	145058539	145058539	Missense_Mutation	SNP	T	C	T	PARP10	c.A1555G	p.S519G
XH_P38	8	145065682	145065682	Silent	SNP	G	A	G	GRINA	c.G291A	p.G97G
XH_P38	8	145583707	145583707	Silent	SNP	C	T	C	SLCS2A2	c.C555T	p.L185L
XH_P38	8	145603114	145603114	Missense_Mutation	SNP	A	C	A	ADCK5	c.A51C	p.R17S
XH_P38	8	145640720	145640720	Silent	SNP	C	G	C	SLC39A4	c.G483C	p.L161L
XH_P38	8	145661320	145661320	Silent	SNP	G	A	G	TONSL	c.C2496T	p.A832A
XH_P38	8	145661675	145661675	Missense_Mutation	SNP	G	A	G	TONSL	c.C2141T	p.A714V
XH_P38	8	145729727	145729727	Missense_Mutation	SNP	C	A	C	GPT	c.C40A	p.H14N
XH_P38	8	145732017	145732017	Missense_Mutation	SNP	C	G	C	GPT	c.C1265G	p.A422R
XH_P38	8	145737816	145737816	Missense_Mutation	SNP	C	T	C	RECQL4	c.G3014A	p.R1005Q
XH_P38	8	145747920	145747920	Missense_Mutation	SNP	T	G	T	LRRRC24	c.A1481C	p.E494A
XH_P38	8	145752900	145752900	Silent	SNP	C	T	C	C8orf82	c.G477A	p.P159P
XH_P38	9	712040	712040	In_Frame_Ins	INS	-	AGCTGT	-	KANK1	c.800_801insAGCT	p.A267delinsAAV
XH_P38	9	841971	841971	Missense_Mutation	SNP	T	A	T	DMRT1	c.T133A	p.S45T

XH_P38	9	2718351	2718351	Silent	SNP	G	A	G	KCNV2	c.G612A	p.E204E
XH_P38	9	4564432	4564432	Silent	SNP	G	A	G	SLC1A1	c.G414A	p.T138T
XH_P38	9	5050706	5050706	Silent	SNP	C	T	C	JAK2	c.C42T	p.H14H
XH_P38	9	5763354	5763354	Missense_Mutation	SNP	T	C	T	RIC1	c.T2216C	p.I739T
XH_P38	9	6007767	6007767	Silent	SNP	C	A	C	KIAA2026	c.G21T	p.P7P
XH_P38	9	6015011	6015011	Silent	SNP	T	C	T	RANBP6	c.A597G	p.T199T
XH_P38	9	18681821	18681821	Silent	SNP	A	G	A	ADAMTSL1	c.A1353G	p.T451T
XH_P38	9	18777191	18777191	Silent	SNP	G	T	G	ADAMTSL1	c.G2964T	p.P988P
XH_P38	9	19058048	19058048	Missense_Mutation	SNP	G	A	G	HAUS6	c.C2612T	p.S871F
XH_P38	9	19516280	19516280	Silent	SNP	G	C	G	SLC24A2	c.C1806G	p.L602L
XH_P38	9	20346570	20346570	Silent	SNP	G	A	G	MLLT3	c.C1569T	p.I523I
XH_P38	9	21227621	21227621	Missense_Mutation	SNP	T	C	T	IFNA17	c.A552G	p.I184M
XH_P38	9	32784414	32784414	Missense_Mutation	SNP	G	A	G	TMEM215	c.G233A	p.R78H
XH_P38	9	34242094	34242094	Missense_Mutation	SNP	T	A	T	UBAP1	c.T1263A	p.N421K
XH_P38	9	34310927	34310927	Missense_Mutation	SNP	T	C	T	KIF24	c.A418G	p.M140V
XH_P38	9	34311195	34311195	Missense_Mutation	SNP	G	C	G	KIF24	c.C150G	p.D50E
XH_P38	9	34500821	34500821	Missense_Mutation	SNP	G	A	G	DNAI1	c.G1015A	p.V339I
XH_P38	9	34637329	34637329	Silent	SNP	C	T	C	SIGMAR1	c.G240A	p.Q80Q
XH_P38	9	34726182	34726182	Missense_Mutation	SNP	A	G	A	FAM205A	c.T1055C	p.F352S
XH_P38	9	35560358	35560366	In_Frame_Del	DEL	GAAGAGGAA	-	GAAGAGGAA	RUSC2	c.1087_1095del	p.363_365del
XH_P38	9	35704150	35704150	Silent	SNP	C	T	C	TLN1	c.G6069A	p.A2023A
XH_P38	9	37442190	37442190	Missense_Mutation	SNP	G	A	G	ZBTB5	c.C359T	p.T120M
XH_P38	9	37740637	37740637	Silent	SNP	T	C	T	FRMPD1	c.T2112C	p.A704A
XH_P38	9	37745413	37745413	Silent	SNP	G	A	G	FRMPD1	c.G3384A	p.E1128E
XH_P38	9	37948724	37948724	Silent	SNP	T	C	T	SHB	c.A1254G	p.G418G
XH_P38	9	38068532	38068532	Silent	SNP	A	G	A	SHB	c.T111C	p.P37P
XH_P38	9	38595886	38595886	Missense_Mutation	SNP	T	C	T	ANKRD18A	c.A1451G	p.N484S
XH_P38	9	39118196	39118196	Missense_Mutation	SNP	C	A	C	CNTNAP3	c.G2141T	p.G714V
XH_P38	9	71002491	71002491	Silent	SNP	C	T	C	PGM5	c.C684T	p.D228D
XH_P38	9	71628207	71628207	Missense_Mutation	SNP	G	C	G	PRKACG	c.C802G	p.H268D
XH_P38	9	72741247	72741247	Silent	SNP	C	T	C	MAMDC2	c.C816T	p.Y272Y
XH_P38	9	72755129	72755131	In_Frame_Del	DEL	AAA	-	AAA	MAMDC2	c.1063_1065del	p.355_355del
XH_P38	9	73028223	73028223	Silent	SNP	C	T	C	KLf9	c.G57A	p.S19S
XH_P38	9	77377410	77377410	Missense_Mutation	SNP	C	T	C	TRPM6	c.G4162A	p.V1388I
XH_P38	9	77502160	77502160	Missense_Mutation	SNP	G	A	G	TRPM6	c.C5T	p.T2I
XH_P38	9	78773953	78773953	Silent	SNP	G	A	G	PCSK5	c.G1485A	p.S495S
XH_P38	9	79320847	79320847	Missense_Mutation	SNP	G	C	G	PRUNE2	c.C6343G	p.Q2115E
XH_P38	9	80851350	80851350	Silent	SNP	G	C	G	CEP78	c.G84C	p.S28S
XH_P38	9	84605747	84605747	Missense_Mutation	SNP	G	A	G	SPATA31D1	c.G362A	p.R121H
XH_P38	9	88692336	88692336	Silent	SNP	C	T	C	GOLM1	c.G300A	p.Q100Q
XH_P38	9	90588903	90588903	Silent	SNP	C	T	C	CDK20	c.G123A	p.E41E
XH_P38	9	90744737	90744737	Missense_Mutation	SNP	G	A	G	SPATA31C2	c.C3215T	p.A1072V
XH_P38	9	90747121	90747121	Silent	SNP	G	A	G	SPATA31C2	c.C831T	p.G277G
XH_P38	9	90749692	90749692	Silent	SNP	C	T	C	SPATA31C2	c.G180A	p.K60K
XH_P38	9	91606390	91606390	Silent	SNP	G	A	G	C9orf47	c.G252A	p.P84P
XH_P38	9	93641151	93641151	Silent	SNP	T	C	T	SYK	c.T1428C	p.N476N
XH_P38	9	94486688	94486688	Silent	SNP	G	A	G	ROR2	c.C2088T	p.Y696Y
XH_P38	9	94495608	94495608	Missense_Mutation	SNP	T	C	T	ROR2	c.A733G	p.T245A
XH_P38	9	95838070	95838070	Silent	SNP	G	C	G	SUSD3	c.G93C	p.T31T
XH_P38	9	95993170	95993170	Silent	SNP	A	G	A	WNK2	c.A855G	p.T285T
XH_P38	9	96051785	96051785	Silent	SNP	C	T	C	WNK2	c.C4749T	p.F1583F
XH_P38	9	96097673	96097673	Silent	SNP	G	A	G	C9orf129	c.C348T	p.G116G
XH_P38	9	96214928	96214928	Missense_Mutation	SNP	G	A	G	FAM120AOS	c.C64T	p.L22F
XH_P38	9	96714491	96714491	Silent	SNP	C	G	C	BARX1	c.G720C	p.P240P
XH_P38	9	98638288	98638288	Missense_Mutation	SNP	A	G	A	ERCC6L2	c.A1G	p.M1V
XH_P38	9	99180243	99180243	Silent	SNP	G	A	G	ZNF367	c.C72T	p.H24H
XH_P38	9	99700727	99700727	Missense_Mutation	SNP	T	A	T	NUTM2G	c.T1522A	p.S508T
XH_P38	9	100194406	100194406	Missense_Mutation	SNP	T	C	T	TDRD7	c.T227C	p.V76A
XH_P38	9	100672338	100672338	Missense_Mutation	SNP	C	T	C	TRMO	c.G970A	p.V324M
XH_P38	9	101748356	101748356	Missense_Mutation	SNP	A	G	A	COL15A1	c.A610G	p.M204V
XH_P38	9	102591042	102591042	Missense_Mutation	SNP	A	G	A	NR4A3	c.A718G	p.S240G
XH_P38	9	104309445	104309445	Silent	SNP	T	C	T	RNF20	c.T921C	p.T307Y
XH_P38	9	104449063	104449063	Silent	SNP	C	T	C	GRIN3A	c.G1119A	p.G373G
XH_P38	9	107331722	107331722	Missense_Mutation	SNP	G	C	G	OR13C8	c.G274C	p.V92L
XH_P38	9	110249648	110249648	Missense_Mutation	SNP	G	A	G	KLf4	c.C1027T	p.H343Y
XH_P38	9	110250186	110250186	Silent	SNP	C	A	C	KLf4	c.G489T	p.A163A
XH_P38	9	111653574	111653574	Silent	SNP	C	G	C	ELP1	c.G2022C	p.L674L
XH_P38	9	111727670	111727670	Missense_Mutation	SNP	C	G	C	CTNNA1	c.G1579C	p.E527Q
XH_P38	9	111755008	111755008	Silent	SNP	C	T	C	CTNNA1	c.G423A	p.V141V
XH_P38	9	113166792	113166792	Missense_Mutation	SNP	A	T	A	SVEP1	c.T9481A	p.F3161I
XH_P38	9	113169126	113169126	Silent	SNP	G	A	G	SVEP1	c.C8754T	p.H2918H
XH_P38	9	113169630	113169630	Silent	SNP	T	C	T	SVEP1	c.A8250G	p.A2750A
XH_P38	9	113169631	113169631	Missense_Mutation	SNP	G	A	G	SVEP1	c.C8249T	p.A2750V
XH_P38	9	113208250	113208250	Missense_Mutation	SNP	T	G	T	SVEP1	c.A4330C	p.M1444L
XH_P38	9	114246717	114246717	Missense_Mutation	SNP	C	T	C	KIAA0368	c.G196A	p.E66K
XH_P38	9	115652836	115652836	Silent	SNP	G	A	G	SLC46A2	c.C126T	p.L42L
XH_P38	9	115968797	115968797	Missense_Mutation	SNP	C	T	C	FKBP15	c.G316A	p.A106T
XH_P38	9	116060124	116060124	Missense_Mutation	SNP	T	C	T	RNF183	c.A341G	p.Q114R
XH_P38	9	116060221	116060221	Missense_Mutation	SNP	C	T	C	RNF183	c.G244A	p.A82T
XH_P38	9	116153900	116153900	Silent	SNP	A	G	A	ALAD	c.T144C	p.Y48Y
XH_P38	9	116346118	116346118	Missense_Mutation	SNP	G	A	G	RG53	c.G389A	p.R130Q
XH_P38	9	116346236	116346236	Silent	SNP	G	A	G	RG53	c.G507A	p.A169A
XH_P38	9	116356776	116356776	Silent	SNP	C	T	C	RG53	c.C57T	p.P19P
XH_P38	9	117050998	117050998	Missense_Mutation	SNP	G	A	G	COL27A1	c.G4061A	p.R1354Q
XH_P38	9	117051534	117051534	Missense_Mutation	SNP	C	T	C	COL27A1	c.C4165T	p.P1389S
XH_P38	9	117139280	117139280	Silent	SNP	T	C	T	AKNA	c.A450G	p.P150P
XH_P38	9	117166246	117166246	Missense_Mutation	SNP	A	G	A	WHRN	c.T1295C	p.V432A
XH_P38	9	117792583	117792583	Missense_Mutation	SNP	C	G	C	TNC	c.G6022C	p.E2008Q
XH_P38	9	117808785	117808785	Missense_Mutation	SNP	T	A	T	TNC	c.A5029T	p.I1677L
XH_P38	9	117848201	117848201	Silent	SNP	T	C	T	TNC	c.A1809G	p.Q603Q
XH_P38	9	118949998	118949998	Silent	SNP	C	T	C	PAPPA	c.C981T	p.C327C
XH_P38	9	119491365	119491365	Missense_Mutation	SNP	C	A	C	ASTN2	c.G2379T	p.R793S
XH_P38	9	123583192	123583192	Silent	SNP	A	G	A	PSMD5	c.T1053C	p.D351D
XH_P38	9	123769200	123769200	Missense_Mutation	SNP	C	T	C	C5	c.G2422A	p.V808I
XH_P38	9	123780005	123780005	Silent	SNP	G	A	G	C5	c.C1650T	p.Y550Y
XH_P38	9	124535282	124535282	Silent	SNP	G	A	G	DAB2IP	c.G2103A	p.P701P
XH_P38	9	124632992	124632992	Missense_Mutation	SNP	T	C	T	TTL11	c.A1787G	p.E596G
XH_P38	9	126132919	126132919	Silent	SNP	G	A	G	CRB2	c.G1587A	p.A529A

XH_P38	9	126133497	126133497	Silent	SNP	C	T	C	CRB2	c.C2076T	p.S692S
XH_P38	9	127618162	127618162	Silent	SNP	G	A	G	WDR38	c.G183A	p.T61T
XH_P38	9	129595667	129595667	Silent	SNP	C	T	C	ZBTB43	c.C879T	p.I293I
XH_P38	9	129854199	129854199	Silent	SNP	G	A	G	ANGPTL2	c.C1032T	p.D344D
XH_P38	9	130164927	130164927	Silent	SNP	G	A	G	SLC2A8	c.G129A	p.P43P
XH_P38	9	130504070	130504070	Silent	SNP	G	A	G	SH2D3C	c.C1611T	p.A537A
XH_P38	9	130677112	130677112	Silent	SNP	G	A	G	ST6GALNAC4	c.C21T	p.L7L
XH_P38	9	130885353	130885353	Silent	SNP	A	G	A	PTGES2	c.T747C	p.N249N
XH_P38	9	131088076	131088076	Missense_Mutation	SNP	G	A	G	COQ4	c.G221A	p.R74Q
XH_P38	9	131670919	131670919	Silent	SNP	T	C	T	LRRC8A	c.T1476C	p.R492R
XH_P38	9	132630570	132630570	Missense_Mutation	SNP	G	A	G	USP20	c.G977A	p.R326Q
XH_P38	9	132638424	132638424	Silent	SNP	C	T	C	USP20	c.C2316T	p.P772P
XH_P38	9	132686143	132686143	Missense_Mutation	SNP	A	G	A	FNBP1	c.T1150C	p.F384L
XH_P38	9	133556993	133557007	In_Frame_Del	DEL	CGCCGCCGC	-	CCGCCGCCGC	PRDM12	c.1041_1055del	p.347_352del
XH_P38	9	133759864	133759864	Silent	SNP	G	A	G	ABL1	c.G2187A	p.T729T
XH_P38	9	133901819	133901819	Missense_Mutation	SNP	C	A	C	LAMC3	c.C521A	p.P174H
XH_P38	9	133914285	133914285	Silent	SNP	G	A	G	LAMC3	c.G1011A	p.T337T
XH_P38	9	134350854	134350854	Missense_Mutation	SNP	G	A	G	PRRC2B	c.G3338A	p.R1113Q
XH_P38	9	134363270	134363270	Silent	SNP	G	C	G	PRRC2B	c.G6012C	p.L2004L
XH_P38	9	134400534	134400534	Missense_Mutation	SNP	A	G	A	UCK1	c.T700C	p.S234P
XH_P38	9	134473655	134473655	Silent	SNP	C	T	C	RAPGEF1	c.G2037A	p.E679E
XH_P38	9	135073877	135073877	Silent	SNP	C	T	C	NTNG2	c.C738T	p.F246F
XH_P38	9	135273607	135273607	Silent	SNP	C	G	C	TTF1	c.G153C	p.L51L
XH_P38	9	135974100	135974100	Silent	SNP	G	A	G	RALGDS	c.C2454T	p.T818T
XH_P38	9	135985796	135985796	Silent	SNP	C	T	C	RALGDS	c.G210A	p.V70V
XH_P38	9	136006421	136006421	Frame_Shift_Del	DEL	G	-	G	RALGDS	c.S0delC	p.P17fs
XH_P38	9	136199466	136199466	Missense_Mutation	SNP	G	A	G	SURF6	c.C523T	p.R175W
XH_P38	9	136199503	136199503	Missense_Mutation	SNP	G	A	G	SURF6	c.C487T	p.R163W
XH_P38	9	136268084	136268084	Missense_Mutation	SNP	A	G	A	STKL1	c.A1417G	p.K473E
XH_P38	9	136505114	136505114	Silent	SNP	A	G	A	DBH	c.A486G	p.E162E
XH_P38	9	136507473	136507473	Missense_Mutation	SNP	G	A	G	DBH	c.G631A	p.A211T
XH_P38	9	136573412	136573412	Silent	SNP	G	A	G	SARDH	c.C1467T	p.H489H
XH_P38	9	136915508	136915508	Silent	SNP	C	T	C	BRD3	c.G702A	p.P234P
XH_P38	9	137619195	137619195	Silent	SNP	C	T	C	COL5A1	c.C738T	p.T246T
XH_P38	9	137711997	137711997	Silent	SNP	G	C	G	COL5A1	c.G4482C	p.P1494P
XH_P38	9	137777727	137777727	Silent	SNP	C	T	C	FCN2	c.C429T	p.H143H
XH_P38	9	137801800	137801800	Silent	SNP	T	C	T	FCN1	c.A825G	p.Q275Q
XH_P38	9	137804360	137804360	Silent	SNP	A	G	A	FCN1	c.T570C	p.N190N
XH_P38	9	138377433	138377433	Silent	SNP	G	A	G	PPP1R26	c.G1077A	p.A359A
XH_P38	9	138516128	138516128	Missense_Mutation	SNP	C	T	C	GLT6D1	c.G646A	p.A216T
XH_P38	9	138516347	138516347	Frame_Shift_Del	DEL	A	-	A	GLT6D1	c.427delT	p.W143fs
XH_P38	9	138714620	138714620	Silent	SNP	G	A	G	CAMSAP1	c.C1887T	p.S629S
XH_P38	9	138903635	138903635	Silent	SNP	G	A	G	NACC2	c.C1491T	p.A497A
XH_P38	9	138908250	138908250	Silent	SNP	C	T	C	NACC2	c.G912A	p.P304P
XH_P38	9	139256495	139256495	Missense_Mutation	SNP	G	T	G	DNLZ	c.C506A	p.P169H
XH_P38	9	139265088	139265088	Silent	SNP	C	T	C	CARD9	c.G693A	p.T231T
XH_P38	9	139265870	139265870	Silent	SNP	G	A	G	CARD9	c.C228T	p.Y76Y
XH_P38	9	139270876	139270876	Missense_Mutation	SNP	G	A	G	SNAPC4	c.C4342T	p.P1448S
XH_P38	9	139273288	139273288	Silent	SNP	C	T	C	SNAPC4	c.G2991A	p.E997E
XH_P38	9	139289825	139289825	Silent	SNP	A	G	A	SNAPC4	c.T396C	p.D132D
XH_P38	9	139298607	139298607	Missense_Mutation	SNP	G	A	G	SDCCAG3	c.C889T	p.R297W
XH_P38	9	139301960	139301960	Silent	SNP	G	A	G	SDCCAG3	c.C237T	p.T79T
XH_P38	9	139311471	139311471	Silent	SNP	C	T	C	PMPCA	c.C309T	p.N103N
XH_P38	9	139350125	139350125	Missense_Mutation	SNP	C	T	C	SEC16A	c.G5785A	p.A1929T
XH_P38	9	139391543	139391543	Silent	SNP	C	T	C	NOTCH1	c.G6648A	p.P2216P
XH_P38	9	139402694	139402694	Silent	SNP	C	A	C	NOTCH1	c.G3315T	p.A1105A
XH_P38	9	139617662	139617662	Silent	SNP	T	C	T	FAM69B	c.T732C	p.L244L
XH_P38	9	139634495	139634495	Nonsense_Mutation	SNP	G	A	G	LCN10	c.C481T	p.Q161X
XH_P38	9	139636334	139636334	Missense_Mutation	SNP	G	A	G	LCN10	c.C256T	p.R86W
XH_P38	9	139693596	139693596	Missense_Mutation	SNP	T	C	T	CCDC183	c.T113C	p.M38T
XH_P38	9	139733769	139733769	Missense_Mutation	SNP	C	T	C	RAB16	c.C1592T	p.P531L
XH_P38	9	139753246	139753246	Missense_Mutation	SNP	C	T	C	MAMDC4	c.C2897T	p.P966L
XH_P38	9	139873565	139873565	Missense_Mutation	SNP	C	G	C	PTGDS	c.C235G	p.L79V
XH_P38	9	139996099	139996099	Missense_Mutation	SNP	G	A	G	MAN1B1	c.G1229A	p.R410H
XH_P38	9	140008934	140008934	Silent	SNP	A	G	A	DPF7	c.T162C	p.P54P
XH_P38	9	140051376	140051376	Silent	SNP	G	A	G	GRIN1	c.G855A	p.V285V
XH_P38	9	140109871	140109871	Missense_Mutation	SNP	C	T	C	NDOR1	c.C1084T	p.R362W
XH_P38	9	140323749	140323749	Missense_Mutation	SNP	C	T	C	NOXA1	c.C526T	p.R176W
XH_P38	9	140372570	140372570	Missense_Mutation	SNP	G	A	G	PNPLA7	c.C2723T	p.P908L
XH_P38	9	140917779	140917779	Missense_Mutation	SNP	G	T	G	CACNA1B	c.G2584T	p.A862S
XH_P38	9	141016262	141016262	Missense_Mutation	SNP	T	G	T	CACNA1B	c.T6644G	p.L2215R
XH_P38	10	429977	429977	Silent	SNP	G	A	G	DIP2C	c.C1866T	p.G622G
XH_P38	10	3150973	3150973	Silent	SNP	C	T	C	PFKP	c.C303T	p.F101F
XH_P38	10	3197856	3197856	Missense_Mutation	SNP	C	G	C	PITRM1	c.G1452C	p.Q484H
XH_P38	10	5415954	5415954	Missense_Mutation	SNP	A	G	A	UCN3	c.A271G	p.R91G
XH_P38	10	5541181	5541181	Missense_Mutation	SNP	T	C	T	CALML5	c.A221G	p.K74R
XH_P38	10	5541183	5541183	Silent	SNP	C	T	C	CALML5	c.G219A	p.A73A
XH_P38	10	5541230	5541230	Missense_Mutation	SNP	T	C	T	CALML5	c.A172G	p.S58G
XH_P38	10	7605243	7605243	Missense_Mutation	SNP	C	T	C	ITIH5	c.G1990A	p.V664I
XH_P38	10	7679393	7679393	Silent	SNP	C	T	C	ITIH5	c.G450A	p.K150K
XH_P38	10	7780646	7780646	Missense_Mutation	SNP	C	G	C	ITIH2	c.C2020G	p.P674A
XH_P38	10	14816448	14816448	Missense_Mutation	SNP	G	A	G	FAM107B	c.C215T	p.A72V
XH_P38	10	15255835	15255835	Silent	SNP	C	T	C	FAM171A1	c.G1752A	p.P584P
XH_P38	10	15255915	15255915	Missense_Mutation	SNP	C	T	C	FAM171A1	c.G1672A	p.G558S
XH_P38	10	15256194	15256194	Missense_Mutation	SNP	G	A	G	FAM171A1	c.C1393T	p.P465S
XH_P38	10	16918972	16918972	Silent	SNP	A	G	A	CUBN	c.T9030C	p.A3010A
XH_P38	10	17216556	17216556	Missense_Mutation	SNP	C	T	C	TRDMT1	c.G68A	p.R23Q
XH_P38	10	19425531	19425531	Missense_Mutation	SNP	A	G	A	MALRD1	c.A1232G	p.Q411R
XH_P38	10	19678449	19678449	Missense_Mutation	SNP	A	G	A	MALRD1	c.A4756G	p.M1586V
XH_P38	10	20506418	20506418	Missense_Mutation	SNP	G	A	G	PLXDC2	c.G1039A	p.V347I
XH_P38	10	21415006	21415006	Missense_Mutation	SNP	T	C	T	C10orf113	c.A214G	p.R72G
XH_P38	10	23481621	23481621	Silent	SNP	C	T	C	PTF1A	c.C162T	p.S54S
XH_P38	10	24813454	24813454	Missense_Mutation	SNP	G	A	G	KIAA1217	c.G1708A	p.A570T
XH_P38	10	27459670	27459670	Silent	SNP	C	T	C	MASTL	c.C1782T	p.I594I
XH_P38	10	29783908	29783908	Missense_Mutation	SNP	A	G	A	SVIL	c.T2498C	p.M833T
XH_P38	10	30316208	30316208	Missense_Mutation	SNP	T	C	C	JCAD	c.A2869G	p.R957G
XH_P38	10	30316872	30316872	Silent	SNP	T	C	T	JCAD	c.A2205G	p.A735A
XH_P38	10	35929131	35929131	Silent	SNP	G	A	G	FZD8	c.C1227T	p.A409A

XH_P38	10	45430462	45430462	Silent	SNP	C	T	C	TMEM72	c.C354T	p.A118A
XH_P38	10	45472899	45472899	Missense_Mutation	SNP	G	A	G	C10orf10	c.C580T	p.R194C
XH_P38	10	45473317	45473317	Silent	SNP	C	T	C	C10orf10	c.G162A	p.L54L
XH_P38	10	45939617	45939617	Silent	SNP	A	G	A	ALOX5	c.A1728G	p.P576P
XH_P38	10	45958676	45958676	Silent	SNP	G	A	G	MARCH8	c.C1011T	p.S337S
XH_P38	10	45958881	45958881	Missense_Mutation	SNP	A	G	A	MARCH8	c.T806C	p.L269S
XH_P38	10	46224381	46224381	Silent	SNP	C	T	C	WASHC2C	c.C198T	p.D66D
XH_P38	10	46321527	46321527	Missense_Mutation	SNP	G	A	G	AGAP4	c.C1828T	p.R610C
XH_P38	10	46321905	46321905	Missense_Mutation	SNP	G	A	G	AGAP4	c.C1450T	p.R484C
XH_P38	10	46968665	46968665	Silent	SNP	G	A	G	SYT15	c.C271T	p.L91L
XH_P38	10	47756065	47756065	Silent	SNP	C	T	C	ANXA8L1	c.C354T	p.D118D
XH_P38	10	49654545	49654545	Silent	SNP	C	T	C	ARHGAP22	c.G1716A	p.A572A
XH_P38	10	50533776	50533776	Silent	SNP	C	G	C	C10orf71	c.C3186G	p.P1062P
XH_P38	10	50534599	50534599	Missense_Mutation	SNP	G	A	G	C10orf71	c.G4009A	p.G1337S
XH_P38	10	52002980	52002980	Silent	SNP	T	G	T	ASAH2	c.A492C	p.S164S
XH_P38	10	52005153	52005153	Silent	SNP	A	G	A	ASAH2	c.T189C	p.A63A
XH_P38	10	52573698	52573698	Silent	SNP	G	A	G	A1CF	c.C1242T	p.L414L
XH_P38	10	54074757	54074757	Silent	SNP	A	G	A	DKK1	c.A318G	p.A106A
XH_P38	10	61831744	61831744	Silent	SNP	A	G	A	ANK3	c.T8895C	p.A2965A
XH_P38	10	63450379	63450379	Silent	SNP	G	A	G	C10orf107	c.G288A	p.E96E
XH_P38	10	64565011	64565011	Silent	SNP	G	A	G	ADO	c.G192A	p.E64E
XH_P38	10	64967951	64967956	In_Frame_Del	DEL	CTAAAC	-	CTAAAC	JMJD1C	c.2816_2821del	p.939_941del
XH_P38	10	64974380	64974380	Missense_Mutation	SNP	G	C	G	JMJD1C	c.C890G	p.T297S
XH_P38	10	70940191	70940191	Silent	SNP	C	T	C	SUPV3L1	c.C144T	p.A48A
XH_P38	10	71026510	71026510	Missense_Mutation	SNP	C	A	C	HKDC1	c.C2751A	p.N917K
XH_P38	10	71168727	71168727	Missense_Mutation	SNP	C	T	C	TACR2	c.G692A	p.G231E
XH_P38	10	71332204	71332204	Missense_Mutation	SNP	A	G	A	NEUROG3	c.T596C	p.F199S
XH_P38	10	71391542	71391542	Missense_Mutation	SNP	G	A	G	C10orf35	c.G43A	p.D15N
XH_P38	10	71678058	71678058	Silent	SNP	C	G	C	COL13A1	c.C843G	p.A281A
XH_P38	10	71874048	71874048	Silent	SNP	G	A	G	A1FM2	c.C1008T	p.D336D
XH_P38	10	72289701	72289701	Silent	SNP	G	A	G	PALD1	c.G345A	p.V151V
XH_P38	10	72358340	72358340	Silent	SNP	C	T	C	PRF1	c.G1137A	p.R379R
XH_P38	10	72358655	72358655	Silent	SNP	G	A	G	PRF1	c.C822T	p.A274A
XH_P38	10	72517837	72517837	Silent	SNP	C	T	C	ADAMTS14	c.C3057T	p.P1019P
XH_P38	10	72520259	72520259	Missense_Mutation	SNP	C	T	C	ADAMTS14	c.C3322T	p.P1108S
XH_P38	10	73051388	73051388	Silent	SNP	T	C	T	UNC5B	c.T1461C	p.D487D
XH_P38	10	73466709	73466709	Silent	SNP	T	C	T	CDH23	c.T3009C	p.S1003S
XH_P38	10	73500599	73500599	Silent	SNP	C	T	C	CDH23	c.C4509T	p.G1503G
XH_P38	10	73520632	73520632	Missense_Mutation	SNP	A	C	A	VSIR	c.T561G	p.D187E
XH_P38	10	73550969	73550969	Missense_Mutation	SNP	G	A	G	CDH23	c.G6130A	p.E2044K
XH_P38	10	73562744	73562744	Silent	SNP	G	A	G	CDH23	c.G852A	p.A284A
XH_P38	10	75406764	75406764	Silent	SNP	G	C	G	SYNPO2L	c.C1974G	p.A658A
XH_P38	10	75406912	75406912	Missense_Mutation	SNP	G	T	G	SYNPO2L	c.C1826A	p.S609Y
XH_P38	10	75407290	75407290	Missense_Mutation	SNP	G	A	G	SYNPO2L	c.C1448T	p.P483L
XH_P38	10	75407649	75407649	Silent	SNP	A	C	A	SYNPO2L	c.T1089G	p.P363P
XH_P38	10	75519905	75519905	Missense_Mutation	SNP	G	T	G	SEC24C	c.G611T	p.R204L
XH_P38	10	81373674	81373674	Silent	SNP	T	C	T	SFTPA1	c.T552C	p.Y184Y
XH_P38	10	81465826	81465826	Silent	SNP	C	T	C	NUTM2B	c.C411T	p.T137T
XH_P38	10	88441431	88441431	Missense_Mutation	SNP	C	T	C	LDB3	c.C560T	p.P187L
XH_P38	10	88696622	88696622	Missense_Mutation	SNP	C	G	C	MMRN2	c.G2728C	p.V910L
XH_P38	10	88719789	88719789	Missense_Mutation	SNP	C	G	C	SNCG	c.C247G	p.R83G
XH_P38	10	88722398	88722398	Nonstop_Mutation	SNP	A	T	A	SNCG	c.A381T	p.X127C
XH_P38	10	89623716	89623716	Missense_Mutation	SNP	G	A	G	PTEN	c.G10A	p.G4R
XH_P38	10	90429652	90429652	Missense_Mutation	SNP	A	G	A	LIPF	c.A382G	p.T128A
XH_P38	10	90438207	90438207	Silent	SNP	A	G	A	LIPF	c.A867G	p.Q289Q
XH_P38	10	90580144	90580144	Silent	SNP	C	T	C	LIPM	c.C1158T	p.H386H
XH_P38	10	91222287	91222287	Missense_Mutation	SNP	A	C	A	SLC16A12	c.T49G	p.W17G
XH_P38	10	91404448	91404448	Silent	SNP	C	G	C	PANK1	c.G612C	p.L204L
XH_P38	10	91404832	91404832	Silent	SNP	T	C	T	PANK1	c.A228G	p.A76A
XH_P38	10	91497631	91497631	Missense_Mutation	SNP	T	A	T	KIF20B	c.T3033A	p.D1011E
XH_P38	10	94822686	94822686	Silent	SNP	C	T	C	CYP26C1	c.C639T	p.T213T
XH_P38	10	95123725	95123725	Missense_Mutation	SNP	G	A	G	MYOF	c.C2822T	p.T941M
XH_P38	10	95276742	95276742	Missense_Mutation	SNP	G	C	G	CEP55	c.G730C	p.A244P
XH_P38	10	96493058	96493058	Missense_Mutation	SNP	C	T	C	CYP2C18	c.C977T	p.T326M
XH_P38	10	96541616	96541616	Silent	SNP	G	A	G	CYP2C19	c.G681A	p.P227P
XH_P38	10	96602622	96602622	Silent	SNP	C	T	C	CYP2C19	c.C990T	p.V330V
XH_P38	10	97174537	97174537	Missense_Mutation	SNP	C	A	C	SORBS1	c.G497T	p.G166V
XH_P38	10	98806512	98806512	Silent	SNP	G	C	G	SLIT1	c.C1752G	p.A584A
XH_P38	10	99126249	99126249	Silent	SNP	G	A	G	RRP12	c.C3045T	p.D1015D
XH_P38	10	99141205	99141205	Silent	SNP	A	G	A	RRP12	c.T1056C	p.A352A
XH_P38	10	99219885	99219885	Silent	SNP	G	A	G	MMS19	c.C2280T	p.A760A
XH_P38	10	99240048	99240048	Missense_Mutation	SNP	C	T	C	MMS19	c.G329A	p.R110Q
XH_P38	10	99332488	99332488	Silent	SNP	A	C	A	ANKRD2	c.A24C	p.A8A
XH_P38	10	99439556	99439556	Missense_Mutation	SNP	A	C	A	AVP1	c.T107G	p.L36R
XH_P38	10	99473729	99473729	Silent	SNP	C	G	G	MARVELD1	c.C96G	p.G32G
XH_P38	10	100018844	100018844	Silent	SNP	G	A	G	LOXL4	c.C843T	p.H281H
XH_P38	10	102988345	102988345	Silent	SNP	G	A	G	LBX1	c.C228T	p.R76R
XH_P38	10	104230437	104230437	Silent	SNP	C	G	C	MFSD13A	c.C267G	p.L89L
XH_P38	10	104386934	104386934	Silent	SNP	T	C	T	SUFU	c.T1299C	p.I433I
XH_P38	10	105217976	105217976	Missense_Mutation	SNP	C	T	C	CALHM1	c.G533A	p.R178H
XH_P38	10	105344451	105344451	Missense_Mutation	SNP	G	A	G	NEURL1	c.G808A	p.G270S
XH_P38	10	108380213	108380213	Silent	SNP	G	A	G	SORCS1	c.C2769T	p.Y923Y
XH_P38	10	114849264	114849264	Missense_Mutation	SNP	T	C	T	TCF7L2	c.T589C	p.S197P
XH_P38	10	115393948	115393948	Missense_Mutation	SNP	C	T	C	NRAP	c.G1345A	p.D449N
XH_P38	10	115439641	115439642	Frame_Shift_Del	DEL	TT	-	TT	CASP7	c.128_129del	p.L43fs
XH_P38	10	116602805	116602805	Silent	SNP	A	G	A	FAM160B1	c.A636G	p.E212E
XH_P38	10	118969346	118969346	Missense_Mutation	SNP	T	C	T	KCNK18	c.T691C	p.S231P
XH_P38	10	119133968	119133968	Silent	SNP	G	C	G	PDZB8	c.C771G	p.S257S
XH_P38	10	119134058	119134058	Silent	SNP	T	C	T	PDZB8	c.A681G	p.G227G
XH_P38	10	121196335	121196335	Missense_Mutation	SNP	G	A	G	GRK5	c.G911A	p.R304H
XH_P38	10	121685689	121685689	Missense_Mutation	SNP	G	A	G	SEC23IP	c.G2263A	p.V755M
XH_P38	10	122216862	122216862	Silent	SNP	C	T	C	PLPP4	c.C45T	p.F15F
XH_P38	10	122645376	122645376	Silent	SNP	A	T	A	WDR11	c.A1899T	p.A633A
XH_P38	10	123687456	123687456	Silent	SNP	G	A	G	ATE1	c.C9T	p.F3F
XH_P38	10	123842195	123842195	Silent	SNP	C	T	C	TACC2	c.C180T	p.T60T
XH_P38	10	123970587	123970587	Missense_Mutation	SNP	C	T	C	TACC2	c.C881T	p.P294L
XH_P38	10	124896963	124896963	Silent	SNP	C	T	C	HMX3	c.C790T	p.L264L
XH_P38	10	126715075	126715075	Silent	SNP	T	C	T	CTBP2	c.A1254G	p.A418A

XH_P38	10	126715744	126715744	Silent	SNP	G	A	G	CTBP2	c.C585T	p.D195D
XH_P38	10	127462833	127462833	Silent	SNP	C	T	C	MMP21	c.G264A	p.A88A
XH_P38	10	129160458	129160458	Silent	SNP	G	A	G	DOCK1	c.G3414A	p.S1138S
XH_P38	10	129216658	129216658	Silent	SNP	T	C	T	DOCK1	c.T4545C	p.I151S
XH_P38	10	129535789	129535789	Silent	SNP	C	T	C	FOXI2	c.C252T	p.A84A
XH_P38	10	129899778	129899778	Missense_Mutation	SNP	G	C	G	MKI67	c.C8369G	p.T2790S
XH_P38	10	129901946	129901946	Missense_Mutation	SNP	T	G	T	MKI67	c.A7078C	p.T2360P
XH_P38	10	129904477	129904477	Missense_Mutation	SNP	C	T	C	MKI67	c.G4547A	p.R1516Q
XH_P38	10	129905896	129905896	Missense_Mutation	SNP	T	A	T	MKI67	c.A3128T	p.E1043V
XH_P38	10	129906468	129906468	Silent	SNP	C	T	C	MKI67	c.G2556A	p.Q852Q
XH_P38	10	129906903	129906903	Silent	SNP	C	T	C	MKI67	c.G2121A	p.T707T
XH_P38	10	129906980	129906980	Missense_Mutation	SNP	C	T	C	MKI67	c.G2044A	p.G682S
XH_P38	10	129907544	129907544	Missense_Mutation	SNP	G	C	G	MKI67	c.C1480G	p.L494V
XH_P38	10	129914272	129914272	Splice_Site	SNP	C	T	C	MKI67		
XH_P38	10	133918372	133918372	Silent	SNP	G	A	G	JAKMIP3	c.G60A	p.A20A
XH_P38	10	133950642	133950642	Silent	SNP	T	C	T	JAKMIP3	c.T1020C	p.D340D
XH_P38	10	134623959	134623959	Missense_Mutation	SNP	T	C	T	CFAP46	c.A7618G	p.S2540G
XH_P38	10	134624504	134624504	Silent	SNP	C	T	C	CFAP46	c.G7533A	p.A2511A
XH_P38	10	134942166	134942166	Silent	SNP	A	G	A	ADGRA1	c.A543G	p.S181S
XH_P38	10	134942340	134942340	Silent	SNP	C	T	C	ADGRA1	c.C717T	p.A239A
XH_P38	10	135012429	135012429	Missense_Mutation	SNP	T	A	T	KNDC1	c.T2417A	p.V806D
XH_P38	10	135012430	135012430	Silent	SNP	T	C	T	KNDC1	c.T2418C	p.V806V
XH_P38	10	135044263	135044263	Silent	SNP	C	G	C	UTF1	c.C471G	p.R157R
XH_P38	10	135051653	135051653	Missense_Mutation	SNP	A	G	A	VENTX	c.A235G	p.M79V
XH_P38	10	135053465	135053465	Missense_Mutation	SNP	G	A	G	VENTX	c.G432A	p.M144I
XH_P38	10	135139635	135139635	Missense_Mutation	SNP	G	A	G	CALY	c.C104T	p.P35L
XH_P38	11	290494	290494	Missense_Mutation	SNP	C	T	C	PGGHG	c.C364T	p.R122C
XH_P38	11	403764	403764	Silent	SNP	C	T	C	PKP3	c.C2070T	p.D690D
XH_P38	11	403980	403980	Silent	SNP	G	A	G	PKP3	c.G2115A	p.P705P
XH_P38	11	404317	404317	Silent	SNP	C	T	C	PKP3	c.C2352T	p.F784F
XH_P38	11	406954	406954	Silent	SNP	G	A	G	SIGIRR	c.C768T	p.P256P
XH_P38	11	420983	420983	Silent	SNP	C	G	C	ANO9	c.G1020C	p.L340L
XH_P38	11	433453	433453	Missense_Mutation	SNP	G	A	G	ANO9	c.C211T	p.R71W
XH_P38	11	490036	490036	Silent	SNP	G	A	G	PTDS22	c.G642A	p.A214A
XH_P38	11	494942	494942	Silent	SNP	G	C	G	RNH1	c.C1239G	p.A413A
XH_P38	11	562421	562421	Missense_Mutation	SNP	G	A	G	RASSF7	c.G467A	p.R156Q
XH_P38	11	563257	563257	Silent	SNP	G	A	G	RASSF7	c.G891A	p.Q297Q
XH_P38	11	721570	721570	Silent	SNP	C	T	C	EPS8L2	c.C774T	p.I258I
XH_P38	11	772490	772490	Silent	SNP	G	A	G	GATD1	c.C129T	p.A43A
XH_P38	11	802379	802379	Missense_Mutation	SNP	T	C	T	PIDD1	c.A992G	p.Q331R
XH_P38	11	804212	804212	Silent	SNP	C	A	C	PIDD1	c.G177T	p.L59L
XH_P38	11	1013987	1013987	In_Frame_Ins	SNP	G	A	G	MUC6	c.C7054T	p.R2352W
XH_P38	11	1016513	1016513	In_Frame_Ins	INS	-	ATCGCCTTCTGT	-	MUC6	5288insACAGAA	2096delinsQQKAM
XH_P38	11	1027811	1027811	Missense_Mutation	SNP	C	T	C	MUC6	c.G1855A	p.V619M
XH_P38	11	1087972	1087972	Silent	SNP	C	T	C	MUC2	c.C3447T	p.N1149N
XH_P38	11	1090343	1090343	Silent	SNP	T	C	T	MUC2	c.T3639C	p.C1213C
XH_P38	11	1092388	1092388	Missense_Mutation	SNP	A	C	A	MUC2	c.A4207C	p.T1403P
XH_P38	11	1093769	1093769	Missense_Mutation	SNP	G	A	G	MUC2	c.G5588A	p.R1863Q
XH_P38	11	1246941	1246941	Missense_Mutation	SNP	A	G	A	MUC5B	c.A101G	p.E34G
XH_P38	11	1247458	1247458	Missense_Mutation	SNP	C	T	C	MUC5B	c.C151T	p.R51W
XH_P38	11	1267443	1267443	Silent	SNP	G	C	G	MUC5B	c.G9333C	p.T3111T
XH_P38	11	1481930	1481930	Missense_Mutation	SNP	A	G	A	BRSK2	c.A2188G	p.T730A
XH_P38	11	1578090	1578090	Silent	SNP	G	A	G	DUSP8	c.C1536T	p.L512L
XH_P38	11	1857762	1857762	Silent	SNP	C	T	C	SYT8	c.C669T	p.T223T
XH_P38	11	2016717	2016717	Silent	SNP	T	A	T	HOTS	c.T291A	p.I97I
XH_P38	11	2320865	2320865	Frame_Shift_Ins	INS	-	G	-	C11orf21	c.T219dupC	p.T74fs
XH_P38	11	2797237	2797237	Silent	SNP	G	A	G	KCNQ1	c.G1638A	p.S546S
XH_P38	11	3249984	3249984	Missense_Mutation	SNP	C	T	C	MRGPRE	c.G46A	p.G16S
XH_P38	11	3660914	3660914	Missense_Mutation	SNP	A	G	A	ART5	c.T745C	p.T249H
XH_P38	11	3681519	3681519	Missense_Mutation	SNP	T	C	T	ART1	c.T770C	p.L257P
XH_P38	11	4608542	4608542	Missense_Mutation	SNP	C	T	C	OR52I2	c.C500T	p.T167M
XH_P38	11	4615508	4615508	Silent	SNP	C	G	C	OR52I1	c.C240G	p.S80S
XH_P38	11	4703321	4703321	Silent	SNP	G	A	G	OR51E2	c.C621T	p.G207G
XH_P38	11	4703654	4703654	Silent	SNP	A	G	A	OR51E2	c.T288C	p.C96C
XH_P38	11	4703762	4703762	Silent	SNP	G	T	G	OR51E2	c.C180A	p.L60L
XH_P38	11	4945196	4945196	Missense_Mutation	SNP	T	G	T	OR51G1	c.A374C	p.Y125S
XH_P38	11	5345128	5345128	Missense_Mutation	SNP	G	A	G	OR51B2	c.C400T	p.L134F
XH_P38	11	5423931	5423931	Silent	SNP	C	T	C	OR51J1	c.C105T	p.S35S
XH_P38	11	5510553	5510553	Missense_Mutation	SNP	C	T	C	OR52D1	c.C617T	p.A206V
XH_P38	11	5537045	5537045	Silent	SNP	T	G	T	UBQLNL	c.A627C	p.P209P
XH_P38	11	5537161	5537161	Missense_Mutation	SNP	A	G	A	UBQLNL	c.T511C	p.C171R
XH_P38	11	5632018	5632018	Missense_Mutation	SNP	C	A	C	TRIM6	c.C388A	p.L130M
XH_P38	11	5757785	5757785	Silent	SNP	C	T	C	OR56B1	c.C39T	p.S13S
XH_P38	11	5842356	5842356	Missense_Mutation	SNP	A	G	A	OR52N2	c.A791G	p.H264R
XH_P38	11	5906143	5906143	Silent	SNP	T	C	T	OR52E4	c.T621C	p.Y207Y
XH_P38	11	6129152	6129152	Silent	SNP	T	C	T	OR56B4	c.T144C	p.N48N
XH_P38	11	6238960	6238960	Missense_Mutation	SNP	C	A	C	FAM160A2	c.G1856T	p.R619L
XH_P38	11	6281267	6281267	Missense_Mutation	SNP	C	T	C	CCKBR	c.C109T	p.L37F
XH_P38	11	6415463	6415463	Missense_Mutation	SNP	G	A	G	SMPD1	c.G1522A	p.G508R
XH_P38	11	6422834	6422834	Silent	SNP	G	A	G	APBB1	c.C813T	p.I271I
XH_P38	11	6453232	6453232	Missense_Mutation	SNP	C	T	C	HPX	c.G851A	p.R284H
XH_P38	11	6585207	6585207	Silent	SNP	G	A	G	DNHD1	c.G10137A	p.L3379L
XH_P38	11	6942726	6942726	Missense_Mutation	SNP	G	C	G	OR2D3	c.G494C	p.W165S
XH_P38	11	6953858	6953858	Missense_Mutation	SNP	A	G	A	ZNF215	c.A355G	p.M119V
XH_P38	11	6976996	6976996	Missense_Mutation	SNP	C	T	C	ZNF215	c.C788T	p.S263F
XH_P38	11	7022038	7022038	Silent	SNP	A	G	A	ZNF214	c.T876C	p.F292F
XH_P38	11	7059981	7059981	Missense_Mutation	SNP	G	A	G	NLRP14	c.G164A	p.R55Q
XH_P38	11	7110548	7110548	Missense_Mutation	SNP	C	T	C	RBMXL2	c.C197T	p.A66V
XH_P38	11	7949860	7949860	Missense_Mutation	SNP	G	A	G	OR10A6	c.C350T	p.A117V
XH_P38	11	8251921	8251921	Silent	SNP	G	C	G	LMO1	c.C153G	p.A51A
XH_P38	11	8707233	8707233	Silent	SNP	C	T	C	RPL27A	c.C327T	p.Y109Y
XH_P38	11	8751640	8751640	Missense_Mutation	SNP	G	C	G	ST5	c.C1197G	p.D399E
XH_P38	11	10064452	10064452	Missense_Mutation	SNP	A	G	A	SBF2	c.T218C	p.I73T
XH_P38	11	10647702	10647702	Silent	SNP	G	A	G	MRV11	c.C234T	p.L78L
XH_P38	11	10650329	10650329	Silent	SNP	C	T	C	MRV11	c.G594A	p.R198R
XH_P38	11	11373960	11373960	Missense_Mutation	SNP	C	T	C	CSNK2A3	c.G707A	p.R236H
XH_P38	11	14865551	14865551	Silent	SNP	A	G	A	PDE3B	c.A2499G	p.L833L
XH_P38	11	17449929	17449929	Silent	SNP	C	T	C	ABCC8	c.G1947A	p.K649K

XH_P38	11	17981047	17981047	Silent	SNP	C	T	C	SERGEF	c.G981A	p.S327S
XH_P38	11	19955500	19955500	Silent	SNP	A	G	A	NAV2	c.A1518G	p.K506K
XH_P38	11	20529886	20529886	Missense_Mutation	SNP	G	A	G	PRMT3	c.G1337A	p.S446N
XH_P38	11	26587133	26587133	Silent	SNP	T	C	T	MUC15	c.A273G	p.S91S
XH_P38	11	34482908	34482908	Silent	SNP	C	T	C	CAT	c.C1167T	p.D389D
XH_P38	11	36103228	36103228	Silent	SNP	A	G	A	LDLRAD3	c.A72G	p.P24P
XH_P38	11	44089352	44089352	Missense_Mutation	SNP	G	A	G	ACCS	c.G175A	p.D59N
XH_P38	11	44129290	44129290	Silent	SNP	C	A	C	EXT2	c.C127A	p.R43R
XH_P38	11	44289071	44289071	Silent	SNP	G	A	G	ALX4	c.C879T	p.L293L
XH_P38	11	44636833	44636833	Silent	SNP	G	A	G	CD82	c.G273A	p.E91E
XH_P38	11	45307634	45307634	Missense_Mutation	SNP	C	T	C	SYT13	c.C125A	p.R42Q
XH_P38	11	45975130	45975130	Missense_Mutation	SNP	C	T	C	PHF21A	c.G1040A	p.R347H
XH_P38	11	46338965	46338965	Silent	SNP	C	T	C	CREB3L1	c.C1185T	p.P395P
XH_P38	11	46564032	46564032	Missense_Mutation	SNP	C	T	C	AMBRA1	c.G1535A	p.R512Q
XH_P38	11	47355475	47355475	Missense_Mutation	SNP	G	C	G	MYBPC3	c.C2992G	p.Q998E
XH_P38	11	47380422	47380422	Missense_Mutation	SNP	C	T	C	SP1	c.G469A	p.G157R
XH_P38	11	48239182	48239182	Missense_Mutation	SNP	C	A	C	OR4B1	c.C821A	p.T274K
XH_P38	11	49080252	49080252	Splice_Site	SNP	C	T	C	TRIM64C	.	.
XH_P38	11	49197416	49197416	Silent	SNP	A	G	A	FOLH1	c.T90C	p.S30S
XH_P38	11	49974670	49974670	Silent	SNP	C	T	C	OR4C13	c.C696T	p.H232H
XH_P38	11	51515912	51515912	Missense_Mutation	SNP	C	T	C	OR4C46	c.C631T	p.L211F
XH_P38	11	55322638	55322638	Missense_Mutation	SNP	C	T	C	OR4C15	c.C856T	p.R286C
XH_P38	11	55406022	55406022	Nonsense_Mutation	SNP	C	G	C	OR4P4	c.C189G	p.Y63X
XH_P38	11	55418693	55418693	Missense_Mutation	SNP	T	C	T	OR4S2	c.T314C	p.F105S
XH_P38	11	56128081	56128081	Missense_Mutation	SNP	A	G	A	OR8J1	c.A359G	p.Y120C
XH_P38	11	56185327	56185327	Missense_Mutation	SNP	T	C	T	OR5R1	c.A382G	p.S128G
XH_P38	11	56380134	56380134	Missense_Mutation	SNP	C	G	C	OR5M1	c.G845C	p.S282T
XH_P38	11	56431216	56431216	Nonsense_Mutation	SNP	C	T	C	OR5AR1	c.C55T	p.Q19X
XH_P38	11	57075940	57075940	Silent	SNP	G	T	G	TNKS1BP1	c.C4245A	p.S1415S
XH_P38	11	57081197	57081197	Missense_Mutation	SNP	G	C	G	TNKS1BP1	c.C965G	p.T322S
XH_P38	11	57996084	57996084	Silent	SNP	G	A	G	OR10Q1	c.C264T	p.N88N
XH_P38	11	58170738	58170738	Missense_Mutation	SNP	A	G	A	OR5B3	c.T145C	p.W49R
XH_P38	11	60699230	60699230	Silent	SNP	G	A	G	TMEM132A	c.G1089A	p.A363A
XH_P38	11	61487690	61487690	Silent	SNP	G	A	G	DAGLA	c.G63A	p.P21P
XH_P38	11	61505168	61505168	Silent	SNP	G	A	G	DAGLA	c.G1524A	p.A508A
XH_P38	11	61511498	61511498	Missense_Mutation	SNP	C	T	C	DAGLA	c.C2666T	p.P889L
XH_P38	11	61658800	61658800	Silent	SNP	C	T	C	FADS3	c.G54A	p.A18A
XH_P38	11	61895741	61895741	Silent	SNP	A	G	A	INCENP	c.A108G	p.E36E
XH_P38	11	61897359	61897359	Silent	SNP	C	T	C	INCENP	c.C360T	p.V120V
XH_P38	11	61908440	61908440	Missense_Mutation	SNP	T	C	T	INCENP	c.T1517C	p.M506T
XH_P38	11	61913196	61913196	Missense_Mutation	SNP	G	T	G	INCENP	c.G1920T	p.E640D
XH_P38	11	62285818	62285818	Silent	SNP	G	A	G	AHNAK	c.C16071T	p.N5357N
XH_P38	11	62288649	62288649	Missense_Mutation	SNP	G	C	G	AHNAK	c.C13240G	p.L4414V
XH_P38	11	62290140	62290140	Missense_Mutation	SNP	T	C	T	AHNAK	c.A11749G	p.N3917D
XH_P38	11	62293822	62293822	Silent	SNP	C	T	C	AHNAK	c.G8067A	p.K2689K
XH_P38	11	62296892	62296892	Missense_Mutation	SNP	T	C	T	AHNAK	c.A4997G	p.K1666R
XH_P38	11	63988045	63988045	Silent	SNP	G	A	G	FERMT3	c.G1449A	p.P483P
XH_P38	11	64034911	64034911	Silent	SNP	G	A	G	PLCB3	c.G3387A	p.P1129P
XH_P38	11	64066999	64066999	Missense_Mutation	SNP	C	T	C	KCNK4	c.C983T	p.P328L
XH_P38	11	64109148	64109148	Silent	SNP	G	A	G	CCDC88B	c.G609A	p.E203E
XH_P38	11	64110668	64110668	Silent	SNP	G	A	G	CCDC88B	c.G1080A	p.S360S
XH_P38	11	64122853	64122853	Silent	SNP	G	A	G	CCDC88B	c.G4287A	p.A1429A
XH_P38	11	64496357	64496357	Silent	SNP	G	T	G	RASGRP2	c.C1749A	p.G583G
XH_P38	11	64597506	64597506	Missense_Mutation	SNP	T	C	T	CDC42BPG	c.A3404G	p.Q1135R
XH_P38	11	64606177	64606177	Silent	SNP	C	T	C	CDC42BPG	c.G1074A	p.G358G
XH_P38	11	64695360	64695360	Silent	SNP	G	A	G	PPP2R5B	c.G483A	p.S161S
XH_P38	11	64789194	64789194	Missense_Mutation	SNP	T	C	T	ARL2	c.T341C	p.V114A
XH_P38	11	64855986	64855986	Missense_Mutation	SNP	A	G	A	TMEM262	c.T260C	p.V87A
XH_P38	11	64882789	64882789	Missense_Mutation	SNP	C	T	C	TM75F2	c.C896T	p.T299I
XH_P38	11	64972286	64972286	Missense_Mutation	SNP	G	C	G	CAPN1	c.G1298C	p.R433P
XH_P38	11	64981472	64981472	Silent	SNP	G	C	G	SLC22A20	c.G129C	p.T43T
XH_P38	11	64981853	64981853	Missense_Mutation	SNP	G	T	G	SLC22A20	c.G438T	p.M146I
XH_P38	11	65349962	65349962	Missense_Mutation	SNP	G	T	G	EHBPL1L	c.G1819T	p.A607S
XH_P38	11	65351074	65351074	Silent	SNP	G	A	G	EHBPL1L	c.G2931A	p.A977A
XH_P38	11	65386206	65386206	Missense_Mutation	SNP	C	G	C	PCNX3	c.C1373G	p.S458C
XH_P38	11	65392695	65392695	Silent	SNP	C	T	C	PCNX3	c.C2973T	p.L991L
XH_P38	11	65417434	65417434	Silent	SNP	G	A	G	SIPA1	c.G2760A	p.A920A
XH_P38	11	65628334	65628334	Missense_Mutation	SNP	G	A	G	MUS81	c.G110A	p.R37H
XH_P38	11	65629932	65629932	Silent	SNP	T	C	T	MUS81	c.T537C	p.A179A
XH_P38	11	65629934	65629934	Missense_Mutation	SNP	G	C	G	MUS81	c.G539C	p.R180P
XH_P38	11	65631973	65631973	Silent	SNP	G	A	G	MUS81	c.G1068A	p.R356R
XH_P38	11	65685317	65685317	Silent	SNP	G	A	G	C11orf68	c.C495T	p.H165H
XH_P38	11	65793454	65793454	Missense_Mutation	SNP	C	T	C	CATSPER1	c.G397A	p.G133S
XH_P38	11	65793797	65793797	Silent	SNP	G	A	G	CATSPER1	c.C54T	p.N18N
XH_P38	11	65826704	65826704	Silent	SNP	G	A	G	SF3B2	c.G1215A	p.K405K
XH_P38	11	66033430	66033430	Missense_Mutation	SNP	C	T	C	KLC2	c.C1318T	p.P440S
XH_P38	11	66062023	66062023	Silent	SNP	G	T	G	TMEM151A	c.G306T	p.P102P
XH_P38	11	66206169	66206169	Silent	SNP	C	T	C	MRPL11	c.G57A	p.V19V
XH_P38	11	66335832	66335832	Silent	SNP	G	A	G	CTSF	c.C126T	p.P42P
XH_P38	11	66512290	66512290	In_Frame_Ins	INS	-	GGC	-	C11orf80	c.77_78insGGC	p.G26delinsGA
XH_P38	11	66807561	66807561	Missense_Mutation	SNP	A	C	A	SYT12	c.A163C	p.N55H
XH_P38	11	67075131	67075131	Silent	SNP	C	T	C	SSH3	c.C714T	p.S238S
XH_P38	11	67135006	67135006	Silent	SNP	A	T	A	CLCF1	c.T78A	p.P26P
XH_P38	11	67160961	67160961	Missense_Mutation	SNP	A	G	A	RAD9A	c.A1G	p.M1V
XH_P38	11	67164791	67164791	Silent	SNP	T	C	T	RAD9A	c.T786C	p.G262G
XH_P38	11	67171736	67171736	Silent	SNP	C	T	C	TBC1D10C	c.C63T	p.S21S
XH_P38	11	67172911	67172911	Silent	SNP	C	T	C	TBC1D10C	c.C294T	p.R98R
XH_P38	11	67176898	67176898	Missense_Mutation	SNP	A	G	A	TBC1D10C	c.A820G	p.R274G
XH_P38	11	67188466	67188466	Silent	SNP	C	T	C	CARNS1	c.C1033T	p.L345L
XH_P38	11	67209515	67209515	Silent	SNP	C	T	C	CORO1B	c.G246A	p.T82T
XH_P38	11	68029253	68029253	Missense_Mutation	SNP	C	T	C	C11orf24	c.G1210A	p.V404M
XH_P38	11	68115489	68115489	Missense_Mutation	SNP	A	G	A	LRP5	c.A266G	p.Q89R
XH_P38	11	68174122	68174122	Silent	SNP	G	A	G	LRP5	c.G189A	p.E63E
XH_P38	11	68682402	68682402	Missense_Mutation	SNP	A	G	A	IGHMBP2	c.A823G	p.I275V
XH_P38	11	68701948	68701948	Silent	SNP	C	T	C	IGHMBP2	c.C1554T	p.V518V
XH_P38	11	68704028	68704028	Missense_Mutation	SNP	C	T	C	IGHMBP2	c.C2080T	p.R694W
XH_P38	11	69063510	69063510	Missense_Mutation	SNP	G	A	G	MYEOV	c.G419A	p.R140Q
XH_P38	11	69063728	69063728	Missense_Mutation	SNP	G	C	G	MYEOV	c.G637C	p.G213R

XH_P38	11	71276769	71276769	Missense_Mutation	SNP	G	A	G	KRTAP5-10	c.G136A	p.V46I
XH_P38	11	72288599	72288599	Silent	SNP	G	A	G	PDE2A	c.C2634T	p.Y878Y
XH_P38	11	72408055	72408055	Missense_Mutation	SNP	G	C	C	ARAP1	c.C2221G	p.Q741E
XH_P38	11	72466071	72466071	Silent	SNP	C	A	G	STARD10	c.G747T	p.L249L
XH_P38	11	72946020	72946020	Silent	SNP	C	T	C	P2RY2	c.C816T	p.R272R
XH_P38	11	72946140	72946140	Missense_Mutation	SNP	G	C	G	P2RY2	c.G936C	p.R312S
XH_P38	11	73020363	73020363	Missense_Mutation	SNP	C	T	C	ARHGEF17	c.C680T	p.A227V
XH_P38	11	73669367	73669367	Missense_Mutation	SNP	G	A	G	DNAJB13	c.G74A	p.R25H
XH_P38	11	73689104	73689104	Missense_Mutation	SNP	G	A	G	UCP2	c.C164T	p.A55V
XH_P38	11	73717254	73717254	Silent	SNP	A	G	A	UCP3	c.T297C	p.Y99Y
XH_P38	11	73825503	73825503	Silent	SNP	T	C	T	C2CD3	c.A1656G	p.P552P
XH_P38	11	73978243	73978243	Nonsense_Mutation	SNP	G	A	G	P4HA3	c.C1678T	p.Q560X
XH_P38	11	73988167	73988167	Missense_Mutation	SNP	C	T	C	P4HA3	c.G1198A	p.D400N
XH_P38	11	74109166	74109166	Missense_Mutation	SNP	A	G	A	PGM2L1	c.T41C	p.L14P
XH_P38	11	74413872	74413872	Silent	SNP	A	G	A	CHRD2	c.T892C	p.L298L
XH_P38	11	75277582	75277582	Missense_Mutation	SNP	C	T	C	SERPINH1	c.C188T	p.A63V
XH_P38	11	76371418	76371418	Missense_Mutation	SNP	C	T	C	LRRC32	c.G1219A	p.A407T
XH_P38	11	76372052	76372052	Silent	SNP	A	G	A	LRRC32	c.T585C	p.G195G
XH_P38	11	76895771	76895792	Frame_Shift_Del	DEL	GGGGACACC	-	CGGGGACACCA	MYO7A	c.3514_3535del	p.G1172fs
XH_P38	11	76910766	76910766	Silent	SNP	C	T	C	MYO7A	c.C4755T	p.S1585S
XH_P38	11	76912636	76912636	Missense_Mutation	SNP	A	T	A	MYO7A	c.A4996T	p.S1666C
XH_P38	11	76917220	76917220	Silent	SNP	A	G	A	MYO7A	c.A5715G	p.Y1905K
XH_P38	11	77639511	77639511	Silent	SNP	T	A	T	INTS4	c.A1248T	p.L416L
XH_P38	11	77790655	77790655	Missense_Mutation	SNP	G	C	G	NDUFC2	c.C136G	p.L46V
XH_P38	11	77907888	77907888	Silent	SNP	G	A	G	USP35	c.G597A	p.L199L
XH_P38	11	78372536	78372536	Silent	SNP	G	A	G	TENM4	c.C7509T	p.L2503L
XH_P38	11	78614532	78614532	Missense_Mutation	SNP	C	T	C	TENM4	c.G530A	p.T177Q
XH_P38	11	82973004	82973004	Silent	SNP	C	T	C	CCDC90B	c.G369A	p.S123S
XH_P38	11	86161388	86161388	Missense_Mutation	SNP	C	G	C	ME3	c.G972C	p.K324N
XH_P38	11	89537258	89537258	Missense_Mutation	SNP	C	T	C	TRIM49	c.G380A	p.R127H
XH_P38	11	92088177	92088177	Silent	SNP	C	T	C	FAT3	c.C2899T	p.L967L
XH_P38	11	93913149	93913149	Silent	SNP	C	T	C	PANX1	c.C927T	p.Y309Y
XH_P38	11	94261280	94261280	Missense_Mutation	SNP	G	A	G	C11orf97	c.G281A	p.R94K
XH_P38	11	94320237	94320237	Silent	SNP	T	C	T	PIWIL4	c.T738C	p.F246F
XH_P38	11	94326710	94326710	Silent	SNP	G	A	G	PIWIL4	c.G1053A	p.S151L
XH_P38	11	94337220	94337220	Silent	SNP	C	T	C	PIWIL4	c.C1636T	p.L546L
XH_P38	11	94533373	94533373	Silent	SNP	C	T	C	AMOTL1	c.C867T	p.P289P
XH_P38	11	95825797	95825797	Silent	SNP	A	G	A	MAML2	c.T1398C	p.S466S
XH_P38	11	106888608	106888608	Silent	SNP	G	A	G	GUCY1A2	c.C174T	p.A58A
XH_P38	11	108464209	108464209	Missense_Mutation	SNP	T	C	T	EXPH5	c.A55G	p.R19G
XH_P38	11	111896242	111896242	Missense_Mutation	SNP	G	A	G	DLAT	c.G46A	p.A16T
XH_P38	11	113270828	113270828	Missense_Mutation	SNP	G	A	G	ANKK1	c.G2137A	p.E713K
XH_P38	11	113283477	113283477	Silent	SNP	A	G	A	DRD2	c.T852C	p.H284H
XH_P38	11	116728630	116728630	Missense_Mutation	SNP	G	C	G	SIK3	c.C3227G	p.P1076R
XH_P38	11	116729161	116729161	Missense_Mutation	SNP	T	C	T	SIK3	c.A2696G	p.Y899C
XH_P38	11	117042377	117042377	Missense_Mutation	SNP	G	A	G	PAFAH1B2	c.G451A	p.V151M
XH_P38	11	117074109	117074109	Silent	SNP	G	A	G	TAGLN	c.G267A	p.K89K
XH_P38	11	117097952	117097952	Silent	SNP	C	T	C	PCSK7	c.G690A	p.T230T
XH_P38	11	117100257	117100257	Missense_Mutation	SNP	C	T	C	PCSK7	c.G304A	p.A102T
XH_P38	11	117267884	117267884	Missense_Mutation	SNP	A	G	A	CEP164	c.A3365G	p.Q1122R
XH_P38	11	117789539	117789539	Silent	SNP	T	C	C	TMPPRS513	c.A36G	p.A12A
XH_P38	11	118514625	118514625	Silent	SNP	C	T	C	PHLDB1	c.C2844T	p.S948S
XH_P38	11	118769442	118769442	Silent	SNP	A	G	A	BCL9L	c.T4182C	p.P1394P
XH_P38	11	118922200	118922200	Silent	SNP	G	A	G	HYOU1	c.C1476T	p.N492N
XH_P38	11	119005132	119005132	Missense_Mutation	SNP	C	T	C	HINFP	c.C1478T	p.A493V
XH_P38	11	119216275	119216275	Missense_Mutation	SNP	G	C	G	MFRP	c.C496G	p.P166A
XH_P38	11	119535677	119535677	In_Frame_Ins	INS	-	CCT	-	NECTIN1	1333_1334insA	p.G445delinsEG
XH_P38	11	121038810	121038810	Silent	SNP	C	T	C	TECTA	c.C5634T	p.S1878S
XH_P38	11	122665437	122665437	Silent	SNP	A	G	A	UBASH3B	c.A1008G	p.S336S
XH_P38	11	123886865	123886865	Missense_Mutation	SNP	T	A	T	OR10G4	c.T584A	p.V195E
XH_P38	11	123909342	123909342	Silent	SNP	G	A	G	OR10G7	c.C367T	p.L123L
XH_P38	11	124266906	124266906	Missense_Mutation	SNP	C	T	C	OR8B3	c.G342A	p.M114I
XH_P38	11	124765361	124765361	Missense_Mutation	SNP	G	A	G	ROBO4	c.C593T	p.P198L
XH_P38	11	124857578	124857578	Missense_Mutation	SNP	G	T	G	CCDC15	c.G1456T	p.V486F
XH_P38	11	125365285	125365285	Missense_Mutation	SNP	T	C	T	LOC403312	c.T61C	p.S21P
XH_P38	11	125476252	125476252	Silent	SNP	C	G	C	STT3A	c.C396G	p.L132L
XH_P38	11	125547869	125547869	Missense_Mutation	SNP	C	T	C	ACRV1	c.G376A	p.G126R
XH_P38	11	126135973	126135973	Silent	SNP	C	T	C	SRPRA	c.G852A	p.A284A
XH_P38	11	126162468	126162468	Missense_Mutation	SNP	G	A	G	TIRAP	c.G164A	p.S55N
XH_P38	11	126174038	126174038	Silent	SNP	C	T	C	DCPS	c.C63T	p.H21H
XH_P38	11	126278203	126278203	Silent	SNP	T	C	C	ST3GAL4	c.T436C	p.L146L
XH_P38	11	128844354	128844354	Missense_Mutation	SNP	A	G	A	ARHGAP32	c.T1649C	p.L550S
XH_P38	11	130058817	130058817	Silent	SNP	G	A	G	ST14	c.G423A	p.S141S
XH_P38	11	130068491	130068491	Silent	SNP	G	C	G	ST14	c.G1659C	p.G553G
XH_P38	11	130078470	130078470	Silent	SNP	G	A	G	ST14	c.G2160A	p.P720P
XH_P38	11	130339312	130339312	Silent	SNP	T	C	T	ADAMTS15	c.T1698C	p.N566N
XH_P38	11	133805585	133805585	Silent	SNP	C	T	C	IGSF9B	c.G894A	p.S298S
XH_P38	11	133814191	133814191	Silent	SNP	A	G	A	IGSF9B	c.T333C	p.Y111Y
XH_P38	12	274647	274647	Silent	SNP	T	C	T	IQSEC3	c.T1848C	p.F161F
XH_P38	12	300332	300332	Missense_Mutation	SNP	T	C	T	SLC6A12	c.A1747G	p.K583E
XH_P38	12	653594	653594	Silent	SNP	C	T	C	B4GALNT3	c.C441T	p.Y147Y
XH_P38	12	662838	662838	Silent	SNP	T	C	T	B4GALNT3	c.T1749C	p.P583P
XH_P38	12	974355	974355	Frame_Shift_Ins	INS	-	C	-	WNK1	c.2220dupC	p.L740fs
XH_P38	12	994014	994014	Silent	SNP	C	T	C	WNK1	c.C3303T	p.T1101T
XH_P38	12	1702561	1702561	Silent	SNP	G	A	G	FBXL14	c.C672T	p.S224S
XH_P38	12	2944024	2944024	Silent	SNP	G	C	G	NRIP2	c.C126G	p.P42P
XH_P38	12	2968169	2968169	Missense_Mutation	SNP	A	G	A	FOXMI	c.T1882C	p.S628P
XH_P38	12	3789452	3789452	Missense_Mutation	SNP	C	T	C	CRACR2A	c.G292A	p.A98T
XH_P38	12	6030302	6030302	Silent	SNP	T	C	T	ANO2	c.A438G	p.G146G
XH_P38	12	6184646	6184646	Silent	SNP	G	A	G	VWF	c.C729T	p.P243P
XH_P38	12	6426747	6426747	Missense_Mutation	SNP	T	G	T	PLEKHG6	c.T806G	p.M269R
XH_P38	12	6483851	6483851	Silent	SNP	G	A	G	SCNN1A	c.C276T	p.P92P
XH_P38	12	6638116	6638116	Silent	SNP	C	T	C	NCAPD2	c.C3483T	p.N1161N
XH_P38	12	6781677	6781677	Silent	SNP	C	T	C	ZNF384	c.G933A	p.T311T
XH_P38	12	6933223	6933223	Silent	SNP	C	T	C	GPR162	c.C159T	p.C53C
XH_P38	12	7047017	7047017	Silent	SNP	A	G	A	ATN1	c.A2304G	p.K768K
XH_P38	12	7249598	7249598	Missense_Mutation	SNP	T	C	T	C1RL	c.A727G	p.I243V
XH_P38	12	7280880	7280880	Missense_Mutation	SNP	C	G	C	RPB5	c.G208C	p.E70Q

XH_P38	12	7528471	7528471	Silent	SNP	G	A	G	CD163L1	c.C2541T	p.N847N
XH_P38	12	7585247	7585247	Silent	SNP	T	C	T	CD163L1	c.A561G	p.G187G
XH_P38	12	8200622	8200622	Missense_Mutation	SNP	A	G	A	FOXJ2	c.A962G	p.Q321R
XH_P38	12	9312951	9312951	Missense_Mutation	SNP	G	A	G	PZP	c.C3008T	p.T1003M
XH_P38	12	10069302	10069302	Missense_Mutation	SNP	C	T	C	CLEC2A	c.G407A	p.G136D
XH_P38	12	10131939	10131939	Silent	SNP	C	T	C	CLEC12A	c.C967T	p.H32H
XH_P38	12	10332197	10332197	Missense_Mutation	SNP	G	T	G	TMEM52B	c.G8T	p.W3L
XH_P38	12	10954632	10954632	Missense_Mutation	SNP	C	A	C	TAS2R7	c.G538T	p.A180S
XH_P38	12	10954916	10954916	Missense_Mutation	SNP	A	G	A	TAS2R7	c.T254C	p.I85T
XH_P38	12	11150240	11150240	Missense_Mutation	SNP	T	C	T	TAS2R20	c.A235G	p.K79E
XH_P38	12	11175087	11175087	Silent	SNP	G	A	G	TAS2R19	c.C84T	p.A28A
XH_P38	12	14019128	14019128	Silent	SNP	C	T	C	GRIN2B	c.G15A	p.A5A
XH_P38	12	22602796	22602796	Silent	SNP	A	G	A	C2CD5	c.T2901C	p.D967D
XH_P38	12	27064232	27064232	Silent	SNP	C	T	C	INTS13	c.G1824A	p.E608E
XH_P38	12	29709853	29709853	Missense_Mutation	SNP	T	C	T	TMTC1	c.A1613G	p.Q538R
XH_P38	12	30868002	30868002	Silent	SNP	C	T	C	CAPRIN2	c.G2373A	p.V791V
XH_P38	12	30881809	30881809	Missense_Mutation	SNP	T	C	T	CAPRIN2	c.A556G	p.M186V
XH_P38	12	30888001	30888001	Missense_Mutation	SNP	T	C	T	CAPRIN2	c.A710G	p.K237R
XH_P38	12	31135579	31135579	Missense_Mutation	SNP	T	C	T	TSPAN11	c.T569C	p.V190A
XH_P38	12	44148259	44148259	Missense_Mutation	SNP	T	C	T	PUS7L	c.A790G	p.K264E
XH_P38	12	44180295	44180295	Missense_Mutation	SNP	G	A	G	IRAK4	c.G910A	p.A304T
XH_P38	12	44191625	44191625	Silent	SNP	G	A	G	TWF1	c.C495T	p.D165D
XH_P38	12	45444516	45444516	Silent	SNP	G	A	G	DBX2	c.C195T	p.A65A
XH_P38	12	47629368	47629368	Silent	SNP	G	T	G	PCED1B	c.G522T	p.G174G
XH_P38	12	48919659	48919659	Missense_Mutation	SNP	T	C	T	OR851	c.T245C	p.L82P
XH_P38	12	48919796	48919796	Missense_Mutation	SNP	C	T	C	OR851	c.C382T	p.R128C
XH_P38	12	48920006	48920006	Missense_Mutation	SNP	G	A	G	OR851	c.G592A	p.A198T
XH_P38	12	49221622	49221622	Silent	SNP	G	A	G	CACNB3	c.G1272A	p.E424E
XH_P38	12	49230035	49230035	Silent	SNP	T	G	T	DDX23	c.A1251C	p.I417I
XH_P38	12	49390677	49390677	Missense_Mutation	SNP	T	C	T	DDN	c.A1982G	p.E661G
XH_P38	12	49425978	49425978	Silent	SNP	T	C	T	KMT2D	c.A12510G	p.P4170P
XH_P38	12	49434074	49434074	Silent	SNP	C	A	C	KMT2D	c.G7479T	p.G2493G
XH_P38	12	49689009	49689009	Missense_Mutation	SNP	G	A	G	PRPH	c.G26A	p.R9Q
XH_P38	12	49691250	49691250	Silent	SNP	A	G	A	PRPH	c.A1107G	p.K369K
XH_P38	12	51236802	51236802	Missense_Mutation	SNP	T	C	T	TMPRSS12	c.T55C	p.Y19H
XH_P38	12	52369191	52369191	Silent	SNP	C	T	C	ACVR1B	c.C234T	p.A78A
XH_P38	12	52448157	52448157	Silent	SNP	G	A	G	NR4A1	c.G45A	p.P15P
XH_P38	12	52635360	52635360	Silent	SNP	G	A	G	KRT7	c.G798A	p.A266A
XH_P38	12	52685213	52685213	Missense_Mutation	SNP	T	G	T	KRT81	c.A37C	p.S13R
XH_P38	12	52699548	52699548	Silent	SNP	T	C	T	KRT86	c.T1002C	p.A334A
XH_P38	12	52777502	52777502	Silent	SNP	A	G	A	KRT84	c.T627C	p.N209N
XH_P38	12	52824352	52824352	Silent	SNP	G	A	G	KRT75	c.C1008T	p.A336A
XH_P38	12	52886478	52886478	Silent	SNP	T	C	T	KRT6A	c.A495G	p.E165E
XH_P38	12	52994896	52994896	Missense_Mutation	SNP	A	G	A	KRT72	c.T341C	p.M114T
XH_P38	12	52995020	52995020	Missense_Mutation	SNP	C	T	C	KRT72	c.G217A	p.G73S
XH_P38	12	53164848	53164848	Silent	SNP	G	A	G	KRT76	c.C1419T	p.N473N
XH_P38	12	53189543	53189543	Missense_Mutation	SNP	C	T	C	KRT3	c.G284A	p.G95D
XH_P38	12	53645615	53645615	Nonsense_Mutation	SNP	C	A	C	MFSD5	c.C99A	p.Y33X
XH_P38	12	53645616	53645616	Missense_Mutation	SNP	C	G	C	MFSD5	c.C100G	p.R34G
XH_P38	12	53671005	53671005	Missense_Mutation	SNP	G	A	G	ESPL1	c.G2079A	p.M693I
XH_P38	12	53682457	53682457	Missense_Mutation	SNP	G	A	G	ESPL1	c.G4682A	p.R1561Q
XH_P38	12	53777171	53777171	Silent	SNP	A	G	A	SP1	c.A1296G	p.Q432Q
XH_P38	12	54379670	54379670	Silent	SNP	C	T	C	HOXC10	c.C627T	p.P209P
XH_P38	12	55523685	55523685	Missense_Mutation	SNP	C	T	C	OR9K2	c.C133T	p.R45C
XH_P38	12	55863224	55863224	Missense_Mutation	SNP	C	G	C	OR6C70	c.G699C	p.K233N
XH_P38	12	55886489	55886489	Missense_Mutation	SNP	T	G	T	OR6C68	c.T328A	p.F110I
XH_P38	12	56415298	56415298	Silent	SNP	C	T	C	IKZF4	c.C21T	p.L7L
XH_P38	12	57585144	57585144	Silent	SNP	C	T	C	LRP1	c.C7278T	p.A2426A
XH_P38	12	57593101	57593101	Silent	SNP	G	A	G	LRP1	c.G9783A	p.T3261T
XH_P38	12	58009796	58009796	Silent	SNP	C	T	C	ARHGEF25	c.C1326T	p.L442L
XH_P38	12	58015494	58015494	Missense_Mutation	SNP	G	A	G	SLC26A10	c.G577A	p.A193T
XH_P38	12	58176614	58176614	Silent	SNP	T	C	T	TSFM	c.T30C	p.F10F
XH_P38	12	59313936	59313936	Silent	SNP	T	G	T	LRIG3	c.A81C	p.S27S
XH_P38	12	62946739	62946739	Missense_Mutation	SNP	A	C	A	MON2	c.A2995C	p.K999Q
XH_P38	12	65672558	65672558	Silent	SNP	C	A	C	MSRB3	c.C10A	p.R4R
XH_P38	12	66696410	66696410	Silent	SNP	C	T	C	HELB	c.C27T	p.R9R
XH_P38	12	69646914	69646914	Silent	SNP	G	A	G	CPSF6	c.G354A	p.R118R
XH_P38	12	70037520	70037520	Missense_Mutation	SNP	G	A	G	BEST3	c.C1148T	p.P383L
XH_P38	12	70953277	70953277	Silent	SNP	T	C	T	PTPRB	c.A3636G	p.A1212A
XH_P38	12	72372862	72372862	Silent	SNP	A	G	A	TPH2	c.A936G	p.P312P
XH_P38	12	75902186	75902186	Silent	SNP	T	C	T	KRR1	c.A126G	p.E42E
XH_P38	12	78362303	78362303	Missense_Mutation	SNP	A	G	A	NAV3	c.A492G	p.L164M
XH_P38	12	94243853	94243853	Silent	SNP	C	T	C	CRADD	c.C406T	p.L136L
XH_P38	12	94543506	94543506	Silent	SNP	C	T	C	PLXNC1	c.C759T	p.Y253Y
XH_P38	12	94972290	94972290	Silent	SNP	C	T	C	TMCC3	c.G918A	p.E306E
XH_P38	12	96337225	96337225	Silent	SNP	C	T	C	AMDHD1	c.C49T	p.L17L
XH_P38	12	96346594	96346594	Silent	SNP	T	C	T	AMDHD1	c.T237C	p.I79I
XH_P38	12	97023939	97023939	Missense_Mutation	SNP	A	T	A	CFAP54	c.A4172T	p.N1391I
XH_P38	12	97254620	97254620	Silent	SNP	G	A	G	CFAP54	c.G9195A	p.P3065P
XH_P38	12	99007623	99007623	Missense_Mutation	SNP	C	T	C	IKBIP	c.G793A	p.G265S
XH_P38	12	102036305	102036305	Silent	SNP	C	T	C	MYBPC1	c.C621T	p.D207D
XH_P38	12	10224436	10224436	Silent	SNP	C	T	C	GNPTAB	c.G18A	p.L6L
XH_P38	12	104100617	104100617	Silent	SNP	C	T	C	STAB2	c.C4044T	p.C1348C
XH_P38	12	104171742	104171742	Silent	SNP	C	T	C	NT5DC3	c.G1512A	p.L504L
XH_P38	12	104186995	104186995	Silent	SNP	G	A	G	NT5DC3	c.C966T	p.F322F
XH_P38	12	108985785	108985785	Silent	SNP	C	T	C	TMEM119	c.G375A	p.S125S
XH_P38	12	109017898	109017898	Missense_Mutation	SNP	C	T	C	SELPLG	c.G234A	p.M78I
XH_P38	12	109182049	109182049	Silent	SNP	T	C	T	SSH1	c.A2865G	p.T955T
XH_P38	12	110841379	110841379	Silent	SNP	G	A	G	ANAPC7	c.C156T	p.N52N
XH_P38	12	112580071	112580071	Silent	SNP	C	T	C	TRAFD1	c.C822T	p.G274G
XH_P38	12	113379599	113379599	Silent	SNP	A	G	A	OAS3	c.A402G	p.T134T
XH_P38	12	113565889	113565889	Silent	SNP	G	A	G	RASAL1	c.C217T	p.L73L
XH_P38	12	113592306	113592306	Frame_Shift_Ins	INS	-	C	-	CFAP73	c.557dupC	p.A186fs
XH_P38	12	118020115	118020115	Silent	SNP	G	A	G	KSR2	c.C1134T	p.L378L
XH_P38	12	120741382	120741382	Silent	SNP	G	A	G	SIRT4	c.G18A	p.A6A
XH_P38	12	120762837	120762837	Silent	SNP	A	G	A	PLA2G1B	c.T222C	p.Y74Y
XH_P38	12	120907271	120907271	Silent	SNP	G	T	G	SRSF9	c.C142A	p.R48R
XH_P38	12	121878659	121878659	Silent	SNP	C	T	C	KDM2B	c.G3363A	p.Q1121Q

XH_P38	12	121880520	121880520	Silent	SNP	G	A	G	KDM2B	c.C2517T	p.D839D
XH_P38	12	121881848	121881848	Silent	SNP	G	A	G	KDM2B	c.C2325T	p.Y775Y
XH_P38	12	122079441	122079441	Silent	SNP	T	C	T	ORA1	c.T804C	p.T268T
XH_P38	12	122255356	122255356	Missense_Mutation	SNP	C	T	C	SETD1B	c.C3058T	p.R1020W
XH_P38	12	122392038	122392038	Missense_Mutation	SNP	C	T	C	WDR66	c.C1333T	p.L445F
XH_P38	12	124819027	124819027	Missense_Mutation	SNP	G	A	G	NCOR2	c.C6518T	p.P2173L
XH_P38	12	128899673	128899673	Missense_Mutation	SNP	A	G	A	TMEM132C	c.A482G	p.H161R
XH_P38	12	129278864	129278864	Silent	SNP	A	G	A	SLC15A4	c.T1611C	p.F537F
XH_P38	12	130185054	130185054	Missense_Mutation	SNP	A	T	A	TMEM132D	c.T269A	p.L90Q
XH_P38	12	130941150	130941150	Silent	SNP	G	C	G	RIMBP2	c.C198G	p.G66G
XH_P38	12	131306314	131306314	Missense_Mutation	SNP	C	G	C	STX2	c.G125C	p.S42T
XH_P38	12	132402020	132402020	Silent	SNP	T	C	T	ULK1	c.T2247C	p.P749P
XH_P38	12	132514288	132514288	Silent	SNP	C	G	C	EP400	c.C5424G	p.S1808S
XH_P38	12	132547162	132547162	Silent	SNP	G	A	G	EP400	c.G8250A	p.T2750T
XH_P38	12	132561987	132561987	Silent	SNP	C	T	C	EP400	c.C9141T	p.A3047A
XH_P38	12	132626425	132626425	Missense_Mutation	SNP	G	A	G	DDX51	c.C965T	p.A322V
XH_P38	12	133196596	133196596	Silent	SNP	T	C	T	P2RX2	c.T252C	p.T84T
XH_P38	12	133208979	133208979	Silent	SNP	T	C	T	POLE	c.A6252G	p.S2084S
XH_P38	12	133294333	133294333	Silent	SNP	C	T	C	PGAM5	c.C534T	p.G178G
XH_P38	12	133295353	133295353	Missense_Mutation	SNP	C	T	C	PGAM5	c.C725T	p.P242L
XH_P38	12	133306710	133306710	Missense_Mutation	SNP	C	T	C	ANKLE2	c.G2038A	p.F680K
XH_P38	12	133357412	133357412	Missense_Mutation	SNP	T	C	T	GOLGA3	c.A3554G	p.K1185R
XH_P38	12	133378440	133378440	Silent	SNP	C	T	C	GOLGA3	c.G1713A	p.L571L
XH_P38	13	19748038	19748038	Missense_Mutation	SNP	C	T	C	TUBA3C	c.G1318A	p.V440M
XH_P38	13	19751229	19751229	Silent	SNP	T	C	T	TUBA3C	c.A894G	p.P298P
XH_P38	13	24895437	24895437	Missense_Mutation	SNP	G	A	G	C1QTNF9	c.G533A	p.R178Q
XH_P38	13	28008980	28008980	Missense_Mutation	SNP	C	T	C	GTFA3	c.C682T	p.R228C
XH_P38	13	28009920	28009920	Missense_Mutation	SNP	G	C	G	MTIF3	c.C729G	p.F243L
XH_P38	13	28542961	28542961	Silent	SNP	C	G	C	CDX2	c.G183C	p.P61P
XH_P38	13	28674628	28674628	Missense_Mutation	SNP	T	C	T	FLT3	c.A20G	p.D7G
XH_P38	13	33703656	33703656	Silent	SNP	T	C	T	STARD13	c.A1134G	p.E378E
XH_P38	13	36385031	36385031	Silent	SNP	G	T	G	DCLK1	c.C708A	p.P236P
XH_P38	13	36402426	36402426	Silent	SNP	A	G	A	DCLK1	c.T327C	p.Y109Y
XH_P38	13	36801415	36801415	Missense_Mutation	SNP	C	T	C	CCDC169	c.G349A	p.G117R
XH_P38	13	36886469	36886469	Silent	SNP	T	C	T	SPG20	c.A1629G	p.A543A
XH_P38	13	39586343	39586343	Silent	SNP	G	C	G	PROSER1	c.C2589G	p.G863G
XH_P38	13	39587166	39587166	Silent	SNP	A	G	A	PROSER1	c.T2223C	p.P741P
XH_P38	13	39587677	39587677	Missense_Mutation	SNP	A	G	A	PROSER1	c.T1712C	p.V571A
XH_P38	13	41134122	41134122	Silent	SNP	C	T	C	FOXO1	c.G1506A	p.S502S
XH_P38	13	42772717	42772717	Silent	SNP	G	T	G	DGKH	c.G1536T	p.P512P
XH_P38	13	43148565	43148565	Silent	SNP	T	C	T	TNFSF11	c.T126C	p.P42P
XH_P38	13	44411432	44411432	Missense_Mutation	SNP	A	G	A	CCDC122	c.T443C	p.I148T
XH_P38	13	44457925	44457925	Missense_Mutation	SNP	A	G	A	LACC1	c.A760G	p.I254V
XH_P38	13	45841502	45841502	Silent	SNP	G	A	G	GTTF22	c.G621A	p.K207K
XH_P38	13	50204880	50204880	Silent	SNP	G	A	G	ARL11	c.G297A	p.S99S
XH_P38	13	52515354	52515354	Missense_Mutation	SNP	A	G	A	ATP7B	c.T2798C	p.V933A
XH_P38	13	53235671	53235671	Silent	SNP	A	T	A	SUGT1	c.A390T	p.P130P
XH_P38	13	53421432	53421432	Silent	SNP	C	A	C	PCDH8	c.G1140T	p.G380G
XH_P38	13	53422553	53422553	Missense_Mutation	SNP	A	G	A	PCDH8	c.T19C	p.W7R
XH_P38	13	76055602	76055602	Missense_Mutation	SNP	G	A	G	TBC1D4	c.C302T	p.A101V
XH_P38	13	76055820	76055820	Silent	SNP	G	C	G	TBC1D4	c.C84G	p.P28P
XH_P38	13	88329472	88329472	Missense_Mutation	SNP	T	A	T	SLITRK5	c.T1829A	p.L610Q
XH_P38	13	99575568	99575568	Silent	SNP	G	A	G	DOCK9	c.C477T	p.V159V
XH_P38	13	103391634	103391634	Missense_Mutation	SNP	C	T	C	CCDC168	c.G11413A	p.V3805I
XH_P38	13	103400083	103400083	Silent	SNP	G	A	G	CCDC168	c.C2964T	p.S988S
XH_P38	13	103402522	103402522	Silent	SNP	C	T	C	CCDC168	c.G525A	p.T175T
XH_P38	13	108922556	108922556	Missense_Mutation	SNP	G	A	G	TNFSF13B	c.G313A	p.A105T
XH_P38	13	110435953	110435953	Silent	SNP	A	G	A	IRS2	c.T2448C	p.C816C
XH_P38	13	110436232	110436232	Silent	SNP	G	A	G	IRS2	c.C2169T	p.S723S
XH_P38	13	111156506	111156506	Missense_Mutation	SNP	G	T	G	COL4A2	c.G4297T	p.A1433S
XH_P38	13	111160304	111160304	Silent	SNP	G	A	G	COL4A2	c.G4617A	p.A1539A
XH_P38	13	111290630	111290630	Missense_Mutation	SNP	T	C	T	NAXD	c.T935C	p.I312T
XH_P38	13	111298392	111298392	Silent	SNP	A	G	A	CARS2	c.T1239C	p.D413D
XH_P38	13	113728781	113728781	Silent	SNP	G	A	G	MCF2L	c.G1020A	p.A340A
XH_P38	13	113751159	113751159	Missense_Mutation	SNP	G	A	G	MCF2L	c.G3364A	p.D1122N
XH_P38	13	113795264	113795264	Silent	SNP	G	T	G	F10	c.G402T	p.G134G
XH_P38	13	114498153	114498153	Frame_Shift_Ins	INS	-	GT	-	TMEM255B	c.285_286insGT	p.G95fs
XH_P38	13	114622597	114622597	Missense_Mutation	SNP	A	G	A	LINC00452	c.A503G	p.L168S
XH_P38	13	115047305	115047305	Missense_Mutation	SNP	G	A	G	UPF3A	c.G191A	p.R64K
XH_P38	13	115064423	115064423	Missense_Mutation	SNP	G	A	G	UPF3A	c.G856A	p.A286T
XH_P38	13	115090019	115090019	Silent	SNP	G	A	G	CHAMP1	c.G702A	p.P234P
XH_P38	13	115090193	115090193	Silent	SNP	G	A	G	CHAMP1	c.G876A	p.P292P
XH_P38	13	115091399	115091399	Silent	SNP	T	C	T	CHAMP1	c.T2082C	p.S694S
XH_P38	14	20852817	20852817	Missense_Mutation	SNP	G	A	G	TEP1	c.C2839T	p.R947C
XH_P38	14	20898347	20898347	Missense_Mutation	SNP	C	T	C	KLHL33	c.G488A	p.R163H
XH_P38	14	20898442	20898442	Silent	SNP	C	T	C	KLHL33	c.G393A	p.Q131Q
XH_P38	14	21550499	21550499	Silent	SNP	G	T	G	ARHGEF40	c.G1206T	p.T402T
XH_P38	14	21551058	21551058	Silent	SNP	G	A	G	ARHGEF40	c.G1413A	p.A471A
XH_P38	14	21560632	21560632	Missense_Mutation	SNP	C	T	C	ZNFX2	c.G824A	p.R275H
XH_P38	14	21623290	21623290	Missense_Mutation	SNP	T	C	T	OR5AU1	c.A895G	p.I299V
XH_P38	14	21770730	21770730	Missense_Mutation	SNP	A	G	A	RPGRIP1	c.A574G	p.K192E
XH_P38	14	23371055	23371055	Missense_Mutation	SNP	G	C	G	RBM23	c.C1182G	p.F394L
XH_P38	14	23530622	23530622	Silent	SNP	T	C	T	ACIN1	c.A1302G	p.S434S
XH_P38	14	23745533	23745533	Missense_Mutation	SNP	C	T	C	HOMEZ	c.G904A	p.A302T
XH_P38	14	23992742	23992742	Missense_Mutation	SNP	T	G	T	ZFH2	c.A6409C	p.S2137R
XH_P38	14	23994517	23994517	Missense_Mutation	SNP	A	G	A	ZFH2	c.T4634C	p.V1545A
XH_P38	14	24002602	24002602	Missense_Mutation	SNP	T	C	T	ZFH2	c.A1933G	p.T645A
XH_P38	14	24423090	24423090	Silent	SNP	A	G	A	DHR54	c.A93G	p.A31A
XH_P38	14	24731043	24731043	Silent	SNP	C	T	C	TGM1	c.G366A	p.S122S
XH_P38	14	24785092	24785092	Missense_Mutation	SNP	G	T	G	LTB4R	c.G235T	p.A79S
XH_P38	14	24785784	24785784	Silent	SNP	C	T	C	LTB4R	c.C927T	p.G309G
XH_P38	14	24839083	24839083	Missense_Mutation	SNP	G	C	G	NFATC4	c.G479C	p.G160A
XH_P38	14	24845841	24845841	Missense_Mutation	SNP	T	C	T	NFATC4	c.T2188C	p.S730P
XH_P38	14	24878370	24878370	Missense_Mutation	SNP	C	T	C	NYNRIN	c.C1370T	p.T457M
XH_P38	14	24883887	24883887	Missense_Mutation	SNP	G	A	G	NYNRIN	c.G2932A	p.A978T
XH_P38	14	24901249	24901249	Missense_Mutation	SNP	A	C	A	KHNYN	c.A905C	p.K302T
XH_P38	14	31355096	31355096	Missense_Mutation	SNP	C	G	C	COCH	c.C1055G	p.T352S
XH_P38	14	37135752	37135752	Silent	SNP	C	T	C	PAX9	c.C717T	p.H239H

XH_P38	14	38060905	38060905	Missense_Mutation	SNP	A	C	A	FOXA1	c.T1084G	p.S362A
XH_P38	14	38679473	38679473	Silent	SNP	C	T	C	SSTR1	c.C879T	p.V293V
XH_P38	14	38723905	38723905	Silent	SNP	C	T	C	CLEC14A	c.G1323A	p.P441P
XH_P38	14	39901186	39901186	Silent	SNP	G	A	G	FBXO33	c.C181T	p.L61L
XH_P38	14	44974966	44974966	Missense_Mutation	SNP	G	A	G	FSCB	c.C1225T	p.P409S
XH_P38	14	44975052	44975052	Missense_Mutation	SNP	A	G	A	FSCB	c.T1139C	p.L380P
XH_P38	14	44975606	44975606	Missense_Mutation	SNP	G	T	G	FSCB	c.C585A	p.H195Q
XH_P38	14	51101982	51101982	Nonsense_Mutation	SNP	G	T	G	SAV1	c.C1071A	p.Y357X
XH_P38	14	51378591	51378591	Splice_Site	DEL	T	-	T	PYGL	.	.
XH_P38	14	53619500	53619500	Missense_Mutation	SNP	C	G	C	DDHD1	c.G317C	p.G106A
XH_P38	14	59105188	59105188	Silent	SNP	C	T	C	DACT1	c.C268T	p.L90L
XH_P38	14	59112732	59112732	Missense_Mutation	SNP	C	T	C	DACT1	c.C1280T	p.A427V
XH_P38	14	59789727	59789727	Silent	SNP	G	A	G	DAAM1	c.G558A	p.K186K
XH_P38	14	60976537	60976537	Missense_Mutation	SNP	C	A	C	SIX6	c.C421A	p.H141N
XH_P38	14	61180466	61180466	Missense_Mutation	SNP	G	A	G	SIX4	c.C2005T	p.L669F
XH_P38	14	64699917	64699917	Missense_Mutation	SNP	C	T	C	ESR2	c.G1258A	p.E420K
XH_P38	14	64701690	64701690	Silent	SNP	C	T	C	ESR2	c.G1131A	p.A377A
XH_P38	14	64988279	64988279	Silent	SNP	A	G	A	ZBTB1	c.A57G	p.E19E
XH_P38	14	65035067	65035067	Missense_Mutation	SNP	G	T	G	PPP1R36	c.G435T	p.R145S
XH_P38	14	65260078	65260078	Missense_Mutation	SNP	C	T	C	SPTB	c.G2303A	p.G768D
XH_P38	14	68029118	68029118	Missense_Mutation	SNP	C	A	C	PLEKHH1	c.C770A	p.P257H
XH_P38	14	68249803	68249803	Missense_Mutation	SNP	A	C	A	ZFYVE26	c.T4066G	p.C1356G
XH_P38	14	70171418	70171418	Silent	SNP	T	C	T	SUSD6	c.T417C	p.F139F
XH_P38	14	70924852	70924852	Silent	SNP	A	C	A	ADAM21	c.A636C	p.L121L
XH_P38	14	71374702	71374702	Silent	SNP	G	A	G	PCNX1	c.G135A	p.L45L
XH_P38	14	73717720	73717720	Missense_Mutation	SNP	G	A	G	PAPLN	c.G571A	p.A191T
XH_P38	14	74196581	74196581	Silent	SNP	G	A	G	ELMSAN1	c.C1857T	p.I619I
XH_P38	14	75378038	75378038	Missense_Mutation	SNP	T	G	T	RPS6KL1	c.A577C	p.I193L
XH_P38	14	75388183	75388183	Missense_Mutation	SNP	C	T	C	RPS6KL1	c.G62A	p.R21Q
XH_P38	14	76045691	76045691	Silent	SNP	C	T	C	FLVCR2	c.C376T	p.L126L
XH_P38	14	76368544	76368544	Missense_Mutation	SNP	T	C	T	TTL5	c.T3800C	p.F1267S
XH_P38	14	76905777	76905777	Silent	SNP	C	A	C	ESRRB	c.C81A	p.I27I
XH_P38	14	76964655	76964655	Missense_Mutation	SNP	C	T	C	ESRRB	c.C1156T	p.P386S
XH_P38	14	77708804	77708804	Silent	SNP	C	T	C	TMEM63C	c.C1179T	p.D393D
XH_P38	14	78398004	78398004	Silent	SNP	C	T	C	ADCK1	c.C1146T	p.S382S
XH_P38	14	81610583	81610583	Missense_Mutation	SNP	G	C	G	TSHR	c.G2181C	p.E727D
XH_P38	14	86089363	86089363	Missense_Mutation	SNP	G	A	G	FLRT2	c.G1505A	p.R502H
XH_P38	14	88407888	88407888	Missense_Mutation	SNP	A	G	A	GALC	c.T1616C	p.J539T
XH_P38	14	88652389	88652389	Silent	SNP	C	T	C	KCNK10	c.G1107A	p.A369A
XH_P38	14	88938652	88938652	Missense_Mutation	SNP	A	G	A	PTPN21	c.T2807C	p.V936A
XH_P38	14	88946622	88946622	Missense_Mutation	SNP	G	A	G	PTPN21	c.C1153T	p.L385F
XH_P38	14	91681888	91681888	Silent	SNP	G	A	G	C14orf159	c.G1704A	p.P568P
XH_P38	14	91773494	91773494	Missense_Mutation	SNP	G	A	G	CCDC88C	c.C3083T	p.A1028V
XH_P38	14	92436176	92436176	Silent	SNP	C	T	C	TRIP11	c.G5778A	p.S1926S
XH_P38	14	93412743	93412743	Silent	SNP	G	A	G	ITPK1	c.C834T	p.F278F
XH_P38	14	93650465	93650465	Silent	SNP	A	C	A	MOAP1	c.T123G	p.A41A
XH_P38	14	94187832	94187832	Silent	SNP	C	T	C	PRIMA1	c.G420A	p.S140S
XH_P38	14	94756450	94756450	Missense_Mutation	SNP	T	A	T	SERPINA10	c.A481T	p.T161S
XH_P38	14	94935901	94935901	Missense_Mutation	SNP	G	C	G	SERPINA9	c.C223G	p.Q75E
XH_P38	14	95053849	95053849	Silent	SNP	T	C	T	SERPINA5	c.T150C	p.F50F
XH_P38	14	95884323	95884323	Missense_Mutation	SNP	G	A	G	SYNE3	c.C2768T	p.A923V
XH_P38	14	96922766	96922766	Missense_Mutation	SNP	A	G	A	AK7	c.A1103G	p.H368R
XH_P38	14	97299853	97299853	Silent	SNP	A	G	A	VRK1	c.A45G	p.A15A
XH_P38	14	99182535	99182535	Missense_Mutation	SNP	C	T	C	C14orf177	c.C7T	p.R3W
XH_P38	14	100380948	100380948	Missense_Mutation	SNP	T	C	T	EML1	c.T1666C	p.S556P
XH_P38	14	100615961	100615961	Missense_Mutation	SNP	C	T	C	DEGS2	c.G169A	p.A57T
XH_P38	14	100625902	100625902	Missense_Mutation	SNP	C	T	C	DEGS2	c.G23A	p.S8N
XH_P38	14	100795139	100795139	Missense_Mutation	SNP	G	T	G	SLC25A47	c.G404T	p.R135L
XH_P38	14	100808845	100808845	Silent	SNP	G	A	G	WARS	c.C880T	p.L294L
XH_P38	14	101004432	101004432	Silent	SNP	G	A	G	BEGAIN	c.C1656T	p.A552A
XH_P38	14	101010204	101010204	Silent	SNP	T	C	T	BEGAIN	c.A342G	p.S114S
XH_P38	14	101350523	101350523	Silent	SNP	G	A	G	RTL1	c.C603T	p.P201P
XH_P38	14	103342049	103342049	Missense_Mutation	SNP	T	C	T	TRAF3	c.T386C	p.M129T
XH_P38	14	103570354	103570354	Missense_Mutation	SNP	G	T	G	EXOC3L4	c.G1126T	p.A376S
XH_P38	14	103573871	103573871	Silent	SNP	G	A	G	EXOC3L4	c.G1692A	p.P564P
XH_P38	14	103987728	103987728	Silent	SNP	C	G	C	CKB	c.G525C	p.A175A
XH_P38	14	104029378	104029378	Missense_Mutation	SNP	C	G	C	APOPT1	c.C79G	p.P27A
XH_P38	14	104165753	104165753	Missense_Mutation	SNP	G	A	G	XRCC3	c.C722T	p.T241M
XH_P38	14	104643421	104643421	Silent	SNP	T	C	T	KIF26A	c.T4296C	p.L1432L
XH_P38	14	104643721	104643721	Silent	SNP	C	A	C	KIF26A	c.C4596A	p.A1532A
XH_P38	14	104643859	104643859	Silent	SNP	A	G	A	KIF26A	c.A4734G	p.R1578R
XH_P38	14	104644099	104644099	Silent	SNP	T	C	T	KIF26A	c.T4974C	p.S1558S
XH_P38	14	104646103	104646103	Silent	SNP	G	A	G	KIF26A	c.G5625A	p.P1875P
XH_P38	14	105060632	105060632	Missense_Mutation	SNP	T	C	T	TMEM179	c.A623G	p.H208R
XH_P38	14	105071055	105071055	Silent	SNP	G	A	G	TMEM179	c.C24T	p.F8F
XH_P38	14	105196365	105196365	Silent	SNP	T	C	T	ADSSL1	c.T136C	p.L46L
XH_P38	14	105211221	105211221	Silent	SNP	C	T	C	ADSSL1	c.C531T	p.N177N
XH_P38	14	105222037	105222037	Silent	SNP	C	T	C	SIVA1	c.C189T	p.A63A
XH_P38	14	105239894	105239894	Silent	SNP	C	T	C	AKT1	c.G726A	p.E242E
XH_P38	14	105405942	105405942	Silent	SNP	G	A	G	AHNAK2	c.C15546T	p.L5182L
XH_P38	14	105406238	105406238	Missense_Mutation	SNP	A	C	A	AHNAK2	c.T15250G	p.Y5084D
XH_P38	14	105407031	105407031	Silent	SNP	A	G	A	AHNAK2	c.T14457C	p.S4819S
XH_P38	14	105407208	105407208	Silent	SNP	T	C	T	AHNAK2	c.A14280G	p.V4760V
XH_P38	14	105407798	105407798	Missense_Mutation	SNP	T	C	T	AHNAK2	c.A13690G	p.T4564A
XH_P38	14	105408030	105408030	Silent	SNP	A	G	A	AHNAK2	c.T13458C	p.D4486D
XH_P38	14	105410352	105410352	Silent	SNP	T	C	T	AHNAK2	c.A11136G	p.S3712S
XH_P38	14	105411153	105411153	Silent	SNP	G	A	G	AHNAK2	c.C10335T	p.P3445P
XH_P38	14	105411260	105411260	Missense_Mutation	SNP	A	G	A	AHNAK2	c.T10228C	p.S3410P
XH_P38	14	105412138	105412138	Missense_Mutation	SNP	A	G	A	AHNAK2	c.T9350C	p.L1317P
XH_P38	14	105413223	105413223	Silent	SNP	A	G	A	AHNAK2	c.T8265C	p.D2755D
XH_P38	14	105414629	105414629	Missense_Mutation	SNP	G	A	G	AHNAK2	c.C6859T	p.P2287S
XH_P38	14	105414804	105414804	Silent	SNP	A	G	A	AHNAK2	c.T6684C	p.F2228F
XH_P38	14	105415933	105415933	Missense_Mutation	SNP	G	A	G	AHNAK2	c.C5555T	p.P1852L
XH_P38	14	105416010	105416010	Silent	SNP	T	C	T	AHNAK2	c.A5478G	p.T1826T
XH_P38	14	105417527	105417527	Missense_Mutation	SNP	C	T	C	AHNAK2	c.G3961A	p.V1321M
XH_P38	14	105417548	105417548	Missense_Mutation	SNP	G	C	G	AHNAK2	c.C3940G	p.L1314V
XH_P38	14	105419446	105419446	Missense_Mutation	SNP	T	G	T	AHNAK2	c.A2042C	p.K681T
XH_P38	14	105420215	105420215	Missense_Mutation	SNP	T	C	T	AHNAK2	c.A1273G	p.T425A

XH_P38	14	105461067	105461067	Silent	SNP	C	T	C	C14orf79	c.C949T	p.L317L
XH_P38	14	105478102	105478102	Silent	SNP	G	A	G	CDC4	c.C165T	p.N55N
XH_P38	14	105611282	105611282	Silent	SNP	A	G	A	JAG2	c.T2955C	p.A985A
XH_P38	14	105613039	105613039	Silent	SNP	C	T	C	JAG2	c.G2388A	p.S796S
XH_P38	14	105615648	105615648	Missense_Mutation	SNP	C	T	C	JAG2	c.G1498A	p.D500N
XH_P38	15	24921376	24921376	Missense_Mutation	SNP	G	A	G	NPAP1	c.G362A	p.R121H
XH_P38	15	27018797	27018797	Silent	SNP	G	A	G	GABRB3	c.C75T	p.P25P
XH_P38	15	28511093	28511093	Silent	SNP	G	A	G	HERC2	c.C1626T	p.S542S
XH_P38	15	29415560	29415560	Silent	SNP	G	A	G	FAM189A1	c.C1602T	p.D534D
XH_P38	15	29416901	29416901	Missense_Mutation	SNP	A	G	A	FAM189A1	c.T1292C	p.V431A
XH_P38	15	32322929	32322929	Silent	SNP	G	A	G	CHRNA7	c.G132A	p.A44A
XH_P38	15	33023098	33023098	Silent	SNP	C	G	C	GREM1	c.C207G	p.P69P
XH_P38	15	34113010	34113010	Silent	SNP	C	T	C	RYR3	c.C10797T	p.F3599F
XH_P38	15	34648935	34648935	Missense_Mutation	SNP	G	T	G	NUTM1	c.G2696T	p.S899I
XH_P38	15	34649631	34649631	Missense_Mutation	SNP	G	A	G	NUTM1	c.G3392A	p.R1131H
XH_P38	15	37329154	37329154	Missense_Mutation	SNP	C	A	C	MEIS2	c.G722T	p.G241V
XH_P38	15	40583560	40583560	Silent	SNP	G	T	G	PLCB2	c.C2731A	p.R911R
XH_P38	15	40627845	40627845	Silent	SNP	G	A	G	C15orf52	c.C1119T	p.S373S
XH_P38	15	40633138	40633138	Silent	SNP	A	T	A	C15orf52	c.T15A	p.A5A
XH_P38	15	40656141	40656141	Silent	SNP	T	C	T	DISP2	c.T435C	p.H145H
XH_P38	15	40662501	40662501	Silent	SNP	G	A	G	DISP2	c.G4188A	p.T1396T
XH_P38	15	41146880	41146880	Silent	SNP	T	C	T	SPINT1	c.T1110C	p.S370S
XH_P38	15	41148516	41148516	Missense_Mutation	SNP	G	A	G	SPINT1	c.G1331A	p.S444N
XH_P38	15	42149472	42149472	Missense_Mutation	SNP	T	C	T	SPTBN5	c.A8585G	p.Q2862R
XH_P38	15	42158022	42158022	Missense_Mutation	SNP	C	T	C	SPTBN5	c.G6902A	p.R2301Q
XH_P38	15	42170578	42170578	Silent	SNP	G	A	G	SPTBN5	c.C3432T	p.H1144H
XH_P38	15	42178122	42178122	Missense_Mutation	SNP	T	C	T	SPTBN5	c.A1331G	p.D444G
XH_P38	15	42185482	42185482	Nonsense_Mutation	SNP	G	A	G	SPTBN5	c.C214T	p.Q72X
XH_P38	15	42287578	42287578	Silent	SNP	G	A	G	PLA2G4E	c.C1227T	p.T409T
XH_P38	15	42979105	42979105	Missense_Mutation	SNP	A	G	A	STARD9	c.A5329G	p.R1777G
XH_P38	15	42982819	42982819	Missense_Mutation	SNP	A	G	A	STARD9	c.A9043G	p.R3015G
XH_P38	15	42983155	42983155	Missense_Mutation	SNP	G	A	G	STARD9	c.G9379A	p.V3127M
XH_P38	15	42983943	42983943	Silent	SNP	C	G	C	STARD9	c.C10167G	p.R3389R
XH_P38	15	42984858	42984858	Silent	SNP	G	T	G	STARD9	c.G11082T	p.L3694L
XH_P38	15	43018559	43018559	Silent	SNP	C	T	C	CDAN1	c.G3153A	p.E1051E
XH_P38	15	43023161	43023161	Missense_Mutation	SNP	C	T	C	CDAN1	c.G1969A	p.G657S
XH_P38	15	43023482	43023482	Missense_Mutation	SNP	T	C	T	CDAN1	c.A1787G	p.Q596R
XH_P38	15	43028511	43028511	Silent	SNP	G	C	G	CDAN1	c.C558G	p.P186P
XH_P38	15	43028626	43028626	Missense_Mutation	SNP	G	A	G	CDAN1	c.C443T	p.A148V
XH_P38	15	43028749	43028749	Missense_Mutation	SNP	T	A	T	CDAN1	c.A320T	p.Q107L
XH_P38	15	43531411	43531411	Missense_Mutation	SNP	G	C	G	TGM5	c.C809G	p.A270G
XH_P38	15	43545728	43545728	Silent	SNP	G	A	G	TGM5	c.C414T	p.Y138Y
XH_P38	15	43621947	43621947	Silent	SNP	A	G	A	LCMT2	c.T741C	p.R247R
XH_P38	15	43622265	43622265	Missense_Mutation	SNP	C	A	C	LCMT2	c.G423T	p.R141S
XH_P38	15	43661802	43661802	Missense_Mutation	SNP	T	C	T	ZSCAN29	c.A310G	p.R104G
XH_P38	15	43748304	43748304	Silent	SNP	A	G	A	TP53BP1	c.T2502C	p.D834D
XH_P38	15	43814780	43814780	Missense_Mutation	SNP	C	G	C	MAP1A	c.C1109G	p.P370R
XH_P38	15	43817406	43817406	Silent	SNP	T	C	T	MAP1A	c.T3735C	p.D1245D
XH_P38	15	43893072	43893072	Silent	SNP	G	A	G	STRC	c.C4842T	p.F1614F
XH_P38	15	43924420	43924420	Missense_Mutation	SNP	C	T	C	CATSPER2	c.G1550A	p.R517H
XH_P38	15	43924422	43924422	Silent	SNP	T	C	T	CATSPER2	c.A1548G	p.E516E
XH_P38	15	44069069	44069069	Missense_Mutation	SNP	G	C	G	ELL3	c.C31G	p.Q11E
XH_P38	15	45444518	45444518	Silent	SNP	A	G	A	DUOX1	c.A3228G	p.T1076T
XH_P38	15	45968435	45968435	Missense_Mutation	SNP	T	C	T	SQOR	c.T791C	p.I264T
XH_P38	15	48053229	48053229	Silent	SNP	C	A	C	SEMA6D	c.C276A	p.P92P
XH_P38	15	48058071	48058071	Missense_Mutation	SNP	G	A	G	SEMA6D	c.G1433A	p.S478N
XH_P38	15	51397262	51397262	Missense_Mutation	SNP	C	T	C	TNFAIP8L3	c.G112A	p.A38T
XH_P38	15	52230365	52230365	Missense_Mutation	SNP	T	A	T	LEO1	c.A1809T	p.E603D
XH_P38	15	52402026	52402026	Missense_Mutation	SNP	G	A	G	BC12L10	c.C704T	p.P235L
XH_P38	15	52534344	52534344	Silent	SNP	G	A	G	MYO5C	c.C2457T	p.R819R
XH_P38	15	52605941	52605941	Silent	SNP	G	C	G	MYO5A	c.C5439G	p.T1813T
XH_P38	15	54003091	54003091	Missense_Mutation	SNP	G	A	G	WDR72	c.C917T	p.P306L
XH_P38	15	55652305	55652305	Missense_Mutation	SNP	T	C	T	CCPG1	c.A1666G	p.K556E
XH_P38	15	56208178	56208178	Silent	SNP	C	T	C	NEDD4	c.G852A	p.L284L
XH_P38	15	57836715	57836715	Silent	SNP	C	T	C	CGNL1	c.C3420T	p.Y1140Y
XH_P38	15	58000981	58000981	Silent	SNP	C	T	C	GCOM1	c.C183T	p.A61A
XH_P38	15	58834741	58834741	Silent	SNP	G	T	G	LIPC	c.G465T	p.V155V
XH_P38	15	59453384	59453384	Silent	SNP	T	C	T	MYO1E	c.A2673G	p.A891A
XH_P38	15	62990971	62990971	Silent	SNP	C	T	C	TLN2	c.C1492T	p.L498L
XH_P38	15	63125789	63125789	Silent	SNP	G	A	G	TLN2	c.G7089A	p.S2363S
XH_P38	15	65321795	65321795	Missense_Mutation	SNP	A	T	A	MTFMT	c.T157A	p.F53I
XH_P38	15	65622651	65622651	Missense_Mutation	SNP	C	T	C	IGDCC3	c.G1838A	p.R613K
XH_P38	15	65667724	65667724	Silent	SNP	A	G	A	IGDCC3	c.T120C	p.A40A
XH_P38	15	65688198	65688198	Missense_Mutation	SNP	C	T	C	IGDCC4	c.G1301A	p.R434Q
XH_P38	15	66996307	66996307	Silent	SNP	C	T	C	SMAD6	c.C711T	p.H237H
XH_P38	15	68609647	68609647	Missense_Mutation	SNP	G	T	G	ITGA11	c.C2671A	p.Q891K
XH_P38	15	69238392	69238392	Silent	SNP	T	C	T	SPESP1	c.T519C	p.Y173Y
XH_P38	15	69325581	69325581	Silent	SNP	C	T	C	NOX5	c.C735T	p.C245C
XH_P38	15	69327825	69327825	Silent	SNP	C	T	C	NOX5	c.C903T	p.T301T
XH_P38	15	69709748	69709748	Silent	SNP	C	A	C	KIF23	c.C108A	p.G36G
XH_P38	15	70345626	70345626	Silent	SNP	C	T	C	TLF3	c.G1704A	p.T568T
XH_P38	15	72492965	72492965	Missense_Mutation	SNP	G	A	G	PKM	c.C1117T	p.R373C
XH_P38	15	74001993	74001993	Silent	SNP	T	C	T	CD276	c.T855C	p.A285A
XH_P38	15	74220084	74220084	Silent	SNP	G	T	G	LOXL1	c.G960T	p.A320A
XH_P38	15	74328141	74328141	Missense_Mutation	SNP	G	T	G	PML	c.G2195T	p.G732V
XH_P38	15	74467856	74467856	Silent	SNP	G	A	G	ISLR	c.G657A	p.T219T
XH_P38	15	74622533	74622533	Missense_Mutation	SNP	A	G	A	CCDC33	c.A73G	p.M25V
XH_P38	15	74703022	74703022	Silent	SNP	G	A	G	SEMA7A	c.C1902T	p.A634A
XH_P38	15	74706943	74706943	Silent	SNP	G	A	G	SEMA7A	c.C1197T	p.V399V
XH_P38	15	74709975	74709975	Silent	SNP	G	A	G	SEMA7A	c.C465T	p.Y155Y
XH_P38	15	74836829	74836829	In Frame Ins	INS	-	AATGGT	-	ARID3B	52_553insAATG	Q184delinsONG
XH_P38	15	74908132	74908132	Missense_Mutation	SNP	G	A	G	CLK3	c.G337A	p.A113T
XH_P38	15	75015305	75015305	Missense_Mutation	SNP	C	T	C	CYP1A1	c.G134A	p.G45D
XH_P38	15	75189930	75189930	Silent	SNP	A	G	A	MPI	c.A981G	p.V327V
XH_P38	15	75979782	75979782	Silent	SNP	G	T	G	CSPG4	c.C3624A	p.R1208R
XH_P38	15	76136768	76136768	Missense_Mutation	SNP	C	T	C	UBE2Q2	c.C74T	p.P25L
XH_P38	15	76496232	76496232	Missense_Mutation	SNP	G	A	G	TMEM266	c.G1172A	p.R391H
XH_P38	15	76496340	76496340	Missense_Mutation	SNP	C	T	C	TMEM266	c.C1280T	p.P427L

XH_P38	15	78369972	78369972	Missense_Mutation	SNP	G	C	G	TBC1D2B	c.C23G	p.A8G
XH_P38	15	78566680	78566680	Missense_Mutation	SNP	G	A	G	DNAJA4	c.G560A	p.R187H
XH_P38	15	78921762	78921762	Silent	SNP	G	A	G	CHRN84	c.C885T	p.I295I
XH_P38	15	79069121	79069121	Silent	SNP	A	G	A	ADAMTS7	c.T1530C	p.A510A
XH_P38	15	79082108	79082108	Silent	SNP	C	T	C	ADAMTS7	c.G1101A	p.Q367Q
XH_P38	15	79254511	79254511	Missense_Mutation	SNP	C	T	C	RASGRF1	c.G1445A	p.R482Q
XH_P38	15	79296172	79296172	Silent	SNP	G	A	G	RASGRF1	c.C117T	p.P39P
XH_P38	15	80873642	80873642	Silent	SNP	C	G	C	ARNT2	c.C1815G	p.T605T
XH_P38	15	81578139	81578139	Missense_Mutation	SNP	C	T	C	IL16	c.C1300T	p.P434S
XH_P38	15	82934942	82934942	Missense_Mutation	SNP	T	C	T	GOLGA6L10	c.A638G	p.E213G
XH_P38	15	85402610	85402610	Silent	SNP	G	A	G	ALPK3	c.G4560A	p.E1520E
XH_P38	15	85467275	85467275	Silent	SNP	C	T	C	SLC28A1	c.C1017T	p.H339H
XH_P38	15	85478696	85478696	Missense_Mutation	SNP	C	T	C	SLC28A1	c.C1528T	p.R510C
XH_P38	15	86284342	86284342	Silent	SNP	C	T	C	AKAP13	c.C3537T	p.L1179L
XH_P38	15	86800209	86800209	Silent	SNP	C	T	C	AGBL1	c.C861T	p.P287P
XH_P38	15	86806029	86806029	Silent	SNP	C	T	C	AGBL1	c.C990T	p.D330D
XH_P38	15	88476365	88476365	Silent	SNP	G	A	G	NTRK3	c.C1473T	p.A491A
XH_P38	15	89169614	89169614	Silent	SNP	A	G	A	AEN	c.A174G	p.E58E
XH_P38	15	89421249	89421249	Silent	SNP	G	A	G	HAPLN3	c.C1035T	p.P345P
XH_P38	15	89694986	89694986	Silent	SNP	G	A	G	ABHD2	c.G273A	p.S91S
XH_P38	15	89760391	89760391	Silent	SNP	T	G	T	RLBP1	c.A306C	p.A102A
XH_P38	15	90168108	90168108	Missense_Mutation	SNP	C	T	C	TICRR	c.C4564T	p.R1522C
XH_P38	15	90172234	90172234	Missense_Mutation	SNP	C	T	C	KIF7	c.G3637A	p.G1213S
XH_P38	15	90176073	90176073	Missense_Mutation	SNP	C	A	C	KIF7	c.G2873T	p.S958I
XH_P38	15	90176432	90176432	Silent	SNP	T	G	T	KIF7	c.A2658C	p.A886A
XH_P38	15	90246336	90246336	Silent	SNP	A	G	A	WDR93	c.A459G	p.L153L
XH_P38	15	90293776	90293776	Silent	SNP	A	C	A	MESP1	c.T687G	p.P229P
XH_P38	15	90628537	90628537	Silent	SNP	G	A	G	IDH2	c.C660T	p.T220T
XH_P38	15	90768320	90768320	Silent	SNP	C	T	C	SEMA4B	c.C901T	p.L301L
XH_P38	15	90902172	90902172	Missense_Mutation	SNP	C	T	C	ZNF774	c.C194T	p.P65L
XH_P38	15	91424255	91424255	Missense_Mutation	SNP	A	G	A	FURIN	c.A1777G	p.S593G
XH_P38	15	92459385	92459385	Missense_Mutation	SNP	G	A	G	SLCO3A1	c.G343A	p.V115I
XH_P38	15	93588289	93588289	Missense_Mutation	SNP	G	A	G	RGMA	c.C1244T	p.A415V
XH_P38	15	97327393	97327393	Nonsense_Mutation	SNP	C	T	C	SPATA8	c.C100T	p.R34X
XH_P38	15	100252805	100252805	Silent	SNP	G	T	G	MEF2A	c.G1119T	p.G373G
XH_P38	15	101549194	101549194	Silent	SNP	G	C	G	LRRK1	c.G915C	p.R305R
XH_P38	16	304514	304514	Silent	SNP	C	T	C	FAM234A	c.C102T	p.N34N
XH_P38	16	309998	309998	Missense_Mutation	SNP	C	T	C	FAM234A	c.C416T	p.A139V
XH_P38	16	320759	320759	Missense_Mutation	SNP	C	T	C	RGS11	c.G499A	p.V167M
XH_P38	16	324052	324052	Silent	SNP	A	G	A	RGS11	c.T387C	p.D129D
XH_P38	16	325290	325290	Silent	SNP	C	G	C	RGS11	c.G204C	p.S68S
XH_P38	16	334580	334580	Silent	SNP	G	C	G	PDIA2	c.G393C	p.P131P
XH_P38	16	419154	419154	Silent	SNP	G	A	G	MRPL28	c.C355T	p.L119L
XH_P38	16	420140	420140	Missense_Mutation	SNP	G	A	G	MRPL28	c.C797T	p.H27Y
XH_P38	16	718232	718232	Silent	SNP	C	T	C	RHOT2	c.C33T	p.G11G
XH_P38	16	726716	726716	Silent	SNP	C	T	C	RHBDL1	c.C441T	p.N147N
XH_P38	16	732188	732188	Silent	SNP	G	A	G	STUB1	c.G477A	p.L159L
XH_P38	16	737269	737269	Silent	SNP	C	T	C	WDR24	c.G807A	p.T269T
XH_P38	16	765861	765861	Missense_Mutation	SNP	G	A	G	METRNL	c.G382A	p.A128T
XH_P38	16	813650	813650	Silent	SNP	G	A	G	MSLN	c.G138A	p.A46A
XH_P38	16	839084	839084	Missense_Mutation	SNP	A	C	A	CHTF18	c.A245C	p.Q82P
XH_P38	16	842450	842450	Silent	SNP	C	T	C	CHTF18	c.C1338T	p.N446N
XH_P38	16	847743	847743	Missense_Mutation	SNP	C	T	C	CHTF18	c.C2783T	p.P928L
XH_P38	16	855717	855717	Missense_Mutation	SNP	C	G	C	PRR25	c.C275G	p.T92S
XH_P38	16	929711	929711	Silent	SNP	C	T	C	LMF1	c.G756A	p.A252A
XH_P38	16	1004605	1004605	Silent	SNP	A	G	A	LMF1	c.T255C	p.L85L
XH_P38	16	1034954	1034954	Silent	SNP	T	C	T	SOX8	c.T909C	p.Y303Y
XH_P38	16	1143567	1143567	Silent	SNP	G	A	G	C1QTNF8	c.C693T	p.Y231Y
XH_P38	16	1252259	1252259	Silent	SNP	A	G	A	CACNA1H	c.A1809G	p.R603R
XH_P38	16	1254369	1254369	Missense_Mutation	SNP	C	T	C	CACNA1H	c.C2362T	p.R788C
XH_P38	16	1488646	1488646	Silent	SNP	A	G	A	CCDC154	c.T999C	p.R333R
XH_P38	16	1524850	1524850	Silent	SNP	A	G	A	CLCN7	c.T126C	p.P42P
XH_P38	16	1555589	1555589	Missense_Mutation	SNP	A	G	A	TELO2	c.A2021G	p.Q674R
XH_P38	16	1559838	1559838	Silent	SNP	T	C	T	TELO2	c.T2415C	p.A805A
XH_P38	16	1574863	1574863	Silent	SNP	G	A	G	IFT140	c.C2919T	p.A973A
XH_P38	16	1814440	1814440	Missense_Mutation	SNP	A	G	A	MAPK8IP3	c.A2239G	p.T747A
XH_P38	16	1841033	1841033	Silent	SNP	G	A	G	IGFALS	c.C1500T	p.Y500Y
XH_P38	16	1842386	1842386	Silent	SNP	C	T	C	IGFALS	c.G147A	p.A49A
XH_P38	16	1877494	1877494	Silent	SNP	T	C	T	FAHD1	c.T264C	p.A88A
XH_P38	16	1877558	1877558	Missense_Mutation	SNP	G	A	G	FAHD1	c.G328A	p.D110N
XH_P38	16	1995898	1995898	Missense_Mutation	SNP	C	T	C	RPL3L	c.G985A	p.D329N
XH_P38	16	2048796	2048796	Silent	SNP	C	T	C	ZNF598	c.G2268A	p.R756R
XH_P38	16	2049728	2049728	Missense_Mutation	SNP	C	T	C	ZNF598	c.G1822A	p.A608T
XH_P38	16	2050192	2050192	Missense_Mutation	SNP	G	T	G	ZNF598	c.C1358A	p.S453Y
XH_P38	16	2160494	2160494	Silent	SNP	C	T	C	PKD1	c.G4674A	p.T1558T
XH_P38	16	2367336	2367336	Silent	SNP	G	A	G	ABCA3	c.C1059T	p.F353F
XH_P38	16	2812647	2812647	Silent	SNP	C	T	C	SRRM2	c.C2118T	p.S706S
XH_P38	16	3119020	3119020	Silent	SNP	A	G	A	IL32	c.A204G	p.R68R
XH_P38	16	3140616	3140616	Silent	SNP	T	C	T	ZSCAN10	c.A408G	p.E136E
XH_P38	16	3191339	3191339	Silent	SNP	C	G	C	ZNF213	c.C1371G	p.P457P
XH_P38	16	3297073	3297073	Silent	SNP	A	G	A	MEFV	c.T897C	p.D299D
XH_P38	16	3299749	3299749	Silent	SNP	G	A	G	MEFV	c.C309T	p.R103R
XH_P38	16	3613126	3613126	Silent	SNP	C	T	C	NLRC3	c.G1812A	p.L604L
XH_P38	16	3614575	3614575	Silent	SNP	G	A	G	NLRC3	c.C363T	p.T121T
XH_P38	16	3639139	3639139	Silent	SNP	A	G	A	SLX4	c.T4500C	p.N1500N
XH_P38	16	3639977	3639977	Missense_Mutation	SNP	G	A	G	SLX4	c.C3662T	p.A1221V
XH_P38	16	3707023	3707023	Missense_Mutation	SNP	C	G	C	DNASE1	c.C460G	p.P154A
XH_P38	16	3778337	3778337	Silent	SNP	G	A	G	CREBBP	c.C6597T	p.P2199P
XH_P38	16	3820667	3820667	Silent	SNP	C	T	C	CREBBP	c.G2670A	p.P890P
XH_P38	16	4016943	4016943	Silent	SNP	A	G	A	ADCY9	c.T2895C	p.S965S
XH_P38	16	4511926	4511926	Missense_Mutation	SNP	G	A	G	NMRAL1	c.C755T	p.P252L
XH_P38	16	4743793	4743793	Silent	SNP	G	A	G	NUDT16L1	c.G66A	p.P22P
XH_P38	16	4787935	4787935	Missense_Mutation	SNP	G	C	G	C16orf71	c.G264C	p.E88D
XH_P38	16	4935185	4935185	Silent	SNP	C	T	C	PPL	c.G3471A	p.K1157K
XH_P38	16	8953081	8953081	Silent	SNP	C	G	C	CARHSP1	c.G105C	p.R35R
XH_P38	16	10837913	10837913	Missense_Mutation	SNP	C	G	C	NUBP1	c.C115G	p.P39A
XH_P38	16	11056378	11056378	Silent	SNP	C	T	C	CLEC16A	c.C276T	p.Y92Y
XH_P38	16	15815351	15815351	Silent	SNP	G	A	G	MYH11	c.C4506T	p.L1502L

XH_P38	16	16263663	16263663	Silent	SNP	G	A	G	ABCC6	c.C2835T	p.P945P
XH_P38	16	17228363	17228363	Missense_Mutation	SNP	G	A	G	XYLT1	c.C1994T	p.T665M
XH_P38	16	17232233	17232233	Silent	SNP	C	T	C	XYLT1	c.G1743A	p.P581P
XH_P38	16	19079037	19079037	Silent	SNP	G	A	G	COQ7	c.G51A	p.P17P
XH_P38	16	20360101	20360101	Silent	SNP	G	A	G	UMOD	c.C522T	p.C174C
XH_P38	16	20441053	20441053	Missense_Mutation	SNP	C	G	C	ACSM5	c.C1055G	p.P352R
XH_P38	16	20635418	20635418	Silent	SNP	C	T	C	ACSM1	c.G1647A	p.K549K
XH_P38	16	20636814	20636814	Silent	SNP	G	A	G	ACSM1	c.C1458T	p.S486S
XH_P38	16	20810067	20810067	Missense_Mutation	SNP	T	C	T	ERI2	c.A1055G	p.Y352C
XH_P38	16	20873767	20873767	Silent	SNP	T	G	T	DCUN1D3	c.A94C	p.R32R
XH_P38	16	21008690	21008690	Silent	SNP	T	C	T	DNAH3	c.A6378G	p.K2126K
XH_P38	16	23464226	23464226	Silent	SNP	G	A	G	COG7	c.C90T	p.S30S
XH_P38	16	23717689	23717689	Missense_Mutation	SNP	C	T	C	ERN2	c.G551A	p.R184H
XH_P38	16	27374400	27374400	Missense_Mutation	SNP	A	G	A	IL4R	c.A1727G	p.Q576R
XH_P38	16	27974487	27974487	Silent	SNP	T	C	T	GSG1L	c.A387G	p.A129A
XH_P38	16	28123226	28123226	Silent	SNP	G	A	G	XPO6	c.C2253T	p.H751H
XH_P38	16	28488943	28488943	Missense_Mutation	SNP	T	C	T	CLN3	c.A911G	p.H304R
XH_P38	16	28506872	28506872	Silent	SNP	A	G	A	APOBR	c.A510G	p.E170E
XH_P38	16	28508447	28508447	Silent	SNP	A	G	A	APOBR	c.A2085G	p.A695A
XH_P38	16	28513403	28513403	Missense_Mutation	SNP	A	G	A	IL27	c.T356C	p.L119P
XH_P38	16	28603655	28603655	Missense_Mutation	SNP	T	G	T	SULT1A2	c.A704C	p.N235T
XH_P38	16	28883241	28883241	Missense_Mutation	SNP	A	G	A	SH2B1	c.A442G	p.T148A
XH_P38	16	28885108	28885108	Silent	SNP	C	G	C	SH2B1	c.C2238G	p.P746P
XH_P38	16	28898793	28898793	Silent	SNP	T	C	T	ATP2A1	c.T303C	p.T101T
XH_P38	16	28925721	28925721	Missense_Mutation	SNP	C	T	C	RABEP2	c.G730A	p.G244S
XH_P38	16	30594109	30594109	Missense_Mutation	SNP	G	T	G	ZNF785	c.C990A	p.H330Q
XH_P38	16	30724960	30724960	Missense_Mutation	SNP	C	G	C	SRCAP	c.C2421G	p.F807L
XH_P38	16	30794289	30794289	Missense_Mutation	SNP	C	T	C	ZNF629	c.G1360A	p.G454S
XH_P38	16	31341863	31341863	Missense_Mutation	SNP	G	C	G	ITGAM	c.G3213C	p.E1071D
XH_P38	16	31483546	31483546	Splice_Site	SNP	T	A	T	TGFB111	.	.
XH_P38	16	50188027	50188027	Silent	SNP	C	T	C	PAPD5	c.C450T	p.N150N
XH_P38	16	50733585	50733585	Missense_Mutation	SNP	G	A	G	NOD2	c.G179A	p.R60H
XH_P38	16	50745929	50745929	Missense_Mutation	SNP	C	T	C	NOD2	c.C2026T	p.R676C
XH_P38	16	53262964	53262964	Silent	SNP	C	T	C	CHD9	c.C2238T	p.I746I
XH_P38	16	53504721	53504721	Silent	SNP	T	C	T	RBL2	c.T2590C	p.L864L
XH_P38	16	55734106	55734106	Missense_Mutation	SNP	T	C	T	SLC6A2	c.T1331C	p.I444T
XH_P38	16	56368689	56368689	Silent	SNP	C	T	C	GNAO1	c.C513T	p.T171T
XH_P38	16	56701294	56701294	Splice_Site	SNP	T	A	T	MT1G	.	.
XH_P38	16	56839439	56839439	Silent	SNP	C	T	C	NUP93	c.C15T	p.Y5Y
XH_P38	16	57068106	57068106	Missense_Mutation	SNP	A	G	A	NLRC5	c.A2570G	p.H857R
XH_P38	16	57068107	57068107	Silent	SNP	C	T	C	NLRC5	c.C2571T	p.H857H
XH_P38	16	57180158	57180158	Silent	SNP	C	A	C	CPNE2	c.C1464A	p.R488R
XH_P38	16	57760824	57760824	Silent	SNP	C	T	C	DRC7	c.C1860T	p.S620S
XH_P38	16	57762401	57762401	Missense_Mutation	SNP	T	C	T	DRC7	c.T2101C	p.C701R
XH_P38	16	57950057	57950057	Silent	SNP	G	A	G	CNGB1	c.C2175T	p.N725N
XH_P38	16	57996932	57996932	Silent	SNP	G	A	G	CNGB1	c.C327T	p.G109G
XH_P38	16	58030741	58030741	Missense_Mutation	SNP	G	A	G	ZNF319	c.C1429T	p.R477C
XH_P38	16	58318604	58318604	Missense_Mutation	SNP	T	C	T	PRSS54	c.A247G	p.S83G
XH_P38	16	58327646	58327646	Silent	SNP	A	G	A	PRSS54	c.T75C	p.Y25Y
XH_P38	16	58542901	58542901	Silent	SNP	G	A	G	NDRG4	c.G819A	p.T273T
XH_P38	16	58713798	58713798	Missense_Mutation	SNP	G	A	G	SLC38A7	c.C233T	p.T78I
XH_P38	16	60392994	60392994	Missense_Mutation	SNP	T	G	T	LOC729159	c.A613C	p.T205P
XH_P38	16	60393058	60393058	Silent	SNP	C	T	C	LOC729159	c.G549A	p.A183A
XH_P38	16	60393404	60393404	Missense_Mutation	SNP	T	A	T	LOC729159	c.A203T	p.D68V
XH_P38	16	65022234	65022234	Missense_Mutation	SNP	C	T	C	CDH11	c.G447A	p.M149I
XH_P38	16	66638804	66638804	Silent	SNP	G	A	G	CMTM3	c.G96A	p.P32P
XH_P38	16	67911517	67911517	Silent	SNP	T	C	T	EDC4	c.T747C	p.C249C
XH_P38	16	68026486	68026486	Missense_Mutation	SNP	T	G	T	DPEP2	c.A317C	p.D106A
XH_P38	16	68732049	68732049	Missense_Mutation	SNP	A	C	A	CDH3	c.A2334C	p.R778S
XH_P38	16	68857441	68857441	Silent	SNP	T	C	T	CDH1	c.T1893C	p.A631A
XH_P38	16	70211218	70211218	Silent	SNP	G	A	G	CLEC18C	c.G291A	p.A97A
XH_P38	16	70512510	70512510	Missense_Mutation	SNP	C	A	C	FUK	c.C2886A	p.S962R
XH_P38	16	71712786	71712786	Silent	SNP	A	G	A	PHLP2	c.T1140C	p.F380F
XH_P38	16	72993831	72993831	Missense_Mutation	SNP	A	C	A	ZFH3	c.T214G	p.S72A
XH_P38	16	74447025	74447025	Missense_Mutation	SNP	T	C	T	CLEC18B	c.A586G	p.I196V
XH_P38	16	75258617	75258617	Missense_Mutation	SNP	C	T	C	CTR81	c.C511T	p.P171S
XH_P38	16	81010073	81010073	Missense_Mutation	SNP	C	T	C	CMC2	c.G157A	p.V53I
XH_P38	16	81077016	81077016	Missense_Mutation	SNP	A	G	A	ATMIN	c.A445G	p.K149E
XH_P38	16	81087679	81087679	Missense_Mutation	SNP	C	G	C	C16orf46	c.G1164C	p.K388N
XH_P38	16	81249927	81249927	Missense_Mutation	SNP	C	T	C	PKD1L2	c.G386A	p.G129D
XH_P38	16	81971403	81971403	Silent	SNP	T	C	T	PLCG2	c.T3093C	p.N1031N
XH_P38	16	84012104	84012104	Missense_Mutation	SNP	T	C	T	NECAB2	c.T59C	p.L20S
XH_P38	16	84229436	84229436	Silent	SNP	G	A	G	ADAD2	c.G1068A	p.S356S
XH_P38	16	84229580	84229580	Silent	SNP	C	T	C	ADAD2	c.C1212T	p.A404A
XH_P38	16	84229883	84229883	Missense_Mutation	SNP	C	T	C	ADAD2	c.C1433T	p.T478I
XH_P38	16	84256619	84256619	Missense_Mutation	SNP	C	T	C	KCNG4	c.G764A	p.C255Y
XH_P38	16	84270381	84270381	Silent	SNP	G	A	G	KCNG4	c.C711T	p.S237S
XH_P38	16	84476200	84476200	Missense_Mutation	SNP	A	T	A	ATP2C2	c.A943T	p.M315L
XH_P38	16	84520292	84520292	Silent	SNP	C	T	C	TLDC1	c.G903A	p.K301K
XH_P38	16	87446368	87446368	Silent	SNP	C	T	C	ZCCHC14	c.G1548A	p.P516P
XH_P38	16	87723838	87723838	Silent	SNP	T	C	T	JPH3	c.T1872C	p.H624H
XH_P38	16	88747995	88747995	Missense_Mutation	SNP	G	C	G	SNAI3	c.C204G	p.I68M
XH_P38	16	88779032	88779032	Silent	SNP	G	C	G	CTU2	c.G195C	p.V65V
XH_P38	16	88803124	88803124	Missense_Mutation	SNP	T	C	T	PIEZO1	c.A1219G	p.R407G
XH_P38	16	88870967	88870967	Silent	SNP	T	C	T	CDT1	c.T243C	p.S81S
XH_P38	16	88876190	88876190	Silent	SNP	G	A	G	APRT	c.C459T	p.C153C
XH_P38	16	89245890	89245890	Missense_Mutation	SNP	G	T	G	CDH15	c.G109T	p.A37S
XH_P38	16	89256695	89256695	Silent	SNP	G	A	G	CDH15	c.G1023A	p.S341S
XH_P38	16	89258747	89258747	Missense_Mutation	SNP	A	C	A	CDH15	c.A1750C	p.K584Q
XH_P38	16	89347486	89347486	Missense_Mutation	SNP	C	T	C	ANKRD11	c.G5464A	p.D1822N
XH_P38	16	89349519	89349519	Missense_Mutation	SNP	G	A	G	ANKRD11	c.C3431T	p.P1144L
XH_P38	16	89350038	89350038	Missense_Mutation	SNP	G	A	G	ANKRD11	c.C2912T	p.A971L
XH_P38	16	89644001	89644001	Missense_Mutation	SNP	T	C	T	CPNE7	c.T229C	p.A717V
XH_P38	16	89789898	89789898	Missense_Mutation	SNP	T	C	T	ZNF276	c.T787C	p.W263R
XH_P38	16	89986154	89986154	Missense_Mutation	SNP	G	A	G	MC1R	c.G488A	p.R163Q
XH_P38	16	89986545	89986545	Silent	SNP	C	T	C	MC1R	c.C879T	p.I293I
XH_P38	16	90037828	90037828	Missense_Mutation	SNP	G	A	G	CENPBD1	c.C503T	p.T168I
XH_P38	16	90086206	90086206	Silent	SNP	C	T	C	DBNDD1	c.G321A	p.P107P

XH_P38	17	617869	617869	Silent	SNP	G	A	G	VP553	c.C81T	p.I271
XH_P38	17	1494567	1494567	Silent	SNP	G	A	G	SLC43A2	c.C516T	p.A172A
XH_P38	17	1611433	1611433	Silent	SNP	A	G	A	TLC02	c.T426C	p.S142S
XH_P38	17	1674429	1674429	Silent	SNP	T	C	T	SERPINF1	c.T390C	p.T130T
XH_P38	17	3324810	3324810	Missense_Mutation	SNP	A	G	A	OR3A3	c.A949G	p.K317E
XH_P38	17	3422073	3422073	Missense_Mutation	SNP	C	T	C	TRPV3	c.G1882A	p.A628T
XH_P38	17	3476990	3476990	Silent	SNP	G	A	G	TRPV1	c.C2040T	p.I680I
XH_P38	17	3654980	3654980	Silent	SNP	A	G	A	ITGAE	c.T1857C	p.N619N
XH_P38	17	3657175	3657175	Missense_Mutation	SNP	T	C	T	ITGAE	c.A1429G	p.I477V
XH_P38	17	3828702	3828702	Silent	SNP	T	C	T	ATP2A3	c.A3102G	p.R1034R
XH_P38	17	4337412	4337412	Silent	SNP	C	G	C	SPNS3	c.C150G	p.V50V
XH_P38	17	4391132	4391132	Silent	SNP	C	T	C	SPNS3	c.C1101T	p.N367N
XH_P38	17	4575596	4575598	In_Frame_Del	DEL	TCC	-	TCC	PELP1	c.2838_2840del	p.946_947del
XH_P38	17	4641755	4641755	Silent	SNP	C	T	C	CXCL16	c.G306A	p.G102G
XH_P38	17	4798399	4798399	Missense_Mutation	SNP	G	A	G	MINK1	c.G2836A	p.D946N
XH_P38	17	4936972	4936972	Missense_Mutation	SNP	G	A	G	SLC52A1	c.C812T	p.A217V
XH_P38	17	4937351	4937351	Silent	SNP	G	T	G	SLC52A1	c.C433A	p.R145R
XH_P38	17	5037281	5037281	Missense_Mutation	SNP	T	C	T	USP6	c.T484C	p.Y162H
XH_P38	17	5044794	5044794	Missense_Mutation	SNP	G	A	G	USP6	c.G1573A	p.V525I
XH_P38	17	5058808	5058808	Missense_Mutation	SNP	G	A	G	USP6	c.G2735A	p.R912Q
XH_P38	17	5404262	5404262	Silent	SNP	G	C	G	LOC728392	c.C156G	p.L5L
XH_P38	17	6930139	6930139	Silent	SNP	C	T	C	BCL6B	c.C1170T	p.G390G
XH_P38	17	6941625	6941625	Silent	SNP	C	T	C	SLC16A13	c.C498T	p.Y166Y
XH_P38	17	6945087	6945087	Missense_Mutation	SNP	G	T	G	SLC16A11	c.C1327A	p.P443T
XH_P38	17	6945483	6945483	Missense_Mutation	SNP	C	T	C	SLC16A11	c.G1018A	p.G340S
XH_P38	17	6945940	6945940	Silent	SNP	A	G	A	SLC16A11	c.T561C	p.L187L
XH_P38	17	7080316	7080316	Silent	SNP	C	T	C	ASGR1	c.G150A	p.K50K
XH_P38	17	7131010	7131010	Missense_Mutation	SNP	T	C	T	DVL2	c.A1195G	p.M399V
XH_P38	17	7154582	7154582	Missense_Mutation	SNP	T	C	T	CTDNEP1	c.A34G	p.T12A
XH_P38	17	7197633	7197633	Missense_Mutation	SNP	A	G	A	YBX2	c.T187C	p.S63P
XH_P38	17	7230845	7230845	Missense_Mutation	SNP	G	T	G	NEURL4	c.C641A	p.P214H
XH_P38	17	7287538	7287538	Missense_Mutation	SNP	G	A	G	TNK1	c.G832A	p.V278I
XH_P38	17	7293715	7293715	Missense_Mutation	SNP	C	T	C	PLSCR3	c.G877A	p.V293I
XH_P38	17	7318920	7318920	Silent	SNP	C	T	C	NLGN2	c.C1128T	p.Y376Y
XH_P38	17	7320581	7320581	Silent	SNP	C	T	C	NLGN2	c.C1971T	p.P657P
XH_P38	17	7366348	7366348	Missense_Mutation	SNP	A	C	A	ZBTB4	c.T1953G	p.D651E
XH_P38	17	7690345	7690345	Silent	SNP	C	T	C	DNAH2	c.C6597T	p.P2199P
XH_P38	17	7910025	7910025	Silent	SNP	C	T	C	GUCY2D	c.C1371T	p.C457C
XH_P38	17	7942901	7942901	Silent	SNP	C	G	C	ALOX15B	c.C345G	p.T115T
XH_P38	17	7951149	7951149	Silent	SNP	C	T	C	ALOX15B	c.C1545T	p.G515G
XH_P38	17	7951878	7951878	Missense_Mutation	SNP	A	G	A	ALOX15B	c.A1804G	p.I602V
XH_P38	17	7999957	7999957	Silent	SNP	G	A	G	ALOXE3	c.C2520T	p.S840S
XH_P38	17	8026364	8026364	Silent	SNP	C	T	C	HE57	c.G123A	p.E41E
XH_P38	17	8046772	8046772	Missense_Mutation	SNP	C	G	C	PER1	c.G2884C	p.A962P
XH_P38	17	8048283	8048283	Silent	SNP	G	A	G	PER1	c.C2247T	p.G749G
XH_P38	17	8053085	8053085	Silent	SNP	T	G	T	PER1	c.A639C	p.T213T
XH_P38	17	8092694	8092694	Silent	SNP	T	G	T	BORCS6	c.A765C	p.P255P
XH_P38	17	8132763	8132763	Missense_Mutation	SNP	T	C	T	CTC1	c.A3013G	p.I1005V
XH_P38	17	8161149	8161149	Missense_Mutation	SNP	C	T	C	PFAS	c.C1100T	p.P367L
XH_P38	17	8167600	8167600	Missense_Mutation	SNP	T	C	T	PFAS	c.T1862C	p.L621P
XH_P38	17	8168224	8168224	Silent	SNP	T	C	T	PFAS	c.T2061C	p.S687S
XH_P38	17	8700982	8700982	Missense_Mutation	SNP	C	T	C	MFS06L	c.G1457A	p.R486H
XH_P38	17	8926418	8926418	Missense_Mutation	SNP	C	T	C	NTN1	c.C728T	p.T243M
XH_P38	17	9549381	9549381	Silent	SNP	C	T	C	USP43	c.C432T	p.T144T
XH_P38	17	9632247	9632247	Silent	SNP	A	G	A	USP43	c.A3297G	p.R1099R
XH_P38	17	11671913	11671913	Missense_Mutation	SNP	G	G	G	DNAH9	c.G7314C	p.Q2438H
XH_P38	17	11757556	11757556	Silent	SNP	C	G	C	DNAH9	c.C9744G	p.P3248P
XH_P38	17	11786951	11786951	Silent	SNP	T	C	T	DNAH9	c.T10855S	p.L3619L
XH_P38	17	12666520	12666520	Missense_Mutation	SNP	C	A	A	MYOCD	c.C2376A	p.S792R
XH_P38	17	13504255	13504255	Silent	SNP	C	T	C	HS3ST3A1	c.G192A	p.G64G
XH_P38	17	13980350	13980350	Missense_Mutation	SNP	G	A	G	COX10	c.G476A	p.R159Q
XH_P38	17	15234563	15234563	Nonsense_Mutation	SNP	G	A	G	TEKT3	c.C340T	p.R114X
XH_P38	17	16321032	16321032	Missense_Mutation	SNP	G	C	G	TRPV2	c.G50C	p.G17A
XH_P38	17	16346932	16346932	Silent	SNP	G	T	G	LRRC75A	c.C1005A	p.G335G
XH_P38	17	16594011	16594011	Silent	SNP	C	T	C	CCDC144A	c.C297T	p.I99I
XH_P38	17	17250159	17250159	Silent	SNP	C	T	C	NTSM	c.C585T	p.T195T
XH_P38	17	18167397	18167397	Missense_Mutation	SNP	G	T	G	MIEF2	c.G610T	p.A204S
XH_P38	17	18167684	18167684	Missense_Mutation	SNP	G	A	G	MIEF2	c.G971A	p.G324E
XH_P38	17	18284262	18284262	Missense_Mutation	SNP	G	A	G	EVPLL	c.G11A	p.S4N
XH_P38	17	18881572	18881572	Silent	SNP	C	T	C	FAM83G	c.G1407A	p.R469R
XH_P38	17	19318460	19318460	Silent	SNP	C	T	C	RNF112	c.C1236T	p.R412R
XH_P38	17	19608773	19608773	Silent	SNP	G	A	G	SLC47A2	c.C885T	p.Y295Y
XH_P38	17	20798992	20798992	Silent	SNP	C	T	C	CCDC144NL	c.G342A	p.K114K
XH_P38	17	20799119	20799119	Missense_Mutation	SNP	A	G	A	CCDC144NL	c.T215C	p.L72P
XH_P38	17	21207844	21207844	Silent	SNP	C	T	C	MAP2K3	c.C588T	p.A196A
XH_P38	17	25909850	25909850	Silent	SNP	G	T	G	KSR1	c.G288T	p.L96L
XH_P38	17	26093543	26093543	Missense_Mutation	SNP	T	C	T	NOS2	c.A2239G	p.T747A
XH_P38	17	27052358	27052358	Silent	SNP	C	T	C	TLCD1	c.G183A	p.T61T
XH_P38	17	27065211	27065211	Silent	SNP	T	C	T	NEK8	c.T1170C	p.G390G
XH_P38	17	27075423	27075423	Silent	SNP	C	T	C	TRAF4	c.C606T	p.F202F
XH_P38	17	27085564	27085564	Silent	SNP	A	G	A	FAM222B	c.T1413C	p.L471L
XH_P38	17	29508775	29508775	Silent	SNP	G	A	G	NF1	c.G702A	p.L234L
XH_P38	17	29646032	29646032	Silent	SNP	G	A	G	EVIA2	c.C69T	p.S23S
XH_P38	17	29855661	29855661	Silent	SNP	G	A	G	RAB11FIP4	c.G738A	p.E246E
XH_P38	17	30533970	30533970	Silent	SNP	A	G	A	RHOT1	c.A1458G	p.E486E
XH_P38	17	30625205	30625205	Missense_Mutation	SNP	G	A	G	RHBDL3	c.G739A	p.V247M
XH_P38	17	31266554	31266554	Missense_Mutation	SNP	G	A	G	TMEM98	c.G473A	p.R158Q
XH_P38	17	32963043	32963043	Silent	SNP	G	A	G	TMEM132E	c.G1995A	p.T665T
XH_P38	17	33520964	33520964	Silent	SNP	C	T	C	SLC35G3	c.G363A	p.A121A
XH_P38	17	33884804	33884804	Missense_Mutation	SNP	T	C	T	SLFN14	c.A278G	p.Q93R
XH_P38	17	34072898	34072898	Missense_Mutation	SNP	C	T	C	GAS2L2	c.G1618A	p.A540T
XH_P38	17	34340284	34340284	Missense_Mutation	SNP	C	T	C	CCL23	c.G367A	p.V123M
XH_P38	17	34416537	34416537	Silent	SNP	G	A	G	CCL3	c.C180T	p.P60P
XH_P38	17	34432663	34432663	Silent	SNP	A	G	A	CCL4	c.A237G	p.E79E
XH_P38	17	34432664	34432664	Missense_Mutation	SNP	T	A	T	CCL4	c.C238A	p.S80T
XH_P38	17	34854280	34854280	Missense_Mutation	SNP	G	A	G	MYO19	c.C1987T	p.L663F
XH_P38	17	34958598	34958598	Missense_Mutation	SNP	G	C	G	MRM1	c.G359C	p.C120S
XH_P38	17	35902225	35902225	Silent	SNP	C	G	C	SYNRG	c.G2433C	p.P811P

XH_P38	17	35937637	35937637	Missense_Mutation	SNP	T	C	T	SYNRG	c.A664G	p.T222A
XH_P38	17	36047350	36047350	Missense_Mutation	SNP	G	A	G	HNF1B	c.C1307T	p.A436V
XH_P38	17	36490940	36490940	Missense_Mutation	SNP	G	A	G	GPR179	c.C1621T	p.R541C
XH_P38	17	36614489	36614489	Silent	SNP	C	T	C	ARHGAP23	c.C207T	p.A69A
XH_P38	17	37054772	37054772	Silent	SNP	C	T	C	LASP1	c.C189T	p.N63N
XH_P38	17	37070658	37070658	Silent	SNP	A	G	A	LASP1	c.A270G	p.S90S
XH_P38	17	37334243	37334243	Silent	SNP	G	A	G	CACNB1	c.C1140T	p.C380C
XH_P38	17	38024839	38024839	Silent	SNP	C	T	C	ZPBP2	c.C90T	p.G30G
XH_P38	17	38457151	38457151	Missense_Mutation	SNP	G	A	G	CDC6	c.G1321A	p.V441I
XH_P38	17	39079288	39079288	Missense_Mutation	SNP	C	T	C	KRT23	c.G811A	p.G271R
XH_P38	17	39140221	39140221	Missense_Mutation	SNP	C	T	C	KRT40	c.G305A	p.S102N
XH_P38	17	39140417	39140417	Missense_Mutation	SNP	T	C	T	KRT40	c.A109G	p.T37A
XH_P38	17	39186031	39186031	Silent	SNP	C	T	C	KRTAP1-4	c.G300A	p.P100P
XH_P38	17	39190954	39190954	In_Frame_Ins	INS	-	5GCTGGCAGCA	-	KRTAP1-3	ACCAGCTGCTG	delinsCETSCCOPSCC
XH_P38	17	39274069	39274069	Missense_Mutation	SNP	G	C	G	KRTAP4-11	c.C499G	p.R167G
XH_P38	17	39316880	39316880	Missense_Mutation	SNP	G	A	G	KRTAP4-4	c.C64T	p.R22C
XH_P38	17	39346139	39346139	Missense_Mutation	SNP	A	G	A	KRTAP9-1	c.A1G	p.M1V
XH_P38	17	39619193	39619193	Missense_Mutation	SNP	C	T	C	KRT32	c.G1106A	p.R369Q
XH_P38	17	39623363	39623363	Missense_Mutation	SNP	T	C	T	KRT32	c.A215G	p.Q72R
XH_P38	17	39633349	39633349	Missense_Mutation	SNP	G	C	G	KRT35	c.C1327G	p.P443A
XH_P38	17	39637244	39637244	Missense_Mutation	SNP	A	G	A	KRT35	c.T106C	p.S36P
XH_P38	17	39643646	39643646	Missense_Mutation	SNP	G	A	G	KRT36	c.C944T	p.T315M
XH_P38	17	39671724	39671724	Missense_Mutation	SNP	T	C	T	KRT15	c.A1247G	p.K416R
XH_P38	17	39967442	39967442	Missense_Mutation	SNP	T	C	T	P3H4	c.A557G	p.Q186R
XH_P38	17	40274873	40274873	Missense_Mutation	SNP	A	C	A	HSPB9	c.A5C	p.Q2P
XH_P38	17	40459737	40459737	Silent	SNP	C	T	C	STAT5A	c.C1812T	p.D604D
XH_P38	17	40556985	40556985	Missense_Mutation	SNP	C	T	C	CACVIN1	c.G893A	p.R298H
XH_P38	17	42164885	42164885	Missense_Mutation	SNP	G	C	G	HDAC5	c.C1782G	p.D594E
XH_P38	17	42267949	42267949	Missense_Mutation	SNP	G	A	G	TMUB2	c.G623A	p.R208H
XH_P38	17	42427630	42427630	Silent	SNP	T	C	T	GRN	c.T384C	p.D128D
XH_P38	17	42477189	42477189	Silent	SNP	A	G	A	GPATCH8	c.T2022C	p.D674D
XH_P38	17	45810919	45810919	Missense_Mutation	SNP	C	G	C	TBX21	c.C99G	p.H33Q
XH_P38	17	46801724	46801724	Missense_Mutation	SNP	T	G	T	PRAC2	c.T102G	p.C34W
XH_P38	17	46802008	46802008	Missense_Mutation	SNP	C	G	C	PRAC2	c.C236G	p.T79R
XH_P38	17	46805443	46805443	Silent	SNP	A	G	A	HOXB13	c.T513C	p.S171S
XH_P38	17	46894377	46894377	Missense_Mutation	SNP	A	C	A	TTLL6	c.T58G	p.W20G
XH_P38	17	48153093	48153093	Silent	SNP	C	G	C	ITGA3	c.C1668G	p.L556L
XH_P38	17	48174908	48174908	Silent	SNP	C	T	C	PKD2	c.C48T	p.S16S
XH_P38	17	48437456	48437456	Missense_Mutation	SNP	C	G	C	XYLT2	c.C2402G	p.T801R
XH_P38	17	48561852	48561852	Missense_Mutation	SNP	C	T	C	RSAD1	c.C1157T	p.A386V
XH_P38	17	48917333	48917333	Silent	SNP	C	T	C	WFIKN2	c.C405T	p.S135S
XH_P38	17	56540267	56540267	Missense_Mutation	SNP	C	T	C	HSF5	c.G1418A	p.S473N
XH_P38	17	57287454	57287454	Silent	SNP	A	G	A	SMG8	c.A42G	p.A14A
XH_P38	17	57963537	57963537	Missense_Mutation	SNP	A	G	A	TUBD1	c.T227C	p.M76T
XH_P38	17	59485555	59485555	Silent	SNP	C	T	C	TBX2	c.C1827T	p.S609S
XH_P38	17	59533868	59533868	Missense_Mutation	SNP	G	C	G	TBX4	c.G17C	p.G6A
XH_P38	17	59534987	59534987	Silent	SNP	T	G	T	TBX4	c.T276G	p.A92A
XH_P38	17	59560463	59560463	Silent	SNP	C	T	C	TBX4	c.C1224T	p.D408D
XH_P38	17	60769803	60769803	Silent	SNP	A	G	A	MRC2	c.A4431G	p.Q1477Q
XH_P38	17	61771128	61771128	Silent	SNP	C	G	C	MAP3K3	c.C1860G	p.L620L
XH_P38	17	62007498	62007498	Silent	SNP	A	G	A	CD79B	c.T366C	p.C122C
XH_P38	17	62018773	62018773	Silent	SNP	T	C	T	SCN4A	c.A4869G	p.T1623T
XH_P38	17	62121452	62121452	Missense_Mutation	SNP	T	C	T	ERN1	c.A2830G	p.T944A
XH_P38	17	62228250	62228250	Missense_Mutation	SNP	A	G	A	TEX2	c.T3212C	p.L1071S
XH_P38	17	63554586	63554586	Silent	SNP	G	A	G	AXIN2	c.C153T	p.V51V
XH_P38	17	64210757	64210757	Missense_Mutation	SNP	C	A	C	APOH	c.G796T	p.V266L
XH_P38	17	66039350	66039350	Silent	SNP	A	G	A	KPNA2	c.A801G	p.V267V
XH_P38	17	66596769	66596769	Silent	SNP	C	T	C	FAM20A	c.G39A	p.L13L
XH_P38	17	66904001	66904001	Missense_Mutation	SNP	A	C	A	ABCA8	c.T2038G	p.C680G
XH_P38	17	70119808	70119808	Frame_Shift_Del	DEL	C	-	C	SOX9	c.810delC	p.F270fs
XH_P38	17	71192663	71192663	Silent	SNP	G	A	G	COG1	c.G333A	p.Q111Q
XH_P38	17	71197748	71197748	Silent	SNP	G	A	G	COG1	c.G1782A	p.E594E
XH_P38	17	71205854	71205854	Missense_Mutation	SNP	A	G	A	FAM104A	c.T275C	p.I92T
XH_P38	17	71232687	71232687	Missense_Mutation	SNP	T	C	T	C17orf80	c.T1066C	p.F356L
XH_P38	17	71233130	71233130	Silent	SNP	A	G	A	C17orf80	c.A1509G	p.S503S
XH_P38	17	71364601	71364601	Silent	SNP	G	A	G	SDK2	c.C5112T	p.N1704N
XH_P38	17	71412118	71412118	Missense_Mutation	SNP	C	T	C	SDK2	c.G2200A	p.G734R
XH_P38	17	71746796	71746796	Missense_Mutation	SNP	A	G	A	LOC100134391	c.A143G	p.Y48C
XH_P38	17	72306291	72306291	Missense_Mutation	SNP	G	A	G	DNAI2	c.G1447A	p.V483I
XH_P38	17	72346868	72346868	Missense_Mutation	SNP	C	T	C	KIF19	c.C1411T	p.R471W
XH_P38	17	72349067	72349067	Silent	SNP	C	T	C	KIF19	c.C2088T	p.S696S
XH_P38	17	72368550	72368550	Silent	SNP	T	C	T	GPR142	c.T936C	p.N312N
XH_P38	17	72613589	72613589	Missense_Mutation	SNP	T	G	T	CD300E	c.A56C	p.K19T
XH_P38	17	72815981	72815981	Silent	SNP	C	T	C	TMEM104	c.C729T	p.I243I
XH_P38	17	72943126	72943126	Silent	SNP	G	A	G	OTOP3	c.G1122A	p.A374A
XH_P38	17	72956124	72956124	Silent	SNP	G	A	G	HID1	c.C948T	p.A316A
XH_P38	17	73750859	73750859	Silent	SNP	C	G	C	ITGB4	c.C4311G	p.P1437P
XH_P38	17	73831016	73831016	Silent	SNP	G	A	G	UNC13D	c.C1977T	p.T659T
XH_P38	17	73839137	73839137	Silent	SNP	G	A	G	UNC13D	c.C279T	p.P93P
XH_P38	17	74077797	74077797	Nonsense_Mutation	SNP	C	T	C	ZACN	c.C841T	p.Q281X
XH_P38	17	76118767	76118767	Silent	SNP	G	A	G	TMC6	c.C1146T	p.T382T
XH_P38	17	76121031	76121031	Missense_Mutation	SNP	C	T	C	TMC6	c.G572A	p.G191D
XH_P38	17	76230729	76230729	Silent	SNP	T	C	T	TMEM235	c.T246C	p.C82C
XH_P38	17	76435208	76435208	Silent	SNP	G	A	G	DNAH17	c.C11769T	p.D3923D
XH_P38	17	76521134	76521134	Missense_Mutation	SNP	C	T	C	DNAH17	c.G3821A	p.R1274Q
XH_P38	17	77707358	77707358	Silent	SNP	C	T	C	ENPP7	c.C306T	p.T102T
XH_P38	17	77758691	77758691	Silent	SNP	G	A	G	CBX2	c.G1449A	p.P483P
XH_P38	17	77984141	77984141	Silent	SNP	C	T	C	TBC1D16	c.G597A	p.G199G
XH_P38	17	78055758	78055758	Silent	SNP	T	G	T	CCDC40	c.T1890G	p.A630A
XH_P38	17	78071052	78071052	Silent	SNP	T	C	T	CCDC40	c.T3030C	p.D1010D
XH_P38	17	78078709	78078709	Silent	SNP	T	C	T	GAA	c.T324C	p.C108C
XH_P38	17	78082504	78082504	Silent	SNP	G	A	G	GAA	c.G1203A	p.Q401Q
XH_P38	17	78092063	78092063	Silent	SNP	G	A	G	GAA	c.G2553A	p.G851G
XH_P38	17	78171944	78171944	Missense_Mutation	SNP	G	C	G	CARD14	c.G930C	p.R310S
XH_P38	17	78311508	78311508	Silent	SNP	G	A	G	RNF213	c.G4650A	p.A1550A
XH_P38	17	78319380	78319380	Silent	SNP	G	C	G	RNF213	c.G7245C	p.P2415P
XH_P38	17	78327358	78327358	Silent	SNP	G	A	G	RNF213	c.G10470A	p.E3490E
XH_P38	17	78354661	78354661	Silent	SNP	C	T	C	RNF213	c.C13671T	p.H4557H

XH_P38	17	78396004	78396004	Splice_Site	SNP	A	G	A	ENDOV	.	.
XH_P38	17	78820329	78820329	Silent	SNP	C	T	C	RPTOR	c.C1269T	p.G423G
XH_P38	17	79089590	79089590	Missense_Mutation	SNP	A	G	A	BAIAP2	c.A1556G	p.Q519R
XH_P38	17	79166384	79166384	Silent	SNP	C	T	C	CEP131	c.G2331A	p.A777A
XH_P38	17	79170578	79170578	Missense_Mutation	SNP	C	T	C	CEP131	c.G1822A	p.A608T
XH_P38	17	79220016	79220016	Silent	SNP	T	C	T	SLC38A10	c.A2700G	p.A900A
XH_P38	17	79226362	79226362	Silent	SNP	G	A	G	SLC38A10	c.C1578T	p.H526H
XH_P38	17	79632363	79632363	Silent	SNP	C	T	C	OXLD1	c.G312A	p.A104A
XH_P38	17	79637367	79637367	Missense_Mutation	SNP	C	G	C	CCDC137	c.C381G	p.H127Q
XH_P38	17	79639550	79639550	Missense_Mutation	SNP	G	A	G	CCDC137	c.G686A	p.R229Q
XH_P38	17	79662067	79662067	Silent	SNP	A	G	A	HGS	c.A1089G	p.E363E
XH_P38	17	79668135	79668135	Missense_Mutation	SNP	G	T	G	HGS	c.G2197T	p.A733S
XH_P38	17	79671714	79671714	Missense_Mutation	SNP	T	C	T	MRPL12	c.T313C	p.S105P
XH_P38	17	79682558	79682558	Silent	SNP	T	C	T	SLC25A10	c.T264C	p.R88R
XH_P38	17	79687361	79687361	Silent	SNP	C	T	C	SLC25A10	c.C1035T	p.P345P
XH_P38	17	79804369	79804369	Missense_Mutation	SNP	G	A	G	P4HB	c.C992T	p.S331L
XH_P38	17	79899272	79899272	Missense_Mutation	SNP	A	G	A	MYADML2	c.T346C	p.S116P
XH_P38	17	79952700	79952700	Silent	SNP	G	A	G	ASPSCR1	c.G147A	p.E49E
XH_P38	17	79954544	79954544	Missense_Mutation	SNP	T	A	T	ASPSCR1	c.T524A	p.L175Q
XH_P38	17	79974731	79974731	Silent	SNP	T	C	T	ASPSCR1	c.T1305C	p.D435D
XH_P38	17	79994600	79994600	Silent	SNP	C	T	C	DCXR	c.G339A	p.S113S
XH_P38	17	80006957	80006957	Missense_Mutation	SNP	A	C	A	RFNG	c.T864G	p.H288Q
XH_P38	17	80008392	80008392	Silent	SNP	G	T	G	RFNG	c.C459A	p.A153A
XH_P38	17	80012449	80012449	Silent	SNP	G	A	G	GPS1	c.G372A	p.T124T
XH_P38	17	80039481	80039481	Silent	SNP	G	A	G	FASN	c.C6402T	p.I2134I
XH_P38	17	80043739	80043739	Silent	SNP	A	G	A	FASN	c.T3741C	p.A1247A
XH_P38	17	80059596	80059596	Missense_Mutation	SNP	T	C	T	CCDC57	c.A2710G	p.R904G
XH_P38	17	80350331	80350331	Silent	SNP	G	A	G	OGFOD3	c.C903T	p.I301I
XH_P38	17	80395073	80395073	Missense_Mutation	SNP	G	A	G	HEXDC	c.G733A	p.G245S
XH_P38	17	80899281	80899281	Silent	SNP	G	A	G	TBCD	c.G3486A	p.A1162A
XH_P38	18	580609	580609	Silent	SNP	A	G	A	CETN1	c.A201G	p.E67E
XH_P38	18	2656248	2656248	Silent	SNP	G	C	G	SMCHD1	c.G174C	p.A58A
XH_P38	18	2891478	2891478	Silent	SNP	T	C	T	EMILIN2	c.T1353C	p.N451N
XH_P38	18	3215156	3215156	Silent	SNP	C	G	C	MYOM1	c.G66C	p.V22V
XH_P38	18	3215158	3215158	Missense_Mutation	SNP	C	G	C	MYOM1	c.G64C	p.V22L
XH_P38	18	3729175	3729175	Silent	SNP	C	T	C	DLGAP1	c.G645A	p.P215P
XH_P38	18	5443840	5443840	Silent	SNP	G	T	G	EPB41L3	c.C526A	p.R176R
XH_P38	18	7023371	7023371	Silent	SNP	A	G	A	LAMA1	c.T2493C	p.C831C
XH_P38	18	7034508	7034508	Missense_Mutation	SNP	T	G	T	LAMA1	c.A2021C	p.N674T
XH_P38	18	7955213	7955213	Silent	SNP	G	A	G	PTPRM	c.G933A	p.G311G
XH_P38	18	8784612	8784612	Missense_Mutation	SNP	A	G	A	MTCL1	c.A1502G	p.Q501R
XH_P38	18	10696227	10696227	Silent	SNP	C	T	C	PIEZO2	c.G6696A	p.P2232P
XH_P38	18	10758023	10758023	Silent	SNP	G	A	G	PIEZO2	c.C3792T	p.N1264N
XH_P38	18	10787047	10787047	Silent	SNP	G	A	G	PIEZO2	c.C2305T	p.L769L
XH_P38	18	11886563	11886563	Missense_Mutation	SNP	C	G	C	MPPE1	c.G736C	p.A246P
XH_P38	18	12127887	12127887	Silent	SNP	G	A	G	ANKRD62	c.G2703A	p.Q901Q
XH_P38	18	12254956	12254956	Splice_Site	SNP	G	A	G	CIDEA	.	.
XH_P38	18	13826088	13826088	Silent	SNP	C	T	C	MCSR	c.C324T	p.D108D
XH_P38	18	14542648	14542648	Missense_Mutation	SNP	C	A	C	POTEC	c.G498T	p.M166I
XH_P38	18	19053049	19053049	Missense_Mutation	SNP	A	G	A	GREB1L	c.A2240G	p.K747R
XH_P38	18	21120444	21120444	Missense_Mutation	SNP	T	C	T	NPC1	c.A2572G	p.I858V
XH_P38	18	23865998	23865998	Missense_Mutation	SNP	G	T	G	TAF4B	c.G1125T	p.Q375H
XH_P38	18	28584268	28584268	Silent	SNP	A	G	A	DSC3	c.T1953C	p.T651T
XH_P38	18	30349691	30349691	Silent	SNP	C	T	C	KLHL14	c.G864A	p.P288P
XH_P38	18	30350404	30350404	Silent	SNP	G	A	G	KLHL14	c.C151T	p.L51L
XH_P38	18	30350405	30350405	Silent	SNP	C	A	C	KLHL14	c.G150T	p.V50V
XH_P38	18	42643270	42643270	Missense_Mutation	SNP	G	T	G	SETBP1	c.G4398T	p.E1466D
XH_P38	18	44104437	44104437	Missense_Mutation	SNP	T	C	T	LOXHD1	c.A1247G	p.E416G
XH_P38	18	44641603	44641603	Missense_Mutation	SNP	T	C	T	HDHD2	c.A242G	p.D81G
XH_P38	18	45566669	45566669	Silent	SNP	C	T	C	ZBTB7C	c.G810A	p.L270L
XH_P38	18	46163049	46163049	Missense_Mutation	SNP	C	T	C	CTIF	c.C245T	p.P82L
XH_P38	18	46343666	46343666	Silent	SNP	C	T	C	CTIF	c.C1446T	p.C482C
XH_P38	18	46447817	46447817	Silent	SNP	G	C	G	SMAD7	c.C642G	p.G214G
XH_P38	18	46448129	46448129	Silent	SNP	G	A	G	SMAD7	c.C330T	p.L110L
XH_P38	18	47369758	47369758	Silent	SNP	C	T	C	MYO5B	c.G4464A	p.L1488L
XH_P38	18	48327815	48327815	Silent	SNP	G	A	G	MRO	c.C531T	p.A177A
XH_P38	18	52265308	52265308	Missense_Mutation	SNP	A	C	A	DYNAP	c.A409C	p.T137P
XH_P38	18	54815025	54815025	Missense_Mutation	SNP	G	T	G	BOD1L2	c.G482T	p.G161V
XH_P38	18	55104016	55104016	Silent	SNP	T	C	T	ONECUT2	c.T1068C	p.F356F
XH_P38	18	61650865	61650865	Silent	SNP	G	A	G	SERPINB8	c.G477A	p.L159L
XH_P38	18	70209177	70209177	Silent	SNP	C	T	C	CBLN2	c.G219A	p.S73S
XH_P38	18	72124435	72124435	Nonsense_Mutation	SNP	G	T	G	FAM69C	c.C60A	p.C20X
XH_P38	18	72176083	72176083	Missense_Mutation	SNP	T	C	T	CNDP2	c.T376C	p.Y126H
XH_P38	18	72178161	72178161	Silent	SNP	T	C	T	CNDP2	c.T318C	p.Y106Y
XH_P38	18	72226578	72226578	Silent	SNP	C	A	C	CNDP1	c.C174A	p.A58A
XH_P38	18	72998899	72998899	Missense_Mutation	SNP	G	A	G	TSHZ1	c.G1537A	p.A513T
XH_P38	18	74208486	74208486	Splice_Site	DEL	G	-	G	C18orf65	.	.
XH_P38	18	74680208	74680208	Silent	SNP	C	T	C	ZNF236	c.C5457T	p.D1819D
XH_P38	18	74962810	74962810	Silent	SNP	G	T	G	GALR1	c.G306T	p.V102V
XH_P38	18	77478011	77478011	Silent	SNP	C	T	G	CTDP1	c.C2055T	p.S685S
XH_P38	18	77623691	77623691	In_Frame_Ins	INS	-	GGC	-	KCNG2	c.24_25insGGC	p.P8delinsPG
XH_P38	19	362283	362283	Missense_Mutation	SNP	C	T	C	THEG	c.G985A	p.D329N
XH_P38	19	371250	371250	Silent	SNP	G	A	G	THEG	c.C636T	p.A212A
XH_P38	19	464140	464140	Missense_Mutation	SNP	C	T	C	ODF3L2	c.G574A	p.A192T
XH_P38	19	501900	501900	Missense_Mutation	SNP	C	A	C	MADCAM1	c.C899A	p.P300H
XH_P38	19	532066	532066	Silent	SNP	C	T	C	CDC34	c.C135T	p.I45I
XH_P38	19	582310	582310	Missense_Mutation	SNP	C	G	C	BSG	c.C534G	p.D178E
XH_P38	19	605171	605171	Silent	SNP	T	C	T	HCN2	c.T1167C	p.P389P
XH_P38	19	613307	613307	Silent	SNP	C	T	C	HCN2	c.C1644T	p.A548A
XH_P38	19	619021	619021	Silent	SNP	G	C	G	POLRMT	c.C3243G	p.P1081P
XH_P38	19	621712	621712	Silent	SNP	A	G	A	POLRMT	c.T1986C	p.A662A
XH_P38	19	622336	622336	Missense_Mutation	SNP	T	G	T	POLRMT	c.A1664C	p.E555A
XH_P38	19	625198	625198	Silent	SNP	A	G	A	POLRMT	c.T879C	p.T293T
XH_P38	19	632915	632915	Missense_Mutation	SNP	G	A	G	POLRMT	c.C112T	p.P38S
XH_P38	19	652275	652275	Silent	SNP	G	A	G	RNF126	c.C156T	p.A52A
XH_P38	19	852918	852918	Missense_Mutation	SNP	G	A	G	ELANE	c.G110A	p.R37Q
XH_P38	19	880066	880066	Silent	SNP	G	A	G	MED16	c.C1224T	p.S408S
XH_P38	19	900951	900951	Missense_Mutation	SNP	A	G	A	R3HDM4	c.T353C	p.V118A

XH_P38	19	1003439	1003439	Missense_Mutation	SNP	G	A	G	GRIN3B	c.G737A	p.R246H
XH_P38	19	1004808	1004808	Silent	SNP	C	T	C	GRIN3B	c.C1308T	p.D436D
XH_P38	19	1009551	1009577	In_Frame_Del	DEL	AGAGGCCCCA	-	GGAGGCCCCAC	GRIN3B	c.3082_3108del	p.1028_1036del
XH_P38	19	1042809	1042809	Missense_Mutation	SNP	A	G	A	ABCA7	c.A563G	p.E188G
XH_P38	19	1049305	1049305	Silent	SNP	C	A	C	ABCA7	c.C2421A	p.V807V
XH_P38	19	1051214	1051214	Silent	SNP	A	G	A	ABCA7	c.A2745G	p.V915V
XH_P38	19	1052005	1052005	Silent	SNP	C	T	C	ABCA7	c.C3027T	p.A1009A
XH_P38	19	1055191	1055191	Missense_Mutation	SNP	G	A	G	ABCA7	c.G4046A	p.R1349Q
XH_P38	19	1071312	1071312	Missense_Mutation	SNP	C	T	C	ARHGAP45	c.C25T	p.P95
XH_P38	19	1077985	1077985	Missense_Mutation	SNP	A	G	A	ARHGAP45	c.A220G	p.S74G
XH_P38	19	1612340	1612340	Missense_Mutation	SNP	C	T	C	TCF3	c.G1679A	p.R560Q
XH_P38	19	1783261	1783261	Silent	SNP	C	T	C	ATP8B3	c.G3558A	p.K1186K
XH_P38	19	1819112	1819112	Missense_Mutation	SNP	A	G	A	REXO1	c.T2669C	p.V890A
XH_P38	19	1827624	1827624	Silent	SNP	G	A	G	REXO1	c.C1164T	p.S388S
XH_P38	19	1880950	1880950	Missense_Mutation	SNP	T	C	T	ABHD17A	c.A430G	p.K144E
XH_P38	19	1924133	1924133	Silent	SNP	C	T	C	SCAMP4	c.C408T	p.G136G
XH_P38	19	1969882	1969882	Silent	SNP	G	T	G	CSNK1G2	c.G111T	p.S37S
XH_P38	19	2110746	2110746	Silent	SNP	G	A	G	AP3D1	c.C2949T	p.S983S
XH_P38	19	2116649	2116649	Silent	SNP	A	G	A	AP3D1	c.T1956C	p.R652R
XH_P38	19	2120910	2120910	Missense_Mutation	SNP	T	C	T	AP3D1	c.A1432G	p.I478V
XH_P38	19	2226772	2226772	Missense_Mutation	SNP	G	C	G	DOT1L	c.G4252C	p.V1418L
XH_P38	19	2226855	2226855	Silent	SNP	C	T	C	DOT1L	c.C4335T	p.A1445A
XH_P38	19	2252990	2252990	Missense_Mutation	SNP	C	G	C	JSRP1	c.G449C	p.G150A
XH_P38	19	2290499	2290499	Missense_Mutation	SNP	C	T	C	LINGO3	c.G1277A	p.R426H
XH_P38	19	2433890	2433890	Silent	SNP	A	G	A	LMNB2	c.T1416C	p.G472G
XH_P38	19	2767192	2767192	Silent	SNP	G	T	G	SGTA	c.C234A	p.P78P
XH_P38	19	2805172	2805172	Missense_Mutation	SNP	G	A	G	THOP1	c.G748A	p.E250K
XH_P38	19	3062857	3062857	Silent	SNP	T	C	T	AES	c.A69G	p.L23L
XH_P38	19	3594993	3594993	Silent	SNP	G	A	G	TBXA2R	c.C1065T	p.S355S
XH_P38	19	3595794	3595794	Silent	SNP	A	G	A	TBXA2R	c.T924C	p.V308Y
XH_P38	19	3613159	3613159	Silent	SNP	C	T	C	CACTIN	c.G1683A	p.P561P
XH_P38	19	3728609	3728609	Missense_Mutation	SNP	G	A	G	TJP3	c.G56A	p.R19H
XH_P38	19	3752515	3752515	Silent	SNP	G	A	G	APBA3	c.C1386T	p.A462A
XH_P38	19	3752563	3752563	Silent	SNP	G	A	G	APBA3	c.C1338T	p.A446A
XH_P38	19	3831765	3831765	Missense_Mutation	SNP	G	A	G	ZFR2	c.C491T	p.S164L
XH_P38	19	4012947	4012947	Silent	SNP	C	T	C	PIA54	c.C54T	p.S18S
XH_P38	19	4013229	4013229	Silent	SNP	C	T	C	PIA54	c.C336T	p.Y112Y
XH_P38	19	4207940	4207940	Silent	SNP	G	A	G	ANKRD24	c.G807A	p.A269A
XH_P38	19	4217510	4217510	Missense_Mutation	SNP	A	T	A	ANKRD24	c.A2353T	p.T785S
XH_P38	19	4318432	4318432	Missense_Mutation	SNP	G	A	G	FSD1	c.G889A	p.V297M
XH_P38	19	4446378	4446378	Missense_Mutation	SNP	C	T	C	UBXN6	c.G794A	p.R265Q
XH_P38	19	4454000	4454000	Silent	SNP	G	A	G	UBXN6	c.C15T	p.A5A
XH_P38	19	4525046	4525046	Missense_Mutation	SNP	A	G	A	PLIN5	c.T763C	p.C255R
XH_P38	19	4793216	4793216	Silent	SNP	C	A	C	FEM1A	c.C1350A	p.A450A
XH_P38	19	4852137	4852137	Silent	SNP	C	T	C	PLIN3	c.G525A	p.S175S
XH_P38	19	5455735	5455735	Missense_Mutation	SNP	G	A	G	ZNRF4	c.G233A	p.R78Q
XH_P38	19	5831672	5831672	Missense_Mutation	SNP	G	C	G	FUT6	c.C907G	p.R303G
XH_P38	19	6007045	6007045	Silent	SNP	G	A	G	RFK2	c.C1305T	p.P435P
XH_P38	19	6007724	6007724	Silent	SNP	G	A	G	RFK2	c.C1149T	p.D383D
XH_P38	19	6008188	6008188	Missense_Mutation	SNP	A	C	A	RFK2	c.T988G	p.F330V
XH_P38	19	6312290	6312290	Missense_Mutation	SNP	T	C	T	ACER1	c.A220G	p.M74V
XH_P38	19	6375831	6375831	Silent	SNP	G	A	G	PSPN	c.C30T	p.S10S
XH_P38	19	6415662	6415662	Missense_Mutation	SNP	C	T	C	KHSRP	c.G1771A	p.V591I
XH_P38	19	6427408	6427408	Silent	SNP	G	A	G	SLC25A41	c.C729T	p.R243R
XH_P38	19	6665336	6665336	Silent	SNP	G	A	G	TNFSF14	c.C216T	p.S72S
XH_P38	19	6678462	6678462	Silent	SNP	G	A	G	CSF3	c.C4635T	p.Y1545Y
XH_P38	19	6755155	6755155	Missense_Mutation	SNP	T	C	T	SH2D3A	c.A668G	p.D223G
XH_P38	19	7056590	7056590	Missense_Mutation	SNP	C	T	C	MBD3L3	c.G370A	p.G124S
XH_P38	19	7125297	7125297	Silent	SNP	G	A	G	INSR	c.C3219T	p.H1073H
XH_P38	19	7532252	7532252	Silent	SNP	G	C	G	ARHGEF18	c.G2598C	p.A866A
XH_P38	19	7542118	7542118	Silent	SNP	G	A	G	PEX11G	c.C513T	p.A171A
XH_P38	19	7547074	7547074	Missense_Mutation	SNP	A	C	A	PEX11G	c.T273G	p.C91W
XH_P38	19	7682305	7682305	Silent	SNP	G	A	G	CAMSAP3	c.G3306A	p.A1102A
XH_P38	19	7747293	7747293	Missense_Mutation	SNP	T	G	T	TRAPPC5	c.T154G	p.S52A
XH_P38	19	7755056	7755056	Silent	SNP	G	A	G	FCER2	c.C714T	p.H238H
XH_P38	19	7964727	7964727	Silent	SNP	G	A	G	LRRC8E	c.G933A	p.E311E
XH_P38	19	8321946	8321946	Silent	SNP	T	C	T	CERS4	c.T726C	p.S242S
XH_P38	19	8389520	8389520	Silent	SNP	C	T	C	KANK3	c.G2277A	p.L759L
XH_P38	19	8398975	8398975	Missense_Mutation	SNP	C	T	C	KANK3	c.G1453A	p.A485T
XH_P38	19	8468337	8468337	Silent	SNP	C	T	C	RAB11B	c.C552T	p.R184R
XH_P38	19	8486884	8486884	Missense_Mutation	SNP	G	A	G	MARCH2	c.G160A	p.A54T
XH_P38	19	8564153	8564153	Missense_Mutation	SNP	G	T	G	PRAM1	c.C539A	p.P180H
XH_P38	19	8575765	8575765	Missense_Mutation	SNP	C	G	C	ZNF414	c.G1069C	p.A357P
XH_P38	19	8576670	8576670	Silent	SNP	C	T	C	ZNF414	c.G705A	p.P235P
XH_P38	19	8650043	8650043	Silent	SNP	G	T	G	ADAMTS10	c.C1476A	p.A492A
XH_P38	19	8996340	8996340	Silent	SNP	G	A	G	MUC16	c.C41232T	p.N13744N
XH_P38	19	9024871	9024871	Missense_Mutation	SNP	C	T	C	MUC16	c.G36991A	p.E12331K
XH_P38	19	9048342	9048342	Missense_Mutation	SNP	C	T	C	MUC16	c.G33289A	p.V11097M
XH_P38	19	9049726	9049726	Silent	SNP	G	A	G	MUC16	c.C31905T	p.D10635D
XH_P38	19	9056982	9056982	Missense_Mutation	SNP	G	A	G	MUC16	c.C30464T	p.T10155I
XH_P38	19	9058907	9058907	Missense_Mutation	SNP	G	C	G	MUC16	c.C28539G	p.H9513Q
XH_P38	19	9060656	9060656	Silent	SNP	C	T	C	MUC16	c.G26790A	p.E8930E
XH_P38	19	9063678	9063678	Missense_Mutation	SNP	T	G	T	MUC16	c.A23768C	p.D7923A
XH_P38	19	9065632	9065632	Missense_Mutation	SNP	T	C	T	MUC16	c.A21814G	p.I7272V
XH_P38	19	9072313	9072313	Missense_Mutation	SNP	A	G	A	MUC16	c.T15133C	p.S5045P
XH_P38	19	9072742	9072742	Missense_Mutation	SNP	T	C	T	MUC16	c.A14704G	p.I4902V
XH_P38	19	9074950	9074950	Missense_Mutation	SNP	G	T	G	MUC16	c.C12496A	p.H4166N
XH_P38	19	9075217	9075217	Missense_Mutation	SNP	T	A	T	MUC16	c.A12229T	p.T4077S
XH_P38	19	9075346	9075346	Missense_Mutation	SNP	T	A	T	MUC16	c.A12100T	p.I4034F
XH_P38	19	9075584	9075584	Silent	SNP	T	A	T	MUC16	c.A11862T	p.T3954T
XH_P38	19	9075737	9075737	Silent	SNP	T	C	T	MUC16	c.A11709G	p.V3903V
XH_P38	19	9076278	9076278	Missense_Mutation	SNP	G	A	G	MUC16	c.C11168T	p.T3723M
XH_P38	19	9077264	9077264	Silent	SNP	T	G	T	MUC16	c.A10182C	p.V3394V
XH_P38	19	9077436	9077436	Missense_Mutation	SNP	G	A	G	MUC16	c.C10010T	p.S3337L
XH_P38	19	9362343	9362343	Silent	SNP	C	T	C	OR7E24	c.C624T	p.S208S
XH_P38	19	9362443	9362443	Missense_Mutation	SNP	C	T	C	OR7E24	c.C724T	p.P242S
XH_P38	19	10071347	10071347	Missense_Mutation	SNP	C	T	C	COL5A3	c.G5071A	p.V1691I
XH_P38	19	10077419	10077419	Missense_Mutation	SNP	C	G	C	COL5A3	c.G4462C	p.A1488P

XH_P38	19	10078589	10078589	Silent	SNP	T	C	T	COL5A3	c.A4395G	p.K1465K
XH_P38	19	10088271	10088271	Missense_Mutation	SNP	C	G	C	COL5A3	c.G3125C	p.R1042P
XH_P38	19	10089262	10089262	Silent	SNP	G	A	G	COL5A3	c.C3006T	p.P1002P
XH_P38	19	10265725	10265725	Silent	SNP	G	A	G	DNMT1	c.C1452T	p.A484A
XH_P38	19	10407169	10407169	Silent	SNP	G	C	G	ICAM5	c.G2652C	p.L884L
XH_P38	19	10445806	10445806	Silent	SNP	C	T	C	ICAM3	c.G90A	p.E30E
XH_P38	19	10556897	10556897	Silent	SNP	C	T	C	PDE4A	c.C324T	p.F108F
XH_P38	19	10664632	10664632	Missense_Mutation	SNP	A	G	A	KR11	c.T2125C	p.S709P
XH_P38	19	10668673	10668673	Missense_Mutation	SNP	A	G	A	KR11	c.T1352C	p.L451P
XH_P38	19	10692051	10692051	Silent	SNP	G	A	G	AP1M2	c.C564T	p.S188S
XH_P38	19	11170839	11170839	Silent	SNP	T	C	T	SMARCA4	c.T4797C	p.D1599D
XH_P38	19	11230881	11230881	Silent	SNP	T	C	T	LDLR	c.T1455C	p.V485V
XH_P38	19	11465316	11465316	Missense_Mutation	SNP	G	C	G	CCDC159	c.G833C	p.C278S
XH_P38	19	11508177	11508177	Missense_Mutation	SNP	G	A	G	RGL3	c.C1843T	p.R615C
XH_P38	19	11516007	11516007	Silent	SNP	T	G	T	RGL3	c.A1092C	p.A364A
XH_P38	19	11942362	11942362	Missense_Mutation	SNP	A	G	A	ZNF440	c.A371G	p.N124S
XH_P38	19	11942615	11942615	Silent	SNP	A	C	A	ZNF440	c.A624C	p.A208A
XH_P38	19	12502787	12502787	Missense_Mutation	SNP	G	A	G	ZNF799	c.C425T	p.T142M
XH_P38	19	12541214	12541214	Missense_Mutation	SNP	G	T	G	ZNF443	c.C1772A	p.P591Q
XH_P38	19	12541795	12541795	Missense_Mutation	SNP	C	A	C	ZNF443	c.G1191T	p.Q397H
XH_P38	19	12865392	12865392	Missense_Mutation	SNP	C	T	C	BEST2	c.C274T	p.R92C
XH_P38	19	13035006	13035006	Silent	SNP	G	A	G	FARSA	c.C1347T	p.P449P
XH_P38	19	13318673	13318690	In_Frame_Del	DEL	TCGCTGCTGCT	-	CTGCTGCTGCTG	CACNA1A	c.6958_6975del	p.2320_2325del
XH_P38	19	14000170	14000170	Missense_Mutation	SNP	T	C	T	C19orf57	c.A1145G	p.Q382R
XH_P38	19	14000400	14000400	Silent	SNP	A	G	A	C19orf57	c.T915C	p.P305P
XH_P38	19	14000870	14000870	Missense_Mutation	SNP	C	T	C	C19orf57	c.G445A	p.G149R
XH_P38	19	14065341	14065341	Silent	SNP	T	C	T	DCAF15	c.T234C	p.H78H
XH_P38	19	14142705	14142705	Silent	SNP	C	T	C	IL27RA	c.C21T	p.A7A
XH_P38	19	14165598	14165598	Missense_Mutation	SNP	C	T	C	PALM3	c.G841A	p.V281M
XH_P38	19	14185226	14185226	Missense_Mutation	SNP	T	C	T	MISP3	c.T593C	p.V198A
XH_P38	19	14512489	14512489	Missense_Mutation	SNP	G	A	G	ADGRE5	c.G821A	p.R274Q
XH_P38	19	14580328	14580328	Missense_Mutation	SNP	A	G	A	PKN1	c.A2152G	p.I718V
XH_P38	19	14581063	14581063	Silent	SNP	A	G	A	PKN1	c.A2382G	p.P794R
XH_P38	19	14584317	14584317	Silent	SNP	G	A	G	PTGER1	c.C816T	p.A272A
XH_P38	19	14827830	14827830	Missense_Mutation	SNP	C	A	C	ZNF333	c.C752A	p.A251E
XH_P38	19	14829749	14829749	Missense_Mutation	SNP	C	T	C	ZNF333	c.C1610T	p.A537V
XH_P38	19	15133733	15133733	Missense_Mutation	SNP	C	G	C	CCDC105	c.C1302G	p.D434E
XH_P38	19	15220904	15220904	Missense_Mutation	SNP	G	A	G	SYDE1	c.G619A	p.G207S
XH_P38	19	15271771	15271771	Missense_Mutation	SNP	G	A	G	NOTCH3	c.C6668T	p.A2223V
XH_P38	19	15565046	15565046	Silent	SNP	G	A	G	RASAL3	c.C2193T	p.T731T
XH_P38	19	15807837	15807837	Missense_Mutation	SNP	T	A	T	CYP4F12	c.T1517A	p.M506K
XH_P38	19	15996820	15996820	Silent	SNP	G	A	G	CYP4F2	c.C1029T	p.H343H
XH_P38	19	16025176	16025176	Missense_Mutation	SNP	C	T	C	CYP4F11	c.G1336A	p.D446N
XH_P38	19	16040292	16040292	Silent	SNP	A	G	A	CYP4F11	c.T318C	p.I106I
XH_P38	19	16591464	16591464	Silent	SNP	G	A	G	CALR3	c.C972T	p.Y324Y
XH_P38	19	16620363	16620363	Silent	SNP	G	A	G	C19orf44	c.G1203A	p.A401A
XH_P38	19	16630994	16630994	Silent	SNP	T	G	T	CHERP	c.A2428C	p.R810R
XH_P38	19	16666101	16666101	Silent	SNP	G	C	G	SLC35E1	c.C864G	p.P288P
XH_P38	19	16942396	16942396	Missense_Mutation	SNP	G	A	G	SIN3B	c.G319A	p.G107R
XH_P38	19	17283657	17283657	Silent	SNP	C	T	C	MYO9B	c.C2025T	p.I675I
XH_P38	19	17306163	17306163	Silent	SNP	C	T	C	MYO9B	c.C3927T	p.A1309A
XH_P38	19	17337555	17337555	Silent	SNP	C	A	C	OCEL1	c.C123A	p.T41T
XH_P38	19	17392629	17392629	Missense_Mutation	SNP	G	A	G	ANKLE1	c.G62A	p.G21E
XH_P38	19	17439034	17439034	Silent	SNP	C	T	C	ANO8	c.G2163A	p.P721P
XH_P38	19	17622614	17622614	Silent	SNP	C	T	C	PGLS	c.C133T	p.L45L
XH_P38	19	17837425	17837425	Missense_Mutation	SNP	C	G	C	MAP15	c.C1154G	p.S385C
XH_P38	19	17837685	17837685	Missense_Mutation	SNP	C	T	C	MAP15	c.C1414T	p.R472C
XH_P38	19	17837952	17837952	Nonsense_Mutation	SNP	C	T	C	MAP15	c.C1681T	p.R561X
XH_P38	19	17838807	17838807	Missense_Mutation	SNP	C	T	C	MAP15	c.C2536T	p.R846C
XH_P38	19	17919024	17919024	Silent	SNP	A	T	A	B3GNT3	c.A408T	p.V136V
XH_P38	19	18285944	18285944	Missense_Mutation	SNP	G	A	G	IFI30	c.G227A	p.R76Q
XH_P38	19	18288069	18288069	Silent	SNP	A	G	A	IFI30	c.A603G	p.P201P
XH_P38	19	18304700	18304700	Missense_Mutation	SNP	A	G	A	MPV17L2	c.A214G	p.M72V
XH_P38	19	18305824	18305824	Silent	SNP	C	T	C	MPV17L2	c.C492T	p.P164P
XH_P38	19	18329240	18329240	Silent	SNP	T	C	T	PDE4C	c.A1038G	p.E346E
XH_P38	19	18368810	18368810	Missense_Mutation	SNP	G	T	G	KIAA1683	c.C3284A	p.P1095H
XH_P38	19	18375563	18375563	Silent	SNP	G	A	G	KIAA1683	c.C2787T	p.P929P
XH_P38	19	18376407	18376407	Missense_Mutation	SNP	T	A	T	KIAA1683	c.A1943T	p.Y648F
XH_P38	19	18377274	18377274	Missense_Mutation	SNP	A	G	A	KIAA1683	c.T1076C	p.M359T
XH_P38	19	18377496	18377496	Missense_Mutation	SNP	C	G	C	KIAA1683	c.G854C	p.S285T
XH_P38	19	18377647	18377647	Missense_Mutation	SNP	G	C	G	KIAA1683	c.C703G	p.L235V
XH_P38	19	18377761	18377761	Missense_Mutation	SNP	A	G	A	KIAA1683	c.T589C	p.C197R
XH_P38	19	18538742	18538742	Silent	SNP	A	C	A	SSBP4	c.A229C	p.R77R
XH_P38	19	18545786	18545786	Silent	SNP	G	T	G	ISYNA1	c.C1230A	p.T410T
XH_P38	19	18679379	18679379	Missense_Mutation	SNP	C	G	C	KXD1	c.C469G	p.P157A
XH_P38	19	18710535	18710535	Silent	SNP	G	A	G	CRLF1	c.C237T	p.N79N
XH_P38	19	18726856	18726856	Silent	SNP	T	C	T	TMEM59L	c.T480C	p.L160L
XH_P38	19	19165023	19165023	Missense_Mutation	SNP	C	T	C	ARMC6	c.C841T	p.R281C
XH_P38	19	19351431	19351431	Silent	SNP	G	A	G	NCAN	c.G3429A	p.T1143T
XH_P38	19	19369435	19369435	Silent	SNP	A	G	A	HAPLN4	c.T714C	p.S238S
XH_P38	19	19380996	19380996	Silent	SNP	G	T	G	TM6SF2	c.C387A	p.G129G
XH_P38	19	19606634	19606634	Silent	SNP	G	A	G	GATAD2A	c.G696A	p.S232S
XH_P38	19	19625547	19625547	Silent	SNP	A	G	A	TSSK6	c.T690C	p.Y230Y
XH_P38	19	19654117	19654117	Silent	SNP	G	C	G	CILP2	c.G1038C	p.L346L
XH_P38	19	19744692	19744692	Missense_Mutation	SNP	G	A	G	GMIP	c.C2305T	p.P769S
XH_P38	19	19767899	19767899	Silent	SNP	T	C	T	ATP13A1	c.A810G	p.L270L
XH_P38	19	20044069	20044069	Missense_Mutation	SNP	G	T	G	ZNF93	c.G305T	p.R102I
XH_P38	19	21909733	21909733	Missense_Mutation	SNP	C	T	C	ZNF100	c.G736A	p.E246K
XH_P38	19	21990859	21990859	Missense_Mutation	SNP	C	G	C	ZNF43	c.G1785C	p.Y595N
XH_P38	19	22155520	22155520	Silent	SNP	A	G	A	ZNF208	c.T2316C	p.T772T
XH_P38	19	22155757	22155757	Silent	SNP	G	A	G	ZNF208	c.C2079T	p.Y693Y
XH_P38	19	23545447	23545447	Missense_Mutation	SNP	A	G	A	ZNF91	c.T238C	p.Y80H
XH_P38	19	23557502	23557502	Missense_Mutation	SNP	G	A	G	ZNF91	c.C95T	p.T32I
XH_P38	19	24310032	24310032	Missense_Mutation	SNP	A	T	A	ZNF254	c.A975T	p.E325D
XH_P38	19	30164969	30164969	Missense_Mutation	SNP	C	T	C	PLEKHF1	c.C223T	p.R75C
XH_P38	19	33098632	33098632	Missense_Mutation	SNP	G	C	G	ANKRD27	c.C2282G	p.P761R
XH_P38	19	33333155	33333155	Silent	SNP	G	A	G	SLC7A9	c.C1143T	p.A381A
XH_P38	19	33353464	33353464	Silent	SNP	G	A	G	SLC7A9	c.C507T	p.S169S

XH_P38	19	33487071	33487071	Silent	SNP	G	T	G	RHPN2	c.C1281A	p.A427A
XH_P38	19	33882222	33882222	Silent	SNP	G	A	G	PEPD	c.C1008T	p.H336H
XH_P38	19	34712618	34712618	Missense_Mutation	SNP	G	A	G	LSM14A	c.G1343A	p.R448Q
XH_P38	19	35422808	35422808	Missense_Mutation	SNP	C	T	C	ZNF30	c.C71T	p.S24F
XH_P38	19	35449409	35449409	Silent	SNP	G	A	G	ZNF792	c.C1350T	p.H450H
XH_P38	19	35550832	35550832	Silent	SNP	G	A	G	HPN	c.G345A	p.S115S
XH_P38	19	35660508	35660508	Missense_Mutation	SNP	G	A	G	FXYS	c.G434A	p.R145H
XH_P38	19	35850169	35850169	Missense_Mutation	SNP	G	A	G	FFAR3	c.C377A	p.R126Q
XH_P38	19	35850264	35850264	Missense_Mutation	SNP	G	A	G	FFAR3	c.G472A	p.D158N
XH_P38	19	35850560	35850560	Silent	SNP	G	A	G	FFAR3	c.G768A	p.A256A
XH_P38	19	35998362	35998362	Silent	SNP	T	G	T	DMKN	c.A943C	p.R315R
XH_P38	19	36048741	36048741	Silent	SNP	G	T	G	ATP4A	c.C1509A	p.I503I
XH_P38	19	36206271	36206271	Missense_Mutation	SNP	C	T	C	ZBTB32	c.C743T	p.S248L
XH_P38	19	36218478	36218478	Silent	SNP	C	T	C	KMT2B	c.C4257T	p.G1419G
XH_P38	19	36224705	36224705	Missense_Mutation	SNP	A	G	A	KMT2B	c.A7091G	p.D2364G
XH_P38	19	36340175	36340175	Missense_Mutation	SNP	C	T	C	NPHS1	c.G803A	p.R268Q
XH_P38	19	36342482	36342482	Silent	SNP	G	A	G	NPHS1	c.C151T	p.L51L
XH_P38	19	36370011	36370011	Silent	SNP	G	A	G	APLP1	c.G1749A	p.V583V
XH_P38	19	36387881	36387881	Missense_Mutation	SNP	A	G	A	NFKBID	c.T131C	p.V44A
XH_P38	19	36394272	36394272	Silent	SNP	T	C	T	HCS1	c.T63C	p.T21T
XH_P38	19	36593649	36593649	Silent	SNP	C	T	C	WDR62	c.C3231T	p.P1077P
XH_P38	19	37264068	37264068	Missense_Mutation	SNP	A	G	A	LOC728485	c.A35G	p.N12S
XH_P38	19	37618208	37618208	Silent	SNP	A	G	A	ZNF420	c.A315G	p.E105E
XH_P38	19	37854239	37854239	Silent	SNP	G	A	G	HKR1	c.G1362A	p.T454T
XH_P38	19	38055553	38055553	Missense_Mutation	SNP	T	C	T	ZNF571	c.A1777G	p.K593E
XH_P38	19	38189616	38189616	Silent	SNP	T	C	T	ZNF607	c.A1413G	p.T471T
XH_P38	19	38229824	38229824	Missense_Mutation	SNP	T	C	T	ZNF573	c.A1303G	p.M435V
XH_P38	19	38375985	38375985	Missense_Mutation	SNP	G	A	G	WDR87	c.C8326T	p.R2776W
XH_P38	19	38379699	38379699	Missense_Mutation	SNP	C	A	C	WDR87	c.G4612T	p.A1538S
XH_P38	19	38655235	38655235	Missense_Mutation	SNP	C	A	C	SIPA1L3	c.C3897A	p.D1299E
XH_P38	19	38684261	38684261	Missense_Mutation	SNP	G	C	G	SIPA1L3	c.G4681C	p.A1561P
XH_P38	19	38800165	38800165	Silent	SNP	C	T	C	YIFB	c.G132A	p.L44L
XH_P38	19	38817486	38817486	Silent	SNP	T	C	T	KCNK6	c.T576C	p.F192F
XH_P38	19	38817876	38817876	Missense_Mutation	SNP	G	A	G	KCNK6	c.G775A	p.V259M
XH_P38	19	38827960	38827960	Missense_Mutation	SNP	T	C	T	CATSPERG	c.T86C	p.L29P
XH_P38	19	38948769	38948769	Silent	SNP	C	T	C	RYR1	c.C2004T	p.D668D
XH_P38	19	38956803	38956803	Silent	SNP	G	A	G	RYR1	c.G2943A	p.T981T
XH_P38	19	39307103	39307103	Missense_Mutation	SNP	C	T	C	ECH1	c.G649A	p.G217R
XH_P38	19	39402455	39402455	Missense_Mutation	SNP	C	G	C	CCER2	c.G99C	p.E33D
XH_P38	19	39798900	39798900	Silent	SNP	G	A	G	LRFN1	c.C1689T	p.G563G
XH_P38	19	39913634	39913634	Missense_Mutation	SNP	G	A	G	PLEKHG2	c.G1763A	p.R588H
XH_P38	19	39915958	39915958	Missense_Mutation	SNP	A	G	A	PLEKHG2	c.A3653G	p.K1218R
XH_P38	19	40196627	40196627	Missense_Mutation	SNP	G	A	G	LGALS14	c.G80A	p.R27H
XH_P38	19	40331067	40331067	Silent	SNP	C	T	C	FBL	c.G270A	p.P90P
XH_P38	19	40357683	40357683	Silent	SNP	T	G	T	FCGBP	c.A15630C	p.A5210A
XH_P38	19	40376881	40376881	Missense_Mutation	SNP	G	C	G	FCGBP	c.C11541G	p.D3847E
XH_P38	19	40392585	40392585	Missense_Mutation	SNP	T	G	T	FCGBP	c.A7919C	p.E2640A
XH_P38	19	40886993	40886993	Missense_Mutation	SNP	C	T	C	HIPK4	c.G905A	p.R302Q
XH_P38	19	41003463	41003463	Missense_Mutation	SNP	C	T	C	SPTBN4	c.C736T	p.R246C
XH_P38	19	41082868	41082868	Silent	SNP	T	C	T	SHKBP1	c.T63C	p.I21I
XH_P38	19	41197997	41197997	Silent	SNP	G	A	G	COQ8B	c.C1455T	p.D485D
XH_P38	19	41349774	41349774	Missense_Mutation	SNP	A	G	A	CYP2A6	c.T1412C	p.I471T
XH_P38	19	41349874	41349874	Missense_Mutation	SNP	T	A	T	CYP2A6	c.A1312T	p.N438Y
XH_P38	19	41356310	41356310	Silent	SNP	G	A	G	CYP2A6	c.C22T	p.L8L
XH_P38	19	41383217	41383217	Missense_Mutation	SNP	T	C	T	CYP2A7	c.A886G	p.T296A
XH_P38	19	41858921	41858921	Missense_Mutation	SNP	G	A	G	TGFB1	c.C29T	p.P10L
XH_P38	19	41889748	41889748	Silent	SNP	T	C	T	TMEM91	c.T489C	p.A163A
XH_P38	19	41903220	41903220	Missense_Mutation	SNP	G	A	G	EXOSC5	c.C14T	p.T5M
XH_P38	19	41928652	41928652	Silent	SNP	C	T	C	BCKDHA	c.C972T	p.F324F
XH_P38	19	41930396	41930396	Silent	SNP	A	G	A	BCKDHA	c.A1221G	p.L407L
XH_P38	19	41932084	41932084	Silent	SNP	G	T	G	B3GNT8	c.C600A	p.A200A
XH_P38	19	41932120	41932120	Silent	SNP	C	T	C	B3GNT8	c.G564A	p.V188V
XH_P38	19	41932275	41932275	Missense_Mutation	SNP	T	C	T	B3GNT8	c.A409G	p.S137G
XH_P38	19	41932612	41932612	Silent	SNP	C	T	C	B3GNT8	c.G72A	p.E24E
XH_P38	19	42572987	42572987	Missense_Mutation	SNP	C	T	C	ZNF574	c.C124T	p.R42W
XH_P38	19	42911769	42911769	Missense_Mutation	SNP	G	A	G	LIPE	c.C1831T	p.R611C
XH_P38	19	43372386	43372386	Silent	SNP	T	C	T	PSG1	c.A831G	p.E277E
XH_P38	19	43999432	43999432	Silent	SNP	A	T	A	PHLDB3	c.T1011A	p.S337S
XH_P38	19	44001345	44001345	Silent	SNP	C	T	C	PHLDB3	c.G750A	p.E250E
XH_P38	19	44118188	44118188	Missense_Mutation	SNP	A	C	A	SRRM5	c.A1915C	p.S639R
XH_P38	19	44118353	44118353	Missense_Mutation	SNP	G	A	G	SRRM5	c.G2080A	p.D694N
XH_P38	19	44500701	44500701	Missense_Mutation	SNP	C	T	C	ZNF155	c.C692T	p.P231L
XH_P38	19	44622362	44622362	Missense_Mutation	SNP	G	A	G	ZNF225	c.G37A	p.V13M
XH_P38	19	45029208	45029208	Missense_Mutation	SNP	G	A	G	CEACAM20	c.C122T	p.A41V
XH_P38	19	45412079	45412079	Missense_Mutation	SNP	C	T	C	APOE	c.C526T	p.R176C
XH_P38	19	45567708	45567708	Missense_Mutation	SNP	G	C	G	CLASRP	c.G1043C	p.R348P
XH_P38	19	45655486	45655486	Missense_Mutation	SNP	G	C	G	NKPD1	c.C2209G	p.Q737E
XH_P38	19	45818783	45818783	Frame_Shift_Del	DEL	T	-	T	CKM	c.421delA	p.T141fs
XH_P38	19	45885787	45885787	Missense_Mutation	SNP	C	T	C	PPP1R13L	c.G2446A	p.G816R
XH_P38	19	45912002	45912002	Missense_Mutation	SNP	A	C	A	CD3EAP	c.A782C	p.K261T
XH_P38	19	46024584	46024584	Silent	SNP	T	G	T	VASP	c.T348G	p.G116G
XH_P38	19	46124517	46124517	Missense_Mutation	SNP	C	T	C	EML2	c.G1070A	p.R357H
XH_P38	19	46269076	46269076	Missense_Mutation	SNP	G	A	G	SIX5	c.C1903T	p.P635S
XH_P38	19	46327053	46327053	Silent	SNP	C	T	C	SYMPK	c.G2571A	p.T857T
XH_P38	19	46375779	46375779	Silent	SNP	C	T	C	FOXA3	c.C516T	p.N172N
XH_P38	19	46387503	46387503	Silent	SNP	T	C	T	IRF2BP1	c.A1530G	p.L510L
XH_P38	19	46388379	46388379	Silent	SNP	C	G	C	IRF2BP1	c.G654C	p.R218R
XH_P38	19	46394187	46394187	Silent	SNP	C	T	C	MYPOP	c.G894A	p.L298Q
XH_P38	19	46663890	46663890	Silent	SNP	A	G	A	IGFL2	c.A93G	p.P31P
XH_P38	19	46914921	46914921	Missense_Mutation	SNP	G	A	G	CCDC8	c.C1147T	p.H383Y
XH_P38	19	46998253	46998253	Missense_Mutation	SNP	G	C	G	PNMA8B	c.C470G	p.P157R
XH_P38	19	47124591	47124591	Missense_Mutation	SNP	G	T	G	PTGIR	c.C1107A	p.S369R
XH_P38	19	47225265	47225265	Silent	SNP	G	A	G	STRN4	c.C2091T	p.N697N
XH_P38	19	47249604	47249604	Silent	SNP	G	C	G	STRN4	c.C84G	p.P28P
XH_P38	19	47258842	47258842	Silent	SNP	C	T	C	FKRP	c.C135T	p.A45A
XH_P38	19	47588325	47588325	Silent	SNP	G	A	G	ZC3H4	c.C1095T	p.D365D
XH_P38	19	47778530	47778530	Silent	SNP	C	T	C	INAFM1	c.C354T	p.S118S
XH_P38	19	47878858	47878858	Missense_Mutation	SNP	C	T	C	DHX34	c.C2200T	p.R734C

XH_P38	19	48047821	48047821	Silent	SNP	C	T	C	ZNF541	c.G1965A	p.A655A
XH_P38	19	48305357	48305357	Missense_Mutation	SNP	G	A	G	TPRX1	c.C911T	p.P304L
XH_P38	19	48697961	48697961	Silent	SNP	C	T	C	C19orf68	c.C640T	p.L214L
XH_P38	19	48715153	48715153	Silent	SNP	T	C	T	CARD8	c.A1428G	p.Q476Q
XH_P38	19	48800751	48800751	Missense_Mutation	SNP	C	A	C	CCDC114	c.G1495T	p.A499S
XH_P38	19	49218111	49218111	Silent	SNP	G	T	G	MAMSTR	c.C171A	p.P57P
XH_P38	19	49218602	49218602	Silent	SNP	C	T	C	MAMSTR	c.G33A	p.A11A
XH_P38	19	49219014	49219014	Silent	SNP	C	T	C	MAMSTR	c.G108A	p.P36P
XH_P38	19	49232226	49232226	Missense_Mutation	SNP	G	A	G	RASIP1	c.C1801T	p.R601C
XH_P38	19	49254504	49254504	Missense_Mutation	SNP	G	A	G	FUT1	c.C35T	p.A12V
XH_P38	19	49261267	49261267	Silent	SNP	C	T	C	FGF21	c.C420T	p.H140H
XH_P38	19	49377424	49377424	Missense_Mutation	SNP	G	A	G	PPP1R15A	c.G934A	p.G312S
XH_P38	19	49513273	49513273	Silent	SNP	C	T	C	RUVBL2	c.C511T	p.L171L
XH_P38	19	49519466	49519466	Silent	SNP	A	G	A	LHB	c.T285C	p.G95G
XH_P38	19	49657889	49657889	In_Frame_Ins	INS	-	TCC	-	HRC	.605_606insGG	p.E202delinsEE
XH_P38	19	49699866	49699866	Silent	SNP	C	T	C	TRPM4	c.C1318T	p.L440L
XH_P38	19	49867913	49867913	Missense_Mutation	SNP	G	A	G	DKK1	c.G85A	p.A29T
XH_P38	19	49930721	49930721	Missense_Mutation	SNP	T	C	T	GFY	c.T1034C	p.V345A
XH_P38	19	49930786	49930786	Missense_Mutation	SNP	C	A	C	GFY	c.C1099A	p.P367T
XH_P38	19	50091798	50091798	Missense_Mutation	SNP	G	T	G	PRRG2	c.G346T	p.G116C
XH_P38	19	50097784	50097784	Silent	SNP	T	C	T	PRR12	c.T273C	p.L91L
XH_P38	19	50098423	50098423	Silent	SNP	G	A	G	PRR12	c.G831A	p.P277P
XH_P38	19	50099422	50099422	Silent	SNP	C	T	C	PRR12	c.C1830T	p.A610A
XH_P38	19	50165549	50165549	Missense_Mutation	SNP	C	T	C	IRF3	c.G200A	p.R67H
XH_P38	19	50193163	50193163	Silent	SNP	A	G	A	ADM5	c.A69G	p.A23A
XH_P38	19	50322482	50322482	Silent	SNP	C	G	C	MED25	c.C234G	p.P78P
XH_P38	19	50354211	50354211	Missense_Mutation	SNP	C	T	C	PTOV1	c.C74T	p.S25L
XH_P38	19	50364721	50364721	Missense_Mutation	SNP	A	C	A	PNKP	c.T1433G	p.V478G
XH_P38	19	50383636	50383636	Missense_Mutation	SNP	T	C	T	TBC1D17	c.T197C	p.L66P
XH_P38	19	50393269	50393269	Silent	SNP	A	G	A	IL41	c.T1362C	p.F454F
XH_P38	19	50436269	50436269	Missense_Mutation	SNP	G	A	G	ATF5	c.G769A	p.V257M
XH_P38	19	50863023	50863023	Silent	SNP	A	G	A	NAPSA	c.T765C	p.P255P
XH_P38	19	50865535	50865535	Missense_Mutation	SNP	A	G	A	NAPSA	c.T119C	p.I40T
XH_P38	19	50918758	50918758	Silent	SNP	C	T	C	POLD1	c.C2706T	p.I902I
XH_P38	19	50983419	50983419	Missense_Mutation	SNP	G	A	G	EMC10	c.G349A	p.G117R
XH_P38	19	51021944	51021944	Silent	SNP	C	T	C	LRRC4B	c.G1026A	p.A342A
XH_P38	19	51159571	51159571	Missense_Mutation	SNP	T	G	T	C19orf81	c.T229G	p.S77A
XH_P38	19	51170706	51170706	Missense_Mutation	SNP	A	G	A	SHANK1	c.T4511C	p.V1504A
XH_P38	19	51171188	51171188	Silent	SNP	G	A	G	SHANK1	c.C4029T	p.T1343T
XH_P38	19	51297825	51297825	Missense_Mutation	SNP	G	A	G	ACPT	c.G973A	p.A325T
XH_P38	19	51297826	51297826	Missense_Mutation	SNP	C	A	C	ACPT	c.C974A	p.A325D
XH_P38	19	51323232	51323232	Missense_Mutation	SNP	T	C	T	KLK1	c.A556G	p.K186E
XH_P38	19	51330932	51330932	Silent	SNP	G	T	G	KLK15	c.C180A	p.A60A
XH_P38	19	51535130	51535130	Splice_Site	SNP	A	G	A	KLK12	-	-
XH_P38	19	51840579	51840579	Missense_Mutation	SNP	G	A	G	VSIG10L	c.C2218T	p.R740W
XH_P38	19	51841335	51841335	Silent	SNP	G	A	G	VSIG10L	c.C1857T	p.P619P
XH_P38	19	51844807	51844807	Silent	SNP	C	T	C	VSIG10L	c.G495A	p.P165P
XH_P38	19	51850290	51850290	Missense_Mutation	SNP	G	A	G	ETFB	c.C734T	p.T245M
XH_P38	19	51871195	51871195	Silent	SNP	G	A	G	CLDND2	c.C255T	p.C85C
XH_P38	19	51875225	51875225	Silent	SNP	G	T	G	NGK7	c.C408A	p.G136G
XH_P38	19	51960940	51960940	Missense_Mutation	SNP	A	G	A	SIGLEC8	c.T508C	p.T170P
XH_P38	19	52000672	52000672	Missense_Mutation	SNP	G	A	G	SIGLEC12	c.C1079T	p.T360M
XH_P38	19	52001485	52001485	Missense_Mutation	SNP	G	A	G	SIGLEC12	c.C838T	p.H280Y
XH_P38	19	52002729	52002729	Silent	SNP	G	A	G	SIGLEC12	c.C696T	p.G232G
XH_P38	19	52003331	52003331	Missense_Mutation	SNP	G	C	G	SIGLEC12	c.C297G	p.H99Q
XH_P38	19	52033206	52033206	Missense_Mutation	SNP	G	A	G	SIGLEC6	c.C628T	p.L210F
XH_P38	19	52034469	52034469	Silent	SNP	C	T	C	SIGLEC6	c.G264A	p.K88K
XH_P38	19	52220351	52220351	Silent	SNP	G	A	G	HAS1	c.C795T	p.D265D
XH_P38	19	52520607	52520607	Missense_Mutation	SNP	C	T	C	ZNF614	c.G244A	p.G82R
XH_P38	19	52569057	52569057	Missense_Mutation	SNP	C	T	C	ZNF841	c.G1730A	p.S577N
XH_P38	19	52937339	52937339	Silent	SNP	G	A	G	ZNF534	c.G147A	p.E49E
XH_P38	19	53117531	53117531	Missense_Mutation	SNP	C	T	C	ZNF83	c.G287A	p.S96N
XH_P38	19	53117809	53117809	Silent	SNP	C	A	C	ZNF83	c.G9T	p.G3G
XH_P38	19	53269614	53269614	Silent	SNP	G	A	G	ZNF600	c.C1395T	p.T465T
XH_P38	19	53303705	53303705	Missense_Mutation	SNP	T	G	T	ZNF28	c.A1393C	p.A465Q
XH_P38	19	53761775	53761775	Silent	SNP	C	T	C	VN1R2	c.C147T	p.R49R
XH_P38	19	53854397	53854397	Missense_Mutation	SNP	G	C	G	ZNF845	c.G469C	p.E157Q
XH_P38	19	53958126	53958126	Missense_Mutation	SNP	T	G	T	ZNF761	c.T365G	p.I122S
XH_P38	19	53959615	53959615	Silent	SNP	G	A	G	ZNF761	c.G1854A	p.T618T
XH_P38	19	53959804	53959804	Silent	SNP	T	C	T	ZNF761	c.T2043C	p.H681H
XH_P38	19	53994802	53994802	Missense_Mutation	SNP	A	T	A	ZNF813	c.A1316T	p.Y439F
XH_P38	19	53995004	53995004	Silent	SNP	G	A	G	ZNF813	c.G1518A	p.R506R
XH_P38	19	54561792	54561792	Silent	SNP	G	A	G	VSTM1	c.C123T	p.A41A
XH_P38	19	54744771	54744771	Silent	SNP	A	G	A	LILRA6	c.T891C	p.Y297Y
XH_P38	19	54744921	54744921	Silent	SNP	A	G	A	LILRA6	c.T741C	p.S247S
XH_P38	19	54755918	54755918	Missense_Mutation	SNP	C	G	C	LILRB5	c.G1328C	p.R443P
XH_P38	19	54782201	54782201	Missense_Mutation	SNP	C	T	C	LILRB2	c.G823A	p.A275T
XH_P38	19	54848741	54848741	Silent	SNP	T	C	T	LILRA4	c.A882G	p.R294R
XH_P38	19	54930361	54930361	Silent	SNP	C	T	C	TTYH1	c.C186T	p.I62I
XH_P38	19	55106696	55106696	Missense_Mutation	SNP	C	T	C	LILRA1	c.C490T	p.H164Y
XH_P38	19	55174498	55174498	Missense_Mutation	SNP	T	C	T	LILRB4	c.T13C	p.F5L
XH_P38	19	55451050	55451050	Silent	SNP	C	T	C	NLRP7	c.G1137A	p.K379K
XH_P38	19	55451232	55451232	Missense_Mutation	SNP	C	T	C	NLRP7	c.G955A	p.V319I
XH_P38	19	55485899	55485899	Silent	SNP	G	A	G	NLRP2	c.G312A	p.K104K
XH_P38	19	55525497	55525497	Missense_Mutation	SNP	A	G	A	GP6	c.T1816C	p.F606L
XH_P38	19	55525894	55525894	Silent	SNP	G	A	G	GP6	c.C1419T	p.P473P
XH_P38	19	55539061	55539061	Silent	SNP	A	G	A	GP6	c.T495C	p.F165F
XH_P38	19	55598724	55598724	Missense_Mutation	SNP	A	G	A	EP58L1	c.A1625G	p.K542R
XH_P38	19	55716800	55716800	Silent	SNP	A	G	A	PTPRH	c.T513C	p.T171T
XH_P38	19	55964720	55964720	Silent	SNP	G	A	G	ISOC2	c.C363T	p.S121S
XH_P38	19	56113512	56113512	Missense_Mutation	SNP	C	A	C	ZNF524	c.C34A	p.P12T
XH_P38	19	56244004	56244004	Nonsense_Mutation	INS	-	TGTTTT	-	NLRP9	92_1193insAAA	p.L398delinsX
XH_P38	19	56321517	56321517	Silent	SNP	T	C	T	NLRP11	c.A162G	p.G54G
XH_P38	19	56369593	56369593	Silent	SNP	T	C	T	NLRP4	c.T834C	p.A278A
XH_P38	19	56490816	56490816	Frame_Shift_Ins	INS	-	TCTGGACTTGAA	-	NLRP8	GAGACATCTGGA	p.R959fs
XH_P38	19	56538976	56538976	Missense_Mutation	SNP	C	G	G	NLRP5	c.G1377C	p.M459I
XH_P38	19	56552456	56552456	Silent	SNP	G	T	G	NLRP5	c.G2955T	p.L985L
XH_P38	19	57065189	57065189	Silent	SNP	T	C	T	ZFP28	c.T1035C	p.F345F

XH_P38	19	57132968	57132968	Missense_Mutation	SNP	G	A	G	ZNF71	c.G313A	p.V105I
XH_P38	19	57931553	57931553	Silent	SNP	C	T	C	ZNF17	c.C693T	p.S231S
XH_P38	19	58058739	58058739	Silent	SNP	T	C	T	ZNF550	c.A873G	p.Q291Q
XH_P38	19	58213952	58213952	Missense_Mutation	SNP	C	A	C	ZNF154	c.G365T	p.G122V
XH_P38	19	58233733	58233733	Silent	SNP	C	T	C	ZNF671	c.G45A	p.V15V
XH_P38	19	58491627	58491627	Missense_Mutation	SNP	T	C	T	ZNF606	c.A151G	p.S51G
XH_P38	19	58572979	58572979	Missense_Mutation	SNP	G	A	G	ZNF135	c.G101A	p.G34D
XH_P38	19	58578578	58578578	Silent	SNP	C	T	C	ZNF135	c.C762T	p.Y254Y
XH_P38	19	58596134	58596134	Missense_Mutation	SNP	G	A	G	ZSCAN18	c.C1043T	p.A348V
XH_P38	19	58850341	58850341	Silent	SNP	G	C	G	ZSCAN22	c.G1125C	p.T375T
XH_P38	19	58991743	58991743	Missense_Mutation	SNP	G	A	G	ZNF446	c.G1003A	p.E335K
XH_P38	19	58991900	58991900	Missense_Mutation	SNP	G	A	G	ZNF446	c.G1160A	p.R387H
XH_P38	19	59028939	59028939	Silent	SNP	G	A	G	ZBTB45	c.C102T	p.D34D
XH_P38	19	59061357	59061357	Silent	SNP	C	T	C	TRIM28	c.C2148T	p.P716P
XH_P38	19	59074429	59074429	Silent	SNP	C	T	C	MZF1	c.G1215A	p.T405T
XH_P38	19	59082368	59082368	Missense_Mutation	SNP	C	T	C	MZF1	c.G389A	p.R130Q
XH_P38	19	59082605	59082605	Missense_Mutation	SNP	C	T	C	MZF1	c.G152A	p.R51H
XH_P38	20	76962	76962	Silent	SNP	T	C	T	DEFB125	c.T375C	p.S125S
XH_P38	20	239804	239804	Missense_Mutation	SNP	T	C	T	DEFB132	c.T145C	p.C49R
XH_P38	20	377226	377226	Silent	SNP	C	T	C	TRIB3	c.C969T	p.A323A
XH_P38	20	741847	741847	Silent	SNP	A	G	A	SLC52A3	c.T1233C	p.S411S
XH_P38	20	744308	744308	Missense_Mutation	SNP	T	C	T	SLC52A3	c.A907G	p.I303V
XH_P38	20	745963	745963	Silent	SNP	G	A	G	SLC52A3	c.C456T	p.P152P
XH_P38	20	1293247	1293247	Missense_Mutation	SNP	C	T	C	SDCBP2	c.G289A	p.V97M
XH_P38	20	1350709	1350709	Silent	SNP	T	C	T	FKBP1A	c.A258G	p.P86P
XH_P38	20	2321105	2321105	Missense_Mutation	SNP	G	C	G	TGM3	c.G1960C	p.G654R
XH_P38	20	2380323	2380323	Silent	SNP	G	A	G	TGM6	c.G789A	p.K263K
XH_P38	20	2384434	2384434	Missense_Mutation	SNP	G	A	G	TGM6	c.G1301A	p.R434H
XH_P38	20	2739583	2739583	Silent	SNP	T	C	T	EBF4	c.T1755C	p.F585F
XH_P38	20	2945759	2945759	Missense_Mutation	SNP	C	T	C	PTPRA	c.C326T	p.P109L
XH_P38	20	3090848	3090848	Missense_Mutation	SNP	T	G	T	UBOX5	c.A1525C	p.T509P
XH_P38	20	3147468	3147468	Silent	SNP	G	A	G	LZT53	c.C342T	p.N114N
XH_P38	20	3655219	3655219	Missense_Mutation	SNP	T	C	T	ADAM33	c.A532G	p.T178A
XH_P38	20	3684022	3684022	Silent	SNP	A	G	A	SIGLEC1	c.T1050C	p.N350N
XH_P38	20	3684729	3684729	Missense_Mutation	SNP	T	C	T	SIGLEC1	c.A716G	p.K239R
XH_P38	20	3732633	3732633	Silent	SNP	C	T	C	HSPA12B	c.C1623T	p.C541C
XH_P38	20	3759936	3759936	Silent	SNP	G	A	G	SPEF1	c.C285T	p.C95C
XH_P38	20	5903485	5903485	Missense_Mutation	SNP	G	A	G	CHGB	c.G695A	p.R232Q
XH_P38	20	5904289	5904289	Missense_Mutation	SNP	G	A	G	CHGB	c.G1499A	p.R500K
XH_P38	20	5923223	5923223	Missense_Mutation	SNP	C	T	C	TRMT6	c.G367A	p.E123K
XH_P38	20	6032927	6032927	Silent	SNP	C	T	C	LRRN4	c.G519A	p.Q173Q
XH_P38	20	6033033	6033033	Missense_Mutation	SNP	G	A	G	LRRN4	c.C413T	p.P138L
XH_P38	20	10620275	10620275	Silent	SNP	G	A	G	JAG1	c.C3528T	p.Y1176Y
XH_P38	20	10653469	10653469	Silent	SNP	C	T	C	JAG1	c.G267A	p.G89G
XH_P38	20	16360492	16360492	Missense_Mutation	SNP	C	T	C	KIF16B	c.G2155A	p.E171K
XH_P38	20	17462411	17462411	Missense_Mutation	SNP	G	A	G	PCSK2	c.G1508A	p.R503Q
XH_P38	20	18142564	18142564	Silent	SNP	A	G	A	KAT14	c.A783G	p.K261K
XH_P38	20	20484043	20484043	Silent	SNP	A	G	A	RALGAP2	c.T5160C	p.H1720H
XH_P38	20	21284236	21284236	Silent	SNP	T	C	T	XRN2	c.T60C	p.P20P
XH_P38	20	23016970	23016970	Missense_Mutation	SNP	T	G	T	SSTR4	c.T850G	p.F284V
XH_P38	20	23028724	23028724	Missense_Mutation	SNP	G	A	G	THBD	c.C1418T	p.A473V
XH_P38	20	23424660	23424660	Silent	SNP	G	C	G	CSTL1	c.G309C	p.L103L
XH_P38	20	23546639	23546639	Missense_Mutation	SNP	T	G	T	CST9L	c.A326C	p.H109P
XH_P38	20	23731426	23731426	Silent	SNP	C	T	C	CST1	c.G78A	p.E26E
XH_P38	20	23805953	23805953	Missense_Mutation	SNP	C	T	C	CST2	c.G236A	p.G79D
XH_P38	20	23860178	23860178	Missense_Mutation	SNP	A	G	A	CST5	c.T136C	p.C46R
XH_P38	20	24964556	24964556	Missense_Mutation	SNP	T	C	T	APMAP	c.A195G	p.I65M
XH_P38	20	25062684	25062684	Missense_Mutation	SNP	G	C	G	VXS1	c.C49G	p.L17V
XH_P38	20	30720826	30720826	Missense_Mutation	SNP	C	T	C	TM95F4	c.C26T	p.P9L
XH_P38	20	31022469	31022469	Missense_Mutation	SNP	G	A	G	ASXL1	c.G1954A	p.G652S
XH_P38	20	33591006	33591006	Silent	SNP	G	A	G	TRPC4AP	c.C2337T	p.L779L
XH_P38	20	33874720	33874720	Missense_Mutation	SNP	C	T	C	FAM83C	c.G1862A	p.R621Q
XH_P38	20	34022387	34022387	Missense_Mutation	SNP	A	C	A	GDF5	c.T826G	p.S276A
XH_P38	20	34145209	34145209	Silent	SNP	C	T	C	ERGIC3	c.C1086T	p.I362I
XH_P38	20	35128751	35128751	Missense_Mutation	SNP	G	A	G	DLGAP4	c.G128A	p.R43Q
XH_P38	20	35443691	35443691	Silent	SNP	G	A	G	SOGA1	c.C2154T	p.S718S
XH_P38	20	39990632	39990632	Missense_Mutation	SNP	G	A	G	EMILIN3	c.C1577T	p.T526I
XH_P38	20	41306600	41306600	Silent	SNP	A	G	A	PTPRT	c.T1059C	p.D353D
XH_P38	20	42743454	42743454	Silent	SNP	A	G	A	JPH2	c.T2073C	p.F691F
XH_P38	20	42744587	42744587	Silent	SNP	G	C	G	JPH2	c.C1728G	p.P576P
XH_P38	20	43139956	43139956	Missense_Mutation	SNP	T	C	T	SERINC3	c.A449G	p.Y150C
XH_P38	20	43629911	43629911	Missense_Mutation	SNP	T	C	T	ISK4	c.T1064C	p.I355T
XH_P38	20	44184498	44184498	Missense_Mutation	SNP	A	G	A	WFDC8	c.T287C	p.M96T
XH_P38	20	44506918	44506918	Missense_Mutation	SNP	C	T	C	ZSWIM3	c.C1721T	p.P574L
XH_P38	20	44520562	44520562	Nonsense_Mutation	INS	-	GGTTGACTCCA	-	CTSA	TAGGGGTTGTA	QLQLYQPRIGVV
XH_P38	20	44581348	44581348	Silent	SNP	G	A	G	ZNF335	c.C2703T	p.S901S
XH_P38	20	48522392	48522392	Missense_Mutation	SNP	G	A	G	SPATA2	c.C1327T	p.L443F
XH_P38	20	48600809	48600809	Silent	SNP	G	A	G	SNAI1	c.G531A	p.T177T
XH_P38	20	49225058	49225058	Missense_Mutation	SNP	C	T	C	RIPOR3	c.G824A	p.R275Q
XH_P38	20	49576348	49576348	Silent	SNP	A	G	A	MOC53	c.A969G	p.K323K
XH_P38	20	50803444	50803444	Silent	SNP	C	T	C	ZFP64	c.G213A	p.S71S
XH_P38	20	52192637	52192637	Missense_Mutation	SNP	T	C	T	ZNF217	c.A2666G	p.D889G
XH_P38	20	52198340	52198340	Silent	SNP	T	A	T	ZNF217	c.A1026T	p.A342A
XH_P38	20	56098733	56098733	Missense_Mutation	SNP	T	C	T	CTCF	c.A529G	p.T177A
XH_P38	20	56099114	56099114	Missense_Mutation	SNP	C	G	C	CTCF	c.G148C	p.E50Q
XH_P38	20	56137895	56137895	Missense_Mutation	SNP	G	C	G	PCK1	c.G550C	p.V184L
XH_P38	20	56138686	56138686	Silent	SNP	C	T	C	PCK1	c.C864T	p.C288C
XH_P38	20	56139403	56139403	Silent	SNP	T	C	T	PCK1	c.T1140C	p.G380G
XH_P38	20	56190634	56190634	Missense_Mutation	SNP	C	T	C	ZBP1	c.G37A	p.E13K
XH_P38	20	57245580	57245580	Missense_Mutation	SNP	G	A	G	STX16	c.G557A	p.R186Q
XH_P38	20	58514300	58514300	Silent	SNP	G	A	G	PPP1R3D	c.C687T	p.P229P
XH_P38	20	60511860	60511860	Silent	SNP	C	T	C	CDH4	c.C2499T	p.Y833Y
XH_P38	20	60699716	60699716	Silent	SNP	G	A	G	LSM14B	c.G171A	p.A57A
XH_P38	20	60791422	60791422	Silent	SNP	C	T	C	HRH3	c.G978A	p.P326P
XH_P38	20	60893639	60893639	Silent	SNP	G	C	G	LAMA5	c.C7110G	p.T2370T
XH_P38	20	61039958	61039958	Silent	SNP	T	C	T	GATA5	c.A1128G	p.P376P
XH_P38	20	61040453	61040453	Silent	SNP	C	G	C	GATA5	c.G981C	p.S327S
XH_P38	20	61040951	61040951	Silent	SNP	C	T	C	GATA5	c.G852A	p.K284K

XH_P38	20	61048549	61048549	Silent	SNP	G	A	G	GATA5	c.C609T	p.D203D
XH_P38	20	61440971	61440971	Silent	SNP	G	A	G	OGFR	c.G354A	p.T118T
XH_P38	20	61512185	61512185	Missense_Mutation	SNP	G	C	G	DIDO1	c.C5123G	p.S1708C
XH_P38	20	61525293	61525293	Silent	SNP	C	T	C	DIDO1	c.G2826A	p.P942P
XH_P38	20	61528271	61528271	Missense_Mutation	SNP	C	T	C	DIDO1	c.G1666A	p.A56T
XH_P38	20	62126299	62126299	Silent	SNP	C	T	C	EEF1A2	c.G480A	p.P160P
XH_P38	20	62165528	62165528	Missense_Mutation	SNP	G	A	G	PTK6	c.C371T	p.A124V
XH_P38	20	62191321	62191321	Silent	SNP	A	G	A	HELZ2	c.T6078C	p.N2026N
XH_P38	20	62191937	62191937	Silent	SNP	G	A	G	HELZ2	c.C5688T	p.C1896C
XH_P38	20	62193019	62193019	Silent	SNP	C	T	C	HELZ2	c.G5064A	p.P1688P
XH_P38	20	62193445	62193445	Missense_Mutation	SNP	G	A	G	HELZ2	c.C4802T	p.T1601M
XH_P38	20	62194713	62194713	Missense_Mutation	SNP	A	C	A	HELZ2	c.T3755G	p.L1252R
XH_P38	20	62195220	62195220	Missense_Mutation	SNP	C	T	C	HELZ2	c.G3248A	p.R1083Q
XH_P38	20	62195672	62195672	Silent	SNP	C	T	C	HELZ2	c.G2796A	p.L932L
XH_P38	20	62196033	62196033	Missense_Mutation	SNP	C	T	C	HELZ2	c.G2435A	p.R812K
XH_P38	20	62196182	62196182	Silent	SNP	G	C	G	HELZ2	c.C2286G	p.A762A
XH_P38	20	62198977	62198977	Silent	SNP	G	A	G	HELZ2	c.C27T	p.A9A
XH_P38	20	62221766	62221766	Silent	SNP	C	T	C	GMEB2	c.G1269A	p.P423P
XH_P38	20	62236148	62236148	Silent	SNP	T	C	T	GMEB2	c.A177G	p.A59A
XH_P38	20	62320929	62320929	Silent	SNP	C	T	C	RTEL1	c.C1284T	p.R428R
XH_P38	20	62326159	62326159	Missense_Mutation	SNP	G	A	G	RTEL1	c.G2506A	p.A836T
XH_P38	20	62422080	62422080	Missense_Mutation	SNP	T	C	T	ZBTB46	c.A31G	p.T11A
XH_P38	21	30971183	30971183	Silent	SNP	G	A	G	GRIK1	c.C747T	p.D249D
XH_P38	21	33684178	33684178	Silent	SNP	C	G	C	MRAP	c.C213G	p.T71T
XH_P38	21	33688865	33688865	Silent	SNP	A	G	A	URB1	c.T6546C	p.A2182A
XH_P38	21	33719695	33719695	Silent	SNP	C	T	C	URB1	c.G3438A	p.K1466K
XH_P38	21	33726326	33726326	Silent	SNP	G	A	G	URB1	c.C2332T	p.L778L
XH_P38	21	35773137	35773137	Silent	SNP	C	T	C	C21orf140	c.G234A	p.A78A
XH_P38	21	35893737	35893737	Missense_Mutation	SNP	T	C	T	RCAN1	c.A481G	p.R161G
XH_P38	21	37507501	37507501	Missense_Mutation	SNP	G	A	G	CBR3	c.G11A	p.C4Y
XH_P38	21	37507769	37507769	Silent	SNP	C	T	C	CBR3	c.C279T	p.V93V
XH_P38	21	37609571	37609571	Silent	SNP	T	C	T	DOPEY2	c.T2634C	p.R878R
XH_P38	21	37617533	37617533	Silent	SNP	C	T	C	DOPEY2	c.C3255T	p.S1085S
XH_P38	21	37692589	37692589	Silent	SNP	A	T	A	MORC3	c.A27T	p.I9I
XH_P38	21	40191431	40191431	Silent	SNP	T	G	T	ETS2	c.T816G	p.T272T
XH_P38	21	43161022	43161022	Silent	SNP	C	T	C	RIPK4	c.G2331A	p.T777T
XH_P38	21	43161877	43161877	Silent	SNP	C	T	C	RIPK4	c.G1476A	p.A492A
XH_P38	21	43162150	43162150	Silent	SNP	G	A	G	RIPK4	c.C1203T	p.G401G
XH_P38	21	43164232	43164232	Silent	SNP	C	A	C	RIPK4	c.G1005T	p.L335L
XH_P38	21	43236176	43236176	Silent	SNP	G	A	G	PRDM15	c.C2388T	p.H796H
XH_P38	21	43327856	43327856	Silent	SNP	A	G	A	C2CD2	c.T591C	p.F197F
XH_P38	21	43539293	43539293	Missense_Mutation	SNP	G	A	G	UMODL1	c.G2716A	p.V906I
XH_P38	21	43803167	43803167	Missense_Mutation	SNP	T	C	T	TMPRSS3	c.A376G	p.L126V
XH_P38	21	44179145	44179145	Missense_Mutation	SNP	G	A	G	PDE9A	c.G196A	p.G66R
XH_P38	21	44485350	44485350	Silent	SNP	G	A	G	CBS	c.C384T	p.Y128Y
XH_P38	21	44589215	44589215	Silent	SNP	C	T	C	CRYAA	c.C6T	p.D2D
XH_P38	21	44840138	44840138	Silent	SNP	G	A	G	LOC102724428	c.C948T	p.G316G
XH_P38	21	45528919	45528919	Missense_Mutation	SNP	G	A	G	PWP2	c.G73A	p.D25N
XH_P38	21	45553596	45553596	Missense_Mutation	SNP	T	C	T	C21orf33	c.T17C	p.V6A
XH_P38	21	45709568	45709568	Silent	SNP	C	T	C	AIRE	c.C681T	p.G227G
XH_P38	21	45959195	45959195	Missense_Mutation	SNP	G	A	G	KRTAP10-1	c.C839T	p.P280L
XH_P38	21	45959312	45959312	Missense_Mutation	SNP	C	T	C	KRTAP10-1	c.G722A	p.R241Q
XH_P38	21	45959733	45959733	Missense_Mutation	SNP	C	T	C	KRTAP10-1	c.G301A	p.V101M
XH_P38	21	45970812	45970812	Missense_Mutation	SNP	G	A	G	KRTAP10-2	c.C530T	p.P177L
XH_P38	21	45978483	45978483	Missense_Mutation	SNP	G	A	G	KRTAP10-3	c.C116T	p.P39L
XH_P38	21	46011432	46011432	In_Frame_Ins	INS	-	TGGCAGCAGGT	-	KRTAP10-6	AAGTCCACCTGG12delinsVQHLPPSC	
XH_P38	21	46011583	46011583	Nonsense_Mutation	SNP	G	T	G	KRTAP10-6	c.C783A	p.C261X
XH_P38	21	46021335	46021335	Missense_Mutation	SNP	G	A	G	KRTAP10-7	c.G799A	p.V267M
XH_P38	21	46057810	46057810	Missense_Mutation	SNP	C	G	G	KRTAP10-10	c.C476G	p.P159R
XH_P38	21	46057961	46057961	Silent	SNP	C	T	C	KRTAP10-10	c.C627T	p.C209C
XH_P38	21	46233836	46233836	Missense_Mutation	SNP	C	A	C	SUMO3	c.G205T	p.V69F
XH_P38	21	46876173	46876173	Silent	SNP	C	T	C	COL18A1	c.C729T	p.P243P
XH_P38	21	46896381	46896381	Silent	SNP	G	T	G	COL18A1	c.G1455T	p.V485V
XH_P38	21	46897878	46897878	Missense_Mutation	SNP	C	T	C	COL18A1	c.C1760T	p.P587L
XH_P38	21	46910210	46910210	Missense_Mutation	SNP	G	A	G	COL18A1	c.G2521A	p.V841I
XH_P38	21	46924383	46924383	Silent	SNP	C	T	C	COL18A1	c.C3321T	p.P1107P
XH_P38	21	47410931	47410931	Silent	SNP	T	C	T	COL6A1	c.T1095C	p.G365G
XH_P38	21	47423040	47423040	Missense_Mutation	SNP	A	G	A	COL6A1	c.A2441G	p.R814R
XH_P38	21	47423790	47423790	Missense_Mutation	SNP	C	T	C	COL6A1	c.C2950T	p.R984C
XH_P38	21	47532440	47532440	Silent	SNP	C	T	C	COL6A2	c.C663T	p.P221P
XH_P38	21	47552386	47552386	Missense_Mutation	SNP	G	A	G	COL6A2	c.G2980A	p.A994T
XH_P38	21	47635176	47635176	Missense_Mutation	SNP	T	C	T	LSS	c.A689G	p.H230R
XH_P38	21	47635627	47635627	Silent	SNP	C	G	C	LSS	c.G624C	p.P208P
XH_P38	21	47786524	47786524	Missense_Mutation	SNP	A	G	A	PCNT	c.A2281G	p.T761A
XH_P38	21	47836653	47836653	Missense_Mutation	SNP	C	T	C	PCNT	c.C6467T	p.P2156L
XH_P38	21	47851753	47851753	Missense_Mutation	SNP	A	G	A	PCNT	c.A8021G	p.Q2674R
XH_P38	21	47863757	47863757	Missense_Mutation	SNP	A	C	A	PCNT	c.A9144C	p.R3048S
XH_P38	21	47910523	47910523	Silent	SNP	A	G	A	DIP2A	c.A174G	p.P58P
XH_P38	22	16287372	16287372	Missense_Mutation	SNP	C	T	C	POTEH	c.G514A	p.V172I
XH_P38	22	17990852	17990852	Missense_Mutation	SNP	G	A	G	CECR2	c.G389A	p.R130H
XH_P38	22	18607020	18607020	Silent	SNP	C	T	C	TUBA8	c.C126T	p.Y42Y
XH_P38	22	18650682	18650682	Missense_Mutation	SNP	C	T	C	USP18	c.C506T	p.T169M
XH_P38	22	18905991	18905991	Missense_Mutation	SNP	T	C	T	PRODH	c.A941G	p.N314S
XH_P38	22	19132061	19132061	Silent	SNP	C	T	C	DGCR14	c.G93A	p.A31A
XH_P38	22	19711403	19711403	Missense_Mutation	SNP	C	T	C	GP1BB	c.C37T	p.L13F
XH_P38	22	19751829	19751829	Silent	SNP	C	T	C	TBX1	c.C664T	p.L222L
XH_P38	22	19766782	19766782	Missense_Mutation	SNP	C	T	C	TBX1	c.C1049T	p.T350M
XH_P38	22	19789541	19789541	Missense_Mutation	SNP	A	C	A	GNB1L	c.T715G	p.W239G
XH_P38	22	19808769	19808769	Missense_Mutation	SNP	C	T	C	GNB1L	c.G110A	p.R37H
XH_P38	22	20103915	20103915	Nonsense_Mutation	SNP	C	T	C	RANBP1	c.C208T	p.R70X
XH_P38	22	20307256	20307256	Silent	SNP	G	A	G	DGCR6L	c.C177T	p.T59T
XH_P38	22	20759672	20759672	Missense_Mutation	SNP	G	A	G	ZNF74	c.G263A	p.G88E
XH_P38	22	20761192	20761192	Missense_Mutation	SNP	G	T	G	ZNF74	c.G1656T	p.K552N
XH_P38	22	20761193	20761193	Missense_Mutation	SNP	C	T	C	ZNF74	c.C1657T	p.L553F
XH_P38	22	20784050	20784050	Missense_Mutation	SNP	T	A	T	SCARF2	c.A1273T	p.T425S
XH_P38	22	20800835	20800835	Silent	SNP	A	G	A	KLHL22	c.T1434C	p.D478D
XH_P38	22	20920814	20920819	In_Frame_Del	DEL	CAGCAG	-	CAGCAG	MED15	c.538_543del	p.180_181del
XH_P38	22	20940085	20940085	Silent	SNP	G	A	G	MED15	c.G1869A	p.P623P

XH_P38	22	21385277	21385277	Silent	SNP	C	T	C	SLC7A4	c.G825A	p.S275S
XH_P38	22	21385843	21385843	Silent	SNP	G	A	G	SLC7A4	c.C259T	p.L87L
XH_P38	22	21982892	21982892	Missense_Mutation	SNP	C	T	C	YDIC	c.G787A	p.A263T
XH_P38	22	22288560	22288560	Missense_Mutation	SNP	G	A	G	PPM1F	c.C394T	p.R132C
XH_P38	22	22312790	22312790	Missense_Mutation	SNP	C	G	C	TOP3B	c.G1773C	p.Q591H
XH_P38	22	22318538	22318538	Missense_Mutation	SNP	C	T	C	TOP3B	c.G1093A	p.D365N
XH_P38	22	22318671	22318671	Silent	SNP	G	A	G	TOP3B	c.C960T	p.H320H
XH_P38	22	22869439	22869439	Silent	SNP	A	G	A	ZNF280A	c.T516C	p.D172D
XH_P38	22	23406099	23406099	Missense_Mutation	SNP	G	A	A	RSPH14	c.C634T	p.R212C
XH_P38	22	24583988	24583988	Silent	SNP	G	A	G	SUSD2	c.G2226A	p.L742L
XH_P38	22	24988920	24988920	Silent	SNP	C	T	C	LRRC75B	c.G87A	p.E29E
XH_P38	22	25144912	25144912	Missense_Mutation	SNP	C	T	C	PIWIL3	c.G1411A	p.V471I
XH_P38	22	26164413	26164413	Missense_Mutation	SNP	C	T	C	MYO18B	c.C530T	p.P177L
XH_P38	22	26422454	26422454	Silent	SNP	T	C	T	MYO18B	c.T6517C	p.L2173L
XH_P38	22	26422683	26422683	Missense_Mutation	SNP	C	T	C	MYO18B	c.C6746T	p.A2249V
XH_P38	22	26702015	26702015	Silent	SNP	A	C	A	SEZ6L	c.A1419C	p.T473T
XH_P38	22	28495028	28495028	Missense_Mutation	SNP	T	C	T	TTC28	c.A3422G	p.Y1141C
XH_P38	22	29446077	29446077	Silent	SNP	G	C	G	ZNRF3	c.G1908C	p.V636V
XH_P38	22	29446611	29446611	Silent	SNP	A	C	A	ZNRF3	c.A2442C	p.P814P
XH_P38	22	30163526	30163526	Missense_Mutation	SNP	A	G	A	UQCRI10	c.A139G	p.I47V
XH_P38	22	30189642	30189642	Missense_Mutation	SNP	C	T	C	ASCC2	c.G1484A	p.R495Q
XH_P38	22	30403167	30403167	Nonsense_Mutation	SNP	C	T	C	MTMR3	c.C736T	p.R246X
XH_P38	22	30689998	30689998	Silent	SNP	G	A	G	TBC1D10A	c.C828T	p.L276L
XH_P38	22	30766580	30766580	Missense_Mutation	SNP	G	A	G	CCDC157	c.G686A	p.G229E
XH_P38	22	30823196	30823196	Silent	SNP	T	C	T	MTFP1	c.T234C	p.T78T
XH_P38	22	30864610	30864610	Missense_Mutation	SNP	A	G	A	SEC14L3	c.T308C	p.I103T
XH_P38	22	30888504	30888504	Silent	SNP	C	T	C	SEC14L4	c.G621A	p.S207S
XH_P38	22	30975861	30975861	Missense_Mutation	SNP	C	T	C	PES1	c.G1216A	p.A406T
XH_P38	22	31032920	31032920	Silent	SNP	A	G	A	SLC35E4	c.A483G	p.P161P
XH_P38	22	31266546	31266546	Silent	SNP	T	C	T	OSBP2	c.T210C	p.A70A
XH_P38	22	31535995	31535995	Missense_Mutation	SNP	C	G	C	PLA2G3	c.G346C	p.E116Q
XH_P38	22	32754306	32754306	Missense_Mutation	SNP	T	C	T	RFPL3	c.T248C	p.M83T
XH_P38	22	32756407	32756407	Missense_Mutation	SNP	A	G	A	RFPL3	c.A542G	p.Y181C
XH_P38	22	32756555	32756555	Silent	SNP	G	C	G	RFPL3	c.G690C	p.T230T
XH_P38	22	32784051	32784051	Silent	SNP	T	C	T	RTCB	c.A1446G	p.V482V
XH_P38	22	33253292	33253292	Silent	SNP	C	T	C	TIMP3	c.C261T	p.S87S
XH_P38	22	36537893	36537893	Silent	SNP	A	G	A	APOL3	c.T564C	p.N188N
XH_P38	22	37329999	37329999	Silent	SNP	C	T	C	CSF2RB	c.C1278T	p.S426S
XH_P38	22	37387257	37387257	Missense_Mutation	SNP	T	C	T	TEX33	c.A806G	p.Y269C
XH_P38	22	37469591	37469591	Silent	SNP	G	A	G	TMPRSS6	c.C1536T	p.D512D
XH_P38	22	37480797	37480797	Silent	SNP	C	T	C	TMPRSS6	c.G1056A	p.S352S
XH_P38	22	37480861	37480861	Missense_Mutation	SNP	G	A	G	TMPRSS6	c.C992T	p.T331M
XH_P38	22	37485724	37485724	Missense_Mutation	SNP	T	C	T	TMPRSS6	c.A730G	p.K244E
XH_P38	22	37622815	37622815	Silent	SNP	A	G	A	RAC2	c.T477C	p.A159A
XH_P38	22	37637653	37637653	Silent	SNP	G	C	G	RAC2	c.C81G	p.A27A
XH_P38	22	37770066	37770066	Silent	SNP	G	T	G	ELFN2	c.C1509A	p.I503I
XH_P38	22	37770357	37770357	Silent	SNP	A	G	A	ELFN2	c.T1218C	p.F406F
XH_P38	22	37771158	37771158	Silent	SNP	G	A	G	ELFN2	c.C417T	p.I139I
XH_P38	22	38061821	38061821	Silent	SNP	C	T	C	PDXP	c.C834T	p.L278L
XH_P38	22	38130459	38130459	Missense_Mutation	SNP	G	T	G	TRIOBP	c.G4116T	p.F1372D
XH_P38	22	38131069	38131069	Missense_Mutation	SNP	C	T	C	TRIOBP	c.C4726T	p.R1576C
XH_P38	22	38168725	38168725	Missense_Mutation	SNP	G	A	G	TRIOBP	c.G1915A	p.A639T
XH_P38	22	38382304	38382304	Missense_Mutation	SNP	G	A	G	POLR2F	c.G437A	p.G146D
XH_P38	22	38493186	38493186	Splice_Site	SNP	C	T	C	BAIAP2L2	.	.
XH_P38	22	38642038	38642038	Silent	SNP	G	A	G	TMEM184B	c.C261T	p.I87I
XH_P38	22	39095987	39095987	Silent	SNP	A	G	A	JOSD1	c.T6C	p.S2S
XH_P38	22	39122038	39122038	Silent	SNP	C	T	C	GTBPBP1	c.C1101T	p.N367N
XH_P38	22	39125529	39125529	Silent	SNP	G	A	G	GTBPBP1	c.G1779A	p.S593S
XH_P38	22	39134715	39134715	Silent	SNP	T	C	T	SUN2	c.A1887G	p.Q629Q
XH_P38	22	39138332	39138332	Missense_Mutation	SNP	G	A	G	SUN2	c.C1105T	p.R369C
XH_P38	22	39477566	39477566	Missense_Mutation	SNP	A	G	A	APOBEC3G	c.A356G	p.H119R
XH_P38	22	39498038	39498038	Missense_Mutation	SNP	G	C	G	APOBEC3H	c.G534C	p.E178D
XH_P38	22	39883736	39883736	Silent	SNP	G	C	G	MGAT3	c.G384C	p.P128P
XH_P38	22	41489077	41489077	Silent	SNP	C	A	C	EP300	c.C69A	p.L23L
XH_P38	22	41626225	41626225	Silent	SNP	C	T	C	L3MBTL2	c.C2088T	p.V696V
XH_P38	22	42089630	42089630	Missense_Mutation	SNP	A	G	A	C22orf46	c.A380G	p.Q127R
XH_P38	22	42095644	42095644	Silent	SNP	C	T	C	MEI1	c.C102T	p.R34R
XH_P38	22	42276742	42276742	Missense_Mutation	SNP	G	C	G	SREBF2	c.G1784C	p.G595A
XH_P38	22	42306472	42306472	Missense_Mutation	SNP	T	C	T	SHISA8	c.A751G	p.T251A
XH_P38	22	42322716	42322716	Missense_Mutation	SNP	G	C	G	TNFRSF13C	c.C62G	p.P21R
XH_P38	22	42341934	42341934	Silent	SNP	A	G	A	CENPM	c.T111C	p.N37N
XH_P38	22	42525756	42525756	Silent	SNP	G	A	G	CYP2D6	c.C336T	p.F112F
XH_P38	22	42526694	42526694	Missense_Mutation	SNP	G	A	G	CYP2D6	c.C100T	p.P34S
XH_P38	22	42950033	42950033	Missense_Mutation	SNP	G	A	G	SERHL2	c.G7A	p.E3K
XH_P38	22	43568512	43568512	Missense_Mutation	SNP	C	T	C	TLL12	c.G1390A	p.V464M
XH_P38	22	43576904	43576904	Silent	SNP	G	A	G	TLL12	c.C390T	p.H130H
XH_P38	22	44287629	44287629	Silent	SNP	G	A	G	PNPLA5	c.C132T	p.R44R
XH_P38	22	45128232	45128232	Silent	SNP	T	C	T	PRR5	c.T231C	p.R77R
XH_P38	22	45132687	45132687	Missense_Mutation	SNP	G	A	G	PRR5	c.G442A	p.V148M
XH_P38	22	45723854	45723854	Silent	SNP	C	G	C	FAM118A	c.C432G	p.V144V
XH_P38	22	46318952	46318952	Silent	SNP	G	A	G	WNT7B	c.C834T	p.C278C
XH_P38	22	47085924	47085924	Silent	SNP	G	A	G	CERK	c.C1506T	p.D502D
XH_P38	22	50280655	50280655	Silent	SNP	C	T	C	ZBED4	c.C3345T	p.S1115S
XH_P38	22	50301476	50301476	Silent	SNP	T	C	T	ALG12	c.A885G	p.A295A
XH_P38	22	50307139	50307139	Silent	SNP	G	A	G	ALG12	c.C189T	p.V63V
XH_P38	22	50468933	50468933	Missense_Mutation	SNP	G	T	G	TTL8	c.C2177A	p.A726E
XH_P38	22	50636350	50636350	Missense_Mutation	SNP	C	T	C	TRABD	c.C782T	p.S261L
XH_P38	22	50658698	50658698	Missense_Mutation	SNP	T	A	T	TUBGCP6	c.A4090T	p.S1364C
XH_P38	22	50716167	50716167	Silent	SNP	G	A	G	PLXNB2	c.C5049T	p.S1683S
XH_P38	22	50719251	50719251	Silent	SNP	A	G	A	PLXNB2	c.T3915C	p.P1305P
XH_P38	22	50720622	50720622	Silent	SNP	C	T	C	PLXNB2	c.G3108A	p.Q1036Q
XH_P38	22	50722134	50722134	Missense_Mutation	SNP	T	C	T	PLXNB2	c.A2467G	p.I823V
XH_P38	22	50879447	50879447	Silent	SNP	T	G	T	PP6R2	c.T2493G	p.A831A
XH_P38	22	50921149	50921166	In_Frame_Del	DEL	CTGGGGCCCC	-	CTGGGGCCCCCG	ADM2	c.264_281del	p.88_94del
XH_P38	22	50928026	50928026	Silent	SNP	G	A	G	MIOX	c.G702A	p.L234L
XH_P38	22	50944128	50944128	Silent	SNP	G	A	G	LMF2	c.C891T	p.H297H
XH_P38	22	50960682	50960682	Splice_Site	SNP	C	T	C	NCAPH2	.	.
XH_P38	22	50964236	50964236	Missense_Mutation	SNP	G	A	G	TYMP	c.C1412T	p.S471L

XH_P38	22	51064039	51064039	Missense_Mutation	SNP	G	C	G	ARSA	c.C1178G	p.T393S
XH_P38	X	9905342	9905342	Silent	SNP	A	G	A	SHROOM2	c.A261G	p.T87T
XH_P38	X	9912792	9912792	Missense_Mutation	SNP	A	G	A	SHROOM2	c.A928G	p.I310V
XH_P38	X	11130193	11130193	Missense_Mutation	SNP	C	T	C	HCCS	c.C13T	p.P5S
XH_P38	X	18342034	18342034	Silent	SNP	G	A	G	SCML2	c.C342T	p.D114D
XH_P38	X	26157583	26157583	Missense_Mutation	SNP	G	A	G	MAGEB18	c.G481A	p.G161S
XH_P38	X	30327105	30327105	Missense_Mutation	SNP	C	T	C	NR0B1	c.G376A	p.V126M
XH_P38	X	34148761	34148761	Silent	SNP	C	A	C	FAM47A	c.G1635T	p.P545P
XH_P38	X	37061416	37061416	Missense_Mutation	SNP	C	T	C	FTHP18	c.G346A	p.G116S
XH_P38	X	37967868	37967868	Silent	SNP	T	C	T	SYTL5	c.T1416C	p.Y472Y
XH_P38	X	48690416	48690416	Silent	SNP	G	T	G	PCSK1N	c.C450A	p.L150L
XH_P38	X	48690546	48690546	Missense_Mutation	SNP	G	A	G	PCSK1N	c.C320T	p.A107V
XH_P38	X	48751471	48751471	Silent	SNP	A	G	A	TIMM17B	c.T228C	p.I76I
XH_P38	X	49021052	49021052	Silent	SNP	C	T	C	MAGIX	c.C204T	p.S68S
XH_P38	X	49034491	49034491	Missense_Mutation	SNP	C	T	C	PRICKLE3	c.G602A	p.R201H
XH_P38	X	53284002	53284002	Missense_Mutation	SNP	G	A	G	IQSEC2	c.C1111T	p.R371C
XH_P38	X	53641647	53641647	Silent	SNP	T	C	T	HUWE1	c.A2109G	p.S703S
XH_P38	X	57935520	57935520	Silent	SNP	G	A	G	ZXDA	c.C1335T	p.T445T
XH_P38	X	66766208	66766208	Missense_Mutation	SNP	G	A	G	AR	c.G1220A	p.R407H
XH_P38	X	69478942	69478942	Missense_Mutation	SNP	T	G	T	P2RY4	c.A533C	p.N178T
XH_P38	X	79698574	79698574	Missense_Mutation	SNP	T	A	T	FAM46D	c.T536A	p.V179D
XH_P38	X	92927634	92927634	Missense_Mutation	SNP	G	C	G	NAP1L3	c.C670G	p.P224A
XH_P38	X	100808342	100808342	Silent	SNP	C	T	C	ARMCX1	c.C429T	p.P143P
XH_P38	X	106310827	106310827	Missense_Mutation	SNP	C	T	C	RBM41	c.G1172A	p.R391Q
XH_P38	X	107449782	107449782	Missense_Mutation	SNP	C	T	C	COL4A6	c.G575A	p.G119E
XH_P38	X	129306113	129306113	Missense_Mutation	SNP	C	T	C	RAB33A	c.C77T	p.S26L
XH_P38	X	134994054	134994054	Silent	SNP	G	A	G	SAGE1	c.G2463A	p.R821K
XH_P38	X	148798223	148798223	Silent	SNP	T	C	T	MAGEA11	c.T990C	p.L330L
XH_P38	X	149639109	149639109	Missense_Mutation	SNP	G	C	G	MAML1	c.G1189C	p.G397R
XH_P38	X	150349122	150349122	Missense_Mutation	SNP	C	A	C	GPR50	c.C1067A	p.P356H
XH_P38	X	152482198	152482198	Silent	SNP	G	A	G	MAGEA1	c.C813T	p.L271L
XH_P38	X	152482917	152482917	Missense_Mutation	SNP	T	C	T	MAGEA1	c.A94G	p.T32A
XH_P38	X	152845465	152845465	Silent	SNP	G	A	G	ATP2B3	c.G3372A	p.S1124S
XH_P38	X	153278829	153278829	Missense_Mutation	SNP	G	A	G	IRAK1	c.C1358T	p.S453L
XH_P38	X	153284192	153284192	Missense_Mutation	SNP	A	G	A	IRAK1	c.T587C	p.F196S
XH_P38	X	153284483	153284483	Silent	SNP	G	A	G	IRAK1	c.C483T	p.V161V
XH_P38	X	153588165	153588165	Missense_Mutation	SNP	G	A	G	FLNA	c.C3914T	p.T1305M
XH_P38	X	153648592	153648592	Missense_Mutation	SNP	C	T	C	TAZ	c.C556T	p.R186C
XH_P38	Y	16952598	16952598	Missense_Mutation	SNP	C	A	C	NLGN4Y	c.C1403A	p.T468N
XH_P38	1	1119410	1119410	Missense_Mutation	SNV	G	A	A	TTL10	c.1199G>A	P.R400H
XH_P38	1	1354800	1354800	Missense_Mutation	SNV	C	T	T	ANKRD65	c.880G>A	P.E294K
XH_P38	1	145576112	145576112	Splice_Site	SNV	C	T	T	PIA53	c.24+10C>T	
XH_P38	1	152084175	152084175	Missense_Mutation	INDEL	-	TGCTCGCGCTCT	TGCTCGCGCTCT	TCHH	dupGGAGAGCGC06_L507insERREQQ	
XH_P38	1	161167854	161167854	Silent	SNV	G	A	A	ADAMTS4	c.564C>T	P.S188S
XH_P38	1	182353547	182353547	Missense_Mutation	SNV	T	G	G	GLUL	c.1115A>C	P.K372T
XH_P38	1	1855896	1855896	Missense_Mutation	SNV	G	A	A	CFAP74	c.4168C>T	P.R1390W
XH_P38	1	1918384	1918384	Silent	SNV	C	T	T	CFAP74	c.387G>A	P.A129A
XH_P38	1	203024722	203024722	Silent	SNV	A	T	T	PPFIA4	c.1992A>T	P.P664P
XH_P38	1	2434022	2434022	Missense_Mutation	SNV	C	A	A	PLCH2	c.3052C>A	P.P1018T
XH_P38	1	3697733	3697733	Silent	SNV	A	G	G	LRRC47	c.1671T>C	P.D557D
XH_P38	1	43232316	43232316	Silent	SNV	G	A	A	P3H1	c.327C>T	P.F109F
XH_P38	1	45469555	45469555	Missense_Mutation	SNV	G	A	A	HECTD3	c.2401C>T	P.R801W
XH_P38	1	50887065	50887065	Silent	SNV	G	A	A	DMRTA2	c.144C>T	P.G48G
XH_P38	1	53527917	53527917	Missense_Mutation	SNV	C	G	G	PODN	c.26C>G	P.A9G
XH_P38	1	55073681	55073681	Silent	SNV	A	G	G	ACOT11	c.1569A>G	P.R523R
XH_P38	1	70493890	70493890	Missense_Mutation	SNV	C	G	G	LRRC7	c.1717C>G	P.P573A
XH_P38	10	135053465	135053465	Missense_Mutation	SNV	G	A	A	VENTX	c.432G>A	P.M144I
XH_P38	10	72358340	72358340	Silent	SNV	C	T	T	PRF1	c.1137G>A	P.R379R
XH_P38	10	81465826	81465826	Silent	SNV	C	T	T	NUTM2B	c.411C>T	P.T137T
XH_P38	11	10064452	10064452	Missense_Mutation	SNV	A	G	G	SBF2	c.218T>C	P.I73T
XH_P38	11	119216275	119216275	Missense_Mutation	SNV	G	C	C	MFRP	c.496C>G	P.P166A
XH_P38	11	1267443	1267443	Silent	SNV	G	C	C	MUC5B	c.9333G>C	P.T3111T
XH_P38	11	45307634	45307634	Missense_Mutation	SNV	C	T	T	SYT13	c.125G>A	P.R42Q
XH_P38	11	49080252	49080252	Splice_Site	SNV	C	T	T	TRIM64C	c.412+1G>A	
XH_P38	11	6585207	6585207	Silent	SNV	G	A	A	DNHD1	c.10137G>A	P.L3379L
XH_P38	11	68029253	68029253	Missense_Mutation	SNV	C	T	T	C11orf24	c.1210G>A	P.V404M
XH_P38	11	73020363	73020363	Missense_Mutation	SNV	C	T	T	ARHGEF17	c.680C>T	P.A227V
XH_P38	11	75277582	75277582	Missense_Mutation	SNV	C	T	T	SERPINH1	c.188C>T	P.A63V
XH_P38	12	53189543	53189543	Missense_Mutation	SNV	C	T	T	KRT3	c.284G>A	P.G95D
XH_P38	12	56415298	56415298	Silent	SNV	C	T	T	IKZF4	c.21C>T	P.L7L
XH_P38	12	78362303	78362303	Missense_Mutation	SNV	A	G	G	NAV3	c.492A>G	P.I164M
XH_P38	12	8200622	8200622	Missense_Mutation	SNV	A	G	G	FOXJ2	c.962A>G	P.Q321R
XH_P38	13	111156506	111156506	Missense_Mutation	SNV	G	T	T	COL4A2	c.4297G>T	P.A1433S
XH_P38	13	114498153	114498153	Frame_Shift_Ins	INDEL	-	GT	GT	TMEM255B	c.287_288dupT	P.V97fs
XH_P38	14	101350523	101350523	Silent	SNV	G	A	A	RTL1	c.603C>T	P.P201P
XH_P38	14	38060905	38060905	Missense_Mutation	SNV	A	C	C	FOXA1	c.1084T>G	P.S362A
XH_P38	14	51101982	51101982	Nonsense_Mutation	SNV	G	T	T	SAV1	c.1071C>A	P.Y357*
XH_P38	15	101549194	101549194	Silent	SNV	G	C	C	LRRK1	c.915G>C	P.R305R
XH_P38	15	43814780	43814780	Missense_Mutation	SNV	C	G	G	MAP1A	c.1109C>G	P.P370R
XH_P38	15	55652305	55652305	Missense_Mutation	SNV	T	C	C	CCPG1	c.1666A>G	P.K556E
XH_P38	15	79254511	79254511	Missense_Mutation	SNV	C	T	T	RASGRF1	c.3749G>A	P.R1250Q
XH_P38	15	90172234	90172234	Missense_Mutation	SNV	C	T	T	KIF7	c.3637G>A	P.G1213S
XH_P38	15	91424255	91424255	Missense_Mutation	SNV	A	G	G	FURIN	c.1777A>G	P.S593G
XH_P38	16	1143567	1143567	Silent	SNV	G	A	A	C1QTNF8	c.693C>T	P.Y231Y
XH_P38	16	23464226	23464226	Silent	SNV	G	A	A	COG7	c.90C>T	P.S30S
XH_P38	16	30724960	30724960	Missense_Mutation	SNV	C	G	G	SRCAP	c.2421C>G	P.F807L
XH_P38	16	3614575	3614575	Silent	SNV	G	A	A	NLRC3	c.363C>T	P.T121T
XH_P38	16	4935185	4935185	Silent	SNV	C	T	T	PPL	c.3471G>A	P.K1157K
XH_P38	16	50733585	50733585	Missense_Mutation	SNV	G	A	A	NOD2	c.179G>A	P.R60H
XH_P38	16	718232	718232	Silent	SNV	C	T	T	RHOT2	c.33C>T	P.G111G
XH_P38	17	16594011	16594011	Silent	SNV	C	T	T	CCDC144A	c.297C>T	P.I99I
XH_P38	17	36490940	36490940	Missense_Mutation	SNV	G	A	A	GPR179	c.1621C>T	P.R541C
XH_P38	17	39190954	39190954	Missense_Mutation	INDEL	-	GGCTGGCAGCAG	GGCTGGCAGCAG	KRTAP1-3	ACCACTGCTGCTG	Q41insETSCCPSSCC
XH_P38	17	4798399	4798399	Missense_Mutation	SNV	G	A	A	MINK1	c.2887G>A	P.D963N
XH_P38	17	7318920	7318920	Silent	SNV	C	T	T	NLGN2	c.1128C>T	P.Y376Y
XH_P38	17	73838701	73838701	Splice_Site	SNV	A	C	C	UNC13D	c.389-7T>G	
XH_P38	17	79804369	79804369	Missense_Mutation	SNV	G	A	A	P4HB	c.992C>T	P.S331L
XH_P38	18	44641603	44641603	Missense_Mutation	SNV	T	C	C	HDHD2	c.242A>G	P.D81G

XH_P38	18	5443840	5443840	Silent	SNV	G	T	T	EPB41L3	c.526C>A	P.R176R
XH_P38	18	580609	580609	Silent	SNV	A	G	G	CETN1	c.201A>G	P.E67E
XH_P38	19	17837685	17837685	Missense_Mutation	SNV	C	T	T	MAP1S	c.1414C>T	P.R472C
XH_P38	19	2120910	2120910	Missense_Mutation	SNV	T	C	C	AP3D1	c.1432A>G	P.I478V
XH_P38	19	2805172	2805172	Missense_Mutation	SNV	G	A	A	THOP1	c.748G>A	P.E250K
XH_P38	19	3110339	3110339	Splice_Site	SNV	C	T	T	GNA11	c.321+8C>T	
XH_P38	19	41003463	41003463	Missense_Mutation	SNV	C	T	T	SPTBN4	c.736C>T	P.R246C
XH_P38	19	45567708	45567708	Missense_Mutation	SNV	G	C	C	CLASRP	c.1043G>C	P.R348P
XH_P38	19	46998253	46998253	Missense_Mutation	SNV	G	C	C	PNMAL2	c.470C>G	P.P157R
XH_P38	19	47124591	47124591	Missense_Mutation	SNV	G	T	T	PTGIR	c.1107C>A	P.S369R
XH_P38	19	47778530	47778530	Silent	SNV	C	T	T	INAFM1	c.354C>T	P.S118S
XH_P38	19	4793216	4793216	Silent	SNV	C	A	A	FEM1A	c.1350C>A	P.A450A
XH_P38	19	50436269	50436269	Missense_Mutation	SNV	G	A	A	ATF5	c.769G>A	P.V257M
XH_P38	19	54744921	54744921	Silent	SNV	A	G	G	LILRB3	c.741T>C	P.S247S
XH_P38	19	56113512	56113512	Missense_Mutation	SNV	C	A	A	ZNF524	c.34C>A	P.P12T
XH_P38	19	58596134	58596134	Missense_Mutation	SNV	G	A	A	ZSCAN18	c.1619C>T	P.A540V
XH_P38	19	652275	652275	Silent	SNV	S2A	A	A	RNF126	c.156C>T	P.A52A
XH_P38	19	7682305	7682305	Silent	SNV	G	A	A	CAMSAP3	c.3387G>A	P.A1129A
XH_P38	19	852918	852918	Missense_Mutation	SNV	G	A	A	ELANE	c.110G>A	P.R37Q
XH_P38	19	8650043	8650043	Silent	SNV	G	T	T	ADAMTS10	c.1476C>A	P.A492A
XH_P38	2	11053416	11053416	Silent	SNV	C	T	T	KCNF1	c.864C>T	P.A288A
XH_P38	2	1795716	1795716	Missense_Mutation	SNV	G	T	T	MYT1L	c.3484C>A	P.Q1162K
XH_P38	2	179605497	179605497	Missense_Mutation	SNV	C	T	T	TTN	c.11512G>A	P.V3838I
XH_P38	2	200813030	200813030	Splice_Site	SNV	G	A	A	TYW5	c.233+11C>T	
XH_P38	2	31805765	31805765	Missense_Mutation	SNV	G	A	A	SRD5A2	c.205C>T	P.P69S
XH_P38	2	70315174	70315174	Missense_Mutation	SNV	T	A	A	PCBP1	c.299T>C	P.L100Q
XH_P38	2	70408526	70408526	Missense_Mutation	SNV	T	C	C	C2orf42	c.592A>G	P.K198E
XH_P38	2	71211259	71211259	Nonsense_Mutation	SNV	G	T	T	ANKRD53	c.910G>T	P.G304*
XH_P38	20	62198977	62198977	Silent	SNV	G	A	A	HEL22	c.1734C>T	P.A578A
XH_P38	21	37617533	37617533	Silent	SNV	C	T	T	DOPEY2	c.3255C>T	P.S1085S
XH_P38	21	46057810	46057810	Missense_Mutation	SNV	C	G	G	KRTAP10-10	c.476C>G	P.P159R
XH_P38	21	46897878	46897878	Missense_Mutation	SNV	C	T	T	COL18A1	c.1760C>T	P.P587L
XH_P38	21	47423790	47423790	Missense_Mutation	SNV	C	T	T	COL6A1	c.2950C>T	P.P984C
XH_P38	22	19711403	19711403	Missense_Mutation	SNV	C	T	T	GP1BB	c.37C>T	P.L13F
XH_P38	22	21830934	21830934	Splice_Site	SNV	G	A	A	PI4KAP2	n.1620C>T	
XH_P38	22	37480861	37480861	Missense_Mutation	SNV	G	A	A	TMPRSS6	c.992C>T	P.T331M
XH_P38	22	38131069	38131069	Missense_Mutation	SNV	C	T	T	TRIOBP	c.4726C>T	P.R1576G
XH_P38	22	38168725	38168725	Missense_Mutation	SNV	G	A	A	TRIOBP	c.7054G>A	P.A2352T
XH_P38	22	41489077	41489077	Silent	SNV	C	A	A	EP300	c.69C>A	P.L23L
XH_P38	22	41626225	41626225	Silent	SNV	C	T	T	L3MBTL2	c.2088C>T	P.V696V
XH_P38	22	45821971	45821971	Silent	SNV	G	T	T	RIBC2	c.816G>T	P.V272V
XH_P38	3	122003711	122003711	Silent	SNV	C	T	T	CASR	c.2910C>T	P.S970S
XH_P38	3	128200073	128200073	Missense_Mutation	SNV	G	A	A	GATA2	c.1232C>T	P.A411V
XH_P38	3	13376973	13376973	Missense_Mutation	SNV	G	C	C	NUP210	c.3824C>G	P.S1275W
XH_P38	3	48677316	48677316	Silent	SNV	G	A	A	CELSR3	c.9702C>T	P.P3234P
XH_P38	3	50224060	50224060	Missense_Mutation	SNV	G	C	C	SEMA3F	c.1531G>C	P.V511L
XH_P38	3	50264608	50264608	Missense_Mutation	SNV	A	C	C	GNAI2	c.53A>C	P.H18P
XH_P38	3	52378506	52378506	Splice_Site	SNV	G	A	A	DNAH1	c.1287G>A	P.S429S
XH_P38	3	99513875	99513875	Missense_Mutation	SNV	A	G	G	COL8A1	c.1130A>G	P.K377R
XH_P38	4	16188159	16188159	Splice_Site	SNV	G	A	A	TAPT1	c.915C>T	P.S305S
XH_P38	4	1823989	1823989	Silent	SNV	G	A	A	LETM1	c.1527C>T	P.T509T
XH_P38	4	37591815	37591815	Missense_Mutation	SNV	C	G	G	C4orf19	c.138C>G	P.S46R
XH_P38	4	53728701	53728701	Silent	SNV	C	A	A	RASL11B	c.27C>A	P.T9T
XH_P38	4	6303479	6303479	Missense_Mutation	SNV	C	T	T	WFS1	c.1957C>T	P.R653C
XH_P38	4	7056450	7056450	Missense_Mutation	SNV	C	T	T	TADA2B	c.932C>T	P.A311V
XH_P38	5	1033594	1033594	Missense_Mutation	SNV	G	A	A	NKD2	c.310G>A	P.G104R
XH_P38	5	1037916	1037916	Splice_Site	SNV	G	A	A	NKD2	c.*31-4G>A	
XH_P38	5	141233796	141233796	Silent	SNV	C	T	T	PCDH1	c.3525G>A	P.P1175P
XH_P38	5	41000886	41000886	Missense_Mutation	SNV	G	T	T	MROH2B	c.4244C>A	P.A1415E
XH_P38	6	109775021	109775021	Missense_Mutation	SNV	C	T	T	MICAL1	c.286G>A	P.G96R
XH_P38	6	116574994	116574994	Missense_Mutation	SNV	C	G	G	TSPYL4	c.178G>C	P.G60R
XH_P38	6	1313258	1313258	Missense_Mutation	SNV	G	C	C	FOXQ1	c.319G>C	P.E107Q
XH_P38	6	158492691	158492691	Silent	SNV	C	T	T	SYNJ2	c.1287C>T	P.G429G
XH_P38	6	159653094	159653094	Missense_Mutation	SNV	G	T	T	FNDC1	c.1550G>T	P.G517V
XH_P38	6	160679666	160679666	Missense_Mutation	SNV	A	G	G	SLC22A2	c.124T>C	P.F42L
XH_P38	6	165715587	165715587	Missense_Mutation	SNV	G	A	A	C6orf118	c.224C>T	P.T75M
XH_P38	6	34857302	34857302	Frame_Shift_Ins	INDEL	-	GGCGGC	GGCGGC	ANKS1A	c.138dupGGCGG	P.G45_G46dup
XH_P38	6	43030791	43030791	Missense_Mutation	SNV	G	A	A	KLC4	c.395G>A	P.R132H
XH_P38	6	50683193	50683193	Missense_Mutation	SNV	G	A	A	TFAP2D	c.404G>A	P.G135D
XH_P38	mcf_ha	2619903	2619903	Missense_Mutation	SNV	C	T	T	HLA-C	c.343G>A	P.G115R
XH_P38	7	100459443	100459443	Missense_Mutation	SNV	C	A	A	SLC12A9	c.1621C>A	P.P541T
XH_P38	7	154667694	154667694	Silent	SNV	C	T	T	DPP6	c.1770C>T	P.G590G
XH_P38	7	16734506	16734506	Nonsense_Mutation	SNV	C	G	G	BZW2	c.699C>G	P.Y233*
XH_P38	7	16816718	16816718	Missense_Mutation	SNV	G	T	T	TSPAN13	c.283G>T	P.A95S
XH_P38	7	90233544	90233544	Missense_Mutation	SNV	A	T	T	CDK14	c.104A>T	P.D35V
XH_P38	8	144697070	144697070	Missense_Mutation	SNV	T	C	C	TSTA3	c.295A>G	P.M99V
XH_P38	8	145009203	145009203	Silent	SNV	G	A	A	PLEC	c.882C>T	P.D294D
XH_P38	8	145640720	145640720	Silent	SNV	C	G	G	SLC39A4	c.558G>C	P.L186L
XH_P38	8	19363123	19363123	Silent	SNV	G	A	A	CSGALNACT1	c.223C>T	P.L75L
XH_P38	8	28932797	28932797	Splice_Site	SNV	C	A	A	KIF13B	c.4521+1G>T	
XH_P38	8	75233158	75233158	Missense_Mutation	SNV	G	T	T	JPH1	c.365C>A	P.T122N
XH_P38	8	77618751	77618751	Missense_Mutation	SNV	C	A	A	ZFHX4	c.2428C>A	P.H810N
XH_P38	9	114246717	114246717	Missense_Mutation	SNV	C	T	T	KIAA0368	c.196G>A	P.E66K
XH_P38	9	130164927	130164927	Silent	SNV	G	A	A	SLC2A8	c.618G>A	P.P206P
XH_P38	9	134363270	134363270	Silent	SNV	G	C	C	PRRC2B	c.6012G>C	P.L2004L
XH_P38	9	134400534	134400534	Missense_Mutation	SNV	A	G	G	UCK1	c.658T>C	P.S220P
XH_P38	9	139298607	139298607	Missense_Mutation	SNV	G	A	A	SDCCAG3	c.1108C>T	P.R370W
XH_P38	9	139636334	139636334	Missense_Mutation	SNV	G	A	A	LCN10	c.256C>T	P.R86W
XH_P38	9	18777191	18777191	Silent	SNV	G	T	T	ADAMTSL1	c.2964G>T	P.P988P
XH_P38	X	100808342	100808342	Silent	SNV	C	T	T	ARMCX1	c.429C>T	P.P143P
XH_P38	X	106310827	106310827	Missense_Mutation	SNV	C	T	T	RBM41	c.1172G>A	P.R391Q
XH_P38	X	107449782	107449782	Missense_Mutation	SNV	C	T	T	COL4A6	c.575G>A	P.G192E
XH_P38	X	153588165	153588165	Missense_Mutation	SNV	G	A	A	FLNA	c.3914C>T	P.T1305M
XH_P38	X	26157583	26157583	Missense_Mutation	SNV	G	A	A	MAGEB18	c.481G>A	P.G161S
XH_P38	X	34148761	34148761	Silent	SNV	C	A	A	FAM47A	c.1635G>T	P.P545P
XH_P38	X	48690546	48690546	Missense_Mutation	SNV	G	A	A	PCSK1N	c.320C>T	P.A107V
XH_P38	X	66766208	66766208	Missense_Mutation	SNV	G	A	A	AR	c.1220G>A	P.R407H
XH_P38	X	79698574	79698574	Missense_Mutation	SNV	T	A	A	FAM46D	c.536T>A	P.V179D

XH_P39	12	25398284	25398284	Missense_Mutation	SNP	C	T	T	KRAS	c.35G>A	p.G12D
XH_P39	17	7578190	7578190	Missense_Mutation	SNP	T	C	C	TP53	c.659A>G	p.Y220C
XH_P39		-	-	Frame_Shift_Ins	INS	-	-	-	RBM10	c.1844_1845dup	p.V616Mfs*89
XH_P39	1	3742991	3742991	In_Frame_Ins	INS	-	TGTTTATTGTAA	-	CEP104	2198insTTACAA	G733delinsVTINR
XH_P39	1	9669937	9669937	Missense_Mutation	SNP	A	C	A	TMEM201	c.A1433C	p.Q478P
XH_P39	1	12853415	12853415	Silent	SNP	A	G	A	PRAMEF1	c.A39G	p.A13A
XH_P39	1	12855647	12855647	Silent	SNP	C	T	C	PRAMEF1	c.C192T	p.D64D
XH_P39	1	12855648	12855648	Missense_Mutation	SNP	A	G	A	PRAMEF1	c.A193G	p.M65V
XH_P39	1	19518825	19518825	Frame_Shift_Ins	INS	-	GTATGTGT	-	UBR4	0_1251insACAC	p.S417fs
XH_P39	1	19518826	19518826	Nonsense_Mutation	INS	-	GATTATAATTTA	-	UBR4	sAAATATAAATT	A17_L418delinsKIX
XH_P39	1	25785324	25785324	Nonsense_Mutation	INS	-	CATTATTAAATC	-	TMEM57	96insATCATTAT	65_D366delinsKIIIX
XH_P39	1	25785325	25785325	Missense_Mutation	SNP	G	T	G	TMEM57	c.G1096T	p.D366Y
XH_P39	1	41847542	41847542	Silent	SNP	G	A	G	FOXO6	c.G669A	p.P223P
XH_P39	1	44423731	44423731	Silent	SNP	T	G	T	IPO13	c.T1623G	p.P541P
XH_P39	1	46184960	46184960	Nonsense_Mutation	INS	-	TATTTTAAATTT	-	IPP	AAATGAAATTT	delinsYYVSTKMKIKNTX
XH_P39	2	3605849	3605849	Missense_Mutation	SNP	A	C	A	RNASEH1	c.T2G	p.M1R
XH_P39	2	9633940	9633940	Frame_Shift_Ins	INS	-	GGAGCTTGGGA	-	ADAM17	1929insTCCAA	p.K643fs
XH_P39	2	15378741	15378741	Nonsense_Mutation	INS	-	AAGTTA	-	NBAS	793_5794insTAA	p.P1932delinsX
XH_P39	2	15378742	15378742	Nonsense_Mutation	INS	-	ATTATGTCG	-	NBAS	2_5793insCGAC	31_P1932delinsNDX
XH_P39	2	27888093	27888093	Frame_Shift_Ins	INS	-	AGGTTATTTATT	-	SLC4A1AP	nsAAAAAGGTTAT	p.M318fs
XH_P39	2	37235963	37235963	Frame_Shift_Ins	INS	-	CAGATGGTGAGT	-	HEATR5B	313insTACTCAC	p.K1438fs
XH_P39	2	84897554	84897554	Missense_Mutation	SNP	G	C	G	DNAH6	c.G6409C	p.E2137Q
XH_P39	2	86711206	86711206	Frame_Shift_Ins	INS	-	TTAA	-	KDM3A	1019_3020insTT	p.V1007fs
XH_P39	2	107049646	107049646	Frame_Shift_Ins	INS	-	GTAAGG	-	RGPD3	00_2301insCCT	p.G767fs
XH_P39	2	141243055	141243055	Silent	SNP	G	A	G	LRP1B	c.C9282T	p.V3094V
XH_P39	2	149227341	149227341	Missense_Mutation	SNP	G	A	G	MBD5	c.G1829A	p.G610D
XH_P39	2	166003406	166003406	Frame_Shift_Ins	INS	-	G	-	SCN3A	1513_1514ins	p.K505fs
XH_P39	2	166003408	166003408	Frame_Shift_Ins	INS	-	GCTTTTATAGTTT	-	SCN3A	ATACAAAAACTA	p.K504fs
XH_P39	2	166896083	166896083	Frame_Shift_Ins	INS	-	AACAATCAGG	-	SCN1A	2439insSCCTGA	p.A813fs
XH_P39	2	166896085	166896085	Missense_Mutation	SNP	C	T	C	SCN1A	c.G2437A	p.A813T
XH_P39	2	179498013	179498013	Missense_Mutation	SNP	C	A	C	TTN	c.G15792T	p.E5264D
XH_P39	2	182347352	182347352	Frame_Shift_Ins	INS	-	ACCTTTTACCTT	-	ITGA4	CATATTACCTTT	p.V339fs
XH_P39	2	182347354	182347354	Nonsense_Mutation	INS	-	TAAAGATA	-	ITGA4	17_1018insTAA	339_F340delinsVX
XH_P39	2	219452034	219452034	Missense_Mutation	SNP	C	T	C	CNOT9	c.C437T	p.T146M
XH_P39	2	219452035	219452035	Silent	SNP	G	A	G	CNOT9	c.G438A	p.T146T
XH_P39	2	233244626	233244626	Missense_Mutation	SNP	A	C	A	ALPP	c.A637C	p.I213L
XH_P39	2	234704662	234704662	Missense_Mutation	SNP	T	G	T	MROH2A	c.T1118G	p.M373R
XH_P39	2	238939217	238939217	Frame_Shift_Ins	INS	-	TATAA	-	UBE2F	278_279insTAT	p.I93fs
XH_P39	2	238939219	238939219	In_Frame_Ins	INS	-	CTTGTTTATGT	-	UBE2F	31insTCTGTGTG	D94delinsVLCVY
XH_P39	3	27472823	27472823	Frame_Shift_Ins	INS	-	GTTTTTTTCTT	-	SLC4A7	6insTAAAGAAA	p.E372fs
XH_P39	3	38354964	38354964	Missense_Mutation	SNP	T	G	T	SLC22A14	c.T1151G	p.M384R
XH_P39	3	39227011	39227011	Missense_Mutation	SNP	G	T	G	XIRP1	c.C3926A	p.T1309K
XH_P39	3	49848183	49848183	Splice_Site	SNP	A	C	A	UBA7	-	-
XH_P39	3	105495375	105495375	Missense_Mutation	SNP	G	T	G	CBLB	c.C515A	p.T172K
XH_P39	3	118931445	118931445	In_Frame_Ins	INS	-	AAGACAGCTTG	-	B4GALT4	nsTAAAGAAAGC	329delinsLRKLSCY
XH_P39	3	121351315	121351315	In_Frame_Ins	INS	-	GGCTCA	-	HCL51	92_993insTGAG	p.P311delinsPEP
XH_P39	3	123987839	123987839	Missense_Mutation	SNP	A	C	A	KALRN	c.A700C	p.K234Q
XH_P39	3	133467286	133467286	Missense_Mutation	SNP	T	G	T	TF	c.T74G	p.V252fs
XH_P39	3	134968196	134968196	Silent	SNP	C	G	C	EPH81	c.C2709G	p.L903L
XH_P39	3	137880741	137880741	In_Frame_Del	DEL	TCG	-	TCG	DBR1	c.1623_1625del	p.S41_542del
XH_P39	3	158526978	158526978	Nonsense_Mutation	SNP	G	T	G	MFSD1	c.G481T	p.E161X
XH_P39	3	183524847	183524847	Silent	SNP	A	T	A	YEATS2	c.A3978T	p.P1326P
XH_P39	3	195513398	195513398	In_Frame_Ins	INS	-	GGCGTGACCGG	-	MUC4	3CATCCACCGG	delinsTSSASTGHATPLPVTG
XH_P39	3	195515449	195515449	Missense_Mutation	SNP	A	T	A	MUC4	c.T3002A	p.V1001E
XH_P39	3	195789794	195789794	In_Frame_Ins	INS	-	GTGTATAAATA	-	TFRC	89insTTTATTAT	A163delinsSLFITV
XH_P39	3	195789795	195789795	Frame_Shift_Ins	INS	-	ATTTACTATTAT	-	TFRC	insCTAATAAGT	p.S163fs
XH_P39	4	436577	436577	Missense_Mutation	SNP	T	C	T	ZNF721	c.A1679G	p.E560G
XH_P39	4	38829080	38829080	Missense_Mutation	SNP	C	T	C	TLR6	c.G2015A	p.C672Y
XH_P39	4	38933160	38933160	Frame_Shift_Ins	INS	-	GGATCTCTGTGA	-	FAM114A1	530insTGGAGCT	p.K210fs
XH_P39	4	40434705	40434725	In_Frame_Del	DEL	GCGGCGGCT	-	TGCGGCGGCTG	RBM47	c.1278_1298del	p.426_433del
XH_P39	4	71099858	71099858	Missense_Mutation	SNP	C	T	C	FDCSP	c.C212T	p.P71L
XH_P39	4	71698877	71698877	In_Frame_Ins	INS	-	ATCCCCAAAAAGC	-	GRSF1	ATTATGGCTTTT	8delinsRLWLFGLIAL
XH_P39	4	71698879	71698879	Missense_Mutation	SNP	G	A	G	GRSF1	c.C140T	p.A47V
XH_P39	4	72121018	72121018	Frame_Shift_Ins	INS	-	GATACAC	-	SLC4A4	55_156insGATA	p.K52fs
XH_P39	4	83788085	83788085	In_Frame_Ins	INS	-	CTTTTATACCA	-	SEC31A	58insTTTGGTGA	A353delinsLWYKKS
XH_P39	4	83788086	83788086	Frame_Shift_Ins	INS	-	TGTT	-	SEC31A	056_1057insAA	p.P353fs
XH_P39	4	109584406	109584406	Missense_Mutation	SNP	T	C	T	OSTC	c.T449C	p.L150S
XH_P39	4	119951422	119951422	In_Frame_Ins	INS	-	ATGCTACTTCAC	-	SYNP02	193insAATGCTA	A498delinsKCYFTW
XH_P39	4	119951424	119951424	Missense_Mutation	SNP	G	T	G	SYNP02	c.G1494T	p.R498S
XH_P39	4	122743786	122743786	Nonsense_Mutation	INS	-	TGTGTGGAATTA	-	CCNA2	229insTAATTC	p.D77delinsX
XH_P39	4	122743787	122743787	Nonsense_Mutation	INS	-	TATAAATTATAG	-	CCNA2	ATCATCTAATAA	p.K76delinsNIX
XH_P39	4	156643278	156643278	Frame_Shift_Ins	INS	-	ACTCTTTTCCATT	-	GUCY1A3	TTCTTAACCTCTT	p.T602fs
XH_P39	4	166946559	166946559	Frame_Shift_Ins	INS	-	CTACAAGAATC	-	TLL1	insAACTCTACA	p.R378fs
XH_P39	4	169312697	169312697	Nonsense_Mutation	INS	-	TTGT	-	DDX60L	908_3909insAC	303_R1304delinsX
XH_P39	4	169312699	169312699	Nonsense_Mutation	INS	-	TTTTCATAGTTAG	-	DDX60L	AAACCCTAACTA	A803_R1304delinsKPX
XH_P39	5	55075881	55075881	Nonsense_Mutation	INS	-	ATTTAATTTAAG	-	DDX4	insAAATTTAAT	A142_G143delinsQIX
XH_P39	5	63509638	63509638	Frame_Shift_Ins	INS	-	GGACAATTCAGT	-	RNF180	86insGGACAAT	p.N162fs
XH_P39	5	70806652	70806652	Frame_Shift_Ins	INS	-	CCTCTCGT	-	BDP1	33_3734insCCTC	p.S1245fs
XH_P39	5	71495041	71495041	Silent	SNP	T	C	T	MAP1B	c.T5481C	p.G1827G
XH_P39	5	75591727	75591727	Missense_Mutation	SNP	G	C	G	SV2C	c.G1462C	p.E488Q
XH_P39	5	93159953	93159953	Frame_Shift_Ins	INS	-	TGGTA	-	FAM172A	476_477insTAC	p.E159fs
XH_P39	5	93159955	93159955	In_Frame_Ins	INS	-	ACTCTTTAAGTT	-	FAM172A	nsCATAACTTTAA	159delinsHNLSIE
XH_P39	5	96121618	96121618	Missense_Mutation	SNP	C	G	C	ERAP1	c.G1817C	p.G606A
XH_P39	5	98229235	98229235	Silent	SNP	G	A	G	CHD1	c.C1876T	p.L626L
XH_P39	5	140789355	140789355	Missense_Mutation	SNP	C	T	C	PCDHGB6	c.C1586T	p.A529V
XH_P39	5	147889180	147889180	Silent	SNP	G	A	G	HTR4	c.C915T	p.S305S
XH_P39	5	156479444	156479444	Frame_Shift_Del	DEL	T	-	T	HAVCR1	c.601delA	p.S201fs
XH_P39	6	10709602	10709602	In_Frame_Ins	INS	-	CTTTTAAAAAAA	-	PAK1IP1	1097insCTTTTA	G366delinsAFKKS
XH_P39	6	10709604	10709604	Silent	SNP	C	A	C	PAK1IP1	c.C1098A	p.G366G
XH_P39	6	17539587	17539587	Missense_Mutation	SNP	G	A	G	CAP2	c.G724A	p.G242R
XH_P39	6	26043718	26043718	Silent	SNP	T	G	T	HIST1H2BB	c.A168C	p.S565
XH_P39	6	26124130	26124130	Missense_Mutation	SNP	C	A	C	HIST1H2BC	c.G3T	p.M1I
XH_P39	6	26216704	26216704	Silent	SNP	T	G	T	HIST1H2BG	c.A168C	p.S565
XH_P39	6	27100350	27100350	Missense_Mutation	SNP	C	A	C	HIST1H2BJ	c.G180T	p.M60I
XH_P39	6	27861408	27861408	Silent	SNP	A	C	A	HIST1H2BO	c.A168C	p.S565
XH_P39	6	28269232	28269232	In_Frame_Ins	INS	-	GAAGTGTGA	-	PGBD1	1_1602insGAAC	L534delinsLNCD
XH_P39	6	38831780	38831780	In_Frame_Ins	INS	-	AGTTTTACTCTA	-	DNAH8	nsGTAAAGTTTTT	148delinsCKVLLVNI
XH_P39	6	64423432	64423432	Frame_Shift_Ins	INS	-	TGTGAATCACT	-	PHF3	5949insTGTGA	p.G1983fs

XH_P39	6	117116999	117116999	Splice_Site	INS	-	ATTTATTTTGGT	-	GPRC6A	-	-
XH_P39	6	147527119	147527119	Missense_Mutation	SNP	G	A	G	STXBPS	c.G163A	p.G55R
XH_P39	6	147527120	147527120	Frame_Shift_Ins	INS	-	AAAATCTTTAT	-	STXBPS	nsAAGAAAAATCT	p.G55fs
XH_P39	7	15725798	15725803	In_Frame_Del	DEL	TTGGTGG	-	TTGGTGG	MEOX2	c.225_230del	p.75_77del
XH_P39	7	22533322	22533322	Nonsense_Mutation	INS	-	TTGGTTTACCT	-	STEAP1B	218insAGGTAA	L73_P74delinsX
XH_P39	7	27169932	27169934	In_Frame_Del	DEL	GCA	-	GCA	HOXA4	c.419_421del	p.140_141del
XH_P39	7	38247205	38247205	Missense_Mutation	SNP	A	C	A	STARD3NL	c.A100C	p.M34L
XH_P39	7	47876635	47876635	Missense_Mutation	SNP	A	C	A	PKD1L1	c.T5827G	p.V1943D
XH_P39	7	63981679	63981679	Missense_Mutation	SNP	C	A	A	ZN680	c.G1453T	p.A485S
XH_P39	7	72413243	72413243	Missense_Mutation	SNP	A	C	A	POM121	c.A1916C	p.H639P
XH_P39	7	73280015	73280015	Missense_Mutation	SNP	A	C	A	TMEM270	c.A610C	p.I204L
XH_P39	7	73513478	73513478	Missense_Mutation	SNP	A	C	A	LIMK1	c.A416C	p.H139P
XH_P39	7	73790509	73790509	Missense_Mutation	SNP	C	T	C	CLIP2	c.C1673T	p.A558V
XH_P39	7	86822549	86822549	Frame_Shift_Ins	INS	-	AAGACAGTTG	-	DMTF1	1267insAAGAC	p.T422fs
XH_P39	7	87743933	87743933	Missense_Mutation	SNP	A	C	A	ADAM22	c.A505C	p.I169L
XH_P39	7	100867238	100867238	Nonstop_Mutation	SNP	G	C	G	ZNH1T	c.G464C	p.X155S
XH_P39	7	107577674	107577674	Frame_Shift_Ins	INS	-	SGATTTAACGAT	-	LAMB1	8810insTATCGT	p.K1270fs
XH_P39	8	1626555	1626555	Missense_Mutation	SNP	C	T	C	DLGAP2	c.C2464T	p.R822W
XH_P39	8	19363099	19363099	Missense_Mutation	SNP	T	G	T	CSGALNACT1	c.A247C	p.K83Q
XH_P39	8	24774966	24774966	Frame_Shift_Ins	INS	-	ATTCCTCT	-	NEFM	70_471insATTCC	p.Q157fs
XH_P39	8	24774968	24774968	Nonsense_Mutation	SNP	G	T	G	NEFM	c.G472T	p.E158X
XH_P39	8	27657119	27657119	Missense_Mutation	SNP	G	A	G	ESCO2	c.G1559A	p.E520K
XH_P39	8	37968287	37968287	Missense_Mutation	SNP	C	T	C	ASH2L	c.C104T	p.A35V
XH_P39	8	87549843	87549843	Nonsense_Mutation	INS	-	CTAACTCTATAG	-	CPNE3	insAGTCTAACTC	D171delinsEVX
XH_P39	8	87549845	87549845	In_Frame_Ins	INS	-	ATA	-	CPNE3	c.514_515insATA	p.G172delinsDR
XH_P39	8	94746140	94746140	Missense_Mutation	SNP	T	G	T	RBM12B	c.A2499C	p.E833D
XH_P39	8	104924318	104924318	Missense_Mutation	SNP	G	A	G	RIMS2	c.G1295A	p.R432H
XH_P39	8	119936842	119936842	Frame_Shift_Ins	INS	-	CAATGTACAAAT	-	TNFRSF11B	977insAATTGTG	p.L326fs
XH_P39	8	120629800	120629800	Silent	SNP	A	G	A	ENPP2	c.T483C	p.F161F
XH_P39	8	134025902	134025902	Missense_Mutation	SNP	T	G	T	TG	c.T6455G	p.V2152G
XH_P39	8	139207526	139207526	In_Frame_Ins	INS	-	TATTCTTACATT	-	FAM135B	848insAATGTAA	L283delinsQCKNI
XH_P39	8	139207527	139207527	Missense_Mutation	SNP	G	C	G	FAM135B	c.C847G	p.L283V
XH_P39	8	143784276	143784276	Missense_Mutation	SNP	G	A	G	LY6K	c.G232A	p.A78T
XH_P39	9	8449812	8449812	Nonsense_Mutation	INS	-	ATTTTACTA	-	PTPRD	7_2638insTAGTA	p.K880delinsX
XH_P39	9	27185588	27185588	In_Frame_Ins	INS	-	ATC	-	TEK	c.847_848insATC	p.A283delinsDP
XH_P39	9	35906348	35906353	In_Frame_Del	DEL	CTGCTG	-	CTGCTG	HRCT1	c.64_69del	p.22_23del
XH_P39	9	35906526	35906526	Missense_Mutation	SNP	A	C	A	HRCT1	c.A242C	p.H81P
XH_P39	9	86322510	86322510	Missense_Mutation	SNP	C	T	C	UBQLN1	c.G85A	p.A29T
XH_P39	9	100092968	100092968	In_Frame_Ins	INS	-	GAG	-	CCDC180	2325_2326insGAG	p.E775delinsEE
XH_P39	9	100823193	100823193	Frame_Shift_Ins	INS	-	ATCTTTATTATT	-	NANS	nsACCATCTTTAT	p.L88fs
XH_P39	9	105767853	105767853	In_Frame_Ins	INS	-	CTTGTA	-	CYLC2	40_941insCTTG	D314delinsACN
XH_P39	10	17113559	17113559	In_Frame_Ins	INS	-	TCTTTG	-	CUBN	90_2491insCAAB	F831delinsORF
XH_P39	10	17113560	17113560	Nonsense_Mutation	INS	-	GTGTATATTATA	-	CUBN	ATTTTATAATA	B830_1831delinsPX
XH_P39	10	26463315	26463315	Frame_Shift_Ins	INS	-	CTTTTCC	-	MYO3A	22_4123insCTTT	p.F1374fs
XH_P39	10	26463317	26463317	Missense_Mutation	SNP	A	T	A	MYO3A	c.A4124T	p.K1375M
XH_P39	10	30918618	30918618	Missense_Mutation	SNP	A	C	A	LYZL2	c.T17G	p.L6R
XH_P39	10	43090101	43090101	Silent	SNP	T	C	T	ZNF33B	c.A318G	p.Q106Q
XH_P39	10	61958155	61958155	Missense_Mutation	SNP	A	C	A	ANK3	c.T1581G	p.H527Q
XH_P39	10	73406494	73406494	Silent	SNP	T	G	T	CDH23	c.T1569G	p.P523P
XH_P39	10	77161110	77161112	In_Frame_Del	DEL	CCT	-	CCT	ZNFS03	c.66_68del	p.22_23del
XH_P39	10	102116326	102116326	Frame_Shift_Ins	INS	-	TGTGAAGATCCA	-	SCD	TAGTGTGGGAAG	p.L229fs
XH_P39	10	105793962	105793962	Silent	SNP	T	G	T	COL17A1	c.A3897C	p.S1299S
XH_P39	10	115400028	115400028	Silent	SNP	C	T	C	NRAP	c.G1281A	p.T427T
XH_P39	10	115970727	115970727	Splice_Site	INS	-	AGCAAGTACTG	-	TDRD1	-	-
XH_P39	10	116925343	116925343	Frame_Shift_Del	DEL	A	-	A	ATRN1L	c.1030delA	p.N344fs
XH_P39	11	5322472	5322472	Silent	SNP	G	C	G	OR51B4	c.C705G	p.L235L
XH_P39	11	5566066	5566066	Frame_Shift_Ins	INS	-	AAGGTTATACT	-	OR52H1	8insAAAAGTATA	p.L230fs
XH_P39	11	5566068	5566068	Missense_Mutation	SNP	A	T	A	OR52H1	c.T686A	p.I229N
XH_P39	11	13399958	13399958	Nonsense_Mutation	SNP	C	T	C	ARNTL	c.C1486T	p.R496X
XH_P39	11	18427068	18427068	Missense_Mutation	SNP	G	C	G	LDHA	c.G609C	p.E203D
XH_P39	11	48387900	48387900	Nonsense_Mutation	INS	-	TCTA	-	OR4C5	117_118insTAG	Q40_N41delinsX
XH_P39	11	59982088	59982088	Splice_Site	INS	-	TGATTAATCCIT	-	MS4A4E	-	-
XH_P39	11	62289913	62289913	Silent	SNP	T	A	T	AHNAK	c.A11976T	p.P3992P
XH_P39	11	65314941	65314941	Silent	SNP	C	T	C	LTBP3	c.G2076A	p.R692R
XH_P39	11	66411364	66411384	In_Frame_Del	DEL	GCTGCAGCA	-	TGCTGCAGCAG	RBM14-RBM4	c.781_801del	p.261_267del
XH_P39	11	67059646	67059646	Missense_Mutation	SNP	T	G	T	ANKRD13D	c.T726G	p.F242L
XH_P39	11	69978027	69978027	Missense_Mutation	SNP	T	G	T	ANO1	c.T1100G	p.M367R
XH_P39	11	84245762	84245762	Frame_Shift_Ins	INS	-	T	-	DLG2	c.54_55insA	p.Q19fs
XH_P39	11	84245763	84245763	Nonsense_Mutation	INS	-	TTGGGACATAT	-	DLG2	nsAAAAATATGTC	Y18_Q19delinsX
XH_P39	11	89537461	89537461	Silent	SNP	G	T	G	TRIM49	c.C177A	p.T59T
XH_P39	11	89608809	89608809	Frame_Shift_Del	DEL	C	-	C	TRIM64B	c.377delG	p.S126fs
XH_P39	11	102272887	102272887	Missense_Mutation	SNP	T	A	T	TMEM123	c.A208T	p.T70S
XH_P39	11	102272889	102272889	In_Frame_Ins	INS	-	ACATCTCAGATA	-	TMEM123	206insTATCTGA	S69delinsSEMFC
XH_P39	11	129991605	129991605	Nonsense_Mutation	INS	-	AAAATAAACCTT	-	APLP2	14insCAAAATA	T205_T206delinsPKX
XH_P39	12	4479620	4479715	In_Frame_Del	DEL	GGGGTCATC	-	CGGGGTCATCCG	FGF23	c.550_645del	p.184_215del
XH_P39	12	28702099	28702099	In_Frame_Ins	INS	-	TCCTTCAACTCAG	-	CCDC91	CTTTATCTCTCA	4delinsIFFILQLSIFFS
XH_P39	12	52885381	52885381	Missense_Mutation	SNP	C	G	C	KRT6A	c.G680C	p.S227T
XH_P39	12	53189741	53189741	Missense_Mutation	SNP	A	C	A	KRT3	c.T86G	p.M29R
XH_P39	12	55863522	55863522	In_Frame_Ins	INS	-	GACACACAT	-	OR6C70	D_401insATGTG	M134delinsNVCL
XH_P39	12	56349890	56349890	Frame_Shift_Ins	INS	-	SGTATTCTTCCTA	-	PMEL	CTAGATAGGAA	p.V404fs
XH_P39	12	76424934	76424934	Frame_Shift_Del	DEL	C	-	C	PHLDA1	c.588delG	p.Q196fs
XH_P39	12	76424936	76424940	Frame_Shift_Del	DEL	GTTGC	-	GTTGC	PHLDA1	c.582_586del	p.Q194fs
XH_P39	12	80014962	80014962	Frame_Shift_Ins	INS	-	ATGCCTTCTTAA	-	PAWR	42insGTAAGGA	p.E181fs
XH_P39	12	88589225	88589225	In_Frame_Ins	INS	-	GGC	-	TMTCT3	2544_2545insGG	p.E848delinsEG
XH_P39	12	88589226	88589226	In_Frame_Ins	INS	-	TCTTTCAGC	-	TMTCT3	5_2546insTCTTT	B849delinsFQL
XH_P39	12	120760039	120760039	Nonsense_Mutation	INS	-	CTCTTTTATTTT	-	PLA2G1B	4insTAAAAATA	K135delinsIKKEX
XH_P39	12	120760041	120760041	Frame_Shift_Ins	INS	-	TA	-	PLA2G1B	c.401_402insTA	p.N134fs
XH_P39	12	123834966	123834966	Nonsense_Mutation	INS	-	TTTTTTTTT	-	SBNO1	2_23insAAAAAA	p.L8delinsX
XH_P39	12	123834968	123834968	Frame_Shift_Ins	INS	-	GATAG	-	SBNO1	c.20_21insCTAT	p.D7fs
XH_P39	13	21742534	21742534	Silent	SNP	G	A	G	SKA3	c.C336T	p.K112H
XH_P39	13	24465533	24465533	Missense_Mutation	SNP	A	C	A	C1QTNF9B	c.T897G	p.D299E
XH_P39	13	52602637	52602637	Nonsense_Mutation	INS	-	CTTTTAAGTTTTT	-	ALG11	TGTAATCTTTTAA	H64_K465delinsMX
XH_P39	13	103515080	103515080	In_Frame_Ins	INS	-	GCACAC	-	BIVM-ERC5	81_1582insGCA	P527delinsPAH
XH_P39	14	21109695	21109695	Frame_Shift_Ins	INS	-	ATTCATTCTTCTAC	-	OR651	insAAGTAGAA	p.R52fs
XH_P39	14	23550017	23550017	Frame_Shift_Ins	INS	-	GAAGGTGTTT	-	ACIN1	581insAAACAC	p.A194fs
XH_P39	14	24773346	24773346	Nonsense_Mutation	SNP	C	T	C	NOP9	c.C1510T	p.R504X
XH_P39	14	45414507	45414507	Missense_Mutation	SNP	C	G	C	KLHL28	c.G667C	p.D223H
XH_P39	14	45716107	45716107	Frame_Shift_Ins	INS	-	CA	-	MIS18BP1	c.382_383insTG	p.E128fs

XH_P39	14	45716109	45716109	Frame_Shift_Ins	INS	-	5AGGTAGTTTT	-	MIS18BP1	insCATAAACT	p.Q127fs
XH_P39	14	64655376	64655376	Frame_Shift_Ins	INS	-	CTTACACCTG	-	SYNE2	17822insCTTA	p.L5941fs
XH_P39	14	73440797	73440797	Missense_Mutation	SNP	T	G	T	ZFYVE1	c.A847C	p.I283L
XH_P39	14	93154538	93154543	In_Frame_Del	DEL	GCGGGC	-	GCGGGC	RIN3	c.2674_2679del	p.892_893del
XH_P39	14	99723924	99723924	Missense_Mutation	SNP	G	C	G	BCL11B	c.C308G	p.S103C
XH_P39	14	105239855	105239855	Silent	SNP	A	C	A	AKT1	c.T765G	p.A255A
XH_P39	15	28456220	28456220	Missense_Mutation	SNP	G	A	G	HERC2	c.C6997T	p.L2333F
XH_P39	15	32976867	32976867	Frame_Shift_Ins	INS	-	AATCATCATTAT	-	SCG5	7insACATTCATC	p.K162fs
XH_P39	15	41813966	41813966	Missense_Mutation	SNP	A	C	A	RPAP1	c.T3008G	p.L1003R
XH_P39	15	45426449	45426449	Silent	SNP	A	C	A	DUOX1	c.A249C	p.S83S
XH_P39	15	62266576	62266576	In_Frame_Ins	INS	-	5AAAGTAAATG	-	VPS13C	2320insCATTTT	1774delinsHFTFI
XH_P39	15	75942496	75942496	Missense_Mutation	SNP	T	G	T	SNX33	c.T1053G	p.D351E
XH_P39	15	76646321	76646321	Missense_Mutation	SNP	A	C	A	SCAPER	c.T4016G	p.M1339R
XH_P39	15	82934774	82934774	Missense_Mutation	SNP	T	C	T	GOLGA6L10	c.A806G	p.E269G
XH_P39	16	1867220	1867220	Missense_Mutation	SNP	A	C	A	HAGH	c.T485G	p.M162R
XH_P39	16	4312339	4312339	Missense_Mutation	SNP	T	G	T	TFAP4	c.A340C	p.K144Q
XH_P39	16	11444642	11444642	Frame_Shift_Ins	INS	-	TTTTTTTTTCTT	-	RM12	440insTTTTTTT	p.P147fs
XH_P39	16	18549933	18549933	Nonsense_Mutation	INS	-	AGAACTTAAGA	-	NOMO2	35insCTTCTTAAT	879_Q380delinsLSX
XH_P39	16	18549935	18549935	Frame_Shift_Ins	INS	-	TA	-	NOMO2	1132_1133insT	p.H378fs
XH_P39	16	20811290	20811290	Missense_Mutation	SNP	C	T	C	ER12	c.G632A	p.R211Q
XH_P39	16	24835005	24835005	Silent	SNP	G	A	G	TNRC6A	c.G5619A	p.P1873P
XH_P39	16	30615809	30615809	Missense_Mutation	SNP	G	A	G	ZNFB69	c.C1279T	p.R427W
XH_P39	16	30776374	30776374	Silent	SNP	A	C	A	RNF40	c.A765C	p.S255S
XH_P39	18	13731869	13731869	Frame_Shift_Ins	INS	-	AACTCTTTTCTC	-	RNMT	54insAAACTCTT	p.S118fs
XH_P39	18	13731871	13731871	Missense_Mutation	SNP	A	T	A	RNMT	c.A355T	p.T119S
XH_P39	18	14542693	14542693	Silent	SNP	C	T	C	POTEC	c.G453A	p.K151K
XH_P39	18	14763838	14763838	Frame_Shift_Ins	INS	-	5TGTCCTGTAG	-	ANKRD30B	insAGGTGTCTCC	p.S325fs
XH_P39	18	34081926	34081926	Missense_Mutation	SNP	G	C	G	FHOD3	c.G369C	p.L123F
XH_P39	18	42532125	42532125	Silent	SNP	G	A	G	SETBP1	c.G2820A	p.R940R
XH_P39	18	47107855	47107855	Silent	SNP	G	A	G	LIPG	c.G642A	p.Q214Q
XH_P39	18	47107857	47107857	Frame_Shift_Ins	INS	-	CATCCTGCATGC	-	LIPG	5GGCTCATCTCTG	p.D215fs
XH_P39	19	4512945	4512945	Missense_Mutation	SNP	C	T	C	PLIN4	c.G985A	p.G329S
XH_P39	19	4512946	4512946	Silent	SNP	A	G	A	PLIN4	c.T984C	p.T328T
XH_P39	19	9578459	9578459	Silent	SNP	C	T	C	ZNFS60	c.G846A	p.P282P
XH_P39	19	10404443	10404443	Missense_Mutation	SNP	T	G	T	ICAM5	c.T1535G	p.L512R
XH_P39	19	11152147	11152147	Silent	SNP	G	A	G	SMARCA4	c.G4245A	p.R1415R
XH_P39	19	11728278	11728278	In_Frame_Ins	INS	-	TTC	-	ZNFB67	630_631insTTGp	A210delinsAF
XH_P39	19	11728279	11728279	Frame_Shift_Ins	INS	-	TAAG	-	ZNFB67	631_632insTAA	p.S211fs
XH_P39	19	14554333	14554333	Missense_Mutation	SNP	T	G	T	PKN1	c.T374G	p.L125R
XH_P39	19	14991480	14991480	Frame_Shift_Ins	INS	-	ACCCCTTTATC	-	OR7A17	688insGATAAA	p.S230fs
XH_P39	20	126205	126205	Nonsense_Mutation	INS	-	TATATAGATTAT	-	DEFB126	5GAATTATATAG	V70_F71delinsEX
XH_P39	20	2464269	2464352	In_Frame_Del	DEL	TCATCCAAGT	-	CTCATCCAAGTG	ZNFB343	c.985_1068del	p.329_356del
XH_P39	20	3785276	3785276	Silent	SNP	T	G	T	CD25B	c.T975G	p.T329S
XH_P39	20	13107302	13107302	In_Frame_Ins	INS	-	ACCACTGTT	-	SPTLC3	7_1218insACCA	P406delinsPPVL
XH_P39	20	13107304	13107304	Frame_Shift_Ins	INS	-	ATTGGCTTCTTT	-	SPTLC3	5GATTATTTCG	p.I407fs
XH_P39	20	21686604	21686604	Missense_Mutation	SNP	G	A	G	PAX1	c.G254A	p.G85D
XH_P39	20	31652645	31652645	Silent	SNP	T	G	T	BPIFB3	c.T918G	p.P306P
XH_P39	20	33587406	33587406	Missense_Mutation	SNP	C	G	G	MYH7B	c.C4699G	p.L1567V
XH_P39	20	62679626	62679626	Missense_Mutation	SNP	C	T	C	SOX18	c.G1048A	p.A350T
XH_P39	21	30927553	30927553	Nonsense_Mutation	INS	-	GGACTGGTTAG	-	GRIK1	10insAAACTAAC	670_K671delinsINX
XH_P39	21	33038833	33038833	Splice_Site	SNP	T	G	T	SOD1	.	.
XH_P39	21	33073424	33073424	Nonsense_Mutation	INS	-	TATCACTCAACT	-	SCAF4	insTCAAGTTGA	206_A207delinsSSX
XH_P39	21	43339039	43339039	Missense_Mutation	SNP	C	G	C	C2CD2	c.G58C	p.D20H
XH_P39	22	18226640	18226640	Nonsense_Mutation	INS	-	T	C	BID	c.G152A	p.W51X
XH_P39	22	25294219	25294219	Missense_Mutation	SNP	A	C	A	SGSM1	c.A2120C	p.Q707P
XH_P39	22	26873066	26873066	Frame_Shift_Ins	INS	-	AGTTTAGGAAG	-	HP54	5cCATAAATCTTCT	p.I52fs
XH_P39	22	26873067	26873067	Silent	SNP	C	T	C	HP54	c.G153A	p.Q51Q
XH_P39	22	29610951	29610951	Silent	SNP	A	C	A	EMID1	c.A138C	p.S46S
XH_P39	22	37578616	37578616	Missense_Mutation	SNP	C	T	C	C1QTNF6	c.G449A	p.R150H
XH_P39	22	38134717	38134717	Nonsense_Mutation	INS	-	TAGATCCAT	-	TRIOBP	5_5176insTAGA	Q1725delinsQX
XH_P39	22	38134719	38134719	Missense_Mutation	SNP	C	T	C	TRIOBP	c.C5177T	p.A1726V
XH_P39	22	38493187	38493187	Splice_Site	SNP	T	G	T	BAIAP2L2	.	.
XH_P39	22	39357586	39357586	Silent	SNP	T	C	T	APOBEC3A	c.T369C	p.R123R
XH_P39	22	40082147	40082147	Missense_Mutation	SNP	T	G	T	CACNA1I	c.T6304G	p.C2102G
XH_P39	22	40697177	40697185	In_Frame_Del	DEL	GCAGCAGCA	-	GCAGCAGCA	TNRC6B	c.3630_3638del	p.1210_1213del
XH_P39	22	46725381	46725381	Missense_Mutation	SNP	G	A	G	GTSE1	c.G2053A	p.E68SK
XH_P39	22	47068862	47068862	Missense_Mutation	SNP	A	C	A	GRAMD4	c.A1207C	p.G403Q
XH_P39	X	17745550	17745550	Frame_Shift_Ins	INS	-	AGTAAAGA	-	NHS	0_2731insAGTA	p.L910fs
XH_P39	X	17745551	17745551	Nonsense_Mutation	INS	-	TGAACCTCCAA	-	NHS	732insCTTGAAC	p.H911delinsPX
XH_P39	X	30864729	30864729	Silent	SNP	G	A	G	TAB3	c.C1743T	p.N581N
XH_P39	X	40570533	40570533	Missense_Mutation	SNP	G	C	G	MED14	c.C910G	p.Q304E
XH_P39	X	47775310	47775310	Missense_Mutation	SNP	C	T	C	ZNFB1	c.C1265T	p.A422V
XH_P39	X	48921924	48921924	Missense_Mutation	SNP	A	C	A	CCDC120	c.A453C	p.E151D
XH_P39	X	50350728	50350728	Silent	SNP	T	C	T	SHROOM4	c.A3414G	p.E1138E
XH_P39	X	50377866	50377866	Missense_Mutation	SNP	T	G	T	SHROOM4	c.A1207C	p.I403L
XH_P39	X	57618845	57618845	Missense_Mutation	SNP	G	C	G	ZXDB	c.G364C	p.E122Q
XH_P39	1	44423731	44423731	Silent	SNV	T	G	G	IPO13	c.1623T>G	p.P541P
XH_P39	1	9669937	9669937	Missense_Mutation	SNV	A	C	C	TMEM201	c.1433A>C	p.Q478P
XH_P39	10	105793962	105793962	Silent	SNV	T	G	G	COL17A1	c.3897A>C	p.S1299S
XH_P39	10	115400028	115400028	Silent	SNV	C	T	T	NRAP	c.1386G>A	p.T462T
XH_P39	10	116925343	116925343	Frame_Shift_Del	INDEL	A	-	-	ATRNL1	c.1031delA	p.N344fs
XH_P39	10	30918618	30918618	Missense_Mutation	SNV	A	C	C	LYZL2	c.177>G	p.L16R
XH_P39	10	61958155	61958155	Missense_Mutation	SNV	A	C	C	ANK3	c.1632T>G	p.H544Q
XH_P39	10	73406494	73406494	Silent	SNV	T	G	G	CDH23	c.1569T>G	p.P523P
XH_P39	11	13399958	13399958	Nonsense_Mutation	SNV	C	T	T	ARNTL	c.1486C>T	p.P496*
XH_P39	11	67059646	67059646	Missense_Mutation	SNV	T	G	G	ANKRD13D	c.726T>G	p.F242L
XH_P39	11	69978027	69978027	Missense_Mutation	SNV	T	G	G	ANO1	c.1100T>G	p.M367R
XH_P39	12	53189741	53189741	Missense_Mutation	SNV	A	C	C	KRT3	c.86T>G	p.M29R
XH_P39	13	24465533	24465533	Missense_Mutation	SNV	A	C	C	C1QTNF9B	c.897T>G	p.D299E
XH_P39	14	105239855	105239855	Silent	SNV	A	C	C	AKT1	c.765T>G	p.A255A
XH_P39	14	45414507	45414507	Missense_Mutation	SNV	C	G	G	KLHL28	c.667G>C	p.D223H
XH_P39	14	73440797	73440797	Missense_Mutation	SNV	T	G	G	ZFYVE1	c.2050A>C	p.I684L
XH_P39	15	41813966	41813966	Missense_Mutation	SNV	A	C	C	RPAP1	c.3008T>G	p.L1003R
XH_P39	15	42622881	42622881	Splice_Site	SNV	G	C	C	GANC	c.1741+11G>C	.
XH_P39	15	45426449	45426449	Silent	SNV	A	C	C	DUOX1	c.249A>C	p.S83S
XH_P39	15	75942496	75942496	Missense_Mutation	SNV	T	G	G	SNX33	c.1053T>G	p.D351E
XH_P39	15	76646321	76646321	Missense_Mutation	SNV	A	C	C	SCAPER	c.3278T>G	p.M1093R
XH_P39	16	1867220	1867220	Missense_Mutation	SNV	A	C	C	HAGH	c.450T>G	p.D150E

XH_P39	16	20811290	20811290	Missense_Mutation	SNV	C	T	T	ERI2	c.632G>A	P.R211Q
XH_P39	16	30776374	30776374	Silent	SNV	A	C	C	RNF40	c.765A>C	P.S255S
XH_P39	16	4312339	4312339	Missense_Mutation	SNV	T	G	G	TFAP4	c.340A>C	P.K114Q
XH_P39	18	42532125	42532125	Silent	SNV	G	A	A	SETBP1	c.2820G>A	P.R940R
XH_P39	19	10404443	10404443	Missense_Mutation	SNV	T	G	G	ICAM5	c.1535T>G	P.L512R
XH_P39	19	14554333	14554333	Missense_Mutation	SNV	T	G	G	PKN1	c.374T>G	P.L125R
XH_P39	2	141243055	141243055	Silent	SNV	G	A	A	LRP1B	c.9282C>T	P.V3094V
XH_P39	2	179498013	179498013	Missense_Mutation	SNV	C	A	A	TTN	c.38064G>T	P.E12688D
XH_P39	2	233244626	233244626	Missense_Mutation	SNV	A	C	C	ALPP	c.637A>C	P.I213L
XH_P39	2	234704662	234704662	Missense_Mutation	SNV	T	G	G	MROH2A	c.1118T>G	P.M373R
XH_P39	2	3605849	3605849	Nonsense_Mutation	SNV	A	C	C	RNA5EH1	c.2T>G	P.M1?
XH_P39	2	86711206	86711206	Frame_Shift_Ins	INDEL	-	TTAA	TTAA	KDM3A	022_3025dupA	P.C1009fs
XH_P39	20	31652645	31652645	Silent	SNV	T	G	G	BPIFB3	c.918T>G	P.P306P
XH_P39	20	3785276	3785276	Silent	SNV	T	G	G	CDC25B	c.1359T>G	P.P453P
XH_P39	21	33038833	33038833	Splice_Site	SNV	T	G	G	SOD1	c.239+2T>G	
XH_P39	21	43339039	43339039	Missense_Mutation	SNV	C	G	G	C2CD2	c.523G>C	P.D175H
XH_P39	22	18226640	18226640	Nonsense_Mutation	SNV	C	T	T	BID	c.152G>A	P.W51*
XH_P39	22	25294219	25294219	Missense_Mutation	SNV	A	C	C	SGSM1	c.2468A>C	P.Q823P
XH_P39	22	29610951	29610951	Silent	SNV	A	C	C	EMID1	c.138A>C	P.S46S
XH_P39	22	38493187	38493187	Splice_Site	SNV	T	G	G	BAIAP2L2	c.466-2A>C	
XH_P39	22	40082147	40082147	Missense_Mutation	SNV	T	G	G	CACNA1I	c.6304T>G	P.C2102G
XH_P39	22	47068862	47068862	Missense_Mutation	SNV	A	C	C	GRAMD4	c.1207A>C	P.K403Q
XH_P39	3	123987839	123987839	Missense_Mutation	SNV	A	C	C	KALRN	c.700A>C	P.K234Q
XH_P39	3	133467286	133467286	Missense_Mutation	SNV	T	G	G	TF	c.74T>G	P.V25G
XH_P39	3	158526978	158526978	Nonsense_Mutation	SNV	G	T	T	MFS1	c.481G>T	P.E161*
XH_P39	3	183524847	183524847	Silent	SNV	A	T	T	YEATS2	c.3978A>T	P.P1326P
XH_P39	3	38354964	38354964	Missense_Mutation	SNV	T	G	G	SLC22A14	c.1151T>G	P.M384R
XH_P39	3	39227011	39227011	Missense_Mutation	SNV	G	T	T	XIRP1	c.3926C>A	P.T1309K
XH_P39	3	49848183	49848183	Splice_Site	SNV	A	C	C	UBA7	c.1311+2T>G	
XH_P39	4	38829080	38829080	Missense_Mutation	SNV	C	T	T	TLR6	c.2015G>A	P.C672Y
XH_P39	4	71099858	71099858	Missense_Mutation	SNV	C	T	T	FDCSP	c.212C>T	P.P711L
XH_P39	4	76812997	76812997	Splice_Site	SNV	A	C	C	PPEF2	c.183+7T>G	
XH_P39	5	150110967	150110967	Splice_Site	SNV	T	C	C	DCTN4	c.632+11A>G	
XH_P39	5	176520559	176520559	Splice_Site	SNV	T	G	G	FGFR4	c.1397+7T>G	
XH_P39	6	17539587	17539587	Missense_Mutation	SNV	G	A	A	CAP2	c.724G>A	P.G242R
XH_P39	6	26043718	26043718	Silent	SNV	T	G	G	HIST1H2BB	c.168A>C	P.S56S
XH_P39	6	26124130	26124130	Nonsense_Mutation	SNV	C	A	A	HIST1H2BC	c.3G>T	P.M1?
XH_P39	6	26216704	26216704	Silent	SNV	T	G	G	HIST1H2BG	c.168A>C	P.S56S
XH_P39	6	27861408	27861408	Silent	SNV	A	C	C	HIST1H2BO	c.168A>C	P.S56S
XH_P39	7	101943978	101943978	Missense_Mutation	SNV	C	A	A	SH2B2	c.273C>A	P.D91E
XH_P39	7	38247205	38247205	Missense_Mutation	SNV	A	C	C	STAR3DNL	c.100A>C	P.M34L
XH_P39	7	72413243	72413243	Missense_Mutation	SNV	A	C	C	POM121	c.1916A>C	P.H639P
XH_P39	7	73280015	73280015	Missense_Mutation	SNV	A	C	C	WBSCR28	c.610A>C	P.I204L
XH_P39	7	73513478	73513478	Missense_Mutation	SNV	A	C	C	LIMK1	c.416A>C	P.H139P
XH_P39	7	87743933	87743933	Missense_Mutation	SNV	A	C	C	ADAM22	c.505A>C	P.I169L
XH_P39	8	104924318	104924318	Missense_Mutation	SNV	G	A	A	RIMS2	c.1730G>A	P.R577H
XH_P39	8	120629800	120629800	Silent	SNV	A	G	G	ENPP2	c.483T>C	P.F161F
XH_P39	8	134025902	134025902	Missense_Mutation	SNV	T	G	G	TG	c.6455T>G	P.V2152G
XH_P39	8	27657119	27657119	Missense_Mutation	SNV	G	A	A	ESCO2	c.1559G>A	P.R520K
XH_P39	8	37968287	37968287	Missense_Mutation	SNV	C	T	T	ASH2L	c.239C>T	P.A80V
XH_P39	9	35906526	35906526	Missense_Mutation	SNV	A	C	C	HRCT1	c.242A>C	P.H81P
XH_P39	X	47041617	47041617	Frame_Shift_Ins	INDEL	-	TA	TA	RBM10	1844_1845dup	P.V616fs
XH_P39	X	47775310	47775310	Missense_Mutation	SNV	C	T	T	ZNF81	c.1265C>T	P.A422V
XH_P39	X	50377866	50377866	Missense_Mutation	SNV	T	G	G	SHROOM4	c.1207A>C	P.I403L
XH_P40	10	123274774	123274774	Missense_Mutation	SNP	A	G	G	FGFR2	c.1144T>C	p.C382R
XH_P40	3	52443601	52443601	Missense_Mutation	SNP	C	T	T	BAP1	c.91G>A	p.E31K
XH_P40	1	36291563	36291563	In_Frame_Ins	INS	-	CAA	-	AGO4	-662_663insCA	p.I221delinsIN
XH_P40	1	67266861	67266861	Nonsense_Mutation	INS	-	TAAGGGATTAA	-	INSL5	insAATTAAATCC	p.F15delinsX
XH_P40	1	90058348	90058348	Frame_Shift_Ins	INS	-	ATAAATTGAA	-	LRR8B	2159insATAAA	p.G720fs
XH_P40	1	110172025	110172025	Missense_Mutation	SNP	A	G	A	AMPD2	c.A1580G	p.E527G
XH_P40	1	110295810	110295810	Frame_Shift_Ins	INS	-	AATCCAGCA	-	EP58L3	1030insTGCTG	p.T344fs
XH_P40	1	114964245	114964245	Frame_Shift_Ins	INS	-	AGATATT	-	TRIM33	73_1874insAAT	p.G625fs
XH_P40	1	152186938	152186938	Silent	SNP	T	C	T	HRNR	c.A7167G	p.S2389S
XH_P40	1	152191783	152191783	Missense_Mutation	SNP	G	C	G	HRNR	c.C2322G	p.H774Q
XH_P40	1	152283291	152283291	Silent	SNP	A	G	A	FLG	c.T4071C	p.H1357H
XH_P40	1	152327425	152327425	Missense_Mutation	SNP	A	G	A	FLG2	c.T2837C	p.F946S
XH_P40	1	152327427	152327427	Silent	SNP	A	T	A	FLG2	c.T2835A	p.T945T
XH_P40	1	154548297	154548306	Frame_Shift_Del	DEL	TGCTTTTGTC	-	TGCTTTTGTC	CHRN2	c.1398_1407del	p.F466fs
XH_P40	1	155287978	155287978	In_Frame_Ins	INS	-	AAT	-	FDPS	c.67_68insAAT	p.A23delinsES
XH_P40	1	182874710	182874710	Nonsense_Mutation	INS	-	TTATATTTTAA	-	SHCBP1L	257insGTAATAA	p.419_G420delinsRX
XH_P40	1	227843106	227843106	Silent	SNP	G	C	G	ZNF678	c.G1320C	p.A440A
XH_P40	1	227947187	227947187	Splice_Site	INS	-	AATT	-	SNAP47	-	-
XH_P40	1	228528833	228528833	Missense_Mutation	SNP	G	A	G	OBSCN	c.G17735A	p.R5912H
XH_P40	1	248814136	248814136	Nonsense_Mutation	INS	-	CTTCCTC	-	OR2T27	9_50insGAGGA	p.L17_F18delinsX
XH_P40	1	248814137	248814137	Missense_Mutation	SNP	A	T	A	OR2T27	c.T49A	p.L17M
XH_P40	2	74592757	74592757	Silent	SNP	G	T	G	DCTN1	c.C2512A	p.R838R
XH_P40	2	74592759	74592759	Missense_Mutation	SNP	A	C	A	DCTN1	c.T2510G	p.V837G
XH_P40	2	113742529	113742529	Nonsense_Mutation	SNP	G	A	G	IL36G	c.G308A	p.W103X
XH_P40	2	120388404	120388410	Frame_Shift_Del	DEL	AAACATC	-	AAACATC	CFAP221	c.1901_1907del	p.K634fs
XH_P40	2	131521725	131521725	Missense_Mutation	SNP	G	A	G	AMER3	c.G2080A	p.A694T
XH_P40	2	163039951	163039951	In_Frame_Ins	INS	-	ATCTTT	-	FAP	66_1767insAAAB	p.D589delinsEKI
XH_P40	2	187516811	187516811	Frame_Shift_Ins	INS	-	AGGTTGA	-	ITGAV	92_1393insAGG	p.V464fs
XH_P40	2	202358592	202358592	In_Frame_Ins	INS	-	AGA	-	C2CD6	2471_2472insT	p.H824delinsHL
XH_P40	2	202358593	202358593	Missense_Mutation	SNP	T	A	T	C2CD6	c.A2471T	p.H824L
XH_P40	2	210685341	210685341	Frame_Shift_Ins	INS	-	TCAT	-	UNC80	269_2270insTC	p.G757fs
XH_P40	2	228243869	228243869	Frame_Shift_Ins	INS	-	TGGA	-	TM4SF20	115_116insTCC	p.Q39fs
XH_P40	3	9935002	9935002	Missense_Mutation	SNP	T	A	T	JAGN1	c.T493A	p.Y165N
XH_P40	3	100605165	100605165	Missense_Mutation	SNP	A	T	A	AB13BP	c.T485A	p.F162Y
XH_P40	3	100605167	100605171	Frame_Shift_Del	DEL	TCTGT	-	TCTGT	AB13BP	c.483delA	p.R161fs
XH_P40	3	118931431	118931431	Frame_Shift_Del	DEL	T	-	T	B4GALT4	c.1000delA	p.I334fs
XH_P40	3	118931432	118931432	Silent	SNP	A	G	A	B4GALT4	c.T999C	p.Y333Y
XH_P40	3	120050217	120050217	In_Frame_Ins	INS	-	TAG	-	LRR5C8	c.945_946insCT	p.V316delinsLV
XH_P40	3	130116488	130116488	Silent	SNP	G	A	G	COL6A5	c.G3630A	p.T1210L
XH_P40	3	130116489	130116489	Frame_Shift_Ins	INS	-	ATATATATACAT	-	COL6A5	632insCATATAT	p.F1211fs
XH_P40	3	130735111	130735111	In_Frame_Ins	INS	-	CTGTTTCTCAT	-	ASTE1	TACTGATGAGA	p.delinsHFTDEKTAGR
XH_P40	3	180321110	180321110	Frame_Shift_Ins	INS	-	TAACG	-	TTC14	485_486insTAA	p.T162fs
XH_P40	3	182871872	182871872	Frame_Shift_Ins	INS	-	TTATC	-	LAMP3	356_357insGAT	p.P119fs
XH_P40	3	195510912	195510912	Frame_Shift_Ins	INS	-	ATGCTGAGGAA	-	MUC4	CGACACTTCTCT	p.L2513fs

XH_P40	4	104096047	104096047	In_Frame_Ins	INS	-	CCTCTTTTTTTT	-	CENPE	AAAAAAAAAAAdelinsKKKKKKEADLC
XH_P40	4	113482063	113482063	Nonsense_Mutation	INS	-	CATTA	-	ZGRF1	511_4612insTA1538_11539delinsX
XH_P40	4	140624661	140624666	In_Frame_Del	DEL	CTGGGG	-	CTGGGG	MGST2	c.78_83del p.26_28del
XH_P40	4	154502589	154502589	Missense_Mutation	SNP	C	T	C	TMEM131L	c.C769T p.R257C
XH_P40	4	154502590	154502590	In_Frame_Ins	INS	-	TTTTAT	-	TMEM131L	770_771insTTTT p.R257delinsRF
XH_P40	5	36227629	36227629	Silent	SNP	T	C	T	NADK2	c.A339G p.E113E
XH_P40	5	37148323	37148323	In_Frame_Ins	INS	-	AGA	-	CSorf42	8258_8259insT p.K2753delinsNL
XH_P40	5	37148325	37148325	Nonsense_Mutation	INS	-	A	-	CSorf42	c.8256_8257insT p.K2753delinsX
XH_P40	5	55075881	55075881	Nonsense_Mutation	INS	-	AAATTTAAAT	-	DDX4	c.425insAAATT142_G143delinsQIX
XH_P40	5	74060873	74060873	Missense_Mutation	SNP	A	G	A	GFNM2	c.T59C p.L20P
XH_P40	5	100238578	100238578	Frame_Shift_Ins	INS	-	ATGAG	-	ST8SIA4	c.81_82insCTCA p.T28fs
XH_P40	5	111531357	111531357	Splice_Site	INS	-	CAAAAGCCAGTT	-	EPB41L4A	.
XH_P40	5	126860330	126860330	Nonsense_Mutation	INS	-	AGAATTAGA	-	PRRC1	c.212insAGAAT p.P71delinsQNX
XH_P40	5	126860331	126860331	Missense_Mutation	SNP	C	A	C	PRRC1	c.C212A p.P71Q
XH_P40	5	145838618	145838683	In_Frame_Del	DEL	CCCAGGCCA	-	GCCCAGGCCAC	TCERG1	c.610_675del p.204_225del
XH_P40	5	147795520	147795520	Missense_Mutation	SNP	A	T	A	FBXO38	c.A1294T p.I432F
XH_P40	5	172517895	172517895	Missense_Mutation	SNP	C	G	C	CREBRF	c.C713G p.A238G
XH_P40	5	176830374	176830374	Missense_Mutation	SNP	G	A	G	F12	c.C1412T p.A471V
XH_P40	5	178140425	178140441	Frame_Shift_Del	DEL	TTGTGGGT	-	TTTGTGGGTGC	ZNF354A	c.312_328del p.S104fs
XH_P40	5	178309821	178309821	Frame_Shift_Ins	INS	-	GGTTTGCT	-	ZNF354B	8_369insGGTTT p.R123fs
XH_P40	5	178541030	178541030	Silent	SNP	G	T	G	ADAMTS2	c.C3474A p.T1158T
XH_P40	5	178541031	178541031	Missense_Mutation	SNP	G	T	G	ADAMTS2	c.C3473A p.T1158N
XH_P40	6	35764600	35764600	Nonsense_Mutation	SNP	T	A	T	CLP5	c.A28T p.K10X
XH_P40	6	41774256	41774256	Missense_Mutation	SNP	G	A	G	USP49	c.C466T p.R156W
XH_P40	6	43497052	43497052	Missense_Mutation	SNP	G	A	G	POLR1C	c.G988A p.E330K
XH_P40	6	43497053	43497053	Missense_Mutation	SNP	A	G	A	POLR1C	c.A989G p.E330G
XH_P40	6	70890352	70890352	Splice_Site	INS	-	T	-	COL19A1	.
XH_P40	6	70890354	70890354	Missense_Mutation	SNP	G	C	G	COL19A1	c.G2714C p.G905A
XH_P40	6	87971226	87971226	Frame_Shift_Ins	INS	-	ACTTG	-	ZNF292	879_7880insAC p.S2627fs
XH_P40	6	117663625	117663625	In_Frame_Ins	INS	-	GCG	-	ROS1	4606_4607insC p.Y1536delinsSH
XH_P40	6	117663627	117663627	Frame_Shift_Ins	INS	-	G	-	ROS1	c.4604_4605ins p.Y1535fs
XH_P40	6	159465019	159465019	Nonsense_Mutation	SNP	A	T	A	TAGAP	c.T72A p.C24X
XH_P40	7	2752130	2752130	Missense_Mutation	SNP	C	T	C	AMZ1	c.C1115T p.A372V
XH_P40	7	29186557	29186557	Silent	SNP	A	T	A	CHN2	c.A255T p.L85L
XH_P40	7	34979922	34979922	In_Frame_Ins	INS	-	TGTTGCTT	-	DPY19L1	7_1488insAAAG F496delinsLKQH
XH_P40	7	34979923	34979923	Missense_Mutation	SNP	A	T	A	DPY19L1	c.T1487A p.F496Y
XH_P40	7	45123066	45123066	Missense_Mutation	SNP	G	T	G	NACAD	c.C2713A p.P905T
XH_P40	7	55873063	55873063	In_Frame_Ins	INS	-	AGGATA	-	SEPT14	1006_1007insTAT p.A336delinsVSS
XH_P40	7	63680237	63680237	Missense_Mutation	SNP	G	A	G	ZNF735	c.G808A p.A270T
XH_P40	7	63720712	63720712	Frame_Shift_Ins	INS	-	A	-	ZNF679	c.153_154insA p.N51fs
XH_P40	7	63720713	63720713	In_Frame_Ins	INS	-	TTACTA	-	ZNF679	154_155insTTAC p.L52delinsLTM
XH_P40	7	64167505	64167505	Missense_Mutation	SNP	A	G	A	ZNF107	c.A934G p.K312E
XH_P40	7	64389272	64389272	Silent	SNP	T	C	T	ZNF273	c.T1566C p.A522A
XH_P40	7	64438774	64438774	Missense_Mutation	SNP	C	T	C	ERV3-1-ZNF117	c.G1175A p.R392K
XH_P40	7	64438775	64438775	Missense_Mutation	SNP	T	C	T	ERV3-1-ZNF117	c.A1174G p.R392G
XH_P40	7	82582707	82582707	Missense_Mutation	SNP	G	A	G	PCLO	c.C7562T p.T2521I
XH_P40	7	82582708	82582708	Frame_Shift_Ins	INS	-	TACATTGCCA	-	PCLO	7561insTGCCA p.T2521fs
XH_P40	7	83675713	83675713	Frame_Shift_Ins	INS	-	AGAGATTAAA	-	SEMA3A	594insTTTAAT p.D198fs
XH_P40	7	87079391	87079391	Frame_Shift_Ins	INS	-	GACT	-	ABC84	725_726insAGT p.S242fs
XH_P40	7	91670097	91670097	Frame_Shift_Ins	INS	-	CATTTTG	-	AKAP9	102_4803insCAT p.H1601fs
XH_P40	7	91670099	91670099	Missense_Mutation	SNP	C	A	C	AKAP9	c.C4804A p.Q1602K
XH_P40	7	95739378	95739378	Missense_Mutation	SNP	A	G	A	DYNC111	c.A1804G p.T602A
XH_P40	7	100641110	100641110	Silent	SNP	A	G	A	MUC12	c.A7266G p.A2422A
XH_P40	7	100678075	100678075	Silent	SNP	C	T	C	MUC17	c.C3378T p.V1126V
XH_P40	7	100682765	100682765	Missense_Mutation	SNP	A	G	A	MUC17	c.A8068G p.R2690G
XH_P40	7	107399020	107399020	Frame_Shift_Ins	INS	-	AGGAGGA	-	CBLL1	10_871insAGGA p.N290fs
XH_P40	7	117007497	117007497	Missense_Mutation	SNP	G	T	G	ASZ1	c.C560A p.P187H
XH_P40	7	117007498	117007498	Missense_Mutation	SNP	G	A	G	ASZ1	c.C559T p.P187S
XH_P40	7	129497375	129497375	Missense_Mutation	SNP	T	C	T	UBE2H	c.A64G p.N22D
XH_P40	7	129497377	129497377	Missense_Mutation	SNP	A	G	A	UBE2H	c.T62C p.I21T
XH_P40	7	143417904	143417904	Missense_Mutation	SNP	C	T	C	TCAF2	c.C1129T p.H377Y
XH_P40	7	143417905	143417905	Missense_Mutation	SNP	A	G	A	TCAF2	c.A1130G p.H377R
XH_P40	8	52321782	52321782	Missense_Mutation	SNP	C	T	C	PXNDL	c.G2402A p.R801H
XH_P40	8	71646395	71646395	Nonsense_Mutation	INS	-	CGATAAT	-	XKR9	58_859insCGAT186_M287delinsPRX
XH_P40	8	80678440	80678440	Frame_Shift_Ins	INS	-	G	-	HEY1	c.58dupC p.Q20fs
XH_P40	8	94934493	94934493	Missense_Mutation	SNP	G	A	G	PDP1	c.G206A p.R69K
XH_P40	8	95751984	95751984	Missense_Mutation	SNP	G	A	G	DPY19L4	c.G577A p.G193R
XH_P40	8	95751985	95751985	Missense_Mutation	SNP	G	T	G	DPY19L4	c.G578T p.G193V
XH_P40	9	35906586	35906586	In_Frame_Ins	INS	-	CCCCACGCCAC	-	HRCT1	ACCACCCCCACCdelinsHHHHHPHRTPHHL
XH_P40	9	133911583	133911583	Silent	SNP	C	T	C	LAMC3	c.C840T p.C280C
XH_P40	9	135251335	135251335	Silent	SNP	A	G	A	TF1F	c.C1140C p.S380S
XH_P40	10	73963275	73963275	Nonsense_Mutation	INS	-	TTATTTTTTATT	-	ASCC1	AAAAAAAAATAAA74_G75delinsKKXX
XH_P40	10	75301490	75301490	Nonsense_Mutation	INS	-	TTATATA	-	USP54	78_579insTATA193_A194delinsHX
XH_P40	10	75301492	75301492	Frame_Shift_Ins	INS	-	T	-	USP54	c.576_577insA p.Q193fs
XH_P40	10	119043385	119043385	Frame_Shift_Ins	INS	-	CA	-	PDZD8	2858_2859insT p.K953fs
XH_P40	11	721564	721564	Splice_Site	SNP	G	A	G	EPS8L2	.
XH_P40	11	1643082	1643082	Missense_Mutation	SNP	T	C	T	KRTAP5-4	c.A242G p.Y81C
XH_P40	11	5799215	5799215	Missense_Mutation	SNP	A	C	A	OR52N5	c.T650G p.V217G
XH_P40	11	5799216	5799216	In_Frame_Ins	INS	-	TATTGT	-	OR52N5	48_649insACA p.V217delinsTIV
XH_P40	11	10793127	10793133	Frame_Shift_Del	DEL	TGAGATT	-	TGAGATT	CTR9	c.2408_2414del p.M803fs
XH_P40	11	31128473	31128473	Missense_Mutation	SNP	G	T	G	DCDC1	c.C479A p.S160Y
XH_P40	11	31128474	31128474	Frame_Shift_Ins	INS	-	TG	-	DCDC1	c.477_478insCA p.S160fs
XH_P40	11	32861758	32861758	In_Frame_Ins	INS	-	CTATGA	-	PRRG4	22_423insCTATb.T141delinsTYD
XH_P40	11	57958845	57958845	Nonsense_Mutation	INS	-	GGT	-	OR9Q2	c.883_884insGG p.K295delinsRX
XH_P40	11	63326001	63326001	Missense_Mutation	SNP	A	T	A	HRASLS2	c.T250A p.Y84N
XH_P40	11	107375437	107375437	Frame_Shift_Ins	INS	-	TGTTTGT	-	ALKB8H	50_1951insACA p.L651fs
XH_P40	11	118130851	118130851	In_Frame_Ins	INS	-	ATAAAAGAA	-	MP2L2	1_502insTTCTT p.I168delinsFFVI
XH_P40	12	26553192	26553192	Splice_Site	INS	-	ATT	-	ITPR2	.
XH_P40	12	30805220	30805220	Frame_Shift_Ins	INS	-	CATATATTTTTC	-	IPO8	63insATGAAAAA p.M488fs
XH_P40	12	39750685	39750685	Frame_Shift_Ins	INS	-	ACTCTTA	-	KIF21A	17_1418insTAA p.E473fs
XH_P40	12	48538876	48538876	Missense_Mutation	SNP	C	A	C	PFKM	c.C2055A p.N685K
XH_P40	12	48538877	48538877	Missense_Mutation	SNP	T	G	T	PFKM	c.T2056G p.W686G
XH_P40	12	48919508	48919508	Missense_Mutation	SNP	C	G	C	OR8S1	c.C94G p.L32V
XH_P40	12	52699116	52699116	Silent	SNP	C	T	C	KRT86	c.C828T p.A276A
XH_P40	12	53162773	53162775	In_Frame_Del	DEL	ACT	-	ACT	KRT76	c.1639_1641del p.547_547del
XH_P40	12	55945266	55945266	In_Frame_Ins	INS	-	AAA	-	OR6C4	c.256_257insAA p.G86delinsER
XH_P40	12	55945268	55945268	Frame_Shift_Ins	INS	-	TG	-	OR6C4	c.258_259insTG p.G86fs
XH_P40	12	56552476	56552476	Frame_Shift_Ins	INS	-	CT	-	MYL6	c.12_13insCT p.F4fs

XH_P40	12	56552477	56552477	Missense_Mutation	SNP	A	G	A	MYL6	c.A13G	p.T5A
XH_P40	12	99065383	99065383	Frame_Shift_Ins	INS	-	AAGTAACAAA	-	APAF1	1647insAAGTA	p.F549fs
XH_P40	12	104492124	104492124	Frame_Shift_Ins	INS	-	GA	-	HCFC2	1744_1745insG	p.E582fs
XH_P40	12	113663128	113663128	Silent	SNP	C	T	C	TPCN1	c.C78T	p.S26S
XH_P40	12	123741557	123741557	Frame_Shift_Ins	INS	-	TAATATTTTATA	-	C12orf65	81insATAATATT	p.I160fs
XH_P40	12	124288363	124288363	Frame_Shift_Ins	INS	-	GGACTATC	-	DNAH10	6_2417insGGAC	p.I806fs
XH_P40	13	20398952	20398952	In_Frame_Ins	INS	-	AAAAATAAAG	-	ZMYM5	4_1675insCTTTA	F559delinsLYF
XH_P40	13	52656375	52656375	Missense_Mutation	SNP	T	C	T	NEK5	c.A1646G	p.Q549R
XH_P40	14	22133706	22133706	Missense_Mutation	SNP	A	G	A	OR4E2	c.A410G	p.N137S
XH_P40	14	22133707	22133707	Missense_Mutation	SNP	C	A	C	OR4E2	c.C411A	p.N137K
XH_P40	14	61915947	61915947	Missense_Mutation	SNP	A	T	A	PRKCH	c.A679T	p.N227Y
XH_P40	14	61915948	61915948	Frame_Shift_Ins	INS	-	TCCCT	-	PRKCH	680_681insTCC	p.N227fs
XH_P40	14	73967325	73967325	Missense_Mutation	SNP	A	G	A	HEATR4	c.T2215C	p.S739P
XH_P40	14	77703043	77703043	Missense_Mutation	SNP	T	A	T	TMEM63C	c.T619A	p.C207S
XH_P40	14	77703045	77703045	Silent	SNP	C	T	C	TMEM63C	c.C621T	p.C207C
XH_P40	14	77951245	77951245	Frame_Shift_Del	DEL	A	-	A	ISM2	c.159delT	p.D53fs
XH_P40	14	77951246	77951246	Missense_Mutation	SNP	T	C	T	ISM2	c.A158G	p.D53G
XH_P40	15	42984180	42984180	Frame_Shift_Ins	INS	-	ATCA	-	STAR9D	1404_10405insA	p.P3468fs
XH_P40	15	55651850	55651850	Nonsense_Mutation	INS	-	GTGTGTC	-	CCPG1	20_2121insGCA	7707_1708delinsX
XH_P40	15	56959020	56959020	Nonsense_Mutation	INS	-	AGGAATTATA	-	ZNF280D	1671insTTAA	557_N558delinsSX
XH_P40	15	59971947	59971947	Nonsense_Mutation	INS	-	AATG	-	BNIP2	501_502insCAT	168_K169delinsHX
XH_P40	15	59971949	59971949	Missense_Mutation	SNP	C	A	C	BNIP2	c.G500T	p.G167V
XH_P40	15	65369354	65369354	Silent	SNP	C	T	C	KBTBD13	c.C201T	p.G67G
XH_P40	15	65983112	65983112	Missense_Mutation	SNP	G	A	G	DENND4A	c.C3688T	p.R1230W
XH_P40	15	65983114	65983114	Nonsense_Mutation	INS	-	TAGG	-	DENND4A	1685_3686insCC	229_R1230delinsPX
XH_P40	15	91346947	91346947	In_Frame_Ins	INS	-	TGG	-	BLM	3555_3556insTQ	1185delinsLW
XH_P40	15	91346948	91346948	Frame_Shift_Ins	INS	-	C	-	BLM	3556_3557ins	p.K1186fs
XH_P40	15	91795713	91795713	In_Frame_Ins	INS	-	CCCACCTTA	-	SV2B	4_295insCCCAC	1098delinsYPTL
XH_P40	16	2979707	2979707	Missense_Mutation	SNP	C	G	C	FLYWCH1	c.C21G	p.S7R
XH_P40	16	4431434	4431434	Missense_Mutation	SNP	C	T	C	VASN	c.C556T	p.P186S
XH_P40	16	4882183	4882183	Nonsense_Mutation	INS	-	AGTG	-	GLYR1	333_334insCAC	112_S113delinsHX
XH_P40	16	4882185	4882185	Missense_Mutation	SNP	C	T	C	GLYR1	c.G332A	p.R111H
XH_P40	16	24801707	24801707	In_Frame_Ins	INS	-	ACACACAAACAA	-	TNRC6A	1745insACACAC	2582delinsHTQT
XH_P40	16	28734598	28734598	Frame_Shift_Ins	INS	-	CCTAG	-	E1F3C	890_891insCCTA	p.E297fs
XH_P40	16	67337112	67337112	Missense_Mutation	SNP	G	T	G	KCTD19	c.C580A	p.L194M
XH_P40	17	1559963	1559963	Frame_Shift_Del	DEL	CT	-	CT	PRPF8	c.5597_5598del	p.K1866fs
XH_P40	17	7481720	7481720	Frame_Shift_Ins	INS	-	ACCT	-	E1F4A1	1137_1138insAC	p.E379fs
XH_P40	17	15609786	15609786	In_Frame_Del	DEL	TGGAGA	-	TGGAGA	ZNF286A	c.182_187del	p.61_63del
XH_P40	17	26962276	26962276	Missense_Mutation	SNP	A	G	A	KIAA0100	c.T2329C	p.F777L
XH_P40	17	26962277	26962277	Frame_Shift_Ins	INS	-	GA	-	KIAA0100	2327_2328insT	p.G776fs
XH_P40	17	29622577	29622577	Frame_Shift_Ins	INS	-	AGGC	-	OMG	772_773insGCC	p.I258fs
XH_P40	17	34182319	34182319	Silent	SNP	G	T	G	HEATR9	c.C1341A	p.T447T
XH_P40	17	34182320	34182320	Missense_Mutation	SNP	G	C	G	HEATR9	c.C1340G	p.T447S
XH_P40	17	36656872	36656872	Splice_Site	DEL	T	-	T	ARHGAP23	-	-
XH_P40	17	39197538	39197538	Missense_Mutation	SNP	G	T	G	KRTAP1-1	c.C112A	p.R38S
XH_P40	17	40255769	40255769	Silent	SNP	T	C	T	DXH58	c.A1611G	p.A537A
XH_P40	17	55028239	55028239	In_Frame_Ins	INS	-	GGGTGA	-	COIL	163_364insTCAC	T122delinsSPT
XH_P40	17	56620687	56620687	Frame_Shift_Ins	INS	-	C	-	C17orf47	c.860_861insG	p.V287fs
XH_P40	17	56620688	56620688	Missense_Mutation	SNP	A	T	A	C17orf47	c.T860A	p.V287D
XH_P40	17	80047551	80047551	Missense_Mutation	SNP	G	T	G	FASN	c.C1922A	p.A641D
XH_P40	17	80739547	80739547	In_Frame_Ins	INS	-	CTC	-	TBCD	721_722insCTG	p.F241delinsSL
XH_P40	18	2892320	2892320	Frame_Shift_Ins	INS	-	TT	-	EMILIN2	2195_2196insT	p.K732fs
XH_P40	18	2892321	2892321	Frame_Shift_Ins	INS	-	CT	-	EMILIN2	2196_2197insC	p.K732fs
XH_P40	18	14837262	14837262	Frame_Shift_Ins	INS	-	CC	-	ANKRD30B	2543_2544insC	p.I848fs
XH_P40	18	14837263	14837263	Frame_Shift_Ins	INS	-	GGGA	-	ANKRD30B	544_2545insGG	p.I848fs
XH_P40	18	18629834	18629834	Missense_Mutation	SNP	G	T	G	ROCK1	c.C183A	p.D61E
XH_P40	18	18629835	18629835	Missense_Mutation	SNP	T	G	T	ROCK1	c.A182C	p.D61A
XH_P40	18	19031075	19031075	Frame_Shift_Del	DEL	C	-	C	GREB1L	c.1812delC	p.V604fs
XH_P40	18	19031077	19031077	In_Frame_Del	DEL	GTTTCC	-	GTTTCC	GREB1L	c.1814_1819del	p.605_607del
XH_P40	18	24081188	24081188	Frame_Shift_Del	DEL	A	-	A	KCTD1	c.12delT	p.P4fs
XH_P40	18	24081190	24081190	Frame_Shift_Del	DEL	GTCTTGACAT	-	GTCTTGACAT	KCTD1	c.1825_1834del	p.M609fs
XH_P40	19	2994946	2994946	Missense_Mutation	SNP	C	T	C	TL66	c.C1294T	p.R432C
XH_P40	19	6495551	6495551	Missense_Mutation	SNP	C	T	C	TUBB4A	c.G743A	p.R248H
XH_P40	19	12089789	12089789	Silent	SNP	G	A	G	ZNF763	c.G1059A	p.T353T
XH_P40	19	13319692	13319694	In_Frame_Del	DEL	GAT	-	GAT	CACNA1A	c.6659_6661del	p.2220_2221del
XH_P40	19	20044949	20044949	Silent	SNP	G	A	G	ZNF93	c.G1185A	p.K395K
XH_P40	19	20229329	20229329	Silent	SNP	C	T	C	ZNF90	c.C966T	p.F322F
XH_P40	19	20229793	20229793	Missense_Mutation	SNP	A	G	A	ZNF90	c.A1430G	p.E477G
XH_P40	19	21240552	21240552	Missense_Mutation	SNP	T	A	T	ZNF430	c.T1435A	p.S479T
XH_P40	19	21300463	21300463	Silent	SNP	A	G	A	ZNF714	c.A993G	p.K331K
XH_P40	19	21477016	21477016	Missense_Mutation	SNP	A	G	A	ZNF708	c.T560C	p.L187P
XH_P40	19	21719801	21719801	Missense_Mutation	SNP	A	G	A	ZNF429	c.A754G	p.K252E
XH_P40	19	21909734	21909734	Missense_Mutation	SNP	G	T	G	ZNF100	c.C735A	p.D245E
XH_P40	19	21910155	21910155	Missense_Mutation	SNP	G	T	G	ZNF100	c.C314A	p.T105K
XH_P40	19	21910156	21910156	Missense_Mutation	SNP	T	C	T	ZNF100	c.A313G	p.T105A
XH_P40	19	21910190	21910190	Silent	SNP	T	C	T	ZNF100	c.A279G	p.K93K
XH_P40	19	22272001	22272001	Silent	SNP	G	A	G	ZNF257	c.G1221A	p.G407G
XH_P40	19	22363998	22363998	Missense_Mutation	SNP	T	C	T	ZNF676	c.A521G	p.N174S
XH_P40	19	22363999	22363999	Missense_Mutation	SNP	T	A	T	ZNF676	c.A520T	p.N174Y
XH_P40	19	22497365	22497365	Silent	SNP	T	C	T	ZNF729	c.T1146C	p.G382G
XH_P40	19	22499603	22499603	Silent	SNP	G	A	G	ZNF729	c.G3384A	p.G1128K
XH_P40	19	22499604	22499604	Missense_Mutation	SNP	G	A	G	ZNF729	c.G3385A	p.E1129K
XH_P40	19	22847758	22847758	Silent	SNP	T	C	T	ZNF492	c.T1287C	p.A429A
XH_P40	19	22941867	22941867	Missense_Mutation	SNP	T	C	T	ZNF99	c.A844G	p.K282E
XH_P40	19	22941868	22941868	Silent	SNP	C	T	C	ZNF99	c.G843A	p.G281G
XH_P40	19	23158787	23158787	Missense_Mutation	SNP	T	G	T	ZNF728	c.A1352C	p.H451P
XH_P40	19	23544630	23544630	Missense_Mutation	SNP	T	C	T	ZNF91	c.A1055G	p.D352G
XH_P40	19	24310546	24310546	Missense_Mutation	SNP	T	G	T	ZNF254	c.T1489G	p.S497A
XH_P40	19	32959712	32959712	Nonsense_Mutation	INS	-	ATCACTA	-	DPY19L3	90_1691insATC	564_1565delinsYHX
XH_P40	19	32959713	32959713	Nonsense_Mutation	SNP	G	A	G	DPY19L3	c.G1691A	p.W564X
XH_P40	19	38910606	38910606	Missense_Mutation	SNP	C	T	C	RASGRP4	c.G515A	p.G172D
XH_P40	19	41025947	41025947	Nonsense_Mutation	SNP	G	A	G	SPTBN4	c.G3543A	p.W1181X
XH_P40	19	42603941	42603941	Frame_Shift_Ins	INS	-	AA	-	POU2F2	c.335_336insTT	p.L112fs
XH_P40	19	42603943	42603943	Missense_Mutation	SNP	G	T	G	POU2F2	c.C334A	p.L112M
XH_P40	19	53014994	53014994	Missense_Mutation	SNP	T	C	T	ZNF578	c.T1360C	p.S454P
XH_P40	19	54377109	54377109	Missense_Mutation	SNP	C	T	C	MYADM	c.C326T	p.A109V
XH_P40	19	58050159	58050159	Nonsense_Mutation	INS	-	GTG	-	ZNF549	1748_1749insG	p.Y583delinsX
XH_P40	20	5996064	5996064	Missense_Mutation	SNP	C	G	C	CRLS1	c.C205G	p.L69V

XH_P40	20	20493629	20493629	Missense_Mutation	SNP	T	C	T	RALGAP2	c.A4384G	p.I1462V
XH_P40	20	62065229	62065229	Missense_Mutation	SNP	G	T	G	KCNQ2	c.C1051A	p.L351I
XH_P40	21	37602927	37602927	Silent	SNP	C	T	C	DOPEY2	c.C1845T	p.D615D
XH_P40	21	45500009	45500009	Splice_Site	INS	-	CTGAACACTACTAC	-	TRAPPC10	.	.
XH_P40	22	19969135	19969135	Silent	SNP	C	T	C	ARVCF	c.G495A	p.P165R
XH_P40	22	20918792	20918792	In_Frame_Ins	INS	-	CAG	-	MED15	c.294_295insCA	p.F98delinsFQ
XH_P40	22	40706836	40706836	Missense_Mutation	SNP	C	T	C	TNRC6B	c.C3944T	p.P1315L
XH_P40	X	20174313	20174313	In_Frame_Ins	INS	-	GCATATCAATAT	-	RP56KA3	2014insATATTG	L672delinsLIC
XH_P40	X	49957965	49957965	In_Frame_Ins	INS	-	AAG	-	AKAP4	1398_1399insC	p.F467delinsLF
XH_P40	X	49957966	49957966	Missense_Mutation	SNP	T	A	T	AKAP4	c.A1398T	p.E466D
XH_P40	X	69385735	69385735	Missense_Mutation	SNP	A	T	A	IGBP1	c.A924T	p.E308D
XH_P40	X	70598174	70598174	In_Frame_Ins	INS	-	GATGAT	-	TAF1	83_1084insGAT	E361delinsEDD
XH_P40	X	79932453	79932453	Silent	SNP	T	G	T	BRWD3	c.A5064C	p.G1688G
XH_P40	X	101857132	101857132	Frame_Shift_Ins	INS	-	T	-	ARMCX5	c.63_64insT	p.G21fs
XH_P40	X	108781337	108781337	Frame_Shift_Ins	INS	-	TAGCTCTATAT	-	NXT2	80insTAGTCTCT	p.E27fs
XH_P40	X	133379598	133379598	In_Frame_Ins	INS	-	TTAGGG	-	CCDC160	68_769insTTAG	N256delinsNLG
XH_P40	X	138678916	138678916	Frame_Shift_Ins	INS	-	TGTA	-	MCF5	951_1952insTA	p.651fs
XH_P40	X	140994592	140994699	In_Frame_Del	DEL	CTCCTCTCTCT	-	CTCCTCTCTCTCC	MAGEC1	c.1402_1509del	p.468_503del
XH_P40	X	153539506	153539506	Frame_Shift_Ins	INS	-	TC	-	TKTL1	c.419_420insTC	p.C140fs
XH_P40	1	110172025	110172025	Missense_Mutation	SNV	A	G	G	AMPD2	c.1937A>G	P.646G
XH_P40	11	1643082	1643082	Missense_Mutation	SNV	T	C	C	KRTAP5-4	c.242A>G	P.Y81C
XH_P40	11	63326001	63326001	Missense_Mutation	SNV	A	T	T	HRASLS2	c.250T>A	P.Y84N
XH_P40	12	52699116	52699116	Silent	SNV	C	T	T	KRT86	c.828C>T	P.A276A
XH_P40	16	2979707	2979707	Missense_Mutation	SNV	C	G	G	FLYWCH1	c.21C>G	P.S7R
XH_P40	16	4431434	4431434	Missense_Mutation	SNV	C	T	T	VASN	c.556C>T	P.P186S
XH_P40	16	67337112	67337112	Missense_Mutation	SNV	G	T	T	KCTD19	c.580C>A	P.L194M
XH_P40	17	40255769	40255769	Silent	SNV	T	C	C	DHX58	c.1611A>G	P.A537A
XH_P40	17	80047551	80047551	Missense_Mutation	SNV	G	T	T	FASN	c.1922C>A	P.A641D
XH_P40	19	17303546	17303546	Splice_Site	SNV	G	A	A	MYO9B	c.2812-9G>A	P.P186S
XH_P40	19	21719801	21719801	Missense_Mutation	SNV	A	G	G	ZNFA429	c.946A>G	P.K316E
XH_P40	19	2994946	2994946	Missense_Mutation	SNV	C	T	T	TL6	c.1663C>T	P.R555C
XH_P40	19	38910606	38910606	Missense_Mutation	SNV	C	T	T	RASGRP4	c.515G>A	P.G172D
XH_P40	20	62065229	62065229	Missense_Mutation	SNV	G	T	T	KCNQ2	c.1051C>A	P.L351I
XH_P40	21	37602927	37602927	Silent	SNV	C	T	T	DOPEY2	c.1845C>T	P.D615D
XH_P40	21	46923918	46923918	Splice_Site	SNV	C	T	T	COL18A1	c.3224-7C>T	
XH_P40	8	74791040	74791040	Splice_Site	SNV	C	G	G	UBE2W	c.102+3G>C	
XH_P40	9	35906586	35906586	Frame_Shift_Ins	INDEL	-	CCCCACCGCCAC	CCCCACCGCCAC	HRCT1	c.CACCTCCACCA	110insTPHLLHHHPHRRH
XH_P41	9	21971153	21971153	Nonsense_Mutation	SNP	C	A	A	CDKN2A	c.205G>T	p.E69*
XH_P41	1	27101453	27101453	Nonsense_Mutation	SNP	C	T	T	ARID1A	c.4735C>T	p.Q1579*
XH_P41	1	-	-	Frame_Shift_Ins	INS	-	-	-	BAP1	c.1833_1834dup	P.K612Rfs*6
XH_P41	1	16262538	16262538	Missense_Mutation	SNP	G	A	A	SPEN	c.9803G>A	p.R3268H
XH_P41	6	151687760	151687760	Missense_Mutation	SNP	C	A	A	ZBTB2	c.441G>T	p.K147N
XH_P41	1	1417574	1417574	Missense_Mutation	SNP	A	G	A	ATAD3B	c.A433G	p.T145A
XH_P41	1	2491306	2491306	Missense_Mutation	SNP	G	A	G	TNFRSF14	c.G349A	p.A117T
XH_P41	1	38463504	38463504	Silent	SNP	C	T	C	FHL3	c.G216A	p.P72P
XH_P41	1	62971488	62971488	Splice_Site	SNP	C	A	C	DOCK7	.	.
XH_P41	1	89473491	89473491	Frame_Shift_Ins	INS	-	AACAA	-	GBP3	301_1302insTT	p.T434fs
XH_P41	1	100329981	100329981	Frame_Shift_Ins	INS	-	GTTC	-	AGL	500_501insGT	p.G167fs
XH_P41	1	100329983	100329984	Frame_Shift_Del	DEL	CT	-	CT	AGL	c.502_503del	p.L168fs
XH_P41	1	110230504	110230504	Missense_Mutation	SNP	G	T	G	GSTM1	c.G9T	p.M3I
XH_P41	1	151090727	151090727	In_Frame_Ins	INS	-	TGC	-	GABPB2	1108_1109insTG	p.S370delinsLP
XH_P41	1	152052196	152052196	Frame_Shift_Ins	INS	-	TCCCTGCCCCAG	-	LOC100131107	c.SGGAACGTGGGG	p.L363fs
XH_P41	1	152128561	152128561	Silent	SNP	A	G	A	RPTN	c.T1014C	p.G338G
XH_P41	1	152192514	152192514	Missense_Mutation	SNP	T	C	T	HRNR	c.A1591G	p.S531G
XH_P41	1	152329328	152329328	Missense_Mutation	SNP	A	G	A	FLG2	c.T934C	p.Y312H
XH_P41	1	152329330	152329339	Frame_Shift_Del	DEL	CTAAATTGAT	-	CTAAATTGAT	FLG2	c.923_932del	p.N308fs
XH_P41	1	154223643	154223643	Missense_Mutation	SNP	C	T	C	UBAP2L	c.C1340T	p.A447V
XH_P41	1	158943530	158943530	Missense_Mutation	SNP	A	T	A	PYHIN1	c.A1453T	p.T485S
XH_P41	1	160604665	160604665	Nonsense_Mutation	INS	-	CATTTCCTTAT	-	SLAMF1	438insATAAAGA	p.L146delinsIX
XH_P41	1	162336877	162336877	Missense_Mutation	SNP	C	T	C	NOS1AP	c.C256T	p.R86C
XH_P41	1	169080657	169080657	Silent	SNP	C	A	C	ATP1B1	c.C147A	p.I49I
XH_P41	1	171553263	171553263	In_Frame_Ins	INS	-	GTT	-	PRRC2C	7572_7573insG	b.E2524delinsEV
XH_P41	1	171553264	171553264	Missense_Mutation	SNP	C	A	C	PRRC2C	c.C7573A	p.H2525N
XH_P41	1	186086679	186086679	Frame_Shift_Ins	INS	-	AAGAC	-	HMCN1	772_11773insA	p.P3924fs
XH_P41	1	186273365	186273365	In_Frame_Ins	INS	-	CATCTGTTTATC	-	PRG4	23insACATCTTG	108delinsNILFML
XH_P41	1	200818796	200818796	Missense_Mutation	SNP	A	G	A	CAMSAP2	c.A2851G	p.S951G
XH_P41	1	228476488	228476488	Frame_Shift_Ins	INS	-	CA	-	OBSCN	10238_10239ins	p.A3413fs
XH_P41	1	228584722	228584722	In_Frame_Ins	INS	-	ACATCA	-	TRIM11	84_785insTGAT	p.P262delinsLMS
XH_P41	1	231881247	231881247	Splice_Site	SNP	T	C	T	DISC1	.	.
XH_P41	1	248129253	248129253	Nonsense_Mutation	INS	-	ATACGTTTGAAT	-	OR2AK2	621insATACGT	T207delinsTVVX
XH_P41	1	248814136	248814136	Nonsense_Mutation	INS	-	CTTCCTCT	-	OR2T27	9_50insAGAGGA	L17_F18delinsX
XH_P41	2	14774372	14774372	Missense_Mutation	SNP	G	A	G	FAM84A	c.G269A	p.R90Q
XH_P41	2	20482714	20482714	Missense_Mutation	SNP	A	C	A	PUM2	c.T1546G	p.S516A
XH_P41	2	47748292	47748292	Silent	SNP	A	G	A	KCNK12	c.T1047C	p.G349G
XH_P41	2	51255107	51255107	Missense_Mutation	SNP	G	A	G	NRXN1	c.C305T	p.T102M
XH_P41	2	101869588	101869588	Silent	SNP	G	T	G	CNOT11	c.G162T	p.P54P
XH_P41	2	102968212	102968212	Missense_Mutation	SNP	A	G	A	IL1RL1	c.A1502G	p.Q501R
XH_P41	2	175264810	175264810	Missense_Mutation	SNP	T	A	T	SCRN3	c.T299A	p.L100Q
XH_P41	2	175264811	175264811	Frame_Shift_Ins	INS	-	AACCAGAAAAG	-	SCRN3	301insAACCAG	p.L100fs
XH_P41	2	178415786	178415786	Frame_Shift_Ins	INS	-	GA	-	ITC30B	1705_1706insT	p.K569fs
XH_P41	2	178415787	178415787	Nonsense_Mutation	INS	-	TTATGA	-	ITC30B	704_1705insTCA	p.K569delinsSX
XH_P41	2	179343146	179343146	Silent	SNP	C	T	C	FKBP7	c.G81A	p.K27K
XH_P41	2	202358592	202358592	Frame_Shift_Ins	INS	-	AGAAGTT	-	C2CD6	71_2472insAAC	p.H824fs
XH_P41	2	234394466	234394466	Nonsense_Mutation	SNP	C	A	C	USP40	c.G3388T	p.E1130X
XH_P41	2	234394467	234394467	Frame_Shift_Ins	INS	-	GATGTTTG	-	USP40	6_3387insCAAA	p.L1129fs
XH_P41	2	238275725	238275725	Missense_Mutation	SNP	A	G	A	COL6A3	c.T3284C	p.I1095T
XH_P41	2	241570294	241570294	Missense_Mutation	SNP	G	A	G	GPR35	c.G925A	p.A309T
XH_P41	3	12859004	12859004	Missense_Mutation	SNP	A	C	A	CAND2	c.A2294C	p.H765P
XH_P41	3	135721000	135721000	Missense_Mutation	SNP	A	G	A	PPP2R3A	c.A660G	p.L220M
XH_P41	3	154033018	154033018	In_Frame_Ins	INS	-	AAAAAT	-	DHX36	419_420insATT	p.L140delinsLFF
XH_P41	3	154033020	154033020	Missense_Mutation	SNP	G	T	G	DHX36	c.C418A	p.L140I
XH_P41	3	184966252	184966252	Frame_Shift_Ins	INS	-	ATTTA	-	EHHADH	127_128insTAA	p.H43fs
XH_P41	3	184966254	184966254	Missense_Mutation	SNP	G	T	G	EHHADH	c.C126A	p.D42E
XH_P41	4	961373	961373	Silent	SNP	G	A	G	DGKQ	c.C951T	p.V317V
XH_P41	4	983809	983809	Silent	SNP	C	T	C	SLC26A1	c.G918A	p.S306S
XH_P41	4	166388971	166388971	Frame_Shift_Ins	INS	-	TTATTATTATGT	-	CPE	37insCTTATTAT	p.L212fs
XH_P41	5	23526373	23526373	Silent	SNP	A	G	A	PRDM9	c.A1176G	p.S392S
XH_P41	5	55075881	55075881	Nonsense_Mutation	INS	-	AAATTTAATT	-	DDX4	425insAAATT	42_G143delinsQIX

XH_P41	5	66459878	66459878	Missense_Mutation	SNP	G	C	G	MAST4	c.G4088C	p.R1363P
XH_P41	5	86668011	86668011	Frame_Shift_Ins	INS	-	G	-	RASA1	c.1776dupG	p.Q592fs
XH_P41	5	112824048	112824048	In_Frame_Ins	INS	-	GCC	-	MCC	c.63_64insGGC	p.S22delinsGS
XH_P41	5	115177803	115177803	Frame_Shift_Ins	INS	-	A	-	AP31	c.70dupA	p.Y23fs
XH_P41	5	115177805	115177805	Splice_Site	INS	-	CAACAGCAAAAT	-	AP31	-	-
XH_P41	5	132198248	132198248	Nonsense_Mutation	INS	-	ACATGT	-	GDF9	97_398insACAT	G133delinsDMX
XH_P41	5	149466156	149466172	Splice_Site	DEL	TTCCCTTTTA	-	CTTCCCTTTTAG	CSF1R	-	-
XH_P41	5	178140425	178140441	Frame_Shift_Del	DEL	TTTGTGGGT	-	TTTGTGGGTGG	ZNF354A	c.312_328del	p.S104fs
XH_P41	6	17541240	17541240	Nonsense_Mutation	INS	-	AATTAATAAAAA	-	CAP2	54insAAATTAATAA	N289delinsKNX
XH_P41	6	31324151	31324151	Missense_Mutation	SNP	C	T	C	HLA-B	c.G412A	p.D138N
XH_P41	6	31324200	31324200	Missense_Mutation	SNP	G	C	G	HLA-B	c.C363G	p.S121R
XH_P41	6	33756793	33756793	Missense_Mutation	SNP	T	A	T	LEMD2	c.A101T	p.K34M
XH_P41	6	41562693	41562693	Missense_Mutation	SNP	G	A	G	FOXP4	c.G1622A	p.R541Q
XH_P41	6	42236611	42236611	In_Frame_Ins	INS	-	TAT	-	TRERF1	717_718insAT	p.L240delinsIL
XH_P41	6	91246115	91246115	Missense_Mutation	SNP	C	T	C	MAP3K7	c.G1216A	p.G406R
XH_P41	6	127797179	127797179	Silent	SNP	G	A	G	SOGA3	c.C1992T	p.A664A
XH_P41	6	151674784	151674784	In_Frame_Ins	INS	-	ACT	-	AKAP12	4964_4965insAp	S1655delinsRL
XH_P41	6	157100283	157100283	Missense_Mutation	SNP	G	A	G	ARID1B	c.G1220A	p.G407D
XH_P41	7	34014376	34014376	Nonsense_Mutation	INS	-	AAGACA	-	BMPER	56_557insAAGA	p.C186delinsX
XH_P41	7	64004135	64004135	Frame_Shift_Ins	INS	-	T	-	ZNF680	c.202_203insA	p.G68fs
XH_P41	7	75959188	75959188	Silent	SNP	G	A	G	YWHAG	c.C450T	p.S150S
XH_P41	7	91670097	91670097	Frame_Shift_Ins	INS	-	CATTT	-	AKAP9	802_4803insCA	p.H1601fs
XH_P41	7	92244577	92244577	Frame_Shift_Ins	INS	-	TTGTGT	-	CDK6	57_858insAAAC	p.A286fs
XH_P41	7	100642572	100642572	Missense_Mutation	SNP	C	T	C	MUC12	c.C8728T	p.P2910S
XH_P41	7	100643293	100643293	Missense_Mutation	SNP	G	A	G	MUC12	c.G9494A	p.G3150D
XH_P41	7	100647304	100647304	Frame_Shift_Ins	INS	-	ATTC	-	MUC12	1460_13461insA	p.S4487fs
XH_P41	7	100676418	100676418	Missense_Mutation	SNP	A	G	A	MUC17	c.A1721G	p.N574S
XH_P41	7	100676419	100676419	Silent	SNP	C	T	C	MUC17	c.C1722T	p.N574N
XH_P41	7	150700402	150700402	Missense_Mutation	SNP	T	C	T	NOS3	c.T1756C	p.W586R
XH_P41	8	52733148	52733148	Silent	SNP	C	T	C	PCMTD1	c.G609A	p.K203K
XH_P41	8	95751962	95751962	Frame_Shift_Ins	INS	-	GATATAAA	-	DPY19L4	5_556insGATAT	p.L185fs
XH_P41	8	105361493	105361493	Frame_Shift_Del	DEL	G	-	G	DCSTAMP	c.713delG	p.C238fs
XH_P41	8	105361494	105361494	Nonsense_Mutation	SNP	T	A	T	DCSTAMP	c.T714A	p.C238X
XH_P41	8	110131301	110131301	Missense_Mutation	SNP	G	A	G	TRHR	c.G814A	p.V272I
XH_P41	8	110131302	110131302	Nonsense_Mutation	INS	-	CAATTAG	-	TRHR	15_816insCAAT	T72_1273delinsVNX
XH_P41	8	144942903	144942903	Missense_Mutation	SNP	T	C	T	EPPK1	c.A4519G	p.T1507A
XH_P41	8	145661320	145661320	Silent	SNP	G	A	G	TONSL	c.C2496T	p.A832A
XH_P41	9	13150667	13150667	Frame_Shift_Ins	INS	-	TTTT	-	MPDZ	472_3473insAA	p.P1158fs
XH_P41	9	13150668	13150668	Nonsense_Mutation	INS	-	TTTATTTATTTAT	-	MPDZ	72insAATAAATA	P1158delinsKNX
XH_P41	9	86617261	86617261	In_Frame_Ins	INS	-	AATACTCCT	-	RM11	10_1361insAATA	R454delinsKYSW
XH_P41	9	134346218	134346218	Missense_Mutation	SNP	C	T	C	PRRC2B	c.C1955T	p.P652L
XH_P41	9	139581797	139581797	Missense_Mutation	SNP	G	A	G	AGPAT2	c.C13T	p.P5S
XH_P41	10	12197888	12197888	In_Frame_Ins	INS	-	GCTATT	-	SEC61A2	408_509insGCTA	V170delinsGYF
XH_P41	10	71835435	71835435	Silent	SNP	G	A	G	H2AFY2	c.G21A	p.K7K
XH_P41	10	102768605	102768605	Frame_Shift_Ins	INS	-	AC	-	PDZD7	2720_2721insG	p.A907fs
XH_P41	10	102768606	102768606	Missense_Mutation	SNP	G	T	G	PDZD7	c.C2720A	p.A907D
XH_P41	10	129904962	129904962	Silent	SNP	G	T	G	MKI67	c.C4062A	p.I1354I
XH_P41	10	129904963	129904963	Missense_Mutation	SNP	A	T	A	MKI67	c.T4061A	p.I1354N
XH_P41	11	280816	280816	Missense_Mutation	SNP	A	T	A	NLRP6	c.A1082T	p.Y361F
XH_P41	11	280817	280817	Silent	SNP	T	C	T	NLRP6	c.T1083C	p.Y361Y
XH_P41	11	771034	771034	Silent	SNP	A	G	A	GATD1	c.T357C	p.T191T
XH_P41	11	1019404	1019404	In_Frame_Ins	INS	-	ATTCAGTGA	-	MUC6	10_3901insTCAC	V1301delinsSLNV
XH_P41	11	1090970	1090970	Missense_Mutation	SNP	C	A	C	MUC2	c.C3865A	p.P1289T
XH_P41	11	1090972	1090972	Silent	SNP	G	C	G	MUC2	c.G3867C	p.P1289P
XH_P41	11	1309956	1309956	Silent	SNP	C	T	C	TOLLIP	c.G267A	p.P89P
XH_P41	11	6341365	6341365	Silent	SNP	C	T	C	CAVIN3	c.G342A	p.G114G
XH_P41	11	11906119	11906119	Missense_Mutation	SNP	A	G	A	USP47	c.A145G	p.I49V
XH_P41	11	18195528	18195528	Missense_Mutation	SNP	T	A	T	MRGPRX4	c.T725A	p.M242K
XH_P41	11	18195529	18195529	Frame_Shift_Ins	INS	-	T	-	MRGPRX4	c.726_727insT	p.M242fs
XH_P41	11	20622975	20622975	Missense_Mutation	SNP	G	A	G	SLC6A5	c.G304A	p.G102S
XH_P41	11	46564282	46564282	Missense_Mutation	SNP	G	A	G	AMBRA1	c.C1285T	p.R429C
XH_P41	11	62297689	62297689	Silent	SNP	A	T	A	AHNAK	c.T4200A	p.P1400P
XH_P41	11	62644260	62644260	Silent	SNP	A	G	A	SLC3A2	c.A210G	p.E70E
XH_P41	11	65810749	65810749	Silent	SNP	T	C	T	GAL3ST3	c.A525G	p.V175V
XH_P41	11	71146577	71146577	Silent	SNP	G	A	G	DHCR7	c.C1272T	p.G424G
XH_P41	11	76255690	76255690	Frame_Shift_Ins	INS	-	TGTTAGT	-	EMSY	10_3101insTGT	p.P1034fs
XH_P41	11	88042451	88042454	Frame_Shift_Del	DEL	AAGT	-	AAGT	CTSC	c.S18_521del	p.N173fs
XH_P41	11	95595477	95595477	Frame_Shift_Ins	INS	-	ATTAATTG	-	MTMR2	5_316insCAATT	p.T106fs
XH_P41	11	100998623	100998623	Silent	SNP	G	A	G	PGR	c.C1179T	p.G393G
XH_P41	11	107375842	107375842	Missense_Mutation	SNP	G	T	G	ALKBH8	c.C1546A	p.Q516K
XH_P41	11	107375843	107375843	Silent	SNP	C	T	C	ALKBH8	c.G1545A	p.K515K
XH_P41	11	117153552	117153552	Frame_Shift_Ins	INS	-	AGTACTT	-	RNF214	36_1937insAGT	p.G646fs
XH_P41	11	119020753	119020753	Silent	SNP	C	T	C	ABCG4	c.C78T	p.D26D
XH_P41	12	31242051	31242074	In_Frame_Del	DEL	TCGGCTGGT	-	TTCCGGCTGGTC	DDX11	c.758_781del	p.253_261del
XH_P41	12	56092319	56092319	Missense_Mutation	SNP	C	T	C	ITGA7	c.G1052A	p.R351H
XH_P41	12	56745081	56745081	Silent	SNP	G	T	G	STAT2	c.C936A	p.L312L
XH_P41	12	56745082	56745082	Frame_Shift_Ins	INS	-	TTTCTCG	-	STAT2	34_935insCAGA	p.L312fs
XH_P41	12	56814867	56814867	Nonsense_Mutation	INS	-	A	-	TIMELESS	12916_2917ins	E973_E974delinsX
XH_P41	12	56814869	56814869	Frame_Shift_Ins	INS	-	TC	-	TIMELESS	2914_2915insG	p.E972fs
XH_P41	12	58157922	58157922	Frame_Shift_Ins	INS	-	CCTG	-	CYP27B1	173_1174insCA	p.C392fs
XH_P41	12	85449603	85449603	Silent	SNP	G	A	G	LRRIQ1	c.G1032A	p.R344R
XH_P41	12	85449604	85449604	In_Frame_Ins	INS	-	TTTTTCTTTTC	-	LRRIQ1	034insTTTTTTT	T1345delinsFFFFL
XH_P41	12	111926295	111926295	Missense_Mutation	SNP	T	C	T	ATXN2	c.A1838G	p.K613R
XH_P41	12	123741557	123741557	Frame_Shift_Ins	INS	-	ATAATATTTTA	-	C12orf65	481insATAATA	p.E160fs
XH_P41	12	123741559	123741559	Nonsense_Mutation	SNP	C	A	C	C12orf65	c.C482A	p.S161X
XH_P41	12	132325239	132325239	Missense_Mutation	SNP	G	A	G	MMP17	c.G544A	p.A182T
XH_P41	13	32835796	32835796	Missense_Mutation	SNP	C	T	C	FRY	c.C7460T	p.S2487F
XH_P41	13	52524194	52524194	Frame_Shift_Ins	INS	-	TT	-	ATP7B	2192_2193insA	p.D731fs
XH_P41	13	52524196	52524196	Missense_Mutation	SNP	C	T	C	ATP7B	c.G2191A	p.D731N
XH_P41	13	76448005	76448005	Silent	SNP	T	C	T	LMO7DN	c.T213C	p.P71P
XH_P41	13	103390160	103390160	Frame_Shift_Ins	INS	-	GAAAGAC	-	CCDC168	86_12887insGT	p.I4296fs
XH_P41	14	21992205	21992205	Frame_Shift_Ins	INS	-	TG	-	SALL2	1656_1657insC	p.L553fs
XH_P41	14	23738174	23738185	Splice_Site	DEL	CAGTAACACT	-	TCAGTAACACTA	RNF212B	-	-
XH_P41	14	54878280	54878280	Nonsense_Mutation	INS	-	SACAATCTATAA	-	CDKN3	63insTGACAATC	N51delinsNDNLX
XH_P41	14	70527623	70527623	Frame_Shift_Ins	INS	-	AAAT	-	SLC8A3	1817_1818insAT	p.E606fs
XH_P41	14	71275774	71275779	In_Frame_Del	DEL	CCTCCT	-	CCTCCT	MAP3K9	c.110_115del	p.37_39del
XH_P41	14	77732902	77732902	Missense_Mutation	SNP	T	A	T	NGB	c.A433T	p.S145C
XH_P41	14	101200780	101200780	Silent	SNP	T	C	T	DLK1	c.T699C	p.C233C

XH_P41	14	105410601	105410601	Missense_Mutation	SNP	C	G	C	AHNAK2	c.G10887C	p.L3629F
XH_P41	14	105410862	105410862	Silent	SNP	T	C	T	AHNAK2	c.A10626G	p.K3542K
XH_P41	15	39910106	39910106	Missense_Mutation	SNP	G	A	G	FSIP1	c.C1529T	p.S510F
XH_P41	15	90760791	90760791	Missense_Mutation	SNP	T	C	T	SEMA4B	c.T46C	p.S16P
XH_P41	16	2049003	2049003	Missense_Mutation	SNP	A	T	A	ZNF598	c.T2173A	p.C725S
XH_P41	16	21215490	21215490	Missense_Mutation	SNP	G	A	G	郑2	c.C833T	p.P278L
XH_P41	16	30939947	30939947	Missense_Mutation	SNP	G	A	G	FBXL19	c.G847A	p.E283K
XH_P41	16	31519547	31519547	Missense_Mutation	SNP	C	T	C	C16orf58	c.G148A	p.V50I
XH_P41	16	67681962	67681962	Missense_Mutation	SNP	A	G	A	CARMIL2	c.A1079G	p.Y360C
XH_P41	16	67943557	67943557	Missense_Mutation	SNP	G	A	G	PSKH1	c.G905A	p.R302H
XH_P41	16	84225156	84225156	Missense_Mutation	SNP	C	T	C	ADAD2	c.C320T	p.P107L
XH_P41	16	89916879	89916879	In_Frame_Ins	INS	-	AAG	-	SPIRE2	c.456_457insAAp	p.P152delinsPK
XH_P41	17	4883785	4883785	Frame_Shift_Ins	INS	-	TTGTA	-	CAMTA2	837_838insTAC	p.P280fs
XH_P41	17	11513803	11513803	Silent	SNP	G	A	G	DNAH9	c.G705A	p.E235E
XH_P41	17	11513805	11513805	Frame_Shift_Ins	INS	-	CCAAA	-	DNAH9	707_708insCCA	p.S236fs
XH_P41	17	29632364	29632364	Frame_Shift_Ins	INS	-	AACAAATAACT	-	EV12B	264insAGTTAT	p.S88fs
XH_P41	17	37657597	37657597	Silent	SNP	G	C	G	CDK12	c.G2514C	p.S838S
XH_P41	17	37657598	37657598	Nonsense_Mutation	INS	-	AATA	-	CDK12	515_2516insAA	839_M840delinsX
XH_P41	17	40725578	40725578	Frame_Shift_Ins	INS	-	AGGTG	-	PSMC3IP	211_212insCAC	p.K71fs
XH_P41	17	48559559	48559559	Silent	SNP	A	G	A	RSAD1	c.A582G	p.V194V
XH_P41	17	56620445	56620472	Frame_Shift_Del	DEL	AACATGGATG	-	AAACATGGATGA	C17orf47	c.1076_1103del	p.S539fs
XH_P41	17	76121864	76121864	Missense_Mutation	SNP	A	G	A	TMC6	c.T373C	p.W125R
XH_P41	17	79009061	79009061	Silent	SNP	C	T	C	BAIAP2	c.C7T	p.L3L
XH_P41	17	79202951	79202951	Frame_Shift_Del	DEL	C	-	C	TEPSIN	c.1355delG	p.G452fs
XH_P41	17	80739547	80739547	In_Frame_Ins	INS	-	CTC	-	TBCD	c.721_722insCTp	p.F241delinsSL
XH_P41	18	9211707	9211708	Frame_Shift_Del	DEL	GC	-	GC	ANKRD12	c.508_509del	p.A170fs
XH_P41	18	9211708	9211708	In_Frame_Ins	INS	-	AAA	-	ANKRD12	509_510insAA	p.A170delinsAN
XH_P41	19	1014398	1014398	Silent	SNP	A	G	A	TMEM259	c.T300C	p.H100H
XH_P41	19	1456961	1456961	Missense_Mutation	SNP	G	A	G	APC2	c.G923A	p.R308H
XH_P41	19	4510960	4510960	Frame_Shift_Ins	INS	-	CA	-	PLIN4	2969_2970insT	p.A990fs
XH_P41	19	5455990	5455990	Missense_Mutation	SNP	G	A	G	ZNRF4	c.G488A	p.R163H
XH_P41	19	5687977	5687977	Missense_Mutation	SNP	A	G	A	HSD11B1L	c.A547G	p.S183G
XH_P41	19	6380378	6380381	Frame_Shift_Del	DEL	CTGT	-	CTGT	GTFF21	c.1465_1468del	p.T489fs
XH_P41	19	7676008	7676008	Silent	SNP	G	A	G	CAMSAP3	c.G1077A	p.P359P
XH_P41	19	14199554	14199554	Frame_Shift_Ins	INS	-	G	-	SAMD1	c.1068_1069ins	p.T357fs
XH_P41	19	14199555	14199555	Nonsense_Mutation	INS	-	TT	-	SAMD1	1067_1068insAV	356_T357delinsX
XH_P41	19	14508037	14508037	Splice_Site	INS	-	ATGACCTGG	-	ADGRE5	-	
XH_P41	19	15659002	15659002	Missense_Mutation	SNP	G	T	G	CYP4F22	c.G1220T	p.R407L
XH_P41	19	15659003	15659003	Frame_Shift_Ins	INS	-	TCCTCT	-	CYP4F22	221_1222insTC	p.R407fs
XH_P41	19	20229289	20229289	Missense_Mutation	SNP	A	G	A	ZNF90	c.A926G	p.E309G
XH_P41	19	20229479	20229479	Missense_Mutation	SNP	T	A	T	ZNF90	c.T1116A	p.D372E
XH_P41	19	20229480	20229480	Missense_Mutation	SNP	A	G	A	ZNF90	c.A1117G	p.K373E
XH_P41	19	20727555	20727555	Missense_Mutation	SNP	C	T	C	ZNF737	c.G1454A	p.R485Q
XH_P41	19	20727556	20727556	Missense_Mutation	SNP	G	C	G	ZNF737	c.C1453G	p.R485S
XH_P41	19	21366637	21366637	Missense_Mutation	SNP	T	C	T	ZNF431	c.T1534C	p.S512P
XH_P41	19	21366639	21366639	Silent	SNP	T	C	T	ZNF431	c.T1536C	p.S512S
XH_P41	19	21720133	21720133	Missense_Mutation	SNP	T	A	T	ZNF429	c.T1086A	p.N362K
XH_P41	19	23543701	23543701	Missense_Mutation	SNP	T	C	T	ZNF91	c.A1984G	p.T662A
XH_P41	19	30935350	30935350	Missense_Mutation	SNP	G	A	G	ZNF536	c.G881A	p.R294H
XH_P41	19	33424507	33424507	Nonsense_Mutation	SNP	C	A	C	CEP89	c.G736T	p.E246G
XH_P41	19	33424508	33424508	Frame_Shift_Ins	INS	-	GTTGTGA	-	CEP89	34_735insTACG	p.E245fs
XH_P41	19	40228590	40228590	Missense_Mutation	SNP	C	T	C	CLC	c.G3A	p.M1I
XH_P41	19	50393269	50393269	Silent	SNP	A	G	A	IL41	c.T1362C	p.F454F
XH_P41	19	53572841	53572841	Missense_Mutation	SNP	G	T	G	ZNF160	c.C946A	p.H316N
XH_P41	19	53855011	53855011	Silent	SNP	C	T	C	ZNF845	c.C1083T	p.D361D
XH_P41	19	53855012	53855012	Missense_Mutation	SNP	A	G	A	ZNF845	c.A1084G	p.K362E
XH_P41	19	56196794	56196794	Silent	SNP	C	T	C	EPN1	c.C261T	p.T87T
XH_P41	19	57176198	57176198	Silent	SNP	T	G	T	ZNF835	c.A369C	p.S123S
XH_P41	19	57176304	57176304	Missense_Mutation	SNP	T	G	T	ZNF835	c.A263C	p.E88A
XH_P41	19	58355650	58355650	Frame_Shift_Ins	INS	-	TCGAG	-	ZNF587B	149_1150insTCG	p.H383fs
XH_P41	20	1617017	1617017	Frame_Shift_Ins	INS	-	T	-	SIRPG	c.564_565insA	p.L189fs
XH_P41	20	1617018	1617018	Silent	SNP	C	T	C	SIRPG	c.G564A	p.E188E
XH_P41	20	35672606	35672606	In_Frame_Ins	INS	-	CATTTT	-	RB1L	71_372insAAAA	M124delinsKW
XH_P41	20	4768913	4768913	Nonsense_Mutation	INS	-	TGAAC TAG	-	CSE1L	9_860insTGAAC	287_R288delinsLNX
XH_P41	20	50769183	50769183	Silent	SNP	G	A	G	ZFP64	c.C1386T	p.A462A
XH_P41	20	60885047	60885047	Missense_Mutation	SNP	C	A	C	LAMA5	c.G10825T	p.A3609S
XH_P41	20	61981134	61981134	Silent	SNP	G	A	G	CHRNA4	c.C1629T	p.S543S
XH_P41	21	41173194	41173194	Silent	SNP	T	A	T	IGSF5	c.T1134A	p.A378A
XH_P41	21	46066764	46066764	Missense_Mutation	SNP	C	T	C	KRTAP10-11	c.C389T	p.S130F
XH_P41	22	19838816	19838816	Missense_Mutation	SNP	T	G	T	RTL10	c.A969C	p.K323N
XH_P41	22	32586994	32586994	Missense_Mutation	SNP	C	T	C	RFPL2	c.G719A	p.R240H
XH_P41	22	41721837	41721837	Missense_Mutation	SNP	A	T	A	ZC3H7B	c.A200T	p.D67V
XH_P41	22	50898026	50898026	Silent	SNP	G	A	G	SBF1	c.C3561T	p.Y1187Y
XH_P41	X	3235393	3235393	Missense_Mutation	SNP	C	T	C	MXRA5	c.G6329A	p.R2110H
XH_P41	X	18942536	18942536	Missense_Mutation	SNP	T	A	T	PHKA2	c.A1677T	p.R559S
XH_P41	X	48854582	48854582	Frame_Shift_Ins	INS	-	GTCTG	-	GRIPAP1	181_182insCAG	p.K61fs
XH_P41	X	101970836	101970836	Missense_Mutation	SNP	A	T	A	RM CX5-GPRAS	c.A1039T	p.N347Y
XH_P41	X	151366249	151366249	In_Frame_Ins	INS	-	TGA	-	GABRA3	c.786_787insTCp	p.V263delinsSV
XH_P41	Y	9304636	9304636	Silent	SNP	C	T	C	TSPY1	c.C27T	p.Y9Y
XH_P41	1	110230504	110230504	Missense_Mutation	SNV	G	T	T	GSTM1	c.96>T	p.M3I
XH_P41	1	154223643	154223643	Missense_Mutation	SNV	C	T	T	UBAP2L	c.1340C>T	p.A447V
XH_P41	1	169080657	169080657	Silent	SNV	C	A	A	ATP1B1	c.147C>A	p.I19T
XH_P41	1	200818796	200818796	Missense_Mutation	SNV	A	G	G	CAMSAP2	c.2932A>G	p.S978G
XH_P41	1	62971488	62971488	Splice_Site	SNV	C	A	A	DOCK7	c.4450-1G>T	
XH_P41	10	71835435	71835435	Silent	SNV	G	A	A	H2AFY2	c.21G>A	p.K7K
XH_P41	11	11906119	11906119	Missense_Mutation	SNV	A	G	G	USP47	c.349A>G	p.I117V
XH_P41	12	111926295	111926295	Missense_Mutation	SNV	T	C	C	ATXN2	c.1910A>G	p.K637R
XH_P41	12	56092319	56092319	Missense_Mutation	SNV	C	T	T	ITGAT	c.1052G>A	p.R351H
XH_P41	13	32835796	32835796	Missense_Mutation	SNV	C	T	T	FRY	c.7460C>T	p.S2487F
XH_P41	14	77732902	77732902	Missense_Mutation	SNV	T	A	A	NGB	c.433A>T	p.S145C
XH_P41	15	25422059	25422059	Splice_Site	SNV	C	T	T	SNORD115-4	n.81C>T	
XH_P41	15	39910106	39910106	Missense_Mutation	SNV	G	A	A	FSIP1	c.1529C>T	p.S510F
XH_P41	16	21215490	21215490	Missense_Mutation	SNV	G	A	A	郑2	c.833C>T	p.P278L
XH_P41	16	30939947	30939947	Missense_Mutation	SNV	G	A	A	FBXL19	c.847G>A	p.E283K
XH_P41	16	67036963	67036963	Splice_Site	SNV	G	T	T	CES4A	c.397-10G>T	
XH_P41	16	67681962	67681962	Missense_Mutation	SNV	A	G	G	CARMIL2	c.1079A>G	p.Y360C
XH_P41	16	67943557	67943557	Missense_Mutation	SNV	G	A	A	PSKH1	c.905G>A	p.R302H
XH_P41	19	1456961	1456961	Missense_Mutation	SNV	G	A	A	APC2	c.926G>A	p.R309H

XH_P41	19	40228590	40228590	Nonsense_Mutation	SNV	C	T	T	CLC	c.3G>A	P.M1?
XH_P41	19	6380378	6380381	Frame_Shift_Del	INDEL	CTGT	-	-	GTF2F1	465_1468delAC	P.T489fs
XH_P41	2	14774372	14774372	Missense_Mutation	SNV	G	A	A	FAM84A	c.269G>A	P.R90Q
XH_P41	2	179343146	179343146	Silent	SNV	C	T	T	FKBP7	c.81G>A	P.K27K
XH_P41	2	20482714	20482714	Missense_Mutation	SNV	A	C	C	PUM2	c.1546T>G	P.S516A
XH_P41	2	238275725	238275725	Missense_Mutation	SNV	A	G	G	COL6A3	c.5105T>C	P.I1702T
XH_P41	2	241570294	241570294	Missense_Mutation	SNV	G	A	A	GPR35	c.1018G>A	P.A340T
XH_P41	21	41173194	41173194	Silent	SNV	T	A	A	IGSF5	c.1134T>A	P.A378A
XH_P41	22	19838816	19838816	Missense_Mutation	SNV	T	G	G	C22orf29	c.969A>C	P.K323N
XH_P41	22	41721837	41721837	Missense_Mutation	SNV	A	T	T	ZC3H7B	c.200A>T	P.D67V
XH_P41	3	135721000	135721000	Missense_Mutation	SNV	A	G	G	PPP2R3A	c.660A>G	P.I220M
XH_P41	3	141259371	141259371	Splice_Site	SNV	A	G	G	RASA2	c.451-4A>G	
XH_P41	3	52437209	52437209	Frame_Shift_Ins	INDEL	-	TC	TC	BAP1	1833_1834dupC	P.K612fs
XH_P41	5	140569168	140569168	Missense_Mutation	SNV	A	G	G	PCDH89	c.2276A>G	P.Q759R
XH_P41	5	86668011	86668011	Splice_Site	INDEL	-	G	G	RASA1	c.1776+1dupG	
XH_P41	6	157100283	157100283	Missense_Mutation	SNV	G	A	A	ARID1B	c.1220G>A	P.G407D
XH_P41	6	33756793	33756793	Missense_Mutation	SNV	T	A	A	LEM2	c.101A>T	P.K34M
XH_P41	9	139581797	139581797	Missense_Mutation	SNV	G	A	A	AGPAT2	c.13C>T	P.P55
XH_P41	9	21971153	21971153	Missense_Mutation	SNV	C	A	A	CDKN2A	c.248G>T	P.G83V
XH_P41	X	101970836	101970836	Missense_Mutation	SNV	A	T	T	GPRASP2	c.1039A>T	P.N347Y
XH_P42	1	1895207	1895207	Missense_Mutation	SNP	G	A	G	CFAP74	c.C1675T	p.R559W
XH_P42	1	1961713	1961713	Missense_Mutation	SNP	G	A	G	GABRD	c.G1351A	p.A451T
XH_P42	1	2428372	2428372	Missense_Mutation	SNP	G	A	G	PLCH2	c.G1958A	p.R653H
XH_P42	1	6313981	6313981	Missense_Mutation	SNP	G	A	G	GPR153	c.C583T	p.L195F
XH_P42	1	12183393	12183393	Silent	SNP	G	A	G	TNFRSF8	c.G666A	p.P222P
XH_P42	1	16461628	16461628	Silent	SNP	G	A	G	EPHA2	c.C1323T	p.D441D
XH_P42	1	26608828	26608828	Missense_Mutation	SNP	G	A	G	UBXN11	c.C1165T	p.P389S
XH_P42	1	27333320	27333320	Silent	SNP	C	G	C	FAM46B	c.G393C	p.R131R
XH_P42	1	27622882	27622882	Frame_Shift_Ins	INS	-	TCACAGCTTCCA	-	WDC1	TTACCTCACAGC	p.H313fs
XH_P42	1	36769473	36769473	Missense_Mutation	SNP	G	A	G	THRAP3	c.G2720A	p.R907Q
XH_P42	1	38289478	38289478	Missense_Mutation	SNP	C	A	C	MTF1	c.G1075T	p.G359C
XH_P42	1	38289479	38289479	Nonsense_Mutation	INS	-	ATGAATCATTCTA	-	MTF1	774insCTAGAATp.Q358delinsHX	
XH_P42	1	40125028	40125028	Missense_Mutation	SNP	C	T	C	NT5C1A	c.G872A	p.R291Q
XH_P42	1	43632906	43632906	Nonsense_Mutation	INS	-	AAATCAACTCTA	-	EBNA1BP2	TACTTTAGAGTTp.V180delinsQVLX	
XH_P42	1	45120834	45120834	Silent	SNP	G	A	G	TMEM53	c.C12T	p.P4F
XH_P42	1	48865171	48865171	In_Frame_Ins	INS	-	AGATAAACCTCC	-	SPATA6	0insATGGAGGTp.197delinsNGGLSV	
XH_P42	1	52269589	52269589	Missense_Mutation	SNP	G	A	G	NRDC	c.C2210T	p.A737V
XH_P42	1	65278469	65278469	Nonsense_Mutation	INS	-	TTCTCTATTCTT	-	RAVER2	AAGTATTTCCTCTp.64_R565delinsKX	
XH_P42	1	66384459	66384459	Silent	SNP	G	A	G	PDE4B	c.G222A	p.P74P
XH_P42	1	84956144	84956144	Missense_Mutation	SNP	G	A	G	RPF1	c.G605A	p.R202H
XH_P42	1	94037342	94037342	In_Frame_Ins	INS	-	CTTTCATGAGAC	-	BCAR3	nsCAGCTCTTCATp.296delinsSALMKAL	
XH_P42	1	104120374	104120374	Frame_Shift_Ins	INS	-	TAGTAACCTCTT	-	AMY2B	sATTAATAGTAA	p.G418fs
XH_P42	1	115165718	115165718	Missense_Mutation	SNP	G	T	G	DENND2C	c.C946A	p.P316T
XH_P42	1	115165719	115165719	Frame_Shift_Ins	INS	-	TTTTTTTTATTTT	-	DENND2C	5insCAAAAATAA	p.V315fs
XH_P42	1	115596024	115596024	Silent	SNP	G	A	G	TSPAN2	c.C501T	p.V167V
XH_P42	1	144852477	144852477	Missense_Mutation	SNP	G	A	G	PDE4DIP	c.C7508T	p.P2503L
XH_P42	1	149761715	149761715	Frame_Shift_Ins	INS	-	A	-	FCGR1A	c.665_666insA	p.G222fs
XH_P42	1	149761716	149761716	In_Frame_Ins	INS	-	TAAACAGGCAA	-	FCGR1A	7insGCTAAACA222delinsGAKOAT	
XH_P42	1	150531134	150531134	Silent	SNP	G	A	G	ADAMTSL4	c.G2568A	p.P856P
XH_P42	1	151090631	151090631	In_Frame_Ins	INS	-	CTCTCT	-	GABPB2	012_1013insCTCp.V338delinsALF	
XH_P42	1	152192634	152192634	Missense_Mutation	SNP	G	A	G	HRNR	c.C1471T	p.H491Y
XH_P42	1	152328411	152328411	Silent	SNP	A	G	A	FLG2	c.T1851C	p.S617S
XH_P42	1	152328507	152328507	Silent	SNP	C	T	C	FLG2	c.G1755A	p.S585S
XH_P42	1	153004942	153005013	In_Frame_Del	DEL	CAAAAGTGCC	-	CCCAAGATGCC	SPRR1B	c.121_192del	p.41_64del
XH_P42	1	153751918	153751918	In_Frame_Ins	INS	-	AGGGCA	-	SLC27A3	28_229insAGGp.743delinsPGH	
XH_P42	1	153751919	153751919	Frame_Shift_Ins	INS	-	GGGCTGGAATG	-	SLC27A3	AAGGCAGGGCTp.p.743fs	
XH_P42	1	155448205	155448205	Missense_Mutation	SNP	G	A	G	ASH1L	c.C4456T	p.R1486C
XH_P42	1	156131148	156131148	Silent	SNP	C	T	C	SEMA4A	c.C426T	p.G142G
XH_P42	1	159002473	159002473	In_Frame_Ins	INS	-	TTTTTTCTTTAT	-	IFI16	6GTTTGTTTTTT85delinsSGLFFSLSESI	
XH_P42	1	165173169	165173169	Missense_Mutation	SNP	C	A	C	LMX1A	c.G1097T	p.G366V
XH_P42	1	167787436	167787436	In_Frame_Ins	INS	-	GTTTTGAAGGT	-	ADCY10	TTCTTCACCTTCp.99delinsSSSPSKTNQ	
XH_P42	1	175372616	175372616	Silent	SNP	C	A	C	TNR	c.G636T	p.G212G
XH_P42	1	176708870	176708870	Missense_Mutation	SNP	G	A	G	PAPPA2	c.G3907A	p.D1303N
XH_P42	1	182775328	182775328	Missense_Mutation	SNP	G	A	G	NPL	c.G191A	p.R64H
XH_P42	1	185958761	185958761	Frame_Shift_Ins	INS	-	TTTTTGTTTGTTT	-	HMCN1	insGGTTTTTTTG	p.V1064fs
XH_P42	1	200143208	200143208	Frame_Shift_Ins	INS	-	AGGTGTCAGGA	-	NR5A2	GTAGAAGGTGT	p.L427fs
XH_P42	1	201180243	201180243	Silent	SNP	A	G	A	IGFN1	c.A6222G	p.T2074L
XH_P42	1	205589575	205589575	Missense_Mutation	SNP	G	A	G	ELK4	c.C599T	p.P200L
XH_P42	1	205904864	205904864	Missense_Mutation	SNP	G	A	G	SLC26A9	c.C85T	p.R29W
XH_P42	1	216692679	216692679	Missense_Mutation	SNP	C	T	C	ESRRG	c.G194A	p.R65Q
XH_P42	1	226353673	226353673	Frame_Shift_Ins	INS	-	ATTCACATACAA	-	ACBD3	TTTTCTGTATAG	p.T105fs
XH_P42	1	228399737	228399737	Missense_Mutation	SNP	C	T	C	OBSCN	c.C253T	p.R85C
XH_P42	1	228456389	228456389	Missense_Mutation	SNP	G	A	G	OBSCN	c.G5020A	p.V1674M
XH_P42	1	228491389	228491389	Silent	SNP	A	G	A	OBSCN	c.A13752G	p.R4584R
XH_P42	1	229771085	229771085	Missense_Mutation	SNP	G	A	G	URB2	c.G725A	p.R242Q
XH_P42	1	229771573	229771573	Missense_Mutation	SNP	A	C	A	URB2	c.A1213C	p.I405L
XH_P42	1	234582716	234582716	Nonsense_Mutation	INS	-	AGATACCAAGAC	-	TARBP1	TTGTTCCTCTCTGp.657delinsISCFSWYLYX	
XH_P42	1	240370169	240370169	Missense_Mutation	SNP	T	C	T	FMN2	c.T2057C	p.L686P
XH_P42	1	245019801	245019801	Missense_Mutation	SNP	C	T	C	HNRNP1	c.G1813A	p.G605K
XH_P42	2	1271333	1271333	Missense_Mutation	SNP	A	T	A	SNTG2	c.A1274T	p.Q425L
XH_P42	2	20130190	20130190	Nonsense_Mutation	INS	-	ATAAAATCTGC	-	WDR35	TAAATGAGCAGp.030delinsPNNNSHX	
XH_P42	2	21363730	21363730	Frame_Shift_Ins	INS	-	TTTTCTCTAC	-	TDRD15	3392insTTTTCT	p.I1131fs
XH_P42	2	25469148	25469148	Missense_Mutation	SNP	G	A	G	DNMT3A	c.C854T	p.T285M
XH_P42	2	25991687	25991687	Frame_Shift_Ins	INS	-	A	-	ASXL2	c.S54_555insT	p.S185fs
XH_P42	2	25991688	25991688	Nonsense_Mutation	INS	-	TTATTTTAAAT	-	ASXL2	ATATAATTTTAAAB85_1186delinsNIIIX	
XH_P42	2	26534743	26534743	Missense_Mutation	SNP	G	A	G	ADGRF3	c.C1256T	p.T419M
XH_P42	2	32476162	32476162	Silent	SNP	G	A	G	NLR4	c.C771T	p.N257N
XH_P42	2	37121148	37121148	In_Frame_Ins	INS	-	CACTCTAGATT	-	STRN	nsATGAATCTAGp.275delinsNESRSAG	
XH_P42	2	43452622	43452622	Silent	SNP	G	A	G	ZFP36L2	c.C321T	p.G107G
XH_P42	2	54952290	54952290	Missense_Mutation	SNP	C	T	C	EML6	c.C92T	p.T31M
XH_P42	2	55570910	55570910	Nonsense_Mutation	INS	-	ATTTAAATAGAT	-	CCDC88A	07insTTATCTATp.003_K404delinsLSIX	
XH_P42	2	55570912	55570912	In_Frame_Ins	INS	-	TGAAGTGTGATT	-	CCDC88A	AACATAAAATACp.02delinsKHKNYFMIR	
XH_P42	2	61729415	61729415	Nonsense_Mutation	INS	-	TAGTCAGACTCA	-	XP01	GATATTGAGTCp.111delinsKSFYRX	
XH_P42	2	73496580	73496597	In_Frame_Del	DEL	GGCGGGCGG	-	GCGGCGGGCGG	FBXO41	c.162_179del	p.54_60del
XH_P42	2	74642137	74642137	Silent	SNP	C	T	C	C2orf81	c.G882A	p.L294L
XH_P42	2	96078703	96078703	Nonstop_Mutation	SNP	T	G	T	FAHD2A	c.T943G	p.X315G
XH_P42	2	97350122	97350122	In_Frame_Ins	INS	-	CAG	-	FER1L5	1728_1729insCp.5576delinsSQ	
XH_P42	2	97350124	97350124	Frame_Shift_Ins	INS	-	CCCCCAGACACC	-	FER1L5	731insTCCCCCA	p.N577fs

XH_P42	2	97637976	97637976	Missense_Mutation	SNP	G	A	G	FAM178B	c.C226T	p.R76C
XH_P42	2	97749494	97749494	Nonstop_Mutation	SNP	A	C	A	FAHD2B	c.T943G	p.X315G
XH_P42	2	98422114	98422114	Missense_Mutation	SNP	A	T	A	TMEM131	c.T2108A	p.V703E
XH_P42	2	98422116	98422116	Frame_Shift_Ins	INS	-	CTCCAAGTCTTC	-	TMEM131	nsTAAGGAAGA	p.K702fs
XH_P42	2	108487406	108487406	Missense_Mutation	SNP	A	C	A	RGPD4	c.A2946C	p.E982D
XH_P42	2	111556219	111556219	Silent	SNP	G	A	G	ACOXL	c.G378A	p.A126A
XH_P42	2	112740484	112740484	Missense_Mutation	SNP	A	G	A	MERTK	c.A1210G	p.R404G
XH_P42	2	118854300	118854300	Silent	SNP	G	A	G	INSIG2	c.G168A	p.T56T
XH_P42	2	128394147	128394147	Missense_Mutation	SNP	G	A	G	MYO7B	c.G6073A	p.V2025I
XH_P42	2	135872863	135872863	Missense_Mutation	SNP	G	A	G	RAB3GAP1	c.G560A	p.R187Q
XH_P42	2	137928506	137928506	Missense_Mutation	SNP	G	A	G	THSD7B	c.G1721A	p.R574H
XH_P42	2	159526360	159526360	Missense_Mutation	SNP	G	A	G	PKP4	c.G2857A	p.A953T
XH_P42	2	163361125	163361125	Frame_Shift_Ins	INS	-	ACCATGAAACA	-	KCNH7	35insATGTTTCA	p.S312fs
XH_P42	2	166848681	166848681	Missense_Mutation	SNP	C	T	C	SCN1A	c.G5104A	p.D1702N
XH_P42	2	166903302	166903302	Nonsense_Mutation	INS	-	TAGTTTAATTAT	-	SCN1A	insTAAAAATAAT	452_K453delinsKX
XH_P42	2	170042152	170042152	Nonsense_Mutation	SNP	G	A	G	LRP2	c.C9706T	p.R3236X
XH_P42	2	171264321	171264321	Frame_Shift_Ins	INS	-	TGGGGTTCTTG	-	MYO3B	2618insTGGGG	p.Q873fs
XH_P42	2	171264323	171264323	Frame_Shift_Ins	INS	-	AAAAATAGAGA	-	MYO3B	2620insAAAAA	p.Q873fs
XH_P42	2	179431635	179431635	Silent	SNP	G	A	G	TTN	c.C52029T	p.N17343N
XH_P42	2	197637788	197637788	Nonsense_Mutation	SNP	G	A	G	UTF3C3	c.C1921T	p.R641X
XH_P42	2	201437158	201437158	Frame_Shift_Ins	INS	-	CATCTTTATCATT	-	SGO2	2090insCATCTT	p.N697fs
XH_P42	2	207395608	207395608	Splice_Site	INS	-	ACTGCAGCTATT	-	ADAM23	.	.
XH_P42	2	208632543	208632543	Silent	SNP	G	A	G	FZD5	c.C921T	p.Y307Y
XH_P42	2	209113113	209113113	Missense_Mutation	SNP	G	A	G	IDH1	c.C394T	p.R132C
XH_P42	2	216298165	216298165	Nonsense_Mutation	INS	-	ATGGTACAGCTT	-	FN1	7insATAAGCTGT	D99_K100delinsEX
XH_P42	2	219528006	219528006	Missense_Mutation	SNP	G	A	G	BCS1L	c.G797A	p.R266Q
XH_P42	2	220336975	220336975	Missense_Mutation	SNP	G	A	G	SPFG	c.G3862A	p.A1288T
XH_P42	2	220424188	220424188	Missense_Mutation	SNP	A	C	A	OBSL1	c.T2985G	p.D995E
XH_P42	3	8590324	8590324	Missense_Mutation	SNP	G	A	G	LMCD1	c.G239A	p.R80H
XH_P42	3	14964556	14964556	Missense_Mutation	SNP	G	A	G	FGD5	c.G3811A	p.V1271M
XH_P42	3	40573747	40573747	Nonsense_Mutation	SNP	T	G	T	ZNF621	c.T486G	p.Y162X
XH_P42	3	47158243	47158243	Nonsense_Mutation	INS	-	ATGAGAAGACG	-	SETD2	CTTAATCGTCTT	442_K1443delinsLSX
XH_P42	3	49323757	49323757	Silent	SNP	T	C	T	USP4	c.A1833G	p.G611G
XH_P42	3	49323759	49323759	Splice_Site	INS	-	CTGTTCTGAAAC	-	USP4	.	.
XH_P42	3	51263088	51263088	Missense_Mutation	SNP	C	T	C	DOCK3	c.C1261T	p.R421C
XH_P42	3	72971477	72971477	Frame_Shift_Ins	INS	-	TATACAAAGAA	-	GXYLT2	92insATATACAA	p.L197fs
XH_P42	3	72971479	72971479	Frame_Shift_Ins	INS	-	TGAGCACAGAA	-	GXYLT2	594insTGAGCA	p.F198fs
XH_P42	3	78766995	78766995	Nonsense_Mutation	INS	-	SACAGTCAGCTC	-	ROBO1	TAGCCGAGCTGAp	K193delinsKX
XH_P42	3	89390983	89390983	Missense_Mutation	SNP	A	G	A	EPHA3	c.A1049G	p.D350G
XH_P42	3	97983363	97983363	Missense_Mutation	SNP	C	T	C	OR5H6	c.C235T	p.L79F
XH_P42	3	100605135	100605135	Nonsense_Mutation	INS	-	TTACCTAATTTT	-	ABI3BP	insTTAAAAAATA	72_E173delinsKNX
XH_P42	3	111851949	111851949	Frame_Shift_Ins	INS	-	CTTGCTGTGTG	-	GCSAM	nsGACAACACAG	p.R7fs
XH_P42	3	111851951	111851951	Missense_Mutation	SNP	A	T	A	GCSAM	c.T17A	p.L6Q
XH_P42	3	121351315	121351315	Silent	SNP	G	A	G	HLCS1	c.C993T	p.P331P
XH_P42	3	123219515	123219515	Missense_Mutation	SNP	G	A	G	HACD2	c.C196T	p.P665
XH_P42	3	126137618	126137618	Splice_Site	SNP	G	A	G	CFAP100	.	.
XH_P42	3	132389893	132389893	Nonsense_Mutation	INS	-	ATACATTATACT	-	UBA5	CTCTAATACATT	103_A104delinsTLX
XH_P42	3	134911453	134911453	Frame_Shift_Ins	INS	-	CTCATTGTAACT	-	EPHB1	CTCTCTCTCAT	p.L640fs
XH_P42	3	141163728	141163728	Frame_Shift_Ins	INS	-	TTTCTCTTTTCT	-	ZBTB38	99insAGTTTCT	p.V833fs
XH_P42	3	150128693	150128693	Missense_Mutation	SNP	C	T	C	TSC22D2	c.C1566T	p.P519L
XH_P42	3	151163773	151163773	Nonsense_Mutation	INS	-	GCACAATCAGTT	-	IGSF10	996insAACTGAA	332_E1333delinsX
XH_P42	3	169644898	169644898	Frame_Shift_Ins	INS	-	AATGTCTG	-	SAMD7	8_849insAATGT	p.S283fs
XH_P42	3	195481086	195481086	Missense_Mutation	SNP	G	A	G	MUC4	c.C2465T	p.A822V
XH_P42	3	195516676	195516676	Missense_Mutation	SNP	G	A	G	MUC4	c.C1775T	p.T592M
XH_P42	4	10446803	10446803	Frame_Shift_Ins	INS	-	AAAGGAGAGT	-	ZNF518B	9_1150insACTCT	p.R384fs
XH_P42	4	17586746	17586746	Missense_Mutation	SNP	G	A	G	LAP3	c.G691A	p.E231K
XH_P42	4	22403140	22403140	Frame_Shift_Ins	INS	-	SCTTGGCAGATG	-	ADGRA3	TGCCAGCATCTG	p.V799fs
XH_P42	4	25759189	25759189	Missense_Mutation	SNP	C	T	C	SEL1L3	c.G3121A	p.A1041T
XH_P42	4	37962629	37962629	Nonstop_Mutation	INS	-	TCA	-	PTTG2	574_575insTCp	p.192delinsFR
XH_P42	4	37962630	37962630	Frame_Shift_Ins	INS	-	CCCCCTTCACCT	-	PTTG2	TGGGCCCCCTC	92delinsCWAPLHX
XH_P42	4	41748011	41748028	In_Frame_Del	DEL	CCGCCGCTG	-	GCCGCCGCTGCC	PHOX2B	c.741_758del	p.247_253del
XH_P42	4	47427774	47427774	Silent	SNP	C	T	C	GABRB1	c.C1164T	p.S388S
XH_P42	4	75937865	75937865	Frame_Shift_Ins	INS	-	TCCACAAACAC	-	PARM1	AGCTCTCCACAA	p.S92fs
XH_P42	4	79359739	79359739	Missense_Mutation	SNP	G	A	G	FRAS1	c.G5233A	p.D1745N
XH_P42	4	79359740	79359740	In_Frame_Ins	INS	-	ATTCTCT	-	FRAS1	34_523SinsATT	D1745delinsEFL
XH_P42	4	108969841	108969841	Frame_Shift_Ins	INS	-	AAAGCATAAAA	-	LEF1	8insACCTTTTAA	p.M383fs
XH_P42	4	114275990	114275990	Silent	SNP	C	A	C	ANK2	c.C6216A	p.S2072S
XH_P42	4	114275992	114275992	In_Frame_Ins	INS	-	CTCTCTGTTTTG	-	ANK2	219insCCCTCTCT	2073delinsLSVFE
XH_P42	4	129864317	129864317	Nonsense_Mutation	INS	-	CACTGACAAGCC	-	SCLT1	nsTGTGGGCTTG	9_E490delinsLWACQX
XH_P42	4	140811064	140811096	In_Frame_Del	DEL	TGCTGTCTGC	-	SCTGCTGTCTGC	MAML3	c.1494_1514del	p.498_505del
XH_P42	4	155410587	155410587	Missense_Mutation	SNP	G	A	G	DCHS2	c.C1921T	p.P641S
XH_P42	4	156632189	156632189	Missense_Mutation	SNP	T	C	T	GUCY1A3	c.T872C	p.M221T
XH_P42	4	156632191	156632191	Frame_Shift_Ins	INS	-	TGAACGGAAG	-	GUCY1A3	TTATATGAAACG	p.F292fs
XH_P42	4	173942679	173942679	Missense_Mutation	SNP	C	A	C	GALNTL6	c.C1541A	p.T514N
XH_P42	4	185686065	185686065	Silent	SNP	G	A	G	ACSL1	c.C1272T	p.Y424Y
XH_P42	5	896885	896885	Missense_Mutation	SNP	G	A	G	TRIP13	c.G364A	p.A122T
XH_P42	5	23527777	23527777	Silent	SNP	C	T	C	PRDM9	c.C2580T	p.Y860Y
XH_P42	5	36226646	36226646	Missense_Mutation	SNP	G	A	G	NADK2	c.C409T	p.R137C
XH_P42	5	43613231	43613231	Frame_Shift_Ins	INS	-	AA	-	NNT	c.373_374insAA	p.V125fs
XH_P42	5	43613232	43613232	Frame_Shift_Ins	INS	-	ATCTCTTTGG	-	NNT	375insATCTCT	p.V125fs
XH_P42	5	56177849	56177854	In_Frame_Del	DEL	CAACAA	-	CAACAA	MAP3K1	c.2822_2827del	p.941_943del
XH_P42	5	64521983	64521983	Missense_Mutation	SNP	G	A	G	ADAMT56	c.C1997T	p.A666V
XH_P42	5	82834077	82834078	Frame_Shift_Del	DEL	TA	-	TA	VCAN	c.2294_2295del	p.L765fs
XH_P42	5	90136557	90136557	Frame_Shift_Ins	INS	-	A	-	ADGRV1	16774_16775ins	p.P5592fs
XH_P42	5	90136558	90136558	Frame_Shift_Ins	INS	-	ATATTACAAAA	-	ADGRV1	ATTACTAATATT	p.P5592fs
XH_P42	5	101816059	101816059	Frame_Shift_Ins	INS	-	TAATGAA	-	SLC6A1	37_438insTTCA	p.A146fs
XH_P42	5	102895168	102895168	Frame_Shift_Ins	INS	-	TT	-	NUDT12	c.153_154insAA	p.C52fs
XH_P42	5	102895169	102895169	Nonsense_Mutation	INS	-	CATTCTGTAGGA	-	NUDT12	TGGTTCTCAACG	M51delinsILGSX
XH_P42	5	130982900	130982900	Splice_Site	INS	-	CTCCTTGACATG	-	FNIP1	.	.
XH_P42	5	138773156	138773156	Frame_Shift_Ins	INS	-	ACCCCAA	-	DNAJC18	31_132insTTGGG	p.A44fs
XH_P42	5	138773158	138773158	Nonsense_Mutation	INS	-	AGCTGTCTCTCA	-	DNAJC18	130insTGAGGA	p.A44delinsX
XH_P42	5	140207965	140207965	Missense_Mutation	SNP	G	C	G	PCDH46	c.G289C	p.G97R
XH_P42	5	140573626	140573626	Missense_Mutation	SNP	G	A	G	PCDH810	c.G1501A	p.A501T
XH_P42	5	140725547	140725547	Silent	SNP	C	T	C	PCDHGA3	c.C1947T	p.H649H
XH_P42	5	147788744	147788744	Nonsense_Mutation	INS	-	ATACATTATAAA	-	FBXO38	ATACTATACAT	309delinsVFYYTLX
XH_P42	5	161309615	161309615	Missense_Mutation	SNP	G	A	G	GABRA1	c.G611A	p.R204H
XH_P42	6	4892315	4892315	Silent	SNP	G	A	G	CDYL	c.G393A	p.K131K
XH_P42	6	28227727	28227727	Missense_Mutation	SNP	C	T	C	NKAPL	c.C578T	p.S193L

XH_P42	6	37620032	37620032	Missense_Mutation	SNP	G	A	G	MDGA1	c.C1067T	p.S356L
XH_P42	6	42656069	42656069	Missense_Mutation	SNP	G	A	G	UBR2	c.G4969A	p.G1657R
XH_P42	6	42832824	42832824	Silent	SNP	A	T	A	BICRAL	c.A2880T	p.A960A
XH_P42	6	42986447	42986447	Missense_Mutation	SNP	G	C	G	KLHDC3	c.G810C	p.K270N
XH_P42	6	43100271	43100271	Silent	SNP	C	T	C	PTK7	c.C1098T	p.H366H
XH_P42	6	54254679	54254679	Frame_Shift_Ins	INS	-	ACATACCTTTGGT	-	TINAG	insGAAACACATAC	p.I463fs
XH_P42	6	75823413	75823413	Frame_Shift_Ins	INS	-	TATATATATATT	-	COL12A1	insCAAATAAATAT	p.L1418fs
XH_P42	6	75892823	75892823	Missense_Mutation	SNP	G	A	G	COL12A1	c.C1834T	p.L612F
XH_P42	6	85472394	85472394	Missense_Mutation	SNP	G	A	G	TBX18	c.C365T	p.L122L
XH_P42	6	94066754	94066754	Frame_Shift_Ins	INS	-	A	-	EPHA7	c.1004_1005ins	p.P335fs
XH_P42	6	94066756	94066756	Nonsense_Mutation	INS	-	TCACATCGTTTC	-	EPHA7	1003insGAAACG	P335delinsETMX
XH_P42	6	116265573	116265573	Nonsense_Mutation	INS	-	TTTGTGTTTAATT	-	FRK	insCTAATTAAAA	B25_I326delinsTNX
XH_P42	6	136597648	136597648	Splice_Site	INS	-	TTAAGAACTTCC	-	BCLAF1	.	.
XH_P42	6	137243670	137243670	Missense_Mutation	SNP	G	A	G	SLC35D3	c.G104A	p.R35H
XH_P42	6	146993502	146993502	Frame_Shift_Ins	INS	-	C	-	ADGB	c.986_987insC	p.E329fs
XH_P42	6	146993504	146993504	In_Frame_Ins	INS	-	AAACAT	-	ADGB	88_989insAAAC	p.I330delinsKTL
XH_P42	6	151766776	151766776	Frame_Shift_Ins	INS	-	GGTTCTAAATG	-	RMND1	171insCCATTTAC	p.K57fs
XH_P42	6	152565769	152565769	Nonsense_Mutation	INS	-	TAGAAAAAAT	-	SYNE1	19382insATT	G1_L6462delinsDFFX
XH_P42	6	152565770	152565770	Frame_Shift_Ins	INS	-	ACTTT	-	SYNE1	380_19381insA	p.G6461fs
XH_P42	6	153292503	153292503	Missense_Mutation	SNP	C	T	C	FBXO5	c.G1001A	p.R334H
XH_P42	6	160525985	160525985	Missense_Mutation	SNP	G	A	G	IGF2R	c.G7345A	p.D2449N
XH_P42	6	160819096	160819096	In_Frame_Ins	INS	-	TGTGTCAATGCG	-	SLC22A3	nsGTCGTGTGTCAT	72delinsSVSMRG
XH_P42	6	160819098	160819098	Missense_Mutation	SNP	G	T	G	SLC22A3	c.G517T	p.G173C
XH_P42	6	170871055	170871058	Frame_Shift_Del	DEL	GCAG	-	GCAG	TBP	c.171_174del	p.Q57fs
XH_P42	7	1786409	1786409	Missense_Mutation	SNP	C	T	C	ELFN1	c.C2177T	p.P726L
XH_P42	7	6193562	6193562	Missense_Mutation	SNP	G	A	G	USP42	c.G2377A	p.A793T
XH_P42	7	14017062	14017062	In_Frame_Ins	INS	-	ATAAGA	-	ETV1	104_105insCTCT	Q35delinsHLM
XH_P42	7	15725798	15725803	In_Frame_Del	DEL	TGGTGG	-	TGGTGG	MEOX2	c.225_230del	p.75_77del
XH_P42	7	17379766	17379766	Missense_Mutation	SNP	C	A	C	AHR	c.C2317A	p.Q773K
XH_P42	7	17379767	17379767	Frame_Shift_Ins	INS	-	AAAAAT	-	AHR	318_2319insAA	p.Q773fs
XH_P42	7	20193994	20193994	Nonsense_Mutation	INS	-	AGTCGTACTAAC	-	MACC1	GAAAAAGTTAGT	723_M7724delinsTSX
XH_P42	7	27239446	27239463	In_Frame_Del	DEL	CGCCCGCCG	-	CGCCCGCCCGCC	HOXA13	c.234_251del	p.78_84del
XH_P42	7	30185905	30185905	Missense_Mutation	SNP	C	A	C	MTURN	c.C275A	p.S92Y
XH_P42	7	64378072	64378072	In_Frame_Ins	INS	-	TATTTACCAACT	-	ZNF273	17insATATTTAC	N72delinsNFTNL
XH_P42	7	66532390	66532390	Missense_Mutation	SNP	G	A	G	TYW1	c.G1274A	p.R425Q
XH_P42	7	72849516	72849516	Silent	SNP	G	A	G	FZD9	c.G1179A	p.T393T
XH_P42	7	76110029	76110029	Missense_Mutation	SNP	C	A	C	DTX2	c.C203A	p.A68E
XH_P42	7	77539717	77539717	Frame_Shift_Ins	INS	-	AATTTCC	-	PHTF2	53_654insAATT	p.F218fs
XH_P42	7	94992089	94992089	Missense_Mutation	SNP	C	T	C	PON3	c.G760A	p.D254N
XH_P42	7	97823848	97823848	Silent	SNP	G	A	G	LMTK2	c.G4071A	p.T1357T
XH_P42	7	99227017	99227017	Missense_Mutation	SNP	G	A	G	ZSCAN25	c.G1009A	p.E337K
XH_P42	7	99312214	99312214	Silent	SNP	T	C	T	CYP3A7	c.A762G	p.K254K
XH_P42	7	99506310	99506323	Frame_Shift_Del	DEL	TCTTCTTCGT	-	CTTCTTCTTCGTC	TRIM4	c.602_615del	p.E201fs
XH_P42	7	100635142	100635142	Missense_Mutation	SNP	G	A	G	MUC12	c.G1298A	p.R433H
XH_P42	7	100635243	100635245	In_Frame_Del	DEL	CCC	-	CCC	MUC12	c.1399_1401del	p.467_467del
XH_P42	7	100676246	100676246	Missense_Mutation	SNP	T	C	T	MUC17	c.T1549C	p.S517P
XH_P42	7	100680017	100680017	Missense_Mutation	SNP	A	G	A	MUC17	c.A5320G	p.I1774V
XH_P42	7	103301862	103301862	Missense_Mutation	SNP	T	G	T	RELN	c.A1402C	p.T468P
XH_P42	7	104807824	104807824	Missense_Mutation	SNP	G	A	G	SRPK2	c.C481T	p.H161Y
XH_P42	7	107708510	107708510	Nonsense_Mutation	INS	-	AAATGT	-	LAMB4	396_2397insACA	p.C799delinsX
XH_P42	7	107708511	107708511	In_Frame_Ins	INS	-	AAGACTGTG	-	LAMB4	5_2396insCACAC	C799delinsSQSC
XH_P42	7	131859651	131859651	Missense_Mutation	SNP	A	C	A	PLXNA4	c.T3903G	p.H1301Q
XH_P42	7	139090511	139090511	Missense_Mutation	SNP	G	A	G	C7orf55-LUC7L	c.G488A	p.R163Q
XH_P42	7	139257835	139257835	Silent	SNP	G	A	G	HPK2	c.C3354T	p.P1118P
XH_P42	7	141362520	141362520	Missense_Mutation	SNP	A	T	A	KIAA1147	c.T1304A	p.L435Q
XH_P42	8	3076841	3076841	Missense_Mutation	SNP	G	T	G	CSMD1	c.C4608A	p.S1536R
XH_P42	8	3076842	3076842	Nonsense_Mutation	INS	-	GATACAAATTA	-	CSMD1	307insATTAATT	p.S1536delinsNX
XH_P42	8	14095166	14095166	Frame_Shift_Ins	INS	-	CTGTCCGGTTA	-	SGCZ	257insTAACCG	p.S86fs
XH_P42	8	20072400	20072400	Silent	SNP	G	A	G	ATP6V1B2	c.G999A	p.T333T
XH_P42	8	22105698	22105698	Frame_Shift_Ins	INS	-	GAAGGGCGAG	-	POLR3D	CCAGAGAAGAGG	p.D131fs
XH_P42	8	41794972	41794972	Frame_Shift_Ins	INS	-	GATGCTGATGG	-	KAT6A	3154insACCATC	p.S1052fs
XH_P42	8	41906091	41906091	Silent	SNP	G	A	G	KAT6A	c.C405T	p.F135F
XH_P42	8	67590068	67590068	Missense_Mutation	SNP	T	C	T	C8orf44	c.T125C	p.M42T
XH_P42	8	106813386	106813386	Missense_Mutation	SNP	C	T	C	ZFPM2	c.C1076T	p.T359I
XH_P42	8	141566055	141566055	Missense_Mutation	SNP	A	C	A	AGO2	c.T1209G	p.D403E
XH_P42	8	144732584	144732584	Frame_Shift_Ins	INS	-	GA	-	ZNF623	c.542_543insGA	p.C181fs
XH_P42	8	144732585	144732585	Frame_Shift_Ins	INS	-	CTTCC	-	ZNF623	543_544insCTT	p.C181fs
XH_P42	8	144942124	144942124	Silent	SNP	G	A	G	EPPK1	c.C5298T	p.Y1766Y
XH_P42	9	78910321	78910321	Nonsense_Mutation	INS	-	ACTTATGTTGAT	-	PCSK5	7insATGACTTAT	1106delinsHDLX
XH_P42	9	111625023	111625023	Missense_Mutation	SNP	G	A	G	ACTL7A	c.G421A	p.V141M
XH_P42	9	111674598	111674598	Missense_Mutation	SNP	G	A	G	ELP1	c.C88T	p.R30V
XH_P42	9	113550104	113550104	Missense_Mutation	SNP	T	C	T	MUSK	c.T1625C	p.I542T
XH_P42	9	114134864	114134864	Nonsense_Mutation	INS	-	TACATTCTCTT	-	KIAA0368	nsGAAAGAGAA	G5_A1637delinsRKRRMX
XH_P42	9	114134866	114134866	Silent	SNP	A	G	A	KIAA0368	c.T4905C	p.I1635I
XH_P42	9	117106079	117106079	Silent	SNP	G	A	G	AKNA	c.C3309T	p.H1103H
XH_P42	9	121929544	121929544	Nonsense_Mutation	SNP	G	A	G	BRINP1	c.C2104T	p.R702X
XH_P42	9	127074839	127074839	Missense_Mutation	SNP	G	A	G	NEK6	c.G196A	p.E66K
XH_P42	9	127670752	127670752	Splice_Site	INS	-	TAGAAGGGGATT	-	GOLGA1	.	.
XH_P42	9	139793340	139793340	Missense_Mutation	SNP	G	A	G	TRAF2	c.G148A	p.G50S
XH_P42	9	139906715	139906715	Splice_Site	SNP	A	C	A	ABCA2	.	.
XH_P42	9	140002059	140002059	Missense_Mutation	SNP	G	A	G	MAN1B1	c.G1841A	p.R614H
XH_P42	10	3209169	3209169	Silent	SNP	C	T	C	PITRM1	c.G129A	p.R43R
XH_P42	10	5415732	5415732	Missense_Mutation	SNP	G	C	G	UCN3	c.G49C	p.G17R
XH_P42	10	5415733	5415733	Missense_Mutation	SNP	G	C	G	UCN3	c.G50C	p.G17A
XH_P42	10	15883594	15883630	Frame_Shift_Del	DEL	ACCAAAGCA	-	AACCAAAGCAT	MINDY3	c.236_240del	p.E79fs
XH_P42	10	18874964	18874964	Frame_Shift_Ins	INS	-	CT	-	NSUN6	c.412_413insAG	p.A138fs
XH_P42	10	21806398	21806398	Silent	SNP	C	T	C	SKIDA1	c.G354A	p.P118P
XH_P42	10	27815803	27815803	Silent	SNP	T	A	T	RAB18	c.T171A	p.A57A
XH_P42	10	45939661	45939661	Missense_Mutation	SNP	C	A	C	ALOX5	c.C1772A	p.T591K
XH_P42	10	49659056	49659056	Silent	SNP	G	A	G	ARHGAP22	c.C846T	p.S282S
XH_P42	10	58120143	58120143	Missense_Mutation	SNP	C	T	C	ZWINT	c.G43A	p.V15I
XH_P42	10	58120144	58120144	Frame_Shift_Ins	INS	-	TGGCTGGCAGT	-	ZWINT	2insAACTGCCA	p.E14fs
XH_P42	10	69565508	69565508	Frame_Shift_Ins	INS	-	AAATTGAGAT	-	DNAJC12	335insATCTGA	p.M121fs
XH_P42	10	70644586	70644586	Missense_Mutation	SNP	G	A	G	STOX1	c.G1034A	p.R345Q
XH_P42	10	75184521	75184521	Missense_Mutation	SNP	C	A	C	MS5S1	c.G1173T	p.E391D
XH_P42	10	75529130	75529130	Missense_Mutation	SNP	C	T	C	SEC24C	c.C2450T	p.A817V
XH_P42	10	86273726	86273726	In_Frame_Ins	INS	-	CCA	-	CCSER2	1128_1129insC	p.K376delinsKLP
XH_P42	10	86273728	86273728	In_Frame_Ins	INS	-	ATTGAGTTCTTT	-	CCSER2	11nsCATATTGAG	377delinsSILSLV

XH_P42	10	88418345	88418345	Missense_Mutation	SNP	G	A	G	OPN4	c.G529A	p.A177T
XH_P42	10	95660860	95660860	Silent	SNP	G	A	G	SLC35G1	c.G711A	p.S237S
XH_P42	10	98155720	98155720	Missense_Mutation	SNP	G	A	G	TLI2	c.C1442T	p.P481L
XH_P42	10	99156022	99156022	Missense_Mutation	SNP	G	A	G	RRP12	c.C406T	p.R136C
XH_P42	10	116200820	116200820	Missense_Mutation	SNP	A	G	A	ABLIM1	c.T743C	p.F248S
XH_P42	10	126631247	126631247	Nonsense_Mutation	INS	-	AATAATTAGGAC	-	ZRANB1	CTATAAATAATT62	S63delinsSVKX
XH_P42	10	129903076	129903076	Missense_Mutation	SNP	T	C	T	MKI67	c.A5948G	p.K1983R
XH_P42	11	613452	613452	Missense_Mutation	SNP	A	C	A	IRF7	c.T1030G	p.F344V
XH_P42	11	800232	800232	Missense_Mutation	SNP	G	A	G	PIDD1	c.C2173T	p.R725C
XH_P42	11	1017514	1017514	Missense_Mutation	SNP	A	G	A	MUC6	c.T5287C	p.S1763P
XH_P42	11	1261452	1261452	Missense_Mutation	SNP	G	A	G	MUC5B	c.G3817A	p.V1273I
XH_P42	11	1265450	1265450	Missense_Mutation	SNP	A	C	A	MUC5B	c.A7340C	p.E2447A
XH_P42	11	1265451	1265451	Silent	SNP	G	A	G	MUC5B	c.G7341A	p.E2447E
XH_P42	11	1606138	1606138	Silent	SNP	T	G	T	KRTAP5-1	c.A342C	p.G114G
XH_P42	11	1774802	1774802	Silent	SNP	G	A	G	CTSD	c.C1170T	p.I390I
XH_P42	11	4661117	4661117	In_Frame_Ins	INS	-	TGCGAAGCCCC	-	OR51D1	TGTATGCAGAA8delinsDFVCRSPSSW	
XH_P42	11	6587042	6587042	In_Frame_Ins	INS	-	GCTCTTCTT	-	DNHD1	4_10875insGCTE3625delinsEFLF	
XH_P42	11	6588165	6588165	Missense_Mutation	SNP	G	A	G	DNHD1	c.G11426A	p.R809H
XH_P42	11	8013361	8013361	Nonsense_Mutation	INS	-	ATAGGGTTTATT	-	EIF3F	399insATAGGGT133	C134delinsKX
XH_P42	11	8662434	8662434	Silent	SNP	A	C	A	TRIM66	c.T1053G	p.P351P
XH_P42	11	9606861	9606861	Missense_Mutation	SNP	G	A	G	WEE1	c.G703A	p.E235K
XH_P42	11	10822295	10822295	Nonsense_Mutation	SNP	C	A	C	EIF4G2	c.G1513T	p.E505X
XH_P42	11	11643052	11643052	Frame_Shift_Ins	INS	-	TGTCGGGCGCCC	-	GALNT18	AGCCGGCGCCCC	p.G30fs
XH_P42	11	19955108	19955108	Missense_Mutation	SNP	G	A	G	NAV2	c.G1126A	p.E376K
XH_P42	11	20066919	20066919	Missense_Mutation	SNP	G	A	G	NAV2	c.G863A	p.R288Q
XH_P42	11	33360980	33360980	Nonsense_Mutation	INS	-	TAAGTCACAGAC	-	HIPK3	4insAATAAGTC1505	L506delinsKX
XH_P42	11	33373759	33373759	Missense_Mutation	SNP	G	A	G	HIPK3	c.G3056A	p.R1019H
XH_P42	11	33596398	33596398	Missense_Mutation	SNP	G	A	G	KIAA1549L	c.G3490A	p.V1164I
XH_P42	11	46369238	46369238	Missense_Mutation	SNP	C	A	C	DGKZ	c.C29A	p.A10D
XH_P42	11	48185115	48185115	Missense_Mutation	SNP	G	A	G	PTPRJ	c.G3664A	p.V1222I
XH_P42	11	49075312	49075312	Missense_Mutation	SNP	G	C	G	TRIM64C	c.C1307G	p.S436C
XH_P42	11	59575205	59575205	Missense_Mutation	SNP	G	A	G	MRPL16	c.C239T	p.T80M
XH_P42	11	62546426	62546426	In_Frame_Ins	INS	-	GAAGCCTTT	-	TAF6L	2_523insGAAGCG174delinsQEAF	
XH_P42	11	62761028	62761028	Missense_Mutation	SNP	G	A	G	SLC22A8	c.C1028T	p.T343M
XH_P42	11	64064379	64064379	Silent	SNP	G	A	G	KCNK4	c.G219A	p.A73A
XH_P42	11	64514214	64514214	Missense_Mutation	SNP	G	A	G	PYGM	c.C2182T	p.R728C
XH_P42	11	66290955	66290955	Missense_Mutation	SNP	G	A	G	BB51	c.G589A	p.E287K
XH_P42	11	66411364	66411384	In_Frame_Del	DEL	GCTGCAGCA	-	TGCTGCAGCAG	RBM14-RBM4	c.781_801del	p.261_267del
XH_P42	11	66512290	66512290	Frame_Shift_Ins	INS	-	GC	-	C11orf80	c.77_78insGC	p.G26fs
XH_P42	11	66639562	66639562	Silent	SNP	G	A	G	PC	c.C69T	p.P23P
XH_P42	11	67190888	67190888	Nonsense_Mutation	INS	-	AGCTGACCTGG	-	CARN51	1insACTAGCTG434	V435delinsYX
XH_P42	11	71293831	71293839	In_Frame_Del	DEL	CCACAGCCCC	-	CCACAGCCCC	KRTAP5-11	c.45_53del	p.15_18del
XH_P42	11	86152464	86152464	Nonsense_Mutation	INS	-	CTTTTAAACTTT	-	ME3	2insCAGAAAGTT	K558delinsQKVX
XH_P42	11	89608840	89608840	Missense_Mutation	SNP	C	G	C	TRIM64B	c.G346C	p.E116Q
XH_P42	11	102585439	102585439	Silent	SNP	G	A	G	MMP8	c.C1038T	p.G346G
XH_P42	11	102984928	102984928	Frame_Shift_Ins	INS	-	CTCTCC	-	DYNC2H1	463_464insSCCT	p.N155fs
XH_P42	11	108043676	108043676	Nonsense_Mutation	INS	-	TGATGATCATT	-	NPAT	35insCAAATGG6A	A68delinsQMDHXX
XH_P42	11	117789257	117789257	Silent	SNP	G	A	G	TMPPRS513	c.C318T	p.S106S
XH_P42	11	118130871	118130871	Missense_Mutation	SNP	G	C	G	MPZL2	c.C482G	p.A161G
XH_P42	11	118130872	118130872	Frame_Shift_Ins	INS	-	TTACGATTTT	-	MPZL2	481insAAAATC	p.A161fs
XH_P42	11	118962124	118962124	Missense_Mutation	SNP	G	A	G	HMBS	c.G500A	p.R167Q
XH_P42	11	124745572	124745572	Silent	SNP	G	A	G	ROBO3	c.G2412A	p.T804T
XH_P42	11	129785616	129785616	Missense_Mutation	SNP	G	T	G	PRDM10	c.C2207A	p.T736K
XH_P42	12	306585	306585	Frame_Shift_Ins	INS	-	CT	-	SLC6A12	1032_1033insA	p.S345fs
XH_P42	12	306587	306587	Nonsense_Mutation	INS	-	TCAGCAAGAGA	-	SLC6A12	5CATTCTCTCTTT4	S345delinsTLLSXX
XH_P42	12	4835874	4835874	Missense_Mutation	SNP	G	A	G	GALNT8	c.G388A	p.E130K
XH_P42	12	6166079	6166079	Missense_Mutation	SNP	G	A	G	VWF	c.C1889T	p.A630V
XH_P42	12	7301789	7301789	Missense_Mutation	SNP	G	A	G	CLSTN3	c.G2069A	p.G690D
XH_P42	12	9243846	9243846	Missense_Mutation	SNP	G	A	G	A2M	c.C1970T	p.A657V
XH_P42	12	9317737	9317737	Missense_Mutation	SNP	G	A	G	PZP	c.C2485T	p.R829W
XH_P42	12	11420289	11420289	In_Frame_Ins	INS	-	CAATGACAGTA	-	PRB3	767insTACCTGT	K256delinsIPVIE
XH_P42	12	14804407	14804407	Silent	SNP	G	A	G	GUCY2C	c.C1644T	p.Y548Y
XH_P42	12	49167304	49167304	Missense_Mutation	SNP	G	A	G	ADCY6	c.C2569T	p.P857S
XH_P42	12	52162755	52162755	Missense_Mutation	SNP	G	A	G	SCN8A	c.G3008A	p.R1003H
XH_P42	12	53162773	53162775	In_Frame_Del	DEL	ACT	-	ACT	KRT76	c.1639_1641del	p.547_547del
XH_P42	12	54645964	54645964	Missense_Mutation	SNP	A	G	A	CBX5	c.C185C	p.L62P
XH_P42	12	54645965	54645965	Frame_Shift_Ins	INS	-	CTCTTGTTACTT	-	CBX5	CAGAAAGTAAC	p.L62fs
XH_P42	12	57691141	57691141	Frame_Shift_Ins	INS	-	TACTCTAAATTT	-	R3HDM2	5GAAATAAAATTT	p.Q177fs
XH_P42	12	57906602	57906602	Nonsense_Mutation	INS	-	TTTCTCTTGCTT	-	MARS	3insTTTTTTCTCT	G608delinsLFLCLX
XH_P42	12	70150438	70150438	Frame_Shift_Ins	INS	-	CTCTCTGCATTA	-	RAB3IP	06insTCTCTCTG	p.Q169fs
XH_P42	12	71974178	71974178	In_Frame_Ins	INS	-	ATAATTAATAT	-	LGR5	5insCGGATAATT	K485delinsKRIIKYS
XH_P42	12	81205269	81205283	In_Frame_Del	DEL	TGCTGCTGC	-	5TTGCTGCTGCTC	LIN7A	c.450_464del	p.150_155del
XH_P42	12	81741459	81741459	Frame_Shift_Ins	INS	-	TGTTAAGATTAA	-	PPFIA2	insCATTAACTCT	p.L262fs
XH_P42	12	89984864	89984864	Frame_Shift_Ins	INS	-	AAAGAAACAAA	-	ATP2B1	3560insTTTGT	p.N1187fs
XH_P42	12	96077480	96077480	Silent	SNP	G	A	G	NTN4	c.C1188T	p.S396S
XH_P42	12	99056345	99056345	Frame_Shift_Ins	INS	-	ACACTTATCTAA	-	APAF1	790insACACTTA	p.M263fs
XH_P42	12	99056347	99056347	Splice_Site	SNP	G	C	G	APAF1	.	.
XH_P42	12	99793512	99793512	Silent	SNP	G	A	G	ANKS1B	c.C1653T	p.N551N
XH_P42	12	99793514	99793514	Nonsense_Mutation	INS	-	AAGACTGAAGT	-	ANKS1B	ATAAACTACTTC	p.N551delinsSX
XH_P42	12	108958154	108958154	Missense_Mutation	SNP	G	A	G	ISCU	c.G214A	p.V72I
XH_P42	12	117624340	117624368	Frame_Shift_Del	DEL	AATGTCACT	-	TCAATGTCACTGA	FBXO21	c.384_412del	p.C127fs
XH_P42	12	120295450	120295450	Silent	SNP	G	A	G	CIT	c.C291T	p.F98T
XH_P42	12	123641404	123641404	Missense_Mutation	SNP	G	A	G	MPHOSPH9	c.C3502T	p.R1168C
XH_P42	12	129467603	129467603	Missense_Mutation	SNP	A	C	A	GLT1D1	c.A769C	p.I257L
XH_P42	12	133306450	133306450	Silent	SNP	T	C	T	ANKLE2	c.A2298G	p.R766R
XH_P42	12	133306452	133306452	In_Frame_Ins	INS	-	TGACATTTCACT	-	ANKLE2	insGAAAGTGA766delinsEEMSAR	
XH_P42	13	24864814	24864814	Missense_Mutation	SNP	G	A	G	SPATA13	c.G577A	p.E193K
XH_P42	13	25671214	25671214	Missense_Mutation	SNP	T	G	T	PABPC3	c.T878G	p.V293G
XH_P42	13	33684863	33684863	Missense_Mutation	SNP	G	A	G	STAR13	c.C2435T	p.T812M
XH_P42	13	77626027	77626027	Silent	SNP	G	A	G	MYCBP2	c.C1367AT	p.C4558C
XH_P42	13	101710394	101710394	Silent	SNP	C	T	C	NALCN	c.G4833A	p.Q1611Q
XH_P42	14	21109695	21109695	Frame_Shift_Ins	INS	-	ATTCTATTTCTAC	-	OR6S1	insAAGTAGAA	p.R52fs
XH_P42	14	22038771	22038771	Nonsense_Mutation	INS	-	AACCTCACTT	-	OR10G3	105insAAGTGA	Y35_136delinsX
XH_P42	14	23818628	23818628	Missense_Mutation	SNP	G	A	G	SLC22A17	c.C379T	p.R127C
XH_P42	14	23892844	23892844	Frame_Shift_Ins	INS	-	GTGCAGGAGAGA	-	MYH7	insTGAATTTCTCC	p.Q1004fs
XH_P42	14	24769398	24769398	Missense_Mutation	SNP	G	A	G	NOP9	c.G238A	p.E80K
XH_P42	14	31597213	31597213	Splice_Site	INS	-	TTCTTATATGG	-	HECTD1	.	.
XH_P42	14	39644510	39644510	Silent	SNP	G	A	G	PNN	c.G27A	p.Q9Q

XH_P42	14	70263556	70263556	Nonsense_Mutation	INS	-	GTAGTCTCTGT	-	SLC10A1	CTGGGACAGGA	V107delinsSLGQELHX
XH_P42	14	72961875	72961875	Silent	SNP	G	A	G	RG56	c.G765A	p.T255T
XH_P42	14	74444027	74444027	Nonsense_Mutation	INS	-	CCTGGCCCCAG	-	ENTPD5	AGGAATCTGGGG	insVKDLTKGTGARNKQKEX
XH_P42	14	76249769	76249769	Frame_Shift_Ins	INS	-	A	-	TTLL5	c.2883dupA	p.P961fs
XH_P42	14	76249771	76249771	Nonsense_Mutation	INS	-	TGAACACAGTCT	-	TTLL5	TTTCTACTGAACA	62_C963delinsQFYX
XH_P42	14	105518023	105518023	Missense_Mutation	SNP	G	A	G	GPR132	c.C424T	p.R142W
XH_P42	15	25650612	25650612	Nonsense_Mutation	SNP	G	A	G	UBE3A	c.C58T	p.R20X
XH_P42	15	31776619	31776619	Silent	SNP	G	A	G	OTUD7A	c.C1659T	p.N533N
XH_P42	15	32928506	32928506	Missense_Mutation	SNP	G	A	G	ARHGAP11A	c.G965A	p.R322Q
XH_P42	15	40594721	40594721	Missense_Mutation	SNP	C	A	C	PLCB2	c.G321T	p.M107I
XH_P42	15	40917015	40917015	Nonsense_Mutation	INS	-	AAATAAGAGTT	-	KNL1	AGCTGGAAATAA	18_A1519delinsTVX
XH_P42	15	52684136	52684136	Frame_Shift_Ins	INS	-	GATATACTAATG	-	MYO5A	33insTTCATTAG	p.E511fs
XH_P42	15	69324073	69324073	Missense_Mutation	SNP	G	A	G	NOX5	c.G457A	p.G153S
XH_P42	16	1129641	1129641	Missense_Mutation	SNP	C	T	C	SSTR5	c.C773T	p.A258V
XH_P42	16	1143512	1143512	Missense_Mutation	SNP	C	T	C	C1QTNF8	c.G748A	p.A250T
XH_P42	16	1633353	1633353	Missense_Mutation	SNP	G	A	G	IFT140	c.C1394T	p.A465V
XH_P42	16	1779576	1779600	Frame_Shift_Del	DEL	CGCGGGCGCG	-	CGCGGGCGCGCG	MAPK8IP3	c.599_602del	p.R200fs
XH_P42	16	1823356	1823356	Missense_Mutation	SNP	G	A	G	EME2	c.G128A	p.G43D
XH_P42	16	3076719	3076719	Missense_Mutation	SNP	G	A	G	THOC6	c.G523A	p.A175T
XH_P42	16	4851574	4851574	Missense_Mutation	SNP	G	T	G	ROGDI	c.C130A	p.R44S
XH_P42	16	14041970	14041970	In_Frame_Ins	INS	-	ACTACGGATTCT	-	ERCC4	8insCAGACTACG	839delinsPQTTDLSL
XH_P42	16	24564879	24564879	Splice_Site	INS	-	TA	-	RBBP6	-	-
XH_P42	16	24829973	24829973	Missense_Mutation	SNP	G	C	G	TNRC6A	c.G4885C	p.A1629P
XH_P42	16	24834957	24834957	Silent	SNP	G	A	G	TNRC6A	c.G5571A	p.S1857S
XH_P42	16	29855905	29855905	Missense_Mutation	SNP	G	A	G	MVP	c.G1528A	p.A510T
XH_P42	16	29917169	29917169	Frame_Shift_Ins	INS	-	TTCTGTCTCCAT	-	ASPHD1	CTGCTGTCTCTG	p.A375fs
XH_P42	16	31195693	31195704	In_Frame_Del	DEL	GTGGAGGTG	-	GTGGAGGTGGA	FUS	c.496_507del	p.166_169del
XH_P42	16	49407930	49407930	Missense_Mutation	SNP	G	A	G	C16orf78	c.G80A	p.R27H
XH_P42	16	50102759	50102759	Nonsense_Mutation	INS	-	TTCTATTTTATG	-	HEATR3	TTTATTTCTATT	V128delinsLTFISIFSHIX
XH_P42	16	50187912	50187929	In_Frame_Del	DEL	GGCGTCTCTCG	-	GGCGTCTCTCGC	PAPD5	c.335_352del	p.112_118del
XH_P42	16	53729299	53729299	Frame_Shift_Ins	INS	-	AA	-	RPGRIP1L	c.301_302insTT	p.E101fs
XH_P42	16	53729300	53729300	In_Frame_Ins	INS	-	AATTTTTTT	-	RPGRIP1L	301insAAAAA	E101delinsKKIE
XH_P42	16	56501135	56501135	Nonsense_Mutation	INS	-	AATTAATGTGCA	-	OGFOD1	CCTGAAATTAAT	38_P239delinsGGPX
XH_P42	16	69963403	69963403	Silent	SNP	G	A	G	WWP2	c.G939A	p.T313T
XH_P42	16	75446564	75446564	In_Frame_Ins	INS	-	GGAAGCTGGCC	-	CFDP1	5CTCTGGGCCAGC	91delinsLWASFLND
XH_P42	16	77317892	77317892	Silent	SNP	G	A	G	ADAMTS18	c.C3111T	p.Y1037Y
XH_P42	16	88874629	88874649	In_Frame_Del	DEL	CCACATCAC	-	CCACATCACACTG	CDT1	c.C1584_1604del	p.528_535del
XH_P42	17	4876953	4876953	Missense_Mutation	SNP	G	A	G	CAMTA2	c.C2134T	p.R712W
XH_P42	17	7733722	7733722	Silent	SNP	T	C	T	DNAH2	c.T11958C	p.C3986C
XH_P42	17	10295905	10295905	Nonsense_Mutation	INS	-	TGACTATTTATT	-	MYH8	22insTAAATAAA	K1841delinsINXK
XH_P42	17	17697390	17697390	Silent	SNP	G	A	G	RAI1	c.G1128A	p.P376P
XH_P42	17	18238949	18238949	Silent	SNP	C	G	C	SHMT1	c.G441C	p.L147L
XH_P42	17	28789055	28789055	Nonsense_Mutation	INS	-	TTTAAATATATA	-	CPD	AAAATGTTTTAA	G1018delinsEKMFKIX
XH_P42	17	30661542	30661542	Missense_Mutation	SNP	G	C	G	C17orf75	c.C817G	p.H273D
XH_P42	17	30815085	30815085	Missense_Mutation	SNP	T	G	T	CDK5R1	c.T447G	p.S149R
XH_P42	17	33331309	33331309	Frame_Shift_Ins	INS	-	TG	-	LIG3	2814_2815insT	p.F938fs
XH_P42	17	33884431	33884431	Frame_Shift_Ins	INS	-	TATCATCCACCC	-	SLFN14	ATTGGGGGTGGA	p.T217fs
XH_P42	17	33884433	33884433	Missense_Mutation	SNP	T	A	T	SLFN14	c.A649T	p.T217S
XH_P42	17	34853557	34853557	Nonsense_Mutation	SNP	C	T	C	ZNHIT3	c.C394T	p.Q132X
XH_P42	17	38990896	38990896	Frame_Shift_Ins	INS	-	CTCTGTGTGT	-	TMEM99	129insCTCTGT	p.G43fs
XH_P42	17	39041136	39041136	Nonsense_Mutation	INS	-	AAACACAGAGTA	-	KRT20	TTTCTACTCTGTG	1delinsLVFPTLCLASRX
XH_P42	17	39262084	39262113	In_Frame_Del	DEL	CCCAGCTGCA	-	CCCAGCTGCAG	KRTAP4-9	c.444_473del	p.148_158del
XH_P42	17	39334071	39334085	In_Frame_Del	DEL	AGGTGGTGCC	-	ACAGGTGGTGCTT	KRTAP4-2	c.332_346del	p.111_116del
XH_P42	17	48741188	48741188	Missense_Mutation	SNP	G	A	G	ABCC3	c.G1145A	p.B3C2H
XH_P42	17	48755467	48755467	Missense_Mutation	SNP	G	A	G	ABCC3	c.G3592A	p.G1198R
XH_P42	17	80195180	80195180	Silent	SNP	C	T	C	SLC16A3	c.C534T	p.G178G
XH_P42	18	5291808	5291808	Silent	SNP	G	A	G	ZBTB14	c.C399T	p.P133P
XH_P42	18	10487808	10487808	Missense_Mutation	SNP	G	A	G	APCDD1	c.G1318A	p.G440S
XH_P42	18	10807258	10807258	Frame_Shift_Ins	INS	-	AATCGATACTC	-	PIEZO2	932insGAGTAT	p.K311fs
XH_P42	18	13731869	13731869	In_Frame_Ins	INS	-	AACTCTTTTCTCT	-	RNMT	54insAAACTCTT	5118delinsSNSFLF
XH_P42	18	21128073	21128073	Splice_Site	INS	-	ACTTGG	-	NPC1	-	-
XH_P42	18	21662968	21662968	Nonsense_Mutation	INS	-	TAATGTGCTCAA	-	TTC39C	insGTTAATGTG	303_L304delinsSX
XH_P42	18	32398238	32398238	Missense_Mutation	SNP	G	A	G	DTNA	c.G70A	p.G24R
XH_P42	18	43447707	43447707	Frame_Shift_Ins	INS	-	ATGAT	-	EPG5	231_6232insAT	p.R2078fs
XH_P42	18	44561387	44561387	Silent	SNP	G	A	G	ELOA2	c.C249T	p.T83T
XH_P42	18	60646095	60646095	Missense_Mutation	SNP	C	T	C	PHLPP1	c.C4585T	p.R1529C
XH_P42	18	74091961	74091961	Silent	SNP	C	T	C	ZNFS16	c.G2109A	p.T703T
XH_P42	19	1119019	1119019	Silent	SNP	C	T	C	SBN02	c.G1347A	p.A449A
XH_P42	19	1881527	1881527	Frame_Shift_Del	DEL	G	-	G	ABHD17A	c.39delC	p.F13fs
XH_P42	19	2834374	2834374	Missense_Mutation	SNP	G	A	G	ZNFS54	c.G1141A	p.G381R
XH_P42	19	3494029	3494029	Silent	SNP	G	A	G	DOHH	c.C348T	p.I161I
XH_P42	19	8201077	8201077	Frame_Shift_Ins	INS	-	AGGCAGGCGGG	-	FBN3	TGACTGCCCGCC	p.V488fs
XH_P42	19	9271308	9271308	Silent	SNP	C	T	C	ZNFS17	c.C891T	p.T297T
XH_P42	19	10781681	10781681	Missense_Mutation	SNP	G	A	G	ILF3	c.G35A	p.R12H
XH_P42	19	12975891	12975891	Nonsense_Mutation	INS	-	GTGAGCTTTGAT	-	MAST1	GACAAAGTGAGC	L513delinsPDKX
XH_P42	19	15052698	15052698	Missense_Mutation	SNP	C	T	C	OR7C2	c.C398T	p.T133M
XH_P42	19	17306101	17306101	Missense_Mutation	SNP	G	A	G	MYO9B	c.G3865A	p.D1289N
XH_P42	19	18260385	18260385	Missense_Mutation	SNP	G	A	G	MAST3	c.G3779A	p.R1260Q
XH_P42	19	18377490	18377490	Missense_Mutation	SNP	C	T	C	KIAA1683	c.G860A	p.R287Q
XH_P42	19	19033268	19033268	Missense_Mutation	SNP	G	A	G	DDX49	c.G581A	p.R194Q
XH_P42	19	19790215	19790215	Silent	SNP	G	A	G	ZNFI01	c.G57A	p.T19T
XH_P42	19	19905748	19905748	Silent	SNP	C	T	C	ZNF506	c.G852A	p.E284E
XH_P42	19	21300656	21300739	In_Frame_Del	DEL	CCTCAAACCT	-	ATCCTCAAACCTT	ZNFI714	c.1186_1269del	p.396_423del
XH_P42	19	22154475	22154475	Missense_Mutation	SNP	T	C	T	ZNFI208	c.A3361G	p.S1121G
XH_P42	19	22155223	22155223	Silent	SNP	T	C	T	ZNFI208	c.A2613G	p.K871K
XH_P42	19	22155786	22155786	Missense_Mutation	SNP	T	C	T	ZNFI208	c.A2050G	p.K684E
XH_P42	19	22156945	22156945	Silent	SNP	G	A	G	ZNFI208	c.C891T	p.V297V
XH_P42	19	22363785	22363785	Nonsense_Mutation	INS	-	BCTTTGCCACAT	-	ZNFI676	TGAAGAATGTG	BRVHTGEEKPYKCECGKAFSX
XH_P42	19	22499036	22499119	In_Frame_Del	DEL	TGAAGCATA	-	TATGAAGCATAA	ZNFI729	c.2817_2900del	p.939_967del
XH_P42	19	22940944	22940944	Silent	SNP	C	T	C	ZNFI99	c.G1767A	p.G589G
XH_P42	19	22940945	22940945	Missense_Mutation	SNP	C	G	C	ZNFI99	c.G1766C	p.G589A
XH_P42	19	22942154	22942154	Nonsense_Mutation	INS	-	AGAAAAACATGA	-	ZNFI99	ATTATCTCATGT	delinsYHLHICRVSVQYELSHVFX
XH_P42	19	23927344	23927344	Silent	SNP	T	C	T	ZNFI681	c.A1008G	p.K36K
XH_P42	19	30935540	30935540	Silent	SNP	G	A	G	ZNFI536	c.G1071A	p.A357A
XH_P42	19	31769124	31769124	In_Frame_Ins	INS	-	ACAAACCTT	-	TSHZ3	1575insAAAG	S525delinsSKFV
XH_P42	19	31769125	31769125	Missense_Mutation	SNP	G	C	G	TSHZ3	c.C1574G	p.S525C
XH_P42	19	38968362	38968362	Missense_Mutation	SNP	G	A	G	RYR1	c.G4306A	p.V1436M
XH_P42	19	41778080	41778080	Missense_Mutation	SNP	G	A	G	HNRNPUL1	c.G245A	p.R82Q

XH_P42	19	41858919	41858921	In_Frame_Del	DEL	GCG	-	GCG	TGFB1	c.29_31del	p.10_11del
XH_P42	19	44117798	44117798	Missense_Mutation	SNP	T	C	T	SRRM5	c.T1525C	p.C509R
XH_P42	19	45315634	45315634	Missense_Mutation	SNP	G	T	G	BCAM	c.G419T	p.R140L
XH_P42	19	46914960	46915031	In_Frame_Del	DEL	TGTTTATCT	-	TCTGGTTATCTG	CCDC8	c.1037_1108del	p.346_370del
XH_P42	19	48981737	48981737	Missense_Mutation	SNP	A	C	A	CYTH2	c.A1000C	p.I334L
XH_P42	19	48989869	48989056	Frame_Shift_Del	DEL	CGGGGTCGG	-	GCGGGGTCGGG	LMTK3	c.4454_4531del	p.G1485fs
XH_P42	19	49539046	49539046	Missense_Mutation	SNP	C	T	C	CGB1	c.G289A	p.V97M
XH_P42	19	51135659	51135659	Silent	SNP	A	C	A	SYT3	c.T558G	p.P186P
XH_P42	19	51645628	51645633	In_Frame_Del	DEL	TGCTGC	-	TGCTGC	SIGLEC7	c.2_7del	p.1_3del
XH_P42	19	53553922	53553922	Frame_Shift_Ins	INS	-	CCATCTGGGAG	-	ERVV-2	CAAGGGCCATCT	p.F473fs
XH_P42	19	53959648	53959648	Silent	SNP	C	T	C	ZNF761	c.C1887T	p.T629T
XH_P42	19	55748337	55748337	Missense_Mutation	SNP	C	T	C	PPP6R1	c.G1753A	p.A585T
XH_P42	19	56934541	56934541	Nonsense_Mutation	INS	-	GATGATTCTC	-	ZNF583	515insGATGAT	172_1173delinsGX
XH_P42	19	56934998	56934998	Missense_Mutation	SNP	T	A	T	ZNF583	c.T971A	p.F324Y
XH_P42	19	56934999	56934999	Silent	SNP	C	T	C	ZNF583	c.C972T	p.F324F
XH_P42	19	57931832	57931832	Silent	SNP	T	C	T	ZNF17	c.T972C	p.H324H
XH_P42	19	58118220	58118220	Missense_Mutation	SNP	G	T	G	ZNF530	c.G1327T	p.V443F
XH_P42	20	278688	278693	In_Frame_Del	DEL	CGGCGG	-	CGGCGG	ZCHCH3	c.461_466del	p.154_156del
XH_P42	20	20018061	20018061	In_Frame_Ins	INS	-	GACTTCTCTGG	-	CRNKL1	1802insCCAGAG	E601delinsARESQ
XH_P42	20	20018063	20018063	Frame_Shift_Ins	INS	-	TGAGTTTGTCCT	-	CRNKL1	1800insAGACA	p.F600fs
XH_P42	20	25657512	25657512	Nonsense_Mutation	INS	-	SGATTTTCCCTCT	-	ZNF337	GGCCAGAGGGA	139delinsVKARGKILQKX
XH_P42	20	35207182	35207182	Missense_Mutation	SNP	C	T	C	TGIF2	c.C5T	p.S2L
XH_P42	20	35521385	35521385	Nonsense_Mutation	SNP	G	A	G	SAMHD1	c.C1831T	p.R611X
XH_P42	20	44520238	44520243	In_Frame_Del	DEL	CTGCTG	-	CTGCTG	CTSA	c.85_90del	p.29_30del
XH_P42	20	44856221	44856221	Missense_Mutation	SNP	G	A	G	CDH22	c.C596T	p.T199M
XH_P42	20	45129987	45130070	In_Frame_Del	DEL	TGTGTGATT	-	CTGTGTGTATTT	ZNF334	c.1908_1991del	p.636_664del
XH_P42	20	47351146	47351146	Missense_Mutation	SNP	A	C	A	PREX1	c.T456G	p.H152Q
XH_P42	20	47841502	47841502	Missense_Mutation	SNP	C	T	C	DDX27	c.C580T	p.R194W
XH_P42	20	57415750	57415750	Missense_Mutation	SNP	G	A	G	GNAS	c.C589A	p.E197K
XH_P42	20	58467350	58467350	Nonsense_Mutation	INS	-	AACAAAAA	-	SYCP2	TCACCATTTTTT	V687delinsIKTHX
XH_P42	21	18937956	18937956	Missense_Mutation	SNP	G	A	G	CXADR	c.G1044A	p.M348I
XH_P42	21	31768494	31768494	Frame_Shift_Ins	INS	-	CTGCTCTGGAA	-	KRTAP13-1	ACTGCTGCTCTG	p.Y30fs
XH_P42	21	31964824	31964874	In_Frame_Del	DEL	CGGAGGCT	-	ACGGAGGCGCTG	KRTAP6-3	c.60_110del	p.20_37del
XH_P42	21	33073424	33073424	Nonsense_Mutation	INS	-	TATCACTCAACT	-	SCAF4	insTCAAGTTGA	206_A207delinsSSX
XH_P42	21	34399564	34399564	Missense_Mutation	SNP	C	T	C	OLIG2	c.C394T	p.R132C
XH_P42	21	42866441	42866441	Missense_Mutation	SNP	G	A	G	TMPPRS2	c.C191T	p.P64L
XH_P42	21	47851916	47851916	Silent	SNP	G	A	G	PCNT	c.G8538A	p.T2846T
XH_P42	22	18301185	18301185	Silent	SNP	G	A	G	MICAL3	c.C4242T	p.S1414S
XH_P42	22	23915483	23915483	Frame_Shift_Ins	INS	-	TTCTTATCTCTCA	-	IGLL1	insTATGAGAGA	p.E204fs
XH_P42	22	32239093	32239093	Missense_Mutation	SNP	G	A	G	DEPDC5	c.G2294A	p.R765Q
XH_P42	22	38119489	38119489	Missense_Mutation	SNP	C	T	C	TRIOBP	c.C926T	p.T309I
XH_P42	22	38120532	38120532	Missense_Mutation	SNP	G	A	G	TRIOBP	c.G1969A	p.D657N
XH_P42	22	38120873	38120873	Silent	SNP	A	T	A	TRIOBP	c.A2310T	p.T770T
XH_P42	22	38694938	38694938	Frame_Shift_Ins	INS	-	T	-	CSNK1E	c.737_738insA	p.S246fs
XH_P42	22	38694939	38694939	In_Frame_Ins	INS	-	AGTCAC	-	CSNK1E	36_737insGTGA	S246delinsCDS
XH_P42	22	47068805	47068805	Missense_Mutation	SNP	G	A	G	GRAMD4	c.G1150A	p.A384T
XH_P42	22	51159651	51159651	Silent	SNP	C	T	C	SHANK3	c.C3348T	p.P1116P
XH_P42	X	17745550	17745550	Frame_Shift_Ins	INS	-	AGTAAAGA	-	NHS	0_2731insAGTA	p.L910fs
XH_P42	X	17745551	17745551	Nonsense_Mutation	INS	-	TGAACCTCCAA	-	NHS	732insCTTGAA	p.H911delinsPX
XH_P42	X	47466365	47466365	Missense_Mutation	SNP	C	T	C	SYN1	c.G506A	p.R169Q
XH_P42	X	69626872	69626872	Missense_Mutation	SNP	G	A	G	KIF4A	c.G3202A	p.E1068K
XH_P42	X	70613188	70613188	Missense_Mutation	SNP	T	C	T	TAF1	c.T3149C	p.V1050A
XH_P42	X	71363227	71363227	Missense_Mutation	SNP	G	T	G	NHSL2	c.G3481T	p.G1161W
XH_P42	X	73811809	73811809	Silent	SNP	T	C	T	RLIM	c.A1341G	p.G447G
XH_P42	X	90691714	90691714	Missense_Mutation	SNP	C	T	C	PABPC5	c.C1138T	p.R380C
XH_P42	X	91132563	91132563	Missense_Mutation	SNP	G	T	G	PCDH11X	c.G1324T	p.G442C
XH_P42	X	117570755	117570755	Nonsense_Mutation	INS	-	TAACATAGTCAA	-	WDR44	insTGATAACAT	623_F624delinsVITX
XH_P42	X	118723709	118723709	Frame_Shift_Ins	INS	-	TAGATAGGCTCC	-	NKRF	insTACGGGAGC	p.R560fs
XH_P42	X	118979176	118979176	Missense_Mutation	SNP	C	T	C	UPF3R	c.G454A	p.G152R
XH_P42	X	135122245	135122245	Missense_Mutation	SNP	C	T	C	SLC9A6	c.C1738T	p.P580S
XH_P42	X	151303809	151303809	Missense_Mutation	SNP	G	A	G	MAGEA10	c.C284T	p.S95L
XH_P42	1	156131148	156131148	Silent	SNV	C	T	T	SEMA4A	c.822C>T	p.G274G
XH_P42	1	165173169	165173169	Missense_Mutation	SNV	C	A	A	LMX1A	c.1097G>T	P.G366V
XH_P42	1	1895207	1895207	Missense_Mutation	SNV	G	A	A	CFAP74	c.1675C>T	P.R559W
XH_P42	1	205492433	205492433	Splice_Site	SNV	G	T	T	CDK18	c.130>8G>T	
XH_P42	1	228491389	228491389	Silent	SNV	A	G	G	OBSCN	c.13752A>G	P.R4584R
XH_P42	1	229771573	229771573	Missense_Mutation	SNV	A	C	C	URB2	c.1213A>C	P.I405L
XH_P42	1	240370169	240370169	Missense_Mutation	SNV	T	C	C	FMN2	c.2069T>C	P.L690P
XH_P42	1	245019801	245019801	Missense_Mutation	SNV	C	T	T	HNRNPU	c.1813G>A	P.E605K
XH_P42	1	27333320	27333320	Silent	SNV	C	G	G	FAM46B	c.393G>C	P.R131R
XH_P42	1	34092187	34092187	Splice_Site	SNV	G	A	A	CSMD2	c.5201-6C>T	
XH_P42	1	40125028	40125028	Missense_Mutation	SNV	C	T	T	NT5C1A	c.872G>A	P.R291Q
XH_P42	1	60330284	60330284	Splice_Site	INDEL	-	T	T	HOOK1	c.1627-12dupT	
XH_P42	1	6313981	6313981	Missense_Mutation	SNV	G	A	A	GPR153	c.583C>T	P.L195F
XH_P42	10	116200820	116200820	Missense_Mutation	SNV	A	G	G	ABLM1	c.1835T>C	P.F612S
XH_P42	10	134694542	134694542	Splice_Site	SNV	G	A	A	CFAP46	c.3628-6C>T	
XH_P42	10	27815803	27815803	Silent	SNV	T	A	A	RAB18	c.171T>A	P.A57A
XH_P42	10	3209169	3209169	Silent	SNV	C	T	T	PITRM1	c.225G>A	P.R75R
XH_P42	10	45939661	45939661	Missense_Mutation	SNV	C	A	A	ALOX5	c.1772C>A	P.T591K
XH_P42	10	68535286	68535286	Splice_Site	SNV	C	A	A	CTNNA3	c.1048-4G>T	
XH_P42	10	75529130	75529130	Missense_Mutation	SNV	C	T	T	SEC24C	c.2450C>T	P.A817V
XH_P42	11	102585439	102585439	Splice_Site	SNV	G	A	A	MMPB	c.969C>T	P.G323G
XH_P42	11	8662434	8662434	Silent	SNV	A	C	C	TRIM66	c.1053T>G	P.P351P
XH_P42	11	9606861	9606861	Missense_Mutation	SNV	G	A	A	WEE1	c.1345G>A	P.E449K
XH_P42	12	117624340	117624368	Frame_Shift_Del	INDEL	AATGTCAC	-	-	FBXO21	GGCTTCAGTGA	p.C128fs
XH_P42	12	129467603	129467603	Missense_Mutation	SNV	A	C	C	GLT1D1	c.769A>C	P.I257L
XH_P42	12	54645964	54645964	Missense_Mutation	SNV	A	G	G	CBX5	c.185T>C	P.L62P
XH_P42	13	101710394	101710394	Silent	SNV	C	T	T	NALCN	c.4920G>A	P.Q1640Q
XH_P42	14	23818628	23818628	Missense_Mutation	SNV	G	A	A	SLC22A17	c.379C>T	P.R127C
XH_P42	15	40594721	40594721	Missense_Mutation	SNV	C	A	A	PLCB2	c.321G>T	P.M107I
XH_P42	16	4851574	4851574	Missense_Mutation	SNV	G	T	T	ROGDI	c.130C>A	P.R44S
XH_P42	16	49407930	49407930	Missense_Mutation	SNV	G	A	A	C16orf78	c.80G>A	P.R27H
XH_P42	17	18238949	18238949	Silent	SNV	C	G	G	SHMT1	c.441G>C	P.L147L
XH_P42	17	30815085	30815085	Missense_Mutation	SNV	T	G	G	CDK5R1	c.447T>G	P.S149R
XH_P42	17	7733722	7733722	Silent	SNV	T	C	C	DNAH2	c.11958T>C	P.C3986C
XH_P42	19	22156945	22156945	Silent	SNV	G	A	A	ZNF208	c.891C>T	P.V297V
XH_P42	19	38968362	38968362	Missense_Mutation	SNV	G	A	A	RYR1	c.4306G>A	P.V1436M
XH_P42	19	45315634	45315634	Missense_Mutation	SNV	G	T	T	BCAM	c.419G>T	P.R140L

XH_P42	19	51135659	51135659	Silent	SNV	A	C	C	SYT3	c.558T>G	P.P186P
XH_P42	19	55014961	55014961	Splice_Site	SNV	G	A	A	LAIR2	c.70+10G>A	
XH_P42	19	9271308	9271308	Silent	SNV	C	T	T	ZNF317	c.891C>T	P.T297T
XH_P42	2	108487406	108487406	Missense_Mutation	SNV	A	C	C	RGPD4	c.2946A>C	P.E982D
XH_P42	2	112740484	112740484	Missense_Mutation	SNV	A	G	G	MERTK	c.1210A>G	P.R404G
XH_P42	2	12713333	12713333	Missense_Mutation	SNV	A	T	T	SNTG2	c.1274A>T	P.Q425L
XH_P42	2	209113113	209113113	Missense_Mutation	SNV	G	A	A	IDH1	c.394C>T	P.R132C
XH_P42	2	220336975	220336975	Missense_Mutation	SNV	G	A	A	SPFG	c.3862G>A	P.A1288T
XH_P42	2	220424188	220424188	Missense_Mutation	SNV	A	C	C	OBSL1	c.2985T>G	P.D995E
XH_P42	2	25469148	25469148	Missense_Mutation	SNV	G	A	A	DNMT3A	c.1310C>T	P.T437M
XH_P42	2	54952290	54952290	Missense_Mutation	SNV	C	T	T	EML6	c.92C>T	P.T31M
XH_P42	2	74642137	74642137	Silent	SNV	C	T	T	C2orf81	c.1086G>A	P.L362L
XH_P42	2	96078703	96078703	Nonstop_Mutation	SNV	T	G	G	FAHD2A	c.943T>G	P.Ter315Gext*?
XH_P42	2	97749494	97749494	Nonstop_Mutation	SNV	A	C	C	FAHD2B	c.943T>G	P.Ter315Gext*?
XH_P42	20	35207182	35207182	Missense_Mutation	SNV	C	T	T	TGIF2	c.5C>T	P.S2L
XH_P42	20	47351146	47351146	Missense_Mutation	SNV	A	C	C	PREX1	c.456T>G	P.H152Q
XH_P42	20	56189933	56189933	Splice_Site	SNV	G	A	A	ZBP1	c.502+10C>T	P.D995E
XH_P42	20	57415750	57415750	Missense_Mutation	SNV	G	A	A	GNAS	c.589G>A	P.E197K
XH_P42	21	18937956	18937956	Missense_Mutation	SNV	G	A	A	CXADR	c.1044G>A	P.M348I
XH_P42	21	34399564	34399564	Missense_Mutation	SNV	C	T	T	OLIG2	c.394C>T	P.R132C
XH_P42	21	42866441	42866441	Missense_Mutation	SNV	G	A	A	TMPPRS2	c.191C>T	P.P64L
XH_P42	22	38120873	38120873	Silent	SNV	A	T	T	TRIOBP	c.2310A>T	P.T770T
XH_P42	22	47068805	47068805	Missense_Mutation	SNV	G	A	A	GRAMD4	c.1150G>A	P.A384T
XH_P42	22	51159651	51159651	Silent	SNV	C	T	T	SHANK3	c.3348C>T	P.P1116P
XH_P42	3	126137618	126137618	Splice_Site	SNV	G	A	A	CFAP100	c.650+1G>A	
XH_P42	3	150128693	150128693	Missense_Mutation	SNV	C	T	T	TSC22D2	c.1556C>T	P.P519L
XH_P42	3	40573747	40573747	Nonsense_Mutation	SNV	T	G	G	ZNF621	c.486T>G	P.Y162*
XH_P42	3	89390983	89390983	Missense_Mutation	SNV	A	G	G	EPHA3	c.1049A>G	P.D350G
XH_P42	3	97983363	97983363	Missense_Mutation	SNV	C	T	T	OR5H6	c.235C>T	P.L79F
XH_P42	4	173942679	173942679	Missense_Mutation	SNV	C	A	A	GALNTL6	c.1541C>A	P.T514N
XH_P42	4	47427774	47427774	Silent	SNV	C	T	T	GABRB1	c.1164C>T	P.S388S
XH_P42	6	28227727	28227727	Missense_Mutation	SNV	C	T	T	NKAPL	c.578C>T	P.S193L
XH_P42	6	42832824	42832824	Silent	SNV	A	T	T	GLTSCR1L	c.2880A>T	P.A960A
XH_P42	6	85472394	85472394	Missense_Mutation	SNV	G	A	A	TBX18	c.365C>T	P.P122L
XH_P42	7	103301862	103301862	Missense_Mutation	SNV	T	G	G	RELN	c.1402A>C	P.T468P
XH_P42	7	131859651	131859651	Missense_Mutation	SNV	A	C	C	PLXNA4	c.3903T>G	P.H1301Q
XH_P42	7	141362520	141362520	Missense_Mutation	SNV	A	T	T	KIAA1147	c.1304T>A	P.L435Q
XH_P42	7	1786409	1786409	Missense_Mutation	SNV	C	T	T	ELFN1	c.2177C>T	P.P726L
XH_P42	7	30185905	30185905	Missense_Mutation	SNV	C	A	A	MTURN	c.275C>A	P.S92Y
XH_P42	7	6193562	6193562	Missense_Mutation	SNV	G	A	A	USP42	c.2377G>A	P.A793T
XH_P42	7	76110029	76110029	Missense_Mutation	SNV	C	A	A	DTX2	c.203C>A	P.A68E
XH_P42	7	94992089	94992089	Missense_Mutation	SNV	C	T	T	PON3	c.760G>A	P.D254N
XH_P42	7	99312214	99312214	Silent	SNV	T	C	C	CYP3A7	c.762A>G	P.K254K
XH_P42	8	141566055	141566055	Missense_Mutation	SNV	A	C	C	AGO2	c.1209T>G	P.D403E
XH_P42	9	113550104	113550104	Missense_Mutation	SNV	T	C	C	MUSK	c.1655T>C	P.I552T
XH_P42	9	139793340	139793340	Missense_Mutation	SNV	G	A	A	TRAF2	c.148G>A	P.G50S
XH_P42	9	139906715	139906715	Splice_Site	SNV	A	C	C	ABCA2	c.5299+2T>G	
XH_P42	X	135122245	135122245	Missense_Mutation	SNV	C	T	T	SLC9A6	c.1738C>T	P.P580S
XH_P42	X	70613188	70613188	Missense_Mutation	SNV	T	C	C	TAF1	c.3086T>C	P.V1029A
XH_P42	X	71363227	71363227	Missense_Mutation	SNV	G	T	T	NHSL2	c.3481G>T	P.G1161W
XH_P42	X	91132563	91132563	Missense_Mutation	SNV	G	T	T	PCDH11X	c.1324G>T	
XH_P43	1	3544132	3544132	In_Frame_Ins	INS	-	TTTATTTTGTGT	-	TPRG1L	TAGTTTTTATT	delinsKTACSFYFCYFLFLF
XH_P43	1	9649032	9649032	Missense_Mutation	SNP	G	T	G	TMEM201	c.G44T	p.G15V
XH_P43	1	10364381	10364381	Missense_Mutation	SNP	A	T	A	KIF1B	c.A3138T	p.Q1046H
XH_P43	1	10364382	10364382	Nonsense_Mutation	INS	-	TCTGTATGATG	-	KIF1B	140insTTCTGTT	delinsL417_R1048delinsLLX
XH_P43	1	12939747	12939747	Missense_Mutation	SNP	G	A	G	PRAMEF4	c.C1055T	p.A352V
XH_P43	1	17085498	17085498	Missense_Mutation	SNP	G	T	G	MST1L	c.C1193A	p.S398Y
XH_P43	1	19518825	19518825	Frame_Shift_Ins	INS	-	GTATGTGT	-	UBR4	0_1251insACAC	p.S417fs
XH_P43	1	19518826	19518826	Nonsense_Mutation	INS	-	GATTATAATTTA	-	UBR4	sAAATATAAATT	delinsL417_R1418delinsKIX
XH_P43	1	19585040	19585040	Frame_Shift_Ins	INS	-	A	-	MRT04	c.563_564insA	p.R188fs
XH_P43	1	19585042	19585042	Missense_Mutation	SNP	G	C	G	MRT04	c.G565C	p.V189L
XH_P43	1	24981595	24981595	Nonsense_Mutation	INS	-	ATAAGATATTC	-	SRRM1	91insGAATAAA	delinsL430_S431delinsVEX
XH_P43	1	25558601	25558601	Frame_Shift_Ins	INS	-	CAATTTA	-	SYF2	25_126insTAA	p.L42fs
XH_P43	1	25558603	25558603	Missense_Mutation	SNP	G	T	G	SYF2	c.C124A	p.L42M
XH_P43	1	26644536	26644536	Missense_Mutation	SNP	A	C	A	CD52	c.A28C	p.T10P
XH_P43	1	31208069	31208069	Nonsense_Mutation	INS	-	TCATTCATTATT	-	LAPTMS	sCTGAATAAATC	delinsL217_C218delinsTEX
XH_P43	1	32689637	32689637	Silent	SNP	C	T	C	E1F31	c.C99T	p.I331
XH_P43	1	38463766	38463766	Nonsense_Mutation	SNP	C	A	C	FHL3	c.G46T	p.E16X
XH_P43	1	40688334	40688334	Missense_Mutation	SNP	C	T	C	RLF	c.C899T	p.T300M
XH_P43	1	40922690	40922690	Missense_Mutation	SNP	G	A	G	ZFP69B	c.G287A	p.R96Q
XH_P43	1	43002200	43002203	Frame_Shift_Del	DEL	AGAG	-	AGAG	CDC30	c.45_48del	p.K15fs
XH_P43	1	43825958	43825958	Silent	SNP	G	A	G	CDC20	c.G651A	p.L217L
XH_P43	1	43825959	43825959	Missense_Mutation	SNP	C	A	C	CDC20	c.C652A	p.Q218K
XH_P43	1	47725975	47725975	Silent	SNP	G	A	G	STIL	c.C3066T	p.N1022N
XH_P43	1	54284720	54284720	Silent	SNP	C	A	C	NDC1	c.G507T	p.L169L
XH_P43	1	54284721	54284721	In_Frame_Ins	INS	-	ATTTAGGAAAA	-	NDC1	insAATATTTTC	delinsL69delinsQYFPKYM
XH_P43	1	54606798	54606798	Missense_Mutation	SNP	G	A	G	CDCP2	c.C736T	p.R246C
XH_P43	1	54606898	54606898	Silent	SNP	G	T	G	CDCP2	c.C636A	p.T212T
XH_P43	1	54694151	54694151	Splice_Site	SNP	C	A	C	SSBP3	.	
XH_P43	1	63097073	63097073	Frame_Shift_Ins	INS	-	TTTTTTTGAG	-	DOCK7	1120insCTCAA	p.K374fs
XH_P43	1	63097075	63097075	Frame_Shift_Ins	INS	-	GGAG	-	DOCK7	117_1118insCT	p.N373fs
XH_P43	1	67340463	67340463	Splice_Site	SNP	C	T	C	WDR78	.	
XH_P43	1	70654958	70654958	Splice_Site	INS	-	CTGTTCTTGATG	-	LRRC40	.	
XH_P43	1	74492500	74492500	Missense_Mutation	SNP	T	G	T	LRR1Q3	c.A1872C	p.K624N
XH_P43	1	74663954	74663954	Missense_Mutation	SNP	G	T	G	PGT	c.G31T	p.G11C
XH_P43	1	75065499	75065499	Missense_Mutation	SNP	C	G	C	ERICH3	c.G1606C	p.D536H
XH_P43	1	85824449	85824449	Missense_Mutation	SNP	C	T	C	DDAH1	c.G85A	p.G29R
XH_P43	1	89521788	89521788	Missense_Mutation	SNP	A	C	A	GBP1	c.T1279G	p.Y427D
XH_P43	1	89587518	89587518	Silent	SNP	C	A	C	GBP2	c.G132T	p.V44V
XH_P43	1	94497565	94497565	Frame_Shift_Ins	INS	-	TC	-	ABCA4	3896_3897insG	p.P1299fs
XH_P43	1	94497567	94497567	Frame_Shift_Ins	INS	-	T	-	ABCA4	3894_3895ins	p.P1299fs
XH_P43	1	100731947	100731947	Missense_Mutation	SNP	G	A	G	RTCA	c.G16A	p.V6M
XH_P43	1	104166750	104166750	Frame_Shift_Ins	INS	-	TAGTAACCTCTT	-	AMY2A	sATTAATAGTAA	p.G418fs
XH_P43	1	117504042	117504042	Nonsense_Mutation	INS	-	GTTTAAACAATT	-	PTGFRN	2insCTTGTTTTA	delinsL464delinsLLFX
XH_P43	1	143767566	143767566	Missense_Mutation	SNP	A	G	A	PPIAL4G	c.T283C	p.S95P
XH_P43	1	145296546	145296546	Missense_Mutation	SNP	G	C	G	NBP10	c.G468C	p.Q156H
XH_P43	1	145606316	145606316	Frame_Shift_Del	DEL	AGCAGCATC	-	CAGCAGCATCT	POLR3C	c.654_676del	p.S218fs
XH_P43	1	146756150	146756150	Missense_Mutation	SNP	G	A	G	CHD1L	c.G1220A	p.R407Q

XH_P43	1	147124342	147124342	Frame_Shift_Ins	INS	-	GGTTG	-	ACP6	790_791insCAA	p.L264fs
XH_P43	1	150064184	150064184	Nonsense_Mutation	SNP	C	T	C	VPS45	c.C889T	p.R297X
XH_P43	1	150484223	150484223	Missense_Mutation	SNP	G	T	G	ECM1	c.G1080T	p.R360S
XH_P43	1	150923438	150923438	Missense_Mutation	SNP	T	G	T	SETD81	c.T2085G	p.N695K
XH_P43	1	150956517	150956517	Missense_Mutation	SNP	C	T	C	ANXA9	c.C239T	p.S80L
XH_P43	1	151090631	151090631	Frame_Shift_Ins	INS	-	CTCTCTT	-	GABPB2	12_1013insCTC	p.V338fs
XH_P43	1	151380666	151380666	Frame_Shift_Ins	INS	-	TGGTTTTTAA	-	POGZ	2000insTTAA	p.D667fs
XH_P43	1	151380667	151380667	In_Frame_Ins	INS	-	CAG	-	POGZ	1998_1999insC	p.D667delinsD
XH_P43	1	151552157	151552157	Missense_Mutation	SNP	G	T	G	TUFT1	c.G882T	p.K294N
XH_P43	1	152052197	152052197	Frame_Shift_Ins	INS	-	CCCTGCCCCAG	-	LOC100131107	nsGGAACCTGGG	p.L363fs
XH_P43	1	152052199	152052199	Frame_Shift_Ins	INS	-	GCTGCTC	-	LOC100131107	4_1085insGAG	p.A362fs
XH_P43	1	152127272	152127272	Missense_Mutation	SNP	C	T	C	RPTN	c.G2303A	p.R768H
XH_P43	1	152191626	152191626	In_Frame_Ins	INS	-	AGAGGA	-	HRNR	178_2479insTCG	p.G827delinsSSG
XH_P43	1	152191732	152191732	Silent	SNP	G	A	G	HRNR	c.C2373T	p.H791H
XH_P43	1	152192008	152192008	Silent	SNP	G	A	G	HRNR	c.C2097T	p.S699S
XH_P43	1	152275818	152275818	Silent	SNP	A	T	A	FLG	c.T11544A	p.G3484G
XH_P43	1	152276660	152276660	Nonsense_Mutation	SNP	G	A	G	FLG	c.C10702T	p.Q3568X
XH_P43	1	152280504	152280504	Missense_Mutation	SNP	G	T	G	FLG	c.C6858A	p.H2286Q
XH_P43	1	152282812	152282812	Missense_Mutation	SNP	T	G	T	FLG	c.A4550C	p.Y1517S
XH_P43	1	152286132	152286132	Silent	SNP	G	A	G	FLG	c.C1230T	p.S410S
XH_P43	1	152944594	152944594	Silent	SNP	C	T	C	SPRR4	c.C228T	p.S76S
XH_P43	1	153924549	153924549	Missense_Mutation	SNP	C	A	C	CRTC2	c.G942T	p.M314I
XH_P43	1	154940728	154940728	Silent	SNP	G	A	G	SHC1	c.C756T	p.I252I
XH_P43	1	159002411	159002411	Frame_Shift_Ins	INS	-	AT	-	IFI16	1091_1092insA	p.T364fs
XH_P43	1	159002413	159002413	Frame_Shift_Ins	INS	-	CATTGTGAGA	-	IFI16	14insTTTCATTGT	p.F365fs
XH_P43	1	159283723	159283723	Nonsense_Mutation	INS	-	TTATAAATATGT	-	OR10J3	TTAGTACATATT	143_524delinsKNX
XH_P43	1	161023103	161023103	Silent	SNP	G	A	G	ARHGAP30	c.C78T	p.V480A
XH_P43	1	168056880	168056880	Missense_Mutation	SNP	A	C	A	GPR161	c.T1033G	p.C345G
XH_P43	1	171509822	171509822	Nonsense_Mutation	INS	-	CTGATTTAGATT	-	PRRC2C	5AGTTTCTGATT	11071delinsTSFX
XH_P43	1	171510220	171510220	Frame_Shift_Ins	INS	-	CAGGTGTGTTTT	-	PRRC2C	18610insCAGGT	p.S1203fs
XH_P43	1	173721045	173721045	Missense_Mutation	SNP	G	A	G	KLHL20	c.G740A	p.R247H
XH_P43	1	173910423	173910423	Missense_Mutation	SNP	C	G	C	RC3H1	c.G3231C	p.E1077D
XH_P43	1	173947722	173947722	Nonsense_Mutation	INS	-	A	-	RC3H1	c.1005_1006ins	E336_L337delinsX
XH_P43	1	173947723	173947723	Nonsense_Mutation	INS	-	TATTTAATACTTT	-	RC3H1	5TATAAAAGTAGT	E336delinsQQYKYX
XH_P43	1	175304899	175304899	Frame_Shift_Ins	INS	-	TCATTAAATAGTC	-	TNR	180insGAGACTAT	p.K60fs
XH_P43	1	179816750	179816750	Nonsense_Mutation	INS	-	TACTTAATTAAT	-	TOR1AIP2	CAATCATTAAAT	92_T193delinsPIIKX
XH_P43	1	180399375	180399375	Frame_Shift_Ins	INS	-	FATGTGTATATG	-	ACBD6	nsTACACATATA	p.L136fs
XH_P43	1	180399377	180399377	Frame_Shift_Ins	INS	-	ATATA	-	ACBD6	404_405insTAT	p.K135fs
XH_P43	1	183909846	183909846	Silent	SNP	G	A	G	COLGALT2	c.C1473T	p.A491A
XH_P43	1	186123054	186123054	Missense_Mutation	SNP	T	G	T	HMCN1	c.T15191G	p.V5064G
XH_P43	1	196397391	196397391	Frame_Shift_Ins	INS	-	TT	-	KN2T	c.827_828insAA	p.Q276fs
XH_P43	1	196397393	196397393	Nonsense_Mutation	INS	-	GGAGGAGTTTTT	-	KN2T	1826insTAAAAAT	1276_L277delinsX
XH_P43	1	196973898	196973898	Missense_Mutation	SNP	T	G	T	CFHR5	c.T1438G	p.S480A
XH_P43	1	197072532	197072532	Missense_Mutation	SNP	G	A	G	ASPM	c.C5849T	p.A1950V
XH_P43	1	197876348	197876348	Nonstop_Mutation	SNP	T	G	T	C1orf53	c.T436G	p.X146G
XH_P43	1	197898307	197898307	Frame_Shift_Ins	INS	-	TTTTTCTTTCTT	-	LHX9	TTTTTTCTTTTCT	p.T371fs
XH_P43	1	197898309	197898309	In_Frame_Ins	INS	-	ATA	-	LHX9	1114_1115insA	p.V372delinsDI
XH_P43	1	201180652	201180652	Missense_Mutation	SNP	A	G	A	IGFN1	c.A6631G	p.K2211E
XH_P43	1	201836000	201836000	Missense_Mutation	SNP	G	A	G	IPO9	c.G1768A	p.V590I
XH_P43	1	201868916	201868916	Missense_Mutation	SNP	G	A	G	LMOD1	c.C1225T	p.R409W
XH_P43	1	203819046	203819046	Missense_Mutation	SNP	C	T	C	ZC3H11A	c.C1831T	p.R611W
XH_P43	1	205156740	205156740	Missense_Mutation	SNP	G	A	G	DSTYK	c.C460T	p.R154C
XH_P43	1	205241087	205241087	Silent	SNP	C	T	C	TMCC2	c.C1290T	p.A430A
XH_P43	1	207317197	207317197	Missense_Mutation	SNP	G	T	G	C48PA	c.G1479T	p.R493S
XH_P43	1	210977432	210977432	Missense_Mutation	SNP	A	C	A	KNCH1	c.T1458G	p.H486Q
XH_P43	1	212798568	212798568	Nonsense_Mutation	SNP	G	T	G	FAM71A	c.G349T	p.E117X
XH_P43	1	214171209	214171209	Missense_Mutation	SNP	G	A	G	PROX1	c.G1331A	p.R444H
XH_P43	1	218475844	218475844	Frame_Shift_Ins	INS	-	AATAA	-	RRP15	348_349insAAT	p.K116fs
XH_P43	1	225541540	225541552	Frame_Shift_Del	DEL	CTATAAAATTT	-	CCTATAAAATTTTC	DNAH14	11290_11302d	p.P3764fs
XH_P43	1	227300490	227300490	Frame_Shift_Ins	INS	-	GTAATATAATAT	-	CDC42BPA	insTTATATATTA	p.T591fs
XH_P43	1	227842621	227842621	Missense_Mutation	SNP	C	G	C	ZNF678	c.C835G	p.L279V
XH_P43	1	228434277	228434277	Missense_Mutation	SNP	G	A	G	OBSCN	c.G3806A	p.R1269Q
XH_P43	1	228487799	228487799	Missense_Mutation	SNP	C	T	C	OBSCN	c.C13691T	p.S5464L
XH_P43	1	228492129	228492129	Silent	SNP	C	A	C	OBSCN	c.C14128A	p.R4710R
XH_P43	1	230824202	230824208	Frame_Shift_Del	DEL	GTGTGCC	-	GTGTGCC	COG2	c.1685_1691de	p.C562fs
XH_P43	1	234601434	234601434	Missense_Mutation	SNP	C	A	C	TARBP1	c.G1269T	p.M423I
XH_P43	1	234601435	234601435	In_Frame_Ins	INS	-	CTCCTTTGTTTT	-	TARBP1	AAGAAAAAACCA	23delinsTRKNNKGETL
XH_P43	1	237774206	237774206	Silent	SNP	C	A	C	RVR2	c.C4828A	p.R1610R
XH_P43	1	237777676	237777676	Missense_Mutation	SNP	G	T	G	RVR2	c.G5248T	p.G1750W
XH_P43	1	241262027	241262027	Missense_Mutation	SNP	T	A	T	RG57	c.A114T	p.K38N
XH_P43	1	241262029	241262029	Nonsense_Mutation	INS	-	TTATAAAATGCT	-	RG57	1CACAGGCATT	8_N39delinsYTTGILX
XH_P43	1	247162680	247162680	Nonsense_Mutation	INS	-	CTCTCATAGTTTA	-	ZNF695	1CCTATAAACCTA	77_N78delinsPYKLX
XH_P43	1	247921607	247921607	Missense_Mutation	SNP	C	T	C	OR1C1	c.G102A	p.M34I
XH_P43	1	247921608	247921608	Missense_Mutation	SNP	A	C	A	OR1C1	c.T101G	p.M34R
XH_P43	2	24181213	24181213	Frame_Shift_Ins	INS	-	A	-	UBXN2A	c.30dupA	p.I10fs
XH_P43	2	25190127	25190127	Silent	SNP	G	A	G	DNAJC27	c.C123T	p.F41F
XH_P43	2	27164917	27164917	Missense_Mutation	SNP	G	A	G	DPYSL5	c.G1189A	p.G397R
XH_P43	2	27804879	27804879	Missense_Mutation	SNP	C	T	C	C2orf16	c.C5440T	p.R1814C
XH_P43	2	33505109	33505109	Missense_Mutation	SNP	T	C	T	LTBP1	c.T2018C	p.I673T
XH_P43	2	37247965	37247965	Missense_Mutation	SNP	G	T	G	HEATR5B	c.C3868A	p.L1290I
XH_P43	2	44051236	44051236	Frame_Shift_Ins	INS	-	CCTAAAT	-	ABCG5	139_1140insATT	p.V380fs
XH_P43	2	45233593	45233593	Missense_Mutation	SNP	G	T	G	SIX2	c.C592A	p.H198N
XH_P43	2	46607605	46607605	Missense_Mutation	SNP	G	C	G	EPAS1	c.G1794C	p.E598D
XH_P43	2	48027493	48027493	Missense_Mutation	SNP	C	T	C	MSH6	c.C1981T	p.R661C
XH_P43	2	54587612	54587612	Frame_Shift_Del	DEL	G	-	G	C2orf73	c.777delG	p.K259fs
XH_P43	2	60688491	60688491	Missense_Mutation	SNP	A	G	A	BC11A	c.T1556C	p.L519P
XH_P43	2	70488476	70488476	Missense_Mutation	SNP	G	A	G	PCYOX1	c.G452A	p.R151H
XH_P43	2	71170817	71170817	Frame_Shift_Del	DEL	C	-	C	ATP6V1B1	c.148delC	p.P50fs
XH_P43	2	88082721	88082721	In_Frame_Ins	INS	-	GAAAGGGGC	-	RGPD1	7_3798insGCCC	11266delinsMPLS
XH_P43	2	88888397	88888397	Nonsense_Mutation	INS	-	ACTGTTATATAC	-	EIF2AK3	1ATAAAGTATAT	p.Y245delinsX
XH_P43	2	96574314	96574314	Missense_Mutation	SNP	T	A	T	ANKRD36C	c.A2970T	p.R990S
XH_P43	2	96614313	96614313	Missense_Mutation	SNP	C	G	C	ANKRD36C	c.G1327C	p.A443P
XH_P43	2	97297208	97297208	Missense_Mutation	SNP	A	G	A	KANSL3	c.T227C	p.V76A
XH_P43	2	98418984	98418984	Frame_Shift_Ins	INS	-	TGTAGTATTG	-	TMEM131	2558insCAATA	p.L853fs
XH_P43	2	98732163	98732163	Missense_Mutation	SNP	G	A	G	VWA3B	c.G245A	p.G82D
XH_P43	2	105859235	105859235	Missense_Mutation	SNP	C	A	C	GPR45	c.C920A	p.T307N
XH_P43	2	108488215	108488215	Missense_Mutation	SNP	G	A	G	RGPD4	c.G3755A	p.C1252Y
XH_P43	2	108609550	108609550	Nonsense_Mutation	INS	-	SAATGTAATATA	-	SLCSA7	AAAAGAAATGTA	134delinsNKNKVIKX

XH_P43	2	109383055	109383055	Silent	SNP	C	T	C	RANBP2	c.C6060T	p.P2020P
XH_P43	2	110015097	110015097	Missense_Mutation	SNP	G	T	G	SH3RF3	c.G997T	p.A333S
XH_P43	2	110015099	110015103	Frame_Shift_Del	DEL	TGCAT	-	TGCAT	SH3RF3	c.999_1003del	p.A333fs
XH_P43	2	135756498	135756498	Silent	SNP	C	A	C	MAP3K19	c.G384T	p.T128T
XH_P43	2	137917848	137917848	Missense_Mutation	SNP	A	T	A	THSD7B	c.A1435T	p.I479F
XH_P43	2	155102459	155102459	Nonsense_Mutation	INS	-	AAAACCAATTTA	-	GALNT13	2insTAAACCA	M274delinsKTNLX
XH_P43	2	160628521	160628521	Silent	SNP	T	C	T	CD302	c.A366G	p.V122V
XH_P43	2	163059589	163059589	Missense_Mutation	SNP	C	G	C	FAP	c.G1039C	p.D347H
XH_P43	2	163374321	163374321	Missense_Mutation	SNP	G	A	G	KCNH7	c.C811T	p.R271W
XH_P43	2	171850405	171850405	In_Frame_Ins	INS	-	GGTTGGTTTCTT	-	TLK1	insAAAAAGAA	633delinsEKENKHS
XH_P43	2	171906643	171906643	Frame_Shift_Ins	INS	-	ACAATTGAGTG	-	TLK1	nsTCATCACTCA	p.K162fs
XH_P43	2	172641804	172641804	Missense_Mutation	SNP	C	T	C	SLC25A12	c.G2017A	p.A673T
XH_P43	2	173332218	173332218	Missense_Mutation	SNP	C	T	C	ITGA6	c.C317T	p.T106M
XH_P43	2	179318291	179318291	Nonsense_Mutation	INS	-	AAAATACAAAG	-	DFNB59	TCTTAAAAATACT	52_S53delinsTSX
XH_P43	2	179428837	179428837	Missense_Mutation	SNP	C	T	C	TTN	c.G54827A	p.R18276Q
XH_P43	2	179476574	179476574	Frame_Shift_Ins	INS	-	ACATGTGA	-	TTN	6_23267insTCA	p.E775fs
XH_P43	2	17956813	17956813	Frame_Shift_Ins	INS	-	GTTTTTACTGTT	-	TTN	7960insAACACAG	p.P9320fs
XH_P43	2	179613977	179613977	Missense_Mutation	SNP	C	G	C	TTN	c.G13150C	p.D4384H
XH_P43	2	183104914	183104914	Missense_Mutation	SNP	C	G	C	PDE1A	c.G219C	p.M73I
XH_P43	2	183948243	183948243	Missense_Mutation	SNP	A	C	A	DUSP19	c.A234C	p.Q78H
XH_P43	2	186659084	186659084	Missense_Mutation	SNP	G	T	G	FSIP2	c.G7221T	p.K2407N
XH_P43	2	190428890	190428890	Missense_Mutation	SNP	A	C	A	SLC40A1	c.T822G	p.T274Q
XH_P43	2	191841728	191841728	Nonsense_Mutation	INS	-	GGTGATTA	-	STAT1	6_1897insTAAT	P633_Y634delinsX
XH_P43	2	200213696	200213696	Frame_Shift_Ins	INS	-	TCITTT	-	SATB2	900_901insAAA	p.Q301fs
XH_P43	2	200213697	200213697	In_Frame_Ins	INS	-	CAA	-	SATB2	899_900insTTG	p.P300delinsPC
XH_P43	2	201436479	201436485	Frame_Shift_Del	DEL	AAAGAAA	-	AAAGAAA	SGO2	c.1410_1416del	p.L470fs
XH_P43	2	201437158	201437158	Frame_Shift_Ins	INS	-	CATCTTTATC	-	SGO2	2090insCATCT	p.N697fs
XH_P43	2	206921261	206921272	In_Frame_Del	DEL	CTGCTGCGG	-	GCTGCTGCGGAG	INO80D	c.614_625del	p.205_209del
XH_P43	2	207516603	207516603	Missense_Mutation	SNP	T	G	T	DYTN	c.A1676C	p.Q559P
XH_P43	2	207575286	207575286	Frame_Shift_Ins	INS	-	GACTTGTGCAT	-	DYTN	56insATGCACA	p.T19fs
XH_P43	2	210560205	210560205	Frame_Shift_Ins	INS	-	TTTAAACATCT	-	MAP2	3312insTTTTTA	p.K1104fs
XH_P43	2	218762667	218762667	Frame_Shift_Ins	INS	-	TT	-	TNS1	c.21_22insAA	p.E8fs
XH_P43	2	218762668	218762668	In_Frame_Ins	INS	-	TCITTTGTTT	-	TNS1	21insAAACAA	p.M7delinsINKE
XH_P43	2	228147097	228147097	Silent	SNP	G	A	G	COL4A3	c.G2505A	p.T835T
XH_P43	2	230678968	230678968	Nonsense_Mutation	INS	-	ACAGTTTCTAT	-	TRIP12	sAAATATAGAA	257_K258delinsKIX
XH_P43	2	231861033	231861059	In_Frame_Del	DEL	AGCCCTGA	-	CTAGCCCTGAAT	SPATA3	c.85_111del	p.29_37del
XH_P43	2	233273233	233273233	Missense_Mutation	SNP	G	A	G	ALPPL2	c.G806A	p.R269H
XH_P43	2	236957796	236957796	Missense_Mutation	SNP	G	A	G	AGAP1	c.G1826A	p.R609Q
XH_P43	2	239164301	239164301	Nonsense_Mutation	SNP	G	A	G	PER2	c.C2317T	p.R773X
XH_P43	2	240078397	240078397	Silent	SNP	C	T	C	HDAC4	c.G684A	p.P228P
XH_P43	3	9489446	9489446	Nonsense_Mutation	INS	-	ATTCACITTAAG	-	SETD5	60insCTATTTCAC	20_R621delinsSYSIX
XH_P43	3	12944315	12944315	Silent	SNP	T	A	T	IQSEC1	c.A2763T	p.R921R
XH_P43	3	12944317	12944319	In_Frame_Del	DEL	GCT	-	GCT	IQSEC1	c.2759_2761del	p.920_921del
XH_P43	3	19384153	19384153	Missense_Mutation	SNP	C	G	C	KCNH8	c.C517G	p.H173D
XH_P43	3	19384154	19384154	In_Frame_Ins	INS	-	TTATATATTTTA	-	KCNH8	19insTTTATATA	H173delinsHLYIFI
XH_P43	3	19574988	19574988	In_Frame_Ins	INS	-	TTATTCCTACTTA	-	KCNH8	insTCTTTTATTTCT	907delinsFSFIPTVL
XH_P43	3	19574990	19574990	Missense_Mutation	SNP	G	T	G	KCNH8	c.G2723T	p.C908F
XH_P43	3	25635199	25635199	Splice_Site	INS	-	AAAAAATTGAT	-	RARB	-	-
XH_P43	3	25778885	25778885	Frame_Shift_Ins	INS	-	GTAAT	-	NGLY1	942_943insATT	p.C315fs
XH_P43	3	32746387	32746387	In_Frame_Ins	INS	-	TCATTCCTCAATA	-	CNOT10	stATATCATTTCC	68delinsVYHSKYIS
XH_P43	3	32776413	32776413	Nonsense_Mutation	INS	-	AAATAAGGCTC	-	CNOT10	tATTTTAAATAA	487_5488delinsIFX
XH_P43	3	33134547	33134547	Missense_Mutation	SNP	G	A	G	TMPE	c.C1141T	p.R381W
XH_P43	3	37368218	37368218	Nonsense_Mutation	INS	-	TCTATTTCAATA	-	GOLGA4	2insGACTCTATT	1614delinsRTLFXQX
XH_P43	3	40251559	40251559	Frame_Shift_Ins	INS	-	TGTTGCTTCTT	-	MYRIP	1320insTGTGTG	p.Q40fs
XH_P43	3	44448997	44448997	Missense_Mutation	SNP	A	C	A	TCAIM	c.A1314C	p.L438F
XH_P43	3	44611483	44611483	Missense_Mutation	SNP	C	T	C	ZKSCAN7	c.C428T	p.S143F
XH_P43	3	49568441	49568441	Missense_Mutation	SNP	C	T	C	DAG1	c.C497T	p.S166L
XH_P43	3	50327623	50327623	Silent	SNP	G	C	G	IFRD2	c.C558G	p.A186A
XH_P43	3	52089926	52089962	Frame_Shift_Del	DEL	CCCGGGCTCG	-	CGCCGGGGCTCGG	DUSP7	c.421_457del	p.A141fs
XH_P43	3	52422952	52422952	Missense_Mutation	SNP	C	T	C	DNAH1	c.C9494T	p.T3165M
XH_P43	3	78663944	78663944	In_Frame_Ins	INS	-	TAT	-	ROBO1	3988_3989insA	R1330delinsHR
XH_P43	3	78663946	78663946	Frame_Shift_Ins	INS	-	AT	-	ROBO1	3986_3987insA	p.R1329fs
XH_P43	3	93595881	93595881	Missense_Mutation	SNP	A	C	A	PROS1	c.T1799G	p.L600R
XH_P43	3	96706748	96706748	Missense_Mutation	SNP	T	C	T	EPHA6	c.T1025C	p.L342P
XH_P43	3	107491556	107491556	Frame_Shift_Ins	INS	-	CAATTATATCTG	-	BBX	nsTTTTCAATTAT	p.E330fs
XH_P43	3	111688712	111688712	Frame_Shift_Ins	INS	-	CATCTATA	-	PHLDB2	2_3363insCATC	p.W1121fs
XH_P43	3	111688713	111688713	Frame_Shift_Ins	INS	-	CTAATTA	-	PHLDB2	63_3364insCTAA	p.W1121fs
XH_P43	3	113045448	113045448	Nonsense_Mutation	INS	-	GCATATGACTTA	-	CFAP44	360insTAAGAT	454_N1455delinsX
XH_P43	3	119379059	119379059	Missense_Mutation	SNP	C	A	C	POPD2	c.G212T	p.S71I
XH_P43	3	122134051	122134051	Silent	SNP	A	G	A	WDR5B	c.T325C	p.L109L
XH_P43	3	123688991	123688991	Missense_Mutation	SNP	G	A	G	ROPN1	c.C194T	p.P65L
XH_P43	3	126735436	126735436	Missense_Mutation	SNP	A	C	A	PLXNA1	c.A3091C	p.N1031H
XH_P43	3	128856021	128856021	Missense_Mutation	SNP	A	G	A	ISY1	c.T437C	p.M146T
XH_P43	3	133553479	133553479	Nonsense_Mutation	SNP	G	A	G	RAB6B	c.C502T	p.R168X
XH_P43	3	134911453	134911453	In_Frame_Ins	INS	-	TCTCATTTGTAAC	-	EPHB1	GTCTTCTCTCAT	40delinsQSSLIUTILL
XH_P43	3	134960062	134960062	Missense_Mutation	SNP	G	A	G	EPHB1	c.G2419A	p.V807I
XH_P43	3	135870841	135870841	Missense_Mutation	SNP	C	G	C	MSL2	c.G660C	p.L220F
XH_P43	3	136183801	136183801	Missense_Mutation	SNP	T	C	T	STAG1	c.A1235G	p.D412G
XH_P43	3	136183803	136183803	Frame_Shift_Ins	INS	-	GTATACATGGTG	-	STAG1	33insTTCACCAT	p.E411fs
XH_P43	3	142522994	142522994	Nonsense_Mutation	INS	-	CCTGTAAAGACA	-	TRPC1	832insACCTGTA	11_H612delinsHLX
XH_P43	3	142747362	142747362	Missense_Mutation	SNP	G	A	G	U2SURP	c.G257A	p.R86H
XH_P43	3	146239452	146239452	Missense_Mutation	SNP	A	G	A	PLSCR1	c.T617C	p.V206A
XH_P43	3	146239454	146239454	Nonsense_Mutation	INS	-	AGATGATTT	-	PLSCR1	4_615insAAATC	p.Y205delinsX
XH_P43	3	150421527	150421527	In_Frame_Ins	INS	-	CCTCCTCCTCCT	-	ERIC6	GAGGAGGAGG	53delinsEEEEEEEE
XH_P43	3	151163773	151163773	Nonsense_Mutation	INS	-	AGCAACATCAGT	-	IGSF10	8996insAACTGA	1332_E1333delinsX
XH_P43	3	151598857	151598857	Missense_Mutation	SNP	G	A	G	SUCNR1	c.G526A	p.A176T
XH_P43	3	153840760	153840760	Nonsense_Mutation	INS	-	AGATTTACTATT	-	ARHGEF26	nsGTTGGATTTA	D328delinsCWIVLFX
XH_P43	3	155198891	155198891	Missense_Mutation	SNP	G	A	G	PLCH1	c.C4924T	p.R1642W
XH_P43	3	156395703	156395703	Frame_Shift_Ins	INS	-	CATTTCCTAAT	-	TIPARP	18insCCATTTC	p.F73fs
XH_P43	3	168834129	168834129	Missense_Mutation	SNP	G	C	G	MECOM	c.C967G	p.P323A
XH_P43	3	169820389	169820389	Missense_Mutation	SNP	C	T	C	PHC3	c.G2675A	p.R892H
XH_P43	3	175293954	175293954	Silent	SNP	C	T	C	NAALADL2	c.C1779T	p.Y593Y
XH_P43	3	180377470	180377470	In_Frame_Ins	INS	-	TGTTAAAGTAG	-	CCDC39	4insAACTACTT	202delinsNYFTKA
XH_P43	3	180377472	180377472	Missense_Mutation	SNP	C	T	C	CCDC39	c.G602A	p.S201N
XH_P43	3	189526258	189526258	Silent	SNP	G	A	G	TP63	c.G240A	p.P80P
XH_P43	3	190573409	190573409	Missense_Mutation	SNP	G	A	G	GMNC	c.C680T	p.P227L
XH_P43	3	195509196	195509196	Missense_Mutation	SNP	G	C	G	MUC4	c.C9255G	p.H3085Q
XH_P43	4	436577	436577	Missense_Mutation	SNP	T	C	T	ZNF721	c.A1679G	p.E560G

XH_P43	4	437481	437481	Missense_Mutation	SNP	A	T	A	ZNF721	c.T775A	p.S259T
XH_P43	4	4419094	4419094	Missense_Mutation	SNP	T	G	T	NSG1	c.T490G	p.W164G
XH_P43	4	6863603	6863603	Silent	SNP	G	T	G	KIAA0232	c.G1494T	p.L498L
XH_P43	4	8271771	8271771	Frame_Shift_Del	DEL	C	-	C	HTRA3	c.76delC	p.P26fs
XH_P43	4	8271987	8272030	Frame_Shift_Del	DEL	5CAGGCGGCG	-	7GCAGGCGGCGCA	HTRA3	c.292_335del	p.A98fs
XH_P43	4	8451440	8451440	Frame_Shift_Del	DEL	A	-	A	TRMT44	c.S6delA	p.D19fs
XH_P43	4	10492148	10492148	Silent	SNP	C	T	C	CLNK	c.G1230A	p.R410R
XH_P43	4	10492149	10492149	Nonsense_Mutation	INS	-	ATTTCAAAGTT	-	CLNK	nsAAATAAACTT	R410delinsKINFX
XH_P43	4	13590395	13590395	Frame_Shift_Ins	INS	-	A	-	BOD1L1	c.8230_8231ins	p.D2744fs
XH_P43	4	13590396	13590396	In_Frame_Ins	INS	-	AGTCAGAATGG	-	BOD1L1	8230insACCATTT	D2744delinsTILTD
XH_P43	4	15575868	15575868	Silent	SNP	A	G	A	CC2D2A	c.A3690G	p.R1230R
XH_P43	4	22438160	22438160	Nonsense_Mutation	SNP	C	T	C	ADGRA3	c.G1190A	p.W397X
XH_P43	4	24839843	24839843	Missense_Mutation	SNP	C	T	C	CCDC149	c.G424A	p.V142M
XH_P43	4	39868503	39868503	Nonsense_Mutation	INS	-	TTGTATTATTTAA	-	PDSSA	20insTATTAAAAA	874_875delinsYX
XH_P43	4	42145575	42145575	Frame_Shift_Ins	INS	-	TTTCT	-	BEND4	923_924insAGA	p.S308fs
XH_P43	4	42145576	42145576	In_Frame_Ins	INS	-	TATGTGTATGT	-	BEND4	TATACACATAC	98delinsYYTTYTMST
XH_P43	4	48525064	48525064	Missense_Mutation	SNP	C	T	C	FRYL	c.G7375A	p.D2459N
XH_P43	4	48584726	48584726	Frame_Shift_Ins	INS	-	GTACCAGA	-	FRYL	3_1774insTCTG	p.L592fs
XH_P43	4	55593428	55593428	In_Frame_Ins	INS	-	ACATTGTAC	-	KIT	5_1586insACAT	p.F529delinsYIVL
XH_P43	4	55593430	55593430	Frame_Shift_Ins	INS	-	TT	-	KIT	.1587_1588insT	p.F529fs
XH_P43	4	57182477	57182477	Frame_Shift_Ins	INS	-	TTCTCTCT	-	KIAA1211	99_2810insTTCT	p.P937fs
XH_P43	4	57796632	57796632	In_Frame_Ins	INS	-	TCGAGTTCTGG	-	REST	609insTTTCGAG	9536delinsDFRVLV
XH_P43	4	68374654	68374654	Missense_Mutation	SNP	A	T	A	CENPC	c.T1782A	p.F594L
XH_P43	4	70146261	70146261	Missense_Mutation	SNP	G	A	G	UGT2B28	c.G43A	p.G15S
XH_P43	4	71698131	71698131	Nonsense_Mutation	INS	-	TTTCTAATATT	-	GRSF1	TCTATAAATATT	p.M74delinsNLX
XH_P43	4	81124307	81124309	In_Frame_Del	DEL	GCG	-	GCG	PRDM8	c.1691_1693del	p.S64_565del
XH_P43	4	85716106	85716106	Nonsense_Mutation	INS	-	TATATATAATTT	-	WDFY3	AACTCTAAATTA	1066delinsQKQINSKLYIIYX
XH_P43	4	85724611	85724611	Nonsense_Mutation	INS	-	TGAGTATGATTA	-	WDFY3	CTCATATAATCA	813_H814delinsX
XH_P43	4	88535211	88535211	Frame_Shift_Ins	INS	-	TTTGTTAATATT	-	DSPF	insCTTCTTTGGT	p.N466fs
XH_P43	4	96222837	96222837	Missense_Mutation	SNP	G	T	G	UNC5C	c.C410A	p.P137H
XH_P43	4	99966407	99966407	Missense_Mutation	SNP	G	A	G	METAP1	c.G733A	p.A245T
XH_P43	4	108622425	108622425	Frame_Shift_Ins	INS	-	TAGGCGTAAGCA	-	PAPSS1	instATGCTTACG	p.T26fs
XH_P43	4	113199106	113199106	Missense_Mutation	SNP	G	A	G	TIFA	c.C467T	p.P156L
XH_P43	4	114275990	114275990	Silent	SNP	C	A	C	ANK2	c.C6216A	p.S2072S
XH_P43	4	114275991	114275991	Frame_Shift_Ins	INS	-	TCCTCTCTGTT	-	ANK2	6218insTCTCT	p.L2073fs
XH_P43	4	114290876	114290876	Missense_Mutation	SNP	G	A	G	ANK2	c.G5270A	p.R1757Q
XH_P43	4	119219902	119219902	Missense_Mutation	SNP	C	T	C	PRSS12	c.G1823A	p.G608D
XH_P43	4	119256799	119256799	Nonsense_Mutation	INS	-	GAAAGTGCTCTA	-	PRSS12	ATAAATAAGAC	6217_1218delinsLX
XH_P43	4	123151130	123151130	Silent	SNP	G	A	G	KIAA1109	c.G3087A	p.S1029S
XH_P43	4	123179958	123179958	Frame_Shift_Ins	INS	-	TTGACAAATATT	-	KIAA1109	TATTCCTTGACA	p.S2241fs
XH_P43	4	125591483	125591483	Silent	SNP	A	G	A	ANKRD50	c.T2412C	p.L804L
XH_P43	4	128854242	128854242	Nonsense_Mutation	INS	-	AATCAGATTATG	-	MFS08	761insACATAAT	154_D255delinsNIIIX
XH_P43	4	146435902	146435902	Frame_Shift_Ins	INS	-	AGAGAGATTTC	-	SMAD1	ACAGCAGAAAGT	p.G46fs
XH_P43	4	147560458	147560469	In_Frame_Del	DEL	5CGGCGGCGG	-	5GCGGCGGCGGGA	POU4F2	c.166_177del	p.S6_59del
XH_P43	4	164247261	164247261	Nonsense_Mutation	INS	-	TTGTTTTATATT	-	NPY1R	saATAAAATATAA	149_P150delinsKX
XH_P43	4	166235300	166235300	Nonsense_Mutation	INS	-	TATATCATATTAT	-	KLHL2	GAGATTTTATATC	1365delinsKRFISYX
XH_P43	4	177632786	177632786	Missense_Mutation	SNP	G	C	G	VEGFC	c.C571G	p.P191A
XH_P43	4	185603415	185603415	Missense_Mutation	SNP	T	G	T	PRIMPOL	c.T496G	p.L166V
XH_P43	5	447798	447798	Missense_Mutation	SNP	G	A	G	EXOC3	c.G295A	p.V99I
XH_P43	5	5182420	5182420	Splice_Site	SNP	T	C	T	ADAMTS16	-	-
XH_P43	5	13769150	13769162	Frame_Shift_Del	DEL	7GTGCCACAA	-	5CTGTCCACAATC	DNAHS	c.9804_9816del	p.A3268fs
XH_P43	5	14406745	14406745	Nonsense_Mutation	INS	-	AAAATATAGTT	-	TRIO	24insATAAAAT	1641delinsAKVYSX
XH_P43	5	14461165	14461165	Silent	SNP	C	T	C	TRIO	c.C5241T	p.P1747P
XH_P43	5	23521272	23521272	Nonsense_Mutation	INS	-	AATTTCTTATAGT	-	PRDM9	3insGAATTTTCTT	64_S165delinsHEFLX
XH_P43	5	35065918	35065918	Missense_Mutation	SNP	T	A	T	PRLR	c.A839T	p.E280V
XH_P43	5	40681119	40681119	Frame_Shift_Ins	INS	-	CCTACTTTCTGG	-	PTGER4	insATCCTACTTT	p.S8fs
XH_P43	5	40853422	40853422	Frame_Shift_Ins	INS	-	ATTTGAGC	-	CARD6	8_1989insATT	p.N663fs
XH_P43	5	40853424	40853424	Missense_Mutation	SNP	A	T	A	CARD6	c.A1990T	p.T645S
XH_P43	5	41381971	41381971	Missense_Mutation	SNP	C	G	C	PLCXD3	c.G769C	p.V257L
XH_P43	5	43613100	43613100	Frame_Shift_Ins	INS	-	TGATGTT	-	NNT	42_243insTGAT	p.N81fs
XH_P43	5	43613102	43613102	Silent	SNP	T	C	T	NNT	c.T244C	p.L82L
XH_P43	5	54327310	54327310	Nonsense_Mutation	SNP	C	A	A	GZMK	c.C482A	p.S161X
XH_P43	5	56177849	56177854	In_Frame_Del	DEL	CAACAA	-	CAACAA	C	c.2822_2827del	p.941_943del
XH_P43	5	78671978	78671978	Missense_Mutation	SNP	C	G	C	HOMER1	c.G529C	p.D177H
XH_P43	5	79950724	79950724	In_Frame_Ins	INS	-	CCGCCGCGGC	-	MSH3	3_179insCCGCCG	A60delinsAAAA
XH_P43	5	94859466	94859466	Frame_Shift_Ins	INS	-	ATAAATGAAAT	-	TTC37	AAAAATATTTT	p.D509fs
XH_P43	5	112174620	112174620	Nonsense_Mutation	SNP	C	G	C	APC	c.C3275G	p.S1092X
XH_P43	5	112175951	112175951	Frame_Shift_Ins	INS	-	A	-	APC	c.4607dupA	p.E1536fs
XH_P43	5	112824048	112824048	Missense_Mutation	SNP	T	C	T	MCC	c.A64G	p.S22G
XH_P43	5	115238594	115238594	Missense_Mutation	SNP	C	A	C	AP3S1	c.C154A	p.L52I
XH_P43	5	122718538	122718538	Nonsense_Mutation	INS	-	TTTAATCTCTA	-	CEP120	1828insTAGAG	P610_C611delinsX
XH_P43	5	122718540	122718540	Frame_Shift_Ins	INS	-	TT	-	CEP120	1825_1826insA	p.A609fs
XH_P43	5	130764910	130764910	Splice_Site	SNP	C	G	C	RAPGEF6	-	-
XH_P43	5	135692506	135692506	Silent	SNP	G	A	G	TRPC7	c.C570T	p.I190I
XH_P43	5	139060444	139060444	Frame_Shift_Ins	INS	-	ATTGG	-	CXXC5	836_337insATTG	p.A112fs
XH_P43	5	139742029	139742029	Splice_Site	INS	-	TAAA	-	SLC4A9	-	-
XH_P43	5	139742030	139742030	Frame_Shift_Ins	INS	-	ACCC	-	SLC4A9	720_721insACC	p.R240fs
XH_P43	5	140053882	140053882	In_Frame_Ins	INS	-	5GTTATTTTATTG	-	HARS	ATAATCAATAAA	883delinsVIINKTIIK
XH_P43	5	140482016	140482016	Missense_Mutation	SNP	G	A	G	PCDHB3	c.G1783A	p.D595N
XH_P43	5	140763194	140763194	Frame_Shift_Ins	INS	-	TATTTTACATT	-	PCDHGA7	insCATTATTTT	p.S243fs
XH_P43	5	141041803	141041803	Silent	SNP	T	G	T	ARAP3	c.A2820C	p.V940V
XH_P43	5	145894881	145894881	Missense_Mutation	SNP	C	T	C	GPR151	c.G796A	p.E266K
XH_P43	5	148632392	148632392	Missense_Mutation	SNP	C	T	C	ABLM3	c.C1597T	p.R533C
XH_P43	5	149406316	149406316	Missense_Mutation	SNP	G	A	G	HMGXB3	c.G1508A	p.R503K
XH_P43	5	150413184	150413184	Silent	SNP	C	T	C	TNP1	c.G1605A	p.S535S
XH_P43	5	150885608	150885608	Missense_Mutation	SNP	G	A	G	FAT2	c.C12568T	p.R4190C
XH_P43	5	153054066	153054066	Missense_Mutation	SNP	A	G	A	GRIA1	c.A466G	p.M156V
XH_P43	5	153190634	153190634	Missense_Mutation	SNP	C	G	C	GRIA1	c.C2330G	p.S777W
XH_P43	5	154292518	154292518	Frame_Shift_Del	DEL	C	-	C	GEMIN5	c.1933delG	p.A645fs
XH_P43	5	156376669	156376682	Frame_Shift_Del	DEL	CAGCAGGAC	-	GTACAGCAGGACA	TIMD4	c.740_753del	p.T247fs
XH_P43	5	156479558	156479572	In_Frame_Del	DEL	GAACAGTCG	-	GGAACAGTCGT	HAVCR1	c.473_487del	p.L158_163del
XH_P43	5	157078575	157078575	Missense_Mutation	SNP	G	C	G	SOX30	c.C512G	p.P171R
XH_P43	5	167881085	167881085	Missense_Mutation	SNP	G	T	G	WWC1	c.G2638T	p.D880Y
XH_P43	5	169116272	169116272	Nonsense_Mutation	SNP	C	T	C	DOCK2	c.C778T	p.R260X
XH_P43	5	172750383	172750383	Silent	SNP	C	A	C	STC2	c.G345T	p.R115R
XH_P43	5	174938489	174938489	Missense_Mutation	SNP	G	T	G	SFXN1	c.G470T	p.S157V
XH_P43	5	176823786	176823786	Silent	SNP	C	T	C	SLC34A1	c.C1227T	p.G409G
XH_P43	5	177547473	177547473	Missense_Mutation	SNP	A	C	A	N4BP3	c.A625C	p.S209R

XH_P43	5	178418947	178418970	In_Frame_Del	DEL	CCAGTGCCT	-	TCCAGTGCCT	GRM6	c.619_642del	p.207_214del
XH_P43	6	7298173	7298173	In_Frame_Ins	INS	-	ACAGAGTCTTAC	-	SSR1	478insGTAAGAA	L160delinsVRLCL
XH_P43	6	26390390	26390390	Silent	SNP	G	A	G	BTN2A2	c.G252A	p.K84K
XH_P43	6	28270005	28270005	Frame_Shift_Ins	INS	-	ACACTTTTACTAT	-	PGBD1	ATCATACACTTT	p.F792fs
XH_P43	6	34574504	34574504	Frame_Shift_Ins	INS	-	A	-	C6orf106	c.490_491insT	p.P164fs
XH_P43	6	34574506	34574506	Frame_Shift_Ins	INS	-	AGGT	-	C6orf106	488_489insACC	p.D163fs
XH_P43	6	42162482	42162482	Frame_Shift_Ins	INS	-	STCTCTTCTCTTC	-	GUCA18	insGGAAGAGA	p.K26fs
XH_P43	6	42626555	42626555	Missense_Mutation	SNP	G	C	G	UBR2	c.G3235C	p.D1079H
XH_P43	6	47759569	47759569	Nonsense_Mutation	SNP	C	A	C	OPN5	c.C282A	p.C94X
XH_P43	6	47759571	47759571	Frame_Shift_Ins	INS	-	ACAGATTTCCTA	-	OPN5	5insACACAGATT	p.F95fs
XH_P43	6	52661078	52661078	Silent	SNP	A	C	A	GSTA1	c.T174G	p.V58V
XH_P43	6	56394321	56394321	Silent	SNP	C	T	C	DST	c.G9651A	p.V3217V
XH_P43	6	56505023	56505023	Missense_Mutation	SNP	G	C	G	DST	c.C797G	p.S266C
XH_P43	6	70098725	70098725	In_Frame_Ins	INS	-	AATAGTTTT	-	ADGRB3	1_4512insAATA	E1504delinsEIVL
XH_P43	6	70098727	70098727	Frame_Shift_Ins	INS	-	TTTT	-	ADGRB3	4513_4514insTT	p.K1505fs
XH_P43	6	71665561	71665561	Missense_Mutation	SNP	C	G	C	B3GAT2	c.G572C	p.S191T
XH_P43	6	74354251	74354251	Missense_Mutation	SNP	C	T	C	SLC17A5	c.G170A	p.R57H
XH_P43	6	75861640	75861640	Missense_Mutation	SNP	C	T	C	COL12A1	c.G451A	p.D151N
XH_P43	6	75904568	75904568	Frame_Shift_Ins	INS	-	TGTTATTGAGTT	-	COL12A1	TGTTAAACTCAA	p.I57fs
XH_P43	6	76744431	76744440	Frame_Shift_Del	DEL	GTCCTGATA	-	GTCCTGATAT	IMP61	c.132_141del	p.E44fs
XH_P43	6	78173072	78173072	Frame_Shift_Ins	INS	-	CAAT	-	HTR1B	c.48_49insATTG	p.E17fs
XH_P43	6	78173073	78173073	Frame_Shift_Ins	INS	-	CCTTTGT	-	HTR1B	7_48insACAA	p.S16fs
XH_P43	6	88126526	88126526	In_Frame_Ins	INS	-	AAACAAAAT	-	CFAP206	2_613insAAACA	G204delinsGKON
XH_P43	6	88126527	88126527	In_Frame_Ins	INS	-	ATA	-	CFAP206	613_614insAT	p.G205delinsDR
XH_P43	6	89793782	89793782	Frame_Shift_Ins	INS	-	A	-	PNRC1	c.851_852insA	p.F284fs
XH_P43	6	89793784	89793784	Frame_Shift_Ins	INS	-	TTCTGTCTGTTT	-	PNRC1	TGCTTTTCTGTC	p.S285fs
XH_P43	6	90340611	90340611	Missense_Mutation	SNP	G	A	G	ANKRD6	c.G1880A	p.R627Q
XH_P43	6	90410477	90410477	In_Frame_Ins	INS	-	GATTTTCTTTTC	-	MDN1	sCCCAGAAAAG	842delinsHPKKNLNR
XH_P43	6	90422329	90422329	Frame_Shift_Ins	INS	-	ATTATTTAAT	-	MDN1	7395insAATAA	p.L245fs
XH_P43	6	90422331	90422331	Nonsense_Mutation	INS	-	GATGTTTTTA	-	MDN1	7393insTAAAA	465_N246delinsX
XH_P43	6	102503416	102503416	In_Frame_Ins	INS	-	GAAAAGAGAGG	-	GRIK2	sCCTAAGAAAAC	41delinsEPKKREVMM
XH_P43	6	121577425	121577425	Silent	SNP	T	G	T	TBC1D32	c.A1740C	p.T580T
XH_P43	6	131915465	131915465	In_Frame_Ins	INS	-	ATATCCTTTTTAT	-	MED23	nsCACAAATAAAA	1002delinsVTIKRILS
XH_P43	6	131915467	131915467	Missense_Mutation	SNP	C	T	C	MED23	c.G3004A	p.V1002M
XH_P43	6	132270606	132270606	Missense_Mutation	SNP	A	T	A	CTG3	c.T848A	p.F283Y
XH_P43	6	136582430	136582430	Frame_Shift_Ins	INS	-	AATTTTTTCTCTC	-	BCLAF1	577insGAGAGA	p.E859fs
XH_P43	6	152565769	152565769	Nonsense_Mutation	INS	-	TAGAAAAAAT	-	SYNE1	1_19382insATT	61_L6462delinsDFFX
XH_P43	6	152565771	152565771	Frame_Shift_Ins	INS	-	CTTTATT	-	SYNE1	79_19380insAA	p.D6460fs
XH_P43	6	152651648	152651648	Silent	SNP	C	T	C	SYNE1	c.G13959A	p.A4653A
XH_P43	6	152711507	152711507	Missense_Mutation	SNP	G	T	G	SYNE1	c.C8106A	p.S2702R
XH_P43	6	152711508	152711508	Frame_Shift_Ins	INS	-	TGTGTCT	-	SYNE1	4_8105insAGAA	p.S2702fs
XH_P43	6	152765647	152765647	Missense_Mutation	SNP	C	T	C	SYNE1	c.G3757A	p.E1253K
XH_P43	7	1132250	1132250	Nonsense_Mutation	SNP	C	T	C	GPFR1	c.C886T	p.Q296X
XH_P43	7	12409717	12409717	In_Frame_Ins	INS	-	AGAGATTAGACA	-	VWDE	1870insTGCTA	S624delinsCLIS
XH_P43	7	20825146	20825172	In_Frame_Del	DEL	GGCTGCTGCC	-	GGCTGCTGCCG	SP8	c.264_290del	p.88_97del
XH_P43	7	21646154	21646154	Missense_Mutation	SNP	G	T	G	DNAH11	c.G3759T	p.L1253F
XH_P43	7	21658797	21658797	Missense_Mutation	SNP	G	A	G	DNAH11	c.G4334A	p.R1445Q
XH_P43	7	25266558	25266558	In_Frame_Ins	INS	-	ATGCTGAGTGAT	-	NPVF	226insATCACTC	P76delinsITQHP
XH_P43	7	40133929	40133929	Missense_Mutation	SNP	G	A	G	CDK13	c.G3889A	p.G1297R
XH_P43	7	44047000	44047000	Missense_Mutation	SNP	C	T	C	SPDY1	c.C766T	p.P256S
XH_P43	7	44611308	44611308	Silent	SNP	G	A	G	DDX56	c.C673T	p.L225L
XH_P43	7	44611309	44611309	Frame_Shift_Ins	INS	-	ATCT	-	DDX56	671_672insAGA	p.Q224fs
XH_P43	7	45688277	45688277	Missense_Mutation	SNP	C	A	C	ADCY1	c.C1029A	p.H343Q
XH_P43	7	48259015	48259015	In_Frame_Ins	INS	-	AATCATTAT	-	ABCA13	2_353insAATCA	p.I118delinsKSLL
XH_P43	7	57528754	57528754	In_Frame_Ins	INS	-	ATCTTCTCA	-	ZNF716	7_588insATCTTC	M196delinsSSQ
XH_P43	7	57528755	57528755	Frame_Shift_Ins	INS	-	TATCA	-	ZNF716	588_589insTAT	p.M196fs
XH_P43	7	64864248	64864248	Missense_Mutation	SNP	A	C	A	ZNF92	c.A993C	p.K331N
XH_P43	7	84636181	84636181	Silent	SNP	A	G	A	SEMA3D	c.T1845C	p.P615P
XH_P43	7	86813934	86813934	Missense_Mutation	SNP	A	C	A	DMTF1	c.A778C	p.I260L
XH_P43	7	87537395	87537395	Missense_Mutation	SNP	G	T	G	DBF4	c.G1243T	p.D415Y
XH_P43	7	88963540	88963540	Frame_Shift_Ins	INS	-	ATGGAGATGGT	-	ZNF804B	insGTTTATGGAA	p.D415fs
XH_P43	7	91670082	91670082	Missense_Mutation	SNP	G	A	G	AKAP9	c.G4784A	p.R1596Q
XH_P43	7	94028370	94028370	Missense_Mutation	SNP	G	A	G	COL1A2	c.G106A	p.G36R
XH_P43	7	95739378	95739378	Missense_Mutation	SNP	A	G	A	DYNC11	c.A1804G	p.7602A
XH_P43	7	96747146	96747146	Silent	SNP	C	T	C	SDHAF3	c.C111T	p.D37D
XH_P43	7	98649918	98649918	Missense_Mutation	SNP	G	A	G	SMURF1	c.C631T	p.R211W
XH_P43	7	99171042	99171042	Frame_Shift_Ins	INS	-	TTCT	-	ZNF655	311_1312insTT	p.E437fs
XH_P43	7	99171044	99171044	Frame_Shift_Ins	INS	-	TTGTTTAATA	-	ZNF655	1314insTTGTT	p.C438fs
XH_P43	7	99705122	99705122	In_Frame_Ins	INS	-	CCTTTG	-	TA6F	91_1892insCAAB	S631delinsTKG
XH_P43	7	100678230	100678230	Missense_Mutation	SNP	A	G	A	MUC17	c.A3533G	p.N1178S
XH_P43	7	100679374	100679374	Missense_Mutation	SNP	C	A	C	MUC17	c.C4677A	p.D1559E
XH_P43	7	100682351	100682351	Missense_Mutation	SNP	A	G	A	MUC17	c.A7654G	p.I2552V
XH_P43	7	107571837	107571837	Silent	SNP	T	G	T	LAMB1	c.A4501C	p.R1501R
XH_P43	7	107577674	107577674	In_Frame_Ins	INS	-	GGA	-	LAMB1	3809_3810insTG	K1270delinsNP
XH_P43	7	107577675	107577675	Nonsense_Mutation	INS	-	TTAACGATATG	-	LAMB1	3809insCATATG	70_L1271delinsTYRX
XH_P43	7	111387455	111387455	Frame_Shift_Ins	INS	-	GGTTTCATGAAT	-	DOCK4	434insGATTCAAT	p.N1478fs
XH_P43	7	111400375	111400375	Nonsense_Mutation	INS	-	TGAATAGAACTT	-	DOCK4	997insTAAGTTCT	333_E1334delinsX
XH_P43	7	111644163	111644163	Missense_Mutation	SNP	C	A	C	DOCK4	c.G61T	p.V21F
XH_P43	7	111644165	111644165	Nonsense_Mutation	INS	-	ATTTTAAAGCTGA	-	DOCK4	TAATCAGCTTAA	720_V21delinsLIIX
XH_P43	7	117243663	117243663	Missense_Mutation	SNP	C	T	C	CFTR	c.C2735T	p.S912L
XH_P43	7	119915032	119915032	Missense_Mutation	SNP	G	A	G	KCN2D	c.G346A	p.D116N
XH_P43	7	127528040	127528040	Missense_Mutation	SNP	G	A	G	SDN1	c.G1429A	p.D477N
XH_P43	7	128415040	128415040	Missense_Mutation	SNP	C	T	C	OPN1SW	c.G521A	p.R174Q
XH_P43	7	138969128	138969128	Frame_Shift_Ins	INS	-	GATACAGT	-	UBN2	7_3478insGATA	p.G1159fs
XH_P43	7	138969130	138969130	Missense_Mutation	SNP	A	G	A	UBN2	c.A3479G	p.K1160R
XH_P43	7	141643752	141643752	In_Frame_Ins	INS	-	TTCTTATGG	-	CLEC5A	1_152insCCATAA	p.F51delinsSRI
XH_P43	7	143956137	143956137	Frame_Shift_Ins	INS	-	AATCCCCCTTA	-	OR2A7	585insTAAGGG	p.E195fs
XH_P43	7	150325467	150325467	Missense_Mutation	SNP	T	A	T	GIMAP6	c.A429T	p.R143S
XH_P43	7	150654543	150654543	Missense_Mutation	SNP	A	G	A	KCNH2	c.T964C	p.S322P
XH_P43	7	150654544	150654544	Missense_Mutation	SNP	G	C	G	KCNH2	c.C963G	p.D321E
XH_P43	7	151680085	151680085	Frame_Shift_Ins	INS	-	AAATTTATTTAA	-	GALNTL5	nsCAAAAATTTA	p.H128fs
XH_P43	7	158534471	158534471	Frame_Shift_Ins	INS	-	AGGCCTCGGCG	-	ESY2	92insCATCGCCG	p.G664fs
XH_P43	8	28385465	28385465	Silent	SNP	C	A	C	FZD3	c.C1188A	p.S396S
XH_P43	8	35425698	35425698	Silent	SNP	G	A	G	UNC5D	c.G390A	p.Q130Q
XH_P43	8	35425699	35425699	Missense_Mutation	SNP	T	G	T	UNC5D	c.T391G	p.C131G
XH_P43	8	36780071	36780071	Missense_Mutation	SNP	C	A	C	KCNU1	c.C2660A	p.T887K
XH_P43	8	37728030	37728030	Nonsense_Mutation	INS	-	ATAATTA	-	RAB11FIP1	38_1639insTAA	547_M548delinsX
XH_P43	8	37728032	37728032	Nonsense_Mutation	INS	-	CCTTACTACTGTT	-	RAB11FIP1	AACTAAACAAGT	6_P547delinsITQVX

XH_P43	8	42720633	42720633	Splice_Site	INS	-	TATTATTATTAT	-	RNF170	-	-	-
XH_P43	8	53062428	53062428	Frame_Shift_Ins	INS	-	AAGAGGTATTG	-	ST18	1916insACAATA	p.T639fs	-
XH_P43	8	53568744	53568744	Nonsense_Mutation	INS	-	TATAAAATTAAM	-	RB1CC1	5insTATTTTAAT	R15_R121delinsDILUX	-
XH_P43	8	53568746	53568746	In_Frame_Ins	INS	-	AGTGATTCG	-	RB1CC1	2_3643insCGAA	D1215delinsRITD	-
XH_P43	8	66539568	66539568	Silent	SNP	C	G	C	ARMC1	c.G66C	p.R22R	-
XH_P43	8	66695068	66695068	Missense_Mutation	SNP	G	A	G	PDE7A	c.C149T	p.A50V	-
XH_P43	8	66695069	66695069	Nonsense_Mutation	INS	-	TCATGGAGTTTA	-	PDE7A	nsCTCTAAACTCC	A50_I51delinsLX	-
XH_P43	8	77690663	77690663	Missense_Mutation	SNP	C	A	C	ZFH4	c.C3313A	p.P110ST	-
XH_P43	8	87549843	87549843	Nonsense_Mutation	INS	-	CTAACTCTATAG	-	CPNE3	insAGTCTTAACCT	D171delinsEVX	-
XH_P43	8	94746720	94746720	Missense_Mutation	SNP	G	T	G	RBM12B	c.C1919A	p.T640K	-
XH_P43	8	95186404	95186404	Missense_Mutation	SNP	T	C	T	CDH17	c.A509G	p.Q170R	-
XH_P43	8	102701604	102701604	Missense_Mutation	SNP	C	T	C	NCALD	c.G515A	p.G172E	-
XH_P43	8	102701605	102701605	Frame_Shift_Ins	INS	-	TTTTG	-	NCALD	513_514insCAA	p.G172fs	-
XH_P43	8	126448435	126448435	Nonsense_Mutation	SNP	C	T	C	TRIB1	c.C343T	p.R115X	-
XH_P43	8	142367220	142367220	Silent	SNP	G	A	G	GPR20	c.C804T	p.P268P	-
XH_P43	8	145577673	145577673	Missense_Mutation	SNP	C	T	C	TMEM249	c.G383A	p.R128H	-
XH_P43	9	990882	990896	In_Frame_Del	DEL	CTCGGATTC	-	CTCGGATTCCTCA	DMRT3	c.1296_1310del	p.432_437del	-
XH_P43	9	5300378	5300378	Missense_Mutation	SNP	T	G	T	RLN2	c.A23C	p.N8T	-
XH_P43	9	8449792	8449792	Frame_Shift_Ins	INS	-	TT	-	PTPRD	2657_2658insA	p.N886fs	-
XH_P43	9	8449813	8449813	Frame_Shift_Ins	INS	-	TTACTATTATGG	-	PTPRD	insTCTCCATAAT	p.R879fs	-
XH_P43	9	12702360	12702360	Nonsense_Mutation	INS	-	TTT	-	TYRP1	1003_1004insT	p.Q335delinsLX	-
XH_P43	9	12702361	12702361	In_Frame_Ins	INS	-	ATAGCATGAAT	-	TYRP1	TTATACATAGCA	delinsQNFIHSMNMKYR	-
XH_P43	9	21305070	21305070	Silent	SNP	A	G	A	IFNA5	c.T186C	p.P62P	-
XH_P43	9	33395216	33395216	Missense_Mutation	SNP	T	G	T	AQP7	c.A1C	p.M1L	-
XH_P43	9	33541216	33541216	Missense_Mutation	SNP	G	C	G	ANKRD18B	c.G880C	p.G294R	-
XH_P43	9	37948674	37948674	Missense_Mutation	SNP	C	T	C	SHB	c.G1304A	p.R435Q	-
XH_P43	9	38578116	38578116	In_Frame_Ins	INS	-	TGGAAAAAGAT	-	ANKRD18A	277insATATCTT	A759delinsAVLFPY	-
XH_P43	9	38601182	38601182	Frame_Shift_Ins	INS	-	A	-	ANKRD18A	c.881dupT	p.V294fs	-
XH_P43	9	38601184	38601184	In_Frame_Ins	INS	-	CATAATTTTCATA	-	ANKRD18A	stTCAATATGAA	94delinsFNMKLCV	-
XH_P43	9	74674269	74674269	Silent	SNP	G	A	G	C9orf57	c.C45T	p.L15L	-
XH_P43	9	75435918	75435925	Frame_Shift_Del	DEL	CTCATCTCT	-	CTCATCTCT	TMC1	c.1924_1931del	p.L642fs	-
XH_P43	9	75545867	75545867	Missense_Mutation	SNP	C	A	C	ALDH1A1	c.G240T	p.M80I	-
XH_P43	9	77354811	77354811	Missense_Mutation	SNP	C	T	C	TRPM6	c.G5300A	p.R1767Q	-
XH_P43	9	88247699	88247699	Missense_Mutation	SNP	A	C	A	AGTPBP1	c.T2049G	p.I683M	-
XH_P43	9	98734848	98734848	Nonsense_Mutation	INS	-	CTTTTGGATTTA	-	ERCC6L2	GCCTTTCTTTTG	R951delinsNMLFFWIX	-
XH_P43	9	106896830	106896830	Missense_Mutation	SNP	C	A	C	SMC2	c.C3243A	p.N1081K	-
XH_P43	9	106896831	106896831	Missense_Mutation	SNP	C	A	C	SMC2	c.C3244A	p.L1082I	-
XH_P43	9	112020470	112020470	Missense_Mutation	SNP	A	G	A	EPB41L4B	c.T739C	p.W247R	-
XH_P43	9	112918685	112918685	Missense_Mutation	SNP	G	A	G	AKAP2	c.G2656A	p.G886R	-
XH_P43	9	123476543	123476551	In_Frame_Del	DEL	CGCGCGCGG	-	CGCGCGCGG	MEGF9	c.86_94del	p.29_32del	-
XH_P43	9	123935712	123935712	Nonsense_Mutation	INS	-	TGATTTTTCAGA	-	CNTRL	4954insTGATT	651_K1652delinsLX	-
XH_P43	9	125512494	125512494	Missense_Mutation	SNP	G	A	G	OR1L6	c.C368A	p.R123Q	-
XH_P43	9	131708608	131708608	Silent	SNP	G	A	G	DOLK	c.C975T	p.S325S	-
XH_P43	9	136597690	136597690	Missense_Mutation	SNP	T	A	T	SARDH	c.A365T	p.E122V	-
XH_P43	9	140140167	140140167	Silent	SNP	A	T	A	FAM166A	c.T195A	p.I65I	-
XH_P43	9	140140169	140140169	Missense_Mutation	SNP	T	A	T	FAM166A	c.A193T	p.I65F	-
XH_P43	9	140261078	140261078	Missense_Mutation	SNP	T	A	T	EXD3	c.A523T	p.I175F	-
XH_P43	10	6148182	6148182	Missense_Mutation	SNP	G	C	G	RBM17	c.G486C	p.E162D	-
XH_P43	10	7618752	7618752	Missense_Mutation	SNP	G	A	G	ITIH5	c.C1000T	p.R334W	-
XH_P43	10	15658534	15658534	Missense_Mutation	SNP	G	T	G	ITGA8	c.C1379A	p.T460K	-
XH_P43	10	15658535	15658535	Frame_Shift_Ins	INS	-	GCATTTTTCAC	-	ITGA8	1378insGTAA	p.T460fs	-
XH_P43	10	33068012	33068012	Missense_Mutation	SNP	G	A	G	CCDC7	c.G3013A	p.E1005K	-
XH_P43	10	35333790	35333790	Silent	SNP	A	G	A	CUL2	c.T324C	p.R108R	-
XH_P43	10	45478054	45478054	Missense_Mutation	SNP	G	A	G	RASSF4	c.G224A	p.R75Q	-
XH_P43	10	50122025	50122025	Missense_Mutation	SNP	C	T	C	LRRC18	c.G176A	p.R59Q	-
XH_P43	10	51769004	51769004	Frame_Shift_Ins	INS	-	GTATTTCCT	-	AGAP6	9_1120insGTAT	p.D373fs	-
XH_P43	10	60560808	60560808	Splice_Site	INS	-	TG	-	BICC1	-	-	-
XH_P43	10	61836206	61836206	Frame_Shift_Ins	INS	-	ATCAATATGGT	-	ANK3	4433insACCAT	p.I1478fs	-
XH_P43	10	64968934	64968934	Nonsense_Mutation	SNP	A	C	A	JMJD1C	c.T2099G	p.L700X	-
XH_P43	10	70509434	70509434	Frame_Shift_Ins	INS	-	AAAA	-	CCAR1	065_106insAA	p.S355fs	-
XH_P43	10	70509435	70509435	In_Frame_Ins	INS	-	ACTAATATTCTA	-	CCAR1	067insTACTAAT	L356delinsLULI	-
XH_P43	10	73857142	73857142	Missense_Mutation	SNP	C	T	C	ASCC1	c.G1024A	p.V342I	-
XH_P43	10	77807000	77807000	Missense_Mutation	SNP	G	A	G	LRMDA	c.G253A	p.V85M	-
XH_P43	10	81061895	81061895	Missense_Mutation	SNP	G	A	G	ZMIZ1	c.G2051A	p.P684Q	-
XH_P43	10	87628910	87628910	Missense_Mutation	SNP	G	C	G	GRID1	c.C808G	p.L270V	-
XH_P43	10	91498109	91498109	Frame_Shift_Ins	INS	-	TTGTTTTCATCC	-	KIF20B	insTCTATTGTTT	p.E1171fs	-
XH_P43	10	103920516	103920516	In_Frame_Ins	INS	-	TGGCTT	-	NOLC1	37_1438insTGG	S479delinsSWL	-
XH_P43	10	104230572	104230582	Frame_Shift_Del	DEL	GATGGCTTC	-	TGATGGCTTC	MFS13A	c.402_412del	p.Y134fs	-
XH_P43	10	105344801	105344801	Silent	SNP	G	A	G	NEURL1	c.G1158A	p.V386V	-
XH_P43	10	105762627	105762627	Frame_Shift_Ins	INS	-	TTTGCTCTTTTT	-	SLK	1692insTTTGCC	p.D564fs	-
XH_P43	10	105762741	105762741	Frame_Shift_Ins	INS	-	CACATCACCTTG	-	SLK	1806insCACAT	p.I602fs	-
XH_P43	10	108339147	108339147	Silent	SNP	G	A	G	SORCS1	c.C3351T	p.F1117F	-
XH_P43	10	115978190	115978190	Missense_Mutation	SNP	C	T	C	TDRD1	c.C2341T	p.R781C	-
XH_P43	10	116201544	116201544	In_Frame_Ins	INS	-	ATTTTAACCTCC	-	ABLIM1	3insAGGGAGG	T221delinsAGRLKF	-
XH_P43	10	116201546	116201546	Splice_Site	SNP	C	G	C	ABLIM1	-	-	-
XH_P43	10	118689512	118689512	Nonsense_Mutation	INS	-	ATTACTCATG	-	SHTN1	680insCATGAG	227_K228delinsAX	-
XH_P43	10	119044825	119044825	Silent	SNP	T	G	T	PDZD8	c.A1419C	p.S473S	-
XH_P43	10	121691665	121691665	Missense_Mutation	SNP	C	T	C	SEC23IP	c.C2593T	p.R865C	-
XH_P43	10	123843656	123843656	Silent	SNP	G	A	G	TACC2	c.G1641A	p.P547P	-
XH_P43	10	124273779	124273779	Silent	SNP	C	T	C	HTRA1	c.C1347T	p.S449S	-
XH_P43	10	124697270	124697270	Missense_Mutation	SNP	C	T	C	C10orf88	c.G1054A	p.E352K	-
XH_P43	10	126138461	126138461	Missense_Mutation	SNP	T	C	T	NKX1-2	c.A52G	p.I18V	-
XH_P43	10	129905363	129905363	Missense_Mutation	SNP	T	C	T	MKI67	c.A3661G	p.K1221E	-
XH_P43	10	129905515	129905515	Missense_Mutation	SNP	C	T	C	MKI67	c.G3509A	p.R1170Q	-
XH_P43	10	129906976	129906976	In_Frame_Ins	INS	-	5GAATGAAGAA	-	MKI67	2048insCTTCTT	K683delinsTSSFQ	-
XH_P43	10	129914032	129914032	Missense_Mutation	SNP	G	A	G	MKI67	c.C640T	p.R214C	-
XH_P43	11	1265450	1265450	Missense_Mutation	SNP	A	C	A	MUC5B	c.A7340C	p.E2447A	-
XH_P43	11	1265451	1265451	Silent	SNP	G	A	A	MUC5B	c.G7341A	p.E2447A	-
XH_P43	11	6190877	6190877	In_Frame_Ins	INS	-	TGT	-	OR52B2	c.679_680insAC	p.V227delinsDM	-
XH_P43	11	6190878	6190878	Frame_Shift_Ins	INS	-	CATATCT	-	OR52B2	78_679insAGAT	p.V227fs	-
XH_P43	11	6243730	6243730	In_Frame_Ins	INS	-	CTTCTTTTGCTT	-	FAM160A2	133insAGGCAAR	378delinsQAKEG	-
XH_P43	11	6340722	6340722	Silent	SNP	G	A	G	CAVIN3	c.C457T	p.L153L	-
XH_P43	11	6587042	6587042	In_Frame_Ins	INS	-	GCTCTTCTT	-	DNHD1	4_10875insGCT	E3625delinsELFL	-
XH_P43	11	6587044	6587044	Missense_Mutation	SNP	A	G	A	DNHD1	c.A10876G	p.R3626G	-
XH_P43	11	6623244	6623244	Missense_Mutation	SNP	G	A	G	RRP8	c.C301T	p.P101S	-
XH_P43	11	7686733	7686733	Frame_Shift_Ins	INS	-	AG	-	CYBSR2	c.702_703insCT	p.E235fs	-
XH_P43	11	7686734	7686734	Frame_Shift_Ins	INS	-	AA	-	CYBSR2	c.701_702insTT	p.K234fs	-
XH_P43	11	12951874	12951874	Splice_Site	SNP	G	C	G	TEAD1	-	-	-

XH_P43	11	15726805	15726805	In_Frame_Ins	INS	-	CACATTCTAAAG	-	LOC102724957	8insTCACATTC	5106delinsSHILKY
XH_P43	11	33360981	33360981	In_Frame_Ins	INS	-	AAGTCACAGAG	-	HIPK3	1515insAAGTCA	MS05delinsISHRE
XH_P43	11	45952726	45952726	Frame_Shift_Ins	INS	-	TTAACGTGATTA	-	PHF21A	696insTTAATCA	p.K566fs
XH_P43	11	51412011	51412011	Frame_Shift_Ins	INS	-	GAGCAAT	-	OR4A5	84_385insATTG	p.L129fs
XH_P43	11	55655604	55655604	Nonsense_Mutation	SNP	C	T	C	TRIM51	c.C604T	p.R202X
XH_P43	11	57093913	57093913	Frame_Shift_Ins	INS	-	ACAT	-	SSRP1	097_2098insAT	p.S700fs
XH_P43	11	57093915	57093915	Frame_Shift_Ins	INS	-	TCTCCTGT	-	SSRP1	5_2096insACAG	p.S699fs
XH_P43	11	57971509	57971509	Frame_Shift_Ins	INS	-	TGGTGAAAT	-	OR152	4_145insATTCA	p.V49fs
XH_P43	11	59189907	59189907	Frame_Shift_Ins	INS	-	CTCTATGGTTAA	-	OR5A2	20insGTAACCA	p.M174fs
XH_P43	11	59245190	59245190	Frame_Shift_Ins	INS	-	CCTCTTTA	-	OR4D10	88_289insCCTCT	p.H96fs
XH_P43	11	59626550	59626550	Missense_Mutation	SNP	C	G	C	TCN1	c.G747C	p.Q249H
XH_P43	11	60470907	60470907	Silent	SNP	G	A	G	MS4A8	c.G276A	p.T92T
XH_P43	11	62287783	62287783	Silent	SNP	C	T	C	AHNAK	c.G14106A	p.A4702A
XH_P43	11	62287963	62287963	Silent	SNP	G	A	G	AHNAK	c.C13926T	p.D4642D
XH_P43	11	62294964	62294964	Missense_Mutation	SNP	T	C	T	AHNAK	c.A6925G	p.T2309A
XH_P43	11	62295474	62295474	Missense_Mutation	SNP	A	C	A	AHNAK	c.T6415G	p.L2139V
XH_P43	11	62295475	62295475	Silent	SNP	A	C	A	AHNAK	c.T6414G	p.S2138S
XH_P43	11	66296856	66296856	Silent	SNP	G	T	G	ZDHHC24	c.C663A	p.R221R
XH_P43	11	66411364	66411384	In_Frame_Del	DEL	GCTGCAGCA	-	TGCTGCAGCAG	RBM14-RBM4	c.781_801del	p.261_267del
XH_P43	11	66482734	66482734	Missense_Mutation	SNP	G	C	G	SPTN2	c.C442G	p.L148V
XH_P43	11	67254524	67254524	Silent	SNP	G	A	G	AIP	c.G147A	p.V49V
XH_P43	11	68029953	68029953	In_Frame_Ins	INS	-	CAGCCT	-	C11orf24	09_510insAGGC	T170delinsTGW
XH_P43	11	71238675	71238675	In_Frame_Ins	INS	-	GTCAGATGCTG	-	KRTAP5-7	TGCCAGTCCAG	delinsSCCQSRCCNP
XH_P43	11	73824935	73824935	Nonsense_Mutation	INS	-	TTCTAATTACTG	-	C2CD3	CAAATGAGTAA	78delinsKSQMSNX
XH_P43	11	74717292	74717292	Missense_Mutation	SNP	A	C	A	NEU3	c.A1141C	p.N381H
XH_P43	11	77910752	77910752	Silent	SNP	G	A	G	USP35	c.G918A	p.S306S
XH_P43	11	100909962	100909962	Frame_Shift_Ins	INS	-	T	-	PGR	c.1888dupA	p.1630fs
XH_P43	11	100909964	100909964	Nonsense_Mutation	INS	-	GGCTTTGAGTTT	-	PGR	insATAAAAACTC	629_1630delinsLX
XH_P43	11	101833918	101833918	In_Frame_Ins	INS	-	TGAATGACT	-	CEP126	2_2153insTGAA	G718delinsVND
XH_P43	11	101833920	101833920	Frame_Shift_Ins	INS	-	TCAGCATTGTTT	-	CEP126	55insTTTTCAGCA	p.G718fs
XH_P43	11	101834168	101834168	Frame_Shift_Ins	INS	-	CTTAGTTTTAGAV	-	CEP126	2403insCTTAGT	p.C801fs
XH_P43	11	103048478	103048478	Frame_Shift_Ins	INS	-	T	-	DYNC2H1	c.6068_6069ins	p.D2023fs
XH_P43	11	103048479	103048479	Nonsense_Mutation	INS	-	AATATGTTCATA	-	DYNC2H1	5AAAGAAATATG	023_M2024delinsDX
XH_P43	11	105880453	105880453	Nonsense_Mutation	SNP	C	A	C	MSANTD4	c.G847T	p.G283X
XH_P43	11	105880454	105880454	Nonsense_Mutation	INS	-	TCAGGTGATATA	-	MSANTD4	46insTTATATCAB2	G283delinsHYITX
XH_P43	11	111625799	111625799	Frame_Shift_Ins	INS	-	GTGGAAATGTTA	-	PPP2R1B	nsAATGTAACAT	p.P161fs
XH_P43	11	116636107	116636107	Missense_Mutation	SNP	C	T	C	BUD13	c.G293A	p.R98H
XH_P43	11	116741066	116741066	Frame_Shift_Ins	INS	-	CCTCGCTTCATA	-	SIK3	645insTATGAAC	p.D549fs
XH_P43	11	118352691	118352691	In_Frame_Ins	INS	-	TTTGCTGTCTTT	-	KMT2A	3897insTTTGCT	S1299delinsSLSF
XH_P43	11	120744909	120744923	In_Frame_Del	DEL	GAACTACCT	-	ATGAACTACCTG	GRIK4	c.1041_1055del	p.347_352del
XH_P43	11	120957678	120957678	Frame_Shift_Ins	INS	-	CTTTAAAAAA	-	TBCEL	c.1149insCTTTA	p.M383fs
XH_P43	11	120957679	120957679	Missense_Mutation	SNP	G	T	G	TBCEL	c.G1149T	p.M383I
XH_P43	11	124095538	124095538	Nonsense_Mutation	INS	-	GACCTTTGGTTT	-	OR8G2P	TAGATGACCTTT	N47_148delinsMIX
XH_P43	12	6122690	6122690	Frame_Shift_Ins	INS	-	CATAAGATT	-	VWF	5577insAAATC	p.T1859fs
XH_P43	12	9089483	9089483	Silent	SNP	C	T	C	PHC1	c.C2400T	p.C800C
XH_P43	12	10762506	10762506	In_Frame_Ins	INS	-	TTAATTTTAA	-	MAGOHB	9_50insTAAAT	p.K17delinsIKLK
XH_P43	12	10762508	10762508	Frame_Shift_Ins	INS	-	TCTT	-	MAGOHB	c.47_48insAAGA	p.L16fs
XH_P43	12	11149642	11149642	Missense_Mutation	SNP	A	G	A	TAS2R20	c.T833C	p.I278T
XH_P43	12	11174668	11174668	Frame_Shift_Ins	INS	-	TGTTATTGGCC	-	TAS2R19	503insGGCAAA	p.L168fs
XH_P43	12	15803897	15803897	Nonsense_Mutation	SNP	G	A	G	EP58	c.C1294T	p.R432X
XH_P43	12	18872553	18872553	In_Frame_Ins	INS	-	TATGTAAGGTA	-	PLC21	nsTAAATACCTTA	H23delinsHKYLTYP
XH_P43	12	19646858	19646858	Missense_Mutation	SNP	C	A	C	AEBP2	c.C1112A	p.S371Y
XH_P43	12	19646860	19646860	Nonsense_Mutation	INS	-	ATGAGTGAATA	-	AEBP2	115insAATGAG	372_5373delinsQX
XH_P43	12	21958990	21958990	Frame_Shift_Ins	INS	-	GTGTTGAATTA	-	ABCC9	insTACATAATT	p.N1485fs
XH_P43	12	22671011	22671011	In_Frame_Ins	INS	-	AAATTTGTTTCTA	-	C2CD5	AGAAATAGAAAT	7delinsLURNRNKFLKK
XH_P43	12	27067449	27067449	Silent	SNP	G	A	G	INTS13	c.C1311T	p.I437I
XH_P43	12	39751096	39751096	Frame_Shift_Ins	INS	-	T	-	KIF21A	c.1358_1359ins	p.I453fs
XH_P43	12	39751097	39751097	Frame_Shift_Ins	INS	-	CAGTCTGTGG	-	KIF21A	1358insCCACA	p.I453fs
XH_P43	12	46245680	46245680	Silent	SNP	T	G	T	ARID2	c.T3774G	p.V1258V
XH_P43	12	48441827	48441827	Missense_Mutation	SNP	C	T	C	SEN1	c.G1648A	p.D550N
XH_P43	12	51686040	51686040	Missense_Mutation	SNP	G	T	G	BIN2	c.C850A	p.L284I
XH_P43	12	52139801	52139801	In_Frame_Ins	INS	-	AGT	-	SCN8A	2113_2114insA	p.T705delinsKS
XH_P43	12	52139802	52139802	In_Frame_Ins	INS	-	TATAAAGGT	-	SCN8A	1_2115insTATAA	T705delinsTIKV
XH_P43	12	52631309	52631309	Missense_Mutation	SNP	A	C	A	KRT7	c.A553C	p.N185H
XH_P43	12	52681868	52681868	Missense_Mutation	SNP	C	T	C	KRT81	c.G800A	p.R267Q
XH_P43	12	54982248	54982248	Missense_Mutation	SNP	T	G	T	PPP1R1A	c.A25C	p.K9Q
XH_P43	12	56822422	56822422	Frame_Shift_Del	DEL	GAGCCAAGT	-	AGAGCCAAGTG	TIMELESS	c.1306_1316del	p.G436fs
XH_P43	12	57637978	57637978	Missense_Mutation	SNP	G	A	G	STAC3	c.C331T	p.P111S
XH_P43	12	57637979	57637979	Frame_Shift_Ins	INS	-	CTTAACATTAA	-	STAC3	30insATTAAATG	p.T110fs
XH_P43	12	64011087	64011087	Silent	SNP	C	T	C	DPY19L2	c.G1215A	p.T405T
XH_P43	12	76784358	76784358	Nonsense_Mutation	INS	-	AAATCTTAAATG	-	OSBP18	4insTTCATTAA	312_E313delinsFIX
XH_P43	12	88505113	88505113	Nonsense_Mutation	INS	-	TTATTTTATTTT	-	CEP290	AAAGTAAATAAT	K745_E746delinsX
XH_P43	12	89745528	89745528	Frame_Shift_Ins	INS	-	CA	-	DUSP6	c.288_289insTG	p.L97fs
XH_P43	12	99060074	99060074	Missense_Mutation	SNP	G	A	G	APAF1	c.G1268A	p.R423H
XH_P43	12	100691833	100691833	Silent	SNP	A	G	A	SCYL2	c.A360G	p.E120E
XH_P43	12	109967771	109967771	Missense_Mutation	SNP	G	A	G	UBE3B	c.G2704A	p.G902R
XH_P43	12	110874004	110874149	In_Frame_Del	DEL	CTCTGGATG	-	AGCTCTGGATGC	ARPC3	c.380_385del	p.127_129del
XH_P43	12	111856340	111856340	Missense_Mutation	SNP	G	T	G	SH2B3	c.G391T	p.G131W
XH_P43	12	112171758	112171758	Missense_Mutation	SNP	C	T	C	ACAD10	c.C1426T	p.P476S
XH_P43	12	112326720	112326720	Missense_Mutation	SNP	G	A	G	MAPKAPK5	c.G1132A	p.D378N
XH_P43	12	112673558	112673558	Frame_Shift_Ins	INS	-	AGATTATG	-	HECTD4	2_5073insCAT	p.Q1691fs
XH_P43	12	112681241	112681241	Missense_Mutation	SNP	C	T	C	HECTD4	c.G4472A	p.R1491Q
XH_P43	12	116399156	116399156	Missense_Mutation	SNP	G	A	G	MED13L	c.C6548T	p.P2183L
XH_P43	12	117693790	117693790	Missense_Mutation	SNP	C	A	C	NOS1	c.G2584T	p.G862C
XH_P43	12	118636987	118636987	Missense_Mutation	SNP	C	T	C	TAOK3	c.G1063A	p.V355M
XH_P43	12	119631647	119631647	Nonsense_Mutation	INS	-	TTTATTTCATT	-	HSPB8	CACGATTTTATT	193delinsSKHTLFIYCCX
XH_P43	12	119631649	119631649	Missense_Mutation	SNP	G	T	G	HSPB8	c.G577T	p.V193F
XH_P43	12	120634618	120634618	Silent	SNP	C	T	C	RPLP0	c.G912A	p.S304S
XH_P43	12	121701611	121701611	Missense_Mutation	SNP	C	G	C	CAMKK2	c.G757C	p.E253Q
XH_P43	12	121701612	121701612	Nonsense_Mutation	INS	-	TTTTCTGTGAGA	-	CAMKK2	AAATATCTGACA	52_E253delinsVNIX
XH_P43	12	125397130	125397130	Silent	SNP	C	T	C	UBC	c.G1188A	p.E396E
XH_P43	13	21563023	21563023	Missense_Mutation	SNP	C	T	C	LATS2	c.G896A	p.G299D
XH_P43	13	21714712	21714712	Silent	SNP	A	G	A	SAP18	c.A21G	p.G7G
XH_P43	13	24444305	24444305	Frame_Shift_Ins	INS	-	GATAATATAAT	-	MIPEP	nsTACTATTATA	p.K211fs
XH_P43	13	24798696	24798696	Frame_Shift_Ins	INS	-	ACTT	-	SPATA13	629_1630insAC	p.G543fs
XH_P43	13	25419175	25419175	Frame_Shift_Ins	INS	-	G	-	RNF17	c.3059_3060ins	p.T1020fs
XH_P43	13	25419177	25419177	Frame_Shift_Ins	INS	-	ATTTTCAAAATAT	-	RNF17	insCAACATTTTCG	p.M1021fs
XH_P43	13	25479711	25479711	Missense_Mutation	SNP	G	A	G	CENP1	c.C2465T	p.P822L

XH_P43	13	32786510	32786510	Nonsense_Mutation	INS	-	GTAGACATCTG	-	FRY	4674insGTAGA	558_D1559delinsSX
XH_P43	13	32869537	32869537	Missense_Mutation	SNP	G	C	G	FRY	c.G8982C	p.Q2994H
XH_P43	13	32890558	32890558	Splice_Site	SNP	G	A	G	BRCA2	.	.
XH_P43	13	32893318	32893318	Nonsense_Mutation	SNP	G	T	G	BRCA2	c.G172T	p.E58X
XH_P43	13	36049333	36049333	Missense_Mutation	SNP	G	A	G	MAB21L1	c.C943T	p.R315W
XH_P43	13	38237678	38237678	Silent	SNP	G	A	G	TRP4	c.C1044T	p.F348F
XH_P43	13	41943342	41943342	Missense_Mutation	SNP	C	G	C	NAA16	c.C1870G	p.Q624E
XH_P43	13	42457556	42457556	In_Frame_Ins	INS	-	CTCCTT	-	VWA8	46_1047insAAG	H349delinsQRS
XH_P43	13	47409350	47409350	Silent	SNP	G	A	G	HTR2A	c.C786T	p.A262A
XH_P43	13	49841849	49841849	Nonsense_Mutation	INS	-	AAGGTAATTAT	-	CDADC1	TACGAAAGGTA	K218delinsKYERX
XH_P43	13	52539089	52539089	Silent	SNP	G	A	G	ATP7B	c.C1788T	p.S596S
XH_P43	13	52603233	52603233	Nonsense_Mutation	INS	-	TCACCTCAAGGG	-	UTP14C	nsATTTTCACTCAB	L99delinsSFSLKGX
XH_P43	13	95813446	95813446	Missense_Mutation	SNP	T	C	T	ABCC4	c.A2311G	p.I771V
XH_P43	13	96282320	96282320	Missense_Mutation	SNP	C	T	C	DZIP1	c.G733A	p.V245I
XH_P43	13	96547518	96547518	In_Frame_Ins	INS	-	GGT	-	UGGT2	2674_2675insAA	p.F892delinsYL
XH_P43	13	96547519	96547519	In_Frame_Ins	INS	-	AATAAAAGACAT	-	UGGT2	674insATATGTC	F892delinsICLLF
XH_P43	13	99042309	99042309	Nonsense_Mutation	INS	-	CTAAACTCTAGT	-	FARP1	65insACTAAACT	L1318delinsLTKLX
XH_P43	13	99520227	99520227	Silent	SNP	C	T	C	DOCK9	c.G3132A	p.K1044K
XH_P43	14	21109695	21109695	Frame_Shift_Ins	INS	-	ATTCATTCTCTAC	-	OR6S1	5insAAGTAGAA	p.R52fs
XH_P43	14	23549879	23549884	In_Frame_Del	DEL	TCCTCC	-	TCCTCC	ACIN1	c.714_719del	p.238_240del
XH_P43	14	23744820	23744820	Frame_Shift_Del	DEL	A	-	A	HOMEZ	c.1617delIT	p.D539fs
XH_P43	14	23744822	23744829	Frame_Shift_Del	DEL	CATCTTCC	-	CATCTTCC	HOMEZ	c.1608_1615de	p.E536fs
XH_P43	14	24710078	24710078	Missense_Mutation	SNP	C	T	C	TINF2	c.G608A	p.C203Y
XH_P43	14	31765237	31765237	Nonsense_Mutation	INS	-	TTTTTATTTTITAG	-	HEATR5A	TAAATCTAAAAA	L1834delinsLNLKIKKLX
XH_P43	14	38296543	38296543	Nonsense_Mutation	INS	-	FATGATTATTATA	-	TTC6	5319insTATGAT	73_Y1774delinsIMIX
XH_P43	14	38296544	38296544	Nonsense_Mutation	INS	-	FGGGGAATGATG	-	TTC6	20insATTGGGGG	73_Y1774delinsIGEX
XH_P43	14	38679763	38679763	In_Frame_Ins	INS	-	GCAGGG	-	SSTR1	69_1170insGCA	T390delinsTQG
XH_P43	14	45716108	45716108	Nonsense_Mutation	INS	-	CTAAGAGGGTTA	-	MIS18BP1	382insCTAACCT	28_Q129delinsLTSX
XH_P43	14	53175199	53175199	Splice_Site	INS	-	CT	-	PSMC6	.	.
XH_P43	14	53175200	53175200	Splice_Site	INS	-	TACAATTGGAAC	-	PSMC6	.	.
XH_P43	14	60585282	60585282	Missense_Mutation	SNP	G	A	G	PCNX4	c.G1112A	p.R371Q
XH_P43	14	62207739	62207739	In_Frame_Ins	INS	-	AGTCTAAATCTG	-	HIF1A	1999insAGTCTA	P666delinsPSLNL
XH_P43	14	64421614	64421614	Frame_Shift_Ins	INS	-	ACTATATCAATA	-	SYNE2	nsTCCACTATAT	p.P256fs
XH_P43	14	64519922	64519922	In_Frame_Ins	INS	-	TTTCTTCAAGTTG	-	SYNE2	insATTTTCTTCT	0097delinsLIFSSSSF
XH_P43	14	64935463	64935463	Frame_Shift_Ins	INS	-	TCTCTTG	-	AKAP5	51_352insTCTC	p.S117fs
XH_P43	14	64935657	64935657	Missense_Mutation	SNP	T	G	T	AKAP5	c.T545G	p.L182R
XH_P43	14	69727055	69727055	Missense_Mutation	SNP	G	C	G	GALNT16	c.G48C	p.W16C
XH_P43	14	70633744	70633744	Missense_Mutation	SNP	C	T	C	SLC8A3	c.G1396A	p.V466M
XH_P43	14	70926287	70926287	Nonsense_Mutation	INS	-	ATGATAGTCAAT	-	ADAM21	2insAAATGATA	6691_L692delinsX
XH_P43	14	75277114	75277114	Missense_Mutation	SNP	G	A	G	YLP1M1	c.G5219A	p.R1740Q
XH_P43	14	81380742	81380742	Missense_Mutation	SNP	C	T	C	CEP128	c.G158A	p.R53Q
XH_P43	14	81743648	81743648	Silent	SNP	C	T	C	STON2	c.G2007A	p.A669A
XH_P43	14	88857781	88857781	Missense_Mutation	SNP	T	A	T	SPATA7	c.T76A	p.L26M
XH_P43	14	91444862	91444862	Frame_Shift_Ins	INS	-	TTGGGGT	-	RPS6KA5	81_182insACCC	p.G61fs
XH_P43	14	91444863	91444863	Frame_Shift_Ins	INS	-	TTAAGTT	-	RPS6KA5	80_181insAACT	p.G61fs
XH_P43	14	93940627	93940627	Silent	SNP	G	A	G	UNC79	c.G336A	p.P112P
XH_P43	14	94088171	94088171	In_Frame_Ins	INS	-	AGTTCTATT	-	UNC79	1_4062insAGTT	P1354delinsPVLFF
XH_P43	14	102695866	102695866	Silent	SNP	G	A	G	MOK	c.C1020T	p.S340S
XH_P43	14	104208350	104208350	Silent	SNP	C	T	C	PPP1R13B	c.G1599A	p.A533A
XH_P43	14	105408863	105408863	Missense_Mutation	SNP	C	T	C	AHNAK2	c.G12625A	p.G4209R
XH_P43	14	105412902	105412902	Silent	SNP	A	C	A	AHNAK2	c.T8586G	p.G2862G
XH_P43	14	105413869	105413869	Missense_Mutation	SNP	C	T	C	AHNAK2	c.G7619A	p.G2540D
XH_P43	14	105459315	105459315	Missense_Mutation	SNP	G	C	G	C14orf79	c.G730C	p.E244Q
XH_P43	15	29415603	29415603	Missense_Mutation	SNP	G	C	G	FAM189A1	c.C1559G	p.T520S
XH_P43	15	34355251	34355251	Silent	SNP	C	T	C	CHRM5	c.C333T	p.Y111Y
XH_P43	15	35084695	35084695	Frame_Shift_Ins	INS	-	GTGATACTCTTT	-	ACT1C	1insATAAAGAGT	p.I177fs
XH_P43	15	40648332	40648332	In_Frame_Ins	INS	-	GGCCCTGCGGG	-	PHGR1	CCAGGGCCCTG	delinsGHGPGPCGPPPL
XH_P43	15	41227160	41227160	Missense_Mutation	SNP	G	C	G	DL4	c.G1085C	p.S362T
XH_P43	15	42280287	42280287	Missense_Mutation	SNP	C	A	C	PLA2G4E	c.G1791T	p.E597D
XH_P43	15	43020984	43020984	In_Frame_Ins	INS	-	CCATTCTCT	-	CDAN1	2670insAGAG	V890delinsVENG
XH_P43	15	43584209	43584209	Missense_Mutation	SNP	A	G	A	TGM7	c.T526C	p.F176L
XH_P43	15	43783889	43783889	Frame_Shift_Ins	INS	-	ATTAGATAGTAT	-	TP53BP1	TTACAATACTAT	p.P117fs
XH_P43	15	49716762	49716762	Nonsense_Mutation	INS	-	CAATTGTGCGAT	-	FGF7	AGTATCCATTGTG	00delinsVSIHLICVX
XH_P43	15	50773953	50773953	In_Frame_Ins	INS	-	CTTTTC	-	USP8	263_1264insCTT	b.E421delinsELF
XH_P43	15	50773955	50773955	Frame_Shift_Ins	INS	-	CTCTGAGG	-	USP8	5_1266insCTCT	p.Q422fs
XH_P43	15	64687675	64687675	Frame_Shift_Ins	INS	-	TAAT	-	TRIP4	350_351insTAA	p.A117fs
XH_P43	15	65686806	65686806	Frame_Shift_Ins	INS	-	G	-	IGDC4	c.1656dupC	p.S553fs
XH_P43	15	66625559	66625559	Nonsense_Mutation	INS	-	TTGGTATCTTG	-	DIS3L	CTGTATTGGT	899_R900delinsX
XH_P43	15	71535393	71535393	Silent	SNP	A	C	A	THSD4	c.A870C	p.S290S
XH_P43	15	73029926	73029926	Nonstop_Mutation	INS	-	C	-	BB54	1042_1043ins	p.X348delinsS
XH_P43	15	73029927	73029927	Nonstop_Mutation	INS	-	TCCTTTTTTGCTGT	-	BB54	044insTTCTTTT	X348delinsYSFLL
XH_P43	15	73995313	73995313	Missense_Mutation	SNP	A	G	A	CD276	c.A181G	p.I61V
XH_P43	15	74315486	74315486	Missense_Mutation	SNP	G	A	G	PML	c.G920A	p.R307H
XH_P43	15	75761254	75761254	Silent	SNP	C	T	C	PTPN9	c.G1638A	p.T546T
XH_P43	15	78390781	78390781	Missense_Mutation	SNP	T	A	T	SH2D7	c.T488A	p.V163E
XH_P43	15	78453948	78453948	Silent	SNP	C	T	C	IDH3A	c.C315T	p.A105A
XH_P43	15	78474408	78474408	Nonsense_Mutation	INS	-	ATC	-	ACSBG1	961_962insGA	p.Y321delinsX
XH_P43	15	78474410	78474410	Frame_Shift_Ins	INS	-	TCAGAATT	-	ACSBG1	9_960insAATT	p.S320fs
XH_P43	15	78841219	78841219	In_Frame_Ins	INS	-	CATACATTTATT	-	PSMA4	sAACACATACAT	169delinsQTHFICI
XH_P43	15	78894018	78894018	Silent	SNP	G	A	G	CHRNA3	c.C966T	p.T322T
XH_P43	15	79183876	79183876	Missense_Mutation	SNP	C	T	C	MORF4L1	c.C136T	p.R46W
XH_P43	15	83218245	83218245	Missense_Mutation	SNP	G	A	G	CPEB1	c.C1139T	p.A380V
XH_P43	15	86199015	86199015	Missense_Mutation	SNP	G	A	G	AKAP13	c.G662A	p.R221Q
XH_P43	15	86312758	86312758	Missense_Mutation	SNP	G	A	G	KLHL25	c.C284T	p.P95L
XH_P43	15	90171666	90171666	Missense_Mutation	SNP	C	T	C	KIF7	c.G4016A	p.R1339Q
XH_P43	15	91425070	91425070	Missense_Mutation	SNP	G	A	G	FURIN	c.G2347A	p.E783K
XH_P43	15	91425072	91425072	Frame_Shift_Ins	INS	-	CTGCCCTA	-	FURIN	9_2350insCTGC	p.E783fs
XH_P43	16	746821	746821	Silent	SNP	G	C	G	FBXL16	c.C585G	p.V195V
XH_P43	16	3029648	3029648	Splice_Site	SNP	C	T	C	PKMYT1	.	.
XH_P43	16	3139353	3139353	Silent	SNP	C	T	C	ZSCAN10	c.G900A	p.T300T
XH_P43	16	3299749	3299749	Silent	SNP	G	A	G	MEFV	c.C309T	p.R103R
XH_P43	16	3562401	3562401	Missense_Mutation	SNP	G	C	G	CLUAP1	c.G418C	p.A140P
XH_P43	16	9196983	9196983	Frame_Shift_Ins	INS	-	GAAAAAGAAAA	-	C16orf72	insAAAAAGAAAA	p.K150fs
XH_P43	16	10989530	10989530	Silent	SNP	C	T	C	CIITA	c.C204T	p.P68P
XH_P43	16	15917162	15917162	Missense_Mutation	SNP	G	A	G	MYH11	c.C452T	p.P151L
XH_P43	16	22545369	22545380	In_Frame_Del	DEL	CCCTCAGCTC	-	ACCCTCAGCTCC	NP1PB5	c.1065_1076de	p.355_359del
XH_P43	16	24564880	24564883	Splice_Site	DEL	TATA	-	TATA	RBBP6	.	.
XH_P43	16	28990578	28990594	Frame_Shift_Del	DEL	GGAGCGGA	-	CGGAGCGGAT	SPNS1	c.481_497del	p.Q161fs

XH_P43	16	31075742	31075742	Silent	SNP	G	A	G	ZNF668	c.C39T	p.P13P
XH_P43	16	31202423	31202424	Frame_Shift_Del	DEL	GG	-	GG	FUS	c.1530_1531del	p.M510fs
XH_P43	16	31202424	31202424	Frame_Shift_Ins	INS	-	CTATCAT	-	FUS	31_1532insCTA	p.D511fs
XH_P43	16	46638178	46638178	Nonsense_Mutation	INS	-	AGGTATGTGTTT	-	SHCBP1	sAACCAACACAC	K258delinsLTKHIPX
XH_P43	16	56448254	56448254	Frame_Shift_Ins	INS	-	TTTTTAAACTTT	-	AMFR	ATACAAAGTTT	p.V86fs
XH_P43	16	67660556	67660556	Missense_Mutation	SNP	C	G	C	CTCF	c.C472G	p.Q158E
XH_P43	16	67855093	67855093	Missense_Mutation	SNP	C	G	C	TSNAXIP1	c.C239G	p.P80R
XH_P43	16	70815812	70815812	Silent	SNP	A	T	A	VAC14	c.T204A	p.T68T
XH_P43	16	71884705	71884705	Silent	SNP	T	C	T	ATXN1L	c.T1062C	p.A354A
XH_P43	16	89935977	89935977	Missense_Mutation	SNP	G	A	G	SPIRE2	c.G1809A	p.M603I
XH_P43	17	1198880	1198880	Silent	SNP	C	T	C	TUSC5	c.C483T	p.I161I
XH_P43	17	4462855	4462855	Frame_Shift_Ins	INS	-	AACTTAGGGAG	-	GGT6	341insACTCCCTA	p.A114fs
XH_P43	17	7291913	7291913	Frame_Shift_Ins	INS	-	AATACCCCATGC	-	TNK1	CACACAATCACC	p.K561fs
XH_P43	17	7306646	7306646	In_Frame_Ins	INS	-	CCAGCTTTTACT	-	TMEM256	181insAGTAAAA	C61delinsKSKWSC
XH_P43	17	8077885	8077885	Silent	SNP	G	A	G	TMEM107	c.C324T	p.F108F
XH_P43	17	8396211	8396211	Frame_Shift_Ins	INS	-	STTTAAAAATAAT	-	MYH10	4248insGATTAT	p.D1416fs
XH_P43	17	13980352	13980352	Frame_Shift_Ins	INS	-	CTGAAGATGTT	-	COX10	479insCTGAAG	p.L160fs
XH_P43	17	15522806	15522806	Frame_Shift_Ins	INS	-	AGTTAAATAG	-	CDRT1	21insCTATTTA	p.R7fs
XH_P43	17	15522807	15522807	In_Frame_Ins	INS	-	TTATAT	-	CDRT1	19_20insATATA	p.R7delinsNIR
XH_P43	17	16062179	16062179	Frame_Shift_Ins	INS	-	GTTTGAATGT	-	NCOR1	300insACATTCA	p.L100fs
XH_P43	17	16062181	16062181	Missense_Mutation	SNP	G	T	G	NCOR1	c.C298A	p.L100I
XH_P43	17	17174313	17174313	Nonsense_Mutation	INS	-	ATACTATTCAAG	-	COP53	5GAATACCTTGA	5_F46delinsKLGILEX
XH_P43	17	17409546	17409546	Nonsense_Mutation	SNP	G	A	G	PEN1	c.C679T	p.R227X
XH_P43	17	18022373	18022373	Missense_Mutation	SNP	A	C	A	MYO15A	c.A259C	p.M87L
XH_P43	17	20921337	20921337	Frame_Shift_Ins	INS	-	T	-	USP22	c.607_608insA	p.F203fs
XH_P43	17	20921338	20921338	Frame_Shift_Ins	INS	-	ACCTTTTGTAGT	-	USP22	AACCTTACTACAA	p.F203fs
XH_P43	17	21319786	21319786	Missense_Mutation	SNP	G	C	G	KCNJ12	c.G1132C	p.E378Q
XH_P43	17	27248819	27248819	Missense_Mutation	SNP	G	C	G	PHF12	c.C723G	p.S241R
XH_P43	17	27248820	27248820	In_Frame_Ins	INS	-	AGACCATGTATC	-	PHF12	722insCATACAT	241delinsTYMVC
XH_P43	17	28512493	28512493	Missense_Mutation	SNP	A	T	A	NSRP1	c.A1316T	p.E439V
XH_P43	17	28512494	28512494	Frame_Shift_Ins	INS	-	CATTATTTTCAT	-	NSRP1	nsTTTATCATTAT	p.E439fs
XH_P43	17	28789055	28789055	Nonsense_Mutation	INS	-	TTTAAATATAA	-	CPD	AAAATGTTTAA	G1018delinsKMFKIX
XH_P43	17	29161784	29161784	Frame_Shift_Ins	INS	-	GGAGGTCATAG	-	ATAD5	insAGGGAGGTT	p.L229fs
XH_P43	17	37844195	37844195	Missense_Mutation	SNP	G	C	G	PGAP3	c.C73G	p.R25G
XH_P43	17	37985695	37985695	Frame_Shift_Ins	INS	-	A	-	IKZF3	c.107_108insT	p.E36fs
XH_P43	17	37985696	37985696	Frame_Shift_Ins	INS	-	AAAAGTAATA	-	IKZF3	5_107insATTAC	p.E36fs
XH_P43	17	38240932	38240932	In_Frame_Ins	INS	-	ACTACTCTCTCT	-	THRA	441insACTACTCT	K147delinsKLFL
XH_P43	17	38240933	38240933	Silent	SNP	G	A	G	THRA	c.G441A	p.K147K
XH_P43	17	38792256	38792256	Nonsense_Mutation	INS	-	GTTATATTGAG	-	SMARCE1	ATCTTACTCAAT	6_S157delinsDKSYSIX
XH_P43	17	39186047	39186047	Missense_Mutation	SNP	G	A	G	KRTAP1-4	c.C284T	p.A95V
XH_P43	17	39186179	39186179	Frame_Shift_Del	DEL	C	-	C	KRTAP1-4	c.152delIG	p.G51fs
XH_P43	17	39595598	39595598	Missense_Mutation	SNP	G	A	G	KRT38	c.C589T	p.R197C
XH_P43	17	40766624	40766624	Silent	SNP	G	A	G	TUBG1	c.G1107A	p.S369S
XH_P43	17	42452041	42452041	Nonsense_Mutation	SNP	G	A	G	ITGA2B	c.C2929T	p.R977X
XH_P43	17	43138716	43138764	Frame_Shift_Del	DEL	ACCTCCGCTC	-	ACCTCCGCTGC	NMT1	c.19_67del	p.T7fs
XH_P43	17	44590528	44590528	Silent	SNP	G	A	G	LRR37A2	c.G450A	p.L150L
XH_P43	17	45234303	45234303	Missense_Mutation	SNP	G	C	G	CD27	c.C635G	p.A212G
XH_P43	17	46685437	46685437	Missense_Mutation	SNP	G	A	G	HOXB7	c.C421T	p.R141C
XH_P43	17	46801827	46801827	Missense_Mutation	SNP	T	C	T	PRAC2	c.T55C	p.F19L
XH_P43	17	46986015	46986015	Silent	SNP	G	A	G	UBE2Z	c.G150A	p.A50A
XH_P43	17	59999180	59999180	Nonsense_Mutation	INS	-	TTAAGTAAATTA	-	INTS2	ATAATATAATT	147_5148delinsEX
XH_P43	17	60038437	60038437	Frame_Shift_Ins	INS	-	CCAAATAGGTAT	-	MED13	nsACAAATACCT	p.L1757fs
XH_P43	17	62290231	62290231	Silent	SNP	G	A	G	TEX2	c.C1347T	p.L449L
XH_P43	17	64062934	64062934	Nonsense_Mutation	INS	-	TGGATATATTTA	-	CEP112	nsTATATAAATA	4_E265delinsLYKVIHX
XH_P43	17	65103456	65103456	Missense_Mutation	SNP	C	G	C	HELZ	c.G5073C	p.Q169H
XH_P43	17	65103458	65103458	In_Frame_Ins	INS	-	ATATCAGTATT	-	HELZ	nsTCAATAAATA	691delinsSINTDIFQ
XH_P43	17	65340883	65340883	In_Frame_Ins	INS	-	GTGGAAAGA	-	PSMD12	1_862insTCTTGT	L288delinsSFHL
XH_P43	17	65888128	65888128	Frame_Shift_Ins	INS	-	TT	-	BPTF	.2033_2034insT	p.K678fs
XH_P43	17	65888129	65888129	Nonsense_Mutation	INS	-	TAACCACC	-	BPTF	4_2035insTAAC	678_L679delinsKX
XH_P43	17	65889816	65889816	Frame_Shift_Ins	INS	-	ATGATCACTTCC	-	BPTF	2387insATGATC	p.L796fs
XH_P43	17	66547263	66547263	Nonstop_Mutation	SNP	T	G	T	PRKAR1A	c.T1012G	p.X338E
XH_P43	17	74774329	74774329	Frame_Shift_Ins	INS	-	ACAGTGTCTT	-	MFS011	1090insACAGT	p.L363fs
XH_P43	17	76989736	76989736	Missense_Mutation	SNP	C	T	C	CANT1	c.G1102A	p.G368S
XH_P43	17	77808613	77808613	Silent	SNP	C	T	C	CBX4	c.G828A	p.A276A
XH_P43	17	79986289	79986289	Missense_Mutation	SNP	G	A	G	LRR345	c.G1142A	p.R381Q
XH_P43	18	6873480	6873480	Missense_Mutation	SNP	A	G	A	ARHGAP28	c.A550G	p.I184V
XH_P43	18	10807258	10807258	Frame_Shift_Ins	INS	-	AATCGATACTCT	-	PIEZO2	32insTAGAGTA	p.K311fs
XH_P43	18	12127844	12127844	Nonsense_Mutation	INS	-	TGTTAATAATAT	-	ANKRD62	nsATTTTGTAA	N887delinsKFCX
XH_P43	18	12697366	12697366	Frame_Shift_Ins	INS	-	SGTGTAGTATC	-	CEP17	37insCCATACCT	p.L113fs
XH_P43	18	13737124	13737124	Silent	SNP	A	C	A	RNMT	c.A669C	p.L223L
XH_P43	18	13737125	13737125	Missense_Mutation	SNP	G	T	G	RNMT	c.G670T	p.V224F
XH_P43	18	14105082	14105082	Frame_Shift_Del	DEL	TTCTCTC	-	TTCTCTC	ZNF519	c.1451_1457del	p.G484fs
XH_P43	18	14513764	14513764	Missense_Mutation	SNP	C	T	C	POTEC	c.G1430A	p.R477Q
XH_P43	18	14763838	14763838	In_Frame_Ins	INS	-	AGG	-	ANKRD30B	.974_975insAG	p.S325delins5G
XH_P43	18	14763840	14763840	Frame_Shift_Ins	INS	-	TTCTGTGA	-	ANKRD30B	6_977insTTCTCT	p.G326fs
XH_P43	18	39637989	39637989	Frame_Shift_Ins	INS	-	TCATAAAGAATA	-	PIK3C3	nsCTCTTCATAA	p.C739fs
XH_P43	18	40853812	40853812	Nonsense_Mutation	INS	-	STCTAAGGAATT	-	SYT4	insAAAAATTC	94_K195delinsKIPX
XH_P43	18	42532021	42532021	Missense_Mutation	SNP	C	T	C	SETBP1	c.C2716T	p.P906S
XH_P43	18	43447707	43447707	In_Frame_Ins	INS	-	ATGATT	-	EPG5	31_6232insAAT	R2078delinsNHR
XH_P43	18	55328538	55328538	Missense_Mutation	SNP	C	T	C	ATP8B1	c.G2575A	p.E859K
XH_P43	18	77796710	77796710	Silent	SNP	G	A	G	RBFA	c.G201A	p.S67S
XH_P43	19	1020899	1020899	Missense_Mutation	SNP	T	G	T	TMEM259	c.A97C	p.N33H
XH_P43	19	1487972	1487972	Missense_Mutation	SNP	C	A	C	PCSK4	c.G507T	p.W169C
XH_P43	19	3936622	3936622	Frame_Shift_Ins	INS	-	TTCTGATTCITTT	-	NMRK2	ATTTTCTTGATT	p.L26fs
XH_P43	19	4231187	4231187	Splice_Site	SNP	G	A	G	EBI3	-	-
XH_P43	19	5258034	5258034	Missense_Mutation	SNP	C	T	C	PTPRS	c.G673A	p.V225M
XH_P43	19	5699108	5699108	Missense_Mutation	SNP	C	T	C	LONP1	c.G1027A	p.A343T
XH_P43	19	5772919	5772919	Silent	SNP	G	T	G	CATSPERD	c.G1884T	p.P628P
XH_P43	19	8436202	8436202	Missense_Mutation	SNP	G	A	G	ANGPTL4	c.G721A	p.D241N
XH_P43	19	8670540	8670540	Missense_Mutation	SNP	A	T	A	ADAMTS10	c.T56A	p.M19K
XH_P43	19	8953438	8953438	Missense_Mutation	SNP	G	C	G	MBD3L1	c.G84C	p.L28F
XH_P43	19	9090970	9090970	Missense_Mutation	SNP	G	A	G	MUC16	c.C845T	p.A282V
XH_P43	19	10398859	10398859	Nonstop_Mutation	SNP	G	C	G	ICAM4	c.G818C	p.X273S
XH_P43	19	12637605	12637605	Silent	SNP	A	G	A	ZNF564	c.T1317C	p.H439H
XH_P43	19	14507991	14507991	Missense_Mutation	SNP	C	T	C	ADGRE5	c.C581T	p.P194L
XH_P43	19	15281611	15281611	Missense_Mutation	SNP	T	G	T	NOTCH3	c.A4762C	p.N1588H
XH_P43	19	19655153	19655153	Missense_Mutation	SNP	C	T	C	CILP2	c.C1799T	p.S600L
XH_P43	19	20003167	20003167	Missense_Mutation	SNP	A	G	A	ZNF253	c.A883G	p.R295G

XH_P43	19	20044867	20044867	Missense_Mutation	SNP	A	C	A	ZNF93	c.A1103C	p.H368P
XH_P43	19	20044868	20044868	Silent	SNP	T	C	T	ZNF93	c.T1104C	p.H368H
XH_P43	19	20117561	20117561	Silent	SNP	G	A	G	ZNF682	c.C654T	p.I218I
XH_P43	19	20736554	20736554	Missense_Mutation	SNP	T	C	T	ZNF737	c.A91G	p.N31D
XH_P43	19	20807161	20807161	Missense_Mutation	SNP	A	G	A	ZNF626	c.T1522C	p.S508P
XH_P43	19	20807162	20807162	Silent	SNP	A	G	A	ZNF626	c.T1521C	p.N507N
XH_P43	19	21131797	21131797	Frame_Shift_Ins	INS	-	TGTCT	-	ZNF85	285_286insTGT	p.S95fs
XH_P43	19	21477016	21477016	Missense_Mutation	SNP	A	G	A	ZNF708	c.T560C	p.L187P
XH_P43	19	21606915	21606915	Missense_Mutation	SNP	A	G	A	ZNF493	c.A1070G	p.E357G
XH_P43	19	21607169	21607169	Missense_Mutation	SNP	C	G	C	ZNF493	c.C1324G	p.H442D
XH_P43	19	21607171	21607171	Missense_Mutation	SNP	C	G	C	ZNF493	c.C1326G	p.H442Q
XH_P43	19	21909896	21909896	Silent	SNP	G	A	G	ZNF100	c.C573T	p.C191C
XH_P43	19	21990759	21990759	Missense_Mutation	SNP	A	T	A	ZNF43	c.T1885A	p.S629T
XH_P43	19	21991587	21991587	Missense_Mutation	SNP	A	T	A	ZNF43	c.T1057A	p.L353I
XH_P43	19	22154589	22154589	Missense_Mutation	SNP	C	T	C	ZNF208	c.G3247A	p.E1083K
XH_P43	19	22155433	22155433	Missense_Mutation	SNP	A	T	A	ZNF208	c.T2403A	p.D801E
XH_P43	19	22155434	22155434	Missense_Mutation	SNP	T	C	T	ZNF208	c.A2402G	p.D801G
XH_P43	19	22363643	22363643	Silent	SNP	C	T	C	ZNF676	c.G876A	p.S292S
XH_P43	19	22497596	22497596	Silent	SNP	A	C	A	ZNF729	c.A1377C	p.P459P
XH_P43	19	22497922	22497922	Missense_Mutation	SNP	G	C	G	ZNF729	c.G1703C	p.G568A
XH_P43	19	22498426	22498426	Missense_Mutation	SNP	C	G	C	ZNF729	c.C2207G	p.A736G
XH_P43	19	22586302	22586302	In_Frame_Ins	INS	-	TAAATTTTATTTC	-	ZNF98	AGAGAAATAAA	5delinsKKRNKIYRVF
XH_P43	19	22941856	22941856	Silent	SNP	A	G	A	ZNF99	c.T855C	p.Y285Y
XH_P43	19	22941917	22941917	Missense_Mutation	SNP	A	G	A	ZNF99	c.T794C	p.V265A
XH_P43	19	23040555	23040555	Missense_Mutation	SNP	A	G	A	ZNF723	c.A862G	p.K288E
XH_P43	19	23544418	23544418	Missense_Mutation	SNP	A	T	A	ZNF91	c.T1267A	p.F423I
XH_P43	19	36054384	36054384	Missense_Mutation	SNP	C	T	C	ATP4A	c.G58A	p.G20R
XH_P43	19	37904451	37904451	In_Frame_Ins	INS	-	TCATTACATACA	-	ZNF569	AGCCCTATGTAT	ORSHTEKGPYVCNCGKAFSQFSMLI
XH_P43	19	38102592	38102592	Nonsense_Mutation	INS	-	TAATT	-	ZNF540	315_316insTAA	105_510delinsRX
XH_P43	19	38102594	38102594	Frame_Shift_Ins	INS	-	TTGGTCT	-	ZNF540	17_318insTTGG	p.5106fs
XH_P43	19	38886412	38886412	Missense_Mutation	SNP	C	A	C	SPRED3	c.C860A	p.A287D
XH_P43	19	39965193	39965193	Missense_Mutation	SNP	G	A	G	SUPTSH	c.G2847A	p.M949I
XH_P43	19	46521350	46521350	Silent	SNP	G	T	G	CCDC61	c.G1383T	p.V461V
XH_P43	19	49206338	49206338	Missense_Mutation	SNP	C	T	C	FUT2	c.C125T	p.P42L
XH_P43	19	49228005	49228005	Silent	SNP	G	A	G	RASIP1	c.C2340T	p.N780N
XH_P43	19	50148325	50148325	Silent	SNP	G	A	G	SCAF1	c.G42A	p.S14S
XH_P43	19	50166616	50166616	Silent	SNP	G	A	G	IRF3	c.C321T	p.Y107Y
XH_P43	19	51274851	51274851	Missense_Mutation	SNP	A	C	A	GNR32	c.A994C	p.R332P
XH_P43	19	51628529	51628529	Missense_Mutation	SNP	A	G	A	SIGLEC9	c.A298G	p.K100E
XH_P43	19	52033119	52033119	Missense_Mutation	SNP	G	A	G	SIGLEC6	c.C715T	p.P239S
XH_P43	19	52941718	52941718	In_Frame_Ins	INS	-	ATTCACACCTTG	-	ZNF534	CGGAATTCACA	7delinsFRRNSHLVRH
XH_P43	19	53270991	53270991	Silent	SNP	C	T	C	ZNF600	c.G18A	p.L6L
XH_P43	19	53270992	53270992	Missense_Mutation	SNP	A	G	A	ZNF600	c.T17C	p.L6S
XH_P43	19	53344035	53344118	In_Frame_Del	DEL	CTCCAGTAT	-	CTCTCCAGTATG	ZNF468	c.1429_1512del	p.477_504del
XH_P43	19	54444729	54444729	Missense_Mutation	SNP	T	G	T	CACNG7	c.T430G	p.S144A
XH_P43	19	55386792	55386792	Missense_Mutation	SNP	G	T	G	FCAR	c.G41T	p.C14F
XH_P43	19	56284031	56284031	Frame_Shift_Ins	INS	-	GTAAAAATTGA	-	RFPL4AL1	351insGTTAAA	p.S117fs
XH_P43	19	57065489	57065489	In_Frame_Ins	INS	-	STTTTGTTATGA	-	ZFP28	36insGGTTTGG	445delinsEGFVMS
XH_P43	19	58050159	58050159	Nonsense_Mutation	INS	-	GTGTGGATTTTG	-	ZNF549	1749insGTGTGG	p.Y583delinsX
XH_P43	19	58324676	58324676	Missense_Mutation	SNP	A	G	A	ZNF552	c.T146C	p.L49P
XH_P43	19	58966859	58966859	Missense_Mutation	SNP	G	A	G	ZNF324B	c.G548A	p.R183Q
XH_P43	20	3026345	3026345	Frame_Shift_Ins	INS	-	GTCCC	-	GNRH2	326_327insGTC	p.E109fs
XH_P43	20	13398163	13398163	In_Frame_Ins	INS	-	CCAGCATATCTA	-	TASP1	9insAATAGATA	237delinsNRYAGF
XH_P43	20	20616238	20616238	Nonsense_Mutation	INS	-	TTATTGATTGTT	-	RALGAP2	ACTCTAACAACT	77_V278delinsNQX
XH_P43	20	33703671	33703671	In_Frame_Ins	INS	-	AGAAAA	-	EDEM2	190_1191insTTT	p.V397delinsVFL
XH_P43	20	33703673	33703673	In_Frame_Ins	INS	-	ACTGTT	-	EDEM2	88_1189insAAC	p.V397delinsNSV
XH_P43	20	34526940	34526940	Silent	SNP	C	T	C	PHF20	c.C262T	p.N874N
XH_P43	20	34618348	34618348	Missense_Mutation	SNP	G	C	G	CNB2	c.G1497C	p.Q499H
XH_P43	20	34618349	34618349	Frame_Shift_Ins	INS	-	CTTCCCT	-	CNB2	98_1499insCTTT	p.L500fs
XH_P43	20	36841667	36841667	Missense_Mutation	SNP	G	A	G	KIAA1755	c.C2333T	p.P778L
XH_P43	20	36841668	36841668	In_Frame_Ins	INS	-	CAC	-	KIAA1755	2331_2332insG	p.P778delinsVP
XH_P43	20	37175041	37175041	Missense_Mutation	SNP	C	T	C	RALGAPB	c.C2870T	p.A957V
XH_P43	20	37581026	37581026	Missense_Mutation	SNP	C	T	C	FAM83D	c.C1621T	p.R541W
XH_P43	20	45140726	45140726	Missense_Mutation	SNP	A	T	A	ZNF334	c.T16A	p.F6I
XH_P43	20	48257153	48257153	Nonsense_Mutation	INS	-	AGGTAAATCTG	-	B4GALT5	CCTTTCAGATT	9_E220delinsPSFOIX
XH_P43	20	50090603	50090603	Missense_Mutation	SNP	C	T	C	NFATC2	c.G1562A	p.R521Q
XH_P43	20	50140273	50140273	Silent	SNP	G	A	G	NFATC2	c.C447T	p.P149P
XH_P43	20	52199025	52199025	Missense_Mutation	SNP	C	T	C	ZNF217	c.G341A	p.R114Q
XH_P43	20	57042528	57042528	Silent	SNP	G	A	G	APCDD1L	c.C375T	p.A125A
XH_P43	20	60770984	60770984	Missense_Mutation	SNP	G	A	G	MTG2	c.G331A	p.G111S
XH_P43	20	61828070	61828070	Frame_Shift_Ins	INS	-	TTTCTATGTATT	-	YTHDF1	nsTTATAATACA	p.N557fs
XH_P43	20	62195670	62195670	Missense_Mutation	SNP	C	T	C	HELZ2	c.G2798A	p.R933Q
XH_P43	20	62679559	62679559	Missense_Mutation	SNP	G	C	G	SOX18	c.C1115G	p.A372G
XH_P43	21	10934053	10934053	In_Frame_Ins	INS	-	TAATAACATTTTC	-	TPTE	nsAAGGAAAAT	170delinsKKRMLLP
XH_P43	21	33073424	33073424	Nonsense_Mutation	INS	-	FATCACTCAACTT	-	SCAF4	insTCAAGTTGA	206_A207delinsSSX
XH_P43	21	35138252	35138252	Missense_Mutation	SNP	G	A	G	ITSN1	c.G862A	p.V288I
XH_P43	21	35190725	35190725	Missense_Mutation	SNP	T	G	T	ITSN1	c.T2867G	p.F956C
XH_P43	21	37602811	37602811	Missense_Mutation	SNP	G	A	G	DOPEY2	c.G1729A	p.E577K
XH_P43	22	21965219	21965219	Missense_Mutation	SNP	C	T	C	UBE2L3	c.C101T	p.P34L
XH_P43	22	26164876	26164876	Frame_Shift_Ins	INS	-	TCCTTCTCTG	-	MYO18B	994insTCCTTC	p.P331fs
XH_P43	22	26873065	26873065	Frame_Shift_Ins	INS	-	TAAAGTTTAGGA	-	HP54	insACTTCTCTAA	p.I52fs
XH_P43	22	26873067	26873067	Missense_Mutation	SNP	C	A	C	HP54	c.G153T	p.Q51H
XH_P43	22	32108425	32108425	Silent	SNP	G	T	G	PRR14L	c.C5400A	p.L1800L
XH_P43	22	32506183	32506183	In_Frame_Ins	INS	-	CACAAA	-	SLCSA1	97_1598insCAC	p.H533delinsPQN
XH_P43	22	32506185	32506185	Nonsense_Mutation	INS	-	AGGTCATAG	-	SLCSA1	9_1600insAGGT	p.H533delinsHRSX
XH_P43	22	40831528	40831528	In_Frame_Ins	INS	-	CATTTA	-	MKL1	37_38insTAAAT	p.Q13delinsLNE
XH_P43	22	40831529	40831529	Missense_Mutation	SNP	G	C	G	MKL1	c.C37G	p.Q13E
XH_P43	22	41542790	41542790	Nonsense_Mutation	INS	-	AAAATTATTTTAT	-	EP300	nsCCACAAAATA	1701delinsPTKYFX
XH_P43	22	50192252	50192252	Nonsense_Mutation	INS	-	AATTCCTCGTTTTT	-	BRD1	TAAATAAAACG	80_K581delinsVKX
XH_P43	X	9864732	9864732	Nonsense_Mutation	SNP	C	A	C	SHROOM2	c.C2784A	p.Y928X
XH_P43	X	22117166	22117166	In_Frame_Ins	INS	-	TATTGTCTTTTT	-	PHEX	77insCTATTGTC	L326delinsPIVFFF
XH_P43	X	43542796	43542796	Missense_Mutation	SNP	G	A	G	MAOA	c.G109A	p.V37I
XH_P43	X	43572030	43572030	Frame_Shift_Ins	INS	-	GTGATAATATTA	-	MAOA	AGTAGTGATAA	p.1164fs
XH_P43	X	46502762	46502762	Missense_Mutation	SNP	T	G	T	SLC9A7	c.A1525C	p.M509L
XH_P43	X	53421734	53421734	Missense_Mutation	SNP	A	C	A	SMC1A	c.T2937G	p.I979M
XH_P43	X	63444220	63444220	Silent	SNP	G	A	G	ASB12	c.C952T	p.L318L
XH_P43	X	66766357	66766357	In_Frame_Del	DEL	GGCGGCGGCG	-	CGGCGGCGGCGG	AR	c.1369_1401del	p.457_467del
XH_P43	X	71425692	71425692	In_Frame_Ins	INS	-	AAT	-	ERCC6L	2924_2925insA	p.V975delinsVF

XH_P43	X	71425694	71425694	In_Frame_Ins	INS	-	CCAGTAGTGTAA	-	ERCC6L	2923insTTACAC	/975delinsLHWVV
XH_P43	X	74291457	74291457	Frame_Shift_Ins	INS	-	CTTGATGGTTTG	-	ABC87	ATTATCAAAACCA	p.T325fs
XH_P43	X	84510808	84510808	Splice_Site	INS	-	GACCACATGTTC	-	ZNF711		
XH_P43	X	100630257	100630257	Missense_Mutation	SNP	G	T	G	BTX	c.C16A	p.L6M
XH_P43	X	100808244	100808244	Frame_Shift_Ins	INS	-	AGATTITTCG	-	ARMCX1	332insAGATT	p.L111fs
XH_P43	X	106396711	106396711	Frame_Shift_Ins	INS	-	G	-	NUP62CL	c.367_368insC	p.V123fs
XH_P43	X	106396712	106396712	Nonsense_Mutation	INS	-	TTATTAACCTAT	-	NUP62CL	sTAAATAAGTT	/123_N124delinsX
XH_P43	X	114425154	114425154	Missense_Mutation	SNP	G	A	G	RBMXL3	c.G1150A	p.G384R
XH_P43	X	118123554	118123554	In_Frame_Ins	INS	-	CAATGTGGG	-	LONRF3	_1121insCAATG	K374delinsTMWVE
XH_P43	X	123019835	123019835	Frame_Shift_Ins	INS	-	TTCTTCCTTAT	-	XIAP	324insTTCCTC	p.S108fs
XH_P43	X	123019837	123019837	Frame_Shift_Ins	INS	-	AT	-	XIAP	c.325_326insAT	p.G109fs
XH_P43	X	123539055	123539055	Silent	SNP	G	A	G	TENM1	c.C5196T	p.S1732S
XH_P43	X	138864863	138864863	Nonsense_Mutation	INS	-	GAAAAATGATAC	-	ATP11C	AATAAGAGTAT	602delinsNNKSIIIFX
XH_P43	X	148037594	148037594	In_Frame_Ins	INS	-	TTGTGTTCTGGA	-	AFF2	943insTTGTGTTT	A314delinsAFVSG
XH_P43	X	148037596	148037596	Missense_Mutation	SNP	C	T	C	AFF2	c.C944T	p.T315I
XH_P43	X	153130395	153130395	Missense_Mutation	SNP	C	T	C	L1CAM	c.G2912A	p.R971Q
XH_P43	1	100731947	100731947	Missense_Mutation	SNV	G	A	A	RTCA	c.16G>A	p.V6M
XH_P43	1	145296546	145296546	Missense_Mutation	SNV	G	C	C	NBPF10	c.468G>C	P.Q156H
XH_P43	1	145606316	145606338	Frame_Shift_Del	INDEL	AGCAGCATC	-	-	POLR3C	SATGAAGATGC	P.D219fs
XH_P43	1	150484223	150484223	Missense_Mutation	SNV	G	T	T	ECM1	c.1080G>T	P.R360S
XH_P43	1	150923438	150923438	Missense_Mutation	SNV	T	G	G	SETDB1	c.2085T>G	P.N695K
XH_P43	1	150956517	150956517	Missense_Mutation	SNV	C	T	T	ANXA9	c.239C>T	P.S80L
XH_P43	1	151552157	151552157	Missense_Mutation	SNV	G	T	T	TUFT1	c.882G>T	P.K294N
XH_P43	1	153924549	153924549	Missense_Mutation	SNV	C	A	A	CRTC2	c.942G>T	P.M314I
XH_P43	1	168056880	168056880	Missense_Mutation	SNV	A	C	C	GPR161	c.1327T>G	P.C443G
XH_P43	1	17085498	17085498	Missense_Mutation	SNV	G	T	T	MST1L	c.1193C>A	P.S398Y
XH_P43	1	173910423	173910423	Missense_Mutation	SNV	C	G	G	RC3H1	c.3231G>C	P.I1077D
XH_P43	1	186123054	186123054	Missense_Mutation	SNV	T	G	G	HMCN1	c.15191T>G	P.V5064G
XH_P43	1	196973898	196973898	Missense_Mutation	SNV	T	G	G	CFHR5	c.1438T>G	P.S480A
XH_P43	1	197876348	197876348	Nonstop_Mutation	SNV	T	G	G	C1orf53	c.436T>G	P.Ter146Gext*?
XH_P43	1	205156534	205156534	Splice_Site	SNV	T	G	G	DSTYK	c.654+12A>C	
XH_P43	1	207317197	207317197	Missense_Mutation	SNV	G	T	T	C4BPA	c.1479G>T	P.R493S
XH_P43	1	210977432	210977432	Missense_Mutation	SNV	A	C	C	KCNH1	c.1458T>G	P.H486Q
XH_P43	1	212798568	212798568	Nonsense_Mutation	SNV	G	T	T	FAM71A	c.349G>T	P.E117*
XH_P43	1	225541540	225541552	Frame_Shift_Del	INDEL	TATAAAATT	-	-	DNAH14	11305delATATAA	P.13765fs
XH_P43	1	227842621	227842621	Missense_Mutation	SNV	C	G	G	ZNF678	c.835C>G	P.L279V
XH_P43	1	230824202	230824208	Frame_Shift_Del	INDEL	GTGTGCC	-	-	COG2	85_1691delGTG	P.C562fs
XH_P43	1	237774206	237774206	Silent	SNV	C	A	A	RYR2	c.4828C>A	P.R1610R
XH_P43	1	237777676	237777676	Missense_Mutation	SNV	G	T	T	RYR2	c.5248G>T	P.G1750W
XH_P43	1	26644536	26644536	Missense_Mutation	SNV	A	C	C	CD52	c.28A>C	P.T10P
XH_P43	1	38463766	38463766	Nonsense_Mutation	SNV	C	A	A	FHL3	c.46G>T	P.E16*
XH_P43	1	43825958	43825958	Silent	SNV	G	A	A	CCD20	c.651G>A	P.L217L
XH_P43	1	43825959	43825959	Missense_Mutation	SNV	C	A	A	CDC20	c.652C>A	P.Q218K
XH_P43	1	54606898	54606898	Silent	SNV	G	T	T	CDCP2	c.636C>A	P.T212T
XH_P43	1	74492500	74492500	Missense_Mutation	SNV	T	G	G	LRRIQ3	c.1872A>C	P.K624N
XH_P43	1	74663954	74663954	Missense_Mutation	SNV	G	T	T	FPGT-TNNI3K	c.31G>T	P.G11C
XH_P43	1	75065499	75065499	Missense_Mutation	SNV	C	G	G	ERICH3	c.1606G>C	P.D536H
XH_P43	1	89521788	89521788	Missense_Mutation	SNV	A	C	C	GBP1	c.1279T>G	P.Y427D
XH_P43	1	89587518	89587518	Silent	SNV	C	A	A	GBP2	c.132G>T	P.V44V
XH_P43	10	105344801	105344801	Silent	SNV	G	A	A	NEURL1	c.1158G>A	P.V386V
XH_P43	10	106917053	106917053	Splice_Site	SNV	C	A	A	SORCS3	c.1629+11C>A	
XH_P43	10	119044825	119044825	Silent	SNV	T	G	G	PDZD8	c.1419A>C	P.S473S
XH_P43	10	124273779	124273779	Silent	SNV	C	T	T	HTRA1	c.1347C>T	P.S449S
XH_P43	10	126138461	126138461	Missense_Mutation	SNV	T	C	C	NKX1-2	c.52A>G	P.I18V
XH_P43	10	35333790	35333790	Silent	SNV	A	G	G	CUL2	c.513T>C	P.R171R
XH_P43	10	6148182	6148182	Missense_Mutation	SNV	G	C	C	RBM17	c.486G>C	P.E162D
XH_P43	10	7618752	7618752	Missense_Mutation	SNV	G	A	A	ITIH5	c.1642C>T	P.R548W
XH_P43	10	87628910	87628910	Missense_Mutation	SNV	G	C	C	GRID1	c.808C>G	P.L270V
XH_P43	11	120744909	120744923	Missense_Mutation	INDEL	GAACCTACCT	-	-	GRIK4	S9delAACTACCT	N349_M353del
XH_P43	11	17140870	17140870	Splice_Site	SNV	T	C	C	PIK3C2A	c.2847-10A>G	
XH_P43	11	17661017	17661017	Splice_Site	SNV	A	G	G	OTOG	c.7971+7A>G	
XH_P43	11	59626550	59626550	Missense_Mutation	SNV	C	G	G	TCN1	c.747G>C	P.Q249H
XH_P43	11	60470907	60470907	Silent	SNV	G	A	A	MS4A8	c.276G>A	P.T92T
XH_P43	11	6623244	6623244	Missense_Mutation	SNV	G	A	A	RRP8	c.301C>T	P.P101S
XH_P43	11	66482734	66482734	Missense_Mutation	SNV	G	C	C	SPTBN2	c.442C>G	P.L148V
XH_P43	11	74717292	74717292	Missense_Mutation	SNV	A	C	C	NEU3	c.1141A>C	P.N381H
XH_P43	12	100691833	100691833	Silent	SNV	A	G	G	SCYL2	c.360A>G	P.E120E
XH_P43	12	11149642	11149642	Missense_Mutation	SNV	A	G	G	TAS2R20	c.833T>C	P.L278T
XH_P43	12	111856340	111856340	Missense_Mutation	SNV	G	T	T	SH2B3	c.391G>T	P.G131W
XH_P43	12	112171758	112171758	Missense_Mutation	SNV	C	T	T	ACAD10	c.1519C>T	P.P507S
XH_P43	12	114385128	114385128	Splice_Site	SNV	C	T	T	RBM19	c.1407+11G>A	
XH_P43	12	117693790	117693790	Missense_Mutation	SNV	C	A	A	NOS1	c.2584G>T	P.G862C
XH_P43	12	46245680	46245680	Silent	SNV	T	G	G	ARID2	c.3774T>G	P.V1258V
XH_P43	12	51686040	51686040	Missense_Mutation	SNV	G	T	T	BIN2	c.772C>A	P.L258I
XH_P43	12	52631309	52631309	Missense_Mutation	SNV	A	C	C	KRT7	c.553A>C	P.N185H
XH_P43	12	7970637	7970637	Splice_Site	INDEL	-	CCCTATCTATGT	CCCTATCTATGT	SLC2A14	CATAGATACATAGATAAGGTGGAGTTTA	
XH_P43	12	89745528	89745528	Frame_Shift_Ins	INDEL	-	CA	CA	DUSP6	-287_288dupTG	P.L97fs
XH_P43	13	21563023	21563023	Missense_Mutation	SNV	C	T	T	LATS2	c.896G>A	P.G299D
XH_P43	13	21714712	21714712	Silent	SNV	A	G	G	SAP18	c.21A>G	P.G7G
XH_P43	13	32869537	32869537	Missense_Mutation	SNV	G	C	C	FRY	c.8982G>C	P.Q2994H
XH_P43	13	32890558	32890558	Splice_Site	SNV	G	A	A	BRCA2	c.-39-1G>A	
XH_P43	13	32893318	32893318	Nonsense_Mutation	SNV	G	T	T	BRCA2	c.172G>T	P.E58*
XH_P43	13	41943342	41943342	Missense_Mutation	SNV	C	G	G	NAA16	c.1870C>G	P.Q624E
XH_P43	13	95813446	95813446	Missense_Mutation	SNV	T	C	C	ABCC4	c.2452A>G	P.I818V
XH_P43	13	99520227	99520227	Silent	SNV	C	T	T	DOCK9	c.3129G>A	P.K1043K
XH_P43	14	105459315	105459315	Missense_Mutation	SNV	G	C	C	C14orf79	c.730G>C	P.E244Q
XH_P43	14	24710078	24710078	Missense_Mutation	SNV	C	T	T	TINF2	c.608G>A	P.C203Y
XH_P43	14	64935657	64935657	Missense_Mutation	SNV	T	G	G	AKAP5	c.545T>G	P.L182R
XH_P43	14	65253884	65253884	Splice_Site	SNV	G	A	A	SPTB	c.2805-6C>T	
XH_P43	14	69727055	69727055	Missense_Mutation	SNV	G	C	C	GALNT16	c.48G>C	P.W16C
XH_P43	14	88857781	88857781	Missense_Mutation	SNV	T	A	A	SPATA7	c.76T>A	P.L26M
XH_P43	15	29415603	29415603	Missense_Mutation	SNV	G	C	C	FAM189A1	c.1559C>G	P.T520S
XH_P43	15	33999266	33999266	Splice_Site	SNV	C	T	T	RYR3	c.6619+11C>T	
XH_P43	15	42280287	42280287	Missense_Mutation	SNV	C	A	A	PLA2G4E	c.1791G>T	P.E597D
XH_P43	15	43584209	43584209	Missense_Mutation	SNV	A	G	G	TGM7	c.526T>C	P.F176L
XH_P43	15	71535393	71535393	Silent	SNV	A	C	C	THSD4	c.870A>C	P.S290S
XH_P43	15	74315486	74315486	Missense_Mutation	SNV	G	A	A	PML	c.920G>A	P.R307H
XH_P43	15	78390781	78390781	Missense_Mutation	SNV	T	A	A	SH2D7	c.488T>G	P.V163E

XH_P43	15	78416044	78416044	Splice_Site	SNV	T	G	G	CIB2	n.406+3A>C	
XH_P43	16	28990578	28990594	Frame_Shift_Del	INDEL	GGAGCCGGA	-	-	SPN51	delGGAGCCGGA	P.R184fs
XH_P43	16	3029648	3029648	Splice_Site	SNV	C	T	T	PKMYT1	c.10+1G>A	
XH_P43	16	3562401	3562401	Missense_Mutation	SNV	G	C	C	CLUAP1	c.418G>C	P.A140P
XH_P43	16	67660556	67660556	Missense_Mutation	SNV	C	G	G	CTCF	c.1456C>G	P.Q486E
XH_P43	16	70815812	70815812	Silent	SNV	A	T	T	VAC14	c.906T>A	P.T302T
XH_P43	16	71884705	71884705	Silent	SNV	T	C	C	ATXN1L	c.1062T>C	P.A354A
XH_P43	16	746821	746821	Silent	SNV	G	C	C	FBXL16	c.585C>G	P.V195V
XH_P43	16	89935977	89935977	Missense_Mutation	SNV	G	A	A	SPIRE2	c.1809G>A	P.M603I
XH_P43	17	18022373	18022373	Missense_Mutation	SNV	A	C	C	MYO15A	c.259A>C	P.M87L
XH_P43	17	37844195	37844195	Missense_Mutation	SNV	G	C	C	PGAP3	c.73C>G	P.R25G
XH_P43	17	39186047	39186047	Missense_Mutation	SNV	G	A	A	KRTAP1-4	c.284C>T	P.A95V
XH_P43	17	42452041	42452041	Nonsense_Mutation	SNV	G	A	A	ITGA2B	c.2929C>T	P.R977*
XH_P43	17	43138716	43138764	Frame_Shift_Del	INDEL	ACCTCCGCT	-	-	NMT1	GGCACCTCCGC	P.A8fs
XH_P43	17	44590528	44590528	Silent	SNV	G	A	A	LRRC37A2	c.450G>A	P.L150L
XH_P43	17	46801827	46801827	Missense_Mutation	SNV	T	C	C	PRAC2	c.55T>C	P.F19L
XH_P43	17	46986015	46986015	Silent	SNV	G	A	A	UBE2Z	c.150G>A	P.A50A
XH_P43	17	61473294	61473294	Splice_Site	SNV	G	C	C	TANC2	c.3015+5G>C	
XH_P43	17	66547263	66547263	Nonstop_Mutation	SNV	T	G	G	PRKAR1A	c.1012T>G	P.Ter338Ext**?
XH_P43	18	42532021	42532021	Missense_Mutation	SNV	C	T	T	SETBP1	c.2716C>T	P.P906S
XH_P43	18	52946773	52946773	Splice_Site	SNV	G	C	C	TCF4	c.655+9C>G	
XH_P43	18	6873480	6873480	Missense_Mutation	SNV	A	G	G	ARHGAP28	c.550A>G	P.I184V
XH_P43	19	1020899	1020899	Missense_Mutation	SNV	T	G	G	TMEM259	c.97A>C	P.N33H
XH_P43	19	1487972	1487972	Missense_Mutation	SNV	C	A	A	PCSK4	c.507G>T	P.W169C
XH_P43	19	15281611	15281611	Missense_Mutation	SNV	T	G	G	NOTCH3	c.4762A>C	P.N1588H
XH_P43	19	38886412	38886412	Missense_Mutation	SNV	C	A	A	SPRED3	c.860C>A	P.A287D
XH_P43	19	39965193	39965193	Missense_Mutation	SNV	G	A	A	SUPT5H	c.2859G>A	P.M953I
XH_P43	19	41105127	41105127	Frame_Shift_Del	INDEL	G	-	-	LTBP4	c.173delG	P.G58fs
XH_P43	19	4231187	4231187	Splice_Site	SNV	G	A	A	EBI3	c.68-1G>A	
XH_P43	19	46521350	46521350	Silent	SNV	G	T	T	CCDC61	c.1383G>T	P.V461V
XH_P43	19	52033119	52033119	Missense_Mutation	SNV	G	A	A	SIGLEC6	c.715C>T	P.P239S
XH_P43	19	54444729	54444729	Missense_Mutation	SNV	T	G	G	CACNG7	c.430T>G	P.S144A
XH_P43	19	55386792	55386792	Missense_Mutation	SNV	G	T	T	FCAR	c.41G>T	P.C14F
XH_P43	19	55665534	55665534	Missense_Mutation	SNV	T	C	C	TNNI3	c.410A>G	P.K137R
XH_P43	19	5772919	5772919	Silent	SNV	G	T	T	CATSPERD	c.1884G>T	P.P628P
XH_P43	19	8436202	8436202	Missense_Mutation	SNV	G	A	A	ANGPTL4	c.721G>A	P.D241N
XH_P43	19	8670540	8670540	Missense_Mutation	SNV	A	T	T	ADAMTS10	c.56T>A	P.M19K
XH_P43	19	8953438	8953438	Missense_Mutation	SNV	G	C	C	MBD3L1	c.84G>C	P.L28F
XH_P43	2	135756498	135756498	Silent	SNV	C	A	A	MAP3K19	c.384G>T	P.T128T
XH_P43	2	137917848	137917848	Missense_Mutation	SNV	A	T	T	THSD7B	c.1435A>T	P.I479F
XH_P43	2	160628521	160628521	Silent	SNV	T	C	C	LY75-CD302	c.5463A>G	P.V1821V
XH_P43	2	163059589	163059589	Missense_Mutation	SNV	C	G	G	FAP	c.1039G>C	P.D347H
XH_P43	2	172641804	172641804	Missense_Mutation	SNV	C	T	T	SLC25A12	c.2017G>A	P.A673T
XH_P43	2	179613977	179613977	Missense_Mutation	SNV	C	G	G	TTN	c.13150G>C	P.D4384H
XH_P43	2	183104914	183104914	Missense_Mutation	SNV	C	G	G	PDE1A	c.321G>C	P.M107I
XH_P43	2	183948243	183948243	Missense_Mutation	SNV	A	C	C	DUSP19	c.234A>C	P.Q78H
XH_P43	2	186659084	186659084	Missense_Mutation	SNV	G	T	T	FSIP2	c.7221G>T	P.K2407N
XH_P43	2	190428890	190428890	Missense_Mutation	SNV	A	C	C	SLC40A1	c.822T>G	P.H274Q
XH_P43	2	206921261	206921272	Missense_Mutation	INDEL	CTGCTCGCG	-	-	INO80D	525delCTCCGCGAP.P205_Q208del	
XH_P43	2	207516603	207516603	Missense_Mutation	SNV	T	G	G	DYTN	c.1676A>C	P.Q559P
XH_P43	2	220418415	220418415	Splice_Site	SNV	G	T	T	OBSL1	c.4877-7C>A	
XH_P43	2	228147097	228147097	Silent	SNV	G	A	A	COL4A3	c.2505G>A	P.T835T
XH_P43	2	24181213	24181213	Frame_Shift_Ins	INDEL	-	A	A	UBXN2A	c.33dupA	P.E12fs
XH_P43	2	33505109	33505109	Missense_Mutation	SNV	T	C	C	LTBP1	c.2018T>C	P.I673T
XH_P43	2	37247965	37247965	Missense_Mutation	SNV	G	T	T	HEATR5B	c.3868C>A	P.L1290I
XH_P43	2	39440536	39440536	Splice_Site	SNV	C	T	T	CDKL4	c.363+5G>A	
XH_P43	2	45233593	45233593	Missense_Mutation	SNV	G	T	T	SIX2	c.592C>A	P.H198N
XH_P43	2	46607605	46607605	Missense_Mutation	SNV	G	C	C	EPAS1	c.1794G>C	P.E598D
XH_P43	2	48027493	48027493	Missense_Mutation	SNV	C	T	T	MSH6	c.2371C>T	P.R791C
XH_P43	2	60688491	60688491	Missense_Mutation	SNV	A	G	G	BCL11A	c.1556T>C	P.L519P
XH_P43	2	71170817	71170817	Frame_Shift_Del	INDEL	C	-	-	ATP6V1B1	c.151delC	P.L51fs
XH_P43	2	97297208	97297208	Missense_Mutation	SNV	A	G	G	KANSL3	c.227T>C	P.V76A
XH_P43	2	98732163	98732163	Missense_Mutation	SNV	G	A	A	VWA3B	c.245G>A	P.G82D
XH_P43	20	45140726	45140726	Missense_Mutation	SNV	A	T	T	ZNF334	c.16T>A	P.F6I
XH_P43	21	35138252	35138252	Missense_Mutation	SNV	G	A	A	ITSN1	c.862G>A	P.V288I
XH_P43	21	35190725	35190725	Missense_Mutation	SNV	T	G	G	ITSN1	c.2882T>G	P.F961C
XH_P43	3	119379059	119379059	Missense_Mutation	SNV	C	A	A	POPOC2	c.212G>T	P.S71I
XH_P43	3	122134051	122134051	Silent	SNV	A	G	G	WDR5B	c.325T>C	P.L109L
XH_P43	3	126735436	126735436	Missense_Mutation	SNV	A	C	C	PLXNA1	c.3091A>C	P.N1031H
XH_P43	3	151598857	151598857	Missense_Mutation	SNV	G	A	A	SUCNR1	c.526G>A	P.A176T
XH_P43	3	44448997	44448997	Missense_Mutation	SNV	A	C	C	TCAM1	c.882A>C	P.L294F
XH_P43	3	50327623	50327623	Silent	SNV	G	C	C	IFRD2	c.558C>G	P.A186A
XH_P43	3	93595881	93595881	Missense_Mutation	SNV	A	C	C	PROS1	c.1799T>G	P.L600R
XH_P43	3	96706748	96706748	Missense_Mutation	SNV	T	C	C	EPHA6	c.1025T>C	P.L342P
XH_P43	4	113199106	113199106	Missense_Mutation	SNV	G	A	A	TIFA	c.467C>T	P.P156L
XH_P43	4	119219902	119219902	Missense_Mutation	SNV	C	T	T	PRSS12	c.1823G>A	P.G608D
XH_P43	4	15575868	15575868	Silent	SNV	A	G	G	CC2D2A	c.3690A>G	P.R1230R
XH_P43	4	177632786	177632786	Missense_Mutation	SNV	G	C	C	VEGFC	c.571C>G	P.P191A
XH_P43	4	185603415	185603415	Missense_Mutation	SNV	T	G	G	PRIMPOL	c.634T>G	P.L212V
XH_P43	4	187149410	187149410	Splice_Site	SNV	A	T	T	KLKB1	c.58+3A>T	
XH_P43	4	22438160	22438160	Nonsense_Mutation	SNV	C	T	T	ADGRA3	c.1190G>A	P.W397*
XH_P43	4	24839843	24839843	Missense_Mutation	SNV	C	T	T	CCDC149	c.424G>A	P.V142M
XH_P43	4	4419094	4419094	Missense_Mutation	SNV	T	G	G	NSG1	c.490T>G	P.W164G
XH_P43	4	48525064	48525064	Missense_Mutation	SNV	C	T	T	FRYL	c.7375G>A	P.D2459N
XH_P43	4	6863603	6863603	Silent	SNV	G	T	T	KIAA0232	c.1494G>T	P.L498L
XH_P43	4	8271771	8271771	Frame_Shift_Del	INDEL	C	-	-	HTRA3	c.78delC	P.A27fs
XH_P43	4	8271987	8272030	Frame_Shift_Del	INDEL	5CAGGCGGCG	-	-	HTRA3	1GCTGCAGGCGCG	P.N99fs
XH_P43	4	8451440	8451440	Frame_Shift_Del	INDEL	A	-	-	TRMT44	c.779delA	P.D260fs
XH_P43	4	96222837	96222837	Missense_Mutation	SNV	G	T	T	UNC5C	c.410C>A	P.P137H
XH_P43	4	99966407	99966407	Missense_Mutation	SNV	G	A	A	METAP1	c.733G>A	P.A245T
XH_P43	5	112174620	112174620	Nonsense_Mutation	SNV	C	G	G	APC	c.3329C>G	P.S1110*
XH_P43	5	112175951	112175951	Frame_Shift_Ins	INDEL	-	A	A	APC	c.4666dupA	P.T1556fs
XH_P43	5	115238594	115238594	Missense_Mutation	SNV	C	A	A	AP3S1	c.292C>A	P.L98I
XH_P43	5	130764910	130764910	Splice_Site	SNV	C	G	G	RAPGEF6	c.4490-1G>C	
XH_P43	5	13769150	13769162	Frame_Shift_Del	INDEL	TGTCCACAA	-	-	DNAH5	816delCATTGTG	P.I3269fs
XH_P43	5	141041803	141041803	Silent	SNV	T	G	G	ARAP3	c.2820A>C	P.V940V
XH_P43	5	149406316	149406316	Missense_Mutation	SNV	G	A	A	HMGXB3	c.1508G>A	P.R503K
XH_P43	5	153054066	153054066	Missense_Mutation	SNV	A	G	G	GRIA1	c.706A>G	P.M236V

XH_P43	5	153190634	153190634	Missense_Mutation	SNV	C	G	G	GRIA1	c.2570C>G	P.S857W
XH_P43	5	156376669	156376682	Frame_Shift_Del	INDEL	CAGCAGGA	-	-	TIMD4	53delCTGTCCTG	P.T247fs
XH_P43	5	157078575	157078575	Missense_Mutation	SNV	G	C	C	SOX30	c.512C>G	P.P171R
XH_P43	5	167881085	167881085	Missense_Mutation	SNV	G	T	T	WWC1	c.2638G>T	P.D880Y
XH_P43	5	169116272	169116272	Nonsense_Mutation	SNV	C	T	T	DOCK2	c.778C>T	P.R260*
XH_P43	5	172750383	172750383	Silent	SNV	C	A	A	STC2	c.345G>T	P.R115R
XH_P43	5	177547473	177547473	Missense_Mutation	SNV	A	C	C	N4BP3	c.625A>C	P.S209R
XH_P43	5	178418947	178418970	Missense_Mutation	INDEL	CCCACTGCC	-	-	GRM6	CGTGAGGGCACT	P.1207_N214del
XH_P43	5	34937739	34937739	Splice_Site	SNV	C	T	T	DNAJC21	c.743+4C>T	
XH_P43	5	41381971	41381971	Missense_Mutation	SNV	C	G	G	PLCXD3	c.769G>C	P.V257L
XH_P43	5	5182420	5182420	Splice_Site	SNV	T	C	C	ADAMTS16	c.763+2T>C	
XH_P43	6	121577425	121577425	Silent	SNV	T	G	G	TBC1D32	c.1740A>C	P.T580T
XH_P43	6	132270606	132270606	Missense_Mutation	SNV	A	T	T	CTGF	c.848T>A	P.F283Y
XH_P43	6	152765647	152765647	Missense_Mutation	SNV	C	T	T	SYNE1	c.3757G>A	P.E1253K
XH_P43	6	26390390	26390390	Silent	SNV	G	A	A	BTN2A2	c.882G>A	P.K294K
XH_P43	6	52661078	52661078	Silent	SNV	A	C	C	GSTA1	c.174T>G	P.V58V
XH_P43	6	56505023	56505023	Missense_Mutation	SNV	G	C	C	DST	c.2309C>G	P.S770C
XH_P43	6	76744431	76744440	Frame_Shift_Del	INDEL	GTCTCTGATA	-	-	IMPG1	141delATATCA	P.E44fs
XH_P43	7	107571837	107571837	Silent	SNV	T	G	G	LAM81	c.4501A>C	P.R1501R
XH_P43	7	1132250	1132250	Nonsense_Mutation	SNV	C	T	T	GP296*	c.886C>T	P.Q296*
XH_P43	7	128531043	128531043	Missense_Mutation	SNV	C	A	A	KCP	c.1894G>T	P.G632C
XH_P43	7	150325467	150325467	Missense_Mutation	SNV	T	A	A	GIMAP6	c.219A>T	P.R73S
XH_P43	7	45688277	45688277	Missense_Mutation	SNV	C	A	A	ADCY1	c.354C>A	P.H118Q
XH_P43	7	84636181	84636181	Silent	SNV	A	G	G	SEMA3D	c.1845T>C	P.P615P
XH_P43	7	86813934	86813934	Missense_Mutation	SNV	A	C	C	DMTF1	c.778A>C	P.I260L
XH_P43	7	91670082	91670082	Missense_Mutation	SNV	G	A	A	AKAP9	c.4787G>A	P.R1596G
XH_P43	8	35425698	35425698	Silent	SNV	G	A	A	UNC5D	c.390G>A	P.Q130Q
XH_P43	8	35425699	35425699	Missense_Mutation	SNV	T	G	G	UNC5D	c.391T>G	P.C131G
XH_P43	8	36780071	36780071	Missense_Mutation	SNV	C	A	A	KCNU1	c.2660C>A	P.T887K
XH_P43	8	77690663	77690663	Missense_Mutation	SNV	C	A	A	ZFXH4	c.3313C>A	P.P1105T
XH_P43	8	95186404	95186404	Missense_Mutation	SNV	T	C	C	CDH17	c.509A>G	P.Q170R
XH_P43	9	112020470	112020470	Missense_Mutation	SNV	A	G	G	EPB41L4B	c.739T>C	P.W247R
XH_P43	9	125512494	125512494	Missense_Mutation	SNV	G	A	A	OR1L6	c.368G>C	P.T213Q
XH_P43	9	136597690	136597690	Missense_Mutation	SNV	T	A	A	SARDH	c.365A>T	P.E122V
XH_P43	9	140100370	140100370	Splice_Site	SNV	G	T	T	NDOR1	c.135+6G>T	
XH_P43	9	74674269	74674269	Silent	SNV	G	A	A	C9orf57	c.45C>T	P.L15L
XH_P43	9	75435918	75435925	Frame_Shift_Del	INDEL	CTCATCCT	-	-	TMC1	6_1933delCATC	P.P1643fs
XH_P43	9	75545867	75545867	Missense_Mutation	SNV	C	A	A	ALDH1A1	c.240G>C	P.M80I
XH_P43	9	88247699	88247699	Missense_Mutation	SNV	A	C	C	AGTPBP1	c.2049T>G	P.P1683M
XH_P43	9	990882	990896	Missense_Mutation	INDEL	TCGGATTTC	-	-	DMRT3	14delCGGATTTP	P.R434_P438del
XH_P43	X	100630257	100630257	Missense_Mutation	SNV	G	T	T	BTX	c.16C>A	P.L6M
XH_P43	X	46502762	46502762	Missense_Mutation	SNV	T	G	G	SLC9A7	c.1525A>C	P.M509L
XH_P43	X	48676620	48676620	Splice_Site	SNV	C	T	T	HDAC6	c.2037-7C>T	
XH_P43	X	9864732	9864732	Nonsense_Mutation	SNV	C	A	A	SHROOM2	c.2784C>A	P.Y928*
XH_P44	11	108236192	108236192	Missense_Mutation	SNP	A	G	G	ATM	c.9128A>G	p.K3043R
XH_P44	3	178952006	178952006	Missense_Mutation	SNP	T	C	C	PIK3CA	c.3061T>C	p.V1021H
XH_P44	1	1722017	1722017	Nonsense_Mutation	INS	-	GCTAAATTTTAA	-	GNB1	AAAGTTTAAAT	P.7_173delinsEKFIX
XH_P44	1	1722019	1722019	Nonsense_Mutation	INS	-	TGGATTA	-	GNB1	13_214insTAAT	P.7_173delinsX
XH_P44	1	3742991	3742991	Nonsense_Mutation	INS	-	TAACCTAAAATA	-	CEP104	AAAGGATATTTT	P.573delinsAERIFX
XH_P44	1	7309649	7309649	In_Frame_Ins	INS	-	AAGTCTCTACAG	-	CAMTA1	nsTAAAGTCTCT	P.104delinsSKSLYRK
XH_P44	1	8074451	8074451	Frame_Shift_Ins	INS	-	CTCTCTCTGG	-	ERRF1	208insCCAGAGA	p.A70fs
XH_P44	1	10318685	10318685	Frame_Shift_Ins	INS	-	AGTTTACTTTTC	-	KIF1B	9insCAAGTTTAA	p.T106fs
XH_P44	1	10318687	10318687	In_Frame_Ins	INS	-	TAAATACAC	-	KIF1B	321insTAAAT	P.1M107delinsIKYT
XH_P44	1	10363382	10363382	Frame_Shift_Ins	INS	-	CGAAGAAAAAG	-	KIF1B	140insTCGAAG	p.K713fs
XH_P44	1	10384842	10384842	In_Frame_Ins	INS	-	AAGCCATCAAA	-	KIF1B	2427insAAGCCAA	P.1M809delinsISHQK
XH_P44	1	10421817	10421817	Nonsense_Mutation	INS	-	TATCTGAGGTAA	-	KIF1B	TATTTTATTCTGA	P.1367delinsAFIFIX
XH_P44	1	10435047	10435047	Frame_Shift_Ins	INS	-	TT	-	KIF1B	5094_5095insT	p.11698fs
XH_P44	1	10435049	10435049	In_Frame_Ins	INS	-	CTGCCAAAG	-	KIF1B	5_5097insCTGCC	P.11699delinsICQS
XH_P44	1	11204783	11204783	In_Frame_Ins	INS	-	AGTGTA	-	MTOR	793_4794insTAC	P.1E1598delinsDTL
XH_P44	1	11204785	11204785	Missense_Mutation	SNP	C	T	C	MTOR	c.G4792A	p.E1598K
XH_P44	1	12333066	12333066	Nonsense_Mutation	INS	-	AATAACTAAAT	-	VPS13D	ATAGCAAAATA	P.4_K705delinsKKNKX
XH_P44	1	12337562	12337562	In_Frame_Ins	INS	-	TGTCAATCCAT	-	VPS13D	8insTTGTGTCAA	P.1306delinsSCVKIS
XH_P44	1	12359400	12359400	In_Frame_Ins	INS	-	AATTAATAATG	-	VPS13D	TAAACAATAAT	P.104delinsREFIKQLKSYRAYSM
XH_P44	1	14108446	14108446	Nonsense_Mutation	INS	-	AAAGCTTGGG	-	PRDM2	3554insAAAGC	P.185_D118delinsX
XH_P44	1	14108448	14108448	Frame_Shift_Ins	INS	-	ATGCT	-	PRDM2	555_3556insAT	p.L1185fs
XH_P44	1	14108709	14108709	Nonsense_Mutation	INS	-	AGTTAAGCCTTT	-	PRDM2	7insTAAAGTTAA	P.1H1272delinsHX
XH_P44	1	15987142	15987142	Nonsense_Mutation	INS	-	TCTTGTCATG	-	RSC1A1	AGATATTCTTGG	P.60delinsTKFLVMX
XH_P44	1	16254851	16254851	In_Frame_Ins	INS	-	ATAATATGTACG	-	SPEN	ACTCTCAATAA	P.16delinsHSHNMYDLG
XH_P44	1	16256942	16256942	Nonsense_Mutation	INS	-	TGCTAGATCAT	-	SPEN	8insTCTGCTAG	P.1403delinsLLESX
XH_P44	1	17355193	17355193	Frame_Shift_Ins	INS	-	AC	-	SDHB	c.324_325insGT	p.N109fs
XH_P44	1	17355195	17355195	Frame_Shift_Ins	INS	-	TATTAGTTTTT	-	SDHB	323insAAAAAC	p.G108fs
XH_P44	1	19408061	19408061	Nonsense_Mutation	INS	-	GCTCACTATTC	-	UBR4	15015insGAAAT	P.1R5005delinsRKX
XH_P44	1	19428130	19428130	In_Frame_Ins	INS	-	AAAGTTATGGG	-	UBR4	07insATTCCCCA	P.303delinsPHNFNE
XH_P44	1	19482862	19482862	Nonsense_Mutation	INS	-	GTAGCTGTGAT	-	UBR4	975insGATCAC	P.1992_H1993delinsX
XH_P44	1	19514033	19514033	Frame_Shift_Ins	INS	-	AA	-	UBR4	1395_1396insT	p.H466fs
XH_P44	1	19514035	19514035	Splice_Site	INS	-	TGCTCT	-	UBR4	.	.
XH_P44	1	19559434	19559434	Frame_Shift_Ins	INS	-	TGGTGAAGGA	-	EMC1	1562insTCCTT	p.G521fs
XH_P44	1	19559435	19559435	Frame_Shift_Ins	INS	-	AAGG	-	EMC1	1560_1561insCC	p.G521fs
XH_P44	1	20964528	20964528	Frame_Shift_Ins	INS	-	CCTAGGA	-	PINK1	81_582insCCTAG	p.P194fs
XH_P44	1	21299578	21299578	Frame_Shift_Ins	INS	-	8ATTGTATGGG	-	EIF4G3	8insATGCCATA	p.P114fs
XH_P44	1	21307678	21307678	In_Frame_Ins	INS	-	CGTGGAAGCT	-	EIF4G3	5sAAAACAGTTCA	P.25delinsKVTHTSP
XH_P44	1	22304940	22304940	Nonsense_Mutation	INS	-	GGACCTCCCG	-	CELA3B	TTTGGGGACCC	P.10delinsPPLCFWGPSRX
XH_P44	1	23418654	23418654	In_Frame_Ins	INS	-	AGACTACGTGG	-	LUZP1	TGTTTCTCCAAC	P.10delinsLFLQRLSCSR
XH_P44	1	23419847	23419847	Nonsense_Mutation	INS	-	GAGAGGTAGAA	-	LUZP1	TTCCCTCTCTAC	P.103delinsIFPFVLSIFX
XH_P44	1	24077955	24077955	Nonsense_Mutation	INS	-	TCTGTAGTGGT	-	ELOA	939insTCTGTAG	P.13_N314delinsDLX
XH_P44	1	24981595	24981595	Nonsense_Mutation	INS	-	AATAAAGTATTG	-	SRRM1	291insGAATAAA	P.430_5431delinsVEX
XH_P44	1	25715554	25715554	Nonsense_Mutation	INS	-	ATTGTGTAA	-	RHCE	5_537insTTAAC	p.S179delinsSX
XH_P44	1	25715556	25715556	In_Frame_Ins	INS	-	TGCTGG	-	RHCE	34_535insCCAG	P.5179delinsPAS
XH_P44	1	26161642	26161642	Frame_Shift_Ins	INS	-	5GAAAAATAGT	-	AUNIP	CCACAACATAT	p.P306fs
XH_P44	1	26582311	26582311	Frame_Shift_Ins	INS	-	G	-	CEP85	c.705_706insG	p.C235fs
XH_P44	1	26582312	26582312	In_Frame_Ins	INS	-	8GTCTTGGGTT	-	CEP85	7insTGGTTCTTG	P.236delinsLVGLW
XH_P44	1	26691706	26691706	In_Frame_Ins	INS	-	ATACCCACT	-	ZNF683	331insAGTGG	P.111delinsSGVP
XH_P44	1	26800627	26800627	Splice_Site	INS	-	TGTTTTTTGATG	-	HMG2	.	.
XH_P44	1	27106002	27106002	In_Frame_Ins	INS	-	ATTCTCTGAAGC	-	ARID1A	514insTATTCTCT	P.1871delinsHYSYKL
XH_P44	1	28477260	28477260	Silent	SNP	G	A	G	PTAFR	c.C273T	p.N91N
XH_P44	1	29040775	29040775	Nonsense_Mutation	INS	-	AAAGACTTTTGTG	-	GMEB1	AAAGAAAAAGAC	P.95delinsVYKKEKTLCRGXK
XH_P44	1	31414971	31414971	Splice_Site	INS	-	GAATCTTGTGG	-	PUM1	.	.
XH_P44	1	32505141	32505141	Nonsense_Mutation	INS	-	AAAATAATTGAC	-	KHDRB51	nsTTATAAAAAA	P.162_G363delinsLIXK

XH_P44	1	32745564	32745564	In_Frame_Ins	INS	-	CCAGTCTCCTT	-	LCK	1012insCCCAGT	L337delinsLPSLL
XH_P44	1	32745566	32745566	Missense_Mutation	SNP	T	C	T	LCK	c.T1013C	p.I338T
XH_P44	1	33412076	33412076	Nonsense_Mutation	INS	-	TGAAAGTTCTTA	-	RNF19B	ATGTTAATAAGA	V358delinsGCX
XH_P44	1	34046379	34046379	In_Frame_Ins	INS	-	TCITTTCTCATAC	-	CSMD2	61insAGATTGAC	2454delinsQYKEKRG
XH_P44	1	34401550	34401550	Frame_Shift_Ins	INS	-	AGGT	-	CSMD2	522_523insACC	p.P175fs
XH_P44	1	35559637	35559637	Nonsense_Mutation	INS	-	SGTTCTCTCATTC	-	ZMYM1	50insGGTTCTCTT	417_L18delinsRFLHX
XH_P44	1	35579369	35579369	In_Frame_Ins	INS	-	SCITTAGGTA	-	ZMYM1	714insAGCTTTAA	I571delinsISFRYF
XH_P44	1	35972472	35972472	In_Frame_Ins	INS	-	AGGTAAGCATGTG	-	KIAA0319L	407insGCATGCT	T136delinsSMLTS
XH_P44	1	35972474	35972474	Missense_Mutation	SNP	T	A	T	KIAA0319L	c.A405T	p.Q135H
XH_P44	1	36202564	36202564	Missense_Mutation	SNP	G	T	G	CLSPN	c.C3668A	p.T1223K
XH_P44	1	36202566	36202566	In_Frame_Ins	INS	-	TTCTTTCTTTTT	-	CLSPN	insGAAAAAAG	222delinsQKKRKKD
XH_P44	1	36301571	36301571	Frame_Shift_Ins	INS	-	TTTAT	-	AG04	701_1702insTT	p.N567fs
XH_P44	1	36301573	36301573	Frame_Shift_Ins	INS	-	ACTATATACTGT	-	AG04	insCCTACTATA	p.N568fs
XH_P44	1	36904502	36904502	In_Frame_Ins	INS	-	ATGCAATGGTTG	-	OSCP1	122insGAACCA	T41delinsGTIAY
XH_P44	1	38027786	38027786	Frame_Shift_Ins	INS	-	AATGGAAT	-	DNAL1	7_748insAATGC	p.V249fs
XH_P44	1	38288266	38288266	Frame_Shift_Ins	INS	-	T	-	MTF1	1293_1294ins	p.Q432fs
XH_P44	1	38288268	38288268	Frame_Shift_Ins	INS	-	CATCAGCT	-	MTF1	1_1292insAGCT	p.P431fs
XH_P44	1	38348540	38348540	In_Frame_Ins	INS	-	TAGTTGTCTCCC	-	INPP5B	378insGGGAGA	293delinsGETTM
XH_P44	1	38484931	38484931	In_Frame_Ins	INS	-	CTCACTTATAT	-	UTP11	TGGTCTCACTT	delinsHRIWSHFILDSSR
XH_P44	1	39358876	39358876	Silent	SNP	A	T	A	RHBDL2	c.T870A	p.P290P
XH_P44	1	39358878	39358878	In_Frame_Ins	INS	-	TTTTATTAGAAA	-	RHBDL2	insATCITTTCTAA	P290delinsFLIKPP
XH_P44	1	39751004	39751004	Frame_Shift_Ins	INS	-	CACCT	-	MACF1	310_1311insCA	p.Q437fs
XH_P44	1	39751006	39751006	In_Frame_Ins	INS	-	ACAGATACTCTT	-	MACF1	313insAACAGAT	N438delinsKQILFH
XH_P44	1	39785351	39785351	In_Frame_Ins	INS	-	AAGTTCTCGCTT	-	MACF1	377insCAAGTTC	T1326delinsTSSRFL
XH_P44	1	39851327	39851327	Frame_Shift_Ins	INS	-	AAAAACAGATCTA	-	MACF1	385insAAAAACA	p.E2628fs
XH_P44	1	39853499	39853499	Frame_Shift_Ins	INS	-	ATCTTCTATCCAT	-	MACF1	3800insATCTTC	p.T2933fs
XH_P44	1	39853500	39853500	Frame_Shift_Ins	INS	-	GCAC	-	MACF1	3800_8801insGC	p.E2934fs
XH_P44	1	39898264	39898264	In_Frame_Ins	INS	-	CACATTTCAATT	-	MACF1	1210insCCACAT	T373delinsTTFQFL
XH_P44	1	39907872	39907872	Frame_Shift_Ins	INS	-	AGTGTTAT	-	MACF1	1_12652insAGT	p.H4217fs
XH_P44	1	39907873	39907873	Frame_Shift_Ins	INS	-	T	-	MACF1	12652_12653in	p.Q4218fs
XH_P44	1	40207572	40207572	Nonsense_Mutation	INS	-	CAATGAACAGGG	-	PIIE	181insCAATGAAP	A60delinsAQX
XH_P44	1	40703432	40703432	Missense_Mutation	SNP	A	T	A	RLF	c.A3058T	p.S1020C
XH_P44	1	40703433	40703433	Frame_Shift_Ins	INS	-	ACTGGAAACATT	-	RLF	insCCATACTGGG	p.S1020fs
XH_P44	1	40705906	40705906	Nonsense_Mutation	INS	-	TAGGTTTGTAAAG	-	RLF	5533insTAGGTT	P1844delinsPX
XH_P44	1	40705907	40705907	Missense_Mutation	SNP	C	T	C	RLF	c.C5533T	p.P1845S
XH_P44	1	40775989	40775989	In_Frame_Ins	INS	-	SGATTCCTGCTT	-	COL9A2	5insACAAGCAG	229delinsTSRNPNG
XH_P44	1	40923099	40923099	Frame_Shift_Ins	INS	-	GAGCCCATCC	-	ZFP69B	425insGAGCC	p.V142fs
XH_P44	1	40929232	40929232	Frame_Shift_Ins	INS	-	CCTTACATTTA	-	ZFP69B	1577insCCTTAA	p.L526fs
XH_P44	1	40961084	40961084	Frame_Shift_Ins	INS	-	5AATAAAATTATA	-	ZFP69	338insGAATAAA	p.A313fs
XH_P44	1	41012624	41012624	Nonsense_Mutation	INS	-	ACTTCTATTATA	-	ZNF684	GTATAACTTCTA	T211delinsKRFLQYNFYIYX
XH_P44	1	42048025	42048025	Missense_Mutation	SNP	G	A	G	HIVEP3	c.C244AT	p.P815L
XH_P44	1	42657102	42657102	Nonsense_Mutation	INS	-	TCTTGATTAAAA	-	FOXJ3	sATAAAATTTTAA	74_Q375delinsNKFX
XH_P44	1	42880573	42880573	Frame_Shift_Ins	INS	-	ATCGT	-	RIMKLA	104_1105insAT	p.A368fs
XH_P44	1	43055136	43055136	Frame_Shift_Ins	INS	-	GTATGTGTCTAT	-	CCDC30	5GTAGGGGTATG	p.E455fs
XH_P44	1	43240471	43240471	Frame_Shift_Ins	INS	-	TTAGACTATGCT	-	C1orf50	AAAAATAGACT	p.P116fs
XH_P44	1	43632865	43632865	In_Frame_Ins	INS	-	TTTTATTCTTAA	-	EBNA1BP2	GTATTTTAAAGA	delinsAPLYFNKNSLNH
XH_P44	1	43719817	43719817	Frame_Shift_Ins	INS	-	CAAACATTITA	-	CFAP57	3808insCAAAC	p.P1269fs
XH_P44	1	43806146	43806146	Frame_Shift_Ins	INS	-	CCTAGAGATA	-	MPL	943insCTCTAGA	p.F314fs
XH_P44	1	43868846	43868846	Splice_Site	INS	-	AGTTTCACCTATA	-	SZT2	.	.
XH_P44	1	43896275	43896275	In_Frame_Ins	INS	-	TGAAAACTCCAG	-	SZT2	4419insTGAAAA	1473delinsSENSR
XH_P44	1	44121427	44121427	Frame_Shift_Ins	INS	-	TCCAGGAAGCA	-	KDM4A	insGAGTCCAGG	p.N102fs
XH_P44	1	44149406	44149406	Nonsense_Mutation	INS	-	ACGTACCAAC	-	KDM4A	AAATACCAGTAA	R597delinsQYHVPNX
XH_P44	1	44422622	44422622	In_Frame_Ins	INS	-	ACACCTGCA	-	IP013	5_1246insACAC	D415delinsDTPA
XH_P44	1	44590507	44590507	Frame_Shift_Ins	INS	-	TTTTTGGTTTT	-	KLF17	115insTTTTTGG	p.M381fs
XH_P44	1	44590509	44590509	Missense_Mutation	SNP	C	A	C	KLF17	c.C116A	p.S39Y
XH_P44	1	45155575	45155575	Missense_Mutation	SNP	C	T	C	C1orf228	c.C206T	p.T69I
XH_P44	1	45155576	45155576	Splice_Site	INS	-	CAACTCCAT	-	C1orf228	.	.
XH_P44	1	45292163	45292163	Frame_Shift_Ins	INS	-	TGCT	-	PTCHK2	972_2973insAG	p.L991fs
XH_P44	1	45808951	45808951	Silent	SNP	C	G	C	TOE1	c.C1110G	p.V370V
XH_P44	1	45808952	45808952	Missense_Mutation	SNP	T	G	T	TOE1	c.T1111G	p.C371G
XH_P44	1	45812388	45812388	Frame_Shift_Ins	INS	-	TTTTGTATTAT	-	TESK2	607insATAATA	p.Q203fs
XH_P44	1	45812390	45812390	Missense_Mutation	SNP	A	T	A	TESK2	c.T605A	p.L202Q
XH_P44	1	46073974	46073974	Frame_Shift_Ins	INS	-	CTGATCCAGCCT	-	NASP	00insTTCTGATC	p.T400fs
XH_P44	1	46087389	46087389	Nonsense_Mutation	INS	-	TTTCTA	-	CCDC17	04_1105insTAG	p.M369delinsX
XH_P44	1	46725766	46725766	In_Frame_Ins	INS	-	TTTTTTTTTGAG	-	RAD54L	insTTTTTTTTTTTT	T134delinsLFFFFEM
XH_P44	1	47399901	47399901	Silent	SNP	C	T	C	CYP4A11	c.G1035A	p.E345E
XH_P44	1	47399902	47399902	Missense_Mutation	SNP	T	C	T	CYP4A11	c.A1034G	p.E345G
XH_P44	1	47400147	47400147	In_Frame_Ins	INS	-	CAGCCTCCT	-	CYP4A11	875insAGGAG	L292delinsQEA
XH_P44	1	49511473	49511473	Splice_Site	INS	-	AGGTTTGGGT	-	AGBL4	.	.
XH_P44	1	52306000	52306000	Nonsense_Mutation	INS	-	CAAAAAGGAAG	-	NRDC	TATATACTCTCT	77delinsDQKITVYFLFAIKXX
XH_P44	1	52902577	52902577	Nonsense_Mutation	SNP	G	A	G	ZCHC11	c.C4012T	p.R1338X
XH_P44	1	52941060	52941060	Frame_Shift_Ins	INS	-	ACCAGCAAAAGC	-	ZCHC11	71insCTGCTTTT	p.K724fs
XH_P44	1	52947206	52947206	Frame_Shift_Ins	INS	-	AGTACCAAGAT	-	ZCHC11	1737insATCTTC	p.E579fs
XH_P44	1	53250636	53250636	Frame_Shift_Ins	INS	-	TATTGATCTATT	-	ZYG11B	1181insTATTCA	p.D394fs
XH_P44	1	54254855	54254855	Nonsense_Mutation	INS	-	TGTTTATATAG	-	ND1	ATGATCTATATA	1delinsSKYIFQNDLYKTIKX
XH_P44	1	54262641	54262641	Frame_Shift_Ins	INS	-	A	-	ND1	1278_1279ins	p.T427fs
XH_P44	1	54262642	54262642	In_Frame_Ins	INS	-	GATATGTTATA	-	ND1	8insTCTATAAAC	426delinsNPITISS
XH_P44	1	55119265	55119265	In_Frame_Ins	INS	-	5AATGGGGTTTC	-	MROH7	567insGAATGGG	5222delinsSEWGL
XH_P44	1	55562839	55562839	Frame_Shift_Ins	INS	-	TACTACCCGCT	-	USP24	5722insAGCGG	p.W1908fs
XH_P44	1	55643718	55643718	In_Frame_Ins	INS	-	ATTTATTCTCTT	-	USP24	412insAAGAGA	D138delinsKRIND
XH_P44	1	55643720	55643720	In_Frame_Ins	INS	-	TCT	-	USP24	409_410insAG	p.T137delinsKT
XH_P44	1	59126881	59126881	Frame_Shift_Ins	INS	-	TAGCAGATTATT	-	MYSM1	289insTAATAAT	p.K763fs
XH_P44	1	60373578	60373578	Nonsense_Mutation	INS	-	GCACATTCTTCA	-	CYP2J2	883insTGAAGA	p.S295delinsX
XH_P44	1	62675751	62675751	Frame_Shift_Ins	INS	-	AACCTCTTCTCT	-	L1TD1	1306insAACCTC	p.E435fs
XH_P44	1	62911040	62911040	Nonsense_Mutation	SNP	G	T	G	USP1	c.G1189T	p.E397X
XH_P44	1	62911042	62911042	Nonsense_Mutation	INS	-	AACTCTTGATTTC	-	USP1	TATTTTAACTCT	T97delinsEPIVNSX
XH_P44	1	63024889	63024889	Frame_Shift_Ins	INS	-	TGGGGTGGAAG	-	DOCK7	ATAACATCTTCC	p.D734fs
XH_P44	1	63050524	63050524	Missense_Mutation	SNP	G	T	G	DOCK7	c.C1826A	p.P609Q
XH_P44	1	63284972	63284972	Frame_Shift_Ins	INS	-	TTTGACAGTGTG	-	ATGAC	392insTTTTGACA	p.W231fs
XH_P44	1	64102012	64102012	Nonsense_Mutation	INS	-	TTTCAATGAGTT	-	PGM1	TTTTATTTTTCAA	3345delinsGFFYQX
XH_P44	1	65130277	65130277	Nonsense_Mutation	INS	-	CTACCTA	-	CACHD1	03_1304insCTAA	435_Y436delinsPTX
XH_P44	1	65255159	65255159	In_Frame_Ins	INS	-	ACATATAATTGAT	-	RAVER2	TGATAAACATAA	5delinsLYDKHNLIIYI
XH_P44	1	65858477	65858477	In_Frame_Ins	INS	-	TGTTTTTGTGCT	-	DNAJC6	1833insTGCTTT	A611delinsAAFV
XH_P44	1	65858479	65858479	Missense_Mutation	SNP	T	G	T	DNAJC6	c.T1834G	p.S612A
XH_P44	1	65860632	65860632	Nonsense_Mutation	INS	-	ATTTGTTATCTA	-	DNAJC6	1956insATTGTG	L652delinsLFVIX
XH_P44	1	66081833	66081833	Frame_Shift_Ins	INS	-	SGCTGAGAGGC	-	LEPR	9insAAGGCTGA	p.T713fs
XH_P44	1	67299827	67299827	Frame_Shift_Ins	INS	-	5ATGACAAATTT	-	WDR78	38insCAAATTT	p.S580fs
XH_P44	1	67891833	67891833	In_Frame_Ins	INS	-	TTTTTTGTGATAG	-	SERBP1	449insCTCTACA	E150delinsALQKK

XH_P44	1	68173355	68173355	Frame_Shift_Ins	INS	-	TCCA	-	GNG12	c.14_15insTGGG	p.T5fs
XH_P44	1	68173356	68173356	In_Frame_Ins	INS	-	GAT	-	GNG12	c.13_14insATC	p.T5delinsNP
XH_P44	1	70397219	70397219	In_Frame_Ins	INS	-	TACAGCATCTGT	-	LRRC7	54insCTACAGCA	R188delinsSYSICS
XH_P44	1	70654913	70654913	In_Frame_Ins	INS	-	AATTTAGGCTTTG	-	LRRC40	95insCCAAAGGCC	E65delinsQSLNL
XH_P44	1	74507263	74507263	Frame_Shift_Ins	INS	-	GACCAAGGAGCAT	-	LRRIQ3	352insTAGTCTCT	p.E451fs
XH_P44	1	75055529	75055529	In_Frame_Ins	INS	-	TGGGTTGGAGC	-	ERIC3	1962insCCTCCA	V654delinsVLQPR
XH_P44	1	75672375	75672375	In_Frame_Ins	INS	-	TAATTCTAAGAA	-	SLC44A5	9insGACTTCTTA	687delinsDFLELST
XH_P44	1	78098700	78098700	Frame_Shift_Ins	INS	-	A	-	ZZZ3	c.339_340insT	p.P114fs
XH_P44	1	78098702	78098702	Nonsense_Mutation	INS	-	GAGAAAAAGGG	-	ZZZ3	nsAATTTCCCTTT	113_114delinsX
XH_P44	1	78207312	78207312	Frame_Shift_Ins	INS	-	ATAGG	-	USP33	c.70_71insCCTA	p.Q24fs
XH_P44	1	78207314	78207314	Frame_Shift_Ins	INS	-	ACTGTGCAGG	-	USP33	69insCCTGACA	p.I23fs
XH_P44	1	78395143	78395143	Frame_Shift_Ins	INS	-	TTTCAATGCCCTT	-	NEXN	816insTTTCAAT	p.R272fs
XH_P44	1	78479163	78479163	Frame_Shift_Ins	INS	-	GATCACCATCTA	-	DNAJB4	96insGGATCACC	p.I99fs
XH_P44	1	79002283	79002283	Nonsense_Mutation	INS	-	GTGATGCTATTG	-	PTGFR	ACAGAGTGATG	831delinsPQSDAIVX
XH_P44	1	79116059	79116059	In_Frame_Ins	INS	-	TAGATAATATGT	-	IFI44	AAACAGATAA	siYFPLNIKKQICYSKYCIYAS
XH_P44	1	82436215	82436215	Nonsense_Mutation	INS	-	AAAGAAAACTCA	-	ADGRL2	nsCACAAAAAGAA	967delinsNTKENSX
XH_P44	1	82447661	82447661	Splice_Site	INS	-	AACAA	-	ADGRL2		
XH_P44	1	84373335	84373335	Nonsense_Mutation	INS	-	GATCCTTTCAT	-	TTL7	15insTTATGGA	R572delinsIMERIX
XH_P44	1	85397248	85397248	Missense_Mutation	SNP	C	G	C	MCOLN2	c.G1339C	p.E447Q
XH_P44	1	85397249	85397249	Frame_Shift_Ins	INS	-	GGTTTTGTGG	-	MCOLN2	1338insCCACA	p.F446fs
XH_P44	1	85564318	85564318	Nonsense_Mutation	INS	-	ACATAAATTAGT	-	WDR63	5GAAAAACATAA	W448delinsPVQGTKX
XH_P44	1	85647928	85647928	Nonsense_Mutation	INS	-	AAATTAGATAT	-	SYDE2	ATGTGTAATAAT	799_N80delinsEX
XH_P44	1	85648243	85648243	Nonsense_Mutation	INS	-	TGAAAGTGACTC	-	SYDE2	CCATAAGAGTCA	94_P695delinsPVPX
XH_P44	1	86821041	86821041	Frame_Shift_Ins	INS	-	AACATAACTTCT	-	ODF2L	7insTAAAGAAG	p.S486fs
XH_P44	1	87036864	87036864	Nonsense_Mutation	INS	-	AGAGATAAATCT	-	CLC4	ATAGAAAGAGAT	5429delinsSYAEX
XH_P44	1	89449278	89449278	Missense_Mutation	SNP	C	T	C	RBMXL1	c.G232A	p.A78T
XH_P44	1	90048294	90048294	In_Frame_Ins	INS	-	TTC	-	LRRC8B	c.85_86insTTC	p.Y29delinsFH
XH_P44	1	90048296	90048296	In_Frame_Ins	INS	-	TTGAAACTA	-	LRRC8B	7_88insTTGAAA	p.Y29delinsYCLK
XH_P44	1	91989958	91989958	In_Frame_Ins	INS	-	ATG	-	CDC7	1691_1692insA	p.L564delinsLV
XH_P44	1	91989960	91989960	In_Frame_Ins	INS	-	AGTCTTCTCTGA	-	CDC7	94insCAGTCTCT	565delinsSVFSEM
XH_P44	1	92446477	92446477	Frame_Shift_Ins	INS	-	CT	-	BRDT	1354_1355insC	p.G452fs
XH_P44	1	92446478	92446478	Nonsense_Mutation	INS	-	TTATTAACCTTT	-	BRDT	1356insTTATTA	G452delinsGYX
XH_P44	1	93705001	93705001	In_Frame_Ins	INS	-	GCAGAAATATCT	-	CCDC18	nsTATCAGCAAA	912delinsNISKISSW
XH_P44	1	93705003	93705003	In_Frame_Ins	INS	-	ATTTTAAAT	-	CCDC18	7_2738insATTT	T913delinsNFKS
XH_P44	1	94342443	94342443	Frame_Shift_Ins	INS	-	AG	-	DNTTIP2	1047_1048insC	p.V350fs
XH_P44	1	94342444	94342444	Frame_Shift_Ins	INS	-	TAAGTGTCTAGT	-	DNTTIP2	47insTTCACCTA	p.S349fs
XH_P44	1	94528837	94528837	Frame_Shift_Ins	INS	-	AAAGTCAGTGG	-	ABCA4	91insTTCCCACTG	p.E531fs
XH_P44	1	97236394	97236394	In_Frame_Ins	INS	-	AAT	-	PTBP2	c.263_264insAA	p.N88delinsKL
XH_P44	1	97236396	97236396	Nonsense_Mutation	INS	-	AATCTATTCTAGA	-	PTBP2	TAAGCAATCTAT	89_190delinsNIX
XH_P44	1	97243288	97243288	In_Frame_Ins	INS	-	TACTAGTCTCACT	-	PTBP2	425insTACTAGT	L142delinsLVHF
XH_P44	1	99358650	99358650	Frame_Shift_Ins	INS	-	TTGTCTTTTTTTT	-	PLPPR5	insGAAAAAAA	p.T310fs
XH_P44	1	100606035	100606035	Frame_Shift_Ins	INS	-	TAATTGAACCTTG	-	TRMT13	67insTAATTGA	p.N156fs
XH_P44	1	100613783	100613783	Frame_Shift_Ins	INS	-	CCACATCATCT	-	TRMT13	1152insCCACA	p.N384fs
XH_P44	1	100681750	100681750	Frame_Shift_Ins	INS	-	TTCTTTTCTTTTT	-	DBT	AAAAAAAAGAA	p.K187fs
XH_P44	1	101705434	101705434	Nonsense_Mutation	INS	-	AAGAGGATATA	-	S1PR1	nsCAGAAAGAGG	A298delinsVQKRIX
XH_P44	1	103380346	103380346	Nonsense_Mutation	INS	-	ATTAATCTCTTA	-	COL11A1	AATTTCTTAAAG	A164delinsNFX
XH_P44	1	103400060	103400060	Frame_Shift_Ins	INS	-	CACCTCTCTTCTT	-	COL11A1	GAGTGAAGAAA	p.K1066fs
XH_P44	1	103544295	103544295	Frame_Shift_Ins	INS	-	GAGAG	-	COL11A1	406_407insCTC	p.V136fs
XH_P44	1	103544296	103544296	In_Frame_Ins	INS	-	AGTAAAGAGGT	-	COL11A1	406insAACCTCT	V136delinsNLFTV
XH_P44	1	104166524	104166524	Nonsense_Mutation	SNP	G	T	G	AMY2A	c.G1138T	p.G380X
XH_P44	1	108703875	108703875	Missense_Mutation	SNP	A	C	A	SLC25A24	c.T439G	p.W147G
XH_P44	1	108703876	108703876	Frame_Shift_Ins	INS	-	CTCCCTCTCCC	-	SLC25A24	438insGGGAGA	p.E146fs
XH_P44	1	109276076	109276076	Frame_Shift_Ins	INS	-	AAAAA	-	FNDC7	262_2063insAA	p.D688fs
XH_P44	1	109276078	109276078	Nonsense_Mutation	INS	-	AGCAAATAGTCT	-	FNDC7	5insATAAGCAAA	688delinsDISKLXV
XH_P44	1	109365991	109365991	Splice_Site	INS	-	ATAATCACTACT	-	AKNAD1		
XH_P44	1	109766671	109766671	Splice_Site	SNP	G	T	G	SARS		
XH_P44	1	110256337	110256337	Frame_Shift_Ins	INS	-	AGACGCTCCA	-	GSTM5	315insAGACGT	p.M105fs
XH_P44	1	110257830	110257830	In_Frame_Ins	INS	-	CCA	-	GSTM5	c.535_536insCC	p.L179delinsPL
XH_P44	1	110257831	110257831	Missense_Mutation	SNP	T	G	T	GSTM5	c.T536G	p.L179R
XH_P44	1	111146169	111146169	In_Frame_Ins	INS	-	TAGCAACTGTA	-	KCNA2	36insGGTACAG	A122delinsKVQLAV
XH_P44	1	112999207	112999207	Missense_Mutation	SNP	G	A	G	CTTNBP2NL	c.G1093A	p.G365S
XH_P44	1	112999208	112999208	Frame_Shift_Ins	INS	-	CCTCTTTTCTCT	-	CTTNBP2NL	1095insCCTCTC	p.G365fs
XH_P44	1	113058875	113058875	Frame_Shift_Ins	INS	-	AAAGTGCCCTTT	-	WNT2B	TATTCAAGGTG	p.R81fs
XH_P44	1	113063112	113063112	Frame_Shift_Ins	INS	-	AAAGAATCGCTT	-	WNT2B	nsTAAAAAGGAAT	p.E294fs
XH_P44	1	113464750	113464750	Nonsense_Mutation	INS	-	TCATTGGGA	-	SLC16A1	2_223insTCCAA	p.175delinsSKX
XH_P44	1	113464752	113464752	Frame_Shift_Ins	INS	-	CATTAGTTTAT	-	SLC16A1	221insATAAAC	p.P74fs
XH_P44	1	114225812	114225812	In_Frame_Ins	INS	-	ACA	-	MAGI3	3622_3623insA	L1208delinsHL
XH_P44	1	114225813	114225813	Nonsense_Mutation	INS	-	TGAAGACGAAG	-	MAGI3	624insTTGAAGA	208_L1209delinsLX
XH_P44	1	114226375	114226375	In_Frame_Ins	INS	-	CTTTTTCCTCACT	-	MAGI3	186insGCTTTTTT	1395delinsSAFFQL
XH_P44	1	114226377	114226377	Missense_Mutation	SNP	G	T	G	MAGI3	c.G4187T	p.S1396I
XH_P44	1	114254637	114254637	In_Frame_Ins	INS	-	CTGTCTCCAATT	-	PHTF1	24insAATTGGAG	V8delinsVIGDR
XH_P44	1	114255954	114255954	In_Frame_Ins	INS	-	SAAGACTGGAA	-	PHTF1	730insGTCTCCAG	A244delinsVPVFM
XH_P44	1	115144767	115144767	Nonsense_Mutation	INS	-	SAAGGGGTATGT	-	DENND2C	AATAAATCATAT	p.F515delinsLX
XH_P44	1	115168514	115168514	Missense_Mutation	SNP	C	A	C	DENND2C	c.G92T	p.R31M
XH_P44	1	115168515	115168515	Nonsense_Mutation	INS	-	GATCAAAG	-	DENND2C	0_91insCTTTGAR	R31_A32delinsLX
XH_P44	1	115275369	115275369	Nonsense_Mutation	INS	-	TTATATTCAAGT	-	CSDE1	5TATAAATCTGA	D272delinsNFNLVXX
XH_P44	1	115593158	115593158	Nonsense_Mutation	INS	-	AATGAAATCTG	-	TSPAN2	GCACACAGATT	82delinsPANRHFHYX
XH_P44	1	116206534	116206534	In_Frame_Ins	INS	-	CCCCAG	-	VANGL1	51_452insCCCC	p.F151delinsSPV
XH_P44	1	116206536	116206536	In_Frame_Ins	INS	-	GTC	-	VANGL1	c.453_454insGT	p.F151delinsFV
XH_P44	1	117504016	117504016	Silent	SNP	C	T	C	PTGFRN	c.C1365T	p.S455S
XH_P44	1	117637951	117637951	Nonsense_Mutation	INS	-	CTCTTCTCTAAA	-	TF2	98insAGCTCTTT	9_L1000delinsESSFX
XH_P44	1	118003235	118003235	Splice_Site	INS	-	TAAAAGGAGAC	-	MAN1A2		
XH_P44	1	118166435	118166435	Frame_Shift_Ins	INS	-	TCTGTCTGCAG	-	FAM46C	6insAGTCTGTC	p.N315fs
XH_P44	1	118449137	118449137	Frame_Shift_Ins	INS	-	AGGAGCATTTCG	-	GDAP2	627insACGAAGT	p.D209fs
XH_P44	1	118462816	118462816	Nonsense_Mutation	INS	-	TTCTTGCTCACTA	-	GDAP2	scCTATAGTGAC	55_V56delinsNLX
XH_P44	1	118640445	118640445	Frame_Shift_Ins	INS	-	GAGC	-	SPAG17	858_859insGCT	p.N287fs
XH_P44	1	118640446	118640446	Frame_Shift_Ins	INS	-	AGGC	-	SPAG17	857_858insGCC	p.E286fs
XH_P44	1	119575710	119575710	In_Frame_Ins	INS	-	AAAAAGAAAAG	-	WARS2	5TATAAATCTTTT	03delinsYNNFFLGK
XH_P44	1	120269715	120269715	Frame_Shift_Ins	INS	-	CA	-	PHGDH	c.500_501insCA	p.P167fs
XH_P44	1	120269717	120269717	Missense_Mutation	SNP	G	C	G	PHGDH	c.G502C	p.G168R
XH_P44	1	120436727	120436727	Frame_Shift_Ins	INS	-	GGAAACAAACC	-	ADAM30	2233insSGGTTT	p.K745fs
XH_P44	1	120436729	120436729	In_Frame_Ins	INS	-	TGC	-	ADAM30	2230_2231insG	p.S744delinsCT
XH_P44	1	120458175	120458175	Frame_Shift_Ins	INS	-	ACTTTTGTA	-	NOTCH2	7170insTTTACA	p.H2390fs
XH_P44	1	120458826	120458826	Frame_Shift_Ins	INS	-	CCACCACATT	-	NOTCH2	6519insAATGT	p.P2173fs
XH_P44	1	144873996	144873996	Nonsense_Mutation	INS	-	GGTTTGGAGCT	-	PDE4DIP	47insAACAGTCA	p.L181delinsX
XH_P44	1	144879273	144879273	In_Frame_Ins	INS	-	TGAAAATGTGT	-	PDE4DIP	nsAACTTACACA	555delinsNLHFNQE
XH_P44	1	144882814	144882814	In_Frame_Ins	INS	-	GAA	-	PDE4DIP	3693_3694insT	D1232delinsFD
XH_P44	1	144882816	144882816	Frame_Shift_Ins	INS	-	AATAA	-	PDE4DIP	691_3692insTT	p.S1231fs

XH_P44	1	144911889	144911889	Silent	SNP	G	T	G	PDE4DIP	c.C2709A	p.S903S
XH_P44	1	144911891	144911891	Frame_Shift_Ins	INS	-	TTGAGGTTATTG	-	PDE4DIP	707insGCAATAA	p.S903fs
XH_P44	1	145015902	145015902	Frame_Shift_Ins	INS	-	GTGG	-	PDE4DIP	185_186insCTCA	p.K62fs
XH_P44	1	145015904	145015904	Frame_Shift_Ins	INS	-	ATGGA	-	PDE4DIP	183_184insTCC	p.K62fs
XH_P44	1	145330777	145330777	Missense_Mutation	SNP	A	T	A	NBPF20	c.A6691T	p.T2231S
XH_P44	1	145330778	145330778	Missense_Mutation	SNP	C	G	C	NBPF20	c.C6692G	p.T2231S
XH_P44	1	145533436	145533436	In_Frame_Ins	INS	-	GAATGGCACTG	-	ITGA10	CCCACGAATGGG7delinsFPPRMALEDE	
XH_P44	1	145539039	145539039	Frame_Shift_Ins	INS	-	TCTCACCCTGA	-	ITGA10	2551insTCTCA	p.A850fs
XH_P44	1	145748555	145748555	Frame_Shift_Ins	INS	-	GAAGAAGAAA	-	PDZK1	429insGAAGAA	p.G143fs
XH_P44	1	145748556	145748556	Silent	SNP	C	A	C	PDZK1	c.C429A	p.G143G
XH_P44	1	146757139	146757139	Frame_Shift_Ins	INS	-	GCACCTGG	-	CHD1L	1_1382insGCAC	p.K461fs
XH_P44	1	147127361	147127361	Nonsense_Mutation	INS	-	GGTTTAAATTAC	-	ACP6	2insAGTGTAAATT188_1189delinsSVIX	
XH_P44	1	149290968	149290968	In_Frame_Ins	INS	-	TGAGCT	-	FAM231D	40_441insTGAGCT1147delinsTEL	
XH_P44	1	149761715	149761715	Nonsense_Mutation	INS	-	CTAAACAGGCA	-	FCGR1A	insATGCTAAAC222_L223delinsGCX	
XH_P44	1	150443101	150443101	Frame_Shift_Ins	INS	-	AAAATAC	-	RPRD2	99_1600insAAA	p.Q533fs
XH_P44	1	150443103	150443103	In_Frame_Ins	INS	-	GGCCTATTTTAT	-	RPRD2	1602insGGCCTA5534delinsRAYFI	
XH_P44	1	150812072	150812072	Missense_Mutation	SNP	C	T	C	ARNT	c.G286A	p.E96K
XH_P44	1	150812073	150812073	Frame_Shift_Ins	INS	-	GTTTTTTGGACA	-	ARNT	85insTTGTCCAA	p.T95fs
XH_P44	1	151258875	151258875	Frame_Shift_Ins	INS	-	AAAAGAGAGTT	-	ZNF687	109insAAAAGA	p.G36fs
XH_P44	1	151258877	151258877	Missense_Mutation	SNP	C	T	C	ZNF687	c.C110T	p.P37L
XH_P44	1	151288434	151288434	In_Frame_Ins	INS	-	GCCACTGCC	-	PI4KB	524insGGCAG175delinsWQWH	
XH_P44	1	151288436	151288436	In_Frame_Ins	INS	-	CAT	-	PI4KB	521_522insATp.F174delinsLC	
XH_P44	1	151611567	151611567	Frame_Shift_Ins	INS	-	TGATCTCCACCC	-	SNX27	nsCCTGTATCT	p.H172fs
XH_P44	1	151630901	151630901	Nonsense_Mutation	INS	-	AAATAAATCAC	-	SNX27	ATACAAATTAATK245delinsKHTX	
XH_P44	1	151780070	151780070	Frame_Shift_Ins	INS	-	AACC	-	RORC	371_1372insGG	p.H458fs
XH_P44	1	152086554	152086554	Nonsense_Mutation	INS	-	AAGGAATGGTG	-	TCHH	AAACCACCATTC	p.M1delinsIX
XH_P44	1	152128671	152128671	Nonsense_Mutation	INS	-	SACAGAAAAGG	-	RPTN	CACTGGCCTTTT	Q303delinsHWPFSLIX
XH_P44	1	152191195	152191195	Silent	SNP	G	A	G	HRNR	c.C2910T	p.S970S
XH_P44	1	152193411	152193411	Missense_Mutation	SNP	T	C	T	HRNR	c.A694G	p.S232G
XH_P44	1	152275658	152275658	Nonsense_Mutation	INS	-	TTAGACACTCTC	-	FLG	1704insTGAGAG902_G3903delinsX	
XH_P44	1	152278216	152278216	Frame_Shift_Ins	INS	-	ACCACATCCCA	-	FLG	9146insTGGGA	p.R3049fs
XH_P44	1	152280040	152280040	Frame_Shift_Ins	INS	-	CCAGGGAC	-	FLG	1_7322insGTCC	p.S2441fs
XH_P44	1	152280322	152280322	Missense_Mutation	SNP	C	G	C	FLG	c.G7040C	p.G2347A
XH_P44	1	152285046	152285046	Frame_Shift_Ins	INS	-	A	-	FLG	2315_2316ins	p.Q772fs
XH_P44	1	152285047	152285047	Frame_Shift_Ins	INS	-	CCCAA	-	FLG	314_2315insTTC	p.Q772fs
XH_P44	1	152324114	152324114	Missense_Mutation	SNP	C	T	C	FLG2	c.G6148A	p.A2050T
XH_P44	1	152327955	152327955	Silent	SNP	G	A	G	FLG2	c.C2307T	p.S769S
XH_P44	1	152484091	152484091	In_Frame_Ins	INS	-	TTTATTATTATG	-	LCESA	AGAATTTATTATdelinsKMTRIYYDDYY	
XH_P44	1	153303372	153303372	Frame_Shift_Ins	INS	-	TCCTGTGCCTCT	-	PGLYRP4	nsAAAGGAGGC	p.Q331fs
XH_P44	1	153791293	153791293	Frame_Shift_Ins	INS	-	GTGATTTTTTTT	-	GATAD2B	ATTAAAAAAA	p.L191fs
XH_P44	1	153921831	153921831	Nonsense_Mutation	INS	-	GTGACTTCAACC	-	CRTC2	434insAGGTTTGA78_T479delinsSGX	
XH_P44	1	154300608	154300608	Silent	SNP	G	A	G	ATP8B2	c.G90A	p.L30L
XH_P44	1	154961072	154961072	Frame_Shift_Ins	INS	-	TCCAACCTGGG	-	FLAD1	865insTCCAAC	p.A288fs
XH_P44	1	155039875	155039875	Frame_Shift_Ins	INS	-	ACCTCAACCCGA	-	EFNA4	29insTACCTCAA	p.Q143fs
XH_P44	1	155041516	155041516	Frame_Shift_Ins	INS	-	TATGACCT	-	EFNA4	1_492insTATGA	p.S164fs
XH_P44	1	155167967	155167967	Frame_Shift_Ins	INS	-	TTTTCTTTACTA	-	THBS3	759insATAGTAA	p.A587fs
XH_P44	1	155208006	155208006	In_Frame_Ins	INS	-	CAGGCTTCC	-	GBA	419insGGAAG	N140delinsRKP
XH_P44	1	155227385	155227385	Missense_Mutation	SNP	T	G	T	SCAMP3	c.A503C	p.N168T
XH_P44	1	155227386	155227386	In_Frame_Ins	INS	-	ATCCCA	-	SCAMP3	01_502insTGGG	N168delinsWDN
XH_P44	1	155408389	155408389	In_Frame_Ins	INS	-	AAGAGAATAAT	-	ASH1L	TACCTTTTATTAT53delinsITFFYSLALLP	
XH_P44	1	155449636	155449636	In_Frame_Ins	INS	-	GCCTTCATC	-	ASH1L	3025insGATGA51009delinsDEGS	
XH_P44	1	155630317	155630317	Nonsense_Mutation	INS	-	TATCTTCA	-	YY1AP1	0_1351insTGAA451_V452delinsX	
XH_P44	1	155698904	155698904	In_Frame_Ins	INS	-	AAT	-	DAP3	573_574insAA	p.V191delinsVN
XH_P44	1	155698905	155698905	Frame_Shift_Ins	INS	-	TTTCTTTTCTTT	-	DAP3	575insCTTTCTTT	p.V192fs
XH_P44	1	155733196	155733196	Frame_Shift_Ins	INS	-	TG	-	GON4L	4632_4633insC	p.T1545fs
XH_P44	1	155733197	155733197	Nonsense_Mutation	INS	-	TAGATTAT	-	GON4L	1_4632insATAA	M1544delinsIX
XH_P44	1	155735089	155735089	Frame_Shift_Ins	INS	-	A	-	GON4L	c.4174dupT	p.S1392fs
XH_P44	1	155735091	155735091	In_Frame_Ins	INS	-	GGGCCAGAA	-	GON4L	2_4173insTCTCT	S1391delinsSSGP
XH_P44	1	155736348	155736348	Silent	SNP	T	A	T	GON4L	c.A2916T	p.L972L
XH_P44	1	155736349	155736349	In_Frame_Ins	INS	-	TGGTGCTCC	-	GON4L	2915insGGAAG	L972delinsRSTI
XH_P44	1	155737298	155737298	Frame_Shift_Ins	INS	-	AAAATAATAG	-	GON4L	2681insCTATT	p.G894fs
XH_P44	1	155737299	155737299	Missense_Mutation	SNP	C	G	C	GON4L	c.G2680C	p.G894R
XH_P44	1	155823262	155823262	In_Frame_Ins	INS	-	ACAAGGTCTCT	-	GON4L	0insCTAGAGACT	104delinsLELYT
XH_P44	1	155823490	155823490	Frame_Shift_Ins	INS	-	AGGTGTGTGATG	-	GON4L	32insACATCAAC	p.L28fs
XH_P44	1	155838327	155838327	In_Frame_Ins	INS	-	TCGGCAGTTTG	-	SYT11	GTCTCTCCGCA2delinsFVSPHDFDF	
XH_P44	1	155899107	155899107	Frame_Shift_Ins	INS	-	ATGTTTTTATTG	-	KIAA0907	CCTCCAATAAAA	p.E148fs
XH_P44	1	156351685	156351685	Frame_Shift_Ins	INS	-	TAACTCTCAT	-	RHBG	930insTAACCT	p.A310fs
XH_P44	1	156351687	156351687	Frame_Shift_Ins	INS	-	TCCT	-	RHBG	931_932insTCC	p.G311fs
XH_P44	1	156502883	156502883	Frame_Shift_Ins	INS	-	GTATCT	-	IQGAP3	31_3992insAGG	p.A1331fs
XH_P44	1	156509745	156509745	Frame_Shift_Ins	INS	-	ICAGGAAAGGAG	-	IQGAP3	77insGTCTCCTT	p.N926fs
XH_P44	1	156509746	156509746	Nonsense_Mutation	INS	-	A	-	IQGAP3	2775_2776ins	N926_K927delinsX
XH_P44	1	156518519	156518519	Missense_Mutation	SNP	A	G	A	IQGAP3	c.T1847C	p.L616T
XH_P44	1	156518520	156518520	Nonsense_Mutation	INS	-	TTCTGCTTA	-	IQGAP3	1846insTAAG	p.L616delinsX
XH_P44	1	156708486	156708486	Missense_Mutation	SNP	G	A	G	MRPL24	c.C11T	p.S4F
XH_P44	1	156708487	156708487	In_Frame_Ins	INS	-	GTGGTTCAAGTT	-	MRPL24	0insAACTTGAA	S4delinsNLNHS
XH_P44	1	156821565	156821565	Frame_Shift_Ins	INS	-	AA	-	INSRR	c.956_957insTT	p.K319fs
XH_P44	1	156821566	156821566	In_Frame_Ins	INS	-	TTTCCATCATCC	-	INSRR	956insGGATGAT	319delinsRMMXK
XH_P44	1	157497680	157497680	In_Frame_Ins	INS	-	AATATCACTCAG	-	FCRL5	1687insCTGAGT	V563delinsLSDIV
XH_P44	1	157670258	157670258	Frame_Shift_Ins	INS	-	A	-	FCRL3	c.21_22insT	p.L8fs
XH_P44	1	157670259	157670259	Nonsense_Mutation	INS	-	ATAATTTTTCAG	-	FCRL3	5sCATCTGAAAA	p.L7delinsLIX
XH_P44	1	157737213	157737213	Frame_Shift_Ins	INS	-	TGTCCAGT	-	FCRL2	9_970insACTCG	p.L324fs
XH_P44	1	157771978	157771978	Nonsense_Mutation	INS	-	TCAACTCA	-	FCRL1	2_613insTGAAG	p.V205delinsX
XH_P44	1	157771980	157771980	Missense_Mutation	SNP	G	A	G	FCRL1	c.C611T	p.P204L
XH_P44	1	158299426	158299426	Frame_Shift_Ins	INS	-	AAGTGTAT	-	CD1B	19_620insATCA	p.A207fs
XH_P44	1	158299428	158299428	Silent	SNP	C	T	C	CD1B	c.G618A	p.E206E
XH_P44	1	158390302	158390302	Nonsense_Mutation	INS	-	AGTCAGATTGTC	-	OR10K2	AAGATGACAATC	9_Y120delinsKMTIX
XH_P44	1	158450077	158450077	Frame_Shift_Ins	INS	-	G	-	OR10R2	c.4111dupG	p.V137fs
XH_P44	1	158450079	158450079	Frame_Shift_Ins	INS	-	GCCTTTATCCAG	-	OR10R2	13insGGCTTTTAT	p.M138fs
XH_P44	1	158517372	158517372	Missense_Mutation	SNP	C	A	C	OR6Y1	c.G524T	p.G175V
XH_P44	1	158517374	158517374	Frame_Shift_Ins	INS	-	CTTTTCACTATG	-	OR6Y1	22insCATAGTG	p.C174fs
XH_P44	1	158532760	158532760	Frame_Shift_Ins	INS	-	CTACTGCCTGAG	-	OR6P1	35insCCTCAGGC	p.L212fs
XH_P44	1	158549505	158549505	Nonsense_Mutation	INS	-	CCTTGTCAAACA	-	OR10X1	85insGTGTTTGA	M62_G63delinsSVX
XH_P44	1	158615050	158615050	In_Frame_Ins	INS	-	CTATGCTTTCTA	-	SPTA1	CGGTATAGAAA74delinsNRYRKHSTM	
XH_P44	1	158618435	158618435	In_Frame_Ins	INS	-	TTTATTCTGTATC	-	SPTA1	78insTGTACAA	1193delinsVYKNKY
XH_P44	1	158639229	158639229	Frame_Shift_Ins	INS	-	TGATCTTATAGC	-	SPTA1	2insTTTGGCTAA	p.K601fs
XH_P44	1	158669713	158669713	Frame_Shift_Ins	INS	-	STTGAGATTTCTG	-	OR6K2	CTATACAGAAATC	p.S244fs
XH_P44	1	158670166	158670166	Frame_Shift_Ins	INS	-	CATATCTTCT	-	OR6K2	277insAGAAGA	p.F93fs
XH_P44	1	158670167	158670167	Frame_Shift_Ins	INS	-	T	-	OR6K2	c.275_276insA	p.S92fs

XH_P44	1	158687092	158687092	Frame_Shift_Ins	INS	-	ATGATCT	-	OR6K3	13_814insAGAT	p.A272fs
XH_P44	1	158724778	158724778	Frame_Shift_Ins	INS	-	TCTGTAATGAGT	-	OR6K6	4insTTTCTGTAA	p.P58fs
XH_P44	1	158725331	158725331	In_Frame_Ins	INS	-	STCAGGACACAC	-	OR6K6	727insGTCAAGGA	A242delinsAVRTQ
XH_P44	1	158914751	158914751	Nonsense_Mutation	INS	-	TGCCCTCTACTA	-	PYHIN1	79insATTGCCTC	6_A427delinsEIASIX
XH_P44	1	158988414	158988414	Frame_Shift_Ins	INS	-	TTTTTCTCCATTT	-	IF16	insATTTTCTTCTC	p.I259fs
XH_P44	1	159169565	159169565	In_Frame_Ins	INS	-	TCITTTCTCTCT	-	CADM3	78insTTCTTTTCTC	6326delinsSSFPFS
XH_P44	1	159409559	159409559	Missense_Mutation	SNP	G	T	G	OR101	c.G11T	p.C4F
XH_P44	1	159409560	159409560	Frame_Shift_Ins	INS	-	CTTTCTTACTC	-	OR101	13insCTTTCCTA	p.C4fs
XH_P44	1	160094210	160094210	Missense_Mutation	SNP	A	C	A	ATP1A2	c.A620C	p.H207P
XH_P44	1	160094212	160094212	Frame_Shift_Del	DEL	G	-	G	ATP1A2	c.622delG	p.G208fs
XH_P44	1	160134124	160134124	Frame_Shift_Ins	INS	-	C	-	ATP1A4	c.958dupC	p.L319fs
XH_P44	1	160134126	160134126	Nonsense_Mutation	INS	-	GACATAGAG	-	ATP1A4	960insGACATA	p.L320delinsLTX
XH_P44	1	160183020	160183020	In_Frame_Ins	INS	-	AGCTGAGTT	-	PEA15	7_228insAGCTGA	p.K76delinsKAE
XH_P44	1	160325734	160325734	Frame_Shift_Ins	INS	-	TC	-	NCSTN	1123_1124insT	p.A375fs
XH_P44	1	160325736	160325736	Frame_Shift_Ins	INS	-	CTTCA	-	NCSTN	125_1126insCT	p.A375fs
XH_P44	1	160607197	160607197	In_Frame_Ins	INS	-	CTG	-	SLAMF1	198_199insCAG	p.A67delinsQA
XH_P44	1	160607199	160607199	Frame_Shift_Ins	INS	-	GTTGAGGC	-	SLAMF1	6_197insGCCTC	p.M66fs
XH_P44	1	160784403	160784403	In_Frame_Ins	INS	-	AAAGGGGAC	-	LY9	925insAAAGG	P308delinsPKGD
XH_P44	1	160970009	160970009	Frame_Shift_Ins	INS	-	AAGGCAATTG	-	F11R	1insAAACAAAT	p.M124fs
XH_P44	1	161059074	161059074	Frame_Shift_Ins	INS	-	AAAAGCCA	-	NECTIN4	2_13insTGGCT	p.L5fs
XH_P44	1	161059076	161059076	Missense_Mutation	SNP	G	T	G	NECTIN4	c.C11A	p.S4Y
XH_P44	1	161141832	161141832	Frame_Shift_Ins	INS	-	ACTGACTCCTCC	-	B4GALT3	6insAGGAGGAC	p.M319fs
XH_P44	1	161197057	161197057	Frame_Shift_Ins	INS	-	TAGACTGG	-	TOMM40L	3_194insTAGAC	p.T65fs
XH_P44	1	161332288	161332288	Frame_Shift_Ins	INS	-	CCACAGATTGG	-	SDHC	nsAAACCCACAG	p.S103fs
XH_P44	1	162302831	162302831	Frame_Shift_Ins	INS	-	A	-	NOS1AP	c.354_355insA	p.S118fs
XH_P44	1	162302832	162302832	Frame_Shift_Ins	INS	-	AAACACT	-	NOS1AP	55_356insAAAC	p.Q119fs
XH_P44	1	162353443	162353443	In_Frame_Ins	INS	-	AGAACTTTG	-	C1orf226	9_790insAGAAAC	G263delinsGRTL
XH_P44	1	162492339	162492339	Frame_Shift_Ins	INS	-	CCACCTTTAAT	-	UHMK1	1038insCCACC	X346delinsYHLX
XH_P44	1	162560173	162560173	Missense_Mutation	SNP	T	A	T	UAP1	c.T1230A	p.D410E
XH_P44	1	162560174	162560174	Frame_Shift_Ins	INS	-	TTTCTTTTTCAA	-	UAP1	232insTTTCTT	p.S411fs
XH_P44	1	162825087	162825087	Frame_Shift_Ins	INS	-	GAACAAGTCTC	-	CCDC190	77insTAGGACC	p.H126fs
XH_P44	1	164776906	164776906	Nonsense_Mutation	INS	-	GAGTAGTGAGG	-	PBX1	TTGCAGAGTAG	W277delinsDIFAEX
XH_P44	1	165380007	165380007	Missense_Mutation	SNP	T	G	T	RXRg	c.A476C	p.E159A
XH_P44	1	165380009	165380009	Nonsense_Mutation	INS	-	TTTACCAGGCT	-	RXRg	nsATAAAGCGGT	158_159delinsVX
XH_P44	1	166818903	166818903	Frame_Shift_Ins	INS	-	TT	-	POGK	c.733_734insTT	p.A245fs
XH_P44	1	166818905	166818905	In_Frame_Ins	INS	-	TTTCT	-	POGK	735_736insTTCT	A245delinsAFP
XH_P44	1	168160728	168160728	Nonsense_Mutation	INS	-	AAATTGGGTGT	-	TIPRL	6TTCTAAATTGGG	9_V170delinsSTQFX
XH_P44	1	169391478	169391478	Frame_Shift_Ins	INS	-	SACTTGGAGGAC	-	CCDC181	5TTCTCTCTCTCC	p.R64fs
XH_P44	1	169489811	169489811	Frame_Shift_Ins	INS	-	AAAACCTTTTGTG	-	F5	5TGTTCACAAA	p.R2047fs
XH_P44	1	169492554	169492554	Nonsense_Mutation	INS	-	FACAAATTAGAG	-	F5	5TGCTTCTCTAA	7_T1978delinsCFSNLX
XH_P44	1	169510493	169510493	Nonsense_Mutation	INS	-	AGATGGCCCT	-	F5	3835insAGGGG	79_L1280delinsRGIX
XH_P44	1	169511337	169511337	Frame_Shift_Ins	INS	-	AGCCTCACTTCT	-	F5	1insTCAGGAAG	p.G997fs
XH_P44	1	169511819	169511819	Nonsense_Mutation	INS	-	GTGATCTGTTAC	-	F5	9insAGAGTAACAA	B37delinsRVTDHX
XH_P44	1	169512066	169512066	Frame_Shift_Ins	INS	-	CCAGCCCATATT	-	F5	2insAGAAATATG	p.T754fs
XH_P44	1	169526002	169526002	Nonsense_Mutation	INS	-	AACCAAACTTAG	-	F5	AAATATCTAAGT	78_N279delinsQNIX
XH_P44	1	169526098	169526098	Frame_Shift_Ins	INS	-	TTCTCTG	-	F5	7_738insCGAG	p.T246fs
XH_P44	1	169526100	169526100	In_Frame_Ins	INS	-	TCC	-	F5	735_736insGG	p.T246delinsGT
XH_P44	1	169762075	169762075	Nonsense_Mutation	INS	-	GCAAAGCACAT	-	METTL18	2insTAATGTGTC	254delinsNNVLX
XH_P44	1	169762323	169762323	Frame_Shift_Ins	INS	-	A	-	METTL18	c.S13dupT	p.T172fs
XH_P44	1	169762325	169762325	Nonsense_Mutation	INS	-	ACTATATAAATG	-	METTL18	nsCGGCATTAT	C171delinsSAFIX
XH_P44	1	169762620	169762620	Frame_Shift_Ins	INS	-	TGTGGATCAGG	-	METTL18	7insAAACCTGAT	p.Q73fs
XH_P44	1	169798546	169798546	Frame_Shift_Ins	INS	-	AGAAATTCCTTA	-	C1orf112	insCAAAGAAAT	p.C289fs
XH_P44	1	171033345	171033345	In_Frame_Ins	INS	-	GCAATTTTGAAC	-	MROH9	2451insGCATT	L817delinsLHFVT
XH_P44	1	171086539	171086539	Frame_Shift_Ins	INS	-	AACCTGGAGATG	-	FMO3	88insCAAACCTG	p.A456fs
XH_P44	1	171302025	171302025	Nonsense_Mutation	INS	-	GGTG	-	FMO4	805_806insGGT	69_G270delinsWX
XH_P44	1	171302026	171302026	Nonsense_Mutation	INS	-	TAGGTCTACAT	-	FMO4	GTACATAGGCT	269_G270delinsX
XH_P44	1	171501716	171501716	Frame_Shift_Ins	INS	-	TCATCTCATCAC	-	PRRC2C	sATATTTCATCT	p.L495fs
XH_P44	1	171509822	171509822	Nonsense_Mutation	INS	-	CTGATTTAGATT	-	PRRC2C	5AGTTTCTGATT	11071delinsTSFX
XH_P44	1	171544129	171544129	In_Frame_Ins	INS	-	ATATCCATT	-	PRRC2C	1_6812insATAT	T272delinsNIHS
XH_P44	1	171544131	171544131	Frame_Shift_Ins	INS	-	C	-	PRRC2C	c.6813_6814ins	p.T2721fs
XH_P44	1	171544250	171544250	In_Frame_Ins	INS	-	AATAAAACGGAA	-	PRRC2C	ATCTGCAATAAA	B11delinsPSAIKRTFY
XH_P44	1	172411143	172411143	Frame_Shift_Ins	INS	-	TCAAGGAAGAC	-	PIGC	520insAGTCTTC	p.I207fs
XH_P44	1	172546916	172546916	Missense_Mutation	SNP	T	A	T	SUCO	c.T1186A	p.S396T
XH_P44	1	172546917	172546917	Frame_Shift_Ins	INS	-	TATGTACTTGAT	-	SUCO	88insCTTTATGTA	p.S396fs
XH_P44	1	172579213	172579213	In_Frame_Ins	INS	-	TCAATTTTGTAC	-	SUCO	nsTTTTTTTCAAT	630delinsOFFQCTC
XH_P44	1	173010678	173010678	Nonsense_Mutation	INS	-	ATCAACACACAAA	-	TNFSF18	5TTCTGTTTGTG	3_D144delinsFCCLX
XH_P44	1	173556950	173556950	Nonsense_Mutation	INS	-	CTCTCTCTTATCT	-	SLC9C2	TTCAAGATAAGA	26_S127delinsRKX
XH_P44	1	174418208	174418208	In_Frame_Ins	INS	-	TGGAAGAAAT	-	GPR52	9_960insTGGAAT	S320delinsSGRI
XH_P44	1	174418210	174418210	Missense_Mutation	SNP	A	T	A	GPR52	c.A961T	p.N321Y
XH_P44	1	174769633	174769633	Nonsense_Mutation	INS	-	GAGCACTAAGT	-	RABGAP1L	insCATGAGCAC	L55_A56delinsPX
XH_P44	1	175087942	175087942	Frame_Shift_Ins	INS	-	T	-	TNN	c.2632_2633ins	p.D878fs
XH_P44	1	175087943	175087943	Frame_Shift_Ins	INS	-	TTCTCTGT	-	TNN	3_2634insTTCT	p.D878fs
XH_P44	1	175331838	175331838	Nonsense_Mutation	INS	-	ATACTAAACGTT	-	TNR	816insTAAACGT	p.R606delinsX
XH_P44	1	175375683	175375683	In_Frame_Ins	INS	-	AGATGCTGGAG	-	TNR	58insCTCTCCAG	T56delinsTSPA5R
XH_P44	1	176118200	176118200	In_Frame_Ins	INS	-	5TTATCAGTAAG	-	RFDW2	TCAATCTTACTG	18delinsVNLTDNFS
XH_P44	1	179013344	179013344	Frame_Shift_Ins	INS	-	AATCAGGAAAA	-	FAM20B	63insCAATCAGC	p.V121fs
XH_P44	1	179078526	179078526	Frame_Shift_Ins	INS	-	CTACAGCATGCT	-	ABL2	3insTCAGCATG	p.K605fs
XH_P44	1	179318041	179318041	In_Frame_Ins	INS	-	CCCAAGAACA	-	SOAT1	05insTTCCCAA	D368delinsDFPKNI
XH_P44	1	179318044	179318044	Frame_Shift_Del	DEL	GC	-	GC	SOAT1	c.1107_1108del	p.W369fs
XH_P44	1	179609152	179609152	Frame_Shift_Ins	INS	-	TTAAT	-	TDRD5	364_365insTTAA	p.G122fs
XH_P44	1	179609153	179609153	In_Frame_Ins	INS	-	CTCATT	-	TDRD5	365_366insCTCA	G122delinsGSL
XH_P44	1	179965957	179965957	In_Frame_Ins	INS	-	TGGAAGTGCAAT	-	CEP350	nsAATTGGAAGG	222delinsEIGRTM
XH_P44	1	179989270	179989270	Nonsense_Mutation	INS	-	TTAAACCAACAT	-	CEP350	GTTAACCTAAAC	67_A788delinsMLVNX
XH_P44	1	179989272	179989272	Missense_Mutation	SNP	C	T	C	CEP350	c.C2363T	p.A788V
XH_P44	1	179989422	179989422	Missense_Mutation	SNP	G	A	G	CEP350	c.G2513A	p.R838K
XH_P44	1	179989424	179989424	Frame_Shift_Ins	INS	-	GGCTGTGG	-	CEP350	5_2516insGGCT	p.I839fs
XH_P44	1	179989911	179989911	Frame_Shift_Ins	INS	-	ATCATCATCAAA	-	CEP350	3insAGATCATC	p.D1001fs
XH_P44	1	179989913	179989913	Nonsense_Mutation	INS	-	CATGA	-	CEP350	D04_3005insCA	D02_Q1003delinsAX
XH_P44	1	180047745	180047745	Frame_Shift_Ins	INS	-	TATCTATTTCAC	-	CEP350	CTGGGTATTCTA	p.S1972fs
XH_P44	1	180804106	180804106	Frame_Shift_Ins	INS	-	C	-	XPR1	c.1231_1232ins	p.E411fs
XH_P44	1	180804108	180804108	Frame_Shift_Ins	INS	-	CAGTGGC	-	XPR1	33_1234insCAG	p.E411fs
XH_P44	1	180832993	180832993	Nonsense_Mutation	INS	-	AATTACTACTATT	-	XPR1	GAGAAAAATTAC	86delinsKRENNYIX
XH_P44	1	18255938	18255938	Frame_Shift_Del	DEL	CC	-	CC	RNASEL	c.3_4del	p.M1fs
XH_P44	1	18255939	18255939	Frame_Shift_Ins	INS	-	GAGGAAGAAGA	-	RNASEL	3insTCTTCTTC	p.M1fs
XH_P44	1	182841573	182841573	In_Frame_Ins	INS	-	CAG	-	DHX9	1659_1660insC	p.E553delinsEQ
XH_P44	1	182841574	182841574	Nonsense_Mutation	INS	-	AGCCTAATAGTT	-	DHX9	1insGTAGCCTTA	p.Y554delinsLX
XH_P44	1	183209334	183209334	Splice_Site	INS	-	AGTAAATTAGA	-	LAMC2	.	.
XH_P44	1	183230341	183230341	Nonsense_Mutation	INS	-	TCACAGCC	-	NMNAT2	8_749insGGCTG	50_K251delinsWLX

XH_P44	1	183536456	183536456	Frame_Shift_Ins	INS	-	TTTATTTTTCCT	-	NCF2	nsAAAGGAAAA	p.R165fs
XH_P44	1	183536458	183536459	Frame_Shift_Del	DEL	GG	-	GG	NCF2	c.492_493del	p.H164fs
XH_P44	1	183617070	183617070	Frame_Shift_Ins	INS	-	GAATACACAGAA	-	APOBEC4	7insTGTTCTGTG	p.L283fs
XH_P44	1	183711416	183711416	Frame_Shift_Ins	INS	-	CGAAGCAAAATT	-	RGL1	GACATCGAAGCA	p.T42fs
XH_P44	1	184775137	184775137	In_Frame_Ins	INS	-	AAGTCGACGTAG	-	FAM129A	1389insGTCACCT	Q463delinsQSLDL
XH_P44	1	184787827	184787827	Frame_Shift_Ins	INS	-	T	-	FAM129A	c.1117_1118ins	p.V373fs
XH_P44	1	184787829	184787829	In_Frame_Ins	INS	-	AGCCTT	-	FAM129A	15_1116insAAGb	E372delinsERL
XH_P44	1	184863270	184863270	Frame_Shift_Ins	INS	-	TACAAGGCTAT	-	FAM129A	257insATAGCC	p.W86fs
XH_P44	1	185109142	185109142	Frame_Shift_Ins	INS	-	AGATGAAAAATT	-	TRMT1L	c.TAGAAAAATTTT	p.A202fs
XH_P44	1	185109333	185109333	In_Frame_Ins	INS	-	ATGTAAGTAGA	-	TRMT1L	stCTTTTCTACTT	38delinsVFSTYMKMS
XH_P44	1	185951446	185951446	In_Frame_Ins	INS	-	GTAATA	-	HMCN1	15_2716insGTA	Q905delinsQVI
XH_P44	1	185951447	185951447	Frame_Shift_Ins	INS	-	TACTGCAGTAGT	-	HMCN1	17insATTACTGC	p.Q906fs
XH_P44	1	185985234	185985234	Nonsense_Mutation	INS	-	TAACGTGCTCTAA	-	HMCN1	insACTGTAACTGC	S85_D1686delinsKLX
XH_P44	1	186043937	186043937	In_Frame_Ins	INS	-	ATTTGTGCATGA	-	HMCN1	8205insATTGTG	T2735delinsAFVHD
XH_P44	1	186106053	186106053	In_Frame_Ins	INS	-	ATAATAGGAGGA	-	HMCN1	13567insATAAT	W4522delinsVIIGG
XH_P44	1	186107067	186107067	Frame_Shift_Ins	INS	-	CTGGGGCAATCC	-	HMCN1	8insTACACTGGG	p.A4629fs
XH_P44	1	186113470	186113470	Nonsense_Mutation	INS	-	TGAACCAATGA	-	HMCN1	insAAACTGGAAC	A697_P4698delinsX
XH_P44	1	186120398	186120398	In_Frame_Ins	INS	-	TAAACACTCTCA	-	HMCN1	14676insTAAAA	F4892delinsFKTFY
XH_P44	1	186120400	186120400	Missense_Mutation	SNP	C	T	C	HMCN1	c.C14677T	p.L4893F
XH_P44	1	186286733	186286733	Splice_Site	INS	-	AACTGTGTTGTG	-	TPR	-	-
XH_P44	1	186310503	186310503	Frame_Shift_Ins	INS	-	GAGTGAGAAAA	-	TPR	3769insCTTTTC	p.A1257fs
XH_P44	1	186310504	186310504	In_Frame_Ins	INS	-	GGT	-	TPR	3767_3768insA	M1256delinsLP
XH_P44	1	186359977	186359977	Frame_Shift_Ins	INS	-	A	-	C1orf27	c.514dupA	p.N171fs
XH_P44	1	186359979	186359979	Nonsense_Mutation	INS	-	GATGTAGTCTAA	-	C1orf27	insTATGATGTAA	2_K173delinsTMMX
XH_P44	1	186901963	186901963	In_Frame_Ins	INS	-	TTTTTAAAGAA	-	PLA2G4A	CTAATTTTTTAA	A49delinsMPNFLKEEN
XH_P44	1	192998530	192998530	In_Frame_Ins	INS	-	TAA	-	UCHL5	c.421_422insTT	p.N141delinsIN
XH_P44	1	192998532	192998532	In_Frame_Ins	INS	-	GGAGAC	-	UCHL5	19_420insGTCT	H140delinsQSP
XH_P44	1	193045063	193045063	Frame_Shift_Ins	INS	-	CCATGATATAAA	-	TROVE2	nsCTTCCATGA	p.V232fs
XH_P44	1	196395091	196395091	In_Frame_Ins	INS	-	ATGTGTTTAAAG	-	KCNT2	AAACATACTTTAA	8delinsQTYFNTSCNT
XH_P44	1	196887421	196887421	Frame_Shift_Ins	INS	-	T	-	CFHR4	c.881_882insT	p.K294fs
XH_P44	1	196887422	196887422	Nonsense_Mutation	INS	-	TAGTTATTAATT	-	CFHR4	5TTAATAGTTAT	4_T295delinsKVNSYX
XH_P44	1	197029552	197029552	Nonsense_Mutation	INS	-	TTTTAGCAATCT	-	F13B	ATTAAAGATTG	0_D251delinsYKDCX
XH_P44	1	197060105	197060105	Nonsense_Mutation	INS	-	GGTTTATTAATCA	-	ASPM	ACTTCTTGATTA	H1587delinsYFLINLLX
XH_P44	1	197065269	197065269	Frame_Shift_Ins	INS	-	GAGTGTAAAG	-	ASPM	nsCAAATACTTTT	p.K1364fs
XH_P44	1	197070511	197070511	Nonsense_Mutation	INS	-	CTAATTCACTGA	-	ASPM	5TAGAATTGACTG	2624_H2625delinsX
XH_P44	1	197070890	197070890	Nonsense_Mutation	INS	-	CAAGCACC	-	ASPM	0_7491insGGTG	p.V2497delinsX
XH_P44	1	197070892	197070892	Frame_Shift_Ins	INS	-	ATGTATAGGCA	-	ASPM	8insATAGTCCCT	p.V2497fs
XH_P44	1	197071661	197071661	Frame_Shift_Ins	INS	-	A	-	ASPM	c.6719_6720ins	p.R2240fs
XH_P44	1	197071662	197071662	Nonsense_Mutation	INS	-	ATTACATATGAG	-	ASPM	19insTATCTCAT	A0_H2241delinsISHMX
XH_P44	1	197072034	197072034	Frame_Shift_Ins	INS	-	GAAGAGAAACAT	-	ASPM	5AATTGTATGTT	p.M2116fs
XH_P44	1	197072329	197072329	Frame_Shift_Ins	INS	-	TAAAGATGTAGAC	-	ASPM	052insGCTCTAC	p.L2018fs
XH_P44	1	197073101	197073101	Frame_Shift_Ins	INS	-	TCAGAGATGGT	-	ASPM	8insCTGTACCAT	p.S1760fs
XH_P44	1	197112055	197112055	Frame_Shift_Ins	INS	-	AAGCAAAAAGA	-	ASPM	27insACATCTTT	p.6443fs
XH_P44	1	197112894	197112894	In_Frame_Ins	INS	-	CTTGCCACTCTC	-	ASPM	188insGAGAGTG	163delinsREWQA
XH_P44	1	197128537	197128537	Frame_Shift_Ins	INS	-	ACTTTAATGGT	-	ZBTB41	2682insAACCAT	p.D894fs
XH_P44	1	197128539	197128539	Frame_Shift_Ins	INS	-	TT	-	ZBTB41	2679_2680insA	p.D894fs
XH_P44	1	197168936	197168936	Frame_Shift_Ins	INS	-	GAGGA	-	ZBTB41	667_668insTCC	p.E223fs
XH_P44	1	197168937	197168937	In_Frame_Ins	INS	-	CTCTGGAAGTGA	-	ZBTB41	667insTTCACTT	E223delinsFTSRE
XH_P44	1	197390359	197390359	Frame_Shift_Ins	INS	-	GTTAATAATAAA	-	CRB1	66insCTGTAAA	p.F355fs
XH_P44	1	197404281	197404281	Frame_Shift_Ins	INS	-	CAGA	-	CRB1	952_2953insCA	p.C984fs
XH_P44	1	197404283	197404283	Nonsense_Mutation	INS	-	TAGCATATAA	-	CRB1	2955insTAGCA	B85_S986delinsLSIX
XH_P44	1	198222272	198222272	Nonsense_Mutation	INS	-	ACACTGACGAC	-	NEK7	nsCTACACACTG	A54_L55delinsPTHX
XH_P44	1	200378074	200378074	Frame_Shift_Ins	INS	-	CAAGAGGACAT	-	ZNF281	8insTATGTGTCC	p.L254fs
XH_P44	1	200826957	200826957	Nonsense_Mutation	INS	-	TGTTGAAAGTCT	-	CAMSAP2	8insTGCTGTTGA	387delinsMLLKVX
XH_P44	1	200882708	200882708	Frame_Shift_Ins	INS	-	TACACATTTTCT	-	C1orf106	8insCTTTACACA	p.P563fs
XH_P44	1	201181463	201181463	In_Frame_Ins	INS	-	TACCCAATA	-	IGFN1	2_7443insTACC	A2481delinsATQY
XH_P44	1	201181465	201181465	Missense_Mutation	SNP	G	C	G	IGFN1	c.G7444C	p.A2482P
XH_P44	1	201181869	201181869	Frame_Shift_Ins	INS	-	TTCCA	-	IGFN1	848_7849insTT	p.A2616fs
XH_P44	1	201750251	201750251	In_Frame_Ins	INS	-	SAGAAAAAGGCA	-	NAV1	nsAAAGAGAAAA	102delinsKREKGRV
XH_P44	1	201772792	201772792	In_Frame_Ins	INS	-	TATTGAGTCCCA	-	NAV1	AACATTATTATGA	6delinsKHLSPNHV
XH_P44	1	201778340	201778340	Frame_Shift_Ins	INS	-	GTAAAGTTTGA	-	NAV1	075insAGTTAA	p.V1025fs
XH_P44	1	201972399	201972399	Nonsense_Mutation	INS	-	TTTAACTTACT	-	RNPEP	92insATTTAACA	A97_W198delinsGIX
XH_P44	1	201972401	201972402	Frame_Shift_Del	DEL	GG	-	GG	RNPEP	c.593_594del	p.W198fs
XH_P44	1	202703001	202703001	Frame_Shift_Ins	INS	-	TT	-	KDM5B	3301_3302insA	p.G1101fs
XH_P44	1	202703003	202703003	In_Frame_Ins	INS	-	GCGTATCCG	-	KDM5B	3300insCGGA	L1100delinsLGVA
XH_P44	1	203012559	203012559	Frame_Shift_Ins	INS	-	CTTC	-	PPFIA4	269_270insCTT	p.C90fs
XH_P44	1	203316899	203316899	Frame_Shift_Ins	INS	-	CTGATCTT	-	FMO4	9_500insAAGAT	p.L167fs
XH_P44	1	203768161	203768161	In_Frame_Ins	INS	-	CACAACATGTG	-	ZBED6	1512insCACAA	C5504delinsSTTCC
XH_P44	1	203816457	203816457	Frame_Shift_Ins	INS	-	AGAGTCCAACAGA	-	ZC3H11A	189insCAGTCC	p.R396fs
XH_P44	1	203819115	203819115	Nonsense_Mutation	INS	-	ATCTGGTACCTC	-	ZC3H11A	ATTAAAACTCGG	K635delinsDRIKWYLYX
XH_P44	1	205138650	205138650	Frame_Shift_Ins	INS	-	TATGATTGTTG	-	DSTYK	GTGTCTCAACA	p.A322fs
XH_P44	1	206325436	206325436	Frame_Shift_Ins	INS	-	CAAGAGTGCTT	-	CTSE	437insCAAGAA	p.L146fs
XH_P44	1	206325438	206325438	Splice_Site	SNP	G	C	G	CTSE	-	-
XH_P44	1	207196132	207196132	In_Frame_Ins	INS	-	GGACCT	-	C1orf116	38_239insAGG	p.T80delinsKVP
XH_P44	1	207241600	207241600	Frame_Shift_Ins	INS	-	ACTTGGTCTGTA	-	PKFB2	34insAACTTGGT	p.A311fs
XH_P44	1	207300167	207300167	Frame_Shift_Ins	INS	-	TGATGTGCAAGT	-	C4BPA	5AATGTGCATGT	p.V272fs
XH_P44	1	207646301	207646301	Nonsense_Mutation	INS	-	AATGAAGCTGG	-	CR2	756insAAATGA	A85_W586delinsTKX
XH_P44	1	209880464	209880464	Frame_Shift_Ins	INS	-	GCAAGAGATGG	-	HSD11B1	509insGCAAGA	p.S170fs
XH_P44	1	209961989	209961989	Frame_Shift_Ins	INS	-	ATCTTCTCCTTC	-	IRF6	5insAGAAGGAA	p.V299fs
XH_P44	1	210187063	210187063	Nonsense_Mutation	INS	-	TAAGTTAGCTTA	-	SYT14	AACATTAAAGTT	A60delinsKETPNIKLAYLYIX
XH_P44	1	210334350	210334350	Frame_Shift_Ins	INS	-	AC	-	SYT14	1631_1632insA	p.Q544fs
XH_P44	1	210334351	210334351	In_Frame_Ins	INS	-	TATCACAAATAT	-	SYT14	1633insTATCAC	Q544delinsQVHKY
XH_P44	1	212274335	212274335	In_Frame_Ins	INS	-	ATCCAAATGAAG	-	DTL	nsACAGATCCAA	A97delinsAIQMIKIF
XH_P44	1	213181793	213181793	Frame_Shift_Ins	INS	-	ATTTTGTGCGAG	-	ANGEL2	ACGTCTGCATCA	p.N8fs
XH_P44	1	213303191	213303191	In_Frame_Ins	INS	-	GCCTCG	-	RPS6KC1	58_759insGCTC	p.F253delinsLLC
XH_P44	1	213303193	213303193	Frame_Shift_Ins	INS	-	C	-	RPS6KC1	c.760_761insC	p.Y254fs
XH_P44	1	213415040	213415040	Frame_Shift_Ins	INS	-	TTTTCTCCAAA	-	RPS6KC1	827insTTTTCT	p.C276fs
XH_P44	1	213415042	213415042	Silent	SNP	C	T	C	RPS6KC1	c.C828T	p.C276C
XH_P44	1	214170752	214170752	Missense_Mutation	SNP	G	T	G	PROX1	c.G874T	p.V292F
XH_P44	1	214170754	214170754	In_Frame_Ins	INS	-	ATTTTCATT	-	PROX1	6_877insATTITT	b.V292delinsVIF
XH_P44	1	214818582	214818582	Frame_Shift_Ins	INS	-	TTATGGATATCT	-	CENPF	0insGATTATGG	p.N1890fs
XH_P44	1	214818784	214818784	Frame_Shift_Ins	INS	-	TTATCTCC	-	CENPF	71_5872insTTAT	p.T1957fs
XH_P44	1	214818786	214818786	Missense_Mutation	SNP	G	A	G	CENPF	c.G5873A	p.S1958N
XH_P44	1	215777614	215777614	Missense_Mutation	SNP	A	T	A	KCTD3	c.A1279T	p.I427F
XH_P44	1	215793605	215793605	Frame_Shift_Ins	INS	-	GGCTG	-	KCTD3	387_2088insGG	p.K696fs
XH_P44	1	215793715	215793715	Nonsense_Mutation	INS	-	GAAATACAG	-	KCTD3	7_2198insGAAA	p.F733delinsX
XH_P44	1	215848282	215848282	Nonsense_Mutation	INS	-	TAAATATTAGT	-	USH2A	ATACTCAACTAAB	24_P4325delinsHIX
XH_P44	1	215955495	215955495	Frame_Shift_Ins	INS	-	TGGTGTTAAGTA	-	USH2A	0629insCTACTT	p.R3543fs

XH_P44	1	215955496	215955496	Frame_Shift_Ins	INS	-	GT	-	USH2A	0627_10628ins	p.R3543fs
XH_P44	1	216262439	216262439	Frame_Shift_Ins	INS	-	TGTTGAATTTGC	-	USH2A	801insGGCAAA	p.Q1601fs
XH_P44	1	218475846	218475846	In_Frame_Ins	INS	-	AAGTGGTCCTTT	-	RRP15	insTAAAGTTGG	117delinsNKSQPPF
XH_P44	1	220146700	220146700	In_Frame_Ins	INS	-	TTTTTACTTGTA	-	EPRS	CCATAATACAAAG	375delinsTIQVKNPE
XH_P44	1	220146702	220146702	Missense_Mutation	SNP	C	T	C	EPRS	c.G4122A	p.M1374I
XH_P44	1	220152861	220152861	Frame_Shift_Ins	INS	-	GACTGTGTGTAT	-	EPRS	808insAATACAC	p.Q1270fs
XH_P44	1	220195781	220195781	Frame_Shift_Ins	INS	-	TACCACATTATT	-	EPRS	CTTAGAAATAAT	p.K341fs
XH_P44	1	220809279	220809279	In_Frame_Ins	INS	-	AACTGATCTACT	-	MARK1	1316insAACTCGA	1439delinsQLIVF
XH_P44	1	221912805	221912805	Frame_Shift_Ins	INS	-	CAAAGAA	-	DUSP10	81_282insTTCT	p.T94fs
XH_P44	1	221912807	221912807	Missense_Mutation	SNP	T	A	T	DUSP10	c.A280T	p.T94S
XH_P44	1	222801282	222801282	Silent	SNP	G	T	G	MI3	c.G720T	p.V240V
XH_P44	1	222801283	222801283	Frame_Shift_Ins	INS	-	TATAATTATGAA	-	MI3	TACATTATAATT	p.P241fs
XH_P44	1	222802020	222802020	In_Frame_Ins	INS	-	AAATCCATCGTA	-	MI3	CTCTCTAAATCC	86delinsELSKISVSL
XH_P44	1	223116548	223116548	Nonsense_Mutation	INS	-	SGTGTGAGCTGT	-	DISP1	384insGGTGTGA	C128delinsWVX
XH_P44	1	223175940	223175940	Nonsense_Mutation	INS	-	CAAAAGCTAAA	-	DISP1	AGTTACAAAAG	8_A159delinsRESYKX
XH_P44	1	223176321	223176321	Frame_Shift_Ins	INS	-	TGCTCTCCCCCTT	-	DISP1	854insTGCTCTCT	p.T285fs
XH_P44	1	223178567	223178567	In_Frame_Ins	INS	-	SAGGTTCTAATT	-	DISP1	00insAGAGGTT	1033delinsARGSNS
XH_P44	1	223984118	223984118	Frame_Shift_Ins	INS	-	AATCCAGAATCC	-	TP53BP2	23insATGGATTCT	p.L708fs
XH_P44	1	224599220	224599220	Frame_Shift_Ins	INS	-	TGTAAGTTAATA	-	WDR26	TGATAAATATTA	p.N340fs
XH_P44	1	224606096	224606096	Frame_Shift_Ins	INS	-	GTITTTTCTGTTAT	-	WDR26	7insAGATAAACGA	p.M279fs
XH_P44	1	225156575	225156575	Frame_Shift_Ins	INS	-	CTCAACACACT	-	DNAH14	617insCTCAAC	p.R206fs
XH_P44	1	225156577	225156577	Silent	SNP	G	C	G	DNAH14	c.G618C	p.R206R
XH_P44	1	225230676	225230676	Nonsense_Mutation	INS	-	CAACATATAACT	-	DNAH14	529insACAACAT	p.C543delinsX
XH_P44	1	225394895	225394895	Frame_Shift_Ins	INS	-	CCACTGCCCTCT	-	DNAH14	6347insCCACT	p.M2116fs
XH_P44	1	225591016	225591016	Frame_Shift_Ins	INS	-	AATGCTATTGAT	-	LBR	ATAAACATCAA	p.V613fs
XH_P44	1	225692726	225692726	In_Frame_Ins	INS	-	SAATAGAAGATC	-	ENAH	nsAAAGGATCT	523delinsEKDLFNF
XH_P44	1	225692728	225692728	Missense_Mutation	SNP	A	C	A	ENAH	c.T1566G	p.I522M
XH_P44	1	226567651	226567651	Frame_Shift_Ins	INS	-	TTACATTAACT	-	PARP1	5insTGAAGTTA	p.K505fs
XH_P44	1	227204722	227204722	Nonsense_Mutation	INS	-	AACTCTCATTGAT	-	CDC42BPA	297insGATCAAT	33_D1434delinsDQX
XH_P44	1	227842194	227842194	In_Frame_Ins	INS	-	AAAAATAAAAAA	-	ZNF678	9insATAAAAAAT	E136delinsEIKKS
XH_P44	1	227842547	227842547	Frame_Shift_Ins	INS	-	ATTTGTATGGC	-	ZNF678	TTTCACATTGTGT	p.H254fs
XH_P44	1	227842983	227842983	Frame_Shift_Ins	INS	-	TGTAA	-	ZNF678	197_1198insTG	p.T399fs
XH_P44	1	227842985	227842985	Nonsense_Mutation	INS	-	TATGATTCTCT	-	ZNF678	CTCCAGTATTGAA	0_E401delinsGFSPVX
XH_P44	1	227946929	227946929	Frame_Shift_Ins	INS	-	AAGGAGTAATA	-	SNAP47	ATTTTTAAGGAG	p.S244fs
XH_P44	1	228482587	228482587	Silent	SNP	G	A	G	OBSCN	c.G11502A	p.R3834R
XH_P44	1	228487117	228487117	Frame_Shift_Ins	INS	-	CACATGCA	-	OBSCN	8_13369insCAC	p.D4456fs
XH_P44	1	229584927	229584927	Nonsense_Mutation	INS	-	TAGTCTGTATC	-	NUP133	insGATTGTATCA	N1065delinsRLYQDX
XH_P44	1	229790097	229790097	In_Frame_Ins	INS	-	AGATA	-	URB2	4339_4340insAG	P1447delinsQT
XH_P44	1	229790098	229790098	Nonsense_Mutation	INS	-	TCTTTA	-	URB2	340_4341insTCT	P1447delinsPLX
XH_P44	1	230814778	230814778	Silent	SNP	G	A	G	COG2	c.G1146A	p.L382L
XH_P44	1	230814779	230814779	In_Frame_Ins	INS	-	AAGATCTTT	-	COG2	7_1148insAAGA	P383delinsQDLS
XH_P44	1	231298885	231298951	Frame_Shift_Del	DEL	CTGGAGCAC	-	CTGGAGCACGA	TRIM67	c.170_236del	p.L57fs
XH_P44	1	231401514	231401514	Frame_Shift_Ins	INS	-	TTCTGTGAACAA	-	GNPAT	71insCTTCTCGTA	p.G190fs
XH_P44	1	231488888	231488888	In_Frame_Ins	INS	-	AGG	-	SPRNT	1251_1252insAG	p.F417delinsFFR
XH_P44	1	231488890	231488890	In_Frame_Ins	INS	-	TGTTGC	-	SPRNT	53_1254insTGT	D418delinsDVA
XH_P44	1	231700511	231700512	Frame_Shift_Del	DEL	AC	-	AC	TSNAX	c.733_734del	p.T245fs
XH_P44	1	232144667	232144667	Nonsense_Mutation	INS	-	GGCATAAAAATG	-	DISC1	ACAAAGGCATAC	G605delinsETKAX
XH_P44	1	232941332	232941332	Missense_Mutation	SNP	A	G	A	MAP10	c.A563G	p.E188G
XH_P44	1	232942932	232942932	Nonsense_Mutation	INS	-	TCAGCTTTAAAG	-	MAP10	GATTTGTGACGT	1_5722delinsIRICQLX
XH_P44	1	232943268	232943268	Frame_Shift_Ins	INS	-	AGTTTAGTTTCT	-	MAP10	TATTTTCAGTTTA	p.C833fs
XH_P44	1	232943499	232943499	Frame_Shift_Ins	INS	-	GAATGTCAATT	-	MAP10	nsATAAGAAATG	p.A910fs
XH_P44	1	232943500	232943500	Frame_Shift_Ins	INS	-	SAATGTCATTAT	-	MAP10	insTAAGAATGT	p.G911fs
XH_P44	1	232943855	232943855	Nonsense_Mutation	INS	-	TGTTTAAACAGA	-	MAP10	ACTTCTTGTTTT	9_Q1030delinsNYFLFX
XH_P44	1	233335981	233335981	Frame_Shift_Ins	INS	-	SGCTAGTTAGG	-	PCNX2	AAGAAAAACCTA	p.PCN5fs
XH_P44	1	233489667	233489667	Nonsense_Mutation	INS	-	CAGTATGCATTG	-	MAP3K21	GAAATCCAGTAT	368delinsSQKSMHSFX
XH_P44	1	233518407	233518407	Nonsense_Mutation	INS	-	GGTGAGGGGC	-	MAP3K21	3062insGGTGA	021_1102delinsRX
XH_P44	1	234593464	234593464	Frame_Shift_Ins	INS	-	TTTG	-	TARBP1	670_1671insCA	p.M557fs
XH_P44	1	234593465	234593465	In_Frame_Ins	INS	-	ATTGTATATTGT	-	TARBP1	DinsAAGCAAAAT	557delinsKANIQYL
XH_P44	1	234601434	234601434	Missense_Mutation	SNP	C	A	C	TARBP1	c.G1269T	p.M423I
XH_P44	1	234601435	234601435	Frame_Shift_Ins	INS	-	CTTTGTTTTTTCT	-	TARBP1	AAACAAGAAAA	p.M423fs
XH_P44	1	236738185	236738185	Frame_Shift_Ins	INS	-	CAGGAACAGCG	-	HEATR1	3103insCGCTG	p.L1035fs
XH_P44	1	236766674	236766674	Frame_Shift_Ins	INS	-	AGTGTCTGGAGT	-	HEATR1	SinsCCACTCCAG	p.C49fs
XH_P44	1	236897786	236897786	Nonsense_Mutation	INS	-	AACA	-	ACTN2	751_752insAAC	251_Y252delinsX
XH_P44	1	236897787	236897787	Missense_Mutation	SNP	G	T	G	ACTN2	c.G752T	p.C251F
XH_P44	1	237777597	237777597	Frame_Shift_Ins	INS	-	SATCTGTAGAAG	-	RYR2	170insAGATCTG	p.N1723fs
XH_P44	1	237819146	237819146	Missense_Mutation	SNP	T	A	T	RYR2	c.T7991A	p.L2664Q
XH_P44	1	237819147	237819147	Frame_Shift_Ins	INS	-	AAAAGAAAGCT	-	RYR2	7993insAAAAAG	p.L2664fs
XH_P44	1	238049159	238049159	Frame_Shift_Ins	INS	-	C	-	ZP4	c.866_867insG	p.V289fs
XH_P44	1	238049160	238049160	Frame_Shift_Ins	INS	-	AATCCTTATT	-	ZP4	866insAAATAA	p.V289fs
XH_P44	1	238053896	238053896	Nonsense_Mutation	INS	-	AGTCTAAGTTAT	-	ZP4	nsGTTATAACTTA	p.S14delinsVITX
XH_P44	1	241680613	241680613	Nonsense_Mutation	INS	-	AGTAAGTAGGCT	-	FH	AATACAGCCTAC	S46_Q47delinsX
XH_P44	1	241798477	241798477	Nonsense_Mutation	INS	-	TGTTAGTCGTTA	-	CHML	CTACATAACGA	p.K198delinsFX
XH_P44	1	242451691	242451691	Nonsense_Mutation	INS	-	AATCATATGTCA	-	PLD5	insGAGTGACAT	B4_N95delinsLDIX
XH_P44	1	243456426	243456426	Frame_Shift_Ins	INS	-	SCATATGCTTCT	-	SDCCAG8	AAAAGCATATG	p.E194fs
XH_P44	1	244715939	244715939	Frame_Shift_Ins	INS	-	SAATAAAATGAT	-	CATSPERE	AAGAGAAATAAA	p.R133fs
XH_P44	1	244803350	244803350	Nonsense_Mutation	INS	-	AATAGCTAGCTA	-	CATSPERE	nsTTTGAATAGC	L790delinsLFEX
XH_P44	1	247013305	247013305	Frame_Shift_Ins	INS	-	C	-	AHCTF1	c.6002_6003ins	p.E2001fs
XH_P44	1	247013306	247013306	Nonsense_Mutation	INS	-	AAGAAAAAA	-	AHCTF1	1_6002insTTTT	E2001delinsVF5X
XH_P44	1	247013835	247013835	Frame_Shift_Ins	INS	-	GAAA	-	AHCTF1	5472_5473insTT	p.N1825fs
XH_P44	1	247013836	247013836	Nonsense_Mutation	INS	-	TATAAATGA	-	AHCTF1	1_5472insTCAT	E1824delinsDHLX
XH_P44	1	247024457	247024457	Frame_Shift_Ins	INS	-	AGTTTATAATAA	-	AHCTF1	5insATTCTATTAT	p.D1292fs
XH_P44	1	247150733	247150733	Nonsense_Mutation	INS	-	CATATCTTACTAA	-	ZNF695	4insGATTAGTA	362_Q363delinsDX
XH_P44	1	247150735	247150735	Frame_Shift_Ins	INS	-	TCATAAG	-	ZNF695	81_1082insCTTA	p.F361fs
XH_P44	1	247263800	247263800	Frame_Shift_Ins	INS	-	AAAAATAAATAA	-	ZNF695	013insCATTATT	p.G338fs
XH_P44	1	247320067	247320067	In_Frame_Ins	INS	-	AAGGTGTAGGA	-	ZNF124	stACTTTTCTTAC	286delinsVLSYTLHS
XH_P44	1	247320068	247320068	Frame_Shift_Ins	INS	-	TT	-	ZNF124	c.855_856insAA	p.A286fs
XH_P44	1	247695843	247695843	Splice_Site	INS	-	ATGTCCTA	-	OR2C3	.	.
XH_P44	1	247769485	247769485	Frame_Shift_Ins	INS	-	GCAAG	-	OR2G3	598_599insGCA	p.F200fs
XH_P44	1	247769486	247769486	Nonsense_Mutation	INS	-	TAACATAAGGTC	-	OR2G3	600insTAACATA	00_V201delinsFNX
XH_P44	1	247921598	247921598	Frame_Shift_Ins	INS	-	AATATCTT	-	OR1C1	0_111insAAGA	p.A37fs
XH_P44	1	247921599	247921599	Frame_Shift_Ins	INS	-	A	-	OR1C1	c.109_110insT	p.A37fs
XH_P44	1	247921705	247921705	Missense_Mutation	SNP	C	G	C	OR1C1	c.G4C	p.E2Q
XH_P44	1	247921707	247921707	Frame_Shift_Ins	INS	-	GGCTGCC	-	OR1C1	.1_2insGGCAGC	p.M1fs
XH_P44	1	248004976	248004976	Missense_Mutation	SNP	A	T	A	OR11L1	c.T223A	p.S75T
XH_P44	1	248004977	248004977	Frame_Shift_Ins	INS	-	TCCTG	-	OR11L1	221_222insCAG	p.T74fs
XH_P44	1	248031322	248031322	Nonsense_Mutation	INS	-	TAAAAATT	-	TRIM58	8_829insTAAAA	276_C277delinsAX
XH_P44	1	248031324	248031324	Missense_Mutation	SNP	G	C	G	TRIM58	c.G830C	p.C277S
XH_P44	1	248129390	248129390	Frame_Shift_Ins	INS	-	ACATACAATGTA	-	OR2AK2	sAAACACATACA	p.V253fs

XH_P44	1	248343767	248343767	In_Frame_Ins	INS	-	GAGGAGGAA	-	OR2M2	481insGAGGA	A160delinsAEEE
XH_P44	1	248343769	248343769	Frame_Shift_Ins	INS	-	ATGGGGGTGTCT	-	OR2M2	3insACATGGGG	p.V161fs
XH_P44	1	248487095	248487095	Nonsense_Mutation	INS	-	CTTTTATTGTCT	-	OR2M7	AAGAGAGACAA	C259_I260delinsX
XH_P44	1	248512316	248512316	Nonsense_Mutation	SNP	T	A	T	OR14C36	c.T240A	p.C80X
XH_P44	1	248512317	248512317	Frame_Shift_Ins	INS	-	GAGAAATCCA	-	OR14C36	242insGAGAAA	p.V81fs
XH_P44	1	248569608	248569608	In_Frame_Ins	INS	-	SATATAAGGTAA	-	OR2T1	314insGATATAA	L105delinsRVKVI
XH_P44	1	248616565	248616565	In_Frame_Ins	INS	-	GCATCT	-	OR2T2	67_468insGCA	b.D156delinsEHL
XH_P44	1	248652023	248652023	Frame_Shift_Ins	INS	-	GGATTTGAGT	-	OR2T5	135insGGATT	p.G45fs
XH_P44	1	248652025	248652025	Missense_Mutation	SNP	A	T	A	OR2T5	c.A136T	p.N46Y
XH_P44	1	248685898	248685898	Silent	SNP	G	A	G	OR2G6	c.G951A	p.X317X
XH_P44	1	248756316	248756316	Nonsense_Mutation	INS	-	TGTGAAAGAAC	-	OR2T10	ACTTAAGTTCTT	252delinsNLS5FTLX
XH_P44	1	248789720	248789720	Frame_Shift_Ins	INS	-	GACGTCA	-	OR2T11	9_710insTGAC	p.T237fs
XH_P44	1	248789722	248789722	Silent	SNP	G	A	G	OR2T11	c.C708T	p.T236T
XH_P44	1	248790271	248790271	Frame_Shift_Ins	INS	-	TC	-	OR2T11	c.158_159insGA	p.H53fs
XH_P44	1	248790273	248790273	In_Frame_Ins	INS	-	TAACCTCT	-	OR2T11	157insAGAGG	H53delinsRGLH
XH_P44	1	248844806	248844806	Frame_Shift_Ins	INS	-	TTGAATGGGAG	-	OR14I1	GTCTTCTCCCA	p.I267fs
XH_P44	2	7030374	7030374	In_Frame_Ins	INS	-	ATATAACCTTTC	-	RSAD2	TTAAATATAAA	69delinsLKYKLSKT
XH_P44	2	8897901	8897901	Frame_Shift_Ins	INS	-	CACCCAGAGGT	-	KIDINS220	insCAGTACCTC	p.S1011fs
XH_P44	2	8999008	8999008	Nonsense_Mutation	INS	-	TACGACCTTTTC	-	MBOAT2	nsCTTGAAAAGG	p.L322delinsPX
XH_P44	2	10050931	10050931	Nonsense_Mutation	INS	-	CTATAAACATCTA	-	TAF1B	8insTTCTTAAAA	T86_F87delinsTSX
XH_P44	2	10927529	10927529	In_Frame_Ins	INS	-	GGT	-	PDIAB	1034_1035insA	p.L345delinsLP
XH_P44	2	10927530	10927530	Nonsense_Mutation	INS	-	TAGGTGTGTTG	-	PDIAB	AAACAAACAAC	45delinsQTKQQTXX
XH_P44	2	11335112	11335112	Frame_Shift_Ins	INS	-	ACTGGTACCTTT	-	ROCK2	GTGTCTAAAGG	p.N1077fs
XH_P44	2	11725298	11725298	Frame_Shift_Ins	INS	-	TTTGTAAATGTT	-	GREB1	4insTTTTGTGA	p.N305fs
XH_P44	2	11725300	11725300	Silent	SNP	C	T	C	GREB1	c.C915T	p.N305N
XH_P44	2	11905740	11905740	Missense_Mutation	SNP	G	A	G	LPIN1	c.G73A	p.A25T
XH_P44	2	15536595	15536595	Frame_Shift_Ins	INS	-	GGGAGTGA	-	NBAS	5_3076insTCAC	p.K1026fs
XH_P44	2	15536597	15536597	Frame_Shift_Ins	INS	-	TTTCTCAA	-	NBAS	3_3074insTTGA	p.D1025fs
XH_P44	2	15674755	15674755	Nonsense_Mutation	INS	-	TCATGCTTATCTA	-	NBAS	insGATAGATAA	420_Q221delinsDRX
XH_P44	2	17942783	17942783	Nonsense_Mutation	INS	-	AATAACATTTTA	-	GEN1	AATGTAATAAC	Y94delinsYQKRX
XH_P44	2	17942785	17942785	Missense_Mutation	SNP	G	A	G	GEN1	c.G284A	p.G95E
XH_P44	2	17946235	17946235	Frame_Shift_Ins	INS	-	AA	-	GEN1	c.420_421insAA	p.A140fs
XH_P44	2	17946236	17946236	Nonsense_Mutation	INS	-	5TTATGTTTCTTT	-	GEN1	TGTGGTTATGTG	T141_L142delinsX
XH_P44	2	18112553	18112553	In_Frame_Ins	INS	-	CAGAAGGCAGA	-	KCNS3	9insTACAGAAG	E93delinsDTEGRV
XH_P44	2	18112851	18112851	Frame_Shift_Ins	INS	-	CGTCTCTGGT	-	KCNS3	577insCGTTC	p.L192fs
XH_P44	2	20132169	20132169	Frame_Shift_Ins	INS	-	GGAAA	-	WDR35	697_2698insTT	p.K900fs
XH_P44	2	20132170	20132170	Frame_Shift_Ins	INS	-	AAATATTT	-	WDR35	6_2697insAAAT	p.W899fs
XH_P44	2	20478579	20478579	Frame_Shift_Ins	INS	-	TC	-	PUM2	1553_1554insG	p.V518fs
XH_P44	2	20478581	20478581	Splice_Site	INS	-	TTTCATCATATGG	-	PUM2	-	-
XH_P44	2	20494277	20494277	In_Frame_Ins	INS	-	CATACAGTTGAT	-	PUM2	844insATCAACT	P282delinsNCMP
XH_P44	2	21225438	21225438	In_Frame_Ins	INS	-	TTTCGTGAAGAA	-	APOB	856insTATTCTT	4286delinsYSSRRA
XH_P44	2	21231695	21231695	In_Frame_Ins	INS	-	AATTGAAGTACC	-	APOB	nsAAGTAGGTAC	682delinsKVGTSIVC
XH_P44	2	21255429	21255429	Silent	SNP	A	T	A	APOB	c.T1149A	p.V383V
XH_P44	2	21255430	21255430	Frame_Shift_Ins	INS	-	TTTCTCCT	-	APOB	7_1148insAGGA	p.V383fs
XH_P44	2	21362777	21362777	Missense_Mutation	SNP	G	A	G	TDRD15	c.G2438A	p.G813E
XH_P44	2	21362779	21362779	Frame_Shift_Ins	INS	-	TATTAACAGCT	-	TDRD15	2441insTATTAA	p.K814fs
XH_P44	2	21364193	21364193	Frame_Shift_Ins	INS	-	TTTGTGTTTTGTA	-	TDRD15	TCTTCATTTTGT	p.D1285fs
XH_P44	2	24302427	24302427	Frame_Shift_Ins	INS	-	AAAGTGTGGTTG	-	TP53I3	3insATGAACCA	p.W235fs
XH_P44	2	26679355	26679355	Frame_Shift_Ins	INS	-	CAGCCTCTTGTA	-	DRC1	194insCCAGCCT	p.P731fs
XH_P44	2	26679357	26679357	Frame_Shift_Ins	INS	-	AG	-	DRC1	2195_2196insA	p.T732fs
XH_P44	2	26683010	26683010	Frame_Shift_Ins	INS	-	ACACAACACACA	-	OTOF	3807insTGTGT	p.W1269fs
XH_P44	2	27591890	27591890	Missense_Mutation	SNP	G	C	G	EIF2B4	c.C464G	p.A155G
XH_P44	2	27591891	27591891	Nonsense_Mutation	INS	-	TCATCCTGTTTT	-	EIF2B4	463insAAAAACAG	A155delinsKTGX
XH_P44	2	27677447	27677447	Nonsense_Mutation	INS	-	TTTCATGATTATC	-	IFT172	2insCAAGATAAT	F1151delinsSRX
XH_P44	2	27686003	27686003	Frame_Shift_Ins	INS	-	AGTCAGACCAT	-	IFT172	1983insATGGT	p.H661fs
XH_P44	2	27686005	27686005	Missense_Mutation	SNP	G	T	G	IFT172	c.C1981A	p.H661N
XH_P44	2	27800280	27800280	Missense_Mutation	SNP	G	C	G	C2orf16	c.G841C	p.A281P
XH_P44	2	27800281	27800281	Frame_Shift_Ins	INS	-	ATTTCTCTACAGT	-	C2orf16	ACAGATTCTCTCT	p.A281fs
XH_P44	2	27801022	27801022	In_Frame_Ins	INS	-	TGTTAGGCCCA	-	C2orf16	584insTTGTTTAACT	528delinsTLAPL
XH_P44	2	27802163	27802163	Nonsense_Mutation	INS	-	5ATGTCTCTGAA	-	C2orf16	sGGTAGATGTC	5908delinsCGRCLX
XH_P44	2	27825409	27825409	Frame_Shift_Ins	INS	-	ATCAGAGGAGA	-	ZNF512	AAAATATCAGAC	p.K221fs
XH_P44	2	27825411	27825411	Missense_Mutation	SNP	C	A	C	ZNF512	c.C664A	p.L221I
XH_P44	2	27850455	27850455	Frame_Shift_Ins	INS	-	AAGACACGGGA	-	CCDC121	98insCTCCCGT	p.R233fs
XH_P44	2	27850457	27850457	Silent	SNP	T	A	T	CCDC121	c.A696T	p.R232R
XH_P44	2	27878393	27878393	Nonsense_Mutation	INS	-	ATTTCACTACTT	-	SUPT7L	GCAAAAAGTAC	K139delinsSKYX
XH_P44	2	29416119	29416119	Nonsense_Mutation	INS	-	AGAAAATATCAT	-	ALK	ATTTTTATGATA	12_N1613delinsFLX
XH_P44	2	29436868	29436868	Frame_Shift_Ins	INS	-	5TTTTTTTGAGC	-	ALK	insTCTCTCACAA	p.E1242fs
XH_P44	2	32476025	32476025	In_Frame_Ins	INS	-	GGAGAC	-	NLR4	707_908insGTCT	D303delinsGLH
XH_P44	2	32640637	32640637	Nonsense_Mutation	INS	-	TTACTCATAATA	-	BIRC6	insACTTTTACTC	0_N761delinsNFYSX
XH_P44	2	32754833	32754833	Nonsense_Mutation	INS	-	GATTCTGAAACC	-	BIRC6	2037insTGATTC	012_I4013delinsVX
XH_P44	2	36691676	36691676	Splice_Site	SNP	G	A	G	CRIM1	-	-
XH_P44	2	36691677	36691677	Nonsense_Mutation	INS	-	TAACATAAGGCT	-	CRIM1	871insTAACATA	290_C291delinsRX
XH_P44	2	37543631	37543631	In_Frame_Ins	INS	-	TTT	-	PRKD3	c.36_37insAAA	p.S13delinsKS
XH_P44	2	38908525	38908525	Nonsense_Mutation	INS	-	ATTTAAAGACAA	-	GALM	TCAATATTTAAA	50_T151delinsVFNIX
XH_P44	2	39213173	39213173	Frame_Shift_Ins	INS	-	AAAATGAGAACT	-	SOS1	94insGGAGTTCT	p.S1265fs
XH_P44	2	39251230	39251230	Frame_Shift_Ins	INS	-	AAAACCTTTTCAT	-	SOS1	123insTATGAA	p.Q375fs
XH_P44	2	39262536	39262536	Missense_Mutation	SNP	A	C	A	SOS1	c.T970G	p.L324V
XH_P44	2	39262537	39262537	Nonsense_Mutation	INS	-	GTGTTTCTGTTT	-	SOS1	AAAGAAAACAG	4323_L324delinsX
XH_P44	2	40656129	40656129	Nonsense_Mutation	INS	-	TGTAACATATTTT	-	SLC8A1	insATCAAAATAT	B1_R432delinsHQXK
XH_P44	2	42180410	42180410	Frame_Shift_Ins	INS	-	AAGGTACAAAC	-	C2orf91	6insGTGTTTGTG	p.F9fs
XH_P44	2	42580484	42580484	Splice_Site	INS	-	TTA	-	COX7A2L	-	-
XH_P44	2	43814114	43814114	In_Frame_Ins	INS	-	GCAAGTGT	-	THADA	9_330insAACAC	F110delinsLTLA
XH_P44	2	43927174	43927174	In_Frame_Ins	INS	-	AATTCTGGGAGA	-	PLEKH2	1078insAATTCT	Q359delinsQNSGR
XH_P44	2	44203368	44203368	Missense_Mutation	SNP	G	T	G	LRPPRC	c.C651A	p.S217R
XH_P44	2	44203370	44203370	Splice_Site	INS	-	TGAATTTTITAGA	-	LRPPRC	-	-
XH_P44	2	44556142	44556142	In_Frame_Ins	INS	-	5TTTAAGTAGCC	-	PREPL	77insGAGGCTA	M426delinsRGVLNL
XH_P44	2	45829127	45829127	Frame_Shift_Ins	INS	-	TGTGAGTGTGCT	-	SRBD1	insTACCAGCAC	p.S59fs
XH_P44	2	46707812	46707812	In_Frame_Ins	INS	-	TGTATGGAGCAG	-	TMEM247	5GTGGTGATGG	insRQHEVVMQQLQWEQ
XH_P44	2	46842097	46842097	Frame_Shift_Ins	INS	-	CAGAGCA	-	PIGF	26_207insTGCT	p.K69fs
XH_P44	2	46842098	46842098	Nonsense_Mutation	INS	-	ATAATATTGTGA	-	PIGF	insGGCTCACAA	K69delinsRLTILX
XH_P44	2	47389752	47389752	In_Frame_Ins	INS	-	ATGTTTCCACTAA	-	CALM2	GCTTTAGTGA	8delinsKALVETKQ
XH_P44	2	48027927	48027927	In_Frame_Ins	INS	-	TCA	-	MSH6	2415_2416insT	p.S805delinsSS
XH_P44	2	48027928	48027928	In_Frame_Ins	INS	-	GGGAGACCCAA	-	MSH6	2417insGGGAG	D806delinsGETQH
XH_P44	2	48028233	48028233	In_Frame_Ins	INS	-	ATTTTCTCT	-	MSH6	1_2722insATT	b.F907delinsFI
XH_P44	2	48066091	48066091	Nonsense_Mutation	INS	-	AGTTAATAGCA	-	FBX011	TCAGTTGCTATT	K166delinsHNQSVAINX
XH_P44	2	48808724	48808724	In_Frame_Ins	INS	-	AGTAGGCTCTTG	-	STON1	5TTCTAAGTGAG	B18delinsLSES
XH_P44	2	54159184	54159184	Frame_Shift_Ins	INS	-	TATTTCTGTTC	-	PSME4	04insAGGAACA	p.L368fs
XH_P44	2	54876898	54876898	Frame_Shift_Ins	INS	-	T	-	SPTBN1	c.5310_5311ins	p.L1770fs

XH_P44	2	54876900	54876900	Frame_Shift_Ins	INS	-	GCAAGATG	-	SPTBN1	2_5313insGCAA	p.N1717fs
XH_P44	2	54882345	54882345	In_Frame_Ins	INS	-	NGCTTTTCAAAA	-	SPTBN1	nsATCAAGCTTT	974delinsEIKLFKKC
XH_P44	2	55197229	55197229	In_Frame_Ins	INS	-	AAATGTTGGTCT	-	EML6	5insGCTAAATGT	p.X1959delinsCX
XH_P44	2	55252547	55252547	Frame_Shift_Ins	INS	-	CATTCCTACTAC	-	RTN4	ACAAAAATGTAG	p.H690fs
XH_P44	2	55481323	55481323	Frame_Shift_Ins	INS	-	T	-	MTIF2	c.517_518insA	p.P173fs
XH_P44	2	55481324	55481324	Frame_Shift_Ins	INS	-	TTTTGTACTTCT	-	MTIF2	17insAGAAAGT	p.P173fs
XH_P44	2	58390205	58390205	Frame_Shift_Ins	INS	-	CCAGACAGTAT	-	FANCL	ATGCAATACTG	p.V265fs
XH_P44	2	58459210	58459210	Frame_Shift_Ins	INS	-	ATTTA	-	FANCL	133_134insTAA	p.D45fs
XH_P44	2	58459211	58459211	Frame_Shift_Ins	INS	-	AAAGTGCTTTTA	-	FANCL	ATGTTTAAAAAGC	p.D45fs
XH_P44	2	61144141	61144141	Frame_Shift_Ins	INS	-	ACCTTGAATAGC	-	REL	25insAACCTTGA	p.1175fs
XH_P44	2	61433196	61433196	In_Frame_Ins	INS	-	GGCTCAATAATTA	-	USP34	STAATGTAATTA	delinsHGVNVMISQLRNF
XH_P44	2	61441779	61441779	Frame_Shift_Ins	INS	-	TG	-	USP34	.8097_8098insC	p.M2700fs
XH_P44	2	61441780	61441780	Nonsense_Mutation	INS	-	TTCAATTACATCC	-	USP34	97insAGGATGT	2699delinsQGCNXX
XH_P44	2	61633034	61633034	In_Frame_Ins	INS	-	TATGTAAATAA	-	USP34	51insCCTATTTTT	5121delinsPILHTS
XH_P44	2	61719303	61719303	In_Frame_Ins	INS	-	TATCAATCTGTA	-	XPO1	4insACATACAGA	585delinsYIQIDTS
XH_P44	2	63609225	63609225	Frame_Shift_Ins	INS	-	TATTTTTCATGTA	-	WDPCP	ACTCATCAATGA	p.V321fs
XH_P44	2	67631163	67631163	Frame_Shift_Ins	INS	-	ATCATCT	-	ETAA1	49_1350insATC	p.K450fs
XH_P44	2	67631164	67631164	Nonsense_Mutation	INS	-	TAAATGCATCAA	-	ETAA1	1insTAGTAAATG	p.K450delinsKX
XH_P44	2	67631792	67631792	Frame_Shift_Ins	INS	-	ACAGGGGCTTT	-	ETAA1	9insTTAACAGG	p.K660fs
XH_P44	2	67631896	67631896	Frame_Shift_Ins	INS	-	TCTACATCATCT	-	ETAA1	83insCATCTACA	p.H694fs
XH_P44	2	68273165	68273165	Frame_Shift_Ins	INS	-	TTCTCTTACCTT	-	C1D	GAAAAAGGTAA	p.A72fs
XH_P44	2	68273166	68273166	In_Frame_Ins	INS	-	ATAATTGGTATT	-	C1D	215insATAACCA	A72delinsEYQLS
XH_P44	2	69093078	69093078	Frame_Shift_Ins	INS	-	ATACGAAGGCAT	-	BMP10	0insCCATGCCTT	p.G320fs
XH_P44	2	69581645	69581645	Nonsense_Mutation	INS	-	TGGGCCCTCTAA	-	GFPT1	61insTTTTAGAG	I221_I222delinsFX
XH_P44	2	70106074	70106074	In_Frame_Ins	INS	-	TGTAAAGATGGG	-	GMCL1	sCTCACTGTAAC	96delinsPHKMGTV
XH_P44	2	70890783	70890783	Frame_Shift_Ins	INS	-	CT	-	ADD2	1954_1955insA	p.R652fs
XH_P44	2	71061139	71061139	Frame_Shift_Ins	INS	-	CAGAGTTAAAA	-	CD207	ATCAGTTTTTAA	p.M68fs
XH_P44	2	71577299	71577299	Frame_Shift_Ins	INS	-	ATCAGAGATTGA	-	ZNF638	6insGAATCAGA	p.K405fs
XH_P44	2	71650563	71650563	Frame_Shift_Ins	INS	-	TTTTAGGGTTAA	-	ZNF638	ATGCTGTTTTAG	p.M1307fs
XH_P44	2	71654070	71654070	In_Frame_Ins	INS	-	CCCCTTTTCTTC	-	ZNF638	insTTTTCCCTCT	691delinsVFPFFFKK
XH_P44	2	73678581	73678581	Nonsense_Mutation	INS	-	5GAAGGAGAGG	-	ALMS1	insGTAGGAAGG	642delinsSRKERLX
XH_P44	2	73680933	73680933	Frame_Shift_Ins	INS	-	G	-	ALMS1	.7276_7277ins	p.S2426fs
XH_P44	2	73680934	73680934	Frame_Shift_Ins	INS	-	TGGGCTTTTCCTC	-	ALMS1	278insTTGGGC	p.S2426fs
XH_P44	2	74042803	74042803	Nonsense_Mutation	INS	-	CTTATTCTTAG	-	C2orf78	54insCTCTATT	B5_Q48delinsALISX
XH_P44	2	74042805	74042805	Frame_Shift_Ins	INS	-	GCATTTT	-	C2orf78	55_1456insGCA	p.V485fs
XH_P44	2	74043031	74043031	Nonsense_Mutation	INS	-	TGATTTACCTTG	-	C2orf78	82insCCTGATT	561_I562delinsTX
XH_P44	2	74043033	74043033	Frame_Shift_Ins	INS	-	C	-	C2orf78	.1683_1684ins	p.R561fs
XH_P44	2	74682979	74682979	Frame_Shift_Ins	INS	-	ACCTCTT	-	INO80B	86_287insACCT	p.R96fs
XH_P44	2	77746865	77746865	Frame_Shift_Ins	INS	-	CTCCGCAATC	-	LRR1M4	133insGATTGC	p.I45fs
XH_P44	2	80782944	80782944	In_Frame_Ins	INS	-	AATAATACTAAA	-	CTNNA2	TGCTTAATAATA	235delinsACLIUKLY
XH_P44	2	80808930	80808930	Frame_Shift_Ins	INS	-	A	-	CTNNA2	.1030_1031ins	p.G344fs
XH_P44	2	80808932	80808932	Frame_Shift_Ins	INS	-	CTAAATATCCC	-	CTNNA2	1033insCTAAA	p.G344fs
XH_P44	2	85097903	85097903	Nonsense_Mutation	INS	-	CACACAGTGTCT	-	TRABD2A	15insTGACAGC	E39_L40delinsX
XH_P44	2	85769311	85769311	Frame_Shift_Ins	INS	-	GACAACCAAGC	-	MAT2A	AATGAGACAAC	p.V195fs
XH_P44	2	85858014	85858014	Frame_Shift_Ins	INS	-	AAGCTCTCCAA	-	USP39	6insCCAAGCTC	p.E195fs
XH_P44	2	86831654	86831654	In_Frame_Ins	INS	-	AGTAGTGAGAA	-	RNF103	TACTCTCTTCTC	57delinsILPSHYSKC
XH_P44	2	87214083	87214083	Frame_Shift_Ins	INS	-	ACTTGGCAACG	-	RGPD1	4038insTACTTGC	p.A1346fs
XH_P44	2	88082491	88082491	Missense_Mutation	SNP	C	T	C	RGPD1	c.G4028A	p.S1343N
XH_P44	2	88082492	88082492	In_Frame_Ins	INS	-	TTCGAGATGGAG	-	RGPD1	4027insCTCCAT	I1343delinsLHLQS
XH_P44	2	88409928	88409928	In_Frame_Ins	INS	-	GGGCTTAATGTC	-	SMYD1	2insCAAGGGGCT	444delinsIKGLMSW
XH_P44	2	88885488	88885488	In_Frame_Ins	INS	-	ACACCA	-	EIF2AK3	67_1068insTGG	N35delinsNGV
XH_P44	2	88885489	88885489	Frame_Shift_Ins	INS	-	GCTCTCC	-	EIF2AK3	6_1067insGGAA	p.N356fs
XH_P44	2	95847811	95847811	Missense_Mutation	SNP	T	A	T	ZNF2	c.T998A	p.V333D
XH_P44	2	95847812	95847812	Nonsense_Mutation	INS	-	5CTGTGTAAGGC	-	ZNF2	000insGCTGTG	V333delinsVAVX
XH_P44	2	96521778	96521778	Frame_Shift_Ins	INS	-	TTCTGATT	-	ANKRD36C	8_5329insAATC	p.H1777fs
XH_P44	2	96604752	96604752	Nonsense_Mutation	SNP	G	A	G	ANKRD36C	c.C1543T	p.Q515X
XH_P44	2	96610419	96610419	Frame_Shift_Ins	INS	-	TAATTTTACAATC	-	ANKRD36C	1447insCATTGT	p.K483fs
XH_P44	2	96949571	96949571	In_Frame_Ins	INS	-	TGTCCTCTTTAT	-	SNRNP200	4564insATAAAG	P1522delinsIKRTP
XH_P44	2	97784171	97784171	Frame_Shift_Ins	INS	-	GTCAGCTACTAT	-	ANKRD36	AAGAGCTCAGCT	p.1335fs
XH_P44	2	97820452	97820452	Frame_Shift_Ins	INS	-	TTTGCTCTTATA	-	ANKRD36	5insTAATTTGTCT	p.K412fs
XH_P44	2	97869953	97869953	Frame_Shift_Ins	INS	-	CTCTCTGCCTGT	-	ANKRD36	8015insCCTCCTC	p.V1005fs
XH_P44	2	97869955	97869955	Nonsense_Mutation	INS	-	AGCGTA	-	ANKRD36	16_3017insAGC	p.L1006delinsX
XH_P44	2	97911232	97911232	Frame_Shift_Ins	INS	-	TTTTCACAATTC	-	ANKRD36	9insTTCTTTTCA	p.A1636fs
XH_P44	2	97911233	97911233	Frame_Shift_Ins	INS	-	T	-	ANKRD36	.4909_4910ins	p.A1637fs
XH_P44	2	98411496	98411496	Nonsense_Mutation	INS	-	CATTTAACACTG	-	TMEM131	3283insCAGTGT	L1095delinsQCX
XH_P44	2	98419171	98419171	In_Frame_Ins	INS	-	GGTAAGTATTG	-	TMEM131	5insCAAGCAATA	829delinsQAILTLI
XH_P44	2	98422071	98422071	In_Frame_Ins	INS	-	AGGCCGCCACTT	-	TMEM131	51insAAAAAGTG	F717delinsLKVAAAS
XH_P44	2	98422073	98422073	Frame_Shift_Ins	INS	-	AG	-	TMEM131	.2148_2149insC	p.F171fs
XH_P44	2	98732169	98732169	Nonsense_Mutation	INS	-	CTAAA	-	VWA3B	251_252insCTAA	F84_P85delinsFX
XH_P44	2	98732171	98732171	In_Frame_Ins	INS	-	AAGTATTCTAG	-	VWA3B	nsATGAAGTATT	85delinsHEVFLGA
XH_P44	2	98914477	98914477	Frame_Shift_Ins	INS	-	AGTTATAACACT	-	VWA3B	7insTGAGTTAT	p.P746fs
XH_P44	2	99256445	99256445	Frame_Shift_Ins	INS	-	ATAATAGATTTTT	-	MGAT4A	ACACAAAAATC	p.P255fs
XH_P44	2	100019520	100019520	Frame_Shift_Ins	INS	-	GGAAGAAGCTCT	-	REV1	insGCAGAGAGT	p.K1071fs
XH_P44	2	102456441	102456441	Nonsense_Mutation	INS	-	AAAGATCGAAA	-	MAP4K4	5insGTAAAGAT	312delinsSKDRKX
XH_P44	2	107041671	107041671	Frame_Shift_Ins	INS	-	TCCGGTGACTTT	-	RGPD3	752insCAAAGTC	p.V918fs
XH_P44	2	108488282	108488282	Frame_Shift_Ins	INS	-	GCTCTGCC	-	RGPD4	2_3823insGCTC	p.A1274fs
XH_P44	2	108922035	108922035	Frame_Shift_Ins	INS	-	GAATT	-	SULT1C2	762_763insGAA	p.S254fs
XH_P44	2	108922037	108922037	In_Frame_Ins	INS	-	ATG	-	SULT1C2	.764_765insATC	p.S255delinsSC
XH_P44	2	109087387	109087387	Frame_Shift_Ins	INS	-	TGCTGTCTTACA	-	GCC2	sTGTTATGCTGT	p.L534fs
XH_P44	2	109088375	109088375	Frame_Shift_Ins	INS	-	TTCTGATCCCAT	-	GCC2	591insCTTCTGA	p.M864fs
XH_P44	2	109369511	109369511	In_Frame_Ins	INS	-	CTACACTC	-	RANBP2	3_1814insCTAC	A.Y605delinsSTLN
XH_P44	2	109369513	109369513	Silent	SNP	T	C	T	RANBP2	c.T1815C	p.V605Y
XH_P44	2	109380829	109380829	In_Frame_Ins	INS	-	TTCTTTCCATTCT	-	RANBP2	5insCGTTCTTTCT	278delinsPRSFHSL
XH_P44	2	109383459	109383459	Frame_Shift_Ins	INS	-	AGCCCCCT	-	RANBP2	64_6465insAGC	p.H2155fs
XH_P44	2	109383703	109383703	Frame_Shift_Ins	INS	-	CATTGTGCAAA	-	RANBP2	6709insCATTTC	p.D2236fs
XH_P44	2	109383705	109383705	Missense_Mutation	SNP	G	A	G	RANBP2	c.G6710A	p.S2237N
XH_P44	2	109384264	109384264	Frame_Shift_Ins	INS	-	CCTC	-	RANBP2	7269_7270insCC	p.F2423fs
XH_P44	2	109384265	109384265	Frame_Shift_Ins	INS	-	CACCTGGATACCT	-	RANBP2	271insCCACTGG	p.K2424fs
XH_P44	2	111419349	111419349	Frame_Shift_Ins	INS	-	TGTTGAAAAAGC	-	BUB1	nsCTTGCTTTTTCT	p.T232fs
XH_P44	2	111551298	111551298	Frame_Shift_Ins	INS	-	CATGCTCT	-	ACOXL	1_232insCATGC	p.W77fs
XH_P44	2	111744708	111744708	Frame_Shift_Ins	INS	-	TAACACTATTATG	-	ACOXL	CTTCAATTAATA	p.A361fs
XH_P44	2	112560017	112560017	Frame_Shift_Ins	INS	-	GCCTTTTATTTT	-	ANAPC1	209insAAAAAT	p.F1403fs
XH_P44	2	112994162	112994162	Frame_Shift_Ins	INS	-	AAATATATGCAC	-	ZC3H8	481insTGTGCAT	p.R161fs
XH_P44	2	113258879	113258879	Frame_Shift_Ins	INS	-	AGGATTA	-	TTL	56_567insAGGA	p.P189fs
XH_P44	2	113258882	113258882	Frame_Shift_Del	DEL	TG	-	TG	TTL	c.569_570del	p.L190fs
XH_P44	2	113410371	113410371	Frame_Shift_Ins	INS	-	TGACTGATAACA	-	SLC20A1	55insGTGACTGA	p.A218fs
XH_P44	2	113418743	113418743	Nonsense_Mutation	INS	-	CCCTAAGATCTA	-	SLC20A1	ATAACCCCTTAA	607delinsSLFAITPKIYFIFX
XH_P44	2	113514018	113514018	Nonsense_Mutation	INS	-	AAAAGCACAGA	-	CKAP2L	insAAGTCTGTG	7145_E146delinsX

XH_P44	2	113742505	113742505	In_Frame_Ins	INS	-	CAAATCCAGAGA	-	IL36G	285insCAAATCC	L95delinsLKSRO
XH_P44	2	114508107	114508107	Nonsense_Mutation	INS	-	GTTCCTTTAAGG	-	SLC35F5	ACCGTCCTTAA	p.T98delinsTX
XH_P44	2	116497401	116497401	Frame_Shift_Ins	INS	-	GACTGTGTATTG	-	DPP10	TCTAGACTGTG	p.P8fs
XH_P44	2	118854225	118854225	Frame_Shift_Ins	INS	-	C	-	INSIG2	c.93_94insC	p.R31fs
XH_P44	2	118854227	118854227	In_Frame_Ins	INS	-	TACCAC	-	INSIG2	95_96insTACCAC	p.G32delinsGTT
XH_P44	2	120620219	120620219	In_Frame_Ins	INS	-	GCCAGAGGTAG	-	PTPN4	TTTATGCCAGAG	82delinsPFMPPEVAN
XH_P44	2	122144748	122144748	Frame_Shift_Ins	INS	-	TGTTCTCTCGTT	-	CLASP1	DinsAAGAACGA	p.T1080fs
XH_P44	2	122159193	122159193	Frame_Shift_Ins	INS	-	GAATATAC	-	CLASP1	07_2708insGTA	p.D903fs
XH_P44	2	122159195	122159195	Frame_Shift_Ins	INS	-	TATCT	-	CLASP1	705_2706insAG	p.D902fs
XH_P44	2	122215334	122215334	Splice_Site	SNP	C	G	C	CLASP1		
XH_P44	2	122363393	122363393	Frame_Shift_Ins	INS	-	A	-	CLASP1	c.78_79insT	p.L27fs
XH_P44	2	122363395	122363395	Frame_Shift_Ins	INS	-	GTGGC	-	CLASP1	c.76_77insGCCA	p.E26fs
XH_P44	2	128066293	128066293	In_Frame_Ins	INS	-	AGAATTGCGAA	-	MAP3K2	5TTAATCTTCGCA	01delinsVLLIFALTSY
XH_P44	2	128262753	128262753	Frame_Shift_Ins	INS	-	TAAGGGAGAG	-	IWS1	6insATCCTCTCC	p.L242fs
XH_P44	2	128495586	128495586	Frame_Shift_Ins	INS	-	TGCTTCTAAAAC	-	WDR33	tsGTCCTTTTGA	p.K256fs
XH_P44	2	128522470	128522470	Frame_Shift_Ins	INS	-	G	-	WDR33	c.557_558insC	p.K186fs
XH_P44	2	128522471	128522471	Nonsense_Mutation	INS	-	AGAGATGTACT	-	WDR33	57insCAGTACAB6	Y187delinsTVHLX
XH_P44	2	128712809	128712809	In_Frame_Ins	INS	-	CTTTCC	-	SAP130	64_2065insGGAB	T689delinsGKT
XH_P44	2	128747311	128747311	Nonsense_Mutation	INS	-	GTCTTATAATT	-	SAP130	5TAGAGAAATTA62	P563delinsLEKLX
XH_P44	2	130872873	130872873	Missense_Mutation	SNP	C	T	C	POTEF	c.G550A	p.P184R
XH_P44	2	130872874	130872874	Frame_Shift_Ins	INS	-	ATATGTAATTTG	-	POTEF	9insAACAAATTA	p.L183fs
XH_P44	2	131245674	131245674	In_Frame_Ins	INS	-	AAATCAGCGAAG	-	POTEF	CTCATTGTTCG	47delinsTHCSLIFIF
XH_P44	2	133541747	133541747	In_Frame_Ins	INS	-	AAGGGAACCTCT	-	NCKAP5	2637insAGAAG	P879delinsPEVPF
XH_P44	2	133542266	133542266	Frame_Shift_Ins	INS	-	GAGTAATCCAG	-	NCKAP5	118insCCTGGA	p.K706fs
XH_P44	2	135711817	135711817	Missense_Mutation	SNP	G	C	G	CCNT2	c.G1792C	p.V598L
XH_P44	2	135711818	135711818	Frame_Shift_Ins	INS	-	TTTCCTTTT	-	CCNT2	1794insTTTCC	p.V598fs
XH_P44	2	135893182	135893182	Frame_Shift_Ins	INS	-	AAAGCTTAGTT	-	RAB3GAP1	604insGAAAGC	p.K535fs
XH_P44	2	135965358	135965358	Frame_Shift_Ins	INS	-	AGCTCCCATTAG	-	ZRANB3	nsTGTTCTAATG	p.T883fs
XH_P44	2	136540358	136540358	Nonsense_Mutation	INS	-	TATATCTATCAAC	-	UBXN4	9insCATTATATC	N6_7477delinsDHYIYX
XH_P44	2	136540359	136540359	Frame_Shift_Ins	INS	-	T	-	UBXN4	c.1429_1430ins	p.D477fs
XH_P44	2	136566499	136566499	Frame_Shift_Ins	INS	-	GGCA	-	LCT	417_3418insTG	p.V1140fs
XH_P44	2	136566501	136566501	In_Frame_Ins	INS	-	GAA	-	LCT	3415_3416insT	p.D1139delinsVH
XH_P44	2	136567508	136567508	Frame_Shift_Ins	INS	-	ACCCAAG	-	LCT	08_2409insCTTG	p.D803fs
XH_P44	2	136678128	136678128	Nonsense_Mutation	INS	-	GAAACATATATA	-	DARS	TCTTTATATATA	85delinsGKSLYICSX
XH_P44	2	138759736	138759736	Nonsense_Mutation	INS	-	SGTTTCTAGTAT	-	HNMT	TTTTTGTTTCTCT	K135delinsHTAFFGFX
XH_P44	2	138771542	138771542	In_Frame_Ins	INS	-	TCTTTTCTTCA	-	HNMT	TATTATCTTTCT	241delinsFSLFSICR
XH_P44	2	141291635	141291635	Frame_Shift_Ins	INS	-	TTAAAACCTCTTA	-	LRP1B	17insTATAAGAG	p.G2573fs
XH_P44	2	141816521	141816521	In_Frame_Ins	INS	-	STTCTATGATAC	-	LRP1B	39insTCTATCAT	1447delinsSLIETI
XH_P44	2	150325191	150325191	Frame_Shift_Ins	INS	-	TCCTTGCTTTTC	-	LYPD6	tsTTCTCCTTGC	p.E84fs
XH_P44	2	152320279	152320279	Frame_Shift_Ins	INS	-	CCTTTTATTC	-	RIF1	4246insCCTTT	p.R1415fs
XH_P44	2	152320281	152320281	Missense_Mutation	SNP	G	T	G	RIF1	c.G4247T	p.R1416L
XH_P44	2	152320697	152320697	Frame_Shift_Ins	INS	-	C	-	RIF1	c.4663_4664ins	p.D1555fs
XH_P44	2	152320698	152320698	Nonsense_Mutation	INS	-	TTAGCAC	-	RIF1	64_4665insTTAC	555_5155delinsDX
XH_P44	2	152354172	152354172	Silent	SNP	T	G	T	NEB	c.A24268C	p.R8090R
XH_P44	2	152354173	152354173	Silent	SNP	T	C	T	NEB	c.A24267G	p.E0809E
XH_P44	2	152402504	152402504	In_Frame_Ins	INS	-	AGGGGTTTTGCA	-	NEB	AAAATCATGCA	42delinsYKIMQNPSSA
XH_P44	2	152411468	152411468	Nonsense_Mutation	INS	-	ATATATACTTTT	-	NEB	4266insAAAAGA	56_V4757delinsKRLX
XH_P44	2	152419290	152419290	Frame_Shift_Ins	INS	-	GC	-	NEB	3586_13587ins	p.K4529fs
XH_P44	2	152419291	152419291	Nonsense_Mutation	INS	-	CTCAAAACAAAC	-	NEB	13586insCTTTTG	129_A4530delinsTLFX
XH_P44	2	152424921	152424921	Missense_Mutation	SNP	C	A	C	NEB	c.G12506T	p.R4169L
XH_P44	2	152424922	152424922	In_Frame_Ins	INS	-	TCTCTACAAGG	-	NEB	505insTTCTCTTG	4169delinsFLVEIR
XH_P44	2	152483713	152483713	Frame_Shift_Ins	INS	-	GG	-	NEB	9384_9385insC	p.Y3129fs
XH_P44	2	152483714	152483714	Nonsense_Mutation	INS	-	TAAGACAGGGC	-	NEB	34insATAGCCCT	128_Y3129delinsIX
XH_P44	2	152499351	152499351	Nonsense_Mutation	INS	-	AGCTGTTGCTAA	-	NEB	3insCTGTTAGC	731_T2732delinsNCX
XH_P44	2	153473665	153473665	Nonsense_Mutation	INS	-	TATGGTTCTGA	-	FMNL2	TTATAATATGG	5delinsMVMFIWFX
XH_P44	2	153535960	153535960	In_Frame_Ins	INS	-	AACTAGGATAC	-	PRPF40A	STCTGTGATCT	61delinsSGILVSV
XH_P44	2	153535962	153535962	Nonsense_Mutation	SNP	T	A	T	PRPF40A	c.A481T	p.K161X
XH_P44	2	154997011	154997011	Frame_Shift_Ins	INS	-	CAGAGATACAG	-	GALNT13	insATACAGAGA	p.L102fs
XH_P44	2	158157501	158157501	Frame_Shift_Ins	INS	-	GGAATGATCTCA	-	GALNT5	80insAGGGAATC	p.A810fs
XH_P44	2	158991285	158991285	Frame_Shift_Ins	INS	-	TCTTTTCTCTCCA	-	UPP2	5CTTCTCTTTTC	p.L279fs
XH_P44	2	159195539	159195539	Missense_Mutation	SNP	T	A	T	CCDC148	c.A107T	p.Q36L
XH_P44	2	159195541	159195541	Frame_Shift_Ins	INS	-	GAGTCTCA	-	CCDC148	4_105insTAGAA	p.Q35fs
XH_P44	2	159663588	159663588	Frame_Shift_Ins	INS	-	ATTATTATTATTA	-	DAPL1	9insTTATTATTA	p.K56fs
XH_P44	2	160205726	160205726	Frame_Shift_Ins	INS	-	TTCTCTGATTAT	-	BAZ2B	nsAGTTATATAA	p.51607fs
XH_P44	2	160243011	160243011	Nonsense_Mutation	INS	-	AGATTTGTGTCA	-	BAZ2B	TAACCTGACACG	1072delinsGVTX
XH_P44	2	160801555	160801555	Nonsense_Mutation	INS	-	TCITTAGCATT	-	PLA2R1	DinsTTAAATGCG	Q1334delinsFKCX
XH_P44	2	162875320	162875320	Frame_Shift_Ins	INS	-	C	-	DPD4	c.1338_1339ins	p.C447fs
XH_P44	2	162875321	162875321	Frame_Shift_Ins	INS	-	CACAAACACACA	-	DPD4	88insGGTGTGTG	p.546fs
XH_P44	2	163228584	163228584	Nonsense_Mutation	INS	-	TATTT	-	KCNH7	345_3346insAA	116_K1117delinsKX
XH_P44	2	163228586	163228586	Frame_Shift_Ins	INS	-	TCTCTACTTGAC	-	KCNH7	tsCTGAGTCAAG	p.L1115fs
XH_P44	2	165349642	165349642	Nonsense_Mutation	INS	-	GGCGAAACAT	-	GRB14	66insGTAATGTT	422_F423delinsRX
XH_P44	2	165349644	165349644	Nonsense_Mutation	SNP	T	A	T	GRB14	c.A1264T	p.R422X
XH_P44	2	166245849	166245849	Nonsense_Mutation	INS	-	CTTCTTCAGTA	-	SCN2A	534insACCTTCT	5_M1846delinsHFLQX
XH_P44	2	166747382	166747382	Nonsense_Mutation	INS	-	GGGGTGAGTTAT	-	TTC21B	TGTCAAAATAC	p.P1023delinsX
XH_P44	2	166848798	166848798	Missense_Mutation	SNP	A	T	A	SCN1A	c.T4987A	p.L1663M
XH_P44	2	166848799	166848799	Frame_Shift_Ins	INS	-	TTCTCTGGTTGTC	-	SCN1A	6insACCACAACC	p.A1662fs
XH_P44	2	167162394	167162394	Frame_Shift_Ins	INS	-	GC	-	SCN9A	c.503_504insGC	p.L168fs
XH_P44	2	167162395	167162395	In_Frame_Ins	INS	-	TGGAAT	-	SCN9A	02_503insATTCC	p.L168delinsHSI
XH_P44	2	167289055	167289055	In_Frame_Ins	INS	-	ATTGCTTAGTGG	-	SCN7A	6insTCACCACTA	789delinsSPLNSQD
XH_P44	2	167301511	167301511	Splice_Site	INS	-	CATTATTCCCAT	-	SCN7A		
XH_P44	2	168096418	168096418	Nonsense_Mutation	INS	-	AATCTTAGGACT	-	XIRP2	7insTAATCTTAC	p.A82delinsAX
XH_P44	2	168099597	168099597	Frame_Shift_Ins	INS	-	TATACATCTT	-	XIRP2	c.1030insTATAC	p.E343fs
XH_P44	2	168099599	168099599	Nonsense_Mutation	INS	-	ACTGGTAGTCT	-	XIRP2	2insGGGACTGG	344delinsWGLVVF
XH_P44	2	168100310	168100310	Missense_Mutation	SNP	G	T	G	XIRP2	c.G1742T	p.G581V
XH_P44	2	168100312	168100312	In_Frame_Ins	INS	-	ATGTTGAGTTTC	-	XIRP2	ATCTAGATGTTG	82delinsDLDFEQTW
XH_P44	2	168100673	168100673	In_Frame_Ins	INS	-	TTATTTTTTCTCT	-	XIRP2	5TACCTATTATT	2delinsCTYFFFLND
XH_P44	2	168102041	168102041	Frame_Shift_Ins	INS	-	TCACCTTCT	-	XIRP2	3474insTCACC	p.Q1158fs
XH_P44	2	168102042	168102042	In_Frame_Ins	INS	-	TTTCTTTTATCT	-	XIRP2	5insGCTTTCTTT	1158delinsQAFFYL
XH_P44	2	168103387	168103387	In_Frame_Ins	INS	-	GTGGGAGTTG	-	XIRP2	nsACTCTGTGTG	607delinsDSVWSCFS
XH_P44	2	168105014	168105014	Nonsense_Mutation	INS	-	ATTACTTTTTTCT	-	XIRP2	ATCACCAATACT	50delinsTPSQPAHHYFFULX
XH_P44	2	170034420	170034420	Frame_Shift_Ins	INS	-	GGAAGAC	-	LRP2	5_10286insGTC	p.T3429fs
XH_P44	2	170034421	170034421	Frame_Shift_Ins	INS	-	A	-	LRP2	10284_10285ins	p.T3429fs
XH_P44	2	170066059	170066059	Nonsense_Mutation	INS	-	TGCTTATTT	-	LRP2	2_6373insAAAT	p.R2125delinsKX
XH_P44	2	170066061	170066061	In_Frame_Ins	INS	-	AATGATACGGT	-	LRP2	371insACACCGT	2124delinsNTVSFI
XH_P44	2	170134403	170134403	Nonsense_Mutation	INS	-	GACCTGCTCTAT	-	LRP2	34insAAATAGAC	542_M543delinsKX
XH_P44	2	170163907	170163907	In_Frame_Ins	INS	-	SGTGATGTTCTG	-	LRP2	CTTATCAGAAC	44delinsYSQNTPNP
XH_P44	2	170367325	170367325	Frame_Shift_Ins	INS	-	CCAACATCAC	-	KLHL41	c.1038insCCAAC	p.Q346fs
XH_P44	2	170367326	170367326	Missense_Mutation	SNP	G	C	G	KLHL41	c.G1038C	p.Q346H

XH_P44	2	170592635	170592635	Frame_Shift_Ins	INS	-	GACC	-	KLHL23	111_1112insGA	p.V371fs
XH_P44	2	170606130	170606130	Frame_Shift_Ins	INS	-	T	-	KLHL23	1565_1566ins	p.T522fs
XH_P44	2	170606131	170606131	Frame_Shift_Ins	INS	-	AGCACAATCCA	-	KLHL23	1567insAGCAC	p.T522fs
XH_P44	2	170753219	170753219	Nonsense_Mutation	INS	-	AGTTTATGTTTT	-	UBR3	CACATTAGTTTT	C481delinsRKKHSFNFX
XH_P44	2	170804134	170804134	Nonsense_Mutation	INS	-	TTTAAATAATAA	-	UBR3	AATAAAATTTAAp.N998delinsKX	
XH_P44	2	170850902	170850902	In_Frame_Ins	INS	-	ACTCGAATTAT	-	UBR3	CAAGCAACTCGp.85delinsPKOLELFHY	
XH_P44	2	170863662	170863662	Missense_Mutation	SNP	G	A	G	UBR3	c.G4192A	p.E1398K
XH_P44	2	170863663	170863663	Nonsense_Mutation	INS	-	AAACAAAATCCT	-	UBR3	94insATAAACAA398_V1399delinsEX	
XH_P44	2	171687681	171687681	Nonsense_Mutation	INS	-	ATTAACCATGCT	-	GAD1	insAATATTAAACC	p.L176delinsX
XH_P44	2	171917623	171917623	Frame_Shift_Ins	INS	-	ATGTTGCCCTTA	-	TLK1	3insATAAGGGC	p.R29fs
XH_P44	2	171917625	171917625	Missense_Mutation	SNP	C	G	C	TLK1	c.G84C	p.K28N
XH_P44	2	172314989	172314989	Splice_Site	INS	-	AAAGAAAATGTC	-	DCAF17	-	-
XH_P44	2	173338913	173338913	Frame_Shift_Ins	INS	-	TTGACCTT	-	ITGA6	6_907insTTGAC	p.L302fs
XH_P44	2	173885351	173885351	Frame_Shift_Ins	INS	-	AA	-	RAPGEF4	1501_1502insA	p.V501fs
XH_P44	2	173885352	173885352	In_Frame_Ins	INS	-	AGAGATGCCAGA	-	RAPGEF4	1503insAGAGATV501delinsVEMPE	
XH_P44	2	174131392	174131392	Nonsense_Mutation	INS	-	GCTG	-	MAP3K20	317_2318insGC773_R774delinsCX	
XH_P44	2	174131394	174131394	Frame_Shift_Ins	INS	-	T	-	MAP3K20	c.2319_2320ins	p.Y773fs
XH_P44	2	175618347	175618347	Frame_Shift_Ins	INS	-	AGTCACTGTGA	-	CHRNA1	62insCTCACAG	p.I221fs
XH_P44	2	178386023	178386023	Frame_Shift_Ins	INS	-	AAAAACAAGAA	-	AGP5	1725insAAAAAC	p.A575fs
XH_P44	2	178481878	178481878	Frame_Shift_Ins	INS	-	GAAAGAAAGAAT	-	TTIC30A	52insTGCATTCT	p.E518fs
XH_P44	2	179255936	179255936	Nonsense_Mutation	INS	-	CATCATTCCTCG	-	OSBP6L	TAATAACATCAV782_R783delinsX	
XH_P44	2	179325962	179325962	Frame_Shift_Ins	INS	-	AGCTGTGAACG	-	DFNB59	AGTAAAGCTGT	p.A340fs
XH_P44	2	179393607	179393607	In_Frame_Ins	INS	-	AAGGAATCGTC	-	TTN	76insACTTGACG6559delinsHLTIPSL	
XH_P44	2	179395942	179395942	Frame_Shift_Ins	INS	-	CGATGAGGGCA	-	TTN	7820insTTGCC	p.K26069fs
XH_P44	2	179396882	179396882	Frame_Shift_Ins	INS	-	TGATA	-	TTN	264_77265insTA	p.E2575fs
XH_P44	2	179396884	179396884	Frame_Shift_Ins	INS	-	TTTTCAG	-	TTN	2_77263insCTG	p.E2575fs
XH_P44	2	179398883	179398883	In_Frame_Ins	INS	-	GGTGTGAGAGA	-	TTN	insAGACTTCTC088delinsVDFSHTFN	
XH_P44	2	179402490	179402490	Frame_Shift_Ins	INS	-	AACACTGAGCAC	-	TTN	GAGTATAGTGC	p.K24083fs
XH_P44	2	179403806	179403806	Frame_Shift_Ins	INS	-	GT	-	TTN	71660_71661ins	p.I23887fs
XH_P44	2	179403807	179403807	Frame_Shift_Ins	INS	-	AAGAAAT	-	TTN	59_71660insAT	p.I23887fs
XH_P44	2	179410288	179410288	Nonsense_Mutation	INS	-	AAATTTTAGAAT	-	TTN	54insTAAATTTCT	2785delinsNSKNXSX
XH_P44	2	179417418	179417418	Frame_Shift_Ins	INS	-	GGGAAACCCCA	-	TTN	4insTGGTTTGGG	p.K21005fs
XH_P44	2	179421865	179421865	Frame_Shift_Ins	INS	-	CATCGATTCTTA	-	TTN	0821insATAAGp.P20274fs	
XH_P44	2	179424354	179424354	Nonsense_Mutation	INS	-	CCCTCAGATAGC	-	TTN	TCCTTTGCTATC	9770delinsSLSFAlX
XH_P44	2	179427121	179427121	Frame_Shift_Ins	INS	-	CATTCAA	-	TTN	42_56543insTTC	p.C18848fs
XH_P44	2	179432938	179432938	Frame_Shift_Ins	INS	-	AATCTGAAGAA	-	TTN	6insTGCCTCTCT	p.S16909fs
XH_P44	2	179447315	179447315	Nonsense_Mutation	INS	-	TCATTTTATTTTT	-	TTN	stTTTAAAAAAAT	12891delinsNFKXX
XH_P44	2	179466177	179466177	Frame_Shift_Ins	INS	-	TATATTATTATA	-	TTN	CGTTGTTTATAA	p.I9451fs
XH_P44	2	179472279	179472279	In_Frame_Ins	INS	-	ATGATGGAGGA	-	TTN	5941insCTTCTC	8647delinsDFLHHL
XH_P44	2	179477118	179477118	In_Frame_Ins	INS	-	AAACCGACA	-	TTN	8_22939insTGT	V7647delinsCRFV
XH_P44	2	179484429	179484429	Nonsense_Mutation	INS	-	AGATTTCACAGT	-	TTN	TTAAATAACCTGT	D6475delinsTSLNNCEIX
XH_P44	2	179498367	179498367	Frame_Shift_Ins	INS	-	A	-	TTN	15523_15524ins	p.K5175fs
XH_P44	2	179498368	179498368	Nonsense_Mutation	INS	-	TAGTTCA	-	TTN	22_15523insTG	6175_T5176delinsX
XH_P44	2	179532414	179532414	Nonsense_Mutation	INS	-	ATGTAAACCTAC	-	TTN	580insTTAGTAG	860_K11861delinsDX
XH_P44	2	179536874	179536874	Nonsense_Mutation	INS	-	TAGATGATAGTA	-	TTN	TCAATATTACT	0383_H10384delinsX
XH_P44	2	179544634	179544634	Frame_Shift_Ins	INS	-	T	-	TTN	29834_29835ins	p.V9945fs
XH_P44	2	179544635	179544635	Frame_Shift_Ins	INS	-	AGAGACTTCAT	-	TTN	29834insATGA	p.V9945fs
XH_P44	2	179579750	179579750	Frame_Shift_Ins	INS	-	TTTCCAAATCCT	-	TTN	2431insAGGAT	p.V7477fs
XH_P44	2	179579752	179579752	Frame_Shift_Ins	INS	-	TGAAT	-	TTN	428_22429insA	p.V7477fs
XH_P44	2	179585268	179585268	Frame_Shift_Ins	INS	-	GTGGCCATGAT	-	TTN	9489insAATCA	p.Q6497fs
XH_P44	2	179585270	179585270	Nonsense_Mutation	INS	-	CACA	-	TTN	486_19487insT	96_Q6497delinsMX
XH_P44	2	179588014	179588014	In_Frame_Ins	INS	-	TTAGGT	-	TTN	87_17988insAC	S5996delinsSPN
XH_P44	2	179588016	179588016	Frame_Shift_Del	DEL	AA	-	AA	TTN	17985_17986del	p.H5995fs
XH_P44	2	179610466	179610466	Frame_Shift_Ins	INS	-	GAAATAATCTCT	-	TTN	CTCATAGAGA	p.V554fs
XH_P44	2	179612872	179612872	In_Frame_Ins	INS	-	GTGAACAATAAT	-	TTN	TTTGTACTTATT	2delinsMFVLICSPGF
XH_P44	2	179616698	179616698	Frame_Shift_Ins	INS	-	ATAAAGCTGAG	-	TTN	insTCACTCTCAG	p.D3477fs
XH_P44	2	179641015	179641015	Frame_Shift_Ins	INS	-	AAGGCCTGAG	-	TTN	5438insCTCAG	p.R1813fs
XH_P44	2	182339943	182339943	In_Frame_Ins	INS	-	TTTTCTGTTAAC	-	ITGA4	sGTATTTTTTCTG	162delinsSIFLLTTS
XH_P44	2	182766830	182766830	Frame_Shift_Ins	INS	-	ACGCATTG	-	SSFA2	1_592insACGCA	p.K197fs
XH_P44	2	182766892	182766892	Nonsense_Mutation	INS	-	TCGAGTTAAAGT	-	SSFA2	54insTTCGAGTT	18_E219delinsTSXX
XH_P44	2	184016360	184016360	Frame_Shift_Ins	INS	-	ATCTAGTTTAA	-	NUP35	AAAAATCTTAG	p.S174fs
XH_P44	2	186662034	186662034	Nonsense_Mutation	INS	-	GTTTTAGGTTCT	-	FSIP2	0172insGGTTT	891_I3392delinsWFX
XH_P44	2	186669373	186669373	Missense_Mutation	SNP	C	A	C	FSIP2	c.C15340A	p.P5114T
XH_P44	2	186669375	186669375	Nonsense_Mutation	INS	-	ATTTTITGAAC	-	FSIP2	15343insATTT	14_H5115delinsPIFX
XH_P44	2	186670599	186670599	Frame_Shift_Ins	INS	-	STATCTTATATC	-	FSIP2	16567insGTATC	p.E5522fs
XH_P44	2	186670601	186670601	Missense_Mutation	SNP	A	T	A	FSIP2	c.A16568T	p.N5523I
XH_P44	2	186673538	186673538	Frame_Shift_Ins	INS	-	TTGTTCG	-	FSIP2	05_19506insTTC	p.E6502fs
XH_P44	2	186673539	186673539	Frame_Shift_Ins	INS	-	GTATG	-	FSIP2	506_19507insG	p.E6502fs
XH_P44	2	187702131	187702131	Frame_Shift_Ins	INS	-	A	-	ZSWIM2	c.644_645insT	p.S215fs
XH_P44	2	187702132	187702132	Nonsense_Mutation	INS	-	GTGACGACTGCT	-	ZSWIM2	saATAAGCAGTC	215_K216delinsXX
XH_P44	2	189872811	189872811	Frame_Shift_Ins	INS	-	AGGAGTGAAGG	-	COL3A1	3469insAGGAG	p.H1156fs
XH_P44	2	189931473	189931473	Frame_Shift_Ins	INS	-	ATGGTATTACAG	-	COL5A2	437insCCTGAA	p.A479fs
XH_P44	2	190339992	190339992	Nonsense_Mutation	INS	-	AGTACACTTTA	-	WDR75	5TTACTAAGTACB1	S782delinsEFCYX
XH_P44	2	190618880	190618880	In_Frame_Ins	INS	-	GACCTTGACCTT	-	OSGEPL1	nsCACAAGGTCA	267delinsNTRSRSW
XH_P44	2	191301163	191301163	Frame_Shift_Ins	INS	-	5GAATAGCAGAT	-	MFSD6	9insAGGAATAG	p.L136fs
XH_P44	2	196723474	196723474	In_Frame_Ins	INS	-	GAATGAACAAG	-	DNAH7	nsCATAGCTTGT	2597delinsSIACSFAl
XH_P44	2	196729425	196729425	Frame_Shift_Ins	INS	-	TG	-	DNAH7	6953_6954insC	p.F2318fs
XH_P44	2	196729426	196729426	Frame_Shift_Ins	INS	-	AGATTTAAAAGT	-	DNAH7	6953insCACCTT	p.F2318fs
XH_P44	2	196737189	196737189	In_Frame_Ins	INS	-	GAAATGGGATT	-	DNAH7	TCACATAATCCC	40delinsFSHNPISITGK
XH_P44	2	197541453	197541453	Nonsense_Mutation	INS	-	AGAGCTCTTATT	-	CCDC150	439insCAGAGTC	480delinsAESLFX
XH_P44	2	197565845	197565845	Nonsense_Mutation	INS	-	TTTGTATTTAA	-	CCDC150	6TTGGTTTGTGA	6delinsSLLVYNFFCX
XH_P44	2	197565847	197565847	Missense_Mutation	SNP	G	T	G	CCDC150	c.G1638T	p.K546N
XH_P44	2	197631417	197631417	Nonsense_Mutation	INS	-	ACTTCAATTCAT	-	GTF3C3	0insAGATGAA	804_S805delinsRX
XH_P44	2	198404835	198404835	In_Frame_Ins	INS	-	TAATTTGGAAT	-	HSPE1-MOB4	GAAGTAATTTG	54delinsREVWVKYL
XH_P44	2	198404836	198404836	Frame_Shift_Ins	INS	-	CA	-	HSPE1-MOB4	c.163_164insCA	p.Q55fs
XH_P44	2	200136960	200136960	Nonsense_Mutation	INS	-	CAGGATACACCT	-	SATB2	176insTAGGTG	726_P727delinsX
XH_P44	2	200213702	200213702	Frame_Shift_Ins	INS	-	G	-	SATB2	c.894_895insC	p.S299fs
XH_P44	2	200213704	200213704	In_Frame_Ins	INS	-	TTGAGATAG	-	SATB2	2_893insCTATC	p.L298delinsPISI
XH_P44	2	202356291	202356291	Frame_Shift_Ins	INS	-	A	-	C2CD6	c.4772_4773ins	p.K1591fs
XH_P44	2	202357813	202357813	Nonsense_Mutation	INS	-	GGACATATCAC	-	C2CD6	51insTTGGTGAT	51085delinsLGDMSX
XH_P44	2	202358613	202358613	In_Frame_Ins	INS	-	ATGAAGAAAAAT	-	C2CD6	nsTCAGCATTTT	017delinsDQHFHLHI
XH_P44	2	203061655	203061655	Missense_Mutation	SNP	T	A	T	KIAA2012	c.T3320A	p.L1107Q
XH_P44	2	203061657	203061657	Frame_Shift_Ins	INS	-	GATCATTTTT	-	KIAA2012	c_3323insGATCA	p.L1108fs
XH_P44	2	203142698	203142698	Nonsense_Mutation	INS	-	TAGGCTAGTAAT	-	NOP58	9insGTTAGGCTA	F50_Q51delinsCX
XH_P44	2	203142701	203142702	Frame_Shift_Del	DEL	CA	-	CA	NOP58	c.151_152del	p.Q51fs
XH_P44	2	204037552	204037552	Frame_Shift_Ins	INS	-	TTTTTCCCTGT	-	NBEAL1	13insTATTTTTTC	p.K2071fs
XH_P44	2	204231683	204231683	Frame_Shift_Ins	INS	-	AAACCAAACTA	-	AB12	202insAAACCA	p.T67fs
XH_P44	2	204305023	204305023	In_Frame_Ins	INS	-	AAACTCAAT	-	RAPH1	9_2890insATTGA	S964delinsIEFS

XH_P44	2	204313554	204313554	Nonsense_Mutation	INS	-	TGCCTACGTTT	-	RAPH1	insTGAAAAACG473delinsPEKRRHX
XH_P44	2	204735538	204735538	Frame_Shift_Ins	INS	-	T	-	CTLA4	c.339_340insT p.N113fs
XH_P44	2	204735539	204735539	Frame_Shift_Ins	INS	-	ATGCTCCT	-	CTLA4	0_341insATGCT p.L114fs
XH_P44	2	206869261	206869261	Missense_Mutation	SNP	A	T	A	INO80D	c.T2915A p.L972H
XH_P44	2	206869263	206869263	In_Frame_Ins	INS	-	CTG	-	INO80D	2912_2913insCp.Q971delinsHR
XH_P44	2	206874445	206874445	Nonsense_Mutation	INS	-	AAAACCATTAG	-	INO80D	insTATACTAAA539_P540delinsIYX
XH_P44	2	207012543	207012543	Frame_Shift_Ins	INS	-	A	-	NDUFS1	c.20_21insT p.E7fs
XH_P44	2	207012544	207012544	Frame_Shift_Ins	INS	-	GGCATTGGTAA	-	NDUFS1	nsTCTTTACCAAT p.E7fs
XH_P44	2	207169695	207169695	Frame_Shift_Ins	INS	-	AAATGCACCA	-	ZDBF2	.444insAAATGC p.P148fs
XH_P44	2	207170172	207170172	Frame_Shift_Ins	INS	-	TGCTGGT	-	ZDBF2	20_921insTGCT p.A307fs
XH_P44	2	207170173	207170173	Silent	SNP	A	G	A	ZDBF2	c.A921G p.A307A
XH_P44	2	207170958	207170958	In_Frame_Ins	INS	-	AATATGCCTTGC	-	ZDBF2	7insGCTAATATG569delinsRLICLAF
XH_P44	2	207171648	207171648	Nonsense_Mutation	INS	-	TTACTTCATCCA	-	ZDBF2	insAGATTTACTT799_S800delinsX
XH_P44	2	207172048	207172048	Nonsense_Mutation	INS	-	TTTAAACAGTAC	-	ZDBF2	TACTTCTTTAAACB2_D933delinsELLLX
XH_P44	2	207173160	207173160	In_Frame_Ins	INS	-	CTTTAACGGTTT	-	ZDBF2	TTATTCTCTTAA03delinsAYFFNGFSQ
XH_P44	2	207175330	207175330	Nonsense_Mutation	INS	-	ATTTTTCTTTTCA	-	ZDBF2	CTAATTATTTTTC26_F2027delinsPLVX
XH_P44	2	207527702	207527702	Nonsense_Mutation	INS	-	GTAGCAGTGCT	-	DYTN	sATTACAGACAC E521delinsQSTATYX
XH_P44	2	207564611	207564611	Frame_Shift_Ins	INS	-	TGATTTCCTGG	-	DYTN	559insCCAGGA p.L187fs
XH_P44	2	208420432	208420432	In_Frame_Ins	INS	-	CTTATTCAAAT	-	CREB1	74insCTTATTCAM25delinsTYSNL
XH_P44	2	209113237	209113237	Frame_Shift_Ins	INS	-	AAGCAAGGTA	-	IDH1	270insTACCTT p.Q90fs
XH_P44	2	209113239	209113239	In_Frame_Ins	INS	-	ATGCATATATG	-	IDH1	AGTTATACATATdelinsTVIHICISQFQ
XH_P44	2	209136308	209136308	Nonsense_Mutation	INS	-	ACTATGATCTG	-	PIKFYVE	6insAACCTAGAG22_S23delinsTTMIX
XH_P44	2	209215666	209215666	Nonsense_Mutation	INS	-	CTTAAGTTCTT	-	PIKFYVE	07insCACCTTAAGB69_F1870delinsTTX
XH_P44	2	209308238	209308238	In_Frame_Ins	INS	-	GAT	-	PTH2R	c.342_343insGA p.A114delinsAD
XH_P44	2	209308240	209308240	Nonsense_Mutation	INS	-	TTATATGATATA	-	PTH2R	GTCCTTTTATATG15delinsTQVLMIX
XH_P44	2	210557643	210557643	Frame_Shift_Ins	INS	-	GTCTTTTITA	-	MAP2	750insGTCTT p.L250fs
XH_P44	2	210557645	210557645	Missense_Mutation	SNP	G	C	G	MAP2	c.G751C p.D251H
XH_P44	2	210558441	210558441	Frame_Shift_Ins	INS	-	CATAACATGTTC	-	MAP2	TTTCCCCATAAC p.T516fs
XH_P44	2	210558981	210558981	In_Frame_Ins	INS	-	ATGGACACCTTC	-	MAP2	8insCTCATGGAA69delinsDSVWTL
XH_P44	2	210560371	210560371	Frame_Shift_Ins	INS	-	CTCTCTCGCGT	-	MAP2	478insGCTCTCT p.S1159fs
XH_P44	2	211302592	211302592	Frame_Shift_Ins	INS	-	AGGTACTGTGTG	-	LANCL1	AAATACACACAC p.S232fs
XH_P44	2	211515128	211515128	In_Frame_Ins	INS	-	AGTGTAGGGGG	-	CP51	SGGTAAAGTGT98delinsVKCRGSV
XH_P44	2	214013348	214013348	Frame_Shift_Ins	INS	-	TTTCCACCTTGA	-	IKZF2	CATTCAAAGGTG p.E2fs
XH_P44	2	215815791	215815791	Nonsense_Mutation	INS	-	ATTATTGGCCAG	-	ABCA12	CTGTACCTGGCC904delinsLYLANNX
XH_P44	2	215865528	215865528	Frame_Shift_Ins	INS	-	ATGATGTGAAG	-	ABCA12	insAACACTTTAC p.S709fs
XH_P44	2	216240409	216240409	Nonsense_Mutation	INS	-	CAGATCTTTTA	-	FN1	ACACTTAAAG3_Y1794delinsTLKRIX
XH_P44	2	216273137	216273137	In_Frame_Ins	INS	-	FATGTTAATCTA	-	FN1	12insTTAAGAT T771delinsKINIA
XH_P44	2	216930200	216930200	Nonsense_Mutation	INS	-	CATGCTCTTAAT	-	PECR	CTCTAAATAAAG87_N88delinsISXX
XH_P44	2	217315777	217315777	Frame_Shift_Ins	INS	-	AACAAATGAGA	-	SMARCA1	1insTAAACCAA p.K687fs
XH_P44	2	219330831	219330831	Nonsense_Mutation	INS	-	AACTAATGTGT	-	USP37	GTGCTCAACAC Q791delinsH5KCSHX
XH_P44	2	219452396	219452396	In_Frame_Ins	INS	-	BAACTACGCTG	-	CNOT9	9insAGATTACAC173delinsSDSHSY
XH_P44	2	219494349	219494349	Frame_Shift_Ins	INS	-	CTCATCTGCA	-	PLCD4	1083insGCTACA p.L361fs
XH_P44	2	219604884	219604884	Frame_Shift_Ins	INS	-	ACAGTTAGATTG	-	TTLL4	92insTCACAGTT p.E531fs
XH_P44	2	220037510	220037510	Frame_Shift_Ins	INS	-	AAGTCTTTCGTT	-	CNPPD1	031insAACGA p.R344fs
XH_P44	2	222347338	222347338	Frame_Shift_Ins	INS	-	AAATAATGAAT	-	EPHA4	ATTATAATTCAI p.P300fs
XH_P44	2	223484450	223484450	Nonsense_Mutation	INS	-	TCATCTGGGTT	-	FARS8	ATGAAGAACCCCA420_F421delinsKX
XH_P44	2	225376133	225376133	Frame_Shift_Ins	INS	-	CA	-	CUL3	c.622_623insTG p.K208fs
XH_P44	2	225376134	225376134	Nonsense_Mutation	INS	-	TTTACATTAAATG	-	CUL3	22insGATTAAAT208_T209delinsDX
XH_P44	2	225710346	225710346	In_Frame_Ins	INS	-	ATAAATAGCAAT	-	DOCK10	nsACAATAATGCF44delinsHNNAIYYL
XH_P44	2	225740758	225740758	In_Frame_Ins	INS	-	AATGATGTGGG	-	DOCK10	10insTCCCAACA304delinsSQHHLL
XH_P44	2	225740760	225740760	Missense_Mutation	SNP	C	T	C	DOCK10	c.G908A p.G303D
XH_P44	2	227906867	227906867	Frame_Shift_Ins	INS	-	CTTCTTCTCTTG	-	COL4A4	GAAGAGAAAGA p.K1168fs
XH_P44	2	228399742	228399742	Splice_Site	INS	-	TTCCAAATCATT	-	AGFG1	.
XH_P44	2	228883492	228883492	Frame_Shift_Ins	INS	-	CAACAATCTTG	-	SPHKAP	2078insCAAGA p.N693fs
XH_P44	2	228884154	228884154	Frame_Shift_Ins	INS	-	TACTCTTCTCCA	-	SPHKAP	AGCAGATGGAA p.E472fs
XH_P44	2	230636313	230636313	Frame_Shift_Ins	INS	-	GCAAGGAAGAA	-	TRIP12	469insATTCTCT p.S1565fs
XH_P44	2	230638979	230638979	Splice_Site	INS	-	SAGTGCACATAT	-	TRIP12	.
XH_P44	2	230662472	230662472	Missense_Mutation	SNP	A	T	A	TRIP12	c.T2523A p.D841E
XH_P44	2	230724165	230724165	Frame_Shift_Ins	INS	-	CA	-	TRIP12	c.223_224insTG p.S75fs
XH_P44	2	230724166	230724166	In_Frame_Ins	INS	-	CAACAA	-	TRIP12	22_223insTTGT p.S75delinsL
XH_P44	2	231077649	231077649	Frame_Shift_Ins	INS	-	ATCCCAGCATCT	-	SP110	10insAAGATGC p.L137fs
XH_P44	2	231157498	231157498	Frame_Shift_Ins	INS	-	AAATCCCC	-	SP140	1_1622insAAAT p.M541fs
XH_P44	2	231314912	231314912	Frame_Shift_Ins	INS	-	CTCTTACTTCTCT	-	SP100	TCTCTCTCTTAC p.Q229fs
XH_P44	2	231338148	231338148	Missense_Mutation	SNP	C	A	C	SP100	c.C1539A p.D513E
XH_P44	2	231338149	231338149	Frame_Shift_Ins	INS	-	TCTCTTTTCTCTT	-	SP100	1541insTCTCTT p.M514fs
XH_P44	2	231379899	231379899	Frame_Shift_Ins	INS	-	CAGC	-	SP100	184_2185insCA p.A728fs
XH_P44	2	231379901	231379901	Frame_Shift_Ins	INS	-	GGTAC	-	SP100	186_2187insG p.K729fs
XH_P44	2	232028367	232028367	In_Frame_Ins	INS	-	TTAATCTCTGTG	-	PSMD1	CTTTTCTTAATC03delinsTFLNLCAFE
XH_P44	2	233659607	233659607	Frame_Shift_Ins	INS	-	AAGC	-	GIGYF2	414_1415insAA p.V472fs
XH_P44	2	233659608	233659608	Frame_Shift_Ins	INS	-	AC	-	GIGYF2	1415_1416insA p.V472fs
XH_P44	2	234421232	234421232	Frame_Shift_Ins	INS	-	AGGTATCTTA	-	USP40	2453insTAAGA p.G818fs
XH_P44	2	234421234	234421234	Missense_Mutation	SNP	A	C	A	USP40	c.T2451G p.N817K
XH_P44	2	234526800	234526800	Frame_Shift_Ins	INS	-	STATGAGGTGTG	-	UGT1A8	AGAGTGTATGAG p.P149fs
XH_P44	2	234545987	234545987	Silent	SNP	T	G	T	UGT1A10	c.T819G p.G273G
XH_P44	2	234545988	234545988	In_Frame_Ins	INS	-	FAGGAAAGAGG	-	UGT1A10	nsACATAGGAAA274delinsDIGKRSS
XH_P44	2	234628017	234628017	Frame_Shift_Ins	INS	-	C	-	UGT1A4	c.552dupC p.G184fs
XH_P44	2	234628019	234628019	Missense_Mutation	SNP	A	T	A	UGT1A4	c.A553T p.T185S
XH_P44	2	234638386	234638386	Frame_Shift_Ins	INS	-	CAAAG	-	UGT1A3	514_615insCAA p.M205fs
XH_P44	2	234638388	234638388	Nonsense_Mutation	INS	-	AGTAG	-	UGT1A3	516_617insAGT206_F207delinsKX
XH_P44	2	234713188	234713188	Missense_Mutation	SNP	A	C	A	MROH2A	c.A1948C p.I650L
XH_P44	2	234713189	234713189	Frame_Shift_Ins	INS	-	CAACCAGTTC	-	MROH2A	1950insCAACC p.I650fs
XH_P44	2	234750781	234750781	In_Frame_Ins	INS	-	AGA	-	HJURP	c.389_390insTC p.W130delinsCL
XH_P44	2	234750783	234750783	Missense_Mutation	SNP	A	G	A	HJURP	c.T388C p.W130R
XH_P44	2	237489923	237489923	Nonsense_Mutation	INS	-	TTCAGGTAGTA	-	ACKR3	16insCTTCAGG72_L273delinsVFRX
XH_P44	2	238247736	238247736	Nonsense_Mutation	INS	-	CAGTTAGCTTTT	-	COL6A3	ATGGCAAAAGC3_D2224delinsHGKXS
XH_P44	2	240985350	240985350	Missense_Mutation	SNP	A	G	A	OR6B3	c.T140C p.L47P
XH_P44	2	240985351	240985351	In_Frame_Ins	INS	-	CTTCTCCTTGTG	-	OR6B3	39insACAAAGGL47delinsTKEKL
XH_P44	2	241066247	241066247	In_Frame_Ins	INS	-	CAT	-	COP59	c.491_492insATp.P164delinsPW
XH_P44	2	241066248	241066248	Frame_Shift_Ins	INS	-	CATA	-	COP59	490_491insTAT p.P164fs
XH_P44	2	242194575	242194575	Splice_Site	INS	-	GTTTGAC	-	HDLBP	.
XH_P44	2	242594006	242594006	In_Frame_Ins	INS	-	TTTTTTTTTTTTT	-	ATG4B	ATCTTTTTTTTTT10delinsRIFFFFFLN
XH_P44	3	361545	361545	Frame_Shift_Ins	INS	-	TTTTTTTTTTTTT	-	CHL1	insTTTTTTTTTTTT p.S29fs
XH_P44	3	3214549	3214549	Nonsense_Mutation	INS	-	SAGCCTTCATAT	-	CRBN	nsCAAAATATGA45_E146delinsDKIX
XH_P44	3	7620422	7620422	In_Frame_Ins	INS	-	ACATGGTAGTG	-	GRM7	30insTTACATGG61delinsAYMVVC
XH_P44	3	8578942	8578942	Frame_Shift_Ins	INS	-	TTGGG	-	LMCD1	203_204insTTGG p.K68fs
XH_P44	3	8578944	8578944	In_Frame_Ins	INS	-	CTGCAT	-	LMCD1	05_206insCTGG p.I69delinsTAF
XH_P44	3	8981258	8981258	Frame_Shift_Ins	INS	-	ATCCCTCTCCTCT	-	RAD18	nsACAGAGGAG p.E228fs
XH_P44	3	10123061	10123061	In_Frame_Ins	INS	-	CACAATGACAA	-	FANCD2	nsAAACACAAT046delinsEKHNEQFL

XH_P44	3	10146359	10146359	In_Frame_Ins	INS	-	AAATCATTAGCA	-	FANCD2OS	TCCCTGCTAATG	34delinsSLLMLQK
XH_P44	3	10312552	10312552	Frame_Shift_Ins	INS	-	AGGGAGCTGGA	-	TATDN2	1687insAGGGA	p.G562fs
XH_P44	3	10428197	10428197	Splice_Site	INS	-	ACCCT	-	ATP2B2	.	.
XH_P44	3	12421380	12421380	Frame_Shift_Ins	INS	-	AGAACATAACCA	-	PPARG	insAAAGAACAT	p.D59fs
XH_P44	3	12641888	12641888	Nonsense_Mutation	INS	-	CCTGCCAATTAG	-	RAF1	861insCTAATTG	p.S287delinsSX
XH_P44	3	12641890	12641890	Missense_Mutation	SNP	A	G	A	RAF1	c.T859C	p.S287P
XH_P44	3	15604996	15604996	Frame_Shift_Ins	INS	-	TACCAAACAGAA	-	HACL1	AGGGTGTTCTG	p.F443fs
XH_P44	3	16640098	16640098	Frame_Shift_Ins	INS	-	GGCC	-	DAZL	c.70_71insGGCC	p.A24fs
XH_P44	3	16640100	16640100	Silent	SNP	A	T	A	DAZL	c.T69A	p.T23T
XH_P44	3	19295357	19295357	Frame_Shift_Ins	INS	-	G	-	KCNH8	c.288_289insG	p.E96fs
XH_P44	3	19295359	19295359	Frame_Shift_Ins	INS	-	ACTCAGCAAC	-	KCNH8	291insACTCAG	p.I97fs
XH_P44	3	19926070	19926070	Frame_Shift_Ins	INS	-	TGTCCTCTGTCT	-	EFHB	nsGGACAGACA	p.N657fs
XH_P44	3	21706428	21706428	Frame_Shift_Ins	INS	-	AAAGAGATTTCG	-	ZNF385D	nsGGATCGAATC	p.F39fs
XH_P44	3	25778885	25778885	Frame_Shift_Ins	INS	-	GT	-	NGLY1	c.942_943insAC	p.C315fs
XH_P44	3	25778886	25778886	Frame_Shift_Ins	INS	-	TACCAACCTTCC	-	NGLY1	sACCTGGAAGG	p.N314fs
XH_P44	3	25833226	25833226	Nonsense_Mutation	INS	-	A	-	OXSM	c.715_716insA	C239_1240delinsX
XH_P44	3	25833227	25833227	In_Frame_Ins	INS	-	AAAAAATGGGCT	-	OXSM	GGACAAAAAAT	89delinsWDKKWANF
XH_P44	3	27233665	27233665	Frame_Shift_Ins	INS	-	ATAGTTACATGC	-	NEK10	AATATTGCATGT	p.M99fs
XH_P44	3	27418299	27418299	Frame_Shift_Ins	INS	-	AGTGCCAA	-	SLC4A7	8_3229insTTGC	p.D1077fs
XH_P44	3	27460052	27460052	Frame_Shift_Ins	INS	-	AACTATGAACAT	-	SLC4A7	1200insCATGTG	p.D400fs
XH_P44	3	27473146	27473146	Frame_Shift_Ins	INS	-	CCAGAACTACTG	-	SLC4A7	93insCCAGTAGT	p.A265fs
XH_P44	3	32483407	32483407	In_Frame_Ins	INS	-	TGCTATTATAATC	-	CMTM7	insAACTGCTATT	V79delinsELLILQL
XH_P44	3	32737292	32737292	In_Frame_Ins	INS	-	ACCACGTTT	-	CNOT10	5_176insACACG	L59delinsHHVL
XH_P44	3	33894176	33894176	Nonsense_Mutation	INS	-	ACAAAAAAGAC	-	PDCD6IP	insCTAAACAAA	618_K619delinsTX
XH_P44	3	33905541	33905541	Frame_Shift_Ins	INS	-	AAAAAC	-	PDCD6IP	179_2180insAA	p.I727fs
XH_P44	3	33905542	33905542	In_Frame_Ins	INS	-	CTAGATCTACAA	-	PDCD6IP	nsAAAACTAGAT	272delinsIKLDLQYD
XH_P44	3	36874666	36874666	Frame_Shift_Ins	INS	-	AGGATGAAAACT	-	TRANK1	76insACAGTTTT	p.P2092fs
XH_P44	3	37034060	37034060	Frame_Shift_Ins	INS	-	TGGAATGTCAT	-	EPM2AIP1	AATGAATGACA	p.R170fs
XH_P44	3	37105245	37105245	Frame_Shift_Ins	INS	-	TTAAGGAG	-	LRRFIP2	73_774insCTCCT	p.E258fs
XH_P44	3	37105247	37105247	Nonsense_Mutation	INS	-	ATATAGT	-	LRRFIP2	71_772insACTA	258_1259delinsTIX
XH_P44	3	37366354	37366354	Frame_Shift_Ins	INS	-	TTCCATCTTTTT	-	GOLGA4	nsACTTTTTTCCA	p.S993fs
XH_P44	3	37366627	37366627	Frame_Shift_Ins	INS	-	TTTTGGTTTGTT	-	GOLGA4	insTTCTTTTGGG	p.G1084fs
XH_P44	3	37368728	37368728	Frame_Shift_Ins	INS	-	TGGGTACAATTA	-	GOLGA4	52insTCTGGGTA	p.E1784fs
XH_P44	3	38168106	38168106	In_Frame_Ins	INS	-	AGGAAA	-	ACAA1	612_613insTTTC	R205delinsFPR
XH_P44	3	38287706	38287706	Frame_Shift_Ins	INS	-	AGTGTTCCTTAA	-	OXSR1	sCACACAGTGT	p.T417fs
XH_P44	3	38548445	38548445	Nonsense_Mutation	INS	-	TGCATTTGAGAA	-	EXOGL	2insACTGCATT	61_V162delinsNCIX
XH_P44	3	38548447	38548447	In_Frame_Ins	INS	-	AACAAGAACATC	-	EXOGL	484insAACAAAG	161delinsINKNM
XH_P44	3	38592323	38592323	Missense_Mutation	SNP	C	T	C	SCN5A	c.G5486A	p.R1829H
XH_P44	3	38988380	38988380	Frame_Shift_Ins	INS	-	CTGGG	-	SCN11A	285_286insCCC	p.R96fs
XH_P44	3	38988382	38988382	Frame_Shift_Ins	INS	-	CCTA	-	SCN11A	283_284insTAG	p.N95fs
XH_P44	3	39107362	39107362	Nonsense_Mutation	INS	-	ACTGAAAGCTTA	-	WDR48	51insTACTGAAA	B84_85delinsLLKAX
XH_P44	3	39111231	39111231	Frame_Shift_Ins	INS	-	A	-	WDR48	c.422_423insA	p.T141fs
XH_P44	3	39111232	39111232	Frame_Shift_Ins	INS	-	CTCTTTATCTTG	-	WDR48	24insCCTCTTTA	p.T141fs
XH_P44	3	39431961	39431961	Frame_Shift_Ins	INS	-	ACACAAAAACA	-	SLC25A38	240insACACAA	p.T80fs
XH_P44	3	39431962	39431962	In_Frame_Ins	INS	-	ACAATA	-	SLC25A38	40_241insACAA	p.T80delinsTTI
XH_P44	3	40208370	40208370	Missense_Mutation	SNP	T	A	T	MYRIQ	c.T23A	p.LRQ
XH_P44	3	40208371	40208371	Frame_Shift_Ins	INS	-	AAATTCTCT	-	MYRIQ	4_25insAAATTC	p.L8fs
XH_P44	3	41795922	41795922	Nonsense_Mutation	INS	-	AATATTCCACC	-	ULK4	1346insGGTGA	449_4450delinsRX
XH_P44	3	41996208	41996208	Missense_Mutation	SNP	T	C	T	ULK4	c.A44G	p.K15R
XH_P44	3	41996210	41996210	In_Frame_Ins	INS	-	ATGAGTAAATAA	-	ULK4	ATATGTTTATTA	14delinsRVVYYSLF
XH_P44	3	42679833	42679833	In_Frame_Ins	INS	-	AAGATGATCTGC	-	NKTR	AATCTAAAGATG	79delinsNLNLMICSR
XH_P44	3	42680288	42680288	Frame_Shift_Ins	INS	-	TTTGATGTGAA	-	NKTR	893insCTTTGAT	p.D1031fs
XH_P44	3	42681107	42681107	Missense_Mutation	SNP	G	C	G	NKTR	c.G3911C	p.S1304T
XH_P44	3	42681108	42681108	In_Frame_Ins	INS	-	TCTTCC	-	NKTR	912_3913insTCT	S1304delinsSSS
XH_P44	3	43381847	43381847	Frame_Shift_Ins	INS	-	AATTAACATATAG	-	SNRK	insAGAATTAAC	p.P61fs
XH_P44	3	44286392	44286392	Frame_Shift_Ins	INS	-	TAGAGGACTGTG	-	TOPAZ1	895insCTAGAGG	p.V798fs
XH_P44	3	44346806	44346806	In_Frame_Ins	INS	-	TTTCTGGCTATA	-	TOPAZ1	4033insTTTCTG	A1344delinsAFLAI
XH_P44	3	44449077	44449077	In_Frame_Ins	INS	-	GCCAAATATATC	-	TCAlM	5insAAGGCCAA	465delinsQRNPYTF
XH_P44	3	44490085	44490085	Frame_Shift_Ins	INS	-	NTCAGAGAATTC	-	ZNF445	78insTATGAATT	p.R360fs
XH_P44	3	44636043	44636043	Frame_Shift_Ins	INS	-	TGAGTACTTTA	-	ZNF660	CTTCTGTGAGTA	p.H120fs
XH_P44	3	44763426	44763426	Nonsense_Mutation	INS	-	ATAAGGTGTGT	-	ZNF502	TGATGAATAAG	p.H373delinsLX
XH_P44	3	44795062	44795062	Frame_Shift_Ins	INS	-	AAAAATAGTAGC	-	KIAA1143	291insSGGCTACT	p.K97fs
XH_P44	3	44986759	44986759	Frame_Shift_Ins	INS	-	AATTTTTGTGCTA	-	ZDHHC3	ATTATTGACCAA	p.T111fs
XH_P44	3	45127465	45127465	Silent	SNP	G	T	G	CDCP1	c.C2176A	p.R726R
XH_P44	3	46063154	46063154	Frame_Shift_Ins	INS	-	AACCTCTTCTT	-	XCR1	286insAAGAAG	p.V96fs
XH_P44	3	46245155	46245155	In_Frame_Ins	INS	-	GCAGACATT	-	CCR1	9_650insAATGT	1217delinsKCLL
XH_P44	3	46245578	46245578	Frame_Shift_Ins	INS	-	TCTT	-	CCR1	226_227insAAG	p.L76fs
XH_P44	3	46245580	46245580	Frame_Shift_Ins	INS	-	C	-	CCR1	c.224_225insG	p.N75fs
XH_P44	3	47125486	47125486	Frame_Shift_Ins	INS	-	AAAGGAGCCAA	-	SETD2	5652insCTTGGC	p.L1884fs
XH_P44	3	47165487	47165487	Frame_Shift_Ins	INS	-	ATTCTCTCAAAA	-	SETD2	TTCTTTTTTTGAG	p.A169fs
XH_P44	3	47727586	47727586	Frame_Shift_Ins	INS	-	TTTGTGTTTGTG	-	SMARCC1	ACAAAAACAAC	p.T446fs
XH_P44	3	47957484	47957484	Frame_Shift_Ins	INS	-	AACACCTT	-	MAP4	2_1833insAAGG	p.Q611fs
XH_P44	3	47957721	47957721	In_Frame_Ins	INS	-	CAA	-	MAP4	1595_1596insTG	K532delinsNW
XH_P44	3	47957723	47957723	In_Frame_Ins	INS	-	AAAGACATG	-	MAP4	3_1594insCATG	K532delinsHVFK
XH_P44	3	48491576	48491576	Missense_Mutation	SNP	G	T	G	ATRIP	c.G102T	p.K34N
XH_P44	3	48491577	48491577	Splice_Site	INS	-	AAAATACCCACT	-	ATRIP	.	.
XH_P44	3	48697796	48697796	Nonsense_Mutation	INS	-	GATCACTGCTA	-	CELSR3	2272insTAGCA	M758_K759delinsX
XH_P44	3	49139679	49139679	In_Frame_Ins	INS	-	TTGTCCCTTTG	-	QARS	557insCAAAGGC	E186delinsAKGTK
XH_P44	3	49308675	49308675	Frame_Shift_Ins	INS	-	TTTGAATTCAT	-	C3orf62	2insCAATGGAA	p.T248fs
XH_P44	3	49413019	49413019	Frame_Shift_Ins	INS	-	TTTTTCATAACAA	-	RHOA	TCAGTTGTTATG	p.A2fs
XH_P44	3	49721577	49721577	In_Frame_Ins	INS	-	ATGTGTGCTAGTA	-	MST1	2062insTCACTG	V688delinsSLTHV
XH_P44	3	50005731	50005731	Nonsense_Mutation	INS	-	AAATCCCTTCCC	-	RBM6	CTGATAAATCC	1292delinsNLINFPFX
XH_P44	3	50129611	50129611	In_Frame_Ins	INS	-	ATCCAAATA	-	RBM5	3_154insATCCA	p.Y51delinsYIQI
XH_P44	3	50129612	50129612	Nonsense_Mutation	INS	-	AAAGTGTAAAAA	-	RBM5	nsTTTAAAGGTG	p.D52delinsVX
XH_P44	3	51392352	51392352	Frame_Shift_Ins	INS	-	T	-	DOCK3	c.4148dupT	p.L1383fs
XH_P44	3	51436239	51436239	Nonsense_Mutation	INS	-	AAAAATGACAA	-	DCAF1	TCCCTGTTGTCA	360_D1361delinsSX
XH_P44	3	51455650	51455650	Frame_Shift_Ins	INS	-	TATGTATTTTCC	-	DCAF1	sACATGGGAAA	p.D1011fs
XH_P44	3	51667735	51667735	Frame_Shift_Ins	INS	-	CAGAAAAAGGAT	-	RAF54L2	AAAAACAGAAA	p.F323fs
XH_P44	3	52595959	52595959	Frame_Shift_Ins	INS	-	TGAACCTTTTATT	-	PBRM1	112insAAATAA	p.S1371fs
XH_P44	3	52668801	52668801	Missense_Mutation	SNP	G	A	G	PBRM1	c.C1118T	p.A373V
XH_P44	3	52668802	52668802	Nonsense_Mutation	INS	-	ITCAGTATAATT	-	PBRM1	nsATAAAATTAT	T73_E374delinsKLKY
XH_P44	3	52786176	52786176	Frame_Shift_Ins	INS	-	AAGGACCAGG	-	NEK4	873insCCTGG	p.D291fs
XH_P44	3	52819126	52819126	In_Frame_Ins	INS	-	ATTTTTTTTTTT	-	ITIH1	611insATTTTTT	V204delinsDFFF
XH_P44	3	52819128	52819128	Silent	SNP	C	T	C	ITIH1	c.C612T	p.V204V
XH_P44	3	52964958	52964958	In_Frame_Ins	INS	-	GGA	-	SFMBT1	793_794insTC	p.K265delinsIQ
XH_P44	3	52964959	52964959	In_Frame_Ins	INS	-	TTTTTCCAGAGT	-	SFMBT1	nsTCTACTCTGG	265delinsSTLETK
XH_P44	3	53126622	53126622	Frame_Shift_Ins	INS	-	TCTGATAATGT	-	RF1	221insCACATT	p.V407fs
XH_P44	3	53326509	53326509	Frame_Shift_Ins	INS	-	AGAAACTCAGG	-	DCP1A	insCAACTGAG	p.E166fs

XH_P44	3	53757876	53757876	In_Frame_Ins	INS	-	CGGTTGAAAG	-	CACNA1D	insAAACCGGTT	650delinsKPVEKR
XH_P44	3	54786692	54786692	Frame_Shift_Ins	INS	-	TCTTTTAAACCA	-	CACNA2D3	insTTGATCTTTT	p.C412fs
XH_P44	3	56026106	56026106	Frame_Shift_Ins	INS	-	GATTATATACTCT	-	ERC2	sCTGAAGAAGTA	p.K745fs
XH_P44	3	56468770	56468770	In_Frame_Ins	INS	-	TATTAAAGACTTT	-	ERC2	266insAAAGCTC	A89delinsESLNT
XH_P44	3	56681112	56681112	Frame_Shift_Ins	INS	-	ATCCCATATTGA	-	FAM208A	sAGTATCAATAT	p.H155fs
XH_P44	3	57135325	57135325	Missense_Mutation	SNP	C	T	C	IL17RD	c.G1046G	p.R349K
XH_P44	3	57135326	57135326	Missense_Mutation	SNP	T	C	T	IL17RD	c.A1045G	p.R349G
XH_P44	3	57282380	57282380	Splice_Site	INS	-	CGGATCGGGTG	-	APPL1	-	-
XH_P44	3	57545602	57545602	Frame_Shift_Ins	INS	-	CAAGGCTACTG	-	PDE12	GTGAGCCAAGG	p.L567fs
XH_P44	3	58395877	58395877	Missense_Mutation	SNP	A	C	A	PXK	c.A1045C	p.N349H
XH_P44	3	58395878	58395878	Frame_Shift_Ins	INS	-	GTGTTTATCTT	-	PXK	TTCACTGTGTT	p.N349fs
XH_P44	3	58853662	58853662	Nonsense_Mutation	INS	-	TTAAATAGACAC	-	C3orf67	1insTACTGTCTA	A84_A285delinsVLSIX
XH_P44	3	58853664	58853664	Splice_Site	SNP	T	C	T	C3orf67	-	-
XH_P44	3	64004528	64004528	Frame_Shift_Ins	INS	-	T	-	PSMD6	c.568dupA	p.M190fs
XH_P44	3	64004530	64004530	Nonsense_Mutation	INS	-	AGGGTTGATAT	-	PSMD6	TCAAAAATATC	p.S189delinsRX
XH_P44	3	64527294	64527294	Nonsense_Mutation	INS	-	TCATGGGTTATT	-	ADAMT59	116insAAATAAC	706_L1707delinsKX
XH_P44	3	64527559	64527559	Nonsense_Mutation	INS	-	ATCACACCTCAT	-	ADAMT59	CAAAAAATAGG	D169delinsHKXK
XH_P44	3	64527561	64527561	Missense_Mutation	SNP	G	T	G	ADAMT59	c.C5066A	p.T1689N
XH_P44	3	64608208	64608208	Frame_Shift_Ins	INS	-	CACATTCTAGGT	-	ADAMT59	360insAACCTAC	p.M787fs
XH_P44	3	65347006	65347006	Frame_Shift_Ins	INS	-	TGCTTGCTTACG	-	MAG1I	nsCCACGTAAAG	p.D1168fs
XH_P44	3	65376967	65376967	Frame_Shift_Ins	INS	-	TAAA	-	MAG1I	265_226insTT	p.H756fs
XH_P44	3	65376968	65376968	Frame_Shift_Ins	INS	-	TGGGTAA	-	MAG1I	64_226insTTAC	p.L755fs
XH_P44	3	69047229	69047229	Frame_Shift_Ins	INS	-	GGTATGTATGT	-	EOGT	764insCACATAC	p.N255fs
XH_P44	3	69097236	69097236	Frame_Shift_Ins	INS	-	AAAAAC	-	TMF1	619_620insGTT	p.M207fs
XH_P44	3	69097237	69097237	Frame_Shift_Ins	INS	-	CACGTAG	-	TMF1	18_619insCTCA	p.M207fs
XH_P44	3	69153769	69153769	Frame_Shift_Ins	INS	-	ACTCCCTCTCTC	-	ARL6IP5	ATTACACTCCCT	p.183fs
XH_P44	3	69168864	69168864	In_Frame_Ins	INS	-	AGTAAAGGGA	-	LMOD3	sCACATCTCTT	E14delinsSTIPLPVM
XH_P44	3	71021798	71021798	In_Frame_Ins	INS	-	TATGCTTATTGG	-	FOXP1	60insTGCAATA	H420delinsHAISIS
XH_P44	3	73114657	73114657	Nonsense_Mutation	INS	-	TGATTTTCAAA	-	PPP4R2	TAATTGTATT	89_E290delinsMLLX
XH_P44	3	73114846	73114846	In_Frame_Ins	INS	-	TTCTATTCACAGT	-	PPP4R2	57insTCTTCATT	p.V352fs
XH_P44	3	73657828	73657828	Frame_Shift_Ins	INS	-	TGGGGGTG	-	PDZRN3	0_731insCACCC	p.E244fs
XH_P44	3	73657829	73657829	Nonsense_Mutation	INS	-	ATTCTTTTT	-	PDZRN3	730insAAAAAG	44_T245delinsKKXK
XH_P44	3	74474003	74474003	Nonsense_Mutation	INS	-	TCTAAACAATCG	-	CNTN3	TGAGTCGATTGT	99_S150delinsHESIVX
XH_P44	3	77651608	77651608	In_Frame_Ins	INS	-	TCAATGCTACTA	-	ROBO2	TGAAGTCAATG	34delinsGSEVNATING
XH_P44	3	81695571	81695571	Frame_Shift_Ins	INS	-	ATATAGAATGTG	-	GBE1	4insTGGACATTG	p.Q252fs
XH_P44	3	87018085	87018085	Nonsense_Mutation	INS	-	CTTTCA	-	VGLL3	91_592insTGAA	p.A198delinsX
XH_P44	3	88040809	88040809	In_Frame_Ins	INS	-	TCC	-	HTR1F	1_910_911insTC	p.I304delinsIL
XH_P44	3	88040811	88040811	In_Frame_Ins	INS	-	CTTGCT	-	HTR1F	12_913insCTTG	p.I304delinsLA
XH_P44	3	93762074	93762074	In_Frame_Ins	INS	-	TGCTTTCTCCAT	-	ARL13B	94insCTGCTCTT	S231delinsSLFSI
XH_P44	3	93779978	93779978	Missense_Mutation	SNP	C	A	C	DHFR2	c.G378T	p.M126I
XH_P44	3	93779979	93779979	Frame_Shift_Ins	INS	-	TGTTTTTCTGGTT	-	DHFR2	ACTTAAACCAGA	p.M126fs
XH_P44	3	97251313	97251313	In_Frame_Ins	INS	-	NTTAAACCCAGC	-	EPHA6	9insGATTAAAC	F163delinsLKPNT
XH_P44	3	97591027	97591027	Frame_Shift_Ins	INS	-	GGTATTCACAG	-	CRYBG3	990insGGTATT	p.N330fs
XH_P44	3	97592756	97592756	Nonsense_Mutation	INS	-	ATTATGCTCATAT	-	CRYBG3	TTCTCTATTATG	E907delinsNQTSLLCSYLLX
XH_P44	3	97806600	97806600	Frame_Shift_Ins	INS	-	A	-	OR5AC2	c.584_585insA	p.S195fs
XH_P44	3	97806601	97806601	Frame_Shift_Ins	INS	-	ACCAGGAGGAA	-	OR5AC2	86insCACGAGGA	p.S195fs
XH_P44	3	97868564	97868564	In_Frame_Ins	INS	-	AGGAACAGGGG	-	OR5H14	6insCCAGGAAC	112delinsCQEQGY
XH_P44	3	98072914	98072914	Nonsense_Mutation	INS	-	AA	-	OR5K4	c.217_218insAA	C73_S74delinsX
XH_P44	3	98072915	98072915	Frame_Shift_Ins	INS	-	GAGTGAT	-	OR5K4	18_219insGAGT	p.C73fs
XH_P44	3	98110028	98110028	In_Frame_Ins	INS	-	AAAAATAAATG	-	OR5K3	AGAGAAAAATAA	3delinsQDRENKIVPY
XH_P44	3	98518569	98518569	Frame_Shift_Ins	INS	-	CACAGCAG	-	DCBLD2	4_1975insTTCC	p.G659fs
XH_P44	3	99649733	99649733	Nonsense_Mutation	INS	-	CATCTAAAGG	-	FILIP1L	132insCCTTTA	B44_D45delinsSLX
XH_P44	3	99649735	99649735	Missense_Mutation	SNP	A	G	A	FILIP1L	c.T130C	p.S44P
XH_P44	3	99891173	99891173	In_Frame_Ins	INS	-	ATACAGGGACAG	-	CM5S1	nsTCTATACAGG	180delinsVLYRDR
XH_P44	3	100092401	100092401	Frame_Shift_Ins	INS	-	ATTGTTTGGGT	-	TOMM70	insATGAACCA	p.A439fs
XH_P44	3	100535606	100535606	Frame_Shift_Ins	INS	-	TC	-	ABI3BP	2752_2753insG	p.K918fs
XH_P44	3	100535608	100535608	In_Frame_Ins	INS	-	TCAAAATATTAA	-	ABI3BP	nsCATGTTAAAT	E17delinsPMLNNLIL
XH_P44	3	100549434	100549434	Nonsense_Mutation	INS	-	TAAATTTTAAAC	-	ABI3BP	nsTGTGGTTAA	A702_T703delinsCGX
XH_P44	3	100963584	100963584	In_Frame_Ins	INS	-	AAACTAGTTTTA	-	IMP2G	691insACTAAAA	531delinsTKTSFL
XH_P44	3	101062784	101062784	Frame_Shift_Ins	INS	-	GC	-	SEN7P	1359_1360insG	p.F454fs
XH_P44	3	101062785	101062785	Nonsense_Mutation	INS	-	NGATCTCAGGT	-	SEN7P	ATGCTAACCTGA	3_F454delinsDMLTX
XH_P44	3	101384251	101384251	Frame_Shift_Ins	INS	-	AGTTGACCAAC	-	ZBTB11	180insGGTTGG	p.S394fs
XH_P44	3	101481363	101481363	Frame_Shift_Ins	INS	-	TTTATTTTTATT	-	CEP97	nsCCTTATTTTAT	p.K59fs
XH_P44	3	101572587	101572587	In_Frame_Ins	INS	-	TTTATTTCAGA	-	NFKBIZ	sAGGACTGATAT	06delinsKGLYSRVG
XH_P44	3	107491806	107491806	Frame_Shift_Ins	INS	-	TT	-	BBX	1238_1239insT	p.A413fs
XH_P44	3	107491807	107491807	Nonsense_Mutation	INS	-	CTTCTGTAACCT	-	BBX	1240insCTTCTG	A413delinsALLX
XH_P44	3	107492480	107492480	Frame_Shift_Ins	INS	-	TTTCTCTCTCT	-	BBX	1913insTTTTCTT	p.R638fs
XH_P44	3	107517503	107517503	Frame_Shift_Ins	INS	-	TGCTAAATTTG	-	BBX	79insCATGTCTA	p.K493fs
XH_P44	3	108272543	108272543	In_Frame_Ins	INS	-	TGA	-	KIAA1524	2358_2359insT	p.R787delinsSR
XH_P44	3	108272544	108272544	Frame_Shift_Ins	INS	-	ATAA	-	KIAA1524	2357_2358insTT	p.Q786fs
XH_P44	3	108366895	108366895	Frame_Shift_Ins	INS	-	AAAA	-	DZIP3	898_1899insAA	p.I633fs
XH_P44	3	108366896	108366896	Frame_Shift_Ins	INS	-	ATCTTACTCTTT	-	DZIP3	00insATATCTTA	p.I633fs
XH_P44	3	108688528	108688528	Frame_Shift_Ins	INS	-	GTAGGACTGTA	-	MORC1	stCAAGATACAG	p.M864fs
XH_P44	3	111356984	111356984	Frame_Shift_Ins	INS	-	AAAATTTCCATTA	-	CD96	7insATAAAATT	p.G482fs
XH_P44	3	111604101	111604101	Frame_Shift_Ins	INS	-	CTTACATAAGGA	-	PHLDB2	stAGAACTTACA	p.A393fs
XH_P44	3	111835704	111835704	Silent	SNP	T	C	T	C3orf52	c.T612C	p.S204S
XH_P44	3	111835706	111835706	Frame_Shift_Ins	INS	-	CCATCAC	-	C3orf52	14_615insCCAT	p.L205fs
XH_P44	3	111842494	111842494	In_Frame_Ins	INS	-	AGTTTTCCCAT	-	GCSAM	300insAATGGG	E100delinsEMGKL
XH_P44	3	112546473	112546473	Silent	SNP	G	A	G	CD200R1L	c.C171T	p.I57I
XH_P44	3	113045448	113045448	Nonsense_Mutation	INS	-	SCATATGATCTT	-	CFAP44	360insTAAGAT	A454_N1455delinsX
XH_P44	3	113049228	113049228	Frame_Shift_Ins	INS	-	TAAGGGGTGAA	-	CFAP44	3903insTTTCA	p.G1301fs
XH_P44	3	113166932	113166932	Frame_Shift_Ins	INS	-	ATGGAGTGAGG	-	SPICE1	nsTTTTATTCTCA	p.S793fs
XH_P44	3	113172698	113172698	In_Frame_Ins	INS	-	CATATGAATAAT	-	SPICE1	nsATAATATTAT	86delinsNNIIMCL
XH_P44	3	113376020	113376020	Frame_Shift_Ins	INS	-	CAGCAA	-	USF3	08_4509insTTTC	p.H1503fs
XH_P44	3	113503279	113503279	Nonsense_Mutation	INS	-	GGCTAAGGAAA	-	ATP6V1A	sAGCAGCTAAG	A40_L141delinsNSSX
XH_P44	3	113563465	113563465	Nonsense_Mutation	INS	-	AATGTTTAGAA	-	GRAMD1C	44insAAATGTT	A48_H49delinsLVX
XH_P44	3	113563467	113563467	Nonsense_Mutation	INS	-	TTTTTGCTTCAA	-	GRAMD1C	ATACGTTTTTGC	p.H49delinsOX
XH_P44	3	113765579	113765579	Nonsense_Mutation	INS	-	GTCTCTAATTTG	-	CCDC191	80insGGAATTA	A44_V45delinsGNX
XH_P44	3	118649044	118649044	Frame_Shift_Ins	INS	-	GTGACTCTTTT	-	IGSF11	31insTAAAGAA	p.C44fs
XH_P44	3	119099830	119099830	Frame_Shift_Ins	INS	-	GTCTCTGTGGT	-	ARHGAP31	9insCAGTTTTCTG	p.Y143fs
XH_P44	3	120357322	120357322	In_Frame_Ins	INS	-	TTAAITTTATAAT	-	HGD	TTTTCTATTATA	A29delinsSFHYKLSL
XH_P44	3	120424944	120424944	Nonsense_Mutation	INS	-	TCTCTTTTCTCT	-	RABL3	stCAGAAGAA	A96_L97delinsNPX
XH_P44	3	121192269	121192269	Frame_Shift_Ins	INS	-	ATTAACACATGT	-	POLQ	sACAAACCAATG	p.T2157fs
XH_P44	3	121195436	121195436	Frame_Shift_Ins	INS	-	AACCA	-	POLQ	355_635insTG	p.Q2119fs
XH_P44	3	121195438	121195438	Nonsense_Mutation	INS	-	CTTTGGGAATA	-	POLQ	4insGAATATTC	118_Q2119delinsX
XH_P44	3	121208048	121208048	Frame_Shift_Ins	INS	-	BATAGTTTCTAT	-	POLQ	ATCCAGATAGA	p.T1244fs
XH_P44	3	121228977	121228977	Frame_Shift_Ins	INS	-	ATAGAGCTGCT	-	POLQ	GTATGAGCAGG	p.E575fs
XH_P44	3	121410016	121410016	Frame_Shift_Ins	INS	-	AACTTAACCAA	-	GOLGB1	insGCTGTGGT	p.K2652fs

XH_P44	3	121413075	121413075	Frame_Shift_Ins	INS	-	AGTACTGTGA	-	GOLGB1	6055insTCACA	p.V2019fs
XH_P44	3	121415128	121415128	Frame_Shift_Ins	INS	-	CA	-	GOLGB1	4001_4002insT	p.S1334fs
XH_P44	3	121415130	121415130	Frame_Shift_Ins	INS	-	GAACACAAAG	-	GOLGB1	insGGAGACTTT	p.S1334fs
XH_P44	3	121417537	121417537	Frame_Shift_Ins	INS	-	CG	-	GOLGB1	1592_1593insC	p.I531fs
XH_P44	3	121417538	121417538	Frame_Shift_Ins	INS	-	GCTAAAC	-	GOLGB1	91_1592insGTT	p.I531fs
XH_P44	3	121647402	121647402	Frame_Shift_Ins	INS	-	GGCAACACATA	-	SLC15A2	TACAATGGCAAC	p.Q416fs
XH_P44	3	122419658	122419658	In_Frame_Ins	INS	-	TTTCATGTTTGT	-	PARP14	TCTATTTTCATG	3delinsSLYFHLFNEV
XH_P44	3	122437793	122437793	In_Frame_Ins	INS	-	ATTTCATCT	-	PARP14	5_4796insATTTC	1599delinsNFIS
XH_P44	3	122437795	122437795	Silent	SNP	G	T	G	PARP14	c.G4797T	p.T1599T
XH_P44	3	123419020	123419020	Missense_Mutation	SNP	C	T	C	MYLK	c.G2767A	p.A923T
XH_P44	3	123674897	123674897	Frame_Shift_Ins	INS	-	CATACTATTCCT	-	CCDC14	nsCCAAAGGAAT	p.D123fs
XH_P44	3	124376643	124376643	Frame_Shift_Ins	INS	-	TCATAAATCTGA	-	KALRN	CCAGTCATAAA	p.I280fs
XH_P44	3	124854614	124854614	In_Frame_Ins	INS	-	GATATGGGCTT	-	SLC12A8	AAGCTAAGCCCC	12delinsKAKPISKV
XH_P44	3	124896777	124896777	Frame_Shift_Ins	INS	-	TTGTAGGTGTG	-	SLC12A8	32insTCACACC	p.S144fs
XH_P44	3	124952398	124952398	Frame_Shift_Ins	INS	-	GAAGCGGTAT	-	ZNF148	1172insATACC	p.V391fs
XH_P44	3	124952784	124952784	Splice_Site	INS	-	T	-	ZNF148	.	.
XH_P44	3	125032288	125032288	Nonsense_Mutation	INS	-	ATAAGATTATTA	-	ZNF148	197insTTTAATA	E66_367delinsVX
XH_P44	3	125032289	125032289	Frame_Shift_Ins	INS	-	AGAAACATAATT	-	ZNF148	6insAAAAATTATG	p.E66fs
XH_P44	3	125170222	125170222	Frame_Shift_Ins	INS	-	TGTTTACCAATT	-	SNX4	TAGAGAAATTG	p.K411fs
XH_P44	3	125769894	125769894	Splice_Site	INS	-	CTTGGCATT	-	SLC41A3	.	.
XH_P44	3	129155440	129155440	Nonsense_Mutation	INS	-	AAAGCATATTA	-	MBD4	AATGTTTAATAC	D350delinsDIMFNSAX
XH_P44	3	129156594	129156594	Frame_Shift_Ins	INS	-	GAATGTGTTAA	-	MBD4	304insTTAACC	p.T102fs
XH_P44	3	129156595	129156595	Nonsense_Mutation	INS	-	GCATTTTAGTTA	-	MBD4	AAATATACTAA	01_1102delinsNLX
XH_P44	3	129370327	129370327	Silent	SNP	T	C	T	TMCC1	c.A1440G	p.R480R
XH_P44	3	129547102	129547102	Frame_Shift_Ins	INS	-	ACAGGAAG	-	TMCC1	9_120insCTTCC	p.N40fs
XH_P44	3	129547103	129547103	Frame_Shift_Ins	INS	-	C	-	TMCC1	c.118_119insG	p.N40fs
XH_P44	3	130142736	130142736	Missense_Mutation	SNP	G	A	G	COL6A5	c.G5155A	p.G1719R
XH_P44	3	130142737	130142737	Frame_Shift_Ins	INS	-	CTCTTTGTGACA	-	COL6A5	157insCCTCTTT	p.G1719fs
XH_P44	3	130447527	130447527	Frame_Shift_Ins	INS	-	TGATAGTATAG	-	PIK3R4	5TACCAACTATA	p.E529fs
XH_P44	3	130694328	130694328	Nonsense_Mutation	INS	-	GATTAATAATTG	-	ATP2C1	insTGAAAGATTAA	517_R518delinsLX
XH_P44	3	130799345	130799345	Frame_Shift_Ins	INS	-	TGTGTATCCTAA	-	NEK11	insATCTGTGTA	p.L83fs
XH_P44	3	131306343	131306343	In_Frame_Ins	INS	-	AAACAGAAAG	-	CPNE4	insTAACCTTTCT	273delinsANLSVLL
XH_P44	3	131306345	131306345	Missense_Mutation	SNP	C	A	C	CPNE4	c.G817T	p.A273S
XH_P44	3	132182653	132182653	Nonsense_Mutation	INS	-	TGCTAA	-	DNAJC13	84_1885insTGG	L628delinsLX
XH_P44	3	132182655	132182655	Nonsense_Mutation	INS	-	TTAATATT	-	DNAJC13	86_1887insTTAA	629_N630delinsTX
XH_P44	3	132319273	132319273	Nonsense_Mutation	INS	-	TACTCAAACCTT	-	ACKR4	insGTTACTCAA	Y11_Y12delinsX
XH_P44	3	132390676	132390676	Nonsense_Mutation	INS	-	ATTATTAATTTG	-	UBA5	TAAATATTATTA	2_S123delinsVSKYYX
XH_P44	3	132400801	132400801	Nonsense_Mutation	INS	-	AAAAGAATTTTG	-	NPHP3	TAATAGGAAAA	T1317delinsYNRKILLNNX
XH_P44	3	132403632	132403632	Frame_Shift_Ins	INS	-	CCCTTCTTTG	-	NPHP3	3336insCAAAG	p.A1112fs
XH_P44	3	132403634	132403634	In_Frame_Ins	INS	-	ATA	-	NPHP3	3333_3334insT	p.A1112delinsYA
XH_P44	3	135721961	135721961	Frame_Shift_Ins	INS	-	G	-	PPP2R3A	c.1621_1622ins	p.N541fs
XH_P44	3	135722039	135722039	Frame_Shift_Ins	INS	-	CAAAATCATTA	-	PPP2R3A	insATTCCAAATC	p.V567fs
XH_P44	3	136323310	136323310	Nonsense_Mutation	INS	-	GTATAAGCAAT	-	STAG1	insTGATTTGCTT	74delinsTVLLYTX
XH_P44	3	136664617	136664617	In_Frame_Ins	INS	-	GCACACTAGGT	-	NCK1	ATCTGGCACACT	6delinsRIWHTRRSF
XH_P44	3	136664799	136664799	In_Frame_Ins	INS	-	SCATTCTCTCATG	-	NCK1	sCACTGCATTTC	137delinsSLHFSMTI
XH_P44	3	139085930	139085930	Frame_Shift_Ins	INS	-	CAATGG	-	COPB2	02_1603insCCA	p.I535fs
XH_P44	3	139085932	139085932	In_Frame_Ins	INS	-	TTTTGAGCAAGA	-	COPB2	1insCCCTCTTGG	534delinsSLLKTF
XH_P44	3	141012004	141012004	Frame_Shift_Ins	INS	-	AGTGACATCA	-	PXYLP1	1401insAGTGA	p.S467fs
XH_P44	3	141162496	141162496	Nonsense_Mutation	INS	-	GTTTGGAGATTI	-	ZBTB38	7insATTGTTTGG	422delinsFVWRFK
XH_P44	3	141162498	141162498	Frame_Shift_Ins	INS	-	G	-	ZBTB38	c.1268_1269ins	p.T423fs
XH_P44	3	141274712	141274712	Missense_Mutation	SNP	G	T	G	RASA2	c.G642T	p.K214N
XH_P44	3	141274713	141274713	Nonsense_Mutation	INS	-	AGCTTTAGGCAT	-	RASA2	sTATAAGCTTTTA	p.K215delinsIX
XH_P44	3	141678682	141678682	Frame_Shift_Ins	INS	-	TGTTAAAACCTT	-	TFDP2	77insAAAGGTTT	p.K159fs
XH_P44	3	142131493	142131493	Nonsense_Mutation	INS	-	TCATGAAAAAAT	-	XRN1	insTGGAAAGTTT	E537delinsWKFCLTX
XH_P44	3	142754945	142754945	Frame_Shift_Ins	INS	-	CTTTTATTTTGG	-	U2SURP	ACAAACTTTTAT	p.E279fs
XH_P44	3	148782629	148782629	In_Frame_Ins	INS	-	GATTGAATTTGG	-	HLTF	ATACTACCCA	89delinsVILPNSISFIM
XH_P44	3	149042767	149042767	Frame_Shift_Ins	INS	-	TTCTGCGACAGA	-	TM45F18	AAAGATCTGTG	p.S104fs
XH_P44	3	149089552	149089552	Frame_Shift_Ins	INS	-	CTTT	-	TM45F1	515_516insAAA	p.I172fs
XH_P44	3	149089553	149089553	Frame_Shift_Ins	INS	-	TGTCAGTACAAC	-	TM45F1	5insGCTTGTATC	p.I172fs
XH_P44	3	149684339	149684339	Frame_Shift_Ins	INS	-	ATTCTGTTCACT	-	PFN2	ACAAAAGTGAA	p.H120fs
XH_P44	3	151105924	151105924	Frame_Shift_Ins	INS	-	CTGGGTTCTCTT	-	MED12L	311insGCTGGG	p.G1770fs
XH_P44	3	151107784	151107784	Silent	SNP	C	T	C	MED12L	c.C5364T	p.N1788N
XH_P44	3	151155945	151155945	Frame_Shift_Ins	INS	-	GATGTGGTCTC	-	IGSF10	485insGAGACC	p.I162fs
XH_P44	3	151164539	151164539	Missense_Mutation	SNP	G	C	G	IGSF10	c.C3230G	p.A1077G
XH_P44	3	151164540	151164540	Frame_Shift_Ins	INS	-	AACATCCA	-	IGSF10	8_3229insTGA	p.A1077fs
XH_P44	3	151164743	151164743	Nonsense_Mutation	INS	-	GACATTGCTAG	-	IGSF10	3026insTCTAGC	009_F1010delinsLX
XH_P44	3	151165063	151165063	Frame_Shift_Ins	INS	-	AGTACAGTTAAC	-	IGSF10	2706insTTGTTAA	p.E902fs
XH_P44	3	153840760	153840760	Frame_Shift_Ins	INS	-	TTGGATTTACTT	-	ARHGEF26	80insGTTGGATT	p.F327fs
XH_P44	3	154055949	154055949	Frame_Shift_Ins	INS	-	TAACTCTGATGG	-	GPR149	sTATCACCATCA	p.G579fs
XH_P44	3	154886570	154886570	Nonsense_Mutation	INS	-	TCCTTTGTTAAAG	-	MME	5insSCATCTTTG	85_G656delinsLHLCX
XH_P44	3	157082291	157082291	Nonsense_Mutation	INS	-	TCATTATCCAA	-	VEPH1	138insTTTGGAA	80_T381delinsFGX
XH_P44	3	157082292	157082292	In_Frame_Ins	INS	-	AAACTCACT	-	VEPH1	5_1137insAGTGb	I379delinsVSF
XH_P44	3	158363489	158363489	In_Frame_Ins	INS	-	AGAGGACAGAC	-	GFNM1	154insAGAGGA	I51delinsIRGQT
XH_P44	3	161220925	161220925	Frame_Shift_Ins	INS	-	FACTAATTAGGA	-	OTOL1	AACTACTAAT	p.D210fs
XH_P44	3	164716449	164716449	In_Frame_Ins	INS	-	ATAGTTGTCTCC	-	SI	GGCTTGAGAGAC	3delinsNTGLETTMHDG
XH_P44	3	164764790	164764790	Frame_Shift_Ins	INS	-	GG	-	SI	c.1725_1726insC	p.K576fs
XH_P44	3	164764791	164764791	Frame_Shift_Ins	INS	-	SACAGTTTCATA	-	SI	5insCTCTATGA	p.Q575fs
XH_P44	3	164786606	164786606	Frame_Shift_Ins	INS	-	AC	-	SI	c.386_387insGT	p.K129fs
XH_P44	3	164786607	164786607	Frame_Shift_Ins	INS	-	AAAGACATTTG	-	SI	386insTCAAATG	p.K129fs
XH_P44	3	166958689	166958689	Nonsense_Mutation	INS	-	CAAGGCTACAA	-	ZBBX	ATTAGTTGTAG	K737delinsTYNFTFISLX
XH_P44	3	167510545	167510545	Frame_Shift_Ins	INS	-	TAAAGATTACT	-	SERPINI1	nsAAATAAAAA	p.M217fs
XH_P44	3	168833508	168833508	Frame_Shift_Ins	INS	-	G	-	MECOM	c.1587_1588ins	p.L530fs
XH_P44	3	168833509	168833509	Frame_Shift_Ins	INS	-	GTGTATGGAA	-	MECOM	c.1587insTTCCA	p.S529fs
XH_P44	3	169525484	169525484	Nonsense_Mutation	INS	-	TTGGTGCACTAC	-	LRR34	71insTAGTATGG	I91_T92delinsX
XH_P44	3	169574576	169574576	Frame_Shift_Ins	INS	-	GAAGGATATGT	-	LRR31	c.TCCTACATACC	p.L135fs
XH_P44	3	169802488	169802488	Nonsense_Mutation	INS	-	TAAATAATTTT	-	GPR160	AGAAATAAAAT	K243delinsKLKLX
XH_P44	3	169835108	169835108	Nonsense_Mutation	INS	-	TTGTAATTTTAT	-	PHC3	CTTGAATAAA	88_E689delinsTFLKX
XH_P44	3	169835200	169835200	Frame_Shift_Ins	INS	-	GCAAGCATATTT	-	PHC3	71insACAAATAT	p.P657fs
XH_P44	3	169847165	169847165	In_Frame_Ins	INS	-	GTCTCCTCACCC	-	PHC3	059insGGTGGAA	353delinsMVEET
XH_P44	3	170244473	170244473	Frame_Shift_Ins	INS	-	GTTAGGGCCAG	-	SLC7A14	insAACCTGGCC	p.P85fs
XH_P44	3	170716069	170716069	Frame_Shift_Ins	INS	-	GGCCTTTACCC	-	SLC2A2	930insGGGTAA	p.Q310fs
XH_P44	3	170716071	170716071	In_Frame_Ins	INS	-	TTACATATTTT	-	SLC2A2	928insAAAAAAT	Q310delinsKKCEQ
XH_P44	3	172835325	172835325	Frame_Shift_Ins	INS	-	AGTGATA	-	SPATA16	6_197insTGTAC	p.T66fs
XH_P44	3	172835327	172835327	Missense_Mutation	SNP	C	A	C	SPATA16	c.G195T	p.M65I
XH_P44	3	173322719	173322719	Frame_Shift_Ins	INS	-	TCACTGCT	-	NLGN1	1_332insTCACT	p.T111fs
XH_P44	3	173996773	173996773	Frame_Shift_Ins	INS	-	C	-	NLGN1	c.982_983insC	p.V328fs
XH_P44	3	173996774	173996774	Frame_Shift_Ins	INS	-	CAAGAAAC	-	NLGN1	3_984insCAAGA	p.V328fs
XH_P44	3	173998475	173998475	Nonsense_Mutation	INS	-	ACAAAACGGTT	-	NLGN1	ACCTCTACAAA	9delinsDISQYTSKRLGLVX

XH_P44	3	174974311	174974311	Missense_Mutation	SNP	C	T	C	NAALADL2	c.C931T	p.L311F
XH_P44	3	179051287	179051287	Frame_Shift_Ins	INS	-	ACCAA	-	ZNF639	535_536insACC	p.L179fs
XH_P44	3	179051288	179051288	Frame_Shift_Ins	INS	-	CAAAATATATCA	-	ZNF639	37insACAAAATA	p.L179fs
XH_P44	3	179447994	179447994	Frame_Shift_Ins	INS	-	GAAACGTTTATC	-	USP13	107insTGAAAC	p.P369fs
XH_P44	3	180369266	180369266	Frame_Shift_Ins	INS	-	CTCC	-	CCDC39	089_109insGG	p.T364fs
XH_P44	3	180369268	180369268	Missense_Mutation	SNP	A	C	A	CCDC39	c.T1088G	p.I363R
XH_P44	3	182812381	182812381	Frame_Shift_Ins	INS	-	TGTATCAAAATC	-	MCCCI	sAGAGATTGAT	p.E4fs
XH_P44	3	182817187	182817187	In_Frame_Ins	INS	-	TTATCGATA	-	LAMP3	5_357insTATCG	p.P119delinsPIDK
XH_P44	3	182817187	182817187	Missense_Mutation	SNP	G	C	G	LAMP3	c.C355G	p.P119A
XH_P44	3	183754560	183754560	In_Frame_Ins	INS	-	TTTGAGATGCT	-	HTR3D	393insTTTGACAG	p.R131delinsLQML
XH_P44	3	184039208	184039208	Frame_Shift_Ins	INS	-	SGTACTACTCCA	-	EIF4G1	249insSGCTATAC	p.N83fs
XH_P44	3	184040370	184040370	In_Frame_Ins	INS	-	TCTTATTTA	-	EIF4G1	9_1060insTCTTA	p.P353delinsPSVL
XH_P44	3	184040372	184040372	Frame_Shift_Ins	INS	-	TCCTT	-	EIF4G1	061_1062insTC	p.A354fs
XH_P44	3	184090427	184090427	Frame_Shift_Ins	INS	-	TTCTACTTCTCT	-	THPO	nsAGGAGAAAG	p.T312fs
XH_P44	3	184090757	184090757	Frame_Shift_Ins	INS	-	CCATCCTCCT	-	THPO	606insAGGAGG	p.L202fs
XH_P44	3	185155411	185155411	Frame_Shift_Ins	INS	-	TCACC	-	MAP3K13	652_653insTCA	p.A218fs
XH_P44	3	185637255	185637255	Nonsense_Mutation	INS	-	AAACTAAATGTA	-	TRA2B	ACTTTATACATT	p.152delinsINIQRLTYFSFRX
XH_P44	3	18597721	18597721	Silent	SNP	G	A	G	DGKG	c.C711T	p.D237D
XH_P44	3	186459500	186459500	Missense_Mutation	SNP	C	T	C	KNG1	c.C1315T	p.H439Y
XH_P44	3	186459502	186459502	Nonsense_Mutation	INS	-	ATGAATGTATTA	-	KNG1	nsTAAGATGAAT	p.H439delinsHX
XH_P44	3	186507043	186507043	Nonsense_Mutation	INS	-	ATCAGAACGTTA	-	EIF4A2	AAAGAATCAGAA	p.V403delinsVX
XH_P44	3	186760832	186760832	Frame_Shift_Ins	INS	-	TGGTTTGCATT	-	ST6GAL1	TTCTCTGTTTGT	p.K114fs
XH_P44	3	186915474	186915474	Frame_Shift_Ins	INS	-	AGTTTGTGGGTG	-	RTP1	72insGAGTTTGT	p.A57fs
XH_P44	3	186915476	186915476	Frame_Shift_Ins	INS	-	AT	-	RTP1	c.173_174insAT	p.K58fs
XH_P44	3	190936715	190936715	Nonsense_Mutation	INS	-	TGTAACATCTTA	-	OSTN	nsATCATGTAACT	p.S95delinsLIMX
XH_P44	3	193854445	193854445	Frame_Shift_Ins	INS	-	TTGTTTGTGTCT	-	HE51	nsTTTTTTGTGTG	p.I50fs
XH_P44	3	195245915	195245915	Frame_Shift_Ins	INS	-	T	-	PPP1R2	c.392_393insA	p.A131fs
XH_P44	3	195245916	195245916	Frame_Shift_Ins	INS	-	CTAAGATAATGT	-	PPP1R2	92insTACATTAT	p.A131fs
XH_P44	3	195511992	195511992	Frame_Shift_Ins	INS	-	GCTG	-	MUC4	458_6459insCA	p.V2153fs
XH_P44	3	195516956	195516956	Missense_Mutation	SNP	T	C	T	MUC4	c.A1495G	p.T499A
XH_P44	3	195516957	195516957	In_Frame_Ins	INS	-	ACA	-	MUC4	1493_1494insTG	p.T498delinsTV
XH_P44	3	196199062	196199062	Frame_Shift_Del	DEL	T	-	T	RNF168	c.1344delA	p.L448fs
XH_P44	3	196807977	196807977	Frame_Shift_Ins	INS	-	GCCA	-	DLG1	600_1601insTG	p.K534fs
XH_P44	3	196807978	196807978	Frame_Shift_Ins	INS	-	GGTG	-	DLG1	599_1600insCA	p.K534fs
XH_P44	3	196812573	196812573	Nonsense_Mutation	INS	-	TTTTTAATTGTG	-	DLG1	5TTGTACAAAT	p.N490delinsLHVVTNX
XH_P44	3	197423867	197423867	Frame_Shift_Ins	INS	-	CTGCCATTTC	-	RUBCN	1315insGAAAT	p.S439fs
XH_P44	3	197585729	197585729	Nonsense_Mutation	INS	-	TTTACTAA	-	LRCH3	59_1670insTTTA	p.S57_C558delinsVYX
XH_P44	3	197585730	197585730	In_Frame_Ins	INS	-	CTA	-	LRCH3	1670_1671insCP	p.G557delinsGY
XH_P44	3	197680875	197680875	Frame_Shift_Ins	INS	-	AACAAAATCTT	-	RPL35A	TATAAAACAAA	p.N56fs
XH_P44	4	155389	155389	Missense_Mutation	SNP	A	T	A	ZNF718	c.A914T	p.H305L
XH_P44	4	155390	155390	Nonsense_Mutation	INS	-	STGTTGAGTTAG	-	ZNF718	5insTTGTTGTTGA	p.O5_A306delinsHLXC
XH_P44	4	155691	155691	Frame_Shift_Ins	INS	-	GA	-	ZNF718	1216_1217insG	p.V406fs
XH_P44	4	155692	155692	Frame_Shift_Ins	INS	-	ATTCTTACATT	-	ZNF718	TTTCCACATTCT	p.V406fs
XH_P44	4	366804	366804	In_Frame_Ins	INS	-	TTATAACCTCCT	-	ZNF141	351insTTATAAC	p.H117delinsHYNLL
XH_P44	4	366806	366806	Missense_Mutation	SNP	G	T	G	ZNF141	c.G352T	p.A118S
XH_P44	4	367538	367538	Frame_Shift_Ins	INS	-	AGTA	-	ZNF141	084_1085insAG	p.L362fs
XH_P44	4	367540	367540	In_Frame_Ins	INS	-	ATTCTCTTATGT	-	ZNF141	087insAATTCTC	p.362delinsLNSLMF
XH_P44	4	619677	619677	Nonsense_Mutation	SNP	C	T	C	PDE8X	c.C262T	p.Q88X
XH_P44	4	1388662	1388662	Silent	SNP	G	C	G	CRIPAK	c.G363C	p.P121P
XH_P44	4	2698310	2698310	In_Frame_Ins	INS	-	TTTCTACTTGT	-	FAM193A	2625insTTTCTA	p.K875delinsNFYLL
XH_P44	4	2701874	2701874	Frame_Shift_Ins	INS	-	TACAGCTCTTAG	-	FAM193A	nsTTTTTTACAGC	p.F1034fs
XH_P44	4	2956164	2956164	Nonsense_Mutation	INS	-	TTTT	-	NOP14	598_599insAAA	p.S200_K201delinsX
XH_P44	4	2956165	2956165	Frame_Shift_Ins	INS	-	TTTGAGAGCTGAC	-	NOP14	98insACTACGTC	p.S200fs
XH_P44	4	4239640	4239640	Frame_Shift_Ins	INS	-	T	-	TMEM128	c.420_421insA	p.V141fs
XH_P44	4	4239641	4239641	Nonsense_Mutation	INS	-	AATTATCCATTCA	-	TMEM128	0insATGAATGG	p.H140delinsQX
XH_P44	4	4440216	4440216	In_Frame_Ins	INS	-	AGCAAAGGAAG	-	STX18	STCTGCTTCTCT	p.P92delinsLPLLYA
XH_P44	4	5759851	5759851	Nonstop_Mutation	INS	-	GACT	-	EVC	607_1608insGA	p.X536delinsWT
XH_P44	4	6086688	6086688	Frame_Shift_Ins	INS	-	TAGGAACCTATC	-	JAKMIP1	stAAAGATAAG	p.Q115fs
XH_P44	4	6864285	6864285	In_Frame_Ins	INS	-	KACAGAGTTTAT	-	KIAO232	77insAACACAGA	p.T726delinsKQEFIP
XH_P44	4	8467242	8467242	Frame_Shift_Ins	INS	-	AAGGCTCTTCAC	-	TRMT44	TTTTGAAGTCT	p.G242fs
XH_P44	4	13603397	13603397	Frame_Shift_Ins	INS	-	ATAATGATGCA	-	BOD1L1	5127insTGCAT	p.G1709fs
XH_P44	4	13603914	13603914	Frame_Shift_Ins	INS	-	GGAAAAGGATG	-	BOD1L1	610insATCATCC	p.P1537fs
XH_P44	4	13605738	13605738	Nonsense_Mutation	INS	-	AGCACATAGTA	-	BOD1L1	insTGTGACTAT	p.T9_E930delinsCTMCX
XH_P44	4	13616325	13616325	Frame_Shift_Ins	INS	-	AACAGCAAGACA	-	BOD1L1	69insCTGCTTTC	p.P223fs
XH_P44	4	15518365	15518365	Frame_Shift_Ins	INS	-	STGTCAACATAT	-	CC2D2A	sATTCTGTGTCA	p.T379fs
XH_P44	4	15554922	15554922	Frame_Shift_Ins	INS	-	TGCTGTTTAGAA	-	CC2D2A	CAGGATGCTGT	p.F827fs
XH_P44	4	15602920	15602920	Nonsense_Mutation	INS	-	CAGCTTTTAT	-	CC2D2A	TCTACTCAGCT	p.S1580delinsFFSYAFYX
XH_P44	4	15689956	15689956	Nonsense_Mutation	INS	-	CACCATATTAG	-	FAM200B	ACACAGCACCAAT	p.S2delinsDSTQHHYX
XH_P44	4	15991418	15991418	Frame_Shift_Ins	INS	-	CCACCTTGCTC	-	PROM1	1986insGAGCA	p.K662fs
XH_P44	4	20525443	20525443	Nonsense_Mutation	INS	-	TTAACTTTAATA	-	SLIT2	AACATTTTAACT	p.T01delinsNTNLTUIX
XH_P44	4	20706325	20706325	In_Frame_Ins	INS	-	AAAGCTCTGTAC	-	PACRGL	96insAAAGCTCT	p.H32delinsQKLC
XH_P44	4	20706327	20706327	Missense_Mutation	SNP	A	T	A	PACRGL	c.A97T	p.R33W
XH_P44	4	20711376	20711376	Frame_Shift_Ins	INS	-	ATGTG	-	PACRGL	346_347insATG	p.L116fs
XH_P44	4	20726498	20726498	Nonsense_Mutation	INS	-	CTTGTTTATAGT	-	PACRGL	insCCCCCTGTTT	p.Q226delinsHPLFX
XH_P44	4	22389696	22389696	Frame_Shift_Ins	INS	-	AAAGTAGCAGAA	-	ADGRA3	98insATTCTGCG	p.G1200fs
XH_P44	4	24531364	24531364	Frame_Shift_Ins	INS	-	CAGTGGGATGT	-	DHX15	insTCAACAATC	p.Y710fs
XH_P44	4	25416288	25416288	Nonsense_Mutation	INS	-	AGAAAAATTTA	-	ANAPC4	5AAATGAGAAA	p.C600delinsREKEMRXX
XH_P44	4	36126590	36126590	Splice_Site	INS	-	AGAACTCACCT	-	ARAP2	.	
XH_P44	4	36286166	36286166	Frame_Shift_Ins	INS	-	TGTTGCCATT	-	DTHD1	466insTGTTCG	p.P155fs
XH_P44	4	36310040	36310040	Frame_Shift_Ins	INS	-	AATGACAGTGTCA	-	DTHD1	sGGAAAAATGCA	p.E384fs
XH_P44	4	37636572	37636572	Nonsense_Mutation	INS	-	CTGGTGTGAGT	-	RELL1	TAGGACTCACA	p.T206delinsIX
XH_P44	4	38798825	38798825	Frame_Shift_Ins	INS	-	5ATCTGGCCTGAG	-	TLR1	628insACCAGG	p.S543fs
XH_P44	4	39217802	39217802	Frame_Shift_Ins	INS	-	CAAAATAAAT	-	WDR19	742insCAAAAT	p.R247fs
XH_P44	4	39217804	39217804	Missense_Mutation	SNP	C	A	C	WDR19	c.C743A	p.A248D
XH_P44	4	39436045	39436045	Frame_Shift_Ins	INS	-	AATATTATTGAT	-	KLK	42insAAAAATAT	p.K347fs
XH_P44	4	40356503	40356503	In_Frame_Ins	INS	-	CTGGCTGCTTTG	-	CHRNA9	407insTCTGGCG	p.469delinsVPGCFQ
XH_P44	4	40356505	40356505	Missense_Mutation	SNP	A	G	A	CHRNA9	c.A1408G	p.M470V
XH_P44	4	41652611	41652611	Frame_Shift_Ins	INS	-	ACACTGACTTT	-	LIMCH1	1370insACACT	p.P457fs
XH_P44	4	42145992	42145992	In_Frame_Ins	INS	-	ACTTCTGCCTTTT	-	BEND4	CTCAAAAGGCG	p.S9delinsPSKQKQFVV
XH_P44	4	42457378	42457378	Frame_Shift_Ins	INS	-	GATA	-	ATP8A1	2707_2708insTA	p.E903fs
XH_P44	4	42457379	42457379	In_Frame_Ins	INS	-	AGGCAGAGAAG	-	ATP8A1	2707insCCTTCT	p.E903delinsPSLPE
XH_P44	4	42524264	42524264	Silent	SNP	C	T	C	ATP8A1	c.G1815A	p.Q605Q
XH_P44	4	42524265	42524265	Nonsense_Mutation	INS	-	ATTTGGATCAA	-	ATP8A1	CAAACTTGATC	p.S05delinsPNLDPLX
XH_P44	4	46053572	46053572	Missense_Mutation	SNP	C	A	C	GABRG1	c.G1000T	p.D334Y
XH_P44	4	46053573	46053573	Frame_Shift_Ins	INS	-	AATATTATTGTG	-	GABRG1	ACAAACACATA	p.M333fs
XH_P44	4	46979605	46979605	In_Frame_Ins	INS	-	TTTCTTCTCTTC	-	GABRA4	5insGGAAAGGA	p.106delinsGKERKK
XH_P44	4	46979606	46979606	Missense_Mutation	SNP	G	T	G	GABRA4	c.C315A	p.D105E
XH_P44	4	47405655	47405655	Nonsense_Mutation	INS	-	CACCATCTTGTA	-	GABRB1	sTAGACACCATCT	p.S254_T255delinsSX

XH_P44	4	47853949	47853949	Nonsense_Mutation	INS	-	TGGGTTATCTC	-	NFXL1	432insAGAGAT	c811_N812delinsX
XH_P44	4	47853951	47853951	Missense_Mutation	SNP	C	G	C	NFXL1	c.G2430C	p.Q810H
XH_P44	4	48076029	48076029	Nonsense_Mutation	INS	-	TCACATACCTTC	-	TXK	sGTGAAGAAGG	p.K427delinsMX
XH_P44	4	48140724	48140724	Frame_Shift_Ins	INS	-	TCCTTCATGGT	-	TEC	770insAACCATG	p.A590fs
XH_P44	4	48422228	48422228	Frame_Shift_Ins	INS	-	TTAAATTACAA	-	SLAIN2	1448insTTAAA	p.S483fs
XH_P44	4	48422230	48422230	Frame_Shift_Ins	INS	-	GATGATTG	-	SLAIN2	9_1450insGATG	p.S483fs
XH_P44	4	48517177	48517177	Frame_Shift_Ins	INS	-	A	-	FRYL	c.7804_7805ins	p.E2602fs
XH_P44	4	48517178	48517178	Nonsense_Mutation	INS	-	TGTTTCAGCTCG	-	FRYL	GATTACAGACT	T2603delinsNTQSMITDX
XH_P44	4	48584640	48584640	Nonsense_Mutation	INS	-	TAATAGTCTGT	-	FRYL	sGAGTGAACAGA	G620_F621delinsX
XH_P44	4	53610604	53610604	Nonsense_Mutation	INS	-	TCTATATAAATT	-	ERVMER34-1	CGAATAATTTA	B62_Y363delinsSEX
XH_P44	4	56744232	56744232	Frame_Shift_Ins	INS	-	AAAC	-	EXOC1	224_1225insAA	p.K408fs
XH_P44	4	56744233	56744233	Splice_Site	INS	-	ACAATAAAAAAG	-	EXOC1	.	.
XH_P44	4	57265517	57265517	Nonsense_Mutation	INS	-	ATAATAAATTAA	-	PPAT	insAAAGTTAAT	B55_T356delinsKSX
XH_P44	4	57832898	57832898	Nonsense_Mutation	INS	-	AAATAGCCACAC	-	NOA1	sTAGCTGTGTG	551delinsIAVWLFX
XH_P44	4	62453159	62453159	Splice_Site	INS	-	ATTACATGTGT	-	ADGRL3	.	.
XH_P44	4	68606421	68606421	Frame_Shift_Ins	INS	-	C	-	GNRHR	c.763_764insG	p.K255fs
XH_P44	4	68606423	68606423	In_Frame_Ins	INS	-	TGATTGATA	-	GNRHR	1_762insTATCA	S254delinsSINH
XH_P44	4	68780424	68780424	Nonsense_Mutation	INS	-	TATATTATATGT	-	TMPRS511A	TAAAGAACATA	B6_A327delinsvKNIX
XH_P44	4	69964374	69964374	In_Frame_Ins	INS	-	CTTCAGGTAAAT	-	UGT2B7	AATTACTTCAGG	delinsHKITSKGLKGV
XH_P44	4	70146411	70146411	Missense_Mutation	SNP	G	A	G	UGT2B28	c.G193A	p.D65N
XH_P44	4	70146412	70146412	In_Frame_Ins	INS	-	GTCACGTGTTCT	-	UGT2B28	195insGTCACTG	D65delinsESLFL
XH_P44	4	70346573	70346573	Nonsense_Mutation	INS	-	AAGAGATTAA	-	UGT2B4	366insTAATTTAA	p.P456delinsX
XH_P44	4	70346575	70346575	Missense_Mutation	SNP	T	G	T	UGT2B4	c.A1364C	p.K455T
XH_P44	4	70823406	70823406	In_Frame_Ins	INS	-	AGT	-	CSN2	c.257_258insAC	p.P86delinsPL
XH_P44	4	70823408	70823408	Frame_Shift_Ins	INS	-	TGCC	-	CSN2	255_256insGGC	p.P86fs
XH_P44	4	71200946	71200946	In_Frame_Ins	INS	-	TGGGAGCAATG	-	CAB51	191insTGGGAGC	T64delinsMGAMS
XH_P44	4	71346959	71346959	Frame_Shift_Ins	INS	-	CT	-	MUC7	c.498_499insCT	p.T166fs
XH_P44	4	71346961	71346961	Frame_Shift_Ins	INS	-	ATTTTATCTGG	-	MUC7	01insTATTTTAA	p.A167fs
XH_P44	4	71509605	71509605	Frame_Shift_Ins	INS	-	CTTGTTTGTGAT	-	ENAM	3insTCCCTTGG	p.P821fs
XH_P44	4	72319301	72319301	Frame_Shift_Ins	INS	-	TTTT	-	SLC4A4	280_1281insTT	p.S427fs
XH_P44	4	72319303	72319303	Frame_Shift_Ins	INS	-	ACCAAAATTAGG	-	SLC4A4	3insGTCAACAA	p.A428fs
XH_P44	4	72338670	72338670	In_Frame_Ins	INS	-	5AAAAATGTTTA	-	SLC4A4	AGAAAGAAAAA	delinsWKKERKMFRFLLL
XH_P44	4	73957480	73957480	In_Frame_Ins	INS	-	CCAGC	-	ANKRD17	11_5112insGGC	S1704delinsGAX
XH_P44	4	73957482	73957482	Missense_Mutation	SNP	T	A	T	ANKRD17	c.A5110T	p.S1704C
XH_P44	4	73986025	73986025	Nonsense_Mutation	INS	-	ACATTGTCTGAT	-	ANKRD17	AAACAATCAG	B42delinsAETNQTMX
XH_P44	4	74303968	74303968	In_Frame_Ins	INS	-	ATT	-	AFP	c.215_216insAT	p.T72delinsTF
XH_P44	4	74303970	74303970	Nonsense_Mutation	INS	-	AATTATGTAAAA	-	AFP	TGTAAAAATTATG	A73_T74delinsDLX
XH_P44	4	74853370	74853370	Splice_Site	INS	-	TAGTCTCATGGA	-	PPBP	.	.
XH_P44	4	76452388	76452388	In_Frame_Ins	INS	-	TATTACACTGTA	-	THAP6	8insCCATTACAC	T169delinsCPLHCS
XH_P44	4	77065419	77065419	Nonsense_Mutation	INS	-	GATACTAGCTGA	-	NUP54	TAATGTCAGCTA	G60_F61delinsX
XH_P44	4	77100854	77100854	In_Frame_Ins	INS	-	5TAAGTAGATT	-	SCARB2	8insAAAAATCT	V143delinsESLTVL
XH_P44	4	79432614	79432614	Missense_Mutation	SNP	G	A	G	FRAS1	c.G9967A	p.A3323T
XH_P44	4	79432615	79432615	Nonsense_Mutation	INS	-	TATTGACTTTTA	-	FRAS1	sGTAATTATTGA	B323_T3324delinsSAX
XH_P44	4	79832699	79832699	In_Frame_Ins	INS	-	TTCTGTGTACATT	-	BMP2K	2999insTTCCTG	T1000delinsILVHS
XH_P44	4	80246816	80246816	Frame_Shift_Ins	INS	-	AGACGCAC	-	NAA11	15_216insGTGC	p.I72fs
XH_P44	4	80246818	80246818	Missense_Mutation	SNP	T	A	T	NAA11	c.A214T	p.I72F
XH_P44	4	80328215	80328215	Frame_Shift_Ins	INS	-	AA	-	GK2	.1139_1140insT	p.L380fs
XH_P44	4	80328217	80328217	Frame_Shift_Ins	INS	-	TGAAATTCGT	-	GK2	.1138insACGAA	p.L380fs
XH_P44	4	82010940	82010940	Nonsense_Mutation	INS	-	TGTATTACATTA	-	PRKG2	GCAAAATAGTA	T7_H318delinsEKQIMX
XH_P44	4	84338009	84338009	Nonsense_Mutation	INS	-	CTATAGATACAA	-	HELQ	2insCTTTTGTATC	B8_Q959delinsLVLX
XH_P44	4	84338011	84338011	Missense_Mutation	SNP	G	A	G	HELQ	c.C2870T	p.A957V
XH_P44	4	84348842	84348842	Nonsense_Mutation	INS	-	CCTATTATATGC	-	HELQ	sAAAAAGCATA	L783delinsLSKIX
XH_P44	4	84508469	84508469	Nonsense_Mutation	INS	-	CTAAAAAAGCT	-	GPAT3	2insCACTAAAAAT	B1_P182delinsPLKX
XH_P44	4	85553020	85553020	Nonsense_Mutation	INS	-	TCAAATTAATTAG	-	CD51	TTAATTCAATTA	T210_F211delinsLHX
XH_P44	4	85731070	85731070	Nonsense_Mutation	INS	-	ATTAGTTCAT	-	WDFY3	ACTGCAATGAGA	T772_Y773delinsQX
XH_P44	4	85742544	85742544	Nonsense_Mutation	INS	-	GCAATTGAAAC	-	WDFY3	AGAAGTGTGTTT	T428_Q249delinsSX
XH_P44	4	86898843	86898843	In_Frame_Ins	INS	-	ACA	-	ARHGAP24	c.348_349insAC	p.E116delinsET
XH_P44	4	86898844	86898844	In_Frame_Ins	INS	-	AATATTGGAT	-	ARHGAP24	350insAATTATT	G117delinsELFGC
XH_P44	4	87728887	87728887	Frame_Shift_Ins	INS	-	TGCACTTTAAAC	-	PTPN13	nsAGCATGTGAT	p.M2116fs
XH_P44	4	87808910	87808910	Splice_Site	INS	-	TACTCTGTGTCC	-	C4orf36	.	.
XH_P44	4	87968299	87968299	Frame_Shift_Ins	INS	-	TGTGAATGGG	-	AFF1	592insTGTGAA	p.E197fs
XH_P44	4	88085210	88085210	Nonsense_Mutation	INS	-	TTAAATGTGTGC	-	KLHL8	10insTAGCAAC	B7_L338delinsLATFX
XH_P44	4	88535039	88535039	Nonsense_Mutation	INS	-	AGGAAGAATAA	-	DSPP	226insGAGGAA	A409_G410delinsSX
XH_P44	4	88583720	88583720	Missense_Mutation	SNP	A	G	A	DMP1	c.A742G	p.S248G
XH_P44	4	88583722	88583722	Frame_Shift_Ins	INS	-	GCTCTTCACTCT	-	DMP1	745insGCTCTCT	p.S248fs
XH_P44	4	88584078	88584078	In_Frame_Ins	INS	-	sGAGTTGCTGTT	-	DMP1	01insTGGAGTT	T367delinsSGVAVF
XH_P44	4	89034587	89034587	In_Frame_Ins	INS	-	TATTGTTTATCTT	-	ABCG2	GAGTGGAAGATA	4delinsGKVKITNNWK
XH_P44	4	89338629	89338629	In_Frame_Ins	INS	-	sGAAATTTTTTTC	-	HERC6	512insTGGAAAT	A537delinsMWKFFS
XH_P44	4	89576446	89576446	In_Frame_Ins	INS	-	CTATCACACAAA	-	HERC3	546insCTATCAC	A182delinsAYHNN
XH_P44	4	90169810	90169810	Nonsense_Mutation	INS	-	TAGGAAGAA	-	GPRIN3	1_1452insTTCT	G484delinsGSSX
XH_P44	4	96762448	96762448	Frame_Shift_Ins	INS	-	TCATACTGTGTC	-	PDHA2	148insCTCATAC	p.K383fs
XH_P44	4	100052911	100052911	In_Frame_Ins	INS	-	AGGTGTGGATT	-	ADH4	587insAAATCCA	T196delinsKIH7S
XH_P44	4	100235117	100235117	In_Frame_Ins	INS	-	CTTGGAAGATTG	-	ADH1B	689insGCATCTT	F230delinsCIFQV
XH_P44	4	100496091	100496091	Nonsense_Mutation	INS	-	GAGGAAACTTTA	-	MTTP	CAATGAGGAAA	C10delinsHPMRKLX
XH_P44	4	102751319	102751319	In_Frame_Ins	INS	-	TGGCTT	-	BANK1	35_336insTGGG	E112delinsDGL
XH_P44	4	102751320	102751320	Missense_Mutation	SNP	A	C	A	BANK1	c.A336C	p.E112D
XH_P44	4	103964538	103964538	Frame_Shift_Ins	INS	-	GTGTTCACTCTT	-	SLC9B2	sAAAAAAAGAT	p.S297fs
XH_P44	4	103964592	103964592	Nonsense_Mutation	INS	-	TTGATGTCTTAA	-	SLC9B2	TAAGTAAAGAC	V279delinsDIFX
XH_P44	4	104070070	104070070	In_Frame_Ins	INS	-	TTTGTAGTGAAA	-	CENPE	9insTTCTTTAC	T233delinsVSFTTNG
XH_P44	4	106156794	106156794	Frame_Shift_Ins	INS	-	AGGACTCTGG	-	TET2	1696insAGGAC	p.I655fs
XH_P44	4	106588630	106588630	In_Frame_Ins	INS	-	SATTGATGTCAT	-	ARHGEF38	nsAGAAGATTGA	G540delinsQKIDVIFL
XH_P44	4	107237745	107237745	In_Frame_Ins	INS	-	CAC	-	AIMP1	c.41_42insCAC	p.R14delinsRT
XH_P44	4	107237747	107237747	Frame_Shift_Ins	INS	-	CTTTCTC	-	AIMP1	43_44insCTTTC	p.T15fs
XH_P44	4	109861774	109861774	Nonsense_Mutation	INS	-	AAGTGA	-	COL25A1	580_581insTCA	G194delinsVTX
XH_P44	4	109861775	109861775	Missense_Mutation	SNP	C	G	C	COL25A1	c.G580C	p.G194R
XH_P44	4	110791078	110791078	In_Frame_Ins	INS	-	CTGGAGATTCT	-	LRIT3	74insCTCTGGA	A391delinsFLWRF
XH_P44	4	110909010	110909010	Frame_Shift_Ins	INS	-	CATTAAAGATG	-	EGF	nsACTGCATTAA	p.C826fs
XH_P44	4	110909012	110909012	Silent	SNP	T	C	T	EGF	c.T2478C	p.C826C
XH_P44	4	111471041	111471041	Frame_Shift_Ins	INS	-	AT	-	ENPEP	2500_2501insA	p.R834fs
XH_P44	4	113108028	113108028	Frame_Shift_Ins	INS	-	TGAGTCTTCAAC	-	C4orf32	4insTGTGAGTCT	p.F111fs
XH_P44	4	113479438	113479438	Nonsense_Mutation	INS	-	AACAGTAATGG	-	ZGRF1	ATTAGCCATT	A605_L1606delinsX
XH_P44	4	113524836	113524836	Frame_Shift_Ins	INS	-	TGTGAAAATAGT	-	ZGRF1	AACTAATACTATT	p.G940fs
XH_P44	4	114158299	114158299	Frame_Shift_Ins	INS	-	TGCTAGAG	-	ANK2	0_641insTGCTA	p.N214fs
XH_P44	4	114158301	114158301	Frame_Shift_Ins	INS	-	TTAGTTCTAA	-	ANK2	643insTTAGTT	p.N214fs
XH_P44	4	114274888	114274888	Frame_Shift_Ins	INS	-	GT	-	ANK2	5114_5115insG	p.R1705fs
XH_P44	4	114274889	114274889	Frame_Shift_Ins	INS	-	GTTCACT	-	ANK2	15_5116insGTT	p.R1705fs
XH_P44	4	114275730	114275730	Frame_Shift_Ins	INS	-	ACAGGTGAGTG	-	ANK2	sGTGATACAGG	p.E1986fs
XH_P44	4	114279784	114279784	In_Frame_Ins	INS	-	CTAACTGGAGCT	-	ANK2	5011nsATCTAAC	B337delinsKSNWTC

XH_P44	4	114823515	114823515	Frame_Shift_Ins	INS	-	TTTAGAAAACGT	-	ARSJ	15insCCACGTTT	p.K572fs
XH_P44	4	115589422	115589422	Frame_Shift_Ins	INS	-	ACTTACAACATT	-	UGT8	insAACAACTTAC	p.A408fs
XH_P44	4	119239644	119239644	Frame_Shift_Ins	INS	-	ATAAATACACCA	-	PRSS12	39insTTTGGTGT	p.V347fs
XH_P44	4	119665296	119665296	Nonsense_Mutation	INS	-	TTTATGATTATAG	-	SEC24D	845insCCATATAA	p.1616delinsHLX
XH_P44	4	119944683	119944683	Nonsense_Mutation	INS	-	TTTAAATCCACCT	-	SYNP02	205insTTTTTAAT	p.E68_V69delinsEFX
XH_P44	4	119944685	119944685	Frame_Shift_Ins	INS	-	TAAC	-	SYNP02	206_207insTAA	p.V69fs
XH_P44	4	120192991	120192991	Nonsense_Mutation	INS	-	ACATTTAATGTT	-	USP53	CTATCAACATT	p.G660delinsKNTNINIX
XH_P44	4	121738061	121738061	Frame_Shift_Ins	INS	-	TCTTACCTGCAT	-	PRDM5	59insTATGCAGG	p.A223fs
XH_P44	4	121774674	121774674	Nonsense_Mutation	INS	-	ACAGCTCATATA	-	PRDM5	AATTAATATATG	p.V67_L68delinsX
XH_P44	4	121958377	121958377	Frame_Shift_Ins	INS	-	CAGCAACATG	-	NDNF	749insCATGTT	p.F250fs
XH_P44	4	122592728	122592728	Frame_Shift_Ins	INS	-	CCTA	-	ANXA5	694_695insTAG	p.N232fs
XH_P44	4	122605918	122605918	In_Frame_Ins	INS	-	TAA	-	ANXA5	c.102_103insTTA	p.E35delinsLE
XH_P44	4	122605920	122605920	In_Frame_Ins	INS	-	TATCAG	-	ANXA5	00_101insCTGAb	p.D34delinsADN
XH_P44	4	122824178	122824178	Frame_Shift_Ins	INS	-	CCAGGGTAGG	-	TRPC3	2073insCCTAC	p.K691fs
XH_P44	4	123207926	123207926	Frame_Shift_Ins	INS	-	CACA	-	KIAA1109	268_9269insCA	p.R3090fs
XH_P44	4	123207927	123207927	Nonsense_Mutation	INS	-	TTTCCTCTCTCTG	-	KIAA1109	CAACCATTCCTC	p.delinsRYVNHSSFCQ5X
XH_P44	4	123270451	123270451	In_Frame_Ins	INS	-	AAATGAAAAAAA	-	KIAA1109	AACTAAAAAATG	p.73delinsVQLKNEKKVI
XH_P44	4	123978396	123978396	Silent	SNP	C	A	C	SPATA5	c.C2163A	p.S721S
XH_P44	4	123978398	123978398	Frame_Shift_Ins	INS	-	CTTAAAGAGACA	-	SPATA5	nsAGTGCTTAAA	p.I722fs
XH_P44	4	126240277	126240277	Frame_Shift_Ins	INS	-	TGAGATCCATGG	-	FAT4	12insATTAGAGAT	p.E904fs
XH_P44	4	126328275	126328275	Frame_Shift_Ins	INS	-	AGGCTTTTGGC	-	FAT4	AAGGAAGGCTT	p.11850fs
XH_P44	4	126373444	126373444	Frame_Shift_Ins	INS	-	G	-	FAT4	11279_11280ins	p.N3760fs
XH_P44	4	126373446	126373446	Frame_Shift_Ins	INS	-	CCCCCTG	-	FAT4	81_11282insCC	p.R3761fs
XH_P44	4	128564844	128564844	Frame_Shift_Ins	INS	-	G	-	INTU	c.315_316insG	p.K105fs
XH_P44	4	128564845	128564845	Frame_Shift_Ins	INS	-	FAATCTTAATAG	-	INTU	817insTAATCTTA	p.K106fs
XH_P44	4	128694723	128694723	Nonsense_Mutation	INS	-	GAACATTCATAC	-	SLC25A31	6TAGAGAACATT	p.G314delinsGX
XH_P44	4	140262179	140262179	Frame_Shift_Ins	INS	-	ACAGCCATTTA	-	NAA15	359insACAGCC	p.L120fs
XH_P44	4	141310400	141310400	Nonsense_Mutation	INS	-	ATAAAGTGCGC	-	CLGN	GTAATGTGCCAA	p.404delinsICNPVLLFX
XH_P44	4	142155004	142155004	Frame_Shift_Ins	INS	-	CAAGGCATT	-	ZNF330	c.645insCAAGG	p.Y215fs
XH_P44	4	142155006	142155006	Frame_Shift_Ins	INS	-	TT	-	ZNF330	c.646_647insTT	p.E216fs
XH_P44	4	144460047	144460047	In_Frame_Ins	INS	-	CCACATGCAAT	-	SMARCA5	27insCTCCACA	p.1576delinsSPHAM
XH_P44	4	145040848	145040848	In_Frame_Ins	INS	-	CATCAACAGCA	-	GYPA	insCTATGCTGTT	p.42delinsLCLLMIE
XH_P44	4	146031577	146031577	Frame_Shift_Ins	INS	-	AGGAACTCTGGT	-	ABCE1	GCCTTAGGGAATC	p.A198fs
XH_P44	4	146058894	146058894	Frame_Shift_Ins	INS	-	GTGAGAAGTGA	-	OTUD4	2838insCTCACT	p.S946fs
XH_P44	4	148743963	148743963	Frame_Shift_Ins	INS	-	AATGTTTATTCC	-	ARHGAP10	insAAAAATGTTT	p.E80fs
XH_P44	4	148984376	148984376	Frame_Shift_Ins	INS	-	TACTGTCTCTCT	-	ARHGAP10	6insCTTACTGT	p.V702fs
XH_P44	4	149357538	149357538	In_Frame_Ins	INS	-	TAA	-	NR3C2	c.474_475insTTA	p.T159delinsLT
XH_P44	4	149357539	149357539	In_Frame_Ins	INS	-	CATGAAATCCTC	-	NR3C2	nsATTGAGGAT	p.158delinsKLRSICY
XH_P44	4	151023840	151023840	In_Frame_Ins	INS	-	GATTTTATTATG	-	DCLK2	AATTTGATTTTAA	p.11delinsAKFDIFSMII
XH_P44	4	151207182	151207182	Nonsense_Mutation	INS	-	ACTATTAAATT	-	LRBA	TTTAAATAATTTA	p.E2673delinsDFKX
XH_P44	4	151773830	151773830	Frame_Shift_Ins	INS	-	GAGGAAGATGA	-	LRBA	nsTAATCATCATC	p.L71011fs
XH_P44	4	152096054	152096054	Frame_Shift_Ins	INS	-	GAAAAATCAGC	-	SH3D19	2insACTGCTGAT	p.P154fs
XH_P44	4	153691475	153691475	Frame_Shift_Ins	INS	-	TGATTTTITTTG	-	TIGD4	AGACTCAACAA	p.L228fs
XH_P44	4	153793686	153793686	Frame_Shift_Ins	INS	-	GAATCGCTGAG	-	ARFIP1	nsCTGGAAATCG	p.L95fs
XH_P44	4	154471288	154471288	Nonsense_Mutation	INS	-	ACATGGCTATT	-	TMEM131L	4insTGACATGG	p.1101_1102delinsGX
XH_P44	4	154624990	154624990	In_Frame_Ins	INS	-	GTT	-	TLR2	c.931_932insGT	p.T311delinsSS
XH_P44	4	154624991	154624991	Frame_Shift_Ins	INS	-	GAAAAATGGAA	-	TLR2	33insTGAAAAA	p.T311fs
XH_P44	4	155506841	155506841	In_Frame_Ins	INS	-	TTTTTTTGCT	-	FGA	0insCTAGCACACA	p.58delinsSLAQKQT
XH_P44	4	159533353	159533353	In_Frame_Ins	INS	-	CCACTTACCTTA	-	RXFP1	10insACCACCTTA	p.1170delinsLPLTLS
XH_P44	4	159533354	159533354	Splice_Site	SNP	G	A	G	RXFP1	-	-
XH_P44	4	164247537	164247537	Frame_Shift_Ins	INS	-	TCTCGGTTCT	-	NPY1R	170insAGAAACC	p.G57fs
XH_P44	4	166986891	166986891	Frame_Shift_Ins	INS	-	AAGTT	-	TLL1	064_2065insAA	p.L688fs
XH_P44	4	166986893	166986893	Frame_Shift_Ins	INS	-	GAGATTTT	-	TLL1	6_2067insGAG	p.H689fs
XH_P44	4	169312779	169312779	In_Frame_Ins	INS	-	TGTCCTTCTCTT	-	DDX6L	27insTAAAGGA	p.4276delinsVKGRTO
XH_P44	4	169433029	169433029	Nonsense_Mutation	INS	-	GAGGGAGTAC	-	PALLD	nsTGAGAGGGA	p.5_P126delinsSERESX
XH_P44	4	169633057	169633057	In_Frame_Ins	INS	-	ATCTCAGATGGT	-	PALLD	2insGATCTCAG	p.267delinsDLRWF
XH_P44	4	170043403	170043403	Frame_Shift_Ins	INS	-	GTCTGATACAT	-	SH3RF1	nsAGCTCATGTA	p.P398fs
XH_P44	4	170523768	170523768	Nonsense_Mutation	INS	-	TGGACATCTTAA	-	NEK1	CATTTTAAAGATG	p.V5_R6delinsETFX
XH_P44	4	172735762	172735762	In_Frame_Ins	INS	-	ACAAACGCACAC	-	GALNTL6	82insACAAACG	p.M11delinsKRTV
XH_P44	4	172735764	172735764	Missense_Mutation	SNP	G	T	G	GALNTL6	c.G33T	p.M11I
XH_P44	4	174169513	174169513	Frame_Shift_Ins	INS	-	GTGCTCTGTGCT	-	GALNT7	10insGGTGTCTC	p.L170fs
XH_P44	4	174312549	174312549	In_Frame_Ins	INS	-	AGTGATTGCTC	-	SCRG1	17insAGGCAAT	p.A70delinsQAIHF
XH_P44	4	177113918	177113918	Nonsense_Mutation	INS	-	AGGGAATTACT	-	SPATA4	nsAAGAAATTAAT	p.V184delinsKEVISLX
XH_P44	4	177632805	177632805	Splice_Site	INS	-	TGAAATTACTG	-	VEGFC	-	-
XH_P44	4	178262750	178262750	Frame_Shift_Ins	INS	-	TCGAAAGTCAC	-	NEIL3	24insCTCGAAA	p.F275fs
XH_P44	4	183245376	183245376	In_Frame_Ins	INS	-	AGTCTCATTTGG	-	TENM3	204insAGTCTCA	p.H68delinsQVSLA
XH_P44	4	184182361	184182361	Missense_Mutation	SNP	G	A	G	WWC2	c.G1585A	p.A529T
XH_P44	4	185606776	185606776	Nonsense_Mutation	INS	-	ATAAGCTGAAAG	-	PRIMPOL	ATTACAATAGCT	p.7_D328delinsYKLQX
XH_P44	4	186111525	186111525	Nonsense_Mutation	INS	-	ATTTTATTATTG	-	CFAP97	TCCCAACAATAA	p.6_Q277delinsHSQXQ
XH_P44	4	186329132	186329132	Nonsense_Mutation	INS	-	TAATCTTAATTTT	-	UFSP2	TGAAAAAAAT	p.60delinsQKMKMKNX
XH_P44	4	186380337	186380337	Frame_Shift_Ins	INS	-	AGCAACAAT	-	CCDC110	c.1293insATTG	p.S431fs
XH_P44	4	186510900	186510900	Frame_Shift_Ins	INS	-	GAGAGAAGACA	-	SORBS2	86insAATTGCTC	p.D962fs
XH_P44	4	187004325	187004325	Nonsense_Mutation	INS	-	GGGAGAATGAG	-	TLR3	5insTAAGGGAG	p.495_D496delinsVX
XH_P44	4	187004769	187004769	Frame_Shift_Ins	INS	-	AAATCGAGAA	-	TLR3	1930insAAATC	p.R643fs
XH_P44	4	187004936	187004936	Nonsense_Mutation	INS	-	TGGAAGTGTGT	-	TLR3	nsATGCTGGAAG	p.A700delinsRCWKVCX
XH_P44	4	187173309	187173309	Frame_Shift_Ins	INS	-	CAACAATCTCAA	-	KLKB1	4insTTACACAA	p.W428fs
XH_P44	4	187179342	187179342	Nonsense_Mutation	INS	-	GTAGAAAGTTAC	-	KLKB1	nsAATAGTAGAA	p.31_A632delinsKIIX
XH_P44	4	187524855	187524855	Frame_Shift_Ins	INS	-	AGGATACTGAA	-	FAT1	nsAATACATTCA	p.Q3609fs
XH_P44	4	187525108	187525108	Frame_Shift_Ins	INS	-	CTGTTCTCTGT	-	FAT1	10572insACAGA	p.Q3524fs
XH_P44	4	187539825	187539825	Nonsense_Mutation	INS	-	TTCTATACCTTA	-	FAT1	nsACTGTAAGG	p.2639delinsTVKX
XH_P44	4	187557905	187557905	Frame_Shift_Ins	INS	-	nsAGTGTITTTGTG	-	FAT1	8806insTCACAA	p.E1269fs
XH_P44	4	187627869	187627869	Nonsense_Mutation	INS	-	TTTTTTTTTTTAA	-	FAT1	nsATGGTTAAAAA	p.38_E1039delinsDGX
XH_P44	4	189012748	189012748	Missense_Mutation	SNP	T	G	T	TRIML2	c.A1093C	p.K365Q
XH_P44	4	189012749	189012749	Frame_Shift_Ins	INS	-	GTGTAAAA	-	TRIML2	91_1092insTTTT	p.E364fs
XH_P44	5	453963	453963	Frame_Shift_Ins	INS	-	TCTCTCTCCCTTT	-	EXOC3	844insTTCTCTCT	p.L281fs
XH_P44	5	5462595	5462595	Frame_Shift_Ins	INS	-	ATTTCAGGAGA	-	ICE1	nsAGGATATTTC	p.K1050fs
XH_P44	5	5466606	5466606	Nonsense_Mutation	INS	-	nsAGATTATCTAA	-	ICE1	3insCAAGGATT	p.18_K2019delinsPKIIX
XH_P44	5	6616929	6616929	In_Frame_Ins	INS	-	AAATCTTCA	-	NSUN2	5_827insTGAAG	p.A276delinsVKIS
XH_P44	5	9043089	9043089	In_Frame_Ins	INS	-	CCTATTTTCTCTG	-	SEMA5A	ACTTGTCAGAAA	p.delinsQWTCQKNRMTIK
XH_P44	5	10426559	10426559	Missense_Mutation	SNP	G	A	G	MARCH6	c.G2116A	p.A706T
XH_P44	5	10426560	10426560	Nonsense_Mutation	INS	-	TAGTCAAAGTGG	-	MARCH6	AAAAATAGTCA	p.A706delinsAQKX
XH_P44	5	10973751	10973751	In_Frame_Ins	INS	-	TTTTTTTCTCTCT	-	CTNND2	TTTGCAGGAGA	p.7delinsTKFAGEKNKTE
XH_P44	5	10988294	10988294	Frame_Shift_Ins	INS	-	5CTGCTGAGCAG	-	CTNND2	61insTCTGCTC	p.E754fs
XH_P44	5	13770865	13770865	Frame_Shift_Ins	INS	-	ATGTAGTGGG	-	DNAH5	9598insCCCA	p.A3200fs
XH_P44	5	13770866	13770866	Silent	SNP	C	T	C	DNAH5	c.G9597A	p.L3199L
XH_P44	5	13770955	13770955	Nonsense_Mutation	INS	-	GGCTTAGGG	-	DNAH5	7_9508insCCCTA	p.S3170delinsPX
XH_P44	5	13814918	13814918	Nonsense_Mutation	INS	-	TGCAATTTTATG	-	DNAH5	CATTAGCATAAA	p.42_A2343delinsEHX
XH_P44	5	13901442	13901442	Frame_Shift_Ins	INS	-	G	-	DNAH5	c.1970_1971ins	p.K657fs

XH_P44	5	13901443	13901443	Frame_Shift_Ins	INS	-	TTGTAAGGCAG	-	DNAH5	1970insTCTGCC	p.K657fs
XH_P44	5	14497977	14497977	Frame_Shift_Ins	INS	-	CACTGCACTCA	-	TRIO	8042insTCACTG	p.Y2681fs
XH_P44	5	14497979	14497979	Nonsense_Mutation	SNP	T	A	T	TRIO	c.T8043A	p.Y2681X
XH_P44	5	14673813	14673813	Frame_Shift_Ins	INS	-	TGAT	-	OTULIN	215_216insTGA	p.E72fs
XH_P44	5	14673815	14673815	Nonsense_Mutation	INS	-	CTAATAAAAAA	-	OTULIN	218insTCAATAAR73	G74delinsX
XH_P44	5	16458679	16458679	Nonsense_Mutation	INS	-	GGTTATGATTC	-	ZNF622	1109insGAATC6370	E371delinsX
XH_P44	5	16458681	16458681	In_Frame_Ins	INS	-	AAT	-	ZNF622	1106_1107insA	p.P369delinsPF
XH_P44	5	23526662	23526662	In_Frame_Ins	INS	-	SATTGCGTTCTA	-	PRDM9	nsGAGTGATTGC89	delinsGVIAFYML
XH_P44	5	31302397	31302397	In_Frame_Ins	INS	-	TATGTACCTATT	-	CDH6	2insGTATGTAC332	E53delinsMYLLI
XH_P44	5	31323114	31323114	Frame_Shift_Ins	INS	-	AGGAAAGATT	-	CDH6	2073insAGGAA	p.D691fs
XH_P44	5	31323115	31323115	Missense_Mutation	SNP	C	A	C	CDH6	c.C2073A	p.D691E
XH_P44	5	31515280	31515280	Frame_Shift_Ins	INS	-	GGGCTGGATAA	-	DROSHA	994insTTTATCCA	p.K332fs
XH_P44	5	32097459	32097459	Frame_Shift_Ins	INS	-	GCTTTTC	-	PDZD2	20_7921insGCT	p.G2640fs
XH_P44	5	32263251	32263251	Frame_Shift_Ins	INS	-	CATTTTCCCGA	-	MTMR12	insATTCCGGGA	p.V227fs
XH_P44	5	32780891	32780891	Nonsense_Mutation	INS	-	TAAATCTTAAC	-	NPR3	sATTCCTAAATT0	M421delinsAFLNSX
XH_P44	5	34823627	34823627	Frame_Shift_Ins	INS	-	CTTCT	-	RAI14	593_1594insCT	p.L531fs
XH_P44	5	34823628	34823628	Nonsense_Mutation	INS	-	CTAAGGACTTCT	-	RAI14	insCACACTAAGG32	E53delinsAHX
XH_P44	5	34823793	34823793	Frame_Shift_Ins	INS	-	GGACTTCTTC	-	RAI14	1760insGGACT	p.K587fs
XH_P44	5	34823795	34823795	Missense_Mutation	SNP	A	T	A	RAI14	c.A1761T	p.K587N
XH_P44	5	34922844	34922844	Nonsense_Mutation	INS	-	GGAGTAAGCTT	-	BRX1	GATATGGAGTAGA	p.G161delinsAX
XH_P44	5	34998834	34998834	Nonsense_Mutation	INS	-	AAATAAATCCTA	-	AGXT2	insCTAAATTAGGA37	A438delinsTNX
XH_P44	5	35712913	35712913	Splice_Site	INS	-	ATTTGGTAGTGG	-	SPEF2	-	-
XH_P44	5	35874593	35874593	Frame_Shift_Ins	INS	-	AAAGGCATTGA	-	IL7R	50insAAAAGGC	p.F250fs
XH_P44	5	35921153	35921153	Frame_Shift_Ins	INS	-	CCTTGTGACA	-	CAPSL	70insTGTGACA	p.D24fs
XH_P44	5	35921155	35921155	Missense_Mutation	SNP	G	T	G	CAPSL	c.C68A	p.T23N
XH_P44	5	36037921	36037921	Frame_Shift_Ins	INS	-	TG	-	UGT3A2	1170_1171insC	p.K391fs
XH_P44	5	36037922	36037922	In_Frame_Ins	INS	-	ACTGTATTTTCT	-	UGT3A2	GTCTAGAAAAA	OdelinsPCPRKYSFNLK
XH_P44	5	36168512	36168512	Nonsense_Mutation	INS	-	CTTCAAGCATT	-	SKP2	ACATACTTCAAG	L213delinsNTYFKHX
XH_P44	5	36985167	36985167	Nonsense_Mutation	INS	-	TAATGCTGGCC	-	NIPBL	86insATTAAATGp	R629delinsHX
XH_P44	5	36985930	36985930	In_Frame_Ins	INS	-	TTTTTCTCTGT	-	NIPBL	9insAGGTTTTTT	B83delinsSGFFSVD
XH_P44	5	37020911	37020911	Frame_Shift_Ins	INS	-	AGAAACTTTTTT	-	NIPBL	51insCTAAGAAA	p.C1754fs
XH_P44	5	37022450	37022450	Frame_Shift_Ins	INS	-	A	-	NIPBL	c.5532_5533ins	p.Q1844fs
XH_P44	5	37022451	37022451	Frame_Shift_Ins	INS	-	ACACTTCATGGC	-	NIPBL	34insAAACACTT	p.L1845fs
XH_P44	5	37169029	37169029	In_Frame_Ins	INS	-	AATAAT	-	C5orf42	996_7097insATT	L2366delinsHYF
XH_P44	5	37169030	37169030	Frame_Shift_Ins	INS	-	TTGTAGCTGGGC	-	C5orf42	996insTGCCCAAG	p.L2366fs
XH_P44	5	37213825	37213825	Nonsense_Mutation	INS	-	GCATAGTATCTC	-	C5orf42	GTGTTTCAGATAp	S920delinsMFQILCX
XH_P44	5	37341270	37341270	Nonsense_Mutation	INS	-	TATTGGGTCTT	-	NUP155	1168insAAGAC	90_R391delinsKTQX
XH_P44	5	37396543	37396543	In_Frame_Ins	INS	-	GGGTATTTTTTA	-	WDR70	CAACTGGGTATT	delinsPINNWVFFNFK
XH_P44	5	38481905	38481905	Frame_Shift_Ins	INS	-	AGCCACTTCAA	-	LIFR	3086insTTGAG	p.R1029fs
XH_P44	5	38510801	38510801	In_Frame_Ins	INS	-	CTGGAGTGGGC	-	LIFR	ACCCCCCACTC	252delinsTPPHSRRI
XH_P44	5	38904577	38904577	Frame_Shift_Ins	INS	-	AA	-	OSMR	1257_1258insA	p.S419fs
XH_P44	5	38950085	38950085	Frame_Shift_Ins	INS	-	C	-	RICTOR	c.3864dupG	p.P1289fs
XH_P44	5	38950087	38950087	In_Frame_Ins	INS	-	ACAGTTTTGAGT	-	RICTOR	3863insACTCAA	1288delinsDSKLL
XH_P44	5	39311365	39311365	Nonsense_Mutation	INS	-	AGTCTTAAGAA	-	C9	insGTATTCTTA9	Y330delinsVFLRLX
XH_P44	5	40854259	40854259	Frame_Shift_Ins	INS	-	AACTCTGTTA	-	CARD6	2826insAACTC	p.F942fs
XH_P44	5	40980011	40980011	Frame_Shift_Ins	INS	-	CTCGAGCTTAG	-	C7	2351insCTCTGA	p.A784fs
XH_P44	5	41160411	41160411	Frame_Shift_Ins	INS	-	AGATAAG	-	C6	16_1517insCTT	p.N506fs
XH_P44	5	41160413	41160413	Missense_Mutation	SNP	G	T	G	C6	c.C1515A	p.N505K
XH_P44	5	41201725	41201725	Nonsense_Mutation	INS	-	GAGGGGGTTTA	-	C6	ATAAAATAAACp	P79_180delinsIKX
XH_P44	5	41201727	41201727	Missense_Mutation	SNP	C	T	C	C6	c.G233A	p.C78Y
XH_P44	5	43175139	43175139	Frame_Shift_Ins	INS	-	TCATGTGT	-	ZNF131	9_940insTCATG	p.H313fs
XH_P44	5	43299044	43299044	Nonsense_Mutation	INS	-	SAGAAGATATTA	-	HMGCS1	AGAGTTAATATC	N8_A9delinsKESX
XH_P44	5	52161585	52161585	Missense_Mutation	SNP	G	T	G	ITGA1	c.G558T	p.W186C
XH_P44	5	52397275	52397275	Frame_Shift_Ins	INS	-	TATTCATGTATTA	-	MOC52	AAAAATAATACA	p.P97fs
XH_P44	5	54618290	54618290	Missense_Mutation	SNP	A	T	A	SKIV2L2	c.A270T	p.L90f
XH_P44	5	54618291	54618291	Frame_Shift_Ins	INS	-	TTGTATTTTCATT	-	SKIV2L2	TGCATTTGTATT	p.S91fs
XH_P44	5	54624627	54624627	In_Frame_Ins	INS	-	ACA	-	SKIV2L2	1503_504insAC	p.T168delinsTQ
XH_P44	5	54624629	54624629	Frame_Shift_Ins	INS	-	CAGGC	-	SKIV2L2	505_506insCAG	p.V169fs
XH_P44	5	54641023	54641023	In_Frame_Ins	INS	-	AAT	-	SKIV2L2	1107_1108insA	p.K369delinsKN
XH_P44	5	54641024	54641024	Frame_Shift_Ins	INS	-	AAACATAAGAT	-	SKIV2L2	AAAGCAAAACAT	p.G370fs
XH_P44	5	54931444	54931444	In_Frame_Ins	INS	-	STACTACATGCC	-	SLC38A9	20insCTGGCATC	340delinsTWHVVH
XH_P44	5	54952590	54952590	In_Frame_Ins	INS	-	AACCAA	-	SLC38A9	20_521insTTGG	H174delinsLGY
XH_P44	5	54952591	54952591	Frame_Shift_Ins	INS	-	CAATAGGTTGT	-	SLC38A9	520insCAACCC	p.H174fs
XH_P44	5	56189482	56189482	In_Frame_Ins	INS	-	GGATTTTCTGCT	-	MAP3K1	GTGGGAGGATT	5delinsQKWEDFLLSKS
XH_P44	5	57751390	57751390	Frame_Shift_Del	DEL	T	-	T	PLK2	c.1601delA	p.H534fs
XH_P44	5	59284391	59284391	In_Frame_Ins	INS	-	AGG	-	PDE4D	c.195_196insCC	p.E66delinsPE
XH_P44	5	59284393	59284393	Frame_Shift_Ins	INS	-	ACATTTCAT	-	PDE4D	194insATAGAA	p.S65fs
XH_P44	5	60790102	60790102	Frame_Shift_Ins	INS	-	GCCTTCAAC	-	ZSWIM6	8_1199insGCC	p.K400fs
XH_P44	5	60827543	60827543	Frame_Shift_Ins	INS	-	AG	-	ZSWIM6	2236_2237insA	p.L746fs
XH_P44	5	60827545	60827545	Frame_Shift_Ins	INS	-	TCTT	-	ZSWIM6	2238_2239insT	p.L746fs
XH_P44	5	60982895	60982895	Nonsense_Mutation	INS	-	CACTGCAAAAGA	-	C5orf64	insGAACACTGCA	Y75_N76delinsX
XH_P44	5	61677063	61677063	Nonsense_Mutation	INS	-	ACAGACAGTATA	-	KIF2A	TTATTCAAGAG	655delinsKIHLYSQTQVX
XH_P44	5	63496763	63496763	Frame_Shift_Ins	INS	-	CAGTAAAGCAGC	-	RNF180	insGACAGTAA	p.V43fs
XH_P44	5	63496765	63496765	Missense_Mutation	SNP	T	C	T	RNF180	c.T131C	p.I44T
XH_P44	5	63665567	63665567	In_Frame_Ins	INS	-	AGCCCATTAAT	-	RNF180	6insTAAAGCCCA	569delinsLKPIKFN
XH_P44	5	64020259	64020259	In_Frame_Ins	INS	-	ATATAGACA	-	SREK1IP1	9_420insTGTC	K140delinsNVYVM
XH_P44	5	64314065	64314065	Frame_Shift_Ins	INS	-	ATGTCTGGAGT	-	CWC27	7insAACATGTC	p.L446fs
XH_P44	5	65058897	65058897	In_Frame_Ins	INS	-	AGTATACTGGG	-	NLN	ATCAAAGTATAC	38delinsTYQSILGYNL
XH_P44	5	65350105	65350105	In_Frame_Ins	INS	-	CTTGCTCCTGAC	-	ERBIN	60insACTTGCTC	V987delinsDLLTI
XH_P44	5	66456392	66456392	Frame_Shift_Ins	INS	-	TC	-	MAST4	2974_2975insT	p.K992fs
XH_P44	5	66456393	66456393	Frame_Shift_Ins	INS	-	AGAGATGAGAG	-	MAST4	insGAACAGAGA	p.K992fs
XH_P44	5	67591280	67591280	In_Frame_Ins	INS	-	TATTTGTTATTA	-	PIK3R1	insACGTATTTCG	230delinsKRICYUL
XH_P44	5	68471290	68471290	In_Frame_Ins	INS	-	AAAGTCCTAATA	-	CCNB1	1010insAAAGTC	V337delinsESPNM
XH_P44	5	70806381	70806381	In_Frame_Ins	INS	-	GTCTCATTTTCA	-	BDP1	3463insGTCTCC	S1154delinsSVSIS
XH_P44	5	70922538	70922538	Frame_Shift_Ins	INS	-	TTAAAAACAAA	-	MCCC2	697insTTAAAA	p.I232fs
XH_P44	5	70922540	70922540	Nonsense_Mutation	INS	-	CTCTAAATGTTT	-	MCCC2	99insCCTCTAA	A233_R234delinsVLX
XH_P44	5	71489938	71489938	Frame_Shift_Ins	INS	-	GAAGAGAAAGAA	-	MAP1B	TTAAGAGAAAG	p.G126fs
XH_P44	5	71493616	71493616	Frame_Shift_Ins	INS	-	TTCAATA	-	MAP1B	56_4057insTTCA	p.T1352fs
XH_P44	5	71493617	71493617	Frame_Shift_Ins	INS	-	AGACTCGGATCT	-	MAP1B	58insCAGACTC	p.D1353fs
XH_P44	5	71495564	71495564	Frame_Shift_Ins	INS	-	GTGTGTGTTCTG	-	MAP1B	5insTTCTGTGTT	p.G2002fs
XH_P44	5	71528338	71528338	Frame_Shift_Ins	INS	-	ATGTGTGTTTAT	-	MRPS27	ATACAATAAAC	p.V119fs
XH_P44	5	72383914	72383914	Frame_Shift_Ins	INS	-	ACCAAGGG	-	FCHO2	1_2332insACCA	p.C777fs
XH_P44	5	72383916	72383916	Nonstop_Mutation	SNP	G	T	G	FCHO2	c.G2333T	p.X778L
XH_P44	5	72469306	72469306	Frame_Shift_Ins	INS	-	CTTAGAGTGGAG	-	TMEM174	37insTCTTAGAG	p.L79fs
XH_P44	5	72857071	72857071	Frame_Shift_Ins	INS	-	AGAAGGAAAT	-	ANKRA2	nsACAGAATTC	p.V111fs
XH_P44	5	72864425	72864425	Nonsense_Mutation	INS	-	TACAAGATGAA	-	UTP15	GAATCTACAAG	K104delinsKCESTRX
XH_P44	5	72873828	72873828	Frame_Shift_Ins	INS	-	ATTCAAAATACAC	-	UTP15	5TTCATTCAA	p.R158fs
XH_P44	5	74400422	74400422	In_Frame_Ins	INS	-	TACAATAAAAA	-	ANKRD31	1insGCCTTTTTT	1597delinsKPFLLYL

XH_P44	5	75428097	75428097	Missense_Mutation	SNP	C	G	C	SV2C	c.C522G	p.F174L
XH_P44	5	75428098	75428098	Frame_Shift_Ins	INS	-	TTCATAC	-	SV2C	23_524insTTCA	p.V175fs
XH_P44	5	76733243	76733243	Frame_Shift_Ins	INS	-	TTGTTTTGAGG	-	WDR41	1insTTCCCTCAA	p.L337fs
XH_P44	5	78602281	78602281	Frame_Shift_Ins	INS	-	ATCATTGACCC	-	JMY	insAGTATCAC	p.Q655fs
XH_P44	5	78610668	78610668	Missense_Mutation	SNP	A	G	A	JMY	c.A2653G	p.R885G
XH_P44	5	79025124	79025124	In_Frame_Ins	INS	-	TATCTTCCTTT	-	CMYA5	537insTATCTTC	T179delinsTIFFL
XH_P44	5	79029672	79029672	Frame_Shift_Ins	INS	-	GGTT	-	CMYA5	084_5085insGG	p.P1695fs
XH_P44	5	79029674	79029674	Frame_Shift_Ins	INS	-	TTCTTAT	-	CMYA5	86_5087insTTC	p.A1696fs
XH_P44	5	79030813	79030813	Frame_Shift_Ins	INS	-	GGACTAAGAC	-	CMYA5	6insCTAGGACT	p.P2075fs
XH_P44	5	79031674	79031674	Nonsense_Mutation	INS	-	TAATCTTCCTTA	-	CMYA5	7insCCATAATCT	F2362delinsFPX
XH_P44	5	79032237	79032237	Nonsense_Mutation	INS	-	GTAGATCT	-	CMYA5	9_7650insGTAC	G550_G2551delinsEX
XH_P44	5	79033774	79033774	Nonsense_Mutation	INS	-	TAATGTTTTATG	-	CMYA5	GCTCTTTAATG	062delinsNLLFNVLX
XH_P44	5	79034051	79034051	Nonsense_Mutation	INS	-	GAATAAATGAT	-	CMYA5	GGGCTGAATA	P3156delinsNCLNKK
XH_P44	5	79734470	79734470	Frame_Shift_Ins	INS	-	TG	-	ZFYVE16	1966_1967insT	p.P656fs
XH_P44	5	79734471	79734471	In_Frame_Ins	INS	-	ATTGAAATATAT	-	ZFYVE16	1968insATTGAA	P656delinsPLKYI
XH_P44	5	80600774	80600774	In_Frame_Ins	INS	-	ACA	-	ZCHC9	198_199insAC	p.E66delinsET
XH_P44	5	80600775	80600775	Frame_Shift_Ins	INS	-	GCTATATC	-	ZCHC9	9_200insGCTAT	p.Y67fs
XH_P44	5	80640733	80640733	Frame_Shift_Ins	INS	-	TCTCTTCTCTC	-	ACOT12	901insGAGAGA	p.P301fs
XH_P44	5	80640734	80640734	Frame_Shift_Ins	INS	-	CTTCCTT	-	ACOT12	9_900insAAGG	p.F300fs
XH_P44	5	82815488	82815488	Frame_Shift_Ins	INS	-	CATTTGTGGTTG	-	VCAN	364insCCATTTG	p.1455fs
XH_P44	5	82815945	82815945	Frame_Shift_Ins	INS	-	GTTACAGGGAA	-	VCAN	821insAGTTTACA	p.S607fs
XH_P44	5	82816166	82816166	Frame_Shift_Ins	INS	-	TGTGGATGGTG	-	VCAN	042insGTGTGG	p.T681fs
XH_P44	5	82816354	82816354	Missense_Mutation	SNP	G	C	G	VCAN	c.G2229C	p.M743I
XH_P44	5	82816508	82816508	In_Frame_Ins	INS	-	TCTCTTGTATT	-	VCAN	4insATCTCTTCT	795delinsDLFLYFI
XH_P44	5	82816716	82816716	Frame_Shift_Ins	INS	-	FAATATTTTCATC	-	VCAN	TGTTGTAATAT	p.Q864fs
XH_P44	5	82835102	82835102	In_Frame_Ins	INS	-	TGCTGACTGTGA	-	VCAN	3320insTGCTGA	P1107delinsLTVT
XH_P44	5	82836286	82836286	Frame_Shift_Ins	INS	-	TGTGGTCTACTA	-	VCAN	4insGTTTGTGG	p.M1501fs
XH_P44	5	82836795	82836795	Frame_Shift_Ins	INS	-	ATTTTTATCCGA	-	VCAN	insTAGTATTTTT	p.E1671fs
XH_P44	5	86703989	86703989	Nonsense_Mutation	INS	-	ATAATCATCTCC	-	CNNH	ACAACGAGGATC	58delinsCYNNEDDYEFX
XH_P44	5	86707128	86707128	Frame_Shift_Ins	INS	-	ATTCAAGTCTC	-	CNNH	AAAGTGAGACT	p.1451fs
XH_P44	5	89938763	89938763	Frame_Shift_Ins	INS	-	CTTGGTTTCC	-	ADGRV1	2459insCTTGG	p.N820fs
XH_P44	5	89981675	89981675	Frame_Shift_Ins	INS	-	TCTACTATTATT	-	ADGRV1	TTTCCCTCTACTA	p.G2118fs
XH_P44	5	90074280	90074280	Frame_Shift_Ins	INS	-	CCCCAATCTCC	-	ADGRV1	12704insCCCC	p.Y4235fs
XH_P44	5	90670060	90670060	Frame_Shift_Ins	INS	-	TAGATGTGCC	-	ARRDC3	44insGGGGGAC	p.F82fs
XH_P44	5	94204054	94204054	In_Frame_Ins	INS	-	AGCCCAATGTAT	-	MCTP1	sAAATGATACA	40delinsKMIHWLRC
XH_P44	5	94764392	94764392	Nonsense_Mutation	INS	-	TGGTAGATATA	-	FAM81B	sGAGTTGGTAG	F248_V249delinsX
XH_P44	5	94814134	94814134	Frame_Shift_Ins	INS	-	TATTTTGGGGTT	-	TTC37	insCACAAACCC	p.V1409fs
XH_P44	5	95099314	95099314	Frame_Shift_Ins	INS	-	CAGTTTAACTTC	-	RHOBTB3	2insGATCAGTTT	p.T384fs
XH_P44	5	95234086	95234086	Nonsense_Mutation	INS	-	ACTATTAACATG	-	ELL2	383insTCATGTT	K461delinsNHVX
XH_P44	5	95730719	95730719	Frame_Shift_Ins	INS	-	C	-	PCSK1	1732_1733ins	p.I578fs
XH_P44	5	95730720	95730720	Frame_Shift_Ins	INS	-	GGTAGACAATG	-	PCSK1	32insCTACATTG	p.I578fs
XH_P44	5	98215312	98215312	Frame_Shift_Ins	INS	-	TTAATTTGCTGT	-	CHD1	81insAAACAGCA	p.Q1061fs
XH_P44	5	98224935	98224935	In_Frame_Ins	INS	-	TGTGCTCTTCT	-	CHD1	2188insGAAAG	L730delinsRKAPL
XH_P44	5	98224936	98224936	Frame_Shift_Ins	INS	-	AATGGTCTCAGT	-	CHD1	187insAACTGAG	p.I729fs
XH_P44	5	100192011	100192011	Nonsense_Mutation	INS	-	TTCCGTATTTT	-	ST8SIA4	ATTATAAAATA	B9_F199delinsVTIHK
XH_P44	5	10288111	10288111	Frame_Shift_Ins	INS	-	TCTCTGACTGA	-	NUDT12	sACCAATACAGT	p.T344fs
XH_P44	5	102894870	102894870	Frame_Shift_Ins	INS	-	GTTGT	-	NUDT12	451_452insACA	p.F151fs
XH_P44	5	102894871	102894871	In_Frame_Ins	INS	-	TGTATTTGC	-	NUDT12	0_451insGCAAA	F151delinsANTF
XH_P44	5	108380427	108380427	In_Frame_Ins	INS	-	CTCTATGGCTAG	-	FER	ACTTTACTCTATG	8delinsSNFTLWLGIH
XH_P44	5	108714443	108714443	Frame_Shift_Ins	INS	-	AAAAGTTAGA	-	PIA2	1_745insTCTAAC	p.V249fs
XH_P44	5	110097366	110097366	Frame_Shift_Ins	INS	-	TGCTTGTCTAT	-	SLC25A46	899insTCGTTT	p.G300fs
XH_P44	5	110461423	110461423	Nonsense_Mutation	INS	-	TCCTTTTATACCI	-	WDR36	CAGTTTTCCTTT	I880delinsITVFLYPKK
XH_P44	5	110461425	110461425	Frame_Shift_Ins	INS	-	TATAT	-	WDR36	638_2639insTA	p.I880fs
XH_P44	5	111504782	111504782	Nonsense_Mutation	INS	-	TCATCAGGTTA	-	EPB41L4A	sTATTACTAACCT	87_I588delinsLLLT
XH_P44	5	111600688	111600688	Nonsense_Mutation	INS	-	AC	-	EPB41L4A	c.458_459insGT	I153_K154delinsX
XH_P44	5	111600689	111600689	Nonsense_Mutation	INS	-	ATTTTAACTCTA	-	EPB41L4A	8insTTTAGAGT	p.V153delinsFX
XH_P44	5	112174356	112174356	Frame_Shift_Ins	INS	-	ACTTCTGTCT	-	APC	3012insACTCT	p.D1004fs
XH_P44	5	112174358	112174358	Missense_Mutation	SNP	A	C	A	APC	c.A3013C	p.T1005P
XH_P44	5	112176928	112176928	Frame_Shift_Ins	INS	-	TGACTTTTCCCT	-	APC	84insTGTGACTT	p.A1861fs
XH_P44	5	112179748	112179748	Frame_Shift_Ins	INS	-	CCCACGGT	-	APC	3_8404insCCCA	p.K2801fs
XH_P44	5	112203228	112203228	Nonsense_Mutation	INS	-	ATTGAATATCAC	-	SRP19	ATCAAAATTGAAT	9_K120delinsKSSNX
XH_P44	5	112915359	112915359	Frame_Shift_Ins	INS	-	AAAA	-	YTHDC2	421_2422insAA	p.L807fs
XH_P44	5	112915360	112915360	In_Frame_Ins	INS	-	ATCACAATGTAA	-	YTHDC2	2423insATCAC	A808delinsDHMLN
XH_P44	5	113698631	113698631	In_Frame_Ins	INS	-	ACC	-	KCNN2	159_160insAC	p.A53delinsAT
XH_P44	5	113831641	113831641	Missense_Mutation	SNP	A	G	A	KCNN2	c.A458G	p.E153G
XH_P44	5	114462484	114462484	Nonsense_Mutation	INS	-	TATCGCTGAGT	-	TRIM36	sAGAACTACTCA	80delinsRTLSDMX
XH_P44	5	114956251	114956251	Nonsense_Mutation	INS	-	CATGCACTAACT	-	TMED7	TCATCAGTTAGT	7_F108delinsSSVSAX
XH_P44	5	114956253	114956253	Missense_Mutation	SNP	T	C	T	TMED7	c.A317G	p.Y106C
XH_P44	5	115469821	115469821	Frame_Shift_Ins	INS	-	GT	-	COMMD10	c.414_415insGT	p.K138fs
XH_P44	5	115469822	115469822	Frame_Shift_Ins	INS	-	ATCTT	-	COMMD10	415_416insATC	p.L139fs
XH_P44	5	118502444	118502444	Nonsense_Mutation	INS	-	AAATATATTATG	-	DMXL1	CAGTAAAAATTA	L1703delinsPSKNYIRX
XH_P44	5	118970251	118970251	In_Frame_Ins	INS	-	sAGGTTTCTGGT	-	FAM170A	8insGGAGGTTT	4223delinsRRFLVD
XH_P44	5	122911588	122911588	Nonsense_Mutation	INS	-	AAAGAAATAAA	-	CSNK1G3	66insAAAGAA	A89_Y90delinsQKKX
XH_P44	5	122911590	122911590	In_Frame_Ins	INS	-	GAAATTGTT	-	CSNK1G3	7_268insGAAAT	p.P89delinsPEIV
XH_P44	5	123980191	123980191	Frame_Shift_Ins	INS	-	ACAG	-	ZNF608	868_3869insCT	p.S1290fs
XH_P44	5	123980192	123980192	In_Frame_Ins	INS	-	TATCTCTGGTACG	-	ZNF608	3868insCGTACC	S1290delinsRTRIS
XH_P44	5	123983778	123983778	In_Frame_Ins	INS	-	ATGGATGCCA	-	ZNF608	9insAGCTTGGC	6767delinsSLASIFG
XH_P44	5	125896792	125896792	Frame_Shift_Ins	INS	-	CTTCTTCTGTTT	-	ALDH7A1	2AGCAACAGAA	p.G299fs
XH_P44	5	126156797	126156797	In_Frame_Ins	INS	-	ATAAAACAATTC	-	LMNB1	7insATAAAAC	242delinsKNKTIH
XH_P44	5	126734469	126734469	Frame_Shift_Ins	INS	-	TAATTGTTTCA	-	MEGF10	2insAATAATTGT	p.S254fs
XH_P44	5	126771176	126771176	Frame_Shift_Ins	INS	-	AACAGCATCCT	-	MEGF10	2100insAACAG	p.S700fs
XH_P44	5	126860553	126860553	Frame_Shift_Ins	INS	-	GAAGGAA	-	PRRC1	4_435insGAAGG	p.H145fs
XH_P44	5	126889577	126889577	Frame_Shift_Ins	INS	-	GGTATTTTTAGA	-	PRRC1	AATTAAGGTATT	p.X463delinsX
XH_P44	5	127640737	127640737	Frame_Shift_Ins	INS	-	ACTACTATGCTC	-	FBN2	insACAGAGACA	p.S1904fs
XH_P44	5	127670914	127670914	Nonsense_Mutation	INS	-	GTTGTATATTTA	-	FBN2	3921insATAAAT	307_C1308delinsRX
XH_P44	5	127670916	127670916	Missense_Mutation	SNP	G	T	G	FBN2	c.C3919A	p.R1307S
XH_P44	5	130897714	130897714	Frame_Shift_Ins	INS	-	AAACATGATAC	-	RAPGEF6	GTAAGTGTATC	p.R103fs
XH_P44	5	132228738	132228738	Frame_Shift_Ins	INS	-	AAAA	-	AF4	2379_2380insTT	p.P794fs
XH_P44	5	132228739	132228739	Nonsense_Mutation	INS	-	AATTAGTCTTCC	-	AF4	AATAAGGGAAG	A.K793delinsKKX
XH_P44	5	132270014	132270014	Nonsense_Mutation	INS	-	SACTACGTGAAG	-	AF4	43insGCTTCACG	48_M249delinsCFTX
XH_P44	5	133644068	133644068	Frame_Shift_Ins	INS	-	CCCCAGTGTGAG	-	CDKL3	40insCCTCACAC	p.K80fs
XH_P44	5	134344570	134344570	Missense_Mutation	SNP	C	T	C	CATSPER3	c.C175T	p.R239W
XH_P44	5	137426529	137426529	Nonsense_Mutation	INS	-	CCAAAGGTTAG	-	WNT8A	sAAGACCAAGC	C293_L294delinsX
XH_P44	5	137502370	137502370	Frame_Shift_Ins	INS	-	GGCATT	-	BRD8	10_711insAAAT	p.F237fs
XH_P44	5	137502372	137502372	Frame_Shift_Del	DEL	AC	-	AC	BRD8	c.708_709del	p.Q236fs
XH_P44	5	137525579	137525579	Frame_Shift_Ins	INS	-	A	-	CDC23	1440_1441ins	p.T481fs
XH_P44	5	137525580	137525580	Frame_Shift_Ins	INS	-	ATTTTAAAGTGC	-	CDC23	440insTGCAC	p.L480fs
XH_P44	5	137626429	137626429	Frame_Shift_Ins	INS	-	AGAGAAAGTAT	-	CDC25C	TAAGAAATACT	p.G182fs

XH P44	5	137722077	137722077	Missense_Mutation	SNP	A	C	A	KDM3B	c.A1147C	p.T383P
XH P44	5	137722078	137722078	In_Frame_Ins	INS	-	GCCTTCTCTCTT	-	KDM3B	sCTCTATGCTTCT	83delinsTSMLSLFFF
XH P44	5	138209140	138209140	Frame_Shift_Ins	INS	-	CTCCACCTTT	-	LRRTM2	1110insAAAGT	p.M370fs
XH P44	5	138643806	138643806	Nonsense_Mutation	INS	-	CAGGAGTAATC	-	MATR3	703insCAGGAG	34_F23delinsSQEX
XH P44	5	138764248	138764248	Nonsense_Mutation	INS	-	ACTTGATTTTACC	-	DNAJC18	2insAGGTAAAA	p.G118delinsRX
XH P44	5	139267073	139267073	Frame_Shift_Ins	INS	-	ACTCC	-	NRG2	723_724insGGA	p.M242fs
XH P44	5	139715456	139715456	Splice_Site	INS	-	AGGAGTCTTTT	-	HBEGF	.	.
XH P44	5	139906599	139906599	Nonsense_Mutation	INS	-	ATTCTGATTTAAA	-	ANKHD1	28insATATTCGT	76_L1677delinsKYSYX
XH P44	5	139907597	139907597	In_Frame_Ins	INS	-	ATTAAAGTCTCTC	-	ANKHD1	228insAATTAAAG	34_743delinsKLVNSF
XH P44	5	139908590	139908590	In_Frame_Ins	INS	-	CGGGTA	-	ANKHD1	59_6060insCGG	S2020delinsSGY
XH P44	5	140048341	140048341	Frame_Shift_Ins	INS	-	G	-	WDR55	c.525_526insG	p.A175fs
XH P44	5	140048342	140048342	In_Frame_Ins	INS	-	TCTCCTTACCCA	-	WDR55	527insTCTCCTT	L176delinsSLPM
XH P44	5	140073250	140073250	Frame_Shift_Ins	INS	-	AATCTATGTT	-	HARS2	184insAATCTA	p.K61fs
XH P44	5	140501829	140501829	Frame_Shift_Ins	INS	-	CATTCAATTCCA	-	PCDH84	nsAGACATTCAA	p.L83fs
XH P44	5	140515496	140515496	Frame_Shift_Ins	INS	-	TATCAAGCTGCA	-	PCDH85	81insATATCAAG	p.F160fs
XH P44	5	140552673	140552673	In_Frame_Ins	INS	-	GGATCAGTCTT	-	PCDH87	58insTTGGATCA	L86delinsLWLSLS
XH P44	5	140580121	140580121	Frame_Shift_Ins	INS	-	ACTT	-	PCDH811	774_775insACT	p.G258fs
XH P44	5	140580123	140580123	In_Frame_Ins	INS	-	TAGTAA	-	PCDH811	76_777insTAGTb	S259delinsSSK
XH P44	5	140580677	140580677	Frame_Shift_Ins	INS	-	TATTT	-	PCDH811	330_1331insTA	p.V444fs
XH P44	5	140580679	140580679	In_Frame_Ins	INS	-	GGATTTGGGACTG	-	PCDH811	33insTGGGATTG	444delinsVWDWTG
XH P44	5	140699137	140699137	In_Frame_Ins	INS	-	GACAGC	-	TA7F	74_475insGCTG	S159delinsAVS
XH P44	5	140699139	140699139	Missense_Mutation	SNP	T	A	T	TA7F	c.A473T	p.E158V
XH P44	5	140699485	140699485	Frame_Shift_Ins	INS	-	GAAGAGAAGGT	-	TA7F	127insACCTTC	p.L43fs
XH P44	5	140735784	140735784	Frame_Shift_Ins	INS	-	AGTGGCTTTTAC	-	PCDHGA4	111insCAGTGGG	p.D370fs
XH P44	5	140783732	140783732	Nonsense_Mutation	INS	-	TATTTCAATAAAAT	-	PCDHGA9	sATTTCCATTTCAs	T406delinsYHFIKX
XH P44	5	140802046	140802046	Nonsense_Mutation	INS	-	AGAAGAGGTTGA	-	PCDHGA11	ATTAATAGAGAG	p.S418delinsNX
XH P44	5	140810395	140810395	Silent	SNP	G	A	G	PCDHGA12	c.G69A	p.L23L
XH P44	5	140870409	140870409	Frame_Shift_Ins	INS	-	AGATGTTTGTGT	-	PCDHGCS	603insAGATGT	p.V534fs
XH P44	5	145859650	145859650	Frame_Shift_Ins	INS	-	TTGTTACAAAGT	-	TCERG1	CAAATATTGTTTA	p.K606fs
XH P44	5	146258290	146258290	Missense_Mutation	SNP	A	T	A	PPP2R2B	c.T58A	p.C20S
XH P44	5	146991919	146991919	Frame_Shift_Ins	INS	-	TAGTTTCCCCCTT	-	JAKMIP2	3insAGGAAGGGG	p.E767fs
XH P44	5	147019223	147019223	Nonsense_Mutation	INS	-	TTTTAAAGATAG	-	JAKMIP2	CTCAACTATCTT	5459delinsVLNVLX
XH P44	5	147661734	147661734	Frame_Shift_Ins	INS	-	TATCATCTCTTCA	-	SPINK13	CATCCTATCATC	p.P59fs
XH P44	5	148730535	148730535	Nonsense_Mutation	INS	-	AAGAACAATAGT	-	GRPEL2	AACCCACAGAAC	3_T124delinsTEPKNX
XH P44	5	148897414	148897414	Nonsense_Mutation	INS	-	TTTGTATGATTTT	-	CSNK1A1	AACAAAAATCAK	73delinsRIKTKQSSKX
XH P44	5	148999976	148999976	Frame_Shift_Ins	INS	-	TCTTGAACCTCA	-	ARHGEF37	5insCTTCTTGAA	p.V318fs
XH P44	5	150110652	150110652	In_Frame_Ins	INS	-	AATTGTTTGAAA	-	DCTN4	507insTTTCAAA	E169delinsDFKQL
XH P44	5	150110654	150110654	Nonsense_Mutation	INS	-	GTCAACTTTCTA	-	DCTN4	AAATATAGAAAG	E169delinsKIX
XH P44	5	150113019	150113019	Missense_Mutation	SNP	A	T	A	DCTN4	c.T448A	p.Y150N
XH P44	5	150113021	150113021	Frame_Shift_Ins	INS	-	GTAGGCACCTG	-	DCTN4	446insCAGTGC	p.E149fs
XH P44	5	150666954	150666954	In_Frame_Ins	INS	-	TTGTAAAAAGCTA	-	SLC36A3	ATAATTAGCTTT	87delinsLISFYNLW
XH P44	5	150925130	150925130	Missense_Mutation	SNP	G	T	G	FAT2	c.C5558A	p.P1853H
XH P44	5	150925131	150925131	Frame_Shift_Ins	INS	-	CTGAATCCTGCT	-	FAT2	557insAAGCAG	p.P1853fs
XH P44	5	150932844	150932844	Missense_Mutation	SNP	A	T	A	FAT2	c.T4050A	p.D1350E
XH P44	5	151166162	151166162	Splice_Site	INS	-	TAATTTTCTT	-	G3BP1	.	.
XH P44	5	151166163	151166163	Splice_Site	INS	-	TTTT	-	G3BP1	.	.
XH P44	5	153407813	153407813	Frame_Shift_Ins	INS	-	TTTTTTTGGGGG	-	FAM114A2	16insCCCCCAA	p.A106fs
XH P44	5	154251381	154251381	Nonsense_Mutation	INS	-	AGTTTATCTGAT	-	CNOT8	gAGTAGTTTAT	p.F83delinsX
XH P44	5	154394256	154394256	Frame_Shift_Ins	INS	-	TAAAGATGGCAT	-	KIF4B	3insTGTAAGAT	p.D279fs
XH P44	5	156378688	156378688	Nonsense_Mutation	INS	-	GTATATTAGTCT	-	TIMD4	sTAGCAGACTAA	172_T173delinsX
XH P44	5	156770439	156770439	In_Frame_Ins	INS	-	CACCTC	-	FINDC9	55_106insAGG	W36delinsRVW
XH P44	5	157181948	157181948	In_Frame_Ins	INS	-	GACCAAATTCCTT	-	LSM11	AAAAAGACCAA	3delinsYRKRPNLSLM
XH P44	5	158139316	158139316	In_Frame_Ins	INS	-	GTGCTAAAGGCA	-	EBF1	402insGGTGCCCT	/434delinsVVPLAP
XH P44	5	158697583	158697583	Frame_Shift_Ins	INS	-	AAACATCATCAT	-	UBLCP1	ATTAAACAACATC	p.V127fs
XH P44	5	159519665	159519665	Nonsense_Mutation	INS	-	CACAGATTTTCTA	-	PWWP2A	92insCTAGAAAp	V664delinsYX
XH P44	5	159520834	159520834	Frame_Shift_Ins	INS	-	AAAAGGTAGTAA	-	PWWP2A	5TTGCACTACTAA	p.P275fs
XH P44	5	159521013	159521013	In_Frame_Ins	INS	-	TAAATGTAAAA	-	PWWP2A	sACTGTTTTTAC	215delinsHCFYVYHT
XH P44	5	159855658	159855658	Nonsense_Mutation	INS	-	GGAGGTAAGTGT	-	PTTG1	CATTAGGAAGTb	P194delinsLTFIRKX
XH P44	5	161116127	161116127	Nonsense_Mutation	INS	-	AAATAAAATAAT	-	GABRA6	5GAGAAAAATAA	33_K134delinsKRKX
XH P44	5	161580348	161580348	Frame_Shift_Ins	INS	-	TGGGCGG	-	GABRG2	78_1379insTGG	p.Y460fs
XH P44	5	161580350	161580350	Frame_Shift_Ins	INS	-	ATCAA	-	GABRG2	380_1381insAT	p.Y460fs
XH P44	5	162900462	162900462	Nonsense_Mutation	INS	-	AGTATTAATAAA	-	HMMR	sACTGAGTATTA	E181delinsENDX
XH P44	5	162943708	162943708	In_Frame_Ins	INS	-	AATAAA	-	MAT2B	11_712insAATA	K237delinsKNK
XH P44	5	162943710	162943710	Nonsense_Mutation	INS	-	TTAAAGCTGACT	-	MAT2B	ATAATTTAAAGC	38_M239delinsSKX
XH P44	5	166802420	166802420	Nonsense_Mutation	INS	-	TGGTTCCTAGGG	-	TENM2	3insGTTGGTCC	8_N149delinsEVGSX
XH P44	5	167631567	167631567	Frame_Shift_Ins	INS	-	ATGTGTA	-	TENM2	59_3070insATG	p.D1023fs
XH P44	5	167631569	167631569	Frame_Shift_Ins	INS	-	GG	-	TENM2	3071_3072insG	p.F1024fs
XH P44	5	167921652	167921652	Frame_Shift_Ins	INS	-	TCAGATACGTGC	-	RARS	7insTATCAGATA	p.K192fs
XH P44	5	168180101	168180101	Missense_Mutation	SNP	A	T	A	SLIT3	c.T1832A	p.M611K
XH P44	5	168180102	168180102	Missense_Mutation	SNP	T	C	T	SLIT3	c.A1831G	p.M611V
XH P44	5	169309770	169309770	Frame_Shift_Ins	INS	-	TTTTTTTTCAT	-	FAM196B	1133insGTGAAA	p.H378fs
XH P44	5	169309771	169309771	Missense_Mutation	SNP	G	T	G	FAM196B	c.C1132A	p.H378N
XH P44	5	169310639	169310639	Frame_Shift_Ins	INS	-	AGGTTCCAGAGT	-	FAM196B	nsTATCATCTGG	p.K88fs
XH P44	5	169685158	169685158	Frame_Shift_Ins	INS	-	5GAAATGACGGT	-	LCP2	3insTACCCCTGA	p.P328fs
XH P44	5	170238999	170238999	Frame_Shift_Ins	INS	-	TTTAGAGGCTCA	-	GABRP	sAAAAAGTTTAGA	p.1354fs
XH P44	5	170239001	170239001	Missense_Mutation	SNP	C	G	C	GABRP	c.C1062G	p.I354M
XH P44	5	171638989	171638989	Nonsense_Mutation	INS	-	TCCTTTTTTA	-	UBTD2	550insTAAAAA	p.A184delinsX
XH P44	5	171638991	171638991	Frame_Shift_Ins	INS	-	GTTCCTGTGTGT	-	UBTD2	548insACAACA	p.A183fs
XH P44	5	172517807	172517807	Frame_Shift_Ins	INS	-	CTTTTGTTC	-	CREBRF	626insCTTTTG	p.S209fs
XH P44	5	172517809	172517809	Silent	SNP	A	C	A	CREBRF	c.A627C	p.S209S
XH P44	5	173370054	173370054	Splice_Site	INS	-	C	-	CPEB4	.	.
XH P44	5	174936187	174936187	Missense_Mutation	SNP	G	T	G	SFXN1	c.G317T	p.C106F
XH P44	5	174936189	174936189	In_Frame_Ins	INS	-	TTATGCTCTGGG	-	SFXN1	AAAGTTTATGC	107delinsKSLCSGWV
XH P44	5	175933915	175933915	Frame_Shift_Ins	INS	-	ACTCT	-	FAF2	302_1303insAC	p.T434fs
XH P44	5	176395894	176395894	Nonsense_Mutation	INS	-	5CTGTAAATTAAG	-	UIMC1	ATCATCTCTTAAT	B8_P289delinsNHPX
XH P44	5	176684025	176684025	Frame_Shift_Ins	INS	-	TTCATAAGAAAA	-	NSD1	4840insTTCATA	p.K1613fs
XH P44	5	176719038	176719038	Nonsense_Mutation	INS	-	GTAGCAATAAT	-	NSD1	sGATACGTAGC	14_K2115delinsTDTX
XH P44	5	176795910	176795910	Frame_Shift_Ins	INS	-	CTCT	-	RG514	1042_1043insCT	p.G348fs
XH P44	5	176795911	176795911	In_Frame_Ins	INS	-	ATT	-	RG514	1043_1044insA	p.G348delinsGF
XH P44	5	176816722	176816722	Frame_Shift_Ins	INS	-	G	-	SLC34A1	1019_1020ins	p.P340fs
XH P44	5	176816723	176816723	In_Frame_Ins	INS	-	5GGGTTTTTTTT	-	SLC34A1	1021insAGGGGT	P340delinsPRGFFL
XH P44	5	178310019	178310019	Frame_Shift_Ins	INS	-	CTGAGACTAAAT	-	ZNF354B	sTTGGCTGAGAC	p.F189fs
XH P44	5	178359093	178359093	Nonsense_Mutation	INS	-	AAGGGAGGATC	-	ZFP2	0insGTAAGGGA	p.H260delinsQX
XH P44	5	178994554	178994554	Nonsense_Mutation	INS	-	AAAAAGACACCT	-	RUFY1	insCAGAAAGAA	4_L125delinsHRKDTX
XH P44	5	179048323	179048323	Frame_Shift_Ins	INS	-	AAATGGATTGGC	-	HNRNP1	CAACACCAATC	p.F58fs
XH P44	5	179193739	179193739	Frame_Shift_Ins	INS	-	TGGG	-	MAML1	728_1729insTG	p.G576fs
XH P44	5	179193740	179193740	In_Frame_Ins	INS	-	TGG	-	MAML1	1729_1730insTG	p.Q577delinsLE
XH P44	5	179393963	179393963	In_Frame_Ins	INS	-	TGTATAATTAAT	-	RNF130	TTCTTATTAATT	B31delinsFLLIHKH

XH_P44	5	179994992	179994992	Frame_Shift_Ins	INS	-	GGCAC	-	CNOT6	D16_1017insGG	p.I339fs
XH_P44	5	179994993	179994993	Nonsense_Mutation	INS	-	AAATCACATTAC	-	CNOT6	018insTAAATCA	339_E340delinsIX
XH_P44	5	180166732	180166732	Frame_Shift_Ins	INS	-	CCTGTATTTCTG	-	OR2Y1	AACTTCAGAAAT	p.S109fs
XH_P44	5	180277987	180277987	Frame_Shift_Ins	INS	-	AAGAACTGTAA	-	ZFP62	TCACATTTCACAC	p.E170fs
XH_P44	5	180335794	180335794	Frame_Shift_Ins	INS	-	TAAATCATCAAA	-	BTN18	9insGATAAATCA	p.K86fs
XH_P44	5	180666130	180666130	Frame_Shift_Ins	INS	-	TTGTGTTTTTTT	-	RACK1	AAACAAAAAAAC	p.H191fs
XH_P44	5	180687313	180687313	Missense_Mutation	SNP	C	A	C	TRIM52	c.G502T	p.D168Y
XH_P44	6	6167798	6167798	In_Frame_Ins	INS	-	TGAAAGAAAGTA	-	F13A1	801insTTTACTCT	601delinsFTSKE
XH_P44	6	7570756	7570756	Frame_Shift_Ins	INS	-	AAACACTCAAC	-	DSP	662insAAAAACC	p.M545fs
XH_P44	6	7581613	7581613	Frame_Shift_Ins	INS	-	GTCACTCTCAC	-	DSP	5191insGTCAAT	p.E1730fs
XH_P44	6	7584273	7584273	Frame_Shift_Ins	INS	-	CG	-	DSP	4981_4982insC	p.I1661fs
XH_P44	6	10530051	10530051	Frame_Shift_Ins	INS	-	TTTTTCCTTTTAA	-	GCNT2	8insTATTTTTTCC	p.T303fs
XH_P44	6	10796305	10796305	Nonsense_Mutation	INS	-	GAGATCACTTAA	-	MAK	insAATTTTAAAGT	57_P358delinsNFKX
XH_P44	6	10990615	10990615	Nonsense_Mutation	INS	-	GTTCAGAGGGCT	-	ELOVL2	TAAAAAGCCCTC	89delinsHIKSPLTSKI
XH_P44	6	11103982	11103982	Frame_Shift_Ins	INS	-	TTCCCAAGATAA	-	ERVFRD-1	2insCAATTATCT	p.Q521fs
XH_P44	6	11104421	11104421	Missense_Mutation	SNP	T	G	T	ERVFRD-1	c.A1123C	p.T375P
XH_P44	6	11104422	11104422	Nonsense_Mutation	INS	-	AATCAATCAGG	-	ERVFRD-1	122insTTCCTGA	p.I374delinsISX
XH_P44	6	11575773	11575773	Frame_Shift_Ins	INS	-	TTTCATCAAAAC	-	TMEM170B	79insTTTCATCA	p.S126fs
XH_P44	6	12125367	12125367	Frame_Shift_Ins	INS	-	TGTAATGTTGG	-	HIVEP1	340insTTGTAA	p.L1780fs
XH_P44	6	12130040	12130040	In_Frame_Ins	INS	-	CTTTACAACTCTC	-	HIVEP1	125insGCTTTTAC	2042delinsGFTTSY
XH_P44	6	12164681	12164681	Missense_Mutation	SNP	T	G	T	HIVEP1	c.T8144G	p.V2715G
XH_P44	6	12164683	12164683	Missense_Mutation	SNP	A	C	A	HIVEP1	c.A8146C	p.I2716L
XH_P44	6	17130966	17130966	In_Frame_Ins	INS	-	ATT	-	STMND1	685_686insAT	p.P229delinsHS
XH_P44	6	17130967	17130967	Frame_Shift_Ins	INS	-	ATGGCTTCTCT	-	STMND1	687insATGGCT	p.P229fs
XH_P44	6	17662291	17662291	Frame_Shift_Ins	INS	-	TTTA	-	NUP153	225_1226insTA	p.E409fs
XH_P44	6	17662292	17662292	Nonsense_Mutation	INS	-	CTAGTTAAACA	-	NUP153	CCATAACTTGTGT	E409delinsCGPX
XH_P44	6	18258273	18258273	Nonsense_Mutation	INS	-	AGACTGAGGTG	-	DEK	AGTATATACCTC	delinsKSFNKVIPOSAQX
XH_P44	6	20546738	20546738	Frame_Shift_Ins	INS	-	ATGAAGTACTAT	-	CDKAL1	tsAGGATGAAGT	p.S53fs
XH_P44	6	20548930	20548930	Nonsense_Mutation	INS	-	GTAAGTTTCATT	-	CDKAL1	AAAAAGTAAGT	T95delinsKKVSIEX
XH_P44	6	20781478	20781478	Frame_Shift_Ins	INS	-	GTCAAAAGGAA	-	CDKAL1	insACTGTCAAA	p.I207fs
XH_P44	6	24448394	24448394	In_Frame_Ins	INS	-	AGGGAATTTGTG	-	GPLD1	1489insCCACA	S497delinsPQFP
XH_P44	6	24448395	24448395	Frame_Shift_Ins	INS	-	TGCGTTTT	-	GPLD1	7_1488insAAAA	p.M496fs
XH_P44	6	24658876	24658876	Frame_Shift_Ins	INS	-	TC	-	TDP2	c.337_338insGA	p.M113fs
XH_P44	6	24658878	24658878	Nonsense_Mutation	INS	-	AATTAAGATGAT	-	TDP2	insGCAATCATCT	S112delinsRQSSX
XH_P44	6	24830892	24830892	Frame_Shift_Ins	INS	-	CTCTTCAGTGTG	-	RIPOR2	351insTCACACT	p.P784fs
XH_P44	6	25594728	25594728	Frame_Shift_Ins	INS	-	TAGATTTAAGA	-	CARMIL1	3093insTAGAT	p.T1031fs
XH_P44	6	25594730	25594730	Frame_Shift_Ins	INS	-	CTGTGATT	-	CARMIL1	4_3095insCTGT	p.K1032fs
XH_P44	6	25850824	25850824	In_Frame_Ins	INS	-	GTATGATT	-	SLC17A3	1_622insAAATC	P208delinsKSYP
XH_P44	6	25983601	25983601	Frame_Shift_Ins	INS	-	TTCTGTGAT	-	TRIM38	4_1085insTTCC	p.G362fs
XH_P44	6	26043791	26043791	Nonsense_Mutation	INS	-	CTGTTTCAGTTC	-	HIST1H2BB	CTAGAACTGAA	R32_S33delinsLX
XH_P44	6	26091594	26091594	In_Frame_Ins	INS	-	GAACATGTG	-	HFE	9_130insGAACAB	S43delinsSEHV
XH_P44	6	26104218	26104218	Frame_Shift_Ins	INS	-	TTGCAAGTTGAA	-	HIST1H4C	4insTTTGCAAGT	p.G15fs
XH_P44	6	26108065	26108065	Nonsense_Mutation	INS	-	ACTCCTAAAAT	-	HIST1H1T	257insAGTTTTTA	p.L86delinsQFX
XH_P44	6	26285680	26285680	Nonsense_Mutation	INS	-	CATTTTCAACCA	-	HIST1H4H	CTTTGGTTGAA	16_K17delinsAFGX
XH_P44	6	26637759	26637759	Frame_Shift_Ins	INS	-	AAGA	-	ZNF322	1022_1023insTC	p.K341fs
XH_P44	6	26637760	26637760	In_Frame_Ins	INS	-	GAGGACAAA	-	ZNF322	1_1022insTTTG	K341delinsCPQ
XH_P44	6	27368202	27368202	Nonsense_Mutation	INS	-	ACTTTATATGAG	-	ZNF391	sGCAACTTTTATA	p.Y18delinsX
XH_P44	6	27419498	27419498	In_Frame_Ins	INS	-	SAAACCTTATAA	-	ZNF184	ATTACAGTTATAA	4delinsHYSYKVSLOQY
XH_P44	6	28093439	28093439	Missense_Mutation	SNP	A	G	A	ZSCAN16	c.A218G	p.E73G
XH_P44	6	28093440	28093440	In_Frame_Ins	INS	-	GATTTATCC	-	ZSCAN16	9_220insGATTTC	p.E73delinsEDLS
XH_P44	6	28097373	28097373	Frame_Shift_Ins	INS	-	TCACAATGTAA	-	ZSCAN16	693insTCACAA	p.R231fs
XH_P44	6	28227697	28227697	Nonsense_Mutation	INS	-	CTGCATAGCAG	-	NKAPL	9insTTCTGCATA	S183delinsSSAX
XH_P44	6	28244185	28244185	Frame_Shift_Ins	INS	-	ATATATACCACC	-	ZSCAN26	ATTAAATATATA	p.A42fs
XH_P44	6	28359148	28359148	Frame_Shift_Ins	INS	-	AAAAAATGCTAT	-	ZSCAN12	9insCTGATAGCA	p.C307fs
XH_P44	6	34496565	34496565	Nonsense_Mutation	INS	-	TCCTCCTTCTCTG	-	PACIN1	368insTCTCCCTQ	23_Q124delinsSLXX
XH_P44	6	35803246	35803246	Frame_Shift_Ins	INS	-	CCTTTTTCAGG	-	SRPK1	1803insCCTGAA	p.T601fs
XH_P44	6	35838123	35838123	In_Frame_Ins	INS	-	ATAAGAATATG	-	SRPK1	AGATCCATATT	9delinsYDKIHILKIPP
XH_P44	6	36181799	36181799	Frame_Shift_Ins	INS	-	GC	-	BRPF3	2625_2626insG	p.R875fs
XH_P44	6	36359586	36359586	In_Frame_Ins	INS	-	CAG	-	PXT1	365_366insCTG	Q122delinsHW
XH_P44	6	36359587	36359587	Frame_Shift_Ins	INS	-	TTGTGTAA	-	PXT1	4_365insTTCAA	p.Q122fs
XH_P44	6	36454923	36454923	Frame_Shift_Ins	INS	-	TTTCTTTACAGG	-	KCTD20	AATTTTTCCTTTA	p.Q245fs
XH_P44	6	36931061	36931061	Nonsense_Mutation	INS	-	GAGTCTGATGCT	-	PI16	944insGAGTCTCTG	p.I315delinsRVX
XH_P44	6	38560523	38560523	Nonsense_Mutation	INS	-	TCATTTTCC	-	BTBD9	466insGGAAP	K156delinsGKX
XH_P44	6	38560525	38560525	Nonsense_Mutation	INS	-	TT	-	BTBD9	c.463_464insAA	155_K156delinsX
XH_P44	6	38709604	38709604	Nonsense_Mutation	INS	-	ATACCAATAAT	-	DNAH8	TGTTCAATACCA	p.G412delinsVX
XH_P44	6	38831741	38831741	Frame_Shift_Ins	INS	-	AAACGGGA	-	DNAH8	3_6404insAAAC	p.V2135fs
XH_P44	6	38877467	38877467	Frame_Shift_Ins	INS	-	CAGAGGGGTT	-	DNAH8	9688insCAGAG	p.T3229fs
XH_P44	6	39046967	39046967	Missense_Mutation	SNP	T	A	T	GLP1R	c.T1034A	p.I345N
XH_P44	6	39046969	39046969	Nonsense_Mutation	INS	-	CACACGCAT	-	GLP1R	5_1037insCACAA	K346delinsTHAX
XH_P44	6	42224783	42224783	Frame_Shift_Ins	INS	-	TTGCCAGGTG	-	TRERF1	2454insCACCT	p.S818fs
XH_P44	6	42796516	42796516	Nonsense_Mutation	INS	-	AAAAAATAAACA	-	BICRAL	46insAAAAAAT	149_T150delinsX
XH_P44	6	42890790	42890790	Silent	SNP	T	C	T	PTCR	c.T84C	p.S28S
XH_P44	6	42890793	42890794	Frame_Shift_Del	DEL	GG	-	GG	PTCRA	c.87_88del	p.L29fs
XH_P44	6	42976481	42976481	Frame_Shift_Ins	INS	-	TTGGACATTAT	-	PPP2R5D	760insTTGGAC	p.E253fs
XH_P44	6	42986651	42986651	Frame_Shift_Ins	INS	-	ATTGTAGCCAAC	-	KLHDC3	372insATTGTAG	p.R291fs
XH_P44	6	43025943	43025943	Frame_Shift_Ins	INS	-	ATGTAATTAATA	-	MRPL2	25insTTTTTAAT	p.P42fs
XH_P44	6	43146590	43146590	Missense_Mutation	SNP	G	T	G	SRF	c.G789T	p.Q263H
XH_P44	6	43146591	43146591	In_Frame_Ins	INS	-	TGTGTGTGTATG	-	SRF	791insTGTGTGT	264delinsMCVVV
XH_P44	6	43310598	43310598	Frame_Shift_Ins	INS	-	ATACCCCTATCTG	-	ZNF318	092insCAGATA	p.E1031fs
XH_P44	6	43415570	43415570	Missense_Mutation	SNP	G	A	G	ABCC10	c.G3770A	p.G1257D
XH_P44	6	44219849	44219849	In_Frame_Ins	INS	-	GAC	-	HSP90AB1	1576_1577insGp	K526delinsRQ
XH_P44	6	44278174	44278174	Frame_Shift_Ins	INS	-	STTGAGAACTCA	-	AAR52	6insTCTGAGTTC	p.A252fs
XH_P44	6	44413494	44413494	Nonsense_Mutation	INS	-	AAAAATACACTA	-	CDC5L	nsAAGCAAAAAT	B2_K733delinsKAKIHX
XH_P44	6	45515011	45515011	Nonsense_Mutation	INS	-	GTAGGTGTGGT	-	RUNX2	1428insGTAGG	H76_M477delinsRX
XH_P44	6	45515013	45515013	Missense_Mutation	SNP	A	G	A	RUNX2	c.A1429G	p.M477V
XH_P44	6	46521510	46521510	In_Frame_Ins	INS	-	ACACTTTTCTCTG	-	CYP39A1	6insTCAGAGAA	272delinsPQRKVF
XH_P44	6	46658946	46658946	Frame_Shift_Ins	INS	-	TGCAAGTCTCTT	-	TDRD6	insGTCTTGCAAC	p.L1027fs
XH_P44	6	46660165	46660165	Frame_Shift_Ins	INS	-	CATATCATATCT	-	TDRD6	sCAGCACATATC	p.M1434fs
XH_P44	6	46660894	46660894	Frame_Shift_Ins	INS	-	TATAATAATGTC	-	TDRD6	GTGCCCTATAAT	p.I1677fs
XH_P44	6	46806790	46806790	Frame_Shift_Ins	INS	-	CCCAATTTCAAG	-	MEP1A	2159insTCCCAT	p.G720fs
XH_P44	6	46806792	46806792	Frame_Shift_Ins	INS	-	TGTAT	-	MEP1A	160_2161insTG	p.G720fs
XH_P44	6	46825982	46825982	In_Frame_Ins	INS	-	TTTTATCAC	-	ADGRF5	7_3658insGTGA	S122delinsVKS
XH_P44	6	46825984	46825984	Nonsense_Mutation	INS	-	CATTATAATTTA	-	ADGRF5	656insCTAAATTT	19_S122delinsTKLX
XH_P44	6	46846133	46846133	In_Frame_Ins	INS	-	GTAGAATGGAAC	-	ADGRF5	1046insCTTCCA	V349delinsASILL
XH_P44	6	46846134	46846134	In_Frame_Ins	INS	-	GAAGGAAAAAT	-	ADGRF5	045insTATTTTT	V349delinsLFLPV
XH_P44	6	46977555	46977555	Nonsense_Mutation	INS	-	CGAGGCTTTGTT	-	ADGRF1	nsCCAAAAACAA	S540delinsSKTKPRX
XH_P44	6	47678563	47678563	Frame_Shift_Ins	INS	-	TTCTGGAGATTT	-	ADGRF4	sTTCATTCTGGA	p.K81fs
XH_P44	6	47847624	47847624	Frame_Shift_Ins	INS	-	TCCTGTCTGGTC	-	PTCHD4	6insAGACCAGA	p.T319fs

XH_P44	6	49803150	49803150	Frame_Shift_Ins	INS	-	A	-	CRISP1	c.628_629insT	p.P210fs
XH_P44	6	49803151	49803151	In_Frame_Ins	INS	-	GAGATGTCT	-	CRISP1	7_628insAGACA	P210delinsRHP
XH_P44	6	50696983	50696983	Nonsense_Mutation	INS	-	ATCATGACTAAG	-	TFAP2D	842insATCATGA	R281delinsHDX
XH_P44	6	51619698	51619698	Frame_Shift_Ins	INS	-	TTATTTTAAAG	-	PKHD1	insTATTCCTTAA	p.D2894fs
XH_P44	6	51619700	51619700	Missense_Mutation	SNP	A	T	A	PKHD1	c.T8679A	p.H2893Q
XH_P44	6	51751987	51751987	Frame_Shift_Ins	INS	-	CTGTGCAATTTT	-	PKHD1	053insGAAAAAT	p.Q2351fs
XH_P44	6	51936934	51936934	Frame_Shift_Ins	INS	-	C	-	PKHD1	c.580_581insG	p.I194fs
XH_P44	6	51936936	51936936	Frame_Shift_Ins	INS	-	CCTTATCTTT	-	PKHD1	579insAAAGAT	p.I193fs
XH_P44	6	51947315	51947315	Frame_Shift_Ins	INS	-	TCATGTGAATA	-	PKHD1	AAAGCATATTCA	p.P52fs
XH_P44	6	52548932	52548932	Nonsense_Mutation	INS	-	ATAAAGTGCTCT	-	TMEM14A	0insGATAAAGT	p.I77delinsRX
XH_P44	6	54002934	54002934	Nonsense_Mutation	INS	-	CCAACCTTGAGG	-	MLIP	sCTCTTCCCAAC	T8_5679delinsPLFPTX
XH_P44	6	54806276	54806276	Frame_Shift_Ins	INS	-	TCCTCCAAGTTA	-	FAM83B	508insCTCCTCC	p.S836fs
XH_P44	6	55638995	55638995	In_Frame_Ins	INS	-	AAGAATAAAA	-	BMP5	8_879insTTTAT	G293delinsGLFL
XH_P44	6	55922554	55922554	Frame_Shift_Ins	INS	-	AG	-	COL21A1	c.968_969insCT	p.G323fs
XH_P44	6	55922555	55922555	Nonsense_Mutation	INS	-	CATTAATTAAT	-	COL21A1	8insAGATTTAAT	323_1324delinsEIX
XH_P44	6	56350271	56350271	Splice_Site	INS	-	GATTATTCGAG	-	DST	-	-
XH_P44	6	56366034	56366034	Splice_Site	INS	-	TTTCAAGTTTAT	-	DST	-	-
XH_P44	6	56371530	56371530	Frame_Shift_Ins	INS	-	AGGA	-	DST	427_11428insT	p.G3810fs
XH_P44	6	56371531	56371531	Frame_Shift_Ins	INS	-	GGACTGC	-	DST	26_11427insGC	p.L3809fs
XH_P44	6	56483825	56483825	Frame_Shift_Ins	INS	-	TCAGGAAGAAAT	-	DST	5007insGATGTTCT	p.Q1669fs
XH_P44	6	56963866	56963866	Nonsense_Mutation	INS	-	CACCCCTGTAGA	-	ZNFA51	4insTACACCCCT	B8_139delinsPTPLX
XH_P44	6	64431415	64431415	Frame_Shift_Ins	INS	-	T	-	EYS	c.8511dupA	p.E2838fs
XH_P44	6	64431417	64431417	Frame_Shift_Ins	INS	-	GTTGCTGTGTA	-	EYS	0insAGTACACA	p.I2837fs
XH_P44	6	66205201	66205201	Nonsense_Mutation	INS	-	GGACACATTATT	-	EYS	03insAAATAAT	Q35_P36delinsKX
XH_P44	6	69349283	69349283	Frame_Shift_Ins	INS	-	ACATAATACATG	-	ADGRB3	17insACATAAT	p.V239fs
XH_P44	6	70410746	70410746	Frame_Shift_Ins	INS	-	TAGCTGTATCTT	-	LMBRD1	099insAAAGATA	p.Y367fs
XH_P44	6	70962004	70962004	Frame_Shift_Ins	INS	-	T	-	COL9A1	-1049_1050ins	p.A350fs
XH_P44	6	70962005	70962005	Nonsense_Mutation	INS	-	TCTTCCATTCAT	-	COL9A1	049insAATGAAT	350_P351delinsEX
XH_P44	6	71234299	71234299	Frame_Shift_Ins	INS	-	GATTCTG	-	FAM135A	13_1414insGAT	p.E471fs
XH_P44	6	71234301	71234301	Frame_Shift_Ins	INS	-	TTCC	-	FAM135A	415_1416insTT	p.N472fs
XH_P44	6	71569101	71569101	Nonsense_Mutation	INS	-	AAATTAACGTGTG	-	SMAP1	nsAGCAAAATTA	p.L420delinsX
XH_P44	6	73839572	73839572	In_Frame_Ins	INS	-	CTATGTGTGTTA	-	KCNQ5	nsAGTACTATGT	426delinsRVLLCLIV
XH_P44	6	74118985	74118985	Frame_Shift_Ins	INS	-	TGTCTATGTAC	-	DDX43	95insATTGTGCA	p.A398fs
XH_P44	6	74118987	74118987	Missense_Mutation	SNP	A	T	A	DDX43	c.A1196T	p.D399V
XH_P44	6	74190072	74190072	Missense_Mutation	SNP	C	T	C	MT01	c.C1186T	p.H396Y
XH_P44	6	74190073	74190073	Missense_Mutation	SNP	A	G	A	MT01	c.A1187G	p.H396R
XH_P44	6	74202041	74202041	In_Frame_Ins	INS	-	TATTTCTTTTTT	-	MT01	insAGATTATTTCT	574delinsKRLFLFFF
XH_P44	6	75828787	75828787	Frame_Shift_Ins	INS	-	TTTATATTTAAT	-	COL12A5	TCCATAATTAATA	p.K1278fs
XH_P44	6	76024057	76024057	Frame_Shift_Ins	INS	-	AAAGAGATGAG	-	FILIP1	1491insACTCAT	p.D497fs
XH_P44	6	76024059	76024059	Missense_Mutation	SNP	C	G	C	FILIP1	c.G1489C	p.D497H
XH_P44	6	76072588	76072588	Frame_Shift_Ins	INS	-	AGATATCTTCACA	-	FILIP1	2insAATGTGAAC	p.P108fs
XH_P44	6	76331289	76331289	Nonsense_Mutation	INS	-	TTGTTTTACTAA	-	SEN6	insTCTGTTTTTAAG	B2_N33delinsCFYX
XH_P44	6	80745089	80745089	Nonsense_Mutation	INS	-	TCGTCTTCTTCT	-	TTK	TTGTTATCTGCTG	626delinsVICFFX
XH_P44	6	82924111	82924111	Frame_Shift_Ins	INS	-	AGTAATT	-	IBTK	36_2037insAAT	p.Q679fs
XH_P44	6	82924113	82924113	In_Frame_Ins	INS	-	STATGATTTCTC	-	IBTK	TATAAAAGAGA	79delinsRYKREIPTTQ
XH_P44	6	83823123	83823123	Nonsense_Mutation	INS	-	TATGCTTCTGAG	-	DOPEY1	AAAGTATGCTCT	55delinsLESMLLRX
XH_P44	6	86251758	86251758	Frame_Shift_Ins	INS	-	GTGGTTCCTATG	-	SNX14	ATATAACAATGG	p.F421fs
XH_P44	6	88066209	88066209	Frame_Shift_Ins	INS	-	TTTGATACATC	-	C6orf163	3insTGTTTTGAT	p.Q181fs
XH_P44	6	88066211	88066211	Missense_Mutation	SNP	G	T	G	C6orf163	c.G544T	p.A182S
XH_P44	6	88272484	88272484	Frame_Shift_Ins	INS	-	T	-	RARS2	c.232_233insA	p.V78fs
XH_P44	6	88272485	88272485	In_Frame_Ins	INS	-	ATCTTGATATT	-	RARS2	CAAAGAAATATC	8delinsPKKYQDLKV
XH_P44	6	88367705	88367705	Frame_Shift_Ins	INS	-	TGGGTTTTGTGT	-	ORC3	TCAAAATGGGT	p.N411fs
XH_P44	6	90333206	90333206	Nonsense_Mutation	INS	-	AACATTTGGCTT	-	ANKRD6	5GTGGAACATT	66_S267delinsVGX
XH_P44	6	90406151	90406151	Frame_Shift_Ins	INS	-	CCATGTCACTG	-	MDN1	9311insAACTGA	p.R3104fs
XH_P44	6	90410477	90410477	Nonsense_Mutation	INS	-	TTTTCTTTCTG	-	MDN1	ATCACCCAGAAA	E2843delinsHITQKRKIX
XH_P44	6	90418269	90418269	In_Frame_Ins	INS	-	CCTGAGAAGTT	-	MDN1	344insACAACCT	Q2615delinsHNFSGS
XH_P44	6	90459421	90459421	Frame_Shift_Ins	INS	-	A	-	MDN1	c.3455_3456ins	p.E1152fs
XH_P44	6	90459422	90459422	Frame_Shift_Ins	INS	-	GTGAATGTCAG	-	MDN1	GAGGCTCTGAC	p.E1152fs
XH_P44	6	90499612	90499612	Missense_Mutation	SNP	G	A	G	MDN1	c.C1117T	p.R373C
XH_P44	6	90576596	90576596	Frame_Shift_Ins	INS	-	GTGAAATGTAT	-	CASP8AP2	88insCTGTGAAT	p.L1196fs
XH_P44	6	90605750	90605750	Missense_Mutation	SNP	T	G	T	GJA10	c.T1563G	p.D521E
XH_P44	6	90605751	90605751	Frame_Shift_Ins	INS	-	T	-	GJA10	c.1564_1565ins	p.G522fs
XH_P44	6	96053870	96053870	In_Frame_Ins	INS	-	GAC	-	MANEA	c.978_979insGA	p.T326delinsTD
XH_P44	6	96053872	96053872	Frame_Shift_Ins	INS	-	AAACTGT	-	MANEA	80_981insAAAC	p.N327fs
XH_P44	6	97339198	97339198	In_Frame_Ins	INS	-	TGAGCTCCCTGA	-	NDUFAF4	310insTCAGGGA	1104delinsSGSSI
XH_P44	6	97339200	97339200	Missense_Mutation	SNP	A	T	A	NDUFAF4	c.T308A	p.M103K
XH_P44	6	99893912	99893912	Frame_Shift_Ins	INS	-	GTTACAAAATTC	-	USP45	sTCAGTGAAATT	p.Q521fs
XH_P44	6	101214580	101214580	Frame_Shift_Ins	INS	-	TATAGTGAACTT	-	ASCC3	AAATAAAAGTT	p.I533fs
XH_P44	6	105406148	105406148	Frame_Shift_Ins	INS	-	AAAGATTAAAA	-	LIN28B	CATTCAAGAT	p.V62fs
XH_P44	6	105816892	105816892	Frame_Shift_Ins	INS	-	CATGAGTGAATA	-	PREP	03insATATTCAC	p.E201fs
XH_P44	6	105816894	105816894	In_Frame_Ins	INS	-	TTT	-	PREP	c.600_601insAA	p.E201delinsKE
XH_P44	6	106967130	106967130	Silent	SNP	T	C	T	CRYBG1	c.T823C	p.L275L
XH_P44	6	106967131	106967131	Frame_Shift_Ins	INS	-	GATATATAAC	-	CRYBG1	825insGATATA	p.L275fs
XH_P44	6	107100256	107100256	Nonsense_Mutation	INS	-	TAAACTGTATTT	-	QRS1	sATTTTAAACTG	44_G245delinsYFX
XH_P44	6	109294675	109294675	Frame_Shift_Ins	INS	-	GATTTCTTACTCT	-	ARMC2	2068insAGTTCT	p.R689fs
XH_P44	6	109415148	109415148	Nonsense_Mutation	INS	-	GGTGTGTATGAT	-	SESN1	nsGTTTACATAAA	43_E44delinsKFTX
XH_P44	6	111540102	111540102	In_Frame_Ins	INS	-	sATTTTACATACA	-	SLC16A10	CACITTTGATTTT	91delinsIHFDFTIIN
XH_P44	6	111696761	111696761	In_Frame_Ins	INS	-	AGAAAAACAAG	-	REV3L	7insATTACTTG	E933delinsITCF5LE
XH_P44	6	111709060	111709060	Nonsense_Mutation	INS	-	TATAATTTTATAT	-	REV3L	AAGAAAAATATA	p.L335delinsX
XH_P44	6	112476129	112476129	Nonsense_Mutation	INS	-	TACTTTAAAT	-	LAMA4	1980insAATTTA	660_Q661delinsTIX
XH_P44	6	112476130	112476130	Frame_Shift_Ins	INS	-	CTATGTAGTAA	-	LAMA4	ATGATAGTTTAC	p.T660fs
XH_P44	6	117113407	117113407	Nonsense_Mutation	INS	-	CTACCTTTTTCAT	-	GPRC6A	466insATGAAA	822_K823delinsQX
XH_P44	6	117114352	117114352	Nonsense_Mutation	INS	-	AGCTTTTTCATTG	-	GPRC6A	21insCCAATGA	A.M507delinsIQX
XH_P44	6	117121928	117121928	Nonsense_Mutation	INS	-	GAGTCCCTATTTA	-	GPRC6A	insGCTAAATAG	281_D282delinsSX
XH_P44	6	117708090	117708090	Frame_Shift_Ins	INS	-	TACTTGTGTTAAG	-	ROS1	sATTTTCTTAAC	p.P696fs
XH_P44	6	117709111	117709111	Frame_Shift_Ins	INS	-	AGAAATGAGAA	-	ROS1	6insCTCATTTCT	p.T616fs
XH_P44	6	118588189	118588189	Nonsense_Mutation	INS	-	CTGAAATAAATG	-	SLC35F1	AGACTCTGAAT	70delinsMYLKQTLKX
XH_P44	6	121625559	121625559	Frame_Shift_Ins	INS	-	CTTAGCTATGTG	-	TBC1D32	TAATTCACATAG	p.N296fs
XH_P44	6	124604232	124604232	Frame_Shift_Ins	INS	-	TTATAACTGTTG	-	NKAIN2	AGCAATTATAAC	p.I46fs
XH_P44	6	125366487	125366487	Nonsense_Mutation	INS	-	GTAATTTTAAAG	-	RNF217	TTGTGTGTAAT	B39delinsRNKGLCVIFKITX
XH_P44	6	126203677	126203677	Nonsense_Mutation	INS	-	AAACTAACCTAA	-	NCOA7	TTTAGAAACTAA	p.R123delinsLX
XH_P44	6	127611317	127611317	Frame_Shift_Ins	INS	-	ATTGTGAGGAA	-	ECHDC1	8insTGCTTCCTC	p.Q126fs
XH_P44	6	12771265	12771265	Frame_Shift_Ins	INS	-	TAAAGGCTCTTC	-	KIAA0408	TTCTTCAAGAGC	p.K123fs
XH_P44	6	128306937	128306937	Frame_Shift_Ins	INS	-	AAAATAAAAGT	-	PTPRK	77insCCAACCTT	p.G1059fs
XH_P44	6	128306938	128306938	Frame_Shift_Ins	INS	-	TGTAAGTAGT	-	PTPRK	c.3176insACTAC	p.G1059fs
XH_P44	6	129609185	129609185	Frame_Shift_Ins	INS	-	GGCAATGTGTTA	-	LAMA2	732insGGGCA	p.D911fs
XH_P44	6	129722460	129722460	Missense_Mutation	SNP	C	T	C	LAMA2	c.C5537T	p.A1846V
XH_P44	6	129722461	129722461	Frame_Shift_Ins	INS	-	sACTTCTCTGAG	-	LAMA2	sTCTCTGACTTTC	p.A1846fs

XH_P44	6	130442078	130442078	Nonsense_Mutation	INS	-	GAAAATGTAGC	-	L3MBTL3	ATTCTGGAAAA	522delinsELFWKMX
XH_P44	6	131925437	131925437	Missense_Mutation	SNP	C	A	C	MED23	c.G1637T	p.R546M
XH_P44	6	131925439	131925439	Nonsense_Mutation	INS	-	TGGAGCTTATGG	-	MED23	635insTCCATAAA	445_R546delinsTPX
XH_P44	6	132030992	132030992	Frame_Shift_Ins	INS	-	GGAGAGAA	-	CTAGE9	55_1166insTTCT	p.389fs
XH_P44	6	132030994	132030994	Silent	SNP	A	T	A	CTAGE9	c.T1164A	p.T388T
XH_P44	6	132031505	132031505	Missense_Mutation	SNP	T	G	T	CTAGE9	c.A653C	p.Q218P
XH_P44	6	132031506	132031506	Frame_Shift_Ins	INS	-	CAAAACAAAGG	-	CTAGE9	652insTCCTTTG	p.Q218fs
XH_P44	6	132791185	132791185	Nonsense_Mutation	INS	-	AAGATGCTTAG	-	STX7	5ATTACTCTAAGCA	Q148delinsITX
XH_P44	6	132874381	132874381	Missense_Mutation	SNP	A	C	A	TAAR8	c.A550C	p.N184H
XH_P44	6	132874382	132874382	Frame_Shift_Ins	INS	-	CCGTC	-	TAAR8	551_552insCCG	p.N184fs
XH_P44	6	132874739	132874739	Nonsense_Mutation	INS	-	ACTTGTCTACTAG	-	TAAR8	ATTCTACTTTGCA	A304delinsSLRMILLCYX
XH_P44	6	132966446	132966446	Frame_Shift_Ins	INS	-	GGTTTATGCA	-	TAAR1	697insTGCATA	p.I233fs
XH_P44	6	132966764	132966764	Nonsense_Mutation	INS	-	ATGTTATGTGTCT	-	TAAR1	5AATAGACACAT	7_P128delinsNRHITX
XH_P44	6	132967052	132967052	Frame_Shift_Ins	INS	-	SGTATTTTGGAG	-	TAAR1	ACTCTCTCAAAA	p.V31fs
XH_P44	6	132967054	132967054	Missense_Mutation	SNP	A	T	A	TAAR1	c.T89A	p.M30K
XH_P44	6	133013630	133013630	Missense_Mutation	SNP	T	C	T	VNN1	c.A920G	p.H307R
XH_P44	6	133013631	133013631	Nonsense_Mutation	INS	-	CTATTATCTACA	-	VNN1	919insTGTAGAT	H307delinsCRX
XH_P44	6	133077049	133077049	Missense_Mutation	SNP	C	G	C	VNN2	c.G470C	p.G157A
XH_P44	6	133077051	133077051	In_Frame_Ins	INS	-	AAGAAAAAGAC	-	VNN2	insAAGTGCAT	N156delinsKSVIFFI
XH_P44	6	133108690	133108690	Frame_Shift_Ins	INS	-	TAACTTGGTTT	-	SLC18B1	84insGAAACCAA	p.V128fs
XH_P44	6	135787219	135787219	Frame_Shift_Ins	INS	-	GGAAAAAGAAA	-	AH1	5TTCTTTTTTCTT	p.P161fs
XH_P44	6	135787221	135787221	Silent	SNP	C	T	C	AH1	c.G480A	p.C160K
XH_P44	6	136597486	136597486	Frame_Shift_Ins	INS	-	AAAGAGAC	-	BCLAF1	10_1171insGTCT	p.391fs
XH_P44	6	136597487	136597487	Frame_Shift_Ins	INS	-	GGATA	-	BCLAF1	169_1170insTA	p.Q390fs
XH_P44	6	136687121	136687121	Frame_Shift_Ins	INS	-	CTCTCTC	-	MAP7	2_743insGAGA	p.T248fs
XH_P44	6	137015426	137015426	Nonsense_Mutation	INS	-	AGAGTGTAAAC	-	MAP3K5	5sTAATACTTTAA	369_K370delinsX
XH_P44	6	138192471	138192471	In_Frame_Ins	INS	-	ACTAGCTGGCCG	-	TNFAIP3	108insACTAGCT	I36delinsLAGP
XH_P44	6	138754532	138754532	Frame_Shift_Ins	INS	-	CTTCTCTCTC	-	NHSL1	962insGAAGAG	p.D321fs
XH_P44	6	138754534	138754534	Silent	SNP	A	G	A	NHSL1	c.T960C	p.L320L
XH_P44	6	138893010	138893010	Frame_Shift_Ins	INS	-	GTCAATTTGTT	-	NHSL1	39insAACAAAT	p.Q13fs
XH_P44	6	139101117	139101117	Frame_Shift_Ins	INS	-	AAACCAAAAGA	-	CCDC28A	insCAGAAACCA	p.A196fs
XH_P44	6	139222246	139222246	Frame_Shift_Ins	INS	-	TCCTG	-	ECT2L	576_2577insTC	p.P859fs
XH_P44	6	139222247	139222247	In_Frame_Ins	INS	-	TGT	-	ECT2L	2577_2578insTC	p.P859delinsPC
XH_P44	6	139591683	139591683	Nonsense_Mutation	INS	-	AATAATTTTACC	-	TXLNB	5sAGGAGGTAAT	A9_L200delinsQGGKIX
XH_P44	6	144033293	144033293	Frame_Shift_Ins	INS	-	5AACTCTCACATA	-	PHACTR2	5ATTGGAATCTC	p.S63fs
XH_P44	6	144075017	144075017	Frame_Shift_Ins	INS	-	ACTGTTTCCACC	-	PHACTR2	5CTGCACTGTTT	p.P141fs
XH_P44	6	144165755	144165755	Splice_Site	INS	-	ACGGGAATAAA	-	LTV1	-	-
XH_P44	6	144765421	144765421	Nonsense_Mutation	INS	-	5ATAATAGAACT	-	UTRN	8insAACATAAT	506_G507delinsLTX
XH_P44	6	144854396	144854396	Nonsense_Mutation	INS	-	GTGGTATCAAT	-	UTRN	insTATTGTGGT	8_L297delinsSIVVSIX
XH_P44	6	146264556	146264556	In_Frame_Ins	INS	-	5TAAAGTTTTC	-	SHPRH	TGAAGAAGCAA	54delinsMKKQNF
XH_P44	6	149699888	149699888	Nonsense_Mutation	INS	-	GTAAGGCTCAA	-	TAB2	GTAATGTAAAGG	79_T280delinsQELX
XH_P44	6	149826711	149826711	Frame_Shift_Ins	INS	-	ATAAAGAAATTG	-	PP14	AAAATGTTCAAT	p.Y435fs
XH_P44	6	151766630	151766630	Frame_Shift_Ins	INS	-	ACTTCTTCATCA	-	RMND1	insCCTTGATGA	p.R106fs
XH_P44	6	151857573	151857573	Nonsense_Mutation	INS	-	TCCAGGATGGT	-	CCDC170	79insCTCCAGG	A0_S61delinsPPGWX
XH_P44	6	152265493	152265493	Frame_Shift_Ins	INS	-	AAAAAATAGTT	-	ESR1	nsAAAAAAAAT	p.V316fs
XH_P44	6	152555087	152555087	Frame_Shift_Ins	INS	-	CTCTCCG	-	SYNE1	7_20328insCGG	p.K6776fs
XH_P44	6	152555089	152555089	Frame_Shift_Ins	INS	-	TATTAATATTA	-	SYNE1	0326insCTTAAT	p.K6776fs
XH_P44	6	152716722	152716722	In_Frame_Ins	INS	-	CCTTGAATG	-	SYNE1	1_7662insCATTG	K2554delinsNIQG
XH_P44	6	152784004	152784004	In_Frame_Ins	INS	-	AAAAAATGTATT	-	SYNE1	0insTTCAATAC	714delinsFNTFFYD
XH_P44	6	152819900	152819900	Frame_Shift_Ins	INS	-	GTTTCTTTCT	-	SYNE1	937insAGAAAG	p.A313fs
XH_P44	6	152861127	152861127	Nonsense_Mutation	INS	-	5AAACTATTTC	-	SYNE1	TGGATGAAATB	T34delinsNWMKX
XH_P44	6	153019142	153019142	Frame_Shift_Ins	INS	-	5GAATCCACAT	-	MYCT1	5TCTTGAATTC	p.L35fs
XH_P44	6	154412293	154412293	Frame_Shift_Ins	INS	-	5AATGTTAGTGT	-	OPRM1	5AGAGAATGTTA	p.V184fs
XH_P44	6	155131308	155131308	Frame_Shift_Ins	INS	-	TGTCCTATATT	-	SCAF2	387insTTGTCTT	p.K462fs
XH_P44	6	155154158	155154158	Frame_Shift_Ins	INS	-	TATATCTACAG	-	SCAF8	5CTCTCTTATATC	p.F1149fs
XH_P44	6	158735280	158735280	Frame_Shift_Ins	INS	-	TTTCAATGGTAT	-	TULP4	ATTCTTTCAATG	p.L18fs
XH_P44	6	160526039	160526039	Frame_Shift_Ins	INS	-	TCATTCTCATCT	-	IGF2R	400insTTTCATTC	p.A2467fs
XH_P44	6	161527734	161527734	In_Frame_Ins	INS	-	TTAGTCCCAACT	-	MAP3K4	nsCCTCATTAGT	299delinsTSLVPITV
XH_P44	6	162622247	162622247	Nonsense_Mutation	INS	-	TTTCTGGATTTCT	-	PRKN	insAAAGAAATCT	150_K151delinsX
XH_P44	6	165809873	165809873	Frame_Shift_Ins	INS	-	TTCCAGATATTA	-	PDE10A	54insCATAATAT	p.T452fs
XH_P44	6	167344591	167344591	Missense_Mutation	SNP	C	G	C	RNASET2	c.G508C	p.D170H
XH_P44	6	167344592	167344592	Frame_Shift_Ins	INS	-	GGTGTGTG	-	RNASET2	6_507insCACAC	p.K169fs
XH_P44	6	170627847	170627847	In_Frame_Ins	INS	-	5GATATTACTTG	-	FAM120B	nsCTGTGGATAT	469delinsLVDITCLS
XH_P44	6	170627849	170627849	In_Frame_Ins	INS	-	AAAGTTAT	-	FAM120B	7_1408insAAAG	A469delinsPKVI
XH_P44	7	4014137	4014137	Nonsense_Mutation	SNP	G	T	G	SDK1	c.G1954T	p.E652X
XH_P44	7	4014139	4014139	Nonsense_Mutation	INS	-	AGCAACTAACAA	-	SDK1	AAAGCAAGCAAA	652delinsEKASNX
XH_P44	7	6797535	6797535	Frame_Shift_Ins	INS	-	TAGATTAT	-	RSPH10B	7_228insTAGAT	p.S76fs
XH_P44	7	6797536	6797536	Frame_Shift_Ins	INS	-	AGAGAGAC	-	RSPH10B	8_229insAGAGAA	p.S76fs
XH_P44	7	7398398	7398398	In_Frame_Ins	INS	-	TACAGCAGATA	-	COL28A1	CTCAAATATAGT	82delinsTLKYSVFLG
XH_P44	7	7480452	7480452	Frame_Shift_Ins	INS	-	CAACCAAAATATT	-	COL28A1	5TTCTGAATATT	p.Q564fs
XH_P44	7	7571289	7571289	Frame_Shift_Ins	INS	-	AGATCGTCTGG	-	COL28A1	371insCCAGAC	p.M124fs
XH_P44	7	7571291	7571291	Frame_Shift_Ins	INS	-	GGTACCTAATG	-	COL28A1	369insCATTAG	p.S123fs
XH_P44	7	7636050	7636050	Frame_Shift_Ins	INS	-	CTAACAAA	-	MIOS	9_2360insCTAA	p.L787fs
XH_P44	7	12396998	12396998	Frame_Shift_Ins	INS	-	TGACTATTCTTT	-	VWDE	73insACAAAGAA	p.V1025fs
XH_P44	7	12644251	12644251	Nonsense_Mutation	INS	-	ATATACATAATT	-	SCIN	GAGGTATATACA	210delinsVEVYTX
XH_P44	7	17873778	17873778	Frame_Shift_Ins	INS	-	TGGAGTCCAAAT	-	SNX13	5TTTTATATTGG	p.R498fs
XH_P44	7	17873780	17873780	Frame_Shift_Ins	INS	-	GTAATATA	-	SNX13	1_1492insTATA	p.R498fs
XH_P44	7	21470100	21470100	Frame_Shift_Ins	INS	-	GTGTTTGAGAT	-	SP4	1267insGTGTTT	p.Q422fs
XH_P44	7	21470101	21470101	Missense_Mutation	SNP	C	T	C	SP4	c.C1267T	p.P423S
XH_P44	7	21550879	21550879	Missense_Mutation	SNP	G	A	G	SP4	c.G2296A	p.E766K
XH_P44	7	21550881	21550881	Nonsense_Mutation	INS	-	CAGTAAATGGCC	-	SP4	2299insCAGTAA	A9_E766delinsEQX
XH_P44	7	21609840	21609840	Nonsense_Mutation	INS	-	CAAGTTCTAGAA	-	DNAH11	349insACAAGTT	50_R451delinsHKFX
XH_P44	7	21646147	21646147	Nonsense_Mutation	INS	-	ACTC	-	DNAH11	3752_3753insAC	1251_1252delinsX
XH_P44	7	21646149	21646149	Frame_Shift_Ins	INS	-	ATTTCTTTCTT	-	DNAH11	3755insATTTCT	p.I1252fs
XH_P44	7	21677273	21677273	Frame_Shift_Ins	INS	-	ATAAAAATAAA	-	DNAH11	GTTTTTATAAAA	p.A1590fs
XH_P44	7	21757520	21757520	Frame_Shift_Ins	INS	-	GGACACGT	-	DNAH11	1_7112insGGAC	p.I2371fs
XH_P44	7	21940706	21940706	Frame_Shift_Ins	INS	-	TTGTCAAGTGGT	-	DNAH11	13386insTTGTG	p.A4462fs
XH_P44	7	24882014	24882014	Frame_Shift_Ins	INS	-	CTTTGTAGTCAT	-	OSBPL3	insCATAATGACT	p.N362fs
XH_P44	7	24905821	24905821	Frame_Shift_Ins	INS	-	5GAGTCTGCTGT	-	OSBPL3	insCCAAGACACAG	p.S139fs
XH_P44	7	25266534	25266534	Frame_Shift_Ins	INS	-	GCTGAGTGATT	-	NPVF	50insAAATCAC	p.S84fs
XH_P44	7	26236581	26236581	In_Frame_Ins	INS	-	TTTTTGTTCT	-	HNRNPA2B1	321insGAACA	A107delinsMKNKN
XH_P44	7	26236582	26236582	Frame_Shift_Ins	INS	-	TATATAAGGGC	-	HNRNPA2B1	320insGCCTTT	p.I107fs
XH_P44	7	27835809	27835809	Nonsense_Mutation	INS	-	GATATACAAAG	-	TAX1BP1	ATCCTAGATATA	delinsSIHLIDQRIIRYKX
XH_P44	7	28843895	28843895	Nonsense_Mutation	INS	-	ACTCACATTTTC	-	CREB5	AAATGACTCAC	A122_M123delinsIX
XH_P44	7	29546942	29546942	Frame_Shift_Ins	INS	-	FTCTCAAGTAACT	-	CHN2	insAGTCTCAGC	p.I170fs
XH_P44	7	31378257	31378257	In_Frame_Ins	INS	-	CCATGTCTCA	-	NEUROD6	5_626insTGAACT	P209delinsLNMA
XH_P44	7	31887597	31887597	Nonsense_Mutation	INS	-	GTCTTATTTCTC	-	PDE1C	AAAAAGAGAAA	B22delinsCIKKKEKX
XH_P44	7	32910204	32910204	Frame_Shift_Ins	INS	-	TTGTAACCTC	-	KBTBD2	625insGGAGTT	p.R209fs

XH_P44	7	35242265	35242265	Frame_Shift_Ins	INS	-	AA	-	TBX20	.1120_1121insT	p.S374fs
XH_P44	7	35242267	35242267	Frame_Shift_Ins	INS	-	ATAGGACAGG	-	TBX20	.1119insCCTGT	p.A373fs
XH_P44	7	35922129	35922129	Nonsense_Mutation	INS	-	CTACGCTAGTCT	-	SEPT7	559insCTACGCT	p.I186delinsLRX
XH_P44	7	37901745	37901745	Frame_Shift_Ins	INS	-	ATCCTCTTTTAG	-	NME8	nsTGAATCTCTCT	p.Q129fs
XH_P44	7	38433696	38433696	Nonsense_Mutation	INS	-	ACATTATTATCAC	-	AMPH	891insTCTGATA	p.S464delinsIX
XH_P44	7	39612055	39612055	In_Frame_Ins	INS	-	TAAAC	-	YAE1D1	31_432insTAAAC	.H144delinsHKT
XH_P44	7	39612057	39612057	Frame_Shift_Ins	INS	-	TTTATAATTCA	-	YAE1D1	434insTTTATA	p.V145fs
XH_P44	7	40027618	40027618	Nonsense_Mutation	INS	-	GCTAGGAGAA	-	CDK13	TAGTGTGTAGG	p.V45delinsQXSX
XH_P44	7	42949445	42949445	Nonsense_Mutation	INS	-	AAGTAAGTTATT	-	C7orf25	9insATAAAATAAG	p.S410delinsYKX
XH_P44	7	44153778	44153780	In_Frame_Del	DEL	AGA	-	AGA	AEBP1	c.3395_3397del	p.1132_1133del
XH_P44	7	44737280	44737280	Nonsense_Mutation	INS	-	STAATAATTAGG	-	OGDH	nsGAGGTAATA	p.A750delinsRGNXX
XH_P44	7	47698762	47698762	In_Frame_Ins	INS	-	ACTCT	-	C7orf65	892_393insACTC	p.A131delinsALL
XH_P44	7	47892788	47892788	Frame_Shift_Ins	INS	-	ATAAACAAACT	-	PKD1L1	insGAGCAGTTT	p.K1633fs
XH_P44	7	48015231	48015231	Frame_Shift_Ins	INS	-	CTCTT	-	HUS1	518_519insAAG	p.M173fs
XH_P44	7	48015232	48015232	Frame_Shift_Ins	INS	-	ATGAACATTGT	-	HUS1	AAAGATACAATG	p.M173fs
XH_P44	7	48313756	48313756	In_Frame_Ins	INS	-	TTGAAGATGAC	-	ABCA13	nsATATTTTGAA	p.498delinsKYFEDDLV
XH_P44	7	48319285	48319285	Frame_Shift_Ins	INS	-	TGTTTGTGATA	-	ABCA13	5insGCTGTTTT	p.F2832fs
XH_P44	7	48411960	48411960	Frame_Shift_Ins	INS	-	SAGAAAAAACCC	-	ABCA13	nsAAAAAGAGAA	p.13667fs
XH_P44	7	48654969	48654969	Nonsense_Mutation	INS	-	AAACAATAAGG	-	ABCA13	5CTTTTGAAAAC	p.N4945delinsSFX
XH_P44	7	51133135	51133135	Frame_Shift_Ins	INS	-	CTTCTCT	-	COBL	7_1108insAGAA	p.A370fs
XH_P44	7	54617597	54617597	Frame_Shift_Ins	INS	-	C	-	VSTM2A	c.369dupC	p.G123fs
XH_P44	7	54617599	54617599	Frame_Shift_Ins	INS	-	TGGC	-	VSTM2A	370_371insTGG	p.L124fs
XH_P44	7	55863688	55863688	In_Frame_Ins	INS	-	GCTTGCTTATTG	-	SEPT14	7insATACAATAA	p.406delinsYTISKPI
XH_P44	7	55872974	55872974	Nonsense_Mutation	INS	-	GCCTTTACAAA	-	SEPT14	CTATAATTTTGT	p.6_F367delinsLQTHLX
XH_P44	7	57529400	57529400	Nonsense_Mutation	INS	-	TTAAGGGTTGAA	-	ZNF716	TGTTTCTTAAGG	p.E412delinsELSVYSX
XH_P44	7	63537926	63537926	Frame_Shift_Ins	INS	-	TCCTCATCAGA	-	ZNF727	00insCTCCCTCA	p.F167fs
XH_P44	7	63680384	63680384	In_Frame_Ins	INS	-	STGTAGTACCGC	-	ZNF735	TTATGTGTAGT	p.19delinsLCLVVPLED
XH_P44	7	63726546	63726546	Frame_Shift_Ins	INS	-	AATCACAAGTTA	-	ZNF679	insAAAAATCACA	p.T179fs
XH_P44	7	63982052	63982052	Frame_Shift_Ins	INS	-	CC	-	ZNF680	1079_1080insG	p.N360fs
XH_P44	7	63982053	63982053	Frame_Shift_Ins	INS	-	GCAACTCTTGC	-	ZNF680	1079insGCAAG	p.N360fs
XH_P44	7	64292272	64292272	Frame_Shift_Ins	INS	-	TTTTCCATAT	-	ZNF138	.212insTTTTCC	p.T71fs
XH_P44	7	64388600	64388600	Silent	SNP	C	A	C	ZNF273	c.C894A	p.V298V
XH_P44	7	64388601	64388601	In_Frame_Ins	INS	-	GCAACATGA	-	ZNF273	5_89insGCAAC	p.F299delinsCNMI
XH_P44	7	64388952	64388952	Frame_Shift_Ins	INS	-	TTTTTGTCTGT	-	ZNF273	5TAGGGTTTTGT	p.T416fs
XH_P44	7	64864170	64864170	Frame_Shift_Ins	INS	-	ACATTCT	-	ZNF92	15_916insACAT	p.S305fs
XH_P44	7	64864537	64864537	In_Frame_Ins	INS	-	5TTATCTTCCAT	-	ZNF92	5TAGGGTTTATC	p.8delinsICRVLYPYDFS
XH_P44	7	66237009	66237009	Nonsense_Mutation	INS	-	5AAGGAGGGAG	-	RABGEF1	56insTGAAGGAG	p.E55_E56delinsEX
XH_P44	7	76908398	76908398	In_Frame_Ins	INS	-	TTC	-	CCDC146	1674_1675insTp	p.N558delinsNF
XH_P44	7	76908399	76908399	Frame_Shift_Ins	INS	-	CATTTTTTCTCT	-	CCDC146	567insCATTTTT	p.S559fs
XH_P44	7	77256676	77256676	Nonsense_Mutation	INS	-	AAGCAGATTTAA	-	PTPN12	AGGTGAAGCAC	p.30_Q431delinsYTRX
XH_P44	7	77824311	77824311	Frame_Shift_Ins	INS	-	A	-	MAGI2	c.2148_2149ins	p.L717fs
XH_P44	7	77824312	77824312	Frame_Shift_Ins	INS	-	CTGGTCTAAAT	-	MAGI2	nsGATAATTTTAA	p.N716fs
XH_P44	7	80091870	80091870	Nonsense_Mutation	INS	-	TAGTCTAGATCT	-	GNAT3	ACAAGGATCTA	p.223_C224delinsSX
XH_P44	7	81589125	81589125	In_Frame_Ins	INS	-	GAAACTATTAG	-	CACNA2D1	7insAGTCTAAT	p.996delinsQSN5FLF
XH_P44	7	81964561	81964561	Nonsense_Mutation	SNP	C	A	C	CACNA2D1	c.G184T	p.E62X
XH_P44	7	81964562	81964562	Nonsense_Mutation	INS	-	TTTTTTTATATT	-	CACNA2D1	1TAGTAATATAA	p.Y61_E62delinsX
XH_P44	7	82544518	82544518	In_Frame_Ins	INS	-	TGGCCA	-	PCLO	83_12784insTG	p.T4262delinsWPT
XH_P44	7	82546120	82546120	Nonsense_Mutation	INS	-	AAAGAGGCCCTA	-	PCLO	11182insTAGGCG	p.P3728delinsX
XH_P44	7	82579033	82579033	Nonsense_Mutation	INS	-	TAATCATGTGT	-	PCLO	71insGAAACAC	p.Y3624delinsX
XH_P44	7	82579864	82579864	In_Frame_Ins	INS	-	TGATCCCCGAA	-	PCLO	40insAAACTTCG	p.3347delinsKTSGIIC
XH_P44	7	82582204	82582204	Frame_Shift_Ins	INS	-	ATTATAAATCTTA	-	PCLO	CACACTAAGAT	p.V2689fs
XH_P44	7	82582206	82582206	Frame_Shift_Ins	INS	-	ATCATCAA	-	PCLO	2_8063insTTGA	p.S5268fs
XH_P44	7	82583892	82583892	Frame_Shift_Ins	INS	-	TAACACACAGTT	-	PCLO	77insATAAACTG	p.S2126fs
XH_P44	7	82584360	82584360	Frame_Shift_Ins	INS	-	TAGTGGACCTG	-	PCLO	7insTACCAGGT	p.D1970fs
XH_P44	7	83021958	83021958	In_Frame_Ins	INS	-	TTCCCTCTTTTG	-	SEMA3E	7insTTTCAAAG	p.467delinsVKEGKT
XH_P44	7	84649562	84649562	Frame_Shift_Ins	INS	-	TCCTCTAAGCATA	-	SEMA3D	490insATATGCT	p.L497fs
XH_P44	7	86468495	86468495	Silent	SNP	C	A	C	GRM3	c.C1665A	p.P555P
XH_P44	7	86988642	86988642	Frame_Shift_Ins	INS	-	CAAAAGAT	-	CROT	6_237insCAAAA	p.N79fs
XH_P44	7	87073085	87073085	Frame_Shift_Ins	INS	-	GGCTTTGTTGT	-	ABCBA	1124insACAAC	p.P375fs
XH_P44	7	87073087	87073087	In_Frame_Ins	INS	-	AGTGTG	-	ABCBA	21_1122insCAC	p.N374delinsNLT
XH_P44	7	87476340	87476340	Frame_Shift_Ins	INS	-	TTTATTGAATGA	-	SLC25A40	NACTATTATTCTA	p.K185fs
XH_P44	7	87910338	87910338	Frame_Shift_Ins	INS	-	CAGCTAAGACT	-	STEAP4	7insTATAGTCTTA	p.S171fs
XH_P44	7	88424080	88424080	In_Frame_Ins	INS	-	AAGTTC	-	TEX47	76_177insGAA	p.N59delinsKNF
XH_P44	7	88963746	88963746	In_Frame_Ins	INS	-	GTTTTATCTAAA	-	ZNF804B	nsTTTCTGTTTTA	p.84delinsSVLSKDF
XH_P44	7	88964070	88964070	Frame_Shift_Ins	INS	-	GT	-	ZNF804B	1774_1775insG	p.A592fs
XH_P44	7	88964071	88964071	In_Frame_Ins	INS	-	TTCTCT	-	ZNF804B	775_1776insTTC	p.A592delinsASF
XH_P44	7	88964815	88964815	Frame_Shift_Ins	INS	-	AAATTACCTCTG	-	ZNF804B	7insAGCAAATTA	p.S840fs
XH_P44	7	89861900	89861900	Frame_Shift_Ins	INS	-	AAAGACTGAA	-	STEA2P	GAACAAATGAA	p.L479fs
XH_P44	7	91503095	91503095	In_Frame_Ins	INS	-	5GAACTGTGAAT	-	MTERF1	AAACATTTACACA	p.8delinsGITVYQFLRIK
XH_P44	7	91630927	91630927	Frame_Shift_Ins	INS	-	GTTTTCATTTC	-	AKAP9	TGCCGTGTTTT	p.S566fs
XH_P44	7	91631836	91631836	In_Frame_Ins	INS	-	ACATGTCTCTCA	-	AKAP9	ATTTTCAACATG	p.59delinsVFSTCLOQFS
XH_P44	7	91670135	91670135	Nonsense_Mutation	INS	-	AATCTCATCATG	-	AKAP9	CACTGAAATCTG	p.614delinsLDTEISSX
XH_P44	7	91690690	91690690	Nonsense_Mutation	INS	-	ATACTACTGAAT	-	AKAP9	AAAGATATACTA	p.S1907delinsEDFKIKIYYX
XH_P44	7	91708730	91708730	Nonsense_Mutation	INS	-	CACTCATCAAAC	-	AKAP9	CTTGATCACTCA	p.428_E2429delinsHSX
XH_P44	7	91709316	91709316	In_Frame_Ins	INS	-	GACAGAAATTTT	-	AKAP9	nsATCTTGACAG	p.2623delinsILTEFCI
XH_P44	7	91712766	91712766	Frame_Shift_Ins	INS	-	TTCTTTTCTAA	-	AKAP9	CTCATCTCTTT	p.E2815fs
XH_P44	7	91924392	91924392	In_Frame_Ins	INS	-	AAA	-	ANKIB1	c.100_101insAA	p.L34delinsQI
XH_P44	7	91924393	91924393	In_Frame_Ins	INS	-	TTTAAACAC	-	ANKIB1	1_102insTTTTA	p.L34delinsLNT
XH_P44	7	92027776	92027776	Missense_Mutation	SNP	A	T	A	ANKIB1	c.A2783T	p.E928V
XH_P44	7	92027778	92027778	Frame_Shift_Ins	INS	-	TAACCTGT	-	ANKIB1	85_2786insTAA	p.N929fs
XH_P44	7	92355078	92355078	In_Frame_Ins	INS	-	TCCATGTCTCTA	-	CDK6	AACTATAGAGAC	p.33delinsLTLETWKR
XH_P44	7	92732647	92732647	In_Frame_Ins	INS	-	TAT	-	SAMD9	2763_2764insA	p.A922delinsIA
XH_P44	7	92732649	92732649	In_Frame_Ins	INS	-	CCT	-	SAMD9	2761_2762insAc	p.L921delinsQV
XH_P44	7	92826707	92826707	Nonsense_Mutation	INS	-	TAGTTGTGTTAA	-	HEPACAM2	ATAATATTAAAC	p.A69_K370delinsNIX
XH_P44	7	92844927	92844927	In_Frame_Ins	INS	-	TGAAAT	-	HEPACAM2	65_466insATT	p.L156delinsSL
XH_P44	7	92844929	92844929	In_Frame_Ins	INS	-	AAAGTGATA	-	HEPACAM2	3_464insTATCA	p.T155delinsSLS
XH_P44	7	93516207	93516207	Frame_Shift_Ins	INS	-	TTTTTTTATATA	-	TFPI2	TAGTTATATATA	p.L186fs
XH_P44	7	94183859	94183859	Frame_Shift_Ins	INS	-	CTAAAGATATTA	-	CASD1	sATATTCTAAAA	p.F700fs
XH_P44	7	94540068	94540068	Frame_Shift_Ins	INS	-	AAACATCTTT	-	PPP1R9A	.644insAAACA	p.P215fs
XH_P44	7	94540070	94540070	Silent	SNP	C	G	C	PPP1R9A	c.C645G	p.P215P
XH_P44	7	94540492	94540492	Nonsense_Mutation	INS	-	CAGGAATTAG	-	PPP1R9A	1068insCAGGA	p.A357delinsARNX
XH_P44	7	94913379	94913379	Nonsense_Mutation	INS	-	AAAGTTTGACAT	-	PPP1R9A	sAGTAAAAAGT	p.Q076_Q1077delinsEX
XH_P44	7	94919517	94919517	Nonsense_Mutation	INS	-	ALGGTGTAAACA	-	PPP1R9A	CTCTGATGGTG	p.E1059delinsALX
XH_P44	7	95434146	95434146	Nonsense_Mutation	INS	-	AGTTAGATCTG	-	DYNC111	AATTAAGTTAG	p.E36delinsKQIKLILVX
XH_P44	7	96639235	96639235	Frame_Shift_Ins	INS	-	TCCACCTCTTTC	-	DLX6	59insTTCACCT	p.P253fs
XH_P44	7	97820068	97820068	Frame_Shift_Ins	INS	-	G	-	LMTK2	c.1027_1028insC	p.F343fs
XH_P44	7	98535444	98535444	Splice_Site	INS	-	ACTTATCTTTACT	-	TRRAP	.	.
XH_P44	7	98655109	98655109	Frame_Shift_Ins	INS	-	AGTTCAC	-	SMURF1	58_269insGTGA	p.Q90fs

XH_P44	7	99091480	99091480	Frame_Shift_Ins	INS	-	AGACAAAGTACA	-	ZNF394	sAGGTGTGTACT	p.I453fs
XH_P44	7	99129051	99129051	Missense_Mutation	SNP	C	A	C	ZKSCAN5	c.C1480A	p.H494N
XH_P44	7	99474446	99474446	Frame_Shift_Ins	INS	-	C	-	OR2AE1	c.210_211insG	p.L71fs
XH_P44	7	99474447	99474447	In_Frame_Ins	INS	-	GCATTCTCC	-	OR2AE1	c.210insGGAGAG	p.D70delinsEENA
XH_P44	7	99569630	99569630	Splice_Site	INS	-	ACAGGGG	-	AZGP1	-	-
XH_P44	7	99662124	99662124	Frame_Shift_Ins	INS	-	ATCTTTGCACCT	-	ZSCAN21	1307insATTCTT	p.R436fs
XH_P44	7	99689295	99689295	In_Frame_Ins	INS	-	ATTAAA	-	COP56	67_868insATTAA	p.M289delinsMik
XH_P44	7	99689296	99689296	Frame_Shift_Ins	INS	-	GGGA	-	COP56	868_869insGGG	p.A290fs
XH_P44	7	99695843	99695843	Frame_Shift_Ins	INS	-	GAAGGGATTAC	-	MCM7	insGATGTAATC	p.I88fs
XH_P44	7	100552037	100552037	In_Frame_Ins	INS	-	CTCACTTGATAGA	-	MUC3A	AGTGAACCTCACT	p.73delinsVNSLVDVS
XH_P44	7	100552566	100552566	Frame_Shift_Ins	INS	-	STCCATATATGT	-	MUC3A	GAAGTGTCAT	p.V1049fs
XH_P44	7	100635516	100635516	Missense_Mutation	SNP	C	T	C	MUC12	c.C1672T	p.P558S
XH_P44	7	100635518	100635518	Silent	SNP	C	A	C	MUC12	c.C1674A	p.P558P
XH_P44	7	100641110	100641110	Silent	SNP	A	G	A	MUC12	c.A7266G	p.A2422A
XH_P44	7	100648213	100648213	Frame_Shift_Ins	INS	-	GGTGTGTGG	-	MUC12	14370insGGTG	p.L4790fs
XH_P44	7	100648214	100648214	Silent	SNP	C	T	C	MUC12	c.C14370T	p.L4790L
XH_P44	7	100675608	100675608	Frame_Shift_Ins	INS	-	STGCTGGCAGG	-	MUC17	2insGGTGCTGG	p.I304fs
XH_P44	7	100677079	100677079	In_Frame_Ins	INS	-	CCGCAGTTGTA	-	MUC17	83insTCCGCACT	p.794delinsTFRSCR
XH_P44	7	100682694	100682694	Frame_Shift_Ins	INS	-	GGACTGTTGGA	-	MUC17	998insAGGACT	p.T2666fs
XH_P44	7	100682970	100682970	Frame_Shift_Ins	INS	-	GGAGTGCTTCTT	-	MUC17	insTAATGGAGT	p.V2758fs
XH_P44	7	100684419	100684419	Missense_Mutation	SNP	T	C	T	MUC17	c.T9722C	p.I3241T
XH_P44	7	100685104	100685104	Silent	SNP	G	A	G	MUC17	c.G10407A	p.P3469P
XH_P44	7	100685505	100685505	Frame_Shift_Ins	INS	-	GC	-	MUC17	0808_10809ins	p.R3603fs
XH_P44	7	100685506	100685506	Frame_Shift_Ins	INS	-	TATTTGTTAATG	-	MUC17	10810insTATTTG	p.R3603fs
XH_P44	7	100686669	100686669	Frame_Shift_Ins	INS	-	GGAGTTGAGG	-	MUC17	73insGTGGGAG	p.F3991fs
XH_P44	7	100686872	100686872	Nonsense_Mutation	INS	-	AAAAGATGTG	-	MUC17	TAGTTGAAAAA	p.059_H4060delinsX
XH_P44	7	100695217	100695217	Nonsense_Mutation	INS	-	STGTTGAAACAC	-	MUC17	78insTGTGTTG	p.9_M4360delinsQWCX
XH_P44	7	100959814	100959814	In_Frame_Ins	INS	-	CTCTGTCCA	-	IFT22	126insTGGAC	p.S42delinsSGQS
XH_P44	7	102953029	102953029	Frame_Shift_Ins	INS	-	TGTTT	-	DNAJC2	593_1694insAA	p.R565fs
XH_P44	7	102953031	102953031	Frame_Shift_Ins	INS	-	ACATGTGTCAA	-	DNAJC2	nsATTGTTGAAC	p.S564fs
XH_P44	7	102964067	102964067	Nonsense_Mutation	INS	-	TTGCTTAACCTA	-	DNAJC2	nsACCTAGGTTA	p.E233delinsTX
XH_P44	7	103019746	103019746	In_Frame_Ins	INS	-	AAG	-	SLC26A5	1524_1525insC	p.N509delinsLN
XH_P44	7	103019747	103019747	Frame_Shift_Ins	INS	-	ACATAAAC	-	SLC26A5	3_1524insGTTT	p.I508fs
XH_P44	7	103179728	103179728	Frame_Shift_Ins	INS	-	AAACACAAGTG	-	RELN	977insTGCACT	p.D2326fs
XH_P44	7	103180853	103180853	Nonsense_Mutation	INS	-	ATCGATCAGGT	-	RELN	21insTGACCTG	p.P2241delinsX
XH_P44	7	103205901	103205901	Nonsense_Mutation	INS	-	AATTGTCAT	-	RELN	3_5034insATGA	p.N1678delinsKX
XH_P44	7	103276830	103276830	Nonsense_Mutation	INS	-	CAGTTTATTAGG	-	RELN	155insTCTCAAT	p.T19_L72delinsSQX
XH_P44	7	103301968	103301968	Frame_Shift_Ins	INS	-	AGCAGAAGCCT	-	RELN	1296insCAGGCT	p.D432fs
XH_P44	7	104730627	104730627	Frame_Shift_Ins	INS	-	AATCCTTTTTAG	-	KMT2E	ATAAGCAATCC	p.T510fs
XH_P44	7	105904055	105904055	In_Frame_Ins	INS	-	CATCAATACTAC	-	NAMPT	752insGTAGTAT	p.T251delinsSSIDA
XH_P44	7	106513362	106513362	In_Frame_Ins	INS	-	TCTGGC	-	PIK3CG	66_2267insTCT	p.K756delinsWQ
XH_P44	7	106513363	106513363	Frame_Shift_Ins	INS	-	GGGCACATCAT	-	PIK3CG	268insAGGGCAG	p.K756fs
XH_P44	7	107115734	107115734	Frame_Shift_Ins	INS	-	STCACTTGGGCC	-	GPR22	230insGTCACT	p.D410fs
XH_P44	7	107577670	107577670	Frame_Shift_Ins	INS	-	ATGG	-	LAMB1	813_3814insCC	p.S1272fs
XH_P44	7	107601715	107601715	Frame_Shift_Ins	INS	-	CCCC	-	LAMB1	044_2045insGG	p.L682fs
XH_P44	7	107601716	107601716	In_Frame_Ins	INS	-	AGAAAGGATTTA	-	LAMB1	044insAAATAAAT	p.682delinsNKSFPL
XH_P44	7	108113022	108113022	Frame_Shift_Ins	INS	-	GATGAGTATAT	-	PNPLA8	ATAAGCATATA	p.N724fs
XH_P44	7	110763549	110763549	Nonsense_Mutation	INS	-	GTGATTAATATA	-	LRRN3	sAGTTGTGATTA	p.241_S242delinsKLX
XH_P44	7	113520053	113520053	In_Frame_Ins	INS	-	GGCAGCAAAGA	-	PPP1R3A	094insCTTCTTTG	p.365delinsTSLLPV
XH_P44	7	113558764	113558764	Frame_Shift_Ins	INS	-	TCCTTTAAGATT	-	PPP1R3A	AAATCAATCTTA	p.T96fs
XH_P44	7	116395468	116395468	Frame_Shift_Ins	INS	-	AAAGAGCAGA	-	MET	472insAAAGAG	p.D157fs
XH_P44	7	116395469	116395469	Frame_Shift_Ins	INS	-	GCAGC	-	MET	472_473insGCA	p.F158fs
XH_P44	7	116423488	116423488	Frame_Shift_Ins	INS	-	CTTTTGCTTTAA	-	MET	2474insCTTTTG	p.L825fs
XH_P44	7	116869897	116869897	Nonsense_Mutation	INS	-	ACTGTAGA	-	ST7	1_1652insACTG	p.L551delinsHCX
XH_P44	7	117180330	117180330	In_Frame_Ins	INS	-	CATCATATGACC	-	CFTR	nsTCCACATCAT	p.49delinsAPHMTCV
XH_P44	7	117431519	117431519	In_Frame_Ins	INS	-	CTTTT	-	CTTNBP2	30_1731insAAAA	p.A577delinsAKG
XH_P44	7	117431521	117431521	Frame_Shift_Ins	INS	-	TCTT	-	CTTNBP2	728_1729insAA	p.A577fs
XH_P44	7	120450614	120450614	In_Frame_Ins	INS	-	CCCTTATTTCAC	-	TSPAN12	nsCATGTGAAAT	p.124delinsPCEIKGK
XH_P44	7	120629891	120629891	Frame_Shift_Ins	INS	-	AT	-	CPED1	c.216_217insAT	p.F72fs
XH_P44	7	120629892	120629892	Frame_Shift_Ins	INS	-	CTGCTTAAGAA	-	CPED1	18insCCTGCTT	p.L73fs
XH_P44	7	120911477	120911477	In_Frame_Ins	INS	-	TTA	-	CPED1	2861_2862insT	p.F954delinsFY
XH_P44	7	120911478	120911478	Nonsense_Mutation	INS	-	TGGGATTAGT	-	CPED1	2863insTGGG	p.A4_H955delinsFWDX
XH_P44	7	121756975	121756975	Nonsense_Mutation	INS	-	CGTTTAAATAGT	-	AAS5	nsCATCAGATTAT	p.H42_V243delinsHQYX
XH_P44	7	122001016	122001016	Frame_Shift_Ins	INS	-	TTCCCTTAGGGA	-	CADPS2	316insCTCCCTA	p.G1106fs
XH_P44	7	122033359	122033359	Nonsense_Mutation	INS	-	ATTTGAGTTTTT	-	CADPS2	AGCTTAAAAACT	p.N971delinsLLAX
XH_P44	7	123097544	123097544	In_Frame_Ins	INS	-	GGTATATATAAG	-	IQUB	AAATCTCTTATA	p.95delinsVQISYIYLLFN
XH_P44	7	123101657	123101657	Nonsense_Mutation	INS	-	GTGCCAATTAT	-	IQUB	1761insATAAT	p.S587delinsVX
XH_P44	7	123101659	123101659	Missense_Mutation	SNP	C	G	C	IQUB	c.G1759C	p.V587L
XH_P44	7	123302076	123302076	Frame_Shift_Ins	INS	-	TA	-	LMOD2	c.436_437insTA	p.G146fs
XH_P44	7	123302077	123302077	In_Frame_Ins	INS	-	CACATGGCAAGT	-	LMOD2	438insCACATGG	p.146delinsGTWQV
XH_P44	7	123332717	123332717	Frame_Shift_Ins	INS	-	ATGCACCTGT	-	WASL	1031insTAACA	p.P344fs
XH_P44	7	126249452	126249452	In_Frame_Ins	INS	-	NATTTGGCCCTT	-	GRM8	TCATAAAAGGGG	p.4delinsNDFIKGQNLKGI
XH_P44	7	127014587	127014587	Frame_Shift_Ins	INS	-	A	-	ZNF800	c.802_803insT	p.K268fs
XH_P44	7	127014588	127014588	Frame_Shift_Ins	INS	-	TCTCCTAAAAAA	-	ZNF800	802insTTTTTTAG	p.K268fs
XH_P44	7	127732091	127732091	In_Frame_Ins	INS	-	GAGAAGAAAGG	-	SNP1	715insGAGAAG	p.E905delinsERRKG
XH_P44	7	128141905	128141905	Nonsense_Mutation	INS	-	AGTTCATGTTTAC	-	METTL2B	73insAAGTTTCA	p.1358delinsQVHVX
XH_P44	7	129813560	129813560	Nonsense_Mutation	INS	-	TTAAATTCGAAA	-	TMEM209	AAACACATTTC	p.8delinsRNIVGNFTPIX
XH_P44	7	129841907	129841907	Missense_Mutation	SNP	T	A	T	TMEM209	c.A356T	p.D119V
XH_P44	7	129841908	129841908	Frame_Shift_Ins	INS	-	ACCCATTATAA	-	TMEM209	355insTTTAAAT	p.D119fs
XH_P44	7	130038762	130038762	Frame_Shift_Ins	INS	-	TAAAAAC	-	CEP41	27_828insGTTT	p.S276fs
XH_P44	7	130038764	130038764	Missense_Mutation	SNP	T	A	T	CEP41	c.A826T	p.S276C
XH_P44	7	130301931	130301931	Frame_Shift_Ins	INS	-	ATTTTTT	-	COPG2	28_329insAAAA	p.T110fs
XH_P44	7	130301933	130301933	Nonsense_Mutation	INS	-	CTTTATTATGTT	-	COPG2	27insAACATAAA	p.A09_T110delinsLTX
XH_P44	7	131815321	131815321	Frame_Shift_Ins	INS	-	TTGCTCTGCC	-	PLXNA4	5602insGGGAC	p.L1868fs
XH_P44	7	134617950	134617950	Frame_Shift_Ins	INS	-	GAACAAC	-	CALD1	12_413insGAAC	p.N138fs
XH_P44	7	135073590	135073590	Nonsense_Mutation	INS	-	CTTTCATTAGGC	-	CNOT4	TTAAAGGCCTA	p.Q559delinsCX
XH_P44	7	135080522	135080522	Nonsense_Mutation	INS	-	TCAGGTATATAA	-	CNOT4	TATTTGTATATA	p.E329delinsTIVYLMX
XH_P44	7	135369002	135369002	Missense_Mutation	SNP	G	C	G	SLC13A4	c.C1616G	p.T539R
XH_P44	7	135369003	135369003	Nonsense_Mutation	INS	-	CTTTCAAAGCTT	-	SLC13A4	615insTAAGCTT	p.T539_L540delinsX
XH_P44	7	135376065	135376065	Nonsense_Mutation	SNP	G	A	G	SLC13A4	c.C1330T	p.Q444X
XH_P44	7	135421943	135421943	In_Frame_Ins	INS	-	CTAATTGT	-	FAM180A	81insACAAAT	p.V27delinsVQIR
XH_P44	7	135421945	135421945	Missense_Mutation	SNP	C	G	C	FAM180A	c.G79C	p.V27L
XH_P44	7	136700347	136700347	In_Frame_Ins	INS	-	ACTGCCAGAAG	-	CHRM2	6insGAACCTGCC	p.N245delinsNELPEE
XH_P44	7	137341283	137341283	In_Frame_Ins	INS	-	ATTTGATATCAT	-	DGKI	GTAAATGATA	p.04delinsRKMISNYTS
XH_P44	7	138603453	138603453	Nonsense_Mutation	INS	-	AAACATCATAT	-	KIAA1549	919insATATGA	p.307_S308delinsIX
XH_P44	7	138968522	138968522	Frame_Shift_Ins	INS	-	AAAGAAGTGTGA	-	UBN2	2insAGGAAGAA	p.K957fs
XH_P44	7	139083427	139083427	Frame_Shift_Ins	INS	-	GACAAATATAA	-	c7orf55-LUC7L	nsCATAGACAAA	p.F80fs
XH_P44	7	139092080	139092080	Frame_Shift_Ins	INS	-	AAACAAT	-	c7orf55-LUC7L	71_672insAAAC	p.K224fs

XH_P44	7	139092081	139092081	Nonsense_Mutation	INS	-	ACCATATAAT	-	c7orf55-LUC7L	673insACCATAT	24_L225delins	KTIX
XH_P44	7	139299193	139299193	Frame_Shift_Ins	INS	-	AAGG	-	HIPK2	1828_1829insCC	p.V610fs	
XH_P44	7	139299194	139299194	In_Frame_Ins	INS	-	CCCTCCAT	-	HIPK2	1828insATGAC	p.V610delins	MRRV
XH_P44	7	139741610	139741610	In_Frame_Ins	INS	-	TGTTTGTCTCG	-	PARP12	1016insCAGGAC	F339delins	SGQNI
XH_P44	7	140501356	140501356	In_Frame_Ins	INS	-	TTTCATACGATT	-	BRAF	716insAATCGTAR	239delins	QSYGR
XH_P44	7	140501358	140501358	Frame_Shift_Ins	INS	-	TATAGAGA	-	BRAF	3_714insTCTCT	p.V238fs	
XH_P44	7	141464484	141464484	Frame_Shift_Ins	INS	-	CACCAAGACAG	-	TAS2R3	527insCACCAAC	p.S176fs	
XH_P44	7	141672839	141672839	Frame_Shift_Ins	INS	-	AGGGGTGATGG	-	TAS2R38	nsACAAACCATCA	p.T217fs	
XH_P44	7	141919904	141919904	Nonsense_Mutation	INS	-	ATTTAACAAAAA	-	MGAM2	ATTACAATTAA	1865_P1866delins	X
XH_P44	7	141954986	141954986	Frame_Shift_Ins	INS	-	TTTCTATCATTT	-	PRSS58	sgAGAAAATGA	p.T109fs	
XH_P44	7	142573386	142573386	Frame_Shift_Ins	INS	-	CTAATCTCAAA	-	TRPV6	77insATATTGA	p.L359fs	
XH_P44	7	142573388	142573388	Missense_Mutation	SNP	G	T	G	TRPV6	c.C1075A	p.L359I	
XH_P44	7	143043262	143043262	Frame_Shift_Ins	INS	-	TCCC	-	CLCN1	2202_2203insTC	p.S734fs	
XH_P44	7	143091299	143091299	Frame_Shift_Ins	INS	-	TCITT	-	EPHA1	189_2490insAA	p.M830fs	
XH_P44	7	143091300	143091300	Frame_Shift_Ins	INS	-	C	-	EPHA1	12488_2489ins	p.M830fs	
XH_P44	7	143633043	143633043	Frame_Shift_Ins	INS	-	G	-	OR2F2	c.718_719insG	p.T240fs	
XH_P44	7	143633044	143633044	In_Frame_Ins	INS	-	GAGTTCACAGG	-	OR2F2	nsTAGGAGTTCA	40delins	TRSSQDM
XH_P44	7	143792621	143792621	Frame_Shift_Ins	INS	-	GT	-	OR2A12	c.421_422insGT	p.T141fs	
XH_P44	7	143792623	143792623	Frame_Shift_Ins	INS	-	GTCCAAGTAGA	-	OR2A12	insAGAGTCCAA	p.T141fs	
XH_P44	7	143929704	143929704	In_Frame_Ins	INS	-	CCTCAT	-	OR2A1	32_233insATGA	p.P78delins	HEA
XH_P44	7	143929705	143929705	Frame_Shift_Ins	INS	-	AAAT	-	OR2A1	231_232insATT	p.P78fs	
XH_P44	7	144060577	144060577	Frame_Shift_Ins	INS	-	ATATCTGGTCT	-	ARHGEF5	816insATATCT	p.Q272fs	
XH_P44	7	144071849	144071849	In_Frame_Ins	INS	-	TTA	-	ARHGEF5	4165_4166insTb	R1389delins	LS
XH_P44	7	144071850	144071850	Frame_Shift_Ins	INS	-	ATTCTCTTCT	-	ARHGEF5	4167insATTCT	p.R1389fs	
XH_P44	7	144463030	144463030	Frame_Shift_Ins	INS	-	SACTCCGAAGG	-	TPK1	nsCTCCTTCGG	p.C20fs	
XH_P44	7	149543324	149543324	In_Frame_Ins	INS	-	GAAAGTAGGAG	-	ZNFR82	222insGAAAGTA	S74delins	RRKVG
XH_P44	7	150217369	150217369	Missense_Mutation	SNP	C	A	C	GIMAP7	c.C307A	p.R103S	
XH_P44	7	150217371	150217371	In_Frame_Ins	INS	-	AAT	-	GIMAP7	309_310insAA	p.R103delins	RN
XH_P44	7	150439827	150439827	Frame_Shift_Ins	INS	-	CCCCGATGTTCT	-	GIMAP1-GIMAP	01insTCCCAG	p.Q200fs	
XH_P44	7	150439829	150439829	Missense_Mutation	SNP	C	T	C	GIMAP1-GIMAP	c.C602T	p.A201V	
XH_P44	7	151053006	151053006	Nonsense_Mutation	INS	-	TTTCTATGTTAA	-	NUB1	TCCATTCTCTAT	p.K214delins	RX
XH_P44	7	151842382	151842382	Splice_Site	INS	-	GTATGTTTCTGT	-	KMT2C	.	.	
XH_P44	7	151851434	151851434	Silent	SNP	T	A	T	KMT2C	c.A12057T	p.P4019P	
XH_P44	7	151851436	151851436	In_Frame_Ins	INS	-	TCTTAT	-	KMT2C	54_1205insAT	p.P4019delins	RP
XH_P44	7	151859317	151859317	Frame_Shift_Ins	INS	-	CATTCTACCTC	-	KMT2C	45insGAGAGGT	p.K3782fs	
XH_P44	7	151877180	151877180	Nonsense_Mutation	INS	-	AGTATG	-	KMT2C	80_718insCAT	Q2394delins	PYX
XH_P44	7	151877182	151877183	Frame_Shift_Del	DEL	CT	-	CT	KMT2C	c.7178_7179de	p.Q2393fs	
XH_P44	7	151878461	151878461	Frame_Shift_Ins	INS	-	GTTTAC	-	KMT2C	83_6484insGTAA	p.P2162fs	
XH_P44	7	151878604	151878604	Frame_Shift_Ins	INS	-	TCTACACAACT	-	KMT2C	CAAGTCAGTTTG	p.R2114fs	
XH_P44	7	151927080	151927080	Frame_Shift_Ins	INS	-	TATAAATCTTAT	-	KMT2C	904insTATAAGA	p.Q968fs	
XH_P44	7	151932944	151932944	Frame_Shift_Ins	INS	-	T	-	KMT2C	12726_2727ins	p.R909fs	
XH_P44	7	151932945	151932945	Nonsense_Mutation	INS	-	CTTATCTTCTA	-	KMT2C	2726insTAGAAA	R909delins	IERX
XH_P44	7	154759614	154759614	Nonsense_Mutation	INS	-	TAGATGTAACT	-	PAXIP1	GAACACAGTTA	E603delins	VNTVSTX
XH_P44	7	156451263	156451263	Frame_Shift_Ins	INS	-	TTAGTTGTGCTA	-	RNF32	sCAAGTTAGTTG	p.K228fs	
XH_P44	7	156743306	156743306	Frame_Shift_Ins	INS	-	TCCCGAAATAT	-	NOM1	876insCTCCAG	p.G292fs	
XH_P44	7	157023974	157023974	Nonsense_Mutation	INS	-	AGGAGGAAAG	-	UBE3C	nsGGTGAGGAG	812_5813delins	GX
XH_P44	7	158727201	158727201	Frame_Shift_Ins	INS	-	CCTAAATCAA	-	WDR60	1267insSCCTAA	p.N722fs	
XH_P44	7	158727202	158727202	Frame_Shift_Ins	INS	-	ATATTTA	-	WDR60	67_2168insATA	p.V723fs	
XH_P44	8	1828299	1828299	Frame_Shift_Ins	INS	-	AATGCACAAATA	-	ARHGEF10	30insAAATGCAC	p.I310fs	
XH_P44	8	2824238	2824238	Nonsense_Mutation	INS	-	SACTTTAAGGTC	-	CSMD1	AGTATAACACCT	T2985delins	KTVX
XH_P44	8	3263740	3263740	Frame_Shift_Ins	INS	-	C	-	CSMD1	c.2074_2075ins	p.P692fs	
XH_P44	8	3263741	3263741	Nonsense_Mutation	INS	-	ACTGTGTTAGC	-	CSMD1	1074insAGCTAA	692_693delins	SX
XH_P44	8	6378824	6378824	Nonsense_Mutation	INS	-	AGGGGAAATAT	-	ANGPT2	ATAACATATATT	p.S173delins	X
XH_P44	8	7215856	7215856	In_Frame_Ins	INS	-	AAAGCTCTGGC	-	ZNFR705G	SinsAAGCCAGA	182delins	KARALT
XH_P44	8	7217762	7217762	Nonsense_Mutation	INS	-	GGGTAAACATT	-	ZNFR705G	nsATGAAAGTTT	P78delins	MKVX
XH_P44	8	9437892	9437892	Frame_Shift_Ins	INS	-	A	-	TNKS	c.897_898insA	p.I299fs	
XH_P44	8	9437893	9437893	In_Frame_Ins	INS	-	CACCCATCTGTA	-	TNKS	899insCACCCAT	V300delins	AFICM
XH_P44	8	9578053	9578053	In_Frame_Ins	INS	-	AACTATCTTCTT	-	TNKS	920insGAACCTA	T640delins	RNYLLF
XH_P44	8	9578055	9578055	Missense_Mutation	SNP	G	A	G	TNKS	c.G1921A	p.E641K	
XH_P44	8	9592967	9592967	Nonsense_Mutation	INS	-	TATGTAATAAG	-	TNKS	CATACATATGTA	P873delins	KEKKYIHM
XH_P44	8	12583321	12583321	Frame_Shift_Ins	INS	-	CCCACCTCATCT	-	LONRF1	045insAAGATGA	p.S682fs	
XH_P44	8	17157661	17157661	Frame_Shift_Ins	INS	-	ATAGTGGAAG	-	MTMR7	93insGTCTCTGC	p.H565fs	
XH_P44	8	17402085	17402085	Frame_Shift_Ins	INS	-	TACAGTAGTCA	-	SLC7A2	AATCATACAGTA	p.P168fs	
XH_P44	8	17581198	17581198	Frame_Shift_Ins	INS	-	TCTGAAGTGAT	-	MTU51	insCACCATCAC	p.S811fs	
XH_P44	8	17827209	17827209	Nonsense_Mutation	INS	-	TGAATTAATAAG	-	PCM1	TTAAATGAAATP	91_P1180delins	LALKX
XH_P44	8	18656864	18656864	Splice_Site	INS	-	GGTGCTCGGAG	-	PSD3	.	.	
XH_P44	8	22052044	22052044	Missense_Mutation	SNP	A	T	A	BMP1	c.A1384T	p.I462F	
XH_P44	8	22052045	22052045	Frame_Shift_Ins	INS	-	CTTCC	-	BMP1	385_1386insCT	p.I462fs	
XH_P44	8	22105454	22105454	In_Frame_Ins	INS	-	TTTCAGTTTGCT	-	POLR3D	GATTTTTTCAGT	8delins	GRIFSVCFTL
XH_P44	8	23539147	23539147	Frame_Shift_Ins	INS	-	AAGATATGGTT	-	NKX3-1	292insAACCAT	p.H98fs	
XH_P44	8	24188685	24188685	Frame_Shift_Ins	INS	-	AATATAGTCATA	-	ADAM28	GAGAAAAATATA	p.S376fs	
XH_P44	8	24254926	24254926	Missense_Mutation	SNP	A	G	A	ADAMDEC1	c.A347G	p.K116R	
XH_P44	8	24254927	24254927	Frame_Shift_Ins	INS	-	TAGAGACTATATA	-	ADAMDEC1	insTATAGAGAC	p.K116fs	
XH_P44	8	24774966	24774966	Frame_Shift_Ins	INS	-	ATTCCTCTGTAA	-	NEFM	471insATTCTCT	p.Q157fs	
XH_P44	8	24810342	24810342	Frame_Shift_Ins	INS	-	CCAGC	-	NEFL	612_1613insGC	p.A538fs	
XH_P44	8	24810344	24810344	Frame_Shift_Ins	INS	-	G	-	NEFL	1610_1611ins	p.Q537fs	
XH_P44	8	24811776	24811776	Nonsense_Mutation	INS	-	TTTAAA	-	NEFL	87_1088insTTT	p.S363delins	IX
XH_P44	8	24811778	24811778	Nonsense_Mutation	INS	-	SGATGATTATT	-	NEFL	nsAATATAATAA	362_5363delins	KIX
XH_P44	8	25266412	25266412	In_Frame_Ins	INS	-	GAACAGGCA	-	DOCK5	5361insGAACP	P1787delins	PNRH
XH_P44	8	25766060	25766060	Nonsense_Mutation	INS	-	ATTCACTGCTAC	-	EBF2	nsGGAGTAGGAC	188delins	RSSSEX
XH_P44	8	27610035	27610035	Nonsense_Mutation	INS	-	GAAGGTTGTCT	-	CCDC25	34insTAGACCAAC	I12_Q13delins	X
XH_P44	8	27634030	27634030	Frame_Shift_Ins	INS	-	AAGTAAGCTCT	-	ESCO2	06insTAAGTAA	p.P69fs	
XH_P44	8	27634032	27634032	Silent	SNP	A	T	A	ESCO2	c.A207T	p.P69P	
XH_P44	8	27634461	27634461	In_Frame_Ins	INS	-	CTGTGACAATGC	-	ESCO2	637insCTGTCACT	P212delins	FLSQW
XH_P44	8	27898693	27898693	Nonsense_Mutation	INS	-	GAGGTAAGAGG	-	NUGGC	insCTAACTCTT	6_E497delins	LTLYLFX
XH_P44	8	27925104	27925104	In_Frame_Ins	INS	-	ATGGCTATCAAA	-	NUGGC	5TCCATTGTGATA	Q13delins	FLHAIINN
XH_P44	8	29927225	29927225	Frame_Shift_Ins	INS	-	5CTATGTTAATG	-	SARAF	insAGGCATTAA	p.S39fs	
XH_P44	8	29927312	29927312	In_Frame_Ins	INS	-	TGTGGTTGCTA	-	SARAF	nsACATAGCAAC	10delins	LNIAITTY
XH_P44	8	32617766	32617766	Frame_Shift_Ins	INS	-	TGCTATAGAGA	-	NRG1	insATTGTGCTAT	p.V216fs	
XH_P44	8	33247313	33247313	Frame_Shift_Ins	INS	-	AC	-	FUT10	c.379_380insGT	p.T127fs	
XH_P44	8	33247314	33247314	In_Frame_Ins	INS	-	GTG	-	FUT10	1378_379insCA	p.T127delins	HT
XH_P44	8	38067927	38067927	In_Frame_Ins	INS	-	ATTACCATA	-	BAG4	2_1183insATTAG	G394delins	GITI
XH_P44	8	38110596	38110596	Nonsense_Mutation	INS	-	TTAAATGATTTA	-	DDHD2	nsGAACATATAAT	T614delins	TYKX
XH_P44	8	38205090	38205090	Frame_Shift_Ins	INS	-	ATATATGAATGG	-	NSD3	00insTCCATTCA	p.S200fs	
XH_P44	8	38205091	38205091	Nonsense_Mutation	INS	-	ATTAGTTAAGAA	-	NSD3	insTATTCTCTAA	S200delins	IFLN
XH_P44	8	38386106	38386106	Frame_Shift_Ins	INS	-	AAATCAT	-	C8orf86	49_50insATTGAT	p.S17fs	
XH_P44	8	38840059	38840059	Frame_Shift_Ins	INS	-	GGTTTGTGCCT	-	HTRA4	158insTGGTTTC	p.L386fs	
XH_P44	8	39506044	39506044	Frame_Shift_Ins	INS	-	TAAACAACACTC	-	ADAM18	CACATCTAAACA	p.N386fs	

XH_P44	8	39806681	39806681	In_Frame_Ins	INS	-	AAATTCCTCAT	-	IDO2	AAAGAAATTCCTC	2delinsKLKEIPFSFL
XH_P44	8	39873084	39873084	Frame_Shift_Ins	INS	-	GTGCTGAGTGG	-	IDO2	7insAGGTGCTG	p.D409fs
XH_P44	8	41834784	41834784	Nonsense_Mutation	INS	-	TTA	-	KAT6A	1104_1105insTA	p.T369delinsX
XH_P44	8	41834785	41834785	Nonsense_Mutation	INS	-	AAACAAATAGTA	-	KAT6A	TACAGAATACTA	T369delinsHIVQNTICFX
XH_P44	8	41906446	41906446	Nonsense_Mutation	INS	-	GGTCAGAAAGGA	-	KAT6A	DinsCATCCTCTCT	p.L17delinsTSFX
XH_P44	8	42019852	42019852	Nonsense_Mutation	INS	-	CAACAGAAATA	-	AP3M2	QinsTTCAACAAW	167delinsQITEX
XH_P44	8	42024842	42024842	Frame_Shift_Ins	INS	-	CTTTTCTGCCCT	-	AP3M2	5insTGCTTTTTC	p.S322fs
XH_P44	8	42175259	42175259	In_Frame_Ins	INS	-	TCGTCAGCAAGA	-	IKKB	1205insTGTTCA	R402delinsLFSKR
XH_P44	8	48882505	48882505	Frame_Shift_Ins	INS	-	AGCTTCCCATATC	-	MC4M	1323insACCTTC	p.F441fs
XH_P44	8	53536350	53536350	Frame_Shift_Ins	INS	-	TTAGGAATAAT	-	RB1CC1	GAATTTATTAT	p.K1590fs
XH_P44	8	53569061	53569061	In_Frame_Ins	INS	-	AAAGACAGACA	-	RB1CC1	8insTTTTGTCT	1110delinsFLSVFLK
XH_P44	8	53569579	53569579	Nonsense_Mutation	INS	-	AGTTACAGGAA	-	RB1CC1	AGTTTTAATTC	937_E938delinsKPKX
XH_P44	8	55538237	55538237	Missense_Mutation	SNP	G	T	G	RP1	c.G1795T	p.G599C
XH_P44	8	55538238	55538238	Nonsense_Mutation	INS	-	CACCTGACT	-	RP1	6_1797insCACT	G599delinsGTX
XH_P44	8	55538674	55538674	Frame_Shift_Ins	INS	-	TATTCTCTCAT	-	RP1	3insGTTTATTCT	p.C744fs
XH_P44	8	55539423	55539423	In_Frame_Ins	INS	-	AGTTGGATATG	-	RP1	82insAAAGTTG	994delinsLKLMD
XH_P44	8	55540926	55540926	In_Frame_Ins	INS	-	ATATTACAGGGT	-	RP1	nsTTTTTATATTC	495delinsHFYIQLS
XH_P44	8	55542152	55542152	Frame_Shift_Ins	INS	-	CTCATGAAAAG	-	RP1	11insTCCTCATG	p.A1904fs
XH_P44	8	56436018	56436018	Silent	SNP	G	A	G	XKR4	c.G1185A	p.S395S
XH_P44	8	56436019	56436019	Frame_Shift_Ins	INS	-	AAGACTCTTAAT	-	XKR4	87insCAAGACT	p.V396fs
XH_P44	8	56699331	56699331	Frame_Shift_Ins	INS	-	A	-	TGS1	c.S95_S96insA	p.L199fs
XH_P44	8	56699333	56699333	Frame_Shift_Ins	INS	-	GCTCCCATCTT	-	TGS1	6ATGTTGCTCCC	p.L199fs
XH_P44	8	56911002	56911002	In_Frame_Ins	INS	-	CTCCAATAATGG	-	LYN	1086insCTCCAA	1362delinsINSNG
XH_P44	8	57218276	57218276	Frame_Shift_Ins	INS	-	ACTTTAAAAATA	-	SDR16C5	insAGGTATTTT	p.P195fs
XH_P44	8	61764783	61764783	In_Frame_Ins	INS	-	GCA	-	CHD7	5871_5872insG	A1957delinsAA
XH_P44	8	61764785	61764785	Frame_Shift_Ins	INS	-	TTGCAATACAGA	-	CHD7	874insCTTGCAA	p.L1958fs
XH_P44	8	62489419	62489419	Splice_Site	INS	-	ATTCTCTACAG	-	ASPH	-	-
XH_P44	8	63978585	63978585	Frame_Shift_Ins	INS	-	GGTAAATGTATA	-	TPA	sAAAAATACAT	p.V144fs
XH_P44	8	67062641	67062641	Frame_Shift_Ins	INS	-	ATTTAAAGCAGT	-	TRIM55	ATTAGATTTAA	p.H309fs
XH_P44	8	67062643	67062643	Frame_Shift_Ins	INS	-	ATGCTAT	-	TRIM55	27_928insATGC	p.H309fs
XH_P44	8	67356934	67356934	Frame_Shift_Ins	INS	-	TACATTTTTTAAA	-	ADHFE1	CGTTGTACATT	p.L102fs
XH_P44	8	67488573	67488573	In_Frame_Ins	INS	-	GA AAAATGCGA	-	MYBL1	nsCCCACTCGCA	80delinsTSHFSLL
XH_P44	8	67547318	67547318	In_Frame_Ins	INS	-	5GAAATGGTTTC	-	VCPIP1	087insAAGAAAC	1029delinsGRNHL
XH_P44	8	67577383	67577383	In_Frame_Ins	INS	-	CCAGTACCA	-	VCPIP1	1811insTGGTA	R604delinsMVLG
XH_P44	8	68062140	68062140	Nonsense_Mutation	INS	-	AAGCCATTAT	-	CSPP1	AAAAATAAGCC	N695delinsRKXX
XH_P44	8	68950491	68950491	Frame_Shift_Ins	INS	-	AAGAAGCAAG	-	PREX2	804insAAGAAC	p.F268fs
XH_P44	8	71646513	71646513	Nonsense_Mutation	INS	-	FAAGCAATCTT	-	XKR9	nsAAATAAAGCA	6_L327delinsEIKQSX
XH_P44	8	72184066	72184066	Frame_Shift_Ins	INS	-	GCAAAAGGGCTT	-	EYA1	GAAACAGACCC	p.G265fs
XH_P44	8	72967983	72967983	Nonsense_Mutation	INS	-	AGTTACAGTCTCT	-	TRPA1	802insAAGAAGG	34_F435delinsGRSX
XH_P44	8	74209577	74209577	Frame_Shift_Ins	INS	-	SAGCTTCAAATT	-	RDH10	ACAGTGAGCTTC	p.A146fs
XH_P44	8	74209579	74209579	Missense_Mutation	SNP	G	C	G	RDH10	c.G440C	p.G147A
XH_P44	8	74440034	74440034	Nonsense_Mutation	INS	-	ATTATTTTAGACT	-	STAU2	ACAAGAAAGTCT	Y409delinsQTRSLKX
XH_P44	8	75263620	75263620	In_Frame_Ins	INS	-	AAAATAAGTAA	-	GDAP1	ACACAAATAAA	9delinsEHKISNEM
XH_P44	8	77767269	77767269	Silent	SNP	G	A	G	ZFH4	c.G8112A	p.Q2704Q
XH_P44	8	77767270	77767270	Frame_Shift_Ins	INS	-	TTTTCATAGAGT	-	ZFH4	4insTATTTTCA	p.A2705fs
XH_P44	8	79652261	79652261	Frame_Shift_Ins	INS	-	TTCTTCTTCTCT	-	IL7	AGAAAGAAAGA	p.K68fs
XH_P44	8	81412363	81412363	Frame_Shift_Ins	INS	-	ATTAACTGGTTT	-	ZBTB10	ATCTCTATTAA	p.S536fs
XH_P44	8	82627265	82627265	Nonsense_Mutation	INS	-	CAGAAACTGTGT	-	ZFAND1	23insTAACAAG	V75_A76delinsX
XH_P44	8	87076719	87076719	Frame_Shift_Ins	INS	-	CCTGAGCAATGA	-	PSKH2	TCGACTCATTGC	p.L109fs
XH_P44	8	90955529	90955529	Frame_Shift_Ins	INS	-	TTC	-	NBN	135_2136insGG	p.H712fs
XH_P44	8	90955531	90955531	Nonsense_Mutation	INS	-	TTACAGAGCAT	-	NBN	34insTAATGCT	p.H712delinsX
XH_P44	8	91094923	91094923	Nonsense_Mutation	INS	-	AATCTTATCTCT	-	CALB1	nsAAGAAGATAA	p.M1delinsIRRX
XH_P44	8	93027004	93027004	Frame_Shift_Ins	INS	-	ATAGTGT	-	RUNX1T1	59_160insACAC	p.P54fs
XH_P44	8	94747903	94747903	In_Frame_Ins	INS	-	ATATGCTTTGT	-	RBM12B	nsATCACAAAAG	246delinsITKAYLV
XH_P44	8	94935374	94935374	In_Frame_Ins	INS	-	TGCTCATTAGAC	-	PDP1	1088insTGGTCA	363delinsVVRH
XH_P44	8	95521981	95521981	Nonsense_Mutation	INS	-	TCTATGTTTTAT	-	VIRMA	14insTAATAAA	p.D127delinsX
XH_P44	8	95538875	95538875	Frame_Shift_Ins	INS	-	C	-	VIRMA	1596_1597ins	p.K533fs
XH_P44	8	95538876	95538876	Frame_Shift_Ins	INS	-	TCTTTTGGAATC	-	VIRMA	TTTGAGGATTCT	p.Q532fs
XH_P44	8	95780763	95780763	Missense_Mutation	SNP	T	G	T	DPY19L4	c.T1316G	p.V439G
XH_P44	8	95780765	95780765	In_Frame_Ins	INS	-	CTATCC	-	DPY19L4	18_1319insCTA	p.L44delinsTIL
XH_P44	8	95902778	95902778	Frame_Shift_Ins	INS	-	GTCTTTTTTGAG	-	CCNE2	AGTACCTCAAA	p.S106fs
XH_P44	8	100182360	100182360	In_Frame_Ins	INS	-	TGACAA	-	VPS13B	02_2303insTGA	Y768delinsLTN
XH_P44	8	100403909	100403909	In_Frame_Ins	INS	-	CGCTTTTTTTTT	-	VPS13B	3060insCGCTTT	P1020delinsPAFFF
XH_P44	8	100990172	100990172	Frame_Shift_Ins	INS	-	AA	-	RGS22	2948_2949insT	p.A983fs
XH_P44	8	100990173	100990173	Frame_Shift_Ins	INS	-	CTCAATGATAG	-	RGS22	8insATACTATCA	p.A983fs
XH_P44	8	101020726	101020726	Frame_Shift_Ins	INS	-	AACCATTCAGGT	-	RGS22	TAGTAAACCTG	p.E565fs
XH_P44	8	101300294	101300294	Missense_Mutation	SNP	G	T	G	RNF19A	c.C109A	p.Q37K
XH_P44	8	101300295	101300295	Frame_Shift_Ins	INS	-	TACAAATACCTC	-	RNF19A	8insAAGAGGTA	p.R36fs
XH_P44	8	101534999	101534999	In_Frame_Ins	INS	-	TTG	-	ANKRD46	470_471insCA	p.S157delinsSN
XH_P44	8	101535000	101535000	Splice_Site	INS	-	TTATTA	-	ANKRD46	-	-
XH_P44	8	101730401	101730401	Frame_Shift_Ins	INS	-	G	-	PABPC1	c.300dupC	p.L101fs
XH_P44	8	101730403	101730403	Frame_Shift_Ins	INS	-	TCCAAGGGCTA	-	PABPC1	299insTAGCCC	p.N100fs
XH_P44	8	101936396	101936396	Silent	SNP	G	A	G	YWHAZ	c.C549T	p.N183N
XH_P44	8	101936397	101936397	Frame_Shift_Ins	INS	-	TTTTTATTTAAA	-	YWHAZ	stGTATTTAATA	p.N183fs
XH_P44	8	102555658	102555658	Nonsense_Mutation	INS	-	ACATTAATTTTT	-	GRHL2	3insAAACATTAA	54_Y55delinsYKH
XH_P44	8	102676744	102676744	Frame_Shift_Ins	INS	-	CCCAGCCTCAT	-	GRHL2	1714insCCCAG	p.K571fs
XH_P44	8	102701588	102701588	In_Frame_Ins	INS	-	AGACTTCGT	-	NCALD	531insACGAA	P177delinsPSRL
XH_P44	8	102701590	102701590	Frame_Shift_Ins	INS	-	T	-	NCALD	c.S28_S29insA	p.P177fs
XH_P44	8	103307940	103307940	Nonsense_Mutation	INS	-	AAGGTGAGTTAA	-	UBR5	36insAATTAACT	246_Q1247delinsNX
XH_P44	8	103341620	103341620	Frame_Shift_Ins	INS	-	TAACCAATGAA	-	UBR5	6insTCTTTTCTT	p.T369fs
XH_P44	8	103372376	103372376	Nonsense_Mutation	INS	-	TACAATTAATCT	-	UBR5	nsCCTAGATTAA	03_P104delinsSLDX
XH_P44	8	105361114	105361114	Missense_Mutation	SNP	G	A	G	DCSTAMP	c.G334A	p.E112K
XH_P44	8	105361115	105361115	In_Frame_Ins	INS	-	TCTCCC	-	DCSTAMP	35_336insTCTC	p.E112delinsDLP
XH_P44	8	105510013	105510013	Frame_Shift_Ins	INS	-	GCTTTTGATT	-	LRP12	710insAATCAA	p.V237fs
XH_P44	8	106813682	106813682	Missense_Mutation	SNP	C	A	C	ZFPM2	c.C1372A	p.P458T
XH_P44	8	106813683	106813683	In_Frame_Ins	INS	-	GGTGCAATT	-	ZFPM2	8_1374insGGTG	P458delinsPVHF
XH_P44	8	106815607	106815607	Frame_Shift_Ins	INS	-	G	-	ZFPM2	3297_3298ins	p.E1099fs
XH_P44	8	106815608	106815608	Nonsense_Mutation	INS	-	CTGGCCTTTAGG	-	ZFPM2	3299insCTGGCC	Q110delinsPGLX
XH_P44	8	107726168	107726168	Frame_Shift_Ins	INS	-	ACTTAAAATATA	-	OXR1	891insGACTTAA	p.E630fs
XH_P44	8	108970494	108970494	Frame_Shift_Ins	INS	-	AAAA	-	RSPO2	228_229insTTT	p.G77fs
XH_P44	8	108970495	108970495	In_Frame_Ins	INS	-	AAGTATTTA	-	RSPO2	7_228insTAAAT	p.E76delinsDKYL
XH_P44	8	109482091	109482091	Frame_Shift_Ins	INS	-	ACTCTGTCTCAT	-	EMC2	nsTTTACTCTGT	p.Q143fs
XH_P44	8	110477000	110477000	Frame_Shift_Ins	INS	-	AGCAATTGTCTC	-	PKHD1L1	940insCAGCAT	p.L2647fs
XH_P44	8	113585869	113585869	In_Frame_Ins	INS	-	CAGAGG	-	CSMD3	90_3591insCCT	D1197delinsDLC
XH_P44	8	113585870	113585870	Frame_Shift_Ins	INS	-	AAGTAATTTTG	-	CSMD3	590insTCAAAA	p.D1197fs
XH_P44	8	116599495	116599495	Nonsense_Mutation	INS	-	ATTTTAAATAA	-	TRPS1	sAGGAATATTTT	02_I803delinsEGLIX
XH_P44	8	116616443	116616443	Nonsense_Mutation	INS	-	GTCTGTCAAGG	-	TRPS1	1726insCCTTG	576_577delinsPX
XH_P44	8	117658775	117658775	Frame_Shift_Ins	INS	-	TTCAGTG	-	EIF3H	95_896insCACT	p.E299fs

XH_P44	8	117658777	117658777	Silent	SNP	C	T	C	EIF3H	c.G894A	p.E298E
XH_P44	8	117669517	117669517	Nonsense_Mutation	INS	-	AGTGCTGCTTGC	-	EIF3H	494insGCAAGCA	K165delinsSKQH
XH_P44	8	118169959	118169959	In_Frame_Ins	INS	-	TTTCTCTGG	-	SLC30A8	8_449insTTTCC	C150delinsFSLG
XH_P44	8	118169961	118169961	Missense_Mutation	SNP	C	G	C	SLC30A8	c.C450G	p.C150W
XH_P44	8	120810077	120810077	In_Frame_Ins	INS	-	AAATTTTTTAAAT	-	TA2	CTACATTTTAA	delinsVFLHKNFKTKF
XH_P44	8	121211775	121211775	Frame_Shift_Ins	INS	-	TTTGTAAATAAC	-	COL14A1	8insATTTTGTGA	p.R283fs
XH_P44	8	123964227	123964227	Frame_Shift_Ins	INS	-	TTGG	-	ZHX2	477_478insTTG	p.T159fs
XH_P44	8	123964228	123964228	In_Frame_Ins	INS	-	GTTTTTTGG	-	ZHX2	8_479insGTTTT	N160delinsSFLD
XH_P44	8	124250056	124250056	Frame_Shift_Ins	INS	-	AGAGGTTTCTCT	-	C8orf76	ACAAGAGAAAA	p.L113fs
XH_P44	8	124265864	124265864	Frame_Shift_Ins	INS	-	GAAAA	-	ZHX1	322_232insTT	p.L775fs
XH_P44	8	124265866	124265866	Nonsense_Mutation	INS	-	AGGAAGATGAA	-	ZHX1	21insAACTTCAT	6774_L775delinsX
XH_P44	8	124267665	124267665	Nonsense_Mutation	INS	-	ACCTACAAAT	-	ZHX1	1_522insATTGTAp	S174delinsSLX
XH_P44	8	124382250	124382250	Nonsense_Mutation	INS	-	AGTTTGTAAACAA	-	ATAD2	ATTATTTGTAC	E249delinsKLFVTNLGX
XH_P44	8	125463334	125463334	Nonsense_Mutation	INS	-	AAATTC	-	TRMT12	66_167insAAAT	S56_V57delinsX
XH_P44	8	125989634	125989634	Nonsense_Mutation	INS	-	AGGCTGGAAC	-	ZNF572	1125insAGGCTC	375_R376delinsX
XH_P44	8	125989636	125989636	Nonsense_Mutation	SNP	A	T	A	ZNF572	c.A1126T	p.R376X
XH_P44	8	126087344	126087344	Frame_Shift_Ins	INS	-	AAGATTAGGATC	-	WASHC5	8insGGGATCCTA	p.L144fs
XH_P44	8	128753036	128753036	Nonsense_Mutation	INS	-	TGCTGATGTGT	-	MYC	1198insTGCTG	899_E400delinsLCX
XH_P44	8	132958873	132958873	Missense_Mutation	SNP	C	G	C	EFR3A	c.C251G	p.T84R
XH_P44	8	132958875	132958875	Frame_Shift_Ins	INS	-	TGAAATAAGTC	-	EFR3A	54insCTGAAAT	p.N85fs
XH_P44	8	132962329	132962329	Nonsense_Mutation	INS	-	AAAGTAACAAAC	-	EFR3A	AAAAAAGTAA	124_R125delinsIX
XH_P44	8	132982861	132982861	Frame_Shift_Ins	INS	-	TTGCAATTTTGA	-	EFR3A	CTAGTATTGCAT	p.I341fs
XH_P44	8	132998498	132998498	Nonsense_Mutation	INS	-	ACAACCTTTAAAC	-	EFR3A	AAAAAAACAAC	607_K608delinsAX
XH_P44	8	133883798	133883798	Splice_Site	INS	-	GATAGAACCTGC	-	TG	-	-
XH_P44	8	133899588	133899588	In_Frame_Ins	INS	-	GAGGGCATTTTC	-	TG	nsAATTGTGAGGG	57delinsRNLRAFWF
XH_P44	8	134057335	134057335	Silent	SNP	G	A	G	SLA	c.C54T	p.H18H
XH_P44	8	134057337	134057337	Frame_Shift_Ins	INS	-	CCTTCATGATAT	-	SLA	AAGCATATCATC	p.H18fs
XH_P44	8	134274407	134274407	In_Frame_Ins	INS	-	AAATACTTTTTTA	-	NDRG1	AGTTAAAAAGT	delinsTTVKYKLEQ
XH_P44	8	135614834	135614834	Silent	SNP	C	T	C	ZFAT	c.G942A	p.A314A
XH_P44	8	139145014	139145014	Missense_Mutation	SNP	T	C	T	FAM135B	c.A4043G	p.N1348S
XH_P44	8	139145015	139145015	Frame_Shift_Ins	INS	-	CG	-	FAM135B	4041_4042insC	p.N1348fs
XH_P44	8	139164906	139164907	Frame_Shift_Del	DEL	GG	-	GG	FAM135B	c.1811_1812del	p.A604fs
XH_P44	8	139164907	139164907	Nonsense_Mutation	INS	-	CTTCATCCAT	-	FAM135B	1811insATGGAG	604_I605delinsDGX
XH_P44	8	141900864	141900864	Nonsense_Mutation	INS	-	TTTTCCATGAGA	-	PTK2	GATGTCTCATG	Y13_D14delinsX
XH_P44	8	143928094	143928094	Nonsense_Mutation	INS	-	AATAATTGATTI	-	GML	nsGAAAAATAAT	N155delinsNENNX
XH_P44	8	144733265	144733265	Frame_Shift_Ins	INS	-	CCTTCCCACA	-	ZNF623	1224insCCTTC	p.C408fs
XH_P44	8	144733487	144733487	Frame_Shift_Ins	INS	-	TTCTCCACGTGT	-	ZNF623	nsACTCTCTCTC	p.T482fs
XH_P44	8	144990499	144990510	In_Frame_Del	DEL	AGCCGGTGC	-	GAGCCGGTGC	PLEC	13437_13448del	p.4479_4483del
XH_P44	8	145989851	145989851	In_Frame_Ins	INS	-	GCAGAGTCCAGG	-	ZNF34	1263insGCTGGG	H421delinsQLDSA
XH_P44	8	146067532	146067532	In_Frame_Ins	INS	-	GATAACTTTTTT	-	ZNF7	63insAGATAACT	251delinsSDNFEW
XH_P44	9	339091	339091	Frame_Shift_Ins	INS	-	AGAAATTAGGA	-	DOCK8	TTTTCATAGAAA	p.D435fs
XH_P44	9	3856124	3856124	Frame_Shift_Ins	INS	-	AAGT	-	GLIS3	892_1893insAC	p.S631fs
XH_P44	9	4576632	4576632	Frame_Shift_Ins	INS	-	ATCATGCTAGCC	-	SLC1A1	8insCAATCATG	p.I354fs
XH_P44	9	4685127	4685127	Frame_Shift_Ins	INS	-	AATTTTCTTAAAT	-	CDC37L1	AGTTCAAATTTT	p.T128fs
XH_P44	9	4849493	4849493	Frame_Shift_Ins	INS	-	TATCAAAATCCA	-	RCL1	7insAATATCAA	p.M119fs
XH_P44	9	5089799	5089799	In_Frame_Ins	INS	-	AAATTTTATAAT	-	JAK2	ACAAATAAATT	50delinsITNKFVNYI
XH_P44	9	5720669	5720669	In_Frame_Ins	INS	-	CTCTCCCTTTCG	-	RIC1	insCACCTCTCCC	213delinsAHLSPCI
XH_P44	9	5738513	5738513	Missense_Mutation	SNP	A	T	A	RIC1	c.A876T	p.L292F
XH_P44	9	5738515	5738515	In_Frame_Ins	INS	-	ACAAAG	-	RIC1	78_879insACAA	E293delinsEQR
XH_P44	9	5797933	5797933	Splice_Site	INS	-	CCTCCTT	-	ERMP1	-	-
XH_P44	9	5919869	5919869	Nonsense_Mutation	INS	-	AAAATTTTCAAT	-	KIAA2026	ATAAACATTGAA	43_K2044delinsNKHX
XH_P44	9	5920152	5920152	In_Frame_Ins	INS	-	GTCTCCAGCTAC	-	KIAA2026	44insGAGTAGCT	1948delinsKSSVRL
XH_P44	9	6493875	6493875	Frame_Shift_Ins	INS	-	TTTAAATGCAAT	-	UHRF2	nsAAAAATTTAA	p.A516fs
XH_P44	9	6606621	6606621	Frame_Shift_Ins	INS	-	AGAA	-	GLDC	683_684insTTC	p.Q228fs
XH_P44	9	6606622	6606622	In_Frame_Ins	INS	-	TGA	-	GLDC	c.682_683insTC	p.Q228delinsLK
XH_P44	9	6986655	6986655	Frame_Shift_Ins	INS	-	GGAAGGTACACT	-	KDM4C	GATATAGAAGG	p.K556fs
XH_P44	9	8449832	8449832	In_Frame_Ins	INS	-	GTCTGAAAGGA	-	PTPRD	CTTAATTTCTCT	3delinsNLISFQTFAW
XH_P44	9	13126687	13126687	Nonsense_Mutation	INS	-	AGAGAAATTAGG	-	MPDZ	sCATAACCCCAA	A1485delinsHNPNLSLX
XH_P44	9	14841546	14841546	Nonsense_Mutation	INS	-	GACTTTTATAGA	-	FREM1	TAGATATCTATAp	G594delinsT
XH_P44	9	16436442	16436442	Frame_Shift_Ins	INS	-	TTTCTAAGCATTA	-	BNC2	624insTTATGC	p.S542fs
XH_P44	9	19326072	19326072	In_Frame_Ins	INS	-	AAAAACTACCCC	-	DENN4C	701insAAAAAAC	D667delinsEKNYPF
XH_P44	9	19516195	19516195	In_Frame_Ins	INS	-	CGTCAATACAGG	-	SLC24A2	1891insCCTGTA	V631delinsPVLTV
XH_P44	9	19786007	19786007	Frame_Shift_Ins	INS	-	AAGTGGGCATTA	-	SLC24A2	8insCATTATGCC	p.V286fs
XH_P44	9	19786009	19786009	Missense_Mutation	SNP	C	T	C	SLC24A2	c.G856A	p.V286I
XH_P44	9	20354850	20354850	Frame_Shift_Ins	INS	-	TAGTTTGTTTT	-	MLLT3	1450insAAAAG	p.Q484fs
XH_P44	9	20354851	20354851	In_Frame_Ins	INS	-	CATGTG	-	MLLT3	48_1449insCAC	K483delinsNTW
XH_P44	9	20740316	20740316	In_Frame_Ins	INS	-	CCCAACCACTTAT	-	FOCAD	sCAAAACCACCAA	23delinsNQTTNLSI
XH_P44	9	21077563	21077563	Nonsense_Mutation	INS	-	GGAATCTCAAGC	-	IFNB1	AGTTCCTTAGGA	2_I103delinsEVPX
XH_P44	9	21227906	21227906	Frame_Shift_Ins	INS	-	GAAATACAGCC	-	IFNA17	67insGGGCTGT	p.N89fs
XH_P44	9	21239802	21239802	Nonsense_Mutation	INS	-	AAAATTCTACAT	-	IFNA14	nsTTCAATGTAG	5_R46delinsFNVFFFX
XH_P44	9	21409325	21409325	Frame_Shift_Ins	INS	-	CAACCTCCAGAT	-	IFNA8	51insTCAACCTC	p.F50fs
XH_P44	9	27158135	27158135	In_Frame_Ins	INS	-	GCATCAGAT	-	TEK	9_360insGCATC	Q120delinsQHQI
XH_P44	9	27185586	27185586	Frame_Shift_Ins	INS	-	ATATTACCATC	-	TEK	sAGCCATATTCA	p.V282fs
XH_P44	9	27185588	27185588	In_Frame_Ins	INS	-	ATC	-	TEK	1847_848insATAp	A283delinsDP
XH_P44	9	27218795	27218795	Missense_Mutation	SNP	T	A	T	TEK	c.T2639A	p.L880Q
XH_P44	9	27218796	27218796	Frame_Shift_Ins	INS	-	CAAAGAAACAG	-	TEK	2641insCAAAG	p.L880fs
XH_P44	9	27949601	27949601	Frame_Shift_Ins	INS	-	TAGAATGCAGTG	-	LINGO2	969insGCATCTG	p.L357fs
XH_P44	9	32449030	32449030	Frame_Shift_Ins	INS	-	TTACAAAAGAC	-	ACO1	insAGGTTTACA	p.T836fs
XH_P44	9	32633477	32633477	Frame_Shift_Ins	INS	-	TAGTGGATATTT	-	TAFL1	ACCACAAAATA	p.E701fs
XH_P44	9	33073723	33073723	Frame_Shift_Ins	INS	-	GATCTTGTTCTG	-	SMU1	8insAACAGAAC	p.V36fs
XH_P44	9	33548608	33548608	Frame_Shift_Ins	INS	-	TTTCATGTCTA	-	ANKRD18B	1634insTTTCA	p.G545fs
XH_P44	9	33944615	33944615	Nonsense_Mutation	INS	-	CCCCAGCTTCTA	-	UBAP2	2insTTAGAAAGCT	p.P164delinsPX
XH_P44	9	34089582	34089582	Nonsense_Mutation	INS	-	TACTACTACTTT	-	DCAF12	GTGAAAAAGTA	A_5345delinsLVKKYEX
XH_P44	9	34089584	34089584	Silent	SNP	G	T	G	DCAF12	c.C1029A	p.I343I
XH_P44	9	34098415	34098415	Nonsense_Mutation	INS	-	GTGAGAAATTAAT	-	DCAF12	insGTTATAATT	H234delinsQLX
XH_P44	9	34242066	34242066	Frame_Shift_Ins	INS	-	CAGAGTCAAGT	-	UBAP1	6insCATCAGAG	p.V412fs
XH_P44	9	34343203	34343203	Frame_Shift_Ins	INS	-	TTATTATTATTAT	-	NUDT2	TTTATTATTATT	p.L70fs
XH_P44	9	34497154	34497154	Frame_Shift_Ins	INS	-	ACTACCTCTCTC	-	DNAI1	1insCCACTACCC	p.M290fs
XH_P44	9	34724515	34724515	Frame_Shift_Ins	INS	-	CCAGAAG	-	FAM205A	21_2722insCTTC	p.I908fs
XH_P44	9	34724909	34724909	Frame_Shift_Ins	INS	-	AGGAACAAATG	-	FAM205A	7_2328insCATTG	p.T776fs
XH_P44	9	34993329	34993329	Nonsense_Mutation	INS	-	TAAATGAAAG	-	DNAJB5	nsTCTGTAAATQ	D5_D106delinsPSVKK
XH_P44	9	35092517	35092517	Frame_Shift_Ins	INS	-	CT	-	PIGO	1366_1367insA	p.A456fs
XH_P44	9	35092519	35092519	Frame_Shift_Ins	INS	-	TCCTCCCTTTTC	-	PIGO	65insAGAAAAAG	p.T455fs
XH_P44	9	35398264	35398264	Frame_Shift_Ins	INS	-	TCATTTTTAA	-	UNC13B	3565insTCATT	p.F1188fs
XH_P44	9	35398265	35398265	Nonsense_Mutation	INS	-	CTGGGTGGT	-	UNC13B	3566insCTGG	E1189delinsAGWX
XH_P44	9	35616677	35616677	Frame_Shift_Ins	INS	-	TGTTGCTTCTCTC	-	CDY2	insTTCAGGAAG	p.T91fs
XH_P44	9	35722213	35722213	In_Frame_Ins	INS	-	CTAAGA	-	TLN1	50_851insTCTT	p.K284delinsLE
XH_P44	9	36223390	36223390	In_Frame_Ins	INS	-	TTGGTAACGTT	-	GENE	61insCAACAGT	K354delinsTNVTKD

XH_P44	9	36223392	36223392	Frame_Shift_Ins	INS	-	TTAGG	-	GNE	058_1059insCC	p.L353fs
XH_P44	9	38578116	38578116	Frame_Shift_Ins	INS	-	AAAGATATGGTA	-	ANKRD18A	AAGTTCTACCA	p.A759fs
XH_P44	9	40706040	40706040	Nonsense_Mutation	INS	-	GTGG	-	SPATA31A3	697_3698insGG	233_Q1234delinsSX
XH_P44	9	40706041	40706041	Frame_Shift_Ins	INS	-	GGAG	-	SPATA31A3	698_3699insGG	p.N1233fs
XH_P44	9	40773199	40773199	Silent	SNP	C	T	C	ZNF658	c.G2076A	p.E692E
XH_P44	9	40774925	40774925	Frame_Shift_Ins	INS	-	TGGAGGAA	-	ZNF658	9_350insTTCT	p.K117fs
XH_P44	9	40774927	40774927	Frame_Shift_Ins	INS	-	TTTTGAA	-	ZNF658	47_348insTTCA	p.Q116fs
XH_P44	9	43627263	43627263	Frame_Shift_Ins	INS	-	TTACCCCTCTA	-	SPATA31A6	1424insTAGAG	p.R475fs
XH_P44	9	73235251	73235251	Missense_Mutation	SNP	T	A	T	TRPM3	c.A1345T	p.T449S
XH_P44	9	73235252	73235252	Frame_Shift_Ins	INS	-	GACA	-	TRPM3	343_1344insTG	p.K448fs
XH_P44	9	74360146	74360146	Frame_Shift_Ins	INS	-	GTGAGAGGAG	-	TMEM2	22insCTCTCCTC	p.Q274fs
XH_P44	9	74365220	74365220	Frame_Shift_Ins	INS	-	GTGTGTATATGC	-	TMEM2	ATGTGCATATAC	p.P24fs
XH_P44	9	77693279	77693279	Frame_Shift_Ins	INS	-	AG	-	NMRK1	c.3_4insCT	p.G2fs
XH_P44	9	77693280	77693280	In_Frame_Ins	INS	-	TTATTTCTT	-	NMRK1	2_3insAAGAAATp.M1delinsIRNK	
XH_P44	9	78973803	78973803	In_Frame_Ins	INS	-	TGCTCTCTC	-	PCSK5	8_5549insTGCT	E1850delinsVL5Q
XH_P44	9	78973804	78973804	Missense_Mutation	SNP	A	T	A	PCSK5	c.A5549T	p.E1850V
XH_P44	9	79117786	79117786	Frame_Shift_Ins	INS	-	ATTTCACGTGTA	-	GCNT1	90insAATTTCAC	p.L163fs
XH_P44	9	79117788	79117788	Missense_Mutation	SNP	C	A	C	GCNT1	c.C491A	p.A164D
XH_P44	9	79118584	79118584	Frame_Shift_Ins	INS	-	G	-	GCNT1	1287_1288ins	p.X429delinsX
XH_P44	9	79324208	79324208	Frame_Shift_Ins	INS	-	GATGAAAATGA	-	PRUNE2	982insGTTCATT	p.E994fs
XH_P44	9	79841508	79841508	Nonsense_Mutation	INS	-	CAATAAGAAATT	-	VPS13A	GTGCAACATAAC	451_E452delinsHX
XH_P44	9	79995586	79995586	In_Frame_Ins	INS	-	AATTATGGATAT	-	VPS13A	nsCTGTAATTATTC	092delinsDCNYGYNI
XH_P44	9	80880430	80880430	Frame_Shift_Ins	INS	-	CTACACCCCT	-	CEP78	1772insCTACA	p.N591fs
XH_P44	9	84300775	84300775	Frame_Shift_Ins	INS	-	GGATTGATGGT	-	TLE1	nsTACTACCATCA	p.K54fs
XH_P44	9	84606472	84606472	In_Frame_Ins	INS	-	AAAAGATGGTG	-	SPATA31D1	1088insAAAAGA	A363delinsEKMVS
XH_P44	9	84606473	84606473	Missense_Mutation	SNP	C	T	C	SPATA31D1	c.C1088T	p.A363V
XH_P44	9	84607223	84607223	Frame_Shift_Ins	INS	-	AAGG	-	SPATA31D1	838_1839insAA	p.A613fs
XH_P44	9	84607225	84607225	In_Frame_Ins	INS	-	AGA	-	SPATA31D1	1840_1841insA	p.R614delinsQR
XH_P44	9	84608213	84608213	Nonsense_Mutation	INS	-	TGTTTAATTGG	-	SPATA31D1	2829insTGTTTA	D943delinsDVX
XH_P44	9	84609466	84609466	Nonsense_Mutation	INS	-	GGAAATTCGTA	-	SPATA31D1	082insGGGAAA	p.F1361fs
XH_P44	9	86281319	86281319	Frame_Shift_Ins	INS	-	AATGCTTTGTTA	-	UBQLN1	8insTATTAAACA	p.G426fs
XH_P44	9	86616907	86616907	Nonsense_Mutation	INS	-	CGTTAGAATTG	-	RM1	nsGTTTTCGTTA	L336delinsCFRX
XH_P44	9	86617158	86617158	Frame_Shift_Ins	INS	-	TT	-	RM1	1257_1258insT	p.K419fs
XH_P44	9	86617159	86617159	Nonsense_Mutation	INS	-	AGGATTATGTGA	-	RM1	GTATTAGGATTG	L421delinsRSIRIMX
XH_P44	9	86914627	86914627	Missense_Mutation	SNP	A	T	A	SLC28A3	c.T538A	p.S180T
XH_P44	9	86914629	86914629	Frame_Shift_Ins	INS	-	CCTA	-	SLC28A3	535_536insTAG	p.S179fs
XH_P44	9	88193952	88193952	Silent	SNP	G	A	G	AGTPBP1	c.C3381T	p.F1127F
XH_P44	9	88954996	88954996	Frame_Shift_Ins	INS	-	TCGCGTCCATTG	-	ZCHC6	3insTTGAAATG	p.D388fs
XH_P44	9	90746185	90746185	Nonsense_Mutation	INS	-	ATTTCAG	-	SPATA31C2	66_1767insCTG	p.E589delinsDX
XH_P44	9	91083498	91083498	Frame_Shift_Ins	INS	-	A	-	SPIN1	c.567_568insA	p.D189fs
XH_P44	9	91083499	91083499	Frame_Shift_Ins	INS	-	CTGAAAT	-	SPIN1	58_569insCTGA	p.L190fs
XH_P44	9	94118410	94118410	Frame_Shift_Ins	INS	-	GTCTTTTGTTTG	-	AUH	nsGTTCAACCA	p.A97fs
XH_P44	9	95233043	95233043	In_Frame_Ins	INS	-	TATTAATAATA	-	ASPN	292insTATTATT	N98delinsYYLIN
XH_P44	9	95233044	95233044	Frame_Shift_Ins	INS	-	CATGTAAATGT	-	ASPN	91insTACATTTT	p.T97fs
XH_P44	9	95610784	95610784	Nonsense_Mutation	INS	-	AGCCTATCATAA	-	ZNF484	TAAGGTTATGA	V59_S60delinsVX
XH_P44	9	96439004	96439004	Silent	SNP	C	A	C	PHF2	c.C2961A	p.T987T
XH_P44	9	97062426	97062426	Frame_Shift_Ins	INS	-	A	-	ZNF169	c.13_14insA	p.G5fs
XH_P44	9	97062427	97062427	In_Frame_Ins	INS	-	ATCTGT	-	ZNF169	14_15insATCTG	p.G5delinsGSV
XH_P44	9	99130587	99130587	Nonsense_Mutation	INS	-	CTCTCTATTTTA	-	SLC35D2	3AACTTAAAAAT	A63_F54delinsGNLXK
XH_P44	9	99228000	99228000	Missense_Mutation	SNP	G	A	G	HABP4	c.G683A	p.R28K
XH_P44	9	99580371	99580371	In_Frame_Ins	INS	-	ACACAGGAGAG	-	ZNF782	2insAGTTCTCTC	621delinsQFSPVCS
XH_P44	9	100693386	100693386	Nonsense_Mutation	INS	-	GTACCAAGAAAT	-	HEMGN	CAGATATTTCTT	97delinsVQIQLFTFX
XH_P44	9	100823193	100823193	Frame_Shift_Ins	INS	-	TCATCTTTATTTA	-	NANS	3insACCATCTT	p.L88fs
XH_P44	9	100919878	100919878	Frame_Shift_Ins	INS	-	TCCTCTGAATAT	-	CORO2A	nsTTATATTGCA	p.K22fs
XH_P44	9	102778704	102778704	In_Frame_Ins	INS	-	ATTCTTCACCTT	-	ERP44	nsGCAAAAGGTGA	221delinsSKGEESL
XH_P44	9	103092231	103092231	Frame_Shift_Ins	INS	-	AGAA	-	TEX10	479_1480insTT	p.Q494fs
XH_P44	9	103092232	103092232	Frame_Shift_Ins	INS	-	TTTTTCCCTTG	-	TEX10	1479insCAAGG	p.M493fs
XH_P44	9	103261121	103261121	Nonsense_Mutation	INS	-	AATAAGACATAA	-	SANTD3-TMEF	nsTGTAATAAGA	165_G166delinsVX
XH_P44	9	103348334	103348334	Frame_Shift_Ins	INS	-	AAAAACA	-	CAVIN4	96_697insAAAA	p.E232fs
XH_P44	9	103348336	103348336	In_Frame_Ins	INS	-	CATATTAGT	-	CAVIN4	8_699insCATAT	R233delinsSILV
XH_P44	9	104125062	104125062	Nonsense_Mutation	INS	-	CTAGAATAATTI	-	BAAT	AATGAGAAATT	002_Q303delinsKTX
XH_P44	9	104152876	104152876	In_Frame_Ins	INS	-	TCATCTTTTTTT	-	MRPL50	GAGAAAAAAA	7delinsYEKKDDTFL
XH_P44	9	104170383	104170383	Nonsense_Mutation	INS	-	AAATAAAGTCAA	-	ZNF189	nsAACAAATAAA	R97delinsRNKX
XH_P44	9	104170899	104170899	In_Frame_Ins	INS	-	TCCACAGTAATT	-	ZNF189	GTITTTCCACAG	9delinsTKGFSVTILU
XH_P44	9	104171349	104171349	In_Frame_Ins	INS	-	TCCACACTCAAT	-	ZNF189	8insTTTTCCACA	419delinsTFSTLNT
XH_P44	9	105767870	105767870	Frame_Shift_Ins	INS	-	TCCTTCTTGAAT	-	CYL2	CTTGCCCTCTCT	p.A319fs
XH_P44	9	106892013	106892013	Nonsense_Mutation	INS	-	ATACTTTTGAATC	-	SMC2	nsTTTAACTACTT	p.N960delinsIX
XH_P44	9	107289258	107289258	Nonsense_Mutation	INS	-	TAATCATTTCTTA	-	OR13C4	CGCATAAGAAA	P79delinsRSRIRNDX
XH_P44	9	107299014	107299014	In_Frame_Ins	INS	-	TACATCTCTCTC	-	OR13C3	insCAGAGGAGG	K27delinsNRGGCI
XH_P44	9	107367264	107367264	Frame_Shift_Ins	INS	-	GT	-	OR13C2	c.644_645insAC	p.I215fs
XH_P44	9	107367265	107367265	Frame_Shift_Ins	INS	-	AAACACCTAC	-	OR13C2	c.644insGTAGG	p.I215fs
XH_P44	9	107593292	107593292	Nonsense_Mutation	INS	-	ACTTTTATCTT	-	ABCA1	1806insAAGAT	602_A603delinsQRX
XH_P44	9	108358924	108358924	Nonsense_Mutation	INS	-	AGTTAATTAAGT	-	FTKN	AGTAAGTTAAT	51_S52delinsSVSX
XH_P44	9	111640981	111640981	Nonsense_Mutation	INS	-	TCATGTGTTTAA	-	ELP1	GAATAATTAATA	K859delinsWNNX
XH_P44	9	111662634	111662634	Frame_Shift_Ins	INS	-	TTAGGCTTTCTT	-	ELP1	AGAATAAGAAAC	p.S330fs
XH_P44	9	111855800	111855800	Missense_Mutation	SNP	C	T	C	TMEM245	c.G871A	p.G291R
XH_P44	9	111855802	111855802	In_Frame_Ins	INS	-	GTTCTTTGTCT	-	TMEM245	869insAGAACAAT	T290delinsKNKEP
XH_P44	9	111938959	111938959	Frame_Shift_Ins	INS	-	TT	-	EPB41L4B	2504_2505insA	p.S835fs
XH_P44	9	111938960	111938960	In_Frame_Ins	INS	-	AAGTATTATTATG	-	EPB41L4B	4insTTTCAATAA	835delinsSINTYS
XH_P44	9	112144722	112144722	Silent	SNP	C	A	C	PTPN3	c.G1392T	p.G464G
XH_P44	9	112144724	112144724	Frame_Shift_Ins	INS	-	TTCAAAGTTTTT	-	PTPN3	90insAAAAA	ACT p.G464fs
XH_P44	9	112219643	112219643	In_Frame_Ins	INS	-	TAT	-	PTPN3	174_175insAT	p.H59delinsIH
XH_P44	9	112219645	112219645	Frame_Shift_Ins	INS	-	CAGCTGTTTCTG	-	PTPN3	73insGAGAAAC	p.V58fs
XH_P44	9	113065977	113065977	In_Frame_Ins	INS	-	TGTAGTGTCTC	-	TXNDC8	CCAGTGGAAACA	1delinsDQWNTVF
XH_P44	9	113168587	113168587	Frame_Shift_Ins	INS	-	TCTCCAAACA	-	SVEP1	9293insTGTTT	p.G3098fs
XH_P44	9	113197640	113197640	Nonsense_Mutation	INS	-	TCTACTTTTGTG	-	SVEP1	CTAGTTACAAA	A0_S1591delinsTSYKXK
XH_P44	9	114090215	114090215	Frame_Shift_Ins	INS	-	AGAAACAAGGC	-	OR2K2	499insGCCTTG	p.P167fs
XH_P44	9	114090694	114090694	Frame_Shift_Ins	INS	-	TGTTCACATC	-	OR2K2	5GCAGATGTGTA	p.T7fs
XH_P44	9	114412156	114412156	Nonsense_Mutation	INS	-	TTGGGGTTTCTC	-	DNAJC25	914insTTGGGGG	5_E306delinsWGF
XH_P44	9	114412157	114412157	Frame_Shift_Ins	INS	-	T	-	DNAJC25	c.914_915insT	p.K305fs
XH_P44	9	114480506	114480506	Nonsense_Mutation	INS	-	GATTTGATTGTA	-	C9orf84	TGATTATACAT	p.I629delinsX
XH_P44	9	114486108	114486108	Missense_Mutation	SNP	T	A	T	C9orf84	c.A1609T	p.R537W
XH_P44	9	114486110	114486110	Frame_Shift_Ins	INS	-	GCCCTAC	-	C9orf84	96_1607insGTAC	p.E536fs
XH_P44	9	114911575	114911575	In_Frame_Ins	INS	-	TTGTGGTATATA	-	SUSD1	TATCTATATAC	8delinsLSYIPQYHYA
XH_P44	9	114911577	114911577	Frame_Shift_Ins	INS	-	TTATTTT	-	SUSD1	19_320insAAAA	p.R107fs
XH_P44	9	115932129	115932129	In_Frame_Ins	INS	-	GTG	-	FKBP15	2859_2860insC	p.R954delinsHR
XH_P44	9	115932131	115932131	Nonsense_Mutation	INS	-	AGGGAAGTA	-	FKBP15	7_2858insTACT	R953delinsLPX
XH_P44	9	116181437	116181437	Frame_Shift_Ins	INS	-	A	-	C9orf43	c.337_338insA	p.L113fs

XH_P44	9	116181439	116181439	Frame_Shift_Ins	INS	-	CACACTGCAAAT	-	C9orf43	40insGCACACTG	p.L113fs
XH_P44	9	116191565	116191565	Frame_Shift_Ins	INS	-	NATGGGGTGT	-	C9orf43	5GAAAAATGGG	p.I429fs
XH_P44	9	117104005	117104005	Missense_Mutation	SNP	C	T	C	AKNA	c.G3518A	p.G1173E
XH_P44	9	119413993	119413993	In_Frame_Ins	INS	-	ATATCATCATCA	-	ASTN2	42insTGATGATC	14delinsHDDMM
XH_P44	9	120475252	120475252	Frame_Shift_Ins	INS	-	AATACTTTGAAT	-	TLR4	47insAAATACTT	p.N82fs
XH_P44	9	120476478	120476478	Frame_Shift_Ins	INS	-	CTTATTCATCTG	-	TLR4	nsTGGTCTTATT	p.E491fs
XH_P44	9	123476543	123476551	In_Frame_Del	DEL	CGCGCGCGG	-	CGCGCGCGG	MEGF9	c.86_94del	p.29_32del
XH_P44	9	123550208	123550208	In_Frame_Ins	INS	-	AAAAATTTATGA	-	FBXW2	TTTTCTCATATA	10delinsVFLIKFYKN
XH_P44	9	123550209	123550209	Frame_Shift_Ins	INS	-	AGACTGCTTTTA	-	FBXW2	TGTTTTAAAGAA	p.D10fs
XH_P44	9	123912590	123912590	Frame_Shift_Ins	INS	-	T	-	CNTRL	-2136_2137ins	p.A712fs
XH_P44	9	123912591	123912591	Frame_Shift_Ins	INS	-	TCAAAGAAATAA	-	CNTRL	138insTCAAAG	p.P713fs
XH_P44	9	123920126	123920126	Frame_Shift_Ins	INS	-	ATACATCAACGG	-	CNTRL	950insATACATC	p.C983fs
XH_P44	9	123949270	123949270	In_Frame_Ins	INS	-	TTGCATTTTATT	-	RAB14	nsTATAATAAAA	104delinsSIKKCT
XH_P44	9	125033255	125033255	In_Frame_Ins	INS	-	ATATTATTGCGC	-	MRRF	nsAAAAATATTATT	V29delinsENICLI
XH_P44	9	125289265	125289265	Frame_Shift_Ins	INS	-	ATGATGGTTTTT	-	OR1N1	AAGACAAAAAC	p.L103fs
XH_P44	9	125316344	125316344	Frame_Shift_Ins	INS	-	AGCTCGTTTACA	-	OR1N2	sCATCAGCTCGT	p.I299fs
XH_P44	9	125330214	125330214	Frame_Shift_Ins	INS	-	AAGCT	-	OR1L8	542_543insAGC	p.D181fs
XH_P44	9	125424618	125424618	Nonsense_Mutation	INS	-	TGTAGTGGAAG	-	OR1L1	sGTGATGTAGTG	8_209delinsMVMX
XH_P44	9	125486820	125486820	Silent	SNP	T	G	T	OR1L4	c.T552G	p.P184P
XH_P44	9	125486822	125486822	Frame_Shift_Ins	INS	-	CGATG	-	OR1L4	554_555insCGA	p.V185fs
XH_P44	9	125512749	125512749	Missense_Mutation	SNP	T	G	T	OR1L6	c.T623G	p.I208S
XH_P44	9	125512751	125512751	Frame_Shift_Ins	INS	-	TTCCCAAA	-	OR1L6	5_626insTTCCC	p.V209fs
XH_P44	9	125513049	125513049	Frame_Shift_Ins	INS	-	CT	-	OR1L6	c.923_924insCT	p.R308fs
XH_P44	9	125513051	125513051	Frame_Shift_Ins	INS	-	GGTCTCAG	-	OR1L6	5_926insGGTCT	p.I309fs
XH_P44	9	126202734	126202734	Nonsense_Mutation	INS	-	TTTTACATCTTT	-	DENN1A	ACATTTAAAGAT	p.E465delinsX
XH_P44	9	128246821	128246821	Frame_Shift_Ins	INS	-	TGCTCTCTTTTT	-	MAPKAP1	82insAAAAAAGA	p.D178fs
XH_P44	9	131287614	131287614	Missense_Mutation	SNP	G	T	G	GLE1	c.G1041T	p.K347N
XH_P44	9	131287615	131287615	Frame_Shift_Ins	INS	-	CATACAAGTCA	-	GLE1	sATACCTCATAC	p.L348fs
XH_P44	9	131362384	131362384	Missense_Mutation	SNP	C	T	C	SPTAN1	c.C3509T	p.S1170F
XH_P44	9	131374486	131374486	Nonsense_Mutation	INS	-	SAGAAGAGAATC	-	SPTAN1	insTAAGAGAAG	F.1643delinsFX
XH_P44	9	131479136	131479136	Frame_Shift_Ins	INS	-	T	-	PKN3	-1919_1920ins	p.E640fs
XH_P44	9	131479137	131479137	Frame_Shift_Ins	INS	-	GTTTCTTTTCAT	-	PKN3	1921insGTTTCT	p.E640fs
XH_P44	9	131733139	131733139	In_Frame_Ins	INS	-	TACTCTCTCTTTA	-	NUP188	016insTTACTCT	S339delinsITLPR
XH_P44	9	131733140	131733140	Missense_Mutation	SNP	G	C	G	NUP188	c.G1016C	p.S39T
XH_P44	9	132687436	132687436	In_Frame_Ins	INS	-	AAAAAATAAGG	-	FNPB1	90insTACCTTAT	D264delinsYLIFD
XH_P44	9	133574782	133574782	Splice_Site	INS	-	A	-	EXOSC2	.	.
XH_P44	9	134477523	134477523	In_Frame_Ins	INS	-	TTTTTTTGT	-	RAPGEF1	TCTAAAAACAA	40delinsVSKKKKEIR
XH_P44	9	135201879	135201879	Frame_Shift_Ins	INS	-	GAGTGAAAAATG	-	SETX	ATACTCTCATTT	p.V1702fs
XH_P44	9	135203357	135203357	Frame_Shift_Ins	INS	-	TC	-	SETX	3627_3628insG	p.S1210fs
XH_P44	9	135203358	135203358	Frame_Shift_Ins	INS	-	TGGCAAAACTG	-	SETX	3627insCAGTT	p.N1209fs
XH_P44	9	135205392	135205392	Frame_Shift_Ins	INS	-	GAACATAAAAT	-	SETX	93insGAATTTTA	p.V531fs
XH_P44	10	1063122	1063122	Frame_Shift_Ins	INS	-	TTATCCCTGTTA	-	GPBP4	61insAGTTATCC	p.H620fs
XH_P44	10	5009221	5009221	Nonsense_Mutation	INS	-	CAATAGACCACA	-	AKR1C1	CAAACTAATG	9_V120delinsLLQNX
XH_P44	10	5043818	5043818	Nonsense_Mutation	INS	-	TAGACTATAGAA	-	AKR1C2	TCTATTCTATA	9_H48delinsLSFYSLCX
XH_P44	10	5782359	5782359	Frame_Shift_Ins	INS	-	AGATGTTCCTTG	-	FAM208B	insTGTAGATGT	p.S661fs
XH_P44	10	5789576	5789576	Frame_Shift_Ins	INS	-	TTCT	-	FAM208B	8949_3950insTT	p.E1317fs
XH_P44	10	5789578	5789578	Nonsense_Mutation	INS	-	ATTTGAGAAT	-	FAM208B	3952insATTGTC	B17_V1318delinsEIX
XH_P44	10	5959607	5959607	Frame_Shift_Ins	INS	-	AGTAAGCATAT	-	FBXO18	TAGGAAGTAA	p.I570fs
XH_P44	10	5967407	5967407	Frame_Shift_Ins	INS	-	AGGAAACAAC	-	FBXO18	2675insAGGAA	p.V892fs
XH_P44	10	6157433	6157433	In_Frame_Ins	INS	-	TTTTAAATGATT	-	RBM17	TTTTCTTTTAA	4delinsEFSLNDFSEW
XH_P44	10	11299718	11299718	In_Frame_Ins	INS	-	GTTTAAATA	-	CELF2	7_68insGTTTTAA	L23delinsCFNM
XH_P44	10	11299720	11299720	Frame_Shift_Ins	INS	-	TAATGCTGTAA	-	CELF2	CATGTAATGCTG	p.L23fs
XH_P44	10	12071057	12071057	In_Frame_Ins	INS	-	SAGTTTTCCTCT	-	UPF2	ACTAGGAGGA	8delinsISLGGKLNLF
XH_P44	10	12148385	12148385	In_Frame_Ins	INS	-	TTTTGTTGTTG	-	DHTKD1	038insTTTTTGT	F679delinsFFLVC
XH_P44	10	12148386	12148386	Missense_Mutation	SNP	A	T	A	DHTKD1	c.A2038T	p.I680F
XH_P44	10	13169843	13169843	Missense_Mutation	SNP	G	A	G	OPTN	c.G1341A	p.M447I
XH_P44	10	13169844	13169844	Frame_Shift_Ins	INS	-	TTCTGCCTGT	-	OPTN	1343insTTCTGC	p.K448fs
XH_P44	10	13225085	13225085	Frame_Shift_Ins	INS	-	TTTTTTT	-	MCM10	83_1084insTTT	p.K361fs
XH_P44	10	13225086	13225086	Frame_Shift_Ins	INS	-	TTATTCAAAAT	-	MCM10	85insTTGTTATT	p.D362fs
XH_P44	10	13251278	13251278	Frame_Shift_Ins	INS	-	AGGTGACATTG	-	MCM10	TGTTCAAGGTG	p.E865fs
XH_P44	10	13655837	13655837	Frame_Shift_Ins	INS	-	TACTCTTAAAG	-	PRPF18	ACAATCATCTCT	p.T226fs
XH_P44	10	14950561	14950561	In_Frame_Ins	INS	-	AGATGACAGTC	-	DCLRE1C	580insTTGACTG	N527delinsIDCHLY
XH_P44	10	15145765	15145765	Frame_Shift_Ins	INS	-	TTTTGTCTTTTT	-	RPP38	nsGTGTTTGT	p.S151fs
XH_P44	10	15145767	15145767	Silent	SNP	C	T	C	RPP38	c.C454T	p.L152L
XH_P44	10	15170444	15170444	Frame_Shift_Ins	INS	-	GGAGCGAAAGA	-	NMT2	nsAATCTCTTCT	p.S302fs
XH_P44	10	15879237	15879237	Frame_Shift_Ins	INS	-	GTTGTGAAATG	-	MINDY3	GACAGCATTTCA	p.V8fs
XH_P44	10	16824041	16824041	Frame_Shift_Ins	INS	-	TTCTTTTCTTTT	-	RSU1	CAAAAAAAGAA	p.K51fs
XH_P44	10	16911797	16911797	Nonsense_Mutation	INS	-	ACTGTTACCTTT	-	CUBN	AAGCAGAAAGG	Y3099delinsLNKAERX
XH_P44	10	17756686	17756686	Frame_Shift_Ins	INS	-	TATTTTAGGCTG	-	STAM	sATTGTTATT	p.N413fs
XH_P44	10	18280172	18280172	Frame_Shift_Ins	INS	-	GTGTGAATATA	-	SLC39A12	nsCCAGTGTTGA	p.G320fs
XH_P44	10	18289687	18289687	Frame_Shift_Ins	INS	-	CC	-	SLC39A12	1290_1291insC	p.S430fs
XH_P44	10	18289688	18289688	Nonsense_Mutation	INS	-	ACACTTGA	-	SLC39A12	1_1292insACAC	31_S432delinsYTX
XH_P44	10	18787337	18787337	Nonsense_Mutation	INS	-	TGAAGTAAAA	-	CACNB2	insTTCTGAAGT	A74_E75delinsHFX
XH_P44	10	19338053	19338053	Nonsense_Mutation	INS	-	AAGTAAGTCCA	-	MALRD1	GTAATAAGTAA	2_D63delinsSCNXX
XH_P44	10	19377075	19377075	Frame_Shift_Ins	INS	-	AAAGTGAGCTAT	-	MALRD1	59insGAAGTGA	p.E186fs
XH_P44	10	19422875	19422875	Nonsense_Mutation	INS	-	GCTCTTTAATT	-	MALRD1	ATACATGCTCTT	1_1402delinsTYMLFX
XH_P44	10	19435257	19435257	Frame_Shift_Ins	INS	-	CAATATCTCAGG	-	MALRD1	543insCAATAT	p.T514fs
XH_P44	10	22676915	22676915	In_Frame_Ins	INS	-	TATATAGCATCC	-	SPAG6	77insCTATATAG	H259delinsSHVIAS
XH_P44	10	25312235	25312235	Nonsense_Mutation	INS	-	GATAATTTGGTT	-	THNSL1	AAAAGATAATT	A29delinsQTKNNKRX
XH_P44	10	27964305	27964305	Nonsense_Mutation	INS	-	TTTTAATTATCC	-	MXK	ATTGGGATAAT	p.Y304delinsX
XH_P44	10	30317059	30317059	Frame_Shift_Ins	INS	-	AAGGACTTCTCT	-	JCAD	2018insAGGAA	p.R673fs
XH_P44	10	31138384	31138384	Frame_Shift_Ins	INS	-	GAGT	-	ZNF438	949_950insACT	p.F317fs
XH_P44	10	31138386	31138386	Frame_Shift_Ins	INS	-	AAAATGAT	-	ZNF438	17_948insATCA	p.G316fs
XH_P44	10	31139084	31139084	Frame_Shift_Ins	INS	-	CTCCTGTACAAA	-	ZNF438	insGATTGTGAC	p.Q84fs
XH_P44	10	31791412	31791412	Frame_Shift_Ins	INS	-	GTTTTCTAAAT	-	ZEB1	CAAGGTTTCTT	p.P132fs
XH_P44	10	31810558	31810558	In_Frame_Ins	INS	-	GTTTAGAGGTG	-	ZEB1	74insAGGTTTAC	691delinsERRFGD
XH_P44	10	32562180	32562180	Nonsense_Mutation	INS	-	TGCTCCCTATTT	-	EPC1	sTTTTAAAAATAG	p.O592delinsFX
XH_P44	10	32576113	32576113	In_Frame_Ins	INS	-	AAAGATGGAGG	-	EPC1	065insATCCTCC	Q355delinsQSSIFR
XH_P44	10	32833228	32833228	Nonsense_Mutation	INS	-	ACATTTCTCAAA	-	CCDC7	TGAATAACATT	78_K379delinsQTTEX
XH_P44	10	33208921	33208921	Frame_Shift_Ins	INS	-	TTTGGAG	-	ITGB1	60_1361insCTC	p.V454fs
XH_P44	10	33208922	33208922	Nonsense_Mutation	INS	-	AAATTATTT	-	ITGB1	9_1360insAAAT	p.V454delinsKX
XH_P44	10	38343988	38343988	Nonsense_Mutation	INS	-	TCTGACATATA	-	ZNF33A	nsGTTTCTGAC	18_K319delinsRVSX
XH_P44	10	38344377	38344377	Nonsense_Mutation	INS	-	TGTCGAGTGAG	-	ZNF33A	1344insTGTCCG	A48_C49delinsDVEX
XH_P44	10	38407238	38407238	Nonsense_Mutation	INS	-	TGTTTAATGAGG	-	ZNF37A	160insATGTTTA	A87_C388delinsDVX
XH_P44	10	38407239	38407239	In_Frame_Ins	INS	-	TGAATCTCT	-	ZNF37A	0_1161insTGAA	A387delinsAEFL
XH_P44	10	38407598	38407598	Nonsense_Mutation	INS	-	TTCTTAGATGT	-	ZNF37A	520insGTCTCTTA	507_S508delinsSSX
XH_P44	10	43292456	43292456	Frame_Shift_Ins	INS	-	TCCAACCC	-	BMS1	4_1765insTCCA	p.F588fs
XH_P44	10	43315860	43315860	In_Frame_Ins	INS	-	TATGTA	-	BMS1	57_2758insTAT	V919delinsVYV

XH_P44	10	43326414	43326414	Nonsense_Mutation	INS	-	5AATATTAACGTG	-	BMS1	0insATGAATAT	240_Q1241delinsKX
XH_P44	10	43651229	43651229	Nonsense_Mutation	INS	-	AAAAGATCACT	-	CSGALNACT2	3insCTAAAGA	p.L211delinsLX
XH_P44	10	43882800	43882800	Frame_Shift_Ins	INS	-	TCGGGAGA	-	HNRNPF	2_533insTCTCC	p.H178fs
XH_P44	10	43882802	43882802	Silent	SNP	C	A	C	HNRNPF	c.G531T	p.G177G
XH_P44	10	44053460	44053460	Frame_Shift_Ins	INS	-	ACCTTCAAGTTA	-	ZNF239	5AGTTTAACTTG	p.P23fs
XH_P44	10	44053462	44053462	Missense_Mutation	SNP	C	G	C	ZNF239	c.G66C	p.E22D
XH_P44	10	44111892	44111892	Frame_Shift_Ins	INS	-	TTCTATTCTACAT	-	ZNF485	TAATGTCTTATT	p.E43fs
XH_P44	10	46148447	46148447	Nonsense_Mutation	INS	-	TAATCTCTGCTCT	-	ZFAND4	5CAAAGGCGAGG	2_183delinsSKGRRX
XH_P44	10	46148449	46148449	Nonsense_Mutation	INS	-	ATCTCTCTAT	-	ZFAND4	243insATAGGA	Y81_C82delinsX
XH_P44	10	50121511	50121511	Frame_Shift_Del	DEL	C	-	C	LRRC18	c.690delG	p.T230fs
XH_P44	10	50121513	50121527	In_Frame_Del	DEL	GTGGCCATGT	-	GTGGCCATGTG	LRRC18	c.674_688del	p.225_230del
XH_P44	10	50666985	50666985	In_Frame_Ins	INS	-	AAGGAAGAAGA	-	ERCC6	358insTTTCTTC	1453delinsVSSSLK
XH_P44	10	50666986	50666986	In_Frame_Ins	INS	-	TCTTCT	-	ERCC6	56_4357insAGA	E1453delinsRRE
XH_P44	10	51027505	51027505	Frame_Shift_Ins	INS	-	T	-	PARG	c.1569_1570ins	p.E524fs
XH_P44	10	51027506	51027506	Nonsense_Mutation	INS	-	TCATCTTTTGAT	-	PARG	ATAAACATCAAA	3_E524delinsKEINIKEX
XH_P44	10	51363103	51363103	Frame_Shift_Ins	INS	-	AATATT	-	PARG	44_645insAAAT	p.S215fs
XH_P44	10	51363105	51363105	Nonsense_Mutation	INS	-	AGCC	-	PARG	642_643insGGG	215_P216delinsGX
XH_P44	10	52573730	52573730	In_Frame_Ins	INS	-	ATCCCTACTCAA	-	A1CF	1210insTTGAGT	Q404delinsLSRDQ
XH_P44	10	52573731	52573731	Frame_Shift_Ins	INS	-	GGTTTTCCTTT	-	A1CF	TATTAAGAA	p.Y403fs
XH_P44	10	55943355	55943355	Splice_Site	INS	-	ACATGTGCA	-	PCDH15	.	.
XH_P44	10	61828823	61828823	In_Frame_Ins	INS	-	5AAGAAAAAA	-	ANK3	816insCATCTTT	8939delinsASFFLLQ
XH_P44	10	61828825	61828825	Silent	SNP	T	A	T	ANK3	c.A11814T	p.P3938P
XH_P44	10	62545439	62545439	Frame_Shift_Ins	INS	-	CTGTATTCAAAA	-	CDK1	5GAGCGTGATT	p.M71fs
XH_P44	10	63173285	63173285	Frame_Shift_Ins	INS	-	CTTA	-	TMEM26	613_614insTAA	p.P205fs
XH_P44	10	63173286	63173286	Frame_Shift_Ins	INS	-	GAAGTAGATT	-	TMEM26	5insTTCAATCTA	p.P205fs
XH_P44	10	63760063	63760063	In_Frame_Ins	INS	-	AACACT	-	ARID5B	16_717insAAC	5239delinsRTL
XH_P44	10	63851660	63851660	In_Frame_Ins	INS	-	5AACACAAGTCA	-	ARID5B	10insGGAACAC	570delinsLEHSS
XH_P44	10	63851662	63851662	Silent	SNP	T	C	T	ARID5B	c.T1711C	p.L571L
XH_P44	10	63957814	63957814	Nonsense_Mutation	INS	-	FAGAAAACTCT	-	RTKN2	583insTTAAGAG	p.K561delinsNX
XH_P44	10	63959533	63959533	In_Frame_Ins	INS	-	GAATTAAATACAA	-	RTKN2	ATTATTTTGTAT	insKTCIHYFVLIHLNMS
XH_P44	10	64136182	64136182	In_Frame_Ins	INS	-	AAA	-	ZNF365	230_231insAA	p.S77delinsSK
XH_P44	10	64136184	64136184	In_Frame_Ins	INS	-	TGTTGCTTACT	-	ZNF365	5CCTTCTGTGTC	78delinsAFCCITLK
XH_P44	10	64565121	64565121	Missense_Mutation	SNP	T	A	T	ADO	c.T302A	p.F101Y
XH_P44	10	64966806	64966806	Frame_Shift_Ins	INS	-	TAGTGATATACA	-	JMJD1C	TATTTTGTATAT	p.T1322fs
XH_P44	10	64968884	64968884	Frame_Shift_Ins	INS	-	CACATATCTTAA	-	JMJD1C	nsAATCTTAAGA	p.L171fs
XH_P44	10	64973781	64973781	Nonsense_Mutation	INS	-	CTAGCAAACTC	-	JMJD1C	9insATGGAGTT	7_P498delinsMEFDX
XH_P44	10	64974733	64974733	Frame_Shift_Ins	INS	-	GTCAGAACAG	-	JMJD1C	c.537insCTGTC	p.E179fs
XH_P44	10	67726490	67726490	Silent	SNP	A	T	A	CTNNA3	c.T2280A	p.T260S
XH_P44	10	67726492	67726492	Frame_Shift_Ins	INS	-	ATCTTTTAGGTA	-	CTNNA3	nsATTTTACCTA	p.S760fs
XH_P44	10	69804244	69804244	Frame_Shift_Ins	INS	-	TAAGAGTTTGG	-	HERC4	803insACCAAA	p.D101fs
XH_P44	10	69804246	69804246	In_Frame_Ins	INS	-	TGCTTATG	-	HERC4	0_301insCATAA	D101delinsHKQD
XH_P44	10	70045146	70045146	In_Frame_Ins	INS	-	CCAATAAGTGTT	-	PBLD	713insAACACTT	5238delinsKHLGG
XH_P44	10	70333384	70333384	Frame_Shift_Ins	INS	-	GAATTTTATTCT	-	TET1	5AAGAGGAATT	p.P430fs
XH_P44	10	70405788	70405788	Nonsense_Mutation	INS	-	TATGTGAGTTGG	-	TET1	3303insTATGTG	E1101delinsDMX
XH_P44	10	70405790	70405790	In_Frame_Ins	INS	-	AGG	-	TET1	3304_3305insA	S1102delinsSKG
XH_P44	10	70496741	70496741	Frame_Shift_Ins	INS	-	T	-	CCAR1	c.183dupT	p.Y61fs
XH_P44	10	70496743	70496743	Frame_Shift_Ins	INS	-	ACAAT	-	CCAR1	184_185insACA	p.Q62fs
XH_P44	10	70516235	70516235	Missense_Mutation	SNP	G	A	G	CCAR1	c.G1786A	p.E596K
XH_P44	10	70516236	70516236	Frame_Shift_Ins	INS	-	AAAATTCTAAAA	-	CCAR1	788insAAAAATT	p.E596fs
XH_P44	10	70968522	70968522	Frame_Shift_Ins	INS	-	GACAACCTCTCA	-	SUPV3L1	06insTGGACAA	p.P369fs
XH_P44	10	72619212	72619212	In_Frame_Ins	INS	-	AAGAAG	-	SGPL1	71_572insAAGA	p.I191delinsKEV
XH_P44	10	72619213	72619213	Nonsense_Mutation	INS	-	ATATGGTTAAAA	-	SGPL1	sATAAATATGGT	I191_A192delinsIX
XH_P44	10	73973046	73973046	Frame_Shift_Ins	INS	-	AAATTTGAGATG	-	ASCC1	5CAAACTCTCA	p.L4fs
XH_P44	10	75105004	75105004	Splice_Site	INS	-	AATA	-	CFAP70	.	.
XH_P44	10	75185772	75185772	Frame_Shift_Ins	INS	-	AACTTTTCTTTT	-	MS551	AAAAAAAAG	p.M289fs
XH_P44	10	75258652	75258652	Frame_Shift_Ins	INS	-	A	-	USP54	c.4603_4604ins	p.P1535fs
XH_P44	10	75258654	75258654	Frame_Shift_Ins	INS	-	TTTCTGTTGTTG	-	USP54	2insTAGAACAA	p.H1534fs
XH_P44	10	75530739	75530739	Silent	SNP	G	A	G	SEC24C	c.G3171A	p.K1057K
XH_P44	10	75530741	75530741	Nonsense_Mutation	INS	-	TTTATCTTATG	-	SEC24C	4insTCATTTATCC	E1059delinsHLSLWX
XH_P44	10	75868814	75868814	In_Frame_Ins	INS	-	CCACCTGCT	-	VCL	5_2646insCCAC	D882delinsDHLL
XH_P44	10	76781843	76781843	Frame_Shift_Ins	INS	-	GT	-	KAT6B	2677_2678insG	p.E893fs
XH_P44	10	76781844	76781844	Frame_Shift_Ins	INS	-	AAAATGGT	-	KAT6B	8_2679insAAAA	p.E893fs
XH_P44	10	78761219	78761219	Frame_Shift_Ins	INS	-	TTCCCTCTGATT	-	KCNMA1	12insAAATCAG	p.A738fs
XH_P44	10	78869988	78869988	Frame_Shift_Ins	INS	-	TTCTTGGTGTAT	-	KCNMA1	12insAATACAC	p.V304fs
XH_P44	10	86131621	86131621	Frame_Shift_Ins	INS	-	CTGATCGGTTTG	-	CCSER2	14insGCTGATCG	p.T271fs
XH_P44	10	86131756	86131756	Nonsense_Mutation	INS	-	TGAAGGTGG	-	CCSER2	1_949insTGAAG	p.R316delinsRX
XH_P44	10	86273648	86273648	Nonsense_Mutation	INS	-	TAAGTTTGCTCT	-	CCSER2	TAATGTTTAAAGT	50_K351delinsLQX
XH_P44	10	88768459	88768459	In_Frame_Ins	INS	-	CAAAAAATGGG	-	AGAP11	1insTTCAAAAA	150delinsGKNVWV
XH_P44	10	88950344	88950344	Frame_Shift_Ins	INS	-	AATTTCTCCTCC	-	FAM35A	413insAAATTT	p.F804fs
XH_P44	10	90342033	90342033	Frame_Shift_Ins	INS	-	GATTAGC	-	RNLS	49_150insGCTA	p.H50fs
XH_P44	10	90342035	90342035	Frame_Shift_Ins	INS	-	AATGGAACATA	-	RNLS	5insTACTATTGT	p.H50fs
XH_P44	10	90353841	90353841	Nonsense_Mutation	INS	-	5TTCTTTTAAAT	-	LIPJ	GAAGAGTCTTTA	90delinsKNVESLX
XH_P44	10	90365451	90365451	Missense_Mutation	SNP	A	T	A	LIPJ	c.A857T	p.H286L
XH_P44	10	90365452	90365452	Frame_Shift_Ins	INS	-	CTTTTCCTTTGGA	-	LIPJ	359insCTTTTCC	p.H286fs
XH_P44	10	90522063	90522063	Splice_Site	INS	-	AATTAATAAATA	-	LIPN	.	.
XH_P44	10	91479375	91479375	Frame_Shift_Ins	INS	-	TACAAACAGGA	-	KIF20B	635insATACAA	p.T545fs
XH_P44	10	92509098	92509098	In_Frame_Ins	INS	-	TGCATCCCA	-	HTR7	2_793insTGGGA	A265delinsWDAA
XH_P44	10	93220243	93220243	Nonsense_Mutation	INS	-	TGCATACTAAT	-	HECTD2	329insTGCATAC	10_S111delinsVHTX
XH_P44	10	93389703	93389703	Frame_Shift_Ins	INS	-	GAAAACTATTTT	-	PPP1R3C	TTATAAAAAATAC	p.N312fs
XH_P44	10	94407980	94407980	Nonsense_Mutation	INS	-	ATCCCAACAGG	-	KIF11	CTGGATATCCCA	854delinsQCCEASSSDIIX
XH_P44	10	95093644	95093644	Nonsense_Mutation	INS	-	TCATTTTACAGG	-	MYOF	insACACCTGTA	P1517delinsPHLX
XH_P44	10	95557433	95557433	Frame_Shift_Ins	INS	-	CGCTGGGAAC	-	LG1	1404insCGCTG	p.E468fs
XH_P44	10	95557435	95557435	Silent	SNP	T	C	T	LG1	c.T1405C	p.L469L
XH_P44	10	95791060	95791060	Frame_Shift_Ins	INS	-	AAGCTGTCATT	-	PLCE1	258insAAGCTG	p.S86fs
XH_P44	10	95892177	95892177	Frame_Shift_Ins	INS	-	CT	-	PLCE1	c.529_530insCT	p.S177fs
XH_P44	10	95892178	95892178	Nonsense_Mutation	INS	-	TGTAGATCTGT	-	PLCE1	insCATTGTAGAT	7_T178delinsSIVDLX
XH_P44	10	96322615	96322615	Frame_Shift_Ins	INS	-	TTATACTTACCTA	-	HELLS	nsCTATTATACT	p.S139fs
XH_P44	10	96448004	96448004	Frame_Shift_Ins	INS	-	AGTACATACAC	-	CYP2C18	55insCAGTACT	p.L152fs
XH_P44	10	97096853	97096853	Nonsense_Mutation	INS	-	CTCCCTTCACAT	-	SORBS1	8064insATGTGA	A1022delinsMX
XH_P44	10	97117530	97117530	Nonsense_Mutation	INS	-	ATTTTCTTACCGG	-	SORBS1	5ATGGCCGGTAA	868delinsKWPVRKX
XH_P44	10	97775993	97775993	Frame_Shift_Ins	INS	-	AA	-	CC2D2B	c.444_445insAA	p.E148fs
XH_P44	10	97775995	97775995	Nonsense_Mutation	INS	-	TGACTTGGAGCA	-	CC2D2B	47insTTGACTTG	149_A150delinsHX
XH_P44	10	98405239	98405239	Frame_Shift_Ins	INS	-	CAAACTTCTCTC	-	PIK3AP1	5insAACAGAGG	p.E456fs
XH_P44	10	98408606	98408606	In_Frame_Ins	INS	-	AATACGAACAG	-	PIK3AP1	95insATCTGTT	332delinsNLFEVW
XH_P44	10	98742431	98742431	In_Frame_Ins	INS	-	TTCTGG	-	LCOR	14_2215insTTC	T738delinsTFW
XH_P44	10	99023362	99023362	Nonsense_Mutation	INS	-	TTGGCTAGTTAA	-	ARHGAP19	TAAACTTAACTA	143_V144delinsNX
XH_P44	10	99969066	99969066	In_Frame_Ins	INS	-	TGGAATCTGTA	-	R3HC11	5insGAATGGAA	B99delinsGMESVSF
XH_P44	10	100904126	100904126	Frame_Shift_Ins	INS	-	AACITGTTTTTGT	-	HPSE2	nsCCCCAAAAA	p.K160fs

XH_P44	10	101503023	101503023	Nonsense Mutation	INS	-	ATATGGTAGAAG	-	CUTC	GTATATATGGT	elinsTEKKNVYMVEGKX
XH_P44	10	101658027	101658027	Nonsense Mutation	INS	-	GGGC	-	DNMBP	631_1632insGCY544_I545delinsX	
XH_P44	10	101658028	101658028	In_Frame_Ins	INS	-	GTGATGAAG	-	DNMBP	0_1631insCTTCA_Y544delinsSSSH	
XH_P44	10	102013295	102013295	Frame_Shift_Ins	INS	-	TTAACCATATAA	-	CWF19L1	GATGTTATATGG	p.G32fs
XH_P44	10	102265241	102265241	Nonsense Mutation	INS	-	CTCACCAT	-	SEC31B	5_1056insATGG52_F353delinsSWX	
XH_P44	10	102276694	102276694	Nonsense Mutation	INS	-	STTAGGTACGTC	-	SEC31B	6insAGACGTAC16_E7delinsRTRX	
XH_P44	10	102684696	102684696	Frame_Shift_Ins	INS	-	TTCTG	-	SLF2	938_1939insTTG	p.S646fs
XH_P44	10	103364925	103364925	In_Frame_Ins	INS	-	ACCAAAGAGAA	-	DPDC	134insACCAAGAP145delinsHQREA	
XH_P44	10	103755109	103755109	Frame_Shift_Ins	INS	-	TTAAACTGTGGA	-	C10orf76	154insCTCCACA	p.E385fs
XH_P44	10	103920405	103920405	In_Frame_Ins	INS	-	CCAAATTGG	-	NOLC1	5_1327insCCAA	S442delinsSPNW
XH_P44	10	103920552	103920552	Frame_Shift_Ins	INS	-	TTTCATCATCCTC	-	NOLC1	474insCTTCATC	p.E491fs
XH_P44	10	104117875	104117875	Frame_Shift_Ins	INS	-	TTTGCTAAAGTA	-	GBF1	20insCTTTGCTA	p.M240fs
XH_P44	10	104126947	104126947	Frame_Shift_Ins	INS	-	GGAGAGGTACC	-	GBF1	2540insGGAGA	p.N847fs
XH_P44	10	104127316	104127316	Frame_Shift_Ins	INS	-	TGCC	-	GBF1	541_2642insTG	p.K881fs
XH_P44	10	104127318	104127318	Splice_Site	SNP	G	C	G	GBF1	.	.
XH_P44	10	104129698	104129698	In_Frame_Ins	INS	-	AAAGTTCTCTGG	-	GBF1	97insCAAAGTT	1099delinsTKVLWI
XH_P44	10	104247960	104247960	Missense Mutation	SNP	G	A	G	ACTR1A	c.C262T	p.R88C
XH_P44	10	104632344	104632344	Frame_Shift_Ins	INS	-	AAATCTTATACAT	-	AS3MT	CACTAAATCTTA	p.T104fs
XH_P44	10	104853757	104853757	Frame_Shift_Ins	INS	-	AGTCT	-	NT5C2	386_387insAGA	p.P129fs
XH_P44	10	104853759	104853759	Nonsense Mutation	INS	-	AGCAGTGTGTA	-	NT5C2	ATATACTAACAA	129_L130delinsIYX
XH_P44	10	105165854	105165854	Frame_Shift_Ins	INS	-	AATCAACACTCC	-	PDCD11	nsTCAAATTCAA	p.Q226fs
XH_P44	10	105762295	105762295	In_Frame_Ins	INS	-	CTGTTGAGTTTA	-	SLK	nsTTTGCTGTGG	453delinsNFAVEFIF
XH_P44	10	105762626	105762626	Missense Mutation	SNP	G	T	G	SLK	c.G1690T	p.D564Y
XH_P44	10	105762627	105762627	Frame_Shift_Ins	INS	-	TGCCTCTTTTTC	-	SLK	92insTTTGCTCT	p.D564fs
XH_P44	10	105762741	105762741	Frame_Shift_Ins	INS	-	CACATCATTCTG	-	SLK	1806insCACAT	p.1602fs
XH_P44	10	105763024	105763024	In_Frame_Ins	INS	-	CCTGGTTCCTCA	-	SLK	9insGTTCTCTGG	696delinsVVPSSSL
XH_P44	10	105838341	105838341	Frame_Shift_Ins	INS	-	GCTAGTATATT	-	COL17A1	nsGTAATATAC	p.V19fs
XH_P44	10	106019392	106019392	In_Frame_Ins	INS	-	ATG	-	GSTO1	202_203insAT	p.P68delinsHA
XH_P44	10	112344132	112344132	In_Frame_Ins	INS	-	CCGTTCTTCTCTG	-	SMC3	284insTCGGTTC	428delinsDPFFPG
XH_P44	10	112344134	112344134	Nonsense Mutation	SNP	A	T	A	SMC3	c.A1285T	p.K429X
XH_P44	10	113926255	113926255	Frame_Shift_Ins	INS	-	CTGTAAA	-	GPAM	25_1126insTTTTA	p.E376fs
XH_P44	10	113926257	113926257	Frame_Shift_Ins	INS	-	GGACTATGATAA	-	GPAM	24insCCTTTATCA	p.N375fs
XH_P44	10	114889731	114889731	Frame_Shift_Ins	INS	-	T	-	TCF7L2	c.108_109insT	p.L36fs
XH_P44	10	114889733	114889733	In_Frame_Ins	INS	-	AACTTTCTCTGT	-	TCF7L2	insAAAAAATTTN	37delinsKTFESVP
XH_P44	10	115534738	115534738	In_Frame_Ins	INS	-	CTAGCATCAAAT	-	PLEKH51	0insGCTAGCAT	T223delinsTASIKF
XH_P44	10	115609113	115609113	Nonsense Mutation	INS	-	AAAGTCAAAGTC	-	DCLRE1A	1751insGACTTT	p.N584delinsRLX
XH_P44	10	115609115	115609115	Frame_Shift_Ins	INS	-	C	-	DCLRE1A	1748_1749ins	p.I583fs
XH_P44	10	115917438	115917438	In_Frame_Ins	INS	-	AAAAATAATACA	-	CCDC186	84insAATGTATT	L212delinsNVFILL
XH_P44	10	115922699	115922699	In_Frame_Ins	INS	-	5AAAGTGTGTG	-	CCDC186	329insCACACAC	E110delinsAHTFQ
XH_P44	10	115922700	115922700	In_Frame_Ins	INS	-	AAGATAAAT	-	CCDC186	7_328insATTTA	p.E110delinsLYLE
XH_P44	10	115947769	115947769	Frame_Shift_Ins	INS	-	TCTCCCAAATATA	-	TDRD1	10insATTCTCCCA	p.N60fs
XH_P44	10	115962882	115962882	Frame_Shift_Ins	INS	-	GG	-	TDRD1	c.748_749insGG	p.I250fs
XH_P44	10	115962883	115962883	In_Frame_Ins	INS	-	TATTTCAAAAAA	-	TDRD1	GACTTTATTTC	50delinsIDFISKMKM
XH_P44	10	116595395	116595395	Frame_Shift_Ins	INS	-	TTAATAAC	-	FAM160B1	4_395insTTAAT	p.V132fs
XH_P44	10	116595397	116595397	Nonsense Mutation	INS	-	AATTTTCAATCAA	-	FAM160B1	ATAAAATTTTCA	B32_Q133delinsVSEX
XH_P44	10	116735053	116735053	Frame_Shift_Ins	INS	-	ACCCAAAAGTA	-	TRUB1	966insACCCAA	p.P322fs
XH_P44	10	116931009	116931009	Frame_Shift_Ins	INS	-	CATAAAGATGT	-	ATRN1L	TCCATACATAAA	p.A436fs
XH_P44	10	118351378	118351378	Frame_Shift_Ins	INS	-	TTTGTTTAGAA	-	PNLIPRP1	146insTTTGT	p.P49fs
XH_P44	10	118700048	118700048	Frame_Shift_Ins	INS	-	CC	-	SHTN1	c.606_607insGG	p.L203fs
XH_P44	10	118700049	118700049	In_Frame_Ins	INS	-	CCITTT	-	SHTN1	05_606insAAAA	L202delinsLKG
XH_P44	10	119798648	119798648	Nonsense Mutation	INS	-	AGGTAAGCTTAA	-	RAB11FIP2	00insTATTAAGG	F7_D368delinsLSLPX
XH_P44	10	120450901	120450901	In_Frame_Ins	INS	-	TTTGATTITGTG	-	CACUL1	5CTTCCACAAAA	01delinsLPQNNLIA
XH_P44	10	120488899	120488899	Nonsense Mutation	INS	-	ATATAAATTTAT	-	CACUL1	ACATTTATAAAT	C170delinsQHSPRKHLX
XH_P44	10	120817553	120817553	Nonsense Mutation	INS	-	ACGGAGTATTAT	-	EIF3A	892insGATAAT	F531_K632delinsRX
XH_P44	10	121347713	121347713	Nonsense Mutation	INS	-	AGAATGGAGTTT	-	TIAL1	AAATAAACTCC	D27_L28delinsLXX
XH_P44	10	123974950	123974950	Frame_Shift_Ins	INS	-	TTAACGCTATT	-	TACC2	nsACTTTTAAACA	p.S521fs
XH_P44	10	124593427	124593427	In_Frame_Ins	INS	-	AAGTGCAAGTG	-	CUZD1	112insGCCACTT	471delinsCHLHFD
XH_P44	10	124753620	124753620	In_Frame_Ins	INS	-	TATGAAAT	-	IKZF5	5_936insATTTTG	S312delinsRFSY
XH_P44	10	126138353	126138353	Missense Mutation	SNP	C	T	C	NKX1-2	c.G160A	p.E54K
XH_P44	10	127520062	127520062	Nonsense Mutation	INS	-	CTATTTGAAAAA	-	BCCIP	5GAATCTATTGT	163delinsVEQLDKFLNDIX
XH_P44	10	127526859	127526859	In_Frame_Ins	INS	-	GTGGATGATACC	-	DHX32	1979insGGTATC	K660delinsRYHPQ
XH_P44	10	127542662	127542662	Missense Mutation	SNP	C	A	C	DHX32	c.G960T	p.K320N
XH_P44	10	127548346	127548346	Nonsense Mutation	INS	-	TTTTAATAACTA	-	DHX32	5TATGTTAGTTA	5_N226delinsLKPVCX
XH_P44	10	129902350	129902350	Frame_Shift_Ins	INS	-	AGAAGGCCAA	-	MKI67	6674insTTGGC	p.P2225fs
XH_P44	10	129903713	129903713	Frame_Shift_Ins	INS	-	CCAGACCCAGTG	-	MKI67	11insCCCATCTGG	p.V1771fs
XH_P44	10	129904227	129904227	In_Frame_Ins	INS	-	AAAGCGTTTAA	-	MKI67	7insTTCCTTAA	599delinsDSLNALM
XH_P44	10	129907680	129907680	Frame_Shift_Ins	INS	-	ATACAGAAATTT	-	MKI67	1344insCAATTT	p.N448fs
XH_P44	10	131639249	131639249	In_Frame_Ins	INS	-	CGTCCAAAT	-	EBF3	2_1393insATTTG	P465delinsWTP
XH_P44	10	134151166	134151166	In_Frame_Ins	INS	-	5AAAGAACCAC	-	LRRC27	GAAAGAAAAG	03delinsIRKKRTRTP
XH_P44	10	134161716	134161716	Missense Mutation	SNP	G	A	G	LRRC27	c.G401A	p.R134H
XH_P44	10	135439504	135439504	Splice_Site	INS	-	AGCCCTCACT	-	FRG2B	.	.
XH_P44	11	3744548	3744548	Nonsense Mutation	INS	-	GATATTCAACAT	-	NUP98	036insTATGTTG	579_N680delinsICX
XH_P44	11	4389127	4389127	Nonsense Mutation	INS	-	TTTTATTTCCTA	-	OR52B4	sCATATAGGAA	133_Y134delinsSIX
XH_P44	11	4608370	4608370	In_Frame_Ins	INS	-	TAAGGAGGAAG	-	OR52I2	29insCAAGGAG	K110delinsSTRKE
XH_P44	11	4790729	4790729	Nonsense Mutation	INS	-	TGTCCTGTGATA	-	OR51F1	AGATATATGAC	140_S141delinsSEX
XH_P44	11	4791048	4791048	Frame_Shift_Ins	INS	-	TAGGTATCCTCT	-	OR51F1	0insCAGAGGAT	p.C34fs
XH_P44	11	4967553	4967553	In_Frame_Ins	INS	-	AGATTTAACAGT	-	OR51A4	778insACTGTTA	A260delinsTVKSA
XH_P44	11	4976547	4976547	In_Frame_Ins	INS	-	GGCTTTTTTGGG	-	OR51A2	7insCTCCAAAA	133delinsLOKSHR
XH_P44	11	5172793	5172793	Nonsense Mutation	INS	-	TCTACGTGACTA	-	OR52A1	7insATTAGTCAC	9_H270delinsSLVTX
XH_P44	11	5173163	5173163	In_Frame_Ins	INS	-	GATATTATACAC	-	OR52A1	AAACTGTGATA	6delinsKNCDDYLDV
XH_P44	11	5345238	5345238	Frame_Shift_Ins	INS	-	GTCTTTTTCATT	-	OR51B2	TGAAAAATGAAA	p.L97fs
XH_P44	11	5364536	5364536	Nonsense Mutation	INS	-	TTTGTGCTGGAT	-	OR51B5	AGATAATCAGC	p.L73delinsLRX
XH_P44	11	5373361	5373361	In_Frame_Ins	INS	-	AGGATAGAGGT	-	OR51B6	625insAGGATAG	D208delinsDRIEV
XH_P44	11	5373363	5373363	Missense Mutation	SNP	T	A	T	OR51B6	c.T626A	p.F209Y
XH_P44	11	5373456	5373456	Frame_Shift_Ins	INS	-	AGGCGAACAA	-	OR51B6	720insAGGCGA	p.V240fs
XH_P44	11	5411085	5411085	Nonsense Mutation	INS	-	GATAGTAGA	-	OR51M1	7_458insGATAG	p.V153delinsGX
XH_P44	11	5411087	5411087	Silent	SNP	G	A	G	OR51M1	c.G459A	p.V153V
XH_P44	11	5603105	5603105	Frame_Shift_Ins	INS	-	SCGGAAGACTG	-	OR52B6	00insGGCGGAA	p.G333fs
XH_P44	11	5632387	5632387	Frame_Shift_Ins	INS	-	AGGTCCAGATA	-	TRIM6	8insGAAGGTCCA	p.V253fs
XH_P44	11	5686217	5686217	Frame_Shift_Ins	INS	-	CCCCTTCT	-	TRIM5	3_1304insAGAA	p.P435fs
XH_P44	11	5686218	5686218	Frame_Shift_Ins	INS	-	T	-	TRIM5	1302_1303ins	p.P435fs
XH_P44	11	5776676	5776676	Missense Mutation	SNP	C	T	C	OR52N4	c.C706T	p.R236W
XH_P44	11	5776677	5776677	Nonsense Mutation	INS	-	AAAGTAAAGGG	-	OR52N4	TGAGGAAAGTA	236_Q237delinsRX
XH_P44	11	5862422	5862422	In_Frame_Ins	INS	-	GTCTCTCTTAGC	-	OR52E6	6insATGCTAAG	236delinsMLRETL
XH_P44	11	6424414	6424414	Frame_Shift_Ins	INS	-	G	-	APBB1	c.404_405insC	p.E135fs
XH_P44	11	6424415	6424415	Nonsense Mutation	INS	-	TTAGTTCAGAAC	-	APBB1	04insTGTTCTGA	135_E136delinsVFXX
XH_P44	11	6790032	6790032	Frame_Shift_Ins	INS	-	ATCCCTGA	-	OR2AG2	6_157insTCAGG	p.A53fs
XH_P44	11	6790034	6790034	Frame_Shift_Ins	INS	-</					

XH_P44	11	6806862	6806862	Frame_Shift_Ins	INS	-	AGGGTCAT	-	OR2AG1	4_595insAGGG	p.M198fs
XH_P44	11	6898145	6898145	Frame_Shift_Ins	INS	-	AATCTAG	-	OR10A4	57_268insAATC	p.Q89fs
XH_P44	11	6898147	6898147	Frame_Shift_Ins	INS	-	TCATATGTTATT	-	OR10A4	AAATCTCATATG	p.D90fs
XH_P44	11	6898707	6898707	In_Frame_Ins	INS	-	AGAAGAAGTGG	-	OR10A4	830insAGAAGAA	277delinsQKKWF
XH_P44	11	6942464	6942464	Frame_Shift_Ins	INS	-	GCCTG	-	OR2D3	232_233insGCC	p.F78fs
XH_P44	11	6977027	6977027	In_Frame_Ins	INS	-	GAAAAAATACT	-	ZNF215	820insGAAAAAA	L273delinsLEKNT
XH_P44	11	7063690	7063690	Frame_Shift_Ins	INS	-	ATCAGAGCTGGT	-	NLRP14	insAAATCAGAG	p.G145fs
XH_P44	11	7818238	7818238	Nonsense_Mutation	INS	-	ATACTACTCTCTT	-	OR5P2	ATAGAAGGAAC84	R85delinsEEX
XH_P44	11	7847312	7847312	Nonsense_Mutation	INS	-	GGAGCTCGCATC	-	OR5P3	AGATGATGCAGD70	I71delinsRX
XH_P44	11	8662001	8662001	Frame_Shift_Ins	INS	-	A	-	TRIM66	1485_1486ins	p.P496fs
XH_P44	11	8662002	8662002	In_Frame_Ins	INS	-	ACC	-	TRIM66	1484_1485insGp	S495delinsRV
XH_P44	11	8717052	8717052	Nonsense_Mutation	INS	-	AACAGGTGTTA	-	ST5	2077insTAACA693	T694delinsX
XH_P44	11	8718128	8718128	Frame_Shift_Ins	INS	-	TA	-	ST5	1877_1878insT	p.T626fs
XH_P44	11	8718129	8718129	Frame_Shift_Ins	INS	-	AAACT	-	ST5	876_1877insAG	p.T626fs
XH_P44	11	8959339	8959339	In_Frame_Ins	INS	-	ATAATATCACAA	-	ASCL3	CCCATTTTGTGA24	delinsTPFCDIHFY
XH_P44	11	9051593	9051593	Splice_Site	INS	-	ATGTAGATGTT	-	SCUBE2	-	-
XH_P44	11	9113009	9113014	In_Frame_Del	DEL	GCAGCA	-	GCAGCA	SCUBE2	c.62_67del	p.21_23del
XH_P44	11	9229112	9229112	Frame_Shift_Ins	INS	-	TGTTATTCAAT	-	DENND5A	AGTATATTGAA	p.T59fs
XH_P44	11	9735126	9735126	Frame_Shift_Ins	INS	-	AAAGACAAAGC	-	SWAP70	55insGAAAGAC	p.I118fs
XH_P44	11	9879938	9879938	Frame_Shift_Ins	INS	-	AAAAAAACTCT	-	SBF2	1935insAGAGT	p.L645fs
XH_P44	11	9879940	9879940	Frame_Shift_Ins	INS	-	CTAC	-	SBF2	932_1933insGT	p.L645fs
XH_P44	11	10051381	10051381	Nonsense_Mutation	INS	-	AGGTCATGAGGT	-	SBF2	AATTAACCTCAT8	N149delinsSKLTSX
XH_P44	11	10582213	10582213	In_Frame_Ins	INS	-	SATAATTCATAG	-	LYVE1	5GGATTCTATGA78	delinsGFVELSVI
XH_P44	11	10582215	10582215	Frame_Shift_Ins	INS	-	CCTGTCTT	-	LYVE1	9_530insAAGAC	p.T177fs
XH_P44	11	10781816	10781816	Frame_Shift_Ins	INS	-	CCCTCTCTCTAT	-	CTR9	90insCCCTCTCC	p.K230fs
XH_P44	11	10821134	10821134	Nonsense_Mutation	INS	-	CAGTGCCTGTAC	-	EIF4G2	insGCATACAGG725	delinsQHTGHX
XH_P44	11	10875217	10875217	Nonsense_Mutation	INS	-	GTTTTCTACAG	-	ZBED5	CACTGAGTGTAG142	6delinsKNHX
XH_P44	11	10875503	10875503	Frame_Shift_Ins	INS	-	GAGGAAATGGG	-	ZBED5	990insCCCCATT	p.K330fs
XH_P44	11	11373969	11373969	Nonsense_Mutation	INS	-	GCACCCCT	-	CSNK2A3	7_698insAGGGG233	H234delinsX
XH_P44	11	12263933	12263933	Frame_Shift_Ins	INS	-	ATACACCTCA	-	MICAL2	2511insATACA	p.S837fs
XH_P44	11	12951873	12951873	Frame_Shift_Ins	INS	-	TAGAATCCATT	-	TEAD1	TATACATAGAA	p.L389fs
XH_P44	11	12951875	12951875	Splice_Site	SNP	T	G	T	TEAD1	-	-
XH_P44	11	14502425	14502425	Frame_Shift_Ins	INS	-	SAATTTTTTAA	-	COPB1	sATATTTTTTAA	p.V364fs
XH_P44	11	14502427	14502427	Missense_Mutation	SNP	C	G	C	COPB1	c.G1090C	p.V364L
XH_P44	11	17527495	17527495	Frame_Shift_Ins	INS	-	CAGA	-	USH1C	2014_2015insTC	p.T672fs
XH_P44	11	17650783	17650783	Frame_Shift_Ins	INS	-	TCTGACAAACAT	-	OTOG	CCATCATCTGTAC	p.Q2223fs
XH_P44	11	18108563	18108563	Missense_Mutation	SNP	G	T	G	SAAL1	c.C892A	p.L298I
XH_P44	11	18591911	18591911	Frame_Shift_Ins	INS	-	ATACTGCATTTT	-	UEVLD	41insGAAATG	p.N47fs
XH_P44	11	18637393	18637393	Frame_Shift_Ins	INS	-	GCTGAGAAGA	-	SPTY2D1	428insTCTTCT	p.Y143fs
XH_P44	11	18637395	18637395	Missense_Mutation	SNP	C	A	C	SPTY2D1	c.G426T	p.E142D
XH_P44	11	19173867	19173867	In_Frame_Ins	INS	-	GAAGTGAAGAA	-	ZDHHC13	ATTCAGAACTGA19	delinsKYEELRNFF
XH_P44	11	20070657	20070657	Missense_Mutation	SNP	C	G	C	NAV2	c.C1544G	p.S515C
XH_P44	11	20070658	20070658	Frame_Shift_Ins	INS	-	TGTAGAGAGG	-	NAV2	1546insGTAG	p.S515fs
XH_P44	11	20411345	20411345	In_Frame_Ins	INS	-	NCCTAAAACCAA	-	PRMT3	insTACCTAAAAA	L28delinsLYLKPI
XH_P44	11	20939779	20939779	Nonsense_Mutation	INS	-	IGACATCCAGT	-	NELL1	insCAAGACACA2	C163delinsPKTHQX
XH_P44	11	26569001	26569001	Nonsense_Mutation	INS	-	TAATTAATCCAA	-	ANO3	56insTTAATTA252	L253delinsCX
XH_P44	11	26569003	26569003	Missense_Mutation	SNP	C	A	C	ANO3	c.C575A	p.L253M
XH_P44	11	27520330	27520330	Frame_Shift_Ins	INS	-	TG	-	LIN7C	c.459_460insCA	p.E154fs
XH_P44	11	27520331	27520331	Frame_Shift_Ins	INS	-	GAAAAAGTAAA	-	LIN7C	9insCCTTTTACT	p.H153fs
XH_P44	11	27680043	27680043	In_Frame_Ins	INS	-	AGGAATACAAA	-	BDNF	9insTTTTTGTAT	E23delinsDFCIPP
XH_P44	11	28119474	28119474	Frame_Shift_Ins	INS	-	TATTTGTT	-	KIF18A	0_21insAACAA	p.D7fs
XH_P44	11	28119476	28119476	In_Frame_Ins	INS	-	ATTGGGATTTA	-	KIF18A	insATTAAATCCD7	delinsIKSQID
XH_P44	11	30352636	30352636	In_Frame_Ins	INS	-	TTAGGTCATGGC	-	ARL14EP	nsGGTTTAGGTC47	delinsGGGLHGL
XH_P44	11	30928205	30928205	Frame_Shift_Ins	INS	-	G	-	DCDC1	c.1306_1307ins	p.M436fs
XH_P44	11	30928206	30928206	Nonsense_Mutation	INS	-	GTGTCTTTTA	-	DCDC1	1306insTAAAA436	R437delinsX
XH_P44	11	31131841	31131841	In_Frame_Ins	INS	-	GCTTGG	-	DCDC1	09_410insCCAA	D137delinsAKH
XH_P44	11	31131843	31131843	Frame_Shift_Ins	INS	-	CTGGTTTT	-	DCDC1	7_408insAAAA	p.S136fs
XH_P44	11	31703477	31703477	Missense_Mutation	SNP	T	C	T	ELP4	c.T1286C	p.M429T
XH_P44	11	32635267	32635267	In_Frame_Ins	INS	-	SATGTTGGAAAC	-	CCDC73	7insATCCTTTCC86	delinsYPFOHPH
XH_P44	11	32636042	32636042	Frame_Shift_Ins	INS	-	GAAAAACTATGT	-	CCDC73	22insACACATAC	p.P608fs
XH_P44	11	33076258	33076258	Nonsense_Mutation	INS	-	AAAAGCAGAGA	-	TCP11L1	insCCTAAAAAGC	L95_P96delinsSX
XH_P44	11	33564550	33564550	Frame_Shift_Ins	INS	-	GCTGTTTCTGT	-	KIAA1549L	551insGCTGTT	p.Q184fs
XH_P44	11	33566325	33566325	Frame_Shift_Ins	INS	-	A	-	KIAA1549L	c.1896dupA	p.S632fs
XH_P44	11	33566327	33566327	Nonsense_Mutation	INS	-	GTGACTACTGTG	-	KIAA1549L	8insGAGGTGAC633	K634delinsX
XH_P44	11	33881074	33881074	Frame_Shift_Ins	INS	-	TGGGGGTTTGA	-	LMO2	05insCTCAAAAC	p.R102fs
XH_P44	11	35250771	35250771	Frame_Shift_Ins	INS	-	IAGTGAGGTCCC	-	CD44	15insAAGTGAG	p.Q305fs
XH_P44	11	35308484	35308484	Frame_Shift_Ins	INS	-	A	-	SLC1A2	c.1105_1106ins	p.P369fs
XH_P44	11	35308485	35308485	Frame_Shift_Ins	INS	-	5CCACCTGAATT	-	SLC1A2	105insAAATTCA	p.P369fs
XH_P44	11	40136571	40136571	Frame_Shift_Ins	INS	-	ATATAAACAGTG	-	LRR4C4	2insTCCCACTGT	p.Y424fs
XH_P44	11	43905557	43905557	Nonsense_Mutation	INS	-	TAAACTACTTTC	-	ALKBH3	CTTCTTAAAAC70	delinsFLKLLHX
XH_P44	11	45991409	45991409	Frame_Shift_Ins	INS	-	AAAGGGAACAT	-	PHF21A	TTAGAAATAGTT	p.I219fs
XH_P44	11	46369371	46369371	Splice_Site	INS	-	AAAGCCA	-	DGK2	-	-
XH_P44	11	46884283	46884283	In_Frame_Ins	INS	-	AGAAGTGAATG	-	LRP4	9insATTACATT753	delinsKLHVSLL
XH_P44	11	46898083	46898083	Frame_Shift_Ins	INS	-	GTGACAGTACAC	-	LRP4	70insCACTGTAC	p.M1157fs
XH_P44	11	46898891	46898891	Splice_Site	INS	-	CTTCAACAA	-	LRP4	-	-
XH_P44	11	47298402	47298402	Frame_Shift_Ins	INS	-	CC	-	MADD	1083_1084insC	p.A361fs
XH_P44	11	47298403	47298403	Frame_Shift_Ins	INS	-	CCCAATC	-	MADD	84_1085insCCC	p.S362fs
XH_P44	11	47707599	47707599	Frame_Shift_Ins	INS	-	AGCGTGGTTTAA	-	AGBL2	CAATTCTTAAAA	p.L545fs
XH_P44	11	47746242	47746242	Frame_Shift_Ins	INS	-	AGGAAGATACCC	-	FNBP4	103insGGGGTA	p.N701fs
XH_P44	11	47862068	47862068	In_Frame_Ins	INS	-	TTGGATTCTCGT	-	NUP160	GGATAACGAGA29	delinsRDNENPNF
XH_P44	11	48328599	48328599	Nonsense_Mutation	INS	-	AATCACTGTCCT	-	OR4S1	CACGTAATCAC5	M276delinsVAHTX
XH_P44	11	49059510	49059510	Nonsense_Mutation	INS	-	CTCATTCTGATT	-	TRIM49B	1341insCTCATTT47	C448delinsFSFX
XH_P44	11	49075417	49075417	Frame_Shift_Ins	INS	-	CTTTTGCTTTTG	-	TRIM64C	1202insCAAAG	p.Q401fs
XH_P44	11	49190768	49190768	Frame_Shift_Ins	INS	-	TTTGATTAGCTT	-	FOLH1	27insGAAGCTAA	p.N143fs
XH_P44	11	49974493	49974493	Frame_Shift_Ins	INS	-	C	-	OR4C13	c.520dupC	p.D173fs
XH_P44	11	49974495	49974495	Nonsense_Mutation	INS	-	TGAATAAGATAG	-	OR4C13	22insTTGAATAA	174_F175delinsHX
XH_P44	11	50003742	50003742	Missense_Mutation	SNP	G	A	G	OR4C12	c.C296T	p.A99V
XH_P44	11	50003743	50003743	Frame_Shift_Ins	INS	-	CATACCCCTTGGT	-	OR4C12	sAGAGACCAAG	p.A99fs
XH_P44	11	50004032	50004032	Nonsense_Mutation	INS	-	5CTCCTAAGTTG	-	OR4C12	nsATCAACTTAG	p.E2delinsESTX
XH_P44	11	51515816	51515816	Frame_Shift_Ins	INS	-	GGTTAGGGGTA	-	OR4C46	36insAGGTTAG	p.L179fs
XH_P44	11	55340048	55340048	Frame_Shift_Ins	INS	-	TCTT	-	OR4C16	445_446insTCT	p.G149fs
XH_P44	11	55340049	55340049	Nonsense_Mutation	INS	-	ACACTAATA	-	OR4C16	5_447insACACTA	G149delinsGHX
XH_P44	11	55406419	55406419	Frame_Shift_Ins	INS	-	CTCCAAAAAAA	-	OR4P4	nsATGCCTCCAA	p.L196fs
XH_P44	11	55406421	55406421	Silent	SNP	A	G	A	OR4P4	c.A588G	p.L196L
XH_P44	11	55432779	55432779	Missense_Mutation	SNP	C	A	C	OR4C6	c.C137A	p.T46N
XH_P44	11	55432781	55432781	Nonsense_Mutation	INS	-	TTTAAAGGGA	-	OR4C6	AATAATTTAAAA	p.I47delinsKX
XH_P44	11	55588014	55588014	Silent	SNP	C	T	C	OR5D18	c.C909T	p.T303T
XH_P44	11	55588015	55588015	Nonsense_Mutation	INS	-	GTTGATGTAAGT	-	OR5D18	911insGTTGATG	p.E304delinsGX

XH_P44	11	55606695	55606695	Nonsense_Mutation	INS	-	TTTTGGGTTAAT	-	OR5D16	69insATTTTGGG	56_C157delinsA	ILGX
XH_P44	11	55872685	55872685	Frame_Shift_Ins	INS	-	ACTGGAGAAGC	-	OR8H2	168insACTGGA	p.L56fs	
XH_P44	11	55872687	55872687	Missense_Mutation	SNP	C	G	C	OR8H2	c.C169G	p.H57D	
XH_P44	11	55904677	55904677	Nonsense_Mutation	INS	-	TATCTTATTTCAA	-	OR8J3	CAATATTGAAAT	73_1174delinsTKQYX	
XH_P44	11	55927522	55927522	In_Frame_Ins	INS	-	ATTGTTGAGCAT	-	OR8K5	2insGTATGCTC	791delinsSMLNNS	
XH_P44	11	56020603	56020603	Nonsense_Mutation	INS	-	AAGAGTAGAAG	-	OR5T3	AGTAGAAGAGT	p.I310delinsKX	
XH_P44	11	56085982	56085982	Frame_Shift_Ins	INS	-	A	-	OR8K3	c.200_201insA	p.A67fs	
XH_P44	11	56085984	56085984	Nonsense_Mutation	INS	-	AATAGCTTTCCT	-	OR8K3	insGTCAATAGC	p.F68delinsCQX	
XH_P44	11	56086564	56086564	Frame_Shift_Ins	INS	-	A	-	OR8K3	c.782_783insA	p.P261fs	
XH_P44	11	56086565	56086565	Frame_Shift_Ins	INS	-	GAAGGATAAAG	-	OR8K3	84insAGAAGGA	p.P261fs	
XH_P44	11	56185007	56185007	Frame_Shift_Ins	INS	-	TTACACAGTGG	-	OR5R1	insTCACCACTG	p.Q234fs	
XH_P44	11	56344492	56344492	In_Frame_Ins	INS	-	AAAATTGCAGTT	-	OR5M10	insCTAAACTGCA	236delinsLNCNFTK	
XH_P44	11	56344676	56344676	In_Frame_Ins	INS	-	CAGTCTTTT	-	OR5M10	c.522insAAAAAG	p.I174delinsIKDC	
XH_P44	11	56344678	56344678	Frame_Shift_Ins	INS	-	AC	-	OR5M10	c.519_520insGT	p.I174fs	
XH_P44	11	56431375	56431375	Nonsense_Mutation	INS	-	AGTTTTTTGATG	-	OR5AR1	nsATTTAGTTTTT	72_Y73delinsDLVFX	
XH_P44	11	56756910	56756910	Frame_Shift_Ins	INS	-	TTGGG	-	OR5AK2	522_523insTTGG	p.I174fs	
XH_P44	11	56756911	56756911	In_Frame_Ins	INS	-	GTG	-	OR5AK2	c.523_524insGTp	N175delinsSD	
XH_P44	11	57093899	57093899	In_Frame_Ins	INS	-	CTTAAGGATGTA	-	SSRP1	2112insTACATC	A704delinsATSLR	
XH_P44	11	57319961	57319961	Nonsense_Mutation	INS	-	TAGGTTGTTAGT	-	UBE2L6	AATGACTAACAA	V112delinsHTQTNDX	
XH_P44	11	57971171	57971171	In_Frame_Ins	INS	-	TGTAGGCGT	-	OR1S2	2_483insACGCC	S161delinsSRLQ	
XH_P44	11	58206924	58206924	Nonsense_Mutation	INS	-	TAATTATAAAG	-	OR5B12	GAACTCTTTATA	K234delinsILLX	
XH_P44	11	58207151	58207151	Frame_Shift_Ins	INS	-	CCTTACT	-	OR5B12	73_474insAGTA	p.T158fs	
XH_P44	11	58207152	58207152	Frame_Shift_Ins	INS	-	AGTTTCCATCTT	-	OR5B12	73insAAAGATG	p.T158fs	
XH_P44	11	58379144	58379144	Nonsense_Mutation	INS	-	AGTTATCACTGA	-	ZFP91	CTTAGAGTTATC	263_E264delinsAX	
XH_P44	11	58722819	58722819	Frame_Shift_Ins	INS	-	ACCTCAGTGC	-	GLYATL1	485insACCTCA	p.G162fs	
XH_P44	11	58722821	58722821	Frame_Shift_Ins	INS	-	AGTA	-	GLYATL1	486_487insAGT	p.F162fs	
XH_P44	11	58877144	58877144	Nonsense_Mutation	INS	-	ATTTAGCTTACT	-	FAM111B	insCTATTTAGCT	16_D17delinsAIX	
XH_P44	11	58979181	58979181	Nonsense_Mutation	INS	-	TTTAGGGCTTTT	-	MPEG1	58insCAAAAG	T386delinsTKPKX	
XH_P44	11	58979753	58979753	Frame_Shift_Ins	INS	-	C	-	MPEG1	c.585_586insG	p.I196fs	
XH_P44	11	58979754	58979754	Frame_Shift_Ins	INS	-	ACCTC	-	MPEG1	584_585insGAG	p.E195fs	
XH_P44	11	59132372	59132372	Frame_Shift_Ins	INS	-	SGAAGAAATAC	-	OR5AN1	42insAGGAAGA	p.I147fs	
XH_P44	11	60183262	60183262	Frame_Shift_Ins	INS	-	TTGATCATTTTG	-	MS4A14	TGTAATTGATCA	p.M257fs	
XH_P44	11	60184222	60184222	Frame_Shift_Ins	INS	-	CTGCTTTGGAG	-	MS4A14	31insTTTCTGCTT	p.E577fs	
XH_P44	11	60565942	60565942	Missense_Mutation	SNP	A	C	A	MS4A10	c.A677C	p.Y262S	
XH_P44	11	60565944	60565944	Frame_Shift_Ins	INS	-	TGTTCTTGAAA	-	MS4A10	680insTGTTCT	p.Q227fs	
XH_P44	11	61081081	61081081	Frame_Shift_Ins	INS	-	T	-	DDB1	c.1958_1959ins	p.S653fs	
XH_P44	11	61730552	61730552	Frame_Shift_Ins	INS	-	GTTGGTTGGTG	-	BEST1	insGTATGTTGG	p.C582fs	
XH_P44	11	62285278	62285278	Frame_Shift_Ins	INS	-	AGGTGGAAGGA	-	AHNAK	16611insCTCCT	p.A5537fs	
XH_P44	11	62286425	62286425	Missense_Mutation	SNP	A	C	A	AHNAK	c.T15464G	p.J1555R	
XH_P44	11	62286427	62286427	In_Frame_Ins	INS	-	GAAGGAGAC	-	AHNAK	1_15462insGTC	K5154delinsKSPS	
XH_P44	11	62289235	62289235	Silent	SNP	G	A	G	AHNAK	c.C12654T	p.D4218D	
XH_P44	11	62290030	62290030	Silent	SNP	A	G	A	AHNAK	c.T11859C	p.D3953D	
XH_P44	11	62291024	62291024	In_Frame_Ins	INS	-	AGG	-	AHNAK	0864_1086insp	V3622delinsAF	
XH_P44	11	62291025	62291025	Nonsense_Mutation	INS	-	TCAGAGGGTAA	-	AHNAK	10864insTTTAC	V3622delinsFTLX	
XH_P44	11	62293072	62293072	In_Frame_Ins	INS	-	GGAGAGGGCCCC	-	AHNAK	317insCTGGGCC	2939delinsIWLFS	
XH_P44	11	62297856	62297856	Missense_Mutation	SNP	A	C	A	AHNAK	c.T4033G	p.L1345V	
XH_P44	11	62297857	62297857	Silent	SNP	G	A	G	AHNAK	c.C4032T	p.S1344A	
XH_P44	11	62444227	62444227	Frame_Shift_Ins	INS	-	ATAGACCTGAG	-	UBXN1	saGAAACTCAGG	p.L301fs	
XH_P44	11	63486935	63486935	Frame_Shift_Ins	INS	-	TTTTAGCCTC	-	RTN3	626insTTTTAG	p.A209fs	
XH_P44	11	63487413	63487413	Nonsense_Mutation	INS	-	GTGCTAGTTTT	-	RTN3	1104insGTGCT	68_M369delinsECX	
XH_P44	11	63487415	63487415	In_Frame_Ins	INS	-	GAT	-	RTN3	1105_1106insG	p.M369delinsRL	
XH_P44	11	63991775	63991775	Frame_Shift_Ins	INS	-	CTTCTCTAACCA	-	TRPT1	41insTGGTTAG	p.G181fs	
XH_P44	11	64567080	64567080	Frame_Shift_Ins	INS	-	ATGAGCCGGTG	-	MAP4K2	991insTCACCGG	p.Q331fs	
XH_P44	11	64715280	64715280	Missense_Mutation	SNP	T	A	T	MAJIN	c.A361T	p.S121C	
XH_P44	11	64900650	64900650	In_Frame_Ins	INS	-	AATGTTCCTCACT	-	SVYV1	206insAGTGGAA	L69delinsQWHL	
XH_P44	11	66411364	66411364	In_Frame_Del	DEL	GCTGCAGCA	-	TCGCTGCAGCAG	RBM14-RBM4	c.781_801del	p.261_267del	
XH_P44	11	66813340	66813340	In_Frame_Ins	INS	-	GTCCTTTATTAT	-	SYT12	740insGTCCTTT	V247delinsGPLL	
XH_P44	11	66999319	66999319	Frame_Shift_Ins	INS	-	TCCAAATCTACC	-	KDM2A	insAACTCCAAA	p.F456fs	
XH_P44	11	68363644	68363644	In_Frame_Ins	INS	-	ACAAAGGCTCCT	-	PP6R3	1910insACAAAA	S637delinsNKRSC	
XH_P44	11	69488060	69488060	Nonsense_Mutation	INS	-	TTTATTTCGATA	-	ORA0V1	TGAATATCGGAA	28delinsSITLNIEYKX	
XH_P44	11	69588249	69588249	Nonsense_Mutation	INS	-	STAGGTGTAAG	-	FGF4	TAATATCTTAC	p.F150delinsX	
XH_P44	11	71209538	71209538	Frame_Shift_Ins	INS	-	CGAGCTTC	-	NADSYN1	4_2035insCGAC	p.L678fs	
XH_P44	11	73072193	73072193	Missense_Mutation	SNP	G	A	G	ARHGEF17	c.G4481A	p.R1494H	
XH_P44	11	74009291	74009291	In_Frame_Ins	INS	-	TGA	-	P4HA3	c.682_683insTC	p.D228delinsVN	
XH_P44	11	74009293	74009293	In_Frame_Ins	INS	-	ACTTTACAATCA	-	P4HA3	681insTGATTGT	E227delinsDDCKV	
XH_P44	11	74056623	74056623	Nonsense_Mutation	INS	-	ACACTTGTTTCA	-	PGM2L1	AGAGACTGAACT	70_K371delinsIKRDX	
XH_P44	11	74651911	74651911	Frame_Shift_Ins	INS	-	ACTCTCAAAGTG	-	XRR1	ATATGCATCTTA	p.G5fs	
XH_P44	11	74800597	74800597	In_Frame_Ins	INS	-	CACCTGCACT	-	OR2AT4	c.162insAGTGC	V54delinsVVQW	
XH_P44	11	76062167	76062167	Frame_Shift_Ins	INS	-	A	-	THAP12	c.2026_2027ins	p.N676fs	
XH_P44	11	76062168	76062168	In_Frame_Ins	INS	-	TAAACTCTATA	-	THAP12	26insTGTATAG	N676delinsCIEFNN	
XH_P44	11	76115029	76115029	Frame_Shift_Ins	INS	-	TCGGCCTGTGG	-	LOC100506127	709insTCGGCC	p.S236fs	
XH_P44	11	76255507	76255507	In_Frame_Ins	INS	-	ACATTITTC	-	EMSY	7_2918insACAT	F973delinsVIFL	
XH_P44	11	76255588	76255588	In_Frame_Ins	INS	-	GTCTCTCGCTGT	-	EMSY	99insAGTTCTCT	1000delinsKFLAVF	
XH_P44	11	77066792	77066792	Frame_Shift_Ins	INS	-	GGATACTATGT	-	PAK1	93insTAACATAG	p.P231fs	
XH_P44	11	77387961	77387961	Nonsense_Mutation	INS	-	JAAGCAGATTCA	-	RSF1	GTATTCTTGAAT	N1074delinsLVFLNLX	
XH_P44	11	77413154	77413154	Frame_Shift_Ins	INS	-	ACCAATAGAGAC	-	RSF1	nsACTTTGTCTCT	p.L374fs	
XH_P44	11	77612489	77612489	In_Frame_Ins	INS	-	GCACAACACTG	-	INTS4	nsAAGTCCAGTG	736delinsKSSVLYV	
XH_P44	11	77820625	77820625	Frame_Shift_Ins	INS	-	GCTCTTCC	-	ALG8	D_901insGGAAC	p.L301fs	
XH_P44	11	77820627	77820627	Missense_Mutation	SNP	C	A	C	ALG8	c.G899T	p.G300V	
XH_P44	11	82644202	82644202	Nonsense_Mutation	SNP	A	T	A	DDIAS	c.A1822T	p.K608X	
XH_P44	11	82644203	82644203	Nonsense_Mutation	INS	-	AGTTTGCTTTGA	-	DDIAS	324insCAGTTTG	K608delinsSSLX	
XH_P44	11	82876956	82876956	Nonsense_Mutation	INS	-	TGTTCATGTTAA	-	PCF11	8insAAATGTTTC	A339delinsNKCSCX	
XH_P44	11	82876972	82876972	Frame_Shift_Ins	INS	-	TTGC	-	PCF11	c.033_1034insTT	p.K345fs	
XH_P44	11	82876973	82876973	Frame_Shift_Ins	INS	-	AAACAACCTGAAG	-	PCF11	1035insAACAA	p.K345fs	
XH_P44	11	82879852	82879852	In_Frame_Ins	INS	-	AAATCATCTTCG	-	PCF11	369insAAATCA	P956delinsPKIIFV	
XH_P44	11	82880266	82880266	In_Frame_Ins	INS	-	ATCTCAAACCAC	-	PCF11	283insAATCTCA	1094delinsSNLKPP	
XH_P44	11	82880268	82880268	Missense_Mutation	SNP	T	G	T	PCF11	c.T3284G	p.V1095G	
XH_P44	11	87013450	87013450	In_Frame_Ins	INS	-	AAAAAAAATTA	-	TMEM135	nsCTCAAAAAA	200delinsTQKKLIV	
XH_P44	11	88301031	88301031	Frame_Shift_Ins	INS	-	ATTGCTTTCATTG	-	GRM5	820insGAATGA	p.T607fs	
XH_P44	11	89133400	89133400	Nonsense_Mutation	INS	-	TTTGTAGGGTG	-	NOX4	cATAGCACCTC	307_A308delinsAX	
XH_P44	11	89133402	89133402	Missense_Mutation	SNP	A	T	A	NOX4	c.T917A	p.F306Y	
XH_P44	11	89892452	89892452	In_Frame_Ins	INS	-	ATA	-	NAALAD2	c.936_937insAT	p.A312delinsAI	
XH_P44	11	89892454	89892454	In_Frame_Ins	INS	-	CAGTAAGTAA	-	NAALAD2	GAAATCAGTAA	B13delinsKSVKIR	
XH_P44	11	92086719	92086719	In_Frame_Ins	INS	-	CATCGTACACTT	-	FAT3	nsCTCACATCGT	481delinsAHVHFFL	
XH_P44	11	92087872	92087872	Frame_Shift_Ins	INS	-	T	-	FAT3	c.2594_2595ins	p.E865fs	
XH_P44	11	92087873	92087873	Nonsense_Mutation	INS	-	AGGAGATAGAG	-	FAT3	insTTAAGGAGA	E865delinsELRRX	
XH_P44	11	92532346	92532346	Frame_Shift_Ins	INS	-	TTGTGTAAAGTG	-	FAT3	168insTTTGTG	p.A2056fs	
XH_P44	11	92532347	92532347	Silent	SNP	C	G	C	FAT3	c.C6168G	p.A2056A	

XH_P44	11	92918974	92918974	Frame_Shift_Ins	INS	-	AGACACAAATAT	-	SLC36A4	TCCTTATATTGT	p.D21fs
XH_P44	11	93417238	93417238	Frame_Shift_Ins	INS	-	GGGCC	-	CEP295	58_1059insGG	p.G353fs
XH_P44	11	93417240	93417240	Missense_Mutation	SNP	G	C	G	CEP295	c.G1060C	p.A354P
XH_P44	11	93432089	93432089	Frame_Shift_Ins	INS	-	ATGGTACTGTCA	-	CEP295	AGGGAATGGTA	p.L1337fs
XH_P44	11	93469396	93469396	Missense_Mutation	SNP	T	A	T	TA1D	c.A768T	p.E256D
XH_P44	11	93469397	93469397	Frame_Shift_Ins	INS	-	AAGATAAATGTG	-	TA1D	TATATCCACATT	p.E256fs
XH_P44	11	93527174	93527174	Nonsense_Mutation	INS	-	ICAGATCGAGAT	-	MED17	TTATCCAGATC	8delinsRYLFQIEICILYX
XH_P44	11	93913106	93913106	Nonsense_Mutation	INS	-	CAGTATAATGAT	-	PANX1	5insAACAGTATA	95_F296delinsTVX
XH_P44	11	94335129	94335129	Frame_Shift_Ins	INS	-	AAGAGATTGAAC	-	PIW1L4	TCATGAAGAAGGA	p.V517fs
XH_P44	11	95516426	95516426	Frame_Shift_Ins	INS	-	ACCATCATCACC	-	FAM76B	nsGATGGTGAT	p.V122fs
XH_P44	11	95712550	95712550	Frame_Shift_Ins	INS	-	AGTGATGCTGAT	-	MAML2	insTGAAATCAG	p.Q1011fs
XH_P44	11	96098305	96098305	Nonsense_Mutation	INS	-	TTTTATTTCATAA	-	CCDC82	5ATTATTITATGA	407delinsVLGLFMKX
XH_P44	11	96117248	96117248	Nonsense_Mutation	INS	-	TTTTAATCAAGT	-	CCDC82	AGAATACCTTGAT	p.E222delinsX
XH_P44	11	99942522	99942522	Nonsense_Mutation	INS	-	TTTTTTGTAGTTA	-	CNTN5	ACAATTTTTTTTG	8_K389delinsKEITIFLX
XH_P44	11	101375385	101375385	Nonsense_Mutation	INS	-	GTAAAGGTTATG	-	TRPC6	5CGAACATAACG	A106delinsAEHNLYX
XH_P44	11	101833293	101833293	Frame_Shift_Ins	INS	-	TTGGGGCTCTCA	-	CEP126	528insGTTGGG	p.N509fs
XH_P44	11	102477401	102477401	In_Frame_Ins	INS	-	TATGCAGCA	-	MMP20	7_818insTGCTG	R273delinsLHR
XH_P44	11	102477403	102477403	Frame_Shift_Ins	INS	-	AG	-	MMP20	c.815_816insCT	p.P272fs
XH_P44	11	102710939	102710939	Frame_Shift_Ins	INS	-	CTGTTCTTAGC	-	MMP3	TAGAAGCTAAG	p.P279fs
XH_P44	11	103027317	103027317	In_Frame_Ins	INS	-	TGATTGTAACTTG	-	DYNC2H1	46insCTGATTTG	1315delinsSLIVTS
XH_P44	11	103866942	103866942	Nonsense_Mutation	INS	-	GTAGAGATTAAC	-	PDGFD	AGAAAATTGATG	21_T122delinsIENX
XH_P44	11	104763208	104763208	Frame_Shift_Ins	INS	-	CTCTTAATGGG	-	PCP4	insCTGCCAATTG	p.R94fs
XH_P44	11	104871094	104871094	Frame_Shift_Ins	INS	-	CAAATAAAGTAC	-	CASP5	20insTGACTTT	p.K140fs
XH_P44	11	105925169	105925169	Frame_Shift_Ins	INS	-	TATTATCTATATG	-	KBTBD3	TCGTGATATAGA	p.V4fs
XH_P44	11	107224439	107224439	Nonsense_Mutation	INS	-	AGGTAAAGAAGT	-	CWF19L2	TATAAATACTTT	Y633delinsDNKYFLPX
XH_P44	11	107260908	107260908	Nonsense_Mutation	INS	-	CAAGTGAAGATG	-	CWF19L2	CAACAACACTTT	588_R589delinsVX
XH_P44	11	107375399	107375399	Nonsense_Mutation	INS	-	AGTGCTACTAA	-	ALKBH8	CTACATTTAGTA	664delinsHDLHLVALYX
XH_P44	11	108043676	108043676	Nonsense_Mutation	INS	-	TGATGATCCATT	-	NPAT	35insCAAATGGG	A680delinsQMDHHX
XH_P44	11	108357108	108357108	Frame_Shift_Ins	INS	-	GT	-	KDEL2C	c.459_460insAC	p.L154fs
XH_P44	11	108357109	108357109	Nonsense_Mutation	INS	-	ATTGATAATACA	-	KDEL2C	TTAAACTGTATT	p.T153delinsTX
XH_P44	11	108381144	108381144	Nonsense_Mutation	INS	-	TAAAAAGCATTG	-	EXPH5	GAACATTAAATG	6_Q1509delinsPX
XH_P44	11	108381464	108381464	Silent	SNP	T	A	T	EXPH5	c.A4206T	p.S1402S
XH_P44	11	108381465	108381465	Frame_Shift_Ins	INS	-	ATTTTCAACAGG	-	EXPH5	205insGTGGTTG	p.S1402fs
XH_P44	11	110007771	110007771	In_Frame_Ins	INS	-	GTGGTTACGTGT	-	ZC3H12C	406insGTTGTTA	E135delinsEVTVC
XH_P44	11	111959612	111959612	Nonsense_Mutation	INS	-	TTTGAAGTCTT	-	SDHD	5GTTTTTTTGAAGS	H26delinsLFEVFX
XH_P44	11	113609999	113609999	Nonsense_Mutation	INS	-	CCAGTTATATAA	-	ZW10	TAAAATTATATA	A564delinsLHSPYKIX
XH_P44	11	113848548	113848548	In_Frame_Ins	INS	-	5AAAGGACCTAT	-	HTR3A	nsGTAGAAAGGA	47delinsLVERTYA
XH_P44	11	114393101	114393101	Frame_Shift_Ins	INS	-	CAATGCTTATAT	-	NXPE1	TAGTGAATATAA	p.X269fs
XH_P44	11	116657737	116657737	Nonsense_Mutation	INS	-	CATTAGTTAATG	-	ZPR1	TCATGATTAAAC	A70delinsAHDHX
XH_P44	11	116658287	116658287	Frame_Shift_Ins	INS	-	GTGAAATGCTT	-	ZPR1	TTTACAAAGCAT	p.H82fs
XH_P44	11	116728887	116728887	Frame_Shift_Ins	INS	-	GCCCAAGAATTT	-	SIK3	2970insCAATTCT	p.A990fs
XH_P44	11	116741066	116741066	Frame_Shift_Ins	INS	-	CCCTGCCCTCAT	-	SIK3	645insTATGAAC	p.D549fs
XH_P44	11	117056896	117056896	Frame_Shift_Ins	INS	-	ACTTCTG	-	SIDT2	19_920insACTT	p.P307fs
XH_P44	11	117340664	117340664	Frame_Shift_Ins	INS	-	GGGTGGGAA	-	DSCAML1	5_3166insTTCC	p.Q1056fs
XH_P44	11	118342657	118342657	Frame_Shift_Ins	INS	-	AGGTCTCCCACG	-	KMT2A	84insAGGTTCTC	p.S261fs
XH_P44	11	118342659	118342659	Missense_Mutation	SNP	C	G	C	KMT2A	c.C785G	p.A262G
XH_P44	11	118342742	118342742	Missense_Mutation	SNP	C	G	C	KMT2A	c.C868G	p.L290V
XH_P44	11	118342743	118342743	In_Frame_Ins	INS	-	GGGAGG	-	KMT2A	69_870insGGGA	L290delinsLGG
XH_P44	11	118352658	118352658	Frame_Shift_Ins	INS	-	TCACAACACTGC	-	KMT2A	5GTTCTTCCACAA	p.T1288fs
XH_P44	11	118367059	118367059	Frame_Shift_Ins	INS	-	GGGAAAAAGAA	-	KMT2A	TTTCAAGGAAA	p.T1881fs
XH_P44	11	118376309	118376309	Frame_Shift_Ins	INS	-	TAAAGTCTGGT	-	KMT2A	703insGTAAAGT	p.N3234fs
XH_P44	11	118468528	118468528	Frame_Shift_Ins	INS	-	GTATTTGGCAG	-	ARCN1	85insGGTATT	p.K362fs
XH_P44	11	118656914	118656914	Missense_Mutation	SNP	C	T	C	DDX6	c.G47A	p.S16N
XH_P44	11	118656915	118656915	In_Frame_Ins	INS	-	CCAAATAGA	-	DDX6	5_46insTCTATT	p.S16delinsSIWS
XH_P44	11	118968614	118968614	Nonsense_Mutation	INS	-	AATAGATCTCAG	-	PDAGT1	58insACCTGAGAG	p.L290delinsE
XH_P44	11	120346192	120346192	In_Frame_Ins	INS	-	ACGGCTTGTATT	-	ARHGEF12	TGGAGACGCGT	6delinsEMETRLNFMIM
XH_P44	11	120349062	120349062	Nonsense_Mutation	INS	-	5AAAAGGTAGAC	-	ARHGEF12	GAATAGAAAAG	225_E1226delinsX
XH_P44	11	120350764	120350764	Nonsense_Mutation	INS	-	AGTTGTGAATAT	-	ARHGEF12	5GTTATAGTTGTG	p.S1269delinsX
XH_P44	11	121178187	121178187	Frame_Shift_Ins	INS	-	TCCACCTG	-	SC5D	6_867insTCACC	p.K289fs
XH_P44	11	122828088	122828088	In_Frame_Ins	INS	-	TTCTTTGTGTC	-	C11orf63	nsAACCTTCTTTG	67delinsQNLCCY
XH_P44	11	123676732	123676732	In_Frame_Ins	INS	-	TTTCTCTCTCTG	-	OR6M1	26insCAGAGAG	E109delinsAERRK
XH_P44	11	123847838	123847838	In_Frame_Ins	INS	-	TCAACCCATTCA	-	OR10S1	1insAATGAATG	187delinsQMNGLS
XH_P44	11	123909236	123909236	Nonsense_Mutation	INS	-	TTTCAATTACCTG	-	OR10G7	73insTCAGGTA	158_T159delinsLRX
XH_P44	11	124413404	124413404	Frame_Shift_Ins	INS	-	TTTCTCTGCTTC	-	OR8B12	CAAAGAAGCAG	p.G49fs
XH_P44	11	125514124	125514124	Nonsense_Mutation	INS	-	TATGTTAATGTC	-	CHEK1	AGTATTATTGTT	A370delinsTLVLCX
XH_P44	11	128856559	128856559	Frame_Shift_Ins	INS	-	TTTGTGG	-	ARHGAP32	13_214insCCAC	p.E72fs
XH_P44	11	128856560	128856560	In_Frame_Ins	INS	-	ACTTTGTCTG	-	ARHGAP32	2_213insCAGCA	H71delinsHSKV
XH_P44	11	128933907	128933907	Frame_Shift_Ins	INS	-	ATAGT	-	ARHGAP32	732_733insACT	p.G245fs
XH_P44	11	128933909	128933909	Frame_Shift_Ins	INS	-	TTTA	-	ARHGAP32	730_731insTAA	p.K244fs
XH_P44	11	129752386	129752386	Frame_Shift_Ins	INS	-	AA	-	NFRKB	1116_1117insT	p.Q373fs
XH_P44	11	129752387	129752387	Nonsense_Mutation	INS	-	CAATCTAGG	-	NFRKB	5_1116insCCTAG	S372delinsSLDX
XH_P44	11	130131289	130131289	Frame_Shift_Ins	INS	-	G	-	ZBTB44	c.479_480insC	p.L160fs
XH_P44	11	130131290	130131290	Nonsense_Mutation	INS	-	TGGCTGATTAT	-	ZBTB44	179insCATAATC	A160_S161delinsTX
XH_P44	11	134055381	134055381	Nonsense_Mutation	INS	-	ATAGCTATTCTA	-	NCAPD3	2086insTATGAA	596_K697delinsYEX
XH_P44	12	427602	427602	Frame_Shift_Ins	INS	-	GAAAGCTGATAG	-	KDM5A	2567insCTATC	p.F856fs
XH_P44	12	432361	432361	Nonsense_Mutation	INS	-	SAGATTAATGGG	-	KDM5A	AATCAACCCATT	P721delinsQSTHX
XH_P44	12	994357	994357	Frame_Shift_Ins	INS	-	CT	-	WNK1	3646_3647insC	p.S1216fs
XH_P44	12	2926465	2926465	Frame_Shift_Ins	INS	-	ACTTGTAATCCC	-	ITFG2	174insACTTGTG	p.T58fs
XH_P44	12	2977897	2977897	Frame_Shift_Ins	INS	-	A	-	FOXM1	c.674_675insT	p.S225fs
XH_P44	12	2977898	2977898	Frame_Shift_Ins	INS	-	TGATAAACAAAT	-	FOXM1	4insACATTGTGT	p.S225fs
XH_P44	12	6626153	6626153	Nonsense_Mutation	INS	-	ACTTTTTCCATT	-	NCAPD2	5insATAACTTTT	B_V384delinsHNFFHX
XH_P44	12	7528576	7528576	Missense_Mutation	SNP	C	A	C	CD163L1	c.G2436T	p.M812I
XH_P44	12	7528577	7528577	Frame_Shift_Ins	INS	-	GTTGGAGT	-	CD163L1	4_2435insACTC	p.M812fs
XH_P44	12	7559389	7559389	Nonsense_Mutation	INS	-	AGGTAAGACT	-	CD163L1	1_856insAGTCTT	86_L287delinsSLTX
XH_P44	12	7585328	7585328	Frame_Shift_Ins	INS	-	5GATGACATTTT	-	CD163L1	180insTAAATG	p.L160fs
XH_P44	12	7917938	7917938	Silent	SNP	G	A	G	NANOGNB	c.G57A	p.A19A
XH_P44	12	8212764	8212764	Frame_Shift_Ins	INS	-	ACATGTTT	-	C3AR1	7_18insAAACA	p.A6fs
XH_P44	12	9073614	9073614	Frame_Shift_Ins	INS	-	ACTCT	-	PHC1	259_260insACT	p.P87fs
XH_P44	12	9229444	9229444	Frame_Shift_Ins	INS	-	C	-	A2M	c.2989_2990insC	p.K997fs
XH_P44	12	9229445	9229445	Nonsense_Mutation	INS	-	CAATTACGATGG	-	A2M	2989insCCATCG	p.K997delinsPSX
XH_P44	12	9356548	9356548	Splice_Site	SNP	C	T	C	PZP	.	.
XH_P44	12	10217381	10217381	Frame_Shift_Ins	INS	-	AGGAGAGAAGG	-	CELC9A	insAAAAGGAGA	p.W174fs
XH_P44	12	10762506	10762506	In_Frame_Ins	INS	-	TATATTTTA	-	MAGOHB	9_50insTAAATG	p.K17delinsIKK
XH_P44	12	10762508	10762508	Frame_Shift_Ins	INS	-	TCTT	-	MAGOHB	c.47_48insAAGA	p.L16fs
XH_P44	12	10958798	10958798	Frame_Shift_Ins	INS	-	GATGCATA	-	TAS2R8	1_782insTATGC	p.T261fs
XH_P44	12	10958800	10958800	Frame_Shift_Ins	INS	-	TTTAAATATT	-	TAS2R8	1_780insAAATT	p.M260fs
XH_P44	12	10978242	10978242	Frame_Shift_Ins	INS	-	5AACAGCAAGC	-	TAS2R10	nsTTTAGCTTGC	p.S209fs
XH_P44	12	11214231	11214231	Missense_Mutation	SNP	C	A	C	TAS2R46	c.G663T	p.M221I

XH_P44	12	11339408	11339408	In_Frame_Ins	INS	-	ATTGTTATGCTT	-	TAS2R42	ATAAGAAGCAT	46delinsNIRSIIT	IIIPF
XH_P44	12	11506238	11506238	Nonsense_Mutation	INS	-	CAGTCATCATAGG	-	PRB1	00insTCCTAGAT	134_G135delinsSX	
XH_P44	12	12311935	12311935	Frame_Shift_Ins	INS	-	GGGTTATTGTG	-	LRP6	sAACCAAAACAA	p.L873fs	
XH_P44	12	12814531	12814531	Missense_Mutation	SNP	C	A	C	GPR19	c.G852T	p.L284F	
XH_P44	12	12814533	12814533	Frame_Shift_Ins	INS	-	TACGTTGGCATT	-	GPR19	50insAAATGCCA	p.L284fs	
XH_P44	12	13103204	13103204	Frame_Shift_Ins	INS	-	TGTTGCAATCA	-	GPRC5D	5insAATGATTTG	p.L39fs	
XH_P44	12	14577932	14577932	Frame_Shift_Ins	INS	-	AAGGTAC	-	ATF7IP	83_1084insAAG	p.S361fs	
XH_P44	12	15637140	15637140	Nonsense_Mutation	INS	-	GCTGTAGCATTC	-	PTPRO	309insGCTGTAG	N.103delinsLX	
XH_P44	12	18658376	18658376	Frame_Shift_Ins	INS	-	CAAAAAATGAG	-	PIK3C2G	TAACAACAAAAA	p.T1061fs	
XH_P44	12	18872555	18872555	Nonsense_Mutation	INS	-	ATGTAAGGTATT	-	PLCZ1	insTAAATACCTT	H23_Q24delinsX	
XH_P44	12	19436520	19436520	Nonsense_Mutation	INS	-	GTAATGTTTGGT	-	PLEKHA5	79insTGGTAATG	26_D427delinsSWX	
XH_P44	12	20766621	20766621	In_Frame_Ins	INS	-	CAGGCAAGAAA	-	PDE3A	291insCAGGCAA	L97delinsLRQEN	
XH_P44	12	20766622	20766622	Silent	SNP	T	G	T	PDE3A	c.T291G	p.L97L	
XH_P44	12	20903711	20903711	In_Frame_Ins	INS	-	TACTTTAATCTAG	-	SLCO1C1	ACCACCTTACTTTA	6delinsSETTYFNLVTV	
XH_P44	12	21028400	21028400	Frame_Shift_Ins	INS	-	GCTCCAACCC	-	SLCO1B3	876insGCTCCA	p.K292fs	
XH_P44	12	21448728	21448728	Splice_Site	INS	-	ATGTTGTTTTCTA	-	SLCO1A2	.	.	
XH_P44	12	21721945	21721945	Splice_Site	INS	-	GGATTTTGTTTT	-	GY52	.	.	
XH_P44	12	23689565	23689565	Frame_Shift_Ins	INS	-	GTGAACATATT	-	SOX5	nsAACAAATATG	p.P218fs	
XH_P44	12	23689567	23689567	Missense_Mutation	SNP	T	A	T	SOX5	c.A650T	p.Q217L	
XH_P44	12	25257395	25257395	In_Frame_Ins	INS	-	TTTTTCTTGGCA	-	LRMP	nsTTATTTTCTTCT	B83delinsLIFSWHIQ	
XH_P44	12	25357095	25357095	Frame_Shift_Ins	INS	-	AGAATTGGCCAT	-	ETFRF1	CTTAAAGGAATTG	p.L41fs	
XH_P44	12	26568415	26568415	Nonsense_Mutation	INS	-	AGGTATTGCTAT	-	ITPR2	insGGTAATAGCG	876_R2377delinsWX	
XH_P44	12	26636816	26636816	Frame_Shift_Ins	INS	-	CC	-	ITPR2	5826_5827insG	p.Q1943fs	
XH_P44	12	26636817	26636817	In_Frame_Ins	INS	-	GACATTTTACT	-	ITPR2	5826insAGTAA	1942delinsVKVMS	
XH_P44	12	26752988	26752988	In_Frame_Ins	INS	-	GTG	-	ITPR2	B732_3733insCp	F1245delinsHF	
XH_P44	12	26752989	26752989	In_Frame_Ins	INS	-	ATATCTTTTTTT	-	ITPR2	B732insAAAAAA	N1244delinsKKDKI	
XH_P44	12	27849773	27849773	Frame_Shift_Ins	INS	-	TTGC	-	REP15	278_279insTTG	p.W93fs	
XH_P44	12	27849775	27849775	In_Frame_Ins	INS	-	TGC	-	REP15	280_281insTG	p.I94delinsML	
XH_P44	12	29921001	29921001	Nonsense_Mutation	INS	-	AGAGTTCACTCA	-	TMT1C1	0insTTTGAGTG	p.I104delinsFEX	
XH_P44	12	30815337	30815337	Frame_Shift_Ins	INS	-	AAACTGTATAGG	-	IP08	064insACCTATA	p.T355fs	
XH_P44	12	30816540	30816540	Nonsense_Mutation	INS	-	TCAGGGTTTGG	-	IP08	nsAATTCCAAC	L288delinsNSKPX	
XH_P44	12	30906612	30906612	Frame_Shift_Ins	INS	-	CGATGAGACCT	-	CAPRIN2	sATATAGGTCCTC	p.R29fs	
XH_P44	12	31237922	31237922	Missense_Mutation	SNP	G	C	G	DDX11	c.G500C	p.R167T	
XH_P44	12	31862326	31862326	In_Frame_Ins	INS	-	TTTATGATTTTGT	-	AMN1	nsTTCCAAAAATC	R24delinsSSKNLKP	
XH_P44	12	31862327	31862327	Nonsense_Mutation	INS	-	AATGGTATA	-	AMN1	0_71insTATACC	p.R24delinsVHX	
XH_P44	12	32135424	32135424	Frame_Shift_Ins	INS	-	GTTTATCTCTA	-	KIAA1551	nsCTTCTGTTTTA	p.K512fs	
XH_P44	12	32135624	32135624	Missense_Mutation	SNP	A	C	A	KIAA1551	c.A1735C	p.N579H	
XH_P44	12	32135625	32135625	Frame_Shift_Ins	INS	-	CATTGAGTCTTA	-	KIAA1551	37insTACATTGA	p.N579fs	
XH_P44	12	32136427	32136427	Frame_Shift_Ins	INS	-	CACACAGCTAT	-	KIAA1551	9insGACACTAC	p.G846fs	
XH_P44	12	32136429	32136429	In_Frame_Ins	INS	-	GTTCG	-	KIAA1551	40_2541insGTT	N.847delinsKFC	
XH_P44	12	32136722	32136722	Missense_Mutation	SNP	A	G	A	KIAA1551	c.A2833G	p.N945D	
XH_P44	12	32136723	32136723	In_Frame_Ins	INS	-	CTCATTTCTGCTT	-	KIAA1551	2835insCTCATTT	N945delinsNSFCF	
XH_P44	12	32735395	32735395	Frame_Shift_Ins	INS	-	TCTTATCTGTATC	-	FGD4	B16insTCTTATC	p.E105fs	
XH_P44	12	39087604	39087604	In_Frame_Ins	INS	-	TTG	-	CPNE8	997_998insCA	p.N333delinsTN	
XH_P44	12	39087606	39087606	Frame_Shift_Ins	INS	-	AAAAGGATTTG	-	CPNE8	996insCAAATC	p.M332fs	
XH_P44	12	40012639	40012639	Frame_Shift_Ins	INS	-	TCGATGGACC	-	ABCD2	779insGGTCCA	p.A260fs	
XH_P44	12	40728946	40728946	Missense_Mutation	SNP	G	T	G	LRRK2	c.G5935T	p.A1979S	
XH_P44	12	40728948	40728948	Frame_Shift_Ins	INS	-	CCTTCTTTAAA	-	LRRK2	5938insCCTTCT	p.A1979fs	
XH_P44	12	40740715	40740715	Frame_Shift_Ins	INS	-	CATACACTTAGG	-	LRRK2	71insGGCATACA	p.G2090fs	
XH_P44	12	41410603	41410603	Frame_Shift_Ins	INS	-	AGAGGAAAAA	-	CNTN1	2272insAGAGG	p.V57fs	
XH_P44	12	41967404	41967404	In_Frame_Ins	INS	-	ATGTTTGCATAT	-	PDZRN4	050insGATGTTT	N.683delinsWDVCIS	
XH_P44	12	42554617	42554617	Nonsense_Mutation	INS	-	ATGACAGATAC	-	YAF2	911insTGATCTCT	64_N65delinsMYLSX	
XH_P44	12	44130274	44130274	Nonsense_Mutation	INS	-	CTGTCAGT	-	PUS7L	5_696insACTGA	232_R233delinsX	
XH_P44	12	44130276	44130276	Missense_Mutation	SNP	A	T	A	PUS7L	c.T694A	p.Y232N	
XH_P44	12	44148326	44148326	Frame_Shift_Ins	INS	-	AA	-	PUS7L	c.722_723insTT	p.H241fs	
XH_P44	12	44148327	44148327	Nonsense_Mutation	INS	-	AGGAAAAAGTTA	-	PUS7L	TATATATAACTT	441_R242delinsLYIX	
XH_P44	12	44338084	44338084	Frame_Shift_Ins	INS	-	AGAGTAAATACT	-	TMEM117	ATCTCTAGAGTAA	p.L117fs	
XH_P44	12	45209901	45209901	In_Frame_Ins	INS	-	GAG	-	NELL2	202_203insCT	p.K68delinsTQ	
XH_P44	12	45209902	45209902	Nonsense_Mutation	INS	-	CTGTGTTTTTCAT	-	NELL2	insTAATGAAAAA	K68_A69delinsX	
XH_P44	12	45822991	45822991	Frame_Shift_Ins	INS	-	TTGTGTCTAATC	-	ANO6	ATGCCATTGTGT	p.L877fs	
XH_P44	12	46243553	46243553	Frame_Shift_Ins	INS	-	SAITTTGGAAAG	-	ARID2	5TGATGATTTTG	p.P636fs	
XH_P44	12	46244749	46244749	Nonsense_Mutation	INS	-	GTAGCTACC	-	ARID2	8_2844insGTAG	p.L948delinsLX	
XH_P44	12	46321699	46321699	Frame_Shift_Ins	INS	-	AAAAAGAAATGA	-	SCAF11	5insGCGATTCA	p.H595fs	
XH_P44	12	48142709	48142709	Nonsense_Mutation	INS	-	TTCCCTGTGTCT	-	RAPGEF3	1insATGACACACp	V307delinsVX	
XH_P44	12	48391973	48391973	Nonsense_Mutation	INS	-	CACCTTCAGGG	-	COL2A1	14insTCCTTGA	538_E39delinsGPX	
XH_P44	12	48596453	48596453	In_Frame_Ins	INS	-	AGACAAACC	-	OR10AD1	2_623insSGGTTT	N.1208delinsRFVF	
XH_P44	12	48596917	48596917	In_Frame_Ins	INS	-	GAACCTGCTGGT	-	OR10AD1	159insACAGGG	D53delinsEPGSS	
XH_P44	12	48739240	48739240	In_Frame_Ins	INS	-	GAGAAATGAGAG	-	ZNF641	insTTTACTCTCA	98delinsNLLFSFW	
XH_P44	12	49054372	49054372	Frame_Shift_Ins	INS	-	GCCTTATTATT	-	KANSL2	ACCATTATAATA	p.F335fs	
XH_P44	12	49087739	49087739	Frame_Shift_Ins	INS	-	AAAG	-	CCNT1	1257_1258insCT	p.Y420fs	
XH_P44	12	49087741	49087741	Missense_Mutation	SNP	G	C	G	CCNT1	c.C1256G	p.A419G	
XH_P44	12	49460041	49460041	Frame_Shift_Ins	INS	-	TTTGTTTA	-	RHEBL1	6_347insTAAAC	p.G116fs	
XH_P44	12	49460043	49460043	Frame_Shift_Ins	INS	-	T	-	RHEBL1	c.344_345insA	p.V115fs	
XH_P44	12	49959428	49959428	Nonsense_Mutation	INS	-	TCAGAT	-	MCRS1	10_211insATCT	p.D71delinsIX	
XH_P44	12	50503280	50503280	In_Frame_Ins	INS	-	BATTCTCTGGCT	-	GPD1	50insTGATTCTC	320delinsHDSLAW	
XH_P44	12	50571742	50571742	Frame_Shift_Ins	INS	-	BATGTGCTAGTCA	-	LIMA1	nsGATCTAGATC	p.K160fs	
XH_P44	12	50744890	50744890	Missense_Mutation	SNP	G	A	G	FAM186A	c.C572S	p.H1909Y	
XH_P44	12	50744891	50744891	Frame_Shift_Ins	INS	-	TCGAGACACTT	-	FAM186A	724insAAAGTG	p.Q1908fs	
XH_P44	12	50747903	50747903	Frame_Shift_Ins	INS	-	AGCAACCCTTGT	-	FAM186A	insAAACACAAG	p.E904fs	
XH_P44	12	50747905	50747905	Frame_Shift_Ins	INS	-	ATTTT	-	FAM186A	709_2710insAA	p.E904fs	
XH_P44	12	50748209	50748209	In_Frame_Ins	INS	-	CTATGAGAAGA	-	FAM186A	TCACTTATCTCT	2delinsDHLSSHSPAS	
XH_P44	12	51054072	51054072	Nonsense_Mutation	SNP	C	T	C	DIP2B	c.C937T	p.Q133X	
XH_P44	12	51054073	51054073	Nonsense_Mutation	INS	-	AAAAAAAAGGT	-	DIP2B	AAAAAAAAGGAA	B_S134delinsQKKKKRX	
XH_P44	12	52470869	52470869	Frame_Shift_Ins	INS	-	TTCTTCTTCTG	-	ATG101	553insTCTTCT	p.D184fs	
XH_P44	12	52842659	52842659	In_Frame_Ins	INS	-	AAGCTGTAAAG	-	KRT6B	ACTATACTTTTA	90delinsRLVFYSFDQ	
XH_P44	12	52864288	52864288	Splice_Site	INS	-	AACCAGCATTC	-	KRT6C	.	.	
XH_P44	12	52981617	52981617	Missense_Mutation	SNP	C	T	C	KRT72	c.G982A	p.A328T	
XH_P44	12	53072422	53072422	Frame_Shift_Ins	INS	-	GAAGATAGTCTA	-	KRT1	710insCTAGACT	p.N237fs	
XH_P44	12	53072424	53072424	In_Frame_Ins	INS	-	GTT	-	KRT1	707_708insAA	p.N236delinsKT	
XH_P44	12	53096757	53096757	Frame_Shift_Ins	INS	-	TTAATTCTATCT	-	KRT77	2insAAAGATAG	p.D154fs	
XH_P44	12	53594062	53594062	Frame_Shift_Ins	INS	-	AATTTGT	-	ITGB7	55_166insACAA	p.L56fs	
XH_P44	12	53594064	53594064	In_Frame_Ins	INS	-	GAATTGGGAGA	-	ITGB7	insCTTTCTCCCA	55delinsTFSQFMV	
XH_P44	12	53677263	53677263	Frame_Shift_Ins	INS	-	AAGGGAGAAGA	-	ESPL1	019insAAAGGG	p.E1006fs	
XH_P44	12	53684248	53684248	Frame_Shift_Ins	INS	-	ATCTTACC	-	ESPL1	9_5360insATCC	p.M1787fs	
XH_P44	12	54405116	54405116	Frame_Shift_Ins	INS	-	CCAGTCTGGTTA	-	HOXC8	1insCCCCAGTCT	p.N227fs	
XH_P44	12	54765350	54765350	Nonsense_Mutation	INS	-	A	-	ZNF385A	c.S10_S11insST	171_E172delinsX	
XH_P44	12	54903679	54903679	Nonsense_Mutation	INS	-	ACACTGTAAATT	-	NCKAP1L	ATACTACACTGT	166delinsRYTTYTVNYMX	
XH_P44	12	55039454	55039454	Frame_Shift_Ins	INS	-	AGGGGTGCCCAT	-	DCD	35insCATGGGCA	p.A45fs	

XH_P44	12	55524107	55524107	Silent	SNP	T	C	T	OR9K2	c.T555C	p.T185T	
XH_P44	12	55524109	55524109	Nonsense_Mutation	INS	-	AAGTTGAT	-	OR9K2	7_558insAAGT	86_M187delinsRSX	
XH_P44	12	55725609	55725609	Frame_Shift_Ins	INS	-	CTTGTTTG	-	OR6C3	5_126insCTTG	p.I42fs	
XH_P44	12	55725611	55725611	Nonsense_Mutation	INS	-	TTTAATAATTTTT	-	OR6C3	TATGTTTTAATA	H3_T44delinsIMFX	
XH_P44	12	56088245	56088245	Missense_Mutation	SNP	A	T	A	ITGA7	c.T2351A	p.V784E	
XH_P44	12	56194648	56194648	Frame_Shift_Ins	INS	-	AAGAAGAAACA	-	SARNP	GGGCTTTGTTTC	p.D58fs	
XH_P44	12	56215825	56215825	Nonsense_Mutation	INS	-	TCITTTTCTTTT	-	DNAJC14	5insAATAAAAAAG	p.T682delinsKX	
XH_P44	12	56330210	56330210	Frame_Shift_Ins	INS	-	TACCTTCCCTGA	-	DGKA	8insCTACCTCC	p.Y13fs	
XH_P44	12	56558465	56558465	Missense_Mutation	SNP	C	T	C	SMARCC2	c.G3190A	p.A1064T	
XH_P44	12	56571830	56571830	Frame_Shift_Ins	INS	-	ACATAACAAGTA	-	SMARCC2	58insGGTACTTG	p.K453fs	
XH_P44	12	56992501	56992501	Missense_Mutation	SNP	G	T	G	BAZ2A	c.C5613A	p.N1871K	
XH_P44	12	56992502	56992502	Frame_Shift_Ins	INS	-	TCCTACATCCCT	-	BAZ2A	2insGAAAGGGA	p.N1871fs	
XH_P44	12	57005777	57005777	Frame_Shift_Ins	INS	-	GACTC	-	BAZ2A	388_1389insGGA	p.V463fs	
XH_P44	12	57037687	57037687	In_Frame_Ins	INS	-	GTT	-	ATP5B	540_541insAA	p.E181delinsNE	
XH_P44	12	57037688	57037688	In_Frame_Ins	INS	-	TTCTGAGTT	-	ATP5B	540insAACTCA	Q180delinsQTQK	
XH_P44	12	57113667	57113667	Nonsense_Mutation	INS	-	GCCTCTGTAATC	-	NACA	47insTTGATTAC	549_G550delinsAX	
XH_P44	12	57397688	57397688	Nonsense_Mutation	INS	-	CATGTGTGAAC	-	ZBTB39	5AACTTAGTTTC	B38_E339delinsRTX	
XH_P44	12	57457066	57457066	Frame_Shift_Ins	INS	-	SAGTCTATTTTT	-	NEMP1	insAAAAAAAAT	p.E199fs	
XH_P44	12	57650289	57650289	Nonsense_Mutation	INS	-	TACCTCCT	-	R3HDM2	8_2359insAGGA	787_R788delinsRRX	
XH_P44	12	57861216	57861216	Missense_Mutation	SNP	G	T	G	GLI1	c.G629T	p.C210F	
XH_P44	12	57861217	57861217	Frame_Shift_Ins	INS	-	GAGAG	-	GLI1	630_631insGAG	p.C210fs	
XH_P44	12	58340789	58340789	Frame_Shift_Ins	INS	-	AATCCATTCT	-	ATP23	90insAATCCA	p.K30fs	
XH_P44	12	58340791	58340791	Frame_Shift_Ins	INS	-	TTCAAATTCT	-	ATP23	92insTTCAAAT	p.D31fs	
XH_P44	12	60169035	60169035	In_Frame_Ins	INS	-	CTTATTTTTAGAC	-	SLC16A7	5CAGTCTTATTT	320delinsASLIFRLR	
XH_P44	12	60169037	60169037	In_Frame_Ins	INS	-	GTGGT	-	SLC16A7	61_962insGTGG	p.I321delinsSGF	
XH_P44	12	62954589	62954589	Frame_Shift_Ins	INS	-	ACTGTATATGGT	-	MON2	9insTGACTGTA	p.A1243fs	
XH_P44	12	64472852	64472852	Frame_Shift_Ins	INS	-	AATTCAC	-	SRGAP1	79_1280insAAT	p.K427fs	
XH_P44	12	64472854	64472854	In_Frame_Ins	INS	-	TCTATT	-	SRGAP1	1281_1282insTCT	p.K427delinsKSI	
XH_P44	12	64811875	64811875	In_Frame_Ins	INS	-	GTAGTGATTTGT	-	XPOT	251insGTAGTGTA	184delinsSSDLL	
XH_P44	12	65137024	65137024	Frame_Shift_Ins	INS	-	GTITTTCTTCA	-	GNS	689insTGAAAG	p.A230fs	
XH_P44	12	65137026	65137026	Silent	SNP	G	A	G	GNS	c.C687T	p.I229I	
XH_P44	12	66703601	66703601	Missense_Mutation	SNP	A	G	A	HELB	c.A893G	p.Y298C	
XH_P44	12	66718850	66718850	Nonsense_Mutation	INS	-	TAGAAGTTTTCA	-	HELB	5ACAAATAGAA	72_M873delinsHXK	
XH_P44	12	66839254	66839254	Frame_Shift_Ins	INS	-	TATCTTTGAATG	-	GRIP1	233insCCATTCA	p.G411fs	
XH_P44	12	66839256	66839256	Missense_Mutation	SNP	C	T	C	GRIP1	c.G1231A	p.G411R	
XH_P44	12	67699314	67699314	Frame_Shift_Ins	INS	-	CGTGAGG	-	CAND1	186_1867insCGTG	p.E622fs	
XH_P44	12	67699316	67699316	Frame_Shift_Ins	INS	-	GGAAGAC	-	CAND1	186_1869insGGA	p.I623fs	
XH_P44	12	68707453	68707453	Frame_Shift_Ins	INS	-	GATACTGTAAAC	-	MDM1	5AGCAGGTTAAAC	p.T492fs	
XH_P44	12	69233395	69233395	In_Frame_Ins	INS	-	AGTTTGGCTTTC	-	MDM2	insTCCAGTTTGG	218delinsFSSLAfS	
XH_P44	12	69991425	69991425	In_Frame_Ins	INS	-	AATGGTTCTAAG	-	CC2	insCATAATGGT	323delinsAHNKSGL	
XH_P44	12	70070828	70070828	Nonsense_Mutation	INS	-	GATT	-	BEST3	416_417insAAT	139_T140delinsX	
XH_P44	12	70070830	70070830	In_Frame_Ins	INS	-	ACATGTAAT	-	BEST3	4_415insATTACA	Y139delinsTCY	
XH_P44	12	70736038	70736038	Frame_Shift_Ins	INS	-	AAAAGAGATTT	-	CNOT2	1242insAAAAG	p.D414fs	
XH_P44	12	70736039	70736039	Nonsense_Mutation	INS	-	TAA	-	CNOT2	1242_1243insT	p.D414delinsDX	
XH_P44	12	72050830	72050830	Missense_Mutation	SNP	C	G	C	ZFC3H1	c.G850C	p.E284Q	
XH_P44	12	72050832	72050832	In_Frame_Ins	INS	-	TTGGCAGTG	-	ZFC3H1	7_848insCACTG	K283delinsTLPK	
XH_P44	12	72070654	72070654	Nonsense_Mutation	INS	-	GGGTTGAACAT	-	THAP2	TTAGAGGGTTG	K151delinsKLEGX	
XH_P44	12	72070759	72070759	In_Frame_Ins	INS	-	AGTAGTACT	-	THAP2	8_559insAGTAG	T186delinsTSST	
XH_P44	12	72288645	72288645	Frame_Shift_Ins	INS	-	TAAAACAGAGT	-	TBC1D15	38insCTAAAC	p.G279fs	
XH_P44	12	72866914	72866914	Nonsense_Mutation	INS	-	TTTTTTTATACAT	-	TRHDE	404insGTTTTTTT	p.Y468delinsX	
XH_P44	12	75824646	75824646	Frame_Shift_Ins	INS	-	ATTTTAAAGTAC	-	GLP1R12	5GCCAATTTTAA	p.V247fs	
XH_P44	12	75824837	75824837	Frame_Shift_Ins	INS	-	TTTCATATAAAG	-	GLP1R12	TTGATTTCATAT	p.E311fs	
XH_P44	12	76740383	76740383	In_Frame_Ins	INS	-	AAGAACAATTC	-	BBS10	82insTGGAAATT	G461delinsVELFLS	
XH_P44	12	77419575	77419575	Frame_Shift_Ins	INS	-	AGCTTTCATTTT	-	E2F7	328insTAAAAATC	p.P77fs	
XH_P44	12	78452873	78452873	Missense_Mutation	SNP	G	A	G	NAV3	c.G2614A	p.D872N	
XH_P44	12	78452874	78452874	Nonsense_Mutation	INS	-	AAATATATTCTA	-	NAV3	TTACTCAATAAT	72_V873delinsDFQX	
XH_P44	12	79679632	79679632	Nonsense_Mutation	INS	-	GACTCTCCAAG	-	SYT1	3insCTTGACTCTC	C78_I79delinsSX	
XH_P44	12	80214932	80214932	Nonsense_Mutation	INS	-	TACTTTTGTTATT	-	PPP1R12A	AAAATAATAACA	08delinsNKTKIKILLRCRVX	
XH_P44	12	81043422	81043422	Nonsense_Mutation	INS	-	TTTAAAGTCACT	-	PTPRQ	CAGCTTTTAAAA	428_L1829delinsTAFX	
XH_P44	12	81283103	81283103	Frame_Shift_Ins	INS	-	TA	-	LIN7A	c.127_128insTA	p.G43fs	
XH_P44	12	81283104	81283104	Nonsense_Mutation	INS	-	ACAGTTGAAATT	-	LIN7A	5TAAACAATTTCA	G43_E44delinsX	
XH_P44	12	82793026	82793026	Frame_Shift_Ins	INS	-	TTTCTGTTTCTC	-	METTL25	4insATTTCCTGT	p.S241fs	
XH_P44	12	82824726	82824726	Nonsense_Mutation	INS	-	AACAGTAGTTAA	-	METTL25	AGTAAAAACAGT	58_W359delinsRNX	
XH_P44	12	85450427	85450427	In_Frame_Ins	INS	-	TAATTCTTGCAA	-	LRR1Q1	7insCTTTAATTC	19delinsDFNSCGX	
XH_P44	12	85677588	85677588	Nonsense_Mutation	INS	-	AATCAATAAGT	-	ALX1	AATTAATCAAT	H155delinsHLNX	
XH_P44	12	88442134	88442134	In_Frame_Ins	INS	-	TTGTCT	-	C12orf29	13_914insTTGTG	p.N305delinsIVY	
XH_P44	12	88442136	88442136	In_Frame_Ins	INS	-	CTTCCC	-	C12orf29	15_916insCTTCC	N305delinsNLP	
XH_P44	12	88471581	88471581	In_Frame_Ins	INS	-	TGA	-	CEP290	5478_5479insTG	Q1827delinsSQ	
XH_P44	12	88471582	88471582	Nonsense_Mutation	INS	-	TGTGTTTATAGT	-	CEP290	CTAGACATATA	826_Q1827delinsLX	
XH_P44	12	91445296	91445296	Splice_Site	INS	-	AATCTAAAAATT	-	KERA	.	.	
XH_P44	12	93171863	93171863	In_Frame_Ins	INS	-	CCCTCATAGGTA	-	EEA1	3747insTACCTA	11249delinsNTVRG	
XH_P44	12	93245039	93245039	Missense_Mutation	SNP	G	C	G	EEA1	c.C646G	p.Q216E	
XH_P44	12	93245040	93245040	Frame_Shift_Ins	INS	-	TATGTTTTCCTT	-	EEA1	45insAAAGCAA	p.L215fs	
XH_P44	12	95453729	95453729	Nonsense_Mutation	INS	-	CATTTAACAT	-	NR2C1	5AAAAATTAGT	106delinsLWEKISX	
XH_P44	12	95645799	95645799	Nonsense_Mutation	INS	-	AATAAAACACAC	-	VEZT	CTCTAAATAAAA	40_C41delinsKLX	
XH_P44	12	95927425	95927425	Frame_Shift_Ins	INS	-	TTCAAGGTGTTG	-	USP44	insACTCAACACC	p.A203fs	
XH_P44	12	95927890	95927890	In_Frame_Ins	INS	-	AAGAAGATA	-	USP44	2_143insTATCC	b.A48delinsVSFS	
XH_P44	12	95927891	95927891	Frame_Shift_Ins	INS	-	TAATGGGTAA	-	USP44	142insTTACCC	p.A48fs	
XH_P44	12	96384250	96384250	In_Frame_Ins	INS	-	AGCTTAGAAGT	-	HAL	62insTGACTTCTA	P51delinsLTSKL5	
XH_P44	12	96660957	96660957	Frame_Shift_Ins	INS	-	TATTAGTTGCCA	-	ELK3	TAGAGATTAGT	X84delinsCDRDX	
XH_P44	12	96912787	96912787	Missense_Mutation	SNP	G	C	G	CFAP54	c.G880C	p.A294P	
XH_P44	12	96974716	96974716	Frame_Shift_Ins	INS	-	AT	-	CFAP54	2908_2909insA	p.S970fs	
XH_P44	12	96974717	96974717	Frame_Shift_Ins	INS	-	AGCC	-	CFAP54	909_2910insAG	p.S970fs	
XH_P44	12	99007696	99007696	Frame_Shift_Ins	INS	-	GAAAGAAATTG	-	IKBP1	720insGCAATT	p.N240fs	
XH_P44	12	100452623	100452623	Frame_Shift_Ins	INS	-	AGTGTGAGCC	-	UHRF1BP1L	2432insGGCTCT	p.V811fs	
XH_P44	12	100657521	100657521	Nonsense_Mutation	INS	-	TATATTTTATTTA	-	DEPDC4	5GGTCTAAATAA	H103delinsLSKX	
XH_P44	12	101017551	101017551	Frame_Shift_Ins	INS	-	NTGTGATGTCTG	-	GAS2L3	CAATATGTGAT	p.V323fs	
XH_P44	12	101381395	101381395	Missense_Mutation	SNP	C	A	C	ANO4	c.C681A	p.D227E	
XH_P44	12	101381396	101381396	Nonsense_Mutation	INS	-	TCTAG	-	ANO4	682_683insTCTA	228_E229delinsLX	
XH_P44	12	101576672	101576672	Nonsense_Mutation	INS	-	AATGTTGTATC	-	SLCSA8	AACATTGATACA	58_A359delinsNIKHX	
XH_P44	12	102155457	102155457	In_Frame_Ins	INS	-	AAGAAAAAAGT	-	GNPTAB	300insGGACTTT	5934delinsGLF5FS	
XH_P44	12	102164320	102164320	Frame_Shift_Ins	INS	-	TTCTC	-	GNPTAB	976_977insGAG	p.N326fs	
XH_P44	12	102164322	102164322	Frame_Shift_Ins	INS	-	GC	-	GNPTAB	c.974_975insGC	p.D325fs	
XH_P44	12	104056726	104056726	Nonsense_Mutation	INS	-	GGTGTCTATTAT	-	STAB2	AGGGTAGGTTG	658_P659delinsGGX	
XH_P44	12	104152966	104152966	Nonsense_Mutation	INS	-	SAGCAGAGCTT	-	STAB2	7164insGAGCAC	p.Y2388delinsX	
XH_P44	12	104171809	104171809	Frame_Shift_Ins	INS	-	AGTGTTCCTT	-	NTSDC3	1445insAAAGC	p.T482fs	
XH_P44	12	104359839	104359839	Splice_Site	SNP	G	C	G	TDG	.	.	
XH_P44	12	104515060	104515060	Frame_Shift_Ins	INS	-	TTTTGGTGAG	-	NFYB	TGAATCTTCACC	p.A157fs	

XH_P44	12	104698090	104698090	Silent	SNP	C	T	C	EID3	c.C378T	p.F126F
XH_P44	12	105322287	105322287	Frame_Shift_Ins	INS	-	CAACACATGGA	-	SLC41A2	nsTACTCCATGT	p.R7fs
XH_P44	12	105527575	105527575	Nonsense_Mutation	INS	-	ATAAATATTACA	-	WASHC4	AAAGAGATAAA	9_5410delinsVVKRX
XH_P44	12	105571035	105571035	Missense_Mutation	SNP	A	G	A	APL2	c.T1658C	p.I53T
XH_P44	12	105571036	105571036	In_Frame_Ins	INS	-	TGCTTTTITTTT	-	APL2	657insGAAAAA	1553delinsEKAI
XH_P44	12	106480656	106480656	In_Frame_Ins	INS	-	AGCATGTATGG	-	NUAK1	sATTCCTCATACA	23delinsEFHSHPM
XH_P44	12	106898028	106898028	In_Frame_Ins	INS	-	AAACAAACAA	-	POLR3B	95insTTAAACA	1032delinsVKQTKS
XH_P44	12	106898030	106898030	Silent	SNP	C	G	C	POLR3B	c.C3096G	p.G1032G
XH_P44	12	106903238	106903238	Frame_Shift_Ins	INS	-	A	-	POLR3B	c.3139_3140ins	p.R1047fs
XH_P44	12	106903240	106903240	Nonsense_Mutation	INS	-	STTTAAAGCATG	-	POLR3B	142insGTTTAA	1047_1048delinsRVX
XH_P44	12	107371653	107371653	Frame_Shift_Ins	INS	-	C	-	MTERF2	c.839_840insG	p.D280fs
XH_P44	12	107371654	107371654	Frame_Shift_Ins	INS	-	GAATAAAGGAT	-	MTERF2	9insTCCATCCTT	p.D280fs
XH_P44	12	107391407	107391407	Frame_Shift_Ins	INS	-	GTACCTTCTAAT	-	CRY1	sTTAGGATTAGA	p.P451fs
XH_P44	12	108686305	108686305	Frame_Shift_Ins	INS	-	TCCTCATCATC	-	CMKLR1	435insGATGAT	p.V145fs
XH_P44	12	108931971	108931971	In_Frame_Ins	INS	-	GTCC	-	SART3	70_1071insGGG	Q357delinsQGT
XH_P44	12	108931973	108931973	In_Frame_Ins	INS	-	GGGTTT	-	SART3	68_1069insAAA	Q357delinsKPQ
XH_P44	12	109577399	109577399	Nonsense_Mutation	INS	-	AGGATTACATA	-	ACACB	ATTTTAGGATT	63_64delinsETFX
XH_P44	12	110989759	110989759	Nonsense_Mutation	INS	-	GCGAGGTGTGA	-	PPTC7	8insCTATCACAC	0_8delinsSHSAX
XH_P44	12	111923574	111923574	Nonsense_Mutation	INS	-	TGCAGAGATTCA	-	ATXN2	013insCTGAATC	671_672delinsHX
XH_P44	12	112326790	112326790	Frame_Shift_Ins	INS	-	AAAAATAACAA	-	MAPKAPK5	3insCAGAAAAA	p.1401fs
XH_P44	12	112485593	112485593	Frame_Shift_Ins	INS	-	TTATTTTAAAGT	-	NAA25	c.CTAATTCTTTAA	p.S628fs
XH_P44	12	112631416	112631416	Nonsense_Mutation	INS	-	CTTTATCTCATC	-	HECTD4	410insAGATGA	804_12805delinsRX
XH_P44	12	112631418	112631418	Missense_Mutation	SNP	G	T	G	HECTD4	c.C8408A	p.S2803Y
XH_P44	12	112743892	112743892	Frame_Shift_Ins	INS	-	CTTTGTTGGAG	-	HECTD4	sACAACTCCAAA	p.V293fs
XH_P44	12	112846370	112846370	Frame_Shift_Ins	INS	-	AAAGAAAAAGAT	-	RPL6	1insCCTCTTTTT	p.N31fs
XH_P44	12	113405980	113405980	Splice_Site	INS	-	CA	-	OAS3	-	-
XH_P44	12	113405981	113405981	Splice_Site	INS	-	ACACAG	-	OAS3	-	-
XH_P44	12	116406820	116406820	Frame_Shift_Ins	INS	-	AACT	-	MED13L	149_6150insAG	p.S2050fs
XH_P44	12	116406822	116406822	Frame_Shift_Ins	INS	-	CTAT	-	MED13L	147_6148insAT	p.S2050fs
XH_P44	12	116421342	116421342	Nonsense_Mutation	INS	-	CTACCTCTCTCT	-	MED13L	5insTGAAAGAA	12_Y1513delinsLKKRX
XH_P44	12	116445411	116445411	Frame_Shift_Ins	INS	-	CTCTGTCCCCAT	-	MED13L	43insTATGGGG	p.K681fs
XH_P44	12	116675341	116675341	In_Frame_Ins	INS	-	TCCTTTTCCAGT	-	MED13L	2insTAACCTGGA	K81delinsITGKGQ
XH_P44	12	118467624	118467624	In_Frame_Ins	INS	-	TACCAAGGTGAT	-	RFC5	912insTACCAAAA	D304delinsDTKVI
XH_P44	12	118517193	118517193	Frame_Shift_Ins	INS	-	TTTCCACTTGAC	-	VSIG10	83insTGTCAAG	p.I295fs
XH_P44	12	120510504	120510504	Frame_Shift_Ins	INS	-	CACCAAGTTCA	-	BICDL1	CCAAGACACCA	p.Q427fs
XH_P44	12	121001215	121001215	Frame_Shift_Ins	INS	-	AAGAACTAATA	-	RNF10	5GGGAAAGAAC	p.P445fs
XH_P44	12	121441997	121441997	Frame_Shift_Ins	INS	-	ACCAATCAAGG	-	C12orf43	52insGGCCTTGA	p.F218fs
XH_P44	12	121693587	121693587	Nonsense_Mutation	INS	-	TGGGTAGTTAG	-	CAMKK2	7insTGTCAACT	p.G273delinsCX
XH_P44	12	121768474	121768474	Frame_Shift_Ins	INS	-	AGATTTAGAAT	-	ANAPC5	7insCCCATTTCTA	p.S246fs
XH_P44	12	121779871	121779871	Nonsense_Mutation	INS	-	TGTGTGTGATT	-	ANAPC5	AATAAAATCAC	E99_E100delinsXX
XH_P44	12	121858089	121858089	Frame_Shift_Ins	INS	-	CTTCCAAAAAGT	-	RNF34	03insCCTTCCAA	p.D34fs
XH_P44	12	122243997	122243997	Frame_Shift_Ins	INS	-	ACTCATC	-	SETD1B	30_531insACTC	p.E177fs
XH_P44	12	122243999	122243999	Missense_Mutation	SNP	C	A	C	SETD1B	c.C532A	p.I178M
XH_P44	12	122359540	122359540	Frame_Shift_Ins	INS	-	CCTCTCCTCCTC	-	WDR66	30insTCCTCTCC	p.L110fs
XH_P44	12	122359541	122359541	Missense_Mutation	SNP	G	T	G	WDR66	c.G330T	p.L110F
XH_P44	12	123068985	123068985	Frame_Shift_Ins	INS	-	AACACATTAAAT	-	KNTC1	5insTCAACACA	p.L1142fs
XH_P44	12	123087622	123087622	Frame_Shift_Ins	INS	-	AGAGCAATGTT	-	KNTC1	4insTTAAGAGC	p.K1645fs
XH_P44	12	123187196	123187196	Frame_Shift_Ins	INS	-	GAAGATGACAG	-	HCAR2	635insCCTGTCA	p.I212fs
XH_P44	12	123187198	123187198	Silent	SNP	A	G	A	HCAR2	c.T633C	p.I211I
XH_P44	12	123200794	123200794	In_Frame_Ins	INS	-	CCACTTTGA	-	HCAR3	0_491insTCAAA	K164delinsIKVE
XH_P44	12	123201151	123201151	Frame_Shift_Ins	INS	-	ATCTCTGCGCTT	-	HCAR3	4insGAAGGCA	p.N45fs
XH_P44	12	123706370	123706370	In_Frame_Ins	INS	-	AAA	-	MPHOSPH9	c.420_421insTT	p.N141delinsFN
XH_P44	12	123706371	123706371	In_Frame_Ins	INS	-	TACAAATCTAAA	-	MPHOSPH9	insGTCTTTAGAT	140delinsGSLDLYR
XH_P44	12	123810856	123810856	In_Frame_Ins	INS	-	CGAGAG	-	SBN01	17_1718insCTC	Q573delinsP
XH_P44	12	124111617	124111617	In_Frame_Ins	INS	-	ATTGTATTGATG	-	EIF2B1	AATCTCTCATCA	delinsVDKNLHQYNLCS
XH_P44	12	124111619	124111619	Missense_Mutation	SNP	C	G	C	EIF2B1	c.G454C	p.V152L
XH_P44	12	124191300	124191300	Frame_Shift_Ins	INS	-	ACATCTGCCAGT	-	TCTN2	95insCAACATCT	p.Q598fs
XH_P44	12	125497177	125497177	In_Frame_Ins	INS	-	GGGTAC	-	BR13BP	11_312insGGG	p.L104delinsLGT
XH_P44	12	125497179	125497179	In_Frame_Ins	INS	-	ATC	-	BR13BP	c.313_314insAT	p.D105delinsDH
XH_P44	12	125570959	125570959	Nonsense_Mutation	INS	-	STTCAATGCAG	-	AACS	cACCTGTTTCAA	G149delinsNPPTCFNAGYX
XH_P44	12	125900140	125900140	Frame_Shift_Ins	INS	-	TTTCTGTTTAATC	-	TMEM132B	sTTAATTTTCTG	p.A336fs
XH_P44	12	126138411	126138411	Nonsense_Mutation	INS	-	TTACTAGTTGCTT	-	TMEM132B	insAACTTACTAT	G310delinsELTIASX
XH_P44	12	129190233	129190233	Missense_Mutation	SNP	G	T	G	TMEM132C	c.G720T	p.G907V
XH_P44	12	132522632	132522632	Frame_Shift_Ins	INS	-	AAGCCCC	-	EP400	98_6199insAAG	p.P2066fs
XH_P44	12	133778907	133778907	Nonsense_Mutation	INS	-	ACAATTAGTCAC	-	ZNF268	nsAGAAACAATTAY	212_1213delinsX
XH_P44	13	20233412	20233412	In_Frame_Ins	INS	-	CTGCTGCCTGCC	-	MPHOSPH8	1775insCTGCTG	Y592delinsSAAACH
XH_P44	13	20346663	20346663	Frame_Shift_Ins	INS	-	C	-	PSPC1	c.392_393insG	p.E131fs
XH_P44	13	20346664	20346664	Frame_Shift_Ins	INS	-	GTCTTTTCATTG	-	PSPC1	392insCACTGA	p.E131fs
XH_P44	13	23905665	23905665	Frame_Shift_Ins	INS	-	STGGTGATATCT	-	SACS	1909insTAGAT	p.T3970fs
XH_P44	13	23906601	23906601	Nonsense_Mutation	INS	-	AGTCAAGGTGA	-	SACS	insACTCCTCACC	58_L3659delinsHSSPX
XH_P44	13	23930017	23930017	Frame_Shift_Ins	INS	-	GTTTAGAGTGA	-	SACS	293insTCACTC	p.D98fs
XH_P44	13	23930018	23930018	In_Frame_Ins	INS	-	TTCCAG	-	SACS	91_292insCTCG	p.D98delinsLED
XH_P44	13	25008923	25008923	Frame_Shift_Ins	INS	-	AG	-	PARP4	4355_4356insC	p.G1452fs
XH_P44	13	25008924	25008924	In_Frame_Ins	INS	-	TGCTTTTGA	-	PARP4	4355insTAAA	G1452delinsVKSR
XH_P44	13	26789156	26789156	Missense_Mutation	SNP	T	G	T	RNF6	c.A863C	p.N288T
XH_P44	13	26789158	26789158	Frame_Shift_Ins	INS	-	AGAAGGAGAAG	-	RNF6	51insATTCTTCTC	p.S287fs
XH_P44	13	27241791	27241791	In_Frame_Ins	INS	-	AATAATATTTTT	-	WASF3	sACCAATAATAA	136delinsNQIFFIV
XH_P44	13	27333083	27333083	Frame_Shift_Ins	INS	-	CTTCCCTT	-	GPR12	1_882insAAGG	p.S294fs
XH_P44	13	29012441	29012441	Nonsense_Mutation	INS	-	TTTACAAACACC	-	FLT1	30insAGGTGTT	44_1145delinsRCLX
XH_P44	13	29287213	29287213	Nonsense_Mutation	INS	-	TGAAGTTTATAT	-	SLC46A3	TAACCTATAAAA	222_K223delinsX
XH_P44	13	31712565	31712565	Frame_Shift_Ins	INS	-	ACTTCTCCAT	-	HSPH1	2121insATTGGA	p.Q707fs
XH_P44	13	31713241	31713241	Missense_Mutation	SNP	G	A	G	HSPH1	c.C1756T	p.H586Y
XH_P44	13	31713242	31713242	Frame_Shift_Ins	INS	-	ATTAATTATTATG	-	HSPH1	5insATGTAATA	p.D585fs
XH_P44	13	32313834	32313834	Frame_Shift_Ins	INS	-	CT	-	RFXP2	c.85_86insCT	p.N29fs
XH_P44	13	32313835	32313835	Frame_Shift_Ins	INS	-	ATTCTATTAGG	-	RFXP2	87insATTCTATT	p.N29fs
XH_P44	13	32745358	32745358	In_Frame_Ins	INS	-	SAATAGAGAGCC	-	FRY	8insTATGAATAG	701delinsHMNREP
XH_P44	13	32786510	32786510	Nonsense_Mutation	INS	-	TAGACATCTGT	-	FRY	674insGTAGAC	558_D1559delinsSX
XH_P44	13	32835946	32835946	Frame_Shift_Ins	INS	-	TGTCACACATTC	-	FRY	insACATGTTTCA	p.S2537fs
XH_P44	13	32906957	32906957	Frame_Shift_Ins	INS	-	GAATCTAATAGT	-	BRCA2	insATTGTAATG	p.R448fs
XH_P44	13	32911464	32911464	In_Frame_Ins	INS	-	TTCTTCTAGATT	-	BRCA2	973insGTCTCTT	N991delinsKFLSLIS
XH_P44	13	33628117	33628117	Frame_Shift_Ins	INS	-	AAATTTATCTCT	-	KL	sATGGCAAAATT	p.L345fs
XH_P44	13	33681012	33681012	Nonsense_Mutation	INS	-	ATTAGTGTGCTT	-	STARD13	sTATGAAAGCA	p.H918delinsLX
XH_P44	13	33687067	33687067	Nonsense_Mutation	INS	-	TATAGATAGATG	-	STARD13	nsCCTACCTATC	643delinsVLPVLYX
XH_P44	13	36905706	36905706	Frame_Shift_Ins	INS	-	T	-	SPG20	c.837_838insA	p.P280fs
XH_P44	13	36905708	36905708	Frame_Shift_Ins	INS	-	TTGTGTGTATCA	-	SPG20	36insATGATCA	p.V279fs
XH_P44	13	37427764	37427764	Frame_Shift_Ins	INS	-	TATAAAATGTT	-	SMAD9	1insCTGAACATT	p.S314fs
XH_P44	13	37447005	37447005	Nonsense_Mutation	INS	-	GTCCTATCAAC	-	SMAD9	50insTGTGATA	154_S155delinsCX
XH_P44	13	37580133	37580133	Frame_Shift_Ins	INS	-	GAGATTAC	-	EXOSC8	5_316insGAGA	p.A105fs

XH_P44	13	37596408	37596408	Frame_Shift_Ins	INS	-	TGGTAAGTTTG	-	SUPT20H	insAATGCAAAC	p.546fs
XH_P44	13	38211292	38211292	Frame_Shift_Ins	INS	-	ACGAAGATTA	-	TRPC4	2163insTAATC	p.R721fs
XH_P44	13	39358933	39358933	Frame_Shift_Ins	INS	-	AGAATTCAAAAC	-	FREM2	CAGAGAGAAAT	p.D2003fs
XH_P44	13	39588017	39588017	Frame_Shift_Ins	INS	-	AACTCTT	-	PROSER1	71_1372insAAG	p.V458fs
XH_P44	13	39588018	39588018	Missense_Mutation	SNP	G	C	G	PROSER1	c.C1371G	p.5457R
XH_P44	13	39588503	39588503	Missense_Mutation	SNP	A	C	A	PROSER1	c.T886G	p.S296A
XH_P44	13	39588504	39588504	Frame_Shift_Ins	INS	-	TCTACCA	-	PROSER1	84_885insTGGT	p.P295fs
XH_P44	13	40175347	40175347	Frame_Shift_Ins	INS	-	GAATTCAGTTT	-	LHPF	insGAAACTGAA	p.S3fs
XH_P44	13	41133994	41133994	Frame_Shift_Ins	INS	-	AATCCATCAT	-	FOXO1	1634insATGAT	p.T545fs
XH_P44	13	42872842	42872842	Frame_Shift_Ins	INS	-	AAAA	-	AKAP11	525_526insAAA	p.D175fs
XH_P44	13	42872844	42872844	Frame_Shift_Ins	INS	-	CAAATACAAAA	-	AKAP11	TAATTTCAAATA	p.T176fs
XH_P44	13	42876618	42876618	Frame_Shift_Ins	INS	-	C	-	AKAP11	c.3736_3737ins	p.L1246fs
XH_P44	13	42876620	42876620	Nonsense_Mutation	INS	-	TAGTATTTTGTG	-	AKAP11	8739insTAGTAT	246_N1247delinsLX
XH_P44	13	42877042	42877042	Frame_Shift_Ins	INS	-	TCTACTTTATAAT	-	AKAP11	TTCTCTTCTACT	p.T1387fs
XH_P44	13	42877145	42877145	Nonsense_Mutation	INS	-	ACTGTTCTCTCT	-	AKAP11	stAACCACTGTT	421_D1422delinsAX
XH_P44	13	45768505	45768505	In_Frame_Ins	INS	-	CTCTCTGTAATGC	-	KCTD4	CAGGAGCATTAC	6delinsNQEHYRFL
XH_P44	13	46543785	46543785	Frame_Shift_Ins	INS	-	TGTGCAATGGTA	-	ZC3H13	insTTCTTACCAT	p.K965fs
XH_P44	13	46559803	46559803	Frame_Shift_Ins	INS	-	GAATAAAGGAT	-	ZC3H13	insCTCATTCCTT	p.R450fs
XH_P44	13	46708363	46708363	Nonsense_Mutation	INS	-	TTGTTTGTGATG	-	LCP1	TGATGAACATCA	insFINEMADEHQNNNESFKQNX
XH_P44	13	46730701	46730701	Nonsense_Mutation	INS	-	ACCATCAACAAT	-	LCP1	insTTAAITGGTTG	121_E122delinsDX
XH_P44	13	46946399	46946399	In_Frame_Ins	INS	-	AGGTAATTTTGA	-	RUBCNL	sACCTACTAAAA	71delinsHLLKLPS
XH_P44	13	47255967	47255967	In_Frame_Ins	INS	-	AAATAATTGGAC	-	LRCH1	AATTTAAATATT	24delinsKEFKYLDNVT
XH_P44	13	47255969	47255969	Frame_Shift_Ins	INS	-	STACACTTTTAT	-	LRCH1	574insGTACACT	p.V225fs
XH_P44	13	48881479	48881479	Frame_Shift_Ins	INS	-	TAGTGAAAAATA	-	RB1	insCACAGTGAA	p.P67fs
XH_P44	13	49772506	49772506	Frame_Shift_Ins	INS	-	GGGATTTCCTAT	-	FNDC3A	nsAATGGGGAT	p.V872fs
XH_P44	13	50065955	50065955	In_Frame_Ins	INS	-	ACCACGTCATGT	-	SETDB2	2095insACCCAG	5698delinsGTQSC
XH_P44	13	51948351	51948351	Nonsense_Mutation	INS	-	TATTAGCTATTAT	-	INTS6	AGAACATAATA	9_H700delinsLEHNSX
XH_P44	13	52544856	52544856	In_Frame_Ins	INS	-	TATCAGTAGCC	-	ATP7B	15insAGGGCTA	439delinsRATDKH
XH_P44	13	52603142	52603142	Frame_Shift_Ins	INS	-	ATCCATTTCCTT	-	UTP14C	203insATCCATT	p.L68fs
XH_P44	13	52603515	52603515	Nonsense_Mutation	INS	-	CTTGATTGTGAC	-	UTP14C	sCCTCTTTGAT	H192delinsHLLX
XH_P44	13	52604544	52604544	In_Frame_Ins	INS	-	CCTCCT	-	UTP14C	604_1605insCCT	Q53delinsHLL
XH_P44	13	52605055	52605055	In_Frame_Ins	INS	-	CTTCCCTCTCTG	-	UTP14C	116insGCTTCCC	1705delinsTASLFS
XH_P44	13	52674001	52674001	Frame_Shift_Ins	INS	-	TTGTTTGTGTTG	-	NEK5	04insAACAAACA	p.Q302fs
XH_P44	13	52674003	52674003	Missense_Mutation	SNP	A	G	A	NEK5	c.T902C	p.I301T
XH_P44	13	52725324	52725324	Missense_Mutation	SNP	C	G	C	NEK3	c.G505C	p.V169L
XH_P44	13	52725325	52725325	Nonsense_Mutation	INS	-	CTATATTGCTAA	-	NEK3	TATAGATTAGCA	168_V169delinsX
XH_P44	13	53036022	53036022	Frame_Shift_Ins	INS	-	AGTCT	-	CKAP2	064_1065insAG	p.S355fs
XH_P44	13	53036024	53036024	Frame_Shift_Ins	INS	-	TCTTATTATACC	-	CKAP2	067insTTTCTTAT	p.R356fs
XH_P44	13	58299376	58299376	Frame_Shift_Ins	INS	-	C	-	PCDH17	c.3428_3429ins	p.D1143fs
XH_P44	13	58299377	58299377	Frame_Shift_Ins	INS	-	GTCAAGTGGGC	-	PCDH17	3430insGTCAG	p.D1143fs
XH_P44	13	60545279	60545279	Frame_Shift_Ins	INS	-	GAATTGGTTAAA	-	DIAPH3	TTACCTTTAACC	p.A293fs
XH_P44	13	67799906	67799906	Frame_Shift_Ins	INS	-	AACACCTT	-	PCDH9	6_2667insAAGG	p.E889fs
XH_P44	13	67799908	67799908	Missense_Mutation	SNP	C	G	C	PCDH9	c.G265C	p.E889Q
XH_P44	13	67802154	67802154	Frame_Shift_Ins	INS	-	AAACAGAAAGAT	-	PCDH9	ATAGGTATCTT	p.P140fs
XH_P44	13	74420229	74420229	Frame_Shift_Ins	INS	-	TTTGGAGGATG	-	KLF12	405insCATCTG	p.S135fs
XH_P44	13	76379814	76379814	Nonsense_Mutation	INS	-	GACTTTGAAGTT	-	LMO7	JAGAGGACTTTG	139_W140delinsX
XH_P44	13	76414605	76414605	Nonsense_Mutation	INS	-	TTTGAATTTTAA	-	LMO7	2858insTTTGA	953_K954delinsLX
XH_P44	13	76414607	76414607	Missense_Mutation	SNP	G	T	G	LMO7	c.G2859T	p.Q953H
XH_P44	13	77531916	77531916	Nonsense_Mutation	INS	-	ATTCTCTTAATG	-	ACOD1	insACAATTCTC	0_Q411delinsSTILLMX
XH_P44	13	77581543	77581543	Frame_Shift_Ins	INS	-	AAGAAGTACTA	-	FBXL3	nsGGAATTAGTA	p.N342fs
XH_P44	13	77672728	77672728	Frame_Shift_Ins	INS	-	AAGGATTCTACA	-	MYCBP2	61insTCTGTAGA	p.S2854fs
XH_P44	13	77740630	77740630	Frame_Shift_Ins	INS	-	STATATTAGTA	-	MYCBP2	sACCTTACTATA	p.T2058fs
XH_P44	13	77779665	77779665	Frame_Shift_Ins	INS	-	T	-	MYCBP2	c.3657_3658ins	p.Q1220fs
XH_P44	13	78320796	78320796	In_Frame_Ins	INS	-	TAAATAACAA	-	SLAIN1	ACCTATAAAAT	9delinsPETYKITNSTL
XH_P44	13	79916891	79916891	Missense_Mutation	SNP	C	T	C	RBM26	c.G2263A	p.V755I
XH_P44	13	79916893	79916893	Frame_Shift_Ins	INS	-	ACCATTGTATGT	-	RBM26	261insTACATAC	p.E754fs
XH_P44	13	79927320	79927320	Frame_Shift_Ins	INS	-	TGCCTCCCCTA	-	RBM26	332insATAGTGG	p.V678fs
XH_P44	13	79940803	79940803	Nonsense_Mutation	INS	-	ATTAAGTATAT	-	RBM26	DinsAGTGATAT	p.P367delinsQX
XH_P44	13	86370405	86370405	Nonsense_Mutation	INS	-	AAATGACAATG	-	SLITRK6	AAATAGCATTTG	0_T81delinsLNSIVIX
XH_P44	13	92380886	92380886	Missense_Mutation	SNP	G	T	G	GPC5	c.G1121T	p.R374M
XH_P44	13	92380888	92380888	Frame_Shift_Ins	INS	-	TCACCTCAATAT	-	GPC5	TTGCTTTCACT	p.N375fs
XH_P44	13	96489411	96489411	Frame_Shift_Ins	INS	-	TTGATGATTCAC	-	UGGT2	330insAGTGAA	p.P1444fs
XH_P44	13	96489413	96489413	Frame_Shift_Ins	INS	-	G	-	UGGT2	c.4327dupC	p.L1443fs
XH_P44	13	96536885	96536885	Nonsense_Mutation	INS	-	TTCTTATCAGCT	-	UGGT2	TGTAATAGCTG	80_S1031delinsNCNSX
XH_P44	13	96636081	96636081	Frame_Shift_Ins	INS	-	AGGTAGTATGG	-	UGGT2	69insAAACCATA	p.E357fs
XH_P44	13	99340752	99340752	Nonsense_Mutation	INS	-	TATATAGTCCAA	-	SLC15A1	TTCTCTTGGAC	6_T517delinsFLWTIX
XH_P44	13	99540714	99540714	In_Frame_Ins	INS	-	GAATATTGGCA	-	DOCK9	DinsAAATCCGAA	627delinsQIAILA
XH_P44	13	99966465	99966465	Nonsense_Mutation	INS	-	TCATGTCCTAAA	-	UBAC2	ATGATTCAATG	3delinsLIFYDSCPKX
XH_P44	13	99966467	99966467	Missense_Mutation	SNP	G	A	G	UBAC2	c.G401A	p.G134E
XH_P44	13	101910882	101910882	Nonsense_Mutation	INS	-	GCTGAATCATTG	-	NALCN	91insGACAATG	864_V365delinsRQX
XH_P44	13	102029303	102029303	In_Frame_Ins	INS	-	GATGTTTGG	-	NALCN	9_480insCCAAA	F160delinsFQTS
XH_P44	13	102029305	102029305	Nonsense_Mutation	INS	-	TACTATACACTG	-	NALCN	nsACACAGTGAT	60_E161delinsTXQ
XH_P44	13	103383402	103383402	Nonsense_Mutation	INS	-	TCAAATAGATC	-	CCDC168	AAATCAAGATC	p.L6549delinsLX
XH_P44	13	103387124	103387124	Frame_Shift_Ins	INS	-	C	-	CCDC168	15922_15923ins	p.L5308fs
XH_P44	13	103387125	103387125	Frame_Shift_Ins	INS	-	GATATAACTT	-	CCDC168	15922insAAGT	p.L5308fs
XH_P44	13	103388348	103388348	In_Frame_Ins	INS	-	CAG	-	CCDC168	4698_14699ins	p.L4900delinsTV
XH_P44	13	103388349	103388349	Missense_Mutation	SNP	T	A	T	CCDC168	c.A14698T	p.I4900L
XH_P44	13	103389015	103389015	Nonsense_Mutation	INS	-	AGGCCAAAGACA	-	CCDC168	14032insATGTC	8_K4679delinsMSLPX
XH_P44	13	103389759	103389759	Frame_Shift_Ins	INS	-	KAGTAGAAGTGG	-	CCDC168	nsATAATCCACA	p.L4430fs
XH_P44	13	103392292	103392292	In_Frame_Ins	INS	-	AAGGAATTCCT	-	CCDC168	10755insAGGA	3585delinsQGNNSF
XH_P44	13	103393253	103393253	Frame_Shift_Ins	INS	-	AAGAAAAATAT	-	CCDC168	9794insTATATT	p.A3265fs
XH_P44	13	103393255	103393255	Missense_Mutation	SNP	C	A	C	CCDC168	c.G9792T	p.E3264D
XH_P44	13	103396266	103396266	Nonsense_Mutation	INS	-	CA	-	CCDC168	6780_6781insT	261_F2262delinsX
XH_P44	13	103396268	103396268	Nonsense_Mutation	INS	-	GTCATATTA	-	CCDC168	8_6779insTAAT	A2260delinsVIX
XH_P44	13	103396438	103396438	In_Frame_Ins	INS	-	ACTATGAAGGAA	-	CCDC168	ACTTCTTTCTCT	3delinsDDFFSFIVKHL
XH_P44	13	103396721	103396721	In_Frame_Ins	INS	-	AAAAGCAACAC	-	CCDC168	326insCGGTGTT	2109delinsTVLLFL
XH_P44	13	103400869	103400869	Nonsense_Mutation	INS	-	AAAATTCAGAGT	-	CCDC168	TGTATTCACTTG	27delinsHTFCILHNFYFGX
XH_P44	13	103402624	103402624	Frame_Shift_Ins	INS	-	G	-	CCDC168	c.422_423insC	p.S141fs
XH_P44	13	103402625	103402625	Frame_Shift_Ins	INS	-	TCTAGATTCAC	-	CCDC168	22insCAGTGAA	p.S141fs
XH_P44	13	103518257	103518257	Frame_Shift_Ins	INS	-	TGCAATCATCAA	-	BIVM-ERCC5	TGATCCTGCAAT	p.N732fs
XH_P44	13	103527860	103527860	Frame_Shift_Ins	INS	-	TTCTCTCC	-	BIVM-ERCC5	38_3169insTTCT	p.Q1056fs
XH_P44	13	103527861	103527861	Missense_Mutation	SNP	A	C	A	BIVM-ERCC5	c.A3169C	p.K1057Q
XH_P44	13	103528130	103528130	In_Frame_Ins	INS	-	ATTGTTATGCC	-	BIVM-ERCC5	AAGGTATTGTT	SDSDSSKKVFMPLFVWFRFALSS
XH_P44	13	108861358	108861358	Nonsense_Mutation	INS	-	CTTGTTTACGTC	-	LIG4	TTCCCTCAGCTAA	53_F754delinsHSLSX
XH_P44	13	109496824	109496824	Frame_Shift_Ins	INS	-	TAAGAAATATT	-	MYO16	TTTCAGATAAGA	p.S411fs
XH_P44	13	110815819	110815819	Nonsense_Mutation	INS	-	GTGGTTTCTCAA	-	COL4A1	40insACTTATGA	414_P1415delinsTX
XH_P44	13	111158796	111158796	Silent	SNP	G	A	G	COL4A2	c.G4437A	p.P1479P
XH_P44	13	111545550	111545550	Frame_Shift_Ins	INS	-	TTATTTT	-	ANKRD10	09_610insAAAA	p.V204fs

XH_P44	13	111545552	111545552	In_Frame_Ins	INS	-	CTGTAATATGTT	-	ANKRD10	AAGAAAAACATA	172delinsKTTYRKE
XH_P44	14	19378165	19378165	Frame_Shift_Ins	INS	-	CATCTGGGAA	-	OR11H12	73insACATCTTC	p.H191fs
XH_P44	14	20181627	20181627	Frame_Shift_Ins	INS	-	AGCTGTGTGG	-	OR11H2	49insCCCAACA	p.I150fs
XH_P44	14	20181713	20181713	Frame_Shift_Ins	INS	-	TTATTGACCATG	-	OR11H2	8insAACATGGTC	p.S121fs
XH_P44	14	20249253	20249253	Missense_Mutation	SNP	T	C	T	OR4M1	c.T772C	p.Y258H
XH_P44	14	20249254	20249254	Nonsense_Mutation	INS	-	GGAGAGAG	-	OR4M1	3774insGGAGAG	2581259delinsX
XH_P44	14	20344725	20344725	Frame_Shift_Ins	INS	-	CCATT	-	OR4K2	299300insCCA	p.Q100fs
XH_P44	14	20344726	20344726	Frame_Shift_Ins	INS	-	TTGCCAC	-	OR4K2	300301insTGC	p.Q100fs
XH_P44	14	20404561	20404561	Frame_Shift_Ins	INS	-	AATAGACACAA	-	OR4K1	insGAAATAGAC	p.V246fs
XH_P44	14	20444233	20444233	Frame_Shift_Ins	INS	-	AAAAGAAATAG	-	OR4K15	57insCAAAAGAA	p.F186fs
XH_P44	14	20483223	20483223	Frame_Shift_Ins	INS	-	TTGGC	-	OR4K14	129130insGCC	p.L44fs
XH_P44	14	20483224	20483224	Frame_Shift_Ins	INS	-	GACTTGCACTC	-	OR4K14	129insGATGCA	p.L43fs
XH_P44	14	20767592	20767592	Frame_Shift_Ins	INS	-	AG	-	TTC5	c.411_412insCT	p.S138fs
XH_P44	14	20767594	20767594	Missense_Mutation	SNP	A	G	A	TTC5	c.T410C	p.V137A
XH_P44	14	20876090	20876090	In_Frame_Ins	INS	-	ACCATC	-	TEP1	80509insGATG	T170delinsRW5
XH_P44	14	21360186	21360186	In_Frame_Ins	INS	-	CTGTGGGGG	-	RNASE3	1342insCTGTGG	N114delinsNCGG
XH_P44	14	21469431	21469431	Frame_Shift_Ins	INS	-	CGAAGATA	-	SLC39A2	3624insCGAAG	p.F114fs
XH_P44	14	21526500	21526500	In_Frame_Ins	INS	-	TGATGCTCATG	-	RNASE8	ATTGATGATGC	50delinsLLMLLMAE
XH_P44	14	21623112	21623112	Frame_Shift_Ins	INS	-	AGTGATTTCTCT	-	OR5AU1	AGGAAAGGAA	p.R358fs
XH_P44	14	21793501	21793501	Nonsense_Mutation	INS	-	CTTTGGGAAAT	-	RPGRIIP1	7insAGGCTTTGG	p.S776delinsX
XH_P44	14	21822659	21822659	Nonsense_Mutation	INS	-	A	-	SUPT16H	c.2700_2701ins	901W902delinsX
XH_P44	14	21822660	21822660	Frame_Shift_Ins	INS	-	AATATGAGTAG	-	SUPT16H	tsTATGTACTACT	p.L900fs
XH_P44	14	21859208	21859208	In_Frame_Ins	INS	-	TTTTTTTTTTTT	-	CHD8	tsTCTCAAAAAA	360delinsRLKKKNP
XH_P44	14	21862614	21862614	Nonsense_Mutation	INS	-	CCCTAACC	-	CHD8	D5421insGGTT	1807R1808delinsX
XH_P44	14	21876962	21876962	In_Frame_Ins	INS	-	TACTCTATTTTT	-	CHD8	tsTTAAAAAA	796delinsFKNRVCR
XH_P44	14	21876964	21876964	Frame_Shift_Ins	INS	-	TTTAACATTTTT	-	CHD8	GAAAAA	p.A795fs
XH_P44	14	21969269	21969269	Nonsense_Mutation	INS	-	AGCAATCTT	-	METTL3	1902insAAGAT	R301delinsQDCX
XH_P44	14	21991982	21991982	Frame_Shift_Ins	INS	-	A	-	SALL2	c.1879dupT	p.S627fs
XH_P44	14	21991984	21991984	In_Frame_Ins	INS	-	TTCCACCAAT	-	SALL2	71878insATTGG	A626delinsALVN
XH_P44	14	23282267	23282267	Frame_Shift_Ins	INS	-	SAGGAATGCTC	-	SLC7A7	TTGTACAGAGACA	p.F174fs
XH_P44	14	23392010	23392010	In_Frame_Ins	INS	-	CTAGAGCTTCTG	-	PRMT5	1007insCAGAAAG	H336delinsPEALD
XH_P44	14	24004011	24004011	Missense_Mutation	SNP	A	C	A	ZFHX2	c.T524G	p.F175C
XH_P44	14	24004012	24004012	In_Frame_Ins	INS	-	CACAGTCTCATG	-	ZFHX2	523insCATGAG	F175delinsHETVF
XH_P44	14	24029216	24029216	Frame_Shift_Ins	INS	-	AACCC	-	AP1G2	3431044insGG	p.S348fs
XH_P44	14	24534215	24534215	Silent	SNP	G	A	G	CARMIL3	c.G3129A	p.L1043P
XH_P44	14	24590623	24590623	Frame_Shift_Ins	INS	-	ACTCACATACT	-	DCAF11	CATTACACTCAC	p.R432fs
XH_P44	14	24607726	24607726	Nonsense_Mutation	INS	-	SAAGAAGGAGG	-	PSME1	527insGAAGAAG	p.Y209delinsX
XH_P44	14	24775342	24775342	Frame_Shift_Ins	INS	-	CTACCCCTAG	-	CIDEB	338insTAGGG	p.S113fs
XH_P44	14	31177268	31177268	In_Frame_Ins	INS	-	CTTGAGAAATTC	-	SCFD1	AAGGGCTCTGAG	57delinsQKLENFCC
XH_P44	14	31589057	31589057	Missense_Mutation	SNP	C	T	C	HECTD1	c.G5254A	p.E1752K
XH_P44	14	31589058	31589058	Frame_Shift_Ins	INS	-	GTATGCAGGTT	-	HECTD1	5253insTAACCTC	p.Y1751fs
XH_P44	14	31644277	31644277	Nonsense_Mutation	INS	-	AAACTTTTAAAG	-	HECTD1	TATAATCTTAAA	81149delinsHSHLX
XH_P44	14	31782318	31782318	Frame_Shift_Ins	INS	-	TTTTGTTTTGA	-	HEATR5A	nsCCTGTCAAAA	p.R1433fs
XH_P44	14	33004799	33004799	Frame_Shift_Ins	INS	-	ACTATTCCATCA	-	AKAP6	65insTACTATTCT	p.H122fs
XH_P44	14	33015339	33015339	Frame_Shift_Ins	INS	-	ITGGTTCGTTTG	-	AKAP6	1insTGATGGTTG	p.R494fs
XH_P44	14	35182661	35182661	Frame_Shift_Ins	INS	-	STACTTTTAAAA	-	CF12	ITGCATTTTAAA	p.L20fs
XH_P44	14	35182663	35182663	Frame_Shift_Ins	INS	-	TTATT	-	CF12	c.56_57insAATA	p.V19fs
XH_P44	14	35234117	35234117	In_Frame_Ins	INS	-	GAGGAGGAAGA	-	BAZ1A	476insACTCTTC	1159delinsVSSSL
XH_P44	14	35786487	35786487	Frame_Shift_Ins	INS	-	ACCTATACACAA	-	PSMA6	insTCACCTATAC	p.L160fs
XH_P44	14	35786489	35786489	In_Frame_Ins	INS	-	TTTACT	-	PSMA6	481482insTTTA	V161delinsVVF
XH_P44	14	36096385	36096385	Frame_Shift_Ins	INS	-	TC	-	RALGAP1A	6626_6627insG	p.Q2209fs
XH_P44	14	36096387	36096387	Nonsense_Mutation	INS	-	CATTTTATTTTC	-	RALGAP1A	AGAACAGAAAAA	D92210delinsKNRXX
XH_P44	14	39648436	39648436	Missense_Mutation	SNP	G	A	G	PNN	c.G640A	p.E214K
XH_P44	14	39648438	39648438	Nonsense_Mutation	INS	-	AGCCTGCCTTAA	-	PNN	33insTAGCCTGC	p.E214delinsEX
XH_P44	14	39650984	39650984	Frame_Shift_Ins	INS	-	ACTACTACTAGT	-	PNN	CTCCTACTACTCT	p.1691fs
XH_P44	14	45578953	45578953	Nonsense_Mutation	INS	-	CATGTACAGTGT	-	PRPF39	ATGCACATGTAC	383delinsSPKYAHVQCX
XH_P44	14	45665736	45665736	Frame_Shift_Ins	INS	-	TG	-	FANCM	5624_5625insT	p.D1875fs
XH_P44	14	45665737	45665737	Nonsense_Mutation	INS	-	CCCTGA	-	FANCM	25_5626insCCC	D1875delinsDPX
XH_P44	14	45712069	45712069	Nonsense_Mutation	INS	-	GGGCACTTAACT	-	MIS18BP1	nsTAAAGTTTAA	p.Q185delinsX
XH_P44	14	50085514	50085514	Frame_Shift_Ins	INS	-	TGCAAGAGAAG	-	RPL36AL	TTGTTCTCTCTCT	p.V103fs
XH_P44	14	50175943	50175943	Nonsense_Mutation	INS	-	AACAATAAAGG	-	KLHDC1	64insAAACAATA	L55W56delinsX
XH_P44	14	51111714	51111714	Frame_Shift_Ins	INS	-	CACAAATAAGA	-	SAV1	nsGCCCTCTTAT	p.A185fs
XH_P44	14	52471157	52471157	In_Frame_Ins	INS	-	CTT	-	C14orf166	c.658_659insCT	p.N220delinsTY
XH_P44	14	52471159	52471159	In_Frame_Ins	INS	-	TGTCAAAACCAA	-	C14orf166	TCCTGTGTCAAA	20delinsNLLCQNQEY
XH_P44	14	52741623	52741623	Nonsense_Mutation	INS	-	TGTGGAAAGGT	-	PTGDR	2insTGATGTGG	41delinsMMWKGX
XH_P44	14	53175231	53175231	Frame_Shift_Ins	INS	-	STAAGTCTACTT	-	PSMC6	TTTACGTAAAGTC	p.E80fs
XH_P44	14	55509997	55509997	Nonsense_Mutation	INS	-	ACATTTTACTAA	-	SOC54	39insTACATTTT	H80delinsHIFYX
XH_P44	14	55510449	55510449	Frame_Shift_Ins	INS	-	ATTTCCTCGTTT	-	SOC54	1insATATTTCTT	p.S230fs
XH_P44	14	56130728	56130728	Frame_Shift_Ins	INS	-	GCCCACCTTCCA	-	KTN1	AAGACGCCAC	p.M1049fs
XH_P44	14	57052571	57052571	Frame_Shift_Ins	INS	-	GA	-	TMEM260	c.285_286insGA	p.N95fs
XH_P44	14	57052572	57052572	Nonsense_Mutation	INS	-	ATGTTTGAATAG	-	TMEM260	nsTAAATGTTTGG	L96delinsLVNX
XH_P44	14	57741170	57741170	Frame_Shift_Ins	INS	-	TCGTTTTTCAA	-	AP5M1	284insTCGTTT	p.P95fs
XH_P44	14	57741487	57741487	Frame_Shift_Ins	INS	-	ACTGACACTAAT	-	AP5M1	1insCCACTGACA	p.T200fs
XH_P44	14	58954816	58954816	Frame_Shift_Ins	INS	-	AGGATGG	-	KIAA0586	63097insAGG	p.H1032fs
XH_P44	14	58954817	58954817	Frame_Shift_Ins	INS	-	TGATACATTGCT	-	KIAA0586	098insATGATAC	p.P1033fs
XH_P44	14	59961901	59961901	Nonsense_Mutation	INS	-	ATATTTAAATGCT	-	JKAMP	TTGCAATATTTA	p.Y133delinsYX
XH_P44	14	60591918	60591918	Frame_Shift_Ins	INS	-	ATAACGAGCTCA	-	PCNX4	328insAATAACG	p.T776fs
XH_P44	14	60712681	60712681	Frame_Shift_Ins	INS	-	TCCTGTCTGTGT	-	PPM1A	117insTCTGTCT	p.K39fs
XH_P44	14	60752440	60752440	Frame_Shift_Ins	INS	-	AGTTATA	-	PPM1A	33_934insAGTT	p.Y311fs
XH_P44	14	60752442	60752442	Frame_Shift_Ins	INS	-	AGTGAATAAGTT	-	PPM1A	5TTCTAGTGAAA	p.L312fs
XH_P44	14	60921775	60921775	Nonsense_Mutation	INS	-	ATTTAAATCAGC	-	C14orf39	5CCTTTAGCTGA	B3G484delinsTAFSX
XH_P44	14	61518643	61518643	Frame_Shift_Ins	INS	-	AACATATACAA	-	SLC38A6	5AGAGAAACATA	p.V397fs
XH_P44	14	62207717	62207717	Frame_Shift_Ins	INS	-	ATTGGGATATAG	-	HIF1A	5CATCCATTGGG	p.1659fs
XH_P44	14	64066028	64066028	Frame_Shift_Ins	INS	-	CAGGATGTGAC	-	WDR89	CTTCTCTGACAT	p.T211fs
XH_P44	14	64447450	64447450	In_Frame_Ins	INS	-	AAACAGGAAGA	-	SYNE2	5TAGGAAACACAG	50delinsVGKQEEGS
XH_P44	14	64460682	64460682	Frame_Shift_Ins	INS	-	TCAAAATCCTCT	-	SYNE2	77insCCTCAAAA	p.W926fs
XH_P44	14	64491941	64491941	Silent	SNP	G	A	G	SYNE2	c.G6054A	p.L2018L
XH_P44	14	64491942	64491942	Nonsense_Mutation	INS	-	AATAAGCAAAA	-	SYNE2	ATACAAAATAA	19D2020delinsNTKX
XH_P44	14	64497810	64497810	Frame_Shift_Ins	INS	-	TT	-	SYNE2	c.6956_6957insT	p.N2319fs
XH_P44	14	64497812	64497812	Frame_Shift_Ins	INS	-	AACCAATGCTG	-	SYNE2	6959insAACCA	p.T2320fs
XH_P44	14	64518891	64518891	In_Frame_Ins	INS	-	ATTCCTCTTTCT	-	SYNE2	261insAATTCTT	2754delinsKFFFSF
XH_P44	14	64655356	64655356	Frame_Shift_Ins	INS	-	5CCTCTCTTAA	-	SYNE2	32insTTTGCTCT	p.Y5934fs
XH_P44	14	64749687	64749687	Nonsense_Mutation	INS	-	AAGCAAGATCG	-	ESR2	7insAGCGATCTT	p.S6delinsX
XH_P44	14	65246559	65246559	Frame_Shift_Ins	INS	-	AGTGCTTTTGT	-	SPTB	4357insACAAA	p.D1453fs
XH_P44	14	66096299	66096299	Frame_Shift_Ins	INS	-	TTTATTTTCTATC	-	FUT8	ATCTTTTATTTT	p.V28fs
XH_P44	14	67745963	67745963	Frame_Shift_Ins	INS	-	ATGCTATGAAA	-	MPP5	AATAATGCTATG	p.P26fs
XH_P44	14	69521308	69521308	Frame_Shift_Ins	INS	-	CCCCCAGATCAA	-	DCAF5	392insTTTGATC	p.K698fs
XH_P44	14	70235573	70235573	In_Frame_Ins	INS	-	CATACAGTCAA	-	SRSF5	7insGCCATACAC	586delinsCHTVKP

XH_P44	14	70839839	70839839	Frame_Shift_Ins	INS	-	C	-	SYNJ2BP	c.306dupG	p.Q103fs
XH_P44	14	70839841	70839841	Frame_Shift_Ins	INS	-	TGCTCTT	-	SYNJ2BP	34_305insAAAG	p.V102fs
XH_P44	14	71063420	71063420	Splice_Site	INS	-	TTTTTTTTGATTG	-	MED6	-	-
XH_P44	14	71445258	71445258	Frame_Shift_Ins	INS	-	CTGCTGAAGTG	-	PCNX1	205insACTGCTC	p.5735fs
XH_P44	14	71500215	71500215	In_Frame_Ins	INS	-	GTACTATAAGCT	-	PCNX1	96insTGGTACTA	1099delinsLVKLH
XH_P44	14	73659547	73659547	Nonsense_Mutation	INS	-	ACATTAGATAT	-	PSEN1	1249delinsLPNIRYX	-
XH_P44	14	73743752	73743752	Nonsense_Mutation	INS	-	TCCCTTCTTTAA	-	NUMB	438_439delinsAX	-
XH_P44	14	73963351	73963351	Nonsense_Mutation	INS	-	TTTTCTCCCATC	-	HEATR4	579insGATGGG	4860_4861delinsX
XH_P44	14	74516619	74516619	Missense_Mutation	SNP	A	T	A	BBOF1	c.A1007T	p.Q336L
XH_P44	14	74516621	74516621	Frame_Shift_Ins	INS	-	GGGTITGGATTI	-	BBOF1	10insAGGGTTI	p.M337fs
XH_P44	14	75150153	75150153	Frame_Shift_Ins	INS	-	TTTTAAAAATAA	-	AREL1	27insATTATTTT	p.V109fs
XH_P44	14	75150155	75150155	In_Frame_Ins	INS	-	CTTTAT	-	AREL1	24_325insATAA	109delinsKV
XH_P44	14	75329392	75329392	Frame_Shift_Ins	INS	-	ATTGTTGG	-	PROX2	5_1146insCCAA	p.W382fs
XH_P44	14	75329394	75329394	Missense_Mutation	SNP	A	C	A	PROX2	c.T1144G	p.W382G
XH_P44	14	75329519	75329519	Frame_Shift_Ins	INS	-	AGTCTACCCCTT	-	PROX2	19insGAAGGGG	p.I340fs
XH_P44	14	75515096	75515096	Frame_Shift_Ins	INS	-	CAAGTTAGAAA	-	MLH3	insAACATTCTA	p.N421fs
XH_P44	14	75537655	75537655	Frame_Shift_Ins	INS	-	AGAA	-	ZC2HC1C	379_380insAGA	p.P127fs
XH_P44	14	75537656	75537656	Frame_Shift_Ins	INS	-	AAC	-	ZC2HC1C	380_381insAAC	p.P127fs
XH_P44	14	75570661	75570661	Nonsense_Mutation	INS	-	GTACATGCTATA	-	NEK9	insGCTATATAG	551_552delinsAIX
XH_P44	14	75573403	75573403	Nonsense_Mutation	SNP	C	A	C	NEK9	c.G1330T	p.E44X
XH_P44	14	75573404	75573404	In_Frame_Ins	INS	-	GAGAAGTGTTA	-	NEK9	329insATTAACTA	434delinsELTLI
XH_P44	14	75587282	75587282	Frame_Shift_Ins	INS	-	ACACITT	-	NEK9	54_45insAAAG	p.M152fs
XH_P44	14	77255604	77255604	Frame_Shift_Ins	INS	-	CGGTCTC	-	ANGEL1	9_1980insGAGA	p.L660fs
XH_P44	14	77255605	77255605	Missense_Mutation	SNP	A	T	A	ANGEL1	c.T1979A	p.L660Q
XH_P44	14	77872299	77872299	Nonsense_Mutation	INS	-	ATTTCACCTCTA	-	NOXRED1	ACTGTTAGAGG	88_89delinsYKNXC
XH_P44	14	77872301	77872301	Missense_Mutation	SNP	G	T	G	NOXRED1	c.C860A	p.T287K
XH_P44	14	77873984	77873984	Frame_Shift_Ins	INS	-	CTCTTAGAGTTG	-	NOXRED1	CAACCAACTCTA	p.E118fs
XH_P44	14	81558951	81558951	In_Frame_Ins	INS	-	TAATCTTATTC	-	TSHR	ATAGCTTAATCT	82delinsQYSLIFLFLK
XH_P44	14	81659065	81659065	Frame_Shift_Ins	INS	-	AAAGAAGTAAGT	-	GTf2A1	73insAACTTAC	p.T244fs
XH_P44	14	81744010	81744010	Frame_Shift_Ins	INS	-	TGCCGTTTCC	-	STON2	1645insGGGAA	p.L549fs
XH_P44	14	81744012	81744012	Missense_Mutation	SNP	C	T	C	STON2	c.G1643A	p.R548H
XH_P44	14	88477479	88477479	Frame_Shift_Ins	INS	-	TGCTGTT	-	GPR65	38_289insTGCT	p.M96fs
XH_P44	14	88477480	88477480	Missense_Mutation	SNP	A	C	A	GPR65	c.A289C	p.N97H
XH_P44	14	88936057	88936057	In_Frame_Ins	INS	-	TTTTTATGTGAG	-	PTPN21	1insTCACTCACA	007delinsSHSKNP
XH_P44	14	88967626	88967626	Frame_Shift_Ins	INS	-	TAAGATCATAG	-	PTPN21	674insTCTATGA	p.K225fs
XH_P44	14	89039343	89039343	In_Frame_Ins	INS	-	ACACCATACTCT	-	ZC3H14	389insACACCA	130delinsNTTIC
XH_P44	14	89085129	89085129	Silent	SNP	T	A	T	EML5	c.A5403T	p.A1801A
XH_P44	14	89085130	89085130	In_Frame_Ins	INS	-	CTCCCCCTTCT	-	EML5	402insAGGAAA	1801delinsEERGA
XH_P44	14	89091417	89091417	In_Frame_Ins	INS	-	CCTTCT	-	EML5	94_4795insAGA	1599delinsRRH
XH_P44	14	89091418	89091418	Frame_Shift_Ins	INS	-	TTTGATTC	-	EML5	3_4794insGAAT	p.D1598fs
XH_P44	14	89163277	89163277	Nonsense_Mutation	INS	-	TGGATTGTCTAG	-	EML5	insCTAGCTAGCA	53_54delinsTSX
XH_P44	14	90429682	90429682	Missense_Mutation	SNP	A	T	A	TDP1	c.A224T	p.K75I
XH_P44	14	90429684	90429684	Frame_Shift_Ins	INS	-	TCGCTTCTCT	-	TDP1	227insTCGCT	p.R76fs
XH_P44	14	90729760	90729760	In_Frame_Ins	INS	-	AAGGGGAGTGT	-	PSMC1	ATGGAAGGGGG	85delinsNGKGSVAV
XH_P44	14	91444843	91444843	In_Frame_Ins	INS	-	GGTAAGTGT	-	RPS6KA5	10_201insACACT	167delinsRHLPL
XH_P44	14	91444844	91444844	In_Frame_Ins	INS	-	GTATATGACACTT	-	RPS6KA5	ATAAAAAGCTCT	67delinsHKSDNNC
XH_P44	14	91875096	91875096	Frame_Shift_Ins	INS	-	CCTTGTGTTG	-	CCDC88C	177insCAAAAC	p.T59fs
XH_P44	14	91927945	91927945	Frame_Shift_Ins	INS	-	TTCCCAATTGAA	-	PPP4R3A	454insCTTCAAT	p.E485fs
XH_P44	14	91927947	91927947	Nonsense_Mutation	INS	-	TCTCAACAATA	-	PPP4R3A	1452insTTATTG	184_485delinsNYCX
XH_P44	14	92136184	92136184	Nonsense_Mutation	INS	-	ATTCTAATCTGG	-	CATSPERB	261insACAGTTT	421_422delinsTSX
XH_P44	14	92136186	92136186	Missense_Mutation	SNP	C	T	C	CATSPERB	c.G1259A	p.S420N
XH_P44	14	92403411	92403411	Frame_Shift_Ins	INS	-	A	-	FBLN5	c.258_259insT	p.P87fs
XH_P44	14	92471452	92471452	Nonsense_Mutation	INS	-	AACTGGAGATTA	-	TRIP11	insAGTTTAATC	855_1956delinsQVX
XH_P44	14	92471769	92471769	Nonsense_Mutation	INS	-	AAAGAAGGAA	-	TRIP11	CTCATCTTCTCT	851delinsLHIFLLLLX
XH_P44	14	92622924	92622924	Frame_Shift_Ins	INS	-	AA	-	CPSF2	1085_1086insA	p.L362fs
XH_P44	14	92622926	92622926	Frame_Shift_Ins	INS	-	ACATTTCATCCA	-	CPSF2	8insATACATTTT	p.C536fs
XH_P44	14	92625489	92625489	Nonsense_Mutation	INS	-	AACAAATTAAT	-	CPSF2	CATATTAACAA	161delinsNTYX
XH_P44	14	93154538	93154538	In_Frame_Del	DEL	GGCGGC	-	GGCGGC	RIN3	c.2674_2679del	p.892_893del
XH_P44	14	93650564	93650564	Frame_Shift_Ins	INS	-	TACATTTTTAAG	-	MOAP1	TCTGCTTAAAA	p.88fs
XH_P44	14	93760331	93760331	Missense_Mutation	SNP	G	T	G	BTBD7	c.C1035A	p.S345R
XH_P44	14	93760903	93760903	Frame_Shift_Ins	INS	-	TGGTTGA	-	BTBD7	52_463insTCAA	p.V155fs
XH_P44	14	93760905	93760905	Frame_Shift_Ins	INS	-	CTTTTGGT	-	BTBD7	10_461insACCAA	p.P154fs
XH_P44	14	94545740	94545740	Frame_Shift_Ins	INS	-	GAGCAGTTTGG	-	DDX24	CTGGTCCAAAC	p.E117fs
XH_P44	14	94545950	94545950	Frame_Shift_Ins	INS	-	AAAAGATCAAG	-	DDX24	9insAACTTGAT	p.L47fs
XH_P44	14	94731781	94731781	Nonsense_Mutation	INS	-	TTCTTACTTGTG	-	PPP4R4	5AAATATCTTAA	6672delinsPNILTWX
XH_P44	14	94732198	94732198	Nonsense_Mutation	INS	-	AGATGGCTTTAG	-	PPP4R4	insCACAGATGG	704delinsKRWLX
XH_P44	14	94936027	94936027	Frame_Shift_Ins	INS	-	TTCTTGGGCA	-	SERPINA9	105insATTGCCCA	p.F69fs
XH_P44	14	94936028	94936028	In_Frame_Ins	INS	-	ACCTGACCT	-	SERPINA9	204insAGGTC	168delinsSEQV
XH_P44	14	94964361	94964361	Nonsense_Mutation	INS	-	AAATATATTTTC	-	SERPINA12	5GAAAGAAATAT	25_K12delinsRKXIK
XH_P44	14	96779746	96779746	Frame_Shift_Ins	INS	-	GTTGTTGTGTT	-	ATG2B	ATTAACAAACAC	p.D1223fs
XH_P44	14	100157484	100157484	Frame_Shift_Ins	INS	-	ACTAGGCCAC	-	CYP46A1	CTTATTACTAGG	p.D62fs
XH_P44	14	102466435	102466435	Frame_Shift_Ins	INS	-	CGTTTCGG	-	DYNC1H1	4_3915insCGTT	p.E1305fs
XH_P44	14	102466436	102466436	Frame_Shift_Ins	INS	-	TTCT	-	DYNC1H1	3915_3916insTT	p.E1305fs
XH_P44	14	102486334	102486334	Nonsense_Mutation	INS	-	TTAAGAAGATA	-	DYNC1H1	AAATATTTAAG	5_P2817delinsLYLRRX
XH_P44	14	102486336	102486336	Missense_Mutation	SNP	C	A	C	DYNC1H1	c.C8450A	p.P2817H
XH_P44	14	102675261	102675261	Nonsense_Mutation	INS	-	GTGACTGTGCTA	-	WDR20	AACTCGTGACTT	1191delinsGNSX
XH_P44	14	104026661	104026661	In_Frame_Ins	INS	-	GAAAGAAAGC	-	BAG5	41insCAGCTTTC	281delinsQLSFLK
XH_P44	14	104026663	104026663	Frame_Shift_Ins	INS	-	TG	-	BAG5	c.838_839insCA	p.E280fs
XH_P44	14	104407851	104407851	Frame_Shift_Ins	INS	-	TAAATTACATTI	-	RD3L	2insTTAAATGTA	p.Y61fs
XH_P44	14	104493059	104493059	Nonsense_Mutation	INS	-	CAATAAAACCTA	-	TDRD9	1066insCCAATA	122_L1023delinsSQX
XH_P44	14	105406089	105406089	Frame_Shift_Ins	INS	-	CCCTTTCAGA	-	AHNAK2	15399insTCTGA	p.K513fs
XH_P44	15	23006812	23006812	Nonsense_Mutation	INS	-	TAAATAGGGCC	-	NIPAZ	15CCAGGGCCCT	5_L146delinsIQPIX
XH_P44	15	24922863	24922863	Frame_Shift_Ins	INS	-	GGAGGAGGGG	-	NPAP1	1850insGGAGG	p.T617fs
XH_P44	15	24922864	24922864	Missense_Mutation	SNP	C	A	C	NPAP1	c.C1850A	p.T617K
XH_P44	15	25599748	25599748	In_Frame_Ins	INS	-	GGGGTGTGTGA	-	UBE3A	147insAATCACAA	1716delinsKSHTPL
XH_P44	15	28386650	28386650	Nonsense_Mutation	INS	-	CTGTACTAAAA	-	HERC2	1943insGTTTTA	881_13982delinsAFX
XH_P44	15	28386652	28386652	Missense_Mutation	SNP	C	T	C	HERC2	c.G11941A	p.A3981T
XH_P44	15	28424336	28424336	In_Frame_Ins	INS	-	CCTAAT	-	HERC2	70_8971insATT	A2991delinsIRA
XH_P44	15	28424338	28424338	Nonsense_Mutation	INS	-	GTGCTCTT	-	HERC2	8_8969insAAGG	990_A2991delinsX
XH_P44	15	30919142	30919142	Frame_Shift_Ins	INS	-	CAGACCGCTTG	-	ARHGAP11B	TTACACAGACCC	p.T40fs
XH_P44	15	32908524	32908524	Frame_Shift_Ins	INS	-	ACCCGCTT	-	ARHGAP11A	2_113insACCCG	p.A38fs
XH_P44	15	32917824	32917824	Frame_Shift_Ins	INS	-	ATTATCTTCTCT	-	ARHGAP11A	6insTTATTATCC	p.Q95fs
XH_P44	15	32917826	32917826	Missense_Mutation	SNP	G	C	G	ARHGAP11A	c.G287C	p.S96T
XH_P44	15	32929431	32929431	Frame_Shift_Ins	INS	-	CTTCATCACTGG	-	ARHGAP11A	1insTTCTTCAT	p.L630fs
XH_P44	15	33359180	33359180	Frame_Shift_Ins	INS	-	GAGACAG	-	FMN1	105_906insCTGT	p.D302fs
XH_P44	15	33359181	33359181	Missense_Mutation	SNP	T	C	T	FMN1	c.A905G	p.D302G
XH_P44	15	33381139	33381139	In_Frame_Ins	INS	-	TTAATA	-	FMN1	103_1904insTAT	1635delinsLNL
XH_P44	15	33381141	33381141	In_Frame_Ins	INS	-	ATGTAATTGTG	-	FMN1	TATATACACAAT	634delinsFIYTIKY

XH_P44	15	33443476	33443476	Frame_Shift_Ins	INS	-	TTGAT	-	FMN1	971_1972insAT	p.E658fs
XH_P44	15	33443477	33443477	Silent	SNP	C	T	C	FMN1	c.G1971A	p.K657K
XH_P44	15	33445664	33445664	Frame_Shift_Ins	INS	-	CGCTCTC	-	FMN1	51_1452insGAG	p.Q484fs
XH_P44	15	34060905	34060905	Nonsense_Mutation	INS	-	AAACAGTTATAG	-	RYR3	53insGAAACAG	p.F2918delinsX
XH_P44	15	34130649	34130649	Frame_Shift_Ins	INS	-	ATTGACAACAT	-	RYR3	12454insATTGA	p.F4151fs
XH_P44	15	34355061	34355061	Nonsense_Mutation	INS	-	TAAATAGTGT	-	CHRM5	TACAGTAAATAdelinsKNFTVNSVRFX	
XH_P44	15	34355235	34355235	Nonsense_Mutation	INS	-	AAGGA	-	CHRM5	317_318insAAGV106_L107delinsX	
XH_P44	15	34395361	34395361	In_Frame_Ins	INS	-	CAGTAAAGAAC	-	PGBD4	0insCTCAGTAAAdelinsSSVKN	
XH_P44	15	34536226	34536226	Nonsense_Mutation	INS	-	CCGTGTTGTCTC	-	SLC12A6	5CCTAAGAGACACp.649_7650delinsPX	
XH_P44	15	35045171	35045171	Frame_Shift_Ins	INS	-	TTGCTGTAAGT	-	GJD2	5sTGCCACTTACp.p.1E58fs	
XH_P44	15	38805156	38805157	Frame_Shift_Del	DEL	AA	-	AA	RASGRP1	c.676_677del	p.F226fs
XH_P44	15	38805157	38805157	Frame_Shift_Ins	INS	-	TGTTTTTTCCCT	-	RASGRP1	6insGAGGGAAp.p.F226fs	
XH_P44	15	40301878	40301878	In_Frame_Ins	INS	-	GAA	-	EIF2AK4	3640_3641insGA.G1214delinsGR	
XH_P44	15	40491909	40491909	Nonsense_Mutation	INS	-	TATGTTACTAAT	-	BUB1B	83insTATATGTTp.61_E462delinsHCYX	
XH_P44	15	40502363	40502363	Frame_Shift_Ins	INS	-	AGGAGAAGACA	-	BUB1B	2338insAGGAGp.p.K779fs	
XH_P44	15	40502364	40502364	Nonsense_Mutation	INS	-	AATTCC	-	BUB1B	338_2339insAATp.L780delinsX	
XH_P44	15	41679757	41679757	Frame_Shift_Ins	INS	-	GCTAGTATGTA	-	NDUFAF1	AGAGAAATACATp.p.V290fs	
XH_P44	15	41820464	41820464	Nonsense_Mutation	INS	-	TCTTAAGCCT	-	RPAP1	1229insAGGCTp.110_L411delinsEAX	
XH_P44	15	42041839	42041839	Frame_Shift_Ins	INS	-	AC	-	MGA	5407_5408insA	p.S1803fs
XH_P44	15	42041841	42041841	Frame_Shift_Ins	INS	-	GACT	-	MGA	409_5410insGA	p.S1803fs
XH_P44	15	42740441	42740441	Nonsense_Mutation	INS	-	CAACTTCTA	-	ZNF106	9_450insTAGAAp.S150delinsSRX	
XH_P44	15	42743385	42743385	Frame_Shift_Ins	INS	-	GAAAAACCTGA	-	ZNF106	1016insTTCAGG	p.G339fs
XH_P44	15	42749381	42749381	Missense_Mutation	SNP	C	A	C	ZNF106	c.G23T	p.C8F
XH_P44	15	42749382	42749382	Frame_Shift_Ins	INS	-	GGAAGAGGAAG	-	ZNF106	AATCTCTCTTCTp.p.C8fs	
XH_P44	15	42980291	42980291	Missense_Mutation	SNP	G	C	G	STARD9	c.G6515C	p.G2172A
XH_P44	15	42980293	42980293	Frame_Shift_Ins	INS	-	TACACTC	-	STARD9	17_6518insTAC	p.S2173fs
XH_P44	15	42982525	42982525	In_Frame_Ins	INS	-	TACCTTCTT	-	STARD9	9_8750insTACCp.P2917delinsLPS	
XH_P44	15	42984346	42984346	Frame_Shift_Ins	INS	-	AGTTTCTCTCG	-	STARD9	10571insAGTTp.p.P3524fs	
XH_P44	15	43621555	43621555	In_Frame_Ins	INS	-	TTAAGAGTGAAG	-	LCMT2	7ATTATCTCTCACTp.78delinsVILLTKMKM	
XH_P44	15	43707906	43707906	Frame_Shift_Ins	INS	-	CTGCTATAAAGT	-	TP53BP1	975insGACTTTA	p.T1659fs
XH_P44	15	43714280	43714280	In_Frame_Ins	INS	-	GGTGCAGACAG	-	TP53BP1	873insCCCTGTCTp.1291delinsDPVCT	
XH_P44	15	43814792	43814792	Frame_Shift_Ins	INS	-	AGGTCCT	-	MAP1A	21_1122insAGG	p.P374fs
XH_P44	15	43818616	43818616	Frame_Shift_Ins	INS	-	GCTTC	-	MAP1A	945_4946insGC	p.E1649fs
XH_P44	15	43818617	43818617	Frame_Shift_Ins	INS	-	TCCTTCT	-	MAP1A	46_4947insTCC	p.E1649fs
XH_P44	15	43818833	43818833	Nonsense_Mutation	INS	-	GGCT	-	MAP1A	162_5163insGGp.721_T1722delinsX	
XH_P44	15	43818835	43818835	Missense_Mutation	SNP	A	T	A	MAP1A	c.A5164T	p.T1722S
XH_P44	15	44889091	44889091	Frame_Shift_Ins	INS	-	GACATAGGCCT	-	SPG11	52insAAAAAGCC	p.R1351fs
XH_P44	15	45270825	45270825	Frame_Shift_Ins	INS	-	GTGAGAAGATT	-	TERB2	7TACCAGTGAGAp.p.X221delinsX	
XH_P44	15	45453048	45453048	Nonsense_Mutation	INS	-	ATTCCATGAGGA	-	DUOX1	717insCATTTCCA	p.39_S1240delinsGIPX
XH_P44	15	45456058	45456058	Nonsense_Mutation	INS	-	SATGAAGTAGA	-	DUOX1	4476insGATGAAp.H1492delinsQMXX	
XH_P44	15	45559984	45559984	In_Frame_Ins	INS	-	AGACTA	-	SLC28A2	89_1190insAGA.L397delinsQTM	
XH_P44	15	48784758	48784758	Nonsense_Mutation	INS	-	ACAGCTCTTCAAC	-	FBN1	4insTATTGTAAAp.p.P918delinsPIX	
XH_P44	15	48905282	48905282	Nonsense_Mutation	INS	-	TACTTTGATGG	-	FBN1	AACTCCCATCAp.8delinsSNSHQSNX	
XH_P44	15	49031379	49031379	Frame_Shift_Ins	INS	-	AAGGAGGC	-	CEP152	1_4032insGCCT	p.N1344fs
XH_P44	15	49048356	49048356	Frame_Shift_Ins	INS	-	AGAGTGAGAGA	-	CEP152	4089insCTTCTCT	p.Q1030fs
XH_P44	15	49048358	49048358	Missense_Mutation	SNP	C	T	C	CEP152	c.G3087A	p.M1029I
XH_P44	15	49304055	49304055	Frame_Shift_Ins	INS	-	G	-	SECISBP2L	c.1601_1602ins	p.1534fs
XH_P44	15	49304057	49304057	Frame_Shift_Ins	INS	-	AGGGAGATGGT	-	SECISBP2L	TCITTTAACCATC	p.1534fs
XH_P44	15	49327770	49327770	Frame_Shift_Ins	INS	-	GTAACAGAGGA	-	SECISBP2L	nsCTGATCTCTCT	p.S97fs
XH_P44	15	51289866	51289866	Frame_Shift_Ins	INS	-	AAAAATAAAA	-	AP4E1	2466insAAAAA	p.A822fs
XH_P44	15	51289868	51289868	Frame_Shift_Ins	INS	-	TAATAAT	-	AP4E1	67_2468insTAA	p.K823fs
XH_P44	15	51503153	51503153	Frame_Shift_Ins	INS	-	GT	-	CYP19A1	1363_1364insA	p.1455fs
XH_P44	15	51503155	51503155	In_Frame_Ins	INS	-	ACACTC	-	CYP19A1	61_1362insGAGp.L454delinsLSV	
XH_P44	15	51766690	51766690	Nonsense_Mutation	INS	-	ACTTTTATTTT	-	DMXL2	TTCTATAAAAATp.1718delinsMLFLX	
XH_P44	15	51792113	51792113	In_Frame_Ins	INS	-	GTACATTGGAC	-	DMXL2	8insCCAGTCCAAp.103delinsPSPNVLN	
XH_P44	15	51792115	51792115	Missense_Mutation	SNP	C	T	C	DMXL2	c.G3306A	p.M1102I
XH_P44	15	51792182	51792182	In_Frame_Ins	INS	-	AGTAAT	-	DMXL2	38_3239insATT	p.G1080delinsDYC
XH_P44	15	51792183	51792183	Frame_Shift_Ins	INS	-	TGTT	-	DMXL2	237_3238insAA	p.G1080fs
XH_P44	15	52356821	52356821	Frame_Shift_Ins	INS	-	GC	-	MAPK6	1790_1791insG	p.F597fs
XH_P44	15	52529756	52529756	In_Frame_Ins	INS	-	GAGCAAACTCAGA	-	MYO5C	791insAATCTGAp.A931delinsNULCSA	
XH_P44	15	52676520	52676520	Splice_Site	INS	-	CAGATCTTCCCT	-	MYO5C	-	
XH_P44	15	52885931	52885931	Frame_Shift_Ins	INS	-	AACC	-	FAM214A	672_2673insGG	p.E891fs
XH_P44	15	52885933	52885933	Nonsense_Mutation	INS	-	GATGGTACTAAAT	-	FAM214A	7TACATTTTGTAGT	p.891_S892delinsKX
XH_P44	15	52901950	52901950	In_Frame_Ins	INS	-	AAACTTGTTATT	-	FAM214A	1182insAAATACp.5394delinsRNTSF	
XH_P44	15	54557665	54557665	Frame_Shift_Ins	INS	-	STCTTTTGGGCT	-	UNC13C	8790insGTCTT	p.L1263fs
XH_P44	15	54557666	54557666	In_Frame_Ins	INS	-	TAG	-	UNC13C	3790_3791insTAp.N1264delinsID	
XH_P44	15	54557668	54557668	In_Frame_Ins	INS	-	GCATCC	-	UNC13C	92_3793insGCAp.N1264delinsNAS	
XH_P44	15	55710197	55710235	Frame_Shift_Del	DEL	CTTTTGTGAT	-	CTCTTTTGTGATTC	DNAAF4	c.1144_1182del	p."382fs
XH_P44	15	55838601	55838601	Frame_Shift_Ins	INS	-	TTGTACAAACGA	-	PYG01	0insCCTGCTTTG	p.A294fs
XH_P44	15	56208689	56208689	Missense_Mutation	SNP	A	C	A	NEDD4	c.T341G	p.F114C
XH_P44	15	56208690	56208690	Frame_Shift_Ins	INS	-	GATCCTTTTGT	-	NEDD4	340insACAAA	p.F114fs
XH_P44	15	56387729	56387729	Missense_Mutation	SNP	T	G	T	RFK7	c.A2197C	p.N733H
XH_P44	15	56387730	56387730	In_Frame_Ins	INS	-	CACAGGACACAT	-	RFK7	2196insATGTGTp.732delinsLCVLV	
XH_P44	15	56387983	56387983	In_Frame_Ins	INS	-	ACAGAAGGTTT	-	RFK7	943insTTGAACCP.648delinsVEPSVY	
XH_P44	15	56735850	56735850	In_Frame_Ins	INS	-	AGAGCAAGCTAA	-	MNS1	7TACTTTTAGCTT	p.7delinsNLLLCASYIFQ
XH_P44	15	57484445	57484445	Frame_Shift_Ins	INS	-	TTCCACCTCACAC	-	TCF12	TTTTCTCCACCC	p.S160fs
XH_P44	15	59182582	59182582	Frame_Shift_Ins	INS	-	ATAA	-	SLTM	922_1923insTT	p.R641fs
XH_P44	15	59182583	59182583	Frame_Shift_Ins	INS	-	TGAATTAGGTAC	-	SLTM	22insTAGTACCT	p.R641fs
XH_P44	15	59809012	59809012	Nonsense_Mutation	INS	-	CCATAATATCTG	-	FAM81A	66insGCCATAAT	p.319delinsSHNIVX
XH_P44	15	60741575	60741575	Frame_Shift_Ins	INS	-	GATGGAAAGA	-	ICE2	9_1180insTCTTT	p.T394fs
XH_P44	15	60741577	60741577	Frame_Shift_Ins	INS	-	GCTGT	-	ICE2	177_1178insAC	p.M393fs
XH_P44	15	60741807	60741807	Frame_Shift_Ins	INS	-	ATGACTATAGAT	-	ICE2	TAATATATCTAT	p.S316fs
XH_P44	15	60742039	60742039	Frame_Shift_Ins	INS	-	TT	-	ICE2	c.715_716insAA	p.M239fs
XH_P44	15	60742041	60742041	Splice_Site	INS	-	CTAATTCTAGAA	-	ICE2	-	
XH_P44	15	62256116	62256116	Frame_Shift_Ins	INS	-	AATTGGATTGTA	-	VPS13C	5GAAGCATACAA	p.D1040fs
XH_P44	15	62273628	62273628	Nonsense_Mutation	INS	-	AACTAAATGTA	-	VPS13C	TAAGTCTACATT	p.650_L651delinsKX
XH_P44	15	63927045	63927045	Missense_Mutation	SNP	C	T	C	HERC1	c.G12457A	p.G4153S
XH_P44	15	63927046	63927046	Nonsense_Mutation	INS	-	AATTGATAATTTT	-	HERC1	AACAGTTAAATp.G4153delinsETVKIINX	
XH_P44	15	64067265	64067265	Nonsense_Mutation	INS	-	ATGACCATATTA	-	HERC1	sGCATTAAATATG	p.86_S187delinsLHX
XH_P44	15	64404883	64404883	Nonsense_Mutation	INS	-	CAATTCGTTATT	-	SNX1	272insCAAATCGp.1_A92delinsANRYX	
XH_P44	15	64791753	64791753	Frame_Shift_Ins	INS	-	ATCTTAGAGT	-	ZNF609	136insATCTTA	p.D45fs
XH_P44	15	64792259	64792259	Frame_Shift_Ins	INS	-	C	-	ZNF609	c.641_642insC	p.S214fs
XH_P44	15	64792260	64792260	Missense_Mutation	SNP	T	A	T	ZNF609	c.T642A	p.S214R
XH_P44	15	64966875	64966875	Frame_Shift_Ins	INS	-	CTTGACTTCTTG	-	ZNF609	23insTGCTTGTA	p.G608fs
XH_P44	15	64968157	64968157	Nonsense_Mutation	INS	-	TGGATGACCG	-	ZNF609	3105insTGGATp.D35_L1036delinsAGX	
XH_P44	15	65445954	65445954	Frame_Shift_Ins	INS	-	G	-	CLPX	c.1634_1635ins	p.D545fs
XH_P44	15	65445955	65445955	Frame_Shift_Ins	INS	-	CTTCCA	-	CLPX	3_1634insTGG	p.D545fs
XH_P44	15	65917404	65917404	In_Frame_Ins	INS	-	GCTCCTTGG	-	SLC24A1	5_987insGCTCC	p.T329delinsTLG

XH_P44	15	65942863	65942863	Nonsense_Mutation	INS	-	AAC TAGTGC	-	SLC24A1	7358insAACTAA	p.E119delinsENX
XH_P44	15	65942865	65942865	In_Frame_Ins	INS	-	TAATTC	-	SLC24A1	59360insTAAT	p.E120delinsDNS
XH_P44	15	65983680	65983680	In_Frame_Ins	INS	-	AAGAGG	-	DENND4A	193120insCT	p.M1040delinsL
XH_P44	15	65983682	65983682	Nonsense_Mutation	INS	-	AACGTATGAAC	-	DENND4A	18insCTGTCTCA	p.M1040delinsFIRX
XH_P44	15	66618621	66618621	Missense_Mutation	SNP	G	T	G	DIS3L	c.G1742T	p.R581L
XH_P44	15	66618622	66618622	Frame_Shift_Ins	INS	-	TTCT	-	DIS3L	7431744insTT	p.R581fs
XH_P44	15	67664588	67664588	In_Frame_Ins	INS	-	AATCCTAGCACT	-	IQCH	8insGAATCCTAA	p.46delinsMNPSTD
XH_P44	15	69548644	69548644	Frame_Shift_Ins	INS	-	TAACA	-	GLCE	499500insTAA	p.P167fs
XH_P44	15	69548646	69548646	Frame_Shift_Ins	INS	-	T	-	GLCE	c.502dupT	p.P167fs
XH_P44	15	69553581	69553581	Nonsense_Mutation	INS	-	AATACCATTCT	-	GLCE	TTCTCTAATACCA	p.D249delinsPNTPIHX
XH_P44	15	69732766	69732766	Nonsense_Mutation	INS	-	TATTTCTAAAA	-	KIF23	TCTCTTTATTTCT	p.9556delinsPNLFI5X
XH_P44	15	70959917	70959917	Frame_Shift_Ins	INS	-	TTAATGG	-	UACA	663067insCCA	p.E1023fs
XH_P44	15	70959918	70959918	Frame_Shift_Ins	INS	-	ACAA	-	UACA	30653066insTT	p.K1022fs
XH_P44	15	72172892	72172892	Nonsense_Mutation	INS	-	TAGTTAGACTG	-	MYO9A	5406insCCAGCTC	p.2A1803delinsAQSNX
XH_P44	15	72231250	72231250	In_Frame_Ins	INS	-	TAAAT	-	MYO9A	20232insATT	p.P774delinsHFT
XH_P44	15	72231251	72231251	Frame_Shift_Ins	INS	-	GCCTTACA	-	MYO9A	92320insTGT	p.P774fs
XH_P44	15	72324917	72324917	Frame_Shift_Ins	INS	-	TTTCT	-	MYO9A	852853insAGA	p.A285fs
XH_P44	15	72324919	72324919	In_Frame_Ins	INS	-	TATGCATACATT	-	MYO9A	GAACAAATGTA	p.284delinsRTNVCIIY
XH_P44	15	72645518	72645518	Frame_Shift_Ins	INS	-	GTTAGAGAGGG	-	HEXA	461insCCCTCT	p.F154fs
XH_P44	15	72645520	72645520	Splice_Site	SNP	C	A	C	HEXA		
XH_P44	15	72953887	72953887	Frame_Shift_Ins	INS	-	CTGGATGG	-	GOLGA6B	9740insCTGGA	p.M247fs
XH_P44	15	73536815	73536815	In_Frame_Ins	INS	-	AAAATCTATCA	-	NEO1	83insATAAAAA	p.528delinsHKNLSV
XH_P44	15	74743189	74743189	Frame_Shift_Ins	INS	-	TG	-	UBL7	c.483484insCA	p.D162fs
XH_P44	15	74743190	74743190	Frame_Shift_Ins	INS	-	TCAGTTTAGGT	-	UBL7	CACGAAACCTAA	p.Q161fs
XH_P44	15	75819599	75819599	Frame_Shift_Ins	INS	-	CTAAGTGTCTCT	-	PTPN9	GAGGAGGAACA	p.T23fs
XH_P44	15	76165830	76165830	In_Frame_Ins	INS	-	CCACATTCCATT	-	UBE2Q2	5insCCCACATT	p.135delinsSPHSIQ
XH_P44	15	76646424	76646424	Frame_Shift_Ins	INS	-	CTCGAGT	-	SCAPER	23913insAATC	p.F1305fs
XH_P44	15	77473755	77473755	Frame_Shift_Ins	INS	-	TCTGGGTAACAG	-	PEAK1	sGGTTCTGTTC	p.S172fs
XH_P44	15	78789637	78789637	Frame_Shift_Ins	INS	-	TGTGCACTTTAT	-	IREB2	insAAATGTGCA	p.P167fs
XH_P44	15	79307740	79307740	Nonsense_Mutation	INS	-	CTTTGGCTTAG	-	RASGRF1	insAAACTAAGC	p.N585delinsKNX
XH_P44	15	79586770	79586770	Frame_Shift_Ins	INS	-	TGTGAAAGAGG	-	ANKRD34C	145insGTGTGA	p.L382fs
XH_P44	15	79586772	79586772	Silent	SNP	A	G	A	ANKRD34C	c.A1146G	p.L382L
XH_P44	15	79750156	79750156	Frame_Shift_Ins	INS	-	GTTTCATGCTT	-	KIAA1024	1668insGTTC	p.C556fs
XH_P44	15	81591950	81591950	In_Frame_Ins	INS	-	ATTACATCATAC	-	IL16	insTGCAATTACAT	p.L60delinsLCITSYS
XH_P44	15	81627318	81627318	Splice_Site	INS	-	A	-	TMC3		
XH_P44	15	81631111	81631111	Nonsense_Mutation	INS	-	CATTCAAAAATC	-	TMC3	CTAAGTGATTTT	p.6561657delinsPKX
XH_P44	15	83331491	83331491	Frame_Shift_Ins	INS	-	CTTGTTGTTTTC	-	AP3B2	635insGAAACA	p.P879fs
XH_P44	15	83805386	83805386	Frame_Shift_Ins	INS	-	TTTAATGTCAGA	-	TM65F1	83insCTTTAATG	p.F328fs
XH_P44	15	83932574	83932574	Frame_Shift_Ins	INS	-	A	-	BNC1	c.1407dupT	p.V470fs
XH_P44	15	83932576	83932576	Nonsense_Mutation	INS	-	AGCTCAGATGA	-	BNC1	6insTCTTCATCT	p.69V470delinsVFIX
XH_P44	15	84241372	84241372	Frame_Shift_Ins	INS	-	AAGTACTTACCA	-	SH3GL3	1insCGAAGTAC	p.D60fs
XH_P44	15	85164537	85164537	Frame_Shift_Ins	INS	-	C	-	ZSCAN2	c.1111112ins	p.F371fs
XH_P44	15	85164539	85164539	Frame_Shift_Ins	INS	-	CCAC	-	ZSCAN2	1131114insCC	p.F371fs
XH_P44	15	85164714	85164714	Frame_Shift_Ins	INS	-	TTTACATTCTGT	-	ZSCAN2	89insTTCTTTACA	p.S430fs
XH_P44	15	85325971	85325971	In_Frame_Ins	INS	-	ATA	-	ZNF592	c.6566insATA	p.T22delinsTY
XH_P44	15	85399835	85399835	Nonsense_Mutation	INS	-	TGAAAAACAG	-	ALPK3	2473insTGAA	p.T824delinsTX
XH_P44	15	86807834	86807834	Frame_Shift_Ins	INS	-	GCCTTGGTCC	-	AGBL1	1433insGCCTT	p.M478fs
XH_P44	15	89836232	89836232	Nonsense_Mutation	INS	-	AGGGTATGACT	-	FANCI	0insGTAAAGG	p.3F744delinsAVRVX
XH_P44	15	90380906	90380906	Frame_Shift_Ins	INS	-	TTTGTAATTCCT	-	AP3S2	insGGAGGAAT	p.T132fs
XH_P44	15	90774710	90774710	Frame_Shift_Ins	INS	-	TGAG	-	CIB1	344345insCTC	p.R115fs
XH_P44	15	90774712	90774712	Missense_Mutation	SNP	T	C	T	CIB1	c.A343G	p.R115G
XH_P44	15	90897986	90897986	Missense_Mutation	SNP	G	T	G	ZNF774	c.G94T	p.A32S
XH_P44	15	90897987	90897987	Nonsense_Mutation	INS	-	CTGAGGTAAAT	-	ZNF774	96insCTGAGGT	p.A32L33delinsAX
XH_P44	15	93486167	93486167	Frame_Shift_Ins	INS	-	AACTCACAAACA	-	CHD2	22insAAACTCAC	p.Y307fs
XH_P44	15	99758904	99758904	Frame_Shift_Ins	INS	-	GAGGT	-	TTC23	469470insACC	p.A157fs
XH_P44	15	99758905	99758905	Frame_Shift_Ins	INS	-	ACTGTGTAAA	-	TTC23	469insTTTACA	p.A157fs
XH_P44	15	101562156	101562156	In_Frame_Ins	INS	-	GCCTTCTCTCTG	-	LRRK1	1847insGCCTT	p.K616delinsSLSPE
XH_P44	15	101562157	101562157	Missense_Mutation	SNP	A	G	A	LRRK1	c.A1847G	p.K616R
XH_P44	15	102185366	102185366	Splice_Site	INS	-	A	-	TM2D3		
XH_P44	16	1270585	1270585	Missense_Mutation	SNP	G	A	G	CACNA1H	c.G6635A	p.R2212H
XH_P44	16	1616173	1616173	Frame_Shift_Ins	INS	-	GTCCTTCAGG	-	IFT140	1890insCCTGA	p.Q630fs
XH_P44	16	2815145	2815145	Frame_Shift_Ins	INS	-	TATATCTTTCA	-	SRRM2	insTAGGTATATC	p.S1539fs
XH_P44	16	3293304	3293304	Frame_Shift_Ins	INS	-	AAATAACAAAT	-	MEFV	83insCTAATTTT	p.S728fs
XH_P44	16	3367297	3367297	In_Frame_Ins	INS	-	TCAAGGCACAT	-	ZNF75A	insACATCAAGG	p.107delinsHIKAHS
XH_P44	16	3593478	3593478	Nonsense_Mutation	INS	-	TCGCTAT	-	NLR3	852886insATAC	p.962A963delinsGX
XH_P44	16	4937208	4937208	Frame_Shift_Ins	INS	-	CTGCTGAAAGTG	-	PPL	35insTTCACTTT	p.K845fs
XH_P44	16	10524915	10524915	Nonsense_Mutation	INS	-	TCTTTCTCTGA	-	ATF7IP2	ACTTTTCTCTGA	p.1delinsEILNIFYX
XH_P44	16	10575961	10575961	Frame_Shift_Ins	INS	-	GTCAATTGTCAG	-	ATF7IP2	AAAGTGGTCAA	p.L635fs
XH_P44	16	11444642	11444642	Frame_Shift_Ins	INS	-	TTTTTTTCTCT	-	RM12	440insTTTTTTT	p.P147fs
XH_P44	16	11824628	11824628	Frame_Shift_Ins	INS	-	G	-	TXNDC11	c.571572insC	p.F191fs
XH_P44	16	11824629	11824629	Nonsense_Mutation	INS	-	TTTAAGAGAAT	-	TXNDC11	nsACTCTATTCTC	p.1G192delinsTLFSX
XH_P44	16	14041695	14041695	Frame_Shift_Ins	INS	-	AACTATGCTTTG	-	ERCC4	243insCAACTAT	p.M748fs
XH_P44	16	14648004	14648004	Nonsense_Mutation	INS	-	SAATGTTAATAT	-	PARN	ACCTTGAATATT	p.5P396delinsQLKPX
XH_P44	16	14680189	14680189	Nonsense_Mutation	INS	-	AAAAAATTAGC	-	PARN	ACCCAGCTAAT	p.1delinsTHHTQLIFYFLX
XH_P44	16	15185221	15185221	Frame_Shift_Ins	INS	-	SATGGCTGCAG	-	RRN3	3insTATCTGCAG	p.T68fs
XH_P44	16	15814050	15814050	Silent	SNP	G	A	G	MYH11	c.C4911T	p.P1637T
XH_P44	16	15854432	15854432	Silent	SNP	G	T	G	MYH11	c.C1213A	p.R405R
XH_P44	16	15854434	15854434	Nonsense_Mutation	INS	-	ATCCCTCACT	-	MYH11	1211insAGTGA	p.404R405delinsEX
XH_P44	16	18549933	18549933	Nonsense_Mutation	INS	-	ACTTAAGAAAG	-	NOMO2	sACTAATCTTTC	p.9Q380delinsTNL5X
XH_P44	16	18846427	18846427	Nonsense_Mutation	INS	-	GTTATCTTGGTT	-	SMG1	AAACACAAACCA	p.2706delinsKTQPRX
XH_P44	16	18849915	18849915	Frame_Shift_Ins	INS	-	TGTATTGTGTA	-	SMG1	GTCTATTTAACA	p.G2348fs
XH_P44	16	18851113	18851113	In_Frame_Ins	INS	-	TGTCCTCCAGA	-	SMG1	CCAAGTCTGGA	p.84delinsLP5LEGQRK
XH_P44	16	19451643	19451643	Frame_Shift_Ins	INS	-	GGAGTGGTAAA	-	TMCS	284insGGAGTG	p.S95fs
XH_P44	16	20043415	20043415	Frame_Shift_Ins	INS	-	AAAACCTATAA	-	GRP139	704insTATAG	p.S235fs
XH_P44	16	20043417	20043417	Silent	SNP	G	A	G	GRP139	c.C702T	p.T234T
XH_P44	16	20481042	20481042	Splice_Site	INS	-	AAGCCAACAGT	-	ACSM2A		
XH_P44	16	20809302	20809302	Frame_Shift_Ins	INS	-	G	-	ER12	c.18191820ins	p.V607fs
XH_P44	16	21261364	21261364	In_Frame_Ins	INS	-	GAGGAGTGTTC	-	ANKS4B	nsGTAGAGGAG	p.159delinsNVEECFP
XH_P44	16	23632791	23632791	In_Frame_Ins	INS	-	GTGTG	-	PALB2	043005insCAA	p.E1002delinsATQ
XH_P44	16	23632792	23632792	Frame_Shift_Ins	INS	-	GTTGTGTGTGT	-	PALB2	004insAACAAAC	p.E1002fs
XH_P44	16	24373029	24373029	Missense_Mutation	SNP	T	A	T	CACNG3	c.T793A	p.F265I
XH_P44	16	24373030	24373030	Frame_Shift_Ins	INS	-	GAAAGAGAAGG	-	CACNG3	795insGAAAGA	p.F265fs
XH_P44	16	24573244	24573244	Nonsense_Mutation	INS	-	GAGTGCTGTTCT	-	RBBP6	2insCAGGAGTG	p.351delinsPGVFLFX
XH_P44	16	24580749	24580749	In_Frame_Ins	INS	-	TTTCATACCACT	-	RBBP6	AATATTTTTCAT	p.1delinsNLVNIHFTLTVFS
XH_P44	16	24581503	24581503	Frame_Shift_Ins	INS	-	TTTCTCTCTTTT	-	RBBP6	391insCTTTTCT	p.S1130fs
XH_P44	16	24581504	24581504	Frame_Shift_Ins	INS	-	CTGGTTT	-	RBBP6	913392insCTG	p.M1131fs
XH_P44	16	24801713	24801713	Nonsense_Mutation	INS	-	TTAGAACCATAG	-	TNRC6A	751insATTAGAA	p.584S585delinsNX
XH_P44	16	25251979	25251979	In_Frame_Ins	INS	-	AAA	-	ZKSCAN2	20612062insT	p.E688delinsFE

XH_P44	16	25251981	25251981	Frame_Shift_Ins	INS	-	TGGAGAAAGC	-	ZKSCAN2	2060insGCTTT	p.I687fs
XH_P44	16	27364000	27364000	Missense_Mutation	SNP	G	C	G	IL4R	c.G653C	p.S218T
XH_P44	16	27364002	27364002	Frame_Shift_Ins	INS	-	TGTTTAAGAG	-	IL4R	656insTGTTTA	p.T219fs
XH_P44	16	27689113	27689113	Missense_Mutation	SNP	G	T	G	KIA00556	c.G604T	p.D202Y
XH_P44	16	27752102	27752102	Frame_Shift_Ins	INS	-	TTTTCCAGTT	-	KIA00556	2485insTTTTCC	p.R828fs
XH_P44	16	28493651	28493651	Missense_Mutation	SNP	C	A	C	CLN3	c.G659T	p.R220L
XH_P44	16	28550201	28550201	Frame_Shift_Ins	INS	-	TGGAACCTCAG	-	NUPR1	28insCTGAAGT	p.A10fs
XH_P44	16	28855587	28855587	Frame_Shift_Ins	INS	-	GCATT	-	TUFM	885_886insAAT	p.T296fs
XH_P44	16	28970331	28970331	Frame_Shift_Ins	INS	-	AAAGAGGTTCTT	-	NFATC2IP	012insAAAAAGAC	p.S337fs
XH_P44	16	30544467	30544467	Missense_Mutation	SNP	A	G	A	ZNF747	c.T349C	p.S117P
XH_P44	16	30724688	30724688	Frame_Shift_Ins	INS	-	AAGG	-	SRCAP	290_2291insAA	p.N764fs
XH_P44	16	30724690	30724690	Frame_Shift_Ins	INS	-	AGTAATCAGG	-	SRCAP	2293insAGTAA	p.N764fs
XH_P44	16	31196420	31196420	Silent	SNP	C	T	C	FUS	c.C681T	p.G227G
XH_P44	16	31201659	31201659	Frame_Shift_Ins	INS	-	ATTCCTTACCTAC	-	FUS	GGAGAATTCTT	p.P410fs
XH_P44	16	46615876	46615876	Missense_Mutation	SNP	T	G	T	SHCBP1	c.A1550C	p.K517T
XH_P44	16	46615878	46615878	Frame_Shift_Ins	INS	-	TTTGCTGTATTG	-	SHCBP1	548insACAATAC	p.G516fs
XH_P44	16	47117526	47117526	Frame_Shift_Ins	INS	-	ATTCCT	-	NETO2	52_1163insAGG	p.P388fs
XH_P44	16	47117527	47117527	Frame_Shift_Ins	INS	-	TGAAATTT	-	NETO2	1_1162insAAAT	p.P388fs
XH_P44	16	47684827	47684827	In_Frame_Ins	INS	-	CATGCATT	-	PHKB	5_1967insCATG	p.L656delinsPCIL
XH_P44	16	48385712	48385712	In_Frame_Ins	INS	-	SAGAAAAAGTT	-	LONP2	sAGGAGAGAGAA	p.X809delinsX
XH_P44	16	48399304	48399304	Frame_Shift_Ins	INS	-	TTTCAAGATGGA	-	SlAH1	5insCTCCATCTT	p.R29fs
XH_P44	16	48587545	48587545	Nonsense_Mutation	INS	-	ATCAATTGAAGA	-	N4BP1	5insCTCTCTTCA	p.I642delinsTLFNX
XH_P44	16	48594905	48594905	In_Frame_Ins	INS	-	SATTTGAACAC	-	N4BP1	549insATGTGTT	p.550delinsNVFOIR
XH_P44	16	50112872	50112872	Nonsense_Mutation	INS	-	TCCTTTAGATTCT	-	HEATR3	TAATGCTCTTTA	p.E97_G98delinsEX
XH_P44	16	50136341	50136341	In_Frame_Ins	INS	-	CAAGTACCACT	-	HEATR3	1223insCAAGTA	p.M408delinsTSTNL
XH_P44	16	51172999	51172999	Frame_Shift_Ins	INS	-	CCCTGCTC	-	SALL1	2_2843insGAGC	p.K948fs
XH_P44	16	53289661	53289661	In_Frame_Ins	INS	-	GTGTGTGACTCT	-	CHD9	4180insGTTGTT	p.1393delinsEVDVS
XH_P44	16	53338419	53338419	Nonsense_Mutation	INS	-	SAAGACTGAGG	-	CHD9	5502insGAAGAC	p.S2167delinsSEDX
XH_P44	16	53358483	53358483	Frame_Shift_Ins	INS	-	CAGTACTTGCA	-	CHD9	371insGCAGTTA	p.P2790fs
XH_P44	16	53860153	53860153	Frame_Shift_Ins	INS	-	AGATACCGGA	-	FTO	502insAGATAC	p.A167fs
XH_P44	16	56309985	56309985	Splice_Site	INS	-	AAAGCTACCTAA	-	GNAO1		
XH_P44	16	56388958	56388958	In_Frame_Ins	INS	-	CATAGGTATTGG	-	GNAO1	1059insCATAGG	p.L353delinsFIGIG
XH_P44	16	56938368	56938368	In_Frame_Ins	INS	-	TTCTTATAGAGT	-	SLC12A3	6insAAATCTCTTA	p.982delinsINSYRVVS
XH_P44	16	58552800	58552800	Frame_Shift_Ins	INS	-	G	-	SETD6	c.1289_1290ins	p.D430fs
XH_P44	16	58552801	58552801	Frame_Shift_Ins	INS	-	AATTAGATGTAC	-	SETD6	c.TCTTTAATTAG	p.D430fs
XH_P44	16	58579374	58579374	Frame_Shift_Ins	INS	-	TTGTCTTCTTCT	-	CNOT1	3insAGGGAAGA	p.T1338fs
XH_P44	16	66812825	66812825	Nonsense_Mutation	INS	-	SGAAGGAAGTA	-	TERB1	94insAATACCTTC	p.S265_S266delinsX
XH_P44	16	66824920	66824920	Frame_Shift_Ins	INS	-	G	-	TERB1	c.33_34insC	p.M12fs
XH_P44	16	66824921	66824921	Frame_Shift_Ins	INS	-	GATTTATTTTA	-	TERB1	33insTAAATA	p.E11fs
XH_P44	16	66887317	66887317	Nonsense_Mutation	INS	-	TTATTATTCTCAC	-	CA7	CCTCATTATTATTA	p.D182delinsDPHLFTHX
XH_P44	16	66967608	66967608	Frame_Shift_Ins	INS	-	C	-	FAM96B	c.256_257insG	p.F86fs
XH_P44	16	66967609	66967609	Frame_Shift_Ins	INS	-	GAATAAAGATCT	-	FAM96B	56insCAGATCT	p.F86fs
XH_P44	16	67405090	67405090	Frame_Shift_Ins	INS	-	ACTCCAACCTCG	-	LRR36	077insAACTCCA	p.N359fs
XH_P44	16	67645917	67645917	Frame_Shift_Ins	INS	-	AACTTATTTTAA	-	CTCF	insAAAAAAGCTTA	p.D282fs
XH_P44	16	67645919	67645919	Missense_Mutation	SNP	C	G	C	CTCF	c.C847G	p.R283G
XH_P44	16	68157013	68157013	Frame_Shift_Ins	INS	-	ATGGACAGAAG	-	NFATC3	1228insATGGA	p.T409fs
XH_P44	16	68157015	68157015	Missense_Mutation	SNP	C	A	C	NFATC3	c.C1229A	p.P410H
XH_P44	16	68225524	68225524	Frame_Shift_Ins	INS	-	ATGAGAAGCT	-	NFATC3	2953insATGAG	p.G984fs
XH_P44	16	68597236	68597236	Frame_Shift_Ins	INS	-	GGTCTTCC	-	ZFP90	6_547insGGTCT	p.P182fs
XH_P44	16	69177253	69177253	Frame_Shift_Ins	INS	-	ACGAAACAACAT	-	UTP4	51insTACGAAAC	p.L150fs
XH_P44	16	69272113	69272113	Frame_Shift_Ins	INS	-	ATACTTTTGTG	-	NFAT5	ACTCATCATACT	p.Q1111fs
XH_P44	16	69745107	69745107	Silent	SNP	G	A	G	NQO1	c.C381T	p.D127D
XH_P44	16	69745108	69745108	Frame_Shift_Ins	INS	-	TGGATCATTTT	-	NQO1	insTTAAAAATG	p.D127fs
XH_P44	16	70162871	70162871	Nonsense_Mutation	INS	-	AGAAGACCTGT	-	PDPB	54insTGAAGA	p.G51_152delinsGX
XH_P44	16	70170269	70170269	Frame_Shift_Ins	INS	-	ACCCTCTACT	-	PDPB	871insACCCCT	p.S290fs
XH_P44	16	70305876	70305876	Splice_Site	SNP	C	A	C	AARS		
XH_P44	16	70560588	70560588	Nonsense_Mutation	INS	-	CAAGCCCTATTA	-	SF3B3	30insCAAGCCCT	p.R10delinsSKPYX
XH_P44	16	71784162	71784162	Frame_Shift_Ins	INS	-	AATATGGTGATC	-	AP1G1	58insAAGATCAC	p.A453fs
XH_P44	16	71784164	71784164	Missense_Mutation	SNP	A	T	A	AP1G1	c.T1356A	p.H452Q
XH_P44	16	72094160	72094160	Nonsense_Mutation	INS	-	TTAAAAATATTC	-	HP	sAGTTTAAAAAT	p.L139delinsQFX
XH_P44	16	72188313	72188313	Nonsense_Mutation	INS	-	SGTACCTGCAGA	-	PMFBP1	insATTTCTGCAG	p.E71delinsSAGTX
XH_P44	16	72831642	72831642	Frame_Shift_Ins	INS	-	AGAGGGCCAATC	-	ZFH3X	2197insGATTG	p.L733fs
XH_P44	16	73161449	73161449	Nonsense_Mutation	INS	-	CAAAAAATATTA	-	C16orf47	07insCTAAATAT	p.E69_P70delinsDX
XH_P44	16	74526993	74526993	Frame_Shift_Ins	INS	-	T	-	GLG1	c.1062_1063ins	p.Y355fs
XH_P44	16	74526994	74526994	Frame_Shift_Ins	INS	-	ATAAACGTTAGT	-	GLG1	062insAACTAAC	p.D354fs
XH_P44	16	75204090	75204090	In_Frame_Ins	INS	-	IGCAAATGTCTTT	-	ZFP1	insTGGGGCAAAT	p.C28delinsFGQMSFH
XH_P44	16	75448523	75448523	Nonsense_Mutation	INS	-	TAGGATTAACCT	-	CFDP1	c.AAAGAAAGTTAA	p.45delinsTKLILKX
XH_P44	16	77465457	77465457	Frame_Shift_Ins	INS	-	CTGGCTTGGT	-	ADAMTS18	230insACCAAG	p.S27fs
XH_P44	16	78064646	78064646	Frame_Shift_Ins	INS	-	TGTGAAGTGTA	-	CLEC3A	sAAGATGTGAAC	p.V116fs
XH_P44	16	81295888	81295888	Frame_Shift_Ins	INS	-	ATCCTTGATGGC	-	BCO1	nsTCTATCCTTG	p.K157fs
XH_P44	16	82033434	82033434	Frame_Shift_Ins	INS	-	CTACTGCTTTC	-	SDR42E1	nsAAAGCAAAG	p.T155fs
XH_P44	16	84115434	84115434	Frame_Shift_Ins	INS	-	AAGCACAGTA	-	MBTPS1	1366insAATTTCT	p.V456fs
XH_P44	16	84115436	84115436	Missense_Mutation	SNP	C	T	C	MBTPS1	c.G1364A	p.G455E
XH_P44	16	84125417	84125417	Frame_Shift_Ins	INS	-	AATTGAGTGG	-	MBTPS1	883insCCAATC	p.Y295fs
XH_P44	16	84126882	84126882	Frame_Shift_Ins	INS	-	TGTCGACCTAAC	-	MBTPS1	7insAACTTAGGT	p.V253fs
XH_P44	16	84163877	84163877	Nonsense_Mutation	INS	-	GCTTCTAAGGT	-	HSDL1	ATCTGACCTTAG	p.127_S128delinsNIX
XH_P44	16	84922934	84922934	In_Frame_Ins	INS	-	CTT	-	CRISPLD2	1404_1405insC	p.Y468delinsYL
XH_P44	16	84922935	84922935	In_Frame_Ins	INS	-	ATGCCT	-	CRISPLD2	105_1406insATG	p.V469delinsDAL
XH_P44	16	89809256	89809256	Frame_Shift_Ins	INS	-	IGACAAATATGT	-	FANCA	17insGCCACATA	p.E1239fs
XH_P44	17	1585290	1585290	Frame_Shift_Ins	INS	-	AGAAGGA	-	PRPF8	76_477insTCCT	p.R159fs
XH_P44	17	1703397	1703397	Frame_Shift_Ins	INS	-	AC	-	SMYD4	1290_1291insG	p.H431fs
XH_P44	17	1782981	1782981	Frame_Shift_Ins	INS	-	AAGAAAGCTAG	-	RPA1	81insCAAGAGAA	p.L360fs
XH_P44	17	1798359	1798359	Frame_Shift_Ins	INS	-	AT	-	RPA1	c.1716_1717insA	p.F572fs
XH_P44	17	1798361	1798361	Nonsense_Mutation	INS	-	AGGTAGTAATGG	-	RPA1	719insAAGGTAA	p.V574delinsRRX
XH_P44	17	2201229	2201229	Frame_Shift_Ins	INS	-	TTGGGACCAATA	-	SMG6	nsTAATTATTAG	p.R656fs
XH_P44	17	2201341	2201341	Frame_Shift_Ins	INS	-	TTCT	-	SMG6	855_1856insAG	p.L619fs
XH_P44	17	2201342	2201342	Nonsense_Mutation	INS	-	GTGACGATGGA	-	SMG6	55insAATCCATC	p.L619delinsNPSX
XH_P44	17	2202868	2202868	Frame_Shift_Ins	INS	-	CTGATGATGAA	-	SMG6	1179insCTTCATC	p.E393fs
XH_P44	17	2966296	2966296	Frame_Shift_Ins	INS	-	CAGTGATGAT	-	OR1D5	606insATACAT	p.T202fs
XH_P44	17	2966656	2966656	In_Frame_Ins	INS	-	TTCTCTCTG	-	OR1D5	246insCAGGA	p.L82delinsLRK
XH_P44	17	2966658	2966658	Missense_Mutation	SNP	G	C	G	OR1D5	c.C244G	p.L82V
XH_P44	17	3195854	3195854	Frame_Shift_Ins	INS	-	CAATG	-	OR3A1	c.22_23insCATTT	p.N8fs
XH_P44	17	3422070	3422070	Nonsense_Mutation	INS	-	TGGTGCA	-	TRPV3	84_1885insTGA	p.V629_L630delinsX
XH_P44	17	3985795	3985795	Frame_Shift_Ins	INS	-	CCAA	-	ZZEF1	649_2650insTT	p.V884fs
XH_P44	17	3985797	3985797	Frame_Shift_Ins	INS	-	TGGTAAAAATA	-	ZZEF1	48insTTATTAT	p.N883fs
XH_P44	17	4009086	4009086	Nonsense_Mutation	INS	-	AGTCTTTAAAA	-	ZZEF1	ATATATTTTTAA	p.B2_P433delinsRLUIYFX
XH_P44	17	4684143	4684143	In_Frame_Ins	INS	-	ACCTTACTTTATC	-	TM4SF5	sCTTCACCTTAC	p.79delinsGLHLTSL
XH_P44	17	4789236	4789236	In_Frame_Ins	INS	-	CAC	-	MINK1	c.670_671insCA	p.I224delinsTL

XH_P44	17	4789237	4789237	Frame_Shift_Ins	INS	-	TGCCTTGC	-	MINK1	1_672insTGCT	p.I224fs
XH_P44	17	4858775	4858775	Frame_Shift_Ins	INS	-	CCTTCCCATACT	-	EN03	13insTCCTCTCC	p.A204fs
XH_P44	17	4995227	4995227	In_Frame_Ins	INS	-	GACTCTCTCGAA	-	ZFP3	429insGACTCTCTC	143delinsWTLN
XH_P44	17	5086174	5086174	Missense_Mutation	SNP	A	G	A	ZNF594	c.T1378C	p.Y460H
XH_P44	17	5086175	5086175	Silent	SNP	G	A	G	ZNF594	c.C1377T	p.P459P
XH_P44	17	5238574	5238574	Frame_Shift_Ins	INS	-	CTGGCCAATGT	-	RABEP1	35insTCTGGCCA	p.A112fs
XH_P44	17	5290095	5290095	In_Frame_Ins	INS	-	GGATGACCTTCT	-	NUP88	2143insAGAAGG	L715delinsRRSSL
XH_P44	17	7405260	7405260	In_Frame_Ins	INS	-	CCCAT	-	POLR2A	91_2392insCC	R797delinsRPH
XH_P44	17	7495895	7495895	In_Frame_Ins	INS	-	GCAGAGTCT	-	FXR2	1_1752insAGAC	R584delinsRDSA
XH_P44	17	7646833	7646833	Silent	SNP	G	A	G	DNAH2	c.G2523A	p.K841K
XH_P44	17	7678641	7678641	In_Frame_Ins	INS	-	CAATTCTAAGAA	-	DNAH2	03insACCAATTCT	1601delinsLPILRS
XH_P44	17	7736047	7736047	In_Frame_Ins	INS	-	AATCCGTATTATT	-	DNAH2	nsATTCAAAATCCG	93delinsHSNPVYLFM
XH_P44	17	7810769	7810769	Frame_Shift_Ins	INS	-	TA	-	CHD3	5064_5065insT	p.E1688fs
XH_P44	17	7810770	7810770	Missense_Mutation	SNP	C	G	C	CHD3	c.C5065G	p.P1689A
XH_P44	17	8131610	8131610	Nonsense_Mutation	INS	-	T	-	CTC1	3541_3542ins	181_G1182delinsX
XH_P44	17	8131611	8131611	In_Frame_Ins	INS	-	TTCCCTTCTTTGG	-	CTC1	sAACACCAAGG	181delinsNTKEGKLC
XH_P44	17	10295921	10295921	Nonsense_Mutation	INS	-	A	-	MYH8	c.5505dupT	1836_11837delinsX
XH_P44	17	10295923	10295923	Frame_Shift_Ins	INS	-	ATGTAAGGAGT	-	MYH8	GTCTTTACTCT	p.R1835fs
XH_P44	17	11835443	11835443	Frame_Shift_Ins	INS	-	CATTACCATATA	-	DNAH9	55insAACATTAC	p.N385fs
XH_P44	17	12908405	12908405	Frame_Shift_Del	DEL	T	-	T	ELAC2	c.764delA	p.E255fs
XH_P44	17	12908407	12908407	Frame_Shift_Del	DEL	T	-	T	ELAC2	c.762delA	p.E254fs
XH_P44	17	15234782	15234782	Nonsense_Mutation	INS	-	TAACCAACTATC	-	TEKT3	21insTGATAGT	N41_L42delinsX
XH_P44	17	15234783	15234783	Silent	SNP	G	A	G	TEKT3	c.C120T	p.S40S
XH_P44	17	15458621	15458621	Frame_Shift_Ins	INS	-	ACATTTCTTTAT	-	TVP23C	CTATATAAAGAA	p.N24fs
XH_P44	17	15492341	15492341	Frame_Shift_Ins	INS	-	AGTGATCA	-	CDRT1	6_2207insTGAT	p.T736fs
XH_P44	17	15532464	15532464	In_Frame_Ins	INS	-	TCCAAT	-	TRIM16	69_770insATTG	R257delinsHWR
XH_P44	17	15619691	15619691	In_Frame_Ins	INS	-	AGT	-	ZNF286A	560_561insAG	p.H187delinsQV
XH_P44	17	15619693	15619693	Frame_Shift_Ins	INS	-	STCATAGACACT	-	ZNF286A	insGAGTCATAG	p.T188fs
XH_P44	17	15620332	15620332	Nonsense_Mutation	INS	-	TGTGTTGCAAGT	-	ZNF286A	sCTGATGTGT	p.H401delinsLX
XH_P44	17	15965556	15965556	In_Frame_Ins	INS	-	AGG	-	NCOR1	5297_5298insC	p.S1766delinsSL
XH_P44	17	15965557	15965557	In_Frame_Ins	INS	-	TTTTTTTGTGTG	-	NCOR1	5297insACAACA	1766delinsNNKKS
XH_P44	17	16456597	16456597	Nonsense_Mutation	INS	-	STGGGAAAGAG	-	ZNF287	sCTAAACTCTTT	p.I239delinsYAX
XH_P44	17	16638133	16638133	Frame_Shift_Ins	INS	-	CTATCGAAAC	-	CCDC144A	2549insCTATC	p.F850fs
XH_P44	17	16638453	16638453	Frame_Shift_Ins	INS	-	ATTCTTTTCTTTC	-	CCDC144A	9insATCATTTCT	p.V956fs
XH_P44	17	16692466	16692466	Frame_Shift_Ins	INS	-	GGATTCAAGTG	-	FAM106CP	253insGGATTCA	p.A84fs
XH_P44	17	17163711	17163711	In_Frame_Ins	INS	-	SAGAGAACTCTC	-	COPS3	525insGAGAGT	N175delinsKRVLS
XH_P44	17	17786158	17786158	Nonsense_Mutation	INS	-	ACTATCCTTTTT	-	TOM1L2	871insAAAAAGG	P124delinsQKQX
XH_P44	17	17786159	17786159	Missense_Mutation	SNP	G	C	G	TOM1L2	c.C370G	p.T124A
XH_P44	17	18023440	18023440	Silent	SNP	C	A	C	MYO15A	c.C1326A	p.G442G
XH_P44	17	18244122	18244122	Frame_Shift_Ins	INS	-	ACATATATTAGT	-	SHMT1	sAGAAACTAATA	p.N37fs
XH_P44	17	18565413	18565413	Missense_Mutation	SNP	C	T	C	ZNF286B	c.G1406A	p.C469Y
XH_P44	17	18565414	18565414	Nonsense_Mutation	INS	-	AAATACCTTGAG	-	ZNF286B	405insCACTCAA	C469delinsHSSIX
XH_P44	17	18682577	18682577	In_Frame_Ins	INS	-	ACGAACCTCA	-	FBXW10	5_2967insACGA	A989delinsARTQ
XH_P44	17	26962253	26962253	In_Frame_Ins	INS	-	NGCACTTCTCATC	-	KIAA0100	sAACCCATGAG	784delinsTHEKCS
XH_P44	17	26966597	26966597	Frame_Shift_Ins	INS	-	C	-	KIAA0100	c.1078dupG	p.V360fs
XH_P44	17	26966599	26966599	In_Frame_Ins	INS	-	GGAAAT	-	KIAA0100	076_1077insAAT	p.S359delinsRIP
XH_P44	17	27061990	27061990	Nonsense_Mutation	INS	-	TTGTTGTTTTTT	-	NEK8	TGTTGTTGTTGT	I153delinsVVVVFVFX
XH_P44	17	27246284	27246284	Frame_Shift_Ins	INS	-	TTGT	-	PHF12	845_846insACA	p.R282fs
XH_P44	17	27246285	27246285	In_Frame_Ins	INS	-	ATA	-	PHF12	844_845insTA	p.R282delinsLC
XH_P44	17	27963790	27963790	Frame_Shift_Ins	INS	-	CAAAAATTTCTC	-	SSH2	77insAAGAGGA	p.S459fs
XH_P44	17	28270646	28270646	Nonsense_Mutation	INS	-	STAATCACAGTG	-	EFCAB5	sAGGTAATCACA	p.M1delinsKRX
XH_P44	17	28380782	28380782	In_Frame_Ins	INS	-	TTTGCTTGTGTG	-	EFCAB5	nsGCTTTTGGCC	548delinsGLPCCS
XH_P44	17	28381123	28381123	In_Frame_Ins	INS	-	FTTGCTTGATCC	-	EFCAB5	nsACTCTCTGCT	661delinsLTCLILV
XH_P44	17	28512639	28512639	In_Frame_Ins	INS	-	CTTTGTTGGGA	-	NSRP1	GTCTCTCATTTT	8delinsMFLILLDSLW
XH_P44	17	28525512	28525512	Frame_Shift_Ins	INS	-	T	-	SLC6A4	c.1854dupA	p.E619fs
XH_P44	17	28525514	28525514	In_Frame_Ins	INS	-	GTATGATCA	-	SLC6A4	2_1853insTGAT	T618delinsMIIP
XH_P44	17	28776748	28776748	Nonsense_Mutation	INS	-	TTAAAAAGTCT	-	CPD	311insTTTTAA	p.K770delinsKFX
XH_P44	17	29162511	29162511	Frame_Shift_Ins	INS	-	KGATGTCATTTT	-	ATAD5	413insAGAGTG	p.L471fs
XH_P44	17	29195431	29195431	Splice_Site	INS	-	CTTCTCTG	-	ATAD5	.	.
XH_P44	17	29221917	29221917	Frame_Shift_Ins	INS	-	GTATTCAATTAT	-	ATAD5	5522insGTATTC	p.A1841fs
XH_P44	17	29221919	29221919	Frame_Shift_Ins	INS	-	STCTATTACCCAC	-	ATAD5	sAGCTTGCTCAT	p.A1841fs
XH_P44	17	30216406	30216406	Frame_Shift_Ins	INS	-	TTTGTATTTTTAA	-	UTP6	CTACTAAAAATA	p.A147fs
XH_P44	17	30315416	30315416	Frame_Shift_Ins	INS	-	C	-	SUZ12	c.1032_1033ins	p.D344fs
XH_P44	17	30315417	30315417	Nonsense_Mutation	INS	-	GCAACAGGTG	-	SUZ12	1034insGCAAC	45_5346delinsSNRX
XH_P44	17	30349530	30349530	Frame_Shift_Ins	INS	-	ATCTGCAGGTT	-	LRRC37B	366insCATCTG	p.P455fs
XH_P44	17	33591870	33591870	Frame_Shift_Ins	INS	-	TCTGTGCTTTTC	-	SLFN5	08insGCTCTGTG	p.P603fs
XH_P44	17	33591872	33591872	Silent	SNP	G	A	G	SLFN5	c.G1809A	p.P603P
XH_P44	17	33679874	33679874	Frame_Shift_Ins	INS	-	AAAGCAAT	-	SLFN11	6_2207insATTG	p.P736fs
XH_P44	17	34182176	34182176	Missense_Mutation	SNP	G	A	G	HEATR9	c.C1484T	p.A495V
XH_P44	17	34182177	34182177	Nonsense_Mutation	INS	-	TACTATCTTCC	-	HEATR9	ATTACGGAAGAA	A495delinsHGRX
XH_P44	17	34641530	34641530	Frame_Shift_Ins	INS	-	CACCTGATTATC	-	CLCL1	CCACTCACTGG	p.L86fs
XH_P44	17	34851239	34851239	Frame_Shift_Ins	INS	-	AAGTGGAACA	-	ZNHIT3	insTTCAAGTGG	p.E97fs
XH_P44	17	34871732	34871733	Frame_Shift_Del	DEL	GA	-	GA	MYO19	c.515_516del	p.I172fs
XH_P44	17	35580446	35580446	Frame_Shift_Ins	INS	-	TTTCAGTAGTTT	-	ACACA	AAATAGAAACT	p.M1089fs
XH_P44	17	35614779	35614779	In_Frame_Ins	INS	-	AATAGGAATCAT	-	ACACA	1387insATGAT	P463delinsMIPIP
XH_P44	17	36520701	36520701	Frame_Shift_Ins	INS	-	GAAGTCAATTTT	-	SOC57	ACCAGGAAGTC	p.T307fs
XH_P44	17	37437708	37437708	Frame_Shift_Ins	INS	-	G	-	FBXL20	c.533_534insC	p.D178fs
XH_P44	17	37437710	37437710	Nonsense_Mutation	INS	-	CAAGACCAGTAT	-	FBXL20	2insCAATACTGG	8_E179delinsQVWSX
XH_P44	17	37455309	37455309	Frame_Shift_Ins	INS	-	TTCTTTTGGAGC	-	FBXL20	TCAAAGCTCCA	p.R88fs
XH_P44	17	37566816	37566816	In_Frame_Ins	INS	-	AAATCA	-	MED1	57_1658insTGA	p.G553delinsVIC
XH_P44	17	37566818	37566818	Silent	SNP	T	A	T	MED1	c.A1656T	p.T552T
XH_P44	17	37580067	37580067	In_Frame_Ins	INS	-	TCT	-	MED1	858_859insAG	p.S287delinsRS
XH_P44	17	37580069	37580069	Nonsense_Mutation	INS	-	ACTTGTATATAA	-	MED1	57insATTATATAA	286_5287delinsHLX
XH_P44	17	37604105	37604105	Nonsense_Mutation	INS	-	FCCTTATATGAA	-	MED1	insTTTCATATAA	p.K26delinsNFX
XH_P44	17	38282571	38282571	Nonsense_Mutation	INS	-	CAGATACTTAGC	-	MSL1	nsACACAGATAC	9_E40delinsHTDTX
XH_P44	17	38548474	38548474	Frame_Shift_Ins	INS	-	TTGAGTCTTAT	-	TOP2A	ATGTTAATAAG	p.P1362fs
XH_P44	17	38556284	38556284	Nonsense_Mutation	INS	-	C	-	TOP2A	c.3035_3036ins	T012_D1013delinsX
XH_P44	17	38556285	38556285	In_Frame_Ins	INS	-	TATACACGC	-	TOP2A	3035insCGCT	Y1012delinsCVVN
XH_P44	17	38556540	38556540	Frame_Shift_Ins	INS	-	CAGGTGCTTTTT	-	TOP2A	1insTCAAAAAG	p.E974fs
XH_P44	17	38573045	38573045	Frame_Shift_Ins	INS	-	GTAATAC	-	TOP2A	23_124insGTAT	p.H42fs
XH_P44	17	38573047	38573047	Nonsense_Mutation	INS	-	ACTTATGGTAA	-	TOP2A	CATGATTACCAT	1delinsVIMITIKCSYX
XH_P44	17	38854541	38854541	Frame_Shift_Ins	INS	-	TTTAATTGTTT	-	KRT24	1526insAAACA	p.G509fs
XH_P44	17	38854542	38854542	Nonsense_Mutation	INS	-	AAATTACTTTT	-	KRT24	ACTTGCAAAAGT	509_K510delinsNX
XH_P44	17	38955904	38955904	Nonsense_Mutation	INS	-	AAGGTGAGAAA	-	KRT28	CTGTGATTCTCT	L82delinsQICDFSPYSX
XH_P44	17	39140211	39140211	Frame_Shift_Ins	INS	-	TCTATGTTTGG	-	KRT40	sTAAAGCAAACC	p.E105fs
XH_P44	17	39254068	39254142	In_Frame_Del	DEL	CACTGGGGG	-	AGCACTGGGGCT	KRTAP4-8	c.195_269del	p.G5_90del
XH_P44	17	39458839	39458839	In_Frame_Ins	INS	-	TGTGATGCT	-	KRTAP29-1	1_265insAGCAT	p.A89delinsSITA
XH_P44	17	39464382	39464382	Frame_Shift_Ins	INS	-	TCCAGCCAACCT	-	KRTAP16-1	4insTCCAGTTGG	p.R375fs

XH_P44	17	39464384	39464384	Silent	SNP	A	T	A	KRTAP16-1	c.T1122A	p.P374P
XH_P44	17	40725340	40725340	In_Frame_Ins	INS	-	TCTTTG	-	PSMC3IP	36_337insCAAA	R113delinsQRR
XH_P44	17	40855840	40855840	Splice_Site	INS	-	TCTAATCTGCTT	-	EZH1	.	.
XH_P44	17	40947983	40947983	Frame_Shift_Ins	INS	-	TCTCTGA	-	WNK4	55_2356insTCTC	p.5785fs
XH_P44	17	41243681	41243681	Frame_Shift_Ins	INS	-	AAATTCCAAGT	-	BRCA1	6insTATACTTG	p.T1242fs
XH_P44	17	41244532	41244532	Frame_Shift_Ins	INS	-	CTATGCTTAGA	-	BRCA1	2875insCTTAA	p.H959fs
XH_P44	17	41245243	41245243	Frame_Shift_Ins	INS	-	GCAGAAGAGG	-	BRCA1	12164insCCTCT	p.I722fs
XH_P44	17	41245245	41245245	Missense_Mutation	SNP	C	A	C	BRCA1	c.G2162T	p.S721I
XH_P44	17	41349082	41349082	Nonsense_Mutation	INS	-	ATCTAAACCTTTG	-	NBR1	923insTATCTAA	641_P642delinsAIX
XH_P44	17	41584980	41584980	In_Frame_Ins	INS	-	TAAGAACTCTGAT	-	DHX8	TAATCTTAAGAA	87delinsHNLKNIKIM
XH_P44	17	41987003	41987003	Frame_Shift_Ins	INS	-	ATAATGGAAAG	-	MPP2	15cCCCTTCCATT	p.W3fs
XH_P44	17	41987004	41987004	Missense_Mutation	SNP	C	G	C	MPP2	c.G8C	p.W3S
XH_P44	17	42225693	42225693	Frame_Shift_Ins	INS	-	CTCCTAT	-	C17orf53	22_523insCTCC	p.L174fs
XH_P44	17	42225695	42225695	Missense_Mutation	SNP	A	C	A	C17orf53	c.A524C	p.E175A
XH_P44	17	42293279	42293279	Frame_Shift_Ins	INS	-	ATGAGCAACC	-	UBTF	313insGGTTGG	p.L105fs
XH_P44	17	42541907	42541907	Frame_Shift_Ins	INS	-	AC	-	GPATCH8	c.50_51insGT	p.N17fs
XH_P44	17	42541908	42541908	Nonsense_Mutation	INS	-	AAGTCACTGTTA	-	GPATCH8	56GCTTAACAGTG	118delinsRGLTVTX
XH_P44	17	42786200	42786200	Frame_Shift_Ins	INS	-	CTCTCTATTCT	-	DBF4B	3insTCTCTCAT	p.P4fs
XH_P44	17	42807370	42807370	Frame_Shift_Ins	INS	-	TCCAGAACTAA	-	DBF4B	3GAGTCCAGAA	p.P108fs
XH_P44	17	42807422	42807422	In_Frame_Ins	INS	-	TCCAATGCTTTA	-	DBF4B	1insGAATCAATG	125delinsPESMSLN
XH_P44	17	43315931	43315931	Frame_Shift_Ins	INS	-	GCCTT	-	FMNL1	895_896insGCC	p.V299fs
XH_P44	17	44408849	44408849	Frame_Shift_Ins	INS	-	TTGTTCTGTGGG	-	LRR37A	07insGGTTGTTCT	p.F1402fs
XH_P44	17	44408851	44408851	Missense_Mutation	SNP	T	C	T	LRR37A	c.T4208C	p.M1403T
XH_P44	17	44590687	44590687	Frame_Shift_Ins	INS	-	AGAACTGCTCT	-	LRR37A2	610insAGAACT	p.S203fs
XH_P44	17	45753797	45753797	Nonsense_Mutation	INS	-	TGCTCAAGTTA	-	KPNB1	1insGAATGTCA	500delinsKECCGX
XH_P44	17	46030413	46030413	Frame_Shift_Ins	INS	-	GCCA	-	PRR15L	187_188insTGG	p.T63fs
XH_P44	17	46030414	46030414	Frame_Shift_Ins	INS	-	A	-	PRR15L	c.186_187insT	p.T63fs
XH_P44	17	46262165	46262165	Silent	SNP	G	T	G	SKAP1	c.C487A	p.R163R
XH_P44	17	46262166	46262166	Frame_Shift_Ins	INS	-	CTCCCCCTCTCA	-	SKAP1	AAATTGAGAAG	p.V162fs
XH_P44	17	46868895	46868895	Nonsense_Mutation	INS	-	CTGGCTCACCTA	-	TTL6	148insTAGGTGA	p.E50delinsX
XH_P44	17	46926658	46926658	Nonsense_Mutation	INS	-	ATCCATTAAATC	-	CALCOCO2	ATTATATCCATT	K82delinsKNVHX
XH_P44	17	47376287	47376287	Splice_Site	INS	-	CAATATGAATC	-	ZNF652	.	.
XH_P44	17	47783639	47783639	Frame_Shift_Ins	INS	-	GAGTCTTCCTCT	-	SLC35B1	CCTGAGGGAAG	p.A22fs
XH_P44	17	48263690	48263690	Silent	SNP	G	A	G	COL1A1	c.C3993T	p.T1331T
XH_P44	17	48755278	48755278	Frame_Shift_Ins	INS	-	TGGAGGGAGA	-	ABCC3	sGCTGATGGAG	p.S1184fs
XH_P44	17	48940834	48940834	Frame_Shift_Ins	INS	-	CAAC	-	TOB1	127_128insGT	p.F43fs
XH_P44	17	48940836	48940839	Frame_Shift_Del	DEL	AGTG	-	AGTG	TOB1	c.123_126del	p.A41fs
XH_P44	17	49064530	49064530	Frame_Shift_Ins	INS	-	G	-	SPAG9	c.2410_2411ins	p.E804fs
XH_P44	17	49064531	49064531	In_Frame_Ins	INS	-	TGAATAGTAAG	-	SPAG9	ATATGGCTTAC	04delinsTYGILLRTSE
XH_P44	17	49097589	49097589	Frame_Shift_Ins	INS	-	ATGTTAGTATTA	-	SPAG9	1insAATATAATAC	p.V184fs
XH_P44	17	49097590	49097590	In_Frame_Ins	INS	-	TAA	-	SPAG9	c.549_550insTTA	p.V184delinsLV
XH_P44	17	51901572	51901572	Frame_Shift_Ins	INS	-	CATCC	-	KIF2B	178_179insCA	p.E393fs
XH_P44	17	51901573	51901573	Missense_Mutation	SNP	G	T	G	KIF2B	c.G1179T	p.E393D
XH_P44	17	55918611	55918611	In_Frame_Ins	INS	-	TACAGAAACTT	-	MRPS23	6insCCAAGTTT	576delinsPSFCSS
XH_P44	17	56582168	56582168	Nonsense_Mutation	SNP	A	C	A	MTMR4	c.T1271G	p.L424X
XH_P44	17	56582169	56582169	Missense_Mutation	SNP	A	C	A	MTMR4	c.T1270G	p.L424V
XH_P44	17	56634401	56634401	Nonsense_Mutation	INS	-	ACCATTTGTTTTC	-	TEX14	TGACTGAAACAA	1443_1444delinsX
XH_P44	17	56694927	56694927	In_Frame_Ins	INS	-	GCCCTATTGAA	-	TEX14	TCCCTCAATAG	03delinsLSLNRGKGKE
XH_P44	17	57288537	57288537	Frame_Shift_Ins	INS	-	AGAAATGT	-	SMG8	5_1126insAGA	p.G375fs
XH_P44	17	57288538	57288538	Missense_Mutation	SNP	C	T	C	SMG8	c.C1126T	p.P376S
XH_P44	17	57290446	57290446	In_Frame_Ins	INS	-	TGGGAAATTTGA	-	SMG8	63insACTGGGA	N754delinsNTGKLI
XH_P44	17	57721846	57721846	In_Frame_Ins	INS	-	AACATCTACATT	-	CLTC	ACAATAACATCT	84delinsGHNNIYIML
XH_P44	17	57725718	57725718	Frame_Shift_Ins	INS	-	TTTGTCATCTTT	-	CLTC	0insGCTTTGTCA	p.S217fs
XH_P44	17	58124749	58124749	Missense_Mutation	SNP	C	A	C	HEATR6	c.G2690T	p.S897I
XH_P44	17	58124750	58124750	Frame_Shift_Ins	INS	-	AGTGCCCATTTG	-	HEATR6	9insTTACAATGG	p.S897fs
XH_P44	17	59668303	59668303	In_Frame_Ins	INS	-	AGAGGAGAG	-	NACA2	8_239insCTCTC	p.M80delinsLLL
XH_P44	17	59668304	59668304	Frame_Shift_Ins	INS	-	GAAGAGGA	-	NACA2	37_238insTCCTC	p.M80fs
XH_P44	17	60028360	60028360	Splice_Site	INS	-	TCCTAAATAATG	-	MED13	.	.
XH_P44	17	60042783	60042783	Frame_Shift_Ins	INS	-	GTATGAACATTG	-	MED13	428insTTACTGT	p.Q1476fs
XH_P44	17	60059882	60059882	Frame_Shift_Ins	INS	-	GA	-	MED13	3481_3482insT	p.K1161fs
XH_P44	17	60059883	60059883	Frame_Shift_Ins	INS	-	GCACCTGTGAA	-	MED13	31insCTTTTCAC	p.K1161fs
XH_P44	17	60088337	60088337	Missense_Mutation	SNP	T	A	T	MED13	c.A1541T	p.N514I
XH_P44	17	60088339	60088339	Nonsense_Mutation	INS	-	CTGTAGAACCTA	-	MED13	ATACTGTAGGTT	N514delinsTYTVGSTASX
XH_P44	17	60447662	60447662	In_Frame_Ins	INS	-	CTGGTGGGTTGT	-	EFCAB3	14insCTGGTGGG	M5delinsTGGLL
XH_P44	17	60814264	60814264	Frame_Shift_Ins	INS	-	TGATGGAGTG	-	MARCH10	TACAATCACCTC	p.3222fs
XH_P44	17	61498654	61498654	In_Frame_Ins	INS	-	TGGCTTGGA	-	TANC2	1_5312insTGGC	P1771delinsLAWT
XH_P44	17	61498656	61498656	Silent	SNP	G	A	G	TANC2	c.G5313A	p.P1771P
XH_P44	17	61884006	61884006	Nonsense_Mutation	INS	-	GATCTAGCATTT	-	DDX42	ACCTGGATCTAG	C0821delinsTWIX
XH_P44	17	61895505	61895505	Frame_Shift_Ins	INS	-	TGTGTTGTTGAC	-	DDX42	1insAGCTGTGTT	p.D855fs
XH_P44	17	61902790	61902790	Nonsense_Mutation	INS	-	TTTTTAGG	-	FTSJ3	6_407insCCTAA	136_1137delinsSX
XH_P44	17	61902792	61902792	Missense_Mutation	SNP	A	T	A	FTSJ3	c.T405A	p.H135Q
XH_P44	17	61908204	61908204	Missense_Mutation	SNP	G	C	G	PSMC5	c.G564C	p.K188N
XH_P44	17	61908205	61908205	Frame_Shift_Ins	INS	-	CTTC	-	PSMC5	565_566insCTT	p.T189fs
XH_P44	17	62500847	62500847	Frame_Shift_Ins	INS	-	AACAATAAATTT	-	DDX5	AAAAAAAATTT	p.K53fs
XH_P44	17	64062934	64062934	Nonsense_Mutation	INS	-	TTTATATAGGCT	-	CEP112	ATGGAAGCCTAT	265delinsPSYGLYKVIHX
XH_P44	17	65105671	65105671	Frame_Shift_Ins	INS	-	CCCAACATGCT	-	HELZ	1insAAAAAGCAT	p.H1351fs
XH_P44	17	65850822	65850822	In_Frame_Ins	INS	-	ACA	-	BPTF	1380_1381insA	p.P460delinsPT
XH_P44	17	65907199	65907199	Frame_Shift_Ins	INS	-	G	-	BPTF	c.3200dupG	p.R1067fs
XH_P44	17	65908116	65908116	Frame_Shift_Ins	INS	-	TTCTCTC	-	BPTF	16_4117insTTCT	p.V1372fs
XH_P44	17	65908117	65908117	In_Frame_Ins	INS	-	AAGTCC	-	BPTF	17_4118insAAG	N1373delinsKVH
XH_P44	17	65909163	65909163	Nonsense_Mutation	INS	-	TACCTTGATCAC	-	BPTF	164insCTACCTT	21_V1722delinsFLPX
XH_P44	17	65925589	65925589	Frame_Shift_Ins	INS	-	CGTGTTGG	-	BPTF	36_6137insCGTG	p.T2046fs
XH_P44	17	65925591	65925591	In_Frame_Ins	INS	-	GGGTTTTAT	-	BPTF	3_6139insGGGT	T2046delinsTGfY
XH_P44	17	65941803	65941803	Frame_Shift_Ins	INS	-	TTTTGCTTTGAT	-	BPTF	30insGGTTTTGTG	p.A2327fs
XH_P44	17	65941977	65941977	Frame_Shift_Ins	INS	-	ACATGGGATGA	-	BPTF	1sAGGGACATGG	p.I2385fs
XH_P44	17	66253090	66253090	Frame_Shift_Ins	INS	-	SGCAAGAGAGA	-	AMZ2	ATCAGGCAAGA	p.L297fs
XH_P44	17	66881345	66881345	Frame_Shift_Ins	INS	-	AAGGG	-	ABCA8	420_3421insCC	p.S1141fs
XH_P44	17	66881347	66881347	In_Frame_Ins	INS	-	AGGGGT	-	ABCA8	18_3419insACC	L1140delinsVPL
XH_P44	17	66980317	66980317	Splice_Site	INS	-	TTCTCTTTCTCTG	-	ABCA9	.	.
XH_P44	17	67183996	67183996	Frame_Shift_Ins	INS	-	AGTATATGAAA	-	ABCA10	1insTGTTTTTTCA	p.K719fs
XH_P44	17	67218038	67218038	Splice_Site	INS	-	ATCCCTAATGTCT	-	ABCA10	.	.
XH_P44	17	68129037	68129037	Missense_Mutation	SNP	C	T	C	KCNJ16	c.C914T	p.A305V
XH_P44	17	68129404	68129404	Frame_Shift_Ins	INS	-	TTCAAACT	-	KCNJ16	1_1282insTTCA	p.S427fs
XH_P44	17	68129405	68129405	In_Frame_Ins	INS	-	GTTCACTTTGTA	-	KCNJ16	TAAGCAGTTCA	28delinsVSSSLCNTS
XH_P44	17	71166054	71166054	Frame_Shift_Ins	INS	-	T	-	SSTR2	c.597dupT	p.G199fs
XH_P44	17	71166056	71166056	Frame_Shift_Ins	INS	-	AGGATGTA	-	SSTR2	8_599insAGGA	p.E200fs
XH_P44	17	71231951	71231951	Nonsense_Mutation	INS	-	GATCAGTAGGT	-	C17orf80	CTTTTGTATCAG	D1011delinsKLFDDQX
XH_P44	17	71232328	71232328	Missense_Mutation	SNP	G	T	G	C17orf80	c.G707T	p.S236I

XH_P44	17	71232330	71232330	Frame_Shift_Ins	INS	-	TTAGTATTTTTT	-	C1orf80	DinsGTTT	AGTAT	p.D237fs
XH_P44	17	74287649	74287649	Frame_Shift_Ins	INS	-	AGGTT	-	QRICH2	560_2661insAA		p.H887fs
XH_P44	17	76046445	76046445	Nonsense_Mutation	INS	-	CTTTCCCATTTGA	-	TNRC6C	3insATCCTTTCC	L434delinsLILSHX	
XH_P44	17	76094461	76094461	Nonsense_Mutation	INS	-	AAACTCAAGTAA	-	TNRC6C	4345insAAACTC	G1448delinsGKLKX	
XH_P44	17	78350316	78350316	Nonsense_Mutation	INS	-	TTGTGTGAATTC	-	RNF213	3402insATTGTG	T67_L4468delinsNIVX	
XH_P44	17	78350318	78350318	Frame_Shift_Ins	INS	-	CTTA	-	RNF213	403_13404insC	p.L4468fs	
XH_P44	17	78797015	78797015	Frame_Shift_Ins	INS	-	TACACACACGTG	-	RPTOR	AAACATACACA	p.H376fs	
XH_P44	17	80724237	80724237	In_Frame_Ins	INS	-	AGCTAC	-	TBCD	28_429insAGCT	D143delinsEAT	
XH_P44	17	80730362	80730362	Frame_Shift_Ins	INS	-	AAAAAAA	-	TBCD	7_618insAAAAA	p.A206fs	
XH_P44	17	80730364	80730364	Missense_Mutation	SNP	G	C	G	TBCD	c.G619C	p.A207P	
XH_P44	18	624942	624942	Frame_Shift_Ins	INS	-	C	-	CLUL1	c.333_334insC	p.D111fs	
XH_P44	18	624943	624943	In_Frame_Ins	INS	-	CCC	-	CLUL1	c.334_335insCC	p.S112delinsSP	
XH_P44	18	2890927	2890927	Nonsense_Mutation	INS	-	GTTTCATTATCTG	-	EMILIN2	3insGGTTTCATT	E268delinsGFII	CX
XH_P44	18	2892264	2892264	Frame_Shift_Ins	INS	-	ACCCACCTTAGT	-	EMILIN2	40insTCACCCAC	p.C713fs	
XH_P44	18	6966179	6966179	Nonsense_Mutation	INS	-	CTAGTCTTTATA	-	LAMA1	3ATATCTATAAA	B39_G2340delinsKCX	
XH_P44	18	8085869	8085869	Silent	SNP	A	T	A	PTPRM	c.A1752T	p.S584S	
XH_P44	18	8085871	8085871	Splice_Site	INS	-	TGGACTCAGAT	-	PTPRM	.	.	
XH_P44	18	9254725	9254725	Frame_Shift_Ins	INS	-	TG	-	ANKRD12	1391_1392insT	p.E464fs	
XH_P44	18	9254727	9254727	Nonsense_Mutation	INS	-	TCTACTTTAAATC	-	ANKRD12	TGTTTTTTACTT	465delinsLFFTFKX	
XH_P44	18	10672816	10672816	In_Frame_Ins	INS	-	GGC	-	PIEZO2	7876_7877insG	Y2626delinsCH	
XH_P44	18	10672817	10672817	Frame_Shift_Ins	INS	-	TTAATCCAATTC	-	PIEZO2	nsCATGGGATTG	p.Y2626fs	
XH_P44	18	10715691	10715691	Nonsense_Mutation	INS	-	GGCAACTTTAT	-	PIEZO2	039insAATAAA	G680_L1681delinsEX	
XH_P44	18	12358831	12358831	In_Frame_Ins	INS	-	GAAGTTGGATTA	-	AFG3L2	ATAAGTAATCAA	delinsLSISNQT	SQNYN
XH_P44	18	13049434	13049434	Nonsense_Mutation	INS	-	ACTA	-	CEP192	644_2645insAC	B82_S883delinsYX	
XH_P44	18	13049435	13049435	Nonsense_Mutation	INS	-	CCCTTGAAAAAGT	-	CEP192	646insCCCTTG	B82_S883delinsCPX	
XH_P44	18	13069179	13069179	Frame_Shift_Ins	INS	-	CCGAGAATTCT	-	CEP192	sCTTTTCCCGAG	p.K1685fs	
XH_P44	18	14851876	14851876	Frame_Shift_Ins	INS	-	ATTTATTTTCC	-	ANKRD30B	3577insATTTTA	p.S1192fs	
XH_P44	18	14851877	14851877	Missense_Mutation	SNP	G	T	G	ANKRD30B	c.G3577T	p.V1193F	
XH_P44	18	18547887	18547887	Frame_Shift_Ins	INS	-	TTTGTTTCAGAT	-	ROCK1	8insCAGTCTGA	p.L1006fs	
XH_P44	18	19153797	19153797	Frame_Shift_Ins	INS	-	CAGCACAATAA	-	ESCO1	1008insTTATTG	p.P336fs	
XH_P44	18	19437161	19437161	Frame_Shift_Ins	INS	-	AAACAATGACA	-	MIB1	737insAAAAACA	p.M912fs	
XH_P44	18	19762934	19762934	In_Frame_Ins	INS	-	SCATTAATAAGCT	-	GATA6	tsATTGGCACTA	G17delinsTLALKALI	
XH_P44	18	19996228	19996228	Nonsense_Mutation	INS	-	ATTTTATTCTAA	-	CTAGE1	insACAATTAGA	G16_S517delinsHNX	
XH_P44	18	19996927	19996927	Frame_Shift_Ins	INS	-	TTAAAGTAATGA	-	CTAGE1	ATTCAAGTCATTA	p.L283fs	
XH_P44	18	21141445	21141445	In_Frame_Ins	INS	-	GGAGGC	-	NPC1	09_510insGCC	D170delinsEPP	
XH_P44	18	21479329	21479329	Missense_Mutation	SNP	G	A	G	LAMA3	c.G1087A	p.E363K	
XH_P44	18	21735890	21735890	Frame_Shift_Ins	INS	-	GACCATTTCCTCT	-	CABYR	32insTGACCAT	p.S44fs	
XH_P44	18	21819248	21819248	Nonsense_Mutation	INS	-	STGTGTCTGTT	-	OSBPL1A	TTAATAACATGAp	S78delinsSLITX	
XH_P44	18	21897326	21897326	Frame_Shift_Ins	INS	-	TGTG	-	OSBPL1A	770_771insCAC	p.V257fs	
XH_P44	18	21897327	21897327	Frame_Shift_Ins	INS	-	AATCAGTT	-	OSBPL1A	9_770insAACTG	p.V257fs	
XH_P44	18	23901068	23901068	Missense_Mutation	SNP	T	A	T	TAF4B	c.T2052A	p.D684E	
XH_P44	18	23901070	23901070	Frame_Shift_Ins	INS	-	CTCAGAAAAATA	-	TAF4B	2055insCTCAG	p.A685fs	
XH_P44	18	24442386	24442386	Nonsense_Mutation	INS	-	GCATCTTTAGCT	-	AQP4	tsAAATAGCTAA	G47_M48delinsENXS	
XH_P44	18	25543347	25543347	In_Frame_Ins	INS	-	AGGATTTTTTTT	-	CDH2	tsCTAGGAAAAAA	799delinsLKGKILLG	
XH_P44	18	28588079	28588079	Frame_Shift_Ins	INS	-	ACTTTAAAGAC	-	DS3	1566insGTCTT	p.E522fs	
XH_P44	18	28588081	28588081	Nonsense_Mutation	INS	-	TTCTGTCTCTCT	-	DS3	64insTAAGAGAG	p.E522delinsCX	
XH_P44	18	28605791	28605791	Frame_Shift_Ins	INS	-	TGCATCTCTCT	-	DS3	TAAGAAGAGAG	p.E189fs	
XH_P44	18	28906954	28906954	Nonsense_Mutation	INS	-	SGGAAATTGGT	-	DSG1	TAATTGGGAAA	8delinsMFNWENWX	
XH_P44	18	28968973	28968973	In_Frame_Ins	INS	-	AAAGAAACAAT	-	DSG4	0insGCAAGAA	G170delinsRQRNNF	
XH_P44	18	28980883	28980883	Frame_Shift_Ins	INS	-	CATTTTTACTCT	-	DSG4	insTCATCATTTT	p.L439fs	
XH_P44	18	28992959	28992959	Frame_Shift_Ins	INS	-	AATAACAGCAAT	-	DSG4	82insAGAATAAC	p.T861fs	
XH_P44	18	29122778	29122778	Nonsense_Mutation	INS	-	CCTTTG	-	DSG2	97_2298insCTC	B76delinsALX	
XH_P44	18	29122780	29122780	Frame_Shift_Ins	INS	-	AA	-	DSG2	2299_2300insA	p.L767fs	
XH_P44	18	29246274	29246274	Frame_Shift_Ins	INS	-	SATGTATGAACC	-	B4GALT6	sCACACGTTTCAT	p.T59fs	
XH_P44	18	29790627	29790627	Nonsense_Mutation	INS	-	CAGAAGCCTAA	-	MEP1B	AAATGACAGAA	B61_Y362delinsEKX	
XH_P44	18	29793179	29793179	In_Frame_Ins	INS	-	TTCTCT	-	MEP1B	236_1237insTTCT	L412delinsLFS	
XH_P44	18	29793181	29793181	In_Frame_Ins	INS	-	AATAGC	-	MEP1B	38_1239insAAT	B.G413delinsGIA	
XH_P44	18	29797807	29797807	Nonsense_Mutation	INS	-	ATGAAACTA	-	MEP1B	0_1971insATGA	p.V657delinsVX	
XH_P44	18	29890249	29890249	In_Frame_Ins	INS	-	GAAGCTCTCTG	-	GAREM1	0insTACAGAGAG	100delinsNTEAVR	
XH_P44	18	31263464	31263464	In_Frame_Ins	INS	-	TAT	-	ASXL3	c.811_812insTA	p.T271delinsLS	
XH_P44	18	31263465	31263465	Frame_Shift_Ins	INS	-	KATGTATATTTCA	-	ASXL3	GTGAACATGTA	p.T271fs	
XH_P44	18	31325803	31325803	Nonsense_Mutation	INS	-	TAGGTTCTGCTG	-	ASXL3	5992insTAGGTT	B.K1997delinsKX	
XH_P44	18	32395971	32395971	Nonsense_Mutation	INS	-	AAACATGTTTAC	-	DTNA	sTTATTAACATCA	V234delinsVLLNX	
XH_P44	18	34327071	34327071	Frame_Shift_Ins	INS	-	AT	-	FHOD3	3629_3630insA	p.K1210fs	
XH_P44	18	34327072	34327072	Frame_Shift_Ins	INS	-	ATATTTACAGCC	-	FHOD3	sCAACATATTTT	p.K1210fs	
XH_P44	18	34647332	34647332	Frame_Shift_Ins	INS	-	GTTT	-	KIAA1328	732_733insGT	p.L244fs	
XH_P44	18	34647333	34647333	Frame_Shift_Ins	INS	-	AAGAATTAATTC	-	KIAA1328	34insAAAGAAAT	p.Q245fs	
XH_P44	18	34740269	34740269	In_Frame_Ins	INS	-	AGCACA	-	KIAA1328	23_1124insAGG	V375delinsEHI	
XH_P44	18	34740270	34740270	Nonsense_Mutation	INS	-	TATTTAAATTTCA	-	KIAA1328	5insAGATATTTTA	V375delinsVDIX	
XH_P44	18	39550386	39550386	In_Frame_Ins	INS	-	ATGCCATTCTTT	-	PIK3C3	309insATGCCA	T103delinsTCHSF	
XH_P44	18	42530854	42530854	In_Frame_Ins	INS	-	GCC	-	SETBP1	1549_1550insG	p.K517delinsSQ	
XH_P44	18	42530855	42530855	Frame_Shift_Ins	INS	-	AG	-	SETBP1	1550_1551insA	p.K517fs	
XH_P44	18	43311070	43311070	Frame_Shift_Ins	INS	-	AAAGCCTCTATC	-	SLC14A1	CCCTGAAAGCC	p.L137fs	
XH_P44	18	43572144	43572144	Frame_Shift_Ins	INS	-	CTAATAGAATTG	-	PSTPIP2	TTTACACAATTC	p.L256fs	
XH_P44	18	43796392	43796392	Frame_Shift_Ins	INS	-	GTTC	-	C18orf25	546_547insGT	p.L182fs	
XH_P44	18	43796393	43796393	In_Frame_Ins	INS	-	TTCTCT	-	C18orf25	547_548insTTCT	p.L183delinsILF	
XH_P44	18	43820140	43820140	Frame_Shift_Ins	INS	-	ACTTTATAGATC	-	C18orf25	86insCACITTTAT	p.L295fs	
XH_P44	18	43820142	43820142	Frame_Shift_Ins	INS	-	TATT	-	C18orf25	887_888insTAT	p.N296fs	
XH_P44	18	44087608	44087608	Frame_Shift_Ins	INS	-	AAAATCTA	-	LOXHD1	1_302insTAGAT	p.R101fs	
XH_P44	18	44087609	44087609	Frame_Shift_Ins	INS	-	CAATCCAAGTTT	-	LOXHD1	01insAAAACCTTG	p.R101fs	
XH_P44	18	44656695	44656695	In_Frame_Ins	INS	-	GTG	-	HDHD2	c.44_45insCAC	p.L15delinsIT	
XH_P44	18	44656696	44656696	In_Frame_Ins	INS	-	GTATGTTTTTTTG	-	HDHD2	sAAACAAAAAA	G115delinsKTKNILL	
XH_P44	18	47017935	47017935	In_Frame_Ins	INS	-	GAAATTGAGAA	-	RPL17	CTACTTCTCAAT	G3delinsTTSQFHKR	
XH_P44	18	48447550	48447550	Frame_Shift_Ins	INS	-	CCTTACAATCA	-	ME2	insTTTCCCTTAC	p.L350fs	
XH_P44	18	48702993	48702993	Frame_Shift_Ins	INS	-	TCCA	-	MEX3C	707_1708insTG	p.H570fs	
XH_P44	18	50589756	50589756	Nonsense_Mutation	INS	-	ATTCAAATCAAT	-	DCC	ATTTATAATTCA	G57delinsGIENIYNHSLSSX	
XH_P44	18	50589831	50589831	Splice_Site	INS	-	TCTGCCACAAG	-	DCC	.	.	
XH_P44	18	53018157	53018157	Nonsense_Mutation	INS	-	GGTACGTTAACT	-	TCF4	sAGCTGTATAACG	p.Y19delinsX	
XH_P44	18	55355738	55355738	Nonsense_Mutation	INS	-	TCATGACCTTTA	-	ATP8B1	ACTTTTTAAAGG	V408delinsTFX	
XH_P44	18	56008350	56008350	Silent	SNP	C	T	C	NEDD4L	c.C783T	p.Y261Y	
XH_P44	18	56246907	56246907	In_Frame_Ins	INS	-	ACATGGATGAAT	-	ALPK2	1101insATTCACT	G367delinsGFIHV	
XH_P44	18	56246909	56246909	Missense_Mutation	SNP	C	A	C	ALPK2	c.G1099T	p.G367C	
XH_P44	18	56247177	56247177	In_Frame_Ins	INS	-	GTG	-	ALPK2	c.830_831insCA	p.S277delinsST	
XH_P44	18	56247179	56247179	Frame_Shift_Ins	INS	-	ATGGG	-	ALPK2	828_829insCCC	p.S277fs	
XH_P44	18	56278980	56278980	Nonsense_Mutation	INS	-	ACTCCATCTCTA	-	ALPK2	TCATAGAGGAT	T17_L18delinsKSX	
XH_P44	18	56414818	56414818	Frame_Shift_Ins	INS	-	CAAA	-	MALT1	186_2187insCA	p.S729fs	
XH_P44	18	56414819	56414819	Frame_Shift_Ins	INS	-	CCTCAAG	-	MALT1	87_2188insCCTC	p.S729fs	
XH_P44	18	56651416	56651416	Missense_Mutation	SNP	T	G	T	ZNF532	c.T3624G	p.C1208W	

XH_P44	18	56651418	56651418	Frame_Shift_Ins	INS	-	A	-	ZNF532	c.3626_3627ins	p.G1209fs
XH_P44	18	56892869	56892869	Frame_Shift_Ins	INS	-	AAAAACAAAA	-	GRP	286insAAAAAC	p.N95fs
XH_P44	18	59777097	59777097	Nonsense_Mutation	INS	-	TC1TTGTGTATC	-	PIGN	ATAAAAGATAC	p.515_L516delinsLX
XH_P44	18	60036355	60036355	Frame_Shift_Ins	INS	-	TCCTCCTCTAT	-	TNFRSF11A	c.1164insTCTTC	p.C388fs
XH_P44	18	60241466	60241466	Nonsense_Mutation	INS	-	GAAATAAACAT	-	ZCHC2	insGCTAGAAAT	p.718_M719delinsCX
XH_P44	18	60563191	60563191	In_Frame_Ins	INS	-	GTATTA	-	PHLPP1	c.91_2392insGTAb	p.T797delinsTVL
XH_P44	18	60563192	60563192	Frame_Shift_Ins	INS	-	CAGAAAATGTA	-	PHLPP1	2393insCAGAA	p.L798fs
XH_P44	18	61570378	61570378	Frame_Shift_Ins	INS	-	GTTC	-	SERPINB2	c.1087_1088insGT	p.N363fs
XH_P44	18	61570380	61570380	Nonsense_Mutation	INS	-	TC1TCTCAATTG	-	SERPINB2	saATGCTCTCTC	p.E364delinsNNALLIX
XH_P44	18	64172416	64172416	Frame_Shift_Ins	INS	-	SGATGAAAGCT	-	CDH19	insATCATAGCT	p.T651fs
XH_P44	18	64235873	64235873	Frame_Shift_Ins	INS	-	T	-	CDH19	c.269_270insA	p.F90fs
XH_P44	18	64235874	64235874	In_Frame_Ins	INS	-	GGAAGCAGGTTT	-	CDH19	AATTTTAAACCT	p.0delinsSNFKPASLLI
XH_P44	18	65178942	65178942	In_Frame_Ins	INS	-	AATGTACCAGAC	-	DSEL	TAAATGCTCTGG	p.78delinsPKCSGTFFK
XH_P44	18	66351710	66351710	Frame_Shift_Ins	INS	-	TACAGAGACCTC	-	TMX3	binsAAGAGGTC	p.A109fs
XH_P44	18	67688017	67688017	Frame_Shift_Ins	INS	-	ACTCA	-	RTTN	c.250_325insTG	p.H1084fs
XH_P44	18	67688018	67688018	Frame_Shift_Ins	INS	-	TGAAATAATCT	-	RTTN	c.3250insAGATT	p.H1084fs
XH_P44	18	71822545	71822545	Frame_Shift_Ins	INS	-	AG	-	TIMM21	c.369_370insAG	p.G123fs
XH_P44	18	71822546	71822546	Silent	SNP	T	C	T	TIMM21	c.C370C	p.L124L
XH_P44	18	73122840	73122840	Frame_Shift_Ins	INS	-	TTGAGGGGCA	-	SMIM21	285insTGCCCC	p.R95fs
XH_P44	19	5604815	5604815	In_Frame_Ins	INS	-	TTGAAAGATAA	-	SAFB2	c.429insCTTTACT	p.M477delinsLYFSIM
XH_P44	19	5641825	5641825	Frame_Shift_Ins	INS	-	TC	-	SAFB	c.414_415insTC	p.E138fs
XH_P44	19	5641827	5641827	In_Frame_Ins	INS	-	CAGCATGAGATC	-	SAFB	nsTTACAGCATG	p.39delinsLYMRSN
XH_P44	19	7083359	7083359	Frame_Shift_Ins	INS	-	ATCT	-	ZNF557	c.897_898insATC	p.K299fs
XH_P44	19	7083361	7083361	In_Frame_Ins	INS	-	TGCTGAAGG	-	ZNF557	c.900insTGCTGA	p.A300delinsAAEG
XH_P44	19	7809019	7809019	Frame_Shift_Ins	INS	-	SGAGGTGTATTA	-	CD209	binsTTTTAATAC	p.W193fs
XH_P44	19	7809020	7809020	Nonsense_Mutation	SNP	C	T	C	CD209	c.G578A	p.W193X
XH_P44	19	8550805	8550805	Missense_Mutation	SNP	C	T	C	HNRNPM	c.C1088T	p.A363V
XH_P44	19	9012854	9012854	Frame_Shift_Ins	INS	-	CCCATGTTCAA	-	MUC16	c.38590insTTGA	p.T12864fs
XH_P44	19	9045757	9045757	Nonsense_Mutation	INS	-	TCGTGTTTCAAA	-	MUC16	c.4insAAGTTTGA	p.G11959delinsQSFENRX
XH_P44	19	9047147	9047147	Frame_Shift_Ins	INS	-	AACCAAGCACAA	-	MUC16	c.4484insGTGTG	p.P11495fs
XH_P44	19	9047149	9047149	Silent	SNP	A	G	A	MUC16	c.C34482C	p.H11494H
XH_P44	19	9047702	9047702	Frame_Shift_Ins	INS	-	CCACCAAGTCC	-	MUC16	c.33929insGGAG	p.T11310fs
XH_P44	19	9049355	9049355	In_Frame_Ins	INS	-	TTCTAGGGCAGI	-	MUC16	c.32276insACTGC	p.10759delinsHCPRT
XH_P44	19	9057983	9057983	In_Frame_Ins	INS	-	ACAAGTGCACTG	-	MUC16	c.29463insGACTG	p.9821delinsRTALV
XH_P44	19	9061326	9061326	Missense_Mutation	SNP	G	A	G	MUC16	c.C26120T	p.T8707I
XH_P44	19	9061327	9061327	In_Frame_Ins	INS	-	CTC	-	MUC16	c.5118_26119insGp	p.T8707delinsET
XH_P44	19	9061506	9061506	Missense_Mutation	SNP	A	T	A	MUC16	c.C25940A	p.V8647E
XH_P44	19	9061507	9061507	Frame_Shift_Ins	INS	-	TGGATTAAGGG	-	MUC16	c.25939insCCCT	p.V8647fs
XH_P44	19	9064344	9064344	Nonsense_Mutation	INS	-	TCATCTTCAAGT	-	MUC16	c.102insAACTTCTG	p.P7701delinsQTX
XH_P44	19	9068877	9068877	Frame_Shift_Ins	INS	-	TTAAGGAACA	-	MUC16	c.18569insTGTG	p.D6190fs
XH_P44	19	9071132	9071132	In_Frame_Ins	INS	-	ACAAATACT	-	MUC16	c.8_16314insAGT	p.S5438delinsSVFV
XH_P44	19	9071133	9071133	Nonsense_Mutation	INS	-	CTTTTCTT	-	MUC16	c.16313insAAGAp	p.S5438delinsX
XH_P44	19	9072417	9072417	Frame_Shift_Ins	INS	-	CCAACAACCTCG	-	MUC16	c.5029insCAGAG	p.F5010fs
XH_P44	19	9073192	9073192	Missense_Mutation	SNP	G	C	G	MUC16	c.C14254G	p.L4752V
XH_P44	19	9073193	9073193	Frame_Shift_Ins	INS	-	CATCTCTCCATA	-	MUC16	c.4253insTTATGG	p.V4751fs
XH_P44	19	9073357	9073357	In_Frame_Ins	INS	-	CTCAGTTCT	-	MUC16	c.14089insAGAA	p.D4697delinsRTED
XH_P44	19	9073359	9073359	Nonsense_Mutation	INS	-	CTTCTTC	-	MUC16	c.6_14087insGA	p.D4697delinsX
XH_P44	19	9076140	9076140	Frame_Shift_Ins	INS	-	CAGC	-	MUC16	c.305_11306insG	p.L3769fs
XH_P44	19	9076142	9076142	Frame_Shift_Ins	INS	-	TT	-	MUC16	c.1303_11304ins	p.M3768fs
XH_P44	19	9077301	9077301	Nonsense_Mutation	INS	-	CATCTCCCTCAAT	-	MUC16	c.0145insATTGA	p.382_T3383delinsYX
XH_P44	19	9083236	9083236	Frame_Shift_Ins	INS	-	CT	-	MUC16	c.8578_8579insA	p.L2860fs
XH_P44	19	9083237	9083237	Frame_Shift_Ins	INS	-	AAACCCCT	-	MUC16	c.7_8578insAGGG	p.L2860fs
XH_P44	19	9084742	9084742	Nonsense_Mutation	INS	-	CACCTATTCTCT	-	MUC16	c.sCATCAAGAGA	p.8_K2359delinsPSREX
XH_P44	19	9085655	9085655	Nonsense_Mutation	INS	-	ACAGGTCCTT	-	MUC16	c.61600insAAAA	p.L2055delinsKDLX
XH_P44	19	9086655	9086655	Frame_Shift_Ins	INS	-	AGCACTGAAAT	-	MUC16	c.160insTATTTTC	p.S1720fs
XH_P44	19	9086904	9086904	Frame_Shift_Ins	INS	-	T	-	MUC16	c.4910_4911ins	p.G1637fs
XH_P44	19	9226423	9226423	Nonsense_Mutation	INS	-	AACCACAACCAC	-	OR7G1	c.17insGTGGTTG	p.Q6delinsRGCGX
XH_P44	19	9226424	9226424	Nonsense_Mutation	SNP	G	A	G	OR7G1	c.C16T	p.Q6X
XH_P44	19	9237290	9237290	In_Frame_Ins	INS	-	CAC1TTTCTGTG	-	OR7G3	c.7insTCACAGAA	p.113delinsSQKKWG
XH_P44	19	9406468	9406468	Frame_Shift_Ins	INS	-	GTTTGTCTCG	-	ZNF699	c.1612insCAGGA	p.K538fs
XH_P44	19	9525288	9525288	Frame_Shift_Ins	INS	-	AA	-	ZNF266	c.c.312_313insTT	p.T105fs
XH_P44	19	9525289	9525289	Nonsense_Mutation	INS	-	GGAAAGAGGATT	-	ZNF266	c.TATCTAAATCTC	p.104_T105delinsNIX
XH_P44	19	9676949	9676949	Nonsense_Mutation	INS	-	TACTAAACATT	-	ZNF121	c.sTTTTTAAATGTG	p.G280delinsGFX
XH_P44	19	9721274	9721274	Frame_Shift_Ins	INS	-	TTGGGAAGCAT	-	ZNF561	c.CAGCAAAATGCTT	p.H286fs
XH_P44	19	9730116	9730116	Frame_Shift_Ins	INS	-	G	-	ZNF561	c.c.16_17insC	p.L6fs
XH_P44	19	9730118	9730118	Nonsense_Mutation	INS	-	ATTATTTATTTA	-	ZNF561	c.TAAATAAATAA	p.p.Y5_L6delinsX
XH_P44	19	9869412	9869412	Nonsense_Mutation	INS	-	CATATAAGATCT	-	ZNF846	c.TGTGAGATCTTA	p.Y114delinsSPLX
XH_P44	19	11211016	11211016	Nonsense_Mutation	INS	-	TGTCAACAAAGG	-	LDLR	nsACTTGCTCAAC	p.62delinsTLVNKGX
XH_P44	19	11548888	11548888	In_Frame_Ins	INS	-	TAAAGACCCC	-	PRKCSH	c.294insTAAGAA	p.D98delinsDKSP
XH_P44	19	11916891	11916891	Frame_Shift_Ins	INS	-	AAGTCTCACTC	-	ZNF491	c.124insAAGTCT	p.T41fs
XH_P44	19	11917205	11917205	In_Frame_Ins	INS	-	TGG	-	ZNF491	c.c.437_438insTG	p.Y146delinsYG
XH_P44	19	11917206	11917206	Frame_Shift_Ins	INS	-	TCCTCTAAAAATT	-	ZNF491	c.39insTTCTCTAA	p.Y146fs
XH_P44	19	11978556	11978556	In_Frame_Ins	INS	-	TTTGTGCCATAT	-	ZNF439	c.insGGCTTTGGT	p.88delinsHGFPGYS
XH_P44	19	12059884	12059884	Frame_Shift_Ins	INS	-	CCATCCCCAC	-	ZNF700	c.1055insCCATC	p.F352fs
XH_P44	19	12059972	12059972	Frame_Shift_Ins	INS	-	KCGAAGAGAAC	-	ZNF700	c.sGTGCTACGAAG	p.Q381fs
XH_P44	19	12060335	12060335	Frame_Shift_Ins	INS	-	TGCTTGC	-	ZNF700	c.D5_1506insTGC	p.I502fs
XH_P44	19	12060336	12060336	Frame_Shift_Ins	INS	-	TTTAT	-	ZNF700	c.506_1507insTT	p.I502fs
XH_P44	19	12125986	12125986	Nonsense_Mutation	INS	-	ATAATGTAACC	-	ZNF433	c.CACATTGGTTA	p.C567delinsTLPHWLHLX
XH_P44	19	12184962	12184962	Frame_Shift_Ins	INS	-	KCCCATTTACTCTC	-	ZNF844	c.21insACCCATT	p.L40fs
XH_P44	19	12223576	12223576	Nonsense_Mutation	INS	-	TCCTTACATTCA	-	ZNF788	c.CCCACATTCTCTA	p.Q406delinsFPHLSHSX
XH_P44	19	12244127	12244127	Frame_Shift_Ins	INS	-	CACCTGAGGATTA	-	ZNF20	c.AGGGTTTATCTC	p.F289fs
XH_P44	19	12298079	12298079	Frame_Shift_Ins	INS	-	TGGTGATATATCC	-	ZNF136	c.TTATATGGTGTA	p.R230fs
XH_P44	19	12384292	12384292	Frame_Shift_Ins	INS	-	ATTTCCTCGGTT	-	ZNF44	c.78insGAACCAAG	p.K260fs
XH_P44	19	12460988	12460988	Frame_Shift_Ins	INS	-	AATGTCAACAAT	-	ZNF442	c.sACCACATTGTT	p.D471fs
XH_P44	19	12461177	12461177	Frame_Shift_Ins	INS	-	TCTCAACATA	-	ZNF442	c.1222insTATGT	p.K408fs
XH_P44	19	12461178	12461178	Nonsense_Mutation	INS	-	AAGGACT	-	ZNF442	c.20_1221insAGT	p.C407_K408delinsX
XH_P44	19	12461586	12461586	Nonsense_Mutation	INS	-	TGTCTAGTTCA	-	ZNF442	c.binsAGTGAAC	p.T71_K272delinsSVNX
XH_P44	19	12461588	12461588	Missense_Mutation	SNP	A	C	A	ZNF442	c.C.T811G	p.S5271A
XH_P44	19	12501902	12501902	Frame_Shift_Ins	INS	-	A	-	ZNF799	c.c.1309_1310ins	p.R437fs
XH_P44	19	12501903	12501903	Nonsense_Mutation	INS	-	CATTTGGTAAC	-	ZNF799	c.09insAAGTTAC	p.R437delinsKLPKX
XH_P44	19	12541593	12541593	Frame_Shift_Ins	INS	-	GTCATTATGAT	-	ZNF443	c.1393insATCAT	p.R465fs
XH_P44	19	12691522	12691522	In_Frame_Ins	INS	-	TGTTAATGCTGT	-	ZNF490	c.7insCTGACAGCA	p.456delinsTDSITL
XH_P44	19	12691718	12691718	Nonsense_Mutation	INS	-	ACACAAAAGAA	-	ZNF490	c.GTATGAATTCTT	p.E391delinsPVX
XH_P44	19	12692060	12692060	Frame_Shift_Ins	INS	-	AA	-	ZNF490	c.c.828_829insTT	p.P277fs
XH_P44	19	12692061	12692061	Frame_Shift_Ins	INS	-	GTGGGAGAGCC	-	ZNF490	c.828insGGCTCT	p.K276fs
XH_P44	19	13264286	13264286	Missense_Mutation	SNP	A	G	A	IER2	c.C286G	p.M96V
XH_P44	19	14952355	14952355	Frame_Shift_Ins	INS	-	A	-	OR7A10	c.c.334_335insT	p.N12fs
XH_P44	19	14952357	14952357	Frame_Shift_Ins	INS	-	AGGCATTT	-	OR7A10	c.2_333insAAATG	p.D111fs

XH_P44	19	15052796	15052796	In_Frame_Ins	INS	-	AGCCTGCAAAAG	-	OR7C2	497insAGCCTGC	166delinsQPAKV
XH_P44	19	15571915	15571915	Frame_Shift_Ins	INS	-	CAAAATGAAGC	-	RASAL3	562insGCTTCA	p.T188fs
XH_P44	19	15659002	15659002	Missense_Mutation	SNP	G	T	G	CYP4F22	c.G1220T	p.R407L
XH_P44	19	15659003	15659003	In_Frame_Ins	INS	-	TCCTCTCTCTCTCT	-	CYP4F22	insTCTCTCTCTCTCT	407delinsRSLSLSLSL
XH_P44	19	15789150	15789150	In_Frame_Ins	INS	-	GTGTTTGAGAAAG	-	CYP4F12	nsAGGGTGTGTTTG	93delinsGGCLRRD
XH_P44	19	18309625	18309625	Frame_Shift_Ins	INS	-	CAAGAGGCATC	-	RAB3A	82insAGATGCC	p.A128fs
XH_P44	19	18311245	18311245	Missense_Mutation	SNP	C	T	C	RAB3A	c.G239A	p.G80E
XH_P44	19	18311246	18311246	Nonsense_Mutation	INS	-	TCCTTTCTTTTGAC	-	RAB3A	TCCTCTCAAGAAAG	G80_Q81delinsX
XH_P44	19	19822740	19822740	In_Frame_Ins	INS	-	TTTGTAGGTGTA	-	ZNF14	CATTGCTTACAC	odelinsNHAYTQKAYL
XH_P44	19	19905446	19905446	Frame_Shift_Ins	INS	-	TAAACCTACAA	-	ZNF506	TTATATTGTAG	p.K385fs
XH_P44	19	20002545	20002545	Silent	SNP	G	A	G	ZNF253	c.G261A	p.K87K
XH_P44	19	20002546	20002546	Nonsense_Mutation	INS	-	TACAAACTACAT	-	ZNF253	nsTTATACAAAC	T88delinsLIQTTX
XH_P44	19	20003438	20003438	Nonsense_Mutation	INS	-	CTCTACATCTGT	-	ZNF253	CACATTCTCTAC	N386delinsPHSLHLX
XH_P44	19	20044887	20044887	Frame_Shift_Ins	INS	-	TT	-	ZNF93	.1123_1124insT	p.G375fs
XH_P44	19	20044888	20044888	Frame_Shift_Ins	INS	-	AGGATTGGTT	-	ZNF93	1125insAGGA	p.G375fs
XH_P44	19	20044962	20044962	Frame_Shift_Ins	INS	-	TAGT	-	ZNF93	198_1199insTA	p.E400fs
XH_P44	19	20045021	20045021	Nonsense_Mutation	INS	-	AGGGTTGAGG	-	ZNF93	CTACTAAGGGT	19_T420delinsHVXX
XH_P44	19	20116846	20116846	Frame_Shift_Ins	INS	-	AAGTGTAAATGAT	-	ZNF682	nsTGTGTATCAT	p.A457fs
XH_P44	19	20116978	20116978	Nonsense_Mutation	INS	-	TA	-	ZNF682	1236_1237insT	K413_I414delinsX
XH_P44	19	20116980	20116980	Frame_Shift_Ins	INS	-	AAATGTAAAGA	-	ZNF682	GCCACATCTCTT	p.K412fs
XH_P44	19	20727918	20727918	Missense_Mutation	SNP	C	G	C	ZNF737	c.G1091C	p.S364T
XH_P44	19	21132231	21132231	Nonsense_Mutation	INS	-	TTTCTTATGTTT	-	ZNF85	TGAATTTTCTTA	R241delinsQYEF5VXX
XH_P44	19	21239848	21239848	Nonsense_Mutation	INS	-	TAACATTCTTTGT	-	ZNF430	ATCATAACATTG	F244delinsFSSSX
XH_P44	19	21300098	21300098	Frame_Shift_Ins	INS	-	CATGGAATATT	-	ZNF714	TATCACATGGAA	p.K210fs
XH_P44	19	21300136	21300136	Frame_Shift_Ins	INS	-	C	-	ZNF714	c.666_667insC	p.H222fs
XH_P44	19	21300138	21300138	Frame_Shift_Ins	INS	-	ATTTTTTACAT	-	ZNF714	669insATTTTT	p.T223fs
XH_P44	19	21719461	21719461	Missense_Mutation	SNP	A	T	A	ZNF429	c.A414T	p.R138S
XH_P44	19	21719463	21719463	Missense_Mutation	SNP	G	T	G	ZNF429	c.G416T	p.C139F
XH_P44	19	21719944	21719944	Frame_Shift_Ins	INS	-	C	-	ZNF429	c.897_898insC	p.H299fs
XH_P44	19	21719946	21719946	Frame_Shift_Ins	INS	-	AGGGCTTCTCTG	-	ZNF429	TTTTGTAGGGCT	p.T300fs
XH_P44	19	21720600	21720600	Frame_Shift_Ins	INS	-	GGTT	-	ZNF429	553_1554insGC	p.S518fs
XH_P44	19	21720602	21720602	Nonsense_Mutation	INS	-	ATTTTTTTATGAC	-	ZNF429	ATGAAATTTTTT	20delinsLSTMFFMTVKVX
XH_P44	19	21910173	21910173	Missense_Mutation	SNP	A	T	A	ZNF100	c.T296A	p.V99E
XH_P44	19	21990703	21990704	Frame_Shift_Del	DEL	GC	-	GC	ZNF43	c.1940_1941del	p.G647fs
XH_P44	19	22156106	22156106	Missense_Mutation	SNP	A	C	A	ZNF208	c.T1730G	p.V577G
XH_P44	19	22271610	22271610	In_Frame_Ins	INS	-	CAACATTCATCA	-	ZNF257	31insGCAACATT	F277delinsLQHSY
XH_P44	19	22496827	22496827	In_Frame_Ins	INS	-	TCCTGCATATGT	-	ZNF729	TCACATCTTGCA	3delinsMSTSCICSQY
XH_P44	19	22497910	22497910	Nonsense_Mutation	INS	-	TGAGAAATGGTT	-	ZNF729	592insCTGAGAA	564_1565delinsVX
XH_P44	19	22498406	22498406	Frame_Shift_Ins	INS	-	CGGTTTCTTTC	-	ZNF729	2188insCGGTT	p.V729fs
XH_P44	19	22498408	22498408	Frame_Shift_Ins	INS	-	AAATTATCTTATG	-	ZNF729	nsGTATGAATTA	p.H730fs
XH_P44	19	22574713	22574713	Nonsense_Mutation	INS	-	TAACAACCTCTC	-	ZNF98	4insTAGAGGAG	A442_F443delinsX
XH_P44	19	22941531	22941531	Missense_Mutation	SNP	G	C	G	ZNF99	c.C1180G	p.Q394E
XH_P44	19	22942016	22942016	Nonsense_Mutation	INS	-	AGAAAACTACG	-	ZNF99	ATTATCTGATGT	233delinsMNYLMFSKXG
XH_P44	19	23040533	23040533	Frame_Shift_Ins	INS	-	NTTCTTTCATGT	-	ZNF723	ATATGATTTCTT	p.T280fs
XH_P44	19	23329228	23329228	Nonsense_Mutation	INS	-	CTTTATATTTGT	-	ZNF730	CACATTCTTTAT	N462delinsLPHSLYLX
XH_P44	19	23926984	23926984	Nonsense_Mutation	INS	-	ATCGACTCTCAA	-	ZNF681	68insTTTTGAGG	456delinsSGFEDRX
XH_P44	19	24102238	24102238	Frame_Shift_Ins	INS	-	GTATATATGATA	-	ZNF726	CAGTGATATATA	p.T23fs
XH_P44	19	24115842	24115842	Frame_Shift_Ins	INS	-	TGTA	-	ZNF726	924_925insTGT	p.I308fs
XH_P44	19	24115844	24115844	Frame_Shift_Ins	INS	-	CTTCAGTATGAG	-	ZNF726	CTTTTCTTCAGT	p.G309fs
XH_P44	19	24116004	24116004	Nonsense_Mutation	INS	-	ATTGATTAAAG	-	ZNF726	TGAGGATTGAT	362_H363delinsIX
XH_P44	19	24310111	24310111	Frame_Shift_Ins	INS	-	C	-	ZNF254	c.1054_1055ins	p.E352fs
XH_P44	19	24310112	24310112	Frame_Shift_Ins	INS	-	CTCTTATGCTAG	-	ZNF254	56insTCCTCTTA	p.E352fs
XH_P44	19	29698665	29698665	Nonsense_Mutation	INS	-	TTTATGTACCT	-	UQCRF51	CTTGAGGTGAC	V205delinsVLRX
XH_P44	19	33202818	33202818	Nonsense_Mutation	INS	-	CATCGAGTATTA	-	NUDT19	TAATTCCTCGA	H362delinsKILIPSSILX
XH_P44	19	33331155	33331155	Silent	SNP	G	A	G	SLC7A9	c.C1143T	p.A381A
XH_P44	19	33870306	33870306	Frame_Shift_Ins	INS	-	ATCTTCACAT	-	CEBP6	162insATCTTC	p.K54fs
XH_P44	19	34710618	34710618	Frame_Shift_Ins	INS	-	GT	-	LSM14A	c.972_973insGT	p.K324fs
XH_P44	19	34710620	34710620	Frame_Shift_Ins	INS	-	TTCTCAAAATTC	-	LSM14A	975insTTCTCAA	p.L325fs
XH_P44	19	35175419	35175419	Frame_Shift_Ins	INS	-	AGCACTGCCTTT	-	ZNF302	nsCAAAAGCACTG	p.K159fs
XH_P44	19	35251440	35251440	Frame_Shift_Ins	INS	-	AGAAGTTGAGT	-	ZNF599	266insACTCAA	p.T89fs
XH_P44	19	35434324	35434324	Nonsense_Mutation	SNP	G	T	G	ZNF30	c.G457T	p.E153X
XH_P44	19	35434325	35434325	Frame_Shift_Ins	INS	-	GCTCAGTAAT	-	ZNF30	459insGCTCAG	p.E153fs
XH_P44	19	36674043	36674043	Nonsense_Mutation	INS	-	ACATCAAAGAAT	-	ZNF565	825insAATTCTT	T275_E276delinsGILX
XH_P44	19	36674045	36674045	Missense_Mutation	SNP	C	A	C	ZNF565	c.G823T	p.G275C
XH_P44	19	36727787	36727787	Frame_Shift_Ins	INS	-	GC	-	ZNF146	c.445_446insGC	p.I149fs
XH_P44	19	36727788	36727788	Frame_Shift_Ins	INS	-	TCTCG	-	ZNF146	446_447insTCTC	p.I149fs
XH_P44	19	36940425	36940425	Frame_Shift_Ins	INS	-	TAAACATCAAAG	-	ZNF566	GGATCTTTTGAT	p.I133fs
XH_P44	19	37130451	37130451	Frame_Shift_Ins	INS	-	AGAATGTGGAA	-	ZNF461	nsGTCTTCCAC	p.I243fs
XH_P44	19	37130453	37130453	Missense_Mutation	SNP	C	T	C	ZNF461	c.G725A	p.R242K
XH_P44	19	37368718	37368718	Frame_Shift_Ins	INS	-	AAAGGCC	-	ZNF345	86_987insAAAG	p.L329fs
XH_P44	19	37368719	37368719	In_Frame_Ins	INS	-	TACCAC	-	ZNF345	87_988insTACC	b.L329delinsLYH
XH_P44	19	37619889	37619889	In_Frame_Ins	INS	-	GGG	-	ZNF420	1783_1784insGG	p.I595delinsRV
XH_P44	19	37619890	37619890	Frame_Shift_Ins	INS	-	TTTTCTC	-	ZNF420	84_1785insTTT	p.I595fs
XH_P44	19	37853830	37853830	In_Frame_Ins	INS	-	TTTCCCCCA	-	HKR1	3_954insTTTCCC	A318delinsAFPQ
XH_P44	19	37854139	37854139	Frame_Shift_Ins	INS	-	TGTGTCCTCTTG	-	HKR1	1263insTGTGTC	p.K421fs
XH_P44	19	37903761	37903761	In_Frame_Ins	INS	-	TGAGTGTGGCA	-	ZNF569	1322insTTGCCA	H441delinsLATLN
XH_P44	19	37975780	37975780	Nonsense_Mutation	INS	-	ATCTGTGCTAA	-	ZNF570	nsGATGATCTGT	R378delinsWIMCCX
XH_P44	19	38027942	38027942	Frame_Shift_Ins	INS	-	AAATGGAATTC	-	ZNF793	nsGCACAAATGG	p.D128fs
XH_P44	19	38102855	38102855	Frame_Shift_Ins	INS	-	GACGATTTTCTT	-	ZNF540	79insAGACGAT	p.S193fs
XH_P44	19	38104133	38104133	In_Frame_Ins	INS	-	ATTATATAGGCT	-	ZNF540	857insCATTTATA	Y619delinsYIYRAF
XH_P44	19	38126357	38126357	In_Frame_Ins	INS	-	GAA	-	ZFP30	1084_1085insT	p.T362delinsIP
XH_P44	19	38126358	38126358	Frame_Shift_Ins	INS	-	TGAAAGGCCTTT	-	ZFP30	4insTCTAAAGG	p.T362fs
XH_P44	19	38134176	38134176	Frame_Shift_Ins	INS	-	CTTCCACTTATC	-	ZFP30	25insTGATAAGT	p.R75fs
XH_P44	19	38229649	38229649	Frame_Shift_Ins	INS	-	TGTAAGACCGTA	-	ZNF573	ACTCTTTACGGT	p.P493fs
XH_P44	19	38383648	38383648	Frame_Shift_Ins	INS	-	AAGGATGAAAG	-	WDR87	2695insCTTTC	p.V899fs
XH_P44	19	38383650	38383650	Missense_Mutation	SNP	C	G	C	WDR87	c.G2693C	p.S898T
XH_P44	19	38847150	38847150	Missense_Mutation	SNP	C	T	C	CATSPERG	c.C1162T	p.P388S
XH_P44	19	38847151	38847151	Frame_Shift_Ins	INS	-	TT	-	CATSPERG	.1163_1164insT	p.P388fs
XH_P44	19	39076799	39076799	Nonsense_Mutation	INS	-	CTCGCTCTCTCA	-	RYR1	nsCCTAATCTCC	T74_T4975delinsHPX
XH_P44	19	39879776	39879776	Frame_Shift_Ins	INS	-	TGACTAGACCC	-	PAF1	94insTGGGTCTG	p.Q165fs
XH_P44	19	40554662	40554662	Frame_Shift_Ins	INS	-	TTATGTCTGGTC	-	ZNF780B	1insTGACCAGC	p.Q17fs
XH_P44	19	40580574	40580574	Frame_Shift_Ins	INS	-	TGTGGTTCAAAC	-	ZNF780A	nsTAACGTTTGA	p.K592fs
XH_P44	19	41798170	41798170	Missense_Mutation	SNP	C	A	C	HNRNPUL1	c.C753A	p.D251E
XH_P44	19	42083820	42083820	Missense_Mutation	SNP	C	A	C	CEACAM21	c.C333A	p.N111K
XH_P44	19	42083821	42083821	Frame_Shift_Ins	INS	-	GGCTAGGAAAG	-	CEACAM21	GTGAGGCTAGC	p.V112fs
XH_P44	19	42265366	42265366	Nonsense_Mutation	INS	-	GATTTGAAGG	-	CEACAM6	635insGATTTC	p.S212delinsX
XH_P44	19	42265367	42265367	Missense_Mutation	SNP	C	G	C	CEACAM6	c.C635G	p.S212C
XH_P44	19	42301579	42301579	Missense_Mutation	SNP	G	C	G	CEACAM3	c.G123C	p.M41I

XH_P44	19	42301581	42301581	Nonsense_Mutation	INS	-	GGTCCCAATAT	-	CEACAM3	ACATGGGTCC	42delinsPIHGSQYX
XH_P44	19	42582931	42582931	In_Frame_Ins	INS	-	TCCTAATACCTT	-	ZNF574	444insTCTCAAT	T148delinsTPNTL
XH_P44	19	43372441	43372441	Frame_Shift_Ins	INS	-	GTCTG	-	PSG1	775_776insCAGA	p.L259fs
XH_P44	19	43372442	43372442	Frame_Shift_Ins	INS	-	AGTCTCTG	-	PSG1	4_775insCAGAC	p.L259fs
XH_P44	19	43411278	43411278	Frame_Shift_Ins	INS	-	TGATAGTCAAAG	-	PSG6	CAGAGACTTTGA	p.G346fs
XH_P44	19	43680266	43680266	Nonsense_Mutation	INS	-	AAACGACCCCT	-	PSG5	TTTCATAGGGTCC	55_5156delinsNSX
XH_P44	19	44352509	44352509	Frame_Shift_Ins	INS	-	TG	-	ZNF283	1339_1340insT	p.L447fs
XH_P44	19	44352511	44352511	Frame_Shift_Ins	INS	-	TGGATTCTTTCA	-	ZNF283	1342insTGGATT	p.L447fs
XH_P44	19	44469460	44469460	Frame_Shift_Ins	INS	-	CATCCTTG	-	ZNF221	4_285insCATCC	p.Q95fs
XH_P44	19	44469462	44469462	Frame_Shift_Ins	INS	-	T	-	ZNF221	c.286_287insT	p.R96fs
XH_P44	19	44514931	44514931	Frame_Shift_Ins	INS	-	TCATTGCATGT	-	ZNF230	741insTCATTG	p.T247fs
XH_P44	19	44514933	44514933	Nonsense_Mutation	SNP	G	T	G	ZNF230	c.G742T	p.G248X
XH_P44	19	44536531	44536531	Frame_Shift_Ins	INS	-	CCTCTGATGAAT	-	ZNF222	5insACCCCTCTGA	p.G275fs
XH_P44	19	44537125	44537125	Missense_Mutation	SNP	G	T	G	ZNF222	c.G1418T	p.R473L
XH_P44	19	44537126	44537126	Frame_Shift_Ins	INS	-	CCACATCTTTAC	-	ZNF222	1insTCCACAT	p.R473fs
XH_P44	19	44570988	44570988	In_Frame_Ins	INS	-	TAATGTTTCTCTC	-	ZNF223	nsATTATAAATG	B39delinsTIMFLSH
XH_P44	19	44590460	44590460	In_Frame_Ins	INS	-	TTTCTG	-	ZNF284	829_830insTTTC	H277delinsLSD
XH_P44	19	44590462	44590462	Frame_Shift_Ins	INS	-	GAAGA	-	ZNF284	831_832insGAA	p.H277fs
XH_P44	19	44636593	44636593	Frame_Shift_Ins	INS	-	TG	-	ZNF225	1826_1827insT	p.S609fs
XH_P44	19	44653037	44653037	Frame_Shift_Ins	INS	-	AATAG	-	ZNF234	129_130insAAT	p.A43fs
XH_P44	19	44653038	44653038	Frame_Shift_Ins	INS	-	CTTCAAT	-	ZNF234	30_131insCTTC	p.L44fs
XH_P44	19	44891993	44891993	Nonsense_Mutation	INS	-	ATGATACAGATG	-	ZNF285	4insAGGATCTG	V138_Q139delinsX
XH_P44	19	44892220	44892220	Frame_Shift_Ins	INS	-	TGACCAG	-	ZNF285	6_187insCTCGG	p.L63fs
XH_P44	19	44934119	44934119	Frame_Shift_Ins	INS	-	ATTTGGTCGAAG	-	ZNF229	19insACTTCGAC	p.D273fs
XH_P44	19	46206288	46206288	Frame_Shift_Ins	INS	-	CTTTTTTTTTTTT	-	QPCTL	49insACTTTTTTTT	p.A283fs
XH_P44	19	47425126	47425126	In_Frame_Ins	INS	-	TTTGAAATGGTC	-	ARHGAP35	95insGCTTAGA	L065delinsELRMVF
XH_P44	19	47585552	47585552	Nonsense_Mutation	INS	-	ATCTCATTTAACT	-	ZC3H4	219insTGTAA	A407_D408delinsCX
XH_P44	19	49793601	49793601	In_Frame_Ins	INS	-	GAACAAAGTA	-	SLC6A16	1990insGTACTT	L664delinsVLCF1
XH_P44	19	49793946	49793946	Frame_Shift_Ins	INS	-	TCCTTTTCTCTT	-	SLC6A16	7insCCAAAGAGA	p.P619fs
XH_P44	19	49956673	49956673	Missense_Mutation	SNP	G	A	G	ALDH16A1	c.G85A	p.P354T
XH_P44	19	50243098	50243098	Frame_Shift_Ins	INS	-	TATTTATTTTAA	-	TSKS	nsTTAATTAATA	p.T572fs
XH_P44	19	50462136	50462136	Missense_Mutation	SNP	C	T	C	SIGLEC11	c.G1127A	p.G376D
XH_P44	19	50550250	50550250	Nonsense_Mutation	INS	-	GGGTGAAGGC	-	ZNF473	AGCTCTGGGTG	38_F839delinsAFRX
XH_P44	19	50958892	50958892	Frame_Shift_Ins	INS	-	GCTGACCCCTGA	-	MYBPC2	CTTCTGCTGAC	p.L777fs
XH_P44	19	51466776	51466776	Missense_Mutation	SNP	T	A	T	KLK6	c.A227T	p.N76I
XH_P44	19	51466777	51466777	In_Frame_Ins	INS	-	GGGAGTGGGA	-	KLK6	226insTCCCCAG	N76delinsFPLPN
XH_P44	19	51639455	51639455	In_Frame_Ins	INS	-	AAACTGCAAAAA	-	SIGLEC9	41insAAAACTG	p.X480delinsX
XH_P44	19	51656437	51656437	Missense_Mutation	SNP	C	T	C	SIGLEC7	c.C1060T	p.P354S
XH_P44	19	51656438	51656438	Frame_Shift_Ins	INS	-	ACAAGTTGTT	-	SIGLEC7	1062insACAAC	p.P354fs
XH_P44	19	52131340	52131340	Nonsense_Mutation	INS	-	CAGTTTACTGTG	-	SIGLEC5	744insCACAGTA	L248delinsTVNX
XH_P44	19	52519978	52519978	Frame_Shift_Ins	INS	-	GAGAAAAATCTT	-	ZNF614	8insTGTAAGATT	p.E291fs
XH_P44	19	52658179	52658179	Frame_Shift_Ins	INS	-	ATCCCCCTTATT	-	ZNF836	757insCAATAAA	p.T191fs
XH_P44	19	52663755	52663755	In_Frame_Ins	INS	-	CCCTTTTTTGAA	-	ZNF836	AGACATTCAA	A35delinsEDIQKGD5
XH_P44	19	52825845	52825845	Frame_Shift_Ins	INS	-	CCAGTATGAAT	-	ZNF480	TTTCTCTCCAGT	p.L405fs
XH_P44	19	52919808	52919808	Nonsense_Mutation	INS	-	TACATTGTGAAG	-	ZNF528	04insGTTACATT	B8_A569delinsLHLHX
XH_P44	19	53015232	53015232	In_Frame_Ins	INS	-	CATTTG	-	ZNF578	98_1599insCAT	H533delinsHIC
XH_P44	19	53015234	53015234	Frame_Shift_Ins	INS	-	AGATTTCTCTC	-	ZNF578	1601insAGATT	p.T534fs
XH_P44	19	53058466	53058466	Frame_Shift_Ins	INS	-	GATTT	-	ZNF808	297_2298insGA	p.N766fs
XH_P44	19	53058467	53058467	Frame_Shift_Ins	INS	-	TCTCCACCAT	-	ZNF808	2299insTCTCC	p.N766fs
XH_P44	19	53085674	53085674	In_Frame_Ins	INS	-	ATCTTCATCATG	-	ZNF701	insAACATCTTCA	121delinsRTSSCI
XH_P44	19	53085676	53085676	Missense_Mutation	SNP	A	T	A	ZNF701	c.A364T	p.S122C
XH_P44	19	53086276	53086276	Frame_Shift_Ins	INS	-	CCTAAATGGATT	-	ZNF701	TGTCTCTCAAT	p.G322fs
XH_P44	19	53116429	53116429	In_Frame_Ins	INS	-	ACATACAATAAT	-	ZNF83	nsTATAAATAT	63delinsGINYCM5Y
XH_P44	19	53209281	53209281	Frame_Shift_Ins	INS	-	ATAGACTTCATG	-	ZNF611	TCCACCATGAAC	p.Y343fs
XH_P44	19	53209944	53209944	Nonsense_Mutation	INS	-	AACTATGGGAA	-	ZNF611	4insTTATTCCCA	22_N123delinsLFPX
XH_P44	19	53217296	53217296	In_Frame_Ins	INS	-	SCCTCAGCCTCC	-	ZNF611	2insCAGGAGGC	L54delinsFRRLRQ
XH_P44	19	53269555	53269555	Frame_Shift_Ins	INS	-	AGACTTCATAG	-	ZNF600	insACCACTATGA	p.L485fs
XH_P44	19	53270533	53270533	In_Frame_Ins	INS	-	GTCAAAATTCAG	-	ZNF600	6insGGCTGAAT	159delinsGLNFDQ
XH_P44	19	53384568	53384568	In_Frame_Ins	INS	-	GTGACCAAG	-	ZNF320	0_811insCCTTG	K271delinsPCHK
XH_P44	19	53391429	53391429	Frame_Shift_Ins	INS	-	T	-	ZNF320	c.92_93insA	p.T31fs
XH_P44	19	53453962	53453962	Frame_Shift_Ins	INS	-	ATAAATGTGGC	-	ZNF816	5insTCTTGCCAC	p.L356fs
XH_P44	19	53643737	53643737	Frame_Shift_Ins	INS	-	GAGATTCTTTGA	-	ZNF347	7insTTTTCAAG	p.R783fs
XH_P44	19	53854549	53854549	In_Frame_Ins	INS	-	CTTTTCTCCATT	-	ZNF845	2insTATCTTTCTC	207delinsEYLSFPF
XH_P44	19	53856440	53856440	Nonsense_Mutation	INS	-	TGT	-	ZNF845	2512_2513insT	Qp.K838delinsMX
XH_P44	19	53856441	53856441	In_Frame_Ins	INS	-	AGGGAT	-	ZNF845	13_2514insAGG	K838delinsKGM
XH_P44	19	53959195	53959195	Nonsense_Mutation	INS	-	AAACTGTAAGC	-	ZNF761	GATCTGAAACT	478_5479delinsKIX
XH_P44	19	53959648	53959648	Silent	SNP	C	T	C	ZNF761	c.C188T	p.T629T
XH_P44	19	54081038	54081038	In_Frame_Ins	INS	-	CTTCTGATGCTG	-	ZNF331	5insGATCTTCTG	408delinsVDLML5
XH_P44	19	54135365	54135365	Missense_Mutation	SNP	C	A	C	DPRX	c.C5A	p.P2Q
XH_P44	19	54135366	54135366	Frame_Shift_Ins	INS	-	TTCTTTTTTTCTT	-	DPRX	CTTTTCTTTTTT	p.P2fs
XH_P44	19	54140183	54140183	Missense_Mutation	SNP	G	T	G	DPRX	c.G517T	p.A173S
XH_P44	19	54140185	54140185	In_Frame_Ins	INS	-	GTGATTCTTGAA	-	DPRX	520insGTGATT	A173delinsAVILE
XH_P44	19	54403688	54403688	Frame_Shift_Ins	INS	-	TGCATGGGCTTA	-	PRKCG	390insGTGCATG	p.E463fs
XH_P44	19	54647477	54647477	Frame_Shift_Ins	INS	-	TAGCTTCTTAAT	-	CNOT3	nsCTTGAGCTTC	p.L84fs
XH_P44	19	55494630	55494632	In_Frame_Del	DEL	GAA	-	GAA	NLRP2	c.1498_1500del	p.500_500del
XH_P44	19	55790886	55790886	In_Frame_Ins	INS	-	GCC	-	HSPBP1	228_229insGG	p.S77delinsGS
XH_P44	19	56156080	56156080	Frame_Shift_Ins	INS	-	TTGAGACCATG	-	ZNF581	44insGTTGAGA	p.P48fs
XH_P44	19	56156082	56156082	Missense_Mutation	SNP	A	G	A	ZNF581	c.A145G	p.R49G
XH_P44	19	56435987	56435987	Frame_Shift_Ins	INS	-	TATTTCTTATTA	-	NLRP13	6insTTTAATAAG	p.Q142fs
XH_P44	19	56953392	56953392	Frame_Shift_Ins	INS	-	AAAAACTATACA	-	ZNF667	2insTCTGTATAC	p.H324fs
XH_P44	19	56953394	56953394	Frame_Shift_Ins	INS	-	CAAT	-	ZNF667	969_970insATT	p.H324fs
XH_P44	19	56953733	56953733	Frame_Shift_Ins	INS	-	TGTACATAAAAG	-	ZNF667	31insTCTTTTAT	p.Q211fs
XH_P44	19	57088665	57088665	Frame_Shift_Ins	INS	-	TTTTTAA	-	ZNF470	68_869insTTTTT	p.G290fs
XH_P44	19	57088666	57088666	Frame_Shift_Ins	INS	-	TTTCTTATCTGT	-	ZNF470	0insCTTTTCTTA	p.G290fs
XH_P44	19	57286555	57286555	Frame_Shift_Ins	INS	-	CGGAATTTCATA	-	ZIM2	085insATATGA	p.A362fs
XH_P44	19	57867697	57867697	Frame_Shift_Ins	INS	-	GTTCTCG	-	ZNF304	50_461insGTTCT	p.F154fs
XH_P44	19	57889173	57889173	Frame_Shift_Ins	INS	-	CTGATGTCTA	-	ZNF547	830insCTGATG	p.F277fs
XH_P44	19	57967159	57967159	Frame_Shift_Ins	INS	-	TTGTCTCTCATCA	-	VN1R1	5insCATGATGAG	p.L232fs
XH_P44	19	58018201	58018201	In_Frame_Ins	INS	-	CCC	-	ZNF773	c.735_736insCC	p.P245delinsPP
XH_P44	19	58018203	58018203	Frame_Shift_Ins	INS	-	CTTT	-	ZNF773	737_738insCTT	p.Y246fs
XH_P44	19	58048864	58048864	Frame_Shift_Ins	INS	-	GGGATGGAAG	-	ZNF549	5CATTTGGGATG	p.E151fs
XH_P44	19	58084420	58084420	Nonsense_Mutation	INS	-	AAAGCTTCAGCC	-	ZNF416	52insAGGCTGA	A84_L285delinsQGX
XH_P44	19	58152805	58152805	Frame_Shift_Ins	INS	-	CAAGTGTGTC	-	ZNF211	769insCAAGTC	p.E256fs
XH_P44	19	58187892	58187892	Frame_Shift_Ins	INS	-	GTCCTTGCCCTT	-	ZSCAN4	80insGGTCTCTG	p.L127fs
XH_P44	19	58189550	58189550	Nonsense_Mutation	INS	-	ACATCTCTTAA	-	ZSCAN4	0insTGACATCT	Qp.Q193delinsQX
XH_P44	19	58199045	58199045	In_Frame_Ins	INS	-	CTGATAAGGCC	-	ZNF551	1319insCTGATA	L440delinsTDKAF
XH_P44	19	58216349	58216349	Splice_Site	INS	-	CTCTTTTCTCTAT	-	ZNF154	.	.
XH_P44	19	58232560	58232560	Nonsense_Mutation	INS	-	TTTTTAGCAGTA	-	ZNF671	AGACTTACTGCT	200_T201delinsDX

XH_P44	19	58290876	58290876	Frame_Shift_Ins	INS	-	TG	-	ZNF586	c.921_922insTG	p.H307fs
XH_P44	19	58290878	58290878	Nonsense_Mutation	INS	-	CTCATAAGGCC	-	ZNF586	924insCTCATAA	08_Q309delinsHSX
XH_P44	19	58352780	58352780	In_Frame_Ins	INS	-	AGTTTCCAC	-	ZNF587B	8_739insAGTTT	E246delinsESFH
XH_P44	19	58385600	58385600	In_Frame_Ins	INS	-	ACG	-	ZNF814	1157_1158insCG	G386delinsGV
XH_P44	19	58385602	58385602	Frame_Shift_Ins	INS	-	GGAGAAAG	-	ZNF814	55_115insCTTT	p.G386fs
XH_P44	19	58421206	58421206	Nonsense_Mutation	INS	-	GATGGATGTT	-	ZNF417	437insAACATC	146_Y147delinsX
XH_P44	19	58639476	58639476	In_Frame_Ins	INS	-	GTGAATTGATGA	-	ZNF329	395insATTTCATC	R465delinsRFINSL
XH_P44	19	58639477	58639477	Missense_Mutation	SNP	C	G	C	ZNF329	c.G1394C	p.R465T
XH_P44	19	58945011	58945011	Frame_Shift_Ins	INS	-	AAGATTCAATCC	-	ZNF132	insCTCAGGTAT	p.K600fs
XH_P44	20	76893	76893	In_Frame_Ins	INS	-	TTCAAAGCTACC	-	DEFB125	GGGGTTCAAAG	02delinsFLGFKATCR
XH_P44	20	1460484	1460484	In_Frame_Ins	INS	-	ACAATACATAT	-	SIRPB2	5TACAAATATGT	04delinsDTNMYCCI
XH_P44	20	1902349	1902349	Frame_Shift_Ins	INS	-	GCTCATT	-	SIRPA	45_746insGCTC	p.T249fs
XH_P44	20	1961145	1961145	In_Frame_Ins	INS	-	CAGCTCAGC	-	PDYN	589insGCTGA	S197delinsAEELS
XH_P44	20	2464779	2464779	Frame_Shift_Ins	INS	-	TAAGTCCATCCT	-	ZNF343	TATTGAGGATG	p.R186fs
XH_P44	20	2465116	2465116	Frame_Shift_Ins	INS	-	CGAGG	-	ZNF343	220_221insCCTC	p.W74fs
XH_P44	20	2465118	2465118	Missense_Mutation	SNP	A	C	A	ZNF343	c.T219G	p.C73W
XH_P44	20	2840427	2840427	Frame_Shift_Ins	INS	-	AGGGAAGGATG	-	VPS16	117insAGGGAA	p.A39fs
XH_P44	20	3543080	3543080	Frame_Shift_Ins	INS	-	TA	-	ATRN	1257_1258insT	p.Y419fs
XH_P44	20	3543081	3543081	Nonsense_Mutation	INS	-	AAAGAGCTTAGC	-	ATRN	TGTCCAAAGAG	Y421delinsKMSKELRAX
XH_P44	20	3565508	3565508	Frame_Shift_Ins	INS	-	AGTCAAAAATA	-	ATRN	insCTTAGAGTCA	p.W939fs
XH_P44	20	3944654	3944654	Frame_Shift_Ins	INS	-	AAAAATTAAGAT	-	RNF24	AAGCCATCTTAA	p.D4fs
XH_P44	20	5903631	5903631	In_Frame_Ins	INS	-	TATGTGCTTCT	-	CHGB	842insTATGTG	P281delinsLCVFS
XH_P44	20	7963064	7963064	Frame_Shift_Ins	INS	-	GCAGTTTGTG	-	TMX4	884insTACAAA	p.E295fs
XH_P44	20	7980403	7980403	Nonsense_Mutation	INS	-	TTACACTAAGCC	-	TMX4	3insTGGCTTAG	G148delinsVAX
XH_P44	20	9400517	9400517	In_Frame_Ins	INS	-	TTTTTATCC	-	PLCB4	9_2080insTTTT	T693delinsTFLS
XH_P44	20	9404441	9404441	In_Frame_Ins	INS	-	AATGAATGT	-	PLCB4	0_2331insAATG	D777delinsEMNV
XH_P44	20	9404443	9404443	In_Frame_Ins	INS	-	AAGAT	-	PLCB4	32_2333insAAG	N778delinsDY
XH_P44	20	9510382	9510382	Nonsense_Mutation	INS	-	TCGTCTACATA	-	LAMP5	insTAATCGTTCT	209delinsLNRSTX
XH_P44	20	10023941	10023941	Nonsense_Mutation	INS	-	CACAACACACAT	-	ANKEF1	sCAGTCACAACC	G174delinsNSHNHIX
XH_P44	20	10030325	10030325	Frame_Shift_Ins	INS	-	ATCTAAATTTCT	-	ANKEF1	1109insATCTAA	p.A370fs
XH_P44	20	11904177	11904177	In_Frame_Ins	INS	-	ACTCTTTTA	-	BTBD3	9_980insACTCT	L327delinsHSFI
XH_P44	20	13756543	13756543	Frame_Shift_Ins	INS	-	TGAT	-	ESF1	010_1011insAT	p.D337fs
XH_P44	20	13756545	13756545	Frame_Shift_Ins	INS	-	AAATTTTGATATC	-	ESF1	sTATTCATATC	p.D337fs
XH_P44	20	13830174	13830174	Nonsense_Mutation	INS	-	AGACCTTCTCGT	-	SEL1L2	insCTAAGCAGG	V563delinsTKQEVX
XH_P44	20	14306675	14306675	In_Frame_Ins	INS	-	GAAAGGATGAC	-	FLRT3	478insTAGTCAT	T493delinsVILSS
XH_P44	20	14306868	14306868	Nonsense_Mutation	INS	-	CTTACAAAACC	-	FLRT3	AAATTGGGGTTT	A430delinsGKLGLFX
XH_P44	20	14306996	14306996	Frame_Shift_Ins	INS	-	TATAACAGAAA	-	FLRT3	57insTTGTTTCT	p.T386fs
XH_P44	20	16355028	16355028	Frame_Shift_Ins	INS	-	5AACTACTTTGT	-	KIF16B	224insTACAAA	p.K1075fs
XH_P44	20	16355030	16355030	Frame_Shift_Ins	INS	-	5GAGGGCTCTAT	-	KIF16B	222insAATAGAC	p.I1074fs
XH_P44	20	16385473	16385473	Frame_Shift_Ins	INS	-	ACAGTTTTGCAT	-	KIF16B	insGAAATGCA	p.M590fs
XH_P44	20	17950946	17950946	In_Frame_Ins	INS	-	TCTTCATATGGG	-	MGME1	CCACTTCTTCAT	8delinsLVHFFWVHF
XH_P44	20	18531793	18531793	Nonsense_Mutation	INS	-	GCTTCTGAC	-	SEC23B	5_1967insGCTTC	F656delinsCFX
XH_P44	20	19261698	19261698	Nonsense_Mutation	SNP	G	T	G	SLC24A3	c.G238T	p.G80X
XH_P44	20	19261700	19261700	Frame_Shift_Ins	INS	-	AGGCTTC	-	SLC24A3	40_241insAGGC	p.G80fs
XH_P44	20	19664840	19664840	Frame_Shift_Ins	INS	-	TCATCTTCTTTG	-	SLC24A3	923insTCATTCT	p.S308fs
XH_P44	20	19665995	19665995	In_Frame_Ins	INS	-	TCCAG	-	SLC24A3	14_1315insTCC	F438delinsFST
XH_P44	20	20269451	20269451	Frame_Shift_Ins	INS	-	CACCTCTCATTT	-	CFAP61	96insATCATCT	p.S999fs
XH_P44	20	20269453	20269453	In_Frame_Ins	INS	-	TTCCA	-	CFAP61	97_2998insTTC	S999delinsSFP
XH_P44	20	30037933	30037933	In_Frame_Ins	INS	-	GATTGTCTT	-	DEFB123	0_161insGATTG	p.V54delinsGLSL
XH_P44	20	30365410	30365410	In_Frame_Ins	INS	-	5CAGTCCCTTTGT	-	TPX2	52insTCCAGTCC	T284delinsTPVLL
XH_P44	20	32217658	32217658	In_Frame_Ins	INS	-	TTT	-	CBFA2T2	1166_1167insT	P.K389delinsNS
XH_P44	20	32217659	32217659	Frame_Shift_Ins	INS	-	5GTTTCTTAAAG	-	CBFA2T2	168insGGTTCC	p.K389fs
XH_P44	20	32295769	32295769	Nonsense_Mutation	INS	-	AATCAATAGAGA	-	PXMP4	CTCTTTCTCTAT	1delinsTFLGPFPLYX
XH_P44	20	32848322	32848322	Frame_Shift_Ins	INS	-	TGTTGGAG	-	ASIP	2_143insTGGTG	p.ASIP
XH_P44	20	33331131	33331131	Missense_Mutation	SNP	G	A	G	NCOA6	c.C2929T	p.P977S
XH_P44	20	33331132	33331132	Frame_Shift_Ins	INS	-	AAACAAGAA	-	NCOA6	7_2928insTTCTT	p.Q976fs
XH_P44	20	33337821	33337821	Nonsense_Mutation	INS	-	ACTACA	-	NCOA6	76_2177insTGT	p.Q726delinsLX
XH_P44	20	33337823	33337823	Frame_Shift_Ins	INS	-	ATAACGATGTCA	-	NCOA6	75insACTGACAT	p.K725fs
XH_P44	20	33703692	33703692	Nonsense_Mutation	INS	-	CTGTTAGTTCGG	-	EDEM2	170insCCGGAAC	90_F391delinsSPNX
XH_P44	20	34053961	34053961	In_Frame_Ins	INS	-	AATTTTCCATTG	-	CEP250	425insAATTTTC	T142delinsKFSIA
XH_P44	20	34060551	34060551	Frame_Shift_Ins	INS	-	CCACC	-	CEP250	104_1105insCC	p.S368fs
XH_P44	20	34218888	34218888	Nonsense_Mutation	INS	-	TTCAGTTTCAG	-	CPNE1	930insCTGAAA	310_T311delinsPX
XH_P44	20	34241356	34241356	Frame_Shift_Ins	INS	-	CAAAATGCC	-	RBM12	8_1889insGGCA	p.N630fs
XH_P44	20	34243128	34243128	Frame_Shift_Ins	INS	-	G	-	RBM12	c.116_117insC	p.E39fs
XH_P44	20	34243129	34243129	Nonsense_Mutation	INS	-	AGTTACTGC	-	RBM12	5_116insGCAGT	E39delinsGSNX
XH_P44	20	34596348	34596348	Frame_Shift_Ins	INS	-	AAAA	-	CNBD2	100_1101insAA	p.I367fs
XH_P44	20	34596350	34596350	Frame_Shift_Ins	INS	-	TGTGGCTTCCA	-	CNBD2	103insCTGTGG	p.R368fs
XH_P44	20	34611608	34611608	In_Frame_Ins	INS	-	GTTTCGCTGTG	-	CNBD2	1343insGTTTCC	I448delinsSFAVV
XH_P44	20	35395197	35395197	In_Frame_Ins	INS	-	GAGTGCAGT	-	DSN1	5_156insACTGCG	F52delinsLHSS
XH_P44	20	35672548	35672548	Frame_Shift_Ins	INS	-	CTCCCTAGCTGT	-	RBL1	insTTACAGTCA	p.D144fs
XH_P44	20	36641191	36641191	Frame_Shift_Ins	INS	-	TGGG	-	TTI1	027_1028insCC	p.E343fs
XH_P44	20	36641192	36641192	In_Frame_Ins	INS	-	CCAAAA	-	TTI1	26_1027insTTT	E343delinsFWE
XH_P44	20	36641546	36641546	Frame_Shift_Ins	INS	-	GATAATTGAGTC	-	TTI1	73insACACTAC	p.F225fs
XH_P44	20	36642043	36642043	In_Frame_Ins	INS	-	ACT	-	TTI1	175_176insAG	p.T59delinsKS
XH_P44	20	36642045	36642045	Frame_Shift_Ins	INS	-	GCACATT	-	TTI1	73_174insAATG	p.F58fs
XH_P44	20	39704907	39704907	Nonsense_Mutation	INS	-	5GTTCAAGTAGA	-	TOP1	53insAGGTTCAA	B4_D85delinsRRFKX
XH_P44	20	39729964	39729964	Frame_Shift_Ins	INS	-	GTAG	-	TOP1	279_1280insGT	p.I427fs
XH_P44	20	39729966	39729966	Frame_Shift_Ins	INS	-	CCACCTT	-	TOP1	81_1282insCCA	p.I427fs
XH_P44	20	39750644	39750644	Splice_Site	SNP	A	T	A	TOP1	.	.
XH_P44	20	39832718	39832718	Missense_Mutation	SNP	A	C	A	ZHX3	c.T839G	p.V280G
XH_P44	20	39832719	39832719	In_Frame_Ins	INS	-	GGAAAAAGA	-	ZHX3	7_838insTCTTT	V280delinsFSV
XH_P44	20	41420046	41420046	In_Frame_Ins	INS	-	TTTTACCAT	-	PTPRT	275insATGGT	L92delinsHGKM
XH_P44	20	41420047	41420047	Frame_Shift_Ins	INS	-	GTTTATTTTT	-	PTPRT	274insAAAAAT	p.L92fs
XH_P44	20	42328634	42328634	Frame_Shift_Ins	INS	-	CTGT	-	MYBL2	829_830insCTG	p.I277fs
XH_P44	20	42355293	42355293	Frame_Shift_Ins	INS	-	CGCTAAT	-	GTSF1L	41_42insATTAG	p.H144fs
XH_P44	20	42355295	42355295	Frame_Shift_Ins	INS	-	CC	-	GTSF1L	c.39_40insGG	p.H144fs
XH_P44	20	42935437	42935437	Nonsense_Mutation	INS	-	GCTAATCTATTT	-	FITM2	TTGAAAAATAG	206_L207delinsYIX
XH_P44	20	43547679	43547679	Frame_Shift_Ins	INS	-	AGGCTTA	-	PABPC1L	86_637insAGGC	p.S212fs
XH_P44	20	44682338	44682352	Frame_Shift_Del	DEL	TGGAGATGG	-	GTGGAAGATGGT	SLC12A5	c.2738_2748del	p.V913fs
XH_P44	20	44695758	44695758	Nonsense_Mutation	INS	-	TAGTCTCTAAGC	-	NCOA5	nsAGTGCCTAG	p.Q84delinsSAX
XH_P44	20	44695760	44695760	Missense_Mutation	SNP	A	T	A	NCOA5	c.T248A	p.I83N
XH_P44	20	45130033	45130033	Frame_Shift_Ins	INS	-	TAAAACTTATAT	-	ZNF334	TACATTTATAAG	p.I649fs
XH_P44	20	45130882	45130882	Frame_Shift_Ins	INS	-	G	-	ZNF334	c.1095_1096ins	p.V366fs
XH_P44	20	45130884	45130884	Nonsense_Mutation	INS	-	ATCAGCCCT	-	ZNF334	1094insAGGG	V365delinsEGX
XH_P44	20	46267871	46267871	Frame_Shift_Ins	INS	-	CAAGAATGCTCT	-	NCOA3	33insCCCAAGA	p.M878fs
XH_P44	20	47258704	47258704	Splice_Site	SNP	A	T	A	PREX1	.	.
XH_P44	20	47587811	47587811	Frame_Shift_Ins	INS	-	AAAATGTCAAAC	-	ARFGEF2	AAGAAAAAATG	p.P449fs
XH_P44	20	47602090	47602090	In_Frame_Ins	INS	-	CAGCAG	-	ARFGEF2	16_2217insCAG	A739delinsASS

XH_P44	20	47688907	47688907	Nonsense_Mutation	INS	-	AATGCTAACATA	-	CSE1L	ACTCTAATGCTA	Z86delinsEFQHTTLM	TX
XH_P44	20	47708662	47708662	Nonsense_Mutation	INS	-	ACCTCTGGAACA	-	CSE1L	AAACCAACCTCT	759_K760delins	PX
XH_P44	20	47734946	47734946	Splice_Site	INS	-	ATTGCGTIT	-	STAU1	.	.	
XH_P44	20	47892370	47892370	Nonsense_Mutation	INS	-	AAAGAATGACT	-	ZNF1	CCATAGCATCTC	E3_R4delins	PX
XH_P44	20	47991402	47991402	Frame_Shift_Ins	INS	-	GTCT	-	KCNB1	694_695insAGA	p.V232fs	
XH_P44	20	49510144	49510144	In_Frame_Ins	INS	-	TATGTACAATCT	-	ADNP	CATTACAGATTG	69delinsITDCTCT	YFP
XH_P44	20	50286578	50286578	Nonsense_Mutation	INS	-	TCATTGTTTTTT	-	ATP9A	CTTAAAAAAA	S417delins	SEYAX
XH_P44	20	50782537	50782537	Frame_Shift_Ins	INS	-	AGGCCCTTGA	-	ZFP64	314insTTCAAA	p.H105fs	
XH_P44	20	51870395	51870395	Frame_Shift_Ins	INS	-	CTTTTATTTCTC	-	TSH2Z	insCTTCTTTTAT	p.L130fs	
XH_P44	20	51870396	51870396	Silent	SNP	G	T	G	TSH2Z	c.G390T	p.L130L	
XH_P44	20	55047460	55047460	Frame_Shift_Ins	INS	-	GGGCTTGCTC	-	RTFDC1	149insGGGTCT	p.M50fs	
XH_P44	20	55213056	55213056	Frame_Shift_Ins	INS	-	TAATACTAATAG	-	TFAP2C	41insTTTAAATAC	p.K447fs	
XH_P44	20	56094398	56094398	Frame_Shift_Ins	INS	-	TCCACCTGTTT	-	CTCF	4insAAACAGGT	p.F2fs	
XH_P44	20	56098747	56098747	Nonsense_Mutation	INS	-	ATTATACATGAA	-	CTCF	ATTGATTTCAGT	172delinsILLISV	XV
XH_P44	20	56793727	56793731	Frame_Shift_Del	DEL	TCTCC	-	TCTCC	ANKRD60	c.858_862del	p.G286fs	
XH_P44	20	57598831	57598831	In_Frame_Ins	INS	-	ATCGTCCAGGT	-	TUBB1	350insATCGTCC	L117delins	HRPRL
XH_P44	20	58494633	58494633	Nonsense_Mutation	INS	-	AGCATTTATCT	-	SYCP2	TACCAGAAATAA	p.K106delins	TIX
XH_P44	20	62326425	62326425	Missense_Mutation	SNP	G	A	G	RTEL1	c.G2681A	p.S894N	
XH_P44	20	62891375	62891375	Nonsense_Mutation	INS	-	TGAAAATAATAC	-	PCMTD2	ATTCTGAAATAA	K19_E20delins	KFX
XH_P44	21	10910398	10910398	Nonsense_Mutation	INS	-	TTTGCTTTACTAC	-	TPTE	SAATTGTAGTA	B15_L316delins	ELX
XH_P44	21	11097638	11097638	Frame_Shift_Ins	INS	-	TTGTATTTTTTAA	-	BAGE	CTACTAAAAATA	p.L8fs	
XH_P44	21	26965208	26965208	Frame_Shift_Ins	INS	-	ATATTTTATAAA	-	MRPL39	37insGTTTATAA	p.E279fs	
XH_P44	21	26965210	26965210	In_Frame_Ins	INS	-	AGGTTTATG	-	MRPL39	4_835insCATAA	E279delins	HKPE
XH_P44	21	30380934	30380934	Frame_Shift_Ins	INS	-	AGACTTAAAAA	-	RWDD2B	nsCAATGTTTTA	p.T26fs	
XH_P44	21	30698966	30698966	Frame_Shift_Ins	INS	-	TTCCCTTGATACC	-	BACH1	22insTTTCCCTTG	p.Q274fs	
XH_P44	21	30714840	30714840	Nonsense_Mutation	INS	-	GATCACATGGAC	-	BACH1	3insTAAGATCA	C33delinsV	VRSHGVX
XH_P44	21	31709551	31709551	Frame_Shift_Ins	INS	-	T	-	KRTAP27-1	c.435_436insA	p.S146fs	
XH_P44	21	31709552	31709552	Nonsense_Mutation	INS	-	ATTCTTTAAATA	-	KRTAP27-1	TTTTTTATTTAA	A45_S146delins	TFPIX
XH_P44	21	33074602	33074602	In_Frame_Ins	INS	-	TGTTACAGATA	-	SCAF4	insGTTTATACTG	123delins	VYVTITTT
XH_P44	21	33949209	33949209	Frame_Shift_Ins	INS	-	AAAAGTAC	-	21orf59-TCP10	2_523insGTACT	p.L175fs	
XH_P44	21	33949211	33949211	Nonsense_Mutation	INS	-	AATTTG	-	21orf59-TCP10	20_521insCAAA	R174delins	TNX
XH_P44	21	34003586	34003586	Frame_Shift_Ins	INS	-	CACTGGACTT	-	SYNJ1	4300insAAGTC	p.W1434fs	
XH_P44	21	34003588	34003588	Missense_Mutation	SNP	C	A	C	SYNJ1	c.G4298T	p.G1433V	
XH_P44	21	34003848	34003848	Frame_Shift_Ins	INS	-	ACAGTTTTGATC	-	SYNJ1	nsGTAGATCA	p.P1346fs	
XH_P44	21	34617328	34617328	Frame_Shift_Ins	INS	-	TT	-	IFNAR2	c.170_171insTT	p.K57fs	
XH_P44	21	34617329	34617329	In_Frame_Ins	INS	-	AGTCAATTAACG	-	IFNAR2	nsGTAAGTCAAT	K57delins	KVSLTS
XH_P44	21	34889747	34889747	Nonsense_Mutation	INS	-	TTTGCTTCTCTC	-	GART	nsGAAGAGAGA	F624_S625delins	X
XH_P44	21	34926657	34926657	In_Frame_Ins	INS	-	TCATATTTATTA	-	SON	CAACATCATAT	7delinsDKSTS	LYLLTKLR
XH_P44	21	35279724	35279724	In_Frame_Ins	INS	-	STTGTTTTCATTT	-	ATP5O	nsTAAAAATGA	A121delins	IKMKQTS
XH_P44	21	35893943	35893943	Frame_Shift_Ins	INS	-	TCTGTATTCTT	-	RCAN1	197insAAGAAT	p.G66fs	
XH_P44	21	37445090	37445090	Frame_Shift_Ins	INS	-	CTCCCTTCTTT	-	CBR1	745insCTCCCT	p.A248fs	
XH_P44	21	37571537	37571537	Frame_Shift_Ins	INS	-	TCTTAGTA	-	DOPEY2	8_309insTCTTA	p.L103fs	
XH_P44	21	37584295	37584295	Frame_Shift_Ins	INS	-	TTGGGAAA	-	DOPEY2	4_805insTTGGG	p.P268fs	
XH_P44	21	37584297	37584297	Missense_Mutation	SNP	T	A	T	DOPEY2	c.T806A	p.L269H	
XH_P44	21	37741983	37741983	Nonsense_Mutation	INS	-	STAATTGGCAGC	-	MORC3	nsTCTTGTAATT	T702_Q703delins	FLX
XH_P44	21	37742058	37742058	In_Frame_Ins	INS	-	TCATCT	-	MORC3	179_2180insTCAP	p.S727delins	LC
XH_P44	21	37742060	37742060	Frame_Shift_Ins	INS	-	AGATTTAT	-	MORC3	1_2182insAGAT	p.S727fs	
XH_P44	21	38269390	38269390	Frame_Shift_Ins	INS	-	CATTGATCATCC	-	HLCS	AAGAGAGGATG	p.V407fs	
XH_P44	21	40568675	40568675	Frame_Shift_Ins	INS	-	AAGCAAAAGTAG	-	BRWD1	TTTCTAACTACT	p.A2107fs	
XH_P44	21	40778114	40778114	Nonsense_Mutation	INS	-	AAAGAAAATAA	-	LCA5L	insATAATTATT	569_570delins	QX
XH_P44	21	41684244	41684244	Nonsense_Mutation	INS	-	STTGATTGTCAG	-	DSCAM	TCACCTCTGCACA	delinsTWLMILC	SPLTINWLX
XH_P44	21	41711327	41711327	Frame_Shift_Ins	INS	-	CGTAAGAGGTG	-	DSCAM	226insGCACCT	p.J409fs	
XH_P44	21	43223030	43223030	In_Frame_Ins	INS	-	AGACATTCTGT	-	PRDM15	2896insAACAGA	A966delins	NRMSA
XH_P44	21	43413723	43413723	In_Frame_Ins	INS	-	SGTGAAAAGAA	-	ZBTB21	482insTTTCTTT	K161delins	SFHQX
XH_P44	21	43413725	43413725	Silent	SNP	T	G	T	ZBTB21	c.A480C	p.G160G	
XH_P44	21	44520724	44520724	In_Frame_Ins	INS	-	CACTCCATCTCG	-	U2AF1L5	nsACCAAGATGG	61delins	RPDGVGD
XH_P44	21	46011298	46011298	Silent	SNP	G	A	G	KRTAP10-6	c.C1068T	p.S356S	
XH_P44	21	46923945	46923945	Frame_Shift_Ins	INS	-	TTAATGGTGCC	-	COL18A1	TTTTTTGTTAATG	p.L1082fs	
XH_P44	22	16449442	16449442	Frame_Shift_Ins	INS	-	ATTGACCATGTT	-	OR11H1	sACACAACATGG	p.S121fs	
XH_P44	22	17072016	17072016	Silent	SNP	G	A	G	CCT8L2	c.C1425T	p.N475N	
XH_P44	22	17072017	17072017	In_Frame_Ins	INS	-	CTGGAA	-	CCT8L2	23_1424insTTCT	N475delins	IPD
XH_P44	22	18374372	18374372	Frame_Shift_Ins	INS	-	TTTTTATTTTTGT	-	MICAL3	AAAAAAACAAA	p.L525fs	
XH_P44	22	18374374	18374374	Frame_Shift_Ins	INS	-	ATTTTTTT	-	MICAL3	0_1571insAAAA	p.L524fs	
XH_P44	22	18382305	18382305	Nonsense_Mutation	INS	-	AGCGTGAACAA	-	MICAL3	sAAGAGTTGTTCT	286_E287delins	X
XH_P44	22	21570373	21570373	Missense_Mutation	SNP	C	T	C	GGT2	c.G589A	p.G197S	
XH_P44	22	24953757	24953757	Frame_Shift_Ins	INS	-	STCAGTTCATCT	-	SNRPD3	116insGTCACTG	p.M39fs	
XH_P44	22	24953759	24953759	Missense_Mutation	SNP	G	C	G	SNRPD3	c.G117C	p.M39I	
XH_P44	22	26105932	26105932	Splice_Site	INS	-	GAATGTCACGAT	-	GRK3	.	.	
XH_P44	22	26899743	26899743	Nonsense_Mutation	INS	-	TGTTATTGTACA	-	TFIP11	nsACATGTACAA	1148delins	HWQX
XH_P44	22	26902853	26902853	In_Frame_Ins	INS	-	AGGGAGAGAA	-	TFIP11	7_158insTTTCT	G53delins	VSPW
XH_P44	22	28490181	28490181	In_Frame_Ins	INS	-	TCTGTCTTTATTC	-	TT2C8	AAAAAGAAATAA	73delins	SKKNDRPL
XH_P44	22	29750843	29750843	In_Frame_Ins	INS	-	AGCCTCTT	-	AP1B1	734insGAGAA	T245delins	RRGS
XH_P44	22	29885359	29885359	Missense_Mutation	SNP	A	G	A	NEFH	c.A1730G	p.E577G	
XH_P44	22	29886210	29886210	Frame_Shift_Ins	INS	-	TGGCCCTCTCTG	-	NEFH	insGTCTTGGCC	p.K861fs	
XH_P44	22	30384550	30384550	Missense_Mutation	SNP	A	T	A	MTMR3	c.A292T	p.R98W	
XH_P44	22	30384552	30384552	Splice_Site	INS	-	AGTACTCAAGTC	-	MTMR3	.	.	
XH_P44	22	32046759	32046759	Frame_Shift_Ins	INS	-	AAACATA	-	PISD	70_71insTAGTG	p.H24fs	
XH_P44	22	32046761	32046761	In_Frame_Ins	INS	-	TAGAGTTAAAT	-	PISD	AACTCATTTAAC	3delins	LLTLTITTT
XH_P44	22	32112227	32112227	Nonsense_Mutation	INS	-	CACATGATGATA	-	PRR14L	GTGGAATATCA	K534delins	KWNIMX
XH_P44	22	32179957	32179957	Frame_Shift_Ins	INS	-	CTCTTTTITTTTC	-	DEPDC5	549insCTTCTTT	p.D183fs	
XH_P44	22	32217621	32217621	Silent	SNP	A	G	A	DEPDC5	c.A2004G	p.G668G	
XH_P44	22	32217622	32217622	Frame_Shift_Ins	INS	-	TACAGATGTT	-	DEPDC5	2006insTACAG	p.R669fs	
XH_P44	22	36142607	36142607	Frame_Shift_Ins	INS	-	T	-	RBFOX2	c.897_898insA	p.V300fs	
XH_P44	22	36142609	36142609	Splice_Site	INS	-	CTTCTTGTTTCT	-	RBFOX2	.	.	
XH_P44	22	36889806	36889806	Nonsense_Mutation	INS	-	AAATTACAACTG	-	FOXRED2	69insTGAGTTG	p.P557delins	X
XH_P44	22	38877434	38877434	Frame_Shift_Ins	INS	-	AAAAGAA	-	KDELR3	59_570insAAAA	p.F190fs	
XH_P44	22	38877435	38877435	Frame_Shift_Ins	INS	-	ATAAT	-	KDELR3	570_571insATA	p.F190fs	
XH_P44	22	39475019	39475019	Frame_Shift_Ins	INS	-	AAAAAAAAGAG	-	APOBEC3G	nsCAAAAAAAA	p.W23fs	
XH_P44	22	39482428	39482428	Nonsense_Mutation	INS	-	CTGGAGTGT	-	POBEC3G	9_680insCTGGA	E227delins	AGVX
XH_P44	22	40060900	40060900	Missense_Mutation	SNP	C	T	C	CACNA1	c.C3718T	p.R1240W	
XH_P44	22	40068242	40068242	Frame_Shift_Ins	INS	-	TTTCTTATTATG	-	CACNA1	insCCTTTTCTT	p.F1491fs	
XH_P44	22	40760930	40760930	Frame_Shift_Ins	INS	-	CTCATGATCAT	-	ADSL	sAAGCCTCATG	p.V413fs	
XH_P44	22	40760932	40760932	Missense_Mutation	SNP	G	T	G	ADSL	c.G1240T	p.V414F	
XH_P44	22	40762502	40762502	Frame_Shift_Ins	INS	-	TTTTACTCCAAC	-	ADSL	255insCTTTTAC	p.K418fs	
XH_P44	22	40762503	40762503	Missense_Mutation	SNP	G	C	G	ADSL	c.G1255C	p.V419L	
XH_P44	22	41320447	41320447	Frame_Shift_Ins	INS	-	TTAATACTACT	-	XPNPEP3	sGCTATTATAA	p.L440fs	
XH_P44	22	41605932	41605932	Frame_Shift_Ins	INS	-	AGATGGG	-	L3MBTL2	7_258insAGATG	p.E86fs	
XH_P44	22	41605934	41605934	Missense_Mutation	SNP	C	T	C	L3MBTL2	c.C259T	p.P87S	

XH_P44	22	42114192	42114192	Nonsense_Mutation	INS	-	CATGCTTAATCT	-	MEI1	8insTGCATGCTT	6_G217delinsSACLIX
XH_P44	22	42607640	42607640	Frame_Shift_Ins	INS	-	CAAGCCCT	-	TCF20	1_3672insAGGC	p.A1224fs
XH_P44	22	42807574	42807574	Frame_Shift_Ins	INS	-	GGACT	-	NFAM1	289_290insAGT	p.T97fs
XH_P44	22	43213831	43213831	Frame_Shift_Ins	INS	-	TTAAAAGAAGG	-	ARFGAP3	CTTTTCTCTCTT	p.L238fs
XH_P44	22	45946455	45946455	Missense_Mutation	SNP	G	T	G	FBLN1	c.G1657T	p.A553S
XH_P44	22	47116872	47116872	Nonsense_Mutation	INS	-	ATTTTATTTAT	-	CERK	sATAAATAAATA	E61_E62delinsEX
XH_P44	22	50279312	50279312	Frame_Shift_Ins	INS	-	GCTTCGAGGTCT	-	ZBED4	003insAGCTTCG	p.L668fs
XH_P44	22	50946058	50946058	Missense_Mutation	SNP	G	A	G	LMF2	c.C47T	p.A16V
XH_P44	22	51065691	51065691	Missense_Mutation	SNP	G	A	G	ARSA	c.C368T	p.L213V
XH_P44	X	2951244	2951244	Frame_Shift_Ins	INS	-	STATGATACCAT	-	ARSH	508insGTATGA	p.F503fs
XH_P44	X	6069378	6069378	Missense_Mutation	SNP	G	T	G	NLGN4X	c.C130A	p.Q44K
XH_P44	X	6069380	6069380	In_Frame_Ins	INS	-	ACCATGTGTTCAA	-	NLGN4X	nsATCTTGAACA	A43delinsDLEHRSS
XH_P44	X	11206955	11206955	Nonsense_Mutation	INS	-	GTGAAAACCTGG	-	ARHGAP6	insTATCCAGTT	4_K145delinsYPVFTX
XH_P44	X	11272821	11272821	Frame_Shift_Ins	INS	-	CTCTT	-	ARHGAP6	54_55insAAGA	p.F19fs
XH_P44	X	11272822	11272822	Missense_Mutation	SNP	A	C	A	ARHGAP6	c.T54G	p.D18E
XH_P44	X	13727462	13727462	Nonsense_Mutation	INS	-	GCATAATATA	-	RAB9A	598insGCATAA	99_C200delinsSAX
XH_P44	X	13727464	13727464	Nonsense_Mutation	INS	-	AATTCTTTT	-	RAB9A	9_600insAATTC	200_C201delinsX
XH_P44	X	16850834	16850834	Frame_Shift_Ins	INS	-	GTGGCCCT	-	TXLNG	7_558insGTGGC	p.A186fs
XH_P44	X	20227524	20227524	Splice_Site	INS	-	ACCA	-	RP56KA3	CTATTTT	
XH_P44	X	22117166	22117166	Frame_Shift_Ins	INS	-	CTATTGCTTTTT	-	PHEX	977insCTATTGT	p.L326fs
XH_P44	X	24007008	24007008	In_Frame_Ins	INS	-	TTATTGGGAAG	-	KLHL15	insTAAACTTCCC	282delinsINFPTP
XH_P44	X	24024700	24024700	Frame_Shift_Ins	INS	-	GGCTGCCATGT	-	KLHL15	111insACATGG	p.L37fs
XH_P44	X	24229461	24229461	Nonsense_Mutation	INS	-	AGATCCCTTGTG	-	ZFX	sATGGAAGATCC	7_R568delinsNGRSFVX
XH_P44	X	24859875	24859875	Nonsense_Mutation	INS	-	AATGACTTCTCT	-	POLA1	844insAAATGAC	A1281delinsDKX
XH_P44	X	26157809	26157809	In_Frame_Ins	INS	-	TCAAATCAACAC	-	MAGEB18	708insTCAAATC	L236delinsLQINT
XH_P44	X	26212871	26212871	In_Frame_Ins	INS	-	CACCAAAATG	-	MAGEB6	3_909insCACCA	A1303delinsTTKC
XH_P44	X	27479267	27479267	In_Frame_Ins	INS	-	GTGTGGTTCGT	-	PPP4R3CP	2147insAACGAAM	716delinsKRTTL
XH_P44	X	27479650	27479650	In_Frame_Ins	INS	-	AATTGG	-	PPP4R3CP	763_1764insCCA	A588delinsAQF
XH_P44	X	27479652	27479652	Nonsense_Mutation	INS	-	AAGAAATATGT	-	PPP4R3CP	CCATAAAACATAP	p.A588delinsPX
XH_P44	X	27998985	27998985	Frame_Shift_Ins	INS	-	TGAGATGT	-	DCAF8L1	6_467insCACTC	p.Q156fs
XH_P44	X	27998987	27998987	Nonsense_Mutation	SNP	C	T	C	DCAF8L1	c.G465A	p.W155X
XH_P44	X	32404514	32404514	Nonsense_Mutation	INS	-	CTATGTATATGT	-	DMD	3TATACATATAC	188delinsYYTYYTX
XH_P44	X	38024127	38024127	Nonsense_Mutation	INS	-	ACTATATATGTC	-	SRPX	TAAGTGACATAT	K163delinsIHRX
XH_P44	X	40513715	40513715	Frame_Shift_Ins	INS	-	GA	-	MED14	4191_4192insT	p.Q1398fs
XH_P44	X	40513716	40513716	Nonsense_Mutation	INS	-	TTTTTGTTAG	-	MED14	4191insCTAAC	397_Q1398delinsHX
XH_P44	X	41203645	41203645	In_Frame_Ins	INS	-	TGAAAAAGCTAA	-	DDX3X	nsCAATGAAAAA	324delinsSMKKLII
XH_P44	X	41554966	41554966	Frame_Shift_Ins	INS	-	AGTTA	-	GPR34	80_81insAGTT	p.T27fs
XH_P44	X	41554967	41554967	Nonsense_Mutation	INS	-	TAACATAAAAGTG	-	GPR34	insTTTTAACTAA	27_N28delinsTFNX
XH_P44	X	45011133	45011133	Missense_Mutation	SNP	G	C	G	Cxorf36	c.C1066G	p.Q356E
XH_P44	X	45011134	45011134	Frame_Shift_Ins	INS	-	A	-	Cxorf36	c.1064_1065ins	p.K355fs
XH_P44	X	46359703	46359703	Frame_Shift_Ins	INS	-	5AAAAACCTTAC	-	ZNF674	sACATTGTGAAG	p.Y441fs
XH_P44	X	47307952	47307952	Frame_Shift_Ins	INS	-	AGAGAAACCC	-	ZNF41	595insGGGTT	p.T320fs
XH_P44	X	47307953	47307953	Frame_Shift_Ins	INS	-	TATATGTACAC	-	ZNF41	958insTCTGTAC	p.T320fs
XH_P44	X	47774919	47774919	Missense_Mutation	SNP	C	G	C	ZNF81	c.C874G	p.P292A
XH_P44	X	47774920	47774920	Frame_Shift_Ins	INS	-	ATTGCTTTTA	-	ZNF81	876insATTGCT	p.P292fs
XH_P44	X	48672897	48672897	Nonsense_Mutation	INS	-	TTAATTATTAA	-	HDAC6	858insTTAATA	1286_L287delinsHX
XH_P44	X	48672899	48672899	Frame_Shift_Ins	INS	-	A	-	HDAC6	c.859_860insA	p.L287fs
XH_P44	X	48681460	48681460	Frame_Shift_Ins	INS	-	CTTCCCTG	-	HDAC6	1_2652insCTTC	p.5884fs
XH_P44	X	49071679	49071679	Frame_Shift_Ins	INS	-	ATCTCCACATAA	-	CACNA1F	insGGGATTATG	p.K1155fs
XH_P44	X	49645750	49645750	Frame_Shift_Ins	INS	-	GTGCAGGACAT	-	USP27X	41insTGTGCAGG	p.A280fs
XH_P44	X	52677315	52677315	Frame_Shift_Ins	INS	-	TAGTCCATAAG	-	SSX7	insCATCTTATGG	p.T154fs
XH_P44	X	53115156	53115156	Frame_Shift_Ins	INS	-	GAATTGCTCAT	-	TSPYL2	583insTGAATTG	p.N528fs
XH_P44	X	53115327	53115327	Frame_Shift_Ins	INS	-	GTTCGTGGTCT	-	TSPYL2	1754insGTTTCC	p.D585fs
XH_P44	X	53115329	53115329	Frame_Shift_Ins	INS	-	CA	-	TSPYL2	1755_1756insC	p.D585fs
XH_P44	X	53457721	53457721	Frame_Shift_Ins	INS	-	GCTCTGGAGTG	-	RIBC1	697insGCTCTG	p.A232fs
XH_P44	X	53584360	53584360	Nonsense_Mutation	INS	-	TGTTCTGGTTA	-	HUWE1	sGATAATAACCA	p.T2730delinsRX
XH_P44	X	53631646	53631646	Nonsense_Mutation	INS	-	CAGTCCAATTA	-	HUWE1	TCATCTCTAAAT	82_A883delinsEISSX
XH_P44	X	54161531	54161531	Nonsense_Mutation	INS	-	CTGTATTATTTT	-	FAM120C	349insCAAAATA	450_P451delinsAKX
XH_P44	X	54359650	54359650	In_Frame_Ins	INS	-	AAA	-	WNK3	c.456_457insTT	p.L153delinsFL
XH_P44	X	54359652	54359652	Nonsense_Mutation	INS	-	ATGGTC	-	WNK3	54_455insGACG	E152delinsGPX
XH_P44	X	54839982	54839982	In_Frame_Ins	INS	-	SAGTTCAGGACG	-	MAGED2	1271insGAGTTC	424delinsRVDDQ
XH_P44	X	70053425	70053425	Frame_Shift_Ins	INS	-	TGCTTCCTTTGT	-	TEX11	sAAGAACAAAGC	p.F182fs
XH_P44	X	70757818	70757818	Frame_Shift_Ins	INS	-	AGTTTGAGAT	-	OGT	359insAGTTTG	p.P120fs
XH_P44	X	71684461	71684461	Frame_Shift_Ins	INS	-	TTCTCAGCTTAG	-	HDAC8	insTCTTAAGCT	p.K195fs
XH_P44	X	73812702	73812702	Frame_Shift_Ins	INS	-	AACATCCTTT	-	RLIM	448insAAAGGA	p.Q150fs
XH_P44	X	73812704	73812704	Missense_Mutation	SNP	C	G	C	RLIM	c.G446C	p.S149T
XH_P44	X	73960748	73960748	Frame_Shift_Ins	INS	-	GATATGAGCA	-	KIAA2022	3_3644insTGCTC	p.N1215fs
XH_P44	X	73962762	73962762	In_Frame_Ins	INS	-	ACGCTAGTAATC	-	KIAA2022	CTTTATGATTAA	4delinsFFMITSVPLI
XH_P44	X	77266676	77266676	Nonsense_Mutation	INS	-	GTTAATATGTAT	-	ATP7A	574insAGTTAAT	p.L625delinsX
XH_P44	X	77301054	77301054	In_Frame_Ins	INS	-	CCTCTTGGTGGT	-	ATP7A	ATTATCTCTCT	26delinsSAFILLVVEIF
XH_P44	X	77301947	77301947	In_Frame_Ins	INS	-	AGAAAGAAGAT	-	ATP7A	50insAAAGAAA	1383delinsRKERRF
XH_P44	X	79952315	79952315	Nonsense_Mutation	INS	-	CTATTGTATATT	-	BRWD3	CTCTAAATATA	97_P998delinsPVLX
XH_P44	X	83126554	83126554	Frame_Shift_Ins	INS	-	CTTGAGTAAGAA	-	CYL1	TTATTCTTGAGT	p.P50fs
XH_P44	X	84525882	84525882	Frame_Shift_Ins	INS	-	AGTTGGCATTC	-	ZNF711	335insTAGTTG	p.T445fs
XH_P44	X	84525884	84525884	Missense_Mutation	SNP	C	T	C	ZNF711	c.C136G	p.H446Y
XH_P44	X	99943437	99943437	Nonsense_Mutation	INS	-	AGACTATAGGTG	-	SYTLA	CTAAGCACCTAT	E307delinsLSTYSLNX
XH_P44	X	100117658	100117658	Nonsense_Mutation	INS	-	TCTTCTATATCT	-	NOX1	sCCAAGGATATA	p.T126delinsTX
XH_P44	X	100169529	100169529	Nonsense_Mutation	INS	-	STTGCTGATTC	-	XKRX	insAATAGAATC	883_A384delinsKX
XH_P44	X	100653786	100653786	Nonsense_Mutation	INS	-	AACTTTAAGAA	-	GLA	GAACATTCTTA	N263delinsRKHSX
XH_P44	X	101909048	101909048	Frame_Shift_Ins	INS	-	TACAAAGAAA	-	GPRASP1	208insTACAAA	p.569fs
XH_P44	X	101909169	101909169	Missense_Mutation	SNP	A	G	A	GPRASP1	c.A328G	p.R110G
XH_P44	X	101909171	101909171	Frame_Shift_Ins	INS	-	CATCATTTCTCT	-	GPRASP1	331insCATCAT	p.R110fs
XH_P44	X	101909583	101909583	Nonsense_Mutation	INS	-	TCTCTCTCTTTG	-	GPRASP1	43insGTCTCTCT	48_S249delinsGLLLX
XH_P44	X	101911110	101911110	Frame_Shift_Ins	INS	-	CTTATTATTTGT	-	GPRASP1	sCAAGACTTATT	p.D757fs
XH_P44	X	101912985	101912985	Nonsense_Mutation	INS	-	AGTAGTCTTTT	-	GPRASP1	5insCTGAGTAG	K1382delinsTEX
XH_P44	X	103420390	103420390	Nonsense_Mutation	INS	-	AATTTTAAGATA	-	FAM199X	CATACAAATTTTA	delinsENYRIHTILRYNX
XH_P44	X	105279334	105279334	Frame_Shift_Ins	INS	-	ACTACAGAAGGG	-	SERPINA7	TTTACCCCTCTC	p.S222fs
XH_P44	X	106109220	106109220	Nonsense_Mutation	INS	-	FAAAAATAAATA	-	TBC1D8B	TTCTATTAAAAA	3_5874delinsNSSFPYX
XH_P44	X	107402838	107402838	Nonsense_Mutation	INS	-	AAAGAATGGA	-	COL4A6	c.4495insTCCAT	99_Q1500delinsSILX
XH_P44	X	109695360	109695360	In_Frame_Ins	INS	-	AACTCTAAAGCTC	-	RTL9	16insGAATCTA	P505delinsPESKAL
XH_P44	X	111090659	111090659	Frame_Shift_Ins	INS	-	GC	-	TRPC5	1382_1383insG	p.N461fs
XH_P44	X	111090660	111090660	Frame_Shift_Ins	INS	-	TTACTCT	-	TRPC5	81_1382insGAA	p.N461fs
XH_P44	X	112058984	112058984	Frame_Shift_Ins	INS	-	AGCCTATT	-	AMOT	3_994insAATAG	p.S332fs
XH_P44	X	115590056	115590056	In_Frame_Ins	INS	-	GTTGTTAATAG	-	SLC6A14	nsAGCTAGTTGT	522delinsELVNVRSI
XH_P44	X	118239107	118239107	Frame_Shift_Ins	INS	-	TTTTCCATCCA	-	KIAA1210	916insTGGATG	p.P306fs
XH_P44	X	118239108	118239108	Silent	SNP	G	A	G	KIAA1210	c.C915T	p.N305N
XH_P44	X	118257544	118257544	Splice_Site	INS	-	AAGGCTTTTTCT	-	KIAA1210	.	.
XH_P44	X	118257546	118257546	Silent	SNP	C	T	C	KIAA1210	c.G480A	p.E160E

XH_P44	X	119694376	119694376	Nonsense_Mutation	INS	-	AATAAGAGTATA	-	CUL4B	insTTAATATACT	0_L41delinsLIYSYFX
XH_P44	X	122766869	122766869	Missense_Mutation	SNP	C	A	C	THOC2	c.G2159T	p.R720I
XH_P44	X	122766871	122766871	In_Frame_Ins	INS	-	TACATGTTTTTA	-	THOC2	2157insTAAAAA	1719delinsIKNMY
XH_P44	X	122770004	122770004	Frame_Shift_Ins	INS	-	ATTTGTGGTTG	-	THOC2	insCTACAAACCA	p.A648fs
XH_P44	X	127186132	127186132	Frame_Shift_Ins	INS	-	TTTGAATCCTAG	-	ACTR1	4insCCTAGGATT	p.S18fs
XH_P44	X	128642068	128642068	Frame_Shift_Ins	INS	-	ACTGAAACAGCCG	-	SMARCA1	5ACACCCGGCTG	p.A272fs
XH_P44	X	130416711	130416711	Nonsense_Mutation	INS	-	ACTGTTTTTATT	-	IGSF1	TTGATAATAAAA	T310delinsVDNKNCSX
XH_P44	X	132160095	132160095	Frame_Shift_Ins	INS	-	AAGGAAACAAA	-	USP26	5TTTCTTTTGT	p.K718fs
XH_P44	X	132160096	132160096	Frame_Shift_Ins	INS	-	GATGA	-	USP26	152_2153insTC	p.K718fs
XH_P44	X	132351569	132351569	Frame_Shift_Ins	INS	-	GAAGA	-	TFDP3	718_719insTCT	p.E240fs
XH_P44	X	133379376	133379376	Missense_Mutation	SNP	A	G	A	CCDC160	c.A546G	p.I182M
XH_P44	X	133379377	133379377	Frame_Shift_Ins	INS	-	TTCTCTTGTTCT	-	CCDC160	548insTTCTCTCT	p.F183fs
XH_P44	X	133927918	133927918	Frame_Shift_Ins	INS	-	T	-	FAM122B	c.103_104insA	p.L35fs
XH_P44	X	133927920	133927920	Nonsense_Mutation	INS	-	TCCTAAAATGAT	-	FAM122B	GCACATCATTTT	4_L35delinsDSTSFx
XH_P44	X	134425455	134425455	In_Frame_Ins	INS	-	CTTCTCACTTTT	-	ZNF75D	539insAAAAAGTG	E213delinsEKVRR
XH_P44	X	134494786	134494786	Frame_Shift_Ins	INS	-	GAATTCTCTGAT	-	ZNF449	43insATGAATTC	p.T448fs
XH_P44	X	135312740	135312740	Nonsense_Mutation	INS	-	ATCTTAGCAACA	-	MAP7D3	TTTCTGTGTGGC	483_K484delinsQX
XH_P44	X	135322643	135322643	Nonsense_Mutation	INS	-	TCA	-	MAP7D3	483_484insTG	p.N162delinsX
XH_P44	X	135322644	135322644	Nonsense_Mutation	INS	-	STCCCATGTTAT	-	MAP7D3	TGTAATAATAAC	61_N162delinsAVKX
XH_P44	X	135431898	135431898	Frame_Shift_Ins	INS	-	TGTTGATAATGA	-	ADGRG4	hsAAGATGTGTGA	p.L2011fs
XH_P44	X	135441571	135441571	Frame_Shift_Ins	INS	-	CATAAATGTCAA	-	ADGRG4	5TAGTTCATAAA	p.L2367fs
XH_P44	X	135593932	135593932	Frame_Shift_Ins	INS	-	TTCTTCAACTCT	-	HTATSF1	29insTTTCTCTC	p.S676fs
XH_P44	X	135593933	135593933	Frame_Shift_Ins	INS	-	CAAGAACATTTT	-	HTATSF1	030insTCAAGAA	p.D677fs
XH_P44	X	135829737	135829737	Frame_Shift_Ins	INS	-	ATGCTTGAATTT	-	ARHGEF6	64insAAAAATTC	p.D88fs
XH_P44	X	138699835	138699835	Nonsense_Mutation	INS	-	CTTCTCAGAGG	-	MCF2	TATAACCTCTGAP	p.L240delinsTIX
XH_P44	X	140996156	140996156	In_Frame_Ins	INS	-	GAACCTTGATAT	-	MAGEC1	2967insGAACCT	5989delinsRNLYI
XH_P44	X	142716575	142716575	Nonsense_Mutation	INS	-	CAAGGGTGCTCT	-	SLITRK4	350insTGAGACA	784_Q785delinsX
XH_P44	X	147106484	147106484	Frame_Shift_Ins	INS	-	CTCTCCCACTTC	-	FMR1NB	3insTGCTCTCCC	p.K244fs
XH_P44	X	148037403	148037403	Frame_Shift_Ins	INS	-	GTTC	-	AFF2	751_752insGT	p.L251fs
XH_P44	X	148037405	148037405	In_Frame_Ins	INS	-	GATGTCACTTGG	-	AFF2	4insGGATGTGCA	25delinsLNGCHFV
XH_P44	X	148037594	148037594	Frame_Shift_Ins	INS	-	TTTCTGGAATTT	-	AFF2	5TTTGTTCCTGG	p.A314fs
XH_P44	X	148037596	148037596	Missense_Mutation	SNP	C	G	C	AFF2	c.C944G	p.Q315fs
XH_P44	X	149983373	149983373	Frame_Shift_Ins	INS	-	A	-	CD99L2	c.238_239insT	p.T80fs
XH_P44	X	149983374	149983374	Nonsense_Mutation	INS	-	AACTGAAAGAC	-	CD99L2	ATAAAGCTCTT	Q80_D81delinsX
XH_P44	X	151283993	151283993	Frame_Shift_Ins	INS	-	TTGAT	-	AGEA10-MAGE	19_20insATCA	p.S7fs
XH_P44	X	151283995	151283995	In_Frame_Ins	INS	-	ATT	-	AGEA10-MAGE	c.17_18insAAT	p.K6delinsKM
XH_P44	X	151870144	151870144	Frame_Shift_Ins	INS	-	TTTTGCGATT	-	MAGEA6	835insTTTTTG	p.L278fs
XH_P44	X	154159502	154159502	In_Frame_Ins	INS	-	AAATAATGATTC	-	F8	nsACTTTGAATC	855delinsTLNHYFLH
XH_P44	X	154743862	154743862	Frame_Shift_Ins	INS	-	CCACAGTATTAT	-	TMLHE	TAATTATAATAC	p.Q141fs
XH_P44	Y	21869192	21869192	Frame_Shift_Ins	INS	-	SCTCCATCTCAT	-	KDM5D	669insTATAGA	p.R1223fs
XH_P44	I	104166524	104166524	Nonsense_Mutation	SNV	G	T	T	AMY2A	c.1138G>T	P.G380*
XH_P44	I	155330089	155330089	Splice_Site	SNV	T	C	C	ASH1L	c.6795+3A>G	
XH_P44	I	161332111	161332111	Splice_Site	SNV	G	T	T	SDHC	c.406-8G>T	
XH_P44	I	185984573	185984573	Splice_Site	INDEL	-	CTCCTTTAATAC	CTCCTTTAATAC	HMCN1	insCATTTCCTCCTTTAATACTAGGT	
XH_P44	I	215777614	215777614	Missense_Mutation	SNV	A	T	T	KCTD3	c.1279A>T	P.I427F
XH_P44	I	227260005	227260005	Splice_Site	INDEL	-	TGTTTAATGATT	TGTTTAATGATT	CDC42BP	ACTATGAAATCATTAACAAACATGCATA	
XH_P44	I	42657102	42657102	Frame_Shift_Ins	INDEL	-	TCTTGATTAAAT	TCTTGATTAAAT	FOXJ3	5ATAAATTTTAA	P.5408fs
XH_P44	I	43632865	43632865	Missense_Mutation	INDEL	-	TTTATTCTTAAAT	TTTATTCTTAAAT	EBNA1BP2	GTATTTTAAAGAA	H249insPLPKMNSLNH
XH_P44	I	116595395	116595395	Frame_Shift_Ins	INDEL	-	TTAATAAC	TTAATAAC	FAM160B1	5_396insTAATA	P.Q133fs
XH_P44	I	120795787	120795787	Splice_Site	INDEL	-	CTGATGAAGAT	CTGATGAAGAT	EIF3A	7insCATCCATCTTCATCAGTCTCA	
XH_P44	I	126138353	126138353	Missense_Mutation	SNV	C	T	T	NKX1-2	c.160G>A	P.E54K
XH_P44	I	64565121	64565121	Missense_Mutation	SNV	T	A	A	ADO	c.302T>A	P.F101Y
XH_P44	I	75258951	75258951	Splice_Site	SNV	G	A	A	USP54	c.4310-5C>T	
XH_P44	I	75258952	75258952	Splice_Site	INDEL	-	GATCTTTTCCATT	GATCTTTTCCATT	USP54	10-6insGAAGATGGAAAGATCA	
XH_P44	I	86273648	86273648	Frame_Shift_Ins	INDEL	-	TAAGTTTGCTTC	TAAGTTTGCTTC	CCSER2	AATGTTTAAAGT	P.K924fs
XH_P44	I	57094887	57094887	Splice_Site	INDEL	-	ATGGGGGAACG	ATGGGGGAACG	SSRP1	TATTTTTTTTCGTTCCCACTACCTTCAAAAT	
XH_P44	I	55725609	55725609	Frame_Shift_Ins	INDEL	-	CTTGTTTG	CTTGTTTG	OR6C3	6_127insTGTGT	P.I43fs
XH_P44	I	55725611	55725611	Frame_Shift_Ins	INDEL	-	TTTAATATTTTTT	TTTAATATTTTTT	OR6C3	ATGTTTAAATAT	P.T44fs
XH_P44	I	66703601	66703601	Missense_Mutation	SNV	A	G	G	HELB	c.893A>G	P.Y298C
XH_P44	I	96912787	96912787	Missense_Mutation	SNV	G	C	C	CFAP54	c.880G>C	P.A294P
XH_P44	I	100953867	100953867	Splice_Site	INDEL	-	AATGTAACATT	AATGTAACATT	PCCA	GTTAATCGAATGTAACTTTTGAAATATT	
XH_P44	I	103528130	103528130	Frame_Shift_Ins	INDEL	-	ATTGTATTATGCC	ATTGTATTATGCC	ERCC5	TCTGGGTTTTT	SSKVFVMPFLVWFRFLSSSSSSDD
XH_P44	I	49033978	49033978	Splice_Site	INDEL	-	TAGTCACTTTTAC	TAGTCACTTTTAC	RB1	6+10insATTAGTCATTTTTACTGT	
XH_P44	I	24534215	24534215	Silent	SNV	G	A	A	CARMIL3	c.3129G>A	P.P1043P
XH_P44	I	23006812	23006812	Frame_Shift_Ins	INDEL	-	TAAATAGGGCC	TAAATAGGGCC	NIP2A	5CCAGGGCCCT	P.L165fs
XH_P44	I	49304055	49304055	Frame_Shift_Ins	INDEL	-	G	G	SECISBP2L	c.1736_1737insT	P.L580fs
XH_P44	I	49304057	49304057	Frame_Shift_Ins	INDEL	-	AGGGAGATGGT	AGGGAGATGGT	SECISBP2L	TCTTTAACATC	P.I579fs
XH_P44	I	1270585	1270585	Missense_Mutation	SNV	G	A	A	CACNA1H	c.6635G>A	P.R2212H
XH_P44	I	15814050	15814050	Silent	SNV	G	A	A	MYH11	c.4932C>T	P.I1644I
XH_P44	I	30544467	30544467	Missense_Mutation	SNV	A	G	G	ZNF747	c.349T>C	P.S117P
XH_P44	I	31201659	31201659	Frame_Shift_Ins	INDEL	-	ATTCTTTACCTAG	ATTCTTTACCTAG	FUS	GGAGAATTTCT	P.5412fs
XH_P44	I	65105671	65105671	Frame_Shift_Ins	INDEL	-	CCCAACAATGCT	CCCAACAATGCT	HELZ	insAAAAAGCAT	P.H1350fs
XH_P44	I	65941977	65941977	Frame_Shift_Ins	INDEL	-	ACATGGGATGA	ACATGGGATGA	BPTF	5AGGGACATGG	P.I2511fs
XH_P44	I	47101968	47101968	Splice_Site	INDEL	-	ATTACAAGTTAA	ATTACAAGTTAA	LIPG	3+9insTGATTACAAGTTAAGT	
XH_P44	I	66542031	66542031	Splice_Site	INDEL	-	CTTCATTTAGCT	CTTCATTTAGCT	CCDC102B	5sATTAGTCCTTCATTAGCTTTAGTGT	
XH_P44	I	13264286	13264286	Missense_Mutation	SNV	A	G	G	IER2	c.286A>G	P.M96V
XH_P44	I	49956673	49956673	Missense_Mutation	SNV	G	A	A	ALDH16A1	c.85G>A	P.A29T
XH_P44	I	207175330	207175330	Frame_Shift_Ins	INDEL	-	ATTTTCTTTTCA	ATTTTCTTTTCA	ZDBF2	CTAATTATTTTC	P.F2025fs
XH_P44	I	48027927	48027927	Frame_Shift_Ins	INDEL	-	TCA	TCA	MSH6	2805_2806insT	P.S935dup
XH_P44	I	48027928	48027928	Missense_Mutation	INDEL	-	GGGAGACCCAA	GGGAGACCCAA	MSH6	2807insGGGAG	936delinsGETQH
XH_P44	I	30384550	30384550	Missense_Mutation	SNV	A	T	T	MTMR3	c.292A>T	P.R98W
XH_P44	I	30384552	30384552	Splice_Site	INDEL	-	AGTACTCAAGT	AGTACTCAAGT	MTMR3	5ATCAACAGTACTCAAGTGATTAC	
XH_P44	I	122404174	122404174	Splice_Site	INDEL	-	TAAAGATTG	TAAAGATTG	PARP14	321+10insTAAAGATTG	
XH_P44	I	129370327	129370327	Silent	SNV	T	C	C	TMCC1	c.1959A>G	P.R653R
XH_P44	I	172735881	172735881	Splice_Site	SNV	C	A	A	GALNTL6	c.138+12C>A	
XH_P44	I	184182361	184182361	Missense_Mutation	SNV	G	A	A	WWC2	c.1585G>A	P.A529T
XH_P44	I	22438270	22438270	Splice_Site	INDEL	-	TAATCAGGTAAC	TAATCAGGTAAC	ADGRA3	CTTTCTAGTTACCTGATTAAACATATAAGAA	
XH_P44	I	113831641	113831641	Missense_Mutation	SNV	A	G	G	KCN2	c.458A>G	P.E153G
XH_P44	I	134344570	134344570	Missense_Mutation	SNV	C	T	T	CATSPER3	c.715C>T	P.R239W
XH_P44	I	140810395	140810395	Silent	SNV	G	A	A	PCDHGA12	c.69G>A	P.L23L
XH_P44	I	52161585	52161585	Missense_Mutation	SNV	G	T	T	ITGA1	c.558G>T	P.W186C
XH_P44	I	161471022	161471022	Splice_Site	INDEL	-	TTTAATCTCTCT	TTTAATCTCTCT	MAP3K4	2insACTCCTTTAATCTCTCTCTGT	
XH_P44	I	64940723	64940723	Splice_Site	INDEL	-	ATCTTCAATCC	ATCTTCAATCC	EYS	TACAAAAGGGTAAGAAAGATTGATTACCTTTT	
XH_P44	I	79700580	79700580	Splice_Site	SNV	T	G	G	PHIP	c.2319+5A>C	
XH_P44	I	134274407	134274407	Frame_Shift_Ins	INDEL	-	AAATACCTTTTA	AAATACCTTTTA	NDRG1	CAGTTAAAAAG	0delinsTVVKYKLEQ
XH_P44	I	62489419	62489419	Splice_Site	INDEL	-	ATTCTCTACAG	ATTCTCTACAG	ASPH	5TGATTTCTGTAGAGAAATAGAA	
XH_P44	I	89128957	89128957	Splice_Site	INDEL	-	AGTTCTCATTC	AGTTCTCATTC	MMP16	10insGAATGAATGAGAACTGTG	
XH_P44	I	131362384	131362384	Missense_Mutation	SNV	C	T	T	SPTAN1	c.3569C>T	P.S1190F

XH_P44	9	8449832	8449832	Frame_Shift_Ins	INDEL	-	GTCTGAAAGGA	GTCTGAAAGGA	PTPRD	CTTAATTCCTT	94delinsNLISFOTFAW
XH_P44	X	148037594	148037594	Frame_Shift_Ins	INDEL	-	TTTCTGGAATTT	TTTCTGGAATTT	AFF2	insTTTGTTCCTG	P.T641fs
XH_P44	X	24229461	24229461	Frame_Shift_Ins	INDEL	-	AGATCCTTTGTG	AGATCCTTTGTG	ZFX	sATGGAAGATCC	P.M796fs
XH_P45	1	909723	909723	Missense_Mutation	SNP	G	A	G	PLEKHN1	c.G1576A	p.E526K
XH_P45	1	42047604	42047604	Silent	SNP	C	T	C	HIVEP3	c.G2865A	p.G955G
XH_P45	1	42047605	42047605	Missense_Mutation	SNP	C	T	C	HIVEP3	c.G2864A	p.G955E
XH_P45	1	43850740	43850740	Silent	SNP	C	T	C	MED8	c.G513A	p.S171S
XH_P45	1	120165808	120165808	Silent	SNP	G	A	G	ZNF697	c.C1158T	p.C386C
XH_P45	1	143906122	143906122	Missense_Mutation	SNP	C	A	C	FAM72C	c.G245T	p.G82V
XH_P45	1	152323466	152323466	Missense_Mutation	SNP	A	C	A	FLG2	c.T6796G	p.V2266G
XH_P45	1	156551665	156551665	Missense_Mutation	SNP	C	G	C	TTC24	c.C509G	p.P170R
XH_P45	1	157772407	157772407	Missense_Mutation	SNP	G	T	G	FCRL1	c.C367A	p.Q123K
XH_P45	1	179363112	179363112	Missense_Mutation	SNP	G	A	G	AXDND1	c.G938A	p.R313Q
XH_P45	1	179852003	179852003	Missense_Mutation	SNP	G	T	G	TOR1AIP1	c.G366T	p.M122I
XH_P45	1	182856531	182856531	Missense_Mutation	SNP	G	A	G	DHX9	c.G3775A	p.G1259S
XH_P45	1	182856532	182856532	Frame_Shift_Ins	INS	-	AA	-	DHX9	3776_3777insA	p.G1259fs
XH_P45	1	183520049	183520049	In_Frame_Ins	INS	-	CTATTA	-	SMG7	71_3172insCTA	D1057delinsDLL
XH_P45	1	186273365	186273365	In_Frame_Ins	INS	-	CATCTGTTTATG	-	PRG4	23insACATCTTG	108delinsNILFML
XH_P45	1	201437771	201437771	Silent	SNP	G	A	G	PHLDA3	c.C144T	p.G48G
XH_P45	1	212148632	212148632	Nonsense_Mutation	INS	-	TCTGAGGCAAC	-	INTS7	TGCTGAGTTGC	515delinsSSEKICX
XH_P45	1	214819459	214819459	Silent	SNP	A	C	A	CENPF	c.A6546C	p.A2182A
XH_P45	1	223178705	223178705	Silent	SNP	C	T	C	DISP1	c.C3237T	p.V1079V
XH_P45	1	227152761	227152761	Missense_Mutation	SNP	C	T	C	COQ8A	c.C238T	p.H80Y
XH_P45	1	227152778	227152778	Missense_Mutation	SNP	T	G	T	COQ8A	c.T255G	p.H85Q
XH_P45	1	249142545	249142545	Missense_Mutation	SNP	C	T	C	ZNF672	c.C1072T	p.R358W
XH_P45	2	11798684	11798684	Missense_Mutation	SNP	C	T	C	NTSR2	c.G1154A	p.R385Q
XH_P45	2	98177189	98177189	Silent	SNP	G	A	G	ANKRD36B	c.C804T	p.D268D
XH_P45	2	99438796	99438796	Missense_Mutation	SNP	G	A	G	KIAA1211L	c.C1940T	p.P647L
XH_P45	2	108487160	108487160	Splice_Site	DEL	G	-	G	RGPD4	.	.
XH_P45	2	131377636	131377636	Silent	SNP	C	T	C	POTFJ	c.C718T	p.L240L
XH_P45	2	201501684	201501684	Silent	SNP	T	C	T	AOX1	c.T2397C	p.H799H
XH_P45	2	220435402	220435402	Missense_Mutation	SNP	C	T	C	OBSL1	c.G553A	p.E18SK
XH_P45	3	44776636	44776636	Frame_Shift_Ins	INS	-	SAGTCTTACATT	-	ZNF501	AGATTGAGTCTT	p.T241fs
XH_P45	3	119379085	119379085	In_Frame_Ins	INS	-	SCCCAAAGATG	-	POPCD2	SGCGCTCATCTT	insLCCCWRSSGLPKASL
XH_P45	3	182872043	182872043	Frame_Shift_Ins	INS	-	ACTGAAG	-	LAMP3	85_186insCTTCA	p.Q62fs
XH_P45	4	367133	367133	Silent	SNP	C	A	C	ZNF141	c.C679A	p.R227R
XH_P45	4	1730122	1730122	Silent	SNP	G	A	G	TACC3	c.G993A	p.S331S
XH_P45	4	13605800	13605800	Frame_Shift_Ins	INS	-	AGTACACAGAAC	-	BOD1L1	724insCCTTCTG	p.L908fs
XH_P45	4	71099933	71099933	Splice_Site	INS	-	C	-	FDCSP	.	.
XH_P45	4	85657363	85657363	Missense_Mutation	SNP	C	T	C	WDFY3	c.G6875A	p.R2292Q
XH_P45	4	85657364	85657364	Silent	SNP	G	T	G	WDFY3	c.C6874A	p.R2292R
XH_P45	4	109584437	109584437	Silent	SNP	G	A	G	OSTC	c.G480A	p.S160S
XH_P45	4	128818048	128818048	Frame_Shift_Ins	INS	-	ACTATACAGTAG	-	PLK4	701insTACTATA	p.N900fs
XH_P45	4	140046374	140046374	Nonsense_Mutation	INS	-	STAATTTGTGCG	-	ELF2	CTCTATGCACAA	61_M62delinsSVIX
XH_P45	5	15936681	15936681	Missense_Mutation	SNP	G	A	G	FBXL7	c.G721A	p.E241K
XH_P45	5	36251469	36251469	Missense_Mutation	SNP	C	T	C	RANBP3L	c.G1228A	p.E410K
XH_P45	5	149216256	149216256	Silent	SNP	C	T	C	PPARGC1B	c.C1211T	p.G707G
XH_P45	5	175535641	175535641	Missense_Mutation	SNP	G	A	G	FAM153B	c.G665A	p.G222E
XH_P45	6	26056440	26056440	Missense_Mutation	SNP	C	T	C	HIST1H1C	c.G217A	p.V73M
XH_P45	6	42072919	42072919	Missense_Mutation	SNP	C	T	C	C6orf132	c.G2731A	p.E911K
XH_P45	6	143090985	143090985	Missense_Mutation	SNP	C	G	C	HIVEP2	c.G4891C	p.D1631H
XH_P45	7	5265491	5265491	Missense_Mutation	SNP	G	A	G	WIP1	c.G601A	p.G201S
XH_P45	7	15405182	15405182	Missense_Mutation	SNP	C	A	C	AGMO	c.G1220T	p.G407V
XH_P45	7	39649581	39649582	Frame_Shift_Del	DEL	TT	-	TT	YAE1D1	c.617_618del	p.T06fs
XH_P45	7	57188238	57188238	Missense_Mutation	SNP	C	T	C	ZNF479	c.G884A	p.R295K
XH_P45	7	64169028	64169028	Frame_Shift_Ins	INS	-	G	-	ZNF107	-2457_2458insG	p.R819fs
XH_P45	7	64169029	64169029	Missense_Mutation	SNP	A	C	A	ZNF107	c.A2458C	p.T820P
XH_P45	7	64292354	64292354	Missense_Mutation	SNP	G	A	G	ZNF138	c.G293A	p.R98H
XH_P45	7	76029798	76029798	Missense_Mutation	SNP	C	T	C	SSCAD	c.G280A	p.V94I
XH_P45	7	100675718	100675718	Frame_Shift_Ins	INS	-	TCAACACCACA	-	MUC17	1022insTCAAC	p.A341fs
XH_P45	7	100684419	100684419	Missense_Mutation	SNP	T	C	T	MUC17	c.T9722C	p.I3241T
XH_P45	7	117188877	117188877	Missense_Mutation	SNP	G	T	G	CFR1	c.G1392T	p.K464N
XH_P45	7	143090920	143090920	Missense_Mutation	SNP	G	A	G	EPHA1	c.C2540T	p.P847L
XH_P45	8	10465894	10465894	In_Frame_Ins	INS	-	CCTCCCATCTCG	-	RP1L1	AGAGGCAGAAAT	insDVEPPEAEWEVQPESEG
XH_P45	8	75157007	75157007	Silent	SNP	G	A	G	JPH1	c.C1662T	p.Y554Y
XH_P45	8	133187777	133187777	Missense_Mutation	SNP	C	T	C	KCNQ3	c.G496A	p.V166I
XH_P45	8	144874523	144874523	Missense_Mutation	SNP	C	T	C	SCRIB	c.G4381A	p.A1461T
XH_P45	9	71836286	71836286	Missense_Mutation	SNP	G	A	G	TJP2	c.G838A	p.D280N
XH_P45	9	88624819	88624819	Silent	SNP	C	T	C	NAA35	c.C1263T	p.I421I
XH_P45	9	116811587	116811587	Missense_Mutation	SNP	G	A	G	ZNF618	c.G1906A	p.E636K
XH_P45	9	130580435	130580435	Silent	SNP	C	T	C	ENG	c.G1650A	p.T550T
XH_P45	10	8007521	8007521	In_Frame_Ins	INS	-	TTTCTCTCT	-	TAF3	8_2049insTTTCT	P683delinsPFSL
XH_P45	10	88912127	88912127	Missense_Mutation	SNP	C	A	C	FAM35A	c.C1016A	p.S339Y
XH_P45	10	129904386	129904386	Silent	SNP	C	T	C	MKI67	c.G4638A	p.T1546T
XH_P45	11	609242	609242	Silent	SNP	C	T	C	PHRF1	c.C3786T	p.G1262G
XH_P45	11	1651346	1651346	Silent	SNP	C	T	C	KRTAP5-5	c.C276T	p.C92C
XH_P45	11	10536511	10536511	Silent	SNP	G	A	G	RNF141	c.C645T	p.N215N
XH_P45	11	31703413	31703413	Silent	SNP	C	T	C	ELP4	c.C1222T	p.L408L
XH_P45	11	31703414	31703414	Missense_Mutation	SNP	T	G	T	ELP4	c.T1223G	p.L408R
XH_P45	11	62289981	62289981	Missense_Mutation	SNP	C	T	C	AHNAK	c.G11908A	p.V3970I
XH_P45	11	62295116	62295116	Missense_Mutation	SNP	C	G	C	AHNAK	c.G6773C	p.G2258A
XH_P45	11	64601971	64601971	Missense_Mutation	SNP	C	T	C	CDC42BPG	c.G2254A	p.E752K
XH_P45	11	68773443	68773443	Missense_Mutation	SNP	G	A	G	MRGPRF	c.C335T	p.A112V
XH_P45	11	76062520	76062520	Missense_Mutation	SNP	T	A	T	THAP12	c.A1674T	p.R558S
XH_P45	11	85712094	85712094	Missense_Mutation	SNP	C	T	C	PICALM	c.G1001A	p.R334H
XH_P45	12	7636271	7636271	Frame_Shift_Ins	INS	-	GGGA	-	CD163	779_2780insTC	p.N927fs
XH_P45	12	7636272	7636272	Splice_Site	SNP	C	T	C	CD163	.	.
XH_P45	12	10962149	10962149	Missense_Mutation	SNP	C	T	C	TAS2R9	c.G526A	p.G176S
XH_P45	12	11546058	11546058	Silent	SNP	G	A	G	PRB2	c.C954T	p.P318P
XH_P45	12	53162773	53162775	In_Frame_Del	DEL	ACT	-	ACT	KRT76	c.1639_1641del	p.547_547del
XH_P45	12	57567621	57567621	Silent	SNP	G	A	G	LRP1	c.G3405A	p.S1135S
XH_P45	12	70954714	70954714	Nonsense_Mutation	INS	-	CACGGTGCCCCAC	-	PTPRB	ATGAGGCTGGG	83delinsEKVYEAAGHRGSCSX
XH_P45	12	104121124	104121124	Missense_Mutation	SNP	C	T	C	STAB2	c.C4931T	p.A1644V
XH_P45	12	109639409	109639409	Missense_Mutation	SNP	G	A	G	ACACB	c.G2816A	p.R939K
XH_P45	12	125397652	125397652	Silent	SNP	T	C	T	UBC	c.A666G	p.V222V
XH_P45	13	50279847	50279847	Missense_Mutation	SNP	C	A	C	KPNA3	c.G1282T	p.V428F
XH_P45	14	59113387	59113387	Silent	SNP	G	A	G	DACT1	c.G1935A	p.S645S
XH_P45	14	71275774	71275779	In_Frame_Del	DEL	CCTCCT	-	CCTCCT	MAP3K9	c.110_115del	p.37_39del

XH_P45	14	97031383	97031383	Missense_Mutation	SNP	G	A	G	PAPOLA	c.G1484A	p.R495Q
XH_P45	14	105413588	105413588	Missense_Mutation	SNP	G	C	G	AHNAK2	c.C7900G	p.L2634V
XH_P45	15	24921537	24921537	Missense_Mutation	SNP	G	A	G	NPAP1	c.G523A	p.E175K
XH_P45	15	75982185	75982185	Silent	SNP	T	C	T	CSPG4	c.A1221G	p.P407P
XH_P45	15	90336303	90336303	Missense_Mutation	SNP	T	A	T	ANPEP	c.A2212T	p.N738Y
XH_P45	16	1291545	1291545	Missense_Mutation	SNP	C	T	C	TPSAB1	c.C344T	p.T115I
XH_P45	16	1291547	1291552	In_Frame_Del	DEL	GCCCAG	-	GCCCAG	TPSAB1	c.346_351del	p.116_117del
XH_P45	16	2230709	2230709	Missense_Mutation	SNP	G	A	G	CASKIN1	c.C2660T	p.A887V
XH_P45	16	3778907	3778907	Silent	SNP	G	A	G	CREBBP	c.C6027T	p.A2009A
XH_P45	16	27364014	27364014	Missense_Mutation	SNP	A	C	A	IL4R	c.A667C	p.N223H
XH_P45	16	27364015	27364015	Frame_Shift_Ins	INS	-	GC	-	IL4R	c.668_669insGC	p.N223fs
XH_P45	16	66946227	66946227	Missense_Mutation	SNP	G	A	G	CDH16	c.C1175T	p.A392V
XH_P45	17	1557187	1557187	Nonsense_Mutation	INS	-	ACCTAA	-	PRPF8	10_6111insTTAb	S2037delinsSX
XH_P45	17	4936297	4936297	Silent	SNP	G	A	G	SLC52A1	c.C1302T	p.H434H
XH_P45	17	7809273	7809273	Missense_Mutation	SNP	C	T	C	CHD3	c.C4501T	p.R1501W
XH_P45	17	15458614	15458614	In_Frame_Ins	INS	-	TGAATAATT	-	TVP23C	6_77insAATTAT	p.P26delinsQLFT
XH_P45	17	38068586	38068586	Missense_Mutation	SNP	C	T	C	GSDMB	c.G400A	p.E134K
XH_P45	17	40266570	40266570	Missense_Mutation	SNP	G	A	G	KAT2A	c.C2072T	p.P691L
XH_P45	17	48431278	48431278	Silent	SNP	C	T	C	XYLT2	c.C423T	p.H141H
XH_P45	17	55962727	55962727	Missense_Mutation	SNP	C	T	C	CUEDC1	c.G199A	p.E67K
XH_P45	17	56348148	56348148	Frame_Shift_Ins	INS	-	GAGATCTGGGCC	-	MPO	GGCCCTGGCCCA	p.1703fs
XH_P45	17	57157227	57157227	In_Frame_Ins	INS	-	TTG	-	TRIM37	1_401_402insCA	p.V134delinsVK
XH_P45	17	57157229	57157229	Missense_Mutation	SNP	C	G	C	TRIM37	c.G400C	p.V134L
XH_P45	18	14851839	14851839	Missense_Mutation	SNP	C	A	C	ANKRD30B	c.C3539A	p.P1180H
XH_P45	18	33751074	33751074	Missense_Mutation	SNP	C	G	C	ELP2	c.C2065G	p.Q689E
XH_P45	18	76753611	76753611	Silent	SNP	C	T	C	SALL3	c.C1620T	p.Y540Y
XH_P45	19	7267569	7267569	Missense_Mutation	SNP	C	T	C	INSR	c.G439A	p.E147K
XH_P45	19	7620584	7620584	Missense_Mutation	SNP	G	A	G	PNPLA6	c.G3028A	p.G1010R
XH_P45	19	10225013	10225013	Missense_Mutation	SNP	G	A	G	P2RY11	c.G724A	p.E242K
XH_P45	19	12638185	12638185	Missense_Mutation	SNP	C	T	C	ZNF564	c.G737A	p.R246K
XH_P45	19	17893940	17893940	Silent	SNP	C	T	C	FCHO1	c.C1902T	p.T634T
XH_P45	19	19906093	19906093	Silent	SNP	A	G	A	ZNF506	c.T507C	p.Y169Y
XH_P45	19	21476874	21476874	Silent	SNP	G	A	G	ZNF708	c.C702T	p.H234H
XH_P45	19	21719866	21719866	Silent	SNP	T	A	T	ZNF429	c.T819A	p.G273G
XH_P45	19	21991985	21991985	Missense_Mutation	SNP	A	G	A	ZNF43	c.T659C	p.F220S
XH_P45	19	21991986	21991986	Missense_Mutation	SNP	A	G	A	ZNF43	c.T658C	p.F220L
XH_P45	19	22847485	22847485	Silent	SNP	G	A	G	ZNF492	c.G1014A	p.K338K
XH_P45	19	23542824	23542824	Missense_Mutation	SNP	A	C	A	ZNF91	c.T2861G	p.I954R
XH_P45	19	23543355	23543355	Missense_Mutation	SNP	C	T	C	ZNF91	c.G2330A	p.R777H
XH_P45	19	23926839	23926839	Missense_Mutation	SNP	A	G	A	ZNF681	c.T1513C	p.S505P
XH_P45	19	44223788	44223788	Missense_Mutation	SNP	G	A	G	IRGC	c.G1078A	p.A360T
XH_P45	19	44611162	44611162	Silent	SNP	G	A	G	ZNF224	c.G849A	p.T283T
XH_P45	19	48800557	48800557	Silent	SNP	G	A	G	CCDC114	c.C1689T	p.G563G
XH_P45	19	50827179	50827179	Missense_Mutation	SNP	G	A	G	KCN3	c.C1031T	p.T344M
XH_P45	19	53643561	53643561	Nonstop_Mutation	SNP	C	A	C	ZNF347	c.G2523T	p.X841Y
XH_P45	19	53643562	53643562	Nonstop_Mutation	SNP	T	A	T	ZNF347	c.A2522T	p.X841L
XH_P45	19	54080841	54080841	Missense_Mutation	SNP	G	A	G	ZNF331	c.G1027A	p.V343I
XH_P45	20	3363139	3363139	Frame_Shift_Ins	INS	-	TCAGCCTCCT	-	C20orf194	98insAGGAGG	p.R33fs
XH_P45	20	31395666	31395666	Missense_Mutation	SNP	G	A	G	DNMT3B	c.G2042A	p.R681Q
XH_P45	20	34320005	34320005	In_Frame_Ins	INS	-	ATG	-	RBM39	1_153_154insCA	p.S52delinsHS
XH_P45	21	34100309	34100309	Missense_Mutation	SNP	C	G	C	SYNJ1	c.G43C	p.G15R
XH_P45	22	20812233	20812233	Silent	SNP	G	A	G	KLHL22	c.C1167T	p.H389H
XH_P45	22	50615772	50615772	Missense_Mutation	SNP	G	A	G	PANX2	c.G631A	p.E211K
XH_P45	22	50616578	50616578	Frame_Shift_Ins	INS	-	TCAGGCATTGCC	-	PANX2	ACGAATTCAGG	p.R479fs
XH_P45	X	20060641	20060641	In_Frame_Ins	INS	-	TGA	-	MAP7D2	1_727_728insTC	p.P243delinsLT
XH_P45	X	135582958	135582958	Missense_Mutation	SNP	G	T	G	HTATSF1	c.G551T	p.G184V
XH_P45	1	120165808	120165808	Silent	SNV	G	A	A	ZNF697	c.1158C>T	P.C386C
XH_P45	1	179852003	179852003	Missense_Mutation	SNV	G	T	T	TOR1AIP1	c.366G>T	P.M122I
XH_P45	1	214819459	214819459	Silent	SNV	A	C	C	CENPF	c.6546A>C	P.A2182A
XH_P45	11	10536511	10536511	Silent	SNV	G	A	A	RNF141	c.645C>T	P.N215N
XH_P45	11	1651346	1651346	Silent	SNV	C	T	T	KRTAP5-5	c.276C>T	P.C92C
XH_P45	12	10962149	10962149	Missense_Mutation	SNV	C	T	T	TAS2R9	c.526G>A	P.G176S
XH_P45	12	109639409	109639409	Missense_Mutation	SNV	G	A	A	ACACB	c.2816G>A	P.R939K
XH_P45	15	24921537	24921537	Missense_Mutation	SNV	G	A	A	NPAP1	c.523G>A	P.E175K
XH_P45	15	90336303	90336303	Missense_Mutation	SNV	T	A	A	ANPEP	c.2212A>T	P.N738Y
XH_P45	17	48431278	48431278	Silent	SNV	C	T	T	XYLT2	c.423C>T	P.H141H
XH_P45	18	14851839	14851839	Missense_Mutation	SNV	C	A	A	ANKRD30B	c.3539C>A	P.P1180H
XH_P45	19	21719866	21719866	Silent	SNV	T	A	A	ZNF429	c.1011T>A	P.G337G
XH_P45	19	53643561	53643561	Nonstop_Mutation	SNV	C	A	A	ZNF347	c.2523G>T	P.Ter841Yext**?
XH_P45	19	53643562	53643562	Nonstop_Mutation	SNV	T	A	A	ZNF347	c.2522A>T	P.Ter841Lext**?
XH_P45	2	108487160	108487160	Frame_Shift_Del	INDEL	G	-	-	RGPD4	c.2702delG	P.G901fs
XH_P45	2	11798684	11798684	Missense_Mutation	SNV	C	T	T	NTRS2	c.1154G>A	P.R385Q
XH_P45	2	201501684	201501684	Silent	SNV	T	C	C	AOX1	c.2397T>C	P.H799H
XH_P45	2	220435402	220435402	Missense_Mutation	SNV	C	T	T	OBSL1	c.553G>A	P.E185K
XH_P45	21	34100309	34100309	Missense_Mutation	SNV	C	G	G	SYNJ1	c.43G>C	P.G15R
XH_P45	6	143090985	143090985	Missense_Mutation	SNV	C	G	G	HIVEP2	c.4891G>C	P.D1631H
XH_P45	7	143090920	143090920	Missense_Mutation	SNV	G	A	A	EPHA1	c.2540C>T	P.P847L
XH_P45	7	15405182	15405182	Missense_Mutation	SNV	C	A	A	AGMO	c.1220G>T	P.G407V
XH_P45	7	57188238	57188238	Missense_Mutation	SNV	C	T	T	ZNF479	c.884G>A	P.R295K
XH_P45	8	133187777	133187777	Missense_Mutation	SNV	C	T	T	KCNQ3	c.496G>A	P.V166I
XH_P45	X	38535121	38535121	Splice_Site	SNV	G	A	A	TSPAN7	c.597+7G>A	
XH_P46	-	-	-	Frame_Shift_Ins	INS	-	-	-	FBXW7	c.544dup	p.S182Ffs*74
XH_P46	12	25398284	25398284	Missense_Mutation	SNP	C	T	T	KRAS	c.35G>A	p.G12D
XH_P46	17	7577570	7577570	Missense_Mutation	SNP	C	G	G	TP53	c.711G>C	p.M237I
XH_P46	8	31498185	31498185	Missense_Mutation	SNP	C	A	A	NRG1	c.685C>A	p.P229T
XH_P46	X	70347827	70347827	Missense_Mutation	SNP	G	T	T	MED12	c.3066G>T	p.M1022I
XH_P46	-	-	-	Frame_Shift_Ins	INS	-	-	-	RNF43	c.327_328insCA	p.E110Qfs*49
XH_P46	-	-	-	Frame_Shift_Del	INS	-	-	-	RNF43	c.118del	P.R40Dfs*11
XH_P46	1	1139317	1139317	Missense_Mutation	SNP	C	T	C	TNFRSF18	c.G422A	p.R141Q
XH_P46	1	1722017	1722017	In_Frame_Ins	INS	-	AGA	-	GNB1	1_215_216insTC	p.E72delinsDL
XH_P46	1	3544132	3544132	Frame_Shift_Ins	INS	-	TGTAGTITTTAT	-	TPRG1L	CGGCTTGTAGT	p.N180fs
XH_P46	1	8074451	8074451	Frame_Shift_Ins	INS	-	CCTCTCTCTGG	-	ERF11	208insCCAGAG	p.A70fs
XH_P46	1	11140899	11140899	Frame_Shift_Ins	INS	-	TGTGTGTGTGT	-	EXOSC10	ACACACACACA	p.N503fs
XH_P46	1	12908041	12908041	Missense_Mutation	SNP	C	A	C	HNRNPCL1	c.G102T	p.E34D
XH_P46	1	14108709	14108709	Nonsense_Mutation	INS	-	AGTTAAGCCTTT	-	PRDM2	7insTAAAGTTAA	H.1272delinsHX
XH_P46	1	19071410	19071410	Missense_Mutation	SNP	G	A	G	PAX7	c.G1505A	p.G502D
XH_P46	1	25785324	25785324	Nonsense_Mutation	INS	-	TTAATCTTTTACT	-	TMEM57	CATTATTTAATC	65_D36delinsKIII
XH_P46	1	26800627	26800627	Splice_Site	INS	-	TGTTTTTGTATG	-	HMG2	.	.

XH_P46	1	28128324	28128324	Nonsense_Mutation	INS	-	AATAAATTGCT	-	STX12	AAATTAATAAA	142_ A143delinsX
XH_P46	1	28343741	28343741	Nonsense_Mutation	INS	-	TCTTCACT	-	EYA3	371insAGTGA	124_ N125delinsX
XH_P46	1	28343743	28343743	Missense_Mutation	SNP	G	C	G	EYA3	c.C369G	p.S123R
XH_P46	1	28948546	28948546	Nonsense_Mutation	INS	-	TTTGTGTGTTT	-	TAF12	ATTAACAAACAA	6delinsSYIKTNKKSX
XH_P46	1	33060810	33060810	Nonsense_Mutation	INS	-	GAATTTTATTA	-	ZBTB8A	CGAAGAAATTT	H32delinsKRRKKFYX
XH_P46	1	33060812	33060812	Silent	SNP	C	T	C	ZBTB8A	c.C98T1	p.S327S
XH_P46	1	33558956	33558956	In_Frame_Ins	INS	-	CCC	-	AZIN2	241_ 242insCC	p.K81delinsTQ
XH_P46	1	33558958	33558958	Missense_Mutation	SNP	A	T	A	AZIN2	c.A243T	p.K81N
XH_P46	1	35454261	35454261	Missense_Mutation	SNP	A	G	A	ZMYM6	c.T2422C	p.S808P
XH_P46	1	35454262	35454262	Frame_Shift_Ins	INS	-	SAGAGTCAAAGT	-	ZMYM6	21insCCACTTTG	p.K807fs
XH_P46	1	35580088	35580088	Frame_Shift_Ins	INS	-	ACAAATAGTG	-	ZMYM1	2433insACAAA	p.I811fs
XH_P46	1	38484957	38484957	Frame_Shift_Ins	INS	-	TTAAACCATTTG	-	UTP11	nsAGTTTAAACC	p.T157fs
XH_P46	1	39353635	39353635	In_Frame_Ins	INS	-	TGCCATATT	-	RHBDL2	972insAATATC	P324delinsPIWQ
XH_P46	1	39353637	39353637	Frame_Shift_Ins	INS	-	TAGCT	-	RHBDL2	969_ 970insAGC	p.P324fs
XH_P46	1	40562846	40562846	Missense_Mutation	SNP	C	G	C	PPT1	c.G65C	p.R22P
XH_P46	1	40703241	40703241	Nonsense_Mutation	INS	-	TTCTTATGTCTC	-	RLF	58insATTCTTTA	956_ G957delinsX
XH_P46	1	40735788	40735788	Frame_Shift_Ins	INS	-	AAGACAATGGG	-	ZMPSTE24	AGCTTAAGACAA	p.V206fs
XH_P46	1	40961047	40961047	Frame_Shift_Ins	INS	-	TA	-	ZFP69	c.900_ 901insTA	p.F300fs
XH_P46	1	40961049	40961049	Frame_Shift_Ins	INS	-	ACATCATCAT	-	ZFP69	903insACATCA	p.R301fs
XH_P46	1	43055136	43055136	In_Frame_Ins	INS	-	AGGGGTATGTGT	-	CCDC30	66insGTAGGGT	455delinsEVGVVS
XH_P46	1	45232592	45232592	Frame_Shift_Ins	INS	-	AGCTTGTTTTTTT	-	KIF2C	944insAGCTTG	p.Q648fs
XH_P46	1	45981376	45981376	Silent	SNP	G	A	G	PRDX1	c.C210T	p.N70N
XH_P46	1	46206963	46206963	Frame_Shift_Ins	INS	-	SCAATGGATTCT	-	IPP	34insCAGAAATC	p.I112fs
XH_P46	1	46726537	46726537	Nonsense_Mutation	SNP	G	T	G	RAD54L	c.G616T	p.E206X
XH_P46	1	46726538	46726538	Frame_Shift_Ins	INS	-	CCTC	-	RAD54L	617_ 618insCT	p.E206fs
XH_P46	1	52399108	52399108	Silent	SNP	A	T	A	RAB3B	c.T354A	p.T118T
XH_P46	1	52399109	52399109	Nonsense_Mutation	INS	-	TTGTTTATATT	-	RAB3B	sTACAAATATAA	18_ Q119delinsQIX
XH_P46	1	52704563	52704563	Frame_Shift_Ins	INS	-	AACCTTCATTTG	-	ZFYVE9	75insATAACCTT	p.P492fs
XH_P46	1	54262816	54262816	Frame_Shift_Ins	INS	-	GGTGAGAATTA	-	NDC1	1104insTAATT	p.E368fs
XH_P46	1	60476099	60476099	Nonsense_Mutation	INS	-	ATAGCTAGGTAT	-	C1orf87	1157insATACCT	R38delinsNTX
XH_P46	1	61554336	61554336	Nonsense_Mutation	INS	-	TCATGTTTTTGA	-	NFIA	5CTTTTCATGTT	F182delinsYAFHVF
XH_P46	1	62675863	62675863	Frame_Shift_Ins	INS	-	AGCAACTTTTAC	-	L1TD1	insGCTTAGCA	p.V473fs
XH_P46	1	62941477	62941477	In_Frame_Ins	INS	-	TTTTCTTTAAAA	-	DOCK7	5insACCTTTTAA	912delinsQPFKEKA
XH_P46	1	63024889	63024889	Nonsense_Mutation	INS	-	GGGGTGGGAAGA	-	DOCK7	AATAACATCTTC	34_ P735delinsDKX
XH_P46	1	63063611	63063611	Frame_Shift_Ins	INS	-	TTGGCTCTGGAG	-	ANGPTL3	5insTTTTGGCTC	p.E125fs
XH_P46	1	67098767	67098767	Missense_Mutation	SNP	G	C	G	SGIP1	c.G89C	p.R30T
XH_P46	1	75684309	75684309	Nonsense_Mutation	INS	-	TTTTACAATCCC	-	SLC44A5	1377insGGGATT	L459delinsLGLX
XH_P46	1	77629619	77629619	Nonsense_Mutation	INS	-	GTTTTAAAAAGA	-	PIGK	GTTTTCTTTTAA	N167delinsNSQFFFX
XH_P46	1	84867733	84867733	In_Frame_Ins	INS	-	TATCTCTCATTTG	-	DNASE2B	TAATATATCTCT	delinsHTLIYLSFLFHG
XH_P46	1	85128148	85128148	Missense_Mutation	SNP	T	A	T	SSX2IP	c.A658T	p.T220S
XH_P46	1	85128150	85128150	Nonsense_Mutation	INS	-	IGAATAATTAAAA	-	SSX2IP	ACATATTTTTAA	19delinsTTFYNSYX
XH_P46	1	85491913	85491913	Nonsense_Mutation	INS	-	T	-	MCOLN3	c.718_ 719insA	C240_ L241delinsX
XH_P46	1	91404951	91404951	Frame_Shift_Ins	INS	-	GA	-	ZNF644	1959_ 1960insT	p.N654fs
XH_P46	1	91404952	91404952	Nonsense_Mutation	INS	-	AAAACCTAAGT	-	ZNF644	959insTACTTAG	53_ N654delinsNTX
XH_P46	1	92446883	92446883	Frame_Shift_Ins	INS	-	TTGCTCAG	-	BRDT	1_ 1672insTTGC	p.E557fs
XH_P46	1	92647815	92647815	In_Frame_Ins	INS	-	TTCCAGCAGATTC	-	KIAA1107	3037insTTCACG	1012delinsKFTTF
XH_P46	1	92647817	92647817	Missense_Mutation	SNP	A	T	A	KIAA1107	c.A3038T	p.N1013I
XH_P46	1	94997961	94997961	Nonsense_Mutation	INS	-	AGGTTTTTTGTT	-	F3	sTAACCAACAAA	223_ V224delinsX
XH_P46	1	97215229	97215229	Nonsense_Mutation	INS	-	TTCTAAGCCTGA	-	PTBP2	ATCATCTAAGC	1delinsVTVLNHSPKPEVLYX
XH_P46	1	100681751	100681751	Missense_Mutation	SNP	T	A	T	DBT	c.A560T	p.K187M
XH_P46	1	100681753	100681753	Frame_Shift_Ins	INS	-	TTTTCTTTTCTTT	-	DBT	AAAAAAAGAAA	p.1186fs
XH_P46	1	104166750	104166750	Frame_Shift_Ins	INS	-	TAGTAACCTCTT	-	AMY2A	sATTAATAGTAA	p.G418fs
XH_P46	1	109466728	109466728	Frame_Shift_Ins	INS	-	ACTATATTCT	-	GPSM2	1708insACTAT	p.L569fs
XH_P46	1	109466730	109466730	Missense_Mutation	SNP	C	T	C	GPSM2	c.C1709T	p.P570L
XH_P46	1	109816242	109816242	Silent	SNP	C	T	C	CELSR2	c.C8694T	p.L2898I
XH_P46	1	110200396	110200396	Nonsense_Mutation	INS	-	GATAGAT	-	GSTM4	62_ 263insGATAG	888_ RH8delinsGX
XH_P46	1	111495401	111495401	Nonsense_Mutation	INS	-	GTCTTCAAAC	-	LRIF1	105insAGTTTGA	p.135delinsVX
XH_P46	1	115216703	115216703	Frame_Shift_Ins	INS	-	GTTGTCTC	-	AMPD1	7_ 1888insGAA	p.S630fs
XH_P46	1	115216705	115216705	Splice_Site	SNP	T	C	T	AMPD1	.	.
XH_P46	1	117122285	117122285	Missense_Mutation	SNP	G	C	G	IGSF3	c.C3063G	p.D1021E
XH_P46	1	117617767	117617767	Nonsense_Mutation	INS	-	TAATTAATCTT	-	TTF2	562insTAATTA	187_ Q188delinsXK
XH_P46	1	117617769	117617769	Frame_Shift_Ins	INS	-	T	-	TTF2	c.S63_ 564insT	p.Q188fs
XH_P46	1	117618192	117618192	Missense_Mutation	SNP	C	T	C	TTF2	c.C986T	p.A329V
XH_P46	1	118449137	118449137	Frame_Shift_Ins	INS	-	GGAGCATTTTCG	-	GDAP2	527insACGAAAT	p.D209fs
XH_P46	1	144879219	144879219	Frame_Shift_Ins	INS	-	ATTTAAATGGTA	-	PDE4DIP	717insCTACCAT	p.S1573fs
XH_P46	1	145330777	145330777	Missense_Mutation	SNP	A	T	A	NBPF20	c.A6691T	p.T2231S
XH_P46	1	145330778	145330778	Missense_Mutation	SNP	C	G	C	NBPF20	c.C6692G	p.T2231S
XH_P46	1	145354364	145354364	Silent	SNP	A	G	A	NBPF10	c.A7779G	p.S2593S
XH_P46	1	148010146	148010146	Nonsense_Mutation	INS	-	ATCATTTAGTAA	-	NBPF19	3227insTTACTA	E1076delinsVTXK
XH_P46	1	151090631	151090631	Frame_Shift_Ins	INS	-	CTCTCTT	-	GABPB2	12_ 1013insCTC	p.V338fs
XH_P46	1	152279841	152279841	Missense_Mutation	SNP	G	C	G	FLG	c.C7521G	p.H2507Q
XH_P46	1	152325990	152325990	Silent	SNP	A	G	A	FLG2	c.T4272C	p.H1424H
XH_P46	1	152327434	152327434	Frame_Shift_Ins	INS	-	AT	-	FLG2	2827_ 2828insA	p.G943fs
XH_P46	1	152327436	152327436	Frame_Shift_Ins	INS	-	TATGGTCAACA	-	FLG2	6insCCATGTTG	p.S942fs
XH_P46	1	152328398	152328398	Missense_Mutation	SNP	T	C	T	FLG2	c.A1864G	p.S622G
XH_P46	1	152328411	152328411	Silent	SNP	A	G	A	FLG2	c.T1851C	p.S617S
XH_P46	1	152328908	152328908	Nonsense_Mutation	INS	-	CAATCATCTGGC	-	FLG2	1354insGCCAGAG	T452delinsARX
XH_P46	1	153800595	153800595	Nonsense_Mutation	INS	-	ATCCTAAAGA	-	GATAD2B	229insTCTTTA	77_ K78delinsSLGX
XH_P46	1	153982585	153982585	Nonsense_Mutation	INS	-	ATATCTGTAGTTT	-	NUP210L	AGATGAAACTAG	N1599delinsQMKLQIX
XH_P46	1	155314064	155314064	Frame_Shift_Ins	INS	-	T	-	ASH1L	c.7890_ 7891ins	p.E2631fs
XH_P46	1	155314065	155314065	Splice_Site	INS	-	ATAATACTAAT	-	ASH1L	.	.
XH_P46	1	155737298	155737298	Frame_Shift_Ins	INS	-	AAAATAATAG	-	GON4L	2681insCTATT	p.G894fs
XH_P46	1	155737299	155737299	Missense_Mutation	SNP	C	G	C	GON4L	c.G2680C	p.G894R
XH_P46	1	156532441	156532441	Missense_Mutation	SNP	T	G	T	IQGAP3	c.A815C	p.Q272P
XH_P46	1	156532443	156532443	In_Frame_Ins	INS	-	AAGCTT	-	IQGAP3	12_ 813insAAGG	S271delinsRSF
XH_P46	1	156708485	156708485	Frame_Shift_Ins	INS	-	AAGTG	-	MRPL24	11_ 12insCACT	p.S4fs
XH_P46	1	158747024	158747024	In_Frame_Ins	INS	-	ACTTCTCTCTTA	-	OR6N2	TGATAAAGAAAG	34delinsIMIKKVVIR
XH_P46	1	159505633	159505633	Frame_Shift_Ins	INS	-	GTCTTTGGC	-	OR10J5	165insGCCAAA	p.L55fs
XH_P46	1	160000746	160000746	Frame_Shift_Ins	INS	-	CTCTGGAAAG	-	PIGM	nsAGCTCTTTCC	p.L262fs
XH_P46	1	169565266	169565266	In_Frame_Ins	INS	-	TCATCTCCC	-	SELP	1998insGGGAG	T666delinsTGDD
XH_P46	1	169565267	169565267	Missense_Mutation	SNP	G	T	G	SELP	c.C1997A	p.T666N
XH_P46	1	171509822	171509822	Nonsense_Mutation	INS	-	TGATTGTAGATT	-	PRRC2C	AGTTTCTGATT	71_ Q1072delinsTSFX
XH_P46	1	171511136	171511136	Frame_Shift_Ins	INS	-	TTTCTCTAGCTG	-	PRRC2C	526insCTTTCTC	p.R1509fs
XH_P46	1	176659395	176659395	Missense_Mutation	SNP	T	G	T	PAPPA2	c.T2260G	p.C754G
XH_P46	1	179816750	179816750	Nonsense_Mutation	INS	-	SGTAGTGAGACA	-	TOR1AIIP2	ACTATGTCTCA	192_ T193delinsLX
XH_P46	1	182856511	182856511	Frame_Shift_Ins	INS	-	CCATCTCCATAC	-	DXH9	756insACCATCT	p.G1252fs
XH_P46	1	183212377	183212377	Frame_Shift_Ins	INS	-	TTTAAAGCTTAT	-	LAMC2	25insATTTTAAA	p.M1142fs
XH_P46	1	183511399	183511399	Frame_Shift_Ins	INS	-	AAATAAAT	-	SMG7	8_ 1479insAAAT	p.N493fs

XH_P46	1	183511400	183511400	Nonsense_Mutation	INS	-	TATATAAAAAAC	-	SMG7	30insCATATATA	93_N494delinsNHIX
XH_P46	1	185966595	185966595	Frame_Shift_Ins	INS	-	CC	-	HMCN1	3813_3814insC	p.Y1271fs
XH_P46	1	185966597	185966597	Frame_Shift_Ins	INS	-	TCACATAGTAC	-	HMCN1	3816insTCACA	p.N1272fs
XH_P46	1	197030151	197030151	Nonsense_Mutation	INS	-	ATTTTTAATTATC	-	F13B	CAACATAATTAA	9_F170delinsRLSLTX
XH_P46	1	197070185	197070185	In_Frame_Ins	INS	-	GTAGAAATGGTCA	-	ASPM	8196insTGACCA	2732delinsSDHST
XH_P46	1	197071967	197071967	Nonsense_Mutation	INS	-	ATTTAGAACTCT	-	ASPM	ATCATTAGAGTT	88_M2139delinsTHHX
XH_P46	1	197091723	197091723	Frame_Shift_Ins	INS	-	TCCTCCTGCATA	-	ASPM	3insATTATGCA	p.V1131fs
XH_P46	1	197128938	197128938	Nonsense_Mutation	INS	-	AAAAATATACTC	-	ZBTB41	1insTAAGAGTA	p.E761delinsX
XH_P46	1	201180243	201180243	Silent	SNP	A	G	A	IGFN1	c.A6222G	p.L2074L
XH_P46	1	206821209	206821209	Nonsense_Mutation	INS	-	GGTGGTGTTTA	-	DYRK3	nsTGAGGTGGT	10_Q222delinsQX
XH_P46	1	207273216	207273216	In_Frame_Ins	INS	-	AGTGTGTTGTT	-	C4BPB	GTTCAGTGTG	34delinsDLFSVCLVL
XH_P46	1	210187033	210187033	In_Frame_Ins	INS	-	GTGTGTTCAATTC	-	SYT14	insACAGTTGTT	139delinsMTVVQFI
XH_P46	1	210187035	210187035	Missense_Mutation	SNP	T	A	T	SYT14	c.T119A	p.L40Q
XH_P46	1	215793709	215793709	Frame_Shift_Ins	INS	-	TCATGGGTGGT	-	KCTD3	2insCTTCATGG	p.E731fs
XH_P46	1	220142158	220142158	Missense_Mutation	SNP	C	T	C	EPRS	c.G4529A	p.R1510H
XH_P46	1	222892296	222892296	Nonsense_Mutation	INS	-	AAGGGAATTAA	-	BROX	2insCTAAGGGA	144_E45delinsLX
XH_P46	1	226252147	226252147	Frame_Shift_Ins	INS	-	CCAAATCTGGAA	-	H3F3a	6insCCCAAAATCT	p.S32fs
XH_P46	1	228285343	228285343	Missense_Mutation	SNP	G	A	G	ARF1	c.G311A	p.R104H
XH_P46	1	228612922	228612922	Silent	SNP	G	A	G	HIST3H3	c.C105T	p.G35G
XH_P46	1	230819382	230819382	Splice_Site	INS	-	TTTTTTTTTTTTT	-	COG2	.	.
XH_P46	1	231298885	231298951	Frame_Shift_Del	DEL	CTGGAGCAC	-	CTGGAGCACG	TRIM67	c.170_236del	p.L57fs
XH_P46	1	232942845	232942845	Nonsense_Mutation	INS	-	ATCTCTCTATA	-	MAP10	nsTATTATCTTC	139delinsEYLSLX
XH_P46	1	235918909	235918909	Frame_Shift_Ins	INS	-	TTCTTTTCTTTTC	-	LYST	5AAAAGAAAAG	p.Q2366fs
XH_P46	1	235918911	235918911	Missense_Mutation	SNP	G	T	G	LYST	c.C7096A	p.Q2366K
XH_P46	1	236389778	236389778	Frame_Shift_Ins	INS	-	CC	-	ERO1B	c.842_843insGG	p.K281fs
XH_P46	1	236389779	236389779	Frame_Shift_Ins	INS	-	CTCTG	-	ERO1B	841_842insCAG	p.K281fs
XH_P46	1	236762906	236762906	Nonsense_Mutation	INS	-	AGGGATTAAAT	-	HEATR1	378insATTAA	126_N127delinsX
XH_P46	1	237732569	237732569	Frame_Shift_Ins	INS	-	TCACACACAACA	-	RYR2	549insATCAACA	p.L1183fs
XH_P46	1	237880610	237880610	In_Frame_Ins	INS	-	AAT	-	RYR2	0436_10437ins	p.N3479delinsKI
XH_P46	1	237880611	237880611	Nonsense_Mutation	INS	-	AAATAATTTTCTC	-	RYR2	TTTGAAGATAA	3479delinsNLLFX
XH_P46	1	243333025	243333025	Nonsense_Mutation	SNP	C	T	C	CEP170	c.G1454A	p.W485X
XH_P46	1	243333027	243333027	Frame_Shift_Ins	INS	-	AACATATTACACA	-	CEP170	insAATATGTGA	p.R484fs
XH_P46	1	243581312	243581312	Frame_Shift_Ins	INS	-	CATCATACCA	-	SDCCAG8	_1494insCATCA	p.L498fs
XH_P46	1	244715960	244715960	Frame_Shift_Ins	INS	-	CA	-	CATSPERE	c.420_421insCA	p.L140fs
XH_P46	1	244715961	244715961	Frame_Shift_Ins	INS	-	TTGTACAGTTG	-	CATSPERE	22insCTGTGAC	p.L141fs
XH_P46	1	245021508	245021508	Nonsense_Mutation	INS	-	TCTGTTTCATT	-	HNRNPU	2insGTAATGA	414_1415delinsKX
XH_P46	1	245025943	245025943	Frame_Shift_Ins	INS	-	TATGAAATGC	-	HNRNPU	_724insGCATT	p.L242fs
XH_P46	1	247150499	247150499	Nonsense_Mutation	INS	-	ATGGCATAGTCT	-	ZN6F95	5TATTAAAGACT	140_C441delinsRYX
XH_P46	1	248343396	248343396	Missense_Mutation	SNP	G	A	G	OR2M2	c.G109A	p.V37M
XH_P46	1	248436342	248436342	Nonsense_Mutation	INS	-	TGAATTTATTA	-	OR2T33	AAATATTATAA	R259delinsLKYX
XH_P46	1	248525107	248525107	Nonsense_Mutation	INS	-	SGTTAAAGTAAT	-	OR2T4	nsTGGGGTTAAA	75_V76delinsAWGX
XH_P46	1	248637240	248637240	Frame_Shift_Ins	INS	-	GGGAAATGGTA	-	OR2T3	590insGGGAAA	p.V197fs
XH_P46	1	248737482	248737482	In_Frame_Ins	INS	-	CATGATGGT	-	OR2T34	5_577insACCAT	5193delinsTIM5
XH_P46	1	248790041	248790041	Nonsense_Mutation	INS	-	STTAGCATCTTC	-	OR2T11	insATAGAAGAT	10_V131delinsHRRCK
XH_P46	2	11773043	11773043	Silent	SNP	G	T	G	GREB1	c.G4845T	p.L1615L
XH_P46	2	15736874	15736874	In_Frame_Ins	INS	-	CATCTCAATCTAC	-	DDX1	CTCATCTTCTA	delinsSSHNSLDYY
XH_P46	2	17773449	17773449	In_Frame_Ins	INS	-	TCT	-	VSNL1	c.108_109insTC	p.K36delinsKS
XH_P46	2	17773450	17773450	In_Frame_Ins	INS	-	CCTCCTCTCT	-	VSNL1	9_110insCCTCC	D37delinsASFV
XH_P46	2	21365376	21365376	Frame_Shift_Ins	INS	-	CCAA	-	TDRD15	4037_5038insCC	p.L1679fs
XH_P46	2	21365377	21365377	Nonsense_Mutation	INS	-	TCTAAACCTTTTT	-	TDRD15	9insCATTTCTAAA	80_D1681delinsAFX
XH_P46	2	27702415	27702415	Nonsense_Mutation	INS	-	CAGCT	-	IFT172	965_966insAGC	322_K323delinsX
XH_P46	2	27702417	27702417	Frame_Shift_Ins	INS	-	TTAT	-	IFT172	963_964insATA	p.Y322fs
XH_P46	2	32703884	32703884	Frame_Shift_Ins	INS	-	ACTGAACAAT	-	BIRC6	725insACTGA	p.A2417fs
XH_P46	2	38525714	38525714	In_Frame_Ins	INS	-	GTTTGCGGTCA	-	ATL2	1insCATGACCG	231delinsHDKQC
XH_P46	2	38545760	38545760	Frame_Shift_Ins	INS	-	TC	-	ATL2	c.6_7insGA	p.T3fs
XH_P46	2	38545761	38545761	In_Frame_Ins	INS	-	TTC	-	ATL2	c.5_6insGAA	p.D2delinsEN
XH_P46	2	40657059	40657059	In_Frame_Ins	INS	-	5GAAGGTTTGCT	-	SLC8A1	2insTAAGCAA	121delinsVSKP5Q
XH_P46	2	44065795	44065795	Silent	SNP	G	A	G	ABCG5	c.C24T	p.T8T
XH_P46	2	44079818	44079818	Missense_Mutation	SNP	G	A	G	ABCG8	c.G775A	p.A259T
XH_P46	2	54081026	54081026	Nonsense_Mutation	INS	-	TATTTTCAAGT	-	GPR75	8insTGACTTGA	p.K290delinsX
XH_P46	2	54150464	54150464	Frame_Shift_Ins	INS	-	5GATAAGTTTTT	-	PSME4	CAAGAAAAAAA	p.A634fs
XH_P46	2	55756110	55756110	Nonsense_Mutation	INS	-	TACTGCAAAACA	-	CFAP36	TATTTCTACTGCA	1128delinsTISTAKQX
XH_P46	2	64779805	64779805	Frame_Shift_Ins	INS	-	ATTAATTTTATG	-	AFTHP	insTCTATTAA	p.D399fs
XH_P46	2	67631175	67631175	Frame_Shift_Ins	INS	-	TTTTTCAATGACC	-	ETAA1	1362insTTTTTCA	p.R454fs
XH_P46	2	67631708	67631708	Frame_Shift_Ins	INS	-	CTTCCTTTATTT	-	ETAA1	insATATCTTCT	p.T632fs
XH_P46	2	70890783	70890783	Frame_Shift_Ins	INS	-	CT	-	ADD2	1954_1955insA	p.R652fs
XH_P46	2	71360565	71360565	Frame_Shift_Ins	INS	-	CCATCCTCTTC	-	MPHOSPH10	628insCCATCC	p.E209fs
XH_P46	2	71650264	71650264	Frame_Shift_Ins	INS	-	ACTATCAAGTTG	-	ZN6F38	nsAGGGACTATC	p.S1207fs
XH_P46	2	73678490	73678490	In_Frame_Ins	INS	-	ATGCCAGTT	-	ALMS1	3_4834insATGCG	1611delinsAMPV
XH_P46	2	73799643	73799643	Frame_Shift_Ins	INS	-	AAAGAATAGTT	-	ALMS1	TAAGGAAAGA	p.S3546fs
XH_P46	2	73799911	73799911	Nonsense_Mutation	INS	-	AATCTGCTCTAG	-	ALMS1	nsGGTATAATCT	335_Q3636delinsLVX
XH_P46	2	85276629	85276629	Frame_Shift_Ins	INS	-	ATCAAAAGACA	-	KCMF1	743insATCAAA	p.L248fs
XH_P46	2	85554483	85554483	Silent	SNP	A	G	A	TGOLN2	c.T372C	p.S124S
XH_P46	2	86075267	86075267	In_Frame_Ins	INS	-	TGTGATAAGGTA	-	ST3GAL5	310insTACCTTA	T104delinsYLIT
XH_P46	2	86075268	86075268	Frame_Shift_Ins	INS	-	SGTTTTTTTTGTT	-	ST3GAL5	nsACAAACAAAA	p.K103fs
XH_P46	2	88885490	88885490	Missense_Mutation	SNP	T	G	T	EIF2AK3	c.A1066C	p.N356H
XH_P46	2	96616509	96616509	Missense_Mutation	SNP	T	C	T	ANKRD36C	c.A1283G	p.E428G
XH_P46	2	96616511	96616511	Frame_Shift_Ins	INS	-	AAGCA	-	ANKRD36C	280_1281insTG	p.E427fs
XH_P46	2	97784176	97784176	In_Frame_Ins	INS	-	5GTGCGCAGAGG	-	ANKRD36	409insSGGTGCGCA	1136delinsHGRRG
XH_P46	2	98413404	98413404	Frame_Shift_Ins	INS	-	CTTAAAGATATT	-	TMEM131	CACITTTAAATCT	p.G972fs
XH_P46	2	100910699	100910699	Frame_Shift_Ins	INS	-	AATTT	-	LONRF2	748_1749insAA	p.E583fs
XH_P46	2	100910701	100910701	Nonsense_Mutation	INS	-	TTTATCCCCATT	-	LONRF2	747insAAATGGG	83_H584delinsKWGX
XH_P46	2	101186095	101186095	Frame_Shift_Ins	INS	-	ACACATTTTCATT	-	PDC13	nsGACACACATT	p.V94fs
XH_P46	2	107053128	107053128	Splice_Site	INS	-	TAGTGCGTAGG	-	RGPD3	.	.
XH_P46	2	108487743	108487743	Frame_Shift_Ins	INS	-	CATCATCTTTCT	-	RGPD4	284insTCATCAT	p.K1095fs
XH_P46	2	108487916	108487916	Nonsense_Mutation	INS	-	STTTTACCCCTG	-	RGPD4	57insTAGTTTATA	152_T1153delinsKX
XH_P46	2	109087221	109087221	In_Frame_Ins	INS	-	TCTAAGTCTTCC	-	GCC2	437insCTCTAAG	1479delinsNSKSSR
XH_P46	2	109087796	109087796	Frame_Shift_Ins	INS	-	TCTTCATGGGAA	-	GCC2	TCCATTTCTTCA	p.V671fs
XH_P46	2	109383459	109383459	Frame_Shift_Ins	INS	-	AGCCCCCTTCT	-	RANBP2	6465insAGCCC	p.H2155fs
XH_P46	2	111551298	111551298	Frame_Shift_Ins	INS	-	CATGCTTC	-	ACOXL	1_232insCATGC	p.W77fs
XH_P46	2	113258879	113258879	Frame_Shift_Ins	INS	-	AGGATTA	-	TTL	56_567insAGGA	p.P189fs
XH_P46	2	113785482	113785482	Nonstop_Mutation	INS	-	G	-	IL36B	c.471_472insC	p.X158delinsL
XH_P46	2	113785484	113785484	Frame_Shift_Ins	INS	-	AAACC	-	IL36B	469_470insGGG	p.L157fs
XH_P46	2	122217656	122217656	Missense_Mutation	SNP	C	T	C	CLASP1	c.G1078A	p.D360N
XH_P46	2	122217657	122217657	Nonsense_Mutation	INS	-	GGAAAAGTGAA	-	CLASP1	7insGAATTTTCA	359_D360delinsX
XH_P46	2	122363393	122363393	Frame_Shift_Ins	INS	-	A	-	CLASP1	c.78_79insT	p.L27fs
XH_P46	2	122363395	122363395	Frame_Shift_Ins	INS	-	GTGGC	-	CLASP1	c.76_77insGCCA	p.E26fs
XH_P46	2	128046441	128046441	Splice_Site	INS	-	TAAATCACACC	-	ERCC3	.	.

XH_P46	2	130872873	130872873	Missense_Mutation	SNP	C	T	C	POTEF	c.G550A	p.G184R
XH_P46	2	132290242	132290242	Missense_Mutation	SNP	G	C	G	CCDC74A	c.G566C	p.G189A
XH_P46	2	135744825	135744825	Nonsense_Mutation	INS	-	TAAAAAGCAATG	-	MAP3K19	8insAATGATTG	426delinsEMIAFX
XH_P46	2	135744999	135744999	Nonsense_Mutation	INS	-	TCAGAAATTTTGTG	-	MAP3K19	104insCACAAA	68_V369delinsITKFX
XH_P46	2	135957970	135957970	Missense_Mutation	SNP	C	G	C	ZRANB3	c.G3176C	p.R1059T
XH_P46	2	135957971	135957971	Frame_Shift_Ins	INS	-	TAAAAAATGTAT	-	ZRANB3	3175insGTACAT	p.R1059fs
XH_P46	2	136567212	136567212	Missense_Mutation	SNP	G	A	G	LCT	c.C2705T	p.T902M
XH_P46	2	138771542	138771542	In_Frame_Ins	INS	-	ATCTTCTCTTCA	-	HNMT	ATTATTCTTTTC	241delinsSFLSFCICR
XH_P46	2	140995854	140995854	Nonsense_Mutation	INS	-	AAAGTACAATTA	-	LRP1B	7insGTCCATAAT	14476delinsSPX
XH_P46	2	145156509	145156509	Nonsense_Mutation	INS	-	CTCATCTGAAA	-	ZE82	5TGAGTTTTCAG	p.N725delinsX
XH_P46	2	149526755	149526755	Nonsense_Mutation	INS	-	TAAAAATCATTG	-	EPC2	ATAGTTAAAA	92_D393delinsNFLX
XH_P46	2	149526757	149526757	Nonsense_Mutation	INS	-	TTAGT	-	EPC2	178_1179insTTA	393_P394delinsDX
XH_P46	2	152487273	152487273	Nonsense_Mutation	INS	-	AAATATTACATT	-	NEB	4insTAAAAATGTA	p.P2972delinsX
XH_P46	2	160035287	160035287	Missense_Mutation	SNP	A	G	A	TANC1	c.A1520G	p.K507R
XH_P46	2	162274270	162274270	Missense_Mutation	SNP	C	T	C	TBR1	c.C776T	p.A259V
XH_P46	2	165771720	165771720	In_Frame_Ins	INS	-	GCAGCTTCA	-	SLC38A11	5_386insTGAAG	K129delinsMKLQ
XH_P46	2	166775930	166775930	Nonsense_Mutation	INS	-	AGTATTTTGTGT	-	TTC21B	6GCTAAACACACA	A510delinsATGX
XH_P46	2	166892645	166892645	Frame_Shift_Ins	INS	-	ATACTCTCATGC	-	SCN1A	42insCAGCATGA	p.T1114fs
XH_P46	2	167141232	167141232	Frame_Shift_Ins	INS	-	GATGACAGCGT	-	SCN9A	1705insTACGCT	p.E569fs
XH_P46	2	168103379	168103379	Nonsense_Mutation	INS	-	ATTTTAGCCCTTT	-	XIRP2	5CATCAATTTTAA	04_11605delinsRHQFX
XH_P46	2	170059415	170059415	In_Frame_Ins	INS	-	GTGTGAATG	-	LRP2	9_8060insCATTG	N2687delinsFTFH
XH_P46	2	170151215	170151215	Nonsense_Mutation	INS	-	AGTTTGAAGTC	-	LRP2	433insTGACTTC	P145_1146delinsX
XH_P46	2	170349508	170349508	Nonsense_Mutation	INS	-	GAA	-	BB55	511_512insGA	p.S171delinsX
XH_P46	2	170349509	170349509	Nonsense_Mutation	INS	-	TCAAAATAATTAT	-	BB55	5ATTACTCAAAT	S171delinsSLKX
XH_P46	2	170667455	170667455	In_Frame_Ins	INS	-	TAAATGATC	-	SS8	8_899insTAAAT	E300delinsVNDQ
XH_P46	2	170804206	170804206	In_Frame_Ins	INS	-	ATCCCT	-	UBR3	65_306insATC	D1022delinsESL
XH_P46	2	170804208	170804208	Frame_Shift_Ins	INS	-	TTGTCTC	-	UBR3	67_3068insTTG	p.N1023fs
XH_P46	2	179392030	179392030	In_Frame_Ins	INS	-	ATCTTTCTGAAC	-	TTN	90insACAGTTCA	6830delinsIQFRKIS
XH_P46	2	179413366	179413366	Frame_Shift_Ins	INS	-	AT	-	TTN	65791_65792ins	p.L21931fs
XH_P46	2	179413367	179413367	Frame_Shift_Ins	INS	-	AGTATGGTGT	-	TTN	65791insAACAA	p.L21931fs
XH_P46	2	179427343	179427343	Nonsense_Mutation	INS	-	5AAGCAACATATA	-	TTN	221insAGATATA	774_V18775delinsQIX
XH_P46	2	179433822	179433822	In_Frame_Ins	INS	-	IGGGAAGAATAT	-	TTN	9842insAGATAT	16614delinsKDLPL
XH_P46	2	179466177	179466177	Frame_Shift_Ins	INS	-	TTGAAGTATATT	-	TTN	352insATAATAT	p.19451fs
XH_P46	2	179472150	179472150	In_Frame_Ins	INS	-	GGGACAGAAGAT	-	TTN	70insTTATATCT	B690delinsAYILVPQ
XH_P46	2	179536874	179536874	Nonsense_Mutation	INS	-	AGATGATAGTA	-	TTN	TCAAATATTACT	P383_H10384delinsX
XH_P46	2	179556814	179556814	Missense_Mutation	SNP	G	T	G	TTN	c.C27959A	p.P9320H
XH_P46	2	179556815	179556815	Nonsense_Mutation	INS	-	TTTACTGTTTGT	-	TTN	958insGACAAA	P9320delinsDKQX
XH_P46	2	179574422	179574422	Frame_Shift_Ins	INS	-	ATGAGCATTTCT	-	TTN	TATCATAAAGAA	p.I8298fs
XH_P46	2	179578885	179578885	In_Frame_Ins	INS	-	CTTCATCAT	-	TTN	7_22768insATGA	G7590delinsMMKE
XH_P46	2	179587253	179587253	Nonsense_Mutation	INS	-	5TGCGTTCATAT	-	TTN	29insGAAATATC	L77_A6178delinsEIX
XH_P46	2	179588365	179588365	Frame_Shift_Ins	INS	-	TGCTC	-	TTN	729_17730insGA	p.V5910fs
XH_P46	2	179638312	179638312	Frame_Shift_Ins	INS	-	AGAA	-	TTN	7332_7333insTT	p.V2445fs
XH_P46	2	179638314	179638314	In_Frame_Ins	INS	-	TCAAAATGT	-	TTN	0_7331insACAT	R2444delinsHLSL
XH_P46	2	182394374	182394374	Nonsense_Mutation	INS	-	CAGAAATTTTAA	-	ITGA4	nsTAGTCAGAAT	846delinsHSQNFx
XH_P46	2	182394376	182394376	Splice_Site	SNP	G	C	G	ITGA4	.	.
XH_P46	2	182766830	182766830	Frame_Shift_Ins	INS	-	ACGCATT	-	SSFA2	91_592insACGC	p.K197fs
XH_P46	2	186657686	186657686	Nonsense_Mutation	INS	-	TGACACAGATGT	-	FSIP2	ATAAAATGAACA	Y1941delinsYYPX
XH_P46	2	186658847	186658847	Nonsense_Mutation	INS	-	GTGCTTCTTCT	-	FSIP2	SinsTGAGTGTCT	p.F2328delinsFX
XH_P46	2	186661348	186661348	Frame_Shift_Ins	INS	-	TTTTTTGTTTAAC	-	FSIP2	36insATTTTTCG	p.T3162fs
XH_P46	2	186670276	186670276	In_Frame_Ins	INS	-	GAGAGAGACAAA	-	FSIP2	nsATGAGGAGAA	415delinsNEERTKFV
XH_P46	2	186670278	186670278	Missense_Mutation	SNP	C	G	C	FSIP2	c.C16245G	p.I5415M
XH_P46	2	190531333	190531333	Frame_Shift_Ins	INS	-	CTTCAACC	-	ASNSD1	5_476insCTTCA	p.V159fs
XH_P46	2	191353542	191353542	Frame_Shift_Ins	INS	-	ACTAGGCACCT	-	MFSD6	791insAACTAG	p.F597fs
XH_P46	2	196545675	196545675	Frame_Shift_Ins	INS	-	TCATTGCTAG	-	SLC39A10	910insTCATTG	p.G303fs
XH_P46	2	197672240	197672240	Nonsense_Mutation	INS	-	CTATATCTACATT	-	C2orf66	281insAATGAGT	p.S94delinsX
XH_P46	2	201438327	201438327	Nonsense_Mutation	INS	-	TAGTGTTTATT	-	SGO2	3259insTAGTGTG	O86_D1087delinsIX
XH_P46	2	201438329	201438329	In_Frame_Ins	INS	-	TTGGCATTCAAG	-	SGO2	ATGTCTTGCGCA	87delinsDNVLAFKFLF
XH_P46	2	202358613	202358613	In_Frame_Ins	INS	-	TCATGAAGAAA	-	C2CD6	1insGCATTTTCT	817delinsEHLFHEI
XH_P46	2	202519634	202519634	Nonsense_Mutation	INS	-	AGTATTTCTAAC	-	MPP4	AATATGGTAGAT	36_G437delinsLKX
XH_P46	2	205986663	205986663	Frame_Shift_Ins	INS	-	TTTTTCTA	-	PARDB3	55_1156insTTCT	p.D385fs
XH_P46	2	205986665	205986665	Frame_Shift_Ins	INS	-	TCACGTTTCTGT	-	PARDB3	58insGTTTCAGG	p.L386fs
XH_P46	2	206166320	206166320	Nonsense_Mutation	INS	-	ACGCTAACAT	-	PARDB3	2319insACGCT	773_K774delinsKRX
XH_P46	2	206166322	206166322	Nonsense_Mutation	SNP	A	T	A	PARDB3	c.A2320T	p.K774X
XH_P46	2	207170422	207170422	Nonsense_Mutation	INS	-	ATTTAACTCTTAA	-	ZDBF2	1171insATTTAA	B90_931delinsEIX
XH_P46	2	208420432	208420432	Frame_Shift_Ins	INS	-	CTTATTCAAAT	-	CREB1	74insCTTATTCA	p.M25fs
XH_P46	2	209113237	209113237	In_Frame_Ins	INS	-	TGAGAAATGCAAT	-	IDH1	ACATATATGCAT	delinsHIQLIYYAFLNFIPCL
XH_P46	2	210559001	210559001	Frame_Shift_Ins	INS	-	CTCGCTGGCTC	-	MAP2	2108insCTGCC	p.N703fs
XH_P46	2	210559002	210559002	In_Frame_Ins	INS	-	ATGCTT	-	MAP2	08_2109insATG	N703delinsKCF
XH_P46	2	210560132	210560132	Frame_Shift_Ins	INS	-	TT	-	MAP2	3238_3239insT	p.P1080fs
XH_P46	2	210560133	210560133	Frame_Shift_Ins	INS	-	TCTGCTTT	-	MAP2	39_3240insTCTG	p.P1080fs
XH_P46	2	210574849	210574849	Frame_Shift_Ins	INS	-	AGGTATTTTAGAA	-	MAP2	TTCTAAGGTAT	p.R292fs
XH_P46	2	211473273	211473273	Frame_Shift_Ins	INS	-	AAGAAAAATTTA	-	CP51	029insAAGAAA	p.S343fs
XH_P46	2	218673384	218673384	Frame_Shift_Ins	INS	-	AGTCTTTCCAC	-	TNS1	nsTATAGTGGGA	p.R1637fs
XH_P46	2	219320394	219320394	Frame_Shift_Ins	INS	-	CC	-	USP37	2760_2761insG	p.T921fs
XH_P46	2	219320395	219320395	Nonsense_Mutation	INS	-	AATATTTTCTCTC	-	USP37	50insATGAGAGA	G920_1921delinsLX
XH_P46	2	223795471	223795471	Nonsense_Mutation	INS	-	TATCAATTTTAA	-	ACSL3	574insTTTATCAA	R558delinsSLSIX
XH_P46	2	228476241	228476241	Nonsense_Mutation	INS	-	TTTTTTTTTTTT	-	C2orf83	TCTCAAAAAAAA	8_T109delinsSVSKXX
XH_P46	2	230675901	230675901	In_Frame_Ins	INS	-	AAA	-	TRIP12	5970_971insTT	p.S324delinsIC
XH_P46	2	230675902	230675902	Nonsense_Mutation	INS	-	TTACTG	-	TRIP12	69_970insCAGTG	p.S324delinsQX
XH_P46	2	233681744	233681744	Splice_Site	INS	-	GATCCACACAG	-	GIGYF2	.	.
XH_P46	2	239237645	239237645	Nonsense_Mutation	INS	-	CACGTAACAAAT	-	TRAF3IP1	578insCACGTAAK	193delinsTRNKX
XH_P46	2	241631616	241631616	Silent	SNP	T	C	T	AQP12A	c.T249C	p.T83T
XH_P46	3	404959	404959	Frame_Shift_Ins	INS	-	AGATTGTATATG	-	CHL1	insACCAAGATTG	p.G493fs
XH_P46	3	9032232	9032232	Silent	SNP	C	T	C	SRGAP3	c.G2778A	p.G926G
XH_P46	3	12618174	12618174	In_Frame_Ins	INS	-	AACCTTTATTAC	-	MKRN2	774insAACCTTA	S258delinsRTLFT
XH_P46	3	19384150	19384150	Frame_Shift_Ins	INS	-	ATTATATATTTT	-	KCNH8	nsATGATTTTATAT	p.Y172fs
XH_P46	3	25677572	25677572	In_Frame_Ins	INS	-	CTT	-	TOP2B	691_692insAA	p.T231delinsKA
XH_P46	3	25677574	25677574	Nonsense_Mutation	INS	-	TATTTTATTTCAC	-	TOP2B	0insGAGTGAATA	230_T231delinsX
XH_P46	3	27233665	27233665	Frame_Shift_Ins	INS	-	AGTTAGAAAAAT	-	NEK10	96insCTATTTTTC	p.M99fs
XH_P46	3	27233667	27233667	Silent	SNP	G	T	G	NEK10	c.C294A	p.V98V
XH_P46	3	37365568	37365568	In_Frame_Ins	INS	-	TTTTGACTG	-	GOLGA4	1_2192insTTTTG	H731delinsLLTD
XH_P46	3	37367776	37367776	Frame_Shift_Ins	INS	-	AA	-	GOLGA4	4399_4400insA	p.L1467fs
XH_P46	3	37367777	37367777	Frame_Shift_Ins	INS	-	CTTCATCATACT	-	GOLGA4	ATTTTTCTTCAT	p.L1467fs
XH_P46	3	37368312	37368312	In_Frame_Ins	INS	-	CAATTCTTTGTG	-	GOLGA4	936insCCAAATTC	1645delinsEPILCV
XH_P46	3	38101275	38101275	Missense_Mutation	SNP	G	A	G	DLEC1	c.G605A	p.R202Q
XH_P46	3	38103826	38103826	Frame_Shift_Ins	INS	-	GG	-	DLEC1	c.840_841insGG	p.P280fs
XH_P46	3	38103828	38103828	Frame_Shift_Ins	INS	-	CTTATTCTAT	-	DLEC1	2_843insCTTATT	p.K281fs
XH_P46	3	40574484	40574484	Frame_Shift_Ins	INS	-	A	-	ZNF621	5_1223_1224ins	p.P408fs

XH_P46	3	40574486	40574486	In_Frame_Ins	INS	-	TGAAGG	-	ZNF621	25_122insTGA	S409delinsLKA
XH_P46	3	41504680	41504680	Frame_Shift_Ins	INS	-	C	-	ULK4	2384_2385ins	p.N795fs
XH_P46	3	41504682	41504682	In_Frame_Ins	INS	-	GAATGTATAAT	-	ULK4	CTATAGAAATTA	95delinsSIELYLLNN
XH_P46	3	44284520	44284520	Nonsense_Mutation	INS	-	TTGTGAGG	-	TOPAZ1	2_523insTTGTG	174_L175delinsKLX
XH_P46	3	44284522	44284522	Frame_Shift_Ins	INS	-	ATCA	-	TOPAZ1	524_525insATC	p.L175fs
XH_P46	3	44488364	44488364	Silent	SNP	G	T	G	ZNF445	c.C2799A	p.S933s
XH_P46	3	44612043	44612043	Frame_Shift_Ins	INS	-	ACTTCCTTATAT	-	ZKSCAN7	9insCAACTTCCT	p.R330fs
XH_P46	3	44636043	44636043	Frame_Shift_Ins	INS	-	TCCCTTCTGTG	-	ZNF660	359insTCCTCT	p.H120fs
XH_P46	3	44636044	44636044	Frame_Shift_Ins	INS	-	GTACTTTATTG	-	ZNF660	360insGTACTT	p.H120fs
XH_P46	3	44636431	44636431	In_Frame_Ins	INS	-	CTTTTTTCTCT	-	ZNF660	47insACTTTTTT	N249delinsKLFFLC
XH_P46	3	44700428	44700428	Frame_Shift_Ins	INS	-	AATCCCATCACA	-	ZNF35	574insAATCCCA	p.E191fs
XH_P46	3	44795062	44795062	Frame_Shift_Ins	INS	-	AAAAATAGTAGC	-	KIAA1143	291insGGCTACT	p.K97fs
XH_P46	3	45030658	45030658	Nonsense_Mutation	INS	-	CAACATTACTAT	-	EXOSC7	ACAACAACACTTA	p.G28delinsGX
XH_P46	3	45030660	45030660	Missense_Mutation	SNP	G	A	G	EXOSC7	c.G86A	p.C29Y
XH_P46	3	46751074	46751079	In_Frame_Del	DEL	AAGAAG	-	AAGAAG	TMIE	c.367_372del	p.123_124del
XH_P46	3	47719796	47719796	Nonsense_Mutation	INS	-	TTT	-	SMARCC1	1462_1463insA	p.L488delinsX
XH_P46	3	47719798	47719798	Nonsense_Mutation	INS	-	TGTTTCCTTTCA	-	SMARCC1	ATGAAATGAAAY	487_L488delinsX
XH_P46	3	48338292	48338292	Nonsense_Mutation	INS	-	TGCTTGATAAT	-	NME6	CTGATATTATCA	K40_F41delinsYX
XH_P46	3	51475867	51475867	Frame_Shift_Ins	INS	-	AG	-	DCAF1	c.313_314insCT	p.V105fs
XH_P46	3	51475868	51475868	Frame_Shift_Ins	INS	-	AAAAGTTGGGT	-	DCAF1	313insAACCAA	p.V105fs
XH_P46	3	54604116	54604116	Silent	SNP	C	T	C	CACNA2D3	c.C873T	p.F291F
XH_P46	3	56207536	56207536	Nonsense_Mutation	INS	-	ATTTTTTTTACT	-	ERC2	insGGAAGGTAA	R363delinsGRX
XH_P46	3	69245509	69245509	Nonsense_Mutation	INS	-	AATAATAAGTA	-	FRMD4B	ATTGACATACTT	77_M378delinsAVX
XH_P46	3	73114282	73114282	Nonsense_Mutation	INS	-	TCACTGTAAT	-	PPP4R2	748insTCACTG	49_E250delinsESLX
XH_P46	3	77530284	77530284	Nonsense_Mutation	INS	-	GTTAGTCTTCAC	-	ROBO2	2insTAGTTAGTC	194_K195delinsSSX
XH_P46	3	77530286	77530286	Nonsense_Mutation	INS	-	AATTCATTGAA	-	ROBO2	584insAATTCAT	95_S196delinsKFIX
XH_P46	3	77623837	77623837	Frame_Shift_Ins	INS	-	CCTCATAACT	-	ROBO2	TTTCTGTCTCAT	p.Q270fs
XH_P46	3	78676530	78676530	Frame_Shift_Ins	INS	-	AATTAACATA	-	ROBO1	3516insTAGT	p.Q1172fs
XH_P46	3	89259247	89259247	Frame_Shift_Ins	INS	-	TCTTCCCACTG	-	EPHA3	392insTCTTCC	p.H131fs
XH_P46	3	89259249	89259249	Missense_Mutation	SNP	T	A	T	EPHA3	c.T393A	p.H131Q
XH_P46	3	97591053	97591053	In_Frame_Ins	INS	-	CCTCGATAT	-	CRYBG3	5_1016insCCTCG	G339delinsASIW
XH_P46	3	99643208	99643208	In_Frame_Ins	INS	-	ATACAAAGATA	-	FILIP1L	71insATTATCT	1157delinsFIFVS
XH_P46	3	100556016	100556016	Splice_Site	INS	-	ATTTCAGATTGCT	-	AB13BP	71insAACATTA	p.L157fs
XH_P46	3	100963584	100963584	In_Frame_Ins	INS	-	AAACTAGTTTTA	-	IMP2	591insACTAAAA	531delinsTKTSFL
XH_P46	3	105377954	105377954	Frame_Shift_Ins	INS	-	T	-	CBLB	c.1749_1750ins	p.A584fs
XH_P46	3	105377955	105377955	Frame_Shift_Ins	INS	-	GCCAT	-	CBLB	748_1749insATC	p.I583fs
XH_P46	3	108776232	108776232	Frame_Shift_Ins	INS	-	TGAACAACCTGA	-	MORC1	33insCATCAAGT	p.K378fs
XH_P46	3	112989792	112989792	Splice_Site	SNP	G	A	G	BOC	-	-
XH_P46	3	113176139	113176139	Nonsense_Mutation	INS	-	GACATTTAATTA	-	SPICE1	TAAAAATTAATTA	1_Q502delinsNKINX
XH_P46	3	113376020	113376020	Frame_Shift_Ins	INS	-	CAGCAAA	-	USF3	308_4509insTTTC	p.H1503fs
XH_P46	3	113376579	113376579	Nonsense_Mutation	INS	-	CACGATTATTTC	-	USF3	950insGGAAAT	17_K1318delinsWXX
XH_P46	3	119451310	119451310	Frame_Shift_Ins	INS	-	T	-	MAATS1	c.810_811insT	p.L270fs
XH_P46	3	119451311	119451311	Nonsense_Mutation	INS	-	ATATTGTTCGA	-	MAATS1	2insAAATATTGT	71_T272delinsKILFX
XH_P46	3	120424944	120424944	Nonsense_Mutation	INS	-	CTTCTTTCTCT	-	RAB13	CTAGAGAAGAA	96_L97delinsNPX
XH_P46	3	121208725	121208725	In_Frame_Ins	INS	-	TAATAAAACATC	-	POLQ	953insATGATGT	1018delinsNDVLLS
XH_P46	3	122942530	122942530	In_Frame_Ins	INS	-	AACATTATTATA	-	SEC22A	stCTTAAACATT	103delinsLTLFIYS
XH_P46	3	123665760	123665760	Nonsense_Mutation	INS	-	AAGAAAATGAG	-	CCDC14	GTAGAACCTCATT	212_K213delinsKX
XH_P46	3	124952375	124952375	Frame_Shift_Ins	INS	-	TAACACAAGCA	-	ZNF148	195insCTGCTG	p.R393fs
XH_P46	3	130095213	130095213	Frame_Shift_Ins	INS	-	TTAATTAAGA	-	COL6A5	202insTTATT	p.Y67fs
XH_P46	3	130095214	130095214	Frame_Shift_Ins	INS	-	TGTGCTGGTGTT	-	COL6A5	3insTAGTGCTG	p.R68fs
XH_P46	3	130447527	130447527	Frame_Shift_Ins	INS	-	BATAGTATAGT	-	PIK3R4	CATACCAACTAT	p.E529fs
XH_P46	3	131271330	131271330	Frame_Shift_Ins	INS	-	TAACAGAGCAG	-	CPNE4	1176insCTGCT	p.S392fs
XH_P46	3	132419280	132419280	Frame_Shift_Ins	INS	-	FACTTCAGTAAC	-	NPHP3	insCGTAGTTAC	p.Q547fs
XH_P46	3	135721851	135721851	Nonsense_Mutation	INS	-	5CTACTCATCTTA	-	PPP2R3A	5AACATGCTACT	5505delinsRTCYSX
XH_P46	3	138374332	138374332	Nonsense_Mutation	INS	-	GTTATAAAGGG	-	PIK3CB	548insTTCCCTT	L550delinsFPLX
XH_P46	3	142269112	142269112	Missense_Mutation	SNP	C	A	C	ATR	c.G2838T	p.M946I
XH_P46	3	142269113	142269113	Nonsense_Mutation	INS	-	ACTTAAGTTTAA	-	ATR	837insCTTAAAC	946_T947delinsTX
XH_P46	3	146311891	146311891	Frame_Shift_Ins	INS	-	AATTAGCATTTGT	-	PLSCR5	69insAACAAATG	p.I90fs
XH_P46	3	149469271	149469271	Nonsense_Mutation	INS	-	5GTTTATAATTG	-	COMMD2	AAAAATCAATTA	K50delinsSMSSKNQLX
XH_P46	3	150285814	150285814	Frame_Shift_Ins	INS	-	TAACAACAAAAC	-	EIF2A	3insCATAAACAA	p.T164fs
XH_P46	3	150908695	150908695	Frame_Shift_Ins	INS	-	CAAGAATTCCCT	-	MED12L	946insTCAAGAA	p.K649fs
XH_P46	3	151535309	151535309	Frame_Shift_Ins	INS	-	TCATTGGACTTA	-	AADAC	295insTCTATGG	p.R98fs
XH_P46	3	151535311	151535311	Missense_Mutation	SNP	A	G	A	AADAC	c.A296G	p.K99R
XH_P46	3	157081235	157081235	Frame_Shift_Ins	INS	-	TTTTTTTCCC	-	VEPH1	1653insGGGAA	p.L551fs
XH_P46	3	160803594	160803594	Frame_Shift_Ins	INS	-	GGAAATTGGAGG	-	B3GALNT1	CAAAAACCTCCA	p.I317fs
XH_P46	3	164777012	164777012	Frame_Shift_Ins	INS	-	5TAAAAATGAT	-	SI	22insAATATCAT	p.L408fs
XH_P46	3	169847202	169847202	Frame_Shift_Ins	INS	-	CTTCCATCCCA	-	PHC3	1022insTGGGA	p.N341fs
XH_P46	3	172115243	172115243	Frame_Shift_Ins	INS	-	CATTCACTCTTA	-	FNDC3B	94insCACATTCA	p.L1198fs
XH_P46	3	180377470	180377470	In_Frame_Ins	INS	-	TGGTAAAGTAG	-	CCDC39	4insCAACTACTT	202delinsNYFTKA
XH_P46	3	183493744	183493749	In_Frame_Del	DEL	GGAGGA	-	GGAGGA	YEATS2	c.2410_2415del	p.804_805del
XH_P46	3	184023944	184023944	Splice_Site	INS	-	ACCCTACTGC	-	PSMD2	-	-
XH_P46	3	194140665	194140665	Nonsense_Mutation	INS	-	CAGCTTTTCTTAC	-	ATP13A3	45insGCTAAGAA	p.Y1115delinsX
XH_P46	3	195514222	195514222	Missense_Mutation	SNP	A	G	A	MUC4	c.T4229C	p.L1410P
XH_P46	3	196612373	196612373	Frame_Shift_Ins	INS	-	5AATTTCCTCTG	-	SENPS	nsATAGAAATTTG	p.S107fs
XH_P46	3	196888592	196888592	In_Frame_Ins	INS	-	ACATTTGGGAT	-	DLG1	5ATTAAATCCCAA	167delinsLLNPKCLS
XH_P46	3	196888594	196888594	Missense_Mutation	SNP	G	T	G	DLG1	c.C499A	p.L167I
XH_P46	4	1066809	1066809	Frame_Shift_Ins	INS	-	AATATTTTATATG	-	RNF212	insGTACATAAA	p.N249fs
XH_P46	4	1388755	1388755	Silent	SNP	C	G	C	CRIPAK	c.C456G	p.P152P
XH_P46	4	2209736	2209736	Missense_Mutation	SNP	G	C	G	POLN	c.C692G	p.S231C
XH_P46	4	37848718	37848718	Frame_Shift_Ins	INS	-	ACTCTAAAGT	-	PGM2	1175insACTCT	p.G392fs
XH_P46	4	38830154	38830154	Frame_Shift_Ins	INS	-	TGAGAGTA	-	TLR6	0_941insTACTC	p.N314fs
XH_P46	4	38830156	38830156	Silent	SNP	C	A	C	TLR6	c.G939T	p.T313T
XH_P46	4	39344088	39344088	Splice_Site	INS	-	AGTTGAAGCTT	-	RFC1	-	-
XH_P46	4	39450080	39450080	Frame_Shift_Ins	INS	-	ATTCTTTTATGA	-	KLH	nsCATTTATCTT	p.E970fs
XH_P46	4	39456492	39456492	Nonsense_Mutation	INS	-	ATAGAAAATGGA	-	RPL9	5AACTCTCCATT	155_N156delinsX
XH_P46	4	39846408	39846408	Nonsense_Mutation	INS	-	TTGGTTTATCTT	-	PDSSA	5AATAAAAGATA	139_V114delinsEX
XH_P46	4	39924367	39924367	Nonsense_Mutation	INS	-	ATATTGATTAAC	-	PDSSA	GATATGTTAATC	7_S178delinsSYMIX
XH_P46	4	39924369	39924369	Splice_Site	SNP	C	T	C	PDSSA	-	-
XH_P46	4	42553247	42553247	Frame_Shift_Ins	INS	-	ATACTCAAATTA	-	ATP8A1	25insAATAATTT	p.G509fs
XH_P46	4	48608568	48608568	In_Frame_Ins	INS	-	GTGTAAATTAAT	-	FRYL	insAAAATTAAT	210delinsKINHLE
XH_P46	4	48608569	48608569	Silent	SNP	C	T	C	FRYL	c.G627A	p.K209K
XH_P46	4	56309990	56309990	In_Frame_Ins	INS	-	AGAAATAAAGC	-	CLOCK	766insGAGCTTT	1589delinsRALFL
XH_P46	4	57367932	57367932	In_Frame_Ins	INS	-	TTT	-	SRP72	1738_1739insT	p.I580delinsI
XH_P46	4	57367934	57367934	In_Frame_Ins	INS	-	ACTGTTTTT	-	SRP72	0_1741insACTGB	I580delinsITVF
XH_P46	4	68704023	68704023	Nonsense_Mutation	INS	-	AGCTAAATATA	-	TMPRSS11D	ATATGGTATATT	4_D115delinsAIWYIX
XH_P46	4	70146409	70146409	Nonsense_Mutation	INS	-	TTTCTCATCTACTA	-	UGT2B28	5TTTCTTCTCAT	5delinsFKSFLSHYIQRX
XH_P46	4	71115135	71115135	Frame_Shift_Ins	INS	-	5CCAAAACCTGC	-	C5N3	CGTCGCCCAAAC	p.P170fs
XH_P46	4	71201164	71201164	Frame_Shift_Ins	INS	-	TTTTT	-	CAB51	408_409insTTT	p.S136fs

XH_P46	4	71201165	71201165	Frame_Shift_Ins	INS	-	TGTCAGTTTGT	-	CABS1	0insGCTGTCAG	p.T137fs
XH_P46	4	71698131	71698131	Nonsense_Mutation	INS	-	TAATATTTATAG	-	GRSF1	AAAACTTATAAA	K75delinsTYKIKYX
XH_P46	4	74351727	74351727	Frame_Shift_Ins	INS	-	TTCCCTC	-	AFM	19_420insTCC	p.P140fs
XH_P46	4	74351729	74351729	Missense_Mutation	SNP	A	C	A	AFM	c.A421C	p.T141P
XH_P46	4	77084482	77084482	Missense_Mutation	SNP	T	A	T	SCARB2	c.A865T	p.T289S
XH_P46	4	80327784	80327784	Frame_Shift_Ins	INS	-	A	-	GK2	-1570_1571ins	p.P524fs
XH_P46	4	80327785	80327785	In_Frame_Ins	INS	-	ATATTGGGTGTG	-	GK2	AAAAAACACAC	delinsVKKNTPNISTVP
XH_P46	4	82355115	82355115	Frame_Shift_Ins	INS	-	TTTGCACTTAAT	-	RASGEF1B	077insTATTAAG	p.K359fs
XH_P46	4	83838373	83838373	In_Frame_Ins	INS	-	AGAATA	-	THAP9	08_1009insAGAp	P336delinsPRI
XH_P46	4	83838375	83838375	Missense_Mutation	SNP	T	A	T	THAP9	c.T1010A	p.L337H
XH_P46	4	83989669	83989669	Frame_Shift_Ins	INS	-	A	-	COPS4	-1081_1082ins	p.F361fs
XH_P46	4	83989670	83989670	Nonsense_Mutation	INS	-	AAGTTAACTGGG	-	COPS4	BinsTTTAAGTTA	F361delinsFLSX
XH_P46	4	84383753	84383753	Missense_Mutation	SNP	C	T	C	ABRAXAS1	c.G772A	p.D258N
XH_P46	4	84383755	84383755	In_Frame_Ins	INS	-	ATGTTACCTGT	-	ABRAXAS1	TGCAAACAGGT	57delinsLQTGEHSK
XH_P46	4	86491844	86491844	Frame_Shift_Ins	INS	-	ATTTCAACTCCC	-	ARHGAP24	151insATTCAA	p.Y50fs
XH_P46	4	88533950	88533950	Frame_Shift_Ins	INS	-	GTCCCCATTCC	-	DSP	613insGTCCCC	p.C204fs
XH_P46	4	88733000	88733000	Missense_Mutation	SNP	A	T	A	IBSP	c.A892T	p.S298C
XH_P46	4	88733001	88733001	Frame_Shift_Ins	INS	-	GTGCCGTTTATG	-	IBSP	94insGTGCCGT	p.S298fs
XH_P46	4	88766968	88766968	Silent	SNP	C	G	C	MEPE	c.C948G	p.T316T
XH_P46	4	88766970	88766970	Frame_Shift_Ins	INS	-	TGCTTTTGCTTT	-	MEPE	nsGGGTGCTTTT	p.L317fs
XH_P46	4	88996100	88996100	In_Frame_Ins	INS	-	CCGCTGGTA	-	PKD2	9_2660insCGCG	G887delinsAAGR
XH_P46	4	103245406	103245406	Splice_Site	SNP	C	G	C	SLC39A8	-	-
XH_P46	4	106156989	106156989	Frame_Shift_Ins	INS	-	ATCTCGTGT	-	TET2	1891insATCTC	p.K630fs
XH_P46	4	110865083	110865083	Frame_Shift_Ins	INS	-	TA	-	EGF	c.S95_596insTA	p.S199fs
XH_P46	4	110865084	110865084	Frame_Shift_Ins	INS	-	AAGTGATTTC	-	EGF	597insAAGTGA	p.S199fs
XH_P46	4	113475121	113475121	Frame_Shift_Ins	INS	-	ATAGG	-	ZGRF1	041_5042insCC	p.E1681fs
XH_P46	4	113475123	113475123	Frame_Shift_Ins	INS	-	AAGAGGAAAGT	-	ZGRF1	40insTACTACTT	p.S1680fs
XH_P46	4	113482070	113482070	Nonsense_Mutation	INS	-	GTTCAGGAATA	-	ZGRF1	5insGAGTTATTC	K1535delinsKSYSX
XH_P46	4	114279189	114279189	Frame_Shift_Ins	INS	-	CATCAGTTTTTG	-	ANK2	9416insCATCAG	p.R3139fs
XH_P46	4	120442196	120442196	Nonsense_Mutation	INS	-	TATATTTCGTTA	-	PDE5A	TTTAATTAAACGAp	S601delinsSSLINEX
XH_P46	4	121742465	121742465	Frame_Shift_Ins	INS	-	CCTTT	-	PRDM5	335_336insAAA	p.D112fs
XH_P46	4	121742467	121742467	Frame_Shift_Ins	INS	-	GTTGATTGTCT	-	PRDM5	CTAGAAGACAA	p.D112fs
XH_P46	4	123179999	123179999	Splice_Site	INS	-	AACAAACGGCT	-	KIAA1109	-	-
XH_P46	4	123193516	123193516	Nonsense_Mutation	INS	-	TAAATGAAAAAT	-	KIAA1109	TATAAGTAAATG	K2802delinsLLYKX
XH_P46	4	126371180	126371180	Frame_Shift_Ins	INS	-	CTGATTGGGAT	-	FAT4	AATATTCTGAT	p.L3005fs
XH_P46	4	138451054	138451054	Frame_Shift_Ins	INS	-	AGGAATTGTGT	-	PCDH18	89insTAAACACA	p.D730fs
XH_P46	4	139966460	139966460	In_Frame_Ins	INS	-	GTT	-	NOCT	1128_1129insG	p.L376delinsLV
XH_P46	4	139966462	139966462	Missense_Mutation	SNP	A	G	A	NOCT	c.A1130G	p.D377G
XH_P46	4	139980489	139980489	Frame_Shift_Ins	INS	-	GGAAA	-	ELF2	162_1163insTT	p.N388fs
XH_P46	4	139980490	139980490	Nonsense_Mutation	INS	-	AAGACAG	-	ELF2	61_1162insCTG	388_1389delinsLSX
XH_P46	4	141484493	141484493	Frame_Shift_Ins	INS	-	TTTGAAG	-	UCP1	4_505insCTTCT	p.G169fs
XH_P46	4	146059706	146059706	Frame_Shift_Ins	INS	-	TGATCTTGAAT	-	OTUD4	026insAGATTCA	p.P676fs
XH_P46	4	146064542	146064542	Nonsense_Mutation	INS	-	GGAAATGTTATA	-	OTUD4	nsATTTCTATAAC	488delinsYFYNIPX
XH_P46	4	148743963	148743963	Frame_Shift_Ins	INS	-	AAAATGTTTATT	-	ARHGAP10	241insAAAAATGT	p.E80fs
XH_P46	4	148800487	148800487	In_Frame_Ins	INS	-	AAA	-	ARHGAP10	937_938insAA	p.L313delinsQL
XH_P46	4	148800488	148800488	In_Frame_Ins	INS	-	CAGCAATAC	-	ARHGAP10	8_939insCAGCA	L313delinsLSNT
XH_P46	4	149075973	149075973	Frame_Shift_Ins	INS	-	AAAGATCTTCC	-	NR3C2	094insTGGAAG	p.P698fs
XH_P46	4	151336694	151336694	Nonsense_Mutation	INS	-	CCCTTGCTCTCC	-	LRBA	0insCAGAAGAG	N2365delinsQKSKGX
XH_P46	4	151511939	151511939	Frame_Shift_Ins	INS	-	TTTGTGAATAAT	-	LRBA	stGAAAAATTATT	p.E2040fs
XH_P46	4	155507895	155507895	In_Frame_Ins	INS	-	ACCAAAACC	-	FGA	6_686insGGTTT	V229delinsGFWF
XH_P46	4	156632376	156632376	In_Frame_Ins	INS	-	TGTTGCTTTTCA	-	GUCY1A3	060insCTTGTTG	353delinsWLGAFH
XH_P46	4	156643278	156643278	Frame_Shift_Ins	INS	-	TCCTAACTCTTT	-	GUCY1A3	5insACTTCTTAA	p.T602fs
XH_P46	4	157689061	157689061	Nonsense_Mutation	INS	-	STTTTGTTTTTT	-	PDGFC	nsTTTAAAAAAC	262_1263delinsVX
XH_P46	4	157689062	157689062	Nonsense_Mutation	SNP	C	A	C	PDGFC	c.G784T	p.E262X
XH_P46	4	169312779	169312779	In_Frame_Ins	INS	-	TGTCCTTCTTTT	-	DDX60L	27insTAAAGAG	A276delinsVKGRTQ
XH_P46	4	175898094	175898094	Frame_Shift_Ins	INS	-	CAGCGCTTCACA	-	ADAM29	419insCAGCGC	p.H473fs
XH_P46	4	186111972	186111972	Frame_Shift_Ins	INS	-	AACACAAGTATA	-	CFAP97	9insTTTATACT	p.G127fs
XH_P46	4	186274725	186274725	Frame_Shift_Ins	INS	-	CAGAACTACCA	-	SNX25	062insCAGAAA	p.M687fs
XH_P46	4	186329132	186329132	Nonsense_Mutation	INS	-	TAATCTTAATTTT	-	UFSP2	TGAAAAAAAT	60delinsQKMKMKNX
XH_P46	4	186379790	186379790	Frame_Shift_Ins	INS	-	C	-	CCDC110	-1839_1840ins	p.S614fs
XH_P46	4	186379792	186379792	Nonsense_Mutation	INS	-	TGAAGACAAAA	-	CCDC110	338insTATTTTG	613delinsVFCLQX
XH_P46	4	186380549	186380549	Frame_Shift_Ins	INS	-	GAAAGAGTAC	-	CCDC110	81insATAGTAC	p.Q361fs
XH_P46	4	186384152	186384152	Nonsense_Mutation	INS	-	ACTTTACTTTTGT	-	CCDC110	7insGACAAAAAG	p.L56delinsX
XH_P46	4	187172907	187172907	Nonsense_Mutation	INS	-	AATTTT	-	KLKB1	036_1037insAAT	K346delinsKFX
XH_P46	4	187172909	187172909	Frame_Shift_Ins	INS	-	ATGGCAGGGTT	-	KLKB1	039insAATGGC	p.K346fs
XH_P46	4	187549778	187549778	Nonsense_Mutation	INS	-	GAAAGCACCAA	-	FAT1	nsTCCCATTTGGT	488delinsIPLVLSLX
XH_P46	4	187629442	187629442	Nonsense_Mutation	INS	-	ACTGGATTGTG	-	FAT1	40insTAAACAA	p.H514delinsX
XH_P46	5	730558	730558	Nonsense_Mutation	INS	-	TTCTTTCTTTAA	-	ZDHHC11B	5sGTGTTTAAAGAp	S350delinsCVX
XH_P46	5	5461951	5461951	In_Frame_Ins	INS	-	TTTTACTACTTT	-	ICE1	2505insTTTTTAC	P835delinsPPTTF
XH_P46	5	5461953	5461953	Frame_Shift_Ins	INS	-	T	-	ICE1	-2506_2507ins	p.D836fs
XH_P46	5	5463271	5463271	Frame_Shift_Ins	INS	-	TGGAAAGTCTAT	-	ICE1	25insTGTGGAA	p.E1275fs
XH_P46	5	7886739	7886739	In_Frame_Ins	INS	-	AAACATAAGAA	-	MTRR	70insAAAAACA	357delinsQKHKK
XH_P46	5	13736034	13736034	Frame_Shift_Ins	INS	-	A	-	DNAH5	11462_11463in	p.T3821fs
XH_P46	5	13736035	13736035	In_Frame_Ins	INS	-	GTAGAATTGAT	-	DNAH5	11462insAATCA	T3821delinsKSILP
XH_P46	5	15936569	15936569	Missense_Mutation	SNP	A	T	A	FBXL7	c.A609T	p.K203N
XH_P46	5	16675232	16675232	In_Frame_Ins	INS	-	AAGGTAAGGCA	-	MYO10	4694insATGCTT	1565delinsHALPF
XH_P46	5	32126652	32126652	Frame_Shift_Ins	INS	-	ACTTCTGGTTT	-	GOLPH3	563insAAACCA	p.T188fs
XH_P46	5	34823663	34823663	Nonsense_Mutation	INS	-	TGCTCTGAGTTT	-	RAI14	CGTATTTGCTCT	543delinsPRICSEFLX
XH_P46	5	38431305	38431307	In_Frame_Del	DEL	ACT	-	ACT	EGFLAM	c.1379_1381de	p.460_461del
XH_P46	5	39376931	39376931	Frame_Shift_Ins	INS	-	A	-	DAB2	-1894_1895ins	p.E632fs
XH_P46	5	39376932	39376932	Nonsense_Mutation	INS	-	TTTGGTGATAAC	-	DAB2	94insTAGTTATC	632_1633delinsX
XH_P46	5	41927335	41927335	In_Frame_Ins	INS	-	TAAACTACCAT	-	FBXO4	ATAACTAAATCT	137delinsLTKSTINN
XH_P46	5	43175139	43175139	Frame_Shift_Ins	INS	-	TCATGTGT	-	ZNF131	9_940insTCATG	p.H313fs
XH_P46	5	43613100	43613100	Frame_Shift_Ins	INS	-	TGATGT	-	NNT	42_243insTGAT	p.N81fs
XH_P46	5	43613101	43613101	Frame_Shift_Ins	INS	-	CTGA	-	NNT	243_244insCTG	p.N81fs
XH_P46	5	56179506	56179506	Frame_Shift_Ins	INS	-	ACATTATTGTG	-	MAP3K1	stACAAACATT	p.Q1273fs
XH_P46	5	64100132	64100132	Nonsense_Mutation	INS	-	AGGTTTTTTTTT	-	CWC27	AACTAGGTTTTT	286_K287delinsAFX
XH_P46	5	64314065	64314065	In_Frame_Ins	INS	-	ATGCTCGGAGT	-	CWC27	7insAACATGCTC	46delinsKHWWSLF
XH_P46	5	68616209	68616209	Nonsense_Mutation	INS	-	AAAAATAATAA	-	CCDC125	ATATGGTTATT	8_G54delinsEYGYLFX
XH_P46	5	68651571	68651571	Frame_Shift_Ins	INS	-	TTTGTGTTGTTT	-	AK6	AAACAAACAA	p.D74fs
XH_P46	5	68660946	68660946	Frame_Shift_Ins	INS	-	ATAACATGTATA	-	TAF9	insAAGTATACA	p.S207fs
XH_P46	5	72857092	72857092	Missense_Mutation	SNP	G	A	G	ANKRA2	c.C311T	p.S104F
XH_P46	5	72857094	72857094	Nonsense_Mutation	INS	-	TCTGTCACTTG	-	ANKRA2	309insCAAGTGA	A03_S104delinsTKX
XH_P46	5	78587085	78587085	Missense_Mutation	SNP	T	A	T	JMY	c.T1490A	p.I497K
XH_P46	5	78587086	78587086	Frame_Shift_Ins	INS	-	CAAAATCC	-	JMY	91_1492insCAA	p.I497fs
XH_P46	5	79031434	79031434	In_Frame_Ins	INS	-	TCCTTTTCTCTCA	-	CMYA5	847insTTCCTTT	2282delinsSFPFPQ
XH_P46	5	79473862	79473862	In_Frame_Ins	INS	-	CTTATGTTCAAG	-	SERINC5	220insCCTGAAC	K74delinsPEHHK
XH_P46	5	82816508	82816508	Frame_Shift_Ins	INS	-	A	-	VCAN	-2383_2384ins	p.V795fs

XH_P46	5	82816509	82816509	In_Frame_Ins	INS	-	TTCTGTATTTC	-	VCAN	5insCTCTCTCTG795delinsVSSCISS
XH_P46	5	82833217	82833217	Nonsense_Mutation	INS	-	SGTCTATTTCAA	-	VCAN	5GTATAGGTCTA78_Q479delinsVXX
XH_P46	5	108380427	108380427	In_Frame_Ins	INS	-	CTCTATGGGCTAG	-	FER	ACTTACTCTATG8delinsSNFTLWLGH
XH_P46	5	112174324	112174324	Frame_Shift_Ins	INS	-	FTCTCATCTGTGC	-	APC	80insTTTCTCTCA p.A993fs
XH_P46	5	112176376	112176376	Frame_Shift_Ins	INS	-	TAATACATTCTT	-	APC	32insAAATAATAC p.R1677fs
XH_P46	5	112176378	112176378	Frame_Shift_Ins	INS	-	TATTTCAA	-	APC	3_5034insTATT p.S1678fs
XH_P46	5	112203228	112203228	Nonsense_Mutation	INS	-	CATCAAAATTGAA	-	SRP19	58insTCATCAAA9_K120delinsKSSNX
XH_P46	5	114588943	114588943	Frame_Shift_Ins	INS	-	GCATTGCC	-	PGTG18	9_150insGGCAAC p.I50fs
XH_P46	5	114607044	114607044	In_Frame_Ins	INS	-	AGTCTAGTGGG	-	CCDC112	nsTCTTCCCACT800delinsSPLDYNL
XH_P46	5	114878777	114878777	Frame_Shift_Ins	INS	-	T	-	FEM1C	c.413dupA p.H138fs
XH_P46	5	114878779	114878779	In_Frame_Ins	INS	-	TATGATGTTTG	-	FEM1C	ATTACCAACA8delinsSITKHRNTH
XH_P46	5	115813816	115813816	In_Frame_Ins	INS	-	GGATGGATAAA	-	SEMA6A	nsCTTCTTTATC488delinsLPLSIHNM
XH_P46	5	123983834	123983834	Frame_Shift_Ins	INS	-	AAGGACAAAGA	-	ZNF608	243insCTTCTT p.Q748fs
XH_P46	5	135583406	135583406	In_Frame_Ins	INS	-	TGGCT	-	TRPC7	48_1249insAAGb.P417delinsKPP
XH_P46	5	137498970	137498970	In_Frame_Ins	INS	-	TTTTTCTTGTT	-	BRD8	insGAGAACCAAG605delinsENKKKEK
XH_P46	5	140228733	140228733	Frame_Shift_Ins	INS	-	TTTGCGTTAATG	-	PCDHA9	54insGTTGTCG p.G218fs
XH_P46	5	140731787	140731787	Missense_Mutation	SNP	G	A	G	PCDHGB1	c.G1960A p.A654T
XH_P46	5	140768296	140768296	Missense_Mutation	SNP	G	A	G	PCDHGB4	c.G845A p.S282N
XH_P46	5	145895416	145895416	Frame_Shift_Ins	INS	-	CATCATGA	-	GPR151	0_261insTCATG p.L87fs
XH_P46	5	147493994	147493994	Frame_Shift_Ins	INS	-	AGAATTTT	-	SPINK5	7_1958insAGAA p.V653fs
XH_P46	5	149360264	149360264	Missense_Mutation	SNP	C	T	C	SLC26A2	c.C1108T p.P370S
XH_P46	5	149360705	149360705	Frame_Shift_Ins	INS	-	C	-	SLC26A2	c.1549_1550ins p.V517fs
XH_P46	5	150682871	150682871	Silent	SNP	C	T	C	SLC36A3	c.G45A p.L15L
XH_P46	5	150924653	150924653	Nonsense_Mutation	INS	-	TTGCAGAAGAT	-	FAT2	5035insAATCTTC012_H2013delinsX
XH_P46	5	153065831	153065831	Missense_Mutation	SNP	G	T	G	GRIA1	c.G836T p.G279V
XH_P46	5	153407793	153407793	Frame_Shift_Ins	INS	-	GGAACTTGTTA	-	FAM114A2	AACACTAACAC p.K112fs
XH_P46	5	154396318	154396318	Frame_Shift_Ins	INS	-	CTGTTTTC	-	KIF4B	9_2900insCTG p.D967fs
XH_P46	5	154396319	154396319	Frame_Shift_Ins	INS	-	AGTTTGG	-	KIF4B	0_2901insAGT p.D967fs
XH_P46	5	156378688	156378688	Nonsense_Mutation	INS	-	ATGCGTATATTA	-	TIMD4	514insTAATATA p.V172delinsX
XH_P46	5	156378690	156378690	Missense_Mutation	SNP	A	T	A	TIMD4	c.T512A p.V171D
XH_P46	5	156479644	156479644	Nonsense_Mutation	INS	-	AACGGTCTCTAC	-	HAVCR1	0insGGTAGAG434_V135delinsRX
XH_P46	5	158697623	158697623	Frame_Shift_Ins	INS	-	TATCCTTAATAT	-	UBLCP1	CATATTATCCTT p.L140fs
XH_P46	5	161115992	161115992	In_Frame_Ins	INS	-	CTTAATATTTCTC	-	GABRA6	5TTTCTCTTAATA88delinsTFNLNPL
XH_P46	5	161115994	161115994	Missense_Mutation	SNP	G	T	G	GABRA6	c.G265T p.D89Y
XH_P46	5	173317354	173317354	In_Frame_Ins	INS	-	CTGACT	-	CPEB4	18_619insCTGA p.L206delinsLT
XH_P46	5	176477820	176477820	Missense_Mutation	SNP	G	A	G	ZNF346	c.G292A p.D98N
XH_P46	5	178310140	178310140	In_Frame_Ins	INS	-	TTCAATCTTTTC	-	ZNF354B	688insTTCAATC L229delinsLNFNF
XH_P46	5	180582464	180582464	Frame_Shift_Ins	INS	-	AGTACATGGGGG	-	OR2V2	23insAAGTACAT p.P174fs
XH_P46	6	7581096	7581096	Frame_Shift_Ins	INS	-	TTTTCAT	-	DSP	73_4674insTTT p.R1558fs
XH_P46	6	7581097	7581097	Silent	SNP	G	C	G	DSP	c.G4674C p.R1558R
XH_P46	6	8097636	8097636	In_Frame_Ins	INS	-	TTCTCTCTCAGCT	-	EEF1E1	2insCAGCTGAGAL51delinsPAEREV
XH_P46	6	11005710	11005710	Nonsense_Mutation	INS	-	ATTTGATATTAT	-	ELOVL2	150insAATAATAW50_L51delinsX
XH_P46	6	11005711	11005711	In_Frame_Ins	INS	-	TTTCTGAA	-	ELOVL2	3_149insTTTCACTW50delinsFSER
XH_P46	6	11103981	11103981	Frame_Shift_Ins	INS	-	TTTTCCCAGATA	-	ERVFRD-1	53insATTATCTG p.Q521fs
XH_P46	6	12121009	12121009	Frame_Shift_Ins	INS	-	TTGGGAGGGGA	-	HIVEP1	982insTTGGGAG p.N327fs
XH_P46	6	25773745	25773745	Nonsense_Mutation	INS	-	ATAAAGGGATG	-	SLC17A4	831insATAAAGG p.C277delinsX
XH_P46	6	26184065	26184065	Silent	SNP	C	A	C	HIST1H2BE	c.C42A p.G34G
XH_P46	6	27279773	27279773	Silent	SNP	C	T	C	POM121L2	c.G177A p.R59R
XH_P46	6	28214856	28214856	Frame_Shift_Ins	INS	-	AAAGCCTGTTAG	-	ZKSCAN4	4insCAGTAACAG p.M68fs
XH_P46	6	34826087	34826087	Frame_Shift_Ins	INS	-	GAGAAAATGAA	-	UHRF1BP1	5insACAGAGAA p.P652fs
XH_P46	6	34826089	34826089	Silent	SNP	T	A	T	UHRF1BP1	c.T1956A p.P652P
XH_P46	6	38994426	38994426	In_Frame_Ins	INS	-	GTCTCAGTGTT	-	DNAH8	insCATTGTGCTC607delinsTFVSVFRF
XH_P46	6	43025944	43025944	Missense_Mutation	SNP	G	A	G	MRPL2	c.C124T p.P42S
XH_P46	6	43025945	43025945	Missense_Mutation	SNP	C	A	C	MRPL2	c.G123T p.Q41H
XH_P46	6	43307358	43307358	Frame_Shift_Ins	INS	-	ACATATTCTAT	-	ZNF318	4378insATAGAA p.H1460fs
XH_P46	6	43307360	43307360	Frame_Shift_Ins	INS	-	TA	-	ZNF318	4375_4376insT p.P1459fs
XH_P46	6	43310598	43310598	Frame_Shift_Ins	INS	-	ATACCCCTATCTC	-	ZNF318	092insCAGATA p.E1031fs
XH_P46	6	45459696	45459696	Frame_Shift_Ins	INS	-	AG	-	RUNX2	c.662_663insAG p.D221fs
XH_P46	6	45459697	45459697	In_Frame_Ins	INS	-	CAAGCATCAATA	-	RUNX2	664insCAAGCATD221delinsDQASI
XH_P46	6	51612806	51612806	Missense_Mutation	SNP	G	A	G	PKHD1	c.C9608T p.S5203L
XH_P46	6	51947315	51947315	Nonsense_Mutation	INS	-	AAAAAAAGTTTC	-	PKHD1	6insATGAAACTP52_N53delinsPX
XH_P46	6	52764783	52764783	Frame_Shift_Ins	INS	-	TTTT	-	GSTA3	362_363insAA p.I121fs
XH_P46	6	52764785	52764785	In_Frame_Ins	INS	-	GAAAAATGA	-	GSTA3	0_361insTCAAT p.I121delinsNFI
XH_P46	6	56334734	56334734	Frame_Shift_Ins	INS	-	T	-	DST	14628_14629ins p.C4877fs
XH_P46	6	56334735	56334735	Frame_Shift_Ins	INS	-	ATGCACA	-	DST	27_14628insTG p.K4876fs
XH_P46	6	56420265	56420265	Missense_Mutation	SNP	T	G	T	DST	c.A7145C p.K2382T
XH_P46	6	56420267	56420267	Frame_Shift_Ins	INS	-	TCAGTGAAGAG	-	DST	8insCCTCTCTCTC p.I2381fs
XH_P46	6	56918465	56918465	Frame_Shift_Ins	INS	-	CT	-	KIAA1586	1087_1088insC p.D363fs
XH_P46	6	56918466	56918466	In_Frame_Ins	INS	-	TTCTTGTTGCAC	-	KIAA1586	1089insTTCTTG363delinsDSSCT
XH_P46	6	62390907	62390907	Frame_Shift_Ins	INS	-	GGCGTGACATT	-	KHORB52	AGGTGCAATGT p.A337fs
XH_P46	6	71571588	71571588	In_Frame_Ins	INS	-	ATGGAGCTT	-	B3GAT2	9_830insAAGCT L277delinsQAPF
XH_P46	6	74118985	74118985	Frame_Shift_Ins	INS	-	ATTT	-	DDX43	194_1195insAT p.A398fs
XH_P46	6	74118986	74118986	Frame_Shift_Ins	INS	-	TCATTGT	-	DDX43	95_1196insTCA p.D399fs
XH_P46	6	76022348	76022348	Frame_Shift_Ins	INS	-	AGTGACCTAATA	-	FILIP1	200insCTATTAG p.I1067fs
XH_P46	6	79650872	79650872	Frame_Shift_Ins	INS	-	AG	-	PHIP	5003_5004insC p.Y1668fs
XH_P46	6	79650873	79650873	Frame_Shift_Ins	INS	-	AGTGTTAAGGAC	-	PHIP	nsTACTTCTCCTT p.Y1668fs
XH_P46	6	80197020	80197020	Frame_Shift_Ins	INS	-	GTGAAGGAAGA	-	LCA5	795insCTTCTTC p.E599fs
XH_P46	6	87969421	87969421	Frame_Shift_Ins	INS	-	AATGTTTTTGTA	-	ZNF292	CTGTAAATGTT p.L2025fs
XH_P46	6	87970754	87970754	Frame_Shift_Ins	INS	-	AGGCTATTITTC	-	ZNF292	GAATAAGGCTT p.S2469fs
XH_P46	6	87994339	87994339	Frame_Shift_Ins	INS	-	GTGATTGTGT	-	GJB7	insTCAACACAA p.H98fs
XH_P46	6	90425449	90425449	Silent	SNP	G	A	G	MDN1	c.C6783T p.P2261P
XH_P46	6	90466084	90466084	Frame_Shift_Ins	INS	-	C	-	MDN1	2727_2728ins p.L910fs
XH_P46	6	90466085	90466085	Frame_Shift_Ins	INS	-	ATGGCAGGATTA	-	MDN1	TAATAATAATC p.E909fs
XH_P46	6	90572321	90572321	Frame_Shift_Ins	INS	-	CATTAGTGCA	-	CASP8AP2	894insCATTAG p.T298fs
XH_P46	6	90572805	90572805	Frame_Shift_Ins	INS	-	TATTTCAITCTTG	-	CASP8AP2	78insGTTATTTC p.N459fs
XH_P46	6	90578433	90578433	Frame_Shift_Ins	INS	-	TGTTACTTCTAT	-	CASP8AP2	425insCTGTTC p.K1808fs
XH_P46	6	97001326	97001326	Missense_Mutation	SNP	T	A	T	UFL1	c.T2332A p.S778T
XH_P46	6	97001327	97001327	Frame_Shift_Ins	INS	-	TAATACA	-	UFL1	83_2334insTAA p.S778fs
XH_P46	6	112443397	112443397	Nonsense_Mutation	INS	-	CACCTTAATCCT	-	LAMA4	ATAATAGGATT p.K1432delinsTX
XH_P46	6	117128274	117128274	Frame_Shift_Ins	INS	-	SAATATAAATAA	-	GPCR6A	CACATCTATT p.A198fs
XH_P46	6	117128276	117128276	Missense_Mutation	SNP	C	A	C	GPCR6A	c.G592T p.A198S
XH_P46	6	128643204	128643204	Frame_Shift_Ins	INS	-	TTGTTGGTGGT	-	PTPRK	75insAAACCACC p.F159fs
XH_P46	6	131277278	131277278	Frame_Shift_Ins	INS	-	CTTAGATTGG	-	EPB41L2	348insCCAAATC p.I16fs
XH_P46	6	131277280	131277280	Nonsense_Mutation	INS	-	TA	-	EPB41L2	c.345_346insTAA116_P117delinsX
XH_P46	6	131915465	131915465	In_Frame_Ins	INS	-	ATAATATCCTTT	-	MED23	06insAAAAAG1002delinsVKRILS
XH_P46	6	131915467	131915467	Missense_Mutation	SNP	C	T	C	MED23	c.G3004A p.V1002M
XH_P46	6	132031090	132031090	Nonsense_Mutation	INS	-	CAAAGCAGGT	-	CTAGE9	1068insAACCTG66_K357delinsITCFX
XH_P46	6	132061463	132061463	Missense_Mutation	SNP	G	C	G	ENPP3	c.G2400C p.W800C

XH_P46	6	133072589	133072589	Frame_Shift_Ins	INS	-	GTACTGGCAGG	-	VNN2	5insTTACTGTGCC	p.L299fs
XH_P46	6	133079008	133079008	Nonsense_Mutation	INS	-	ATCATTTTTTATTT	-	VNN2	5insAAAAATAAA	p.S5_F6delinsSKX
XH_P46	6	133079009	133079009	In_Frame_Ins	INS	-	CTTGTTTTGAAC	-	VNN2	14insGTTCAAAA	p.S5delinsCSKQA
XH_P46	6	135787219	135787219	Frame_Shift_Ins	INS	-	GGAAAAAGAAAC	-	AH1	5TTCTTTTCTTT	p.p161fs
XH_P46	6	135787221	135787221	Silent	SNP	C	T	C	AH1	c.G480A	p.p160K
XH_P46	6	136882724	136882724	Nonsense_Mutation	INS	-	TCAGGTGTTTA	-	MAP3K5	TATCTAATAAAC	L1313delinsLSPYLINTX
XH_P46	6	142630752	142630752	In_Frame_Ins	INS	-	5AAAAATAATCC	-	ADGRG6	AAAGAAAAATAA	p.25delinsAKENKSMH
XH_P46	6	143094481	143094481	Frame_Shift_Ins	INS	-	TATTCCTCCTT	-	HIVEP2	1395insAAGGA	p.p.R465fs
XH_P46	6	146127422	146127422	Frame_Shift_Ins	INS	-	TC	-	FBXO30	c.119_120insGA	p.p.V40fs
XH_P46	6	146127423	146127423	In_Frame_Ins	INS	-	TATGAAAAT	-	FBXO30	8_119insATTIT	p.V40delinsDFHI
XH_P46	6	146480661	146480661	Missense_Mutation	SNP	G	T	G	GRM1	c.G878T	p.p.G293V
XH_P46	6	146993502	146993502	Frame_Shift_Ins	INS	-	C	-	ADGB	c.986_987insC	p.p.E329fs
XH_P46	6	146993504	146993504	In_Frame_Ins	INS	-	AAACAT	-	ADGB	88_989insAAAC	p.L330delinsKTL
XH_P46	6	151674402	151674402	In_Frame_Ins	INS	-	TACTGCTTTTGG	-	AKAP12	583insTTTACTG	p.L528delinsVYCFWS
XH_P46	6	151674404	151674404	Silent	SNP	A	T	A	AKAP12	c.A4584T	p.p.A1528A
XH_P46	6	151766560	151766560	Frame_Shift_Ins	INS	-	AAAACAAAATAC	-	RMND1	nsACCTGTATTTT	p.p.S129fs
XH_P46	6	151790036	151790036	In_Frame_Ins	INS	-	CTAATATTAAAT	-	ARMT1	nsCGGTCTAATA	p.L254delinsSANIKSV
XH_P46	6	152763329	152763329	Missense_Mutation	SNP	C	T	C	SYNE1	c.G3910A	p.p.A1304T
XH_P46	6	155154158	155154158	Frame_Shift_Ins	INS	-	CTCTC	-	SCAF8	445_3446insCT	p.p.F1149fs
XH_P46	6	155154160	155154160	In_Frame_Ins	INS	-	ATATCTACAGGA	-	SCAF8	3448insATATCT	p.F1149delinsFISTG
XH_P46	7	286468	286468	Nonsense_Mutation	INS	-	CCCTTCCTCCTC	-	FAM20C	5TGAGCCCTCC	p.L7_D31delinsLDRX
XH_P46	7	4900584	4900584	In_Frame_Ins	INS	-	AGAAAA	-	PAPOLB	857_858insTTT	p.V28delinsVFL
XH_P46	7	4900586	4900586	Nonsense_Mutation	INS	-	AACATTAGAA	-	PAPOLB	856insTCTCAA	p.L286_1287delinsFX
XH_P46	7	6692398	6692398	In_Frame_Del	DEL	TTACGCACCC	-	GTTACGCACCGA	ZNF316	c.1171_1338del	p.p.391_446del
XH_P46	7	12254638	12254638	Nonsense_Mutation	INS	-	TCAAACAT	-	TMEM106B	2_203insTCAAA	p.G68delinsVKLX
XH_P46	7	12254639	12254639	In_Frame_Ins	INS	-	TAA	-	TMEM106B	c.203_204insTA	p.p.G68delinsGK
XH_P46	7	12680054	12680054	Frame_Shift_Ins	INS	-	ACAGCACTCTTA	-	SCIN	CTTTACAGCA	p.p.T251fs
XH_P46	7	15725798	15725798	In_Frame_Del	DEL	TGGTGG	-	TGGTGG	MEOX2	c.225_230del	p.p.75_77del
XH_P46	7	21470332	21470332	Frame_Shift_Ins	INS	-	AGGCT	-	SP4	498_1499insAG	p.p.G500fs
XH_P46	7	23018049	23018049	Frame_Shift_Ins	INS	-	TTTGTTTTTTCAT	-	FAM126A	72insATGAAAA	p.p.H58fs
XH_P46	7	23240203	23240203	Frame_Shift_Ins	INS	-	GAGTTTG	-	NUPL2	11_1112insGAG	p.p.T371fs
XH_P46	7	23240204	23240204	Missense_Mutation	SNP	C	T	C	NUPL2	c.C1112T	p.p.T371I
XH_P46	7	23556134	23556134	Frame_Shift_Ins	INS	-	TG	-	TRA2A	c.183_184insCA	p.p.R62fs
XH_P46	7	23556135	23556135	Frame_Shift_Ins	INS	-	TTTTAGGGGAG	-	TRA2A	183insCTCCCC	p.p.R61fs
XH_P46	7	23651120	23651120	Nonsense_Mutation	INS	-	CTCTTAATCTGTA	-	CCDC126	ATTAGTCTTAAT	p.L1delinsEENKKNISISLNLYQX
XH_P46	7	25175856	25175856	In_Frame_Ins	INS	-	ATAACA	-	C7orf31	407_1508insGTG	p.H503delinsLLY
XH_P46	7	25175858	25175858	Frame_Shift_Ins	INS	-	TAATTCCTTCGT	-	C7orf31	56GCAATACGAAC	p.p.E502fs
XH_P46	7	25266558	25266558	In_Frame_Ins	INS	-	ATGCTGAGTGAT	-	NPVF	226insATCACTC	p.P76delinsITQHP
XH_P46	7	26236582	26236582	Missense_Mutation	SNP	A	T	A	HNRNPA2B1	c.T320A	p.p.L107N
XH_P46	7	26236584	26236584	Nonsense_Mutation	INS	-	ATATAAGGGCTT	-	HNRNPA2B1	5AAGCAAGCCC	p.L106_1107delinsGX
XH_P46	7	27140366	27140366	Nonsense_Mutation	INS	-	TGATCATATAAT	-	HOXA2	insTACAATTATA	p.L70_L371delinsDTIX
XH_P46	7	27582672	27582672	Nonsense_Mutation	INS	-	TGCTCAGATTTT	-	HIBADH	5TTTTAAATCT	p.L78delinsNKCFKIX
XH_P46	7	31125053	31125053	Frame_Shift_Ins	INS	-	TAAATCT	-	ADCYAP1R1	2_603insTAAAT	p.p.S201fs
XH_P46	7	40132777	40132777	Frame_Shift_Ins	INS	-	TCTGTTTTTCAC	-	CDK13	30insTGTCGT	p.p.S1210fs
XH_P46	7	47921648	47921648	Frame_Shift_Ins	INS	-	TTTCTCT	-	PKD1L1	0_3301insAGAA	p.p.L1101fs
XH_P46	7	47921649	47921649	Frame_Shift_Ins	INS	-	ACTTTTCTGTTT	-	PKD1L1	300insTAAACG	p.p.S1100fs
XH_P46	7	50121485	50121485	In_Frame_Ins	INS	-	ATG	-	ZBPB	c.218_219insCA	p.p.Y73delinsYL
XH_P46	7	50121487	50121487	In_Frame_Ins	INS	-	GATAGTGT	-	ZBPB	5_217insAACAC	p.p.Y73delinsNTIV
XH_P46	7	57529119	57529119	Frame_Shift_Ins	INS	-	CTTATGTTTAGT	-	ZNF716	53insTCTTATGT	p.p.H318fs
XH_P46	7	63538259	63538259	Frame_Shift_Ins	INS	-	TTCTGTATGGTA	-	ZNF727	3insTCTTCTGTA	p.p.H278fs
XH_P46	7	64166829	64166829	Nonsense_Mutation	INS	-	TACAAACTACAT	-	ZNF107	nsATTATACAAAG	p.H87delinsKILQTTX
XH_P46	7	64167954	64167954	In_Frame_Ins	INS	-	TATCTTATGTCT	-	ZNF107	ATGAATTATCTT	p.L1delinsS5MNVLMSSKS
XH_P46	7	74564919	74564919	In_Frame_Ins	INS	-	GGC	-	GF2F1RD2	2666_2667insG	p.P.E889delinsEA
XH_P46	7	74564920	74564920	Frame_Shift_Ins	INS	-	CAGTT	-	GF2F1RD2	667_2668insCA	p.p.E889fs
XH_P46	7	75614177	75614177	Silent	SNP	G	A	G	POR	c.G1149A	p.p.P383P
XH_P46	7	82582537	82582537	Frame_Shift_Ins	INS	-	CAAGACTGAGG	-	PCLO	7732insCCTCA	p.p.E2578fs
XH_P46	7	86988642	86988642	Frame_Shift_Ins	INS	-	CAAAAGAT	-	CROT	6_237insCAAAA	p.p.N79fs
XH_P46	7	87537448	87537448	Nonsense_Mutation	INS	-	TTTCACTTTTCAG	-	DBF4	TATTATTTTCAC	p.L432_P433delinsSX
XH_P46	7	87757987	87757987	Frame_Shift_Ins	INS	-	CCACCTACTCAG	-	ADAM22	ATTCTCCACCTA	p.p.L249fs
XH_P46	7	87910338	87910338	In_Frame_Ins	INS	-	CAGCTAAGACTA	-	STEAP4	nsCTATAGTCTT	p.L171delinsSYSLSR
XH_P46	7	88963244	88963244	In_Frame_Ins	INS	-	GTTTGCAGTACC	-	ZNF804B	949insGTTTGCA	p.D316delinsDVCS
XH_P46	7	91630751	91630751	Missense_Mutation	SNP	C	T	C	AKAP9	c.C1520T	p.p.S507F
XH_P46	7	91630753	91630753	Frame_Shift_Ins	INS	-	TTCTTGTTCCAT	-	AKAP9	TTGTGTTTCTTG	p.p.Q508fs
XH_P46	7	91708868	91708868	Frame_Shift_Ins	INS	-	TCTTCTTCTCAT	-	AKAP9	2insATTCTTCT	p.p.L274fs
XH_P46	7	92764616	92764616	Frame_Shift_Ins	INS	-	STAAAGATAAAA	-	SAMD9L	9insTATTTTATC	p.p.R223fs
XH_P46	7	92764617	92764617	Missense_Mutation	SNP	C	T	C	SAMD9L	c.G668A	p.p.R223Q
XH_P46	7	92821589	92821589	Frame_Shift_Ins	INS	-	AGTGGAAGTACA	-	HEPACAM2	1302insATCTAG	p.p.L434fs
XH_P46	7	94539584	94539584	Frame_Shift_Ins	INS	-	GTGTATT	-	PPP1R9A	59_160insGTGT	p.p.Q53fs
XH_P46	7	94539586	94539586	In_Frame_Ins	INS	-	GAA	-	PPP1R9A	c.161_162insGA	p.p.S54delinsRN
XH_P46	7	94881159	94881159	Nonsense_Mutation	INS	-	AAGAAAAATGAT	-	PPP1R9A	2417insAAGAAA	p.L806delinsQEKX
XH_P46	7	97498378	97498378	Missense_Mutation	SNP	C	T	C	ASNS	c.G28A	p.p.A10T
XH_P46	7	98506466	98506466	Silent	SNP	C	T	C	TRRAP	c.C1231T	p.p.L411L
XH_P46	7	99129716	99129716	In_Frame_Ins	INS	-	CTTGCTCTC	-	ZKSCAN5	5_2146insCTTG	p.L715delinsLTVF
XH_P46	7	99170811	99170811	Frame_Shift_Ins	INS	-	TTTATGTGCGAT	-	ZNF655	31insTCTTTTATG	p.p.Y360fs
XH_P46	7	99315230	99315230	In_Frame_Ins	INS	-	TTGTGAGAAATC	-	CYP3A7	insTCAGATTTC	p.L117delinsAQISHQH
XH_P46	7	99669412	99669412	In_Frame_Ins	INS	-	GGAGAAAAA	-	ZNF3	5_716insTTTTT	p.E239delinsVFLQ
XH_P46	7	99669413	99669413	In_Frame_Ins	INS	-	CCTATGAATGTA	-	ZNF3	715insTACATTC	p.E239delinsVIHRE
XH_P46	7	99673220	99673220	Frame_Shift_Ins	INS	-	CCCTCC	-	ZNF3	8_89insGGAAG	p.p.K30fs
XH_P46	7	100676021	100676021	Nonsense_Mutation	INS	-	FAGGAAGTGAAC	-	MUC17	nsGTTGTAGGAA	p.L2_A443delinsSCRXC
XH_P46	7	100676075	100676075	In_Frame_Ins	INS	-	ACAGGAGTTATT	-	MUC17	1379insACAGGA	p.S460delinsNRSYC
XH_P46	7	100682694	100682694	Frame_Shift_Ins	INS	-	AGGACTG	-	MUC17	97_7998insAGG	p.p.T2666fs
XH_P46	7	102960107	102960107	In_Frame_Ins	INS	-	TTTTTTTGGTTTT	-	DNAJC2	insCAAAAAACCC	p.97delinsDKPKNR
XH_P46	7	104752717	104752717	Frame_Shift_Ins	INS	-	GGCAG	-	KMT2E	514_4515insGG	p.p.N1505fs
XH_P46	7	104752719	104752719	Missense_Mutation	SNP	C	T	C	KMT2E	c.C4516T	p.p.L1506F
XH_P46	7	104782896	104782896	Frame_Shift_Ins	INS	-	CACCTCGTTG	-	SRPK2	1069insCAACG	p.p.E357fs
XH_P46	7	111400359	111400359	Nonsense_Mutation	INS	-	CCATCATCTTAA	-	DOCK4	5TAAAAATTAAAG	p.R1338delinsKLRLX
XH_P46	7	112424161	112424161	In_Frame_Ins	INS	-	GCCATAAAGTAT	-	TMEM168	nsAATATACCTT	p.L240delinsEYIFMAV
XH_P46	7	113517923	113517923	Frame_Shift_Ins	INS	-	CCCCAACATTTC	-	PPP1R3A	4insTCCAATG	p.p.L1075fs
XH_P46	7	113518471	113518471	In_Frame_Ins	INS	-	AAACCTGAAGAA	-	PPP1R3A	2676insTTCTTC	p.L7892delinsTSSGL
XH_P46	7	115582075	115582075	Missense_Mutation	SNP	C	G	C	TFEC	c.G334C	p.p.G112R
XH_P46	7	115582076	115582076	Frame_Shift_Ins	INS	-	GAATTGGG	-	TFEC	2_333insCCCAA	p.p.K111fs
XH_P46	7	116340302	116340302	In_Frame_Ins	INS	-	CTAGAGTTTCCC	-	MET	1165insCTAGAG	p.H388delinsHLEFP
XH_P46	7	127015066	127015066	In_Frame_Ins	INS	-	AGAAAAAGAA	-	ZNF800	3_324insTTCTT	p.K108delinsNSFL
XH_P46	7	128394609	128394609	Nonsense_Mutation	INS	-	TGAGCTTAGCCA	-	CALU	5ACTCTGGAAGT	p.B3_K84delinsELWTX
XH_P46	7	129841907	129841907	Missense_Mutation	SNP	T	A	T	TMEM209	c.A356T	p.p.D119V
XH_P46	7	129841909	129841909	In_Frame_Ins	INS	-	CCCATT	-	TMEM209	53_354insAATG	p.H118delinsQMG
XH_P46	7	134346517	134346517	Frame_Shift_Ins	INS	-	TTTCAAATGGG	-	BPGM	259insTTTCAA	p.p.R86fs
XH_P46	7	141408744	141408744	Nonsense_Mutation	INS	-	CAGCTACAAAC	-	WEE2	nsTAACAGCTAC	p.p.N62delinsNX

XH_P46	7	143792326	143792326	Nonsense_Mutation	INS	-	AAATAAAAAACA	-	OR2A12	hsAGAAAAATAAA42	I43delinsGRKK
XH_P46	7	143884412	143884412	Frame_Shift_Ins	INS	-	CAATGTATTTT	-	ARHGEF35	065insTAAAAA	p.V355fs
XH_P46	7	143884414	143884414	Missense_Mutation	SNP	C	A	C	ARHGEF35	c.G1063T	p.V355L
XH_P46	7	144060555	144060555	Nonsense_Mutation	INS	-	GAGAAATAATATC	-	ARHGEF5	794insGAGAAAT	V262delinsGEX
XH_P46	7	149512992	149512992	Missense_Mutation	SNP	G	T	G	SSPO	c.G10895T	p.G3632V
XH_P46	7	150700402	150700402	Missense_Mutation	SNP	T	C	T	NOS3	c.T1756C	p.W586R
XH_P46	7	151860149	151860149	Frame_Shift_Ins	INS	-	C	-	KMT2C	10512_10513ins	p.N3505fs
XH_P46	7	151860151	151860151	Frame_Shift_Ins	INS	-	GTATTCTGATAT	-	KMT2C	511insTTATATC	p.T3504fs
XH_P46	7	151873992	151873992	In_Frame_Ins	INS	-	GTTCGCTC	-	KMT2C	8546insGAGG	V2849delinsGGKL
XH_P46	7	151875020	151875020	Frame_Shift_Ins	INS	-	GGCCAGACTT	-	KMT2C	7518insAAGTC	p.Q2506fs
XH_P46	8	7190443	7190443	Missense_Mutation	SNP	G	A	G	USP17L1	c.G535A	p.G179S
XH_P46	8	7195831	7195831	In_Frame_Ins	INS	-	IAGAGAAGTAAT	-	USP17L4	96insTAAGAGA	T399delinsREVIS
XH_P46	8	18656864	18656864	Splice_Site	INS	-	GGTGTCTGGAG	-	PSD3	.	.
XH_P46	8	19678014	19678014	Silent	SNP	G	A	G	INTS10	c.G426A	p.T142T
XH_P46	8	21931335	21931335	In_Frame_Ins	INS	-	TTTTTTTTCTTT	-	DMTN	705insTTTTTTT	P235delinsPFFSF
XH_P46	8	22105455	22105455	Missense_Mutation	SNP	C	A	C	POLR3D	c.C295A	p.R99S
XH_P46	8	22105456	22105456	In_Frame_Ins	INS	-	GATTTTTTCAGT	-	POLR3D	297insGATTTTT	R99delinsRIFSV
XH_P46	8	24207483	24207483	In_Frame_Ins	INS	-	AATTATATTAA	-	ADAM28	8insGATAATTAT	G99delinsQDNYINI
XH_P46	8	25346120	25346120	Frame_Shift_Ins	INS	-	TATATTACCCAA	-	CDCA2	tsATACATATAT	p.V514fs
XH_P46	8	25346122	25346122	Nonsense_Mutation	SNP	C	T	C	CDCA2	c.C1543T	p.Q515X
XH_P46	8	30703099	30703099	In_Frame_Ins	INS	-	ATATCA	-	TEX15	83_4584insTGA	T1528delinsTDI
XH_P46	8	30703101	30703101	Frame_Shift_Ins	INS	-	GATTCAAATGTG	-	TEX15	nsGCTTCACATT	p.T1528fs
XH_P46	8	30938664	30938664	In_Frame_Ins	INS	-	TTC	-	WRN	1121_1122insT	p.F374delinsFS
XH_P46	8	30938666	30938666	Frame_Shift_Ins	INS	-	AATATCCTTTAG	-	WRN	124insAAATATC	p.E375fs
XH_P46	8	41805377	41805377	Nonsense_Mutation	INS	-	ATATTCTCCTAG	-	KAT6A	94insTCTTAGGA	L599delinsNPRRIX
XH_P46	8	42720633	42720633	Splice_Site	INS	-	ATTATTATTATTA	-	RNF170	.	.
XH_P46	8	48612984	48612984	In_Frame_Ins	INS	-	STCTGTCCATCT	-	SPIDR	ACAGTGTCTGT	elinsWFPTSVHLSVCLL
XH_P46	8	52320887	52320887	Silent	SNP	C	T	C	PXDNL	c.G3297A	p.P1099P
XH_P46	8	52336280	52336280	Frame_Shift_Ins	INS	-	TCCTATACTTCT	-	PXDNL	CAGAAAGAAAG	p.Q505fs
XH_P46	8	52733242	52733242	Missense_Mutation	SNP	C	T	C	PCMTD1	c.G515A	p.R172H
XH_P46	8	53586477	53586477	Missense_Mutation	SNP	G	C	G	RB1CC1	c.C930G	p.D310E
XH_P46	8	55538237	55538237	Missense_Mutation	SNP	G	T	G	RP1	c.G1795T	p.G599C
XH_P46	8	55538238	55538238	Nonsense_Mutation	INS	-	GCAGACTGTTT	-	RP1	ACTTAAGCAGAG	99_N600delinsGTX
XH_P46	8	62538834	62538834	Nonstop_Mutation	SNP	A	T	A	ASPH	c.T883A	p.C295K
XH_P46	8	62538836	62538836	Nonsense_Mutation	INS	-	CTGAATTTATG	-	ASPH	ACACACATAAA94	X295delinsKHTX
XH_P46	8	69020551	69020551	Nonsense_Mutation	INS	-	GCAGTTGAACA	-	PREX2	TAAAAAGCAGT	75_S976delinsKSSX
XH_P46	8	72234486	72234486	In_Frame_Ins	INS	-	AGTTTT	-	EYA1	20_121insAAA	p.F41delinsKTF
XH_P46	8	72234488	72234488	Nonsense_Mutation	INS	-	TTTAAGATACAA	-	EYA1	119insTTGTATC	S40delinsIVSX
XH_P46	8	75227278	75227278	Silent	SNP	G	A	G	JPH1	c.C957T	p.T319T
XH_P46	8	77765154	77765154	Frame_Shift_Ins	INS	-	G	-	ZFHx4	5997_5998ins	p.S1999fs
XH_P46	8	77765156	77765156	Frame_Shift_Ins	INS	-	TGTTTTCGTT	-	ZFHx4	6000insTGT	p.P2000fs
XH_P46	8	77765977	77765977	Nonsense_Mutation	INS	-	GAATCTTTATTT	-	ZFHx4	5821insGAATCT	T274_Q2275delinsX
XH_P46	8	77776305	77776305	Nonsense_Mutation	INS	-	AACGTGT	-	ZFHx4	55_10356insAAG	452_D3453delinsX
XH_P46	8	82606346	82606346	Frame_Shift_Ins	INS	-	TGTTTGT	-	SLC10A5	51_862insACAA	p.G288fs
XH_P46	8	82606347	82606347	Frame_Shift_Ins	INS	-	AAACTGTTGCT	-	SLC10A5	861insAGCAAC	p.I287fs
XH_P46	8	98703408	98703408	In_Frame_Ins	INS	-	TGATTGCTTGAC	-	MTDH	TTTTCTATGATTG	7delinsSHFYDCLTYIV
XH_P46	8	100155314	100155314	Frame_Shift_Ins	INS	-	TTGT	-	VPS13B	764_1765insTT	p.S588fs
XH_P46	8	100155316	100155316	Frame_Shift_Ins	INS	-	CTTAA	-	VPS13B	766_1767insCT	p.S589fs
XH_P46	8	101078492	101078492	In_Frame_Ins	INS	-	ACAGTACTAGT	-	RGS22	ACCACCTAAGTA	8delinsAPTTKYCTVK
XH_P46	8	103662520	103662520	Nonsense_Mutation	INS	-	ATGAGAGAAAGCT	-	KLF10	AATAAAAGCTT	F17_F418delinsHFXK
XH_P46	8	104898201	104898201	In_Frame_Ins	INS	-	TATGCTTCTCT	-	RIMS2	799insTATGCC	H266delinsHYAFS
XH_P46	8	105025830	105025830	Missense_Mutation	SNP	C	T	C	RIMS2	c.C2722T	p.P908S
XH_P46	8	106813385	106813385	Missense_Mutation	SNP	A	T	A	ZFPM2	c.A1075T	p.T359S
XH_P46	8	106813387	106813387	Frame_Shift_Ins	INS	-	TGAAAATGGAA	-	ZFPM2	AGGAGTGAA	p.T359fs
XH_P46	8	106813682	106813682	Missense_Mutation	SNP	C	A	C	ZFPM2	c.C1372A	p.P458T
XH_P46	8	106813683	106813683	In_Frame_Ins	INS	-	GGTGCAATT	-	ZFPM2	3_1374insGGTG	P458delinsPVHF
XH_P46	8	108315585	108315585	In_Frame_Ins	INS	-	AGAGATACTCTG	-	ANGPT1	219insCAGAGT	K73delinsNRVSL
XH_P46	8	110255499	110255499	In_Frame_Ins	INS	-	GAGAGA	-	NUDCD1	403_1404insCTC	K468delinsNLS
XH_P46	8	110255501	110255501	Nonsense_Mutation	INS	-	A	-	NUDCD1	1401_1402ins	K468_F469delinsX
XH_P46	8	113237123	113237123	Frame_Shift_Ins	INS	-	GGAATGAT	-	CSMD3	3_10494insATC	p.V3498fs
XH_P46	8	113237125	113237125	Frame_Shift_Ins	INS	-	AGAAGAG	-	CSMD3	91_10492insCT	p.V3498fs
XH_P46	8	113871448	113871448	In_Frame_Ins	INS	-	TAAAAATAATAC	-	CSMD3	9insATTGATTAT	4570delinsIVLFLFS
XH_P46	8	113871450	113871450	Missense_Mutation	SNP	G	C	G	CSMD3	c.C1367G	p.T456R
XH_P46	8	113988377	113988377	Frame_Shift_Ins	INS	-	GAGCTTCGAGTT	-	CSMD3	nsTAACAACCTGC	p.G344fs
XH_P46	8	118169959	118169959	In_Frame_Ins	INS	-	TTTCCTTGG	-	SLC30A8	8_449insTTTCC	C150delinsFSLG
XH_P46	8	118169961	118169961	Missense_Mutation	SNP	C	G	C	SLC30A8	c.C450G	p.C150W
XH_P46	8	120795866	120795866	Frame_Shift_Ins	INS	-	IATAAAGGAAAT	-	TA2F	AATAGCTATTTC	p.S623fs
XH_P46	8	120803700	120803700	Splice_Site	INS	-	GGATTATTAGTT	-	TA2F	.	.
XH_P46	8	124335194	124335194	Nonsense_Mutation	INS	-	TTTCCAATCTATA	-	ATAD2	TAAGTTATAGA	72_T1373delinsIKLX
XH_P46	8	125988959	125988959	In_Frame_Ins	INS	-	TTATAATGTTGT	-	ZNF572	nsTGCTTATAAT	L50delinsHAYNVVV
XH_P46	8	125988961	125988961	Nonsense_Mutation	SNP	C	T	C	ZNF572	c.C451T	p.Q151X
XH_P46	8	125989015	125989015	In_Frame_Ins	INS	-	GTGGCTCATGTC	-	ZNF572	506insGTGGCTC	F169delinsGCLCL
XH_P46	8	131073058	131073058	Frame_Shift_Ins	INS	-	SAACCTATTCC	-	ASAP1	9insTGCGGAAT	p.K987fs
XH_P46	8	132982861	132982861	Frame_Shift_Ins	INS	-	CATGTTTCTAGT	-	EFR3A	023insACATGTT	p.I341fs
XH_P46	8	134026000	134026000	In_Frame_Ins	INS	-	TTTCATCAAAATC	-	TG	554insCTTTCATC	T185delinsPFKISW
XH_P46	8	144732321	144732321	Frame_Shift_Ins	INS	-	AAATCATCTTTCC	-	ZNF623	nsACAAAATCATG	p.T93fs
XH_P46	8	144732322	144732322	Missense_Mutation	SNP	G	A	G	ZNF623	c.G280A	p.A94T
XH_P46	9	117998	117998	Missense_Mutation	SNP	G	T	G	FOXD4	c.C122A	p.A41E
XH_P46	9	1056868	1056868	Frame_Shift_Ins	INS	-	TTGCTTGGTG	-	DMRT2	1282insTTGCT	p.S427fs
XH_P46	9	8528771	8528771	Nonsense_Mutation	INS	-	TTTCTCTCTCCTT	-	PTPRD	AAATAAGGAGAA	P122delinsLKLIRREKNX
XH_P46	9	12775861	12775861	In_Frame_Ins	INS	-	GGC	-	LURAP1L	147_148insGG	p.G49delinsGG
XH_P46	9	15478527	15478527	Nonsense_Mutation	INS	-	TCAATTTATATA	-	PSIP1	GTATCTATATAA93	R194delinsVSIX
XH_P46	9	17340935	17340935	In_Frame_Ins	INS	-	TCAAATAAAAG	-	CNTLN	AATGTTTCAAA	elinsESINIMFIQKGYPSKY
XH_P46	9	32541729	32541729	In_Frame_Ins	INS	-	AGACTGTGATAT	-	TOPORS	nsAAGACATATC	B67delinsKTYHSLYQ
XH_P46	9	33464075	33464075	Missense_Mutation	SNP	C	T	C	NOL6	c.G2864A	p.R955H
XH_P46	9	33548825	33548825	In_Frame_Ins	INS	-	TTTCCT	-	ANKRD18B	350_1851insTTT	Q617delinsHFL
XH_P46	9	33548826	33548826	Missense_Mutation	SNP	G	T	G	ANKRD18B	c.G1851T	p.Q617H
XH_P46	9	34611209	34611209	Missense_Mutation	SNP	G	A	G	RPP25L	c.C85T	p.R29W
XH_P46	9	35957901	35957901	Frame_Shift_Ins	INS	-	TGTT	-	OR2S2	194_195insAAC	p.G65fs
XH_P46	9	35957902	35957902	Frame_Shift_Ins	INS	-	ATCTCTTT	-	OR2S2	3_194insAAAAA	p.G65fs
XH_P46	9	38414186	38414186	In_Frame_Ins	INS	-	STAAAAATGTTT	-	IGFBPL1	AAAGAAAAACA	delinsLTKRKTFLPLTSV
XH_P46	9	43628048	43628048	In_Frame_Ins	INS	-	ATGTCGTGG	-	SPATA31A6	8_639insCCACG	P213delinsPHDI
XH_P46	9	67968555	67968555	In_Frame_Ins	INS	-	GCC	-	ANKRD20A1	2114_2115insG	Q705delinsQP
XH_P46	9	67968556	67968556	Nonsense_Mutation	INS	-	GTCTAG	-	ANKRD20A1	15_2116insGTC	Q705delinsQVX
XH_P46	9	79968486	79968486	Nonsense_Mutation	INS	-	AATATTTGTAGA	-	VPS13A	TGAATTAATAT	A2488delinsATKX
XH_P46	9	79984315	79984315	Nonsense_Mutation	INS	-	ACTCTTTTTTTT	-	VPS13A	ATCACTACTCTT	2846_E2847delinsX
XH_P46	9	86292842	86292842	Nonsense_Mutation	INS	-	STATCTTTATAAA	-	UBQLN1	ATAGTTTATAAA	p.N302delinsIX
XH_P46	9	86518860	86518860	Nonsense_Mutation	INS	-	AGGAAATGTAAT	-	KIF27	3insTTATTACAT	A192delinsAAYISX

XH_P46	9	86616907	86616907	Nonsense_Mutation	INS	-	GTTAGAATTGT	-	RM1	gTTTTTCGTTAG	B6_Q337delinsCFRX
XH_P46	9	86617643	86617643	Frame_Shift_Ins	INS	-	ACTTCACTGTTC	-	RM1	sCTTTCACCTTCA	p.C581fs
XH_P46	9	88631574	88631574	Frame_Shift_Ins	INS	-	G	-	NAA35	c.1689_1690ins	p.T53fs
XH_P46	9	88631575	88631575	Nonsense_Mutation	INS	-	CATTAGATAAT	-	NAA35	nsTCACTTCACTAA	K564delinsIHX
XH_P46	9	88938026	88938026	Frame_Shift_Ins	INS	-	ACAAGTTGGC	-	ZCHC6	c.2270insGCCAA	p.D757fs
XH_P46	9	90749868	90749868	Frame_Shift_Ins	INS	-	TT	-	SPATA31C2	c.c3_4insAA	p.E2fs
XH_P46	9	90749869	90749869	In_Frame_Ins	INS	-	TTTCTTTTATT	-	SPATA31C2	3insAATAAAAAAG	p.M1delinsIIKK
XH_P46	9	95030563	95030563	Nonsense_Mutation	INS	-	TTATCTCTTCT	-	IARS	nsTTCTAGAAAG	442_K434delinsFX
XH_P46	9	99285637	99285637	Nonsense_Mutation	INS	-	TTTTTATATTTA	-	CDC14B	0insTTATAAATA	347delinsVINIKNX
XH_P46	9	100692724	100692724	Frame_Shift_Ins	INS	-	AA	-	HEMGN	c.952_953insTT	p.S318fs
XH_P46	9	100692726	100692726	Frame_Shift_Ins	INS	-	TACCAAGAAAC	-	HEMGN	95insTGTTTCT	p.E317fs
XH_P46	9	104152876	104152876	Frame_Shift_Ins	INS	-	TGTATCATCTTT	-	MRPL50	sAAAAAAAAGA	p.L117fs
XH_P46	9	107331943	107331943	Frame_Shift_Ins	INS	-	GA	-	OR13C8	c.495_496insGA	p.Q165fs
XH_P46	9	107331944	107331944	Frame_Shift_Ins	INS	-	CATCAGG	-	OR13C8	c.496_497insCATC	p.L166fs
XH_P46	9	107361519	107361519	Frame_Shift_Ins	INS	-	AACAGTGT	-	OR13C5	c.5_176insACACT	p.M59fs
XH_P46	9	107380358	107380358	In_Frame_Ins	INS	-	AAACTA	-	OR13C9	c.27_128insTAGT	p.G43delinsVVC
XH_P46	9	107380360	107380360	Frame_Shift_Ins	INS	-	T	-	OR13C9	c.125dupA	p.N42fs
XH_P46	9	111662604	111662604	In_Frame_Ins	INS	-	TTCTGTTAGCTT	-	ELP1	GAATAAGCTA	delinsPLNKANRKLRS
XH_P46	9	113168587	113168587	In_Frame_Ins	INS	-	TCT	-	SVEP1	c.9292_9293insA	p.G3098delinsES
XH_P46	9	114454772	114454772	Nonsense_Mutation	INS	-	GAATACTCCTTT	-	C9orf84	6insAGAAAAAGG	L059_L106delinsX
XH_P46	9	114841005	114841005	Splice_Site	INS	-	GCTTTTATCATC	-	SUSD1	.	.
XH_P46	9	125377936	125377936	Frame_Shift_Ins	INS	-	CATAGAGGCAAT	-	OR1Q1	2insGCATAGGA	p.S307fs
XH_P46	9	125621373	125621373	Missense_Mutation	SNP	G	C	G	RC3H2	c.C1858G	p.P620A
XH_P46	9	125621374	125621374	Nonsense_Mutation	INS	-	CTCATCTGTC	-	RC3H2	1857insGACAG	p.619_P620delinsX
XH_P46	9	125898771	125898771	Nonsense_Mutation	INS	-	TAATCTATTATA	-	STRBP	9insAATTATAAT	p.L493delinsLIX
XH_P46	9	135202348	135202348	Missense_Mutation	SNP	C	T	C	SETX	c.G4637A	p.G1546D
XH_P46	10	882435	882435	Frame_Shift_Ins	INS	-	TCCT	-	LARP4B	657_658insAGC	p.V220fs
XH_P46	10	882437	882437	Frame_Shift_Ins	INS	-	AATAAGATAGT	-	LARP4B	656insCACTATC	p.L219fs
XH_P46	10	5773155	5773155	Frame_Shift_Ins	INS	-	TCCTTTTCTGTT	-	FAM208B	1194insTCCTTT	p.K398fs
XH_P46	10	5773156	5773156	Missense_Mutation	SNP	A	C	A	FAM208B	c.A1194C	p.K398N
XH_P46	10	5815864	5815864	Nonsense_Mutation	INS	-	AAGTTAGTA	-	GD12	4_625insTACTA	p.P209delinsYX
XH_P46	10	7866474	7866474	Nonsense_Mutation	INS	-	TTTAATAGATT	-	TAf3	61insATTATAA	p.120_K121delinsRIX
XH_P46	10	8007267	8007267	Frame_Shift_Ins	INS	-	CAGTTTTCCTTT	-	TAf3	95insCCCAAGTT	p.V598fs
XH_P46	10	12071297	12071297	Nonsense_Mutation	INS	-	TGAACAGCAATA	-	UPF2	nsATTTTATAGCT	198_S199delinsFX
XH_P46	10	15145523	15145523	Nonsense_Mutation	INS	-	ATCTTGACTGT	-	RPP38	AGAATATCTTG	delinsPLFKESREKCMTX
XH_P46	10	24873666	24873666	In_Frame_Ins	INS	-	CAC	-	ARHGAP21	5551_5552insG	p.D1851delinsGD
XH_P46	10	24873668	24873668	Frame_Shift_Ins	INS	-	TACCAATAAAC	-	ARHGAP21	5550insCGTTTA	p.S1850fs
XH_P46	10	25887273	25887273	In_Frame_Ins	INS	-	AGT	-	GRP158	c.2718_2719insAA	p.I906delinsIS
XH_P46	10	25887275	25887275	In_Frame_Ins	INS	-	TGTGGG	-	GRP158	20_2721insTGT	p.A907delinsAVG
XH_P46	10	27366469	27366469	Frame_Shift_Ins	INS	-	TTGAGATGAT	-	ANKRD26	c.875insATCATC	p.L292fs
XH_P46	10	27366470	27366470	Splice_Site	INS	-	A	-	ANKRD26	.	.
XH_P46	10	31139084	31139084	Frame_Shift_Ins	INS	-	AACCTCCTGTA	-	ZNF438	c.250insTACAGG	p.Q84fs
XH_P46	10	32098204	32098204	Frame_Shift_Ins	INS	-	GAAC	-	ARHGAP12	c.925_926insGT	p.S642fs
XH_P46	10	32098206	32098206	Nonsense_Mutation	INS	-	TTTACATTAAAT	-	ARHGAP12	4insTGATTAAAT	p.642_G643delinsX
XH_P46	10	38345128	38345128	Frame_Shift_Ins	INS	-	TG	-	ZNF33A	c.2094_2095insT	p.P698fs
XH_P46	10	43285933	43285933	Frame_Shift_Ins	INS	-	AG	-	BMS1	c.610_611insAG	p.H204fs
XH_P46	10	43285935	43285935	Frame_Shift_Ins	INS	-	CACCTACACTA	-	BMS1	613insCACCTA	p.H204fs
XH_P46	10	44112619	44112619	Frame_Shift_Ins	INS	-	G	-	ZNF485	c.855_856insG	p.H285fs
XH_P46	10	44112620	44112620	Nonsense_Mutation	INS	-	AAGGATTGAGT	-	ZNF485	sCTTAAAGGAT	p.T286delinsTX
XH_P46	10	61835609	61835609	Nonsense_Mutation	SNP	G	C	G	ANK3	c.C5030G	p.S1677X
XH_P46	10	61835610	61835610	In_Frame_Ins	INS	-	GTCAATGTTTCT	-	ANK3	29insCAGAAAC	p.677delinsQKHMTS
XH_P46	10	64973806	64973806	Frame_Shift_Ins	INS	-	ACTTCCCACCTGT	-	JMJD1C	464insCACAGTC	p.K488fs
XH_P46	10	69804268	69804268	In_Frame_Ins	INS	-	GATTGTCTATT	-	HERC4	TATAAAAAATAG	3delinsEYIKIANQSI
XH_P46	10	71018716	71018716	Splice_Site	INS	-	CTCAGTTTCTTCA	-	HKDC1	.	.
XH_P46	10	75406859	75406859	Missense_Mutation	SNP	G	A	G	SYNP02L	c.C1879T	p.R627W
XH_P46	10	75526118	75526118	Frame_Shift_Ins	INS	-	AACTTATTGTT	-	SEC24C	1619insAACTT	p.A540fs
XH_P46	10	75526120	75526120	Silent	SNP	A	T	A	SEC24C	c.A1620T	p.A540A
XH_P46	10	76744920	76744920	Nonsense_Mutation	INS	-	GCAAGTACAGC	-	KAT6B	908insAGCAAGT	p.636_D637delinsX
XH_P46	10	76744922	76744922	Missense_Mutation	SNP	G	A	G	KAT6B	c.G1909A	p.D637N
XH_P46	10	76788960	76788960	Frame_Shift_Ins	INS	-	TTCTCCTCCTTG	-	KAT6B	CTCAATTCTCTC	p.L1277fs
XH_P46	10	81373728	81373728	Silent	SNP	C	T	C	SFTPA1	c.C606T	p.D202D
XH_P46	10	85997420	85997420	Missense_Mutation	SNP	C	T	C	LRIT1	c.G145A	p.D49N
XH_P46	10	91484915	91484915	In_Frame_Ins	INS	-	AAC	-	KIF20B	2001_2002insA	p.F667delinsEN
XH_P46	10	91484916	91484916	Splice_Site	INS	-	AAC	-	KIF20B	.	.
XH_P46	10	96448005	96448005	In_Frame_Ins	INS	-	AGTACATACACA	-	CYP2C18	456insAGTACAT	p.L152delinsLVHHT
XH_P46	10	96740981	96740981	Frame_Shift_Ins	INS	-	AAAAATCTGTAG	-	CYP2C9	ATTAAGAAAAAT	p.R335fs
XH_P46	10	98741906	98741906	Silent	SNP	C	T	C	LCOR	c.C1689T	p.D53D
XH_P46	10	98741908	98741908	Nonsense_Mutation	INS	-	ATTGATTTTTGA	-	LCOR	592insTATTGAT	p.N564delinsNIDFX
XH_P46	10	98742739	98742739	Missense_Mutation	SNP	C	T	C	LCOR	c.C2522T	p.A841V
XH_P46	10	98742741	98742741	In_Frame_Ins	INS	-	CACTGG	-	LCOR	24_2525insCAC	p.C842delinsSLG
XH_P46	10	99023362	99023362	Nonsense_Mutation	INS	-	TCCTAGTTAAGT	-	ARHGAP19	AATTAACCTTAA	p.143_V144delinsNX
XH_P46	10	101563802	101563802	Silent	SNP	G	A	G	ABCC2	c.G1236A	p.A412R
XH_P46	10	101563804	101563804	Frame_Shift_Ins	INS	-	TCCTATTATACC	-	ABCC2	39insACTCTCAT	p.K413fs
XH_P46	10	102300472	102300472	Frame_Shift_Ins	INS	-	TTACTTATCCTT	-	HIF1AN	11insCTTACTTA	p.L170fs
XH_P46	10	102300474	102300474	Missense_Mutation	SNP	A	T	A	HIF1AN	c.A512T	p.N171I
XH_P46	10	102684107	102684107	Nonsense_Mutation	INS	-	AAATTTTCTCTT	-	SLF2	TTTTATAAATTT	p.50delinsICFINFSFX
XH_P46	10	105108703	105108703	Frame_Shift_Ins	INS	-	C	-	PCGF6	c.413_414insG	p.K138fs
XH_P46	10	105108705	105108705	Frame_Shift_Ins	INS	-	AAGGTAAGAAGA	-	PCGF6	TATATCTTCTTT	p.K138fs
XH_P46	10	121602852	121602853	Frame_Shift_Del	DEL	GG	-	GG	MCMBP	c.913_914del	p.P305fs
XH_P46	10	121602853	121602853	Frame_Shift_Ins	INS	-	ACATTAATTCTC	-	MCMBP	8insAAGAGAAAT	p.P305fs
XH_P46	10	129901930	129901930	In_Frame_Ins	INS	-	AGAAAGTAGAA	-	MKI67	7094insCTTCTA	p.2365delinsTSTFW
XH_P46	10	129906052	129906069	In_Frame_Del	DEL	AAAGCCAGT	-	TTAAAGCCAGTC	MKI67	c.2955_2972del	p.985_991del
XH_P46	10	129907216	129907216	Missense_Mutation	SNP	T	G	T	MKI67	c.A1808C	p.D603A
XH_P46	10	129907217	129907217	Missense_Mutation	SNP	C	G	C	MKI67	c.G1807C	p.D603H
XH_P46	10	129907679	129907679	Missense_Mutation	SNP	C	A	C	MKI67	c.G1345T	p.V449L
XH_P46	10	129907681	129907681	Frame_Shift_Ins	INS	-	ACAGAAATGT	-	MKI67	c.1343insCAATT	p.N448fs
XH_P46	11	1258193	1258194	Frame_Shift_Del	DEL	TG	-	TG	MUC5B	c.3096_3097del	p.N1032fs
XH_P46	11	3380588	3380588	Frame_Shift_Ins	INS	-	AAAAAATAAAC	-	TRIM195	34insTTTGTTTA	p.Y478fs
XH_P46	11	3781847	3781847	Nonsense_Mutation	INS	-	CATTTACTTTGG	-	NUP98	9insAATCAAAG	p.G366delinsNPXK
XH_P46	11	4936668	4936668	In_Frame_Ins	INS	-	TTCTACATCTCT	-	OR51G2	nsAATAAGAAATG	76delinsNKNVREL
XH_P46	11	4967552	4967552	In_Frame_Ins	INS	-	AAGATTAA	-	OR51A4	c.8_779insTAA	p.A260delinsVKSS
XH_P46	11	4976543	4976543	Frame_Shift_Ins	INS	-	CTTACACCTGT	-	OR51A2	401insCAGGGT	p.Y134fs
XH_P46	11	5662458	5662458	Nonstop_Mutation	INS	-	TGAAATGTCT	-	TRIM34	c.813insTGAAAT	p.X271delinsYENV
XH_P46	11	6977057	6977057	Frame_Shift_Ins	INS	-	AAGGAGGGTTAC	-	ZNF215	sGTTAAAGGAG	p.N283fs
XH_P46	11	6977366	6977366	Frame_Shift_Ins	INS	-	TGTCCCATTTT	-	ZNF215	insTTATGTCC	p.K386fs
XH_P46	11	7335021	7335021	Frame_Shift_Ins	INS	-	TATATACTGTG	-	SYT9	CTGCTTATATAA	p.L298fs
XH_P46	11	7817711	7817711	Nonsense_Mutation	INS	-	TTTTC	-	OR5P2	c.778_779insGAA	p.T260delinsX
XH_P46	11	7817713	7817713	Nonsense_Mutation	INS	-	AACTTAATAAGC	-	OR5P2	AGATATGCTTAT	p.F260delinsKYASMLIKFX

XH_P46	11	8662056	8662056	Frame_Shift_Ins	INS	-	GTGCATA	-	TRIM66	30_1431insTATG	p.Q477fs
XH_P46	11	10582213	10582213	In_Frame_Ins	INS	-	SATAATTCATAG	-	LYVE1	sGGATTCTATGA	78delinsGFYELSVI
XH_P46	11	10781843	10781843	In_Frame_Ins	INS	-	TACATCATACCA	-	CTR9	717insTACATCA	A239delinsATSYH
XH_P46	11	10781845	10781845	Missense_Mutation	SNP	G	A	G	CTR9	c.G718A	p.V240I
XH_P46	11	10785372	10785372	Frame_Shift_Ins	INS	-	TATGTACAAAA	-	CTR9	GACCAATATGT	p.I380fs
XH_P46	11	10875995	10875995	Frame_Shift_Ins	INS	-	GCTTGTTTGTAG	-	ZBED5	98insTCTACAAA	p.S166fs
XH_P46	11	18428876	18428876	Frame_Shift_Ins	INS	-	CTTACAGTCTCT	-	LDHA	AAGACTTACAG	p.L260fs
XH_P46	11	19905858	19905858	Nonsense_Mutation	INS	-	GATTGATTGTAT	-	NAV2	nsGTTTCTGAT	63_S264delinsVYX
XH_P46	11	22279301	22279301	Splice_Site	INS	-	ATGGTTCCTCT	-	ANOS	.	.
XH_P46	11	26587082	26587082	Frame_Shift_Ins	INS	-	ACCACAACA	-	MUC15	324insTGTTTG	p.T108fs
XH_P46	11	27390626	27390626	Frame_Shift_Ins	INS	-	CTTATCTGCAAA	-	LGR4	insATCTTTGCA	p.I524fs
XH_P46	11	30517069	30517069	Splice_Site	INS	-	ACAT	-	MPPED2	.	.
XH_P46	11	32953756	32953756	Nonsense_Mutation	INS	-	AAAGTTGAATCC	-	QSER1	566insAAAGTTG	p.I189delinsKSX
XH_P46	11	33054852	33054852	Nonsense_Mutation	INS	-	GTGATTGGATAT	-	DEPDC7	CAAATGTGATT	delinsNTVSNLEPLHLMX
XH_P46	11	33308137	33308137	In_Frame_Ins	INS	-	CAAAATCAC	-	HIPK3	7_178insCAAA	T.G59delinsGQIH
XH_P46	11	33308139	33308139	Missense_Mutation	SNP	G	A	G	HIPK3	c.G179A	p.S60N
XH_P46	11	34680473	34680473	Frame_Shift_Ins	INS	-	CTCCTCACCTCAT	-	EHF	830insCTCCTCA	p.N277fs
XH_P46	11	43457871	43457871	Frame_Shift_Ins	INS	-	GGTTTT	-	TTC17	09_2410insGGT	p.A803fs
XH_P46	11	46465146	46465146	In_Frame_Ins	INS	-	AGTTCTGGCTCA	-	AMBRA1	5CTGGTGAGCC	delinsLYLLVSQNSKIHGA
XH_P46	11	46782280	46782280	Frame_Shift_Ins	INS	-	GTAAATGTATTG	-	CKAP5	76insTTACAATA	p.R1426fs
XH_P46	11	46782281	46782281	In_Frame_Ins	INS	-	CAAAATG	-	CKAP5	74_4275insCAT	K1425delinsNIW
XH_P46	11	51412207	51412207	Nonsense_Mutation	INS	-	TTTGCTTCCTT	-	OR4A5	189insAAGGAA	C63_L64delinsX
XH_P46	11	51412209	51412209	Missense_Mutation	SNP	A	T	A	OR4A5	c.T187A	p.C63S
XH_P46	11	55860958	55860958	Frame_Shift_Ins	INS	-	TAATCAAATT	-	OR8I2	176insTAATCA	p.M59fs
XH_P46	11	55860960	55860960	In_Frame_Ins	INS	-	ACT	-	OR8I2	c.177_178insAC	p.M59delinsMT
XH_P46	11	55927269	55927269	Missense_Mutation	SNP	A	C	A	OR8K5	c.T525G	p.S175R
XH_P46	11	55927270	55927270	Frame_Shift_Ins	INS	-	TCTATAAGCTCT	-	OR8K5	24insAAGAGCTT	p.S175fs
XH_P46	11	55999912	55999912	Nonsense_Mutation	INS	-	TATCAATAAAG	-	OR5T2	750insACTTTAT	150_L251delinsILYX
XH_P46	11	56344676	56344676	Frame_Shift_Ins	INS	-	C	-	OR5M10	c.521_522insG	p.I174fs
XH_P46	11	56344677	56344677	Frame_Shift_Ins	INS	-	GTCTTTTATAC	-	OR5M10	521insGTATAA	p.I174fs
XH_P46	11	57148139	57148139	In_Frame_Ins	INS	-	GAACCTTCTCT	-	PRG3	5AAAAAGAGAA	15delinsKRRKFQV
XH_P46	11	57254662	57254662	Missense_Mutation	SNP	G	A	G	SLC43A1	c.C1439T	p.T480I
XH_P46	11	58125925	58125925	Nonsense_Mutation	INS	-	GATTCAAGTCTT	-	OR5B17	CATTAAAGACT	F206delinsLHHX
XH_P46	11	58207309	58207309	Frame_Shift_Ins	INS	-	TCCTCTCTTGAC	-	OR5B12	AGAGAGTCAAG	p.I106fs
XH_P46	11	58920491	58920491	Frame_Shift_Ins	INS	-	CTTTAAAAACAA	-	FAM111A	51insTCCTTTAA	p.Q450fs
XH_P46	11	60511243	60511243	In_Frame_Ins	INS	-	AATTTTTTCTTC	-	M54A18	insATAATTTTT	287delinsHNFFLP
XH_P46	11	60609700	60609700	Frame_Shift_Del	DEL	T	-	T	CCDC86	c.103delT	p.F35fs
XH_P46	11	62289899	62289899	Silent	SNP	G	A	G	AHNAK	c.C12900T	p.I4300I
XH_P46	11	62289934	62289934	Nonsense_Mutation	INS	-	AAATGGATGTT	-	AHNAK	1955insTTAACA	K3985delinsNX
XH_P46	11	62292999	62292999	Missense_Mutation	SNP	G	A	G	AHNAK	c.C8890T	p.P2964S
XH_P46	11	62546426	62546426	In_Frame_Ins	INS	-	GAAGCCTTT	-	TAF6L	2_523insGAAGCC	Q174delinsQEAF
XH_P46	11	63486801	63486801	In_Frame_Ins	INS	-	CCCTGAGGCTTT	-	RTN3	492insCCCTGAG	S164delinsSPEAF
XH_P46	11	65350451	65350451	Frame_Shift_Ins	INS	-	CCTCAGTCTCTG	-	EHBP1L1	09insTACCTCAG	p.E770fs
XH_P46	11	66444183	66444183	Frame_Shift_Ins	INS	-	AGAATCACAAA	-	RBM4B	368insTTTGTG	p.D123fs
XH_P46	11	66999319	66999319	Frame_Shift_Ins	INS	-	AACTCCAATC	-	KDM2A	1368insAACTC	p.F456fs
XH_P46	11	67926176	67926176	Frame_Shift_Ins	INS	-	ATGGGTGCCCA	-	KMT5B	917insTGGGGA	p.T306fs
XH_P46	11	71942604	71942606	In_Frame_Del	DEL	CCG	-	CCG	INPPL1	c.1560_1562del	p.S20_S21del
XH_P46	11	73811719	73811719	In_Frame_Ins	INS	-	CCTTGAAGG	-	C2CD3	2_2583insCCTTC	V861delinsVLQG
XH_P46	11	73811721	73811721	Frame_Shift_Ins	INS	-	TTTT	-	C2CD3	580_2581insAA	p.V861fs
XH_P46	11	73814541	73814541	Frame_Shift_Ins	INS	-	CA	-	C2CD3	2214_2215insT	p.D739fs
XH_P46	11	73814542	73814542	Frame_Shift_Ins	INS	-	SAGGAATATAGG	-	C2CD3	14insCCCTCTATA	p.Q738fs
XH_P46	11	76956536	76956536	Frame_Shift_Ins	INS	-	CTATCTCAGTAT	-	GDPD4	insAAATCTGA	p.F292fs
XH_P46	11	85346821	85346821	Nonsense_Mutation	INS	-	CAACTAAACCAT	-	TMEM126B	371insCAACTAA	K124delinsTTKPY
XH_P46	11	96117607	96117607	In_Frame_Ins	INS	-	TTGAAGATGAA	-	CCDC82	05insCCTTCTATC	N102delinsTTFINH
XH_P46	11	96124000	96124000	Frame_Shift_Ins	INS	-	AATCCTTCCTT	-	JRKL	188insAATCCT	p.S63fs
XH_P46	11	96124001	96124001	Missense_Mutation	SNP	G	C	G	JRKL	c.G188C	p.S63T
XH_P46	11	96125208	96125208	Frame_Shift_Ins	INS	-	AATCTTCTTCCA	-	JRKL	1396insAATCTT	p.E465fs
XH_P46	11	105880453	105880453	Nonsense_Mutation	SNP	C	A	C	MSANTD4	c.G847T	p.G283X
XH_P46	11	105880454	105880454	Nonsense_Mutation	INS	-	TCAGGTGATATA	-	MSANTD4	46insTTATATCAB2	G283delinsHYITX
XH_P46	11	108151881	108151881	Nonsense_Mutation	INS	-	TACTCACTAATC	-	ATM	563insCTACTCAH	I188delinsPTHX
XH_P46	11	108173746	108173746	Missense_Mutation	SNP	C	T	C	ATM	c.C5486T	p.P1829L
XH_P46	11	108173748	108173748	Frame_Shift_Ins	INS	-	AGTTAAACTA	-	ATM	insATACAGTTA	p.M1830fs
XH_P46	11	108593990	108593990	In_Frame_Ins	INS	-	GTTTATAGGTGT	-	DDX10	7insTATGTTTAT	589delinsDMFIGVI
XH_P46	11	110451788	110451788	In_Frame_Ins	INS	-	GAGTTTTAT	-	ARHGAP20	2_1813insATAAA	P605delinsIKLP
XH_P46	11	110451790	110451790	Missense_Mutation	SNP	T	A	T	ARHGAP20	c.A1811T	p.Q604L
XH_P46	11	111953628	111953628	Frame_Shift_Ins	INS	-	TCTGCTGTTATA	-	C11orf57	15insATCTGCTG	p.T272fs
XH_P46	11	114278281	114278281	Missense_Mutation	SNP	T	A	T	RBM7	c.T193A	p.S65T
XH_P46	11	114392822	114392822	In_Frame_Ins	INS	-	TTAAAGAATCT	-	NPXPE1	6insAACAGATTG	362delinsETDSFKF
XH_P46	11	117115272	117115272	Frame_Shift_Ins	INS	-	GATGAGATTGG	-	RNF214	5ATATGATGAG	p.R264fs
XH_P46	11	118239494	118239494	Missense_Mutation	SNP	G	C	G	UBE4A	c.G270C	p.R90S
XH_P46	11	118239495	118239495	Frame_Shift_Ins	INS	-	AAAGTTTATT	-	UBE4A	272insAAAGTT	p.I91fs
XH_P46	11	118344722	118344722	In_Frame_Ins	INS	-	CGCTATTCTCCT	-	KMT2A	849insCCGCTTA	950delinsPAYSPF
XH_P46	11	120198298	120198298	Nonsense_Mutation	INS	-	AATCTTCTATT	-	TMEM136	insAAGAATCTTC	L72delinsQESSIX
XH_P46	11	123778030	123778030	Frame_Shift_Ins	INS	-	ATGTTAGGCTTG	-	OR8D4	insTGATTGTTAC	p.R298fs
XH_P46	11	123909236	123909236	Nonsense_Mutation	INS	-	TTCATTTACCTG	-	OR10G7	73insTCAGGTAAT	158_T159delinsLRX
XH_P46	11	125547860	125547860	Missense_Mutation	SNP	G	T	G	ACRV1	c.C385A	p.P129T
XH_P46	11	125547862	125547864	In_Frame_Del	DEL	TGT	-	TGT	ACRV1	c.381_383del	p.127_128del
XH_P46	12	1291182	1291182	Frame_Shift_Ins	INS	-	AT	-	ERC1	1967_1968insA	p.D656fs
XH_P46	12	1291183	1291183	Frame_Shift_Ins	INS	-	CACTTTTTTTTT	-	ERC1	1969insCACTTTT	p.D656fs
XH_P46	12	10762532	10762532	Nonsense_Mutation	INS	-	ACCTCCTAGTAG	-	MAGOH8	insCACTACTAGG	V8delinsVTTTRX
XH_P46	12	10954751	10954751	In_Frame_Ins	INS	-	ATTAGCTGTGAT	-	TAS2R7	6CAAAATCACAA	40delinsPKITANSV
XH_P46	12	10958840	10958840	Nonsense_Mutation	INS	-	TTAATAGTCTAT	-	TAS2R8	5GAGAAATAGAC	247_Y248delinsX
XH_P46	12	10961948	10961948	Missense_Mutation	SNP	C	T	C	TAS2R9	c.G727A	p.V243M
XH_P46	12	11506837	11506837	Missense_Mutation	SNP	T	C	T	PRB1	c.A200G	p.K67R
XH_P46	12	12284807	12284807	Frame_Shift_Ins	INS	-	AAGATTTATA	-	LRP6	7_3918insTATAA	p.R1306fs
XH_P46	12	16425693	16425693	Frame_Shift_Ins	INS	-	AGGCTTATGA	-	SLC15A5	386insTCATAA	p.A129fs
XH_P46	12	18891225	18891225	Frame_Shift_Ins	INS	-	TCTTCTCT	-	CAP2A3	23_24insTCTTCT	p.R8fs
XH_P46	12	21926390	21926390	Missense_Mutation	SNP	C	T	C	KCNJ8	c.G161A	p.G54E
XH_P46	12	25656721	25656721	In_Frame_Ins	INS	-	ATG	-	LMNTD1	c.950_951insCA	K317delinsNM
XH_P46	12	25656723	25656723	Frame_Shift_Ins	INS	-	GAATGATAAGC	-	LMNTD1	949insGCTTAT	p.K317fs
XH_P46	12	26639241	26639241	In_Frame_Ins	INS	-	SAGAATACAACC	-	ITPR2	5607insGGTTG	E1869delinsEVVFS
XH_P46	12	26639243	26639243	Nonsense_Mutation	SNP	C	A	C	ITPR2	c.G5605T	p.E1869X
XH_P46	12	27081724	27081724	Frame_Shift_Ins	INS	-	AATTTAACATTTT	-	INTS13	15insAAAAATGT	p.Y139fs
XH_P46	12	30869570	30869570	Frame_Shift_Ins	INS	-	ACATGTTCTCCC	-	CAPRIN2	231insTGAGGGA	p.Q744fs
XH_P46	12	32138030	32138030	Nonsense_Mutation	INS	-	TTTAGTTTATC	-	KIAA1551	4142insTTAG	381_V1382delinsIX
XH_P46	12	39734119	39734119	Frame_Shift_Ins	INS	-	AATAA	-	KIF21A	118_2119insTTA	p.E707fs
XH_P46	12	39734121	39734121	In_Frame_Ins	INS	-	GTA	-	KIF21A	2116_2117insT	p.S706delinsLP
XH_P46	12	40012657	40012657	Missense_Mutation	SNP	A	C	A	ABCD2	c.T761G	p.I254S

XH_P46	12	40012659	40012659	Frame_Shift_Ins	INS	-	CTTAGTGTCTTA	-	ABCD2	59insTAAGACA	p.P253fs
XH_P46	12	40076630	40076630	Missense_Mutation	SNP	C	A	C	C12orf40	c.C904A	p.Q302K
XH_P46	12	40076632	40076632	Frame_Shift_Ins	INS	-	TCCTATTTCCTA	-	C12orf40	07insTCCTATT	p.Q302fs
XH_P46	12	44149036	44149036	In_Frame_Ins	INS	-	AGAAGATGGAA	-	PUS7L	tsTTCTTCATCT	T5delinsFFHLRLT
XH_P46	12	46318839	46318839	Nonsense_Mutation	INS	-	CTCAAGTTTAAT	-	SCAF11	ATATTGATTAA	193_T1194delinsLYX
XH_P46	12	46320437	46320437	Frame_Shift_Ins	INS	-	5AAAAAGTGAA	-	SCAF11	insTCCTGTTTCA	p.H1016fs
XH_P46	12	48064102	48064102	Frame_Shift_Ins	INS	-	TTTTTTGTTTGT	-	RPAP3	TAAGTACAAC	p.E404fs
XH_P46	12	49087739	49087739	Frame_Shift_Ins	INS	-	AAAG	-	CCNT1	1257_1258insCT	p.Y420fs
XH_P46	12	49087741	49087741	Missense_Mutation	SNP	G	C	G	CCNT1	c.C1256G	p.A419G
XH_P46	12	49088200	49088200	Frame_Shift_Ins	INS	-	CAGAAGCAGAA	-	CCNT1	7insCTATTCTGC	p.K266fs
XH_P46	12	50529623	50529623	Splice_Site	INS	-	CAGACC	-	CERS5		
XH_P46	12	53162773	53162775	In_Frame_Del	DEL	ACT	-	ACT	KRT76	c.1639_1641del	p.547_547del
XH_P46	12	54687073	54687073	Nonsense_Mutation	INS	-	ATCCCTCAACTA	-	NFE2	207insTAGTTGA	p.S69delinsSSX
XH_P46	12	54687074	54687074	Nonsense_Mutation	SNP	G	T	G	NFE2	c.C206A	p.S69X
XH_P46	12	55524109	55524109	Nonsense_Mutation	INS	-	AAGTTGAT	-	OR9K2	7_558insAAGTT	86_M187delinsRSX
XH_P46	12	55524110	55524110	Frame_Shift_Ins	INS	-	CTTGGGTTCAAT	-	OR9K2	ATAGCCTTGGG	p.S186fs
XH_P46	12	55725588	55725588	Frame_Shift_Ins	INS	-	ATAAAAGATAT	-	OR6C3	AATAGATAAAAC	p.S35fs
XH_P46	12	55863601	55863601	Missense_Mutation	SNP	T	A	T	OR6C70	c.A322T	p.T108S
XH_P46	12	55863603	55863603	In_Frame_Ins	INS	-	CCCTTCAGCTCA	-	OR6C70	DinsCTGAGCTGA	107delinsAELKGI
XH_P46	12	57925857	57925971	In_Frame_Del	DEL	TTGAGACTTG	-	GTTGAGACTTGA	DCTN2	c.1034_1066del	p.345_356del
XH_P46	12	59268083	59268083	In_Frame_Ins	INS	-	TCCAAGTTGTG	-	LRIG3	89insCACACAA	897delinsHTTWSM
XH_P46	12	65226073	65226073	Missense_Mutation	SNP	G	A	G	TBC1D30	c.G583A	p.D195N
XH_P46	12	65226074	65226074	In_Frame_Ins	INS	-	ACAATATTT	-	TBC1D30	4_585insACAAT	D195delinsEQVF
XH_P46	12	72366496	72366496	Splice_Site	INS	-	CATTAAGTATTA	-	TPH2		
XH_P46	12	76424934	76424934	Frame_Shift_Del	DEL	C	-	C	PHLDA1	c.588delG	p.Q196fs
XH_P46	12	76424936	76424940	Frame_Shift_Del	DEL	GTTGC	-	GTTGC	PHLDA1	c.582_586del	p.Q194fs
XH_P46	12	85450168	85450168	Frame_Shift_Ins	INS	-	ATCTACATTTC	-	LRRIQ1	8insTCTATCTAC	p.D533fs
XH_P46	12	86198817	86198817	Frame_Shift_Ins	INS	-	AATGTTTGTTTA	-	RASSF9	971insTTAAACA	p.K324fs
XH_P46	12	88487715	88487715	Frame_Shift_Ins	INS	-	TATTATAAGTTT	-	CEP290	insGATAAAACT	p.I1047fs
XH_P46	12	91365772	91365772	Frame_Shift_Ins	INS	-	ATTCGTGTAGG	-	EPYC	607insCCCTACA	p.I169fs
XH_P46	12	91365774	91365774	In_Frame_Ins	INS	-	AATAAATTT	-	EPYC	4_505insAAATTT	L169delinsKFL
XH_P46	12	94796978	94796978	In_Frame_Ins	INS	-	CCT	-	CEP83	384_385insAG	p.P129delinsRP
XH_P46	12	94796979	94796979	Frame_Shift_Ins	INS	-	CTGAT	-	CEP83	383_384insATC	p.T128fs
XH_P46	12	100452367	100452367	Frame_Shift_Ins	INS	-	GAAGATGAAG	-	UHRF1BP1L	88insCTACTTTC	p.D896fs
XH_P46	12	102041901	102041901	Frame_Shift_Ins	INS	-	TTTTTGTCTTGT	-	MYBP1C	stTTTTGTTTTGT	p.V339fs
XH_P46	12	102155457	102155457	In_Frame_Ins	INS	-	AAGAAAAAAGT	-	GNPTAB	300insGGACTTT	5934delinsGLF5FS
XH_P46	12	104373714	104373714	In_Frame_Ins	INS	-	CCCTTCTTCTCT	-	TDG	8insTTCCTTCTCT	S91delinsSSLSFL
XH_P46	12	104373716	104373716	Missense_Mutation	SNP	A	G	A	TDG	c.A274G	p.K92E
XH_P46	12	104379506	104379506	In_Frame_Ins	INS	-	AGCGTGGAGTT	-	TDG	stTGAGAGCGTG	64delinsLEVSLRV
XH_P46	12	104383285	104383285	Frame_Shift_Ins	INS	-	GAA	-	GLT8D2	c.950_951insTC	p.R317fs
XH_P46	12	104383287	104383287	Frame_Shift_Ins	INS	-	GAAAAACA	-	GLT8D2	8_949insTGTIT	p.R317fs
XH_P46	12	108134857	108134857	In_Frame_Ins	INS	-	TAGAGGGATTG	-	PRDM4	790insTACAATC	0597delinsQLSLYK
XH_P46	12	108147867	108147867	Nonsense_Mutation	INS	-	AACITTTATCCTG	-	PRDM4	insTTCAGGATA	55_N56delinsPSGX
XH_P46	12	108911005	108911005	Missense_Mutation	SNP	T	C	T	FICD	c.T256C	p.S86P
XH_P46	12	109894070	109894070	Silent	SNP	C	T	C	KCTD10	c.G579A	p.L193L
XH_P46	12	111748092	111748092	Silent	SNP	C	T	C	CUX2	c.C1506T	p.G502G
XH_P46	12	112846370	112846370	Frame_Shift_Ins	INS	-	AGAAAAAGAAG	-	RPL6	tsTCTCCTCTT	p.N31fs
XH_P46	12	113645308	113645308	In_Frame_Ins	INS	-	GGGTTTTTCTCT	-	IQCD	64insGAGGAA	N222delinsEEKPN
XH_P46	12	113645309	113645309	Frame_Shift_Ins	INS	-	GATTGATTTTT	-	IQCD	3insAAAAAAA	p.N221fs
XH_P46	12	120760118	120760118	Nonsense_Mutation	INS	-	TTATTTTTTCTAC	-	PLA2G1B	CCACCTAGAAAA	K109delinsSTX
XH_P46	12	120760120	120760120	Missense_Mutation	SNP	C	T	C	PLA2G1B	c.G323A	p.S108N
XH_P46	12	121154755	121154755	Frame_Shift_Ins	INS	-	CTCTCTCTGTGA	-	UNC119B	insCACTCTTCTC	p.N185fs
XH_P46	12	123087627	123087627	Frame_Shift_Ins	INS	-	TTTGG	-	KNTC1	938_4939insTT	p.K1646fs
XH_P46	12	123087629	123087629	Frame_Shift_Ins	INS	-	ATCCA	-	KNTC1	940_4941insAT	p.L1647fs
XH_P46	12	124144425	124144425	Frame_Shift_Ins	INS	-	CATTCTCT	-	GTTF2H3	89_640insCATTC	p.F213fs
XH_P46	12	124158327	124158327	Missense_Mutation	SNP	G	A	G	TCTN2	c.G430A	p.A144T
XH_P46	12	124158328	124158328	Frame_Shift_Ins	INS	-	AGAGATGACA	-	TCTN2	432insAGAGAT	p.A144fs
XH_P46	13	32826083	32826083	Frame_Shift_Ins	INS	-	AG	-	FRY	7239_7240insA	p.N2413fs
XH_P46	13	32826084	32826084	Nonsense_Mutation	INS	-	AATTGTAAATA	-	FRY	ATTAAAAATTGT	S2415delinsQLKIVKYX
XH_P46	13	37580133	37580133	Frame_Shift_Ins	INS	-	GAGATTAC	-	EXOSC8	5_316insGAGA	p.A105fs
XH_P46	13	42793925	42793925	Frame_Shift_Ins	INS	-	GTACTACTAAAA	-	DGKH	03insATGTACTA	p.Q901fs
XH_P46	13	42877145	42877145	Nonsense_Mutation	INS	-	CAACTGTTCTTC	-	AKAP11	4insTAACAACCTG	421_D1422delinsAX
XH_P46	13	45768204	45768204	Nonsense_Mutation	INS	-	CAAGTAATTACC	-	KCTD4	9insCAGGTAATT	67_1168delinsQVITX
XH_P46	13	46946422	46946422	In_Frame_Ins	INS	-	CTTGTT	-	RUBCNL	88_189insAACAP	p.P63delinsPTR
XH_P46	13	46946424	46946424	Missense_Mutation	SNP	G	T	G	RUBCNL	c.C187A	p.P63T
XH_P46	13	47409272	47409272	Nonsense_Mutation	INS	-	TGGTTGCTCTAG	-	HTR2A	864insCTAGAGC	p.S288delinsSX
XH_P46	13	51943130	51943130	Frame_Shift_Ins	INS	-	AACACCAATA	-	INTS6	2421insTATTT	p.E807fs
XH_P46	13	51952475	51952475	Frame_Shift_Ins	INS	-	GAGT	-	INTS6	501_1502insAC	p.F501fs
XH_P46	13	52604504	52604504	Frame_Shift_Ins	INS	-	TTCAATTTCCTGA	-	UTP14C	565insCTTCAAT	p.Q522fs
XH_P46	13	60545279	60545279	Frame_Shift_Ins	INS	-	ATGAGAAGAT	-	DIAPH3	5_877insATCTTC	p.A293fs
XH_P46	13	73348174	73348174	Frame_Shift_Ins	INS	-	AGGACGGAGAA	-	DIS3	2insTAATTCTCC	p.K214fs
XH_P46	13	74420229	74420229	Frame_Shift_Ins	INS	-	TTTGGAGGATG	-	KLF12	405insCATCTCT	p.S135fs
XH_P46	13	75884169	75884169	In_Frame_Ins	INS	-	TTTGTGAGGTGG	-	TBC1D4	3insTAACACCT	71delinsNNHLTKW
XH_P46	13	76379844	76379844	Frame_Shift_Ins	INS	-	CAACCGGTTAAG	-	LMO7	ACATCCAACCGG	p.R149fs
XH_P46	13	77641998	77641998	Frame_Shift_Ins	INS	-	GTTATTG	-	MYCBP2	72_12173insCA	p.V4058fs
XH_P46	13	77641999	77641999	Frame_Shift_Ins	INS	-	CT	-	MYCBP2	2171_12172ins	p.V4058fs
XH_P46	13	77670533	77670533	Frame_Shift_Ins	INS	-	TATTGTGTTGTG	-	MYCBP2	AGAGTTACACA	p.G3290fs
XH_P46	13	77779671	77779671	Missense_Mutation	SNP	C	G	C	MYCBP2	c.G3652C	p.E1218Q
XH_P46	13	77779672	77779672	Frame_Shift_Ins	INS	-	AGGTAGAGGAG	-	MYCBP2	1insTATTCTCTCT	p.E1217fs
XH_P46	13	79940854	79940854	Frame_Shift_Ins	INS	-	GTAGATATTATA	-	RBM26	insAAACTATAA	p.P350fs
XH_P46	13	103389260	103389260	Frame_Shift_Ins	INS	-	TAGTTGTACTTC	-	CCDC168	3787insAGAAGT	p.L4596fs
XH_P46	13	103389262	103389262	Frame_Shift_Ins	INS	-	GC	-	CCDC168	3784_13785ins	p.F4595fs
XH_P46	13	103395331	103395331	In_Frame_Ins	INS	-	CTAAGATAC	-	CCDC168	5_7716insGTAT	12572delinsMYLR
XH_P46	13	103398339	103398339	Frame_Shift_Ins	INS	-	AAAAGGACACAG	-	CCDC168	4708insCTGTT	p.D1570fs
XH_P46	13	112722813	112722881	In_Frame_Del	DEL	GCGCACCAAG	-	GCGCGACCAAG	SOX1	c.841_909del	p.281_303del
XH_P46	14	20502563	20502563	Nonsense_Mutation	INS	-	CTATGAGAGTCA	-	OR4K13	TATTATGACTCC	9_1120delinsNIMTPX
XH_P46	14	20612027	20612027	Frame_Shift_Ins	INS	-	ATAAAATACGTT	-	OR4N5	TAATAATAAAAT	p.I45fs
XH_P46	14	21897289	21897289	Frame_Shift_Ins	INS	-	TCTCTGAACCTG	-	CHD8	9insCCTCAGTT	p.K350fs
XH_P46	14	23456809	23456809	Frame_Shift_Ins	INS	-	AAGAGGAAGAT	-	C14orf93	1232insCATCTT	p.F411fs
XH_P46	14	23548835	23548835	Nonsense_Mutation	INS	-	CTCCACTAGAT	-	ACIN1	1763insTCTAGT	588_M589delinsIX
XH_P46	14	23745214	23745214	In_Frame_Ins	INS	-	ACCCAGCAG	-	HOMEZ	2_1223insCTGC	R408delinsPAGC
XH_P46	14	24590623	24590623	In_Frame_Ins	INS	-	ACACTCACATAC	-	DFAC11	ATCATTCACACT	32delinsRIUILLTYFI
XH_P46	14	31785056	31785056	Nonsense_Mutation	INS	-	AGAGACTCTCCG	-	HEATR5A	TAGACTACGGAA	G1380delinsHXK
XH_P46	14	34985654	34985654	In_Frame_Ins	INS	-	TTTTTTTTTCTTT	-	EAPP	tsTCAAGAAAAA	240delinsDQRKKKG
XH_P46	14	39649959	39649959	Frame_Shift_Ins	INS	-	GTCTACCTTCA	-	PNN	1047insGTCTA	p.A349fs
XH_P46	14	39716999	39716999	Frame_Shift_Ins	INS	-	TT	-	MIAT2	1221_1222insT	p.G407fs
XH_P46	14	39717000	39717000	Frame_Shift_Ins	INS	-	CTTTCTT	-	MIAT2	22_1223insCTT	p.A408fs
XH_P46	14	45542655	45542655	Frame_Shift_Ins	INS	-	AAAATATACTAA	-	TOGARAM1	2055insAAAAATA	p.I1685fs

XH_P46	14	45644941	45644941	Frame_Shift_Ins	INS	-	A	-	FANCM	c.2906_2907ins	p.S969fs
XH_P46	14	45644943	45644943	In_Frame_Ins	INS	-	GTAGGCTCTTCT	-	FANCM	970delinsLVGLD	
XH_P46	14	45693308	45693308	Frame_Shift_Ins	INS	-	TAGCAATAAGGG	-	MIS18BP1	482insCCCCCTTA	p.F828fs
XH_P46	14	45693310	45693310	Frame_Shift_Ins	INS	-	AA	-	MIS18BP1	.2479_2480insT	p.E827fs
XH_P46	14	51224473	51224473	In_Frame_Ins	INS	-	CAGAGACAGGA	-	NIN	3275insTTCCTG	1092delinsLPVSE
XH_P46	14	52734696	52734696	Missense_Mutation	SNP	G	T	G	PTGDR	c.G164T	p.R55L
XH_P46	14	53175199	53175199	Splice_Site	INS	-	CT	-	PSMC6	.	.
XH_P46	14	53175200	53175200	Splice_Site	INS	-	TACAATTGTGAAC	-	PSMC6	.	.
XH_P46	14	58830893	58830893	Missense_Mutation	SNP	T	C	T	ARID4A	c.T2086C	p.C696R
XH_P46	14	60749815	60749815	In_Frame_Ins	INS	-	CATCCTCCA	-	PPM1A	4_395insCATCC	.V132delinsASSI
XH_P46	14	61346441	61346441	Frame_Shift_Del	DEL	A	-	A	MNAT1	c.571delA	p.I191fs
XH_P46	14	64453331	64453331	Frame_Shift_Ins	INS	-	AG	-	SYNE2	2309_2310insA	p.L770fs
XH_P46	14	64453333	64453333	In_Frame_Ins	INS	-	GGCCAGGGC	-	SYNE2	.2312insGGCCAK	771delinsRPGQ
XH_P46	14	64519922	64519922	In_Frame_Ins	INS	-	AGTTCCTTTTCT	-	SYNE2	TCTTCAAGTTCC	7delinsLIFSSSFSFSNT
XH_P46	14	64520079	64520079	Frame_Shift_Ins	INS	-	CTTTCTC	-	SYNE2	48_9449insCTT	p.D3150fs
XH_P46	14	64520080	64520080	In_Frame_Ins	INS	-	ATTCTC	-	SYNE2	449_9450insATT	.D3150delinsEFS
XH_P46	14	70839835	70839835	Frame_Shift_Ins	INS	-	GTCTTTCCCTCTC	-	SYNJ2BP	11insGAGAGGG	p.N104fs
XH_P46	14	71206734	71206734	Nonsense_Mutation	INS	-	ACCTTTTAGTCA	-	MAP3K9	nsATGTGACTAA	266delinsVYTKRX
XH_P46	14	75266132	75266132	Missense_Mutation	SNP	G	A	G	YLPM1	c.G4132A	p.E1378K
XH_P46	14	75266133	75266133	In_Frame_Ins	INS	-	CTTCTATCATAC	-	YLPM1	4134insCTTCTA	1378delinsDFYHT
XH_P46	14	77493831	77493831	In_Frame_Del	DEL	GCG	-	GCG	IRF2BPL	c.303_305del	p.101_102del
XH_P46	14	77493833	77493911	Frame_Shift_Del	DEL	GCGCGCGCT	-	CGCGCGCGCTTC	IRF2BPL	c.225_303del	p.P75fs
XH_P46	14	89341451	89341451	Nonsense_Mutation	INS	-	CAAAATTATGTT	-	TTC8	CTTGCCAAAATT	279delinsTPLKLCX
XH_P46	14	91444862	91444862	Frame_Shift_Ins	INS	-	TTTGGGT	-	RPS6KA5	81_182insACCC	p.G61fs
XH_P46	14	91444863	91444863	Frame_Shift_Ins	INS	-	TTAAGTT	-	RPS6KA5	80_181insAACT	p.G61fs
XH_P46	14	92403411	92403411	Frame_Shift_Ins	INS	-	AGGTATTTTTCG	-	FBLN5	59insAGCAAAA	p.P87fs
XH_P46	14	92609404	92609404	Silent	SNP	G	A	G	CPSF2	c.G447A	p.P149P
XH_P46	14	93154538	93154543	In_Frame_Del	DEL	GCGCGC	-	GCGCGC	RIN3	c.2674_2679del	p.892_893del
XH_P46	14	93940540	93940540	Nonsense_Mutation	INS	-	TGCTCACCGTG	-	UNC79	CTAAGTGCTCA	R84delinsLRPQVFSX
XH_P46	14	94088973	94088973	Frame_Shift_Ins	INS	-	TACTTGATACAAG	-	UNC79	64insCTTACTTG	p.T1621fs
XH_P46	14	94517700	94517700	In_Frame_Ins	INS	-	CTGTTC	-	DDX24	16_2417insGAAP	K808delinsRTE
XH_P46	14	95577763	95577763	Frame_Shift_Ins	INS	-	TT	-	DICER1	2146_2147insA	p.G716fs
XH_P46	14	95577764	95577764	Nonsense_Mutation	INS	-	CTAATGTAG	-	DICER1	5_2146insTACA	G.716delinsLHX
XH_P46	14	96788567	96788567	Frame_Shift_Ins	INS	-	GCCTGAATATT	-	ATG2B	1insTATAATATT	p.E921fs
XH_P46	14	102445810	102445810	Frame_Shift_Ins	INS	-	ACTGAATCAAG	-	DYNCH1	0insCTACTGAAT	p.E167fs
XH_P46	14	105268595	105268595	Missense_Mutation	SNP	G	A	G	ZBTB42	c.G1061A	p.R354Q
XH_P46	15	23021316	23021316	Missense_Mutation	SNP	T	A	T	NIP2	c.A21T	p.K7N
XH_P46	15	23021318	23021318	Nonsense_Mutation	INS	-	GTTAACTACTCA	-	NIP2	9insCTGAGTAG	K7_Y8delinsLSXX
XH_P46	15	23685922	23685922	In_Frame_Ins	INS	-	ATCTTCTCTACT	-	GOLGA6L2	5AAGCAGTAGGA	67delinsEAVGEDAG
XH_P46	15	23812402	23812402	Frame_Shift_Ins	INS	-	AACTCAC	-	MKRN3	73_1474insAAC	p.Q491fs
XH_P46	15	23889402	23889402	In_Frame_Ins	INS	-	ACATTCTTTTATGT	-	MAGEL2	ACACCAACATAA	8delinsKSTPHKKCTLW
XH_P46	15	24922857	24922857	Frame_Shift_Ins	INS	-	TGGAAGGGACT	-	NPAP1	1844insTGGAA	p.G615fs
XH_P46	15	25220508	25220508	Frame_Shift_Ins	INS	-	C	-	SNRPN	c.7_8insC	p.V3fs
XH_P46	15	25220509	25220509	Frame_Shift_Ins	INS	-	TTTCTCTGTAC	-	SNRPN	_9insTTTCTCTG	p.V3fs
XH_P46	15	30009040	30009040	Frame_Shift_Ins	INS	-	TGTTTTGTITTT	-	TJP1	nsCTTTAAAAAC	p.I1246fs
XH_P46	15	30009042	30009042	Frame_Shift_Ins	INS	-	TG	-	TJP1	.3734_3735insC	p.R1245fs
XH_P46	15	30010728	30010728	In_Frame_Ins	INS	-	ATGTCTTTAGTG	-	TJP1	3378insCACTAA	G.1126delinsGTKDI
XH_P46	15	35149201	35149201	Nonsense_Mutation	INS	-	AATTCTAGTTTC	-	AQR	0insAATGAAAC	417_11418delinsKX
XH_P46	15	40914922	40914922	Frame_Shift_Ins	INS	-	CTTTTCC	-	KNL1	60_2461insCTT	p.K820fs
XH_P46	15	40916383	40916383	Frame_Shift_Ins	INS	-	TTAGG	-	KNL1	921_3922insTTA	p.N1307fs
XH_P46	15	40916385	40916385	Frame_Shift_Ins	INS	-	TTTCTTCAAG	-	KNL1	.3924insTTTCT	p.V1308fs
XH_P46	15	40917419	40917419	Nonsense_Mutation	INS	-	TGTATTATAGTT	-	KNL1	sAGAGCTGTATT	1653_11654delinsX
XH_P46	15	42702857	42702857	Silent	SNP	C	T	C	CAPN3	c.C261T	p.N87N
XH_P46	15	42749380	42749380	Nonsense_Mutation	INS	-	GGAAGAAGATT	-	ZNF106	CAAAATAAATCT	p.C8_99delinsSX
XH_P46	15	43577055	43577055	Nonsense_Mutation	SNP	G	A	G	TGM7	c.C961T	p.R321X
XH_P46	15	43815899	43815899	Missense_Mutation	SNP	A	T	A	MAP1A	c.A2228T	p.Y743F
XH_P46	15	43815900	43815900	Frame_Shift_Ins	INS	-	TGTTCTG	-	MAP1A	29_2230insTGT	p.Y743fs
XH_P46	15	50773945	50773945	Frame_Shift_Ins	INS	-	GTTGCTCATGGT	-	USP8	nsGATTGTTGCT	p.K419fs
XH_P46	15	51696744	51696744	Nonsense_Mutation	INS	-	AACTGAGTAGT	-	GLDN	78insTAAACTGAA	359_V360delinsYX
XH_P46	15	54305653	54305653	Frame_Shift_Ins	INS	-	GTTGGTGAGAG	-	UNC13C	64insATGTTGGT	p.R185fs
XH_P46	15	55484958	55484958	In_Frame_Ins	INS	-	TGAAGTCCGGA	-	RSL24D1	55insATTCCCAA	T52delinsNSQLHP
XH_P46	15	55484960	55484960	Missense_Mutation	SNP	C	G	C	RSL24D1	c.G153C	p.W51C
XH_P46	15	55651859	55651859	Frame_Shift_Ins	INS	-	TGGCCACTGAG	-	CCPG1	2112insCTCAG	p.V704fs
XH_P46	15	55710197	55710235	Frame_Shift_Del	DEL	CTTTTGTGAT	-	TCITTTTGTGATTC	DNAAF4	c.1144_1182del	p.*382fs
XH_P46	15	55710487	55710487	Frame_Shift_Ins	INS	-	AAATTCCTTC	-	C15orf65	.86insAAATTC	p.V29fs
XH_P46	15	62254093	62254093	Splice_Site	INS	-	TAATCAGTTCAC	-	VPS13C	.	.
XH_P46	15	64791850	64791850	Frame_Shift_Ins	INS	-	CTTTCTTAATT	-	ZNF609	.233insCTTTCC	p.V78fs
XH_P46	15	64966298	64966298	Frame_Shift_Ins	INS	-	TAAGAAGAGAA	-	ZNF609	nsATTATTAAAGA	p.N415fs
XH_P46	15	66618334	66618334	Frame_Shift_Ins	INS	-	TTCATCT	-	DIS3L	55_1456insTTC	p.K485fs
XH_P46	15	66618336	66618336	Missense_Mutation	SNP	A	G	A	DIS3L	c.A1457G	p.D486G
XH_P46	15	72190246	72190246	In_Frame_Ins	INS	-	AAAGAGAACAC	-	MYO9A	4598insAGTGT	11533delinsKCSLF
XH_P46	15	83438626	83438626	Silent	SNP	C	G	C	FSD2	c.G1278C	p.V426V
XH_P46	15	83438628	83438628	In_Frame_Ins	INS	-	TTTTTTTGTGAGA	-	FSD2	nsCTCATCTCAAA	426delinsLUSKKNV
XH_P46	15	83805292	83805292	Silent	SNP	C	A	C	TM6SF1	c.C888A	p.V296V
XH_P46	15	84566757	84566757	Nonsense_Mutation	INS	-	TTAGACAAATA	-	ADAMTSL3	insACTTTTAGAA	639_K540delinsDFX
XH_P46	15	85326004	85326004	In_Frame_Ins	INS	-	TCAGTTTTA	-	ZNF592	8_99insTCAGTT	p.P33delinsPQFY
XH_P46	15	100996217	100996217	Frame_Shift_Ins	INS	-	TAAGAAATTGC	-	CERS3	nsAAAAGCAATT	p.H294fs
XH_P46	16	787292	787292	Missense_Mutation	SNP	G	A	G	NARFL	c.C200T	p.S67L
XH_P46	16	2550856	2550856	Missense_Mutation	SNP	G	A	G	TBC1D24	c.G1559A	p.R520H
XH_P46	16	3070405	3070405	Missense_Mutation	SNP	C	G	C	TNFRSF12A	c.C7G	p.R3G
XH_P46	16	3367315	3367315	In_Frame_Ins	INS	-	CATTTCCTCC	-	ZNF75A	7_338insCATTTC	K.113delinsTFLQ
XH_P46	16	8844296	8844296	In_Frame_Ins	INS	-	TTATTTTATTATGA	-	ABAT	17insTTTATTTTT	H72delinsHFFVE
XH_P46	16	9857996	9857996	Frame_Shift_Ins	INS	-	TGCC	-	GRIN2A	404_3405insGG	p.F1135fs
XH_P46	16	9857998	9857998	Missense_Mutation	SNP	A	C	A	GRIN2A	c.T3403G	p.F1135V
XH_P46	16	10525170	10525170	Missense_Mutation	SNP	A	T	A	ATF7IP2	c.A693T	p.K231N
XH_P46	16	10525172	10525172	Frame_Shift_Ins	INS	-	TTACTTTTCTCTC	-	ATF7IP2	96insTTTACTTT	p.T232fs
XH_P46	16	20809543	20809543	Frame_Shift_Ins	INS	-	TCATATTGTGAA	-	ER12	579insGTCACA	p.L527fs
XH_P46	16	21156663	21156663	Nonsense_Mutation	INS	-	TTATTATTATTAT	-	DNAH3	AAATAAAATAAT	P96_F97delinsLXK
XH_P46	16	24581503	24581503	Frame_Shift_Ins	INS	-	TTTTTCTCCTTC	-	RBBP6	391insCTTTTTC	p.S1130fs
XH_P46	16	24581504	24581504	Frame_Shift_Ins	INS	-	TGTTTGTGTTTC	-	RBBP6	392insCTGGTTT	p.M1131fs
XH_P46	16	28734842	28734842	Frame_Shift_Ins	INS	-	CACCTTAACCA	-	EIF3C	1011insCACCT	p.L337fs
XH_P46	16	30015913	30015913	Nonsense_Mutation	SNP	G	T	G	INOB8E	c.G538T	p.E180X
XH_P46	16	31075463	31075474	In_Frame_Del	DEL	TGGCTGCGC	-	GTGGCTGCGCC	ZNF668	c.307_318del	p.103_106del
XH_P46	16	31927531	31927531	Nonsense_Mutation	INS	-	CTACATGCTTTA	-	ZNF267	5ATTTGCTACAT	654_T655delinsHX
XH_P46	16	46615886	46615886	Frame_Shift_Ins	INS	-	ATTGCTGTATT	-	SHCBP1	insATAAAATAC	p.A514fs
XH_P46	16	53644906	53644906	In_Frame_Ins	INS	-	AAGACT	-	RPGRIP1L	33_3434insAGT	L1145delinsQSL
XH_P46	16	53644908	53644908	Frame_Shift_Ins	INS	-	AACAGGTGGA	-	RPGRIP1L	.3432insTCAAC	p.I1144fs
XH_P46	16	58043834	58043834	Frame_Shift_Ins	INS	-	AAGCAGAGGAG	-	USB1	8insGAAGCAGA	p.Y89fs

XH_P46	16	58579395	58579395	Frame_Shift_Ins	INS	-	GGATTGTTCTT	-	CNOT1	3992insAAGAA	p.T1331fs
XH_P46	16	69726174	69726174	Nonsense_Mutation	INS	-	ATCTGCTGCTGT	-	NFAT5	5GCTGAATCTG	798_Q799delinsGX
XH_P46	16	71713359	71713359	Frame_Shift_Ins	INS	-	CAGCA	-	PHLPP2	969_970insTGC	p.L324fs
XH_P46	16	71713361	71713361	Missense_Mutation	SNP	G	T	G	PHLPP2	c.C968A	p.T323N
XH_P46	16	71792817	71792817	In_Frame_Ins	INS	-	CATTATGTATTT	-	AP1G1	TGACTAAATAC	delinsNTMTKYINVNTLA
XH_P46	16	72110351	72110351	Nonsense_Mutation	INS	-	TTTAAATAATT	-	HPR	insAGTTTTTAAAb	L140delinsQFX
XH_P46	16	81078215	81078215	In_Frame_Ins	INS	-	IAGACTACGATG	-	ATMIN	45insAAAGACT	548delinsTKDYDD
XH_P46	16	84125384	84125385	Frame_Shift_Del	DEL	GG	-	GG	MBTPS1	c.915_916del	p.N305fs
XH_P46	16	84125385	84125385	In_Frame_Ins	INS	-	TTTTTTTTTTTTTT	-	MBTPS1	nsAAAAAAATAA	305delinsKKKKKN
XH_P46	16	85840516	85840516	Frame_Shift_Ins	INS	-	AAACACACGG	-	COX4I1	281insAAACAC	p.L94fs
XH_P46	17	3030361	3030361	Frame_Shift_Ins	INS	-	GT	-	OR1G1	c.484_485insAC	p.L162fs
XH_P46	17	3030364	3030365	Frame_Shift_Del	DEL	AG	-	AG	OR1G1	c.481_482del	p.L161fs
XH_P46	17	4576196	4576196	Missense_Mutation	SNP	G	A	G	PELP1	c.C2240T	p.S747L
XH_P46	17	4925967	4925967	Missense_Mutation	SNP	G	A	G	KIF1C	c.G2591A	p.R864H
XH_P46	17	5013013	5013013	In_Frame_Ins	INS	-	GCTGGAGGA	-	ZNF232	3_174insTCCTC	58delinsDPPA
XH_P46	17	6553696	6553696	Missense_Mutation	SNP	G	A	G	MED31	c.C86T	p.A29V
XH_P46	17	6553697	6553697	Frame_Shift_Ins	INS	-	ACAGATTTTTTT	-	MED31	nsAAAAAAATAA	p.A29fs
XH_P46	17	9281937	9281937	In_Frame_Ins	INS	-	GATTAAATGGTTT	-	STX8	TTCCCAACCAT	2delinsTISQTNLCKH
XH_P46	17	10596149	10596149	In_Frame_Ins	INS	-	TGATGTTAAATG	-	SCO1	TCTAACATTTAA	65delinsDLTFNKT
XH_P46	17	11835443	11835443	In_Frame_Ins	INS	-	ACATTACCATA	-	DNAH9	155insAACATTAA	N385delinsKTLPIY
XH_P46	17	15458621	15458621	Frame_Shift_Ins	INS	-	TTCTTTATATAG	-	TVP23C	GAAACTATATA	p.N24fs
XH_P46	17	16638832	16638832	Frame_Shift_Ins	INS	-	TC	-	CCDC144A	3247_3248insT	p.N1083fs
XH_P46	17	16638833	16638833	Frame_Shift_Ins	INS	-	AACTCTC	-	CCDC144A	48_3249insAAC	p.N1083fs
XH_P46	17	26676189	26676189	Splice_Site	INS	-	GTACCCTGTGAT	-	POLDIP2	-	-
XH_P46	17	28296214	28296214	In_Frame_Ins	INS	-	TCCATGTGTGCT	-	EFCAB5	insTCTTCCATGT	143delinsFLPCVLW
XH_P46	17	28380543	28380543	In_Frame_Ins	INS	-	CAGAAATTGTA	-	EFCAB5	insGCACAGAA	468delinsEHRNCNI
XH_P46	17	28512639	28512639	Frame_Shift_Ins	INS	-	TTTCTCATTTTG	-	NSRP1	63insTGTTTCTC	p.R488fs
XH_P46	17	28512641	28512641	Frame_Shift_Ins	INS	-	AT	-	NSRP1	1464_1465insA	p.R488fs
XH_P46	17	33348687	33348687	Frame_Shift_Ins	INS	-	GTTCCCC	-	RFFL	3_294insGGGG	p.R98fs
XH_P46	17	35563783	35563783	Missense_Mutation	SNP	C	T	C	ACACA	c.G3577A	p.E1193K
XH_P46	17	35563785	35563785	In_Frame_Ins	INS	-	ATTTAATTTTGT	-	ACACA	5insCATACAAA	1192delinsAVKIKYY
XH_P46	17	35981295	35981295	Frame_Shift_Ins	INS	-	ACATATGCTCAC	-	DDX52	378insAGTGAG	p.A460fs
XH_P46	17	37564198	37564198	Frame_Shift_Ins	INS	-	5AAAAGAGAA	-	MED1	CTTTTACTTTCTT	p.A1426fs
XH_P46	17	37618895	37618895	Nonsense_Mutation	INS	-	TATCATCAT	-	CDK12	1_572insTATCA	p.K191delinsSSX
XH_P46	17	37618897	37618897	Missense_Mutation	SNP	G	C	G	CDK12	c.G573C	p.K191N
XH_P46	17	39262015	39262015	Silent	SNP	T	C	T	KRTAP4-9	c.T375C	p.C125C
XH_P46	17	39595539	39595539	Silent	SNP	A	G	A	KRT38	c.T648C	p.D216D
XH_P46	17	40725340	40725340	In_Frame_Ins	INS	-	TCTTTG	-	PSMC3IP	36_337insCAAA	R113delinsQRR
XH_P46	17	42744257	42744257	Nonsense_Mutation	INS	-	TAGAATGATCA	-	MEIOC	ACAGTTAGAATG	C326delinsCDSX
XH_P46	17	45753797	45753797	Nonsense_Mutation	INS	-	TGTCAGGTTAA	-	KPNB1	1insGAATGTCAA	500delinsKECGX
XH_P46	17	45755717	45755717	Frame_Shift_Ins	INS	-	TGAATTAAGT	-	KPNB1	1857insTGAAT	p.S619fs
XH_P46	17	46700340	46700340	Missense_Mutation	SNP	A	T	A	HOXB9	c.T675A	p.S225R
XH_P46	17	46700341	46700341	Frame_Shift_Ins	INS	-	TCTCTCTAGTGT	-	HOXB9	74insCACCTAGA	p.S225fs
XH_P46	17	49075935	49075935	Frame_Shift_Ins	INS	-	TAAAT	-	SPAG9	236_1237insAT	p.P413fs
XH_P46	17	49075936	49075936	Nonsense_Mutation	INS	-	ATAAAAAAATCA	-	SPAG9	236insATGATT	412_P413delinsKX
XH_P46	17	49280526	49280526	Frame_Shift_Ins	INS	-	TGGAAAGTGTA	-	MBTD1	803insTTACACT	p.T268fs
XH_P46	17	51901963	51901963	Silent	SNP	G	A	G	KIF2B	c.G1569A	p.G523G
XH_P46	17	54921456	54921456	Frame_Shift_Ins	INS	-	C	-	DGKE	c.541_542insC	p.E181fs
XH_P46	17	54921457	54921457	Nonsense_Mutation	INS	-	AAGGTTTGAAC	-	DGKE	3insATAAGGTT	p.E181delinsEX
XH_P46	17	56620517	56620517	Missense_Mutation	SNP	A	C	A	C17orf47	c.T1031G	p.V344G
XH_P46	17	56620518	56620518	In_Frame_Ins	INS	-	TTCCCTAGATCT	-	C17orf47	1030insAGATCT	V344delinsRSREV
XH_P46	17	60042783	60042783	Frame_Shift_Ins	INS	-	GTATGAACAGTA	-	MED13	428insTTACTGT	p.Q1476fs
XH_P46	17	61877897	61877897	Frame_Shift_Ins	INS	-	AGAAGAAA	-	DDX42	1_542insAGAAG	p.L181fs
XH_P46	17	61877898	61877898	Nonsense_Mutation	INS	-	GAATTAAAC	-	DDX42	2_543insGAATT	p.L181delinsLN
XH_P46	17	62856364	62856364	Nonsense_Mutation	INS	-	TGCTCCTCAGA	-	LRR37A3	5AATGTCTCTGAA	8_S419delinsQMF
XH_P46	17	65110497	65110497	Silent	SNP	G	A	G	HELZ	c.C3864T	p.S1288S
XH_P46	17	65732870	65732870	Nonsense_Mutation	INS	-	ACCACTCATACA	-	NOL11	AAAAAACCACTC	199_L200delinsIX
XH_P46	17	65908116	65908116	Frame_Shift_Ins	INS	-	TTCCCTC	-	BPTF	16_4117insTTC	p.V1372fs
XH_P46	17	65908118	65908118	Frame_Shift_Ins	INS	-	AGTCCAT	-	BPTF	18_4119insAGT	p.N1373fs
XH_P46	17	65908383	65908383	Frame_Shift_Ins	INS	-	CTTGTTTTTTTA	-	BPTF	84insGACTTGG	p.A1461fs
XH_P46	17	67022605	67022605	In_Frame_Ins	INS	-	TTT	-	ABCA9	2053_2054insA	p.R685delinsKR
XH_P46	17	67022607	67022607	Frame_Shift_Ins	INS	-	TGTTTTTTTTC	-	ABCA9	2052insGAAAA	p.D684fs
XH_P46	17	67124926	67124926	In_Frame_Ins	INS	-	AGCTTTTATTCT	-	ABCA6	TGTTTAGAATA	18delinsKLFRKALSL
XH_P46	17	72287269	72287269	In_Frame_Ins	INS	-	ATCTGGCATTCT	-	DNAI2	722insATCTGGG	I241delinsNLAFL
XH_P46	18	580417	580417	Silent	SNP	C	T	C	CETN1	c.C9T	p.S3S
XH_P46	18	3188940	3188940	Frame_Shift_Ins	INS	-	T	-	MYOM1	c.S76dupA	p.S193fs
XH_P46	18	3188942	3188942	Frame_Shift_Ins	INS	-	TGTTCTTTTTTTT	-	MYOM1	sAAAAAAATAA	p.A192fs
XH_P46	18	3457452	3457452	Frame_Shift_Ins	INS	-	TTTTGTCTCTCA	-	TGIF1	3insTTTTTTGTCT	p.S114fs
XH_P46	18	7044813	7044813	Frame_Shift_Ins	INS	-	AGTC	-	LAMA1	883_884insGAC	p.N295fs
XH_P46	18	7044815	7044815	Nonsense_Mutation	INS	-	TATTAATTTTAC	-	LAMA1	CAAAAGTAAAA	4_N295delinsCKQKX
XH_P46	18	7888279	7888279	Frame_Shift_Ins	INS	-	TTTCCTTCATT	-	PTPRM	137insTTTCTCT	p.P124fs
XH_P46	18	10807272	10807272	In_Frame_Ins	INS	-	TCTAGTGT	-	PIEZO2	7_918insAACAC	R306delinsRTL
XH_P46	18	13053080	13053080	Frame_Shift_Ins	INS	-	TTCTCCA	-	CEP192	80_3181insTTC	p.E1060fs
XH_P46	18	13731869	13731869	Frame_Shift_Ins	INS	-	AACTCTTTTCTC	-	RNMT	54insAAACTCT	p.S118fs
XH_P46	18	13731871	13731871	Missense_Mutation	SNP	A	T	A	RNMT	c.A355T	p.T119S
XH_P46	18	18629840	18629840	Nonsense_Mutation	INS	-	TCCTTTAGACAT	-	ROCK1	nsACAATGTCTA	p.Y59delinsX
XH_P46	18	19154047	19154047	Missense_Mutation	SNP	G	A	G	ESCO1	c.C758T	p.T253I
XH_P46	18	19154048	19154048	Frame_Shift_Ins	INS	-	AATTGGAAGAG	-	ESCO1	7insGGTCTCTC	p.T253fs
XH_P46	18	19996228	19996228	Nonsense_Mutation	INS	-	ATTTTATTCTAA	-	CTAGE1	insACAATTAGA	16_S517delinsHNX
XH_P46	18	21739788	21739788	In_Frame_Ins	INS	-	AAAAATTTGCAG	-	CABYR	AAAAAAATTT	0delinsAIKKNFAGIK
XH_P46	18	21739790	21739790	Frame_Shift_Ins	INS	-	TTTGTC	-	CABYR	D2_603insTTTG	p.V201fs
XH_P46	18	22056862	22056862	Nonsense_Mutation	INS	-	AATATAAT	-	HRH4	5_246insAATAT	S82_E83delinsSIX
XH_P46	18	22056863	22056863	In_Frame_Ins	INS	-	AATGTGTATGTT	-	HRH4	247insAATGTGT	S82delinsSNVYV
XH_P46	18	22806039	22806039	Missense_Mutation	SNP	T	A	T	ZNF521	c.A1183T	p.T395S
XH_P46	18	23872293	23872293	Nonsense_Mutation	INS	-	TAAATTTTATTT	-	TAF4B	0insATTTTAAATT	p.G563delinsGIX
XH_P46	18	28710536	28710536	Nonsense_Mutation	INS	-	STTTGTTAATTC	-	DSC1	AAAAAGAGAA	T876delinsHIKENX
XH_P46	18	29790620	29790620	Nonsense_Mutation	INS	-	ATAAATCGC	-	MEP1B	5_1077insATAA	p.I359delinsIX
XH_P46	18	42529990	42529990	Missense_Mutation	SNP	G	A	G	SETPB1	c.G685A	p.G229R
XH_P46	18	43492336	43492336	In_Frame_Ins	INS	-	CTCTTCTCTGT	-	EPG5	sTAGAGACAGA	301delinsIETEKESS
XH_P46	18	47107855	47107855	Silent	SNP	G	A	G	LIPG	c.G642A	p.Q214Q
XH_P46	18	47107857	47107857	Frame_Shift_Ins	INS	-	CATCCTGCATGC	-	LIPG	3GGCTCATCTCG	p.D215fs
XH_P46	18	47480783	47480783	Nonsense_Mutation	INS	-	ATTCATATATAT	-	MYO5B	568insTATATAT	23_W524delinsIYIX
XH_P46	18	54424389	54424389	Frame_Shift_Ins	INS	-	CATCATCAAGG	-	WDR7	6insCTTCATCAT	p.A855fs
XH_P46	18	71928174	71928174	Frame_Shift_Ins	INS	-	AGTAAACTACTT	-	CYB5A	insAAAAAGTAG	p.D88fs
XH_P46	18	72347148	72347148	Missense_Mutation	SNP	G	T	G	ZNF407	c.G4173T	p.L1391F
XH_P46	18	72347149	72347149	Frame_Shift_Ins	INS	-	ATCAATACTAAT	-	ZNF407	75insTCATCAAT	p.K1392fs
XH_P46	19	1428963	1428963	Silent	SNP	G	A	G	DAZAP1	c.G669A	p.P223P
XH_P46	19	5244098	5244098	Missense_Mutation	SNP	C	T	C	PTPRS	c.G1345A	p.V449I

XH_P46	19	9016693	9016693	In_Frame_Ins	INS	-	GGT	-	MUC16	8043_38044ins	S12682delinsT5
XH_P46	19	9057539	9057539	In_Frame_Ins	INS	-	CTCTCCTCTCTT	-	MUC16	7insAAAAAGAG	969delinsRRKRGGRD
XH_P46	19	9067030	9067030	Frame_Shift_Ins	INS	-	GCATCCTTCCA	-	MUC16	20416insTGGAA	p.M6806fs
XH_P46	19	9075089	9075089	In_Frame_Ins	INS	-	CCTCTA	-	MUC16	56_12357insTA	T4119delinsTRG
XH_P46	19	9075090	9075090	Missense_Mutation	SNP	G	C	G	MUC16	c.C12356G	p.T4119R
XH_P46	19	9084739	9084739	Frame_Shift_Ins	INS	-	CACTAACACCT	-	MUC16	076insTAGGTG	p.K2359fs
XH_P46	19	9325138	9325138	Frame_Shift_Ins	INS	-	AATTCACATGTG	-	OR7D4	ATTACACATGGC	p.I126fs
XH_P46	19	9577251	9577251	Nonstop_Mutation	INS	-	TTTTTTTTTTTTC	-	ZNF560	nsCATCAAAAAA	685delinsSSKKKKE
XH_P46	19	12060390	12060390	In_Frame_Ins	INS	-	ACCACA	-	ZNF700	60_1561insACCP	F520delinsFTT
XH_P46	19	12060391	12060391	Frame_Shift_Ins	INS	-	TGCTTGC	-	ZNF700	61_1562insTGC	p.Y521fs
XH_P46	19	14826993	14826993	Frame_Shift_Ins	INS	-	TCCACTCCTTA	-	ZNF333	671insTCCACT	p.Q224fs
XH_P46	19	14991480	14991480	Nonsense_Mutation	INS	-	CCCTTTATCTAC	-	OR7A17	8insCTGTAGATA	230_A231delinsLX
XH_P46	19	14991572	14991572	Frame_Shift_Ins	INS	-	AC	-	OR7A17	c.595_596insGT	p.M199fs
XH_P46	19	14991574	14991574	Frame_Shift_Ins	INS	-	ACACA	-	OR7A17	593_594insTGT	p.G198fs
XH_P46	19	15659038	15659038	Frame_Shift_Ins	INS	-	AGAAACAGTC	-	CYP4F22	1257insAGAAA	p.R419fs
XH_P46	19	21240004	21240004	Frame_Shift_Ins	INS	-	GATTTGT	-	ZNF430	87_888insGATT	p.T296fs
XH_P46	19	21240005	21240005	Frame_Shift_Ins	INS	-	ACAT	-	ZNF430	888_889insACA	p.T296fs
XH_P46	19	21300607	21300607	Nonsense_Mutation	INS	-	CTCTCCAGAATG	-	ZNF714	AGATTTCCTCTC	delinsHIVHCISLQNELSYVX
XH_P46	19	21720600	21720600	In_Frame_Ins	INS	-	TCTCCACTATGA	-	ZNF429	GGTTTCTCTCCA	18delinsRVSLHYEFF
XH_P46	19	21990645	21990645	Missense_Mutation	SNP	G	T	G	ZNF43	c.C1999A	p.Q667K
XH_P46	19	22000717	22000717	Frame_Shift_Ins	INS	-	TATG	-	ZNF43	c.6_7insCATA	p.R3fs
XH_P46	19	22000718	22000718	Frame_Shift_Ins	INS	-	TTTTCATTCT	-	ZNF43	6insAGAATGTGA	p.R2fs
XH_P46	19	22155633	22155633	Missense_Mutation	SNP	C	T	C	ZNF208	c.G2203A	p.V735I
XH_P46	19	22156714	22156714	Silent	SNP	G	A	G	ZNF208	c.C1122T	p.C374C
XH_P46	19	22497275	22497275	Frame_Shift_Ins	INS	-	AATTTAAAGGCA	-	ZNF729	057insAATTTAA	p.E352fs
XH_P46	19	22497401	22497401	Nonsense_Mutation	INS	-	GGTTTCTCTCCA	-	ZNF729	5TTGTAGGTTTT	894_K395delinsHLX
XH_P46	19	22499077	22499077	Frame_Shift_Ins	INS	-	TCATGTGTTTCT	-	ZNF729	9insTTATCTCATC	p.K953fs
XH_P46	19	22499079	22499079	Missense_Mutation	SNP	C	G	C	ZNF729	c.C2860G	p.H954D
XH_P46	19	23040068	23040068	Nonsense_Mutation	INS	-	CATAGCAAAATA	-	ZNF723	76insGCATAGCA	25_H126delinsMAX
XH_P46	19	23544308	23544308	Nonsense_Mutation	INS	-	TGCTGGAAAGA	-	ZNF91	AGAGTTTCTTTG	K459delinsNLX
XH_P46	19	23837076	23837076	Nonsense_Mutation	INS	-	GGAGAGCAACC	-	ZNF675	5GTAGGGTTGCG	R220delinsMX
XH_P46	19	24309520	24309520	Nonsense_Mutation	INS	-	ATTGAAATACT	-	ZNF254	ATCAGATTGAA	65_E156delinsYLSHX
XH_P46	19	24310638	24310638	In_Frame_Ins	INS	-	ACA	-	ZNF254	1581_1582insAA	p.F527delinsFT
XH_P46	19	24310639	24310639	Nonsense_Mutation	INS	-	TATGAAATATCT	-	ZNF254	CTTCAGTATGAA	delinsFVGLFSEMNLYMFSKX
XH_P46	19	34710618	34710618	Frame_Shift_Ins	INS	-	GT	-	LSM14A	c.972_973insGT	p.K324fs
XH_P46	19	34710619	34710619	Frame_Shift_Ins	INS	-	TTCTCAAAATTC	-	LSM14A	74insTTCTCAA	p.L325fs
XH_P46	19	35232174	35232174	Silent	SNP	T	A	T	ZNF181	c.T888A	p.I296I
XH_P46	19	35232176	35232176	Frame_Shift_Ins	INS	-	TTTTCTCTCTATT	-	ZNF181	891insTTTTCTCT	p.T297fs
XH_P46	19	36674043	36674043	Nonsense_Mutation	INS	-	ACATCAAGAAT	-	ZNF565	825insAATTTCTT	875_E276delinsGILX
XH_P46	19	37240020	37240020	In_Frame_Ins	INS	-	ACACTAATTCAA	-	ZNF850	5insATGTTGAAT	609delinsDVELVLS
XH_P46	19	37487541	37487541	Silent	SNP	A	T	A	ZNF568	c.A756T	p.G252G
XH_P46	19	37487542	37487542	Nonsense_Mutation	INS	-	ATCTAATTTCTA	-	ZNF568	758insATCTAAT	83_C254delinsDLISX
XH_P46	19	37733627	37733627	Frame_Shift_Ins	INS	-	CATAAAGCTTCT	-	ZNF383	TATTTTCATAAAC	p.I163fs
XH_P46	19	37854139	37854139	Frame_Shift_Ins	INS	-	TGTCTCCTCTG	-	HKR1	1263insTGTGTC	p.K421fs
XH_P46	19	37975057	37975057	Nonsense_Mutation	INS	-	GGGTTAAT	-	ZNF570	7_408insGGGTT	36_T137delinsWGX
XH_P46	19	38795550	38795550	In_Frame_Ins	INS	-	GAAGGAGAAGG	-	C19orf33	8insAAGAAGGA	K89delinsKKKEKD
XH_P46	19	44418320	44418320	Frame_Shift_Ins	INS	-	AAATGCGAGAAG	-	ZNF45	68insCACTTCTC	p.K423fs
XH_P46	19	44514931	44514931	Frame_Shift_Ins	INS	-	TCATTGCATGT	-	ZNF230	741insTCATTG	p.T247fs
XH_P46	19	44514933	44514933	Nonsense_Mutation	SNP	G	T	G	ZNF230	c.G742T	p.G248X
XH_P46	19	44636100	44636100	Nonsense_Mutation	INS	-	ATGAAGCGTTT	-	ZNF225	nsATAAATGAAG	P.445delinsYKX
XH_P46	19	44681637	44681637	Frame_Shift_Ins	INS	-	GGTTTTCTCTCA	-	ZNF226	TTGAATGGTTT	p.Q741fs
XH_P46	19	44777932	44777932	In_Frame_Ins	INS	-	TGTCTCTCT	-	ZNF233	9_1120insTTGT	G373delinsGLSL
XH_P46	19	44777934	44777934	Missense_Mutation	SNP	G	A	G	ZNF233	c.G1121A	p.R374K
XH_P46	19	44980743	44980743	Nonsense_Mutation	INS	-	TATTTTAAAGGTA	-	ZNF180	ATGTACTACTCT	627delinsLHVLXP
XH_P46	19	44980745	44980745	Missense_Mutation	SNP	A	T	A	ZNF180	c.T1878A	p.H626Q
XH_P46	19	47951365	47951365	Silent	SNP	G	A	G	SLC8A2	c.C1464T	p.G488G
XH_P46	19	50204584	50204584	Missense_Mutation	SNP	G	A	G	CPT1C	c.G464A	p.R155H
XH_P46	19	50958892	50958892	In_Frame_Ins	INS	-	CTGACCCCTGA	-	MYBPC2	TTCTCTGCTGAC	77delinsPFLTPDPSSL
XH_P46	19	52271947	52271947	Silent	SNP	T	C	T	PR2	c.T36C	p.Y12Y
XH_P46	19	52568916	52568916	Frame_Shift_Ins	INS	-	TTCTGCT	-	ZNF841	70_1871insAGC	p.I624fs
XH_P46	19	52568918	52568918	Nonsense_Mutation	INS	-	TCATCAGATGAT	-	ZNF841	869insCATCATC	623_I624delinsCLIX
XH_P46	19	52620264	52620264	Frame_Shift_Ins	INS	-	GTCAGGGGGAT	-	ZNF616	153insCATCCCC	p.K51fs
XH_P46	19	52663785	52663785	In_Frame_Ins	INS	-	TGTGCCCTTAGT	-	ZNF836	75insACTAAGGG	L25delinsLLRAQ
XH_P46	19	53014600	53014600	Frame_Shift_Ins	INS	-	ATTTT	-	ZNF578	966_967insATT	p.K322fs
XH_P46	19	53014602	53014602	Frame_Shift_Ins	INS	-	TCTCATGTGTA	-	ZNF578	969insTCTCATG	p.S323fs
XH_P46	19	53057106	53057106	In_Frame_Ins	INS	-	ATTACAGGGGAT	-	ZNF808	5AAGAATTTCAG	3delinsMKNSGDYSQ
XH_P46	19	53209281	53209281	Frame_Shift_Ins	INS	-	ATAGACTTCATG	-	ZNF611	TCCACCATGAAC	p.Y343fs
XH_P46	19	53576713	53576713	Frame_Shift_Ins	INS	-	A	-	ZNF160	c.320_321insT	p.C107fs
XH_P46	19	53576714	53576714	Frame_Shift_Ins	INS	-	GAGGGAATAGG	-	ZNF160	20insCCCTATTG	p.C107fs
XH_P46	19	53911686	53911686	In_Frame_Ins	INS	-	CAACTTGAT	-	ZNF765	9_720insCAACT	H240delinsHNLI
XH_P46	19	53911688	53911688	Frame_Shift_Ins	INS	-	TCAATTTTCT	-	ZNF765	1_722insTCAATT	p.T241fs
XH_P46	19	53994798	53994798	In_Frame_Ins	INS	-	AAGCTTTGTGAC	-	ZNF813	3insTGAAAGCTT	438delinsKALSHS
XH_P46	19	53994800	53994800	Silent	SNP	C	T	C	ZNF813	c.C1314T	p.P438P
XH_P46	19	56320507	56320507	Frame_Shift_Ins	INS	-	AAGGCCAACTGG	-	NLRP11	72insTAGCAGTT	p.Q391fs
XH_P46	19	56435986	56435986	Frame_Shift_Ins	INS	-	ATTTCTTATTAA	-	NLRP13	5TTATTTTAAATA	p.E143fs
XH_P46	19	57641066	57641066	Frame_Shift_Ins	INS	-	AATCTGTCTTATA	-	USP29	5sAAGGAATCTG	p.F341fs
XH_P46	19	58049281	58049281	In_Frame_Ins	INS	-	CCCTGCTTC	-	ZNF549	0_871insCCCTG	S290delinsSPCF
XH_P46	19	58050159	58050159	Nonsense_Mutation	INS	-	GTGTGGAT	-	ZNF549	8_1749insGTGT	583_K584delinsX
XH_P46	19	58146094	58146094	In_Frame_Ins	INS	-	CTTCACAGAAAT	-	ZNF211	nsAACTTCACAA	L63delinsLNFTIEK
XH_P46	19	58187892	58187892	In_Frame_Ins	INS	-	GGTCTTGCGCTT	-	ZSCAN4	380insGGTCTCTT	I127delinsRSLAL
XH_P46	19	58420272	58420272	Frame_Shift_Ins	INS	-	TATGGGAAATCG	-	ZNF417	71insAACGATT	p.H457fs
XH_P46	19	58472902	58472902	Frame_Shift_Ins	INS	-	TTCTTCTTCTTT	-	C19orf18	9insGAAGAAAG	p.E130fs
XH_P46	19	58579264	58579264	Frame_Shift_Ins	INS	-	GTGTGATC	-	ZNF135	4_1485insGTGT	p.C495fs
XH_P46	20	210245	210245	In_Frame_Ins	INS	-	GTGATACAAAG	-	DEFB129	GTGCTGTGATGA	delinsKNSSAVIQRKHLS
XH_P46	20	11904177	11904177	In_Frame_Ins	INS	-	ACTCTTTA	-	BTBD3	9_980insACTCT	L327delinsHSFI
XH_P46	20	15967743	15967743	Missense_Mutation	SNP	G	C	G	MACROD2	c.G388C	p.V130L
XH_P46	20	15967745	15967745	Frame_Shift_Ins	INS	-	ATTTTATTTTCAT	-	MACROD2	TTTCAATTTTITA	p.V130fs
XH_P46	20	17240916	17240916	Missense_Mutation	SNP	A	T	A	PCS2	c.A209T	p.Y70F
XH_P46	20	17240917	17240917	In_Frame_Ins	INS	-	AACTTTCTG	-	PCS2	0_211insAACTT	p.Y70delinsYNFL
XH_P46	20	17950945	17950945	Frame_Shift_Ins	INS	-	G	-	MGME1	c.444dupG	p.L148fs
XH_P46	20	17950947	17950947	Frame_Shift_Ins	INS	-	CCACTTCTCAT	-	MGME1	446insCCACTTC	p.L149fs
XH_P46	20	19673974	19673974	In_Frame_Ins	INS	-	AATTAACCTTA	-	SLC24A3	897insGAATTAA	N466delinsRIKPY
XH_P46	20	19674028	19674028	In_Frame_Ins	INS	-	TAAACCTTATTA	-	SLC24A3	nsGAATTAAACC	484delinsRIKPYVIA
XH_P46	20	19674030	19674030	Silent	SNP	G	T	G	SLC24A3	c.G1452T	p.T484T
XH_P46	20	31021297	31021297	Frame_Shift_Ins	INS	-	ATAAATCTGTGT	-	ASXL1	297insAATAAAT	p.Q432fs
XH_P46	20	32664877	32664877	Silent	SNP	C	T	C	RALY	c.C654T	p.G218G
XH_P46	20	34065899	34065899	Nonsense_Mutation	INS	-	AAATGGTTAGTT	-	CEP250	2insACAAATGG	7_E58delinsKTNGX
XH_P46	20	34243128	34243128	Frame_Shift_Ins	INS	-	TACTGCCACCA	-	RBM12	AGAAGTGGTGG	p.E39fs

XH_P46	20	35315985	35315985	Missense_Mutation	SNP	A	T	A	NDRG3	c.T194A	p.F65Y
XH_P46	20	35315986	35315986	Frame_Shift_Ins	INS	-	TTTTCTCTCCTTG	-	NDRG3	93insCAAGGAG	p.F65fs
XH_P46	20	36694658	36694658	In_Frame_Ins	INS	-	TACAAATCACAC	-	RPRD1B	AAATATACAAAT	77delinsEKIYKSHRY
XH_P46	20	37146216	37146216	Frame_Shift_Ins	INS	-	CTCACTATTCTT	-	RALGAPB	sATCTACTCACT	p.S373fs
XH_P46	20	40161804	40161804	Frame_Shift_Ins	INS	-	GT	-	CHD6	c.438_439insAC	p.Q147fs
XH_P46	20	40161806	40161806	Nonsense_Mutation	INS	-	ACTTAGCATTAT	-	CHD6	sCTAAATAATGG	46_Q147delinsTKX
XH_P46	20	43836911	43836911	Frame_Shift_Ins	INS	-	AGTGAGGTTTG	-	SEMG1	74insGAGTGAG	p.K325fs
XH_P46	20	49366531	49366531	Frame_Shift_Ins	INS	-	GTGGCTTTTTC	-	PARD6B	6insATGTGGCT	p.L209fs
XH_P46	20	49508441	49508441	Missense_Mutation	SNP	T	C	T	ADNP	c.A2810G	p.E937G
XH_P46	20	49508442	49508442	Nonsense_Mutation	INS	-	GGAAAAGTTGA	-	ADNP	9insCCTTCAAC	7_T938delinsPSTFPX
XH_P46	20	50769535	50769535	Missense_Mutation	SNP	T	G	T	ZFP64	c.A1034C	p.K345T
XH_P46	20	51870396	51870396	Silent	SNP	G	C	G	TSH22	c.G390C	p.L130L
XH_P46	20	51870397	51870397	Frame_Shift_Ins	INS	-	CTTTTATTTTCTT	-	TSH22	92insTCTTTTAT	p.S131fs
XH_P46	20	57242651	57242651	Frame_Shift_Ins	INS	-	TTTACTCTCTCT	-	STX16	239insTTTACTC	p.E80fs
XH_P46	20	57242653	57242653	Frame_Shift_Ins	INS	-	AT	-	STX16	c.240_241insAT	p.E80fs
XH_P46	20	58467447	58467447	Frame_Shift_Ins	INS	-	AGGAAGAAATA	-	SYCP2	2insTATGATATT	p.K654fs
XH_P46	21	18971136	18971136	Frame_Shift_Ins	INS	-	GCACGTAAATAG	-	BTG3	18insCCTATTTTA	p.G106fs
XH_P46	21	30434830	30434830	In_Frame_Ins	INS	-	GATGGTGTAA	-	CCT8	70insTATTAAACA	257delinsVLTPSS
XH_P46	21	34668613	34668613	Frame_Shift_Ins	INS	-	C	-	IL10RB	c.929_930insC	p.G310fs
XH_P46	21	34668615	34668615	Frame_Shift_Ins	INS	-	CTATTTTATTTTA	-	IL10RB	AAAATCTATTTTA	p.D311fs
XH_P46	21	34878388	34878388	Frame_Shift_Ins	INS	-	TAATAATCTCTC	-	GART	TGATAGAGAGA	p.D826fs
XH_P46	21	35279724	35279724	In_Frame_Ins	INS	-	TTTGTTTTCATT	-	ATP50	nsTAAAAATGAA	121delinsIKMKQTS
XH_P46	21	40590563	40590563	Frame_Shift_Ins	INS	-	ATTGAGGTTTC	-	BRWD1	6insACAGAAAC	p.A1136fs
XH_P46	21	43711690	43711690	Missense_Mutation	SNP	C	T	C	ABCG1	c.C1613T	p.A538V
XH_P46	21	45971162	45971162	Silent	SNP	C	T	C	KRTAP10-2	c.G180A	p.A60A
XH_P46	21	47316126	47316126	Silent	SNP	C	T	C	PCBP3	c.C15T	p.D5D
XH_P46	22	18650781	18650781	Nonsense_Mutation	INS	-	TTAACTCTTTTT	-	USP18	606insTTAACTC	202_S203delinsDX
XH_P46	22	21065113	21065113	Missense_Mutation	SNP	C	T	C	PI4KA	c.G5957A	p.G1986D
XH_P46	22	29025793	29025793	Nonsense_Mutation	INS	-	AAATTTTACCTA	-	TTTC28	CTTCATAGGTA	3_G44delinsNLHRX
XH_P46	22	30221716	30221716	In_Frame_Ins	INS	-	TCCTTCACTGGA	-	ASCC2	nsGGATCCAGTG	45delinsKDPVKEV
XH_P46	22	32012744	32012744	Frame_Shift_Del	DEL	G	-	G	SFI1	c.3149delG	p.R1050fs
XH_P46	22	36889843	36889843	Frame_Shift_Ins	INS	-	AATAATGGATAA	-	FOXRED2	insCATATTATCC	p.E544fs
XH_P46	22	40391329	40391329	Missense_Mutation	SNP	G	T	G	FAM83F	c.G283T	p.A95S
XH_P46	22	42141938	42141938	Nonsense_Mutation	INS	-	TGCCTTTAAATA	-	MEI1	89insTTTGCTT	30_A531delinsICLX
XH_P46	22	45757863	45757863	In_Frame_Ins	INS	-	ACGGAGTCT	-	SMC1B	3_2564insAGAC	A855delinsETPS
XH_P46	22	45757865	45757865	Splice_Site	INS	-	CTTTG	-	SMC1B	.	.
XH_P46	X	20069060	20069060	Frame_Shift_Ins	INS	-	GGTTAATAACGT	-	MAP7D2	ATAAGACGTTA	p.H200fs
XH_P46	X	24229461	24229461	Frame_Shift_Ins	INS	-	GAAGATCCTTT	-	ZFX	0insATGGGAAGA	p.M567fs
XH_P46	X	27765400	27765400	In_Frame_Del	DEL	GAGGAGGAG	-	GAGGAGGAG	DCAF8L2	c.388_396del	p.130_132del
XH_P46	X	32361392	32361392	Frame_Shift_Ins	INS	-	TGATGCATTTC	-	DMD	75insAAGGAAAT	p.S525fs
XH_P46	X	38024127	38024127	Nonsense_Mutation	INS	-	ACCTAACACTACTA	-	SRPX	88insTAGTATG	63_C164delinsIVCX
XH_P46	X	41485934	41485934	Nonsense_Mutation	INS	-	CTTTTCACTTTTA	-	CASK	insATTAAATGA	313_S314delinsYX
XH_P46	X	53634542	53634542	In_Frame_Ins	INS	-	GTATTTTTCTTT	-	HUWE1	38insCAAGAGAA	813delinsTKKYF
XH_P46	X	56276728	56276728	Frame_Shift_Ins	INS	-	CTGTTTCTCTCT	-	KLF8	insATCTGTTTCT	p.V24fs
XH_P46	X	67454353	67454353	Nonsense_Mutation	INS	-	TCATCCCATAT	-	OPHN1	nsCAGATAATGG	K154delinsNRX
XH_P46	X	74291457	74291457	Nonsense_Mutation	INS	-	ACTTGATGGTTT	-	ABC87	TTATCAACACCAT	25delinsNHYQTIKX
XH_P46	X	78216223	78216223	Nonsense_Mutation	INS	-	GTAAAAATGGTT	-	P2RY10	207insGTAAAAA	A69_170delinsAX
XH_P46	X	78216224	78216224	Silent	SNP	C	A	C	P2RY10	c.C207A	p.A99A
XH_P46	X	79973173	79973173	Nonsense_Mutation	INS	-	CCATATTATTC	-	BRWD3	TCACTGGAAATA	40_M711delinsHSLX
XH_P46	X	84525882	84525882	Frame_Shift_Ins	INS	-	TAGTTGG	-	ZNFX11	84_1335insTAG	p.T445fs
XH_P46	X	84525883	84525883	In_Frame_Ins	INS	-	ATT	-	ZNFX11	1335_1336insA	p.T445delinsTL
XH_P46	X	100403118	100403118	In_Frame_Ins	INS	-	TCATCAGGTCAT	-	CENPI	nsACTCCCATCA	688delinsYSHQVIYI
XH_P46	X	102317920	102317920	Frame_Shift_Ins	INS	-	AATTGAATATTG	-	BEX1	3insCACAAATAT	p.K95fs
XH_P46	X	114141709	114141709	Frame_Shift_Ins	INS	-	T	-	HTR2C	c.1109dupT	p.L370fs
XH_P46	X	114141711	114141711	In_Frame_Ins	INS	-	CAGCAC	-	HTR2C	10_111insCAG	L370delinsLQH
XH_P46	X	117043403	117043403	Nonsense_Mutation	INS	-	ATAAAAATGTAG	-	KLHL13	CCCTAACTACA	403_T404delinsEPX
XH_P46	X	123195171	123195171	In_Frame_Ins	INS	-	AAGACGTGTAC	-	STAG2	1515insAAGAC	CE505delinsERRVR
XH_P46	X	129373599	129373599	Nonsense_Mutation	INS	-	SAATGTTTATT	-	ZNFX280C	60insTAAATAAA	b.E150delinsDKX
XH_P46	X	135313108	135313108	Frame_Shift_Ins	INS	-	AAAAAGGATTT	-	MAP7D3	1326insTAAATC	p.K442fs
XH_P46	X	139866207	139866207	In_Frame_Ins	INS	-	AAGACTTGGATT	-	CDR1	325insAATCCAA	P109delinsNPSP
XH_P46	X	140996156	140996156	In_Frame_Ins	INS	-	GAACCTGTA	-	MAGEC1	5_2967insGAAC	S989delinsNRQTY
XH_P46	Y	15418118	15418118	Nonsense_Mutation	INS	-	TGACATGTATG	-	UTY	nsTAAAACTAAC	917_R918delinsX
XH_P46	1	109816242	109816242	Silent	SNV	C	T	T	CELSR2	c.8694C>T	P.12898I
XH_P46	1	1139317	1139317	Missense_Mutation	SNV	C	T	T	TNFRSF18	c.422G>A	P.1411Q
XH_P46	1	12908041	12908041	Missense_Mutation	SNV	C	A	A	HNRNPCL1	c.102G>T	P.E34D
XH_P46	1	176659395	176659395	Missense_Mutation	SNV	T	G	G	PAPPA2	c.2260T>G	P.C754G
XH_P46	1	220142158	220142158	Missense_Mutation	SNV	C	T	T	EPRS	c.4529G>A	P.R1510H
XH_P46	1	228612922	228612922	Silent	SNV	G	A	A	HIST3H3	c.105C>T	P.G35fs
XH_P46	1	231298885	231298851	Frame_Shift_Del	INDEL	CTGGAGCAC	-	-	TRIM67	GCACGACGCTG	p.A61fs
XH_P46	1	40562846	40562846	Missense_Mutation	SNV	C	G	G	PPT1	c.65G>C	P.R22P
XH_P46	1	67098767	67098767	Missense_Mutation	SNV	G	C	C	SGIP1	c.89G>C	P.R30T
XH_P46	10	85997420	85997420	Missense_Mutation	SNV	C	T	T	LRIT1	c.145G>A	P.D49N
XH_P46	11	57254662	57254662	Missense_Mutation	SNV	G	A	A	SLC43A1	c.1439C>T	P.T480I
XH_P46	11	60609700	60609700	Frame_Shift_Del	INDEL	T	-	-	CCDC86	c.104delT	P.F35fs
XH_P46	11	71942604	71942606	Missense_Mutation	INDEL	CCG	-	-	INPPL1	1560_1562delC	P.R521del
XH_P46	12	102041901	102041901	Frame_Shift_Ins	INDEL	-	TTTTTGTTCTGT	TTTTTGTTCTGT	MYBPC1	sTTTTGTTTTTG	P.S366fs
XH_P46	12	108911005	108911005	Missense_Mutation	SNV	T	C	C	FICD	c.256T>C	P.S86P
XH_P46	12	109894070	109894070	Silent	SNV	C	T	T	KCTD10	c.579G>A	P.L193L
XH_P46	12	111748092	111748092	Silent	SNV	C	T	T	CUX2	c.1506C>T	P.G502G
XH_P46	12	21926390	21926390	Missense_Mutation	SNV	C	T	T	KCNJ8	c.161G>A	P.G54E
XH_P46	12	56825396	56825396	Splice_Site	SNV	G	A	A	TIMELESS	c.688-8C>T	.
XH_P46	14	52734696	52734696	Missense_Mutation	SNV	G	T	T	PTGDR	c.164G>T	P.R55L
XH_P46	14	58830893	58830893	Missense_Mutation	SNV	T	C	C	ARID4A	c.2086T>C	P.C696R
XH_P46	14	77257712	77257717	Splice_Site	INDEL	GCAGAG	-	-	ANGEL1	9-8_1619-3delCTCTGC	.
XH_P46	15	83805292	83805292	Silent	SNV	C	A	A	TM65F1	c.888C>A	P.V296V
XH_P46	16	30015913	30015913	Nonsense_Mutation	SNV	G	T	T	INO80E	c.538G>T	P.E180*
XH_P46	16	3070405	3070405	Missense_Mutation	SNV	C	G	G	TNFRSF12A	c.70C>G	P.R3G
XH_P46	16	787292	787292	Missense_Mutation	SNV	G	A	A	NARFL	c.200C>T	P.S67L
XH_P46	17	51901963	51901963	Silent	SNV	G	A	A	KIF2B	c.1569G>A	P.G523G
XH_P46	17	56492821	56492821	Frame_Shift_Del	INDEL	T	-	-	RNF43	c.118delA	P.R40fs
XH_P46	18	22806039	22806039	Missense_Mutation	SNV	T	A	A	ZNFX521	c.1183A>T	P.T395S
XH_P46	18	580417	580417	Silent	SNV	C	T	T	CETN1	c.9C>T	P.S3S
XH_P46	19	1428963	1428963	Silent	SNV	G	A	A	DAZAP1	c.669G>A	P.P23P
XH_P46	19	24310638	24310638	Frame_Shift_Ins	INDEL	-	ACA	ACA	ZNFX254	1713_1714insA	F571_W572insT
XH_P46	19	24310639	24310639	Frame_Shift_Ins	INDEL	-	TATGAATTATCT	TATGAATTATCT	ZNFX254	CTTCAGTATGAA	P.W572fs
XH_P46	19	47951365	47951365	Silent	SNV	G	A	A	SLC8A2	c.1464C>T	P.G488G
XH_P46	19	52271947	52271947	Silent	SNV	T	C	C	FPR2	c.36T>C	P.Y12Y
XH_P46	19	5244098	5244098	Missense_Mutation	SNV	C	T	T	PTPRS	c.1384G>A	P.V462I

XH_P46	2	11773043	11773043	Silent	SNV	G	T	T	GREB1	c.4845G>T	P.L1615L
XH_P46	2	136567212	136567212	Missense_Mutation	SNV	G	A	A	LCT	c.2705C>T	P.T902M
XH_P46	2	160035287	160035287	Missense_Mutation	SNV	A	G	G	TANC1	c.2099A>G	P.K700R
XH_P46	2	44065795	44065795	Silent	SNV	G	A	A	ABCG5	c.24C>T	P.T8T
XH_P46	2	55481167	55481167	Splice_Site	SNV	G	A	A	MTIF2	c.664+10C>T	
XH_P46	20	50769535	50769535	Missense_Mutation	SNV	T	G	G	ZFP64	c.1196A>C	P.K399T
XH_P46	22	32012744	32012744	Frame_Shift_Del	INDEL	G	-	-	SF1	c.3316delG	P.A1106fs
XH_P46	22	40391329	40391329	Missense_Mutation	SNV	G	T	T	FAM83F	c.283G>T	P.A95S
XH_P46	3	112989792	112989792	Splice_Site	SNV	G	A	A	BOC	c.667+1G>A	
XH_P46	3	44488364	44488364	Silent	SNV	G	T	T	ZNF445	c.2799C>A	P.S933S
XH_P46	3	54604116	54604116	Silent	SNV	C	T	T	CACNA2D3	c.873C>T	P.F291F
XH_P46	4	153271233	153271233	Frame_Shift_Ins	INDEL	-	A	A	FBXW7	c.544dupT	P.S182fs
XH_P46	4	189061781	189061781	Splice_Site	SNV	G	A	A	TRIML1	c.504+4G>A	
XH_P46	4	2209736	2209736	Missense_Mutation	SNV	G	C	C	POLN	c.692C>G	P.S231C
XH_P46	4	84383753	84383753	Missense_Mutation	SNV	C	T	T	FAM175A	c.1099G>A	P.D367N
XH_P46	5	140768296	140768296	Missense_Mutation	SNV	G	A	A	PCDHGB4	c.845G>A	P.S282N
XH_P46	5	150682871	150682871	Silent	SNV	C	T	T	SLC36A3	c.45G>A	P.L15L
XH_P46	5	153065831	153065831	Missense_Mutation	SNV	G	T	T	GR1A	c.1076G>T	P.G359V
XH_P46	5	15936569	15936569	Missense_Mutation	SNV	A	T	T	FBXL7	c.609A>T	P.K203N
XH_P46	6	132061463	132061463	Missense_Mutation	SNV	G	C	C	ENPP3	c.2400G>C	P.W800C
XH_P46	6	146480661	146480661	Missense_Mutation	SNV	G	T	T	GRM1	c.878G>T	P.G293V
XH_P46	6	152763329	152763329	Missense_Mutation	SNV	C	T	T	SYNE1	c.3910G>A	P.A1304T
XH_P46	6	51612806	51612806	Missense_Mutation	SNV	G	A	A	PKHD1	c.9608C>T	P.S3203L
XH_P46	7	98506466	98506466	Silent	SNV	C	T	T	TRRAP	c.1231C>T	P.L411L
XH_P46	7	98534907	98534907	Splice_Site	SNV	G	T	T	TRRAP	c.4233+7G>T	
XH_P46	8	52320887	52320887	Silent	SNV	C	T	T	PXDNL	c.3297G>A	P.P1099P
XH_P46	X	99840075	99840075	Splice_Site	SNV	C	A	A	TNMD	c.48+12C>A	
XH_P47	1	12853415	12853415	Silent	SNP	A	G	A	PRAMEF1	c.A39G	p.A13A
XH_P47	1	27023743	27023743	Frame_Shift_Ins	INS	-	G	-	ARID1A	c.850dupG	p.G283fs
XH_P47	1	40092730	40092730	Missense_Mutation	SNP	G	A	G	HEYL	c.C436T	p.R146W
XH_P47	1	62676036	62676036	Silent	SNP	C	T	C	L1TD1	c.C1590T	p.H530H
XH_P47	1	62910675	62910675	Frame_Shift_Ins	INS	-	TTTACTTCTCT	-	USP1	insATTTTACT	p.T275fs
XH_P47	1	65330568	65330568	Missense_Mutation	SNP	G	A	G	JAK1	c.C1078T	p.R360W
XH_P47	1	76779531	76779531	Frame_Shift_Ins	INS	-	ATCTCACTATA	-	ST6GALNAC3	61insATCTCAC	p.L20fs
XH_P47	1	89476781	89476781	Missense_Mutation	SNP	G	A	G	GBP3	c.C766T	p.R256W
XH_P47	1	104166750	104166750	Frame_Shift_Ins	INS	-	TTAATAGTAACT	-	AMY2A	254insATTAAATA	p.G418fs
XH_P47	1	117078587	117078587	Missense_Mutation	SNP	C	A	C	CD58	c.G628T	p.G210C
XH_P47	1	145360684	145360684	Silent	SNP	C	T	C	NBPF19	c.C8490T	p.Y2830Y
XH_P47	1	151396659	151396659	Frame_Shift_Ins	INS	-	AAGA	-	POGZ	1003_1004insTC	p.A335fs
XH_P47	1	152275416	152275416	Silent	SNP	T	A	T	FLG	c.A11946T	p.A3982A
XH_P47	1	155235680	155235680	Missense_Mutation	SNP	C	A	C	CLK2	c.G220T	p.D74Y
XH_P47	1	161495788	161495788	Missense_Mutation	SNP	G	T	G	HSPA6	c.G1340T	p.G447V
XH_P47	1	173010670	173010670	Nonsense_Mutation	INS	-	AACTCTAGAAAT	-	TNFSF18	TATTCAATTCTT65	Q147delinsKIFNFX
XH_P47	1	200818331	200818331	Frame_Shift_Ins	INS	-	CTTGGTACTT	-	CAMSAP2	2387insCTTGG	p.R796fs
XH_P47	1	204588573	204588573	Missense_Mutation	SNP	C	T	C	LRRN2	c.G548A	p.R183H
XH_P47	1	214820283	214820283	In_Frame_Ins	INS	-	ATTITTGCTTTTA	-	CENPF	1insTCTATTTT	2457delinsLFLLLG
XH_P47	1	216108091	216108091	Silent	SNP	G	A	G	USH2A	c.C1761T	p.S2389S
XH_P47	1	226065175	226065175	Missense_Mutation	SNP	C	T	C	TMEM63A	c.G106A	p.A36T
XH_P47	1	234614162	234614162	Missense_Mutation	SNP	G	T	G	TARBP1	c.C688A	p.L230M
XH_P47	1	243333027	243333027	Silent	SNP	A	G	A	CEP170	c.T1452C	p.R484R
XH_P47	1	248437002	248437002	Missense_Mutation	SNP	C	T	C	OR2T33	c.G115A	p.G39S
XH_P47	2	1499889	1499889	Missense_Mutation	SNP	G	A	G	TPO	c.G1616A	p.G539D
XH_P47	2	10132240	10132240	Frame_Shift_Ins	INS	-	AAAGTCCCACT	-	GRHL1	insTGTTAAAGT	p.D476fs
XH_P47	2	73799626	73799626	Frame_Shift_Ins	INS	-	ACGGG	-	ALMS1	519_10620insAC	p.D3540fs
XH_P47	2	73799627	73799627	Frame_Shift_Ins	INS	-	AG	-	ALMS1	0620_10621ins	p.D3540fs
XH_P47	2	84777064	84777064	Silent	SNP	G	A	A	DNAH6	c.G1368A	p.A456T
XH_P47	2	85571829	85571829	Missense_Mutation	SNP	G	A	G	RETSAT	c.C1144T	p.R382W
XH_P47	2	96559342	96559342	Silent	SNP	G	A	G	ANKRD36C	c.C3789T	p.T1263D
XH_P47	2	98319259	98319259	Nonsense_Mutation	INS	-	CTGTGGTTTTTG	-	LINC01125	GAGCACTGTGG65	X266delinsSALSX
XH_P47	2	113127775	113127775	Missense_Mutation	SNP	G	C	G	RGPD5	c.C5278G	p.P1760A
XH_P47	2	148701092	148701092	Splice_Site	SNP	C	A	C	ORC4	-	
XH_P47	2	168100673	168100673	In_Frame_Ins	INS	-	CTGTACCTATTA	-	XIRP2	2106insCTGTAG	1702delinsICTYY
XH_P47	2	168100982	168100982	Missense_Mutation	SNP	A	G	A	XIRP2	c.A2414G	p.R805G
XH_P47	2	196593033	196593033	Missense_Mutation	SNP	T	G	T	SLC39A10	c.T2297G	p.V766G
XH_P47	2	196593035	196593035	Frame_Shift_Ins	INS	-	AGCAAGCAATT	-	SLC39A10	CTGTAAAGCAA	p.T767fs
XH_P47	2	222298928	222298928	Silent	SNP	A	G	A	EPHA4	c.T2277C	p.Y759Y
XH_P47	3	7728109	7728109	Missense_Mutation	SNP	G	C	G	GRM7	c.G2764C	p.V922L
XH_P47	3	14861829	14861838	Frame_Shift_Del	DEL	GAGGAGGGA	-	GGAGGAGGAG	FGD5	c.1251_1260del	p.L417fs
XH_P47	3	41504680	41504680	Frame_Shift_Ins	INS	-	C	-	ULK4	-2384_2385ins	p.N795fs
XH_P47	3	41504682	41504682	Nonsense_Mutation	INS	-	AAGAATGTATAA	-	ULK4	TATAGAATTATA	K796delinsYRIIHSFKX
XH_P47	3	47050016	47050016	Missense_Mutation	SNP	T	C	T	NBEAL2	c.T7885C	p.Y2629H
XH_P47	3	71021798	71021798	Frame_Shift_Ins	INS	-	CTTATGCTTA	-	FOXP1	1260insTAAGC	p.H420fs
XH_P47	3	71179736	71179736	In_Frame_Ins	INS	-	CTTCTAACTCCT	-	FOXP1	99insAGGAGTTA	Q33delinsQGVRR
XH_P47	3	98518631	98518631	In_Frame_Ins	INS	-	TTTAAAAACATC	-	DCBLD2	nsATGTGATGTT	38delinsNMVFLKKS
XH_P47	3	110852553	110852553	Missense_Mutation	SNP	G	T	G	NECTIN3	c.G1141T	p.A381S
XH_P47	3	110852554	110852554	Frame_Shift_Ins	INS	-	GTTCACATTAGA	-	NECTIN3	TTTACTGTTTCCA	p.A381fs
XH_P47	3	132319393	132319393	Missense_Mutation	SNP	T	C	T	ACKR4	c.T152C	p.S51A
XH_P47	3	133698460	133698460	Silent	SNP	C	T	C	SLCO2A1	c.G99A	p.V33V
XH_P47	3	137880741	137880743	In_Frame_Del	DEL	TCG	-	TCG	DBR1	c.1623_1625del	p.541_542del
XH_P47	3	146239651	146239651	Frame_Shift_Ins	INS	-	CATGGACCACT	-	PLSCR1	AAAATAAGTGG	p.S182fs
XH_P47	3	147114005	147114005	Missense_Mutation	SNP	C	T	C	ZIC4	c.G472A	p.A158T
XH_P47	3	151535309	151535309	Frame_Shift_Ins	INS	-	CTATGGACTTA	-	AADAC	295insTCTATGG	p.R98fs
XH_P47	3	165504041	165504041	Frame_Shift_Ins	INS	-	AACTCTTACTATA	-	BCHE	576insTATAGTA	p.Q526fs
XH_P47	3	183906036	183906036	Missense_Mutation	SNP	G	A	G	ABCF3	c.G659A	p.R220Q
XH_P47	3	185198046	185198046	Missense_Mutation	SNP	A	G	A	MAP3K13	c.A1907G	p.Q636R
XH_P47	3	194062381	194062381	Missense_Mutation	SNP	C	T	C	CPN2	c.G1051A	p.A351T
XH_P47	4	41748011	41748028	In_Frame_Del	DEL	CCGCCGCTG	-	GCCGCCGCTGCC	PHOX2B	c.741_758del	p.247_253del
XH_P47	4	47939190	47939190	Frame_Shift_Ins	INS	-	C	-	CNGA1	c.1527_1528ins	p.L510fs
XH_P47	4	47939191	47939191	Frame_Shift_Ins	INS	-	TGATAATGTAC	-	CNGA1	AGAGATGTACA	p.Y509fs
XH_P47	4	62935870	62935870	Missense_Mutation	SNP	T	A	T	ADGRL3	c.T3706A	p.S1236T
XH_P47	4	62936364	62936364	In_Frame_Ins	INS	-	ATTATACCAAGAA	-	ADGRL3	nsACACCATTATA	B83delinsPHHYTRRR
XH_P47	4	83852181	83852181	Nonsense_Mutation	INS	-	CAAAAAATATAAA	-	LIN54	GTTGAGTTTATA	566_1567delinsSX
XH_P47	4	114275936	114275936	Nonsense_Mutation	INS	-	TTTATGTTTATG	-	ANK2	5163insTTTTATG	G4_R205delinsQFYVX
XH_P47	4	114277509	114277509	Frame_Shift_Ins	INS	-	AAGAGCCCCCTT	-	ANK2	CAGGGAAGAGCA	p.K2579fs
XH_P47	4	123207926	123207926	Frame_Shift_Ins	INS	-	CACA	-	KIAA1109	268_9269insCA	p.R3090fs
XH_P47	4	123207927	123207927	Nonsense_Mutation	INS	-	TTCTCTCTCTCG	-	KIAA1109	CAACCATTCCTC	delinsRYVNHSSFCQSX
XH_P47	4	126372500	126372500	Missense_Mutation	SNP	C	A	C	FAT4	c.C10335A	p.F3445L
XH_P47	4	140811081	140811081	Frame_Shift_Del	DEL	C	-	C	MAML3	c.1509delG	p.Q503fs

XH_P47	4	140811083	140811096	Frame_Shift_Del	DEL	TGCTGCTGC	-	CTGCTGCTGCTG	MAML3	c.1494_1507del	p.Q498fs
XH_P47	4	146461191	146461191	In_Frame_Ins	INS	-	GTTACCCAAACT	-	SMAD1	TAGCAGTTACCC	12delinsPIAVTQTL
XH_P47	4	153691312	153691312	Missense_Mutation	SNP	C	G	C	TIGD4	c.G845C	p.R282T
XH_P47	4	166946559	166946559	Frame_Shift_Ins	INS	-	CTACAAGAATC	-	TL1	insAACTCTCAAA	p.R378fs
XH_P47	4	188924186	188924186	Silent	SNP	C	T	C	ZFP42	c.C225T	p.C75C
XH_P47	5	56177849	56177854	In_Frame_Del	DEL	CAACAA	-	CAACAA	MAP3K1	c.2822_2827del	p.941_943del
XH_P47	5	74400949	74400949	Frame_Shift_Ins	INS	-	T	-	ANKRD31	c.4263dupA	p.Q1422fs
XH_P47	5	89990181	89990181	Silent	SNP	G	A	G	ADGRV1	c.G7608A	p.E2536E
XH_P47	5	102895168	102895168	Frame_Shift_Ins	INS	-	TT	-	NUDT12	c.153_154insAA	p.C53fs
XH_P47	5	102895169	102895169	Nonsense_Mutation	INS	-	ATTCGTTAGGAA	-	NUDT12	CTTGGTTCTCTAA	M51delinsSLGSX
XH_P47	5	113829120	113829120	Missense_Mutation	SNP	A	G	A	KCNN2	c.A359G	p.E120G
XH_P47	5	137593359	137593359	Missense_Mutation	SNP	G	A	G	GFR3	c.C754T	p.C252W
XH_P47	5	140223201	140223201	Silent	SNP	G	A	G	PCDHA8	c.G2295A	p.P765P
XH_P47	5	140719676	140719676	Missense_Mutation	SNP	G	A	G	PCDHGA2	c.G1138A	p.A380T
XH_P47	5	140725547	140725547	Silent	SNP	C	T	C	PCDHGA3	c.C1947T	p.H649H
XH_P47	5	150133216	150133216	In_Frame_Ins	INS	-	GTG	-	DCTN4	c.209_210insCA	p.C70delinsCT
XH_P47	5	150133217	150133217	Nonsense_Mutation	INS	-	TATA	-	DCTN4	208_209insTAT	C70_A71delinsLX
XH_P47	5	153783750	153783750	Silent	SNP	G	A	G	GALNT10	c.G1143A	p.P381P
XH_P47	5	156734867	156734867	Missense_Mutation	SNP	C	A	C	CYFIP2	c.C816A	p.F272L
XH_P47	6	27861453	27861453	Silent	SNP	T	C	T	HIST1H2BO	c.T213C	p.F71F
XH_P47	6	135517027	135517027	In_Frame_Ins	INS	-	CTTCTGCTCTCT	-	MYB	insTTTCTCTCTG	329delinsSSVLSL
XH_P47	6	135517029	135517029	In_Frame_Ins	INS	-	TTTCTACAC	-	MYB	7_98insTTTCTTA	L329delinsLFH
XH_P47	6	161027559	161027559	Missense_Mutation	SNP	G	A	G	LPA	c.C2735T	p.A912V
XH_P47	6	168370510	168370510	Nonsense_Mutation	INS	-	TCTAGTTTGTCC	-	AFDN	GTGTTTCTTAGT	D9_F1710delinsTGCFX
XH_P47	7	6836259	6836259	Missense_Mutation	SNP	C	T	C	RSPH10B	c.C2294T	p.T765M
XH_P47	7	20738083	20738083	Missense_Mutation	SNP	A	T	A	ABCBS	c.A729T	p.E243D
XH_P47	7	26246130	26246130	In_Frame_Ins	INS	-	CTGACAATACT	-	CBX3	8insTGCTGACA	D56delinsDADNTC
XH_P47	7	26246132	26246132	Splice_Site	SNP	T	G	T	CBX3	-	-
XH_P47	7	37927910	37927910	Missense_Mutation	SNP	C	T	C	NME8	c.C1279T	p.P427S
XH_P47	7	44797065	44797109	In_Frame_Del	DEL	CACTGCCACCG	-	CACTGCCACCG	ZM122	c.457_501del	p.153_167del
XH_P47	7	91631845	91631845	Nonsense_Mutation	INS	-	TTTTCTAACAAT	-	AKAP9	ATCTGTTTTTCT	L872delinsHLFFX
XH_P47	7	100675934	100675934	Missense_Mutation	SNP	A	C	A	MUC17	c.A1237C	p.T413P
XH_P47	7	100676390	100676390	Missense_Mutation	SNP	C	T	C	MUC17	c.C1693T	p.P565S
XH_P47	7	100676391	100676391	Missense_Mutation	SNP	C	A	C	MUC17	c.C1694A	p.P565H
XH_P47	7	100676518	100676518	Silent	SNP	T	C	T	MUC17	c.T1821C	p.A607A
XH_P47	7	100679469	100679469	Missense_Mutation	SNP	A	G	A	MUC17	c.A4772G	p.N1591S
XH_P47	7	100681195	100681195	Missense_Mutation	SNP	G	A	G	MUC17	c.G6498A	p.M2166I
XH_P47	7	100682920	100682920	Missense_Mutation	SNP	G	A	G	MUC17	c.G8223A	p.M2741I
XH_P47	7	100682922	100682922	Missense_Mutation	SNP	G	C	G	MUC17	c.G8225C	p.R2742P
XH_P47	7	106762395	106762395	Splice_Site	INS	-	ACTTAAAAATAA	-	PRKAR2B	-	-
XH_P47	7	107314664	107314664	Silent	SNP	C	T	C	SLC26A4	c.C471T	p.P157P
XH_P47	8	16021694	16021694	Frame_Shift_Del	DEL	G	-	G	MSR1	c.697delC	p.Q233fs
XH_P47	8	25346120	25346120	Frame_Shift_Ins	INS	-	TATATTACCCAA	-	CDCA2	insATACATATT	p.V514fs
XH_P47	8	28385332	28385332	Nonsense_Mutation	INS	-	ATAGGCGTTTCA	-	FZD3	insATAATAGGC	p.1352delinsIX
XH_P47	9	21971114	21971114	Frame_Shift_Ins	INS	-	CGGGTGAGAGT	-	CDKN2A	insCGCCACTCTC	p.V82fs
XH_P47	9	27185588	27185588	Frame_Shift_Ins	INS	-	AT	-	TEK	c.847_848insAT	p.A283fs
XH_P47	9	35722212	35722212	Frame_Shift_Ins	INS	-	CCTAAGA	-	TLN1	51_852insTCTTA	p.K284fs
XH_P47	9	137593102	137593102	Missense_Mutation	SNP	C	T	C	COL5A1	c.C577T	p.R193C
XH_P47	9	139400096	139400096	Missense_Mutation	SNP	C	T	C	NOTCH1	c.G4252A	p.A1418T
XH_P47	10	26463315	26463315	Frame_Shift_Ins	INS	-	CTTTTTC	-	MYO3A	22_4123insCTTT	p.F1374fs
XH_P47	10	26463317	26463317	Missense_Mutation	SNP	A	T	A	MYO3A	c.A4124T	p.R1375M
XH_P47	10	65225357	65225357	Missense_Mutation	SNP	C	A	C	JMJD1C	c.G66T	p.E22D
XH_P47	10	121485844	121485844	Missense_Mutation	SNP	C	T	C	INPP5F	c.C70T	p.R24C
XH_P47	11	46387982	46387982	Missense_Mutation	SNP	G	A	G	DGK2	c.G176A	p.C59Y
XH_P47	11	47612315	47612340	Frame_Shift_Del	DEL	AGGCGCTGG	-	CAGGCGCTGGG	C1QTNF4	c.23_48del	p.L8fs
XH_P47	11	62289981	62289981	Missense_Mutation	SNP	C	T	C	AHNAK	c.G11908A	p.V3970I
XH_P47	11	66411364	66411384	In_Frame_Del	DEL	GCTGCAGCA	-	TGCTGCAGCAG	RBM14-RBM4	c.781_801del	p.261_267del
XH_P47	11	118376152	118376152	In_Frame_Ins	INS	-	ATTGCTACCCAT	-	KMT2A	insAGGATTGCT	182delinsKGLPPMS
XH_P47	11	130068963	130068963	Silent	SNP	C	T	C	ST14	c.C1806T	p.C602C
XH_P47	12	4920759	4920759	Silent	SNP	C	A	C	KCNA6	c.C1552A	p.R518R
XH_P47	12	25398284	25398284	Missense_Mutation	SNP	C	T	C	KRAS	c.G35A	p.G12D
XH_P47	12	32993967	32993967	Silent	SNP	G	A	G	PKP2	c.C1551T	p.C517C
XH_P47	12	56525271	56525271	Missense_Mutation	SNP	T	A	T	ESY1	c.G725A	p.V242D
XH_P47	12	57850082	57850082	Nonsense_Mutation	SNP	G	A	G	INHBE	c.G504A	p.W168X
XH_P47	12	59274453	59274453	In_Frame_Ins	INS	-	AAAATTAAGATT	-	LRIG3	1531insAATCTT	V511delinsNLNFV
XH_P47	12	93772199	93772199	Splice_Site	INS	-	GCTGC	-	NUDT4	-	-
XH_P47	12	125396398	125396398	Silent	SNP	A	G	A	UBC	c.T1920C	p.D640D
XH_P47	12	125397358	125397358	Silent	SNP	T	C	T	UBC	c.A960G	p.E320E
XH_P47	13	25744858	25744858	Silent	SNP	G	A	G	AMER2	c.C900T	p.A300A
XH_P47	13	28712860	28712910	In_Frame_Del	DEL	CCCCGCCGGG	-	CCCCGCCGGGG	PAN3	c.66_116del	p.22_39del
XH_P47	13	32911464	32911464	Frame_Shift_Ins	INS	-	TTTCCTTAGTATT	-	BRCA2	973insGTTCCTT	p.N991fs
XH_P47	13	77641983	77641983	Frame_Shift_Ins	INS	-	CGATGAT	-	MYCBP2	87_12188insATC	p.R4063fs
XH_P47	13	95121252	95121252	Missense_Mutation	SNP	C	T	C	DCT	c.G343A	p.G115S
XH_P47	13	100622668	100622673	In_Frame_Del	DEL	GGCGGC	-	GGCGGC	ZIC5	c.1257_1262del	p.419_421del
XH_P47	13	110435300	110435302	In_Frame_Del	DEL	GGT	-	GGT	IRS2	c.3099_3101del	p.1033_1034del
XH_P47	14	23886479	23886479	Nonsense_Mutation	SNP	C	A	C	MYH7	c.G4402T	p.E1468H
XH_P47	14	75150153	75150153	Frame_Shift_Ins	INS	-	TTTTT	-	AREL1	326_327insAAA	p.V109fs
XH_P47	14	75150154	75150154	Frame_Shift_Ins	INS	-	AAAATAATAC	-	AREL1	326insGTATT	p.V109fs
XH_P47	14	76249769	76249769	Frame_Shift_Ins	INS	-	A	-	TTL5	c.2883dupA	p.P961fs
XH_P47	14	76249771	76249771	Nonsense_Mutation	INS	-	TGAACACAGTCT	-	TTL5	TTTTACTGAACA	62_C963delinsQFYX
XH_P47	14	89105173	89105173	Missense_Mutation	SNP	A	T	A	EML5	c.T4316A	p.I439K
XH_P47	15	25926179	25926179	Missense_Mutation	SNP	C	T	C	ATP10A	c.G3535A	p.A1179T
XH_P47	15	32323160	32323160	Missense_Mutation	SNP	C	G	C	CHRNA7	c.C115G	p.P39A
XH_P47	15	50822116	50822116	Nonsense_Mutation	SNP	G	A	G	USP50	c.C814T	p.Q272X
XH_P47	15	102185366	102185366	Splice_Site	INS	-	A	-	TM2D3	-	-
XH_P47	16	4625401	4625401	Missense_Mutation	SNP	C	T	C	C16orf96	c.C920T	p.A307V
XH_P47	16	8995057	8995057	Silent	SNP	G	A	G	USP7	c.C2034T	p.P678P
XH_P47	16	29395397	29395453	In_Frame_Del	DEL	TGAGGGTGG	-	CTGAGGGTGGG	NP1B11	c.800_856del	p.267_286del
XH_P47	16	29810469	29810479	Frame_Shift_Del	DEL	CGCTCTCTCC	-	CGCTCTCTCCC	KIF22	c.519_529del	p.Q173fs
XH_P47	16	88500071	88500071	Missense_Mutation	SNP	T	A	T	ZNF469	c.T6109A	p.25037T
XH_P47	17	5085647	5085647	Silent	SNP	A	G	A	ZNF594	c.T1905C	p.G635G
XH_P47	17	6531494	6531494	Nonsense_Mutation	SNP	G	A	G	KIA00753	c.C661T	p.R221X
XH_P47	17	7577089	7577094	In_Frame_Del	DEL	GCGCGG	-	GCGCGG	TP53	c.448_453del	p.150_151del
XH_P47	17	17697094	17697108	In_Frame_Del	DEL	CAGCAGCAG	-	GCAGCAGCAGC	RAI1	c.832_846del	p.278_282del
XH_P47	17	19186563	19186563	Missense_Mutation	SNP	C	T	C	EPN2	c.C131T	p.A44V
XH_P47	17	28512493	28512493	Missense_Mutation	SNP	A	T	A	NSRP1	c.A1316T	p.E439V
XH_P47	17	28512495	28512495	In_Frame_Ins	INS	-	TATTTTCATATCT	-	NSRP1	TATCATTATTTT	440delinsFIIFISFLP
XH_P47	17	36623139	36623139	Silent	SNP	G	A	G	ARHGAP23	c.G1215A	p.P405P

XH_P47	17	38519757	38519757	Missense_Mutation	SNP	G	A	G	GJD3	c.C311T	p.A104V
XH_P47	17	39254142	39254142	Silent	SNP	A	G	A	KRTAP4-8	c.T195C	p.C65C
XH_P47	17	39421886	39421886	Missense_Mutation	SNP	A	G	A	KRTAP9-6	c.A257G	p.Y86C
XH_P47	17	45916181	45916181	Missense_Mutation	SNP	G	A	G	SCRN2	c.C748T	p.R250W
XH_P47	17	56342311	56342311	Frame_Shift_Ins	INS	-	CGCCTTCGCTT	-	LPO	insCCTTCGCTT	p.N416fs
XH_P47	17	56342312	56342312	Missense_Mutation	SNP	A	C	A	LPO	c.A1247C	p.N416T
XH_P47	17	72915691	72915691	Missense_Mutation	SNP	C	T	C	USH1G	c.G931A	p.D311N
XH_P47	17	79792784	79792784	Missense_Mutation	SNP	G	A	G	PPP1R27	c.C46T	p.R16W
XH_P47	18	13731870	13731870	Silent	SNP	T	A	T	RNMT	c.T354A	p.S118S
XH_P47	18	13731871	13731871	Frame_Shift_Ins	INS	-	ACTCTTTTCT	-	RNMT	c.356insACTCTT	p.T119fs
XH_P47	18	47107855	47107855	Silent	SNP	G	A	G	LIPG	c.G642A	p.Q214Q
XH_P47	18	47107857	47107857	In_Frame_Ins	INS	-	ATCCTGCATGCT	-	LIPG	GGCTCATCTCGG15delinsEGLIHAFYL	
XH_P47	18	50589788	50589788	Frame_Shift_Ins	INS	-	GCAGCATGCAAG	-	DCC	sCCTCAGCAGCA	p.N367fs
XH_P47	19	5212372	5212372	Missense_Mutation	SNP	G	A	G	PTPRS	c.C3404T	p.A1135V
XH_P47	19	14627780	14627780	Missense_Mutation	SNP	T	A	T	DNAJB1	c.A290T	p.D97V
XH_P47	19	21366540	21366540	Silent	SNP	C	T	C	ZNFA31	c.C1437T	p.H479H
XH_P47	19	22155646	22155646	Silent	SNP	A	G	A	ZNFA208	c.T2190C	p.F730F
XH_P47	19	22941617	22941617	Missense_Mutation	SNP	T	C	T	ZNFA99	c.A1094G	p.E365G
XH_P47	19	23543210	23543210	Silent	SNP	C	T	C	ZNFA91	c.G2475A	p.E825E
XH_P47	19	23543701	23543701	Missense_Mutation	SNP	T	C	T	ZNFA91	c.A1984G	p.T662A
XH_P47	19	24310638	24310638	In_Frame_Ins	INS	-	TTCTCTTCAGTA	-	ZNFA254	TAGGGTTCTCTCT	delinsFTFVGFLFSMNYLM
XH_P47	19	37130868	37130868	Nonsense_Mutation	INS	-	TTAATCATAAGT	-	ZNFA461	AGACAACTTATG4	M105delinsDLNX
XH_P47	19	44981600	44981600	Silent	SNP	C	T	C	ZNFA180	c.G1023A	p.S341S
XH_P47	19	50243430	50243430	Missense_Mutation	SNP	C	T	C	TSKS	c.G1508A	p.R503H
XH_P47	19	53058449	53058449	Silent	SNP	G	A	G	ZNFA808	c.G2280A	p.E760E
XH_P47	19	53958558	53958558	Missense_Mutation	SNP	G	A	G	ZNFA761	c.G797A	p.G266D
XH_P47	19	53958559	53958559	Silent	SNP	T	A	T	ZNFA761	c.T798A	p.G266G
XH_P47	19	53958603	53958603	Missense_Mutation	SNP	A	G	A	ZNFA761	c.A842G	p.Q281R
XH_P47	19	54697134	54697134	Missense_Mutation	SNP	G	A	G	TSEN34	c.G850A	p.V284I
XH_P47	19	57640488	57640488	Frame_Shift_Ins	INS	-	C	-	USP29	c.445_446insC	p.F149fs
XH_P47	19	57640490	57640490	Frame_Shift_Ins	INS	-	TTTTTACA	-	USP29	c.7_448insTTTTT	p.F149fs
XH_P47	20	239936	239936	Missense_Mutation	SNP	G	A	G	DEFB132	c.G277A	p.V93I
XH_P47	20	3767122	3767184	Frame_Shift_Del	DEL	CCGGGGCCCC	-	CCCGGGGGCCCCG	CENPB	NM_001810	wholegene
XH_P47	20	44236763	44236763	Nonsense_Mutation	INS	-	TTTTTTTTAACTT	-	WFDC9	insGGAAGTTAA	M86_L87delinsGSX
XH_P47	20	46279837	46279842	In_Frame_Del	DEL	CAGCAG	-	CAGCAG	NCOA3	c.3760_3765del	p.1254_1255del
XH_P47	20	48712801	48712801	Missense_Mutation	SNP	G	A	G	UBE2V1	c.C178T	p.R60C
XH_P47	21	41414574	41414574	Frame_Shift_Ins	INS	-	TTTGATGATAC	-	DSCAM	5410insGTATC	p.T1804fs
XH_P47	X	71426280	71426281	Frame_Shift_Del	DEL	AT	-	AT	ERCC6L	c.2336_2337del	p.D779fs
XH_P47	1	117078587	117078587	Missense_Mutation	SNV	C	A	A	CD58	c.628G>T	P.G210C
XH_P47	1	152275416	152275416	Silent	SNV	T	A	A	FLG	c.11946A>T	P.A3982A
XH_P47	1	155235680	155235680	Missense_Mutation	SNV	C	A	A	CLK2	c.904G>T	P.D302Y
XH_P47	1	216108091	216108091	Silent	SNV	G	A	A	USH2A	c.7167C>T	P.S2389S
XH_P47	1	27023743	27023743	Frame_Shift_Ins	INDEL	-	G	G	ARID1A	c.854dupG	P.T286fs
XH_P47	1	40092730	40092730	Missense_Mutation	SNV	G	A	A	HEVL	c.436C>T	P.R146W
XH_P47	1	62676036	62676036	Silent	SNV	C	T	T	LITD1	c.1590C>T	P.H530H
XH_P47	1	65330568	65330568	Missense_Mutation	SNV	G	A	A	JAK1	c.1078C>T	P.R360W
XH_P47	10	121485844	121485844	Missense_Mutation	SNV	C	T	T	INPP5F	c.70C>T	P.R24C
XH_P47	11	46387982	46387982	Missense_Mutation	SNV	G	A	A	DGKZ	c.176G>A	P.C59Y
XH_P47	12	25398284	25398284	Missense_Mutation	SNV	C	T	T	KRAS	c.35G>A	P.G12D
XH_P47	12	4920759	4920759	Silent	SNV	C	A	A	KCNAB6	c.1552C>A	P.R518R
XH_P47	12	56525271	56525271	Missense_Mutation	SNV	T	A	A	ESYT1	c.725T>A	P.V242D
XH_P47	12	58024975	58024975	Splice_Site	SNV	G	A	A	B4GALNT1	c.383+8C>T	
XH_P47	12	94772826	94772826	Splice_Site	SNV	T	A	A	CEP83	c.550-8A>T	
XH_P47	13	25744858	25744858	Silent	SNV	G	A	A	AMER2	c.900C>T	P.A300A
XH_P47	13	95121252	95121252	Missense_Mutation	SNV	C	T	T	DCT	c.343G>A	P.G115S
XH_P47	14	89105173	89105173	Missense_Mutation	SNV	A	T	T	EML5	c.4316T>A	P.J1439K
XH_P47	15	32323160	32323160	Missense_Mutation	SNV	C	G	G	CHRNA7	c.115C>G	P.P39A
XH_P47	15	50822116	50822116	Nonsense_Mutation	SNV	G	A	A	USP50	c.814C>T	P.Q272*
XH_P47	16	88500071	88500071	Missense_Mutation	SNV	T	A	A	ZNFA469	c.6109T>A	P.S2037T
XH_P47	17	45916181	45916181	Missense_Mutation	SNV	G	A	A	SCRN2	c.748C>T	P.R250W
XH_P47	17	72915691	72915691	Missense_Mutation	SNV	C	T	T	USH1G	c.931G>A	P.D311N
XH_P47	19	14627780	14627780	Missense_Mutation	SNV	T	A	A	DNAJB1	c.290A>T	P.D97V
XH_P47	19	50243430	50243430	Missense_Mutation	SNV	C	T	T	TSKS	c.1508G>A	P.R503H
XH_P47	2	168100982	168100982	Missense_Mutation	SNV	A	G	G	XIRP2	c.3080A>G	P.D1027G
XH_P47	2	222298928	222298928	Silent	SNV	A	G	G	EPHA4	c.2430T>C	P.Y810Y
XH_P47	2	33335824	33335824	Splice_Site	SNV	T	C	C	LTBP1	c.1033+6T>C	
XH_P47	20	48712801	48712801	Missense_Mutation	SNV	G	A	A	UBE2V1	c.178C>T	P.R60C
XH_P47	3	133698460	133698460	Splice_Site	SNV	C	T	T	SLCO2A1	c.99G>A	P.V33V
XH_P47	3	147114005	147114005	Missense_Mutation	SNV	C	T	T	ZIC4	c.472G>A	P.A158T
XH_P47	3	14861829	14861838	Frame_Shift_Del	INDEL	AGAGGAGGA	-	-	FGD5	1261delAGAGGA	P.E418fs
XH_P47	3	185198046	185198046	Missense_Mutation	SNV	A	G	G	MAP3K13	c.2528A>G	P.Q843R
XH_P47	3	194062381	194062381	Missense_Mutation	SNV	C	T	T	CPN2	c.1051G>A	P.A351T
XH_P47	3	47050016	47050016	Missense_Mutation	SNV	T	C	C	NBEAL2	c.7885T>C	P.Y2629H
XH_P47	3	7728109	7728109	Missense_Mutation	SNV	G	C	C	GRM7	c.2764G>C	P.V922L
XH_P47	4	126372500	126372500	Missense_Mutation	SNV	C	A	A	FAT4	c.10329C>A	P.F3443L
XH_P47	4	62935870	62935870	Missense_Mutation	SNV	T	A	A	ADGRL3	c.3706T>A	P.S1236T
XH_P47	5	113829120	113829120	Missense_Mutation	SNV	A	G	G	KCNN2	c.359A>G	P.E120G
XH_P47	5	137593359	137593359	Missense_Mutation	SNV	G	A	A	GFRA3	c.754C>T	P.R252W
XH_P47	5	140223201	140223201	Silent	SNV	G	A	A	PCDHA8	c.2295G>A	P.P765P
XH_P47	5	140719676	140719676	Missense_Mutation	SNV	G	A	A	PCDHGA2	c.1138G>A	P.A380T
XH_P47	5	153783750	153783750	Silent	SNV	G	A	A	GALNT10	c.1143G>A	P.P381P
XH_P47	5	156734867	156734867	Missense_Mutation	SNV	C	A	A	CYFIP2	c.894C>A	P.F298L
XH_P47	5	89990181	89990181	Silent	SNV	G	A	A	ADGRV1	c.7608G>A	P.E2536E
XH_P47	6	161027559	161027559	Missense_Mutation	SNV	G	A	A	LPA	c.2735C>T	P.A912V
XH_P47	6	2970988	2970988	Splice_Site	SNV	T	A	A	SERPINB6	c.47+4A>T	
XH_P47	7	107314664	107314664	Silent	SNV	C	T	T	SLC26A4	c.471C>T	P.P157P
XH_P47	7	20738083	20738083	Missense_Mutation	SNV	A	T	T	ABCB5	c.2064A>T	P.E688D
XH_P47	9	21971114	21971114	Frame_Shift_Ins	INDEL	-	CGGGTGAGAGT	CGGGTGAGAGT	CDKN2A	upCGCCACTCTC	P.R82fs
XH_P47	X	71426280	71426281	Frame_Shift_Del	INDEL	AT	-	-	ERCC6L	2336_2337delA	P.D779fs
XH_P48		-	-	Frame_Shift_Del	INS	-	-	-	ARID1A	c.4534del	P.Q1512Rfs+15
XH_P48	11	108205694	108205694	Splice_Site	SNP	A	G	G	ATM	c.8011-2A>G	
XH_P48	20	54948572	54948572	Missense_Mutation	SNP	G	A	A	AURKA	c.746C>T	p.S249L
XH_P48	3	52441415	52441415	Missense_Mutation	SNP	C	A	A	BAP1	c.437G>T	p.R146M
XH_P48	3	52584626	52584626	Nonsense_Mutation	SNP	G	A	A	PBRM1	c.4387C>T	p.Q1463*
XH_P48	1	9775822	9775822	Missense_Mutation	SNP	G	A	G	PIK3CD	c.G365A	p.G122D
XH_P48	1	12520290	12520290	Silent	SNP	G	T	G	VP513D	c.G12426T	p.S4142S
XH_P48	1	19244917	19244917	Missense_Mutation	SNP	G	A	G	IFFO2	c.C902T	p.T301M
XH_P48	1	26608815	26608892	In_Frame_Del	DEL	GGGGCCCGG	-	CTGGGGCCCGG	UBXN11	c.1101_1178del	p.367_393del

XH_P48	1	38227571	38227571	Missense_Mutation	SNP	G	A	G	EPHA10	c.C356T	p.A119V
XH_P48	1	44595426	44595426	Silent	SNP	G	A	G	KLF17	c.G483A	p.S161S
XH_P48	1	52897088	52897088	Frame_Shift_Ins	INS	-	TCCCA	-	ZCCHC11	307_4308insTGC	p.Q1436fs
XH_P48	1	52897090	52897090	Frame_Shift_Ins	INS	-	CACAATA	-	ZCCHC11	05_4306insTAT	p.Q1436fs
XH_P48	1	52956450	52956450	Missense_Mutation	SNP	C	T	C	ZCCHC11	c.G1342A	p.D48N
XH_P48	1	62910675	62910675	Frame_Shift_Ins	INS	-	TTTTTACTTCTTC	-	USP1	5insATTITTTTAC	p.T275fs
XH_P48	1	104120374	104120374	Frame_Shift_Ins	INS	-	TAGTAACCTCTT	-	AMY2B	sATTAATAGTAA	p.G418fs
XH_P48	1	109814029	109814029	Silent	SNP	C	T	C	CELSR2	c.C7698T	p.F2566F
XH_P48	1	119964589	119964589	Silent	SNP	G	A	G	HSDB32	c.G465A	p.P155P
XH_P48	1	149898455	149898455	Silent	SNP	G	A	G	SF3B4	c.C519T	p.T173T
XH_P48	1	151011281	151011281	Missense_Mutation	SNP	C	T	C	BNIP1	c.C212T	p.T71I
XH_P48	1	151090631	151090631	In_Frame_Ins	INS	-	CTC	-	GABPB2	1012_1013insC	p.V338delinsAL
XH_P48	1	155028726	155028726	Splice_Site	SNP	G	A	G	ADAM15	.	.
XH_P48	1	155152211	155152211	Silent	SNP	C	T	C	TRIM46	c.C1011T	p.T337T
XH_P48	1	158687092	158687092	Frame_Shift_Ins	INS	-	ATGATCT	-	OR6K3	13_814insAGAT	p.A272fs
XH_P48	1	159284421	159284421	Frame_Shift_Ins	INS	-	CTCTCTCTCTA	-	OR10J3	29insTAGAAGA	p.T10fs
XH_P48	1	161021110	161021121	In_Frame_Del	DEL	CCACGGGCC	-	GGCCAGGGCCAA	ARHGAP30	c.872_883del	p.291_295del
XH_P48	1	161179685	161179685	Nonsense_Mutation	INS	-	ATATAGTTT	-	NDUFS2	5_667insATATA	M222delinsMIX
XH_P48	1	161179686	161179686	Frame_Shift_Ins	INS	-	TACAA	-	NDUFS2	567_668insTAC	p.H223fs
XH_P48	1	169345860	169345860	Silent	SNP	C	T	C	BLZF1	c.C111T	p.S37S
XH_P48	1	169510051	169510051	Nonsense_Mutation	INS	-	CCITCATCTCC	-	F5	4277insGGAGA	M26_M1427delinsRRX
XH_P48	1	169510052	169510052	Missense_Mutation	SNP	G	T	G	F5	c.C4276A	p.Q1426K
XH_P48	1	196658707	196658707	Nonsense_Mutation	SNP	C	A	C	CFH	c.C1122A	p.C374A
XH_P48	1	197128938	197128938	In_Frame_Ins	INS	-	TGGAAAAATATA	-	ZBTB41	2281insTATATT	E761delinsYIFPE
XH_P48	1	202735617	202735617	Missense_Mutation	SNP	C	G	C	KDM5B	c.G727C	p.V243L
XH_P48	1	203455841	203455841	Silent	SNP	C	T	C	PRELP	c.C981T	p.N327N
XH_P48	1	210857135	210857135	Missense_Mutation	SNP	C	T	C	KCNH1	c.G2377A	p.E793K
XH_P48	1	214556970	214556970	Missense_Mutation	SNP	C	T	C	PTPN14	c.G2228A	p.R743H
XH_P48	1	229568310	229568310	Missense_Mutation	SNP	C	A	C	ACTA1	c.G447T	p.R149S
XH_P48	1	229568312	229568312	Silent	SNP	T	G	T	ACTA1	c.A445C	p.R149R
XH_P48	1	235918911	235918911	Missense_Mutation	SNP	G	T	G	LYST	c.C7096A	p.Q2366K
XH_P48	1	245530204	245530204	Silent	SNP	C	T	C	KIF26B	c.C534T	p.N178N
XH_P48	1	247464181	247464181	Silent	SNP	G	A	G	ZNF496	c.C1404T	p.C468C
XH_P48	1	247875599	247875599	Silent	SNP	G	A	G	OR6F1	c.C459T	p.F153F
XH_P48	1	248525127	248525127	Frame_Shift_Ins	INS	-	ATTGTGTGTGTG	-	OR2T4	46insAATTGTGT	p.H82fs
XH_P48	1	248525128	248525128	Missense_Mutation	SNP	C	G	C	OR2T4	c.C246G	p.H82Q
XH_P48	2	47657021	47657021	Missense_Mutation	SNP	G	A	G	MSH2	c.G1217A	p.R406Q
XH_P48	2	85843529	85843529	Missense_Mutation	SNP	C	T	C	USP39	c.C211T	p.R71W
XH_P48	2	98351053	98351053	Silent	SNP	C	T	C	ZAP70	c.C39T	p.S13S
XH_P48	2	109382974	109382974	Silent	SNP	C	T	C	RANBP2	c.C5979T	p.S1993S
XH_P48	2	109988072	109988072	Missense_Mutation	SNP	G	C	G	SH3RF3	c.G880C	p.D294H
XH_P48	2	109988074	109988074	Frame_Shift_Ins	INS	-	TATCAATTCAG	-	SH3RF3	883insTATCCA	p.D294fs
XH_P48	2	141130660	141130680	In_Frame_Del	DEL	CACCGGAACT	-	RACACCGGAACT	LRP1	10665_10685del	3555_3562del
XH_P48	2	143986215	143986215	Frame_Shift_Ins	INS	-	AT	-	ARHGAP15	c.362_363insAT	p.K121fs
XH_P48	2	143986216	143986216	Nonsense_Mutation	INS	-	CTGTATCTATAA	-	ARHGAP15	TCATACTGTATC	Q122delinsKLLILYLX
XH_P48	2	171264319	171264319	Frame_Shift_Ins	INS	-	GGGG	-	MYO3B	615_2616insGG	p.L872fs
XH_P48	2	171264320	171264320	Nonsense_Mutation	INS	-	GAGAAAAATAG	-	MYO3B	7insTCTTGAGAA	L872delinsLSX
XH_P48	2	175300997	175300997	Silent	SNP	G	A	G	GPR155	c.C2376T	p.N792N
XH_P48	2	179395889	179395889	Silent	SNP	G	A	G	TTN	c.C78258T	p.D26086D
XH_P48	2	179399194	179399194	Frame_Shift_Ins	INS	-	ATGGGTGCTGGG	-	TTN	4953insCTCCAG	p.V24985fs
XH_P48	2	179570009	179570009	Silent	SNP	A	T	A	TTN	c.T25764A	p.P8588P
XH_P48	2	183699643	183699643	In_Frame_Ins	INS	-	ACATCA	-	FRZB	10_911insTGAT	S304delinsMMM
XH_P48	2	183699645	183699645	Frame_Shift_Ins	INS	-	TTCTATT	-	FRZB	08_909insAATA	p.S303fs
XH_P48	2	187559047	187559047	Silent	SNP	G	A	G	FAM171B	c.G147A	p.Q49Q
XH_P48	2	189873670	189873670	Silent	SNP	G	A	G	COL3A1	c.G3546A	p.G1182G
XH_P48	2	198949301	198949301	Frame_Shift_Ins	INS	-	SCCTCAAACTCT	-	PLCL1	061insGCTTCA	p.L354fs
XH_P48	2	203991404	203991404	Missense_Mutation	SNP	G	C	G	NBEAL1	c.G3023C	p.R1008P
XH_P48	2	232323043	232323043	Missense_Mutation	SNP	T	A	T	NCL	c.A1223T	p.E408V
XH_P48	2	232343529	232343534	In_Frame_Del	DEL	TGCTGTC	-	TGCTGTC	ALPP	c.17_22del	p.6_8del
XH_P48	3	39142554	39142554	Missense_Mutation	SNP	G	A	G	GORASP1	c.C103T	p.R35C
XH_P48	3	45030659	45030659	Nonsense_Mutation	INS	-	CAACAACATTAC	-	EXOSC7	insAACAAACAAC	C29_E30delinsX
XH_P48	3	45030660	45030660	Missense_Mutation	SNP	G	T	G	EXOSC7	c.G86T	p.C29F
XH_P48	3	45067909	45067909	Missense_Mutation	SNP	G	T	G	CLEC3B	c.G55T	p.V19F
XH_P48	3	56591278	56591278	Frame_Shift_Ins	INS	-	GGGGCAAGCA	-	CDC66	9insGGGGCAAG	p.L3fs
XH_P48	3	114070652	114070652	Silent	SNP	G	A	G	ZBTB20	c.C273T	p.L91L
XH_P48	3	122829811	122829811	Missense_Mutation	SNP	G	T	G	PDIA5	c.G501T	p.K167N
XH_P48	3	124732416	124732416	In_Frame_Ins	INS	-	AGAGGAGGAGG	-	HEG1	007insCTCTCC	S669delinsSSSSSS
XH_P48	3	128780785	128780785	Missense_Mutation	SNP	C	T	C	GP9	c.C203T	p.P68L
XH_P48	3	130159656	130159656	In_Frame_Ins	INS	-	CAATTCTT	-	COL6A5	4_6475insCAAA	L2158delinsQLI
XH_P48	3	130159658	130159658	Missense_Mutation	SNP	A	T	A	COL6A5	c.A6476T	p.Y2159F
XH_P48	3	151156071	151156071	In_Frame_Ins	INS	-	GGGCATAGCAA	-	IGSF10	TTACTTGTGCTA	20delinsRLYLCPH
XH_P48	4	1980404	1980404	Missense_Mutation	SNP	G	A	G	NSD2	c.G3866A	p.G1289D
XH_P48	4	40434705	40434725	In_Frame_Del	DEL	GCGGCGGCT	-	TGCGGCGGCTG	RBM47	c.1278_1298del	p.426_433del
XH_P48	4	41748011	41748028	In_Frame_Del	DEL	CCGCGCTG	-	GCCGCGCTGCC	PHOX2B	c.741_758del	p.247_253del
XH_P48	4	70146409	70146409	Frame_Shift_Ins	INS	-	CAAGTCACTG	-	UGT2B28	192insCAAGTC	p.F64fs
XH_P48	4	71024600	71024600	Missense_Mutation	SNP	T	C	T	PRR27	c.T631C	p.S211P
XH_P48	4	71232641	71232641	In_Frame_Ins	INS	-	TGG	-	SMR3A	335_336insTGG	p.Y112delinsYG
XH_P48	4	71232643	71232643	Frame_Shift_Ins	INS	-	GGAGAAATCAA	-	SMR3A	insCAGGGAGAA	p.P113fs
XH_P48	4	71698877	71698877	In_Frame_Ins	INS	-	ATCCCAAAAAGC	-	GRSF1	ATTATGGCTTTT	8delinsRLWFLGIIAL
XH_P48	4	71698879	71698879	Missense_Mutation	SNP	G	A	G	GRSF1	c.C140T	p.A47V
XH_P48	4	73968171	73968171	Frame_Shift_Ins	INS	-	TTAAAAATTATA	-	ANKRD17	3742insTATAA	p.L1248fs
XH_P48	4	74124031	74124031	Missense_Mutation	SNP	C	T	C	ANKRD17	c.G355A	p.E119K
XH_P48	4	74853058	74853058	Silent	SNP	C	T	C	PPBP	c.G318A	p.L106L
XH_P48	4	77661599	77661599	Missense_Mutation	SNP	G	A	G	SHROOM3	c.G2273A	p.R758Q
XH_P48	4	108969841	108969841	In_Frame_Ins	INS	-	TAAAGCATAAAA	-	LEF1	8insCCTTTTAT	M383delinsTFLCFIL
XH_P48	4	187126435	187126435	Missense_Mutation	SNP	C	A	C	CYP4V2	c.C1069A	p.H357N
XH_P48	5	16701210	16701210	Silent	SNP	G	A	G	MYO10	c.C3294T	p.D1098D
XH_P48	5	32101308	32101308	Silent	SNP	G	A	G	PDZD2	c.G8316A	p.T2772T
XH_P48	5	39202348	39202348	In_Frame_Ins	INS	-	CAAAACCCAC	-	FYB	1_745insGTGGT	K249delinsVVLK
XH_P48	5	39202349	39202349	Frame_Shift_Ins	INS	-	CCAGG	-	FYB	743_744insCCTC	p.L248fs
XH_P48	5	41934295	41934295	Nonsense_Mutation	INS	-	AAGTGTGAGAA	-	FBXO4	CACAAAAGTGT	tsRHNEGDPNTHSVRTHYX
XH_P48	5	43613100	43613100	Frame_Shift_Ins	INS	-	TGATGTTT	-	NNT	42_243insTGAT	p.N81fs
XH_P48	5	43613102	43613102	Silent	SNP	T	C	T	NNT	c.T244C	p.L82L
XH_P48	5	59995898	59995898	Missense_Mutation	SNP	G	A	G	DEPDC1B	c.C23T	p.P8L
XH_P48	5	64492883	64492883	In_Frame_Ins	INS	-	GAAGAAAAATA	-	ADAMT56	tsGAGAAATTATT	91delinsENYFLVQVQ
XH_P48	5	79029891	79029891	Missense_Mutation	SNP	A	C	A	CMY45	c.A5303C	p.E1768A
XH_P48	5	89821057	89821057	Frame_Shift_Ins	INS	-	SATCGAAGTTCA	-	LYSMD3	50insATGAACCT	p.S17fs
XH_P48	5	90074881	90074881	Frame_Shift_Ins	INS	-	ATTTGATTGGA	-	ADGRV1	050insTTATTGT	p.S4350fs

XH_P48	5	90074883	90074883	Silent	SNP	C	T	C	ADGRV1	c.C13051T	p.L4351L
XH_P48	5	120022350	120022350	Frame_Shift_Ins	INS	-	AGAAATGGGG	-	PRR16	862insAGAAAA	p.T287fs
XH_P48	5	129520069	129520069	Missense_Mutation	SNP	C	T	C	CHSY3	c.C1234T	p.R412C
XH_P48	5	140167861	140167861	Silent	SNP	G	A	G	PCDHA1	c.G1986A	p.T662T
XH_P48	5	140256501	140256501	Missense_Mutation	SNP	G	A	G	PCDHA12	c.G1444A	p.A482T
XH_P48	5	140573473	140573473	Missense_Mutation	SNP	G	A	G	PCDH810	c.G1348A	p.A450T
XH_P48	5	140789268	140789268	Missense_Mutation	SNP	C	T	C	PCDHGB6	c.C1499T	p.A500V
XH_P48	5	141309829	141309829	Nonsense_Mutation	INS	-	AAACAAGATAAA	-	KIA0413	CCAGGAACAAG	248delinsFPGTRX
XH_P48	5	150278015	150278015	Silent	SNP	C	T	C	ZNF300	c.G9A	p.E3E
XH_P48	5	156479460	156479477	In_Frame_Del	DEL	GTGTCTGTTG	-	CGTTGTCGTTGG	HAVCR1	c.568_585del	p.190_195del
XH_P48	5	157214758	157214758	Nonsense_Mutation	INS	-	GTTTGGAGCTG	-	CLINT1	AGGTTCCACAGCT	delinsRTGSMFDELGRLFTAPKLX
XH_P48	5	169680208	169680208	Nonsense_Mutation	INS	-	CTCCCTTTGTT	-	LCP2	AATAAAACAAA	387_R388delinsIKX
XH_P48	6	7583735	7583735	Frame_Shift_Ins	INS	-	TTCCCTTCAATA	-	DSP	4444insTTCCCTC	p.F1481fs
XH_P48	6	16306711	16306711	Missense_Mutation	SNP	G	A	G	ATXN1	c.C2297T	p.P766L
XH_P48	6	33638300	33638300	Silent	SNP	G	A	G	ITPR3	c.G2388A	p.P796P
XH_P48	6	36689438	36689438	Silent	SNP	T	C	T	RAB44	c.T1527C	p.S509S
XH_P48	6	56483868	56483868	In_Frame_Ins	INS	-	CTGTTCCCGCGG	-	DST	1964insCGCGGG	1655delinsTRGTE
XH_P48	6	85457795	85457795	Frame_Shift_Ins	INS	-	TG	-	TBX18	c.781_782insCA	p.H261fs
XH_P48	6	85457797	85457797	Frame_Shift_Ins	INS	-	ATCTTTGT	-	TBX18	9_780insACAAA	p.L260fs
XH_P48	6	112015616	112015616	Missense_Mutation	SNP	G	A	G	FYN	c.C1226T	p.A409V
XH_P48	6	169634853	169634853	Missense_Mutation	SNP	A	T	A	TBHS2	c.T1627A	p.C543S
XH_P48	7	14017062	14017062	Frame_Shift_Ins	INS	-	AAGATGATTGTA	-	ETV1	5insAATCAAAATC	p.Q35fs
XH_P48	7	30062395	30062395	Frame_Shift_Ins	INS	-	AGCA	-	FKBP14	234_235insTGC	p.L79fs
XH_P48	7	30062397	30062397	Frame_Shift_Ins	INS	-	AATGATGAGCTT	-	FKBP14	nsGAGAAAGCTC	p.L78fs
XH_P48	7	30962248	30962248	Missense_Mutation	SNP	A	C	A	AQP1	c.A619C	p.S207R
XH_P48	7	63538640	63538640	In_Frame_Ins	INS	-	TTTCCACATTC	-	ZNF727	1214insTTTCCA	F405delinsFSTFI
XH_P48	7	63726518	63726518	Silent	SNP	A	C	A	ZNF679	c.A507C	p.S169S
XH_P48	7	63726519	63726519	In_Frame_Ins	INS	-	TATCTTCTGGT	-	ZNF679	509insTATCTTC	N170delinsSSWV
XH_P48	7	75511413	75511413	Missense_Mutation	SNP	C	T	C	RHBDD2	c.C445T	p.R149C
XH_P48	7	86415744	86415744	Silent	SNP	C	T	C	GRM3	c.C636T	p.Y212Y
XH_P48	7	97820068	97820068	Frame_Shift_Ins	INS	-	GTGTGTTGTTG	-	LMTK2	1028insGTGTTG	p.F343fs
XH_P48	7	100642572	100642572	Missense_Mutation	SNP	C	T	C	MUC12	c.C8728T	p.P2910S
XH_P48	7	100676465	100676465	Frame_Shift_Del	DEL	A	-	A	MUC17	c.1768delA	p.T590fs
XH_P48	7	100678156	100678156	Silent	SNP	A	G	A	MUC17	c.A3459G	p.S1153S
XH_P48	7	100678157	100678157	Missense_Mutation	SNP	C	A	C	MUC17	c.C3460A	p.P1154T
XH_P48	7	100679025	100679025	Missense_Mutation	SNP	T	C	T	MUC17	c.T4328C	p.I1443T
XH_P48	7	100680862	100680862	Silent	SNP	T	G	T	MUC17	c.T6165G	p.L2055L
XH_P48	7	100682285	100682285	Missense_Mutation	SNP	C	T	C	MUC17	c.C7588T	p.P2530S
XH_P48	7	121653375	121653380	In_Frame_Del	DEL	TGATGA	-	TGATGA	PTPRZ1	c.4275_4280del	p.1425_1427del
XH_P48	7	127977184	127977184	Splice_Site	INS	-	A	-	RBM28	-	-
XH_P48	7	127977186	127977186	In_Frame_Ins	INS	-	GAACACAGGAG	-	RBM28	AACAACCTCTG	3delinsETTPVFMIK
XH_P48	7	148801435	148801435	Nonsense_Mutation	SNP	G	A	G	ZNF425	c.C1528T	p.Q510X
XH_P48	7	149516577	149516577	Missense_Mutation	SNP	C	T	C	SSPO	c.C11980T	p.R3994C
XH_P48	8	1616621	1616621	Missense_Mutation	SNP	G	A	G	DLGAP2	c.G1937A	p.R646H
XH_P48	8	8748825	8748825	Missense_Mutation	SNP	G	A	G	MFHAS1	c.C1744T	p.R582W
XH_P48	8	10555480	10555480	Missense_Mutation	SNP	G	A	G	C8orf74	c.G613A	p.A205T
XH_P48	8	20070343	20070343	Frame_Shift_Ins	INS	-	TCTTTTGGTCT	-	ATP6V1B2	GTGTTTCTTTT	p.L285fs
XH_P48	8	52321924	52321924	Nonsense_Mutation	SNP	G	A	G	PXDNL	c.C2260T	p.Q754X
XH_P48	8	89209477	89209477	Missense_Mutation	SNP	C	T	C	MMP16	c.G191A	p.R64H
XH_P48	8	124105975	124105975	Missense_Mutation	SNP	G	A	G	TBC1D31	c.C349A	p.V117I
XH_P48	9	8449795	8449795	Missense_Mutation	SNP	G	T	G	PTPRD	c.C2655A	p.N885K
XH_P48	9	8449796	8449796	In_Frame_Ins	INS	-	GAGCCA	-	PTPRD	53_2654insTGC	N885delinsMAH
XH_P48	9	35650024	35650024	Missense_Mutation	SNP	G	A	G	SIT1	c.C412T	p.R138W
XH_P48	9	38414187	38414187	Silent	SNP	G	C	G	IGFBPL1	c.C474G	p.V158V
XH_P48	9	91978684	91978684	Silent	SNP	C	T	C	SEMA4D	c.G2064A	p.S688S
XH_P48	9	116183383	116183383	Nonsense_Mutation	INS	-	AGTCCACAGCA	-	C9orf43	GAGAAAGTCCCA	17delinsFPVLNIUWRSPATX
XH_P48	9	123476543	123476551	In_Frame_Del	DEL	CGGCGGCGG	-	CGGCGGCGG	MEGF9	c.86_94del	p.29_32del
XH_P48	9	127920559	127920559	Missense_Mutation	SNP	G	A	G	PPP6C	c.C274T	p.H92Y
XH_P48	9	134312015	134312015	Missense_Mutation	SNP	C	T	C	PRRC2B	c.C302T	p.A101V
XH_P48	9	139701501	139701501	Missense_Mutation	SNP	G	A	G	CCDC183	c.G1469A	p.R490Q
XH_P48	10	49452836	49452836	Silent	SNP	C	T	C	FRMPD2	c.G366A	p.P122P
XH_P48	10	50255037	50255037	Nonsense_Mutation	INS	-	TAAAAATCCAAA	-	VSTM4	insCTATTITGGAT	276delinsNYLDFX
XH_P48	10	70191719	70191719	Missense_Mutation	SNP	T	C	T	DNA2	c.A1883G	p.K628R
XH_P48	10	102265241	102265241	Frame_Shift_Ins	INS	-	CCTACCATGT	-	SEC31B	1056insACATG	p.S352fs
XH_P48	10	112572332	112572332	Missense_Mutation	SNP	G	A	G	RBM20	c.G2177A	p.R726Q
XH_P48	10	120820272	120820272	Missense_Mutation	SNP	G	A	G	EIF3A	c.C1312T	p.R438C
XH_P48	10	125506281	125506281	Silent	SNP	C	T	C	CPXM2	c.G2270A	p.X757X
XH_P48	10	129904528	129904528	Missense_Mutation	SNP	C	T	C	MKI67	c.G4496A	p.C1499Y
XH_P48	11	19970251	19970251	Missense_Mutation	SNP	C	T	C	NAV2	c.C2078T	p.T693M
XH_P48	11	35006258	35006258	Frame_Shift_Ins	INS	-	AAATCATTGTG	-	PDHX	insATAAAATCA	p.I162fs
XH_P48	11	55579515	55579515	Nonsense_Mutation	INS	-	TGTGCTTAGCTC	-	OR5L1	TCATTGTGCTCT	I192delinsDSFVLSXX
XH_P48	11	56058369	56058369	Frame_Shift_Ins	INS	-	CTGCTGAA	-	OR8H1	9_170insTTCAG	p.T57fs
XH_P48	11	57093913	57093913	Frame_Shift_Ins	INS	-	ACAT	-	SSRP1	1097_2098insAT	p.S700fs
XH_P48	11	62289235	62289235	Silent	SNP	G	A	G	AHNAK	c.C12654T	p.D4218D
XH_P48	11	62295157	62295157	Silent	SNP	A	G	A	AHNAK	c.T6732C	p.P2244P
XH_P48	11	62296921	62296921	Silent	SNP	G	A	G	AHNAK	c.C4968T	p.P1656P
XH_P48	11	64622152	64622152	Missense_Mutation	SNP	C	T	C	EHD1	c.G1258A	p.G420R
XH_P48	11	71249250	71249279	In_Frame_Del	DEL	GGGGGCTCC	-	GTGGGGGCTCCA	KRTAP5-8	c.149_178del	p.50_60del
XH_P48	11	71948284	71948284	Missense_Mutation	SNP	C	T	C	INPPL1	c.C2996T	p.P999L
XH_P48	11	116643602	116643602	Missense_Mutation	SNP	C	T	C	BUD13	c.G79A	p.G27R
XH_P48	11	116729011	116729013	In_Frame_Del	DEL	TGT	-	TGT	SIK3	c.2844_2846del	p.948_949del
XH_P48	11	120702655	120702655	Silent	SNP	G	A	G	GRIK4	c.G606A	p.P202P
XH_P48	11	120998539	120998539	Missense_Mutation	SNP	C	T	C	TECTA	c.C1853T	p.T618M
XH_P48	11	126333190	126333190	Missense_Mutation	SNP	C	G	C	KIRREL3	c.G604C	p.D202H
XH_P48	11	129814696	129814696	Silent	SNP	C	T	C	PRDM10	c.G474A	p.S158S
XH_P48	12	7050643	7050643	Silent	SNP	G	A	G	ATN1	c.G3465A	p.L1155L
XH_P48	12	8211836	8211836	Missense_Mutation	SNP	C	G	C	C3AR1	c.G946C	p.D316H
XH_P48	12	46205333	46205333	Silent	SNP	G	A	G	ARID2	c.G417A	p.S139S
XH_P48	12	48921793	48921793	Silent	SNP	C	T	C	OR8S1	c.C987T	p.P329P
XH_P48	12	49446041	49446041	Silent	SNP	G	A	G	KMT2D	c.C1425T	p.P475P
XH_P48	12	49499720	49499720	Missense_Mutation	SNP	C	T	C	LMBR1L	c.G178A	p.V60I
XH_P48	12	53201511	53201511	Silent	SNP	C	T	C	KRT4	c.G1263A	p.E421E
XH_P48	12	65609805	65609805	Frame_Shift_Ins	INS	-	T	-	LEMD3	c.1606_1607ins	p.R536fs
XH_P48	12	65609806	65609806	Frame_Shift_Ins	INS	-	AAGACAAATCTA	-	LEMD3	508insAAAGACA	p.R536fs
XH_P48	12	76424934	76424934	Frame_Shift_Del	DEL	C	-	C	PHLDA1	c.588delG	p.Q196fs
XH_P48	12	76424936	76424940	Frame_Shift_Del	DEL	GTTGC	-	GTTGC	PHLDA1	c.582_586del	p.Q194fs
XH_P48	12	104331531	104331531	Missense_Mutation	SNP	G	A	G	HSP90B1	c.G802A	p.V268I
XH_P48	12	105536308	105536308	Frame_Shift_Ins	INS	-	AAGTCACAAA	-	WASHC4	869insAAAGTCA	p.G623fs

XH_P48	12	133381504	133381504	Silent	SNP	C	T	C	GOLGA3	c.G1395A	p.S465S	
XH_P48	13	49794681	49794681	Missense_Mutation	SNP	C	T	C	MLNR	c.C208T	p.R70W	
XH_P48	13	53217316	53217316	Nonsense_Mutation	INS	-	GCTTTCTAACT	-	HNRNPA11L2	690insGCTTTTC	30_S231delinsGLFX	
XH_P48	13	111935499	111935499	Missense_Mutation	SNP	C	T	C	ARHGEF7	c.C1034T	p.P345L	
XH_P48	14	31067748	31067748	Missense_Mutation	SNP	G	A	G	G2E3	c.G557A	p.R186H	
XH_P48	14	51237623	51237623	Silent	SNP	C	T	C	NIN	c.G1206A	p.S402S	
XH_P48	14	70234970	70234970	Frame_Shift_Ins	INS	-	ATAGCAATGAC	-	SRSF5	98insATAGCAA	p.I33fs	
XH_P48	14	73491142	73491142	Silent	SNP	G	A	G	ZFYVE1	c.C75T	p.S25S	
XH_P48	14	76249770	76249770	Frame_Shift_Ins	INS	-	TTTACTGAACA	-	TTLL5	nsACAATTTTAC	p.P61fs	
XH_P48	14	76249772	76249772	Missense_Mutation	SNP	G	T	G	TTLL5	c.G2885T	p.R962L	
XH_P48	14	89069306	89069306	Frame_Shift_Ins	INS	-	CAAGTTTATAG	-	ZC3H14	AAGTCCCAAGT	p.T370fs	
XH_P48	14	95599763	95599763	Missense_Mutation	SNP	C	T	C	DICER1	c.G33A	p.M11I	
XH_P48	14	105419358	105419358	Silent	SNP	C	T	C	AHNAK2	c.G2130A	p.L710L	
XH_P48	14	105716022	105716022	Silent	SNP	G	A	G	BTBD6	c.G471A	p.L157L	
XH_P48	15	22383148	22383148	Missense_Mutation	SNP	C	T	C	OR4N4	c.C676T	p.R226C	
XH_P48	15	28474440	28474440	Missense_Mutation	SNP	G	A	G	HERC2	c.C5173T	p.R1725W	
XH_P48	15	28949022	28949022	Silent	SNP	C	T	C	GOLGA8M	c.G1242A	p.T414T	
XH_P48	15	34529641	34529641	Silent	SNP	C	T	C	SLC12A6	c.G2868A	p.A956A	
XH_P48	15	48905225	48905225	Missense_Mutation	SNP	C	T	C	FBN1	c.G229A	p.G77R	
XH_P48	15	52684136	52684136	Frame_Shift_Ins	INS	-	GATATACTAATG	-	MYO5A	33insTTCATTAG	p.E511fs	
XH_P48	16	19127388	19127388	Silent	SNP	G	A	G	ITPR1P2	c.G1605A	p.P535P	
XH_P48	16	19718261	19718261	Missense_Mutation	SNP	C	T	C	KNOP1	c.G1279A	p.A427T	
XH_P48	16	24582721	24582721	Nonsense_Mutation	INS	-	GATACTTGACTA	-	RBBP6	233insGGATACT	11_S1412delinsQDTH	
XH_P48	16	27078367	27078367	Silent	SNP	G	A	G	C16orf82	c.G51A	p.G17G	
XH_P48	16	30975994	30975994	Missense_Mutation	SNP	C	T	C	SETD1A	c.C931T	p.R311C	
XH_P48	16	52473381	52473381	In_Frame_Del	DEL	TGC	-	TGC	TOX3	c.1485_1487del	p.495_496del	
XH_P48	16	52473720	52473720	In_Frame_Ins	INS	-	CCATGG	-	TOX3	47_1148insCCAA	1383delinsTMV	
XH_P48	16	56388958	56388958	Frame_Shift_Ins	INS	-	CATAG	-	GNAO1	058_1059insCA	p.L353fs	
XH_P48	16	67470574	67470574	Missense_Mutation	SNP	G	A	G	HSD11B2	c.G886A	p.G296S	
XH_P48	16	87637893	87637893	In_Frame_Ins	INS	-	CTGTGG	-	JPH3	30_431insCTGTG	P144delinsPVA	
XH_P48	16	89351923	89351923	Missense_Mutation	SNP	C	T	C	ANKRD11	c.G1027A	p.V343I	
XH_P48	17	2995996	2995996	Frame_Shift_Ins	INS	-	NTCTACTCCTTT	-	OR1D2	5insGAAAGGAC	p.T99fs	
XH_P48	17	4349436	4349436	Missense_Mutation	SNP	G	A	G	SPN53	c.G115A	p.V39M	
XH_P48	17	4858435	4858435	Silent	SNP	T	C	T	ENO3	c.T381C	p.I27I	
XH_P48	17	5085160	5085160	Frame_Shift_Ins	INS	-	AA	-	ZNF594	2391_2392insT	p.Q798fs	
XH_P48	17	5085389	5085389	Silent	SNP	C	T	C	ZNF594	c.G2163A	p.T721T	
XH_P48	17	7606772	7606772	Missense_Mutation	SNP	G	A	G	WRAP53	c.G1615A	p.G539R	
XH_P48	17	10417165	10417165	Silent	SNP	G	A	G	MYH1	c.C714T	p.T238T	
XH_P48	17	16285335	16285335	Silent	SNP	C	T	C	UBB	c.C114T	p.P38P	
XH_P48	17	16527820	16527820	In_Frame_Ins	INS	-	TTC	-	ZNF624	379_380insGA	M127delinsRM	
XH_P48	17	16527822	16527822	Frame_Shift_Ins	INS	-	CAGACCATTCTC	-	ZNF624	TACAGAGAATG	p.D126fs	
XH_P48	17	26093544	26093544	Silent	SNP	C	T	C	NOS2	c.G2238A	p.P746P	
XH_P48	17	28511908	28511908	Frame_Shift_Ins	INS	-	TCTCTTGTGGTA	-	NSRP1	2insTTTCTCTTG	p.H244fs	
XH_P48	17	29631394	29631394	Frame_Shift_Ins	INS	-	AGCTGATCTTC	-	EV12B	1234insGAAGA	p.K412fs	
XH_P48	17	45234343	45234343	Missense_Mutation	SNP	T	G	T	CDC27	c.A595C	p.N199H	
XH_P48	17	56342311	56342311	Frame_Shift_Ins	INS	-	TCGCTTCGCTT	-	LPO	7insCCTTCGCTT	p.N416fs	
XH_P48	17	56342312	56342312	Missense_Mutation	SNP	A	C	A	LPO	c.A1247C	p.N416T	
XH_P48	17	56572837	56572837	Missense_Mutation	SNP	C	T	C	MTMR4	c.G2666A	p.R889Q	
XH_P48	17	62856031	62856031	Silent	SNP	T	G	T	LRRC37A3	c.A1587C	p.G529G	
XH_P48	17	62856032	62856032	Missense_Mutation	SNP	C	A	C	LRRC37A3	c.G1586T	p.G529V	
XH_P48	17	62856449	62856449	Missense_Mutation	SNP	C	G	C	LRRC37A3	c.G1169C	p.W390S	
XH_P48	17	74449014	74449014	Silent	SNP	G	A	G	UBE2O	c.C210T	p.Y70Y	
XH_P48	17	76212078	76212078	Missense_Mutation	SNP	A	C	A	BIRC5	c.A253C	p.T85P	
XH_P48	18	13731869	13731869	Frame_Shift_Ins	INS	-	AACTCTTTTCTC	-	RNMT	54insAAACTCT	p.S118fs	
XH_P48	18	13731871	13731871	Missense_Mutation	SNP	A	T	A	RNMT	c.A355T	p.T119S	
XH_P48	18	13762106	13762106	Missense_Mutation	SNP	G	A	G	RNMT	c.G1462A	p.A488T	
XH_P48	18	14763838	14763838	In_Frame_Ins	INS	-	GTGTTCTCTGTA	-	ANKRD30B	5insAGGTGTTCT	325delinsSGVPVD	
XH_P48	18	43447706	43447706	Frame_Shift_Ins	INS	-	CTTTTCAT	-	EPG5	2_6233insATGA	p.R2078fs	
XH_P48	18	43447707	43447707	Frame_Shift_Ins	INS	-	ATGAT	-	EPG5	231_6232insAT	p.R2078fs	
XH_P48	19	2850690	2850690	Nonsense_Mutation	INS	-	CAATTCAACATA	-	ZNF555	5sAAAAACAATTCA	F37_Q38delinsX	
XH_P48	19	4298062	4298062	Silent	SNP	C	T	C	TMIGD2	c.G327A	p.A109A	
XH_P48	19	6396559	6396559	Splice_Site	SNP	G	A	G	LOC390877	.	.	
XH_P48	19	17838450	17838450	Missense_Mutation	SNP	A	G	A	MAP15	c.A2179G	p.M727V	
XH_P48	19	20308482	20308482	Silent	SNP	G	A	G	ZNF486	c.G963A	p.P231P	
XH_P48	19	20727555	20727555	Missense_Mutation	SNP	C	T	C	ZNF737	c.G1454A	p.R485Q	
XH_P48	19	20727556	20727556	Missense_Mutation	SNP	G	C	G	ZNF737	c.C1453G	p.R485G	
XH_P48	19	22270841	22270841	Nonsense_Mutation	INS	-	ATAAAACTGTGA	-	ZNF257	AACTATAAAAC	p.K21delinsIX	
XH_P48	19	22271240	22271240	Missense_Mutation	SNP	A	C	A	ZNF257	c.A460C	p.K154Q	
XH_P48	19	22363643	22363643	Silent	SNP	C	T	C	ZNF676	c.G876A	p.S292S	
XH_P48	19	22497365	22497365	Silent	SNP	T	C	T	ZNF729	c.T1146C	p.G382G	
XH_P48	19	23159374	23159374	Silent	SNP	A	G	A	ZNF728	c.T765C	p.H255H	
XH_P48	19	23159375	23159375	Missense_Mutation	SNP	T	G	T	ZNF728	c.A764C	p.H255P	
XH_P48	19	23836292	23836292	Silent	SNP	C	T	C	ZNF675	c.G1443A	p.K481K	
XH_P48	19	23836540	23836540	Missense_Mutation	SNP	T	C	T	ZNF675	c.A1195G	p.K399E	
XH_P48	19	24310035	24310035	Silent	SNP	C	T	C	ZNF254	c.C978T	p.C326C	
XH_P48	19	39034023	39034023	Missense_Mutation	SNP	C	T	C	RYR1	c.C11711T	p.T3904M	
XH_P48	19	42265289	42265289	Missense_Mutation	SNP	C	T	C	CEACAM6	c.C557T	p.P186L	
XH_P48	19	42793204	42793204	Missense_Mutation	SNP	G	A	G	CIC	c.G1096A	p.G366R	
XH_P48	19	44622424	44622424	Silent	SNP	C	T	C	ZNF225	c.C99T	p.Y33Y	
XH_P48	19	45815150	45815150	Silent	SNP	T	C	T	CKM	c.A510G	p.K170K	
XH_P48	19	46327108	46327108	Missense_Mutation	SNP	G	A	G	SYMPK	c.C2516T	p.P839L	
XH_P48	19	47126943	47126943	Silent	SNP	G	A	G	PTGIR	c.C540T	p.G180G	
XH_P48	19	49669431	49669431	Missense_Mutation	SNP	G	A	G	TRPM4	c.G226A	p.G76R	
XH_P48	19	53303666	53303666	Missense_Mutation	SNP	A	G	A	ZNF28	c.T1432C	p.C478R	
XH_P48	19	53303667	53303667	Missense_Mutation	SNP	C	A	C	ZNF28	c.G1431T	p.R477S	
XH_P48	19	53855582	53855582	Missense_Mutation	SNP	C	A	C	ZNF845	c.C1654A	p.Q552K	
XH_P48	19	53885265	53885265	Frame_Shift_Ins	INS	-	CTCTC	-	ZNF525	433_1434insCT	p.F478fs	
XH_P48	19	53885267	53885267	Frame_Shift_Ins	INS	-	TTATG	-	ZNF525	435_1436insTTA	p.K479fs	
XH_P48	19	54314291	54314291	Missense_Mutation	SNP	C	T	C	NLRP12	c.G622A	p.E208K	
XH_P48	19	54745989	54745989	Nonsense_Mutation	SNP	G	A	G	LILRA6	c.C268T	p.Q90X	
XH_P48	20	3129660	3129660	Nonsense_Mutation	INS	-	AGGCTAATGTGT	-	FASTKD5	CAGAACACATT	9_S20delinsPSRTHX	
XH_P48	20	3146192	3146192	Missense_Mutation	SNP	T	C	T	LZT53	c.A1136G	p.Q379R	
XH_P48	20	3181080	3181080	Missense_Mutation	SNP	C	T	C	DDR6K1	c.G316A	p.E106K	
XH_P48	20	3209276	3209276	Missense_Mutation	SNP	G	A	G	SLC4A11	c.C2318T	p.P773L	
XH_P48	20	20180490	20180490	In_Frame_Ins	INS	-	TCCAGAACCCCT	-	CFAP61	TTCAAGTCCAGAA	6delinsFQFQNPYAH	
XH_P48	20	21687201	21687201	Missense_Mutation	SNP	C	T	C	PAX1	c.C412T	p.R138W	
XH_P48	20	48500541	48500541	Missense_Mutation	SNP	G	A	G	SLC9A8	c.G1477A	p.E493K	
XH_P48	20	52775529	52775529	Missense_Mutation	SNP	G	A	G	CYP24A1	c.C1124T	p.P375L	

XH_P48	21	43708018	43708018	Silent	SNP	C	T	C	ABCG1	c.C993T	p.G331G
XH_P48	21	45876639	45876639	Missense_Mutation	SNP	C	T	C	LRR3	c.C112T	p.R38W
XH_P48	21	45959918	45959932	In_Frame_Del	DEL	GGCGCAGCAC	-	GGCGCAGCAGC	KRTAP10-1	c.102_116del	p.34_39del
XH_P48	22	18898452	18898452	Missense_Mutation	SNP	G	-	G	DGCR6	c.G424A	p.V142I
XH_P48	22	19119140	19119140	Silent	SNP	C	T	C	TSSK2	c.C228T	p.Y76Y
XH_P48	22	20800753	20800753	Missense_Mutation	SNP	C	T	C	KLHL22	c.G1516A	p.G506R
XH_P48	22	24981939	24981939	Missense_Mutation	SNP	G	A	G	LRR375B	c.C863T	p.A288V
XH_P48	22	30685456	30685456	Missense_Mutation	SNP	G	A	G	CASTOR1	c.C31T	p.R11W
XH_P48	22	37709524	37709524	Missense_Mutation	SNP	G	A	G	CYTH4	c.G986A	p.R329Q
XH_P48	X	48682589	48682589	Missense_Mutation	SNP	G	A	G	HDAC6	c.G3464A	p.R1155H
XH_P48	X	152087570	152087575	In_Frame_Del	DEL	GAGGAG	-	GAGGAG	ZNF185	c.70_75del	p.24_25del
XH_P48	Y	14968707	14968707	Nonsense_Mutation	INS	-	ACTTAAGATCA	-	USP9Y	TTGTTAACTTAA	8delinsFLERSHSARMTLAKACX
XH_P48	1	196658707	196658707	Nonsense_Mutation	SNV	C	A	A	CFH	c.1122C>A	P.C374*
XH_P48	1	229568310	229568310	Missense_Mutation	SNV	C	A	A	ACTA1	c.447G>T	P.R149S
XH_P48	1	229568312	229568312	Silent	SNV	T	G	G	ACTA1	c.445A>C	P.R149R
XH_P48	1	245530204	245530204	Silent	SNV	C	T	T	KIF26B	c.534C>T	P.N178N
XH_P48	1	247875599	247875599	Silent	SNV	G	A	A	OR6F1	c.459C>T	P.F153F
XH_P48	1	27101252	27101252	Frame_Shift_Del	INDEL	C	-	-	ARID1A	c.4534delC	P.Q1512fs
XH_P48	1	38227571	38227571	Missense_Mutation	SNV	G	A	A	EPHA10	c.356C>T	P.A119V
XH_P48	11	116643602	116643602	Missense_Mutation	SNV	C	T	T	BUD13	c.79G>A	P.G27R
XH_P48	11	126333190	126333190	Missense_Mutation	SNV	C	G	G	KIRREL3	c.604G>C	P.D202H
XH_P48	12	46205333	46205333	Splice_Site	SNV	G	A	A	ARID2	c.417G>A	P.S139S
XH_P48	12	48921793	48921793	Silent	SNV	C	T	T	OR8S1	c.987C>T	P.P329P
XH_P48	12	8211836	8211836	Missense_Mutation	SNV	C	G	G	C3AR1	c.946G>C	P.D316H
XH_P48	13	34398048	34398048	Splice_Site	SNV	C	T	T	RF3C	c.226-6C>T	
XH_P48	16	27078367	27078367	Silent	SNV	G	A	A	C16orf82	c.51G>A	P.G17G
XH_P48	19	17838450	17838450	Missense_Mutation	SNV	A	G	G	MAP15	c.2179A>G	P.M727V
XH_P48	19	46327108	46327108	Missense_Mutation	SNV	G	A	A	SYMPK	c.2516C>T	P.P839L
XH_P48	19	54314291	54314291	Missense_Mutation	SNV	C	T	T	NLRP12	c.622G>A	P.E208K
XH_P48	2	187559047	187559047	Silent	SNV	G	A	A	FAM171B	c.147G>A	P.Q49Q
XH_P48	2	189873670	189873670	Silent	SNV	G	A	A	COL3A1	c.3546G>A	P.G1182G
XH_P48	2	203991404	203991404	Missense_Mutation	SNV	G	C	C	NBEAL1	c.3023G>C	P.R1008P
XH_P48	2	47657021	47657021	Missense_Mutation	SNV	G	A	A	MSH2	c.1217G>A	P.R406Q
XH_P48	20	21687201	21687201	Missense_Mutation	SNV	C	T	T	PAX1	c.412C>T	P.R138W
XH_P48	20	3146192	3146192	Missense_Mutation	SNV	T	C	C	LZTS3	c.1136A>G	P.Q379R
XH_P48	3	122829811	122829811	Missense_Mutation	SNV	G	T	T	PDIA5	c.501G>T	P.K167N
XH_P48	3	45067909	45067909	Missense_Mutation	SNV	G	T	T	CLEC3B	c.55G>T	P.V19F
XH_P48	4	187126435	187126435	Missense_Mutation	SNV	C	A	A	CYP4V2	c.1069C>A	P.H357N
XH_P48	4	71024600	71024600	Missense_Mutation	SNV	T	C	C	PRR27	c.631T>C	P.S211P
XH_P48	5	140256501	140256501	Missense_Mutation	SNV	G	A	A	PCDHA12	c.1444G>A	P.A482T
XH_P48	5	79029891	79029891	Missense_Mutation	SNV	A	C	C	CMYA5	c.5303A>C	P.E1768A
XH_P48	7	30962248	30962248	Missense_Mutation	SNV	A	C	C	AQP1	c.619A>C	P.S207R
XH_P48	7	86415744	86415744	Silent	SNV	C	T	T	GRM3	c.636C>T	P.Y212Y
XH_P48	8	10555480	10555480	Missense_Mutation	SNV	G	A	A	C8orf74	c.613G>A	P.A205T
XH_P48	8	124105975	124105975	Missense_Mutation	SNV	G	A	A	TBC1D31	c.664G>A	P.V222I
XH_P48	8	52321924	52321924	Nonsense_Mutation	SNV	G	A	A	PXDNL	c.2260C>T	P.Q754*
XH_P48	8	89209477	89209477	Missense_Mutation	SNV	C	T	T	MMP16	c.191G>A	P.R64H
XH_P48	9	127920559	127920559	Missense_Mutation	SNV	G	A	A	PPP6C	c.451C>T	P.H151Y
XH_P48	9	38414187	38414187	Silent	SNV	G	C	C	IGFBPL1	c.474C>G	P.V158V
XH_P49	12	25398284	25398284	Missense_Mutation	SNP	C	T	T	KRAS	c.35G>A	p.G12D
XH_P49	2	209113113	209113113	Missense_Mutation	SNP	G	A	A	IDH1	c.394C>T	p.R132C
XH_P49	2	212543784	212543784	Missense_Mutation	SNP	A	T	T	ERBB4	c.1615T>A	p.Y539N
XH_P49	1	6505817	6505879	In_Frame_Del	DEL	CCCCGCCAC	-	CCCCGCCACCC	ESPN	c.1286_1348del	p.429_450del
XH_P49	1	21806606	21806606	Missense_Mutation	SNP	T	G	G	NBPF3	c.T1061G	p.F354C
XH_P49	1	26608815	26608892	In_Frame_Del	DEL	GGGGCCCGG	-	CTGGGGCCCGGGA	UBXN11	c.1101_1178del	p.367_393del
XH_P49	1	39352333	39352333	In_Frame_Ins	INS	-	CCC	-	RHBDL2	.994_995insGGp	A332delinsGA
XH_P49	1	39352335	39352335	Silent	SNP	A	T	A	RHBDL2	c.T993A	p.I331I
XH_P49	1	44071948	44071948	Missense_Mutation	SNP	G	A	G	PTPRF	c.G2609A	p.R870Q
XH_P49	1	47685581	47685581	Silent	SNP	A	C	A	TAL1	c.T330G	p.G110G
XH_P49	1	62676780	62676780	Frame_Shift_Ins	INS	-	CTCTTTGCCCTTC	-	LLTD1	CTATATCTCTTTC	p.R778fs
XH_P49	1	116577828	116577828	Missense_Mutation	SNP	A	T	A	SLC22A15	c.A965T	p.Y322F
XH_P49	1	145281964	145281964	Frame_Shift_Ins	INS	-	AAAT	-	NOTCH2NL	.644_645insAA	p.R215fs
XH_P49	1	145295505	145295505	Silent	SNP	G	C	G	NBPF10	c.G258C	p.L86L
XH_P49	1	151204172	151204172	Missense_Mutation	SNP	C	T	C	PIP5K1A	c.C227T	p.A76V
XH_P49	1	151260439	151260439	Missense_Mutation	SNP	C	T	C	ZNF687	c.C1672T	p.R558C
XH_P49	1	152323605	152323605	Missense_Mutation	SNP	C	G	C	FLG2	c.G6657C	p.Q2219H
XH_P49	1	152327955	152327955	Silent	SNP	G	A	G	FLG2	c.C2307T	p.S769S
XH_P49	1	152328169	152328169	Missense_Mutation	SNP	A	G	A	FLG2	c.T2093C	p.F698S
XH_P49	1	152760050	152760050	Missense_Mutation	SNP	G	A	G	LCE1E	c.G275A	p.S92N
XH_P49	1	155028885	155028885	Missense_Mutation	SNP	C	T	C	ADAM15	c.C968T	p.T323M
XH_P49	1	155447927	155447927	In_Frame_Ins	INS	-	GACACT	-	ASH1L	33_4734insAGT	D1578delinsEV5
XH_P49	1	156513966	156513966	Missense_Mutation	SNP	C	T	C	IQGAP3	c.G2438A	p.R813H
XH_P49	1	160128906	160128906	Frame_Shift_Ins	INS	-	CTCCCTT	-	ATP1A4	.40_641insCTCCC	p.I214fs
XH_P49	1	160784272	160784272	Missense_Mutation	SNP	G	T	G	LY9	c.G793T	p.V265F
XH_P49	1	161495788	161495788	Missense_Mutation	SNP	G	T	G	HSPA6	c.G1340T	p.G447V
XH_P49	1	167059489	167059489	Silent	SNP	G	T	G	GPA33	c.C36A	p.L12L
XH_P49	1	182572417	182572417	Silent	SNP	G	A	G	RGS16	c.C102T	p.C34C
XH_P49	1	183511450	183511450	Nonsense_Mutation	INS	-	AATAACAACCTGA	-	SMG7	TTAAAAATAAC	T511delinsNLKNNNX
XH_P49	1	201178708	201178708	Missense_Mutation	SNP	A	G	A	IGFN1	c.A4687G	p.K1563E
XH_P49	1	214815646	214815646	Nonsense_Mutation	INS	-	GTTTAAATTC	-	CENPF	3966insGTTTT	B22_D1323delinsKFX
XH_P49	1	214815648	214815648	Missense_Mutation	SNP	G	T	G	CENPF	c.G3967T	p.D1323Y
XH_P49	1	221053600	221053600	In_Frame_Ins	INS	-	CATCAACAGCCG	-	HLX	2insGCATCAAC	134delinsQHQQP
XH_P49	1	225594433	225594433	Silent	SNP	G	A	G	LBR	c.C1416T	p.A472A
XH_P49	1	246720806	246720806	Nonsense_Mutation	SNP	G	A	G	TFB2M	c.C433T	p.R145X
XH_P49	1	247039450	247039450	Nonsense_Mutation	SNP	G	A	G	AHCTF1	c.C2977T	p.R993X
XH_P49	2	1926562	1926562	Missense_Mutation	SNP	G	T	G	MYT1L	c.C979A	p.L327M
XH_P49	2	27282121	27282121	Silent	SNP	A	T	A	AGBL5	c.A1938T	p.T646T
XH_P49	2	27282122	27282122	Missense_Mutation	SNP	A	T	A	AGBL5	c.A1939T	p.S647C
XH_P49	2	44021707	44021707	Nonsense_Mutation	INS	-	AAGAATAACTAA	-	DYNC2L1	TATCTAAGAAATA	.44_L145delinsKFX
XH_P49	2	74659644	74659644	Silent	SNP	G	A	G	RTKN	c.C261T	p.G87G
XH_P49	2	97818241	97818241	Missense_Mutation	SNP	T	G	T	ANKRD36	c.T1163G	p.V388G
XH_P49	2	109383732	109383732	Frame_Shift_Ins	INS	-	CTTCAGCTCTCT	-	RANBP2	binsATTTCCTCAG	p.S2246fs
XH_P49	2	182347352	182347352	Frame_Shift_Ins	INS	-	ACATATTACC	-	ITGA4	.1016insACATA	p.V339fs
XH_P49	2	182347354	182347354	Silent	SNP	G	T	G	ITGA4	c.G1017T	p.V339V
XH_P49	2	217142540	217142540	Silent	SNP	G	A	G	MARCH4	c.C720T	p.A240A
XH_P49	3	56651516	56651516	Frame_Shift_Ins	INS	-	TTTGTGTTGTTTC	-	CDC6C	insGTGTTTGTGTT	p.H706fs
XH_P49	3	69271014	69271014	Silent	SNP	C	A	C	FRMD4B	c.G726T	p.V242V
XH_P49	3	137880741	137880743	In_Frame_Del	DEL	TCG	-	TCG	DBR1	c.1623_1625del	p.541_542del

XH_P49	3	160233369	160233369	Splice_Site	SNP	C	A	C	KPNA4	-	-
XH_P49	3	170078979	170078979	Missense_Mutation	SNP	C	T	C	SKIL	c.C860T	p.P287L
XH_P49	3	192516360	192516360	Nonsense_Mutation	SNP	G	A	G	MB21D2	c.C1291T	p.R431X
XH_P49	3	195512139	195512186	In_Frame_Del	DEL	AGAAGAGAG	-	AAGAAGAGAGG	MUC4	c.6265_6312del	p.2089_2104del
XH_P49	4	71232641	71232641	In_Frame_Ins	INS	-	TGG	-	SMR3A	c.335_336insTG	p.V112delinsYG
XH_P49	4	71232643	71232643	Frame_Shift_Ins	INS	-	GGAGAATTCAA	-	SMR3A	insCAGGGAGAA	p.P113fs
XH_P49	4	140811081	140811081	Frame_Shift_Del	DEL	C	-	C	MAML3	c.1509delG	p.Q503fs
XH_P49	4	140811083	140811096	Frame_Shift_Del	DEL	TGCTGCTGCT	-	CTGCTGCTGCTG	MAML3	c.1494_1507del	p.Q498fs
XH_P49	4	158262598	158262598	Missense_Mutation	SNP	C	A	C	GRIA2	c.C2027A	p.P676N
XH_P49	4	190873379	190873379	Missense_Mutation	SNP	A	G	A	FRG1	c.A196G	p.K66E
XH_P49	5	38952475	38952475	Nonsense_Mutation	INS	-	GTATTTGTTACA	-	RICTOR	TACAAATGTAAC	84delinsYKCNKYIX
XH_P49	5	43613100	43613100	Frame_Shift_Ins	INS	-	TGATGTTTC	-	NTT	2_243insTGATG	p.N81fs
XH_P49	5	58289266	58289266	In_Frame_Ins	INS	-	ACA	-	PDE4D	c.275_276insTG	p.L92delinsLV
XH_P49	5	58289268	58289268	Nonsense_Mutation	INS	-	TTCTTAGTTTAA	-	PDE4D	TAATAAAACT	L92_193delinsSX
XH_P49	5	102343295	102343295	Nonsense_Mutation	INS	-	TTGACTCTCTAG	-	PAM	829insTTTGACT	610_F611delinsVX
XH_P49	5	127419934	127419934	Silent	SNP	G	T	G	SLC12A2	c.G288T	p.A96A
XH_P49	5	128797089	128797089	Missense_Mutation	SNP	C	A	C	ADAMTS19	c.C386A	p.P129Q
XH_P49	5	140503078	140503078	Missense_Mutation	SNP	G	A	G	PCDH8A	c.G1498A	p.A500T
XH_P49	5	140574045	140574045	Silent	SNP	C	G	C	PCDH8B10	c.C1920G	p.L640L
XH_P49	5	140795081	140795081	Missense_Mutation	SNP	C	T	C	PCDHGA10	c.C2339T	p.A780V
XH_P49	5	177636395	177636395	Missense_Mutation	SNP	G	A	G	HNRNPAB	c.G734A	p.R245H
XH_P49	6	4995510	4995510	Silent	SNP	A	G	A	RPP40	c.T825C	p.C275C
XH_P49	6	26240753	26240753	Missense_Mutation	SNP	G	A	G	HIST1H4F	c.G100A	p.A34T
XH_P49	6	35280286	35280286	Missense_Mutation	SNP	C	A	C	DEF6	c.C631A	p.Q211K
XH_P49	6	96997335	96997335	Missense_Mutation	SNP	C	G	C	UFL1	c.C1568G	p.S523C
XH_P49	6	152461140	152461140	Missense_Mutation	SNP	C	T	C	SYNE1	c.G1937A	p.R646H
XH_P49	6	152671362	152671362	Missense_Mutation	SNP	G	C	G	SYNE1	c.C11842G	p.P3948A
XH_P49	7	6838148	6838148	In_Frame_Ins	INS	-	TTAGGCTATTTA	-	RSPH10B	8insGTTTTAGGC	863delinsSFRFLIV
XH_P49	7	42977123	42977123	Frame_Shift_Ins	INS	-	ACGTCTATGTT	-	MRPL32	c.516insACGCTC	p.K172fs
XH_P49	7	57528754	57528754	In_Frame_Ins	INS	-	ATCTTCTCA	-	ZNF716	7_588insATCTT	M196delinsSSQ
XH_P49	7	57528755	57528755	Frame_Shift_Ins	INS	-	TATCA	-	ZNF716	588_589insTAT	p.M196fs
XH_P49	7	100676748	100676748	Missense_Mutation	SNP	C	G	C	MUC17	c.C2051G	p.T684S
XH_P49	7	100677833	100677833	Missense_Mutation	SNP	C	A	C	MUC17	c.C3136A	p.R1046S
XH_P49	7	100681022	100681022	Missense_Mutation	SNP	C	G	C	MUC17	c.C6325G	p.L1209V
XH_P49	7	142562074	142562074	Silent	SNP	C	T	C	EPH6	c.C516T	p.S172S
XH_P49	7	151945256	151945256	Nonsense_Mutation	SNP	G	A	G	KMT2C	c.C2263T	p.Q755X
XH_P49	8	27146721	27146721	Missense_Mutation	SNP	G	T	G	TRIM35	c.C743A	p.A248E
XH_P49	8	39634659	39634659	Nonsense_Mutation	SNP	C	A	C	ADAM2	c.G856T	p.E286X
XH_P49	8	41566342	41566342	Missense_Mutation	SNP	A	T	A	ANK1	c.T1952A	p.V651E
XH_P49	8	67590053	67590053	Missense_Mutation	SNP	G	A	G	C8orf44	c.G110A	p.R37Q
XH_P49	8	71646207	71646207	In_Frame_Ins	INS	-	AAAAAAATAAAA	-	XKR9	AAAACAAAAAA	24delinsQNKIKNI
XH_P49	8	116426722	116426722	Silent	SNP	C	T	C	TRP51	c.G3387A	p.P1129P
XH_P49	8	144522387	144522389	In_Frame_Del	DEL	GAG	-	GAG	ZC3H3	c.2637_2639del	p.879_880del
XH_P49	9	27185588	27185588	Frame_Shift_Ins	INS	-	AT	-	TEK	c.847_848insAT	p.A283fs
XH_P49	9	35075746	35075746	Silent	SNP	G	A	G	FANCG	c.C1149T	p.S383S
XH_P49	9	103261137	103261137	Missense_Mutation	SNP	A	C	A	SANTD3-TMEF	c.A509C	p.K170T
XH_P49	9	103261139	103261139	In_Frame_Ins	INS	-	ATTGGCTTTTAA	-	SANTD3-TMEF	5ATATATTGGC	17delinsYVGFLLR
XH_P49	10	49659092	49659092	Silent	SNP	C	T	C	ARHGAP22	c.G810A	p.P270P
XH_P49	10	75294415	75294415	Missense_Mutation	SNP	C	T	C	USP54	c.G1258A	p.G420R
XH_P49	10	79571808	79571808	Missense_Mutation	SNP	C	T	C	DLG5	c.G4196A	p.G1399D
XH_P49	10	121432046	121432046	Missense_Mutation	SNP	G	A	G	BAG3	c.G787A	p.A263T
XH_P49	10	129905618	129905618	In_Frame_Ins	INS	-	AGC	-	MKI67	3405_3406insG	S1136delinsAS
XH_P49	10	133950788	133950788	Missense_Mutation	SNP	G	A	G	JAKMIP3	c.G1063A	p.V355M
XH_P49	11	4967552	4967552	In_Frame_Ins	INS	-	AAGATTATA	-	OR51A4	8_779insTTAAA	A260delinsVKSS
XH_P49	11	55579515	55579515	Nonsense_Mutation	INS	-	TGTGCTAGCTC	-	OR5L1	TCACCTGTGCTT	L192delinsDSLVLSSX
XH_P49	11	59982088	59982088	Splice_Site	INS	-	TGATTAATCCTT	-	MS4A4E	-	-
XH_P49	11	60511243	60511243	In_Frame_Ins	INS	-	AATTTTTTCTTC	-	MS4A18	insATAATTTTTT	287delinsHNFFLPs
XH_P49	11	60670301	60670301	Missense_Mutation	SNP	C	T	C	PRPF19	c.G299A	p.R100H
XH_P49	11	62293810	62293810	Silent	SNP	A	G	A	AHNAK	c.T8079C	p.P2693P
XH_P49	11	62294227	62294227	Silent	SNP	A	G	A	AHNAK	c.T7662C	p.N254N
XH_P49	11	66411364	66411384	In_Frame_Del	DEL	GCTGCAGCA	-	TGCTGCAGCAG	RBM14-RBM4	c.781_801del	p.261_267del
XH_P49	11	68359155	68359155	Missense_Mutation	SNP	G	A	G	PPP6R3	c.G1810A	p.E604K
XH_P49	11	68359157	68359157	Nonsense_Mutation	INS	-	ATAAACACCTAA	-	PPP6R3	TAATAATATAAC	p.E604delinsEX
XH_P49	11	71277138	71277197	In_Frame_Del	DEL	GCTGCCAGT	-	TGCTGCCAGTCT	KRTAP5-10	c.505_564del	p.169_188del
XH_P49	11	118374778	118374778	Frame_Shift_Ins	INS	-	ATGGAATGCT	-	KMT2A	8172insATGGA	p.D2724fs
XH_P49	11	118376151	118376151	Frame_Shift_Ins	INS	-	AAGG	-	KMT2A	544_9545insAA	p.N3182fs
XH_P49	11	118376153	118376153	Frame_Shift_Ins	INS	-	TGCTA	-	KMT2A	546_9547insTG	p.N3182fs
XH_P49	12	39223248	39223248	Missense_Mutation	SNP	C	T	C	CPNE8	c.G340A	p.G114R
XH_P49	12	50747905	50747905	Frame_Shift_Ins	INS	-	ATTTT	-	FAM186A	709_2710insAA	p.E904fs
XH_P49	12	52964517	52964517	Missense_Mutation	SNP	C	T	C	KRT74	c.G944A	p.R315H
XH_P49	12	53162773	53162775	In_Frame_Del	DEL	ACT	-	ACT	KRT76	c.1639_1641del	p.547_547del
XH_P49	12	56559303	56559303	Missense_Mutation	SNP	G	T	G	SMARCC2	c.C2938A	p.P980T
XH_P49	12	57463044	57463044	Nonsense_Mutation	INS	-	TTAATGTGATT	-	NEMP1	8insATAATACAC	3_F174delinsHNTHX
XH_P49	12	85492233	85492233	Silent	SNP	A	T	A	LRRIQ1	c.A2988T	p.L996L
XH_P49	12	117287228	117287228	Missense_Mutation	SNP	C	T	C	RNF21	c.C1310T	p.T437M
XH_P49	12	123333143	123333143	Silent	SNP	C	T	C	HIP1R	c.C288T	p.D96D
XH_P49	12	123834966	123834966	Nonsense_Mutation	INS	-	TTTTTTTTT	-	SBN01	2_23insAAAAAA	p.L8delinsX
XH_P49	12	123834968	123834968	Frame_Shift_Ins	INS	-	GATAG	-	SBN01	20_21insCTAT	p.D7fs
XH_P49	12	124829281	124829281	Missense_Mutation	SNP	C	A	C	NCOR2	c.G4546T	p.A1516S
XH_P49	12	125396296	125396296	Silent	SNP	A	G	A	UBC	c.T2022C	p.T674T
XH_P49	12	133306450	133306450	Silent	SNP	T	C	T	ANKLE2	c.A2298G	p.R766R
XH_P49	12	133306452	133306452	In_Frame_Ins	INS	-	TGACATTTTCACT	-	ANKLE2	insGAAAGTGA	766delinsEEMsAR
XH_P49	13	46543289	46543289	Frame_Shift_Ins	INS	-	A	-	ZC3H13	c.3389dupT	p.F1130fs
XH_P49	13	53217447	53217447	Missense_Mutation	SNP	G	A	G	HNRNP1A12	c.G820A	p.G274R
XH_P49	14	75150153	75150153	Frame_Shift_Ins	INS	-	TAAAAATAATAC	-	AREL1	sAAAGGTATTAT	p.V109fs
XH_P49	14	105416378	105416378	Missense_Mutation	SNP	G	A	G	AHNAK2	c.C5110T	p.R1704W
XH_P49	15	23686518	23686518	Silent	SNP	T	C	T	GOLGA6L2	c.A1104G	p.E368E
XH_P49	15	41854918	41854918	Splice_Site	SNP	T	G	T	TYRO3	-	-
XH_P49	15	55710197	55710235	Frame_Shift_Del	DEL	CTTTTGTGAT	-	TCTTTTGTGATTC	DNAAF4	c.1144_1182del	p.*382fs
XH_P49	15	65684700	65684700	Missense_Mutation	SNP	C	A	A	IGDC24	c.G1894T	p.A632S
XH_P49	15	84909507	84909507	Silent	SNP	C	T	C	GOLGA6L4	c.C1401T	p.A467A
XH_P49	15	85788472	85788472	Missense_Mutation	SNP	G	A	G	GOLGA6L3	c.G1165A	p.D389N
XH_P49	15	89398825	89398825	Silent	SNP	C	T	C	ACAN	c.C3009T	p.T1003T
XH_P49	15	89398826	89398826	Missense_Mutation	SNP	A	G	A	ACAN	c.A3010G	p.T1004A
XH_P49	15	93515552	93515552	Nonsense_Mutation	SNP	C	T	C	CHD2	c.C2410T	p.R804X
XH_P49	16	1440694	1440694	Missense_Mutation	SNP	G	A	G	UNKL	c.C1025T	p.A342V
XH_P49	16	20976195	20976195	Missense_Mutation	SNP	C	T	C	DNAH3	c.G8873A	p.G2958E
XH_P49	16	27215421	27215421	Missense_Mutation	SNP	G	A	G	KDM8	c.G8A	p.R3H

XH_P49	16	57397448	57397448	Missense_Mutation	SNP	C	T	C	CCL22	c.C230T	p.A77V
XH_P49	16	72991713	72991715	In_Frame_Del	DEL	CCA	-	CCA	ZFH3	c.2330_2332del	p.777_778del
XH_P49	17	1961638	1961638	Missense_Mutation	SNP	C	T	C	HIC1	c.C1711T	p.R571W
XH_P49	17	3627502	3627502	Silent	SNP	G	A	G	HASPIN	c.G273A	p.R91R
XH_P49	17	7793996	7793996	Frame_Shift_Ins	INS	-	ATACCATATCTT	-	CHD3	499insATACCAT	p.H166fs
XH_P49	17	9760894	9760894	Splice_Site	SNP	G	T	G	GLP2R	-	-
XH_P49	17	16097954	16097954	Splice_Site	INS	-	AAATTATCTT	-	NCOR1	-	-
XH_P49	17	16285383	16285383	Silent	SNP	T	C	T	UBB	c.T162C	p.R54R
XH_P49	17	18291544	18291544	Silent	SNP	A	G	A	EVPLL	c.A888G	p.P296P
XH_P49	17	27216004	27216004	Silent	SNP	G	A	G	FLOT2	c.C90T	p.G30G
XH_P49	17	28380902	28380902	In_Frame_Ins	INS	-	CCTTCTACT	-	EFCAB5	2_1763insCCTT	p.I588delinsTFYL
XH_P49	17	65888128	65888128	Frame_Shift_Ins	INS	-	TT	-	BPTF	.2033_2034insT	p.K678fs
XH_P49	17	65888129	65888129	Nonsense_Mutation	INS	-	TAACCACC	-	BPTF	4_2035insTAAC	p.678_1679delinsKX
XH_P49	17	78064053	78064145	In_Frame_Del	DEL	CAGGCACG	-	CAGGCACGTG	CCDC40	c.2948_3040del	p.983_1014del
XH_P49	18	13731869	13731869	In_Frame_Ins	INS	-	ACTCTTTCTCTT	-	RNMT	insAAACTCTTT	p.118delinsS5NFLFL
XH_P49	18	13731871	13731871	Missense_Mutation	SNP	A	G	A	RNMT	c.A355G	p.T119A
XH_P49	18	14763840	14763840	Frame_Shift_Ins	INS	-	TTCCTGTA	-	ANKRD30B	6_977insTTCCT	p.G326fs
XH_P49	18	29419411	29419411	Frame_Shift_Ins	INS	-	AAGGTTTGAGC	-	TRAPPC8	AAATAAAGCTCA	p.E1283fs
XH_P49	18	56587569	56587569	Missense_Mutation	SNP	C	T	C	ZNF532	c.C2050T	p.P684s
XH_P49	19	2805117	2805117	Silent	SNP	C	T	C	THOP1	c.C693T	p.C231C
XH_P49	19	3964978	3964978	Missense_Mutation	SNP	G	A	G	DAPK3	c.C74T	p.A25V
XH_P49	19	4366559	4366559	Silent	SNP	G	A	G	SH3GL1	c.C126T	p.V42V
XH_P49	19	5231496	5231496	Silent	SNP	C	T	C	PTPRS	c.G1941A	p.P647P
XH_P49	19	7707889	7707889	Silent	SNP	C	G	C	STXB2	c.C972G	p.S324s
XH_P49	19	8191415	8191415	Missense_Mutation	SNP	G	A	G	FBN3	c.C2491T	p.R831W
XH_P49	19	11465349	11465349	Missense_Mutation	SNP	A	T	A	CCDC159	c.A866T	p.K289M
XH_P49	19	12817546	12817546	Missense_Mutation	SNP	G	A	G	TNPO2	c.C1334T	p.S445L
XH_P49	19	12903507	12903507	Missense_Mutation	SNP	G	A	G	JUNB	c.G922A	p.A308T
XH_P49	19	20727918	20727918	Missense_Mutation	SNP	C	G	C	ZNF737	c.G1091C	p.S364T
XH_P49	19	21300069	21300069	Missense_Mutation	SNP	T	A	T	ZNF714	c.T599A	p.T200Y
XH_P49	19	21476689	21476689	Missense_Mutation	SNP	T	C	T	ZNF708	c.A887G	p.E296G
XH_P49	19	21477189	21477189	Silent	SNP	T	C	T	ZNF708	c.A387G	p.E129E
XH_P49	19	21720507	21720507	Missense_Mutation	SNP	G	C	G	ZNF429	c.G1460C	p.R487T
XH_P49	19	21909915	21909915	Missense_Mutation	SNP	A	G	A	ZNF100	c.T554C	p.F185S
XH_P49	19	21990712	21990795	In_Frame_Del	DEL	TATGTGTAG	-	TTATGTGTAGA	ZNF43	c.1849_1932del	p.617_644del
XH_P49	19	22154797	22154797	Silent	SNP	T	G	T	ZNF208	c.A3039C	p.S1013S
XH_P49	19	22155346	22155346	Silent	SNP	T	C	T	ZNF208	c.A2490G	p.E830E
XH_P49	19	22157238	22157238	Missense_Mutation	SNP	A	G	A	ZNF208	c.T598C	p.S200P
XH_P49	19	22157239	22157239	Missense_Mutation	SNP	A	T	A	ZNF208	c.T597A	p.N199K
XH_P49	19	22171625	22171625	Silent	SNP	T	C	T	ZNF208	c.A90G	p.R30R
XH_P49	19	22363008	22363008	Missense_Mutation	SNP	C	G	C	ZNF676	c.G1511C	p.R504P
XH_P49	19	22497383	22497383	Silent	SNP	T	A	T	ZNF729	c.T1164A	p.S388S
XH_P49	19	22498461	22498461	Missense_Mutation	SNP	T	G	T	ZNF729	c.T2242G	p.S748A
XH_P49	19	22499413	22499413	Missense_Mutation	SNP	A	T	A	ZNF729	c.A3194T	p.E1065V
XH_P49	19	22499464	22499464	Missense_Mutation	SNP	A	G	A	ZNF729	c.A3245G	p.D1082G
XH_P49	19	22499532	22499532	Missense_Mutation	SNP	C	A	C	ZNF729	c.C3313A	p.Q1105K
XH_P49	19	23836540	23836540	Missense_Mutation	SNP	T	C	T	ZNF675	c.A1195G	p.K399E
XH_P49	19	24310638	24310638	Frame_Shift_Ins	INS	-	TCCTTCAGTAT	-	ZNF254	AGGGTTTCTCTT	p.F527fs
XH_P49	19	39088190	39088190	Nonsense_Mutation	INS	-	ACACCTACCTAT	-	MAP4K1	714insAATAGG	p.72_R573delinsNRX
XH_P49	19	43233310	43233310	Missense_Mutation	SNP	A	T	A	PSG3	c.T1208A	p.M403K
XH_P49	19	46095085	46095085	Missense_Mutation	SNP	G	A	G	GPRA	c.C40T	p.R14C
XH_P49	19	49926531	49926536	In_Frame_Del	DEL	CAGCAG	-	CAGCAG	PTH2	c.61_66del	p.21_22del
XH_P49	19	53058737	53058737	Silent	SNP	C	T	C	ZNF808	c.C2568T	p.F856F
XH_P49	19	53058738	53058738	Missense_Mutation	SNP	A	G	A	ZNF808	c.A2569G	p.S857G
XH_P49	19	53854248	53854248	Nonsense_Mutation	INS	-	TTCCACTTAAGT	-	ZNF845	TAGGTTTCCACT	p.107delinsKYKHQX
XH_P49	19	53856223	53856223	Silent	SNP	C	T	C	ZNF845	c.C2295T	p.H765H
XH_P49	19	53959342	53959342	Silent	SNP	C	T	C	ZNF761	c.C1581T	p.C527C
XH_P49	19	58050159	58050159	Nonsense_Mutation	INS	-	GTGTGGAT	-	ZNF549	8_1749insGTGT	p.583_K584delinsX
XH_P49	19	58850358	58850441	In_Frame_Del	DEL	GCACCTGAC	-	CGCACCTGACTC	ZSCAN22	c.1142_1225del	p.381_409del
XH_P49	20	13279730	13279730	Missense_Mutation	SNP	G	A	G	ISM1	c.G1019A	p.R340H
XH_P49	20	42788391	42788391	Silent	SNP	G	A	G	JPH2	c.C1036T	p.L346L
XH_P49	20	44505644	44505644	Silent	SNP	G	A	G	ZSWIM3	c.G447A	p.S149S
XH_P49	21	41711106	41711106	Missense_Mutation	SNP	G	A	G	DSCAM	c.C1447T	p.R483C
XH_P49	21	44592356	44592356	Missense_Mutation	SNP	G	A	G	CCGAA	c.G488A	p.CR163Q
XH_P49	22	38153807	38153818	In_Frame_Del	DEL	CCCGCACCC	-	GCCCGCACCCCA	TRIOBP	c.736_747del	p.246_249del
XH_P49	X	3530324	3530324	Missense_Mutation	SNP	T	C	T	PRKX	c.A994G	p.N332D
XH_P49	X	10106856	10106856	Silent	SNP	C	T	C	WWC3	c.C2964T	p.C988C
XH_P49	X	16870993	16870993	Missense_Mutation	SNP	T	A	T	RBBP7	c.A896T	p.D299V
XH_P49	X	17745550	17745550	Frame_Shift_Ins	INS	-	AGTAAAGA	-	NHS	0_2731insAGTA	p.L910fs
XH_P49	X	17745551	17745551	Nonsense_Mutation	INS	-	TGAACCTCCAA	-	NHS	732insCTTGAA	p.H911delinsPX
XH_P49	X	22117166	22117166	In_Frame_Ins	INS	-	CTATTGCTCTTT	-	PHEX	977insCTATTGT	p.L326delinsPIVFF
XH_P49	X	23411203	23411203	Frame_Shift_Ins	INS	-	GAGAAACC	-	PTCHD1	8_1569insGAGA	p.S523fs
XH_P49	X	49179717	49179717	Silent	SNP	A	G	A	GAGE12J	c.A45G	p.R15R
XH_P49	X	49179719	49179719	Missense_Mutation	SNP	C	G	C	GAGE12J	c.C47G	p.P16R
XH_P49	X	50654021	50654021	Missense_Mutation	SNP	T	A	T	BMP15	c.T238A	p.S80T
XH_P49	X	54784914	54784914	Silent	SNP	C	A	C	ITI6	c.G1593T	p.V531V
XH_P49	X	55748688	55748688	Missense_Mutation	SNP	G	T	G	RRAGB	c.G196T	p.A66S
XH_P49	X	77276481	77276481	Frame_Shift_Ins	INS	-	TCCAATGAATTA	-	ATP7A	TTTGTTTCCAAT	p.F863fs
XH_P49	X	109695944	109695944	Frame_Shift_Ins	INS	-	TTTGTGGG	-	RTL9	99_2100insTTTG	p.Q700fs
XH_P49	X	109695945	109695945	In_Frame_Ins	INS	-	CAG	-	RTL9	2100_2101insC	p.Q700delinsQQ
XH_P49	X	135291512	135291512	Missense_Mutation	SNP	G	T	G	FHL1	c.G799T	p.G267C
XH_P49	X	135312740	135312740	Frame_Shift_Ins	INS	-	ACTAAGAAAGTTT	-	MAP7D3	449insTAAACTT	p.Q483fs
XH_P49	1	116577828	116577828	Missense_Mutation	SNV	A	T	T	SLC22A15	c.965A>T	p.Y322F
XH_P49	1	155028885	155028885	Missense_Mutation	SNV	C	T	T	ADAM15	c.968C>T	p.T323M
XH_P49	1	167059489	167059489	Silent	SNV	G	T	T	GPA33	c.36C>A	p.L12L
XH_P49	1	225594433	225594433	Silent	SNV	G	A	A	LBR	c.1416C>T	p.A472A
XH_P49	1	246720806	246720806	Nonsense_Mutation	SNV	G	A	A	TFB2M	c.433C>T	p.R145*
XH_P49	1	32126732	32126732	Splice_Site	SNV	A	G	G	COL16A1	c.3772-12T>C	-
XH_P49	10	133950788	133950788	Missense_Mutation	SNV	G	A	A	JAKMIP3	c.1279G>A	p.V427M
XH_P49	10	51853613	51853613	Splice_Site	SNV	C	G	G	FAM21A	c.1123-7C>G	-
XH_P49	10	75294415	75294415	Missense_Mutation	SNV	C	T	T	USP54	c.1258G>A	p.G420R
XH_P49	12	123333143	123333143	Silent	SNV	C	T	T	HIP1R	c.288C>T	p.D96D
XH_P49	12	124829281	124829281	Missense_Mutation	SNV	C	A	A	NCOR2	c.4546G>T	p.A1516S
XH_P49	12	39223248	39223248	Missense_Mutation	SNV	C	T	T	CPNE8	c.340G>A	p.G114R
XH_P49	12	56559303	56559303	Missense_Mutation	SNV	G	T	T	SMARCC2	c.3031C>A	p.P1011T
XH_P49	12	85492233	85492233	Silent	SNV	A	T	T	LRRIQ1	c.2988A>T	p.L196L
XH_P49	15	78213671	78213671	Splice_Site	SNV	G	A	A	LOC645752	n.590+7C>T	-
XH_P49	15	84909507	84909507	Silent	SNV	C	T	T	GOLGA6L4	c.1401C>T	p.A467A

XH_P49	16	1440694	1440694	Missense_Mutation	SNV	G	A	A	UNKL	c.1025C>T	P.A342V
XH_P49	16	20976195	20976195	Missense_Mutation	SNV	C	T	T	DNAH3	c.9011G>A	P.G3004E
XH_P49	17	9760894	9760894	Splice_Site	SNV	G	T	T	GLP2R	c.765+1G>T	
XH_P49	19	11465349	11465349	Missense_Mutation	SNV	A	T	T	CCDC159	c.866A>T	P.K289M
XH_P49	19	12903507	12903507	Missense_Mutation	SNV	G	A	A	JUNB	c.922G>A	P.A308T
XH_P49	19	4366559	4366559	Silent	SNV	G	A	A	SH3GL1	c.126C>T	P.V42V
XH_P49	19	46095085	46095085	Missense_Mutation	SNV	G	A	A	GPR4	c.40C>T	P.R14C
XH_P49	19	53456137	53456137	Splice_Site	INDEL	-	A	A	ZNF816	c.64-8dupT	
XH_P49	19	7707889	7707889	Silent	SNV	C	G	G	STXB2	c.972C>G	P.S324S
XH_P49	19	8191415	8191415	Missense_Mutation	SNV	G	A	A	FBN3	c.2491C>T	P.R831W
XH_P49	2	1926562	1926562	Missense_Mutation	SNV	G	T	T	MYT1L	c.979C>A	P.L327M
XH_P49	2	217142540	217142540	Silent	SNV	G	A	A	MARCH4	c.720C>T	P.A240A
XH_P49	2	74659644	74659644	Silent	SNV	G	A	A	RTKN	c.261C>T	P.G87G
XH_P49	20	44505644	44505644	Silent	SNV	G	A	A	ZSWIM3	c.447G>A	P.S149S
XH_P49	21	44592356	44592356	Missense_Mutation	SNV	G	A	A	LOC102724652	c.488G>A	P.R163Q
XH_P49	22	38153807	38153818	Missense_Mutation	INDEL	CCCCCACCCG	-	-	TRIOBP	5894delCCCCAGG	P1962_11965del
XH_P49	3	160233369	160233369	Splice_Site	SNV	C	A	A	KPNA4	c.904-1G>T	
XH_P49	3	170078979	170078979	Missense_Mutation	SNV	C	T	T	SKIL	c.860C>T	P.P287L
XH_P49	3	192516360	192516360	Nonsense_Mutation	SNV	G	A	A	MB21D2	c.1291C>T	P.R431*
XH_P49	4	158262598	158262598	Missense_Mutation	SNV	C	A	A	GRIA2	c.2027C>A	P.1676N
XH_P49	5	128797089	128797089	Missense_Mutation	SNV	C	A	A	ADAMTS19	c.386C>A	P.P129Q
XH_P49	5	179318597	179318597	Splice_Site	SNV	A	C	C	TBC1D9B	c.837-11T>G	
XH_P49	6	152461140	152461140	Missense_Mutation	SNV	C	T	T	SYNE1	c.25259G>A	P.R8420H
XH_P49	6	152671362	152671362	Missense_Mutation	SNV	G	C	C	SYNE1	c.11842C>G	P.P3948A
XH_P49	6	35280286	35280286	Missense_Mutation	SNV	C	A	A	DEF6	c.631C>A	P.Q211K
XH_P49	6	4995510	4995510	Splice_Site	SNV	A	G	G	RPP40	c.825T>C	P.C275C
XH_P49	6	96997335	96997335	Missense_Mutation	SNV	C	G	G	UFL1	c.1568C>G	P.S523C
XH_P49	8	116426722	116426722	Silent	SNV	C	T	T	TRPS1	c.3387G>A	P.P1129P
XH_P49	8	27146721	27146721	Missense_Mutation	SNV	G	T	T	TRIM35	c.743C>A	P.A248E
XH_P49	8	39634659	39634659	Nonsense_Mutation	SNV	C	A	A	ADAM2	c.856G>T	P.E286*
XH_P49	X	135291512	135291512	Missense_Mutation	SNV	G	T	T	FHL1	c.799G>C	P.G267C
XH_P49	X	17745550	17745550	Frame_Shift_Ins	INDEL	-	AGTAAAGA	AGTAAAGA	NHS	3_2794insAGTA	P.H932fs
XH_P49	X	17745551	17745551	In_Frame_Ins	INDEL	-	TGAACTTCCAA	TGAACTTCCAA	NHS	795insCTTGAAC	P32delinsPterTSNV
XH_P49	X	50654021	50654021	Missense_Mutation	SNV	T	A	A	BMP15	c.238T>A	P.S80T
XH_P49	X	54784914	54784914	Silent	SNV	C	A	A	ITIH6	c.1593G>T	P.V531V
XH_P49	X	55748688	55748688	Missense_Mutation	SNV	G	T	T	RRAGB	c.196G>T	P.A66S
XH_P50	12	25398284	25398284	Missense_Mutation	SNP	C	A	A	KRAS	c.35G>T	p.G12V
XH_P50	2	198267484	198267484	Missense_Mutation	SNP	G	A	A	SF3B1	c.1873C>T	p.F625C
XH_P50	1	2333651	2333651	Missense_Mutation	SNP	C	T	C	RER1	c.C371T	p.A124V
XH_P50	1	6279342	6279342	Missense_Mutation	SNP	C	T	C	RNF207	c.C1780T	p.P594S
XH_P50	1	11876733	11876733	Frame_Shift_Ins	INS	-	GGCCAAGATGTA	-	CLCN6	insTTGGCCCAAG	p.G70fs
XH_P50	1	21806710	21806710	Missense_Mutation	SNP	T	G	T	NBPF3	c.T1165G	p.L389V
XH_P50	1	31501697	31501697	Nonsense_Mutation	INS	-	CCTCTCCCATCG	-	PUM1	AGAGCGATGGG	E127delinsEERWERX
XH_P50	1	33060799	33060799	Frame_Shift_Ins	INS	-	TGTCAATGTAA	-	ZBTB8A	69insTTGTCAA	p.D323fs
XH_P50	1	39854271	39854271	Frame_Shift_Ins	INS	-	CTCTCT	-	MACF1	71_9572insCTC	p.L3191fs
XH_P50	1	40735760	40735760	Frame_Shift_Ins	INS	-	AAAA	-	ZMPSTE24	588_589insAAA	p.F196fs
XH_P50	1	40735761	40735761	Nonsense_Mutation	INS	-	AATAAATACAA	-	ZMPSTE24	TGATAAATAAA	p.F197delinsX
XH_P50	1	42049976	42049976	Missense_Mutation	SNP	C	T	T	G	c.G493A	p.H165M
XH_P50	1	43632906	43632906	Nonsense_Mutation	INS	-	TCAACTCTAAG	-	EBNA1BP2	CAGGTACTTTAG	Q181delinsRVAGTLELUX
XH_P50	1	52272550	52272550	Nonsense_Mutation	INS	-	CATGTGATTATC	-	NRDC	26insTAGATAAA	p.E676delinsX
XH_P50	1	52306000	52306000	In_Frame_Ins	INS	-	AGCTTTATT	-	NRDC	7_528insAATAAA	D176delinsEIKL
XH_P50	1	52306002	52306002	Missense_Mutation	SNP	C	T	C	NRDC	c.G526A	p.D176N
XH_P50	1	52499413	52499413	Silent	SNP	G	A	G	KTI12	c.C21T	p.C7C
XH_P50	1	53547798	53547800	In_Frame_Del	DEL	GAA	-	GAA	PODN	c.1951_1953del	p.651_651del
XH_P50	1	62240999	62240999	Frame_Shift_Ins	INS	-	CCAATACAATC	-	PATJ	3insTTTCCAATA	p.A281fs
XH_P50	1	62672944	62672944	Missense_Mutation	SNP	G	T	G	L1TD1	c.G644T	p.R215I
XH_P50	1	62676780	62676780	Frame_Shift_Ins	INS	-	TCCTCTATATCT	-	L1TD1	insTCTCTCTCT	p.R778fs
XH_P50	1	63284825	63284825	Frame_Shift_Ins	INS	-	AAAG	-	ATG4C	544_545insAAA	p.1182fs
XH_P50	1	63284826	63284826	Nonsense_Mutation	INS	-	AGATTAA	-	ATG4C	45_546insAGAT	B2_G183delinsIDX
XH_P50	1	66075787	66075787	Frame_Shift_Ins	INS	-	GGGCCCTG	-	LEPR	0_1911insGGG	p.K637fs
XH_P50	1	66075789	66075789	Missense_Mutation	SNP	G	A	G	LEPR	c.G1912A	p.V638I
XH_P50	1	70644669	70644669	Nonsense_Mutation	INS	-	AAAGGAGCTAA	-	LRR40	CAAGATTAGCT	23_H224delinsKQDX
XH_P50	1	78383422	78383422	Nonsense_Mutation	INS	-	AA	-	NEXN	c.199_200insAA	W67_N68delinsX
XH_P50	1	78383423	78383423	Frame_Shift_Ins	INS	-	ATAAAAAATATT	-	NEXN	5CAATATAAAA	p.W67fs
XH_P50	1	100155294	100155294	Frame_Shift_Ins	INS	-	TCATTGT	-	PALMD	78_1479insTCA	p.N493fs
XH_P50	1	104166788	104166788	Frame_Shift_Ins	INS	-	ATCATTAAATCT	-	AMY2A	92insCAATCAT	p.Q431fs
XH_P50	1	109815303	109815303	Frame_Shift_Ins	INS	-	AAGACGACGAG	-	CELSR2	AGGTCAAGACC	p.L2699fs
XH_P50	1	145305994	145305994	In_Frame_Ins	INS	-	TCTACGTGT	-	NBPF10	5_1636insTCTAC	P545delinsPSTC
XH_P50	1	149761715	149761715	Nonsense_Mutation	INS	-	CTAAACAGGCCA	-	FCGR1A	insATGCTAAAC	222_L223delinsGCX
XH_P50	1	150975177	150975177	Frame_Shift_Ins	INS	-	TGCTGATG	-	MINDY1	0_61insCATCAG	p.S21fs
XH_P50	1	152279476	152279476	Missense_Mutation	SNP	C	T	C	FLG	c.G7886A	p.R2629H
XH_P50	1	152325102	152325102	Silent	SNP	A	T	A	FLG	c.T5160A	p.T1720T
XH_P50	1	154067520	154067520	Nonsense_Mutation	INS	-	CTGCTGAATTA	-	NUP210L	nsAAACTAAATT	693_N694delinsX
XH_P50	1	154171977	154171977	In_Frame_Ins	INS	-	ACATACCTGGAT	-	C1orf189	232insATCCAGG	F78delinsIQVCF
XH_P50	1	155737298	155737298	Nonsense_Mutation	INS	-	AAAATA	-	GON4L	580_2681insATA	G894delinsVFX
XH_P50	1	155737299	155737299	Nonsense_Mutation	SNP	C	A	C	GON4L	c.G2680T	p.G894X
XH_P50	1	158390302	158390302	Frame_Shift_Ins	INS	-	ACTTTAGT	-	OR10K2	4_355insACTAA	p.G119fs
XH_P50	1	158655138	158655138	Splice_Site	SNP	C	A	C	SPTA1	.	.
XH_P50	1	158655139	158655139	Splice_Site	SNP	T	C	T	SPTA1	.	.
XH_P50	1	158687092	158687092	Frame_Shift_Ins	INS	-	ATGATCT	-	OR6K3	13_814insAGAT	p.A272fs
XH_P50	1	159283723	159283723	In_Frame_Ins	INS	-	TTTTCTTT	-	OR10J3	727insAAAGG	A243delinsKGKA
XH_P50	1	159283725	159283725	Frame_Shift_Ins	INS	-	TTTATAAATATG	-	OR10J3	25insACATATT	p.C242fs
XH_P50	1	169510865	169510865	Frame_Shift_Ins	INS	-	TTTAG	-	F5	462_3463insCTA	p.E1155fs
XH_P50	1	169511336	169511336	Frame_Shift_Ins	INS	-	GATA	-	F5	2991_2992insTA	p.H998fs
XH_P50	1	169511338	169511338	Frame_Shift_Ins	INS	-	CT	-	F5	2989_2990insA	p.G997fs
XH_P50	1	169762108	169762108	Frame_Shift_Ins	INS	-	CCAGATTATTAT	-	METTL18	9insCTATAATAA	p.D243fs
XH_P50	1	169762110	169762110	Missense_Mutation	SNP	C	A	C	METTL18	c.G727T	p.D243Y
XH_P50	1	172425611	172425611	Frame_Shift_Ins	INS	-	TCCTCACCTCTC	-	C1orf105	6insTTTCTCTCAC	p.T75fs
XH_P50	1	172425613	172425613	Frame_Shift_Ins	INS	-	TCTC	-	C1orf105	227_228insTCT	p.C76fs
XH_P50	1	175304899	175304899	Frame_Shift_Ins	INS	-	CATTAATAGTCT	-	TNR	insTAAGAGACT	p.K860fs
XH_P50	1	179528893	179528893	Frame_Shift_Ins	INS	-	ATAATGATATG	-	NPHS2	455insCATATC	p.L152fs
XH_P50	1	182827921	182827921	Silent	SNP	C	T	C	DHX9	c.C954T	p.F318F
XH_P50	1	183602293	183602293	Nonsense_Mutation	INS	-	ATAGCCCTATAA	-	ARPC5	sCTACATTATAG	p.I50delinsTTLX
XH_P50	1	186320527	186320527	Frame_Shift_Ins	INS	-	T	-	TPR	c.2544_2545ins	p.S849fs
XH_P50	1	186320528	186320528	Frame_Shift_Ins	INS	-	CAGTAAAGTTA	-	TPR	2544insTAAC	p.I848fs
XH_P50	1	196712732	196712732	Frame_Shift_Ins	INS	-	AAAAGAAGTGG	-	CFH	285insAAAAAGA	p.N1095fs
XH_P50	1	198492676	198492676	Frame_Shift_Ins	INS	-	AATGAGAACT	-	ATP6V1G3	2insTTAAGGTT	p.N68fs
XH_P50	1	214819912	214819912	Frame_Shift_Ins	INS	-	ATTCTCTTTTGA	-	CENPF	000insGATTCTT	p.L2333fs

XH_P50	1	215793715	215793715	Nonsense_Mutation	INS	-	GAAATACAG	-	KCTD3	7_2198insGAAA	p.F733delinsX
XH_P50	1	222801129	222801129	In_Frame_Ins	INS	-	CTTATCCAC	-	MAI3	7_568insCTTATC	p.S189delinsSLIH
XH_P50	1	227842507	227842507	In_Frame_Ins	INS	-	TTTATGTTTTGT	-	ZNf678	insTCTTTTATGT	p.241delinsFFVLLG
XH_P50	1	230805222	230805222	Frame_Shift_Ins	INS	-	ATAAAATCAAAA	-	COG2	nsTATATAAAAT	p.p.239fs
XH_P50	1	247694985	247694985	Missense_Mutation	SNP	G	C	G	OR2C3	c.C289G	p.L277V
XH_P50	1	248789733	248789733	Frame_Shift_Ins	INS	-	C	-	OR2T11	c.696_697insG	p.p.233fs
XH_P50	1	248789734	248789734	In_Frame_Ins	INS	-	ATACCA	-	OR2T11	95_696insTGGb	p.K232delinsNGI
XH_P50	1	248814136	248814136	Nonsense_Mutation	INS	-	CTTCTC	-	OR2T27	9_50insGAGGGA	p.L17_F18delinsX
XH_P50	1	248814137	248814137	Missense_Mutation	SNP	A	T	A	OR127	c.T49A	p.L17M
XH_P50	2	10132240	10132240	Frame_Shift_Ins	INS	-	AAAGTGCCACT	-	GRH1	insTGTTAAAGT	p.p.476fs
XH_P50	2	21228564	21228564	Silent	SNP	A	G	A	APOB	c.T11176C	p.L3726L
XH_P50	2	21228566	21228566	Frame_Shift_Ins	INS	-	ACTCCTTGATTC	-	APOB	1174insGGAATC	p.p.3725fs
XH_P50	2	21364244	21364244	In_Frame_Ins	INS	-	TGGTCTATTTTT	-	TDRD15	6insAATTGGTCT	p.1302delinsSIGLFFF
XH_P50	2	24033367	24033367	Nonsense_Mutation	INS	-	TGATTATTCATT	-	ATAD2B	ATGCTAATGAA58	p.Y759delinsLILEXC
XH_P50	2	44569677	44569677	Nonsense_Mutation	INS	-	TTTAAAGTACTG	-	PREPL	AAAGTCAGTACT	p.211delinsQSQYFKX
XH_P50	2	55561359	55561359	Silent	SNP	G	A	G	CCDC88A	c.C2598T	p.N866N
XH_P50	2	55561361	55561361	In_Frame_Ins	INS	-	TCTATCAGTAAT	-	CCDC88A	nsTGCAAATTCAC	p.866delinsKLLIDSN
XH_P50	2	61719478	61719478	Silent	SNP	G	A	G	XPO1	c.C1705T	p.L569L
XH_P50	2	61719479	61719479	Nonsense_Mutation	INS	-	TTAACACTATTA	-	XPO1	704insATAATAG	p.568_L569delinsKX
XH_P50	2	64196115	64196115	Frame_Shift_Ins	INS	-	GTCTTCTTTCTT	-	VP54	GAAAAAGAAAG	p.p.144fs
XH_P50	2	71211378	71211378	Frame_Shift_Ins	INS	-	TGCAGTGTGCA	-	ANKRD53	AAGGATGCAGT	p.p.343fs
XH_P50	2	71650848	71650848	Frame_Shift_Ins	INS	-	CTATTGAAGAT	-	ZNf638	nsTGTTCTTATT	p.p.1402fs
XH_P50	2	73799626	73799626	Frame_Shift_Ins	INS	-	ACGGGTAGTAT	-	ALMS1	10620insACGG	p.p.3540fs
XH_P50	2	99949585	99949585	Frame_Shift_Ins	INS	-	A	-	TXNDC9	c.88_89insT	p.p.30fs
XH_P50	2	99949587	99949587	Frame_Shift_Ins	INS	-	TATTACTGTT	-	TXNDC9	87insAACAGTA	p.p.129fs
XH_P50	2	108627182	108627182	Nonsense_Mutation	INS	-	TGATTATATATA	-	SLCSA7	94insTTCTGATT	p.A431_L432delinsNFX
XH_P50	2	113590354	113590354	Frame_Shift_Ins	INS	-	AAAAATATTTAA	-	IL1B	insCTTTTAAATA	p.p.117fs
XH_P50	2	113590356	113590356	Missense_Mutation	SNP	C	A	C	IL1B	c.G349T	p.A117S
XH_P50	2	125204474	125204474	Missense_Mutation	SNP	G	A	G	CNTNAP5	c.C878A	p.R293H
XH_P50	2	136690399	136690399	In_Frame_Ins	INS	-	ATATTGACTTTC	-	DARS	8insAAGAAAGT	p.T73delinsKESQYP
XH_P50	2	159312926	159312926	Splice_Site	INS	-	T	-	CCDC148	-	-
XH_P50	2	160128275	160128284	Frame_Shift_Del	DEL	ACTCAGTGT	-	ACTCAGTGT	WDSUB1	c.192_201del	p.p.564fs
XH_P50	2	160879354	160879354	In_Frame_Ins	INS	-	TGTAGTAACACT	-	PLA2R1	nsTAAAAAGTAGT	p.372delinsNKSSYYII
XH_P50	2	165578747	165578747	Frame_Shift_Ins	INS	-	GTTTTGTTTTCTA	-	COBL11	AAAAATAGAAAA	p.p.278fs
XH_P50	2	168115140	168115140	Nonsense_Mutation	INS	-	CTTTTAAATTCAC	-	XLRP2	9insTCACCTTTTA	p.M473delinsHEFX
XH_P50	2	182403985	182403985	Frame_Shift_Ins	INS	-	TTTCTGAAGCAC	-	CERKL	nsGAAACTGCTT	p.p.345fs
XH_P50	2	186658847	186658847	Frame_Shift_Ins	INS	-	TG	-	FSIP2	c.6984_6985insT	p.p.2328fs
XH_P50	2	186658848	186658848	Frame_Shift_Ins	INS	-	GTGTCTT	-	FSIP2	85_6986insGTG	p.p.2329fs
XH_P50	2	196737189	196737189	In_Frame_Ins	INS	-	TGTATTGAAT	-	DNAH7	8insCCCAATTTC	p.2140delinsPISITGK
XH_P50	2	202358592	202358592	Frame_Shift_Ins	INS	-	AGTTTGTGTCAT	-	C2CD6	2insTGTGATGA	p.p.824fs
XH_P50	2	203964422	203964422	Nonsense_Mutation	INS	-	ACATTGTGTAAT	-	NBEAL1	GTGAGCACATT	p.390_P391delinsSX
XH_P50	2	207171368	207171368	Frame_Shift_Ins	INS	-	CTTCAGAGAT	-	ZDBF2	2117insCTTCAC	p.p.1706fs
XH_P50	2	207171370	207171370	Silent	SNP	G	T	G	ZDBF2	c.G2118T	p.L706L
XH_P50	2	207175098	207175098	Nonsense_Mutation	INS	-	GTAACCTT	-	ZDBF2	6_5847insGTA	p.949_C195delinsRX
XH_P50	2	207175330	207175330	Nonsense_Mutation	INS	-	TATTTTCTTTTG	-	ZDBF2	TCTAATTATTTT	p.26_F0227delinsPLVX
XH_P50	2	209035738	209035738	Frame_Shift_Ins	INS	-	AAATG	-	C2orf80	503_504insCAT	p.p.516fs
XH_P50	2	209035740	209035740	Frame_Shift_Ins	INS	-	AGAATAAT	-	C2orf80	51_502insATTAT	p.p.516fs
XH_P50	2	216256500	216256500	Nonsense_Mutation	INS	-	ATATTAACCTAG	-	FN1	4insGCTCTAGG	p.11278delinsMLX
XH_P50	2	216298165	216298165	In_Frame_Ins	INS	-	TGGTACAGCTTA	-	FN1	nsGAATAAGCTG	p.999delinsENKLYHR
XH_P50	2	228389615	228389615	Frame_Shift_Ins	INS	-	TAACATATAAGA	-	AGFG1	9insATTAACTAT	p.p.226fs
XH_P50	2	234526800	234526800	Frame_Shift_Ins	INS	-	CCAGAGTG	-	UGT1A8	7_448insCCAGA	p.p.149fs
XH_P50	2	234526802	234526802	Missense_Mutation	SNP	T	A	T	UGT1A8	c.T449A	p.F150Y
XH_P50	3	4847859	4847859	Frame_Shift_Ins	INS	-	AGACCCAT	-	ITPR1	1_6992insAGAC	p.M2331fs
XH_P50	3	14708937	14708937	Missense_Mutation	SNP	G	A	G	CCDC174	c.G731A	p.R244Q
XH_P50	3	27460042	27460042	Frame_Shift_Ins	INS	-	CATTTTTACT	-	SLC4A7	1210insAGTAA	p.p.V404fs
XH_P50	3	27475501	27475501	Frame_Shift_Ins	INS	-	TGCTTTGTTTCT	-	SLC4A7	2insAAGAAACA	p.p.224fs
XH_P50	3	31663787	31663787	Nonsense_Mutation	INS	-	TGAAGTACATA	-	STT3B	527insCTGAAC	p.509_L510delinsNX
XH_P50	3	40251559	40251559	Frame_Shift_Ins	INS	-	TGTTGCTTCTT	-	MYRIP	1320insGTGTG	p.p.440fs
XH_P50	3	43344816	43344816	Frame_Shift_Ins	INS	-	AAATATT	-	SNRK	1_122insAAATA	p.p.K41fs
XH_P50	3	43344818	43344818	In_Frame_Ins	INS	-	ACT	-	SNRK	c.123_124insAC	p.p.K41delinsKT
XH_P50	3	44285155	44285155	Frame_Shift_Ins	INS	-	TTGGTTT	-	TOPAZ1	57_1158insTTG	p.p.386fs
XH_P50	3	44285157	44285157	Frame_Shift_Ins	INS	-	CTTTGTT	-	TOPAZ1	59_1160insCTT	p.p.387fs
XH_P50	3	44364722	44364722	Frame_Shift_Ins	INS	-	ACCCATTATAGG	-	TOPAZ1	611insTACCCAT	p.p.1153fs
XH_P50	3	52554531	52554531	Missense_Mutation	SNP	G	A	G	STAB1	c.G5615A	p.p.R1872H
XH_P50	3	88189595	88189595	Frame_Shift_Ins	INS	-	ATTGTTT	-	ZNf654	37_2438insATT	p.p.7813fs
XH_P50	3	88189597	88189597	Frame_Shift_Ins	INS	-	CT	-	ZNf654	2439_2440insC	p.p.7813fs
XH_P50	3	97591017	97591017	Missense_Mutation	SNP	G	T	G	CRYBG3	c.G979T	p.A327S
XH_P50	3	97591019	97591019	Frame_Shift_Ins	INS	-	CAATGTG	-	CRYBG3	81_982insCAAT	p.p.A327fs
XH_P50	3	98072961	98072961	Nonsense_Mutation	INS	-	CATAAATGTAA	-	OR5K4	65insACATAAAT	p.E88_D89delinsETX
XH_P50	3	100551174	100551174	Frame_Shift_Ins	INS	-	TGTACATATAAT	-	ABI3BP	993insGATTATA	p.p.R665fs
XH_P50	3	100551176	100551176	Missense_Mutation	SNP	T	A	T	ABI3BP	c.A1991T	p.p.K664I
XH_P50	3	107492413	107492413	Nonsense_Mutation	DEL	C	-	C	BBX	c.1845delC	p.p.C615X
XH_P50	3	107492415	107492420	In_Frame_Del	DEL	AAGGTG	-	AAGGTG	BBX	c.1847_1852del	p.p.616_618del
XH_P50	3	109056323	109056323	Nonsense_Mutation	INS	-	TTATTTTATTTT	-	DPPA4	nsTTAAAAATAA	p.A14_K15delinsAX
XH_P50	3	112731660	112731660	Splice_Site	INS	-	TATTTTCTTATG	-	NEPRO	-	-
XH_P50	3	118931445	118931445	Frame_Shift_Ins	INS	-	AACAA	-	B4GALT4	985_986insTTG	p.p.H329fs
XH_P50	3	118931446	118931446	Frame_Shift_Ins	INS	-	ACAGC	-	B4GALT4	984_985insGCT	p.p.H329fs
XH_P50	3	119634996	119634996	Frame_Shift_Ins	INS	-	ACAGTAATCTTA	-	GSK3B	303insTAAGAA	p.p.S168fs
XH_P50	3	120053953	120053953	Nonsense_Mutation	INS	-	TTCAGTATTCAT	-	LRRC58	3insACATGAAT	p.N221delinsKHEYX
XH_P50	3	120489718	120489718	Frame_Shift_Ins	INS	-	CC	-	GTf2E1	c.592_593insCC	p.p.N198fs
XH_P50	3	120489720	120489720	Frame_Shift_Ins	INS	-	TTTAGATTCTAC	-	GTf2E1	5insCAITTAGAT	p.p.N198fs
XH_P50	3	125170265	125170265	Splice_Site	INS	-	AGGATTCTGT	-	SNX4	-	-
XH_P50	3	125279353	125279353	Frame_Shift_Ins	INS	-	A	-	OSBPL11	c.1024_1025ins	p.p.E342fs
XH_P50	3	125279354	125279354	Nonsense_Mutation	INS	-	AAATTTTAAATT	-	OSBPL11	nsAATTTAAATTA	p.342_1343delinsNX
XH_P50	3	130150671	130150671	Nonsense_Mutation	INS	-	AAAGAGCTCTCT	-	COL6A5	2insATTAAAGC	p.871_51872delinsYX
XH_P50	3	145797021	145797021	In_Frame_Ins	INS	-	TTTTTTTGGTTCT	-	PLOD2	82insCAGAACCC	p.4461delinsTEPKL
XH_P50	3	157082256	157082256	In_Frame_Ins	INS	-	ATCACTCTGTGA	-	VEPH1	1173insTAACAG	p.E391delinsDNRVI
XH_P50	3	169555331	169555331	Frame_Shift_Ins	INS	-	TTTTTTTCTTCT	-	LRIQ4	1596insTTTTTA	p.p.K532fs
XH_P50	3	169555333	169555333	Missense_Mutation	SNP	C	T	C	LRIQ4	c.C1597T	p.p.P533S
XH_P50	3	183952534	183952534	Silent	SNP	G	A	G	VVAWSB2	c.G279A	p.p.G93G
XH_P50	3	186435449	186435449	Frame_Shift_Ins	INS	-	AATTTGACAAT	-	KNG1	119insAATTTG	p.p.A40fs
XH_P50	3	187440335	187440335	Frame_Shift_Del	DEL	G	-	G	BCL6	c.1864delC	p.p.R622fs
XH_P50	3	194336331	194336331	Missense_Mutation	SNP	C	A	C	TMEM44	c.G879T	p.p.L293F
XH_P50	3	195514481	195514481	In_Frame_Ins	INS	-	AGCCTT	-	MUC4	69_3970insAAG	p.G1324delinsKAG
XH_P50	3	196612373	196612373	Frame_Shift_Ins	INS	-	SAATTTTCCTCT	-	SENP5	nsATAGAAATTTT	p.p.S107fs
XH_P50	4	437249	437249	Missense_Mutation	SNP	C	T	C	ZNf72	c.G1007A	p.p.G336E
XH_P50	4	3132146	3132146	Nonsense_Mutation	INS	-	AGTATGATTATT	-	HTT	1983insAGTATG	p.661_K662delinsKVX
XH_P50	4	13606472	13606472	Frame_Shift_Ins	INS	-	CATAAATATAAA	-	BOD1L1	ATCACCTTTTATA	p.p.E684fs

XH_P50	4	15638268	15638268	In_Frame_Ins	INS	-	TTTTCTAGATGA	-	FBXL5	AATATTCATCTAC	insIIINVNEYSSRKIHENILK
XH_P50	4	37848718	37848718	Frame_Shift_Ins	INS	-	ACTCTAAA	-	PGM2	4_1175insACTC	p.G392fs
XH_P50	4	40434705	40434725	In_Frame_Del	DEL	GCGCGCGCTG	-	TGCGCGCGGCTG	RBM47	c.1278_1298del	p.426_433del
XH_P50	4	69964374	69964374	Frame_Shift_Ins	INS	-	TAATTACTTTCAG	-	UGT287	AAGATAATTAC	p.L280fs
XH_P50	4	71115135	71115135	Frame_Shift_Ins	INS	-	CCCAAACCTGCG	-	CSN3	CGTGCCTCCAAA	p.P170fs
XH_P50	4	74043241	74043241	Frame_Shift_Ins	INS	-	SGTATTTAGAAT	-	ANKRD17	GTATCTATTCAA	p.F22fs
XH_P50	4	104116352	104116352	Missense_Mutation	SNP	C	T	C	CENPE	c.G396A	p.M132I
XH_P50	4	106879713	106879713	Frame_Shift_Ins	INS	-	TTTAATTATATA	-	NPNT	sAAATATTTTAA	p.P415fs
XH_P50	4	110880494	110880494	Missense_Mutation	SNP	G	A	G	EGF	c.G967A	p.G323R
XH_P50	4	110880495	110880495	In_Frame_Ins	INS	-	GCAGTGTCTCTC	-	EGF	sATTTAGCAGTGT	23delinsGFSSVLCCQ
XH_P50	4	114274678	114274678	Frame_Shift_Ins	INS	-	CTCTTCCTCA	-	ANK2	1_4905insCTCTT	p.G1635fs
XH_P50	4	121742465	121742465	Frame_Shift_Ins	INS	-	CTTTT	-	PRDM5	335_336insAAA	p.D112fs
XH_P50	4	121742467	121742467	Frame_Shift_Ins	INS	-	GTTGATTGCTTT	-	PRDM5	CTAGAAGACAA	p.D112fs
XH_P50	4	123179958	123179958	Frame_Shift_Ins	INS	-	TTCTTGACAAA	-	KIAA1109	insATATTCTCTG	p.S2241fs
XH_P50	4	140468167	140468167	Nonsense_Mutation	INS	-	TGCCATCAAAG	-	SETD7	CTCTTCTTTGATG	727delinsFFFDGRX
XH_P50	4	142950041	142950041	Nonsense_Mutation	INS	-	CTTTTTTGTGTTG	-	INPP4B	TAATAACAAAC	p.L890delinsQX
XH_P50	4	144465126	144465126	Splice_Site	SNP	G	C	G	SMARCA5	-	-
XH_P50	4	144465127	144465127	Splice_Site	INS	-	CTTTAAGGAAA	-	SMARCA5	-	-
XH_P50	4	144618277	144618277	Nonsense_Mutation	INS	-	CAGAGACAA	-	FREM3	1_3552insTTGT	p.I1184delinsCLX
XH_P50	4	153884187	153884187	Missense_Mutation	SNP	G	A	G	FHDC1	c.G934A	p.G312S
XH_P50	4	154249812	154249812	Missense_Mutation	SNP	G	C	G	TRIM2	c.G2072C	p.S691T
XH_P50	4	154249813	154249813	Frame_Shift_Ins	INS	-	TATGAAATATTI	-	TRIM2	74insTGTATGA	p.S691fs
XH_P50	4	155157600	155157600	Nonsense_Mutation	INS	-	GACCTATTCTA	-	DCHS2	6839insTAGAA	280_F2281delinsLEX
XH_P50	4	155719264	155719264	Frame_Shift_Ins	INS	-	AACCTCATCTTCA	-	RBM46	4insCTAACTCAT	p.E151fs
XH_P50	4	159894390	159894390	Nonsense_Mutation	INS	-	TTGAATCTTTTAT	-	C4orf45	38insATAAAGA	A46_L47delinsAX
XH_P50	4	175184109	175184109	Frame_Shift_Ins	INS	-	CTTTGAGATGCT	-	FBXO8	35insGAGCATCT	p.K45fs
XH_P50	4	177608650	177608650	In_Frame_Ins	INS	-	AATGCT	-	VEGFC	35_836insAGCA	p.I279delinsKHF
XH_P50	4	187179342	187179342	Nonsense_Mutation	INS	-	AATAGTAGAAAG	-	KLKB1	nsATAAAATAGT	31_A632delinsKIIX
XH_P50	5	10256245	10256245	Nonsense_Mutation	INS	-	CTTCACTTTTATG	-	CC75	346insCTTCACT	15_T116delinsKLHFX
XH_P50	5	33751560	33751560	Frame_Shift_Ins	INS	-	CTTTTTTTTTTTA	-	ADAMTS12	insATTAAAAAA	p.Y195fs
XH_P50	5	36976156	36976156	Frame_Shift_Ins	INS	-	ATAGAAGTAACA	-	NIPBL	sATTTCGATAGAA	p.S383fs
XH_P50	5	36985858	36985858	Frame_Shift_Ins	INS	-	TTTTTGTT	-	NIPBL	76_2577insTTTT	p.D859fs
XH_P50	5	36985860	36985860	Frame_Shift_Ins	INS	-	TTATCATG	-	NIPBL	8_2579insTTAT	p.S860fs
XH_P50	5	54416265	54416265	Frame_Shift_Ins	INS	-	AGTT	-	CDC20B	328_1329insAA	p.S443fs
XH_P50	5	54416266	54416266	Nonsense_Mutation	INS	-	TTAATATAATTT	-	CDC20B	nsAACACAAAT	443delinsKHLVX
XH_P50	5	54929718	54929718	Frame_Shift_Ins	INS	-	TAAA	-	SLC38A9	1104_1105insTT	p.N369fs
XH_P50	5	54929720	54929720	Frame_Shift_Ins	INS	-	GTGA	-	SLC38A9	1102_1103insTC	p.D368fs
XH_P50	5	64020298	64020298	Frame_Shift_Ins	INS	-	CTGGCAATATA	-	SREK1IP1	381insTATATTG	p.K127fs
XH_P50	5	64625294	64625294	In_Frame_Ins	INS	-	ATGATGTTATTA	-	ADAMTS6	nsCACAAATAATA	378delinsATIHTSSI
XH_P50	5	68651571	68651571	Frame_Shift_Ins	INS	-	TGTTGTTGTTTG	-	AK6	cAAAAACAAACA	p.D74fs
XH_P50	5	74137492	74137492	Frame_Shift_Ins	INS	-	ACTTTATGGCTT	-	FAM169A	TTAAAGCCATA	p.P4fs
XH_P50	5	94859466	94859466	Frame_Shift_Ins	INS	-	FAAATGAAAATA	-	TTCT37	ATAAAAAATATT	p.D509fs
XH_P50	5	102895168	102895168	Frame_Shift_Ins	INS	-	TTCTT	-	NUDT12	153_154insAAG	p.C52fs
XH_P50	5	102895170	102895170	Splice_Site	INS	-	CGTTAGGAACCA	-	NUDT12	-	-
XH_P50	5	114607044	114607044	In_Frame_Ins	INS	-	AGTCTAGTGGG	-	CCDC112	nsTCTTTCCCAC	800delinsSFPLDYNL
XH_P50	5	123983834	123983834	Frame_Shift_Ins	INS	-	AAGGACAAAGA	-	ZNF608	2243insCTCTCTT	p.Q748fs
XH_P50	5	132545934	132545934	Frame_Shift_Ins	INS	-	SAGTTCTTCTCTC	-	FSTL4	CCACTGAGAGA	p.Q555fs
XH_P50	5	140764484	140764484	Missense_Mutation	SNP	C	T	C	PCDHGA7	c.C2018T	p.A673V
XH_P50	6	7583436	7583436	Frame_Shift_Ins	INS	-	CTTC	-	DSP	1144_4145insCT	p.Y1382fs
XH_P50	6	7583437	7583437	Nonsense_Mutation	INS	-	ATTCTCT	-	DSP	45_4146insATT	382_E1383delinsX
XH_P50	6	7606393	7606393	Frame_Shift_Ins	INS	-	AATGTTAATCA	-	SNRNP48	937insAATGTTT	p.K312fs
XH_P50	6	7606395	7606395	Missense_Mutation	SNP	A	T	A	SNRNP48	c.A938T	p.D313V
XH_P50	6	8430307	8430307	Silent	SNP	G	A	G	SLC35B3	c.C87T	p.S29S
XH_P50	6	8430308	8430308	Nonsense_Mutation	INS	-	AATTTATGGGTA	-	SLC35B3	nsAATACCCATA	29_K30delinsKYPX
XH_P50	6	8430367	8430367	Frame_Shift_Ins	INS	-	SGCATTACTAG	-	SLC35B3	27insACTAGTAA	p.D9fs
XH_P50	6	22287722	22287722	Frame_Shift_Ins	INS	-	CTCC	-	PRL	592_593insGGA	p.N198fs
XH_P50	6	37247342	37247342	Nonsense_Mutation	INS	-	TATTATTGTAAT	-	TBC1D22B	TTGCTTATTATT	K126delinsICLLX
XH_P50	6	38029466	38029466	Frame_Shift_Ins	INS	-	AATAAAG	-	ZFAND3	10_211insAATA	p.N70fs
XH_P50	6	38029468	38029468	Frame_Shift_Ins	INS	-	TGAT	-	ZFAND3	212_213insTGA	p.T71fs
XH_P50	6	46679325	46679325	Frame_Shift_Ins	INS	-	CAATGACCTGCG	-	PLA2G7	AATGAGCAGGT	p.K191fs
XH_P50	6	49456372	49456372	Frame_Shift_Ins	INS	-	TGAATTTGTTC	-	CENPQ	1insTCTGAATT	p.K217fs
XH_P50	6	51936934	51936934	Frame_Shift_Ins	INS	-	C	-	PKHD1	c.580_581insG	p.1194fs
XH_P50	6	51936936	51936936	Frame_Shift_Ins	INS	-	CCTTATCTTT	-	PKHD1	579insAAAGAT	p.1193fs
XH_P50	6	53516782	53516782	Missense_Mutation	SNP	A	T	A	KLHL31	c.T1519A	p.C507S
XH_P50	6	54001630	54001630	Missense_Mutation	SNP	G	T	G	MLIP	c.G730T	p.V244F
XH_P50	6	54001632	54001632	Nonsense_Mutation	INS	-	CTCTAGTTAACT	-	MLIP	733insCTCTAGT	244_L245delinsVLX
XH_P50	6	56366034	56366034	Splice_Site	INS	-	GTGTTTCAAG	-	DST	-	-
XH_P50	6	56418059	56418059	Nonsense_Mutation	INS	-	CTTTAACTT	-	DST	1_7662insAAGT	p.T254delinsTSX
XH_P50	6	56418060	56418060	Frame_Shift_Ins	INS	-	GCAATAGAAT	-	DST	1_7661insATTCT	p.T2554fs
XH_P50	6	70410746	70410746	Frame_Shift_Ins	INS	-	AGCTGTATCTTT	-	LMBRD1	99insATAAAGAT	p.Y367fs
XH_P50	6	75904568	75904568	Frame_Shift_Ins	INS	-	TTAATGTTATTG	-	COL12A1	4insCTCAATAAC	p.I57fs
XH_P50	6	76385167	76385167	Frame_Shift_Ins	INS	-	TAGGTTACAGGG	-	SENPE	89insTTTAGGTT	p.I463fs
XH_P50	6	76412668	76412668	Missense_Mutation	SNP	C	G	C	SENPE	c.C2575G	p.H859D
XH_P50	6	76412669	76412669	In_Frame_Ins	INS	-	ATGACTAAATAT	-	SENPE	77insAATGACT	859delinsQMTKYV
XH_P50	6	87970254	87970254	Nonsense_Mutation	INS	-	AAATGAAGATTI	-	ZNF292	8insAGTAAATGA	p.S2303delinsX
XH_P50	6	94066754	94066754	Frame_Shift_Ins	INS	-	A	-	EPHA7	c.1004_1005ins	p.P335fs
XH_P50	6	94066756	94066756	Nonsense_Mutation	INS	-	TCACATCGTTTC	-	EPHA7	1003insGAAACG	P335delinsETMX
XH_P50	6	96997609	96997609	In_Frame_Ins	INS	-	ATAAGTTTAT	-	UFL1	3insGAGATAAG	1584delinsLEISFIK
XH_P50	6	111694778	111694778	Nonsense_Mutation	INS	-	GTAGCTTTT	-	REV3L	4780insTAAAA	1594_11595delinsX
XH_P50	6	116446642	116446642	In_Frame_Ins	INS	-	TAATATTGAATTG	-	COL10A1	ATATACAAATTC	5delinsNIQFNPL
XH_P50	6	117860539	117860539	Nonsense_Mutation	INS	-	TCCTCTAATCCA	-	DCBLD1	9insTTATCTCTC	66_K367delinsELSLX
XH_P50	6	127794487	127794487	Frame_Shift_Ins	INS	-	GACATTTTCTG	-	SOGA3	783insACAGAA	p.S928fs
XH_P50	6	131926605	131926605	Nonsense_Mutation	INS	-	ATGTGCGTATTA	-	MED23	ATGAAATAATAC	63_N464delinsTMKX
XH_P50	6	132891584	132891584	In_Frame_Ins	INS	-	TATCAACAAAAT	-	TAAR6	sTTGATTATCAC	42delinsVDYHKYR
XH_P50	6	146993502	146993502	Frame_Shift_Ins	INS	-	CAAAAACAT	-	ADGB	987insCAAAA	p.E329fs
XH_P50	6	155131308	155131308	Nonsense_Mutation	INS	-	GTCTTATATTTA	-	SCAF8	87insTTGTCTTA	2_G463delinsKLSVIX
XH_P50	6	155565165	155565165	Frame_Shift_Ins	INS	-	TTTTTTTTTTTTT	-	TIAM2	CTTTTTTTTTTTT	p.E48fs
XH_P50	7	11582714	11582714	Nonsense_Mutation	INS	-	ATGGCTCAAGA	-	THSD7A	1484insGCTCTTT	895_G496delinsSLX
XH_P50	7	25175856	25175856	Frame_Shift_Ins	INS	-	AACAGAATTTC	-	C7orf31	8insGAAGGAAA	p.H503fs
XH_P50	7	27169932	27169934	In_Frame_Del	DEL	GCA	-	GCA	HOXA4	c.419_421del	p.140_141del
XH_P50	7	30062395	30062395	Frame_Shift_Ins	INS	-	AGCA	-	FKBP14	234_235insTGC	p.L79fs
XH_P50	7	30062397	30062397	Frame_Shift_Ins	INS	-	ATGATGAGCTT	-	FKBP14	sAGAGAAAGCT	p.L78fs
XH_P50	7	35674974	35674974	In_Frame_Ins	INS	-	ACTTTTTGTGTT	-	HERPUD2	sATTAAACACAA	23delinsIKPOQVNE
XH_P50	7	44797065	44797109	In_Frame_Del	DEL	ACTGCCACCG	-	CCACTGCCACCG	ZMIZ2	c.457_501del	p.153_167del
XH_P50	7	57528754	57528754	In_Frame_Ins	INS	-	ATCTTCTCA	-	ZNF716	7_588insATCTT	C1M96delinsISSQ
XH_P50	7	57528755	57528755	Frame_Shift_Ins	INS	-	TATCA	-	ZNF716	588_589insTAT	p.M196fs
XH_P50	7	57529400	57529400	Nonsense_Mutation	INS	-	CTTATGTTTCTT	-	ZNF716	insCTATCTTATG	E412delinsELSVVX
XH_P50	7	64864674	64864674	Frame_Shift_Ins	INS	-	T	-	ZNF92	c.1420dupT	p.F473fs

XH_P50	7	64864676	64864676	Nonsense_Mutation	INS	-	TCTCTAGTATGA	-	ZNF92	GGTTTTTCTCTA	S474delinsSHLX
XH_P50	7	66453413	66453413	Frame_Shift_Ins	INS	-	CTTA	-	SBD5	697_698insTAA	p.S233fs
XH_P50	7	66489954	66489954	In_Frame_Ins	INS	-	TTTTTTTTTTTT	-	TYW1	30insTTTTTTTT	S310delinsSFFFF
XH_P50	7	82764924	82764924	Missense_Mutation	SNP	C	T	C	PCLO	c.G1942A	p.G648R
XH_P50	7	87838760	87838760	Frame_Shift_Ins	INS	-	TTCTCTCCAAAT	-	SRI	AAAAAATTTGGG	p.R135fs
XH_P50	7	99631039	99631039	Frame_Shift_Ins	INS	-	GCTTCTAC	-	ZKSCAN1	2_273insGCTTC	p.K91fs
XH_P50	7	99673208	99673208	Frame_Shift_Ins	INS	-	TTCTCT	-	ZNF3	100_101insAGG	p.G34fs
XH_P50	7	100681947	100681947	Missense_Mutation	SNP	A	T	A	MUC17	c.A7250T	p.H2417L
XH_P50	7	100683775	100683775	Silent	SNP	C	A	C	MUC17	c.C9078A	p.C3026G
XH_P50	7	104730655	104730655	Nonsense_Mutation	INS	-	CATTAAATAAT	-	KMT2E	TTTTTTTCATTAA	0_K521delinsKFFSLKX
XH_P50	7	111644163	111644163	Missense_Mutation	SNP	C	A	C	DOCK4	c.G61T	p.V21F
XH_P50	7	111644165	111644165	In_Frame_Ins	INS	-	CATCAT	-	DOCK4	58_59insATGAT	b.T20delinsNDA
XH_P50	7	124464104	124464104	Nonsense_Mutation	INS	-	GCATGGGTATG	-	POT1	nsAATCCCATAC	p.F475delinsX
XH_P50	7	128852055	128852055	Silent	SNP	G	A	G	SMO	c.G2127A	p.R709R
XH_P50	7	132174219	132174219	Missense_Mutation	SNP	G	T	G	PLXNA4	c.C1203A	p.D401E
XH_P50	7	132174220	132174220	Frame_Shift_Ins	INS	-	A	-	PLXNA4	c.1201_1202ins	p.D401fs
XH_P50	7	134618431	134618431	In_Frame_Ins	INS	-	TTTTTAATGACAT	-	CALD1	12insTTTTTTTAA	b.304delinsHFLMTL
XH_P50	7	135376061	135376061	Frame_Shift_Ins	INS	-	GAAGCCAGAGC	-	SLC13A4	insCTATGCTCT	p.E445fs
XH_P50	7	140434569	140434569	Missense_Mutation	SNP	A	C	A	BRAF	c.T2129G	p.I710S
XH_P50	7	141750062	141750062	Nonsense_Mutation	INS	-	TTATGGGATGA	-	MGAM	16insCCTTATGG	b.872delinsFLMDEX
XH_P50	7	141920186	141920186	Missense_Mutation	SNP	G	A	G	MGAM2	c.G5875A	p.D1959N
XH_P50	7	143269947	143269947	Frame_Shift_Ins	INS	-	GAATTTT	-	CTAGE15	37_1038insGAA	p.D346fs
XH_P50	7	143881371	143881371	Frame_Shift_Ins	INS	-	TTCACTCATTT	-	CTAGE4	776insTTCACT	p.L259fs
XH_P50	7	143881373	143881373	Silent	SNP	G	A	G	CTAGE4	c.G777A	p.L259L
XH_P50	7	150269974	150269974	Frame_Shift_Ins	INS	-	CCTTCCTT	-	GIMAP4	16_817insCCTTC	p.Q272fs
XH_P50	8	3165235	3165235	Missense_Mutation	SNP	T	C	T	CSMD1	c.A3932G	p.D1311G
XH_P50	8	10466413	10466413	Missense_Mutation	SNP	G	A	G	RP11	c.C5195T	p.P1732L
XH_P50	8	22398136	22398136	Missense_Mutation	SNP	G	T	G	PPP3CC	c.G1330T	p.G444W
XH_P50	8	24774966	24774966	Frame_Shift_Ins	INS	-	ATTCTCT	-	NEFM	70_471insATTCT	p.Q157fs
XH_P50	8	24774968	24774968	Nonsense_Mutation	SNP	G	T	G	NEFM	c.G472T	p.E158X
XH_P50	8	25346120	25346120	Frame_Shift_Ins	INS	-	TATATTACCCAA	-	CDC42	nsATACATATATT	p.V514fs
XH_P50	8	25346122	25346122	Nonsense_Mutation	SNP	C	T	C	CDC42	c.C1543T	p.Q515X
XH_P50	8	27634219	27634219	Nonsense_Mutation	INS	-	TTTCAGTTGTTT	-	ESCO2	ATTATTTCAGT	b.513delinsYLFQLFX
XH_P50	8	42720633	42720633	Splice_Site	INS	-	A	-	RNF170	.	.
XH_P50	8	63492167	63492167	Frame_Shift_Ins	INS	-	TATTTTCATGTGC	-	NKAIN3	nsATTCTTATTCCA	p.L42fs
XH_P50	8	77764926	77764926	Frame_Shift_Ins	INS	-	AAATATCTTC	-	ZFH4	5770insAAATA	p.Q1923fs
XH_P50	8	95895095	95895095	In_Frame_Ins	INS	-	TTCTGCTTTAA	-	CNE2	nsAACTCTTAAAG	b.6delinsKELLQNNV
XH_P50	8	96259885	96259885	Frame_Shift_Ins	INS	-	TCTGTTTAAAT	-	C8orf37	584insTATTAA	p.Q195fs
XH_P50	8	96259887	96259887	Frame_Shift_Ins	INS	-	GTGTTGATTATG	-	C8orf37	582insCCATAAT	p.L194fs
XH_P50	8	97312024	97312024	In_Frame_Ins	INS	-	TTCTCAGCTCTT	-	PTDSS1	TGTGTTTCTCAG	delinsGSCVSQLFFMHL
XH_P50	8	101253136	101253136	Missense_Mutation	SNP	T	G	T	SPAG1	c.T2667G	p.I889M
XH_P50	8	101253138	101253138	Frame_Shift_Ins	INS	-	GGATCTTTTT	-	SPAG1	2670insGGAT	p.S890fs
XH_P50	8	101535000	101535000	Splice_Site	SNP	C	T	C	ANKRD46	.	.
XH_P50	8	104831857	104831857	Frame_Shift_Ins	INS	-	TTCCATATTTCT	-	RIMS2	123insTTCCATA	p.R41fs
XH_P50	8	104831858	104831858	Splice_Site	SNP	G	C	G	RIMS2	.	.
XH_P50	8	106813387	106813387	Frame_Shift_Ins	INS	-	TGAAATGGGAA	-	ZFPM2	nsAGGAGTGAATA	p.T359fs
XH_P50	8	108264179	108264179	Silent	SNP	G	A	G	ANGPT1	c.C801T	p.N267N
XH_P50	8	110424633	110424633	Nonsense_Mutation	INS	-	TACTTTAACTTT	-	PKHD1L1	nsCTGATTACTTT	b.742_7743delinsPX
XH_P50	8	125332390	125332390	Silent	SNP	C	A	C	TMEM65	c.G558T	p.L186L
XH_P50	8	139648997	139648997	Frame_Shift_Ins	INS	-	TTCTTTTCCTTC	-	COL22A1	nsAAGGAAAGG	p.Q1181fs
XH_P50	8	139648999	139648999	Missense_Mutation	SNP	G	T	G	COL22A1	c.C3541A	p.Q1181K
XH_P50	9	14750209	14750209	Frame_Shift_Ins	INS	-	AAATGCTTAATT	-	FREM1	insAAGAAATTA	p.F361fs
XH_P50	9	26905572	26905572	Nonsense_Mutation	INS	-	AAAAACAC	-	PLAA	55_2256insGTG	b.752_5753delinsX
XH_P50	9	26905574	26905574	In_Frame_Ins	INS	-	ATTAATAAATATC	-	PLAA	nsGGACGGGATAT	b.752delinsGRIFLIDY
XH_P50	9	27185586	27185586	Frame_Shift_Ins	INS	-	ATATTCACCATC	-	TEK	nsAGCCATATTCA	p.V282fs
XH_P50	9	27185588	27185588	In_Frame_Ins	INS	-	ATC	-	TEK	1847_848insAT	b.A283delinsDP
XH_P50	9	35398264	35398264	Frame_Shift_Ins	INS	-	CATTTTAAAGCT	-	UNC13B	565insTCATTTT	p.F1188fs
XH_P50	9	35853506	35853506	Missense_Mutation	SNP	T	C	T	TMEM8B	c.T1088C	p.V363A
XH_P50	9	43853575	43853575	Frame_Shift_Ins	INS	-	AAAAATGACA	-	CNTNAP3B	1836insAAAAA	p.S612fs
XH_P50	9	72365850	72365850	Frame_Shift_Ins	INS	-	ATAGTAGGAA	-	PTAR1	2_103insTTCTCA	p.I35fs
XH_P50	9	72365851	72365851	Silent	SNP	C	G	C	PTAR1	c.G102C	p.L34L
XH_P50	9	78923635	78923635	Frame_Shift_Ins	INS	-	TTTTTTTCTCTTA	-	PCSK5	nsTTAITTTTTTTT	p.C1200fs
XH_P50	9	78923636	78923636	Missense_Mutation	SNP	G	T	G	PCSK5	c.G3599T	p.C1200F
XH_P50	9	86917270	86917270	Silent	SNP	C	A	C	SLC28A3	c.G369T	p.L123L
XH_P50	9	86917272	86917272	In_Frame_Ins	INS	-	AGAGATAGTAG	-	SLC28A3	367insACTACTA	b.L123delinsTTISL
XH_P50	9	94118418	94118418	In_Frame_Ins	INS	-	TCC	-	AUH	281_282insGG	p.I94delinsME
XH_P50	9	94118419	94118419	In_Frame_Ins	INS	-	TTAGATGTTCT	-	AUH	281insAGAACAT	b.I94delinsKNIL
XH_P50	9	96860746	96860746	Frame_Shift_Ins	INS	-	GTGCTTCTCTTT	-	PTPDC1	899insTGTGCTT	p.A633fs
XH_P50	9	103109107	103109107	Nonsense_Mutation	INS	-	TTTTCATATGTT	-	TEX10	TGAGTAACATAA	b.257_K258delinsHEX
XH_P50	9	103947813	103947813	Frame_Shift_Ins	INS	-	AAGCAATAATA	-	PLPPR1	AAAAAGCAAAAT	p.I13fs
XH_P50	9	114989900	114989900	Silent	SNP	G	A	G	PTBP3	c.C954T	p.N318N
XH_P50	9	114989901	114989901	Nonsense_Mutation	INS	-	AATAACTACAA	-	PTBP3	53insTATTGTAG	b.N318delinsLX
XH_P50	9	116930659	116930659	Missense_Mutation	SNP	C	T	C	COL27A1	c.C824T	p.A275V
XH_P50	9	125618144	125618144	Nonsense_Mutation	INS	-	AGAATGAATGTT	-	RC3H2	nsATAGAAAACAT	b.823_5824delinsEX
XH_P50	9	125920648	125920648	Missense_Mutation	SNP	G	T	G	STRBP	c.C854A	p.T285N
XH_P50	9	125920650	125920650	Frame_Shift_Ins	INS	-	AAGGGCTTTATG	-	STRBP	52insTCATAAAG	p.M284fs
XH_P50	9	127670752	127670752	Splice_Site	INS	-	TAGAAGGGATTG	-	GOLGA1	.	.
XH_P50	9	131609088	131609088	Nonsense_Mutation	INS	-	CTGTTGGTAAAG	-	KYAT1	nsAAATACTACCC	b.H49_L50delinsQX
XH_P50	9	137642661	137642661	Missense_Mutation	SNP	C	T	C	COL5A1	c.C1595T	p.A532V
XH_P50	10	22830767	22830767	Silent	SNP	C	T	C	PIP4K2A	c.G825A	p.P275P
XH_P50	10	25839987	25839987	Nonsense_Mutation	INS	-	AATAAAATCTAA	-	GPR158	8insTTAAATAAA	b.p.Y496delinsYX
XH_P50	10	27375495	27375495	Nonsense_Mutation	INS	-	A	-	ANKRD26	c.681dupT	b.C228_H229delinsX
XH_P50	10	27375497	27375497	Nonsense_Mutation	INS	-	TAGTATGTTATG	-	ANKRD26	80insACATAACA	b.C27_K228delinsHITYX
XH_P50	10	31137741	31137741	Frame_Shift_Ins	INS	-	AAAGGAAGTGCA	-	ZNF438	1593insTGCAC	p.N531fs
XH_P50	10	31137743	31137743	Missense_Mutation	SNP	T	A	T	ZNF438	c.A1591T	p.NF531Y
XH_P50	10	38345331	38345331	In_Frame_Ins	INS	-	TGG	-	ZNF33A	2297_2298insTGT	b.Q766delinsHG
XH_P50	10	38345332	38345332	Frame_Shift_Ins	INS	-	AAAT	-	ZNF33A	2298_2299insAA	p.Q766fs
XH_P50	10	50732583	50732583	Frame_Shift_Ins	INS	-	CAGAGGGAGAC	-	ERCC6	893insAGTCTCC	p.A298fs
XH_P50	10	70513785	70513785	Frame_Shift_Ins	INS	-	TACACAAACATT	-	CCAR1	insGGTTACACA	p.N417fs
XH_P50	10	93572950	93572950	Nonsense_Mutation	INS	-	CAAATTAGATGA	-	TNKS2	1insATCAAAATT	b.I137delinsSNX
XH_P50	10	94291615	94291615	Nonsense_Mutation	INS	-	TATATTTTATGT	-	IDE	TATATACATAAA	b.A84_A185delinsYTX
XH_P50	10	120488899	120488899	Frame_Shift_Ins	INS	-	CTTTGTAATTTTG	-	CACUL1	nsAATCAAAATT	p.K169fs
XH_P50	10	129902700	129902700	Silent	SNP	C	T	C	MKI67	c.G6324A	p.Q2108Q
XH_P50	10	129904575	129904575	In_Frame_Ins	INS	-	GAGAAA	-	MKI67	448_4449insTTT	p.C1483delinsCF5
XH_P50	10	129905550	129905550	Silent	SNP	C	T	C	MKI67	c.G3474A	p.V1158V
XH_P50	10	129905551	129905551	Missense_Mutation	SNP	A	G	G	MKI67	c.T3473C	p.V1158A
XH_P50	10	133784428	133784428	Missense_Mutation	SNP	A	C	A	BNIP3	c.T524G	p.L175W
XH_P50	10	133784429	133784429	Frame_Shift_Ins	INS	-	TCTCT	-	BNIP3	522_523insAGA	p.L175fs

XH_P50	11	5686784	5686784	Frame_Shift_Ins	INS	-	AGTTACATTATA	-	TRIM5	insGGATATAAT	p.I333fs
XH_P50	11	9005101	9005101	In_Frame_Ins	INS	-	5GAATTTGCTTT	-	NRIP3	TAATAAAAAGCA	239delinsSNKSKFLE
XH_P50	11	10822531	10822531	Frame_Shift_Ins	INS	-	AGAATACATTA	-	EIF4G2	BinsTCTTTAATG	p.T468fs
XH_P50	11	16036585	16036585	Frame_Shift_Ins	INS	-	ACTAGAGAAAA	-	SOX6	554insGCTTTTC	p.R518fs
XH_P50	11	26569001	26569001	Nonsense_Mutation	INS	-	TAATTAATCCAA	-	ANO3	56insTTAATTAA	252_L253delinsCX
XH_P50	11	33308115	33308115	Nonsense_Mutation	INS	-	TATTAATGTCAA	-	HIPK3	AGAAATATTAAT	NS2delinsKKKYX
XH_P50	11	34991787	34991787	In_Frame_Ins	INS	-	TTTTCGAGGCA	-	PDHX	TGCTTTTTTGCA	delinsDRLLSFCRAHSLK
XH_P50	11	46369302	46369302	Silent	SNP	C	G	C	DGKZ	c.C93G	p.P31P
XH_P50	11	58892340	58892340	In_Frame_Ins	INS	-	TTTTCCAT	-	FAM111B	0_681insTTTTCA	D227delinsDFHI
XH_P50	11	58892342	58892342	Frame_Shift_Ins	INS	-	GGGT	-	FAM111B	682_683insGCC	p.E228fs
XH_P50	11	59245190	59245190	Frame_Shift_Ins	INS	-	CCTC	-	OR4D10	288_289insCCT	p.H96fs
XH_P50	11	59982088	59982088	Splice_Site	INS	-	TGATTAATCCTT	-	MS4A4E	-	-
XH_P50	11	62299214	62299214	Missense_Mutation	SNP	G	C	G	AHNAK	c.C2675G	p.A892G
XH_P50	11	73814541	73814541	Frame_Shift_Ins	INS	-	CA	-	C2CD3	2214_2215insT	p.D739fs
XH_P50	11	73814543	73814543	Frame_Shift_Ins	INS	-	AGAGGAATATA	-	C2CD3	2213insTATAT	p.Q738fs
XH_P50	11	75591057	75591057	Frame_Shift_Ins	INS	-	TTTAC	-	UVRAG	405_406insTTTA	p.L135fs
XH_P50	11	75591058	75591058	In_Frame_Ins	INS	-	ATTATTTC	-	UVRAG	6_407insATTAT	D136delinsDYFN
XH_P50	11	82536159	82536159	In_Frame_Ins	INS	-	TTTGATTTTCTA	-	PRCP	965insTAGAAA	G322delinsVENQS
XH_P50	11	82536161	82536161	Frame_Shift_Ins	INS	-	TGTAATTACC	-	PRCP	963insGGTAA	p.N321fs
XH_P50	11	83170879	83170879	Frame_Shift_Ins	INS	-	TCCTTCATCTG	-	DLG2	CATTGCAGTATG	p.P329fs
XH_P50	11	83182764	83182764	Nonsense_Mutation	INS	-	C	-	DLG2	c.427_428insG	T143_L144delinsX
XH_P50	11	83182765	83182765	Frame_Shift_Ins	INS	-	TTTAATAAAAAA	-	DLG2	TATTATTITTTAT	p.Y143fs
XH_P50	11	84245762	84245762	Frame_Shift_Ins	INS	-	TTTGGGACATAT	-	DLG2	AAAAATATGTCC	p.Q19fs
XH_P50	11	89820188	89820188	Frame_Shift_Ins	INS	-	T	-	UBTF1L	c.1072dupT	p.N357fs
XH_P50	11	89820190	89820190	Frame_Shift_Ins	INS	-	TGGTATCCAT	-	UBTF1L	1074insTTGTA	p.C38fs
XH_P50	11	95519416	95519416	Frame_Shift_Ins	INS	-	CA	-	FAM76B	c.229_230insTG	p.N77fs
XH_P50	11	95519418	95519418	Nonsense_Mutation	INS	-	TAAAGCATACCT	-	FAM76B	5AAGAAAGGTAT	p.C76delinsX
XH_P50	11	101833817	101833817	Frame_Shift_Ins	INS	-	ACCTTTTCTCTT	-	CEP126	1052insACCTTTT	p.A684fs
XH_P50	11	103027365	103027365	Nonsense_Mutation	INS	-	AAAGTTAAGTG	-	DYNC2H1	994insAAAAAGT	L1332delinsKKXS
XH_P50	11	103027367	103027367	Frame_Shift_Ins	INS	-	CTATTTTACA	-	DYNC2H1	3996insCTATT	p.L1332fs
XH_P50	11	110007772	110007772	Missense_Mutation	SNP	A	G	A	ZC3H12C	c.A406G	p.L136V
XH_P50	11	110007774	110007774	In_Frame_Ins	INS	-	GTTACG	-	ZC3H12C	08_409insGTTA	p.L136delinsIVT
XH_P50	11	110035528	110035528	Missense_Mutation	SNP	T	A	T	ZC3H12C	c.T1718A	p.M573fs
XH_P50	11	110035530	110035530	In_Frame_Ins	INS	-	AGCAATGGCCTT	-	ZC3H12C	TCTTTAAGCAAT	delinsHYIFQKWPSIWSS
XH_P50	11	116827759	116827759	In_Frame_Ins	INS	-	AATTGTGTCTTT	-	SIK3	nsTTTAAAGAAC	K99delinsFKEQIKK
XH_P50	11	118344557	118344557	Frame_Shift_Ins	INS	-	GT	-	KMT2A	2683_2684insG	p.K895fs
XH_P50	11	118344558	118344558	In_Frame_Ins	INS	-	AAAGTT	-	KMT2A	84_2685insAAAG	p.K895delinsKKL
XH_P50	11	118897735	118897736	Frame_Shift_Del	DEL	AC	-	AC	SLC37A4	c.695_696del	p.G232fs
XH_P50	11	124412781	124412781	Frame_Shift_Ins	INS	-	TTGCTTATTAGT	-	OR8B12	CACACACTAATA	p.M257fs
XH_P50	12	968566	968566	Frame_Shift_Ins	INS	-	AACACCATTAG	-	WNK1	1557insAACAC	p.N519fs
XH_P50	12	970321	970321	Missense_Mutation	SNP	G	T	G	WNK1	c.G1763T	p.S588I
XH_P50	12	994572	994572	Missense_Mutation	SNP	T	G	T	WNK1	c.T3861G	p.H1287Q
XH_P50	12	994573	994573	In_Frame_Ins	INS	-	TGTGGATGT	-	WNK1	2_3863insTGTG	L288delinsMWMCM
XH_P50	12	7045891	7045891	In_Frame_Ins	INS	-	CAGCAGCAG	-	ATN1	1462insCAGC	Q487delinsQQQQ
XH_P50	12	9094537	9094537	Splice_Site	INS	-	TGACCTCTCCCC	-	M6PR	-	-
XH_P50	12	10762506	10762506	In_Frame_Ins	INS	-	TTAATTTTA	-	MAGOHB	9_50insTAAAT	p.K17delinsIKLK
XH_P50	12	10762508	10762508	Frame_Shift_Ins	INS	-	TCTT	-	MAGOHB	c.47_48insAAGA	p.L16fs
XH_P50	12	10959090	10959090	Missense_Mutation	SNP	G	T	G	TAS2R8	c.C490A	p.H164N
XH_P50	12	10959092	10959092	Nonsense_Mutation	INS	-	ACCTTTAGCTAT	-	TAS2R8	5TAAGATAGCTA	A163_H164delinsIRX
XH_P50	12	18865886	18865886	Missense_Mutation	SNP	C	G	C	PLCZ1	c.G292C	p.D98H
XH_P50	12	18865888	18865888	Frame_Shift_Ins	INS	-	ATCCATG	-	PLCZ1	89_290insCATG	p.I97fs
XH_P50	12	26275216	26275218	In_Frame_Del	DEL	GCG	-	GCG	BHLHE41	c.1230_1232del	p.410_411del
XH_P50	12	30872139	30872139	Nonsense_Mutation	INS	-	TTTGTAATAATT	-	CAPRIN2	54insATAAATT	688_Q689delinsKX
XH_P50	12	39688311	39688311	Nonsense_Mutation	INS	-	TCTTCATTCATG	-	KIF21A	ATTAAACATGA	0_V1611delinsRYCQX
XH_P50	12	39726519	39726519	In_Frame_Ins	INS	-	ATTTTGTTCCTC	-	KIF21A	2622insAGGGAA	T874delinsTGNKI
XH_P50	12	40076802	40076802	Nonsense_Mutation	INS	-	C12orf40	-	C12orf40	1077insGTAAAT	p.N359delinsKX
XH_P50	12	46318839	46318839	In_Frame_Ins	INS	-	TTAGCAACTCAA	-	SCAF11	3578insTTGAGT	Q1193delinsLELLK
XH_P50	12	46318841	46318841	Missense_Mutation	SNP	G	T	G	SCAF11	c.C3576A	p.D1192E
XH_P50	12	49439901	49439901	Missense_Mutation	SNP	G	A	G	KMT2D	c.C4640T	p.A1547V
XH_P50	12	50055833	50055833	Splice_Site	INS	-	CTTATCAAAGTA	-	FMNL3	-	-
XH_P50	12	55688436	55688436	Frame_Shift_Ins	INS	-	G	-	OR6C6	c.580_581insC	p.E194fs
XH_P50	12	55688437	55688437	Frame_Shift_Ins	INS	-	CCCTT	-	OR6C6	579_580insAAG	p.E194fs
XH_P50	12	55945642	55945642	Frame_Shift_Ins	INS	-	CATAATAGTCA	-	OR6C4	633insCATAAT	p.L211fs
XH_P50	12	70070828	70070828	Nonsense_Mutation	INS	-	GATT	-	BEST3	416_417insAAT	T139_L140delinsX
XH_P50	12	70070830	70070830	Frame_Shift_Ins	INS	-	ACAT	-	BEST3	414_415insATG	p.Y139fs
XH_P50	12	70988361	70988361	Nonsense_Mutation	INS	-	AATAAGTCAA	-	PTPRB	7_748insTTGACT	150_H251delinsLTYX
XH_P50	12	75824837	75824837	Frame_Shift_Ins	INS	-	CTGGATTTCATA	-	GLPR1L2	932insCTGGATT	p.E311fs
XH_P50	12	85450107	85450107	Nonsense_Mutation	INS	-	CTGTCTATCTAC	-	LRR1Q1	TATAGTCTGTCT	L2_G513delinsILLUX
XH_P50	12	100806640	100806640	Nonsense_Mutation	INS	-	TTTTTTTAACTTTA	-	SLC17A8	TTTTTTTTTTTTTTT	G378delinsSKFFFFFX
XH_P50	12	110600869	110600869	In_Frame_Ins	INS	-	TAGATGCCTT	-	IFT81	7_258insTAGAT	p.E86delinsDRCL
XH_P50	12	110974887	110974887	Frame_Shift_Ins	INS	-	G	-	PPTC7	c.869_870insC	p.D290fs
XH_P50	12	116457180	116457180	Frame_Shift_Ins	INS	-	CAGACAAATTGT	-	MED13L	58insATACAATT	p.L286fs
XH_P50	12	120760118	120760118	Nonsense_Mutation	INS	-	5TATTATTITTTT	-	PLA2G1B	nsTAGAAAAAAAT	p.K109delinsX
XH_P50	12	123834966	123834966	Nonsense_Mutation	INS	-	TTTTTTTTT	-	SBN01	2_23insAAAAAA	p.L8delinsX
XH_P50	12	123834968	123834968	Frame_Shift_Ins	INS	-	GATAG	-	SBN01	20_21insCTAT	p.D7fs
XH_P50	12	124144425	124144425	Frame_Shift_Ins	INS	-	CATTCCCT	-	GTFF2H3	89_640insCATTC	p.F213fs
XH_P50	13	28931811	28931811	In_Frame_Ins	INS	-	AGTCTG	-	FLT1	27_2128insCAG	G710delinsQTG
XH_P50	13	31037421	31037421	In_Frame_Ins	INS	-	5AAAACTACTAT	-	HMG81	9insGGATAGTA	R73delinsRDSIFQ
XH_P50	13	42877042	42877042	Frame_Shift_Ins	INS	-	TTCTACTTTTATA	-	AKAP11	nsTTCTCTCTCTAC	p.T1387fs
XH_P50	13	46627900	46627900	Nonsense_Mutation	INS	-	ATCAGAGATTATT	-	CPB2	DinsTAAAAATAAA	Y337delinsLKIIIX
XH_P50	13	52605055	52605055	Frame_Shift_Ins	INS	-	GCTTCCC	-	UTP14C	15_2116insSGCT	p.T705fs
XH_P50	13	52674003	52674003	Missense_Mutation	SNP	A	T	A	NEK5	c.T902A	p.K101K
XH_P50	13	52674004	52674004	Frame_Shift_Ins	INS	-	5TTTGTGTGTTC	-	NEK5	01insCAAAACAA	p.I301fs
XH_P50	13	99907754	99907754	Frame_Shift_Ins	INS	-	ACATTTTTTTTCT	-	GRP18	73insAGAAAAA	p.Q125fs
XH_P50	13	103443461	103443461	Frame_Shift_Ins	INS	-	TTGTITTTTCTAA	-	KDEL1	ATACATTAGAAA	p.Q291fs
XH_P50	13	115090560	115090560	Frame_Shift_Ins	INS	-	C	-	CHAMP1	1243_1244insC	p.V415fs
XH_P50	13	115090561	115090561	Frame_Shift_Ins	INS	-	CCTGGAA	-	CHAMP1	14_1245insCCTG	p.V415fs
XH_P50	14	20295722	20295722	In_Frame_Ins	INS	-	CTCTCCTAT	-	OR4N2	5_116insCTCTC	p.L39delinsPLF
XH_P50	14	20388827	20388827	Nonsense_Mutation	INS	-	GATATAATGTGC	-	OR4K5	63insGATATAAT	p.Q21delinsQIX
XH_P50	14	24458283	24458283	Missense_Mutation	SNP	G	T	G	DHR54L2	c.G127T	p.G43W
XH_P50	14	30194864	30194864	Nonsense_Mutation	INS	-	TTAGAAGTTGT	-	PRKD1	281insACAACT	94_Y95delinsSYNF
XH_P50	14	57863532	57863532	In_Frame_Ins	INS	-	GCACCTACACAC	-	NAA30	835insGCACCTA	T278delinsMAPTH
XH_P50	14	60752440	60752440	Frame_Shift_Ins	INS	-	AGTTACTATGT	-	PPM1A	934insAGTTATA	p.Y311fs
XH_P50	14	74404370	74404370	Frame_Shift_Ins	INS	-	CAAAATAAAATA	-	FAM161B	89insTACTATTTA	p.K597fs
XH_P50	14	75150153	75150153	Frame_Shift_Ins	INS	-	TTTTT	-	AREL1	326_327insAAA	p.V109fs
XH_P50	14	75150154	75150154	Frame_Shift_Ins	INS	-	AAAATAATAC	-	AREL1	326insGTATTA	p.V109fs
XH_P50	14	76249769	76249769	Frame_Shift_Ins	INS	-	A	-	TTL5	c.2883dupA	p.P961fs
XH_P50	14	76249771	76249771	Nonsense_Mutation	INS	-	TGAACACAGTCT	-	TTL5	TTTTACTGAACA	G62_C963delinsQFYX

XH_P50	14	94008994	94008994	Silent	SNP	C	T	C	UNC79	c.C1707T	p.F569F
XH_P50	14	95085756	95085756	Missense_Mutation	SNP	A	C	A	SERPINA3	c.A868C	p.M290L
XH_P50	14	95085757	95085757	Missense_Mutation	SNP	T	A	T	SERPINA3	c.T869A	p.M290K
XH_P50	15	28090159	28090159	Missense_Mutation	SNP	C	A	C	OCA2	c.G2306T	p.C769F
XH_P50	15	32688657	32688657	Missense_Mutation	SNP	T	G	T	GOLGA8K	c.A962C	p.E321A
XH_P50	15	40488938	40488938	Frame_Shift_Ins	INS	-	GGTGCTTAGGA	-	BUB1B	insTTCTGGTGC	p.A417fs
XH_P50	15	50773953	50773953	In_Frame_Ins	INS	-	CTTTTC	-	USP8	263_1264insCTT	p.E421delinsELF
XH_P50	15	50773955	50773955	Frame_Shift_Ins	INS	-	CTCTGAGG	-	USP8	5_1266insCTCT	p.Q422fs
XH_P50	15	54919308	54919308	Frame_Shift_Ins	INS	-	G	-	UNC13C	c.6642_6643ins	p.A2214fs
XH_P50	15	54919310	54919310	Nonstop_Mutation	INS	-	TGGATT	-	UNC13C	44_6645insTGG	X2215delinsCGL
XH_P50	15	56132917	56132917	Nonsense_Mutation	INS	-	GTCTTTTTC	-	NEDD4	1_2888insGAAA	p.Y963delinsX
XH_P50	15	56132918	56132918	In_Frame_Ins	INS	-	CTT	-	NEDD4	2886_2887insAA	p.Y963delinsKY
XH_P50	15	56393751	56393751	Missense_Mutation	SNP	T	A	T	RFK7	c.A617T	p.E206V
XH_P50	15	56393753	56393753	Nonsense_Mutation	INS	-	ACATTACTGT	-	RFK7	615insACAGT	#05_E206delinsAQX
XH_P50	15	60770159	60770159	Nonsense_Mutation	INS	-	AATCTATTTTCTT	-	ICE2	ACATAAGAAAA	1_V6delinsVDIRKX
XH_P50	15	62214705	62214705	Frame_Shift_Ins	INS	-	TATGAGTACAT	-	VPS13C	6737insATGTA	p.C2246fs
XH_P50	15	63946322	63946322	Frame_Shift_Ins	INS	-	TGGTTTGATATA	-	HERC1	6insCTATTATAT	p.N3429fs
XH_P50	15	68657093	68657093	Missense_Mutation	SNP	C	T	C	ITGA11	c.G309A	p.M103I
XH_P50	16	818524	818524	Missense_Mutation	SNP	G	A	G	MSLN	c.G1766A	p.G589D
XH_P50	16	2812890	2812890	Silent	SNP	A	G	A	SRRM2	c.A2361G	p.K787K
XH_P50	16	3458697	3458697	Silent	SNP	C	T	C	ZNF174	c.C1002T	p.S334S
XH_P50	16	3534892	3534892	Missense_Mutation	SNP	G	A	G	NAA60	c.G539A	p.R180Q
XH_P50	16	11862341	11862341	Frame_Shift_Ins	INS	-	ACGCAGAGAG	-	ZC3H7A	1190insCTCTC	p.S397fs
XH_P50	16	15180042	15180042	Frame_Shift_Ins	INS	-	TTTTATGAATTT	-	RRN3	6insATAAAATCA	p.A109fs
XH_P50	16	15180043	15180043	Missense_Mutation	SNP	C	T	C	RRN3	c.G325A	p.A109T
XH_P50	16	24580749	24580749	Frame_Shift_Ins	INS	-	ATTTTTCATACCA	-	RBBP6	ATAATATTTTTCT	p.N879fs
XH_P50	16	24582372	24582372	Nonsense_Mutation	INS	-	TTTTTTCCT	-	RBBP6	3_3884insTTTTT	E1295delinsVFSX
XH_P50	16	24582373	24582373	Missense_Mutation	SNP	A	C	A	RBBP6	c.A3884C	p.E1295A
XH_P50	16	24582709	24582709	Frame_Shift_Ins	INS	-	CCTCATGTTGT	-	RBBP6	4221insCCTCA	p.K1407fs
XH_P50	16	48595285	48595285	Nonsense_Mutation	INS	-	ATGGAATACAA	-	N4BP1	cGAGGATGTTGT	B3_D424delinsTISWEX
XH_P50	16	49669843	49669843	Missense_Mutation	SNP	G	A	G	ZNF423	c.C2869T	p.R957C
XH_P50	16	55866934	55866934	Missense_Mutation	SNP	A	C	A	CES1	c.T34G	p.S12A
XH_P50	16	56377755	56377755	Missense_Mutation	SNP	T	A	T	GNAO1	c.T958A	p.Y320N
XH_P50	17	5086248	5086248	Missense_Mutation	SNP	C	T	C	ZNF594	c.G1304A	p.S435N
XH_P50	17	5086250	5086250	Silent	SNP	A	G	A	ZNF594	c.T1302C	p.C434C
XH_P50	17	6553696	6553696	Missense_Mutation	SNP	G	A	G	MED31	c.C86T	p.A29V
XH_P50	17	6553697	6553697	Frame_Shift_Ins	INS	-	CTACAGATTTTT	-	MED31	5insAAAAAATC	p.A29fs
XH_P50	17	8790868	8790868	Silent	SNP	C	T	C	PIK3R5	c.G591A	p.P197P
XH_P50	17	10354722	10354722	Frame_Shift_Ins	INS	-	TGAGACAGTAA	-	MYH4	786insTTTTACT	p.E1262fs
XH_P50	17	10544656	10544656	Frame_Shift_Ins	INS	-	ACATGTTCTATA	-	MYH3	3insGCATATAG	p.T665fs
XH_P50	17	15234782	15234782	Nonsense_Mutation	INS	-	TAAACCACTATCA	-	TEKT3	21insTGATAGT	N41_L42delinsX
XH_P50	17	15234783	15234783	Silent	SNP	G	A	G	TEKT3	c.C120T	p.S40S
XH_P50	17	15620500	15620500	Nonsense_Mutation	INS	-	CTGATGCTTAGT	-	ZNF286A	370insTCTGATG	457_T458delinsLX
XH_P50	17	27185649	27185649	Frame_Shift_Ins	INS	-	ACACACCTTTGT	-	ERAL1	insCCACACACC	p.E255fs
XH_P50	17	29632121	29632121	Frame_Shift_Ins	INS	-	GCTATAATCATC	-	EVI2B	07insTGATGATT	p.Q169fs
XH_P50	17	30521112	30521112	Nonsense_Mutation	INS	-	TAAATTAGTAA	-	RHOT1	TAAAGTAATAAT	A85_Y286delinsEIKX
XH_P50	17	36614457	36614457	Missense_Mutation	SNP	C	T	C	ARHGAP23	c.C175T	p.R59C
XH_P50	17	38548595	38548595	Splice_Site	INS	-	TG	-	TOP2A		
XH_P50	17	39432066	39432066	Silent	SNP	G	T	G	KRTAP9-7	c.G117T	p.V39V
XH_P50	17	42960502	42960502	In_Frame_Ins	INS	-	TTTCTCTGTT	-	EFTUD2	1_346insAACAG	E116delinsNRKE
XH_P50	17	42960503	42960503	Frame_Shift_Ins	INS	-	TAGT	-	EFTUD2	344_345insACT	p.1115fs
XH_P50	17	56694982	56694982	Splice_Site	INS	-	GTCTTACTA	-	TEX14		
XH_P50	17	58034731	58034731	Frame_Shift_Ins	INS	-	CATTAAATGATTA	-	RNF11	ATCAGTAATCA	p.M287fs
XH_P50	17	60447650	60447650	Frame_Shift_Ins	INS	-	AAAAATCTTTAA	-	EFCAB3	insCAAAAATCT	p.M1fs
XH_P50	17	67108413	67108413	In_Frame_Ins	INS	-	GGTAGCTGT	-	ABCA6	2_2043insACAG	D681delinsEQLP
XH_P50	17	78313696	78313696	Silent	SNP	C	T	C	RNF213	c.C5529T	p.A1843A
XH_P50	17	79514221	79514221	Silent	SNP	G	A	G	FAAP100	c.C1887T	p.S629S
XH_P50	18	9255924	9255924	Nonsense_Mutation	INS	-	GGTTTTTCTTTA	-	ANKRD12	TTCTCAGGTTTT	4delinsIASQVFLYFPLX
XH_P50	18	9258456	9258456	In_Frame_Ins	INS	-	CCAGTTTGTTTT	-	ANKRD12	insCTCTCCAGTT	708delinsTLQVFFF
XH_P50	18	10736650	10736650	Frame_Shift_Ins	INS	-	TTAAATTGTAAT	-	PIEZO2	92insTCATTACA	p.E1564fs
XH_P50	18	12697401	12697401	Frame_Shift_Ins	INS	-	TTGTAAATATAT	-	CEP76	2insAAATATAT	p.G101fs
XH_P50	18	12697402	12697402	Missense_Mutation	SNP	C	T	C	CEP76	c.G301A	p.G101R
XH_P50	18	13731869	13731869	Frame_Shift_Ins	INS	-	AACTCTTTTCTC	-	RNMT	54insAAACTCT	p.S118fs
XH_P50	18	14851989	14851989	In_Frame_Ins	INS	-	ATTTCTTTGCTCT	-	ANKRD30B	0insGATTITCTT	1230delinsQYFFVLF
XH_P50	18	18629840	18629840	Nonsense_Mutation	INS	-	TCCTTTAGACAT	-	ROCK1	nsACAATGTCTA	p.Y59delinsX
XH_P50	18	19153731	19153731	Frame_Shift_Ins	INS	-	AG	-	ESCO1	1073_1074insC	p.Q358fs
XH_P50	18	19153733	19153733	In_Frame_Ins	INS	-	ACTCAAAGT	-	ESCO1	1_1072insACTT	Q358delinsTLSQ
XH_P50	18	57022886	57022886	Frame_Shift_Ins	INS	-	ATTCTTTTGACA	-	LMAN1	TCATTGTCAAA	p.A73fs
XH_P50	18	67760029	67760029	Nonsense_Mutation	INS	-	TTTTGACTTTCTC	-	RTTN	TAAAAAGAAAA	393_F394delinsSX
XH_P50	18	71928177	71928177	Frame_Shift_Ins	INS	-	TAAACTACTTTT	-	CYB5A	61insAAAAAGTA	p.D87fs
XH_P50	18	76753822	76753822	Missense_Mutation	SNP	G	A	G	SALL3	c.G1831A	p.A611T
XH_P50	19	6495405	6495405	Missense_Mutation	SNP	C	T	C	TUBB4A	c.G889A	p.G297S
XH_P50	19	8993443	8993443	Silent	SNP	C	T	C	MUC16	c.G41646A	p.L13882L
XH_P50	19	11943349	11943349	Nonsense_Mutation	INS	-	AGGGTTTCTCTC	-	ZNF440	9insATAGGGTT	453_G454delinsSX
XH_P50	19	12089558	12089558	Nonsense_Mutation	INS	-	TAGGGTTT	-	ZNF763	8_829insTAGGG	276_H277delinsAX
XH_P50	19	19137021	19137021	Nonsense_Mutation	INS	-	CAGGTCA	-	SUGP2	85_136insTGAC	V46_P47delinsX
XH_P50	19	21366659	21366659	Frame_Shift_Ins	INS	-	GGACCGGT	-	ZNF431	6_1557insGGAC	p.G519fs
XH_P50	19	21992242	21992242	Frame_Shift_Ins	INS	-	T	-	ZNF43	c.401_402insA	p.V134fs
XH_P50	19	21992244	21992244	In_Frame_Ins	INS	-	AAATGTAAGAA	-	ZNF43	400insTTCTTTA	V134delinsFFTFV
XH_P50	19	22156350	22156350	Missense_Mutation	SNP	G	A	G	ZNF208	c.C1486T	p.P496S
XH_P50	19	22156351	22156351	Missense_Mutation	SNP	T	A	T	ZNF208	c.A1485T	p.K495N
XH_P50	19	22363643	22363643	Silent	SNP	C	T	C	ZNF676	c.G876A	p.S292S
XH_P50	19	22375831	22375831	Silent	SNP	C	T	C	ZNF676	c.G117A	p.V39V
XH_P50	19	22375832	22375832	Nonsense_Mutation	INS	-	TTTTAAAAATTC	-	ZNF676	TCTTAGAAATTT	E40delinsEFLEIKAX
XH_P50	19	22498426	22498426	Missense_Mutation	SNP	C	G	C	ZNF729	c.C2207G	p.A736G
XH_P50	19	22940265	22940265	Missense_Mutation	SNP	A	G	A	ZNF99	c.T2446C	p.S816P
XH_P50	19	22940554	22940554	Silent	SNP	A	G	A	ZNF99	c.T2157C	p.T719T
XH_P50	19	23543927	23543927	Missense_Mutation	SNP	T	A	T	ZNF91	c.A1758T	p.R586S
XH_P50	19	23543928	23543928	Missense_Mutation	SNP	C	G	C	ZNF91	c.G1757C	p.R586T
XH_P50	19	24310638	24310638	Frame_Shift_Ins	INS	-	TCAGTATGAATT	-	ZNF254	TTCTCTTCAGTA	p.F527fs
XH_P50	19	37210568	37210568	In_Frame_Ins	INS	-	GTTGCTCTCTCT	-	ZNF567	TATTGGTTGCTC	delinsCFFSILVALLFLY
XH_P50	19	37482178	37482178	In_Frame_Ins	INS	-	CAGGCC	-	ZNF568	14_315insCAGG	N105delinsNRP
XH_P50	19	37482179	37482179	Missense_Mutation	SNP	T	A	T	ZNF568	c.T315A	p.N51fs
XH_P50	19	44662086	44662086	In_Frame_Ins	INS	-	AATGGTTTTTCC	-	ZNF234	1918insAATGG	L639delinsLNGFS
XH_P50	19	52003310	52003310	Frame_Shift_Ins	INS	-	TCTCTCCACCTG	-	SIGLEC12	TTCCAGGTGGA	p.G106fs
XH_P50	19	52941506	52941506	In_Frame_Ins	INS	-	AGG	-	ZNF534	1709_710insAG	p.T237delinsKA
XH_P50	19	52941507	52941507	Nonsense_Mutation	INS	-	TTTTCCCTAATG	-	ZNF534	711insTTTTCCC	T237delinsTFPX
XH_P50	19	53573079	53573079	Nonsense_Mutation	INS	-	AATCTAACTAT	-	ZNF160	708insATAGTT	T236_E237delinsQX

XH_P50	19	53573081	53573081	Missense_Mutation	SNP	G	C	G	ZNF160	c.C706G	p.H236D
XH_P50	19	53885191	53885191	Frame_Shift_Ins	INS	-	TATGA	-	ZNF525	359_1360insTA	p.S453fs
XH_P50	19	53885192	53885192	Frame_Shift_Ins	INS	-	TTCAAGGTTTGA	-	ZNF525	361insTTTCAAG	p.L454fs
XH_P50	19	55814140	55814140	Silent	SNP	C	T	C	BRSK1	c.C933T	p.S311S
XH_P50	19	57286752	57286752	Frame_Shift_Ins	INS	-	AAACAGTGTGC	-	ZIM2	888insGCACAC	p.K296fs
XH_P50	19	58005234	58005234	Missense_Mutation	SNP	A	T	A	ZNF419	c.A1174T	p.S392C
XH_P50	19	58018201	58018201	In_Frame_Ins	INS	-	CCCTAC	-	ZNF773	735_736insCCCTb.P245delinsPPY	p.S483F
XH_P50	20	3128699	3128699	In_Frame_Ins	INS	-	GCAGAGAA	-	FASTKD5	7_1018insTTCTb.I340delinsFCI	p.S390fs
XH_P50	20	31385071	31385093	Frame_Shift_Del	DEL	TGCTTTTGA	-	5CTGCTTTGACAG	DNMT3B	c.1168_1190del	p.E390fs
XH_P50	20	33703671	33703671	In_Frame_Ins	INS	-	AGAAAA	-	EDEM2	190_1191insTTTb.V397delinsVFL	p.S390fs
XH_P50	20	33703673	33703673	In_Frame_Ins	INS	-	ACTGTT	-	EDEM2	88_1189insAACb.V397delinsNSV	p.S390fs
XH_P50	20	37580853	37580853	Missense_Mutation	SNP	C	T	C	FAM83D	c.C1448T	p.S483F
XH_P50	20	44520238	44520243	In_Frame_Del	DEL	CTGCTG	-	CTGCTG	CTSA	c.85_90del	p.29_30del
XH_P50	20	47685312	47685312	Frame_Shift_Ins	INS	-	ATTATTTTTTTG	-	CSE1L	hsACTTATTATT	p.S210fs
XH_P50	21	10942923	10942923	Nonsense_Mutation	INS	-	TTGATTA	-	TPTE	9_250insTAAATb.R84_V85delinsX	p.S483F
XH_P50	21	10942924	10942924	Frame_Shift_Ins	INS	-	TTGTATTA	-	TPTE	8_249insTAAAT	p.R83fs
XH_P50	21	46066764	46066764	Missense_Mutation	SNP	C	T	C	KRTAP10-11	c.C389T	p.S130F
XH_P50	22	19221009	19221009	Frame_Shift_Ins	INS	-	AAGGTAACGT	-	CLTCL1	1304insACGT	p.L435fs
XH_P50	22	21065645	21065645	Silent	SNP	A	G	A	PI4KA	c.T5907C	p.G1969G
XH_P50	22	36055616	36055616	Nonsense_Mutation	SNP	T	A	T	APOL6	c.T1005A	p.C335X
XH_P50	22	36055618	36055618	In_Frame_Ins	INS	-	TTC	-	APOL6	1007_1008insT	p.V336delinsVS
XH_P50	22	36922180	36922180	Splice_Site	INS	-	TCCTGAATTTCT	-	EIF3D	-	-
XH_P50	22	50658424	50658424	Missense_Mutation	SNP	T	C	T	TUBGCP6	c.A4129G	p.T1377A
XH_P50	X	11157019	11157019	Silent	SNP	G	A	G	ARHGAP6	c.C2349T	p.T783T
XH_P50	X	17745550	17745550	Frame_Shift_Ins	INS	-	AGTAAAGA	-	NHS	0_2731insAGTA	p.L910fs
XH_P50	X	17745551	17745551	Nonsense_Mutation	INS	-	TGAACCTTCCAA	-	NHS	732insCTTGAAC	p.H911delinsPX
XH_P50	X	129055322	129055322	In_Frame_Ins	INS	-	AGGGACAAGGA	-	UTP14A	ATGACAGGGAC	hinsALHSLMTGTRSSSTSS
XH_P50	X	133927918	133927918	Frame_Shift_Ins	INS	-	T	-	FAM122B	c.103_104insA	p.L35fs
XH_P50	X	133927920	133927920	Frame_Shift_Ins	INS	-	AGTTCTT	-	FAM122B	01_102insAAGA	p.D34fs
XH_P50	X	140993642	140993642	Missense_Mutation	SNP	C	T	C	MAGEC1	c.C452T	p.T151I
XH_P50	1	207930551	207930551	Splice_Site	INDEL	-	GT	GT	CD46	86+5_286+6dupGT	-
XH_P50	13	103443461	103443461	Frame_Shift_Ins	INDEL	-	TTGTTTTTCTAA	TTGTTTTTCTAA	KDEL1	ATACATTAGAAA	P.Q72fs
XH_P50	19	24310638	24310638	Frame_Shift_Ins	INDEL	-	TCAGTATGAATT	TCAGTATGAATT	ZNF254	TTCTCTTCAGTA	P.W572fs
XH_P50	5	102895170	102895170	Splice_Site	INDEL	-	CGTTAGGAACCA	CGTTAGGAACCA	NUDT12	AAGCCTTGTTCTCTAA	c.AAGCAATGAAGT
XH_P50	8	108264179	108264179	Silent	SNV	G	A	A	ANGPT1	c.1401C>T	P.N467N
XH_P50	8	125332390	125332390	Silent	SNV	C	A	A	TMEM65	c.558G>T	P.L186L
XH_P50	9	35853506	35853506	Missense_Mutation	SNV	T	C	C	TMEM8B	c.1088T>C	P.V363A
XH_P50	X	11157019	11157019	Silent	SNV	G	A	A	ARHGAP6	c.2889C>T	P.P963T
XH_P51	12	57574227	57574227	Missense_Mutation	SNP	G	A	A	LRP1	c.5351G>A	p.S1784N
XH_P51	13	110435786	110435786	Missense_Mutation	SNP	G	C	C	IRS2	c.2615C>G	p.P872R
XH_P51	14	20923826	20923826	Missense_Mutation	SNP	G	A	A	APEX1	c.22G>A	p.G8R
XH_P51	14	50971559	50971559	Missense_Mutation	SNP	G	A	A	MAP4K5	c.125C>T	p.T42I
XH_P51	16	2124385	2124385	Missense_Mutation	SNP	T	C	C	TSC2	c.2540T>C	p.L847P
XH_P51	17	15965470	15965470	Missense_Mutation	SNP	T	C	C	NCOR1	c.5336A>G	p.N1779S
XH_P51	17	16024548	16024548	Missense_Mutation	SNP	G	A	A	NCOR1	c.1670C>T	p.T557I
XH_P51	18	23658032	23658032	Splice_Site	SNP	A	C	C	S518	c.231+8T>G	-
XH_P51	19	1219423	1219423	Splice_Site	SNP	G	A	A	STK11	c.464+11G>A	-
XH_P51	-	-	-	Frame_Shift_Del	INS	-	-	-	RANBP2	c.8262_8265del	p.E2756Ffs*15
XH_P51	20	57429128	57429128	Missense_Mutation	SNP	G	A	A	GNAS	c.808G>A	p.A270T
XH_P51	22	41572288	41572288	Missense_Mutation	SNP	C	T	T	EP300	c.4817C>T	p.A1606V
XH_P51	5	225639	225639	Missense_Mutation	SNP	C	T	T	SDHA	c.418C>T	p.H140Y
XH_P51	-	-	-	Frame_Shift_Ins	INS	-	-	-	APC	c.5138dup	p.L1713Ffs*3
XH_P51	-	-	-	Frame_Shift_Del	INS	-	-	-	KMT2C	c.7307del	p.P2436Hfs*16
XH_P51	-	-	-	In_Frame_Ins	INS	-	-	-	MED12	c.6223_6228dup	p.Q2075_Q2076dup
XH_P51	-	-	-	Splice_Site	SNP	-	-	-	ATRX	5787-8_5787-5d	-
XH_P51	1	10364381	10364381	Missense_Mutation	SNP	A	T	A	KIF1B	c.A3138T	p.Q1046H
XH_P51	1	10364382	10364382	Nonsense_Mutation	INS	-	TCTGTTATGATG	-	KIF1B	140insTTCTGTT	b.R1048delinsLLX
XH_P51	1	12907844	12907844	Nonsense_Mutation	SNP	G	T	G	HNRNPCL1	c.C299A	p.S100X
XH_P51	1	13183574	13183574	Missense_Mutation	SNP	G	T	G	HNRNPCL2	c.C299A	p.S100Y
XH_P51	1	14105203	14105203	Nonsense_Mutation	INS	-	GATTCAAGTTAT	-	PRDM2	insAATGATTCAAp.V104delinsEX	p.H893fs
XH_P51	1	16255414	16255414	Frame_Shift_Ins	INS	-	TTTTTCCTCCGT	-	SPEN	2680insTATTTCC	p.H893fs
XH_P51	1	16255416	16255416	Missense_Mutation	SNP	C	T	C	SPEN	c.C2681T	p.T894I
XH_P51	1	19671681	19671681	Missense_Mutation	SNP	C	G	C	CAPZB	c.G654C	p.E218D
XH_P51	1	21268266	21268266	Frame_Shift_Ins	INS	-	CAACAGAGA	-	EIF4G3	2_1213insTCTG	p.P405fs
XH_P51	1	21806606	21806606	Missense_Mutation	SNP	T	G	T	NBPF3	c.T1061G	p.F354C
XH_P51	1	25785324	25785324	Nonsense_Mutation	INS	-	CATTATTAAATC	-	TMEM57	96insATCATTTAT	b.D366delinsKIIIX
XH_P51	1	25785325	25785325	Missense_Mutation	SNP	G	T	G	TMEM57	c.G1096T	p.D366Y
XH_P51	1	26361733	26361733	Silent	SNP	C	T	C	EXTL1	c.C1926T	p.F642F
XH_P51	1	27219232	27219232	Frame_Shift_Ins	INS	-	TGTCC	-	GPATCH3	161_1162insGG	p.R388fs
XH_P51	1	35580088	35580088	Frame_Shift_Ins	INS	-	GTTGAACAAAG	-	ZMYM1	AATAGTGTGA	p.I811fs
XH_P51	1	38338723	38338723	Nonsense_Mutation	INS	-	ATGCCTACC	-	INPP5B	1574insGGTA	p.K525delinsRX
XH_P51	1	39318125	39318125	Frame_Shift_Ins	INS	-	RRAGC	-	RRAGC	c.574_575insA	p.F192fs
XH_P51	1	39888208	39888208	Splice_Site	INS	-	CTATTAGACTCT	-	MACF1	-	-
XH_P51	1	40735788	40735788	Frame_Shift_Ins	INS	-	TTAAGACAAATG	-	ZMPSTE24	5CAGCTTAAGAC	p.V206fs
XH_P51	1	52956450	52956450	Missense_Mutation	SNP	C	T	C	ZCCHC11	c.G1342A	p.D448N
XH_P51	1	61554336	61554336	Nonsense_Mutation	INS	-	TCATGTTTTTTG	-	NFIA	GCTTTTCATGTT	b.F182delinsYAFHVFX
XH_P51	1	61818233	61818233	Frame_Shift_Ins	INS	-	AGTGTGTCAT	-	NFIA	813insAGTGT	p.S271fs
XH_P51	1	62910675	62910675	In_Frame_Ins	INS	-	TTTTACTTCTTC	-	USP1	5insATTTTTTACT	b.275delinsTFTFSF
XH_P51	1	71531416	71531416	Nonsense_Mutation	INS	-	CACCTCCATTAC	-	ZRANB2	insTTGGTAATG	b.K318delinsLVMEVX
XH_P51	1	74797152	74797152	Nonsense_Mutation	SNP	C	T	C	FPGT-TNNI3K	c.C463T	p.Q155X
XH_P51	1	78245357	78245357	Missense_Mutation	SNP	C	T	C	MIGA1	c.C17T	p.S6L
XH_P51	1	82409218	82409218	Frame_Shift_Ins	INS	-	GTCAAAATTCAC	-	ADGRL2	4insAAGTCAAA	p.L321fs
XH_P51	1	94514438	94514438	Missense_Mutation	SNP	G	C	G	ABCA4	c.C2729G	p.P910R
XH_P51	1	94514439	94514439	Missense_Mutation	SNP	G	A	G	ABCA4	c.C2728T	p.P910S
XH_P51	1	109823832	109823832	Frame_Shift_Ins	INS	-	AAATCTTCCA	-	PSRC1	561insTGGAA	p.P187fs
XH_P51	1	115166190	115166190	Nonsense_Mutation	INS	-	AATTGTAGGAT	-	DEPND2C	hsTACCATCTCTA	b.N295delinsIPSYNX
XH_P51	1	118492660	118492660	Nonsense_Mutation	INS	-	ACATTTTAAAA	-	WDR3	1654insACATT	b.S1_V552delinsDTFX
XH_P51	1	118492661	118492661	Nonsense_Mutation	INS	-	TAAGAAAGTAT	-	WDR3	55insTCTAAGA	p.V552delinsVX
XH_P51	1	118581947	118581947	Missense_Mutation	SNP	T	C	T	SPAG17	c.A3287G	p.E1096G
XH_P51	1	118584567	118584567	Silent	SNP	G	A	G	SPAG17	c.C2913T	p.G971G
XH_P51	1	120381953	120381953	Missense_Mutation	SNP	T	C	T	NBPF7	c.A692G	p.Y231C
XH_P51	1	144854528	144854528	Silent	SNP	A	T	A	PDE4DIP	c.T7428A	p.I2476I
XH_P51	1	145282025	145282025	In_Frame_Ins	INS	-	TGGCTAGAA	-	NOTCH2NL	5_706insTGGCTA	b.E235delinsEWLE
XH_P51	1	145305994	145305994	Frame_Shift_Ins	INS	-	TCTACGTGTAG	-	NBPF10	1636insTCTAC	p.P545fs
XH_P51	1	145522575	145522575	Frame_Shift_Ins	INS	-	GCTCTGTGTATC	-	PEX11B	CTTTTGCTCTG	p.M132fs
XH_P51	1	147380265	147380265	Silent	SNP	C	T	C	GJA8	c.C183T	p.C61C
XH_P51	1	149290779	149290779	Missense_Mutation	SNP	T	A	T	FAM231D	c.T251A	p.L84H
XH_P51	1	150900412	150900412	Missense_Mutation	SNP	G	T	G	SETDB1	c.G222T	p.E74D

XH_P51	1	150900413	150900413	Frame_Shift_Ins	INS	-	ATTTTAAAGAG	-	SETDB1	CTGAGATTTT	p.V75fs
XH_P51	1	151111164	151111164	Frame_Shift_Ins	INS	-	C	-	SEMA6C	c.397_398insG	p.S133fs
XH_P51	1	151111166	151111166	Missense_Mutation	SNP	G	C	G	SEMA6C	c.C396G	p.D132E
XH_P51	1	152190868	152190868	Silent	SNP	G	A	G	HRNR	c.C323T	p.H1079H
XH_P51	1	152193650	152193650	Frame_Shift_Ins	INS	-	GTCAC	-	HRNR	454_455insGTG	p.T152fs
XH_P51	1	152276391	152276391	Silent	SNP	T	C	T	FLG	c.A10971G	p.R3657R
XH_P51	1	152276393	152276393	Nonsense_Mutation	SNP	G	A	G	FLG	c.C10969T	p.R3657X
XH_P51	1	152276548	152276548	Missense_Mutation	SNP	T	G	T	FLG	c.A10814C	p.N3605T
XH_P51	1	152279383	152279383	In_Frame_Ins	INS	-	GGA	-	FLG	7978_7979insTG	Q2660delinsLQ
XH_P51	1	152280882	152280882	Silent	SNP	C	T	C	FLG	c.G6480A	p.R2160R
XH_P51	1	152281113	152281113	Missense_Mutation	SNP	G	C	G	FLG	c.C6249G	p.S2083R
XH_P51	1	152328399	152328399	Silent	SNP	G	A	G	FLG2	c.C1863T	p.H621H
XH_P51	1	152882761	152882761	In_Frame_Ins	INS	-	CTGGCATGGGG	-	IVL	489insTCTGGCA	163delinsLLAWG
XH_P51	1	153303372	153303372	In_Frame_Ins	INS	-	STCCTGTGCCTC	-	PGLYRP4	3insAGGAGGCA	331delinsQGGTGL
XH_P51	1	153982586	153982586	In_Frame_Ins	INS	-	ATT	-	NUP210L	4791_4792insAA	p.1598delinsNP
XH_P51	1	153982587	153982587	Frame_Shift_Ins	INS	-	ATTTATATCTGT	-	NUP210L	791insTACAGAT	p.T1597fs
XH_P51	1	155207975	155207975	In_Frame_Ins	INS	-	TTTTATTTTCTT	-	GBA	AAAGAGAAAA	0delinsKKKKKKKKV
XH_P51	1	155365321	155365321	Frame_Shift_Ins	INS	-	CC	-	ASH1L	6031_6032insG	p.L2011fs
XH_P51	1	155365322	155365322	Nonsense_Mutation	INS	-	TACTCTGAAGAA	-	ASH1L	ATAAAATCTCTC	2012delinsTVYKILQSKFKX
XH_P51	1	156206089	156206089	Missense_Mutation	SNP	G	A	G	PMF1	c.G172A	p.G58R
XH_P51	1	156535870	156535870	Nonsense_Mutation	INS	-	AACTAACTAAT	-	IQGAP3	sTTAGATTAAAGT	103_D104delinsTX
XH_P51	1	158368808	158368808	Frame_Shift_Ins	INS	-	ACATCTCA	-	OR10T2	8_449insTGAGA	p.G150fs
XH_P51	1	158390535	158390535	Frame_Shift_Ins	INS	-	CTGCTCTCACTC	-	OR10K2	22insGGAGTGA	p.T41fs
XH_P51	1	158736113	158736113	Silent	SNP	G	A	G	OR6N1	c.C360T	p.Y120Y
XH_P51	1	158747024	158747024	In_Frame_Ins	INS	-	TCATCTTCTTCT	-	OR6N2	GATAAAGAGAA	34delinsMIKKKVVIR
XH_P51	1	159825849	159825849	Silent	SNP	G	T	G	VSIG8	c.C795A	p.I265I
XH_P51	1	160000763	160000763	Frame_Shift_Ins	INS	-	CTAATGTTATGG	-	PIGM	ATAAACCATTAAC	p.H256fs
XH_P51	1	160276275	160276275	In_Frame_Ins	INS	-	GTT	-	COPA	1310_1311insAA	p.1437delinsIT
XH_P51	1	160276277	160276277	Nonsense_Mutation	INS	-	TGTTTTTACAGT	-	COPA	sTAAGTACTGTA	437_K438delinsX
XH_P51	1	160518093	160518093	Frame_Shift_Ins	INS	-	AATGACTCCCTT	-	CD84	98insGAAGGGA	p.Q200fs
XH_P51	1	161495096	161495096	Silent	SNP	T	C	T	HSPA6	c.T648C	p.A216A
XH_P51	1	161496107	161496107	Frame_Shift_Ins	INS	-	CACCTCTA	-	HSPA6	9_1660insCACC	p.G553fs
XH_P51	1	162749975	162749975	Missense_Mutation	SNP	C	T	C	DR2	c.C250T	p.T836M
XH_P51	1	163309266	163309266	Frame_Shift_Ins	INS	-	T	-	NUF2	c.605_606insT	p.T202fs
XH_P51	1	163309267	163309267	Nonsense_Mutation	INS	-	AGAAATTGTCTA	-	NUF2	sATGAAGAAATTT	202_1203delinsTRX
XH_P51	1	166926071	166926071	Frame_Shift_Ins	INS	-	ATTTTTTCTCTC	-	ILDR2	AAAGGAGAGAA	p.G133fs
XH_P51	1	171509761	171509761	Frame_Shift_Ins	INS	-	TTTTGGTTTCTC	-	PRRC2C	stCCTTTTTTGG	p.P1050fs
XH_P51	1	171535748	171535748	Nonsense_Mutation	INS	-	TCTTGACCATTC	-	PRRC2C	9insCTTTCTGTA	P2106delinsPLSX
XH_P51	1	173931087	173931087	Nonsense_Mutation	INS	-	TTTATTACATAG	-	RC3H1	TTAAGTCTATGT	660_Q661delinsNX
XH_P51	1	174190274	174190274	Frame_Shift_Ins	INS	-	C	-	RABGAP1L	c.304dupC	p.L101fs
XH_P51	1	174190276	174190276	In_Frame_Ins	INS	-	GGCTTTTCCAA	-	RABGAP1L	6insTGGCTTTTT	1102delinsHGFFQL
XH_P51	1	174957960	174957960	Frame_Shift_Ins	INS	-	TCATCTTACCCT	-	RABGAP1L	95insATCATCTT	p.A198fs
XH_P51	1	175304899	175304899	Frame_Shift_Ins	INS	-	TCATTAAATAGT	-	TNR	80insGAGACTAT	p.K860fs
XH_P51	1	175332878	175332878	Silent	SNP	G	A	G	TNR	c.C1674T	p.F558F
XH_P51	1	179347867	179347867	In_Frame_Ins	INS	-	ACTCTTCTCTTG	-	AXDND1	71insAACTCTTT	4157delinsQTLSP
XH_P51	1	179609152	179609152	Frame_Shift_Ins	INS	-	TTAAT	-	TDRD5	364_365insTTAA	p.G122fs
XH_P51	1	179609153	179609153	Frame_Shift_Ins	INS	-	CATTAAATACCA	-	TDRD5	6insCTCAATTAAT	p.G122fs
XH_P51	1	179620102	179620102	Nonsense_Mutation	INS	-	TAACCATATACA	-	TDRD5	TATAATAACCA	190delinsMNYNHQIQX
XH_P51	1	180063411	180063411	In_Frame_Ins	INS	-	TGAGGCTCTAT	-	CEP350	8172insTGAGGT	2724delinsTEASI
XH_P51	1	182357862	182357862	In_Frame_Ins	INS	-	GGGCTCACTGT	-	GLUL	TGGACAGTGAG	nsCKTRLDSEPKVVEGET
XH_P51	1	182856511	182856511	Frame_Shift_Ins	INS	-	ACCATCTCCA	-	DHX9	_3756insACCAT	p.G1252fs
XH_P51	1	183255845	183255845	Missense_Mutation	SNP	G	T	G	NMNAT2	c.C400A	p.P134T
XH_P51	1	183255847	183255847	Nonsense_Mutation	INS	-	TTAATTAAACAA	-	NMNAT2	AGGGCTTGTTA	83delinsNHVEGLNXX
XH_P51	1	184690464	184690464	Missense_Mutation	SNP	C	G	C	EDEM3	c.G910C	p.G304L
XH_P51	1	184690466	184690466	Nonsense_Mutation	INS	-	AGTTTACCTAA	-	EDEM3	CAAGATTAGGTB	V304delinsLYKQDX
XH_P51	1	186107032	186107032	In_Frame_Ins	INS	-	TTCAATTGGG	-	HMCN1	insGTATATTCTCA	618delinsGIFQLGIL
XH_P51	1	186286733	186286733	Splice_Site	INS	-	CTGTGTTGTGA	-	TPR	.	.
XH_P51	1	186645719	186645719	Nonsense_Mutation	INS	-	AGCTGCTGTGTC	-	PTGS2	sTCAGACAAAG	M285delinsSRQAGX
XH_P51	1	186645721	186645721	Frame_Shift_Ins	INS	-	AACTGCTCAT	-	PTGS2	848insATGAGC	p.G283fs
XH_P51	1	186908300	186908300	Nonsense_Mutation	INS	-	AATAAAGCATG	-	PLA2G4A	7insTAAATAAA	226delinsVKNAXX
XH_P51	1	198201755	198201755	Silent	SNP	G	A	G	NEK7	c.G45A	p.Q13Q
XH_P51	1	198492676	198492676	Nonsense_Mutation	INS	-	ACCTAAATTTAC	-	ATP6V1G3	TAAATGTAAAT	N68_L69delinsFLX
XH_P51	1	200080441	200080441	Frame_Shift_Ins	INS	-	AAGCACA	-	NR5A2	66_1007insAAG	p.G336fs
XH_P51	1	200827006	200827006	Nonsense_Mutation	INS	-	SAGAGTACATTC	-	CAMSAP2	9insATGAGAGT	403_K1404delinsPX
XH_P51	1	201178297	201178297	Missense_Mutation	SNP	G	A	G	IGFN1	c.G4276A	p.E1426K
XH_P51	1	202409914	202409914	Frame_Shift_Ins	INS	-	TT	-	PPP1R12B	1539_1540insT	p.N513fs
XH_P51	1	202409915	202409915	Nonsense_Mutation	INS	-	TTCTGGATCCA	-	PPP1R12B	ATCTTATTTCTGG	delinsNIPSSYFVWQHXX
XH_P51	1	206243243	206243243	Nonsense_Mutation	INS	-	TTTAAACCAACT	-	C1orf186	AAATAGTTGGT	b.E7_V8delinsKX
XH_P51	1	210273632	210273632	Nonsense_Mutation	INS	-	AGTGGTTTTAAT	-	SYT14	91insTAGAGTTT	p.F330delinsFX
XH_P51	1	211960981	211960981	Frame_Shift_Ins	INS	-	AGCTTTTTTTTT	-	LPGAT1	sAAAAA	p.1149fs
XH_P51	1	212560386	212560386	In_Frame_Ins	INS	-	GTATTTGGTGTA	-	TMEM206	190insTACCACA	N64delinsYHKYN
XH_P51	1	215848566	215848566	Frame_Shift_Ins	INS	-	GGAAATGAAATG	-	USH2A	12687insCATT	p.G4229fs
XH_P51	1	215848567	215848567	Frame_Shift_Ins	INS	-	T	-	USH2A	12685_12686ins	p.G4229fs
XH_P51	1	220142295	220142295	In_Frame_Ins	INS	-	ATGGTTTTTGTA	-	EPRS	AATGAATACAA	64delinsEMNTKTLV
XH_P51	1	228433209	228433209	Missense_Mutation	SNP	C	G	C	OBSCN	c.C357G	p.P1193A
XH_P51	1	230795342	230795342	In_Frame_Ins	INS	-	GCAATGATATCA	-	COG2	206insGCAATGA	A69delinsGNDIT
XH_P51	1	230827216	230827216	Nonsense_Mutation	INS	-	CTTAAGATCATT	-	COG2	AAGTTTCTTAAGT	73_P674delinsVSIX
XH_P51	1	231048461	231048461	Nonsense_Mutation	INS	-	TGTACATCTTAT	-	TTC13	CAAGCATAAAG	59_R660delinsFQAX
XH_P51	1	231298885	231298851	Frame_Shift_Del	DEL	CTGGAGCAC	-	CTGGAGCACGA	TRIM67	c.170_236del	p.L57fs
XH_P51	1	235543399	235543399	Missense_Mutation	SNP	G	A	G	TBCE	c.G35A	p.R12Q
XH_P51	1	235916570	235916598	Frame_Shift_Del	DEL	ATAAATAAT	-	ATAAATAATAAC	LYST	c.7230_7234de	p.E2410fs
XH_P51	1	241146391	241146391	Frame_Shift_Ins	INS	-	A	-	RG57	c.213dupT	p.I72fs
XH_P51	1	241146393	241146393	Frame_Shift_Ins	INS	-	CACATACATCTC	-	RG57	12insTGAGATG	p.T71fs
XH_P51	1	241695773	241695773	In_Frame_Ins	INS	-	TAAATCCATTAC	-	KMO	30insTAAATCCA	K10delinsNKSIT
XH_P51	1	241695775	241695775	Missense_Mutation	SNP	G	A	G	KMO	c.G31A	p.V11I
XH_P51	1	245246990	245246990	Missense_Mutation	SNP	G	C	G	EFCAB2	c.G373C	p.D125H
XH_P51	1	247004268	247004268	Missense_Mutation	SNP	G	A	G	AHCTF1	c.C6641T	p.P2214L
XH_P51	1	247004269	247004269	Nonsense_Mutation	INS	-	ACCTATTGTGTA	-	AHCTF1	ATGACTTTACAA	4delinsLMTLQIGVHX
XH_P51	1	247013112	247013112	Nonsense_Mutation	INS	-	FAAAATTTGGTT	-	AHCTF1	nsCAAAATACCA	206delinsQITKFX
XH_P51	1	248525127	248525127	Frame_Shift_Ins	INS	-	GTGTGTGTGTG	-	OR2T4	ATTGTGTGTGT	p.H82fs
XH_P51	1	248801937	248801937	Frame_Shift_Ins	INS	-	AGATGTG	-	OR2T35	22_623insCACA	p.L208fs
XH_P51	2	3756140	3756140	Missense_Mutation	SNP	T	A	T	CDCC2C	c.T289A	p.Y97N
XH_P51	2	9570093	9570093	Frame_Shift_Ins	INS	-	AGTACAAAAACA	-	CP5F3	6insAAGTACAA	p.A15fs
XH_P51	2	15378741	15378741	Nonsense_Mutation	INS	-	AAGTTA	-	NBAS	793_5794insTAA	p.P1932delinsX
XH_P51	2	15378742	15378742	Nonsense_Mutation	INS	-	ATTAGTCG	-	NBAS	2_5793insCGAC	31_P1932delinsNDX
XH_P51	2	15448400	15448400	Frame_Shift_Ins	INS	-	AA	-	NBAS	4736_4737insT	p.S1579fs
XH_P51	2	15448401	15448401	In_Frame_Ins	INS	-	TGATTACATATG	-	NBAS	4736insCATATG	1579delinsTVYIS
XH_P51	2	15736874	15736874	In_Frame_Ins	INS	-	CATTCTAATCTAG	-	DDX1	CTCATCATTCTA	0delinsSSHNSLDY

XH_P51	2	21363072	21363072	Frame_Shift_Ins	INS	-	GTCAACTCTCTT	-	TDRD15	rsACTATGTCAAC	p.N911fs
XH_P51	2	21364804	21364804	Nonsense_Mutation	INS	-	TTT	-	TDRD15	4465_4466insT	p.K1489delinsIX
XH_P51	2	21365664	21365664	In_Frame_Ins	INS	-	GCATCTAAATAT	-	TDRD15	5326insGCATCT	p.1775delinsTASKY
XH_P51	2	25057716	25057716	Silent	SNP	G	A	G	ADCY3	c.C1752T	p.H584H
XH_P51	2	25170521	25170521	Nonsense_Mutation	INS	-	TGTAATTATAGT	-	DNAJC27	GTGACTACTATA	262_N263delinsVX
XH_P51	2	27802466	27802466	In_Frame_Ins	INS	-	ATAAATTCT	-	C2orf16	7_3028insATAAA	Q1009delinsQINS
XH_P51	2	27802468	27802468	Nonsense_Mutation	INS	-	ATTGACAGGTA	-	C2orf16	nsATAGATTGAC	010_V1011delinsEX
XH_P51	2	48036797	48036797	Nonsense_Mutation	INS	-	CTGAATTTTTC	-	FBXO11	GAATAAGTAA	delinsIKERISKNSSEECX
XH_P51	2	48925934	48925934	In_Frame_Ins	INS	-	CAAACTGTCTG	-	LHCGR	86insACAGAA	p.1229fs
XH_P51	2	50724711	50724711	Nonsense_Mutation	INS	-	AGATGGATTAA	-	NRXN1	TATAGAAATTA	p.1843delinsTVIX
XH_P51	2	63053322	63053322	Frame_Shift_Ins	INS	-	A	-	EHBP1	c.413_414insA	p.F138fs
XH_P51	2	63053323	63053323	Frame_Shift_Ins	INS	-	TTTTTCTTTAAT	-	EHBP1	ACTTTTTTTTCT	p.F138fs
XH_P51	2	63832425	63832425	Nonsense_Mutation	INS	-	ATCCATGTCTTT	-	MDH1	CCAAGATCCATG	41delinsQLRIFPRMSLSLDLX
XH_P51	2	69053204	69053204	Frame_Shift_Ins	INS	-	CTCATTTGTCAT	-	ARHGAP25	1799insCTCAT	p.L600fs
XH_P51	2	71043269	71043269	Frame_Shift_Ins	INS	-	TGTGAAGTAATG	-	CLEC4F	GTGGTCATTACT	p.Q415fs
XH_P51	2	71595637	71595637	Nonsense_Mutation	INS	-	TTTCTCTACCA	-	ZNFG38	nsTATAATTTCTT	1708delinsLYNFFYHX
XH_P51	2	71909786	71909786	In_Frame_Ins	INS	-	CAGGACTTA	-	DYSF	1_6142insCAGG	A2047delinsAQDL
XH_P51	2	73471773	73471773	Frame_Shift_Ins	INS	-	CAAA	-	CCT7	287_288insCAA	p.V96fs
XH_P51	2	73471774	73471774	Frame_Shift_Ins	INS	-	ATCTCAT	-	CCT7	88_289insATCT	p.V96fs
XH_P51	2	73496580	73496582	In_Frame_Del	DEL	GCG	-	GCG	FBXO41	c.177_179del	p.59_60del
XH_P51	2	73799911	73799911	Nonsense_Mutation	INS	-	ATAATCTGTCTT	-	ALMS1	5insGGTATAAT	835_Q3636delinsLVX
XH_P51	2	84838942	84838942	Frame_Shift_Ins	INS	-	ATCTTTTCTCTG	-	DNAH6	5ACTGTATCTTT	p.R1147fs
XH_P51	2	86968093	86968093	Silent	SNP	A	C	A	RMND5A	c.A186C	p.T62T
XH_P51	2	96781276	96781276	In_Frame_Ins	INS	-	CTG	-	ADRA2B	1_612_613insCA	p.R205delinsQR
XH_P51	2	96781278	96781278	In_Frame_Ins	INS	-	AGAAGCCACAG	-	ADRA2B	611insTCTGTGGR	R204delinsLCGFC
XH_P51	2	97009009	97009009	In_Frame_Ins	INS	-	AAAAAACAA	-	NCAPH	155insAAAAA	p.52delinsKQTT
XH_P51	2	97009011	97009011	Silent	SNP	G	T	G	NCAPH	c.G156T	p.P52P
XH_P51	2	97853117	97853117	In_Frame_Ins	INS	-	ATACATAATCAC	-	ANKRD36	23insGATACAT	D708delinsGYIITH
XH_P51	2	99185111	99185111	In_Frame_Ins	INS	-	ATGCATTCCATT	-	INPP4A	2349insATGCAT	p.K783delinsKCIPL
XH_P51	2	99949585	99949585	Frame_Shift_Ins	INS	-	A	-	TXNDC9	c.88_89insT	p.D30fs
XH_P51	2	99949587	99949587	Frame_Shift_Ins	INS	-	TATTACTGTT	-	TXNDC9	87insAACAGTA	p.L29fs
XH_P51	2	99988192	99988192	Frame_Shift_Ins	INS	-	5AATGTTTAAAT	-	EIF5B	2insAAGAATG	p.K517fs
XH_P51	2	101186095	101186095	In_Frame_Ins	INS	-	ACACATTTCATT	-	PDCL3	insGACACACAT	94delinsSGHTFHF
XH_P51	2	112539977	112539977	Missense_Mutation	SNP	G	A	G	ANAPC1	c.C5171T	p.A1724V
XH_P51	2	112551673	112551673	Silent	SNP	G	A	G	ANAPC1	c.C4500T	p.S1500S
XH_P51	2	112767580	112767580	Frame_Shift_Ins	INS	-	CTTTCAGA	-	MERTK	6_2017insCTTT	p.P672fs
XH_P51	2	113147803	113147803	Frame_Shift_Ins	INS	-	5AGAAAGATGA	-	RGPD5	719insCATCATC	p.Q907fs
XH_P51	2	113260636	113260636	Frame_Shift_Ins	INS	-	TTCTGCATATTA	-	TTL	54insTTTCTGCA	p.K251fs
XH_P51	2	113260638	113260639	Frame_Shift_Del	DEL	AC	-	AC	TTL	c.755_756del	p.N252fs
XH_P51	2	114000290	114000290	Nonsense_Mutation	INS	-	CAGATTC	-	PAX8	54_455insGAAT	p.152_153delinsX
XH_P51	2	114201410	114201410	In_Frame_Ins	INS	-	CATTTTATAACT	-	CBWD2	09insGCATTTTT	A1103delinsLHFITY
XH_P51	2	122215333	122215333	Frame_Shift_Ins	INS	-	TGTGTGTGTGT	-	CLASP1	1315insACACA	p.H439fs
XH_P51	2	122215334	122215334	Splice_Site	SNP	C	G	C	CLASP1	-	-
XH_P51	2	130868253	130868253	Silent	SNP	T	C	T	POTEF	c.A918G	p.R306R
XH_P51	2	141072631	141072631	In_Frame_Ins	INS	-	ATGTTACAAATA	-	LRP1B	2678insTATATT	p.4226delinsSIFVT
XH_P51	2	152320280	152320280	In_Frame_Ins	INS	-	CTTTTATCCCT	-	RIF1	4247insCTTTTAT	p.1416delinsPFIW
XH_P51	2	152425875	152425875	Missense_Mutation	SNP	C	G	C	NEB	c.G12303C	p.K4101N
XH_P51	2	152541441	152541441	Frame_Shift_Ins	INS	-	TATC	-	NEB	685_2686insGA	p.P896fs
XH_P51	2	152541443	152541443	In_Frame_Ins	INS	-	CATTGT	-	NEB	83_2684insACA	p.A895delinsDNA
XH_P51	2	153417545	153417545	Nonsense_Mutation	INS	-	AGTATGGAAG	-	FMNL2	nsCTTAGTAGTGG	p.L198delinsPX
XH_P51	2	155303251	155303251	Nonsense_Mutation	INS	-	GGAAGGCACAT	-	GALNT13	AAAGATGGAAG	558_V559delinsSGX
XH_P51	2	158595014	158595014	Nonsense_Mutation	INS	-	TATATAGAAGG	-	ACVR1	insTAAACCCCTT	C445_K446delinsX
XH_P51	2	158595015	158595015	Missense_Mutation	SNP	C	G	C	ACVR1	c.G1332C	p.M444I
XH_P51	2	160806155	160806155	In_Frame_Ins	INS	-	5GGAATTGTAGC	-	PLA2R1	3insCATGCTACA	1225delinsSHATIPTS
XH_P51	2	163208900	163208900	Missense_Mutation	SNP	T	A	T	GCA	c.T323A	p.I108N
XH_P51	2	163291936	163291936	Missense_Mutation	SNP	C	T	C	KCNH7	c.G1705A	p.V569I
XH_P51	2	166172107	166172107	Frame_Shift_Ins	INS	-	CTCCATTTTATTC	-	SCN2A	1insATTCTCCAT	p.R504fs
XH_P51	2	166892558	166892558	Missense_Mutation	SNP	C	A	C	SCN1A	c.G3429T	p.E1143D
XH_P51	2	167162394	167162394	Frame_Shift_Ins	INS	-	TGGAATGTCTGT	-	SCN1A	nsAAATACAGAC	p.L198fs
XH_P51	2	168100279	168100279	Frame_Shift_Ins	INS	-	5TTGATCTAGAT	-	XIRP2	2insAAGTTGAT	p.R571fs
XH_P51	2	168101172	168101172	In_Frame_Ins	INS	-	TGAATGGCATA	-	XIRP2	05insCTTGAATG	868delinsDLEWHT
XH_P51	2	170031853	170031853	Frame_Shift_Ins	INS	-	TTTATGAAGTTT	-	LRP2	AAAAA	p.D3540fs
XH_P51	2	170367063	170367063	In_Frame_Ins	INS	-	TTTTTCTACATT	-	KLHL41	sCTTCTTTTCTTA	259delinsSFSFRL
XH_P51	2	178481522	178481522	Nonsense_Mutation	INS	-	TTGCTTATTTTTG	-	TTC30A	8insTTCAAAAT	36_E637delinsDSKX
XH_P51	2	179433822	179433822	In_Frame_Ins	INS	-	TGGGAAGAATAT	-	TTN	3842insAGATAT	p.16614delinsKDILPL
XH_P51	2	179439490	179439490	Missense_Mutation	SNP	C	T	C	TTN	c.G44174A	p.R14725H
XH_P51	2	179631224	179631224	Frame_Shift_Ins	INS	-	TTTTTTTCAC	-	TTN	9449insGTGAA	p.Y3150fs
XH_P51	2	180047856	180047856	Frame_Shift_Ins	INS	-	ATACGTCTGCAG	-	SESTD1	AAACCTGCAGA	p.N39fs
XH_P51	2	185801306	185801306	Frame_Shift_Ins	INS	-	AA	-	ZNFR04A	1183_1184insA	p.G395fs
XH_P51	2	185801307	185801307	Nonsense_Mutation	INS	-	TAATAATAATGC	-	ZNFR04A	185insGTAATAA	395_P396delinsGX
XH_P51	2	186654966	186654966	Frame_Shift_Ins	INS	-	TCAGTTTGATA	-	FSIP2	TTTAGTTACAGT	p.W1035fs
XH_P51	2	186658847	186658847	Nonsense_Mutation	INS	-	TCTTCTACTAC	-	FSIP2	GTCTTCTTTATC	328_T232delinsFX
XH_P51	2	196737189	196737189	In_Frame_Ins	INS	-	TGTTATTGAAAT	-	DNAH7	3insCCCATTTTCA	2140delinsPISITGK
XH_P51	2	197171284	197171284	Frame_Shift_Ins	INS	-	A	-	HECW2	1_1673_1674ins	p.T558fs
XH_P51	2	197171285	197171285	Frame_Shift_Ins	INS	-	AAATTTATTTCTC	-	HECW2	673insTGAGAA	p.T558fs
XH_P51	2	197584337	197584337	In_Frame_Ins	INS	-	TATTTTATAGGTC	-	CCDC150	nsTATTTTATTTT	04delinsVYFIRWF
XH_P51	2	197584338	197584338	Frame_Shift_Ins	INS	-	TT	-	CCDC150	2113_2114insT	p.Q705fs
XH_P51	2	200213706	200213706	In_Frame_Ins	INS	-	GTGGCATTCC	-	SATB2	0_891insGAATG	p.L297delinsLNAT
XH_P51	2	202358092	202358092	Nonsense_Mutation	INS	-	TTAGTGAA	-	C2CD6	1_2972insTTCA	991_1992delinsIHX
XH_P51	2	202358094	202358094	Frame_Shift_Ins	INS	-	AGATGAAATAA	-	C2CD6	2970insTTATT	p.Q990fs
XH_P51	2	203061654	203061654	Frame_Shift_Ins	INS	-	AGGGATCAAT	-	KIAA2012	3320insAGGGA	p.L1107fs
XH_P51	2	203948089	203948089	Nonsense_Mutation	INS	-	CATATTAATCT	-	NBEAL1	833insCATATT	p.1278delinsTYX
XH_P51	2	206630233	206630233	In_Frame_Ins	INS	-	AGTTTCTGTTAG	-	NRP2	344insAAGTTTC	p.5781delinsSKFLLA
XH_P51	2	207174503	207174503	Nonsense_Mutation	INS	-	TCACACGCTCT	-	ZDBF2	ATTATATCCACA	delinsPLELYPQLLSSESIX
XH_P51	2	209113237	209113237	In_Frame_Ins	INS	-	TGAGAATGCAAT	-	IDH1	ACATATATGCA	delinsHIQLYIAFANFIPCL
XH_P51	2	209200854	209200854	Nonsense_Mutation	INS	-	ATTTTGTGATTTT	-	PIKFYVE	TTATTAATTTTTT	4_S1485delinsLLILFDX
XH_P51	2	209200856	209200856	Silent	SNP	G	A	G	PIKFYVE	c.G4452A	p.Q1484Q
XH_P51	2	210565028	210565028	Frame_Shift_Ins	INS	-	AA	-	MAP2	c.482_483insAA	p.P161fs
XH_P51	2	210565030	210565030	Nonsense_Mutation	INS	-	AATAGT	-	MAP2	84_485insAATA	p.5162delinsKX
XH_P51	2	210896226	210896226	Missense_Mutation	SNP	A	C	A	KANS1L1	c.T2074G	p.C692G
XH_P51	2	210896228	210896228	Nonsense_Mutation	INS	-	GTTTCACCTAAA	-	KANS1L1	5AGACATTTGAG	1_C692delinsKTFEX
XH_P51	2	211471523	211471523	Frame_Shift_Ins	INS	-	AGAAACCTCTCT	-	CP51	8insTTAGAAACC	p.S233fs
XH_P51	2	215818750	215818750	Nonsense_Mutation	INS	-	TCTAAGCTTTTCT	-	ABCA12	CCAATGGGAAAA	1delinsYYQWKSOLDYX
XH_P51	2	216240409	216240409	Frame_Shift_Ins	INS	-	TCTCAGATTCTT	-	FN1	insTTAAAGCAA	p.L1793fs
XH_P51	2	218762667	218762667	Frame_Shift_Ins	INS	-	TCTCTTTGTTTA	-	TNS1	2insATAAACAAA	p.E8fs
XH_P51	2	220264605	220264605	Missense_Mutation	SNP	G	A	G	DNPEP	c.C43T	p.L15F
XH_P51	2	230656595	230656595	Nonsense_Mutation	INS	-	CACCATGTATAA	-	TRIP12	GTACATTATACA	3_H1124delinsALNFIX
XH_P51	2	232030689	232030689	Silent	SNP	C	A	C	PSMD1	c.C2580A	p.V860V

XH_P51	2	232030690	232030690	Frame_Shift_Ins	INS	-	GGTAGTGGTCG	-	PSMD1	nsAAGAGGTAG	p.L861fs
XH_P51	3	383700	383700	Frame_Shift_Ins	INS	-	CATTTCTTTTA	-	CHL1	CTTTTCATTTC	p.F205fs
XH_P51	3	7620570	7620570	Silent	SNP	A	C	A	GRM7	c.A1977C	p.R659R
XH_P51	3	15071914	15071914	In_Frame_Ins	INS	-	GATACCTTAGCT	-	NR2C2	GCATTGTATACC	insFAHRAFDLAKALNTT
XH_P51	3	19491744	19491744	In_Frame_Ins	INS	-	TGTTTGGAAACG	-	KCNH8	CTTGGTGTGTTG	delinsHALVFGNVTAI
XH_P51	3	19491746	19491746	Frame_Shift_Ins	INS	-	ATACAGA	-	KCNH8	24_1525insATA	p.L508fs
XH_P51	3	23960000	23960000	Nonsense_Mutation	INS	-	GG	-	RPL15	c.242_243insGG	Y81_G82delinsX
XH_P51	3	23960001	23960001	Frame_Shift_Ins	INS	-	TACTCACACAG	-	RPL15	244insTACTCA	p.Y81fs
XH_P51	3	30029670	30029670	Frame_Shift_Ins	INS	-	GTAGCCC	-	RBMS3	31_1082insGTAA	p.I361fs
XH_P51	3	30029672	30029672	Silent	SNP	T	A	T	RBMS3	c.T1083A	p.I361I
XH_P51	3	32776413	32776413	Nonsense_Mutation	INS	-	TAAAAAAGGCT	-	CNOT10	15TATTTTAAAAAT	487_5488delinsIFX
XH_P51	3	37034060	37034060	Nonsense_Mutation	INS	-	TGGAATGTCAT	-	EPM2AIP1	TAATGAATGACA	R170delinsNNEX
XH_P51	3	37045944	37045944	Frame_Shift_Ins	INS	-	TTTCTTTTCAGTC	-	MLH1	1GAGTTTTCCTT	p.A120fs
XH_P51	3	37170629	37170629	Frame_Shift_Ins	INS	-	TAAATGTGATAT	-	LRRFIP2	15ACAAATATCA	p.R34fs
XH_P51	3	37170630	37170630	Missense_Mutation	SNP	C	T	C	LRRFIP2	c.G101A	p.R34K
XH_P51	3	37365707	37365707	In_Frame_Ins	INS	-	TTT	-	GOLGA4	2330_2331insT	p.A777delinsAF
XH_P51	3	37365709	37365709	Frame_Shift_Ins	INS	-	CTTTTCATTCAT	-	GOLGA4	TAAAGTCTTTTC	p.H778fs
XH_P51	3	44544132	44544132	Frame_Shift_Ins	INS	-	CTTTTAAACTTT	-	ZNFR52	TAAAAAGTTTAA	p.E15fs
XH_P51	3	46965153	46965153	Nonsense_Mutation	INS	-	GTCACTT	-	CCDC12	19_250insAAGT	E84_K85delinsKX
XH_P51	3	47163043	47163043	In_Frame_Ins	INS	-	ATTGGGAAGATG	-	SETD2	11insTCTCATCTT	984delinsLSSSQWS
XH_P51	3	47318794	47318794	In_Frame_Ins	INS	-	5AAGAATTGACA	-	KIF9	ACAAATGCAAT	4delinsNKCQFCV
XH_P51	3	47956342	47956342	Missense_Mutation	SNP	T	C	T	MAP4	c.A1964G	p.N655S
XH_P51	3	47956344	47956344	Nonsense_Mutation	INS	-	ACAGGGAACATA	-	MAP4	TGTCCTAGTTC	4_N655delinsCRHCLX
XH_P51	3	48215815	48215815	Missense_Mutation	SNP	C	T	C	CDC25A	c.G769A	p.A257T
XH_P51	3	48310120	48310120	Frame_Shift_Ins	INS	-	TGTGATAAATC	-	ZNFS89	940insTGTGAT	p.F313fs
XH_P51	3	48493257	48493257	Nonsense_Mutation	INS	-	ACTTTGTTTTAAC	-	ATRIP	AGGTACTTTGTT	5_E76delinsQEKTTX
XH_P51	3	49699508	49699508	Nonsense_Mutation	INS	-	AAGACGTAGAG	-	BSN	5AGGCCAAAGAb	Y3410delinsYX
XH_P51	3	49724906	49724906	Missense_Mutation	SNP	C	T	C	MST1	c.G361A	p.V121I
XH_P51	3	53694211	53694211	Silent	SNP	C	T	C	CACNA1D	c.C675T	p.N252N
XH_P51	3	57303683	57303683	Frame_Shift_Ins	INS	-	TTCTCTGTGCAT	-	APPL1	1insCCAATTCTTC	p.E700fs
XH_P51	3	73651572	73651572	Missense_Mutation	SNP	G	T	G	PDZRN3	c.C851A	p.S284Y
XH_P51	3	78766995	78766995	Nonsense_Mutation	INS	-	AGACAGTCAGC	-	ROBO1	GCCGAGCTGAC	K193delinsKPSX
XH_P51	3	97591053	97591053	In_Frame_Ins	INS	-	CCTCGATAT	-	CRYBG3	5_1016insCCTCG	G339delinsASIW
XH_P51	3	98217448	98217448	Nonsense_Mutation	INS	-	AGAAGAATGACA	-	OR5K2	1insGTAAAGAA	8_K309delinsVRRIX
XH_P51	3	99567142	99567142	Nonsense_Mutation	INS	-	TCITTTTCTTTAC	-	FLIP1L	8insATGTAAATG	86_T887delinsCKX
XH_P51	3	108282064	108282064	Nonsense_Mutation	INS	-	ATTGAAGACTTC	-	KIAA1524	TACAATGAAGT	15delinsITMKSSIHX
XH_P51	3	111263901	111263901	Frame_Shift_Ins	INS	-	A	-	CD96	c.71dupA	p.E24fs
XH_P51	3	111831984	111831984	Nonsense_Mutation	SNP	T	A	T	C3orf52	c.T641A	p.T124X
XH_P51	3	112730155	112730155	In_Frame_Ins	INS	-	TAC	-	NEPRO	148_149insGT	p.F50delinsCI
XH_P51	3	112730157	112730157	Nonsense_Mutation	INS	-	CACATAC	-	NEPRO	46_147insGTAT	Y49_F50delinsX
XH_P51	3	119177071	119177071	Frame_Shift_Ins	INS	-	TTGTTTTTCTTAA	-	TMEM39A	AATTATTAAAGAA	p.G44fs
XH_P51	3	119379206	119379206	In_Frame_Ins	INS	-	SCCAAAAGATG	-	POPCD2	5CTTCTATCTTTT	2delinsMLLSFWLPE
XH_P51	3	121340966	121340966	In_Frame_Ins	INS	-	CCTCCATTTTCC	-	FBXO40	691insCCTCCCTCA	A230delinsAPPIs
XH_P51	3	123665933	123665933	Frame_Shift_Ins	INS	-	ACAGTGAAGGAT	-	CCDC14	62insCATCTCTTC	p.Y154fs
XH_P51	3	124398320	124398320	Missense_Mutation	SNP	G	A	G	KALRN	c.G2239A	p.E747K
XH_P51	3	124462896	124462896	Nonsense_Mutation	INS	-	TCACATGACTTC	-	UMPS	1409insTCACAT	70_W471delinsVTX
XH_P51	3	124854614	124854614	Nonsense_Mutation	INS	-	CTAAATTTTGT	-	SLC12A8	AAATAACAAAAA	G213delinsYHIHQIKX
XH_P51	3	130159562	130159562	In_Frame_Ins	INS	-	TGTCATAAGTGA	-	COL6A5	1insGGTTGTGCAT	127delinsLVVISDE
XH_P51	3	134911453	134911453	Frame_Shift_Ins	INS	-	CTCATTGTAAC	-	EPHB1	1TCTCTCTCATTC	p.L640fs
XH_P51	3	135721693	135721693	Frame_Shift_Ins	INS	-	TGTTTGGGAATG	-	PPP2R3A	TGGAGTGTGTTTC	p.F451fs
XH_P51	3	140785450	140785450	Silent	SNP	C	T	C	SPS8A	c.C504T	p.D168D
XH_P51	3	145797021	145797021	In_Frame_Ins	INS	-	TTTTTGGTTCGT	-	PIOD2	2insACACAGAAAC	461delinsNTEPKKL
XH_P51	3	148744726	148744726	Missense_Mutation	SNP	C	T	C	GYG1	c.C788T	p.T263I
XH_P51	3	148744727	148744727	Nonsense_Mutation	INS	-	AGAACAAAGTA	-	GYG1	15GGGAGAAACA	263delinsTGRTKX
XH_P51	3	151083726	151083726	Nonsense_Mutation	INS	-	TCTA	-	MED12L	169_3170insTC	O57_C105delinsFX
XH_P51	3	151083727	151083727	In_Frame_Ins	INS	-	TAACGACATAGG	-	MED12L	1insGATTAAACGA	O57delinsWINDIAN
XH_P51	3	151163319	151163319	Nonsense_Mutation	INS	-	TCTGTTACATTC	-	IGSF10	50insTAGAATGT	484_A1485delinsX
XH_P51	3	151163773	151163773	Nonsense_Mutation	INS	-	AGCACAATCAGT	-	IGSF10	3996insAACTGA	1332_E1333delinsX
XH_P51	3	154886570	154886570	Nonsense_Mutation	INS	-	TCCTTTTAAAG	-	MME	1insCCATCTTTG	5_G656delinsLHLCX
XH_P51	3	155198921	155198921	Missense_Mutation	SNP	T	C	T	PLCH1	c.A4894G	p.L1632E
XH_P51	3	155198922	155198922	In_Frame_Ins	INS	-	TTAATGCGTTTG	-	PLCH1	3insATACAAACCG	631delinsLYKRINR
XH_P51	3	155232562	155232562	Missense_Mutation	SNP	G	A	G	PLCH1	c.C1546T	p.R516W
XH_P51	3	157131835	157131835	In_Frame_Ins	INS	-	GTAAGTTTGGCT	-	VEPH1	741insAGCCAAAC	D247delinsEAKLT
XH_P51	3	158402343	158402343	Nonsense_Mutation	INS	-	TAAAAATGTTT	-	GFN1	AATTTTTTTAAAA	99_S60delinsQKX
XH_P51	3	160135688	160135688	Missense_Mutation	SNP	G	C	G	SMC4	c.G1615C	p.A539P
XH_P51	3	160135689	160135689	In_Frame_Ins	INS	-	ATACATTTTATA	-	SMC4	1617insATACAT	A539delinsAYILY
XH_P51	3	160679649	160679649	Frame_Shift_Ins	INS	-	CGCATCTTTTAG	-	PPM1L	45insTCGTGATT	p.S48fs
XH_P51	3	167293805	167293805	Silent	SNP	G	A	G	WDR49	c.C1410T	p.N470N
XH_P51	3	170929023	170929023	Missense_Mutation	SNP	T	A	T	TNIK	c.A188T	p.E63V
XH_P51	3	170929024	170929024	Frame_Shift_Ins	INS	-	TAACCTTTTATTG	-	TNIK	AAACACAATAAA	p.E63fs
XH_P51	3	178938869	178938869	Missense_Mutation	SNP	G	T	G	PIK3CA	c.G2111T	p.P1704M
XH_P51	3	178938870	178938870	Nonsense_Mutation	INS	-	SATTAATAAACA	-	PIK3CA	13insTGATTAA	p.R704delinsRX
XH_P51	3	179287915	179287915	Nonsense_Mutation	SNP	G	T	G	ACTL6A	c.G163T	p.E55X
XH_P51	3	179287916	179287916	Frame_Shift_Ins	INS	-	ATTATATTTTGT	-	ACTL6A	15TTTTATTATAT	p.E55fs
XH_P51	3	180666252	180666252	Frame_Shift_Ins	INS	-	GTTCTAATTAC	-	FXR1	389insGTCTCTA	p.T130fs
XH_P51	3	183035999	183035999	In_Frame_Ins	INS	-	CTTCTTTAGTGA	-	MCF2L2	15AAGTCACATA	204delinsKSLKKKE
XH_P51	3	195518002	195518002	In_Frame_Ins	INS	-	GAGGTCTCCAA	-	MUC4	CTTCTGGAGG	0delinsTTSWRTSIQD
XH_P51	4	437167	437167	Silent	SNP	G	A	G	ZNFR721	c.C1089T	p.C363C
XH_P51	4	437749	437749	Silent	SNP	T	C	T	ZNFR721	c.A507G	p.E169E
XH_P51	4	9784393	9784393	Missense_Mutation	SNP	G	A	G	DRD5	c.G740A	p.R247H
XH_P51	4	15689418	15689418	Frame_Shift_Ins	INS	-	CTTTTGCCACAC	-	FAM200B	9insCTCTTTTGGC	p.F273fs
XH_P51	4	20706429	20706429	In_Frame_Ins	INS	-	AAGCTCTGTACC	-	PACRGL	200insAAGCTCT	I67delinsKALYL
XH_P51	4	39314448	39314448	In_Frame_Ins	INS	-	GAC	-	RFC1	1306_1307insG	p.K436delinsSQ
XH_P51	4	39314449	39314449	Frame_Shift_Ins	INS	-	AGTGATTTTAA	-	RFC1	1TTAAACTTAAAT	p.K436fs
XH_P51	4	42448637	42448637	Missense_Mutation	SNP	G	A	G	ATP8A1	c.C2876T	p.T959I
XH_P51	4	46930766	46930766	Nonsense_Mutation	INS	-	TAACA	-	GABRA4	930_931insGTG	311_A312delinsCX
XH_P51	4	46930768	46930768	In_Frame_Ins	INS	-	TTTATTGGGTTG	-	GABRA4	9insAACAAACCC	310delinsKQPNKP
XH_P51	4	57366772	57366772	In_Frame_Ins	INS	-	GCAGGTTTGG	-	SRP72	1567insGCAG	R522delinsRAGL
XH_P51	4	70146430	70146430	Missense_Mutation	SNP	C	A	C	UGT2B28	c.C212A	p.T71N
XH_P51	4	70146432	70146432	Nonsense_Mutation	INS	-	AAAGTAAATAT	-	UGT2B28	15insCAAAGATA	72_K73delinsPKX
XH_P51	4	71509605	71509605	Frame_Shift_Ins	INS	-	TTTGTATGGATT	-	ENAM	CCTGGTTTGTGA	p.P821fs
XH_P51	4	73012828	73012828	In_Frame_Ins	INS	-	GGC	-	NPFFR2	1868_869insGG	p.K290delinsRQ
XH_P51	4	73012829	73012829	In_Frame_Ins	INS	-	TGCATTGTC	-	NPFFR2	9_870insTGCAT	K290delinsNALs
XH_P51	4	76924783	76924783	Nonsense_Mutation	INS	-	TAAAGGCTATGA	-	CXCL9	GACAATCATAGG	Q117delinsDNHLSX
XH_P51	4	83826023	83826023	Nonsense_Mutation	INS	-	TTTTTAATCCAA	-	THAP9	5insTTTTTTTTAA	72_S73delinsDFFX
XH_P51	4	90034394	90034394	Nonsense_Mutation	INS	-	GTGTCTAATATT	-	TIGD2	TTTAAAGTGCTCA	90delinsHFKCLIFX
XH_P51	4	123161371	123161371	Frame_Shift_Ins	INS	-	CTTTCATCACTG	-	KIAA1109	535insGCCTTCA	p.V1512fs
XH_P51	4	126355476	126355476	Silent	SNP	C	A	C	FAT4	c.C7095A	p.A2365A

XH_P51	5	34922844	34922844	In_Frame_Ins	INS	-	CCT	-	BRX1	c.481_482insCC	b.G161delinsAC
XH_P51	5	34922845	34922845	Frame_Shift_Ins	INS	-	GATATGGAGTA	-	BRX1	insAAAGATATG	p.G161fs
XH_P51	5	36265153	36265153	Silent	SNP	G	A	G	RANBP3L	c.C316T	p.L106L
XH_P51	5	37327835	37327835	Frame_Shift_Ins	INS	-	TATTCTCTTA	-	NUP155	1920insTAAGAA	p.G640fs
XH_P51	5	42759266	42759266	Frame_Shift_Ins	INS	-	CAAATGCTATTGT	-	CCDC152	nsGTCAAATGCA	p.V15fs
XH_P51	5	56177849	56177854	In_Frame_Del	DEL	CAACAA	-	CAACAA	MAP3K1	c.2822_2827del	p.941_943del
XH_P51	5	68616209	68616209	Nonsense_Mutation	INS	-	AAAAATAAATAA	-	CCDC125	ATATGGTTATTB	g.654delinsEYGYLFX
XH_P51	5	75427950	75427950	In_Frame_Ins	INS	-	CTTCTTTACTGTT	-	SV2C	76insCCTTCTTTA	g.5125delinsSPSLF
XH_P51	5	79033590	79033590	In_Frame_Ins	INS	-	GTCTTCACCTTTT	-	CMYAS	GTAAAGTCTTCA	g.101delinsHCKVFTFCIC
XH_P51	5	102895168	102895168	Frame_Shift_Ins	INS	-	TT	-	NUDT12	c.153_154insAA	p.C52fs
XH_P51	5	102895169	102895169	Nonsense_Mutation	INS	-	ATTCGTTAGGAA	-	NUDT12	CTTGGTTCCTAA	M51delinsISLGSX
XH_P51	5	121355972	121355972	Nonsense_Mutation	INS	-	ATTGATATTAAAT	-	SFRBP1	TGGAATTGATA	g.81delinsIHNSKEKIX
XH_P51	5	121488546	121488546	Frame_Shift_Ins	INS	-	TGTGGTAAGGA	-	ZNF474	ACATATGTGGT	p.C287fs
XH_P51	5	123983905	123983905	Frame_Shift_Ins	INS	-	AAACACCA	-	ZNF608	1_2172insTGGG	p.K724fs
XH_P51	5	138209068	138209068	In_Frame_Ins	INS	-	TGTTCA	-	LRRTM2	81_1182insTGA	d.394delinsDEH
XH_P51	5	138209346	138209346	Frame_Shift_Ins	INS	-	ACAATGGCTTTA	-	LRRTM2	904insATAAAGC	p.S302fs
XH_P51	5	138643806	138643806	Nonsense_Mutation	INS	-	CAGGAGTAATC	-	MATR3	703insCAGGAG	g.34_F235delinsSQEX
XH_P51	5	138651795	138651795	Frame_Shift_Ins	INS	-	SAATACAATAA	-	MATR3	AAAAGAATACA	p.T61fs
XH_P51	5	139876855	139876855	In_Frame_Ins	INS	-	TTTCCAAGTATT	-	ANKHD1	nsTTGGTTTCCA	g.99delinsLWFP5ILW
XH_P51	5	140070865	140070865	Frame_Shift_Ins	INS	-	GGCCTCTGCTG	-	HARS	CAAGCAGCAGA	p.E9fs
XH_P51	5	140188914	140188914	Silent	SNP	G	A	G	PCDH4A	c.G2142A	p.T714T
XH_P51	5	140431471	140431471	Frame_Shift_Ins	INS	-	CTCA	-	PCDH81	416_417insCTC	p.L139fs
XH_P51	5	140476277	140476277	Missense_Mutation	SNP	C	G	C	PCDH82	c.C1903G	p.R635G
XH_P51	5	140572418	140572418	Frame_Shift_Ins	INS	-	AGGGGTCTTT	-	PCDH810	294insAGGGG	p.P98fs
XH_P51	5	140579549	140579549	Nonsense_Mutation	INS	-	AAGGATTTTAA	-	PCDH811	203insAAGGAT	g.568_N69delinsX
XH_P51	5	140588659	140588659	In_Frame_Ins	INS	-	ACCAAATCC	-	PCDH812	D_181insACCAA	b.560delinsSTKS
XH_P51	5	140865128	140865128	Missense_Mutation	SNP	G	T	G	PCDHGC4	c.G388T	p.A130S
XH_P51	5	140868999	140868999	Frame_Shift_Ins	INS	-	AAGTCTCTATG	-	PCDHGC5	193insAAGTCTC	p.L64fs
XH_P51	5	147661781	147661781	Nonsense_Mutation	INS	-	TCTGATTGTA	-	SPINK13	224insTCTGAT	g.75_V76delinsFX
XH_P51	5	149505011	149505011	Silent	SNP	G	A	G	PDGFRB	c.C1804T	p.L602L
XH_P51	5	175717557	175717557	Missense_Mutation	SNP	C	T	C	SIMC1	c.C1030T	p.H344Y
XH_P51	6	562826	562826	Frame_Shift_Ins	INS	-	ACCTTTTTCATCC	-	EXOC2	ATACAGGATGA	p.E603fs
XH_P51	6	1390406	1390420	In_Frame_Del	DEL	CGGGCGGCGG	-	CGGGCGGCGG	FOX2	c.224_238del	p.75_80del
XH_P51	6	4032190	4032190	Frame_Shift_Ins	INS	-	TTCTTTTGTGTTT	-	PRPF4B	CTCTTTTCTTTT	p.E147fs
XH_P51	6	10586886	10586886	Frame_Shift_Ins	INS	-	CAGATTCTCTAT	-	GCNT2	65insACAGATT	p.P222fs
XH_P51	6	10709610	10709610	Silent	SNP	A	T	A	PAK1IP1	c.A1104T	p.I368I
XH_P51	6	10724865	10724865	Frame_Shift_Ins	INS	-	TATTTCTCAC	-	TMEM14C	9_20insTATTCTT	p.V7fs
XH_P51	6	10724867	10724867	Splice_Site	INS	-	TACCA	-	TMEM14C	.	.
XH_P51	6	11103981	11103981	Frame_Shift_Ins	INS	-	TTTTCCCAGATA	-	ERVFRD-1	63insATTATCTG	p.Q521fs
XH_P51	6	11191331	11191331	Silent	SNP	C	T	C	NEDD9	c.G324A	p.P108P
XH_P51	6	17675556	17675556	Nonsense_Mutation	INS	-	TTATAATTTATC	-	NUP153	AGAATGATAAA	g.5209delinsSETEX
XH_P51	6	18161675	18161675	Missense_Mutation	SNP	G	A	G	KDM1B	c.G205A	p.A69T
XH_P51	6	18236780	18236780	Nonsense_Mutation	INS	-	ATGTATCTCTAG	-	DEK	gTAAACTAAGGA	g.283_K284delinsINX
XH_P51	6	24533903	24533903	Nonsense_Mutation	INS	-	AAAATAACTG	-	ALDH5A1	1572insAAAAAT	g.524_L525delinsX
XH_P51	6	25652698	25652698	Missense_Mutation	SNP	C	T	C	SCGN	c.C67T	p.R23C
XH_P51	6	25914888	25914888	In_Frame_Ins	INS	-	AAAAATATAAGC	-	SLC17A2	074insAAGCTTA	g.358delinsSVLVS
XH_P51	6	25914890	25914890	Missense_Mutation	SNP	C	T	C	SLC17A2	c.G1072A	p.V358I
XH_P51	6	26043725	26043725	Missense_Mutation	SNP	C	T	C	HIST1H2BB	c.G161A	p.G54D
XH_P51	6	26199811	26199811	Missense_Mutation	SNP	C	A	C	HIST1H2BF	c.C25A	p.P9T
XH_P51	6	26273495	26273495	Missense_Mutation	SNP	G	C	G	HIST1H2BI	c.G292C	p.A98P
XH_P51	6	26273496	26273496	Frame_Shift_Ins	INS	-	CTCATT	-	HIST1H2BI	93_294insCTCA	p.A98fs
XH_P51	6	26452090	26452090	In_Frame_Ins	INS	-	CAGCCATTTTTCT	-	BTN3A3	77insTCAGCCAT	g.5192delinsGSAIFP
XH_P51	6	28269232	28269232	In_Frame_Ins	INS	-	GAACTGTGA	-	PGBD1	1_1602insGAAC	g.1534delinsLNCD
XH_P51	6	37336596	37336596	Frame_Shift_Ins	INS	-	CAAGGATATAT	-	RNF8	78insACAAGGA	p.G193fs
XH_P51	6	39856467	39856467	Nonsense_Mutation	INS	-	TAGACTAGTAT	-	DAAM2	nsTAGATTAGAC	p.5691delinsSX
XH_P51	6	43006195	43006195	In_Frame_Ins	INS	-	GGATTCCGACG	-	CUL7	GCCTCATCGTCC	g.2delinsNCLIVRLKAHG
XH_P51	6	43308578	43308578	Frame_Shift_Ins	INS	-	GATGAAACCC	-	ZNF318	nsTATAATGGGT	p.11149fs
XH_P51	6	44254254	44254254	Frame_Shift_Ins	INS	-	AAAGCATCTTA	-	TCTE1	293insTAAAGT	p.K98fs
XH_P51	6	46977570	46977570	Frame_Shift_Ins	INS	-	GTCGT	-	ADGRF1	500_1601insACC	p.C534fs
XH_P51	6	46977571	46977571	Frame_Shift_Ins	INS	-	TTTGC	-	ADGRF1	599_1600insGCC	p.C534fs
XH_P51	6	46979811	46979811	Frame_Shift_Ins	INS	-	CCTTCAAGCACA	-	ADGRF1	48insCCTGTGCT	p.S350fs
XH_P51	6	52303345	52303345	Frame_Shift_Ins	INS	-	GTACCTATAACA	-	EFHC1	insCAGTACCTA	p.Y177fs
XH_P51	6	55198712	55198712	Nonsense_Mutation	INS	-	ATAACACTAAT	-	GFRAL	insACATAACAC	g.96_197delinsHITLX
XH_P51	6	64422419	64422419	Frame_Shift_Ins	INS	-	TTTGTACTGAAT	-	PHF3	CTCTTTGTTTGA	p.1645fs
XH_P51	6	97339198	97339198	In_Frame_Ins	INS	-	TGAGCTCCCTGA	-	NDUFAF4	310insTCAGGG	g.1104delinsSGSSI
XH_P51	6	97610011	97610011	Frame_Shift_Ins	INS	-	GGTTAAAACTG	-	MMS22L	ACATCTCAGTT	p.S801fs
XH_P51	6	112390713	112390713	Nonsense_Mutation	INS	-	GAACACATGTAG	-	WISP3	AGTTTTGAAGAA	g.9338delinsVNSFENMX
XH_P51	6	123127437	123127437	Missense_Mutation	SNP	G	C	G	SMPDL3A	c.G586C	p.E196Q
XH_P51	6	125366487	125366487	Frame_Shift_Ins	INS	-	GTAGAAATCAA	-	RNF217	014insAGTAGA	p.R338fs
XH_P51	6	132619048	132619048	Frame_Shift_Ins	INS	-	AATTAGTTCTAA	-	MOXD1	insAGTTTATAGA	p.S519fs
XH_P51	6	144996999	144996999	Nonsense_Mutation	INS	-	CAAGTGTTAGG	-	UTRN	ATAATGCAAGT	g.446_52547delinsNRX
XH_P51	6	160174562	160174562	Frame_Shift_Ins	INS	-	TTTTCATCTCAA	-	WTAP	4insTATTTTCAT	p.L175fs
XH_P51	6	160174564	160174564	Silent	SNP	G	A	G	WTAP	c.G525A	p.L175L
XH_P51	7	1275562	1275562	Missense_Mutation	SNP	G	A	G	UNCX	c.G545A	p.C182Y
XH_P51	7	1784418	1784418	Silent	SNP	C	T	C	ELFN1	c.C186T	p.I62I
XH_P51	7	5239240	5239240	Frame_Shift_Ins	INS	-	CAGACAATATTA	-	WIP12	nsATACAGACAA	p.K36fs
XH_P51	7	5940560	5940560	Frame_Shift_Ins	INS	-	TAAAAATGCAAA	-	CC21	nsATTTTAAAAAT	p.L129fs
XH_P51	7	5963575	5963575	In_Frame_Ins	INS	-	TCGTTTCGTT	-	CC21	5_1376insTCGT	g.1459delinsIVRY
XH_P51	7	6180585	6180585	Nonsense_Mutation	INS	-	ATACAAAACCTGG	-	USP42	nsTAGAAATCAAA	g.255_P256delinsDX
XH_P51	7	6189416	6189416	In_Frame_Ins	INS	-	TCATAC	-	USP42	89_1590insTCAB	g.1530delinsFHT
XH_P51	7	6189417	6189417	Silent	SNP	G	A	G	USP42	c.G1590A	p.L530L
XH_P51	7	6845669	6845669	Splice_Site	SNP	C	T	C	CCZ1B	.	.
XH_P51	7	7278319	7278319	Nonsense_Mutation	INS	-	AACTTCTGATA	-	C1GALT1	nsTTCTAACTTTC	g.218_A219delinsEFX
XH_P51	7	12384057	12384057	Frame_Shift_Ins	INS	-	TGATGAAGGTG	-	VWDE	80insTATCACTT	p.V1194fs
XH_P51	7	21675711	21675711	Nonsense_Mutation	INS	-	AAATGTGAGTGC	-	DNAH11	nsGTAGATGTGT	g.75_E1576delinsSRMX
XH_P51	7	21940868	21940868	In_Frame_Ins	INS	-	CGTGGACAGAA	-	DNAH11	CCACCCCGGTG	g.6delinsAEPPTWTEPILQ
XH_P51	7	26246130	26246130	In_Frame_Ins	INS	-	CTGACAATACT	-	CBX3	8insTGCTGACA	g.956delinsDADNTC
XH_P51	7	27239007	27239007	Silent	SNP	G	A	G	HOXA13	c.C690T	p.F230F
XH_P51	7	31378366	31378366	In_Frame_Ins	INS	-	GCGTATGAATCC	-	NEUROD6	517insGGATTCA	g.173delinsGFIRT
XH_P51	7	31691620	31691620	Frame_Shift_Ins	INS	-	TT	-	CCDC129	2779_2780insT	p.Q927fs
XH_P51	7	31691621	31691621	In_Frame_Ins	INS	-	AAAGAGAAT	-	CCDC129	2781insAAAG	g.927delinsQKRM
XH_P51	7	40118403	40118403	Missense_Mutation	SNP	G	T	G	CDK13	c.G2982T	p.Q994H
XH_P51	7	42977166	42977166	Nonsense_Mutation	INS	-	TCACITTTAA	-	MRPL32	8_559insTCAC	g.178delinsTSLX
XH_P51	7	45724630	45724630	Frame_Shift_Ins	INS	-	TATTGAATCTCT	-	ADCY1	37insTATATTGA	p.I679fs
XH_P51	7	45724632	45724632	Missense_Mutation	SNP	G	T	G	ADCY1	c.G2038T	p.V680L
XH_P51	7	47921648	47921648	Frame_Shift_Ins	INS	-	TTTCTCT	-	PKD1L1	D_3301insAGAA	p.L1101fs
XH_P51	7	47921649	47921649	Frame_Shift_Ins	INS	-	AA	-	PKD1L1	3299_3300insT	p.S1100fs
XH_P51	7	63538228	63538228	Silent	SNP	T	C	T	ZNF727	c.T801C	p.C267C

XH_P51	7	63808630	63808630	Nonsense_Mutation	INS	-	TAAATACCACA	-	ZNF736	5ATAATAAAATA130_N131delinsX
XH_P51	7	64167823	64167823	Frame_Shift_Ins	INS	-	TTTTAAGGATC	-	ZNF107	insTAAGTTTAA p.E418fs
XH_P51	7	64864545	64864545	In_Frame_Ins	INS	-	ATATGATTCTCT	-	ZNF92	TCTTCCATATGA delinsGFIFHMSLMFS
XH_P51	7	77885338	77885338	In_Frame_Ins	INS	-	CCA	-	MAGI2	1968_1969insTCb.L657delinsWL
XH_P51	7	77885339	77885339	Frame_Shift_Ins	INS	-	TGTTTGTG	-	MAGI2	7_1968insGACAA p.N656fs
XH_P51	7	82582537	82582537	In_Frame_Ins	INS	-	CAAGACTGAGG	-	PCLO	7732insACCTCAE2578delinsTSVLE
XH_P51	7	88965095	88965095	Frame_Shift_Ins	INS	-	TCTGTCGTGCT	-	ZNF804B	2800insTCTGTG p.Q933fs
XH_P51	7	91630663	91630663	Frame_Shift_Ins	INS	-	GTCTCTTTGCGAC	-	AKAP9	TTCTTGGTCTCT p.Y478fs
XH_P51	7	91924392	91924392	In_Frame_Ins	INS	-	AATTTTAAACAT	-	ANKB1	01insAAATTTTAA p.L34delinsQIFNTV
XH_P51	7	92821589	92821589	Frame_Shift_Ins	INS	-	AGTGGACTAGA	-	HEPACAM2	302insATCTAG p.L434fs
XH_P51	7	98649946	98649946	Frame_Shift_Ins	INS	-	TTTTTTTTTGAG	-	SMURF1	sTTGTCTCAAAA p.P201fs
XH_P51	7	99262917	99262917	Frame_Shift_Ins	INS	-	AAAGGTACAATT	-	CYP3A5	sATGGGAATTGT p.M181fs
XH_P51	7	99662038	99662038	Frame_Shift_Ins	INS	-	TGTGTCTGTAG	-	ZSCAN21	21insAGTGTGT p.Q407fs
XH_P51	7	100678246	100678246	Silent	SNP	T	C	T	MUC17	c.T3549C p.T1183T
XH_P51	7	100678314	100678314	Missense_Mutation	SNP	T	G	T	MUC17	c.T3617G p.V1206G
XH_P51	7	102427887	102427887	Missense_Mutation	SNP	T	C	T	FAM185A	c.T686C p.V229A
XH_P51	7	103202100	103202100	Missense_Mutation	SNP	A	T	A	RELN	c.T5408A p.L1803N
XH_P51	7	103293161	103293161	Frame_Shift_Ins	INS	-	SAAGCCCTATTT	-	RELN	insTACAAATAA p.P534fs
XH_P51	7	104717497	104717497	Missense_Mutation	SNP	G	C	G	KMT2E	c.G856C p.E286Q
XH_P51	7	104730627	104730627	Frame_Shift_Ins	INS	-	TAAGCAATCCTT	-	KMT2E	TAATTATAAGCA p.T510fs
XH_P51	7	107240863	107240863	Missense_Mutation	SNP	G	T	G	BCAP29	c.G502T p.D168Y
XH_P51	7	107240864	107240864	Frame_Shift_Ins	INS	-	CGTCAGTCTTTC	-	BCAP29	04insACGTGACAG p.P168fs
XH_P51	7	107577674	107577674	Frame_Shift_Ins	INS	-	SGATTAAACGAT	-	LAMB1	8810insTATCGT p.K1270fs
XH_P51	7	107799961	107799961	Nonsense_Mutation	INS	-	ACATTTTTCATT	-	NRCAM	261insAAAAATGA087_D1088delinsAKX
XH_P51	7	107799962	107799962	Missense_Mutation	SNP	G	T	G	NRCAM	c.C3260A p.A1087D
XH_P51	7	113558486	113558486	Nonsense_Mutation	INS	-	GAGGATATATCT	-	PPP1R3A	TATGTAAGATAT189_F190delinsX
XH_P51	7	117251821	117251821	Nonsense_Mutation	INS	-	TGGTTAAAAAG	-	CFTR	3327insTGGTTA09_F1110delinsLIGX
XH_P51	7	117431781	117431781	Frame_Shift_Ins	INS	-	ACAAAACGTGGG	-	CTTNBP2	469insGCCACAC p.N490fs
XH_P51	7	124537267	124537267	Splice_Site	INS	-	AAATTCATTCTT	-	POT1	.
XH_P51	7	127015066	127015066	Frame_Shift_Ins	INS	-	ATTCAATCTAG	-	ZNF800	CTCGCTAGAA p.K108fs
XH_P51	7	141351404	141351404	In_Frame_Ins	INS	-	TTGTGATACATT	-	AGK	1127insTTGTGA p.P376delinsLVHIS
XH_P51	7	143269947	143269947	Frame_Shift_Ins	INS	-	GAATTTTCATT	-	CTAGE15	1038insGAATT p.D346fs
XH_P51	7	143807610	143807610	In_Frame_Ins	INS	-	CACCAT	-	OR2A2	35_936insCACGCT312delinsTMT
XH_P51	7	143807612	143807612	Frame_Shift_Ins	INS	-	C	-	OR2A2	c.937_938insC p.V313fs
XH_P51	7	149462760	149462760	Silent	SNP	G	A	G	ZNF467	c.C831T p.C277C
XH_P51	8	17722257	17722257	Nonsense_Mutation	INS	-	GAAAAATACCTC	-	FGL1	insAATGAGTAT261_H262delinsX
XH_P51	8	18656864	18656864	Splice_Site	INS	-	TGTTGTCTGGA	-	PSD3	.
XH_P51	8	59477592	59477592	Nonsense_Mutation	INS	-	AATAAGAATATA	-	SODCBP	AAAAATAAGAA K21delinsKHKKX
XH_P51	8	67567766	67567766	Frame_Shift_Ins	INS	-	TCTTAATTGTAA	-	VCPIP1	ATTATATTACAA p.R806fs
XH_P51	8	77764925	77764925	Nonsense_Mutation	INS	-	CTTATAAATTCCT	-	ZFHx4	CCTTCACTTATA23_Y1924delinsHLHX
XH_P51	8	77765726	77765726	Frame_Shift_Ins	INS	-	GGTAGGACAGAT	-	ZFHx4	ACCCGGGTAGG p.D2190fs
XH_P51	8	81412363	81412363	Frame_Shift_Ins	INS	-	ATTAACCTGGTTT	-	ZBTB10	ATCTCTATTAAAC p.S536fs
XH_P51	8	87076531	87076531	Missense_Mutation	SNP	C	A	C	PSKH2	c.G515T p.R172M
XH_P51	8	91078178	91078178	Frame_Shift_Ins	INS	-	CCAAAGCCAG	-	CALB1	398insCTGGCT p.K133fs
XH_P51	8	91078179	91078179	Frame_Shift_Ins	INS	-	GTAA	-	CALB1	396_397insTTA p.K133fs
XH_P51	8	93004024	93004024	In_Frame_Ins	INS	-	GAACTTAATCTC	-	RUNX1T1	3insTCAAGTTAA241delinsPQVKFR
XH_P51	8	94809634	94809634	Frame_Shift_Ins	INS	-	CATAT	-	TMEM67	036_2037insCA p.E679fs
XH_P51	8	94809636	94809636	Frame_Shift_Ins	INS	-	CCTGAAAAAGT	-	TMEM67	AAAAACACTGAA p.L680fs
XH_P51	8	99101949	99101949	Frame_Shift_Ins	INS	-	GAAC	-	ERICH5	704_705insGAA p.Q235fs
XH_P51	8	99101951	99101951	In_Frame_Ins	INS	-	TCTCAG	-	ERICH5	06_707insTCTC p.F236delinsFSV
XH_P51	8	103373850	103373850	Silent	SNP	G	T	G	UBR5	c.C67A p.R23R
XH_P51	8	105261005	105261005	Frame_Shift_Ins	INS	-	AGCCCAAGTA	-	RIMS2	362insAGCCCA p.L121fs
XH_P51	8	113516192	113516192	Frame_Shift_Ins	INS	-	5CCCATTTGTTAG	-	CSMD3	TAACCACTAAC p.P1533fs
XH_P51	8	120807825	120807825	In_Frame_Ins	INS	-	GAGAATATTTTA	-	TAF2	8insAACTTAAAT380delinsNLNLF
XH_P51	8	126015628	126015628	Nonsense_Mutation	INS	-	TTAAAAAATAAA	-	SQLE	5CTGTTTAAAAAA p.P169delinsRCLKKKRX
XH_P51	8	133092144	133092144	Frame_Shift_Ins	INS	-	GGTAAGATGCA	-	HHLA1	746insTGCATC p.T249fs
XH_P51	8	133806818	133806818	In_Frame_Ins	INS	-	AACAATAAATAC	-	PHF20L1	247insACAATA E82delinsENNKY
XH_P51	8	133806819	133806819	Frame_Shift_Ins	INS	-	TCCAT	-	PHF20L1	247_248insTCC p.D83fs
XH_P51	8	139601616	139601616	In_Frame_Ins	INS	-	TTTTTCTTTCTTT	-	COL22A1	sGATAAAAGAA587delinsTIERKKK
XH_P51	8	143957129	143957129	Silent	SNP	G	T	G	CYP11B1	c.C1120A p.R374R
XH_P51	8	146068308	146068308	Frame_Shift_Ins	INS	-	TTTCT	-	ZNF7	528_1529insTT p.A510fs
XH_P51	9	3271103	3271103	In_Frame_Ins	INS	-	AATAAATTAGAG	-	RFX3	102insATCTCTAA368delinsINLLV
XH_P51	9	5920444	5920444	In_Frame_Ins	INS	-	CTCCTATATCTA	-	KIAA2026	52insGTAGATAT1851delinsRRYKEN
XH_P51	9	5920445	5920445	Missense_Mutation	SNP	G	T	G	KIAA2026	c.C5551A p.H1851N
XH_P51	9	5922669	5922669	Nonsense_Mutation	INS	-	CCTTTATCAAA	-	KIAA2026	ACTTATATTGGA F1110delinsNVLKIKVX
XH_P51	9	6536172	6536172	Silent	SNP	C	T	C	GLDC	c.G2730A p.S910S
XH_P51	9	8449821	8449821	Missense_Mutation	SNP	C	T	C	PTPRD	c.G2629A p.D877N
XH_P51	9	13183576	13183576	Frame_Shift_Ins	INS	-	ACGTTGGTGGT	-	MPDZ	insTATCCAACCA p.T830fs
XH_P51	9	13206023	13206023	In_Frame_Ins	INS	-	ATCTGCATCTTTT	-	MPDZ	stCACAAAAGA56delinsSQMQICL
XH_P51	9	14859414	14859414	Nonsense_Mutation	INS	-	CTTTAATGCC	-	FREM1	398insGGCATT133_1134delinsRHX
XH_P51	9	16738418	16738418	Missense_Mutation	SNP	C	G	C	BNC2	c.G69C p.E23D
XH_P51	9	19597253	19597253	Frame_Shift_Ins	INS	-	C	-	SLC24A2	c.1102_1103ins p.K368fs
XH_P51	9	19597254	19597254	In_Frame_Ins	INS	-	CTGCATTTTGTG	-	SLC24A2	02insGACAAAAA368delinsDKNAEK
XH_P51	9	26923315	26923315	Silent	SNP	T	A	T	PLAA	c.A900T p.S300S
XH_P51	9	27524793	27524793	Frame_Shift_Ins	INS	-	T	-	IFNK	c.459_460insT p.R153fs
XH_P51	9	27524794	27524794	Frame_Shift_Ins	INS	-	ACTCT	-	IFNK	460_461insACT p.V154fs
XH_P51	9	34725246	34725246	Frame_Shift_Ins	INS	-	ATGCCAAC	-	FAM205A	0_1991insGTTG p.P664fs
XH_P51	9	35398264	35398264	Frame_Shift_Ins	INS	-	TCATTTTAA	-	UNC13B	3565insTCATT p.F1188fs
XH_P51	9	35398265	35398265	Nonsense_Mutation	INS	-	CTGGGTGGT	-	UNC13B	3566insCTGGGE1189delinsAGWX
XH_P51	9	35609478	35609478	Silent	SNP	C	T	C	TESK1	c.C1140T p.S380S
XH_P51	9	43625429	43625429	In_Frame_Ins	INS	-	AAACATCAAGC	-	SPATA31A6	258insTTGCTTGA1086delinsNCLMFS
XH_P51	9	75309593	75309593	In_Frame_Ins	INS	-	TCACATCTGTA	-	TMC1	insTTCTCCACAT867delinsLHVMG
XH_P51	9	79954748	79954748	Frame_Shift_Ins	INS	-	G	-	VPS13A	c.6578_6579ins p.I2193fs
XH_P51	9	88204559	88204559	In_Frame_Ins	INS	-	TTAACC	-	AGTPBP1	61_2762insGGG p.Q921delinsRLK
XH_P51	9	88204560	88204560	Frame_Shift_Ins	INS	-	ATAATGGAAATC	-	AGTPBP1	sATTATCATTTCC p.Q921fs
XH_P51	9	90537466	90537466	Missense_Mutation	SNP	G	A	G	SPATA31C1	c.G2644A p.A882T
XH_P51	9	90753358	90753358	Frame_Shift_Ins	INS	-	TT	-	SPATA31C2	c.3_4insAA p.E2fs
XH_P51	9	90753359	90753359	In_Frame_Ins	INS	-	TTTCTTTTATT	-	SPATA31C2	binsAATAAAAAAG p.M1delinsIKRK
XH_P51	9	95012553	95012553	Nonsense_Mutation	INS	-	CTCTAGTATCC	-	IARS	448insAGGATA16_K817delinsKGYX
XH_P51	9	95072486	95072502	Frame_Shift_Del	DEL	AGAGTCCAT	-	GAGAGTCCATG	NOL8	c.2523_2529del p.F841fs
XH_P51	9	97062425	97062425	Frame_Shift_Ins	INS	-	AAGATCTGTGT	-	ZNF169	13insAAGATCT p.G4fs
XH_P51	9	98734848	98734848	Nonsense_Mutation	INS	-	CTTTTGGATTTA	-	ERCC6L2	TCCTTTCTTTTGG R951delinsNMLFFWIX
XH_P51	9	105767852	105767852	In_Frame_Ins	INS	-	TTTACA	-	CYLC2	39_940insTTTA p.A313delinsAFT
XH_P51	9	105767853	105767853	In_Frame_Ins	INS	-	CTTGTA	-	CYLC2	40_941insCTTG p.D314delinsACN
XH_P51	9	107513359	107513359	Frame_Shift_Ins	INS	-	CATTACTCATGT	-	NIPSNAP3A	AGACTCATTACT p.H61fs
XH_P51	9	120475904	120475904	Missense_Mutation	SNP	T	A	T	TLR4	c.T898A p.F300I
XH_P51	9	120476821	120476821	Frame_Shift_Ins	INS	-	AACA	-	TLR4	815_1816insAA p.H605fs
XH_P51	9	125659686	125659686	Nonsense_Mutation	INS	-	TTTTTTGTGATT	-	RC3H2	ACATAAATCACAA335_T36delinsTX

XH_P51	9	135173644	135173644	Silent	SNP	C	T	C	SETX	c.G5604A	p.P1868P
XH_P51	9	139794876	139794876	Frame Shift Ins	INS	-	TTTTTTTTTTTT	-	TRAF2	1insCTTTTTTTT	p.A90fs
XH_P51	9	139973033	139973033	Missense_Mutation	SNP	G	A	G	UAP1L1	c.G574A	p.A192T
XH_P51	10	294956	294956	Nonsense_Mutation	INS	-	CATTATCTACTG	-	ZMYND11	5AGTATCATAT	63_F454delinsESIITX
XH_P51	10	871095	871095	Nonsense_Mutation	INS	-	TGATCATTTTAT	-	LARP4B	1GAGTTATAAAA	5delinsPVNKNGFMCX
XH_P51	10	1042095	1042095	Frame Shift Ins	INS	-	ACCT	-	GTPBP4	373_374insACT	p.R125fs
XH_P51	10	1042096	1042096	Frame Shift Ins	INS	-	AAGAACAATTT	-	GTPBP4	375insAAGAAC	p.R125fs
XH_P51	10	5494870	5494870	Frame Shift Ins	INS	-	AT	-	NET1	c.419_420insAT	p.K140fs
XH_P51	10	5494872	5494872	Frame Shift Ins	INS	-	AGGTTGCCGTAT	-	NET1	22insAAGGTTGC	p.L141fs
XH_P51	10	21804217	21804217	Frame Shift Ins	INS	-	STTTTGGGAAGAT	-	SKIDA1	5insAATATCTCT	p.H845fs
XH_P51	10	24909657	24909657	Frame Shift Ins	INS	-	G	-	ARHGAP21	c.1166_1167insT	p.Y389fs
XH_P51	10	24909658	24909658	Nonsense_Mutation	INS	-	ACTCGTTCATGG	-	ARHGAP21	ATAATCCCATG	389_K390delinsSIX
XH_P51	10	25312935	25312935	Nonsense_Mutation	INS	-	TAAGTAAGTCTT	-	THNSL1	AAATTTAAGTA	51_D262delinsSKFKX
XH_P51	10	27329030	27329030	Nonsense_Mutation	INS	-	GGCCCTCAATA	-	ANKRD26	TTACATATTGA	746_L747delinsTLX
XH_P51	10	30317059	30317059	Frame Shift Ins	INS	-	AAGGACT	-	JCAD	17_2018insAGT	p.R673fs
XH_P51	10	30748263	30748263	Nonsense_Mutation	INS	-	TTTTCTTTTCCTT	-	MAP3K8	ATTCTTTTTTCT	369_E370delinsLX
XH_P51	10	32329384	32329384	Frame Shift Ins	INS	-	AAACGTTACCTC	-	KIF5B	CAATGGAGGTA	p.D72fs
XH_P51	10	33015699	33015699	Frame Shift Ins	INS	-	ATTATTTACACTG	-	CCDC7	1insTTGATTATT	p.S869fs
XH_P51	10	33199189	33199189	Frame Shift Ins	INS	-	A	-	ITGB1	c.2125_2126ins	p.G709fs
XH_P51	10	33199190	33199190	Frame Shift Ins	INS	-	ATGGGAAATATG	-	ITGB1	CTTAAACATATT	p.G709fs
XH_P51	10	35805537	35805537	In Frame Ins	INS	-	AGTACAAAAAC	-	CCNY	1nsAACACATACA	92delinsKNSKTKTL
XH_P51	10	38121835	38121835	Missense_Mutation	SNP	T	A	T	ZNF248	c.A448T	p.L150F
XH_P51	10	45430177	45430177	Missense_Mutation	SNP	G	C	G	TMEM72	c.G69C	p.E23D
XH_P51	10	46322265	46322265	In Frame Ins	INS	-	AGTCCTCAT	-	AGAP4	9_1090insATGA	P364delinsMRT
XH_P51	10	51769019	51769019	Frame Shift Ins	INS	-	CATTT	-	AGAP6	134_1133insCA	p.S378fs
XH_P51	10	69832808	69832808	In Frame Ins	INS	-	AGTTTGAACATAT	-	HERC4	5CATATAGTTAC	E20delinsHIVTTRE
XH_P51	10	70098417	70098417	Frame Shift Ins	INS	-	A	-	HNRNP3	c.16_17insA	p.R6fs
XH_P51	10	70098418	70098418	Nonsense_Mutation	INS	-	TTTTTCTATATCT	-	HNRNP3	TAAGTTTTTCTA	R6delinsRKFFYIX
XH_P51	10	70776125	70776125	Nonsense_Mutation	INS	-	GCTGACTTATTA	-	KIF18P	1insAGTGCTGAC	L607delinsOCX
XH_P51	10	71265949	71265949	Nonsense_Mutation	INS	-	TGTTCTCTAGAG	-	SPAN15	1sGTACTGTCTCT	943_Y144delinsSTVLX
XH_P51	10	72643772	72643772	Missense_Mutation	SNP	C	T	C	PCBD1	c.G250A	p.G84S
XH_P51	10	74666408	74666408	In Frame Ins	INS	-	TCCACCATC	-	OIT3	9_600insTCCAC	L200delinsLPPS
XH_P51	10	76744920	76744920	Nonsense_Mutation	INS	-	GCAAGTACAGC	-	KAT6B	908insAGCAAGT	7636_D637delinsX
XH_P51	10	78647070	78647070	Nonsense_Mutation	INS	-	TTTACACATATT	-	KCNMA1	ATGCAAAATATG	14_E1115delinsCKVYX
XH_P51	10	79784808	79784808	Frame Shift Ins	INS	-	GTTTATT	-	POLR3A	10_411insAATA	p.L137fs
XH_P51	10	88232471	88232471	Nonsense_Mutation	INS	-	GATTTAAATATG	-	WAPL	1insCTAGCATATT	591_A592delinsNX
XH_P51	10	91498831	91498831	Frame Shift Ins	INS	-	FAAACCACTTTTC	-	KIF20B	3894insTAACCC	p.Q1298fs
XH_P51	10	91498832	91498832	Missense_Mutation	SNP	G	T	G	KIF20B	c.G3894T	p.Q1298H
XH_P51	10	93726497	93726497	In Frame Ins	INS	-	AATATTCTCATG	-	BTAF1	4insCTAAATATT	545delinsSKYSHGI
XH_P51	10	102539335	102539335	In Frame Ins	INS	-	TGACTG	-	PAX2	91_492insTGAC	T164delinsTDC
XH_P51	10	103868810	103868810	Nonsense_Mutation	INS	-	CAGTTTTTTCTCA	-	LDB1	81insATGAGAA	327_F328delinsTX
XH_P51	10	104632344	104632344	Frame Shift Ins	INS	-	AACCACTAAAT	-	AS3MT	311insAACCACT	p.L104fs
XH_P51	10	105762500	105762500	In Frame Ins	INS	-	TCTTCTCTTCTTC	-	SLK	565insCTCTTCTCT	L522delinsPLLSFI
XH_P51	10	105765668	105765668	Splice Site	INS	-	AGGAATACT	-	SLK	-	-
XH_P51	10	112262536	112262536	Frame Shift Ins	INS	-	AG	-	DUSP5	c.437_438insAG	p.L146fs
XH_P51	10	112262538	112262538	Nonsense_Mutation	INS	-	AATCAATA	-	DUSP5	9_440insAATCA	147_Q148delinsX
XH_P51	10	121608956	121608956	Frame Shift Ins	INS	-	TA	-	MCMBP	c.706_707insTA	p.G236fs
XH_P51	10	121608958	121608958	Missense_Mutation	SNP	C	A	C	MCMBP	c.G705T	p.K235N
XH_P51	10	124377771	124377771	Silent	SNP	C	T	C	DMBT1	c.C2859T	p.H953H
XH_P51	10	134188673	134188673	Missense_Mutation	SNP	C	T	C	LRRC27	c.C1520T	p.P507L
XH_P51	11	1028703	1028703	Missense_Mutation	SNP	G	A	G	MUC6	c.C1534T	p.R512C
XH_P51	11	5664548	5664548	In Frame Ins	INS	-	ATATATATATAT	-	TRIM34	1nsAAAAATATAT	359delinsTKIYIYI
XH_P51	11	5686784	5686784	Frame Shift Ins	INS	-	AGTTACATTATA	-	TRIM5	1insGGATATAAT	p.I333fs
XH_P51	11	6472654	6472654	Frame Shift Ins	INS	-	AAGATTCTGCT	-	TRIM3	1191insAGCAG	p.E397fs
XH_P51	11	6816731	6816731	Nonsense_Mutation	INS	-	TTTCTTATTTCTG	-	OR6A2	5AGGCCAGAA	p.L70delinsQX
XH_P51	11	10875998	10875998	In Frame Ins	INS	-	GTGCAAAAG	-	ZBED5	4_495insCTTTTCT	61165delinsFCT
XH_P51	11	20483678	20483678	Frame Shift Ins	INS	-	AGGAAAAACAA	-	PRMT3	1040insAGGAA	p.P347fs
XH_P51	11	20483680	20483680	Silent	SNP	G	C	G	PRMT3	c.G1041C	p.P347P
XH_P51	11	22387222	22387222	Frame Shift Ins	INS	-	CTTCTCTTTTGGC	-	SLC17A6	879insCTTCTCT	p.L293fs
XH_P51	11	28119330	28119330	Frame Shift Ins	INS	-	GGGCCTTACTG	-	KIF18A	165insCAGTAA	p.H55fs
XH_P51	11	32956466	32956466	In Frame Ins	INS	-	SGTTCTGTTTAT	-	QSER1	ACTCTTGTTTCT	92delinsQTLGFCYYLM
XH_P51	11	34093506	34093506	Frame Shift Ins	INS	-	TTTC	-	CAPRIN1	c.338_339insTTC	p.Q113fs
XH_P51	11	34093507	34093507	Nonsense_Mutation	INS	-	TTTTGA	-	CAPRIN1	339_340insTTTT	Q113delinsQFX
XH_P51	11	47861497	47861497	Missense_Mutation	SNP	C	T	C	NUP160	c.G646A	p.A216T
XH_P51	11	49080632	49080632	Frame Shift Ins	INS	-	SACAATATCTGT	-	TRIM64C	33insCACAGATA	p.N11fs
XH_P51	11	49974093	49974093	In Frame Ins	INS	-	TTGAGTTTGGG	-	OR4C13	1AAGTTTGTGAGT	40delinsSKFEFWRF
XH_P51	11	58126539	58126539	In Frame Ins	INS	-	AGTAACCTGTCT	-	OR5B17	4insAGACAGGT	E2delinsRQVTE
XH_P51	11	58190685	58190685	Frame Shift Ins	INS	-	GG	-	OR5B2	c.49_50insCC	p.S17fs
XH_P51	11	58206924	58206924	Nonsense_Mutation	INS	-	AGGATTCATATT	-	OR5B12	5TTAAATATGA	234_A235delinsKIX
XH_P51	11	61026259	61026259	Missense_Mutation	SNP	C	T	C	VWCE	c.G2756A	p.R919H
XH_P51	11	62292349	62292349	Silent	SNP	G	A	G	AHNAK	c.C9540T	p.D3180D
XH_P51	11	62444408	62444408	Missense_Mutation	SNP	G	A	G	UBXN1	c.C544T	p.L182F
XH_P51	11	63487898	63487898	Missense_Mutation	SNP	A	C	A	RTN3	c.A1588C	p.N530H
XH_P51	11	73120693	73120693	Frame Shift Ins	INS	-	TCCATCCCTTTCC	-	FAM168A	34insGGAAAGG	p.T145fs
XH_P51	11	73120695	73120695	Nonsense_Mutation	SNP	G	C	G	FAM168A	c.C432G	p.Y144X
XH_P51	11	87025562	87025562	Silent	SNP	C	T	C	TMEM135	c.C984T	p.S328S
XH_P51	11	93104374	93104374	In Frame Ins	INS	-	CCATTT	-	DEUP1	717_718insCCAT	p.L239delinsLPF
XH_P51	11	94759020	94759020	Missense_Mutation	SNP	G	A	G	KDM4E	c.G299A	p.R100H
XH_P51	11	101762183	101762183	Missense_Mutation	SNP	C	T	C	ANGPTL5	c.G994A	p.G332S
XH_P51	11	104971508	104971508	Splice Site	INS	-	ATAATTCACCCA	-	CARD17	-	-
XH_P51	11	118374206	118374206	Frame Shift Ins	INS	-	TCCCATATGTTCC	-	KMT2A	5CTAGATCCCAT	p.E2533fs
XH_P51	11	118374778	118374778	Frame Shift Ins	INS	-	TGGAATGTTCTTC	-	KMT2A	172insATTGGAA	p.D2724fs
XH_P51	11	123848134	123848134	Frame Shift Ins	INS	-	ATTGCCTACTTCT	-	OR10S1	65insAGAAGTA	p.V89fs
XH_P51	11	124910495	124910495	Missense_Mutation	SNP	G	A	G	CCDC15	c.G2744A	p.R915Q
XH_P51	12	332325	332325	Missense_Mutation	SNP	C	T	C	SLC6A13	c.G1111A	p.E371K
XH_P51	12	4385289	4385289	Frame Shift Ins	INS	-	TGAGGAA	-	CCND2	4_315insTGAG	p.C105fs
XH_P51	12	4385291	4385291	Frame Shift Ins	INS	-	TGCGAAGAAGAA	-	CCND2	1GAAGTGCGAAG	p.M106fs
XH_P51	12	10780283	10780283	Frame Shift Ins	INS	-	GATG	-	STYK1	c.673_674insCAT	p.E225fs
XH_P51	12	10780284	10780284	In Frame Ins	INS	-	ATTAATATTCTCA	-	STYK1	1CACTTGAGAATA	1delinsYPLENINMRNME
XH_P51	12	11174277	11174277	Frame Shift Ins	INS	-	AC	-	TAS2R19	c.893_894insGT	p.T298fs
XH_P51	12	12312003	12312003	In Frame Ins	INS	-	GTG	-	LRP6	2550_2551insCA	p.S851delinsHS
XH_P51	12	13237846	13237846	Frame Shift Ins	INS	-	TCTT	-	GSG1	816_817insAAG	p.E273fs
XH_P51	12	15262210	15262210	Missense_Mutation	SNP	T	C	T	RERG	c.A377G	p.Y126C
XH_P51	12	15803941	15803941	Splice Site	INS	-	T	-	EP58	-	-
XH_P51	12	18891347	18891347	Frame Shift Ins	INS	-	AACATTCAGACT	-	CAP2A3	5insTTAACATTC	p.E49fs
XH_P51	12	19427854	19427854	Nonsense_Mutation	INS	-	TCCTTTGTTTTTTT	-	PLEKHA5	TCATTTCTTGT	303delinsLLISLFFX
XH_P51	12	26218047	26218047	In Frame Ins	INS	-	TTTCTC	-	RASSF8	720_721insTTCT	p.L240delinsFL
XH_P51	12	26218049	26218049	Frame Shift Ins	INS	-	T	-	RASSF8	c.722_723insT	p.K241fs

XH_P51	12	26568363	26568363	Frame_Shift_Ins	INS	-	ATGTTTTCTTTT	-	ITPR2	insGAATAAAAG	p.R2393fs
XH_P51	12	30881785	30881785	Frame_Shift_Ins	INS	-	TCTTTTTTTTTT	-	CAPRIN2	AAAAAAAAAAAA	p.K194fs
XH_P51	12	30881787	30881787	Missense_Mutation	SNP	G	A	G	CAPRIN2	c.C578T	p.T193I
XH_P51	12	32134066	32134066	Frame_Shift_Ins	INS	-	TTTGATATAGTA	-	KIAA1551	GTCGGTTTGATA	p.I59fs
XH_P51	12	32137985	32137985	Frame_Shift_Ins	INS	-	TTTTTTTCTTTTG	-	KIAA1551	sCTCAATTTTTT	p.L1366fs
XH_P51	12	32886735	32886735	Nonsense_Mutation	INS	-	TAGCTTTAAAT	-	DNM1L	TACTCTAGCTTTA	808_1309delinsNLLX
XH_P51	12	32890042	32890042	Nonsense_Mutation	SNP	C	T	C	DNM1L	c.C934T	p.Q312X
XH_P51	12	32893136	32893136	Frame_Shift_Ins	INS	-	CATCATATCT	-	DNM1L	1238insCATCA	p.S413fs
XH_P51	12	32893138	32893138	Missense_Mutation	SNP	T	A	T	DNM1L	c.T1239A	p.S413R
XH_P51	12	41966300	41966300	Nonsense_Mutation	INS	-	ATAAGTGATTC	-	PDZRN4	TTCAAAATAAGT	A315delinsAFKX
XH_P51	12	42512805	42512805	Silent	SNP	G	T	G	GXYLT1	c.C390A	p.G130G
XH_P51	12	46318839	46318839	In_Frame_Ins	INS	-	TTA	-	SCAF11	3577_3578insTA	Q1193delinsLK
XH_P51	12	46318840	46318840	Frame_Shift_Ins	INS	-	CAACTCAA	-	SCAF11	6_3577insTTGA	p.Q1193fs
XH_P51	12	46321413	46321413	Frame_Shift_Ins	INS	-	AAGGTGTAAAC	-	SCAF11	71insACAGTTTC	p.H691fs
XH_P51	12	47629680	47629680	Silent	SNP	G	A	G	PCED1B	c.G834A	p.P278P
XH_P51	12	49065719	49065719	Nonsense_Mutation	INS	-	TTATGTAAGTAT	-	KANSL2	CGCCGATACCTTA	11_V192delinsAPILTX
XH_P51	12	49446023	49446023	Frame_Shift_Ins	INS	-	CTGTGCCACCA	-	KMT2D	443insTGGTGGG	p.E481fs
XH_P51	12	51382182	51382182	Silent	SNP	G	A	G	SLC11A2	c.C1600T	p.L534L
XH_P51	12	51442149	51442149	Missense_Mutation	SNP	T	A	T	LETMD1	c.T10A	p.S4T
XH_P51	12	51873913	51873913	Silent	SNP	C	T	C	SLC4A8	c.C2151T	p.D717D
XH_P51	12	53205697	53205697	Missense_Mutation	SNP	G	A	G	KRT4	c.C527T	p.T176M
XH_P51	12	54382998	54382998	In_Frame_Ins	INS	-	GAGAGGAAG	-	HOXC10	798insGAGAG	K266delinsKRG
XH_P51	12	54757616	54757616	In_Frame_Ins	INS	-	GCTCCT	-	GPR84	19_20insAGGAC	p.A7delinsEEP
XH_P51	12	54757618	54757618	Missense_Mutation	SNP	G	C	G	GPR84	c.C18G	p.D6E
XH_P51	12	55688773	55688773	Frame_Shift_Ins	INS	-	TATCTCTCTTAC	-	OR6C6	CAAGTGTAAAGAC	p.T82fs
XH_P51	12	56295873	56295873	Missense_Mutation	SNP	G	T	G	PYM1	c.C395A	p.A132E
XH_P51	12	56676760	56676760	Missense_Mutation	SNP	C	T	C	CS	c.G283A	p.G95S
XH_P51	12	57906594	57906594	Frame_Shift_Ins	INS	-	GTCC	-	MARS	814_1815insGT	p.D605fs
XH_P51	12	57906596	57906596	Missense_Mutation	SNP	A	T	A	MARS	c.A1816T	p.M606L
XH_P51	12	62954528	62954528	Nonsense_Mutation	INS	-	ACTAGGTACTA	-	MON2	68insTGACTAGG	1223delinsMTRYX
XH_P51	12	64011087	64011087	Silent	SNP	C	T	C	DPY19L2	c.G1215A	p.T405T
XH_P51	12	65226073	65226073	Missense_Mutation	SNP	G	A	G	TBC1D30	c.G583A	p.D195N
XH_P51	12	65226074	65226074	Nonsense_Mutation	INS	-	CAAAAATAACT	-	TBC1D30	TATTTTCAAAAA	A196delinsEQYFQKX
XH_P51	12	65634790	65634790	Frame_Shift_Ins	INS	-	ATTTTCTCTAT	-	LEM03	26insTCATTTTT	p.L742fs
XH_P51	12	65634791	65634791	Silent	SNP	G	T	G	LEM03	c.G2226T	p.L742L
XH_P51	12	66707889	66707889	Missense_Mutation	SNP	T	A	T	HELB	c.T1804A	p.S602T
XH_P51	12	66707890	66707890	Nonsense_Mutation	INS	-	AAAATTAATAGC	-	HELB	D6insCAAAATTT	D2_V603delinsSKNX
XH_P51	12	70149378	70149378	In_Frame_Ins	INS	-	GAATCAGGAAC	-	RAB31P	TGTATGAATCAG	delinsGVYESGTQEQT
XH_P51	12	72164452	72164452	Nonsense_Mutation	INS	-	ATGTAATGTTTT	-	RAB21	sCAATATGTAAT	I101delinsDQVVMFX
XH_P51	12	82147850	82147850	Missense_Mutation	SNP	C	T	C	PPFIA2	c.G151A	p.E51K
XH_P51	12	82793022	82793022	In_Frame_Ins	INS	-	CAAAAAGAGGC	-	METT125	AAGGCACAAAAA	240delinsSRTKSLG
XH_P51	12	83251309	83251310	Frame_Shift_Del	DEL	TT	-	TT	TMTC2	c.604_605del	p.F202fs
XH_P51	12	85449885	85449885	In_Frame_Ins	INS	-	CAATATTTCTTT	-	LRRIQ1	GTTTCACAAATA	delinsLFPVSEQSFFLH
XH_P51	12	88442134	88442134	In_Frame_Ins	INS	-	TTGTCT	-	C12orf29	13_914insTTGT	p.N305delinsIVV
XH_P51	12	88442136	88442136	Frame_Shift_Ins	INS	-	CTTC	-	C12orf29	915_916insCTT	p.N305fs
XH_P51	12	90049618	90049618	Frame_Shift_Ins	INS	-	CTATATA	-	ATP2B1	45_46insTATATA	p.N16fs
XH_P51	12	90049620	90049620	Nonsense_Mutation	INS	-	AAATGAGCATGC	-	ATP2B1	ATAAGCATGCTCT	K15_N16delinsIX
XH_P51	12	93173078	93173078	Splice_Site	INS	-	CTTCTTTTTCAC	-	EEA1	-	-
XH_P51	12	99028181	99028181	Missense_Mutation	SNP	G	T	G	IKBIP	c.C190A	p.Q64K
XH_P51	12	99175904	99175904	Nonsense_Mutation	INS	-	AGCAGTCAGTTT	-	ANKS1B	5AAGTAAACTGAG	999_K100delinsQX
XH_P51	12	100041961	100041961	Silent	SNP	C	T	C	FAM71C	c.C9T	p.D3D
XH_P51	12	102558385	102558385	Frame_Shift_Ins	INS	-	CATAA	-	PARBPB	422_423insCAT	p.L141fs
XH_P51	12	102558386	102558386	Nonsense_Mutation	INS	-	CAGTAAAAAT	-	PARBPB	424insCAGTAA	41_V142delinsLQX
XH_P51	12	104373718	104373718	Frame_Shift_Ins	INS	-	CT	-	TDG	c.276_277insCT	p.K92fs
XH_P51	12	107078680	107078680	Missense_Mutation	SNP	C	T	C	RFK4	c.C89T	p.T30M
XH_P51	12	112036797	112036797	Frame_Shift_Del	DEL	C	-	C	ATXN2	c.522delG	p.Q174fs
XH_P51	12	112036799	112036800	Frame_Shift_Del	DEL	GC	-	GC	ATXN2	c.519_520del	p.Q173fs
XH_P51	12	112654155	112654155	Missense_Mutation	SNP	T	G	T	HECTD4	c.A7004C	p.Y2335S
XH_P51	12	112654157	112654157	Frame_Shift_Ins	INS	-	CCTCAATT	-	HECTD4	1_7002insAATG	p.H2334fs
XH_P51	12	112673558	112673558	Frame_Shift_Ins	INS	-	AGATTATG	-	HECTD4	2_5073insCAT	p.Q1691fs
XH_P51	12	118405915	118405915	In_Frame_Ins	INS	-	CTGGCC	-	KSR2	58_59insCGCCG	p.N20delinsSAD
XH_P51	12	120785257	120785257	Frame_Shift_Ins	INS	-	GGCAGTGGCCT	-	MS11	5GGGAGAGAGGC	p.R284fs
XH_P51	12	120785259	120785259	Silent	SNP	A	G	A	MS11	c.T849C	p.V283V
XH_P51	12	122657270	122657270	Frame_Shift_Ins	INS	-	TAAATCATT	-	IL31	184insAATGAT	p.V62fs
XH_P51	12	123461515	123461515	Missense_Mutation	SNP	C	T	C	OGFOD2	c.C401T	p.S134L
XH_P51	12	123741459	123741459	Frame_Shift_Ins	INS	-	TTTATTACTATT	-	C12orf65	GCTTTTTTATT	p.H128fs
XH_P51	12	123950480	123950480	Frame_Shift_Ins	INS	-	CTTTTAATTTGT	-	SNRNP35	94insTCCTTTAA	p.T131fs
XH_P51	12	124416643	124416643	Frame_Shift_Ins	INS	-	AGAC	-	DNAH10	930_12931insA	p.Q4310fs
XH_P51	12	124416645	124416645	Missense_Mutation	SNP	A	T	A	DNAH10	c.A12932T	p.Y4311F
XH_P51	12	132249227	132249227	Frame_Shift_Ins	INS	-	AAAGTTCTAGTA	-	SFSWAP	CCAAGAAAGATT	p.K649fs
XH_P51	12	133732280	133732280	Frame_Shift_Ins	INS	-	CACAGTTGCTTT	-	ZNF10	ATGTACACAGTT	p.V150fs
XH_P51	12	21370389	21370389	Missense_Mutation	SNP	C	A	C	XP04	c.G2623T	p.A875S
XH_P51	12	21370391	21370391	Frame_Shift_Ins	INS	-	ACAGGTAAATG	-	XP04	ACGTTACATTTT	p.K874fs
XH_P51	12	25487030	25487030	In_Frame_Ins	INS	-	CTG	-	CENPJ	133_134insCA	p.R45delinsPG
XH_P51	12	31714404	31714404	In_Frame_Ins	INS	-	GAAGAGAGAAC	-	HSPH1	569insAGGTTCT	D557delinsRFLSD
XH_P51	12	32367005	32367006	Frame_Shift_Del	DEL	GG	-	GG	RXFP2	c.1494_1495de	p.L498fs
XH_P51	12	32367006	32367006	Frame_Shift_Ins	INS	-	TTCATCTTATA	-	RXFP2	1496insTTTCA	p.Y499fs
XH_P51	12	37446999	37446999	Missense_Mutation	SNP	G	A	G	SMAD9	c.C466T	p.L156F
XH_P51	12	37447000	37447000	Frame_Shift_Ins	INS	-	TCCTT	-	SMAD9	464_465insAAG	p.S155fs
XH_P51	12	38320568	38320568	Frame_Shift_Ins	INS	-	GAAAT	-	TRPC4	402_403insATT	p.Q135fs
XH_P51	12	38320569	38320569	Frame_Shift_Ins	INS	-	A	-	TRPC4	c.401_402insT	p.K134fs
XH_P51	12	41767878	41767878	Frame_Shift_Ins	INS	-	CAGCC	-	KBTBD7	515_516insGGC	p.N172fs
XH_P51	12	41767879	41767879	Nonsense_Mutation	INS	-	CCACTGCACAGC	-	KBTBD7	5TGTAAGCTGTGC	172_C173delinsMX
XH_P51	12	46544565	46544565	Nonsense_Mutation	INS	-	ATTTTCTACTAT	-	ZC3H13	2504insATAGTA	R835delinsNSRKK
XH_P51	12	47470002	47470002	Nonsense_Mutation	INS	-	AACTATTGCTGG	-	HTR2A	5TTTCCAGCAAT	A_115delinsVCFQXX
XH_P51	12	76370851	76370851	Nonsense_Mutation	INS	-	TATAGGTGAGTA	-	LM07	TCAAATATAGGT	43_F144delinsAQIX
XH_P51	12	96530095	96530095	Frame_Shift_Ins	INS	-	TGCTG	-	UGGT2	243_244insCA	p.T1082fs
XH_P51	12	103388132	103388132	Missense_Mutation	SNP	C	G	C	CCDC168	c.G14915C	p.S4972T
XH_P51	12	103388133	103388133	In_Frame_Ins	INS	-	CAAAAGAGAAAA	-	CCDC168	nsCTGAATCTTTT	972delinsLNLSLFFS
XH_P51	12	103528199	103528199	In_Frame_Ins	INS	-	GTTTTCCTTTAT	-	BIVM-ERC5C	8insTTCTGTTT	169delinsFFVLPYQ
XH_P51	12	20296052	20296052	Nonsense_Mutation	INS	-	A	-	OR4N2	c.445_446insA	V149_L150delinsX
XH_P51	12	20296054	20296054	Frame_Shift_Ins	INS	-	AGATTAT	-	OR4N2	47_448insAGAT	p.W149fs
XH_P51	12	21991984	21991984	Silent	SNP	G	A	G	SALL2	c.C1878T	p.A626A
XH_P51	12	21991985	21991985	Frame_Shift_Ins	INS	-	TTCAC	-	SALL2	376_1877insGTG	p.A626fs
XH_P51	12	22038549	22038549	Silent	SNP	G	T	G	OR10G3	c.C327A	p.G109G
XH_P51	12	23103273	23103273	Nonsense_Mutation	INS	-	GACCATTAGTCA	-	OR6J1	44insATGACTA	V148_V149delinsX
XH_P51	12	23314498	23314498	Missense_Mutation	SNP	G	A	G	MMP14	c.G1340A	p.S447N
XH_P51	12	23445709	23445709	Nonsense_Mutation	INS	-	ACTTTA	-	AJUBA	94_1195insTAA	p.A399delinsX

XH_P51	14	24736007	24736007	Frame_Shift_Ins	INS	-	AGCCCT	-	RABGGTA	1_1442insAGG	p.A481fs
XH_P51	14	36169458	36169458	Missense_Mutation	SNP	G	T	G	RALGAPA1	c.C2317A	p.R773S
XH_P51	14	36169459	36169459	Frame_Shift_Ins	INS	-	CAAAATTTGCTT	-	RALGAPA1	316insTAAGCA	p.I772fs
XH_P51	14	39510041	39510041	Frame_Shift_Ins	INS	-	GTTTGTG	-	SEC23A	86_2037insCAC	p.E679fs
XH_P51	14	39543686	39543686	In_Frame_Ins	INS	-	TTG	-	SEC23A	1035_1036insCp.D346delinsQD	
XH_P51	14	39543687	39543687	Frame_Shift_Ins	INS	-	AGTCATTATTTC	-	SEC23A	1035insCAAAAT	p.I345fs
XH_P51	14	50262568	50262568	Frame_Shift_Ins	INS	-	TAGGAGATTATG	-	NEMF	97insGCCATAA	p.T833fs
XH_P51	14	56078986	56078986	Frame_Shift_Ins	INS	-	GTACTTTTGTC	-	KTN1	221insGTACTT	p.E74fs
XH_P51	14	56101350	56101350	Nonsense_Mutation	INS	-	GATGA	-	KTN1	435_1436insGA	p.479_480delinsGX
XH_P51	14	56101351	56101351	In_Frame_Ins	INS	-	CATAAATAG	-	KTN1	5_1437insCATAA	p.A479delinsAINS
XH_P51	14	60749815	60749815	Frame_Shift_Ins	INS	-	CATCCTCCAT	-	PPM1A	1_395insCATCCT	p.V132fs
XH_P51	14	60752480	60752480	Nonstop_Mutation	INS	-	TTG	-	PPM1A	c.973_974insTTG	p.X325delinsFE
XH_P51	14	60752481	60752481	In_Frame_Ins	INS	-	GAATATTTT	-	PPM1A	4_975insGAATA	p.X325delinsX
XH_P51	14	64655341	64655341	Nonsense_Mutation	INS	-	ATTCATTTTAAT	-	SYNE2	787insTCATTCA	p.C5930delinsFHSFX
XH_P51	14	64989054	64989054	Frame_Shift_Ins	INS	-	G	-	ZBTB1	c.832_833insG	p.S278fs
XH_P51	14	64989055	64989055	In_Frame_Ins	INS	-	TGTTCTGTT	-	ZBTB1	3_834insGTTC	p.S278delinsVLF
XH_P51	14	71206734	71206734	Nonsense_Mutation	INS	-	TCTACCTTTT	-	MAP3K9	797insAAAGGV	p.G267delinsX
XH_P51	14	73138001	73138001	In_Frame_Ins	INS	-	GTT	-	DPF3	1081_1082insA	p.A361delinsEP
XH_P51	14	73138002	73138002	Nonsense_Mutation	INS	-	ATATTTTTTTTA	-	DPF3	TTTCATTAATAAA	p.A361delinsFHX
XH_P51	14	75538072	75538072	Frame_Shift_Ins	INS	-	GTTGCCCTGG	-	ZC2HC1C	297insGTTGCC	p.I266fs
XH_P51	14	75587280	75587280	Missense_Mutation	SNP	C	A	C	NEK9	c.G457T	p.V153L
XH_P51	14	75587282	75587282	In_Frame_Ins	INS	-	ACACCTTTTATT	-	NEK9	455insAAATAAA	p.M152delinsKIKVL
XH_P51	14	76249769	76249769	Frame_Shift_Ins	INS	-	A	-	TTL5	c.2883dupA	p.P961fs
XH_P51	14	76249771	76249771	Nonsense_Mutation	INS	-	TGAACACAGTCT	-	TTL5	TTTTACTGAACA	p.C963delinsQFYX
XH_P51	14	77493762	77493762	In_Frame_Del	DEL	TCGCTG	-	TCGCTG	IRF2BPL	c.369_374del	p.I23_125del
XH_P51	14	77948765	77948765	Silent	SNP	A	G	A	ISM2	c.T873C	p.D291D
XH_P51	14	81682849	81682849	Frame_Shift_Ins	INS	-	GATGAACGTATA	-	GTF2A1	AACTATACGTTG	p.Y14fs
XH_P51	14	88477825	88477825	Nonsense_Mutation	INS	-	ATAAAATTCATG	-	GPR65	5insTGTAAAAA	p.H212delinsLX
XH_P51	14	91196540	91196540	Frame_Shift_Ins	INS	-	AATG	-	TTC7B	c.576_577insCAT	p.V193fs
XH_P51	14	91196541	91196541	Splice_Site	INS	-	CAAGTTTAGTTA	-	TTC7B	.	.
XH_P51	14	96993858	96993858	Frame_Shift_Ins	INS	-	TTTTGCATCCTA	-	PAPOLA	AATTATTTTGCA	p.E141fs
XH_P51	14	100742956	100742956	Frame_Shift_Ins	INS	-	TTTAAATTTTACT	-	YY1	CCCCCATTTTAA	p.L345fs
XH_P51	14	103969487	103969487	Nonsense_Mutation	INS	-	ATGAAGCTAGT	-	MARK3	2066insATTGA	p.F689_690delinsHX
XH_P51	14	104139522	104139522	Frame_Shift_Ins	INS	-	ATTTCTCAAATTC	-	KLC1	insAGAATTTCTC	p.L387fs
XH_P51	14	105410029	105410029	Missense_Mutation	SNP	A	G	A	AHNAK2	c.T11459C	p.V3820A
XH_P51	14	105996050	105996050	In_Frame_Del	DEL	GCCGCC	-	GCCGCC	TMEM121	c.879_884del	p.293_295del
XH_P51	15	27222278	27222278	Frame_Shift_Ins	INS	-	AAAGAAA	-	GABRG3	83_184insAAAG	p.K61fs
XH_P51	15	27222279	27222279	In_Frame_Ins	INS	-	ACAAATACGAA	-	GABRG3	185insACAAAT	p.L62delinsHKIRM
XH_P51	15	28478906	28478906	Frame_Shift_Ins	INS	-	TTAT	-	HERC2	254_4255insAT	p.C1419fs
XH_P51	15	28515961	28515961	Frame_Shift_Ins	INS	-	G	-	HERC2	c.1136_1137ins	p.L379fs
XH_P51	15	28515962	28515962	In_Frame_Ins	INS	-	GCTTTTCTGGT	-	HERC2	insAATACAGAA	p.B79delinsQYKKQV
XH_P51	15	34396044	34396044	Frame_Shift_Ins	INS	-	ATCAGTCCTA	-	PGBD4	c.1313insATCAG	p.L438fs
XH_P51	15	40488938	40488938	Frame_Shift_Ins	INS	-	TCTGGTGCTTA	-	BUB1B	252insTCTGG	p.A417fs
XH_P51	15	40915312	40915312	Frame_Shift_Ins	INS	-	TAATAAAGGTC	-	KNL1	insTCTCTAATAA	p.V950fs
XH_P51	15	40916868	40916868	Nonsense_Mutation	INS	-	TTTGGTACTGGT	-	KNL1	CTGTCTTTGGT	p.A469delinsNCPLVLVX
XH_P51	15	40916870	40916870	Missense_Mutation	SNP	G	A	G	KNL1	c.G4408A	p.A1470T
XH_P51	15	41863285	41863285	Frame_Shift_Ins	INS	-	AGCCACCA	-	TYRO3	4_1495insAGCC	p.S498fs
XH_P51	15	43903135	43903135	Nonsense_Mutation	INS	-	TGTCTAGACT	-	STRC	4insATTAGCTA	p.V1119delinsALVX
XH_P51	15	48782169	48782169	Silent	SNP	G	A	G	FBN1	c.C2961T	p.A987A
XH_P51	15	50189512	50189512	Nonsense_Mutation	INS	-	TGGAATTTTATT	-	ATP8B4	ATAAATAAATAA	p.T2_893delinsKKINKX
XH_P51	15	55972369	55972369	Nonsense_Mutation	INS	-	TACATGCATACC	-	PRTG	TAATGGTATGCG	p.N286delinsX
XH_P51	15	56132854	56132854	Nonsense_Mutation	INS	-	TGGAATCTGTGG	-	NEDD4	5ACATACCACAG	p.F984delinsX
XH_P51	15	56390461	56390461	Frame_Shift_Ins	INS	-	ATATAATTAAT	-	RFK7	nsTACTATTAA	p.R309fs
XH_P51	15	57730654	57730654	Frame_Shift_Ins	INS	-	GTAGAGGCAGC	-	CGNL1	GGAATGTAGAG	p.Q153fs
XH_P51	15	59368396	59368396	Missense_Mutation	SNP	C	T	C	RNF111	c.C1930T	p.H644Y
XH_P51	15	59466354	59466354	Missense_Mutation	SNP	C	T	C	MYO1E	c.G2135A	p.M712Q
XH_P51	15	62945479	62945479	Nonsense_Mutation	INS	-	TATTCCTAAACA	-	TLN2	TTTGTTATTCTC	p.E161delinsVSSX
XH_P51	15	65916784	65916784	In_Frame_Ins	INS	-	AACATT	-	SLC24A1	c.66_367insAAC	p.I122delinsNI
XH_P51	15	65943011	65943011	Frame_Shift_Ins	INS	-	CATCTTCCTGCG	-	SLC24A1	506insCATCTTC	p.K169fs
XH_P51	15	66625188	66625188	Frame_Shift_Ins	INS	-	TC	-	DIS3L	2418_2419insT	p.K806fs
XH_P51	15	66625189	66625189	Frame_Shift_Ins	INS	-	TTTTCTGTGG	-	DIS3L	2420insCTTTTCC	p.I807fs
XH_P51	15	68468914	68468914	Nonsense_Mutation	INS	-	BTACAGTTTAG	-	PIAS1	104insAGTTTACA	p.S468delinsSVTVX
XH_P51	15	69728578	69728578	Frame_Shift_Ins	INS	-	AAAGATTGCTT	-	KIF23	TGAAGCAAGA	p.Q348fs
XH_P51	15	74174030	74174030	Missense_Mutation	SNP	G	A	G	TBC1D21	c.G106A	p.G365
XH_P51	15	78885517	78885517	Frame_Shift_Ins	INS	-	AACGGTAAGTG	-	CHRNA3	1406insTCACTT	p.E469fs
XH_P51	15	81651731	81651731	Frame_Shift_Ins	INS	-	CAGACAGTATA	-	TMC3	476insTATACT	p.T159fs
XH_P51	15	83793482	83793482	Frame_Shift_Ins	INS	-	TTTTCCAGTAA	-	TM65F1	nsATACTTTTCCA	p.V221fs
XH_P51	15	83805386	83805386	Frame_Shift_Ins	INS	-	TTTAATGTCAGA	-	TM65F1	83insCTTTAATG	p.F328fs
XH_P51	15	84245438	84245438	Frame_Shift_Ins	INS	-	TTCTATTAAAT	-	SH3GL3	3insATTCTATT	p.F121fs
XH_P51	15	84566757	84566757	Nonsense_Mutation	INS	-	TTAGACAAATA	-	ADAMTSL3	insACTTTTAGA	p.B39_K540delinsDFX
XH_P51	15	85681050	85681050	Frame_Shift_Ins	INS	-	TGGCTGCAGAA	-	PDE8A	GGATGGTGGCT	p.L756fs
XH_P51	15	89074384	89074384	Missense_Mutation	SNP	G	A	G	DET1	c.C553T	p.R185W
XH_P51	15	91293011	91293011	Frame_Shift_Ins	INS	-	SATACATTGTTA	-	BLM	514insGATACAT	p.T171fs
XH_P51	15	91424593	91424593	Missense_Mutation	SNP	G	A	G	FURIN	c.G1870A	p.D624N
XH_P51	15	91479513	91479513	Splice_Site	INS	-	CTGAGGCTGA	-	UNC45A	.	.
XH_P51	15	91542243	91542243	Frame_Shift_Ins	INS	-	AGGAAGAG	-	VPS33B	84_1735insCTCT	p.A579fs
XH_P51	15	93540250	93540250	Frame_Shift_Ins	INS	-	TCTCTGCTTAT	-	CHD2	insTATATCTCTG	p.K1220fs
XH_P51	16	1910461	1910461	In_Frame_Ins	INS	-	AATGGCTTTGGT	-	MEIOB	ACTAAACCAAA	p.delinsQSTKTKAFHVT
XH_P51	16	2259379	2259379	Missense_Mutation	SNP	T	C	T	BRICD5	c.A671G	p.Y224C
XH_P51	16	3533570	3533570	Frame_Shift_Ins	INS	-	CCAC	-	NAA60	350_351insCCA	p.N117fs
XH_P51	16	3533572	3533572	Frame_Shift_Ins	INS	-	AGGACCATGCG	-	NAA60	insCCCAGGACC	p.G118fs
XH_P51	16	15811079	15811079	Missense_Mutation	SNP	C	T	C	MYH11	c.G5422A	p.V1808I
XH_P51	16	18853092	18853092	Frame_Shift_Ins	INS	-	GTGAAATACTTG	-	SMG1	AGTCTACAAGTA	p.E2164fs
XH_P51	16	19548544	19548544	In_Frame_Ins	INS	-	TGCTGTTCTTTT	-	CCP110	554insTTGCCTG	p.N518delinsNCLFFS
XH_P51	16	30234381	30234381	Missense_Mutation	SNP	G	A	G	NPIP13	c.C3386T	p.S1129L
XH_P51	16	31927531	31927531	Nonsense_Mutation	INS	-	TTGCTACATGCT	-	ZNF267	AAAGATTTCGTA	p.H654delinsHX
XH_P51	16	50756613	50756613	In_Frame_Ins	INS	-	TTACATTACAGA	-	NOD2	2715insTTACAT	p.L905delinsLYTD
XH_P51	16	53488708	53488708	Frame_Shift_Ins	INS	-	TCAATTAATTAT	-	RBL2	insCATTTCAATT	p.A378fs
XH_P51	16	53515737	53515737	Frame_Shift_Ins	INS	-	CCGAATACAGT	-	RBL2	CCCTCGCCGAA	p.S1056fs
XH_P51	16	56501135	56501135	Nonsense_Mutation	INS	-	AATTAATGTGCA	-	OGFOD1	CCTGAAATTAAT	p.B38_P239delinsGGPX
XH_P51	16	57250087	57250087	Splice_Site	INS	-	TTATCCATTGGG	-	RSPRY1	.	.
XH_P51	16	58314639	58314639	Frame_Shift_Ins	INS	-	GAAGACATAT	-	PRSS54	380insATATGT	p.M127fs
XH_P51	16	58314641	58314641	Frame_Shift_Ins	INS	-	TG	-	PRSS54	c.377_378insCA	p.M126fs
XH_P51	16	58579395	58579395	Frame_Shift_Ins	INS	-	GATTGTTCTCT	-	CNOT1	992insAAGAAG	p.T1331fs
XH_P51	16	66887334	66887334	Frame_Shift_Ins	INS	-	ATTTACTACTA	-	CA7	3insTATTTACT	p.M187fs
XH_P51	16	67982038	67982038	Silent	SNP	G	A	G	SLC12A4	c.C1797N	p.F593F
XH_P51	16	68009812	68009812	In_Frame_Ins	INS	-	ACAAGCATA	-	DPEP3	4_1395insTATG	p.Q465delinsHMLV
XH_P51	16	76592536	76592536	Nonsense_Mutation	INS	-	ACTATTTTCCAC	-	CNTNAP4	CATAACACTATT	p.Q1167delinsKSSX

XH_P51	16	77369663	77369663	Nonsense_Mutation	INS	-	TGGCTACATAA	-	ADAMTS18	TAACCATTATGT	N445delinsHKYVX
XH_P51	16	88958375	88958375	Missense_Mutation	SNP	G	A	G	CBFA2T3	c.C368T	p.S123L
XH_P51	16	89294098	89294098	In_Frame_Ins	INS	-	AATTCT	-	ZNF778	18_1319insAAT	p.V440delinsEFL
XH_P51	16	89294100	89294100	Frame_Shift_Ins	INS	-	CATGTTTGATT	-	ZNF778	1321insCATGT	p.V440fs
XH_P51	17	767289	767289	Missense_Mutation	SNP	A	G	A	NXN	c.T2C	p.M1T
XH_P51	17	3195854	3195854	Frame_Shift_Ins	INS	-	CAATG	-	OR3A1	22_23insCATTT	p.N8fs
XH_P51	17	3953100	3953100	In_Frame_Ins	INS	-	GTGTTTGTITTA	-	ZZEF1	17insAATAAAA	p.1973delinsNKTNTE
XH_P51	17	5085160	5085160	Frame_Shift_Ins	INS	-	AA	-	ZNF594	2391_2392insT	p.Q798fs
XH_P51	17	12656062	12656062	Frame_Shift_Ins	INS	-	CTGACCTGTCAG	-	MYOCD	CCTCCTCTGACC	p.P486fs
XH_P51	17	15619691	15619691	Frame_Shift_Ins	INS	-	AG	-	ZNF286A	c.560_561insAG	p.H187fs
XH_P51	17	15619692	15619692	Nonsense_Mutation	INS	-	TAGAGTCATAG	-	ZNF286A	562insTAGAGT	p.187_1188delinsHX
XH_P51	17	26856176	26856176	Missense_Mutation	SNP	G	A	G	FOXN1	c.G764A	p.R255Q
XH_P51	17	29162971	29162971	Nonsense_Mutation	INS	-	TGAAAAAAGCTCTG	-	ATAD5	TGCTTTTGAATAA	p.K624delinsKCCFX
XH_P51	17	29632121	29632121	Frame_Shift_Ins	INS	-	CATCATTGTACTT	-	EVI2B	TCCAAGATACA	p.Q169fs
XH_P51	17	31322658	31322658	Frame_Shift_Ins	INS	-	CA	-	SPACA3	c.266_267insCA	p.L89fs
XH_P51	17	31322660	31322660	Missense_Mutation	SNP	T	A	T	SPACA3	c.T268A	p.Y90N
XH_P51	17	37618897	37618897	Missense_Mutation	SNP	G	C	G	CDK12	c.G573C	p.K191N
XH_P51	17	37627338	37627338	Frame_Shift_Ins	INS	-	TCAATAAAAAACA	-	CDK12	sACAGATCAATA	p.K418fs
XH_P51	17	37627340	37627340	Missense_Mutation	SNP	G	A	G	CDK12	c.G1255A	p.E419K
XH_P51	17	38285635	38285635	Frame_Shift_Ins	INS	-	GC	-	MSL1	c.341_342insGC	p.C114fs
XH_P51	17	38548490	38548490	Frame_Shift_Ins	INS	-	TATGTTGATACT	-	TOP2A	GTGAACAGTATC	p.P1356fs
XH_P51	17	38556298	38556298	Frame_Shift_Ins	INS	-	GGTGAGAGTAA	-	TOP2A	insACCATTACTC	p.C1008fs
XH_P51	17	39551507	39551507	Missense_Mutation	SNP	T	C	T	KRT31	c.A866G	p.Q289R
XH_P51	17	39580756	39580756	In_Frame_Ins	INS	-	AGACCA	-	KRT37	19_20insTGGTC	p.17delinsMVS
XH_P51	17	39580758	39580758	Frame_Shift_Ins	INS	-	AAGTT	-	KRT37	c.17_18insAACT	p.S6fs
XH_P51	17	39921232	39921232	Missense_Mutation	SNP	G	A	G	JUP	c.C997T	p.R333C
XH_P51	17	41170185	41170185	Frame_Shift_Ins	INS	-	AGTCGTGTGAT	-	VAT1	CGACTATCACAA	p.V212fs
XH_P51	17	41349082	41349082	Nonsense_Mutation	INS	-	ATCTAAACTTTG	-	NBR1	923insTATCTAA	p.641_662delinsAIX
XH_P51	17	42475056	42475056	Frame_Shift_Ins	INS	-	GATGGGA	-	GPATCH8	54_4155insTCC	p.V1385fs
XH_P51	17	42828603	42828603	Frame_Shift_Ins	INS	-	TTCTCA	-	DBF4B	830_1831insTC	p.L610fs
XH_P51	17	42828604	42828604	Frame_Shift_Ins	INS	-	TTTACCTGCTGC	-	DBF4B	GATACCTTTACC	p.A611fs
XH_P51	17	42882714	42882714	Nonsense_Mutation	INS	-	AGATGCTTCA	-	GJC1	472insTGAAGC	p.158_1159delinsX
XH_P51	17	44061055	44061055	Missense_Mutation	SNP	G	T	G	MAPT	c.G885T	p.Q295H
XH_P51	17	45219654	45219654	Frame_Shift_Ins	INS	-	TTTGTITTA	-	CDC27	5_1136insTAA	p.G379fs
XH_P51	17	45219655	45219655	In_Frame_Ins	INS	-	TATGTTGTT	-	CDC27	5_1135insAACA	p.G379delinsNNIG
XH_P51	17	45452060	45452060	Missense_Mutation	SNP	G	C	G	EFCAB13	c.G812C	p.R271T
XH_P51	17	49097589	49097589	Nonsense_Mutation	INS	-	ATGGTTTAAATT	-	SPAG9	ACAAAAAATTTTA	p.V184delinsDNIX
XH_P51	17	54912351	54912351	Silent	SNP	G	A	G	DGKE	c.G195A	p.T65T
XH_P51	17	56342311	56342311	Frame_Shift_Ins	INS	-	GCCTTCCGCTT	-	LPO	7insCCTTCGCTT	p.N416fs
XH_P51	17	56342312	56342312	Missense_Mutation	SNP	A	C	A	LPO	c.A1247C	p.N416T
XH_P51	17	56621371	56621371	Frame_Shift_Ins	INS	-	AGAGCAA	-	C17orf47	76_177insTTGC	p.T59fs
XH_P51	17	60484558	60484558	Frame_Shift_Ins	INS	-	CCACGATGTG	-	EFCAB3	853insCCAGCA	p.R284fs
XH_P51	17	61994806	61994806	Nonsense_Mutation	INS	-	CTATAATATTAT	-	GH1	insCCATAAATAT	p.133_1134delinsPX
XH_P51	17	62533891	62533891	In_Frame_Ins	INS	-	AATAATCTAGCA	-	CEP95	ATTTCCTAATAAT	p.6delinsSKIFNNLATAA
XH_P51	17	62856031	62856031	Silent	SNP	T	G	T	LRR37A3	c.A1587C	p.G529G
XH_P51	17	62856032	62856032	Missense_Mutation	SNP	C	A	C	LRR37A3	c.G1586T	p.G529V
XH_P51	17	65103456	65103456	Missense_Mutation	SNP	C	G	C	HELZ	c.G5073C	p.Q1691H
XH_P51	17	65103458	65103458	In_Frame_Ins	INS	-	ATATCAGTATT	-	HELZ	nsTCAATAAATAA	p.691delinsSINTDIFQ
XH_P51	17	65337042	65337042	Frame_Shift_Ins	INS	-	TCGCTGAAT	-	PSMD12	1228insATTCA	p.Q410fs
XH_P51	17	65337044	65337044	Missense_Mutation	SNP	G	C	G	PSMD12	c.C1226G	p.S409C
XH_P51	17	66925302	66925302	In_Frame_Ins	INS	-	TAAAGCTTGGG	-	ABCA8	ATAATTTTCAAG	p.88delinsNNFQAFKS
XH_P51	17	67282158	67282158	Nonsense_Mutation	INS	-	TGTAAATGCCA	-	ABCA5	TAATAATTGGCA	p.8_179delinsLHFNFX
XH_P51	17	71231945	71231945	Nonsense_Mutation	INS	-	ATTTTAAATCGTT	-	C17orf80	GTGGGATTTTAA	p.108delinsASGLIVX
XH_P51	17	73237730	73237730	Silent	SNP	G	A	G	GG3	c.C429T	p.L143L
XH_P51	17	73664694	73664694	Frame_Shift_Ins	INS	-	ACAATGTAAGA	-	SAP30BP	GAGGTACAAATG	p.S69fs
XH_P51	17	73945597	73945597	Frame_Shift_Ins	INS	-	TAAGTCTTTTTT	-	ACOX1	AACAACAAAAAA	p.V483fs
XH_P51	17	78110087	78110087	Frame_Shift_Ins	INS	-	TTGTGTTGTGTG	-	EIF4A3	AAAACCCACAA	p.P344fs
XH_P51	17	78197101	78197101	In_Frame_Ins	INS	-	GGA	-	SLC26A11	478_479insGG	p.A160delinsGT
XH_P51	17	78197102	78197102	In_Frame_Ins	INS	-	SAGCGGGGACC	-	SLC26A11	GGTGGAGCCGG	p.0delinsAGWSRDQLD
XH_P51	17	80195474	80195474	Silent	SNP	C	T	C	SLC16A3	c.C828T	p.F276F
XH_P51	18	619263	619263	Nonsense_Mutation	INS	-	AATTGTTCTCTTA	-	CLUL1	158insAATTGTTT	p.L53_1754delinsX
XH_P51	18	9530888	9530888	Frame_Shift_Ins	INS	-	TCTCATTTCCTA	-	RALBP1	405insTTCTCAT	p.S468fs
XH_P51	18	10807258	10807258	Frame_Shift_Ins	INS	-	AATCGATACTCT	-	PIEZO2	932insTAGAGTA	p.K311fs
XH_P51	18	12125675	12125675	Nonsense_Mutation	INS	-	GACATATTATGA	-	ANKRD62	6insAATGACATAT	p.7619delinsKX
XH_P51	18	12325450	12325450	Missense_Mutation	SNP	C	T	C	TUBB6	c.C551T	p.T184I
XH_P51	18	14105629	14105629	Missense_Mutation	SNP	T	C	T	ZNF519	c.A910G	p.S304G
XH_P51	18	18547825	18547827	In_Frame_Del	DEL	AAA	-	AAA	ROCK1	c.3078_3080del	p.1026_1027del
XH_P51	18	21494499	21494499	Frame_Shift_Ins	INS	-	CAAATAAATAAT	-	LAMA3	1insTTTCAAATA	p.A820fs
XH_P51	18	21698152	21698152	Nonsense_Mutation	INS	-	CTAAGAAATTAT	-	TTC39C	AAACCACTAAGAA	p.4_175delinsKFNLTXX
XH_P51	18	22057402	22057402	Frame_Shift_Ins	INS	-	CATG	-	HRH4	785_786insCAT	p.N262fs
XH_P51	18	22057404	22057404	Frame_Shift_Ins	INS	-	C	-	HRH4	c.788dupC	p.S263fs
XH_P51	18	28911739	28911739	Nonsense_Mutation	INS	-	ATATCTTAGCTC	-	DSG1	sATGGATATCTT	p.1198delinsWIWX
XH_P51	18	29419411	29419411	Frame_Shift_Ins	INS	-	AAGGTTTGAGC	-	TRAPPC8	AAATAAAGCTCA	p.E1283fs
XH_P51	18	43667319	43667319	Missense_Mutation	SNP	G	T	G	ATPSA1	c.C789A	p.D263E
XH_P51	18	43667321	43667321	Frame_Shift_Ins	INS	-	TAAGGCATTG	-	ATPSA1	787insCAATGC	p.D263fs
XH_P51	18	44027560	44027560	Nonsense_Mutation	SNP	C	T	C	RNF165	c.C520T	p.Q174X
XH_P51	18	44554806	44554806	Missense_Mutation	SNP	C	G	C	ELOA3B	c.G1408C	p.A470P
XH_P51	18	72021289	72021289	Nonsense_Mutation	INS	-	GCACTATTAGA	-	C18orf63	8insACTGCACT	p.96_1795delinsLHYX
XH_P51	19	804908	804908	Missense_Mutation	SNP	C	T	C	PTBP1	c.C686T	p.A229V
XH_P51	19	5455764	5455764	Missense_Mutation	SNP	G	T	G	ZNRF4	c.G262T	p.V88F
XH_P51	19	8953551	8953551	Frame_Shift_Ins	INS	-	GACTTTCATC	-	MBD3L1	198insGACTTT	p.C66fs
XH_P51	19	9049212	9049212	Nonsense_Mutation	INS	-	NCAACTATTCCA	-	MUC16	2419insTTTGA	p.807_110808delinsLEX
XH_P51	19	9049413	9049413	In_Frame_Ins	INS	-	GACAACCTCCAT	-	MUC16	32218insATGGA	p.10740delinsMEVVQ
XH_P51	19	9058383	9058383	In_Frame_Ins	INS	-	TCCACATTA	-	MUC16	2_29063insTAAT	p.19688delinsVMWR
XH_P51	19	9578810	9578810	Frame_Shift_Ins	INS	-	AGATA	-	ZNF560	494_495insTAT	p.P165fs
XH_P51	19	9578812	9578812	Frame_Shift_Ins	INS	-	CT	-	ZNF560	c.492_493insAG	p.P165fs
XH_P51	19	11943349	11943349	Nonsense_Mutation	INS	-	BTTCCTCTCCAG	-	ZNF440	ATAGGGTTTCTC	p.453_1454delinsSX
XH_P51	19	12089559	12089559	Frame_Shift_Ins	INS	-	TCTCCGGTGTG	-	ZNF763	830insTCTCCGG	p.H277fs
XH_P51	19	13004308	13004308	Frame_Shift_Ins	INS	-	AACTCAGCTA	-	GCDH	GAATAAACCTCA	p.A116fs
XH_P51	19	14992160	14992160	In_Frame_Ins	INS	-	CACCTACA	-	OR7A17	7_8insTGTTGATG	p.P3delinsLCSA
XH_P51	19	15366119	15366119	Nonsense_Mutation	INS	-	TTATAATATCTG	-	BRD4	36insCACAGAT	p.79_1680delinsTQILX
XH_P51	19	19790249	19790249	In_Frame_Ins	INS	-	TTTGACTTTTCTT	-	ZNF101	2insGTTTGACTTT	p.131delinsSLTLFV
XH_P51	19	20003438	20003438	Frame_Shift_Ins	INS	-	ACATTCTCTACA	-	ZNF253	2insGCCACATTC	p.P385fs
XH_P51	19	22497090	22497090	Missense_Mutation	SNP	A	C	A	ZNF729	c.A871C	p.T291P
XH_P51	19	22941766	22941766	Silent	SNP	G	A	G	ZNF99	c.C945T	p.C315C
XH_P51	19	22941917	22941917	Missense_Mutation	SNP	A	G	A	ZNF99	c.T794C	p.V265A
XH_P51	19	23544724	23544724	Missense_Mutation	SNP	T	C	T	ZNF91	c.A961G	p.K321E
XH_P51	19	24102268	24102268	Frame_Shift_Ins	INS	-	ATAGAAT	-	ZNF726	97_98insATAGA	p.M33fs

XH_P51	19	24115468	24115468	Nonsense_Mutation	INS	-	CTCTTAGTATT	-	ZNF726	insAATCTTCTTA	M184delinsKSSX
XH_P51	19	24115887	24115914	Frame_Shift_Del	DEL	AACCCCTAACT	-	CAACCCCTAACTA	ZNF726	c.969_996del	p.V323fs
XH_P51	19	24309932	24309932	Missense_Mutation	SNP	G	C	G	ZNF254	c.G875C	p.R292P
XH_P51	19	29698665	29698665	Frame_Shift_Ins	INS	-	C	-	UQCRFS1	c.614_615insG	p.V205fs
XH_P51	19	29698666	29698666	Frame_Shift_Ins	INS	-	GTCTTTATGTCA	-	UQCRFS1	14insGTGACAT	p.V205fs
XH_P51	19	32844763	32844763	Frame_Shift_Ins	INS	-	TTTGACAGT	-	ZNF507	1028insTTTGG	p.E343fs
XH_P51	19	33502663	33502663	Frame_Shift_Ins	INS	-	ACATTGGGTATT	-	RHPN2	5insATAAATACC	p.M172fs
XH_P51	19	36297412	36297412	Silent	SNP	A	G	A	PRODH2	c.T1149C	p.Y383Y
XH_P51	19	36727787	36727787	In_Frame_Ins	INS	-	GCTTCTCGCCAG	-	ZNF146	446insGCTTCTCT	1149delinsFSFV
XH_P51	19	37210338	37210338	Frame_Shift_Ins	INS	-	ATCCATTATA	-	ZNF567	620insATCCAT	p.S207fs
XH_P51	19	37210340	37210340	Nonsense_Mutation	INS	-	CACTAA	-	ZNF567	21_622insCAC	p.S207delinsSHX
XH_P51	19	37487664	37487664	Frame_Shift_Ins	INS	-	GG	-	ZNF568	c.879_880insGG	p.P293fs
XH_P51	19	37487666	37487666	In_Frame_Ins	INS	-	TCTGATTTCTCT	-	ZNF568	882insTCTGATT	Q294delinsHLISL
XH_P51	19	37880484	37880484	Frame_Shift_Ins	INS	-	TTCTTTACATTC	-	ZNF527	tsTTACATTCTTT	p.L511fs
XH_P51	19	40149282	40149282	Missense_Mutation	SNP	G	A	G	LGALS16	c.G275A	p.R92H
XH_P51	19	40149284	40149284	Frame_Shift_Ins	INS	-	CAAAATCCC	-	LGALS16	7_278insCAAA	p.I93fs
XH_P51	19	40328485	40328485	Splice_Site	SNP	T	A	T	FBL	.	.
XH_P51	19	40399735	40399735	Missense_Mutation	SNP	C	T	C	FCGBP	c.G5960A	p.C1987Y
XH_P51	19	43579694	43579694	Missense_Mutation	SNP	G	A	G	PSG2	c.C521T	p.P174L
XH_P51	19	43679576	43679576	Nonsense_Mutation	INS	-	GTCTCTACAGAC	-	PSG5	AGAGAGTCTGT	2_S253delinsQGEESLX
XH_P51	19	44662086	44662086	Frame_Shift_Ins	INS	-	AATGGTTTTCCTC	-	ZNF234	1918insAATGGT	p.L639fs
XH_P51	19	44778267	44778267	Nonsense_Mutation	INS	-	AC	-	ZNF233	1454_1455insA	485_D486delinsX
XH_P51	19	44778269	44778269	Frame_Shift_Ins	INS	-	AAGCCTTTATC	-	ZNF233	1457insAAGCC	p.D486fs
XH_P51	19	44980777	44980777	Frame_Shift_Ins	INS	-	GTGTCTCAAA	-	ZNF180	1846insTTTGA	p.T616fs
XH_P51	19	44980779	44980779	Frame_Shift_Ins	INS	-	TG	-	ZNF180	1843_1844insC	p.K615fs
XH_P51	19	46057149	46057149	Missense_Mutation	SNP	G	A	G	OPA3	c.C163T	p.R55W
XH_P51	19	49657890	49657895	In_Frame_Del	DEL	TCCTCC	-	TCCTCC	HRC	c.600_605del	p.200_202del
XH_P51	19	52658179	52658179	Frame_Shift_Ins	INS	-	TCCCTTTATTTG	-	ZNF836	7insCTCCAATA	p.T919fs
XH_P51	19	53884809	53884809	Frame_Shift_Ins	INS	-	GT	-	ZNF525	c.977_978insGT	p.P326fs
XH_P51	19	53884812	53884813	Frame_Shift_Del	DEL	AT	-	AT	ZNF525	c.980_981del	p.H327fs
XH_P51	19	56127315	56127315	Silent	SNP	G	A	G	ZNF865	c.G2331A	p.A777A
XH_P51	19	57037175	57037175	Frame_Shift_Ins	INS	-	ACATTCTTTACAT	-	ZNF471	3insTCCACATTC	p.F506fs
XH_P51	19	57641066	57641066	Frame_Shift_Ins	INS	-	TCTGTCTATAT	-	USP29	AGGAATCTGTG	p.F341fs
XH_P51	19	57911113	57911113	Frame_Shift_Ins	INS	-	CTCCAGTGTGA	-	ZNF548	1459insCTCCAG	p.F486fs
XH_P51	19	58367524	58367524	Missense_Mutation	SNP	G	T	G	ZNF587	c.G83T	p.W28L
XH_P51	19	58367525	58367525	Frame_Shift_Ins	INS	-	AAACCACATCCA	-	ZNF587	35insAAACCACA	p.W28fs
XH_P51	19	58370398	58370398	Frame_Shift_Ins	INS	-	TTCTGCTTGTGA	-	ZNF587	16insCTTCTGCT	p.Q205fs
XH_P51	19	58453341	58453341	Nonsense_Mutation	INS	-	GTCACTCA	-	ZNF256	835insTGAGG	p.S279delinsX
XH_P51	19	58805904	58805904	Frame_Shift_Ins	INS	-	TCAAGTATTCT	-	ZNF8	CTGCTTCAAGT	p.I244fs
XH_P51	20	2816753	2816753	Nonsense_Mutation	INS	-	CCTTTTTGTAG	-	PCED1A	nsTATCTACAAA	299delinsLSTKKGX
XH_P51	20	2841142	2841142	Frame_Shift_Ins	INS	-	CAGCTCC	-	VPS16	17_418insCAGC	p.E139fs
XH_P51	20	5903631	5903631	Frame_Shift_Ins	INS	-	TATGTGTCTT	-	CHGB	842insTATGTG	p.P281fs
XH_P51	20	13279730	13279730	Missense_Mutation	SNP	G	A	G	ISM1	c.G1019A	p.R340H
XH_P51	20	20180491	20180491	Missense_Mutation	SNP	A	T	A	CFAP61	c.A1877T	p.Y626F
XH_P51	20	20180492	20180492	Frame_Shift_Ins	INS	-	TCCAGAACCCCT	-	CFAP61	nsCAGTTCAGAT	p.Y626fs
XH_P51	20	30366774	30366774	Missense_Mutation	SNP	G	T	G	TPX2	c.G1041T	p.K347N
XH_P51	20	30366776	30366776	In_Frame_Ins	INS	-	AAAAGGCCCT	-	TPX2	1044insAAAA	K348delinsKGL
XH_P51	20	31021297	31021297	Frame_Shift_Ins	INS	-	ATAAATCTGTGT	-	ASXL1	297insAATAAAT	p.Q432fs
XH_P51	20	33203844	33203844	Splice_Site	INS	-	TTACTAACCCGT	-	PIGU	.	.
XH_P51	20	33703671	33703671	In_Frame_Ins	INS	-	AGAAAA	-	EDEM2	190_1191insTTT	b.V397delinsVFL
XH_P51	20	33703673	33703673	In_Frame_Ins	INS	-	ACTGTT	-	EDEM2	88_1189insAAC	V397delinsNSV
XH_P51	20	34242644	34242644	Nonsense_Mutation	INS	-	AGCACCTA	-	RBM12	0_601insTAGGT	1201_M202delinsX
XH_P51	20	34243128	34243128	Nonsense_Mutation	INS	-	AGTTACTGCCAC	-	RBM12	insGTGGTGGCA	9_L40delinsEWWQX
XH_P51	20	39792428	39792428	Frame_Shift_Ins	INS	-	GGTTGGACAGG	-	PLCG1	sCTTGGGTTTGG	p.M322fs
XH_P51	20	49626281	49626295	In_Frame_Del	DEL	CCCTCGCTGT	-	GCCCTCGCTGTC	KCN61	c.S81_595del	p.194_199del
XH_P51	20	58449064	58449064	Frame_Shift_Ins	INS	-	AGATATATCTGA	-	SYCP2	TACCTTCAGATA	p.T1134fs
XH_P51	21	10906966	10906966	Missense_Mutation	SNP	G	A	G	TPTE	c.C1181T	p.A394V
XH_P51	21	16338661	16338661	Missense_Mutation	SNP	C	A	C	NR1P	c.G1853T	p.G618V
XH_P51	21	16339227	16339227	Nonsense_Mutation	INS	-	ATAACACTTCTC	-	NR1P	sCAATTGAAGA	29_G430delinsSNX
XH_P51	21	27348281	27348281	Nonsense_Mutation	INS	-	ATATTTG	-	APP	91_892insCAA	298_A299delinsQIX
XH_P51	21	27348282	27348282	Nonsense_Mutation	INS	-	CCAATTATTTC	-	APP	1insCTTGAAATA	97_K298delinsNLKX
XH_P51	21	30419601	30419601	Frame_Shift_Ins	INS	-	TGGATTTAATAT	-	USP16	38insGTTGGATT	p.C656fs
XH_P51	21	33064731	33064731	Nonsense_Mutation	INS	-	AGGTTTAT	-	SCAF4	9_1500insATAA	500_D501delinsLX
XH_P51	21	33073452	33073452	Frame_Shift_Ins	INS	-	TCTGTATCCCTT	-	SCAF4	ACAGAAAGGAT	p.P196fs
XH_P51	21	34804640	34804640	In_Frame_Ins	INS	-	TGGACACATTTT	-	IFNGR2	719insTGGACA	D240delinsVDTFY
XH_P51	21	36171692	36171692	Frame_Shift_Ins	INS	-	TATTATTAGTA	-	RUNX1	nsGTTTTACTCA	p.I264fs
XH_P51	21	37742058	37742058	In_Frame_Ins	INS	-	TCATCT	-	MORC3	179_2180insTCA	p.S727delinsLIC
XH_P51	21	37742060	37742060	Frame_Shift_Ins	INS	-	AGATTTAT	-	MORC3	1_2182insAGAT	p.S727fs
XH_P51	21	45959923	45959923	Silent	SNP	G	A	G	KRTAP10-1	c.C111T	p.C37C
XH_P51	22	28290612	28290612	Frame_Shift_Ins	INS	-	AAGTCTAGTACG	-	PITPNB	nsCAGACGTACT	p.D129fs
XH_P51	22	30866065	30866065	Missense_Mutation	SNP	A	G	A	SEC14L3	c.T175C	p.Y59H
XH_P51	22	30891588	30891588	Frame_Shift_Ins	INS	-	T	-	SEC14L4	c.215_216insA	p.V72fs
XH_P51	22	30891589	30891589	In_Frame_Ins	INS	-	CTT	-	SEC14L4	214_215insAA	p.V72delinsEV
XH_P51	22	31059731	31059731	Frame_Shift_Ins	INS	-	TTCCC	-	DUSP18	259_260insGGG	p.A87fs
XH_P51	22	32352315	32352315	Frame_Shift_Ins	INS	-	TCCCTTCAACAT	-	YVHAH	8insCTTCCCTTC	p.L93fs
XH_P51	22	44161190	44161190	Missense_Mutation	SNP	T	C	T	EFCAB6	c.A435G	p.I145M
XH_P51	22	46653415	46653415	Frame_Shift_Ins	INS	-	TTCCCTTTCATG	-	PKDREJ	805insGCATGA	p.F1935fs
XH_P51	22	46653417	46653417	Missense_Mutation	SNP	A	G	A	PKDREJ	c.T5803C	p.F1935L
XH_P51	X	3241511	3241511	Missense_Mutation	SNP	T	C	T	MXRA5	c.A2215G	p.K739E
XH_P51	X	12939633	12939633	Nonsense_Mutation	INS	-	CTACTGACT	-	TLR8	4_2475insTAC	D825delinsDYX
XH_P51	X	13778433	13778433	In_Frame_Ins	INS	-	ACAAAA	-	OFD1	34_1735insACA	G578delinsGTK
XH_P51	X	13778435	13778435	Frame_Shift_Ins	INS	-	CCAA	-	OFD1	736_1737insCC	p.S579fs
XH_P51	X	14625379	14625379	Frame_Shift_Ins	INS	-	GACATACG	-	GLRA2	4_705insGACAT	p.H235fs
XH_P51	X	18926165	18926165	In_Frame_Ins	INS	-	TTATACCTCTTA	-	PHKA2	2370insTAAGAG	S790delinsSKRYN
XH_P51	X	20190952	20190952	Missense_Mutation	SNP	T	C	T	RP56KA3	c.A126S	p.Y422C
XH_P51	X	22291465	22291465	In_Frame_Ins	INS	-	CAGGCATCT	-	ZNF645	7_358insCAGGC	Q119delinsQOAS
XH_P51	X	22291467	22291467	Frame_Shift_Ins	INS	-	TT	-	ZNF645	c.359_360insTT	p.C120fs
XH_P51	X	23697398	23697398	Nonsense_Mutation	INS	-	GAAATACACAC	-	PRDX4	4insATGAAATA	p.T198delinsTX
XH_P51	X	38262965	38262965	In_Frame_Ins	INS	-	TGTAGC	-	OTC	35_636insTGTA	G212delinsGVA
XH_P51	X	47774919	47774919	Missense_Mutation	SNP	C	G	C	ZNF81	c.C874G	p.P292A
XH_P51	X	47774920	47774920	Nonsense_Mutation	INS	-	TTATTATGAATA	-	ZNF81	TGCTTTTATTAT	2_Q293delinsPLLLLX
XH_P51	X	50051956	50051956	In_Frame_Ins	INS	-	AACATAATGGCTT	-	CNBN3	8insAAACTAAT	1263delinsKNGFL
XH_P51	X	64737955	64737955	Silent	SNP	T	A	T	LAS1L	c.A1662T	p.T54T
XH_P51	X	71895979	71895979	Missense_Mutation	SNP	C	T	C	PHKA1	c.G559A	p.G187R
XH_P51	X	71895981	71895981	Nonsense_Mutation	INS	-	ATTATATGCCAT	-	PHKA1	nsCTTATGGCAT	86_G187delinsPYGIX
XH_P51	X	72804332	72804332	Nonsense_Mutation	INS	-	CCACCAATAAAA	-	CHIC1	32insACCACCAA	V144_L145delinsDX
XH_P51	X	72804333	72804333	Frame_Shift_Ins	INS	-	A	-	CHIC1	c.432_433insA	p.W144fs
XH_P51	X	74291447	74291447	Nonsense_Mutation	INS	-	TCTGTATCAG	-	ABCB7	984insCTGATA	328_K329delinsFX

XH_P51	X	84362814	84362814	Missense_Mutation	SNP	T	G	T	SATL1	c.A1161C	p.R387S
XH_P51	X	84362816	84362818	In_Frame_Del	DEL	TCA	-	TCA	SATL1	c.1157_1159del	p.386_387del
XH_P51	X	91642909	91642909	Frame_Shift_Ins	INS	-	GTGAAATTACAA	-	PCDH11X	DinsGAATTGAAA	p.D1070fs
XH_P51	X	100117658	100117658	Nonsense_Mutation	INS	-	CTTCTATATCCT	-	NOX1	SCCAAGGATATA	T127delinsTSLQGYRRX
XH_P51	X	100403118	100403118	In_Frame_Ins	INS	-	CCATCAGGTCAT	-	CENPI	hsACTCCCATCAC	688delinsVSHQVIVI
XH_P51	X	100604918	100604918	Frame_Shift_Ins	INS	-	AGACAGACTGA	-	BTX	1407insTTCAGT	p.K469fs
XH_P51	X	100667205	100667205	Frame_Shift_Ins	INS	-	ATTAATAGAAA	-	HNRNP2	AAACTATTAATA	p.T77fs
XH_P51	X	100667681	100667681	Frame_Shift_Ins	INS	-	ATTCTTCCCTTG	-	HNRNP2	6insCTATTCTTT	p.A235fs
XH_P51	X	101970590	101970590	Frame_Shift_Ins	INS	-	GTTCCTCT	-	RMCX5-GPRAS	93_794insGTCTC	p.N265fs
XH_P51	X	102842091	102842091	Frame_Shift_Ins	INS	-	TTCCTTTATCCT	-	TCEAL4	489insTTTCCTTT	p.A163fs
XH_P51	X	103267740	103267740	Splice_Site	SNP	A	T	A	H2BFWT	-	-
XH_P51	X	105167270	105167270	Nonsense_Mutation	INS	-	TTTCATTTTCTTC	-	NRK	sGTAGCTTTTCAT	924_D925delinsX
XH_P51	X	105451465	105451465	Frame_Shift_Ins	INS	-	GACTTCTTGT	-	MUM1L1	2041insGACTT	p.A680fs
XH_P51	X	106038910	106038910	Frame_Shift_Ins	INS	-	TGATTTATGCTA	-	RNF128	ATTATATGATT	p.N392fs
XH_P51	X	108781327	108781327	Frame_Shift_Ins	INS	-	TAAATTTTTCAC	-	NXT2	nsTTTAAATTT	p.N23fs
XH_P51	X	114856604	114856604	Frame_Shift_Ins	INS	-	ATAAAATTTTTC	-	PLS3	CTTACATAAAAT	p.L40fs
XH_P51	X	118604940	118604940	Missense_Mutation	SNP	G	C	G	SLC25A5	c.G816C	p.K272N
XH_P51	X	129150016	129150016	Nonsense_Mutation	INS	-	ATGGGACAT	-	BCORL1	3269insATGG	R1090delinsHGTX
XH_P51	X	132352223	132352223	Missense_Mutation	SNP	T	A	T	TFDP3	c.A65T	p.Q22L
XH_P51	X	133906305	133906305	Frame_Shift_Ins	INS	-	CCAT	-	FAM122B	607_608insATG	p.I203fs
XH_P51	X	135405275	135405275	In_Frame_Ins	INS	-	AAAAATCCAGC	-	ADGRG4	0insAAAAAAAT	137delinsQKNPAL
XH_P51	X	135954464	135954464	Nonsense_Mutation	INS	-	TAGAGTGAGGTT	-	RBMX	81insTAACCTCA94	S195delinsVTSXLX
XH_P51	X	137717733	137717733	Frame_Shift_Ins	INS	-	TTTCTCACATGG	-	FGF13	5GCAACCATGTG	p.Q162fs
XH_P51	X	138644155	138644155	Frame_Shift_Ins	INS	-	ATGGTGTGACTT	-	F9	98insTCATGGTT	p.M399fs
XH_P51	X	138708911	138708911	Frame_Shift_Ins	INS	-	TTAAGTGTAA	-	MC2	26insCTTTAAAC	p.D109fs
XH_P51	X	138708912	138708912	Missense_Mutation	SNP	C	T	C	MC2	c.G325A	p.D109N
XH_P51	X	140995380	140995380	Silent	SNP	T	C	T	MAGEC1	c.T2190C	p.P730P
XH_P51	X	144904117	144904117	Frame_Shift_Ins	INS	-	C	-	SLITRK2	c.175dupC	p.Q58fs
XH_P51	X	147733581	147733581	Nonsense_Mutation	INS	-	ACTTGCTTATTT	-	AFF2	CAAAAACCTTGC	137delinsENKNLIX
XH_P51	X	149826456	149826456	Frame_Shift_Ins	INS	-	G	G	MTM1	c.1216_1217ins	p.L406fs
XH_P51	X	151337014	151337014	Nonsense_Mutation	INS	-	ATTCAATCTGGT	-	GABRA3	5insTAGACCAGA	p.A389delinsX
XH_P51	X	154293983	154293983	Nonsense_Mutation	INS	-	TCTACGAAGATA	-	MTCP1	87insATATCTTC	Q63_Q64delinsISX
XH_P51	X	154293985	154293985	Missense_Mutation	SNP	G	C	G	MTCP1	c.C185G	p.T62S
XH_P51	X	154305554	154305554	In_Frame_Ins	INS	-	ATTGCATTTTAT	-	BRCC3	ATAGAATTGCA	102delinsTIEHLFIII
XH_P51	X	154456712	154456712	In_Frame_Ins	INS	-	5GACATTTAAAA	-	VBP1	1insAGGCATTT	147delinsGLHLKQ
XH_P51	1	118581947	118581947	Missense_Mutation	SNV	T	C	C	SPAG17	c.3287A>G	P.E1096G
XH_P51	1	118584567	118584567	Silent	SNV	G	A	A	SPAG17	c.2913C>T	P.G971G
XH_P51	1	12907844	12907844	Nonsense_Mutation	SNV	G	T	T	HNRNPCL1	c.299C>A	P.S100*
XH_P51	1	13183574	13183574	Missense_Mutation	SNV	G	T	T	HNRNPCL2	c.299C>A	P.S100Y
XH_P51	1	147380265	147380265	Silent	SNV	C	T	T	GJA8	c.183C>T	P.C61C
XH_P51	1	17532878	17532878	Silent	SNV	G	A	A	TNR	c.1674C>T	P.P558F
XH_P51	1	19671681	19671681	Missense_Mutation	SNV	C	G	G	CAP2B	c.654G>C	P.E218D
XH_P51	1	235916570	235916598	Frame_Shift_Del	INDEL	ATAAATAAT	-	-	LYST	CTTAACGTGATT	P.F2411fs
XH_P51	1	245246990	245246990	Missense_Mutation	SNV	G	C	C	EFCAB2	c.373G>C	P.D125H
XH_P51	1	78245357	78245357	Missense_Mutation	SNV	C	T	T	MIGA1	c.17C>T	P.S6L
XH_P51	10	124377771	124377771	Silent	SNV	C	T	T	DMBT1	c.4743C>T	P.H1581H
XH_P51	10	134188673	134188673	Missense_Mutation	SNV	C	T	T	LRRC27	c.1520C>T	P.P507L
XH_P51	10	38121835	38121835	Missense_Mutation	SNV	T	A	A	ZNF248	c.448A>T	P.I150F
XH_P51	10	45430177	45430177	Missense_Mutation	SNV	G	C	C	TMEM72	c.423G>C	P.E141D
XH_P51	10	72643772	72643772	Missense_Mutation	SNV	C	T	T	PCBD1	c.250G>A	P.G84S
XH_P51	11	118509875	118509875	Splice_Site	SNV	C	T	T	PHLDB1	c.2647-5C>T	-
XH_P51	11	62444408	62444408	Missense_Mutation	SNV	G	A	A	UBXN1	c.721C>T	P.L241F
XH_P51	11	87025562	87025562	Silent	SNV	C	T	T	TMEM135	c.984C>T	P.S328S
XH_P51	12	100041961	100041961	Silent	SNV	C	T	T	FAM71C	c.9C>T	P.D3D
XH_P51	12	107078680	107078680	Missense_Mutation	SNV	C	T	T	RF4	c.89C>T	P.T30M
XH_P51	12	32890042	32890042	Nonsense_Mutation	SNV	C	T	T	DNM1L	c.1543C>T	P.Q515*
XH_P51	12	51382182	51382182	Silent	SNV	G	A	A	SLC11A2	c.1612C>T	P.L538L
XH_P51	12	56676760	56676760	Missense_Mutation	SNV	C	T	T	CS	c.283G>A	P.G95S
XH_P51	12	65637256	65637256	Splice_Site	SNV	A	G	G	LEMED3	c.2384+7A>G	-
XH_P51	12	82147850	82147850	Missense_Mutation	SNV	C	T	T	PPFIA2	c.151G>A	P.E51K
XH_P51	12	83251309	83251310	Frame_Shift_Del	INDEL	TT	-	-	TMTC2	c.605_606delTT	P.F202fs
XH_P51	14	23314498	23314498	Missense_Mutation	SNV	G	A	A	MMP14	c.1340G>A	P.S447N
XH_P51	14	77948765	77948765	Silent	SNV	A	G	G	ISM2	c.873T>C	P.D291D
XH_P51	15	48782169	48782169	Silent	SNV	G	A	A	FBN1	c.2961C>T	P.A987A
XH_P51	15	59368396	59368396	Missense_Mutation	SNV	C	T	T	RNF111	c.1930C>T	P.H644Y
XH_P51	15	74174030	74174030	Missense_Mutation	SNV	G	A	A	TBC1D21	c.106G>A	P.G36S
XH_P51	15	89074384	89074384	Missense_Mutation	SNV	G	A	A	DET1	c.553C>T	P.R185W
XH_P51	16	67982038	67982038	Silent	SNV	G	A	A	SLC12A4	c.1773C>T	P.F591F
XH_P51	16	88958375	88958375	Missense_Mutation	SNV	G	A	A	CBFA2T3	c.626C>T	P.S209L
XH_P51	17	44061055	44061055	Missense_Mutation	SNV	G	T	T	MAPT	c.885G>T	P.Q295H
XH_P51	17	45452060	45452060	Missense_Mutation	SNV	G	C	C	EFCAB13	c.812G>C	P.R271T
XH_P51	18	12325450	12325450	Missense_Mutation	SNV	C	T	T	TUBB6	c.662C>T	P.T221I
XH_P51	18	44027560	44027560	Nonsense_Mutation	SNV	C	T	T	RNF165	c.520C>T	P.Q174*
XH_P51	19	36297412	36297412	Silent	SNV	A	G	G	PRODH2	c.1149T>C	P.Y383Y
XH_P51	19	40328485	40328485	Splice_Site	SNV	T	A	A	FB1	c.550-2A>T	-
XH_P51	19	40399735	40399735	Missense_Mutation	SNV	C	T	T	FCGBP	c.5960G>A	P.C1987Y
XH_P51	19	5455764	5455764	Missense_Mutation	SNV	G	T	T	ZNRF4	c.262G>C	P.V88F
XH_P51	19	56127315	56127315	Silent	SNV	G	A	A	ZNF865	c.2331G>A	P.A777A
XH_P51	19	57672168	57672168	Splice_Site	SNV	G	A	A	DUXA	c.26-3C>T	-
XH_P51	2	109389469	109389472	Frame_Shift_Del	INDEL	TCAA	-	-	RANBP2	262_8265delAT	P.E2756fs
XH_P51	2	112539977	112539977	Missense_Mutation	SNV	G	A	A	ANAPC1	c.5171C>T	P.A1724V
XH_P51	2	152425875	152425875	Missense_Mutation	SNV	C	G	G	NEB	c.17442G>C	P.K5814N
XH_P51	2	163208900	163208900	Missense_Mutation	SNV	T	A	A	GCA	c.245T>A	P.I82N
XH_P51	2	220264605	220264605	Missense_Mutation	SNV	G	A	A	DNPEP	c.43C>T	P.L15F
XH_P51	2	241660459	241660459	Splice_Site	SNV	C	T	T	KIF1A	c.4744-4G>A	-
XH_P51	2	25057716	25057716	Silent	SNV	G	A	A	ADCY3	c.1752C>T	P.H584H
XH_P51	2	3756140	3756140	Missense_Mutation	SNV	T	A	A	DCDC2C	c.289T>A	P.Y97N
XH_P51	2	86968093	86968093	Silent	SNV	A	C	C	RMND5A	c.186A>C	P.T62T
XH_P51	20	58468574	58468574	Splice_Site	SNV	C	G	G	SYCP2	c.1735+5G>C	-
XH_P51	21	16338661	16338661	Missense_Mutation	SNV	C	A	A	NRIP1	c.1853G>T	P.G618V
XH_P51	22	30866065	30866065	Missense_Mutation	SNV	A	G	G	SEC14L3	c.175T>C	P.Y59H
XH_P51	22	44161190	44161190	Missense_Mutation	SNV	T	C	C	EFCAB6	c.435A>G	P.I145M
XH_P51	3	111263901	111263901	Frame_Shift_Ins	INDEL	-	A	A	CD96	c.76dupA	P.T26fs
XH_P51	3	111831984	111831984	Nonsense_Mutation	SNV	T	A	A	C3orf52	c.641T>A	P.L214*
XH_P51	3	140785450	140785450	Silent	SNV	C	T	T	SPSB4	c.504C>T	P.D168D
XH_P51	3	167293805	167293805	Silent	SNV	G	A	A	WDR49	c.387C>T	P.D129N
XH_P51	3	48215815	48215815	Missense_Mutation	SNV	C	T	T	CDC25A	c.889G>A	P.A297T
XH_P51	3	53694211	53694211	Silent	SNV	C	T	T	CACNA1D	c.675C>T	P.N225N

XH_P51	3	73651572	73651572	Missense_Mutation	SNV	G	T	T	PDZRN3	c.851C>A	P.S284Y
XH_P51	3	7620570	7620570	Silent	SNV	A	C	C	GRM7	c.1977A>C	P.R659R
XH_P51	4	126355476	126355476	Silent	SNV	C	A	A	FAT4	c.7095C>A	P.A2365A
XH_P51	4	42448637	42448637	Missense_Mutation	SNV	G	A	A	ATP8A1	c.2876C>T	P.T959I
XH_P51	5	112176427	112176427	Frame_Shift_Ins	INDEL	-	T	T	APC	c.5138dupT	P.L1713fs
XH_P51	5	140476277	140476277	Missense_Mutation	SNV	C	G	G	PCDH2	c.1903C>G	P.R635G
XH_P51	5	149505011	149505011	Silent	SNV	G	A	A	PDGFRB	c.1804C>T	P.L602L
XH_P51	5	36265153	36265153	Silent	SNV	G	A	A	RANBP3L	c.463C>T	P.L155L
XH_P51	6	57246959	57246959	Missense_Mutation	SNV	C	T	T	PRIM2	c.686C>T	P.A229V
XH_P51	7	104717497	104717497	Missense_Mutation	SNV	G	C	C	KMT2E	c.856G>C	P.E286Q
XH_P51	7	1275562	1275562	Missense_Mutation	SNV	G	A	A	UNCX	c.545G>A	P.C182Y
XH_P51	7	151877054	151877054	Frame_Shift_Del	INDEL	G	-	-	KMT2C	c.7307delC	P.P2436fs
XH_P51	7	27239007	27239007	Silent	SNV	G	A	A	HOXA13	c.690C>T	P.F230F
XH_P51	7	40118403	40118403	Missense_Mutation	SNV	G	T	T	CDK13	c.2982G>T	P.Q994H
XH_P51	7	5396537	5396537	Splice_Site	SNV	C	T	T	TNRC18	c.5194+10G>A	
XH_P51	7	63538228	63538228	Silent	SNV	T	C	C	ZNFX727	c.801T>C	P.C267C
XH_P51	8	103373850	103373850	Silent	SNV	G	T	T	UBR5	c.67C>A	P.R23R
XH_P51	9	120475904	120475904	Missense_Mutation	SNV	T	A	A	TLR4	c.1378T>A	P.F460I
XH_P51	9	26923315	26923315	Silent	SNV	T	A	A	PLAA	c.900A>T	P.S300S
XH_P51	X	103267740	103267740	Splice_Site	SNV	A	T	T	H2BFWT	c.491+2T>A	
XH_P51	X	118604940	118604940	Missense_Mutation	SNV	G	C	C	SLC25A5	c.816G>C	P.K272N
XH_P51	X	132352223	132352223	Missense_Mutation	SNV	T	A	A	TFDP3	c.65A>T	P.Q22L
XH_P51	X	140995380	140995380	Silent	SNV	T	C	C	MAGEC1	c.2190T>C	P.P730P
XH_P51	X	144904117	144904117	Frame_Shift_Ins	INDEL	-	C	C	SLITRK2	c.181dupC	P.Q61fs
XH_P51	X	20190952	20190952	Missense_Mutation	SNV	T	C	C	RPS6KA3	c.1265A>G	P.Y422C
XH_P51	X	64737955	64737955	Silent	SNV	T	A	A	LAS1L	c.1788A>T	P.T596T
XH_P52	17	29546122	29546122	Nonsense_Mutation	SNP	C	T	T	NF1	c.1627C>T	p.Q543*
XH_P52	17	7578534	7578534	Missense_Mutation	SNP	C	A	A	TP53	c.396G>T	p.K132N
XH_P52	20	57430245	57430245	Missense_Mutation	SNP	C	T	T	GNAS	c.1738C>T	p.R580W
XH_P52	X	53227063	53227063	Splice_Site	SNP	G	A	A	KDM5C	c.2517-5C>T	-
XH_P52	1	8977738	8977738	Silent	SNP	C	T	C	KLHL17	c.C715T	p.L239L
XH_P52	1	914847	914847	Silent	SNP	G	A	G	PERM1	c.C1563T	p.A521A
XH_P52	1	1147485	1147485	Silent	SNP	C	T	C	TNFRSF4	c.G471A	p.P157P
XH_P52	1	1153113	1153113	Silent	SNP	G	A	G	SDF4	c.C984T	p.L328L
XH_P52	1	3649562	3649562	Silent	SNP	G	A	G	TP73	c.G1440A	p.A480A
XH_P52	1	8073643	8073643	Missense_Mutation	SNP	G	A	G	ERRF1	c.C1016T	p.P339L
XH_P52	1	8424831	8424831	Silent	SNP	G	A	G	RERE	c.C1515T	p.Y505Y
XH_P52	1	16260916	16260916	Silent	SNP	C	T	C	SPEN	c.C8181T	p.A2727A
XH_P52	1	19180948	19180948	Missense_Mutation	SNP	C	T	C	TAS1R2	c.G1016A	p.R339H
XH_P52	1	19510645	19510645	Nonsense_Mutation	INS	-	AGCTGCTTAA	-	UBR4	963insATTATAAC	655 N656delinsIX
XH_P52	1	24419496	24419496	Missense_Mutation	SNP	A	G	A	MYOM3	c.T1031C	p.MY344T
XH_P52	1	26513975	26513975	Splice_Site	INS	-	ACTTCCAGACT	-	CNKS1R	-	-
XH_P52	1	28792974	28792974	Missense_Mutation	SNP	G	A	G	PHACTR4	c.G548A	p.R183K
XH_P52	1	31215364	31215364	Silent	SNP	T	C	T	LAPTM5	c.A120G	p.S40S
XH_P52	1	31468044	31468044	Missense_Mutation	SNP	A	T	A	PUM1	c.T744A	p.D248E
XH_P52	1	32669603	32669603	Silent	SNP	G	A	G	CCDC28B	c.G288A	p.L96L
XH_P52	1	36773405	36773405	Silent	SNP	T	G	T	SH3D21	c.T138G	p.P46P
XH_P52	1	38338795	38338795	Missense_Mutation	SNP	A	G	A	INPP5B	c.T1502C	p.M501T
XH_P52	1	39854271	39854271	Frame_Shift_Ins	INS	-	CTCTTCT	-	MACF1	71_9572insCTC	p.L3191fs
XH_P52	1	41847669	41847669	Missense_Mutation	SNP	G	A	G	FOXO6	c.G796A	p.E266K
XH_P52	1	44056806	44056806	Silent	SNP	C	T	C	PTPRF	c.C1113T	p.P371T
XH_P52	1	46087577	46087577	Missense_Mutation	SNP	G	A	G	CCDC17	c.C1058T	p.P353L
XH_P52	1	57233602	57233602	Nonsense_Mutation	INS	-	ACCATCTTATTC	-	C1orf168	nsAAAGAAATAA	N321delinsKKXX
XH_P52	1	67390416	67390416	Missense_Mutation	SNP	G	C	G	WDR78	c.C99G	p.C33W
XH_P52	1	78279445	78279445	Missense_Mutation	SNP	C	T	C	MIG1A	c.C664T	p.R222C
XH_P52	1	110580576	110580576	Nonsense_Mutation	INS	-	TTTATCATAACT	-	STRIP1	45insATTATTCATC	b.L82delinsHLX
XH_P52	1	111060669	111060669	Silent	SNP	T	C	T	KCNA10	c.A741G	p.L247L
XH_P52	1	113057513	113057513	Missense_Mutation	SNP	G	A	G	WNT2B	c.G200A	p.G67E
XH_P52	1	114964257	114964257	Frame_Shift_Ins	INS	-	GAGTTTTTTTTT	-	TRIM33	ATTAAAAAAA	p.H621fs
XH_P52	1	114964259	114964259	Splice_Site	SNP	C	A	C	TRIM33	-	-
XH_P52	1	145438994	145438994	In_Frame_Ins	INS	-	AAATTATT	-	TXNIP	2_193insAAATT	p.K64delinsKKLF
XH_P52	1	145438996	145438996	Frame_Shift_Ins	INS	-	CTTTAAG	-	TXNIP	94_195insCTTTA	p.Q65fs
XH_P52	1	150998002	150998002	Missense_Mutation	SNP	C	A	C	PRUNE1	c.C532A	p.L178M
XH_P52	1	151773851	151773851	Missense_Mutation	SNP	T	A	T	LINGO4	c.A1330T	p.T444S
XH_P52	1	152191944	152191944	Missense_Mutation	SNP	T	C	T	HRNR	c.A2161G	p.S721G
XH_P52	1	152279019	152279019	Silent	SNP	G	A	G	FLG	c.C8343T	p.D2781D
XH_P52	1	152280900	152280900	Nonsense_Mutation	INS	-	AGACACTCAC	-	FLG	6462insGTGAG	154 E2155delinsQX
XH_P52	1	152281522	152281522	Nonsense_Mutation	SNP	C	T	C	FLG	c.G5840A	p.W1947X
XH_P52	1	152285571	152285571	Silent	SNP	G	A	G	FLG	c.C1791T	p.S597S
XH_P52	1	152484091	152484091	Frame_Shift_Ins	INS	-	ATTATTATTATG	-	LCSEA	AGAATTATTATTA	p.K27fs
XH_P52	1	153750769	153750769	Missense_Mutation	SNP	G	A	G	SLC27A3	c.G1678A	p.V560M
XH_P52	1	155149718	155149718	Silent	SNP	G	A	G	TRIM46	c.G483A	p.T161T
XH_P52	1	155260402	155260402	Silent	SNP	G	A	G	PKLR	c.C1686T	p.S562S
XH_P52	1	156287015	156287015	Missense_Mutation	SNP	G	A	G	CCT3	c.C802T	p.R268W
XH_P52	1	156911215	156911215	Missense_Mutation	SNP	C	A	C	ARHGEF11	c.G3343T	p.D1115Y
XH_P52	1	156928654	156928654	Missense_Mutation	SNP	G	T	G	ARHGEF11	c.C1262A	p.T421K
XH_P52	1	156928655	156928655	In_Frame_Ins	INS	-	GCCTGATTC	-	ARHGEF11	1261insGAATG	T421delinsESGT
XH_P52	1	158655096	158655096	Nonsense_Mutation	INS	-	TTTTTCTTTATG	-	SPTA1	ATTAACATAAAG	22 E23delinsDTHX
XH_P52	1	158747024	158747024	In_Frame_Ins	INS	-	ACTTTCTCTTTA	-	OR6N2	ATGATAAAGAAAG	34delinsIMIKKVR
XH_P52	1	159284421	159284421	Nonsense_Mutation	INS	-	CTCTTCTCTATC	-	OR10J3	9insGATAGAAAG	T10 E11delinsRX
XH_P52	1	159898100	159898100	Silent	SNP	A	G	A	IGSF9	c.T3078C	p.S1026S
XH_P52	1	161168004	161168004	Silent	SNP	C	T	C	ADAMTS4	c.G414A	p.S138S
XH_P52	1	161173284	161173284	Nonsense_Mutation	INS	-	TTTTGTITTTTG	-	NDUFS2	5TTTGTITTTTGT	152delinsVFLFCVFVCFXX
XH_P52	1	161681780	161681780	Missense_Mutation	SNP	A	G	A	FCRLA	c.A187G	p.S63G
XH_P52	1	161695747	161695747	Frame_Shift_Ins	INS	-	TCTTTTCTTTCT	-	FCRLB	TCTTTTCTTTT	p.H141fs
XH_P52	1	161723023	161723023	Missense_Mutation	SNP	C	G	C	DUSP12	c.C833G	p.S278C
XH_P52	1	161723025	161723025	Frame_Shift_Ins	INS	-	CGGTATTT	-	DUSP12	5_836insCGGT	p.A279fs
XH_P52	1	162344102	162344102	Silent	SNP	C	T	C	SPATA46	c.G522A	p.R174R
XH_P52	1	171621525	171621525	Missense_Mutation	SNP	C	T	C	MYOC	c.G227A	p.R76K
XH_P52	1	201178630	201178630	Missense_Mutation	SNP	T	C	T	IGFN1	c.T4609C	p.S1537P
XH_P52	1	203468972	203468972	Missense_Mutation	SNP	C	T	C	OPTC	c.C725T	p.A242V
XH_P52	1	207890866	207890866	Missense_Mutation	SNP	T	C	T	CR1L	c.T1472C	p.L491P
XH_P52	1	226074563	226074563	Missense_Mutation	SNP	T	G	T	LEFTY1	c.A965C	p.P322A
XH_P52	1	226736652	226736652	Missense_Mutation	SNP	C	T	C	STUM	c.C47T	p.A16V
XH_P52	1	228402508	228402508	Silent	SNP	C	T	C	OBSCN	c.C1537T	p.L513L
XH_P52	1	228412227	228412227	Silent	SNP	T	C	T	OBSCN	c.T2721C	p.S907S
XH_P52	1	228412228	228412228	Missense_Mutation	SNP	G	A	G	OBSCN	c.G2722A	p.A908T
XH_P52	1	228412308	228412308	Silent	SNP	G	A	G	OBSCN	c.G2802A	p.S934S

XH_P52	1	231557255	231557255	Missense_Mutation	SNP	C	G	C	EGLN1	c.G380C	p.C127S
XH_P52	1	231829577	231829577	Missense_Mutation	SNP	C	T	C	DISC1	c.C73T	p.R25W
XH_P52	1	235377196	235377196	Frame_Shift_Ins	INS	-	A	-	ARID4B	c.1728_1729ins	p.V577fs
XH_P52	1	241933952	241933952	Missense_Mutation	SNP	C	T	C	WDR64	c.C2183T	p.S728L
XH_P52	1	246755170	246755170	Frame_Shift_Ins	INS	-	TGGTTCATATT	-	CNST	c.307insTGGTTC	p.L102fs
XH_P52	1	248185768	248185768	Frame_Shift_Ins	INS	-	AACAATCGTAGA	-	OR2L5	c.TAGGAACAATC	p.I173fs
XH_P52	1	249107350	249107350	Silent	SNP	C	T	C	SH3BP5L	c.G192A	p.A64A
XH_P52	2	21227262	21227262	Missense_Mutation	SNP	C	T	C	APOB	c.G11966A	p.R3989H
XH_P52	2	21364858	21364858	Nonsense_Mutation	INS	-	GTAATTTTAGA	-	TDRD15	c.0insTTGCGTAAAT	p.1507delinsVRKFX
XH_P52	2	27361117	27361117	Frame_Shift_Ins	INS	-	TCCT	-	PRR30	c.80_81insAGGG	p.L27fs
XH_P52	2	27361119	27361119	Missense_Mutation	SNP	G	T	G	PRR30	c.C79A	p.L27I
XH_P52	2	36808536	36808536	Nonsense_Mutation	INS	-	TACATTTTGTTC	-	FE22	c.ACAACAACAA	p.D178delinsPTTKMX
XH_P52	2	36808538	36808538	Missense_Mutation	SNP	G	T	G	FE22	c.C529A	p.P177T
XH_P52	2	39515349	39515349	Missense_Mutation	SNP	G	A	G	MAP4K3	c.C1324T	p.P442S
XH_P52	2	42990101	42990101	Missense_Mutation	SNP	G	C	G	OXER1	c.C1219G	p.L407V
XH_P52	2	44078853	44078853	Silent	SNP	G	A	G	ABCG8	c.G453A	p.V151V
XH_P52	2	71654459	71654459	Frame_Shift_Ins	INS	-	TTAAGCTCTT	-	ZNFX638	c.5461insTTAAG	p.K1820fs
XH_P52	2	73496580	73496580	In_Frame_Del	DEL	GGCGCGGCGG	-	GGCGCGGCGG	FBXO41	c.165_179del	p.55_60del
XH_P52	2	73675227	73675227	In_Frame_Ins	INS	-	CTC	-	ALMS1	c.1570_1571insC	p.S524delinsSP
XH_P52	2	74685789	74685789	Silent	SNP	G	A	G	WBP1	c.G60A	p.P20P
XH_P52	2	103274338	103274338	Missense_Mutation	SNP	T	C	T	SLC9A2	c.C605C	p.I202T
XH_P52	2	103274340	103274340	In_Frame_Ins	INS	-	AAAATAATC	-	SLC9A2	c.7608insAAAAAT	p.T203delinsKNNP
XH_P52	2	108487598	108487598	In_Frame_Ins	INS	-	AATCCCTTG	-	RGPD4	c.3139insAATC	p.E104delinsENPL
XH_P52	2	108487830	108487830	Nonsense_Mutation	INS	-	TACAGAACTTTT	-	RGPD4	c.insGAATACAGA	p.124_G1125delinsX
XH_P52	2	109988080	109988080	Missense_Mutation	SNP	C	A	C	SH3RF3	c.C888A	p.N296K
XH_P52	2	112621469	112621469	Nonsense_Mutation	INS	-	GCTCACCTCTA	-	ANAPC1	c.335insTAGAAGG	p.E279delinsX
XH_P52	2	113955177	113955177	In_Frame_Ins	INS	-	AAGAAACA	-	PSD4	c.2424insAAGA	p.T808delinsTRKH
XH_P52	2	113955179	113955179	Missense_Mutation	SNP	T	A	T	PSD4	c.T2425A	p.L809I
XH_P52	2	152375584	152375584	Splice_Site	INS	-	TGGAACATAAAT	-	NEB	-	-
XH_P52	2	163291934	163291934	Nonsense_Mutation	INS	-	TTGTCTATTAGG	-	KCNH7	c.TCTATCTAATA	p.69_E570delinsVLXS
XH_P52	2	167163583	167163583	Nonsense_Mutation	INS	-	TAGTTTATTAAT	-	SCN9A	c.TGAAATTAATA	p.7_F88delinsILKLINX
XH_P52	2	178416283	178416283	Silent	SNP	A	G	A	TTC30B	c.T1209C	p.N403N
XH_P52	2	179444749	179444749	Frame_Shift_Ins	INS	-	GGATATGTAGT	-	TTN	c.070insTCAACTAG	p.K13357fs
XH_P52	2	179631214	179631214	Silent	SNP	T	C	T	TTN	c.A9459G	p.E3153E
XH_P52	2	179634871	179634871	Silent	SNP	G	A	G	TTN	c.C8419T	p.L2807L
XH_P52	2	200213696	200213696	In_Frame_Ins	INS	-	TCCTTGCAA	-	SATB2	c.901insTTGCA	p.Q301delinsLQRQ
XH_P52	2	207175098	207175098	Nonsense_Mutation	INS	-	GTAACCTTTT	-	ZDBF2	c.5847insGTAA	p.949_C1950delinsRX
XH_P52	2	207629977	207629977	Missense_Mutation	SNP	C	G	C	MDH1B	c.C19C	p.A7P
XH_P52	2	207823120	207823120	Silent	SNP	C	T	C	CPO	c.C363T	p.F121F
XH_P52	2	215890474	215890474	Nonsense_Mutation	SNP	G	A	G	ABCA12	c.C256T	p.R86X
XH_P52	2	219000310	219000310	Silent	SNP	C	T	C	CXCR2	c.C786T	p.L262L
XH_P52	2	220419460	220419460	Missense_Mutation	SNP	T	A	T	OBSL1	c.A4612T	p.R1538W
XH_P52	2	220435375	220435375	Silent	SNP	G	A	G	OBSL1	c.C580T	p.L194L
XH_P52	2	220505265	220505265	Silent	SNP	T	C	T	SLC4A3	c.T3472C	p.L1158L
XH_P52	2	226447663	226447663	Silent	SNP	G	A	G	NYAP2	c.G1530A	p.P510P
XH_P52	2	234731210	234731210	Nonsense_Mutation	SNP	C	T	C	MROH2A	c.C3883T	p.L1295X
XH_P52	2	240951108	240951108	Nonsense_Mutation	INS	-	TGTGGGGTTTA	-	NDUFA10	c.ACCAATAAACCC	p.5_E226delinsQINQX
XH_P52	2	242572888	242572888	Silent	SNP	C	T	C	THAP4	c.G684A	p.A228A
XH_P52	3	11382189	11382189	Nonsense_Mutation	INS	-	AGAGCATGAGC	-	ATG7	c.STCTGAGAGCA	p.E282delinsSTGTLVVX
XH_P52	3	13540035	13540035	Missense_Mutation	SNP	G	A	G	HDAC11	c.C239A	p.R80Q
XH_P52	3	13661319	13661319	Missense_Mutation	SNP	G	A	G	FBLN2	c.G2143A	p.V715M
XH_P52	3	38040912	38040912	Frame_Shift_Del	DEL	C	-	C	VILL	c.1164delC	p.D388fs
XH_P52	3	46008790	46008790	Missense_Mutation	SNP	G	A	G	FYCO1	c.C2036T	p.A679V
XH_P52	3	46009864	46009864	Missense_Mutation	SNP	C	G	C	FYCO1	c.G962C	p.G321A
XH_P52	3	48605185	48605185	Silent	SNP	A	G	A	COL7A1	c.T7941C	p.G2647G
XH_P52	3	48694516	48694516	Silent	SNP	G	A	G	CELSR3	c.C4014T	p.A1338A
XH_P52	3	49690496	49690496	Silent	SNP	C	T	C	BSN	c.C3507T	p.S1169S
XH_P52	3	52366368	52366368	Missense_Mutation	SNP	A	G	A	DNAH1	c.A1244G	p.K415R
XH_P52	3	56835761	56835761	Silent	SNP	G	A	G	ARHGEF3	c.C66T	p.P22P
XH_P52	3	73453495	73453495	Frame_Shift_Ins	INS	-	CCCT	-	PDZRN3	c.63_64insAGGG	p.F22fs
XH_P52	3	121207766	121207766	Frame_Shift_Ins	INS	-	CATTCTCCAAT	-	POLQ	c.4012insATTGG	p.E1338fs
XH_P52	3	121207768	121207768	Missense_Mutation	SNP	G	C	G	POLQ	c.C4010G	p.T1337S
XH_P52	3	121208338	121208338	Frame_Shift_Ins	INS	-	TACCAACAGAA	-	POLQ	c.5TATTTTCTGTT	p.T1147fs
XH_P52	3	121208340	121208340	Silent	SNP	C	A	C	POLQ	c.C3438T	p.V1146V
XH_P52	3	122215306	122215306	Missense_Mutation	SNP	C	T	C	KPNA1	c.G107A	p.R36Q
XH_P52	3	130300843	130300843	Nonsense_Mutation	INS	-	AACTGTGA	-	COL6A6	c.13902insAACT	p.1301_F1302delinsX
XH_P52	3	134911453	134911453	In_Frame_Ins	INS	-	CTCTCATTGTAA	-	EPHB1	c.AGTCTTCTCTCA	p.40delinsQSSLVITL
XH_P52	3	140406947	140406947	Missense_Mutation	SNP	G	A	G	TRIM42	c.G1423A	p.V475M
XH_P52	3	142511775	142511775	Frame_Shift_Ins	INS	-	A	-	TRPC1	c.1445_1446ins	p.M482fs
XH_P52	3	142511776	142511776	Frame_Shift_Ins	INS	-	TTTAAAAATAGA	-	TRPC1	c.5GGTTTTTTTAAA	p.M482fs
XH_P52	3	157177911	157177911	Silent	SNP	T	G	T	VEPH1	c.A588C	p.S196S
XH_P52	3	169644749	169644749	Frame_Shift_Ins	INS	-	TCTCCTCA	-	SAMD7	c.99_700insTCTCC	p.S233fs
XH_P52	3	182871676	182871676	Nonsense_Mutation	INS	-	ACTATAACACTA	-	LAMP3	c.53insATAGTGT	p.85_V186delinsVLX
XH_P52	3	183493744	183493744	In_Frame_Del	DEL	GGAGGA	-	GGAGGA	YEATS2	c.2410_2415del	p.804_805del
XH_P52	3	194062519	194062519	Missense_Mutation	SNP	C	T	C	CPN2	c.G913A	p.A305T
XH_P52	3	194408704	194408704	Silent	SNP	A	G	A	FAM43A	c.A1149G	p.S383S
XH_P52	4	265743	265743	Silent	SNP	G	A	G	ZNFX732	c.C900T	p.T300T
XH_P52	4	436577	436577	Missense_Mutation	SNP	T	C	T	ZNFX721	c.A1679G	p.E560G
XH_P52	4	983060	983060	Missense_Mutation	SNP	T	C	T	SLC26A1	c.A1667G	p.Q556R
XH_P52	4	1330759	1330759	Missense_Mutation	SNP	T	C	T	MAEA	c.T676C	p.W226R
XH_P52	4	2692477	2692477	Silent	SNP	A	T	A	FAM193A	c.A1710T	p.P570P
XH_P52	4	2692479	2692479	In_Frame_Ins	INS	-	TTTTTTTTTTTT	-	FAM193A	c.5CTCCTTTTTTTTT	p.71delinsPSFFFFF
XH_P52	4	4322570	4322570	Missense_Mutation	SNP	G	A	G	ZBTB49	c.G1825A	p.E609K
XH_P52	4	4322665	4322665	Silent	SNP	T	C	T	ZBTB49	c.T1920C	p.S640S
XH_P52	4	6107403	6107403	Missense_Mutation	SNP	G	A	G	JAKMIP1	c.C421T	p.R141C
XH_P52	4	6864763	6864763	Nonsense_Mutation	INS	-	CTTTCATTACAT	-	KIAA0232	c.TGTGGACTTTCA	p.5delinsLHVDHFHVLX
XH_P52	4	17528480	17528480	Silent	SNP	G	A	G	CLRN2	c.G474A	p.A158A
XH_P52	4	24810094	24810094	Missense_Mutation	SNP	G	A	G	CCDC149	c.C1507T	p.R503W
XH_P52	4	39839499	39839499	Nonsense_Mutation	INS	-	GCAGTGACCGA	-	PDS5A	c.TTTCCTCGGTCA	p.5asAAVTVLFFPRSLMLPWVAX
XH_P52	4	40440215	40440215	Silent	SNP	T	C	T	RBM47	c.A696G	p.E232E
XH_P52	4	40440854	40440854	Silent	SNP	G	C	G	RBM47	c.C57G	p.S19S
XH_P52	4	48494870	48494870	Missense_Mutation	SNP	A	G	A	ZAR1	c.A1051G	p.N351D
XH_P52	4	48494872	48494872	Nonsense_Mutation	INS	-	AGCTAGATCTA	-	ZAR1	c.4insTCCAGCTAG	p.N351delinsNSSX
XH_P52	4	54966667	54966667	Silent	SNP	C	T	C	GSX2	c.C156T	p.S52S
XH_P52	4	57220334	57220334	In_Frame_Ins	INS	-	AGA	-	AASDH	c.953_954insTC	p.V318delinsVL
XH_P52	4	57220336	57220336	Nonsense_Mutation	INS	-	FATTGAATATCTA	-	AASDH	c.ATTAAATAGATAT	p.P319delinsYINRYSIFXK
XH_P52	4	57896395	57896395	Missense_Mutation	SNP	A	T	A	POLR2B	c.A3040T	p.M1014L
XH_P52	4	70146409	70146409	Frame_Shift_Ins	INS	-	CAAG	-	UGT2B28	c.191_192insCAA	p.F64fs

XH_P52	4	70146410	70146410	In_Frame_Ins	INS	-	TTTCTCATACTT	-	UGT2B28	GTTCCTCTCTCA	4delinsFHCFFLLIYR
XH_P52	4	71346964	71346964	In_Frame_Ins	INS	-	TATTTTAT	-	MUC7	3_504insTATTT	p.A168delinsAIFI
XH_P52	4	90034393	90034393	In_Frame_Ins	INS	-	ATTTTA	-	TIGD2	268_269insATT	p.Q90delinsHFK
XH_P52	4	90034395	90034395	Frame_Shift_Ins	INS	-	TGTCT	-	TIGD2	270_271insTGT	p.Q90fs
XH_P52	4	95377617	95377617	Missense_Mutation	SNP	A	G	A	PDLIM5	c.A319G	p.K107E
XH_P52	4	95377618	95377618	Missense_Mutation	SNP	A	G	A	PDLIM5	c.A320G	p.K107R
XH_P52	4	103514714	103514714	Frame_Shift_Ins	INS	-	CTAATGGTATTI	-	NFKB1	CTGATTCTAATG	p.S399fs
XH_P52	4	114275298	114275298	Frame_Shift_Ins	INS	-	TTACTTTGTCCT	-	ANK2	25insCTTTACTT	p.H1842fs
XH_P52	4	119948012	119948012	Frame_Shift_Ins	INS	-	GTITTTGTITTT	-	SYNPO2	489insGTTITTT	p.S163fs
XH_P52	4	119948013	119948013	In_Frame_Ins	INS	-	ATTTTCAGA	-	SYNPO2	9_490insATTTTTC	p.S163delinsSIFR
XH_P52	4	141543997	141543997	Silent	SNP	G	A	G	TBC1D9	c.C3153T	p.H1051H
XH_P52	4	144619921	144619921	Silent	SNP	C	T	C	FREM3	c.G1908A	p.G636G
XH_P52	4	155254158	155254158	Missense_Mutation	SNP	C	A	C	DCHS2	c.G3202T	p.V1068L
XH_P52	4	166999165	166999165	Missense_Mutation	SNP	G	A	G	TLL1	c.G2425A	p.G809S
XH_P52	4	170037572	170037572	Missense_Mutation	SNP	G	A	G	SH3RF1	c.C1987T	p.P663S
XH_P52	5	1244425	1244425	Missense_Mutation	SNP	C	T	C	SLC6A18	c.C1433T	p.P478L
XH_P52	5	1255520	1255520	Silent	SNP	G	A	G	TERT	c.C2850T	p.H950H
XH_P52	5	5463200	5463200	Silent	SNP	C	T	C	ICE1	c.C3753T	p.I1251L
XH_P52	5	40853393	40853393	Nonsense_Mutation	INS	-	AAAGTAGCATCT	-	CARD6	AGAACAAGTA3	G654delinsLRTKX
XH_P52	5	74060901	74060901	Missense_Mutation	SNP	A	G	A	GF1M2	c.T31C	p.W11R
XH_P52	5	78181477	78181477	Missense_Mutation	SNP	C	T	C	ARSB	c.G1072A	p.V358M
XH_P52	5	82940460	82940460	Missense_Mutation	SNP	C	T	C	HAPLN1	c.G497A	p.R166Q
XH_P52	5	100238636	100238636	Nonsense_Mutation	SNP	C	T	C	ST8SIA4	c.G24A	p.W8X
XH_P52	5	112257856	112257856	In_Frame_Ins	INS	-	CAACAGGCAGG	-	REEP5	GTGGCCTGCCTC	QLRGRCEVACLLTVLTHCGVKR
XH_P52	5	118969960	118969960	Missense_Mutation	SNP	C	T	C	FAM170A	c.C376T	p.P126S
XH_P52	5	121786936	121786936	Frame_Shift_Ins	INS	-	AAGGTGTG	-	SNCAIP	2_1183insAAGG	p.A394fs
XH_P52	5	121786937	121786937	Missense_Mutation	SNP	C	T	C	SNCAIP	c.C1183T	p.L395F
XH_P52	5	125896792	125896792	In_Frame_Ins	INS	-	TGTTTTTTCTCT	-	ALDH7A1	6insAAGAAGAA	G299delinsEETKTR
XH_P52	5	127622491	127622491	Missense_Mutation	SNP	T	C	T	FBN2	c.A6931G	p.M2311V
XH_P52	5	130726760	130726760	Silent	SNP	G	A	G	CDC42SE2	c.G231A	p.Q77Q
XH_P52	5	130726761	130726761	Frame_Shift_Ins	INS	-	TAAGTAATCTCT	-	CDC42SE2	233insTAAGTAA	p.L78fs
XH_P52	5	140229368	140229368	Missense_Mutation	SNP	G	C	G	PCDHA9	c.G1288C	p.G430R
XH_P52	5	140230370	140230370	Missense_Mutation	SNP	A	C	A	PCDHA9	c.A2290C	p.K764Q
XH_P52	5	140230371	140230371	Missense_Mutation	SNP	A	C	A	PCDHA9	c.A2291C	p.K764T
XH_P52	5	140502960	140502960	Silent	SNP	C	G	C	PCDHB4	c.C1380G	p.R460R
XH_P52	5	140762754	140762754	Silent	SNP	C	T	C	PCDHGA7	c.C288T	p.C96C
XH_P52	5	140763029	140763029	Missense_Mutation	SNP	A	G	A	PCDHGA7	c.A563G	p.E188G
XH_P52	5	140779354	140779354	Missense_Mutation	SNP	A	C	A	PCDHGB5	c.A1660C	p.N554H
XH_P52	5	147510866	147510866	Silent	SNP	T	C	T	SPINK5	c.T3009C	p.G1003G
XH_P52	5	148206646	148206646	Silent	SNP	G	A	G	ADRB2	c.G252A	p.L84L
XH_P52	5	150102536	150102536	Nonsense_Mutation	INS	-	TAGGTTTTTAAT	-	DCTN4	ACTAAATTAATA	224_H225delinsNX
XH_P52	5	150696498	150696498	Silent	SNP	G	A	G	SLC36A2	c.C1332T	p.D444D
XH_P52	5	150946966	150946966	Silent	SNP	G	A	G	FAT9	c.C1527T	p.P502P
XH_P52	5	157078475	157078475	Silent	SNP	C	G	C	SOX30	c.G612C	p.P204P
XH_P52	5	159776637	159776637	Silent	SNP	C	T	C	C1QTNF2	c.G531A	p.K177K
XH_P52	5	180052946	180052946	Silent	SNP	G	A	G	FLT4	c.C1344T	p.Y448Y
XH_P52	6	16328068	16328068	Silent	SNP	T	C	T	ATXN1	c.A474G	p.A158A
XH_P52	6	18171650	18171650	Silent	SNP	G	A	G	KDM1B	c.G474A	p.Q158Q
XH_P52	6	22570064	22570064	Missense_Mutation	SNP	C	T	C	HDGFL1	c.C260T	p.T87M
XH_P52	6	25773745	25773745	Nonsense_Mutation	INS	-	ATAAAGGGATG	-	SLC17A4	831insATAAAGG	p.C277delinsXX
XH_P52	6	26216532	26216532	Nonsense_Mutation	SNP	C	A	C	HIST1H2BG	c.G340T	p.E114X
XH_P52	6	34008406	34008406	Missense_Mutation	SNP	C	T	C	GRM4	c.G940A	p.G314S
XH_P52	6	39024238	39024238	Silent	SNP	C	G	C	GLP1R	c.C144G	p.R48R
XH_P52	6	39158891	39158891	Silent	SNP	C	T	C	KCNK5	c.G1275A	p.T425T
XH_P52	6	43607804	43607804	Nonsense_Mutation	INS	-	CTGTGCTCAGG	-	MAD2L1BP	AGCTGCTGTGCT	nsSSRCKCAQAVLRLWSTLX
XH_P52	6	46657421	46657421	Missense_Mutation	SNP	G	A	G	TDRD6	c.G1556A	p.R519K
XH_P52	6	56484267	56484267	Frame_Shift_Ins	INS	-	TCAGAGAATATA	-	DST	565insCTATATT	p.I1522fs
XH_P52	6	78172260	78172260	Silent	SNP	C	G	G	HTR1B	c.G861C	p.V287V
XH_P52	6	78172992	78172992	Silent	SNP	G	A	G	HTR1B	c.C129T	p.S43S
XH_P52	6	82461727	82461727	In_Frame_Ins	INS	-	GCCGAAGTCGC	-	FAM46A	2insCGGCGACT	p.44delinsGGDFGD
XH_P52	6	83847675	83847675	Nonsense_Mutation	INS	-	TGAGAATTCTCA	-	DOPEY1	888insCTGAGAA	p.K1296delinsNX
XH_P52	6	90642358	90642358	Silent	SNP	G	A	G	BACH2	c.C2295T	p.N765N
XH_P52	6	106555025	106555025	Silent	SNP	G	A	G	PRDM1	c.G1740A	p.P580P
XH_P52	6	109763218	109763218	Missense_Mutation	SNP	C	G	C	SMPD2	c.C266G	p.P89R
XH_P52	6	114378782	114378782	Nonsense_Mutation	INS	-	TAATATTATCTT	-	HS3ST5	TATTAAGATAA	227_A228delinsTYX
XH_P52	6	132891659	132891659	Missense_Mutation	SNP	A	G	A	TAAR6	c.A199G	p.T67A
XH_P52	6	138200252	138200252	Missense_Mutation	SNP	C	T	C	TNFAIP3	c.C1670T	p.P557L
XH_P52	6	138539361	138539361	Nonsense_Mutation	SNP	T	A	T	PBOV1	c.A172T	p.K58X
XH_P52	6	138539362	138539362	Nonsense_Mutation	INS	-	CAAAACTATAC	-	PBOV1	71insGTATAG57	K58delinsDVX
XH_P52	6	146262903	146262903	Silent	SNP	G	A	G	SHPRH	c.C2346T	p.V782V
XH_P52	6	151936677	151936677	Missense_Mutation	SNP	G	A	G	CCDC170	c.G1810A	p.V604I
XH_P52	6	152792863	152792863	Missense_Mutation	SNP	T	A	T	SYN1	c.A1522T	p.M508L
XH_P52	6	160480051	160480051	Frame_Shift_Ins	INS	-	TAGGTTAAACAT	-	IGF2R	TCCACTAGGTT	p.P1004fs
XH_P52	6	161413047	161413047	Silent	SNP	G	A	G	MAP3K4	c.G84A	p.P28P
XH_P52	7	286468	286468	Nonsense_Mutation	INS	-	CCCTTCCTTCCTC	-	FAM20C	GTGAGCCCTTCC	17_D318delinsLDRX
XH_P52	7	4008986	4008986	Silent	SNP	C	T	C	SDK1	c.C1644T	p.A548A
XH_P52	7	15725798	15725803	In_Frame_Del	DEL	TGGTGG	-	TGGTGG	MEOX2	c.225_230del	p.75_77del
XH_P52	7	20199055	20199055	Missense_Mutation	SNP	C	T	C	MACC1	c.G929A	p.C310Y
XH_P52	7	23871865	23871865	Nonsense_Mutation	INS	-	ACAACCTCAACTA	-	STK31	AAAGATACAAC	17delinsVPNPEKOTERYX
XH_P52	7	27222510	27222510	Missense_Mutation	SNP	G	A	G	HOXA11	c.C847T	p.R283C
XH_P52	7	27222512	27222513	Frame_Shift_Del	DEL	TC	-	TC	HOXA11	c.844_845del	p.D282fs
XH_P52	7	36677494	36677494	Nonsense_Mutation	INS	-	CACTACA	-	AOAH	16_317insGTAA	106_K107delinsLX
XH_P52	7	43917013	43917013	Silent	SNP	G	A	G	URGCP	c.C2022T	p.H674H
XH_P52	7	44180652	44180652	Silent	SNP	G	T	G	MYL7	c.C25A	p.R9R
XH_P52	7	51096036	51096036	Missense_Mutation	SNP	G	C	G	COBL	c.C2757G	p.H919Q
XH_P52	7	77539714	77539714	Frame_Shift_Ins	INS	-	TCTTAATTTC	-	PHTF2	651insTCTTAA	p.F217fs
XH_P52	7	99123985	99123985	Missense_Mutation	SNP	G	A	G	ZKSCAN5	c.G1103A	p.R368H
XH_P52	7	99436371	99436371	Silent	SNP	A	G	A	CYP3A43	c.A237G	p.E79E
XH_P52	7	99821634	99821634	Silent	SNP	G	A	G	GATS	c.C282T	p.S94S
XH_P52	7	100634838	100634838	Missense_Mutation	SNP	C	A	C	MUC12	c.C994A	p.P332T
XH_P52	7	100635243	100635243	Missense_Mutation	SNP	C	A	C	MUC12	c.C1399A	p.P467T
XH_P52	7	100645902	100645902	Missense_Mutation	SNP	C	G	C	MUC12	c.C12058G	p.Q4020E
XH_P52	7	100685371	100685371	Silent	SNP	A	T	A	MUC17	c.A10674T	p.P3558P
XH_P52	7	100685372	100685372	Missense_Mutation	SNP	G	A	G	MUC17	c.G10675A	p.A3559T
XH_P52	7	113519356	113519356	Nonsense_Mutation	INS	-	AGGAGTTTGAA	-	PPP1R3A	AGTAGCTTCA	97_P598delinsTILX
XH_P52	7	114298258	114298258	Silent	SNP	T	C	T	FOX2	c.T1401C	p.S467S
XH_P52	7	114655971	114655971	Frame_Shift_Ins	INS	-	CACAACAATCTT	-	MDFC	724insCACAACA	p.G241fs
XH_P52	7	122194737	122194737	Nonsense_Mutation	INS	-	GAATTATTGAA	-	CADPS2	AATGAAATTCAB	Y449delinsNNTLXX

XH_P52	7	128587352	128587381	In_Frame_Del	DEL	CGCCCACTCT	-	CGCCCACTCTG	IRF5	c.502_531del	p.168_177del
XH_P52	7	141954986	141954986	Frame_Shift_Ins	INS	-	TTTCTATCATTTT	-	PRSS58	sGAGAAAAATGA	p.T109fs
XH_P52	7	142651310	142651310	Frame_Shift_Ins	INS	-	TCCTTCTCTTTTC	-	KEL	nsAGGAAAAAGA	p.Q295fs
XH_P52	7	143956137	143956137	Frame_Shift_Ins	INS	-	AATCCCTTCA	-	OR2A7	585insTAAGGG	p.T195fs
XH_P52	7	144062352	144062352	Missense_Mutation	SNP	A	G	A	ARHGEF5	c.A2590G	p.S864G
XH_P52	7	148801346	148801346	Silent	SNP	C	T	C	ZNF425	c.G1617A	p.A539A
XH_P52	7	150704250	150704250	Silent	SNP	C	G	C	NOS3	c.C1998G	p.A666A
XH_P52	7	156469190	156469190	Silent	SNP	A	G	A	RNF32	c.A930G	p.A310A
XH_P52	8	3046428	3046428	Missense_Mutation	SNP	G	C	G	CSMD1	c.C5504G	p.T1835R
XH_P52	8	10467335	10467335	Missense_Mutation	SNP	C	G	C	RP111	c.G4273C	p.D1425H
XH_P52	8	10469340	10469340	Silent	SNP	G	A	G	RP111	c.C2268T	p.N756N
XH_P52	8	12878677	12878677	Silent	SNP	T	C	T	KIAA1456	c.T111C	p.A37A
XH_P52	8	12878807	12878807	Missense_Mutation	SNP	T	G	T	KIAA1456	c.T241G	p.C81G
XH_P52	8	25265657	25265657	Missense_Mutation	SNP	A	C	A	DOCK5	c.A5252C	p.E1751A
XH_P52	8	25265658	25265658	Nonsense_Mutation	INS	-	TATGACTCTTTA	-	DOCK5	54insGTTATGAC	p.T1752delinsEVMTLX
XH_P52	8	37699516	37699516	Silent	SNP	C	T	C	ADGRA2	c.C3660T	p.G1220G
XH_P52	8	52733228	52733228	Missense_Mutation	SNP	G	A	G	PCMTD1	c.C529T	p.R177C
XH_P52	8	56015304	56015304	Missense_Mutation	SNP	C	T	C	XKR4	c.C256T	p.P86S
XH_P52	8	86389403	86389403	Silent	SNP	T	C	T	CA2	c.T259C	p.L87L
XH_P52	8	104898202	104898202	Missense_Mutation	SNP	C	T	C	RIMS2	c.C799T	p.H267Y
XH_P52	8	117783902	117783902	Frame_Shift_Ins	INS	-	CAAAATTCT	-	UTP23	1_572insCAAA	p.S191fs
XH_P52	8	117783903	117783903	Frame_Shift_Ins	INS	-	ATCC	-	UTP23	572_573insATC	p.S191fs
XH_P52	8	121021282	121021282	Silent	SNP	G	A	G	DEPTOR	c.G708A	p.A236A
XH_P52	8	131073058	131073058	In_Frame_Ins	INS	-	AGGAAC	-	ASAP1	58_2959insGTT	p.K987delinsVPK
XH_P52	8	131073060	131073060	Missense_Mutation	SNP	A	C	A	ASAP1	c.T2957G	p.M986G
XH_P52	8	131921955	131921955	Missense_Mutation	SNP	C	T	C	ADCY8	c.G1639A	p.G547R
XH_P52	8	144239783	144239783	Missense_Mutation	SNP	C	G	C	LY6H	c.G370C	p.D124H
XH_P52	8	144877249	144877249	Missense_Mutation	SNP	G	A	G	SCRIB	c.C3805T	p.R1269C
XH_P52	8	144945460	144945460	Silent	SNP	G	A	G	EPK1	c.C1962T	p.I654I
XH_P52	8	145665407	145665407	Missense_Mutation	SNP	C	T	C	TONSL	c.G1477A	p.G493S
XH_P52	8	145676044	145676044	Silent	SNP	G	A	G	CYHR1	c.C933T	p.N311N
XH_P52	9	14810	14810	Silent	SNP	C	G	C	WASHC1	c.G1395C	p.S465S
XH_P52	9	463650	463650	Nonsense_Mutation	INS	-	5AAATTACTTAC	-	DOCK8	insAATGAAATT	p.968_1969delinsQX
XH_P52	9	8528771	8528771	Nonsense_Mutation	INS	-	TTTCTCTCTCTT	-	PTPRD	AAATAAGGAGAG	p.122delinsLKLIRREKNX
XH_P52	9	34725432	34725432	Missense_Mutation	SNP	C	T	C	FAM205A	c.G1805A	p.R602H
XH_P52	9	35906348	35906353	In_Frame_Del	DEL	CTGCTG	-	CTGCTG	HRCT1	c.64_69del	p.22_23del
XH_P52	9	86279960	86279960	Missense_Mutation	SNP	G	A	G	UBQLN1	c.C1349T	p.P450L
XH_P52	9	91083368	91083368	Frame_Shift_Ins	INS	-	AACAGAAATAGAA	-	SPIN1	sATTCAACAGAA	p.G146fs
XH_P52	9	93641151	93641151	Silent	SNP	T	C	T	SYK	c.T1428C	p.N476N
XH_P52	9	104238523	104238523	Silent	SNP	G	A	G	TMEM246	c.C852T	p.A284A
XH_P52	9	105767373	105767373	Frame_Shift_Ins	INS	-	ATTAC	-	CYL2	460_461insATT	p.K154fs
XH_P52	9	105767375	105767375	Frame_Shift_Ins	INS	-	AGATA	-	CYL2	462_463insAGA	p.K154fs
XH_P52	9	105767852	105767852	In_Frame_Ins	INS	-	TTTACA	-	CYL2	39_940insTTT	p.A313delinsAFT
XH_P52	9	105767853	105767853	In_Frame_Ins	INS	-	CTTGTA	-	CYL2	40_941insCTTG	p.D314delinsACN
XH_P52	9	112898488	112898488	Frame_Shift_Ins	INS	-	CGTGACAGGG	-	AKAP2	CGCTCGTGAG	p.A80fs
XH_P52	9	114994482	114994482	Missense_Mutation	SNP	G	A	G	PTBP3	c.C716T	p.P239L
XH_P52	9	115933969	115933969	In_Frame_Ins	INS	-	5TTTGTTGTTTG	-	FKBP15	50insTCAAACAA	p.85delinsAQTNKH
XH_P52	9	115933971	115933971	Missense_Mutation	SNP	C	A	C	FKBP15	c.G2548T	p.A850S
XH_P52	9	129453229	129453229	Silent	SNP	A	G	A	LMX1B	c.A441G	p.E147E
XH_P52	9	130495633	130495633	Missense_Mutation	SNP	C	G	C	TOR2A	c.G624C	p.W208C
XH_P52	9	131469191	131469191	Silent	SNP	G	A	G	PKN3	c.G540A	p.A180A
XH_P52	9	135946599	135946599	Silent	SNP	C	T	C	CEL	c.C1719T	p.P573P
XH_P52	9	136379890	136379890	Silent	SNP	A	G	A	MYMK	c.T534C	p.Y178Y
XH_P52	9	136412170	136412170	Silent	SNP	C	T	C	ADAMTSL2	c.C774T	p.D258D
XH_P52	9	136561367	136561367	Silent	SNP	G	A	G	SARDH	c.C1785T	p.S595S
XH_P52	9	137711997	137711997	Silent	SNP	G	G	G	COL5A1	c.G4482C	p.P1494P
XH_P52	9	139750515	139750515	Missense_Mutation	SNP	A	T	A	MAMDC4	c.A1634T	p.E545V
XH_P52	10	5541181	5541181	Missense_Mutation	SNP	T	C	T	CALML5	c.A221G	p.K74R
XH_P52	10	5541183	5541183	Silent	SNP	C	T	C	CALML5	c.G219A	p.A73A
XH_P52	10	13214710	13214710	Frame_Shift_Ins	INS	-	TTTAATTGTTGT	-	MCM10	8insTGTTTAATT	p.V179fs
XH_P52	10	13214712	13214712	Missense_Mutation	SNP	C	T	C	MCM10	c.C539T	p.P180L
XH_P52	10	26463315	26463315	Frame_Shift_Ins	INS	-	CTTTTTC	-	MYO3A	22_4123insCTTT	p.F1374fs
XH_P52	10	26463317	26463317	Missense_Mutation	SNP	A	T	A	MYO3A	c.A4124T	p.K1375M
XH_P52	10	27688100	27688100	Missense_Mutation	SNP	C	T	C	PTCHD3	c.G1427A	p.R476Q
XH_P52	10	30317059	30317059	Frame_Shift_Ins	INS	-	AAGGACT	-	JCAD	17_2018insAGT	p.R673fs
XH_P52	10	73544086	73544086	Missense_Mutation	SNP	G	A	G	CDH23	c.G5411A	p.R1804Q
XH_P52	10	73767859	73767859	Missense_Mutation	SNP	G	A	G	CHST3	c.G1070A	p.R357Q
XH_P52	10	74890538	74890538	Nonsense_Mutation	INS	-	AAGAAATGAGA	-	NUDT13	TAATTAAGAAAT	p.13_224delinsKRHNX
XH_P52	10	75530064	75530064	Silent	SNP	C	T	C	SEC24C	c.C2889T	p.T963T
XH_P52	10	78647070	78647070	Nonsense_Mutation	INS	-	TTTACACATATT	-	KCNMA1	ATGCAAAATATG	p.14_E1115delinsICKYVX
XH_P52	10	88994266	88994268	In_Frame_Del	DEL	CTC	-	CTC	NUTM2A	c.2438_2440del	p.813_814del
XH_P52	10	98741863	98741863	Nonsense_Mutation	INS	-	GTCTGTGATGGA	-	LCOR	sGAGCTGTCTTG	p.49delinsPSCLDGGX
XH_P52	10	99079214	99079214	Missense_Mutation	SNP	C	T	C	FRAT1	c.C4T	p.P2S
XH_P52	10	101480780	101480780	In_Frame_Ins	INS	-	TTCTCTCTCCAA	-	COX15	6insTTTGGAAG	p.266delinsFGREKG
XH_P52	10	104414960	104414977	In_Frame_Del	DEL	ACGCAGCGC	-	AACGCAGCGCAG	TRIM8	c.694_711del	p.232_237del
XH_P52	10	104934709	104934709	Missense_Mutation	SNP	T	C	T	NT5C2	c.A7G	p.T3A
XH_P52	10	105762762	105762762	Missense_Mutation	SNP	A	G	A	SLK	c.A1826G	p.N609S
XH_P52	10	108367020	108367020	Silent	SNP	C	T	C	SORCS1	c.G3069A	p.A1023A
XH_P52	10	126714714	126714714	Missense_Mutation	SNP	G	C	G	CTBP2	c.C1615G	p.Q539E
XH_P52	10	127426948	127426948	Missense_Mutation	SNP	G	A	G	EDRF1	c.G1813A	p.E605K
XH_P52	10	134942832	134942832	Silent	SNP	G	A	G	ADGRA1	c.G1209A	p.P403P
XH_P52	11	1262907	1262907	Silent	SNP	T	C	T	MUC5B	c.T4797C	p.S1599S
XH_P52	11	1271940	1271940	Silent	SNP	G	A	G	MUC5B	c.G13830A	p.G4610G
XH_P52	11	6520164	6520164	Missense_Mutation	SNP	T	A	T	DNH1D	c.T719A	p.V240E
XH_P52	11	6559701	6559701	Silent	SNP	C	T	C	DNH1D	c.C3087T	p.S1029S
XH_P52	11	8751640	8751640	Missense_Mutation	SNP	G	C	G	ST5	c.C1197G	p.D399E
XH_P52	11	19955278	19955278	Missense_Mutation	SNP	G	C	G	NAV2	c.G1296C	p.K432N
XH_P52	11	45248372	45248372	Silent	SNP	T	C	T	PRDM11	c.T2196C	p.D732D
XH_P52	11	57093913	57093913	Frame_Shift_Ins	INS	-	ACAT	-	SSRP1	097_2098insAT	p.S700fs
XH_P52	11	57093915	57093915	Frame_Shift_Ins	INS	-	TCTCCTG	-	SSRP1	5_2096insCAG	p.S699fs
XH_P52	11	57583452	57583452	Frame_Shift_Ins	INS	-	AAAA	-	CTNND1	490_2491insAA	p.G830fs
XH_P52	11	57583454	57583454	Nonsense_Mutation	INS	-	TCATAAACAGG	-	CTNND1	493insTTCATAA	p.831_V832delinsHSX
XH_P52	11	57983115	57983115	Nonsense_Mutation	INS	-	ACAATAAACAA	-	OR151	900insACAATAA	p.800_F301delinsPQX
XH_P52	11	58379144	58379144	Nonsense_Mutation	INS	-	AGAGTTATCACT	-	ZFP91	nsCTTAGAGTTA	p.263_E264delinsAX
XH_P52	11	62289451	62289451	Silent	SNP	G	A	G	AHNAK	c.C12438T	p.D4146D
XH_P52	11	62295157	62295157	Silent	SNP	A	G	A	AHNAK	c.T6732C	p.P2244P
XH_P52	11	62295701	62295701	Missense_Mutation	SNP	G	C	G	AHNAK	c.C6188G	p.A2063G
XH_P52	11	62297449	62297449	Missense_Mutation	SNP	T	C	T	AHNAK	c.A4440G	p.L1480M

XH_P52	11	65168281	65168281	Silent	SNP	C	T	C	FRMD8	c.C846T	p.F282F
XH_P52	11	68704028	68704028	Missense_Mutation	SNP	C	T	C	IGHMBP2	c.C2080T	p.R694W
XH_P52	11	75298454	75298454	Missense_Mutation	SNP	C	A	C	MAP6	c.G2092T	p.V698F
XH_P52	11	82443672	82443672	Missense_Mutation	SNP	C	G	C	FAM181B	c.G1100C	p.R367P
XH_P52	11	82535963	82535963	Silent	SNP	C	T	C	PRCP	c.G1161A	p.A387A
XH_P52	11	85593692	85593692	Frame_Shift_Ins	INS	-	TC	-	CCDC83	c.317_318insTC	p.E106fs
XH_P52	11	85593694	85593694	Frame_Shift_Ins	INS	-	CTATGTACACTA	-	CCDC83	320insCTATGTGA	p.R107fs
XH_P52	11	102272889	102272889	Nonsense_Mutation	INS	-	ACATCTCAGA	-	TMEM123	206insTCTGAG	569_170delinsX
XH_P52	11	120187999	120187999	Silent	SNP	C	T	C	POU2F3	c.C1203T	p.H401H
XH_P52	11	120998531	120998531	Silent	SNP	C	T	C	TECTA	c.C1845T	p.S615S
XH_P52	11	124739504	124739504	Splice_Site	INS	-	AGGAC	-	ROBO3	-	-
XH_P52	11	132290143	132290143	In_Frame_Ins	INS	-	TTTTGTTTTTTC	-	OPCML	AACAGAAAAA	delinsSRITEKNKKPKKL
XH_P52	12	569586	569599	Frame_Shift_Del	DEL	GTGAAGCTG	-	GGTGAAGCTGCT	B4GALNT3	c.44_57del	p.P15fs
XH_P52	12	1955786	1955786	Silent	SNP	G	A	G	CACNA2D4	c.C2316T	p.F772F
XH_P52	12	6573636	6573636	Nonstop_Mutation	INS	-	AAGTCATTA	-	VAMP1	5_357insTAATG	X119delinsCNDL
XH_P52	12	8374781	8374781	In_Frame_Ins	INS	-	ACG	-	FAM90A1	1031_1032insCTp	T344delinsTV
XH_P52	12	9232268	9232268	Missense_Mutation	SNP	T	C	T	A2M	c.A2548G	p.I850V
XH_P52	12	11150054	11150054	Missense_Mutation	SNP	C	T	C	TAS2R20	c.G421A	p.V141I
XH_P52	12	11183485	11183485	Frame_Shift_Ins	INS	-	GA	-	TAS2R31	c.449_450insTC	p.K150fs
XH_P52	12	11420289	11420289	In_Frame_Ins	INS	-	CAATGACAGGTA	-	PRB3	767insTACCTGT	K256delinsIPVIE
XH_P52	12	13220191	13220191	Missense_Mutation	SNP	G	A	G	FAM234B	c.G1103A	p.R368Q
XH_P52	12	13717508	13717508	Silent	SNP	G	A	G	GRIN2B	c.C2664T	p.T888T
XH_P52	12	32134943	32134943	Missense_Mutation	SNP	A	G	A	KIAA1551	c.A1054G	p.S352G
XH_P52	12	32138031	32138031	Frame_Shift_Ins	INS	-	ACCTCAATTTTT	-	KIAA1551	143insACCTCA	p.N1381fs
XH_P52	12	32138033	32138033	Missense_Mutation	SNP	G	T	G	KIAA1551	c.G4144T	p.V1382L
XH_P52	12	40114672	40114672	Missense_Mutation	SNP	T	G	T	C12orf40	c.T1578G	p.N526K
XH_P52	12	48596416	48596416	Frame_Shift_Ins	INS	-	A	-	OR10AD1	c.659dupT	p.V220fs
XH_P52	12	48596418	48596418	Nonsense_Mutation	INS	-	CCCATCATTT	-	OR10AD1	658insAAATGA	220_H221delinsKX
XH_P52	12	49444545	49444545	Silent	SNP	G	A	G	KMT2D	c.C2826T	p.I942I
XH_P52	12	51707626	51707626	Missense_Mutation	SNP	C	T	C	BIN2	c.G65A	p.S22N
XH_P52	12	52866060	52866060	Missense_Mutation	SNP	C	T	C	KRT6C	c.G545A	p.R182Q
XH_P52	12	52938320	52938320	Missense_Mutation	SNP	C	T	C	KRT71	c.G1568A	p.R523Q
XH_P52	12	52994955	52994955	Silent	SNP	G	A	G	KRT72	c.C282T	p.P94P
XH_P52	12	53162773	53162775	In_Frame_Del	DEL	ACT	-	ACT	KRT76	c.1639_1641del	p.547_547del
XH_P52	12	56558464	56558464	Missense_Mutation	SNP	G	C	G	SMARCC2	c.C3191G	p.A1064G
XH_P52	12	56558465	56558465	Missense_Mutation	SNP	C	T	C	SMARCC2	c.G3190A	p.A1064T
XH_P52	12	57976915	57976915	Missense_Mutation	SNP	G	A	G	KIF5A	c.G3052A	p.D1018N
XH_P52	12	62946922	62946922	Nonsense_Mutation	SNP	C	T	C	MON2	c.C3178T	p.Q1060X
XH_P52	12	68696642	68696642	Nonsense_Mutation	INS	-	TGTAATTATTTT	-	MDM1	25insCAAAATAA	542_A543delinsPKX
XH_P52	12	68696644	68696645	Frame_Shift_Del	DEL	AC	-	AC	MDM1	c.1622_1623del	p.S541fs
XH_P52	12	76424934	76424934	Frame_Shift_Del	DEL	C	-	C	PHLDA1	c.S588delG	p.Q196fs
XH_P52	12	76424936	76424940	Frame_Shift_Del	DEL	GTTGC	-	GTTGC	PHLDA1	c.S582_586del	p.Q194fs
XH_P52	12	93772199	93772199	Splice_Site	INS	-	GCTGCTGGTG	-	NUDT4	-	-
XH_P52	12	94243853	94243853	Silent	SNP	C	T	C	CRADD	c.C406T	p.L136L
XH_P52	12	94976125	94976125	Missense_Mutation	SNP	C	A	C	TMCC3	c.G175T	p.D59Y
XH_P52	12	102079418	102079418	Silent	SNP	G	A	G	MYBP1	c.G3378A	p.S1126S
XH_P52	12	108686305	108686305	Frame_Shift_Ins	INS	-	TCCTCATC	-	CMKLR1	4_435insGATGA	p.V145fs
XH_P52	12	113831813	113831813	Nonsense_Mutation	INS	-	SAATTTTTCATTA	-	SDS	52insTTAATGGGA	221delinsINGKFX
XH_P52	12	117484632	117484632	Missense_Mutation	SNP	T	C	T	TESC	c.A280G	p.M94V
XH_P52	12	120436485	120436485	Missense_Mutation	SNP	G	A	G	BICDL1	c.G590A	p.R197Q
XH_P52	12	120784018	120784018	Missense_Mutation	SNP	C	T	C	MSI1	c.G967A	p.A323T
XH_P52	12	122672307	122672307	Silent	SNP	C	T	C	LRRCA3	c.C582T	p.P194P
XH_P52	12	123834966	123834966	Nonsense_Mutation	INS	-	TTTTTTTTT	-	SBNO1	2_23insAAAAAA	p.L8delinsX
XH_P52	12	123834968	123834968	Frame_Shift_Ins	INS	-	GATAG	-	SBNO1	c.20_21insCTAT	p.D7fs
XH_P52	12	125570959	125570959	In_Frame_Ins	INS	-	ATCCCCACTGTT	-	AACS	443insATCCCCAC	M148delinsNPCTL
XH_P52	12	133393323	133393323	Missense_Mutation	SNP	C	T	C	GOLGA3	c.G209A	p.G70E
XH_P52	13	20398621	20398621	Missense_Mutation	SNP	G	A	G	ZMYM5	c.C2006T	p.T669M
XH_P52	13	25419186	25419186	Frame_Shift_Ins	INS	-	ATACAAAATGCA	-	RNF17	071insAATAACA	p.L1024fs
XH_P52	13	40229970	40229970	Missense_Mutation	SNP	C	T	C	COG6	c.C107T	p.S36L
XH_P52	13	53217314	53217314	Frame_Shift_Ins	INS	-	A	-	HNRNPA1L2	c.687_688insA	p.G229fs
XH_P52	13	53217316	53217316	Nonsense_Mutation	INS	-	GCTTTTCTAA	-	HNRNPA1L2	690insGCTTTT	30_S231delinsGLFX
XH_P52	13	74387319	74387319	Missense_Mutation	SNP	G	A	G	KLF12	c.C776T	p.T259M
XH_P52	13	77641983	77641983	Nonsense_Mutation	INS	-	GATTTTCAATTC	-	MYCBP2	8insCCTGGAATT	53_R4064delinsTWNX
XH_P52	13	77831948	77831948	In_Frame_Ins	INS	-	TCITTTTGTTCCT	-	MYCBP2	sAAATAGGAACA	478delinsLNRNKKKK
XH_P52	13	113527967	113527967	Silent	SNP	G	A	G	ATP11A	c.G3138A	p.S1046S
XH_P52	13	113536132	113536132	Silent	SNP	T	C	T	ATP11A	c.T3330C	p.N1110N
XH_P52	13	115067278	115067278	Frame_Shift_Ins	INS	-	TAAATCATAGTA	-	UPF3A	sGGGAATAAATCA	p.R327fs
XH_P52	14	20852056	20852056	In_Frame_Ins	INS	-	ACTTCCTCT	-	TEP1	3232insAGAG	Q1078delinsRGSQ
XH_P52	14	21992122	21992122	In_Frame_Ins	INS	-	CCTACGCTT	-	SALL2	1740insAGGCC	E580delinsEGVG
XH_P52	14	21992124	21992124	Frame_Shift_Ins	INS	-	AT	-	SALL2	1737_1738insA	p.E580fs
XH_P52	14	23855569	23855569	Silent	SNP	A	G	A	MYH6	c.T4914C	p.A1638A
XH_P52	14	24545366	24545366	Silent	SNP	T	C	T	CPNE6	c.T933C	p.I311I
XH_P52	14	24617238	24617238	Silent	SNP	C	T	C	RNF31	c.C246T	p.Y82Y
XH_P52	14	45716108	45716108	Nonsense_Mutation	INS	-	AAGAGGTTAGT	-	MSI18BP1	insTAAACTAAC	p.E128delinsX
XH_P52	14	52520475	52520475	Silent	SNP	G	A	G	NID2	c.C1251T	p.N417N
XH_P52	14	64908845	64908845	Missense_Mutation	SNP	G	A	G	MTHFD1	c.G1958A	p.R653Q
XH_P52	14	71275774	71275779	In_Frame_Del	DEL	CCTCCT	-	CCTCCT	MAP3K9	c.110_115del	p.37_39del
XH_P52	14	73989117	73989117	Missense_Mutation	SNP	C	T	C	HEATR4	c.G740A	p.R247Q
XH_P52	14	74424908	74424908	Nonsense_Mutation	INS	-	AAAAAATCAGTA	-	COQ6	GATTAAAAAAAT	P181delinsFKIKISNX
XH_P52	14	75052566	75052583	In_Frame_Del	DEL	ACTGTGGTGG	-	GACTGTGGTGGC	LTBP2	c.804_821del	p.268_274del
XH_P52	14	86088869	86088869	Missense_Mutation	SNP	C	G	C	FLRT2	c.C1011G	p.F337L
XH_P52	14	88652389	88652389	Silent	SNP	C	T	C	KCNK10	c.G1107A	p.A369A
XH_P52	14	91444862	91444862	Frame_Shift_Ins	INS	-	TTTGGGT	-	RPS6KA5	81_182insACCC	p.G61fs
XH_P52	14	91444863	91444863	Frame_Shift_Ins	INS	-	TTAAGTT	-	RPS6KA5	80_181insAACT	p.G61fs
XH_P52	14	93708768	93708768	Missense_Mutation	SNP	C	T	C	BTBD7	c.G2197A	p.E733K
XH_P52	14	101350670	101350670	In_Frame_Ins	INS	-	TCT	-	RTL1	455_456insAG	p.E152delinsEE
XH_P52	14	102973911	102973911	Missense_Mutation	SNP	C	T	C	ANKRD9	c.G316A	p.G106S
XH_P52	14	104618546	104618546	Silent	SNP	C	G	C	KIF26A	c.C483G	p.L161L
XH_P52	14	105414578	105414578	Missense_Mutation	SNP	G	C	G	AHNAK2	c.C6910G	p.L2304V
XH_P52	14	105414804	105414804	Silent	SNP	A	G	A	AHNAK2	c.T6684C	p.F2228F
XH_P52	14	105417894	105417894	Missense_Mutation	SNP	C	G	C	AHNAK2	c.G3594C	p.M1198I
XH_P52	14	105418275	105418275	Silent	SNP	T	C	T	AHNAK2	c.A3213G	p.P1071P
XH_P52	14	105930406	105930406	Missense_Mutation	SNP	G	A	G	MTA1	c.G1114A	p.P372I
XH_P52	15	30010728	30010728	In_Frame_Ins	INS	-	ATGTCTTTAGTG	-	TJP1	3378insCACTAA	51126delinsGTKDI
XH_P52	15	50773945	50773945	Frame_Shift_Ins	INS	-	GTTGCTCATGGT	-	USP8	nsGATTGTGTCT	p.K419fs
XH_P52	15	56258734	56258734	Missense_Mutation	SNP	C	T	C	NEDD4	c.G56A	p.R19Q
XH_P52	15	64791850	64791850	Frame_Shift_Ins	INS	-	CTTTCCTA	-	ZNF609	82_233insCTTTC	p.V78fs
XH_P52	15	65412101	65412101	Nonsense_Mutation	INS	-	CATGAGCTCAGT	-	PDCD7	201insGACTGAG	401_L402delinsDX

XH_P52	15	69324003	69324003	Silent	SNP	C	T	C	NOX5	c.C387T	p.S129S
XH_P52	15	73615056	73615056	Silent	SNP	G	A	G	HCN4	c.C3378T	p.S1126S
XH_P52	15	75980112	75980112	Silent	SNP	A	G	A	CSPG4	c.T3294C	p.A1098A
XH_P52	15	76017452	76017452	Missense_Mutation	SNP	C	T	C	ODF3L1	c.C122T	p.A141L
XH_P52	15	77907535	77907535	Silent	SNP	C	G	C	LINGO1	c.G714C	p.L238L
XH_P52	15	79277511	79277511	Silent	SNP	A	G	A	RASGRF1	c.T948C	p.N316N
XH_P52	15	79749155	79749155	Silent	SNP	C	T	C	KIAA1024	c.C666T	p.N222N
XH_P52	15	82532827	82532827	Missense_Mutation	SNP	G	A	G	EF1I	c.C295T	p.R99C
XH_P52	15	82935129	82935129	Missense_Mutation	SNP	C	G	G	GOLGA6L10	c.G451C	p.E151Q
XH_P52	15	86124735	86124735	In_Frame_Ins	INS	-	CAC	-	AKAP13	3436_3437insCA	G1146delinsAR
XH_P52	15	86124736	86124736	Missense_Mutation	SNP	G	T	G	AKAP13	c.G3437T	p.G1146V
XH_P52	15	89391160	89391160	Silent	SNP	C	A	C	ACAN	c.C1623A	p.P541P
XH_P52	15	90196008	90196008	Missense_Mutation	SNP	C	T	C	KIF7	c.G154A	p.D52N
XH_P52	15	91461605	91461605	Missense_Mutation	SNP	C	T	C	MAN2A2	c.C3176T	p.T1059M
XH_P52	15	91795625	91795625	In_Frame_Ins	INS	-	GACATTGCA	-	SV2B	5_207insGACAT	b.F69delinsLT
XH_P52	16	223569	223569	Silent	SNP	G	T	G	HBA2	c.G399T	p.V133V
XH_P52	16	1259077	1259077	Missense_Mutation	SNP	G	A	G	CACNA1H	c.G3409A	p.A1137T
XH_P52	16	1265345	1265345	Missense_Mutation	SNP	C	T	C	CACNA1H	c.C5125T	p.R1709C
XH_P52	16	1506113	1506113	Splice_Site	SNP	C	G	C	CLCN7	-	-
XH_P52	16	2028210	2028210	Missense_Mutation	SNP	G	A	G	TBL3	c.G2123A	p.R708H
XH_P52	16	2287813	2287813	Missense_Mutation	SNP	C	T	C	DNASE1L2	c.C637T	p.R213W
XH_P52	16	2347906	2347906	Missense_Mutation	SNP	C	T	C	ABCA3	c.G1913A	p.R638H
XH_P52	16	3534892	3534892	Missense_Mutation	SNP	G	A	G	NAA60	c.G539A	p.R180Q
XH_P52	16	11260315	11260332	In_Frame_Del	DEL	GGGAGCCCC	-	CGGGAGCCCCAG	CLEC16A	c.2712_2729del	p.904_910del
XH_P52	16	21128599	21128599	Missense_Mutation	SNP	G	T	G	DNAH3	c.C1559A	p.A520E
XH_P52	16	22144318	22144318	Missense_Mutation	SNP	C	T	C	VWA3A	c.C1970T	p.T657I
XH_P52	16	28354179	28354179	Missense_Mutation	SNP	T	G	T	NPIPB6	c.A1027C	p.K343Q
XH_P52	16	28846701	28846701	Missense_Mutation	SNP	C	T	C	ATXN2L	c.C2684T	p.A895V
XH_P52	16	50102759	50102759	Nonsense_Mutation	INS	-	TTCTATTTTAGC	-	HEATR3	TTTATTTCCTATT	V128delinsLTFISIFSHIX
XH_P52	16	50187912	50187929	In_Frame_Del	DEL	GGCGTCCTCC	-	CGGCGTCCTCCG	PAPD5	c.335_352del	p.112_118del
XH_P52	16	57983275	57983277	In_Frame_Del	DEL	TCC	-	TCC	CNGB1	c.1083_1085del	p.361_362del
XH_P52	16	58542901	58542901	Silent	SNP	G	A	G	NDRG4	c.G819A	p.T273T
XH_P52	16	58713798	58713798	Missense_Mutation	SNP	G	A	G	SLC38A7	c.C233T	p.T78I
XH_P52	16	69681120	69681120	Nonsense_Mutation	INS	-	TAAATACACAT	-	NFAT5	sAGAGTAAATAC	30_Q131delinsQEX
XH_P52	16	72993515	72993515	Missense_Mutation	SNP	G	A	G	ZFH3	c.C530T	p.A177V
XH_P52	16	75563330	75563330	Missense_Mutation	SNP	G	A	G	CHST5	c.C953T	p.T318M
XH_P52	16	87678165	87678165	Silent	SNP	G	A	G	JPH3	c.G684A	p.S228S
XH_P52	16	88599023	88599023	Silent	SNP	A	G	A	ZFPM1	c.A948G	p.G316G
XH_P52	16	88902183	88902183	Silent	SNP	G	A	G	GALN5	c.C153T	p.H51H
XH_P52	16	89590528	89590528	Missense_Mutation	SNP	G	A	G	SPG7	c.G491A	p.S164N
XH_P52	16	89717979	89717979	In_Frame_Ins	INS	-	GAGGTA	-	CHMP1A	.82_83insTACCT	b.E28delinsVPO
XH_P52	16	89717980	89717980	Frame_Shift_Ins	INS	-	TATATATATATA	-	CHMP1A	2insATATATATA	p.E28fs
XH_P52	17	3643130	3643130	Nonsense_Mutation	INS	-	TTATTATCTCAA	-	ITGAE	1insATATTGAG	831_E832delinsLRLX
XH_P52	17	4439623	4439623	Silent	SNP	C	T	C	SPNS2	c.C1509T	p.Y503Y
XH_P52	17	4461748	4461748	Nonsense_Mutation	SNP	G	A	G	GGT6	c.C358T	p.R120X
XH_P52	17	4875805	4875805	Missense_Mutation	SNP	C	T	C	CAMTA2	c.G2536A	p.E846K
XH_P52	17	4875806	4875806	Frame_Shift_Ins	INS	-	AGAT	-	CAMTA2	2534_2535insAT	p.S545fs
XH_P52	17	4927256	4927256	Missense_Mutation	SNP	G	A	G	KIF1C	c.G3122A	p.R1041Q
XH_P52	17	5347576	5347576	Silent	SNP	G	A	G	DHX33	c.C1554T	p.Y518Y
XH_P52	17	7129840	7129840	Silent	SNP	T	C	T	DVL2	c.A1662G	p.Q554Q
XH_P52	17	7132556	7132556	Silent	SNP	C	T	C	DVL2	c.G855A	p.Q285Q
XH_P52	17	7154582	7154582	Missense_Mutation	SNP	T	C	T	CTDNEP1	c.A34G	p.T12A
XH_P52	17	7726785	7726785	Nonsense_Mutation	INS	-	TTTTTTTTTTGAG	-	DNAH2	ATTTTTTTTTTTT	3723delinsEFFFFX
XH_P52	17	7809012	7809012	Silent	SNP	G	A	G	CHD3	c.G4389A	p.G1463G
XH_P52	17	10236472	10236472	Missense_Mutation	SNP	C	T	C	MYH13	c.G2093A	p.R698H
XH_P52	17	16692394	16692394	In_Frame_Ins	INS	-	AGCTTCTCTGAA	-	FAM106CP	AAAGAGCTCTCC	60delinsAKELPLRN
XH_P52	17	17124815	17124815	Missense_Mutation	SNP	C	T	C	FLCN	c.G907A	p.G303R
XH_P52	17	20109149	20109149	In_Frame_Ins	INS	-	CATTCA	-	SPECC1	44_154SinsCAT	b.L51SdelinsLIQ
XH_P52	17	20109150	20109150	Frame_Shift_Ins	INS	-	TTTTTCATT	-	SPECC1	5_1546insTTTTT	p.L515fs
XH_P52	17	20911204	20911204	Silent	SNP	G	T	G	USP22	c.C1209A	p.I403I
XH_P52	17	26964143	26964143	In_Frame_Ins	INS	-	TTTTTTTTTTTTC	-	KIAA0100	sACAAGAAAAA	506delinsDKKKKKKT
XH_P52	17	27248819	27248819	Missense_Mutation	SNP	G	C	G	PHF12	c.C723G	p.S241R
XH_P52	17	27248820	27248820	Frame_Shift_Ins	INS	-	AGACCATTGA	-	PHF12	722insTACATG	p.S241fs
XH_P52	17	28380902	28380902	In_Frame_Ins	INS	-	TCTACTTGACCC	-	EFCAB5	3insCCTTCTACT	588delinsFVTLV
XH_P52	17	28512639	28512639	Frame_Shift_Ins	INS	-	TTTCTCATTTTG	-	NSRP1	63insTGTTTCTC	p.R488fs
XH_P52	17	33814758	33814758	Missense_Mutation	SNP	T	C	T	SLFN12L	c.A1G	p.M1V
XH_P52	17	34072898	34072898	Missense_Mutation	SNP	C	T	C	GAS2L2	c.G1618A	p.A540T
XH_P52	17	37381697	37381697	Missense_Mutation	SNP	G	T	G	STAC2	c.C59A	p.P20Q
XH_P52	17	38818215	38818215	Missense_Mutation	SNP	G	A	G	KRT222	c.C178T	p.R60C
XH_P52	17	39296254	39296254	Silent	SNP	C	T	C	KRTAP4-6	c.G486A	p.P162P
XH_P52	17	39334306	39334306	Silent	SNP	G	A	G	KRTAP4-2	c.C111T	p.R37R
XH_P52	17	39681485	39681494	Frame_Shift_Del	DEL	GCAGGACAA	-	TGCAGGACAA	KRT19	c.452_461del	p.L151fs
XH_P52	17	42981654	42981654	Missense_Mutation	SNP	A	G	A	FAM187A	c.A457G	p.K153E
XH_P52	17	48761105	48761105	Silent	SNP	C	T	C	ABCC3	c.C3942T	p.H1314H
XH_P52	17	51901385	51901385	Silent	SNP	C	T	C	KIF2B	c.C991T	p.L331L
XH_P52	17	59560350	59560350	Missense_Mutation	SNP	C	G	C	TBX4	c.C1111G	p.P371A
XH_P52	17	63052634	63052634	Silent	SNP	C	T	C	GNA13	c.G78A	p.E26E
XH_P52	17	65822410	65822410	Silent	SNP	G	A	G	BPTF	c.G570A	p.T190T
XH_P52	17	67522793	67522793	Missense_Mutation	SNP	C	T	C	MAP2K6	c.C656T	p.S219L
XH_P52	17	76046971	76046971	In_Frame_Ins	INS	-	CGCTTT	-	TNRC6C	28_1829insCGG	G610delinsALVW
XH_P52	17	76131070	76131070	Silent	SNP	G	A	G	TMC8	c.G1107A	p.E369E
XH_P52	17	76166939	76166939	Silent	SNP	C	G	C	SYNGR2	c.C141G	p.G47G
XH_P52	17	76178751	76178751	Silent	SNP	C	T	C	TK1	c.G222A	p.E74E
XH_P52	17	76525759	76525759	Missense_Mutation	SNP	G	C	G	DNAH17	c.C3302G	p.A1101G
XH_P52	17	80350331	80350331	Silent	SNP	G	A	G	OGFOD3	c.C903T	p.I301I
XH_P52	18	9258456	9258456	Frame_Shift_Ins	INS	-	TCTCCAGTTTGT	-	ANKRD12	123insCTCTCCA	p.I708fs
XH_P52	18	9886248	9886248	Frame_Shift_Ins	INS	-	GTTCACAGTTGG	-	TXNDC2	78insGTTACAG	p.T26fs
XH_P52	18	13116432	13116432	Missense_Mutation	SNP	G	T	G	CEP192	c.G7346T	p.R2449L
XH_P52	18	13731869	13731869	In_Frame_Ins	INS	-	ACTCTTTTCTCTT	-	RNMT	insAAACTCTTTT	118delinsSNSFLFL
XH_P52	18	19433150	19433150	Frame_Shift_Ins	INS	-	CATCTTTATAT	-	MIB1	2637insCATCT	p.Q879fs
XH_P52	18	29419411	29419411	Nonsense_Mutation	INS	-	TCAAAAAAGGT	-	TRAPPC8	3847insAACCTT	B3_M1284delinsNLFX
XH_P52	18	29419413	29419413	Nonsense_Mutation	INS	-	AGCTTTTATTTTT	-	TRAPPC8	3845insAAAAAT	P1282delinsQKX
XH_P52	18	47107855	47107855	Silent	SNP	G	A	G	LIPG	c.G642A	p.Q214Q
XH_P52	18	50589756	50589756	Frame_Shift_Ins	INS	-	TAGAAAAATATT	-	DCC	68insGATAGAA	p.G356fs
XH_P52	18	56054729	56054729	In_Frame_Ins	INS	-	AAACAACTTTT	-	NEDD4L	124insAAAAACAA	708delinsEKQTF
XH_P52	18	77894844	77894844	Silent	SNP	G	A	G	ADNP2	c.G1548A	p.P516P
XH_P52	19	830854	830854	Silent	SNP	T	C	T	AZU1	c.T507C	p.F169F
XH_P52	19	1010836	1010836	Missense_Mutation	SNP	C	T	C	TMEM259	c.G1376A	p.R459H

XH_P52	19	1082936	1082936	Missense_Mutation	SNP	G	A	G	ARHGAP45	c.G1520A	p.R507Q
XH_P52	19	1085966	1085966	Silent	SNP	A	G	A	ARHGAP45	c.A2277G	p.T759T
XH_P52	19	3206400	3206400	Silent	SNP	G	A	G	NCLN	c.G1473A	p.Q491Q
XH_P52	19	3753769	3753769	Silent	SNP	C	T	C	APBA3	c.G1005A	p.A335A
XH_P52	19	4028553	4028553	Silent	SNP	G	A	G	PIA5A	c.G627A	p.P209P
XH_P52	19	8176009	8176009	Silent	SNP	C	T	C	FBN3	c.G4143A	p.A1381A
XH_P52	19	9077702	9077702	Nonsense_Mutation	INS	-	CAACCTTTAT	-	MUC16	9744insATAAA	248_S3249delinsCX
XH_P52	19	10401994	10401994	Missense_Mutation	SNP	C	A	C	ICAM5	c.C329A	p.A110E
XH_P52	19	13445284	13445284	Missense_Mutation	SNP	C	T	C	CACNA1A	c.G1106A	p.R369Q
XH_P52	19	16339715	16339715	Silent	SNP	C	T	C	AP1M1	c.C1023T	p.I341I
XH_P52	19	17000632	17000632	Missense_Mutation	SNP	G	A	G	F2RL3	c.G358A	p.A120T
XH_P52	19	17953357	17953357	Missense_Mutation	SNP	C	T	C	JAK3	c.G629A	p.R210Q
XH_P52	19	19605126	19605126	Silent	SNP	C	T	C	GATAD2A	c.C558T	p.T186T
XH_P52	19	21240539	21240539	Nonsense_Mutation	INS	-	TTGTAG	-	ZNF430	22_1423insTTG	H474delinsHLX
XH_P52	19	21240541	21240541	Nonsense_Mutation	INS	-	CCAGTATGAATT	-	ZNF430	TTCTCTCCAGTA	5_V476delinsNFSPVX
XH_P52	19	22155005	22155005	Missense_Mutation	SNP	A	G	A	ZNF208	c.T2831C	p.F944S
XH_P52	19	22498184	22498184	Silent	SNP	T	C	T	ZNF729	c.T1965C	p.P655P
XH_P52	19	22498749	22498749	Missense_Mutation	SNP	G	A	G	ZNF729	c.G2530A	p.V844I
XH_P52	19	22499351	22499351	Silent	SNP	G	A	G	ZNF729	c.G3132A	p.G1044G
XH_P52	19	22940554	22940554	Silent	SNP	A	G	A	ZNF99	c.T2157C	p.T719T
XH_P52	19	22941667	22941667	Silent	SNP	T	C	T	ZNF99	c.A1044G	p.K348K
XH_P52	19	23159304	23159304	Missense_Mutation	SNP	C	T	C	ZNF728	c.G835A	p.A279T
XH_P52	19	23543927	23543927	Missense_Mutation	SNP	T	A	T	ZNF91	c.A1758T	p.R586S
XH_P52	19	23543928	23543928	Missense_Mutation	SNP	C	G	C	ZNF91	c.G1757C	p.R586T
XH_P52	19	23544159	23544159	Missense_Mutation	SNP	C	G	C	ZNF91	c.G1526C	p.S509T
XH_P52	19	24310638	24310638	Frame_Shift_Ins	INS	-	TCAGTATGAATT	-	ZNF254	TTCTCTTCAGTA	p.F527fs
XH_P52	19	31769081	31769081	Missense_Mutation	SNP	C	T	C	TSHZ3	c.G1618A	p.G540S
XH_P52	19	35828773	35828773	Silent	SNP	C	T	C	CD22	c.C318T	p.S106S
XH_P52	19	35850560	35850560	Silent	SNP	G	A	G	FFAR3	c.G768A	p.A256A
XH_P52	19	36387881	36387881	Missense_Mutation	SNP	A	G	A	NFKBID	c.T131C	p.V44A
XH_P52	19	37975057	37975057	Nonsense_Mutation	INS	-	GGGTAAATTC	-	ZNF570	408insGGGT	36_T137delinsWGX
XH_P52	19	38798086	38798086	Silent	SNP	T	C	T	YIF1B	c.A726G	p.V242V
XH_P52	19	40023088	40023088	Silent	SNP	T	G	T	EID2B	c.A355C	p.R119R
XH_P52	19	42837775	42837775	Missense_Mutation	SNP	G	A	G	MEGF8	c.G206A	p.R69Q
XH_P52	19	43372386	43372386	Silent	SNP	T	C	T	PSG1	c.A831G	p.E277E
XH_P52	19	43430143	43430143	Nonsense_Mutation	INS	-	TTAGGTGCAGT	-	PSG7	insTAGACTGCA	20_Y221delinsIDCTX
XH_P52	19	44160786	44160786	Missense_Mutation	SNP	G	A	G	PLAUR	c.C317T	p.A106V
XH_P52	19	44622442	44622442	Silent	SNP	G	A	G	ZNF225	c.G117A	p.E39E
XH_P52	19	44636100	44636100	Nonsense_Mutation	INS	-	ATAAATGAAGCC	-	ZNF225	1334insATAAAT	6_F445delinsYKX
XH_P52	19	45206695	45206695	Silent	SNP	G	A	G	CEACAM16	c.G114A	p.T38T
XH_P52	19	46376217	46376217	Silent	SNP	C	A	C	FOXA3	c.C954A	p.P318P
XH_P52	19	46520018	46520018	Frame_Shift_Del	DEL	C	-	C	CCDC61	c.1158delC	p.R386fs
XH_P52	19	50453317	50453317	Silent	SNP	C	T	C	SIGLEC11	c.G1719A	p.S573S
XH_P52	19	51914580	51914580	Frame_Shift_Ins	INS	-	TGAAGATAACAG	-	SIGLEC10	138insTCTGTTA	p.P380fs
XH_P52	19	52857556	52857556	Silent	SNP	G	A	G	ZNF610	c.G243A	p.E81E
XH_P52	19	53645347	53645347	Missense_Mutation	SNP	G	T	G	ZNF347	c.C737A	p.S246Y
XH_P52	19	53855801	53855801	Missense_Mutation	SNP	C	T	C	ZNF845	c.C1873T	p.H625Y
XH_P52	19	54140118	54140118	Nonsense_Mutation	INS	-	TTCTTTTITTTAA	-	DPRX	TTATATTCTTTT	2delinsHFVRLFIYILFFNLX
XH_P52	19	54496300	54496300	Missense_Mutation	SNP	G	A	G	CACNG6	c.G169A	p.V57M
XH_P52	19	55281315	55281315	Missense_Mutation	SNP	G	T	G	KIR2DL1	c.G13T	p.V5F
XH_P52	19	55994240	55994240	Silent	SNP	C	T	C	ZNF628	c.C1680T	p.H560H
XH_P52	19	56011969	56011969	Silent	SNP	C	T	C	SSC5D	c.C2415T	p.D805D
XH_P52	19	56200727	56200727	Missense_Mutation	SNP	A	T	A	EPN1	c.A668T	p.E223V
XH_P52	19	56369314	56369314	Silent	SNP	G	A	G	NLRP4	c.G555A	p.T185T
XH_P52	19	57765027	57765027	In_Frame_Ins	INS	-	TGGGAAACATT	-	ZNF805	AGTGTGGGAA	SEKPYECICGKTCFWSNLRHSII
XH_P52	19	58016051	58016051	Silent	SNP	G	T	G	ZNF773	c.G57T	p.VN19V
XH_P52	19	58018201	58018201	In_Frame_Ins	INS	-	CTACTTTTGGAA	-	ZNF773	6insCCCTACTTT	245delinsPPYFWS
XH_P52	19	58024428	58024428	Missense_Mutation	SNP	C	T	C	ZNF773	c.C298T	p.R100C
XH_P52	19	58049281	58049281	In_Frame_Ins	INS	-	CCCTGCTTC	-	ZNF549	0_871insCCCTG	S290delinsSPCF
XH_P52	19	58132199	58132199	Nonsense_Mutation	INS	-	GTCTTCCTCTTA	-	ZNF134	13insTGCTTCC	5238delinsVSSSYX
XH_P52	19	58849926	58849926	Missense_Mutation	SNP	C	T	C	ZSCAN22	c.C710T	p.T237I
XH_P52	19	58907781	58907781	In_Frame_Del	DEL	ACGCGCCTG	-	CACGCGCCTGG	RNF225	c.325_369del	p.109_123del
XH_P52	20	334213	334213	Missense_Mutation	SNP	C	G	C	NRSN2	c.C549G	p.F183L
XH_P52	20	3846647	3846647	Silent	SNP	C	T	C	MAVS	c.C1053T	p.G351G
XH_P52	20	6022529	6022529	Missense_Mutation	SNP	C	G	C	LRRN4	c.G1362C	p.R454S
XH_P52	20	19673974	19673974	Frame_Shift_Ins	INS	-	ATTAAACCTTAT	-	SLC24A3	7insGAATTAAA	p.N466fs
XH_P52	20	42694409	42694409	Missense_Mutation	SNP	C	A	C	TOX2	c.C964A	p.L322I
XH_P52	20	43850853	43850853	Nonsense_Mutation	INS	-	GTTG	-	SEMG2	580_581insGTT	194_V195delinsCX
XH_P52	20	43850854	43850854	In_Frame_Ins	INS	-	CTTCCACCTAGG	-	SEMG2	582insCTTCCAC	Y194delinsYFHLG
XH_P52	20	44588998	44588998	Frame_Shift_Ins	INS	-	GTGCC	-	ZNF335	368_1869insGG	p.C623fs
XH_P52	20	47244450	47244450	Silent	SNP	G	A	G	PREX1	c.C4818T	p.H1606H
XH_P52	20	47587811	47587811	In_Frame_Ins	INS	-	AAAGAAAAAAT	-	ARFGEF2	46insTAAAGAA	449delinsLKEKMS
XH_P52	20	47587812	47587812	In_Frame_Ins	INS	-	AACAGTATGTTT	-	ARFGEF2	47insAAACAGT	449delinsPNSMFL
XH_P52	20	47865509	47865509	Missense_Mutation	SNP	G	A	G	ZNFX1	c.C4052T	p.T1351I
XH_P52	20	54961390	54961390	In_Frame_Ins	INS	-	AAGTAACAGTG	-	AURKA	242insACACTGT	A81delinsDTVTS
XH_P52	20	56137895	56137895	Missense_Mutation	SNP	G	C	G	PK1	c.G550C	p.V184L
XH_P52	20	57290347	57290347	Missense_Mutation	SNP	C	G	C	NPEPL1	c.C1537G	p.L513V
XH_P52	20	57769739	57769739	Missense_Mutation	SNP	A	G	A	ZNF831	c.A3665G	p.N1222S
XH_P52	20	62324289	62324289	Silent	SNP	C	T	C	RTEL1	c.C2115T	p.F705F
XH_P52	21	18981363	18981363	Nonsense_Mutation	INS	-	AGGAGTTAGTC	-	BTG3	100insGACTAA	L34_T35delinsDX
XH_P52	21	31964916	31964916	Missense_Mutation	SNP	A	C	A	KRTAP6-3	c.A152C	p.Y51S
XH_P52	21	40665947	40665947	Frame_Shift_Ins	INS	-	TT	-	BRWD1	c.620_621insAA	p.D207fs
XH_P52	21	40665949	40665949	Frame_Shift_Ins	INS	-	AATTGAGAAATA	-	BRWD1	CTTACTATTCT	p.D207fs
XH_P52	21	43543114	43543114	Frame_Shift_Ins	INS	-	CCAT	-	UMODL1	169_3170insCC	p.A1057fs
XH_P52	21	45217979	45217979	Missense_Mutation	SNP	C	T	C	RRP1	c.C809T	p.A270V
XH_P52	21	45959256	45959256	Missense_Mutation	SNP	C	G	C	KRTAP10-1	c.G778C	p.A260P
XH_P52	21	45999908	45999908	Missense_Mutation	SNP	A	C	A	KRTAP10-5	c.T548G	p.F183C
XH_P52	21	46047710	46047710	Silent	SNP	T	C	C	KRTAP10-9	c.T622C	p.L208L
XH_P52	21	46602607	46602607	Nonsense_Mutation	SNP	G	T	G	ADARB1	c.G1333T	p.E445X
XH_P52	21	46602608	46602608	In_Frame_Ins	INS	-	TTCTTACCACCT	-	ADARB1	1335insTTCTTA	E445delinsDSVHL
XH_P52	22	18655973	18655973	Silent	SNP	C	T	C	USP18	c.C948T	p.S316S
XH_P52	22	18655975	18655975	Frame_Shift_Ins	INS	-	SACTTTAGAATA	-	USP18	951insGACTTTAG	p.G317fs
XH_P52	22	19365551	19365551	Missense_Mutation	SNP	G	A	G	HIRA	c.C1454T	p.S485L
XH_P52	22	29126456	29126456	Frame_Shift_Ins	INS	-	T	-	CHEK2	c.399_400insA	p.A134fs
XH_P52	22	31338161	31338161	Frame_Shift_Ins	INS	-	CAGAACTAGAC	-	MORC2	524insGTCTAG	p.Y175fs
XH_P52	22	37499392	37499392	Silent	SNP	C	T	C	TMPPRS56	c.G66A	p.A22A
XH_P52	22	37524697	37524697	Silent	SNP	G	A	G	IL2RB	c.C1095T	p.F365F
XH_P52	22	38120965	38120965	Missense_Mutation	SNP	T	C	T	TRIOBP	c.T2402C	p.L801P

XH_P52	22	43435812	43435812	Silent	SNP	C	T	C	TTL1	c.G1242A	p.S414S
XH_P52	22	45279115	45279115	Missense_Mutation	SNP	G	A	G	PHF21B	c.C1285T	p.R429W
XH_P52	X	20069060	20069060	Frame_Shift_Ins	INS	-	GGTAAATAACGT	-	MAP7D2	ATAAGACGTGA	p.H200fs
XH_P52	X	24330386	24330386	Silent	SNP	G	A	G	SUPT20HL2	c.C1047T	p.D349D
XH_P52	X	34149267	34149267	Missense_Mutation	SNP	C	A	C	FAM47A	c.G1129T	p.A377S
XH_P52	X	40448312	40448312	Missense_Mutation	SNP	C	T	C	ATP6AP2	c.C112T	p.P38S
XH_P52	X	48847497	48847497	Silent	SNP	T	C	T	GRIPAP1	c.A483G	p.E161E
XH_P52	X	76709739	76709739	Nonsense_Mutation	INS	-	GGTACTTAGT	-	FGF16	94insGGTACTT31	L32delinsEGTX
XH_P52	X	78011362	78011362	Silent	SNP	C	G	C	LPAR4	c.C996G	p.S32S
XH_P52	X	103267865	103267865	Missense_Mutation	SNP	C	T	C	H2BFWT	c.G368A	p.R123H
XH_P52	X	153135626	153135626	Silent	SNP	G	A	G	L1CAM	c.C861T	p.N287N
XH_P52	1	156911215	156911215	Missense_Mutation	SNV	C	A	A	ARHGEF11	c.3343G>T	P.D1115Y
XH_P52	1	19180948	19180948	Missense_Mutation	SNV	C	T	T	TAS1R2	c.1016G>A	P.R339H
XH_P52	1	203468972	203468972	Missense_Mutation	SNV	C	T	T	OPTC	c.725C>T	P.A242V
XH_P52	1	28792974	28792974	Missense_Mutation	SNV	G	A	A	PHACTR4	c.518G>A	P.R173K
XH_P52	1	41847669	41847669	Missense_Mutation	SNV	G	A	A	FOXO6	c.796G>A	P.E266K
XH_P52	1	8073643	8073643	Missense_Mutation	SNV	G	A	A	ERRF1	c.1016C>T	P.P339L
XH_P52	1	914847	914847	Silent	SNV	G	A	A	PERM1	c.1563C>T	P.A521A
XH_P52	10	127426948	127426948	Missense_Mutation	SNV	G	A	A	EDRF1	c.1915G>A	P.E639K
XH_P52	11	1271940	1271940	Silent	SNV	G	A	A	MUC5B	c.13830G>A	P.G4610G
XH_P52	11	19955278	19955278	Missense_Mutation	SNV	G	C	C	NAV2	c.1296G>C	P.K432N
XH_P52	12	40114672	40114672	Missense_Mutation	SNV	T	G	G	C12orf40	c.1578T>G	P.N526K
XH_P52	12	57976915	57976915	Missense_Mutation	SNV	G	A	A	KIF5A	c.3052G>A	P.D1018N
XH_P52	12	94976125	94976125	Missense_Mutation	SNV	C	A	A	TMCC3	c.175G>T	P.D59Y
XH_P52	13	40229970	40229970	Missense_Mutation	SNV	C	T	T	COG6	c.107C>T	P.S36L
XH_P52	13	74387319	74387319	Missense_Mutation	SNV	G	A	A	KLF12	c.776C>T	P.T259M
XH_P52	14	104618546	104618546	Silent	SNV	C	G	G	KIF26A	c.483C>G	P.L161L
XH_P52	14	52520475	52520475	Silent	SNV	G	A	A	NID2	c.1251C>T	P.N417N
XH_P52	14	86088869	86088869	Missense_Mutation	SNV	C	G	G	FLRT2	c.1011C>G	P.F337L
XH_P52	14	93708768	93708768	Missense_Mutation	SNV	C	T	T	BTBD7	c.3250G>A	P.E1084K
XH_P52	15	73615056	73615056	Silent	SNV	G	A	A	HCN4	c.3378C>T	P.S1126S
XH_P52	16	1259077	1259077	Missense_Mutation	SNV	G	A	A	CACNA1H	c.3409G>A	P.A1137T
XH_P52	16	2028210	2028210	Missense_Mutation	SNV	G	A	A	TBL3	c.2123G>A	P.R708H
XH_P52	16	28354179	28354179	Missense_Mutation	SNV	T	G	G	NPIP6	c.1027A>C	P.K343Q
XH_P52	17	38818215	38818215	Missense_Mutation	SNV	G	A	A	KRT222	c.178C>T	P.R60C
XH_P52	17	39681485	39681494	Frame_Shift_Del	INDEL	GCAGGACA	-	-	KRT19	461delTTGTCC	P.I151fs
XH_P52	19	10401994	10401994	Missense_Mutation	SNV	C	A	A	ICAM5	c.329C>A	P.A110E
XH_P52	19	13397314	13397314	Splice_Site	SNV	C	T	T	CACNA1A	c.3565+3G>A	
XH_P52	19	3206400	3206400	Silent	SNV	G	A	A	NCLN	c.1473G>A	P.Q491Q
XH_P52	19	42837775	42837775	Missense_Mutation	SNV	G	A	A	MEGF8	c.206G>A	P.R69Q
XH_P52	19	44622442	44622442	Silent	SNV	G	A	A	ZNF225	c.117G>A	P.E39E
XH_P52	19	46520018	46520018	Frame_Shift_Del	INDEL	C	-	-	CCDC61	c.1159delC	P.Q387fs
XH_P52	19	53645347	53645347	Missense_Mutation	SNV	G	T	T	ZNF347	c.737C>A	P.S246Y
XH_P52	19	53855801	53855801	Missense_Mutation	SNV	C	T	T	ZNF845	c.1873C>T	P.H625Y
XH_P52	19	56200727	56200727	Missense_Mutation	SNV	A	T	T	EPN1	c.668A>T	P.E223V
XH_P52	19	58016051	58016051	Silent	SNV	G	T	T	ZNF773	c.57G>T	P.V19V
XH_P52	19	58024428	58024428	Missense_Mutation	SNV	C	T	T	ZNF773	c.343C>T	P.R151C
XH_P52	2	21227262	21227262	Missense_Mutation	SNV	C	T	T	APOB	c.11966G>A	P.R3989H
XH_P52	20	3846647	3846647	Silent	SNV	C	T	T	MAVS	c.1053C>T	P.G351G
XH_P52	22	19365551	19365551	Missense_Mutation	SNV	G	A	A	HIRA	c.1454C>T	P.S485L
XH_P52	22	45279115	45279115	Missense_Mutation	SNV	G	A	A	PHF21B	c.1321C>T	P.R441W
XH_P52	3	13661319	13661319	Missense_Mutation	SNV	G	A	A	FBLN2	c.2143G>A	P.V715M
XH_P52	3	169540738	169540738	Splice_Site	SNV	T	G	G	LRRIQ4	c.1020+9T>G	
XH_P52	3	184101308	184101308	Splice_Site	SNV	C	T	T	CHRD	c.1321-3C>T	
XH_P52	3	48605185	48605185	Silent	SNV	A	G	G	COL7A1	c.7941T>C	P.G2647G
XH_P52	4	57896395	57896395	Missense_Mutation	SNV	A	T	T	POLR2B	c.3265A>T	P.M1089L
XH_P52	5	100238636	100238636	Nonsense_Mutation	SNV	C	T	T	ST8SIA4	c.24G>A	P.W8*
XH_P52	5	140762754	140762754	Silent	SNV	C	T	T	PCDHGA7	c.288C>T	P.C96C
XH_P52	5	5463200	5463200	Silent	SNV	C	T	T	ICE1	c.3753C>T	P.L1251L
XH_P52	5	82940460	82940460	Missense_Mutation	SNV	C	T	T	HAPLN1	c.497G>A	P.R166Q
XH_P52	6	34008406	34008406	Missense_Mutation	SNV	C	T	T	GRM4	c.1288G>A	P.G430S
XH_P52	6	46191047	46191047	Splice_Site	SNV	C	T	T	RCAN2	c.572-9G>A	
XH_P52	6	46657421	46657421	Missense_Mutation	SNV	G	A	A	TRDR6	c.1556G>A	P.R519K
XH_P52	7	114298258	114298258	Silent	SNV	T	C	C	FOX2	c.1401T>C	P.S467S
XH_P52	8	121021282	121021282	Silent	SNV	G	A	A	DEPTOR	c.708G>A	P.A236A
XH_P52	8	131921955	131921955	Missense_Mutation	SNV	C	T	T	ADCY8	c.1639G>A	P.G547R
XH_P52	8	144239783	144239783	Missense_Mutation	SNV	C	G	G	LY6H	c.370G>C	P.D124H
XH_P52	8	145676044	145676044	Silent	SNV	G	A	A	CYHR1	c.807C>T	P.N269N
XH_P52	X	78011362	78011362	Silent	SNV	C	G	G	LPAR4	c.996C>G	P.S332S
XH_P53	1	1168256	1168256	Missense_Mutation	SNP	G	A	G	B3GALT6	c.G598A	p.E200K
XH_P53	1	12942047	12942047	Missense_Mutation	SNP	C	T	C	PRAMEF4	c.G503A	p.C168Y
XH_P53	1	22987385	22987438	In_Frame_Del	DEL	CTAAAGGTGG	-	CCTAAAGGTGGC	C1QB	c.268_321del	p.90_107del
XH_P53	1	26671412	26671412	Silent	SNP	T	C	T	CRYBG2	c.A1737G	p.P579P
XH_P53	1	46073304	46073304	Nonsense_Mutation	SNP	G	T	G	NASP	c.G529T	p.E177X
XH_P53	1	54301244	54301244	Missense_Mutation	SNP	A	G	A	NDC1	c.T107C	p.L36P
XH_P53	1	120436655	120436655	Nonsense_Mutation	INS	-	CCCAATATTTTT	-	ADAM30	95insTAAAAAAAE769_	E770delinsX
XH_P53	1	151377752	151377752	Silent	SNP	G	A	G	POGZ	c.C3474T	p.V1158V
XH_P53	1	152327982	152327982	Silent	SNP	T	C	T	FLG2	c.A2280G	p.Q760Q
XH_P53	1	152883009	152883009	Missense_Mutation	SNP	T	C	T	IVL	c.T736C	p.S246P
XH_P53	1	152883011	152883011	Silent	SNP	T	A	T	IVL	c.T738A	p.S246S
XH_P53	1	161495096	161495096	Silent	SNP	T	C	T	HSPA6	c.T648C	p.A216A
XH_P53	1	196759282	196759282	Missense_Mutation	SNP	C	T	C	CFHR3	c.C538T	p.P180S
XH_P53	1	201178297	201178297	Missense_Mutation	SNP	G	A	G	IGFN1	c.G4276A	p.E1426K
XH_P53	1	205033461	205033461	Missense_Mutation	SNP	G	A	G	CNTN2	c.G1252A	p.D418N
XH_P53	1	207110695	207110695	Missense_Mutation	SNP	C	T	C	PIGR	c.G790A	p.A264T
XH_P53	1	237947436	237947436	Missense_Mutation	SNP	G	A	G	RVR2	c.G12424A	p.A4142T
XH_P53	1	248436805	248436805	Silent	SNP	T	A	T	OR2T33	c.A312T	p.T104T
XH_P53	2	25457159	25457159	Missense_Mutation	SNP	C	G	C	DNMT3A	c.G2272C	p.A758P
XH_P53	2	29917793	29917793	Missense_Mutation	SNP	C	T	C	ALK	c.G875A	p.R292H
XH_P53	2	55403038	55403038	Frame_Shift_Ins	INS	-	GT	-	CLHC1	1282_1283insA	p.G428fs
XH_P53	2	128388466	128388468	In_Frame_Del	DEL	CTC	-	CTC	MYO7B	c.4842_4844del	p.1614_1615del
XH_P53	2	131976079	131976079	Missense_Mutation	SNP	A	G	A	POTEE	c.A104G	p.Y35C
XH_P53	2	175440031	175440031	Missense_Mutation	SNP	C	T	C	WIPF1	c.G259A	p.G87R
XH_P53	2	179399194	179399194	Frame_Shift_Ins	INS	-	ATGGGTGCTGGG	-	TTN	4953insCTCCAG	p.V24985fs
XH_P53	2	219543951	219543951	Nonsense_Mutation	INS	-	AAAAACTTTG	-	STK36	746insAAAAAC249_	Y250delinsX
XH_P53	2	220037661	220037661	Missense_Mutation	SNP	T	C	T	CNPPD1	c.A880G	p.N294D
XH_P53	2	241631616	241631616	Silent	SNP	T	C	T	AQP12A	c.T249C	p.T83T
XH_P53	3	9146465	9146465	Missense_Mutation	SNP	G	A	G	SRGAP3	c.C322T	p.R108W

XH_P53	3	13672942	13672942	Missense_Mutation	SNP	G	A	G	FBLN2	c.G3058A	p.G1020R
XH_P53	3	43122452	43122452	Missense_Mutation	SNP	G	A	G	POMGNT2	c.C472T	p.R158C
XH_P53	3	48600247	48600247	Missense_Mutation	SNP	C	T	C	UCN2	c.G311A	p.R104H
XH_P53	3	50816143	50816143	Missense_Mutation	SNP	G	T	G	DOCK3	c.G75T	p.L25F
XH_P53	3	51464969	51464969	Missense_Mutation	SNP	C	G	C	DCAF1	c.G1296C	p.Q432H
XH_P53	3	52422516	52422516	Missense_Mutation	SNP	A	G	A	DNAH1	c.A9254G	p.E3085G
XH_P53	3	52522347	52522347	Missense_Mutation	SNP	C	T	C	NISCH	c.C2839T	p.P947S
XH_P53	3	52526377	52526377	Missense_Mutation	SNP	G	A	G	NISCH	c.C4394A	p.R1465H
XH_P53	3	78766995	78766995	Nonsense_Mutation	INS	-	AGACAGTCAGC	-	ROBO1	GCCGAGCTGAC	K193delinsKPSX
XH_P53	3	87325603	87325603	In_Frame_Ins	INS	-	GTTAATAATCTC	-	POU1F1	5AAAGAGATTAT	Q4delinsKEIINNYQ
XH_P53	3	147114028	147114028	Missense_Mutation	SNP	C	T	C	ZIC4	c.G449A	p.G150D
XH_P53	3	158537482	158537482	Missense_Mutation	SNP	G	C	G	MFSD1	c.G727C	p.A243P
XH_P53	4	38690508	38690508	Silent	SNP	G	A	G	KLF3	c.G360A	p.P120P
XH_P53	4	39267734	39267734	Frame_Shift_Ins	INS	-	GCAGAAGATTG	-	WDR19	nsCTAAGCAGAA	p.L919fs
XH_P53	4	72634067	72634067	Missense_Mutation	SNP	G	A	G	GC	c.C212T	p.T71I
XH_P53	4	119660385	119660385	Missense_Mutation	SNP	C	A	C	SEC24D	c.G2299T	p.G767C
XH_P53	4	146461191	146461191	In_Frame_Ins	INS	-	GTTACCCAAACT	-	SMAD1	TAGCAGTTACCC	12delinsPIAVTQTLT
XH_P53	4	153247288	153247288	Missense_Mutation	SNP	C	T	C	FBXW7	c.G1160A	p.R387H
XH_P53	5	7889262	7889264	In_Frame_Del	DEL	CTA	-	CTA	MTRR	c.1201_1203del	p.401_401del
XH_P53	5	79033383	79033383	Missense_Mutation	SNP	A	C	A	CMYA5	c.A8795C	p.T2932T
XH_P53	5	79033774	79033774	Frame_Shift_Ins	INS	-	5GCTCTTTAATGT	-	CMYA5	87insCTGCTCTT	p.N3062fs
XH_P53	5	86659187	86659187	Frame_Shift_Ins	INS	-	TTATATTTTA	-	RASA1	5_1477insTTATA	p.N492fs
XH_P53	5	112175842	112175842	Silent	SNP	G	A	G	APC	c.G4497A	p.Q1499Q
XH_P53	5	137088929	137088931	In_Frame_Del	DEL	CCG	-	CCG	HNRNPA0	c.825_827del	p.275_276del
XH_P53	5	139060590	139060590	Missense_Mutation	SNP	C	T	C	CXC5	c.C482T	p.T161M
XH_P53	5	140554636	140554636	Silent	SNP	C	T	C	PCDH7	c.C2220T	p.T740T
XH_P53	5	149227049	149227049	Silent	SNP	G	A	G	PPARGC1B	c.G2883A	p.A961A
XH_P53	5	156376667	156376667	Missense_Mutation	SNP	G	T	G	TIMD4	c.C755A	p.S252Y
XH_P53	5	156376668	156376668	Missense_Mutation	SNP	A	C	A	TIMD4	c.T754G	p.S252A
XH_P53	6	52656780	52656780	Splice_Site	INS	-	GAACTGGAGA	-	GSTA1	.	.
XH_P53	6	166944754	166944754	Silent	SNP	G	A	G	RPS6KA2	c.C264T	p.Y88Y
XH_P53	7	1529248	1529248	Missense_Mutation	SNP	C	T	C	INTS1	c.G2236A	p.A746T
XH_P53	7	12254629	12254629	Nonsense_Mutation	SNP	C	T	C	TMEM106B	c.C193T	p.Q65X
XH_P53	7	36406325	36406325	Missense_Mutation	SNP	A	G	A	KIAO0895	c.T127C	p.S43P
XH_P53	7	37283974	37283974	Missense_Mutation	SNP	T	C	T	ELMO1	c.A436G	p.L146V
XH_P53	7	72413243	72413243	Missense_Mutation	SNP	A	C	A	POM121	c.A1916C	p.H639P
XH_P53	7	82582458	82582458	Missense_Mutation	SNP	C	G	C	PCLO	c.G7811C	p.W2604S
XH_P53	7	99081765	99081765	Silent	SNP	A	C	A	ZNF789	c.A213C	p.P71P
XH_P53	7	99081767	99081767	Splice_Site	INS	-	TAACCTACTAAC	-	ZNF789	.	.
XH_P53	7	100679169	100679169	Missense_Mutation	SNP	C	A	C	MUC17	c.C4472A	p.A1491E
XH_P53	7	100680133	100680133	Silent	SNP	C	T	C	MUC17	c.C5436T	p.S1812S
XH_P53	7	100680135	100680135	Missense_Mutation	SNP	C	T	C	MUC17	c.C5438T	p.T1813I
XH_P53	7	100682476	100682476	Silent	SNP	T	C	T	MUC17	c.T7779C	p.T2593T
XH_P53	7	100682941	100682941	Missense_Mutation	SNP	T	A	T	MUC17	c.T8244A	p.D2748E
XH_P53	7	120606733	120606733	Nonsense_Mutation	INS	-	5TGACATGTGAA	-	ING3	5TTGAGTGACATb	S140delinsCLX
XH_P53	7	122194737	122194737	Nonsense_Mutation	INS	-	5AATTATTGAAT	-	CADPS2	AATGAAATTCa	p.L448delinsKK
XH_P53	7	141920186	141920186	Missense_Mutation	SNP	G	A	G	MGAM2	c.G5875A	p.D1959N
XH_P53	8	7274308	7274308	Silent	SNP	A	G	A	DEFB4B	c.T42C	p.F14F
XH_P53	8	16944485	16944485	Nonsense_Mutation	INS	-	ACCCATAATTAA	-	MICU3	TGTTAACCCATa	R259delinsYPLVLVTHNX
XH_P53	8	125072505	125072505	Missense_Mutation	SNP	C	T	C	FER1L6	c.C2959T	p.P987S
XH_P53	9	21971025	21971038	Frame_Shift_Del	DEL	CCCAGGCATG	-	CCCAGGCATCG	CDKN2A	c.320_333del	p.R107fs
XH_P53	9	26905572	26905572	Nonsense_Mutation	INS	-	AAAAACAC	-	PLAA	5_2256insGTG	752_753delinsX
XH_P53	9	26905574	26905574	In_Frame_Ins	INS	-	ATTAATAATATC	-	PLAA	5sGGACGGATAT	752delinsGRIFLIDY
XH_P53	9	27185588	27185588	In_Frame_Ins	INS	-	ATC	-	TEK	5_847_848insATp	A283delinsDP
XH_P53	9	35090143	35090143	Missense_Mutation	SNP	G	A	G	PIGO	c.C2989T	p.R997W
XH_P53	9	35091810	35091810	Missense_Mutation	SNP	C	T	C	PIGO	c.G2074A	p.G692S
XH_P53	9	75532020	75532020	Nonsense_Mutation	INS	-	5CTAACACAATG	-	ALDH1A1	5CCTTGTCATTGT	284_D285delinsX
XH_P53	9	139837261	139837261	Silent	SNP	C	T	C	FBXW5	c.G486A	p.P162P
XH_P53	9	139981571	139981571	Silent	SNP	G	A	G	MAN1B1	c.G120A	p.P40P
XH_P53	10	21104572	21104572	Silent	SNP	A	G	A	NEBL	c.T2223C	p.N741N
XH_P53	10	43651090	43651090	Nonsense_Mutation	INS	-	TTCTTGTAATTC	-	CSGALNACT2	4insATTTCCTGT	65_H166delinsFLX
XH_P53	10	47087071	47087071	Silent	SNP	G	A	G	NPY4R	c.G288A	p.P96P
XH_P53	10	85974073	85974073	Missense_Mutation	SNP	A	C	A	CDHR1	c.A2276C	p.K759T
XH_P53	10	115970727	115970727	Splice_Site	INS	-	AGCAAGTACTG	-	TDRD1	.	.
XH_P53	10	120354138	120354138	Missense_Mutation	SNP	C	T	C	PRLHR	c.G619A	p.D207N
XH_P53	11	804321	804321	Missense_Mutation	SNP	G	A	G	PIDD1	c.C68T	p.S23L
XH_P53	11	992668	992668	Missense_Mutation	SNP	G	A	G	AP2A2	c.G1438A	p.A480T
XH_P53	11	17167235	17167235	Missense_Mutation	SNP	C	T	C	PIK3C2A	c.G544A	p.E182K
XH_P53	11	22297736	22297736	Frame_Shift_Ins	INS	-	CTTCCACTTTTC	-	ANOS	09insTACTTCCA	p.R836fs
XH_P53	11	22297738	22297738	Frame_Shift_Ins	INS	-	CAGAGATTACAG	-	ANOS	511insACAGAGA	p.V837fs
XH_P53	11	45249472	45249472	Missense_Mutation	SNP	G	A	G	PRDM11	c.G3296A	p.R1099H
XH_P53	11	55702935	55702935	Silent	SNP	T	C	T	OR51A	c.A942G	p.S314S
XH_P53	11	55999744	55999744	Silent	SNP	A	G	A	OR5T2	c.T918C	p.A306A
XH_P53	11	56237478	56237478	Missense_Mutation	SNP	A	C	A	OR5M3	c.T496G	p.F166V
XH_P53	11	58275364	58275364	Missense_Mutation	SNP	G	A	G	OR5B21	c.C215T	p.S72L
XH_P53	11	61548192	61548192	Missense_Mutation	SNP	C	T	C	MYRF	c.C2414T	p.A805V
XH_P53	11	62289913	62289913	Silent	SNP	T	A	T	AHNAK	c.A11976T	p.P3992P
XH_P53	11	92532113	92532113	Silent	SNP	C	T	C	FAT3	c.C5934T	p.S1978S
XH_P53	11	94758910	94758910	Silent	SNP	C	T	C	KDM4E	c.C189T	p.I63I
XH_P53	11	95519416	95519416	In_Frame_Ins	INS	-	ATAAAGCATACC	-	FAM76B	AAGAAAGGATAT	delinsRKKKGMYLCYD
XH_P53	11	119045313	119045313	Missense_Mutation	SNP	C	T	C	NLRX1	c.C1001T	p.A334V
XH_P53	11	129744064	129744064	Silent	SNP	C	T	C	NFRKB	c.G2298A	p.S766S
XH_P53	12	1919492	1919492	Silent	SNP	G	A	G	CACNA2D4	c.C2673T	p.F891F
XH_P53	12	2062350	2062350	In_Frame_Ins	INS	-	TGG	-	DCP1B	c.755_756insCC	Q252delinsHQ
XH_P53	12	5154512	5154512	Missense_Mutation	SNP	G	A	G	KCNAS	c.G1199A	p.R400Q
XH_P53	12	29904783	29904783	Missense_Mutation	SNP	G	A	G	TMT1C	c.C754T	p.R252C
XH_P53	12	49666675	49666675	Missense_Mutation	SNP	C	T	C	TUBA1C	c.C1225T	p.R409C
XH_P53	12	52867105	52867105	Silent	SNP	G	A	G	KRT6C	c.C417T	p.T139T
XH_P53	12	52867190	52867190	Missense_Mutation	SNP	C	T	C	KRT6C	c.G332A	p.G111D
XH_P53	12	53162773	53162775	In_Frame_Del	DEL	ACT	-	ACT	KRT76	c.1639_1641del	p.547_547del
XH_P53	12	53853108	53853108	Missense_Mutation	SNP	C	T	C	PCBP2	c.C296T	p.T99I
XH_P53	12	96691090	96691090	Silent	SNP	G	A	G	CDK17	c.C831T	p.Y277Y
XH_P53	12	104373829	104373829	Silent	SNP	C	A	C	TDG	c.C387A	p.T129T
XH_P53	12	122618062	122618062	Silent	SNP	G	A	G	MLXIP	c.G1260A	p.P420P
XH_P53	12	133215747	133215747	Missense_Mutation	SNP	C	T	C	POLE	c.G5516A	p.R1839H
XH_P53	13	42293856	42293856	Frame_Shift_Ins	INS	-	IGATAGGTATCC	-	VWA8	AATACGGGATA	p.S996fs
XH_P53	13	51952518	51952518	Missense_Mutation	SNP	G	A	G	INTS6	c.C1459T	p.R487W
XH_P53	13	72440539	72440541	In_Frame_Del	DEL	GCC	-	GCC	DACH1	c.361_363del	p.121_121del

XH_P53	13	88328670	88328670	Missense_Mutation	SNP	C	T	C	SLITRK5	c.C1027T	p.R343C
XH_P53	13	112722813	112722881	In_Frame_Del	DEL	GCGCACCAG	-	GCGCACCAGAA	SOX1	c.841_909del	p.281_303del
XH_P53	14	52186855	52186855	Silent	SNP	C	T	C	FRMD6	c.C33T	p.S115
XH_P53	14	77605767	77605767	Silent	SNP	C	T	C	ZDHHC22	c.G315A	p.L105L
XH_P53	14	94712839	94712839	Missense_Mutation	SNP	G	A	G	PPP4R4	c.G1331A	p.R444H
XH_P53	15	28171381	28171381	Nonsense_Mutation	INS	-	AAAGTTCTAAAA	-	OCA2	1899insATTTTA633	A634delinsGFX
XH_P53	15	35178833	35178833	Nonsense_Mutation	INS	-	TTTGAGTAGATT	-	AQR	CATTCTAATCTA	904delinsQYHTFX
XH_P53	15	39884814	39884814	Nonsense_Mutation	SNP	C	T	C	THB51	c.C2578T	p.Q860X
XH_P53	15	42042376	42042376	In_Frame_Ins	INS	-	TTG	-	MGA	5944_5945insT	p.Q1982delinsLE
XH_P53	15	42042377	42042377	Frame_Shift_Ins	INS	-	GTTTCTCTCT	-	MGA	5946insGTTT	p.Q1982fs
XH_P53	15	48744850	48744850	Silent	SNP	G	A	G	FBN1	c.C5454T	p.C1818C
XH_P53	15	69003971	69003971	Missense_Mutation	SNP	G	A	G	CORO2B	c.G559A	p.G187S
XH_P53	15	79750637	79750637	Silent	SNP	C	T	C	KIAA1024	c.C2148T	p.N176N
XH_P53	15	82444622	82444622	Missense_Mutation	SNP	G	T	G	EFL1	c.C2020A	p.Q674K
XH_P53	15	100252710	100252715	In_Frame_Del	DEL	CAGCAG	-	CAGCAG	MEF2A	c.1024_1029del	p.342_343del
XH_P53	15	100881250	100881250	Silent	SNP	G	A	G	ADAMTS17	c.C444T	p.G148G
XH_P53	16	2260251	2260251	Frame_Shift_Del	DEL	G	-	G	BRICD5	c.212delC	p.P71fs
XH_P53	16	67964383	67964383	Missense_Mutation	SNP	C	T	C	CTRL	c.G427A	p.A143T
XH_P53	16	87637893	87637893	Frame_Shift_Ins	INS	-	TGCTG	-	JPH3	430_431insTGC	p.P144fs
XH_P53	16	89348521	89348521	Missense_Mutation	SNP	G	A	G	ANKRD11	c.C4429T	p.R1477W
XH_P53	17	3030686	3030686	Frame_Shift_Ins	INS	-	ATTTTTTCATGT	-	OR1G1	50insAACATGAA	p.Q54fs
XH_P53	17	4837274	4837300	In_Frame_Del	DEL	CCGACCATC	-	GCCCACCATCC	GP1BA	c.1375_1401del	p.459_467del
XH_P53	17	7579408	7579430	Frame_Shift_Del	DEL	CAGGAGGGG	-	CCAGGAGGGGG	TP53	c.140_162del	p.A47fs
XH_P53	17	7696331	7696331	Silent	SNP	G	A	G	DNAH2	c.G7377A	p.E2459E
XH_P53	17	10305081	10305081	Nonsense_Mutation	INS	-	TCAGCTCAGCAT	-	MYH8	10insCAATGCTG	p.Q905delinsQCX
XH_P53	17	19641549	19641635	Splice_Site	DEL	CCCTGGTCCC	-	GCCCTGGTCCCG	ALDH3A1	-	-
XH_P53	17	27421999	27422028	In_Frame_Del	DEL	GCAGCTTCT	-	CTGCAGCTTCTC	MYO18A	c.4435_4464del	p.1479_1488del
XH_P53	17	29559195	29559198	Frame_Shift_Del	DEL	AGTT	-	AGTT	NF1	c.3302_3305del	p.Q1101fs
XH_P53	17	39296158	39296158	Silent	SNP	G	A	G	KRTAP4-6	c.C582T	p.C194C
XH_P53	17	39316760	39316834	In_Frame_Del	DEL	AGCACTGGG	-	ACAGCACTGGGG	KRTAP4-4	c.110_184del	p.37_62del
XH_P53	17	42848957	42848957	Silent	SNP	T	A	T	ADAM11	c.T387A	p.A129A
XH_P53	17	45908877	45908877	Missense_Mutation	SNP	T	A	T	MRPL10	c.A1T	p.M1L
XH_P53	17	73831849	73831849	Missense_Mutation	SNP	G	A	G	UNC13D	c.C1606T	p.S36W
XH_P53	17	75494652	75494652	Missense_Mutation	SNP	A	T	A	SEPT9	c.A1337T	p.E464V
XH_P53	17	79634802	79634802	Missense_Mutation	SNP	G	A	G	CCDC137	c.G178A	p.E60K
XH_P53	17	80014797	80014797	Missense_Mutation	SNP	G	A	G	GP51	c.G1336A	p.A446T
XH_P53	18	10705713	10705713	Missense_Mutation	SNP	G	A	G	PIEZO2	c.C5281T	p.R1761C
XH_P53	18	14542654	14542654	Silent	SNP	C	A	C	POTEC	c.G492T	p.T164T
XH_P53	18	30275466	30275466	Nonsense_Mutation	INS	-	ATTACACACATA	-	KLHL14	ACAAGTATGTG	374delinsLUGGAQQQVCVX
XH_P53	18	47107855	47107855	Silent	SNP	G	A	G	LIPG	c.G642A	p.Q214Q
XH_P53	18	47107857	47107857	Frame_Shift_Ins	INS	-	CATCCTGCATGC	-	LIPG	5GGCTCATCTCG	p.D215fs
XH_P53	18	59483373	59483373	Silent	SNP	C	T	C	RNF152	c.G324A	p.K108K
XH_P53	18	60382987	60383043	In_Frame_Del	DEL	CAGCAGCAG	-	GCAGCAGCAGC	PHLPP1	c.71_127del	p.24_43del
XH_P53	19	1802524	1802524	Missense_Mutation	SNP	C	T	C	ATP8B3	c.G866A	p.R289H
XH_P53	19	5914497	5914569	Frame_Shift_Del	DEL	CCCCGGCCCC	-	ACCCCGGGCCCC	CAPS	c.338_341del	p.A113fs
XH_P53	19	5915155	5915228	In_Frame_Del	DEL	CCAGGCAGT	-	CCAGGCAGTTCC	CAPS	c.724_726del	p.242_242del
XH_P53	19	7964875	7964875	Missense_Mutation	SNP	C	T	C	LRR8C8	c.C1081T	p.R361C
XH_P53	19	9060417	9060417	Nonsense_Mutation	INS	-	GCTACATCA	-	MUC16	3_27029insTGA	p.S901delinsLMX
XH_P53	19	10602650	10602650	Frame_Shift_Del	DEL	G	-	G	KEAP1	c.928delC	p.L310fs
XH_P53	19	17267727	17267727	Missense_Mutation	SNP	C	T	C	MYO9B	c.C1208T	p.A403V
XH_P53	19	21991325	21991325	Missense_Mutation	SNP	A	G	A	ZNF43	c.T1319C	p.I440T
XH_P53	19	21991327	21991327	Silent	SNP	G	A	G	ZNF43	c.C1317T	p.H439H
XH_P53	19	22498184	22498184	Silent	SNP	T	C	T	ZNF729	c.T1965C	p.P655P
XH_P53	19	22498749	22498749	Missense_Mutation	SNP	G	A	G	ZNF729	c.G2530A	p.V844I
XH_P53	19	22940554	22940554	Silent	SNP	A	G	A	ZNF99	c.T2157C	p.T719T
XH_P53	19	22940899	22940899	Silent	SNP	G	A	G	ZNF99	c.C1812T	p.H604H
XH_P53	19	22941531	22941531	Missense_Mutation	SNP	G	C	G	ZNF99	c.C1180G	p.Q394E
XH_P53	19	22941917	22941917	Missense_Mutation	SNP	A	G	A	ZNF99	c.T794C	p.V265A
XH_P53	19	36018462	36018462	Missense_Mutation	SNP	T	C	T	SBSN	c.A722G	p.K241R
XH_P53	19	37240172	37240172	Silent	SNP	G	A	G	ZNF850	c.C1674T	p.H558H
XH_P53	19	42503324	42503324	Missense_Mutation	SNP	C	A	C	GRIK5	c.G2642T	p.R881L
XH_P53	19	45176068	45176068	Missense_Mutation	SNP	C	T	C	CEACAM19	c.C256T	p.R86W
XH_P53	19	47575306	47575341	In_Frame_Del	DEL	GGGGGTCCCC	-	GGGGGTCCCCAT	ZC3H4	c.1840_1875del	p.614_625del
XH_P53	20	2843939	2843939	Silent	SNP	C	T	C	VPS16	c.C939T	p.L131L
XH_P53	20	32873409	32873409	Missense_Mutation	SNP	C	T	C	AHCY	c.G1004A	p.R335H
XH_P53	20	50140605	50140605	Missense_Mutation	SNP	C	T	C	NFATC2	c.G115A	p.A39T
XH_P53	22	16277757	16277757	Missense_Mutation	SNP	C	T	C	POTEH	c.G1157A	p.R386H
XH_P53	22	30127278	30127278	Missense_Mutation	SNP	G	T	G	ZMAT5	c.C449A	p.P150H
XH_P53	22	37263475	37263475	Missense_Mutation	SNP	C	T	C	NCF4	c.C313T	p.R105W
XH_P53	22	45110539	45110539	Missense_Mutation	SNP	A	G	A	PRR5	c.A203G	p.N68S
XH_P53	X	71895936	71895936	Nonsense_Mutation	SNP	G	T	G	PHKA1	c.C602A	p.S201X
XH_P53	X	75004861	75004861	Missense_Mutation	SNP	C	T	C	MAGEE2	c.G26A	p.R9H
XH_P53	X	79942454	79942454	Frame_Shift_Ins	INS	-	TGTGAAAGTAG	-	BRWD3	ACACTACTACT	p.W1305fs
XH_P53	X	118723709	118723709	Frame_Shift_Ins	INS	-	TAGATAGGCTCC	-	NKRF	insTACGGGAGC	p.R560fs
XH_P53	X	132351081	132351081	Missense_Mutation	SNP	C	T	C	TFDP3	c.G1207A	p.E403K
XH_P53	X	152815602	152815602	Missense_Mutation	SNP	G	A	G	ATP2B3	c.G1681A	p.V561M
XH_P53	X	153595807	153595807	Missense_Mutation	SNP	G	A	G	FLNA	c.C826T	p.R276W
XH_P53	1	1168256	1168256	Missense_Mutation	SNV	G	A	A	B3GALT6	c.598G>A	P.E200K
XH_P53	1	151377752	151377752	Silent	SNV	G	A	A	POGZ	c.3732C>T	P.V1244V
XH_P53	1	205033461	205033461	Missense_Mutation	SNV	G	A	A	CNTN2	c.1252G>A	P.D418N
XH_P53	1	46073304	46073304	Nonsense_Mutation	SNV	G	T	T	NASP	c.529G>C	P.E177*
XH_P53	1	54301244	54301244	Missense_Mutation	SNV	A	G	G	NDC1	c.107T>C	P.L36P
XH_P53	10	21104572	21104572	Silent	SNV	A	G	G	NEBL	c.2223T>C	P.N741N
XH_P53	10	29169059	29169059	Splice_Site	INDEL	-	C	C	C10orf126	c.211-5dupC	-
XH_P53	11	129744064	129744064	Silent	SNV	C	T	T	NFRKB	c.2223G>A	P.S741S
XH_P53	11	17167235	17167235	Missense_Mutation	SNV	C	T	T	PIK3C2A	c.1684G>A	P.E562K
XH_P53	11	55999744	55999744	Silent	SNV	A	G	G	OR5T2	c.918T>C	P.A306A
XH_P53	11	56237478	56237478	Missense_Mutation	SNV	A	C	C	OR5M3	c.496T>G	P.F166V
XH_P53	11	58275364	58275364	Missense_Mutation	SNV	G	A	A	OR5B21	c.215C>T	P.S72L
XH_P53	12	122618062	122618062	Silent	SNV	G	A	A	MLXIP	c.1260G>A	P.P420P
XH_P53	12	1919492	1919492	Silent	SNV	G	A	A	CACNA2D4	c.2673C>T	P.F891F
XH_P53	12	29904783	29904783	Missense_Mutation	SNV	G	A	A	TMT1C	c.754C>T	P.R252C
XH_P53	12	49666675	49666675	Missense_Mutation	SNV	C	T	T	TUBA1C	c.1225C>T	P.R409C
XH_P53	12	5154512	5154512	Missense_Mutation	SNV	G	A	A	KCNA5	c.1199G>A	P.R400Q
XH_P53	12	53853108	53853108	Missense_Mutation	SNV	C	T	T	PCBP2	c.296C>T	P.T99I
XH_P53	12	96691090	96691090	Silent	SNV	G	A	A	CDK17	c.831C>T	P.DY277Y
XH_P53	14	77605767	77605767	Silent	SNV	C	T	T	ZDHHC22	c.315G>A	P.L105L
XH_P53	15	39884814	39884814	Nonsense_Mutation	SNV	C	T	T	THB51	c.2578C>T	P.Q860*

XH_P53	15	69003971	69003971	Missense_Mutation	SNV	G	A	A	CORO2B	c.559G>A	P.G187S
XH_P53	15	79750637	79750637	Silent	SNV	C	T	T	KIAA1024	c.2148C>T	P.N716N
XH_P53	15	82444622	82444622	Missense_Mutation	SNV	G	T	T	EFL1	c.2020C>A	P.Q674K
XH_P53	17	29559195	29559198	Frame_Shift_Del	INDEL	AGTT	-	-	NF1	303_3306delG	P.Q1101fs
XH_P53	17	4837274	4837300	Missense_Mutation	INDEL	CCGACCATC	-	-	GP1BA	ACCATCTCTGGT	P.P462_5470del
XH_P53	17	65104598	65104598	Splice_Site	SNV	G	A	A	HELZ	c.4724+10C>T	
XH_P53	17	74134210	74134210	Splice_Site	SNV	A	G	G	FOXJ1	c.499-9T>C	
XH_P53	17	75494652	75494652	Missense_Mutation	SNV	A	T	T	SEPT9	c.1673A>T	P.E558V
XH_P53	17	7579408	7579430	Frame_Shift_Del	INDEL	CAGGAGGGG	-	-	TP53	ACCAGCCCCCT	P.A86fs
XH_P53	17	7696331	7696331	Silent	SNV	G	A	A	DNAH2	c.7377G>A	P.E2459E
XH_P53	18	10705713	10705713	Missense_Mutation	SNV	G	A	A	PIEZO2	c.5281C>T	P.R1761C
XH_P53	18	59483373	59483373	Silent	SNV	C	T	T	RNF152	c.324G>A	P.L108K
XH_P53	19	1802524	1802524	Missense_Mutation	SNV	C	T	T	ATP8B3	c.866G>A	P.R289H
XH_P53	2	128388466	128388468	Missense_Mutation	INDEL	CTC	-	-	MYO7B	4844_4846delC	P.S1615del
XH_P53	2	175440031	175440031	Missense_Mutation	SNV	C	T	T	WIPF1	c.259G>A	P.G87R
XH_P53	2	220037661	220037661	Missense_Mutation	SNV	T	C	C	CNPPD1	c.880A>G	P.N294D
XH_P53	2	29917793	29917793	Missense_Mutation	SNV	C	T	T	ALK	c.875G>A	P.R292H
XH_P53	20	2843939	2843939	Silent	SNV	C	T	T	VPS16	c.1371C>T	P.L457L
XH_P53	22	25291187	25291187	Splice_Site	SNV	C	T	T	SGSM1	c.2119-3C>T	
XH_P53	22	30127278	30127278	Missense_Mutation	SNV	G	T	T	ZMAT5	c.449C>A	P.P150H
XH_P53	22	45110539	45110539	Missense_Mutation	SNV	A	G	G	PRR5	c.176A>G	P.N59S
XH_P53	3	13672942	13672942	Missense_Mutation	SNV	G	A	A	FBLN2	c.3199G>A	P.G1067R
XH_P53	3	158537482	158537482	Missense_Mutation	SNV	G	C	C	MFS1D1	c.727G>C	P.A243P
XH_P53	3	19322683	19322683	Splice_Site	SNV	G	T	T	KCNH8	c.311-7G>T	
XH_P53	3	19322684	19322684	Splice_Site	SNV	T	C	C	KCNH8	c.311-6T>C	
XH_P53	3	50816143	50816143	Missense_Mutation	SNV	G	T	T	DOCK3	c.75G>T	P.L25F
XH_P53	4	119660385	119660385	Missense_Mutation	SNV	C	A	A	SEC24D	c.2299G>T	P.G767C
XH_P53	4	153247288	153247288	Missense_Mutation	SNV	C	T	T	FBXW7	c.1514G>A	P.R505H
XH_P53	4	72634067	72634067	Missense_Mutation	SNV	G	A	A	GC	c.212C>T	P.T71I
XH_P53	5	112175842	112175842	Silent	SNV	G	A	A	APC	c.4551G>A	P.Q1517Q
XH_P53	5	149227049	149227049	Silent	SNV	G	A	A	PPARGC1B	c.2883G>A	P.A961A
XH_P53	5	156376667	156376667	Missense_Mutation	SNV	G	T	T	TIMD4	c.755C>A	P.S252Y
XH_P53	5	156376668	156376668	Missense_Mutation	SNV	A	C	C	TIMD4	c.754T>G	P.S252A
XH_P53	5	16769174	16769174	Splice_Site	SNV	T	A	A	MYO10	c.1060+9A>T	
XH_P53	5	7889262	7889264	Missense_Mutation	INDEL	CTA	-	-	MTRR	1202_1204delT	P.L401del
XH_P53	5	79033383	79033383	Missense_Mutation	SNV	A	C	C	CMYA5	c.8795A>C	P.K2932T
XH_P53	5	86659187	86659187	Frame_Shift_Ins	INDEL	-	TTATATTTTA	TTATATTTTA	RASA1	1487dupTATA	P.L497fs
XH_P53	7	36406325	36406325	Missense_Mutation	SNV	A	G	G	KIAA0895	c.127T>C	P.S43P
XH_P53	7	37283974	37283974	Missense_Mutation	SNV	T	C	C	ELMO1	c.436A>G	P.L146V
XH_P53	7	72413243	72413243	Missense_Mutation	SNV	A	C	C	POM121	c.1916A>C	P.H639P
XH_P53	7	82582458	82582458	Missense_Mutation	SNV	C	G	G	PCLO	c.7811G>C	P.W2604S
XH_P53	9	140851291	140851291	Splice_Site	SNV	T	G	G	CACNA1B	c.1243+12T>G	
XH_P53	9	21971025	21971038	Frame_Shift_Del	INDEL	CCAGGACATC	-	-	CDKN2A	3delGCGATGCC	P.R107fs
XH_P53	9	35091810	35091810	Missense_Mutation	SNV	G	T	T	PIGO	c.2074G>A	P.G692S
XH_P53	X	132351081	132351081	Missense_Mutation	SNV	C	T	T	TFDP3	c.1207G>A	P.E403K
XH_P53	X	152815602	152815602	Missense_Mutation	SNV	G	A	A	ATP2B3	c.1681G>A	P.V561M
XH_P53	X	71895936	71895936	Nonsense_Mutation	SNV	G	T	T	PHKA1	c.602C>A	P.S201*
XH_P53	X	75004861	75004861	Missense_Mutation	SNV	C	T	T	MAGEE2	c.26G>A	P.R9H
XH_P54	4	153247208	153247208	Missense_Mutation	SNP	T	G	G	FBXW7	c.1594A>C	p.T532P
XH_P54	16	3786703	3786703	Missense_Mutation	SNP	T	A	A	CREBBP	c.4508A>T	p.Y1503F
XH_P54		-	-	Frame_Shift_Ins	INS	-	-	-	PBRM1	c.3564dupA	P.E189Rfs*6
XH_P54	5	112177244	112177244	Nonsense_Mutation	SNP	G	T	T	APC	c.5953G>T	p.E198S*
XH_P54	15	90631839	90631839	Missense_Mutation	SNP	T	A	A	IDH2	c.514A>T	p.R172W
XH_P54	10	89720870	89720870	Missense_Mutation	SNP	T	G	G	PTEN	c.1021T>G	p.F341V
XH_P54	9	101894987	101894987	Missense_Mutation	SNP	A	C	C	TGFBR1	c.540A>C	p.L180F
XH_P54	7	42063159	42063159	Nonsense_Mutation	SNP	C	A	A	GLI3	c.1405G>T	p.E469*
XH_P54	8	90982707	90982707	Missense_Mutation	SNP	T	G	G	NBN	c.781A>C	p.N261H
XH_P54	1	17087305	17087305	Silent	SNP	G	T	G	MTSL1	c.C279A	p.P93P
XH_P54	1	26149596	26149596	Missense_Mutation	SNP	A	G	A	MTFR1L	c.A1G	p.M1V
XH_P54	1	27023451	27023453	In_Frame_Del	DEL	GCG	-	GCG	ARID1A	c.557_559del	p.186_187del
XH_P54	1	28477386	28477386	Missense_Mutation	SNP	G	T	G	PTAFR	c.C147A	p.F49L
XH_P54	1	50884781	50884781	Silent	SNP	G	A	G	DMRTA2	c.C1185T	p.A395A
XH_P54	1	53547798	53547800	In_Frame_Del	DEL	GAA	-	GAA	PODN	c.1951_1953del	p.651_651del
XH_P54	1	55525272	55525272	Silent	SNP	T	C	T	PCSK9	c.T1617C	p.A339A
XH_P54	1	64475018	64475018	Missense_Mutation	SNP	T	C	T	ROR1	c.T133C	p.S45P
XH_P54	1	65312370	65312370	Missense_Mutation	SNP	A	G	A	JAK1	c.T1949C	p.I650T
XH_P54	1	89655741	89655741	Nonsense_Mutation	SNP	C	A	C	GBP4	c.G1177T	p.E393X
XH_P54	1	92445291	92445291	Missense_Mutation	SNP	C	T	C	BRDT	c.C1126T	p.R376C
XH_P54	1	92946446	92946446	Silent	SNP	C	T	C	GF11	c.G498A	p.A166A
XH_P54	1	111985955	111985955	Silent	SNP	G	T	G	WDR77	c.C489A	p.V163V
XH_P54	1	114246775	114246775	Nonsense_Mutation	INS	-	ACAGAGACGGG	-	PHTF1	GGCCCCGCTCTG	21delinsHQLNAVAPVSVEX
XH_P54	1	147092562	147092562	Silent	SNP	G	A	G	BCL9	c.G2601A	p.T867T
XH_P54	1	149785000	149785000	Silent	SNP	A	G	A	HIST2H3D	c.T237C	p.F79F
XH_P54	1	151105835	151105835	Missense_Mutation	SNP	T	C	T	SEMA6C	c.A1894G	p.I632V
XH_P54	1	152882717	152882717	Missense_Mutation	SNP	G	T	G	IVL	c.G444T	p.K148N
XH_P54	1	154574428	154574428	Missense_Mutation	SNP	T	G	T	ADAR	c.A690C	p.E230D
XH_P54	1	156437998	156437998	Silent	SNP	A	G	A	MEF2D	c.T1320C	p.R440R
XH_P54	1	172559068	172559068	Splice_Site	SNP	T	C	T	SUCO	.	.
XH_P54	1	204129732	204129732	Missense_Mutation	SNP	A	G	A	REN	c.T448C	p.S150P
XH_P54	1	205901138	205901138	Silent	SNP	C	G	C	SLC26A9	c.G402C	p.L134L
XH_P54	1	231298885	231298951	Frame_Shift_Del	DEL	CTGGAGCAC	-	TCTGGAGCACG	TRIM67	c.170_236del	p.L57fs
XH_P54	2	40657236	40657236	Missense_Mutation	SNP	G	A	G	SLC8A1	c.C1821	p.P62L
XH_P54	2	46707812	46707812	In_Frame_Ins	INS	-	TGATGGAGCAG	-	TMEM247	5GTGGTGATGG	4insRQHEVVMLEQLQREQ
XH_P54	2	48040424	48040424	Missense_Mutation	SNP	T	G	T	FBXO11	c.A2176C	p.K726Q
XH_P54	2	50699452	50699452	Silent	SNP	G	A	G	NRXN1	c.C3117T	p.L1039I
XH_P54	2	71219019	71219019	Missense_Mutation	SNP	C	A	C	TEX261	c.G245T	p.G82V
XH_P54	2	79385866	79385866	Missense_Mutation	SNP	C	G	C	REG3A	c.C106C	p.A36P
XH_P54	2	96604747	96604747	Silent	SNP	C	T	C	ANKRD36C	c.G1548A	p.P516P
XH_P54	2	132290899	132290899	Missense_Mutation	SNP	G	T	G	CCDC74A	c.G1056T	p.K352N
XH_P54	2	141739835	141739835	Silent	SNP	G	A	G	LRP1B	c.C2781T	p.C927C
XH_P54	2	162280620	162280620	Missense_Mutation	SNP	A	C	A	TBR1	c.A1931C	p.D644A
XH_P54	2	203383667	203383667	Silent	SNP	A	G	A	BMPR2	c.A744G	p.R248R
XH_P54	2	207026187	207026187	Silent	SNP	T	C	T	EEF1B2	c.T321C	p.D107D
XH_P54	2	207308642	207308642	Missense_Mutation	SNP	C	T	C	ADAM23	c.C52T	p.L18F
XH_P54	2	211018227	211018227	Frame_Shift_Ins	INS	-	T	-	KANSL1L	c.1079dupA	p.N360fs
XH_P54	2	211471502	211471502	Missense_Mutation	SNP	T	G	T	CP51	c.T676G	p.F226V
XH_P54	2	241696841	241696846	In_Frame_Del	DEL	TCCTCC	-	TCCTCC	KIF1A	c.2748_2753del	p.916_918del
XH_P54	2	242275398	242275398	Nonsense_Mutation	SNP	G	T	G	SEPT2	c.G106T	p.E36X

XH_P54	3	1443123	1443123	Missense_Mutation	SNP	G	T	G	CNTN6	c.G2399T	p.S800I
XH_P54	3	42576581	42576581	Silent	SNP	C	T	C	VIPR1	c.C495T	p.V165V
XH_P54	3	48677589	48677589	Silent	SNP	C	T	C	CELSR3	c.G9429A	p.A3143A
XH_P54	3	61975366	61975366	Silent	SNP	T	C	T	PTPRG	c.T258C	p.I86I
XH_P54	3	108298423	108298423	Missense_Mutation	SNP	A	C	A	KIAA1524	c.T662G	p.V221G
XH_P54	3	111312868	111312868	Missense_Mutation	SNP	A	C	A	ZBED2	c.T181G	p.F61V
XH_P54	3	112357517	112357517	Missense_Mutation	SNP	C	A	C	CCDC80	c.G1236T	p.E412D
XH_P54	3	119534175	119534175	Missense_Mutation	SNP	T	G	T	NR12	c.T943G	p.F315V
XH_P54	3	121409820	121409820	Missense_Mutation	SNP	C	A	C	GOLGB1	c.G8151T	p.M2717I
XH_P54	3	123699321	123699321	Missense_Mutation	SNP	T	C	T	ROPN1	c.A8G	p.Q3R
XH_P54	3	128969537	128969537	Missense_Mutation	SNP	A	C	A	COPG1	c.A50C	p.N17T
XH_P54	3	130714921	130714921	Missense_Mutation	SNP	A	C	A	ATP2C1	c.A2077C	p.N693H
XH_P54	3	132244529	132244529	Missense_Mutation	SNP	C	T	C	DNAJC13	c.C6136T	p.P2046S
XH_P54	3	151164791	151164791	Missense_Mutation	SNP	T	C	T	IGSF10	c.A2978G	p.Q993R
XH_P54	3	164710142	164710142	Missense_Mutation	SNP	A	C	A	SI	c.T4885G	p.L1629V
XH_P54	3	184290711	184290711	Silent	SNP	G	A	G	EPHB3	c.G603A	p.S201S
XH_P54	3	195512501	195512501	Missense_Mutation	SNP	G	A	G	MUC4	c.C5950T	p.P1984S
XH_P54	3	195516981	195516981	Silent	SNP	G	A	G	MUC4	c.C1470T	p.S490S
XH_P54	4	1806163	1806163	Silent	SNP	G	T	G	FGFR3	c.G1182T	p.T394T
XH_P54	4	25664333	25664333	Nonsense_Mutation	INS	-	AAGAGCACACG	-	SLC34A2	ATCGGAAGAGC	9delinsNTEIGRAHVX
XH_P54	4	77817956	77817956	Silent	SNP	T	G	T	SOWAHB	c.A1047C	p.S349S
XH_P54	4	94436455	94436455	Missense_Mutation	SNP	C	A	C	GRID2	c.C1801A	p.L601M
XH_P54	4	100510841	100510841	Silent	SNP	A	C	A	MTPP	c.A516C	p.I172I
XH_P54	5	9227058	9227058	Missense_Mutation	SNP	G	A	G	SEMA5A	c.C355T	p.R119W
XH_P54	5	40853720	40853720	Missense_Mutation	SNP	G	T	G	CARD6	c.G2286T	p.R762S
XH_P54	5	74078912	74078912	Silent	SNP	A	C	A	FAM169A	c.T1308G	p.L436L
XH_P54	5	74441843	74441843	Silent	SNP	T	C	T	ANKRD31	c.A3393G	p.Q1131Q
XH_P54	5	79026273	79026273	Missense_Mutation	SNP	T	G	T	CMYA5	c.T1685G	p.L562R
XH_P54	5	82834295	82834295	Missense_Mutation	SNP	C	T	C	VCAN	c.C2512T	p.P838S
XH_P54	5	90006806	90006806	Missense_Mutation	SNP	G	A	G	ADGRV1	c.G8833A	p.G2945S
XH_P54	5	90671401	90671401	Silent	SNP	T	C	T	ARRDC3	c.A540G	p.T180T
XH_P54	5	95761624	95761624	Missense_Mutation	SNP	G	A	G	PCSK1	c.C296T	p.A99V
XH_P54	5	140207965	140207965	Missense_Mutation	SNP	G	C	G	PCDHA6	c.G289C	p.G97R
XH_P54	5	140810735	140810735	Nonsense_Mutation	SNP	G	T	G	PCDHGA12	c.G409T	p.E137X
XH_P54	5	147807242	147807242	Silent	SNP	A	G	A	FBXO38	c.A2385G	p.E795E
XH_P54	5	152870470	152870470	Missense_Mutation	SNP	T	G	T	GRIA1	c.T22G	p.F8V
XH_P54	5	153755840	153755840	Missense_Mutation	SNP	A	G	A	GALNT10	c.A572G	p.H191R
XH_P54	5	162868233	162868233	Silent	SNP	A	G	A	CCNG1	c.A414G	p.L138E
XH_P54	5	167553859	167553859	Nonsense_Mutation	SNP	C	A	C	TENM2	c.C1614A	p.C538X
XH_P54	5	178311215	178311215	Missense_Mutation	SNP	A	C	A	ZNF354B	c.A1762C	p.S588R
XH_P54	6	34826124	34826124	Missense_Mutation	SNP	T	C	T	UHRF1BP1	c.T1991C	p.L664P
XH_P54	6	43100273	43100273	Missense_Mutation	SNP	C	T	C	PTK7	c.C1100T	p.A367V
XH_P54	6	56416987	56416987	Missense_Mutation	SNP	A	T	A	DST	c.T8734A	p.F2912I
XH_P54	6	100838607	100838607	Frame_Shift_Ins	INS	-	G	-	SIM1	c.1930dupC	p.H644fs
XH_P54	6	101296444	101296444	Silent	SNP	G	C	G	ASCC3	c.C381G	p.A127A
XH_P54	6	111665212	111665212	Missense_Mutation	SNP	C	A	C	REV3L	c.G7454T	p.S248S
XH_P54	6	139694661	139694661	Missense_Mutation	SNP	C	T	C	CITED2	c.G421A	p.A141T
XH_P54	6	150464616	150464616	Silent	SNP	T	C	T	PPP1R14C	c.T288C	p.G96G
XH_P54	6	151917494	151917494	Missense_Mutation	SNP	G	A	G	CCDC170	c.G1492A	p.E498K
XH_P54	7	7634710	7634710	Missense_Mutation	SNP	G	A	G	MIOS	c.G2143A	p.E715K
XH_P54	7	21630591	21630591	Missense_Mutation	SNP	T	C	T	DNAH11	c.T2225C	p.I742T
XH_P54	7	77797375	77797375	Silent	SNP	G	A	G	MAGI2	c.C2412T	p.R804R
XH_P54	7	87174276	87174276	Nonsense_Mutation	SNP	C	A	C	ABCB1	c.G1927T	p.E643X
XH_P54	7	96653634	96653634	Missense_Mutation	SNP	T	G	T	DLX5	c.A302C	p.Y101S
XH_P54	7	127991138	127991138	Missense_Mutation	SNP	C	G	C	PRRT4	c.G2472C	p.R824S
XH_P54	7	139416488	139416488	Missense_Mutation	SNP	G	A	G	HIPK2	c.C346T	p.R116C
XH_P54	7	143657858	143657858	Silent	SNP	T	C	T	OR2F1	c.T795C	p.S265S
XH_P54	8	23217710	23217710	Missense_Mutation	SNP	C	A	C	LOXL2	c.G424T	p.G142C
XH_P54	8	72756128	72756128	Missense_Mutation	SNP	G	T	G	MSC	c.C286A	p.P96T
XH_P54	8	86019547	86019547	Missense_Mutation	SNP	C	T	C	LRRC1	c.C17T	p.A6V
XH_P54	8	95538566	95538566	Missense_Mutation	SNP	G	T	G	VIRMA	c.C1906A	p.H636N
XH_P54	8	143833830	143833830	Missense_Mutation	SNP	C	T	C	LYPD2	c.G40A	p.A14T
XH_P54	9	35044077	35044077	Missense_Mutation	SNP	T	G	T	C9orf131	c.T1346G	p.V449G
XH_P54	9	35396547	35396547	Nonsense_Mutation	SNP	G	T	G	UNC13B	c.G3136T	p.I1046X
XH_P54	9	90343177	90343177	Missense_Mutation	SNP	T	C	T	CTSL	c.T262C	p.F88L
XH_P54	9	99700193	99700193	Silent	SNP	C	T	C	NUTM2G	c.C1350T	p.F450F
XH_P54	9	100070326	100070326	Missense_Mutation	SNP	G	A	G	CCDC180	c.G113A	p.G38D
XH_P54	9	104357055	104357055	Missense_Mutation	SNP	C	T	C	PPP3R2	c.C158A	p.R53H
XH_P54	9	107574934	107574934	Missense_Mutation	SNP	A	C	A	ABCA1	c.T3971G	p.L1324R
XH_P54	9	129851332	129851332	Silent	SNP	G	T	G	ANGPTL2	c.C1368A	p.G456G
XH_P54	9	130689479	130689479	Missense_Mutation	SNP	G	T	G	PIP5KL1	c.C603A	p.F201I
XH_P54	9	130716134	130716134	Missense_Mutation	SNP	G	A	G	FAM102A	c.C217T	p.P73S
XH_P54	9	136216831	136216831	Missense_Mutation	SNP	A	C	A	RPL7A	c.A339C	p.R113S
XH_P54	9	140358583	140358583	Missense_Mutation	SNP	G	T	G	PNPLA7	c.C3146A	p.T1049N
XH_P54	10	46272797	46272797	Missense_Mutation	SNP	A	G	A	WASHC2C	c.A2219G	p.K740R
XH_P54	10	50038928	50038928	Missense_Mutation	SNP	T	C	T	WDFY4	c.T6524C	p.L2175S
XH_P54	10	75553649	75553649	Missense_Mutation	SNP	C	A	C	ZSWIM8	c.C2472A	p.S824R
XH_P54	10	77159050	77159050	Silent	SNP	G	A	G	ZNF503	c.C1398T	p.Y466Y
XH_P54	10	100003852	100003852	Missense_Mutation	SNP	A	C	A	R3HCC1L	c.A2274C	p.R758S
XH_P54	10	101190234	101190234	Missense_Mutation	SNP	T	G	T	GOT1	c.A89C	p.D30A
XH_P54	10	102005647	102005647	Missense_Mutation	SNP	G	T	G	CWF19L1	c.C462A	p.F154L
XH_P54	10	124896698	124896698	Silent	SNP	C	A	C	HMX3	c.C525A	p.I175I
XH_P54	11	824052	824052	Missense_Mutation	SNP	T	C	T	PNPLA2	c.T974C	p.M325T
XH_P54	11	1272259	1272259	Missense_Mutation	SNP	G	A	G	MUC5B	c.G14149A	p.A4717T
XH_P54	11	3849251	3849251	Missense_Mutation	SNP	A	C	A	RHOG	c.T118G	p.Y10D
XH_P54	11	4409736	4409736	Missense_Mutation	SNP	T	C	T	TRIM21	c.A529G	p.R177G
XH_P54	11	5067940	5067940	Missense_Mutation	SNP	T	C	T	OR52J3	c.T185C	p.F62S
XH_P54	11	6806883	6806883	Silent	SNP	C	A	C	OR2AG1	c.C615A	p.T205T
XH_P54	11	7021325	7021325	Missense_Mutation	SNP	T	C	T	ZNF214	c.A1589G	p.D530G
XH_P54	11	8662398	8662398	Silent	SNP	G	A	G	TRIM66	c.C1089T	p.C363C
XH_P54	11	8933135	8933135	Missense_Mutation	SNP	G	T	G	AKIP1	c.G139T	p.G47C
XH_P54	11	51515935	51515935	Silent	SNP	C	A	C	OR4C46	c.C654A	p.V218V
XH_P54	11	57798655	57798655	Silent	SNP	T	A	T	OR6Q1	c.T231A	p.S77S
XH_P54	11	63970654	63970654	Frame_Shift_Ins	INS	-	AGCTTCCCAGCT	-	STIP1	GCCTCCAGCTTC	p.A494fs
XH_P54	11	67926352	67926352	Missense_Mutation	SNP	A	C	A	KMT5B	c.T741G	p.N247K
XH_P54	11	68540788	68540788	Missense_Mutation	SNP	C	A	A	CPT1A	c.G1685T	p.C562F
XH_P54	11	70319393	70319393	Missense_Mutation	SNP	C	T	C	SHANK2	c.G3367A	p.V1123M
XH_P54	11	70333348	70333348	Missense_Mutation	SNP	G	T	G	SHANK2	c.C1286A	p.S429Y

XH_P54	11	75115750	75115750	Silent	SNP	C	T	C	RPS3	c.C195T	p.P65P
XH_P54	11	77727935	77727935	Missense_Mutation	SNP	C	T	C	KCTD14	c.G472A	p.A158T
XH_P54	11	100558549	100558549	Missense_Mutation	SNP	T	C	T	ARHGAP42	c.T140C	p.I47T
XH_P54	11	105797521	105797521	Missense_Mutation	SNP	T	G	T	GRIA4	c.T1902G	p.I634M
XH_P54	11	107393259	107393259	Missense_Mutation	SNP	G	C	G	ALKBH8	c.C1062G	p.S534R
XH_P54	11	108384315	108384315	Missense_Mutation	SNP	T	C	T	EXPH5	c.A1355G	p.N452S
XH_P54	12	3806135	3806135	Missense_Mutation	SNP	T	C	T	CRACR2A	c.A31G	p.R11G
XH_P54	12	6969385	6969385	Missense_Mutation	SNP	C	T	C	USP5	c.C1201T	p.R401W
XH_P54	12	7548796	7548796	Missense_Mutation	SNP	C	A	C	CD163L1	c.G1975T	p.D659Y
XH_P54	12	39763556	39763556	Missense_Mutation	SNP	A	G	A	KIF21A	c.T425C	p.F142S
XH_P54	12	47472334	47472334	Missense_Mutation	SNP	T	A	T	AMIGO2	c.A452T	p.N151I
XH_P54	12	48082974	48082974	Silent	SNP	A	G	A	RPAP3	c.T195C	p.Y65Y
XH_P54	12	48458886	48458886	Missense_Mutation	SNP	A	C	A	SEN1	c.T1237G	p.L413V
XH_P54	12	50357929	50357929	Missense_Mutation	SNP	G	T	G	AQP5	c.G583T	p.V195F
XH_P54	12	51447645	51447645	Splice_Site	SNP	T	C	T	LETMD1	.	.
XH_P54	12	53162773	53162775	In_Frame_Del	DEL	ACT	-	ACT	KRT76	c.1639_1641del	p.547_547del
XH_P54	12	54686412	54686412	Missense_Mutation	SNP	T	G	T	NFE2	c.A868C	p.T290P
XH_P54	12	72667178	72667178	Missense_Mutation	SNP	G	T	G	TRHDE	c.G620T	p.G207V
XH_P54	12	76424934	76424934	Frame_Shift_Del	DEL	C	-	C	PHLDA1	c.588delG	p.Q196fs
XH_P54	12	76424936	76424940	Frame_Shift_Del	DEL	GTTGC	-	GTTGC	PHLDA1	c.582_586del	p.Q194fs
XH_P54	12	112674751	112674751	Silent	SNP	T	C	T	HECTD4	c.A5040G	p.S1680S
XH_P54	12	117465917	117465917	Silent	SNP	T	C	T	FBXW8	c.T1539C	p.C513C
XH_P54	12	120784034	120784034	Silent	SNP	G	A	G	MSI1	c.C951T	p.A317A
XH_P54	13	23910331	23910331	Missense_Mutation	SNP	A	T	A	SACS	c.T7243A	p.C2415S
XH_P54	13	33628273	33628273	Silent	SNP	C	T	C	KL	c.C1189T	p.L397L
XH_P54	13	43528085	43528085	Missense_Mutation	SNP	A	G	A	EPST11	c.T181C	p.Y61H
XH_P54	14	21680008	21680008	Missense_Mutation	SNP	T	C	T	HNRNPC	c.A637G	p.N213D
XH_P54	14	23302693	23302693	Missense_Mutation	SNP	T	A	T	MRPL52	c.T221A	p.V74E
XH_P54	14	24780826	24780826	Missense_Mutation	SNP	G	A	G	LTBR42	c.G956A	p.R319H
XH_P54	14	51111571	51111571	Nonsense_Mutation	SNP	G	A	G	SAV1	c.C697T	p.R233X
XH_P54	14	77493785	77493785	Silent	SNP	C	T	C	IRF2BPL	c.G351A	p.Q117Q
XH_P54	14	77493831	77493833	In_Frame_Del	DEL	GCG	-	GCG	IRF2BPL	c.303_305del	p.101_102del
XH_P54	14	93712623	93712623	Nonsense_Mutation	SNP	T	A	T	BTBD7	c.A1078T	p.K360X
XH_P54	14	102348578	102348578	Silent	SNP	A	G	A	PPP2R5C	c.A375G	p.P125P
XH_P54	15	30927337	30927337	Missense_Mutation	SNP	T	A	T	ARHGAP11B	c.T606A	p.N202K
XH_P54	15	33445600	33445600	Missense_Mutation	SNP	T	G	T	FMN1	c.A1516C	p.N506H
XH_P54	15	34824178	34824178	Missense_Mutation	SNP	T	C	T	GOLGA8B	c.A308G	p.E103G
XH_P54	15	42703126	42703126	Missense_Mutation	SNP	T	A	T	CAPN3	c.T313A	p.Y105N
XH_P54	15	43367213	43367213	Silent	SNP	T	G	T	UBR1	c.A492C	p.V164V
XH_P54	15	48058187	48058187	Missense_Mutation	SNP	C	T	C	SEMA6D	c.C1549T	p.R517C
XH_P54	15	52011717	52011717	Silent	SNP	C	T	C	SCG3	c.C705T	p.S235S
XH_P54	15	65983228	65983228	Missense_Mutation	SNP	T	A	T	DENND4A	c.A3572T	p.D1191V
XH_P54	15	76630767	76630767	Silent	SNP	C	T	C	ISL2	c.C423T	p.A141A
XH_P54	15	78453963	78453963	Missense_Mutation	SNP	G	T	G	IDH3A	c.G330T	p.M110I
XH_P54	15	83226579	83226579	Silent	SNP	T	A	T	CPEB1	c.A312T	p.R104R
XH_P54	16	16208777	16208777	Missense_Mutation	SNP	G	C	G	ABCC1	c.G3234C	p.K1078N
XH_P54	16	23573955	23573955	Missense_Mutation	SNP	C	A	C	UBFD1	c.C640A	p.P214T
XH_P54	16	31195695	31195695	Silent	SNP	T	C	T	FUS	c.T498C	p.G166G
XH_P54	16	47581443	47581443	Missense_Mutation	SNP	A	G	A	PHKB	c.A694G	p.T232A
XH_P54	16	55566771	55566771	Missense_Mutation	SNP	C	T	C	LPCAT2	c.C739T	p.L247F
XH_P54	16	66947518	66947518	Splice_Site	INS	-	G	-	CDH16	.	.
XH_P54	16	67986272	67986272	Silent	SNP	C	T	C	SLC12A4	c.G738A	p.S246S
XH_P54	16	74487191	74487191	Silent	SNP	T	G	T	GLG1	c.A3381C	p.V1127V
XH_P54	16	85936728	85936728	Missense_Mutation	SNP	T	C	T	IRF8	c.T107C	p.F36S
XH_P54	17	982075	982075	Missense_Mutation	SNP	A	G	A	ABR	c.T25C	p.F9L
XH_P54	17	1703514	1703514	Missense_Mutation	SNP	T	G	T	SMYD4	c.A1174C	p.N392H
XH_P54	17	3119423	3119423	Missense_Mutation	SNP	G	T	G	OR1A1	c.G509T	p.G170V
XH_P54	17	4200037	4200037	Missense_Mutation	SNP	G	T	G	UBE2G1	c.C222A	p.F74L
XH_P54	17	7750648	7750648	Missense_Mutation	SNP	A	T	A	KDM6B	c.A1135T	p.T379S
XH_P54	17	7750650	7750650	Silent	SNP	C	T	C	KDM6B	c.C1137T	p.T379T
XH_P54	17	7847874	7847874	Missense_Mutation	SNP	A	T	A	CNTR0B	c.A1652T	p.E551V
XH_P54	17	8402721	8402721	Missense_Mutation	SNP	A	C	A	MYH10	c.T3725G	p.V1242G
XH_P54	17	10417165	10417165	Silent	SNP	G	A	G	MYH1	c.C714T	p.T238T
XH_P54	17	17699815	17699815	Missense_Mutation	SNP	G	A	G	RAI1	c.G3553A	p.A1185T
XH_P54	17	26731770	26731770	Silent	SNP	G	A	G	SLC46A1	c.C945T	p.Y315Y
XH_P54	17	27086086	27086086	Silent	SNP	G	A	G	FAM222B	c.C891T	p.P297P
XH_P54	17	33807084	33807084	Nonsense_Mutation	DEL	T	-	T	SLFN12L	c.145delA	p.M49X
XH_P54	17	38978263	38978263	Missense_Mutation	SNP	T	C	T	KRT10	c.A575G	p.E192G
XH_P54	17	43045281	43045281	Missense_Mutation	SNP	T	A	T	KLQ1	c.A136T	p.T46S
XH_P54	17	43319435	43319440	In_Frame_Del	DEL	CCGCCG	-	CCGCCG	FMN1	c.1807_1812del	p.603_604del
XH_P54	17	46655298	46655298	Silent	SNP	G	A	G	HOXB4	c.C384T	p.H128H
XH_P54	17	46675325	46675325	Missense_Mutation	SNP	C	T	C	HOXB6	c.G188A	p.G63D
XH_P54	17	58603282	58603282	Missense_Mutation	SNP	A	G	A	APBP2	c.T11C	p.V4A
XH_P54	17	63221442	63221442	Missense_Mutation	SNP	G	A	G	RG59	c.G1721A	p.R574H
XH_P54	17	67081183	67081183	Missense_Mutation	SNP	C	G	C	ABCA6	c.G4170C	p.R1390S
XH_P54	18	5397084	5397084	Missense_Mutation	SNP	T	G	T	EPB41L3	c.A2148C	p.E176D
XH_P54	18	54278266	54278266	Silent	SNP	A	G	A	TXNL1	c.T798C	p.I266I
XH_P54	18	67425025	67425025	Missense_Mutation	SNP	T	G	T	DOK6	c.T772G	p.S258A
XH_P54	19	1367182	1367182	Nonsense_Mutation	SNP	T	G	T	MUM1	c.T1388G	p.L463X
XH_P54	19	1621174	1621174	Silent	SNP	T	C	T	TCF3	c.A972G	p.T324T
XH_P54	19	3982868	3982868	Silent	SNP	C	T	C	EEF2	c.G549A	p.E183E
XH_P54	19	9058338	9058338	Missense_Mutation	SNP	G	T	G	MUC16	c.C29108A	p.T9703N
XH_P54	19	9067634	9067634	Missense_Mutation	SNP	C	A	C	MUC16	c.G19812T	p.K6604N
XH_P54	19	9085462	9085462	Missense_Mutation	SNP	G	A	G	MUC16	c.C6353T	p.A2118V
XH_P54	19	11097101	11097101	Frame_Shift_Del	DEL	G	-	G	SMARCA4	c.592delG	p.I198fs
XH_P54	19	11577067	11577067	Missense_Mutation	SNP	C	A	C	ELAVL3	c.G253T	p.V85L
XH_P54	19	17362394	17362394	Missense_Mutation	SNP	T	C	T	USHBP1	c.A1727G	p.H576R
XH_P54	19	19416780	19416780	Missense_Mutation	SNP	A	G	A	SUGP1	c.T416C	p.L139P
XH_P54	19	19674356	19674356	Missense_Mutation	SNP	G	C	G	PBX4	c.C994G	p.L332V
XH_P54	19	19744923	19744923	Missense_Mutation	SNP	G	T	G	GMIP	c.C2074A	p.P692T
XH_P54	19	20229513	20229513	Missense_Mutation	SNP	C	A	C	ZNF90	c.C1150A	p.L384I
XH_P54	19	38102914	38102914	Missense_Mutation	SNP	T	C	T	ZNF540	c.T637C	p.C213R
XH_P54	19	38103841	38103841	Missense_Mutation	SNP	A	C	A	ZNF540	c.A1564C	p.S222Q
XH_P54	19	38910627	38910627	Frame_Shift_Del	DEL	G	-	G	RASGRP4	c.536delC	p.P179fs
XH_P54	19	39913476	39913476	Silent	SNP	G	A	G	PLEKHG2	c.G1605A	p.E535E
XH_P54	19	42730237	42730237	Missense_Mutation	SNP	G	A	G	ZNF526	c.G1682A	p.R561H
XH_P54	19	44605335	44605335	Missense_Mutation	SNP	G	T	G	ZNF224	c.G192T	p.K64N
XH_P54	19	45815093	45815093	Silent	SNP	A	G	A	CKM	c.T567C	p.D189D

XH_P54	19	46388993	46388993	Silent	SNP	G	A	G	IRF2BP1	c.C40T	p.L14L
XH_P54	19	46522640	46522640	Missense_Mutation	SNP	C	A	C	PGLYRP1	c.G447T	p.Q149H
XH_P54	19	47935436	47935436	Missense_Mutation	SNP	T	C	T	SLC8A2	c.A2377G	p.T793A
XH_P54	19	50962439	50962439	Silent	SNP	G	C	G	MYBP2C	c.G2667C	p.R889R
XH_P54	19	56538692	56538692	Missense_Mutation	SNP	G	A	G	NLRP5	c.G1093A	p.D365N
XH_P54	19	56549543	56549543	Missense_Mutation	SNP	G	A	G	NLRP5	c.G2768A	p.C923Y
XH_P54	20	1286151	1286151	Missense_Mutation	SNP	C	A	C	SNPH	c.C938A	p.A313D
XH_P54	20	17929597	17929597	Silent	SNP	T	G	T	SNX5	c.A540C	p.S180S
XH_P54	20	19679221	19679221	Missense_Mutation	SNP	A	G	A	SLC24A3	c.A1616G	p.D539G
XH_P54	20	34220523	34220523	Silent	SNP	G	A	G	CPNE1	c.C225T	p.R75R
XH_P54	20	42089666	42089666	Missense_Mutation	SNP	A	G	A	SRSF6	c.A998G	p.K333R
XH_P54	20	44520238	44520243	In_Frame_Del	DEL	CTGCTG	-	CTGCTG	CTSA	c.85_90del	p.29_30del
XH_P54	20	60585091	60585102	Frame_Shift_Del	DEL	TGGCTCTTAC	-	GTGGCTCTTACC	TAF4	c.1761delG	p.T587fs
XH_P54	20	60913399	60913399	Missense_Mutation	SNP	C	A	C	LAMA5	c.G1645T	p.A549S
XH_P54	22	22288558	22288558	Silent	SNP	G	T	G	PPM1F	c.C396A	p.R132R
XH_P54	22	24837443	24837443	Missense_Mutation	SNP	G	A	G	ADORA2A	c.G1225A	p.A409T
XH_P54	22	37334017	37334017	Missense_Mutation	SNP	T	C	T	CSF2RB	c.T2167C	p.S723P
XH_P54	22	37455397	37455397	Silent	SNP	G	A	G	KCTD17	c.G552A	p.Q184Q
XH_P54	22	37964302	37964318	Frame_Shift_Del	DEL	GCCCTTGCA	-	AAGCCCTGCAG	CDC42EP1	c.651_667del	p.P217fs
XH_P54	22	40057211	40057211	Frame_Shift_Ins	INS	-	C	-	CACNA1I	c.2693dupC	p.A898fs
XH_P54	22	45574145	45574145	Missense_Mutation	SNP	A	G	A	NUP50	c.A367G	p.T123A
XH_P54	22	50181275	50181275	Missense_Mutation	SNP	C	A	C	BRD1	c.G2605T	p.A869S
XH_P54	22	50726369	50726369	Missense_Mutation	SNP	C	A	C	PLXNB2	c.G1478T	p.G493V
XH_P54	X	18767912	18767912	Missense_Mutation	SNP	T	G	T	PPEF1	c.T238G	p.L80V
XH_P54	X	23019467	23019467	Silent	SNP	T	C	T	DDX53	c.T1293C	p.G431G
XH_P54	X	24380922	24380922	Silent	SNP	C	A	C	SUPT20HL1	c.C45A	p.I15I
XH_P54	X	24721463	24721463	Silent	SNP	T	C	T	POLA1	c.T264C	p.D88D
XH_P54	X	46918397	46918397	Missense_Mutation	SNP	A	G	A	JADE3	c.A2390G	p.E797G
XH_P54	X	48689846	48689846	Missense_Mutation	SNP	G	T	G	PCSK1N	c.C607A	p.L203I
XH_P54	X	55042032	55042032	Missense_Mutation	SNP	C	A	C	ALAS2	c.G1036T	p.D346Y
XH_P54	X	69665291	69665291	Silent	SNP	G	A	G	DLG3	c.G240A	p.R80R
XH_P54	X	70342686	70342686	Nonsense_Mutation	SNP	C	T	C	MED12	c.C1447T	p.R483X
XH_P54	X	72434324	72434324	Missense_Mutation	SNP	G	T	G	NAP1L2	c.C5A	p.A2D
XH_P54	X	79932788	79932788	Missense_Mutation	SNP	T	G	T	BRWD3	c.A4729C	p.S1577R
XH_P54	X	90691206	90691206	Silent	SNP	A	C	A	PABPC5	c.A630C	p.I20I
XH_P54	X	102931574	102931574	Nonsense_Mutation	SNP	C	A	C	MORF4L2	c.G382T	p.E128X
XH_P54	X	102974177	102974177	Silent	SNP	T	G	T	GLRA4	c.A741C	p.V247V
XH_P54	X	106840647	106840647	Nonsense_Mutation	DEL	C	-	C	FRMPD3	c.1637delC	p.S546X
XH_P54	X	117744269	117744269	Missense_Mutation	SNP	A	T	A	DOCK11	c.A2984T	p.H995L
XH_P54	X	117744270	117744270	Missense_Mutation	SNP	T	G	T	DOCK11	c.T2985G	p.H995Q
XH_P54	X	129146584	129146584	Silent	SNP	G	A	G	BCORL1	c.G117A	p.T39T
XH_P54	X	132160632	132160632	Silent	SNP	G	T	G	USP26	c.C1617A	p.V539V
XH_P54	X	132161092	132161092	Missense_Mutation	SNP	A	C	A	USP26	c.T1157G	p.P386C
XH_P54	X	139865906	139865906	Frame_Shift_Ins	INS	-	A	-	CDR1	c.625dupT	p.S209fs
XH_P54	1	111985955	111985955	Silent	SNV	G	T	T	WDR77	c.681C>A	P.V227V
XH_P54	1	144823826	144823826	Missense_Mutation	SNV	C	G	G	NBPF9	c.1864C>G	P.L622V
XH_P54	1	151105835	151105835	Missense_Mutation	SNV	T	C	C	SEMA6C	c.2014A>G	P.I672V
XH_P54	1	152882717	152882717	Missense_Mutation	SNV	G	T	T	IVL	c.444G>T	P.K148N
XH_P54	1	154574428	154574428	Missense_Mutation	SNV	T	G	G	ADAR	c.690A>C	P.E230D
XH_P54	1	156437998	156437998	Silent	SNV	A	G	G	MEF2D	c.1320T>C	P.R440R
XH_P54	1	165636699	165636699	Splice_Site	SNV	A	C	C	ALDH9A1	c.1208-12T>G	
XH_P54	1	205901138	205901138	Silent	SNV	C	G	G	SLC26A9	c.402G>C	P.L134L
XH_P54	1	247420279	247420279	Silent	SNV	G	C	C	VN1R5	c.906G>C	P.V302V
XH_P54	1	26149596	26149596	Nonsense_Mutation	SNV	A	G	G	MTFR1L	c.1A>G	P.M17
XH_P54	1	92445291	92445291	Missense_Mutation	SNV	C	T	T	BRDT	c.1264C>T	P.R422C
XH_P54	10	100003852	100003852	Missense_Mutation	SNV	A	C	C	R3HCC1L	c.2316A>C	P.R772S
XH_P54	10	46272797	46272797	Missense_Mutation	SNV	A	G	G	FAM21C	c.2219A>G	P.K740R
XH_P54	10	77159050	77159050	Silent	SNV	G	A	A	ZNFS03	c.1398C>T	P.Y466Y
XH_P54	11	107393259	107393259	Missense_Mutation	SNV	G	C	C	ALKBH8	c.1062C>G	P.S354R
XH_P54	11	3849251	3849251	Missense_Mutation	SNV	A	C	C	RHOG	c.118T>G	P.Y40D
XH_P54	11	5067940	5067940	Missense_Mutation	SNV	T	C	C	OR52J3	c.185T>C	P.F62S
XH_P54	11	51515935	51515935	Silent	SNV	C	A	A	OR4C46	c.654C>A	P.V218V
XH_P54	11	57798655	57798655	Silent	SNV	T	A	A	OR6Q1	c.231T>A	P.S77S
XH_P54	11	6806883	6806883	Silent	SNV	C	A	A	OR2AG1	c.615C>A	P.T205T
XH_P54	11	68540788	68540788	Missense_Mutation	SNV	C	A	A	CPT1A	c.1685G>T	P.C562F
XH_P54	11	7021325	7021325	Missense_Mutation	SNV	T	C	C	ZNFX214	c.1589A>G	P.D530G
XH_P54	12	117465917	117465917	Silent	SNV	T	C	C	FBXW8	c.1539T>C	P.C513C
XH_P54	12	39763556	39763556	Missense_Mutation	SNV	A	G	G	KIF21A	c.425T>C	P.F142S
XH_P54	12	47472334	47472334	Missense_Mutation	SNV	T	A	A	AMIGO2	c.452A>T	P.N151I
XH_P54	12	53073536	53073536	Splice_Site	SNV	A	T	T	KRT1	c.591+6T>A	
XH_P54	14	102348578	102348578	Silent	SNV	A	G	G	PPP2R5C	c.468A>G	P.P156P
XH_P54	14	21680008	21680008	Missense_Mutation	SNV	T	C	C	HNRNPC	c.637A>G	P.N213D
XH_P54	14	23302693	23302693	Missense_Mutation	SNV	T	A	A	MRPL52	c.221T>A	P.V74E
XH_P54	14	51111571	51111571	Nonsense_Mutation	SNV	G	A	A	SAV1	c.697C>T	P.R233*
XH_P54	14	93712623	93712623	Nonsense_Mutation	SNV	T	A	A	BTBD7	c.2131A>T	P.K711*
XH_P54	15	52011717	52011717	Silent	SNV	C	T	T	SCG3	c.705C>T	P.S235S
XH_P54	15	65983228	65983228	Missense_Mutation	SNV	T	A	A	DENND4A	c.3701A>T	P.D1234V
XH_P54	15	78453963	78453963	Missense_Mutation	SNV	G	T	T	IDH3A	c.330G>T	P.M110I
XH_P54	16	16208777	16208777	Missense_Mutation	SNV	G	C	C	ABCC1	c.3234G>C	P.K1078N
XH_P54	16	23573955	23573955	Missense_Mutation	SNV	C	A	A	UBFD1	c.640C>A	P.P214T
XH_P54	16	31195695	31195695	Silent	SNV	T	C	C	FUS	c.501T>C	P.G167G
XH_P54	16	47581443	47581443	Missense_Mutation	SNV	A	G	G	PHKB	c.694A>G	P.T232A
XH_P54	16	55566771	55566771	Missense_Mutation	SNV	C	T	T	LPCAT2	c.739C>T	P.L247F
XH_P54	16	66947518	66947518	Splice_Site	INDEL	-	G	G	CDH16	c.781-3dupC	
XH_P54	16	67986272	67986272	Silent	SNV	C	T	T	SLC12A4	c.732G>A	P.S244S
XH_P54	16	74487191	74487191	Silent	SNV	T	G	G	GLG1	c.3381A>C	P.V1127V
XH_P54	16	85936728	85936728	Missense_Mutation	SNV	T	C	C	IRF8	c.107T>C	P.F36S
XH_P54	17	131652	131652	Splice_Site	SNV	G	C	C	RPH3AL	c.352-7C>G	
XH_P54	17	1703514	1703514	Missense_Mutation	SNV	T	G	G	SMYD4	c.1174A>C	P.N392H
XH_P54	17	38978263	38978263	Missense_Mutation	SNV	T	C	C	KRT10	c.575A>G	P.E192G
XH_P54	18	5397084	5397084	Missense_Mutation	SNV	T	G	G	EPB41L3	c.2307A>C	P.E769D
XH_P54	19	1367182	1367182	Nonsense_Mutation	SNV	T	G	G	MUM1	c.1388T>G	P.L463*
XH_P54	19	17362394	17362394	Missense_Mutation	SNV	T	C	C	USHBP1	c.1727A>G	P.H576R
XH_P54	19	19674356	19674356	Missense_Mutation	SNV	G	C	C	PBX4	c.994C>G	P.L332V
XH_P54	19	20229513	20229513	Missense_Mutation	SNV	C	A	A	ZNFX90	c.1150C>A	P.L384I
XH_P54	19	38102914	38102914	Missense_Mutation	SNV	T	C	C	ZNFX540	c.733T>C	P.C245R
XH_P54	19	42730237	42730237	Missense_Mutation	SNV	G	A	A	ZNFX526	c.1682G>A	P.R561H
XH_P54	19	46388993	46388993	Silent	SNV	G	A	A	IRF2BP1	c.40C>T	P.L14L

XH_P54	19	47935436	47935436	Missense_Mutation	SNV	T	C	C	SLC8A2	c.2377A>G	P.T793A
XH_P54	19	5222688	5222688	Splice_Site	SNV	C	G	G	PTPRS	c.3103+12G>C	
XH_P54	19	56538692	56538692	Missense_Mutation	SNV	G	A	A	NLRP5	c.1093G>A	P.D365N
XH_P54	19	56549543	56549543	Missense_Mutation	SNV	G	A	A	NLRP5	c.2768G>A	P.Q923Y
XH_P54	19	9058338	9058338	Missense_Mutation	SNV	G	T	T	MUC16	c.29108C>A	P.T9703N
XH_P54	19	9085462	9085462	Missense_Mutation	SNV	G	A	A	MUC16	c.6353C>T	P.A2118V
XH_P54	2	141739835	141739835	Silent	SNV	G	A	A	LRP1B	c.2781C>T	P.C927C
XH_P54	2	173825479	173825479	Splice_Site	SNV	A	G	G	RAPGEF4	c.106-9A>G	
XH_P54	2	203383667	203383667	Silent	SNV	A	G	G	BMPR2	c.744A>G	P.R248R
XH_P54	2	207026187	207026187	Silent	SNV	T	C	C	EEF1B2	c.321T>C	P.D107D
XH_P54	2	219305595	219305595	Splice_Site	SNV	A	T	T	VIL1	c.2370+10A>T	
XH_P54	2	40657236	40657236	Missense_Mutation	SNV	G	A	A	SLC8A1	c.185C>T	P.P62L
XH_P54	2	71219019	71219019	Missense_Mutation	SNV	C	A	A	TEX261	c.245G>T	P.G82V
XH_P54	2	79385866	79385866	Missense_Mutation	SNV	C	G	G	REG3A	c.106G>C	P.A36P
XH_P54	20	17929597	17929597	Silent	SNV	T	G	G	SNX5	c.540A>C	P.S180S
XH_P54	20	34220523	34220523	Silent	SNV	G	A	A	CPNE1	c.225C>T	P.R75R
XH_P54	20	42089666	42089666	Missense_Mutation	SNV	A	G	G	SRSF6	c.998A>G	P.K333R
XH_P54	20	60913399	60913399	Missense_Mutation	SNV	C	A	A	LAMA5	c.1645G>T	P.A549S
XH_P54	22	22288558	22288558	Silent	SNV	G	T	T	PPM1F	c.396C>A	P.R132R
XH_P54	22	37455397	37455397	Silent	SNV	G	A	A	KCTD17	c.552G>A	P.Q184Q
XH_P54	22	40057211	40057211	Frame_Shift_Ins	INDEL	-	C	C	CACNA1I	c.2698dupC	P.R900fs
XH_P54	22	50726369	50726369	Missense_Mutation	SNV	C	A	A	PLXNB2	c.1478G>T	P.G493V
XH_P54	3	108298423	108298423	Missense_Mutation	SNV	A	C	C	KIAA1524	c.662T>G	P.V221G
XH_P54	3	112548241	112548241	Splice_Site	SNV	A	G	G	CD200R1L	c.47-10T>C	
XH_P54	3	121409820	121409820	Missense_Mutation	SNV	C	A	A	GOLGB1	c.8391G>T	P.M2797I
XH_P54	3	128969537	128969537	Missense_Mutation	SNV	A	C	C	COPG1	c.50A>C	P.N17T
XH_P54	3	130714921	130714921	Missense_Mutation	SNV	A	C	C	ATP2C1	c.2092A>C	P.N698H
XH_P54	3	1443123	1443123	Missense_Mutation	SNV	G	T	T	CNTN6	c.2711G>T	P.S904I
XH_P54	3	14706527	14706527	Splice_Site	SNV	C	A	A	CCDC174	c.486-8C>A	
XH_P54	3	151164791	151164791	Missense_Mutation	SNV	T	C	C	IGSF10	c.2978A>G	P.Q993R
XH_P54	3	195516981	195516981	Silent	SNV	G	A	A	MUC4	c.1470C>T	P.S490S
XH_P54	3	42576581	42576581	Silent	SNV	C	T	T	VIPR1	c.1002C>T	P.V334V
XH_P54	3	57407392	57407392	Silent	SNV	A	G	G	DNAH12	c.5427T>C	P.S1809S
XH_P54	3	61975366	61975366	Silent	SNV	T	C	C	PTPRG	c.258T>C	P.I86I
XH_P54	4	1806163	1806163	Silent	SNV	G	T	T	FGFR3	c.1182G>T	P.T394T
XH_P54	4	77817956	77817956	Silent	SNV	T	G	G	SOWAHB	c.1047A>C	P.S349S
XH_P54	5	140810735	140810735	Nonsense_Mutation	SNV	G	T	T	PCDHGA12	c.409G>T	P.E137*
XH_P54	5	153755840	153755840	Missense_Mutation	SNV	A	G	G	GALNT10	c.572A>G	P.H191R
XH_P54	5	40853720	40853720	Missense_Mutation	SNV	G	T	T	CARD6	c.2286G>T	P.R762S
XH_P54	5	74441843	74441843	Silent	SNV	T	C	C	ANKRD31	c.3393A>G	P.Q1131Q
XH_P54	5	82834295	82834295	Missense_Mutation	SNV	C	T	T	VCAN	c.5473C>T	P.P1825S
XH_P54	5	90006806	90006806	Missense_Mutation	SNV	G	A	A	ADGRV1	c.8833G>A	P.G2945S
XH_P54	6	151917494	151917494	Missense_Mutation	SNV	G	A	A	CCDC170	c.1492G>A	P.E498K
XH_P54	6	34826124	34826124	Missense_Mutation	SNV	T	C	C	UHRF1BP1	c.1991T>C	P.L664P
XH_P54	6	43100273	43100273	Missense_Mutation	SNV	C	T	T	PTK7	c.1100C>T	P.A367V
XH_P54	6	56416987	56416987	Missense_Mutation	SNV	A	T	T	DST	c.10246T>A	P.F3416I
XH_P54	7	7634710	7634710	Missense_Mutation	SNV	G	A	A	MIOS	c.2143G>A	P.E175K
XH_P54	7	96653634	96653634	Missense_Mutation	SNV	T	G	G	DLX5	c.302A>C	P.Y101S
XH_P54	8	23217710	23217710	Missense_Mutation	SNV	C	A	A	LOXL2	c.424G>T	P.G142C
XH_P54	8	95538566	95538566	Missense_Mutation	SNV	G	T	T	KIAA1429	c.1906C>A	P.H636N
XH_P54	9	107574934	107574934	Missense_Mutation	SNV	A	C	C	ABCA1	c.3971T>G	P.L1324R
XH_P54	9	122004503	122004503	Splice_Site	SNV	G	C	C	BRINP1	c.410-9C>G	
XH_P54	9	129851332	129851332	Silent	SNV	G	T	T	ANGPTL2	c.1368C>A	P.G456G
XH_P54	9	140358583	140358583	Missense_Mutation	SNV	G	T	T	PNPLA7	c.3221C>A	P.T1074N
XH_P54	9	35396547	35396547	Nonsense_Mutation	SNV	G	T	T	UNC13B	c.3136G>T	P.E1046*
XH_P54	9	99700193	99700193	Silent	SNV	C	T	T	NUTM2G	c.1350C>T	P.F450F
XH_P54	X	117744269	117744269	Missense_Mutation	SNV	A	T	T	DOCK11	c.2984A>T	P.H995L
XH_P54	X	117744270	117744270	Missense_Mutation	SNV	T	G	G	DOCK11	c.2985T>G	P.H995G
XH_P54	X	23019467	23019467	Silent	SNV	T	C	C	DDX53	c.1293T>C	P.G431G
XH_P54	X	24380922	24380922	Silent	SNV	C	A	A	SUPT20H1	c.45C>A	P.I15I
XH_P54	X	46918397	46918397	Missense_Mutation	SNV	A	G	G	JADE3	c.2390A>G	P.E797G
XH_P54	X	48689846	48689846	Missense_Mutation	SNV	G	T	T	PCSK1N	c.607C>A	P.L203I
XH_P54	X	55042032	55042032	Missense_Mutation	SNV	C	A	A	ALAS2	c.1147G>T	P.P383Y
XH_P54	X	69665291	69665291	Silent	SNV	G	A	A	DLG3	c.240G>A	P.R80R
XH_P55	12	49427695	49427695	Missense_Mutation	SNP	T	C	C	KMT2D	c.10793A>G	p.K3598R
XH_P55	9	21971186	21971186	Nonsense_Mutation	SNP	G	A	A	CDKN2A	c.172C>T	p.R58*
XH_P55	9	98268739	98268739	Missense_Mutation	SNP	C	G	G	PTCH1	c.344G>C	p.G115A
XH_P55	1	1226292	1226292	Silent	SNP	G	A	G	SCNN1D	c.G1935A	p.T645T
XH_P55	1	1246311	1246311	Missense_Mutation	SNP	T	C	T	PUSL1	c.T791C	p.L264P
XH_P55	1	1390875	1390875	Silent	SNP	C	T	C	ATAD3C	c.C414T	p.D138D
XH_P55	1	1635004	1635004	Silent	SNP	T	C	T	CDK11A	c.A1980G	p.K660K
XH_P55	1	1686040	1686040	Missense_Mutation	SNP	G	T	G	NADK	c.C690A	p.N230K
XH_P55	1	1870393	1870393	Missense_Mutation	SNP	G	A	G	CFAP74	c.C2912T	p.T971M
XH_P55	1	7723534	7723534	Silent	SNP	G	A	G	CAMTA1	c.G837A	p.S279S
XH_P55	1	7723957	7723957	Silent	SNP	G	A	G	CAMTA1	c.G1260A	p.S420S
XH_P55	1	9323910	9323910	Missense_Mutation	SNP	G	A	G	H6PD	c.G1391A	p.R464Q
XH_P55	1	15809876	15809876	Silent	SNP	G	A	G	CELA2B	c.G474A	p.T158T
XH_P55	1	16577794	16577794	Missense_Mutation	SNP	C	T	C	FBXO42	c.G1525A	p.A509T
XH_P55	1	17312743	17312743	Missense_Mutation	SNP	C	T	C	ATP13A2	c.G3214A	p.A1072T
XH_P55	1	17313654	17313654	Silent	SNP	C	T	C	ATP13A2	c.G2838A	p.V946V
XH_P55	1	17396703	17396703	Silent	SNP	T	C	T	PADI2	c.A1644G	p.L548L
XH_P55	1	18149566	18149566	Silent	SNP	C	A	C	ACTL8	c.C63A	p.G21G
XH_P55	1	18152582	18152582	Silent	SNP	C	T	C	ACTL8	c.C669T	p.D223D
XH_P55	1	18152646	18152646	Missense_Mutation	SNP	C	T	C	ACTL8	c.C737T	p.R245C
XH_P55	1	20680718	20680718	Missense_Mutation	SNP	G	A	G	VWA5B1	c.G3610A	p.E1204K
XH_P55	1	21806667	21806667	Missense_Mutation	SNP	C	G	C	NBPF3	c.C1122G	p.D374E
XH_P55	1	22965438	22965438	Silent	SNP	A	G	A	CLQA	c.A276G	p.G92G
XH_P55	1	23222928	23222928	Silent	SNP	C	T	C	EPHB2	c.C1722T	p.D574D
XH_P55	1	24201262	24201262	Silent	SNP	A	G	A	CNR2	c.T846C	p.A282A
XH_P55	1	24448084	24448084	Silent	SNP	G	A	G	IL22RA1	c.C936T	p.P312P
XH_P55	1	24448224	24448224	Missense_Mutation	SNP	C	T	C	IL22RA1	c.G796A	p.V266I
XH_P55	1	25291010	25291010	Missense_Mutation	SNP	A	T	A	RUNX3	c.T53A	p.I18N
XH_P55	1	25717365	25717365	Missense_Mutation	SNP	C	G	C	RHCE	c.G676C	p.A226P
XH_P55	1	26672506	26672506	Missense_Mutation	SNP	G	A	G	CRYBG2	c.C643T	p.R215C
XH_P55	1	27676925	27676925	Silent	SNP	G	A	G	SYTL1	c.G954A	p.K318K
XH_P55	1	28733968	28733968	Frame_Shift_Del	DEL	C	-	C	PHACTR4	c.10delC	p.P4fs
XH_P55	1	31349489	31349489	Silent	SNP	G	A	G	SDC3	c.C780T	p.P260P
XH_P55	1	32165495	32165495	Missense_Mutation	SNP	G	T	G	COL16A1	c.C185A	p.T62K

XH_P55	1	32196647	32196647	Silent	SNP	C	G	C	ADGRB2	c.G4035C	p.P1345P
XH_P55	1	32221913	32221913	Silent	SNP	G	A	G	ADGRB2	c.C525T	p.P175P
XH_P55	1	32829281	32829281	Silent	SNP	G	A	G	TSSK3	c.G231A	p.L77L
XH_P55	1	36643701	36643703	In_Frame_Del	DEL	AGA	-	AGA	MAP7D1	c.1496_1498del	p.499_500del
XH_P55	1	40230336	40230336	Missense_Mutation	SNP	C	G	C	BMP8B	c.G827C	p.S276T
XH_P55	1	46810530	46810530	Missense_Mutation	SNP	A	G	A	NSUN4	c.A4G	p.T2A
XH_P55	1	49511431	49511431	Missense_Mutation	SNP	G	A	G	AGBL4	c.C455T	p.P152L
XH_P55	1	54359922	54359922	Silent	SNP	C	T	C	DIO1	c.C39T	p.L13L
XH_P55	1	62738961	62738961	Silent	SNP	G	A	G	KANK4	c.C1815T	p.S605S
XH_P55	1	77685042	77685042	Missense_Mutation	SNP	T	C	T	PIGK	c.A466G	p.T16A
XH_P55	1	78201745	78201745	Silent	SNP	G	T	G	USP33	c.C450A	p.A150A
XH_P55	1	89473492	89473492	Nonsense_Mutation	INS	-	AAAGTGTCAC	-	GBP3	01insTATAGTG	p.T434delinsX
XH_P55	1	92184912	92184912	Missense_Mutation	SNP	C	T	C	TGFBR3	c.G1520A	p.R507Q
XH_P55	1	94466659	94466659	Silent	SNP	A	G	A	ABCA4	c.T6285C	p.D2095D
XH_P55	1	109807082	109807082	Missense_Mutation	SNP	C	T	C	CELSR2	c.C5296T	p.R1766W
XH_P55	1	109815866	109815866	Missense_Mutation	SNP	C	T	C	CELSR2	c.C8417T	p.A2806V
XH_P55	1	110766466	110766466	Missense_Mutation	SNP	G	A	G	KCN4	c.G1559A	p.C520Y
XH_P55	1	110883917	110883917	Silent	SNP	A	G	A	RBM15	c.A1890G	p.R630R
XH_P55	1	114680571	114680571	Missense_Mutation	SNP	C	T	C	SYT6	c.G362A	p.R121H
XH_P55	1	115829313	115829313	Missense_Mutation	SNP	G	A	G	NGF	c.C104T	p.A35V
XH_P55	1	117503940	117503940	Missense_Mutation	SNP	G	A	G	PTGFRN	c.G1289A	p.R430Q
XH_P55	1	117529458	117529458	Missense_Mutation	SNP	G	A	G	PTGFRN	c.G2509A	p.R837I
XH_P55	1	117560818	117560818	Silent	SNP	A	G	A	CD101	c.A1653G	p.Q551Q
XH_P55	1	147380886	147380886	Silent	SNP	C	T	C	GJA8	c.C804T	p.L268L
XH_P55	1	150526044	150526044	Missense_Mutation	SNP	G	C	G	ADAMTS14	c.G577C	p.A193P
XH_P55	1	150830876	150830876	Nonsense_Mutation	SNP	C	A	C	ARNT	c.G49T	p.E17X
XH_P55	1	151288172	151288172	Silent	SNP	G	A	G	PI4KB	c.C786T	p.D262D
XH_P55	1	152187183	152187183	Missense_Mutation	SNP	C	A	C	HRNR	c.G6922T	p.G2308C
XH_P55	1	152188463	152188463	Missense_Mutation	SNP	G	A	G	HRNR	c.C5642T	p.S1881F
XH_P55	1	152191809	152191809	Missense_Mutation	SNP	C	T	C	HRNR	c.G2296A	p.G766S
XH_P55	1	152192825	152192825	Missense_Mutation	SNP	C	T	C	HRNR	c.G1280A	p.G427D
XH_P55	1	152193286	152193286	Missense_Mutation	SNP	G	T	G	HRNR	c.C819A	p.H273Q
XH_P55	1	152281106	152281106	Missense_Mutation	SNP	G	A	G	FLG	c.C6256T	p.R2086C
XH_P55	1	152327329	152327329	Missense_Mutation	SNP	T	C	T	FLG2	c.A2933G	p.E978G
XH_P55	1	152327509	152327509	Missense_Mutation	SNP	T	C	T	FLG2	c.A2753G	p.H918R
XH_P55	1	152552285	152552285	Missense_Mutation	SNP	C	A	C	LCE3D	c.G128T	p.G43V
XH_P55	1	152659471	152659471	Missense_Mutation	SNP	T	G	T	LCE2B	c.T152G	p.I51S
XH_P55	1	152732174	152732174	Missense_Mutation	SNP	T	C	T	KPRP	c.T110C	p.V37A
XH_P55	1	152732567	152732567	Missense_Mutation	SNP	G	A	G	KPRP	c.G503A	p.R168H
XH_P55	1	152733301	152733301	Missense_Mutation	SNP	T	A	T	KPRP	c.T1237A	p.C413S
XH_P55	1	152777908	152777908	Missense_Mutation	SNP	C	T	C	LCE1C	c.G47A	p.C16Y
XH_P55	1	153509890	153509890	Missense_Mutation	SNP	T	C	T	S100A5	c.A161G	p.D54G
XH_P55	1	154516578	154516578	Missense_Mutation	SNP	G	A	G	TDRD10	c.G643A	p.V215I
XH_P55	1	156255456	156255456	Missense_Mutation	SNP	G	A	G	TMEM79	c.G439A	p.V147M
XH_P55	1	156280969	156280969	Silent	SNP	G	A	G	CCT3	c.C1059T	p.L353L
XH_P55	1	156280971	156280971	Missense_Mutation	SNP	G	A	G	CCT3	c.C1057T	p.L353F
XH_P55	1	156446903	156446903	Silent	SNP	T	C	T	MEF2D	c.G456G	p.P252P
XH_P55	1	156450740	156450740	Silent	SNP	G	A	G	MEF2D	c.C282T	p.N94N
XH_P55	1	156499969	156499969	Silent	SNP	T	C	T	IQGAP3	c.A4332G	p.L1444L
XH_P55	1	156518379	156518379	Missense_Mutation	SNP	G	A	G	IQGAP3	c.C1987T	p.R663C
XH_P55	1	161495788	161495788	Missense_Mutation	SNP	G	T	G	HSPA6	c.G1340T	p.G447V
XH_P55	1	161683136	161683136	Missense_Mutation	SNP	G	A	G	FCRLA	c.G392A	p.R131Q
XH_P55	1	161967681	161967681	Missense_Mutation	SNP	A	G	A	OLFML2B	c.T1411C	p.W471R
XH_P55	1	166818566	166818566	Silent	SNP	A	G	A	POGK	c.A396G	p.A132A
XH_P55	1	172502479	172502479	Silent	SNP	T	C	T	SUCO	c.T489C	p.I163I
XH_P55	1	172547465	172547465	Silent	SNP	A	G	A	SUCO	c.A1257G	p.E419E
XH_P55	1	176563791	176563791	Missense_Mutation	SNP	A	C	A	PAPPA2	c.A1051C	p.T351P
XH_P55	1	177001896	177001896	Silent	SNP	C	G	C	ASTN1	c.G561C	p.P187P
XH_P55	1	177915596	177915596	Silent	SNP	G	A	G	SEC16B	c.C1734T	p.T578T
XH_P55	1	179983382	179983382	Silent	SNP	G	A	G	CEP350	c.G1794A	p.Q598Q
XH_P55	1	180199727	180199727	Silent	SNP	T	C	T	LHX4	c.T63C	p.G21G
XH_P55	1	180897569	180897569	Silent	SNP	C	T	C	KIAA1614	c.C1065T	p.T355T
XH_P55	1	185143721	185143721	Missense_Mutation	SNP	A	G	A	SWT1	c.A442G	p.I148V
XH_P55	1	196797357	196797357	Silent	SNP	A	G	A	CFHR1	c.A588G	p.T196T
XH_P55	1	197128938	197128938	In_Frame_Ins	INS	-	TGGAAAAATATA	-	ZBTB41	2281insTATATT	E761delinsYIFPE
XH_P55	1	201035071	201035071	Silent	SNP	G	A	G	CACNA1S	c.C2748T	p.H916H
XH_P55	1	201058551	201058551	Nonsense_Mutation	SNP	G	T	G	CACNA1S	c.C735A	p.C245X
XH_P55	1	201752964	201752964	Frame_Shift_Ins	INS	-	AGTACTCCCGT	-	NAV1	161insCAGTAC	p.A539fs
XH_P55	1	201969082	201969082	Silent	SNP	G	A	G	RNPEP	c.G273A	p.Q91Q
XH_P55	1	203008286	203008286	Silent	SNP	C	G	C	PPFIA4	c.C150G	p.T50T
XH_P55	1	203186950	203186950	Nonsense_Mutation	INS	-	TGGCCCCGCCA	-	CHIT1	GGGACTGGGCG	p.W339delinsX
XH_P55	1	203472112	203472112	Missense_Mutation	SNP	C	T	C	OPTC	c.T803C	p.L268P
XH_P55	1	205041158	205041158	Silent	SNP	C	T	C	CNTN2	c.C2628T	p.S876S
XH_P55	1	205589574	205589574	Silent	SNP	C	T	C	ELK4	c.G600A	p.P200P
XH_P55	1	209791929	209791929	Missense_Mutation	SNP	G	T	G	LAMB3	c.C2777A	p.A926D
XH_P55	1	221912808	221912808	Silent	SNP	T	C	T	DUSP10	c.A279G	p.Q93Q
XH_P55	1	222802376	222802376	Missense_Mutation	SNP	A	G	A	MIA3	c.A1814G	p.K605R
XH_P55	1	223567803	223567803	Missense_Mutation	SNP	G	A	G	CCDC185	c.G986A	p.G329D
XH_P55	1	226125385	226125385	Missense_Mutation	SNP	G	A	G	LEFTY2	c.C857T	p.P286L
XH_P55	1	226923396	226923396	Silent	SNP	G	A	G	ITPKB	c.C1764T	p.S588S
XH_P55	1	226923938	226923938	Missense_Mutation	SNP	A	C	A	ITPKB	c.T1222G	p.S408A
XH_P55	1	228475396	228475396	Silent	SNP	G	A	G	OBSCN	c.G9546A	p.A3182A
XH_P55	1	228560034	228560034	Silent	SNP	C	T	C	OBSCN	c.C21555T	p.Y7185Y
XH_P55	1	228612869	228612869	Missense_Mutation	SNP	C	T	C	HIST3H3	c.G158A	p.R53H
XH_P55	1	229773702	229773702	Silent	SNP	G	A	G	URB2	c.G3342A	p.S1114S
XH_P55	1	232941215	232941215	Missense_Mutation	SNP	A	G	A	MAP10	c.A446G	p.E149G
XH_P55	1	232941677	232941677	Missense_Mutation	SNP	G	T	G	MAP10	c.G908T	p.R303L
XH_P55	1	232942251	232942251	Silent	SNP	A	G	G	MAP10	c.A1482G	p.L494L
XH_P55	1	232942546	232942546	Missense_Mutation	SNP	A	G	A	MAP10	c.A1777G	p.K593E
XH_P55	1	236144951	236144951	Silent	SNP	A	G	A	NID1	c.T3187C	p.L1063L
XH_P55	1	240256822	240256822	Silent	SNP	C	A	C	FMN2	c.C1413A	p.A471A
XH_P55	1	242048674	242048674	Missense_Mutation	SNP	C	T	C	EXO1	c.C2270T	p.P757L
XH_P55	1	246755170	246755170	Frame_Shift_Ins	INS	-	CTATTTCAGAT	-	CNST	TGGTTCTATTGTG	p.L102fs
XH_P55	1	248202344	248202344	Missense_Mutation	SNP	G	C	G	OR2L2	c.G775C	p.V259L
XH_P55	1	248308989	248308989	Missense_Mutation	SNP	C	A	C	OR2M5	c.C540A	p.D180E
XH_P55	1	248366702	248366702	Silent	SNP	G	A	G	OR2M3	c.G333A	p.E111E
XH_P55	2	1520676	1520676	Missense_Mutation	SNP	T	C	T	TPO	c.T2408C	p.V803A
XH_P55	2	3483205	3483205	Silent	SNP	C	T	C	TRAPPC12	c.C2181T	p.F727F

XH_P55	2	20175312	20175312	Silent	SNP	G	A	G	WDR35	c.C549T	p.Y183Y
XH_P55	2	20205848	20205848	Silent	SNP	G	A	G	MATN3	c.C447T	p.A149A
XH_P55	2	29940529	29940529	Silent	SNP	A	T	A	ALK	c.T702A	p.P234P
XH_P55	2	37518045	37518045	Silent	SNP	G	C	G	PRKD3	c.C525G	p.L175L
XH_P55	2	47630435	47630435	Silent	SNP	C	A	C	MSH2	c.C105A	p.R35R
XH_P55	2	55040426	55040426	Silent	SNP	A	G	A	EML6	c.A255G	p.EM5P
XH_P55	2	55436875	55436875	Missense_Mutation	SNP	A	T	A	CLHC1	c.T226A	p.L76M
XH_P55	2	56097896	56097896	Missense_Mutation	SNP	G	A	G	EFEMP1	c.C1279T	p.R427W
XH_P55	2	65298839	65298839	Silent	SNP	A	G	A	CEP68	c.A609G	p.T203T
XH_P55	2	73496580	73496594	In_Frame_Del	DEL	GCGGCGGCCG	-	GCGGCGGCCG	FBXO41	c.165_179del	p.55_60del
XH_P55	2	73677904	73677904	Missense_Mutation	SNP	G	A	G	ALMS1	c.G4247A	p.R1416Q
XH_P55	2	74007136	74007136	Missense_Mutation	SNP	T	C	T	DUSP11	c.A107G	p.D36G
XH_P55	2	74761539	74761539	Missense_Mutation	SNP	T	A	T	LOXL3	c.A760T	p.I254F
XH_P55	2	75113657	75113657	Silent	SNP	C	T	C	HK2	c.C2076T	p.N692N
XH_P55	2	80101321	80101321	Silent	SNP	T	G	T	CTNNA2	c.T705G	p.A235A
XH_P55	2	87016533	87016533	Missense_Mutation	SNP	C	T	C	CD8A	c.G538A	p.A180T
XH_P55	2	95540642	95540642	Missense_Mutation	SNP	G	A	G	TEKT4	c.G289A	p.E97K
XH_P55	2	96604765	96604765	Splice_Site	SNP	T	G	T	ANKRD36C	-	-
XH_P55	2	96993757	96993757	Missense_Mutation	SNP	C	T	C	ITPR1PL1	c.C1412T	p.T471M
XH_P55	2	97847519	97847519	Frame_Shift_Ins	INS	-	TAATCACTCAC	-	ANKRD36	1827insTAATCA	p.Q609fs
XH_P55	2	97911257	97911257	Frame_Shift_Ins	INS	-	TTTT	-	ANKRD36	4933_4934insTT	p.H1645fs
XH_P55	2	97911258	97911258	Frame_Shift_Ins	INS	-	AGTATTT	-	ANKRD36	4934_4935insAGT	p.H1645fs
XH_P55	2	98408918	98408918	Missense_Mutation	SNP	C	T	C	TMEM131	c.G4075A	p.D1359N
XH_P55	2	98928757	98928757	Missense_Mutation	SNP	C	T	C	VWA3B	c.C2801T	p.T934I
XH_P55	2	108487330	108487330	Missense_Mutation	SNP	A	G	A	RGPD4	c.A2870G	p.N957S
XH_P55	2	113832333	113832333	Missense_Mutation	SNP	C	A	C	IL1F10	c.C152A	p.A51D
XH_P55	2	113890304	113890304	Silent	SNP	T	C	T	IL1RN	c.T390C	p.L130S
XH_P55	2	114220055	114220055	Silent	SNP	T	C	T	CBWD2	c.T646C	p.L216L
XH_P55	2	122038783	122038783	Missense_Mutation	SNP	G	A	G	TFPC2L1	c.C127T	p.R43C
XH_P55	2	127821207	127821207	Silent	SNP	G	A	G	BIN1	c.C621T	p.Y207Y
XH_P55	2	133489362	133489362	Silent	SNP	G	A	G	NCKAP5	c.C1434T	p.T478T
XH_P55	2	136393658	136393658	Missense_Mutation	SNP	A	G	A	R3HDM1	c.A640G	p.M214V
XH_P55	2	136555659	136555659	Missense_Mutation	SNP	T	C	T	LCT	c.A4916G	p.N1639S
XH_P55	2	160086468	160086468	Missense_Mutation	SNP	G	A	G	TANC1	c.G3928A	p.G1310S
XH_P55	2	166011048	166011048	Missense_Mutation	SNP	G	T	G	SCN3A	c.C1294A	p.Q432K
XH_P55	2	170591982	170591982	In_Frame_Ins	INS	-	GAGTTTATTTT	-	KLHL23	459insGAGTTT	E153delinsESFL
XH_P55	2	170591984	170591984	Silent	SNP	C	T	C	KLHL23	c.C460T	p.L154L
XH_P55	2	178416283	178416283	Silent	SNP	A	G	A	TTC30B	c.T1209C	p.N403N
XH_P55	2	179451960	179451960	Silent	SNP	A	G	A	TTN	c.T36783C	p.H12261H
XH_P55	2	183605077	183605077	Missense_Mutation	SNP	C	A	C	DNAJC10	c.C901A	p.L301I
XH_P55	2	186658056	186658056	Missense_Mutation	SNP	G	A	G	FSIP2	c.G6193A	p.D2065N
XH_P55	2	186658565	186658565	Missense_Mutation	SNP	G	T	G	FSIP2	c.C6702T	p.E2234D
XH_P55	2	186664963	186664963	Missense_Mutation	SNP	C	A	C	FSIP2	c.C10930A	p.L3644I
XH_P55	2	186665432	186665432	Missense_Mutation	SNP	G	A	G	FSIP2	c.G11399A	p.G3800E
XH_P55	2	196548556	196548556	Frame_Shift_Ins	INS	-	ATTAAAACTACT	-	SLC39A10	TCAGTTATTAA	p.D381fs
XH_P55	2	201437328	201437328	Silent	SNP	C	A	C	SGO2	c.C2259A	p.I753I
XH_P55	2	204732714	204732714	Missense_Mutation	SNP	A	G	A	CTLA4	c.A49G	p.T17A
XH_P55	2	211481257	211481257	Silent	SNP	C	G	C	CP51	c.C1326G	p.G442G
XH_P55	2	215674224	215674224	Missense_Mutation	SNP	G	A	G	BARD1	c.C70T	p.P24S
XH_P55	2	218683154	218683154	Missense_Mutation	SNP	A	G	A	TNS1	c.T3526C	p.W1176R
XH_P55	2	220379560	220379560	Silent	SNP	C	G	C	ASIC4	c.C495G	p.A165A
XH_P55	2	220500178	220500178	Silent	SNP	C	T	C	SLC4A3	c.C2013T	p.V671V
XH_P55	2	232321341	232321341	Splice_Site	SNP	C	T	C	NCL	-	-
XH_P55	2	233757679	233757679	Silent	SNP	G	A	G	NGEF	c.C795T	p.A265A
XH_P55	2	234708903	234708903	Missense_Mutation	SNP	A	T	A	MROH2A	c.A1511T	p.H504L
XH_P55	2	234761225	234761225	Missense_Mutation	SNP	C	T	C	HUURP	c.G226A	p.E76K
XH_P55	2	238277573	238277573	Silent	SNP	C	A	C	COL6A3	c.G2712T	p.G904G
XH_P55	2	241404317	241404317	Silent	SNP	C	T	C	GPC1	c.C1059T	p.P353P
XH_P55	2	241404499	241404499	Silent	SNP	C	T	C	GPC1	c.C1140T	p.S380S
XH_P55	2	242815059	242815059	Missense_Mutation	SNP	C	T	C	RTP5	c.C1352T	p.A451V
XH_P55	3	7620168	7620168	Silent	SNP	A	G	A	GRM7	c.A1575G	p.L525L
XH_P55	3	13383540	13383540	Silent	SNP	A	G	A	NUP210	c.T3048C	p.F1016F
XH_P55	3	13421150	13421150	Missense_Mutation	SNP	C	T	C	NUP210	c.G889A	p.A297T
XH_P55	3	13679391	13679391	Missense_Mutation	SNP	A	G	A	FBLN2	c.A3527G	p.H1176R
XH_P55	3	13896140	13896140	Silent	SNP	A	G	A	WNT7A	c.T459C	p.S153S
XH_P55	3	13896284	13896284	Silent	SNP	C	T	C	WNT7A	c.G315A	p.A105A
XH_P55	3	32031135	32031135	Silent	SNP	A	G	A	ZNF860	c.A564G	p.S188S
XH_P55	3	38170810	38170810	Missense_Mutation	SNP	C	G	C	ACAA1	c.G516C	p.E172D
XH_P55	3	39230171	39230171	Missense_Mutation	SNP	C	T	C	XIRP1	c.G766A	p.A256T
XH_P55	3	45588857	45588857	Silent	SNP	T	C	T	LARS2	c.T2547C	p.A849A
XH_P55	3	46488854	46488854	Silent	SNP	T	C	T	LTF	c.A1116G	p.G372G
XH_P55	3	48691870	48691870	Silent	SNP	C	T	C	CELSR3	c.G5004A	p.T1668T
XH_P55	3	51979083	51979083	Missense_Mutation	SNP	C	T	C	PARP3	c.C725T	p.A242V
XH_P55	3	51994587	51994587	Silent	SNP	T	C	T	PCBP4	c.A210G	p.A70A
XH_P55	3	52556890	52556890	Missense_Mutation	SNP	A	G	A	STAB1	c.A6844G	p.I2282V
XH_P55	3	52852538	52852538	Missense_Mutation	SNP	G	T	G	ITIH4	c.C2002A	p.P668T
XH_P55	3	97594261	97594261	Missense_Mutation	SNP	G	A	G	CRYBG3	c.G4223A	p.G1408E
XH_P55	3	97664725	97664725	Missense_Mutation	SNP	C	T	C	RIOX2	c.G1156A	p.A386T
XH_P55	3	107097081	107097085	Frame_Shift_Del	DEL	AAATG	-	AAATG	CCDC54	c.647_651del	p.Q216fs
XH_P55	3	110863855	110863855	Silent	SNP	A	C	A	NECTIN3	c.A1110C	p.R370R
XH_P55	3	113373982	113373982	Frame_Shift_Ins	INS	-	TTACAAAT	-	USF3	6_6547insATT	p.S2183fs
XH_P55	3	113373983	113373983	Frame_Shift_Ins	INS	-	TA	-	USF3	6545_6546insT	p.N2182fs
XH_P55	3	118945796	118945796	Missense_Mutation	SNP	G	C	G	B4GALT4	c.C346G	p.Q116E
XH_P55	4	843508	843508	Missense_Mutation	SNP	C	T	C	GAK	c.G3652A	p.D1218N
XH_P55	4	994452	994452	Silent	SNP	C	T	C	IDUA	c.C352T	p.L118L
XH_P55	4	1347004	1347004	Missense_Mutation	SNP	G	A	G	UVSSA	c.G737A	p.R246Q
XH_P55	4	3076672	3076672	Silent	SNP	A	G	A	HTT	c.A120G	p.P40P
XH_P55	4	3215835	3215835	Missense_Mutation	SNP	T	C	T	HTT	c.T6925C	p.Y2309H
XH_P55	4	3227419	3227419	Silent	SNP	A	G	A	HTT	c.A7797G	p.L2599L
XH_P55	4	3234980	3234980	Missense_Mutation	SNP	G	A	G	HTT	c.G8356A	p.V2786I
XH_P55	4	3417845	3417845	Silent	SNP	G	C	G	RGS12	c.G480C	p.L160L
XH_P55	4	6304118	6304118	Missense_Mutation	SNP	G	A	G	WFS1	c.G2596A	p.D866N
XH_P55	4	7435486	7435486	Missense_Mutation	SNP	G	T	G	PSAPL1	c.C1121A	p.A374E
XH_P55	4	7435721	7435721	Missense_Mutation	SNP	C	T	C	PSAPL1	c.G886A	p.V296M
XH_P55	4	7436073	7436073	Silent	SNP	C	T	C	PSAPL1	c.G534A	p.A178A
XH_P55	4	13584292	13584292	Silent	SNP	C	T	C	BOD1L1	c.G8502A	p.R2834R
XH_P55	4	20706339	20706339	Nonsense_Mutation	SNP	C	T	C	PACRGL	c.C109T	p.Q37X
XH_P55	4	20706340	20706340	Frame_Shift_Ins	INS	-	AAAAAAAAAAG	-	PACRGL	11insAAAAAAA	p.Q37fs

XH_P55	4	24810094	24810094	Missense_Mutation	SNP	G	A	G	CCDC149	c.C1507T	p.R503W
XH_P55	4	26585881	26585881	Silent	SNP	C	T	C	TBC1D19	c.C66T	p.S225
XH_P55	4	40337523	40337523	Silent	SNP	C	T	C	CHRNA9	c.C39T	p.I131
XH_P55	4	41748011	41748028	In_Frame_Del	DEL	CCGCCGCTG	-	GCCGCCGCTGCC	PHOX2B	c.741_758del	p.247_253del
XH_P55	4	41984778	41984778	Silent	SNP	C	T	C	DCAF4L1	c.C969T	p.H323H
XH_P55	4	57219592	57219592	Silent	SNP	G	A	G	AASDH	c.C99T	p.D33D
XH_P55	4	57333820	57333820	Missense_Mutation	SNP	G	T	G	SRP72	c.G19T	p.G7W
XH_P55	4	57798189	57798189	Silent	SNP	G	A	G	REST	c.G3165A	p.A1055A
XH_P55	4	62936364	62936364	In_Frame_Ins	INS	-	ATTATACCAAG	-	ADGR13	c.ACACCAATTAT	p.B83delinsPHHYTRRR
XH_P55	4	68380215	68380215	Missense_Mutation	SNP	G	A	G	CENPC	c.C1021T	p.L341F
XH_P55	4	76489345	76489345	Missense_Mutation	SNP	C	T	C	C4orf26	c.C89T	p.P30L
XH_P55	4	77033590	77033590	Missense_Mutation	SNP	C	T	C	ART3	c.C1022T	p.S341L
XH_P55	4	79437155	79437155	Silent	SNP	C	T	C	FRAS1	c.C10377T	p.T3459T
XH_P55	4	88584160	88584160	Silent	SNP	G	A	G	DMP1	c.G1182A	p.E394E
XH_P55	4	110902111	110902111	Missense_Mutation	SNP	A	T	A	EGF	c.A2225T	p.D742V
XH_P55	4	114275657	114275657	Silent	SNP	G	T	G	ANK2	c.G5883T	p.L1961L
XH_P55	4	119736796	119736796	Silent	SNP	A	C	A	SEC24D	c.T483G	p.P161P
XH_P55	4	119951647	119951647	Missense_Mutation	SNP	A	G	A	SYNPO2	c.A1717G	p.T573A
XH_P55	4	122254119	122254119	Silent	SNP	G	A	G	QRFR	c.C654T	p.I218I
XH_P55	4	140468167	140468167	Nonsense_Mutation	INS	-	TGCCATCAAAAG	-	SETD7	c.TCTTCTTTGATG	p.T27delinsFFDGRX
XH_P55	4	140640703	140640703	Missense_Mutation	SNP	G	T	G	MAML3	c.C3179A	p.P1060H
XH_P55	4	141294814	141294814	Missense_Mutation	SNP	G	C	G	SCOC	c.G124C	p.V42L
XH_P55	4	146461191	146461191	In_Frame_Ins	INS	-	GTTACCAAACT	-	SMAD1	c.TAGCAGTTACCC	p.12delinsPIAVTQTL
XH_P55	4	151000419	151000419	Silent	SNP	G	A	G	DCLK2	c.G240A	p.G80G
XH_P55	4	154216710	154216710	Silent	SNP	G	A	G	TRIM2	c.G951A	p.T317T
XH_P55	4	154513627	154513627	Missense_Mutation	SNP	A	G	A	TMEM131L	c.A1813G	p.I605V
XH_P55	4	154513722	154513722	Silent	SNP	C	T	C	TMEM131L	c.C1908T	p.H636H
XH_P55	4	155488821	155488821	Silent	SNP	C	T	C	FBG	c.C390T	p.S130S
XH_P55	4	156838566	156838566	In_Frame_Ins	INS	-	ACTGATTGTCAA	-	TD02	c.TGCCAACTGATT	p.6delinsGQLVVKLM
XH_P55	4	169382991	169382991	Silent	SNP	C	T	C	DDX60L	c.G465A	p.T155T
XH_P55	4	184367559	184367561	In_Frame_Del	DEL	CTG	-	CTG	CDKN2AIP	c.722_724del	p.241_242del
XH_P55	5	231111	231111	Silent	SNP	T	C	T	SDHA	c.T747C	p.P249P
XH_P55	5	422955	422955	Missense_Mutation	SNP	C	G	C	AHRR	c.C565G	p.P189A
XH_P55	5	453567	453567	Silent	SNP	G	A	G	EXOC3	c.G447A	p.E149E
XH_P55	5	475104	475104	Missense_Mutation	SNP	A	G	A	SLC9A3	c.T2368C	p.C790R
XH_P55	5	1208964	1208964	Silent	SNP	T	C	T	SLC6A19	c.T306C	p.G102G
XH_P55	5	1878212	1878212	Silent	SNP	G	A	G	IRX4	c.C1431T	p.G477G
XH_P55	5	6633779	6633779	Missense_Mutation	SNP	C	G	C	SRD5A1	c.C116G	p.A39G
XH_P55	5	6656210	6656210	Silent	SNP	G	A	G	SRD5A1	c.G339A	p.T113T
XH_P55	5	14420027	14420027	Silent	SNP	A	C	A	TRIO	c.A5100C	p.T1700T
XH_P55	5	14487702	14487702	Missense_Mutation	SNP	G	A	G	TRIO	c.G6965A	p.G2322D
XH_P55	5	36985241	36985241	In_Frame_Ins	INS	-	GTGCATCATTAC	-	NIPBL	c.1960insGTGCAT	p.D653delinsQVHHY
XH_P55	5	36985243	36985243	Missense_Mutation	SNP	A	T	A	NIPBL	c.A1961T	p.N654I
XH_P55	5	38955796	38955796	Missense_Mutation	SNP	G	A	G	RICTOR	c.C2510T	p.S837F
XH_P55	5	60839907	60839907	Silent	SNP	C	A	C	ZSWIM6	c.C3411A	p.P1137P
XH_P55	5	74962768	74962768	Missense_Mutation	SNP	C	T	C	ANKDD1B	c.C1343T	p.S448L
XH_P55	5	78181477	78181477	Missense_Mutation	SNP	C	T	C	ARSB	c.G1072A	p.V358M
XH_P55	5	79950724	79950724	In_Frame_Ins	INS	-	CCGCAGCGC	-	MSH3	c.179insCCGCA	p.A60delinsAAAP
XH_P55	5	96498783	96498783	Silent	SNP	G	A	G	RIOK2	c.C1641T	p.A547A
XH_P55	5	102895168	102895168	Frame_Shift_Ins	INS	-	TTCTT	-	NUDT12	c.153_154insAAG	p.C52fs
XH_P55	5	102895170	102895170	Splice_Site	INS	-	CGTTAGGAACCA	-	NUDT12	-	-
XH_P55	5	108714077	108714077	Frame_Shift_Ins	INS	-	AC	-	PJA2	c.1110_1111insG	p.H371fs
XH_P55	5	121413208	121413208	Missense_Mutation	SNP	C	T	C	LOX	c.G473A	p.R158Q
XH_P55	5	122425832	122425832	Silent	SNP	G	T	G	PRDM6	c.G123T	p.A41A
XH_P55	5	128956439	128956439	In_Frame_Ins	INS	-	AAAATTTTAAAA	-	ADAMTS19	c.TATAATAAAATT	p.36delinsEYNKILKFTL
XH_P55	5	131607588	131607588	Missense_Mutation	SNP	G	T	G	PDLIM4	c.G775T	p.G259C
XH_P55	5	135207187	135207187	Silent	SNP	G	A	G	SLC25A48	c.G459A	p.A153A
XH_P55	5	139060486	139060486	Silent	SNP	G	A	G	CXC5	c.C378A	p.A126A
XH_P55	5	140182228	140182228	Silent	SNP	G	A	G	PCDHA3	c.G1446A	p.A482A
XH_P55	5	140222891	140222891	Missense_Mutation	SNP	C	T	C	PCDHA8	c.C1985T	p.T662M
XH_P55	5	140250252	140250252	Silent	SNP	T	C	T	PCDHA11	c.T1564C	p.L522L
XH_P55	5	140263026	140263026	Silent	SNP	G	A	G	PCDHA13	c.G1173A	p.P391P
XH_P55	5	140263290	140263290	Silent	SNP	T	G	T	PCDHA13	c.T1437G	p.A479A
XH_P55	5	140480578	140480578	Silent	SNP	A	G	A	PCDHB3	c.A345G	p.Q115Q
XH_P55	5	140481594	140481594	Missense_Mutation	SNP	T	C	T	PCDHB3	c.T1361C	p.I454T
XH_P55	5	140481913	140481913	Silent	SNP	C	T	C	PCDHB3	c.C1680T	p.F560F
XH_P55	5	140998388	140998388	Missense_Mutation	SNP	C	T	C	DIAPH1	c.G94A	p.D32N
XH_P55	5	141335498	141335498	Missense_Mutation	SNP	C	T	C	PCDH12	c.C1919A	p.S640N
XH_P55	5	145506053	145506053	In_Frame_Ins	INS	-	ACTATGTCCAAG	-	LARS	c.TsAAAGCCTTGG	p.933delinsKSLGHSL
XH_P55	5	147040822	147040822	Missense_Mutation	SNP	C	T	C	JAKMIP2	c.C190A	p.V64I
XH_P55	5	148206917	148206917	Silent	SNP	C	A	C	ADRB2	c.C523A	p.R175R
XH_P55	5	149212406	149212406	Missense_Mutation	SNP	C	T	C	PPARGC1B	c.C653T	p.P218L
XH_P55	5	149998128	149998128	Missense_Mutation	SNP	G	A	G	SYNPO	c.G199A	p.D67N
XH_P55	5	151266317	151266317	Missense_Mutation	SNP	T	C	T	GLRA1	c.A217G	p.I73V
XH_P55	5	156727724	156727724	Missense_Mutation	SNP	G	A	G	CYFIP2	c.G311A	p.R104H
XH_P55	5	179193598	179193598	Silent	SNP	C	T	C	MAML1	c.C1587T	p.S529S
XH_P55	6	3015865	3015865	Silent	SNP	C	T	C	NQO2	c.C405T	p.S135S
XH_P55	6	3225759	3225759	Silent	SNP	C	A	C	TUBB2B	c.G564T	p.S188S
XH_P55	6	5431340	5431340	Missense_Mutation	SNP	A	G	A	FARS2	c.A839G	p.N280S
XH_P55	6	18122506	18122506	Missense_Mutation	SNP	G	A	G	NHLRC1	c.C332T	p.T111L
XH_P55	6	26056072	26056072	Silent	SNP	G	C	G	HIST1H1C	c.C585G	p.P195P
XH_P55	6	27839746	27839746	Silent	SNP	T	C	T	HIST1H3I	c.A348G	p.K116K
XH_P55	6	34512064	34512064	Missense_Mutation	SNP	C	T	C	SPDEF	c.G169A	p.A57T
XH_P55	6	36260858	36260858	Silent	SNP	C	T	C	PNPLA1	c.C174T	p.F58F
XH_P55	6	37626142	37626142	Silent	SNP	C	T	C	MDGA1	c.G261A	p.S87S
XH_P55	6	38939405	38939405	Silent	SNP	A	G	A	DNAH8	c.A12489G	p.V4163V
XH_P55	6	39282806	39282806	Missense_Mutation	SNP	G	T	G	KCNK16	c.C761A	p.P254H
XH_P55	6	39283083	39283083	Silent	SNP	G	A	G	KCNK16	c.C786T	p.N262N
XH_P55	6	40998141	40998141	Silent	SNP	G	A	G	UNC5CL	c.C1320T	p.C440C
XH_P55	6	41773723	41773723	Silent	SNP	G	A	G	USP49	c.C999T	p.N333N
XH_P55	6	43020188	43020188	Silent	SNP	G	A	G	CUL7	c.C495T	p.D165D
XH_P55	6	43184132	43184132	Missense_Mutation	SNP	A	C	A	CUL9	c.A6173C	p.H2058P
XH_P55	6	44219163	44219163	Missense_Mutation	SNP	C	T	C	HSP90AB1	c.C1132T	p.R378C
XH_P55	6	44243559	44243559	Silent	SNP	A	G	A	TMEM151B	c.A996G	p.L332L
XH_P55	6	44250165	44250165	Silent	SNP	A	G	A	TCTE1	c.T978C	p.G326G
XH_P55	6	44255459	44255459	Missense_Mutation	SNP	G	A	G	TCTE1	c.C104T	p.P35L
XH_P55	6	52101739	52101739	Missense_Mutation	SNP	T	C	T	IL17F	c.A482G	p.H161R
XH_P55	6	70871832	70871832	Missense_Mutation	SNP	C	T	C	COL19A1	c.C2333T	p.P778L

XH_P55	6	70916888	70916888	Silent	SNP	A	C	A	COL19A1	c.A3339C	p.P1113P
XH_P55	6	75831154	75831154	Missense_Mutation	SNP	C	A	C	COL12A1	c.G3458T	p.C1153F
XH_P55	6	75831155	75831155	Frame_Shift_Ins	INS	-	CTTCTCTTTT	-	COL12A1	3457insAAAAG	p.C1153fs
XH_P55	6	89793894	89793894	Silent	SNP	G	C	G	PNRC1	c.G963C	p.T321T
XH_P55	6	94066754	94066754	Frame_Shift_Ins	INS	-	A	-	EPHA7	c.1004_1005ins	p.P335fs
XH_P55	6	94066756	94066756	Frame_Shift_Ins	INS	-	TCACATCGTTTC	-	EPHA7	003insAGAAAC	p.P335fs
XH_P55	6	128388799	128388799	Silent	SNP	G	T	G	PTPRK	c.C1635A	p.L545L
XH_P55	6	130761725	130761725	Missense_Mutation	SNP	G	A	G	TMEM200A	c.G158A	p.G53D
XH_P55	6	157405844	157405844	Silent	SNP	T	C	T	ARID1B	c.T2047C	p.L683L
XH_P55	6	158927651	158927651	Silent	SNP	A	G	A	TULP4	c.A4557G	p.L1519L
XH_P55	6	170176647	170176647	Silent	SNP	C	T	C	ERMARD	c.C1239T	p.I413I
XH_P55	6	170176648	170176648	Missense_Mutation	SNP	A	G	A	ERMARD	c.A1240G	p.S414G
XH_P55	7	1097449	1097449	Missense_Mutation	SNP	G	A	G	GPR146	c.G298A	p.E100K
XH_P55	7	2577781	2577781	Silent	SNP	T	C	T	BRAT1	c.A1863G	p.E621E
XH_P55	7	2582907	2582907	Missense_Mutation	SNP	C	T	C	BRAT1	c.G329A	p.R110Q
XH_P55	7	2951824	2951824	Silent	SNP	A	G	A	CARD11	c.T3126C	p.I1042I
XH_P55	7	2959172	2959172	Silent	SNP	G	A	G	CARD11	c.C2344T	p.L782L
XH_P55	7	2962293	2962293	Silent	SNP	C	G	C	CARD11	c.G2244C	p.T748T
XH_P55	7	5428786	5428786	Silent	SNP	C	T	C	TNRC18	c.G669A	p.K223K
XH_P55	7	6026988	6026988	Missense_Mutation	SNP	G	A	G	PM52	c.C1090T	p.P364S
XH_P55	7	6456302	6456302	Silent	SNP	C	T	C	DAGLB	c.G996A	p.P332P
XH_P55	7	6693438	6693438	Silent	SNP	C	T	C	ZNF316	c.C2211T	p.H737H
XH_P55	7	7917040	7917040	Silent	SNP	G	A	G	UMAD1	c.G285A	p.P95P
XH_P55	7	11675855	11675855	Silent	SNP	C	T	C	THSD7A	c.G924A	p.R308R
XH_P55	7	11676065	11676065	Missense_Mutation	SNP	G	C	G	THSD7A	c.C714G	p.F238L
XH_P55	7	20824614	20824614	Silent	SNP	C	T	C	SP8	c.G822A	p.S274S
XH_P55	7	20825146	20825172	In_Frame_Del	DEL	GCTGCTGCC	-	GGCTGCTGCCG	SP8	c.264_290del	p.88_97del
XH_P55	7	21956405	21956405	Silent	SNP	G	A	G	CDCA7L	c.C132T	p.C44C
XH_P55	7	30491311	30491311	Silent	SNP	C	T	C	NOD1	c.G1722A	p.A574A
XH_P55	7	30492237	30492237	Missense_Mutation	SNP	C	T	C	NOD1	c.G796A	p.E266K
XH_P55	7	30492550	30492550	Silent	SNP	G	A	G	NOD1	c.C483T	p.D161D
XH_P55	7	38305083	38305083	Silent	SNP	G	A	G	TARP	c.C12T	p.N4N
XH_P55	7	44147485	44147485	Missense_Mutation	SNP	C	A	C	AEBP1	c.C817A	p.P273T
XH_P55	7	44259706	44259706	Silent	SNP	G	A	G	CAMK2B	c.C1305T	p.N435N
XH_P55	7	44259871	44259871	Silent	SNP	C	T	C	CAMK2B	c.G1140A	p.P380P
XH_P55	7	44797065	44797109	In_Frame_Del	DEL	ACTGCCACC	-	CACTGCCACCG	ZMIZ2	c.457_501del	p.153_167del
XH_P55	7	48081095	48081095	Missense_Mutation	SNP	G	T	G	C7orf57	c.G220T	p.A74S
XH_P55	7	48318758	48318758	Missense_Mutation	SNP	C	T	C	ABCA13	c.C7967T	p.A2656V
XH_P55	7	51096974	51096974	Missense_Mutation	SNP	C	T	C	COBL	c.G1819A	p.V607I
XH_P55	7	53103673	53103673	Silent	SNP	C	A	C	POM121L12	c.C309A	p.P103P
XH_P55	7	53104078	53104078	Silent	SNP	G	A	G	POM121L12	c.G714A	p.P238P
XH_P55	7	54617718	54617718	Silent	SNP	G	A	G	VSTM2A	c.G489A	p.C163S
XH_P55	7	63680014	63680014	Frame_Shift_Ins	INS	-	AT	-	ZNF735	c.585_586insAT	p.C195fs
XH_P55	7	63981563	63981563	Silent	SNP	A	G	A	ZNF680	c.T1569C	p.C523C
XH_P55	7	66098384	66098384	Silent	SNP	G	A	G	KCTD7	c.G267A	p.T89T
XH_P55	7	75959188	75959188	Silent	SNP	G	A	G	YWHAG	c.C450T	p.S150S
XH_P55	7	76019476	76019476	Missense_Mutation	SNP	C	T	C	SSC4D	c.G1628A	p.R543H
XH_P55	7	77885320	77885320	Nonsense_Mutation	INS	-	TGCTGAGCCAG	-	MAGI2	CAAAACACTGGC	D664delinsRQTLAQQX
XH_P55	7	82582381	82582381	Missense_Mutation	SNP	C	G	C	PCLO	c.G7888C	p.E2630Q
XH_P55	7	99054204	99054204	Missense_Mutation	SNP	C	T	C	CPSF4	c.C722T	p.A241V
XH_P55	7	99758136	99758136	Silent	SNP	T	G	T	GAL3ST4	c.A876C	p.A292A
XH_P55	7	100180060	100180060	Silent	SNP	G	A	G	LRCH4	c.C243T	p.P81P
XH_P55	7	100304745	100304745	Missense_Mutation	SNP	G	A	G	POP7	c.G292A	p.V98M
XH_P55	7	100638887	100638887	Silent	SNP	A	C	A	MUC12	c.A5043C	p.T1681T
XH_P55	7	100676697	100676697	Missense_Mutation	SNP	C	G	C	MUC17	c.C2000G	p.T667S
XH_P55	7	100677455	100677455	Missense_Mutation	SNP	G	A	G	MUC17	c.G2758A	p.G920R
XH_P55	7	100677457	100677457	Silent	SNP	G	T	G	MUC17	c.G2760T	p.G920G
XH_P55	7	100678625	100678625	Missense_Mutation	SNP	G	A	G	MUC17	c.G3928A	p.V1310I
XH_P55	7	100678626	100678626	Missense_Mutation	SNP	T	C	T	MUC17	c.T3929C	p.V1310A
XH_P55	7	100679316	100679316	Missense_Mutation	SNP	T	A	T	MUC17	c.T4619A	p.V1540D
XH_P55	7	100683474	100683474	Missense_Mutation	SNP	T	G	T	MUC17	c.T8777G	p.V2926G
XH_P55	7	100684253	100684253	Missense_Mutation	SNP	G	A	G	MUC17	c.G9556A	p.A3186T
XH_P55	7	107408245	107408245	Frame_Shift_Ins	INS	-	TCCATTC	-	SLC26A3	70_2171insGAA	p.K724fs
XH_P55	7	124404432	124404432	Missense_Mutation	SNP	G	A	G	GPR37	c.C599T	p.T200M
XH_P55	7	127669857	127669857	Silent	SNP	A	T	A	LRRC4	c.T837A	p.S279S
XH_P55	7	128117227	128117227	Missense_Mutation	SNP	G	A	G	METTL2B	c.G202A	p.V68I
XH_P55	7	128470838	128470838	Silent	SNP	C	T	C	FLNC	c.C147T	p.H49H
XH_P55	7	128491603	128491603	Silent	SNP	T	C	T	FLNC	c.T5664C	p.T1888T
XH_P55	7	128495338	128495338	Silent	SNP	C	T	C	FLNC	c.C7122T	p.D2374D
XH_P55	7	131194328	131194328	Silent	SNP	C	T	C	PODXL	c.G723A	p.S241S
XH_P55	7	131195959	131195959	Missense_Mutation	SNP	C	T	C	PODXL	c.G334A	p.G112S
XH_P55	7	139026152	139026152	Missense_Mutation	SNP	T	G	T	C7orf55-LUC7L	c.T22G	p.S8A
XH_P55	7	141385428	141385428	Missense_Mutation	SNP	C	T	C	KIAA1147	c.G377A	p.R126Q
XH_P55	7	141536209	141536209	Missense_Mutation	SNP	C	T	C	PRSS37	c.G694A	p.A232T
XH_P55	7	143042837	143042837	Silent	SNP	C	T	C	CLCN1	c.C2154T	p.D718D
XH_P55	7	143771557	143771557	Missense_Mutation	SNP	T	C	T	OR2A25	c.T245C	p.V82A
XH_P55	7	144380019	144380019	Missense_Mutation	SNP	G	A	G	TPK1	c.C32T	p.P111L
XH_P55	7	149516486	149516486	Silent	SNP	A	G	A	SSPO	c.A11889G	p.G3963G
XH_P55	7	149558409	149558409	Silent	SNP	G	C	G	ZNF862	c.G2160C	p.L720L
XH_P55	7	149559273	149559273	Silent	SNP	C	T	C	ZNF862	c.C3024T	p.L1008L
XH_P55	7	149559465	149559465	Silent	SNP	C	T	C	ZNF862	c.C3216T	p.G1072G
XH_P55	7	150034378	150034378	Missense_Mutation	SNP	A	G	A	LRRC61	c.A428G	p.N143S
XH_P55	7	150325175	150325175	Missense_Mutation	SNP	C	T	C	GIMAP6	c.G721A	p.G241S
XH_P55	7	150733025	150733025	Silent	SNP	T	A	T	ABCB8	c.T720A	p.R240R
XH_P55	7	150768786	150768786	Silent	SNP	G	A	G	SLCA2	c.G2175A	p.T725T
XH_P55	7	151680085	151680085	Frame_Shift_Ins	INS	-	AAATTTATTTAA	-	GALNTL5	nsCAAAATTTTA	p.H128fs
XH_P55	7	154667643	154667643	Silent	SNP	G	A	G	DPP6	c.G1590A	p.V530V
XH_P55	7	156469123	156469123	Missense_Mutation	SNP	G	A	G	RNF32	c.G863A	p.R288Q
XH_P55	7	158528233	158528233	Silent	SNP	A	G	A	ESYT2	c.T2547C	p.S849S
XH_P55	8	6302183	6302183	Missense_Mutation	SNP	G	C	G	MCPH1	c.G796C	p.D266H
XH_P55	8	6479178	6479178	Silent	SNP	C	A	C	MCPH1	c.C2418A	p.A806A
XH_P55	8	7829924	7829924	Silent	SNP	G	A	G	USP17L8	c.C852T	p.C284C
XH_P55	8	11689119	11689119	Silent	SNP	G	C	G	FDF1	c.G471C	p.L157L
XH_P55	8	11710888	11710888	Missense_Mutation	SNP	G	C	G	CTSB	c.C76G	p.L26V
XH_P55	8	17612639	17612639	Silent	SNP	T	C	T	MTUS1	c.A678G	p.E226E
XH_P55	8	17815138	17815138	Frame_Shift_Ins	INS	-	CACGTTTA	-	PCM1	4_1895insCACG	p.G632fs
XH_P55	8	22471824	22471824	Silent	SNP	G	A	G	CCAR2	c.G924A	p.S308S
XH_P55	8	28980108	28980108	Missense_Mutation	SNP	C	T	C	KIF13B	c.G3535A	p.A1179T

XH_P55	8	37702472	37702472	Silent	SNP	G	A	G	BRF2	c.C796T	p.L266L
XH_P55	8	41166638	41166640	In_Frame_Del	DEL	GCT	-	GCT	SFRP1	c.39_41del	p.13_14del
XH_P55	8	52321686	52321686	Missense_Mutation	SNP	C	T	C	PXDNL	c.G2498A	p.S833N
XH_P55	8	52321843	52321843	Missense_Mutation	SNP	G	C	G	PXDNL	c.C2341G	p.R781G
XH_P55	8	55541042	55541042	Missense_Mutation	SNP	A	G	A	RP1	c.A4600G	p.T1534A
XH_P55	8	65493429	65493429	Missense_Mutation	SNP	T	G	T	BHLHE22	c.T82G	p.S28A
XH_P55	8	69434105	69434105	Missense_Mutation	SNP	T	G	T	C8orf34	c.T708G	p.N236K
XH_P55	8	87241847	87241847	Silent	SNP	G	A	G	SLC7A13	c.C660T	p.G220G
XH_P55	8	98991221	98991221	Missense_Mutation	SNP	A	G	A	MATN2	c.A1066G	p.K356E
XH_P55	8	104427452	104427452	Frame_Shift_Ins	INS	-	ACGCGGAAGCG	-	DCAF13	insGGACGGCGG	p.H78fs
XH_P55	8	117783902	117783902	Frame_Shift_Ins	INS	-	CAAAATCT	-	UTP23	1_572insCAAA	p.S191fs
XH_P55	8	117783903	117783903	Frame_Shift_Ins	INS	-	ATCC	-	UTP23	572_573insATC	p.S191fs
XH_P55	8	133092138	133092138	Missense_Mutation	SNP	G	A	G	HHLA1	c.C752T	p.P251L
XH_P55	8	134144113	134144113	Silent	SNP	C	T	C	TG	c.C7920T	p.Y2640Y
XH_P55	8	135602581	135602581	Silent	SNP	A	G	A	ZFAT	c.T2307C	p.S769S
XH_P55	8	139648997	139648997	In_Frame_Ins	INS	-	TTCTTCTCTTTC	-	COL22A1	5AAGGAAAGG	81delinsQGKERK
XH_P55	8	139648999	139648999	Missense_Mutation	SNP	G	T	G	COL22A1	c.C3541A	p.Q1181K
XH_P55	8	142367559	142367559	Silent	SNP	G	A	G	GPR20	c.C465T	p.P155P
XH_P55	8	143957129	143957129	Silent	SNP	G	T	G	CYP11B1	c.C1120A	p.R374R
XH_P55	8	144620855	144620855	Missense_Mutation	SNP	C	A	A	ZC3H3	c.G682T	p.A228S
XH_P55	8	144660046	144660046	Silent	SNP	G	A	G	NAPRT	c.C294T	p.A98A
XH_P55	8	145001643	145001643	Nonsense_Mutation	SNP	C	A	C	PLEC	c.G3649T	p.E1217X
XH_P55	8	145138331	145138331	Silent	SNP	A	G	A	GPAA1	c.A294G	p.S98S
XH_P55	8	145947776	145947776	Silent	SNP	G	A	G	ZNF251	c.C1269T	p.H423H
XH_P55	9	5081780	5081780	Silent	SNP	G	A	G	JAK2	c.G2043A	p.L681L
XH_P55	9	14784389	14784389	Missense_Mutation	SNP	G	A	G	FREM1	c.C4421T	p.T1474I
XH_P55	9	14859356	14859356	Silent	SNP	T	C	T	FREM1	c.A456G	p.C152Q
XH_P55	9	19786520	19786520	Silent	SNP	G	A	G	SLC24A2	c.C345T	p.H115H
XH_P55	9	21141456	21141456	Missense_Mutation	SNP	C	G	C	IFNW1	c.G114C	p.L38F
XH_P55	9	21350620	21350620	Silent	SNP	G	A	G	IFNA6	c.C267T	p.N89N
XH_P55	9	26905574	26905574	In_Frame_Ins	INS	-	ATTAATAATATC	-	PLAA	tsGGACGGATAT	752delinsGRIFLIDY
XH_P55	9	27548410	27548410	In_Frame_Ins	INS	-	ATGTGTAACCT	-	C9orf72	270insTTAAGTT	424delinsLSYTFK
XH_P55	9	32631762	32631762	Frame_Shift_Ins	INS	-	ATCA	-	TAF1L	815_3816insTG	p.K1272fs
XH_P55	9	32631764	32631764	In_Frame_Ins	INS	-	ATGACTGTCTTT	-	TAF1L	tsTTGGAAAGA	272delinsLEKTVIHK
XH_P55	9	32634588	32634588	Silent	SNP	G	T	G	TAF1L	c.C990A	p.I30I
XH_P55	9	35606884	35606884	Missense_Mutation	SNP	G	A	G	TESK1	c.G44A	p.C15Y
XH_P55	9	36169598	36169598	Silent	SNP	T	C	T	CCIN	c.T99C	p.S33S
XH_P55	9	38396065	38396065	Missense_Mutation	SNP	G	T	G	ALDH1B1	c.G320T	p.R107L
XH_P55	9	86617265	86617265	Missense_Mutation	SNP	A	G	A	RM1	c.A1364G	p.N455S
XH_P55	9	88694179	88694179	Silent	SNP	G	T	G	GOLM1	c.C57A	p.A19A
XH_P55	9	88937852	88937854	In_Frame_Del	DEL	TTT	-	TTT	ZCCHC6	c.2442_2444del	p.814_815del
XH_P55	9	90503628	90503628	Missense_Mutation	SNP	C	G	C	SPATA31E1	c.C4226G	p.P1409R
XH_P55	9	90536780	90536780	Missense_Mutation	SNP	A	G	A	SPATA31C1	c.A1958G	p.P653G
XH_P55	9	96209943	96209943	Missense_Mutation	SNP	T	C	T	FAM120AOS	c.A175G	p.K59E
XH_P55	9	107568688	107568688	Frame_Shift_Del	DEL	T	-	T	ABCA1	c.4298delA	p.E1433fs
XH_P55	9	111617650	111617650	Silent	SNP	G	A	G	ACTL7B	c.C561T	p.Y187Y
XH_P55	9	113168932	113168932	Missense_Mutation	SNP	C	T	C	SVEP1	c.G8948A	p.G2983E
XH_P55	9	114090279	114090279	Silent	SNP	A	G	A	OR2K2	c.T435C	p.A145A
XH_P55	9	114359624	114359624	Missense_Mutation	SNP	C	A	C	PTGR1	c.G79T	p.A27S
XH_P55	9	114694486	114694486	Silent	SNP	A	G	A	UGCG	c.A861G	p.T287T
XH_P55	9	116132334	116132334	Missense_Mutation	SNP	C	T	C	BSPRY	c.C1136T	p.T379I
XH_P55	9	116136198	116136198	Missense_Mutation	SNP	C	T	C	HDHD3	c.G437A	p.G146E
XH_P55	9	116153891	116153891	Missense_Mutation	SNP	C	G	C	ALAD	c.G153C	p.K51N
XH_P55	9	116356373	116356373	Silent	SNP	G	C	G	RG53	c.G174C	p.L58L
XH_P55	9	117051020	117051020	Silent	SNP	A	G	A	COL27A1	c.A4083G	p.G1361G
XH_P55	9	117124731	117124731	Missense_Mutation	SNP	G	A	G	AKNA	c.C1514T	p.PK05L
XH_P55	9	117169033	117169033	Missense_Mutation	SNP	A	G	A	WHRN	c.T785C	p.M262T
XH_P55	9	123632045	123632045	Silent	SNP	A	G	A	PHF19	c.T543C	p.P181S
XH_P55	9	127764304	127764304	Frame_Shift_Ins	INS	-	AATACATTAGAA	-	SCAI	ATGTATATCTAA	p.V362fs
XH_P55	9	135073877	135073877	Silent	SNP	C	T	C	NTNG2	c.C738T	p.F246F
XH_P55	9	135102254	135102254	Silent	SNP	C	T	C	NTNG2	c.C876T	p.H292H
XH_P55	9	136268084	136268084	Missense_Mutation	SNP	A	G	A	STKLD1	c.A1417G	p.K473E
XH_P55	9	136907005	136907005	Silent	SNP	G	A	G	BRD3	c.C1284T	p.P428P
XH_P55	9	137005023	137005023	Silent	SNP	C	T	C	WDR5	c.C24T	p.P8P
XH_P55	9	137642653	137642653	Silent	SNP	C	T	C	COL5A1	c.C1587T	p.G529G
XH_P55	9	137804360	137804360	Silent	SNP	A	G	A	FCN1	c.T570C	p.N190N
XH_P55	9	138379059	138379059	Silent	SNP	G	T	G	PPP1R26	c.G2703T	p.L901L
XH_P55	9	138440525	138440525	Missense_Mutation	SNP	C	G	C	OBP2A	c.C425G	p.P142R
XH_P55	9	138440527	138440527	Missense_Mutation	SNP	T	C	T	OBP2A	c.T293C	p.L98S
XH_P55	9	140174118	140174118	Missense_Mutation	SNP	T	G	T	TOR4A	c.T977G	p.F326C
XH_P55	10	93505	93505	Missense_Mutation	SNP	C	T	C	TUBB8	c.G827A	p.R276Q
XH_P55	10	373048	373048	Silent	SNP	T	C	T	DIP2C	c.A3822G	p.A1274A
XH_P55	10	3172121	3172121	Silent	SNP	C	T	C	PFKP	c.C993T	p.A331A
XH_P55	10	12162869	12162869	Silent	SNP	C	T	C	DHTKD1	c.C2742T	p.L914L
XH_P55	10	13481427	13481427	Silent	SNP	T	A	T	BEND7	c.A1152T	p.S384S
XH_P55	10	15138615	15138615	Missense_Mutation	SNP	C	T	C	C10orf111	c.G209A	p.R70K
XH_P55	10	15658534	15658534	Missense_Mutation	SNP	G	T	G	ITGA8	c.C1379A	p.T460K
XH_P55	10	15658535	15658535	Nonsense_Mutation	INS	-	GCATTTTCTACT	-	ITGA8	1378insGAGTAA	p.T460delinsEX
XH_P55	10	16562570	16562570	Silent	SNP	G	A	G	C1QL3	c.C495T	p.C165C
XH_P55	10	17152994	17152994	Silent	SNP	G	A	G	CUBN	c.C939T	p.N313N
XH_P55	10	21415006	21415006	Missense_Mutation	SNP	T	C	T	C10orf113	c.A214G	p.R72G
XH_P55	10	27688109	27688109	Missense_Mutation	SNP	T	C	T	PTCHD3	c.A1418G	p.D473G
XH_P55	10	35772402	35772402	Silent	SNP	G	A	G	CCNY	c.G225A	p.T75T
XH_P55	10	47701178	47701178	Missense_Mutation	SNP	C	A	C	ANTXL	c.C1754A	p.P585H
XH_P55	10	49933974	49933974	Missense_Mutation	SNP	T	C	T	WDFY4	c.T640C	p.S214P
XH_P55	10	50030533	50030533	Missense_Mutation	SNP	C	T	C	WDFY4	c.C5933T	p.S1978L
XH_P55	10	51769943	51769943	Silent	SNP	G	T	G	AGAP6	c.G2058T	p.V686V
XH_P55	10	61829225	61829225	Nonsense_Mutation	INS	-	GTCAAACAC	-	ANK3	8_11414insGTG	N3805delinsSVX
XH_P55	10	64967951	64967956	In_Frame_Del	DEL	CTAAAC	-	CTAAAC	JMJD1C	c.2816_2821del	p.939_941del
XH_P55	10	64974537	64974537	Missense_Mutation	SNP	A	T	A	JMJD1C	c.T733A	p.S245T
XH_P55	10	70405962	70405962	Missense_Mutation	SNP	G	A	G	TET1	c.G3476A	p.R1159Q
XH_P55	10	70992664	70992664	Missense_Mutation	SNP	C	T	C	HKDC1	c.C371T	p.T124I
XH_P55	10	71332204	71332204	Missense_Mutation	SNP	A	G	A	NEUROG3	c.T596C	p.F199S
XH_P55	10	73044580	73044580	Silent	SNP	G	A	G	UNC5B	c.G408A	p.A136A
XH_P55	10	73498344	73498344	Silent	SNP	T	A	T	CDH23	c.T4299A	p.P1433P
XH_P55	10	73569761	73569761	Silent	SNP	C	T	C	CDH23	c.C2187T	p.R729R
XH_P55	10	75406912	75406912	Missense_Mutation	SNP	G	T	G	SYNPO2L	c.C1826A	p.S609Y
XH_P55	10	104174895	104174895	Silent	SNP	G	A	G	PSD	c.C849T	p.Y283Y

XH_P55	10	104572963	104572963	Missense_Mutation	SNP	T	C	T	WBP1L	c.T967C	p.S323P
XH_P55	10	105361871	105361871	Missense_Mutation	SNP	C	T	C	SH3PXD2A	c.G3020A	p.R1007Q
XH_P55	10	113924340	113924340	Missense_Mutation	SNP	G	A	G	GPAM	c.C1250T	p.P417L
XH_P55	10	116307504	116307504	Silent	SNP	A	G	A	ABLIM1	c.T525C	p.N175N
XH_P55	10	118368606	118368606	Missense_Mutation	SNP	T	C	T	PNLIPRP1	c.T1382C	p.L461P
XH_P55	10	121436068	121436068	Silent	SNP	T	G	T	BAG3	c.T1002G	p.P334P
XH_P55	10	121436286	121436286	Missense_Mutation	SNP	C	T	C	BAG3	c.C1220T	p.P407L
XH_P55	10	121587194	121587194	Frame_Shift_Ins	INS	-	5CATGCTTGAAC	-	INPP5F	2insCAGATGTC	p.Q491fs
XH_P55	10	123662064	123662064	Nonsense_Mutation	INS	-	TGAAGTTCTAA	-	ATE1	ACTAATTAGAAC23_L124delinsSTNX	
XH_P55	10	123846490	123846490	Missense_Mutation	SNP	C	T	C	TACC2	c.C4475T	p.P1492L
XH_P55	10	125804385	125804385	Silent	SNP	A	G	A	CHST15	c.T597C	p.C199C
XH_P55	10	128150096	128150096	Missense_Mutation	SNP	G	T	G	C10orf90	c.C1593A	p.D531E
XH_P55	10	129900858	129900858	Silent	SNP	C	T	C	MKI67	c.G8166A	p.S2722S
XH_P55	10	129906980	129906980	Missense_Mutation	SNP	C	T	C	MKI67	c.G2044A	p.G682S
XH_P55	10	133955427	133955427	Missense_Mutation	SNP	A	G	A	JAKMIP3	c.A1261G	p.M421V
XH_P55	10	134626293	134626293	Missense_Mutation	SNP	C	A	C	CFAP46	c.G7497T	p.L2499F
XH_P55	10	135012162	135012162	Missense_Mutation	SNP	T	C	T	KNDC1	c.T2150C	p.L717P
XH_P55	11	431757	431757	Missense_Mutation	SNP	C	T	C	ANO9	c.G44A	p.R15H
XH_P55	11	1247458	1247458	Missense_Mutation	SNP	C	T	C	MUC5B	c.C151T	p.R51W
XH_P55	11	1252708	1252708	Silent	SNP	G	C	G	MUC5B	c.G1596C	p.L532L
XH_P55	11	1267325	1267325	Missense_Mutation	SNP	T	C	T	MUC5B	c.T9215C	p.F3072S
XH_P55	11	1267562	1267562	Missense_Mutation	SNP	C	T	C	MUC5B	c.C9452T	p.T3151M
XH_P55	11	1271321	1271321	Missense_Mutation	SNP	C	G	C	MUC5B	c.C13211G	p.A4404G
XH_P55	11	1272858	1272858	Silent	SNP	C	T	C	MUC5B	c.C14748T	p.F4916F
XH_P55	11	3249552	3249552	Missense_Mutation	SNP	C	T	C	MRGPRE	c.G478A	p.G160S
XH_P55	11	4471083	4471083	Nonsense_Mutation	SNP	C	T	C	OR52K2	c.C514T	p.R172X
XH_P55	11	4566870	4566870	Silent	SNP	T	C	T	OR52M1	c.T450C	p.S150S
XH_P55	11	4791111	4791111	Missense_Mutation	SNP	T	C	T	OR51F1	c.A37G	p.T13A
XH_P55	11	5080844	5080844	Missense_Mutation	SNP	T	C	T	OR52E2	c.A14G	p.N5S
XH_P55	11	5411239	5411239	Missense_Mutation	SNP	T	C	T	OR51M1	c.T611C	p.I204T
XH_P55	11	5701281	5701281	Missense_Mutation	SNP	G	A	G	TRIM5	c.C127T	p.H43Y
XH_P55	11	6622401	6622401	Missense_Mutation	SNP	T	C	T	RRP8	c.A895G	p.I299V
XH_P55	11	6806827	6806827	Missense_Mutation	SNP	G	T	G	OR2AG1	c.G559T	p.V187L
XH_P55	11	7110548	7110548	Missense_Mutation	SNP	C	T	C	RBMXL2	c.C197T	p.A66V
XH_P55	11	7982432	7982432	Missense_Mutation	SNP	G	A	G	NLRP10	c.C727T	p.R243W
XH_P55	11	8132665	8132665	Nonsense_Mutation	INS	-	CAACCCAAATG	-	RIC3	CAGATCATTTCG_Y48_P49delinsX	
XH_P55	11	16340056	16340056	Silent	SNP	A	C	A	SOX6	c.T381G	p.L127L
XH_P55	11	18955861	18955861	Silent	SNP	C	T	C	MRGPRX1	c.G471A	p.E157E
XH_P55	11	19251289	19251289	Silent	SNP	C	G	C	E2F8	c.G1605C	p.T535T
XH_P55	11	20622975	20622975	Missense_Mutation	SNP	G	A	G	SLC6A5	c.G304A	p.G102S
XH_P55	11	28057957	28057957	Missense_Mutation	SNP	T	C	T	KIF18A	c.A2203G	p.I735V
XH_P55	11	30033764	30033764	Silent	SNP	C	T	C	KCN4A	c.G462A	p.T154T
XH_P55	11	34482908	34482908	Silent	SNP	C	T	C	CAT	c.C1167T	p.D389D
XH_P55	11	44129290	44129290	Silent	SNP	C	A	C	EXT2	c.C127A	p.R43R
XH_P55	11	46724717	46724728	In_Frame_Del	DEL	5TGGTGACAG	-	AGTGGTGACAGA	ZNF408	c.552_563del	p.184_188del
XH_P55	11	46897446	46897446	Missense_Mutation	SNP	G	A	G	LRP4	c.C3608T	p.A1203V
XH_P55	11	51515460	51515460	Missense_Mutation	SNP	C	T	C	OR4C46	c.C179T	p.S60F
XH_P55	11	51515640	51515640	Missense_Mutation	SNP	A	G	A	OR4C46	c.A359G	p.H120R
XH_P55	11	51515912	51515912	Missense_Mutation	SNP	C	T	C	OR4C46	c.C631T	p.L211F
XH_P55	11	55339798	55339798	Silent	SNP	C	T	C	OR4C16	c.C195T	p.S65S
XH_P55	11	56058197	56058197	Silent	SNP	G	A	G	OR8H1	c.C342T	p.L114L
XH_P55	11	56184888	56184888	Missense_Mutation	SNP	G	A	G	OR5R1	c.C821T	p.A274V
XH_P55	11	56185345	56185345	Missense_Mutation	SNP	A	G	A	OR5R1	c.T364C	p.C122R
XH_P55	11	56344993	56344993	Missense_Mutation	SNP	C	A	C	OR5M10	c.G205T	p.V69L
XH_P55	11	57947264	57947264	Silent	SNP	C	G	C	OR9Q1	c.C348G	p.A116A
XH_P55	11	57958775	57958775	Silent	SNP	C	T	C	OR9Q2	c.C813T	p.D271D
XH_P55	11	59982088	59982088	Splice_Site	INS	-	TGATTAATCCTT	-	M54A4E	.	.
XH_P55	11	60704213	60704213	Missense_Mutation	SNP	C	T	C	TMEM132A	c.C2909T	p.A970V
XH_P55	11	61551040	61551040	Silent	SNP	C	T	C	MYRF	c.C2967T	p.T989T
XH_P55	11	61584084	61584084	Silent	SNP	G	A	G	FADS1	c.G30A	p.R10R
XH_P55	11	61722645	61722645	Silent	SNP	C	A	C	BEST1	c.C39A	p.I131
XH_P55	11	61730234	61730234	Silent	SNP	T	C	T	BEST1	c.T1347C	p.T449T
XH_P55	11	62156608	62156608	Silent	SNP	C	T	C	ASRGL1	c.C495T	p.N165N
XH_P55	11	62289670	62289670	Silent	SNP	A	G	A	AHNAK	c.T12219C	p.F4073F
XH_P55	11	62290480	62290480	Silent	SNP	C	T	C	AHNAK	c.G11409A	p.K3803K
XH_P55	11	62293905	62293905	Silent	SNP	G	A	G	AHNAK	c.C7984T	p.L2662L
XH_P55	11	62293906	62293906	Missense_Mutation	SNP	C	G	C	AHNAK	c.G7983C	p.K2661N
XH_P55	11	62296030	62296030	Silent	SNP	A	G	A	AHNAK	c.T5859C	p.G1953G
XH_P55	11	62296271	62296271	Missense_Mutation	SNP	G	A	G	AHNAK	c.C5618T	p.A1873V
XH_P55	11	62298252	62298252	Missense_Mutation	SNP	C	T	C	AHNAK	c.G3637A	p.V1213M
XH_P55	11	63667385	63667385	Missense_Mutation	SNP	A	T	A	MARK2	c.A571T	p.I191F
XH_P55	11	63994230	63994230	Missense_Mutation	SNP	G	T	G	NUDT22	c.G106T	p.G36C
XH_P55	11	64622869	64622869	Silent	SNP	G	C	G	EHF1	c.C1005G	p.L335L
XH_P55	11	65649984	65649984	Silent	SNP	T	C	T	CTSW	c.T525C	p.D175D
XH_P55	11	66031660	66031660	Silent	SNP	C	T	C	KLC2	c.C855T	p.D285D
XH_P55	11	66456274	66456274	Silent	SNP	G	T	G	SPTBN2	c.C6081A	p.A2027A
XH_P55	11	66458980	66458980	Silent	SNP	G	A	G	SPTBN2	c.C5340T	p.N1780N
XH_P55	11	71821634	71821634	Nonsense_Mutation	SNP	C	A	C	ANAPC15	c.G136T	p.E46X
XH_P55	11	76895771	76895792	Frame_Shift_Del	DEL	GGGGACACC	-	CGGGGACACCA	MYO7A	c.3514_3535del	p.G1172fs
XH_P55	11	76910766	76910766	Silent	SNP	C	T	C	MYO7A	c.C4755T	p.S1585S
XH_P55	11	76912636	76912636	Missense_Mutation	SNP	A	T	A	MYO7A	c.A4996T	p.S1666C
XH_P55	11	82443672	82443672	Missense_Mutation	SNP	C	G	C	FAM181B	c.G1100C	p.R367P
XH_P55	11	89537461	89537461	Silent	SNP	G	T	G	TRIM49	c.C177A	p.T59T
XH_P55	11	102593248	102593248	Missense_Mutation	SNP	T	C	T	MMP8	c.A259G	p.K87E
XH_P55	11	103229027	103229027	Silent	SNP	T	C	T	DYNC2H1	c.T12096C	p.D4032D
XH_P55	11	104763208	104763211	Frame_Shift_Del	DEL	TCTT	-	TCTT	CASP12	c.279_282del	p.E93fs
XH_P55	11	104905100	104905100	Missense_Mutation	SNP	T	G	T	CASP1	c.A109C	p.K37Q
XH_P55	11	105880453	105880453	Nonsense_Mutation	SNP	C	A	C	MSANTD4	c.G847T	p.G283X
XH_P55	11	105880454	105880454	Nonsense_Mutation	INS	-	ATCAGGTGATA	-	MSANTD4	846insTATCAC82_G283delinsHITX	
XH_P55	11	110035528	110035528	Missense_Mutation	SNP	T	A	T	ZC3H12C	c.T1718A	p.M573K
XH_P55	11	110035530	110035530	In_Frame_Ins	INS	-	AGCAATGGCCTT	-	ZC3H12C	TCTTTAAGCAATdelinsHYIFKQWPSIWS	
XH_P55	11	114441917	114441917	Missense_Mutation	SNP	G	T	G	NXPE4	c.C1378A	p.H460N
XH_P55	11	116692334	116692334	Missense_Mutation	SNP	C	T	C	APOA4	c.G440A	p.S147N
XH_P55	11	116701535	116701535	Silent	SNP	T	C	T	APOC3	c.T102C	p.G34G
XH_P55	11	116729013	116729013	Silent	SNP	T	C	T	SIK3	c.A2844G	p.Q948Q
XH_P55	11	117391966	117391966	Silent	SNP	G	A	G	DSCAML1	c.C1272T	p.R424R
XH_P55	11	119510644	119510644	Missense_Mutation	SNP	A	C	A	NECTIN1	c.T1082G	p.V361G
XH_P55	11	12098942	12098942	Silent	SNP	C	T	C	TECTA	c.C2256T	p.I752I

XH_P55	11	121475922	121475922	Silent	SNP	T	A	T	SORL1	c.T4752A	p.A1584A
XH_P55	11	124766128	124766128	Silent	SNP	A	G	A	ROBO4	c.T210C	p.H70H
XH_P55	11	129801124	129801124	Silent	SNP	T	C	T	PRDM10	c.A1059G	p.Q353Q
XH_P55	12	475202	475202	Silent	SNP	G	C	G	KDM5A	c.C435G	p.R145R
XH_P55	12	2968169	2968169	Missense_Mutation	SNP	A	G	A	FOXM1	c.T1882C	p.S628P
XH_P55	12	6639088	6639088	Silent	SNP	A	G	A	NCAPD2	c.A3801G	p.V1267V
XH_P55	12	6639981	6639981	Missense_Mutation	SNP	C	G	C	NCAPD2	c.C3962G	p.T1321S
XH_P55	12	6646320	6646320	Silent	SNP	T	C	T	GAPDH	c.T255C	p.D85D
XH_P55	12	6729409	6729409	Missense_Mutation	SNP	C	T	C	LPAR5	c.G1006A	p.A336T
XH_P55	12	6933787	6933787	Silent	SNP	A	G	A	GPR162	c.A723G	p.V241V
XH_P55	12	7528452	7528452	Missense_Mutation	SNP	G	T	G	CD163L1	c.C2560A	p.L854I
XH_P55	12	10762506	10762506	In_Frame_Ins	INS	-	TTAATTITTA	-	MAGOH8	9_50insTAAAAAT	p.K17delinsIKLK
XH_P55	12	10762508	10762508	Frame_Shift_Ins	INS	-	TCTT	-	MAGOH8	c.47_48insAAGA	p.L16fs
XH_P55	12	10999780	10999780	Missense_Mutation	SNP	C	T	C	PRR4	c.G287A	p.R96Q
XH_P55	12	11061122	11061122	Missense_Mutation	SNP	T	C	T	TAS2R13	c.A776G	p.N259S
XH_P55	12	11506281	11506281	Silent	SNP	T	C	T	PRB1	c.A357G	p.Q119Q
XH_P55	12	13061294	13061294	Silent	SNP	C	T	C	GPRC5A	c.C111T	p.A37A
XH_P55	12	22671011	22671011	In_Frame_Ins	INS	-	AATTGTGTTCTA	-	C2CD5	AGAAATAGAAAG7delinsLURNRNKFLKK	
XH_P55	12	26809316	26809316	Silent	SNP	G	A	G	ITPR2	c.C2358T	p.H786H
XH_P55	12	31244748	31244748	Silent	SNP	G	A	G	DDX11	c.G1185A	p.A395A
XH_P55	12	31249861	31249861	Missense_Mutation	SNP	C	G	C	DDX11	c.C1699G	p.Q567E
XH_P55	12	31253995	31253995	Silent	SNP	C	T	C	DDX11	c.C1983T	p.L661L
XH_P55	12	31256905	31256905	Missense_Mutation	SNP	T	C	T	DDX11	c.T2851C	p.C951R
XH_P55	12	42554505	42554505	Silent	SNP	A	G	A	YAF2	c.T303C	p.A101A
XH_P55	12	48578442	48578442	Silent	SNP	C	T	C	CCDC184	c.C537T	p.D179D
XH_P55	12	49390677	49390677	Missense_Mutation	SNP	T	C	T	DDN	c.A1982G	p.E661G
XH_P55	12	49724314	49724412	In_Frame_Del	DEL	TACCTGAGCC	-	GTACCTGAGCCC	TROAP	c.1686_1784del	p.562_595del
XH_P55	12	50348078	50348078	Silent	SNP	T	C	T	AQP2	c.T501C	p.S167S
XH_P55	12	50369305	50369305	Missense_Mutation	SNP	G	A	G	AQP6	c.G700A	p.V234I
XH_P55	12	53070145	53070145	Silent	SNP	G	A	G	KRT1	c.C1389T	p.R463R
XH_P55	12	53086645	53086645	Missense_Mutation	SNP	G	A	G	KRT77	c.C1100T	p.T367M
XH_P55	12	54405116	54405116	Frame_Shift_Ins	INS	-	CCCCAGTC	-	HOXC8	0_681insCCCCA	p.N227fs
XH_P55	12	54974803	54974803	Silent	SNP	C	T	C	PPP1R1A	c.G435A	p.E145E
XH_P55	12	57039080	57039080	Missense_Mutation	SNP	C	T	C	ATP5B	c.G185A	p.R62H
XH_P55	12	57595332	57595332	Silent	SNP	C	T	C	LRP1	c.C10398T	p.C3466C
XH_P55	12	57691140	57691140	Nonsense_Mutation	INS	-	TAAAT	-	R3HDM2	330_531insATTTC	p.Q177delinsQFX
XH_P55	12	57691142	57691142	Frame_Shift_Ins	INS	-	TACCTAAATTTTA	-	R3HDM2	29insATAAATT	p.Q177fs
XH_P55	12	64062132	64062132	Silent	SNP	G	A	G	DPY19L2	c.C42T	p.S14S
XH_P55	12	75824893	75824893	Silent	SNP	G	A	G	GLIPR1L2	c.G987A	p.E329E
XH_P55	12	76424934	76424934	Frame_Shift_Del	DEL	C	-	C	PHLDA1	c.588delG	p.Q196fs
XH_P55	12	76424936	76424940	Frame_Shift_Del	DEL	GTTGC	-	GTTGC	PHLDA1	c.582_586del	p.Q194fs
XH_P55	12	99007623	99007623	Missense_Mutation	SNP	C	T	C	IKBP1	c.G793A	p.G265S
XH_P55	12	104186946	104186946	Silent	SNP	G	T	G	NT5DC3	c.C1015A	p.T339R
XH_P55	12	108954862	108954862	Missense_Mutation	SNP	G	C	G	SART3	c.C69G	p.D23E
XH_P55	12	109717697	109717697	Silent	SNP	A	G	A	FOXN4	c.T1333C	p.L445L
XH_P55	12	110341933	110341933	Missense_Mutation	SNP	A	G	A	TCHP	c.A380G	p.K127R
XH_P55	12	111779792	111779792	Silent	SNP	C	T	C	CUX2	c.C3594T	p.I1198I
XH_P55	12	112589824	112589824	Missense_Mutation	SNP	A	G	G	TRAFD1	c.A1499G	p.D500G
XH_P55	12	120613558	120613558	Missense_Mutation	SNP	T	C	T	GCN1	c.A1033G	p.I345V
XH_P55	12	125298877	125298877	Silent	SNP	G	A	G	SCARB1	c.C501T	p.G167G
XH_P55	12	125396398	125396398	Silent	SNP	A	G	A	UBC	c.T1920C	p.D640D
XH_P55	12	125434716	125434716	Silent	SNP	G	A	G	DHX37	c.C3195T	p.A1065A
XH_P55	12	130839188	130839188	Missense_Mutation	SNP	C	T	C	PIWIL1	c.C1151T	p.P384L
XH_P55	12	132688137	132688137	Silent	SNP	A	G	A	GALNT9	c.T78C	p.Y26Y
XH_P55	12	133303973	133303973	Missense_Mutation	SNP	C	G	C	ANKLE2	c.G2672C	p.G891A
XH_P55	12	133384864	133384864	Missense_Mutation	SNP	G	A	G	GOLGA3	c.C791T	p.P264L
XH_P55	13	20763642	20763642	Missense_Mutation	SNP	C	T	C	GJB2	c.G79A	p.V27I
XH_P55	13	24471048	24471048	Silent	SNP	C	T	C	C1QTNF9B	c.G78A	p.G26G
XH_P55	13	24797703	24797703	Missense_Mutation	SNP	C	G	C	SPATA13	c.C636G	p.I212M
XH_P55	13	25367301	25367301	Silent	SNP	C	T	C	RNF17	c.C1057T	p.L353L
XH_P55	13	26625047	26625047	Silent	SNP	G	A	G	SHISA2	c.C67T	p.L23L
XH_P55	13	30107067	30107067	Silent	SNP	G	C	G	SLC7A1	c.C423G	p.G141G
XH_P55	13	32776603	32776603	Silent	SNP	T	C	T	FRY	c.T3957C	p.L1319L
XH_P55	13	37580139	37580139	Silent	SNP	G	A	G	EXOS8	c.G321A	p.Q107Q
XH_P55	13	39263731	39263731	Silent	SNP	C	T	C	FREM2	c.C2250T	p.D750D
XH_P55	13	40229891	40229891	Missense_Mutation	SNP	G	A	G	COG6	c.G28A	p.A10T
XH_P55	13	41134096	41134096	Missense_Mutation	SNP	G	A	G	FOXO1	c.C1532T	p.A511V
XH_P55	13	43462563	43462563	Frame_Shift_Ins	INS	-	TTGGAAGTATAA	-	EPSTI1	CTCTAATTATAC	p.L352fs
XH_P55	13	46542095	46542095	Frame_Shift_Ins	INS	-	TTCTCTCTGCCT	-	ZC3H13	ATACGAGGCAG	p.R1289fs
XH_P55	13	52603241	52603241	Missense_Mutation	SNP	A	G	A	UTP14C	c.A301G	p.T101A
XH_P55	13	53422553	53422553	Missense_Mutation	SNP	A	G	A	PCDH8	c.T19C	p.W7R
XH_P55	13	103504517	103504517	Silent	SNP	T	C	T	BIVM-ERCC5	c.T138C	p.H46H
XH_P55	13	111164469	111164469	Silent	SNP	C	T	C	COL4A2	c.C5070T	p.A1690A
XH_P55	14	19563532	19563532	Missense_Mutation	SNP	A	G	A	POTEG	c.A1046G	p.H349R
XH_P55	14	20586042	20586042	Missense_Mutation	SNP	G	C	G	OR4K17	c.G477C	p.K159N
XH_P55	14	20847202	20847202	Silent	SNP	A	G	A	TEP1	c.T4866C	p.D1622D
XH_P55	14	20898308	20898308	Missense_Mutation	SNP	C	T	C	KLHL33	c.G527A	p.R176Q
XH_P55	14	21109695	21109695	Frame_Shift_Ins	INS	-	AATTCTATTCTA	-	OR6S1	56insTAGAAAT	p.R52fs
XH_P55	14	21542753	21542753	Silent	SNP	G	A	G	ARHGEF40	c.G864A	p.A288A
XH_P55	14	22102439	22102439	Missense_Mutation	SNP	C	G	C	OR10G2	c.G560C	p.R187P
XH_P55	14	24653954	24653954	Missense_Mutation	SNP	G	A	G	IPO4	c.C1538T	p.A513V
XH_P55	14	24839165	24839165	Silent	SNP	C	T	C	NFATC4	c.C561T	p.D187D
XH_P55	14	24898556	24898556	Missense_Mutation	SNP	G	C	G	KHNYN	c.G49C	p.G17R
XH_P55	14	37051517	37051517	Silent	SNP	C	G	C	NKX2-8	c.G78C	p.P26P
XH_P55	14	39648443	39648443	Frame_Shift_Ins	INS	-	TTAATACTTACG	-	PNN	48insTTTAATAC	p.A216fs
XH_P55	14	39777656	39777656	Missense_Mutation	SNP	A	T	A	MIA2	c.A971T	p.H324L
XH_P55	14	39901157	39901157	Silent	SNP	C	A	C	FBX033	c.G210T	p.S70S
XH_P55	14	44974189	44974189	Missense_Mutation	SNP	C	A	C	FSCB	c.G2002T	p.A668S
XH_P55	14	45432870	45432870	Missense_Mutation	SNP	G	C	G	TOGARAM1	c.G1246C	p.E416Q
XH_P55	14	52186972	52186972	Silent	SNP	A	G	A	FRMD6	c.A150G	p.P50P
XH_P55	14	52735108	52735108	Silent	SNP	C	T	C	PTGDR	c.C576T	p.G192G
XH_P55	14	57052511	57052511	Silent	SNP	G	T	G	TMEM260	c.G225T	p.T75T
XH_P55	14	62229285	62229285	Missense_Mutation	SNP	T	G	T	SNAPC1	c.T107G	p.M36R
XH_P55	14	64554466	64554466	Missense_Mutation	SNP	T	G	T	SYNE2	c.T11562G	p.I3854M
XH_P55	14	65242044	65242044	Silent	SNP	C	T	C	SPTB	c.G4641A	p.A1547A
XH_P55	14	71199452	71199452	Silent	SNP	G	A	G	MAP3K9	c.C1833T	p.N611N
XH_P55	14	71204973	71204973	Silent	SNP	C	T	C	MAP3K9	c.G1059A	p.S353S
XH_P55	14	74428000	74428000	Missense_Mutation	SNP	A	T	A	COQ6	c.A1016T	p.D339V

XH_P55	14	75150153	75150153	Frame_Shift_Ins	INS	-	TTTTAAAAATAA	-	AREL1	27insATTATTTT	p.V109fs
XH_P55	14	75150155	75150155	In_Frame_Ins	INS	-	CTTTAT	-	AREL1	24_325insATAA	p.V109delinsKV
XH_P55	14	75746690	75746690	Silent	SNP	C	T	C	FOS	c.C252T	p.S845
XH_P55	14	76368544	76368544	Missense_Mutation	SNP	T	C	T	TTLL5	c.T3800C	p.F1267S
XH_P55	14	81744736	81744736	Missense_Mutation	SNP	A	G	A	STON2	c.T919C	p.S307P
XH_P55	14	88946622	88946622	Missense_Mutation	SNP	G	A	G	PTPN21	c.C1153T	p.L385F
XH_P55	14	100759277	100759277	Silent	SNP	C	T	C	SLC25A29	c.G57A	p.R19R
XH_P55	14	100795139	100795139	Missense_Mutation	SNP	G	T	G	SLC25A47	c.G404T	p.R135L
XH_P55	14	100996312	100996312	Silent	SNP	T	C	T	WDR25	c.T795C	p.Y265Y
XH_P55	14	101348849	101348849	Silent	SNP	G	A	G	RTL1	c.C2277T	p.H759H
XH_P55	14	103576443	103576443	Silent	SNP	T	C	T	EXOC3L4	c.T2052C	p.T684T
XH_P55	14	103576444	103576444	Missense_Mutation	SNP	C	G	C	EXOC3L4	c.C2053G	p.Q685E
XH_P55	14	105267579	105267579	Silent	SNP	A	G	A	ZBTB42	c.A45G	p.R15R
XH_P55	14	105268104	105268104	Silent	SNP	G	A	G	ZBTB42	c.G570A	p.L190L
XH_P55	14	105414804	105414804	Silent	SNP	A	G	A	AHNAK2	c.T6684C	p.F2228F
XH_P55	14	105478102	105478102	Silent	SNP	G	A	G	CDC4A	c.C165T	p.N55N
XH_P55	14	105517643	105517643	Silent	SNP	G	A	G	GPR132	c.C267T	p.N89N
XH_P55	14	105716034	105716034	Silent	SNP	C	T	C	BTBD6	c.C483T	p.Y161Y
XH_P55	15	22743596	22743596	Nonsense_Mutation	SNP	C	T	C	GOLGA6L1	c.C1981T	p.Q661X
XH_P55	15	31233934	31233934	Silent	SNP	T	A	T	MTMR10	c.A2073T	p.V691V
XH_P55	15	31453147	31453147	Missense_Mutation	SNP	G	A	G	TRPM1	c.C16T	p.R6W
XH_P55	15	32890282	32890282	Silent	SNP	C	T	C	GOLGA8N	c.C495T	p.D165D
XH_P55	15	40648412	40648412	Missense_Mutation	SNP	C	T	C	PHGR1	c.C157T	p.P53S
XH_P55	15	41813279	41813279	Silent	SNP	C	T	C	RPAP1	c.G3105A	p.R1035R
XH_P55	15	41829230	41829230	Silent	SNP	A	G	A	RPAP1	c.T94C	p.L32L
XH_P55	15	43028749	43028749	Missense_Mutation	SNP	T	A	T	CDAN1	c.A320T	p.Q107L
XH_P55	15	43821312	43821312	Silent	SNP	T	C	T	MAP1A	c.T7641C	p.G2547G
XH_P55	15	44038899	44038899	Silent	SNP	C	T	C	PDIA3	c.C162T	p.A54A
XH_P55	15	45388140	45388140	Silent	SNP	G	A	G	DUOX2	c.C3966T	p.S1322S
XH_P55	15	45398438	45398438	Missense_Mutation	SNP	T	C	T	DUOX2	c.A2033G	p.H678R
XH_P55	15	52684136	52684136	Frame_Shift_Ins	INS	-	GATATACTAATG	-	MYO5A	33insTTCAATAG	p.E511fs
XH_P55	15	57731573	57731573	Missense_Mutation	SNP	C	T	C	CGNL1	c.C1376T	p.S459F
XH_P55	15	65621441	65621441	Missense_Mutation	SNP	C	A	C	IGDC3	c.G2251T	p.V751L
XH_P55	15	68628163	68628163	Missense_Mutation	SNP	C	T	C	ITGA11	c.G1297A	p.V433M
XH_P55	15	74032783	74032783	Silent	SNP	A	G	A	C15orf59	c.T357C	p.S119S
XH_P55	15	75932129	75932129	Silent	SNP	G	T	G	IMP3	c.C381A	p.A127A
XH_P55	15	78390414	78390414	Missense_Mutation	SNP	T	C	T	SH2D7	c.T410C	p.M137T
XH_P55	15	84908900	84908900	Missense_Mutation	SNP	G	A	G	GOLGA6L4	c.G794A	p.R265H
XH_P55	15	85405995	85405995	Missense_Mutation	SNP	T	C	T	ALPK3	c.T4865C	p.L1622P
XH_P55	15	85467275	85467275	Silent	SNP	C	T	C	SLC28A1	c.C1017T	p.H339H
XH_P55	15	89398553	89398553	Missense_Mutation	SNP	C	A	C	ACAN	c.C2737A	p.P913T
XH_P55	15	90128966	90128966	Missense_Mutation	SNP	C	T	C	TICRR	c.C1201T	p.R401W
XH_P55	15	90171787	90171787	Missense_Mutation	SNP	C	T	C	KIF7	c.G3895A	p.A1299T
XH_P55	15	91450665	91450665	Missense_Mutation	SNP	G	A	G	MAN2A2	c.G1136A	p.R379H
XH_P55	15	100514614	100514614	Missense_Mutation	SNP	T	C	T	ADAMTS17	c.A3281G	p.N1094S
XH_P55	16	304514	304514	Silent	SNP	C	T	C	FAM234A	c.C102T	p.N34N
XH_P55	16	315008	315008	Missense_Mutation	SNP	A	G	A	FAM234A	c.A1646G	p.Q549R
XH_P55	16	319511	319511	Missense_Mutation	SNP	A	G	A	RG511	c.T728C	p.M243T
XH_P55	16	320759	320759	Missense_Mutation	SNP	C	T	C	RG511	c.G499A	p.V167M
XH_P55	16	347184	347184	Silent	SNP	A	G	A	AXIN1	c.T1827C	p.A609A
XH_P55	16	1664931	1664931	Silent	SNP	T	C	T	CRAMP1	c.T291C	p.D97D
XH_P55	16	1961674	1961674	Missense_Mutation	SNP	G	C	G	HS3ST6	c.C946G	p.L316V
XH_P55	16	2009697	2009697	Silent	SNP	C	T	C	NDUFB10	c.C72T	p.I24I
XH_P55	16	3299749	3299749	Silent	SNP	G	A	G	MEFV	c.C309T	p.R103R
XH_P55	16	3406516	3406516	Silent	SNP	A	G	A	OR2C1	c.A576G	p.T192T
XH_P55	16	3447282	3447282	Missense_Mutation	SNP	C	G	C	ZSCAN32	c.G276C	p.E92D
XH_P55	16	3554799	3554799	Silent	SNP	T	C	T	CLUAP1	c.T102C	p.L34L
XH_P55	16	3640784	3640784	Missense_Mutation	SNP	G	A	G	SLX4	c.C2855T	p.A952V
XH_P55	16	3640785	3640785	Missense_Mutation	SNP	C	T	C	SLX4	c.G2854A	p.A952T
XH_P55	16	4164364	4164364	Silent	SNP	C	T	C	ADCY9	c.G1080A	p.R360R
XH_P55	16	4935146	4935146	Silent	SNP	C	T	C	PPL	c.G3510A	p.V1170V
XH_P55	16	4935636	4935636	Missense_Mutation	SNP	G	A	G	PPL	c.C3020T	p.A1007V
XH_P55	16	11933678	11933678	Silent	SNP	G	C	G	RSL1D1	c.C1020G	p.T340T
XH_P55	16	17228368	17228368	Silent	SNP	G	A	G	XYLT1	c.C1989T	p.A663A
XH_P55	16	19547503	19547503	Missense_Mutation	SNP	C	T	C	CCP110	c.C512T	p.P171L
XH_P55	16	23226787	23226787	Silent	SNP	C	G	C	SCNN1G	c.C1947G	p.L649L
XH_P55	16	23491170	23491170	Nonsense_Mutation	DEL	G	-	G	GGA2	c.1045delC	p.L349X
XH_P55	16	24564880	24564883	Splice_Site	DEL	TATA	-	TATA	RBBP6	.	.
XH_P55	16	27224963	27224963	Missense_Mutation	SNP	C	T	C	KDM8	c.C670T	p.R224W
XH_P55	16	30518041	30518041	Missense_Mutation	SNP	G	C	G	ITGAL	c.G2120C	p.R707T
XH_P55	16	31091199	31091199	Missense_Mutation	SNP	G	A	G	ZNF646	c.G3554A	p.R1185K
XH_P55	16	32265022	32265022	Silent	SNP	G	C	G	TP53TG3D	c.G348C	p.A116A
XH_P55	16	50259176	50259176	Nonsense_Mutation	INS	-	TGCTTTGAT	-	PAPD5	5_1736insTGCT	p.Q579delinsLX
XH_P55	16	55601388	55601388	Silent	SNP	A	G	A	CAPNS2	c.A720G	p.E240E
XH_P55	16	56501135	56501135	Nonsense_Mutation	INS	-	AATTAATGTGCA	-	OGFOD1	CCTGAAATTAAT38	p.P239delinsGGPX
XH_P55	16	57549309	57549309	Silent	SNP	G	A	G	CCDC102A	c.C1467T	p.D489D
XH_P55	16	57992333	57992333	Missense_Mutation	SNP	T	C	T	CNGB1	c.A818G	p.H273R
XH_P55	16	58073845	58073845	Silent	SNP	C	T	C	MMP15	c.C507T	p.R169R
XH_P55	16	58575489	58575489	Silent	SNP	G	A	G	CNOT1	c.C4701T	p.Y1567Y
XH_P55	16	66656102	66656102	Silent	SNP	C	T	C	CMTM4	c.G486A	p.A162A
XH_P55	16	67913573	67913573	Missense_Mutation	SNP	G	A	G	EDC4	c.G1717A	p.V573M
XH_P55	16	68344363	68344363	Missense_Mutation	SNP	A	C	A	SLC7A60S	c.T346G	p.S116A
XH_P55	16	70180088	70180088	Missense_Mutation	SNP	A	T	A	PDPK	c.A1619T	p.Y540F
XH_P55	16	84218565	84218565	Silent	SNP	T	C	T	TAFC1	c.A30G	p.A10A
XH_P55	16	89799950	89799950	Silent	SNP	C	T	C	ZNF276	c.C1341T	p.G447G
XH_P55	16	89965055	89965055	Silent	SNP	G	A	G	TCF25	c.G1113A	p.L371L
XH_P55	16	89986608	89986608	Silent	SNP	A	G	A	MC1R	c.A942G	p.T314T
XH_P55	17	260299	260299	Missense_Mutation	SNP	G	A	G	C17orf97	c.G166A	p.E56K
XH_P55	17	650471	650471	Missense_Mutation	SNP	G	A	G	GEMIN4	c.C812T	p.T271M
XH_P55	17	685640	685640	Missense_Mutation	SNP	G	T	G	MRM3	c.G22T	p.A8S
XH_P55	17	1174094	1174094	Silent	SNP	A	G	A	BHLHA9	c.A237G	p.L79L
XH_P55	17	1782957	1782957	Silent	SNP	C	T	C	RP1A	c.C1056T	p.S352S
XH_P55	17	2930339	2930339	Silent	SNP	G	A	G	RAP1GAP2	c.G2037A	p.P679P
XH_P55	17	2966032	2966032	Missense_Mutation	SNP	C	G	C	OR1D5	c.G870C	p.R290S
XH_P55	17	4436274	4436274	Missense_Mutation	SNP	G	A	G	SPNS2	c.G938A	p.R313H
XH_P55	17	4797305	4797305	Missense_Mutation	SNP	G	A	G	MINK1	c.G2476A	p.V826I
XH_P55	17	4803711	4803711	Nonsense_Mutation	SNP	G	A	G	C17orf107	c.G456A	p.W152X
XH_P55	17	7318935	7318935	Silent	SNP	C	T	C	NLGN2	c.C1143T	p.G381G

XH_P55	17	7412403	7412403	Silent	SNP	T	C	T	POLR2A	c.T3606C	p.F1202F
XH_P55	17	7722365	7722365	Missense_Mutation	SNP	C	T	C	DNAH2	c.C10799T	p.T3600I
XH_P55	17	7736480	7736480	Missense_Mutation	SNP	T	A	T	DNAH2	c.T13070A	p.V4357D
XH_P55	17	7750436	7750436	Missense_Mutation	SNP	C	T	C	KDM6B	c.C923T	p.S308L
XH_P55	17	7754460	7754460	Silent	SNP	C	A	C	KDM6B	c.C3795A	p.I1265I
XH_P55	17	7758522	7758522	Missense_Mutation	SNP	C	T	C	TMEM88	c.C130T	p.L44F
XH_P55	17	8296383	8296383	Missense_Mutation	SNP	C	T	C	RNF222	c.G397A	p.A133T
XH_P55	17	8408131	8408131	Silent	SNP	G	A	G	MYH10	c.C3387T	p.S1129S
XH_P55	17	9725347	9725347	Silent	SNP	A	G	A	SGS1L2	c.T42C	p.P14P
XH_P55	17	11648332	11648332	Silent	SNP	C	T	C	DNAH9	c.C6330T	p.N2110N
XH_P55	17	11672607	11672607	Missense_Mutation	SNP	G	T	G	DNAH9	c.G7513T	p.V2505L
XH_P55	17	15215660	15215660	Silent	SNP	T	C	T	TEKT3	c.A1017G	p.Q339Q
XH_P55	17	15234877	15234877	Missense_Mutation	SNP	G	A	G	TEKT3	c.C26T	p.T9M
XH_P55	17	15532208	15532208	Silent	SNP	G	A	G	TRIM16	c.C1026T	p.N342N
XH_P55	17	16842991	16842991	Missense_Mutation	SNP	G	A	G	TNFRSF13B	c.C752T	p.P251L
XH_P55	17	18047189	18047189	Missense_Mutation	SNP	G	A	G	MYO15A	c.G6052A	p.G2018R
XH_P55	17	18167684	18167684	Missense_Mutation	SNP	G	A	G	MIEF2	c.G971A	p.G324E
XH_P55	17	18221010	18221010	Missense_Mutation	SNP	A	G	A	SMCR8	c.A1907G	p.N636S
XH_P55	17	19186992	19186992	Missense_Mutation	SNP	G	A	G	EPN2	c.G560A	p.G187D
XH_P55	17	20798992	20798992	Silent	SNP	C	T	C	CCDC144NL	c.G342A	p.P114K
XH_P55	17	20799119	20799119	Missense_Mutation	SNP	A	G	A	CCDC144NL	c.T215C	p.L72P
XH_P55	17	25909850	25909850	Silent	SNP	G	T	G	KSR1	c.G288T	p.L96L
XH_P55	17	28511908	28511908	Frame_Shift_Ins	INS	-	TCCTCTGTGGTA	-	NSRP1	2insTTCTCTCTTG	p.H244fs
XH_P55	17	28511910	28511910	Missense_Mutation	SNP	A	T	A	NSRP1	c.A733T	p.S245C
XH_P55	17	29855661	29855661	Silent	SNP	G	A	G	RAB11FIP4	c.G738A	p.E246E
XH_P55	17	32904586	32904586	Missense_Mutation	SNP	C	T	C	C17orf102	c.G464A	p.R155K
XH_P55	17	34257637	34257637	Missense_Mutation	SNP	T	C	T	RDML1	c.A95G	p.H32R
XH_P55	17	35453962	35453962	Missense_Mutation	SNP	C	T	C	ACACA	c.G6575A	p.R2192H
XH_P55	17	36709030	36709030	Missense_Mutation	SNP	G	A	G	SRCIN1	c.C2263T	p.P755S
XH_P55	17	37922259	37922259	Silent	SNP	G	A	G	IKZF3	c.C573T	p.S191S
XH_P55	17	38179492	38179492	Silent	SNP	A	G	A	MED24	c.T2103C	p.I701I
XH_P55	17	39594539	39594539	Silent	SNP	A	G	A	KRT38	c.T1047C	p.C349C
XH_P55	17	39619193	39619193	Missense_Mutation	SNP	C	T	C	KRT32	c.G1106A	p.P369Q
XH_P55	17	39619194	39619194	Missense_Mutation	SNP	G	A	G	KRT32	c.C1105T	p.R369W
XH_P55	17	40714804	40714804	Missense_Mutation	SNP	C	A	C	COASY	c.C164A	p.S55Y
XH_P55	17	40766546	40766546	Silent	SNP	C	G	C	TUBG1	c.C1029G	p.R343R
XH_P55	17	40818451	40818451	Silent	SNP	G	A	G	TUBG2	c.G1107A	p.S369S
XH_P55	17	42453065	42453065	Missense_Mutation	SNP	A	C	A	ITGA2B	c.T2621G	p.I874S
XH_P55	17	42981499	42981499	Missense_Mutation	SNP	C	T	C	FAM187A	c.C302T	p.T101I
XH_P55	17	42981654	42981654	Missense_Mutation	SNP	A	G	A	FAM187A	c.A457G	p.K153E
XH_P55	17	43045249	43045249	Silent	SNP	G	A	G	C1QL1	c.C168T	p.S56S
XH_P55	17	44952531	44952531	Silent	SNP	G	T	G	WNT9B	c.C399T	p.R133R
XH_P55	17	45008570	45008570	Missense_Mutation	SNP	G	A	G	GOSR2	c.G200A	p.R67K
XH_P55	17	45993982	45993982	Missense_Mutation	SNP	C	T	C	SP2	c.C545T	p.A182V
XH_P55	17	46688135	46688135	Missense_Mutation	SNP	G	A	G	HOXB7	c.C146T	p.A49V
XH_P55	17	46802008	46802008	Missense_Mutation	SNP	C	G	C	PRAC2	c.C236G	p.T79R
XH_P55	17	59489893	59489893	Missense_Mutation	SNP	T	C	T	C17orf82	c.T557C	p.L186P
XH_P55	17	61908556	61908556	Silent	SNP	C	T	C	PSMCS	c.C816T	p.L272L
XH_P55	17	62499427	62499430	Frame_Shift_Del	DEL	TCAA	-	TCAA	DDX5	c.686_689del	p.I229fs
XH_P55	17	66596463	66596463	Silent	SNP	C	T	C	FAM20A	c.G345A	p.S115S
XH_P55	17	70645032	70645032	Missense_Mutation	SNP	G	A	G	SLC39A11	c.C860T	p.A287V
XH_P55	17	72346868	72346868	Missense_Mutation	SNP	C	T	C	KIF19	c.C1411T	p.R471W
XH_P55	17	72350362	72350362	Silent	SNP	G	A	G	KIF19	c.G2370A	p.S790S
XH_P55	17	76166939	76166939	Silent	SNP	C	G	G	SYNGR2	c.C141G	p.G47G
XH_P55	17	76420085	76420085	Missense_Mutation	SNP	T	C	T	DNAH17	c.A13291G	p.I4431V
XH_P55	17	76482086	76482086	Missense_Mutation	SNP	C	G	C	DNAH17	c.G7231C	p.D2411H
XH_P55	17	78092063	78092063	Silent	SNP	G	A	G	GAA	c.G2553A	p.G851G
XH_P55	17	78396004	78396004	Splice_Site	SNP	A	G	A	ENDOV	-	-
XH_P55	17	78896529	78896529	Silent	SNP	C	T	C	RPTOR	c.C2052T	p.T684T
XH_P55	17	79682558	79682558	Silent	SNP	T	C	T	SLC25A10	c.T264C	p.R88R
XH_P55	17	80400168	80400168	Missense_Mutation	SNP	C	T	C	HEXDC	c.C1369T	p.R457W
XH_P55	18	2656248	2656248	Silent	SNP	G	C	G	SMCHD1	c.G174C	p.A58A
XH_P55	18	3067278	3067278	Silent	SNP	A	G	A	MYOM1	c.T4752C	p.G1584A
XH_P55	18	5891637	5891637	Silent	SNP	C	A	C	TMEM200C	c.G426T	p.I142P
XH_P55	18	14542949	14542949	Missense_Mutation	SNP	T	C	T	POTEC	c.A197G	p.H66R
XH_P55	18	29797921	29797921	Missense_Mutation	SNP	C	T	C	MEP1B	c.C2084T	p.P695L
XH_P55	18	43246156	43246156	Missense_Mutation	SNP	G	A	G	SLC14A2	c.G1529A	p.R510Q
XH_P55	18	43316538	43316538	Silent	SNP	A	G	A	SLC14A1	c.A192G	p.P64P
XH_P55	18	44549025	44549025	Frame_Shift_Ins	INS	-	GC	-	ELOA3B	1273_1274insG	p.Q425fs
XH_P55	18	47800179	47800179	Missense_Mutation	SNP	G	C	G	MBD1	c.C964G	p.P322A
XH_P55	18	48333203	48333203	Missense_Mutation	SNP	C	G	C	MRO	c.G117C	p.R39S
XH_P55	18	48591919	48591919	Missense_Mutation	SNP	G	A	G	SMAD4	c.G1082A	p.R361H
XH_P55	18	55816791	55816791	Silent	SNP	G	A	G	NEDD4L	c.G24A	p.Q8Q
XH_P55	18	59777079	59777079	Missense_Mutation	SNP	G	A	G	PIGN	c.C1562T	p.A521V
XH_P55	18	74962645	74962645	Silent	SNP	T	C	T	GALR1	c.T141C	p.G47G
XH_P55	19	282753	282753	Missense_Mutation	SNP	G	A	G	PLPP2	c.C539T	p.A180V
XH_P55	19	367089	367089	Missense_Mutation	SNP	G	A	G	THEG	c.C817T	p.H273Y
XH_P55	19	407900	407900	Silent	SNP	A	G	A	C2CD4C	c.T462C	p.A154A
XH_P55	19	422238	422238	Silent	SNP	G	T	G	SHC2	c.C1528A	p.R510R
XH_P55	19	603826	603826	Silent	SNP	C	T	C	HCN2	c.C915T	p.F305F
XH_P55	19	830854	830854	Silent	SNP	T	C	T	AZU1	c.T507C	p.F169F
XH_P55	19	885818	885818	Silent	SNP	A	G	A	MED16	c.T831C	p.F277F
XH_P55	19	991129	991129	Missense_Mutation	SNP	G	A	G	WDR18	c.G790A	p.V264I
XH_P55	19	1004808	1004808	Silent	SNP	C	T	C	GRIN3B	c.C1308T	p.D436D
XH_P55	19	1047002	1047002	Silent	SNP	A	G	A	ABCA7	c.A1824G	p.A608A
XH_P55	19	1047161	1047161	Silent	SNP	A	G	A	ABCA7	c.A1851G	p.G617G
XH_P55	19	1052005	1052005	Silent	SNP	C	T	C	ABCA7	c.C3027T	p.A1009A
XH_P55	19	1054060	1054060	Silent	SNP	A	G	A	ABCA7	c.A3528G	p.L1176L
XH_P55	19	1065018	1065018	Missense_Mutation	SNP	G	T	G	ABCA7	c.G6133T	p.A2045S
XH_P55	19	1272339	1272339	Missense_Mutation	SNP	G	A	G	CIRBP	c.G791A	p.R264H
XH_P55	19	1360575	1360575	Missense_Mutation	SNP	G	A	G	MUM1	c.G658A	p.G220R
XH_P55	19	1615796	1615796	Missense_Mutation	SNP	G	A	G	TCF3	c.C1475T	p.A492V
XH_P55	19	1912817	1912817	Silent	SNP	C	T	C	ADAT3	c.C723T	p.Y241Y
XH_P55	19	1912934	1912934	Silent	SNP	T	C	T	ADAT3	c.T840C	p.T280T
XH_P55	19	2249477	2249477	Missense_Mutation	SNP	G	T	G	AMH	c.G146T	p.S49I
XH_P55	19	2877696	2877696	Missense_Mutation	SNP	G	A	G	ZNFS56	c.G737A	p.R246H
XH_P55	19	4525046	4525046	Missense_Mutation	SNP	A	G	A	PLIN5	c.T763C	p.C255R
XH_P55	19	5783905	5783905	Missense_Mutation	SNP	G	A	G	PRR22	c.C353T	p.P118L

XH_P55	19	5789565	5789565	Missense_Mutation	SNP	T	C	T	DUS3L	c.A553G	p.R185G
XH_P55	19	7694393	7694393	Silent	SNP	G	A	G	XAB2	c.C21T	p.L7L
XH_P55	19	10224526	10224526	Missense_Mutation	SNP	C	T	C	P2RY11	c.C1559T	p.P520L
XH_P55	19	10385540	10385540	Missense_Mutation	SNP	A	T	A	ICAM1	c.A167T	p.K56M
XH_P55	19	10395248	10395248	Silent	SNP	C	T	C	ICAM1	c.C1095T	p.N365N
XH_P55	19	10395683	10395683	Missense_Mutation	SNP	A	G	A	ICAM1	c.A1405G	p.K469E
XH_P55	19	10428432	10428432	Silent	SNP	C	T	C	RAVER1	c.G2058A	p.P686P
XH_P55	19	18329240	18329240	Silent	SNP	T	C	T	PDE4C	c.A1038G	p.E346E
XH_P55	19	18368369	18368369	Missense_Mutation	SNP	G	A	G	KIAA1683	c.C3725T	p.P1242L
XH_P55	19	18368810	18368810	Missense_Mutation	SNP	G	T	G	KIAA1683	c.C3284A	p.P1095H
XH_P55	19	18375608	18375608	Silent	SNP	G	A	G	KIAA1683	c.C2742T	p.A914A
XH_P55	19	18377274	18377274	Missense_Mutation	SNP	A	G	A	KIAA1683	c.T1076C	p.M359T
XH_P55	19	18377496	18377496	Missense_Mutation	SNP	C	G	C	KIAA1683	c.G854C	p.S285T
XH_P55	19	18538742	18538742	Silent	SNP	A	C	A	SSBP4	c.A229C	p.R77R
XH_P55	19	19221651	19221651	Missense_Mutation	SNP	T	G	T	SLC25A42	c.T923G	p.L308R
XH_P55	19	19380996	19380996	Silent	SNP	G	T	G	TM6SF2	c.C387A	p.G129G
XH_P55	19	19625552	19625552	Missense_Mutation	SNP	G	C	G	TSSK6	c.C685G	p.L229V
XH_P55	19	19640198	19640198	Missense_Mutation	SNP	G	A	G	YJEFN3	c.G85A	p.A29T
XH_P55	19	19737686	19737686	Silent	SNP	C	T	C	LPAR2	c.G408A	p.V136V
XH_P55	19	21606876	21606876	Missense_Mutation	SNP	G	A	G	ZNF493	c.G1031A	p.R344Q
XH_P55	19	21948570	21948570	Missense_Mutation	SNP	T	C	T	ZNF100	c.A22G	p.M8V
XH_P55	19	22499413	22499413	Missense_Mutation	SNP	A	T	A	ZNF729	c.A3194T	p.E1065V
XH_P55	19	22940554	22940554	Silent	SNP	A	G	A	ZNF99	c.T2157C	p.T719T
XH_P55	19	23542290	23542290	Missense_Mutation	SNP	A	G	A	ZNF91	c.T3395C	p.L1132P
XH_P55	19	23542291	23542291	Missense_Mutation	SNP	G	C	G	ZNF91	c.C3394G	p.L1132V
XH_P55	19	23542697	23542697	Silent	SNP	G	C	G	ZNF91	c.C2988G	p.G996G
XH_P55	19	23544418	23544418	Missense_Mutation	SNP	A	T	A	ZNF91	c.T1267A	p.F423I
XH_P55	19	23544625	23544625	Missense_Mutation	SNP	C	T	C	ZNF91	c.G1060A	p.A354T
XH_P55	19	23926916	23926916	Missense_Mutation	SNP	T	C	T	ZNF681	c.A1436G	p.A479R
XH_P55	19	24310638	24310638	In_Frame_Ins	INS	-	TTCTCTTCAGTA	-	ZNF254	AGGGTTTCTCTCT	elinsFTFVGGLFSMNYLM
XH_P55	19	30500119	30500124	In_Frame_Del	DEL	TGATGA	-	TGATGA	URI1	c.840_845del	p.280_282del
XH_P55	19	31038995	31038995	Silent	SNP	T	C	T	ZNF536	c.T2469C	p.D823D
XH_P55	19	31039146	31039146	Missense_Mutation	SNP	A	G	A	ZNF536	c.A2620G	p.T874A
XH_P55	19	33517515	33517515	Missense_Mutation	SNP	C	T	C	RHPN2	c.G209A	p.R70Q
XH_P55	19	33696708	33696708	Silent	SNP	T	C	T	LRP3	c.T1032C	p.T344T
XH_P55	19	33696897	33696897	Silent	SNP	C	T	C	LRP3	c.C1221T	p.G407G
XH_P55	19	35510102	35510102	Silent	SNP	G	C	G	GRAMD1A	c.G1200C	p.T400T
XH_P55	19	37039069	37039069	Missense_Mutation	SNP	A	C	A	ZNF529	c.T337G	p.L113V
XH_P55	19	37975057	37975057	Nonsense_Mutation	INS	-	GGGTTAATTC	-	ZNF570	408InsGGGTTA	36 T137delinsWGX
XH_P55	19	38876352	38876352	Missense_Mutation	SNP	G	A	G	GGN	c.C1550T	p.A517V
XH_P55	19	38994910	38994910	Silent	SNP	G	A	G	RYR1	c.G7977A	p.T2659T
XH_P55	19	39002725	39002725	Silent	SNP	A	G	A	RYR1	c.A9186G	p.P3062P
XH_P55	19	39402455	39402455	Missense_Mutation	SNP	C	G	C	CCER2	c.G99C	p.E33D
XH_P55	19	39955533	39955533	Silent	SNP	G	A	G	SUPT5H	c.G708A	p.E236E
XH_P55	19	39996027	39996027	Silent	SNP	C	T	C	DLL3	c.C1029T	p.P343P
XH_P55	19	40730415	40730415	Missense_Mutation	SNP	C	G	C	CNTD2	c.G493C	p.E165Q
XH_P55	19	41008049	41008049	Silent	SNP	A	G	A	SPTBN4	c.A912G	p.V304V
XH_P55	19	41622189	41622189	Silent	SNP	G	A	A	CYP2F1	c.G96A	p.C32P
XH_P55	19	41939297	41939297	Missense_Mutation	SNP	C	G	C	ATP5SL	c.G395C	p.C132S
XH_P55	19	42085873	42085873	Missense_Mutation	SNP	A	G	A	CEACAM21	c.A592G	p.M198V
XH_P55	19	42260569	42260569	Silent	SNP	G	A	G	CEACAM6	c.G126A	p.P42P
XH_P55	19	43371292	43371292	Silent	SNP	A	T	A	PSG1	c.T975A	p.V325V
XH_P55	19	43371294	43371294	Missense_Mutation	SNP	C	A	C	PSG1	c.G973T	p.V325F
XH_P55	19	43433805	43433805	Silent	SNP	A	G	A	PSG7	c.T132C	p.I44I
XH_P55	19	43585122	43585122	Missense_Mutation	SNP	C	T	C	PSG2	c.G341A	p.R114Q
XH_P55	19	44660967	44660967	Silent	SNP	A	G	A	ZNF234	c.A798G	p.G266G
XH_P55	19	44680489	44680489	Silent	SNP	G	A	G	ZNF226	c.G1074A	p.T358T
XH_P55	19	44981883	44981883	Missense_Mutation	SNP	C	G	C	ZNF180	c.G740C	p.C247S
XH_P55	19	45448465	45448465	Missense_Mutation	SNP	T	G	T	APOC4	c.T287G	p.L96R
XH_P55	19	45490570	45490570	Silent	SNP	A	G	A	CLPTM1	c.A885G	p.P295P
XH_P55	19	46997522	46997522	Missense_Mutation	SNP	C	T	C	PNMA8B	c.G1201A	p.V401I
XH_P55	19	47124714	47124714	Silent	SNP	T	G	T	PTGIR	c.A984C	p.S328S
XH_P55	19	47282162	47282162	Silent	SNP	G	A	G	SLC1A5	c.C222T	p.Y74Y
XH_P55	19	47575306	47575341	In_Frame_Del	DEL	GGGGTCCCA	-	GGGGGTCCCAT	ZC3H4	c.1840_1875del	p.614_625del
XH_P55	19	47585517	47585517	Silent	SNP	G	C	G	ZC3H4	c.C1254G	p.L418L
XH_P55	19	49001686	49001686	Silent	SNP	C	T	C	LMTK3	c.G2727A	p.A909A
XH_P55	19	49573518	49573518	Silent	SNP	G	A	G	KCNAB7	c.C1173T	p.P391P
XH_P55	19	49657711	49657719	In_Frame_Del	DEL	CATCATCAT	-	CATCATCAT	HRC	c.776_784del	p.259_262del
XH_P55	19	49686119	49686119	Silent	SNP	G	A	G	TRPM4	c.G486A	p.A162A
XH_P55	19	50059982	50059982	Silent	SNP	C	G	C	NOSIP	c.G549C	p.V183V
XH_P55	19	50455180	50455180	Missense_Mutation	SNP	C	T	C	SIGLEC11	c.G1510A	p.D504N
XH_P55	19	50464023	50464023	Silent	SNP	C	G	C	SIGLEC11	c.G246C	p.T82T
XH_P55	19	52519385	52519385	Missense_Mutation	SNP	C	T	C	ZNF614	c.G1466A	p.G489E
XH_P55	19	53077411	53077411	Missense_Mutation	SNP	T	C	T	ZNF701	c.T11C	p.L4P
XH_P55	19	53085813	53085813	Silent	SNP	T	C	T	ZNF701	c.T501C	p.A167A
XH_P55	19	53086124	53086124	Missense_Mutation	SNP	C	A	C	ZNF701	c.C812A	p.T271K
XH_P55	19	53086598	53086598	Missense_Mutation	SNP	G	A	G	ZNF701	c.G1286A	p.R429H
XH_P55	19	53303148	53303148	Silent	SNP	G	A	G	ZNF28	c.C1950T	p.L650L
XH_P55	19	54782731	54782731	Silent	SNP	G	A	G	LILRB2	c.C543T	p.Y181Y
XH_P55	19	55175740	55175740	Silent	SNP	C	T	C	LILRB4	c.C546T	p.F182F
XH_P55	19	55378083	55378083	Missense_Mutation	SNP	T	C	T	KIR3DL2	c.T1214C	p.L405P
XH_P55	19	56369593	56369593	Silent	SNP	T	C	T	NLRP4	c.T834C	p.A278A
XH_P55	19	56538976	56538976	Missense_Mutation	SNP	G	C	G	NLRP5	c.G1377C	p.M459I
XH_P55	19	56733425	56733425	Missense_Mutation	SNP	C	A	C	ZSCAN5A	c.G659T	p.G220V
XH_P55	19	57335022	57335022	Silent	SNP	G	A	G	PEG3	c.C420T	p.S140S
XH_P55	19	58018618	58018618	Silent	SNP	A	G	A	ZNF773	c.A1152G	p.K384K
XH_P55	19	58421080	58421080	Missense_Mutation	SNP	G	T	G	ZNF417	c.C563A	p.A188E
XH_P55	20	126311	126312	Frame_Shift_Del	DEL	CC	-	CC	DEFB126	c.314_315del	p.T105fs
XH_P55	20	744570	744570	Silent	SNP	G	A	G	SLC52A3	c.C645T	p.P215P
XH_P55	20	2796007	2796007	Silent	SNP	G	A	G	C20orf141	c.G177A	p.L59L
XH_P55	20	3682149	3682149	Silent	SNP	G	A	G	SIGLEC1	c.C1368T	p.S456S
XH_P55	20	4854682	4854682	Silent	SNP	A	G	A	SLC23A2	c.T1002C	p.D334D
XH_P55	20	10633237	10633237	Silent	SNP	G	A	G	JAG1	c.C765T	p.Y255Y
XH_P55	20	17474968	17474968	Silent	SNP	T	C	T	BFSP1	c.A1374G	p.P458P
XH_P55	20	17475217	17475217	Silent	SNP	C	T	C	BFSP1	c.G1125A	p.A375A
XH_P55	20	17600357	17600357	Missense_Mutation	SNP	G	A	G	RRBP1	c.C2297T	p.S766L
XH_P55	20	20007556	20007556	Nonsense_Mutation	INS	-	CATAAATATAGA	-	NAA20	nsACACATAAAAT	A00_E101delinsYTX
XH_P55	20	20616093	20616093	Frame_Shift_Del	DEL	T	-	T	RALGAP2	c.974delA	p.N325fs

XH_P55	20	23731426	23731426	Silent	SNP	C	T	C	CST1	c.G78A	p.E26E
XH_P55	20	30452782	30452782	Silent	SNP	C	T	C	DUSP15	c.G153A	p.P51P
XH_P55	20	36770588	36770588	Silent	SNP	C	T	C	TGM2	c.G630A	p.L210L
XH_P55	20	39986085	39986085	Missense_Mutation	SNP	A	C	A	LPIN3	c.A2040C	p.Q680H
XH_P55	20	40034097	40034097	Silent	SNP	A	G	A	CHD6	c.T7284C	p.T2428T
XH_P55	20	44520238	44520243	In_Frame_Del	DEL	CTGCTG	-	CTGCTG	CTSA	c.85_90del	p.29_30del
XH_P55	20	44587977	44587977	Missense_Mutation	SNP	C	T	C	ZNF335	c.G2116A	p.E706K
XH_P55	20	44644965	44644965	Silent	SNP	G	A	G	MMP9	c.G2082A	p.V694V
XH_P55	20	45014849	45014849	Nonsense_Mutation	INS	-	TTTGCTTAT	-	ELMO2	p.591insATAAG	p.L197delinsLX
XH_P55	20	45216743	45216743	Missense_Mutation	SNP	C	T	C	SLC13A3	c.G926A	p.R309Q
XH_P55	20	45242269	45242269	Silent	SNP	G	C	G	SLC13A3	c.C207G	p.L69L
XH_P55	20	52786219	52786219	Silent	SNP	G	A	G	CYP24A1	c.C552T	p.A184A
XH_P55	20	52788129	52788129	In_Frame_Ins	INS	-	AGC	-	CYP24A1	c.529_530insGC	p.N177delinsSY
XH_P55	20	52788131	52788131	In_Frame_Ins	INS	-	TGAAGCTCCAC	-	CYP24A1	TATTGGTGGAG	76delinsDIGGASSH
XH_P55	20	57244493	57244493	Silent	SNP	G	A	G	STX16	c.G528A	p.Q176Q
XH_P55	20	57268867	57268867	Silent	SNP	C	A	C	NPEPL1	c.C225A	p.T75T
XH_P55	20	61040453	61040453	Silent	SNP	C	G	C	GATA5	c.G981C	p.S327S
XH_P55	20	61040951	61040951	Silent	SNP	C	T	C	GATA5	c.G852A	p.K284K
XH_P55	20	61870727	61870727	Missense_Mutation	SNP	G	C	G	BIRC7	c.G667C	p.E223Q
XH_P55	20	61879009	61879009	Missense_Mutation	SNP	G	T	G	NKAIN4	c.C392A	p.A131D
XH_P55	20	61981315	61981315	Missense_Mutation	SNP	C	T	C	CHRNA4	c.G1448A	p.R483Q
XH_P55	20	62221766	62221766	Silent	SNP	C	T	C	GMEB2	c.G1269A	p.P423P
XH_P55	20	62366650	62366650	Missense_Mutation	SNP	G	T	G	ZGPAT	c.G1131T	p.R377S
XH_P55	21	16337535	16337535	Silent	SNP	A	G	A	NRIP1	c.T2979C	p.S993S
XH_P55	21	19629397	19629397	Missense_Mutation	SNP	A	T	A	CHODL	c.A443T	p.D148V
XH_P55	21	33371123	33371123	Missense_Mutation	SNP	C	T	C	HUNK	c.C1771T	p.R591C
XH_P55	21	34634878	34634878	Missense_Mutation	SNP	G	A	G	IFNAR2	c.G853A	p.A285T
XH_P55	21	34926260	34926260	Missense_Mutation	SNP	C	T	C	SON	c.C4723T	p.R1575C
XH_P55	21	37692589	37692589	Silent	SNP	A	T	A	MORC3	c.A27T	p.I9I
XH_P55	21	43504228	43504228	Silent	SNP	T	C	T	UMODL1	c.T354C	p.P118P
XH_P55	21	43505436	43505436	Missense_Mutation	SNP	G	A	G	UMODL1	c.G517A	p.V173I
XH_P55	21	45993819	45993819	Missense_Mutation	SNP	C	T	C	KRTAP10-4	c.C184T	p.R62C
XH_P55	21	46011324	46011324	Missense_Mutation	SNP	T	C	T	KRTAP10-6	c.A1042G	p.M348V
XH_P55	21	46086377	46086377	Missense_Mutation	SNP	A	G	A	KRTAP12-2	c.T427C	p.S143P
XH_P55	21	46271460	46271460	Missense_Mutation	SNP	T	C	T	PTTG1IP	c.A251G	p.E84G
XH_P55	21	46876173	46876173	Silent	SNP	C	T	C	COL18A1	c.C729T	p.P243P
XH_P55	21	46876306	46876306	Missense_Mutation	SNP	G	A	G	COL18A1	c.G862A	p.A288T
XH_P55	22	16277757	16277757	Missense_Mutation	SNP	C	T	C	POTEH	c.G1157A	p.R386H
XH_P55	22	20819327	20819327	Silent	SNP	C	T	C	KLHL22	c.G930A	p.P310P
XH_P55	22	21213416	21213416	Silent	SNP	A	G	A	SNAP29	c.A18G	p.K6K
XH_P55	22	24325062	24325062	Missense_Mutation	SNP	G	A	G	GSTT2	c.G352A	p.V118M
XH_P55	22	26688507	26688507	Missense_Mutation	SNP	C	T	C	SEZ6L	c.C230T	p.A77V
XH_P55	22	32756407	32756407	Missense_Mutation	SNP	A	G	A	RFPL3	c.A542G	p.Y181C
XH_P55	22	32795641	32795641	Silent	SNP	C	T	C	RTCB	c.G603A	p.Q201Q
XH_P55	22	37499386	37499386	Silent	SNP	C	T	C	TMPPRS6	c.G72A	p.P24P
XH_P55	22	37770066	37770066	Silent	SNP	G	T	G	ELFN2	c.C1509A	p.I503I
XH_P55	22	37900771	37900771	Silent	SNP	A	G	A	CARD10	c.T1389C	p.C463C
XH_P55	22	41645757	41645757	Silent	SNP	C	G	G	RANGAP1	c.G1548C	p.Y1516L
XH_P55	22	42523965	42523965	Silent	SNP	G	A	G	CYP2D6	c.C711T	p.S237S
XH_P55	22	42575703	42575703	Frame_Shift_Ins	INS	-	C	-	TCF20	c.5660dupG	p.C1887fs
XH_P55	22	42575705	42575705	Frame_Shift_Ins	INS	-	CTATTCTGTTTTC	-	TCF20	659insGAAAC	p.C1887fs
XH_P55	22	43614316	43614316	Silent	SNP	C	G	C	SCUBE1	c.G1836C	p.A612A
XH_P55	22	45798386	45798386	Silent	SNP	T	C	T	SMC1B	c.A681G	p.Q227Q
XH_P55	22	50754648	50754648	Silent	SNP	T	C	T	DENN6B	c.A594G	p.A198A
XH_P55	22	50898026	50898026	Silent	SNP	G	A	G	SBF1	c.C3561T	p.Y1187Y
XH_P55	22	51064039	51064039	Missense_Mutation	SNP	G	C	G	ARSA	c.C1178G	p.T393S
XH_P55	22	51142601	51142601	Missense_Mutation	SNP	G	T	G	SHANK3	c.G1654T	p.V552F
XH_P55	X	3228144	3228144	Missense_Mutation	SNP	C	G	C	MXRA5	c.G8100C	p.E2700D
XH_P55	X	9905342	9905342	Silent	SNP	A	G	A	SHROOM2	c.A261G	p.T87T
XH_P55	X	9912792	9912792	Missense_Mutation	SNP	A	G	A	SHROOM2	c.A928G	p.I310F
XH_P55	X	9914947	9914947	Missense_Mutation	SNP	G	C	G	SHROOM2	c.G1326C	p.L442V
XH_P55	X	17745550	17745550	Frame_Shift_Ins	INS	-	AGTAAAGA	-	NHS	p.2731insAGTA	p.L910fs
XH_P55	X	17745551	17745551	Nonsense_Mutation	INS	-	TTGAACCTCCAA	-	NHS	p.732insCTTGAAAC	p.H911delinsPX
XH_P55	X	19764473	19764473	Silent	SNP	C	T	C	SH3KBP1	c.G138A	p.L46L
XH_P55	X	23398214	23398214	Silent	SNP	T	C	T	PTCHD1	c.T858C	p.C286C
XH_P55	X	24073761	24073761	Silent	SNP	C	T	C	EIF2S3	c.C99T	p.H33H
XH_P55	X	30269334	30269334	Missense_Mutation	SNP	C	T	C	MAGEB1	c.C724T	p.R242C
XH_P55	X	36324961	36324961	In_Frame_Ins	INS	-	ATCTCCTCA	-	CFAP47	p.8158insATCTC	p.H2719delinsHSS
XH_P55	X	39932907	39932907	Silent	SNP	T	C	T	BCOR	c.A1692G	p.A564A
XH_P55	X	43603391	43603391	Silent	SNP	T	C	T	MAOA	c.T1410C	p.D470D
XH_P55	X	44938563	44938563	Silent	SNP	G	A	G	KDM6A	c.G2874A	p.Q958Q
XH_P55	X	55103917	55103917	Silent	SNP	G	T	G	PAGE2B	c.G279T	p.G93G
XH_P55	X	63410647	63410647	Silent	SNP	G	A	G	AMER1	c.C2520T	p.A840A
XH_P55	X	69478942	69478942	Missense_Mutation	SNP	T	G	T	P2RY4	c.A533C	p.N178T
XH_P55	X	79960302	79960302	Nonsense_Mutation	INS	-	TATTTTGTTTTT	-	BRWD3	nsTAACAAAAAC	p.866_N867delinsX
XH_P55	X	102755250	102755250	Silent	SNP	G	A	G	RAB40A	c.C435T	p.A145A
XH_P55	X	105153214	105153214	Silent	SNP	C	T	C	NRK	c.C1581T	p.P527P
XH_P55	X	122387309	122387309	Missense_Mutation	SNP	C	T	C	GRIA3	c.C424T	p.R142C
XH_P55	X	129201179	129201179	Silent	SNP	C	T	C	ELF4	c.G1509A	p.T503T
XH_P55	X	129265736	129265736	Missense_Mutation	SNP	C	A	C	AIFM1	c.G470T	p.G157V
XH_P55	X	135312740	135312740	Frame_Shift_Ins	INS	-	ACTAAGAAAGTTT	-	MAP7D3	449insTAAACTT	p.Q483fs
XH_P55	X	135313108	135313108	In_Frame_Ins	INS	-	AAAAAGGGA	-	MAP7D3	5_1326insTCCC	p.K442delinsNPFL
XH_P55	X	153216366	153216366	Silent	SNP	G	A	G	HCFC1	c.C5601T	p.A1867A
XH_P55	X	153284192	153284192	Missense_Mutation	SNP	A	G	A	IRAK1	c.T587C	p.F196S
XH_P55	X	153296444	153296444	Missense_Mutation	SNP	C	T	C	MECP2	c.G871A	p.A291T
XH_P55	X	153609257	153609257	Silent	SNP	C	T	C	EMD	c.C465T	p.Y155Y
XH_P55	Y	21154426	21154426	Missense_Mutation	SNP	G	A	G	CD24	c.C170T	p.A57V
XH_P55	1	1870393	1870393	Missense_Mutation	SNV	G	A	A	CFAP74	c.2912C>T	p.T971M
XH_P55	1	201058551	201058551	Nonsense_Mutation	SNV	G	T	T	CACNA1S	c.735C>A	p.C245*
XH_P55	1	228612869	228612869	Missense_Mutation	SNV	C	T	T	HIST3H3	c.158G>A	P.R53H
XH_P55	1	28733968	28733968	Frame_Shift_Del	INDEL	C	-	-	PHACTR4	c.11delC	P.P4fs
XH_P55	10	12162869	12162869	Silent	SNV	C	T	T	DHTKD1	c.2742C>T	P.L914L
XH_P55	10	51769943	51769943	Silent	SNV	G	T	T	AGAP6	c.2058G>T	P.V686V
XH_P55	11	4471083	4471083	Nonsense_Mutation	SNV	C	T	T	OR52K2	c.514C>T	P.R172*
XH_P55	11	71821634	71821634	Nonsense_Mutation	SNV	C	A	A	ANAPC15	c.136G>T	P.E46*
XH_P55	12	112589824	112589824	Missense_Mutation	SNV	A	G	G	TRAFD1	c.1499A>G	P.D500G
XH_P55	12	130839188	130839188	Missense_Mutation	SNV	C	T	T	PIWIL1	c.1151C>T	P.P384L
XH_P55	12	475202	475202	Silent	SNV	G	C	C	KDM5A	c.435C>G	P.R145R

XH_P55	12	57595332	57595332	Silent	SNV	C	T	T	LRP1	c.10398C>T	P.C3466C
XH_P55	12	7528452	7528452	Missense_Mutation	SNV	G	T	T	CD163L1	c.2560C>A	P.L854I
XH_P55	14	39777656	39777656	Missense_Mutation	SNV	A	T	T	CTAGE5	c.971A>T	P.H324L
XH_P55	16	57992333	57992333	Missense_Mutation	SNV	T	C	C	CNGB1	c.818A>G	P.H273R
XH_P55	16	67913573	67913573	Missense_Mutation	SNV	G	A	A	EDC4	c.1717G>A	P.V573M
XH_P55	17	39619194	39619194	Missense_Mutation	SNV	G	A	A	KRT32	c.1105C>T	P.R369W
XH_P55	17	62499427	62499430	Frame_Shift_Del	INDEL	TCAA	-	-	DDX5	686_689delTTG	P.I229fs
XH_P55	17	80400168	80400168	Silent	SNV	C	T	T	HEXDC	c.1458C>T	P.S486S
XH_P55	18	48591919	48591919	Missense_Mutation	SNV	G	A	A	SMAD4	c.1082G>A	P.R361H
XH_P55	19	18368369	18368369	Missense_Mutation	SNV	G	A	A	KIAA1683	c.3725C>T	P.P1242L
XH_P55	19	2877696	2877696	Missense_Mutation	SNV	G	A	A	ZNF556	c.737G>A	P.R246H
XH_P55	19	40730415	40730415	Missense_Mutation	SNV	C	G	G	CNTD2	c.493G>C	P.E165Q
XH_P55	2	179451960	179451960	Silent	SNV	A	G	G	TTN	c.59055T>C	P.H19685H
XH_P55	2	87016533	87016533	Missense_Mutation	SNV	C	T	T	CD8A	c.538G>A	P.A180T
XH_P55	21	16337535	16337535	Silent	SNV	A	G	G	NRIP1	c.2979T>C	P.S993S
XH_P55	21	19629397	19629397	Missense_Mutation	SNV	A	T	T	CHODL	c.443A>T	P.D148V
XH_P55	3	13679391	13679391	Missense_Mutation	SNV	A	G	G	FBLN2	c.3668A>G	P.H1223R
XH_P55	3	48691870	48691870	Silent	SNV	C	T	T	CELSR3	c.5004G>A	P.T1668T
XH_P55	4	114275657	114275657	Silent	SNV	G	T	T	ANK2	c.5883G>T	P.L1961L
XH_P55	5	149581902	149581902	Splice_Site	SNV	C	T	T	SLC6A7	c.859-8C>T	
XH_P55	6	157405844	157405844	Silent	SNV	T	C	C	ARID1B	c.2086T>C	P.L696L
XH_P55	7	124404432	124404432	Missense_Mutation	SNV	G	A	A	GNAS1	c.599C>T	P.T200M
XH_P55	7	141536209	141536209	Missense_Mutation	SNV	C	T	T	PRSS37	c.694G>A	P.A232T
XH_P55	7	5428786	5428786	Silent	SNV	C	T	T	TNRC18	c.669G>A	P.K223K
XH_P55	7	54617718	54617718	Silent	SNV	G	A	A	VSTM2A	c.489G>A	P.S163S
XH_P55	7	90742001	90742001	Splice_Site	SNV	G	A	A	CDK14	c.1294+5G>A	
XH_P55	8	145001643	145001643	Nonsense_Mutation	SNV	C	A	A	PLEC	c.3772G>T	P.E1258*
XH_P55	8	28980108	28980108	Missense_Mutation	SNV	C	T	T	KIF13B	c.3535G>A	P.A1179T
XH_P55	8	55541042	55541042	Missense_Mutation	SNV	A	G	G	RP1	c.4600A>G	P.T1534A
XH_P55	8	69434105	69434105	Missense_Mutation	SNV	T	G	G	C8orf34	c.837T>G	P.N279K
XH_P55	9	113168932	113168932	Missense_Mutation	SNV	C	T	T	SVEP1	c.8948G>A	P.G2983E
XH_P55	9	21971186	21971186	Missense_Mutation	SNV	G	A	A	CDKN2A	c.215C>T	P.P72L
XH_P55	X	105153214	105153214	Silent	SNV	C	T	T	NRK	c.1581C>T	P.P257P
XH_P557	1	987011	987011	Missense_Mutation	SNP	C	T	C	AGRN	c.C5549T	p.P1850L
XH_P557	1	1168365	1168365	Missense_Mutation	SNP	G	A	A	B3GALT6	c.G707A	p.R236H
XH_P557	1	1246318	1246318	Silent	SNP	C	T	C	PUSL1	c.C798T	p.A266A
XH_P557	1	5927147	5927147	Silent	SNP	G	A	G	NPHP4	c.C1965T	p.D655D
XH_P557	1	6046344	6046344	Silent	SNP	G	A	G	NPHP4	c.C6T	p.N2N
XH_P557	1	8419975	8419975	Missense_Mutation	SNP	C	T	C	RERE	c.G1805A	p.G602E
XH_P557	1	9305594	9305594	Frame_Shift_Ins	INS	-	G	-	H6PD	c.635dupG	p.R212fs
XH_P557	1	16260969	16260969	Missense_Mutation	SNP	-	T	C	SPEN	c.C8234T	p.A2745V
XH_P557	1	17355187	17355187	In_Frame_Ins	INS	-	CGTAACACACAT	-	SDHB	331insATGTGTG	111delinsMCVTL
XH_P557	1	17355189	17355189	In_Frame_Ins	INS	-	CAC	-	SDHB	328_329insGTG	111delinsMCVTL
XH_P557	1	24194627	24194627	Silent	SNP	C	T	C	FUCA1	c.G150A	p.P50P
XH_P557	1	26497120	26497120	Silent	SNP	G	A	G	ZNF593	c.G318A	p.A106A
XH_P557	1	29064804	29064804	Frame_Shift_Ins	INS	-	TA	-	YTHDF2	c.86_87insTA	p.L29fs
XH_P557	1	32264080	32264080	Missense_Mutation	SNP	C	T	C	SPOCD1	c.G470A	p.R157H
XH_P557	1	33480164	33480172	In_Frame_Del	DEL	GGTAGGAAC	-	GGTAGGAAC	AK2	c.323_331del	p.108_111del
XH_P557	1	33841037	33841057	In_Frame_Del	DEL	CTGCTGTGTG	-	GCTGCTGTGTGT	PHC2	c.84_104del	p.28_35del
XH_P557	1	35259961	35259961	Silent	SNP	A	G	A	GJA4	c.A147G	p.Q49Q
XH_P557	1	35575939	35575939	Silent	SNP	G	A	A	ZMYM1	c.G627A	p.K209K
XH_P557	1	36769561	36769561	Silent	SNP	C	T	C	THRAP3	c.C2808T	p.D936D
XH_P557	1	44149406	44149406	Nonsense_Mutation	INS	-	ACCACGTACCAA	-	KDM4A	insAATACCACG	R597delinsQYHVPNX
XH_P557	1	54426079	54426079	Missense_Mutation	SNP	G	A	G	LRRC42	c.G656A	p.L29fs
XH_P557	1	55624648	55624648	Missense_Mutation	SNP	G	A	G	USP24	c.C1130T	p.P377L
XH_P557	1	57159485	57159485	Missense_Mutation	SNP	G	A	G	PRKAA2	c.G523A	p.G175R
XH_P557	1	58999992	58999992	In_Frame_Ins	INS	-	TTATTG	-	OMA1	40_741insCAAT	E247delinsDNK
XH_P557	1	58999994	58999994	Nonsense_Mutation	INS	-	TTTTTATGATGT	-	OMA1	TTAGAACATCAT	F248delinsLEHHKKX
XH_P557	1	61818213	61818213	Frame_Shift_Ins	INS	-	TCTT	-	NFIA	.792_793insTCT	p.R264fs
XH_P557	1	67154853	67154853	Silent	SNP	A	T	A	SGIP1	c.A741T	p.P247P
XH_P557	1	67154855	67154857	In_Frame_Del	DEL	CCA	-	CCA	SGIP1	c.743_745del	p.248_249del
XH_P557	1	67787555	67787555	Frame_Shift_Ins	INS	-	AG	-	IL12RB2	c.347_348insAG	p.A116fs
XH_P557	1	86171840	86171840	Nonsense_Mutation	INS	-	TTTTTTAACTTA	-	ZNHIT6	TTGGTAAGTTAA	delinsPLNIFGKLKKKESNX
XH_P557	1	89528775	89528775	Missense_Mutation	SNP	C	T	C	GBP1	c.G143A	p.R48H
XH_P557	1	92446591	92446591	Frame_Shift_Ins	INS	-	CTGGATTTC	-	BRDT	CATTTTCTTGG	p.1490fs
XH_P557	1	92446593	92446593	Silent	SNP	A	T	A	BRDT	c.A1470T	p.1490I
XH_P557	1	110882083	110882083	Missense_Mutation	SNP	C	T	C	RBM15	c.C56T	p.A19V
XH_P557	1	113062980	113062980	Missense_Mutation	SNP	G	A	G	WNT2B	c.G749A	p.R250Q
XH_P557	1	114483095	114483095	Frame_Shift_Ins	INS	-	TCACAGCTGCAA	-	HIPK1	insATCACAGCT	p.G30fs
XH_P557	1	115165717	115165717	In_Frame_Ins	INS	-	TGTTTTGT	-	DENND2C	CCAAAAACAA	delinsLYVIPKNTKIKKTT
XH_P557	1	117576559	117576559	Missense_Mutation	SNP	C	T	C	CD101	c.C2902T	p.L968F
XH_P557	1	120438486	120438486	Silent	SNP	G	A	G	ADAM30	c.C474T	p.V158V
XH_P557	1	146658682	146658682	Missense_Mutation	SNP	G	A	G	FMO5	c.C1399T	p.P467S
XH_P557	1	149858178	149858178	Missense_Mutation	SNP	C	T	C	HIST2H2BE	c.G13A	p.A5T
XH_P557	1	152327578	152327578	Missense_Mutation	SNP	C	G	C	FLG2	c.G2684C	p.S895T
XH_P557	1	152327579	152327579	Missense_Mutation	SNP	T	A	T	FLG2	c.A2683T	p.S895C
XH_P557	1	156170116	156170116	Frame_Shift_Ins	INS	-	TAGT	-	SLC25A44	478_479insTAG	p.V160fs
XH_P557	1	156437892	156437892	Missense_Mutation	SNP	G	A	G	MEF2D	c.C1426T	p.R476W
XH_P557	1	157095470	157095470	Silent	SNP	A	G	A	ETV3	c.T702C	p.F234F
XH_P557	1	182823275	182823279	Frame_Shift_Del	DEL	AGAAT	-	AGAAT	DHX9	c.588_592del	p.G196fs
XH_P557	1	185270183	185270183	Silent	SNP	G	A	G	IVNS1ABP	c.C1041T	p.I347I
XH_P557	1	185962381	185962381	Missense_Mutation	SNP	C	G	C	HMCN1	c.C3445G	p.L1149V
XH_P557	1	196965192	196965192	Silent	SNP	C	T	C	CFHR5	c.C831T	p.Y277Y
XH_P557	1	201195119	201195119	Missense_Mutation	SNP	C	T	C	IGFN1	c.C10654T	p.H3552Y
XH_P557	1	203276245	203276254	Frame_Shift_Del	DEL	CCACTGGTTT	-	CCACTGGTTT	BTG2	c.156_165del	p.H52fs
XH_P557	1	207133079	207133079	Frame_Shift_Ins	INS	-	AG	-	FCAMR	c.715_716insCT	p.C239fs
XH_P557	1	225586370	225586370	Splice_Site	INS	-	A	-	DNAH14	-	
XH_P557	1	228494696	228494696	Silent	SNP	G	A	G	OBSCN	c.G12021A	p.A4007A
XH_P557	1	235918909	235918909	Frame_Shift_Ins	INS	-	CTTTCTTTTCTT	-	LYST	AAGAAAGAAA	p.Q2366fs
XH_P557	1	235918911	235918911	Missense_Mutation	SNP	G	T	G	LYST	c.C7096A	p.Q2366K
XH_P557	2	3392075	3392075	Silent	SNP	T	C	T	TRAPPC12	c.T681C	p.F227F
XH_P557	2	3392295	3392295	Missense_Mutation	SNP	A	G	A	TRAPPC12	c.A901G	p.S301G
XH_P557	2	3483205	3483205	Silent	SNP	C	T	C	TRAPPC12	c.C2181T	p.F272F
XH_P557	2	39893487	39893487	Frame_Shift_Ins	INS	-	G	-	TMEM178A	c.374dupG	p.R125fs
XH_P557	2	47256405	47256405	Missense_Mutation	SNP	C	T	C	TTC7A	c.C622T	p.R208C
XH_P557	2	54880887	54880887	Frame_Shift_Ins	INS	-	T	-	SPTBN1	c.5681dupT	p.L1894fs
XH_P557	2	85820137	85820137	Missense_Mutation	SNP	C	T	C	VAMP5	c.C208T	p.R70W
XH_P557	2	96963445	96963445	Missense_Mutation	SNP	C	T	C	SNRNP200	c.G1133A	p.R378Q

XH_P557	2	97595044	97595044	Silent	SNP	G	A	G	FAM178B	c.C1092T	p.H364H
XH_P557	2	105889313	105889313	Silent	SNP	G	A	G	TGFBRAP1	c.C1971T	p.L657L
XH_P557	2	109002745	109002745	Missense_Mutation	SNP	T	C	T	SULT1C4	c.T488C	p.V163A
XH_P557	2	112615976	112615976	In_Frame_Ins	INS	-	TTTCCTTTTTTTT	-	ANAPC1	s.CCAAAAAAAA	22delinsAKKKRKEK
XH_P557	2	113940839	113940839	Missense_Mutation	SNP	G	C	G	PSD4	c.G806C	p.G269A
XH_P557	2	128477554	128477554	Missense_Mutation	SNP	C	G	C	WDR33	c.G2045C	p.G682A
XH_P557	2	138208562	138208562	Missense_Mutation	SNP	G	A	G	THSD7B	c.G3107A	p.R1036Q
XH_P557	2	141243024	141243024	Missense_Mutation	SNP	C	T	C	LRP1B	c.G9313A	p.D3105N
XH_P557	2	155295120	155295120	Missense_Mutation	SNP	C	T	C	GALNT13	c.C1412T	p.A471V
XH_P557	2	167133659	167133659	Missense_Mutation	SNP	C	T	C	SCN9A	c.G2675A	p.C892Y
XH_P557	2	170113677	170113677	Missense_Mutation	SNP	T	A	T	LRP2	c.A2596T	p.N866Y
XH_P557	2	175264809	175264809	Frame_Shift_Ins	INS	-	AAACCAAGAAAA	-	SCRN3	99insAAAAACCA	p.L100fs
XH_P557	2	178416701	178416701	Missense_Mutation	SNP	A	G	A	TTC30B	c.T791C	p.L264P
XH_P557	2	179417338	179417338	Frame_Shift_Del	DEL	A	-	A	TTN	c.63094delT	p.S21032fs
XH_P557	2	179417340	179417340	Frame_Shift_Del	DEL	T	-	T	TTN	c.63092delA	p.Q21031fs
XH_P557	2	179489988	179489988	Splice_Site	DEL	CTTGTAATT	-	CTTGTAATTA	TTN	-	-
XH_P557	2	197171230	197171230	Silent	SNP	G	A	G	HECW2	c.C1728T	p.T576T
XH_P557	2	202342470	202342470	Missense_Mutation	SNP	G	A	G	STRADB	c.G677A	p.S226N
XH_P557	2	208425061	208425068	Frame_Shift_Del	DEL	TCAGTTAT	-	TCAGTTAT	CREB1	c.226_233del	p.S76fs
XH_P557	2	220085174	220085174	Frame_Shift_Del	DEL	C	-	C	ATG9A	c.2515delG	p.A7839fs
XH_P557	2	233198609	233198609	Silent	SNP	G	A	G	DIS3L2	c.G2070A	p.A690A
XH_P557	2	234171780	234171780	Missense_Mutation	SNP	G	A	G	ATG16L1	c.G214A	p.G72R
XH_P557	2	234638390	234638390	In_Frame_Ins	INS	-	ATCTGTTGCTCT	-	UGT1A3	AATGAATCTGTT	insTVNMTNMLLSCPMMM
XH_P557	2	241873239	241873239	Missense_Mutation	SNP	G	A	G	CROCC2	c.G1616A	p.R539K
XH_P557	3	9793529	9793529	Missense_Mutation	SNP	G	A	G	OGG1	c.G461A	p.R154H
XH_P557	3	10188287	10188287	Missense_Mutation	SNP	G	A	G	VHL	c.G430A	p.G144R
XH_P557	3	14967578	14967578	Frame_Shift_Ins	INS	-	AA	-	FGD5	.4070_4071insA	p.V1357fs
XH_P557	3	53856575	53856575	In_Frame_Ins	INS	-	AGC	-	CHDH	.797_798insGC	p.L266delinsLL
XH_P557	3	74420362	74420362	Missense_Mutation	SNP	C	T	C	CNTN3	c.G643A	p.V215M
XH_P557	3	113375895	113375895	Frame_Shift_Ins	INS	-	GA	-	USF3	.4633_4634insT	p.T1545fs
XH_P557	3	124211719	124211719	Missense_Mutation	SNP	A	T	A	KALRN	c.A4666T	p.N1556Y
XH_P557	3	124462907	124462907	Silent	SNP	G	A	G	UMPS	c.G1419A	p.A473A
XH_P557	3	133099245	133099245	Silent	SNP	G	A	G	TMEM108	c.G690A	p.P230P
XH_P557	3	136323224	136323246	Frame_Shift_Del	DEL	TAGCTCTCC	-	ATTAGCTCTCCA	STAG1	c.202_224del	p.G68fs
XH_P557	3	164716449	164716449	In_Frame_Ins	INS	-	CCA	-	SI	.4418_4419insTG	K1473delinsNG
XH_P557	3	164716450	164716450	Frame_Shift_Ins	INS	-	AGTTGTCTCCAA	-	SI	.ACTGGCTTGGAG	p.K1473fs
XH_P557	3	182615187	182615206	Frame_Shift_Del	DEL	TGTTGAGTG	-	TCTGGTGAGTGA	ATP11B	c.3145_3152de	p.I1049fs
XH_P557	3	182817182	182817182	Missense_Mutation	SNP	C	T	C	MCCC1	c.G47A	p.R16K
XH_P557	3	184429133	184429133	In_Frame_Ins	INS	-	TTC	-	MAGEF1	.476_477insGA	p.D159delinsEN
XH_P557	3	195513413	195513413	In_Frame_Ins	INS	-	TACTGAGGAATT	-	MUC4	ACCGACAATTC	insSLPVTDNSSVSTGHATP
XH_P557	4	1388759	1388759	Frame_Shift_Ins	INS	-	GCCTGCTCACAC	-	CRIPAK	TGCCGCGCTGCT	p.R154fs
XH_P557	4	3446587	3446587	Missense_Mutation	SNP	C	T	C	HGFAC	c.C883T	p.R295C
XH_P557	4	4304162	4304162	Missense_Mutation	SNP	G	C	G	ZBTB49	c.G599C	p.G200A
XH_P557	4	4304163	4304163	Frame_Shift_Ins	INS	-	TGTTATCAGTGA	-	ZBTB49	ACTTGTGTTATC	p.G200fs
XH_P557	4	13605351	13605351	Frame_Shift_Del	DEL	T	-	T	BOD1L1	c.3173delA	p.N1058fs
XH_P557	4	15518320	15518320	Missense_Mutation	SNP	C	T	C	CC2D2A	c.C1090T	p.P364S
XH_P557	4	41748011	41748028	In_Frame_Del	DEL	CGCCGCTG	-	GCCGCCGCTGCC	PHOX2B	c.741_758del	p.247_253del
XH_P557	4	74853777	74853777	Missense_Mutation	SNP	C	T	T	PPBP	c.G44A	p.R15K
XH_P557	4	76785609	76785609	Missense_Mutation	SNP	T	C	T	PPEF2	c.A1992G	p.I664M
XH_P557	4	83956382	83956382	Missense_Mutation	SNP	C	T	C	COP5A	c.C5T	p.A2V
XH_P557	4	104116366	104116366	Missense_Mutation	SNP	G	A	G	CENPE	c.C382T	p.R128C
XH_P557	4	114251526	114251526	Missense_Mutation	SNP	G	A	G	ANK2	c.G3025A	p.V1009I
XH_P557	4	140306107	140306107	Frame_Shift_Del	DEL	GAATTCT	-	GAATTCT	NAA15	c.2271_2277de	p.R757fs
XH_P557	4	146461191	146461191	In_Frame_Ins	INS	-	GTACCCAAACT	-	SMAD1	TAGCAGTTACCC	12delinsPIAVTQTLL
XH_P557	4	151788916	151788916	Silent	SNP	G	A	G	LRBA	c.C2673T	p.Y891Y
XH_P557	4	166141086	166141086	Silent	SNP	A	G	A	KLHL2	c.A39G	p.V13V
XH_P557	4	175414439	175414439	Frame_Shift_Ins	INS	-	C	-	HPGD	c.320dupG	p.G107fs
XH_P557	4	183673030	183673030	Missense_Mutation	SNP	G	A	G	TENM3	c.G3707A	p.R1236H
XH_P557	4	186318369	186318369	Frame_Shift_Ins	INS	-	CAGT	-	ANKRD37	c.93_94insCAGT	p.K31fs
XH_P557	5	9190451	9190451	Missense_Mutation	SNP	G	A	G	SEMA5A	c.C1201T	p.R401C
XH_P557	5	35065217	35065217	Missense_Mutation	SNP	C	T	C	PRLR	c.G1540A	p.A514T
XH_P557	5	35857128	35857128	Missense_Mutation	SNP	G	C	G	IL7R	c.G49C	p.V17L
XH_P557	5	41842799	41842799	Nonsense_Mutation	SNP	G	A	G	OXC1T	c.C649T	p.R217X
XH_P557	5	66055644	66055644	Missense_Mutation	SNP	G	T	G	MAST4	c.G471T	p.E157D
XH_P557	5	66055645	66055645	Nonsense_Mutation	INS	-	CTCTTCTGCAG	-	MAST4	TCTTCTCTTTCT	58delinsAALPLSAAAX
XH_P557	5	79950708	79950708	Silent	SNP	T	C	T	MSH3	c.T162C	p.A54A
XH_P557	5	112824048	112824048	Missense_Mutation	SNP	T	C	T	MCC	c.A64G	p.S22G
XH_P557	5	123984763	123984763	Silent	SNP	C	T	C	ZNF608	c.G1314A	p.A438A
XH_P557	5	132269985	132269985	Missense_Mutation	SNP	G	A	G	AF4	c.C772T	p.R258W
XH_P557	5	139060486	139060486	Silent	SNP	G	A	G	CXCS	c.G378A	p.A126A
XH_P557	5	140698646	140698646	Silent	SNP	C	T	C	TA7F	c.G966A	p.I322L
XH_P557	5	146703516	146703518	In_Frame_Del	DEL	GGA	-	GGA	STK32A	c.316_318del	p.106_106del
XH_P557	5	147510850	147510850	Frame_Shift_Ins	INS	-	ATTG	-	SPINK5	.993_2994insAT	p.V998fs
XH_P557	5	150632794	150632794	Frame_Shift_Ins	INS	-	G	-	GM2A	c.18dupG	p.Q6fs
XH_P557	5	180219932	180219932	Missense_Mutation	SNP	C	T	C	MGAT1	c.G40A	p.A14T
XH_P557	6	18122358	18122358	Silent	SNP	G	A	G	NHLRC1	c.C480T	p.C160C
XH_P557	6	27101240	27101240	Nonsense_Mutation	INS	-	TAAC	-	HIST1H2AG	.390_391insTAA	130_X131delinsKX
XH_P557	6	31322996	31322996	Silent	SNP	C	T	C	HLA-B	c.G900A	p.P300P
XH_P557	6	39876841	39876841	Missense_Mutation	SNP	C	T	C	MOC51	c.G1140A	p.M380I
XH_P557	6	79650872	79650872	Nonsense_Mutation	INS	-	AGTGTCAAAGTG	-	PHIP	.6004insACACTT	1668_A1669delinsX
XH_P557	6	86215709	86215711	In_Frame_Del	DEL	AAC	-	AAC	SNX14	c.2656_2658de	p.886_886del
XH_P557	6	168443315	168443315	Missense_Mutation	SNP	G	A	G	KIF25	c.G904A	p.V302I
XH_P557	7	21675698	21675698	Silent	SNP	G	A	G	DNAH11	c.G4710A	p.V1570V
XH_P557	7	39504010	39504010	Missense_Mutation	SNP	G	A	G	POU6F2	c.G1693A	p.G565R
XH_P557	7	43918682	43918682	Missense_Mutation	SNP	G	A	G	URGCP	c.C353T	p.A118V
XH_P557	7	48146482	48146482	Missense_Mutation	SNP	G	A	G	UPP1	c.G38A	p.G13D
XH_P557	7	64863860	64863860	Frame_Shift_Ins	INS	-	AC	-	ZNF92	c.605_606insAC	p.I202fs
XH_P557	7	64863862	64863862	Nonsense_Mutation	INS	-	GAATTTTCTTATC	-	ZNF92	AGTATGAATTTT	203_T204delinsLX
XH_P557	7	66489954	66489954	In_Frame_Ins	INS	-	TTTTTTTTTTTTT	-	TYW1	.30insTTTTTTTTT	5310delinsSFFFFF
XH_P557	7	66489956	66489956	Missense_Mutation	SNP	A	T	A	TYW1	c.A931T	p.I311f
XH_P557	7	87168622	87168622	Missense_Mutation	SNP	G	A	G	A8CB1	c.C2359T	p.R787W
XH_P557	7	100676621	100676621	Missense_Mutation	SNP	G	A	G	MUC17	c.G1924A	p.A642T
XH_P557	7	121942102	121942128	In_Frame_Del	DEL	CAGAGGAGG	-	GCAGAGGAGGC	FEZF1	c.1351_1377de	p.451_459del
XH_P557	7	127977184	127977184	Splice_Site	INS	-	A	-	RBM28	-	-
XH_P557	7	127977186	127977186	In_Frame_Ins	INS	-	GAACACAGGAG	-	RBM28	.AACAACTCTCTG	3delinsETTPVFMIK
XH_P557	7	128481295	128481295	Missense_Mutation	SNP	C	T	C	FLNC	c.C1885T	p.R629W
XH_P557	7	128845518	128845518	Frame_Shift_Ins	INS	-	GT	-	SMO	c.815_816insGT	p.A272fs
XH_P557	7	135376061	135376061	Frame_Shift_Ins	INS	-	GAAGCCAGAGC	-	SLC13A4	.insCTATGCTCTC	p.E445fs

XH_P557	7	141764245	141764277	In_Frame_Del	DEL	CTCCCTGGT	-	gCTCCCTGGT	MGAM	c.4407_4439del	1469_1480del
XH_P557	7	142989787	142989787	Silent	SNP	G	A	G	CASP2	c.G378A	p.S126S
XH_P557	7	150269974	150269974	Frame_Shift_Ins	INS	-	CCTTCCTT	-	GIMAP4	c.817insCCTTC	p.Q272fs
XH_P557	7	151902190	151902190	Splice_Site	INS	-	CAT	-	KMT2C	-	-
XH_P557	8	1639784	1639784	Missense_Mutation	SNP	C	A	C	DLGAP2	c.C2788A	p.Q930K
XH_P557	8	19316053	19316053	Silent	SNP	G	A	G	CSGALNACT1	c.C735T	p.F245F
XH_P557	8	22570924	22570924	Missense_Mutation	SNP	C	T	C	PEBP4	c.G643A	p.E215K
XH_P557	8	22880484	22880484	In_Frame_Ins	INS	-	CAC	-	TNFRSF10B	c.1022_1023insG	p.C341delinsWC
XH_P557	8	30669897	30669897	Frame_Shift_Ins	INS	-	C	-	PPP2C8	c.40dupG	p.V14fs
XH_P557	8	52733148	52733148	Silent	SNP	C	T	C	PCMTD1	c.G609A	p.K203K
XH_P557	8	55049147	55049147	Missense_Mutation	SNP	G	A	G	MRPL15	c.G185A	p.R62Q
XH_P557	8	80677734	80677734	Missense_Mutation	SNP	C	T	C	HEY1	c.G334A	p.G112R
XH_P557	8	96166373	96166373	Missense_Mutation	SNP	G	A	G	PLEKHF2	c.G101A	p.R34Q
XH_P557	8	144654783	144654783	Frame_Shift_Ins	INS	-	T	-	MROH6	c.101dupA	p.Q34fs
XH_P557	8	145066886	145066886	Silent	SNP	A	G	A	GRINA	c.A993G	p.L331L
XH_P557	9	27185588	27185588	In_Frame_Ins	INS	-	ATC	-	TEK	c.847_848insATG	p.A283delinsDP
XH_P557	9	33266047	33266047	Nonsense_Mutation	SNP	C	T	C	CHMP5	c.C109T	p.R37X
XH_P557	9	34725047	34725047	Silent	SNP	C	T	C	FAM205A	c.G2190A	p.P730P
XH_P557	9	37800645	37800645	Splice_Site	INS	-	TAAC	-	DCAF10	-	-
XH_P557	9	79324246	79324246	Missense_Mutation	SNP	C	T	C	PRUNE2	c.G2944A	p.E982K
XH_P557	9	86587060	86587060	Silent	SNP	G	A	G	HNRNP	c.C618T	p.Y206Y
XH_P557	9	95610284	95610284	Missense_Mutation	SNP	G	A	G	ZNFA48	c.C677T	p.P226L
XH_P557	9	97873815	97873815	Missense_Mutation	SNP	G	A	G	FANCC	c.C1259T	p.T420M
XH_P557	9	112900341	112900341	In_Frame_Ins	INS	-	GATGCT	-	AKAP2	c.91_2092insGATG	p.E697delinsEDA
XH_P557	9	116930346	116930346	Frame_Shift_Ins	INS	-	TGAC	-	COL27A1	c.511_512insTGA	p.V171fs
XH_P557	9	125315785	125315785	Missense_Mutation	SNP	G	A	G	OR1N2	c.G337A	p.G113R
XH_P557	9	130829180	130829180	Frame_Shift_Del	DEL	TCAGGCAGC	-	CTCAGGCAGCT	NAIF1	c.191_201del	p.G64fs
XH_P557	9	135277175	135277175	In_Frame_Ins	INS	-	ACAGTCCCAACC	-	TTF1	c.1nstTGAGGTTGGG	p.B45delinsVRLGLWK
XH_P557	9	138379777	138379777	Missense_Mutation	SNP	G	A	G	PPP1R26	c.G3421A	p.G1141S
XH_P557	10	27529372	27529375	Frame_Shift_Del	DEL	CAGG	-	CAGG	ACBD5	c.48_51del	p.C16fs
XH_P557	10	43609983	43609983	Silent	SNP	C	T	C	RET	c.C1935T	p.S645S
XH_P557	10	45920506	45920506	Missense_Mutation	SNP	G	A	G	ALOX5	c.G760A	p.E254K
XH_P557	10	88227037	88227037	Missense_Mutation	SNP	G	A	G	WAPL	c.C2351T	p.T784M
XH_P557	10	91371602	91371602	Missense_Mutation	SNP	G	A	G	PANK1	c.C232T	p.R78C
XH_P557	10	98287790	98287790	In_Frame_Ins	INS	-	CTA	-	TM9SF3	c.1538_1539insTAp	p.R513delinsRR
XH_P557	10	102777342	102777342	Nonstop_Mutation	SNP	T	C	T	PDZD7	c.A1553G	p.X518W
XH_P557	10	115661445	115661451	Frame_Shift_Del	DEL	GCCTTAG	-	GCCTTAG	NHLRC2	c.1160_1166del	p.C387fs
XH_P557	10	115884951	115884951	Frame_Shift_Ins	INS	-	T	-	CCDC186	c.2647_2648insG	p.R883fs
XH_P557	10	115884952	115884952	Frame_Shift_Ins	INS	-	TTTGATGAAAT	-	CCDC186	c.sAAACAAATTTTC	p.R883fs
XH_P557	10	124457629	124457629	Nonsense_Mutation	SNP	G	A	G	C10orf120	c.C628T	p.R210X
XH_P557	10	129535882	129535882	Silent	SNP	C	T	C	FOXI2	c.C345T	p.L151I
XH_P557	10	129899769	129899769	Frame_Shift_Ins	INS	-	GCATGAGAACCT	-	MKI67	c.5TGCGAAGGTTG	p.K2793fs
XH_P557	10	134040367	134040367	Silent	SNP	C	T	C	STK32C	c.G615A	p.T205T
XH_P557	11	1020143	1020143	In_Frame_Ins	INS	-	TCT	-	MUC6	c.3754_3755insAa	p.T1252delinsKT
XH_P557	11	6411931	6411936	In_Frame_Del	DEL	CTGGTG	-	CTGGTG	SMPD1	c.103_108del	p.35_36del
XH_P557	11	6415216	6415216	Silent	SNP	G	A	G	SMPD1	c.G1431A	p.P477P
XH_P557	11	9534144	9534147	Splice_Site	DEL	GTAA	-	GTAA	ZNFI43	-	-
XH_P557	11	27390646	27390646	Missense_Mutation	SNP	G	A	G	LGR4	c.C1552T	p.R518C
XH_P557	11	34378381	34378381	Missense_Mutation	SNP	G	C	G	A8TB2	c.C750G	p.H250Q
XH_P557	11	55135837	55135837	Missense_Mutation	SNP	G	A	G	OR4A15	c.G478A	p.E160K
XH_P557	11	62288989	62288989	Silent	SNP	G	A	G	AHNAK	c.C12900T	p.I4300I
XH_P557	11	62295076	62295076	Silent	SNP	G	A	G	AHNAK	c.C6813T	p.D2271D
XH_P557	11	62295933	62295933	Missense_Mutation	SNP	T	C	T	AHNAK	c.A5956G	p.T1986A
XH_P557	11	62298731	62298731	Missense_Mutation	SNP	G	A	G	AHNAK	c.C3158T	p.P1053L
XH_P557	11	62557412	62557412	Missense_Mutation	SNP	G	A	G	TMEM179B	c.G553A	p.V185M
XH_P557	11	62678328	62678328	Frame_Shift_Ins	INS	-	A	-	CHRM1	c.244dupT	p.R82fs
XH_P557	11	72466130	72466130	Silent	SNP	G	A	G	STARD10	c.C688T	p.L230L
XH_P557	11	76061989	76061990	Frame_Shift_Del	DEL	TA	-	TA	THAP12	c.2204_2205del	p.L735fs
XH_P557	11	82892917	82892917	Frame_Shift_Ins	INS	-	TAGC	-	PCF11	c.582_4583insTA	p.I1528fs
XH_P557	11	113849995	113849995	Missense_Mutation	SNP	G	A	G	HTR3A	c.G278A	p.R93Q
XH_P557	11	113934442	113934442	Silent	SNP	C	T	C	ZBTB16	c.C420T	p.G140G
XH_P557	11	115080312	115080323	In_Frame_Del	DEL	GTGGTGGTG	-	TGGTGGTGGTG	CADM1	c.1049_1060del	p.350_354del
XH_P557	11	119045689	119045689	Silent	SNP	G	A	G	NLRX1	c.G1377A	p.T459T
XH_P557	11	120008567	120008567	Missense_Mutation	SNP	C	T	C	TRIM29	c.G173A	p.S58N
XH_P557	11	121000784	121000784	Silent	SNP	T	C	T	TECTA	c.T2805C	p.Y935Y
XH_P557	11	126147070	126147077	Frame_Shift_Del	DEL	GGTAACCTG	-	GGTAACCTG	FOXRED1	c.1206delG	p.K402fs
XH_P557	11	129744104	129744104	Missense_Mutation	SNP	G	A	G	NFRKB	c.C2258T	p.P753L
XH_P557	12	12274234	12274234	In_Frame_Ins	INS	-	TAG	-	LRP6	c.4667_4668insC	p.Y1556delinsYY
XH_P557	12	21995359	21995359	Missense_Mutation	SNP	C	A	A	ABCC9	c.G3362T	p.C1121F
XH_P557	12	25380290	25380290	Silent	SNP	G	A	G	KRAS	c.C168T	p.L56L
XH_P557	12	42863337	42863345	In_Frame_Del	DEL	AACACCTGCG	-	AACACCTGCG	PRICKLE1	c.291_299del	p.97_100del
XH_P557	12	52370133	52370133	Frame_Shift_Del	DEL	C	-	C	ACVR1B	c.354delC	p.H118fs
XH_P557	12	57641928	57641928	Silent	SNP	G	A	G	STAC3	c.C369T	p.Y123Y
XH_P557	12	85450168	85450168	In_Frame_Ins	INS	-	TCTACATTTCT	-	LRRIQ1	c.1nstTCTATCTACA	p.533delinsVYLHLSY
XH_P557	12	104373728	104373728	Frame_Shift_Ins	INS	-	A	-	TDG	c.287dupA	p.E96fs
XH_P557	12	109526161	109526161	Missense_Mutation	SNP	C	T	C	ALKBH2	c.G437A	p.R146Q
XH_P557	12	112098442	112098442	Frame_Shift_Ins	INS	-	CTTATTTTTAAAT	-	BRAP	c.AATAAAATTAAAA	p.V312fs
XH_P557	12	117157653	117157653	Missense_Mutation	SNP	C	T	C	C12orf49	c.G449A	p.R150Q
XH_P557	12	123834966	123834966	Nonsense_Mutation	INS	-	TTTTTTTTT	-	SBN01	c.23insAAAAAA	p.L8delinsX
XH_P557	12	123834968	123834968	Frame_Shift_Ins	INS	-	GATAG	-	SBN01	c.20_21insCTAT	p.D7fs
XH_P557	12	124366286	124366286	Missense_Mutation	SNP	G	A	G	DNAH10	c.G8395A	p.A2799T
XH_P557	12	125396377	125396377	Silent	SNP	A	G	A	UBC	c.T1941C	p.D647D
XH_P557	12	125398191	125398191	Silent	SNP	G	A	G	UBC	c.C127T	p.L43L
XH_P557	13	25370306	25370310	Frame_Shift_Del	DEL	AATAG	-	AATAG	RNF17	c.1272_1276del	p.V424fs
XH_P557	13	37600936	37600936	Frame_Shift_Ins	INS	-	GATC	-	SUPT20H	c.168_1169insGA	p.H390fs
XH_P557	13	52599034	52599034	Frame_Shift_Ins	INS	-	G	-	ALG11	c.1168_1169insG	p.I390fs
XH_P557	13	52599035	52599035	Nonsense_Mutation	INS	-	AGTAGATGAGC	-	ALG11	c.AATAGTAGTAG	p.90_G391delinsHX
XH_P557	13	78236258	78236262	Frame_Shift_Del	DEL	GGTCT	-	GGTCT	LOC100129307	c.500_504del	p.E167fs
XH_P557	13	103385019	103385019	Missense_Mutation	SNP	G	A	G	CCDC168	c.C18028T	p.L6010F
XH_P557	13	110804813	110804813	Missense_Mutation	SNP	G	A	G	COL4A1	c.C4796T	p.A1599V
XH_P557	13	113850537	113850537	In_Frame_Ins	INS	-	TAC	-	PCID2	c.427_428insGT	p.T143delinsST
XH_P557	13	114138283	114138283	Missense_Mutation	SNP	G	A	G	DCUN1D2	c.C92T	p.T31M
XH_P557	14	23398431	23398431	Missense_Mutation	SNP	G	A	G	PRMT5	c.C4T	p.R2W
XH_P557	14	50065118	50065118	Missense_Mutation	SNP	C	T	C	RPS29	c.G53A	p.G18D
XH_P557	14	59814276	59814276	Missense_Mutation	SNP	G	A	G	DAAM1	c.G2095A	p.E699K
XH_P557	14	69376075	69376075	Missense_Mutation	SNP	C	A	C	ACTN1	c.G554T	p.R185L
XH_P557	14	80677791	80677791	Silent	SNP	G	A	G	DIO2	c.C25T	p.L9L
XH_P557	14	105243078	105243078	Missense_Mutation	SNP	G	A	G	AKT1	c.C205T	p.R69W

XH P557	14	105411700	105411700	Missense_Mutation	SNP	A	G	A	AHNAK2	c.T9788C	p.V3263A
XH P557	15	31260193	31260195	In_Frame_Del	DEL	ATG	-	ATG	MTMR10	c.493_495del	p.165_165del
XH P557	15	34654459	34654459	Silent	SNP	G	A	G	LPCAT4	c.C948T	p.G316G
XH P557	15	41165482	41165482	Missense_Mutation	SNP	C	T	C	RHOV	c.G485A	p.R162Q
XH P557	15	41961868	41961868	Missense_Mutation	SNP	G	A	G	MGA	c.G776A	p.R259Q
XH P557	15	43815214	43815214	Frame_Shift_Ins	INS	-	TTTGATCTCTTT	-	MAP1A	44insTTTTTGAT	p.P515fs
XH P557	15	51233687	51233687	Missense_Mutation	SNP	C	T	C	AP4E1	c.C767T	p.S256L
XH P557	15	52258405	52258405	Missense_Mutation	SNP	C	T	C	LEO1	c.G355A	p.E119K
XH P557	15	56735701	56735701	Missense_Mutation	SNP	C	T	C	MNS1	c.G938A	p.R313H
XH P557	15	82935129	82935129	Missense_Mutation	SNP	C	G	C	GOLGA6L10	c.G451C	p.E151Q
XH P557	15	90195966	90195966	Frame_Shift_Ins	INS	-	GG	-	KIF7	c.195_196insCC	p.G66fs
XH P557	15	90344825	90344825	Frame_Shift_Ins	INS	-	G	-	ANPEP	c.1582dupC	p.R528fs
XH P557	15	93173457	93173457	Missense_Mutation	SNP	C	T	C	FAM174B	c.G463A	p.D155N
XH P557	15	99512850	99512850	Missense_Mutation	SNP	C	T	C	PGPEP1L	c.G175A	p.A59T
XH P557	16	1263883	1263883	Silent	SNP	C	T	C	CACNA1H	c.C4863T	p.I1621I
XH P557	16	4445327	4445327	Missense_Mutation	SNP	C	T	C	COR07	c.G323A	p.R108Q
XH P557	16	4777027	4777027	Silent	SNP	G	A	G	ANKS3	c.C322T	p.L108L
XH P557	16	4945324	4945324	Missense_Mutation	SNP	G	A	G	PPL	c.C1180T	p.R394C
XH P557	16	20554248	20554248	Silent	SNP	G	T	G	ACSM2B	c.C1497A	p.P499P
XH P557	16	21689858	21689858	Missense_Mutation	SNP	A	G	A	OTOA	c.A23G	p.Y8C
XH P557	16	24564880	24564883	Splice_Site	DEL	TATA	-	TATA	RBBP6	-	-
XH P557	16	27561001	27561001	Nonsense_Mutation	INS	-	CTA	-	GTF3C1	c.210_211insTA	p.L71delinsX
XH P557	16	30390012	30390012	Silent	SNP	G	A	G	SEPT1	c.C1077T	p.S359S
XH P557	16	31499063	31499063	Nonsense_Mutation	INS	-	AA	-	SLC5A2	c.868_869insAA	290_W291delinsX
XH P557	16	57918303	57918303	Missense_Mutation	SNP	G	A	G	CNGB1	c.C3503T	p.T1168M
XH P557	16	66973200	66973200	Frame_Shift_Ins	INS	-	G	-	CES2	c.555dupG	p.E185fs
XH P557	16	67864336	67864336	Silent	SNP	G	A	G	CENPT	c.C819T	p.A273A
XH P557	16	70534939	70534939	Frame_Shift_Ins	INS	-	TAGC	-	COG4	116_1117insGC	p.Y373fs
XH P557	16	70543922	70543922	Nonsense_Mutation	INS	-	AATCATGTAGTT	-	COG4	c.AAATAAACTAC	447_A248delinsVNX
XH P557	16	86565882	86565882	Missense_Mutation	SNP	G	C	G	MTHFS	c.C887G	p.S296C
XH P557	16	89348452	89348475	In_Frame_Del	DEL	CTGTGATGC	-	CCCTGTGATGCC	ANKRD11	c.4475_4498del	1492_1500del
XH P557	16	89778297	89778298	Frame_Shift_Del	DEL	TG	-	TG	VPS9D1	c.739_740del	p.Q247fs
XH P557	16	90126889	90126889	Silent	SNP	G	A	G	PRDM7	c.C1093T	p.L365L
XH P557	17	4448598	4448598	Frame_Shift_Ins	INS	-	CA	-	MYBBP1A	2115_2116insT	p.V706fs
XH P557	17	7228293	7228293	Silent	SNP	G	A	G	NEURL4	c.C1638T	p.T546T
XH P557	17	7496152	7496152	Missense_Mutation	SNP	G	A	G	FXR2	c.C1589T	p.P530L
XH P557	17	9792910	9792910	Missense_Mutation	SNP	C	T	C	GLP2R	c.C1550T	p.P517L
XH P557	17	12656271	12656271	In_Frame_Ins	INS	-	ACT	-	MYOCD	1666_1667insAp	N556delinsNY
XH P557	17	16526349	16526349	Silent	SNP	G	A	G	ZNF624	c.C1851T	p.C617C
XH P557	17	37441780	37441780	Missense_Mutation	SNP	C	T	C	FBXL20	c.G445A	p.D149N
XH P557	17	38560458	38560458	Missense_Mutation	SNP	C	A	C	TOP2A	c.G2229T	p.K743N
XH P557	17	42156627	42156627	Frame_Shift_Ins	INS	-	T	-	HDAC5	c.2965dupA	p.R989fs
XH P557	17	48244754	48244754	Silent	SNP	C	T	C	SGCA	c.C63T	p.T21T
XH P557	17	48761469	48761469	Splice_Site	INS	-	T	-	ABCC3	-	-
XH P557	17	63221442	63221442	Missense_Mutation	SNP	G	A	G	RG59	c.G1721A	p.R574H
XH P557	17	65909268	65909273	In_Frame_Del	DEL	TCCTTC	-	TCCTTC	BPTF	c.5268_5273del	1756_1758del
XH P557	17	66596510	66596517	Frame_Shift_Del	DEL	GCGGGTGG	-	GCGGGTGG	FAM20A	c.291_298del	p.A97fs
XH P557	17	74077797	74077797	Nonsense_Mutation	SNP	C	T	C	ZACN	c.C841T	p.Q281X
XH P557	17	75486940	75486940	Missense_Mutation	SNP	G	A	G	SEPT9	c.G1043A	p.R348Q
XH P557	17	76166898	76166898	In_Frame_Ins	INS	-	TCT	-	SYNGR2	c.100_101insTC	p.V34delinsVF
XH P557	17	7752194	7752194	Frame_Shift_Ins	INS	-	TACC	-	CBX2	c.84_85insTACC	p.E28fs
XH P557	18	13731869	13731869	In_Frame_Ins	INS	-	ACTCTTTTCTCTT	-	RNMT	insAAACTCTTTT	118delinsSNSFL
XH P557	18	19057153	19057153	Missense_Mutation	SNP	G	A	G	GREB1L	c.G2392A	p.E798K
XH P557	18	32457706	32457706	Missense_Mutation	SNP	G	A	G	DTNA	c.G916A	p.D306N
XH P557	18	44656695	44656695	In_Frame_Ins	INS	-	GTG	-	HDHD2	c.44_45insCAC	p.I15delinsIT
XH P557	18	44656696	44656696	In_Frame_Ins	INS	-	GTTTTTTGTTTT	-	HDHD2	c.AATAAAAAACAA	5delinsNKTKTNILL
XH P557	18	48593441	48593441	Frame_Shift_Ins	INS	-	G	-	SMAD4	c.1193dupG	p.W398fs
XH P557	18	61034290	61034290	Missense_Mutation	SNP	G	A	G	KDSR	c.C62T	p.P21L
XH P557	18	72250823	72250823	Missense_Mutation	SNP	C	T	C	CNDP1	c.C1336T	p.R446W
XH P557	18	77659593	77659593	Missense_Mutation	SNP	G	A	G	KCNQ2	c.G1178A	p.G393D
XH P557	19	2076842	2076842	Missense_Mutation	SNP	C	T	C	MOB3A	c.G592A	p.G198S
XH P557	19	4523873	4523873	Silent	SNP	G	A	G	PLIN5	c.C1059T	p.H353H
XH P557	19	4538623	4538623	Nonsense_Mutation	SNP	G	A	G	LRG1	c.C373T	p.R125X
XH P557	19	8808373	8808373	Missense_Mutation	SNP	G	T	G	ACTL9	c.C679A	p.H227N
XH P557	19	9002519	9002519	Missense_Mutation	SNP	G	T	G	MUC16	c.C40297A	p.H13433N
XH P557	19	9271790	9271790	Missense_Mutation	SNP	G	A	G	ZNFX17	c.G1373A	p.R458Q
XH P557	19	11356502	11356502	Missense_Mutation	SNP	G	A	G	DOCK6	c.C859T	p.R287W
XH P557	19	13058701	13058714	Frame_Shift_Del	DEL	TGATGCCTTC	-	GTGATGCCTTCC	RAD23A	c.112_125del	p.R38fs
XH P557	19	14520117	14520117	Missense_Mutation	SNP	G	A	G	DDX39A	c.C1117T	p.R373W
XH P557	19	17766787	17766787	Silent	SNP	G	A	G	UNC13A	c.C1188T	p.P396P
XH P557	19	19737898	19737898	Missense_Mutation	SNP	G	A	G	LPAR2	c.C196T	p.P66S
XH P557	19	19737899	19737899	Missense_Mutation	SNP	C	A	C	LPAR2	c.G195T	p.Q65H
XH P557	19	20045514	20045514	Nonsense_Mutation	INS	-	CCAGTATGAATT	-	ZNFX93	TTCTCTCCAGTAA	delinsRVS/LQYF/SVXX
XH P557	19	21477431	21477431	Missense_Mutation	SNP	T	C	T	ZNFX08	c.A145G	p.K49E
XH P557	19	22498461	22498461	Missense_Mutation	SNP	T	G	T	ZNFX729	c.T2242G	p.S748A
XH P557	19	23938341	23938341	Frame_Shift_Ins	INS	-	GTTCATTTTTC	-	ZNFX681	5insAGAAAAATG	p.F6fs
XH P557	19	24310638	24310638	Frame_Shift_Ins	INS	-	TCAGTATGAATT	-	ZNFX254	TTCTCTTCAGTA	p.F527fs
XH P557	19	33417851	33417851	Frame_Shift_Ins	INS	-	TA	-	CEP89	1068_1069insT	p.P357fs
XH P557	19	35941124	35941124	Missense_Mutation	SNP	G	A	G	FFAR2	c.G508A	p.D170N
XH P557	19	38852470	38852471	Frame_Shift_Del	DEL	AC	-	AC	CATSPERG	c.1943_1944de	p.Y648fs
XH P557	19	41223770	41223786	Frame_Shift_Del	DEL	ATACTGATG	-	ATATACTGATGG	ITPKC	c.730_746del	p.P244fs
XH P557	19	42342205	42342205	Frame_Shift_Ins	INS	-	TTCCACCTTA	-	LYPD4	237insTAAAGT	p.L79fs
XH P557	19	42342207	42342207	Missense_Mutation	SNP	G	A	G	LYPD4	c.C235T	p.L79F
XH P557	19	42910455	42910455	Silent	SNP	G	A	G	LIPE	c.C2223T	p.Y741Y
XH P557	19	46299138	46299138	In_Frame_Ins	INS	-	TCCTCGCCCTCC	-	RSPH6A	3insGAGGAGG	715delinsEEGET
XH P557	19	46388379	46388379	Silent	SNP	C	G	C	IRF2BP1	c.G654C	p.R218R
XH P557	19	49254466	49254466	Missense_Mutation	SNP	G	A	G	FUT1	c.C73T	p.L25F
XH P557	19	55494075	55494075	Missense_Mutation	SNP	C	T	C	NLRP2	c.C943T	p.R315W
XH P557	19	55739689	55739689	Silent	SNP	G	A	G	TMEM86B	c.C168T	p.P56P
XH P557	19	56539109	56539109	Missense_Mutation	SNP	G	A	G	NLRP5	c.G1510A	p.A504T
XH P557	19	58361416	58361416	Missense_Mutation	SNP	G	A	G	ZNFX587	c.G10A	p.A4T
XH P557	19	59061550	59061550	Missense_Mutation	SNP	C	T	C	TRIM28	c.C2230T	p.R744C
XH P557	20	5987092	5987092	Frame_Shift_Ins	INS	-	C	-	CRLS1	c.201dupC	p.R67fs
XH P557	20	31890796	31890796	Frame_Shift_Ins	INS	-	GG	-	BPIFB1	1056_1057insG	p.Q352fs
XH P557	20	33330510	33330510	Missense_Mutation	SNP	G	C	G	NCOA6	c.C3550G	p.P1184A
XH P557	20	33330512	33330512	Nonsense_Mutation	INS	-	TGATCAACAAG	-	NCOA6	3548insCTTGT	183_P1184delinsPCX
XH P557	20	40033573	40033573	Frame_Shift_Ins	INS	-	TAGT	-	CHD6	7807_7808insAC	p.T2603fs
XH P557	20	42089371	42089371	Missense_Mutation	SNP	C	T	C	SRSF6	c.C703T	p.R235C

XH P557	20	56186938	56186945	Frame_Shift_Del	DEL	GAGGAATC	-	GAGGAATC	ZBP1	c.487_494del	p.D163fs
XH P557	20	62203504	62203504	Missense_Mutation	SNP	G	A	G	HELZ2	c.C235T	p.R79C
XH P557	21	33719695	33719695	Silent	SNP	C	T	C	URB1	c.G3438A	p.K1146K
XH P557	21	37788576	37788576	Missense_Mutation	SNP	C	T	C	CHAF1B	c.C1592T	p.T531M
XH P557	22	17589855	17589855	Silent	SNP	C	T	C	IL17RA	c.C1644T	p.P548P
XH P557	22	31091476	31091479	Frame_Shift_Del	DEL	AACT	-	AACT	OSBP2	c.580_583del	p.N194fs
XH P557	22	32014387	32014387	Missense_Mutation	SNP	C	T	C	SF11	c.C3547T	p.R1183W
XH P557	22	38119755	38119757	In_Frame_Del	DEL	CAA	-	CAA	TRIOBP	c.1192_1194del	p.398_398del
XH P557	22	38536036	38536036	Frame_Shift_Ins	INS	-	C	-	PLA2G6	c.749dupG	p.G250fs
XH P557	22	42525175	42525175	Missense_Mutation	SNP	G	A	G	CYP2D6	c.C365T	p.A122V
XH P557	22	42606257	42606257	Silent	SNP	C	T	C	TCF20	c.G5055A	p.S1685S
XH P557	22	50987778	50987778	Frame_Shift_Ins	INS	-	AT	-	KLHDC7B	c.1183_1184insA	p.R395fs
XH P557	22	50987780	50987783	Frame_Shift_Del	DEL	AGCC	-	AGCC	KLHDC7B	c.1185_1188del	p.R395fs
XH P557	22	51021033	51021033	Missense_Mutation	SNP	C	T	C	CHKB	c.G178A	p.A60T
XH P557	X	47028815	47028815	Frame_Shift_Ins	INS	-	CTAC	-	RBM10	c.119_120insCTA	p.D40fs
XH P557	X	48681964	48681964	Missense_Mutation	SNP	G	A	G	HDAC6	c.G3155A	p.S1052N
XH P557	X	77301017	77301017	Missense_Mutation	SNP	G	A	G	ATP7A	c.G3940A	p.A1314T
XH P557	X	100613313	100613313	Nonsense_Mutation	SNP	G	A	G	BTK	c.C1087T	p.Q363X
XH P557	X	117712515	117712515	Missense_Mutation	SNP	C	T	C	DOCK11	c.C1417T	p.P473S
XH P557	X	119007322	119007322	Missense_Mutation	SNP	G	A	G	NDUFA1	c.G158A	p.R53H
XH P557	X	122336556	122336574	Frame_Shift_Del	DEL	CAAGATCA	-	GCAAGATCATC	GRIA3	c.337_355del	p.C113fs
XH P557	X	125299188	125299188	Silent	SNP	T	G	T	DCAF12L2	c.A720C	p.P240P
XH P557	1	156170116	156170116	Frame_Shift_Ins	INDEL	-	TAGT	TAGT	SLC25A44	c.480_483dupAG	P.A162fs
XH P557	1	16260969	16260969	Missense_Mutation	SNV	C	T	T	SPEN	c.8234C>T	P.A2745V
XH P557	1	182823275	182823279	Frame_Shift_Del	INDEL	AGAAT	-	-	DHX9	c.589_593delGAA	P.E197fs
XH P557	1	185962381	185962381	Missense_Mutation	SNV	C	G	G	HMCN1	c.3445C>G	P.L1149V
XH P557	1	196965192	196965192	Silent	SNV	C	T	T	CFHR5	c.831C>T	P.Y277Y
XH P557	1	203276245	203276254	Frame_Shift_Del	INDEL	CCACTGGTT	-	-	BTG2	c.167delACTGG	P.H53fs
XH P557	1	207133079	207133079	Frame_Shift_Ins	INDEL	-	AG	AG	FCAMR	c.714_715dupC	P.C239fs
XH P557	1	225586370	225586370	Splice_Site	INDEL	-	A	A	DNAH14	c.13332+4dupA	
XH P557	1	32264080	32264080	Missense_Mutation	SNV	C	T	T	SPOCD1	c.1991G>A	P.R664H
XH P557	1	33480164	33480172	Missense_Mutation	INDEL	GGTAGGAAC	-	-	AK2	c.543delGTTCC	P.R142_Y144del
XH P557	1	57159485	57159485	Missense_Mutation	SNV	G	A	A	PRKAA2	c.523G>A	P.G175R
XH P557	1	61818213	61818213	Frame_Shift_Ins	INDEL	-	TCTT	TCTT	NFIA	c.794_797dupCT	P.L266fs
XH P557	1	67154853	67154853	Silent	SNV	A	T	T	SGIP1	c.741A>T	P.P247P
XH P557	1	67154855	67154857	Missense_Mutation	INDEL	CCA	-	-	SGIP1	c.744_746delCA	P.T249del
XH P557	1	9305594	9305594	Frame_Shift_Ins	INDEL	-	G	G	H6PD	c.637dupG	P.V213fs
XH P557	10	129535882	129535882	Silent	SNV	C	T	T	FOXI2	c.345C>T	P.I115I
XH P557	10	27529372	27529375	Frame_Shift_Del	INDEL	CAGG	-	-	ACBD5	c.54_57delCCTG	P.C18fs
XH P557	10	43609983	43609983	Silent	SNV	C	T	T	RET	c.1935C>T	P.S645S
XH P557	10	75511008	75511015	Splice_Site	INDEL	ACTTGGTC	-	-	SEC24C	c.308+15delCTTGGTCA	
XH P557	11	126135985	126136000	Splice_Site	INDEL	GGAGATTAC	-	-	SRPRA	c.9-9delATGTGTAATCTCCTGT	
XH P557	11	55135837	55135837	Missense_Mutation	SNV	G	A	A	OR4A15	c.478G>A	P.E160K
XH P557	11	76061989	76061990	Frame_Shift_Del	INDEL	TA	-	-	THAP12	c.2204_2205delT	P.L735fs
XH P557	11	82892917	82892917	Frame_Shift_Ins	INDEL	-	TAGC	TAGC	PCF11	c.191_4194dupA	P.D1399fs
XH P557	11	9534144	9534147	Splice_Site	INDEL	GTAA	-	-	ZNF143	c.1+4_1521+7delAGTA	
XH P557	12	12274234	12274234	Missense_Mutation	INDEL	-	TAG	TAG	LRP6	c.665_4667dupC	P.Y1556dup
XH P557	12	42863337	42863345	Missense_Mutation	INDEL	AACACCTGC	-	-	PRICKLE1	c.299delGCAGG	P.L97_V99dup
XH P557	12	52370133	52370133	Frame_Shift_Del	INDEL	C	-	-	ACVR1B	c.356delC	P.P119fs
XH P557	13	113850537	113850537	Frame_Shift_Ins	INDEL	-	TAC	TAC	PCID2	c.126-1_427dupG	P.G142_T143insS
XH P557	13	25370306	25370310	Frame_Shift_Del	INDEL	AATAG	-	-	RNF17	c.273_1277delAT	P.L425fs
XH P557	13	78236258	78236262	Frame_Shift_Del	INDEL	GGTCT	-	-	LOC100129307	c.500_504delAGA	P.E167fs
XH P557	14	50582551	50582551	Splice_Site	INDEL	-	CTT	CTT	VCPKMT	c.40+3_450+5dupAAG	
XH P557	14	59814276	59814276	Missense_Mutation	SNV	G	A	A	DAAM1	c.2095G>A	P.E699K
XH P557	14	69376075	69376075	Missense_Mutation	SNV	C	A	A	ACTN1	c.554G>T	P.R185L
XH P557	15	31260193	31260195	Missense_Mutation	INDEL	ATG	-	-	MTMR10	c.493_495delCA	P.H165del
XH P557	16	20554248	20554248	Silent	SNV	G	T	T	ACSM2B	c.1497C>A	P.P499P
XH P557	16	21689858	21689858	Missense_Mutation	SNV	A	G	G	OTOA	c.23A>G	P.Y8C
XH P557	16	4945324	4945324	Missense_Mutation	SNV	G	A	A	PPL	c.1180C>T	P.R394C
XH P557	16	57918303	57918303	Missense_Mutation	SNV	G	A	A	CNGB1	c.3503C>T	P.T1168M
XH P557	16	66973200	66973200	Frame_Shift_Ins	INDEL	-	G	G	CE52	c.556dupG	P.D186fs
XH P557	16	70534939	70534939	Frame_Shift_Ins	INDEL	-	TAGC	TAGC	COG4	c.113_1116dupG	P.Y373fs
XH P557	16	89778297	89778298	Frame_Shift_Del	INDEL	TG	-	-	VPS9D1	c.739_740delCA	P.Q247fs
XH P557	16	90126889	90126889	Silent	SNV	G	A	A	PRDM7	c.1093C>T	P.L365L
XH P557	17	12656271	12656271	Missense_Mutation	INDEL	-	ACT	ACT	MYOCD	c.1667_1669dupA	P.N556_C557insY
XH P557	17	37441780	37441780	Missense_Mutation	SNV	C	T	T	FBXL20	c.445G>A	P.D149N
XH P557	17	38560458	38560458	Missense_Mutation	SNV	C	A	A	TOP2AN	c.2229G>T	P.K743N
XH P557	17	43343925	43343925	Frame_Shift_Ins	INDEL	-	ACA	ACA	MAP3K14	c.2553_2554insTG	P.T851_D852insC
XH P557	17	4448598	4448598	Frame_Shift_Ins	INDEL	-	CA	CA	MYBBP1A	c.2114_2115dupT	P.V706fs
XH P557	17	48761469	48761469	Splice_Site	INDEL	-	T	T	ABCC3	c.4113+2dupT	
XH P557	17	48761471	48761471	Splice_Site	SNV	A	C	C	ABCC3	c.4113+3A>C	
XH P557	17	66596510	66596517	Frame_Shift_Del	INDEL	GCGGGTGG	-	-	FAM20A	c.1_298delCCACC	P.H98fs
XH P557	17	73607936	73608062	Missense_Mutation	INDEL	CACCGAGTC	-	-	MYO15B	c.4391-28_4489del	P.P1497delinsT
XH P557	17	76166898	76166898	Frame_Shift_Ins	INDEL	-	TCT	TCT	SYNR2	c.103_105dupTT	P.F35dup
XH P557	17	77752194	77752194	Frame_Shift_Ins	INDEL	-	TACC	TACC	CBX2	c.186_89dupACC	P.V31fs
XH P557	17	9792910	9792910	Missense_Mutation	SNV	C	T	T	GLP2R	c.1550C>T	P.P517L
XH P557	18	19057153	19057153	Missense_Mutation	SNV	G	A	A	GREB1L	c.2392G>A	P.E798K
XH P557	18	32457706	32457706	Missense_Mutation	SNV	G	A	A	DTNA	c.916G>A	P.D306N
XH P557	18	48593441	48593441	Frame_Shift_Ins	INDEL	-	G	G	SMAD4	c.1195dupG	P.V399fs
XH P557	19	11356502	11356502	Missense_Mutation	SNV	G	A	A	DOCK6	c.859C>T	P.R287W
XH P557	19	13058701	13058714	Frame_Shift_Del	INDEL	TGATGCCTTC	-	-	RAD23A	c.29delATGCCTTC	P.D39fs
XH P557	19	19737898	19737898	Missense_Mutation	SNV	G	A	A	LPAR2	c.196C>T	P.P66S
XH P557	19	19737899	19737899	Missense_Mutation	SNV	C	A	A	LPAR2	c.195G>T	P.Q65H
XH P557	19	33417851	33417851	Frame_Shift_Ins	INDEL	-	TA	TA	CEP89	c.1067_1068dupT	P.P357fs
XH P557	19	38852470	38852471	Frame_Shift_Del	INDEL	AC	-	-	CATSPERG	c.2063_2064delA	P.V688fs
XH P557	19	41223770	41223786	Frame_Shift_Del	INDEL	ATACTGATG	-	-	ITPKC	c.1delTATACTGAT	P.Y245fs
XH P557	19	4538623	4538623	Nonsense_Mutation	SNV	G	A	A	LRG1	c.373C>T	P.R125*
XH P557	19	55494075	55494075	Missense_Mutation	SNV	C	T	T	NLRP2	c.1009C>T	P.R337W
XH P557	19	56539109	56539109	Missense_Mutation	SNV	G	A	A	NLRP5	c.1510G>A	P.A504T
XH P557	2	103348775	103348775	Splice_Site	INDEL	-	CTC	CTC	MFSD9	c.0+3_70+5dupGAG	
XH P557	2	128477554	128477554	Missense_Mutation	SNV	C	G	G	WDR33	c.2045G>C	P.G682A
XH P557	2	141243024	141243024	Missense_Mutation	SNV	C	T	T	LRP1B	c.9313G>A	P.D3105N
XH P557	2	167133659	167133659	Missense_Mutation	SNV	C	T	T	SCN9A	c.2675G>A	P.C892Y
XH P557	2	170113677	170113677	Missense_Mutation	SNV	T	A	A	LRP2	c.2596A>T	P.N866Y
XH P557	2	178416701	178416701	Missense_Mutation	SNV	A	G	G	TTCC30B	c.791T>C	P.L264P
XH P557	2	179417338	179417338	Frame_Shift_Del	INDEL	A	-	-	TTN	c.85366delT	P.S28456fs
XH P557	2	179417340	179417340	Frame_Shift_Del	INDEL	T	-	-	TTN	c.85364delA	P.Q28455fs
XH P557	2	179489988	179489988	Splice_Site	INDEL	CTTGTAATT	-	-	TTN	c.39625+12delTAATTACAAGG	

XH_P557	2	208425061	208425068	Frame_Shift_Del	INDEL	TCAGTTAT	-	-	CREB1	1_238delATTCT	P.I78fs
XH_P557	2	39893487	39893487	Frame_Shift_Ins	INDEL	-	G	G	TMEM178A	c.376dupG	P.D126fs
XH_P557	2	47256405	47256405	Missense_Mutation	SNV	C	T	T	TTC7A	c.1684C>T	P.R562C
XH_P557	2	54880887	54880887	Frame_Shift_Ins	INDEL	-	T	T	SPTBN1	c.5720dupA	P.V1908fs
XH_P557	2	97595044	97595044	Silent	SNV	G	A	A	FAM178B	c.1092C>T	P.H364H
XH_P557	20	31890796	31890796	Frame_Shift_Ins	INDEL	-	GG	GG	BP1FB1	1057_1058dupC	P.H354fs
XH_P557	20	56186938	56186945	Frame_Shift_Del	INDEL	GAGGAATC	-	-	ZBP1	9_716delGATTC	P.D237fs
XH_P557	22	42525175	42525175	Missense_Mutation	SNV	G	A	A	CYP2D6	c.365C>T	P.A122V
XH_P557	22	50987780	50987783	Frame_Shift_Del	INDEL	AGCC	-	-	KLHDC7B	185_1188delAC	P.A396fs
XH_P557	3	10188287	10188287	Missense_Mutation	SNV	G	A	A	VHL	c.430G>A	P.G144R
XH_P557	3	124211719	124211719	Missense_Mutation	SNV	A	T	T	KALRN	c.4816A>T	P.N1606Y
XH_P557	3	136323224	136323246	Frame_Shift_Del	INDEL	TAGCTCTTC	-	-	STAG1	GCCGTGGAAGA	P.G68fs
XH_P557	3	194386921	194386921	Splice_Site	SNV	A	G	G	LSG1	c.434+11T>C	
XH_P557	4	114251526	114251526	Missense_Mutation	SNV	G	A	A	ANK2	c.2998G>A	P.V1000I
XH_P557	4	140306101	140306107	Frame_Shift_Del	INDEL	GAATTCT	-	-	NAA15	73_2279delATTCT	P.N758fs
XH_P557	4	15518320	15518320	Missense_Mutation	SNV	C	T	T	CC2D2A	c.1090C>T	P.P364S
XH_P557	4	175414439	175414439	Frame_Shift_Ins	INDEL	-	C	C	HPGD	c.524dupG	P.V176fs
XH_P557	4	183673030	183673030	Missense_Mutation	SNV	G	A	A	TENM3	c.3707G>A	P.R1236H
XH_P557	4	186318369	186318369	Frame_Shift_Ins	INDEL	-	CAGT	CAGT	ANKRD37	195_98dupAGT	P.P34fs
XH_P557	4	76785609	76785609	Missense_Mutation	SNV	T	C	C	PPEF2	c.1992A>G	P.I664M
XH_P557	5	146703516	146703518	Missense_Mutation	INDEL	GGA	-	-	STK32A	317_319delGA	P.G106del
XH_P557	5	147510850	147510850	Frame_Shift_Ins	INDEL	-	ATTG	ATTG	SPINK5	884_3087dupA	P.P1030fs
XH_P557	5	150632794	150632794	Frame_Shift_Ins	INDEL	-	G	G	GM2A	c.19dupG	P.A7fs
XH_P557	6	39876841	39876841	Missense_Mutation	SNV	C	T	T	MOC51	c.1140G>A	P.M380I
XH_P557	6	86215709	86215711	Missense_Mutation	INDEL	AAC	-	-	SNX14	2788_2790delG	P.V930del
XH_P557	7	128845518	128845518	Frame_Shift_Ins	INDEL	-	GT	GT	SMO	1817_818dupTC	P.F274fs
XH_P557	7	141764245	141764277	Missense_Mutation	INDEL	CTCCCTGGT	-	-	MGAM	AGACGGCTCCCT	L1470_N1480del
XH_P557	7	148506399	148506399	Splice_Site	INDEL	T	-	-	EZH2	c.2110+3delA	
XH_P557	7	151902190	151902190	Frame_Shift_Ins	INDEL	-	CAT	CAT	KMT2C	959_3961dupA	P.D1320dup
XH_P557	7	21675698	21675698	Silent	SNV	G	A	A	DNAH11	c.4710G>A	P.V1570V
XH_P557	7	43918682	43918682	Missense_Mutation	SNV	G	A	A	URGPC	c.380C>T	P.A127V
XH_P557	8	1639784	1639784	Missense_Mutation	SNV	C	A	A	DLGAP2	c.2506C>A	P.Q836G
XH_P557	8	22880484	22880484	Missense_Mutation	INDEL	-	CAC	CAC	TNFRSF10B	1020_1022dupG	Q340_C341insW
XH_P557	8	89179888	89179888	Splice_Site	SNV	A	T	T	MMP16	c.709+10T>A	
XH_P557	9	125315785	125315785	Missense_Mutation	SNV	G	A	A	OR1N2	c.337G>A	P.G113R
XH_P557	9	130829180	130829190	Frame_Shift_Del	INDEL	TCAGGCAGC	-	-	NAIF1	201delAGCTGC	P.E64fs
XH_P557	9	141124270	141124280	Splice_Site	INDEL	TCCCAGGTA	-	-	FAM157B	20+6delCCCAGGTAAC	
XH_P557	9	37800645	37800645	Splice_Site	INDEL	-	TAAC	TAAC	CCAF10	0+4_20+7dupACTA	
XH_P557	X	100613313	100613313	Nonsense_Mutation	SNV	G	A	A	BTK	c.1087C>T	P.Q363*
XH_P557	X	117712515	117712515	Missense_Mutation	SNV	C	T	T	DOCK11	c.1417C>T	P.P473S
XH_P557	X	122336556	122336574	Frame_Shift_Del	INDEL	CAAGATCA	-	-	GRIA3	121_124dupTAC	P.A115fs
XH_P557	X	47028815	47028815	Frame_Shift_Ins	INDEL	-	CTAC	CTAC	RBM10	121_124dupTAC	P.R42fs
XH_P56		-	-	Missense_Mutation	SNP	-	-	-	ATM	036_7037delins	p.A2346I
XH_P56	12	25398284	25398284	Missense_Mutation	SNP	C	T	T	KRAS	c.35G>A	p.G12D
XH_P56	3	89156920	89156920	Missense_Mutation	SNP	C	T	T	EPHA3	c.22C>T	p.L8F
XH_P56	5	1293425	1293425	Splice_Site	SNP	C	T	T	TERT	c.1573+3G>A	-
XH_P56	1	3599688	3599688	Missense_Mutation	SNP	G	A	G	TP73	c.G130A	p.G44R
XH_P56	1	7723711	7723711	Silent	SNP	C	T	T	CAMTA1	c.C1014T	p.S338S
XH_P56	1	12371650	12371650	Missense_Mutation	SNP	C	T	C	VPS13D	c.C6790T	p.R2264W
XH_P56	1	19465698	19465698	Frame_Shift_Ins	INS	-	CACTGAGTCCAC	-	UBR4	10+6delGTCAGTGGAC	p.D2870fs
XH_P56	1	22141030	22141030	Silent	SNP	C	T	C	LDLRAD2	c.C225T	p.D75D
XH_P56	1	38018310	38018310	In_Frame_Ins	INS	-	TTTTTA	-	SNIP1	62_263insTAA	p.R88delinsKR
XH_P56	1	76215194	76215194	Missense_Mutation	SNP	G	A	G	ACADM	c.G232A	p.G78R
XH_P56	1	114354942	114354942	Silent	SNP	T	G	T	RSB1	c.A93C	p.R31R
XH_P56	1	114948281	114948281	Missense_Mutation	SNP	A	G	A	TRIM33	c.T2519C	p.I840T
XH_P56	1	117122285	117122285	Missense_Mutation	SNP	G	C	G	IGSF3	c.C3063G	p.D1021E
XH_P56	1	149858030	149858030	Missense_Mutation	SNP	C	T	C	HIST2H2BE	c.G161A	p.G54D
XH_P56	1	150939039	150939039	Silent	SNP	G	A	G	CERS2	c.C915T	p.P305F
XH_P56	1	152191301	152191301	Frame_Shift_Ins	INS	-	CG	-	HRNR	2803_2804insC	p.K935fs
XH_P56	1	152191302	152191302	Frame_Shift_Ins	INS	-	G	-	HRNR	c.2802dupC	p.K935fs
XH_P56	1	152281770	152281770	Silent	SNP	G	T	G	FLG	c.C5592A	p.V1864V
XH_P56	1	152281771	152281771	Missense_Mutation	SNP	A	G	A	FLG	c.T5591C	p.V1864A
XH_P56	1	152282088	152282088	Missense_Mutation	SNP	C	G	C	FLG	c.G5274C	p.R1758S
XH_P56	1	152283505	152283505	Missense_Mutation	SNP	A	C	A	FLG	c.T3857G	p.L1286W
XH_P56	1	152284055	152284055	Missense_Mutation	SNP	C	T	C	FLG	c.G3307A	p.A1103T
XH_P56	1	152324696	152324696	Missense_Mutation	SNP	C	T	C	FLG2	c.G5566A	p.G1856R
XH_P56	1	152324698	152324698	Missense_Mutation	SNP	C	G	C	FLG2	c.G5564C	p.S1855T
XH_P56	1	152681680	152681680	In_Frame_Ins	INS	-	CTGGGGGGCTG	-	LCEA4	10+6delAGCTCTGGGGG	43delinsSSSGGCC
XH_P56	1	155264115	155264115	Missense_Mutation	SNP	C	T	C	PKLR	c.G1027A	p.E343K
XH_P56	1	169080621	169080621	Silent	SNP	A	G	A	ATP1B1	c.A111G	p.L37L
XH_P56	1	170928671	170928671	Missense_Mutation	SNP	T	C	T	MROH9	c.T221C	p.V74A
XH_P56	1	176175838	176175838	Missense_Mutation	SNP	C	T	C	RWD2	c.G277A	p.A93T
XH_P56	1	180031445	180031445	Nonsense_Mutation	SNP	C	T	C	CEP350	c.C5353T	p.R1785X
XH_P56	1	197069842	197069842	Missense_Mutation	SNP	G	A	G	ASPM	c.C8539T	p.L2847F
XH_P56	1	202287754	202287754	Missense_Mutation	SNP	G	A	G	LGR6	c.G1906A	p.V636M
XH_P56	1	224606084	224606084	Silent	SNP	C	T	C	WDR26	c.G849A	p.R283R
XH_P56	1	226413377	226413377	In_Frame_Ins	INS	-	GCAGCTTTTATT	-	MIXL1	38insAGCAGCTTT	196delinsKAAFI
XH_P56	1	228412227	228412227	Silent	SNP	T	C	T	OBSCN	c.T2721C	p.S907S
XH_P56	1	228412308	228412308	Silent	SNP	G	A	G	OBSCN	c.G2802A	p.S934S
XH_P56	1	231830299	231830299	Silent	SNP	C	T	C	DISC1	c.C795T	p.P265P
XH_P56	1	235377189	235377189	In_Frame_Ins	INS	-	TAATGCACCAAG	-	ARID4B	CCTTTACTTGGT	79delinsFTWCITAD
XH_P56	1	248112823	248112823	Missense_Mutation	SNP	T	C	T	OR2L8	c.T664C	p.F22L
XH_P56	1	248737167	248737167	Missense_Mutation	SNP	G	A	G	OR2T34	c.C892T	p.R298C
XH_P56	2	8822601	8822601	Silent	SNP	G	A	G	ID2	c.G306A	p.P102P
XH_P56	2	24244783	24244783	Silent	SNP	G	A	G	MFS2B	c.G837A	p.R279R
XH_P56	2	24522987	24522987	Frame_Shift_Ins	INS	-	CTGGGCTTTAC	-	ITSN2	5insAACGTAAAC	p.E379fs
XH_P56	2	43818047	43818047	Missense_Mutation	SNP	G	T	G	THADA	c.C218A	p.P73H
XH_P56	2	71891501	71891501	Missense_Mutation	SNP	G	A	G	DYSF	c.G4948A	p.V1650I
XH_P56	2	74043601	74043601	Missense_Mutation	SNP	C	A	C	C2orf18	c.C2251A	p.P751T
XH_P56	2	85843529	85843529	Missense_Mutation	SNP	C	T	C	USP39	c.C211T	p.R71W
XH_P56	2	98165926	98165926	Missense_Mutation	SNP	A	G	A	ANKRD36B	c.T1433C	p.L478S
XH_P56	2	127657553	127657553	In_Frame_Ins	INS	-	CCTGTGGTGAG	-	TEX51	10+6delGAGTCTCTGGG	8delinsNESCGEYAW
XH_P56	2	135988476	135988476	Missense_Mutation	SNP	C	T	C	ZRANB3	c.G1561A	p.D521N
XH_P56	2	160025832	160025832	Missense_Mutation	SNP	A	G	A	TANC1	c.A436G	p.I146V
XH_P56	2	165947635	165947635	Silent	SNP	G	A	G	SCN3A	c.C4881T	p.N1627N
XH_P56	2	170493662	170493662	Missense_Mutation	SNP	G	C	G	PIIG	c.G1894C	p.E632Q
XH_P56	2	178482596	178482596	Silent	SNP	T	G	T	TTCC30A	c.A834C	p.P278P
XH_P56	2	181922458	181922458	Nonsense_Mutation	SNP	C	A	C	UBE2E3	c.C284A	p.S59X

XH_P56	2	219029532	219029532	Missense_Mutation	SNP	G	A	G	CXCR1	c.C403T	p.R135C
XH_P56	2	238991960	238991960	Silent	SNP	A	T	A	SLCY	c.A873T	p.L291L
XH_P56	2	240003870	240003870	Silent	SNP	G	A	G	HDAC4	c.C2565T	p.P855P
XH_P56	2	242756281	242756281	Missense_Mutation	SNP	G	A	G	NEU4	c.G433A	p.A145T
XH_P56	3	24169080	24169080	Missense_Mutation	SNP	C	T	C	THRB	c.G1054A	p.A352T
XH_P56	3	66313795	66313795	Missense_Mutation	SNP	T	G	T	SLC25A26	c.T181G	p.L61V
XH_P56	3	72495654	72495654	Frame_Shift_Ins	INS	-	G	-	RYBP	c.120dupC	p.S41fs
XH_P56	3	98250972	98250972	Missense_Mutation	SNP	C	T	C	GPR15	c.C95T	p.T32I
XH_P56	3	112993367	112993367	Silent	SNP	G	A	G	BOC	c.G1380A	p.P460P
XH_P56	3	119379090	119379090	Missense_Mutation	SNP	A	G	A	POPOC2	c.T181C	p.Y61H
XH_P56	3	122420142	122420142	Missense_Mutation	SNP	G	A	G	PARP14	c.G2741A	p.R914Q
XH_P56	3	124201679	124201679	Missense_Mutation	SNP	G	C	G	KALRN	c.G4060C	p.A1354P
XH_P56	3	124201680	124201680	In_Frame_Ins	INS	-	CTCAGAGTTAC	-	KALRN	TCTCCTCTCAGAA54delinsAFSSQSSHTC	
XH_P56	3	128344375	128344375	Splice_Site	DEL	A	-	A	RPN1	-	
XH_P56	3	130095126	130095126	Silent	SNP	C	G	C	COL6A5	c.C114G	p.S38S
XH_P56	3	137880741	137880741	In_Frame_Del	DEL	TCG	-	TCG	DBR1	c.1623_1625del	p.541_542del
XH_P56	3	138724757	138724757	Silent	SNP	C	G	C	PRR23A	c.G354C	p.S118S
XH_P56	3	179616003	179616003	Missense_Mutation	SNP	A	G	A	PEXS1	c.T53C	p.V18A
XH_P56	3	195507326	195507326	Missense_Mutation	SNP	G	C	G	MUC4	c.C11125G	p.H3709D
XH_P56	4	39757308	39757308	Missense_Mutation	SNP	A	G	A	UBE2K	c.A95G	p.N32S
XH_P56	4	40404215	40404215	Silent	SNP	T	C	T	RBM47	c.A696G	p.E232E
XH_P56	4	41748011	41748028	In_Frame_Del	DEL	CGCCGCTGG	-	GCCGCCGCTGCC	PHOX2B	c.741_758del	p.247_253del
XH_P56	4	57777265	57777265	Missense_Mutation	SNP	C	T	C	REST	c.C461T	p.S154L
XH_P56	4	70079838	70079838	Silent	SNP	T	C	T	UGT2B11	c.A603G	p.L201L
XH_P56	4	80905990	80905990	Frame_Shift_Del	DEL	C	-	C	ANTXR2	c.1069delG	p.A357fs
XH_P56	4	146461191	146461191	In_Frame_Ins	INS	-	GTACCCAAACT	-	SMAD1	TAGCAGTTACCC12delinsPIAVTQTL	
XH_P56	4	170913027	170913027	Silent	SNP	C	T	C	MFAP3L	c.G423A	p.P141P
XH_P56	5	231111	231111	Silent	SNP	T	C	T	SDHA	c.T747C	p.P249P
XH_P56	5	14487614	14487616	In_Frame_Del	DEL	GGC	-	GGC	TRIO	c.6877_6879del	p.2293_2293del
XH_P56	5	32711981	32711981	Silent	SNP	C	T	C	NPR3	c.C99T	p.G33G
XH_P56	5	33467715	33467715	Missense_Mutation	SNP	G	A	G	TAR5	c.G2074A	p.D692N
XH_P56	5	36143277	36143277	Splice_Site	SNP	C	T	C	LMBRD2	-	
XH_P56	5	53815495	53815495	Missense_Mutation	SNP	A	C	A	SNX18	c.A1713C	p.E571D
XH_P56	5	54771275	54771275	Missense_Mutation	SNP	C	G	C	PLPP1	c.G62C	p.G21A
XH_P56	5	79950724	79950724	Missense_Mutation	SNP	G	C	G	MSH3	c.G178C	p.A60P
XH_P56	5	83360532	83360532	Silent	SNP	G	A	G	EDIL3	c.C909T	p.G303G
XH_P56	5	89933649	89933649	Silent	SNP	C	A	C	ADGRV1	c.C2124A	p.G708G
XH_P56	5	94224593	94224593	Missense_Mutation	SNP	C	T	C	MCTP1	c.G1123A	p.D375N
XH_P56	5	121187717	121187717	Missense_Mutation	SNP	G	A	G	FTMT	c.G59A	p.R20H
XH_P56	5	140215088	140215088	Missense_Mutation	SNP	G	A	G	PCDHA7	c.G1120A	p.V374M
XH_P56	5	140530448	140530448	Nonsense_Mutation	SNP	C	T	C	PCDH86	c.C610T	p.C204X
XH_P56	5	160886675	160886675	Missense_Mutation	SNP	C	T	C	GABRB2	c.G413A	p.R138H
XH_P56	5	168176571	168176571	Silent	SNP	C	T	C	SLIT3	c.G2043A	p.R681R
XH_P56	5	177649524	177649524	Silent	SNP	G	A	G	PHYKPL	c.C636T	p.G212G
XH_P56	5	178410151	178410151	Silent	SNP	C	T	C	GRM6	c.G2196A	p.T732T
XH_P56	5	180219039	180219039	Silent	SNP	C	T	C	MGAT1	c.G933A	p.T311T
XH_P56	6	11185790	11185790	Missense_Mutation	SNP	C	T	C	NEDD9	c.G1663A	p.D555N
XH_P56	6	11538534	11538534	Silent	SNP	C	T	C	TMEM170B	c.C24T	p.H8H
XH_P56	6	35430691	35430691	Silent	SNP	C	T	C	FANCE	c.C1509T	p.N503N
XH_P56	6	43323069	43323069	Missense_Mutation	SNP	C	T	C	ZNF318	c.G2003A	p.R668Q
XH_P56	6	52878626	52878627	Frame_Shift_Del	DEL	GG	-	GG	ICK	c.985_986del	p.P329fs
XH_P56	6	52878627	52878627	Frame_Shift_Ins	INS	-	TTATTCTCT	-	ICK	4_985insAGGA	p.P329fs
XH_P56	6	54095524	54095524	Missense_Mutation	SNP	C	T	C	MLIP	c.C1126T	p.P376S
XH_P56	6	102250273	102250273	Missense_Mutation	SNP	A	T	A	GRIK2	c.A1163T	p.D388V
XH_P56	6	108985176	108985176	Frame_Shift_Ins	INS	-	G	-	FOXO3	c.1141dupG	p.D380fs
XH_P56	6	111697475	111697475	Missense_Mutation	SNP	G	A	G	REV3L	c.C2083T	p.R695C
XH_P56	6	135517027	135517027	In_Frame_Ins	INS	-	CTTCTGCTCTCT	-	MYB	insTTTCTTCTGT329delinsLSSVLSL	
XH_P56	6	135517029	135517029	In_Frame_Ins	INS	-	TTTCTACAC	-	MYB	7_988insTTTCTA1329delinsLFLH	
XH_P56	6	144508188	144508188	Missense_Mutation	SNP	G	A	G	STX11	c.G424A	p.A142T
XH_P56	6	151152390	151152390	Missense_Mutation	SNP	G	A	G	PLEKHG1	c.G2026A	p.A676T
XH_P56	6	159044589	159044589	Missense_Mutation	SNP	G	A	G	TMEM181	c.G1315A	p.E439K
XH_P56	6	159065737	159065737	Frame_Shift_Del	DEL	C	-	C	DYNLT1	c.4delG	p.E2fs
XH_P56	6	159653559	159653559	Missense_Mutation	SNP	C	T	C	FNDC1	c.C2015T	p.P672L
XH_P56	6	166572005	166572005	Missense_Mutation	SNP	T	C	T	T	c.A932G	p.N311S
XH_P56	7	2946461	2946461	Silent	SNP	T	C	T	CARD11	c.A3276G	p.R1092R
XH_P56	7	5340182	5340182	Missense_Mutation	SNP	G	A	G	SLC29A4	c.G1339A	p.A447T
XH_P56	7	43916825	43916825	Missense_Mutation	SNP	T	C	T	URGPC	c.A2210G	p.D737G
XH_P56	7	72418992	72418992	Missense_Mutation	SNP	C	T	C	POM121	c.C2983T	p.P995S
XH_P56	7	82584496	82584496	Frame_Shift_Ins	INS	-	C	-	PCLO	-5772_5773ins	p.T1925fs
XH_P56	7	82584497	82584497	Nonsense_Mutation	INS	-	GATTATAAATA	-	PCLO	AGGATTATATTAA1925delinsNRGLYX	
XH_P56	7	89936367	89936367	Missense_Mutation	SNP	C	G	C	CFAP69	c.C2418G	p.S806R
XH_P56	7	94055071	94055071	Missense_Mutation	SNP	G	A	G	COL1A2	c.G2845A	p.G949S
XH_P56	7	98254301	98254301	Silent	SNP	C	T	C	NPTX2	c.C711T	p.Y237Y
XH_P56	7	99796146	99796146	Silent	SNP	A	C	A	STAG3	c.A1119C	p.P373P
XH_P56	7	99821544	99821544	Silent	SNP	G	A	G	GATS	c.C372T	p.S124S
XH_P56	7	100677944	100677944	Missense_Mutation	SNP	T	C	T	MUC17	c.T3247C	p.S1083P
XH_P56	7	102296718	102296718	Silent	SNP	T	C	T	SPDY2	c.T634C	p.T212L
XH_P56	7	139724415	139724415	Missense_Mutation	SNP	G	A	G	PARP12	c.C2051T	p.S684L
XH_P56	7	150912100	150912100	Silent	SNP	C	T	C	ABCF2	c.G1599A	p.Q533Q
XH_P56	7	151945334	151945334	Missense_Mutation	SNP	T	C	T	KMT2C	c.A2185G	p.N729D
XH_P56	7	156469123	156469123	Missense_Mutation	SNP	G	A	G	RNF32	c.G863A	p.R288Q
XH_P56	8	22064904	22064904	Missense_Mutation	SNP	T	C	T	BMP1	c.T2450C	p.V817A
XH_P56	8	24357762	24357762	Silent	SNP	T	C	T	ADAM7	c.T1995C	p.H665H
XH_P56	8	27737198	27737198	Silent	SNP	A	G	A	SCARA5	c.T1239C	p.R413R
XH_P56	8	52733148	52733148	Missense_Mutation	SNP	C	G	C	PCMTD1	c.G609C	p.K203N
XH_P56	8	87076719	87076719	Frame_Shift_Ins	INS	-	CCTGAGCAATGA	-	PSKH2	TCGACTCATTCG	p.L109fs
XH_P56	8	106813385	106813385	Missense_Mutation	SNP	A	T	A	ZFPM2	c.A1075T	p.T359S
XH_P56	8	106813387	106813387	Frame_Shift_Ins	INS	-	TGAAATGGAA	-	ZFPM2	AGGAGTGAAAA	p.T359fs
XH_P56	8	134488007	134488007	Silent	SNP	G	A	G	ST3GAL1	c.C261T	p.T87T
XH_P56	8	142228909	142228909	Missense_Mutation	SNP	G	A	G	SLC45A4	c.C677T	p.P226L
XH_P56	8	144411541	144411541	Missense_Mutation	SNP	G	T	G	TOP1MT	c.C45A	p.N15K
XH_P56	9	32418375	32418375	Missense_Mutation	SNP	G	T	G	ACO1	c.G524T	p.G175V
XH_P56	9	33442323	33442323	Missense_Mutation	SNP	G	A	G	AQP3	c.C686T	p.A229V
XH_P56	9	35398908	35398908	Missense_Mutation	SNP	G	A	G	UNC13B	c.G3704A	p.R1235Q
XH_P56	9	79320596	79320596	Missense_Mutation	SNP	G	T	G	PRUNE2	c.C6594A	p.D2198E
XH_P56	9	79930167	79930167	Splice_Site	SNP	A	T	A	VPS13A	-	
XH_P56	9	90534206	90534206	Missense_Mutation	SNP	T	C	T	SPATA31C1	c.T226C	p.C76R
XH_P56	9	96015256	96015256	Silent	SNP	C	T	C	WNK2	c.C1926T	p.D642D

XH_P56	9	96021312	96021312	Missense_Mutation	SNP	G	A	G	WNK2	c.G2482A	p.V828M
XH_P56	9	96097747	96097747	Missense_Mutation	SNP	C	T	C	C9orf129	c.G274A	p.G925
XH_P56	9	98209594	98209594	Missense_Mutation	SNP	G	A	G	PTCH1	c.C3944T	p.P1315L
XH_P56	9	101748356	101748356	Missense_Mutation	SNP	A	G	A	COL15A1	c.A610G	p.M204V
XH_P56	9	101830849	101830849	Missense_Mutation	SNP	T	C	T	COL15A1	c.T3850C	p.F1284L
XH_P56	9	110249505	110249505	Silent	SNP	C	T	C	KLFA	c.G1170A	p.G390G
XH_P56	9	115030443	115030443	Silent	SNP	G	A	G	PTBP3	c.C36T	p.A12A
XH_P56	9	117050998	117050998	Missense_Mutation	SNP	G	A	G	COL27A1	c.G4061A	p.R1354Q
XH_P56	9	117827141	117827141	Missense_Mutation	SNP	C	A	C	TNC	c.G3272T	p.R1091I
XH_P56	9	119093529	119093529	Nonsense_Mutation	SNP	C	T	C	PAPPA	c.C3154T	p.R1052X
XH_P56	9	140242634	140242634	Silent	SNP	G	C	G	EXD3	c.C1887G	p.A629A
XH_P56	10	12131081	12131081	Missense_Mutation	SNP	T	G	T	DHTKD1	c.T814G	p.Y272D
XH_P56	10	26463315	26463315	Frame_Shift_Ins	INS	-	CTTTTTC	-	MYO3A	22_4123insCTTT	p.F1374fs
XH_P56	10	26463317	26463317	Missense_Mutation	SNP	A	T	A	MYO3A	c.A4124T	p.K1375M
XH_P56	10	43291958	43291958	Missense_Mutation	SNP	G	C	G	BMS1	c.G1266C	p.L422F
XH_P56	10	43292573	43292573	Missense_Mutation	SNP	G	C	G	BMS1	c.G1881C	p.Q627H
XH_P56	10	99531565	99531567	In_Frame_Del	DEL	CCC	-	CCC	SFRP5	c.24_26del	p.8_9del
XH_P56	10	114889731	114889731	Nonsense_Mutation	INS	-	AAAAACTTTCTC	-	TCF7L2	insTAAAAAAAC	p.L36delinsLX
XH_P56	10	135051653	135051653	Missense_Mutation	SNP	A	G	A	VENTX	c.A235G	p.M79V
XH_P56	11	1271381	1271383	In_Frame_Del	DEL	TGA	-	TGA	MUC5B	13271_13273del	p.4424_4425del
XH_P56	11	1769349	1769349	Missense_Mutation	SNP	C	T	C	IFITM10	c.G85A	p.A29T
XH_P56	11	2937871	2937871	Silent	SNP	C	T	C	SLC22A18	c.C262T	p.L88L
XH_P56	11	6816096	6816096	Silent	SNP	G	A	G	OR6A2	c.C844T	p.L282L
XH_P56	11	17632651	17632651	Missense_Mutation	SNP	C	T	C	OTOG	c.C5840T	p.T1947M
XH_P56	11	19955194	19955194	Missense_Mutation	SNP	G	C	G	NAV2	c.G1212C	p.Q404H
XH_P56	11	30942383	30942383	Missense_Mutation	SNP	G	A	G	DCDC1	c.C554T	p.P185L
XH_P56	11	46958292	46958292	Silent	SNP	G	A	G	C11orf49	c.G12A	p.E4E
XH_P56	11	46958293	46958293	Missense_Mutation	SNP	A	G	A	C11orf49	c.A13G	p.R5G
XH_P56	11	47256858	47256858	Silent	SNP	G	A	G	DBB2	c.G918A	p.T306T
XH_P56	11	48387780	48387780	Missense_Mutation	SNP	C	T	C	OR4C5	c.G238A	p.V80M
XH_P56	11	48510786	48510786	Missense_Mutation	SNP	G	T	G	OR4A47	c.G442T	p.V148F
XH_P56	11	65385977	65385977	Missense_Mutation	SNP	C	T	C	PCNX3	c.C1144T	p.R382W
XH_P56	11	65417434	65417434	Silent	SNP	G	A	G	SIPA1	c.G2760A	p.A920A
XH_P56	11	66411364	66411384	In_Frame_Del	DEL	GCTGCAGCA	-	TGCTGCAGCAG	RBM14-RBM4	c.781_801del	p.261_267del
XH_P56	11	67888436	67888447	In_Frame_Del	DEL	SCAGCGGCA	-	GCAGCGCGAG	CHKA	c.198_209del	p.66_70del
XH_P56	11	69063136	69063136	Silent	SNP	C	T	C	MYEOV	c.C45T	p.A15A
XH_P56	11	69063728	69063728	Missense_Mutation	SNP	G	C	G	MYEOV	c.G637C	p.G213R
XH_P56	11	71944012	71944012	Nonsense_Mutation	SNP	C	T	C	INPPL1	c.C1945T	p.R649X
XH_P56	11	74651911	74651911	Frame_Shift_Ins	INS	-	ATGGGACT	-	XRRR1	2_13insAGTCC	p.G5fs
XH_P56	11	75139624	75139624	Missense_Mutation	SNP	C	T	C	KLHL35	c.G929A	p.R310H
XH_P56	11	82874775	82874775	Missense_Mutation	SNP	A	G	A	PCF11	c.A373G	p.I125V
XH_P56	11	118352707	118352707	Frame_Shift_Ins	INS	-	TT	-	KMT2A	.3912_3913insT	p.V1304fs
XH_P56	11	118352708	118352708	Frame_Shift_Ins	INS	-	GACTTTT	-	KMT2A	13_3914insGAC	p.L1305fs
XH_P56	11	119206375	119206375	Silent	SNP	G	A	G	RNF26	c.G543A	p.T181T
XH_P56	12	2062350	2062350	In_Frame_Ins	INS	-	TGG	-	DCP1B	c.755_756insCC	p.Q252delinsHQ
XH_P56	12	11338669	11338669	Missense_Mutation	SNP	C	T	C	TAS2R42	c.G875A	p.R292Q
XH_P56	12	21711172	21711172	Missense_Mutation	SNP	G	A	G	GSY2	c.C1384T	p.R462W
XH_P56	12	23818475	23818475	Missense_Mutation	SNP	T	A	T	SOX5	c.A804T	p.L268F
XH_P56	12	31825298	31825298	Frame_Shift_Ins	INS	-	TTTAATTATTTTA	-	AMN1	insCAATAAAATA	p.E239fs
XH_P56	12	48737166	48737166	Nonsense_Mutation	SNP	G	A	G	ZNFG41	c.C838T	p.R280X
XH_P56	12	53201534	53201534	Missense_Mutation	SNP	C	T	C	KRT4	c.G1240A	p.E414K
XH_P56	12	53204550	53204550	Missense_Mutation	SNP	A	G	A	KRT4	c.T728C	p.V243A
XH_P56	12	55688550	55688550	Missense_Mutation	SNP	G	T	G	OR6C6	c.C467A	p.P156H
XH_P56	12	57548466	57548466	Silent	SNP	C	T	C	LRP1	c.C1209T	p.T403T
XH_P56	12	57589659	57589659	Silent	SNP	C	T	C	LRP1	c.C8574T	p.C2858C
XH_P56	12	64011087	64011087	Silent	SNP	C	T	C	DPY19L2	c.G1215A	p.T405T
XH_P56	12	75601182	75601182	Silent	SNP	G	A	G	KCNC2	c.C582T	p.D194D
XH_P56	12	76424934	76424934	Frame_Shift_Del	DEL	C	-	C	PHLDA1	c.588delG	p.Q196fs
XH_P56	12	76424936	76424940	Frame_Shift_Del	DEL	GTTGC	-	GTTGC	PHLDA1	c.582_586del	p.Q194fs
XH_P56	12	109354738	109354738	Missense_Mutation	SNP	C	T	C	SVOP	c.G380A	p.R127Q
XH_P56	12	111894026	111894026	Frame_Shift_Ins	INS	-	AGTAGAATGT	-	ATXN2	2630insACATT	p.L877fs
XH_P56	12	116406904	116406904	Splice_Site	INS	-	GTTCCTACTGCA	-	MED13L	-	-
XH_P56	12	118681299	118681299	Nonsense_Mutation	INS	-	TTATCAGTATT	-	TAOK3	insTTAAATACTC	p.V73delinsVKYX
XH_P56	12	118681301	118681301	Missense_Mutation	SNP	C	A	C	TAOK3	c.G213T	p.K71N
XH_P56	12	124272495	124272495	Silent	SNP	C	T	C	DNAH10	c.C1383T	p.F461F
XH_P56	12	124798801	124798801	Silent	SNP	C	T	C	RFLNA	c.C138T	p.P46P
XH_P56	12	132547093	132547093	Frame_Shift_Ins	INS	-	G	-	EP400	c.8181_8182ins	p.Q2727fs
XH_P56	12	133733061	133733061	Missense_Mutation	SNP	G	A	G	ZNFG10	c.G1229A	p.C410Y
XH_P56	13	24892981	24892981	Silent	SNP	G	A	G	C1QTNF9	c.G192A	p.P64P
XH_P56	13	25670984	25670984	Frame_Shift_Ins	INS	-	AT	-	PABPC3	c.648_649insAT	p.P216fs
XH_P56	13	28877424	28877424	Silent	SNP	G	A	G	FLT1	c.C3897T	p.H1299H
XH_P56	13	42877873	42877873	Missense_Mutation	SNP	G	A	G	AKAP11	c.G4991A	p.R1664Q
XH_P56	13	77574983	77574983	Missense_Mutation	SNP	A	G	A	CLN5	c.A1103G	p.K368R
XH_P56	13	95363659	95363659	In_Frame_Ins	INS	-	CGGGAAGAAGA	-	SOX21	insACGCGTCTCTCT	p.15delinsARVFFPQS
XH_P56	13	100622668	100622673	In_Frame_Del	DEL	GCGCGG	-	GCGCGG	ZIC5	c.1257_1262del	p.419_421del
XH_P56	13	110435953	110435953	Silent	SNP	A	G	A	IRS2	c.T2448C	p.C816C
XH_P56	14	20528362	20528362	Silent	SNP	A	G	A	OR4L1	c.A159G	p.S53S
XH_P56	14	20528449	20528467	Frame_Shift_Del	DEL	ATTGTGCTCA	-	AGATTGTGCTCA	OR4L1	c.246_264del	p.I82fs
XH_P56	14	23371268	23371268	Silent	SNP	A	G	A	RBM23	c.T1065C	p.A355A
XH_P56	14	23853741	23853741	Silent	SNP	C	T	C	MYH6	c.G5475A	p.E1825E
XH_P56	14	38061912	38061912	Missense_Mutation	SNP	T	C	T	FOXA1	c.A77G	p.Y26C
XH_P56	14	51411029	51411029	Silent	SNP	A	G	A	PYGL	c.T93C	p.S31S
XH_P56	14	53020156	53020156	Silent	SNP	C	T	C	GPR137C	c.C291T	p.T97T
XH_P56	14	60749642	60749642	Frame_Shift_Ins	INS	-	T	-	PPM1A	c.222dupT	p.H74fs
XH_P56	14	61747542	61747542	Silent	SNP	C	G	C	TMEM30B	c.G324C	p.V108V
XH_P56	14	67382766	67382766	Missense_Mutation	SNP	G	C	G	GPNN	c.G436C	p.G146R
XH_P56	14	67787809	67787809	Missense_Mutation	SNP	G	A	G	MPP5	c.G1471A	p.G491S
XH_P56	14	75265453	75265453	Silent	SNP	C	T	C	YLP1	c.C3453T	p.G1151G
XH_P56	14	77493833	77493911	Frame_Shift_Del	DEL	GCGCGCGCT	-	CGCGCGCGCTC	IRF2BPL	c.225_303del	p.P75fs
XH_P56	14	93424571	93424571	Silent	SNP	G	A	G	ITPK1	c.C645T	p.L215L
XH_P56	14	100613141	100613141	Missense_Mutation	SNP	G	A	G	DEGS2	c.C929T	p.A310V
XH_P56	14	105417527	105417527	Missense_Mutation	SNP	C	T	C	AHNAK2	c.G3961A	p.V1321M
XH_P56	14	105420201	105420201	In_Frame_Ins	INS	-	CTCTGTAGTCT	-	AHNAK2	GAGGAAGGACdelinsGDGEEGLQRTTRIT	-
XH_P56	15	22369068	22369068	Nonsense_Mutation	SNP	C	T	C	OR4M2	c.C493T	p.R165X
XH_P56	15	41611955	41611955	Missense_Mutation	SNP	C	T	C	OIP5	c.G413A	p.G138D
XH_P56	15	42579914	42579914	Missense_Mutation	SNP	G	A	G	GANC	c.G227A	p.G76D
XH_P56	15	57535728	57535728	Missense_Mutation	SNP	G	A	G	TCF12	c.G386A	p.G129E
XH_P56	15	72502815	72502815	Missense_Mutation	SNP	T	C	T	PKM	c.A206G	p.H69R

XH_P56	15	82456227	82456227	Missense_Mutation	SNP	T	C	T	EFL1	c.A1696G	p.I566V
XH_P56	15	82935129	82935129	Missense_Mutation	SNP	C	G	C	GOLGA6L10	c.G451C	p.E151Q
XH_P56	15	85400106	85400106	Missense_Mutation	SNP	G	A	G	ALPK3	c.G2743A	p.E915K
XH_P56	15	91557072	91557072	Nonsense_Mutation	SNP	G	A	G	VP53B	c.C238T	p.R80X
XH_P56	16	1270385	1270385	Silent	SNP	C	T	C	CACNA1H	c.C6435T	p.D2145D
XH_P56	16	3534892	3534892	Missense_Mutation	SNP	G	A	G	NAA60	c.G539A	p.R180Q
XH_P56	16	29994922	29994922	Silent	SNP	C	T	C	TAOK2	c.C1359T	p.S453S
XH_P56	16	30005460	30005460	Missense_Mutation	SNP	C	T	C	HIRIP3	c.G1006A	p.E336K
XH_P56	16	30018500	30018500	Silent	SNP	C	T	C	DOC2A	c.G648A	p.Q216Q
XH_P56	16	55527205	55527205	Missense_Mutation	SNP	G	A	G	MMP2	c.G1322A	p.R441Q
XH_P56	16	66943221	66943221	Missense_Mutation	SNP	G	A	G	CDH16	c.C2050T	p.P684S
XH_P56	16	66975745	66975745	Silent	SNP	G	A	G	CES2	c.G1323A	p.T441T
XH_P56	16	67969552	67969552	Frame_Shift_Ins	INS	-	AGGT	-	PSMB10	431_432insACC	p.L144fs
XH_P56	16	79633709	79633709	Missense_Mutation	SNP	C	T	C	MAF	c.G91A	p.E31K
XH_P56	16	89017077	89017077	Missense_Mutation	SNP	A	T	A	LOC100129697	c.A551T	p.H184L
XH_P56	16	89985940	89985940	Missense_Mutation	SNP	G	A	G	MC1R	c.G274A	p.V92M
XH_P56	17	15905291	15905291	Silent	SNP	C	T	C	TTC19	c.C54T	p.L18L
XH_P56	17	18023800	18023800	Silent	SNP	C	T	C	MYO15A	c.C1686T	p.G562G
XH_P56	17	30185832	30185832	Missense_Mutation	SNP	C	T	C	COPR5	c.G8A	p.G3D
XH_P56	17	30221743	30221743	Missense_Mutation	SNP	G	A	G	UTP6	c.C233T	p.S78L
XH_P56	17	32959743	32959743	Silent	SNP	C	T	C	TMEM132E	c.C1503T	p.Y501Y
XH_P56	17	36876025	36876025	Missense_Mutation	SNP	G	A	G	MLLT6	c.G2032A	p.A647T
XH_P56	17	36891788	36891788	Frame_Shift_Ins	INS	-	G	-	PCGF2	c.722_723insC	p.V241fs
XH_P56	17	36891789	36891789	Nonsense_Mutation	INS	-	TCATTCAAAATTC	-	PCGF2	TGAAGAAATTTGA	42delinsASRGPVFAEEFEX
XH_P56	17	39406104	39406104	Silent	SNP	T	G	T	KRTAP9-4	c.T132G	p.V44V
XH_P56	17	39673185	39673185	Missense_Mutation	SNP	C	T	C	KRT15	c.G613A	p.V205I
XH_P56	17	40849742	40849742	Missense_Mutation	SNP	G	A	G	CNTNAP1	c.G3739A	p.E1247K
XH_P56	17	41908674	41908674	Missense_Mutation	SNP	G	A	G	MPP3	c.C235T	p.R79C
XH_P56	17	42239259	42239259	Nonstop_Mutation	SNP	A	C	A	C17orf53	c.A1566C	p.X522C
XH_P56	17	44073947	44073947	Missense_Mutation	SNP	C	T	C	MAPT	c.C565T	p.P189S
XH_P56	17	53038650	53038650	Missense_Mutation	SNP	G	A	G	COX11	c.C686T	p.T229M
XH_P56	17	59485555	59485555	Silent	SNP	C	T	C	TBX2	c.C1827T	p.S609S
XH_P56	17	74077797	74077797	Nonsense_Mutation	SNP	C	T	C	ZACN	c.C841T	p.Q281X
XH_P56	17	76130575	76130575	Missense_Mutation	SNP	A	T	A	TMC8	c.A917T	p.N306I
XH_P56	18	3879385	3879385	Silent	SNP	G	A	G	DLGAP1	c.C684T	p.P228P
XH_P56	19	1119019	1119019	Silent	SNP	C	T	C	SBNO2	c.G1347A	p.A449A
XH_P56	19	9066695	9066695	Missense_Mutation	SNP	C	T	C	MUC16	c.G20751A	p.M6917I
XH_P56	19	9070977	9070977	Nonsense_Mutation	INS	-	ATCATGACAAAA	-	MUC16	16469insTTTTG	R5490delinsLSX
XH_P56	19	11100042	11100042	Missense_Mutation	SNP	G	A	G	SMARCA4	c.G1168A	p.G390R
XH_P56	19	13058812	13058812	Frame_Shift_Del	DEL	A	-	A	RAD23A	c.223delA	p.M75fs
XH_P56	19	13319692	13319694	In_Frame_Del	DEL	GAT	-	GAT	CACNA1A	c.6659_6661del	p.2220_2221del
XH_P56	19	15223218	15223218	Missense_Mutation	SNP	G	A	G	SYDE1	c.G1439A	p.R480H
XH_P56	19	15302325	15302325	Missense_Mutation	SNP	C	T	C	NOTCH3	c.G946A	p.D316N
XH_P56	19	22155473	22155473	Missense_Mutation	SNP	C	T	C	ZNF208	c.G2363A	p.R788Q
XH_P56	19	33623225	33623225	Silent	SNP	G	A	G	WDR88	c.G150A	p.P50P
XH_P56	19	34983953	34983953	Missense_Mutation	SNP	C	T	C	WTIP	c.C781T	p.R261C
XH_P56	19	35435069	35435069	Missense_Mutation	SNP	A	G	A	ZNF30	c.A1202G	p.Y401C
XH_P56	19	35449082	35449082	Silent	SNP	G	A	A	ZNF792	c.C1677T	p.D559D
XH_P56	19	38231072	38231072	Missense_Mutation	SNP	T	A	T	ZNF573	c.A55T	p.I19F
XH_P56	19	38378646	38378646	Missense_Mutation	SNP	T	C	T	WDR87	c.A5665G	p.K1889E
XH_P56	19	38572367	38572367	In_Frame_Ins	INS	-	ACCACC	-	SIPA1L3	62_163insACCA	p.P54delinsPTT
XH_P56	19	38800176	38800176	Missense_Mutation	SNP	G	A	G	YIF1B	c.C121T	p.P41S
XH_P56	19	39369877	39369877	Missense_Mutation	SNP	G	C	G	SIRT2	c.C977G	p.P326R
XH_P56	19	39877162	39877162	Missense_Mutation	SNP	T	A	T	PAF1	c.A1113T	p.E371D
XH_P56	19	39877164	39877164	Frame_Shift_Ins	INS	-	GTGGAGAGAGA	-	PAF1	GGTTTCATCTCT	p.E371fs
XH_P56	19	39964755	39964755	Missense_Mutation	SNP	C	T	C	SUPT5H	c.C2633T	p.P878L
XH_P56	19	44777527	44777527	Silent	SNP	T	C	T	ZNF233	c.T714C	p.N238N
XH_P56	19	45899957	45900033	Frame_Shift_Del	DEL	AAAGGCGTG	-	GAAAGGCGTGG	PPP1R13L	c.482_558del	p.P161fs
XH_P56	19	46388379	46388379	Silent	SNP	C	G	G	IRF2BP1	c.G654C	p.P128R
XH_P56	19	47969310	47969310	Silent	SNP	G	A	G	SLC8A2	c.C351T	p.S117S
XH_P56	19	48198190	48198190	Missense_Mutation	SNP	G	A	G	BICRA	c.G2929A	p.G977R
XH_P56	19	50354211	50354211	Missense_Mutation	SNP	C	T	C	PTOV1	c.C74T	p.S25L
XH_P56	19	53667804	53667804	Missense_Mutation	SNP	C	T	C	ZNF665	c.G1939A	p.V647I
XH_P56	19	54973722	54973722	Missense_Mutation	SNP	C	T	C	LENG9	c.G988A	p.A330T
XH_P56	19	55994240	55994240	Silent	SNP	C	T	C	ZNF628	c.C1680T	p.H560H
XH_P56	19	57176304	57176304	Missense_Mutation	SNP	T	G	T	ZNF835	c.A263C	p.E88A
XH_P56	20	2464742	2464742	Missense_Mutation	SNP	G	A	G	ZNF343	c.C595T	p.R199C
XH_P56	20	33328812	33328812	Missense_Mutation	SNP	A	C	A	NCOA6	c.T5248G	p.S1570A
XH_P56	20	33328813	33328813	Frame_Shift_Ins	INS	-	CA	-	NCOA6	5246_5247insT	p.T1749fs
XH_P56	20	34095984	34095984	Missense_Mutation	SNP	C	T	C	CEP250	c.C4975T	p.R1659C
XH_P56	20	42089647	42089647	Missense_Mutation	SNP	C	T	C	SRSF6	c.C979T	p.R327C
XH_P56	20	42204957	42204957	In_Frame_Ins	INS	-	TTC	-	SGK2	c.967_968insTTG	p.D323delinsVH
XH_P56	20	42204958	42204958	In_Frame_Ins	INS	-	GGTGATCTCCA	-	SGK2	5CATGGGTGATC	3delinsDFAWVILQLFS
XH_P56	20	52193208	52193208	Missense_Mutation	SNP	C	T	C	ZNF217	c.G2095A	p.A699T
XH_P56	20	52193659	52193659	Silent	SNP	G	A	G	ZNF217	c.C1644T	p.T548T
XH_P56	20	55208517	55208517	Missense_Mutation	SNP	C	T	C	TFAP2C	c.C695T	p.S232L
XH_P56	20	62193019	62193019	Silent	SNP	C	T	C	HELZ2	c.G5064A	p.P1688P
XH_P56	20	62195220	62195220	Missense_Mutation	SNP	C	T	C	HELZ2	c.G3248A	p.R1083Q
XH_P56	21	10942717	10942717	Missense_Mutation	SNP	C	T	C	TPTE	c.G310A	p.V104I
XH_P56	21	35773137	35773137	Silent	SNP	C	T	C	C21orf140	c.G234A	p.A78A
XH_P56	21	45999908	45999908	Missense_Mutation	SNP	A	C	A	KRTAP10-5	c.T548G	p.F183C
XH_P56	21	46021335	46021335	Missense_Mutation	SNP	G	A	G	KRTAP10-7	c.G799A	p.V267M
XH_P56	21	46086718	46086718	Missense_Mutation	SNP	G	C	G	KRTAP12-2	c.C86G	p.S29C
XH_P56	21	46086719	46086719	Missense_Mutation	SNP	A	G	A	KRTAP12-2	c.T85C	p.S29P
XH_P56	21	46875665	46875665	Missense_Mutation	SNP	C	T	C	COL18A1	c.C221T	p.A74V
XH_P56	22	16449086	16449086	Missense_Mutation	SNP	A	C	A	OR11H1	c.T719G	p.M240R
XH_P56	22	16449087	16449087	Missense_Mutation	SNP	T	C	T	OR11H1	c.A718G	p.M240V
XH_P56	22	17447218	17447218	Missense_Mutation	SNP	C	A	C	GAB4	c.G1060T	p.A354S
XH_P56	22	18655973	18655973	Silent	SNP	C	T	C	USP18	c.C948T	p.S316S
XH_P56	22	18655975	18655975	Frame_Shift_Ins	INS	-	GACTT	-	USP18	950_951insGAC	p.G317fs
XH_P56	22	20825666	20825666	Missense_Mutation	SNP	C	G	C	KLHL22	c.G364C	p.E122Q
XH_P56	22	50988183	50988183	Missense_Mutation	SNP	G	C	G	KLHDC7B	c.G1588C	p.A530P
XH_P56	X	3241737	3241737	Silent	SNP	C	T	C	MXRA5	c.G1989A	p.T663T
XH_P56	X	42636789	42636789	Missense_Mutation	SNP	G	A	G	PPP1R2P9	c.C542T	p.T181I
XH_P56	X	49179717	49179717	Silent	SNP	A	G	A	GAGE12J	c.A45G	p.R15R
XH_P56	X	55103917	55103917	Silent	SNP	G	T	G	PAGE2B	c.G279T	p.G93G
XH_P56	X	135428334	135428334	Silent	SNP	G	A	G	ADGRG4	c.G2469A	p.T823T
XH_P56	X	147088249	147088249	Missense_Mutation	SNP	C	T	C	FMR1NB	c.C425T	p.A142V

XH_P56	X	151821277	151821277	Missense_Mutation	SNP	T	A	T	GABRQ	c.T1432A	p.F478I
XH_P56	Y	2821990	2821990	Missense_Mutation	SNP	G	A	G	ZFY	c.G13A	p.E5K
XH_P56	Y	9325168	9325168	Missense_Mutation	SNP	G	A	G	TSPY10	c.G229A	p.V77M
XH_P56	1	150939039	150939039	Silent	SNV	G	A	A	CERS2	c.915C>T	p.F305F
XH_P56	1	197069842	197069842	Missense_Mutation	SNV	G	A	A	ASPM	c.8539C>T	p.L2847F
XH_P56	1	224606084	224606084	Silent	SNV	C	T	T	WDR26	c.849G>A	p.R283R
XH_P56	1	7723711	7723711	Silent	SNV	C	T	T	CAMTA1	c.1104C>T	p.S368S
XH_P56	10	43291958	43291958	Missense_Mutation	SNV	G	C	C	BMS1	c.1266G>C	p.L422F
XH_P56	10	43292573	43292573	Missense_Mutation	SNV	G	C	C	BMS1	c.1881G>C	p.P627H
XH_P56	11	108198432	108198432	Missense_Mutation	SNV	G	A	A	ATM	c.7036G>A	p.A2346T
XH_P56	11	108198433	108198433	Missense_Mutation	SNV	C	T	T	ATM	c.7037C>T	p.A2346V
XH_P56	11	1769349	1769349	Missense_Mutation	SNV	C	T	T	IFITM10	c.85G>A	p.A29T
XH_P56	11	2937871	2937871	Silent	SNV	C	T	T	SLC22A18	c.811C>T	p.L271L
XH_P56	11	30942383	30942383	Missense_Mutation	SNV	G	A	A	DCDC5	c.554C>T	p.P185L
XH_P56	11	46958293	46958293	Missense_Mutation	SNV	A	G	G	C11orf49	c.13A>G	p.R5G
XH_P56	11	48510786	48510786	Missense_Mutation	SNV	G	T	T	OR4A47	c.442G>T	p.V148F
XH_P56	11	82874775	82874775	Missense_Mutation	SNV	A	G	G	PCF11	c.373A>G	p.I125V
XH_P56	12	109354738	109354738	Missense_Mutation	SNV	C	T	T	SVOP	c.380G>A	p.R127Q
XH_P56	12	133733061	133733061	Missense_Mutation	SNV	G	A	A	ZNF10	c.1229G>A	p.C410Y
XH_P56	12	23818475	23818475	Missense_Mutation	SNV	T	A	A	SOX5	c.795A>T	p.L265F
XH_P56	12	53201534	53201534	Missense_Mutation	SNV	C	T	T	KRT4	c.1240G>A	p.E414K
XH_P56	12	53204550	53204550	Missense_Mutation	SNV	A	G	G	KRT4	c.728T>C	p.V243A
XH_P56	12	55688550	55688550	Missense_Mutation	SNV	G	T	T	OR6C6	c.467C>A	p.P156H
XH_P56	13	31287981	31287981	Splice_Site	SNV	G	A	A	ALOX5AP	c.116+3G>A	
XH_P56	14	60749642	60749642	Frame_Shift_Ins	INDEL	-	T	T	PPM1A	c.224dupT	p.L75fs
XH_P56	14	61747542	61747542	Silent	SNV	C	G	G	TMEM30B	c.324G>C	p.V108V
XH_P56	14	67382766	67382766	Missense_Mutation	SNV	G	C	C	GPHN	c.436G>C	p.G146R
XH_P56	14	93424571	93424571	Silent	SNV	G	A	A	ITPK1	c.645C>T	p.L215L
XH_P56	15	41611955	41611955	Missense_Mutation	SNV	C	T	T	OIP5	c.413G>A	p.G138D
XH_P56	15	42579914	42579914	Missense_Mutation	SNV	G	A	A	GANC	c.227G>A	p.G76D
XH_P56	15	57535728	57535728	Missense_Mutation	SNV	G	A	A	TCF12	c.584G>A	p.G195E
XH_P56	15	72502815	72502815	Missense_Mutation	SNV	T	C	C	PKM	c.473A>G	p.H158R
XH_P56	15	85400106	85400106	Missense_Mutation	SNV	G	A	A	ALPK3	c.2743G>A	p.E195K
XH_P56	16	89017077	89017077	Missense_Mutation	SNV	A	T	T	LOC100129697	c.551A>T	p.H184L
XH_P56	17	30185832	30185832	Missense_Mutation	SNV	C	T	T	COPRS	c.8G>A	p.G3D
XH_P56	17	30221743	30221743	Missense_Mutation	SNV	G	A	A	UTP6	c.233C>T	p.S78L
XH_P56	17	41908674	41908674	Missense_Mutation	SNV	G	A	A	MPP3	c.160C>T	p.R54C
XH_P56	17	42239259	42239259	Missense_Mutation	SNV	A	C	C	C17orf53	c.1900A>C	p.S634R
XH_P56	17	44073947	44073947	Missense_Mutation	SNV	C	T	T	MAPT	c.1744C>T	p.P582S
XH_P56	17	62223369	62223369	Splice_Site	SNV	C	T	T	SNHG25	n.31+9C>T	
XH_P56	18	3879385	3879385	Silent	SNV	G	A	A	DLGAP1	c.684C>T	p.P228P
XH_P56	19	34983953	34983953	Missense_Mutation	SNV	C	T	T	WTIP	c.781C>T	p.R261C
XH_P56	19	38231072	38231072	Missense_Mutation	SNV	T	A	A	ZNF573	c.55A>T	p.J19F
XH_P56	19	38378646	38378646	Missense_Mutation	SNV	T	C	C	WDR87	c.5665A>G	p.K1889E
XH_P56	19	39369877	39369877	Missense_Mutation	SNV	G	C	C	SIRT2	c.977C>G	p.P326R
XH_P56	19	44777527	44777527	Silent	SNV	T	C	C	ZNF233	c.714T>C	p.N238N
XH_P56	19	48198190	48198190	Missense_Mutation	SNV	G	A	A	GLTSCR1	c.2929G>A	p.G977R
XH_P56	19	54501572	54501572	Splice_Site	SNV	G	A	A	CACNG6	c.406+5G>A	
XH_P56	19	9066695	9066695	Missense_Mutation	SNV	C	T	T	MUC16	c.20751G>A	p.M6917I
XH_P56	2	135988476	135988476	Missense_Mutation	SNV	C	T	T	ZRANB3	c.1561G>A	p.D521N
XH_P56	2	160025832	160025832	Missense_Mutation	SNV	A	G	G	TANC1	c.1015A>G	p.J339V
XH_P56	2	165947635	165947635	Silent	SNV	G	A	A	SCN3A	c.4881C>T	p.N1627N
XH_P56	2	170493662	170493662	Missense_Mutation	SNV	G	C	C	PIIG	c.1894G>C	p.E632Q
XH_P56	2	181922458	181922458	Nonsense_Mutation	SNV	C	A	A	UBE2E3	c.284C>A	p.S95*
XH_P56	2	238991960	238991960	Silent	SNV	A	T	T	SCLY	c.873A>T	p.L291L
XH_P56	2	242756281	242756281	Missense_Mutation	SNV	G	A	A	NEU4	c.433G>A	p.A145T
XH_P56	2	74043601	74043601	Missense_Mutation	SNV	C	A	A	C2orf78	c.2251C>A	p.P751T
XH_P56	22	17447218	17447218	Missense_Mutation	SNV	C	A	A	GAB4	c.1060G>T	p.A354S
XH_P56	3	119379090	119379090	Missense_Mutation	SNV	A	G	G	POPDC2	c.181T>C	p.Y61H
XH_P56	3	130095126	130095126	Silent	SNV	C	G	G	COL6A5	c.114C>G	p.S38S
XH_P56	3	179616003	179616003	Missense_Mutation	SNV	A	G	G	PEX5L	c.119T>C	p.V40A
XH_P56	3	98250972	98250972	Missense_Mutation	SNV	C	T	T	GPR15	c.95C>T	p.T32I
XH_P56	4	170913027	170913027	Silent	SNV	C	T	T	MFAP3L	c.423G>A	p.P141P
XH_P56	4	39757308	39757308	Missense_Mutation	SNV	A	G	G	UBE2K	c.248A>G	p.N83S
XH_P56	4	57777265	57777265	Missense_Mutation	SNV	C	T	T	REST	c.461C>T	p.S154L
XH_P56	5	121187717	121187717	Missense_Mutation	SNV	G	A	A	FTMT	c.59G>A	p.R20H
XH_P56	5	140215088	140215088	Missense_Mutation	SNV	G	A	A	PCDHA7	c.1120G>A	p.V374M
XH_P56	5	168176571	168176571	Silent	SNV	C	T	T	SLIT3	c.2043G>A	p.R681R
XH_P56	5	33467715	33467715	Missense_Mutation	SNV	G	A	A	TARS	c.2074G>A	p.D692N
XH_P56	5	54771275	54771275	Missense_Mutation	SNV	C	G	G	PLPP1	c.62G>C	p.G21A
XH_P56	5	83360532	83360532	Silent	SNV	G	A	A	EDIL3	c.909C>T	p.G303G
XH_P56	5	89933649	89933649	Silent	SNV	C	A	A	ADGRV1	c.2124C>A	p.G708G
XH_P56	6	102250273	102250273	Missense_Mutation	SNV	A	T	T	GRIK2	c.1163A>T	p.D388V
XH_P56	6	11185790	11185790	Missense_Mutation	SNV	C	T	T	NEDD9	c.2110G>A	p.D704N
XH_P56	6	159653559	159653559	Missense_Mutation	SNV	C	T	T	FNDC1	c.2015C>T	p.P672L
XH_P56	7	43916825	43916825	Missense_Mutation	SNV	T	C	C	URGCP	c.2237A>G	p.D746G
XH_P56	7	57188862	57188862	Splice_Site	SNV	G	A	A	ZNF479	c.263-3C>T	
XH_P56	7	98254301	98254301	Silent	SNV	C	T	T	NPTX2	c.711C>T	p.Y237Y
XH_P56	8	24357762	24357762	Silent	SNV	T	C	C	ADAM7	c.1995T>C	p.H665H
XH_P56	9	101830849	101830849	Missense_Mutation	SNV	T	C	C	COL15A1	c.3850T>C	p.F1284L
XH_P56	9	117827141	117827141	Missense_Mutation	SNV	C	A	A	TNC	c.3272G>T	p.R1091I
XH_P56	9	133224404	133224404	Missense_Mutation	SNV	G	A	A	HMCN2	c.2515G>A	p.E839K
XH_P56	9	79320596	79320596	Missense_Mutation	SNV	G	T	T	PRUNE2	c.6594C>A	p.D2198E
XH_P56	9	79930167	79930167	Splice_Site	SNV	A	T	T	VPS13A	c.4296-2A>T	
XH_P56	X	135428334	135428334	Silent	SNV	G	A	A	ADGRG4	c.2469G>A	p.T823T
XH_P56	Y	2821990	2821990	Missense_Mutation	SNV	G	A	A	ZFY	c.13G>A	p.E5K
XH_P57	-	-	-	Frame_Shift_Del	INS	-	-	-	DPYD	c.2534_2535del	p.E845Afs*25
XH_P57	-	-	-	Frame_Shift_Ins	INS	-	-	-	IKBKE	c.18_19dup	p.Y7fs*32
XH_P57	10	43601830	43601830	Missense_Mutation	SNP	G	A	A	RET	c.874G>A	p.V292M
XH_P57	-	-	-	Frame_Shift_Ins	INS	-	-	-	ARID2	c.2460_2463dup	p.I822Vfs*20
XH_P57	12	49427213	49427213	Missense_Mutation	SNP	G	C	C	KMT2D	c.11275C>G	p.Q3759E
XH_P57	-	-	-	Frame_Shift_Ins	INS	-	-	-	KMT2D	c.4561dup	p.I1521Nfs*7
XH_P57	13	108959228	108959228	Missense_Mutation	SNP	A	G	G	TNFSF13B	c.800A>G	p.N267S
XH_P57	-	-	-	Frame_Shift_Ins	INS	-	-	-	TP53	c.159dup	p.F54Vfs*3
XH_P57	17	8110889	8110889	Missense_Mutation	SNP	G	A	A	AURKB	c.206C>T	p.T69M
XH_P57	17	38560458	38560458	Missense_Mutation	SNP	C	A	A	TOP2A	c.2229G>T	p.K743N
XH_P57	-	-	-	Frame_Shift_Ins	INS	-	-	-	GATA6	c.1004_1037dup	p.A348Lfs*126
XH_P57	-	-	-	Frame_Shift_Del	INS	-	-	-	SMAD4	c.1269_1282del	p.A425Lfs*10

XH_P57	2	74327732	74327732	Missense_Mutation	SNP	A	T	T	TET3	c.3817A>T	p.N1273Y
XH_P57	2	170044680	170044680	Missense_Mutation	SNP	C	T	T	LRP2	c.9128G>A	p.R3043H
XH_P57	20	57429085	57429085	Missense_Mutation	SNP	C	T	T	GNAS	c.578C>T	p.S193L
XH_P57	6	152419991	152419991	Missense_Mutation	SNP	G	A	A	ESR1	c.1678G>A	p.V560M
XH_P57	7	42005139	42005139	Missense_Mutation	SNP	T	G	G	GLI3	c.3532A>C	p.K1178Q
XH_P57	1	-	-	In_Frame_Ins	INS	-	-	-	ABL1	2520_2521insCC	Q840_V841insP
XH_P57	1	899336	899336	Silent	SNP	G	A	G	KLHL17	c.G1392A	p.T464T
XH_P57	1	902128	902128	Missense_Mutation	SNP	C	T	C	PLEKHN1	c.C128T	p.A43V
XH_P57	1	906272	906272	Silent	SNP	A	C	A	PLEKHN1	c.A498C	p.A166A
XH_P57	1	909363	909363	Silent	SNP	A	C	A	PLEKHN1	c.A1480C	p.R494R
XH_P57	1	915264	915264	Silent	SNP	G	A	G	PERM1	c.C1146T	p.S382S
XH_P57	1	978974	978974	Missense_Mutation	SNP	G	A	G	AGRN	c.G1660A	p.V554M
XH_P57	1	981345	981345	Silent	SNP	C	T	C	AGRN	c.C2682T	p.D894D
XH_P57	1	981942	981942	Missense_Mutation	SNP	C	A	C	AGRN	c.C3077A	p.T1026N
XH_P57	1	987191	987191	Missense_Mutation	SNP	G	A	G	AGRN	c.G5647A	p.E1883K
XH_P57	1	1007222	1007222	Missense_Mutation	SNP	G	T	G	RNF223	c.C725A	p.P242H
XH_P57	1	1021346	1021346	Silent	SNP	A	G	A	C1orf159	c.T357C	p.I119I
XH_P57	1	1179799	1179799	Missense_Mutation	SNP	C	T	C	C1QTNF12	c.G256A	p.A86T
XH_P57	1	1390875	1390875	Silent	SNP	C	T	C	ATAD3C	c.C414T	p.D138D
XH_P57	1	1562536	1562536	Silent	SNP	G	A	G	MI82	c.G1473A	p.A491A
XH_P57	1	1599812	1599812	Missense_Mutation	SNP	C	T	C	SLC35E2B	c.G934A	p.V312I
XH_P57	1	1643740	1643740	Silent	SNP	C	T	C	CDK11A	c.G558A	p.A186A
XH_P57	1	1666175	1666175	Missense_Mutation	SNP	C	T	C	SLC35E2	c.G686A	p.R229H
XH_P57	1	1686067	1686067	Silent	SNP	C	A	C	NADK	c.G663T	p.T221T
XH_P57	1	1957037	1957037	Silent	SNP	T	C	T	GABRD	c.T330C	p.G110G
XH_P57	1	2103506	2103506	Silent	SNP	C	G	C	PRKC2	c.C525G	p.A175A
XH_P57	1	2130262	2130262	Missense_Mutation	SNP	C	G	C	FAAP20	c.G166C	p.G56R
XH_P57	1	2418625	2418625	Silent	SNP	C	T	C	PLCH2	c.C843T	p.Y281Y
XH_P57	1	2426313	2426313	Missense_Mutation	SNP	G	A	G	PLCH2	c.G1597A	p.V533M
XH_P57	1	3396420	3396420	Missense_Mutation	SNP	G	A	G	ARHGEF16	c.G1933A	p.A645T
XH_P57	1	3548049	3548049	Silent	SNP	C	T	C	WRAP73	c.G1221A	p.S407S
XH_P57	1	3638674	3638674	Silent	SNP	C	T	C	TP73	c.C372T	p.T124T
XH_P57	1	3680333	3680333	Missense_Mutation	SNP	C	T	C	CCDC27	c.C1385T	p.T462M
XH_P57	1	3683914	3683914	Missense_Mutation	SNP	T	A	T	CCDC27	c.T1648A	p.W550R
XH_P57	1	3753136	3753136	Missense_Mutation	SNP	A	T	A	CEP104	c.T1240A	p.L414I
XH_P57	1	5934657	5934657	Silent	SNP	C	T	C	NPHP4	c.G1569A	p.P523P
XH_P57	1	5935110	5935110	Silent	SNP	G	A	G	NPHP4	c.C1332T	p.A444A
XH_P57	1	6038350	6038350	In_Frame_Ins	INS	-	CGG	-	NPHP4	258_259insCC	p.S87delinsPS
XH_P57	1	6269340	6269340	Silent	SNP	A	G	A	RNF207	c.A564G	p.A188A
XH_P57	1	6271125	6271125	Silent	SNP	A	G	A	RNF207	c.A1056G	p.P352P
XH_P57	1	7890064	7890064	Silent	SNP	A	G	A	PER3	c.A3057G	p.T1019T
XH_P57	1	7913430	7913430	Missense_Mutation	SNP	G	A	G	UTS2	c.C62T	p.T21M
XH_P57	1	9324670	9324670	Silent	SNP	A	G	A	H6PD	c.A2151G	p.S717S
XH_P57	1	10328243	10328243	Frame_Shift_Ins	INS	-	AGCC	-	KIF1B	642_643insAGC	p.S214fs
XH_P57	1	10596341	10596341	Silent	SNP	C	T	C	PEX14	c.C156T	p.F52F
XH_P57	1	11008843	11008843	Missense_Mutation	SNP	G	A	G	C1orf127	c.C1349T	p.A450V
XH_P57	1	11008844	11008844	Missense_Mutation	SNP	C	G	C	C1orf127	c.G1348C	p.A450P
XH_P57	1	11087272	11087272	Missense_Mutation	SNP	T	G	T	MASP2	c.A1731C	p.Q577H
XH_P57	1	11097867	11097867	Silent	SNP	C	T	C	MASP2	c.G891A	p.A297A
XH_P57	1	11137661	11137661	Silent	SNP	A	G	A	EXOSC10	c.T1797C	p.A599A
XH_P57	1	11150682	11150682	Silent	SNP	C	T	C	EXOSC10	c.G687A	p.E229E
XH_P57	1	11159823	11159823	Silent	SNP	T	C	T	EXOSC10	c.A666G	p.G22G
XH_P57	1	11771988	11771988	Silent	SNP	A	G	A	DRAXIN	c.A723G	p.L241L
XH_P57	1	11826085	11826085	Missense_Mutation	SNP	G	A	G	C1orf167	c.G242A	p.R81H
XH_P57	1	11838841	11838841	Missense_Mutation	SNP	A	G	A	C1orf167	c.A2464G	p.S822G
XH_P57	1	11845222	11845222	Missense_Mutation	SNP	T	C	T	C1orf167	c.T3443C	p.V1148A
XH_P57	1	11847449	11847449	Missense_Mutation	SNP	G	A	G	C1orf167	c.G3572A	p.R1913H
XH_P57	1	11848068	11848068	Missense_Mutation	SNP	G	C	G	C1orf167	c.G3812C	p.C1271S
XH_P57	1	11854476	11854476	Missense_Mutation	SNP	T	G	T	MTHFR	c.A1409C	p.E470A
XH_P57	1	11854896	11854896	Silent	SNP	G	A	G	MTHFR	c.C1179T	p.S393S
XH_P57	1	11863057	11863057	Silent	SNP	G	A	G	MTHFR	c.C240T	p.P80P
XH_P57	1	11897082	11897082	Silent	SNP	C	T	C	CLCN6	c.C1941T	p.G647G
XH_P57	1	11907648	11907648	Missense_Mutation	SNP	C	T	C	NPPA	c.G94A	p.V32M
XH_P57	1	12009955	12009955	Silent	SNP	C	T	C	PIOD1	c.C294T	p.F98F
XH_P57	1	12010469	12010469	Missense_Mutation	SNP	G	T	G	PIOD1	c.G358T	p.A120S
XH_P57	1	12024235	12024235	Silent	SNP	C	T	C	PIOD1	c.C1206T	p.N402N
XH_P57	1	12026355	12026355	Silent	SNP	A	C	A	PIOD1	c.A1632C	p.A544A
XH_P57	1	12065841	12065841	Silent	SNP	C	T	C	MFN2	c.C1569T	p.S523S
XH_P57	1	12198297	12198297	Silent	SNP	T	C	T	TNFRSF8	c.T1011C	p.S337S
XH_P57	1	13183422	13183422	Missense_Mutation	SNP	T	C	T	HNRNPCL2	c.A451G	p.N151D
XH_P57	1	13448303	13448303	Missense_Mutation	SNP	A	C	A	PRAMEF13	c.T1172G	p.M391R
XH_P57	1	15495110	15495110	Missense_Mutation	SNP	A	G	A	C1orf195	c.T262C	p.Y88H
XH_P57	1	15541607	15541607	Silent	SNP	T	C	T	TMEM51	c.T24C	p.N8N
XH_P57	1	15793913	15793913	Silent	SNP	G	A	G	CELA2A	c.G672A	p.A224A
XH_P57	1	16069071	16069071	Missense_Mutation	SNP	C	T	C	TMEM82	c.C17T	p.S6F
XH_P57	1	16273427	16273431	Frame_Shift_Del	DEL	TACCT	-	TACCT	ZBTB17	c.125_126del	p.K42fs
XH_P57	1	16371067	16371067	Missense_Mutation	SNP	G	T	G	CLCNKB	c.G80T	p.R27L
XH_P57	1	16730308	16730308	Missense_Mutation	SNP	G	T	G	SPATA21	c.C915A	p.H305Q
XH_P57	1	17296361	17296361	Missense_Mutation	SNP	C	G	C	CROCC	c.C5383G	p.R1795G
XH_P57	1	17555508	17555508	Silent	SNP	G	T	G	PADI1	c.G891T	p.T297T
XH_P57	1	17668487	17668487	Silent	SNP	C	T	C	PADI4	c.C702T	p.P234P
XH_P57	1	17914122	17914122	Missense_Mutation	SNP	G	A	G	ARHGEF10L	c.G205A	p.D69N
XH_P57	1	18807953	18807953	Missense_Mutation	SNP	C	A	C	KLHDC7A	c.C478A	p.R160S
XH_P57	1	19422060	19422060	Silent	SNP	G	A	G	UBR4	c.C13605T	p.V4535V
XH_P57	1	19495564	19495564	Frame_Shift_Ins	INS	-	GTCTC	-	UBR4	314_331insGAG	p.D1105fs
XH_P57	1	19566382	19566382	Missense_Mutation	SNP	A	G	A	EMC1	c.T818C	p.L273S
XH_P57	1	19615062	19615062	Missense_Mutation	SNP	C	G	C	AKR7A3	c.G142C	p.V48L
XH_P57	1	19684006	19684006	Silent	SNP	G	C	G	CAPZB	c.C381G	p.G127G
XH_P57	1	20246876	20246876	Missense_Mutation	SNP	C	T	C	PLA2G2E	c.G353A	p.R188H
XH_P57	1	20501582	20501582	Nonsense_Mutation	SNP	G	A	G	PLA2G2C	c.C97T	p.R33X
XH_P57	1	21042094	21042094	Silent	SNP	G	A	G	KIF17	c.C270T	p.Y90Y
XH_P57	1	22109370	22109370	Silent	SNP	G	A	G	USP48	c.C81T	p.H27H
XH_P57	1	22141206	22141206	Missense_Mutation	SNP	A	C	A	LDLRAD2	c.A401C	p.N134T
XH_P57	1	22154845	22154845	Silent	SNP	A	G	A	HSPG2	c.T12315C	p.D4105D
XH_P57	1	22159008	22159008	Silent	SNP	C	A	C	HSPG2	c.G11190T	p.V3730V
XH_P57	1	22161275	22161275	Silent	SNP	G	A	G	HSPG2	c.C10620T	p.V3540V
XH_P57	1	22167696	22167696	Silent	SNP	G	A	G	HSPG2	c.C9414T	p.A3138A
XH_P57	1	22310190	22310190	Silent	SNP	T	C	T	CELA3B	c.T366C	p.N122N

XH_P57	1	22927408	22927408	Silent	SNP	G	A	G	EPHA8	c.G2556A	p.E852E
XH_P57	1	23519633	23519633	Silent	SNP	A	G	A	HTR1D	c.T1080C	p.N360N
XH_P57	1	24083494	24083494	Silent	SNP	C	T	C	ELOA	c.C2214T	p.S738S
XH_P57	1	24416070	24416070	Silent	SNP	G	C	G	MYOM3	c.C1572G	p.P524P
XH_P57	1	24421474	24421474	Missense_Mutation	SNP	G	A	G	MYOM3	c.C797T	p.T266M
XH_P57	1	24432520	24432520	Silent	SNP	G	A	G	MYOM3	c.C450T	p.Y150Y
XH_P57	1	24448084	24448084	Silent	SNP	G	A	G	IL22RA1	c.C936T	p.P312P
XH_P57	1	24460797	24460797	Silent	SNP	T	G	T	IL22RA1	c.A435C	p.P145P
XH_P57	1	24680915	24680915	Silent	SNP	C	T	C	GRHL3	c.C1608T	p.V536V
XH_P57	1	24718075	24718075	Silent	SNP	T	C	T	STPG1	c.A165G	p.Q55Q
XH_P57	1	25634143	25634143	Missense_Mutation	SNP	T	C	T	RHD	c.T1079C	p.L360P
XH_P57	1	25712263	25712263	Missense_Mutation	SNP	G	A	G	RHCE	c.C559T	p.L187F
XH_P57	1	26310438	26310438	Missense_Mutation	SNP	T	C	T	PAFAH2	c.A551G	p.Q184R
XH_P57	1	26357656	26357656	Missense_Mutation	SNP	C	A	C	EXTL1	c.C1135A	p.H379N
XH_P57	1	26510959	26510959	Silent	SNP	G	T	G	CNKSR1	c.G1089T	p.G363G
XH_P57	1	26515956	26515956	Missense_Mutation	SNP	C	A	C	CNKSR1	c.C2080A	p.H694N
XH_P57	1	26608877	26608877	In_Frame_Ins	INS	-	CCGGGA	-	UBXN11	15_1116insTCCG372delinsGPG	
XH_P57	1	26663362	26663362	Missense_Mutation	SNP	C	T	C	CRYBG2	c.G3881A	p.S1294N
XH_P57	1	26671084	26671084	Missense_Mutation	SNP	G	T	G	CRYBG2	c.C2065A	p.P689T
XH_P57	1	26671248	26671248	Missense_Mutation	SNP	A	G	A	CRYBG2	c.T1901C	p.V634A
XH_P57	1	27688633	27688633	Missense_Mutation	SNP	G	A	G	MAP3K6	c.C1340T	p.T447I
XH_P57	1	27709020	27709020	Missense_Mutation	SNP	T	C	T	CD164L2	c.A226G	p.M76V
XH_P57	1	27736478	27736478	Silent	SNP	T	C	T	WASF2	c.A1047G	p.P349P
XH_P57	1	28060574	28060574	Silent	SNP	A	G	A	FAM76A	c.A234G	p.A78A
XH_P57	1	28476862	28476862	Missense_Mutation	SNP	G	T	G	PTAFR	c.C671A	p.A224D
XH_P57	1	32140617	32140617	In_Frame_Ins	INS	-	TGC	-	COL16A1	2849_2850insGGb.H95delinsHQH	
XH_P57	1	32671456	32671456	Silent	SNP	T	C	T	IQCC	c.T174C	p.A58A
XH_P57	1	32829281	32829281	Silent	SNP	G	A	G	TSSK3	c.G231A	p.L77L
XH_P57	1	33099263	33099263	Missense_Mutation	SNP	C	G	C	ZBTB80S	c.G325C	p.E109Q
XH_P57	1	33234307	33234307	Missense_Mutation	SNP	T	C	T	KIAA1522	c.T340C	p.S114P
XH_P57	1	33235641	33235641	Missense_Mutation	SNP	G	C	G	KIAA1522	c.G684C	p.E228D
XH_P57	1	33957130	33957130	Silent	SNP	C	A	C	ZSCAN20	c.C1272A	p.A424A
XH_P57	1	35227147	35227147	Missense_Mutation	SNP	C	T	C	GJB4	c.C292T	p.R98C
XH_P57	1	35260363	35260363	Silent	SNP	C	T	C	GJA4	c.C549T	p.P183P
XH_P57	1	35260769	35260769	Missense_Mutation	SNP	C	T	C	GJA4	c.C955T	p.P319S
XH_P57	1	36316571	36316571	Silent	SNP	A	C	A	AGO4	c.A2394C	p.S798S
XH_P57	1	36640516	36640516	Missense_Mutation	SNP	G	A	G	MAP7D1	c.G757A	p.V253M
XH_P57	1	38185169	38185169	Silent	SNP	G	A	G	EPHA10	c.C2673T	p.P891P
XH_P57	1	38192870	38192870	Missense_Mutation	SNP	G	C	G	EPHA10	c.C1676G	p.S559C
XH_P57	1	38289383	38289383	Silent	SNP	T	C	T	MTF1	c.A1170G	p.T390T
XH_P57	1	39325208	39325208	Silent	SNP	C	T	C	RRAGC	c.G111A	p.A37A
XH_P57	1	39340623	39340623	Frame_Shift_Ins	INS	-	A	-	GJA9	c.1147dupT	p.Y383fs
XH_P57	1	39835817	39835817	Missense_Mutation	SNP	A	G	A	MACF1	c.A6868G	p.M2290V
XH_P57	1	40092464	40092464	Silent	SNP	C	T	C	HEVL	c.G702A	p.R234R
XH_P57	1	40230336	40230336	Missense_Mutation	SNP	C	G	C	BMP8B	c.G827C	p.S276T
XH_P57	1	40923019	40923019	Missense_Mutation	SNP	G	A	G	ZFP69B	c.G344A	p.C115Y
XH_P57	1	40980731	40980731	Missense_Mutation	SNP	G	T	G	EXO5	c.G515T	p.G172V
XH_P57	1	41979348	41979348	Silent	SNP	C	T	C	HIVEP3	c.G5544A	p.S1848S
XH_P57	1	42744175	42744175	Silent	SNP	G	C	G	FOXJ3	c.C213G	p.V71V
XH_P57	1	42915727	42915727	Silent	SNP	C	G	C	ZMYND12	c.G114C	p.G38G
XH_P57	1	43042703	43042703	Silent	SNP	C	T	C	CCDC30	c.C868T	p.L290L
XH_P57	1	43047057	43047057	Silent	SNP	A	G	A	CCDC30	c.A1092G	p.E364E
XH_P57	1	43308488	43308488	Missense_Mutation	SNP	A	C	A	ERMAP	c.A1013C	p.E338A
XH_P57	1	44058217	44058217	Silent	SNP	G	A	G	PTPRF	c.G1758A	p.S586S
XH_P57	1	44415424	44415424	Silent	SNP	A	G	A	IP013	c.A420G	p.P140P
XH_P57	1	44440769	44440769	Silent	SNP	G	C	G	ATP6V0B	c.G57C	p.A19A
XH_P57	1	44447413	44447413	Missense_Mutation	SNP	G	C	G	B4GALT2	c.G366C	p.Q122H
XH_P57	1	44461822	44461822	Missense_Mutation	SNP	C	T	C	CCDC24	c.C512T	p.A171V
XH_P57	1	44468235	44468235	Silent	SNP	G	A	G	SLC6A9	c.C612T	p.L204D
XH_P57	1	45224901	45224901	Silent	SNP	G	A	G	KIF2C	c.G1125A	p.K375K
XH_P57	1	45292866	45292866	Silent	SNP	G	A	G	PTCH2	c.C2487T	p.D829D
XH_P57	1	45793699	45793699	Silent	SNP	G	A	G	HPDL	c.G879A	p.K293K
XH_P57	1	45796899	45796899	Silent	SNP	C	G	C	MUTYH	c.G1002C	p.T334T
XH_P57	1	45810923	45810923	Silent	SNP	G	A	G	TESK2	c.C1056T	p.P352P
XH_P57	1	46073597	46073597	Silent	SNP	A	G	A	NASP	c.A822G	p.V274V
XH_P57	1	46094027	46094027	Silent	SNP	A	G	A	GPBP1L1	c.T1326C	p.S442S
XH_P57	1	46095272	46095272	Silent	SNP	T	C	T	GPBP1L1	c.A1248G	p.K416K
XH_P57	1	46195375	46195375	Missense_Mutation	SNP	T	C	T	IPP	c.A791G	p.K264R
XH_P57	1	46500744	46500744	Missense_Mutation	SNP	G	C	G	MAST2	c.G4400C	p.G1467A
XH_P57	1	46501054	46501054	Silent	SNP	C	G	C	MAST2	c.C4710G	p.P1570P
XH_P57	1	46501495	46501495	Silent	SNP	T	C	T	MAST2	c.T5151C	p.Y1717Y
XH_P57	1	46736380	46736380	Nonsense_Mutation	INS	-	AGGAGCGGCTG	-	RAD54L	AGGAGAGGAGG6RDAAAEADRLQGEELRELTSIVNRX	
XH_P57	1	46738398	46738398	Silent	SNP	G	A	G	RAD54L	c.G1299A	p.P433P
XH_P57	1	46768970	46768970	Missense_Mutation	SNP	C	A	C	LRRC41	c.G25T	p.A9S
XH_P57	1	46775975	46775975	Missense_Mutation	SNP	C	T	C	UQCRH	c.C203T	p.A68V
XH_P57	1	46806550	46806550	Missense_Mutation	SNP	C	T	C	NSUN4	c.C52T	p.L18F
XH_P57	1	46810670	46810670	Silent	SNP	T	C	T	NSUN4	c.T144C	p.D48D
XH_P57	1	46827485	46827485	Silent	SNP	C	T	C	NSUN4	c.C975T	p.P325P
XH_P57	1	46871713	46871713	Silent	SNP	G	A	G	FAAH	c.G789A	p.K263K
XH_P57	1	46874246	46874246	Missense_Mutation	SNP	C	T	C	FAAH	c.C1067T	p.A356V
XH_P57	1	47150211	47150211	Frame_Shift_Del	DEL	GAGCACT	-	GAGCACT	EFCAB14	c.1132_1138del	p.S378fs
XH_P57	1	47395973	47395973	Silent	SNP	G	A	G	CYP4A11	c.C1374T	p.I458I
XH_P57	1	47402458	47402458	Missense_Mutation	SNP	C	T	C	CYP4A11	c.G388A	p.G130S
XH_P57	1	47610590	47610590	Silent	SNP	A	C	A	CYP4A22	c.A876C	p.G292G
XH_P57	1	47746238	47746238	Missense_Mutation	SNP	T	C	T	STIL	c.A1892G	p.D631G
XH_P57	1	48241061	48241061	Missense_Mutation	SNP	G	A	G	TRABD2B	c.C1130T	p.P377L
XH_P57	1	48460108	48460108	Silent	SNP	A	C	A	TRABD2B	c.T264G	p.L88L
XH_P57	1	48694594	48694594	Missense_Mutation	SNP	G	A	G	SLCSA9	c.G307A	p.G103R
XH_P57	1	48697781	48697781	Silent	SNP	C	T	C	SLCSA9	c.C855T	p.F285F
XH_P57	1	48713100	48713100	Missense_Mutation	SNP	C	A	C	SLCSA9	c.C1931A	p.A644E
XH_P57	1	49224584	49224584	Silent	SNP	G	T	G	BEND5	c.C226A	p.R76R
XH_P57	1	49511424	49511424	Silent	SNP	A	G	A	AGBL4	c.T462C	p.H154H
XH_P57	1	53532535	53532535	Missense_Mutation	SNP	G	C	G	PODN	c.G28C	p.A10P
XH_P57	1	53544289	53544289	Silent	SNP	C	T	C	PODN	c.C1251T	p.N417N
XH_P57	1	53927173	53927173	Missense_Mutation	SNP	G	A	G	DMRTB1	c.G605A	p.R202H
XH_P57	1	53972349	53972349	Silent	SNP	G	A	G	GLIS1	c.C1806T	p.P602P
XH_P57	1	53995515	53995515	Silent	SNP	G	A	G	GLIS1	c.C906T	p.A302A
XH_P57	1	54678305	54678305	Missense_Mutation	SNP	C	G	C	MRPL37	c.C964G	p.L322V

XH_P57	1	54690954	54690954	Missense_Mutation	SNP	T	C	T	MRPL37	c.T1351C	p.F451L
XH_P57	1	55060251	55060251	Missense_Mutation	SNP	C	T	C	ACOT11	c.C494T	p.P165L
XH_P57	1	55136529	55136529	Missense_Mutation	SNP	T	C	T	MROH7	c.T80C	p.V27A
XH_P57	1	55224131	55224131	Missense_Mutation	SNP	T	C	T	PARS2	c.A704G	p.N235S
XH_P57	1	55224751	55224751	Missense_Mutation	SNP	C	A	C	PARS2	c.G84T	p.R28S
XH_P57	1	55273580	55273580	Missense_Mutation	SNP	G	T	G	LEXM	c.G376T	p.G126C
XH_P57	1	55569634	55569634	Frame_Shift_Ins	INS	-	T	-	USP24	c.4939dupA	p.S1647fs
XH_P57	1	57171870	57171870	Silent	SNP	T	C	T	PRKAA2	c.T1399C	p.L467L
XH_P57	1	57257817	57257817	Silent	SNP	T	C	T	C1orf168	c.A669G	p.K223K
XH_P57	1	57383358	57383358	Missense_Mutation	SNP	C	T	C	C8A	c.C1724T	p.P575L
XH_P57	1	59042181	59042181	Missense_Mutation	SNP	G	T	G	TACSTD2	c.C648A	p.D216E
XH_P57	1	59247993	59247993	Silent	SNP	C	T	C	JUN	c.G750A	p.Q250Q
XH_P57	1	60505783	60505783	Missense_Mutation	SNP	G	C	G	C1orf87	c.C553G	p.L185V
XH_P57	1	60506744	60506744	Silent	SNP	G	A	G	C1orf87	c.C402T	p.S134S
XH_P57	1	62579823	62579823	Silent	SNP	G	A	G	PATJ	c.G4560A	p.E1520E
XH_P57	1	62579907	62579907	Silent	SNP	C	T	C	PATJ	c.C4644T	p.I1548I
XH_P57	1	63997633	63997633	Silent	SNP	A	T	A	EFCAB7	c.A330T	p.S110S
XH_P57	1	64021096	64021096	Missense_Mutation	SNP	G	A	G	EFCAB7	c.G1124A	p.R375K
XH_P57	1	64624842	64624842	Silent	SNP	A	G	A	ROR1	c.A1353G	p.V451V
XH_P57	1	68614320	68614320	Silent	SNP	G	A	G	WLS	c.C723T	p.I241I
XH_P57	1	70504589	70504589	Missense_Mutation	SNP	G	A	G	LRRC7	c.G2968A	p.G990S
XH_P57	1	70504591	70504591	In_Frame_Ins	INS	-	TTTCTA	-	LRRC7	c.970_2971insTTTb	G990delinsGFL
XH_P57	1	70820008	70820008	Silent	SNP	C	T	C	ANKRD13C	c.G84A	p.E28E
XH_P57	1	70820880	70820880	Silent	SNP	G	A	G	HHLA3	c.G246A	p.A82A
XH_P57	1	72058543	72058543	Silent	SNP	A	T	A	NEGR1	c.T897A	p.A299A
XH_P57	1	75065441	75065441	Missense_Mutation	SNP	C	T	C	ERICH3	c.G1664A	p.R555H
XH_P57	1	77093180	77093180	Missense_Mutation	SNP	C	A	C	STG6ALNAC3	c.C472A	p.L158I
XH_P57	1	79102726	79102726	Missense_Mutation	SNP	C	T	C	IFI44L	c.C886T	p.R296C
XH_P57	1	84403649	84403649	Silent	SNP	C	T	C	TLL7	c.G693A	p.E231E
XH_P57	1	85009894	85009894	Missense_Mutation	SNP	A	G	A	SPATA1	c.A793G	p.K265E
XH_P57	1	85016177	85016177	Silent	SNP	A	G	A	SPATA1	c.A1254G	p.L418L
XH_P57	1	85031630	85031630	Silent	SNP	G	A	G	CTBS	c.C591T	p.I197I
XH_P57	1	89271574	89271574	Silent	SNP	T	C	T	PKN2	c.T1533C	p.S511S
XH_P57	1	89435119	89435119	Missense_Mutation	SNP	C	T	C	KYAT3	c.G29A	p.R10Q
XH_P57	1	89521841	89521841	Missense_Mutation	SNP	G	C	G	GBP1	c.C1226G	p.A409G
XH_P57	1	89522646	89522646	Missense_Mutation	SNP	G	C	G	GBP1	c.C1046G	p.T349S
XH_P57	1	91405699	91405699	Silent	SNP	G	A	G	ZNFG44	c.C1212T	p.T404T
XH_P57	1	92185657	92185657	Silent	SNP	C	T	C	TGFBR3	c.G1203A	p.P401P
XH_P57	1	94466659	94466659	Silent	SNP	A	G	A	ABCA4	c.T6285C	p.D2095D
XH_P57	1	97272456	97272456	Silent	SNP	A	G	A	PTBP2	c.A957G	p.L319L
XH_P57	1	103548497	103548497	Missense_Mutation	SNP	A	C	A	COL11A1	c.T138G	p.D46E
XH_P57	1	109010230	109010230	Silent	SNP	G	A	G	NBPF6	c.G1818A	p.P606P
XH_P57	1	109806834	109806834	Silent	SNP	C	T	C	CELSR2	c.C5136T	p.P1712P
XH_P57	1	109807099	109807099	Silent	SNP	G	A	G	CELSR2	c.G5313A	p.P1771P
XH_P57	1	110086451	110086451	Silent	SNP	G	A	G	GPR61	c.G807A	p.S269S
XH_P57	1	110151395	110151395	Missense_Mutation	SNP	G	T	G	GNAT2	c.C319A	p.L107I
XH_P57	1	110163879	110163879	Missense_Mutation	SNP	G	A	G	AMPD2	c.G244A	p.A82T
XH_P57	1	110466338	110466338	Silent	SNP	C	A	C	CSF1	c.C1095A	p.T365T
XH_P57	1	110709719	110709719	Silent	SNP	T	C	T	SLC6A17	c.T168C	p.D56D
XH_P57	1	110709720	110709720	Missense_Mutation	SNP	G	A	G	SLC6A17	c.G169A	p.A57T
XH_P57	1	110765630	110765630	Silent	SNP	C	G	C	KCNC4	c.C723G	p.T241T
XH_P57	1	110766308	110766308	Silent	SNP	G	A	G	KCNC4	c.G1401A	p.P467P
XH_P57	1	110766466	110766466	Missense_Mutation	SNP	G	A	G	KCNC4	c.G1559A	p.C520Y
XH_P57	1	110921715	110921715	Missense_Mutation	SNP	T	G	T	SLC16A4	c.A460C	p.N154H
XH_P57	1	110950439	110950439	Missense_Mutation	SNP	C	T	C	LAMTOR5	c.G50A	p.S17N
XH_P57	1	111144661	111144661	Silent	SNP	A	G	A	KCNA2	c.T1026C	p.D342D
XH_P57	1	111862074	111862074	Silent	SNP	C	T	C	CHIA	c.C678T	p.L226L
XH_P57	1	111862952	111862952	Missense_Mutation	SNP	T	G	T	CHIA	c.T812G	p.V271G
XH_P57	1	111957245	111957245	Silent	SNP	G	A	G	OVGP1	c.C1878T	p.P626P
XH_P57	1	113059851	113059851	Frame_Shift_Ins	INS	-	C	-	WNT2B	c.514_515insC	p.Y172fs
XH_P57	1	113239382	113239382	Silent	SNP	G	A	G	MOV10	c.G2112A	p.E704E
XH_P57	1	113252779	113252816	Frame_Shift_Del	DEL	AACTGCCTGG	-	TAAGTGCCTGGC	PPM1J	c.1487_1524del	p.1496fs
XH_P57	1	113456734	113456734	Missense_Mutation	SNP	C	T	C	SLC16A1	c.G1282A	p.V428I
XH_P57	1	114438951	114438951	Missense_Mutation	SNP	A	G	A	AP4B1	c.T935C	p.L312S
XH_P57	1	116206423	116206423	Missense_Mutation	SNP	G	A	G	VANGL1	c.G340A	p.A114T
XH_P57	1	116534852	116534852	Silent	SNP	C	T	C	SLC22A15	c.C288T	p.S96S
XH_P57	1	116670774	116670774	Silent	SNP	A	G	A	MA2B1L3	c.A669G	p.G223G
XH_P57	1	117554589	117554589	Splice_Site	INS	-	TAAT	-	CD101	.	.
XH_P57	1	117690406	117690406	Splice_Site	SNP	T	C	T	VTCN1	.	.
XH_P57	1	118584643	118584643	Missense_Mutation	SNP	C	A	C	SPAG17	c.G2837T	p.R946L
XH_P57	1	119923724	119923724	Silent	SNP	T	C	T	HAO2	c.T16C	p.L6L
XH_P57	1	120056870	120056870	Missense_Mutation	SNP	G	A	G	HSD3B1	c.G724A	p.D242N
XH_P57	1	120436630	120436630	Missense_Mutation	SNP	C	T	C	ADAM30	c.G2330A	p.S777N
XH_P57	1	120436632	120436632	Nonsense_Mutation	INS	-	AACAGCTAA	-	ADAM30	c.2328insTTAGC776_5777delinsDX	
XH_P57	1	145365316	145365316	Missense_Mutation	SNP	G	A	G	NBPF10	c.G8471A	p.G2824E
XH_P57	1	145532163	145532163	In_Frame_Ins	INS	-	CTA	-	ITGA10	c.378_379insCTA	p.R126delinsRL
XH_P57	1	145533175	145533175	Silent	SNP	T	C	T	ITGA10	c.T841C	p.L281L
XH_P57	1	145562293	145562293	Missense_Mutation	SNP	G	C	G	ANKRD35	c.G1711C	p.E571Q
XH_P57	1	145588905	145588905	Silent	SNP	G	A	G	NUDT17	c.C343T	p.L115L
XH_P57	1	145761368	145761368	Missense_Mutation	SNP	C	T	C	PDZK1	c.C848T	p.A283V
XH_P57	1	146057292	146057292	Missense_Mutation	SNP	T	C	T	NBPF11	c.A158G	p.N53S
XH_P57	1	149290881	149290881	Missense_Mutation	SNP	C	T	C	FAM231D	c.C353T	p.A118V
XH_P57	1	149908108	149908108	Silent	SNP	A	G	A	MTMR11	c.T81C	p.N27N
XH_P57	1	150483355	150483355	Missense_Mutation	SNP	C	T	C	ECM1	c.C470T	p.T157M
XH_P57	1	150484987	150484987	Missense_Mutation	SNP	G	A	G	ECM1	c.G868A	p.G290S
XH_P57	1	150530993	150530993	Silent	SNP	C	T	C	ADAMTSL4	c.C2427T	p.R809R
XH_P57	1	151112483	151112483	Missense_Mutation	SNP	T	C	T	SEMA6C	c.A202G	p.T68A
XH_P57	1	151373743	151373755	Frame_Shift_Del	DEL	CCAGTGCTAA	-	AGCAGTGCTAA	PSMB4	c.605_617del	p.Q202fs
XH_P57	1	151378211	151378211	Silent	SNP	A	G	A	POGZ	c.T3015C	p.N1005N
XH_P57	1	151395972	151395972	In_Frame_Ins	INS	-	TGA	-	POGZ	c.1293_1294insTGA	p.D432delinsSD
XH_P57	1	151735545	151735545	Silent	SNP	A	G	A	MRPL9	c.T231C	p.H77H
XH_P57	1	151773851	151773851	Missense_Mutation	SNP	T	A	T	LINGO4	c.A1330T	p.T444S
XH_P57	1	151810477	151810477	Missense_Mutation	SNP	A	G	A	C2CD4D	c.T989C	p.I330T
XH_P57	1	152128690	152128690	Silent	SNP	G	A	G	RPTN	c.C885T	p.Y295Y
XH_P57	1	152188287	152188287	Missense_Mutation	SNP	C	G	C	HRNR	c.G5818C	p.G1940R
XH_P57	1	152191709	152191709	Missense_Mutation	SNP	C	G	C	HRNR	c.G2396C	p.S799T
XH_P57	1	152191879	152191879	Silent	SNP	G	A	G	HRNR	c.C226T	p.H742H
XH_P57	1	152192825	152192825	Missense_Mutation	SNP	C	T	C	HRNR	c.G1280A	p.G427D

XH_P57	1	152193544	152193544	Silent	SNP	A	G	A	HRNR	c.T561C	p.H187H
XH_P57	1	152193851	152193851	Missense_Mutation	SNP	C	T	C	HRNR	c.G254A	p.R85H
XH_P57	1	152279406	152279406	Missense_Mutation	SNP	T	G	T	FLG	c.A7956C	p.E2652D
XH_P57	1	152284019	152284019	Missense_Mutation	SNP	C	G	C	FLG	c.G3343C	p.G1115R
XH_P57	1	152285807	152285807	Missense_Mutation	SNP	G	T	G	FLG	c.C1555A	p.H519N
XH_P57	1	152323668	152323668	Silent	SNP	T	A	T	FLG2	c.A6594T	p.G2198G
XH_P57	1	152324099	152324099	Missense_Mutation	SNP	C	T	C	FLG2	c.G6163A	p.G2055R
XH_P57	1	152329369	152329369	Missense_Mutation	SNP	C	G	C	FLG2	c.G893C	p.C298S
XH_P57	1	152883163	152883163	Missense_Mutation	SNP	A	T	A	IVL	c.A890T	p.D297V
XH_P57	1	152944594	152944594	Silent	SNP	C	T	C	SPRR4	c.C228T	p.S76S
XH_P57	1	153004983	153004983	Silent	SNP	C	T	C	SPRR1B	c.C162T	p.P54P
XH_P57	1	153012765	153012765	Missense_Mutation	SNP	T	C	T	SPRR2D	c.A58G	p.T20A
XH_P57	1	153066072	153066072	Silent	SNP	T	C	T	SPRR2E	c.A156G	p.Q52Q
XH_P57	1	153085029	153085029	Missense_Mutation	SNP	G	T	G	SPRR2F	c.C181A	p.P61T
XH_P57	1	153276449	153276449	Missense_Mutation	SNP	T	C	T	PGLYRP3	c.A413G	p.E138G
XH_P57	1	153279598	153279598	Silent	SNP	C	T	C	PGLYRP3	c.G201A	p.L67L
XH_P57	1	153315579	153315579	Silent	SNP	A	G	A	PGLYRP4	c.T459C	p.F153F
XH_P57	1	153509890	153509890	Missense_Mutation	SNP	T	C	T	S100A5	c.A161G	p.D54G
XH_P57	1	153750682	153750682	Missense_Mutation	SNP	G	A	G	SLC27A3	c.G1591A	p.G531R
XH_P57	1	154296076	154296076	Silent	SNP	T	C	T	AQP10	c.T501C	p.T167T
XH_P57	1	154473919	154473919	Missense_Mutation	SNP	T	C	T	SHE	c.A584G	p.Q195R
XH_P57	1	154744807	154744807	Silent	SNP	C	G	C	KCN3	c.G1092C	p.L364L
XH_P57	1	155177615	155177615	Missense_Mutation	SNP	A	C	A	THBS3	c.T53G	p.F18C
XH_P57	1	156236394	156236394	Frame_Shift_Ins	INS	-	T	-	SMG5	c.1192_1193ins	p.R398fs
XH_P57	1	156500033	156500033	Missense_Mutation	SNP	C	T	C	IQGAP3	c.G4268A	p.R1423H
XH_P57	1	156553232	156553232	Frame_Shift_Del	DEL	C	-	C	TTC24	c.C1142delC	p.A381fs
XH_P57	1	156616639	156616639	Missense_Mutation	SNP	G	C	G	BCAN	c.G138C	p.Q46H
XH_P57	1	156622252	156622252	Missense_Mutation	SNP	G	A	G	BCAN	c.G1510A	p.E504K
XH_P57	1	156641537	156641537	Missense_Mutation	SNP	C	T	C	NE5	c.G2443A	p.V815I
XH_P57	1	156879703	156879703	Silent	SNP	T	C	T	PEAR1	c.T1572C	p.C524C
XH_P57	1	156899480	156899480	Missense_Mutation	SNP	G	A	G	LRRC71	c.G1199A	p.G400E
XH_P57	1	157062696	157062696	Silent	SNP	G	T	G	ETV3L	c.C831A	p.L277L
XH_P57	1	158435896	158435896	Missense_Mutation	SNP	C	T	C	OR10K1	c.C545T	p.S182F
XH_P57	1	158532932	158532932	Missense_Mutation	SNP	T	C	T	OR6P1	c.A463G	p.S155G
XH_P57	1	158577167	158577167	Silent	SNP	A	T	A	OR10Z1	c.A939T	p.G313G
XH_P57	1	158813819	158813819	Silent	SNP	A	G	A	MNDA	c.A477G	p.P159P
XH_P57	1	158990247	158990247	Silent	SNP	A	G	A	IFI16	c.A921G	p.Q307Q
XH_P57	1	159024668	159024668	Missense_Mutation	SNP	A	T	A	IFI16	c.A2167T	p.T723S
XH_P57	1	159162378	159162378	Silent	SNP	T	C	T	CADM3	c.T240C	p.D80D
XH_P57	1	159175428	159175428	Missense_Mutation	SNP	C	T	C	ACKR1	c.C205T	p.L69F
XH_P57	1	159275976	159275976	Missense_Mutation	SNP	C	T	C	FCER1A	c.C530T	p.T177M
XH_P57	1	159410007	159410007	Silent	SNP	C	T	C	OR10J1	c.C459T	p.I153I
XH_P57	1	159898100	159898100	Silent	SNP	A	G	A	IGSF9	c.T3078C	p.S1026S
XH_P57	1	160011894	160011894	Silent	SNP	G	A	G	KCN110	c.C429T	p.A143A
XH_P57	1	160098543	160098543	Silent	SNP	G	A	G	ATP1A2	c.G1119A	p.S373S
XH_P57	1	160099931	160099931	Missense_Mutation	SNP	G	A	G	ATP1A2	c.G1501A	p.V501M
XH_P57	1	161017556	161017556	Silent	SNP	C	T	C	ARHGAP30	c.G2724A	p.R908R
XH_P57	1	161071947	161071947	Frame_Shift_Ins	INS	-	T	-	PFND2	c.178dupA	p.T60fs
XH_P57	1	161479745	161479745	Missense_Mutation	SNP	A	G	A	FCGR2A	c.A500G	p.H167R
XH_P57	1	161683136	161683136	Missense_Mutation	SNP	G	A	G	FCRLA	c.G392A	p.R131Q
XH_P57	1	161696782	161696782	Missense_Mutation	SNP	G	C	G	FCRLB	c.G698C	p.R233P
XH_P57	1	162313735	162313735	Silent	SNP	C	T	C	NOS1AP	c.C549T	p.S183S
XH_P57	1	162344102	162344102	Silent	SNP	C	T	C	SPATA46	c.G522A	p.R174R
XH_P57	1	162760622	162760622	Missense_Mutation	SNP	G	C	G	HSD17B7	c.G32C	p.S11T
XH_P57	1	162782145	162782145	Missense_Mutation	SNP	A	G	A	HSD17B7	c.A961G	p.K321E
XH_P57	1	165648709	165648709	Silent	SNP	C	T	C	ALDH9A1	c.G900A	p.A300A
XH_P57	1	167097061	167097061	Missense_Mutation	SNP	A	G	A	DUSP27	c.A2693G	p.Y898C
XH_P57	1	167849414	167849414	Silent	SNP	A	G	A	ADCY10	c.T696C	p.G232G
XH_P57	1	167893759	167893759	Silent	SNP	G	A	G	MPC2	c.C126T	p.F42F
XH_P57	1	167973976	167973976	Silent	SNP	C	T	C	DCAF6	c.C1230T	p.D410D
XH_P57	1	168059866	168059866	Silent	SNP	A	G	A	GPR161	c.T906C	p.G302G
XH_P57	1	169437392	169437392	Missense_Mutation	SNP	A	G	A	SLC19A2	c.T719C	p.I240T
XH_P57	1	169438025	169438025	Silent	SNP	A	G	A	SLC19A2	c.T477C	p.T159T
XH_P57	1	171227216	171227216	Missense_Mutation	SNP	T	C	T	FMO1	c.T2C	p.M1T
XH_P57	1	171509523	171509523	Missense_Mutation	SNP	G	T	G	PRRC2C	c.G2912T	p.G971V
XH_P57	1	171755182	171755182	Missense_Mutation	SNP	G	A	G	METTL13	c.G609A	p.M203I
XH_P57	1	171956803	171956803	Silent	SNP	C	T	C	DNM3	c.C243T	p.A81A
XH_P57	1	172357926	172357926	Silent	SNP	G	A	G	DNM3	c.G2487A	p.T829T
XH_P57	1	175335234	175335234	Silent	SNP	C	T	C	TNR	c.G1095A	p.S365S
XH_P57	1	175375635	175375635	Silent	SNP	G	A	G	TNR	c.C216T	p.N72N
XH_P57	1	179055020	179055020	Silent	SNP	C	T	C	TOR3A	c.C631T	p.L211L
XH_P57	1	179077871	179077871	Missense_Mutation	SNP	C	T	C	ABL2	c.G2468A	p.S823N
XH_P57	1	179621224	179621224	Silent	SNP	G	A	G	TDRD5	c.G717A	p.G239G
XH_P57	1	180064728	180064728	Missense_Mutation	SNP	G	A	G	CEP350	c.G8582A	p.R2861Q
XH_P57	1	180163400	180163400	Silent	SNP	C	T	C	QSOX1	c.C1341T	p.F447F
XH_P57	1	180165699	180165699	Missense_Mutation	SNP	A	C	A	QSOX1	c.A1771C	p.N591H
XH_P57	1	180905352	180905352	Silent	SNP	C	T	C	KIAA1614	c.C2307T	p.S769S
XH_P57	1	180905448	180905448	Missense_Mutation	SNP	G	T	G	KIAA1614	c.G2403T	p.L801F
XH_P57	1	181018252	181018252	Silent	SNP	T	C	T	MR1	c.T132C	p.F44F
XH_P57	1	181702807	181702807	Missense_Mutation	SNP	C	G	C	CACNA1E	c.C3126G	p.D1042E
XH_P57	1	182993025	182993025	Silent	SNP	C	T	C	LAMC1	c.C174T	p.A58A
XH_P57	1	183072590	183072590	Silent	SNP	T	C	T	LAMC1	c.T546C	p.C182C
XH_P57	1	183086567	183086567	Silent	SNP	C	T	C	LAMC1	c.C1677T	p.F559F
XH_P57	1	183086757	183086757	Silent	SNP	A	C	A	LAMC1	c.A1776C	p.A592A
XH_P57	1	183093875	183093875	Silent	SNP	T	C	T	LAMC1	c.T2511C	p.N837N
XH_P57	1	183094547	183094547	Missense_Mutation	SNP	T	C	T	LAMC1	c.T2663C	p.L888P
XH_P57	1	183105534	183105534	Silent	SNP	T	C	T	LAMC1	c.T4128C	p.R1376R
XH_P57	1	183105705	183105705	Silent	SNP	G	A	G	LAMC1	c.G4299A	p.A1433A
XH_P57	1	183617105	183617105	Missense_Mutation	SNP	A	G	A	APOBEC4	c.T812C	p.F271S
XH_P57	1	183909717	183909717	Silent	SNP	G	A	G	COLGALT2	c.C1602T	p.P534P
XH_P57	1	184764912	184764912	Silent	SNP	G	A	G	FAM129A	c.C1986T	p.D662D
XH_P57	1	185135745	185135745	Silent	SNP	A	G	A	SWT1	c.A126G	p.S42S
XH_P57	1	185143721	185143721	Missense_Mutation	SNP	A	G	A	SWT1	c.A442G	p.I148V
XH_P57	1	185240474	185240474	Missense_Mutation	SNP	A	G	A	SWT1	c.A2461G	p.N821D
XH_P57	1	186276661	186276661	Missense_Mutation	SNP	A	G	A	PRG4	c.A1408G	p.T470A
XH_P57	1	186277989	186277989	Silent	SNP	A	G	A	PRG4	c.A2736G	p.P912P
XH_P57	1	186363119	186363119	Missense_Mutation	SNP	C	G	C	C1orf27	c.C656G	p.S219C
XH_P57	1	197872019	197872019	Silent	SNP	G	T	G	C1orf53	c.G240T	p.A80A

XH_P57	1	197896728	197896728	Silent	SNP	T	C	T	LHX9	c.T741C	p.N247N
XH_P57	1	201083930	201083930	Missense_Mutation	SNP	A	G	A	ASCL5	c.T571C	p.S191P
XH_P57	1	201176651	201176651	Missense_Mutation	SNP	C	T	C	IGFN1	c.C2630T	p.T877M
XH_P57	1	201181994	201181994	Missense_Mutation	SNP	A	G	A	IGFN1	c.A7973G	p.D2658G
XH_P57	1	201869257	201869257	Missense_Mutation	SNP	G	A	G	LMOD1	c.C884T	p.T295M
XH_P57	1	201969082	201969082	Silent	SNP	G	A	G	RNPEP	c.G273A	p.Q91Q
XH_P57	1	201981128	201981176	Frame_Shift_Del	DEL	TCAGCTACCC	-	ATCAGCTACCA	ELF3	c.207_255del	p.K69fs
XH_P57	1	202183308	202183308	Missense_Mutation	SNP	C	T	C	LGR6	c.C26T	p.S9L
XH_P57	1	202418235	202418235	In_Frame_Ins	INS	-	CAG	-	PPP1R12B	c.1786_1787insC	p.T596delinsTA
XH_P57	1	202574784	202574784	Silent	SNP	G	A	G	SYT2	c.C117T	p.S39S
XH_P57	1	203008286	203008286	Silent	SNP	C	G	C	PPFIA4	c.C150G	p.T50T
XH_P57	1	203743122	203743122	Silent	SNP	G	A	G	LAX1	c.G462A	p.S154S
XH_P57	1	203743653	203743653	Silent	SNP	C	T	C	LAX1	c.C993T	p.D331D
XH_P57	1	204131186	204131186	Silent	SNP	T	G	T	REN	c.A204C	p.T68T
XH_P57	1	204587240	204587240	Silent	SNP	G	A	G	LRRN2	c.C1881T	p.D627D
XH_P57	1	205053257	205053268	In_Frame_Del	DEL	FCACAGACGG	-	CTCACAGACGGT	TMEM81	c.181_192del	p.G1_64del
XH_P57	1	205632348	205632348	Frame_Shift_Ins	INS	-	G	-	SLC45A3	c.570dupC	p.Y191fs
XH_P57	1	207074905	207074905	Missense_Mutation	SNP	T	C	T	IL24	c.T373C	p.Y125H
XH_P57	1	207087435	207087435	Silent	SNP	C	T	C	FCMR	c.G42A	p.S14S
XH_P57	1	207110936	207110936	Silent	SNP	T	C	T	PIGR	c.A549G	p.V183V
XH_P57	1	207140440	207140440	Silent	SNP	C	T	C	FCAMR	c.C126A	p.A42A
XH_P57	1	208252777	208252777	Missense_Mutation	SNP	G	C	G	PLXNA2	c.C2414G	p.A805G
XH_P57	1	208390469	208390469	Missense_Mutation	SNP	C	T	C	PLXNA2	c.G799A	p.A267T
XH_P57	1	209807972	209807972	Silent	SNP	G	A	G	LAMB3	c.C384T	p.P128P
XH_P57	1	209811886	209811886	Silent	SNP	T	G	T	LAMB3	c.A291C	p.S97S
XH_P57	1	212799949	212799949	Missense_Mutation	SNP	C	T	C	FAM71A	c.C1730T	p.T577M
XH_P57	1	215793834	215793834	Silent	SNP	G	A	G	KCTD3	c.G2316A	p.A772A
XH_P57	1	215848587	215848587	Silent	SNP	T	C	T	USH2A	c.A12666G	p.T4222T
XH_P57	1	216051125	216051125	Missense_Mutation	SNP	G	A	G	USH2A	c.C8656T	p.L2886F
XH_P57	1	221912808	221912808	Silent	SNP	T	C	T	DUSP10	c.A279G	p.Q93Q
XH_P57	1	222802803	222802803	Silent	SNP	T	G	T	MIA3	c.T2241G	p.P747P
XH_P57	1	222833538	222833538	Silent	SNP	C	G	C	MIA3	c.C1629G	p.G543G
XH_P57	1	223567267	223567267	Silent	SNP	C	T	C	CCDC185	c.C450T	p.P150P
XH_P57	1	223567808	223567808	Missense_Mutation	SNP	C	T	C	CCDC185	c.C991T	p.R331W
XH_P57	1	226032919	226032919	Silent	SNP	G	A	G	EPHX1	c.G1239A	p.V413V
XH_P57	1	226054333	226054333	Missense_Mutation	SNP	G	A	G	TMEM63A	c.C616T	p.L206F
XH_P57	1	226074563	226074563	Missense_Mutation	SNP	T	G	T	LEFTY1	c.A965C	p.D322A
XH_P57	1	226108200	226108200	Silent	SNP	C	T	C	PYCR2	c.G696A	p.G232G
XH_P57	1	228399799	228399799	Silent	SNP	C	T	C	OBSCN	c.C315T	p.C105C
XH_P57	1	228400428	228400428	Missense_Mutation	SNP	A	G	A	OBSCN	c.A944G	p.N315S
XH_P57	1	228402508	228402508	Silent	SNP	C	T	C	OBSCN	c.C1537T	p.L513L
XH_P57	1	228404198	228404198	Silent	SNP	G	A	G	OBSCN	c.G2172A	p.A724A
XH_P57	1	228433217	228433217	Silent	SNP	A	G	A	OBSCN	c.A3585G	p.T1195T
XH_P57	1	228434395	228434395	Silent	SNP	T	C	T	OBSCN	c.T3924C	p.A1308A
XH_P57	1	228451826	228451826	Missense_Mutation	SNP	C	T	C	OBSCN	c.C4595T	p.A1532V
XH_P57	1	228468458	228468458	Missense_Mutation	SNP	G	A	G	OBSCN	c.G8158A	p.V2720M
XH_P57	1	228471379	228471379	Silent	SNP	G	C	G	OBSCN	c.G8913C	p.R2971R
XH_P57	1	228475848	228475848	Missense_Mutation	SNP	G	A	G	OBSCN	c.G9898A	p.A3300T
XH_P57	1	228491633	228491633	Missense_Mutation	SNP	G	A	G	OBSCN	c.G13996A	p.V4666I
XH_P57	1	228492044	228492044	Silent	SNP	G	A	G	OBSCN	c.G14043A	p.E4681E
XH_P57	1	228494790	228494790	Missense_Mutation	SNP	G	A	G	OBSCN	c.G12115A	p.G4039R
XH_P57	1	228496014	228496014	Silent	SNP	G	A	G	OBSCN	c.G12669A	p.T4223T
XH_P57	1	228505739	228505739	Missense_Mutation	SNP	G	A	G	OBSCN	c.G13996A	p.G4666S
XH_P57	1	228520973	228520973	Missense_Mutation	SNP	C	G	C	OBSCN	c.C15805G	p.L5269V
XH_P57	1	228550429	228550429	Missense_Mutation	SNP	C	T	C	OBSCN	c.C18814T	p.P6272S
XH_P57	1	228564757	228564757	Missense_Mutation	SNP	C	T	C	OBSCN	c.C23044T	p.R7682C
XH_P57	1	228582643	228582643	Silent	SNP	C	T	C	TRIM11	c.G1170A	p.S390S
XH_P57	1	230384937	230384937	Silent	SNP	T	C	T	GALNT2	c.T711C	p.D237D
XH_P57	1	230461079	230461079	Silent	SNP	G	A	G	PGBD5	c.C1356T	p.C452C
XH_P57	1	231298898	231298898	Silent	SNP	C	A	C	TRIM67	c.C183A	p.A61A
XH_P57	1	232534957	232534957	Silent	SNP	T	C	T	SIPA1L2	c.CA5085G	p.R1695R
XH_P57	1	232539219	232539219	Missense_Mutation	SNP	C	T	C	SIPA1L2	c.G4915A	p.G1639S
XH_P57	1	232581376	232581376	Silent	SNP	G	A	G	SIPA1L2	c.C3252T	p.P1084P
XH_P57	1	232943502	232943502	Silent	SNP	G	T	G	MAP10	c.G2733T	p.G911G
XH_P57	1	233397909	233397909	Missense_Mutation	SNP	T	C	T	PCNX2	c.A362G	p.N121S
XH_P57	1	234509259	234509259	Missense_Mutation	SNP	G	C	G	COA6	c.C47C	p.S16T
XH_P57	1	234546245	234546245	Silent	SNP	C	T	C	TARBP1	c.G3738A	p.T1246T
XH_P57	1	234606998	234606998	Silent	SNP	A	G	A	TARBP1	c.T1035C	p.H345H
XH_P57	1	235940450	235940450	Silent	SNP	C	T	C	LYST	c.G5373A	p.K1791K
XH_P57	1	235955150	235955150	Silent	SNP	G	A	G	LYST	c.C4392T	p.N1464N
XH_P57	1	235972435	235972435	Silent	SNP	T	C	T	LYST	c.A1683G	p.L561L
XH_P57	1	235972867	235972867	Silent	SNP	T	C	T	LYST	c.A1251G	p.Q417Q
XH_P57	1	236208773	236208773	Missense_Mutation	SNP	C	T	C	NID1	c.G736A	p.V246I
XH_P57	1	236413230	236413230	Missense_Mutation	SNP	T	A	T	ERO1B	c.A386T	p.D129V
XH_P57	1	236717926	236717926	Missense_Mutation	SNP	T	C	T	HEATR1	c.A6050G	p.E2017G
XH_P57	1	236719193	236719193	Missense_Mutation	SNP	A	G	A	HEATR1	c.T5561C	p.V1854A
XH_P57	1	236749649	236749649	Missense_Mutation	SNP	T	C	T	HEATR1	c.A1819G	p.M607V
XH_P57	1	238050750	238050750	Missense_Mutation	SNP	G	T	G	ZP4	c.C665A	p.A222E
XH_P57	1	238051793	238051793	Missense_Mutation	SNP	T	C	T	ZP4	c.A418G	p.T140A
XH_P57	1	240256822	240256822	Silent	SNP	C	A	C	FMN2	c.C1413A	p.A471A
XH_P57	1	245849729	245849729	Silent	SNP	G	A	G	KIF26B	c.G3444A	p.P1148P
XH_P57	1	245850506	245850506	Silent	SNP	G	C	G	KIF26B	c.G4221C	p.P1407P
XH_P57	1	245851289	245851289	Silent	SNP	G	T	G	KIF26B	c.G5004T	p.S1668S
XH_P57	1	247264430	247264430	Missense_Mutation	SNP	T	C	T	ZNF669	c.A383G	p.Y128C
XH_P57	1	247587408	247587408	Silent	SNP	C	T	C	NLRP3	c.C663T	p.T221T
XH_P57	1	247615262	247615262	Frame_Shift_Del	DEL	A	-	A	OR2B11	c.23delT	p.F8fs
XH_P57	1	247752161	247752161	Missense_Mutation	SNP	T	C	T	OR2G2	c.T500C	p.L167P
XH_P57	1	247752367	247752367	Missense_Mutation	SNP	A	G	A	OR2G2	c.A706G	p.R236G
XH_P57	1	247769752	247769752	Missense_Mutation	SNP	A	G	A	OR2G3	c.A865G	p.I289V
XH_P57	1	247921100	247921100	Silent	SNP	T	G	T	OR1C1	c.A609C	p.G203G
XH_P57	1	248085108	248085108	Silent	SNP	C	T	C	OR2T8	c.C789T	p.H263H
XH_P57	1	248112627	248112627	Silent	SNP	T	C	T	OR2L8	c.T468C	p.C156C
XH_P57	1	248112815	248112815	Missense_Mutation	SNP	A	G	A	OR2L8	c.A656G	p.Q219R
XH_P57	1	248129240	248129240	Missense_Mutation	SNP	G	A	G	OR2AK2	c.G607A	p.V203M
XH_P57	1	248129512	248129512	Silent	SNP	C	T	C	OR2AK2	c.C879T	p.Y293Y
XH_P57	1	248186000	248186000	Missense_Mutation	SNP	T	C	T	OR2L5	c.T751C	p.Y251H
XH_P57	1	248202344	248202344	Missense_Mutation	SNP	G	C	G	OR2L2	c.G775C	p.V259L
XH_P57	1	248262993	248262993	Missense_Mutation	SNP	A	G	A	OR2L13	c.A316G	p.M106V

XH_P57	1	248367014	248367014	Silent	SNP	T	C	T	OR2M3	c.T645C	p.I215I
XH_P57	1	248367015	248367015	Missense_Mutation	SNP	G	A	G	OR2M3	c.G646A	p.A216T
XH_P57	1	248436809	248436809	Missense_Mutation	SNP	G	A	G	OR2T33	c.C308T	p.P103L
XH_P57	1	248436811	248436811	Silent	SNP	G	C	G	OR2T33	c.C306G	p.L102L
XH_P57	1	248844959	248844959	Missense_Mutation	SNP	T	C	T	OR141I	c.A647G	p.Y216C
XH_P57	1	248845356	248845356	Missense_Mutation	SNP	G	T	G	OR141I	c.C250A	p.L84M
XH_P57	1	249141782	249141782	Silent	SNP	A	T	A	ZNf672	c.A309T	p.T103T
XH_P57	1	249141869	249141869	Silent	SNP	G	C	G	ZNf672	c.G396C	p.L132L
XH_P57	1	249211096	249211096	Missense_Mutation	SNP	G	A	G	PGBD2	c.G313A	p.V105I
XH_P57	1	249211619	249211619	Missense_Mutation	SNP	G	A	G	PGBD2	c.G83A	p.R28Q
XH_P57	2	45611	45611	Missense_Mutation	SNP	C	T	C	FAM110C	c.G775A	p.G259S
XH_P57	2	264981	264981	Missense_Mutation	SNP	C	T	C	ACP1	c.C17T	p.T6I
XH_P57	2	1320143	1320143	Missense_Mutation	SNP	C	T	C	SNTG2	c.C1484T	p.T495M
XH_P57	2	1418192	1418192	Silent	SNP	C	G	C	TPO	c.C12G	p.L4L
XH_P57	2	1652387	1652387	Silent	SNP	G	A	G	PXDn	c.C3165T	p.P1055P
XH_P57	2	1652912	1652912	Silent	SNP	G	C	G	PXDn	c.C2640G	p.R880R
XH_P57	2	1842968	1842968	Silent	SNP	T	C	T	MYT1L	c.A3033G	p.G1011G
XH_P57	2	3673648	3673648	Silent	SNP	G	A	G	COLEC11	c.G159A	p.K53K
XH_P57	2	8870862	8870862	Silent	SNP	T	C	T	KIDINS220	c.A5136G	p.E1712E
XH_P57	2	9634856	9634856	Silent	SNP	A	G	A	ADAM17	c.T1824C	p.S608S
XH_P57	2	10126330	10126330	Missense_Mutation	SNP	G	A	G	GRHL1	c.G1189A	p.V397I
XH_P57	2	10262920	10262920	Missense_Mutation	SNP	T	G	G	RRM2	c.T175G	p.S59A
XH_P57	2	11364528	11364528	Frame_Shift_Ins	INS	-	CAGATAGGTAAT	-	ROCK2	69insCATTACCT	p.H223fs
XH_P57	2	15743344	15743344	Silent	SNP	T	C	T	DDX1	c.T420C	p.H140H
XH_P57	2	15768936	15768936	In_Frame_Ins	INS	-	CGATGTACG	-	DDX1	81849insCGATG	p.I616delinsRCT
XH_P57	2	20132090	20132090	Missense_Mutation	SNP	T	C	T	WDR35	c.A2777G	p.Y926C
XH_P57	2	20133182	20133182	Frame_Shift_Ins	INS	-	AG	-	WDR35	2637_2638insC	p.T880fs
XH_P57	2	21252534	21252534	Missense_Mutation	SNP	G	A	G	APOB	c.C1594T	p.R532W
XH_P57	2	23926233	23926233	Silent	SNP	C	T	C	KLHL29	c.C2283T	p.I761I
XH_P57	2	24149439	24149439	Silent	SNP	G	A	G	ATAD2B	c.C202T	p.L68L
XH_P57	2	24342505	24342505	Silent	SNP	T	C	T	PFN4	c.A303G	p.V101V
XH_P57	2	24344060	24344060	Silent	SNP	T	G	T	PFN4	c.A228C	p.A76A
XH_P57	2	24413298	24413298	Missense_Mutation	SNP	A	G	A	FAM228A	c.A419G	p.Y140C
XH_P57	2	24431184	24431184	Missense_Mutation	SNP	C	T	C	ITSN2	c.G4480A	p.A1494T
XH_P57	2	24432839	24432839	Silent	SNP	A	G	A	ITSN2	c.T4201C	p.L1401L
XH_P57	2	25469502	25469502	Silent	SNP	C	T	C	DNMT3A	c.G810A	p.L270L
XH_P57	2	25965048	25965048	Silent	SNP	C	T	C	ASXL2	c.G4158A	p.A1386A
XH_P57	2	26688662	26688662	Silent	SNP	C	T	C	OTOF	c.G2607A	p.V869V
XH_P57	2	26699159	26699159	Silent	SNP	C	T	C	OTOF	c.G633A	p.S211S
XH_P57	2	26699822	26699822	Silent	SNP	G	A	G	OTOF	c.C543T	p.L181L
XH_P57	2	26739433	26739433	Missense_Mutation	SNP	G	A	G	OTOF	c.C362T	p.T121I
XH_P57	2	27262658	27262658	Silent	SNP	C	T	C	TMEM214	c.C1440T	p.S480S
XH_P57	2	27851918	27851918	Missense_Mutation	SNP	G	A	G	GNP1	c.G35A	p.R12K
XH_P57	2	28805300	28805300	Missense_Mutation	SNP	C	T	C	PLB1	c.C1628T	p.T543M
XH_P57	2	28827608	28827608	Silent	SNP	C	T	C	PLB1	c.C2910T	p.I970I
XH_P57	2	29287926	29287926	In_Frame_Ins	INS	-	GCT	-	C2orf71	3675_3676insAAG	p.E1226delinsSE
XH_P57	2	29295016	29295016	Silent	SNP	A	G	A	C2orf71	c.T2112C	p.N704N
XH_P57	2	29295389	29295389	Missense_Mutation	SNP	G	A	G	C2orf71	c.C1739T	p.T580M
XH_P57	2	29295676	29295676	Silent	SNP	G	A	G	C2orf71	c.C1452T	p.S484S
XH_P57	2	29295866	29295866	Missense_Mutation	SNP	T	C	T	C2orf71	c.A1262G	p.K421R
XH_P57	2	29390381	29390381	Silent	SNP	A	G	A	CLIP4	c.A1698G	p.S566S
XH_P57	2	29449819	29449819	Silent	SNP	C	T	C	ALK	c.G3036A	p.T1012T
XH_P57	2	30381505	30381505	Silent	SNP	T	C	T	YPEL5	c.T162C	p.S54S
XH_P57	2	32402636	32402636	Silent	SNP	C	T	C	SLC30A6	c.C309T	p.N103N
XH_P57	2	32476390	32476390	Silent	SNP	T	G	T	NLRCA	c.A543C	p.R181R
XH_P57	2	33488419	33488419	Silent	SNP	G	A	G	LTBP1	c.G1599A	p.T533T
XH_P57	2	33540248	33540248	Silent	SNP	G	A	G	LTBP1	c.G2664A	p.P888P
XH_P57	2	37035866	37035866	Silent	SNP	G	T	G	VIT	c.G1533T	p.T511T
XH_P57	2	37230728	37230728	Silent	SNP	T	C	T	HEATR5B	c.A5007G	p.V1669V
XH_P57	2	37241050	37241050	Silent	SNP	G	A	G	HEATR5B	c.C4218T	p.S1406S
XH_P57	2	38178877	38178877	Silent	SNP	A	G	A	RMDN2	c.A519G	p.K173K
XH_P57	2	38604351	38604351	Missense_Mutation	SNP	A	G	A	ATL2	c.T52C	p.L178R
XH_P57	2	38916970	38916970	Missense_Mutation	SNP	A	T	A	GALM	c.A568T	p.N190Y
XH_P57	2	39008949	39008949	Missense_Mutation	SNP	G	A	G	GEMIN6	c.G419A	p.G140D
XH_P57	2	40006368	40006368	Silent	SNP	C	A	C	THUMPD2	c.G12T	p.A4A
XH_P57	2	42165754	42165754	Splice_Site	SNP	C	T	C	C2orf91	.	.
XH_P57	2	42275726	42275726	Silent	SNP	C	G	C	PKDCC	c.C387G	p.R129R
XH_P57	2	43458358	43458358	Missense_Mutation	SNP	C	T	C	THADA	c.G5591A	p.S1864N
XH_P57	2	43903066	43903066	Silent	SNP	A	G	A	C1GALT1C1L	c.T396C	p.G132G
XH_P57	2	44021826	44021826	Missense_Mutation	SNP	T	A	T	DYNC2L1I	c.T551A	p.F184Y
XH_P57	2	53943734	53943734	Frame_Shift_Ins	INS	-	A	-	ASB3	c.S31dupT	p.I178fs
XH_P57	2	55130590	55130590	In_Frame_Ins	INS	-	GAAGCATTT	-	EML6	3361insGAAG	p.I1120delinsEAF
XH_P57	2	55155551	55155551	Silent	SNP	C	T	C	EML6	c.C3777T	p.A1259A
XH_P57	2	55449464	55449464	Silent	SNP	T	C	T	CLHC1	c.A84G	p.Q28Q
XH_P57	2	56420006	56420006	Missense_Mutation	SNP	A	T	A	CCDC85A	c.A671T	p.H224L
XH_P57	2	58316814	58316814	Missense_Mutation	SNP	A	G	A	VRK2	c.A145G	p.I49V
XH_P57	2	61577435	61577435	Silent	SNP	T	C	T	USP34	c.A1467G	p.A489A
XH_P57	2	64794728	64794728	Nonsense_Mutation	INS	-	ATTTTGATAATA	-	AFTPH	tsATTTAATTTTG	p.G557delinsFIX
XH_P57	2	68388823	68388823	Silent	SNP	A	G	A	PN01	c.A366G	p.K122K
XH_P57	2	68415767	68415767	Silent	SNP	G	A	A	PPP3R1	c.C99T	p.D33D
XH_P57	2	68613710	68613710	Silent	SNP	G	A	G	PLEK	c.G549A	p.S183S
XH_P57	2	69709919	69709919	Silent	SNP	A	G	A	AAK1	c.T2391C	p.S797S
XH_P57	2	69741609	69741609	Silent	SNP	C	T	C	AAK1	c.G1770A	p.E590E
XH_P57	2	69746296	69746296	Silent	SNP	C	T	C	AAK1	c.G1287A	p.P429P
XH_P57	2	71036482	71036482	Missense_Mutation	SNP	T	C	T	CLEC4F	c.A1691G	p.K564R
XH_P57	2	71220864	71220864	Missense_Mutation	SNP	T	C	T	TEX261	c.A112G	p.T38A
XH_P57	2	71795152	71795152	Silent	SNP	A	T	A	DYSF	c.A2541T	p.S847S
XH_P57	2	71838597	71838597	Silent	SNP	C	A	C	DYSF	c.C3966A	p.I1322I
XH_P57	2	73777449	73777449	Frame_Shift_Ins	INS	-	GATG	-	ALMS1	960_996insGAG	p.D3320fs
XH_P57	2	74074562	74074562	Missense_Mutation	SNP	C	G	G	STAMBP	c.C424G	p.L142V
XH_P57	2	74489318	74489318	Missense_Mutation	SNP	G	A	G	SLC4A5	c.C757T	p.H253Y
XH_P57	2	74642265	74642265	In_Frame_Ins	INS	-	GGGGCGGGTGG	-	C2orf81	GGGGCGGCACCG	p.G2delinsGGATRPSAS
XH_P57	2	74763258	74763258	Silent	SNP	C	G	C	LOXL3	c.G30C	p.L10L
XH_P57	2	75185856	75185856	Missense_Mutation	SNP	G	T	G	POLE4	c.G50T	p.G17V
XH_P57	2	80101372	80101372	Silent	SNP	C	T	C	CTNNA2	c.C756T	p.A252A
XH_P57	2	80529956	80529956	Missense_Mutation	SNP	T	C	T	LRRTM1	c.A989G	p.S30S
XH_P57	2	85824251	85824251	Missense_Mutation	SNP	T	C	T	RNF181	c.T352C	p.Y18H
XH_P57	2	85890553	85890553	Silent	SNP	G	A	G	SFTPB	c.C954T	p.T318T

XH_P57	2	86088311	86088311	Missense_Mutation	SNP	T	C	T	ST3GAL5	c.A242G	p.H81R
XH_P57	2	86259443	86259443	Silent	SNP	C	T	C	POLR1A	c.G4224A	p.G1408G
XH_P57	2	86359513	86359513	Frame_Shift_Ins	INS	-	TGCAAGTAGTAA	-	PTCD3	840insATGCAAG	p.F447fs
XH_P57	2	86371823	86371823	Silent	SNP	A	G	A	IMMT	c.T1842C	p.A614A
XH_P57	2	86406556	86406556	Silent	SNP	C	T	C	IMMT	c.G309A	p.S103S
XH_P57	2	86968138	86968138	Silent	SNP	C	T	C	RMND5A	c.C231T	p.S77S
XH_P57	2	87214163	87214163	Missense_Mutation	SNP	G	T	G	RGPDI	c.G4117T	p.D1373Y
XH_P57	2	88407959	88407959	Silent	SNP	T	C	T	SMYD1	c.T1176C	p.H392H
XH_P57	2	88424066	88424066	Missense_Mutation	SNP	T	C	T	FABP1	c.A280G	p.T94H
XH_P57	2	95940549	95940549	Silent	SNP	G	A	G	PROM2	c.G216A	p.S72S
XH_P57	2	96858817	96858817	Missense_Mutation	SNP	G	A	G	STARD7	c.C742T	p.R248C
XH_P57	2	97613616	97613616	Silent	SNP	T	C	T	FAM178B	c.A1017G	p.T339T
XH_P57	2	97637905	97637905	Missense_Mutation	SNP	T	C	T	FAM178B	c.A297G	p.I99M
XH_P57	2	97849219	97849219	Missense_Mutation	SNP	T	C	T	ANKRD36	c.T1861C	p.W621R
XH_P57	2	97860487	97860487	Missense_Mutation	SNP	T	C	T	ANKRD36	c.T2474C	p.L825S
XH_P57	2	98165920	98165920	Missense_Mutation	SNP	A	G	A	ANKRD36B	c.T1439C	p.I480T
XH_P57	2	98274527	98274527	Silent	SNP	G	C	G	ACTR1B	c.C804G	p.V268V
XH_P57	2	98408918	98408918	Missense_Mutation	SNP	C	T	C	TMEM131	c.G4075A	p.D1359N
XH_P57	2	98611994	98611994	Silent	SNP	G	T	G	TMEM131	c.C132A	p.G44G
XH_P57	2	98853173	98853173	Missense_Mutation	SNP	G	A	G	VWA3B	c.G1624A	p.V542M
XH_P57	2	99013259	99013259	Silent	SNP	C	T	C	CNGA3	c.C1572T	p.S524S
XH_P57	2	99170844	99170844	Silent	SNP	T	C	T	INPP4A	c.T1458C	p.T486T
XH_P57	2	99812108	99812108	Silent	SNP	T	C	T	MRPL30	c.T426C	p.T142T
XH_P57	2	103095404	103095404	Silent	SNP	G	A	G	SLC9A4	c.G363A	p.S121S
XH_P57	2	103095699	103095699	Missense_Mutation	SNP	G	A	G	SLC9A4	c.G658A	p.V220M
XH_P57	2	107040564	107040564	Missense_Mutation	SNP	C	T	C	RGPDI	c.G3859A	p.E1287K
XH_P57	2	107423395	107423395	Silent	SNP	T	G	T	ST6GAL2	c.A1329C	p.I443I
XH_P57	2	107459974	107459974	Missense_Mutation	SNP	C	T	C	ST6GAL2	c.G460A	p.G154R
XH_P57	2	108875198	108875198	Missense_Mutation	SNP	G	A	G	SULT1C3	c.G535A	p.G179R
XH_P57	2	109356978	109356978	Missense_Mutation	SNP	G	C	G	RANBP2	c.G816C	p.L272F
XH_P57	2	109374952	109374952	Silent	SNP	A	G	A	RANBP2	c.A2550G	p.S850S
XH_P57	2	109408208	109408208	Missense_Mutation	SNP	G	A	G	CCDC138	c.G329A	p.R110K
XH_P57	2	109513572	109513572	Missense_Mutation	SNP	T	G	T	EDAR	c.A1138C	p.S380R
XH_P57	2	109746039	109746039	Missense_Mutation	SNP	G	A	G	SH3RF3	c.G43A	p.A15T
XH_P57	2	113309473	113309473	Missense_Mutation	SNP	C	T	C	POLR1B	c.C251T	p.S84L
XH_P57	2	113404708	113404708	Silent	SNP	G	A	G	SLC20A1	c.G303A	p.L101L
XH_P57	2	113819725	113819725	Missense_Mutation	SNP	A	G	A	IL36RN	c.A140G	p.N47S
XH_P57	2	113890304	113890304	Silent	SNP	T	C	T	IL1RN	c.T390C	p.S130S
XH_P57	2	113958972	113958972	Missense_Mutation	SNP	C	T	C	PSD4	c.C3151T	p.R1051W
XH_P57	2	120078778	120078778	Missense_Mutation	SNP	T	C	T	C2orf76	c.A136G	p.I46V
XH_P57	2	121981950	121981950	Silent	SNP	A	G	A	TFCP2L1	c.T1407C	p.D469D
XH_P57	2	122216419	122216419	Silent	SNP	A	G	A	CLASP1	c.T1311C	p.I437I
XH_P57	2	127816695	127816695	Silent	SNP	C	T	C	BIN1	c.G729A	p.S243S
XH_P57	2	127821207	127821207	Silent	SNP	G	A	G	BIN1	c.C621T	p.Y207Y
XH_P57	2	128324358	128324358	Silent	SNP	C	T	C	MYO7B	c.C426T	p.Y142Y
XH_P57	2	128477084	128477084	Missense_Mutation	SNP	G	C	G	WDR33	c.C2515G	p.P839A
XH_P57	2	128522207	128522207	Missense_Mutation	SNP	C	T	C	WDR33	c.G821A	p.R274Q
XH_P57	2	128522383	128522383	Silent	SNP	T	C	T	WDR33	c.A645G	p.P215P
XH_P57	2	128610648	128610648	Silent	SNP	T	C	T	POLR2D	c.A105G	p.S35S
XH_P57	2	128870808	128870808	Silent	SNP	T	C	T	UGGT1	c.T672C	p.N224N
XH_P57	2	128878014	128878014	Silent	SNP	G	A	G	UGGT1	c.G957A	p.K319K
XH_P57	2	129026042	129026042	Silent	SNP	G	A	G	HS6ST1	c.C930T	p.L310L
XH_P57	2	130897234	130897234	Missense_Mutation	SNP	C	T	C	CCDC74B	c.G839A	p.R280H
XH_P57	2	130902549	130902549	Silent	SNP	C	T	C	CCDC74B	c.G21A	p.A7A
XH_P57	2	130925088	130925088	Silent	SNP	C	T	C	SMPD4	c.G633A	p.T211T
XH_P57	2	130949491	130949491	Silent	SNP	A	G	G	TUBA3E	c.C1266T	p.R422R
XH_P57	2	130949553	130949553	Missense_Mutation	SNP	A	G	A	TUBA3E	c.T1204C	p.W402R
XH_P57	2	131113698	131113698	Silent	SNP	C	T	C	PTPN18	c.C18T	p.D6D
XH_P57	2	131258139	131258139	Missense_Mutation	SNP	G	A	G	POTEI	c.C887T	p.A296V
XH_P57	2	131369330	131369330	Silent	SNP	C	T	C	POTEI	c.C225T	p.S75S
XH_P57	2	131520178	131520178	Missense_Mutation	SNP	C	G	C	AMER3	c.C533G	p.A178G
XH_P57	2	133075955	133075955	Silent	SNP	C	T	C	ZNFR806	c.C1416T	p.L472L
XH_P57	2	136437833	136437833	Missense_Mutation	SNP	C	A	C	R3HDM1	c.C1909A	p.P637T
XH_P57	2	136546110	136546110	Silent	SNP	A	G	A	LCT	c.T5568C	p.A1856A
XH_P57	2	136555659	136555659	Missense_Mutation	SNP	T	C	T	LCT	c.A4916G	p.N1639S
XH_P57	2	136561557	136561557	Silent	SNP	G	A	G	LCT	c.C4606T	p.L1536L
XH_P57	2	136575199	136575199	Silent	SNP	G	T	G	LCT	c.C1419A	p.G473G
XH_P57	2	136594158	136594158	Silent	SNP	G	A	G	LCT	c.C582T	p.T194T
XH_P57	2	139429068	139429068	Silent	SNP	G	A	G	NXPH2	c.C219T	p.Y73Y
XH_P57	2	153533260	153533260	Silent	SNP	G	A	G	PRPF40A	c.C690T	p.A230A
XH_P57	2	157407259	157407259	Splice_Site	INS	-	TAAT	-	GPDI	-	-
XH_P57	2	158290914	158290914	Missense_Mutation	SNP	G	C	G	CYTIIP	c.C247G	p.Q83E
XH_P57	2	160604812	160604812	Silent	SNP	C	T	C	MARCH7	c.C843T	p.P281P
XH_P57	2	160605268	160605268	Silent	SNP	T	C	T	MARCH7	c.T1299C	p.P433P
XH_P57	2	160710922	160710922	Silent	SNP	T	C	T	LY75	c.A2544G	p.A848A
XH_P57	2	160729005	160729005	Missense_Mutation	SNP	C	T	C	LY75	c.G2074A	p.D692N
XH_P57	2	160983060	160983060	Silent	SNP	G	C	G	ITGB6	c.C1428G	p.G476G
XH_P57	2	162565292	162565292	Frame_Shift_Del	DEL	GTCATGCA	-	GTCATGCA	SLC4A10	c.34_41del	p.V12fs
XH_P57	2	165987772	165987772	Silent	SNP	T	G	T	SCN3A	c.A2400C	p.V800V
XH_P57	2	165996020	165996020	Silent	SNP	C	T	C	SCN3A	c.G1971A	p.V657V
XH_P57	2	168102211	168102211	Nonsense_Mutation	SNP	C	T	C	XIRP2	c.C3643T	p.R1215X
XH_P57	2	169038488	169038488	Frame_Shift_Ins	INS	-	AA	-	STK39	c.320_321insTT	p.L107fs
XH_P57	2	169952233	169952233	Silent	SNP	T	C	T	DHRS9	c.T916C	p.L306L
XH_P57	2	170403030	170403030	Missense_Mutation	SNP	T	C	T	FASTKD1	c.A1330G	p.M444V
XH_P57	2	170441001	170441001	Splice_Site	SNP	G	A	G	PIIG	-	-
XH_P57	2	171678625	171678625	Silent	SNP	T	C	T	GAD1	c.T111C	p.H37H
XH_P57	2	172822320	172822320	Missense_Mutation	SNP	T	C	T	HAT1	c.T502C	p.C168R
XH_P57	2	173352157	173352157	Silent	SNP	A	T	A	ITGA6	c.A2136T	p.A712A
XH_P57	2	174946760	174946760	Missense_Mutation	SNP	T	C	T	OLA1	c.A287G	p.Y96C
XH_P57	2	175614815	175614815	Silent	SNP	C	T	C	CHRNA1	c.G861A	p.T287T
XH_P57	2	176988290	176988290	In Frame Ins	INS	-	GCA	-	HOXD9	794_795insGCC	p.P265delinsPQ
XH_P57	2	177016728	177016728	Missense_Mutation	SNP	T	C	T	HOXD4	c.T367C	p.S123P
XH_P57	2	177034121	177034121	Silent	SNP	G	T	G	HOXD3	c.G279T	p.P93P
XH_P57	2	177054769	177054769	Missense_Mutation	SNP	G	A	G	HOXD1	c.G886A	p.A296T
XH_P57	2	177193083	177193083	Frame_Shift_Ins	INS	-	TT	-	MTX2	c.348_349insTT	p.E116fs
XH_P57	2	179325816	179325816	Missense_Mutation	SNP	G	A	G	DFNB59	c.G874A	p.G292R
XH_P57	2	179401787	179401787	Missense_Mutation	SNP	G	A	G	TTN	c.C72854T	p.T2428S1
XH_P57	2	179456756	179456756	Missense_Mutation	SNP	G	A	G	TTN	c.C32680T	p.R10894C

XH_P57	2	179474668	179474668	Missense_Mutation	SNP	G	A	G	TTN	c.C24287T	p.A8096V
XH_P57	2	179477717	179477717	Silent	SNP	A	G	A	TTN	c.T22536C	p.H7512H
XH_P57	2	179497025	179497025	Silent	SNP	A	G	A	TTN	c.T16401C	p.N5467N
XH_P57	2	179515483	179515483	Missense_Mutation	SNP	G	C	G	TTN	c.C32402G	p.P10801R
XH_P57	2	179589058	179589058	Missense_Mutation	SNP	G	A	G	TTN	c.C17312T	p.A5771V
XH_P57	2	179593462	179593462	Silent	SNP	C	T	C	TTN	c.G15459A	p.T5153T
XH_P57	2	179644855	179644855	Missense_Mutation	SNP	T	C	T	TTN	c.A3463G	p.K1155E
XH_P57	2	179698945	179698945	Silent	SNP	G	A	G	CCDC141	c.C4548T	p.V1516V
XH_P57	2	180810202	180810202	Missense_Mutation	SNP	C	T	C	CWC22	c.G2381A	p.R794Q
XH_P57	2	182981968	182981968	Silent	SNP	A	G	A	PPP1R1C	c.A276G	p.A92A
XH_P57	2	185801596	185801596	Silent	SNP	C	T	C	ZNF804A	c.C1473T	p.D491D
XH_P57	2	185801917	185801917	Silent	SNP	A	G	A	ZNF804A	c.A1794G	p.K598K
XH_P57	2	185803364	185803364	Missense_Mutation	SNP	C	G	C	ZNF804A	c.C3241G	p.L1081V
XH_P57	2	187373316	187373316	Nonsense_Mutation	INS	-	TTACGAAGGAAC	-	ZC3H15	AGAAGTTACGA	R380delinsERSYEGRX
XH_P57	2	188211112	188211112	Silent	SNP	C	T	C	CALCRL	c.G1185A	p.L395L
XH_P57	2	191184475	191184475	Missense_Mutation	SNP	A	G	A	HIBCH	c.T2C	p.M1T
XH_P57	2	197183367	197183367	Silent	SNP	A	G	A	HECW2	c.T1179C	p.A393A
XH_P57	2	198001319	198001319	Silent	SNP	A	G	A	ANKRD44	c.T258C	p.S865
XH_P57	2	202025621	202025621	Silent	SNP	A	G	A	CFLAR	c.A525G	p.P175P
XH_P57	2	202050677	202050677	Silent	SNP	A	G	A	CASP10	c.A177G	p.S595
XH_P57	2	202082459	202082459	Missense_Mutation	SNP	T	A	T	CASP10	c.T1363A	p.L455I
XH_P57	2	203500378	203500378	Frame_Shift_Ins	INS	-	CCCA	-	FAM117B	468_469insCCD	p.S156fs
XH_P57	2	206364737	206364737	Silent	SNP	T	C	T	PARD3B	c.T2955C	p.S985S
XH_P57	2	207820276	207820276	Missense_Mutation	SNP	G	A	G	CPO	c.G255A	p.M85I
XH_P57	2	207824384	207824384	Missense_Mutation	SNP	T	G	T	CPO	c.T402G	p.S134R
XH_P57	2	207833983	207833983	Silent	SNP	A	G	A	CPO	c.A948G	p.T316T
XH_P57	2	208841964	208841964	Silent	SNP	A	G	A	PLEKHM3	c.T957C	p.T319N
XH_P57	2	210685100	210685100	Silent	SNP	G	A	G	UNC80	c.G2028A	p.A676A
XH_P57	2	210752971	210752971	Silent	SNP	C	T	C	UNC80	c.C4269T	p.V1423V
XH_P57	2	212251864	212251864	Silent	SNP	T	C	T	ERBB4	c.A3147G	p.V1049V
XH_P57	2	214142631	214142631	Nonsense_Mutation	SNP	G	C	G	LOC100130451	c.C245G	p.S82X
XH_P57	2	215865575	215865575	Silent	SNP	T	C	T	ABCA12	c.A2079G	p.P693P
XH_P57	2	219082200	219082200	Silent	SNP	C	T	C	ARPC2	c.C7T	p.L3L
XH_P57	2	219920412	219920412	Silent	SNP	A	G	A	IHH	c.T753C	p.P251P
XH_P57	2	220040330	220040330	Silent	SNP	A	G	A	CNPPD1	c.T243C	p.Y81Y
XH_P57	2	220046975	220046975	Missense_Mutation	SNP	C	A	C	RETREG2	c.C635A	p.P212Q
XH_P57	2	220162054	220162054	Silent	SNP	G	A	G	PTPRN	c.C1902T	p.D634D
XH_P57	2	220193917	220193917	Missense_Mutation	SNP	C	T	C	RESP18	c.G523A	p.A175T
XH_P57	2	220250800	220250800	Silent	SNP	C	T	C	DNPEP	c.G504A	p.L168L
XH_P57	2	220348751	220348751	Missense_Mutation	SNP	C	T	C	SPEG	c.C6566T	p.P2189L
XH_P57	2	220353013	220353013	Silent	SNP	G	A	G	SPEG	c.G7839A	p.P2613P
XH_P57	2	220354365	220354365	Silent	SNP	C	T	C	SPEG	c.C8625T	p.F2875F
XH_P57	2	220355529	220355529	Missense_Mutation	SNP	A	G	A	SPEG	c.A9236G	p.H3079R
XH_P57	2	220356520	220356520	Silent	SNP	G	T	G	SPEG	c.G9390T	p.P3130P
XH_P57	2	220370796	220370802	Splice_Site	DEL	TAGGTAC	-	TAGGTAC	GMPPA	.	.
XH_P57	2	220404579	220404579	Silent	SNP	C	T	C	CHPF	c.G1368A	p.T456T
XH_P57	2	220435386	220435386	Missense_Mutation	SNP	G	C	G	OBSL1	c.C569G	p.A190G
XH_P57	2	225684166	225684166	Silent	SNP	A	G	A	DOCK10	c.T3246C	p.L1082L
XH_P57	2	225709926	225709926	Silent	SNP	A	G	A	DOCK10	c.T2457C	p.S819S
XH_P57	2	227661043	227661043	Silent	SNP	T	C	T	IRS1	c.A2412G	p.A804A
XH_P57	2	228416719	228416719	Missense_Mutation	SNP	G	A	G	AGFG1	c.G1303A	p.G435S
XH_P57	2	232196597	232196597	Silent	SNP	G	A	G	ARMC9	c.G1866A	p.T622T
XH_P57	2	232263127	232263127	Missense_Mutation	SNP	G	A	G	B3GN7T	c.G697A	p.V233I
XH_P57	2	232672202	232672202	Missense_Mutation	SNP	C	T	C	COPS7B	c.C695T	p.P232L
XH_P57	2	233245026	233245026	Missense_Mutation	SNP	G	A	G	ALPP	c.G788A	p.R263H
XH_P57	2	233246466	233246466	Silent	SNP	C	A	C	ALPP	c.C1569A	p.A523A
XH_P57	2	233273107	233273107	Missense_Mutation	SNP	A	G	A	ALPL2	c.A779G	p.H260R
XH_P57	2	233274476	233274476	Missense_Mutation	SNP	G	C	G	ALPL2	c.G1493C	p.R498P
XH_P57	2	233274509	233274509	Missense_Mutation	SNP	C	G	C	ALPL2	c.C1526G	p.P509R
XH_P57	2	233498669	233498669	Silent	SNP	G	T	G	EFHD1	c.G255T	p.P85P
XH_P57	2	233757679	233757679	Silent	SNP	G	A	G	NGEF	c.C795T	p.A265A
XH_P57	2	234591339	234591339	Silent	SNP	G	A	G	UGT1A7	c.G756A	p.L252L
XH_P57	2	234601755	234601755	Silent	SNP	C	T	C	UGT1A6	c.C105T	p.D35D
XH_P57	2	234627608	234627608	Missense_Mutation	SNP	T	G	T	UGT1A4	c.T142G	p.L48V
XH_P57	2	234627914	234627914	Silent	SNP	T	C	T	UGT1A4	c.T448C	p.L150L
XH_P57	2	234628270	234628270	Silent	SNP	G	A	G	UGT1A4	c.G804A	p.P268P
XH_P57	2	234638249	234638249	Silent	SNP	A	G	A	UGT1A3	c.A477G	p.A159A
XH_P57	2	234652347	234652347	Silent	SNP	C	G	C	DNAJB3	c.G216C	p.G72G
XH_P57	2	234652482	234652482	Silent	SNP	C	T	C	DNAJB3	c.G81A	p.A27A
XH_P57	2	234708868	234708868	Missense_Mutation	SNP	G	C	G	MROH2A	c.G1476C	p.K492N
XH_P57	2	234749780	234749780	Missense_Mutation	SNP	G	C	G	HJURP	c.C1391G	p.S464C
XH_P57	2	238245008	238245008	Missense_Mutation	SNP	G	A	G	COL6A3	c.C6914T	p.P2305L
XH_P57	2	238277211	238277211	Missense_Mutation	SNP	C	T	C	COL6A3	c.G3074A	p.R1025Q
XH_P57	2	238277795	238277795	Silent	SNP	A	G	A	COL6A3	c.T2490C	p.I830I
XH_P57	2	238283472	238283472	Missense_Mutation	SNP	T	G	T	COL6A3	c.A1441C	p.K481Q
XH_P57	2	238287357	238287357	Missense_Mutation	SNP	C	T	C	COL6A3	c.G1198A	p.A400T
XH_P57	2	238668783	238668783	Missense_Mutation	SNP	A	G	A	LRRFIP1	c.A656G	p.Q219R
XH_P57	2	238672425	238672425	Missense_Mutation	SNP	G	C	G	LRRFIP1	c.G1901C	p.R634T
XH_P57	2	239006879	239006879	Silent	SNP	C	T	C	SCLY	c.C1245T	p.F415F
XH_P57	2	239057659	239057659	Missense_Mutation	SNP	G	A	G	KLHL30	c.G1351A	p.V451M
XH_P57	2	239165636	239165636	Silent	SNP	C	T	C	PER2	c.G1992A	p.A664A
XH_P57	2	239229372	239229372	Silent	SNP	C	A	C	TRAF3IP1	c.C69A	p.T73T
XH_P57	2	239353001	239353001	Silent	SNP	C	T	C	ASB1	c.C210T	p.D70D
XH_P57	2	240984789	240984789	Missense_Mutation	SNP	C	T	C	OR6B3	c.G701A	p.C234Y
XH_P57	2	241531479	241531479	Silent	SNP	A	G	A	CAPN10	c.A600G	p.P200P
XH_P57	2	241664801	241664801	Silent	SNP	C	T	C	KIF1A	c.G3840A	p.P1280P
XH_P57	2	241713646	241713646	Silent	SNP	A	G	A	KIF1A	c.T991C	p.L1331L
XH_P57	2	241834944	241834944	Silent	SNP	T	C	T	C2orf54	c.A471G	p.V157V
XH_P57	2	241859449	241859449	Silent	SNP	C	T	C	CROCC2	c.C279T	p.N93N
XH_P57	2	242036794	242036794	Missense_Mutation	SNP	C	A	C	MTERF4	c.G5T	p.R2L
XH_P57	2	242066156	242066156	Missense_Mutation	SNP	C	T	C	PASK	c.G2174A	p.G725D
XH_P57	2	242066314	242066314	Silent	SNP	T	C	T	PASK	c.A2016G	p.A672A
XH_P57	2	242066789	242066789	Missense_Mutation	SNP	A	G	A	PASK	c.T1541C	p.L514S
XH_P57	2	242075362	242075362	Silent	SNP	G	A	G	PASK	c.C1230T	p.D410D
XH_P57	2	242350466	242350466	Silent	SNP	A	G	A	FARP2	c.A429G	p.Q143Q
XH_P57	2	242572846	242572846	Silent	SNP	A	G	A	THAP4	c.T726C	p.S242S
XH_P57	2	242757411	242757411	Silent	SNP	C	T	C	NEU4	c.C531T	p.G177G
XH_P57	2	242758203	242758203	Silent	SNP	T	C	T	NEU4	c.T1323C	p.A441A

XH_P57	2	242758326	242758326	Silent	SNP	G	A	G	NEU4	c.G1446A	p.K482K
XH_P57	2	242814009	242814009	Missense_Mutation	SNP	G	A	G	RTP5	c.G302A	p.G101E
XH_P57	3	3887876	3887876	Silent	SNP	T	C	T	LRRN1	c.T1551C	p.N517N
XH_P57	3	4767262	4767262	Silent	SNP	T	C	T	ITPR1	c.T5124C	p.T1708T
XH_P57	3	4842231	4842231	Silent	SNP	C	T	C	ITPR1	c.C685T	p.L2289L
XH_P57	3	4854883	4854883	In_Frame_Ins	INS	-	AGGAAATTTAT	-	ITPR1	38insAAGGAAA	2446delinsRRKFFYD
XH_P57	3	7620789	7620789	Silent	SNP	T	C	T	GRM7	c.T2196C	p.Y732Y
XH_P57	3	9867625	9867625	Silent	SNP	C	T	C	ARPC4-TLL3	c.C1296T	p.R432R
XH_P57	3	9871030	9871030	Missense_Mutation	SNP	T	G	T	ARPC4-TLL3	c.T1934G	p.M645R
XH_P57	3	9918861	9918861	Silent	SNP	C	A	C	CIDEC	c.G96T	p.L32L
XH_P57	3	10050110	10050110	Missense_Mutation	SNP	C	T	C	LOC401052	c.G55A	p.A19T
XH_P57	3	10264480	10264480	Missense_Mutation	SNP	C	G	C	IRAK2	c.C1174G	p.L392V
XH_P57	3	10413601	10413601	Silent	SNP	G	A	G	ATP2B2	c.C1416T	p.G472G
XH_P57	3	10413715	10413715	Silent	SNP	G	A	G	ATP2B2	c.C1302T	p.N434N
XH_P57	3	11468286	11468286	Silent	SNP	T	C	T	ATG7	c.T1884C	p.D628D
XH_P57	3	12776291	12776291	Silent	SNP	C	A	C	TMEM40	c.G456T	p.G152G
XH_P57	3	12810755	12810755	Missense_Mutation	SNP	G	C	G	TMEM40	c.C35G	p.P12R
XH_P57	3	12856856	12856856	Missense_Mutation	SNP	A	G	A	CAND2	c.A944G	p.Q315R
XH_P57	3	12857493	12857493	Missense_Mutation	SNP	C	T	C	CAND2	c.C1148T	p.P383L
XH_P57	3	12859004	12859004	Missense_Mutation	SNP	A	C	A	CAND2	c.A2294C	p.H765P
XH_P57	3	12953129	12953129	Missense_Mutation	SNP	A	G	A	IQSEC1	c.T2416C	p.Y806H
XH_P57	3	12983345	12983345	Missense_Mutation	SNP	C	A	C	IQSEC1	c.G44T	p.S15I
XH_P57	3	13361287	13361287	Missense_Mutation	SNP	C	T	C	NUP210	c.G5359A	p.V1787M
XH_P57	3	13364876	13364876	Silent	SNP	G	T	G	NUP210	c.C4701A	p.T1567T
XH_P57	3	13367406	13367406	Silent	SNP	C	T	C	NUP210	c.G4533A	p.S151S
XH_P57	3	14176347	14176347	Missense_Mutation	SNP	C	T	C	TMEM43	c.C661T	p.R221C
XH_P57	3	14712473	14712473	Silent	SNP	G	A	G	CCDC174	c.G1176A	p.P392P
XH_P57	3	19961331	19961331	Silent	SNP	T	C	T	EFHB	c.A990G	p.S330S
XH_P57	3	25646268	25646268	Missense_Mutation	SNP	G	A	G	TOP2B	c.C4457T	p.T1486M
XH_P57	3	29628639	29628639	Silent	SNP	C	T	C	RBMS3	c.C339T	p.A113A
XH_P57	3	30713246	30713246	Missense_Mutation	SNP	G	A	G	TGFBR2	c.G571A	p.V191I
XH_P57	3	31725316	31725316	Silent	SNP	G	A	G	OSBPL10	c.C1344T	p.H448H
XH_P57	3	31725478	31725478	Silent	SNP	G	A	G	OSBPL10	c.C1182T	p.F394F
XH_P57	3	32031895	32031895	Missense_Mutation	SNP	G	A	G	ZNFR860	c.G1324A	p.V442I
XH_P57	3	33038747	33038747	Silent	SNP	C	G	C	GLB1	c.G1431C	p.L477L
XH_P57	3	35778773	35778773	Silent	SNP	A	G	A	ARPP21	c.A1401G	p.P467P
XH_P57	3	35779750	35779750	Silent	SNP	A	G	A	ARPP21	c.A1527G	p.P509P
XH_P57	3	36931348	36931348	Silent	SNP	A	T	A	TRANK1	c.T747A	p.A249A
XH_P57	3	37560819	37560819	Missense_Mutation	SNP	G	A	G	ITGA9	c.G1210A	p.G404S
XH_P57	3	38170810	38170810	Missense_Mutation	SNP	C	G	C	ACAA1	c.G516C	p.E172D
XH_P57	3	38317497	38317497	Missense_Mutation	SNP	A	G	A	SLC22A13	c.A1147G	p.M383V
XH_P57	3	38763863	38763863	Silent	SNP	G	C	G	SCN10A	c.C3099G	p.T1033T
XH_P57	3	38764998	38764998	Missense_Mutation	SNP	A	G	A	SCN10A	c.T2981C	p.L994P
XH_P57	3	38793989	38793989	Silent	SNP	G	A	G	SCN10A	c.C1476T	p.L492L
XH_P57	3	39111140	39111140	Silent	SNP	C	A	C	WDR48	c.C331A	p.R111R
XH_P57	3	39152345	39152345	Missense_Mutation	SNP	G	A	G	TTCC21A	c.G272A	p.R91Q
XH_P57	3	39185077	39185077	Silent	SNP	G	A	G	CSRN1	c.C1299T	p.S433S
XH_P57	3	39186728	39186728	Silent	SNP	C	T	C	CSRN1	c.G285A	p.R95R
XH_P57	3	39225752	39225752	Missense_Mutation	SNP	C	G	C	XIRP1	c.G1234C	p.V412L
XH_P57	3	39226436	39226436	Missense_Mutation	SNP	C	T	C	XIRP1	c.G550A	p.V184M
XH_P57	3	39226610	39226610	Missense_Mutation	SNP	C	T	C	XIRP1	c.G376A	p.C126S
XH_P57	3	39453851	39453851	In_Frame_Ins	INS	-	GTC	-	RPSA	895_896insGTG	W299delinsCR
XH_P57	3	40231383	40231383	Missense_Mutation	SNP	C	T	C	MYRIP	c.C533T	p.P178L
XH_P57	3	42577733	42577733	Missense_Mutation	SNP	G	T	G	VIPR1	c.G704T	p.R235L
XH_P57	3	42700150	42700150	Silent	SNP	C	T	C	ZBTB47	c.C303T	p.I101I
XH_P57	3	43097765	43097765	Missense_Mutation	SNP	G	A	G	FAM198A	c.G1615A	p.G539S
XH_P57	3	44794881	44794881	Missense_Mutation	SNP	A	C	A	KIAA1143	c.T417G	p.I139M
XH_P57	3	44881909	44881909	Silent	SNP	A	G	A	KIF15	c.A3381G	p.Q1127Q
XH_P57	3	44903434	44903434	Silent	SNP	G	C	G	TMEM42	c.G18C	p.G6G
XH_P57	3	44926861	44926861	Missense_Mutation	SNP	G	A	G	TGM4	c.G64A	p.V22I
XH_P57	3	45557707	45557707	Silent	SNP	G	A	G	LARS2	c.G1983A	p.T661T
XH_P57	3	45837886	45837886	Missense_Mutation	SNP	G	C	G	SLC6A20	c.C26G	p.A9G
XH_P57	3	46399798	46399798	Silent	SNP	T	C	T	CCR2	c.T780C	p.N260N
XH_P57	3	46449978	46449978	Silent	SNP	A	C	A	CCRL2	c.A444C	p.G148G
XH_P57	3	46484964	46484964	Silent	SNP	G	A	G	LTF	c.C1491T	p.N497N
XH_P57	3	46501213	46501213	Missense_Mutation	SNP	T	C	T	LTF	c.A8G	p.K3R
XH_P57	3	47288941	47288941	Missense_Mutation	SNP	G	T	G	KIF9	c.C1155A	p.D385E
XH_P57	3	47958037	47958037	Missense_Mutation	SNP	G	T	G	MAP4	c.C1280A	p.S427Y
XH_P57	3	48461313	48461313	Silent	SNP	C	G	C	PLXNB1	c.G2382C	p.P794P
XH_P57	3	48474249	48474249	Silent	SNP	A	G	A	CCDC51	c.T805C	p.L269L
XH_P57	3	48508585	48508585	Silent	SNP	C	T	C	TREX1	c.C696T	p.Y232Y
XH_P57	3	48638807	48638807	Missense_Mutation	SNP	G	C	G	UQCRC1	c.C800G	p.P267R
XH_P57	3	48669447	48669447	Missense_Mutation	SNP	C	T	C	SLC26A6	c.G553A	p.V185M
XH_P57	3	48681053	48681053	Silent	SNP	C	T	C	CELSR3	c.G8223A	p.G2741G
XH_P57	3	48683218	48683218	Missense_Mutation	SNP	C	T	C	CELSR3	c.G7547A	p.R2516Q
XH_P57	3	48691316	48691316	Missense_Mutation	SNP	T	C	T	CELSR3	c.A5273G	p.Q1758R
XH_P57	3	48694147	48694147	Silent	SNP	G	A	G	CELSR3	c.C4383T	p.C1461C
XH_P57	3	48697654	48697654	Missense_Mutation	SNP	C	G	C	CELSR3	c.G2414C	p.S805T
XH_P57	3	48699519	48699519	Silent	SNP	C	T	C	CELSR3	c.G549A	p.K183K
XH_P57	3	49688419	49688419	Silent	SNP	G	A	G	BSN	c.G1893A	p.A631A
XH_P57	3	50151396	50151403	Frame_Shift_Del	DEL	TGGAACGC	-	TGGAACGC	RBM5	c.1631_1638del	p.M544fs
XH_P57	3	50294487	50294487	Frame_Shift_Ins	INS	-	CAGT	-	GNAI2	599_600insCAC	p.H200fs
XH_P57	3	52183892	52183892	Missense_Mutation	SNP	G	A	G	POC1A	c.C215T	p.S72L
XH_P57	3	52430526	52430526	Missense_Mutation	SNP	G	A	G	DNAH1	c.G11402A	p.G3801D
XH_P57	3	52555957	52555957	Silent	SNP	T	C	T	STAB1	c.T6261C	p.R2087R
XH_P57	3	52556890	52556890	Missense_Mutation	SNP	A	G	A	STAB1	c.A6844G	p.L2282V
XH_P57	3	52567617	52567617	Missense_Mutation	SNP	A	G	A	NTSDC2	c.T137C	p.V46A
XH_P57	3	52584787	52584787	Silent	SNP	T	C	T	PBRM1	c.A4491G	p.P1497P
XH_P57	3	52643685	52643685	Silent	SNP	T	C	T	PBRM1	c.A2211G	p.T737T
XH_P57	3	52740182	52740182	Missense_Mutation	SNP	C	G	C	SPCS1	c.C121G	p.P41A
XH_P57	3	52802402	52802402	Silent	SNP	A	C	A	NEK4	c.T312G	p.P104P
XH_P57	3	52833805	52833805	Missense_Mutation	SNP	C	A	C	ITIH3	c.C943A	p.Q315K
XH_P57	3	53222761	53222761	Silent	SNP	C	T	C	PRKCD	c.C1441T	p.L481L
XH_P57	3	53321631	53321631	Silent	SNP	A	C	A	DCP1A	c.T1239G	p.V413V
XH_P57	3	53796092	53796092	Missense_Mutation	SNP	C	T	C	CACNA1D	c.C3854T	p.A1285V
XH_P57	3	57542173	57542173	Missense_Mutation	SNP	C	T	C	PDE12	c.C67T	p.P23W
XH_P57	3	58512237	58512237	Silent	SNP	A	G	A	ACOX2	c.T1302C	p.C434C
XH_P57	3	58516318	58516318	Silent	SNP	G	A	G	ACOX2	c.C867T	p.N289N

XH_P57	3	62189189	62189189	Missense_Mutation	SNP	G	A	G	PTPRG	c.G1720A	p.G574S
XH_P57	3	62358208	62358208	In_Frame_Ins	INS	-	CCGCCA	-	FEZF2	35_336insTGGC	G112delinsGGG
XH_P57	3	63967900	63967900	Missense_Mutation	SNP	A	G	A	ATXN7	c.A356G	p.K119R
XH_P57	3	66431275	66431275	Silent	SNP	G	A	G	LRIG1	c.C2781T	p.G927G
XH_P57	3	66463340	66463340	Missense_Mutation	SNP	T	C	T	LRIG1	c.A746G	p.K249R
XH_P57	3	69134333	69134333	Frame_Shift_Ins	INS	-	AACT	-	ARL6IP5	135_136insAAC	p.T45fs
XH_P57	3	74349062	74349062	Missense_Mutation	SNP	T	C	T	CNTN3	c.A2123G	p.N708S
XH_P57	3	97595379	97595379	Missense_Mutation	SNP	G	A	G	CRYBG3	c.G5341A	p.V1781M
XH_P57	3	97806616	97806616	Missense_Mutation	SNP	G	A	G	OR5AC2	c.G600A	p.M200I
XH_P57	3	98073313	98073313	Missense_Mutation	SNP	A	G	A	OR5K4	c.A616G	p.I206V
XH_P57	3	98109640	98109640	Missense_Mutation	SNP	G	A	G	OR5K3	c.G131A	p.G44D
XH_P57	3	99513973	99513973	Missense_Mutation	SNP	C	T	C	COL8A1	c.C1228T	p.P410S
XH_P57	3	105421034	105421034	Silent	SNP	C	T	C	CBLB	c.G1716A	p.A572A
XH_P57	3	108475974	108475974	Missense_Mutation	SNP	G	A	G	RETNLB	c.C59T	p.P20L
XH_P57	3	108634973	108634973	Splice_Site	SNP	C	A	C	GUCA1C		
XH_P57	3	108690221	108690221	Missense_Mutation	SNP	G	A	G	MORC1	c.C2506T	p.H836Y
XH_P57	3	111918215	111918215	Missense_Mutation	SNP	C	T	C	SLC9C1	c.G2332A	p.G778S
XH_P57	3	111985107	111985107	Missense_Mutation	SNP	T	C	T	SLC9C1	c.A856G	p.I286V
XH_P57	3	112993367	112993367	Silent	SNP	G	A	G	BOC	c.G1380A	p.P460P
XH_P57	3	112998268	112998268	Silent	SNP	G	A	G	BOC	c.G1989A	p.S663S
XH_P57	3	113176122	113176122	Silent	SNP	G	A	G	SPICE1	c.C1518T	p.P506P
XH_P57	3	113222036	113222036	Silent	SNP	G	A	G	SPICE1	c.C138T	p.P46P
XH_P57	3	118865801	118865801	Silent	SNP	C	T	C	C3orf30	c.C765T	p.S255S
XH_P57	3	118865969	118865969	Silent	SNP	C	T	C	C3orf30	c.C933T	p.Y311Y
XH_P57	3	119133554	119133554	Silent	SNP	G	A	G	ARHGAP31	c.G2778A	p.A926A
XH_P57	3	119305379	119305379	Silent	SNP	T	A	T	ADPRH	c.T225A	p.A75A
XH_P57	3	119334934	119334934	Missense_Mutation	SNP	C	G	C	PLA1A	c.C221G	p.T74S
XH_P57	3	120500093	120500093	Missense_Mutation	SNP	C	T	C	GTFE2E1	c.C1096T	p.P366S
XH_P57	3	121208176	121208176	Missense_Mutation	SNP	T	C	T	POLQ	c.A3602G	p.H1201R
XH_P57	3	121526204	121526204	Silent	SNP	G	A	G	IQCB1	c.C574T	p.L192L
XH_P57	3	122003757	122003757	Missense_Mutation	SNP	G	T	G	CASR	c.G2956T	p.A986S
XH_P57	3	122259640	122259640	Missense_Mutation	SNP	T	C	T	PARP9	c.A1549G	p.I517V
XH_P57	3	122496747	122496747	Missense_Mutation	SNP	T	C	T	HSPBAP1	c.A71G	p.H24R
XH_P57	3	122811208	122811208	Missense_Mutation	SNP	C	G	C	PDIA5	c.C176G	p.A59G
XH_P57	3	123453061	123453061	Missense_Mutation	SNP	A	G	A	MYLK	c.T254C	p.V85A
XH_P57	3	123946895	123946895	Silent	SNP	G	A	G	KALRN	c.G126A	p.K42K
XH_P57	3	124418846	124418846	Silent	SNP	C	T	C	KALRN	c.C2868T	p.S956S
XH_P57	3	124515636	124515636	Missense_Mutation	SNP	C	T	C	ITGB5	c.G1292A	p.R431Q
XH_P57	3	124731689	124731689	Missense_Mutation	SNP	T	A	T	HEG1	c.A2734T	p.T912S
XH_P57	3	124826408	124826408	Missense_Mutation	SNP	T	C	T	SLC12A8	c.A1622G	p.K541R
XH_P57	3	126726705	126726705	Silent	SNP	A	G	A	PLXNA1	c.A2061G	p.H687T
XH_P57	3	126735453	126735453	Silent	SNP	C	T	C	PLXNA1	c.C3108T	p.T1036T
XH_P57	3	126741011	126741011	Silent	SNP	G	A	G	PLXNA1	c.G4122A	p.T1374T
XH_P57	3	126916217	126916217	Missense_Mutation	SNP	G	A	G	C3orf56	c.G689A	p.R230Q
XH_P57	3	127379270	127379270	Silent	SNP	C	T	C	PODXL2	c.C399T	p.T133T
XH_P57	3	128651796	128651796	Missense_Mutation	SNP	G	A	G	KIAA1257	c.C1625T	p.T542M
XH_P57	3	128664664	128664664	Missense_Mutation	SNP	T	C	T	KIAA1257	c.A635G	p.E212G
XH_P57	3	128707606	128707606	Missense_Mutation	SNP	T	C	T	KIAA1257	c.A82G	p.M28V
XH_P57	3	129134242	129134242	Silent	SNP	G	A	G	EFCAB12	c.C684T	p.V228V
XH_P57	3	129137127	129137127	Silent	SNP	G	A	G	EFCAB12	c.C651T	p.T217T
XH_P57	3	129140499	129140499	Missense_Mutation	SNP	T	C	T	EFCAB12	c.A197G	p.E66G
XH_P57	3	129155451	129155451	Missense_Mutation	SNP	C	T	C	MBD4	c.G1036A	p.E346K
XH_P57	3	129289752	129289752	Silent	SNP	C	T	C	PLXND1	c.G3627A	p.Q1209Q
XH_P57	3	129291499	129291499	Silent	SNP	G	A	G	PLXND1	c.C3030T	p.S1010S
XH_P57	3	129302455	129302455	Silent	SNP	G	A	G	PLXND1	c.C2196T	p.S732S
XH_P57	3	129303072	129303072	Silent	SNP	G	A	G	PLXND1	c.C2034T	p.H678H
XH_P57	3	129304797	129304797	Missense_Mutation	SNP	G	A	G	PLXND1	c.C1849T	p.P617S
XH_P57	3	129305460	129305460	Missense_Mutation	SNP	C	T	C	PLXND1	c.G1591A	p.G531S
XH_P57	3	129694681	129694681	Missense_Mutation	SNP	C	G	C	TRH	c.C22G	p.L8V
XH_P57	3	130190531	130190531	Missense_Mutation	SNP	T	C	T	COL6A5	c.T7580C	p.L2527P
XH_P57	3	130190721	130190721	Frame_Shift_Del	DEL	T	-	T	COL6A5	c.7770delT	p.H2590fs
XH_P57	3	130285929	130285929	Missense_Mutation	SNP	C	T	C	COL6A6	c.C1666T	p.P556S
XH_P57	3	130289976	130289976	Missense_Mutation	SNP	C	T	C	COL6A6	c.C2716T	p.R906C
XH_P57	3	130368301	130368301	Silent	SNP	G	A	G	COL6A6	c.G5628A	p.A1876A
XH_P57	3	132051110	132051110	Silent	SNP	A	G	A	ACPP	c.A378G	p.P126P
XH_P57	3	132319924	132319924	Missense_Mutation	SNP	T	C	T	ACKR4	c.T683C	p.M228T
XH_P57	3	133368362	133368362	Missense_Mutation	SNP	T	G	T	TOPBP1	c.A1369C	p.K457Q
XH_P57	3	133474328	133474328	Silent	SNP	G	A	G	TF	c.G624A	p.S208S
XH_P57	3	133547692	133547692	Silent	SNP	G	A	G	RAB6B	c.C567T	p.I189I
XH_P57	3	133670073	133670073	Silent	SNP	T	C	T	SLCO2A1	c.A840G	p.R280R
XH_P57	3	134322916	134322916	Silent	SNP	G	A	G	KY	c.C1443T	p.H481H
XH_P57	3	134327420	134327420	Silent	SNP	C	T	C	KY	c.G1035A	p.P345P
XH_P57	3	134338074	134338074	Missense_Mutation	SNP	C	T	C	KY	c.G500A	p.R167H
XH_P57	3	138191232	138191232	Missense_Mutation	SNP	G	A	G	ESYT3	c.G1768A	p.G590R
XH_P57	3	139075818	139075818	In_Frame_Ins	INS	-	ATC	-	MRPS22	1045_1046insA	p.Y349delinsYH
XH_P57	3	142523349	142523349	Silent	SNP	G	A	G	TRPC1	c.G1929A	p.T643T
XH_P57	3	142681090	142681090	Silent	SNP	T	G	T	PAQR9	c.A1089C	p.V363V
XH_P57	3	142681642	142681642	Silent	SNP	G	A	G	PAQR9	c.C537T	p.G179G
XH_P57	3	145938619	145938619	Missense_Mutation	SNP	T	C	T	PLSCR4	c.A56G	p.N19S
XH_P57	3	147108757	147108757	Missense_Mutation	SNP	G	A	G	ZIC4	c.C347T	p.S116L
XH_P57	3	148562470	148562470	Missense_Mutation	SNP	T	C	T	CPB1	c.C769C	p.F232L
XH_P57	3	150690439	150690439	Silent	SNP	T	A	T	CLRN1	c.A57T	p.A19A
XH_P57	3	151056616	151056616	Silent	SNP	G	A	G	P2RY12	c.C18T	p.N6N
XH_P57	3	151112568	151112568	Silent	SNP	G	A	G	MED12L	c.G5628A	p.S1876S
XH_P57	3	151160772	151160772	Missense_Mutation	SNP	C	G	C	IGSF10	c.G5963C	p.R1988T
XH_P57	3	151161427	151161427	Missense_Mutation	SNP	C	T	C	IGSF10	c.G5308A	p.E1770K
XH_P57	3	153840389	153840389	Missense_Mutation	SNP	T	C	T	ARHGEF26	c.T608C	p.F203S
XH_P57	3	155571275	155571275	Missense_Mutation	SNP	T	C	T	SLC33A1	c.A512G	p.D171G
XH_P57	3	155632314	155632314	Silent	SNP	A	G	A	GMPS	c.A993G	p.T331T
XH_P57	3	156763370	156763370	Missense_Mutation	SNP	G	A	G	LEKR1	c.G1910A	p.R637H
XH_P57	3	156983414	156983414	Silent	SNP	T	C	T	VEPH1	c.A2031G	p.K677K
XH_P57	3	157081324	157081324	Missense_Mutation	SNP	A	G	A	VEPH1	c.T1564C	p.S522P
XH_P57	3	158366900	158366900	Missense_Mutation	SNP	G	A	G	GFM1	c.G643A	p.V215I
XH_P57	3	158383218	158383218	Frame_Shift_Ins	INS	-	AC	-	GFM1	1473_1474insA	p.T491fs
XH_P57	3	158383219	158383219	Missense_Mutation	SNP	G	T	G	GFM1	c.G1474T	p.V492F
XH_P57	3	158537443	158537443	Missense_Mutation	SNP	A	G	A	MFSD1	c.A688G	p.I230V
XH_P57	3	159606676	159606694	Frame_Shift_Del	DEL	ACTATTGGGG	-	GACTATTGGGG	IQCI-SCHIP1	c.566_584del	p.D189fs
XH_P57	3	160143943	160143943	Missense_Mutation	SNP	A	G	A	SMC4	c.A2560G	p.K854E

XH_P57	3	167189607	167189607	Missense_Mutation	SNP	A	C	A	SERPIN2	c.T16G	p.L6V
XH_P57	3	167293773	167293773	Missense_Mutation	SNP	G	C	G	WDR49	c.C1442G	p.A481G
XH_P57	3	167320010	167320010	Missense_Mutation	SNP	T	C	T	WDR49	c.A1180G	p.K394E
XH_P57	3	169500397	169500397	Silent	SNP	T	C	T	MYNN	c.T1365C	p.S455S
XH_P57	3	169513320	169513320	Missense_Mutation	SNP	A	T	A	LRRC34	c.T1048A	p.S350T
XH_P57	3	169539812	169539812	Missense_Mutation	SNP	C	G	C	LRRIQ4	c.C103G	p.Q35E
XH_P57	3	169539990	169539990	Missense_Mutation	SNP	G	A	G	LRRIQ4	c.G281A	p.S94N
XH_P57	3	169572621	169572621	Missense_Mutation	SNP	G	T	G	LRRC31	c.C803A	p.A268E
XH_P57	3	169644710	169644710	Missense_Mutation	SNP	G	C	G	SAMD7	c.G660C	p.E220D
XH_P57	3	171969077	171969077	Missense_Mutation	SNP	C	G	C	FNDC3B	c.C536G	p.T179S
XH_P57	3	172365832	172365832	Missense_Mutation	SNP	T	G	T	NCEH1	c.A307C	p.K103Q
XH_P57	3	175189447	175189447	Silent	SNP	G	A	G	NAALADL2	c.G1554A	p.Q518Q
XH_P57	3	178546026	178546026	Silent	SNP	T	C	T	KCNMB2	c.T288C	p.N96N
XH_P57	3	178968634	178968634	Missense_Mutation	SNP	C	T	C	KCNMB3	c.G145A	p.A49T
XH_P57	3	179137273	179137273	Silent	SNP	A	G	A	GNB4	c.T117C	p.S39S
XH_P57	3	183823729	183823729	Missense_Mutation	SNP	G	T	G	HTR3E	c.G975T	p.L325F
XH_P57	3	183904049	183904049	Silent	SNP	A	G	A	ABCF3	c.A54G	p.Q18Q
XH_P57	3	183976103	183976103	Missense_Mutation	SNP	C	T	C	ECE2	c.C508T	p.R170W
XH_P57	3	184099728	184099728	Missense_Mutation	SNP	C	G	C	CHRD	c.C619G	p.R207G
XH_P57	3	184633247	184633247	Silent	SNP	A	C	A	VP58	c.A2328C	p.V176L
XH_P57	3	185229464	185229464	Silent	SNP	T	C	T	LIPH	c.A1116G	p.K372K
XH_P57	3	186509517	186509517	Silent	SNP	G	A	G	RFC4	c.C798T	p.A266A
XH_P57	3	186943197	186943197	Silent	SNP	G	A	G	MASP1	c.C1656T	p.D552D
XH_P57	3	187088812	187088812	Missense_Mutation	SNP	C	T	C	RTP4	c.C392T	p.T131M
XH_P57	3	192994543	192994543	Missense_Mutation	SNP	A	G	A	ATP13A5	c.T3392C	p.V1131A
XH_P57	3	193334991	193334991	Missense_Mutation	SNP	G	A	G	OPA1	c.G473A	p.S158N
XH_P57	3	193374964	193374964	Silent	SNP	T	C	T	OPA1	c.T2001C	p.A667A
XH_P57	3	193385047	193385047	Silent	SNP	C	T	C	OPA1	c.C2688T	p.R896R
XH_P57	3	194061907	194061907	Nonsense_Mutation	SNP	G	A	G	CPN2	c.C1525T	p.Q509X
XH_P57	3	194325138	194325138	Frame_Shift_Ins	INS	-	-	-	TMEM44	c.1053dupG	p.Q352fs
XH_P57	3	194338424	194338424	Missense_Mutation	SNP	G	C	G	TMEM44	c.C694G	p.R232G
XH_P57	3	195474176	195474176	Silent	SNP	G	A	G	MUC4	c.C3249T	p.F1083F
XH_P57	3	195477791	195477791	Silent	SNP	G	A	G	MUC4	c.C2979T	p.I993I
XH_P57	3	195479256	195479256	Silent	SNP	T	C	T	MUC4	c.A2709G	p.E903E
XH_P57	3	195495916	195495916	Missense_Mutation	SNP	G	C	G	MUC4	c.C645G	p.N215K
XH_P57	3	195497174	195497174	Missense_Mutation	SNP	C	G	C	MUC4	c.G450C	p.M150I
XH_P57	3	195501149	195501149	Missense_Mutation	SNP	C	T	C	MUC4	c.G110A	p.G37D
XH_P57	3	195507591	195507591	Silent	SNP	C	T	C	MUC4	c.G10860A	p.T3620T
XH_P57	3	195507664	195507664	Missense_Mutation	SNP	C	G	C	MUC4	c.G10787C	p.G3596A
XH_P57	3	195508490	195508537	In_Frame_Del	DEL	AAGAAGAGG	-	CAAGAAGAGGA	MUC4	c.9914_9961del	p.3305_3321del
XH_P57	3	195508986	195508986	Silent	SNP	G	A	G	MUC4	c.C9465T	p.V3155V
XH_P57	3	195510707	195510707	Missense_Mutation	SNP	T	G	T	MUC4	c.A7744C	p.T5282P
XH_P57	3	195511142	195511142	Missense_Mutation	SNP	T	C	T	MUC4	c.A7309G	p.N2437D
XH_P57	3	195512287	195512287	Missense_Mutation	SNP	G	A	G	MUC4	c.C6164T	p.S2055F
XH_P57	3	195515008	195515008	Missense_Mutation	SNP	C	G	C	MUC4	c.G3443C	p.G1148A
XH_P57	3	195516630	195516630	Silent	SNP	G	T	G	MUC4	c.C1821A	p.S607S
XH_P57	3	195516878	195516878	Missense_Mutation	SNP	T	C	T	MUC4	c.A1573G	p.T525A
XH_P57	3	195517553	195517553	Missense_Mutation	SNP	A	C	A	MUC4	c.T898G	p.F300V
XH_P57	3	195518112	195518112	In_Frame_Ins	INS	-	CTCCTCGGTAA	-	MUC4	9insTGTACGCA	113delinsVTTCQT
XH_P57	3	195936382	195936382	Silent	SNP	G	A	G	ZDHH19	c.C273T	p.S91S
XH_P57	3	197579466	197579466	Missense_Mutation	SNP	C	T	C	LRCH3	c.C1565T	p.P522L
XH_P57	3	197659160	197659160	Missense_Mutation	SNP	C	G	C	IQCG	c.G529C	p.D177H
XH_P57	3	197665599	197665599	Missense_Mutation	SNP	G	T	G	IQCG	c.C335A	p.A112D
XH_P57	4	517686	517686	Missense_Mutation	SNP	G	A	G	PIGG	c.G1654A	p.G552S
XH_P57	4	663908	663908	Missense_Mutation	SNP	A	G	A	PDE6B	c.A1357G	p.M453V
XH_P57	4	677103	677103	Silent	SNP	G	A	G	MFSD7	c.C693T	p.L231L
XH_P57	4	951947	951947	Missense_Mutation	SNP	T	C	T	TMEM175	c.T932C	p.M311T
XH_P57	4	994414	994414	Missense_Mutation	SNP	G	A	G	IDUA	c.G314A	p.R105Q
XH_P57	4	995305	995305	Silent	SNP	T	C	T	IDUA	c.T543C	p.N181N
XH_P57	4	995919	995919	Silent	SNP	G	C	G	IDUA	c.G942C	p.A314A
XH_P57	4	996888	996888	Silent	SNP	C	T	C	IDUA	c.C1467T	p.R489R
XH_P57	4	1006333	1006333	Silent	SNP	G	A	G	FGFR1	c.G60A	p.P20P
XH_P57	4	1656900	1656900	Silent	SNP	G	A	G	FAM53A	c.C687T	p.L229L
XH_P57	4	1729660	1729660	Silent	SNP	C	T	C	TACC3	c.C531T	p.S177S
XH_P57	4	1730299	1730299	Silent	SNP	A	G	A	TACC3	c.A1170G	p.A390A
XH_P57	4	1732978	1732978	Missense_Mutation	SNP	G	A	G	TACC3	c.G1541A	p.G514E
XH_P57	4	1805478	1805478	Silent	SNP	C	T	C	FGFR3	c.C990T	p.T330T
XH_P57	4	2461817	2461817	Silent	SNP	G	A	G	CFAP99	c.G1509A	p.R503R
XH_P57	4	2743999	2743999	Silent	SNP	A	A	A	TNIP2	c.T1026C	p.A342A
XH_P57	4	2826400	2826400	Silent	SNP	T	C	T	SH3BP2	c.T300C	p.H100H
XH_P57	4	2831383	2831383	Silent	SNP	T	G	T	SH3BP2	c.T750G	p.A250A
XH_P57	4	3039150	3039150	Missense_Mutation	SNP	T	C	T	GRK4	c.T875C	p.V292A
XH_P57	4	3231661	3231661	Silent	SNP	G	A	G	HTT	c.G8157A	p.L2719L
XH_P57	4	3318413	3318413	Silent	SNP	A	G	A	RGS12	c.A516G	p.S172S
XH_P57	4	3319271	3319271	Silent	SNP	C	T	C	RGS12	c.C1374T	p.D458D
XH_P57	4	3446091	3446091	Missense_Mutation	SNP	G	T	G	HGFAC	c.G652T	p.A218S
XH_P57	4	3451109	3451109	Missense_Mutation	SNP	G	A	G	HGFAC	c.G1931A	p.R644Q
XH_P57	4	4249855	4249855	Silent	SNP	G	A	G	TMEM128	c.C75T	p.D25D
XH_P57	4	4861974	4861974	Silent	SNP	C	T	C	MSX1	c.C348T	p.G116G
XH_P57	4	7065903	7065903	Missense_Mutation	SNP	C	T	C	GRPEL1	c.G110A	p.G37D
XH_P57	4	7435194	7435194	Silent	SNP	G	A	G	PSAPL1	c.C1413T	p.G471G
XH_P57	4	7435805	7435805	Missense_Mutation	SNP	C	A	C	PSAPL1	c.G802T	p.A268S
XH_P57	4	7436486	7436486	Missense_Mutation	SNP	C	A	C	PSAPL1	c.G121T	p.A41S
XH_P57	4	7765495	7765495	Silent	SNP	G	T	G	AFAP1	c.C2190A	p.T730T
XH_P57	4	7774610	7774610	Silent	SNP	C	T	C	AFAP1	c.G1938A	p.A646A
XH_P57	4	8443041	8443041	Silent	SNP	C	T	C	TRMT44	c.C492T	p.L164L
XH_P57	4	8594577	8594577	Missense_Mutation	SNP	C	T	C	CPZ	c.C17T	p.P6L
XH_P57	4	9909923	9909923	Missense_Mutation	SNP	G	A	G	SLC2A9	c.C1049T	p.P350L
XH_P57	4	10022992	10022992	Missense_Mutation	SNP	G	A	G	SLC2A9	c.C62T	p.T21I
XH_P57	4	13601977	13601977	Missense_Mutation	SNP	C	A	C	BOD1L1	c.G6547T	p.V2183F
XH_P57	4	15516389	15516389	Silent	SNP	C	T	C	CC2D2A	c.C777T	p.H259H
XH_P57	4	15689928	15689928	Missense_Mutation	SNP	G	A	G	FAM200B	c.G1328A	p.S443N
XH_P57	4	16513650	16513650	Silent	SNP	C	G	C	LD82	c.G693C	p.L231L
XH_P57	4	17711076	17711076	Silent	SNP	T	C	T	FAM184B	c.A333G	p.Q111Q
XH_P57	4	17805379	17805379	Missense_Mutation	SNP	G	A	G	DCAF16	c.C386T	p.T129I
XH_P57	4	25335580	25335580	Missense_Mutation	SNP	T	C	T	ZCHC4	c.T656C	p.I219T
XH_P57	4	25419283	25419283	Silent	SNP	T	C	T	ANAPC4	c.T2124C	p.F708F
XH_P57	4	25419908	25419908	Silent	SNP	G	T	G	ANAPC4	c.G2334T	p.S778S

XH_P57	4	26417136	26417136	Silent	SNP	T	C	T	RBPJ	c.T195C	p.S65S
XH_P57	4	37836302	37836302	Silent	SNP	T	C	T	PGM2	c.T312C	p.S104S
XH_P57	4	37851856	37851856	Missense_Mutation	SNP	A	C	A	PGM2	c.A1464C	p.E488D
XH_P57	4	37962133	37962133	Silent	SNP	G	A	G	PTTG2	c.G78A	p.L26L
XH_P57	4	38776303	38776303	Silent	SNP	T	C	T	TLR10	c.A909G	p.K303K
XH_P57	4	38777173	38777173	Silent	SNP	A	T	A	TLR10	c.T39A	p.I31I
XH_P57	4	38916631	38916631	Silent	SNP	T	C	T	FAM114A1	c.T261C	p.D87D
XH_P57	4	39303925	39303925	Silent	SNP	A	G	A	RFC1	c.T2511C	p.S837S
XH_P57	4	41634859	41634859	Silent	SNP	C	T	C	LIMCH1	c.C1695T	p.G565G
XH_P57	4	42895308	42895308	Missense_Mutation	SNP	G	A	G	GRXCR1	c.G25A	p.E9K
XH_P57	4	47589203	47589203	Silent	SNP	G	A	G	ATP10D	c.G3921A	p.T1307T
XH_P57	4	52709752	52709752	Missense_Mutation	SNP	A	G	A	DCUN1D4	c.A1G	p.M1V
XH_P57	4	52862263	52862263	Missense_Mutation	SNP	G	T	G	LRRC66	c.C925A	p.H309N
XH_P57	4	52938243	52938243	Missense_Mutation	SNP	T	C	T	SPATA18	c.T4C	p.S2P
XH_P57	4	53610272	53610272	Silent	SNP	C	T	C	ERVMER34-1	c.G1416A	p.P472P
XH_P57	4	54011603	54011603	Silent	SNP	C	T	C	SCFD2	c.G1458A	p.T486T
XH_P57	4	57204777	57204777	Missense_Mutation	SNP	A	C	A	AASDH	c.T1633G	p.Y545D
XH_P57	4	57219613	57219613	Silent	SNP	C	T	C	AASDH	c.G78A	p.P26P
XH_P57	4	57333822	57333822	Silent	SNP	G	T	G	SRP72	c.G21T	p.G7G
XH_P57	4	70898907	70898907	Silent	SNP	C	T	C	HTN3	c.C126T	p.G42G
XH_P57	4	71201682	71201682	Missense_Mutation	SNP	C	T	C	CAB51	c.C926T	p.T309I
XH_P57	4	71232388	71232388	Missense_Mutation	SNP	G	A	G	SMR3A	c.G82A	p.G28R
XH_P57	4	71384537	71384537	Missense_Mutation	SNP	C	T	C	AMTN	c.C43T	p.R15W
XH_P57	4	71472426	71472426	Silent	SNP	A	G	A	AMBN	c.A1323G	p.A441A
XH_P57	4	72433545	72433545	Missense_Mutation	SNP	A	C	A	SLC4A4	c.A3220C	p.I1074L
XH_P57	4	75938236	75938236	Silent	SNP	A	G	A	PARM1	c.A645G	p.V215V
XH_P57	4	77660731	77660731	Missense_Mutation	SNP	C	G	C	SHROOM3	c.C1405G	p.P469A
XH_P57	4	78987157	78987157	Missense_Mutation	SNP	A	G	A	FRAS1	c.A95G	p.D32G
XH_P57	4	79400868	79400868	Silent	SNP	C	T	C	FRAS1	c.C8439T	p.D2813D
XH_P57	4	88534065	88534065	Missense_Mutation	SNP	G	A	G	DSPP	c.G727A	p.D243N
XH_P57	4	88535832	88535832	In_Frame_Ins	INS	-	CAGTGACAGCAG	-	DSPP	insTAGCAGTGAG673delinsDSSDSSS	
XH_P57	4	88902692	88902692	Silent	SNP	T	C	T	SPP1	c.T159C	p.D53D
XH_P57	4	88903853	88903853	Silent	SNP	C	T	C	SPP1	c.C627T	p.A209A
XH_P57	4	90169925	90169925	Missense_Mutation	SNP	A	G	A	GPRIN3	c.T1337C	p.V464A
XH_P57	4	91230579	91230579	Missense_Mutation	SNP	G	A	G	CCSER1	c.G1144A	p.G382S
XH_P57	4	95170839	95170839	Missense_Mutation	SNP	G	A	G	SMARCAD1	c.G740A	p.S247N
XH_P57	4	95173779	95173779	Missense_Mutation	SNP	T	C	T	SMARCAD1	c.T902C	p.V301A
XH_P57	4	95197520	95197520	Silent	SNP	C	T	C	SMARCAD1	c.C549T	p.D183D
XH_P57	4	96091414	96091414	Missense_Mutation	SNP	C	T	C	UNC5C	c.G2521A	p.A841T
XH_P57	4	96123981	96123981	Silent	SNP	C	T	C	UNC5C	c.G2037A	p.A679A
XH_P57	4	96127869	96127869	Silent	SNP	T	G	T	UNC5C	c.A1812C	p.P604P
XH_P57	4	100845949	100845949	Nonstop_Mutation	SNP	C	A	G	DNAJB14	c.G329T	p.X110L
XH_P57	4	103555992	103555992	Silent	SNP	A	G	A	MANBA	c.T2368C	p.L790L
XH_P57	4	106510470	106510470	Missense_Mutation	SNP	A	G	A	ARHGEF38	c.A262G	p.M88V
XH_P57	4	107133919	107133919	Silent	SNP	A	G	A	TBCK	c.T1659C	p.G553G
XH_P57	4	107956735	107956735	Missense_Mutation	SNP	A	C	A	DKK2	c.T14G	p.M5R
XH_P57	4	110932474	110932474	Nonsense_Mutation	SNP	C	T	C	EGF	c.C3364T	p.R1122X
XH_P57	4	111543573	111543573	Missense_Mutation	SNP	G	A	G	PITX2	c.C44T	p.A15V
XH_P57	4	113538879	113538879	Silent	SNP	A	G	A	ZGRF1	c.T2319C	p.L773L
XH_P57	4	113565835	113565835	Missense_Mutation	SNP	G	A	G	LARP7	c.G10A	p.E4K
XH_P57	4	115544777	115544777	Silent	SNP	A	G	A	UGT8	c.A741G	p.A247A
XH_P57	4	119736796	119736796	Silent	SNP	A	C	A	SEC24D	c.T483G	p.P161P
XH_P57	4	121706201	121706201	Silent	SNP	A	G	A	PRDM5	c.T1141C	p.L381L
XH_P57	4	121738049	121738049	Silent	SNP	T	C	T	PRDM5	c.A681G	p.L227L
XH_P57	4	122250623	122250623	Missense_Mutation	SNP	T	C	T	QRFRP	c.A1142G	p.N381S
XH_P57	4	124323413	124323413	Frame_Shift_Del	DEL	T	-	T	SPRY1	c.667delT	p.C223fs
XH_P57	4	126237971	126237971	Silent	SNP	C	T	C	FAT4	c.C405T	p.F135F
XH_P57	4	126238924	126238924	Missense_Mutation	SNP	A	T	A	FAT4	c.A1358T	p.Q453L
XH_P57	4	126239986	126239986	Missense_Mutation	SNP	C	T	C	FAT4	c.C2420T	p.A807V
XH_P57	4	126370647	126370647	Missense_Mutation	SNP	G	A	G	FAT4	c.G8482A	p.D2828N
XH_P57	4	128689936	128689936	Silent	SNP	A	G	A	SLC25A31	c.A663G	p.P221P
XH_P57	4	129012181	129012181	Silent	SNP	G	A	G	LARP1B	c.G384A	p.R128R
XH_P57	4	129012638	129012638	Silent	SNP	A	G	A	LARP1B	c.A639G	p.A213A
XH_P57	4	129100643	129100643	Missense_Mutation	SNP	G	A	G	LARP1B	c.G1139A	p.R380H
XH_P57	4	138442663	138442663	Silent	SNP	G	A	G	PCDH18	c.C2925T	p.S975S
XH_P57	4	139964337	139964337	Silent	SNP	G	A	G	NOCT	c.G300A	p.E100E
XH_P57	4	140188094	140188094	Missense_Mutation	SNP	C	T	C	MGARP	c.G382A	p.A128T
XH_P57	4	141294814	141294814	Missense_Mutation	SNP	G	C	G	SCOC	c.G124C	p.V42L
XH_P57	4	144918712	144918712	Missense_Mutation	SNP	C	G	C	GYPB	c.G251C	p.S84T
XH_P57	4	147215092	147215092	Missense_Mutation	SNP	T	C	T	SLC10A7	c.A672G	p.I224M
XH_P57	4	147788709	147788709	Missense_Mutation	SNP	C	T	C	TTC29	c.G826A	p.A276T
XH_P57	4	148605099	148605099	Missense_Mutation	SNP	C	A	G	PRMT9	c.G40T	p.G14C
XH_P57	4	148984321	148984321	Missense_Mutation	SNP	A	G	A	ARHGAP10	c.A2050G	p.M684V
XH_P57	4	151199080	151199080	Missense_Mutation	SNP	G	A	G	LRBA	c.C8390T	p.S2797L
XH_P57	4	151773593	151773593	Missense_Mutation	SNP	G	C	G	LRBA	c.C3269G	p.A1090G
XH_P57	4	151829824	151829824	Silent	SNP	T	C	T	LRBA	c.A1347G	p.A449A
XH_P57	4	152498666	152498666	Missense_Mutation	SNP	C	G	C	FAM160A1	c.C170G	p.P57R
XH_P57	4	154197234	154197234	Silent	SNP	T	G	T	TRIM2	c.T324G	p.T108T
XH_P57	4	154216710	154216710	Silent	SNP	G	A	G	TRIM2	c.G951A	p.T317T
XH_P57	4	154279752	154279752	Missense_Mutation	SNP	A	T	A	MND1	c.A254T	p.K85M
XH_P57	4	155219318	155219318	Missense_Mutation	SNP	C	T	C	DCHS2	c.G4783A	p.E1595K
XH_P57	4	155219361	155219361	Silent	SNP	A	G	A	DCHS2	c.T4740C	p.D1580D
XH_P57	4	155219662	155219662	Missense_Mutation	SNP	G	C	G	DCHS2	c.C4439G	p.T1480R
XH_P57	4	155719189	155719189	Missense_Mutation	SNP	T	G	T	RBM46	c.T378G	p.I126M
XH_P57	4	155720349	155720349	Silent	SNP	C	A	C	RBM46	c.C1035A	p.G345G
XH_P57	4	156706482	156706482	Splice_Site	SNP	G	A	G	GUCY1B3		
XH_P57	4	159791519	159791519	Silent	SNP	G	A	G	FNIP2	c.G1785A	p.A595A
XH_P57	4	165118652	165118652	Missense_Mutation	SNP	C	T	C	ANP32C	c.G212A	p.R71K
XH_P57	4	165118796	165118796	Missense_Mutation	SNP	G	A	G	ANP32C	c.C68T	p.A23V
XH_P57	4	165878248	165878248	Missense_Mutation	SNP	C	T	C	FAM218A	c.C74T	p.A25V
XH_P57	4	169282355	169282355	Missense_Mutation	SNP	T	C	T	DDX60L	c.A4936G	p.M1646V
XH_P57	4	173930333	173930333	Missense_Mutation	SNP	G	A	G	GALNTL6	c.G1376A	p.R459Q
XH_P57	4	174292472	174292472	Missense_Mutation	SNP	G	T	G	SAP30	c.G139T	p.A47S
XH_P57	4	177098285	177098285	Missense_Mutation	SNP	G	A	G	WDR17	c.G3526A	p.A1176T
XH_P57	4	177113836	177113836	Silent	SNP	C	T	C	SPATA4	c.G630A	p.A210A
XH_P57	4	183549831	183549831	Silent	SNP	T	G	T	TENM3	c.T777G	p.G259G
XH_P57	4	183674697	183674697	Silent	SNP	C	T	C	TENM3	c.C3957T	p.G1319G
XH_P57	4	184614874	184614874	Silent	SNP	C	T	C	TRAPPC11	c.C2370T	p.T790T

XH_P57	4	185553507	185553507	Silent	SNP	G	A	G	CASP3	c.C222T	p.L74L
XH_P57	4	186379735	186379735	Missense_Mutation	SNP	T	C	T	CCDC110	c.A1895G	p.Q632R
XH_P57	4	187078866	187078866	Missense_Mutation	SNP	C	T	C	FAM149A	c.C722T	p.P241L
XH_P57	4	187113041	187113041	Missense_Mutation	SNP	C	G	C	CYP4V2	c.C64G	p.L22V
XH_P57	4	187455426	187455426	Missense_Mutation	SNP	G	A	G	MTNR1A	c.C470T	p.A157V
XH_P57	5	224487	224487	Missense_Mutation	SNP	T	C	T	SDHA	c.T163C	p.Y55H
XH_P57	5	344026	344026	Silent	SNP	G	A	G	AHRR	c.G21A	p.P7P
XH_P57	5	422955	422955	Missense_Mutation	SNP	C	G	C	AHRR	c.C565G	p.P189A
XH_P57	5	453567	453567	Silent	SNP	G	A	G	EXOC3	c.G447A	p.E149E
XH_P57	5	475104	475104	Missense_Mutation	SNP	A	G	A	SLC9A3	c.T2368C	p.C790R
XH_P57	5	482186	482186	Silent	SNP	C	G	C	SLC9A3	c.G1416C	p.G472G
XH_P57	5	1208964	1208964	Silent	SNP	T	C	T	SLC6A19	c.T306C	p.G102G
XH_P57	5	1213668	1213668	Missense_Mutation	SNP	G	A	G	SLC6A19	c.G754A	p.V252I
XH_P57	5	1216775	1216775	Silent	SNP	A	G	A	SLC6A19	c.A990G	p.T330T
XH_P57	5	1240757	1240757	Nonsense_Mutation	SNP	C	G	C	SLC6A18	c.C957G	p.Y319X
XH_P57	5	1244425	1244425	Missense_Mutation	SNP	C	T	C	SLC6A18	c.C1433T	p.P478L
XH_P57	5	1255520	1255520	Silent	SNP	G	A	G	TERT	c.C2850T	p.H950H
XH_P57	5	1268697	1268697	Silent	SNP	C	T	C	TERT	c.G2520A	p.L840L
XH_P57	5	1411412	1411412	Silent	SNP	T	C	T	SLC6A3	c.A1215G	p.S405S
XH_P57	5	1494909	1494909	Silent	SNP	C	T	C	LPCAT1	c.G399A	p.A133A
XH_P57	5	1880891	1880891	Missense_Mutation	SNP	C	T	C	IRX4	c.G355A	p.A119T
XH_P57	5	7866967	7866967	Silent	SNP	G	C	G	FASTKD3	c.C1230G	p.A410A
XH_P57	5	7868030	7868030	Missense_Mutation	SNP	T	C	T	FASTKD3	c.A167G	p.K56R
XH_P57	5	13737444	13737444	Missense_Mutation	SNP	G	A	G	DNAH5	c.C11372T	p.T3791I
XH_P57	5	13864728	13864728	Silent	SNP	C	A	C	DNAH5	c.G4374T	p.R1458R
XH_P57	5	13865980	13865980	Silent	SNP	T	C	T	DNAH5	c.A4152G	p.T1384T
XH_P57	5	14498727	14498727	Silent	SNP	G	A	G	TRIO	c.G8310A	p.S2770S
XH_P57	5	16694522	16694522	Missense_Mutation	SNP	C	T	C	MYO10	c.G3758A	p.S1253N
XH_P57	5	31317952	31317952	Silent	SNP	T	C	T	CDH6	c.T1803C	p.H601H
XH_P57	5	32088795	32088795	Silent	SNP	C	T	C	PDZD2	c.C5241T	p.Y1747Y
XH_P57	5	33624430	33624430	Silent	SNP	A	G	A	ADAMTS12	c.T2049C	p.D683D
XH_P57	5	35641582	35641582	Missense_Mutation	SNP	A	C	A	SPEF2	c.A211C	p.N71H
XH_P57	5	35654711	35654711	Silent	SNP	C	T	C	SPEF2	c.C861T	p.D287D
XH_P57	5	35692775	35692775	Missense_Mutation	SNP	T	A	T	SPEF2	c.T1848A	p.N616K
XH_P57	5	35965970	35965970	Missense_Mutation	SNP	A	C	A	UGT3A1	c.T361G	p.C121G
XH_P57	5	36142648	36142648	Silent	SNP	A	G	A	LMBRD2	c.T228C	p.N76N
XH_P57	5	36985303	36985303	Missense_Mutation	SNP	A	G	A	NIPBL	c.A2021G	p.N674S
XH_P57	5	37239884	37239884	Silent	SNP	T	G	T	C5orf42	c.A765C	p.G255G
XH_P57	5	37294473	37294473	Silent	SNP	T	C	T	NUP155	c.A3696G	p.L1232L
XH_P57	5	38921788	38921788	Missense_Mutation	SNP	G	A	G	OSMR	c.G1657A	p.D553N
XH_P57	5	39377132	39377132	Missense_Mutation	SNP	G	A	G	DAB2	c.C1694T	p.P56S1
XH_P57	5	41054934	41054934	Silent	SNP	A	G	A	MROH2B	c.T1042C	p.L348L
XH_P57	5	43122176	43122176	In_Frame_Ins	INS	-	GAATGC	-	ZNF131	21_22insGAATGp.M7delinsMEC	
XH_P57	5	50685678	50685678	Missense_Mutation	SNP	G	A	G	ISL1	c.G677A	p.R226Q
XH_P57	5	53814691	53814691	Silent	SNP	G	A	G	SNX18	c.G909A	p.T303T
XH_P57	5	54404057	54404057	Silent	SNP	C	G	C	GZMA	c.C462G	p.G154G
XH_P57	5	54410099	54410099	Missense_Mutation	SNP	G	A	G	CDC20B	c.C1381T	p.R461W
XH_P57	5	54420799	54420799	Silent	SNP	A	C	A	CDC20B	c.T1047G	p.C349V
XH_P57	5	54528294	54528294	Silent	SNP	C	T	C	CCNO	c.G462A	p.L154L
XH_P57	5	54572163	54572163	Silent	SNP	T	C	T	DHX29	c.A2205G	p.K735K
XH_P57	5	54645411	54645411	Silent	SNP	G	A	G	SKIV2L2	c.G1251A	p.K417K
XH_P57	5	54674296	54674296	Silent	SNP	A	G	A	SKIV2L2	c.A1965G	p.Q655Q
XH_P57	5	57754851	57754851	Silent	SNP	A	G	A	PLK2	c.T339C	p.I113I
XH_P57	5	61694379	61694379	Silent	SNP	T	C	T	DIMT1	c.A405G	p.S135S
XH_P57	5	66479189	66479189	Silent	SNP	G	A	G	CD180	c.C1482T	p.T494T
XH_P57	5	68471247	68471247	Silent	SNP	G	A	G	CCNB1	c.G966A	p.L322L
XH_P57	5	71495041	71495041	Silent	SNP	T	C	T	MAP1B	c.T5481C	p.G1827G
XH_P57	5	71519664	71519664	Missense_Mutation	SNP	C	T	C	MRPS27	c.G683A	p.G228D
XH_P57	5	71524163	71524163	Silent	SNP	A	T	A	MRPS27	c.T456A	p.L152L
XH_P57	5	72868447	72868447	Silent	SNP	T	C	T	UTP15	c.T237C	p.D79D
XH_P57	5	75427935	75427935	Silent	SNP	G	A	G	SV2C	c.G360A	p.R120R
XH_P57	5	75906923	75906923	Missense_Mutation	SNP	C	A	C	IQGAP2	c.C95A	p.P32H
XH_P57	5	77784738	77784738	Silent	SNP	A	G	A	LHFPL2	c.T669C	p.N23N
XH_P57	5	78181423	78181423	Missense_Mutation	SNP	C	T	C	ARSB	c.G1126A	p.V376M
XH_P57	5	79024779	79024779	Missense_Mutation	SNP	A	G	A	CMYA5	c.A191G	p.Y64C
XH_P57	5	79025634	79025634	Missense_Mutation	SNP	G	A	G	CMYA5	c.G1046A	p.G349D
XH_P57	5	79026360	79026360	Missense_Mutation	SNP	G	A	G	CMYA5	c.G1772A	p.G591D
XH_P57	5	79026539	79026539	Missense_Mutation	SNP	A	C	A	CMYA5	c.A1951C	p.S651R
XH_P57	5	79030045	79030045	Silent	SNP	A	G	A	CMYA5	c.A5457G	p.V1819V
XH_P57	5	79030212	79030212	Missense_Mutation	SNP	C	T	C	CMYA5	c.C5624T	p.A1875V
XH_P57	5	79031372	79031372	Missense_Mutation	SNP	G	C	G	CMYA5	c.G6784C	p.V2262L
XH_P57	5	79033306	79033306	Missense_Mutation	SNP	A	C	A	CMYA5	c.A8718C	p.K2906N
XH_P57	5	79034662	79034662	Missense_Mutation	SNP	C	G	C	CMYA5	c.C10074G	p.H3358Q
XH_P57	5	79048562	79048562	Silent	SNP	C	T	C	CMYA5	c.C11055T	p.F3685F
XH_P57	5	79498812	79498812	Missense_Mutation	SNP	G	A	G	SERINC5	c.C88T	p.R30W
XH_P57	5	82833145	82833145	Silent	SNP	G	A	G	VCAN	c.G1362A	p.Q454Q
XH_P57	5	82834630	82834630	Silent	SNP	T	C	T	VCAN	c.T2847C	p.G949G
XH_P57	5	82835545	82835545	Silent	SNP	A	G	A	VCAN	c.A3762G	p.R1254R
XH_P57	5	83360520	83360520	Silent	SNP	C	T	C	EDIL3	c.G921A	p.S307S
XH_P57	5	90020681	90020681	Frame_Shift_Ins	INS	-	TATCTATTCTAAT	-	ADGRV1	rsAACTTATCTAT	p.S3261fs
XH_P57	5	93722036	93722036	Missense_Mutation	SNP	G	A	G	KIAA0825	c.C3530T	p.T1177M
XH_P57	5	93753017	93753017	Missense_Mutation	SNP	C	T	C	KIAA0825	c.G2551A	p.A851T
XH_P57	5	94785958	94785958	Missense_Mutation	SNP	G	A	G	FAM81B	c.G1331A	p.R444H
XH_P57	5	95733112	95733112	Silent	SNP	A	G	A	PCSK1	c.T1650C	p.N550N
XH_P57	5	96031569	96031569	Silent	SNP	A	G	A	CAST	c.A168G	p.Q56Q
XH_P57	5	96086334	96086334	Missense_Mutation	SNP	G	C	G	CAST	c.G1061C	p.C354S
XH_P57	5	96118843	96118843	Frame_Shift_Ins	INS	-	T	-	ERAP1	c.2196dupA	p.L733fs
XH_P57	5	96498783	96498783	Silent	SNP	G	A	G	RIOK2	c.C1641T	p.A547A
XH_P57	5	96503523	96503523	Missense_Mutation	SNP	C	T	C	RIOK2	c.G1045A	p.G349R
XH_P57	5	96513471	96513471	Missense_Mutation	SNP	G	C	G	RIOK2	c.C287G	p.S96C
XH_P57	5	108714298	108714298	Missense_Mutation	SNP	T	C	T	PJA2	c.A890G	p.Q297R
XH_P57	5	110819753	110819753	Silent	SNP	G	C	G	CAMK4	c.G420C	p.S140S
XH_P57	5	112824036	112824036	In_Frame_Ins	INS	-	GCC	-	MCC	c.75_76insGGC	p.S26delinsGS
XH_P57	5	114860397	114860397	Silent	SNP	G	A	G	FEM1C	c.C1462T	p.L488L
XH_P57	5	115811248	115811248	Missense_Mutation	SNP	G	T	G	SEMA6A	c.C1701A	p.D567E
XH_P57	5	118669304	118669304	Silent	SNP	C	T	C	TNFAIP8	c.C45T	p.L15H
XH_P57	5	118861713	118861713	Missense_Mutation	SNP	A	G	A	HSD17B4	c.A1621G	p.I541V
XH_P57	5	121758849	121758849	Silent	SNP	G	A	G	SNCAIP	c.G417A	p.S139S

XH P57	5	122506503	122506503	Silent	SNP	C	T	C	PRDM6	c.C1197T	p.D399D
XH P57	5	126783373	126783373	Silent	SNP	G	A	G	MEGF10	c.G2853A	p.T951T
XH P57	5	131602166	131602166	Silent	SNP	T	C	T	PDLIM4	c.T255C	p.G85G
XH P57	5	131607588	131607588	Missense_Mutation	SNP	G	T	G	PDLIM4	c.G775T	p.G259C
XH P57	5	132158956	132158956	Missense_Mutation	SNP	C	G	C	SHROOM1	c.G2212C	p.D738H
XH P57	5	134681684	134681684	Missense_Mutation	SNP	T	C	T	H2AFY	c.A749G	p.K250R
XH P57	5	135207187	135207187	Silent	SNP	G	A	G	SLC25A48	c.G459A	p.A153A
XH P57	5	135692575	135692575	Silent	SNP	G	A	G	TRPC7	c.C501T	p.P167P
XH P57	5	137726964	137726964	Missense_Mutation	SNP	C	G	C	KDM3B	c.C1643G	p.A548G
XH P57	5	139217320	139217320	Silent	SNP	G	C	G	PSD2	c.G1776C	p.V592V
XH P57	5	139927354	139927366	Frame_Shift_Del	DEL	GGCCCGGGA	-	GGCCCGGGACC	EIF4EBP3	c.32_44del	p.G11fs
XH P57	5	140021482	140021482	Silent	SNP	C	T	C	TMC06	c.C342T	p.V114V
XH P57	5	140023238	140023238	Missense_Mutation	SNP	C	G	C	TMC06	c.C176G	p.T59S
XH P57	5	140048209	140048209	Silent	SNP	T	C	T	WDR55	c.T393C	p.N131N
XH P57	5	140048544	140048544	Missense_Mutation	SNP	C	T	C	WDR55	c.C629T	p.S210F
XH P57	5	140051060	140051060	Frame_Shift_Ins	INS	-	CACC	-	DND1	879_880insGGT	p.I294fs
XH P57	5	140052271	140052271	Silent	SNP	A	G	A	DND1	c.T363C	p.H121H
XH P57	5	140208601	140208601	Missense_Mutation	SNP	G	C	G	PCDHA6	c.G925C	p.D309H
XH P57	5	140228164	140228164	Missense_Mutation	SNP	C	A	C	PCDHA9	c.C84A	p.S28R
XH P57	5	140229086	140229086	Missense_Mutation	SNP	C	G	C	PCDHA9	c.C1006G	p.L336V
XH P57	5	140229368	140229368	Missense_Mutation	SNP	G	C	G	PCDHA9	c.G1288C	p.G430R
XH P57	5	140229526	140229526	Silent	SNP	T	G	T	PCDHA9	c.T1446G	p.A482A
XH P57	5	140237387	140237387	Missense_Mutation	SNP	T	G	T	PCDHA10	c.T1754G	p.V585G
XH P57	5	140237548	140237548	Missense_Mutation	SNP	A	G	A	PCDHA10	c.A1915G	p.T639A
XH P57	5	140250252	140250252	Silent	SNP	T	C	T	PCDHA11	c.T1564C	p.L522L
XH P57	5	140263290	140263290	Silent	SNP	T	G	T	PCDHA13	c.T1437G	p.A479A
XH P57	5	140515483	140515483	Missense_Mutation	SNP	T	C	T	PCDHB5	c.T467C	p.I156T
XH P57	5	140558916	140558916	Missense_Mutation	SNP	C	G	C	PCDHB8	c.C1301G	p.T434R
XH P57	5	140574045	140574045	Silent	SNP	C	G	C	PCDHB10	c.C1920G	p.L640L
XH P57	5	140580493	140580493	Silent	SNP	T	A	T	PCDHB11	c.T1146A	p.V382V
XH P57	5	140594234	140594234	Missense_Mutation	SNP	G	A	G	PCDHB13	c.G539A	p.R180Q
XH P57	5	140723684	140723684	Frame_Shift_Ins	INS	-	G	-	PCDHGA3	c.85dupG	p.S28fs
XH P57	5	140764727	140764727	Missense_Mutation	SNP	C	T	C	PCDHGA7	c.C2261T	p.S754F
XH P57	5	140768428	140768428	Missense_Mutation	SNP	T	C	T	PCDHGB4	c.T977C	p.I362T
XH P57	5	140857906	140857906	Silent	SNP	C	T	C	PCDHGC3	c.C2223T	p.S741S
XH P57	5	141335498	141335498	Missense_Mutation	SNP	C	T	C	PCDH12	c.G1919A	p.S640N
XH P57	5	145317685	145317685	Missense_Mutation	SNP	C	T	C	SH3RF2	c.C194T	p.A65V
XH P57	5	145719271	145719271	Missense_Mutation	SNP	C	T	C	POU4F3	c.C281T	p.T94I
XH P57	5	147466001	147466001	Missense_Mutation	SNP	G	A	G	SPINK5	c.G316A	p.D106N
XH P57	5	147499891	147499891	Missense_Mutation	SNP	G	T	G	SPINK5	c.G2475T	p.E825D
XH P57	5	147805120	147805120	Missense_Mutation	SNP	T	C	T	FBXO38	c.T1774C	p.S592P
XH P57	5	149457678	149457678	Silent	SNP	G	A	G	CSF1R	c.C726T	p.T242T
XH P57	5	149677593	149677593	Silent	SNP	A	G	A	ARSI	c.T894C	p.N298N
XH P57	5	149755744	149755744	Missense_Mutation	SNP	G	C	G	TCOF1	c.G1762C	p.A588P
XH P57	5	149907602	149907602	Silent	SNP	A	G	A	NDST1	c.A750G	p.P250P
XH P57	5	150027814	150027814	Missense_Mutation	SNP	G	A	G	SYNPO	c.G709A	p.D237N
XH P57	5	150578574	150578574	Silent	SNP	A	G	A	CCDC69	c.T303C	p.N101N
XH P57	5	150639409	150639409	Missense_Mutation	SNP	A	G	A	GM2A	c.A175G	p.I59V
XH P57	5	150723747	150723747	Silent	SNP	C	T	C	SLC36A2	c.G246A	p.A82A
XH P57	5	150905398	150905398	Silent	SNP	C	T	C	FAT2	c.G10437A	p.P3479P
XH P57	5	150908813	150908813	Missense_Mutation	SNP	G	A	G	FAT2	c.C9952T	p.R3318W
XH P57	5	151784183	151784183	Silent	SNP	G	A	G	NMUR2	c.C492T	p.L164L
XH P57	5	153149798	153149798	Missense_Mutation	SNP	G	A	G	GRIA1	c.G1853A	p.R618Q
XH P57	5	154395158	154395158	Missense_Mutation	SNP	G	T	G	KIF4B	c.G1739T	p.R580L
XH P57	5	154395458	154395458	Missense_Mutation	SNP	G	A	G	KIF4B	c.G2039A	p.R680H
XH P57	5	154395682	154395682	Missense_Mutation	SNP	G	A	G	KIF4B	c.G2263A	p.V755I
XH P57	5	154396505	154396505	Missense_Mutation	SNP	G	A	G	KIF4B	c.G3086A	p.R1029H
XH P57	5	156589901	156589901	Missense_Mutation	SNP	C	T	C	FAM71B	c.G1375A	p.D459N
XH P57	5	156898690	156898690	Missense_Mutation	SNP	A	G	A	NIPAL4	c.A580G	p.R194G
XH P57	5	159546013	159546013	Missense_Mutation	SNP	T	C	T	PWWP2A	c.A383G	p.E128G
XH P57	5	161119125	161119125	Silent	SNP	C	G	C	GABRA6	c.C1005G	p.A335A
XH P57	5	167858371	167858371	Missense_Mutation	SNP	G	T	G	WWC1	c.G2202T	p.M734I
XH P57	5	167858372	167858372	Missense_Mutation	SNP	T	G	T	WWC1	c.T2203G	p.S735A
XH P57	5	167937607	167937607	Silent	SNP	G	A	G	RARS	c.G1368A	p.S456S
XH P57	5	168123313	168123313	Silent	SNP	A	G	A	SLIT3	c.T3087C	p.C1029C
XH P57	5	168175326	168175326	Missense_Mutation	SNP	G	A	G	SLIT3	c.C2251T	p.P751S
XH P57	5	169435713	169435713	Silent	SNP	A	C	A	DOCK2	c.A3195C	p.L1065L
XH P57	5	169496219	169496219	Missense_Mutation	SNP	T	C	T	DOCK2	c.T4723C	p.W1575R
XH P57	5	169533240	169533240	Silent	SNP	G	A	G	FOX11	c.G279A	p.R93R
XH P57	5	171299917	171299917	Silent	SNP	C	T	C	FBXW11	c.G1134A	p.R378R
XH P57	5	171481606	171481606	Silent	SNP	A	G	A	STK10	c.T2619C	p.C873C
XH P57	5	172197210	172197210	In_Frame_Ins	INS	-	TGT	-	DUSP1	c.466_467insAC	p.S156delinsNS
XH P57	5	175523853	175523853	Missense_Mutation	SNP	C	A	C	FAM153B	c.C160A	p.P54T
XH P57	5	175772208	175772208	Silent	SNP	C	T	C	SIMC1	c.C762T	p.I254I
XH P57	5	175793532	175793532	Silent	SNP	C	T	C	ARL10	c.C333T	p.G111G
XH P57	5	176314639	176314639	Silent	SNP	G	A	G	HK3	c.C1413T	p.A471A
XH P57	5	176637149	176637149	Silent	SNP	G	A	G	NSD1	c.G1749A	p.E583E
XH P57	5	176637576	176637576	Missense_Mutation	SNP	T	C	T	NSD1	c.T2176C	p.S726P
XH P57	5	176795196	176795196	Missense_Mutation	SNP	T	G	T	RGS14	c.T778G	p.S260A
XH P57	5	176916516	176916516	Silent	SNP	C	T	C	PDLIM7	c.G747A	p.P249P
XH P57	5	177035964	177035964	Silent	SNP	T	C	T	B4GALT7	c.T777C	p.H259H
XH P57	5	178540975	178540975	Missense_Mutation	SNP	G	A	G	ADAMTS2	c.C3529T	p.P1177S
XH P57	5	179135353	179135353	Missense_Mutation	SNP	C	A	C	CANX	c.C418A	p.L140M
XH P57	5	179193598	179193598	Silent	SNP	C	T	C	MAML1	c.C1587T	p.S529S
XH P57	5	179201847	179201847	Missense_Mutation	SNP	G	A	G	MAML1	c.G3020A	p.S1007N
XH P57	5	179498641	179498641	Frame_Shift_Ins	INS	-	TGCA	-	RNF130	c.61_62insTGCA	p.S21fs
XH P57	5	179734230	179734230	Silent	SNP	C	G	C	GFPT2	c.G1620C	p.S540S
XH P57	5	180046344	180046344	Missense_Mutation	SNP	G	C	G	FLT4	c.C2670G	p.H890Q
XH P57	5	180057231	180057231	Silent	SNP	C	A	C	FLT4	c.G507T	p.L169L
XH P57	5	180338368	180338368	Missense_Mutation	SNP	A	G	A	BTNL8	c.A79G	p.T27A
XH P57	5	180374534	180374534	Silent	SNP	G	A	G	BTNL8	c.G348A	p.S116S
XH P57	5	180432416	180432416	Silent	SNP	C	T	C	BTNL3	c.C945T	p.P315P
XH P57	5	180622615	180622615	Missense_Mutation	SNP	C	T	C	TRIM7	c.G541A	p.G181S
XH P57	5	180687212	180687212	Silent	SNP	C	T	C	TRIM52	c.G603A	p.L201L
XH P57	6	1313470	1313470	Silent	SNP	C	T	C	FOXQ1	c.C531T	p.F177F
XH P57	6	1395043	1395043	Silent	SNP	T	C	T	FOXF2	c.T1284C	p.Y428Y
XH P57	6	1742794	1742794	Silent	SNP	A	G	A	GMDS	c.T708C	p.D236D
XH P57	6	3015790	3015790	Silent	SNP	A	G	A	NQO2	c.A330G	p.P110P

XH_P57	6	3850420	3850420	Silent	SNP	C	T	C	FAM50B	c.C375T	p.D125D
XH_P57	6	7211818	7211818	Missense_Mutation	SNP	G	A	G	RREB1	c.G583A	p.G195R
XH_P57	6	7230906	7230906	Silent	SNP	C	G	C	RREB1	c.C2574G	p.P858P
XH_P57	6	7231770	7231770	Silent	SNP	A	G	A	RREB1	c.A3438G	p.P1146P
XH_P57	6	7246998	7246998	Missense_Mutation	SNP	G	A	G	RREB1	c.G4150A	p.G1384R
XH_P57	6	7301664	7301664	Missense_Mutation	SNP	G	A	G	SSR1	c.C422T	p.P141L
XH_P57	6	7581636	7581636	Missense_Mutation	SNP	G	A	G	DSP	c.G5213A	p.R1738Q
XH_P57	6	7584943	7584943	Missense_Mutation	SNP	A	G	A	DSP	c.A5651G	p.Y1884C
XH_P57	6	10877476	10877476	Silent	SNP	C	T	C	GCM2	c.G240A	p.S80S
XH_P57	6	11005686	11005686	Silent	SNP	G	A	G	ELOVL2	c.C174T	p.N58N
XH_P57	6	12122773	12122773	Silent	SNP	T	C	T	HIVEP1	c.T2745C	p.T915T
XH_P57	6	13801615	13801615	Missense_Mutation	SNP	T	C	T	MCUR1	c.A646G	p.T216A
XH_P57	6	15496662	15496662	Silent	SNP	C	T	C	JARID2	c.C690T	p.P230P
XH_P57	6	16290761	16290761	Missense_Mutation	SNP	T	A	T	GMPR	c.T766A	p.F256I
XH_P57	6	16306866	16306866	Silent	SNP	G	A	G	ATXN1	c.C2142T	p.D714D
XH_P57	6	17543302	17543302	Silent	SNP	A	G	A	CAP2	c.A1137G	p.K379K
XH_P57	6	17551781	17551781	Silent	SNP	C	T	C	CAP2	c.C1296T	p.I432I
XH_P57	6	17764731	17764731	Silent	SNP	G	C	G	KIF13A	c.C4884G	p.A1628A
XH_P57	6	18161563	18161563	Silent	SNP	G	A	G	KDM1B	c.G93A	p.K31K
XH_P57	6	25967068	25967068	Silent	SNP	C	T	C	TRIM38	c.C318T	p.D106D
XH_P57	6	26017806	26017806	Missense_Mutation	SNP	G	A	G	HIST1H1A	c.C155T	p.S52F
XH_P57	6	26104448	26104448	Silent	SNP	A	G	A	HIST1H4C	c.A273G	p.L91L
XH_P57	6	26107790	26107790	Missense_Mutation	SNP	G	T	G	HIST1H1T	c.C532A	p.Q178K
XH_P57	6	26108282	26108282	Missense_Mutation	SNP	C	G	C	HIST1H1T	c.G40C	p.V14L
XH_P57	6	26204873	26204873	Missense_Mutation	SNP	A	G	A	HIST1H4E	c.A1G	p.M1V
XH_P57	6	26501897	26501897	Silent	SNP	T	C	T	BTN1A1	c.T159C	p.S53S
XH_P57	6	26505362	26505362	Missense_Mutation	SNP	G	A	G	BTN1A1	c.G637A	p.A213T
XH_P57	6	26505403	26505403	Silent	SNP	C	A	C	BTN1A1	c.C678A	p.G226G
XH_P57	6	26509330	26509330	Missense_Mutation	SNP	C	G	C	BTN1A1	c.C1509G	p.D503E
XH_P57	6	26545632	26545632	Silent	SNP	G	A	G	HMGN4	c.G198A	p.G66G
XH_P57	6	26598188	26598188	Silent	SNP	A	G	A	ABT1	c.A288G	p.G96G
XH_P57	6	27791950	27791950	Silent	SNP	T	A	T	HIST1H4J	c.T48A	p.A16A
XH_P57	6	27799258	27799258	Silent	SNP	A	T	A	HIST1H4K	c.T48A	p.A16A
XH_P57	6	31106516	31106516	Missense_Mutation	SNP	C	T	C	PSORS1C1	c.C127T	p.P43S
XH_P57	6	32489753	32489753	Missense_Mutation	SNP	C	G	C	HLA-DRB5	c.G299C	p.R100T
XH_P57	6	32629931	32629931	Missense_Mutation	SNP	C	G	C	HLA-DQB1	c.G474C	p.Q158H
XH_P57	6	33630768	33630768	Frame_Shift_Ins	INS	-	T	-	ITPR3	c.940dupT	p.N313fs
XH_P57	6	33648144	33648144	Silent	SNP	C	T	C	ITPR3	c.C4263T	p.Y1421Y
XH_P57	6	33652167	33652167	Silent	SNP	G	A	G	ITPR3	c.G4971A	p.S1657S
XH_P57	6	33654254	33654254	Silent	SNP	C	T	C	ITPR3	c.C5937T	p.S1979S
XH_P57	6	33660597	33660597	Silent	SNP	C	T	C	ITPR3	c.C7551T	p.I2517I
XH_P57	6	34803949	34803949	Missense_Mutation	SNP	C	T	C	UHRF1BP1	c.C857T	p.P286L
XH_P57	6	34824107	34824107	Missense_Mutation	SNP	A	C	A	UHRF1BP1	c.A1212C	p.K404N
XH_P57	6	35430686	35430686	Missense_Mutation	SNP	G	A	G	FANCE	c.G1504A	p.A502T
XH_P57	6	35705892	35705892	Silent	SNP	T	C	T	ARMC12	c.T252C	p.Y84Y
XH_P57	6	35773782	35773782	Missense_Mutation	SNP	T	C	T	LHFPL5	c.T335C	p.I112T
XH_P57	6	35923246	35923246	Missense_Mutation	SNP	T	C	T	SLC26A8	c.A1600G	p.I534V
XH_P57	6	36260858	36260858	Silent	SNP	C	T	C	PNPLA1	c.C174T	p.F58F
XH_P57	6	36262153	36262153	Missense_Mutation	SNP	G	A	G	PNPLA1	c.G433A	p.A145T
XH_P57	6	36275458	36275458	Missense_Mutation	SNP	T	C	T	PNPLA1	c.T1306C	p.S436P
XH_P57	6	36287312	36287312	Missense_Mutation	SNP	G	C	G	C6orf222	c.C1744G	p.L582V
XH_P57	6	36341294	36341294	Silent	SNP	C	T	C	ETV7	c.G204A	p.G68G
XH_P57	6	36686272	36686272	Silent	SNP	C	T	C	RAB44	c.C735T	p.S245S
XH_P57	6	36689630	36689630	Silent	SNP	C	T	C	RAB44	c.C1719T	p.A573A
XH_P57	6	36689821	36689821	Missense_Mutation	SNP	C	T	C	RAB44	c.C1910T	p.A637V
XH_P57	6	36689961	36689961	Silent	SNP	A	C	A	RAB44	c.A2050C	p.R684R
XH_P57	6	36733132	36733132	Silent	SNP	G	A	G	CPNE5	c.C759T	p.Y253Y
XH_P57	6	36824399	36824399	Silent	SNP	C	T	C	PHL1	c.G243A	p.Q81Q
XH_P57	6	36938432	36938432	Silent	SNP	G	A	G	MTCH1	c.C945T	p.F315F
XH_P57	6	36995222	36995222	Silent	SNP	G	A	G	FGD2	c.G1623A	p.T541T
XH_P57	6	37447798	37447798	Silent	SNP	C	T	C	CMTR1	c.C2385T	p.Y795Y
XH_P57	6	37623626	37623626	Silent	SNP	C	T	C	MDGA1	c.G429A	p.V143V
XH_P57	6	37626142	37626142	Silent	SNP	C	T	C	MDGA1	c.G261A	p.S87S
XH_P57	6	38650628	38650628	Missense_Mutation	SNP	T	G	T	GLO1	c.A332C	p.E111A
XH_P57	6	38705682	38705682	Silent	SNP	C	T	C	DNAH8	c.C1050T	p.A350A
XH_P57	6	38840492	38840492	Missense_Mutation	SNP	G	T	G	DNAH8	c.G7171T	p.A2391S
XH_P57	6	38841083	38841083	Silent	SNP	T	C	T	DNAH8	c.T7551C	p.D2517D
XH_P57	6	39282806	39282806	Missense_Mutation	SNP	G	T	G	KCNK16	c.C761A	p.P254H
XH_P57	6	39283083	39283083	Silent	SNP	G	A	A	KCNK16	c.C786T	p.N262N
XH_P57	6	39284184	39284184	Silent	SNP	A	G	A	KCNK16	c.C769C	p.Y232Y
XH_P57	6	39881120	39881120	Missense_Mutation	SNP	G	A	G	MOC51	c.C698T	p.A233V
XH_P57	6	40998141	40998141	Silent	SNP	G	A	G	UNC5CL	c.C1320T	p.C440C
XH_P57	6	41029109	41029109	Silent	SNP	T	C	T	APOBEC2	c.T174C	p.N58N
XH_P57	6	41029342	41029342	Missense_Mutation	SNP	T	C	T	APOBEC2	c.T407C	p.I136T
XH_P57	6	41162518	41162518	Missense_Mutation	SNP	T	C	T	TREML2	c.A430G	p.S144G
XH_P57	6	41165899	41165899	Silent	SNP	G	A	G	TREML2	c.C324T	p.N108N
XH_P57	6	41533579	41533579	Silent	SNP	C	A	C	FOXP4	c.C81A	p.A27A
XH_P57	6	41555115	41555115	Missense_Mutation	SNP	A	T	A	FOXP4	c.A737T	p.K246M
XH_P57	6	41557567	41557567	Missense_Mutation	SNP	C	T	C	FOXP4	c.C1124T	p.S375L
XH_P57	6	42995126	42995126	Missense_Mutation	SNP	G	A	G	RRP36	c.G539A	p.R180Q
XH_P57	6	43005625	43005625	Missense_Mutation	SNP	G	A	G	CUL7	c.C5150T	p.T1717M
XH_P57	6	43008298	43008298	Silent	SNP	C	T	C	CUL7	c.G4245A	p.L1415L
XH_P57	6	43020188	43020188	Silent	SNP	G	A	G	CUL7	c.C495T	p.D165D
XH_P57	6	43021519	43021519	Silent	SNP	G	A	G	CUL7	c.C78T	p.R26R
XH_P57	6	43152573	43152573	Silent	SNP	A	G	A	CUL9	c.A525G	p.L175L
XH_P57	6	43184132	43184132	Missense_Mutation	SNP	A	C	A	CUL9	c.A6173C	p.H2058P
XH_P57	6	43230970	43230970	Missense_Mutation	SNP	G	C	G	TBKB1	c.G1868C	p.G623A
XH_P57	6	44185264	44185264	Missense_Mutation	SNP	T	A	T	MYMX	c.T56A	p.L19Q
XH_P57	6	44221115	44221127	Frame_Shift_Del	DEL	STAAGTAGCT	-	GTGAAGTAGCTT	HSP90AB1	c.2065delG	p.G689fs
XH_P57	6	44270170	44270170	Silent	SNP	C	T	C	AARS2	c.G2445A	p.A815A
XH_P57	6	46133282	46133282	Missense_Mutation	SNP	T	C	T	ENPP5	c.A566G	p.Y189C
XH_P57	6	47846313	47846313	Missense_Mutation	SNP	C	T	C	PTCHD4	c.G2267A	p.G756E
XH_P57	6	49494241	49494241	Missense_Mutation	SNP	A	G	A	GLYATL3	c.A481G	p.P161D
XH_P57	6	49701439	49701439	Missense_Mutation	SNP	C	A	C	CRISP3	c.G469T	p.A157S
XH_P57	6	51890823	51890823	Missense_Mutation	SNP	G	A	G	PKHD1	c.C3785T	p.A1262V
XH_P57	6	51914956	51914956	Missense_Mutation	SNP	G	A	G	PKHD1	c.C2278T	p.P760C
XH_P57	6	51918923	51918923	Missense_Mutation	SNP	T	C	T	PKHD1	c.A1877G	p.K626R
XH_P57	6	52101739	52101739	Missense_Mutation	SNP	T	C	T	IL17F	c.A482G	p.H161R

XH P57	6	52878637	52878637	Silent	SNP	T	C	T	ICK	c.A975G	p.P325P
XH P57	6	53519857	53519857	Silent	SNP	G	A	G	KLHL31	c.C214T	p.L72L
XH P57	6	54002026	54002026	Missense_Mutation	SNP	T	C	T	MLIP	c.T1126C	p.S376P
XH P57	6	55196587	55196587	Missense_Mutation	SNP	C	T	C	GFRAL	c.C97T	p.R33C
XH P57	6	56327849	56327849	Missense_Mutation	SNP	C	T	C	DST	c.G15124A	p.A5042T
XH P57	6	56463410	56463410	Missense_Mutation	SNP	T	C	T	DST	c.A3923G	p.Q1308R
XH P57	6	56484758	56484758	Silent	SNP	C	T	C	DST	c.G4074A	p.K1358K
XH P57	6	64498055	64498055	Missense_Mutation	SNP	T	A	T	EYS	c.A7666T	p.S2556C
XH P57	6	65622463	65622463	Missense_Mutation	SNP	A	G	A	EYS	c.T2555C	p.L852P
XH P57	6	66005794	66005794	Missense_Mutation	SNP	C	A	C	EYS	c.G1985T	p.R662M
XH P57	6	74073531	74073531	Missense_Mutation	SNP	C	G	C	KHDC3L	c.C602G	p.A201G
XH P57	6	74079024	74079024	Missense_Mutation	SNP	A	G	A	OEEP	c.T275C	p.V92A
XH P57	6	74354175	74354175	Silent	SNP	C	T	C	SLC17A5	c.C246A	p.A82A
XH P57	6	74521947	74521947	Missense_Mutation	SNP	C	T	C	CD109	c.C3491T	p.T1164M
XH P57	6	82461520	82461520	Silent	SNP	A	G	A	FAM46A	c.T339C	p.I113I
XH P57	6	83881740	83881740	Silent	SNP	T	C	T	PGM3	c.A1038G	p.E346E
XH P57	6	88318883	88318883	Missense_Mutation	SNP	G	A	G	ORC3	c.G220A	p.V74I
XH P57	6	88362943	88362943	Silent	SNP	C	T	C	ORC3	c.C1063T	p.L355L
XH P57	6	88853635	88853635	Silent	SNP	C	T	C	CNR1	c.G1359A	p.T453T
XH P57	6	89907883	89907883	Missense_Mutation	SNP	A	G	A	GABRR1	c.T377C	p.M126T
XH P57	6	90338863	90338863	Silent	SNP	C	T	C	ANKRD6	c.C1341T	p.C447C
XH P57	6	90482397	90482397	Missense_Mutation	SNP	T	C	T	MDN1	c.A1978G	p.I660V
XH P57	6	90565242	90565242	Silent	SNP	A	G	A	CASP8AP2	c.A279G	p.K93K
XH P57	6	90660319	90660319	Silent	SNP	T	C	T	BACH2	c.A1506G	p.V502V
XH P57	6	97344676	97344676	Silent	SNP	G	A	G	NDUFAF4	c.C184T	p.L62L
XH P57	6	99825348	99825348	Missense_Mutation	SNP	T	C	T	COQ3	c.A400G	p.K134E
XH P57	6	101296389	101296389	Missense_Mutation	SNP	G	A	G	ASCC3	c.C436T	p.L146F
XH P57	6	107019880	107019880	Silent	SNP	A	G	A	RTN4IP1	c.T882C	p.N294N
XH P57	6	108068003	108068003	Missense_Mutation	SNP	C	T	C	SCML4	c.G203A	p.R68Q
XH P57	6	109591433	109591433	Silent	SNP	T	C	T	C6orf183	c.T1638C	p.N546N
XH P57	6	109770899	109770899	Silent	SNP	G	C	G	MICAL1	c.C1137G	p.R379R
XH P57	6	110146303	110146303	Silent	SNP	G	A	G	FIG4	c.G2559A	p.S853S
XH P57	6	110942500	110942500	Missense_Mutation	SNP	G	A	G	CDK19	c.C1052T	p.A351V
XH P57	6	111650743	111650769	In_Frame_Del	DEL	TTCCCGAGAAA	-	CTCCCGAGAAA	REV3L	c.8207_8233del	p.2736_2745del
XH P57	6	112382313	112382313	Missense_Mutation	SNP	G	T	G	WISP3	c.G222T	p.Q74H
XH P57	6	112493889	112493889	Missense_Mutation	SNP	A	T	A	LAMA4	c.T1475A	p.L492H
XH P57	6	116574455	116574455	Silent	SNP	G	A	G	TSPYL4	c.C171T	p.H239P
XH P57	6	116784850	116784850	Missense_Mutation	SNP	C	G	C	FAM26F	c.C414G	p.N138K
XH P57	6	116938073	116938073	Missense_Mutation	SNP	C	T	C	RSPH4A	c.C287T	p.P96L
XH P57	6	116968690	116968690	In_Frame_Ins	INS	-	AAT	-	ZUF5P	1399_1400insA	p.S467delinsYS
XH P57	6	117591755	117591755	Silent	SNP	T	C	T	VGLL2	c.T441C	p.N147N
XH P57	6	117710661	117710661	Missense_Mutation	SNP	T	C	T	ROS1	c.A1611G	p.I537M
XH P57	6	118886961	118886961	Missense_Mutation	SNP	G	T	G	CEP85L	c.C751A	p.P251T
XH P57	6	119245024	119245024	Silent	SNP	C	T	C	MCN9	c.G573A	p.S191S
XH P57	6	127476516	127476516	Silent	SNP	G	A	G	RSPO3	c.G567A	p.L189L
XH P57	6	128411109	128411109	Silent	SNP	C	T	C	PTPRK	c.G804A	p.K268K
XH P57	6	129635800	129635800	Missense_Mutation	SNP	G	A	G	LAMA2	c.G3412A	p.V1138M
XH P57	6	130374102	130374102	Missense_Mutation	SNP	C	A	C	L3MBTL3	c.C473A	p.T158N
XH P57	6	130381246	130381246	Silent	SNP	T	C	T	L3MBTL3	c.T750C	p.P250P
XH P57	6	131894479	131894479	Silent	SNP	G	A	G	ARG1	c.G57A	p.Q19Q
XH P57	6	132189165	132189165	Missense_Mutation	SNP	A	G	A	ENPP1	c.A1172G	p.K391R
XH P57	6	132206094	132206094	Missense_Mutation	SNP	A	C	A	ENPP1	c.A2335C	p.T779P
XH P57	6	132938842	132938842	Nonsense_Mutation	SNP	C	T	C	TAAR2	c.G368A	p.W123X
XH P57	6	133015227	133015227	Missense_Mutation	SNP	C	T	C	VNN1	c.G436A	p.D146N
XH P57	6	136934321	136934321	Silent	SNP	T	C	T	MAP3K5	c.A2352G	p.T784T
XH P57	6	138753153	138753153	Missense_Mutation	SNP	T	A	T	NHSL1	c.A2341T	p.T781S
XH P57	6	138753155	138753155	Missense_Mutation	SNP	T	G	T	NHSL1	c.A2339C	p.V780S
XH P57	6	139487836	139487836	Silent	SNP	T	C	T	HECA	c.T687C	p.N229N
XH P57	6	142714117	142714117	Silent	SNP	G	A	G	ADGRG6	c.G1257A	p.T419T
XH P57	6	143823157	143823157	Missense_Mutation	SNP	T	C	T	FUCA2	c.A1066G	p.M356V
XH P57	6	144207282	144207282	Silent	SNP	A	G	A	ZC2HC1B	c.A204G	p.Q68Q
XH P57	6	145114993	145114993	Missense_Mutation	SNP	C	T	C	UTRN	c.C8944T	p.P2982S
XH P57	6	145956618	145956618	Missense_Mutation	SNP	G	C	G	EPM2A	c.C481G	p.L161V
XH P57	6	146126419	146126419	Missense_Mutation	SNP	C	T	C	FBXO30	c.G1123A	p.V375M
XH P57	6	146755140	146755140	Silent	SNP	G	A	G	GRM1	c.G2793A	p.K931K
XH P57	6	146755842	146755842	Silent	SNP	C	A	C	GRM1	c.C3495A	p.P1165P
XH P57	6	149795522	149795522	Missense_Mutation	SNP	G	A	G	ZC3H12D	c.C158T	p.P53L
XH P57	6	150210723	150210723	Missense_Mutation	SNP	C	T	C	RAET1E	c.G275A	p.R92H
XH P57	6	150342232	150342232	Missense_Mutation	SNP	G	A	G	RAET1L	c.C440T	p.T147I
XH P57	6	150346532	150346532	Missense_Mutation	SNP	T	C	T	RAET1L	c.A76G	p.R26G
XH P57	6	150390149	150390149	Nonsense_Mutation	SNP	G	C	G	ULBP3	c.C54G	p.Y18X
XH P57	6	150716533	150716533	Missense_Mutation	SNP	T	A	T	IYD	c.T691A	p.F231I
XH P57	6	150716697	150716697	Missense_Mutation	SNP	G	A	G	IYD	c.G794A	p.C265Y
XH P57	6	151055189	151055189	Silent	SNP	C	G	C	PLEKHG1	c.C549G	p.T183T
XH P57	6	151673179	151673179	Missense_Mutation	SNP	A	T	A	AKAP12	c.A3359T	p.K1120I
XH P57	6	151673630	151673630	Silent	SNP	A	G	A	AKAP12	c.A3810G	p.E1270E
XH P57	6	151686905	151686905	Silent	SNP	C	T	C	ZBTB2	c.G1296A	p.E432E
XH P57	6	151914265	151914265	Silent	SNP	T	C	T	CCDC170	c.T1317C	p.L439L
XH P57	6	152646279	152646279	Silent	SNP	G	C	G	SYNE1	c.C15384G	p.A5128A
XH P57	6	153296541	153296541	Missense_Mutation	SNP	G	C	G	FBXO5	c.C181G	p.Q61E
XH P57	6	153315744	153315744	Silent	SNP	T	A	T	MTRF1L	c.A591T	p.G197G
XH P57	6	153323594	153323594	Missense_Mutation	SNP	C	T	C	MTRF1L	c.G227A	p.R76Q
XH P57	6	153323709	153323709	Missense_Mutation	SNP	T	C	T	MTRF1L	c.A112G	p.T38A
XH P57	6	154412347	154412347	Missense_Mutation	SNP	G	A	G	OPRM1	c.G604A	p.V202I
XH P57	6	154763401	154763401	Silent	SNP	G	A	G	CKNSR3	c.C240T	p.N80N
XH P57	6	155578010	155578010	Missense_Mutation	SNP	G	A	G	TIAM2	c.G1636A	p.G546R
XH P57	6	160169258	160169258	Silent	SNP	G	T	G	WTAP	c.G309T	p.P103P
XH P57	6	160328620	160328620	Silent	SNP	C	T	C	MAS1	c.C633T	p.V211V
XH P57	6	160493834	160493834	Silent	SNP	G	A	G	IGF2R	c.G4608A	p.A1536A
XH P57	6	160517481	160517481	Silent	SNP	C	T	C	IGF2R	c.C6666T	p.L2222L
XH P57	6	161054859	161054859	Silent	SNP	A	T	A	LPA	c.T1161A	p.T387T
XH P57	6	161807831	161807831	In_Frame_Ins	INS	-	AAA	-	PRKN	c.714_715insTT	p.T239delinsFT
XH P57	6	166572005	166572005	Missense_Mutation	SNP	T	C	T	T	c.A932G	p.P311S
XH P57	6	166736362	166736362	Silent	SNP	C	T	C	SFT2D1	c.G423A	p.S141S
XH P57	6	166864693	166864693	Silent	SNP	G	A	G	RP56KA2	c.C810T	p.N270N
XH P57	6	166873010	166873010	Silent	SNP	C	T	C	RP56KA2	c.G708A	p.P236P
XH P57	6	167040463	167040463	Silent	SNP	A	G	A	RP56KA2	c.T45C	p.S15S
XH P57	7	930689	930689	Silent	SNP	C	T	C	GET4	c.C591T	p.A197A

XH_P57	7	933428	933428	Silent	SNP	C	T	C	GET4	c.C798T	p.L266L
XH_P57	7	1276250	1276250	Silent	SNP	C	T	C	UNCX	c.C1233T	p.P411P
XH_P57	7	1484852	1484852	Missense_Mutation	SNP	G	A	G	MICALL2	c.C854T	p.S285L
XH_P57	7	2472555	2472555	Missense_Mutation	SNP	C	T	C	CHST12	c.C281T	p.P94L
XH_P57	7	2565976	2565976	Missense_Mutation	SNP	G	A	G	LFNG	c.G920A	p.R307H
XH_P57	7	2951824	2951824	Silent	SNP	A	G	A	CARD11	c.T3126C	p.I1042I
XH_P57	7	2957005	2957005	Silent	SNP	T	C	T	CARD11	c.A2622G	p.P874P
XH_P57	7	2985463	2985463	Silent	SNP	G	A	G	CARD11	c.C348T	p.S116S
XH_P57	7	4308362	4308362	Missense_Mutation	SNP	C	T	C	SDK1	c.C2020T	p.R674C
XH_P57	7	4830426	4830426	Silent	SNP	T	C	T	AP521	c.T2061C	p.S687S
XH_P57	7	4900095	4900095	Silent	SNP	A	G	A	PAPOLB	c.T1347C	p.N449N
XH_P57	7	4900341	4900341	Silent	SNP	G	A	G	PAPOLB	c.C1101T	p.S367S
XH_P57	7	4901062	4901062	Missense_Mutation	SNP	C	T	C	PAPOLB	c.G380A	p.R127Q
XH_P57	7	4901385	4901385	Missense_Mutation	SNP	A	C	A	PAPOLB	c.T57G	p.N19K
XH_P57	7	4955653	4955653	Silent	SNP	C	T	C	MMD2	c.G348A	p.A116A
XH_P57	7	5104972	5104972	Missense_Mutation	SNP	G	C	G	RBAK	c.G1885C	p.G629R
XH_P57	7	5105133	5105133	Silent	SNP	C	T	C	RBAK	c.C2046T	p.N682N
XH_P57	7	5399044	5399044	Silent	SNP	C	G	C	TNRC18	c.G4818C	p.S1606S
XH_P57	7	5410425	5410425	Missense_Mutation	SNP	G	C	G	TNRC18	c.C3800G	p.A1267G
XH_P57	7	5959485	5959485	Missense_Mutation	SNP	G	A	G	CC21	c.G994A	p.V332I
XH_P57	7	6189780	6189780	Silent	SNP	T	C	T	USP42	c.T1953C	p.L651L
XH_P57	7	6193464	6193464	Missense_Mutation	SNP	T	G	T	USP42	c.T2279G	p.L760R
XH_P57	7	6449496	6449496	Missense_Mutation	SNP	T	C	T	DAGLB	c.A1604G	p.Q535R
XH_P57	7	6550293	6550293	Missense_Mutation	SNP	C	T	C	GRID2IP	c.G1600A	p.E534K
XH_P57	7	7493097	7493097	Missense_Mutation	SNP	C	T	C	COL28A1	c.G1414A	p.A472T
XH_P57	7	8009419	8009419	Silent	SNP	C	T	C	GLCC11	c.C438T	p.P146P
XH_P57	7	11521542	11521542	Silent	SNP	T	C	T	THSD7A	c.A1890G	p.P630P
XH_P57	7	11675855	11675855	Silent	SNP	C	T	C	THSD7A	c.G924A	p.R308R
XH_P57	7	11676377	11676377	Silent	SNP	G	A	G	THSD7A	c.C402T	p.P134P
XH_P57	7	18066569	18066569	Missense_Mutation	SNP	C	A	A	PRPS1L1	c.G837T	p.E279D
XH_P57	7	19184732	19184732	Missense_Mutation	SNP	C	A	C	FERD3L	c.G254T	p.G85V
XH_P57	7	20193979	20193979	Missense_Mutation	SNP	T	G	T	MACC1	c.A2183C	p.E728A
XH_P57	7	20197911	20197911	Silent	SNP	C	T	C	MACC1	c.G2073A	p.E691E
XH_P57	7	20201458	20201458	Missense_Mutation	SNP	G	A	G	MACC1	c.C28T	p.R10W
XH_P57	7	20698270	20698270	Missense_Mutation	SNP	A	G	A	ABC85	c.A343G	p.K115E
XH_P57	7	20824614	20824614	Silent	SNP	C	T	C	SP8	c.G822A	p.S274S
XH_P57	7	21639572	21639572	Silent	SNP	A	G	A	DNAH11	c.A2835G	p.Q945Q
XH_P57	7	21775443	21775443	Silent	SNP	G	A	G	DNAH11	c.G7626A	p.T5242T
XH_P57	7	21939032	21939032	Silent	SNP	C	A	C	DNAH11	c.C13128A	p.L4376L
XH_P57	7	24742436	24742436	Silent	SNP	T	C	T	DFNA5	c.A708G	p.A236A
XH_P57	7	29519929	29519929	Missense_Mutation	SNP	A	G	A	CHN2	c.A203G	p.H68R
XH_P57	7	30634630	30634630	Silent	SNP	G	C	G	GARS	c.G93C	p.L31L
XH_P57	7	30695202	30695202	Silent	SNP	C	T	C	CRHR2	c.G1044A	p.S348S
XH_P57	7	30791847	30791847	Silent	SNP	C	T	C	INMT	c.C81T	p.F27F
XH_P57	7	30831144	30831144	Silent	SNP	C	T	C	MINDY4	c.C1027T	p.L343L
XH_P57	7	31683054	31683054	Silent	SNP	G	T	G	CCDC129	c.G2070T	p.G690G
XH_P57	7	31920395	31920395	Silent	SNP	G	A	G	PDE1C	c.C207T	p.A69A
XH_P57	7	33060946	33060946	Silent	SNP	A	G	A	NT5C3A	c.T393C	p.Y131Y
XH_P57	7	33388713	33388713	Missense_Mutation	SNP	G	A	G	BBS9	c.G997A	p.A333T
XH_P57	7	34818113	34818113	Missense_Mutation	SNP	A	T	A	NPSR1	c.A287T	p.N96I
XH_P57	7	34867182	34867182	Silent	SNP	C	T	C	NPSR1	c.C450T	p.F150F
XH_P57	7	34874038	34874038	Missense_Mutation	SNP	C	G	C	NPSR1	c.C525G	p.S175R
XH_P57	7	34889182	34889182	Missense_Mutation	SNP	A	G	A	NPSR1	c.A833G	p.Q278R
XH_P57	7	34917740	34917740	Nonsense_Mutation	SNP	C	T	C	NPSR1	c.C1045T	p.R349X
XH_P57	7	36327317	36327317	Missense_Mutation	SNP	C	T	C	EEPDI	c.C1246T	p.P416S
XH_P57	7	37298800	37298800	Silent	SNP	C	T	C	ELMO1	c.G399A	p.V133V
XH_P57	7	37780799	37780799	Silent	SNP	C	A	C	GPR141	c.C804A	p.I268I
XH_P57	7	37890316	37890316	Silent	SNP	C	T	C	NME8	c.C177T	p.D59D
XH_P57	7	37947164	37947164	Missense_Mutation	SNP	G	T	G	SFRP4	c.C958A	p.P320T
XH_P57	7	37961001	37961001	Silent	SNP	C	A	C	EPDR1	c.C34A	p.R12R
XH_P57	7	38766588	38766588	Missense_Mutation	SNP	T	C	T	VPS41	c.A2330G	p.D777G
XH_P57	7	39606107	39606107	Silent	SNP	G	A	G	YAE1D1	c.G90A	p.A30A
XH_P57	7	40027484	40027484	Missense_Mutation	SNP	A	G	A	CDK13	c.A1498G	p.T500A
XH_P57	7	40127767	40127767	Silent	SNP	G	A	G	CDK13	c.G3072A	p.K1024K
XH_P57	7	43663423	43663423	Missense_Mutation	SNP	G	C	G	STK17A	c.G856C	p.E286Q
XH_P57	7	43843423	43843423	Silent	SNP	G	A	G	BLVRA	c.G609A	p.V203V
XH_P57	7	43916727	43916727	Missense_Mutation	SNP	T	G	T	URGCP	c.A2308C	p.M770L
XH_P57	7	43917013	43917013	Silent	SNP	G	A	G	URGCP	c.C2022T	p.H674H
XH_P57	7	43917274	43917274	Silent	SNP	A	G	A	URGCP	c.T1761C	p.H587H
XH_P57	7	44047066	44047066	Missense_Mutation	SNP	T	C	T	SPDYE1	c.T832C	p.C278R
XH_P57	7	44099664	44099664	Silent	SNP	T	C	T	DBNL	c.T756C	p.A252A
XH_P57	7	44112694	44112694	Silent	SNP	C	T	C	POLM	c.G1494A	p.V498V
XH_P57	7	44153780	44153780	Missense_Mutation	SNP	A	G	A	AEBP1	c.A3397G	p.K1133E
XH_P57	7	44579180	44579180	Silent	SNP	G	C	G	NPC1L1	c.C816G	p.L272L
XH_P57	7	44612229	44612229	Silent	SNP	G	A	G	DDX56	c.C498T	p.D166D
XH_P57	7	44800176	44800176	Missense_Mutation	SNP	G	T	G	ZMI22	c.G1146T	p.L382F
XH_P57	7	45005795	45005795	Silent	SNP	G	A	G	MYO1G	c.C2034T	p.H678H
XH_P57	7	45009723	45009723	Silent	SNP	G	A	G	MYO1G	c.C1248T	p.N416N
XH_P57	7	45015107	45015107	Silent	SNP	G	A	G	MYO1G	c.C540T	p.H180H
XH_P57	7	45016621	45016621	Missense_Mutation	SNP	C	T	C	MYO1G	c.G145A	p.V49M
XH_P57	7	45148667	45148667	Missense_Mutation	SNP	G	A	G	TBRG4	c.C203T	p.P68L
XH_P57	7	45148773	45148773	Missense_Mutation	SNP	C	A	C	TBRG4	c.G97T	p.A33S
XH_P57	7	47859156	47859156	Frame_Shift_Ins	INS	-	T	-	C7orf69	c.331dupT	p.K110fs
XH_P57	7	47879049	47879049	Missense_Mutation	SNP	G	A	G	PKD1L1	c.C5764T	p.R1922W
XH_P57	7	47971626	47971626	Silent	SNP	G	A	G	PKD1L1	c.C426T	p.I142I
XH_P57	7	48285182	48285182	Frame_Shift_Ins	INS	-	TA	-	ABCA13	1464_1465insT	p.K488fs
XH_P57	7	48285183	48285183	Frame_Shift_Ins	INS	-	ACAAATTGATT	-	ABCA13	1466insACAAA	p.D489fs
XH_P57	7	50173777	50173777	Missense_Mutation	SNP	A	G	A	C7orf72	c.A802G	p.T268A
XH_P57	7	51096036	51096036	Missense_Mutation	SNP	G	C	G	COBL	c.C2757G	p.H919Q
XH_P57	7	55540707	55540707	Nonsense_Mutation	SNP	G	A	G	VOPP1	c.C379T	p.R127X
XH_P57	7	56149939	56149939	Silent	SNP	G	A	G	PHKG1	c.C528T	p.C176C
XH_P57	7	63529956	63529956	Silent	SNP	G	A	G	ZNF727	c.G195A	p.A65A
XH_P57	7	64169017	64169017	Frame_Shift_Ins	INS	-	A	-	ZNF107	c.2447dupA	p.E816fs
XH_P57	7	64388472	64388472	Missense_Mutation	SNP	C	A	C	ZNF273	c.C766A	p.H256N
XH_P57	7	64451656	64451656	Silent	SNP	G	A	G	ERV3-1	c.C1749T	p.V583V
XH_P57	7	66459316	66459316	Silent	SNP	G	A	G	SBD5	c.C141T	p.L47L
XH_P57	7	70228020	70228020	Missense_Mutation	SNP	G	T	G	AUTS2	c.G907T	p.A303S
XH_P57	7	70228139	70228139	Silent	SNP	A	G	A	AUTS2	c.A1026G	p.P342P

XH_P57	7	70252283	70252283	Silent	SNP	G	A	G	AUTS2	c.G2325A	p.T775T
XH_P57	7	72209528	72209528	Splice_Site	DEL	A	-	A	TYW1B	-	-
XH_P57	7	73097654	73097654	Missense_Mutation	SNP	C	T	C	DNAJC30	c.G100A	p.G34R
XH_P57	7	73097720	73097720	Missense_Mutation	SNP	G	C	G	DNAJC30	c.C34G	p.L12V
XH_P57	7	73122923	73122923	Silent	SNP	A	G	A	STX1A	c.T204C	p.D68D
XH_P57	7	73151644	73151644	Silent	SNP	A	G	A	ABHD11	c.T201C	p.Y67Y
XH_P57	7	74489486	74489486	Missense_Mutation	SNP	T	C	T	RCC1L	c.A88G	p.R30G
XH_P57	7	74564546	74564546	Missense_Mutation	SNP	G	A	G	GTF2IRD2	c.G2293A	p.A765T
XH_P57	7	75615287	75615287	Silent	SNP	G	A	G	POR	c.G1716A	p.S572S
XH_P57	7	76140186	76140186	Missense_Mutation	SNP	T	C	T	UPK3B	c.T217C	p.S73P
XH_P57	7	76143306	76143306	Missense_Mutation	SNP	G	C	G	UPK3B	c.G669C	p.K223N
XH_P57	7	76144483	76144483	Missense_Mutation	SNP	A	G	A	UPK3B	c.A878G	p.Q293R
XH_P57	7	76871086	76871086	Silent	SNP	G	A	G	CCDC146	c.G318A	p.L106L
XH_P57	7	77365770	77365770	Silent	SNP	A	G	A	RSBN1L	c.A630G	p.E210E
XH_P57	7	83029438	83029438	Silent	SNP	C	T	C	SEMA3E	c.G1092A	p.L364L
XH_P57	7	88963039	88963039	Missense_Mutation	SNP	G	A	G	ZNF804B	c.G743A	p.C248Y
XH_P57	7	89791322	89791322	Frame_Shift_Ins	INS	-	-	-	STEAP1	c.692_693insA	p.A231fs
XH_P57	7	89791324	89791324	Frame_Shift_Ins	INS	-	TTCTTTATTT	-	STEAP1	c.695insTTCTTT	p.L232fs
XH_P57	7	92733766	92733766	Missense_Mutation	SNP	C	A	C	SAMD9	c.G1645T	p.V549L
XH_P57	7	92734451	92734451	Silent	SNP	A	G	A	SAMD9	c.T960C	p.Y320Y
XH_P57	7	92734983	92734983	Missense_Mutation	SNP	A	G	A	SAMD9	c.T428C	p.I143T
XH_P57	7	92760738	92760738	Missense_Mutation	SNP	T	G	T	SAMD9L	c.A4547C	p.N1516T
XH_P57	7	92764982	92764982	Silent	SNP	C	T	C	SAMD9L	c.G303A	p.Q101Q
XH_P57	7	95025600	95025600	Silent	SNP	G	A	G	PON3	c.C63T	p.F21F
XH_P57	7	97847040	97847040	Silent	SNP	G	A	G	TECPR1	c.C3348T	p.H1116H
XH_P57	7	97852399	97852399	Missense_Mutation	SNP	G	A	G	TECPR1	c.C2831T	p.P944L
XH_P57	7	97873994	97873994	Silent	SNP	G	A	G	TECPR1	c.C420T	p.Y140Y
XH_P57	7	98790671	98790671	Missense_Mutation	SNP	G	A	G	KPNA7	c.C607T	p.L203F
XH_P57	7	99445132	99445132	Silent	SNP	C	T	C	CYP3A43	c.C340T	p.L114L
XH_P57	7	99690564	99690564	Silent	SNP	A	T	A	MCM7	c.T1623A	p.T541T
XH_P57	7	99752642	99752642	Missense_Mutation	SNP	C	T	C	C7orf43	c.G928A	p.V310I
XH_P57	7	99818815	99818815	Frame_Shift_Ins	INS	-	CT	-	PVRIG	c.922_923insCT	p.T308fs
XH_P57	7	100075191	100075191	Silent	SNP	G	C	G	TSC22D4	c.C471G	p.T157T
XH_P57	7	100285476	100285476	Missense_Mutation	SNP	C	T	C	GIGYF1	c.G196A	p.A66T
XH_P57	7	100466350	100466350	Missense_Mutation	SNP	C	A	C	TRIP6	c.C597A	p.H199Q
XH_P57	7	100635193	100635193	Missense_Mutation	SNP	C	T	C	MUC12	c.C1349T	p.T450I
XH_P57	7	100682613	100682613	Missense_Mutation	SNP	T	C	T	MUC17	c.T7916C	p.L2639P
XH_P57	7	100683520	100683520	Silent	SNP	C	T	C	MUC17	c.C8823T	p.A2941A
XH_P57	7	100771723	100771723	Missense_Mutation	SNP	G	A	G	SERPINE1	c.G49A	p.V17I
XH_P57	7	101916647	101916647	Silent	SNP	A	G	A	CUX1	c.A1218G	p.A406A
XH_P57	7	101917521	101917521	Missense_Mutation	SNP	G	A	G	CUX1	c.G1342A	p.A448T
XH_P57	7	102112980	102112980	Silent	SNP	G	A	G	LRWD1	c.G1158A	p.T386T
XH_P57	7	102715799	102715799	Missense_Mutation	SNP	T	C	T	ARMC10	c.T80C	p.L27P
XH_P57	7	105103086	105103086	Missense_Mutation	SNP	C	T	C	PUS7	c.G1757A	p.R586H
XH_P57	7	105662821	105662821	Missense_Mutation	SNP	T	C	T	CDHR3	c.T1739C	p.V580A
XH_P57	7	105671267	105671267	Silent	SNP	T	C	T	CDHR3	c.T2070C	p.D690D
XH_P57	7	106685448	106685448	Silent	SNP	G	T	G	PRKAR2B	c.G96T	p.A32A
XH_P57	7	107603431	107603431	Silent	SNP	A	C	C	LAMB1	c.T1776G	p.P592P
XH_P57	7	107706895	107706895	Missense_Mutation	SNP	T	C	T	LAMB4	c.A2597G	p.N866S
XH_P57	7	107872816	107872816	Silent	SNP	G	A	G	NRCAM	c.C381T	p.N127N
XH_P57	7	116339672	116339672	Silent	SNP	C	T	C	MET	c.C534T	p.S178S
XH_P57	7	116340262	116340262	Missense_Mutation	SNP	A	G	A	MET	c.A1124G	p.N375S
XH_P57	7	116528240	116528240	Silent	SNP	C	T	C	CAPZA2	c.C99T	p.F33F
XH_P57	7	117235055	117235055	Silent	SNP	T	G	T	CFR	c.T2562G	p.T854T
XH_P57	7	120969769	120969769	Missense_Mutation	SNP	G	A	G	WNT16	c.G214A	p.G72R
XH_P57	7	120979089	120979089	Missense_Mutation	SNP	C	T	C	WNT16	c.C758T	p.T253I
XH_P57	7	122635357	122635357	Missense_Mutation	SNP	G	A	G	TAS2R16	c.C332T	p.T111I
XH_P57	7	128317658	128317658	Missense_Mutation	SNP	C	T	C	FAM71F2	c.C406T	p.R136W
XH_P57	7	128478103	128478103	Silent	SNP	C	T	C	FLNC	c.C1032T	p.V344V
XH_P57	7	128480123	128480123	Silent	SNP	C	A	C	FLNC	c.C1458A	p.P486P
XH_P57	7	128484816	128484816	Silent	SNP	A	G	A	FLNC	c.A3297G	p.V1099V
XH_P57	7	128487893	128487893	Silent	SNP	G	A	G	FLNC	c.G4431A	p.L1477L
XH_P57	7	128491603	128491603	Silent	SNP	T	C	T	FLNC	c.T5664C	p.L1888T
XH_P57	7	128495338	128495338	Silent	SNP	C	T	C	FLNC	c.C7122T	p.D2374D
XH_P57	7	129950740	129950740	Missense_Mutation	SNP	G	T	G	CPA4	c.G808T	p.G270C
XH_P57	7	130007381	130007381	Missense_Mutation	SNP	T	C	T	CPA5	c.T1007C	p.L1336S
XH_P57	7	130418525	130418525	Silent	SNP	G	A	G	KLF14	c.C336T	p.S112S
XH_P57	7	131195712	131195712	Missense_Mutation	SNP	G	A	G	PODXL	c.C581T	p.S194L
XH_P57	7	131195959	131195959	Missense_Mutation	SNP	C	T	C	PODXL	c.G334A	p.G112S
XH_P57	7	132193201	132193201	Silent	SNP	A	G	A	PLXNA4	c.T252C	p.H84H
XH_P57	7	133580447	133580447	Silent	SNP	G	A	G	EXOC4	c.G1830A	p.V610V
XH_P57	7	134719215	134719215	Silent	SNP	T	C	T	AGBL3	c.T873C	p.D291D
XH_P57	7	134925411	134925411	Silent	SNP	G	A	G	STRA8	c.G201A	p.A67A
XH_P57	7	135279315	135279315	Silent	SNP	A	C	A	NUP205	c.A777C	p.A259A
XH_P57	7	135300783	135300783	Missense_Mutation	SNP	C	G	C	NUP205	c.C2356G	p.L786V
XH_P57	7	135406176	135406176	Silent	SNP	A	G	A	SLC13A4	c.T195C	p.L65L
XH_P57	7	138433937	138433937	Silent	SNP	G	A	G	ATP6V0A4	c.C1155T	p.V385V
XH_P57	7	138601826	138601826	Missense_Mutation	SNP	G	A	G	KIAA1549	c.C2546T	p.S849L
XH_P57	7	138603282	138603282	Missense_Mutation	SNP	T	C	T	KIAA1549	c.A1090G	p.T364A
XH_P57	7	139715574	139715574	Silent	SNP	C	T	C	TBXAS1	c.C1281T	p.P427P
XH_P57	7	139724555	139724555	Silent	SNP	C	T	C	PARP12	c.G1911A	p.P637P
XH_P57	7	139727135	139727135	Silent	SNP	G	A	G	PARP12	c.C1569T	p.F523F
XH_P57	7	139797431	139797431	Missense_Mutation	SNP	G	T	G	KDM7A	c.C1930A	p.R644S
XH_P57	7	140125750	140125750	Missense_Mutation	SNP	T	C	T	RAB19	c.T454C	p.Y152H
XH_P57	7	141464810	141464810	Silent	SNP	C	T	C	TAS2R3	c.C852T	p.L284L
XH_P57	7	141738389	141738389	Nonsense_Mutation	INS	-	AATGAGATTGTG	-	MGAM	2291insAATGA764_L765delinsQX	-
XH_P57	7	141920426	141920426	Missense_Mutation	SNP	C	T	C	MGAM2	c.C6115T	p.P2039S
XH_P57	7	142564250	142564260	Frame_Shift_Del	DEL	CTGTGGTGGC	-	CCTGTGGTGCA	EPH6	c.598_608del	p.P200fs
XH_P57	7	143017768	143017768	Missense_Mutation	SNP	C	T	C	CLCN1	c.C313T	p.R105C
XH_P57	7	143053723	143053723	Missense_Mutation	SNP	C	T	C	FAM131B	c.G721A	p.A241T
XH_P57	7	143771557	143771557	Missense_Mutation	SNP	T	C	T	OR2A25	c.T245C	p.V82A
XH_P57	7	143807542	143807542	Frame_Shift_Ins	INS	-	AT	-	OR2A2	c.867_868insAT	p.Y289fs
XH_P57	7	143882673	143882673	Missense_Mutation	SNP	C	T	C	CTAGE4	c.C2077T	p.L693F
XH_P57	7	143955884	143955884	Missense_Mutation	SNP	A	C	A	OR2A7	c.T838G	p.F280V
XH_P57	7	143955886	143955900	In_Frame_Del	DEL	CTGTGAAAC	-	GTGTGTAACA	OR2A7	c.822_836del	p.274_279del
XH_P57	7	148489820	148489820	Silent	SNP	G	A	G	CUL1	c.G1809A	p.A603A
XH_P57	7	148525904	148525904	Missense_Mutation	SNP	C	G	C	EZH2	c.G436C	p.D146H
XH_P57	7	149191568	149191568	Silent	SNP	C	T	C	ZNF746	c.G51A	p.T17T

XH_P57	7	149484798	149484798	Missense_Mutation	SNP	C	T	C	SSPO	c.C3620T	p.A1207V
XH_P57	7	149509419	149509419	Missense_Mutation	SNP	C	T	C	SSPO	c.C9817T	p.R3273W
XH_P57	7	149511902	149511902	Silent	SNP	C	T	C	SSPO	c.C10452T	p.C3484C
XH_P57	7	149513077	149513077	Silent	SNP	G	C	G	SSPO	c.G10980C	p.S3660S
XH_P57	7	149517978	149517978	Missense_Mutation	SNP	G	T	G	SSPO	c.G12321T	p.Q4107H
XH_P57	7	149523584	149523584	Missense_Mutation	SNP	C	T	C	SSPO	c.C14495T	p.P4832L
XH_P57	7	149543269	149543269	Missense_Mutation	SNP	C	T	C	ZNF862	c.C166T	p.R56C
XH_P57	7	150094853	150094853	Silent	SNP	G	A	G	ZNF775	c.G1284A	p.T428T
XH_P57	7	150439500	150439500	Silent	SNP	C	T	C	GIMAP1-GIMAP	c.C273T	p.A91A
XH_P57	7	150440043	150440043	Silent	SNP	C	T	C	GIMAP1-GIMAP	c.C816T	p.L272L
XH_P57	7	150491156	150491156	Missense_Mutation	SNP	T	C	T	TMEM176B	c.A208G	p.T70A
XH_P57	7	150707738	150707738	Silent	SNP	G	A	G	NOS3	c.G2739A	p.E913E
XH_P57	7	150768786	150768786	Silent	SNP	G	A	G	SLC4A2	c.G2175A	p.T725T
XH_P57	7	150774308	150774308	Missense_Mutation	SNP	G	A	G	FASTK	c.C884T	p.A295V
XH_P57	7	150864240	150864240	Silent	SNP	G	C	G	GBX1	c.C396G	p.A132A
XH_P57	7	150878260	150878260	Silent	SNP	C	G	C	ASB10	c.G870C	p.A290A
XH_P57	7	150878399	150878399	Missense_Mutation	SNP	C	T	C	ASB10	c.G731A	p.R244H
XH_P57	7	150934817	150934817	Frame_Shift_Del	DEL	G	-	G	CHPF2	c.1369delG	p.G457fs
XH_P57	7	151097314	151097314	Silent	SNP	A	G	A	WDR86	c.C177C	p.Y59Y
XH_P57	7	151904421	151904421	Missense_Mutation	SNP	C	T	C	KMT2C	c.G3805A	p.G1269S
XH_P57	7	154681050	154681050	Silent	SNP	C	T	C	DPP6	c.C2052T	p.A684A
XH_P57	7	154681216	154681216	Silent	SNP	G	A	G	DPP6	c.G2106A	p.R702R
XH_P57	7	155255332	155255332	Silent	SNP	T	C	T	EN2	c.T952C	p.L318L
XH_P57	7	155531080	155531080	Missense_Mutation	SNP	A	G	A	RBM33	c.A1720G	p.T574A
XH_P57	7	156742779	156742779	Silent	SNP	C	A	C	NOM1	c.C348A	p.A116A
XH_P57	7	157931091	157931091	Missense_Mutation	SNP	C	T	C	PTPRN2	c.G913A	p.Y305M
XH_P57	7	158540945	158540945	Silent	SNP	C	T	C	ESYT2	c.G1665A	p.V555V
XH_P57	7	158827326	158827326	Silent	SNP	G	A	G	VIPR2	c.C777T	p.N259N
XH_P57	8	195254	195254	Missense_Mutation	SNP	C	A	C	ZNF596	c.C407A	p.T136K
XH_P57	8	196274	196274	Missense_Mutation	SNP	T	G	T	ZNF596	c.T1427G	p.V476G
XH_P57	8	2021421	2021421	Missense_Mutation	SNP	G	T	G	MYOM2	c.G961T	p.V321L
XH_P57	8	2040298	2040298	Silent	SNP	C	T	C	MYOM2	c.C1953T	p.A651A
XH_P57	8	6389889	6389889	Silent	SNP	C	G	C	ANGPT2	c.G408C	p.A136A
XH_P57	8	6500544	6500544	Missense_Mutation	SNP	C	T	C	MCPH1	c.C2482T	p.P828S
XH_P57	8	8234113	8234113	Silent	SNP	G	A	G	PRAG1	c.C1806T	p.P602V
XH_P57	8	8887407	8887407	In_Frame_Ins	INS	-	TAG	-	ER1	c.913_914insTA	p.I305delinsIV
XH_P57	8	10285810	10285810	Silent	SNP	T	C	T	MSRA	c.T576C	p.G192G
XH_P57	8	10467160	10467160	Missense_Mutation	SNP	G	A	G	RP11	c.C4448T	p.A1483V
XH_P57	8	10469340	10469340	Silent	SNP	G	A	G	RP11	c.C2268T	p.N756N
XH_P57	8	11565920	11565920	Silent	SNP	C	T	G	GATA4	c.G99T	p.A33A
XH_P57	8	12958025	12958025	Silent	SNP	C	A	C	DL1	c.C288T	p.A96A
XH_P57	8	17132462	17132462	Missense_Mutation	SNP	A	G	A	VPS37A	c.A562G	p.I188V
XH_P57	8	17206588	17206588	Silent	SNP	G	A	G	MTMR7	c.C471T	p.V157V
XH_P57	8	17739538	17739538	Missense_Mutation	SNP	T	C	T	FGL1	c.A214G	p.I72V
XH_P57	8	17817553	17817553	Missense_Mutation	SNP	G	T	G	PCM1	c.G2071T	p.A691S
XH_P57	8	18725388	18725388	Missense_Mutation	SNP	G	T	G	PSD3	c.C1430A	p.P477H
XH_P57	8	19190491	19190491	Silent	SNP	A	G	A	SH2D4A	c.A72G	p.K24K
XH_P57	8	20005554	20005554	Missense_Mutation	SNP	G	C	G	SLC18A1	c.C1078G	p.L360V
XH_P57	8	21955784	21955784	Missense_Mutation	SNP	A	C	A	FAM160B2	c.A731C	p.N244T
XH_P57	8	21965372	21965372	Silent	SNP	C	T	C	NUDT18	c.G411A	p.A137A
XH_P57	8	21978469	21978469	Silent	SNP	A	G	A	HR	c.T2370C	p.D790D
XH_P57	8	21978578	21978578	Silent	SNP	A	G	A	HR	c.T2367C	p.S789S
XH_P57	8	21984765	21984765	Missense_Mutation	SNP	C	T	C	HR	c.G1190A	p.C397Y
XH_P57	8	21986657	21986657	Silent	SNP	C	T	C	HR	c.G27A	p.K9K
XH_P57	8	21997738	21997738	Silent	SNP	A	T	A	REEP4	c.T129A	p.I43I
XH_P57	8	22273687	22273687	Silent	SNP	T	C	T	SLC39A14	c.T1041C	p.H347H
XH_P57	8	22419422	22419422	Missense_Mutation	SNP	G	A	G	SORBS3	c.G562A	p.G188S
XH_P57	8	23225559	23225559	Silent	SNP	G	A	G	LOXL2	c.C306T	p.Y102Y
XH_P57	8	23423669	23423669	Missense_Mutation	SNP	A	G	A	SLC25A37	c.A259G	p.I87V
XH_P57	8	23429329	23429329	Silent	SNP	T	C	T	SLC25A37	c.T525C	p.F175F
XH_P57	8	26481697	26481697	Missense_Mutation	SNP	G	A	G	DPYSL2	c.G667A	p.A223T
XH_P57	8	26510792	26510792	Silent	SNP	T	C	T	DPYSL2	c.T1821C	p.P607P
XH_P57	8	27362587	27362587	Missense_Mutation	SNP	G	A	G	EPHX2	c.G263A	p.C88Y
XH_P57	8	27528765	27528765	Missense_Mutation	SNP	C	A	C	SCARA3	c.C1718A	p.P573Q
XH_P57	8	27634064	27634064	Missense_Mutation	SNP	C	T	C	ESCO2	c.C239T	p.A80V
XH_P57	8	27668678	27668678	Missense_Mutation	SNP	G	T	G	PBK	c.C602A	p.A201D
XH_P57	8	27767231	27767231	Missense_Mutation	SNP	C	G	C	SCARA5	c.G946C	p.D316H
XH_P57	8	28574803	28574803	Silent	SNP	G	A	G	EXTL3	c.G1227A	p.P409P
XH_P57	8	28998020	28998020	Frame_Shift_Del	DEL	G	-	G	KIF13B	c.2449delC	p.Q817fs
XH_P57	8	28998021	28998021	Missense_Mutation	SNP	T	A	T	KIF13B	c.A2448T	p.L816F
XH_P57	8	30702785	30702785	Missense_Mutation	SNP	T	C	T	TEX15	c.A4898G	p.N1633S
XH_P57	8	30706224	30706224	Missense_Mutation	SNP	A	G	A	TEX15	c.T1459C	p.C487R
XH_P57	8	30706810	30706810	Frame_Shift_Ins	INS	-	T	-	TEX15	c.872dupA	p.N291fs
XH_P57	8	30717452	30717452	Missense_Mutation	SNP	A	G	A	TEX15	c.T662C	p.I221T
XH_P57	8	30973957	30973957	Silent	SNP	G	T	G	WRN	c.G2361T	p.L787L
XH_P57	8	30999280	30999280	Missense_Mutation	SNP	G	T	G	WRN	c.G3222T	p.L1074F
XH_P57	8	37702472	37702472	Silent	SNP	G	A	G	BRF2	c.C796T	p.L266L
XH_P57	8	39682361	39682361	Frame_Shift_Ins	INS	-	CTTGG	-	ADAM2	c.243_244insCCA	p.K82fs
XH_P57	8	41559609	41559609	Silent	SNP	G	A	G	ANK1	c.C2349T	p.T783T
XH_P57	8	48878746	48878751	Frame_Shift_Del	DEL	GACATT	-	GACATT	MCM4	c.833_837del	p.D278fs
XH_P57	8	52321686	52321686	Missense_Mutation	SNP	C	T	C	PXDNL	c.G2498A	p.S833N
XH_P57	8	52321843	52321843	Missense_Mutation	SNP	G	C	G	PXDNL	c.C2341G	p.R781G
XH_P57	8	54163562	54163562	Silent	SNP	C	A	C	OPRK1	c.G36T	p.P12P
XH_P57	8	59571856	59571856	Missense_Mutation	SNP	A	C	A	NSMAF	c.T50G	p.I17S
XH_P57	8	63951312	63951312	Missense_Mutation	SNP	A	G	A	GGH	c.T16C	p.C6R
XH_P57	8	66701147	66701147	Silent	SNP	G	A	G	PDE7A	c.C30T	p.A10A
XH_P57	8	67064613	67064613	Silent	SNP	A	G	A	TRIM55	c.A987G	p.E329E
XH_P57	8	67089425	67089425	Silent	SNP	T	G	T	CRH	c.A288C	p.G96G
XH_P57	8	67380528	67380528	Missense_Mutation	SNP	T	C	T	ADHFE1	c.T1345C	p.C449R
XH_P57	8	68864728	68864728	Silent	SNP	G	A	G	PREX2	c.G99A	p.K33K
XH_P57	8	69104619	69104619	Missense_Mutation	SNP	C	T	C	PREX2	c.C4463T	p.S1488L
XH_P57	8	70978690	70978690	Silent	SNP	C	T	C	PRDM14	c.G963A	p.T321T
XH_P57	8	72211295	72211295	Silent	SNP	T	C	T	EYA1	c.A714G	p.T238T
XH_P57	8	77765865	77765865	Silent	SNP	C	T	C	ZFXH4	c.C6708T	p.Y2236Y
XH_P57	8	86027418	86027418	Missense_Mutation	SNP	A	G	A	LRRCC1	c.A349G	p.T117A
XH_P57	8	95188850	95188850	Missense_Mutation	SNP	T	C	T	CDH17	c.A343G	p.K115E
XH_P57	8	95272605	95272605	Missense_Mutation	SNP	G	C	G	GEM	c.C127G	p.R43G
XH_P57	8	97251798	97251798	Frame_Shift_Ins	INS	-	AT	-	MTERF3	c.1174_1175insA	p.S392fs

XH P57	8	99234772	99234772	Missense_Mutation	SNP	T	G	T	NIPAL2	c.A493C	p.T165P
XH P57	8	101252680	101252680	Missense_Mutation	SNP	T	C	T	SPAG1	c.T2330C	p.M777T
XH P57	8	101253184	101253184	Silent	SNP	G	A	G	SPAG1	c.G2715A	p.S905S
XH P57	8	101271172	101271172	Missense_Mutation	SNP	G	C	G	RNF19A	c.C2129G	p.A710G
XH P57	8	101960850	101960850	Silent	SNP	G	A	G	YWHAZ	c.C268T	p.L90L
XH P57	8	101960851	101960851	Frame_Shift_Ins	INS	-	TTTTGTTTGGTT	-	YWHAZ	57insAAACCAAA	p.E89fs
XH P57	8	102555474	102555474	Missense_Mutation	SNP	A	G	A	GRHL2	c.A26G	p.K9R
XH P57	8	102656413	102656413	Silent	SNP	A	G	A	GRHL2	c.A1524G	p.P508P
XH P57	8	104342244	104342244	Missense_Mutation	SNP	G	A	G	FZD6	c.G988A	p.G330R
XH P57	8	104394744	104394744	Silent	SNP	T	C	T	CTHRC1	c.T606C	p.G202G
XH P57	8	104897809	104897809	Missense_Mutation	SNP	G	A	G	RIMS2	c.G406A	p.E136K
XH P57	8	105105702	105105702	Nonsense_Mutation	SNP	C	T	C	RIMS2	c.C2848T	p.R950X
XH P57	8	107754473	107754473	Silent	SNP	G	A	G	OXR1	c.G369A	p.E123E
XH P57	8	110592147	110592154	Frame_Shift_Del	DEL	CAGAAGGT	-	CAGAAGGT	SYBU	c.218_225del	p.D73fs
XH P57	8	119391791	119391791	Silent	SNP	T	C	T	SAMD12	c.A471G	p.L157L
XH P57	8	119964052	119964052	Missense_Mutation	SNP	G	C	G	TNFRSF11B	c.C9G	p.N3K
XH P57	8	120430428	120430428	Silent	SNP	T	C	T	NOV	c.T441C	p.D147D
XH P57	8	120803637	120803637	Missense_Mutation	SNP	C	G	C	TA2F	c.G1340C	p.S447T
XH P57	8	124658203	124658203	Missense_Mutation	SNP	T	C	T	KLHL38	c.A1522G	p.K508E
XH P57	8	124663895	124663895	Silent	SNP	G	A	G	KLHL38	c.C1272T	p.P424P
XH P57	8	124663987	124663987	Missense_Mutation	SNP	C	G	C	KLHL38	c.G1180C	p.G394R
XH P57	8	124693533	124693533	Missense_Mutation	SNP	G	A	G	ANXA13	c.C898T	p.R300C
XH P57	8	125061895	125061895	Silent	SNP	G	A	G	FER116	c.G2772A	p.K924K
XH P57	8	125463544	125463544	Silent	SNP	T	C	T	TRMT12	c.T376C	p.L126L
XH P57	8	133047071	133047071	Silent	SNP	G	A	G	OC90	c.C690T	p.H230H
XH P57	8	133092138	133092138	Missense_Mutation	SNP	G	A	G	HHLA1	c.C752T	p.P251L
XH P57	8	133900495	133900495	Missense_Mutation	SNP	G	A	G	TG	c.G2443A	p.G815R
XH P57	8	133906136	133906136	Missense_Mutation	SNP	G	C	G	TG	c.G2963C	p.R988P
XH P57	8	134474148	134474148	Silent	SNP	C	T	C	ST3GAL1	c.G819A	p.S273S
XH P57	8	134488007	134488007	Silent	SNP	G	A	G	ST3GAL1	c.C261T	p.T87T
XH P57	8	135524797	135524797	Silent	SNP	G	T	G	ZFAT	c.C3096A	p.I1032I
XH P57	8	135649848	135649848	Missense_Mutation	SNP	G	A	G	ZFAT	c.C268T	p.P90S
XH P57	8	141461062	141461062	Silent	SNP	G	A	G	TRAPP9	c.C411T	p.N137N
XH P57	8	143413136	143413136	Missense_Mutation	SNP	C	T	C	TSNARE1	c.G145A	p.V49I
XH P57	8	143425553	143425553	Silent	SNP	C	T	C	TSNARE1	c.G519A	p.A173A
XH P57	8	143425720	143425720	Missense_Mutation	SNP	T	C	T	TSNARE1	c.A352G	p.T118A
XH P57	8	143427178	143427178	Missense_Mutation	SNP	C	G	C	TSNARE1	c.G164C	p.R55P
XH P57	8	143546035	143546035	Missense_Mutation	SNP	G	C	G	ADGRB1	c.G476C	p.I59P
XH P57	8	143694775	143694775	Silent	SNP	G	C	G	ARC	c.C858G	p.R286R
XH P57	8	143922620	143922620	Missense_Mutation	SNP	C	T	C	GML	c.C160T	p.R54C
XH P57	8	143957163	143957163	Silent	SNP	C	G	C	CYP11B1	c.G1086C	p.L362L
XH P57	8	143961102	143961102	Missense_Mutation	SNP	C	T	C	CYP11B1	c.G128A	p.R43Q
XH P57	8	144239859	144239859	Silent	SNP	A	G	A	LY6H	c.T294C	p.C98C
XH P57	8	144240257	144240257	Silent	SNP	C	G	C	LY6H	c.G213C	p.T71T
XH P57	8	144295782	144295782	Silent	SNP	G	T	G	GPIHBP1	c.G138T	p.V46V
XH P57	8	144413416	144413416	Silent	SNP	G	A	G	TOP1MT	c.C216T	p.D72D
XH P57	8	144457746	144457746	Silent	SNP	C	A	C	RHPN1	c.C84A	p.I28I
XH P57	8	144623574	144623574	Missense_Mutation	SNP	T	C	T	ZC3H3	c.A18G	p.I6M
XH P57	8	144654249	144654249	Missense_Mutation	SNP	G	A	G	MROH6	c.C401T	p.T134I
XH P57	8	144658711	144658711	Silent	SNP	G	A	G	NAPRT	c.C913T	p.L305L
XH P57	8	144662353	144662353	Silent	SNP	G	A	G	EEF1D	c.C564T	p.A188A
XH P57	8	144671244	144671244	Silent	SNP	C	A	C	EEF1D	c.G1008T	p.R336R
XH P57	8	144671922	144671922	Silent	SNP	G	A	G	EEF1D	c.C330T	p.R110R
XH P57	8	144681777	144681777	Missense_Mutation	SNP	G	T	G	TIGD5	c.G1704T	p.M568I
XH P57	8	144688736	144688736	Missense_Mutation	SNP	C	G	C	PYCR3	c.G426C	p.K142N
XH P57	8	144801243	144801243	Silent	SNP	C	T	C	MAPK15	c.C498T	p.P166P
XH P57	8	144808747	144808747	Silent	SNP	G	A	G	FAM83H	c.C2884T	p.L962L
XH P57	8	144941181	144941181	Missense_Mutation	SNP	G	C	G	EPPK1	c.C6241G	p.L2081V
XH P57	8	144944176	144944176	Silent	SNP	T	C	T	EPPK1	c.A3246G	p.E1082E
XH P57	8	144944638	144944638	Silent	SNP	G	A	G	EPPK1	c.C2784T	p.G928G
XH P57	8	144945191	144945191	Missense_Mutation	SNP	T	C	T	EPPK1	c.A2231G	p.Y744C
XH P57	8	144945792	144945792	Missense_Mutation	SNP	T	C	T	EPPK1	c.A1630G	p.K544E
XH P57	8	144946799	144946799	Missense_Mutation	SNP	C	T	C	EPPK1	c.G623A	p.R208Q
XH P57	8	144990528	144990528	Silent	SNP	A	G	A	PLEC	c.T13419C	p.A4473A
XH P57	8	144990921	144990921	Silent	SNP	G	A	G	PLEC	c.C13026T	p.F4342F
XH P57	8	144991176	144991176	Silent	SNP	T	C	T	PLEC	c.A12771G	p.S4257S
XH P57	8	144992103	144992103	Silent	SNP	T	C	T	PLEC	c.A11844G	p.T3948T
XH P57	8	144992361	144992361	Silent	SNP	T	C	T	PLEC	c.A11586G	p.P3862P
XH P57	8	144992862	144992862	Silent	SNP	A	G	A	PLEC	c.T11085C	p.A3695A
XH P57	8	144993324	144993324	Silent	SNP	C	T	C	PLEC	c.G10623A	p.T3541T
XH P57	8	144993377	144993377	Silent	SNP	A	G	A	PLEC	c.T10570C	p.L3524L
XH P57	8	144995188	144995188	Missense_Mutation	SNP	G	A	G	PLEC	c.C8759T	p.T2920M
XH P57	8	144995494	144995494	Missense_Mutation	SNP	C	T	C	PLEC	c.G8453A	p.R2818H
XH P57	8	144995736	144995736	Silent	SNP	G	A	G	PLEC	c.C8211T	p.N2737N
XH P57	8	144996029	144996029	Missense_Mutation	SNP	A	G	A	PLEC	c.T7918C	p.S2640P
XH P57	8	144996408	144996408	Silent	SNP	T	G	T	PLEC	c.A7539C	p.A2513A
XH P57	8	144997656	144997656	Silent	SNP	C	T	C	PLEC	c.G6399A	p.A2133A
XH P57	8	144997927	144997927	Missense_Mutation	SNP	G	A	G	PLEC	c.C6128T	p.A2043V
XH P57	8	144999417	144999417	Silent	SNP	C	T	C	PLEC	c.G4638A	p.A1546A
XH P57	8	145001031	145001031	Missense_Mutation	SNP	T	C	T	PLEC	c.A3923G	p.H1308R
XH P57	8	145001784	145001784	Silent	SNP	A	G	A	PLEC	c.T3508C	p.L1170L
XH P57	8	145007187	145007187	Missense_Mutation	SNP	G	A	G	PLEC	c.C1469T	p.A490V
XH P57	8	145011204	145011204	Silent	SNP	A	G	A	PLEC	c.T336C	p.A112A
XH P57	8	145057868	145057868	Missense_Mutation	SNP	A	G	A	PARP10	c.T1925C	p.V642A
XH P57	8	145058986	145058986	Missense_Mutation	SNP	A	G	A	PARP10	c.T1220C	p.L407P
XH P57	8	145059425	145059425	Missense_Mutation	SNP	T	C	T	PARP10	c.A781G	p.I261V
XH P57	8	145060112	145060112	Silent	SNP	G	A	G	PARP10	c.C249T	p.H83H
XH P57	8	145106274	145106274	Missense_Mutation	SNP	C	T	C	OPLAH	c.G3820A	p.E1274K
XH P57	8	145158050	145158050	Frame_Shift_Ins	INS	-	T	-	SHARPIN	c.279dupA	p.G94fs
XH P57	8	145170289	145170289	Missense_Mutation	SNP	G	C	G	WDR97	c.G4123C	p.A1375P
XH P57	8	145579843	145579851	In_Frame_Del	DEL	GCCATACAG	-	GCCATACAG	FBXL6	c.1249_1257del	p.417_419del
XH P57	8	145741602	145741602	Missense_Mutation	SNP	C	T	C	RECQL4	c.G901A	p.E301K
XH P57	8	145742118	145742118	Frame_Shift_Ins	INS	-	CCAC	-	RECQL4	384_385insGTG	p.P129fs
XH P57	8	145756170	145756170	Silent	SNP	G	A	G	ARHGAP39	c.C2973T	p.D991D
XH P57	8	146157483	146157483	Silent	SNP	G	C	G	ZNF16	c.C690G	p.V230V
XH P57	9	214679	214679	Missense_Mutation	SNP	G	A	G	C9orf66	c.C718T	p.P240S
XH P57	9	370244	370244	Silent	SNP	A	G	A	DOCK8	c.A1608G	p.K536K
XH P57	9	377111	377111	Silent	SNP	G	C	G	DOCK8	c.G2136C	p.L712L

XH_P57	9	841971	841971	Missense_Mutation	SNP	T	A	T	DMRT1	c.T133A	p.S45T
XH_P57	9	990076	990076	Missense_Mutation	SNP	G	A	G	DMRT3	c.G490A	p.A164T
XH_P57	9	1056959	1056959	Missense_Mutation	SNP	G	C	G	DMRT2	c.G1372C	p.E458Q
XH_P57	9	2643634	2643634	Missense_Mutation	SNP	G	C	G	VLDLR	c.G704C	p.R235P
XH_P57	9	4661970	4661971	Frame_Shift_Del	DEL	GA	-	GA	SPATA6L	c.105_106del	p.N35fs
XH_P57	9	5431913	5431913	Missense_Mutation	SNP	A	G	A	PLGRKT	c.T65C	p.M22T
XH_P57	9	6007500	6007500	Silent	SNP	G	A	G	KIAA2026	c.C288T	p.G96G
XH_P57	9	7046901	7046901	Missense_Mutation	SNP	C	G	C	KDM4C	c.C1534G	p.Q512E
XH_P57	9	14846036	14846036	Missense_Mutation	SNP	C	G	C	FREM1	c.G1315C	p.V439L
XH_P57	9	15784631	15784631	Missense_Mutation	SNP	A	G	A	CCDC171	c.A3206G	p.K1069R
XH_P57	9	21384971	21384971	Missense_Mutation	SNP	C	T	C	IFNA2	c.G358A	p.A120T
XH_P57	9	21816758	21816758	Missense_Mutation	SNP	G	A	G	MTAP	c.G166A	p.V56I
XH_P57	9	23692861	23692861	Silent	SNP	G	A	G	ELAVL2	c.C735T	p.D245D
XH_P57	9	23765046	23765046	Silent	SNP	C	T	C	ELAVL2	c.G33A	p.L11L
XH_P57	9	25677698	25677698	Missense_Mutation	SNP	A	C	A	TUSC1	c.T622G	p.S208A
XH_P57	9	25678122	25678122	Silent	SNP	G	C	G	TUSC1	c.C198G	p.A66A
XH_P57	9	26116157	26116157	Silent	SNP	G	A	G	LOC100506422	c.G333A	p.R111R
XH_P57	9	27296705	27296705	Silent	SNP	A	G	A	EQTN	c.T108C	p.D36D
XH_P57	9	32542204	32542204	Silent	SNP	A	G	A	TOPORS	c.T2124C	p.S708S
XH_P57	9	32630472	32630472	Silent	SNP	T	C	T	TAF1L	c.A5106G	p.K1702K
XH_P57	9	32784838	32784838	Silent	SNP	T	C	T	TMEM215	c.T657C	p.C219C
XH_P57	9	33466219	33466219	Silent	SNP	A	C	A	NOL6	c.T2214G	p.V738V
XH_P57	9	33566234	33566234	Silent	SNP	C	T	C	ANKRD18B	c.C2289T	p.A763A
XH_P57	9	33568789	33568789	Silent	SNP	T	G	T	ANKRD18B	c.T2886G	p.L962L
XH_P57	9	33797928	33797928	Frame_Shift_Ins	INS	-	CT	-	PRSS3	c.281_282insCT	p.R94fs
XH_P57	9	33941759	33941759	Missense_Mutation	SNP	T	C	T	UBAP2	c.A1016G	p.N339S
XH_P57	9	34256347	34256347	Silent	SNP	C	T	C	KIF24	c.G3258A	p.G1086G
XH_P57	9	34397545	34397545	Silent	SNP	A	G	A	C9orf24	c.T87C	p.Y29Y
XH_P57	9	34459025	34459025	Missense_Mutation	SNP	G	T	G	DNAI1	c.G22T	p.A8S
XH_P57	9	34622032	34622032	Missense_Mutation	SNP	C	T	C	ARID3C	c.G1123A	p.G375R
XH_P57	9	34622389	34622389	Missense_Mutation	SNP	A	C	A	ARID3C	c.T1003G	p.C335G
XH_P57	9	34637690	34637690	Missense_Mutation	SNP	T	G	T	SIGMAR1	c.A5C	p.Q2P
XH_P57	9	34649442	34649442	Missense_Mutation	SNP	A	G	A	GALT	c.A613G	p.N205D
XH_P57	9	34661994	34661994	Missense_Mutation	SNP	G	A	G	CCL27	c.C286T	p.L96F
XH_P57	9	35043291	35043291	Missense_Mutation	SNP	G	T	G	C9orf131	c.G560T	p.W187L
XH_P57	9	35044493	35044493	Missense_Mutation	SNP	T	A	T	C9orf131	c.T1762A	p.S588T
XH_P57	9	35105257	35105257	Silent	SNP	G	A	G	FAM214B	c.C1578T	p.T526T
XH_P57	9	35674101	35674101	Silent	SNP	T	C	T	CA9	c.T145C	p.L49L
XH_P57	9	35674347	35674347	Missense_Mutation	SNP	A	T	A	CA9	c.A391T	p.R131W
XH_P57	9	35792423	35792423	Silent	SNP	T	C	T	NPR2	c.T18C	p.L6L
XH_P57	9	35818996	35818996	Silent	SNP	G	A	G	FAM221B	c.C1062T	p.C354C
XH_P57	9	36105264	36105264	Silent	SNP	A	G	A	RECK	c.A1560G	p.P520P
XH_P57	9	37692654	37692654	Missense_Mutation	SNP	A	C	A	FRMPD1	c.A16C	p.T6P
XH_P57	9	37729786	37729786	Missense_Mutation	SNP	C	T	C	FRMPD1	c.C674T	p.A225V
XH_P57	9	37731007	37731007	Silent	SNP	C	T	C	FRMPD1	c.C765T	p.D255D
XH_P57	9	37745413	37745413	Silent	SNP	G	A	G	FRMPD1	c.G3384A	p.E1128E
XH_P57	9	40772563	40772563	Silent	SNP	G	A	G	ZNF658	c.C2712T	p.R904R
XH_P57	9	40784155	40784157	In_Frame_Del	DEL	CTC	-	CTC	ZNF658	c.188_190del	p.63_64del
XH_P57	9	42368614	42368614	Missense_Mutation	SNP	A	G	A	ANKRD20A2	c.A200G	p.H67R
XH_P57	9	69206924	69206924	Missense_Mutation	SNP	T	A	T	CBWD6	c.A864T	p.E288D
XH_P57	9	69256816	69256816	Silent	SNP	G	A	G	CBWD5	c.C315T	p.N105N
XH_P57	9	72472831	72472831	Silent	SNP	C	T	C	C9orf135	c.C90T	p.T30T
XH_P57	9	75545882	75545882	Silent	SNP	G	A	G	ALDH1A1	c.C225T	p.S75S
XH_P57	9	77377410	77377410	Missense_Mutation	SNP	C	T	C	TRPM6	c.G4162A	p.V1388I
XH_P57	9	79955345	79955345	Missense_Mutation	SNP	G	A	G	VPS13A	c.G6788A	p.S2263N
XH_P57	9	80851350	80851350	Silent	SNP	G	C	G	CEP78	c.G84C	p.S28S
XH_P57	9	80919756	80919756	Silent	SNP	T	G	T	PSAT1	c.T297G	p.A99A
XH_P57	9	84205860	84205860	Silent	SNP	G	A	G	TLE1	c.C1719T	p.T573T
XH_P57	9	86474115	86474115	Missense_Mutation	SNP	T	C	T	KIF27	c.A2815G	p.N939D
XH_P57	9	86518796	86518796	Missense_Mutation	SNP	T	C	T	KIF27	c.A637G	p.I213V
XH_P57	9	86900926	86900926	Silent	SNP	G	A	G	SLC28A3	c.C1381T	p.L461L
XH_P57	9	90538288	90538288	Nonsense_Mutation	SNP	C	T	C	SPATA31C1	c.C3466T	p.R1156X
XH_P57	9	90749692	90749692	Silent	SNP	C	T	C	SPATA31C2	c.G180A	p.K60K
XH_P57	9	91993724	91993724	Silent	SNP	C	T	C	SEMA4D	c.G2484A	p.T828T
XH_P57	9	92008486	92008486	Frame_Shift_Ins	INS	-	G	-	SEMA4D	c.498dupC	p.V167fs
XH_P57	9	94172975	94172975	Silent	SNP	C	T	C	NFIL3	c.G42A	p.A14A
XH_P57	9	95768448	95768448	Missense_Mutation	SNP	G	A	G	FGD3	c.G823A	p.V275I
XH_P57	9	95782667	95782667	Silent	SNP	C	T	C	FGD3	c.C1455T	p.F485F
XH_P57	9	96052295	96052295	Silent	SNP	C	G	C	WNK2	c.C4902G	p.A1634A
XH_P57	9	96055063	96055063	Silent	SNP	C	T	C	WNK2	c.C5316T	p.D1772D
XH_P57	9	96097669	96097669	Missense_Mutation	SNP	C	T	C	C9orf129	c.G352A	p.G118R
XH_P57	9	96278291	96278291	Silent	SNP	C	T	C	FAM120A	c.C1155T	p.G385G
XH_P57	9	96278474	96278474	Silent	SNP	C	T	C	FAM120A	c.C1338T	p.H446H
XH_P57	9	96318822	96318822	Silent	SNP	C	T	C	FAM120A	c.C2430T	p.L810L
XH_P57	9	96407920	96407920	Silent	SNP	C	T	C	PHF2	c.C309T	p.D103D
XH_P57	9	96415482	96415482	Silent	SNP	A	T	A	PHF2	c.A624T	p.P208P
XH_P57	9	97062852	97062852	Missense_Mutation	SNP	A	T	A	ZNF169	c.A439T	p.R147W
XH_P57	9	97062981	97062981	Missense_Mutation	SNP	C	T	C	ZNF169	c.C568T	p.R190C
XH_P57	9	97082699	97082699	Missense_Mutation	SNP	G	A	G	NUTM2F	c.C1159T	p.P387S
XH_P57	9	98997810	98997810	Missense_Mutation	SNP	C	T	C	HSD17B3	c.G865A	p.G289S
XH_P57	9	100105782	100105782	Missense_Mutation	SNP	C	G	C	CCDC180	c.C2567G	p.S856C
XH_P57	9	100388119	100388119	Missense_Mutation	SNP	G	T	G	TSTD2	c.C326A	p.A109D
XH_P57	9	100897139	100897139	Missense_Mutation	SNP	C	G	C	CORO2A	c.G417C	p.E139D
XH_P57	9	100971348	100971348	Silent	SNP	T	C	T	TBC1D2	c.A372G	p.A124A
XH_P57	9	102591042	102591042	Missense_Mutation	SNP	A	G	A	NR4A3	c.A718G	p.S240G
XH_P57	9	102595069	102595069	Silent	SNP	G	A	G	NR4A3	c.G1050A	p.Q350Q
XH_P57	9	102595685	102595685	Silent	SNP	C	T	C	NR4A3	c.C1203T	p.A401A
XH_P57	9	104324545	104324545	Silent	SNP	G	A	G	RNF20	c.G2769A	p.P923P
XH_P57	9	104335682	104335682	Missense_Mutation	SNP	C	T	C	GRIN3A	c.G3122A	p.R1041Q
XH_P57	9	104385712	104385712	Silent	SNP	A	G	A	GRIN3A	c.T2502C	p.N834N
XH_P57	9	104499987	104499987	Missense_Mutation	SNP	G	A	G	GRIN3A	c.C275T	p.S92L
XH_P57	9	107298444	107298444	Silent	SNP	C	T	C	OR13C3	c.G651A	p.L217L
XH_P57	9	107456933	107456933	Silent	SNP	C	T	C	OR13D1	c.C231T	p.L77L
XH_P57	9	107588033	107588033	Missense_Mutation	SNP	C	T	C	ABCA1	c.G2473A	p.V825I
XH_P57	9	109688010	109688010	Frame_Shift_Ins	INS	-	T	-	ZNF462	c.1818dupT	p.N606fs
XH_P57	9	111727670	111727670	Missense_Mutation	SNP	C	G	C	CTNNA1	c.G1579C	p.E527Q
XH_P57	9	111868885	111868885	Silent	SNP	G	A	G	TMEM245	c.C702T	p.S234S
XH_P57	9	111881856	111881856	Missense_Mutation	SNP	T	C	T	TMEM245	c.A338G	p.H113R

XH P57	9	111881927	111881927	Silent	SNP	T	C	T	TMEM245	c.A267G	p.L89L
XH P57	9	111882167	111882167	Missense_Mutation	SNP	G	C	G	TMEM245	c.C27G	p.D9E
XH P57	9	113459655	113459655	Silent	SNP	C	T	C	MUSK	c.C537T	p.N179N
XH P57	9	114089882	114089882	Missense_Mutation	SNP	C	T	C	OR2K2	c.G832A	p.G278R
XH P57	9	114174415	114174415	Missense_Mutation	SNP	T	C	T	KIAA0368	c.A2627G	p.N876S
XH P57	9	114190337	114190337	Silent	SNP	G	A	G	KIAA0368	c.C1569T	p.F523F
XH P57	9	114195587	114195587	Silent	SNP	G	A	G	KIAA0368	c.C1308T	p.H436H
XH P57	9	115024796	115024796	Silent	SNP	T	C	T	PTBP3	c.A234G	p.T78T
XH P57	9	115216321	115216321	Missense_Mutation	SNP	A	G	A	C9orf147	c.T415C	p.F139L
XH P57	9	115598610	115598610	Missense_Mutation	SNP	A	G	A	SNX30	c.A735G	p.I245M
XH P57	9	115600827	115600827	Silent	SNP	C	T	C	SNX30	c.C864T	p.S288S
XH P57	9	115925104	115925104	Silent	SNP	C	T	C	SLC31A2	c.C339T	p.A113A
XH P57	9	115931692	115931692	Silent	SNP	A	G	A	FKBP15	c.T3297C	p.T1099T
XH P57	9	116136473	116136473	Missense_Mutation	SNP	C	A	C	HDHD3	c.G162T	p.R54S
XH P57	9	116346287	116346287	Silent	SNP	C	T	C	RG53	c.C558T	p.Y186Y
XH P57	9	116791161	116791161	Silent	SNP	T	C	T	ZNFG18	c.T897C	p.C299C
XH P57	9	117002517	117002517	Silent	SNP	C	T	C	COL27A1	c.C2745T	p.I915I
XH P57	9	117122202	117122202	Silent	SNP	C	T	C	AKNA	c.G1908A	p.E636E
XH P57	9	117124731	117124731	Missense_Mutation	SNP	G	A	G	AKNA	c.C1514T	p.P505L
XH P57	9	117169033	117169033	Missense_Mutation	SNP	A	G	A	WHRN	c.T785C	p.M262T
XH P57	9	117186712	117186712	Missense_Mutation	SNP	C	T	C	WHRN	c.G265A	p.A89T
XH P57	9	119461275	119461275	Silent	SNP	G	A	G	TRIM32	c.G1254A	p.V418V
XH P57	9	122001000	122001000	Silent	SNP	G	A	G	BRINP1	c.C618T	p.S206S
XH P57	9	123301346	123301346	Silent	SNP	T	G	T	CDK5RAP2	c.A480C	p.L160L
XH P57	9	123914854	123914854	Missense_Mutation	SNP	C	T	C	CNTRL	c.C2399T	p.S800L
XH P57	9	124048461	124048461	Missense_Mutation	SNP	T	C	T	GSN	c.T40C	p.W14R
XH P57	9	124065224	124065224	Missense_Mutation	SNP	G	A	G	GSN	c.G385A	p.A129T
XH P57	9	124094800	124094800	Silent	SNP	T	C	T	GSN	c.T2268C	p.F756F
XH P57	9	124632992	124632992	Missense_Mutation	SNP	T	C	T	TTL11	c.A1787G	p.E596G
XH P57	9	124914613	124914613	Silent	SNP	C	T	C	NDUFA8	c.G126A	p.E42E
XH P57	9	125273435	125273435	Missense_Mutation	SNP	G	A	G	OR1J2	c.G355A	p.A191T
XH P57	9	125288893	125288893	Missense_Mutation	SNP	C	T	C	OR1N1	c.G680A	p.R227Q
XH P57	9	125316157	125316157	Missense_Mutation	SNP	C	T	C	OR1N2	c.C709T	p.R237C
XH P57	9	125391409	125391409	Silent	SNP	A	G	A	OR1B1	c.T406C	p.L136L
XH P57	9	126135936	126135936	Silent	SNP	G	C	G	CRB2	c.G3126C	p.A1042A
XH P57	9	126219706	126219706	Silent	SNP	A	G	A	DENND1A	c.T1107C	p.D369D
XH P57	9	127262802	127262802	Missense_Mutation	SNP	C	G	C	NR5A1	c.G437C	p.G146A
XH P57	9	129974928	129974929	Frame_Shift_Del	DEL	GG	-	GG	RALGPS1	c.1250_1251del	p.W417fs
XH P57	9	130197414	130197414	Missense_Mutation	SNP	A	G	A	ZNFX7	c.A79G	p.R27G
XH P57	9	130206762	130206762	Silent	SNP	C	T	C	ZNFX7	c.C381T	p.N127N
XH P57	9	130475480	130475480	Missense_Mutation	SNP	C	T	C	CFAP157	c.C1486T	p.P496S
XH P57	9	130511552	130511552	Silent	SNP	G	A	G	SH2D3C	c.C603T	p.S201S
XH P57	9	130513469	130513469	Silent	SNP	A	G	A	SH2D3C	c.T192C	p.H64H
XH P57	9	130529184	130529184	Missense_Mutation	SNP	C	T	C	SH2D3C	c.G307A	p.G103S
XH P57	9	130586621	130586621	Missense_Mutation	SNP	C	G	C	ENG	c.G1096C	p.D366H
XH P57	9	131117383	131117383	Missense_Mutation	SNP	G	A	G	SLC27A4	c.G1376A	p.R459H
XH P57	9	131768785	131768785	Missense_Mutation	SNP	C	T	C	NUP188	c.C5078T	p.T1693M
XH P57	9	131830610	131830610	Frame_Shift_Ins	INS	-	GGTG	-	MIGA2	403_1404insGG	p.T468fs
XH P57	9	132854659	132854659	Missense_Mutation	SNP	C	T	C	GPR107	c.C862T	p.R288W
XH P57	9	133556930	133556930	Silent	SNP	C	T	C	PRDM12	c.C978T	p.P326P
XH P57	9	133787225	133787225	Silent	SNP	A	G	A	FIBCD1	c.T900C	p.D300D
XH P57	9	133924451	133924451	Missense_Mutation	SNP	C	T	C	LAMC3	c.C1564T	p.P522S
XH P57	9	133927878	133927878	Missense_Mutation	SNP	A	G	A	LAMC3	c.A1631G	p.E544G
XH P57	9	133928345	133928345	Silent	SNP	C	T	C	LAMC3	c.C1932T	p.S644S
XH P57	9	134021630	134021630	Silent	SNP	A	G	A	NUP214	c.A1851G	p.T617T
XH P57	9	134351343	134351343	Missense_Mutation	SNP	C	T	C	PRRC2B	c.C3827T	p.A1276V
XH P57	9	135202829	135202829	Missense_Mutation	SNP	T	C	T	SETX	c.A4156G	p.I1386V
XH P57	9	135203231	135203231	Missense_Mutation	SNP	C	T	C	SETX	c.G3754A	p.G1252R
XH P57	9	135763816	135763816	Silent	SNP	C	T	C	SPACA9	c.C487T	p.L163L
XH P57	9	136262342	136262342	Silent	SNP	C	G	C	STKLD1	c.C918G	p.V306V
XH P57	9	136573412	136573412	Silent	SNP	G	A	G	SARDH	c.C1467T	p.H489H
XH P57	9	136672413	136672413	Silent	SNP	C	T	C	VAV2	c.G687A	p.P229P
XH P57	9	137711997	137711997	Silent	SNP	G	C	G	COL5A1	c.G4482C	p.P1494P
XH P57	9	138236031	138236031	Silent	SNP	A	G	A	C9orf62	c.A237G	p.P79P
XH P57	9	138379419	138379419	Silent	SNP	C	T	C	PPP1R26	c.C3063T	p.A1021A
XH P57	9	138391600	138391600	Missense_Mutation	SNP	T	C	T	C9orf116	c.A98G	p.D33G
XH P57	9	138395969	138395969	Missense_Mutation	SNP	A	G	A	MRPS2	c.A881G	p.H294R
XH P57	9	138456155	138456155	Missense_Mutation	SNP	C	A	C	PAEP	c.C310A	p.Q104K
XH P57	9	138516347	138516347	Frame_Shift_Del	DEL	A	-	A	GLTG01	c.427delT	p.W143fs
XH P57	9	138669261	138669261	Silent	SNP	G	A	G	KCNT1	c.G2292A	p.T764T
XH P57	9	138714620	138714620	Silent	SNP	G	A	G	CAMSAP1	c.C1887T	p.S629S
XH P57	9	139612156	139612156	Missense_Mutation	SNP	T	C	T	FAM69B	c.T191C	p.V64A
XH P57	9	139925464	139925464	Missense_Mutation	SNP	G	A	G	FUT7	c.C727T	p.R243C
XH P57	9	140093651	140093651	Missense_Mutation	SNP	G	A	G	TPRN	c.C1513T	p.P505S
XH P57	9	140127798	140127798	Missense_Mutation	SNP	C	T	C	SLC34A3	c.C698T	p.A233V
XH P57	9	140147586	140147586	Missense_Mutation	SNP	C	T	C	STPG3	c.C832T	p.R278C
XH P57	9	140327663	140327663	Missense_Mutation	SNP	C	T	C	NOXA1	c.C689T	p.P230L
XH P57	9	140400456	140400456	Silent	SNP	G	A	G	PNPLA7	c.C1230T	p.P410P
XH P57	9	140611140	140611140	Missense_Mutation	SNP	G	A	G	EHMT1	c.G148A	p.A50T
XH P57	9	141008876	141008876	Silent	SNP	C	T	C	CACNA1B	c.C5583T	p.F1861F
XH P57	10	93816	93816	Silent	SNP	C	T	C	TUBB8	c.G516A	p.S172S
XH P57	10	323283	323283	Silent	SNP	A	G	A	DIP2C	c.T4653C	p.Y1551Y
XH P57	10	871067	871070	Frame_Shift_Del	DEL	CTCT	-	CTCT	LARP4B	c.1419_1422del	p.R473fs
XH P57	10	1046712	1046712	Silent	SNP	G	A	G	GPBP4	c.G750A	p.A250A
XH P57	10	1406029	1406029	Missense_Mutation	SNP	C	T	C	ADARB2	c.G271A	p.G91S
XH P57	10	3150973	3150973	Silent	SNP	C	T	C	PFKP	c.C303T	p.F101F
XH P57	10	5929962	5929962	Missense_Mutation	SNP	G	C	G	ANKRD16	c.C383G	p.A128G
XH P57	10	5931230	5931230	Missense_Mutation	SNP	C	T	C	ANKRD16	c.G88A	p.G30R
XH P57	10	5979117	5979117	Silent	SNP	T	C	T	FBXO18	c.T3006C	p.C1002C
XH P57	10	7605067	7605067	Missense_Mutation	SNP	C	T	C	ITIH5	c.G2165A	p.R722Q
XH P57	10	7780646	7780646	Missense_Mutation	SNP	C	G	C	ITIH2	c.C2020G	p.P674A
XH P57	10	12811723	12811723	Frame_Shift_Ins	INS	-	GT	-	CAMK1D	c.490_491insGT	p.S164fs
XH P57	10	13151224	13151224	Silent	SNP	G	A	G	OPTN	c.G102A	p.T34T
XH P57	10	13375906	13375906	Silent	SNP	T	C	T	SEPHS1	c.A270G	p.T90T
XH P57	10	13653653	13653653	Silent	SNP	A	G	A	PRPF18	c.A549G	p.K183K
XH P57	10	14941635	14941635	In_Frame_Ins	INS	-	TTGTGATTACCT	-	SUV39H2	768insTTGTGATA	T256delinsTCGYL
XH P57	10	15138615	15138615	Missense_Mutation	SNP	C	T	C	C10orf111	c.G209A	p.R70K
XH P57	10	15145569	15145569	Missense_Mutation	SNP	A	G	A	RPP38	c.A256G	p.I86V

XH_P57	10	15256194	15256194	Missense_Mutation	SNP	G	A	G	FAM171A1	c.C1393T	p.P465S
XH_P57	10	16562600	16562600	Silent	SNP	G	A	G	C1QL3	c.C465T	p.H155H
XH_P57	10	16794623	16794623	Silent	SNP	C	T	C	RSU1	c.G354A	p.S118S
XH_P57	10	16918972	16918972	Silent	SNP	A	G	A	CUBN	c.T9030C	p.A3010A
XH_P57	10	17130199	17130199	Silent	SNP	G	A	G	CUBN	c.C1911T	p.L637L
XH_P57	10	17156151	17156151	Missense_Mutation	SNP	A	G	A	CUBN	c.T758C	p.F253S
XH_P57	10	17157572	17157572	Silent	SNP	G	A	G	CUBN	c.C618T	p.Y206Y
XH_P57	10	19392925	19392925	Silent	SNP	A	G	A	MALRD1	c.A615G	p.Q205Q
XH_P57	10	19780557	19780557	Missense_Mutation	SNP	C	A	C	MALRD1	c.C5141A	p.S1714Y
XH_P57	10	21108377	21108377	Silent	SNP	C	T	C	NEBL	c.G2031A	p.R677R
XH_P57	10	21415006	21415006	Missense_Mutation	SNP	T	C	T	C10orf113	c.A214G	p.R72G
XH_P57	10	21805466	21805466	In_Frame_Ins	INS	-	CCTCCT	-	SKIDA1	c.1286insAGG	p.G429delinsEEG
XH_P57	10	22024074	22024074	Silent	SNP	A	T	A	MLLT10	c.A2865T	p.S955S
XH_P57	10	22048330	22048330	Silent	SNP	C	T	C	DNAJC1	c.G1365A	p.A455A
XH_P57	10	22618362	22618362	Missense_Mutation	SNP	G	A	G	BM1	c.G872A	p.S291N
XH_P57	10	23393091	23393091	Missense_Mutation	SNP	A	G	A	MSRB2	c.A137G	p.E46G
XH_P57	10	24721946	24721946	Silent	SNP	A	C	A	KIAA1217	c.A576C	p.G192G
XH_P57	10	25701341	25701341	Missense_Mutation	SNP	C	G	C	GPR158	c.C1274G	p.A425G
XH_P57	10	27317840	27317840	Missense_Mutation	SNP	C	T	C	ANKRD26	c.G3910A	p.V1304I
XH_P57	10	27353007	27353007	Missense_Mutation	SNP	T	C	T	ANKRD26	c.A1273G	p.I425V
XH_P57	10	27381349	27381349	Silent	SNP	T	C	T	ANKRD26	c.A624G	p.V208V
XH_P57	10	27499804	27499804	Silent	SNP	T	C	T	ACBD5	c.A612G	p.A204A
XH_P57	10	28345418	28345418	Silent	SNP	T	C	T	MPP7	c.A1542G	p.K514K
XH_P57	10	29754644	29754644	Missense_Mutation	SNP	T	C	T	SVIL	c.A4735G	p.I1579V
XH_P57	10	29812602	29812602	Silent	SNP	G	T	G	SVIL	c.C1663A	p.R555R
XH_P57	10	29821523	29821523	Silent	SNP	T	C	T	SVIL	c.A1773G	p.K591K
XH_P57	10	29822159	29822159	Silent	SNP	T	C	T	SVIL	c.A1137G	p.L379L
XH_P57	10	29839787	29839787	Missense_Mutation	SNP	A	G	A	SVIL	c.T566C	p.V189A
XH_P57	10	30915859	30915859	Missense_Mutation	SNP	G	A	G	LYZL2	c.C124T	p.R42W
XH_P57	10	31138817	31138817	Missense_Mutation	SNP	G	A	G	ZNF438	c.C517T	p.P173S
XH_P57	10	33475282	33475282	Missense_Mutation	SNP	C	T	C	NRP1	c.G2179A	p.V727I
XH_P57	10	35896957	35896957	Silent	SNP	G	A	G	GJD4	c.G516A	p.K172K
XH_P57	10	43696279	43696279	Silent	SNP	A	G	A	RASGEF1A	c.T541C	p.T181L
XH_P57	10	44111806	44111806	Silent	SNP	G	A	G	ZNF485	c.G42A	p.L14L
XH_P57	10	44788818	44788825	Frame_Shift_Del	DEL	CCGCTGTTT	-	CCGCTGTTT	C10orf142	c.243_250del	p.Y81fs
XH_P57	10	47087609	47087609	Missense_Mutation	SNP	G	A	G	NPY4R	c.G826A	p.V276M
XH_P57	10	47756065	47756065	Silent	SNP	C	T	C	ANXA8L1	c.C354T	p.D118D
XH_P57	10	49383976	49383976	Missense_Mutation	SNP	T	C	T	FRMPD2	c.A2827G	p.I943V
XH_P57	10	49440194	49440194	Missense_Mutation	SNP	C	T	C	FRMPD2	c.G1060A	p.E354K
XH_P57	10	49998780	49998780	Missense_Mutation	SNP	G	A	G	WDFY4	c.G4075A	p.V1359I
XH_P57	10	50040728	50040728	Missense_Mutation	SNP	G	T	G	WDFY4	c.G6637T	p.A2213S
XH_P57	10	50315893	50315893	Missense_Mutation	SNP	A	G	A	VSTM4	c.T203C	p.F68S
XH_P57	10	50533617	50533617	Silent	SNP	T	C	T	C10orf71	c.T3027C	p.G1009G
XH_P57	10	50533776	50533776	Silent	SNP	C	G	C	C10orf71	c.C3186G	p.P1062P
XH_P57	10	50534599	50534599	Missense_Mutation	SNP	G	A	G	C10orf71	c.G4009A	p.G1337S
XH_P57	10	50740626	50740626	Missense_Mutation	SNP	C	T	C	ERCC6	c.G385A	p.V129M
XH_P57	10	50740876	50740876	Silent	SNP	G	C	G	ERCC6	c.C135G	p.L45L
XH_P57	10	50872912	50872912	Silent	SNP	C	T	C	CHAT	c.C1713T	p.I571I
XH_P57	10	50916542	50916542	Missense_Mutation	SNP	C	T	C	C10orf53	c.C353T	p.T118I
XH_P57	10	50950976	50950976	Missense_Mutation	SNP	G	A	G	OGDHL	c.C1283T	p.T428M
XH_P57	10	52005153	52005153	Silent	SNP	A	G	A	ASAH2	c.T189C	p.A63A
XH_P57	10	53458047	53458047	Silent	SNP	A	G	A	CSTF2T	c.T1263C	p.R421R
XH_P57	10	53458998	53458998	Silent	SNP	A	G	A	CSTF2T	c.T312C	p.L104L
XH_P57	10	54074757	54074757	Silent	SNP	A	G	A	DKK1	c.A318G	p.A106A
XH_P57	10	54528266	54528266	Silent	SNP	G	C	G	MBL2	c.C378G	p.L126L
XH_P57	10	55943191	55943204	Frame_Shift_Del	DEL	TGAGTAGTTT	-	GTGAGTAGTTAC	PQDH15	c.1479delG	p.Q493fs
XH_P57	10	59956041	59956041	Missense_Mutation	SNP	C	T	C	IPMK	c.G1047A	p.M349I
XH_P57	10	61665886	61665886	Silent	SNP	C	A	C	CCDC6	c.G297T	p.V99V
XH_P57	10	61831271	61831271	Missense_Mutation	SNP	T	C	T	ANK3	c.A9368G	p.K3123R
XH_P57	10	63170292	63170292	Silent	SNP	A	G	A	TMEM26	c.T895C	p.L299L
XH_P57	10	64565011	64565011	Silent	SNP	G	A	G	ADO	c.G192A	p.E64E
XH_P57	10	64573312	64573312	Silent	SNP	T	G	T	EGR2	c.A1086C	p.R362R
XH_P57	10	68040240	68040240	Silent	SNP	G	T	G	CTNNA3	c.C1872A	p.V624V
XH_P57	10	70225504	70225504	Silent	SNP	G	T	G	DNA2	c.C507A	p.A169A
XH_P57	10	70992635	70992635	Silent	SNP	G	A	G	HKDC1	c.G342A	p.T114T
XH_P57	10	71026510	71026510	Missense_Mutation	SNP	C	A	C	HKDC1	c.C2751A	p.N917K
XH_P57	10	71052083	71052083	Missense_Mutation	SNP	C	T	C	HK1	c.C97T	p.P33S
XH_P57	10	71176012	71176012	Missense_Mutation	SNP	A	G	A	TACR2	c.T68C	p.I23T
XH_P57	10	71391538	71391538	Silent	SNP	T	C	C	C10orf35	c.T39C	p.D13D
XH_P57	10	71874784	71874784	Missense_Mutation	SNP	C	T	C	AIFM2	c.G862A	p.D288N
XH_P57	10	71902488	71902488	Silent	SNP	C	G	C	TYSD1	c.G1419C	p.T473T
XH_P57	10	71905242	71905242	Silent	SNP	T	G	T	TYSD1	c.A1101C	p.V367V
XH_P57	10	72195717	72195717	Silent	SNP	G	A	G	NODAL	c.C216T	p.N72N
XH_P57	10	72326400	72326400	Missense_Mutation	SNP	G	A	G	PALD1	c.G2482A	p.G828R
XH_P57	10	72503344	72503344	Silent	SNP	G	A	G	ADAMTS14	c.G1965A	p.T655T
XH_P57	10	72517830	72517830	Missense_Mutation	SNP	G	A	G	ADAMTS14	c.G3050A	p.S1017N
XH_P57	10	72535007	72535007	Missense_Mutation	SNP	C	T	C	TBATA	c.G713A	p.R238Q
XH_P57	10	73057755	73057755	Silent	SNP	G	C	G	UNC5B	c.G2547C	p.L849L
XH_P57	10	73434906	73434906	Missense_Mutation	SNP	G	A	G	CDH23	c.G1487A	p.S496N
XH_P57	10	75533448	75533448	Silent	SNP	A	G	A	FUT11	c.A1209G	p.K403K
XH_P57	10	75884157	75884157	Silent	SNP	G	T	G	AP3M1	c.C1137A	p.I379I
XH_P57	10	76855412	76855412	Silent	SNP	G	A	G	DUSP13	c.C465T	p.D155D
XH_P57	10	76867899	76867899	Missense_Mutation	SNP	T	C	T	DUSP13	c.A218G	p.K73R
XH_P57	10	81064950	81064950	Silent	SNP	G	C	G	ZMIZ1	c.G2316C	p.L772L
XH_P57	10	81373674	81373674	Silent	SNP	T	C	T	SFTPA1	c.T552C	p.Y184Y
XH_P57	10	81926702	81926702	Missense_Mutation	SNP	G	A	G	ANXA11	c.C688T	p.R230C
XH_P57	10	85961608	85961608	Missense_Mutation	SNP	C	T	C	CDHR1	c.C571T	p.R191C
XH_P57	10	85997105	85997105	Missense_Mutation	SNP	G	T	G	LRIT1	c.C460A	p.L154M
XH_P57	10	88203068	88203068	Silent	SNP	T	C	T	WAPL	c.A3357G	p.T1119T
XH_P57	10	88277457	88277457	Missense_Mutation	SNP	C	T	C	WAPL	c.G370A	p.V124I
XH_P57	10	88414570	88414570	Silent	SNP	G	A	G	OPN4	c.G30A	p.P10P
XH_P57	10	88422151	88422151	Silent	SNP	C	A	C	OPN4	c.C1216A	p.R406R
XH_P57	10	88939962	88939962	Silent	SNP	T	C	T	FAM35A	c.T2094C	p.G698G
XH_P57	10	91162182	91162182	Silent	SNP	C	T	C	IFIT1	c.C150T	p.Y50Y
XH_P57	10	91404832	91404832	Silent	SNP	T	C	T	PANK1	c.A228G	p.A76A
XH_P57	10	91497207	91497207	Missense_Mutation	SNP	A	G	A	KIF20B	c.A2609G	p.N870S
XH_P57	10	91497912	91497912	Missense_Mutation	SNP	A	G	A	KIF20B	c.A3314G	p.K1105R
XH_P57	10	93608142	93608142	Silent	SNP	G	A	G	TNKS2	c.G2361A	p.A787A

XH_P57	10	95083039	95083039	Missense_Mutation	SNP	C	T	C	MYOF	c.G5309A	p.R1770Q
XH_P57	10	95121288	95121288	Silent	SNP	G	A	G	MYOF	c.C2856T	p.S952S
XH_P57	10	95259979	95259979	Missense_Mutation	SNP	C	G	C	CEP55	c.C171G	p.H57Q
XH_P57	10	95326676	95326676	Missense_Mutation	SNP	C	T	C	FFAR4	c.C199T	p.R67C
XH_P57	10	95791613	95791613	Silent	SNP	T	C	T	PLCE1	c.T810C	p.C270C
XH_P57	10	96447920	96447920	Missense_Mutation	SNP	C	T	C	CYP2C18	c.C370T	p.R124W
XH_P57	10	97023725	97023725	Missense_Mutation	SNP	C	A	C	PDLIM1	c.G429T	p.Q143H
XH_P57	10	97141487	97141487	Silent	SNP	G	A	G	SORBS1	c.C978T	p.Y326Y
XH_P57	10	97174352	97174352	Missense_Mutation	SNP	T	C	T	SORBS1	c.A682G	p.T228A
XH_P57	10	97371146	97371146	Silent	SNP	G	A	G	ALDH18A1	c.C1341T	p.S447S
XH_P57	10	97791754	97791754	Nonsense_Mutation	SNP	C	T	C	CC2D2B	c.C958T	p.Q320X
XH_P57	10	98144492	98144492	Silent	SNP	G	A	G	TLL2	c.C2046T	p.S682S
XH_P57	10	98369536	98369536	Silent	SNP	A	G	A	PIK3AP1	c.T2103C	p.S701S
XH_P57	10	98469507	98469507	Missense_Mutation	SNP	C	A	C	PIK3AP1	c.G247T	p.A83S
XH_P57	10	99126540	99126540	Silent	SNP	C	T	C	RRP12	c.G2874A	p.E958E
XH_P57	10	99140570	99140570	Missense_Mutation	SNP	G	A	G	RRP12	c.C1219T	p.P407S
XH_P57	10	99228045	99228045	In_Frame_Ins	INS	-	AGT	-	MMS19	1052_1053insA	p.L351delinsLL
XH_P57	10	99433454	99433454	Silent	SNP	C	T	C	PI4K2A	c.C1395T	p.Y465Y
XH_P57	10	100144782	100144782	Missense_Mutation	SNP	C	T	C	PYROXD2	c.G1597A	p.A533T
XH_P57	10	100190920	100190920	Silent	SNP	G	A	G	HPS1	c.C267T	p.L89L
XH_P57	10	101639616	101639616	Silent	SNP	C	T	C	DNMBP	c.G3396A	p.P1132P
XH_P57	10	101657880	101657880	Silent	SNP	G	A	G	DNMBP	c.C1779T	p.S513N
XH_P57	10	101689378	101689378	Missense_Mutation	SNP	G	C	G	DNMBP	c.C1143G	p.S381R
XH_P57	10	101690379	101690379	Silent	SNP	A	G	A	DNMBP	c.T142C	p.L48L
XH_P57	10	101715303	101715303	Missense_Mutation	SNP	C	T	C	DNMBP	c.G1928A	p.R643H
XH_P57	10	101715899	101715899	Silent	SNP	G	A	G	DNMBP	c.C1332T	p.P444P
XH_P57	10	101716484	101716484	Silent	SNP	G	A	G	DNMBP	c.C747T	p.V249V
XH_P57	10	101823396	101823396	Silent	SNP	C	T	C	CPN1	c.G846A	p.G282G
XH_P57	10	101943529	101943529	Missense_Mutation	SNP	G	C	G	ERLIN1	c.C179G	p.T60R
XH_P57	10	102006681	102006681	Silent	SNP	C	T	C	CWF19L1	c.G309A	p.A103A
XH_P57	10	102295836	102295836	Missense_Mutation	SNP	C	G	C	HIF1AN	c.C121G	p.P41A
XH_P57	10	102744376	102744376	Missense_Mutation	SNP	T	C	T	SEMA4G	c.T1835C	p.M612T
XH_P57	10	102798962	102798962	Silent	SNP	C	A	C	SFXN3	c.C864A	p.A288A
XH_P57	10	103368654	103368654	Missense_Mutation	SNP	T	C	T	DPD	c.T500C	p.L167S
XH_P57	10	103427716	103427716	Missense_Mutation	SNP	G	A	G	FBXW4	c.C436T	p.R146W
XH_P57	10	103825747	103825747	Silent	SNP	G	A	G	HPS6	c.G516A	p.G172G
XH_P57	10	103898986	103898986	Missense_Mutation	SNP	C	G	C	PPRC1	c.C721G	p.Q241E
XH_P57	10	103908648	103908648	Silent	SNP	C	T	C	PPRC1	c.C3900T	p.S1300S
XH_P57	10	104229785	104229785	Silent	SNP	C	T	C	MFSD13A	c.C204T	p.P68P
XH_P57	10	104596924	104596924	Silent	SNP	C	A	C	CYP17A1	c.G195T	p.S65S
XH_P57	10	104814162	104814162	Silent	SNP	T	C	T	CNNM2	c.T1842C	p.S614S
XH_P57	10	104849468	104849468	Silent	SNP	G	A	G	NT5C2	c.C1074T	p.D358D
XH_P57	10	104934709	104934709	Missense_Mutation	SNP	T	C	T	NT5C2	c.A7G	p.T3A
XH_P57	10	105184858	105184858	Missense_Mutation	SNP	G	A	G	PDCD11	c.G2881A	p.D961N
XH_P57	10	106022789	106022789	Missense_Mutation	SNP	C	A	C	GSTO1	c.C335A	p.A112D
XH_P57	10	112266771	112266771	Silent	SNP	C	T	C	DUSP5	c.C607T	p.L203L
XH_P57	10	112404302	112404302	Silent	SNP	G	A	G	RBM20	c.G90A	p.R30R
XH_P57	10	112838892	112838892	Silent	SNP	C	A	C	ADRA2A	c.C1138A	p.R380R
XH_P57	10	114053546	114053546	Silent	SNP	C	G	C	TECTB	c.C534G	p.S178S
XH_P57	10	114200355	114200355	Silent	SNP	G	A	G	ZDHHC6	c.C606T	p.T202T
XH_P57	10	114911641	114911641	Frame_Shift_Ins	INS	-	G	-	TCF7L2	c.731dupG	p.R244fs
XH_P57	10	115381747	115381747	Missense_Mutation	SNP	G	A	G	NRAP	c.C2542T	p.R848C
XH_P57	10	115644040	115644040	Missense_Mutation	SNP	G	A	G	NHLRC2	c.G940A	p.V314I
XH_P57	10	116068193	116068193	Silent	SNP	G	A	G	AFAP1L2	c.C966T	p.D322D
XH_P57	10	116307504	116307504	Silent	SNP	A	G	A	ABLIM1	c.T525C	p.N175N
XH_P57	10	116335246	116335246	Silent	SNP	G	A	G	ABLIM1	c.C312T	p.F104F
XH_P57	10	116602805	116602805	Silent	SNP	A	G	A	FAM160B1	c.A636G	p.E212E
XH_P57	10	116659253	116659253	Missense_Mutation	SNP	A	G	A	FAM160B1	c.A2197G	p.T733A
XH_P57	10	119774598	119774598	Missense_Mutation	SNP	T	A	T	RAB11FIP2	c.A1289T	p.N430I
XH_P57	10	121579040	121579040	Silent	SNP	T	C	T	INPP5F	c.T45C	p.F15F
XH_P57	10	121586520	121586520	Missense_Mutation	SNP	C	T	C	INPP5F	c.C797T	p.A266V
XH_P57	10	121671651	121671651	Silent	SNP	T	C	T	SEC23IP	c.T1287C	p.D429D
XH_P57	10	121685689	121685689	Missense_Mutation	SNP	G	A	G	SEC23IP	c.G2263A	p.V755M
XH_P57	10	121693246	121693246	Silent	SNP	A	G	A	SEC23IP	c.A2970G	p.T990T
XH_P57	10	122216862	122216862	Silent	SNP	C	T	C	PLPP4	c.C45T	p.F15F
XH_P57	10	123310871	123310871	Missense_Mutation	SNP	A	G	A	FGFR2	c.T212C	p.M71T
XH_P57	10	123687456	123687456	Silent	SNP	G	A	G	ATE1	c.C9T	p.F3F
XH_P57	10	123810060	123810060	Silent	SNP	G	A	G	TACC2	c.G141A	p.A47A
XH_P57	10	123842825	123842825	Silent	SNP	C	A	C	TACC2	c.C810G	p.P270P
XH_P57	10	123844558	123844558	Missense_Mutation	SNP	A	G	A	TACC2	c.A2543G	p.Q848R
XH_P57	10	123846490	123846490	Missense_Mutation	SNP	C	T	C	TACC2	c.C4475T	p.P1492L
XH_P57	10	123848113	123848113	Silent	SNP	G	A	G	TACC2	c.G5580A	p.A1860A
XH_P57	10	124066731	124066731	Silent	SNP	T	G	T	BTBD16	c.T822G	p.L274L
XH_P57	10	124094467	124094467	Silent	SNP	T	C	T	BTBD16	c.T1239C	p.D413D
XH_P57	10	124249010	124249010	Silent	SNP	C	T	C	HTRA1	c.C645T	p.I215I
XH_P57	10	125780759	125780759	Missense_Mutation	SNP	G	C	G	CHST15	c.C1360G	p.P454A
XH_P57	10	126714714	126714714	Missense_Mutation	SNP	G	C	G	CTBP2	c.C1615G	p.Q539E
XH_P57	10	126714966	126714966	Missense_Mutation	SNP	A	G	A	CTBP2	c.T1363C	p.Y455H
XH_P57	10	127344606	127344606	Missense_Mutation	SNP	G	A	G	TEX36	c.C424T	p.R142C
XH_P57	10	128150015	128150015	Missense_Mutation	SNP	G	C	G	C10orf90	c.C1674G	p.D558E
XH_P57	10	129899543	129899543	Silent	SNP	C	T	C	MKI67	c.G8604A	p.R2868R
XH_P57	10	129899578	129899578	Missense_Mutation	SNP	T	C	T	MKI67	c.A8569G	p.K2857E
XH_P57	10	129899778	129899778	Missense_Mutation	SNP	G	C	G	MKI67	c.C8369G	p.T2790S
XH_P57	10	129901393	129901393	Missense_Mutation	SNP	T	C	T	MKI67	c.A7631G	p.Q2544R
XH_P57	10	129903016	129903016	Missense_Mutation	SNP	T	C	T	MKI67	c.A6008G	p.N2003S
XH_P57	10	129904917	129904917	Silent	SNP	G	A	G	MKI67	c.C4107T	p.N1369N
XH_P57	10	129906364	129906364	Missense_Mutation	SNP	G	A	G	MKI67	c.C2660T	p.T887I
XH_P57	10	129906468	129906468	Silent	SNP	C	T	C	MKI67	c.G2556A	p.Q852Q
XH_P57	10	129907544	129907544	Missense_Mutation	SNP	G	C	G	MKI67	c.C1480G	p.L494V
XH_P57	10	129910475	129910475	Missense_Mutation	SNP	T	G	T	MKI67	c.A811C	p.I271L
XH_P57	10	133758869	133758869	Silent	SNP	G	A	G	PPP2R2D	c.G231A	p.P77P
XH_P57	10	133761285	133761285	Missense_Mutation	SNP	G	A	G	PPP2R2D	c.G577A	p.G193S
XH_P57	10	133950642	133950642	Silent	SNP	T	C	T	JAKMIP3	c.T1020C	p.D340D
XH_P57	10	134624504	134624504	Silent	SNP	C	T	C	CFAP46	c.G7533A	p.A2511A
XH_P57	10	134942166	134942166	Silent	SNP	A	G	A	ADGRA1	c.A543G	p.S181S
XH_P57	10	134942340	134942340	Silent	SNP	C	T	C	ADGRA1	c.C717T	p.A239A
XH_P57	10	134942832	134942832	Silent	SNP	G	A	G	ADGRA1	c.G1209A	p.P403P
XH_P57	10	134981942	134981942	Silent	SNP	C	T	C	KNDC1	c.C486T	p.A162A

XH_P57	11	233026	233026	Silent	SNP	C	A	C	SIRT3	c.G237T	p.L79L
XH_P57	11	284257	284257	Silent	SNP	G	A	G	NLRP6	c.G2226A	p.A742A
XH_P57	11	396915	396915	Silent	SNP	C	T	C	PKP3	c.C414T	p.N138N
XH_P57	11	433867	433867	Missense_Mutation	SNP	G	A	G	AN09	c.C152T	p.A51V
XH_P57	11	494942	494942	Silent	SNP	G	C	G	RNH1	c.C1239G	p.A413A
XH_P57	11	499059	499059	Silent	SNP	C	T	C	RNH1	c.G570A	p.L190L
XH_P57	11	534242	534242	Silent	SNP	A	G	A	HRAS	c.T81C	p.H27H
XH_P57	11	608360	608360	Silent	SNP	G	A	G	PHRF1	c.G2904A	p.P968P
XH_P57	11	615196	615196	Silent	SNP	C	T	C	IRF7	c.G123A	p.E41E
XH_P57	11	619015	619015	Missense_Mutation	SNP	G	C	G	CDHR5	c.C1526G	p.S509W
XH_P57	11	828916	828916	Missense_Mutation	SNP	G	A	G	CRACR2B	c.G230A	p.R77Q
XH_P57	11	1028042	1028042	Frame_Shift_Ins	INS	-	T	-	MUC6	c.1770_1771ins	p.H591fs
XH_P57	11	1075747	1075747	Missense_Mutation	SNP	T	C	T	MUC2	c.T173C	p.L58P
XH_P57	11	1081141	1081141	Silent	SNP	C	T	C	MUC2	c.C1437T	p.T479T
XH_P57	11	1084362	1084362	Missense_Mutation	SNP	G	A	G	MUC2	c.G2494A	p.G832S
XH_P57	11	1248597	1248597	Silent	SNP	C	T	C	MUC5B	c.C636T	p.G121G
XH_P57	11	1267475	1267475	Missense_Mutation	SNP	T	C	T	MUC5B	c.T9365C	p.M3122T
XH_P57	11	1491416	1491416	Missense_Mutation	SNP	C	T	C	MOB2	c.G793A	p.V265M
XH_P57	11	1619396	1619396	Missense_Mutation	SNP	C	T	C	KRTAP5-2	c.G85A	p.G29R
XH_P57	11	1643252	1643252	Silent	SNP	A	G	A	KRTAP5-4	c.T72C	p.C24C
XH_P57	11	1651140	1651140	Missense_Mutation	SNP	T	C	T	KRTAP5-5	c.T70C	p.C24R
XH_P57	11	2016717	2016717	Silent	SNP	T	A	T	HOTS	c.T291A	p.I97I
XH_P57	11	2906012	2906012	Silent	SNP	C	T	C	CDKN1C	c.G708A	p.E236E
XH_P57	11	3249552	3249552	Missense_Mutation	SNP	C	T	C	MRGPRE	c.G478A	p.G160S
XH_P57	11	3380998	3380998	Missense_Mutation	SNP	C	T	C	ZNF195	c.G1024A	p.E342K
XH_P57	11	3697594	3697594	Missense_Mutation	SNP	C	T	C	NUP98	c.G4976A	p.R1659H
XH_P57	11	4510629	4510629	Missense_Mutation	SNP	C	T	C	OR52K1	c.C499T	p.R167C
XH_P57	11	4661621	4661621	Missense_Mutation	SNP	T	G	T	OR51D1	c.T601G	p.S201A
XH_P57	11	4703321	4703321	Silent	SNP	G	A	G	OR51E2	c.C621T	p.G207G
XH_P57	11	4869649	4869649	Missense_Mutation	SNP	G	A	G	OR51S1	c.C790T	p.L264F
XH_P57	11	4869906	4869906	Missense_Mutation	SNP	A	C	A	OR51S1	c.T533G	p.L178R
XH_P57	11	4976391	4976391	Missense_Mutation	SNP	C	A	C	OR51A2	c.G553T	p.D185Y
XH_P57	11	5021055	5021055	Missense_Mutation	SNP	C	G	C	OR51L1	c.C843G	p.L281M
XH_P57	11	5068297	5068297	Missense_Mutation	SNP	G	A	G	OR52J3	c.G542A	p.C181Y
XH_P57	11	5080359	5080359	Missense_Mutation	SNP	G	A	G	OR52E2	c.C499T	p.R167W
XH_P57	11	5080591	5080591	Silent	SNP	G	T	G	OR52E2	c.C267A	p.I89I
XH_P57	11	5322737	5322737	Missense_Mutation	SNP	A	G	A	OR51B4	c.T440C	p.M147T
XH_P57	11	5323019	5323019	Missense_Mutation	SNP	A	G	A	OR51B4	c.T158C	p.L53P
XH_P57	11	5344902	5344902	Missense_Mutation	SNP	C	G	C	OR51B2	c.G626C	p.C209S
XH_P57	11	5423931	5423931	Silent	SNP	C	T	C	OR51J1	c.C105T	p.S35S
XH_P57	11	5424125	5424125	Missense_Mutation	SNP	G	A	G	OR51J1	c.G299A	p.C100Y
XH_P57	11	5424387	5424387	Frame_Shift_Ins	INS	-	TATC	-	OR51J1	c.561_562insTAT	p.S187fs
XH_P57	11	5537245	5537245	Missense_Mutation	SNP	G	T	G	UBQLNL	c.C427A	p.Q143K
XH_P57	11	5719667	5719667	Silent	SNP	T	C	T	TRIM22	c.T630C	p.D210D
XH_P57	11	5776484	5776484	Nonsense_Mutation	SNP	A	T	A	OR52N4	c.A514T	p.R172X
XH_P57	11	5776595	5776595	Missense_Mutation	SNP	T	G	T	OR52N4	c.T625G	p.W209G
XH_P57	11	5799468	5799468	Missense_Mutation	SNP	C	T	C	OR52N5	c.G397A	p.V133I
XH_P57	11	5809230	5809230	Silent	SNP	G	A	G	OR52N1	c.C817T	p.L273L
XH_P57	11	5862532	5862532	Missense_Mutation	SNP	A	C	A	OR52E6	c.T596G	p.M199R
XH_P57	11	5906205	5906205	Missense_Mutation	SNP	G	A	G	OR52E4	c.G683A	p.R228H
XH_P57	11	5989293	5989293	Silent	SNP	G	A	G	OR56A5	c.C432T	p.V144V
XH_P57	11	6238960	6238960	Missense_Mutation	SNP	C	A	C	FAM160A2	c.G1856T	p.R619L
XH_P57	11	6281267	6281267	Missense_Mutation	SNP	C	T	C	CKK8R	c.C109T	p.L37F
XH_P57	11	6411931	6411942	In_Frame_Del	DEL	FGGTGCTGGG	-	CTGGTGCTGGCC	SMPD1	c.103_114del	p.35_38del
XH_P57	11	6422867	6422867	Silent	SNP	G	A	G	APB81	c.C780T	p.H260H
XH_P57	11	6579106	6579106	Missense_Mutation	SNP	C	A	C	DNHD1	c.C8581A	p.H2861N
XH_P57	11	6588228	6588228	Missense_Mutation	SNP	G	A	G	DNHD1	c.G11489A	p.R3830H
XH_P57	11	6631016	6631016	Silent	SNP	C	T	C	ILK	c.C735T	p.A245A
XH_P57	11	6643976	6643976	Silent	SNP	C	T	C	DCHS1	c.G8931A	p.Q2977Q
XH_P57	11	6644600	6644600	Silent	SNP	C	T	C	DCHS1	c.G8307A	p.A2769A
XH_P57	11	6648424	6648424	Missense_Mutation	SNP	G	A	G	DCHS1	c.C5846T	p.T1949M
XH_P57	11	6651810	6651810	Silent	SNP	A	G	A	DCHS1	c.T4215C	p.L1405L
XH_P57	11	6652618	6652618	Silent	SNP	C	T	C	DCHS1	c.G3696A	p.P1232P
XH_P57	11	6655433	6655433	Silent	SNP	G	A	G	DCHS1	c.C1902T	p.H634H
XH_P57	11	6790028	6790028	Missense_Mutation	SNP	C	G	C	OR2AG2	c.G161C	p.R54P
XH_P57	11	6891758	6891758	Missense_Mutation	SNP	A	C	A	OR10A2	c.A773C	p.K258T
XH_P57	11	6913290	6913290	Missense_Mutation	SNP	A	G	A	OR2D2	c.T442C	p.S148P
XH_P57	11	6942695	6942695	Missense_Mutation	SNP	C	T	C	OR2D3	c.C463T	p.R155W
XH_P57	11	6977175	6977175	Missense_Mutation	SNP	G	C	G	ZNF215	c.G967C	p.V323L
XH_P57	11	6977334	6977334	Missense_Mutation	SNP	A	G	A	ZNF215	c.A1126G	p.M376V
XH_P57	11	7110363	7110363	Silent	SNP	G	A	G	RBMXL2	c.G12A	p.A4A
XH_P57	11	7950024	7950024	Silent	SNP	A	G	A	OR10A6	c.T186C	p.F62F
XH_P57	11	8435077	8435077	Missense_Mutation	SNP	C	T	C	STK33	c.G748A	p.A250T
XH_P57	11	8435078	8435078	Missense_Mutation	SNP	A	C	A	STK33	c.T747G	p.D249E
XH_P57	11	9501063	9501063	Missense_Mutation	SNP	T	G	T	ZNF143	c.T522G	p.L174M
XH_P57	11	10786175	10786175	Silent	SNP	C	T	C	CTR9	c.C1494T	p.T498T
XH_P57	11	12183846	12183846	Silent	SNP	C	T	C	MICAL2	c.C144T	p.N48N
XH_P57	11	12315907	12315907	Missense_Mutation	SNP	G	A	G	MICALCL	c.G929A	p.R310H
XH_P57	11	17409069	17409069	Silent	SNP	G	A	G	KCNJ11	c.C570T	p.A190A
XH_P57	11	17496516	17496516	Silent	SNP	A	G	A	ABCC8	c.T207C	p.P69P
XH_P57	11	17531146	17531146	Silent	SNP	G	A	G	USH1C	c.C1770T	p.A590A
XH_P57	11	17569527	17569527	Missense_Mutation	SNP	C	G	C	OTOG	c.C148G	p.Q50E
XH_P57	11	17593709	17593709	Missense_Mutation	SNP	T	C	T	OTOG	c.T2074C	p.S692P
XH_P57	11	18194944	18194944	Silent	SNP	T	A	T	MRGPRX4	c.T141A	p.V47V
XH_P57	11	18267597	18267597	Splice_Site	INS	-	GGAAA	-	SAA2	-	-
XH_P57	11	20622975	20622975	Missense_Mutation	SNP	G	A	G	SLC6A5	c.G304A	p.G102S
XH_P57	11	20805335	20805335	Silent	SNP	C	T	C	NELL1	c.C294T	p.S98S
XH_P57	11	22271870	22271870	Missense_Mutation	SNP	A	T	A	AN05	c.A963T	p.L321F
XH_P57	11	27679473	27679473	Silent	SNP	C	T	C	BDNF	c.G639A	p.S213S
XH_P57	11	28098605	28098605	Silent	SNP	T	C	T	KIF18A	c.A1374G	p.Q458Q
XH_P57	11	28110151	28110151	Missense_Mutation	SNP	T	C	T	KIF18A	c.A817G	p.T273A
XH_P57	11	31327787	31327787	Frame_Shift_Ins	INS	-	G	-	DCDC1	c.582dupC	p.I195fs
XH_P57	11	32456694	32456694	Silent	SNP	C	A	C	WT1	c.G198T	p.P66P
XH_P57	11	33581306	33581306	Silent	SNP	G	A	G	KIAA1549L	c.G2976A	p.T992T
XH_P57	11	33631423	33631423	Silent	SNP	G	A	G	KIAA1549L	c.G4299A	p.K1433K
XH_P57	11	36472800	36472800	Silent	SNP	A	G	A	PRR5L	c.A243G	p.R81Q
XH_P57	11	36597313	36597313	Missense_Mutation	SNP	A	G	A	RAG1	c.A2459G	p.R820R
XH_P57	11	44089352	44089352	Missense_Mutation	SNP	G	A	G	ACCS	c.G175A	p.D59N

XH_P57	11	44129290	44129290	Silent	SNP	C	A	C	EXT2	c.C127A	p.R43R
XH_P57	11	44286566	44286566	Silent	SNP	G	A	G	ALX4	c.C1074T	p.H358H
XH_P57	11	44636833	44636833	Silent	SNP	G	A	G	CD82	c.G273A	p.E91E
XH_P57	11	45245770	45245770	Missense_Mutation	SNP	G	A	G	PRDM11	c.G745A	p.E249K
XH_P57	11	45949534	45949534	Silent	SNP	C	T	C	LARGE2	c.C1668T	p.F556F
XH_P57	11	47434986	47434986	Silent	SNP	G	A	G	SLC39A13	c.G573A	p.A191A
XH_P57	11	47460306	47460306	Silent	SNP	A	G	A	RAPSN	c.T966C	p.P322P
XH_P57	11	47469439	47469439	Silent	SNP	A	G	A	RAPSN	c.T456C	p.Y152Y
XH_P57	11	47857253	47857253	Missense_Mutation	SNP	T	C	T	NUP160	c.A1051G	p.T351A
XH_P57	11	47869855	47869855	Missense_Mutation	SNP	C	T	C	NUP160	c.G118A	p.A40T
XH_P57	11	48285856	48285856	Silent	SNP	C	T	C	OR4X1	c.C444T	p.G148G
XH_P57	11	49080616	49080616	Missense_Mutation	SNP	T	C	T	TRIM64C	c.A49G	p.I17V
XH_P57	11	49973979	49973979	Missense_Mutation	SNP	C	T	C	OR4C13	c.C5T	p.A2V
XH_P57	11	56019925	56019925	Missense_Mutation	SNP	T	G	T	OR5T3	c.T250G	p.W84G
XH_P57	11	57077464	57077464	Silent	SNP	T	C	T	TNKS18P1	c.A2721G	p.Q907Q
XH_P57	11	57080184	57080184	Missense_Mutation	SNP	G	C	G	TNKS18P1	c.C1978G	p.Q660E
XH_P57	11	57799183	57799183	Silent	SNP	C	T	C	OR6Q1	c.C759T	p.S253S
XH_P57	11	57799371	57799371	Missense_Mutation	SNP	G	C	G	OR6Q1	c.G947C	p.G316A
XH_P57	11	57886435	57886435	Missense_Mutation	SNP	G	T	G	OR9I1	c.C482A	p.T161N
XH_P57	11	57947264	57947264	Silent	SNP	C	G	C	OR9Q1	c.C348G	p.A116A
XH_P57	11	57982584	57982584	Missense_Mutation	SNP	T	C	T	OR1S1	c.T368C	p.I123T
XH_P57	11	57982620	57982620	Missense_Mutation	SNP	A	G	A	OR1S1	c.A404G	p.H135R
XH_P57	11	57983194	57983194	Nonstop_Mutation	SNP	A	G	A	OR1S1	c.A978G	p.X326W
XH_P57	11	58034543	58034543	Missense_Mutation	SNP	C	T	C	OR10W1	c.G788A	p.R263Q
XH_P57	11	58125620	58125620	Missense_Mutation	SNP	T	C	T	OR5B17	c.A923G	p.Y308C
XH_P57	11	58126305	58126305	Missense_Mutation	SNP	A	T	A	OR5B17	c.T238A	p.L80I
XH_P57	11	58318619	58318619	Silent	SNP	C	G	C	LPXN	c.G345C	p.I115L
XH_P57	11	58978684	58978684	Missense_Mutation	SNP	G	A	G	MPEG1	c.C1655T	p.P552L
XH_P57	11	61914260	61914260	Missense_Mutation	SNP	G	A	G	INCENP	c.G2078A	p.R693Q
XH_P57	11	62295075	62295075	Missense_Mutation	SNP	C	T	C	AHNAK	c.G6814A	p.V2272I
XH_P57	11	62402393	62402393	Missense_Mutation	SNP	G	A	G	GANAB	c.C118T	p.R40W
XH_P57	11	62473078	62473078	In_Frame_Ins	INS	-	GCT	-	BSCL2	c.98_99insAGC	p.A33delinsAA
XH_P57	11	62652779	62652779	Silent	SNP	C	T	C	SLC3A2	c.C949T	p.L137L
XH_P57	11	62677529	62677529	Silent	SNP	C	T	C	CHRM1	c.G1044A	p.Q348Q
XH_P57	11	63670097	63670097	Frame_Shift_Ins	INS	-	T	-	MARK2	c.1260dupT	p.S420fs
XH_P57	11	64004692	64004692	Silent	SNP	C	T	C	VEGFB	c.C408T	p.D136D
XH_P57	11	64023971	64023971	Silent	SNP	G	A	G	PLCB3	c.G621A	p.L207L
XH_P57	11	64026685	64026685	Silent	SNP	C	T	C	PLCB3	c.C1293T	p.S431S
XH_P57	11	64326696	64326696	Silent	SNP	C	A	C	SLC22A11	c.C483A	p.G161G
XH_P57	11	64359286	64359286	Silent	SNP	C	T	C	SLC22A12	c.C258T	p.H86H
XH_P57	11	64360274	64360274	Silent	SNP	T	C	T	SLC22A12	c.T426C	p.H142H
XH_P57	11	64418900	64418900	Silent	SNP	G	A	G	NRXN2	c.C2625T	p.I875I
XH_P57	11	64572018	64572018	Missense_Mutation	SNP	T	C	T	MEN1	c.A1636G	p.T546A
XH_P57	11	64572602	64572602	Silent	SNP	G	A	G	MEN1	c.C1269T	p.D423D
XH_P57	11	64603753	64603753	Missense_Mutation	SNP	G	A	G	CDC42BPG	c.C1504T	p.R502W
XH_P57	11	64669565	64669565	Missense_Mutation	SNP	C	A	C	ATGTA	c.G3988T	p.V1330F
XH_P57	11	64757254	64757254	Missense_Mutation	SNP	C	T	C	BATF2	c.G100A	p.A34T
XH_P57	11	65064690	65064690	Missense_Mutation	SNP	G	A	G	POLA2	c.G1747A	p.G583R
XH_P57	11	65168281	65168281	Silent	SNP	C	T	C	FRMD8	c.C846T	p.F282F
XH_P57	11	65380916	65380916	Silent	SNP	G	A	G	MAP3K11	c.C312T	p.G104G
XH_P57	11	65408937	65408937	Missense_Mutation	SNP	C	T	C	SIPA1	c.C545T	p.S182F
XH_P57	11	65546857	65546857	Silent	SNP	A	C	A	AP5B1	c.T1107G	p.L369L
XH_P57	11	65547333	65547333	Missense_Mutation	SNP	G	A	G	AP5B1	c.C631T	p.L211F
XH_P57	11	65547455	65547455	Missense_Mutation	SNP	C	A	C	AP5B1	c.G509T	p.G170V
XH_P57	11	65628334	65628334	Missense_Mutation	SNP	G	A	G	MUS81	c.G110A	p.R37H
XH_P57	11	65629932	65629932	Silent	SNP	T	C	T	MUS81	c.T537C	p.A179A
XH_P57	11	65629934	65629934	Missense_Mutation	SNP	G	C	G	MUS81	c.G539C	p.R180P
XH_P57	11	65631167	65631167	Silent	SNP	C	T	C	MUS81	c.C936T	p.A312A
XH_P57	11	65631973	65631973	Silent	SNP	G	A	A	MUS81	c.G1068A	p.R356R
XH_P57	11	65632262	65632262	Silent	SNP	G	T	G	MUS81	c.G1251T	p.T417T
XH_P57	11	65638719	65638719	Silent	SNP	G	A	G	EFEMP2	c.C276T	p.H92H
XH_P57	11	65652436	65652436	Silent	SNP	G	A	G	FIBP	c.C789T	p.G263G
XH_P57	11	65685317	65685317	Silent	SNP	G	A	G	C11orf68	c.C495T	p.H165H
XH_P57	11	65733393	65733393	Silent	SNP	C	T	C	SART1	c.C774T	p.T258T
XH_P57	11	65793797	65793797	Silent	SNP	G	A	G	CATSPER1	c.C54T	p.N18N
XH_P57	11	65826704	65826704	Silent	SNP	G	A	G	SF3B2	c.G1215A	p.K405K
XH_P57	11	66031660	66031660	Silent	SNP	C	T	C	KLCC	c.C855T	p.D285D
XH_P57	11	66062686	66062712	In_Frame_Del	DEL	GGGGGCCGT	-	CGGGGGCCGTG	TMEM151A	c.969_995del	p.323_332del
XH_P57	11	66099987	66099987	Silent	SNP	C	T	C	RIN1	c.G2112A	p.A704A
XH_P57	11	66610645	66610645	Silent	SNP	G	C	G	C11orf80	c.G1476C	p.V492V
XH_P57	11	66626234	66626234	Missense_Mutation	SNP	T	C	T	LRFN4	c.T1019C	p.V340A
XH_P57	11	67220015	67220015	Missense_Mutation	SNP	C	T	C	GPR152	c.G181A	p.G61R
XH_P57	11	68030173	68030173	Missense_Mutation	SNP	C	A	C	C11orf24	c.G290T	p.G97V
XH_P57	11	68115489	68115489	Missense_Mutation	SNP	A	G	A	LRP5	c.A266G	p.Q89R
XH_P57	11	68177510	68177510	Silent	SNP	C	T	C	LRP5	c.C477T	p.N159N
XH_P57	11	68201295	68201295	Missense_Mutation	SNP	C	T	C	LRP5	c.C2246T	p.A749V
XH_P57	11	68204438	68204438	Missense_Mutation	SNP	G	A	G	LRP5	c.G2339A	p.C780Y
XH_P57	11	68671477	68671477	Silent	SNP	T	C	T	IGHMBP2	c.T57C	p.L19L
XH_P57	11	68678962	68678962	Missense_Mutation	SNP	T	C	T	IGHMBP2	c.T602C	p.L201S
XH_P57	11	68704270	68704270	Silent	SNP	A	G	A	IGHMBP2	c.A2322G	p.E774E
XH_P57	11	68816564	68816564	Silent	SNP	A	G	A	TPCN2	c.A99G	p.Q33Q
XH_P57	11	69063184	69063184	Silent	SNP	G	A	G	MYEOV	c.G93A	p.A31A
XH_P57	11	69063572	69063572	Missense_Mutation	SNP	A	G	A	MYEOV	c.A481G	p.M161V
XH_P57	11	70017120	70017120	Silent	SNP	G	A	G	ANO1	c.G2325A	p.P775P
XH_P57	11	71277083	71277083	Silent	SNP	C	T	C	KRTAP5-10	c.C450T	p.C150C
XH_P57	11	71821236	71821236	Silent	SNP	A	G	A	ANAPC15	c.T216C	p.D72D
XH_P57	11	71941212	71941212	Silent	SNP	A	G	A	INPPL1	c.A987G	p.S329S
XH_P57	11	72288599	72288599	Silent	SNP	G	A	G	PDE2A	c.C2634T	p.Y878Y
XH_P57	11	72290629	72290629	Silent	SNP	G	A	G	PDE2A	c.C2184T	p.I78I
XH_P57	11	72410084	72410084	Missense_Mutation	SNP	T	C	T	ARAP1	c.A1589G	p.E530G
XH_P57	11	72415329	72415329	Silent	SNP	G	A	G	ARAP1	c.C1125T	p.N375N
XH_P57	11	74204479	74204496	In_Frame_Del	DEL	GGCAGGCCCA	-	GGCCAGGCCACC	LIPT2	c.253_270del	p.85_90del
XH_P57	11	74324000	74324000	Frame_Shift_Ins	INS	-	AGAG	-	POLD3	337_338insAGA	p.113fs
XH_P57	11	74800149	74800149	Missense_Mutation	SNP	C	T	C	OR2AT4	c.G610A	p.G204S
XH_P57	11	77378008	77378008	Missense_Mutation	SNP	C	G	C	RSF1	c.G4280C	p.R1427T
XH_P57	11	77909004	77909004	Silent	SNP	C	G	C	USP35	c.C696G	p.A232A
XH_P57	11	82880258	82880258	Missense_Mutation	SNP	G	T	G	PCF11	c.G3274T	p.G1092C
XH_P57	11	85445492	85445492	Missense_Mutation	SNP	A	C	A	SYTL2	c.T877G	p.F293V

XH_P57	11	85447611	85447611	Silent	SNP	T	C	T	SYTL2	c.A516G	p.S172S
XH_P57	11	85456703	85456703	Silent	SNP	T	C	T	SYTL2	c.A366G	p.E122E
XH_P57	11	86123467	86123467	Silent	SNP	G	A	G	CCDC81	c.G987A	p.A329A
XH_P57	11	86161388	86161388	Missense_Mutation	SNP	C	G	C	ME3	c.G972C	p.K324N
XH_P57	11	89531540	89531540	Missense_Mutation	SNP	C	T	C	TRIM49	c.G1117A	p.G373R
XH_P57	11	92703105	92703105	Missense_Mutation	SNP	C	T	C	MTNR1B	c.C214T	p.R72W
XH_P57	11	92901249	92901249	Missense_Mutation	SNP	C	G	C	SLC36A4	c.G224C	p.R75T
XH_P57	11	93529655	93529655	Silent	SNP	G	A	G	MED17	c.G1092A	p.P364P
XH_P57	11	93913036	93913036	Missense_Mutation	SNP	A	G	A	PANX1	c.A814G	p.I272V
XH_P57	11	94113466	94113466	Missense_Mutation	SNP	G	T	G	GPR83	c.C995A	p.P332Q
XH_P57	11	94862577	94862577	Missense_Mutation	SNP	G	T	G	ENDOD1	c.G1337T	p.G446V
XH_P57	11	95825371	95825371	Frame_Shift_Del	DEL	C	-	C	MAML2	c.1824delG	p.G608fs
XH_P57	11	95825797	95825797	Silent	SNP	A	G	A	MAML2	c.T1398C	p.S466S
XH_P57	11	101454192	101454192	Missense_Mutation	SNP	G	A	G	TRPC6	c.C43T	p.P15S
XH_P57	11	102201848	102201848	Silent	SNP	G	A	G	BIRC3	c.G1200A	p.Q400Q
XH_P57	11	102272884	102272884	Missense_Mutation	SNP	C	T	C	TMEM123	c.G211A	p.V71M
XH_P57	11	102584104	102584104	Missense_Mutation	SNP	T	G	T	MMP8	c.A1379C	p.K460T
XH_P57	11	102593273	102593273	Silent	SNP	T	G	T	MMP8	c.A234C	p.P78P
XH_P57	11	102595579	102595579	Missense_Mutation	SNP	G	C	G	MMP8	c.C8G	p.S3C
XH_P57	11	102646042	102646042	Nonsense_Mutation	SNP	G	A	G	MMP10	c.C943T	p.R315X
XH_P57	11	102650246	102650246	Silent	SNP	G	A	G	MMP10	c.C336T	p.H112H
XH_P57	11	103027496	103027496	Frame_Shift_Ins	INS	-	AATTCTGCAGGT	-	DYNC2H1	125insAAATTCT	p.F1375fs
XH_P57	11	106849400	106849400	Silent	SNP	G	A	G	GUCY1A2	c.C432T	p.N144N
XH_P57	11	107799426	107799426	Silent	SNP	C	A	C	RAB39A	c.C132A	p.T44T
XH_P57	11	108009660	108009660	Silent	SNP	C	A	C	ACAT1	c.C471A	p.S157S
XH_P57	11	108159732	108159732	Missense_Mutation	SNP	C	T	C	ATM	c.C4138T	p.H1380Y
XH_P57	11	111154904	111154904	Silent	SNP	C	T	C	C11orf53	c.C111T	p.S37S
XH_P57	11	111597762	111597762	Frame_Shift_Del	DEL	C	-	C	PPP2R1B	c.1739delG	p.R580fs
XH_P57	11	113236975	113236975	Missense_Mutation	SNP	G	A	G	TTIC2	c.G2089A	p.G697S
XH_P57	11	113295162	113295162	Frame_Shift_Ins	INS	-	AA	-	DRD2	c.211_212insTT	p.Y71fs
XH_P57	11	117864047	117864047	Silent	SNP	A	G	A	IL10RA	c.A459G	p.A153A
XH_P57	11	117988082	117988082	Silent	SNP	T	C	T	TMPRSS4	c.T1095C	p.S365S
XH_P57	11	118183445	118183445	Silent	SNP	T	C	T	CD3E	c.T216C	p.D72D
XH_P57	11	118405068	118405068	Missense_Mutation	SNP	A	G	A	TMEM25	c.A581G	p.Q194R
XH_P57	11	118406329	118406336	Frame_Shift_Del	DEL	AGTGTGGA	-	AGTGTGGA	TMEM25	c.1131_1138de	p.T377fs
XH_P57	11	118430519	118430519	Missense_Mutation	SNP	C	T	C	IFT46	c.G26A	p.C9Y
XH_P57	11	118471423	118471423	Silent	SNP	T	C	T	ARCN1	c.T1266C	p.I422I
XH_P57	11	118498080	118498080	Frame_Shift_Ins	INS	-	C	-	PHLDB1	c.542dupC	p.S181fs
XH_P57	11	118773071	118773071	Missense_Mutation	SNP	C	T	C	BCL9L	c.G1381A	p.G461R
XH_P57	11	119050896	119050896	Silent	SNP	C	T	C	NLRX1	c.C2166T	p.S722S
XH_P57	11	119216504	119216504	Missense_Mutation	SNP	C	T	C	MFRP	c.G406A	p.V136M
XH_P57	11	119229964	119229964	Silent	SNP	G	A	G	USP2	c.C309T	p.Y103Y
XH_P57	11	120823608	120823608	Silent	SNP	G	A	G	GRIK4	c.G1635A	p.P545P
XH_P57	11	120989335	120989335	Missense_Mutation	SNP	A	G	A	TECTA	c.A1111G	p.R371G
XH_P57	11	121000774	121000774	Missense_Mutation	SNP	T	C	T	TECTA	c.T2795C	p.V932A
XH_P57	11	121393684	121393684	Missense_Mutation	SNP	G	A	G	SORL1	c.G1582A	p.A528T
XH_P57	11	121498338	121498338	Missense_Mutation	SNP	A	C	A	SORL1	c.A6439C	p.I2147L
XH_P57	11	122671963	122671963	Silent	SNP	T	A	T	UBASH3B	c.T1518A	p.V506V
XH_P57	11	122795688	122795688	Silent	SNP	T	C	T	C11orf63	c.T948C	p.D316D
XH_P57	11	122953804	122953804	Frame_Shift_Del	DEL	A	-	A	CLMP	c.668delT	p.V223fs
XH_P57	11	123813823	123813823	Silent	SNP	G	A	G	OR6T1	c.C723T	p.C241C
XH_P57	11	123813940	123813940	Silent	SNP	G	C	G	OR6T1	c.C606G	p.L202L
XH_P57	11	123814489	123814489	Silent	SNP	A	G	A	OR6T1	c.T57C	p.S19S
XH_P57	11	123886307	123886307	Missense_Mutation	SNP	C	T	C	OR10G4	c.C26T	p.A9V
XH_P57	11	124095414	124095414	Missense_Mutation	SNP	C	G	C	OR8G2P	c.C17G	p.S6C
XH_P57	11	124095525	124095525	Missense_Mutation	SNP	T	C	T	OR8G2P	c.T128C	p.L43P
XH_P57	11	124095647	124095647	Missense_Mutation	SNP	A	C	A	OR8G2P	c.A250C	p.I84L
XH_P57	11	124096247	124096247	Missense_Mutation	SNP	G	A	G	OR8G2P	c.G850A	p.G284R
XH_P57	11	124310752	124310752	Missense_Mutation	SNP	A	T	A	OR8B8	c.T230A	p.I77N
XH_P57	11	124749777	124749777	Silent	SNP	G	A	G	ROBO3	c.G3891A	p.E1297E
XH_P57	11	124794712	124794712	Silent	SNP	C	T	C	HEPACAM	c.G339A	p.Q113Q
XH_P57	11	124857708	124857708	Missense_Mutation	SNP	G	A	G	CCDC15	c.G1586A	p.G529D
XH_P57	11	124955032	124955032	Silent	SNP	T	C	T	SLC37A2	c.T1245C	p.D415D
XH_P57	11	125831701	125831701	Silent	SNP	G	A	G	CDON	c.C3549T	p.V1183V
XH_P57	11	125848261	125848261	Silent	SNP	C	T	C	CDON	c.G3294A	p.T1098T
XH_P57	11	126277216	126277216	Silent	SNP	C	T	C	ST3GAL4	c.C249T	p.Y83Y
XH_P57	11	126278075	126278075	Silent	SNP	C	T	C	ST3GAL4	c.C420T	p.Y140Y
XH_P57	11	128675292	128675292	Silent	SNP	T	A	T	FLI1	c.T108A	p.A36A
XH_P57	11	129794950	129794950	Missense_Mutation	SNP	T	C	T	PRDM10	c.A1447G	p.T483A
XH_P57	11	129802018	129802018	Silent	SNP	T	C	T	PRDM10	c.A1008G	p.E336E
XH_P57	11	129817221	129817221	Silent	SNP	A	G	A	PRDM10	c.T81C	p.S27S
XH_P57	11	130297748	130297748	Missense_Mutation	SNP	G	C	G	ADAMTS8	c.C434G	p.A145G
XH_P57	11	130319732	130319732	Silent	SNP	G	T	G	ADAMTS15	c.G864T	p.T288T
XH_P57	11	134226278	134226278	Silent	SNP	C	T	C	GLB1L2	c.C642T	p.Y214Y
XH_P57	12	427575	427575	Missense_Mutation	SNP	A	G	A	KDMA5A	c.T2594C	p.M865T
XH_P57	12	644337	644337	Missense_Mutation	SNP	G	A	G	B4GALNT3	c.G175A	p.G59S
XH_P57	12	657404	657404	Missense_Mutation	SNP	G	A	G	B4GALNT3	c.G794A	p.R265Q
XH_P57	12	662838	662838	Silent	SNP	T	C	T	B4GALNT3	c.T1749C	p.P583P
XH_P57	12	939302	939302	Silent	SNP	A	G	A	WNK1	c.A1287G	p.A429A
XH_P57	12	993930	993930	Silent	SNP	C	T	C	WNK1	c.C3219T	p.N1073N
XH_P57	12	1192664	1192664	Missense_Mutation	SNP	G	A	G	ERC1	c.G1004A	p.R335Q
XH_P57	12	1887056	1887056	In_Frame_Ins	INS	-	TAC	-	ADIPOR2	328_329insTAA	p.V110delinsVL
XH_P57	12	1893170	1893170	Silent	SNP	C	T	C	ADIPOR2	c.C963T	p.Y321Y
XH_P57	12	4479549	4479549	Missense_Mutation	SNP	G	A	G	FGF23	c.C716T	p.T239M
XH_P57	12	4705317	4705317	Silent	SNP	C	T	C	DYRK4	c.C285T	p.V95V
XH_P57	12	4735737	4735737	Silent	SNP	A	G	A	AKAP3	c.T2331C	p.L777L
XH_P57	12	4791379	4791379	Missense_Mutation	SNP	G	A	G	NDUFA9	c.G809A	p.R270Q
XH_P57	12	4919267	4919267	Silent	SNP	A	G	A	KCNA6	c.A60G	p.G20G
XH_P57	12	5021840	5021840	Silent	SNP	C	G	C	KCNA1	c.C1296G	p.S432S
XH_P57	12	5853474	5853474	Missense_Mutation	SNP	C	T	C	ANO2	c.G1203A	p.M401I
XH_P57	12	6030405	6030405	Missense_Mutation	SNP	A	G	A	ANO2	c.T335C	p.V112A
XH_P57	12	6030437	6030437	Silent	SNP	A	G	A	ANO2	c.T303C	p.Y101Y
XH_P57	12	6128443	6128443	Missense_Mutation	SNP	T	C	T	VWF	c.A4141G	p.T1381A
XH_P57	12	6639009	6639009	Missense_Mutation	SNP	G	A	G	NCAPD2	c.G3722A	p.R1241H
XH_P57	12	6639981	6639981	Missense_Mutation	SNP	C	G	C	NCAPD2	c.C3962G	p.T1321S
XH_P57	12	6646320	6646320	Silent	SNP	T	C	T	GAPDH	c.T255C	p.D85D
XH_P57	12	6647109	6647109	Silent	SNP	T	C	T	GAPDH	c.T759C	p.F253F
XH_P57	12	6933223	6933223	Silent	SNP	C	T	C	GPR162	c.C159T	p.C53C

XH_P57	12	7249598	7249598	Missense_Mutation	SNP	T	C	T	C1RL	c.A727G	p.I243V
XH_P57	12	7254669	7254669	Silent	SNP	A	C	A	C1RL	c.T315G	p.G105G
XH_P57	12	7280880	7280880	Missense_Mutation	SNP	C	G	C	RBP5	c.G208C	p.E70Q
XH_P57	12	7287956	7287956	Silent	SNP	C	T	C	CLSTN3	c.C417T	p.N139N
XH_P57	12	7649653	7649653	Silent	SNP	T	C	T	CD163	c.A855G	p.G285G
XH_P57	12	7867847	7867847	Missense_Mutation	SNP	G	C	G	DPPA3	c.G151C	p.E51Q
XH_P57	12	7966975	7966975	Silent	SNP	C	T	C	SLC2A14	c.G1173A	p.G391G
XH_P57	12	8192590	8192590	Silent	SNP	G	C	G	FOXJ2	c.G162C	p.L54L
XH_P57	12	9010671	9010671	Silent	SNP	G	A	G	A2ML1	c.G1764A	p.V588V
XH_P57	12	11149629	11149629	Silent	SNP	C	T	C	TAS2R20	c.G846A	p.G282G
XH_P57	12	11150054	11150054	Missense_Mutation	SNP	C	T	C	TAS2R20	c.G421A	p.V141I
XH_P57	12	12022389	12022389	Silent	SNP	C	T	C	ETV6	c.C495T	p.S165S
XH_P57	12	12334098	12334098	Missense_Mutation	SNP	A	G	A	LRP6	c.T1252C	p.Y418H
XH_P57	12	12483134	12483134	Missense_Mutation	SNP	T	A	T	MANSC1	c.A1123T	p.N375Y
XH_P57	12	12618690	12618690	Missense_Mutation	SNP	G	A	G	BORCS5	c.G427A	p.D143N
XH_P57	12	12815145	12815145	Missense_Mutation	SNP	T	C	T	GPR19	c.A238G	p.I80V
XH_P57	12	14587301	14587301	Missense_Mutation	SNP	A	G	A	ATF7IP	c.A1586G	p.K529R
XH_P57	12	14849295	14849295	Missense_Mutation	SNP	A	G	A	GUCY2C	c.T88C	p.C30R
XH_P57	12	15819385	15819385	Silent	SNP	G	A	G	EP58	c.C588T	p.P196P
XH_P57	12	21011481	21011481	Missense_Mutation	SNP	C	A	C	SLCO1B3	c.C251A	p.S84Y
XH_P57	12	22627735	22627735	Missense_Mutation	SNP	C	T	C	C2CD5	c.G1993A	p.V665I
XH_P57	12	25311489	25311489	Missense_Mutation	SNP	G	T	G	CASC1	c.C97A	p.R33S
XH_P57	12	26383811	26383811	Silent	SNP	C	T	C	SSPN	c.C225T	p.Y75Y
XH_P57	12	31820716	31820716	Missense_Mutation	SNP	A	T	A	ETFBKMT	c.A581T	p.D194V
XH_P57	12	39695445	39695445	Silent	SNP	G	A	G	KIF21A	c.C4657T	p.L1553L
XH_P57	12	39698641	39698641	Silent	SNP	G	C	G	KIF21A	c.C4431G	p.S1477S
XH_P57	12	41966306	41966306	Silent	SNP	G	A	G	PDZRN4	c.G951A	p.E317E
XH_P57	12	43769228	43769228	Silent	SNP	A	C	A	ADAMTS20	c.T5400G	p.T1800T
XH_P57	12	43769276	43769276	Silent	SNP	T	C	T	ADAMTS20	c.A5352G	p.R1784R
XH_P57	12	43833739	43833739	Silent	SNP	A	G	A	ADAMTS20	c.T2424C	p.I808I
XH_P57	12	46758923	46758923	Frame_Shift_Del	DEL	C	-	C	SLC38A2	c.313delG	p.V105fs
XH_P57	12	47186770	47186770	Missense_Mutation	SNP	C	T	C	SLC38A4	c.G85A	p.G29R
XH_P57	12	47471439	47471439	Silent	SNP	G	A	G	AMIGO2	c.C1347T	p.P449P
XH_P57	12	48376291	48376291	Silent	SNP	G	A	G	COL2A1	c.C2088T	p.G696G
XH_P57	12	48963021	48963021	Missense_Mutation	SNP	T	C	T	LALBA	c.A136G	p.I46V
XH_P57	12	49221622	49221622	Silent	SNP	G	A	G	CACNB3	c.G1272A	p.E424E
XH_P57	12	49230035	49230035	Silent	SNP	T	G	T	DDX23	c.A1251C	p.I417I
XH_P57	12	49360028	49360046	Frame_Shift_Del	DEL	GGCTGGTCTT	-	SCGGCTGGTCTT	WNT10B	c.1002_1020del	p.C334fs
XH_P57	12	49390677	49390677	Missense_Mutation	SNP	T	C	T	DDN	c.A1982G	p.E661G
XH_P57	12	49689335	49689335	Missense_Mutation	SNP	C	A	C	PRPH	c.C352A	p.L118M
XH_P57	12	49951232	49951232	Silent	SNP	T	C	T	KCNH3	c.T2568C	p.G856G
XH_P57	12	49952668	49952668	Silent	SNP	G	A	G	MCRS1	c.C687T	p.L29L
XH_P57	12	49993678	49993678	Missense_Mutation	SNP	C	T	C	FAM186B	c.G1745A	p.R582Q
XH_P57	12	50037745	50037745	Silent	SNP	G	A	G	PRPF40B	c.G2442A	p.E814E
XH_P57	12	50749554	50749554	Missense_Mutation	SNP	G	T	G	FAM186A	c.C1061A	p.P354H
XH_P57	12	51089734	51089734	Silent	SNP	T	A	T	DIP2B	c.T1917A	p.T639T
XH_P57	12	51236802	51236802	Missense_Mutation	SNP	T	C	T	TMPPRSS12	c.T55C	p.Y19H
XH_P57	12	51639824	51639826	In_Frame_Del	DEL	GCT	-	GCT	SMAGP	c.193_195del	p.65_65del
XH_P57	12	51733734	51733734	Silent	SNP	G	A	G	CELA1	c.C519T	p.Y173Y
XH_P57	12	51737607	51737607	Missense_Mutation	SNP	G	A	G	CELA1	c.C130T	p.R44W
XH_P57	12	51773557	51773557	Silent	SNP	G	A	G	GALNT6	c.C9T	p.L3L
XH_P57	12	51863437	51863437	Silent	SNP	C	G	C	SLC4A8	c.C1389G	p.A463A
XH_P57	12	51883711	51883711	Frame_Shift_Ins	INS	-	CATGT	-	SLC4A8	576_2677insCA	p.S892fs
XH_P57	12	52452659	52452659	Silent	SNP	C	G	C	NR4A1	c.C1728G	p.L576L
XH_P57	12	52642518	52642518	Missense_Mutation	SNP	G	A	G	KRT7	c.G1384A	p.A462T
XH_P57	12	52938320	52938320	Missense_Mutation	SNP	C	T	C	KRT71	c.G1568A	p.R523Q
XH_P57	12	52981442	52981442	Missense_Mutation	SNP	C	A	C	KRT72	c.G1157T	p.R386L
XH_P57	12	52984620	52984620	Silent	SNP	C	T	C	KRT72	c.G1089A	p.Q363Q
XH_P57	12	53007492	53007492	Missense_Mutation	SNP	C	T	C	KRT73	c.G964A	p.E322K
XH_P57	12	53069223	53069243	In_Frame_Del	DEL	GGAGCCGTA	-	CGGAGCCGTA	KRT1	c.1669_1689del	p.557_563del
XH_P57	12	53070145	53070145	Silent	SNP	G	A	G	KRT1	c.C1389T	p.R463R
XH_P57	12	53086645	53086645	Missense_Mutation	SNP	G	A	G	KRT77	c.C1100T	p.T1367M
XH_P57	12	53090190	53090190	Silent	SNP	C	T	C	KRT77	c.G783A	p.R261R
XH_P57	12	53091566	53091566	Missense_Mutation	SNP	C	A	C	KRT77	c.G658T	p.G220C
XH_P57	12	53186088	53186088	Missense_Mutation	SNP	G	C	G	KRT3	c.C1123G	p.R375G
XH_P57	12	54115875	54115875	Silent	SNP	C	T	C	CALCOCO1	c.G444A	p.V148V
XH_P57	12	54379670	54379670	Silent	SNP	C	T	C	HOXC10	c.C627T	p.P209P
XH_P57	12	54970454	54970454	Silent	SNP	T	C	T	PDE1B	c.T864C	p.N288N
XH_P57	12	55420747	55420747	Frame_Shift_Ins	INS	-	GG	-	NEUROD4	c.524_525insGG	p.Q175fs
XH_P57	12	55688895	55688895	Missense_Mutation	SNP	A	G	A	OR6C6	c.T122C	p.L41S
XH_P57	12	56030938	56030938	Missense_Mutation	SNP	C	T	C	OR10P1	c.C263T	p.P88L
XH_P57	12	56031273	56031273	Missense_Mutation	SNP	G	A	G	OR10P1	c.G598A	p.V200M
XH_P57	12	56295707	56295707	Silent	SNP	T	C	T	PYM1	c.A561G	p.A187A
XH_P57	12	57039080	57039080	Missense_Mutation	SNP	C	T	C	ATP5B	c.G185A	p.R62H
XH_P57	12	57324068	57324068	Missense_Mutation	SNP	T	C	T	SDR9C7	c.A502G	p.I168V
XH_P57	12	57496678	57496678	Silent	SNP	G	A	G	STAT6	c.C909T	p.I303I
XH_P57	12	57577265	57577265	Silent	SNP	G	A	G	LRP1	c.G5766A	p.S1922S
XH_P57	12	57649840	57649840	Silent	SNP	C	T	C	R3HDM2	c.G2469A	p.K823K
XH_P57	12	57859431	57859431	Silent	SNP	G	A	G	GLI1	c.G192A	p.E64E
XH_P57	12	57865321	57865321	Missense_Mutation	SNP	G	A	G	GLI1	c.G2414A	p.G805D
XH_P57	12	57865821	57865821	Missense_Mutation	SNP	G	C	G	GLI1	c.G2914C	p.E972Q
XH_P57	12	57870155	57870155	Missense_Mutation	SNP	A	C	A	ARHGAP9	c.T118G	p.S40A
XH_P57	12	57985204	57985204	Silent	SNP	C	T	C	PIP4K2C	c.C132T	p.A44A
XH_P57	12	58126234	58126234	Silent	SNP	C	A	C	AGAP2	c.G1746T	p.L582L
XH_P57	12	59270333	59270333	Silent	SNP	C	T	C	LRIG3	c.G2409A	p.T803T
XH_P57	12	59274546	59274546	Nonsense_Mutation	INS	-	GTGGACCATCTA	-	LRIG3	SATATTATTAGATGp.L480delinsDIX	
XH_P57	12	64519806	64519806	Silent	SNP	T	C	T	SRGAP1	c.T2205C	p.S735S
XH_P57	12	64536245	64536245	Silent	SNP	C	T	C	SRGAP1	c.C2982T	p.L994L
XH_P57	12	64712546	64712546	In_Frame_Ins	INS	-	GTT	-	C12orf56	c.702_703insAAp.S235delinsNS	
XH_P57	12	64827294	64827294	Missense_Mutation	SNP	C	T	C	XPOT	c.C2363T	p.A788V
XH_P57	12	65269548	65269548	Missense_Mutation	SNP	A	C	A	TBC1D30	c.A2194C	p.S732R
XH_P57	12	66725160	66725160	Missense_Mutation	SNP	C	T	C	HELB	c.C2897T	p.P966L
XH_P57	12	67700025	67700025	Silent	SNP	T	C	T	CAND1	c.T2577C	p.S859S
XH_P57	12	70037520	70037520	Missense_Mutation	SNP	G	A	G	BEST3	c.C1148T	p.P383L
XH_P57	12	71523134	71523134	Missense_Mutation	SNP	A	C	A	TSPAN8	c.T637G	p.S213A
XH_P57	12	75785100	75785100	Silent	SNP	C	T	C	GLIPR1L2	c.C204T	p.V68V
XH_P57	12	80747209	80747209	Missense_Mutation	SNP	C	G	C	OTOGL	c.C5485G	p.L1829V
XH_P57	12	80761411	80761411	Missense_Mutation	SNP	G	T	G	OTOGL	c.G6375T	p.L1215T

XH_P57	12	88500631	88500631	Missense_Mutation	SNP	C	A	C	CEP290	c.G2638T	p.A880S
XH_P57	12	91502250	91502250	Silent	SNP	A	G	A	LUM	c.T507C	p.N169N
XH_P57	12	94673277	94673277	Silent	SNP	G	A	G	PLXNC1	c.G3627A	p.P1209P
XH_P57	12	94761701	94761701	Silent	SNP	T	C	T	CEP83	c.A1212G	p.R404R
XH_P57	12	94976159	94976159	Silent	SNP	T	C	T	TMCC3	c.A141G	p.V47V
XH_P57	12	96292170	96292170	Missense_Mutation	SNP	C	G	C	CCDC38	c.G607C	p.V203L
XH_P57	12	96641003	96641003	Missense_Mutation	SNP	A	G	A	ELK3	c.A493G	p.K165E
XH_P57	12	97157933	97157933	Missense_Mutation	SNP	C	A	C	CFAP54	c.C8045A	p.P2682H
XH_P57	12	97186242	97186242	Missense_Mutation	SNP	C	A	C	CFAP54	c.C8815A	p.P2939T
XH_P57	12	99007623	99007623	Missense_Mutation	SNP	C	T	C	IKBIP	c.G793A	p.G265S
XH_P57	12	100751196	100751196	Silent	SNP	C	T	C	SLC17A8	c.C27T	p.F9F
XH_P57	12	101603396	101603396	Missense_Mutation	SNP	C	A	C	SLCSA8	c.G231T	p.E77D
XH_P57	12	102517804	102517804	Silent	SNP	G	A	G	PARPBP	c.G138A	p.A46A
XH_P57	12	102545563	102545563	Silent	SNP	A	G	A	PARPBP	c.A603G	p.A201A
XH_P57	12	103696182	103696182	Missense_Mutation	SNP	T	G	T	C12orf42	c.A787C	p.S263R
XH_P57	12	104100617	104100617	Silent	SNP	C	T	C	STAB2	c.C4044T	p.C1348C
XH_P57	12	104136316	104136316	Silent	SNP	C	T	C	STAB2	c.C6015T	p.F2005F
XH_P57	12	105589101	105589101	Silent	SNP	G	A	G	APPL2	c.C1197T	p.T399T
XH_P57	12	107937768	107937768	Missense_Mutation	SNP	G	A	G	BTBD11	c.G1342A	p.G448S
XH_P57	12	108618630	108618630	Missense_Mutation	SNP	C	T	C	WSCD2	c.C797T	p.T266I
XH_P57	12	108954862	108954862	Missense_Mutation	SNP	G	C	G	SART3	c.C69G	p.D23E
XH_P57	12	108986112	108986112	Silent	SNP	G	C	G	TMEM119	c.C48G	p.L16L
XH_P57	12	109605730	109605730	Silent	SNP	C	T	C	ACACB	c.C816T	p.A272A
XH_P57	12	109623516	109623516	Missense_Mutation	SNP	G	A	G	ACACB	c.G1951A	p.A651T
XH_P57	12	110226379	110226379	Silent	SNP	G	A	G	TRPV4	c.C1713T	p.Y171I
XH_P57	12	110238481	110238481	Silent	SNP	G	A	G	TRPV4	c.C795T	p.H265H
XH_P57	12	111160003	111160003	Silent	SNP	G	A	G	PPP1CC	c.C819T	p.C273C
XH_P57	12	114374887	114374887	Missense_Mutation	SNP	T	C	T	RBM19	c.A1993G	p.T665A
XH_P57	12	114386639	114386639	Silent	SNP	A	G	A	RBM19	c.T1275C	p.Y425Y
XH_P57	12	114395651	114395651	Missense_Mutation	SNP	T	C	C	RBM19	c.A776G	p.K259R
XH_P57	12	117993064	117993064	Silent	SNP	C	T	C	KSR2	c.G1341A	p.P447P
XH_P57	12	118020115	118020115	Silent	SNP	G	A	G	KSR2	c.C1134T	p.L378L
XH_P57	12	118506186	118506186	Silent	SNP	A	T	A	VSLG10	c.T1563A	p.L521L
XH_P57	12	120171995	120171995	Silent	SNP	T	C	T	CIT	c.A3198G	p.R1066R
XH_P57	12	120589064	120589064	Silent	SNP	G	C	G	GCN1	c.C4194G	p.A1398A
XH_P57	12	120591143	120591143	Silent	SNP	A	G	A	GCN1	c.T3936C	p.Y1312Y
XH_P57	12	120608031	120608031	Silent	SNP	A	G	A	GCN1	c.T1461C	p.T487T
XH_P57	12	121176083	121176083	Missense_Mutation	SNP	G	A	G	ACADS	c.G625A	p.G209S
XH_P57	12	121600253	121600253	Missense_Mutation	SNP	T	C	T	P2RX7	c.T463C	p.Y155H
XH_P57	12	121622239	121622239	Silent	SNP	C	T	C	P2RX7	c.C1422T	p.P474P
XH_P57	12	121666646	121666646	Missense_Mutation	SNP	A	G	A	P2RX4	c.A643G	p.S215G
XH_P57	12	121691096	121691096	Missense_Mutation	SNP	G	A	G	CAMKK2	c.C1087T	p.R363C
XH_P57	12	121701681	121701681	Silent	SNP	G	A	G	CAMKK2	c.C687T	p.C229P
XH_P57	12	121712077	121712077	Missense_Mutation	SNP	T	A	T	CAMKK2	c.A253T	p.T85S
XH_P57	12	122079295	122079295	Missense_Mutation	SNP	A	G	A	ORAI1	c.A658G	p.S220G
XH_P57	12	122186268	122186268	Silent	SNP	C	T	C	TMEM120B	c.C225T	p.L75L
XH_P57	12	122186317	122186317	Missense_Mutation	SNP	G	A	G	TMEM120B	c.G274A	p.D92N
XH_P57	12	122217457	122217457	Missense_Mutation	SNP	C	T	C	RHOF	c.G583A	p.A195T
XH_P57	12	122217559	122217559	Missense_Mutation	SNP	C	T	C	RHOF	c.G481A	p.A161T
XH_P57	12	122246136	122246136	Silent	SNP	T	C	T	SETD1B	c.T567C	p.Y189Y
XH_P57	12	122247853	122247853	Silent	SNP	C	T	C	SETD1B	c.C1002T	p.P334P
XH_P57	12	122257461	122257461	Silent	SNP	G	A	G	SETD1B	c.G3441A	p.E1147E
XH_P57	12	122261456	122261456	Silent	SNP	G	A	G	SETD1B	c.G4842A	p.A1614A
XH_P57	12	122277891	122277891	Missense_Mutation	SNP	C	A	C	HPD	c.G1018T	p.V340L
XH_P57	12	123470790	123470790	Silent	SNP	G	A	G	PITPNM2	c.C3816T	p.F1272F
XH_P57	12	124826462	124826462	Missense_Mutation	SNP	C	T	C	NCOR2	c.G5065A	p.A1689T
XH_P57	12	124979789	124979789	Silent	SNP	T	G	T	NCOR2	c.A9C	p.G3G
XH_P57	12	125396893	125396893	Silent	SNP	C	G	C	UBC	c.G1425C	p.P475P
XH_P57	12	125397553	125397553	Silent	SNP	T	C	T	UBC	c.A765G	p.K255K
XH_P57	12	125834095	125834095	Silent	SNP	C	A	C	TMEM132B	c.C150A	p.S50S
XH_P57	12	125834395	125834395	Silent	SNP	T	C	T	TMEM132B	c.T450C	p.S150S
XH_P57	12	125900095	125900095	Silent	SNP	T	A	T	TMEM132B	c.T963A	p.G321G
XH_P57	12	126137060	126137060	Missense_Mutation	SNP	C	T	C	TMEM132B	c.C509T	p.A170V
XH_P57	12	129153986	129153986	Missense_Mutation	SNP	G	A	G	TMEM132C	c.G1330A	p.V444I
XH_P57	12	129558926	129558926	Silent	SNP	A	G	A	TMEM132D	c.T2794C	p.L932L
XH_P57	12	129559557	129559557	Silent	SNP	C	T	C	TMEM132D	c.G2163A	p.T721T
XH_P57	12	130941150	130941150	Silent	SNP	G	C	G	RIMBP2	c.C198G	p.G66G
XH_P57	12	132624262	132624262	Missense_Mutation	SNP	C	T	C	DDX51	c.G1892A	p.R631Q
XH_P57	12	132635581	132635581	Silent	SNP	C	T	C	NOC4L	c.C957T	p.H319H
XH_P57	12	132636155	132636155	Silent	SNP	C	T	C	NOC4L	c.C1200T	p.A400A
XH_P57	12	133244162	133244162	Missense_Mutation	SNP	C	T	C	POLE	c.G2246A	p.R749Q
XH_P57	12	133354366	133354366	Missense_Mutation	SNP	C	T	C	GOLGA3	c.G3608A	p.G1203E
XH_P57	13	20221394	20221394	Frame_Shift_Ins	INS	-	AG	-	MPHOSPH8	1181_1182insA	p.E394fs
XH_P57	13	23929842	23929842	Silent	SNP	T	C	T	SACS	c.A468G	p.A156A
XH_P57	13	24465585	24465585	Missense_Mutation	SNP	C	T	C	C1QTNF9B	c.G845A	p.S282N
XH_P57	13	24895437	24895437	Missense_Mutation	SNP	G	A	G	C1QTNF9	c.G533A	p.R178Q
XH_P57	13	25356053	25356053	Silent	SNP	T	C	T	RNF17	c.T582C	p.F194F
XH_P57	13	25367301	25367301	Silent	SNP	C	T	C	RNF17	c.C1057T	p.L353L
XH_P57	13	25670813	25670813	Silent	SNP	C	T	C	PABPC3	c.C477T	p.N159N
XH_P57	13	25670988	25670988	Missense_Mutation	SNP	T	A	T	PABPC3	c.T652A	p.L218I
XH_P57	13	27845134	27845134	Missense_Mutation	SNP	C	A	C	RASL11A	c.C53A	p.S18Y
XH_P57	13	28143229	28143229	Missense_Mutation	SNP	A	G	A	LNK2	c.T592C	p.S198P
XH_P57	13	28674628	28674628	Missense_Mutation	SNP	T	C	T	FLT3	c.A20G	p.D7G
XH_P57	13	29599410	29599410	Missense_Mutation	SNP	C	T	C	MTUS2	c.C605T	p.P202L
XH_P57	13	32360583	32360583	Silent	SNP	A	G	A	RXFP2	c.A921G	p.L307L
XH_P57	13	32371361	32371361	Missense_Mutation	SNP	A	G	A	RXFP2	c.A1738G	p.I580V
XH_P57	13	32676114	32676114	Silent	SNP	A	G	A	FRY	c.A285G	p.T95T
XH_P57	13	32760476	32760476	Silent	SNP	C	A	C	FRY	c.C3399A	p.P1133P
XH_P57	13	32885658	32885658	Silent	SNP	G	A	G	ZAR1L	c.C405T	p.P135P
XH_P57	13	32912299	32912299	Silent	SNP	T	C	T	BRCA2	c.T3807C	p.V1269V
XH_P57	13	33591089	33591089	Missense_Mutation	SNP	C	A	C	KL	c.C511A	p.R171S
XH_P57	13	33634983	33634983	Silent	SNP	C	T	C	KL	c.C1767T	p.H589H
XH_P57	13	33700374	33700374	Silent	SNP	T	G	T	STARD13	c.A1902C	p.S634S
XH_P57	13	33704065	33704065	Missense_Mutation	SNP	T	C	T	STARD13	c.A725G	p.K242R
XH_P57	13	36686138	36686138	Silent	SNP	T	C	T	DCLK1	c.A591G	p.P197P
XH_P57	13	37401827	37401827	Silent	SNP	A	G	A	RFXAP	c.A756G	p.Q252Q
XH_P57	13	37678704	37678704	Missense_Mutation	SNP	T	A	T	CSNK1A1L	c.A690T	p.K230N
XH_P57	13	39343822	39343822	Missense_Mutation	SNP	C	T	C	FREM2	c.C5518T	p.R1840W

XH_P57	13	39546671	39546671	Frame_Shift_Ins	INS	-	TAAC	-	STOML3	289_290insGTT	p.T97fs
XH_P57	13	39586343	39586343	Silent	SNP	G	C	G	PROSER1	c.C2589G	p.G863G
XH_P57	13	39587166	39587166	Silent	SNP	A	G	A	PROSER1	c.T2223C	p.P741P
XH_P57	13	39587677	39587677	Missense_Mutation	SNP	A	G	A	PROSER1	c.T1712C	p.V571A
XH_P57	13	39587865	39587865	Silent	SNP	A	C	A	PROSER1	c.T1524G	p.S508S
XH_P57	13	39587889	39587889	Silent	SNP	T	C	T	PROSER1	c.A1500G	p.L500L
XH_P57	13	41705921	41705921	Missense_Mutation	SNP	C	T	C	KBTBD6	c.G727A	p.A243T
XH_P57	13	42772717	42772717	Silent	SNP	G	T	G	DGKH	c.G1536T	p.P512P
XH_P57	13	44457925	44457925	Missense_Mutation	SNP	A	G	A	LACC1	c.A760G	p.I254V
XH_P57	13	45914196	45914196	Frame_Shift_Ins	INS	-	CATC	-	TP1	123_124insGAT	p.H42fs
XH_P57	13	46067593	46067593	Silent	SNP	G	A	G	COG3	c.G1299A	p.E433E
XH_P57	13	46115731	46115731	Missense_Mutation	SNP	C	A	C	ERICH6B	c.G1957T	p.V653F
XH_P57	13	46170621	46170621	Missense_Mutation	SNP	A	T	A	ERICH6B	c.T520A	p.S174T
XH_P57	13	46539401	46539414	Splice_Site	DEL	SCAAATAGT	-	TGCAAAATAGTTA	ZC3H13	-	-
XH_P57	13	49089344	49089344	Missense_Mutation	SNP	T	C	T	RCBTB2	c.A274G	p.T92A
XH_P57	13	49795277	49795277	Silent	SNP	G	A	G	MLNR	c.G804A	p.G268G
XH_P57	13	50057633	50057633	Silent	SNP	A	G	A	SETDB2	c.A1416G	p.Q472Q
XH_P57	13	51417656	51417656	Missense_Mutation	SNP	G	C	G	DLEU7	c.C127G	p.P43A
XH_P57	13	51948392	51948392	Missense_Mutation	SNP	T	C	T	INT56	c.A2056G	p.T686A
XH_P57	13	52603241	52603241	Missense_Mutation	SNP	A	G	A	UTP14C	c.A301G	p.T101A
XH_P57	13	53217035	53217035	Silent	SNP	C	A	C	HNRNPA1L2	c.C408A	p.I136I
XH_P57	13	53217270	53217270	Missense_Mutation	SNP	A	G	A	HNRNPA1L2	c.A643G	p.N215D
XH_P57	13	76055602	76055602	Missense_Mutation	SNP	G	A	G	TBC1D4	c.C302T	p.A101V
XH_P57	13	76423248	76423248	Missense_Mutation	SNP	T	C	T	LMO7	c.T3485C	p.M1162T
XH_P57	13	77531774	77531774	Missense_Mutation	SNP	G	A	G	ACOD1	c.G1088A	p.S363N
XH_P57	13	77566158	77566158	Silent	SNP	A	G	A	CLN5	c.A72G	p.G24G
XH_P57	13	77751892	77751892	Silent	SNP	C	T	T	MYCBP2	c.G5331A	p.L1777L
XH_P57	13	77780857	77780857	Nonsense_Mutation	INS	-	TTTTTATAGAGTA	-	MYCBP2	ntAAAAATACTC	p.P1174delinsX
XH_P57	13	77780859	77780859	Missense_Mutation	SNP	C	T	C	MYCBP2	c.G3518A	p.S1173N
XH_P57	13	78236177	78236177	Silent	SNP	T	C	T	LOC100129307	c.A585G	p.G195G
XH_P57	13	95034749	95034749	Missense_Mutation	SNP	G	A	G	GPC6	c.G1234A	p.V412M
XH_P57	13	99948178	99948178	Silent	SNP	C	A	C	GPR183	c.G222T	p.V74V
XH_P57	13	102106276	102106276	Silent	SNP	G	C	G	ITGB1	c.G141C	p.S47S
XH_P57	13	103396716	103396716	Missense_Mutation	SNP	C	G	C	CCDC168	c.G6331C	p.E2111Q
XH_P57	13	103397583	103397583	Missense_Mutation	SNP	C	G	C	CCDC168	c.G5464C	p.A1822P
XH_P57	13	103400083	103400083	Silent	SNP	G	A	G	CCDC168	c.C2964T	p.S988S
XH_P57	13	103400729	103400729	Missense_Mutation	SNP	G	A	G	CCDC168	c.C2318T	p.P773L
XH_P57	13	103402522	103402522	Silent	SNP	C	T	C	CCDC168	c.G525A	p.T175T
XH_P57	13	109661359	109661359	Missense_Mutation	SNP	C	G	C	MYO16	c.C2557G	p.P853A
XH_P57	13	110435231	110435231	Missense_Mutation	SNP	C	T	C	IRS2	c.G3170A	p.G1057D
XH_P57	13	110435953	110435953	Silent	SNP	A	G	A	IRS2	c.T2448C	p.C816C
XH_P57	13	110436232	110436232	Silent	SNP	G	A	G	IRS2	c.C2169T	p.S723S
XH_P57	13	111176519	111176519	Silent	SNP	G	T	G	RAB20	c.C198A	p.G66G
XH_P57	13	111896595	111896595	Missense_Mutation	SNP	T	C	T	ARHGEF7	c.T199C	p.C67R
XH_P57	13	112722056	112722079	In_Frame_Del	DEL	GGCGGGGGCG	-	GGCGGGGGGGCG	SOX1	c.84_107del	p.28_36del
XH_P57	13	113140459	113140459	Missense_Mutation	SNP	C	T	C	TUBGCP3	c.G2542A	p.V848M
XH_P57	13	113770068	113770068	Silent	SNP	C	T	C	F7	c.C273T	p.H91H
XH_P57	13	113773159	113773159	Missense_Mutation	SNP	G	A	G	F7	c.G986A	p.R329Q
XH_P57	13	113973832	113973832	Missense_Mutation	SNP	C	T	C	LAMP1	c.C611T	p.A204V
XH_P57	13	113975894	113975894	Silent	SNP	C	T	C	LAMP1	c.C966T	p.N322N
XH_P57	13	113979972	113979972	Frame_Shift_Ins	INS	-	CACT	-	GTRP1	924_925insAGT	p.C309fs
XH_P57	13	114303764	114303764	Silent	SNP	C	T	C	ATP4B	c.G801A	p.A267A
XH_P57	13	115067313	115067313	Missense_Mutation	SNP	A	G	A	UPF3A	c.A1016G	p.H339R
XH_P57	14	20248595	20248595	Silent	SNP	C	T	C	OR4M1	c.C114T	p.I38I
XH_P57	14	20482434	20482434	Missense_Mutation	SNP	C	A	C	OR4K14	c.G919T	p.V307L
XH_P57	14	20502120	20502120	Silent	SNP	C	T	C	OR4K13	c.G798A	p.S266S
XH_P57	14	20847202	20847202	Silent	SNP	A	G	A	TEP1	c.T4866C	p.D1622D
XH_P57	14	20852029	20852029	Missense_Mutation	SNP	A	G	A	TEP1	c.T3259C	p.S1087P
XH_P57	14	20876253	20876253	Missense_Mutation	SNP	A	G	A	TEP1	c.T346C	p.S116P
XH_P57	14	20897064	20897064	Missense_Mutation	SNP	C	T	C	KLHL33	c.G1546A	p.A516T
XH_P57	14	20925154	20925154	Missense_Mutation	SNP	T	G	T	APEX1	c.T444G	p.D148E
XH_P57	14	20978834	20978834	Silent	SNP	G	A	G	RNASE10	c.G204A	p.L68L
XH_P57	14	21215923	21215923	Missense_Mutation	SNP	G	T	G	EDDM3A	c.G184T	p.G62C
XH_P57	14	21469151	21469151	Missense_Mutation	SNP	T	C	T	SLC39A2	c.T343C	p.F115L
XH_P57	14	21500121	21500121	Missense_Mutation	SNP	G	T	G	TPPP2	c.G398T	p.R133L
XH_P57	14	21623303	21623303	Silent	SNP	G	T	G	OR5AU1	c.C882A	p.S294S
XH_P57	14	21769193	21769193	Missense_Mutation	SNP	C	A	C	RPGRI1	c.C287A	p.P96Q
XH_P57	14	23102801	23102801	Frame_Shift_Ins	INS	-	G	-	OR6J1	c.915dupC	p.R306fs
XH_P57	14	23102969	23102969	Missense_Mutation	SNP	G	A	G	OR6J1	c.C748T	p.P250S
XH_P57	14	23240328	23240328	Silent	SNP	T	A	T	OXA1L	c.T1221A	p.R407R
XH_P57	14	23240713	23240713	In_Frame_Ins	INS	-	AGC	-	OXA1L	1434_1435insA	p.P478delinsPS
XH_P57	14	23248112	23248112	Silent	SNP	A	G	A	SLC7A2	c.T660C	p.G220G
XH_P57	14	23745533	23745533	Missense_Mutation	SNP	C	T	C	HOMEZ	c.G904A	p.A302T
XH_P57	14	23894053	23894053	Silent	SNP	A	G	A	MYH7	c.T2604C	p.A868A
XH_P57	14	24029037	24029037	Missense_Mutation	SNP	C	T	C	AP1G2	c.G1136A	p.R379H
XH_P57	14	24569474	24569474	Missense_Mutation	SNP	T	C	T	PKC2	c.T1286C	p.M429T
XH_P57	14	24601553	24601553	Missense_Mutation	SNP	G	A	G	FITM1	c.G400A	p.V134M
XH_P57	14	24653954	24653954	Missense_Mutation	SNP	G	A	G	IPO4	c.C1538T	p.A513V
XH_P57	14	24682767	24682767	Missense_Mutation	SNP	C	T	C	CHMP4A	c.G8A	p.R3Q
XH_P57	14	24702789	24702789	Silent	SNP	C	T	C	GMPR2	c.C246T	p.A82A
XH_P57	14	24784911	24784911	Silent	SNP	T	C	T	LTBR4	c.T54C	p.S18S
XH_P57	14	24839083	24839083	Missense_Mutation	SNP	G	C	G	NFATC4	c.G479C	p.G160A
XH_P57	14	24845841	24845841	Missense_Mutation	SNP	T	C	T	NFATC4	c.T2188C	p.S730P
XH_P57	14	24878370	24878370	Missense_Mutation	SNP	C	T	C	NYNRIN	c.C1370T	p.T457M
XH_P57	14	24898547	24898547	Missense_Mutation	SNP	G	C	G	KHNYN	c.G40C	p.E14Q
XH_P57	14	25076906	25076906	Missense_Mutation	SNP	C	T	C	GZMH	c.G251A	p.R84Q
XH_P57	14	25443879	25443879	Frame_Shift_Ins	INS	-	AGAT	-	STXBP6	145_146insATC	p.C49fs
XH_P57	14	30396622	30396622	In_Frame_Ins	INS	-	CCCGGA	-	PRKD1	96_97insTCCGG	p.P33delinsSGP
XH_P57	14	35263983	35263983	Silent	SNP	T	C	T	BAZ1A	c.A1335G	p.Q445Q
XH_P57	14	35873770	35873770	Silent	SNP	G	A	G	NFKBIA	c.C81T	p.D27D
XH_P57	14	37135752	37135752	Silent	SNP	C	T	C	PAX9	c.C717T	p.H239H
XH_P57	14	38679473	38679473	Silent	SNP	C	T	C	SSTR1	c.C879T	p.V293V
XH_P57	14	39644498	39644498	Silent	SNP	G	A	G	PNN	c.G15A	p.V5V
XH_P57	14	39716201	39716201	Missense_Mutation	SNP	A	G	A	MIA2	c.A423G	p.I141M
XH_P57	14	39722023	39722023	Missense_Mutation	SNP	G	C	G	MIA2	c.G1639C	p.D547H
XH_P57	14	39818028	39818028	Missense_Mutation	SNP	A	G	A	MIA2	c.A1879G	p.I627V
XH_P57	14	39818145	39818145	Missense_Mutation	SNP	G	A	G	MIA2	c.G1996A	p.G666R
XH_P57	14	44975052	44975052	Missense_Mutation	SNP	A	G	A	FSCB	c.T1139C	p.L380P

XH_P57	14	44975606	44975606	Missense_Mutation	SNP	G	T	G	FSCB	c.C585A	p.H195Q
XH_P57	14	45644287	45644287	Missense_Mutation	SNP	A	G	A	FANCM	c.A2252G	p.Y751C
XH_P57	14	50088470	50088470	Frame_Shift_Ins	INS	-	T	-	MGAT2	c.484_485insT	p.Q162fs
XH_P57	14	51204996	51204996	Silent	SNP	C	T	C	NIN	c.G3498A	p.Q1166Q
XH_P57	14	51378591	51378591	Splice_Site	DEL	T	-	T	PYGL	-	-
XH_P57	14	52520368	52520368	Missense_Mutation	SNP	C	T	C	NID2	c.G1358A	p.G453D
XH_P57	14	52735108	52735108	Silent	SNP	C	T	C	PTGDR	c.C576T	p.G192G
XH_P57	14	52937255	52937255	Missense_Mutation	SNP	C	T	C	TXNDC16	c.G1441A	p.E481K
XH_P57	14	52981664	52981664	Missense_Mutation	SNP	G	C	G	TXNDC16	c.C524G	p.A175G
XH_P57	14	53019944	53019944	Missense_Mutation	SNP	A	G	A	GPR137C	c.A79G	p.S27G
XH_P57	14	53529669	53529669	Silent	SNP	A	T	A	DDHD1	c.T1758A	p.T586T
XH_P57	14	55458040	55458040	Missense_Mutation	SNP	A	G	A	WDHD1	c.T863C	p.L288P
XH_P57	14	55615090	55615105	Frame_Shift_Del	DEL	TGAAAAAGT	-	GTGAAAAAGTA	DLGAP5	c.2505_2520del	p.L835fs
XH_P57	14	55619311	55619311	Silent	SNP	A	G	A	DLGAP5	c.T2118C	p.N706N
XH_P57	14	55817708	55817708	Silent	SNP	T	C	T	FBX034	c.T600C	p.Y200Y
XH_P57	14	55864130	55864130	Silent	SNP	A	G	A	ATG14	c.T244C	p.L82L
XH_P57	14	59112732	59112732	Missense_Mutation	SNP	C	T	C	DACT1	c.C1280T	p.A427V
XH_P57	14	59951012	59951012	Missense_Mutation	SNP	G	A	G	L3HYPDH	c.C23T	p.P8L
XH_P57	14	64954683	64954683	Missense_Mutation	SNP	A	G	A	ZBTB25	c.T266C	p.I89T
XH_P57	14	65270357	65270376	Frame_Shift_Del	DEL	ACCAGGCGG	-	GACCAGGCGGTG	SPTB	c.423_442del	p.G141fs
XH_P57	14	65499392	65499392	Missense_Mutation	SNP	G	A	G	CHURC1-FNTB	c.G670A	p.G224S
XH_P57	14	68024134	68024134	Missense_Mutation	SNP	A	T	A	PLEKHH1	c.A338T	p.Q113L
XH_P57	14	68029313	68029313	Missense_Mutation	SNP	G	A	G	PLEKHH1	c.G965A	p.R322Q
XH_P57	14	68042547	68042547	Frame_Shift_Ins	INS	-	G	-	PLEKHH1	c.2178dupG	p.L726fs
XH_P57	14	69352230	69352230	Silent	SNP	G	A	G	ACTN1	c.C1297T	p.L433L
XH_P57	14	70039587	70039587	Silent	SNP	C	T	C	CCDC177	c.G753A	p.S251S
XH_P57	14	70039881	70039881	Missense_Mutation	SNP	C	G	C	CCDC177	c.G459C	p.E153D
XH_P57	14	70171418	70171418	Silent	SNP	T	C	T	SUSD6	c.T417C	p.F139F
XH_P57	14	70418881	70418881	Silent	SNP	G	A	G	SMOC1	c.G126A	p.Q42Q
XH_P57	14	70477508	70477508	Silent	SNP	C	T	C	SMOC1	c.C702T	p.A234A
XH_P57	14	71197250	71197250	Silent	SNP	C	T	C	MAP3K9	c.G2361A	p.P787P
XH_P57	14	74058832	74058832	Missense_Mutation	SNP	C	T	C	ACOT4	c.C169T	p.R57C
XH_P57	14	74523869	74523869	Missense_Mutation	SNP	A	G	A	BBOF1	c.A1486G	p.A496E
XH_P57	14	74523949	74523949	Silent	SNP	G	A	G	BBOF1	c.G1566A	p.Q522Q
XH_P57	14	74976452	74976452	Missense_Mutation	SNP	C	T	C	LTBP2	c.G3262A	p.G1088S
XH_P57	14	74992800	74992800	Silent	SNP	A	G	A	LTBP2	c.T2406C	p.T802T
XH_P57	14	75019002	75019002	Silent	SNP	C	T	C	LTBP2	c.G1287A	p.L429L
XH_P57	14	75022271	75022271	Missense_Mutation	SNP	G	T	G	LTBP2	c.C956A	p.P319Q
XH_P57	14	77786863	77786863	Silent	SNP	C	A	C	POMT2	c.G162T	p.A54A
XH_P57	14	77843977	77843977	Silent	SNP	T	C	T	SAMD15	c.T216C	p.A72A
XH_P57	14	77951255	77951255	Missense_Mutation	SNP	G	T	G	ISM2	c.C149A	p.A50D
XH_P57	14	78353533	78353533	Missense_Mutation	SNP	G	A	G	ADCK1	c.G319A	p.V107M
XH_P57	14	78710044	78710044	Missense_Mutation	SNP	G	A	G	NRXN3	c.G608A	p.G203D
XH_P57	14	81574959	81574959	Silent	SNP	A	G	A	TSHR	c.A696G	p.L232L
XH_P57	14	88407888	88407888	Missense_Mutation	SNP	A	G	A	GALC	c.T1616C	p.I539T
XH_P57	14	91755515	91755515	Missense_Mutation	SNP	C	T	C	CCDC88C	c.G4375A	p.D1459N
XH_P57	14	91773494	91773494	Missense_Mutation	SNP	G	A	G	CCDC88C	c.C3083T	p.A1028V
XH_P57	14	91773568	91773568	Silent	SNP	T	C	T	CCDC88C	c.A3009G	p.L1103L
XH_P57	14	92278836	92278836	Frame_Shift_Ins	INS	-	A	-	TC2N	c.120dupT	p.I41fs
XH_P57	14	92958522	92958522	Missense_Mutation	SNP	A	C	A	SLC24A4	c.A1654C	p.K552Q
XH_P57	14	93199080	93199080	Missense_Mutation	SNP	C	T	C	LGMM	c.G52A	p.V18I
XH_P57	14	93412743	93412743	Silent	SNP	G	A	G	ITPK1	c.C834T	p.F278F
XH_P57	14	93799221	93799221	Silent	SNP	G	A	G	BTBD7	c.C54T	p.G18G
XH_P57	14	94394645	94394645	Missense_Mutation	SNP	G	C	G	FAM181A	c.G14C	p.S5T
XH_P57	14	95029852	95029852	Silent	SNP	G	T	G	SERPINA4	c.G144T	p.L48L
XH_P57	14	95906023	95906023	Silent	SNP	G	A	G	SYNE3	c.C2172T	p.A724A
XH_P57	14	96178688	96178688	Missense_Mutation	SNP	C	T	C	TCL1A	c.G166A	p.V56I
XH_P57	14	96730142	96730142	Silent	SNP	A	G	A	BDKRB1	c.A123G	p.P41P
XH_P57	14	97299853	97299853	Silent	SNP	A	G	A	VRK1	c.A45G	p.A15A
XH_P57	14	100118941	100118941	Silent	SNP	C	T	C	HHIPL1	c.C636T	p.A212A
XH_P57	14	100141689	100141689	Missense_Mutation	SNP	T	C	T	HHIPL1	c.T2075C	p.V692A
XH_P57	14	100996312	100996312	Silent	SNP	T	C	T	WDR25	c.T795C	p.Y265Y
XH_P57	14	102808330	102808330	Silent	SNP	C	T	C	ZNF839	c.C2250T	p.V750V
XH_P57	14	102814945	102814945	Silent	SNP	G	A	G	CINP	c.C588T	p.S196S
XH_P57	14	103342049	103342049	Missense_Mutation	SNP	T	C	T	TRAF3	c.T386C	p.M129T
XH_P57	14	103568614	103568614	Missense_Mutation	SNP	T	A	T	EXOC3L4	c.T554A	p.L185H
XH_P57	14	103568981	103568981	Silent	SNP	A	C	A	EXOC3L4	c.A921C	p.P307P
XH_P57	14	104001032	104001032	Silent	SNP	C	T	C	TRMT61A	c.C744T	p.P248P
XH_P57	14	104028270	104028270	Silent	SNP	T	C	T	BAG5	c.A75G	p.P25P
XH_P57	14	104029449	104029449	Silent	SNP	G	A	G	APOPT1	c.G150A	p.T50T
XH_P57	14	104199036	104199036	Silent	SNP	A	G	A	ZFYVE21	c.A606G	p.T202T
XH_P57	14	104206854	104206854	Silent	SNP	C	T	C	PPP1R13B	c.G1899A	p.T633T
XH_P57	14	105393556	105393556	Missense_Mutation	SNP	G	C	G	PLD4	c.G100C	p.E34Q
XH_P57	14	105408270	105408270	Silent	SNP	G	C	G	AHNAK2	c.C13218G	p.L4406L
XH_P57	14	105410816	105410816	Missense_Mutation	SNP	C	T	C	AHNAK2	c.G10672A	p.E3558K
XH_P57	14	105414804	105414804	Silent	SNP	A	G	A	AHNAK2	c.T6684C	p.F2228F
XH_P57	14	105417036	105417036	Missense_Mutation	SNP	G	C	G	AHNAK2	c.C4452G	p.F1484L
XH_P57	14	105452907	105452907	Silent	SNP	C	T	C	C14orf79	c.C139T	p.L47L
XH_P57	14	105461067	105461067	Silent	SNP	C	T	C	C14orf79	c.C949T	p.L317L
XH_P57	14	105477613	105477613	Silent	SNP	T	C	T	CDC4	c.A654G	p.P218P
XH_P57	14	105995534	105995534	Silent	SNP	G	A	G	TMEM121	c.G363A	p.V121V
XH_P57	15	21051201	21051201	Missense_Mutation	SNP	T	C	T	POTEB	c.A1259G	p.N420S
XH_P57	15	22369373	22369373	Silent	SNP	G	A	G	OR4M2	c.G798A	p.S266S
XH_P57	15	22382655	22382655	Missense_Mutation	SNP	A	C	A	OR4N4	c.A183C	p.L61F
XH_P57	15	22383064	22383064	Missense_Mutation	SNP	C	A	C	OR4N4	c.C592A	p.L198I
XH_P57	15	22743235	22743235	Silent	SNP	A	G	A	GOLGA6L1	c.A1620G	p.R540R
XH_P57	15	24921649	24921649	Missense_Mutation	SNP	T	C	T	NPAP1	c.T635C	p.V212A
XH_P57	15	24921771	24921771	Missense_Mutation	SNP	G	C	G	NPAP1	c.G757C	p.G253R
XH_P57	15	25953198	25953198	Missense_Mutation	SNP	C	T	C	ATP10A	c.G2500A	p.E834K
XH_P57	15	28096538	28096538	Silent	SNP	A	G	A	OCA2	c.T2256C	p.A752A
XH_P57	15	28419659	28419659	Silent	SNP	G	A	G	HERC2	c.C9939T	p.R3313R
XH_P57	15	28502279	28502279	Silent	SNP	A	G	A	HERC2	c.T2445C	p.G815G
XH_P57	15	28632820	28632820	Missense_Mutation	SNP	T	C	T	GOLGA8F	c.T1388C	p.L463P
XH_P57	15	31222820	31222820	Silent	SNP	T	C	T	FAN1	c.T2862C	p.C954C
XH_P57	15	32688214	32688214	Missense_Mutation	SNP	C	T	C	GOLGA8K	c.G1150A	p.A384T
XH_P57	15	34015013	34015013	Silent	SNP	G	A	G	RYR3	c.G6717A	p.G2239G
XH_P57	15	34640510	34640510	Silent	SNP	G	A	G	NUTM1	c.G411A	p.P137P
XH_P57	15	35045057	35045057	Silent	SNP	G	A	G	GJD2	c.C588T	p.S196S

XH_P57	15	35045312	35045312	Silent	SNP	T	A	T	GJD2	c.A333T	p.T111T
XH_P57	15	36946303	36946303	Missense_Mutation	SNP	C	G	C	C15orf41	c.C106G	p.L36V
XH_P57	15	39874781	39874781	Missense_Mutation	SNP	A	G	A	THB51	c.A455G	p.Q152R
XH_P57	15	40494810	40494810	Missense_Mutation	SNP	G	A	G	BUB1B	c.G1649A	p.R550Q
XH_P57	15	40558087	40558087	Silent	SNP	G	A	G	BUB1B-PAK6	c.G249A	p.S835
XH_P57	15	40750740	40750740	Missense_Mutation	SNP	A	G	A	BAHD1	c.A77G	p.E26G
XH_P57	15	40917613	40917613	Silent	SNP	T	C	T	KNL1	c.T5151C	p.P1717P
XH_P57	15	41036410	41036410	Missense_Mutation	SNP	G	T	G	RMDN3	c.C823A	p.Q275K
XH_P57	15	41099899	41099899	Frame_Shift_Ins	INS	-	GGGGC	-	ZFYVE19	c.12_113insGGG	p.W38fs
XH_P57	15	41192558	41192558	Silent	SNP	T	C	T	VPS18	c.T1542C	p.T514T
XH_P57	15	41772795	41772795	Silent	SNP	C	T	C	RTF1	c.C2043T	p.A681A
XH_P57	15	41805237	41805237	Missense_Mutation	SNP	C	T	C	LTK	c.G125A	p.R42Q
XH_P57	15	41819696	41819696	Silent	SNP	T	C	T	RPAP1	c.A1536G	p.A512A
XH_P57	15	41820200	41820200	Missense_Mutation	SNP	C	T	C	RPAP1	c.G1286A	p.R429Q
XH_P57	15	42116076	42116076	Missense_Mutation	SNP	G	T	G	MAPKBP1	c.G4030T	p.G1344C
XH_P57	15	42281719	42281719	Silent	SNP	G	A	G	PLA2G4E	c.C1617T	p.G539G
XH_P57	15	42371752	42371752	Missense_Mutation	SNP	A	T	A	PLA2G4D	c.T1300A	p.S434T
XH_P57	15	42373810	42373810	Missense_Mutation	SNP	G	C	G	PLA2G4D	c.C824G	p.P275R
XH_P57	15	42434254	42434254	Silent	SNP	G	A	G	PLA2G4F	c.C2478T	p.N826N
XH_P57	15	42436305	42436305	Silent	SNP	G	C	G	PLA2G4F	c.C2013G	p.P671P
XH_P57	15	42977676	42977676	Silent	SNP	G	A	G	STARD9	c.G3900A	p.Q1300Q
XH_P57	15	42981377	42981377	Missense_Mutation	SNP	C	T	C	STARD9	c.C7601T	p.P2534L
XH_P57	15	42981806	42981806	Missense_Mutation	SNP	G	A	G	STARD9	c.G8030A	p.R2677H
XH_P57	15	42982340	42982340	Missense_Mutation	SNP	C	T	C	STARD9	c.C8564T	p.T2855I
XH_P57	15	42984892	42984892	Silent	SNP	A	C	A	STARD9	c.A11116C	p.R3706R
XH_P57	15	43017426	43017426	Silent	SNP	T	G	T	CDAN1	c.A3474C	p.L1158L
XH_P57	15	43023482	43023482	Missense_Mutation	SNP	T	C	T	CDAN1	c.A1787G	p.Q596R
XH_P57	15	43027835	43027835	Silent	SNP	G	T	G	CDAN1	c.C816A	p.T272T
XH_P57	15	43028749	43028749	Missense_Mutation	SNP	T	A	T	CDAN1	c.A320T	p.Q107L
XH_P57	15	43044193	43044193	Missense_Mutation	SNP	G	A	G	TTBK2	c.C3251T	p.T1084M
XH_P57	15	43552360	43552360	Missense_Mutation	SNP	G	A	G	TGM5	c.C326T	p.T109M
XH_P57	15	43712876	43712876	Silent	SNP	T	C	T	TP53BP1	c.A4308G	p.P1436P
XH_P57	15	44089414	44089414	Frame_Shift_Ins	INS	-	AG	-	SERINC4	c.772_773insCT	p.M258fs
XH_P57	15	44751350	44751350	Silent	SNP	C	T	C	CTDSP12	c.C138T	p.T46T
XH_P57	15	44944341	44944341	Silent	SNP	G	A	G	SPG11	c.C993T	p.S331S
XH_P57	15	44949329	44949329	Missense_Mutation	SNP	T	C	T	SPG11	c.A833G	p.N278S
XH_P57	15	44967847	44967847	Missense_Mutation	SNP	A	G	A	PATL2	c.T59C	p.L20P
XH_P57	15	45406896	45406896	Missense_Mutation	SNP	T	G	T	DUOXA2	c.T93G	p.F31L
XH_P57	15	49085599	49085599	Frame_Shift_Ins	INS	-	TC	-	CEP152	c.750_751insGA	p.Q251fs
XH_P57	15	50534703	50534703	Silent	SNP	C	T	C	HDC	c.G1644A	p.T548T
XH_P57	15	50534832	50534832	Silent	SNP	A	G	A	HDC	c.T1515C	p.N505N
XH_P57	15	53081221	53081221	Silent	SNP	C	A	C	ONECUT1	c.G861T	p.G287G
XH_P57	15	54003091	54003091	Missense_Mutation	SNP	G	A	G	WDR72	c.C917T	p.P306L
XH_P57	15	56388726	56388726	Frame_Shift_Ins	INS	-	TGAG	-	RFX7	c.199_1200insCT	p.Q400fs
XH_P57	15	57918069	57918069	Silent	SNP	A	G	A	GCOM1	c.A504G	p.A168A
XH_P57	15	58000981	58000981	Silent	SNP	C	T	C	GCOM1	c.C183T	p.A61A
XH_P57	15	58256127	58256127	Missense_Mutation	SNP	C	T	C	ALDH1A2	c.G754A	p.V252I
XH_P57	15	58837957	58837957	Silent	SNP	A	G	A	LIPC	c.A591G	p.G197G
XH_P57	15	62990971	62990971	Silent	SNP	C	T	C	TLN2	c.C1492T	p.L498L
XH_P57	15	64204147	64204147	Missense_Mutation	SNP	G	A	G	DAPK2	c.C992T	p.S331L
XH_P57	15	64962630	64962630	Silent	SNP	A	C	A	ZNF609	c.A1059C	p.P353P
XH_P57	15	65489643	65489643	Missense_Mutation	SNP	C	T	C	CILP	c.G2981A	p.R994Q
XH_P57	15	65676726	65676726	Missense_Mutation	SNP	C	T	C	IGDCC4	c.G3374A	p.C1125Y
XH_P57	15	66411441	66411441	Missense_Mutation	SNP	C	T	C	MEGF11	c.G284A	p.S95N
XH_P57	15	66618342	66618342	Missense_Mutation	SNP	A	G	A	DIS3L	c.A1463G	p.D488G
XH_P57	15	68609647	68609647	Missense_Mutation	SNP	G	T	G	ITGA11	c.C2671A	p.Q891K
XH_P57	15	68612556	68612556	Silent	SNP	T	C	T	ITGA11	c.A2583G	p.S861S
XH_P57	15	68624290	68624290	Silent	SNP	G	A	G	ITGA11	c.C1677T	p.D559D
XH_P57	15	69682021	69682021	Silent	SNP	G	A	G	PAQR5	c.G414A	p.T138T
XH_P57	15	70350607	70350607	Silent	SNP	C	T	C	TLE3	c.G774A	p.G258G
XH_P57	15	72638967	72638967	Missense_Mutation	SNP	C	T	C	HEXA	c.G1231A	p.G411S
XH_P57	15	72668305	72668305	Silent	SNP	G	A	G	HEXA	c.C9T	p.S35
XH_P57	15	73027478	73027478	Missense_Mutation	SNP	T	C	T	BBS4	c.T545C	p.I182T
XH_P57	15	73832892	73832892	Missense_Mutation	SNP	T	C	T	REC114	c.T316C	p.F106L
XH_P57	15	74032783	74032783	Silent	SNP	A	G	A	C15orf59	c.T357C	p.S119S
XH_P57	15	74219546	74219546	Missense_Mutation	SNP	G	T	G	LOXL1	c.G422T	p.R141L
XH_P57	15	74328141	74328141	Missense_Mutation	SNP	G	T	G	PML	c.G2195T	p.G732V
XH_P57	15	74467856	74467856	Silent	SNP	G	A	G	ISLR	c.G657A	p.T219T
XH_P57	15	74473739	74473739	Missense_Mutation	SNP	C	T	C	STRA6	c.G1581A	p.M527I
XH_P57	15	74565181	74565181	Silent	SNP	G	A	G	CCDC33	c.G708A	p.P236P
XH_P57	15	74710305	74710305	Silent	SNP	G	A	G	SEMA7A	c.C336T	p.C112C
XH_P57	15	75499768	75499768	Missense_Mutation	SNP	C	T	C	C15orf39	c.C1379T	p.P460L
XH_P57	15	75521240	75521240	Missense_Mutation	SNP	A	T	A	LOC105376731	c.T193A	p.S65T
XH_P57	15	75932129	75932129	Silent	SNP	G	T	G	IMP3	c.C381A	p.A127A
XH_P57	15	77344793	77344793	Silent	SNP	T	A	T	TSPAN3	c.A411T	p.V137V
XH_P57	15	78770698	78770698	Silent	SNP	C	A	C	IREB2	c.C505A	p.R169R
XH_P57	15	79054773	79054773	Silent	SNP	G	A	G	ADAMTS7	c.C4875T	p.T1625T
XH_P57	15	79064170	79064170	Silent	SNP	C	T	C	ADAMTS7	c.G2133A	p.G711G
XH_P57	15	79068649	79068649	Silent	SNP	G	A	G	ADAMTS7	c.C1587T	p.P529P
XH_P57	15	79069121	79069121	Silent	SNP	A	G	A	ADAMTS7	c.T1530C	p.A510A
XH_P57	15	79092603	79092603	Silent	SNP	G	A	G	ADAMTS7	c.C387T	p.H129H
XH_P57	15	79224747	79224747	Silent	SNP	C	T	C	CTSH	c.G459A	p.A153A
XH_P57	15	79277511	79277511	Silent	SNP	A	G	A	RASGRF1	c.T948C	p.N316N
XH_P57	15	79586361	79586361	Silent	SNP	T	C	T	ANKRD34C	c.T735C	p.P245P
XH_P57	15	80191343	80191343	Missense_Mutation	SNP	G	A	G	ST20	c.C170T	p.P57L
XH_P57	15	80263217	80263217	Missense_Mutation	SNP	C	T	C	BCL2A1	c.G245A	p.G82D
XH_P57	15	81212521	81212521	Silent	SNP	T	C	T	CEMIP	c.T1884C	p.C628C
XH_P57	15	81218024	81218024	Missense_Mutation	SNP	A	G	A	CEMIP	c.A2348G	p.H783R
XH_P57	15	81229192	81229192	Missense_Mutation	SNP	G	A	G	CEMIP	c.G3187A	p.A1063T
XH_P57	15	81440788	81440788	Nonsense_Mutation	INS	-	TGTGA	-	CFAP161	c.820_821insGTG	p.S274delinsVX
XH_P57	15	81440789	81440789	Missense_Mutation	SNP	C	G	C	CFAP161	c.C821G	p.A274G
XH_P57	15	81605655	81605655	Missense_Mutation	SNP	C	T	C	STARD5	c.G584A	p.R195H
XH_P57	15	82555242	82555242	Missense_Mutation	SNP	A	G	A	SAXO2	c.A22G	p.S8G
XH_P57	15	82635194	82635194	Missense_Mutation	SNP	T	C	T	GOLGA6L10	c.A1505G	p.E502G
XH_P57	15	83679041	83679041	Silent	SNP	G	A	G	C15orf40	c.C186T	p.C62C
XH_P57	15	85401106	85401106	Missense_Mutation	SNP	G	A	G	ALPK3	c.G3743A	p.R1248H
XH_P57	15	85402610	85402610	Silent	SNP	G	A	G	ALPK3	c.G4560A	p.E1520E
XH_P57	15	85447431	85447431	Missense_Mutation	SNP	G	A	G	SLC28A1	c.G565A	p.V189I

XH_P57	15	85448875	85448875	Missense_Mutation	SNP	C	A	C	SLC28A1	c.C709A	p.Q237K
XH_P57	15	86123751	86123751	Frame_Shift_Ins	INS	-	TG	-	AKAP13	2452_2453insT	p.L818fs
XH_P57	15	89421405	89421405	Silent	SNP	G	A	G	HAPLN3	c.C879T	p.I293I
XH_P57	15	89444947	89444947	Silent	SNP	G	C	G	MFGE8	c.C573G	p.G191G
XH_P57	15	90168693	90168693	Missense_Mutation	SNP	T	A	T	TICRR	c.T5149A	p.S1717T
XH_P57	15	90170237	90170237	Missense_Mutation	SNP	C	T	C	TICRR	c.C5650T	p.R1884C
XH_P57	15	90196008	90196008	Missense_Mutation	SNP	C	T	C	KIF7	c.G154A	p.D52N
XH_P57	15	90246336	90246336	Silent	SNP	A	G	A	WDR93	c.A459G	p.L153L
XH_P57	15	90335788	90335788	Missense_Mutation	SNP	C	T	C	ANPEP	c.G2255A	p.S752N
XH_P57	15	90344352	90344352	Missense_Mutation	SNP	T	C	T	ANPEP	c.A1809G	p.I603M
XH_P57	15	90349558	90349558	Missense_Mutation	SNP	C	T	C	ANPEP	c.G257A	p.R86Q
XH_P57	15	91161164	91161164	Silent	SNP	G	A	G	CRTC3	c.G663A	p.P221P
XH_P57	15	91185204	91185204	Silent	SNP	G	A	G	CRTC3	c.G1689A	p.A563A
XH_P57	15	91454424	91454424	Silent	SNP	C	T	C	MAN2A2	c.C1899T	p.D633D
XH_P57	15	91499986	91499986	Missense_Mutation	SNP	G	T	G	RCCD1	c.G22T	p.A8S
XH_P57	15	91795203	91795203	Silent	SNP	C	G	C	SV2B	c.C153G	p.L51L
XH_P57	15	91811749	91811749	Silent	SNP	G	A	G	SV2B	c.G954A	p.V318V
XH_P57	15	92987938	92987938	Silent	SNP	C	G	C	STRSIA2	c.C558G	p.P186P
XH_P57	15	93015427	93015427	Missense_Mutation	SNP	G	A	G	C15orf32	c.G49A	p.A17T
XH_P57	15	93588264	93588264	Silent	SNP	G	C	G	RGMA	c.C1269G	p.L423L
XH_P57	15	95013577	95013577	Silent	SNP	G	A	G	MCTP2	c.G2211A	p.T737T
XH_P57	15	99511873	99511873	Missense_Mutation	SNP	G	A	G	PGPEP1L	c.C425T	p.A142V
XH_P57	15	101718529	101718529	Silent	SNP	T	C	T	CHSY1	c.A1473G	p.Q491Q
XH_P57	15	101718950	101718950	Missense_Mutation	SNP	T	C	T	CHSY1	c.A1052G	p.K351R
XH_P57	15	101791359	101791359	Silent	SNP	C	G	C	CHSY1	c.G303C	p.R101R
XH_P57	16	449659	449659	Silent	SNP	G	A	G	NME4	c.G258A	p.S86S
XH_P57	16	450309	450309	Silent	SNP	C	T	C	NME4	c.C429T	p.D143D
XH_P57	16	624114	624114	Missense_Mutation	SNP	A	G	A	PIGQ	c.A40G	p.T14A
XH_P57	16	624713	624713	Silent	SNP	C	T	C	PIGQ	c.C639T	p.C213C
XH_P57	16	633125	633125	Missense_Mutation	SNP	T	C	T	PIGQ	c.T1774C	p.C592R
XH_P57	16	633353	633353	Missense_Mutation	SNP	T	C	T	PIGQ	c.T2002C	p.C668R
XH_P57	16	633354	633354	Missense_Mutation	SNP	G	A	G	PIGQ	c.G2003A	p.C668Y
XH_P57	16	681280	681280	Silent	SNP	G	T	G	WFIKN1	c.G27T	p.P9P
XH_P57	16	718514	718514	Silent	SNP	C	G	C	RHOT2	c.C123G	p.T41T
XH_P57	16	719592	719592	Missense_Mutation	SNP	G	A	G	RHOT2	c.G262A	p.A88T
XH_P57	16	720152	720152	Silent	SNP	T	C	T	RHOT2	c.T306C	p.N102N
XH_P57	16	720960	720960	Silent	SNP	C	T	C	RHOT2	c.C708T	p.N236N
XH_P57	16	721780	721780	Missense_Mutation	SNP	A	G	A	RHOT2	c.A953G	p.C318R
XH_P57	16	1416355	1416355	Silent	SNP	C	T	C	UNKL	c.G435A	p.R145R
XH_P57	16	1591962	1591962	Silent	SNP	G	A	G	TMEM204	c.G321A	p.T107T
XH_P57	16	1608082	1608082	Silent	SNP	A	G	A	IFT140	c.T2253C	p.P751P
XH_P57	16	1614097	1614097	Silent	SNP	A	G	A	IFT140	c.T1968C	p.S665S
XH_P57	16	1814391	1814391	Silent	SNP	T	C	T	MAPK8IP3	c.T2190C	p.D730D
XH_P57	16	1820661	1820666	In_Frame_Del	DEL	GCCAGT	-	GCCAGT	NME3	c.494_499del	p.165_167del
XH_P57	16	1825663	1825668	In_Frame_Del	DEL	GCTCTC	-	GCTCTC	EME2	c.757_762del	p.253_254del
XH_P57	16	2160494	2160494	Silent	SNP	C	T	C	PKD1	c.G4674A	p.T1558T
XH_P57	16	2257105	2257105	Silent	SNP	C	G	C	MLST8	c.C414G	p.P138P
XH_P57	16	2867450	2867450	Silent	SNP	G	C	G	PRSS21	c.G84C	p.P282P
XH_P57	16	2871555	2871555	Silent	SNP	G	A	G	PRSS21	c.G894A	p.P298P
XH_P57	16	2946666	2946666	Silent	SNP	C	T	C	FLYWCH2	c.C216T	p.G72G
XH_P57	16	3017124	3017124	Missense_Mutation	SNP	C	A	C	KREMEN2	c.C737A	p.A246D
XH_P57	16	3017810	3017828	In_Frame_Del	DEL	CTGTCTGCTG	-	GCTGTCTGCTGG	KREMEN2	c.983_1000del	p.328_334del
XH_P57	16	3142911	3142911	Missense_Mutation	SNP	C	G	C	ZSCAN10	c.G28C	p.V10L
XH_P57	16	3165425	3165425	Missense_Mutation	SNP	A	G	A	ZNF205	c.A127G	p.T43A
XH_P57	16	3304573	3304573	Silent	SNP	G	T	G	MEFV	c.C495A	p.A165A
XH_P57	16	3304654	3304654	Silent	SNP	T	C	T	MEFV	c.A414G	p.G138G
XH_P57	16	3304762	3304762	Silent	SNP	A	G	A	MEFV	c.T306C	p.D102D
XH_P57	16	3367023	3367023	Splice_Site	INS	-	TAAA	-	ZNF75A	-	-
XH_P57	16	3613207	3613207	Silent	SNP	G	A	G	NLRC3	c.C1731T	p.S777T
XH_P57	16	3613637	3613637	Missense_Mutation	SNP	G	A	G	NLRC3	c.C1301T	p.P434L
XH_P57	16	3640274	3640274	Missense_Mutation	SNP	G	A	G	SLX4	c.C3365T	p.P1122L
XH_P57	16	3640477	3640477	Silent	SNP	C	T	C	SLX4	c.G3162A	p.S1054S
XH_P57	16	3656557	3656557	Silent	SNP	G	A	G	SLX4	c.C678T	p.H226H
XH_P57	16	3708193	3708193	Silent	SNP	G	A	G	TRAP1	c.C1893T	p.D631D
XH_P57	16	4033373	4033373	Silent	SNP	C	A	C	ADCY9	c.G2379T	p.L793L
XH_P57	16	4310475	4310475	Frame_Shift_Ins	INS	-	CA	-	TFAP4	c.646_647insTG	p.Q216fs
XH_P57	16	4748011	4748011	Missense_Mutation	SNP	C	T	C	ANKS3	c.G1258A	p.A420T
XH_P57	16	4790168	4790168	In_Frame_Ins	INS	-	GCAGATTGGCC	-	C16orf71	292insGCAGAAAT	P97delinsPAELA
XH_P57	16	4802874	4802874	Missense_Mutation	SNP	G	A	G	ZNF500	c.C946T	p.R316W
XH_P57	16	4815602	4815602	Silent	SNP	T	C	T	ZNF500	c.A378G	p.E126E
XH_P57	16	8870314	8870314	Silent	SNP	G	A	G	ABAT	c.G1236A	p.G412G
XH_P57	16	8993587	8993587	Silent	SNP	T	C	T	USP7	c.A2289G	p.E763E
XH_P57	16	9057131	9057131	Missense_Mutation	SNP	C	G	C	USP7	c.G12C	p.Q4H
XH_P57	16	10775855	10775855	Silent	SNP	G	A	G	TEKT5	c.C858T	p.D286D
XH_P57	16	10788406	10788406	Silent	SNP	G	T	G	TEKT5	c.C325A	p.R109R
XH_P57	16	11001743	11001743	Silent	SNP	G	A	G	CIITA	c.G2394A	p.P798P
XH_P57	16	11362729	11362729	Missense_Mutation	SNP	G	A	G	TNP2	c.C391T	p.R131W
XH_P57	16	11369930	11369930	Missense_Mutation	SNP	C	G	C	PRM2	c.G298C	p.A100P
XH_P57	16	11374866	11374866	Silent	SNP	G	T	G	PRM1	c.C139A	p.R47R
XH_P57	16	11647492	11647492	Missense_Mutation	SNP	T	C	T	LITAF	c.A274G	p.I92V
XH_P57	16	11933678	11933678	Silent	SNP	G	C	G	RS1L1D1	c.C1020G	p.T340T
XH_P57	16	11940390	11940390	Silent	SNP	T	C	T	RS1L1D1	c.A603G	p.T201T
XH_P57	16	14859120	14859120	Silent	SNP	G	A	G	NPIPA2	c.G903A	p.A301A
XH_P57	16	14976513	14976513	Silent	SNP	C	T	C	NOMO1	c.C3090T	p.L1030L
XH_P57	16	15122812	15122812	Missense_Mutation	SNP	C	G	C	PDXDC1	c.C1201G	p.L401V
XH_P57	16	15811023	15811023	Silent	SNP	C	T	C	MYH11	c.G5478A	p.L1826L
XH_P57	16	15811062	15811062	Silent	SNP	C	T	C	MYH11	c.G5439A	p.K1813K
XH_P57	16	15818141	15818141	Silent	SNP	A	C	A	MYH11	c.T4242G	p.A1414A
XH_P57	16	20043330	20043330	Silent	SNP	T	C	T	GRP139	c.A789G	p.V263V
XH_P57	16	20552075	20552075	Silent	SNP	G	T	G	ACSM2B	c.C1530A	p.I510I
XH_P57	16	21221430	21221430	Missense_Mutation	SNP	C	A	C	ZIP2	c.G235T	p.D79Y
XH_P57	16	21288900	21288910	In_Frame_Del	DEL	GGTAGCTAC	-	AGGTAGCTACA	CRYM	c.171_176del	p.57_59del
XH_P57	16	21847193	21847193	Missense_Mutation	SNP	G	T	G	NPIP4	c.C2515A	p.P839T
XH_P57	16	21858799	21858799	Missense_Mutation	SNP	G	A	G	NPIP4A	c.C184T	p.H62Y
XH_P57	16	22137603	22137603	Missense_Mutation	SNP	G	A	G	VWA3A	c.G1637A	p.C546Y
XH_P57	16	22237118	22237118	Missense_Mutation	SNP	A	G	A	EEF2K	c.A68G	p.H23R
XH_P57	16	22237273	22237273	Missense_Mutation	SNP	C	G	C	EEF2K	c.C223G	p.P75A
XH_P57	16	22326513	22326513	Missense_Mutation	SNP	A	G	A	POLR3E	c.A518G	p.H173R

XH_P57	16	22826339	22826339	Silent	SNP	A	G	A	HS3T2	c.A408G	p.V136V
XH_P57	16	24788423	24788434	In_Frame_Del	DEL	CAGCCACAG	-	GCAGCCACAGCC	TNRC6A	c.333_344del	p.111_115del
XH_P57	16	24788645	24788645	Missense_Mutation	SNP	T	A	T	TNRC6A	c.T555A	p.N185K
XH_P57	16	24801737	24801737	Missense_Mutation	SNP	G	A	G	TNRC6A	c.G1774A	p.A592T
XH_P57	16	27373872	27373872	Missense_Mutation	SNP	A	C	A	IL4R	c.A1199C	p.E400A
XH_P57	16	27374180	27374180	Missense_Mutation	SNP	T	C	T	IL4R	c.T1507C	p.S503P
XH_P57	16	27374400	27374400	Missense_Mutation	SNP	A	G	A	IL4R	c.A1727G	p.Q576R
XH_P57	16	28354000	28354000	Silent	SNP	G	C	G	NPIP86	c.C1206G	p.P402P
XH_P57	16	28354077	28354077	Missense_Mutation	SNP	G	A	G	NPIP86	c.C1129T	p.R377W
XH_P57	16	28354223	28354223	Missense_Mutation	SNP	G	C	G	NPIP86	c.C983G	p.P328R
XH_P57	16	28620120	28620120	Silent	SNP	C	T	C	SULT1A1	c.G57A	p.P19P
XH_P57	16	28909622	28909622	Silent	SNP	G	A	G	ATP2A1	c.G1239A	p.T413T
XH_P57	16	29891374	29891374	Missense_Mutation	SNP	C	T	C	SEZ6L2	c.G1042A	p.D348N
XH_P57	16	29899123	29899123	Missense_Mutation	SNP	G	T	G	SEZ6L2	c.C713A	p.T238N
XH_P57	16	29900017	29900017	Missense_Mutation	SNP	G	A	G	SEZ6L2	c.C541T	p.R181W
XH_P57	16	30536994	30536994	Missense_Mutation	SNP	A	G	A	ZNF768	c.T467C	p.L156P
XH_P57	16	31090407	31090407	Missense_Mutation	SNP	G	C	G	ZNF646	c.G2762C	p.G921A
XH_P57	16	31091209	31091209	Silent	SNP	T	C	T	ZNF646	c.T3564C	p.T1188T
XH_P57	16	31092075	31092075	Missense_Mutation	SNP	G	A	G	ZNF646	c.G4430A	p.G1477D
XH_P57	16	31096164	31096164	Missense_Mutation	SNP	G	C	G	PRSS53	c.C1216G	p.P406A
XH_P57	16	46642286	46642286	Silent	SNP	G	A	G	SHCBP1	c.C498T	p.N166N
XH_P57	16	46762977	46762977	Silent	SNP	G	A	G	MYLK3	c.C708T	p.D236D
XH_P57	16	47143623	47143623	Splice_Site	SNP	C	A	C	NETO2	.	.
XH_P57	16	49314837	49314837	Silent	SNP	T	G	T	CBLN1	c.A381C	p.I127I
XH_P57	16	49670525	49670525	Silent	SNP	G	T	G	ZNF423	c.C2187A	p.P729P
XH_P57	16	50827518	50827518	Silent	SNP	C	T	C	CYLD	c.C2403T	p.D801D
XH_P57	16	53639438	53639438	Missense_Mutation	SNP	C	T	C	RPGRIP1L	c.G3550A	p.D1184N
XH_P57	16	54967096	54967096	Missense_Mutation	SNP	C	A	C	IRX5	c.C760A	p.P254T
XH_P57	16	55519535	55519535	Silent	SNP	G	C	G	MMP2	c.G528C	p.G176G
XH_P57	16	55536727	55536727	Silent	SNP	C	T	C	MMP2	c.C1656T	p.F552F
XH_P57	16	55601388	55601388	Silent	SNP	A	G	A	CAPNS2	c.A720G	p.E240E
XH_P57	16	55853446	55853446	Splice_Site	SNP	C	A	C	CES1	.	.
XH_P57	16	56370652	56370652	Silent	SNP	C	T	C	GNAO1	c.C603T	p.D201D
XH_P57	16	57416726	57416726	Missense_Mutation	SNP	G	A	G	CX3CL1	c.G721A	p.V241I
XH_P57	16	57717851	57717851	Missense_Mutation	SNP	C	T	C	ADGRG3	c.C529T	p.R177W
XH_P57	16	57760031	57760031	Missense_Mutation	SNP	G	A	G	DRC7	c.G1615A	p.V539M
XH_P57	16	57787906	57787906	Silent	SNP	C	T	C	KATNB1	c.C1227T	p.D409D
XH_P57	16	57849373	57849373	Missense_Mutation	SNP	A	T	A	LOC388282	c.A333T	p.R111S
XH_P57	16	58550484	58550484	Silent	SNP	G	A	G	SETD6	c.G579A	p.L193L
XH_P57	16	60392823	60392823	Missense_Mutation	SNP	G	C	G	LOC729159	c.C784G	p.P262A
XH_P57	16	67265541	67265541	Missense_Mutation	SNP	C	T	C	FHOD1	c.G2384A	p.R795Q
XH_P57	16	67289369	67289369	Frame_Shift_Ins	INS	-	AGTC	-	SLC9A5	425_426insAGT	p.G142fs
XH_P57	16	67691668	67691668	Missense_Mutation	SNP	A	G	A	ACD	c.T1553C	p.V518A
XH_P57	16	67863713	67863713	Missense_Mutation	SNP	C	T	C	CENPT	c.G1141A	p.G381R
XH_P57	16	68373239	68373239	Silent	SNP	C	T	C	PRMT7	c.C369T	p.A123A
XH_P57	16	69973297	69973297	Silent	SNP	C	T	C	WWP2	c.C1177T	p.L393L
XH_P57	16	70365715	70365715	Frame_Shift_Ins	INS	-	G	-	DDX19B	c.662dupG	p.R221fs
XH_P57	16	70395387	70395387	Silent	SNP	C	T	C	DDX19A	c.C360T	p.N120N
XH_P57	16	70710858	70710858	Silent	SNP	C	T	C	MTSS1L	c.G756A	p.S252S
XH_P57	16	71220794	71220794	Missense_Mutation	SNP	G	T	G	HYDIN	c.C86A	p.T29K
XH_P57	16	74419311	74419311	Silent	SNP	C	T	C	NPIP815	c.C321T	p.A107A
XH_P57	16	74425299	74425299	Missense_Mutation	SNP	C	T	C	NPIP815	c.C653T	p.A218V
XH_P57	16	74425447	74425447	Silent	SNP	C	T	C	NPIP815	c.C801T	p.P267P
XH_P57	16	74425622	74425636	In_Frame_Del	DEL	CTCTCCACCC	-	CTCTCTCCACCCCT	NPIP815	c.976_990del	p.326_330del
XH_P57	16	74640753	74640753	Missense_Mutation	SNP	T	A	T	GLG1	c.A240T	p.Q80H
XH_P57	16	74640754	74640754	Missense_Mutation	SNP	T	G	T	GLG1	c.A239C	p.Q80P
XH_P57	16	75149110	75149110	Frame_Shift_Ins	INS	-	T	-	LDHD	c.312_313insA	p.V105fs
XH_P57	16	75513044	75513044	Missense_Mutation	SNP	G	A	G	CHST6	c.C683T	p.T281I
XH_P57	16	75563330	75563330	Missense_Mutation	SNP	G	A	G	CHST5	c.C953T	p.T318M
XH_P57	16	75563746	75563746	Silent	SNP	T	G	T	CHST5	c.A537C	p.P179P
XH_P57	16	75590113	75590113	Silent	SNP	C	G	C	TMEM231	c.G57C	p.R19R
XH_P57	16	76501304	76501304	Missense_Mutation	SNP	G	C	G	CNTNAP4	c.G1152C	p.Q384H
XH_P57	16	77327018	77327018	Silent	SNP	G	A	G	ADAMTS18	c.C2628T	p.C876C
XH_P57	16	77769834	77769834	Missense_Mutation	SNP	G	A	G	NUDT7	c.G299A	p.R100H
XH_P57	16	78466484	78466484	Silent	SNP	G	A	G	WWOX	c.G552A	p.K184K
XH_P57	16	81053707	81053707	In_Frame_Ins	INS	-	ACA	-	CENPN	297_298insAC	p.V99delinsVT
XH_P57	16	81076821	81076821	Missense_Mutation	SNP	T	C	T	ATMIN	c.T250C	p.S84P
XH_P57	16	81094951	81094951	Missense_Mutation	SNP	A	G	A	C16orf46	c.T1003C	p.Y335H
XH_P57	16	81095099	81095099	Silent	SNP	C	G	C	C16orf46	c.G855C	p.A285A
XH_P57	16	81095358	81095358	Missense_Mutation	SNP	A	C	A	C16orf46	c.T596G	p.I199S
XH_P57	16	81248716	81248716	Missense_Mutation	SNP	C	T	C	PKD1L2	c.G547A	p.V183I
XH_P57	16	81737570	81737570	Silent	SNP	C	T	C	CMIP	c.C1689T	p.S563S
XH_P57	16	82033612	82033612	Missense_Mutation	SNP	T	C	T	SDR42E1	c.A286G	p.K96E
XH_P57	16	82101827	82101827	Silent	SNP	C	T	C	HSD17B2	c.C318T	p.G106G
XH_P57	16	83999033	83999033	Silent	SNP	A	G	A	OSGIN1	c.A855G	p.S285S
XH_P57	16	84012104	84012104	Missense_Mutation	SNP	T	C	T	NECAB2	c.T59C	p.L20S
XH_P57	16	84115393	84115393	Silent	SNP	G	A	G	MBTPS1	c.C1407T	p.L469L
XH_P57	16	84158248	84158248	Missense_Mutation	SNP	G	C	G	HSDL1	c.C980G	p.S327C
XH_P57	16	84229517	84229517	Silent	SNP	G	A	G	ADAD2	c.G1149A	p.A383A
XH_P57	16	84256410	84256410	Missense_Mutation	SNP	C	T	C	KCNQ4	c.G973A	p.G325R
XH_P57	16	84270476	84270476	Missense_Mutation	SNP	G	A	G	KCNQ4	c.C616T	p.R206W
XH_P57	16	84691044	84691044	Silent	SNP	C	T	C	KLHL36	c.C631T	p.L211L
XH_P57	16	84693385	84693385	Missense_Mutation	SNP	G	A	G	KLHL36	c.G1157A	p.R386H
XH_P57	16	84906098	84906098	Missense_Mutation	SNP	C	G	C	CRISPLD2	c.C965G	p.T322S
XH_P57	16	84922859	84922859	Silent	SNP	C	T	C	CRISPLD2	c.C1329T	p.A443A
XH_P57	16	85009970	85009970	Silent	SNP	A	G	A	ZDHHC7	c.T906C	p.G302G
XH_P57	16	86565882	86565882	Missense_Mutation	SNP	G	C	G	MTHFSD	c.C887G	p.S296C
XH_P57	16	88017809	88017809	Silent	SNP	C	T	C	BANP	c.C306T	p.V102V
XH_P57	16	88061150	88061150	Silent	SNP	C	T	C	BANP	c.C585T	p.I286I
XH_P57	16	88497937	88497937	Silent	SNP	C	G	G	ZNF469	c.C3975G	p.G1325G
XH_P57	16	88500430	88500430	Silent	SNP	G	T	G	ZNF469	c.G6468T	p.T2156T
XH_P57	16	88501386	88501386	Missense_Mutation	SNP	C	A	C	ZNF469	c.C7424A	p.A2475E
XH_P57	16	88502482	88502482	Silent	SNP	C	T	C	ZNF469	c.C8520T	p.R2840R
XH_P57	16	88552370	88552370	Missense_Mutation	SNP	A	G	A	ZFPM1	c.A64G	p.R22G
XH_P57	16	88594567	88594567	Silent	SNP	C	T	C	ZFPM1	c.C633T	p.C211C
XH_P57	16	88599023	88599023	Silent	SNP	A	G	A	ZFPM1	c.A948G	p.G316G
XH_P57	16	88798819	88798819	Missense_Mutation	SNP	C	T	C	PIEZO1	c.G2915A	p.R972H
XH_P57	16	88803124	88803124	Missense_Mutation	SNP	T	C	T	PIEZO1	c.A1219G	p.R407G

XH_P57	16	89245890	89245890	Missense_Mutation	SNP	G	T	G	CDH15	c.G109T	p.A37S
XH_P57	16	89258747	89258747	Missense_Mutation	SNP	A	C	A	CDH15	c.A1750C	p.K584Q
XH_P57	16	89345573	89345573	Silent	SNP	C	A	C	ANKRD11	c.G7377T	p.T2459T
XH_P57	16	89355034	89355034	Missense_Mutation	SNP	C	T	C	ANKRD11	c.G646A	p.V216I
XH_P57	16	89623393	89623393	Silent	SNP	G	A	G	SPG7	c.G2280A	p.P760P
XH_P57	16	89799950	89799950	Silent	SNP	C	T	C	ZNF276	c.C1341T	p.G447G
XH_P57	16	89805914	89805914	Missense_Mutation	SNP	T	C	T	FANCA	c.A3982G	p.T1328A
XH_P57	16	89809319	89809319	Silent	SNP	T	C	T	FANCA	c.A3654G	p.P1218P
XH_P57	16	89825065	89825065	Silent	SNP	G	A	G	FANCA	c.C2901T	p.S967S
XH_P57	16	89858417	89858417	Silent	SNP	C	A	C	FANCA	c.G1143T	p.T381T
XH_P57	16	89920957	89920957	Silent	SNP	A	G	A	SPIRE2	c.A789G	p.Q263Q
XH_P57	16	89965055	89965055	Silent	SNP	G	A	G	TCF25	c.G1113A	p.L371L
XH_P57	16	89985940	89985940	Missense_Mutation	SNP	G	A	G	MC1R	c.G274A	p.V92M
XH_P57	16	89986608	89986608	Silent	SNP	A	G	A	MC1R	c.A942G	p.T314T
XH_P57	16	90025640	90025640	Missense_Mutation	SNP	G	C	G	DEF8	c.G591C	p.M197I
XH_P57	17	465775	465775	Silent	SNP	G	A	G	VP53	c.C1437T	p.Y479Y
XH_P57	17	1183338	1183338	Missense_Mutation	SNP	C	T	C	TUSC5	c.C43T	p.P15S
XH_P57	17	1370542	1370542	Silent	SNP	C	A	C	MYO1C	c.G3159T	p.L1053L
XH_P57	17	1611433	1611433	Silent	SNP	A	G	A	TLCD2	c.T426C	p.S142S
XH_P57	17	1630584	1630584	Silent	SNP	A	G	A	WDR81	c.A2331G	p.L777L
XH_P57	17	1636934	1636934	Missense_Mutation	SNP	A	G	A	WDR81	c.A994G	p.M332V
XH_P57	17	1655924	1655924	Silent	SNP	T	G	T	SERPINF2	c.T711G	p.L237L
XH_P57	17	1673276	1673276	Missense_Mutation	SNP	C	T	C	SERPINF1	c.C215T	p.T72M
XH_P57	17	1703422	1703422	Silent	SNP	A	G	A	SMYD4	c.T1266C	p.Y422Y
XH_P57	17	1704296	1704296	Missense_Mutation	SNP	C	A	C	SMYD4	c.G392T	p.R131I
XH_P57	17	1731268	1731268	Silent	SNP	T	C	T	SMYD4	c.A21G	p.E7E
XH_P57	17	1733399	1733399	Silent	SNP	A	G	A	RPA1	c.A12G	p.Q4Q
XH_P57	17	2203025	2203025	Missense_Mutation	SNP	T	G	T	SMG6	c.A1022C	p.N341T
XH_P57	17	2600186	2600186	Missense_Mutation	SNP	G	A	G	CLUH	c.C1898T	p.A633V
XH_P57	17	2601836	2601836	Missense_Mutation	SNP	T	C	T	CLUH	c.A1201G	p.I401V
XH_P57	17	2883588	2883588	Missense_Mutation	SNP	C	A	C	RAP1GAP2	c.C559A	p.L187M
XH_P57	17	2966032	2966032	Missense_Mutation	SNP	C	G	C	OR1D5	c.G870C	p.R290S
XH_P57	17	3100827	3100827	Silent	SNP	T	C	T	OR1A2	c.T15C	p.N5N
XH_P57	17	3101578	3101578	Missense_Mutation	SNP	G	T	G	OR1A2	c.G766T	p.G256C
XH_P57	17	3101691	3101691	Missense_Mutation	SNP	G	T	G	OR1A2	c.G879T	p.W293C
XH_P57	17	3422073	3422073	Missense_Mutation	SNP	C	T	C	TRPV3	c.G1882A	p.A628T
XH_P57	17	3431387	3431387	Missense_Mutation	SNP	T	A	T	TRPV3	c.A1435T	p.M479L
XH_P57	17	3475490	3475490	Silent	SNP	C	T	C	TRPV1	c.G2157A	p.K719K
XH_P57	17	3476990	3476990	Silent	SNP	G	A	G	TRPV1	c.C2040T	p.L680I
XH_P57	17	3480910	3480910	Silent	SNP	A	G	A	TRPV1	c.T1695C	p.Y565Y
XH_P57	17	3559823	3559823	Silent	SNP	G	A	G	CTNS	c.G504A	p.T168T
XH_P57	17	3627473	3627473	Missense_Mutation	SNP	C	T	C	HASPIN	c.C244T	p.R82C
XH_P57	17	3628212	3628212	Missense_Mutation	SNP	T	C	T	HASPIN	c.T983C	p.I328T
XH_P57	17	3628362	3628362	Missense_Mutation	SNP	T	C	T	HASPIN	c.T1133C	p.V378A
XH_P57	17	3977532	3977532	Silent	SNP	G	A	G	ZZEF1	c.C3597T	p.A1199A
XH_P57	17	3979949	3979949	Silent	SNP	G	A	G	ZZEF1	c.C3216T	p.P1072P
XH_P57	17	4451453	4451453	Missense_Mutation	SNP	C	T	C	MYBBP1A	c.G1709A	p.R570H
XH_P57	17	4622585	4622585	Frame_Shift_Ins	INS	-	TATC	-	ARRB2	211_212insTAT	p.V71fs
XH_P57	17	4700993	4700993	Missense_Mutation	SNP	C	G	C	PSMB6	c.C319G	p.P107A
XH_P57	17	4712395	4712395	Silent	SNP	A	T	A	PLD2	c.A384T	p.R128R
XH_P57	17	4712617	4712617	Missense_Mutation	SNP	C	T	C	PLD2	c.C514T	p.R172C
XH_P57	17	4836973	4836973	Silent	SNP	A	G	A	GP1BA	c.A1074G	p.R358R
XH_P57	17	5009500	5009500	Silent	SNP	A	G	A	ZNF232	c.T927C	p.L309L
XH_P57	17	5286475	5286475	Frame_Shift_Ins	INS	-	CTTTGACTGGT	-	RABEP1	2448insCTTTGA	p.N816fs
XH_P57	17	5404011	5404011	Missense_Mutation	SNP	T	C	T	LOC728392	c.A266G	p.D89G
XH_P57	17	6406883	6406883	Missense_Mutation	SNP	C	T	C	PITPNM3	c.G130A	p.A44T
XH_P57	17	6916044	6916044	Silent	SNP	C	T	C	RNA5EK	c.C159T	p.C53C
XH_P57	17	6930139	6930139	Silent	SNP	C	T	C	BCL6B	c.C1170T	p.G390G
XH_P57	17	6942111	6942111	Silent	SNP	G	T	G	SLC16A13	c.G984T	p.V328V
XH_P57	17	7099811	7099811	Silent	SNP	G	A	G	DLG4	c.C987T	p.I329I
XH_P57	17	7133162	7133162	Silent	SNP	G	A	G	DVL2	c.C621T	p.S207S
XH_P57	17	7133609	7133609	Silent	SNP	G	A	G	DVL2	c.C405T	p.S135S
XH_P57	17	7224921	7224921	Missense_Mutation	SNP	C	G	C	NEURL4	c.G3051C	p.Q1017H
XH_P57	17	7286326	7286326	Silent	SNP	T	A	T	TNK1	c.T81A	p.L27L
XH_P57	17	7592168	7592168	Missense_Mutation	SNP	C	G	C	WRAP53	c.C202G	p.R68G
XH_P57	17	7592560	7592560	Silent	SNP	C	T	C	WRAP53	c.C450T	p.F150F
XH_P57	17	7637982	7637982	Missense_Mutation	SNP	T	A	T	DNAH2	c.T934A	p.S312T
XH_P57	17	7674784	7674784	Missense_Mutation	SNP	C	T	C	DNAH2	c.C4499T	p.P1500L
XH_P57	17	8022065	8022065	Missense_Mutation	SNP	G	A	G	ALOXE3	c.C32T	p.P111L
XH_P57	17	8026364	8026364	Silent	SNP	C	T	C	HES7	c.G123A	p.E41E
XH_P57	17	8161149	8161149	Missense_Mutation	SNP	C	T	C	PFAS	c.C1100T	p.P367L
XH_P57	17	8402669	8402669	Silent	SNP	C	T	C	MYH10	c.G3777A	p.A1259A
XH_P57	17	8701799	8701799	Missense_Mutation	SNP	G	T	G	MFSD6L	c.C640A	p.P214T
XH_P57	17	9549441	9549441	Silent	SNP	C	T	C	USP43	c.C492T	p.S164S
XH_P57	17	9586165	9586165	Silent	SNP	C	T	C	USP43	c.C1131T	p.S377S
XH_P57	17	9862584	9862584	Missense_Mutation	SNP	G	C	G	GAS7	c.C40G	p.L14V
XH_P57	17	10206595	10206595	Missense_Mutation	SNP	T	C	T	MYH13	c.A5585G	p.H1862R
XH_P57	17	10312762	10312762	Missense_Mutation	SNP	C	G	C	MYH8	c.G1731C	p.E577D
XH_P57	17	10348150	10348150	Missense_Mutation	SNP	G	A	G	MYH4	c.C5533T	p.R1845C
XH_P57	17	10417137	10417137	Splice_Site	SNP	C	T	C	MYH1	.	.
XH_P57	17	10541741	10541741	Silent	SNP	A	G	A	MYH3	c.T3348C	p.I1116I
XH_P57	17	11532835	11532835	Silent	SNP	A	G	A	DNAH9	c.A1452G	p.E484E
XH_P57	17	11651057	11651057	Missense_Mutation	SNP	A	G	A	DNAH9	c.A6584G	p.N2195S
XH_P57	17	14205082	14205082	Missense_Mutation	SNP	G	C	G	HS3ST3B1	c.G247C	p.G83R
XH_P57	17	14248423	14248423	Silent	SNP	T	C	T	HS3ST3B1	c.T633C	p.P211P
XH_P57	17	15134291	15134291	Silent	SNP	G	A	G	PMP22	c.C426T	p.A142A
XH_P57	17	15406197	15406197	Missense_Mutation	SNP	A	T	A	TVP23C	c.T812A	p.L271Q
XH_P57	17	15644506	15644506	Missense_Mutation	SNP	C	T	C	TBC1D26	c.C617T	p.A206V
XH_P57	17	15645289	15645289	Missense_Mutation	SNP	G	A	G	TBC1D26	c.G700A	p.G234S
XH_P57	17	16537207	16537207	Silent	SNP	C	T	C	ZNF624	c.G345A	p.T115T
XH_P57	17	16692262	16692262	Silent	SNP	C	T	C	FAM106CP	c.C48T	p.N16N
XH_P57	17	17109309	17109324	Frame_Shift_Del	DEL	AGAGATCCAA	-	CAGAGATCCAGC	PLD6	c.277_292del	p.S93fs
XH_P57	17	18041507	18041507	Silent	SNP	C	T	C	MYO15A	c.C4954T	p.L1652L
XH_P57	17	18047189	18047189	Missense_Mutation	SNP	G	A	G	MYO15A	c.G6052A	p.G2018R
XH_P57	17	18077175	18077175	Silent	SNP	T	C	T	MYO15A	c.T10431C	p.Y3477Y
XH_P57	17	18148485	18148485	Silent	SNP	G	A	G	FLII	c.C3612T	p.H1204H
XH_P57	17	18159847	18159847	Missense_Mutation	SNP	G	A	G	FLII	c.C206T	p.S69L
XH_P57	17	18167505	18167505	Silent	SNP	T	C	T	MIEF2	c.T792C	p.A264A

XH_P57	17	18219835	18219835	Silent	SNP	T	C	T	SMCR8	c.T732C	p.I244I
XH_P57	17	18220770	18220770	Missense_Mutation	SNP	G	A	G	SMCR8	c.G1667A	p.R556H
XH_P57	17	18221010	18221010	Missense_Mutation	SNP	A	G	A	SMCR8	c.A1907G	p.N636S
XH_P57	17	18996788	18996788	Silent	SNP	G	C	G	LOC388436	c.G207C	p.V69V
XH_P57	17	19458972	19458972	Silent	SNP	C	T	C	SLC47A1	c.C708T	p.L236L
XH_P57	17	19608773	19608773	Silent	SNP	G	A	G	SLC47A2	c.C885T	p.Y295Y
XH_P57	17	19617236	19617236	Silent	SNP	G	T	G	SLC47A2	c.C345A	p.G115G
XH_P57	17	19642952	19642952	Missense_Mutation	SNP	G	C	G	ALDH3A1	c.C985G	p.P329A
XH_P57	17	19812541	19812541	Missense_Mutation	SNP	T	C	T	AKAP10	c.A1762G	p.I588V
XH_P57	17	19861458	19861458	Missense_Mutation	SNP	C	T	C	AKAP10	c.G746A	p.R249H
XH_P57	17	20354836	20354836	Silent	SNP	A	G	A	LGALS9B	c.T879C	p.S293S
XH_P57	17	26824156	26824156	Missense_Mutation	SNP	A	G	A	SLC13A2	c.A1795G	p.I599V
XH_P57	17	26851602	26851602	Missense_Mutation	SNP	C	T	C	FOXN1	c.C205T	p.R69C
XH_P57	17	26864302	26864302	Missense_Mutation	SNP	G	C	G	FOXN1	c.G1795C	p.A599P
XH_P57	17	27613350	27613350	Silent	SNP	T	C	T	NUFIP2	c.A1662G	p.S554S
XH_P57	17	28769470	28769472	Splice_Site	DEL	TGA	-	TGA	CPD	-	-
XH_P57	17	29855661	29855661	Silent	SNP	G	A	G	RAB11FIP4	c.G738A	p.E246E
XH_P57	17	30814717	30814717	Nonsense_Mutation	INS	-	G	-	CDK5R1	c.79_80insG	p.Y27_T28delinsX
XH_P57	17	32906008	32906008	Missense_Mutation	SNP	C	G	C	C17orf102	c.G292C	p.G98R
XH_P57	17	32953258	32953258	Silent	SNP	G	A	G	TMEM132E	c.G180A	p.E60E
XH_P57	17	33286664	33286664	Missense_Mutation	SNP	A	G	A	CCCT68	c.T143C	p.V48A
XH_P57	17	33289046	33289046	Missense_Mutation	SNP	G	C	G	ZNFR80	c.G461C	p.S154T
XH_P57	17	33343582	33343582	In_Frame_Ins	INS	-	AAAGAGATC	-	RRFL	c.693insGATCT	p.D231delinsEISF
XH_P57	17	33433487	33433487	Missense_Mutation	SNP	C	T	C	RAD51D	c.G158A	p.R53Q
XH_P57	17	33520965	33520965	Missense_Mutation	SNP	G	A	G	SLC35G3	c.C362T	p.A121V
XH_P57	17	33768199	33768199	Silent	SNP	G	A	G	SLFN13	c.C2109T	p.D703D
XH_P57	17	33769039	33769039	Missense_Mutation	SNP	G	A	G	SLFN13	c.C1465T	p.R489C
XH_P57	17	33814758	33814758	Missense_Mutation	SNP	T	C	T	SLFN12L	c.A1G	p.M1V
XH_P57	17	34072519	34072519	Missense_Mutation	SNP	A	G	A	GAS2L2	c.T1997C	p.L666P
XH_P57	17	34073301	34073301	Silent	SNP	C	T	C	GAS2L2	c.G1215A	p.E405E
XH_P57	17	34074883	34074883	Missense_Mutation	SNP	G	A	G	GAS2L2	c.C817T	p.R273C
XH_P57	17	34195739	34195739	Missense_Mutation	SNP	T	C	T	HEATR9	c.A8G	p.Y3C
XH_P57	17	34257637	34257637	Missense_Mutation	SNP	T	C	T	RDM1	c.A95G	p.H32R
XH_P57	17	34797746	34797746	Missense_Mutation	SNP	C	T	C	TBC1D38	c.G1390A	p.V464I
XH_P57	17	34854280	34854280	Missense_Mutation	SNP	G	A	G	MYO19	c.C1987T	p.L663F
XH_P57	17	35580489	35580489	Missense_Mutation	SNP	C	G	C	ACACA	c.G3223C	p.V1075L
XH_P57	17	35609866	35609866	Silent	SNP	C	T	C	ACACA	c.G1638A	p.Q546Q
XH_P57	17	35896123	35896123	Silent	SNP	T	C	T	SYNRG	c.A3006G	p.Y1002V
XH_P57	17	35937637	35937637	Missense_Mutation	SNP	T	C	T	SYNRG	c.A664G	p.T222A
XH_P57	17	35956391	35956391	Missense_Mutation	SNP	G	C	G	SYNRG	c.C119G	p.A40G
XH_P57	17	36636008	36636008	Missense_Mutation	SNP	C	T	C	ARHGAP23	c.C2513T	p.P838L
XH_P57	17	38457151	38457151	Missense_Mutation	SNP	G	A	G	CD6C	c.G1321A	p.V441I
XH_P57	17	38645125	38645125	Missense_Mutation	SNP	A	G	A	TNS4	c.T536C	p.L179P
XH_P57	17	38857446	38857446	Missense_Mutation	SNP	C	A	C	KRT24	c.G801T	p.M267I
XH_P57	17	38859601	38859601	Silent	SNP	A	T	A	KRT24	c.T345A	p.A115A
XH_P57	17	38955961	38955961	Missense_Mutation	SNP	G	A	G	KRT28	c.C185T	p.A62V
XH_P57	17	38991003	38991003	Missense_Mutation	SNP	T	C	T	TMEM99	c.T235C	p.Y79H
XH_P57	17	39116728	39116728	Missense_Mutation	SNP	G	A	G	KRT39	c.C1022T	p.T341M
XH_P57	17	39135214	39135214	Silent	SNP	T	C	T	KRT40	c.A1038G	p.Q346Q
XH_P57	17	39137104	39137104	Missense_Mutation	SNP	A	G	A	KRT40	c.T908C	p.M303T
XH_P57	17	39137154	39137154	Missense_Mutation	SNP	C	G	C	KRT40	c.G858C	p.E286D
XH_P57	17	39138712	39138712	Silent	SNP	G	A	G	KRT40	c.C534T	p.Y178Y
XH_P57	17	39140417	39140417	Missense_Mutation	SNP	T	C	T	KRT40	c.A109G	p.T37A
XH_P57	17	39183037	39183037	Missense_Mutation	SNP	C	T	C	KRTAP1-5	c.G371A	p.R124H
XH_P57	17	39274069	39274069	Missense_Mutation	SNP	G	C	G	KRTAP4-11	c.C499G	p.R167G
XH_P57	17	39274518	39274518	Missense_Mutation	SNP	C	T	C	KRTAP4-11	c.G50A	p.R17Q
XH_P57	17	39296254	39296254	Silent	SNP	C	T	C	KRTAP4-6	c.G486A	p.P162P
XH_P57	17	39296361	39296361	Missense_Mutation	SNP	A	G	A	KRTAP4-6	c.T379C	p.S127P
XH_P57	17	39305956	39305956	Missense_Mutation	SNP	G	A	G	KRTAP4-5	c.C64T	p.R22C
XH_P57	17	39316528	39316528	Missense_Mutation	SNP	G	A	G	KRTAP4-4	c.C416T	p.T139I
XH_P57	17	39388811	39388811	Missense_Mutation	SNP	C	A	C	KRTAP9-3	c.C58A	p.Q20K
XH_P57	17	39432066	39432066	Silent	SNP	G	T	G	KRTAP9-7	c.G117T	p.P39V
XH_P57	17	39458893	39458893	Missense_Mutation	SNP	G	A	G	KRTAP29-1	c.C211T	p.R71C
XH_P57	17	39464046	39464046	Missense_Mutation	SNP	G	C	G	KRTAP16-1	c.C1460G	p.A487G
XH_P57	17	39464487	39464487	Missense_Mutation	SNP	G	C	G	KRTAP16-1	c.C1019G	p.P340R
XH_P57	17	39464736	39464736	Missense_Mutation	SNP	C	G	C	KRTAP16-1	c.G770C	p.S257T
XH_P57	17	39465389	39465389	Silent	SNP	T	A	T	KRTAP16-1	c.A117T	p.T39T
XH_P57	17	39503163	39503163	Missense_Mutation	SNP	G	A	G	KRT33A	c.C809T	p.A270V
XH_P57	17	39578424	39578424	Missense_Mutation	SNP	G	T	G	KRT37	c.C917A	p.A306D
XH_P57	17	39595484	39595484	Nonsense_Mutation	SNP	G	A	G	KRT38	c.C703T	p.Q235X
XH_P57	17	39619193	39619193	Missense_Mutation	SNP	C	T	C	KRT32	c.G1106A	p.R369Q
XH_P57	17	39634625	39634625	Silent	SNP	A	G	A	KRT35	c.T987C	p.A329A
XH_P57	17	39637244	39637244	Missense_Mutation	SNP	A	G	A	KRT35	c.T106C	p.S36P
XH_P57	17	39643646	39643646	Missense_Mutation	SNP	G	A	G	KRT36	c.C944T	p.T315M
XH_P57	17	39884065	39884065	Missense_Mutation	SNP	C	A	C	HAP1	c.G1224T	p.L408F
XH_P57	17	39912145	39912145	Missense_Mutation	SNP	T	A	T	JUP	c.A2089T	p.M697L
XH_P57	17	39998141	39998141	Silent	SNP	C	T	C	KLHL10	c.C261T	p.P87P
XH_P57	17	40010979	40010979	Silent	SNP	G	A	G	KLHL11	c.C1140T	p.Y380Y
XH_P57	17	40125864	40125864	Silent	SNP	G	A	G	CNP	c.G1128A	p.G376G
XH_P57	17	40322165	40322165	Silent	SNP	G	A	G	KCNH4	c.C1350T	p.D450D
XH_P57	17	40717719	40717719	Missense_Mutation	SNP	G	A	G	COASY	c.G1528A	p.A510T
XH_P57	17	40864421	40864421	Silent	SNP	C	T	C	EZH1	c.G1305A	p.S435S
XH_P57	17	41573636	41573638	Frame_Shift_Del	DEL	GGT	-	GGT	DHX8	c.1027delG	p.D343fs
XH_P57	17	41879074	41879074	Missense_Mutation	SNP	T	C	T	MPP3	c.A1828G	p.R610G
XH_P57	17	42254417	42254417	Missense_Mutation	SNP	A	G	A	ASB16	c.A881G	p.N294S
XH_P57	17	42287519	42287519	Silent	SNP	C	T	C	UBTF	c.G1488A	p.A496K
XH_P57	17	42336609	42336609	Silent	SNP	A	G	A	SLC4A1	c.T798C	p.F266F
XH_P57	17	42953409	42953409	Silent	SNP	A	G	A	EFTUD2	c.T657C	p.T219T
XH_P57	17	44590611	44590611	Frame_Shift_Ins	INS	-	GG	-	LRR37A2	c.533_534insGG	p.Q178fs
XH_P57	17	44590613	44590613	Frame_Shift_Ins	INS	-	GT	-	LRR37A2	c.535_536insGT	p.T179fs
XH_P57	17	45056301	45056301	Missense_Mutation	SNP	G	T	G	RPRML	c.C73A	p.L25M
XH_P57	17	45368337	45368337	Silent	SNP	A	C	A	ITGB3	c.A1143C	p.V381V
XH_P57	17	46024046	46024046	In_Frame_Ins	INS	-	CAT	-	PNPO	c.684_685insCA	p.D228delinsDH
XH_P57	17	46059071	46059071	Missense_Mutation	SNP	T	C	T	CDK5RAP3	c.T922C	p.S308P
XH_P57	17	46262171	46262171	Missense_Mutation	SNP	C	T	C	SKAP1	c.G481A	p.G161S
XH_P57	17	46923425	46923425	Silent	SNP	C	T	C	CALCO2	c.C210T	p.L70L
XH_P57	17	47921419	47921429	Frame_Shift_Del	DEL	CACTCACCTC	-	CACTCACCTCC	TAC4	c.196_199del	p.G66fs
XH_P57	17	48174908	48174908	Silent	SNP	C	T	C	PDK2	c.C48T	p.S16S

XH_P57	17	48183471	48183471	Silent	SNP	G	T	G	PKD2	c.G555T	p.G185G
XH_P57	17	48433958	48433958	Silent	SNP	T	C	T	XYLT2	c.T1569C	p.Y523Y
XH_P57	17	48452978	48452978	In_Frame_Ins	INS	-	AGC	-	EME1	c.A09_410nsAG	p.K137delinsKQ
XH_P57	17	48546028	48546028	Silent	SNP	C	T	C	CHAD	c.G147A	p.V49V
XH_P57	17	48649993	48649993	Silent	SNP	C	T	C	CACNA1G	c.C825T	p.R275R
XH_P57	17	48913352	48913352	Silent	SNP	G	A	G	WFIKK2	c.G54A	p.A18A
XH_P57	17	48917609	48917609	Silent	SNP	C	T	C	WFIKK2	c.C681T	p.G227G
XH_P57	17	51901494	51901494	Missense_Mutation	SNP	T	C	T	KIF2B	c.T1100C	p.L367S
XH_P57	17	56247101	56247101	Missense_Mutation	SNP	C	A	C	OR4D2	c.C85A	p.L29I
XH_P57	17	56272390	56272390	Silent	SNP	A	G	A	EPX	c.A660G	p.R220R
XH_P57	17	56283519	56283519	Missense_Mutation	SNP	C	T	C	MKS1	c.G992A	p.R331Q
XH_P57	17	56332327	56332327	Missense_Mutation	SNP	G	A	G	LPO	c.G1012A	p.V338M
XH_P57	17	56344867	56344867	Silent	SNP	G	A	G	LPO	c.G1602A	p.P534P
XH_P57	17	56357818	56357818	Missense_Mutation	SNP	C	A	C	MPO	c.G157T	p.V53F
XH_P57	17	56382477	56382477	Missense_Mutation	SNP	C	T	C	TSPOAP1	c.G5309A	p.G1770E
XH_P57	17	56383744	56383744	Missense_Mutation	SNP	T	C	T	TSPOAP1	c.A5003G	p.H1668R
XH_P57	17	56386118	56386118	Silent	SNP	A	G	A	TSPOAP1	c.T4335C	p.D1445D
XH_P57	17	56386358	56386358	Silent	SNP	T	A	T	TSPOAP1	c.A4095T	p.R1365R
XH_P57	17	56388238	56388238	Missense_Mutation	SNP	C	G	C	TSPOAP1	c.G3238C	p.A1080P
XH_P57	17	56396587	56396587	Silent	SNP	T	C	T	TSPOAP1	c.A1383G	p.E461E
XH_P57	17	56448297	56448297	Missense_Mutation	SNP	C	T	C	RNF43	c.G350A	p.R117H
XH_P57	17	56584508	56584508	Missense_Mutation	SNP	T	C	T	MTMR4	c.A838G	p.S280G
XH_P57	17	56618030	56618030	Missense_Mutation	SNP	C	T	C	SEPT4	c.G5A	p.R2K
XH_P57	17	56636908	56636908	Silent	SNP	T	C	T	TEX14	c.A4173G	p.K1391K
XH_P57	17	56690848	56690848	Silent	SNP	T	C	T	TEX14	c.A957G	p.L319L
XH_P57	17	56772341	56772341	Silent	SNP	A	G	A	RAD51C	c.A195G	p.R65R
XH_P57	17	57287454	57287454	Silent	SNP	A	G	A	SMG8	c.A42G	p.A14A
XH_P57	17	59477903	59477903	Silent	SNP	C	A	C	TBX2	c.C366A	p.G122G
XH_P57	17	60493386	60493386	Missense_Mutation	SNP	A	G	A	EFCAB3	c.A1013G	p.Y338C
XH_P57	17	61488943	61488943	Missense_Mutation	SNP	T	C	T	TANC2	c.T3439C	p.S1147P
XH_P57	17	61557200	61557200	Silent	SNP	C	T	C	ACE	c.C582T	p.N194N
XH_P57	17	61566031	61566031	Silent	SNP	G	A	G	ACE	c.G606A	p.T202T
XH_P57	17	61949665	61949665	Missense_Mutation	SNP	G	A	G	CSH2	c.C190T	p.R64C
XH_P57	17	62007498	62007498	Silent	SNP	A	G	A	CD79B	c.T366C	p.C122C
XH_P57	17	62018773	62018773	Silent	SNP	T	C	T	SCN4A	c.A4869G	p.T1623T
XH_P57	17	62020348	62020348	Missense_Mutation	SNP	T	C	T	SCN4A	c.A4126G	p.N1376D
XH_P57	17	62034801	62034801	Silent	SNP	C	T	C	SCN4A	c.G2097A	p.A699A
XH_P57	17	62076077	62076077	Missense_Mutation	SNP	C	G	C	PRR29	c.C71G	p.T24S
XH_P57	17	62079334	62079334	Silent	SNP	A	G	A	PRR29	c.A710G	p.X237X
XH_P57	17	62121480	62121480	Silent	SNP	T	C	T	ERN1	c.A2802G	p.T934T
XH_P57	17	62144222	62144222	Silent	SNP	C	T	C	ERN1	c.G651A	p.L217L
XH_P57	17	63554307	63554307	Silent	SNP	A	G	A	AXIN2	c.T432C	p.I144I
XH_P57	17	65212042	65212042	Missense_Mutation	SNP	C	T	C	HELZ	c.G220A	p.V74M
XH_P57	17	66391276	66391276	Missense_Mutation	SNP	G	A	G	ARSG	c.G1154A	p.R385H
XH_P57	17	66871837	66871837	Missense_Mutation	SNP	C	T	C	ABCA8	c.G4288A	p.G1430S
XH_P57	17	66873743	66873743	Silent	SNP	G	A	G	ABCA8	c.C3996T	p.P1332P
XH_P57	17	67028260	67028260	Silent	SNP	T	C	T	ABCA9	c.A1434G	p.K478K
XH_P57	17	67212031	67212031	Silent	SNP	A	G	A	ABCA10	c.T783C	p.Y261Y
XH_P57	17	71192663	71192663	Silent	SNP	G	A	G	COG1	c.G333A	p.Q111Q
XH_P57	17	71196809	71196809	Missense_Mutation	SNP	A	G	A	COG1	c.A1175G	p.N392S
XH_P57	17	71197748	71197748	Silent	SNP	G	A	G	COG1	c.G1782A	p.E594E
XH_P57	17	71232687	71232687	Missense_Mutation	SNP	T	C	T	C17orf80	c.T1066C	p.F356L
XH_P57	17	71233130	71233130	Silent	SNP	A	G	A	C17orf80	c.A1509G	p.S503S
XH_P57	17	72245220	72245220	Splice_Site	INS	-	T	-	TTYH2		
XH_P57	17	72346868	72346868	Missense_Mutation	SNP	C	T	C	KIF19	c.C1411T	p.R471W
XH_P57	17	72351406	72351406	Silent	SNP	C	T	C	KIF19	c.C2952T	p.H984H
XH_P57	17	72368550	72368550	Silent	SNP	T	C	T	GPR142	c.T936C	p.N312N
XH_P57	17	72469966	72469966	Missense_Mutation	SNP	G	A	G	CD300A	c.G332A	p.R111Q
XH_P57	17	72613589	72613589	Missense_Mutation	SNP	T	G	T	CD300E	c.A56C	p.K19T
XH_P57	17	72937605	72937605	Missense_Mutation	SNP	G	A	G	OTOP3	c.G137A	p.R46Q
XH_P57	17	72949167	72949167	Silent	SNP	T	C	T	HID1	c.A1986G	p.A662A
XH_P57	17	72949649	72949649	Silent	SNP	C	T	C	HID1	c.G1962A	p.P654P
XH_P57	17	73279651	73279651	Silent	SNP	C	T	C	SLC25A19	c.G312A	p.T104T
XH_P57	17	73488794	73488794	Silent	SNP	C	T	C	TMEM94	c.C1866T	p.I622I
XH_P57	17	73498483	73498483	Missense_Mutation	SNP	T	C	T	CASKIN2	c.A2426G	p.E809G
XH_P57	17	73498623	73498623	Silent	SNP	A	G	A	CASKIN2	c.T2286C	p.S762S
XH_P57	17	73518203	73518203	Missense_Mutation	SNP	G	C	C	TSEN4	c.G1041C	p.K347N
XH_P57	17	73518284	73518284	Silent	SNP	G	C	G	TSEN4	c.G1122C	p.R374R
XH_P57	17	73519413	73519413	Missense_Mutation	SNP	C	T	C	TSEN4	c.C1310T	p.A437V
XH_P57	17	73552185	73552185	Missense_Mutation	SNP	G	A	G	LLGL2	c.G134A	p.R45H
XH_P57	17	73565171	73565171	Missense_Mutation	SNP	T	C	T	LLGL2	c.T1435C	p.F479L
XH_P57	17	73566561	73566561	Silent	SNP	G	A	G	LLGL2	c.G2007A	p.P669P
XH_P57	17	73567846	73567846	Missense_Mutation	SNP	C	T	C	LLGL2	c.C2275T	p.P759S
XH_P57	17	73568055	73568055	Silent	SNP	C	T	C	LLGL2	c.C2370T	p.P790P
XH_P57	17	73732412	73732412	Missense_Mutation	SNP	A	T	A	ITGB4	c.A1805T	p.H602L
XH_P57	17	73736879	73736879	Silent	SNP	C	T	C	ITGB4	c.C2566T	p.N852N
XH_P57	17	73750859	73750859	Silent	SNP	C	G	C	ITGB4	c.C4311G	p.P1437P
XH_P57	17	73831594	73831594	Silent	SNP	G	A	G	UNC13D	c.C1744T	p.L582L
XH_P57	17	73837050	73837050	Missense_Mutation	SNP	T	C	T	UNC13D	c.A602G	p.H201R
XH_P57	17	73843040	73843040	Silent	SNP	G	A	G	WBP2	c.C546T	p.A182A
XH_P57	17	73897344	73897344	Missense_Mutation	SNP	G	A	G	MRPL38	c.C602T	p.A201V
XH_P57	17	73917372	73917372	Missense_Mutation	SNP	A	G	A	FBF1	c.T1627C	p.C543R
XH_P57	17	74003981	74003981	Missense_Mutation	SNP	C	T	C	EVPL	c.G5371A	p.G1791S
XH_P57	17	74076415	74076415	Missense_Mutation	SNP	G	A	G	ZACN	c.G454A	p.A152T
XH_P57	17	74163821	74163821	Silent	SNP	G	A	G	RNF157	c.C354T	p.Y118Y
XH_P57	17	74383601	74383601	Silent	SNP	C	T	C	SPHK1	c.C1089T	p.S363S
XH_P57	17	74921072	74921072	Silent	SNP	G	C	G	MGAT5B	c.G1083C	p.R361R
XH_P57	17	75190962	75190962	Silent	SNP	C	T	C	SEC14L1	c.C576T	p.S192S
XH_P57	17	76116777	76116777	Missense_Mutation	SNP	C	T	C	TMC6	c.G1672A	p.V558I
XH_P57	17	76120792	76120792	Missense_Mutation	SNP	T	C	T	TMC6	c.A704G	p.K235R
XH_P57	17	76121864	76121864	Missense_Mutation	SNP	A	G	A	TMC6	c.T373C	p.W125R
XH_P57	17	76354964	76354964	Silent	SNP	G	A	G	SOC53	c.C213T	p.R71R
XH_P57	17	76420085	76420085	Missense_Mutation	SNP	T	C	T	DNAH17	c.A13291G	p.I4431V
XH_P57	17	76480966	76480966	Missense_Mutation	SNP	T	C	T	DNAH17	c.A7633G	p.M2545V
XH_P57	17	76490694	76490694	Missense_Mutation	SNP	C	T	C	DNAH17	c.G6251A	p.R2084Q
XH_P57	17	76503593	76503593	Missense_Mutation	SNP	T	C	T	DNAH17	c.A4531G	p.T1511A
XH_P57	17	76557855	76557855	Silent	SNP	G	A	G	DNAH17	c.C1777T	p.L593L
XH_P57	17	76817090	76817090	Missense_Mutation	SNP	C	T	C	USP36	c.G811A	p.V271I

XH_P57	17	76887763	76887763	Missense_Mutation	SNP	G	A	G	CEP295NL	c.C823T	p.R275W
XH_P57	17	76989782	76989782	Silent	SNP	G	A	G	CANT1	c.C1056T	p.N352N
XH_P57	17	77079574	77079574	Nonsense_Mutation	SNP	C	T	C	ENGASE	c.C1153T	p.R385X
XH_P57	17	77809192	77809192	In_Frame_Ins	INS	-	CCT	-	CBX4	.248_249insAG	p.V83delinsVG
XH_P57	17	78087041	78087041	Missense_Mutation	SNP	G	A	G	GAA	c.G2065A	p.E689K
XH_P57	17	78166351	78166351	Missense_Mutation	SNP	G	T	G	CARD14	c.G578T	p.R193L
XH_P57	17	78184393	78184393	Missense_Mutation	SNP	C	T	C	SGSH	c.G1367A	p.R456H
XH_P57	17	78226506	78226506	Silent	SNP	C	G	C	SLC26A11	c.C1812G	p.L604L
XH_P57	17	78261805	78261805	Silent	SNP	A	G	A	RNF213	c.A453G	p.P151P
XH_P57	17	78341776	78341776	Silent	SNP	G	A	G	RNF213	c.G11988A	p.P3996P
XH_P57	17	78350110	78350110	Missense_Mutation	SNP	G	A	G	RNF213	c.G13195A	p.A4399T
XH_P57	17	78919558	78919558	Silent	SNP	C	T	C	RPTOR	c.C2643T	p.A881A
XH_P57	17	79009061	79009061	Silent	SNP	C	T	C	BAIAP2	c.C7T	p.L3L
XH_P57	17	79354342	79354342	Missense_Mutation	SNP	T	C	T	LOC100130370	c.A466G	p.N16D
XH_P57	17	79511135	79511135	Silent	SNP	A	G	A	FAAP100	c.T2322C	p.T774T
XH_P57	17	79514129	79514129	Missense_Mutation	SNP	G	A	G	FAAP100	c.C1979T	p.P660L
XH_P57	17	79589242	79589242	Silent	SNP	G	A	G	NPLOC4	c.C159T	p.T53T
XH_P57	17	79803540	79803540	Frame_Shift_Ins	INS	-	TC	-	P4HB	.1255_1256insG	p.N419fs
XH_P57	17	79899272	79899272	Missense_Mutation	SNP	A	G	A	MYADML2	c.T346C	p.S116P
XH_P57	17	79899495	79899495	Silent	SNP	G	A	G	MYADML2	c.C123T	p.A41A
XH_P57	17	80051183	80051183	Silent	SNP	A	G	A	FASN	c.T567C	p.N189N
XH_P57	17	80273272	80273272	Silent	SNP	C	T	C	CD7	c.G648A	p.S216S
XH_P57	17	80280865	80280865	Silent	SNP	G	A	G	SECTM1	c.C426T	p.P142P
XH_P57	17	80332897	80332897	Missense_Mutation	SNP	C	T	C	UTS2R	c.C697T	p.R233C
XH_P57	17	80789628	80789628	Missense_Mutation	SNP	T	C	T	ZNF750	c.A703G	p.M235V
XH_P57	18	658035	658035	Silent	SNP	A	G	A	TYMSO5	c.T213C	p.G71G
XH_P57	18	712568	712568	Missense_Mutation	SNP	G	A	G	ENOSF1	c.C20T	p.S7F
XH_P57	18	2939499	2939499	Silent	SNP	G	A	G	LPIN2	c.C801T	p.G267G
XH_P57	18	3729175	3729175	Silent	SNP	C	T	C	DLGAP1	c.G645A	p.P215P
XH_P57	18	5891637	5891637	Silent	SNP	C	A	C	TMEM200C	c.G426T	p.P142P
XH_P57	18	6943264	6943264	Silent	SNP	G	A	G	LAMA1	c.C8982T	p.D2994D
XH_P57	18	6983194	6983194	Silent	SNP	G	T	G	LAMA1	c.C5700A	p.T1900T
XH_P57	18	6985270	6985270	Missense_Mutation	SNP	C	T	C	LAMA1	c.G5626A	p.A1876T
XH_P57	18	6986259	6986259	Silent	SNP	G	A	G	LAMA1	c.C5256T	p.H1752H
XH_P57	18	6993673	6993673	Missense_Mutation	SNP	T	C	T	LAMA1	c.A4975G	p.I1659V
XH_P57	18	6997818	6997818	Missense_Mutation	SNP	A	C	A	LAMA1	c.T4729G	p.S1577A
XH_P57	18	6999489	6999489	Missense_Mutation	SNP	C	T	C	LAMA1	c.G4618A	p.D1540N
XH_P57	18	7888198	7888198	Silent	SNP	C	T	C	PTPRM	c.C291T	p.I97I
XH_P57	18	13056333	13056333	Silent	SNP	C	T	C	CEP192	c.C3744T	p.H1248H
XH_P57	18	13069114	13069114	Silent	SNP	T	A	T	CEP192	c.T4989A	p.A1663A
XH_P57	18	13826007	13826007	Silent	SNP	G	T	G	MC5R	c.G243T	p.A81A
XH_P57	18	13826391	13826391	Missense_Mutation	SNP	C	G	C	MC5R	c.C627G	p.F209L
XH_P57	18	13826508	13826508	Silent	SNP	C	T	C	MC5R	c.C744T	p.T248T
XH_P57	18	14537949	14537949	Missense_Mutation	SNP	A	G	A	POTEC	c.T661C	p.C221R
XH_P57	18	14542648	14542648	Missense_Mutation	SNP	C	A	C	POTEC	c.G498T	p.M166I
XH_P57	18	14850280	14850280	Nonsense_Mutation	SNP	G	T	G	ANKRD30B	c.G3106T	p.E1036X
XH_P57	18	19019528	19019528	Silent	SNP	C	A	C	GREB1L	c.C879A	p.S293S
XH_P57	18	20516917	20516917	Missense_Mutation	SNP	G	A	G	RBBP8	c.G103A	p.V35I
XH_P57	18	21119777	21119777	Silent	SNP	G	A	G	NPC1	c.C2793T	p.N931N
XH_P57	18	21120444	21120444	Missense_Mutation	SNP	T	C	T	NPC1	c.A2572G	p.I858V
XH_P57	18	21481233	21481233	Silent	SNP	C	G	C	LAMA3	c.C1152G	p.A384A
XH_P57	18	21513768	21513768	Silent	SNP	C	T	C	LAMA3	c.C3736T	p.L1246L
XH_P57	18	30349653	30349653	Frame_Shift_Ins	INS	-	A	-	KLHL14	c.901_902insT	p.H301fs
XH_P57	18	32470291	32470291	Missense_Mutation	SNP	G	A	G	DTNA	c.G2062A	p.E688K
XH_P57	18	33557466	33557466	Missense_Mutation	SNP	A	G	A	C18orf21	c.A130G	p.T44A
XH_P57	18	34156497	34156497	Missense_Mutation	SNP	A	G	A	FHOD3	c.A595G	p.I199V
XH_P57	18	34205551	34205551	Silent	SNP	C	T	C	FHOD3	c.C1035T	p.S345S
XH_P57	18	43319519	43319519	Missense_Mutation	SNP	G	A	G	SLC14A1	c.G442A	p.D148N
XH_P57	18	43490602	43490602	Silent	SNP	G	A	G	EPG5	c.C4089T	p.H1363H
XH_P57	18	46447817	46447817	Silent	SNP	G	C	G	SMAD7	c.C642G	p.G214G
XH_P57	18	46448129	46448129	Silent	SNP	G	A	G	SMAD7	c.C330T	p.L110L
XH_P57	18	47429022	47429022	Missense_Mutation	SNP	C	T	C	MYO5B	c.G2753A	p.R918H
XH_P57	18	47431128	47431128	Missense_Mutation	SNP	G	A	G	MYO5B	c.C2485T	p.R829C
XH_P57	18	47800179	47800179	Missense_Mutation	SNP	G	C	G	MBD1	c.C964G	p.P322A
XH_P57	18	47811603	47811603	Silent	SNP	C	T	C	CXXC1	c.G681A	p.T227T
XH_P57	18	48327815	48327815	Silent	SNP	G	A	G	MRO	c.C531T	p.A177A
XH_P57	18	52895531	52895531	Silent	SNP	T	C	T	TCF4	c.A1461G	p.S487S
XH_P57	18	54293658	54293658	Silent	SNP	T	C	T	TXNL1	c.A129G	p.A43A
XH_P57	18	54354098	54354098	Missense_Mutation	SNP	A	G	A	WDR7	c.A610G	p.I204V
XH_P57	18	55226383	55226383	Silent	SNP	G	C	G	FECH	c.C798G	p.P266P
XH_P57	18	55342156	55342156	Missense_Mutation	SNP	T	C	T	ATP8B1	c.A1729G	p.I577V
XH_P57	18	55373767	55373767	Missense_Mutation	SNP	G	C	G	ATP8B1	c.C234G	p.H78Q
XH_P57	18	56246442	56246442	Silent	SNP	T	C	T	ALPK2	c.A1566G	p.G522G
XH_P57	18	56247180	56247180	Silent	SNP	T	C	T	ALPK2	c.A828G	p.L276L
XH_P57	18	56409214	56409214	In_Frame_Ins	INS	-	AGAGCC	-	MALT1	.88_1689insAGAb	p.L563delinsLEP
XH_P57	18	56587802	56587802	Missense_Mutation	SNP	A	C	A	ZNF532	c.A2283C	p.E761D
XH_P57	18	59855000	59855000	Missense_Mutation	SNP	A	G	A	KIAA1468	c.A262G	p.T88A
XH_P57	18	61260204	61260204	Silent	SNP	T	C	T	SERPINB13	c.T498C	p.N166N
XH_P57	18	61585260	61585260	Missense_Mutation	SNP	T	C	T	SERPINB10	c.T296C	p.I99T
XH_P57	18	72176083	72176083	Missense_Mutation	SNP	T	C	T	CNDP2	c.T376C	p.Y126H
XH_P57	18	72178161	72178161	Silent	SNP	T	C	T	CNDP2	c.T318C	p.Y106Y
XH_P57	18	72998899	72998899	Missense_Mutation	SNP	G	A	G	TSHZ1	c.G1537A	p.A513T
XH_P57	18	72999777	72999777	Silent	SNP	C	T	C	TSHZ1	c.C2415T	p.N805N
XH_P57	18	74635105	74635105	Silent	SNP	C	T	C	ZNF236	c.C3636T	p.L1212L
XH_P57	18	74680208	74680208	Silent	SNP	C	T	C	ZNF236	c.C5457T	p.D1819D
XH_P57	18	76753658	76753658	Missense_Mutation	SNP	C	T	C	SALL3	c.C1667T	p.P556L
XH_P57	18	77067000	77067000	Silent	SNP	T	G	T	ATP9B	c.T1539G	p.A513A
XH_P57	18	77208922	77208922	Silent	SNP	C	T	C	NFATC1	c.C111T	p.A37A
XH_P57	19	372661	372661	Missense_Mutation	SNP	C	A	C	THEG	c.G533T	p.R178I
XH_P57	19	407900	407900	Silent	SNP	A	G	A	C2CD4C	c.T462C	p.A154A
XH_P57	19	422238	422238	Silent	SNP	G	T	G	SHC2	c.C1528A	p.R510R
XH_P57	19	496532	496532	Silent	SNP	G	A	G	MADCAM1	c.G33A	p.G11G
XH_P57	19	603832	603832	Silent	SNP	C	T	C	HCN2	c.C921T	p.I307I
XH_P57	19	613307	613307	Silent	SNP	C	T	C	HCN2	c.C1644T	p.A548A
XH_P57	19	746712	746712	Silent	SNP	C	T	C	PALM	c.C930T	p.A310A
XH_P57	19	756985	756985	Silent	SNP	T	G	T	MISP	c.T39G	p.P13P
XH_P57	19	757606	757606	Silent	SNP	T	C	T	MISP	c.T660C	p.P220P
XH_P57	19	821512	821512	Silent	SNP	C	T	C	PLPPR3	c.G48A	p.T16T

XH_P57	19	830854	830854	Silent	SNP	T	C	T	AZU1	c.T507C	p.F169F
XH_P57	19	966693	966693	Silent	SNP	C	T	C	ARID3A	c.C1320T	p.A440A
XH_P57	19	971949	971949	Missense_Mutation	SNP	G	A	G	ARID3A	c.G1666A	p.G556S
XH_P57	19	984554	984554	Silent	SNP	C	G	C	WDR18	c.C201G	p.L67L
XH_P57	19	1005230	1005230	Missense_Mutation	SNP	C	T	C	GRIN3B	c.C1730T	p.T577M
XH_P57	19	1005531	1005531	Silent	SNP	G	C	G	GRIN3B	c.G2031C	p.L677L
XH_P57	19	1009551	1009577	In_Frame_Del	DEL	GGAGGCCCA	-	GGAGGCCCCAC	GRIN3B	c.3082_3108del	p.1028_1036del
XH_P57	19	1049269	1049269	Silent	SNP	G	A	G	ABCA7	c.G2385A	p.L795L
XH_P57	19	1054785	1054785	Silent	SNP	C	T	C	ABCA7	c.C3858T	p.D1286D
XH_P57	19	1113701	1113701	Missense_Mutation	SNP	G	A	G	SBN02	c.C1909T	p.P637S
XH_P57	19	1398750	1398750	Silent	SNP	C	T	C	GAMT	c.G735A	p.A245A
XH_P57	19	1466252	1466252	Silent	SNP	C	A	C	APC2	c.C2949A	p.T983T
XH_P57	19	1469030	1469030	Silent	SNP	A	G	A	APC2	c.A5727G	p.K1909K
XH_P57	19	1535179	1535179	Missense_Mutation	SNP	G	A	G	PLK5	c.G941A	p.R314Q
XH_P57	19	1582656	1582659	Frame_Shift_Del	DEL	AGCT	-	AGCT	MBD3	c.461_464del	p.E154fs
XH_P57	19	1619348	1619348	Silent	SNP	G	A	G	TCF3	c.C1293T	p.G431G
XH_P57	19	1619350	1619350	Missense_Mutation	SNP	C	T	C	TCF3	c.G1291A	p.G431S
XH_P57	19	1811603	1811603	Missense_Mutation	SNP	C	T	C	ATP8B3	c.G133A	p.G45R
XH_P57	19	1819125	1819125	Missense_Mutation	SNP	T	C	T	REX01	c.A2656G	p.S886G
XH_P57	19	1825928	1825930	In_Frame_Del	DEL	CTC	-	CTC	REX01	c.1924_1926del	p.642_642del
XH_P57	19	1827565	1827565	Missense_Mutation	SNP	A	G	A	REX01	c.T1223C	p.V408A
XH_P57	19	1854557	1854557	Silent	SNP	A	G	A	KLF16	c.T660C	p.P220P
XH_P57	19	1912817	1912817	Silent	SNP	C	T	C	ADAT3	c.C723T	p.Y241Y
XH_P57	19	2050823	2050823	Missense_Mutation	SNP	G	T	G	MKNK2	c.C28A	p.Q10K
XH_P57	19	2230406	2230406	Missense_Mutation	SNP	C	A	C	PLEKHJ1	c.G590T	p.S197I
XH_P57	19	2250469	2250469	Silent	SNP	G	A	G	AMH	c.G546A	p.P182P
XH_P57	19	2252990	2252990	Missense_Mutation	SNP	C	G	C	JSRP1	c.G449C	p.G150A
XH_P57	19	2405505	2405505	Silent	SNP	C	T	C	TMPPRS9	c.C702T	p.N234N
XH_P57	19	2422177	2422177	Missense_Mutation	SNP	G	A	G	TMPPRS9	c.G2378A	p.S793N
XH_P57	19	2425196	2425196	Missense_Mutation	SNP	G	A	G	TMPPRS9	c.G2812A	p.E938K
XH_P57	19	2427266	2427266	Silent	SNP	G	A	G	TIMM13	c.C177T	p.D59D
XH_P57	19	3186085	3186085	Silent	SNP	G	T	G	NCLN	c.G57T	p.P19P
XH_P57	19	3281298	3281298	Silent	SNP	G	A	G	CEL5	c.G705A	p.P235P
XH_P57	19	3753874	3753874	Silent	SNP	G	A	G	APBA3	c.C900T	p.I300I
XH_P57	19	4280186	4280186	Silent	SNP	C	T	C	SHD	c.C126T	p.F42F
XH_P57	19	5455890	5455890	Missense_Mutation	SNP	C	T	C	ZNRF4	c.C388T	p.R130W
XH_P57	19	5455989	5455989	Missense_Mutation	SNP	C	T	C	ZNRF4	c.C487T	p.R163C
XH_P57	19	5749130	5749130	Frame_Shift_Ins	INS	-	TA	-	CATSPERD	c.923_924insTA	p.V308fs
XH_P57	19	5831672	5831672	Missense_Mutation	SNP	G	C	G	FUT6	c.C907G	p.R303G
XH_P57	19	5867177	5867177	Missense_Mutation	SNP	G	A	G	FUT5	c.C560T	p.P187L
XH_P57	19	6495736	6495736	Silent	SNP	A	G	A	TUBB4A	c.T558C	p.V186V
XH_P57	19	6669934	6669934	Silent	SNP	G	A	G	TNFSF14	c.C147T	p.A49A
XH_P57	19	7141775	7141775	Silent	SNP	G	A	G	INSR	c.C259Y	p.N853N
XH_P57	19	7565823	7565823	Missense_Mutation	SNP	A	G	A	TEX45	c.A115G	p.M39V
XH_P57	19	7570324	7570324	Splice_Site	INS	-	GA	-	TEX45	.	.
XH_P57	19	7975586	7975586	Silent	SNP	C	T	C	MAP2K7	c.C573T	p.D191D
XH_P57	19	8160334	8160334	Missense_Mutation	SNP	G	A	G	FBN3	c.C5710T	p.L1904F
XH_P57	19	8203328	8203328	Missense_Mutation	SNP	G	A	G	FBN3	c.C986T	p.P329L
XH_P57	19	8321562	8321562	Silent	SNP	C	T	C	CERS4	c.C580T	p.L194L
XH_P57	19	8398975	8398975	Missense_Mutation	SNP	C	T	C	KANK3	c.G1453A	p.A485T
XH_P57	19	8808394	8808394	Missense_Mutation	SNP	G	A	G	ACTL9	c.C658T	p.R220C
XH_P57	19	8995930	8995930	Missense_Mutation	SNP	C	G	C	MUC16	c.G40645C	p.A13549P
XH_P57	19	9005674	9005674	Silent	SNP	G	A	G	MUC16	c.C39732T	p.D13244D
XH_P57	19	9024994	9024994	Missense_Mutation	SNP	C	T	C	MUC16	c.G36868A	p.E12290K
XH_P57	19	9028373	9028373	Missense_Mutation	SNP	G	A	G	MUC16	c.C36419T	p.T12140M
XH_P57	19	9048342	9048342	Missense_Mutation	SNP	C	T	C	MUC16	c.G33289A	p.V11097M
XH_P57	19	9048519	9048519	Missense_Mutation	SNP	C	A	C	MUC16	c.G33112T	p.V11038L
XH_P57	19	9048895	9048895	Missense_Mutation	SNP	A	C	A	MUC16	c.T32736G	p.S10912R
XH_P57	19	9049322	9049322	Missense_Mutation	SNP	G	A	G	MUC16	c.C32309T	p.T10770I
XH_P57	19	9056482	9056482	Missense_Mutation	SNP	C	T	C	MUC16	c.G30964A	p.E10322K
XH_P57	19	9058907	9058907	Missense_Mutation	SNP	G	C	G	MUC16	c.C28539G	p.H9513Q
XH_P57	19	9059159	9059159	Missense_Mutation	SNP	T	G	T	MUC16	c.A28287C	p.K9429N
XH_P57	19	9065203	9065203	Missense_Mutation	SNP	T	C	T	MUC16	c.A22243G	p.S7415G
XH_P57	19	9066259	9066259	Missense_Mutation	SNP	T	C	T	MUC16	c.A21187G	p.T7063A
XH_P57	19	9070079	9070079	Silent	SNP	C	G	C	MUC16	c.G17367C	p.T5789T
XH_P57	19	9075565	9075565	Missense_Mutation	SNP	C	T	C	MUC16	c.G11881A	p.E3961K
XH_P57	19	9075737	9075737	Silent	SNP	T	C	T	MUC16	c.A11709G	p.V3903V
XH_P57	19	9225685	9225685	Missense_Mutation	SNP	T	C	T	OR7G1	c.A755G	p.Y252C
XH_P57	19	9226017	9226017	Missense_Mutation	SNP	C	G	C	OR7G1	c.G423C	p.W141C
XH_P57	19	9226192	9226192	Missense_Mutation	SNP	A	G	A	OR7G1	c.T248C	p.V83A
XH_P57	19	9297381	9297381	Silent	SNP	A	C	A	OR7D2	c.A924C	p.A308A
XH_P57	19	9325116	9325116	Missense_Mutation	SNP	G	A	G	OR7D4	c.C398T	p.T133M
XH_P57	19	9325252	9325252	Missense_Mutation	SNP	G	A	G	OR7D4	c.C262T	p.R88W
XH_P57	19	9361767	9361767	Silent	SNP	G	A	G	OR7E24	c.G48A	p.P16P
XH_P57	19	9415754	9415754	Silent	SNP	T	C	T	ZNFE69	c.A42G	p.R14R
XH_P57	19	9434872	9434872	Silent	SNP	C	T	C	ZNFS59	c.C18T	p.A6A
XH_P57	19	9449888	9449888	Missense_Mutation	SNP	A	G	A	ZNFS59	c.A245G	p.D82G
XH_P57	19	9524272	9524272	Silent	SNP	T	C	T	ZNFE66	c.A1329G	p.K443K
XH_P57	19	10076990	10076990	Missense_Mutation	SNP	G	C	G	COL5A3	c.C4782G	p.I1594M
XH_P57	19	10078589	10078589	Silent	SNP	T	C	T	COL5A3	c.A4395G	p.K1465K
XH_P57	19	10091500	10091500	Silent	SNP	T	C	T	COL5A3	c.A2541G	p.T847T
XH_P57	19	10116375	10116375	Silent	SNP	G	T	G	COL5A3	c.C453A	p.A151A
XH_P57	19	10220616	10220616	Silent	SNP	G	A	G	PPAN	c.G459A	p.A153A
XH_P57	19	10224526	10224526	Missense_Mutation	SNP	C	T	C	P2RY11	c.C1559T	p.P520L
XH_P57	19	10226256	10226256	Silent	SNP	A	G	A	EIF3	c.T846C	p.F282F
XH_P57	19	10370444	10370444	Silent	SNP	A	C	A	MRPL4	c.A891C	p.L297L
XH_P57	19	10488969	10488969	Silent	SNP	G	T	G	TYK2	c.C114A	p.G38G
XH_P57	19	10577843	10577843	Missense_Mutation	SNP	C	A	C	PDE4A	c.C1490A	p.A497E
XH_P57	19	10599965	10599965	Silent	SNP	G	A	G	KEAP1	c.C1611T	p.Y537Y
XH_P57	19	10662779	10662779	Silent	SNP	G	A	G	ATG4D	c.G915A	p.Q305Q
XH_P57	19	10664632	10664632	Missense_Mutation	SNP	A	G	A	KRI1	c.T2125C	p.S709P
XH_P57	19	10670992	10670992	Missense_Mutation	SNP	C	T	C	KRI1	c.G814A	p.E272K
XH_P57	19	10676681	10676681	Missense_Mutation	SNP	T	C	T	KRI1	c.A13G	p.T5A
XH_P57	19	11319636	11319636	Missense_Mutation	SNP	G	A	G	DOCK6	c.C4895T	p.A1632V
XH_P57	19	11486642	11486663	Frame_Shift_Del	DEL	SACCCAGCC	-	TGACCCAGCTC	SWSAP1	c.640_661del	p.A214fs
XH_P57	19	11508177	11508177	Missense_Mutation	SNP	G	A	G	RLG3	c.C1843T	p.R615C
XH_P57	19	11527706	11527706	Missense_Mutation	SNP	G	A	G	RLG3	c.C175T	p.L59F
XH_P57	19	11532450	11532455	In_Frame_Del	DEL	ATAGTT	-	ATAGTT	CCDC151	c.1300_1305del	p.434_435del

XH P57	19	12876964	12876964	Missense_Mutation	SNP	G	C	G	HOOK2	c.C1464G	p.H488Q
XH P57	19	14040420	14040420	Missense_Mutation	SNP	T	A	G	CC2D1A	c.G2657A	p.R886H
XH P57	19	14065341	14065341	Silent	SNP	T	C	T	DCAF15	c.T234C	p.H78H
XH P57	19	14070706	14070706	Frame_Shift_Ins	INS	-	GGCCAGGGCGC	-	DCAF15	sGGTGGGCCCA	p.E480fs
XH P57	19	14083761	14083761	Missense_Mutation	SNP	T	C	T	RFX1	c.A1108G	p.T370A
XH P57	19	14193358	14193358	Silent	SNP	C	T	C	C19orf67	c.G825A	p.S275S
XH P57	19	14512489	14512489	Missense_Mutation	SNP	G	A	G	ADGRE5	c.G821A	p.R274Q
XH P57	19	14829749	14829749	Missense_Mutation	SNP	C	T	C	ZNF333	c.C1610T	p.A537V
XH P57	19	14910210	14910210	Missense_Mutation	SNP	C	G	C	OR7C1	c.G739C	p.V247L
XH P57	19	14991643	14991643	Silent	SNP	G	A	G	OR7A17	c.C525T	p.P175P
XH P57	19	15083693	15083693	Silent	SNP	C	A	C	SLC1A6	c.G30T	p.L10L
XH P57	19	15122045	15122045	Silent	SNP	C	A	C	CCDC105	c.C408A	p.T136T
XH P57	19	15132241	15132241	Silent	SNP	C	T	C	CCDC105	c.C951T	p.N317N
XH P57	19	15198024	15198024	Missense_Mutation	SNP	A	T	A	OR11	c.A148T	p.I50F
XH P57	19	15198441	15198441	Missense_Mutation	SNP	G	T	G	OR11	c.G565T	p.G189C
XH P57	19	15198851	15198851	Silent	SNP	A	T	A	OR11	c.A975T	p.P325P
XH P57	19	15229993	15229993	Silent	SNP	A	G	A	ILVBL	c.T1035C	p.D345D
XH P57	19	15565474	15565474	Missense_Mutation	SNP	C	T	C	RASAL3	c.G1952A	p.R651H
XH P57	19	15648715	15648715	Silent	SNP	G	A	G	CYP4F22	c.G582A	p.A194A
XH P57	19	15763691	15763691	Silent	SNP	G	A	G	CYP4F3	c.G1044A	p.P348P
XH P57	19	15996820	15996820	Silent	SNP	G	A	G	CYP4F2	c.C1029T	p.H343H
XH P57	19	16514682	16514682	Silent	SNP	G	A	G	EPS15L1	c.C1488T	p.P496D
XH P57	19	16625435	16625435	Silent	SNP	G	A	G	C19orf44	c.G1767A	p.A589A
XH P57	19	17088319	17088319	Missense_Mutation	SNP	G	T	G	CPAMD8	c.C1758A	p.D586E
XH P57	19	17362482	17362482	Silent	SNP	G	A	G	USHBP1	c.C1639T	p.L547L
XH P57	19	17392629	17392629	Missense_Mutation	SNP	G	A	G	ANKLE1	c.G62A	p.G21E
XH P57	19	17392894	17392894	Missense_Mutation	SNP	G	A	G	ANKLE1	c.G220A	p.A74T
XH P57	19	17393015	17393015	Missense_Mutation	SNP	C	T	C	ANKLE1	c.C341T	p.A114V
XH P57	19	17394124	17394124	Missense_Mutation	SNP	T	G	T	ANKLE1	c.T680G	p.L227W
XH P57	19	17396549	17396549	Silent	SNP	T	C	T	ANKLE1	c.T1647C	p.G549G
XH P57	19	17412218	17412218	Missense_Mutation	SNP	C	T	C	ABHD8	c.G208A	p.G70R
XH P57	19	17435884	17435884	Silent	SNP	T	C	T	AN08	c.A2973G	p.S991S
XH P57	19	17436152	17436152	Missense_Mutation	SNP	C	T	C	AN08	c.G2705A	p.R902H
XH P57	19	17439034	17439034	Silent	SNP	C	T	C	AN08	c.G2163A	p.P721P
XH P57	19	17444569	17444570	Frame_Shift_Del	DEL	GT	-	GT	AN08	c.146_147del	p.Y49fs
XH P57	19	17448961	17448961	Silent	SNP	A	C	A	GTBPB3	c.A198C	p.T66T
XH P57	19	17450016	17450016	Missense_Mutation	SNP	T	C	T	GTBPB3	c.T845C	p.V282A
XH P57	19	17597765	17597765	Silent	SNP	G	A	G	SLC27A1	c.G561A	p.A187A
XH P57	19	17628587	17628587	Silent	SNP	A	G	A	PGLS	c.A567G	p.T189T
XH P57	19	17691655	17691655	Silent	SNP	G	A	G	COLGALT1	c.G1542A	p.P514P
XH P57	19	17922795	17922795	Missense_Mutation	SNP	G	A	G	B3GNT3	c.G983A	p.C328H
XH P57	19	17932289	17932289	Silent	SNP	C	T	C	INSL3	c.G27A	p.A9A
XH P57	19	18180489	18180489	Silent	SNP	G	A	G	IL12RB1	c.C1056T	p.N352N
XH P57	19	18375563	18375563	Silent	SNP	G	A	G	KIAA1683	c.C2787T	p.P929P
XH P57	19	18375659	18375659	Silent	SNP	C	T	C	KIAA1683	c.G2691A	p.L897L
XH P57	19	18497024	18497024	Missense_Mutation	SNP	G	C	G	GDF15	c.G25C	p.V9L
XH P57	19	18497141	18497141	Missense_Mutation	SNP	T	A	T	GDF15	c.T142A	p.S48T
XH P57	19	18499238	18499238	Silent	SNP	G	T	G	GDF15	c.G420T	p.P140P
XH P57	19	18499422	18499422	Missense_Mutation	SNP	C	G	C	GDF15	c.C604G	p.H202D
XH P57	19	18502835	18502835	Missense_Mutation	SNP	G	A	G	LRRC25	c.C880T	p.P294S
XH P57	19	18778962	18778962	Missense_Mutation	SNP	G	A	G	KLHL26	c.G842A	p.R281H
XH P57	19	18943156	18943156	Silent	SNP	G	A	G	UPF1	c.G138A	p.T46T
XH P57	19	19310037	19310037	Missense_Mutation	SNP	C	T	C	RFKANK	c.C637T	p.R213W
XH P57	19	19737888	19737888	Frame_Shift_Ins	INS	-	TA	-	LPAR2	c.205_206insTA	p.Y69fs
XH P57	19	20044041	20044041	Missense_Mutation	SNP	G	T	G	ZNF93	c.C277T	p.D93Y
XH P57	19	20727463	20727463	Missense_Mutation	SNP	T	C	T	ZNF737	c.A1546G	p.K516E
XH P57	19	20808149	20808149	Silent	SNP	A	G	A	ZNF626	c.T534C	p.C178C
XH P57	19	21606756	21606756	Missense_Mutation	SNP	C	T	C	ZNF493	c.C911T	p.P304L
XH P57	19	22847487	22847487	Missense_Mutation	SNP	G	A	G	ZNF492	c.G1016A	p.C339Y
XH P57	19	22848028	22848028	Missense_Mutation	SNP	G	C	G	ZNF492	c.G1557C	p.K519N
XH P57	19	22940192	22940192	Frame_Shift_Ins	INS	-	G	-	ZNF99	c.2518_2519insG	p.M840fs
XH P57	19	22952111	22952111	Missense_Mutation	SNP	A	G	A	ZNF99	c.T19C	p.W7R
XH P57	19	23040182	23040182	Missense_Mutation	SNP	G	T	G	ZNF723	c.G489T	p.Q163H
XH P57	19	23542697	23542697	Silent	SNP	G	C	G	ZNF91	c.C2988G	p.G996G
XH P57	19	23545250	23545250	Silent	SNP	A	G	A	ZNF91	c.T435C	p.T145T
XH P57	19	30193721	30193721	Silent	SNP	G	A	G	C19orf12	c.C132T	p.T44T
XH P57	19	31038995	31038995	Silent	SNP	T	C	T	ZNF536	c.T2469C	p.D823D
XH P57	19	31769550	31769550	Silent	SNP	C	T	C	TSHZ3	c.G1149A	p.S383S
XH P57	19	31769763	31769763	Silent	SNP	G	A	G	TSHZ3	c.C936T	p.V312V
XH P57	19	33467515	33467515	Missense_Mutation	SNP	T	C	T	FAAP24	c.T290C	p.I97T
XH P57	19	33698448	33698448	Silent	SNP	G	A	G	LRP3	c.G2280A	p.E760E
XH P57	19	33882222	33882222	Silent	SNP	G	A	G	PEPD	c.C1008T	p.H336H
XH P57	19	34868642	34868642	Silent	SNP	A	G	A	GPI	c.A405G	p.G135G
XH P57	19	35501051	35501051	Silent	SNP	T	C	T	GRAMD1A	c.T360C	p.S120S
XH P57	19	35649281	35649281	Silent	SNP	A	G	A	FXDY5	c.A177G	p.P59P
XH P57	19	35790503	35790503	Silent	SNP	G	A	G	MAG	c.G387A	p.E129E
XH P57	19	35836530	35836530	Missense_Mutation	SNP	G	A	G	CD22	c.G1703A	p.G568D
XH P57	19	35842652	35842652	Silent	SNP	G	A	G	FFAR1	c.G198A	p.A66A
XH P57	19	35849883	35849883	Missense_Mutation	SNP	C	G	C	FFAR3	c.C91G	p.L31V
XH P57	19	35850672	35850672	Silent	SNP	T	C	T	FFAR3	c.T880C	p.L294L
XH P57	19	35863141	35863141	Silent	SNP	T	C	T	GPR42	c.T880C	p.L294L
XH P57	19	36134208	36134208	Missense_Mutation	SNP	G	A	G	ETV2	c.G268A	p.D90N
XH P57	19	36159368	36159368	Missense_Mutation	SNP	T	G	T	UPK1A	c.T97G	p.S33A
XH P57	19	36206050	36206050	Missense_Mutation	SNP	A	C	A	ZBTB32	c.A522C	p.R174S
XH P57	19	36206271	36206271	Missense_Mutation	SNP	C	T	C	ZBTB32	c.C743T	p.S248L
XH P57	19	36222857	36222857	Missense_Mutation	SNP	C	T	C	KMT2B	c.C5486T	p.P1829L
XH P57	19	36223747	36223747	Silent	SNP	A	G	A	KMT2B	c.A6297G	p.A2099A
XH P57	19	36230767	36230767	Missense_Mutation	SNP	A	G	A	IGFLR1	c.T565C	p.W189R
XH P57	19	36268771	36268771	Silent	SNP	C	T	C	ARHGAP33	c.C150T	p.A50A
XH P57	19	36273308	36273308	Silent	SNP	G	A	G	ARHGAP33	c.G711A	p.L237L
XH P57	19	36278111	36278111	Missense_Mutation	SNP	C	A	C	ARHGAP33	c.C2236A	p.L746I
XH P57	19	36339044	36339044	Missense_Mutation	SNP	C	T	C	NPH51	c.G1339A	p.E447K
XH P57	19	37210805	37210805	Silent	SNP	C	T	C	ZNF567	c.C1086T	p.Y362Y
XH P57	19	37211478	37211478	Missense_Mutation	SNP	G	A	G	ZNF567	c.G1759A	p.V587I
XH P57	19	37854580	37854580	Missense_Mutation	SNP	C	T	C	HKR1	c.C1703T	p.T568I
XH P57	19	38572597	38572597	Missense_Mutation	SNP	C	T	C	SIPA1L3	c.C392T	p.A131V
XH P57	19	38684261	38684261	Missense_Mutation	SNP	G	C	G	SIPA1L3	c.G4681C	p.A1561P
XH P57	19	38684391	38684391	Missense_Mutation	SNP	C	A	C	SIPA1L3	c.C4811A	p.A1604D

XH_P57	19	38847431	38847431	Silent	SNP	T	C	T	CATSPERG	c.T1245C	p.T415T
XH_P57	19	38851247	38851247	Missense_Mutation	SNP	C	A	C	CATSPERG	c.C1607A	p.T536N
XH_P57	19	38852453	38852453	Silent	SNP	C	T	C	CATSPERG	c.C1926T	p.V642Y
XH_P57	19	38861362	38861362	Missense_Mutation	SNP	T	C	T	CATSPERG	c.T3290C	p.M1097T
XH_P57	19	38876352	38876352	Missense_Mutation	SNP	G	A	G	GGN	c.C1550T	p.A517V
XH_P57	19	38894102	38894102	Missense_Mutation	SNP	G	A	G	FAM98C	c.G190A	p.A64T
XH_P57	19	38896244	38896244	Missense_Mutation	SNP	C	A	C	FAM98C	c.C641A	p.T214K
XH_P57	19	38935280	38935280	Silent	SNP	A	G	A	RYR1	c.A594G	p.L198L
XH_P57	19	39416887	39416887	Silent	SNP	C	T	C	SARS2	c.G321A	p.E107E
XH_P57	19	39789115	39789115	Missense_Mutation	SNP	A	G	A	IFN1	c.A562G	p.N188D
XH_P57	19	39898461	39898461	Missense_Mutation	SNP	T	C	T	ZFP36	c.T121C	p.S41P
XH_P57	19	40196627	40196627	Missense_Mutation	SNP	G	A	G	LGALS14	c.G80A	p.R27H
XH_P57	19	40363020	40363020	Missense_Mutation	SNP	G	A	G	FCGBP	c.C15050T	p.A5017V
XH_P57	19	40363926	40363926	Missense_Mutation	SNP	C	G	C	FCGBP	c.G14716C	p.D4906H
XH_P57	19	40366362	40366362	Silent	SNP	G	C	G	FCGBP	c.C13872G	p.L4624L
XH_P57	19	40367862	40367862	Silent	SNP	T	C	T	FCGBP	c.A13098G	p.P4366P
XH_P57	19	40370471	40370471	Silent	SNP	G	A	G	FCGBP	c.C12195T	p.G4065G
XH_P57	19	40374023	40374023	Missense_Mutation	SNP	C	T	C	FCGBP	c.G12055A	p.V4019M
XH_P57	19	40374025	40374025	Missense_Mutation	SNP	A	C	A	FCGBP	c.T12053G	p.V4018G
XH_P57	19	40384099	40384099	Missense_Mutation	SNP	G	A	G	FCGBP	c.C9511T	p.P3171S
XH_P57	19	40392496	40392496	Missense_Mutation	SNP	C	T	C	FCGBP	c.G8008A	p.G2670R
XH_P57	19	40392585	40392585	Missense_Mutation	SNP	T	G	T	FCGBP	c.A7919C	p.EC2640A
XH_P57	19	40402410	40402410	Silent	SNP	G	A	G	FCGBP	c.C4989T	p.G1663G
XH_P57	19	40420087	40420087	Silent	SNP	G	A	G	FCGBP	c.C2907T	p.A969A
XH_P57	19	40582039	40582039	Missense_Mutation	SNP	T	A	T	ZNF780A	c.A310T	p.I104L
XH_P57	19	40928944	40928944	Silent	SNP	A	G	A	SERTAD1	c.T510C	p.L170L
XH_P57	19	40964312	40964312	Silent	SNP	G	A	G	BLVRB	c.C220T	p.L74L
XH_P57	19	41211056	41211056	Missense_Mutation	SNP	T	C	T	COQ8B	c.A398G	p.H133R
XH_P57	19	41282981	41282981	Silent	SNP	A	T	A	MIA	c.A369T	p.T123T
XH_P57	19	41633946	41633946	Missense_Mutation	SNP	A	C	A	CYP2F1	c.A1435C	p.N479H
XH_P57	19	42083673	42083673	Silent	SNP	T	C	T	CEACAM21	c.T186C	p.L62L
XH_P57	19	42132120	42132120	Silent	SNP	G	A	G	CEACAM4	c.C279T	p.A93A
XH_P57	19	42260569	42260569	Silent	SNP	G	A	G	CEACAM6	c.G126A	p.P42P
XH_P57	19	42880120	42880120	Silent	SNP	C	T	C	MEGF8	c.C7530T	p.Y2510Y
XH_P57	19	43699278	43699278	Missense_Mutation	SNP	A	G	A	PSG4	c.T578C	p.V193A
XH_P57	19	43708100	43708100	Missense_Mutation	SNP	T	A	T	PSG4	c.A368T	p.H123L
XH_P57	19	44156435	44156435	Silent	SNP	A	G	A	PLAUR	c.T561C	p.T187T
XH_P57	19	44515352	44515352	Silent	SNP	T	G	T	ZNF230	c.T1161G	p.T387T
XH_P57	19	44515514	44515514	Missense_Mutation	SNP	C	A	C	ZNF230	c.C1323A	p.D441E
XH_P57	19	44652954	44652954	Missense_Mutation	SNP	G	A	G	ZNF234	c.G46A	p.V16I
XH_P57	19	44660967	44660967	Silent	SNP	A	G	A	ZNF234	c.A798G	p.G266G
XH_P57	19	44933504	44933504	Silent	SNP	G	A	G	ZNF229	c.C1434T	p.T478T
XH_P57	19	44933706	44933706	Missense_Mutation	SNP	C	T	C	ZNF229	c.G1232A	p.S411N
XH_P57	19	45021210	45021210	Missense_Mutation	SNP	G	A	G	CEACAM20	c.C1106T	p.S369F
XH_P57	19	45029208	45029208	Missense_Mutation	SNP	G	A	G	CEACAM20	c.C122T	p.A41V
XH_P57	19	45153329	45153329	Missense_Mutation	SNP	G	A	G	PVR	c.G676A	p.E226K
XH_P57	19	45315539	45315539	Silent	SNP	G	A	G	BCAM	c.G324A	p.G108G
XH_P57	19	45851252	45851252	Missense_Mutation	SNP	G	T	G	KLC3	c.G613T	p.A205S
XH_P57	19	45998247	45998247	Silent	SNP	A	G	A	RTN2	c.T96C	p.S32S
XH_P57	19	46216642	46216642	Missense_Mutation	SNP	G	T	G	FBXO46	c.C112A	p.P38T
XH_P57	19	46376202	46376202	Missense_Mutation	SNP	G	C	G	FOXA3	c.G939C	p.Q313H
XH_P57	19	46388315	46388343	Frame_Shift_Del	DEL	ACAGCGCCAC	-	GACAGCGCCAGT	IRF2BP1	c.690_718del	p.R230fs
XH_P57	19	46511548	46511548	Silent	SNP	T	C	T	CCDC61	c.T540C	p.H180H
XH_P57	19	46520026	46520026	Missense_Mutation	SNP	A	G	A	CCDC61	c.A1166G	p.Q389R
XH_P57	19	46663890	46663890	Silent	SNP	A	G	A	IGFL2	c.A93G	p.P31P
XH_P57	19	46857021	46857021	Silent	SNP	C	T	C	PPP5C	c.C138T	p.N46N
XH_P57	19	47124714	47124714	Silent	SNP	T	G	T	PTGIR	c.A984C	p.S328S
XH_P57	19	47126847	47126847	Silent	SNP	G	A	G	PTGIR	c.C636T	p.R212R
XH_P57	19	47126848	47126848	Missense_Mutation	SNP	C	T	C	PTGIR	c.G635A	p.R212H
XH_P57	19	47127324	47127324	Silent	SNP	C	G	C	PTGIR	c.G159C	p.V53V
XH_P57	19	47258842	47258842	Silent	SNP	C	T	C	FKRP	c.C135T	p.A45A
XH_P57	19	47844955	47844955	Missense_Mutation	SNP	G	A	G	CSAR2	c.G899A	p.R300H
XH_P57	19	47969620	47969620	Missense_Mutation	SNP	G	A	G	SLC8A2	c.C41T	p.A14V
XH_P57	19	48182787	48182787	Silent	SNP	C	T	C	BICRA	c.C360T	p.A120A
XH_P57	19	48183771	48183771	Silent	SNP	C	T	C	BICRA	c.C1344T	p.S448S
XH_P57	19	48184474	48184474	Missense_Mutation	SNP	C	T	C	BICRA	c.C2047T	p.P683S
XH_P57	19	48198675	48198675	Missense_Mutation	SNP	A	G	A	BICRA	c.A3130G	p.T1044A
XH_P57	19	48229404	48229404	Missense_Mutation	SNP	C	T	C	EHD2	c.C838T	p.R280C
XH_P57	19	48244194	48244194	Silent	SNP	A	G	A	EHD2	c.A1137G	p.L379L
XH_P57	19	48244569	48244569	Silent	SNP	G	A	G	EHD2	c.G1512A	p.E504E
XH_P57	19	48255804	48255804	Silent	SNP	A	G	A	NOP53	c.A705G	p.A235A
XH_P57	19	48258141	48258141	Missense_Mutation	SNP	A	G	A	NOP53	c.A1046G	p.H349R
XH_P57	19	48789237	48789237	Nonsense_Mutation	INS	-	AGTCTTCTCTTA	-	ZNF114	357insAGTCTTCTC9_V120delinsPVFSX	
XH_P57	19	48821738	48821738	Missense_Mutation	SNP	C	G	C	CCDC114	c.G155C	p.R52P
XH_P57	19	48869178	48869178	Missense_Mutation	SNP	C	T	C	SYNGR4	c.C79T	p.R27W
XH_P57	19	48949286	48949286	Silent	SNP	G	T	G	GRWD1	c.G24T	p.R8R
XH_P57	19	49079224	49079224	Missense_Mutation	SNP	G	A	G	SULT2B1	c.G53A	p.R18Q
XH_P57	19	49300500	49300500	Silent	SNP	G	A	G	BCAT2	c.C510T	p.L170L
XH_P57	19	49391404	49391404	Missense_Mutation	SNP	C	T	C	TULP2	c.G751A	p.D251N
XH_P57	19	49481243	49481243	Missense_Mutation	SNP	T	C	T	GSY1	c.A1054G	p.M352V
XH_P57	19	49611629	49611629	Missense_Mutation	SNP	A	G	A	SNRNP70	c.A1216G	p.M406V
XH_P57	19	49671832	49671832	Missense_Mutation	SNP	G	A	G	TRPM4	c.G290A	p.R97Q
XH_P57	19	49850606	49850606	Frame_Shift_Ins	INS	-	A	-	TEAD2	c.758dupT	p.L253fs
XH_P57	19	49860521	49860521	Missense_Mutation	SNP	C	A	C	TEAD2	c.G348T	p.Q116H
XH_P57	19	50312653	50312653	Silent	SNP	C	T	C	FUZ	c.G564A	p.L188L
XH_P57	19	50412650	50412650	Missense_Mutation	SNP	C	T	C	NUP62	c.G415A	p.G139S
XH_P57	19	50435747	50435747	Silent	SNP	T	C	T	ATF5	c.T247C	p.L83L
XH_P57	19	50463965	50463965	Nonsense_Mutation	SNP	G	A	G	SIGLEC11	c.C304T	p.R102X
XH_P57	19	50755955	50755955	Silent	SNP	C	T	C	MYH14	c.C1866T	p.V622V
XH_P57	19	50760716	50760716	Silent	SNP	C	G	C	MYH14	c.C2082G	p.R694R
XH_P57	19	50789850	50789850	Missense_Mutation	SNP	G	A	G	MYH14	c.G4528A	p.E1510K
XH_P57	19	50812280	50812280	Nonsense_Mutation	SNP	C	T	C	MYH14	c.C5683T	p.R1895X
XH_P57	19	51412666	51412666	Silent	SNP	C	A	C	KLK4	c.G66T	p.S22S
XH_P57	19	51528041	51528041	Missense_Mutation	SNP	C	T	C	KLK11	c.G50A	p.G17E
XH_P57	19	51628529	51628529	Missense_Mutation	SNP	A	G	A	SIGLEC9	c.A298G	p.K100E
XH_P57	19	51630482	51630482	Missense_Mutation	SNP	C	A	C	SIGLEC9	c.C944A	p.A315E
XH_P57	19	51857738	51857738	Missense_Mutation	SNP	G	A	G	ETFB	c.C155T	p.P52L
XH_P57	19	51984727	51984727	Missense_Mutation	SNP	A	G	A	CEACAM18	c.A481G	p.T161A

XH_P57	19	52004759	52004759	Missense_Mutation	SNP	C	T	C	SIGLEC12	c.G229A	p.A77T
XH_P57	19	52249680	52249680	Missense_Mutation	SNP	T	A	T	FPR1	c.A568T	p.R190W
XH_P57	19	52380625	52380625	Nonsense_Mutation	SNP	G	A	G	ZNF577	c.C193T	p.R65X
XH_P57	19	52569057	52569057	Missense_Mutation	SNP	C	T	C	ZNF841	c.G1730A	p.S577N
XH_P57	19	52856955	52856955	Silent	SNP	C	T	C	ZNF610	c.C84T	p.D28D
XH_P57	19	53770261	53770261	Missense_Mutation	SNP	T	C	T	VN1R4	c.A658G	p.N220D
XH_P57	19	53770569	53770569	Missense_Mutation	SNP	G	C	G	VN1R4	c.C350G	p.A117G
XH_P57	19	53793042	53793042	Missense_Mutation	SNP	G	A	G	BIRC8	c.C586T	p.H196V
XH_P57	19	53793574	53793574	Silent	SNP	A	G	A	BIRC8	c.T54C	p.V18V
XH_P57	19	53854397	53854397	Missense_Mutation	SNP	G	C	G	ZNF845	c.G469C	p.E157Q
XH_P57	19	53958126	53958126	Missense_Mutation	SNP	T	G	T	ZNF761	c.T365G	p.I122S
XH_P57	19	53958263	53958263	Missense_Mutation	SNP	G	A	G	ZNF761	c.G502A	p.V168I
XH_P57	19	53959343	53959343	Missense_Mutation	SNP	G	A	G	ZNF761	c.G1582A	p.G528S
XH_P57	19	53959568	53959568	Missense_Mutation	SNP	G	C	G	ZNF761	c.G1807C	p.E603Q
XH_P57	19	53959804	53959804	Silent	SNP	T	C	T	ZNF761	c.T2043C	p.H681H
XH_P57	19	54080960	54080960	Silent	SNP	G	A	G	ZNF331	c.G1146A	p.P382P
XH_P57	19	54327313	54327313	Missense_Mutation	SNP	C	A	C	NLRP12	c.G116T	p.G39V
XH_P57	19	54394965	54394965	Silent	SNP	T	C	T	PRKCG	c.T567C	p.N189N
XH_P57	19	54409996	54409996	Silent	SNP	C	T	C	PRKCG	c.C1941T	p.F647F
XH_P57	19	54656709	54656709	Silent	SNP	A	T	A	CNOT3	c.A2010T	p.T760T
XH_P57	19	54664209	54664209	Missense_Mutation	SNP	G	C	G	TMC4	c.C2065G	p.Q689E
XH_P57	19	54664752	54664752	Silent	SNP	A	C	A	TMC4	c.T1854G	p.L618L
XH_P57	19	54675643	54675643	Missense_Mutation	SNP	G	A	G	TMC4	c.C307T	p.H103Y
XH_P57	19	54744799	54744799	Missense_Mutation	SNP	G	C	G	LILRA6	c.C863G	p.P288R
XH_P57	19	54755918	54755918	Missense_Mutation	SNP	C	G	C	LILRB5	c.G1328C	p.R443P
XH_P57	19	54871664	54871664	Missense_Mutation	SNP	G	C	G	LAIR1	c.C326G	p.P109R
XH_P57	19	55098667	55098667	Splice_Site	SNP	G	A	G	LILRA2		
XH_P57	19	55106590	55106590	Silent	SNP	A	G	A	LILRA1	c.A384G	p.S128S
XH_P57	19	55106865	55106865	Missense_Mutation	SNP	T	C	T	LILRA1	c.T659C	p.L220P
XH_P57	19	55174498	55174498	Missense_Mutation	SNP	T	C	T	LILRB4	c.T13C	p.P.L51
XH_P57	19	55246739	55246739	Silent	SNP	C	T	C	KIR3DL3	c.C969T	p.H323H
XH_P57	19	55445980	55445980	Missense_Mutation	SNP	T	C	T	NLRP7	c.A2348G	p.Y783C
XH_P57	19	55559715	55559715	Silent	SNP	G	A	G	RDH13	c.C640T	p.L214L
XH_P57	19	55991285	55991285	Splice_Site	INS	-	TGACT	-	ZNF628		
XH_P57	19	56000797	56000797	Silent	SNP	C	T	C	SSC5D	c.C129T	p.T43T
XH_P57	19	56011460	56011460	Silent	SNP	C	T	C	SSC5D	c.C1983T	p.T661T
XH_P57	19	56012108	56012108	Missense_Mutation	SNP	C	T	C	SSC5D	c.C2554T	p.P852S
XH_P57	19	56114045	56114045	Silent	SNP	C	T	C	ZNF524	c.C567T	p.H189H
XH_P57	19	56180115	56180115	Frame_Shift_Ins	INS	-	CT	-	U2AF2	c.902_903insCT	p.G301fs
XH_P57	19	56284197	56284197	Silent	SNP	C	G	C	RFPL4AL1	c.C516G	p.V172V
XH_P57	19	56443519	56443519	Silent	SNP	C	T	C	NLRP13	c.G159A	p.P53P
XH_P57	19	56459342	56459342	Missense_Mutation	SNP	C	T	C	NLRP8	c.C74T	p.P25L
XH_P57	19	56459614	56459614	Missense_Mutation	SNP	G	C	G	NLRP8	c.G346C	p.V116L
XH_P57	19	57065189	57065189	Silent	SNP	T	C	T	ZFP28	c.T1035C	p.F345F
XH_P57	19	57132968	57132968	Missense_Mutation	SNP	G	A	G	ZNF71	c.G131A	p.V105I
XH_P57	19	57175484	57175484	Silent	SNP	A	G	A	ZNF835	c.T1083C	p.P361P
XH_P57	19	57176198	57176198	Silent	SNP	T	G	T	ZNF835	c.A369C	p.S123S
XH_P57	19	57649900	57649900	Missense_Mutation	SNP	C	T	C	ZIM3	c.G82A	p.E28K
XH_P57	19	58002964	58002964	Silent	SNP	G	C	G	ZNF419	c.G162C	p.L54L
XH_P57	19	58117083	58117083	Missense_Mutation	SNP	A	G	A	ZNF530	c.A190G	p.T64A
XH_P57	19	58144715	58144715	Missense_Mutation	SNP	A	G	A	ZNF211	c.A1G	p.M1V
XH_P57	19	58151286	58151286	Missense_Mutation	SNP	T	C	T	ZNF211	c.T224C	p.I75T
XH_P57	19	58198887	58198887	Missense_Mutation	SNP	G	A	G	ZNF551	c.G1160A	p.G387E
XH_P57	19	58928302	58928302	Silent	SNP	T	C	T	ZNF584	c.T417C	p.A139A
XH_P57	19	58929052	58929052	Silent	SNP	G	A	G	ZNF584	c.G1167A	p.K389K
XH_P57	19	58966644	58966644	Silent	SNP	A	T	A	ZNF324B	c.A333T	p.P111P
XH_P57	19	58989495	58989495	Missense_Mutation	SNP	A	C	A	ZNF446	c.A574C	p.N192H
XH_P57	19	58991900	58991900	Missense_Mutation	SNP	G	A	G	ZNF446	c.G1160A	p.R387H
XH_P57	19	59061357	59061357	Silent	SNP	C	T	C	TRIM28	c.C2148T	p.P716P
XH_P57	19	59073613	59073613	Silent	SNP	A	G	A	MZF1	c.T2031C	p.G677G
XH_P57	19	59074429	59074429	Silent	SNP	C	T	C	MZF1	c.G1215A	p.T405T
XH_P57	19	59074653	59074653	Missense_Mutation	SNP	T	C	T	MZF1	c.A991G	p.I331V
XH_P57	19	59082368	59082368	Missense_Mutation	SNP	C	T	C	MZF1	c.G389A	p.P130Q
XH_P57	20	306748	306748	In_Frame_Ins	INS	-	CCA	-	SOX12	c.180_181insCC	p.D60delinsDP
XH_P57	20	333898	333898	Silent	SNP	G	A	G	NRSN2	c.G234A	p.A78A
XH_P57	20	368905	368905	Missense_Mutation	SNP	A	G	A	TRIB3	c.A251G	p.Q84R
XH_P57	20	744615	744615	Silent	SNP	G	A	A	SLC52A3	c.C600T	p.P200P
XH_P57	20	2187943	2187943	Silent	SNP	G	T	G	LOC388780	c.G153T	p.P51P
XH_P57	20	2187944	2187944	Nonsense_Mutation	SNP	C	T	C	LOC388780	c.C154T	p.Q52X
XH_P57	20	2398091	2398091	Missense_Mutation	SNP	T	G	T	TGM6	c.T1550G	p.L517W
XH_P57	20	2463941	2463941	Nonsense_Mutation	SNP	G	A	G	ZNF343	c.C1396T	p.R466X
XH_P57	20	2591232	2591232	Silent	SNP	C	T	C	TMC2	c.C1581T	p.D527D
XH_P57	20	2593863	2593863	Silent	SNP	T	C	T	TMC2	c.T1767C	p.S589S
XH_P57	20	2816138	2816138	Frame_Shift_Ins	INS	-	GGCC	-	PCED1A	c.181_1182insGG	p.P394fs
XH_P57	20	2840929	2840929	Silent	SNP	G	A	G	VPS16	c.G285A	p.E95E
XH_P57	20	2844911	2844911	Silent	SNP	C	T	C	VPS16	c.C1266T	p.I422I
XH_P57	20	3025107	3025107	Missense_Mutation	SNP	C	T	C	GNRH2	c.C47T	p.A16V
XH_P57	20	3640606	3640606	Missense_Mutation	SNP	G	A	G	GFRA4	c.C850T	p.R284C
XH_P57	20	3732633	3732633	Silent	SNP	C	T	C	HSPA12B	c.C1623T	p.C541C
XH_P57	20	3842971	3842971	Missense_Mutation	SNP	A	T	A	MAVS	c.A113T	p.E38V
XH_P57	20	3870130	3870130	Missense_Mutation	SNP	G	A	G	PANK2	c.G383A	p.P128Q
XH_P57	20	4163205	4163205	In_Frame_Ins	INS	-	GGC	-	SMOX	c.1079_1080insGG	p.L360delinsLA
XH_P57	20	4880308	4880308	Silent	SNP	G	A	G	SLC23A2	c.C375T	p.A125A
XH_P57	20	5283376	5283376	Silent	SNP	G	A	G	PROKR2	c.C465T	p.L155L
XH_P57	20	5843812	5843812	Silent	SNP	T	C	T	C20orf196	c.T321C	p.G107G
XH_P57	20	5903223	5903223	Missense_Mutation	SNP	G	A	G	CHGB	c.G433A	p.D145N
XH_P57	20	5943956	5943956	Missense_Mutation	SNP	G	C	G	MCM8	c.G826C	p.A276P
XH_P57	20	5948542	5948542	Missense_Mutation	SNP	G	A	G	MCM8	c.G1094A	p.S365N
XH_P57	20	9547018	9547018	Missense_Mutation	SNP	C	G	C	PAK5	c.G1004C	p.R335P
XH_P57	20	10277621	10277621	Silent	SNP	C	T	C	SNAP25	c.C330T	p.D110D
XH_P57	20	10394046	10394046	Silent	SNP	G	A	G	MKKS	c.C117T	p.P39P
XH_P57	20	10620275	10620275	Silent	SNP	G	A	G	JAG1	c.C3528T	p.Y1176Y
XH_P57	20	10620386	10620386	Silent	SNP	A	G	A	JAG1	c.T3417C	p.Y1139Y
XH_P57	20	10639222	10639222	Silent	SNP	G	A	G	JAG1	c.C588T	p.C196C
XH_P57	20	17596155	17596155	Missense_Mutation	SNP	C	A	C	RRBP1	c.G2672T	p.R891L
XH_P57	20	17600357	17600357	Missense_Mutation	SNP	G	A	G	RRBP1	c.C2297T	p.S766L
XH_P57	20	17932210	17932210	Silent	SNP	C	T	C	SNX5	c.G228A	p.E76E
XH_P57	20	17968923	17968923	Silent	SNP	T	C	T	MGME1	c.T846C	p.D282D

XH_P57	20	18143355	18143355	Silent	SNP	C	T	C	KAT14	c.C1437T	p.P479P
XH_P57	20	18370386	18370386	Silent	SNP	A	G	A	DZANK1	c.T1977C	p.V659V
XH_P57	20	18523002	18523002	Missense_Mutation	SNP	C	G	C	SEC23B	c.C1467G	p.H489Q
XH_P57	20	19955577	19955577	Missense_Mutation	SNP	G	A	G	RIN2	c.G908A	p.R303Q
XH_P57	20	23345069	23345069	Silent	SNP	C	T	C	GZF1	c.C49T	p.L17L
XH_P57	20	23432528	23432528	Silent	SNP	A	G	A	CST11	c.T258C	p.N86N
XH_P57	20	23546639	23546639	Missense_Mutation	SNP	T	G	T	CST9L	c.A326C	p.H109P
XH_P57	20	23804663	23804663	Missense_Mutation	SNP	T	A	T	CST2	c.A420T	p.E140D
XH_P57	20	25259006	25259006	Missense_Mutation	SNP	G	T	G	PYGB	c.G907T	p.A303S
XH_P57	20	25259097	25259115	Frame_Shift_Del	DEL	CATGGTGGC	-	GCATGGTGGCC	PYGB	c.998_999del	p.K333fs
XH_P57	20	30816237	30816237	Silent	SNP	T	C	T	POFUT1	c.T714C	p.H238H
XH_P57	20	30915461	30915461	Silent	SNP	T	C	T	KIF3B	c.T1965C	p.V655Y
XH_P57	20	31427635	31427635	Silent	SNP	C	T	C	MAPRE1	c.C570T	p.D190D
XH_P57	20	31480052	31480052	Missense_Mutation	SNP	G	C	G	EFCAB8	c.G707C	p.R236P
XH_P57	20	31625415	31625415	Silent	SNP	C	T	C	BPIFB6	c.C717T	p.A239A
XH_P57	20	32664926	32664926	Missense_Mutation	SNP	G	A	G	RALY	c.G703A	p.G235S
XH_P57	20	33337751	33337751	Silent	SNP	T	C	T	NCOA6	c.A2247G	p.P749P
XH_P57	20	33874346	33874346	Missense_Mutation	SNP	C	G	C	FAM83C	c.G2236C	p.E746Q
XH_P57	20	35491277	35491277	Silent	SNP	C	A	C	SOGA1	c.G471T	p.G157G
XH_P57	20	35865054	35865054	Silent	SNP	C	T	C	RPN2	c.C1354T	p.L452L
XH_P57	20	36954724	36954724	Missense_Mutation	SNP	C	T	C	BPI	c.C1063T	p.P355S
XH_P57	20	36977970	36977970	Silent	SNP	G	A	G	LBP	c.G144A	p.L48L
XH_P57	20	40040828	40040828	Missense_Mutation	SNP	C	T	C	CHD6	c.G7207A	p.G2403R
XH_P57	20	42743454	42743454	Silent	SNP	A	G	A	JPH2	c.T2073C	p.F691F
XH_P57	20	42825929	42825929	Silent	SNP	C	T	C	OSER1	c.G642A	p.V214V
XH_P57	20	43108846	43108846	Silent	SNP	C	T	C	TTPAL	c.C207T	p.Y69Y
XH_P57	20	43723627	43723627	Missense_Mutation	SNP	T	C	T	KCNS1	c.A1465G	p.I489V
XH_P57	20	43727155	43727155	Silent	SNP	C	T	C	KCNS1	c.G258A	p.E86E
XH_P57	20	43739100	43739100	Missense_Mutation	SNP	G	A	G	WFD5C	c.C308T	p.S103L
XH_P57	20	44047974	44047974	Missense_Mutation	SNP	G	A	G	PIGT	c.G227A	p.R76Q
XH_P57	20	44469290	44469290	Missense_Mutation	SNP	G	A	G	SNX21	c.G460A	p.A154T
XH_P57	20	44469348	44469348	Missense_Mutation	SNP	C	T	C	SNX21	c.C518T	p.S173L
XH_P57	20	44470676	44470676	Silent	SNP	T	C	T	SNX21	c.T594C	p.S198S
XH_P57	20	44505973	44505973	Missense_Mutation	SNP	T	C	T	ZSWIM3	c.T776C	p.V259A
XH_P57	20	44506418	44506418	Silent	SNP	G	A	G	ZSWIM3	c.G1221A	p.R407R
XH_P57	20	44643111	44643111	Missense_Mutation	SNP	G	A	G	MMP9	c.G2003A	p.R668Q
XH_P57	20	44644965	44644965	Silent	SNP	G	A	G	MMP9	c.G2082A	p.V694V
XH_P57	20	45204266	45204266	Silent	SNP	G	A	G	SLC13A3	c.C1128T	p.P376P
XH_P57	20	45717954	45717954	Silent	SNP	C	T	C	EYA2	c.C738T	p.D246D
XH_P57	20	45816757	45816757	Silent	SNP	C	T	C	EYA2	c.C1356T	p.H452H
XH_P57	20	45867852	45867852	Missense_Mutation	SNP	A	G	A	ZMYND8	c.T2099C	p.V700A
XH_P57	20	47244450	47244450	Silent	SNP	G	A	G	PREX1	c.C4818T	p.H1606H
XH_P57	20	47261017	47261017	Silent	SNP	T	C	T	PREX1	c.A3531G	p.R1177R
XH_P57	20	47351095	47351095	Silent	SNP	G	A	G	PREX1	c.C507T	p.R169R
XH_P57	20	47630449	47630449	Silent	SNP	C	T	C	ARFGEF2	c.C4131T	p.I1377I
XH_P57	20	49509184	49509184	Silent	SNP	G	A	G	ADNP	c.C2067T	p.G689G
XH_P57	20	49575419	49575419	Missense_Mutation	SNP	G	A	G	MOC53	c.G40A	p.V14I
XH_P57	20	50140627	50140627	Silent	SNP	G	C	G	NFATC2	c.C93G	p.V313V
XH_P57	20	52198340	52198340	Silent	SNP	T	A	T	ZNF217	c.A1026T	p.A342A
XH_P57	20	52570229	52570229	Silent	SNP	T	C	T	BCAS1	c.A1188G	p.S396S
XH_P57	20	56071399	56071399	Silent	SNP	C	T	C	CTCF	c.G2010A	p.R670R
XH_P57	20	56190634	56190634	Missense_Mutation	SNP	C	T	C	ZBP1	c.G37A	p.E13K
XH_P57	20	57568113	57568113	Silent	SNP	G	A	G	NELFCD	c.G1344A	p.R448R
XH_P57	20	60511860	60511860	Silent	SNP	C	T	C	CDH4	c.C2499T	p.Y833Y
XH_P57	20	60704940	60704940	Missense_Mutation	SNP	C	A	C	LSM14B	c.C527A	p.P176H
XH_P57	20	60791422	60791422	Silent	SNP	C	T	C	HRH3	c.G978A	p.P326P
XH_P57	20	60886768	60886768	Silent	SNP	C	T	C	LAMA5	c.G9708A	p.P3236P
XH_P57	20	60899191	60899191	Missense_Mutation	SNP	C	T	C	LAMA5	c.G5713A	p.D1905N
XH_P57	20	60913127	60913127	Silent	SNP	A	G	A	LAMA5	c.T1836C	p.A612A
XH_P57	20	61288258	61288258	Missense_Mutation	SNP	T	C	T	SLCO4A1	c.T452C	p.I151T
XH_P57	20	61386232	61386232	Missense_Mutation	SNP	G	A	G	NTSR1	c.G910A	p.V304I
XH_P57	20	61443687	61443687	Silent	SNP	G	A	G	OGFR	c.G720A	p.T240T
XH_P57	20	61444939	61444939	Missense_Mutation	SNP	G	C	G	OGFR	c.G1972C	p.G658R
XH_P57	20	61981279	61981279	Missense_Mutation	SNP	C	G	C	CHRNA4	c.G1484C	p.R495P
XH_P57	20	62038277	62038277	Missense_Mutation	SNP	T	G	T	KCNQ2	c.A2255C	p.N752T
XH_P57	20	62038381	62038381	Silent	SNP	C	T	C	KCNQ2	c.G2151A	p.P717P
XH_P57	20	62070966	62070966	Silent	SNP	G	A	G	KCNQ2	c.C912T	p.F304F
XH_P57	20	62126185	62126185	Silent	SNP	A	G	A	EEF1A2	c.T594C	p.G198G
XH_P57	20	62126299	62126299	Silent	SNP	C	T	C	EEF1A2	c.G480A	p.P160P
XH_P57	20	62194727	62194727	Silent	SNP	C	T	C	HELZ2	c.G3741A	p.P1247P
XH_P57	20	62221766	62221766	Silent	SNP	C	T	C	GMEB2	c.G1269A	p.P423P
XH_P57	20	62324289	62324289	Silent	SNP	C	T	C	RTLE1	c.C2115T	p.F705F
XH_P57	20	62421622	62421622	Silent	SNP	A	G	A	ZBTB46	c.T489C	p.A163A
XH_P57	20	62421823	62421823	Silent	SNP	C	T	C	ZBTB46	c.G288A	p.A96A
XH_P57	20	62422080	62422080	Missense_Mutation	SNP	T	C	T	ZBTB46	c.A31G	p.T11A
XH_P57	21	16339570	16339570	Missense_Mutation	SNP	T	A	T	NRIP1	c.A944T	p.V315F
XH_P57	21	19169218	19169218	Missense_Mutation	SNP	G	C	G	C21orf91	c.C345G	p.N115K
XH_P57	21	19713821	19713821	Silent	SNP	C	T	C	TMPPRS515	c.G1473A	p.A491A
XH_P57	21	28212760	28212760	Silent	SNP	G	A	G	ADAMTS1	c.C1500T	p.P500P
XH_P57	21	28216595	28216595	Missense_Mutation	SNP	C	G	C	ADAMTS1	c.G679C	p.A227P
XH_P57	21	28217178	28217178	Silent	SNP	T	G	T	ADAMTS1	c.A96C	p.P32P
XH_P57	21	30357163	30357163	Silent	SNP	G	T	G	LTN1	c.C564A	p.P188P
XH_P57	21	30971183	30971183	Silent	SNP	G	A	G	GRIK1	c.C747T	p.D249D
XH_P57	21	31587793	31587793	Missense_Mutation	SNP	A	G	A	CLDN8	c.T451C	p.S151P
XH_P57	21	31874211	31874211	Silent	SNP	A	G	A	KRTAP19-5	c.T198C	p.Y66Y
XH_P57	21	32201816	32201816	Silent	SNP	G	A	G	KRTAP7-1	c.C201T	p.C67C
XH_P57	21	33688944	33688947	Frame_Shift_Del	DEL	AGCC	-	AGCC	URB1	c.6464_6467del	p.R2155fs
XH_P57	21	33755763	33755763	Silent	SNP	G	A	G	URB1	c.C535T	p.L179L
XH_P57	21	34924805	34924805	Missense_Mutation	SNP	C	T	C	SON	c.C3268T	p.R1090W
XH_P57	21	35467804	35467804	Frame_Shift_Ins	INS	-	GGAT	-	SLCSA3	307_308insGG	p.R103fs
XH_P57	21	38512956	38512956	Silent	SNP	A	G	A	TTC3	c.A825G	p.V275V
XH_P57	21	38563725	38563725	Silent	SNP	G	A	G	TTC3	c.G4185A	p.K1395K
XH_P57	21	38568308	38568308	Silent	SNP	C	T	C	TTC3	c.C4620T	p.H1540H
XH_P57	21	42824661	42824661	Silent	SNP	A	G	A	MX1	c.A1623G	p.A541A
XH_P57	21	42830690	42830690	Silent	SNP	A	G	A	MX1	c.A1509G	p.T503T
XH_P57	21	42852497	42852497	Missense_Mutation	SNP	C	T	C	TMPPRS52	c.G589A	p.V197M
XH_P57	21	42866296	42866296	Silent	SNP	T	C	T	TMPPRS52	c.A336G	p.T112T
XH_P57	21	43221797	43221797	Missense_Mutation	SNP	G	C	G	PRDM15	c.C3140G	p.T1047S

XH_P57	21	43373657	43373657	Missense_Mutation	SNP	G	A	G	C2CD2	c.C101T	p.A34V
XH_P57	21	43491502	43491502	Splice_Site	SNP	G	C	G	UMODL1	.	.
XH_P57	21	43508466	43508466	Silent	SNP	C	T	C	UMODL1	c.C666T	p.N222N
XH_P57	21	43531553	43531553	Missense_Mutation	SNP	A	C	A	UMODL1	c.A2005C	p.T669P
XH_P57	21	43691232	43691232	Silent	SNP	G	A	G	ABCG1	c.G339A	p.L131L
XH_P57	21	43852232	43852232	Silent	SNP	C	T	C	UBASH3A	c.C1077T	p.S359S
XH_P57	21	44180443	44180443	Silent	SNP	C	T	C	PDE9A	c.C252T	p.C84C
XH_P57	21	44514664	44514664	Silent	SNP	T	C	T	U2AF1	c.A492G	p.T164T
XH_P57	21	45708277	45708277	Silent	SNP	C	T	C	AIRE	c.C588T	p.S196S
XH_P57	21	45712977	45712977	Silent	SNP	T	C	T	AIRE	c.T1197C	p.A399A
XH_P57	21	45811343	45811343	Missense_Mutation	SNP	T	G	T	TRPM2	c.T1629G	p.D543E
XH_P57	21	45876716	45876716	Silent	SNP	G	A	G	LRRC3	c.G189A	p.P63P
XH_P57	21	45959557	45959559	In_Frame_Del	DEL	ATC	-	ATC	KRTAP10-1	c.475_477del	p.159_159del
XH_P57	21	45994488	45994488	Missense_Mutation	SNP	G	T	G	KRTAP10-4	c.G853T	p.G285C
XH_P57	21	46011687	46011687	Missense_Mutation	SNP	C	T	C	KRTAP10-6	c.G679A	p.A227T
XH_P57	21	46021335	46021335	Missense_Mutation	SNP	G	A	G	KRTAP10-7	c.G799A	p.V267M
XH_P57	21	46057590	46057590	Missense_Mutation	SNP	A	T	A	KRTAP10-10	c.A256T	p.T86S
XH_P57	21	46066466	46066466	Missense_Mutation	SNP	T	C	T	KRTAP10-11	c.T91C	p.C31R
XH_P57	21	47552386	47552386	Missense_Mutation	SNP	G	A	G	COL6A2	c.G2980A	p.A994T
XH_P57	21	47557222	47557222	Silent	SNP	G	A	G	FTCD	c.C1470T	p.G490G
XH_P57	21	47635627	47635627	Silent	SNP	C	G	C	LSS	c.G624C	p.P208P
XH_P57	21	47641794	47641794	Missense_Mutation	SNP	C	T	C	LSS	c.G284A	p.R95Q
XH_P57	21	47642609	47642609	Silent	SNP	G	A	G	LSS	c.C123T	p.A41A
XH_P57	21	47704896	47704896	Missense_Mutation	SNP	G	A	G	MCM3AP	c.C305T	p.S102L
XH_P57	21	47970581	47970581	Silent	SNP	G	A	G	DIP2A	c.G2751A	p.T917T
XH_P57	21	47974582	47974582	Silent	SNP	A	G	A	DIP2A	c.A3237G	p.T1079T
XH_P57	21	48022230	48022230	Silent	SNP	C	G	C	S100B	c.G99C	p.L33L
XH_P57	22	17590599	17590599	Silent	SNP	C	T	C	IL17RA	c.C2388T	p.P796P
XH_P57	22	17600456	17600456	Missense_Mutation	SNP	C	T	C	CECR6	c.G1562A	p.R521Q
XH_P57	22	17600689	17600689	Silent	SNP	G	A	G	CECR6	c.C1329T	p.L443L
XH_P57	22	18021604	18021604	Missense_Mutation	SNP	C	T	C	CECR2	c.C1472T	p.P491L
XH_P57	22	18095609	18095609	Missense_Mutation	SNP	T	C	T	ATP6V1E1	c.A179G	p.K60R
XH_P57	22	18300879	18300879	Silent	SNP	G	A	G	MICAL3	c.C4548T	p.S1516S
XH_P57	22	18567995	18567997	In_Frame_Del	DEL	TCT	-	TCT	PEX26	c.785_787del	p.262_263del
XH_P57	22	18898523	18898523	Silent	SNP	C	T	C	DGCR6	c.C495T	p.Y165Y
XH_P57	22	18904489	18904489	Silent	SNP	G	A	G	PRODH	c.C1116T	p.Y372Y
XH_P57	22	18910355	18910355	Missense_Mutation	SNP	G	T	G	PRODH	c.C500A	p.T167N
XH_P57	22	19165478	19165478	Silent	SNP	A	G	A	SLC25A1	c.T300C	p.G100G
XH_P57	22	19183787	19183787	Missense_Mutation	SNP	A	G	A	CLTCL1	c.T4181C	p.I1394T
XH_P57	22	19184095	19184095	Missense_Mutation	SNP	T	C	T	CLTCL1	c.A3946G	p.M1316V
XH_P57	22	19423250	19423250	Missense_Mutation	SNP	G	A	G	MRPL40	c.G254A	p.R85H
XH_P57	22	19511265	19511265	Missense_Mutation	SNP	C	T	C	CLDN5	c.G769A	p.A257T
XH_P57	22	19776406	19776406	Silent	SNP	G	A	G	GNB1L	c.C810T	p.T270T
XH_P57	22	20024496	20024505	Frame_Shift_Del	DEL	5CCTGGCAC	-	GCCTGGCACT	TANGO2	c.58_67del	p.A20fs
XH_P57	22	20051108	20051108	Missense_Mutation	SNP	G	C	G	TANGO2	c.G559C	p.D187H
XH_P57	22	20103225	20103225	Silent	SNP	C	T	C	TRMT2A	c.G678A	p.P226P
XH_P57	22	20302276	20302276	Missense_Mutation	SNP	A	T	A	DGCR6L	c.T585A	p.P195K
XH_P57	22	20303664	20303664	Missense_Mutation	SNP	G	A	G	DGCR6L	c.C350T	p.A117V
XH_P57	22	20759672	20759672	Missense_Mutation	SNP	G	A	G	ZNF74	c.G263A	p.G88E
XH_P57	22	20761192	20761192	Missense_Mutation	SNP	G	T	G	ZNF74	c.G1656T	p.K552N
XH_P57	22	20761193	20761193	Missense_Mutation	SNP	C	T	C	ZNF74	c.C1657T	p.L553F
XH_P57	22	20784050	20784050	Missense_Mutation	SNP	T	A	T	SCARF2	c.A1273T	p.T425S
XH_P57	22	20940085	20940085	Silent	SNP	G	A	G	MED15	c.G1869A	p.P623P
XH_P57	22	21341823	21341823	Silent	SNP	C	T	C	LZTR1	c.C351T	p.P137P
XH_P57	22	21370237	21370237	Silent	SNP	T	G	T	P2RX6	c.T93G	p.A31A
XH_P57	22	21982892	21982892	Missense_Mutation	SNP	C	T	C	YDIC	c.G787A	p.A263T
XH_P57	22	22049783	22049783	Silent	SNP	C	T	C	PPIL2	c.C1563T	p.S521S
XH_P57	22	22300281	22300281	Missense_Mutation	SNP	G	A	G	PPM1F	c.C140T	p.T47M
XH_P57	22	22318619	22318619	Missense_Mutation	SNP	G	A	G	TOP3B	c.C1012T	p.R338W
XH_P57	22	22599380	22599380	Silent	SNP	G	A	G	VPREB1	c.G66A	p.L22L
XH_P57	22	23438191	23438191	Silent	SNP	C	T	C	GNAZ	c.C309T	p.D103D
XH_P57	22	23503121	23503121	Missense_Mutation	SNP	G	A	G	RAB36	c.G853A	p.G285S
XH_P57	22	23523630	23523630	Silent	SNP	C	A	C	BCR	c.C483A	p.I161I
XH_P57	22	24086107	24086107	Silent	SNP	A	G	A	ZNF70	c.T1221C	p.I407I
XH_P57	22	26194045	26194045	Silent	SNP	T	C	T	MYO18B	c.T2502C	p.G834G
XH_P57	22	26247456	26247456	Silent	SNP	G	A	G	MYO18B	c.G3798A	p.G1266G
XH_P57	22	26936766	26936766	Silent	SNP	G	A	G	TPST2	c.C831T	p.V277V
XH_P57	22	29446611	29446611	Silent	SNP	A	C	A	ZNRF3	c.A2442C	p.P814P
XH_P57	22	29456733	29456733	Silent	SNP	T	C	T	C22orf31	c.A102G	p.S34S
XH_P57	22	29630337	29630337	Missense_Mutation	SNP	G	A	G	EMID1	c.G1067A	p.R356Q
XH_P57	22	29656389	29656389	Silent	SNP	G	T	G	RHBDD3	c.C909A	p.A303A
XH_P57	22	29885473	29885473	Missense_Mutation	SNP	C	T	C	NEFH	c.C1844T	p.P615L
XH_P57	22	29908072	29908072	Missense_Mutation	SNP	C	T	C	THOC5	c.G1735A	p.V579I
XH_P57	22	30953295	30953295	Missense_Mutation	SNP	C	T	C	GAL3ST1	c.G85A	p.V29M
XH_P57	22	31010417	31010417	Missense_Mutation	SNP	G	A	G	TCN2	c.G509A	p.R170Q
XH_P57	22	31013374	31013374	Missense_Mutation	SNP	C	T	C	TCN2	c.C998T	p.T333M
XH_P57	22	31283577	31283577	Silent	SNP	G	A	G	OSBP2	c.G174A	p.P58P
XH_P57	22	31302233	31302233	Silent	SNP	T	C	T	OSBP2	c.T1290C	p.D430D
XH_P57	22	31333631	31333631	Silent	SNP	T	C	T	MORC2	c.A1437G	p.P479P
XH_P57	22	31342376	31342376	Silent	SNP	G	C	G	MORC2	c.C378G	p.T126T
XH_P57	22	31354653	31354653	Silent	SNP	G	A	G	MORC2	c.C96T	p.A32A
XH_P57	22	31741067	31741067	Silent	SNP	G	A	G	PATZ1	c.C522T	p.T174L
XH_P57	22	31971282	31971282	Missense_Mutation	SNP	T	C	T	SFI1	c.T742C	p.W248R
XH_P57	22	32108824	32108824	Silent	SNP	T	A	T	PRR14L	c.A5001T	p.T1667T
XH_P57	22	32112461	32112461	Missense_Mutation	SNP	T	C	T	PRR14L	c.A1364G	p.A455S
XH_P57	22	32589090	32589090	Missense_Mutation	SNP	C	T	C	RFPL2	c.G172A	p.A58T
XH_P57	22	32754103	32754103	Missense_Mutation	SNP	A	C	A	RFPL3	c.A45C	p.Q15H
XH_P57	22	32784051	32784051	Silent	SNP	T	C	T	RTCB	c.A1446G	p.V482V
XH_P57	22	36122517	36122517	Silent	SNP	T	C	T	APOL5	c.T402C	p.L134L
XH_P57	22	36123083	36123083	Missense_Mutation	SNP	C	T	C	APOL5	c.C968T	p.T323M
XH_P57	22	36690299	36690299	Missense_Mutation	SNP	G	A	G	MYH9	c.C3676T	p.R1226W
XH_P57	22	36900271	36900271	Missense_Mutation	SNP	T	C	T	FOXRED2	c.A923G	p.N308S
XH_P57	22	36900806	36900806	Missense_Mutation	SNP	A	G	A	FOXRED2	c.T535C	p.F179L
XH_P57	22	37603531	37603531	Silent	SNP	G	A	G	SSTR3	c.C312T	p.N104N
XH_P57	22	38221072	38221072	Silent	SNP	G	A	G	GALR3	c.G702A	p.G234G
XH_P57	22	38336756	38336756	Silent	SNP	G	A	G	MICALL1	c.G2511A	p.G837G
XH_P57	22	39357581	39357581	Silent	SNP	C	T	C	APOBEC3A	c.C364T	p.L122L
XH_P57	22	39357634	39357634	Silent	SNP	A	G	A	APOBEC3A	c.A417G	p.A139A

XH_P57	22	39381826	39381826	Missense_Mutation	SNP	A	G	A	POBEC3B	c.A184G	p.K62E
XH_P57	22	39496412	39496412	Silent	SNP	G	C	G	POBEC3H	c.G129C	p.T43T
XH_P57	22	39498038	39498038	Missense_Mutation	SNP	G	C	G	POBEC3H	c.G534C	p.E178D
XH_P57	22	40075400	40075400	Missense_Mutation	SNP	G	A	G	CACNA1I	c.G5239A	p.G1747R
XH_P57	22	40140137	40140137	Silent	SNP	G	T	G	ENTHD1	c.C1371A	p.T457T
XH_P57	22	42473860	42473860	Missense_Mutation	SNP	C	G	C	FAM109B	c.C563G	p.A188G
XH_P57	22	42486723	42486723	Missense_Mutation	SNP	G	A	G	NDUFA6	c.C104T	p.A35V
XH_P57	22	42968514	42968514	Silent	SNP	G	A	G	SERHL2	c.G612A	p.T204T
XH_P57	22	43459855	43459855	Silent	SNP	G	A	G	TTL1	c.C711T	p.F237F
XH_P57	22	43831023	43831023	Silent	SNP	C	T	C	MPPED1	c.C294T	p.T98T
XH_P57	22	43870743	43870743	Silent	SNP	G	A	G	MPPED1	c.G534A	p.P178P
XH_P57	22	44112830	44112830	Frame_Shift_Ins	INS	-	ACAAGTAAGA	-	EFCAB6	c.324insTCTTAC	p.Q108fs
XH_P57	22	44287062	44287062	Silent	SNP	A	G	A	PNPLA5	c.T306C	p.D102D
XH_P57	22	44287629	44287629	Silent	SNP	G	A	G	PNPLA5	c.C132T	p.R44R
XH_P57	22	44386281	44386281	Silent	SNP	C	T	C	SAMM50	c.C1359T	p.G453G
XH_P57	22	44586522	44586522	Silent	SNP	C	T	C	PARVG	c.C480T	p.V160V
XH_P57	22	44594584	44594584	Silent	SNP	C	G	C	PARVG	c.C795G	p.P265P
XH_P57	22	45198009	45198009	Silent	SNP	A	G	A	ARHGAP8	c.A132G	p.P44P
XH_P57	22	45683246	45683246	Silent	SNP	C	T	C	UPK3A	c.C402T	p.V134V
XH_P57	22	45723854	45723854	Silent	SNP	C	G	C	FAM118A	c.C432G	p.V144V
XH_P57	22	45749983	45749983	Missense_Mutation	SNP	G	T	G	SMC1B	c.C3148A	p.L1050M
XH_P57	22	46654197	46654197	Missense_Mutation	SNP	C	A	C	PKDREJ	c.G5023T	p.D1675Y
XH_P57	22	50435480	50435480	Missense_Mutation	SNP	A	G	A	IL17REL	c.T998C	p.L333P
XH_P57	22	50480108	50480108	Missense_Mutation	SNP	C	T	C	TTL8	c.G880A	p.E294K
XH_P57	22	50686830	50686830	Silent	SNP	G	A	G	HDAC10	c.C918T	p.A306A
XH_P57	22	50687178	50687178	Silent	SNP	C	T	C	HDAC10	c.G759A	p.G253G
XH_P57	22	50687595	50687595	Silent	SNP	A	G	A	HDAC10	c.T693C	p.V231V
XH_P57	22	50693889	50693889	Silent	SNP	G	A	G	MAPK12	c.C813T	p.S271S
XH_P57	22	50695370	50695370	Silent	SNP	G	A	G	MAPK12	c.C450T	p.I150I
XH_P57	22	50753334	50753334	Silent	SNP	G	A	G	DENND6B	c.C775T	p.L259L
XH_P57	22	50754466	50754466	Silent	SNP	C	T	C	DENND6B	c.G690A	p.Q230Q
XH_P57	22	50885775	50885775	Silent	SNP	A	G	A	SBF1	c.T5559C	p.T1853T
XH_P57	22	50898026	50898026	Silent	SNP	G	A	G	SBF1	c.C3561T	p.Y1187Y
XH_P57	22	50901009	50901009	Silent	SNP	C	T	C	SBF1	c.G2106A	p.T702T
XH_P57	22	50921149	50921166	In_Frame_Del	DEL	CGGGGCCCCG	-	CTCGGGGCCCCG	ADM2	c.264_281del	p.88_94del
XH_P57	22	50988062	50988062	Silent	SNP	G	T	G	KLHDC7B	c.G1467T	p.V489V
XH_P57	22	50988193	50988193	Missense_Mutation	SNP	A	G	A	KLHDC7B	c.A1598G	p.H533R
XH_P57	22	51009953	51009953	Missense_Mutation	SNP	C	T	C	CPT1B	c.G1489A	p.E497K
XH_P57	X	3228144	3228144	Missense_Mutation	SNP	C	G	C	MXRA5	c.G8100C	p.E2700D
XH_P57	X	3236028	3236028	Silent	SNP	C	T	C	MXRA5	c.G5694A	p.P1898P
XH_P57	X	9863112	9863112	Silent	SNP	A	G	A	SHROOM2	c.A1164G	p.P388P
XH_P57	X	9905419	9905419	Missense_Mutation	SNP	C	T	C	SHROOM2	c.C338T	p.P113L
XH_P57	X	15332558	15332558	Silent	SNP	A	G	A	ASB1	c.T51C	p.R17R
XH_P57	X	19369394	19369394	Missense_Mutation	SNP	C	T	C	PDHA1	c.C308T	p.T103I
XH_P57	X	21861434	21861434	Silent	SNP	A	G	A	M8TPS2	c.A222G	p.Q74Q
XH_P57	X	37028128	37028199	In_Frame_Del	DEL	GCCCCAGAGC	-	CGCCCCAGAGCT	FAM47C	c.1645_1716del	p.549_572del
XH_P57	X	46472826	46472826	Silent	SNP	G	A	G	SLC9A7	c.C1827T	p.Y609Y
XH_P57	X	46618321	46618321	Silent	SNP	C	G	C	SLC9A7	c.G144C	p.A48A
XH_P57	X	46713105	46713105	Silent	SNP	C	T	C	RP2	c.C297T	p.S99S
XH_P57	X	47466361	47466361	Silent	SNP	A	G	A	SYN1	c.T510C	p.N170N
XH_P57	X	48751471	48751471	Silent	SNP	A	G	A	TIMM17B	c.T228C	p.I76I
XH_P57	X	49074374	49074374	Missense_Mutation	SNP	C	T	C	CACNA1F	c.G3019A	p.G1007R
XH_P57	X	49855159	49855159	Missense_Mutation	SNP	A	G	A	CLCN5	c.A1921G	p.I641V
XH_P57	X	53455382	53455382	Silent	SNP	C	T	C	RIBC1	c.C351T	p.G117G
XH_P57	X	55479299	55479299	Silent	SNP	G	A	G	MAGEH1	c.G492A	p.G164G
XH_P57	X	57313357	57313357	Silent	SNP	T	C	T	FAAH2	c.T99C	p.G33G
XH_P57	X	69489530	69489530	Silent	SNP	C	T	C	ARR3	c.C27T	p.S9S
XH_P57	X	69550080	69550080	Silent	SNP	A	G	A	KIF4A	c.A969G	p.T323T
XH_P57	X	70837019	70837019	Silent	SNP	C	T	C	CXCR3	c.G444A	p.L148L
XH_P57	X	75649271	75649306	In_Frame_Del	DEL	CGCCCAACCC	-	GCCGCCCAACCC	MAGEE1	c.948_983del	p.316_328del
XH_P57	X	77268502	77268502	Missense_Mutation	SNP	G	C	G	ATP7A	c.G2299C	p.V767L
XH_P57	X	91873265	91873265	Missense_Mutation	SNP	G	C	G	PCDH11X	c.G3259C	p.A1087P
XH_P57	X	100743826	100743826	Missense_Mutation	SNP	A	G	A	ARMCX4	c.A250G	p.R84G
XH_P57	X	100745825	100745825	Missense_Mutation	SNP	T	C	T	ARMCX4	c.T2249C	p.L750P
XH_P57	X	100749127	100749127	Missense_Mutation	SNP	A	G	A	ARMCX4	c.A5551G	p.L1851V
XH_P57	X	100749585	100749585	Silent	SNP	C	T	C	ARMCX4	c.C6009T	p.H2003H
XH_P57	X	103042882	103042882	Silent	SNP	T	C	T	PLP1	c.T609C	p.D203D
XH_P57	X	106109175	106109175	Frame_Shift_Ins	INS	-	A	-	TBC1D8B	c.2575dupA	p.N858fs
XH_P57	X	107170053	107170053	Missense_Mutation	SNP	G	C	G	MID2	c.G1958C	p.R653P
XH_P57	X	107417730	107417730	Silent	SNP	G	A	G	COL4A6	c.C3078T	p.G1026G
XH_P57	X	107976940	107976940	Missense_Mutation	SNP	G	C	G	IRS4	c.C2635G	p.H879D
XH_P57	X	115573919	115573919	Frame_Shift_Ins	INS	-	TATA	-	SLC6A14	c.411_412insTAT	p.A137fs
XH_P57	X	118603844	118603844	Missense_Mutation	SNP	T	G	T	SLC25A5	c.T332G	p.L111R
XH_P57	X	118893054	118893054	Silent	SNP	C	A	C	SOWAHD	c.C424A	p.R142R
XH_P57	X	118893137	118893137	Silent	SNP	T	C	T	SOWAHD	c.T507C	p.D169D
XH_P57	X	118893413	118893413	Silent	SNP	T	C	T	SOWAHD	c.T783C	p.S261S
XH_P57	X	123034511	123034511	Missense_Mutation	SNP	A	C	A	XIAP	c.A1268C	p.Q423P
XH_P57	X	123480540	123480540	Silent	SNP	C	A	C	SH2D1A	c.C48A	p.G16G
XH_P57	X	123775797	123775797	Missense_Mutation	SNP	T	C	T	TENM1	c.A1921G	p.K641E
XH_P57	X	125686536	125686536	Missense_Mutation	SNP	T	C	T	DCAF12L1	c.A56G	p.D19G
XH_P57	X	125955428	125955428	Silent	SNP	G	A	G	PRR32	c.G807A	p.P269P
XH_P57	X	128901653	128901653	Silent	SNP	G	A	G	XPNP2	c.G1815A	p.L605L
XH_P57	X	129205363	129205363	Frame_Shift_Ins	INS	-	CCTC	-	ELF4	c.563_564insGAG	p.S188fs
XH_P57	X	130678596	130678596	Silent	SNP	C	G	C	OR13H1	c.C549G	p.L183L
XH_P57	X	132438872	132438872	Missense_Mutation	SNP	C	A	C	GPC4	c.G1173T	p.E391D
XH_P57	X	134713855	134713855	Silent	SNP	G	A	G	INTS6L	c.G2151A	p.L717L
XH_P57	X	136112707	136112707	Missense_Mutation	SNP	A	G	A	GPR101	c.T1127C	p.L376P
XH_P57	X	151870081	151870081	Silent	SNP	G	A	G	MAGEA6	c.G771A	p.E257E
XH_P57	X	152823728	152823728	Silent	SNP	G	C	G	ATP2B3	c.G2592C	p.V864V
XH_P57	X	153070999	153070999	Silent	SNP	G	A	G	PDZ4	c.C285T	p.N95N
XH_P57	X	153581932	153581932	Silent	SNP	A	G	A	FLNA	c.T5826C	p.A1942A
XH_P57	X	153667176	153667176	Silent	SNP	T	C	T	GD1I	c.T219C	p.N73N
XH_P57	X	153880830	153880830	Silent	SNP	A	C	A	CTAG2	c.T345G	p.P115P
XH_P57	X	153881525	153881525	Missense_Mutation	SNP	G	C	G	CTAG2	c.C265G	p.Q89E
XH_P57	h_gi0002	129326	129326	Silent	SNP	A	G	A	LOC100288966	c.T957C	p.S319S
XH_P57	1	100750881	100750884	Splice_Site	INDEL	AATG	-	-	RTCA	c.3+4_933+7delATGA	
XH_P57	1	10328243	10328243	Frame_Shift_Ins	INDEL	-	AGCC	AGCC	KIF1B	c.643_646dupAG	P.R216fs
XH_P57	1	113252779	113252816	Frame_Shift_Del	INDEL	AACTGCTG	-	-	PPM1J	c.GAGGGCCAGG	P.I496fs

XH_P57	1	117554589	117554589	Splice_Site	INDEL	-	TAAT	TAAT	CD101	1+4_841+7dupATTA	
XH_P57	1	144617193	144617193	Silent	SNV	T	C	C	NBPf9	c.216T>C	P.N72N
XH_P57	1	145532163	145532163	Missense_Mutation	INDEL	-	CTA	CTA	ITGA10	.417_419dupAC	P.L140dup
XH_P57	1	1559328	1559328	Splice_Site	SNV	G	A	A	MB2	c.764+3G>A	
XH_P57	1	156899480	156899480	Missense_Mutation	SNV	G	A	A	LRRC71	c.1199G>A	P.G400E
XH_P57	1	158532932	158532932	Missense_Mutation	SNV	T	C	C	OR6P1	c.463A>G	P.S155G
XH_P57	1	16273427	16273431	Frame_Shift_Del	INDEL	TACCT	-	-	ZBTB17	25_126+3delAG	P.K42fs
XH_P57	1	167097061	167097061	Missense_Mutation	SNV	A	G	G	DUSP27	c.2693A>G	P.Y898C
XH_P57	1	16913644	16913644	Missense_Mutation	SNV	T	C	C	NBPf1	c.679A>G	P.I227V
XH_P57	1	171509523	171509523	Missense_Mutation	SNV	G	T	T	PRRC2C	c.2912G>T	P.G971V
XH_P57	1	201981128	201981176	Frame_Shift_Del	INDEL	TCAGCTACCC	-	-	ELF3	TCAGCTACCAAC	P.V72fs
XH_P57	1	202418235	202418235	Missense_Mutation	INDEL	-	CAG	CAG	PPP1R12B	788_1790dupA	P.A597dup
XH_P57	1	205053257	205053268	Missense_Mutation	INDEL	TCACAGACGG	-	-	TMEM81	192delACCGTCT	P.T61_E64del
XH_P57	1	206646587	206646587	Frame_Shift_Ins	INDEL	-	TT	TT	IKBKE	c.18_19dupTT	P.Y7fs
XH_P57	1	228400428	228400428	Missense_Mutation	SNV	A	G	G	OBSCN	c.944A>G	P.N315S
XH_P57	1	24432520	24432520	Silent	SNV	G	A	A	MYOM3	c.450C>T	P.Y150Y
XH_P57	1	25712263	25712263	Missense_Mutation	SNV	G	A	A	RHCE	c.559C>T	P.L187F
XH_P57	1	26510959	26510959	Silent	SNV	G	T	T	CNKS1R	c.1089G>T	P.G363G
XH_P57	1	32140617	32140617	Missense_Mutation	INDEL	-	TGC	TGC	COL16A1	847_2849dupG	P.Q949dup
XH_P57	1	33099263	33099263	Missense_Mutation	SNV	C	G	G	ZBTB80S	c.325G>C	P.E109Q
XH_P57	1	3548049	3548049	Silent	SNV	C	T	T	WRAP73	c.1221G>A	P.S407S
XH_P57	1	39325208	39325208	Silent	SNV	C	T	T	RRAGC	c.111G>A	P.A37A
XH_P57	1	42744175	42744175	Silent	SNV	G	C	C	FOXJ3	c.213C>G	P.V71V
XH_P57	1	43002278	43002278	Splice_Site	SNV	A	T	T	CCDC30	c.117+6A>T	
XH_P57	1	47150211	47150217	Frame_Shift_Del	INDEL	GAGCACT	-	-	ECAB14	82_1138delAGT	P.S378fs
XH_P57	1	6038350	6038350	Frame_Shift_Ins	INDEL	-	CGG	CGG	NPHP4	256_258dupCC	P.P86dup
XH_P57	1	6418878	6418878	Splice_Site	SNV	G	A	A	ACOT7	c.20+8C>T	
XH_P57	1	97658712	97658713	Frame_Shift_Del	INDEL	TT	-	-	DPYD	2534_2535delA	P.E845fs
XH_P57	10	101715303	101715303	Missense_Mutation	SNV	C	T	T	DNMBP	c.1928G>A	P.R643H
XH_P57	10	101943529	101943529	Missense_Mutation	SNV	G	C	C	ERLIN1	c.179C>G	P.T60R
XH_P57	10	103898986	103898986	Missense_Mutation	SNV	C	G	G	PPRC1	c.721C>G	P.Q241E
XH_P57	10	125558624	125558624	Splice_Site	SNV	G	C	C	CPXM2	c.738+7C>G	
XH_P57	10	12811723	12811723	Frame_Shift_Ins	INDEL	-	GT	GT	CAMK1D	492_493dupTG	P.D165fs
XH_P57	10	30915859	30915859	Missense_Mutation	SNV	G	A	A	LYZL2	c.124C>T	P.R42W
XH_P57	10	44788818	44788825	Frame_Shift_Del	INDEL	CCGCTGTT	-	-	C10orf142	5_252delGCTG	P.R82fs
XH_P57	10	5468689	5468689	Splice_Site	INDEL	-	TATCT	TATCT	NET1	5+7_195+8insTCTTA	
XH_P57	10	55943191	55943204	Frame_Shift_Del	INDEL	TGAGTAGTTA	-	-	PCDH15	5+13delGGTAA	P.Q535fs
XH_P57	10	71905242	71905242	Silent	SNV	T	G	G	TYSDN1	c.1101A>C	P.V367V
XH_P57	10	75609012	75609012	Splice_Site	INDEL	-	TAA	TAA	CAMK2G	14+6_414+7insTTA	
XH_P57	10	871067	871070	Frame_Shift_Del	INDEL	CTCT	-	-	LARP4B	419_1422delAG	P.E474fs
XH_P57	10	98144492	98144492	Silent	SNV	G	A	A	TLL2	c.2046C>T	P.S682S
XH_P57	10	99140570	99140570	Missense_Mutation	SNV	G	A	A	RRP12	c.1336C>T	P.P446S
XH_P57	10	99228045	99228045	Missense_Mutation	INDEL	-	AGT	AGT	MMS19	1050_1052dupA	P.L351dup
XH_P57	11	102646042	102646042	Nonsense_Mutation	SNV	G	A	A	MMP10	c.943C>T	P.R315*
XH_P57	11	118773071	118773071	Missense_Mutation	SNV	C	T	T	BCL9L	c.1381G>A	P.G461R
XH_P57	11	1248597	1248597	Silent	SNV	C	T	T	MUC5B	c.636C>T	P.G212G
XH_P57	11	4976391	4976391	Missense_Mutation	SNV	C	A	A	OR51A2	c.553G>T	P.D185Y
XH_P57	11	608360	608360	Silent	SNV	G	A	A	PHRF1	c.2904G>A	P.P968P
XH_P57	11	6240194	6240194	Splice_Site	INDEL	-	AGAT	AGAT	FAM160A2	1+3_1271+6dupATCT	
XH_P57	11	62473078	62473078	Missense_Mutation	INDEL	-	GCT	GCT	BSCL2	c.96_98dupAGG	P.A33dup
XH_P57	11	66062686	66062712	Missense_Mutation	INDEL	GGGGGCCGT	-	-	TMEM151A	6GGGCCGTGCCCP.326_P334del	
XH_P57	11	69063184	69063184	Silent	SNV	G	A	A	MYEOV	c.267G>A	P.A89A
XH_P57	11	72410084	72410084	Missense_Mutation	SNV	T	C	C	ARAP1	c.2507A>G	P.E836G
XH_P57	11	74204479	74204496	Missense_Mutation	INDEL	GCCAGGCCA	-	-	LIP2	delCGCGGTGGCC	P.R85_790del
XH_P57	11	74800149	74800149	Missense_Mutation	SNV	C	T	T	OR2A4	c.610G>A	P.G204S
XH_P57	11	77378008	77378008	Missense_Mutation	SNV	C	G	G	RSF1	c.4280G>C	P.R1427T
XH_P57	11	85445492	85445492	Missense_Mutation	SNV	A	C	C	SYTL2	c.877T>G	P.F293V
XH_P57	11	9501063	9501063	Missense_Mutation	SNV	T	G	G	ZNFI43	c.612T>G	P.I204M
XH_P57	12	101603396	101603396	Missense_Mutation	SNV	C	A	A	SLCSA8	c.231G>T	P.E77D
XH_P57	12	122217457	122217457	Missense_Mutation	SNV	C	T	T	RHOE	c.583G>A	P.A195T
XH_P57	12	129558926	129558926	Silent	SNV	A	G	G	TMEM132D	c.2794T>C	P.L932L
XH_P57	12	131466398	131466413	Splice_Site	INDEL	GAATAACTGA	-	-	ADGRD1	1-11delATAACTGATCTGTGA	
XH_P57	12	14849295	14849295	Missense_Mutation	SNV	A	G	G	GUCY2C	c.88T>C	P.C30R
XH_P57	12	1887056	1887056	Missense_Mutation	INDEL	-	TAC	TAC	ADIPOR2	332_334dupTA	P.L111dup
XH_P57	12	46244364	46244364	Frame_Shift_Ins	INDEL	-	AGTT	AGTT	ARID2	460_2463dupG	P.R822fs
XH_P57	12	4791379	4791379	Missense_Mutation	SNV	G	A	A	NDUFA9	c.809G>A	P.R270Q
XH_P57	12	49440064	49440064	Frame_Shift_Ins	INDEL	-	T	T	KMT2D	c.4561dupA	P.L512fs
XH_P57	12	51639824	51639826	Missense_Mutation	INDEL	GCT	-	-	SMAGP	193_195delAG	P.S65del
XH_P57	12	56551525	56551526	Splice_Site	INDEL	GC	-	-	MYL6B	*9+6_*9+7delGC	
XH_P57	12	64827294	64827294	Missense_Mutation	SNV	C	T	T	XPOT	c.2363C>T	P.A788V
XH_P57	12	67700025	67700025	Silent	SNV	T	C	C	CAND1	c.2505T>C	P.S583S
XH_P57	13	20221394	20221394	Frame_Shift_Ins	INDEL	-	AG	AG	MPHOSPH8	1188_1189dupA	P.G397fs
XH_P57	13	33591089	33591089	Missense_Mutation	SNV	C	A	A	KL	c.511C>A	P.R171S
XH_P57	13	39546671	39546671	Frame_Shift_Ins	INDEL	-	TAAC	TAAC	STOML3	259_262dupGT	P.T88fs
XH_P57	13	41705921	41705921	Missense_Mutation	SNV	C	T	T	KBTBD6	c.727G>A	P.A243T
XH_P57	13	45914196	45914196	Frame_Shift_Ins	INDEL	-	CATC	CATC	TP1	225_226insGAT	P.H76fs
XH_P57	13	46539401	46539414	Splice_Site	INDEL	GCAAAAGT	-	-	ZC3H13	74+14delGTAACATTTTGACAG	
XH_P57	13	49795277	49795277	Silent	SNV	G	A	A	MLNR	c.804G>A	P.G268G
XH_P57	14	105410816	105410816	Missense_Mutation	SNV	C	T	T	AHNAK2	c.10972G>A	P.E3658K
XH_P57	14	23894053	23894053	Silent	SNV	A	G	G	MYH7	c.2604T>C	P.A868A
XH_P57	14	25443879	25443879	Frame_Shift_Ins	INDEL	-	AGAT	AGAT	STXBP6	142_145dupAT	P.C49fs
XH_P57	14	59951012	59951012	Missense_Mutation	SNV	G	A	A	L3HYPDH	c.23C>T	P.P8L
XH_P57	14	65270357	65270376	Frame_Shift_Del	INDEL	ACCAGGCCGG	-	-	SPTB	81CAACCAACCCGCC	P.N142fs
XH_P57	14	68042547	68042547	Frame_Shift_Ins	INDEL	-	G	G	PLEKHH1	c.2180dupG	P.C728fs
XH_P57	14	74443720	74443720	Splice_Site	INDEL	-	TAT	TAT	ENTPD5	63+4_553+6dupATA	
XH_P57	14	77951255	77951255	Missense_Mutation	SNV	G	T	T	ISM2	c.149C>A	P.A50D
XH_P57	14	91755515	91755515	Missense_Mutation	SNV	C	T	T	CCDC88C	c.4375G>A	P.D1459N
XH_P57	14	93460191	93460219	Splice_Site	INDEL	TATGTGGTGG	-	-	ITPK1	ACAGTGTGGCCACACATCCGTGGCAGG	
XH_P57	14	94394645	94394645	Missense_Mutation	SNV	G	C	C	FAM181A	c.14G>C	P.S5T
XH_P57	15	45406896	45406896	Missense_Mutation	SNV	T	G	G	DUOXA2	c.93T>G	P.F31L
XH_P57	15	56388726	56388726	Frame_Shift_Ins	INDEL	-	TGAG	TGAG	RFK7	196_1199dupC	P.Q400fs
XH_P57	15	73832892	73832892	Missense_Mutation	SNV	T	C	C	REC114	c.316T>C	P.F106L
XH_P57	15	75499768	75499768	Missense_Mutation	SNV	C	T	T	C15orf39	c.1379C>T	P.P460L
XH_P57	15	78770698	78770698	Silent	SNV	C	A	A	IREB2	c.505C>A	P.R169R
XH_P57	15	83679041	83679041	Silent	SNV	G	A	A	C15orf40	c.186C>T	P.C62C
XH_P57	15	86123751	86123751	Frame_Shift_Ins	INDEL	-	TG	TG	AKAP13	2453_2454insG	P.H819fs
XH_P57	16	1820661	1820666	Missense_Mutation	INDEL	GCCAGT	-	-	NME3	94_499delACTG	P.H165_W166del
XH_P57	16	1825663	1825668	Missense_Mutation	INDEL	GCTCTC	-	-	EME2	59_764delTCTCP	P.L254_A255del

XH_P57	16	21221430	21221430	Missense_Mutation	SNV	C	A	A	ZP2	c.235G>T	P.D79Y
XH_P57	16	21288900	21288910	Missense_Mutation	INDEL	GGTAGCTAC	-	-	CRYM	176delTGTA	P.Y58_L59del
XH_P57	16	22326513	22326513	Missense_Mutation	SNV	A	G	G	POLR3E	c.626A>G	P.H209R
XH_P57	16	2578159	2578182	Splice_Site	INDEL	CCAGGGGCG	-	-	AMDHD2	1ATGGGGCCCCAGGGGGGGGGCTGG	
XH_P57	16	28354000	28354000	Silent	SNV	G	C	C	NP1PB6	c.1206C>G	P.P402P
XH_P57	16	2946666	2946666	Silent	SNV	C	T	T	FLYWCH2	c.216C>T	P.G72G
XH_P57	16	3017810	3017828	Frame_Shift_Del	INDEL	CTGTCTGCTG	-	-	KREMEN2	1delAGCTGTCTGC	P.A329fs
XH_P57	16	3367023	3367023	Splice_Site	INDEL	-	TAAA	TAAA	ZNF75A	4+4_934+7dupAATA	
XH_P57	16	47143623	47143623	Splice_Site	SNV	C	A	A	NETO2	c.634-1G>T	
XH_P57	16	56370652	56370652	Silent	SNV	C	T	T	GNAO1	c.603C>T	P.D201D
XH_P57	16	67289369	67289369	Frame_Shift_Ins	INDEL	-	AGTC	AGTC	SLC9A5	729_732dupAG	P.A245fs
XH_P57	16	70365715	70365715	Frame_Shift_Ins	INDEL	-	G	G	DDX19B	c.790dupG	P.A264fs
XH_P57	16	75513044	75513044	Missense_Mutation	SNV	G	A	A	CHST6	c.683C>T	P.T228I
XH_P57	16	81053707	81053707	Frame_Shift_Ins	INDEL	-	ACA	ACA	CENPN	358_360dupAC	P.T120dup
XH_P57	16	84229517	84229517	Silent	SNV	G	A	A	ADAD2	c.1149G>A	P.A383A
XH_P57	16	84693385	84693385	Missense_Mutation	SNV	G	A	A	KLHL36	c.1157G>A	P.R386H
XH_P57	16	8993587	8993587	Silent	SNV	T	C	C	USP7	c.2289A>G	P.E763E
XH_P57	17	17109309	17109324	Frame_Shift_Del	INDEL	AGAGATCCAA	-	-	PLD6	2delAGCTCTGGA	P.S93fs
XH_P57	17	28769470	28769472	Splice_Site	INDEL	TGA	-	-	CPD	32+2_1632+4delTGA	
XH_P57	17	41573636	41573638	Frame_Shift_Del	INDEL	GGT	-	-	DHX8	300_1300+2delG	P.D434fs
XH_P57	17	4622585	4622585	Frame_Shift_Ins	INDEL	-	TATC	TATC	ARRB2	852_855dupAT	P.P286fs
XH_P57	17	48546028	48546028	Silent	SNV	C	T	T	CHAD	c.147G>A	P.V49V
XH_P57	17	48649993	48649993	Silent	SNV	C	T	T	CACNA1G	c.825C>T	P.R275R
XH_P57	17	56356648	56356648	Splice_Site	SNV	C	T	T	MPO	c.678+10G>A	
XH_P57	17	72245220	72245220	Splice_Site	INDEL	-	T	T	TTYH2	c.-90+2dupT	
XH_P57	17	73732412	73732412	Missense_Mutation	SNV	A	T	T	ITGB4	c.1805A>T	P.H602L
XH_P57	17	73837050	73837050	Missense_Mutation	SNV	T	C	C	UNC13D	c.602A>G	P.T201R
XH_P57	17	7579527	7579527	Frame_Shift_Ins	INDEL	-	C	C	TP53	c.159dupG	P.F54fs
XH_P57	17	76116777	76116777	Missense_Mutation	SNV	C	T	T	TM6C	c.1672G>A	P.V558I
XH_P57	17	77079574	77079574	Nonsense_Mutation	SNV	C	T	T	ENGASE	c.1153C>T	P.R385*
XH_P57	17	78166351	78166351	Missense_Mutation	SNV	G	T	T	CARD14	c.1289G>T	P.R430L
XH_P57	17	79803540	79803540	Frame_Shift_Ins	INDEL	-	TC	TC	P4HB	1254_1255dupG	P.N419fs
XH_P57	17	80273272	80273272	Silent	SNV	C	T	T	CD7	c.648G>A	P.S216S
XH_P57	17	80332897	80332897	Missense_Mutation	SNV	C	T	T	UTS2R	c.697C>T	P.R233C
XH_P57	17	9862584	9862584	Missense_Mutation	SNV	G	C	C	GAS7	c.40C>G	P.L14V
XH_P57	18	12982677	12982680	Splice_Site	INDEL	AAGA	-	-	SEH1L	9+3_919+6delAAGA	
XH_P57	18	13069114	13069114	Silent	SNV	T	A	A	CEP192	c.4989T>A	P.A1663A
XH_P57	18	14850280	14850280	Nonsense_Mutation	SNV	G	T	T	ANKRD30B	c.3106G>T	P.E1036*
XH_P57	18	19019528	19019528	Silent	SNV	C	A	A	GREB1L	c.879C>A	P.S293S
XH_P57	18	47431128	47431128	Missense_Mutation	SNV	G	A	A	MYO5B	c.2485C>T	P.R829C
XH_P57	18	48593518	48593531	Frame_Shift_Del	INDEL	ATGCTGTTCA	-	-	SMAD4	286delGCTGTTCC	P.A425fs
XH_P57	18	54354098	54354098	Missense_Mutation	SNV	A	G	G	WDR7	c.610A>G	P.I204V
XH_P57	18	59855000	59855000	Missense_Mutation	SNV	A	G	G	KIAA1468	c.262A>G	P.T88A
XH_P57	19	11486642	11486663	Frame_Shift_Del	INDEL	SACCCCGACG	-	-	SWSAP1	5CTGGTGACCCC	P.A214fs
XH_P57	19	11532450	11532455	Missense_Mutation	INDEL	ATAGTT	-	-	CCDC151	18_1323delAAC	P.N440_Y441del
XH_P57	19	1582656	1582659	Frame_Shift_Del	INDEL	AGCT	-	-	MBD3	461_464delAGC	P.E154fs
XH_P57	19	16625435	16625435	Silent	SNV	G	A	A	C19orf44	c.1767G>A	P.A589A
XH_P57	19	17436152	17436152	Missense_Mutation	SNV	C	T	T	AN08	c.2705G>A	P.R902H
XH_P57	19	17444569	17444570	Frame_Shift_Del	INDEL	GT	-	-	AN08	c.146_147delAC	P.Y49fs
XH_P57	19	31769550	31769550	Silent	SNV	C	T	T	TSH23	c.1149G>A	P.S383S
XH_P57	19	35842652	35842652	Silent	SNV	G	A	A	FFAR1	c.198G>A	P.A66A
XH_P57	19	46388315	46388343	Frame_Shift_Del	INDEL	ACAGCGCCAC	-	-	IRF2BP1	1CAGCTACTGGC	P.E231fs
XH_P57	19	49671832	49671832	Missense_Mutation	SNV	G	A	A	TRPM4	c.635G>A	P.R212Q
XH_P57	19	50812280	50812280	Nonsense_Mutation	SNV	C	T	T	MYH14	c.5707C>T	P.R1903*
XH_P57	19	50837660	50837660	Splice_Site	INDEL	-	TAC	TAC	NAP5B	930-1_931dupGTA	
XH_P57	19	55445980	55445980	Missense_Mutation	SNV	T	C	C	NLRP7	c.2348A>G	P.Y783C
XH_P57	19	55991285	55991285	Splice_Site	INDEL	-	TGACT	TGACT	ZNF628	7+2_7+3insGACTT	
XH_P57	19	5749130	5749130	Frame_Shift_Ins	INDEL	-	TA	TA	CATSPERD	c.926_927dupTA	P.T310fs
XH_P57	19	7570324	7570324	Splice_Site	INDEL	-	GA	GA	C19orf45	95+6_895+7dupAG	
XH_P57	19	8808394	8808394	Missense_Mutation	SNV	G	A	A	ACTL9	c.658C>T	P.R220C
XH_P57	19	9056482	9056482	Missense_Mutation	SNV	C	T	T	MUC16	c.30964G>A	P.E10322K
XH_P57	2	133075955	133075955	Silent	SNV	C	T	T	ZNF806	c.1416C>T	P.L472L
XH_P57	2	157407259	157407259	Splice_Site	INDEL	-	TAAT	TAAT	GPD2	1+3_971+6dupAATT	
XH_P57	2	162565292	162565299	Frame_Shift_Del	INDEL	GTCATGCA	-	-	SLC4A10	7_44delATGCA	P.M13fs
XH_P57	2	169038488	169038488	Frame_Shift_Ins	INDEL	-	AA	AA	STK39	c.319_320dupT	P.L107fs
XH_P57	2	177193083	177193083	Frame_Shift_Ins	INDEL	-	TT	TT	MTX2	c.319_320dupT	P.L107fs
XH_P57	2	179587377	179587377	Splice_Site	INDEL	-	ATC	ATC	TTN	89+6_21289+8dupGAT	
XH_P57	2	20133182	20133182	Frame_Shift_Ins	INDEL	-	AG	AG	WDR35	c.2670_2671insC	P.T891fs
XH_P57	2	203500378	203500378	Frame_Shift_Ins	INDEL	-	CCA	CCA	FAM117B	475_478dupCA	P.L160fs
XH_P57	2	210752971	210752971	Silent	SNV	C	T	T	UNC80	c.4269C>T	P.V1423V
XH_P57	2	220370796	220370802	Splice_Site	INDEL	TAGGTAC	-	-	GMPPA	+2_993+8delTAGGTAC	
XH_P57	2	232672202	232672202	Missense_Mutation	SNV	C	T	T	COPS7B	c.710C>T	P.P237L
XH_P57	2	239057659	239057659	Missense_Mutation	SNV	G	A	A	KLHL30	c.1351G>A	P.V451M
XH_P57	2	242036794	242036794	Missense_Mutation	SNV	C	A	A	MTERF4	c.5G>T	P.R2L
XH_P57	2	54123933	54123933	Splice_Site	INDEL	-	TC	TC	PSME4	c.88+7_3688+8insGA	
XH_P57	2	69179971	69179971	Splice_Site	INDEL	-	A	A	GKN2	c.12+10dupT	
XH_P57	2	85890553	85890553	Silent	SNV	G	A	A	SFTPB	c.954C>T	P.T318T
XH_P57	20	25259097	25259115	Frame_Shift_Del	INDEL	CATGGTGGG	-	-	PYGB	1delAGGTGCTAGT	P.K333fs
XH_P57	20	2816138	2816138	Frame_Shift_Ins	INDEL	-	GGCC	GGCC	PCED1A	178_1181dupG	P.P395fs
XH_P57	20	306748	306748	Missense_Mutation	INDEL	-	CCA	CCA	SOX12	c.181_182insCA	P.D60_Q61insP
XH_P57	20	30816237	30816237	Silent	SNV	T	C	C	POFUT1	c.714T>C	P.H238H
XH_P57	20	4163205	4163205	Missense_Mutation	INDEL	-	GGC	GGC	SMOX	1081_1082insC	P.L360_Q361insA
XH_P57	20	57568113	57568113	Silent	SNV	G	A	A	NELFCD	c.1344G>A	P.R448R
XH_P57	20	61981279	61981279	Missense_Mutation	SNV	C	G	G	CHRNA4	c.1484G>C	P.R495P
XH_P57	20	62194727	62194727	Silent	SNV	C	T	T	HELZ2	c.5448G>A	P.P1816P
XH_P57	21	33688944	33688947	Frame_Shift_Del	INDEL	AGCC	-	-	URB1	464_6467delGC	P.R2155fs
XH_P57	21	35467804	35467804	Frame_Shift_Ins	INDEL	-	GGAT	GGAT	SLCSA3	309_310insATG	P.S104fs
XH_P57	21	43804075	43804075	Splice_Site	INDEL	T	-	-	TMPPRS53	c.616+4delA	
XH_P57	21	44514664	44514664	Silent	SNV	T	C	C	U2AF1L5	c.492A>G	P.T164T
XH_P57	22	18567995	18567997	Missense_Mutation	INDEL	TCT	-	-	PEX26	c.785_787delTCT	P.C262_Q263delinsR
XH_P57	22	22318619	22318619	Missense_Mutation	SNV	G	A	A	TOP3B	c.1012C>T	P.R338W
XH_P57	22	46654197	46654197	Missense_Mutation	SNV	C	A	A	PKDREJ	c.5023G>T	P.D1675Y
XH_P57	22	11468286	11468286	Silent	SNV	T	C	C	ATG7	c.1884T>C	P.D628D
XH_P57	3	122512460	122512460	Splice_Site	INDEL	-	TG	TG	HSPBAP1	c.64+3_64+4insCA	
XH_P57	3	128707606	128707606	Missense_Mutation	SNV	T	C	C	KIAA1257	c.418A>G	P.M140V
XH_P57	3	12983345	12983345	Missense_Mutation	SNV	C	A	A	IQSEC1	c.44G>T	P.S15I
XH_P57	3	132319924	132319924	Missense_Mutation	SNV	T	C	C	ACKR4	c.683T>C	P.M228T
XH_P57	3	136141604	136141604	Splice_Site	INDEL	C	-	-	STAG1	c.1833+6delG	

XH_P57	3	149089466	149089466	Splice_Site	INDEL	-	TTC	TTC	TM4SF1	4+5_594+7dupGAA	
XH_P57	3	151160772	151160772	Missense_Mutation	SNV	C	G	G	IGSF10	c.5963G>C	P.R1988T
XH_P57	3	151161427	151161427	Missense_Mutation	SNV	C	T	T	IGSF10	c.5308G>A	P.E1770K
XH_P57	3	158383218	158383218	Frame_Shift_Ins	INDEL	-	AC	AC	GFMI	1530_1531insA	P.V511fs
XH_P57	3	158383219	158383219	Missense_Mutation	SNV	G	T	T	GFMI	c.1531G>T	P.V511f
XH_P57	3	159606676	159606694	Frame_Shift_Del	INDEL	ACTATTGGG	-	-	SHIP1	delTGACTATTGG	P.MA09fs
XH_P57	3	186943197	186943197	Silent	SNV	G	A	A	MASP1	c.1656C>T	P.D552D
XH_P57	3	39453851	39453851	Missense_Mutation	INDEL	-	GTC	GTC	RPSA	c.896_897insTC	P.W299delinsCR
XH_P57	3	47288941	47288941	Missense_Mutation	SNV	G	T	T	KIF9	c.1155C>A	P.D385E
XH_P57	3	49040032	49040032	Splice_Site	SNV	G	A	A	P4HTM	c.724+3G>A	
XH_P57	3	50151396	50151403	Frame_Shift_Del	INDEL	TGGAACGC	-	-	RBM5	4_1641delAACG	P.E545fs
XH_P57	3	50294487	50294487	Frame_Shift_Ins	INDEL	-	CAGT	CAGT	GNAI2	733_736dupAG	P.P246fs
XH_P57	3	52183892	52183892	Missense_Mutation	SNV	G	A	A	POC1A	c.215C>T	P.S72L
XH_P57	3	69134333	69134333	Frame_Shift_Ins	INDEL	-	AACT	AACT	ARL6IP5	137_140dupAC	P.Y47fs
XH_P57	4	100057612	100057612	Splice_Site	SNV	T	A	A	ADH4	c.582+5A>T	
XH_P57	4	100057613	100057613	Splice_Site	SNV	T	A	A	ADH4	c.582+4A>T	
XH_P57	4	100845949	100845949	Nonstop_Mutation	SNV	C	A	A	DNAJB14	c.329G>T	P.Ter110Lext*?
XH_P57	4	111543573	111543573	Missense_Mutation	SNV	G	A	A	PITX2	c.44C>T	P.A15V
XH_P57	4	1656900	1656900	Silent	SNV	G	A	A	FAM53A	c.687C>T	P.L229L
XH_P57	4	517686	517686	Missense_Mutation	SNV	G	A	A	PIGG	c.2053G>A	P.G685S
XH_P57	5	126783373	126783373	Silent	SNV	G	A	A	MEGF10	c.2853G>A	P.T951T
XH_P57	5	137726964	137726964	Missense_Mutation	SNV	C	G	G	KDM3B	c.1643C>G	P.A548G
XH_P57	5	139927354	139927366	Frame_Shift_Del	INDEL	GGCCGGGAA	-	-	EIF4EBP3	5delGGGCGCGG	P.G12fs
XH_P57	5	140051060	140051060	Frame_Shift_Ins	INDEL	-	CACC	CACC	DND1	876_879dupGG	P.I294fs
XH_P57	5	140558916	140558916	Missense_Mutation	SNV	C	G	G	PCDH8	c.1301C>G	P.T434R
XH_P57	5	140594234	140594234	Missense_Mutation	SNV	G	A	A	PCDH13	c.539G>A	P.R180Q
XH_P57	5	140768428	140768428	Missense_Mutation	SNV	T	C	C	PCDHGB4	c.977T>C	P.I326T
XH_P57	5	145719271	145719271	Missense_Mutation	SNV	C	T	T	POU4F3	c.281C>T	P.T94I
XH_P57	5	156531674	156531674	Splice_Site	INDEL	-	A	A	HAVCR2	c.478+2dupT	
XH_P57	5	16694522	16694522	Missense_Mutation	SNV	C	T	T	MYO10	c.3758G>A	P.S1253N
XH_P57	5	169496219	169496219	Missense_Mutation	SNV	T	C	C	DOCK2	c.4723T>C	P.W1575R
XH_P57	5	176795196	176795196	Missense_Mutation	SNV	T	G	G	RGS14	c.778T>G	P.S260A
XH_P57	5	2749490	2749490	Splice_Site	SNV	G	A	A	IRX2	c.655+6C>T	
XH_P57	5	41910004	41910004	Splice_Site	SNV	A	T	T	C5orf51	c.354+10A>T	
XH_P57	5	43122176	43122176	Frame_Shift_Ins	INDEL	-	GAATGC	GAATGC	ZNF131	22_27dupGAAT	P.E8_C9dup
XH_P57	5	50685678	50685678	Missense_Mutation	SNV	G	A	A	ISL1	c.677G>A	P.R226Q
XH_P57	5	54528294	54528294	Silent	SNV	C	T	T	CCNO	c.462G>A	P.L154L
XH_P57	6	111650743	111650769	Missense_Mutation	INDEL	TCCCAGAAA	-	-	REV3L	GCTAATTTTCTC	P.S2736_P2744del
XH_P57	6	116968690	116968690	Frame_Shift_Ins	INDEL	-	AAT	AAT	ZUFSP	397_1399dupA	P.Y466dup
XH_P57	6	132189165	132189165	Missense_Mutation	SNV	A	G	G	ENPP1	c.1172A>G	P.K391R
XH_P57	6	145956618	145956618	Missense_Mutation	SNV	G	C	C	EPMA2	c.481C>G	P.L161V
XH_P57	6	154412347	154412347	Missense_Mutation	SNV	G	A	A	OPRM1	c.904G>A	P.V302I
XH_P57	6	161807831	161807831	Frame_Shift_Ins	INDEL	-	AAA	AAA	PARK2	1161_1162insTT	P.T387_T388insf
XH_P57	6	44195083	44195083	Splice_Site	INDEL	-	G	G	SLC29A1	c.29+8dupG	
XH_P57	6	44221115	44221127	Splice_Site	INDEL	TAAGTAGCT	-	-	HSP90AB1	D65+16delAGTAGCTTTGGTA	
XH_P57	6	44270170	44270170	Silent	SNV	C	T	T	AAR5A	c.2445G>A	P.A815A
XH_P57	6	7584943	7584943	Missense_Mutation	SNV	A	G	G	DSP	c.5651A>G	P.Y1884C
XH_P57_mann ha	7	4506084	4506084	Missense_Mutation	SNV	T	C	C	HLA-DPB1	c.190T>C	P.F64L
XH_P57	7	120382663	120382663	Splice_Site	INDEL	-	GAC	GAC	KCND2	7+8_1467+10dupGAC	
XH_P57	7	132193201	132193201	Silent	SNV	A	G	G	PLXNA4	c.252T>C	P.H84H
XH_P57	7	142564250	142564260	Frame_Shift_Del	INDEL	CTGTGGTGC	-	-	EPHB6	610delTTGTGGT	P.V201fs
XH_P57	7	150707738	150707738	Silent	SNV	G	A	A	NOS3	c.2739G>A	P.E913E
XH_P57	7	150715492	150715512	Missense_Mutation	INDEL	CGCACGACC	-	-	ATG9B	ATGCCAGGGTCC	P.C581_Q587del
XH_P57	7	150878399	150878399	Missense_Mutation	SNV	C	T	T	ASB10	c.731G>A	P.AS24H
XH_P57	7	2985463	2985463	Silent	SNV	G	A	A	CARD11	c.348C>T	P.S116S
XH_P57	7	47859156	47859156	Frame_Shift_Ins	INDEL	-	T	T	C7orf69	c.275dupT	P.L92fs
XH_P57	7	4901062	4901062	Missense_Mutation	SNV	C	T	T	PAPOLB	c.380G>A	P.R127Q
XH_P57	7	65154268	65154268	Splice_Site	SNV	T	A	A	INTS4P2	n.768-6T>A	
XH_P57	7	6550293	6550293	Missense_Mutation	SNV	C	T	T	GRID2IP	c.1600G>A	P.E534K
XH_P57	7	74564546	74564546	Missense_Mutation	SNV	G	A	A	GTF2IRD2	c.2293G>A	P.A765T
XH_P57	7	933428	933428	Silent	SNV	C	T	T	GET4	c.798C>T	P.L266L
XH_P57	7	99332635	99332635	Splice_Site	INDEL	-	AGTT	AGTT	CYP3A7	1+7_71+10dupAACT	
XH_P57	8	104897809	104897809	Missense_Mutation	SNV	G	A	A	RIMS2	c.982G>A	P.E328K
XH_P57	8	110592147	110592154	Frame_Shift_Del	INDEL	CAGAAAGGT	-	-	SYBU	5_612delAACCT	P.D202fs
XH_P57	8	124693533	124693533	Missense_Mutation	SNV	G	A	A	ANXA13	c.1021C>T	P.R341C
XH_P57	8	146157483	146157483	Silent	SNV	G	C	C	ZNF16	c.690C>G	P.V230V
XH_P57	8	28998021	28998021	Missense_Mutation	SNV	T	A	A	KIF13B	c.2448A>T	P.L816F
XH_P57	8	8887407	8887407	Missense_Mutation	INDEL	-	TAG	TAG	ER1	914_916dupTAP	P.I305_A306insV
XH_P57	8	89068349	89068349	Splice_Site	INDEL	-	CA	CA	MMP16	173+6_1373+7insTG	
XH_P57	8	97251798	97251798	Frame_Shift_Ins	INDEL	-	AT	AT	MTERF3	1173_1174dupA	P.S392fs
XH_P57	9	100449371	100449371	Splice_Site	INDEL	-	AG	AG	XPA	55+5_555+6dupCT	
XH_P57	9	104499987	104499987	Missense_Mutation	SNV	G	A	A	GRIN3A	c.275C>T	P.S92L
XH_P57	9	109688010	109688010	Frame_Shift_Ins	INDEL	-	T	T	ZNF462	c.1819dupT	P.Y607fs
XH_P57	9	123914854	123914854	Missense_Mutation	SNV	C	T	T	CNTRL	c.4055C>T	P.S1352L
XH_P57	9	129974928	129974929	Frame_Shift_Del	INDEL	GG	-	-	RALGPS1	1251_1252delG	P.W417fs
XH_P57	9	131768785	131768785	Missense_Mutation	SNV	C	T	T	NUP188	c.5078C>T	P.T1693M
XH_P57	9	131830610	131830610	Splice_Site	INDEL	-	GGTG	GGTG	MIGA2	4+3_1404+6dupGGGT	
XH_P57	9	133760139	133760139	Frame_Shift_Ins	INDEL	-	GCC	GCC	ABL1	2463_2464insCC	P.Q821_V822insP
XH_P57	9	136672413	136672413	Silent	SNV	C	T	T	VAV2	c.702G>A	P.P234P
XH_P57	9	139612156	139612156	Missense_Mutation	SNV	T	C	C	FAM69B	c.191T>A	P.V64A
XH_P57	9	140093651	140093651	Missense_Mutation	SNV	G	A	A	TPRN	c.1513C>T	P.P505S
XH_P57	9	140126108	140126108	Splice_Site	SNV	C	T	T	SLC34A3	c.39-8C>T	
XH_P57	9	2643634	2643634	Missense_Mutation	SNV	G	C	C	VLDLR	c.827G>C	P.R276P
XH_P57	9	37800651	37800664	Splice_Site	INDEL	TCGCTCCCTA	-	-	DCAF10	10+20delACTCGCTCCCTACC	
XH_P57	9	4661970	4661971	Frame_Shift_Del	INDEL	GA	-	-	SPATA6L	c.105_106delTC	P.P35fs
XH_P57	9	6540155	6540155	Splice_Site	SNV	G	A	A	GLDC	c.2570-9C>T	
XH_P57	9	96318822	96318822	Silent	SNV	C	T	T	FAM120A	c.2430C>T	P.L810L
XH_P57	X	106109175	106109175	Frame_Shift_Ins	INDEL	-	A	A	TBC1D8B	c.2577dupA	P.D860fs
XH_P57	X	107170053	107170053	Missense_Mutation	SNV	G	C	C	MID2	c.1958G>C	P.R653P
XH_P57	X	115573919	115573919	Frame_Shift_Ins	INDEL	-	TATA	TATA	SLC6A14	412_415dupTA	P.S139fs
XH_P57	X	128901653	128901653	Silent	SNV	G	A	A	XPNPPE2	c.1815G>A	P.L605L
XH_P57	X	151870081	151870081	Silent	SNV	G	A	A	MAGEA6	c.771G>A	P.E257E
XH_P57	X	18963287	18963287	Splice_Site	SNV	A	C	C	PHKA2	c.538-11T>G	
XH_P57	X	46713105	46713105	Silent	SNV	C	T	T	RP2	c.297C>T	P.S99S
XH_P57	X	53455382	53455382	Silent	SNV	C	T	T	RIBC1	c.351C>T	P.G117G
XH_P57	X	70837019	70837019	Silent	SNV	C	T	T	CXCR3	c.444G>A	P.L148L
XH_P61	1	11159837	11159837	Missense_Mutation	SNP	T	C	T	EXOSC10	c.A52G	p.T18A
XH_P61	1	11303178	11303178	Missense_Mutation	SNP	C	T	C	MTOR	c.G1405A	p.A469T

XH_P61	1	17949531	17949531	Missense_Mutation	SNP	T	G	T	ARHGEF10L	c.T395G	p.L132R
XH_P61	1	40424381	40424381	Silent	SNP	T	C	T	MFS02A	c.T276C	p.P92P
XH_P61	1	57173257	57173257	Frame_Shift_Ins	INS	-	TATATGGAAAGT	-	PRKAA2	531insTTATATG	p.H510fs
XH_P61	1	94685922	94685922	Missense_Mutation	SNP	G	A	G	ARHGAP29	c.C40T	p.R14C
XH_P61	1	101004669	101004669	Silent	SNP	C	T	C	GPR88	c.C147T	p.N49N
XH_P61	1	150939603	150939603	Silent	SNP	G	T	G	CERS2	c.C688A	p.R230R
XH_P61	1	152681680	152681680	In_Frame_Ins	INS	-	TCTGGGGGCTAC	-	LCE4A	nsAGCTCTGGGGG43delinsSSSSGGYC	
XH_P61	1	158390477	158390477	Nonsense_Mutation	INS	-	ACCAT	-	OR10K2	179_180insATG	p.Y60_161delinsX
XH_P61	1	158390479	158390479	Missense_Mutation	SNP	A	T	A	OR10K2	c.T178A	p.Y60N
XH_P61	1	160523750	160523750	Missense_Mutation	SNP	G	A	G	CD8A	c.C232T	p.T78M
XH_P61	1	172376914	172376914	Missense_Mutation	SNP	G	A	G	DNM3	c.G2513A	p.R838Q
XH_P61	1	206972324	206972324	Missense_Mutation	SNP	C	T	C	IL19	c.C85T	p.P29S
XH_P61	1	209778962	209778962	Frame_Shift_Ins	INS	-	AAACACT	-	CAMK1G	78_379insAAAC	p.Q126fs
XH_P61	1	227170708	227170708	Silent	SNP	C	T	C	COQ8A	c.C1053T	p.G351G
XH_P61	1	229771573	229771573	Missense_Mutation	SNP	A	C	A	URB2	c.A1213C	p.I405L
XH_P61	1	241755352	241755352	Missense_Mutation	SNP	T	G	T	KMO	c.T1358G	p.L453W
XH_P61	1	244541841	244541841	Silent	SNP	C	G	C	C1orf100	c.C225G	p.L75L
XH_P61	2	24090816	24090816	Frame_Shift_Ins	INS	-	G	-	ATAD2B	1076_1077ins	p.R359fs
XH_P61	2	84897597	84897597	Missense_Mutation	SNP	T	G	T	DNAH6	c.T6452G	p.L2151R
XH_P61	2	100007076	100007076	Missense_Mutation	SNP	G	C	G	EIF5B	c.G2656C	p.D886H
XH_P61	2	131521579	131521579	Missense_Mutation	SNP	C	T	C	AMER3	c.C1934T	p.P645L
XH_P61	2	189904195	189904195	Missense_Mutation	SNP	C	T	C	COL5A2	c.G3728A	p.S1243N
XH_P61	2	220045431	220045431	Missense_Mutation	SNP	G	C	G	RETREG2	c.G595C	p.V199L
XH_P61	2	225681382	225681382	Frame_Shift_Ins	INS	-	ACCTTTTGTTTA	-	DOCK10	saATAATAAACAA	p.E1100fs
XH_P61	3	9489459	9489459	Frame_Shift_Del	DEL	AAAGACTAA	-	CAAAGACTAAAC	SETD5	c.1872_1902del	p.T624fs
XH_P61	3	38908813	38908813	Missense_Mutation	SNP	T	G	T	SCN11A	c.A3950C	p.K1317T
XH_P61	3	124732818	124732818	Silent	SNP	G	A	G	HEG1	c.C1605T	p.Y535Y
XH_P61	3	133099647	133099647	Silent	SNP	C	T	C	TMEM108	c.C1092T	p.F364F
XH_P61	3	195513397	195513397	In_Frame_Ins	INS	-	TTGGCGTGACCT	-	MUC4	TATCCACAGGT	linsDNSSVSTGHATPLPVTG
XH_P61	4	437605	437605	Silent	SNP	T	C	T	ZNFX1	c.A651G	p.G217G
XH_P61	4	110670756	110670756	Missense_Mutation	SNP	T	C	T	CFI	c.A922G	p.R308G
XH_P61	4	156841069	156841069	Missense_Mutation	SNP	C	T	C	TD02	c.C1148T	p.P383L
XH_P61	5	31508798	31508798	Missense_Mutation	SNP	G	A	G	DROSHA	c.C1406T	p.A469V
XH_P61	5	41032877	41032877	Missense_Mutation	SNP	C	T	C	MROH2B	c.G2408A	p.R803Q
XH_P61	5	41917266	41917266	Nonsense_Mutation	INS	-	CAGTAACACA	-	C5orf51	751insCAGTAAP50	L251delinsPQX
XH_P61	5	43644419	43644419	Nonsense_Mutation	INS	-	ACAACGAACC	-	NNT	698insACAACCT33	H234delinsNNX
XH_P61	5	79027561	79027561	Missense_Mutation	SNP	C	G	C	CMYA5	c.C2973G	p.D991E
XH_P61	5	109103350	109103350	Missense_Mutation	SNP	C	T	C	MAN2A1	c.C950T	p.A317V
XH_P61	5	112179088	112179088	Frame_Shift_Ins	INS	-	AAAAAGAAAGA	-	APC	AAAAAATAAAC	p.K2581fs
XH_P61	5	112179089	112179089	Missense_Mutation	SNP	C	A	C	APC	c.C7744A	p.Q2582K
XH_P61	5	118183809	118183809	Silent	SNP	C	T	C	DTWD2	c.G504A	p.L168L
XH_P61	5	140777695	140777695	Missense_Mutation	SNP	A	G	A	PCDHGB5	c.A1G	p.M1V
XH_P61	5	145649079	145649079	Missense_Mutation	SNP	C	G	C	RBM27	c.C2623G	p.Q875E
XH_P61	5	156655340	156655340	Missense_Mutation	SNP	G	A	G	ITK	c.G682A	p.E228K
XH_P61	5	168149276	168149276	Missense_Mutation	SNP	C	T	C	SLIT3	c.G2468A	p.R823Q
XH_P61	5	176950990	176950990	Missense_Mutation	SNP	A	C	A	FAM193B	c.T2340G	p.D780E
XH_P61	5	179226062	179226062	Silent	SNP	C	G	C	MGAT4B	c.G1254C	p.V418V
XH_P61	5	179757737	179757737	Missense_Mutation	SNP	G	T	G	GFPT2	c.C497A	p.T166K
XH_P61	6	35434023	35434023	Silent	SNP	C	T	C	FANCE	c.C1512T	p.I504I
XH_P61	6	44218186	44218186	In_Frame_Ins	INS	-	AAG	-	HSP90AB1	1807_808insAA	p.T269delinsTK
XH_P61	6	65098729	65098729	Missense_Mutation	SNP	C	G	C	EYS	c.G5932C	p.E1978Q
XH_P61	6	74123491	74123491	Silent	SNP	C	T	C	DDX43	c.C1479T	p.F493F
XH_P61	6	76024261	76024261	Silent	SNP	C	T	C	FILIP1	c.G1287A	p.Q429Q
XH_P61	6	110110846	110110846	Missense_Mutation	SNP	C	T	C	FIG4	c.C2146T	p.R716C
XH_P61	7	6797357	6797357	Missense_Mutation	SNP	C	T	C	RSPH10B	c.C49T	p.R17C
XH_P61	7	21646113	21646113	Missense_Mutation	SNP	C	T	C	DNAH11	c.C3718T	p.H1240Y
XH_P61	7	29135824	29135824	Missense_Mutation	SNP	C	T	C	CPVL	c.G298A	p.E100K
XH_P61	7	39500270	39500270	Silent	SNP	C	T	C	POU6F2	c.C1527T	p.L509L
XH_P61	7	63726706	63726706	Missense_Mutation	SNP	G	T	G	ZNFX1	c.G695T	p.R232I
XH_P61	7	64167100	64167100	Missense_Mutation	SNP	G	A	G	ZNFX1	c.G529A	p.A177T
XH_P61	7	72412427	72412427	Missense_Mutation	SNP	G	A	G	POM121	c.G1100A	p.S367N
XH_P61	7	93055823	93055823	Missense_Mutation	SNP	G	A	G	CALCR	c.C1270T	p.R424C
XH_P61	7	100551843	100551843	Frame_Shift_Ins	INS	-	C	-	MUC3A	c.2425dupC	p.T808fs
XH_P61	7	100645566	100645566	Missense_Mutation	SNP	G	A	G	MUC12	c.G11722A	p.E3908K
XH_P61	7	100678788	100678788	Missense_Mutation	SNP	A	C	A	MUC17	c.A4091C	p.N1364T
XH_P61	7	114655819	114655819	Missense_Mutation	SNP	T	G	T	MDFC	c.T571G	p.S191A
XH_P61	7	139168036	139168036	Missense_Mutation	SNP	G	C	G	KLRG2	c.C353G	p.A118G
XH_P61	8	37699407	37699407	Missense_Mutation	SNP	A	G	A	ADGRA2	c.A3551G	p.K1184R
XH_P61	8	105509599	105509599	Missense_Mutation	SNP	C	T	C	LRP12	c.G1124A	p.R375H
XH_P61	8	126369500	126369500	Missense_Mutation	SNP	G	A	G	NSMCE2	c.G458A	p.G153E
XH_P61	8	127568860	127568860	Missense_Mutation	SNP	G	T	G	FAM84B	c.C775A	p.Q259K
XH_P61	8	144998872	144998872	Nonsense_Mutation	INS	-	TCCATCATCTCC	-	PLEC	5ATGGGGAGAGAT	728delinsGEMMGIX
XH_P61	8	145999376	145999376	Missense_Mutation	SNP	G	C	G	ZNFX1	c.C838G	p.P280A
XH_P61	9	5050752	5050752	In_Frame_Ins	INS	-	TAAGTTTCATTA	-	JAK2	ATCGTAAGTTTC	80delinsHRKFHYHV
XH_P61	9	79324135	79324135	In_Frame_Ins	INS	-	TGATTGTTCAC	-	PRUNE2	3055insCTGAA	1019delinsLQQSS
XH_P61	9	80537112	80537112	Missense_Mutation	SNP	T	A	T	GNAQ	c.A286T	p.T96S
XH_P61	9	96429462	96429462	Missense_Mutation	SNP	G	A	G	PHF2	c.G2288A	p.G763D
XH_P61	9	107380470	107380470	Frame_Shift_Ins	INS	-	A	-	OR13C9	c.15_16insT	p.Q6fs
XH_P61	9	107380471	107380471	Frame_Shift_Ins	INS	-	TTACTCTT	-	OR13C9	4_15insAAGAG	p.N5fs
XH_P61	9	138379063	138379063	Missense_Mutation	SNP	G	A	G	PPP1R26	c.G2707A	p.E903K
XH_P61	9	139911046	139911046	Missense_Mutation	SNP	G	A	G	ABCA2	c.C2903T	p.A968V
XH_P61	10	16948390	16948390	Missense_Mutation	SNP	G	C	G	CUBN	c.C7724G	p.P2575R
XH_P61	10	18289686	18289686	Missense_Mutation	SNP	C	T	C	SLC39A12	c.C1289T	p.S430L
XH_P61	10	47087660	47087660	Missense_Mutation	SNP	G	A	G	NPY4R	c.G877A	p.E293K
XH_P61	10	47701175	47701175	Missense_Mutation	SNP	T	C	T	ANTXR1	c.T1751C	p.L584P
XH_P61	10	124457302	124457302	Missense_Mutation	SNP	C	T	C	C10orf120	c.G955A	p.E319K
XH_P61	10	127408454	127408454	Silent	SNP	C	G	C	EDRF1	c.C78G	p.S26S
XH_P61	11	433863	433863	Silent	SNP	C	G	C	ANO9	c.G156C	p.R52R
XH_P61	11	1027177	1027177	Missense_Mutation	SNP	G	A	G	MUC6	c.C2248T	p.R750W
XH_P61	11	2683309	2683309	Silent	SNP	A	C	A	KCNQ1	c.A1512C	p.S504S
XH_P61	11	17629885	17629885	Missense_Mutation	SNP	G	A	G	OTOG	c.G4235A	p.R1412H
XH_P61	11	47296523	47296523	Missense_Mutation	SNP	C	T	C	MADD	c.C472T	p.R158W
XH_P61	11	56185173	56185173	Nonsense_Mutation	INS	-	CTCCT	-	OR5R1	535_536insAGG	179_D180delinsX
XH_P61	11	56185174	56185174	Frame_Shift_Ins	INS	-	CATCTTTTATT	-	OR5R1	535insAATAAA	p.C179fs
XH_P61	11	64005842	64005842	Missense_Mutation	SNP	G	T	G	VEGFB	c.G560T	p.R187L
XH_P61	11	65414067	65414067	Missense_Mutation	SNP	C	T	C	SIPA1	c.C1562T	p.A521V
XH_P61	11	69631166	69631166	Silent	SNP	C	T	C	FGF3	c.C246A	p.E82E
XH_P61	11	89924778	89924778	Missense_Mutation	SNP	C	G	C	NAALAD2	c.C1987G	p.P663A

XH_P61	12	6729733	6729733	Missense_Mutation	SNP	G	A	G	LPAR5	c.C682T	p.R228W
XH_P61	12	46321467	46321467	Silent	SNP	G	A	G	SCAF11	c.C2017T	p.L673L
XH_P61	12	49427679	49427679	Silent	SNP	C	T	C	KMT2D	c.G10809A	p.Q3603Q
XH_P61	12	52995207	52995207	Silent	SNP	G	A	G	KRT72	c.C30T	p.R10R
XH_P61	12	66800158	66800158	Missense_Mutation	SNP	C	T	C	GRIP1	c.G1733A	p.R578Q
XH_P61	12	78569148	78569148	Missense_Mutation	SNP	C	A	C	NAV3	c.C5044A	p.H1682N
XH_P61	12	109725710	109725710	Missense_Mutation	SNP	G	A	G	FOXN4	c.C407T	p.P136L
XH_P61	12	113515808	113515808	Missense_Mutation	SNP	C	T	C	DTX1	c.C839T	p.P280L
XH_P61	12	113836362	113836362	Missense_Mutation	SNP	G	A	G	SDS	c.C383T	p.P128L
XH_P61	12	118848960	118848960	Missense_Mutation	SNP	G	A	G	SUDS3	c.G886A	p.E296K
XH_P61	12	121701655	121701655	Missense_Mutation	SNP	G	A	G	CAMKK2	c.C713T	p.A238V
XH_P61	12	125294749	125294749	Silent	SNP	C	T	C	SCARB1	c.G813A	p.S271S
XH_P61	13	25416217	25416217	Missense_Mutation	SNP	G	C	G	RNF17	c.G2521C	p.D841H
XH_P61	13	25671097	25671097	Frame_Shift_Ins	INS	-	C	-	PABPC3	c.761_762insC	p.K254fs
XH_P61	13	46641466	46641466	Frame_Shift_Ins	INS	-	AG	-	CPB2	c.677_678insCT	p.D226fs
XH_P61	13	60385018	60385018	Missense_Mutation	SNP	C	T	C	DIAPH3	c.G2278A	p.E760K
XH_P61	13	109792778	109792778	Silent	SNP	G	A	G	MYO16	c.G4218A	p.A1406A
XH_P61	13	113201853	113201853	Frame_Shift_Del	DEL	T	-	T	TUBGCP3	c.1249delA	p.M417fs
XH_P61	14	23744827	23744832	In_Frame_Del	DEL	TCCTCC	-	TCCTCC	HOMEZ	c.1605_1610del	p.535_537del
XH_P61	14	42356567	42356567	Missense_Mutation	SNP	G	A	G	LRFN5	c.G739A	p.E247K
XH_P61	14	45642364	45642364	Missense_Mutation	SNP	G	A	G	FANCM	c.G2189A	p.R730H
XH_P61	14	69349764	69349764	Silent	SNP	G	A	G	ACTN1	c.C1644T	p.T548T
XH_P61	14	69358985	69358985	Missense_Mutation	SNP	G	A	G	ACTN1	c.C871T	p.R291C
XH_P61	14	104206674	104206674	Silent	SNP	G	A	G	PPP1R13B	c.C2079T	p.A693A
XH_P61	14	105410279	105410279	Missense_Mutation	SNP	C	T	C	AHNAK2	c.G11209A	p.V3737M
XH_P61	14	105410280	105410280	Silent	SNP	A	G	A	AHNAK2	c.T11208C	p.D3736D
XH_P61	15	22743596	22743596	Nonsense_Mutation	SNP	C	T	C	GOLGA6L1	c.C1981T	p.Q661X
XH_P61	15	23685702	23685702	Silent	SNP	C	T	C	GOLGA6L2	c.G1920A	p.A640A
XH_P61	15	28630276	28630276	Missense_Mutation	SNP	C	A	C	GOLGA8F	c.C919A	p.P307T
XH_P61	15	43102846	43102846	Missense_Mutation	SNP	G	A	G	TTBK2	c.C788T	p.S263F
XH_P61	15	68582301	68582301	Missense_Mutation	SNP	T	C	T	FEM1B	c.T605C	p.I202T
XH_P61	15	69718517	69718517	Missense_Mutation	SNP	G	T	G	KIF23	c.G513T	p.W171C
XH_P61	15	74425465	74425465	Missense_Mutation	SNP	G	A	G	ISLR2	c.G370A	p.A124T
XH_P61	15	88678348	88678348	Silent	SNP	G	A	G	NTRK3	c.C1188T	p.L396L
XH_P61	15	101445745	101445745	Silent	SNP	C	T	C	ALDH1A3	c.C765T	p.F255F
XH_P61	16	22826103	22826103	Missense_Mutation	SNP	G	A	G	HS35T2	c.G172A	p.G58S
XH_P61	16	23479019	23479019	Missense_Mutation	SNP	T	A	T	GGA2	c.A1734T	p.E578D
XH_P61	16	31927264	31927264	Missense_Mutation	SNP	G	A	G	ZNF267	c.G1694A	p.R565Q
XH_P61	16	89777237	89777237	Missense_Mutation	SNP	C	T	C	VPS9D1	c.G1015A	p.E393K
XH_P61	17	5037195	5037195	Missense_Mutation	SNP	G	A	G	USP6	c.G398A	p.R133K
XH_P61	17	7574000	7574000	Nonsense_Mutation	SNP	C	A	C	TP53	c.G631T	p.E211X
XH_P61	17	8925959	8925959	Missense_Mutation	SNP	C	T	C	NTN1	c.C269T	p.S90L
XH_P61	17	10536016	10536016	Missense_Mutation	SNP	G	A	G	MYH3	c.C4733T	p.A1578V
XH_P61	17	18925388	18925388	Missense_Mutation	SNP	G	A	G	GRAP	c.C538T	p.R180C
XH_P61	17	42431897	42431897	Missense_Mutation	SNP	G	A	G	FAM171A2	c.C1685T	p.P562L
XH_P61	17	72368643	72368643	Missense_Mutation	SNP	T	G	T	GPR142	c.T1029G	p.D343E
XH_P61	17	79225347	79225347	Missense_Mutation	SNP	C	T	C	SLC38A10	c.G2011A	p.E671K
XH_P61	18	6956652	6956652	Nonsense_Mutation	SNP	C	A	C	LAMA1	c.G8077T	p.E2693X
XH_P61	18	8825201	8825201	Silent	SNP	A	C	A	MTCL1	c.A3693C	p.P1231P
XH_P61	18	8825203	8825203	Missense_Mutation	SNP	A	C	A	MTCL1	c.A3695C	p.E1232A
XH_P61	19	7997536	7997536	Silent	SNP	G	A	G	TIMM44	c.C963T	p.N321N
XH_P61	19	9084636	9084636	Silent	SNP	G	A	G	MUC16	c.C1719T	p.P2393P
XH_P61	19	12186173	12186173	Nonsense_Mutation	INS	-	AAAGGTTTGTTT	-	ZNF844	rsATTGAAGGTT	C80_G81delinsYX
XH_P61	19	17741031	17741031	Missense_Mutation	SNP	G	T	G	UNC13A	c.C3592A	p.Q1198K
XH_P61	19	22497417	22497417	Missense_Mutation	SNP	G	A	G	ZNF729	c.G1198A	p.G400R
XH_P61	19	34263821	34263821	Silent	SNP	G	A	G	CHST8	c.G1128A	p.R376R
XH_P61	19	39051802	39051802	Missense_Mutation	SNP	T	G	T	RYR1	c.T12317G	p.L4106R
XH_P61	19	46299149	46299149	In_Frame_Ins	INS	-	CTCCTCCCTCTCC	-	RSPH6A	2insGCGAGGAC	E711delinsGEEEE
XH_P61	19	50464171	50464171	Missense_Mutation	SNP	C	T	C	SIGLEC11	c.G98A	p.S33N
XH_P61	19	50721022	50721022	Missense_Mutation	SNP	C	G	C	MYH14	c.C556G	p.L186V
XH_P61	19	53958917	53958917	Missense_Mutation	SNP	G	C	G	ZNF761	c.G1156C	p.E386Q
XH_P61	19	56244577	56244577	Missense_Mutation	SNP	G	A	G	NLRP9	c.C620T	p.P207L
XH_P61	20	18435975	18435975	Silent	SNP	C	T	C	DZANK1	c.C294A	p.K98K
XH_P61	20	32664866	32664866	Missense_Mutation	SNP	G	A	G	RALY	c.G643A	p.G215S
XH_P61	20	45174251	45174251	Missense_Mutation	SNP	A	C	A	OCSTAMP	c.T762G	p.F254L
XH_P61	20	45174252	45174252	Missense_Mutation	SNP	A	C	A	OCSTAMP	c.T761G	p.F254C
XH_P61	20	60503448	60503448	Missense_Mutation	SNP	G	A	G	CDH4	c.G1861A	p.V621M
XH_P61	21	28216628	28216628	Missense_Mutation	SNP	C	G	C	ADAMTS1	c.G646C	p.E216Q
XH_P61	22	24133968	24133968	Missense_Mutation	SNP	G	A	G	SMARCB1	c.G119A	p.R400Q
XH_P61	22	26423243	26423243	Missense_Mutation	SNP	C	T	C	MYO18B	c.C7306T	p.R2436C
XH_P61	22	43088919	43088919	Missense_Mutation	SNP	C	T	C	A4GALT	c.G1039A	p.E347K
XH_P61	22	46832168	46832168	Silent	SNP	C	T	C	CELSR1	c.G4425A	p.R1475R
XH_P61	22	51159557	51159557	Missense_Mutation	SNP	G	A	G	SHANK3	c.G3254A	p.G1085D
XH_P61	X	63412830	63412830	Nonsense_Mutation	SNP	C	A	C	AMER1	c.G337T	p.G113X
XH_P61	X	82763659	82763659	Missense_Mutation	SNP	C	G	C	POU3F4	c.C327G	p.N109K
XH_P61	X	85403694	85403694	Silent	SNP	C	A	C	DACH2	c.C70A	p.R24R
XH_P61	X	91133598	91133598	Missense_Mutation	SNP	C	T	C	PCDH11X	c.C2359T	p.R787C
XH_P61	X	100749184	100749184	Missense_Mutation	SNP	G	A	G	ARMCX4	c.G5608A	p.E1870K
XH_P61	X	105125742	105125742	Frame_Shift_Ins	INS	-	GTTATTAGATGT	-	NRK	3insATTGTTATTA	p.K74fs
XH_P61	X	105153319	105153319	Silent	SNP	G	A	G	NRK	c.G1686A	p.Q562Q
XH_P61	X	152097174	152097174	Missense_Mutation	SNP	C	T	C	ZNF185	c.C883T	p.R295C
XH_P61	1	101004669	101004669	Silent	SNV	C	T	T	GPR88	c.147C>T	P.N49N
XH_P61	1	11159837	11159837	Missense_Mutation	SNV	T	C	C	EXOSC10	c.52A>G	P.T18A
XH_P61	1	11303178	11303178	Missense_Mutation	SNV	C	T	T	MTOR	c.1405G>A	P.A469T
XH_P61	1	160523750	160523750	Missense_Mutation	SNV	G	A	A	CD84	c.575C>T	P.T192M
XH_P61	1	172376914	172376914	Missense_Mutation	SNV	G	A	A	DNM3	c.2513G>A	P.R838Q
XH_P61	1	17949531	17949531	Missense_Mutation	SNV	T	G	G	ARHGEF10L	c.944T>G	P.L315R
XH_P61	1	229771573	229771573	Missense_Mutation	SNV	A	C	C	URB2	c.1213A>C	P.L405L
XH_P61	1	241755352	241755352	Missense_Mutation	SNV	T	G	G	KMO	c.1358T>G	P.L453W
XH_P61	1	244541841	244541841	Silent	SNV	C	G	G	C1orf100	c.225C>G	P.L75L
XH_P61	10	124457302	124457302	Missense_Mutation	SNV	C	T	T	C10orf120	c.955G>A	P.E319K
XH_P61	10	127408454	127408454	Silent	SNV	C	G	G	EDRF1	c.78C>G	P.S26S
XH_P61	10	18289686	18289686	Missense_Mutation	SNV	C	T	T	SLC39A12	c.1691C>T	P.S564L
XH_P61	10	47087660	47087660	Missense_Mutation	SNV	G	A	A	NPY4R	c.877G>A	P.E293K
XH_P61	11	17629885	17629885	Missense_Mutation	SNV	G	A	A	OTOG	c.4235G>A	P.R1412H
XH_P61	11	26833309	26833309	Splice_Site	SNV	A	C	C	KCNQ1	c.1512A>C	P.S504S
XH_P61	11	433863	433863	Silent	SNV	C	G	G	AN09	c.156G>C	P.R52R
XH_P61	11	47296523	47296523	Missense_Mutation	SNV	C	T	T	MADD	c.472C>T	P.R158W

XH_P61	11	64005842	64005842	Missense_Mutation	SNV	G	T	T	VEGFB	c.560G>T	P.R187L
XH_P61	11	65414067	65414067	Missense_Mutation	SNV	C	T	T	SIPA1	c.1562C>T	P.A521V
XH_P61	11	69631166	69631166	Silent	SNV	C	T	T	FGF3	c.246G>A	P.E82E
XH_P61	11	89924778	89924778	Missense_Mutation	SNV	C	G	G	NAALAD2	c.1987C>G	P.P663A
XH_P61	12	109725710	109725710	Missense_Mutation	SNV	G	A	A	FOXN4	c.407C>T	P.P136L
XH_P61	12	113515808	113515808	Missense_Mutation	SNV	C	T	T	DTX1	c.839C>T	P.P280L
XH_P61	12	113836362	113836362	Missense_Mutation	SNV	G	A	A	SDS	c.383C>T	P.P128L
XH_P61	12	118848960	118848960	Missense_Mutation	SNV	G	A	A	SUDS3	c.886G>A	P.E296K
XH_P61	12	125294749	125294749	Silent	SNV	C	T	T	SCARB1	c.813G>A	P.S271S
XH_P61	12	46321467	46321467	Silent	SNV	G	A	A	SCAF11	c.2017C>T	P.L673L
XH_P61	12	52995207	52995207	Silent	SNV	G	A	A	KRT72	c.30C>T	P.R10R
XH_P61	12	66800158	66800158	Missense_Mutation	SNV	C	T	T	GRIP1	c.1733G>A	P.R578Q
XH_P61	12	6729733	6729733	Missense_Mutation	SNV	G	A	A	LPAR5	c.682C>T	P.R228W
XH_P61	12	78569148	78569148	Missense_Mutation	SNV	C	A	A	NAV3	c.5044C>A	P.H1682N
XH_P61	13	109792778	109792778	Silent	SNV	G	A	A	MYO16	c.4218G>A	P.A1406A
XH_P61	13	25416217	25416217	Missense_Mutation	SNV	G	C	C	RNF17	c.2521G>C	P.D841H
XH_P61	13	60385018	60385018	Missense_Mutation	SNV	C	T	T	DIAPH3	c.3067G>A	P.E1023K
XH_P61	14	104206674	104206674	Silent	SNV	G	A	A	PPP1R13B	c.2079C>T	P.A693A
XH_P61	14	23744827	23744832	Missense_Mutation	INDEL	TCCTCC	-	-	HOMEZ	D5_1610delGGAP.E536_E537del	
XH_P61	14	42356567	42356567	Missense_Mutation	SNV	G	A	A	LRFN5	c.739G>A	P.E247K
XH_P61	14	45642364	45642364	Missense_Mutation	SNV	G	A	A	FANCM	c.2267G>A	P.R756H
XH_P61	14	69349764	69349764	Silent	SNV	G	A	A	ACTN1	c.1644C>T	P.T548T
XH_P61	14	69358985	69358985	Missense_Mutation	SNV	G	A	A	ACTN1	c.871C>T	P.R291C
XH_P61	14	96157255	96157255	Splice_Site	SNV	G	T	T	TCL1B	c.333+12G>T	
XH_P61	15	101445745	101445745	Silent	SNV	C	T	T	ALDH1A3	c.1086C>T	P.F362F
XH_P61	15	43102846	43102846	Missense_Mutation	SNV	G	A	A	TTBK2	c.788C>T	P.S263F
XH_P61	15	68582301	68582301	Missense_Mutation	SNV	T	C	C	FEM1B	c.605T>C	P.I202T
XH_P61	15	69718517	69718517	Missense_Mutation	SNV	G	T	T	KIF23	c.513G>T	P.W171C
XH_P61	15	74425465	74425465	Missense_Mutation	SNV	G	A	A	ISLR2	c.370G>A	P.A124T
XH_P61	15	88678348	88678348	Silent	SNV	G	A	A	NTRK3	c.1188C>T	P.L396L
XH_P61	16	22826103	22826103	Missense_Mutation	SNV	G	A	A	HS3ST2	c.172G>A	P.G58S
XH_P61	16	89777237	89777237	Missense_Mutation	SNV	C	T	T	VPS9D1	c.1015G>A	P.E339K
XH_P61	17	18925388	18925388	Missense_Mutation	SNV	G	A	A	GRAP	c.538C>T	P.R180C
XH_P61	17	72368643	72368643	Missense_Mutation	SNV	T	G	G	GPR142	c.1293T>G	P.D431E
XH_P61	17	7574000	7574000	Nonsense_Mutation	SNV	C	A	A	TP53	c.1027G>T	P.E343*
XH_P61	17	79225347	79225347	Missense_Mutation	SNV	C	T	T	SLC38A10	c.2011G>A	P.E671K
XH_P61	17	8925959	8925959	Missense_Mutation	SNV	C	T	T	NTN1	c.269C>T	P.S90L
XH_P61	18	6956652	6956652	Nonsense_Mutation	SNV	C	A	A	LAMA1	c.8077G>T	P.E2693*
XH_P61	18	8825201	8825201	Silent	SNV	A	C	C	MTCL1	c.3693A>C	P.P1231P
XH_P61	18	8825203	8825203	Missense_Mutation	SNV	A	C	C	MTCL1	c.3695A>C	P.E1232A
XH_P61	19	10157798	10157798	Splice_Site	SNV	C	T	T	C3P1	n.1352-3C>T	
XH_P61	19	17741031	17741031	Missense_Mutation	SNV	G	T	T	UNC13A	c.3592C>A	P.Q.1198K
XH_P61	19	22497417	22497417	Missense_Mutation	SNV	G	A	A	ZNF729	c.1198G>A	P.G400R
XH_P61	19	39051802	39051802	Missense_Mutation	SNV	T	G	G	RYR1	c.12332T>G	P.L4111R
XH_P61	19	50464171	50464171	Missense_Mutation	SNV	C	T	T	SIGLEC11	c.98G>A	P.S33N
XH_P61	19	50721022	50721022	Missense_Mutation	SNV	C	G	G	MYH14	c.556C>G	P.L186V
XH_P61	19	53958917	53958917	Missense_Mutation	SNV	G	C	C	ZNF761	c.1156G>C	P.E386Q
XH_P61	19	56244577	56244577	Missense_Mutation	SNV	G	A	A	NLRP9	c.620C>T	P.P207L
XH_P61	19	7997536	7997536	Silent	SNV	G	A	A	TIMM44	c.963C>T	P.N321N
XH_P61	19	9084636	9084636	Silent	SNV	G	A	A	MUC16	c.7179C>T	P.P2393P
XH_P61	2	100007076	100007076	Missense_Mutation	SNV	G	C	C	E1F5B	c.2656G>C	P.D886H
XH_P61	2	131521579	131521579	Missense_Mutation	SNV	C	T	T	AMER3	c.1934C>T	P.P645L
XH_P61	2	189904195	189904195	Missense_Mutation	SNV	C	T	T	COL5A2	c.3728G>A	P.S1243N
XH_P61	2	220045431	220045431	Missense_Mutation	SNV	G	C	C	FAM134A	c.595G>C	P.V199L
XH_P61	2	84897597	84897597	Missense_Mutation	SNV	T	G	G	DNAH6	c.6452T>G	P.L2151R
XH_P61	21	28216628	28216628	Missense_Mutation	SNV	C	G	G	ADAMTS1	c.646G>C	P.E216Q
XH_P61	22	24133968	24133968	Missense_Mutation	SNV	G	A	A	SMARCB1	c.119G>A	P.R40Q
XH_P61	22	26423243	26423243	Missense_Mutation	SNV	C	T	T	MYO18B	c.7306C>T	P.R2436C
XH_P61	22	29707673	29707673	Missense_Mutation	SNV	C	T	T	GAS2L1	c.1232C>T	P.A411V
XH_P61	22	43088919	43088919	Missense_Mutation	SNV	C	T	T	A4GALT	c.1039G>A	P.E347K
XH_P61	22	43227654	43227654	Splice_Site	SNV	C	T	T	ARFGAP3	c.346-12G>A	
XH_P61	22	46832168	46832168	Silent	SNV	C	T	T	CELSR1	c.4425G>A	P.R1475R
XH_P61	3	124732818	124732818	Silent	SNV	G	A	A	HEG1	c.1605C>T	P.Y535Y
XH_P61	3	125696017	125696017	Splice_Site	SNV	G	C	C	ROPN1B	c.396+9G>C	
XH_P61	3	133099647	133099647	Silent	SNV	C	T	T	TMEM108	c.1092C>T	P.F364F
XH_P61	3	38908813	38908813	Missense_Mutation	SNV	T	G	G	SCN11A	c.3950A>C	P.K1317T
XH_P61	3	47037548	47037548	Splice_Site	SNV	C	A	A	NBEAL2	c.2151+7C>A	
XH_P61	3	9489459	9489459	Frame_Shift_Del	INDEL	AAAGACTAA	-	-	SETD5	GCCCAAAGACTA	P.S625fs
XH_P61	4	110670756	110670756	Missense_Mutation	SNV	T	C	C	CFI	c.943A>G	P.R315G
XH_P61	4	156841069	156841069	Missense_Mutation	SNV	C	T	T	TD02	c.1148C>T	P.P383L
XH_P61	5	109103350	109103350	Missense_Mutation	SNV	C	T	T	MAN2A1	c.950C>T	P.A317V
XH_P61	5	145649079	145649079	Missense_Mutation	SNV	C	G	G	RBM27	c.2623C>G	P.Q875E
XH_P61	5	156655340	156655340	Missense_Mutation	SNV	G	A	A	ITK	c.682G>A	P.E228K
XH_P61	5	168149276	168149276	Missense_Mutation	SNV	C	T	T	SLIT3	c.2468G>A	P.R823Q
XH_P61	5	176950990	176950990	Missense_Mutation	SNV	A	C	C	FAM193B	c.2340T>G	P.D780E
XH_P61	5	179226062	179226062	Silent	SNV	C	G	G	MGAT4B	c.1209G>C	P.V403V
XH_P61	5	179757737	179757737	Missense_Mutation	SNV	G	T	T	GFPT2	c.497C>A	P.L166K
XH_P61	5	31508798	31508798	Missense_Mutation	SNV	G	A	A	DROSHA	c.1406C>T	P.A469V
XH_P61	5	41032877	41032877	Missense_Mutation	SNV	C	T	T	MROH2B	c.2408G>A	P.R803Q
XH_P61	5	79027561	79027561	Missense_Mutation	SNV	C	G	G	CMYA5	c.2973C>G	P.D991E
XH_P61	6	110110846	110110846	Missense_Mutation	SNV	C	T	T	FIG4	c.2146C>T	P.R716C
XH_P61	6	35434023	35434023	Splice_Site	SNV	C	T	T	FANCE	c.1512C>T	P.J504I
XH_P61	6	44218186	44218186	Missense_Mutation	INDEL	-	AAG	AAG	HSP90AB1	812_814dupAG	P.K271dup
XH_P61	6	50686792	50686792	Splice_Site	INDEL	C	-	-	TFAP2D	c.538-11delC	
XH_P61	6	65098729	65098729	Missense_Mutation	SNV	C	G	G	EYS	c.5932G>C	P.E1978Q
XH_P61	6	74123491	74123491	Silent	SNV	C	T	T	DDX43	c.1479C>T	P.F493F
XH_P61	6	76024261	76024261	Silent	SNV	C	T	T	FILIP1	c.1296G>A	P.Q432Q
XH_P61	7	100645566	100645566	Missense_Mutation	SNV	G	A	A	MUC12	c.11722G>A	P.E3908K
XH_P61	7	114655819	114655819	Missense_Mutation	SNV	T	G	G	MDFC	c.571T>G	P.S191A
XH_P61	7	139168036	139168036	Missense_Mutation	SNV	G	C	C	KLRG2	c.353C>G	P.A118G
XH_P61	7	29135824	29135824	Missense_Mutation	SNV	C	T	T	CPVL	c.298G>A	P.E100K
XH_P61	7	39500270	39500270	Silent	SNV	C	T	T	POU6F2	c.1527C>T	P.L509L
XH_P61	7	63726706	63726706	Missense_Mutation	SNV	G	T	T	ZNF679	c.695G>T	P.R232I
XH_P61	7	64167100	64167100	Missense_Mutation	SNV	G	A	A	ZNF107	c.418G>A	P.A140T
XH_P61	7	6797357	6797357	Missense_Mutation	SNV	C	T	T	RSPH10B	c.49C>T	P.R17C
XH_P61	7	93055823	93055823	Missense_Mutation	SNV	G	A	A	CALCR	c.1372C>T	P.R458C
XH_P61	8	105509599	105509599	Missense_Mutation	SNV	C	T	T	LRP12	c.1124G>A	P.R375H
XH_P61	8	126369500	126369500	Missense_Mutation	SNV	G	A	A	NSMCE2	c.458G>A	P.G153E

XH_P61	8	127568860	127568860	Missense_Mutation	SNV	G	T	T	FAM84B	c.775C>A	P.Q259K
XH_P61	8	141381290	141381290	Splice_Site	SNV	G	C	C	TRAPP9	c.1135-11C>G	
XH_P61	8	143960438	143960438	Splice_Site	SNV	G	T	T	CYP11B1	c.395+10G>A	
XH_P61	8	144998872	144998872	Frame_Shift_Ins	INDEL	-	CTCCATCATCTCC	CTCCATCATCTCC	PLEC	5ATGGGGGAGATG	IterWGDGDGEMMERWGDGDGEMGCKK
XH_P61	8	145999376	145999376	Missense_Mutation	SNV	G	C	C	ZNF34	c.895C>G	P.P299A
XH_P61	8	37699407	37699407	Missense_Mutation	SNV	A	G	G	ADGRA2	c.3551A>G	P.K1184R
XH_P61	9	131767814	131767814	Splice_Site	SNV	T	G	G	NUP188	c.4737+5T>G	
XH_P61	9	138379063	138379063	Missense_Mutation	SNV	G	A	A	PPP1R26	c.2707G>A	P.E903K
XH_P61	X	100749184	100749184	Missense_Mutation	SNV	G	A	A	ARMCX4	c.5608G>A	P.E1870K
XH_P61	X	105153319	105153319	Silent	SNV	G	A	A	NRK	c.1686G>A	P.Q562Q
XH_P61	X	152097174	152097174	Missense_Mutation	SNV	C	T	T	ZNF185	c.883C>T	P.R295C
XH_P61	X	63412830	63412830	Nonsense_Mutation	SNV	C	A	A	AMER1	c.337G>T	P.G113*
XH_P61	X	82763659	82763659	Missense_Mutation	SNV	C	G	G	POU3F4	c.327C>G	P.N109K
XH_P61	X	85403694	85403694	Silent	SNV	C	A	A	DACH2	c.70C>A	P.R24R
XH_P61	X	91133598	91133598	Missense_Mutation	SNV	C	T	T	PCDH11X	c.2359C>T	P.R787C
XH_P62	1	7798229	7798229	Missense_Mutation	SNP	G	T	T	CAMTA1	c.3869G>T	p.S1290I
XH_P62	13	32893318	32893318	Nonsense_Mutation	SNP	G	T	T	BRCA2	c.172G>T	p.E58*
XH_P62	3	128199863	128199863	Nonsense_Mutation	SNP	T	C	C	GATA2	c.1442A>G	p.*481Vext**19
XH_P62	6	32190351	32190351	Missense_Mutation	SNP	T	C	C	NOTCH4	c.388A>G	p.R130G
XH_P62	1	2411365	2411365	Missense_Mutation	SNP	C	A	C	PLCH2	c.C383A	p.A128D
XH_P62	1	3768888	3768888	Silent	SNP	C	T	C	CEP104	c.G84A	p.A28A
XH_P62	1	11740631	11740631	Missense_Mutation	SNP	T	G	T	MAD2L2	c.A28C	p.N10H
XH_P62	1	11907300	11907300	Missense_Mutation	SNP	C	G	C	NPPA	c.G320C	p.R107P
XH_P62	1	23191621	23191621	Missense_Mutation	SNP	G	A	G	EPHB2	c.G1219A	p.E407K
XH_P62	1	35852628	35852628	Missense_Mutation	SNP	A	G	A	ZMYM4	c.A889G	p.M297V
XH_P62	1	43258495	43258495	Nonsense_Mutation	INS	-	ATTAGTATATTA	-	TMEM269	188insATTAGTA	p.R63delinsHX
XH_P62	1	46487691	46487691	In_Frame_Ins	INS	-	GAGAGATAG	-	MAST2	1361insGAGAA	p.I454delinsREIV
XH_P62	1	47402458	47402458	Missense_Mutation	SNP	C	T	C	CYP4A11	c.G388A	p.G130S
XH_P62	1	47653042	47653042	Missense_Mutation	SNP	A	T	A	PDZK1P1	c.T125A	p.V42D
XH_P62	1	107867524	107867524	Silent	SNP	A	C	A	NTNG1	c.A867C	p.S289S
XH_P62	1	112524306	112524306	Missense_Mutation	SNP	G	A	G	KCND3	c.C1043T	p.A348V
XH_P62	1	119965209	119965209	Missense_Mutation	SNP	G	A	G	HSDB3B2	c.G1085A	p.R362Q
XH_P62	1	120057122	120057122	Missense_Mutation	SNP	G	A	G	HSDB3B1	c.G976A	p.V326I
XH_P62	1	144882849	144882849	Missense_Mutation	SNP	G	A	G	PDE4DIP	c.C3659T	p.A1220V
XH_P62	1	144904697	144904697	Missense_Mutation	SNP	C	T	C	PDE4DIP	c.G3104A	p.R1035Q
XH_P62	1	145311110	145311110	Silent	SNP	G	T	G	NBPF10	c.G1809T	p.R603R
XH_P62	1	152283513	152283513	Silent	SNP	G	A	G	FLG	c.C3849T	p.S1283S
XH_P62	1	152383060	152383060	Silent	SNP	G	A	G	CRNN	c.C498T	p.S166S
XH_P62	1	152383061	152383061	Missense_Mutation	SNP	C	T	C	CRNN	c.G497A	p.S166N
XH_P62	1	152944577	152944577	Missense_Mutation	SNP	C	G	C	SPRR4	c.C211G	p.Q71E
XH_P62	1	156639633	156639633	Silent	SNP	C	T	C	NES	c.G4347A	p.L1449L
XH_P62	1	158390479	158390479	Missense_Mutation	SNP	A	T	A	OR10K2	c.C178A	p.Y60N
XH_P62	1	158604410	158604410	Frame_Shift_Ins	INS	-	ATTTGTTTATT	-	SPTA1	488insAAAAATAA	p.E1830fs
XH_P62	1	161722963	161722963	Missense_Mutation	SNP	C	G	C	DUSP12	c.C773G	p.T258S
XH_P62	1	173743535	173743535	In_Frame_Ins	INS	-	TAAGTG	-	KLHL20	87_1388insTAA	p.Y463delinsLSD
XH_P62	1	173743537	173743537	Nonsense_Mutation	SNP	T	A	T	KLHL20	c.T1389A	p.Y463X
XH_P62	1	201044685	201044685	Missense_Mutation	SNP	C	T	C	CACNA1S	c.G1886A	p.G629E
XH_P62	1	211534436	211534436	Nonsense_Mutation	SNP	G	T	G	TRAF5	c.G628T	p.E210X
XH_P62	1	237756887	237756887	Missense_Mutation	SNP	C	T	C	RYR2	c.C4387T	p.R1463C
XH_P62	1	248084440	248084440	Missense_Mutation	SNP	T	G	T	OR2T8	c.C1212G	p.S41A
XH_P62	2	1459937	1459937	In_Frame_Ins	INS	-	GGAAGAGAC	-	TPO	703insGGAAG	G234delinsGGRD
XH_P62	2	3816956	3816956	Silent	SNP	C	T	C	DCDC2C	c.C909T	p.D303D
XH_P62	2	26407666	26407666	Missense_Mutation	SNP	C	G	C	GAREM2	c.C1718G	p.L240V
XH_P62	2	33817224	33817224	Missense_Mutation	SNP	T	C	T	FAM98A	c.A260G	p.N87S
XH_P62	2	97779601	97779601	Missense_Mutation	SNP	A	G	A	ANKRD36	c.A125G	p.H42R
XH_P62	2	97779611	97779611	Silent	SNP	A	G	A	ANKRD36	c.A135G	p.L45L
XH_P62	2	98373636	98373636	Missense_Mutation	SNP	G	A	G	TMEM131	c.C5578T	p.R1860W
XH_P62	2	114709409	114709409	In_Frame_Ins	INS	-	AAAATAAAATA	-	ACTR3	AGAGAAAAATAA	304delinsGKINIIIF
XH_P62	2	130832756	130832771	Frame_Shift_Del	INDEL	TCCTTTTGCTC	-	CTCTTTTGCTCTC	POTEF	c.2274_2289del	p.A758fs
XH_P62	2	131221328	131221343	Frame_Shift_Del	INDEL	TCCTCTTGCTC	-	CTCTCTTGCTCTC	POTEI	c.2274_2289del	p.A758fs
XH_P62	2	179400436	179400436	Missense_Mutation	SNP	T	G	T	TTN	c.A73711C	p.I24571L
XH_P62	2	183848061	183848061	Nonsense_Mutation	INS	-	TTTAATTATTATT	-	NCKAP1	54insAAATAAT	p.E352delinsKX
XH_P62	2	183848062	183848062	Frame_Shift_Ins	INS	-	AATAA	-	NCKAP1	052_1053insTTA	p.K351fs
XH_P62	2	196933420	196933420	Splice_Site	SNP	C	A	C	DNAH7	-	-
XH_P62	2	220047332	220047332	Missense_Mutation	SNP	A	C	A	RETREG2	c.A992C	p.Q331P
XH_P62	2	234601812	234601812	Missense_Mutation	SNP	T	G	T	UGT1A6	c.T162G	p.H54Q
XH_P62	2	241534720	241534720	Missense_Mutation	SNP	A	T	A	CAPN10	c.A1277T	p.K426M
XH_P62	3	36422206	36422206	Missense_Mutation	SNP	A	C	A	STAC	c.A71C	p.Q24P
XH_P62	3	38315866	38315866	Missense_Mutation	SNP	G	A	G	SLC22A13	c.G482A	p.R161Q
XH_P62	3	40503520	40503520	In_Frame_Ins	INS	-	CTGCTGCTG	-	RPL14	5_446insCTGCTC	T149delinsTAAA
XH_P62	3	42264845	42264845	Silent	SNP	C	T	C	TRAK1	c.C12193T	p.N731N
XH_P62	3	46009684	46009684	Missense_Mutation	SNP	G	A	G	FYCO1	c.C1142T	p.T381M
XH_P62	3	46729759	46729759	Missense_Mutation	SNP	C	T	C	ALS2CL	c.G131A	p.R44K
XH_P62	3	48687987	48687987	Missense_Mutation	SNP	A	C	A	CELSR3	c.T6398G	p.L2133R
XH_P62	3	48697501	48697501	Missense_Mutation	SNP	G	A	G	CELSR3	c.C2567T	p.P856L
XH_P62	3	52729012	52729012	Missense_Mutation	SNP	T	G	T	GLT8D1	c.A965C	p.K322T
XH_P62	3	52817109	52817109	Missense_Mutation	SNP	A	C	A	ITIH1	c.A203C	p.Q68P
XH_P62	3	63973914	63973914	Silent	SNP	G	A	G	ATXN7	c.G840A	p.P280P
XH_P62	3	113374419	113374419	Frame_Shift_Ins	INS	-	TTTTGGTTTTTCT	-	USF3	0insAAAGAAAA	p.I2037fs
XH_P62	3	119246642	119246642	In_Frame_Ins	INS	-	AACAAATTTAAG	-	CD80	843insCTTAATA	R281delinsSLNLL
XH_P62	3	122632117	122632117	Missense_Mutation	SNP	A	C	A	SEMA5B	c.T2261G	p.L754R
XH_P62	3	124732416	124732416	In_Frame_Ins	INS	-	AGAGGAGGAGG	-	HEG1	007insCTCTCC	S669delinsSSSSSS
XH_P62	3	130282194	130282194	Missense_Mutation	SNP	G	A	G	COL6A6	c.G347A	p.R116K
XH_P62	3	195507906	195507906	In_Frame_Ins	INS	-	CTGGTGACAGG	-	MUC4	ACCCCTCTTCCTG	SVSTGHTATPLPVT
XH_P62	3	195509476	195509476	Missense_Mutation	SNP	A	G	A	MUC4	c.T8975C	p.L2992P
XH_P62	3	196529978	196529978	Silent	SNP	C	T	C	PAK2	c.C379T	p.L127L
XH_P62	4	6107567	6107567	Missense_Mutation	SNP	G	A	G	JAKMIP1	c.C257T	p.A86V
XH_P62	4	41633257	41633257	Missense_Mutation	SNP	C	G	C	LIMCH1	c.C1364G	p.A455G
XH_P62	4	62453063	62453063	Silent	SNP	T	C	C	ADGRL3	c.C174C	p.Y58Y
XH_P62	4	71024434	71024463	In_Frame_Del	DEL	5CTGCAGAG	-	TGCTGCAGAGG	PRR27	c.465_494del	p.155_165del
XH_P62	4	78647366	78647366	In_Frame_Ins	INS	-	GATACAAGCATG	-	CNOT6L	1410insCATGCT	T470delinsYMLVS
XH_P62	4	80329070	80329070	Missense_Mutation	SNP	T	G	T	GK2	c.A285C	p.E95D
XH_P62	4	80329071	80329071	Missense_Mutation	SNP	T	G	T	GK2	c.A284C	p.E95A
XH_P62	4	128807355	128807355	Missense_Mutation	SNP	G	A	G	PLK4	c.G734A	p.G245E
XH_P62	4	159791506	159791506	Missense_Mutation	SNP	G	A	G	FNIP2	c.G1772A	p.R591H
XH_P62	4	169611786	169611806	In_Frame_Del	DEL	GGTTCCTGGA	-	GTGGTTCCTGGAG	PALLD	c.222_242del	p.74_81del
XH_P62	5	16463228	16463228	Missense_Mutation	SNP	G	C	G	ZNF622	c.C1038G	p.F346L
XH_P62	5	32355912	32355912	Nonsense_Mutation	INS	-	SCAAATGAGCCA	-	ZFR	AAACGTTGGCTC	O60_E1061delinsCX

XH_P62	5	33576206	33576206	Missense_Mutation	SNP	T	G	T	ADAMTS12	c.A3670C	p.T1224P
XH_P62	5	41917266	41917266	Frame_Shift_Ins	INS	-	AGTAACACAT	-	C5orf51	751insAGTAAC	p.P250fs
XH_P62	5	78411643	78411643	Frame_Shift_Ins	INS	-	AA	-	BHMT	c.87_88insAA	p.P29fs
XH_P62	5	78411644	78411644	Frame_Shift_Ins	INS	-	ATAATTT	-	BHMT	88_89insATAAT	p.V30fs
XH_P62	5	80640737	80640737	Silent	SNP	C	T	C	ACOT12	c.G897A	p.T299T
XH_P62	5	133295223	133295223	Missense_Mutation	SNP	T	A	T	C5orf15	c.A628T	p.I210F
XH_P62	5	139494244	139494244	Missense_Mutation	SNP	A	C	A	PURA	c.A478C	p.K160Q
XH_P62	5	140475862	140475862	Silent	SNP	G	A	G	PCDH82	c.G1488A	p.Q496Q
XH_P62	5	140755343	140755343	Missense_Mutation	SNP	C	A	C	PCDHGA6	c.C1693A	p.P565T
XH_P62	5	142602010	142602010	Nonstop_Mutation	SNP	A	C	A	ARHGAP26	c.A2060C	p.X687S
XH_P62	5	156186255	156186344	In_Frame_Del	DEL	GAGGCAGAA	-	ACGAGGCAGAA	SGCD	c.724_813del	p.242_271del
XH_P62	5	178552066	178552066	Missense_Mutation	SNP	C	T	C	ADAMTS2	c.G2866A	p.A956T
XH_P62	5	179034649	179034683	In_Frame_Del	DEL	TACGTGGGG	-	TGACGTGGGG	RUFY1	c.1648_1659del	p.550_553del
XH_P62	6	36099171	36099171	Missense_Mutation	SNP	T	G	T	MAPK13	c.T243G	p.H81Q
XH_P62	6	41903695	41903695	Missense_Mutation	SNP	T	G	T	CCND3	c.A646C	p.T216P
XH_P62	6	52400580	52400580	Splice_Site	SNP	C	A	C	TRAM2	-	-
XH_P62	6	54806549	54806549	Missense_Mutation	SNP	A	C	A	FAM83B	c.A2780C	p.H927P
XH_P62	6	88170831	88170831	Missense_Mutation	SNP	T	G	T	CFAP206	c.T1586G	p.V529Q
XH_P62	7	2412377	2412377	Missense_Mutation	SNP	G	A	G	EIF3B	c.G1757A	p.R586Q
XH_P62	7	5780686	5780686	Missense_Mutation	SNP	T	G	T	RNF216	c.A962C	p.Q321P
XH_P62	7	8167642	8167642	Silent	SNP	C	A	C	ICA1	c.G966T	p.V322V
XH_P62	7	20683193	20683193	Frame_Shift_Ins	INS	-	SCAAATAAATGT	-	ABCB5	insAAGCAATA	p.L206fs
XH_P62	7	36910077	36910077	Missense_Mutation	SNP	G	A	G	ELMO1	c.C386T	p.P129L
XH_P62	7	57194352	57194352	In_Frame_Ins	INS	-	TAATATATT	-	ZNF479	2_113insAATAT	p.R38delinsQYIR
XH_P62	7	57194353	57194353	Frame_Shift_Ins	INS	-	CTTTT	-	ZNF479	111_112insAAA	p.R38fs
XH_P62	7	73520439	73520439	Silent	SNP	G	T	G	LIMK1	c.G645T	p.L215L
XH_P62	7	99056770	99056770	Missense_Mutation	SNP	T	G	T	ATPSJ2	c.A238C	p.K80Q
XH_P62	7	99097611	99097635	Frame_Shift_Del	DEL	CGTTGGGAC	-	GCGTTGGGACG	ZNF394	c.82_106del	p.A28fs
XH_P62	7	99364010	99364010	Silent	SNP	C	T	C	CYP3A4	c.G852A	p.E284E
XH_P62	7	100678764	100678764	Missense_Mutation	SNP	T	C	T	MUC17	c.T4067C	p.I1356T
XH_P62	7	100683382	100683382	Silent	SNP	T	C	T	MUC17	c.T8685C	p.D2895D
XH_P62	7	100684199	100684199	Missense_Mutation	SNP	T	A	T	MUC17	c.T9502A	p.Y3168N
XH_P62	7	100684200	100684200	Missense_Mutation	SNP	A	G	A	MUC17	c.A9503G	p.Y3168C
XH_P62	7	100684306	100684306	Silent	SNP	A	C	A	MUC17	c.A9609C	p.S5203S
XH_P62	7	100684307	100684307	In_Frame_Ins	INS	-	CTC	-	MUC17	9610_9611insCT	p.S3204delinsSP
XH_P62	7	100731246	100731246	In_Frame_Ins	INS	-	CATTTCATCCAT	-	TRIM56	CATTTCATTCAC	GGSLFHSHSFHFPHSVTFHFIP
XH_P62	7	102760414	102760414	Missense_Mutation	SNP	C	G	C	NAPEPLD	c.G551C	p.S184T
XH_P62	7	134889130	134889130	Frame_Shift_Ins	INS	-	AGAGTCCTTC	-	WDR91	781insGAAGGA	p.F261fs
XH_P62	7	141490560	141490560	Silent	SNP	C	T	C	TAS2R5	c.C399T	p.Y133Y
XH_P62	7	142881278	142881278	Missense_Mutation	SNP	C	A	C	TAS2R39	c.C767A	p.A256D
XH_P62	8	1833806	1833806	Missense_Mutation	SNP	T	C	T	ARHGEF10	c.T1001C	p.I334T
XH_P62	8	6914168	6914168	Missense_Mutation	SNP	G	T	G	DEFA5	c.C52A	p.Q18K
XH_P62	8	24254935	24254935	Missense_Mutation	SNP	C	G	C	ADAMDEC1	c.C356G	p.P119R
XH_P62	8	54708385	54708409	In_Frame_Del	DEL	CATTATGCT	-	CCATTATGCTGA	ATP6V1H	c.624_638del	p.208_213del
XH_P62	8	82606968	82606968	Silent	SNP	T	G	T	SLC10A5	c.A240C	p.S80S
XH_P62	8	87549843	87549843	Nonsense_Mutation	INS	-	ACTCTATAGTAT	-	CPNE3	GTCTAACTCTAT	p.D171delinsEVX
XH_P62	8	87588079	87588079	Missense_Mutation	SNP	C	G	C	CNGB3	c.G2383C	p.G795R
XH_P62	8	101727714	101727714	Missense_Mutation	SNP	G	A	G	PABPC1	c.C619T	p.L207F
XH_P62	8	101727716	101727716	Missense_Mutation	SNP	C	T	C	PABPC1	c.G617A	p.R206H
XH_P62	8	142367555	142367555	Missense_Mutation	SNP	C	A	C	GPR20	c.G469T	p.G157C
XH_P62	8	146017476	146017480	Frame_Shift_Del	DEL	CCCGG	-	CCCGG	RPL8	c.35_39del	p.A12fs
XH_P62	9	7015875	7015875	Missense_Mutation	SNP	T	G	T	KDM4C	c.T1440G	p.H480Q
XH_P62	9	33036669	33036669	Missense_Mutation	SNP	G	A	G	DNAJA1	c.G385A	p.V129I
XH_P62	9	33797962	33797962	Missense_Mutation	SNP	A	T	A	PRSS3	c.A315T	p.K105N
XH_P62	9	35704169	35704169	Missense_Mutation	SNP	T	G	T	TLN1	c.A6050C	p.E2017A
XH_P62	9	71836404	71836404	Missense_Mutation	SNP	C	T	C	TJP2	c.C956T	p.A319V
XH_P62	9	91617005	91617005	Missense_Mutation	SNP	T	G	T	S1PR3	c.T890G	p.I297S
XH_P62	9	95022443	95022443	Missense_Mutation	SNP	C	G	C	IARS	c.G1861C	p.D621H
XH_P62	9	96278331	96278331	Missense_Mutation	SNP	C	T	C	FAM120A	c.C1195T	p.P399S
XH_P62	9	103348339	103348339	Missense_Mutation	SNP	T	C	T	CAVIN4	c.T701C	p.L234P
XH_P62	9	129458648	129458648	Missense_Mutation	SNP	C	T	C	LMX1B	c.C1139T	p.S380L
XH_P62	10	12708754	12708754	Missense_Mutation	SNP	G	T	G	CAMK1D	c.G244T	p.V82F
XH_P62	10	76781906	76781911	In_Frame_Del	DEL	GAAGAA	-	GAAGAA	KAT6B	c.2740_2745del	p.914_915del
XH_P62	10	103901338	103901338	In_Frame_Ins	INS	-	ACA	-	PPRC1	3073_3074insAA	p.L1025delinsHT
XH_P62	10	112039046	112039046	Frame_Shift_Ins	INS	-	TGGTT	-	MXI1	207_208insTGG	p.H69fs
XH_P62	10	126631583	126631583	Frame_Shift_Ins	INS	-	TTATTTCATCAT	-	ZRANB1	2insGTTTATTTC	p.H174fs
XH_P62	11	1079676	1079684	In_Frame_Del	DEL	ACCTGGTGT	-	ACCTGGTGT	MUC2	c.893_901del	p.298_301del
XH_P62	11	2427985	2427985	Missense_Mutation	SNP	T	A	T	TRPM5	c.A3157T	p.T1053S
XH_P62	11	4615448	4615448	Missense_Mutation	SNP	T	G	T	OR52I1	c.T180G	p.H60Q
XH_P62	11	4929147	4929147	Missense_Mutation	SNP	A	C	A	OR51A7	c.A548C	p.D183A
XH_P62	11	6023726	6023726	Missense_Mutation	SNP	G	A	G	OR56A4	c.C653T	p.S218F
XH_P62	11	6806853	6806853	Nonsense_Mutation	SNP	T	G	T	OR2AG1	c.T585G	p.Y195X
XH_P62	11	13408276	13408276	Frame_Shift_Ins	INS	-	AATCATGTCTA	-	ARNTL	1852insAATCA	p.D617fs
XH_P62	11	27016354	27016354	Missense_Mutation	SNP	C	T	C	FIBIN	c.C281T	p.A94V
XH_P62	11	46726037	46726037	Nonsense_Mutation	SNP	G	T	G	ZNF408	c.G763T	p.E255X
XH_P62	11	59271239	59271239	Missense_Mutation	SNP	G	A	G	OR4D11	c.G191A	p.R64H
XH_P62	11	65385824	65385824	Missense_Mutation	SNP	G	T	G	PCNX3	c.G991T	p.A331S
XH_P62	11	71276657	71276657	In_Frame_Ins	INS	-	TGGCTCCGGCT	-	KRTAP5-10	GCTGTGGCTCC	delinsGGCGSGWG
XH_P62	11	82892052	82892052	Missense_Mutation	SNP	G	A	G	PCF11	c.G4379A	p.R1460H
XH_P62	11	93528152	93528152	Missense_Mutation	SNP	G	A	G	MED17	c.G938A	p.R313Q
XH_P62	11	100998724	100998724	Missense_Mutation	SNP	C	A	C	PGR	c.G1078T	p.D360Y
XH_P62	11	116729011	116729013	In_Frame_Del	DEL	TGT	-	TGT	SIK3	c.2844_2846del	p.948_949del
XH_P62	11	117266349	117266349	Frame_Shift_Ins	INS	-	G	-	CEP164	3009_3010insG	p.I1003fs
XH_P62	11	124623761	124623761	Silent	SNP	G	C	G	ESAM	c.C954G	p.A318A
XH_P62	12	2062350	2062350	In_Frame_Ins	INS	-	TGG	-	DCP1B	c.755_756insCC	p.Q252delinsHQ
XH_P62	12	7882286	7882286	Missense_Mutation	SNP	A	T	A	CLEC4C	c.T455A	p.I152K
XH_P62	12	15794757	15794757	In_Frame_Ins	INS	-	TAAAGGATG	-	EP58	5_1576insCATC	p.E526delinsHPLF
XH_P62	12	29450037	29450037	Nonsense_Mutation	INS	-	TGAAGTAAGTCA	-	FAR2	59insATGAAGTA	p.H53_154delinsOX
XH_P62	12	33030969	33030969	Missense_Mutation	SNP	T	C	T	PKP2	c.A845G	p.Q282R
XH_P62	12	52631309	52631309	Missense_Mutation	SNP	A	C	A	KRT7	c.A553C	p.N185H
XH_P62	12	64011087	64011087	Silent	SNP	C	T	C	DPY19L2	c.G1215A	p.T405T
XH_P62	12	89744793	89744802	Frame_Shift_Del	DEL	CTGAAGCCAA	-	CTGAAGCCAC	DUSP6	c.401_410del	p.G134fs
XH_P62	12	121756215	121756215	Silent	SNP	G	A	G	ANAPC5	c.C1422T	p.S474S
XH_P62	12	123214425	123214446	Frame_Shift_Del	DEL	AGCAAAAAG	-	CCAGCAAAAAGAT	HCAR1	c.441_462del	p.T147fs
XH_P62	12	123424767	123424767	Missense_Mutation	SNP	T	G	T	ABC89	c.A1445C	p.K482T
XH_P62	12	124796465	124796465	Missense_Mutation	SNP	T	G	T	RFLNA	c.T66G	p.H22Q
XH_P62	13	23912277	23912277	Missense_Mutation	SNP	A	C	A	SACS	c.T5297G	p.M1766R
XH_P62	13	29598920	29598947	Frame_Shift_Del	DEL	TGGGAGAT	-	TCTGGGAGATAC	MTU52	c.115_142del	p.I39fs

XH_P62	13	41897231	41897231	Missense_Mutation	SNP	C	T	C	NAA16	c.C442T	p.R148C
XH_P62	13	46533734	46533734	Missense_Mutation	SNP	C	T	C	ZC3H13	c.G4723A	p.A1575T
XH_P62	13	96579536	96579536	Missense_Mutation	SNP	C	A	C	UGGT2	c.G2032T	p.V678F
XH_P62	14	23240093	23240093	Nonsense_Mutation	SNP	T	A	T	OXA1L	c.T1094A	p.L365X
XH_P62	14	24534846	24534846	Nonsense_Mutation	SNP	G	T	G	CARMIL3	c.G3412T	p.E1138X
XH_P62	14	33293485	33293485	Frame_Shift_Ins	INS	-	CTCTCTATGTAA	-	AKAP6	5467insCTCTCT	p.F2156fs
XH_P62	14	38259941	38259941	Nonsense_Mutation	SNP	T	G	T	TTC6	c.T3504G	p.Y1168X
XH_P62	14	39796178	39796178	Frame_Shift_Ins	INS	-	GTGAGCCTAAT	-	MAI2	1568insGTGAG	p.L523fs
XH_P62	14	55510717	55510717	Frame_Shift_Ins	INS	-	CCATCAC	-	SOCS4	58_959insCAAT	p.F320fs
XH_P62	14	60976497	60976497	Silent	SNP	C	T	C	SIX6	c.C381T	p.D127D
XH_P62	14	67382785	67382785	Missense_Mutation	SNP	A	C	A	GPHN	c.A455C	p.Q152P
XH_P62	14	74411263	74411263	Missense_Mutation	SNP	T	G	T	FAM161B	c.A889C	p.M297L
XH_P62	14	79181309	79181309	Missense_Mutation	SNP	G	A	G	NRXN3	c.G752A	p.R251Q
XH_P62	14	89124718	89124718	Silent	SNP	C	T	C	EML5	c.G3690A	p.K1230K
XH_P62	14	93760225	93760225	Missense_Mutation	SNP	C	G	C	BTBD7	c.G1141C	p.E381Q
XH_P62	14	105412302	105412302	Missense_Mutation	SNP	A	C	A	AHNAK2	c.T9186G	p.L3062M
XH_P62	14	105939695	105939695	Silent	SNP	T	A	T	CRIP2	c.T111A	p.C37A
XH_P62	15	22841099	22841099	Frame_Shift_Ins	INS	-	TTTATTATATCT	-	TUBGCP5	68insCTTTATTA	p.G156fs
XH_P62	15	31320592	31320592	Missense_Mutation	SNP	G	A	G	TRPM1	c.C3287T	p.A1096V
XH_P62	15	73615439	73615439	Missense_Mutation	SNP	G	A	G	HCN4	c.C2995T	p.R999W
XH_P62	15	79760595	79760595	Missense_Mutation	SNP	G	A	G	KIAA1024	c.G2620A	p.D874N
XH_P62	15	83014106	83014106	Silent	SNP	T	C	T	GOLGA6L10	c.A477G	p.V159V
XH_P62	16	2512676	2512676	Nonsense_Mutation	SNP	G	T	G	C16orf59	c.G907T	p.E303X
XH_P62	16	2819139	2819139	Silent	SNP	C	T	C	SRRM2	c.C7875T	p.S2625S
XH_P62	16	3166446	3166446	Missense_Mutation	SNP	G	T	G	ZNF205	c.G382T	p.L128Y
XH_P62	16	14354860	14354860	Silent	SNP	G	C	G	MKL2	c.G2859C	p.V953V
XH_P62	16	15180043	15180043	Frame_Shift_Ins	INS	-	T	-	RRN3	c.324dupA	p.A109fs
XH_P62	16	15180045	15180045	Nonsense_Mutation	INS	-	TTTTATTTTCTT	-	RRN3	nsAAAAAGAAAD8	A109delinsLKRXX
XH_P62	16	18870425	18870425	Nonsense_Mutation	INS	-	TATTTTITTAGT	-	SMG1	82insAACTAAAB44	S1345delinsQNX
XH_P62	16	28619647	28619647	Silent	SNP	G	A	G	SULT1A1	c.C337T	p.L113L
XH_P62	16	47727353	47727353	Nonsense_Mutation	SNP	C	T	C	PHKB	c.C2830T	p.R944X
XH_P62	16	52480134	52480134	Splice_Site	SNP	C	T	C	TOX3	.	.
XH_P62	16	66968250	66968250	Silent	SNP	C	A	C	FAM96B	c.G18T	p.G6G
XH_P62	16	67354579	67354579	Nonsense_Mutation	INS	-	ATGCCTT	-	KCTD19	12_213insAAGG	Y71_T72delinsX
XH_P62	16	70852449	70852449	Missense_Mutation	SNP	A	C	A	HYDIN	c.T14454G	p.N4818K
XH_P62	16	89628794	89628794	Missense_Mutation	SNP	C	T	C	RPL13	c.C472T	p.R158W
XH_P62	17	17700681	17700681	Silent	SNP	G	C	G	RAI1	c.G4419C	p.L1473L
XH_P62	17	18206030	18206030	Nonsense_Mutation	INS	-	CTCTCTTCCCCA	-	TOP3A	AAGCTGGGGAAAN75delinsPQIKLGKGGX	
XH_P62	17	32905921	32905921	Missense_Mutation	SNP	C	T	C	C17orf102	c.G379A	p.G127R
XH_P62	17	39622060	39622080	In_Frame_Del	DEL	GGGACTCAA	-	AGGGACTCAACC	KRT32	c.653_673del	p.218_225del
XH_P62	17	39978644	39978644	Missense_Mutation	SNP	T	G	T	FKBP10	c.T1733G	p.V578G
XH_P62	17	44592375	44592392	In_Frame_Del	DEL	AGCCCTGGAG	-	CAGCCCTGGAGA	LRR37A2	c.2297_2314del	p.766_772del
XH_P62	17	45214558	45214558	Nonsense_Mutation	SNP	G	A	G	CDCAF2	c.C1690T	p.C564X
XH_P62	17	47587875	47587875	Missense_Mutation	SNP	A	C	A	NGFR	c.A670C	p.I224L
XH_P62	17	65110481	65110481	In_Frame_Ins	INS	-	GGAATCTTG	-	HELZ	9_3880insCAAGK1294delinsQDSK	
XH_P62	17	66547263	66547263	Nonstop_Mutation	SNP	T	G	T	PRKAR1A	c.T1012G	p.X338E
XH_P62	17	76521147	76521147	Missense_Mutation	SNP	T	G	T	DNAH17	c.A3808C	p.K1270Q
XH_P62	17	78093099	78093099	Missense_Mutation	SNP	T	C	T	GAA	c.T2828C	p.M943T
XH_P62	17	79973218	79973218	Missense_Mutation	SNP	G	T	G	ASPSR1	c.G1621T	p.V541L
XH_P62	18	61306965	61306965	Missense_Mutation	SNP	G	A	G	SERPINB4	c.C515T	p.T172M
XH_P62	18	64172380	64172380	Missense_Mutation	SNP	G	T	G	CDH19	c.C1988A	p.7663N
XH_P62	19	463990	463990	Missense_Mutation	SNP	C	T	C	ODF3L2	c.G724A	p.A242T
XH_P62	19	3977563	3977563	Missense_Mutation	SNP	G	T	G	EEF2	c.C2113A	p.H705N
XH_P62	19	7623896	7623896	Missense_Mutation	SNP	G	T	G	PNPLA6	c.G3558T	p.M1186I
XH_P62	19	7623897	7623897	Missense_Mutation	SNP	G	C	G	PNPLA6	c.G3559C	p.A1817P
XH_P62	19	9006370	9006370	Silent	SNP	A	G	A	MUC16	c.T39648C	p.Y13216V
XH_P62	19	9577543	9577543	Nonsense_Mutation	SNP	G	A	G	ZNF560	c.C1762T	p.R588X
XH_P62	19	11240295	11240295	In_Frame_Ins	INS	-	FCCAGCTACTTG	-	LDLR	93insATCCAGG664delinsTIPATW	
XH_P62	19	14043884	14043884	Silent	SNP	A	G	A	PODNL1	c.T900C	p.Y300Y
XH_P62	19	21719959	21719959	Silent	SNP	C	T	C	ZNF429	c.C912T	p.P304P
XH_P62	19	36002370	36002370	In_Frame_Ins	INS	-	CTTCTGCTG	-	DMKN	861insCAGCAAG287delinsGSRS	
XH_P62	19	43766063	43766063	Missense_Mutation	SNP	G	A	G	PSG9	c.C658T	p.R220W
XH_P62	19	44130071	44130071	Silent	SNP	C	T	C	CADM4	c.G747A	p.G249G
XH_P62	19	47549414	47549414	Missense_Mutation	SNP	C	A	C	TMEM160	c.G398T	p.G133V
XH_P62	19	55823355	55823355	Missense_Mutation	SNP	C	A	C	BRSK1	c.C2256A	p.D752E
XH_P62	19	57133546	57133546	Silent	SNP	G	A	G	ZNF71	c.G891A	p.P297P
XH_P62	20	168625	168625	Frame_Shift_Ins	INS	-	T	-	DEFB128	c.183dupA	p.H62fs
XH_P62	20	1552529	1552529	Silent	SNP	G	A	G	SIRPB1	c.C588T	p.R196N
XH_P62	20	1552530	1552530	Nonsense_Mutation	INS	-	CACC	-	SIRPB1	586_587insGGT196_V197delinsRX	
XH_P62	20	4768371	4768371	In_Frame_Ins	INS	-	AAGGCAGCACCA	-	RASSF2	721insTGGTGC	P241delinsWCCLP
XH_P62	20	4768373	4768373	Nonsense_Mutation	INS	-	ATGGCAAAACAT	-	RASSF2	TGTCTTGTITTTT240_P241delinsFX	
XH_P62	20	20279001	20279001	Silent	SNP	C	T	C	CFAP61	c.C3393T	p.Y1131Y
XH_P62	20	37146533	37146533	Missense_Mutation	SNP	G	A	G	RALGAPB	c.G1307A	p.R436Q
XH_P62	20	40743859	40743859	Missense_Mutation	SNP	G	A	G	PTPRT	c.C3079T	p.R1027C
XH_P62	20	40944369	40944369	Silent	SNP	G	A	G	PTPRT	c.C2133T	p.A711A
XH_P62	20	44520238	44520243	In_Frame_Del	DEL	CTGCTG	-	CTGCTG	CTSA	c.85_90del	p.29_30del
XH_P62	20	58467066	58467066	Missense_Mutation	SNP	C	A	C	SYCP2	c.G2343T	p.W781C
XH_P62	20	58467067	58467067	Missense_Mutation	SNP	C	A	C	SYCP2	c.G2342T	p.W781L
XH_P62	20	60911410	60911410	Missense_Mutation	SNP	G	T	G	LAMA5	c.C2309A	p.P770H
XH_P62	20	61468525	61468525	Missense_Mutation	SNP	C	G	C	COL9A3	c.C1694G	p.P565R
XH_P62	21	10916369	10916369	Splice_Site	SNP	C	T	C	TPTE	.	.
XH_P62	21	38538096	38538100	Frame_Shift_Del	DEL	ATTTC	-	ATTTC	TTC3	c.2650_2654del	p.1884fs
XH_P62	22	19961221	19961221	Silent	SNP	G	A	G	ARVCF	c.C2184T	p.A728A
XH_P62	22	22326251	22326251	Nonsense_Mutation	SNP	C	A	C	TOP3B	c.G382T	p.E128X
XH_P62	22	29445816	29445816	Silent	SNP	C	T	C	ZNRF3	c.C1647T	p.S549S
XH_P62	22	37693650	37693650	Nonsense_Mutation	SNP	C	T	C	CYTH4	c.C109T	p.Q37X
XH_P62	22	38247391	38247391	Missense_Mutation	SNP	G	A	G	EIF3L	c.G187A	p.V63I
XH_P62	22	38323558	38323558	Missense_Mutation	SNP	A	G	A	MICALL1	c.A1606G	p.S536G
XH_P62	22	40042696	40042696	Silent	SNP	G	A	G	CACNA1I	c.G1272A	p.T424T
XH_P62	X	5821621	5821621	Silent	SNP	G	A	G	NLGN4X	c.C1098T	p.D366D
XH_P62	X	9900745	9900745	Missense_Mutation	SNP	G	A	G	SHROOM2	c.G3422A	p.G1141E
XH_P62	X	114426308	114426308	Silent	SNP	C	T	C	RBMXL3	c.C2304T	p.S768S
XH_P62	X	140271064	140271064	Missense_Mutation	SNP	C	G	C	LDOC1	c.G143C	p.S48T
XH_P62	X	149639622	149639622	Missense_Mutation	SNP	A	G	A	MAMLD1	c.A1702G	p.T568A
XH_P62	Y	6948818	6948818	Missense_Mutation	SNP	C	G	C	TBL1Y	c.C1001G	p.S334C
XH_P62	1	112524306	112524306	Missense_Mutation	SNV	G	A	A	KCNB3	c.1043C>T	P.A348V
XH_P62	1	11740631	11740631	Missense_Mutation	SNV	T	G	G	MAD2L2	c.28A>C	P.N10H
XH_P62	1	11907300	11907300	Missense_Mutation	SNV	C	G	G	NPPA	c.320G>C	P.R107P

XH_P62	1	145311110	145311110	Silent	SNV	G	T	T	NBPF10	c.1809G>T	P.R603R
XH_P62	1	152383060	152383060	Silent	SNV	G	A	A	CRNN	c.498C>T	P.S166S
XH_P62	1	152383061	152383061	Missense_Mutation	SNV	C	T	T	CRNN	c.497G>A	P.S166N
XH_P62	1	152944577	152944577	Missense_Mutation	SNV	C	G	G	SPRR4	c.211C>G	P.Q71E
XH_P62	1	156639633	156639633	Silent	SNV	C	T	T	NES	c.4347G>A	P.L1449L
XH_P62	1	161722963	161722963	Missense_Mutation	SNV	C	G	G	DUSP12	c.773C>G	P.T258S
XH_P62	1	211534436	211534436	Nonsense_Mutation	SNV	G	T	T	TRAF5	c.628G>T	P.E210*
XH_P62	1	23191621	23191621	Missense_Mutation	SNV	G	A	A	EPHB2	c.1219G>A	P.E407K
XH_P62	1	237756887	237756887	Missense_Mutation	SNV	C	T	T	RYR2	c.4387C>T	P.R1463C
XH_P62	1	2411365	2411365	Missense_Mutation	SNV	C	A	A	PLCH2	c.383C>A	P.A128D
XH_P62	1	35852628	35852628	Missense_Mutation	SNV	A	G	G	ZMYM4	c.1861A>G	P.M621V
XH_P62	1	47653042	47653042	Missense_Mutation	SNV	A	T	T	PDZK1P1	c.125T>A	P.V42D
XH_P62	1	70502319	70502319	Splice_Site	SNV	A	G	G	LRRC7	c.2174+12A>G	
XH_P62	10	12708754	12708754	Missense_Mutation	SNV	G	T	T	CAMK1D	c.244G>T	P.V82F
XH_P62	11	100998724	100998724	Missense_Mutation	SNV	C	A	A	PGR	c.1078G>T	P.D360Y
XH_P62	11	1079676	1079684	Missense_Mutation	INDEL	ACCTGGTGT	-	-	MUC2	c.907delGTAC	P.V300_L302del
XH_P62	11	124623761	124623761	Silent	SNV	G	C	C	ESAM	c.954C>G	P.A318A
XH_P62	11	4615448	4615448	Missense_Mutation	SNV	T	G	G	QR52I1	c.180T>G	P.H60Q
XH_P62	11	46726037	46726037	Nonsense_Mutation	SNV	G	T	T	ZNF408	c.763G>T	P.E255*
XH_P62	11	4929147	4929147	Missense_Mutation	SNV	A	C	C	OR51A7	c.548A>C	P.D183A
XH_P62	11	6806853	6806853	Nonsense_Mutation	SNV	T	G	G	OR2AG1	c.585T>G	P.Y195*
XH_P62	12	123214425	123214446	Frame_Shift_Del	INDEL	TAGCAAAAG	-	-	HCAR1	AGTGTATCTTTT	P.V148fs
XH_P62	12	123424767	123424767	Missense_Mutation	SNV	T	G	G	ABC89	c.1445A>C	P.K482T
XH_P62	12	124796465	124796465	Missense_Mutation	SNV	T	G	G	RFLNA	c.66T>G	P.H22Q
XH_P62	12	33030969	33030969	Missense_Mutation	SNV	T	C	C	PKP2	c.845A>G	P.Q282R
XH_P62	12	52631309	52631309	Missense_Mutation	SNV	A	C	C	KRT7	c.553A>C	P.R185H
XH_P62	12	7882286	7882286	Missense_Mutation	SNV	A	T	T	CLEC4C	c.548T>A	P.I183K
XH_P62	12	89744793	89744802	Frame_Shift_Del	INDEL	CTGAAGCCA	-	-	DUSP6	410delGTGGC	P.G134fs
XH_P62	13	23912277	23912277	Missense_Mutation	SNV	A	C	C	SACS	c.529T>T	P.M1766R
XH_P62	13	96579536	96579536	Missense_Mutation	SNV	C	A	A	UGT2	c.2032G>T	P.V678F
XH_P62	14	105412302	105412302	Missense_Mutation	SNV	A	C	C	AHNAK2	c.9486T>G	P.I3162M
XH_P62	14	105939695	105939695	Silent	SNV	T	A	A	CRIP2	c.111T>A	P.A37A
XH_P62	14	23240093	23240093	Nonsense_Mutation	SNV	T	A	A	OXA1L	c.1094T>A	P.L365*
XH_P62	14	24534846	24534846	Nonsense_Mutation	SNV	G	T	T	CARMIL3	c.3412G>T	P.E1138*
XH_P62	14	38259941	38259941	Nonsense_Mutation	SNV	T	G	G	TTCC	c.3504T>G	P.Y1168*
XH_P62	14	67382785	67382785	Missense_Mutation	SNV	A	C	C	GPHN	c.455A>C	P.Q152P
XH_P62	14	74411263	74411263	Missense_Mutation	SNV	T	G	G	FAM161B	c.889A>C	P.M297L
XH_P62	14	79181309	79181309	Missense_Mutation	SNV	G	A	A	NRXN3	c.752G>A	P.R251Q
XH_P62	14	89124718	89124718	Silent	SNV	C	T	T	EML5	c.3690G>A	P.K1230K
XH_P62	14	93760225	93760225	Missense_Mutation	SNV	C	G	G	BTBD7	c.1141G>C	P.E381Q
XH_P62	15	31320592	31320592	Missense_Mutation	SNV	G	A	A	TRPM1	c.3287C>T	P.A1096V
XH_P62	15	73615439	73615439	Missense_Mutation	SNV	G	A	A	HCN4	c.2995C>T	P.R999W
XH_P62	16	14354860	14354860	Silent	SNV	G	C	C	MKL2	c.2859G>C	P.V953V
XH_P62	16	2512676	2512676	Nonsense_Mutation	SNV	G	T	T	C16orf59	c.907G>T	P.E303*
XH_P62	16	28619647	28619647	Silent	SNV	G	A	A	SULT1A1	c.337C>T	P.L113L
XH_P62	16	3166446	3166446	Missense_Mutation	SNV	G	T	T	ZNF205	c.382G>T	P.D128Y
XH_P62	16	47727353	47727353	Nonsense_Mutation	SNV	C	T	T	PHKB	c.2830C>T	P.R944*
XH_P62	16	66968250	66968250	Silent	SNV	C	A	A	FAM96B	c.18G>T	P.G6G
XH_P62	16	70852449	70852449	Missense_Mutation	SNV	A	C	C	HYDIN	c.14454T>G	P.N4818K
XH_P62	17	17700681	17700681	Silent	SNV	G	C	C	RA1I	c.4419G>C	P.L1473L
XH_P62	17	39622060	39622080	Missense_Mutation	INDEL	GGGAAGCTCAA	-	-	KRT32	CCCAGGTTGAG	P.A218_K224del
XH_P62	17	39978644	39978644	Missense_Mutation	SNV	T	G	G	FKBP10	c.1733T>G	P.V578G
XH_P62	17	44592375	44592392	Missense_Mutation	INDEL	AGCCCTGGAG	-	-	LRRC37A2	delCCTGGAGAA	P.L769_A774del
XH_P62	17	47587875	47587875	Missense_Mutation	SNV	A	C	C	NGFR	c.670A>C	P.I224L
XH_P62	17	66547263	66547263	Nonstop_Mutation	SNV	T	G	G	PRKAR1A	c.1012T>G	P.Ter338Eext*?
XH_P62	17	76521147	76521147	Missense_Mutation	SNV	T	G	G	DNAH17	c.3808A>C	P.K1270Q
XH_P62	17	78093099	78093099	Missense_Mutation	SNV	T	C	C	GAA	c.2828T>C	P.M943T
XH_P62	17	79973218	79973218	Missense_Mutation	SNV	G	T	T	ASPSCR1	c.1621G>T	P.V541L
XH_P62	19	14043884	14043884	Silent	SNV	A	G	G	PODNL1	c.1167T>C	P.Y389Y
XH_P62	19	463990	463990	Missense_Mutation	SNV	C	T	T	ODF3L2	c.724G>A	P.A242T
XH_P62	19	47549414	47549414	Missense_Mutation	SNV	C	A	A	TMEM160	c.398G>T	P.G133V
XH_P62	19	53741817	53741817	Splice_Site	SNV	G	T	T	ZNF677	c.170-7C>A	P.I224L
XH_P62	19	55823355	55823355	Missense_Mutation	SNV	C	A	A	BRSK1	c.2256C>A	P.D752E
XH_P62	19	7623896	7623896	Missense_Mutation	SNV	G	T	T	PNPLA6	c.3588G>T	P.M1196I
XH_P62	19	7623897	7623897	Missense_Mutation	SNV	G	C	C	PNPLA6	c.3589G>C	P.A1197P
XH_P62	19	9577543	9577543	Nonsense_Mutation	SNV	G	A	A	ZNF560	c.2080C>T	P.R694*
XH_P62	2	1271127	1271127	Splice_Site	SNV	T	A	A	SNHG2	c.1078-10T>A	
XH_P62	2	131221328	131221343	Frame_Shift_Del	INDEL	TCCTTGCTC	-	-	POTEL	9delCCAGAGCA	P.Q759fs
XH_P62	2	136562631	136562631	Splice_Site	SNV	A	C	C	LCT	c.4174-4T>G	
XH_P62	2	179400436	179400436	Missense_Mutation	SNV	T	G	G	TTN	c.95983A>C	P.I31995L
XH_P62	2	220047332	220047332	Missense_Mutation	SNV	A	C	C	FAM134A	c.992A>C	P.Q331P
XH_P62	2	234601812	234601812	Missense_Mutation	SNV	T	G	G	UGT1A6	c.162T>G	P.H54Q
XH_P62	2	26407666	26407666	Missense_Mutation	SNV	C	G	G	GAREM2	c.949C>G	P.L317V
XH_P62	2	33817224	33817224	Missense_Mutation	SNV	T	C	C	FAM98A	c.260A>G	P.N875
XH_P62	2	98373636	98373636	Missense_Mutation	SNV	G	A	A	TMEM131	c.5578C>T	P.R1860W
XH_P62	20	20279001	20279001	Silent	SNV	C	T	T	CFAP61	c.3393C>T	P.Y1131Y
XH_P62	20	40743859	40743859	Missense_Mutation	SNV	G	A	A	PTPR	c.3136C>T	P.R1046C
XH_P62	20	58467066	58467066	Missense_Mutation	SNV	C	A	A	SYCP2	c.2343G>T	P.W781C
XH_P62	20	58467067	58467067	Missense_Mutation	SNV	C	A	A	SYCP2	c.2342G>T	P.W781L
XH_P62	20	60911410	60911410	Missense_Mutation	SNV	G	T	T	LAMAS	c.2309C>A	P.P770H
XH_P62	20	61468525	61468525	Missense_Mutation	SNV	C	G	G	COL9A3	c.1694C>G	P.P565R
XH_P62	21	38538096	38538100	Frame_Shift_Del	INDEL	ATTTC	-	-	TTC3	581_3585delTT	P.I1194fs
XH_P62	22	22326251	22326251	Nonsense_Mutation	SNV	C	A	A	TOP3B	c.382G>T	P.E128*
XH_P62	22	38247391	38247391	Missense_Mutation	SNV	G	A	A	EIF3L	c.187G>A	P.V63I
XH_P62	22	38323558	38323558	Missense_Mutation	SNV	A	G	G	MICALL1	c.1606A>G	P.S536G
XH_P62	3	122632117	122632117	Missense_Mutation	SNV	A	C	C	SEMA5B	c.2435T>G	P.L812R
XH_P62	3	130282194	130282194	Missense_Mutation	SNV	G	A	A	COL6A6	c.347G>A	P.R116K
XH_P62	3	38315866	38315866	Missense_Mutation	SNV	G	A	A	SLC22A13	c.482G>A	P.R161Q
XH_P62	3	46729759	46729759	Missense_Mutation	SNV	C	T	T	ALS2CL	c.131G>A	P.R44K
XH_P62	3	48687987	48687987	Missense_Mutation	SNV	A	C	C	CELSR3	c.6398T>G	P.L12133R
XH_P62	3	48697501	48697501	Missense_Mutation	SNV	G	A	A	CELSR3	c.2567C>T	P.P856L
XH_P62	3	52729012	52729012	Missense_Mutation	SNV	T	G	G	GLT8D1	c.965A>C	P.K322T
XH_P62	3	52817109	52817109	Missense_Mutation	SNV	A	C	C	ITIH1	c.641A>C	P.Q214P
XH_P62	4	128807355	128807355	Missense_Mutation	SNV	G	A	A	PLK4	c.734G>A	P.G245E
XH_P62	4	169611786	169611806	Missense_Mutation	INDEL	GGTCTGGGA	-	-	PALLD	delGGTGGTCTGG	P.V458_V464del
XH_P62	4	6107567	6107567	Missense_Mutation	SNV	G	A	A	JAKMIP1	c.257C>T	P.A86V
XH_P62	4	62453063	62453063	Silent	SNV	T	C	C	ADGRL3	c.174T>C	P.Y58Y
XH_P62	4	71024434	71024463	Missense_Mutation	INDEL	CTGCAGAG	-	-	PRR27	TGAGCCTGCTGG	P.G165_V174del

XH_P62	5	133295223	133295223	Missense_Mutation	SNV	T	A	A	C5orf15	c.628A>T	P.I210F
XH_P62	5	139494244	139494244	Missense_Mutation	SNV	A	C	C	PURA	c.478A>C	P.K160Q
XH_P62	5	140755343	140755343	Missense_Mutation	SNV	C	A	A	PCDHGA6	c.1693C>A	P.P565T
XH_P62	5	142602010	142602010	Nonstop_Mutation	SNV	A	C	C	ARHGAP26	c.2279A>C	P.Ter760Sext*?
XH_P62	5	16463228	16463228	Missense_Mutation	SNV	G	C	C	ZN622	c.1038C>G	P.F346L
XH_P62	5	178552066	178552066	Missense_Mutation	SNV	C	T	T	ADAMTS2	c.2866G>A	P.A956T
XH_P62	5	179034649	179034683	Frame_Shift_Del	INDEL	ATACGTGGGG	-	-	RUFY1	AAAGGTACGTG	P.R551fs
XH_P62	5	33576206	33576206	Missense_Mutation	SNV	T	G	G	ADAMTS12	c.3670A>C	P.T1224P
XH_P62	6	36099171	36099171	Missense_Mutation	SNV	T	G	G	MAPK13	c.243T>G	P.H81Q
XH_P62	6	41903695	41903695	Missense_Mutation	SNV	T	G	G	CCND3	c.862A>C	P.T288P
XH_P62	6	54806549	54806549	Missense_Mutation	SNV	A	C	C	FAM83B	c.2780A>C	P.H927P
XH_P62	6	88170831	88170831	Missense_Mutation	SNV	T	G	G	CFAP206	c.1586T>G	P.V529G
XH_P62	qbl_hag	2616630	2616666	Frame_Shift_Del	INDEL	CATGCTGTGA	-	-	HLA-B	SCCATGTACAGC	P.R280fs
XH_P62	7	141490560	141490560	Silent	SNV	C	T	T	TAS2R5	c.399C>T	P.Y133Y
XH_P62	7	5399023	5399023	Splice_Site	SNV	A	G	G	TNRC18	c.4833+6T>C	
XH_P62	7	5780686	5780686	Missense_Mutation	SNV	T	G	G	RNF216	c.962A>C	P.Q321P
XH_P62	7	73520439	73520439	Silent	SNV	G	T	T	LIMK1	c.645G>T	P.L215L
XH_P62	7	99056770	99056770	Missense_Mutation	SNV	T	G	G	ATPSJ2	c.238A>C	P.K80Q
XH_P62	7	99097611	99097635	Frame_Shift_Del	INDEL	CGTTGGGAC	-	-	ZN6394	GGCGCCGTC	P.A28fs
XH_P62	8	100515184	100515184	Splice_Site	SNV	T	G	G	VPS13B	c.4157+6T>G	
XH_P62	8	101727714	101727714	Missense_Mutation	SNV	G	A	A	PABPC1	c.619C>T	P.L207F
XH_P62	8	101727716	101727716	Missense_Mutation	SNV	C	T	T	PABPC1	c.617G>A	P.R206H
XH_P62	8	142367555	142367555	Missense_Mutation	SNV	C	A	A	GPR20	c.469G>T	P.G157C
XH_P62	8	24254935	24254935	Missense_Mutation	SNV	C	G	G	ADAMDEC1	c.356C>G	P.P119R
XH_P62	8	6914168	6914168	Missense_Mutation	SNV	G	T	T	DEFA5	c.52C>A	P.P18K
XH_P62	8	82606968	82606968	Silent	SNV	T	G	G	SLC10A5	c.240A>C	P.S80S
XH_P62	8	87588079	87588079	Missense_Mutation	SNV	C	G	G	CNGB3	c.2383G>C	P.G795R
XH_P62	9	103348339	103348339	Missense_Mutation	SNV	T	C	C	MURC	c.701T>C	P.L234P
XH_P62	9	129458648	129458648	Missense_Mutation	SNV	C	T	T	LMX1B	c.1139C>T	P.S380L
XH_P62	9	35704169	35704169	Missense_Mutation	SNV	T	G	G	TLN1	c.6050A>C	P.E2017A
XH_P62	9	7015875	7015875	Missense_Mutation	SNV	T	G	G	KDM4C	c.2205T>G	P.H735Q
XH_P62	9	91617005	91617005	Missense_Mutation	SNV	T	G	G	S1PR3	c.890T>G	P.I297S
XH_P62	X	149639622	149639622	Missense_Mutation	SNV	A	G	G	MAML1D1	c.1702A>G	P.V568A
XH_P62	X	5821621	5821621	Silent	SNV	G	A	A	NLGN4X	c.1098C>T	P.D366D
XH_P62	Y	6948818	6948818	Missense_Mutation	SNV	C	G	G	TBL1Y	c.1001C>G	P.S334C
XH_P63	12	25398284	25398284	Missense_Mutation	SNP	C	A	A	KRAS	c.35G>T	p.G12V
XH_P63	17	7578263	7578263	Nonsense_Mutation	SNP	G	A	A	TP53	c.586C>T	p.R196*
XH_P63	2	191894583	191894583	Missense_Mutation	SNP	G	A	A	STAT4	c.2230C>T	p.P744S
XH_P63	9	21971167	21971167	Missense_Mutation	SNP	A	G	G	CDKN2A	c.191T>C	p.L64P
XH_P63	1	7880631	7880631	Nonsense_Mutation	INS	-	TTTAGGTTAGT	-	PER3	1889insTTAGG	630_L631delinsIX
XH_P63	1	8074159	8074159	Frame_Shift_Ins	INS	-	ATTTCAAATATG	-	ERRF1	500insTCATATT	p.T167fs
XH_P63	1	2232008	2232008	Silent	SNP	T	C	T	CELA3A	c.T198C	p.D66D
XH_P63	1	26610712	26610712	Frame_Shift_Ins	INS	-	C	-	UBXN11	c.637_638insG	p.F213fs
XH_P63	1	26610713	26610713	Frame_Shift_Ins	INS	-	GTGTC	-	UBXN11	636_637insGAC	p.F213fs
XH_P63	1	28661177	28661177	In_Frame_Ins	INS	-	AGAGCG	-	MED18	23_324insAGAG	p.1108delinsIER
XH_P63	1	32131638	32131638	Silent	SNP	C	T	C	COL13A4	c.G3402A	p.A1134A
XH_P63	1	33797994	33797994	Frame_Shift_Ins	INS	-	TCGGAGAT	-	PHC2	4_165insATCTC	p.S55fs
XH_P63	1	34209095	34209095	Frame_Shift_Ins	INS	-	GAGT	-	CSMD2	958_1959insAC	p.E653fs
XH_P63	1	43665101	43665101	Frame_Shift_Ins	INS	-	GAGGTGCT	-	CFAP57	9_1470insGAGG	p.N490fs
XH_P63	1	46878843	46878843	Frame_Shift_Ins	INS	-	AC	-	FAAH	1562_1563insA	p.E521fs
XH_P63	1	48701546	48701546	Frame_Shift_Ins	INS	-	AAGAT	-	SLCSA9	287_1288insAA	p.V429fs
XH_P63	1	61849014	61849014	Missense_Mutation	SNP	G	C	G	NFIA	c.G1052C	p.R351P
XH_P63	1	65332590	65332590	Frame_Shift_Ins	INS	-	ATAG	-	JAK1	948_949insCTA	p.V317fs
XH_P63	1	65332591	65332591	Frame_Shift_Ins	INS	-	GT	-	JAK1	c.947_948insAC	p.M316fs
XH_P63	1	91843720	91843720	In_Frame_Ins	INS	-	GTAGCTGTA	-	HFM1	5_1257insTACAA	E419delinsDTAT
XH_P63	1	109793706	109793706	Frame_Shift_Ins	INS	-	TCAGA	-	CELSR2	205_1006insTCA	p.S335fs
XH_P63	1	112998721	112998721	Nonsense_Mutation	INS	-	ACTAGCATGGA	-	CTTNBP2NL	608insACTAGC	203_S204delinsHX
XH_P63	1	113124704	113124704	Nonsense_Mutation	INS	-	TATTCTTTTCC	-	ST7L	430insGGAAAAA	44_M145delinsGKEX
XH_P63	1	113124706	113124706	Frame_Shift_Ins	INS	-	TTAT	-	ST7L	427_428insATA	p.L143fs
XH_P63	1	149898374	149898374	Nonsense_Mutation	INS	-	GGTTAAAAATAT	-	SF3B4	nsAAACATATT	100_L201delinsPNIFX
XH_P63	1	152280597	152280597	Silent	SNP	A	G	A	FLG	c.T6765C	p.D225SD
XH_P63	1	152325215	152325215	Missense_Mutation	SNP	G	C	G	FLG2	c.C5047G	p.Q1683E
XH_P63	1	152327469	152327469	Silent	SNP	C	T	C	FLG2	c.G2793A	p.Q931Q
XH_P63	1	155152178	155152178	Frame_Shift_Ins	INS	-	C	-	TRIM46	c.979dupC	p.L326fs
XH_P63	1	156916485	156916485	Missense_Mutation	SNP	C	T	C	ARHGEF11	c.G2543A	p.R848H
XH_P63	1	162557410	162557410	Frame_Shift_Ins	INS	-	AT	-	UAP1	c.980_981insAT	p.N327fs
XH_P63	1	162557411	162557411	Frame_Shift_Ins	INS	-	TCACT	-	UAP1	981_982insTCA	p.N327fs
XH_P63	1	172634937	172634937	In_Frame_Ins	INS	-	CCTTCTTAT	-	FASLG	7_628insCCTTC	H209delinsHPSPY
XH_P63	1	201179954	201179954	Missense_Mutation	SNP	A	C	A	IGFN1	c.A5933C	p.E1978A
XH_P63	1	201193928	201193928	In_Frame_Ins	INS	-	GTCACC	-	IGFN1	12_10413insGT	S3471delinsRSP
XH_P63	1	205116874	205116874	Splice_Site	SNP	C	T	C	DSTYK	-	
XH_P63	1	207286474	207286474	Frame_Shift_Del	DEL	A	-	A	C4BPA	c.104delA	p.Q35fs
XH_P63	1	211654657	211654657	Missense_Mutation	SNP	G	A	G	RD3	c.C101T	p.T34M
XH_P63	1	212799988	212799988	Frame_Shift_Ins	INS	-	GTTACAT	-	FAM71A	9_1770insGTTG	p.T590fs
XH_P63	1	214818263	214818263	Frame_Shift_Ins	INS	-	CAGAAATGCA	-	CENPF	5351insCAGAA	p.L1784fs
XH_P63	1	217955638	217955638	Frame_Shift_Ins	INS	-	ATTTTATATGGA	-	SPATA17	nsCATATTTTATA	p.E282fs
XH_P63	1	229653943	229653943	Nonsense_Mutation	INS	-	CAGAGACTA	-	ABC810	9_2200insTAGT	p.S734delinsX
XH_P63	1	236212256	236212256	Nonsense_Mutation	INS	-	AAGGTTTA	-	NID1	8_259insTAAAC	P87_P88delinsX
XH_P63	1	237619971	237619971	Missense_Mutation	SNP	T	A	T	RVR2	c.T1548A	p.D516E
XH_P63	1	248487682	248487682	In_Frame_Ins	INS	-	TTATGTCTT	-	OR2M7	8_189insAAGAC	L63delinsLRHN
XH_P63	1	248617057	248617153	Frame_Shift_Del	DEL	GACTGTGAT	-	GTGACTGTGATCG	OR2T2	c.959_975del	p.V320fs
XH_P63	1	249211034	249211034	Frame_Shift_Ins	INS	-	ATCAGTGAAT	-	PGBD2	252insATCAGT	p.S84fs
XH_P63	2	1079274	1079274	Missense_Mutation	SNP	C	T	C	SENTG2	c.C143T	p.T48M
XH_P63	2	25042856	25042856	Frame_Shift_Ins	INS	-	GAGAAATTATT	-	ADCY3	8383insAAATAA	p.T1128fs
XH_P63	2	54041757	54041757	Nonsense_Mutation	INS	-	CACATAAGAAAT	-	ERLEC1	insATCTCACTAA	B1_C382delinsKSHX
XH_P63	2	55130592	55130592	Missense_Mutation	SNP	G	A	G	EML6	c.G3362A	p.C1121Y
XH_P63	2	61433252	61433252	Nonsense_Mutation	INS	-	ATAGGTAAGTTA	-	USP34	3054insGTAAC	T18_Q3019delinsKX
XH_P63	2	69093062	69093062	Frame_Shift_Ins	INS	-	GTTTGTAA	-	BMP10	5_976insTTACA	p.T326fs
XH_P63	2	70905837	70905837	Missense_Mutation	SNP	G	A	G	ADD2	c.C1430T	p.T477M
XH_P63	2	109384224	109384224	Frame_Shift_Ins	INS	-	AA	-	RANBP2	7229_7230insA	p.A2410fs
XH_P63	2	109384226	109384226	Frame_Shift_Ins	INS	-	TC	-	RANBP2	7231_7232insT	p.D2411fs
XH_P63	2	109400316	109400316	Frame_Shift_Ins	INS	-	C	-	RANBP2	c.9634_9635insG	p.V3212fs
XH_P63	2	109400318	109400318	Frame_Shift_Ins	INS	-	TCCTCAG	-	RANBP2	96_9637insTCT	p.V3212fs
XH_P63	2	128252519	128252519	In_Frame_Ins	INS	-	TGG	-	IWS1	1727_1728insCp	Q576delinsHQ
XH_P63	2	133075612	133075612	Frame_Shift_Ins	INS	-	AT	-	ZNFR06	c.1073_1074insA	p.P358fs
XH_P63	2	160901461	160901461	Frame_Shift_Ins	INS	-	GGAAGTAT	-	PLAZR1	c.6_317insATAC	p.C106fs
XH_P63	2	162902097	162902097	Frame_Shift_Ins	INS	-	C	-	DPP4	c.310dupG	p.D104fs
XH_P63	2	162902099	162902099	Frame_Shift_Ins	INS	-	GAGTATGCTAT	-	DPP4	809insCATAGCA	p.N103fs

XH_P63	2	167328935	167328935	In_Frame_Ins	INS	-	TTG	-	SCN7A	c.463_464insCA	p.Y155delinsSN
XH_P63	2	167328936	167328936	In_Frame_Ins	INS	-	GTGAGT	-	SCN7A	c.462_463insACTC	p.Y155delinsTHY
XH_P63	2	167760326	167760326	Frame_Shift_Ins	INS	-	CAGAATCC	-	XIRP2	c.4_335insCAGA	p.I112fs
XH_P63	2	179410249	179410249	Frame_Shift_Ins	INS	-	AAATACAATGC	-	TTN	c.58393insAGCAT	p.V22798fs
XH_P63	2	179451930	179451930	Frame_Shift_Ins	INS	-	G	-	TTN	c.36812_36813ins	p.Y12271fs
XH_P63	2	179451932	179451932	Nonsense_Mutation	INS	-	TTATGCTTT	-	TTN	c.36811insAAA	p.Y12271delinsKAX
XH_P63	2	182468581	182468581	Frame_Shift_Ins	INS	-	T	-	CERKL	c.463_464insA	p.F155fs
XH_P63	2	182468582	182468582	In_Frame_Ins	INS	-	TACATGATTAAT	-	CERKL	c.463insATTAAATC	p.F155delinsINHF
XH_P63	2	196884010	196884010	Frame_Shift_Ins	INS	-	GT	-	DNAH7	c.752_753insAC	p.I251fs
XH_P63	2	233393645	233393645	Missense_Mutation	SNP	G	A	G	CHNRD	c.G538A	p.V180M
XH_P63	3	9515069	9515069	Silent	SNP	G	T	G	SETD5	c.G3345T	p.V1115V
XH_P63	3	33038745	33038745	Nonsense_Mutation	INS	-	GTTATTGGC	-	GLB1	c.2_1433insGCCA	p.M478delinsSQX
XH_P63	3	38592908	38592908	Frame_Shift_Ins	INS	-	ACTTCGCT	-	SCN5A	c.0_4901insAGCG	p.M1634fs
XH_P63	3	49753415	49753415	Frame_Shift_Ins	INS	-	T	-	RNF123	c.3312dupT	p.S1104fs
XH_P63	3	52977461	52977461	Missense_Mutation	SNP	C	T	C	SFMBT1	c.G272A	p.R91Q
XH_P63	3	53381457	53381457	Missense_Mutation	SNP	T	G	T	DCP1A	c.A88C	p.T30P
XH_P63	3	111927076	111927076	In_Frame_Ins	INS	-	ATGGAAGTG	-	SLC9C1	c.0_1791insCACT	p.K597delinsNTSI
XH_P63	3	111927078	111927078	Nonsense_Mutation	INS	-	A	-	SLC9C1	c.1788_1789ins	p.K597_H598delinsX
XH_P63	3	130454792	130454792	Frame_Shift_Ins	INS	-	TTAATAGGATCT	-	PIK3R4	c.88insTAGATCCT	p.Q263fs
XH_P63	3	136141872	136141872	Missense_Mutation	SNP	T	A	T	STAG1	c.A1665T	p.K555N
XH_P63	3	142277589	142277589	In_Frame_Ins	INS	-	TAA	-	ATR	c.1761_1762insT	p.E588delinsLE
XH_P63	3	142277590	142277590	Frame_Shift_Ins	INS	-	ATTAAGCTGT	-	ATR	c.1761insACAGC	p.L587fs
XH_P63	3	178922355	178922355	Frame_Shift_Ins	INS	-	AAAAA	-	PIK3CA	c.124_1125insAA	p.R375fs
XH_P63	3	178922357	178922357	Frame_Shift_Ins	INS	-	TAGGTATA	-	PIK3CA	c.6_1127insTAGG	p.V376fs
XH_P63	3	185198246	185198246	Missense_Mutation	SNP	G	C	G	MAP3K13	c.G2107C	p.E703Q
XH_P63	3	185198247	185198247	Missense_Mutation	SNP	A	G	A	MAP3K13	c.A2108G	p.E703G
XH_P63	3	185882769	185882769	Frame_Shift_Ins	INS	-	GTACACA	-	DGKG	c.58_2059insTGTG	p.G687fs
XH_P63	3	186978596	186978596	Nonsense_Mutation	INS	-	ATTGTATGCAT	-	MASP1	c.480insATGCAT	p.Y160_I161delinsX
XH_P63	3	195507899	195507899	In_Frame_Ins	INS	-	AGAAAGCTGGT	-	MUC4	c.TCCTGTCAACAG	p.GHATPLPLPVSFSVSTGDTTLPVTDASSASTGH
XH_P63	4	16215414	16215414	Nonsense_Mutation	SNP	G	A	G	TAPT1	c.C307T	p.R103X
XH_P63	4	17598751	17598751	Frame_Shift_Ins	INS	-	TATTGGAAATA	-	LAP3	c.1072insATTG	p.T357fs
XH_P63	4	54876284	54876284	In_Frame_Ins	INS	-	TGGTGTITTTTT	-	CHIC2	c.476insAAAAAA	p.T159delinsKNTT
XH_P63	4	54876286	54876286	Missense_Mutation	SNP	C	G	C	CHIC2	c.G474C	p.K158N
XH_P63	4	55144089	55144089	Nonsense_Mutation	INS	-	AATATGACTAAT	-	PDGFRA	c.1919insAATATG	p.L40_L64delinsEYDX
XH_P63	4	119948401	119948401	Frame_Shift_Ins	INS	-	CTGGAGATCT	-	SYNP02	c.878insCTGGAC	p.R293fs
XH_P63	4	120240736	120240736	Silent	SNP	G	A	G	FABP2	c.C303T	p.N101N
XH_P63	4	121737677	121737677	In_Frame_Ins	INS	-	GAT	-	PRDM5	c.702_703insAT	p.A235delinsIA
XH_P63	4	121737678	121737678	Frame_Shift_Ins	INS	-	TGTT	-	PRDM5	c.701_702insAAC	p.K234fs
XH_P63	4	152203426	152203426	Nonsense_Mutation	INS	-	ATGAAAAAGTAG	-	PRSS48	c.AGTATATGAAAA	p.I14_V115delinsDSIX
XH_P63	4	155412031	155412031	Silent	SNP	G	A	G	DCHS2	c.C477T	p.D159D
XH_P63	4	155719233	155719233	Frame_Shift_Ins	INS	-	GGCTTCTTCTT	-	RBM46	c.423insGGCTTC	p.C141fs
XH_P63	4	184240834	184240834	Missense_Mutation	SNP	C	A	C	CLDN22	c.G538T	p.G180W
XH_P63	5	11565059	11565059	Missense_Mutation	SNP	A	C	A	CTNND2	c.T11G	p.M4R
XH_P63	5	34043200	34043200	Frame_Shift_Ins	INS	-	CAGAC	-	C1QTNF3	c.30_31insGTCT	p.L11fs
XH_P63	5	37006613	37006613	Nonsense_Mutation	INS	-	TCTGTAAA	-	NIPBL	c.0_4011insTCTG	p.B37_Q1338delinsILX
XH_P63	5	118728705	118728705	Frame_Shift_Ins	INS	-	CTAC	-	TNFAIP8	c.196_197insCTA	p.L66fs
XH_P63	5	140182164	140182164	Missense_Mutation	SNP	C	T	C	PCDH3A	c.C1382T	p.T461M
XH_P63	5	140588732	140588732	In_Frame_Ins	INS	-	CAAAAT	-	PCDHB12	c.53_254insCAAA	p.L85delinsPNF
XH_P63	5	140858151	140858151	Frame_Shift_Del	DEL	T	-	T	PCDHG3C	c.2468delT	p.L823fs
XH_P63	5	162900464	162900464	Nonsense_Mutation	INS	-	ATGACTGAG	-	HMMR	c.1545insATGAC	p.I182delinsNDX
XH_P63	5	162900466	162900466	Silent	SNP	T	A	T	HMMR	c.T546A	p.I182I
XH_P63	5	168179992	168179992	Silent	SNP	C	T	C	SLIT3	c.G1941A	p.G647G
XH_P63	6	7580604	7580604	Frame_Shift_Ins	INS	-	AACT	-	DSP	c.181_4182insAA	p.Q1394fs
XH_P63	6	11185856	11185856	In_Frame_Ins	INS	-	GACGCA	-	NEDD9	c.96_1597insTGG	p.N533delinsCVN
XH_P63	6	36690492	36690492	Missense_Mutation	SNP	G	A	G	RAB44	c.G2581A	p.G861R
XH_P63	6	97681840	97681840	Frame_Shift_Ins	INS	-	A	-	MMS22L	c.349_350insT	p.E117fs
XH_P63	6	97681841	97681841	In_Frame_Ins	INS	-	ATTTATGGGAA	-	MMS22L	c.19insTATCCCA	p.I117delinsYSHKME
XH_P63	6	132636897	132636897	Frame_Shift_Ins	INS	-	AAGTAGTAAAT	-	MOXD1	c.85insTACATTTA	p.S462fs
XH_P63	6	133004445	133004445	Nonsense_Mutation	INS	-	AATAATGCTAAT	-	VNN1	c.TATAAATCTATTAG	p.459_L460delinsLX
XH_P63	7	1539980	1539980	Missense_Mutation	SNP	A	C	A	INTS1	c.C1372G	p.D124E
XH_P63	7	6449609	6449609	Silent	SNP	G	A	G	DAGLB	c.C1491T	p.F497F
XH_P63	7	29035492	29035492	Missense_Mutation	SNP	T	A	T	CPVL	c.A1327T	p.I443F
XH_P63	7	32612969	32612969	Nonsense_Mutation	INS	-	CCTTAGG	-	AVL9	c.09_1510insCCTT	p.W0504delinsEPX
XH_P63	7	80374579	80374579	Nonsense_Mutation	INS	-	AACTTCAA	-	SEMA3C	c.0_1941insTTGA	p.647_L648delinsLX
XH_P63	7	80374581	80374581	Nonsense_Mutation	INS	-	TTTTA	-	SEMA3C	c.938_1939insTAA	p.L647_L648delinsX
XH_P63	7	87079394	87079394	In_Frame_Ins	INS	-	AGG	-	ABC84	c.722_723insCC	p.F241delinsFL
XH_P63	7	90014407	90014407	Nonsense_Mutation	INS	-	TCITTTAA	-	GTPBP10	c.66_867insTCTT	p.289_S290delinsILX
XH_P63	7	90014408	90014408	Missense_Mutation	SNP	G	T	G	GTPBP10	c.G867T	p.M289I
XH_P63	7	100679167	100679167	Silent	SNP	A	T	A	MUC17	c.A4470T	p.T1490T
XH_P63	7	100682351	100682351	Missense_Mutation	SNP	A	G	A	MUC17	c.A7654G	p.I2552V
XH_P63	7	106509376	106509376	Frame_Shift_Ins	INS	-	GTCTTTG	-	PIK3CG	c.70_1371insGTC	p.K457fs
XH_P63	7	106509378	106509378	Missense_Mutation	SNP	G	T	G	PIK3CG	c.G1372T	p.V458F
XH_P63	7	107053020	107053020	Nonsense_Mutation	INS	-	AGACTGTTTTTT	-	COG5	c.insATTAAAAAA	p.230_F231delinsHX
XH_P63	8	7195639	7195639	Frame_Shift_Ins	INS	-	GC	-	USP17L4	c.1003_1004insG	p.Y335fs
XH_P63	8	7195641	7195641	Frame_Shift_Ins	INS	-	A	-	USP17L4	c.1005_1006ins	p.Y335fs
XH_P63	8	17824568	17824568	Frame_Shift_Ins	INS	-	AAGAATCAGTTA	-	PCM1	c.insATCTAAGAA	p.S1101fs
XH_P63	8	22105443	22105443	Missense_Mutation	SNP	C	G	C	POLR3D	c.C283G	p.R95G
XH_P63	8	27328571	27328571	Missense_Mutation	SNP	C	T	C	CHRNA2	c.G5A	p.G2D
XH_P63	8	67488576	67488576	Missense_Mutation	SNP	T	C	T	MYBL1	c.CA1136G	p.D379G
XH_P63	8	73849837	73849837	Silent	SNP	G	A	G	KCNB2	c.G2247A	p.P749P
XH_P63	8	77616719	77616719	Frame_Shift_Ins	INS	-	GCAGGGTATC	-	ZFH4X	c.397insGCAGG	p.V132fs
XH_P63	8	95531686	95531686	Frame_Shift_Ins	INS	-	SGTCTTCTTTTT	-	VIRMA	c.340insAAAAAAA	p.H680fs
XH_P63	8	99560326	99560326	Missense_Mutation	SNP	G	A	G	STK3	c.C679T	p.R227W
XH_P63	8	124142541	124142541	In_Frame_Ins	INS	-	AAATACAGCAAT	-	TBC1D31	c.2060insAAATAC	p.L687delinsQIQQQL
XH_P63	8	145661277	145661277	Missense_Mutation	SNP	G	A	G	TONSL	c.C2539T	p.R847W
XH_P63	9	121517	121517	Missense_Mutation	SNP	T	A	T	CBWD1	c.A1081T	p.T361S
XH_P63	9	2123824	2123824	Frame_Shift_Ins	INS	-	GAGACATTAAT	-	SMARCA2	c.3869insGAGAC	p.E1290fs
XH_P63	9	27359170	27359170	Silent	SNP	G	C	G	MOB3B	c.C483G	p.V161V
XH_P63	9	27359172	27359172	Nonsense_Mutation	INS	-	TTCTATTA	-	MOB3B	c.0_481insTAATA	p.V161_F162delinsX
XH_P63	9	35751347	35751347	Nonsense_Mutation	INS	-	TGAGTGGAGAG	-	RGP1	c.73insATGAGTG	p.191_S192delinsEX
XH_P63	9	79244166	79244166	Frame_Shift_Ins	INS	-	GTTCAGAGATG	-	PRUNE2	c.3insCACATCTCT	p.S295fs
XH_P63	9	91994296	91994296	Frame_Shift_Ins	INS	-	CTTGTGAC	-	SEMA4D	c.1_1912insCTGA	p.V638fs
XH_P63	9	95792215	95792215	In_Frame_Ins	INS	-	GAGGCAAT	-	FGD3	c.7_1618insGAGG	p.K539delinsKEAN
XH_P63	9	131367383	131367383	Missense_Mutation	SNP	G	T	G	SPTAN1	c.C3730T	p.D1244Y
XH_P63	10	21962451	21962451	Frame_Shift_Ins	INS	-	ATCCT	-	MLLT10	c.224_1225insAT	p.E408fs
XH_P63	10	50530736	50530736	In_Frame_Ins	INS	-	ACACG	-	C10orf71	c.46_147insACAC	p.H49delinsQHA
XH_P63	10	55944992	55944992	Frame_Shift_Ins	INS	-	TATGTATGAAT	-	PCDH15	c.TACATACATTCA	p.Y411fs
XH_P63	10	75399717	75399717	In_Frame_Ins	INS	-	ATATATATCTTA	-	MYO21	c.sCCCTAAGATA	p.M20delinsTLRYFL

XH_P63	10	78709071	78709071	Frame_Shift_Ins	INS	-	TGTCAT	-	KCNMA1	3_2214insATG	p.I738fs
XH_P63	10	90703650	90703650	Frame_Shift_Ins	INS	-	AT	-	ACTA2	c.272_273insAT	p.S91fs
XH_P63	10	90703651	90703651	In_Frame_Ins	INS	-	ACTCAAGTA	-	ACTA2	1_272insTACTCTG	p.S91delinsLLES
XH_P63	10	129905616	129905616	In_Frame_Ins	INS	-	GGA	-	MKI6A5	3407_3408insT	p.S1136delinsSP
XH_P63	10	133954073	133954073	In_Frame_Ins	INS	-	CGAGGGTCTCC	-	JAKMIP3	AGGTAACGAGG	delinsDLEEVTRVSCRVLG
XH_P63	11	6636547	6636547	Frame_Shift_Ins	INS	-	GTGAGAA	-	TPP1	79_1280insTTC	p.T427fs
XH_P63	11	7723849	7723849	Frame_Shift_Ins	INS	-	AGAAACCAATG	-	OVCH2	318insCATTGG	p.T106fs
XH_P63	11	8646550	8646550	In_Frame_Ins	INS	-	GCAACT	-	TRIM66	00_2101insAGT	p.Q701delinsSCQ
XH_P63	11	20658768	20658768	In_Frame_Ins	INS	-	CCCTTTGTA	-	SLC6A5	6_1087insCCCT	p.K362delinsKPFV
XH_P63	11	34144094	34144094	In_Frame_Ins	INS	-	CAGAAACAT	-	NAT10	3_654insCAGAA	p.K218delinsNRNI
XH_P63	11	34979030	34979031	Frame_Shift_Del	DEL	GG	-	GG	PDHX	c.397_398del	p.G133fs
XH_P63	11	34979031	34979031	Frame_Shift_Ins	INS	-	TATTTTACT	-	PDHX	3_399insTATTTT	p.G133fs
XH_P63	11	46751000	46751000	Frame_Shift_Ins	INS	-	CCAT	-	F2	543_1544insCC	p.V515fs
XH_P63	11	57971509	57971509	In_Frame_Ins	INS	-	TGTTGA	-	OR1S2	44_145insTCAC	p.V49delinsSPV
XH_P63	11	64109571	64109571	Missense_Mutation	SNP	G	A	G	CCDC88B	c.G781A	p.A261T
XH_P63	11	65143905	65143905	Silent	SNP	G	A	G	SLC25A45	c.C768T	p.Y256Y
XH_P63	11	65302832	65302832	Frame_Shift_Del	DEL	C	-	C	SCYL1	c.1365delC	p.I455fs
XH_P63	11	67132751	67132751	Missense_Mutation	SNP	G	T	G	CLCF1	c.C504A	p.F168L
XH_P63	11	74500745	74500745	Splice_Site	INS	-	AAAAGAAAATA	-	RNF169	-	-
XH_P63	11	89604061	89604061	Nonsense_Mutation	INS	-	TTATGATAATGG	-	TRIM64B	1078insCCATTA	p.S360delinsPLSX
XH_P63	11	119170361	119170361	Nonsense_Mutation	INS	-	TCAGTGA	-	CBL	91_2592insTCAG	p.M85delinsLQX
XH_P63	11	120300187	120300188	Frame_Shift_Del	DEL	TC	-	TC	ARHGEF12	c.567_568del	p.I189fs
XH_P63	11	129744059	129744059	Frame_Shift_Ins	INS	-	GCTTTTTCGTT	-	NFRKB	2303insAACGA	p.V768fs
XH_P63	11	129802117	129802117	Silent	SNP	G	C	G	PRDM10	c.C909G	p.G303G
XH_P63	12	7022073	7022073	Frame_Shift_Ins	INS	-	A	-	LRRC23	c.938_939insA	p.A313fs
XH_P63	12	7022075	7022075	Frame_Shift_Ins	INS	-	GGTTATC	-	LRRC23	40_941insGGTT	p.E314fs
XH_P63	12	7302189	7302189	In_Frame_Ins	INS	-	AGTAGG	-	CLSTN3	45_2146insAGT	p.D715delinsDSR
XH_P63	12	50232483	50232484	Frame_Shift_Del	DEL	CC	-	CC	BCDIN3D	c.549_550del	p.I183fs
XH_P63	12	53238454	53238454	Frame_Shift_Ins	INS	-	CCAAAGAGTGCA	-	KRT78	TCAATTGCACCT	p.M160fs
XH_P63	12	56081987	56081987	Frame_Shift_Ins	INS	-	GATCC	-	ITGA7	067_3068insGG	p.V1023fs
XH_P63	12	56081989	56081989	Silent	SNP	T	A	T	ITGA7	c.A3066T	p.T1022T
XH_P63	12	56478933	56478933	In_Frame_Ins	INS	-	GGAGGT	-	ERBB3	89_390insGGAG	p.A130delinsAEV
XH_P63	12	56527568	56527568	Frame_Shift_Ins	INS	-	CTATTTCCCA	-	ESY1	1_1385insCTATT	p.L462fs
XH_P63	12	66839231	66839231	Frame_Shift_Ins	INS	-	ATTTCCTA	-	GRIP1	5_1256insTAGG	p.T419fs
XH_P63	12	69656333	69656333	Frame_Shift_Ins	INS	-	GA	-	CPSF6	1650_1651insG	p.H550fs
XH_P63	12	96255066	96255066	Nonsense_Mutation	INS	-	GGATCTAATTA	-	SNRPF	AAAAAGGATCT	p.Q43delinsKKGXSNX
XH_P63	12	96407013	96407013	Nonsense_Mutation	INS	-	ACTGTTACTAG	-	LTA4H	1332insCTAGT	p.A44_445delinsDX
XH_P63	12	102116987	102116987	Missense_Mutation	SNP	T	G	T	CHPT1	c.T822G	p.T74M
XH_P63	12	104056668	104056668	Frame_Shift_Ins	INS	-	TCTAATTCTGT	-	STAB2	1915insCTCAA	p.I638fs
XH_P63	12	104056670	104056670	In_Frame_Ins	INS	-	TAT	-	STAB2	1916_1917insT	p.T639delinsTI
XH_P63	12	110941682	110941682	Splice_Site	INS	-	ATGCTTATA	-	RAD9B	-	-
XH_P63	12	120622021	120622021	Frame_Shift_Ins	INS	-	AGAATTGGTA	-	GCN1	1_211insTACCA	p.Q71fs
XH_P63	12	124371834	124371834	Frame_Shift_Ins	INS	-	AACT	-	DNAH10	8615_8616insAA	p.E2872fs
XH_P63	12	124371835	124371835	Frame_Shift_Ins	INS	-	TTT	-	DNAH10	8616_8617insT	p.E2872fs
XH_P63	12	132241107	132241107	Frame_Shift_Ins	INS	-	TA	-	SFSWAP	1638_1639insT	p.A546fs
XH_P63	12	25914187	25914187	Frame_Shift_Ins	INS	-	AGCCTTATGT	-	NUP58	1680insAGCCT	p.N560fs
XH_P63	12	28844853	28844853	Missense_Mutation	SNP	C	A	C	PAN3	c.C1808A	p.P603Q
XH_P63	13	60435662	60435662	In_Frame_Ins	INS	-	GATGAT	-	DIAPH3	26_1827insATC	p.D609delinsESS
XH_P63	13	77625250	77625250	Nonsense_Mutation	INS	-	GTATGCTTTAA	-	MYCBP2	13803insTAAAP	p.Y4601delinsYX
XH_P63	13	79176040	79176040	Missense_Mutation	SNP	G	C	G	POU4F1	c.C770G	p.S257C
XH_P63	13	111953101	111953101	Missense_Mutation	SNP	G	A	G	ARHGEF7	c.G1670A	p.R557H
XH_P63	13	111995227	111995227	Nonsense_Mutation	INS	-	AATGACTCT	-	TEX29	4_365insAATGA	p.G122delinsEX
XH_P63	14	21485882	21485882	Frame_Shift_Ins	INS	-	GAACCTCT	-	NRD2G	6_977insAAGAC	p.I326fs
XH_P63	14	21623898	21623898	Missense_Mutation	SNP	A	T	A	OR5AU1	c.T287A	p.M96K
XH_P63	14	57268630	57268630	Frame_Shift_Ins	INS	-	CTTGGATT	-	OTX2	6_717insAATCC	p.L239fs
XH_P63	14	64908853	64908853	Frame_Shift_Ins	INS	-	ATTCACCGGTA	-	MTHFD1	1967insATTCA	p.L656fs
XH_P63	14	69990964	69990964	In_Frame_Ins	INS	-	CTT	-	PLEKHD1	c.669_670insCT	p.A223delinsAL
XH_P63	14	69990966	69990966	Frame_Shift_Ins	INS	-	AA	-	PLEKHD1	c.671_672insAA	p.R244fs
XH_P63	14	92403481	92403481	Frame_Shift_Ins	INS	-	CTCTCAGC	-	FBLN5	8_189insGCTGA	p.N63fs
XH_P63	14	96937940	96937940	Frame_Shift_Ins	INS	-	TATATGT	-	AK7	05_1406insTAT	p.N469fs
XH_P63	15	34657430	34657430	Splice_Site	INS	-	ACTTTCT	-	LPCAT4	-	-
XH_P63	15	40094389	40094389	Frame_Shift_Ins	INS	-	GTTCCTGGTGT	-	GPR176	357insACACCA	p.M119fs
XH_P63	15	41192186	41192186	Silent	SNP	C	T	C	VPS18	c.C1170T	p.H390H
XH_P63	15	42837375	42837375	Frame_Shift_Ins	INS	-	G	-	LRRC57	c.577dupC	p.L193fs
XH_P63	15	42837377	42837377	Frame_Shift_Ins	INS	-	A	-	LRRC57	c.575dupT	p.M192fs
XH_P63	15	43940257	43940257	Frame_Shift_Ins	INS	-	TATTTCTTCACTA	-	CATSPER2	1insTAGTGAAG	p.M7fs
XH_P63	15	52708377	52708378	Frame_Shift_Del	DEL	CC	-	CC	MYO5A	c.576_577del	p.V192fs
XH_P63	15	63796955	63796955	Missense_Mutation	SNP	T	G	T	USP3	c.T17G	p.L6R
XH_P63	15	64428586	64428586	Nonsense_Mutation	SNP	C	T	C	SNX1	c.C1228T	p.R410X
XH_P63	15	68117238	68117238	In_Frame_Ins	INS	-	GCTCAT	-	SKOR1	36_537insGCTC	p.R179delinsRLI
XH_P63	16	14702948	14702948	Frame_Shift_Ins	INS	-	5AAAGGTAGATC	-	PARN	49insCCATCTAC	p.E150fs
XH_P63	16	14702949	14702949	Missense_Mutation	SNP	C	T	C	PARN	c.G448A	p.E150K
XH_P63	16	20482410	20482410	Frame_Shift_Del	DEL	T	-	T	ACSM2A	c.375delT	p.T125fs
XH_P63	16	20482412	20482413	Frame_Shift_Del	DEL	AT	-	AT	ACSM2A	c.377_378del	p.H126fs
XH_P63	16	22152975	22152975	Frame_Shift_Ins	INS	-	A	-	VWA3A	c.2456_2457ins	p.S819fs
XH_P63	16	22152976	22152976	Frame_Shift_Ins	INS	-	CC	-	VWA3A	2457_2458insC	p.S819fs
XH_P63	16	29393620	29393620	Missense_Mutation	SNP	G	A	G	NPIP811	c.C2633T	p.P878L
XH_P63	16	29393621	29393621	In_Frame_Ins	INS	-	CTC	-	NPIP811	2631_2632insG	p.P878delinsEP
XH_P63	16	29828115	29828115	Missense_Mutation	SNP	C	T	C	PAGR1	c.C269T	p.P90L
XH_P63	16	56466638	56466638	In_Frame_Ins	INS	-	TGTGGT	-	NUDT21	69_670insACCA	p.F224delinsTTF
XH_P63	16	56466639	56466639	In_Frame_Ins	INS	-	GAAAAG	-	NUDT21	668_669insCTTT	p.N223delinsNFS
XH_P63	16	68279444	68279444	Missense_Mutation	SNP	C	T	C	PLA2G15	c.C115T	p.P39S
XH_P63	16	81094914	81094914	In_Frame_Ins	INS	-	TGAGCA	-	C16orf46	39_1040insTGC	p.P347delinsLLT
XH_P63	17	1375225	1375225	Missense_Mutation	SNP	C	T	C	MYO1C	c.G1997A	p.G666H
XH_P63	17	2995884	2995884	Missense_Mutation	SNP	A	C	A	OR1D2	c.T407G	p.M136R
XH_P63	17	2996116	2996116	Missense_Mutation	SNP	C	T	C	OR1D2	c.G175A	p.V59M
XH_P63	17	4634854	4634854	Frame_Shift_Ins	INS	-	AGAGTTTC	-	MED11	0_71insAGAGT	p.I24fs
XH_P63	17	4720033	4720033	Frame_Shift_Ins	INS	-	AGAAGAA	-	PLD2	74_1575insAGAA	p.P525fs
XH_P63	17	8451712	8451712	In_Frame_Ins	INS	-	GTAAACTGATG	-	MYH10	048insTTTCACTA	p.V350delinsFISLPV
XH_P63	17	15973599	15973599	Frame_Shift_Ins	INS	-	TG	-	NCOR1	4440_4441insC	p.E1481fs
XH_P63	17	16667401	16667401	Frame_Shift_Ins	INS	-	GACAAATGCTTA	-	CCDC144A	011insAGACAAA	p.N1337fs
XH_P63	17	16667403	16667403	Missense_Mutation	SNP	C	A	C	CCDC144A	c.C4012A	p.L1338I
XH_P63	17	17697390	17697390	Silent	SNP	G	A	G	RAI1	c.G1128A	p.P376P
XH_P63	17	18673271	18673271	Missense_Mutation	SNP	C	T	C	FBXW10	c.C1879T	p.R627W
XH_P63	17	27613682	27613682	Missense_Mutation	SNP	T	C	T	NUFIP2	c.A1330G	p.T444A
XH_P63	17	38573025	38573025	Frame_Shift_Ins	INS	-	AAATGGATACTC	-	TOP2A	44insAGAGTAT	p.D48fs
XH_P63	17	40838124	40838124	Missense_Mutation	SNP	A	C	A	CNTNAP1	c.A865C	p.N289H
XH_P63	17	42328932	42328932	Frame_Shift_Ins	INS	-	CCCT	-	SLC4A1	335_2336insAG	p.I779fs

XH_P63	17	43559805	43559805	In_Frame_Ins	INS	-	ACAATTCGA	-	PLEKHM1	546insTCGAAT	p.16delinsSNCP
XH_P63	17	48447421	48447421	Missense_Mutation	SNP	C	T	C	MRPL27	c.G212A	p.R71H
XH_P63	17	58275726	58275726	Frame_Shift_Ins	INS	-	GATTGGTGAGT	-	USP32	3329insACTCA	p.T1110fs
XH_P63	17	61910660	61910660	Missense_Mutation	SNP	T	G	T	SMARCD2	c.A1438C	p.K480Q
XH_P63	17	76122702	76122702	Silent	SNP	G	A	G	TMC6	c.C84T	p.S28S
XH_P63	17	78308060	78308060	Frame_Shift_Ins	INS	-	CA	-	RNF213	4299_4300insC	p.E1433fs
XH_P63	18	13073185	13073185	Splice_Site	INS	-	AGATGAAATGT	-	CEP192	-	-
XH_P63	18	14763838	14763838	Frame_Shift_Ins	INS	-	AGGTGTTCCGT	-	ANKRD30B	975insAGGTGT	p.S325fs
XH_P63	18	28671089	28671089	Missense_Mutation	SNP	T	C	T	DS2C	c.A376G	p.K126E
XH_P63	18	28671090	28671090	Frame_Shift_Ins	INS	-	ACAG	-	DS2C	374_375insCTG	p.T125fs
XH_P63	18	48591908	48591916	In_Frame_Del	DEL	TGGAGGAGA	-	TGGAGGAGA	SMAD4	c.1071_1079del	p.357_360del
XH_P63	18	55322551	55322551	Nonsense_Mutation	INS	-	AATGTAATGTTG	-	ATP8B1	6insTAACAACA	p.1936_1937delinsX
XH_P63	19	3750622	3750622	Silent	SNP	A	T	A	TJP3	c.A2700T	p.V900V
XH_P63	19	6456532	6456532	Frame_Shift_Ins	INS	-	T	-	SLC25A23	c.381dupA	p.D128fs
XH_P63	19	6456534	6456534	Frame_Shift_Ins	INS	-	CCCAG	-	SLC25A23	379_380insCTG	p.R127fs
XH_P63	19	8550805	8550805	Missense_Mutation	SNP	C	T	C	HNRNPM	c.C1088T	p.A363V
XH_P63	19	9965434	9965434	Missense_Mutation	SNP	G	A	G	OLFM2	c.C559T	p.P187S
XH_P63	19	11346378	11346378	Frame_Shift_Ins	INS	-	CGGAT	-	DOCK6	449_2450insAT	p.R817fs
XH_P63	19	12186173	12186173	Nonsense_Mutation	INS	-	AAAGGTTTGT	-	ZNF844	nsATTGAAGGTTT	p.C80_81delinsYX
XH_P63	19	15538008	15538008	In_Frame_Ins	INS	-	CCTTCA	-	WIZ	88_989insTGAA	p.5330delinsMKMG
XH_P63	19	17303756	17303756	Missense_Mutation	SNP	G	T	G	MYO9B	c.G3013T	p.A1005S
XH_P63	19	17442023	17442023	Missense_Mutation	SNP	A	T	A	ANO8	c.T705A	p.D235E
XH_P63	19	17442026	17442040	Splice_Site	DEL	CAGGGGACA	-	CCAGGGGACAA	ANO8	-	-
XH_P63	19	18376298	18376298	Silent	SNP	G	A	G	KIAA1683	c.C2052T	p.A684A
XH_P63	19	37368128	37368128	In_Frame_Ins	INS	-	CCCTATGAATGT	-	ZNF345	AAAGACCTCTATG	p.HQRIHTGERPYECKGCKGFSSSGA
XH_P63	19	45375389	45375389	Missense_Mutation	SNP	T	A	T	NECTIN2	c.T758A	p.V253E
XH_P63	19	45375391	45375394	Frame_Shift_Del	DEL	ACCC	-	ACCC	NECTIN2	c.760_763del	p.T254fs
XH_P63	19	46270037	46270037	Missense_Mutation	SNP	G	A	G	SIX5	c.C1180T	p.R394W
XH_P63	19	55175223	55175223	Missense_Mutation	SNP	A	C	A	LILRB4	c.A169C	p.K57Q
XH_P63	19	57326273	57326273	Silent	SNP	G	A	G	PEG3	c.C3537T	p.F1179G
XH_P63	20	20620531	20620531	In_Frame_Ins	INS	-	AAATACTGTG	-	RALGAP2	4insTTCAACAG	p.188delinsPSTVFE
XH_P63	20	20620533	20620533	Missense_Mutation	SNP	G	T	G	RALGAP2	c.C562A	p.P188T
XH_P63	20	43836699	43836699	Frame_Shift_Ins	INS	-	GTAATGCCCTTT	-	SEMG1	62insGGTAATG	p.F254fs
XH_P63	20	47361612	47361612	Frame_Shift_Ins	INS	-	GACTCTAGTTT	-	PREX1	364insAAACTAG	p.H122fs
XH_P63	21	31587890	31587890	Nonsense_Mutation	INS	-	GATTTCAT	-	CLDN8	3_354insATAGA	p.1118delinsIX
XH_P63	21	33067244	33067244	Frame_Shift_Ins	INS	-	A	-	SCAF4	c.1072_1073ins	p.T358fs
XH_P63	22	19210331	19210331	Nonsense_Mutation	INS	-	ATATTATA	-	CLTCL1	3_2294insTATA	p.E765delinsVX
XH_P63	X	14932676	14932676	Silent	SNP	C	A	C	MOSPD2	c.C855A	p.T285T
XH_P63	X	14932677	14932677	Nonsense_Mutation	INS	-	AAGACATTTG	-	MOSPD2	857insAAGACA	p.1286_1287delinsX
XH_P63	X	49050718	49050718	In_Frame_Ins	INS	-	TTGCATGTA	-	SYP	7_328insTACATG	p.V110delinsYMQV
XH_P63	X	54473820	54473823	Frame_Shift_Del	DEL	CCAC	-	CCAC	FGD1	c.2501_2504del	p.G834fs
XH_P63	X	62570280	62570280	Missense_Mutation	SNP	A	C	A	SPIN4	c.T419G	p.M140R
XH_P63	X	69501584	69501584	Frame_Shift_Ins	INS	-	TTAGGAA	-	ARR3	35_1136insTTAG	p.A379fs
XH_P63	X	102755163	102755163	Silent	SNP	C	T	C	RAB40A	c.G522A	p.V174V
XH_P63	X	135288667	135288667	Frame_Shift_Ins	INS	-	TTGT	-	FHL1	c.124_125insTTG	p.H42fs
XH_P63	X	135288668	135288668	Frame_Shift_Ins	INS	-	G	-	FHL1	c.125_126insG	p.H42fs
XH_P63	X	136649696	136649696	Silent	SNP	C	T	C	ZIC3	c.C846T	p.V282V
XH_P63	X	138727794	138727794	Nonsense_Mutation	INS	-	TATCTATGCATT	-	MCF2	4insATAATGCA	p.F55delinsYNAX
XH_P63	X	139038436	139038436	Silent	SNP	T	C	T	Cxorf66	c.A705G	p.E235E
XH_P63	X	139038438	139038438	Frame_Shift_Ins	INS	-	TGAATTAG	-	Cxorf66	2_703insCTAAT	p.E235fs
XH_P63	X	153418531	153418531	Frame_Shift_Ins	INS	-	CAGGAAA	-	OPN1LW	28_529insCAGG	p.S176fs
XH_P63	1	155152178	155152178	Frame_Shift_Ins	INDEL	-	C	C	TRIM46	c.1294dupC	p.H432fs
XH_P63	1	237619971	237619971	Missense_Mutation	SNV	T	A	A	RYR2	c.1548T>A	p.D516E
XH_P63	1	32131638	32131638	Silent	SNV	C	T	T	COL16A1	c.3402G>A	p.A1134A
XH_P63	11	65143905	65143905	Silent	SNV	G	A	A	SLC25A45	c.714C>T	p.Y238Y
XH_P63	15	63796955	63796955	Missense_Mutation	SNV	T	G	G	USP3	c.17T>G	p.L6R
XH_P63	16	29828115	29828115	Missense_Mutation	SNV	C	T	T	PAGR1	c.269C>T	p.P90L
XH_P63	17	2995884	2995884	Missense_Mutation	SNV	A	C	C	OR1D2	c.407T>G	p.M136R
XH_P63	17	40838124	40838124	Missense_Mutation	SNV	A	C	C	CNTNAP1	c.865A>C	p.N289H
XH_P63	17	61910660	61910660	Missense_Mutation	SNV	T	G	G	SMARCD2	c.1438A>C	p.K480Q
XH_P63	18	48591908	48591916	Missense_Mutation	INDEL	TGGAGGAGA	-	-	SMAD4	1080delGGAG	p.G358_D360del
XH_P63	2	70905837	70905837	Missense_Mutation	SNV	G	A	A	ADD2	c.1382C>T	p.T461M
XH_P63	2	95539700	95539700	Splice_Site	SNV	C	A	A	TEK4	c.24-10C>A	-
XH_P63	3	53381457	53381457	Missense_Mutation	SNV	T	G	G	DCP1A	c.88A>C	p.T30P
XH_P63	3	9515069	9515069	Silent	SNV	G	T	T	SETD5	c.3345G>T	p.V1115V
XH_P63	4	120240736	120240736	Silent	SNV	G	A	A	FABP2	c.303C>T	p.N101N
XH_P63	5	11565059	11565059	Missense_Mutation	SNV	A	C	C	CTNND2	c.11T>G	p.M4R
XH_P63	5	140182164	140182164	Missense_Mutation	SNV	C	T	T	PCDHA3	c.1382C>T	p.T461M
XH_P63	5	140858151	140858151	Frame_Shift_Del	INDEL	-	-	-	PCDHGC3	c.2473delT	p.Y825fs
XH_P63	5	168179992	168179992	Silent	SNV	C	T	T	SLIT3	c.1941G>A	p.G647G
XH_P63	7	1539980	1539980	Missense_Mutation	SNV	A	C	C	INTS1	c.372T>G	p.D124E
XH_P63	7	6449609	6449609	Silent	SNV	G	A	A	DAGLB	c.1491C>T	p.F497F
XH_P63	8	67488576	67488576	Missense_Mutation	SNV	T	C	C	MYBL1	c.1136A>G	p.D379G
XH_P63	X	102755163	102755163	Silent	SNV	C	T	T	RAB40A	c.522G>A	p.V174V
XH_P63	X	62570280	62570280	Missense_Mutation	SNV	A	C	C	SPIN4	c.419T>G	p.M140R
XH_P87	1	43888173	43888173	Missense_Mutation	SNV	A	C	C	SZT2	c.1792A>C	p.T598P
XH_P87	10	23729472	23729472	Silent	SNV	G	A	A	OTUD1	c.1086G>A	p.V362V
XH_P87	11	61536746	61536746	Missense_Mutation	SNV	C	T	T	MYRF	c.413C>T	p.S138F
XH_P87	11	62556591	62556591	Missense_Mutation	SNV	T	G	G	TMEM179B	c.193T>G	p.F65V
XH_P87	11	64678637	64678637	Missense_Mutation	SNV	C	G	G	ATG2A	c.1339G>C	p.G447R
XH_P87	11	74705673	74705673	Silent	SNV	C	T	T	NEU3	c.214C>T	p.L72L
XH_P87	12	120791186	120791186	Splice_Site	SNV	A	G	G	MS1	c.653-4T>C	-
XH_P87	12	4554430	4554430	Missense_Mutation	SNV	C	T	T	FGF6	c.307G>A	p.D103N
XH_P87	12	6494542	6494542	Missense_Mutation	SNV	A	C	C	LTBR	c.412A>C	p.P138Q
XH_P87	14	21550253	21550253	Missense_Mutation	SNV	C	T	T	ARHGEF40	c.1084C>T	p.R362W
XH_P87	14	24731564	24731564	Splice_Site	SNV	T	C	C	TGM1	c.-2-4A>G	-
XH_P87	14	38256729	38256729	Missense_Mutation	SNV	A	T	T	TTG6	c.3371A>T	p.D1124V
XH_P87	14	50251828	50251828	Missense_Mutation	SNV	C	A	A	NEMF	c.2992G>T	p.V998L
XH_P87	15	42276808	42276808	Missense_Mutation	SNV	G	T	T	PLA2G4E	c.2212C>A	p.Q738K
XH_P87	15	85403004	85403004	Splice_Site	SNV	C	T	T	ALPK3	c.4572-3C>T	-
XH_P87	15	90631838	90631838	Missense_Mutation	SNV	C	A	A	IDH2	c.515G>T	p.R172M
XH_P87	16	2141861	2141861	Missense_Mutation	SNV	C	G	G	PKD1	c.11455G>C	p.V3819L
XH_P87	16	4815920	4815920	Missense_Mutation	SNV	T	G	G	ZNF500	c.60A>C	p.E20D
XH_P87	17	79096299	79096299	Silent	SNV	G	A	A	AATK	c.1437C>T	p.Y479Y
XH_P87	18	2769704	2769704	Missense_Mutation	SNV	G	A	A	SMCHD1	c.4732G>A	p.A1578T
XH_P87	18	61652418	61652418	Missense_Mutation	SNV	A	T	T	SERPINB8	c.659A>T	p.Y220F
XH_P87	19	16688298	16688298	Missense_Mutation	SNV	C	A	A	MED26	c.343G>T	p.V115L
XH_P87	19	40993598	40993598	Splice_Site	SNV	C	T	T	SPTBN4	c.170-6C>T	-

XH_P87	19	54613437	54613437	Missense_Mutation	SNV	C	T	T	TFPT	c.323G>A	P.R108Q
XH_P87	19	6444316	6444316	Splice_Site	SNV	G	A	A	SLC25A23	c.1072-4C>T	
XH_P87	2	105984159	105984159	Missense_Mutation	SNV	A	C	C	FHL2	c.369T>G	P.H123Q
XH_P87	2	99013386	99013386	Missense_Mutation	SNV	A	C	C	CNGA3	c.1699A>C	P.M567L
XH_P87	20	10256202	10256202	Silent	SNV	G	A	A	SNAP25	c.63G>A	P.L21L
XH_P87	22	50705400	50705400	Silent	SNV	A	C	C	MAPK11	c.573T>G	P.P191P
XH_P87	4	110864525	110864525	Missense_Mutation	SNV	A	G	G	EGF	c.443A>G	P.N148S
XH_P87	4	70504989	70504989	Missense_Mutation	SNV	G	C	C	UGT2A2	c.370C>G	P.L124V
XH_P87	6	11213568	11213568	Silent	SNV	T	C	C	NEDD9	c.405A>G	P.P135P
XH_P87	6	44243155	44243155	Missense_Mutation	SNV	G	A	A	TMEM151B	c.592G>A	P.V198I
XH_P87	7	1484933	1484933	Missense_Mutation	SNV	C	A	A	MICALL2	c.773G>T	P.R258L
XH_P87	7	55259515	55259515	Missense_Mutation	SNV	T	G	G	EGFR	c.2573T>G	P.L858R
XH_P87	7	88962961	88962961	Frame_Shift_Del	INDEL	C	-	-	ZNF804B	c.665delC	P.T222fs
XH_P87	8	142228328	142228328	Missense_Mutation	SNV	G	A	A	SLC45A4	c.1258C>T	P.R420W
XH_P87	8	89053755	89053755	Missense_Mutation	SNV	C	A	A	MMP16	c.1758G>T	P.Q586H
XH_P88	1	118566028	118566028	Missense_Mutation	SNV	G	A	A	SPAG17	c.3968C>T	P.P1323L
XH_P88	1	120166590	120166590	Nonsense_Mutation	SNV	C	A	A	ZNF697	c.376G>T	P.E126*
XH_P88	1	12368548	12368548	Frame_Shift_Del	INDEL	C	-	-	VPS13D	c.6500delC	P.A2167fs
XH_P88	1	12835294	12835294	Missense_Mutation	SNV	C	T	T	PRAMEF12	c.284C>T	P.P95L
XH_P88	1	145560227	145560227	Missense_Mutation	SNV	T	A	A	ANKRD35	c.443T>A	P.L148Q
XH_P88	1	156814912	156814912	Missense_Mutation	SNV	C	A	A	INSRR	c.2393G>T	P.G798V
XH_P88	1	156814913	156814913	Missense_Mutation	SNV	C	A	A	INSRR	c.2392G>T	P.G798C
XH_P88	1	160144370	160144370	Missense_Mutation	SNV	G	T	T	ATP1A4	c.2144G>T	P.G715V
XH_P88	1	169446760	169446760	Missense_Mutation	SNV	C	A	A	SLC19A2	c.440G>T	P.S147I
XH_P88	1	16952260	16952260	Splice_Site	SNV	T	C	C	CROCCP2	n.723+10A>G	
XH_P88	1	170136782	170136782	Missense_Mutation	SNV	C	T	T	METTL11B	c.736C>T	P.R246W
XH_P88	1	171509715	171509715	Missense_Mutation	SNV	A	G	G	PRRC2C	c.3104A>G	P.E1035G
XH_P88	1	175334371	175334371	Missense_Mutation	SNV	A	G	G	TNR	c.1363T>C	P.S455P
XH_P88	1	17942620	17942620	Missense_Mutation	SNV	G	A	A	ARHGEF10L	c.641G>A	P.G214E
XH_P88	1	190067507	190067507	Missense_Mutation	SNV	G	T	T	BRINP3	c.1636C>A	P.P546T
XH_P88	1	193107231	193107231	Missense_Mutation	SNV	G	T	T	CDC73	c.440G>T	P.R147L
XH_P88	1	200943959	200943959	Missense_Mutation	SNV	G	A	A	KIF21B	c.4697C>T	P.A1566V
XH_P88	1	201779178	201779178	Silent	SNV	C	T	T	NAV1	c.3324C>T	P.L108P
XH_P88	1	2161052	2161052	Missense_Mutation	SNV	G	T	T	SKI	c.847G>T	P.A283S
XH_P88	1	225380498	225380498	Frame_Shift_Del	INDEL	G	-	-	DNAH14	c.5706delG	P.W1902fs
XH_P88	1	225380499	225380499	Missense_Mutation	SNV	G	T	T	DNAH14	c.5706G>T	P.W1902C
XH_P88	1	228467010	228467010	Missense_Mutation	SNV	G	T	T	OBSCN	c.7261G>T	P.A2421S
XH_P88	1	229745867	229745867	Missense_Mutation	SNV	C	T	T	TAF5L	c.233G>A	P.R78Q
XH_P88	1	237951332	237951332	Missense_Mutation	SNV	G	A	A	RYR2	c.13373G>A	P.G4458D
XH_P88	1	25634255	25634255	Missense_Mutation	SNV	G	A	A	RHD	c.1191G>A	P.M397I
XH_P88	1	34554788	34554788	Missense_Mutation	SNV	T	A	A	CSMD2	c.194A>T	P.N65I
XH_P88	1	46976147	46976147	Missense_Mutation	SNV	G	A	A	DMBX1	c.169G>A	P.D57N
XH_P88	1	55277591	55277591	Missense_Mutation	SNV	C	A	A	LEXM	c.605C>A	P.P202H
XH_P88	1	6145265	6145265	Missense_Mutation	SNV	G	T	T	KCNAB2	c.283G>T	P.A95S
XH_P88	1	75037471	75037471	Missense_Mutation	SNV	G	A	A	ERIC3	c.3923C>T	P.A1308V
XH_P88	1	8403806	8403806	Splice_Site	SNV	G	C	C	SLC45A1	c.2083-1G>C	
XH_P88	10	100185390	100185390	Missense_Mutation	SNV	G	C	C	HP51	c.1243C>G	P.P415A
XH_P88	10	124608957	124608957	Splice_Site	SNV	T	A	A	FAM24B	c.93-2A>T	
XH_P88	10	125521388	125521388	Missense_Mutation	SNV	T	G	G	CPXM2	c.1777A>C	P.S593R
XH_P88	10	127760107	127760107	Missense_Mutation	SNV	C	A	A	ADAM12	c.1262G>T	P.G421V
XH_P88	10	134021648	134021648	Missense_Mutation	SNV	T	A	A	STK32C	c.1366A>T	P.R456W
XH_P88	10	24832616	24832616	Missense_Mutation	SNV	A	G	G	KIAA1217	c.4417A>G	P.R1473G
XH_P88	10	31809382	31809382	Silent	SNV	G	T	T	ZEB1	c.1071G>T	P.G357G
XH_P88	10	50533979	50533979	Missense_Mutation	SNV	C	T	T	C10orf71	c.3389C>T	P.S1130L
XH_P88	10	71695140	71695140	Missense_Mutation	SNV	G	A	A	COL13A1	c.1730G>A	P.G577E
XH_P88	10	71695141	71695141	Silent	SNV	A	T	T	COL13A1	c.1731A>T	P.G577G
XH_P88	10	81154100	81154100	Missense_Mutation	SNV	C	A	A	ZCCHC24	c.544G>T	P.G182W
XH_P88	10	85984178	85984178	Missense_Mutation	SNV	T	G	G	LRIT2	c.803A>C	P.Q268P
XH_P88	10	90984922	90984922	Missense_Mutation	SNV	C	A	A	LIPA	c.602G>T	P.G201V
XH_P88	10	95072862	95072862	Missense_Mutation	SNV	G	C	C	MYOF	c.5804C>G	P.A1935G
XH_P88	10	97447049	97447049	Missense_Mutation	SNV	C	T	T	TCTN3	c.691G>A	P.A231T
XH_P88	11	103027454	103027454	Missense_Mutation	SNV	T	C	C	DYNC2H1	c.4082T>C	P.L1361S
XH_P88	11	107299677	107299677	Missense_Mutation	SNV	G	T	T	CWF19L2	c.1281C>A	P.D427E
XH_P88	11	116734522	116734522	Silent	SNV	C	T	T	SIK3	c.1344G>A	P.K448K
XH_P88	11	117376421	117376421	Missense_Mutation	SNV	A	G	G	DSCAML1	c.1990T>C	P.F664L
XH_P88	11	119029318	119029318	Missense_Mutation	SNV	G	A	A	ABCG4	c.1219G>A	P.G407S
XH_P88	11	17981057	17981057	Missense_Mutation	SNV	C	T	T	SERGEF	c.971G>A	P.S324N
XH_P88	11	21556065	21556065	Splice_Site	SNV	G	C	C	NELL1	c.1870+5G>C	
XH_P88	11	21556066	21556066	Splice_Site	SNV	C	T	T	NELL1	c.1870+6C>T	
XH_P88	11	379910	379910	Missense_Mutation	SNV	G	T	T	B4GALNT4	c.2533G>T	P.A845S
XH_P88	11	47305930	47305930	Silent	SNV	G	A	A	MADD	c.1971G>A	P.V657V
XH_P88	11	5020978	5020978	Missense_Mutation	SNV	C	A	A	OR51L1	c.766C>A	P.P256T
XH_P88	11	55594737	55594737	Missense_Mutation	SNV	C	A	A	OR5L2	c.43C>A	P.L15I
XH_P88	11	6007208	6007208	Missense_Mutation	SNV	C	T	T	OR52L1	c.953G>A	P.R318H
XH_P88	11	65350799	65350799	Frame_Shift_Ins	INDEL	-	T	T	EHPBP1L1	c.2657dupT	P.Q887fs
XH_P88	11	66333518	66333518	Missense_Mutation	SNV	C	T	T	CTSF	c.842G>A	P.G281E
XH_P88	11	6650972	6650972	Missense_Mutation	SNV	C	T	T	DCHS1	c.4966G>A	P.V1656I
XH_P88	11	78468035	78468035	Frame_Shift_Del	INDEL	G	-	-	TENM4	c.2571delC	P.C858fs
XH_P88	11	82564256	82564256	Missense_Mutation	SNV	T	C	C	PRCP	c.59A>G	P.Y20C
XH_P88	11	86013513	86013513	Missense_Mutation	SNV	G	A	A	HIKESHI	c.23G>A	P.G8E
XH_P88	11	88241995	88241995	Missense_Mutation	SNV	G	A	A	GRM5	c.3308C>T	P.A1103V
XH_P88	11	89135547	89135547	Missense_Mutation	SNV	T	C	C	NOX4	c.793A>G	P.K265E
XH_P88	12	109186276	109186276	Missense_Mutation	SNV	C	A	A	SSH1	c.1679G>T	P.G560V
XH_P88	12	11061429	11061429	Missense_Mutation	SNV	C	A	A	TAS2R13	c.469G>T	P.D157Y
XH_P88	12	111701642	111701642	Splice_Site	SNV	A	T	T	CUX2	c.300A>T	P.P100P
XH_P88	12	120146032	120146032	Silent	SNV	G	A	A	CIT	c.5163C>T	P.P1721P
XH_P88	12	121442854	121442854	Missense_Mutation	SNV	T	A	A	C12orf43	c.497A>T	P.K166M
XH_P88	12	123335415	123335415	Missense_Mutation	SNV	G	A	A	HIP1R	c.472G>A	P.D158N
XH_P88	12	123335416	123335416	Missense_Mutation	SNV	A	G	G	HIP1R	c.473A>G	P.D158G
XH_P88	12	128899982	128899982	Missense_Mutation	SNV	C	A	A	TMEM132C	c.791C>A	P.S264Y
XH_P88	12	1919741	1919741	Missense_Mutation	SNV	C	A	A	CACNA2D4	c.2626G>T	P.D876Y
XH_P88	12	21069046	21069046	Silent	SNV	A	T	T	SLCO1B3	c.1974A>T	P.A658A
XH_P88	12	50367204	50367204	Missense_Mutation	SNV	C	T	T	AQP6	c.248C>T	P.P83L
XH_P88	12	51584254	51584254	Missense_Mutation	SNV	C	T	T	POU6F1	c.682G>A	P.G228R
XH_P88	12	52681775	52681775	Missense_Mutation	SNV	C	T	T	KRT81	c.893G>A	P.R298H
XH_P88	12	5672499	5672499	Missense_Mutation	SNV	A	C	C	ANO2	c.2978T>G	P.M993R
XH_P88	12	66704330	66704330	Missense_Mutation	SNV	G	A	A	HELB	c.1622G>A	P.G541E
XH_P88	12	6700647	6700647	Missense_Mutation	SNV	T	C	C	CHD4	c.3325A>G	P.I1109V

XH_P88	12	6753526	6753526	Missense_Mutation	SNV	C	T	T	ACRBP	c.721G>A	P.G241R
XH_P88	12	70934713	70934713	Missense_Mutation	SNV	C	A	A	PTPRB	c.5519G>T	P.G1840V
XH_P88	12	88433986	88433986	Missense_Mutation	SNV	G	C	C	C12orf29	c.152G>C	P.S51T
XH_P88	13	101315415	101315415	Missense_Mutation	SNV	C	T	T	TMTc4	c.298G>A	P.G100R
XH_P88	13	25672014	25672014	Missense_Mutation	SNV	C	T	T	PABPC3	c.1678C>T	P.P560W
XH_P88	13	27333749	27333749	Frame_Shift_Ins	INDEL	-	T	T	GPR12	c.215dupA	P.N72fs
XH_P88	13	42390911	42390911	Missense_Mutation	SNV	C	A	A	VWA8	c.1870G>T	P.V624F
XH_P88	13	45149543	45149543	Frame_Shift_Ins	INDEL	-	G	G	TSC2D21	c.667dupC	P.H223fs
XH_P88	13	51544059	51544059	Splice_Site	SNV	C	T	T	RNASEH2B	c.742-9C>T	
XH_P88	13	58240881	58240881	Missense_Mutation	SNV	C	A	A	PCDH17	c.2711C>A	P.T904N
XH_P88	13	84455567	84455567	Missense_Mutation	SNV	C	G	G	SLITRK1	c.76G>C	P.E26Q
XH_P88	13	92346009	92346009	Silent	SNV	G	A	A	GPC5	c.894G>A	P.S298S
XH_P88	14	104641874	104641874	Missense_Mutation	SNV	G	T	T	KIF26A	c.2749G>T	P.A917S
XH_P88	14	104642640	104642640	Missense_Mutation	SNV	C	A	A	KIF26A	c.3515C>A	P.T1172N
XH_P88	14	105417221	105417221	Missense_Mutation	SNV	C	A	A	AHNAK2	c.4567G>T	P.V1523L
XH_P88	14	24045127	24045127	Silent	SNV	C	T	T	JPH4	c.918G>A	P.E306E
XH_P88	14	24534858	24534858	Missense_Mutation	SNV	G	A	A	CARMIL3	c.3424G>A	P.G1142R
XH_P88	14	38723886	38723886	Missense_Mutation	SNV	C	G	G	CLEC14A	c.1342G>C	P.E448Q
XH_P88	14	50649224	50649224	Missense_Mutation	SNV	C	A	A	SOS2	c.815G>T	P.S272I
XH_P88	14	51489574	51489574	Silent	SNV	C	T	T	TRIM9	c.1020G>A	P.K340K
XH_P88	14	77844850	77844850	Missense_Mutation	SNV	G	T	T	SAMD15	c.1089G>T	P.E363D
XH_P88	14	77844851	77844851	Missense_Mutation	SNV	A	T	T	SAMD15	c.1090A>T	P.I364L
XH_P88	14	94545835	94545835	Missense_Mutation	SNV	T	C	C	DDX24	c.254A>G	P.E85G
XH_P88	14	94712829	94712829	Missense_Mutation	SNV	A	T	T	PPP4R4	c.1564A>T	P.I522F
XH_P88	14	95557570	95557570	Missense_Mutation	SNV	C	G	G	DICER1	c.5497G>C	P.V1833L
XH_P88	14	95557571	95557571	Silent	SNV	C	T	T	DICER1	c.5496G>A	P.Q1832Q
XH_P88	15	33952400	33952400	Splice_Site	SNV	C	T	T	RYR3	c.4398C>T	P.N1466N
XH_P88	15	42109802	42109802	Splice_Site	SNV	A	T	T	MAPKBP1	c.1801-10A>T	
XH_P88	15	48451820	48451820	Missense_Mutation	SNV	A	C	C	MYEF2	c.707T>G	P.F236C
XH_P88	15	64222622	64222622	Missense_Mutation	SNV	G	C	C	DAPK2	c.616C>G	P.L206V
XH_P88	15	64222623	64222623	Silent	SNV	A	T	T	DAPK2	c.615T>A	P.G205G
XH_P88	15	67786633	67786633	Missense_Mutation	SNV	T	A	A	IQCH	c.2899T>A	P.F967I
XH_P88	15	69003123	69003123	Missense_Mutation	SNV	C	T	T	CORO2B	c.371C>T	P.A124V
XH_P88	15	69006371	69006371	Silent	SNV	C	G	G	CORO2B	c.741C>G	P.L247L
XH_P88	15	81572098	81572098	Missense_Mutation	SNV	A	T	T	IL16	c.1064A>T	P.E355V
XH_P88	15	81625257	81625257	Missense_Mutation	SNV	G	T	T	TMC3	c.2806C>A	P.P936T
XH_P88	15	84611420	84611420	Nonsense_Mutation	SNV	C	A	A	ADAMTSL3	c.2190C>A	P.C730*
XH_P88	15	84611421	84611421	Silent	SNV	C	T	T	ADAMTSL3	c.2191C>T	P.L731L
XH_P88	15	99670824	99670824	Silent	SNV	G	A	A	SYNM	c.2256G>A	P.V752V
XH_P88	16	10273854	10273854	Splice_Site	SNV	C	A	A	GRIN2A	c.414+1G>T	
XH_P88	16	11003051	11003051	Splice_Site	SNV	G	A	A	CIITA	c.2816+7G>A	
XH_P88	16	20809383	20809383	Missense_Mutation	SNV	G	A	A	ERI2	c.1739C>T	P.T580I
XH_P88	16	27514179	27514179	Splice_Site	SNV	C	T	T	GTFC1	c.1907+1G>A	
XH_P88	16	31367262	31367262	Missense_Mutation	SNV	C	A	A	ITGAX	c.86C>A	P.A29D
XH_P88	16	61851450	61851450	Missense_Mutation	SNV	C	T	T	CDH8	c.1210G>A	P.A404T
XH_P88	16	66974433	66974433	Silent	SNV	C	T	T	CES2	c.843C>T	P.G281G
XH_P88	16	67022737	67022737	Splice_Site	SNV	A	T	T	CES4A	c.58+4A>T	
XH_P88	16	68025856	68025856	Missense_Mutation	SNV	A	G	G	DPEP2	c.73T>C	P.C25R
XH_P88	16	68597843	68597843	Missense_Mutation	SNV	G	A	A	ZFP90	c.1153G>A	P.E385K
XH_P88	16	88599826	88599826	Missense_Mutation	SNV	C	T	T	ZFPM1	c.1460C>T	P.S487L
XH_P88	16	89349392	89349392	Silent	SNV	C	T	T	ANKRD11	c.3558G>A	P.K1186K
XH_P88	17	11543667	11543667	Missense_Mutation	SNV	G	T	T	DNAH9	c.1867G>T	P.G623C
XH_P88	17	19287865	19287865	Missense_Mutation	SNV	G	T	T	MFAP4	c.750C>A	P.H250Q
XH_P88	17	27235800	27235800	Splice_Site	SNV	C	A	A	PHF12	c.2458+1G>T	
XH_P88	17	29490210	29490210	Nonsense_Mutation	SNV	A	T	T	NF1	c.295A>T	P.K99*
XH_P88	17	29685517	29685517	Nonsense_Mutation	SNV	A	T	T	NF1	c.7990A>T	P.K2664*
XH_P88	17	32688855	32688855	Missense_Mutation	SNV	G	A	A	CCL1	c.137C>T	P.A46V
XH_P88	17	38935824	38935824	Missense_Mutation	SNV	C	T	T	KRT27	c.902G>A	P.R301Q
XH_P88	17	39643257	39643257	Missense_Mutation	SNV	G	A	A	KRT36	c.1153C>T	P.R385W
XH_P88	17	44828929	44828929	Nonsense_Mutation	SNV	A	T	T	NSF	c.2104A>T	P.K702*
XH_P88	17	4496315	4496315	Silent	SNV	C	T	T	SMTNL2	c.579C>T	P.P193P
XH_P88	17	47109332	47109332	Missense_Mutation	SNV	G	A	A	IGF2BP1	c.398G>A	P.R133K
XH_P88	17	47109333	47109333	Missense_Mutation	SNV	G	T	T	IGF2BP1	c.399G>C	P.R133S
XH_P88	17	48540573	48540573	Silent	SNV	C	T	T	ACSF2	c.924C>T	P.N308N
XH_P88	17	62137824	62137824	Splice_Site	SNV	C	A	A	ERN1	c.1206+5G>T	
XH_P88	17	72584862	72584862	Missense_Mutation	SNV	G	T	T	CD300LD	c.167C>A	P.A56D
XH_P88	17	7557489	7557489	Missense_Mutation	SNV	C	A	A	ATP1B2	c.220C>A	P.Q74K
XH_P88	17	7577556	7577556	Missense_Mutation	SNV	C	A	A	TP53	c.725G>T	P.C242F
XH_P88	17	79096064	79096064	Missense_Mutation	SNV	C	T	T	AATK	c.1672G>A	P.A558T
XH_P88	17	79426306	79426306	Silent	SNV	G	A	A	BAHCC1	c.5673G>A	P.R1891R
XH_P88	17	8738616	8738616	Missense_Mutation	SNV	C	A	A	PIK3R6	c.619G>T	P.A207S
XH_P88	17	9828807	9828807	Missense_Mutation	SNV	T	G	G	GA57	c.932A>C	P.K311T
XH_P88	18	10485535	10485535	Missense_Mutation	SNV	A	T	T	APCDD1	c.851A>T	P.K284M
XH_P88	18	56037692	56037692	Missense_Mutation	SNV	A	G	G	NEDD4L	c.1886A>G	P.E629G
XH_P88	18	8783547	8783547	Missense_Mutation	SNV	G	A	A	MTCL1	c.437G>A	P.R146K
XH_P88	19	10602770	10602770	Missense_Mutation	SNV	C	A	A	KEAP1	c.808G>T	P.A270S
XH_P88	19	10742631	10742631	Splice_Site	SNV	A	C	C	SLC44A2	c.704+4A>C	
XH_P88	19	1122885	1122885	Splice_Site	SNV	G	T	T	SBN02	c.609+8C>A	
XH_P88	19	11230903	11230903	Missense_Mutation	SNV	C	T	T	LDLR	c.1981C>T	P.P661S
XH_P88	19	11660228	11660228	Missense_Mutation	SNV	C	A	A	CNN1	c.592C>A	P.P198T
XH_P88	19	12637600	12637600	Missense_Mutation	SNV	A	G	G	ZNF564	c.1322T>C	P.I441T
XH_P88	19	12958118	12958118	Silent	SNV	C	T	T	MAST1	c.342C>T	P.S114S
XH_P88	19	15567302	15567302	Splice_Site	SNV	C	T	T	RASAL3	c.1576+11G>A	
XH_P88	19	18707846	18707846	Silent	SNV	G	A	A	CRLF1	c.711C>T	P.P237P
XH_P88	19	23542452	23542452	Missense_Mutation	SNV	T	A	A	ZNF91	c.3233A>T	P.P1078V
XH_P88	19	23542453	23542453	Nonsense_Mutation	SNV	C	A	A	ZNF91	c.3232G>T	P.E1078*
XH_P88	19	31769760	31769760	Silent	SNV	G	A	A	TSZH2	c.939C>T	P.A313A
XH_P88	19	3179658	3179658	Missense_Mutation	SNV	G	T	T	S1PR4	c.868G>T	P.D290Y
XH_P88	19	41248364	41248364	Missense_Mutation	SNV	G	A	A	C19orf54	c.1030C>T	P.L344F
XH_P88	19	41248527	41248527	Silent	SNV	G	C	C	C19orf54	c.867C>G	P.S289S
XH_P88	19	44492718	44492718	Splice_Site	SNV	G	A	A	ZNF155	c.15+8G>A	
XH_P88	19	47767944	47767944	Splice_Site	SNV	G	A	A	CCDC9	c.546+1G>A	
XH_P88	19	51162306	51162306	Silent	SNV	C	T	T	C19orf81	c.504C>T	P.L168L
XH_P88	19	53668459	53668459	Missense_Mutation	SNV	T	G	G	ZNF665	c.1284A>C	P.K428N
XH_P88	19	5456781	5456781	Missense_Mutation	SNV	C	T	T	ZNRF4	c.1279C>T	P.P427S
XH_P88	19	54780269	54780269	Missense_Mutation	SNV	C	T	T	LILRB2	c.1522G>A	P.G508R
XH_P88	19	5832415	5832415	Missense_Mutation	SNV	C	T	T	FUT6	c.164G>A	P.G55E
XH_P88	19	7626435	7626435	Missense_Mutation	SNV	C	G	G	PNPLA6	c.4115C>G	P.A1372G

XH_P88	19	9046894	9046894	Silent	SNV	A	G	G	MUC16	c.34737T>C	P.T11579T
XH_P88	19	9070358	9070358	Silent	SNV	C	T	T	MUC16	c.17088G>A	P.E5696E
XH_P88	2	124783255	124783255	Missense_Mutation	SNV	G	A	A	CNTNAP5	c.28G>A	P.V10I
XH_P88	2	128347742	128347742	Silent	SNV	C	T	T	MYO7B	c.1930C>T	P.L644L
XH_P88	2	128466272	128466272	Missense_Mutation	SNV	A	T	T	WDR33	c.3760T>A	P.S1254T
XH_P88	2	166514492	166514492	Missense_Mutation	SNV	C	A	A	CSRN3P	c.370C>A	P.H124N
XH_P88	2	170417229	170417229	Silent	SNV	C	T	T	FASTKD1	c.639G>A	P.V213V
XH_P88	2	171641290	171641290	Missense_Mutation	SNV	G	A	A	ERICH2	c.163G>A	P.E55K
XH_P88	2	179428048	179428048	Missense_Mutation	SNV	C	A	A	TTN	c.77888G>T	P.G25963V
XH_P88	2	179433990	179433990	Silent	SNV	T	C	C	TTN	c.71946A>G	P.E23982E
XH_P88	2	179575356	179575356	Splice_Site	SNV	C	T	T	TTN	c.27511+6G>A	
XH_P88	2	179623733	179623733	Silent	SNV	G	A	A	TTN	c.10281C>T	P.S3427S
XH_P88	2	189872801	189872801	Missense_Mutation	SNV	C	A	A	COL3A1	c.3458C>A	P.T1153N
XH_P88	2	189872802	189872802	Silent	SNV	C	T	T	COL3A1	c.3459C>T	P.T1153T
XH_P88	2	20205608	20205608	Silent	SNV	G	A	A	MATN3	c.687C>T	P.S229S
XH_P88	2	20508157	20508157	Missense_Mutation	SNV	T	A	A	PUM2	c.539A>T	P.Q180L
XH_P88	2	238727553	238727553	Nonsense_Mutation	SNV	G	T	T	RBM44	c.1690G>T	P.E564*
XH_P88	2	32474763	32474763	Missense_Mutation	SNV	G	A	A	NLR4C	c.2170C>T	P.L724F
XH_P88	2	3816940	3816940	Missense_Mutation	SNV	C	T	T	DCDC2C	c.893C>T	P.T298I
XH_P88	2	45620165	45620165	Missense_Mutation	SNV	C	T	T	SRBD1	c.2617G>A	P.E873K
XH_P88	2	49191035	49191035	Missense_Mutation	SNV	C	T	T	FSHR	c.925G>A	P.G309S
XH_P88	2	55571557	55571557	Missense_Mutation	SNV	C	T	T	CCDC88A	c.1135G>A	P.E379K
XH_P88	2	69741736	69741736	Missense_Mutation	SNV	G	T	T	AAK1	c.1643C>A	P.A548D
XH_P88	2	85781327	85781327	Silent	SNV	T	C	C	GGCX	c.828A>G	P.R276R
XH_P88	2	88425811	88425811	Missense_Mutation	SNV	C	T	T	FABP1	c.124G>A	P.V42M
XH_P88	2	96585666	96585666	Missense_Mutation	SNV	A	G	G	ANKRD36C	c.2323T>C	P.S775P
XH_P88	2	99012962	99012962	Nonsense_Mutation	SNV	C	A	A	CNGA3	c.1275C>A	P.Y425*
XH_P88	20	44750900	44750900	Silent	SNV	G	A	A	CD40	c.159G>A	P.E53E
XH_P88	20	44751329	44751329	Missense_Mutation	SNV	A	T	T	CD40	c.337A>T	P.S113C
XH_P88	20	44756876	44756876	Splice_Site	SNV	G	C	C	CD40	c.658+1G>C	
XH_P88	20	9389735	9389735	Missense_Mutation	SNV	C	T	T	PLCB4	c.1870C>T	P.P624S
XH_P88	21	33694217	33694217	Missense_Mutation	SNV	C	T	T	URB1	c.5378G>A	P.R1793Q
XH_P88	21	45113111	45113111	Silent	SNV	G	A	A	RRP1B	c.2124G>A	P.T708T
XH_P88	21	45855099	45855099	Missense_Mutation	SNV	C	T	T	TRPM2	c.4210C>T	P.R1404W
XH_P88	21	45947324	45947324	Missense_Mutation	SNV	G	A	A	TSPPEAR	c.796C>T	P.R266C
XH_P88	22	21400327	21400327	Missense_Mutation	SNV	G	T	T	LRRC74B	c.52G>T	P.A18S
XH_P88	22	24237129	24237223	Frame_Shift_Del	INDEL	GGCGCGGCC	-	-	MIF	GGCGCGCGGCC	P.V95fs
XH_P88	22	26860467	26860467	Missense_Mutation	SNV	C	A	A	HPS4	c.1129G>T	P.A377S
XH_P88	22	31061551	31061551	Splice_Site	SNV	C	A	A	SLC35E4	c.*2+5C>A	
XH_P88	22	41536168	41536168	Silent	SNV	G	A	A	EP300	c.1785G>A	P.P595P
XH_P88	3	108160048	108160048	Silent	SNV	G	A	A	MYH15	c.2775C>T	P.I925I
XH_P88	3	108160050	108160050	Missense_Mutation	SNV	T	C	C	MYH15	c.2773A>G	P.I925V
XH_P88	3	108324283	108324283	Splice_Site	SNV	G	T	T	DZIP3	c.30G>T	P.V10V
XH_P88	3	119134348	119134348	Missense_Mutation	SNV	T	A	A	ARHGAP31	c.3572T>A	P.M1191K
XH_P88	3	119134349	119134349	Missense_Mutation	SNV	G	A	A	ARHGAP31	c.3573G>A	P.M1191I
XH_P88	3	121417093	121417093	Silent	SNV	C	T	T	GOLGB1	c.2277G>A	P.K759K
XH_P88	3	125216218	125216218	Silent	SNV	C	T	T	SNX4	c.564G>A	P.K188K
XH_P88	3	130282481	130282481	Missense_Mutation	SNV	G	A	A	COL6A6	c.634G>A	P.G212R
XH_P88	3	148563260	148563260	Silent	SNV	C	T	T	CPB1	c.828C>T	P.A276A
XH_P88	3	154147088	154147088	Missense_Mutation	SNV	G	A	A	GPR149	c.317C>T	P.T106I
XH_P88	3	160786599	160786599	Frame_Shift_Ins	INDEL	-	T	T	PPM1L	c.357dupT	P.G120fs
XH_P88	3	173997424	173997424	Missense_Mutation	SNV	A	C	C	NLGN1	c.1633A>C	P.N545H
XH_P88	3	18457488	18457488	Splice_Site	SNV	T	A	A	SATB1	c.515+11A>T	
XH_P88	3	18457489	18457489	Splice_Site	SNV	C	A	A	SATB1	c.515+10G>T	
XH_P88	3	193031973	193031973	Missense_Mutation	SNV	A	T	T	ATP13A5	c.2168T>A	P.L723H
XH_P88	3	38739467	38739467	Nonsense_Mutation	SNV	C	T	T	SCN10A	c.5241G>A	P.W1747*
XH_P88	3	46783946	46783946	Missense_Mutation	SNV	G	T	T	PRSS45	c.581C>A	P.T194N
XH_P88	3	49160605	49160605	Missense_Mutation	SNV	G	T	T	LAMB2	c.4184C>A	P.A1395D
XH_P88	3	52090020	52090020	Missense_Mutation	SNV	C	A	A	DUSP7	c.363G>T	P.K121N
XH_P88	3	66432743	66432743	Silent	SNV	G	C	C	LRIG1	c.2571C>G	P.V857V
XH_P88	3	67053698	67053698	Missense_Mutation	SNV	T	G	G	KBTBD8	c.307T>G	P.L103V
XH_P88	4	11401021	11401021	Missense_Mutation	SNV	C	A	A	HS3ST1	c.609G>T	P.W203C
XH_P88	4	140187829	140187829	Missense_Mutation	SNV	T	A	A	MGARP	c.647A>T	P.E216V
XH_P88	4	166910546	166910546	Silent	SNV	C	T	T	TL1	c.183C>T	P.G61G
XH_P88	4	178260931	178260931	Splice_Site	SNV	T	C	C	NEIL3	c.628-6T>C	
XH_P88	4	17839410	17839410	Missense_Mutation	SNV	T	C	C	NCAPG	c.2452T>C	P.S818P
XH_P88	4	187003732	187003732	Missense_Mutation	SNV	C	G	G	TLR3	c.892C>G	P.P298A
XH_P88	4	2835446	2835446	Missense_Mutation	SNV	G	T	T	SH3BP2	c.1571G>T	P.G524V
XH_P88	4	38830610	38830610	Missense_Mutation	SNV	T	A	A	TLR6	c.485A>T	P.D162V
XH_P88	4	54232039	54232039	Missense_Mutation	SNV	C	A	A	SCFD2	c.70G>T	P.A24S
XH_P88	4	54967894	54967894	Missense_Mutation	SNV	C	A	A	GSX2	c.720C>A	P.N240K
XH_P88	4	69968609	69968609	Nonsense_Mutation	SNV	G	T	T	UGT2B7	c.955G>T	P.E319*
XH_P88	4	69968610	69968610	Missense_Mutation	SNV	A	T	T	UGT2B7	c.956A>T	P.E319V
XH_P88	5	1034382	1034382	Silent	SNV	C	T	T	NKD2	c.363C>T	P.D121D
XH_P88	5	13820584	13820584	Missense_Mutation	SNV	G	A	A	DNAH5	c.6712C>T	P.H2238Y
XH_P88	5	13820585	13820585	Missense_Mutation	SNV	G	T	T	DNAH5	c.6711C>A	P.N2237K
XH_P88	5	140529997	140529997	Silent	SNV	G	C	C	PCDH6	c.159G>C	P.L53L
XH_P88	5	141334989	141334989	Missense_Mutation	SNV	G	T	T	PCDH12	c.2428C>A	P.P810T
XH_P88	5	149398241	149398241	Missense_Mutation	SNV	G	T	T	HMGXB3	c.1022G>T	P.G341V
XH_P88	5	156750990	156750990	Missense_Mutation	SNV	C	A	A	CYFIP2	c.1733C>A	P.T578N
XH_P88	5	156750991	156750991	Silent	SNV	C	A	A	CYFIP2	c.1734C>A	P.T578T
XH_P88	5	169671	169671	Missense_Mutation	SNV	C	A	A	PLEKHG4B	c.2625C>A	P.H875Q
XH_P88	5	169672	169672	Missense_Mutation	SNV	T	A	A	PLEKHG4B	c.2626T>A	P.C876S
XH_P88	5	176024694	176024694	Missense_Mutation	SNV	A	T	T	GPRIN1	c.2142T>A	P.S714R
XH_P88	5	178559221	178559221	Splice_Site	SNV	T	A	A	ADAMTS2	c.2290+10A>T	
XH_P88	5	179300230	179300230	Silent	SNV	G	A	A	TBC1D9B	c.2205C>T	P.V735V
XH_P88	5	21854773	21854773	Splice_Site	SNV	A	C	C	CDH12	c.646+7T>G	
XH_P88	5	36195278	36195278	Missense_Mutation	SNV	C	T	T	NADK2	c.1297G>A	P.D433N
XH_P88	5	5200330	5200330	Nonsense_Mutation	SNV	G	T	T	ADAMTS16	c.1399G>T	P.G467*
XH_P88	5	53815148	53815148	Nonsense_Mutation	SNV	C	T	T	SNX18	c.1366C>T	P.Q456*
XH_P88	6	130762087	130762087	Silent	SNV	A	C	C	TMEM200A	c.520A>C	P.R174R
XH_P88	6	132030542	132030542	Missense_Mutation	SNV	G	A	A	CTAGE9	c.1616C>T	P.P539L
XH_P88	6	132722495	132722495	Missense_Mutation	SNV	G	T	T	MOXD1	c.71C>A	P.T24N
XH_P88	6	152763225	152763225	Silent	SNV	C	T	T	SYNE1	c.4014G>A	P.Q1338Q
XH_P88	6	159654096	159654096	Missense_Mutation	SNV	C	T	T	FNDC1	c.2552C>T	P.S851L
XH_P88	6	168315349	168315349	Nonsense_Mutation	SNV	G	T	T	AFDN	c.2209G>T	P.E737*
XH_P88	6	168315350	168315350	Missense_Mutation	SNV	A	T	T	AFDN	c.2210A>T	P.E737V
XH_P88	6	17837213	17837213	Missense_Mutation	SNV	T	A	A	KIF13A	c.1051A>T	P.R351W

XH_P88	6	27420357	27420357	Silent	SNV	A	T	T	ZNF184	c.981T>A	P.I327I
XH_P88	6	27776035	27776035	Missense_Mutation	SNV	G	T	T	HIST1H2AI	c.48G>T	P.K16N
XH_P88	6	27776036	27776036	Missense_Mutation	SNV	A	T	T	HIST1H2AI	c.49A>T	P.T175
XH_P88	6	27835267	27835267	Missense_Mutation	SNV	G	A	A	HIST1H1B	c.41C>T	P.P14L
XH_P88	6	28227194	28227194	Silent	SNV	C	T	T	NKAPL	c.45C>T	P.G15G
XH_P88	6	33636882	33636882	Missense_Mutation	SNV	A	T	T	ITPR3	c.2138A>T	P.Q713L
XH_P88	6	36931221	36931221	Missense_Mutation	SNV	A	C	C	PI16	c.1103A>C	P.E368A
XH_P88	6	42146559	42146559	Missense_Mutation	SNV	C	T	T	GUCA1A	c.371C>T	P.P124L
XH_P88	6	57006817	57006817	Missense_Mutation	SNV	G	C	C	ZNF451	c.928G>C	P.D310H
XH_P88	7	100170519	100170519	Missense_Mutation	SNV	C	T	T	SAP25	c.181G>A	P.G61R
XH_P88	7	100417180	100417180	Splice_Site	SNV	C	T	T	EPHB4	c.1296G>A	P.E432E
XH_P88	7	101200674	101200674	Missense_Mutation	SNV	G	T	T	COL26A1	c.1189G>T	P.V397F
XH_P88	7	103018905	103018905	Silent	SNV	A	T	T	SLC26A5	c.1677T>A	P.T559T
XH_P88	7	103018906	103018906	Missense_Mutation	SNV	G	T	T	SLC26A5	c.1676C>A	P.T559N
XH_P88	7	107336415	107336415	Missense_Mutation	SNV	T	G	G	SLC26A4	c.1475T>G	P.L492R
XH_P88	7	127014210	127014210	Nonsense_Mutation	SNV	C	A	A	ZNF800	c.1180G>T	P.E394*
XH_P88	7	128356939	128356939	Missense_Mutation	SNV	G	T	T	FAM71F1	c.322G>T	P.V108L
XH_P88	7	128494187	128494187	Missense_Mutation	SNV	G	A	A	FLNC	c.6545G>A	P.G2182E
XH_P88	7	128544101	128544101	Splice_Site	SNV	G	A	A	KCP	c.654+8C>T	
XH_P88	7	150417944	150417944	Silent	SNV	C	T	T	GIMAP1	c.852C>T	P.G284G
XH_P88	7	150691042	150691042	Missense_Mutation	SNV	G	C	C	NOS3	c.151G>C	P.E51Q
XH_P88	7	150691043	150691043	Missense_Mutation	SNV	A	T	T	NOS3	c.152A>T	P.E51V
XH_P88	7	21945909	21945909	Missense_Mutation	SNV	C	G	G	CDCA7L	c.817G>C	P.G273R
XH_P88	7	27150189	27150189	Missense_Mutation	SNV	A	C	C	HOXA3	c.71T>G	P.F24C
XH_P88	7	44146455	44146455	Missense_Mutation	SNV	C	A	A	AEBP1	c.564C>A	P.S188R
XH_P88	7	4827912	4827912	Frame_Shift_Del	INDEL	G	-	-	AP521	c.1583delG	P.G528fs
XH_P88	7	57522799	57522799	Missense_Mutation	SNV	G	C	C	ZNF716	c.187G>C	P.D63H
XH_P88	7	66103932	66103932	Nonsense_Mutation	SNV	G	T	T	KCTD7	c.583G>T	P.E195*
XH_P88	7	75066792	75066792	Splice_Site	SNV	C	A	A	POM121C	c.480+1G>T	
XH_P88	7	86416177	86416177	Missense_Mutation	SNV	C	G	G	GRM3	c.1069C>G	P.Q357E
XH_P88	7	99569424	99569424	Silent	SNV	C	T	T	AZGP1	c.282G>A	P.E94E
XH_P88	8	107758091	107758091	Splice_Site	SNV	G	T	T	OXR1	c.2489+1G>T	
XH_P88	8	118174031	118174031	Missense_Mutation	SNV	A	T	T	SLC30A8	c.480A>T	P.Q160H
XH_P88	8	133184947	133184947	Splice_Site	SNV	G	T	T	KCNQ3	c.685-7C>A	
XH_P88	8	134237750	134237750	Missense_Mutation	SNV	C	A	A	WISP1	c.467C>A	P.A156D
XH_P88	8	143356162	143356162	Missense_Mutation	SNV	C	T	T	TSNARE1	c.769G>A	P.A257T
XH_P88	8	144891036	144891036	Missense_Mutation	SNV	G	T	T	SCRIB	c.1858C>A	P.P620T
XH_P88	8	2975983	2975983	Missense_Mutation	SNV	G	A	A	CSMD1	c.6368C>T	P.P2123L
XH_P88	8	39624489	39624489	Frame_Shift_Ins	INDEL	-	C	C	ADAM2	c.1327_1328insG	P.S443fs
XH_P88	8	56015172	56015172	Missense_Mutation	SNV	T	A	A	XKR4	c.124T>A	P.S42T
XH_P88	8	77768080	77768080	Missense_Mutation	SNV	G	T	T	ZFH4	c.8923G>T	P.V2975L
XH_P88	8	88885780	88885780	Silent	SNV	G	A	A	DCAF4L2	c.420C>T	P.S140S
XH_P88	8	91946536	91946536	Missense_Mutation	SNV	T	C	C	NECAB1	c.698T>C	P.L233P
XH_P88	8	95655530	95655530	Splice_Site	SNV	G	T	T	ESRP1	c.262-1G>T	
XH_P88	9	101911461	101911461	Splice_Site	SNV	G	A	A	TGFB1	c.1387-1G>A	
XH_P88	9	104499915	104499915	Missense_Mutation	SNV	C	A	A	GRIN3A	c.347G>T	P.G116V
XH_P88	9	119188315	119188315	Missense_Mutation	SNV	T	A	A	ASTN2	c.991A>T	P.S331C
XH_P88	9	125681880	125681880	Missense_Mutation	SNV	T	G	G	ZBTB26	c.334A>C	P.M112L
XH_P88	9	130913917	130913917	Missense_Mutation	SNV	G	C	C	LCN2	c.276G>C	P.R92S
XH_P88	9	130913918	130913918	Nonsense_Mutation	SNV	A	T	T	LCN2	c.277A>T	P.K93*
XH_P88	9	133339555	133339555	Splice_Site	SNV	G	T	T	ASS1	c.420+1G>T	
XH_P88	9	135251398	135251398	Silent	SNV	T	A	A	TTF1	c.1077A>T	P.G359G
XH_P88	9	138713496	138713496	Missense_Mutation	SNV	G	A	A	CAMSAP1	c.3011C>T	P.A1004V
XH_P88	9	18829846	18829846	Missense_Mutation	SNV	C	T	T	ADAMTSL1	c.4120C>T	P.P1374S
XH_P88	9	2622244	2622244	Missense_Mutation	SNV	C	A	A	VLDLR	c.55C>A	P.P19T
XH_P88	9	428358	428358	Splice_Site	SNV	C	T	T	DOCK8	c.4039-4C>T	
XH_P88	9	88938747	88938747	Missense_Mutation	SNV	G	A	A	ZCCHC6	c.1918C>T	P.L640F
XH_P88	9	88938748	88938748	Silent	SNV	G	A	A	ZCCHC6	c.1917C>T	P.S639S
XH_P88	9	90537428	90537428	Missense_Mutation	SNV	T	A	A	SPATA31C1	c.2606T>A	P.M869K
XH_P88	9	96422826	96422826	Missense_Mutation	SNV	C	T	T	PHF2	c.1682C>T	P.P561L
XH_P88	X	102471131	102471131	Missense_Mutation	SNV	C	T	T	BEX4	c.50C>T	P.A17V
XH_P88	X	122747904	122747904	Missense_Mutation	SNV	C	T	T	THOC2	c.4448G>A	P.R1483K
XH_P88	X	139174569	139174569	Missense_Mutation	SNV	G	A	A	LOC389895	c.668G>A	P.R223Q
XH_P88	X	148584976	148584976	Missense_Mutation	SNV	C	T	T	ID5	c.284G>A	P.R95K
XH_P88	X	15268595	15268595	Missense_Mutation	SNV	A	C	C	ASB9	c.525T>G	P.C175W
XH_P88	X	55650168	55650168	Nonsense_Mutation	SNV	T	A	A	FOXR2	c.24T>A	P.C8*
XH_P88	X	62944563	62944563	Missense_Mutation	SNV	G	A	A	ARHGEF9	c.38C>T	P.A13V
XH_P88	X	83128474	83128474	Missense_Mutation	SNV	A	T	T	CYLC1	c.758A>T	P.Q253L
XH_P88	X	85950118	85950118	Silent	SNV	C	T	T	DACH2	c.828C>T	P.G276G
XH_P88	X	91132824	91132824	Missense_Mutation	SNV	G	C	C	PCDH11X	c.1585G>C	P.D529H
XH_P89	1	161206390	161206390	Splice_Site	SNV	T	A	A	NR1I3	c.-33-2A>T	
XH_P89	1	16260350	16260350	Missense_Mutation	SNV	A	C	C	SPEN	c.7615A>C	P.M2539L
XH_P89	1	16376171	16376171	Silent	SNV	T	G	G	CLCNKB	c.840T>G	P.P280P
XH_P89	1	181745336	181745336	Missense_Mutation	SNV	G	A	A	CACNA1E	c.5239G>A	P.V1747I
XH_P89	1	33772767	33772767	Missense_Mutation	SNV	A	G	G	A3GALT2	c.623T>C	P.F208S
XH_P89	11	113076860	113076860	Missense_Mutation	SNV	C	T	T	NCAM1	c.586C>T	P.R196W
XH_P89	11	119210279	119210279	Missense_Mutation	SNV	T	A	A	C1QTNF5	c.494A>T	P.Q165L
XH_P89	11	120976682	120976682	Splice_Site	SNV	A	T	T	TECTA	c.198+9A>T	
XH_P89	11	64023855	64023855	Nonsense_Mutation	SNV	A	T	T	PLCB3	c.706A>T	P.K236*
XH_P89	11	64419065	64419065	Missense_Mutation	SNV	A	C	C	NRXN2	c.2580T>G	P.I860M
XH_P89	11	6647259	6647259	Missense_Mutation	SNV	T	A	A	DCHS1	c.6623A>T	P.Y2208F
XH_P89	12	110765463	110765463	Silent	SNV	A	C	C	ATP2A2	c.736A>C	P.R246R
XH_P89	12	56565698	56565698	Silent	SNV	G	A	A	SMARCC2	c.1950C>T	P.D650D
XH_P89	12	57650248	57650248	Silent	SNV	C	G	G	R3HDM2	c.2556G>C	P.L852L
XH_P89	13	113798235	113798235	Silent	SNV	C	T	T	F10	c.573C>T	P.S191S
XH_P89	14	102027982	102027982	Missense_Mutation	SNV	C	T	T	DIO3	c.149C>T	P.P50L
XH_P89	14	21560436	21560442	Frame_Shift_Del	INDEL	AGGCCCGG	-	-	ZNF219	c.1020delICGG	P.G339fs
XH_P89	14	26917316	26917316	Missense_Mutation	SNV	G	C	C	NOVA1	c.1373C>G	P.S458C
XH_P89	14	59014668	59014668	Missense_Mutation	SNV	G	T	T	KIAA0586	c.4909G>T	P.A1637S
XH_P89	15	52416756	52416756	Missense_Mutation	SNV	A	G	G	GNB5	c.964T>C	P.F322L
XH_P89	15	90193105	90193105	Missense_Mutation	SNV	A	C	C	KIF7	c.396T>G	P.D132E
XH_P89	16	1497548	1497548	Missense_Mutation	SNV	G	C	C	CLCN7	c.2023C>G	P.L675V
XH_P89	16	65015974	65015974	Silent	SNV	A	G	G	CDH11	c.1230T>C	P.P410P
XH_P89	16	72033670	72033670	Missense_Mutation	SNV	T	G	G	PKD1L3	c.208A>C	P.I70L
XH_P89	17	39503398	39503398	Missense_Mutation	SNV	T	C	C	KRT33A	c.665A>G	P.N222S
XH_P89	17	73518290	73518304	Missense_Mutation	INDEL	CTGGCGGGA	-	-	TSEN54	c.44delGCTGGCGG	P.S377_Y381del
XH_P89	17	7577029	7577029	Frame_Shift_Ins	INDEL	-	CT	CT	TP53	c.907_908dupAG	P.S303fs
XH_P89	18	67531610	67531610	Silent	SNV	T	A	A	CD226	c.951A>T	P.T317T

XH_P89	19	12719966	12719966	Splice_Site	SNV	A	C	C	ZNF490	c.162+6T>G	
XH_P89	19	13919940	13919940	Missense_Mutation	SNV	G	C	C	ZSWIM4	c.918G>C	P.M306I
XH_P89	19	48967551	48967551	Missense_Mutation	SNV	T	G	G	KCNJ14	c.828T>C	P.H276Q
XH_P89	19	8154849	8154849	Splice_Site	SNV	C	T	T	FBN3	c.6185-6G>A	
XH_P89	2	241500140	241500140	Splice_Site	SNV	G	A	A	ANKMY1	c.220+8C>T	
XH_P89	2	27455993	27455993	Missense_Mutation	SNV	T	G	G	CAD	c.2787T>G	P.D929E
XH_P89	2	45233332	45233332	Missense_Mutation	SNV	T	G	G	SIX2	c.853A>C	P.N285H
XH_P89	20	2463830	2463830	Missense_Mutation	SNV	T	G	G	ZNF343	c.1777A>C	P.I593L
XH_P89	22	17589871	17589871	Nonsense_Mutation	SNV	G	T	T	IL17RA	c.1660G>T	P.E554*
XH_P89	22	21380318	21380318	Missense_Mutation	SNV	A	C	C	P2RX6	c.925A>C	P.I309L
XH_P89	3	136574482	136574482	Missense_Mutation	SNV	T	C	C	SLC35G2	c.1180T>C	P.Y394H
XH_P89	3	15276611	15276611	Missense_Mutation	SNV	C	T	T	CAPN7	c.1366C>T	P.P456S
XH_P89	3	183860876	183860876	Missense_Mutation	SNV	G	T	T	EIF2B5	c.1691G>T	P.G564V
XH_P89	3	49152796	49152796	Splice_Site	SNV	T	G	G	USP19	c.1883-2A>C	
XH_P89	3	49941015	49941015	Missense_Mutation	SNV	A	C	C	MST1R	c.28T>G	P.S10A
XH_P89	3	50005251	50005251	Silent	SNV	A	G	G	RBM6	c.393A>G	P.P131P
XH_P89	4	103265814	103265814	Silent	SNV	G	A	A	SLC39A8	c.6C>T	P.A2A
XH_P89	4	152095900	152095900	Missense_Mutation	SNV	T	G	G	SH3D19	c.616A>C	P.I206L
XH_P89	5	454122	454122	Missense_Mutation	SNV	T	G	G	EXOC3	c.1002T>G	P.N334K
XH_P89	5	5190177	5190177	Missense_Mutation	SNV	G	A	A	ADAMTS16	c.1141G>A	P.D381N
XH_P89	6	160176086	160176086	Missense_Mutation	SNV	G	A	A	WTAP	c.634G>A	P.D212N
XH_P89	7	27150189	27150189	Missense_Mutation	SNV	A	C	C	HOXA3	c.71T>G	P.D24C
XH_P89	7	5521463	5521463	Missense_Mutation	SNV	A	C	C	FBXL18	c.2100T>G	P.D700E
XH_P89	7	64363779	64363779	Silent	SNV	C	T	T	ZNF273	c.84C>T	P.L28L
XH_P89	8	104898350	104898350	Missense_Mutation	SNV	G	A	A	RIMS2	c.1523G>A	P.R508H
XH_P89	8	145626954	145626954	Missense_Mutation	SNV	C	A	A	CPSF1	c.176G>T	P.G59V
XH_P89	8	41791689	41791689	Missense_Mutation	SNV	G	C	C	KAT6A	c.4049C>G	P.S1350C
XH_P89	9	133223943	133223943	Missense_Mutation	SNV	A	C	C	HMCN2	c.2362A>C	P.I788L
XH_P89	9	21971096	21971096	Missense_Mutation	SNV	C	A	A	CDKN2A	c.305G>T	P.G102V
XH_P89	9	97062941	97062941	Silent	SNV	A	C	C	ZNF169	c.528A>C	P.S176S
XH_P89	X	139866418	139866418	Missense_Mutation	SNV	A	T	T	CDR1	c.114T>A	P.S38R
XH_P89	X	147744069	147744069	Missense_Mutation	SNV	T	C	C	AF2	c.809T>C	P.L270P
XH_P89	X	29972636	29972636	Splice_Site	SNV	C	A	A	IL1RAPL1	c.1202-3C>A	
XH_P89	X	30260718	30260718	Missense_Mutation	SNV	C	A	A	MAGEB4	c.466C>A	P.Q156K
XH_P89	X	54784819	54784819	Missense_Mutation	SNV	A	T	T	ITIH6	c.1688T>A	P.L563H
XH_P90	1	111434971	111434971	Missense_Mutation	SNV	G	A	A	CD53	c.68G>A	P.C23Y
XH_P90	1	145459672	145459672	Missense_Mutation	SNV	C	T	T	POLR3GL	c.236G>A	P.R79Q
XH_P90	1	151018363	151018363	Splice_Site	SNV	C	T	T	BNIP1	c.692+4C>T	
XH_P90	1	161954007	161954007	Missense_Mutation	SNV	A	C	C	OLFML2B	c.1714T>G	P.Y572D
XH_P90	1	16376171	16376171	Silent	SNV	T	G	G	CLCNKB	c.840T>G	P.P280P
XH_P90	1	19519982	19519982	Missense_Mutation	SNV	G	C	C	UBR4	c.1088C>G	P.P363R
XH_P90	1	202097605	202097605	Missense_Mutation	SNV	A	C	C	GPR37L1	c.1367A>C	P.K456T
XH_P90	1	203678472	203678472	Missense_Mutation	SNV	A	C	C	ATP2B4	c.1601A>C	P.K534T
XH_P90	1	229438743	229438743	Splice_Site	SNV	T	G	G	RAB4A	c.*12+7T>G	
XH_P90	1	27426927	27426927	Silent	SNV	T	G	G	SLC9A1	c.2319A>C	P.G773G
XH_P90	1	7805963	7805963	Missense_Mutation	SNV	T	G	G	CAMTA1	c.4429T>G	P.S1477A
XH_P90	10	123274774	123274774	Missense_Mutation	SNV	A	G	G	FGFR2	c.1144T>C	P.C382R
XH_P90	10	133962974	133962974	Missense_Mutation	SNV	A	C	C	JAKMIP3	c.1907A>C	P.K636T
XH_P90	10	17147527	17147527	Missense_Mutation	SNV	A	G	G	CUBN	c.1159T>C	P.Y387H
XH_P90	10	24832441	24832441	Silent	SNV	T	G	G	KIAA1217	c.4242T>G	P.V1414V
XH_P90	10	43678854	43678854	Missense_Mutation	SNV	A	C	C	CSGALNACT2	c.1493A>C	P.Q498P
XH_P90	10	45936827	45936827	Missense_Mutation	SNV	C	G	G	ALOX5	c.1221C>G	P.I407M
XH_P90	10	50828577	50828577	Missense_Mutation	SNV	A	C	C	CHAT	c.262A>C	P.N88H
XH_P90	10	74994584	74994584	Silent	SNV	A	C	C	FAM149B1	c.1362A>C	P.A454A
XH_P90	11	1027746	1027746	Frame_Shift_Ins	INDEL	-	A	A	MUC6	c.1919dupT	P.P641fs
XH_P90	11	118348884	118348884	Missense_Mutation	SNV	T	G	G	KMT2A	c.3537T>G	P.F1179L
XH_P90	11	2154778	2154778	Missense_Mutation	SNV	C	G	G	IGF2	c.443G>C	P.R148T
XH_P90	11	3819102	3819102	Missense_Mutation	SNV	T	G	G	PGAP2	c.29T>G	P.V10G
XH_P90	11	57982422	57982422	Missense_Mutation	SNV	A	C	C	OR151	c.206A>C	P.H69P
XH_P90	11	59554595	59554595	Missense_Mutation	SNV	C	G	G	STX3	c.200C>G	P.P67R
XH_P90	11	62985044	62985044	Splice_Site	SNV	T	C	C	SLC22A25	c.661+9A>G	
XH_P90	11	64029464	64029464	Missense_Mutation	SNV	A	C	C	PLCB3	c.1954A>C	P.T652P
XH_P90	11	65652592	65652592	Missense_Mutation	SNV	T	G	G	FIBP	c.712A>C	P.X238Q
XH_P90	11	7718249	7718249	Splice_Site	SNV	T	G	G	OVCH2	c.1016+7A>C	
XH_P90	11	78369212	78369212	Missense_Mutation	SNV	A	C	C	TENM4	c.8201T>G	P.V2734G
XH_P90	11	865607	865607	Missense_Mutation	SNV	A	C	C	TSPAN4	c.425A>C	P.Q142P
XH_P90	11	94862519	94862519	Silent	SNV	C	T	T	ENDOD1	c.1279C>T	P.L427L
XH_P90	12	133147929	133147929	Missense_Mutation	SNV	T	G	G	FBRSL1	c.1250T>G	P.F417C
XH_P90	12	33592456	33592456	Nonsense_Mutation	SNV	A	C	C	SYT10	c.2T>G	P.M17C
XH_P90	12	47629129	47629129	Missense_Mutation	SNV	A	C	C	PCED1B	c.283A>C	P.T95P
XH_P90	12	54764756	54764756	Missense_Mutation	SNV	A	C	C	ZNF385A	c.789T>G	P.C263W
XH_P90	13	111767891	111767891	Missense_Mutation	SNV	A	C	C	ARHGEF7	c.18A>C	P.Q6H
XH_P90	13	41507867	41507867	Silent	SNV	T	G	G	ELF1	c.1482A>C	P.G494G
XH_P90	13	45149827	45149827	Missense_Mutation	SNV	G	C	C	TSC22D1	c.384C>G	P.N128K
XH_P90	13	47469856	47469856	Silent	SNV	T	G	G	HTR2A	c.186A>C	P.S62S
XH_P90	13	86368907	86368907	Silent	SNV	A	T	T	SLITRK6	c.1737T>A	P.T579T
XH_P90	13	98642482	98642482	Splice_Site	SNV	T	G	G	IPO5	c.618+6T>G	
XH_P90	14	105268323	105268323	Silent	SNV	G	A	A	ZBTB42	c.789G>A	P.P263P
XH_P90	14	77236312	77236312	Missense_Mutation	SNV	A	C	C	VASH1	c.316A>C	P.I106L
XH_P90	15	34393811	34393811	Missense_Mutation	SNV	A	C	C	EMC7	c.230T>G	P.F77C
XH_P90	15	34393812	34393812	Missense_Mutation	SNV	A	C	C	EMC7	c.229T>G	P.F77V
XH_P90	15	41813089	41813089	Missense_Mutation	SNV	T	G	G	RPAP1	c.3295A>C	P.T1099P
XH_P90	15	68504099	68504099	Missense_Mutation	SNV	T	G	G	CLN6	c.400A>C	P.N134H
XH_P90	16	16251586	16251586	Silent	SNV	T	G	G	ABCC6	c.3816A>C	P.L1272L
XH_P90	16	19651383	19651383	Missense_Mutation	SNV	G	A	A	C16orf62	c.1811G>A	P.R604Q
XH_P90	16	2012870	2012870	Missense_Mutation	SNV	A	C	C	RP52	c.416T>G	P.L139R
XH_P90	16	28997038	28997038	Silent	SNV	C	G	G	LAT	c.105C>G	P.S35S
XH_P90	16	30975420	30975420	Missense_Mutation	SNV	A	C	C	SETD1A	c.645A>C	P.E215D
XH_P90	16	4747103	4747103	Frame_Shift_Del	INDEL	G	-	-	ANKS3	c.1576delC	P.Q526fs
XH_P90	16	67231792	67231792	Silent	SNV	G	A	A	E2F4	c.1104G>A	P.L368L
XH_P90	16	88780134	88780134	Missense_Mutation	SNV	A	C	C	CTU2	c.953A>C	P.Y318S
XH_P90	16	88780136	88780136	Missense_Mutation	SNV	A	C	C	CTU2	c.955A>C	P.N319H
XH_P90	16	89782969	89782969	Missense_Mutation	SNV	T	G	G	VPS9D1	c.332A>C	P.H111P
XH_P90	17	28548781	28548781	Missense_Mutation	SNV	T	G	G	SLC6A4	c.196A>C	P.T66P
XH_P90	17	29298395	29298395	Missense_Mutation	SNV	C	A	A	RNF135	c.304C>A	P.P102T
XH_P90	17	2996124	2996124	Missense_Mutation	SNV	T	G	G	OR1D2	c.167A>C	P.H56P
XH_P90	17	3336741	3336741	Missense_Mutation	SNV	T	G	G	OR1E2	c.395A>C	P.Y132S
XH_P90	17	38519508	38519508	Missense_Mutation	SNV	T	G	G	GJD3	c.560A>C	P.K187T

XH_P90	17	38519847	38519847	Missense_Mutation	SNV	T	G	G	GJD3	c.221A>C	P.H74P
XH_P90	17	4689541	4689541	Missense_Mutation	SNV	A	C	C	VMO1	c.107T>G	P.I36S
XH_P90	17	48193356	48193356	Splice_Site	SNV	C	A	A	SAMD14	c.587+11G>T	
XH_P90	17	650076	650076	Missense_Mutation	SNV	T	G	G	GEMIN4	c.1207A>C	P.T403P
XH_P90	17	66536085	66536085	Nonsense_Mutation	SNV	A	C	C	FAM20A	c.828T>G	P.Y276*
XH_P90	17	67298850	67298850	Splice_Site	SNV	A	C	C	ABCA5	c.1119+9T>G	
XH_P90	17	72920903	72920903	Missense_Mutation	SNV	A	C	C	OTOP2	c.176A>C	P.D59A
XH_P90	17	72920905	72920905	Missense_Mutation	SNV	A	C	C	OTOP2	c.178A>C	P.T60P
XH_P90	17	73914239	73914239	Splice_Site	SNV	A	C	C	FBF1	c.2246+4T>G	
XH_P90	17	76219596	76219596	Missense_Mutation	SNV	A	T	T	BIRC5	c.459A>T	P.K153N
XH_P90	17	79912149	79912149	Missense_Mutation	SNV	A	C	C	NOTUM	c.1167T>G	P.H389Q
XH_P90	18	31320169	31320169	Nonsense_Mutation	SNV	T	G	G	ASXL3	c.2801T>G	P.L934*
XH_P90	19	1037677	1037677	Silent	SNV	A	C	C	CNN2	c.675A>C	P.G225G
XH_P90	19	14938887	14938887	Missense_Mutation	SNV	T	G	G	OR7A5	c.167A>C	P.H56P
XH_P90	19	14952523	14952523	Missense_Mutation	SNV	T	G	G	OR7A10	c.167A>C	P.H56P
XH_P90	19	14992001	14992001	Missense_Mutation	SNV	T	G	G	OR7A17	c.167A>C	P.H56P
XH_P90	19	15752277	15752277	Missense_Mutation	SNV	C	G	G	CYP4F3	c.52C>G	P.P18A
XH_P90	19	18709296	18709296	Missense_Mutation	SNV	T	G	G	CRLF1	c.643A>C	P.N215H
XH_P90	19	20044152	20044152	Missense_Mutation	SNV	T	G	G	ZNF93	c.388T>G	P.Y130D
XH_P90	19	35760526	35760526	Missense_Mutation	SNV	T	G	G	USF2	c.152T>G	P.I51S
XH_P90	19	3765218	3765218	Missense_Mutation	SNV	A	C	C	MRPL54	c.173A>C	P.D58A
XH_P90	19	54625277	54625277	Missense_Mutation	SNV	A	C	C	PRPF31	c.277A>C	P.I93L
XH_P90	19	54974342	54974342	Missense_Mutation	SNV	T	G	G	LENG9	c.368A>C	P.H123P
XH_P90	19	55142731	55142731	Missense_Mutation	SNV	T	A	A	LILRB1	c.44T>A	P.L15Q
XH_P90	19	55703045	55703045	Silent	SNV	G	A	A	PTPRH	c.1788C>T	P.F596F
XH_P90	19	55997795	55997795	Missense_Mutation	SNV	A	C	C	NAT14	c.93A>C	P.E31D
XH_P90	19	55997796	55997796	Missense_Mutation	SNV	A	C	C	NAT14	c.94A>C	P.N32H
XH_P90	19	56104640	56104640	Missense_Mutation	SNV	T	G	G	FIZ1	c.667A>C	P.T223P
XH_P90	19	56104642	56104642	Missense_Mutation	SNV	T	G	G	FIZ1	c.665A>C	P.H222P
XH_P90	19	58437687	58437687	Missense_Mutation	SNV	C	A	A	ZNF418	c.1925G>T	P.C642F
XH_P90	19	59028981	59028981	Silent	SNV	A	C	C	ZBTB45	c.60T>G	P.L20L
XH_P90	19	6427110	6427110	Splice_Site	SNV	T	G	G	SLC25A41	c.526+4A>C	
XH_P90	19	9064836	9064836	Missense_Mutation	SNV	G	T	T	MUC16	c.22610C>A	P.A7537D
XH_P90	19	9296624	9296624	Missense_Mutation	SNV	A	C	C	OR7D2	c.167A>C	P.H56P
XH_P90	19	9361940	9361940	Missense_Mutation	SNV	A	C	C	OR7E24	c.221A>C	P.H74P
XH_P90	2	102955417	102955417	Missense_Mutation	SNV	A	T	T	IL1RL1	c.182A>T	P.E61V
XH_P90	2	113590245	113590245	Frame_Shift_Del	INDEL	G	-	-	IL1B	c.460delC	P.Q154fs
XH_P90	2	182322441	182322441	Silent	SNV	G	T	T	ITGA4	c.60G>T	P.V20V
XH_P90	2	202545609	202545609	Missense_Mutation	SNV	T	G	G	MPP4	c.881A>C	P.D294A
XH_P90	2	207169645	207169645	Silent	SNV	T	G	G	ZDBF2	c.387T>G	P.V129V
XH_P90	2	210880812	210880812	Missense_Mutation	SNV	A	C	C	RPE	c.114A>C	P.K38N
XH_P90	2	56419831	56419831	Missense_Mutation	SNV	A	C	C	CCDC85A	c.496A>C	P.K166Q
XH_P90	2	75101556	75101556	Silent	SNV	A	C	C	HK2	c.855A>C	P.S285S
XH_P90	20	13567891	13567891	Splice_Site	SNV	A	C	C	TASP1	c.97+6T>G	
XH_P90	20	25596738	25596738	Silent	SNV	T	C	C	NANP	c.570A>G	P.T190T
XH_P90	20	33345744	33345744	Silent	SNV	C	T	T	NCOA6	c.807G>A	P.Q269Q
XH_P90	20	41385170	41385170	Missense_Mutation	SNV	T	G	G	PTPRT	c.791A>C	P.K264T
XH_P90	20	44525621	44525621	Missense_Mutation	SNV	A	C	C	CTSA	c.1160A>C	P.Q387P
XH_P90	20	47247273	47247273	Missense_Mutation	SNV	A	C	C	PREX1	c.4586T>G	P.I1529R
XH_P90	20	57766100	57766100	Missense_Mutation	SNV	C	T	T	ZNF831	c.26C>T	P.P9L
XH_P90	20	6021955	6021955	Missense_Mutation	SNV	T	G	G	LRRN4	c.1936A>C	P.T646P
XH_P90	22	24452743	24452743	Silent	SNV	T	G	G	CABIN1	c.1182T>G	P.S394S
XH_P90	22	30823263	30823263	Missense_Mutation	SNV	A	C	C	MTFP1	c.301A>C	P.N101H
XH_P90	22	42782989	42782989	Splice_Site	SNV	G	T	T	NFAM1	c.*43+6C>A	
XH_P90	22	46929778	46929778	Missense_Mutation	SNV	T	G	G	CELSR1	c.3290A>C	P.N1097T
XH_P90	22	46929779	46929779	Missense_Mutation	SNV	T	G	G	CELSR1	c.3289A>C	P.N1097H
XH_P90	22	50696698	50696698	Missense_Mutation	SNV	A	C	C	MAPK12	c.288T>G	P.D96E
XH_P90	22	51182533	51182533	Missense_Mutation	SNV	A	C	C	ACR	c.610A>C	P.I204L
XH_P90	3	133099783	133099783	Missense_Mutation	SNV	A	C	C	TMEM108	c.1228A>C	P.M410L
XH_P90	3	151598623	151598623	Missense_Mutation	SNV	A	C	C	SUCNR1	c.292A>C	P.N98H
XH_P90	3	190366340	190366340	Missense_Mutation	SNV	T	G	G	IL1RAP	c.1559T>G	P.V520G
XH_P90	3	42264865	42264865	Missense_Mutation	SNV	A	C	C	TRAK1	c.2498A>C	P.Q833P
XH_P90	3	58853539	58853539	Splice_Site	SNV	A	C	C	C3orf67	c.760+4T>G	
XH_P90	3	64085227	64085227	Missense_Mutation	SNV	T	G	G	PRICKLE2	c.2035A>C	P.N679H
XH_P90	3	71804200	71804200	Missense_Mutation	SNV	A	C	C	GPR27	c.1000A>C	P.N334H
XH_P90	3	71804201	71804201	Missense_Mutation	SNV	A	C	C	GPR27	c.1001A>C	P.N334T
XH_P90	4	108816945	108816945	Missense_Mutation	SNV	C	T	T	SGMS2	c.236C>T	P.T79M
XH_P90	4	109543131	109543131	Missense_Mutation	SNV	A	C	C	RPL34	c.16A>C	P.T6P
XH_P90	4	109543133	109543133	Silent	SNV	A	C	C	RPL34	c.18A>C	P.T6T
XH_P90	4	70615488	70615488	Missense_Mutation	SNV	T	G	G	SULT1B1	c.326A>C	P.H109P
XH_P90	5	140167136	140167136	Missense_Mutation	SNV	T	G	G	PCDH41	c.1261T>G	P.Y421D
XH_P90	5	176836041	176836041	Splice_Site	SNV	A	C	C	F12	c.115+6T>G	
XH_P90	6	105573417	105573417	Silent	SNV	G	T	T	BVES	c.388C>A	P.R130R
XH_P90	6	105850750	105850750	Missense_Mutation	SNV	T	G	G	PREP	c.17A>C	P.Y6S
XH_P90	6	165715123	165715123	Missense_Mutation	SNV	C	T	T	C6orf118	c.688G>A	P.D230N
XH_P90	6	170598798	170598798	Silent	SNV	T	G	G	DLL1	c.153A>C	P.P51P
XH_P90	6	17987649	17987649	Missense_Mutation	SNV	T	G	G	KIF13A	c.46A>C	P.N16H
XH_P90	6	43250618	43250618	Missense_Mutation	SNV	C	A	A	TTBK1	c.2140C>A	P.L714M
XH_P90	6	44240828	44240828	Missense_Mutation	SNV	C	G	G	TMEM151B	c.161C>G	P.T54S
XH_P90	6	54805082	54805082	Missense_Mutation	SNV	A	G	G	FAM83B	c.1313A>G	P.N438S
XH_P90	7	143097050	143097050	Missense_Mutation	SNV	T	G	G	EPHA1	c.529A>C	P.T177P
XH_P90	7	143771476	143771476	Missense_Mutation	SNV	A	C	C	OR2A25	c.164A>C	P.H55P
XH_P90	7	144015381	144015381	Missense_Mutation	SNV	A	C	C	OR2A1	c.164A>C	P.H55P
XH_P90	7	23731198	23731198	Nonsense_Mutation	SNV	T	G	G	FAM221A	c.620T>G	P.L207*
XH_P90	7	66483133	66483133	Splice_Site	SNV	A	C	C	TYW1	c.861+3A>C	
XH_P90	7	72277656	72277656	Splice_Site	SNV	T	G	G	TYW1B	c.723+3A>C	
XH_P90	7	73097548	73097548	Missense_Mutation	SNV	T	G	G	DNAJC30	c.206A>C	P.Y69S
XH_P90	7	73117253	73117253	Missense_Mutation	SNV	A	C	C	STX1A	c.600T>G	P.S200R
XH_P90	8	123964908	123964908	Silent	SNV	A	C	C	ZHX2	c.1158A>C	P.T386T
XH_P90	8	67425775	67425775	Missense_Mutation	SNV	A	C	C	C8orf46	c.343A>C	P.I115L
XH_P90	8	67509607	67509607	Missense_Mutation	SNV	A	C	C	MYBL1	c.470T>G	P.L157W
XH_P90	8	89128910	89128910	Silent	SNV	T	G	G	MMP16	c.909A>C	P.L303L
XH_P90	9	123667418	123667418	Missense_Mutation	SNV	T	G	G	TRAF1	c.1131A>C	P.E377D
XH_P90	9	131023495	131023495	Missense_Mutation	SNV	A	C	C	GOLGA2	c.1295T>G	P.Y432G
XH_P90	9	133760699	133760699	Missense_Mutation	SNV	A	C	C	ABL1	c.3022A>C	P.T1008P
XH_P90	9	35813273	35813273	Silent	SNV	T	G	G	HINT2	c.390A>C	P.G130G
XH_P90	9	93375818	93375818	Missense_Mutation	SNV	T	G	G	DIRAS2	c.292A>C	P.K98Q
XH_P90	9	98703733	98703733	Splice_Site	SNV	C	G	G	ERCC6L2	c.1785-3C>G	

XH_P90	X	148798322	148798322	Silent	SNV	T	G	G	MAGEA11	c.1089T>G	P.A363A
XH_P90	X	3030328	3030328	Missense_Mutation	SNV	A	C	C	AR5F	c.1504A>C	P.N502H
XH_P90	X	41206603	41206603	Missense_Mutation	SNV	G	A	A	DDX3X	c.1805G>A	P.R602Q
XH_P90	X	48542296	48542296	Silent	SNV	T	G	G	WAS	c.54T>G	P.V18V
XH_P90	X	53310696	53310696	Missense_Mutation	SNV	G	C	C	IQSEC2	c.8C>G	P.P3R
XH_P91	1	145439909	145439909	Missense_Mutation	SNV	A	C	C	TXNIP	c.290A>C	P.N97T
XH_P91	1	16460401	16460401	Missense_Mutation	SNV	G	T	T	EPHA2	c.1692C>A	P.N564K
XH_P91	1	202113631	202113631	Missense_Mutation	SNV	T	G	G	ARL8A	c.70A>C	P.T24P
XH_P91	1	203044863	203044863	Silent	SNV	G	A	A	PPFIA4	c.3552G>A	P.P1184P
XH_P91	1	232941462	232941462	Missense_Mutation	SNV	C	G	G	MAP10	c.693C>G	P.F231L
XH_P91	1	25815718	25815718	Silent	SNV	C	T	T	TMEM57	c.870C>T	P.G290G
XH_P91	1	28208568	28208568	Missense_Mutation	SNV	A	C	C	THEMIS2	c.733A>C	P.K245Q
XH_P91	10	123258042	123258042	Missense_Mutation	SNV	T	C	C	FGFR2	c.1639A>G	P.I547V
XH_P91	10	72520441	72520441	Silent	SNV	T	G	G	ADAMTS14	c.3504T>G	P.P1168P
XH_P91	10	75566473	75566473	Missense_Mutation	SNV	A	G	G	NDST2	c.1190T>C	P.L397P
XH_P91	11	117651411	117651411	Missense_Mutation	SNV	C	T	T	DSCAML1	c.341G>A	P.S114N
XH_P91	11	56344472	56344472	Silent	SNV	A	C	C	ORM5M10	c.726T>G	P.A242A
XH_P91	11	71817052	71817052	Missense_Mutation	SNV	C	T	T	LRTOMT	c.154C>T	P.R52W
XH_P91	13	28712952	28712952	Missense_Mutation	SNV	C	G	G	PAN3	c.158C>G	P.A53G
XH_P91	13	78320911	78320911	Silent	SNV	T	C	C	SLAIN1	c.687T>C	P.P229P
XH_P91	14	88974358	88974358	Missense_Mutation	SNV	C	A	A	PTPN21	c.357G>T	P.Q119H
XH_P91	15	43814169	43814169	Missense_Mutation	SNV	A	C	C	MAP1A	c.498A>C	P.L166F
XH_P91	15	59497624	59497624	Missense_Mutation	SNV	T	G	G	MYO1E	c.1591A>C	P.I531L
XH_P91	16	5115696	5115696	Splice_Site	SNV	A	C	C	C16orf89	c.208+6T>G	
XH_P91	16	90099338	90099338	Splice_Site	SNV	T	G	G	GAS8	c.246+6T>G	
XH_P91	17	10300132	10300132	Missense_Mutation	SNV	C	A	A	MYH8	c.4350G>T	P.R1450S
XH_P91	17	14205001	14205001	Missense_Mutation	SNV	G	T	T	HS3ST3B1	c.166G>T	P.A56S
XH_P91	17	14205002	14205002	Missense_Mutation	SNV	C	T	T	HS3ST3B1	c.167C>T	P.A56V
XH_P91	17	27024649	27024649	Silent	SNV	T	C	C	SUPT6H	c.4221T>C	P.D1407D
XH_P91	17	36716337	36716337	Splice_Site	SNV	T	A	A	SRGIN1	c.1794-4A>T	
XH_P91	17	37829452	37829452	Missense_Mutation	SNV	G	A	A	PGAP3	c.598C>T	P.P200S
XH_P91	17	45745570	45745570	Missense_Mutation	SNV	G	T	T	KPNB1	c.583G>T	P.D195Y
XH_P91	17	72239610	72239610	Splice_Site	SNV	T	G	G	TTYH2	c.731+2T>G	
XH_P91	17	79250883	79250883	Missense_Mutation	SNV	A	C	C	SLC38A10	c.677T>G	P.M226R
XH_P91	17	7979009	7979009	Missense_Mutation	SNV	A	C	C	ALOX12B	c.1558T>G	P.Y520D
XH_P91	17	79912149	79912149	Missense_Mutation	SNV	A	C	C	NOTUM	c.1167T>G	P.H389Q
XH_P91	19	11891730	11891730	Missense_Mutation	SNV	A	C	C	ZNFA41	c.1091A>C	P.H364P
XH_P91	19	12502202	12502202	Missense_Mutation	SNV	T	G	G	ZNFB799	c.1010A>C	P.H337P
XH_P91	19	13002706	13002706	Missense_Mutation	SNV	T	G	G	GCDF	c.189T>G	P.D63E
XH_P91	19	1627417	1627417	Missense_Mutation	SNV	C	T	T	TCF3	c.307G>A	P.G103S
XH_P91	19	39971292	39971292	Missense_Mutation	SNV	C	A	A	TIMM50	c.108C>A	P.D36E
XH_P91	19	44116716	44116716	Missense_Mutation	SNV	A	C	C	SRRM5	c.443A>C	P.H148P
XH_P91	19	55453045	55453045	Missense_Mutation	SNV	G	T	T	NLRP7	c.35C>A	P.T12N
XH_P91	19	57065980	57065980	Missense_Mutation	SNV	G	T	T	ZFP28	c.1826G>T	P.R609M
XH_P91	2	103095615	103095615	Missense_Mutation	SNV	A	C	C	SLC9A4	c.574A>C	P.N192H
XH_P91	2	10942675	10942675	Silent	SNV	T	C	C	PDIA6	c.267A>G	P.R89R
XH_P91	2	133074874	133074874	Missense_Mutation	SNV	G	A	A	ZNFR806	c.335G>A	P.G112D
XH_P91	2	166183388	166183388	Silent	SNV	A	G	G	SCN2A	c.2043A>G	P.R681R
XH_P91	2	179393165	179393165	Splice_Site	INDEL	-	CTTCAGATGTGG	CTTCAGATGTGG	TTN	ATACCATGTCTCCACCTCTGAAGAACTTCAACATTCTTTTCTTTTTC	
XH_P91	2	228211942	228211942	Splice_Site	SNV	T	G	G	MFF	c.594T>G	P.T198T
XH_P91	20	42142493	42142493	Missense_Mutation	SNV	T	G	G	L3MBTL1	c.86T>G	P.L29R
XH_P91	20	43945198	43945198	Missense_Mutation	SNV	G	A	A	RBPLJ	c.1258G>A	P.V420M
XH_P91	22	20456799	20456799	Silent	SNV	G	A	A	RIMBP3	c.4503C>T	P.S1501S
XH_P91	3	170875259	170875259	Missense_Mutation	SNV	C	A	A	TNIK	c.1211G>T	P.R404L
XH_P91	3	183519278	183519278	Missense_Mutation	SNV	C	T	T	YEATS2	c.3464C>T	P.T1155I
XH_P91	3	186272791	186272791	Silent	SNV	C	T	T	TBCD1	c.942G>A	P.Q314Q
XH_P91	4	123280727	123280727	Missense_Mutation	SNV	G	C	C	KIAA1109	c.14651G>C	P.R4884P
XH_P91	4	152021678	152021678	Missense_Mutation	SNV	C	T	T	RPS3A	c.104C>T	P.A35V
XH_P91	5	122281777	122281777	Missense_Mutation	SNV	A	C	C	SNX24	c.172A>C	P.I58L
XH_P91	5	13717526	13717526	Silent	SNV	G	A	A	DNAH5	c.12603C>T	P.F4201F
XH_P91	5	141041803	141041803	Silent	SNV	T	G	G	ARAP3	c.2820A>C	P.V940V
XH_P91	5	149447837	149447837	Missense_Mutation	SNV	T	C	C	CSF1R	c.1567A>G	P.M523V
XH_P91	5	32388694	32388694	Silent	SNV	T	G	G	ZFR	c.2229A>C	P.A743A
XH_P91	5	94620160	94620160	Silent	SNV	G	C	C	MCTP1	c.120C>G	P.G40G
XH_P91	6	154414521	154414521	Silent	SNV	G	A	A	OPRM1	c.1281G>A	P.S427S
XH_P91	7	128488966	128488966	Missense_Mutation	SNV	T	G	G	FLNC	c.4857T>G	P.D1619E
XH_P91	7	157046956	157046956	Nonsense_Mutation	SNV	C	T	T	UBE3C	c.2902C>T	P.Q968*
XH_P91	7	27150189	27150189	Missense_Mutation	SNV	A	C	C	HOXA3	c.71T>G	P.F24C
XH_P91	7	92882072	92882072	Frame_Shift_Del	INDEL	TTAAA	-	-	VP50	120_124delTAA	P.K41fs
XH_P91	8	144790253	144790253	Silent	SNV	C	T	T	CCDC166	c.27G>A	P.P9P
XH_P91	9	16437052	16437052	Missense_Mutation	SNV	T	G	G	BNC2	c.1014A>C	P.Q338H
XH_P91	9	16437053	16437053	Missense_Mutation	SNV	T	G	G	BNC2	c.1013A>C	P.Q338P
XH_P91	X	153005595	153005595	Missense_Mutation	SNV	A	C	C	ABCD1	c.1538A>C	P.K513T
XH_P91	X	24483687	24483687	Splice_Site	SNV	G	A	A	PKD3	c.106+9G>A	
XH_P91	X	49108188	49108188	Missense_Mutation	SNV	A	C	C	FOXP3	c.978T>G	P.N326K
XH_P91	X	54961441	54961441	Missense_Mutation	SNV	A	C	C	PFKFB1	c.1164T>G	P.D388E
XH_P92	1	151397478	151397478	Missense_Mutation	SNV	A	G	G	POGZ	c.1111T>C	P.C371R
XH_P92	1	151787886	151787886	Missense_Mutation	SNV	C	G	G	RORC	c.251G>C	P.R84P
XH_P92	1	156849901	156849901	Missense_Mutation	SNV	G	T	T	NTRK1	c.2157G>T	P.E719D
XH_P92	1	248343781	248343781	Missense_Mutation	SNV	C	G	G	OR2M2	c.494C>G	P.S165C
XH_P92	1	29605640	29605640	Splice_Site	SNV	T	G	G	PTPRU	c.1563+7T>G	
XH_P92	1	29605641	29605641	Splice_Site	SNV	T	G	G	PTPRU	c.1563+8T>G	
XH_P92	10	115375584	115375584	Splice_Site	SNV	G	A	A	NRAP	c.2974-9C>T	
XH_P92	10	55943237	55943237	Nonsense_Mutation	SNV	A	T	T	PCDH15	c.1572T>A	P.Y524*
XH_P92	10	78651384	78651384	Nonsense_Mutation	SNV	C	T	T	KCNMA1	c.3079G>A	P.A1027T
XH_P92	10	78709000	78709000	Missense_Mutation	SNV	T	G	G	KCNMA1	c.2447A>C	P.H816P
XH_P92	11	111784616	111784616	Silent	SNV	C	G	G	HSPB2	c.546C>G	P.P182P
XH_P92	11	17191063	17191063	Missense_Mutation	SNV	T	G	G	PIK3C2A	c.226A>C	P.M76L
XH_P92	11	20940880	20940880	Splice_Site	SNV	A	G	G	NELL1	c.843A>G	P.K281K
XH_P92	11	540803	540803	Missense_Mutation	SNV	G	T	T	LRRCS6	c.119G>T	P.S40I
XH_P92	11	8016855	8016855	Missense_Mutation	SNV	A	C	C	EIF3F	c.937A>C	P.N313H
XH_P92	12	117603304	117603304	Missense_Mutation	SNV	T	C	C	F8X021	c.1312A>G	P.I438V
XH_P92	12	119594508	119594531	Missense_Mutation	INDEL	SCGGGAGCA	-	-	SRRM4	GAGCCGGAGCCP.R588_5595del	
XH_P92	12	52885476	52885476	Nonsense_Mutation	SNV	C	T	T	KRT6A	c.585G>A	P.W195*
XH_P92	12	7188373	7188373	Missense_Mutation	SNV	T	G	G	C1R	c.1347A>C	P.E449D
XH_P92	12	98987790	98987790	Missense_Mutation	SNV	A	C	C	SLC25A3	c.34A>C	P.N12H
XH_P92	13	50296112	50296112	Silent	SNV	C	T	T	KPNA3	c.705G>A	P.P235P
XH_P92	13	58207308	58207308	Missense_Mutation	SNV	A	T	T	PCDH17	c.628A>T	P.T210S

XH_P92	13	99947414	99947414	Missense_Mutation	SNV	A	T	T	GPR183	c.986T>A	P.V329E
XH_P92	14	54896991	54896991	Frame_Shift_Ins	INDEL	-	A	A	CNIH1	c.394dupT	P.Y132fs
XH_P92	15	54435815	54435815	Splice_Site	SNV	A	C	C	UNC13C	c.3007-2A>C	
XH_P92	16	30080653	30080653	Silent	SNV	T	G	G	ALDOA	c.567T>G	P.P189P
XH_P92	16	30666196	30666196	Missense_Mutation	SNV	C	T	T	PRR14	c.905C>T	P.S302F
XH_P92	16	3076384	3076384	Silent	SNV	T	G	G	THOC6	c.381T>G	P.P127P
XH_P92	16	83065735	83065735	Missense_Mutation	SNV	C	G	G	CDH13	c.419C>G	P.T140S
XH_P92	16	88694125	88694125	Missense_Mutation	SNV	T	C	C	ZC3H18	c.2276T>C	P.L759P
XH_P92	17	3664715	3664715	Missense_Mutation	SNV	C	G	G	ITGAE	c.415G>C	P.A139P
XH_P92	17	37822260	37822260	Silent	SNV	T	G	G	TCAP	c.402T>G	P.A134A
XH_P92	17	62856325	62856325	Silent	SNV	G	A	A	LRR37A3	c.1293C>T	P.R431R
XH_P92	17	7100349	7100349	Missense_Mutation	SNV	A	C	C	DLG4	c.801T>G	P.N267K
XH_P92	17	7578416	7578416	Missense_Mutation	SNV	C	A	A	TP53	c.514G>T	P.V172F
XH_P92	19	10165921	10165921	Splice_Site	SNV	A	T	T	C3P1	n.1786-2A>T	
XH_P92	19	1272227	1272227	Missense_Mutation	SNV	G	A	A	CIRBP	c.679G>A	P.E227K
XH_P92	19	36884945	36884945	Silent	SNV	G	A	A	ZFP82	c.300C>T	P.S100S
XH_P92	19	38074876	38074876	Silent	SNV	T	G	G	ZNF571	c.132A>C	P.S44S
XH_P92	19	39409067	39409067	Missense_Mutation	SNV	A	C	C	SARS2	c.917T>G	P.L306R
XH_P92	19	40392073	40392073	Silent	SNV	G	T	T	FCGBP	c.8313C>A	P.S2771S
XH_P92	19	41744391	41744391	Silent	SNV	T	G	G	AXL	c.1011T>G	P.P337P
XH_P92	19	51329945	51329945	Missense_Mutation	SNV	A	T	T	KLK15	c.547T>A	P.Y183N
XH_P92	2	11927241	11927241	Missense_Mutation	SNV	G	A	A	LPIN1	c.1501G>A	P.D501N
XH_P92	2	209113113	209113113	Missense_Mutation	SNV	G	A	A	IDH1	c.394C>T	P.R132C
XH_P92	2	25966130	25966130	Missense_Mutation	SNV	T	A	A	ASXL2	c.3076A>T	P.S1026C
XH_P92	20	23066009	23066009	Missense_Mutation	SNV	T	C	C	CD93	c.821A>G	P.D274G
XH_P92	20	30432554	30432554	Silent	SNV	G	A	A	FOX51	c.792C>T	P.G264G
XH_P92	20	42213636	42213636	Missense_Mutation	SNV	G	A	A	SGK2	c.1084G>A	P.D362N
XH_P92	20	5545719	5545719	Missense_Mutation	SNV	C	T	T	GPCPD1	c.1273G>A	P.V425M
XH_P92	22	37966278	37966282	Frame_Shift_Del	INDEL	TTAAC	-	-	LGALS2	887_391delGTT	P.L130fs
XH_P92	3	122003671	122003671	Missense_Mutation	SNV	A	C	C	CASR	c.2870A>C	P.Q957P
XH_P92	3	131388529	131388529	Missense_Mutation	SNV	C	T	T	CPNE4	c.725G>A	P.R242H
XH_P92	3	134911457	134911457	Missense_Mutation	SNV	C	T	T	EPHB1	c.1922C>T	P.P641L
XH_P92	3	151073780	151073780	Missense_Mutation	SNV	A	C	C	MED12L	c.2509A>C	P.M837L
XH_P92	3	52682399	52682399	Frame_Shift_Ins	INDEL	-	T	T	PBRM1	c.773dupA	P.N258fs
XH_P92	3	73433579	73433579	Missense_Mutation	SNV	T	A	A	PDZRN3	c.1232A>T	P.E411V
XH_P92	4	155226374	155226374	Missense_Mutation	SNV	G	A	A	DCHS2	c.3905C>T	P.S1302F
XH_P92	4	186260522	186260522	Splice_Site	SNV	C	G	G	SNX25	c.1423-11C>G	
XH_P92	4	189068295	189068295	Silent	SNV	G	A	A	TRIML1	c.1176G>A	P.S392S
XH_P92	5	147813037	147813037	Missense_Mutation	SNV	G	T	T	FBXO38	c.1969G>T	P.D657Y
XH_P92	5	16703125	16703125	Missense_Mutation	SNV	C	T	T	MYO10	c.2419G>A	P.V807I
XH_P92	5	169468149	169468149	Missense_Mutation	SNV	G	T	T	DOCK2	c.3756G>T	P.K1252N
XH_P92	5	175530257	175530257	Missense_Mutation	SNV	T	A	A	FAM153B	c.461T>A	P.L154Q
XH_P92	5	179201113	179201113	Silent	SNV	C	T	T	MAML1	c.2286C>T	P.G762G
XH_P92	5	180432732	180432732	Missense_Mutation	SNV	T	C	C	BTNL3	c.1261T>C	P.F421L
XH_P92	6	17292273	17292290	Missense_Mutation	INDEL	CTGCAGCAG	-	-	RBM24	delGCTGCTGCCCP	A158_A163del
XH_P92	7	100276032	100276049	Missense_Mutation	INDEL	TACGCCCTTCA	-	-	GNB2	delACGCCCTTCA	P.239_G244del
XH_P92	9	138457278	138457278	Missense_Mutation	SNV	T	G	G	PAEP	c.378T>G	P.D126E
XH_P92	9	2116003	2116003	Missense_Mutation	SNV	G	T	T	SMARCA2	c.3638G>T	P.R1213L
XH_P92	9	97333774	97333774	Silent	SNV	C	T	T	FBP2	c.537G>A	P.G179G
XH_P92	9	99145841	99145841	Missense_Mutation	SNV	C	A	A	SLC35D2	c.76G>T	P.A26S
XH_P93	1	114483545	114483545	Missense_Mutation	SNV	T	G	G	HIPK1	c.540T>G	P.H180Q
XH_P93	1	156012625	156012625	Silent	SNV	T	G	G	UBQLN4	c.1146A>C	P.S382S
XH_P93	1	29605641	29605641	Splice_Site	SNV	T	G	G	PTPRU	c.1563+8T>G	
XH_P93	11	17191063	17191063	Missense_Mutation	SNV	T	G	G	PIK3C2A	c.226A>C	P.M76L
XH_P93	12	14628869	14628869	Missense_Mutation	SNV	A	C	C	ATF7IP	c.2905A>C	P.T969P
XH_P93	12	98987790	98987790	Missense_Mutation	SNV	A	C	C	SLC25A3	c.34A>C	P.N12H
XH_P93	15	42058630	42058630	Missense_Mutation	SNV	A	C	C	MGA	c.8350A>C	P.K2784Q
XH_P93	16	3076384	3076384	Silent	SNV	T	G	G	THOC6	c.381T>G	P.P127P
XH_P93	16	69970365	69970365	Splice_Site	SNV	A	C	C	WWP2	c.1769+10A>C	
XH_P93	17	7578406	7578406	Missense_Mutation	SNV	C	T	T	TP53	c.524G>A	P.R175H
XH_P93	19	45179618	45179618	Missense_Mutation	SNV	T	G	G	CEACAM19	c.500T>G	P.L167R
XH_P93	20	34458965	34458965	Missense_Mutation	SNV	T	G	G	PHF20	c.1011T>G	P.H337Q
XH_P93	3	14548454	14548454	Missense_Mutation	SNV	A	C	C	GRIP2	c.2250T>G	P.S750R
XH_P93	5	140788648	140788648	Silent	SNV	A	C	C	PCDHGB6	c.879A>C	P.S293S
XH_P93	5	158511688	158511688	Missense_Mutation	SNV	A	C	C	EBF1	c.471T>G	P.H157Q
XH_P93	9	138457278	138457278	Missense_Mutation	SNV	T	G	G	PAEP	c.378T>G	P.D126E
XH_P93	9	35061069	35061069	Missense_Mutation	SNV	A	C	C	VCP	c.1302T>G	P.D434E
XH_P93	X	153175840	153175840	Missense_Mutation	SNV	A	C	C	ARHGAP4	c.1941T>G	P.D647E
XH_P94	1	159842766	159842766	Missense_Mutation	SNV	A	C	C	CFAP45	c.1545T>G	P.D515E
XH_P94	1	16375594	16375594	Missense_Mutation	SNV	T	G	G	CLCNKB	c.128T>G	P.L43R
XH_P94	1	228482650	228482650	Missense_Mutation	SNV	T	G	G	OBSCN	c.11565T>G	P.C3855W
XH_P94	11	76372388	76372388	Missense_Mutation	SNV	A	C	C	LRR32	c.249T>G	P.N83K
XH_P94	11	94730916	94730916	Missense_Mutation	SNV	A	C	C	KDM4D	c.380A>C	P.K127T
XH_P94	17	26096057	26096057	Missense_Mutation	SNV	A	C	C	NOS2	c.1980T>G	P.D660E
XH_P94	17	4905915	4905915	Missense_Mutation	SNV	A	C	C	KIF1C	c.586A>C	P.M196L
XH_P94	17	73495137	73495137	Missense_Mutation	SNV	T	G	G	TMEM94	c.4002T>G	P.N1334K
XH_P94	17	74084149	74084149	Missense_Mutation	SNV	T	G	G	EXOC7	c.1354A>C	P.T452P
XH_P94	19	11942393	11942393	Nonsense_Mutation	SNV	T	G	G	ZNF440	c.402T>G	P.Y134*
XH_P94	19	12015674	12015674	Nonsense_Mutation	SNV	T	G	G	ZNF69	c.462T>G	P.Y154*
XH_P94	19	17311609	17311609	Missense_Mutation	SNV	A	C	C	MYO9B	c.4534A>C	P.K1512Q
XH_P94	20	34219458	34219458	Missense_Mutation	SNV	T	G	G	CPNE1	c.670A>C	P.I224L
XH_P94	21	47817319	47817319	Missense_Mutation	SNV	T	G	G	PCNT	c.4003T>G	P.C1335G
XH_P94	22	24583161	24583161	Splice_Site	SNV	T	G	G	SUSD2	c.1643-9T>G	
XH_P94	3	39185132	39185132	Missense_Mutation	SNV	A	C	C	CSRNP1	c.1244T>G	P.L415W
XH_P94	3	47467541	47467541	Missense_Mutation	SNV	T	G	G	SCAP	c.91A>C	P.J31L
XH_P94	3	52022800	52022800	Silent	SNV	T	G	G	ACY1	c.1020T>G	P.P340P
XH_P94	5	454122	454122	Missense_Mutation	SNV	T	G	G	EXOC3	c.1002T>G	P.N334K
XH_P94	5	79351816	79351816	Silent	SNV	T	G	G	THB54	c.228T>G	P.P76P
XH_P94	8	143561061	143561061	Missense_Mutation	SNV	T	G	G	ADGRB1	c.1734T>G	P.H578Q
XH_P94	9	131589349	131589349	Missense_Mutation	SNV	A	C	C	SPOUT1	c.330T>G	P.D110E
XH_P94	9	37522961	37522961	Silent	SNV	A	C	C	FBXO10	c.1791T>G	P.R597R
XH_P94	X	101908919	101908919	Silent	SNV	T	G	G	GPRASP1	c.78T>G	P.A26A
XH_P95	1	10716795	10716795	Splice_Site	SNV	T	G	G	CASZ1	c.1410-2A>C	
XH_P95	1	155167268	155167268	Missense_Mutation	SNV	C	A	A	THB53	c.2458G>T	P.G820W
XH_P95	1	207075389	207075389	Missense_Mutation	SNV	T	G	G	IL24	c.512T>G	P.F171C
XH_P95	1	22919922	22919922	Nonsense_Mutation	SNV	T	G	G	EPHA8	c.1419T>G	P.Y473*
XH_P95	10	75276669	75276669	Missense_Mutation	SNV	A	G	G	USP54	c.3344T>C	P.F1155S
XH_P95	11	128709896	128709896	Nonsense_Mutation	SNV	A	C	C	KCNJ1	c.300T>G	P.Y100*

XH_P95	11	14865516	14865516	Missense_Mutation	SNV	G	C	C	PDE3B	c.2464G>C	P.D822H
XH_P95	11	61183712	61183712	Missense_Mutation	SNV	A	C	C	CPSF7	c.830T>G	P.L277R
XH_P95	11	66372803	66372803	Splice_Site	SNV	A	C	C	CCS	c.490-7A>C	
XH_P95	12	50642510	50642510	Missense_Mutation	SNV	G	A	A	LIMA1	c.25C>T	P.R9W
XH_P95	12	96350745	96350745	Splice_Site	SNV	T	A	A	AMDHD1	c.587+5T>A	
XH_P95	12	98987790	98987790	Missense_Mutation	SNV	A	C	C	SLC25A3	c.34A>C	P.N12H
XH_P95	13	20567873	20567873	Nonsense_Mutation	SNV	C	T	T	ZMYM2	c.661C>T	P.Q221*
XH_P95	14	72205771	72205771	Missense_Mutation	SNV	C	G	G	SIPA1L1	c.5245C>G	P.Q1749E
XH_P95	15	34048572	34048572	Missense_Mutation	SNV	A	G	G	RYR3	c.8581A>G	P.K2861E
XH_P95	15	34393811	34393811	Missense_Mutation	SNV	A	C	C	EMC7	c.230T>G	P.F77C
XH_P95	15	34393812	34393812	Missense_Mutation	SNV	A	C	C	EMC7	c.229T>G	P.F77V
XH_P95	15	42702005	42702005	Missense_Mutation	SNV	T	G	G	CAPN3	c.2013T>G	P.D671E
XH_P95	16	28944344	28944344	Silent	SNV	G	C	C	CD19	c.468G>C	P.L156L
XH_P95	17	17716082	17716082	Frame_Shift_Ins	INDEL	-	G	G	SREBF1	c.3387dupC	P.G1130fs
XH_P95	17	26963982	26963982	Splice_Site	SNV	C	T	T	KIAA0100	c.1977+1G>A	
XH_P95	17	73486789	73486789	Missense_Mutation	SNV	A	G	G	TMEM94	c.1108A>G	P.K370E
XH_P95	19	1068742	1068742	Splice_Site	SNV	C	T	T	ARHGAP45	c.468C>T	P.D156D
XH_P95	19	18709296	18709296	Missense_Mutation	SNV	T	G	G	CRLF1	c.643A>C	P.N215H
XH_P95	19	36302852	36302852	Splice_Site	SNV	T	G	G	PRODH2	c.825+12A>C	
XH_P95	2	179499998	179499998	Missense_Mutation	SNV	T	C	C	TTN	c.36995A>G	P.D12332G
XH_P95	2	234740876	234740876	Silent	SNV	T	C	C	MROH2A	c.4830T>C	P.Y1610Y
XH_P95	20	62842581	62842581	Silent	SNV	T	G	G	MYT1	c.1314T>G	P.R438R
XH_P95	22	30775813	30775813	Splice_Site	SNV	G	A	A	RNF215	c.1009-11C>T	
XH_P95	22	32108919	32108919	Silent	SNV	T	G	G	PRR14L	c.4906A>C	P.R1636R
XH_P95	22	32108920	32108920	Silent	SNV	T	G	G	PRR14L	c.4905A>C	P.L1635L
XH_P95	22	51182533	51182533	Missense_Mutation	SNV	A	C	C	ACR	c.610A>C	P.I204L
XH_P95	3	178952085	178952085	Missense_Mutation	SNV	A	G	G	PIK3CA	c.3140A>G	P.H1047R
XH_P95	3	185198193	185198193	Missense_Mutation	SNV	C	T	T	MAP3K13	c.2675C>T	P.T892M
XH_P95	4	109543131	109543131	Missense_Mutation	SNV	A	C	C	RPL34	c.16A>C	P.T6P
XH_P95	4	109543133	109543133	Silent	SNV	A	C	C	RPL34	c.18A>C	P.T6T
XH_P95	4	113508641	113508641	Missense_Mutation	SNV	G	C	C	ZGRF1	c.3572C>G	P.A1191G
XH_P95	4	38016173	38016173	Missense_Mutation	SNV	C	T	T	TBC1D1	c.461C>T	P.A154V
XH_P95	5	89947518	89947518	Silent	SNV	A	G	G	ADGRV1	c.3387A>G	P.A1129A
XH_P95	5	93788700	93788700	Missense_Mutation	SNV	A	G	G	KIAA0825	c.2321T>C	P.V774A
XH_P95	6	25665222	25665222	Missense_Mutation	SNV	C	G	G	SCGN	c.298C>G	P.R100G
XH_P95	7	137172409	137172409	Missense_Mutation	SNV	G	A	A	DGKI	c.2275C>T	P.R759C
XH_P95	7	27150189	27150189	Missense_Mutation	SNV	A	C	C	HOXA3	c.71T>G	P.F24C
XH_P95	7	30795230	30795230	Silent	SNV	A	G	G	INMT	c.552A>G	P.S184S
XH_P95	7	4917676	4917676	Missense_Mutation	SNV	A	C	C	RADIL	c.95T>G	P.L32R
XH_P95	X	105921411	105921411	Missense_Mutation	SNV	T	G	G	CXorf57	c.2200T>G	P.L734V
XH_P95	X	107930856	107930856	Missense_Mutation	SNV	T	A	A	COL4A5	c.4442T>A	P.L1481H
XH_P95	X	153132183	153132183	Nonsense_Mutation	SNV	A	C	C	L1CAM	c.2352T>G	P.Y784*
XH_P95	X	49111966	49111966	Missense_Mutation	SNV	A	G	G	FOXP3	c.635T>C	P.V212A
XH_P96	10	102003490	102003490	Missense_Mutation	SNV	C	G	G	CWF19L1	c.1009G>C	P.V337L
XH_P96	11	46563595	46563595	Nonsense_Mutation	SNV	C	A	A	AMBRA1	c.1702G>T	P.E568*
XH_P96	11	6643781	6643781	Missense_Mutation	SNV	A	C	C	DCH52	c.9126T>G	P.D3042E
XH_P96	11	6897982	6897982	Missense_Mutation	SNV	T	A	A	OR10A4	c.104T>A	P.I35N
XH_P96	14	21550424	21550424	Silent	SNV	T	G	G	ARHGEF40	c.1131T>G	P.S377S
XH_P96	14	74061966	74061966	Missense_Mutation	SNV	A	C	C	ACOT4	c.874A>C	P.I292L
XH_P96	19	4200136	4200136	Missense_Mutation	SNV	A	C	C	ANKRD24	c.311A>C	P.H104P
XH_P96	22	30000102	30000102	Splice_Site	SNV	G	T	T	NF2	c.114+1G>T	
XH_P96	22	32352590	32352590	Nonsense_Mutation	SNV	T	G	G	YWHAH	c.552T>G	P.Y184*
XH_P96	4	151770608	151770608	Missense_Mutation	SNV	A	C	C	LRBA	c.4124T>G	P.I1375R
XH_P96	4	80329070	80329070	Missense_Mutation	SNV	T	G	G	GK2	c.285A>C	P.E95D
XH_P96	4	80329071	80329071	Missense_Mutation	SNV	T	G	G	GK2	c.284A>C	P.E95A
XH_P96	5	151178839	151178839	Missense_Mutation	SNV	A	C	C	G3BP1	c.808A>C	P.I270L
XH_P96	8	42128921	42128921	Missense_Mutation	SNV	T	G	G	IKKBK	c.33T>G	P.F11L
XH_P96	9	26094485	26094485	Splice_Site	SNV	T	C	C	LOC100506422	c.-102-6T>C	
XH_P96	9	74365200	74365200	Silent	SNV	C	G	G	TMEM2	c.90G>C	P.G30G
XH_P97	1	120547994	120547994	Missense_Mutation	SNV	T	G	G	NOTCH2	c.373A>C	P.S125R
XH_P97	1	169702014	169702014	Missense_Mutation	SNV	C	T	T	SELE	c.163G>A	P.E55K
XH_P97	1	225391975	225391975	Splice_Site	INDEL	AGTA	-	-	DNAH14	1+3_5911+6delAAGT	
XH_P97	1	248458642	248458642	Missense_Mutation	SNV	G	A	A	OR2T12	c.239C>T	P.A80V
XH_P97	1	40433494	40433494	Missense_Mutation	SNV	A	C	C	MFSD2A	c.1153A>C	P.I385L
XH_P97	1	44085157	44085157	Silent	SNV	G	A	A	PTPRF	c.4011G>A	P.V1337V
XH_P97	10	102250010	102250010	Missense_Mutation	SNV	G	A	A	SEC31B	c.2720C>T	P.T907I
XH_P97	10	131943566	131943566	Missense_Mutation	SNV	C	G	G	GLRX3	c.184C>G	P.Q62E
XH_P97	11	118531414	118531414	Silent	SNV	G	A	A	TREH	c.843C>T	P.L281L
XH_P97	11	60694859	60694859	Missense_Mutation	SNV	G	A	A	TMEM132A	c.284G>A	P.R95Q
XH_P97	11	6632948	6632948	Missense_Mutation	SNV	A	C	C	TAF10	c.334T>G	P.S112A
XH_P97	11	6643781	6643781	Missense_Mutation	SNV	A	C	C	DCH51	c.9126T>G	P.D3042E
XH_P97	11	726681	726681	Missense_Mutation	SNV	T	C	C	EP58L2	c.1997T>C	P.L666P
XH_P97	12	123214792	123214792	Missense_Mutation	SNV	C	T	T	HCAR1	c.95G>A	P.G32D
XH_P97	12	30814198	30814198	Splice_Site	SNV	A	C	C	IP08	c.1143T>G	P.A381A
XH_P97	12	56566384	56566384	Frame_Shift_Ins	INDEL	-	T	T	SMARCC2	c.1847dupA	P.N617fs
XH_P97	12	64017914	64017914	Splice_Site	SNV	G	A	A	DPY19L2	c.862-3C>T	
XH_P97	12	81657134	81657134	Nonsense_Mutation	SNV	C	T	T	PPFIA2	c.3591G>A	P.W1197*
XH_P97	13	45150200	45150200	Missense_Mutation	SNV	G	T	T	TSC22D1	c.11C>A	P.P4Q
XH_P97	14	71524265	71524265	Missense_Mutation	SNV	A	T	T	PCNX1	c.4343A>T	P.H1448L
XH_P97	15	41624670	41624670	Silent	SNV	T	C	C	OIP5	c.90A>G	P.Q30Q
XH_P97	15	45658310	45658310	Missense_Mutation	SNV	A	C	C	GATM	c.525T>G	P.I175M
XH_P97	16	2087823	2087823	Splice_Site	SNV	C	A	A	SLC9A3R2	c.856-4C>A	
XH_P97	16	50666188	50666188	Splice_Site	SNV	G	A	A	NKD1	c.696-4G>A	
XH_P97	17	18243495	18243495	Missense_Mutation	SNV	T	G	G	SHMT1	c.262A>C	P.M88L
XH_P97	17	66547263	66547263	Nonstop_Mutation	SNV	T	G	G	PRKAR1A	c.1012T>G	P.Ter338Eext**?
XH_P97	17	78262114	78262114	Silent	SNV	G	C	C	RNF213	c.762G>C	P.G254G
XH_P97	18	72343995	72343995	Missense_Mutation	SNV	T	G	G	ZNF407	c.1020T>G	P.S340R
XH_P97	19	11172458	11172458	Splice_Site	SNV	A	C	C	SMARCA4	c.4912-2A>C	
XH_P97	19	15568628	15568628	Missense_Mutation	SNV	T	G	G	RASAL3	c.906A>C	P.E302D
XH_P97	19	22940290	22940290	Missense_Mutation	SNV	A	C	C	ZNF99	c.2421T>G	P.H807Q
XH_P97	19	35556830	35556830	Frame_Shift_Del	INDEL	CATTGTGAG	-	-	HPN	CATTGTGAGTTG	P.G373fs
XH_P97	19	9089754	9089754	Silent	SNV	G	T	T	MUC16	c.2061C>A	P.S687S
XH_P97	2	171704297	171704297	Missense_Mutation	SNV	G	A	A	GAD1	c.1114G>A	P.V372I
XH_P97	2	209113112	209113112	Missense_Mutation	SNV	C	A	A	IDH1	c.395G>T	P.R132L
XH_P97	2	234731047	234731047	Missense_Mutation	SNV	T	G	G	MROH2A	c.3720T>G	P.D1240E
XH_P97	2	235951138	235951138	Silent	SNV	C	A	A	SH3BP4	c.1725C>A	P.P575P
XH_P97	2	46770265	46770265	Missense_Mutation	SNV	T	G	G	RHOQ	c.80T>G	P.M27R
XH_P97	20	1144994	1144994	Missense_Mutation	SNV	T	G	G	PSMF1	c.374T>G	P.L125R

XH_P97	20	33609062	33609062	Missense_Mutation	SNV	A	C	C	TRPC4AP	c.1149T>G	P.H383Q
XH_P97	22	36661827	36661827	Silent	SNV	T	G	G	APOL1	c.945T>G	P.G315G
XH_P97	22	40056344	40056344	Splice_Site	SNV	C	T	T	CACNA1I	c.2500-5C>T	
XH_P97	22	42125755	42125755	Silent	SNV	G	C	C	ME1	c.951G>C	P.A317A
XH_P97	3	127379804	127379804	Missense_Mutation	SNV	A	C	C	PODXL2	c.933A>C	P.Q311H
XH_P97	3	130887668	130887668	Splice_Site	SNV	C	G	G	NEK11	c.1177-6C>G	
XH_P97	3	58242353	58242353	Missense_Mutation	SNV	G	A	A	ABHD6	c.40G>A	P.G14S
XH_P97	3	62358079	62358079	Silent	SNV	C	T	T	FEZF2	c.465G>A	P.Q155Q
XH_P97	4	37246735	37246735	Missense_Mutation	SNV	T	G	G	NWD2	c.46T>G	P.S16A
XH_P97	4	39448104	39448104	Silent	SNV	T	G	G	KLB	c.1758T>G	P.L586L
XH_P97	5	134099675	134099675	Missense_Mutation	SNV	A	C	C	DDX46	c.99A>C	P.K33N
XH_P97	5	13777328	13777328	Missense_Mutation	SNV	C	T	T	DNAH5	c.9088G>A	P.V3030I
XH_P97	5	172110981	172111013	Missense_Mutation	INDEL	CGCTCAGCTT	-	-	NEURL1B	AGCTTCACGCTG	A383_D393del
XH_P97	5	179229076	179229076	Missense_Mutation	SNV	A	C	C	MGAT4B	c.36T>G	P.N12K
XH_P97	5	870618	870618	Missense_Mutation	SNV	A	G	G	BRD9	c.1336T>C	P.S446P
XH_P97	6	146264321	146264321	Missense_Mutation	SNV	A	C	C	SHPRH	c.2196T>G	P.D732E
XH_P97	6	47754322	47754322	Missense_Mutation	SNV	G	A	A	OPN5	c.202G>A	P.A68T
XH_P97	7	100365485	100365485	Nonsense_Mutation	SNV	G	A	A	ZAN	c.4892G>A	P.W1631*
XH_P97	7	140111729	140111729	Missense_Mutation	SNV	A	C	C	RAB19	c.257A>C	P.Y86S
XH_P97	7	47408824	47408824	Silent	SNV	C	G	G	TNS3	c.1419G>C	P.R473R
XH_P97	8	139165070	139165070	Missense_Mutation	SNV	C	G	G	FAM135B	c.1648G>C	P.V550L
XH_P97	9	100850240	100850240	Missense_Mutation	SNV	G	A	A	TRIM14	c.841C>T	P.R281C
XH_P97	9	107380272	107380272	Missense_Mutation	SNV	A	G	G	OR13C9	c.214T>C	P.C72R
XH_P97	9	113173374	113173374	Missense_Mutation	SNV	T	G	G	SVEP1	c.6617A>C	P.E2206A
XH_P97	9	15210094	15210094	Missense_Mutation	SNV	A	C	C	TTC39B	c.677T>G	P.L226R
XH_P97	9	34371069	34371069	Missense_Mutation	SNV	C	T	T	KIAA1161	c.1873G>A	P.E625K
XH_P97	9	71006509	71006509	Missense_Mutation	SNV	G	T	T	PGM5	c.757G>T	P.A253S
XH_P97	X	153191592	153191592	Missense_Mutation	SNV	T	C	C	ARHGAP4	c.65A>G	P.K22R
XH_P97	X	78010431	78010431	Nonsense_Mutation	SNV	T	A	A	LPAR4	c.65T>A	P.L22*
XH_P99	1	103488315	103488315	Missense_Mutation	SNV	C	A	A	COL11A1	c.1111G>T	P.D371Y
XH_P99	1	117529460	117529460	Silent	SNV	C	T	T	PTGFRN	c.2511C>T	P.Y837V
XH_P99	1	120385136	120385136	Silent	SNV	G	A	A	NBPF7	c.258C>T	P.L86L
XH_P99	1	183908096	183908096	Silent	SNV	C	T	T	COLGALT2	c.1680G>A	P.T560T
XH_P99	1	196971657	196971657	Missense_Mutation	SNV	C	A	A	CFHR5	c.1193C>A	P.A398D
XH_P99	1	20971000	20971000	Missense_Mutation	SNV	C	T	T	PINK1	c.794C>T	P.P265L
XH_P99	1	240071679	240071679	Missense_Mutation	SNV	C	A	A	CHRM3	c.928C>A	P.R310S
XH_P99	1	42875858	42875858	Missense_Mutation	SNV	G	A	A	RIMKLA	c.685G>A	P.G229S
XH_P99	1	44086156	44086156	Missense_Mutation	SNV	G	A	A	PTPRF	c.4436G>A	P.R1479H
XH_P99	10	27459487	27459487	Missense_Mutation	SNV	G	T	T	MASLT	c.1599G>T	P.M533I
XH_P99	10	81154147	81154147	Missense_Mutation	SNV	C	T	T	ZCCHC24	c.497G>A	P.C166Y
XH_P99	11	119063876	119063876	Missense_Mutation	SNV	G	A	A	CCDC153	c.334C>T	P.L112F
XH_P99	11	46898164	46898164	Missense_Mutation	SNV	G	A	A	LRP4	c.3389C>T	P.A1130V
XH_P99	11	66062418	66062418	Missense_Mutation	SNV	C	T	T	TMEM151A	c.701C>T	P.S234L
XH_P99	12	121686548	121686548	Splice_Site	SNV	C	T	T	CAMKK2	c.1324-11G>A	
XH_P99	12	1702951	1702951	Missense_Mutation	SNV	G	C	C	FBXL14	c.282C>G	P.S94R
XH_P99	12	52369208	52369208	Missense_Mutation	SNV	G	T	T	ACVR1B	c.251G>T	P.C84F
XH_P99	12	6965192	6965192	Missense_Mutation	SNV	G	A	A	USP5	c.316G>A	P.G106R
XH_P99	12	70004467	70004467	Missense_Mutation	SNV	A	T	T	LRRIC10	c.152T>A	P.F51Y
XH_P99	12	9083522	9083522	Splice_Site	SNV	A	C	C	PHC1	c.1104A>C	P.S368S
XH_P99	14	104208438	104208438	Missense_Mutation	SNV	G	A	A	PPP1R13B	c.1511C>T	P.P504L
XH_P99	14	23870003	23870003	Missense_Mutation	SNV	G	A	A	MYH6	c.1325C>T	P.T442M
XH_P99	14	61115716	61115716	Silent	SNV	A	C	C	SIX1	c.192T>G	P.R64R
XH_P99	14	72171986	72171986	Nonsense_Mutation	SNV	C	T	T	SIPA1L1	c.3694C>T	P.R1232*
XH_P99	15	43814170	43814170	Missense_Mutation	SNV	A	C	C	MAP1A	c.499A>C	P.N167H
XH_P99	16	2126142	2126142	Missense_Mutation	SNV	C	T	T	TSC2	c.2713C>T	P.R905W
XH_P99	16	30102201	30102201	Silent	SNV	C	T	T	TBX6	c.231G>A	P.P77P
XH_P99	16	67688413	67688413	Missense_Mutation	SNV	G	A	A	CARMIL2	c.3400G>A	P.D1134N
XH_P99	17	33806550	33806550	Missense_Mutation	SNV	A	C	C	SLFN12L	c.679T>G	P.F227V
XH_P99	17	35921310	35921310	Missense_Mutation	SNV	C	G	G	SYNRG	c.1416G>C	P.E472D
XH_P99	17	7107018	7107018	Missense_Mutation	SNV	G	A	A	DLG4	c.319C>T	P.R107C
XH_P99	18	19751628	19751645	Missense_Mutation	INDEL	CGGCAGCAG	-	-	GATA6	elAGCAGCCGCCG	A178_A183del
XH_P99	18	48255637	48255637	Missense_Mutation	SNV	G	A	A	MAPK4	c.544G>A	P.V182M
XH_P99	18	61564449	61564449	Missense_Mutation	SNV	G	T	T	SERPINB2	c.413G>T	P.R138L
XH_P99	18	66564657	66564657	Nonsense_Mutation	SNV	A	T	T	CCDC102B	c.1255A>T	P.K419*
XH_P99	18	76754712	76754712	Silent	SNV	G	A	A	SALL3	c.2721G>A	P.P907P
XH_P99	19	36883911	36883911	Missense_Mutation	SNV	T	G	G	ZFP82	c.1334A>C	P.H445P
XH_P99	19	472383	472383	Splice_Site	SNV	G	A	A	ODF3L2	c.235+11C>T	
XH_P99	19	9297116	9297116	Missense_Mutation	SNV	G	A	A	OR7D2	c.659G>A	P.R220Q
XH_P99	2	141214067	141214067	Missense_Mutation	SNV	G	T	T	LRP1B	c.9920C>A	P.A3307E
XH_P99	2	179391862	179391862	Missense_Mutation	SNV	A	C	C	TTN	c.102930T>G	P.D34310E
XH_P99	2	21228468	21228468	Missense_Mutation	SNV	C	T	T	APOB	c.11272G>A	P.V3758I
XH_P99	2	26679368	26679368	Missense_Mutation	SNV	C	T	T	DRC1	c.2206C>T	P.R736W
XH_P99	20	210246	210246	Missense_Mutation	SNV	C	A	A	DEFB129	c.386C>A	P.T129N
XH_P99	20	30747817	30747817	Missense_Mutation	SNV	A	G	G	TM9SF4	c.1592A>G	P.Y531C
XH_P99	20	55021046	55021046	Missense_Mutation	SNV	G	A	A	CASS4	c.388G>A	P.V130M
XH_P99	21	27284253	27284253	Missense_Mutation	SNV	T	C	C	APP	c.1709A>G	P.Q570R
XH_P99	21	28338356	28338356	Missense_Mutation	SNV	C	T	T	ADAMTS5	c.355G>A	P.G119R
XH_P99	22	28195222	28195222	Missense_Mutation	SNV	G	A	A	MN1	c.1310C>T	P.A437V
XH_P99	22	50719893	50719893	Silent	SNV	G	A	A	PLXNB2	c.3558C>T	P.R1186R
XH_P99	3	142681287	142681287	Missense_Mutation	SNV	G	A	A	PAQR9	c.892C>T	P.R298C
XH_P99	4	68543347	68543347	Frame_Shift_Del	INDEL	G	-	-	UBA6	c.447delC	P.L151fs
XH_P99	4	79188476	79188476	Missense_Mutation	SNV	G	T	T	FRAS1	c.871G>T	P.V291L
XH_P99	5	1034967	1034967	Missense_Mutation	SNV	G	A	A	NKD2	c.523G>A	P.V175I
XH_P99	5	109973971	109973971	Silent	SNV	C	T	T	TMEM232	c.429G>A	P.S143S
XH_P99	5	112173917	112173917	Nonsense_Mutation	SNV	C	T	T	APC	c.2626C>T	P.R876*
XH_P99	5	112175639	112175639	Nonsense_Mutation	SNV	C	T	T	APC	c.4348C>T	P.R1450*
XH_P99	5	136314405	136314405	Missense_Mutation	SNV	C	T	T	SPOCK1	c.1258G>A	P.V420M
XH_P99	5	177683364	177683364	Missense_Mutation	SNV	G	A	A	COL23A1	c.872C>T	P.A291V
XH_P99	5	180047963	180047963	Missense_Mutation	SNV	C	T	T	FLT4	c.2212G>A	P.V738M
XH_P99	5	63256991	63256991	Missense_Mutation	SNV	C	T	T	HTR1A	c.556G>A	P.A186T
XH_P99	6	152644762	152644762	Silent	SNV	C	T	T	SYNE1	c.15555G>A	P.T5185T
XH_P99	6	7727711	7727711	Missense_Mutation	SNV	C	T	T	BMP6	c.523C>T	P.P175S
XH_P99	6	87970047	87970047	Missense_Mutation	SNV	G	T	T	ZNF292	c.6700G>T	P.V2234F
XH_P99	7	140453136	140453136	Missense_Mutation	SNV	A	T	T	BRAF	c.1799T>A	P.V600E
XH_P99	7	142750347	142750347	Nonsense_Mutation	SNV	C	T	T	OR6V1	c.910C>T	P.Q304*
XH_P99	7	148963903	148963903	Splice_Site	SNV	G	A	A	ZNF783	c.421-7G>A	
XH_P99	7	149516884	149516884	Missense_Mutation	SNV	G	A	A	SSPO	c.12086G>A	P.R4029H
XH_P99	7	43916610	43916610	Missense_Mutation	SNV	C	G	G	URGCP	c.2452G>C	P.V818L

XH_P99	7	4825277	4825277	Missense_Mutation	SNV	G	A	A	AP5Z1	c.1094G>A	P.R365Q
XH_P99	7	73111935	73111935	Splice_Site	SNV	G	A	A	WBSCR22	c.753G>A	P.R251R
XH_P99	8	104933932	104933932	Missense_Mutation	SNV	C	T	T	RIMS2	c.2116C>T	P.R706C
XH_P99	8	143599530	143599530	Missense_Mutation	SNV	C	T	T	ADGRB1	c.2849C>T	P.T950M
XH_P99	8	145235233	145235233	Silent	SNV	G	A	A	MROH1	c.453G>A	P.S151S
XH_P99	8	73849269	73849269	Missense_Mutation	SNV	G	T	T	KCNB2	c.1679G>T	P.C560F
XH_P99	9	101900171	101900171	Missense_Mutation	SNV	C	T	T	TGFBR1	c.605C>T	P.A202V
XH_P99	9	116930019	116930019	Frame_Shift_Ins	INDEL	-	GGAGTCATTCCT	GGAGTCATTCCT	COL27A1	CCGGGAGTCAT	P.F74fs
XH_P99	9	130479979	130479979	Silent	SNV	G	T	T	TTC16	c.315G>T	P.L105L
XH_P99	9	21970973	21970973	Missense_Mutation	SNV	A	G	G	CDKN2A	c.385T>C	P.Y129H
XH_P99	X	152825293	152825293	Missense_Mutation	SNV	G	A	A	ATP2B3	c.2732G>A	P.R911Q
XH_P99	X	55650624	55650624	Silent	SNV	G	A	A	FOXR2	c.480G>A	P.E160E
XH_P99	Y	4968734	4968734	Missense_Mutation	SNV	G	A	A	PCDH11Y	c.3082G>A	P.V1028I

1 **Table S5.** 37 Significantly mutated genes (SMGs) identified by MutSigCV among 160 BTC
2 patients with available WES data (q<0.1).

Gene Symbol	MutsigCV's q-value
TP53	0
KRAS	3.47422E-06
ARID1A	0.03906009
SMAD4	0.000475837
PIK3CA	0.0853317
CDKN2A	0.000110486
MUC4	0
IDH1	2.80915E-05
BAP1	0.000397723
RBM10	0.02217071
PTEN	6.72854E-05
RB1	0.000600933
NF2	2.80915E-05
KRT76	6.0729E-10
CDC27	0.001508177
MAP3K1	0.003202392
PHLDA1	4.12099E-07
RBBP6	0.00676553
RNMT	4.09802E-08
TDG	0.002102845
DBR1	8.31427E-07
MSH3	0.01238534
CTSA	0.000418755
NUDT12	0.000418755
HAVCR1	0
OR10K2	0.04107433
PAN3	0.08188415
RBM47	0.02838428
KRTAP4-11	0
OR6S1	0.02207263
SELPLG	0.03451987
SMR3A	0.08188415
OR10J3	0.0593485
OR5B12	0.07801046
CBX3	0.007363897
LCE4A	0.005556484
DEFB126	0.08845939

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1 **Table S6.** List of 68 putative oncodriver genes in BTCs.

Gene Symbol	
ACVR1B	MUC4
ACVR2A	MYC
AKT3	NCOR1
APC	NF1
ARAF	NRAS
ARID1A	P4HTM
ARID1B	PBRM1
ARID2	PIK3CA
ASXL1	PIK3R1
ATM	PRKCI
BAP1	PTEN
BRAF	RASA1
BRCA1	RB1
BRCA2	RNF43
CCND1	SF3B1
CCND3	SMAD4
CCNE1	STK11
CDK4	TERT
CDKN1B	TGFBR2
CDKN2A	TP53
CTNNB1	WNT5B
DDR2	YEATS4
ECT2	
EGFR	
ELF3	
EPHA2	
ERBB2	
FBXW7	
FGF19	
FGFR1	
FGFR2	
FGFR3	
GNA12	
GNAS	
HSF1	
IDH1	
IDH2	
IKBKB	
KMT2D	
KRAS	
MAP2K4	
MDM2	
MLH1	
MSH2	
MSH3	
MSH6	

2

Table S7. Chromosomal cytobands identified as significantly altered copy number regions by GISTIC2 among 160 BTC patients with available WES data.

Cytoband	chromosome	start	end	type	G-score	-log10(q-value)
1p36.33	1	860260	879955	DEL	0.273016	10.473654
1p36.33	1	879584	894689	DEL	0.273016	10.473654
1p36.33	1	895967	901095	DEL	0.269654	10.259539
1p36.33	1	901877	911245	DEL	0.28243	11.192722
1p36.33	1	910579	917497	DEL	0.28243	11.192722
1p36.33	1	934342	935552	DEL	0.287138	11.549904
1p36.33	1	948803	949920	DEL	0.288483	11.62126
1p36.33	1	955503	991496	DEL	0.329502	14.751935
1p36.33	1	1006346	1009687	DEL	0.335554	15.265508
1p36.33	1	1017198	1051741	DEL	0.336227	15.313454
1p36.33	1	1109264	1133315	DEL	0.348331	16.368436
1p36.33	1	1138888	1142071	DEL	0.292517	11.870463
1p36.33	1	1146706	1149518	DEL	0.292517	11.870463
1p36.33	1	1152288	1167411	DEL	0.289155	11.678967
1p36.33	1	1167629	1170421	DEL	0.294535	11.971889
1p36.33	1	1177826	1182102	DEL	0.278396	10.91084
1p36.33	1	1189289	1209265	DEL	0.272344	10.46069
1p36.33	1	1215816	1227409	DEL	0.272344	10.46069
1p36.33	1	1227756	1244989	DEL	0.266292	10.044307
1p36.33	1	1243947	1247057	DEL	0.266292	10.044307
1p36.33	1	1246965	1260071	DEL	0.266292	10.044307
1p36.33	1	1260136	1264277	DEL	0.266292	10.014472
1p36.33	1	1266694	1270686	DEL	0.270326	10.31747
1p36.33	1	1270656	1284730	DEL	0.270326	10.31747
1p36.33	1	1288069	1297157	DEL	0.268309	10.181588
1p36.33	1	1309110	1310875	DEL	0.268309	10.181588
1p36.33	1	1321091	1334708	DEL	0.266964	10.078695
1p36.33	1	1337288	1342693	DEL	0.268309	10.181588
1p36.33	1	1353800	1357149	DEL	0.283775	11.255068
1p36.33	1	1361508	1363167	DEL	0.283775	11.255068
1p36.33	1	1370241	1378262	DEL	0.278396	10.896155
1p36.33	1	1385069	1405538	DEL	0.269654	10.272593
1p36.33	1	1407143	1433228	DEL	0.262929	9.870514
1p36.33	1	1447531	1470067	DEL	0.265619	9.989204
1p36.33	1	1470554	1475833	DEL	0.283103	11.22098
1p36.33	1	1477053	1510249	DEL	0.351693	16.678664
1p36.33	1	1533392	1535476	DEL	0.39742	20.848753
1p36.33	1	1550795	1565990	AMP	0.39997	2.734703
1p36.33	1	1550795	1565990	DEL	0.43306	24.080021
1p36.33	1	1567474	1570639	DEL	0.414231	22.31697
1p36.33	1	1570603	1590473	DEL	0.288483	11.62126
1p36.33	1	1592939	1624167	DEL	0.288483	11.62126
1p36.33	1	1634169	1655766	DEL	0.288483	11.62126
1p36.33	1	1656277	1677431	DEL	0.18358	5.055508
1p36.33	1	1682671	1711896	DEL	0.18358	5.055508
1p36.33	1	1716729	1822495	DEL	0.165424	4.068408
1p36.33	1	1846266	1848735	DEL	0.174165	4.457965
1p36.33	1	1849029	1850712	DEL	0.17551	4.53515
1p36.33	1	1950780	1962192	DEL	0.169458	4.265361
1p36.33	1	1981909	2116834	DEL	0.163406	3.952709
1p36.33	1	2115903	2144159	DEL	0.163406	3.952709
1p36.33	1	2160134	2241558	DEL	0.155337	3.58476
1p36.33	1	2252692	2323146	DEL	0.162061	3.869288
1p36.32	1	2323267	2336883	DEL	0.171476	4.348633
1p36.32	1	2336236	2345236	DEL	0.171476	4.348633
1p36.32	1	2357419	2436969	DEL	0.171476	4.348633
1p36.32	1	2439972	2458039	DEL	0.162734	3.925206
1p36.32	1	2460184	2461684	DEL	0.174838	4.476867
1p36.32	1	2487078	2496821	DEL	0.17551	4.57487
1p36.32	1	2517930	2522908	DEL	0.171476	4.348633
1p36.32	1	2522078	2564481	DEL	0.171476	4.348633
1p36.32	1	2567415	2718286	DEL	0.173493	4.419351
1p36.32	1	2938046	2939465	DEL	0.173493	4.419351
1p36.32	1	2985732	3355185	DEL	0.17551	4.57487
1p36.32	1	3370990	3397677	DEL	0.203753	6.163696
1p36.32	1	3406484	3528059	DEL	0.242756	8.453529
1p36.32	1	3541566	3546691	DEL	0.209133	6.449333
1p36.32	1	3547331	3569325	DEL	0.214513	6.719543
1p36.32	1	3569084	3652765	DEL	0.225272	7.374203
1p36.32	1	3652548	3663900	DEL	0.225272	7.374203
1p36.32	1	3668962	3688209	DEL	0.218547	7.001254
1p36.32	1	3696784	3713068	DEL	0.250825	9.010626
1p36.32	1	3728645	3773778	DEL	0.235359	8.025602
1p36.32	1	3773845	3801993	DEL	0.24948	8.935172
1p36.32	1	3805689	3816857	DEL	0.24948	8.935172
1p36.32	1	4714792	4852594	DEL	0.256205	9.348487
1p36.31	1	5922871	6052533	DEL	0.256205	9.348487

1p36.31	1	6051526	6161253	DEL	0.239393	8.237752
1p36.31	1	6161853	6240183	DEL	0.222582	7.241513
1p36.31	1	6241329	6269449	DEL	0.250825	8.991867
1p36.31	1	6265535	6281359	DEL	0.245445	8.639947
1p36.31	1	6281253	6296032	DEL	0.245445	8.639947
1p36.31	1	6304252	6305638	DEL	0.254187	9.207825
1p36.31	1	6307406	6321035	DEL	0.252842	9.132738
1p36.31	1	6324329	6454451	DEL	0.252842	9.132738
1p36.31	1	6472478	6484730	DEL	0.259567	9.622622
1p36.31	1	6484848	6521430	DEL	0.269654	10.248387
1p36.31	1	6521211	6526255	DEL	0.276378	10.751425
1p36.31	1	6526152	6580121	DEL	0.276378	10.751425
1p36.31	1	6581407	6614595	DEL	0.271671	10.414385
1p36.31	1	6615241	6639817	DEL	0.271671	10.414385
1p36.31	1	6640061	6649340	DEL	0.246118	8.695328
1p36.31	1	6650784	6674667	DEL	0.248135	8.821287
1p36.31	1	6673745	6684093	DEL	0.246118	8.695328
1p36.31	1	6684926	6695646	DEL	0.24679	8.745565
1p36.31	1	6694228	6761984	DEL	0.244101	8.529884
1p36.31	1	6845384	7829766	DEL	0.210478	6.551994
1p36.23	1	7831329	7841492	DEL	0.22191	7.192195
1p36.23	1	7844380	7905237	DEL	0.22191	7.192195
1p36.23	1	7903143	7913572	DEL	0.240066	8.275015
1p36.23	1	7979907	8000926	DEL	0.233341	7.935143
1p36.23	1	8014351	8045565	DEL	0.233341	7.935143
1p36.23	1	8064464	8086368	DEL	0.239393	8.244846
1p36.23	1	8377886	8404227	DEL	0.239393	8.244846
1p36.23	1	8412457	8877702	DEL	0.231324	7.753318
1p36.23	1	8921061	8939308	DEL	0.242083	8.411046
1p36.23	1	8938894	8939953	DEL	0.242083	8.411046
1p36.23	1	9005926	9035151	DEL	0.231324	7.778547
1p36.23	1	9063359	9086404	DEL	0.232669	7.851003
1p36.23	1	9095166	9148537	DEL	0.235359	8.013472
1p36.23	1	9160364	9189229	DEL	0.238049	8.18386
1p36.22	1	9294834	9331396	DEL	0.228634	7.577115
1p36.22	1	9352939	9429591	DEL	0.236031	8.052374
1p36.22	1	9599541	9645237	DEL	0.236031	8.052374
1p36.22	1	9648932	9674935	DEL	0.235359	8.013472
1p36.22	1	9711790	9789172	DEL	0.240066	8.288369
1p36.22	1	9712668	9714644	DEL	0.240066	8.288369
1p36.22	1	9789084	9884584	DEL	0.222582	7.244674
1p36.22	1	9908334	9970394	DEL	0.234686	7.995693
1p36.22	1	9982173	10003465	DEL	0.234686	7.995693
1p36.22	1	10003486	10045559	DEL	0.231996	7.799771
1p36.22	1	10057264	10076078	DEL	0.239393	8.237752
1p36.22	1	10092890	10241297	DEL	0.215185	6.789789
1p36.22	1	10270863	10441661	DEL	0.241411	8.382301
1p36.22	1	10458649	10480201	DEL	0.229307	7.623487
1p36.22	1	10490159	10512210	DEL	0.238721	8.212265
1p36.22	1	10490159	10512210	DEL	0.238721	8.212265
1p36.22	1	10509776	10511959	DEL	0.238721	8.212265
1p36.22	1	10516579	10532583	DEL	0.238721	8.212265
1p36.22	1	10532345	10690815	DEL	0.235359	8.013472
1p36.22	1	10696661	10856707	DEL	0.227962	7.504581
1p36.22	1	11006528	11042094	DEL	0.231324	7.778547
1p36.22	1	11072414	11085796	DEL	0.232669	7.875639
1p36.22	1	11086580	11107290	DEL	0.256877	9.39139
1p36.22	1	11114641	11120081	DEL	0.250825	9.010626
1p36.22	1	11126675	11159938	DEL	0.221237	7.164318
1p36.22	1	11166592	11322564	DEL	0.238049	8.18386
1p36.22	1	11249398	11256038	DEL	0.238049	8.18386
1p36.22	1	11333263	11356106	DEL	0.237376	8.127697
1p36.22	1	11539223	11597641	DEL	0.22191	7.202565
1p36.22	1	11708424	11715842	DEL	0.236704	8.101167
1p36.22	1	11714432	11723384	DEL	0.236704	8.101167
1p36.22	1	11724181	11734411	DEL	0.234686	7.995693
1p36.22	1	11734537	11751707	DEL	0.234686	7.995693
1p36.22	1	11796141	11814859	DEL	0.234686	7.995693
1p36.22	1	11845780	11866977	DEL	0.231996	7.799771
1p36.22	1	11866207	11903201	DEL	0.233341	7.94133
1p36.22	1	11901074	11908136	DEL	0.239393	8.237752
1p36.22	1	11905766	11908402	DEL	0.239393	8.237752
1p36.22	1	11917521	11918988	DEL	0.239393	8.237752
1p36.22	1	11979648	11986485	DEL	0.231996	7.824242
1p36.22	1	11994262	12035595	DEL	0.223927	7.323854
1p36.22	1	12040238	12073571	DEL	0.223927	7.323854
1p36.22	1	12079523	12092102	DEL	0.232669	7.875639
1p36.22	1	12123434	12204264	DEL	0.254187	9.194133
1p36.22	1	12227060	12269285	DEL	0.245445	8.637373

1p36.22	1	12290124	12572099	DEL	0.241411	8.382301
1p36.22	1	12627939	12677737	DEL	0.247463	8.780599
1p36.21	1	12704566	12727097	DEL	0.262929	9.860044
1p36.21	1	12776118	12788726	DEL	0.264274	9.921517
1p36.21	1	12806163	12823847	DEL	0.289827	11.707138
1p36.21	1	12834984	12838049	DEL	0.303276	12.689234
1p36.21	1	12851546	12856777	DEL	0.305294	12.855428
1p36.21	1	12884468	12891264	DEL	0.305294	12.855428
1p36.21	1	12907261	12908578	DEL	0.304621	12.773846
1p36.21	1	12916941	12921764	DEL	0.305294	12.855428
1p36.21	1	12939045	12946025	DEL	0.305294	12.855428
1p36.21	1	12952727	12958101	DEL	0.305966	12.878415
1p36.21	1	12976450	12980569	DEL	0.305966	12.878415
1p36.21	1	12998181	13117751	DEL	0.305966	12.878415
1p36.21	1	13035543	13038381	DEL	0.305966	12.878415
1p36.21	1	13328196	13331692	DEL	0.29319	11.870463
1p36.21	1	13359819	13369057	DEL	0.292517	11.870463
1p36.21	1	13386646	13390765	DEL	0.292517	11.870463
1p36.21	1	13421176	13428191	DEL	0.292517	11.870463
1p36.21	1	13447414	13452656	DEL	0.292517	11.870463
1p36.21	1	13474689	13477522	DEL	0.292517	11.870463
1p36.21	1	13495254	13498260	DEL	0.292517	11.870463
1p36.21	1	13516066	13526943	DEL	0.292517	11.870463
1p36.21	1	13641973	13648988	DEL	0.292517	11.870463
1p36.21	1	13668269	13673511	DEL	0.292517	11.870463
1p36.21	1	13694889	13698405	DEL	0.292517	11.870463
1p36.21	1	13716092	13719089	DEL	0.292517	11.870463
1p36.21	1	13736907	13747803	DEL	0.292517	11.870463
1p36.21	1	13801445	13840543	DEL	0.291172	11.791899
1p36.21	1	13909960	13944452	DEL	0.291172	11.791899
1p36.21	1	14026693	14151574	DEL	0.192322	5.554185
1p36.21	1	14925200	15444539	DEL	0.198374	5.881779
1p36.21	1	15479028	15546976	DEL	0.194339	5.679759
1p36.21	1	15573768	15726779	DEL	0.17551	4.587313
1p36.21	1	15736391	15756839	DEL	0.197701	5.84149
1p36.21	1	15764935	15775737	DEL	0.196356	5.758546
1p36.21	1	15783223	15798586	DEL	0.196356	5.758546
1p36.21	1	15792404	15817895	DEL	0.196356	5.758546
1p36.21	1	15817327	15853029	DEL	0.195684	5.720412
1p36.21	1	15853308	15918874	DEL	0.194339	5.679759
1p36.21	1	15898848	15911605	DEL	0.194339	5.679759
1p36.21	1	15943995	15995539	DEL	0.202408	6.093196
1p36.21	1	15986364	15988217	DEL	0.202408	6.093196
1p36.21	1	16010827	16061264	DEL	0.200391	5.970401
1p36.21	1	16062900	16067891	DEL	0.207116	6.367275
1p36.21	1	16068917	16074477	DEL	0.228634	7.581833
1p36.21	1	16083102	16113089	DEL	0.228634	7.581833
1p36.21	1	16174359	16266955	DEL	0.201736	6.054854
1p36.13	1	16268364	16302627	DEL	0.180218	4.904653
1p36.13	1	16330731	16335302	DEL	0.188287	5.25632
1p36.13	1	16340523	16346089	DEL	0.187615	5.217794
1p36.13	1	16345370	16360545	DEL	0.187615	5.217794
1p36.13	1	16370272	16383803	DEL	0.201736	6.067772
1p36.13	1	16384264	16400127	DEL	0.209805	6.508411
1p36.13	1	16450832	16482582	DEL	0.203753	6.179204
1p36.13	1	16524349	16539104	DEL	0.204426	6.19691
1p36.13	1	16558195	16563657	DEL	0.21384	6.681712
1p36.13	1	16573334	16678949	DEL	0.21384	6.681712
1p36.13	1	16713612	16763919	DEL	0.206443	6.330183
1p36.13	1	16767167	16786573	DEL	0.211823	6.597158
1p36.13	1	16888814	16940057	DEL	0.215858	6.819517
1p36.13	1	17066768	17299474	DEL	0.240066	8.275015
1p36.13	1	17300997	17307330	DEL	0.236704	8.092226
1p36.13	1	17312453	17338423	DEL	0.225272	7.366607
1p36.13	1	17345217	17380665	DEL	0.206443	6.348678
1p36.13	1	17393256	17445948	DEL	0.200391	5.970401
1p36.13	1	17531621	17572500	DEL	0.203081	6.145609
1p36.13	1	17575593	17610728	DEL	0.204426	6.213619
1p36.13	1	17634690	17690499	DEL	0.202408	6.074248
1p36.13	1	17733256	17766220	DEL	0.204426	6.19691
1p36.13	1	17866330	18024369	DEL	0.203081	6.145609
1p36.13	1	18081808	18153558	DEL	0.210478	6.529394
1p36.13	1	18434240	18704977	DEL	0.205771	6.293533
1p36.13	1	18807424	18812478	DEL	0.214513	6.705862
1p36.13	1	18957500	19075360	DEL	0.206443	6.330183
1p36.13	1	19166093	19186176	DEL	0.210478	6.551994
1p36.13	1	19197926	19229275	DEL	0.215858	6.819517
1p36.13	1	19230775	19283180	DEL	0.205771	6.276526
1p36.13	1	19401000	19536770	DEL	0.160044	3.721385

1p36.13	1	19578033	19586622	DEL	0.204426	6.213619
1p36.13	1	19609052	19615744	DEL	0.215858	6.819517
1p36.13	1	19630459	19638640	DEL	0.209805	6.487421
1p36.13	1	19638820	19655794	DEL	0.206443	6.348678
1p36.13	1	19665267	19812066	DEL	0.205098	6.228164
1p36.13	1	19923477	19956314	DEL	0.205098	6.240448
1p36.13	1	19967048	19984945	DEL	0.214513	6.705862
1p36.13	1	19991780	20006055	DEL	0.211823	6.612127
1p36.13	1	20008706	20126438	DEL	0.202408	6.089385
1p36.13	1	20140523	20141771	DEL	0.21384	6.681712
1p36.13	1	20209006	20239438	DEL	0.205771	6.309414
1p36.13	1	20246502	20250110	DEL	0.213168	6.658472
1p36.13	1	20301925	20306932	DEL	0.21384	6.681712
1p36.13	1	20354672	20417683	DEL	0.212495	6.636263
1p36.12	1	20438432	20446050	DEL	0.21115	6.575465
1p36.12	1	20465819	20476879	DEL	0.209133	6.467798
1p36.12	1	20487746	20503917	DEL	0.214513	6.724944
1p36.12	1	20512578	20522541	DEL	0.212495	6.636263
1p36.12	1	20617412	20681387	DEL	0.215858	6.819517
1p36.12	1	20808884	20812713	DEL	0.210478	6.529394
1p36.12	1	20825943	20834654	DEL	0.210478	6.529394
1p36.12	1	20878932	20881512	DEL	0.211823	6.612127
1p36.12	1	20915441	20945401	DEL	0.211823	6.612127
1p36.12	1	20959948	20978004	DEL	0.207788	6.405468
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1p36.12	1	20990507	21044510	DEL	0.202408	6.089385
1p36.12	1	21046225	21059330	DEL	0.192994	5.625492
1p36.12	1	21069154	21113816	DEL	0.192994	5.625492
1p36.12	1	21132963	21503377	DEL	0.202408	6.07512
1p36.12	1	21543740	21671997	DEL	0.201064	6.01644
1p36.12	1	21766621	21811498	DEL	0.191649	5.503713
1p36.12	1	21835858	21904905	DEL	0.191649	5.503713
1p36.12	1	21922708	21995801	DEL	0.180218	4.904653
1p36.12	1	22004791	22110099	DEL	0.205771	6.276526
1p36.12	1	22138758	22151714	DEL	0.262257	9.771286
1p36.12	1	22148738	22263790	DEL	0.262257	9.771286
1p36.12	1	22303514	22325135	DEL	0.225944	7.413698
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1p36.12	1	22379120	22419437	DEL	0.215858	6.797504
1p36.12	1	22443798	22470462	DEL	0.214513	6.727736
1p36.12	1	22778344	22857650	DEL	0.184925	5.118435
1p36.12	1	22890057	22930087	DEL	0.195684	5.740524
1p36.12	1	22962999	22966101	DEL	0.201064	6.01644
1p36.12	1	22970123	22974603	DEL	0.209133	6.467798
1p36.12	1	22979255	22988031	DEL	0.209133	6.467798
1p36.12	1	23037332	23241818	DEL	0.211823	6.598344
1p36.12	1	23345941	23410182	DEL	0.211823	6.598344
1p36.12	1	23410516	23504301	DEL	0.239393	8.237752
1p36.12	1	23516993	23521222	DEL	0.207116	6.380432
1p36.12	1	23630264	23670829	DEL	0.207116	6.380432
1p36.12	1	23685941	23695935	DEL	0.210478	6.529394
1p36.12	1	23695490	23698332	DEL	0.210478	6.529394
1p36.12	1	23707554	23751233	DEL	0.201736	6.036226
1p36.12	1	23755056	23811061	DEL	0.192994	5.625492
1p36.12	1	23832922	23857712	DEL	0.201064	6.017463
1p36.12	1	23884409	23886285	DEL	0.208461	6.44755
1p36.11	1	23907985	23967058	DEL	0.208461	6.44755
1p36.11	1	24018269	24022915	DEL	0.205771	6.302746
1p36.11	1	24069645	24088549	DEL	0.21115	6.576902
1p36.11	1	24104895	24114722	DEL	0.207116	6.380432
1p36.11	1	24117460	24122029	DEL	0.206443	6.361183
1p36.11	1	24122089	24127271	DEL	0.206443	6.361183
1p36.11	1	24128375	24165110	DEL	0.205098	6.230337
1p36.11	1	24171567	24194784	DEL	0.203081	6.145609
1p36.11	1	24197016	24285549	DEL	0.211823	6.598344
1p36.11	1	24285599	24289952	DEL	0.207788	6.401634
1p36.11	1	24291294	24307417	DEL	0.207788	6.401634
1p36.11	1	24382525	24438665	DEL	0.184925	5.120697
1p36.11	1	24446261	24469611	DEL	0.203753	6.181664
1p36.11	1	24645812	24690972	DEL	0.199719	5.938146
1p36.11	1	24742284	24799466	DEL	0.211823	6.598344
1p36.11	1	24829387	24867530	DEL	0.237376	8.126215
1p36.11	1	24958207	24999758	DEL	0.237376	8.126215
1p36.11	1	25071848	25170815	DEL	0.200391	5.95937
1p36.11	1	25226002	25291612	DEL	0.203753	6.163726
1p36.11	1	25549170	25558993	DEL	0.205771	6.285577
1p36.11	1	25568728	25664704	DEL	0.206443	6.322945
1p36.11	1	25598884	25656936	DEL	0.201064	6.017463
1p36.11	1	25664408	25688852	DEL	0.205771	6.268449

1p36.11	1	25688740	25756683	DEL	0.205771	6.268449
1p36.11	1	25757388	25826700	DEL	0.201064	5.998794
1p36.11	1	25870071	25895377	DEL	0.203753	6.163726
1p36.11	1	25943959	26112698	DEL	0.201064	5.998794
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1p36.11	1	26187701	26197744	DEL	0.208461	6.424215
1p36.11	1	26210672	26233482	DEL	0.211823	6.598344
1p36.11	1	26286258	26324648	DEL	0.200391	5.95937
1p36.11	1	26346375	26362955	DEL	0.202408	6.08657
1p36.11	1	26363743	26372624	DEL	0.217875	6.954475
1p36.11	1	26377795	26394927	DEL	0.22191	7.202565
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1p36.11	1	26485511	26489119	DEL	0.22191	7.202565
1p36.11	1	26496362	26498551	DEL	0.223255	7.26843
1p36.11	1	26503894	26516377	DEL	0.214513	6.737196
1p36.11	1	26517052	26529459	DEL	0.217875	6.954475
1p36.11	1	26560691	26605299	DEL	0.21115	6.582661
1p36.11	1	26605667	26608007	DEL	0.223255	7.26843
1p36.11	1	26607819	26644854	DEL	0.223255	7.26843
1p36.11	1	26644448	26647014	DEL	0.22191	7.179275
1p36.11	1	26648350	26680621	DEL	0.212495	6.636263
1p36.11	1	26688125	26701013	DEL	0.21922	7.065392
1p36.11	1	26737269	26756213	DEL	0.21922	7.065392
1p36.11	1	26758773	26797785	DEL	0.220565	7.133888
1p36.11	1	26798941	26802463	DEL	0.220565	7.133888
1p36.11	1	26856252	26901521	DEL	0.224599	7.344505
1p36.11	1	27022524	27108595	DEL	0.205098	6.227819
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1p36.11	1	27153201	27184093	DEL	0.223927	7.319644
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1p36.11	1	27226729	27273353	DEL	0.221237	7.154335
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1p36.11	1	27425306	27493472	DEL	0.215185	6.756567
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1p35.3	1	28261504	28285668	DEL	0.217875	6.930095
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1p35.3	1	28879597	28905051	DEL	0.259567	9.60778
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1p35.3	1	29138654	29190208	DEL	0.273016	10.479514
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1p35.3	1	29563028	29653325	DEL	0.18089	4.918433
1p35.2	1	31184124	31196434	DEL	0.180218	4.904653
1p35.2	1	31205316	31230667	DEL	0.171476	4.348633
1p35.2	1	31342314	31381608	DEL	0.165424	4.061661

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1p35.2	1	31838472	31849697	DEL	0.154664	3.556518
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1p35.2	1	32192718	32230494	DEL	0.190977	5.471653
1p35.2	1	32256023	32281652	DEL	0.190977	5.471653
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1p34.3	1	35449523	35497569	DEL	0.129784	2.391604
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1p34.3	1	35899091	36023551	DEL	0.125076	2.219334
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1p34.3	1	36038971	36060929	DEL	0.126421	2.320971
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1p34.3	1	36621180	36646450	DEL	0.123731	2.15998
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1p34.3	1	36771988	36790484	DEL	0.129111	2.35934
1p34.3	1	36805225	36851497	DEL	0.138525	2.825135
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1p31.3	1	61330931	61928465	DEL	0.162734	3.903618
1p31.3	1	62146718	62191095	DEL	0.18627	5.173454
1p12	1	1.18E+08	1.19E+08	AMP	0.385091	2.461837
1p12	1	1.19E+08	1.2E+08	AMP	0.447563	3.696626
1p12	1	1.2E+08	1.2E+08	AMP	0.447563	3.696626
1p12	1	1.2E+08	1.2E+08	AMP	0.478799	4.420788
1p12	1	1.2E+08	1.2E+08	AMP	0.478799	4.420788
1p12	1	1.2E+08	1.2E+08	AMP	0.431945	3.347715

1p12	1	1.2E+08	1.2E+08	AMP	0.463181	4.050036
1p12	1	1.2E+08	1.2E+08	AMP	0.463181	4.050036
1p12	1	1.2E+08	1.2E+08	AMP	0.463181	4.050036
1p12	1	1.2E+08	1.2E+08	AMP	0.463181	4.050036
1p12	1	1.2E+08	1.2E+08	AMP	0.494417	4.796174
1p12	1	1.2E+08	1.21E+08	AMP	0.510035	5.184576
1p11.2	1	1.21E+08	1.21E+08	AMP	0.437304	3.454418
1p11.2	1	1.21E+08	1.21E+08	AMP	0.421686	3.130086
1q21.1	1	1.44E+08	1.44E+08	AMP	0.374442	2.260728
1q21.1	1	1.45E+08	1.45E+08	AMP	0.405678	2.826772
1q21.1	1	1.45E+08	1.45E+08	AMP	0.421296	3.130086
1q21.1	1	1.45E+08	1.45E+08	AMP	0.39006	2.542309
1q21.1	1	1.45E+08	1.45E+08	AMP	0.405678	2.826772
1q21.1	1	1.45E+08	1.45E+08	AMP	0.405626	2.826772
1q21.1	1	1.45E+08	1.45E+08	AMP	0.45248	3.805317
1q21.1	1	1.45E+08	1.45E+08	AMP	0.45248	3.805317
1q21.1	1	1.45E+08	1.46E+08	AMP	0.45248	3.805317
1q21.1	1	1.46E+08	1.46E+08	AMP	0.45248	3.805317
1q21.1	1	1.46E+08	1.46E+08	AMP	0.45248	3.805317
1q21.1	1	1.46E+08	1.46E+08	AMP	0.421244	3.130086
1q21.1	1	1.47E+08	1.47E+08	AMP	0.374473	2.260728
1q21.1	1	1.47E+08	1.47E+08	AMP	0.374473	2.260728
1q21.1	1	1.47E+08	1.47E+08	AMP	0.374473	2.260728
1q21.2	1	1.47E+08	1.47E+08	AMP	0.374473	2.260728
1q21.2	1	1.47E+08	1.47E+08	AMP	0.374473	2.260728
1q21.2	1	1.47E+08	1.47E+08	AMP	0.374473	2.260728
1q21.2	1	1.47E+08	1.47E+08	AMP	0.374473	2.260728
1q21.2	1	1.47E+08	1.47E+08	AMP	0.374473	2.260728
1q21.2	1	1.48E+08	1.48E+08	AMP	0.400349	2.734703
1q21.2	1	1.5E+08	1.5E+08	AMP	0.545943	6.080823
1q21.2	1	1.5E+08	1.5E+08	AMP	0.971896	18.30486
1q21.2	1	1.5E+08	1.5E+08	AMP	1.029009	20.361303
1q21.2	1	1.5E+08	1.5E+08	AMP	1.044483	20.965742
1q21.2	1	1.5E+08	1.5E+08	AMP	1.075719	22.180584
1q21.2	1	1.5E+08	1.5E+08	AMP	1.075719	22.180584
1q21.2	1	1.5E+08	1.5E+08	AMP	1.075719	22.180584
1q21.2	1	1.5E+08	1.5E+08	AMP	1.075719	22.180584
1q21.2	1	1.5E+08	1.5E+08	AMP	1.018606	20.054081
1q21.2	1	1.5E+08	1.5E+08	AMP	1.018606	20.054081
1q21.2	1	1.5E+08	1.5E+08	AMP	0.987361	18.905361
1q21.2	1	1.5E+08	1.5E+08	AMP	0.987361	18.905361
1q21.2	1	1.5E+08	1.5E+08	AMP	0.987361	18.905361
1q21.2	1	1.5E+08	1.5E+08	AMP	0.514891	5.310901
1q21.2	1	1.5E+08	1.5E+08	AMP	0.561745	6.479814
1q21.2	1	1.5E+08	1.5E+08	AMP	0.483655	4.534289
1q21.2	1	1.5E+08	1.5E+08	AMP	0.405565	2.826772
1q21.2	1	1.5E+08	1.5E+08	AMP	0.374329	2.260728
1q21.2	1	1.5E+08	1.5E+08	AMP	0.374329	2.260728
1q21.2	1	1.5E+08	1.5E+08	AMP	0.405565	2.826772
1q21.2	1	1.5E+08	1.5E+08	AMP	0.405565	2.826772
1q21.2	1	1.5E+08	1.5E+08	AMP	0.405565	2.826772
1q21.2	1	1.5E+08	1.5E+08	AMP	0.405565	2.826772
1q21.2	1	1.5E+08	1.5E+08	AMP	0.405565	2.826772
1q21.2	1	1.5E+08	1.5E+08	AMP	0.405565	2.826772
1q21.2	1	1.5E+08	1.5E+08	AMP	0.405565	2.826772
1q21.2	1	1.5E+08	1.5E+08	AMP	0.405565	2.826772
1q21.2	1	1.5E+08	1.5E+08	AMP	0.405565	2.826772
1q21.2	1	1.5E+08	1.5E+08	AMP	0.405565	2.826772
1q21.2	1	1.5E+08	1.5E+08	AMP	0.405565	2.826772
1q21.2	1	1.5E+08	1.5E+08	AMP	0.405565	2.826772
1q21.2	1	1.5E+08	1.5E+08	AMP	0.405565	2.826772
1q21.2	1	1.5E+08	1.5E+08	AMP	0.405565	2.826772
1q21.2	1	1.5E+08	1.5E+08	AMP	0.405565	2.826772
1q21.2	1	1.5E+08	1.5E+08	AMP	0.405565	2.826772
1q21.2	1	1.5E+08	1.5E+08	AMP	0.405565	2.826772
1q21.2	1	1.5E+08	1.5E+08	AMP	0.405565	2.826772
1q21.2	1	1.5E+08	1.5E+08	AMP	0.405565	2.826772
1q21.2	1	1.5E+08	1.5E+08	AMP	0.405565	2.826772
1q21.2	1	1.5E+08	1.5E+08	AMP	0.405565	2.826772
1q21.2	1	1.5E+08	1.5E+08	AMP	0.405565	2.826772
1q21.2	1	1.5E+08	1.5E+08	AMP	0.405565	2.826772
1q21.2	1	1.5E+08	1.5E+08	AMP	0.405565	2.826772
1q21.2	1	1.5E+08	1.5E+08	AMP	0.405565	2.826772
1q21.2	1	1.5E+08	1.5E+08	AMP	0.405565	2.826772
1q21.2	1	1.5E+08	1.5E+08	AMP	0.405565	2.826772
1q21.2	1	1.5E+08	1.5E+08	AMP	0.405565	2.826772
1q21.2	1	1.5E+08	1.5E+08	AMP	0.405565	2.826772
1q21.2	1	1.5E+08	1.5E+08	AMP	0.405565	2.826772
1q21.2	1	1.5E+08	1.5E+08	AMP	0.405565	2.826772
1q21.2	1	1.5E+08	1.5E+08	AMP	0.405565	2.826772
1q21.2	1	1.5E+08	1.5E+08	AMP	0.405565	2.826772
1q21.2	1	1.5E+08	1.5E+08	AMP	0.405565	2.826772
1q21.2	1	1.5E+08	1.5E+08	AMP	0.405565	2.826772
1q21.2	1	1.5E+08	1.5E+08	AMP	0.405565	2.826772
1q21.2	1	1.5E+08	1.5E+08	AMP	0.405565	2.826772
1q21.2	1	1.5E+08	1.5E+08	AMP	0.405565	2.826772
1q21.2	1	1.5E+08	1.5E+08	AMP	0.405565	2.826772
1q21.2	1	1.5E+08	1.5E+08	AMP	0.405565	2.826772
1q21.2	1	1.5E+08	1.5E+08	AMP	0.405565	2.826772
1q21.2	1	1.5E+08	1.5E+08	AMP	0.405565	2.826772
1q21.2	1	1.5E+08	1.5E+08	AMP	0.405565	2.826772
1q21.2	1	1.5E+08	1.5E+08	AMP	0.405565	2.826772
1q21.2	1	1.5E+08	1.5E+08	AMP	0.405565	2.826772
1q21.2	1	1.5E+08	1.5E+08	AMP	0.405565	2.826772
1q21.2	1	1.5E+08	1.5E+08	AMP	0.405565	2.826772
1q21.2	1	1.5E+08	1.5E+08	AMP	0.405565	2.826772
1q21.2	1	1.5E+08	1.5E+08	AMP	0.405565	2.826772
1q21.2	1	1.5E+08	1.5E+08	AMP	0.405565	2.826772
1q21.2	1	1.5E+08	1.5E+08	AMP	0.405565	2.826772
1q21.2	1	1.5E+08	1.5E+08	AMP	0.405565	2.826772
1q21.2	1	1.5E+08	1.5E+08	AMP	0.405565	2.826772
1q21.2	1	1.5E+08	1.5E+08	AMP	0.405565	2.826772
1q21.2	1	1.5E+08	1.5E+08	AMP	0.405565	2.826772
1q21.2	1	1.5E+08	1.5E+08	AMP	0.405565	2.826772
1q21.2	1	1.5E+08	1.5E+08	AMP	0.405565	2.826772
1q21.2	1	1.5E+08	1.5E+08	AMP	0.405565	2.826772
1q21.2	1	1.5E+08	1.5E+08	AMP	0.405565	2.826772
1q21.2	1	1.5E+08	1.5E+08	AMP	0.405565	2.826772
1q21.2	1	1.5E+08	1.5E+08	AMP	0.405565	2.826772
1q21.2	1	1.5E+08	1.5E+08	AMP	0.405565	2.826772
1q21.2	1	1.5E+08	1.5E+08	AMP	0.405565	2.826772
1q21.2	1	1.5E+08	1.5E+08	AMP	0.405565	2.826772
1q21.2	1	1.5E+08	1.5E+08	AMP		

[illegible]

[illegible]

[illegible]

1q23.2	1	1.6E+08	1.6E+08	AMP	0.51459	5.292904
1q23.2	1	1.6E+08	1.6E+08	AMP	0.498972	4.901153
1q23.3	1	1.61E+08	1.61E+08	AMP	0.498972	4.901153
1q23.3	1	1.61E+08	1.61E+08	AMP	0.498972	4.901153
1q23.3	1	1.61E+08	1.61E+08	AMP	0.498972	4.901153
1q23.3	1	1.61E+08	1.61E+08	AMP	0.498972	4.901153
1q23.3	1	1.61E+08	1.61E+08	AMP	0.483354	4.522536
1q23.3	1	1.61E+08	1.61E+08	AMP	0.483354	4.522536
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1q23.3	1	1.61E+08	1.61E+08	AMP	0.498972	4.901153
1q23.3	1	1.61E+08	1.61E+08	AMP	0.498972	4.901153
1q23.3	1	1.61E+08	1.61E+08	AMP	0.498972	4.901153
1q23.3	1	1.61E+08	1.61E+08	AMP	0.483268	4.522536
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1q23.3	1	1.61E+08	1.61E+08	AMP	0.467736	4.146257
1q23.3	1	1.61E+08	1.61E+08	AMP	0.467736	4.146257
1q23.3	1	1.61E+08	1.61E+08	AMP	0.452118	3.788967
1q23.3	1	1.61E+08	1.61E+08	AMP	0.452118	3.788967
1q23.3	1	1.61E+08	1.61E+08	AMP	0.4365	3.435456
1q23.3	1	1.61E+08	1.61E+08	AMP	0.452118	3.788967
1q23.3	1	1.61E+08	1.61E+08	AMP	0.452118	3.788967
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1q23.3	1	1.61E+08	1.61E+08	AMP	0.545826	6.066744
1q23.3	1	1.61E+08	1.61E+08	AMP	0.545826	6.066744
1q23.3	1	1.62E+08	1.62E+08	AMP	0.561445	6.479814
1q23.3	1	1.62E+08	1.62E+08	AMP	0.561445	6.479814
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1q23.3	1	1.62E+08	1.62E+08	AMP	0.530208	5.681668
1q23.3	1	1.62E+08	1.62E+08	AMP	0.530208	5.681668
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1q23.3	1	1.62E+08	1.62E+08	AMP	0.608299	7.773481
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1q23.3	1	1.62E+08	1.62E+08	AMP	0.608299	7.773481
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1q23.3	1	1.62E+08	1.62E+08	AMP	0.577063	6.880777
1q23.3	1	1.63E+08	1.63E+08	AMP	0.561445	6.479814
1q23.3	1	1.63E+08	1.63E+08	AMP	0.577063	6.880777
1q23.3	1	1.63E+08	1.63E+08	AMP	0.577063	6.8807

1q24.2	1	1.68E+08	1.68E+08	AMP	0.561445	6.479814
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1q24.2	1	1.69E+08	1.69E+08	AMP	0.561445	6.479814
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1q24.2	1	1.69E+08	1.69E+08	AMP	0.561445	6.479814
1q24.2	1	1.69E+08	1.69E+08	AMP	0.561445	6.479814
1q24.2	1	1.69E+08	1.69E+08	AMP	0.577063	6.880777
1q24.2	1	1.69E+08	1.69E+08	AMP	0.592681	7.319424
1q24.2	1	1.69E+08	1.69E+08	AMP	0.592681	7.319424
1q24.2	1	1.69E+08	1.7E+08	AMP	0.608299	7.773481
1q24.2	1	1.7E+08	1.7E+08	AMP	0.608299	7.773481
1q24.2	1	1.7E+08	1.7E+08	AMP	0.618711	8.056786
1q24.2	1	1.7E+08	1.7E+08	AMP	0.608299	7.773481
1q24.2	1	1.7E+08	1.7E+08	AMP	0.608299	7.773481
1q24.2	1	1.7E+08	1.7E+08	AMP	0.618711	8.056786
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1q24.2	1	1.7E+08	1.7E+08	AMP	0.587475	7.177432
1q24.2	1	1.7E+08	1.7E+08	AMP	0.571857	6.75454
1q24.2	1	1.71E+08	1.71E+08	AMP	0.571857	6.75454
1q24.2	1	1.71E+08	1.71E+08	AMP	0.571857	6.75454
1q24.3	1	1.71E+08	1.71E+08	AMP	0.571857	6.75454
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1q24.3	1	1.71E+08	1.72E+08	AMP	0.571857	6.75454
1q24.3	1	1.72E+08	1.72E+08	AMP	0.556239	6.350227
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1q24.3	1	1.72E+08	1.72E+08	AMP	0.54062	5.950715
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1q24.3	1	1.72E+08	1.72E+08	AMP	0.54062	5.950715
1q24.3	1	1.73E+08	1.73E+08	AMP	0.54062	5.950715
1q25.1	1	1.73E+08	1.73E+08	AMP	0.54062	5.950715
1q25.1	1	1.73E+08	1.73E+08	AMP	0.525166	5.565862
1q25.1	1	1.73E+08	1.73E+08	AMP	0.525166	5.565862
1q25.1	1	1.74E+08	1.74E+08	AMP	0.49385	4.783614
1q25.1	1	1.74E+08	1.74E+08	AMP	0.462614	4.045428
1q25.1	1	1.74E+08	1.74E+08	AMP	0.41584	3.026232
1q25.1	1	1.74E+08	1.74E+08	AMP	0.41584	3.026232
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1q25.1	1	1.74E+08	1.74E+08	AMP	0.41584	3.026232
1q25.1	1	1.74E+08	1.75E+08	AMP	0.447076	3.687345
1q25.1	1	1.74E+08	1.74E+08	AMP	0.41584	3.026232
1q25.1	1	1.75E+08	1.75E+08	AMP	0.447076	3.687345
1q25.1	1	1.75E+08	1.75E+08	AMP	0.452282	3.805317
1q25.1	1	1.75E+08	1.75E+08	AMP	0.483518	4.534289
1q25.1	1	1.75E+08	1.75E+08	AMP	0.483518	4.534289
1q25.1	1	1.75E+08	1.76E+08	AMP	0.483518	4.534289
1q25.1	1	1.76E+08	1.76E+08	AMP	0.504342	5.041368
1q25.2	1	1.76E+08	1.77E+08	AMP	0.483518	4.534289
1q25.2	1	1.77E+08	1.77E+08	AMP	0.483518	4.534289
1q25.2	1	1.78E+08	1.78E+08	AMP	0.4679	4.164895
1q25.2	1	1.78E+08	1.78E+08	AMP	0.4679	4.164895
1q25.2	1	1.79E+08	1.79E+08	AMP	0.421046	3.130086
1q25.2	1	1.79E+08	1.79E+08	AMP	0.421046	3.130086
1q25.2	1	1.79E+08	1.79E+08	AMP	0.421046	3.130086
1q25.2	1	1.79E+08	1.79E+08	AMP	0.374192	2.260728
1q25.2	1	1.79E+08	1.79E+08	AMP	0.374192	2.260728
1q25.2	1	1.79E+08	1.79E+08	AMP	0.368986	2.170574
1q25.2	1	1.79E+08	1.8E+08	AMP	0.368986	2.170574
1q25.2	1	1.8E+08	1.8E+08	AMP	0.368986	2.170574
1q25.2	1	1.8E+08	1.8E+08	AMP	0.368986	2.170574
1q25.2	1	1.8E+08	1.8E+08	AMP	0.368986	2.170574
1q25.2	1	1.8E+08	1.8E+08	AMP	0.368986	2.170574
1q25.2	1	1.8E+08	1.8E+08	AMP	0.368986	2.170574
1q25.2	1	1.8E+08	1.8E+08	AMP	0.368986	2.170574
1q25.2	1	1.8E+08	1.8E+08	AMP	0.384604	2.452057
1q25.2	1	1.8E+08	1.8E+08	AMP	0.384604	2.452057
1q25.2	1	1.8E+08	1.8E+08	AMP	0.400222	2.734703
1q25.3	1	1.81E+08	1.81E+08	AMP	0.41584	3.026232
1q25.3	1	1.81E+08	1.81E+08	AMP	0.405428	2.826772
1q25.3	1	1.81E+08	1.81E+08	AMP	0.405428	2.826772
1q25.3	1	1.81E+08	1.81E+08	AMP	0.405428	2.826772
1q25.3	1	1.81E+08	1.81E+08	AMP	0.421046	3.130086
1q25.3	1	1.81E+08	1.82E+08	AMP	0.4679	4.164895
1q25.3	1	1.82E+08	1.82E+08	AMP	0.421046	3.130086

1q25.3	1	1.82E+08	1.82E+08	AMP	0.421046	3.130086
1q25.3	1	1.82E+08	1.82E+08	AMP	0.405428	2.826772
1q25.3	1	1.82E+08	1.83E+08	AMP	0.405428	2.826772
1q25.3	1	1.83E+08	1.83E+08	AMP	0.405428	2.826772
1q25.3	1	1.83E+08	1.83E+08	AMP	0.405428	2.826772
1q25.3	1	1.83E+08	1.83E+08	AMP	0.405428	2.826772
1q25.3	1	1.83E+08	1.83E+08	AMP	0.41584	3.026232
1q25.3	1	1.83E+08	1.83E+08	AMP	0.41584	3.026232
1q25.3	1	1.83E+08	1.83E+08	AMP	0.41584	3.026232
1q25.3	1	1.83E+08	1.83E+08	AMP	0.405428	2.826772
1q25.3	1	1.83E+08	1.83E+08	AMP	0.421046	3.130086
1q25.3	1	1.83E+08	1.83E+08	AMP	0.421046	3.130086
1q25.3	1	1.83E+08	1.84E+08	AMP	0.421046	3.130086
1q25.3	1	1.84E+08	1.84E+08	AMP	0.421046	3.130086
1q25.3	1	1.84E+08	1.84E+08	AMP	0.421046	3.130086
1q25.3	1	1.84E+08	1.84E+08	AMP	0.421046	3.130086
1q25.3	1	1.84E+08	1.84E+08	AMP	0.421046	3.130086
1q25.3	1	1.84E+08	1.84E+08	AMP	0.473106	4.276863
1q25.3	1	1.84E+08	1.85E+08	AMP	0.473106	4.276863
1q25.3	1	1.85E+08	1.85E+08	AMP	0.473106	4.276863
1q25.3	1	1.85E+08	1.85E+08	AMP	0.473106	4.276863
1q25.3	1	1.85E+08	1.85E+08	AMP	0.457488	3.919138
1q25.3	1	1.85E+08	1.85E+08	AMP	0.457488	3.919138
1q25.3	1	1.85E+08	1.85E+08	AMP	0.51996	5.443497
1q25.3	1	1.85E+08	1.85E+08	AMP	0.629286	8.340644
1q25.3	1	1.86E+08	1.86E+08	AMP	0.769848	12.389332
1q31.1	1	1.86E+08	1.86E+08	AMP	0.707376	10.512157
1q31.1	1	1.86E+08	1.86E+08	AMP	0.691758	10.105903
1q31.1	1	1.86E+08	1.86E+08	AMP	0.660522	9.208694
1q31.1	1	1.86E+08	1.86E+08	AMP	0.660522	9.208694
1q31.1	1	1.86E+08	1.86E+08	AMP	0.660522	9.208694
1q31.1	1	1.87E+08	1.87E+08	AMP	0.660522	9.208694
1q31.1	1	1.87E+08	1.87E+08	AMP	0.660522	9.208694
1q31.2	1	1.92E+08	1.92E+08	AMP	0.644904	8.777787
1q31.2	1	1.92E+08	1.92E+08	AMP	0.644904	8.777787
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1q31.2	1	1.93E+08	1.93E+08	AMP	0.629286	8.340644
1q31.2	1	1.93E+08	1.93E+08	AMP	0.660522	9.208694
1q31.2	1	1.93E+08	1.93E+08	AMP	0.660522	9.208694
1q31.2	1	1.93E+08	1.93E+08	AMP	0.629286	8.340644
1q31.3	1	1.96E+08	1.97E+08	AMP	0.644904	8.777787
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1q31.3	1	1.98E+08	1.98E+08	AMP	0.643703	8.776326
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1q31.3	1	1.98E+08	1.98E+08	AMP	0.643703	8.776326
1q31.3	1	1.98E+08	1.99E+08	AMP	0.643703	8.776326
1q31.3	1	1.99E+08	1.99E+08	AMP	0.643703	8.776326
1q32.1	1	2E+08	2E+08	AMP	0.440669	3.537187
1q32.1	1	2.01E+08	2.01E+08	AMP	0.404019	2.786724
1q32.1	1	2.03E+08	2.03E+08	AMP	0.372991	2.22297
1q32.1	1	2.03E+08	2.03E+08	AMP	0.372991	2.22297
1q32.1	1	2.03E+08	2.03E+08	AMP	0.372991	2.22297
1q32.1	1	2.03E+08	2.03E+08	AMP	0.388609	2.504901
1q32.1	1	2.03E+08	2.03E+08	AMP	0.388609	2.504901
1q32.1	1	2.04E+08	2.04E+08	AMP	0.374192	2.260728
1q32.1	1	2.04E+08	2.04E+08	AMP	0.374192	2.260728
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1q32.1	1	2.04E+08	2.04E+08	AMP	0.405428	2.826772
1q32.1	1	2.04E+08	2.05E+08	AMP	0.405428	2.826772
1q32.1	1	2.05E+08	2.05E+08	AMP	0.38981	2.542309
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1q32.1	1	2.05E+08	2.05E+08	AMP	0.38981	2.542309

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1q32.1	1	2.05E+08	2.05E+08	AMP	0.38981	2.542309
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1q32.1	1	2.06E+08	2.06E+08	AMP	0.38981	2.542309
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1q32.1	1	2.07E+08	2.07E+08	AMP	0.405428	2.826772
1q32.1	1	2.07E+08	2.07E+08	AMP	0.405428	2.826772
1q32.1	1	2.07E+08	2.07E+08	AMP	0.405428	2.826772
1q32.1	1	2.07E+08	2.07E+08	AMP	0.405428	2.826772
1q32.1	1	2.07E+08	2.07E+08	AMP	0.405428	2.826772
1q32.1	1	2.07E+08	2.07E+08	AMP	0.421046	3.130086
1q32.1	1	2.07E+08	2.07E+08	AMP	0.421046	3.130086
1q32.1	1	2.07E+08	2.07E+08	AMP	0.421046	3.130086
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1q32.1	1	2.07E+08	2.07E+08	AMP	0.421046	3.130086
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1q32.1	1	2.07E+08	2.07E+08	AMP	0.421046	3.130086
1q32.2	1	2.07E+08	2.07E+08	AMP	0.421046	3.130086
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1q32.2	1	2.07E+08	2.07E+08	AMP	0.421046	3.130086
1q32.2	1	2.07E+08	2.07E+08	AMP	0.421046	3.130086
1q32.2	1	2.07E+08	2.08E+08	AMP	0.436664	3.454418
1q32.2	1	2.08E+08	2.08E+08	AMP	0.421046	3.130086
1q32.2	1	2.08E+08	2.08E+08	AMP	0.421046	3.130086
1q32.2	1	2.08E+08	2.08E+08	AMP	0.421046	3.130086
1q32.2	1	2.08E+08	2.08E+08	AMP	0.421046	3.130086
1q32.2	1	2.08E+08	2.08E+08	AMP	0.452282	3.805317
1q32.2	1	2.08E+08	2.08E+08	AMP	0.483518	4.534289
1q32.2	1	2.08E+08	2.08E+08	AMP	0.483518	4.534289
1q32.2	1	2.1E+08	2.1E+08	AMP	0.452282	3.805317
1q32.2	1	2.1E+08	2.1E+08	AMP	0.436664	3.454418
1q32.2	1	2.1E+08	2.1E+08	AMP	0.436664	3.454418
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1q32.3	1	2.13E+08	2.13E+08	AMP	0.369031	2.170574
1q32.3	1	2.14E+08	2.14E+08	AMP	0.369031	2.170574
1q32.3	1	2.14E+08	2.15E+08	AMP	0.369031	2.170574
1q41	1	2.15E+08	2.15E+08	AMP	0.369031	2.170574
1q41	1	2.15E+08	2.15E+08	AMP	0.415885	3.026232
1q41	1	2.15E+08	2.15E+08	AMP	0.46274	4.045428
1q41	1	2.16E+08	2.16E+08	AMP	0.509594	5.178139
1q41	1	2.16E+08	2.17E+08	AMP	0.54083	5.950715
1q41	1	2.17E+08	2.17E+08	AMP	0.54083	5.950715
1q41	1	2.18E+08	2.18E+08	AMP	0.509594	5.178139
1q41	1	2.18E+08	2.18E+08	AMP	0.478358	4.4071
1q41	1	2.18E+08	2.19E+08	AMP	0.46274	4.045428
1q41	1	2.19E+08	2.19E+08	AMP	0.447122	3.687345
1q41	1	2.19E+08	2.19E+08	AMP	0.447122	3.687345
1q41	1	2.22E+08	2.22E+08	AMP	0.369031	2.170574
1q42.13	1	2.28E+08	2.28E+08	AMP	0.368867	2.170574
1q42.13	1	2.28E+08	2.28E+08	AMP	0.368867	2.170574
1q42.13	1	2.28E+08	2.28E+08	AMP	0.368867	2.170574
1q42.13	1	2.28E+08	2.28E+08	AMP	0.400103	2.734703
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1q42.13	1	2.28E+08	2.28E+08	AMP	0.400103	2.734703
1q42.13	1	2.28E+08	2.28E+08	AMP	0.400103	2.734703
1q42.13	1	2.28E+08	2.29E+08	AMP	0.550905	6.218078
1q42.13	1	2.29E+08	2.29E+08	AMP	0.415721	3.026232
1q42.13	1	2.29E+08	2.29E+08	AMP	0.446957	3.687345
1q42.13	1	2.29E+08	2.29E+08	AMP	0.488451	4.654156
1q42.13	1	2.29E+08	2.29E+08	AMP	0.488451	4.654156
1q42.13	1	2.29E+08	2.29E+08	AMP	0.488451	4.654156
1q42.13	1	2.29E+08	2.29E+08	AMP	0.400103	2.734703
1q43	1	2.37E+08	2.37E+08	AMP	0.394908	2.617738
1q43	1	2.37E+08	2.38E+08	AMP	0.441762	3.561562
1q43	1	2.38E+08	2.38E+08	AMP	0.441762	3.561562
1q43	1	2.4E+08	2.4E+08	AMP	0.415885	3.026232
1q43	1	2.4E+08	2.41E+08	AMP	0.369031	2.170574
1q43	1	2.41E+08	2.41E+08	AMP	0.369031	2.170574

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1q43	1	2.42E+08	2.42E+08	AMP	0.46274	4.045428
1q43	1	2.42E+08	2.42E+08	AMP	0.384649	2.452057
1q43	1	2.42E+08	2.42E+08	AMP	0.46274	4.045428
1q43	1	2.42E+08	2.42E+08	AMP	0.369031	2.170574
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1q43	1	2.43E+08	2.43E+08	AMP	0.384649	2.452057
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1q44	1	2.45E+08	2.45E+08	AMP	0.400267	2.734703
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1q44	1	2.45E+08	2.45E+08	AMP	0.400267	2.734703
1q44	1	2.49E+08	2.49E+08	AMP	0.371893	2.206365
1q44	1	2.49E+08	2.49E+08	AMP	0.418747	3.068581
1q44	1	2.49E+08	2.49E+08	AMP	0.418747	3.068581
1q44	1	2.49E+08	2.49E+08	AMP	0.387511	2.487286
1q44	1	2.49E+08	2.49E+08	AMP	0.387511	2.487286
2q12.1	2	1.03E+08	1.03E+08	DEL	0.186942	5.193166
2q12.1	2	1.05E+08	1.05E+08	DEL	0.184252	5.078605
2q22.3	2	1.45E+08	1.45E+08	AMP	0.369534	2.181486
2q24.2	2	1.61E+08	1.61E+08	AMP	0.369534	2.181486
2q24.2	2	1.61E+08	1.61E+08	AMP	0.369534	2.181486
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2q24.2	2	1.61E+08	1.61E+08	AMP	0.385152	2.461837
2q24.2	2	1.62E+08	1.62E+08	AMP	0.40077	2.743536
2q24.2	2	1.62E+08	1.62E+08	AMP	0.40077	2.743536
2q24.2	2	1.62E+08	1.62E+08	AMP	0.385152	2.461837
2q24.2	2	1.62E+08	1.63E+08	AMP	0.40077	2.743536
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2q24.2	2	1.63E+08	1.64E+08	AMP	0.40077	2.743536
2q24.3	2	1.64E+08	1.65E+08	AMP	0.40077	2.743536
2q24.3	2	1.65E+08	1.65E+08	AMP	0.40077	2.743536
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2q24.3	2	1.66E+08	1.67E+08	AMP	0.40077	2.743536
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2q24.3	2	1.67E+08	1.67E+08	AMP	0.40077	2.743536
2q24.3	2	1.67E+08	1.67E+08	AMP	0.40077	2.743536
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2q24.3	2	1.67E+08	1.67E+08	AMP	0.40077	2.743536
2q24.3	2	1.67E+08	1.67E+08	AMP	0.40077	2.743536
2q24.3	2	1.68E+08	1.68E+08	AMP	0.40077	2.743536
2q31.1	2	1.72E+08	1.72E+08	DEL	0.134491	2.524586
2q31.1	2	1.72E+08	1.72E+08	DEL	0.134491	2.524586
2q31.2	2	1.79E+08	1.79E+08	AMP	0.369534	2.181486
2q31.2	2	1.79E+08	1.79E+08	AMP	0.369534	2.181486
2q31.2	2	1.79E+08	1.79E+08	AMP	0.385152	2.461837
2q31.2	2	1.79E+08	1.79E+08	AMP	0.541332	5.952
2q31.2	2	1.79E+08	1.8E+08	AMP	0.749572	11.744714
2q31.2	2	1.8E+08	1.8E+08	AMP	0.603804	7.646423
2q31.2	2	1.8E+08	1.8E+08	AMP	0.536126	5.841368
2q31.2	2	1.8E+08	1.81E+08	AMP	0.536126	5.841368
2q31.3	2	1.81E+08	1.81E+08	AMP	0.536126	5.841368
2q31.3	2	1.82E+08	1.82E+08	AMP	0.536126	5.841368
2q31.3	2	1.82E+08	1.82E+08	AMP	0.520508	5.45786
2q31.3	2	1.82E+08	1.83E+08	AMP	0.520508	5.45786
2q31.3	2	1.83E+08	1.83E+08	AMP	0.489272	4.668539
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2q31.3	2	1.83E+08	1.83E+08	AMP	0.489272	4.668539
2q32.1	2	1.83E+08	1.83E+08	AMP	0.473654	4.291441
2q32.1	2	1.84E+08	1.84E+08	AMP	0.4268	3.239278
2q32.1	2	1.84E+08	1.84E+08	AMP	0.379946	2.36057
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2q32.1	2	1.85E+08	1.86E+08	AMP	0.379946	2.36057
2q32.1	2	1.87E+08	1.87E+08	AMP	0.411182	2.92897
2q32.1	2	1.87E+08	1.87E+08	AMP	0.4268	3.239278
2q32.1	2	1.87E+08	1.88E+08	AMP	0.411182	2.92897
2q32.1	2	1.88E+08	1.88E+08	AMP	0.411182	2.92897
2q32.1	2	1.88E+08	1.88E+08	AMP	0.442418	3.578278

2q32.1	2	1.88E+08	1.88E+08	AMP	0.442418	3.578278
2q32.1	2	1.88E+08	1.88E+08	AMP	0.458036	3.935663
2q32.1	2	1.89E+08	1.89E+08	AMP	0.567362	6.628295
2q32.2	2	1.9E+08	1.9E+08	AMP	0.692306	10.114513
2q32.2	2	1.9E+08	1.9E+08	AMP	0.786014	12.866303
2q32.2	2	1.9E+08	1.9E+08	AMP	0.723542	10.957701
2q32.2	2	1.9E+08	1.9E+08	AMP	0.489272	4.668539
2q32.2	2	1.9E+08	1.9E+08	AMP	0.395564	2.638263
2q32.2	2	1.91E+08	1.91E+08	AMP	0.364327	2.083496
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2q32.2	2	1.91E+08	1.91E+08	AMP	0.379946	2.36057
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2q32.2	2	1.92E+08	1.92E+08	AMP	0.379946	2.36057
2q32.3	2	1.93E+08	1.93E+08	AMP	0.411182	2.92897
2q32.3	2	1.93E+08	1.93E+08	AMP	0.379946	2.36057
2q34	2	2.1E+08	2.11E+08	AMP	0.385152	2.461837
2q34	2	2.11E+08	2.11E+08	AMP	0.385152	2.461837
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2q34	2	2.11E+08	2.11E+08	AMP	0.364327	2.083496
2q34	2	2.11E+08	2.11E+08	AMP	0.364327	2.083496
2q34	2	2.11E+08	2.11E+08	AMP	0.379946	2.36057
2q34	2	2.11E+08	2.12E+08	AMP	0.411182	2.92897
2q34	2	2.12E+08	2.13E+08	AMP	0.395564	2.638263
2q34	2	2.14E+08	2.14E+08	AMP	0.395564	2.638263
2q34	2	2.15E+08	2.15E+08	AMP	0.364317	2.083496
2q35	2	2.16E+08	2.16E+08	AMP	0.364317	2.083496
2q37.3	2	2.39E+08	2.39E+08	AMP	0.363777	2.064112
3p21.31	3	46963216	47023500	DEL	0.146595	3.088303
3p21.31	3	47021173	47051193	DEL	0.146595	3.088303
3p21.31	3	47057919	47205457	DEL	0.205098	6.228164
3p21.31	3	48488114	48507115	DEL	0.168113	4.203141
3p21.31	3	48506445	48509044	DEL	0.168113	4.203141
3p21.31	3	48509197	48542259	DEL	0.192322	5.541144
3p21.31	3	48601506	48632700	DEL	0.156009	3.605205
3p21.31	3	48673902	48700348	DEL	0.164079	3.960617
3p21.31	3	48894369	48936426	DEL	0.187615	5.239546
3p21.31	3	48956254	49023815	DEL	0.206443	6.359325
3p21.31	3	49315264	49378145	DEL	0.207788	6.400225
3p21.31	3	49394609	49396033	DEL	0.207788	6.400225
3p21.31	3	49396578	49450431	DEL	0.205771	6.30074
3p21.31	3	49449639	49453908	DEL	0.205771	6.30074
3p21.31	3	49591922	49708978	DEL	0.169458	4.268162
3p21.31	3	49711435	49721396	DEL	0.169458	4.268162
3p21.31	3	49721380	49726934	DEL	0.162734	3.89802
3p21.31	3	49726932	49758962	DEL	0.152647	3.496026
3p21.31	3	49754267	49761349	DEL	0.152647	3.496026
3p21.31	3	49754277	49761384	DEL	0.152647	3.496026
3p21.31	3	49761727	49823975	DEL	0.151974	3.426383
3p21.31	3	49828165	49837268	DEL	0.149285	3.256771
3p21.31	3	50192478	50226508	DEL	0.169458	4.262536
3p21.31	3	50229045	50233949	DEL	0.124404	2.193364
3p21.2	3	50643921	50649262	DEL	0.171476	4.352078
3p21.2	3	50648951	50686720	DEL	0.174838	4.487614
3p14.3	3	58413357	58419584	DEL	0.148612	3.200026
3p14.3	3	58477841	58488087	DEL	0.151302	3.364924
3p14.3	3	58490863	58523046	DEL	0.162061	3.882499
3p14.3	3	58549844	58613337	DEL	0.199046	5.902118
3q21.3	3	1.28E+08	1.28E+08	DEL	0.139198	2.876905
3q26.1	3	1.61E+08	1.61E+08	AMP	0.374832	2.260728
3q26.1	3	1.65E+08	1.65E+08	AMP	0.406068	2.826772
3q26.1	3	1.65E+08	1.65E+08	AMP	0.406068	2.826772
3q26.1	3	1.65E+08	1.66E+08	AMP	0.406068	2.826772
3q26.1	3	1.67E+08	1.67E+08	AMP	0.406068	2.826772
3q26.1	3	1.67E+08	1.67E+08	AMP	0.406068	2.826772
3q26.1	3	1.67E+08	1.67E+08	AMP	0.39045	2.542309
3q26.1	3	1.67E+08	1.68E+08	AMP	0.39045	2.542309
3q26.2	3	1.68E+08	1.68E+08	AMP	0.446689	3.687345

3q26.2	3	1.69E+08	1.69E+08	AMP	0.390459	2.542309
3q27.3	3	1.87E+08	1.87E+08	AMP	0.374523	2.260728
3q27.3	3	1.87E+08	1.87E+08	AMP	0.374523	2.260728
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3q27.3	3	1.87E+08	1.87E+08	AMP	0.390141	2.542309
3q27.3	3	1.88E+08	1.88E+08	AMP	0.390141	2.542309
3q27.3	3	1.88E+08	1.89E+08	AMP	0.390141	2.542309
3q28	3	1.89E+08	1.89E+08	AMP	0.390141	2.542309
3q28	3	1.89E+08	1.9E+08	AMP	0.390141	2.542309
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3q28	3	1.92E+08	1.92E+08	AMP	0.374523	2.260728
3q29	3	1.93E+08	1.93E+08	AMP	0.374523	2.260728
3q29	3	1.93E+08	1.93E+08	AMP	0.374523	2.260728
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3q29	3	1.93E+08	1.93E+08	AMP	0.390141	2.542309
3q29	3	1.93E+08	1.93E+08	AMP	0.405759	2.826772
4p16.3	4	952675	980683	DEL	0.14794	3.153664
4p16.3	4	972861	987228	DEL	0.176183	4.629087
4p16.3	4	980785	998316	DEL	0.176183	4.629087
4p16.3	4	1003724	1020685	DEL	0.176183	4.629087
4p16.3	4	1050038	1107350	DEL	0.133818	2.501365
4p16.3	4	1619642	1686029	DEL	0.264274	9.93495
4p16.3	4	1795034	1810599	DEL	0.178873	4.782882
4p16.3	4	1813206	1857974	DEL	0.176183	4.61564
4p16.3	4	3443614	3451211	AMP	0.373931	2.242657
4p14	4	37245842	37451087	DEL	0.146595	3.08178
4p14	4	37455563	37625117	DEL	0.149285	3.258983
4p14	4	37592422	37687998	DEL	0.149285	3.258983
4q28.1	4	1.29E+08	1.29E+08	DEL	0.15063	3.333669
4q28.2	4	1.29E+08	1.29E+08	DEL	0.151302	3.370733
4q28.2	4	1.29E+08	1.29E+08	DEL	0.202408	6.089385
4q28.2	4	1.29E+08	1.29E+08	DEL	0.205098	6.252359
4q28.2	4	1.29E+08	1.29E+08	DEL	0.205098	6.252359
4q35.1	4	1.84E+08	1.84E+08	DEL	0.151302	3.34691
4q35.2	4	1.91E+08	1.91E+08	DEL	0.83586	72.474168
4q35.2	4	1.91E+08	1.91E+08	DEL	0.852671	74.665649
4q35.2	4	1.91E+08	1.91E+08	DEL	0.852671	74.665649
4q35.2	4	1.91E+08	1.91E+08	DEL	0.869482	76.974703
4q35.2	4	1.91E+08	1.91E+08	DEL	0.960263	89.951707
4q35.2	4	1.91E+08	1.91E+08	DEL	0.960263	89.951707
5p15.33	5	473425	524447	AMP	0.36491	2.091447
5p15.33	5	1008944	1039058	AMP	0.421218	3.130086
5p15.33	5	1050499	1112150	AMP	0.482939	4.522536
5p15.33	5	1201710	1225232	AMP	0.452982	3.814952
5p15.33	5	1225470	1246304	AMP	0.375168	2.260728
5p15.33	5	1253262	1295184	AMP	0.375168	2.260728
5p15.32	5	5140443	5320417	AMP	0.366333	2.112622
5p15.31	5	7396321	7830194	AMP	0.366333	2.112622
5p15.31	5	7830491	7851603	AMP	0.366333	2.112622
5p15.31	5	7851299	7906138	AMP	0.366333	2.112622
5p15.31	5	7859272	7869150	AMP	0.366333	2.112622
5p15.31	5	9035138	9546187	AMP	0.366333	2.112622
5p15.31	5	9629109	9712490	AMP	0.366333	2.112622
5p15.2	5	10353815	10440500	AMP	0.381526	2.373611
5p15.2	5	10564442	10650308	AMP	0.365908	2.100552
5p15.2	5	10679342	10761384	AMP	0.381526	2.373611
5p15.2	5	10971952	11904155	AMP	0.42838	3.260785
5p15.2	5	13690440	13944652	AMP	0.397144	2.65618
5p15.2	5	14143811	14532235	AMP	0.381526	2.373611
5q11.1	5	49692026	49739082	DEL	0.125749	2.2617
5q13.2	5	68710939	68740157	DEL	0.149285	3.276413
5q13.2	5	68788119	68853931	DEL	0.149285	3.276413
5q13.2	5	68856035	68890550	DEL	0.149285	3.276413
5q23.3	5	1.3E+08	1.31E+08	DEL	0.131801	2.458568
5q31.1	5	1.34E+08	1.34E+08	DEL	0.165424	4.093916
5q31.1	5	1.34E+08	1.34E+08	DEL	0.151974	3.400448
5q31.1	5	1.34E+08	1.34E+08	DEL	0.151974	3.400448
5q31.1	5	1.34E+08	1.34E+08	DEL	0.201736	6.058542
5q31.1	5	1.34E+08	1.34E+08	DEL	0.201736	6.058542
5q31.1	5	1.34E+08	1.34E+08	DEL	0.125076	2.238732

[illegible]

6p22.1	6	27775257	27775709	AMP	0.416327	3.029561
6p22.1	6	27775899	27776429	AMP	0.478799	4.420788
6p22.1	6	27777842	27778314	AMP	0.478799	4.420788
6p22.1	6	27782112	27782607	AMP	0.478799	4.420788
6p22.1	6	27782822	27783267	AMP	0.478799	4.420788
6p22.1	6	27791884	27792257	AMP	0.478799	4.420788
6p22.1	6	27798952	27799305	AMP	0.478799	4.420788
6p22.1	6	27805658	27806117	AMP	0.478799	4.420788
6p22.1	6	27806323	27823487	AMP	0.478799	4.420788
6p22.1	6	27833034	27833606	AMP	0.478799	4.420788
6p22.1	6	27834570	27835359	AMP	0.478799	4.420788
6p22.1	6	27839623	27840099	AMP	0.463181	4.050036
6p22.1	6	27840926	27841289	AMP	0.463181	4.050036
6p22.1	6	27858093	27860884	AMP	0.463181	4.050036
6p22.1	6	27860477	27860963	AMP	0.463181	4.050036
6p22.1	6	27861203	27861669	AMP	0.447563	3.696626
6p21.33	6	31777396	31783437	AMP	0.514935	5.310901
6p21.33	6	31783291	31785723	AMP	0.660183	9.208694
6p21.33	6	31795512	31798031	AMP	0.660183	9.208694
6p21.33	6	31802385	31807541	AMP	0.489058	4.668539
6p21.33	6	31825436	31830683	AMP	0.364114	2.083496
6p21.33	6	32006042	32009447	AMP	0.369352	2.170574
6p21.33	6	32008931	32083111	AMP	0.442083	3.578278
6p12.1	6	53659295	53788919	AMP	0.393155	2.570935
6p12.1	6	53794780	54131078	AMP	0.393155	2.570935
6p12.1	6	54172657	54254950	AMP	0.393155	2.570935
6p12.1	6	54711569	54806820	AMP	0.393155	2.570935
6p12.1	6	55039050	55147418	AMP	0.393155	2.570935
6p12.1	6	55192267	55267291	AMP	0.393155	2.570935
6p12.1	6	55299167	55444012	AMP	0.424391	3.168807
6p12.1	6	55618443	55740362	AMP	0.455627	3.868935
6p12.1	6	55921388	56258892	AMP	0.440009	3.51467
6p12.1	6	56322785	56819426	AMP	0.455627	3.868935
6q13	6	73331520	73908574	DEL	0.162061	3.843183
6q13	6	73933267	73935493	DEL	0.234686	7.984074
6q13	6	73951037	74020088	DEL	0.240066	8.275015
6q13	6	74062785	74064018	DEL	0.238721	8.225278
6q13	6	74078278	74104856	DEL	0.25217	9.081285
6q13	6	74104471	74127292	DEL	0.250153	8.975796
6q13	6	74123238	74161999	DEL	0.263602	9.900094
6q13	6	74171301	74218959	DEL	0.297897	12.220689
6q13	6	74225473	74233520	DEL	0.297897	12.220689
6q13	6	74303102	74363878	DEL	0.275033	10.647395
6q13	6	74405508	74538040	DEL	0.153992	3.529002
6q13	6	75794042	75915767	DEL	0.153992	3.529002
6q21	6	1.11E+08	1.11E+08	DEL	0.137853	2.738035
6q21	6	1.11E+08	1.11E+08	DEL	0.137853	2.738035
6q21	6	1.11E+08	1.11E+08	DEL	0.143233	2.977349
6q21	6	1.11E+08	1.11E+08	DEL	0.146595	3.08865
6q21	6	1.11E+08	1.12E+08	DEL	0.146595	3.08865
6q25.1	6	1.5E+08	1.5E+08	DEL	0.198374	5.861136
6q25.1	6	1.5E+08	1.5E+08	DEL	0.125076	2.244507
6q25.1	6	1.5E+08	1.5E+08	DEL	0.198374	5.861136
6q25.1	6	1.5E+08	1.5E+08	DEL	0.192994	5.625492
6q25.1	6	1.5E+08	1.5E+08	DEL	0.180218	4.904653
6q25.1	6	1.5E+08	1.5E+08	DEL	0.180218	4.904653
6q25.1	6	1.5E+08	1.5E+08	DEL	0.182235	4.975786
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6q25.1	6	1.5E+08	1.5E+08	DEL	0.189632	5.369925
6q25.1	6	1.5E+08	1.5E+08	DEL	0.189632	5.369925
6q25.1	6	1.5E+08	1.5E+08	DEL	0.138525	2.790079
6q25.1	6	1.5E+08	1.5E+08	DEL	0.139198	2.833334
6q25.1	6	1.5E+08	1.5E+08	DEL	0.143233	2.978131
6q25.1	6	1.5E+08	1.5E+08	DEL	0.143233	2.978131
6q25.1	6	1.5E+08	1.5E+08	DEL	0.141215	2.910158
6q25.1	6	1.5E+08	1.51E+08	DEL	0.139198	2.855065
6q25.1	6	1.51E+08	1.51E+08	DEL	0.135163	2.578632
6q25.1	6	1.51E+08	1.51E+08	DEL	0.122387	2.11791
6q25.1	6	1.51E+08	1.51E+08	DEL	0.131801	2.458568
6q25.1	6	1.52E+08	1.52E+08	DEL	0.131128	2.437254
6q25.1	6	1.52E+08	1.52E+08	DEL	0.133146	2.489797
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7p22.3	7	1036622	1177896	AMP	0.368285	2.15155
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7p22.3	7	1191707	1200395	AMP	0.368285	2.15155

7p22.3	7	1272543	1276954	AMP	0.399521	2.715132
7p22.3	7	1468101	1499138	AMP	0.399521	2.715132
7p22.3	7	1509913	1545489	AMP	0.493722	4.783614
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7p22.3	7	1606966	1610641	AMP	0.383903	2.428476
7p22.3	7	1727755	1787590	AMP	0.368285	2.15155
7p22.3	7	1855429	2272878	AMP	0.368285	2.15155
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7p22.1	7	5470966	5553429	DEL	0.17551	4.584088
7p22.1	7	5632439	5646286	DEL	0.147267	3.108105
7p22.1	7	5659678	5821370	DEL	0.135163	2.572321
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7p21.3	7	7676149	7758238	AMP	0.541452	5.952
7p21.3	7	8008425	8133902	AMP	0.55707	6.362342
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7p21.3	7	12370511	12443567	AMP	0.614886	7.945251
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7p21.1	7	16639401	16685442	AMP	0.552567	6.242783
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7p21.1	7	19735085	19748710	AMP	0.536164	5.841368
7p21.1	7	19758933	19813221	AMP	0.504928	5.055439
7p21.1	7	20174278	20257027	AMP	0.48931	4.668539
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7p21.1	7	20654830	20816658	AMP	0.427099	3.239278
7p21.1	7	20823906	20826505	AMP	0.411481	2.92897
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7p15.3	7	21582833	21941457	AMP	0.411481	2.92897
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7p15.3	7	22157856	22396763	AMP	0.395863	2.638263
7p15.3	7	22459063	22672544	AMP	0.395863	2.638263
7p15.3	7	22765503	22771621	AMP	0.368074	2.15155
7p15.3	7	22852251	22862470	AMP	0.368074	2.15155
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7p15.3	7	23145353	23217533	AMP	0.368074	2.15155
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7p15.2	7	27233122	27239725	AMP	0.536696	5.841368
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7p15.2	7	27282164	27290112	AMP	0.474224	4.304448
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7p11.2	7	54819943	54827667	AMP	0.457352	3.919138
7p11.2	7	55086714	55324313	AMP	0.504206	5.041368

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7q11.23	7	73113536	73134002	DEL	0.135163	2.622251
7q11.23	7	73150424	73153197	DEL	0.133146	2.479347
7q11.23	7	73183328	73184600	DEL	0.134491	2.525135
7q11.23	7	73213872	73247014	DEL	0.134491	2.525135
7q11.23	7	73248920	73256865	DEL	0.131801	2.458568
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7q11.23	7	75162621	75368280	DEL	0.129784	2.382431
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7q11.23	7	75831216	75916605	DEL	0.125076	2.250924
7q11.23	7	75931861	75933612	DEL	0.133818	2.501365
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7q11.23	7	76018651	76039012	DEL	0.127766	2.340967
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7q31.31	7	1.2E+08	1.2E+08	AMP	0.528638	5.631304
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7q31.32	7	1.22E+08	1.22E+08	AMP	0.411121	2.92897
7q31.32	7	1.22E+08	1.22E+08	AMP	0.411121	2.92897
7q31.32	7	1.22E+08	1.22E+08	AMP	0.38683	2.474991
7q31.32	7	1.22E+08	1.23E+08	AMP	0.38683	2.474991
7q31.32	7	1.22E+08	1.22E+08	AMP	0.38683	2.474991
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7q31.32	7	1.23E+08	1.23E+08	AMP	0.38683	2.474991
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7q31.32	7	1.23E+08	1.23E+08	AMP	0.426739	3.239278
7q31.32	7	1.23E+08	1.23E+08	AMP	0.473593	4.291441
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7q31.33	7	1.24E+08	1.24E+08	AMP	0.426739	3.239278
7q31.33	7	1.24E+08	1.25E+08	AMP	0.426739	3.239278
7q31.33	7	1.26E+08	1.27E+08	AMP	0.369626	2.181486
7q34	7	1.42E+08	1.42E+08	AMP	0.373547	2.242657
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8p23.3	8	182137	197342	DEL	0.134491	2.546745
8p23.3	8	356428	421225	DEL	0.134491	2.546745
8p23.3	8	1993155	2113475	DEL	0.121714	2.028299
8p23.2	8	2792875	4852494	DEL	0.121714	2.041508
8p23.1	8	6264113	6501144	DEL	0.167441	4.183583
8p23.1	8	6357172	6420930	DEL	0.123731	2.1582
8p23.1	8	6565878	6617184	DEL	0.167441	4.183583
8p23.1	8	6728097	6735544	DEL	0.135163	2.581425
8p23.1	8	6782215	6783598	DEL	0.135163	2.581425
8p23.1	8	6793344	6795860	DEL	0.134491	2.557149
8p23.1	8	6835171	6837602	DEL	0.135163	2.622251
8p23.1	8	6854288	6875778	DEL	0.135163	2.622251
8p23.1	8	6873391	6875823	DEL	0.135163	2.622251
8p23.1	8	6912831	6914256	DEL	0.135163	2.622251
8p23.1	8	7213039	7243080	DEL	0.161389	3.821519
8p23.1	8	7272382	7274385	DEL	0.161389	3.821519
8p23.1	8	7286410	7287870	DEL	0.161389	3.821519
8p23.1	8	7300206	7321196	DEL	0.161389	3.821519
8p23.1	8	7327830	7332604	DEL	0.161389	3.821519
8p23.1	8	7340026	7343922	DEL	0.161389	3.821519
8p23.1	8	7345191	7347115	DEL	0.161389	3.821519
8p23.1	8	7353368	7366833	DEL	0.161389	3.821519
8p23.1	8	7669242	7673238	DEL	0.161389	3.821519
8p23.1	8	7679488	7681411	DEL	0.161389	3.821519
8p23.1	8	7682694	7686575	DEL	0.161389	3.821519
8p23.1	8	7693993	7698764	DEL	0.161389	3.821519
8p23.1	8	7705398	7726389	DEL	0.161389	3.821519
8p23.1	8	7738726	7740186	DEL	0.161389	3.821519
8p23.1	8	7752151	7754233	DEL	0.161389	3.821519
8p23.1	8	8175258	8244008	DEL	0.168113	4.192169
8p23.1	8	8559448	8561616	DEL	0.134491	2.562408
8p23.1	8	8640864	8751155	DEL	0.166096	4.101203
8p23.1	8	8859657	8974256	DEL	0.166096	4.101203
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8p23.1	8	10582909	10697357	DEL	0.135836	2.653936
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8p23.1	8	11225911	11296167	DEL	0.121714	2.011432
8p23.1	8	11351510	11422113	DEL	0.128439	2.342739
8p23.1	8	11534468	11617511	DEL	0.138525	2.81501
8p23.1	8	11831446	11832108	DEL	0.121714	2.011432
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8p23.1	8	12039605	12051642	DEL	0.135163	2.622251
8p23.1	8	12168471	12175825	DEL	0.135163	2.622251
8p23.1	8	12282913	12293915	DEL	0.134491	2.525135
8p23.1	8	12579403	12613582	DEL	0.172148	4.365351
8p22	8	12803151	12889012	DEL	0.157354	3.646288
8p22	8	13424352	13425796	DEL	0.121714	2.031388
8p22	8	13947373	15095848	DEL	0.121714	2.052321
8p22	8	17013538	17082308	DEL	0.14794	3.134136
8p22	8	17086737	17104387	DEL	0.147267	3.099116
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8p22	8	17501304	17658426	DEL	0.121714	2.052321
8p22	8	18384811	18942240	DEL	0.121714	2.052321
8p21.3	8	20054878	20084330	DEL	0.135163	2.605025
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8p21.3	8	21971928	21990897	DEL	0.156682	3.637811
8p21.3	8	21995533	21999464	DEL	0.134491	2.525135
8p21.3	8	22022249	22069839	DEL	0.125076	2.207189
8p21.3	8	22077222	22089854	DEL	0.131128	2.425816
8p21.3	8	22102617	22112113	DEL	0.135836	2.703117
8p21.3	8	22132810	22215076	DEL	0.127766	2.338759
8p21.3	8	22224762	22291642	DEL	0.127766	2.338759
8p21.3	8	22435792	22455538	DEL	0.132473	2.468677
8p21.3	8	22477931	22526661	DEL	0.121714	2.052321
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8p21.3	8	23154702	23282841	DEL	0.160716	3.762015
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8p21.2	8	23386318	23432976	DEL	0.160716	3.762015
8p21.2	8	23536206	23540440	DEL	0.135836	2.653936
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8p21.1	8	28351729	28431775	DEL	0.134491	2.531645
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8p21.1	8	28625178	28747759	DEL	0.136508	2.709293
8p12	8	30435835	30515768	DEL	0.174838	4.520863
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8p12	8	30689060	30748122	DEL	0.17551	4.548734
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8q22.2	8	99037079	99058697	AMP	0.535955	5.841368
8q22.2	8	99076539	99105838	AMP	0.535955	5.841368
8q22.2	8	99114572	99129469	AMP	0.535955	5.841368
8q22.2	8	99129525	99172062	AMP	0.535955	5.841368
8q22.2	8	99202061	99306621	AMP	0.535955	5.841368
8q22.2	8	99413631	99955055	AMP	0.535955	5.841368
8q22.2	8	99439250	99445076	AMP	0.535955	5.841368
8q22.2	8	99956631	99964332	AMP	0.520337	5.45786
8q22.2	8	1E+08	1.01E+08	AMP	0.535955	5.841368
8q22.2	8	1.01E+08	1.01E+08	AMP	0.535955	5.841368
8q22.2	8	1.01E+08	1.01E+08	AMP	0.535955	5.841368
8q22.2	8	1.01E+08	1.01E+08	AMP	0.520337	5.45786
8q22.2	8	1.01E+08	1.01E+08	AMP	0.520337	5.45786
8q22.2	8	1.01E+08	1.01E+08	AMP	0.520337	5.45786
8q22.2	8	1.02E+08	1.02E+08	AMP	0.520337	5.45786
8q22.2	8	1.02E+08	1.02E+08	AMP	0.520337	5.45786
8q22.2	8	1.02E+08	1.02E+08	AMP	0.520337	5.45786
8q22.3	8	1.02E+08	1.02E+08	AMP	0.520337	5.45786
8q22.3	8	1.02E+08	1.02E+08	AMP	0.520337	5.45786
8q22.3	8	1.02E+08	1.02E+08	AMP	0.520337	5.45786
8q22.3	8	1.03E+08	1.03E+08	AMP	0.520337	5.45786
8q22.3	8	1.03E+08	1.03E+08	AMP	0.520337	5.45786
8q22.3	8	1.03E+08	1.03E+08	AMP	0.520337	5.45786
8q22.3	8	1.03E+08	1.03E+08	AMP	0.535955	5.841368
8q22.3	8	1.04E+08	1.04E+08	AMP	0.535955	5.841368
8q22.3	8	1.04E+08	1.04E+08	AMP	0.551573	6.230427
8q22.3	8	1.04E+08	1.04E+08	AMP	0.551573	6.230427
8q22.3	8	1.04E+08	1.04E+08	AMP	0.551573	6.230427
8q22.3	8	1.04E+08	1.04E+08	AMP	0.551573	6.230427
8q22.3	8	1.04E+08	1.04E+08	AMP	0.551573	6.230427
8q22.3	8	1.04E+08	1.04E+08	AMP	0.551573	6.230427
8q22.3	8	1.04E+08	1.04E+08	AMP	0.567191	6.628295
8q22.3	8	1.04E+08	1.04E+08	AMP	0.598428	7.497404
8q22.3	8	1.04E+08	1.04E+08	AMP	0.598428	7.497404
8q22.3	8	1.05E+08	1.05E+08	AMP	0.722972	10.957037
8q22.3	8	1.05E+08	1.05E+08	AMP	0.722972	10.957037
8q22.3	8	1.06E+08	1.06E+08	AMP	0.707354	10.512157
8q23.1	8	1.06E+08	1.07E+08	AMP	0.738599	11.405885
8q23.1	8	1.07E+08	1.08E+08	AMP	0.738599	11.405885
8q23.1	8	1.08E+08	1.08E+08	AMP	0.738599	11.405885
8q23.1	8	1.08E+08	1.09E+08	AMP	0.738599	11.405885
8q23.1	8	1.09E+08	1.09E+08	AMP	0.722981	10.957037
8q23.1	8	1.09E+08	1.09E+08	AMP	0.754217	11.900478
8q23.1	8	1.1E+08	1.1E+08	AMP	0.785453	12.866303
8q23.1	8	1.1E+08	1.1E+08	AMP	0.785453	12.866303
8q23.1	8	1.1E+08	1.1E+08	AMP	0.785453	12.866303
8q23.1	8	1.1E+08	1.1E+08	AMP	0.801071	13.319468
8q23.1	8	1.1E+08	1.11E+08	AMP	0.847925	14.638938
8q23.2	8	1.11E+08	1.11E+08	AMP	0.847925	14.638938
8q23.2	8	1.11E+08	1.11E+08	AMP	0.847925	14.638938
8q23.2	8	1.11E+08	1.11E+08	AMP	0.832307	14.31365
8q23.3	8	1.13E+08	1.14E+08	AMP	0.905651	16.139621
8q23.3	8	1.16E+08	1.17E+08	AMP	0.905651	16.139621
8q23.3	8	1.18E+08	1.18E+08	AMP	0.890033	15.911012
8q24.11	8	1.18E+08	1.18E+08	AMP	0.905651	16.139621
8q24.11	8	1.18E+08	1.18E+08	AMP	0.905651	16.139621
8q24.11	8	1.18E+08	1.18E+08	AMP	0.858797	14.910704
8q24.11	8	1.18E+08	1.18E+08	AMP	0.889348	15.911012
8q24.11	8	1.19E+08	1.19E+08	AMP	0.889348	15.911012
8q24.11	8	1.19E+08	1.19E+08	AMP	0.842494	14.506816
8q24.12	8	1.19E+08	1.2E+08	AMP	0.842494	14.506816
8q24.12	8	1.2E+08	1.2E+08	AMP	0.858112	14.885316
8q24.12	8	1.2E+08	1.2E+08	AMP	0.842494	14.506816
8q24.12	8	1.2E+08	1.2E+08	AMP	0.79564	13.126109
8q24.12	8	1.2E+08	1.2E+08	AMP	0.780022	12.692187
8q24.12	8	1.21E+08	1.21E+08	AMP	0.731948	11.205225
8q24.12	8	1.21E+08	1.21E+08	AMP	0.653858	9.04886
8q24.12	8	1.21E+08	1.21E+08	AMP	0.622485	8.175501
8q24.12	8	1.21E+08	1.21E+08	AMP	0.653721	9.04886
8q24.12	8	1.21E+08	1.21E+08	AMP	0.684817	9.905075
8q24.12	8	1.21E+08	1.21E+08	AMP	0.674116	9.610525
8q24.12	8	1.21E+08	1.22E+08	AMP	0.674116	9.610525
8q24.12	8	1.22E+08	1.22E+08	AMP	0.674116	9.610525
8q24.13	8	1.23E+08	1.23E+08	AMP	0.627262	8.3073
8q24.13	8	1.23E+08	1.23E+08	AMP	0.627262	8.3073
8q24.13	8	1.24E+08	1.24E+08	AMP	0.627262	8.3073

8q24.13	8	1.24E+08	1.24E+08	AMP	0.627262	8.3073
8q24.13	8	1.24E+08	1.24E+08	AMP	0.658498	9.175419
8q24.13	8	1.24E+08	1.24E+08	AMP	0.658498	9.175419
8q24.13	8	1.24E+08	1.24E+08	AMP	0.611644	7.877548
8q24.13	8	1.24E+08	1.24E+08	AMP	0.611644	7.877548
8q24.13	8	1.24E+08	1.24E+08	AMP	0.611644	7.877548
8q24.13	8	1.25E+08	1.25E+08	AMP	0.688641	10.003928
8q24.13	8	1.25E+08	1.25E+08	AMP	0.688641	10.003928
8q24.13	8	1.25E+08	1.25E+08	AMP	0.735495	11.303371
8q24.13	8	1.25E+08	1.25E+08	AMP	0.766731	12.282263
8q24.13	8	1.25E+08	1.25E+08	AMP	0.673023	9.561512
8q24.13	8	1.25E+08	1.25E+08	AMP	0.673023	9.561512
8q24.13	8	1.25E+08	1.25E+08	AMP	0.673023	9.561512
8q24.13	8	1.25E+08	1.25E+08	AMP	0.61591	7.964462
8q24.13	8	1.25E+08	1.26E+08	AMP	0.673023	9.561512
8q24.13	8	1.26E+08	1.26E+08	AMP	0.719877	10.857041
8q24.13	8	1.26E+08	1.26E+08	AMP	0.61591	7.964462
8q24.13	8	1.26E+08	1.26E+08	AMP	0.61591	7.964462
8q24.13	8	1.26E+08	1.26E+08	AMP	0.658624	9.175419
8q24.13	8	1.26E+08	1.26E+08	AMP	0.658624	9.175419
8q24.13	8	1.26E+08	1.26E+08	AMP	0.658624	9.175419
8q24.13	8	1.26E+08	1.26E+08	AMP	0.715737	10.74817
8q24.13	8	1.26E+08	1.26E+08	AMP	0.715737	10.74817
8q24.21	8	1.28E+08	1.28E+08	AMP	0.84558	14.588051
8q24.21	8	1.28E+08	1.28E+08	AMP	0.84558	14.588051
8q24.21	8	1.29E+08	1.29E+08	AMP	0.871457	15.336029
8q24.21	8	1.31E+08	1.31E+08	AMP	0.617129	8.015816
8q24.21	8	1.31E+08	1.31E+08	AMP	0.601511	7.589912
8q24.21	8	1.31E+08	1.31E+08	AMP	0.785455	12.866303
8q24.22	8	1.32E+08	1.32E+08	AMP	0.801073	13.319468
8q24.22	8	1.33E+08	1.33E+08	AMP	0.832309	14.31365
8q24.22	8	1.33E+08	1.33E+08	AMP	0.801073	13.319468
8q24.22	8	1.33E+08	1.33E+08	AMP	0.801073	13.319468
8q24.22	8	1.33E+08	1.33E+08	AMP	0.785455	12.866303
8q24.22	8	1.34E+08	1.34E+08	AMP	0.790661	12.981059
8q24.22	8	1.34E+08	1.34E+08	AMP	0.790661	12.981059
8q24.22	8	1.34E+08	1.34E+08	AMP	0.806279	13.459185
8q24.22	8	1.34E+08	1.34E+08	AMP	0.832309	14.31365
8q24.22	8	1.34E+08	1.34E+08	AMP	0.832309	14.31365
8q24.22	8	1.34E+08	1.34E+08	AMP	0.832309	14.31365
8q24.22	8	1.34E+08	1.35E+08	AMP	0.832309	14.31365
8q24.22	8	1.35E+08	1.36E+08	AMP	0.84604	14.591646
8q24.22	8	1.36E+08	1.36E+08	AMP	0.783568	12.826129
8q24.23	8	1.36E+08	1.37E+08	AMP	0.742073	11.519343
8q24.23	8	1.39E+08	1.4E+08	AMP	0.710837	10.631459
8q24.23	8	1.4E+08	1.4E+08	AMP	0.710837	10.631459
8q24.3	8	1.41E+08	1.41E+08	AMP	0.648365	8.889986
8q24.3	8	1.41E+08	1.41E+08	AMP	0.617129	8.015816
8q24.3	8	1.42E+08	1.42E+08	AMP	0.614176	7.929563
8q24.3	8	1.42E+08	1.42E+08	AMP	0.64512	8.785978
8q24.3	8	1.42E+08	1.42E+08	AMP	0.780323	12.716231
8q24.3	8	1.42E+08	1.42E+08	AMP	0.780323	12.716231
8q24.3	8	1.42E+08	1.42E+08	AMP	0.764873	12.231703
8q24.3	8	1.42E+08	1.42E+08	AMP	0.790749	12.981059
8q24.3	8	1.43E+08	1.43E+08	AMP	0.655547	9.075799
8q24.3	8	1.44E+08	1.44E+08	AMP	0.665805	9.346286
8q24.3	8	1.44E+08	1.44E+08	AMP	0.639929	8.660727
8q24.3	8	1.44E+08	1.44E+08	AMP	0.655547	9.075799
8q24.3	8	1.44E+08	1.44E+08	AMP	0.655547	9.075799
8q24.3	8	1.44E+08	1.44E+08	AMP	0.712659	10.665525
8q24.3	8	1.44E+08	1.44E+08	AMP	0.712659	10.665525
8q24.3	8	1.44E+08	1.44E+08	AMP	0.655547	9.075799
8q24.3	8	1.44E+08	1.44E+08	AMP	0.639929	8.660727
8q24.3	8	1.44E+08	1.44E+08	AMP	0.639929	8.660727
8q24.3	8	1.44E+08	1.44E+08	AMP	0.639929	8.660727
8q24.3	8	1.44E+08	1.44E+08	AMP	0.608033	7.773481
8q24.3	8	1.44E+08	1.44E+08	AMP	0.623651	8.195907
8q24.3	8	1.44E+08	1.44E+08	AMP	0.623651	8.195907
8q24.3	8	1.44E+08	1.44E+08	AMP	0.623651	8.195907
8q24.3	8	1.44E+08	1.44E+08	AMP	0.664612	9.332679
8q24.3	8	1.44E+08	1.44E+08	AMP	0.664612	9.332679
8q24.3	8	1.44E+08	1.44E+08	AMP	0.664612	9.332679
8q24.3	8	1.44E+08	1.44E+08	AMP	0.679598	9.761399
8q24.3	8	1.45E+08	1.45E+08	AMP	0.66398	9.317383
8q24.3	8	1.45E+08	1.45E+08	AMP	0.66398	9.317383

8q24.3	8	1.45E+08	1.45E+08	AMP	0.721093	10.91202
8q24.3	8	1.45E+08	1.45E+08	AMP	0.678076	9.709044
8q24.3	8	1.45E+08	1.45E+08	AMP	0.678076	9.709044
8q24.3	8	1.45E+08	1.45E+08	AMP	0.719571	10.857041
8q24.3	8	1.45E+08	1.45E+08	AMP	0.719571	10.857041
8q24.3	8	1.45E+08	1.45E+08	AMP	0.662458	9.265758
8q24.3	8	1.45E+08	1.45E+08	AMP	0.662458	9.265758
8q24.3	8	1.45E+08	1.45E+08	AMP	0.662458	9.265758
8q24.3	8	1.45E+08	1.45E+08	AMP	0.662458	9.265758
8q24.3	8	1.45E+08	1.45E+08	AMP	0.662458	9.265758
8q24.3	8	1.45E+08	1.45E+08	AMP	0.750031	11.771664
8q24.3	8	1.45E+08	1.45E+08	AMP	0.812503	13.655612
8q24.3	8	1.45E+08	1.45E+08	AMP	0.771008	12.430398
8q24.3	8	1.45E+08	1.45E+08	AMP	0.771008	12.430398
8q24.3	8	1.45E+08	1.45E+08	AMP	0.802244	13.326382
8q24.3	8	1.45E+08	1.45E+08	AMP	0.859328	14.911457
8q24.3	8	1.45E+08	1.45E+08	AMP	0.874946	15.437148
8q24.3	8	1.45E+08	1.45E+08	AMP	0.785974	12.866303
8q24.3	8	1.45E+08	1.45E+08	AMP	0.785974	12.866303
8q24.3	8	1.45E+08	1.45E+08	AMP	0.754044	11.900478
8q24.3	8	1.45E+08	1.45E+08	AMP	0.691572	10.105903
8q24.3	8	1.45E+08	1.45E+08	AMP	0.691572	10.105903
8q24.3	8	1.45E+08	1.45E+08	AMP	0.691572	10.105903
8q24.3	8	1.45E+08	1.45E+08	AMP	0.675954	9.649687
8q24.3	8	1.45E+08	1.45E+08	AMP	0.675954	9.649687
8q24.3	8	1.45E+08	1.45E+08	AMP	0.675954	9.649687
8q24.3	8	1.45E+08	1.45E+08	AMP	0.675954	9.649687
8q24.3	8	1.45E+08	1.45E+08	AMP	0.645502	8.785978
8q24.3	8	1.45E+08	1.45E+08	AMP	0.629756	8.352182
8q24.3	8	1.45E+08	1.45E+08	DEL	0.131128	2.448969
8q24.3	8	1.45E+08	1.46E+08	AMP	0.629756	8.352182
8q24.3	8	1.45E+08	1.45E+08	AMP	0.614138	7.929563
8q24.3	8	1.46E+08	1.46E+08	AMP	0.628749	8.340644
8q24.3	8	1.46E+08	1.46E+08	AMP	0.75244	11.854256
8q24.3	8	1.46E+08	1.46E+08	AMP	0.75244	11.854256
8q24.3	8	1.46E+08	1.46E+08	AMP	0.675603	9.649687
8q24.3	8	1.46E+08	1.46E+08	AMP	0.675603	9.649687
8q24.3	8	1.46E+08	1.46E+08	AMP	0.675603	9.649687
8q24.3	8	1.46E+08	1.46E+08	AMP	0.675603	9.649687
8q24.3	8	1.46E+08	1.46E+08	AMP	0.675603	9.649687
8q24.3	8	1.46E+08	1.46E+08	AMP	0.675603	9.649687
8q24.3	8	1.46E+08	1.46E+08	AMP	0.706839	10.512157
8q24.3	8	1.46E+08	1.46E+08	AMP	0.738075	11.405885
8q24.3	8	1.46E+08	1.46E+08	AMP	0.738075	11.405885
8q24.3	8	1.46E+08	1.46E+08	AMP	0.769311	12.389332
8q24.3	8	1.46E+08	1.46E+08	AMP	0.769311	12.389332
8q24.3	8	1.46E+08	1.46E+08	AMP	0.722457	10.957037
8q24.3	8	1.46E+08	1.46E+08	AMP	0.722457	10.957037
8q24.3	8	1.46E+08	1.46E+08	AMP	0.738075	11.405885
8q24.3	8	1.46E+08	1.46E+08	AMP	0.738075	11.405885
8q24.3	8	1.46E+08	1.46E+08	AMP	0.722457	10.957037
8q24.3	8	1.46E+08	1.46E+08	AMP	0.678379	9.709044
8q24.3	8	1.46E+08	1.46E+08	AMP	0.678379	9.709044
8q24.3	8	1.46E+08	1.46E+08	AMP	0.486719	4.603177
8q24.3	8	1.46E+08	1.46E+08	AMP	0.471101	4.229939
8q24.3	8	1.46E+08	1.46E+08	AMP	0.471101	4.229939
8q24.3	8	1.46E+08	1.46E+08	AMP	0.471101	4.229939
8q24.3	8	1.46E+08	1.46E+08	AMP	0.471101	4.229939
8q24.3	8	1.46E+08	1.46E+08	AMP	0.471101	4.229939
8q24.3	8	1.46E+08	1.46E+08	AMP	0.471101	4.229939
8q24.3	8	1.46E+08	1.46E+08	AMP	0.471101	4.229939
8q24.3	8	1.46E+08	1.46E+08	AMP	0.471101	4.229939
9p21.3	9	21440440	21441315	DEL	0.176183	4.637325
9p21.3	9	21455641	21559668	DEL	0.176183	4.637325
9p21.3	9	21480841	21482312	DEL	0.176183	4.637325
9p21.3	9	21802542	21931646	DEL	0.259567	9.610112
9p21.3	9	21967137	21967738	DEL	0.28243	11.166796
9p21.3	9	21967751	21995300	DEL	0.28243	11.166796
9p21.3	9	21994777	22121096	DEL	0.271671	10.394707
9p21.3	9	22002902	22009362	DEL	0.271671	10.394707
9p21.3	9	22446840	22455739	DEL	0.203753	6.176507
9p21.3	9	23690102	23826335	DEL	0.203753	6.176507
9q33.3	9	1.27E+08	1.28E+08	DEL	0.134491	2.525135
9q33.3	9	1.27E+08	1.27E+08	DEL	0.134491	2.525135
9q33.3	9	1.28E+08	1.28E+08	DEL	0.188959	5.324266
9q33.3	9	1.28E+08	1.28E+08	DEL	0.207788	6.395372
9q33.3	9	1.28E+08	1.28E+08	DEL	0.207788	6.395372
9q33.3	9	1.28E+08	1.28E+08	DEL	0.204426	6.19691
9q33.3	9	1.28E+08	1.28E+08	DEL	0.187615	5.239546
9q33.3	9	1.28E+08	1.28E+08	DEL	0.187615	5.239546
9q33.3	9	1.28E+08	1.28E+08	DEL	0.192322	5.584189

9q33.3	9	1.28E+08	1.28E+08	DEL	0.193667	5.654867
9q33.3	9	1.28E+08	1.28E+08	DEL	0.193667	5.654867
9q33.3	9	1.28E+08	1.28E+08	DEL	0.210478	6.543009
9q33.3	9	1.28E+08	1.28E+08	DEL	0.170803	4.327016
9q33.3	9	1.3E+08	1.3E+08	DEL	0.129111	2.359344
9q33.3	9	1.3E+08	1.3E+08	DEL	0.147267	3.099116
9q33.3	9	1.3E+08	1.3E+08	DEL	0.151302	3.370733
9q34.11	9	1.3E+08	1.3E+08	DEL	0.14794	3.149129
9q34.11	9	1.3E+08	1.3E+08	DEL	0.144577	3.036554
9q34.11	9	1.3E+08	1.3E+08	DEL	0.144577	3.036554
9q34.11	9	1.3E+08	1.3E+08	DEL	0.146595	3.08865
9q34.11	9	1.3E+08	1.3E+08	DEL	0.146595	3.08865
9q34.11	9	1.31E+08	1.31E+08	DEL	0.139198	2.888714
9q34.11	9	1.31E+08	1.31E+08	DEL	0.134491	2.535942
9q34.11	9	1.31E+08	1.31E+08	DEL	0.129111	2.359344
9q34.11	9	1.31E+08	1.31E+08	DEL	0.125076	2.225339
9q34.11	9	1.31E+08	1.31E+08	DEL	0.134491	2.556606
9q34.11	9	1.31E+08	1.31E+08	DEL	0.127766	2.340967
9q34.11	9	1.31E+08	1.31E+08	DEL	0.148612	3.200315
9q34.11	9	1.31E+08	1.31E+08	DEL	0.162734	3.93972
9q34.11	9	1.31E+08	1.31E+08	DEL	0.14525	3.04989
9q34.11	9	1.31E+08	1.31E+08	DEL	0.14525	3.04989
9q34.11	9	1.31E+08	1.31E+08	DEL	0.145922	3.063965
9q34.11	9	1.31E+08	1.31E+08	DEL	0.139198	2.85614
9q34.11	9	1.31E+08	1.31E+08	DEL	0.14794	3.162317
9q34.11	9	1.31E+08	1.31E+08	DEL	0.14794	3.123684
9q34.11	9	1.31E+08	1.31E+08	DEL	0.147267	3.112753
9q34.11	9	1.31E+08	1.31E+08	DEL	0.13718	2.72722
9q34.11	9	1.31E+08	1.31E+08	DEL	0.135836	2.653936
9q34.11	9	1.31E+08	1.31E+08	DEL	0.134491	2.536152
9q34.11	9	1.31E+08	1.31E+08	DEL	0.157354	3.659608
9q34.11	9	1.31E+08	1.31E+08	DEL	0.156009	3.601707
9q34.11	9	1.31E+08	1.31E+08	DEL	0.155337	3.573651
9q34.11	9	1.31E+08	1.31E+08	DEL	0.152647	3.462603
9q34.11	9	1.31E+08	1.31E+08	DEL	0.157354	3.659608
9q34.11	9	1.31E+08	1.31E+08	DEL	0.161389	3.799124
9q34.11	9	1.31E+08	1.31E+08	DEL	0.149285	3.258835
9q34.11	9	1.31E+08	1.31E+08	DEL	0.155337	3.573651
9q34.11	9	1.31E+08	1.31E+08	DEL	0.155337	3.573651
9q34.11	9	1.31E+08	1.31E+08	DEL	0.155337	3.559497
9q34.11	9	1.31E+08	1.31E+08	DEL	0.156682	3.629692
9q34.11	9	1.31E+08	1.31E+08	DEL	0.156682	3.629692
9q34.11	9	1.31E+08	1.32E+08	DEL	0.161389	3.784249
9q34.11	9	1.32E+08	1.32E+08	DEL	0.169458	4.260779
9q34.11	9	1.32E+08	1.32E+08	DEL	0.17551	4.560824
9q34.11	9	1.32E+08	1.32E+08	DEL	0.17551	4.560824
9q34.11	9	1.32E+08	1.32E+08	DEL	0.166096	4.12592
9q34.11	9	1.32E+08	1.32E+08	DEL	0.166768	4.167785
9q34.11	9	1.32E+08	1.32E+08	DEL	0.168786	4.212351
9q34.11	9	1.32E+08	1.32E+08	DEL	0.173493	4.40633
9q34.11	9	1.32E+08	1.32E+08	DEL	0.173493	4.40633
9q34.11	9	1.32E+08	1.32E+08	DEL	0.180218	4.90213
9q34.11	9	1.32E+08	1.32E+08	DEL	0.180218	4.90213
9q34.11	9	1.32E+08	1.32E+08	DEL	0.155337	3.573651
9q34.11	9	1.32E+08	1.32E+08	DEL	0.1782	4.744232
9q34.11	9	1.32E+08	1.32E+08	DEL	0.178873	4.779918
9q34.11	9	1.32E+08	1.32E+08	DEL	0.204426	6.193038
9q34.11	9	1.32E+08	1.32E+08	DEL	0.171476	4.340588
9q34.11	9	1.32E+08	1.32E+08	DEL	0.169458	4.244607
9q34.11	9	1.32E+08	1.32E+08	DEL	0.171476	4.340588
9q34.11	9	1.33E+08	1.33E+08	DEL	0.171476	4.340588
9q34.11	9	1.33E+08	1.33E+08	DEL	0.167441	4.18309
9q34.11	9	1.33E+08	1.33E+08	DEL	0.171476	4.340588
9q34.11	9	1.33E+08	1.33E+08	DEL	0.191649	5.486047
9q34.11	9	1.33E+08	1.33E+08	DEL	0.191649	5.486047
9q34.11	9	1.33E+08	1.33E+08	DEL	0.190977	5.453859
9q34.11	9	1.33E+08	1.33E+08	DEL	0.237376	8.144922
9q34.11	9	1.33E+08	1.33E+08	DEL	0.215858	6.799402
9q34.3	9	1.39E+08	1.39E+08	DEL	0.149285	3.293817
9q34.3	9	1.39E+08	1.39E+08	DEL	0.149285	3.293817
9q34.3	9	1.39E+08	1.39E+08	DEL	0.14256	2.952283
9q34.3	9	1.39E+08	1.39E+08	DEL	0.135836	2.689178
9q34.3	9	1.39E+08	1.39E+08	AMP	0.446054	3.669023
9q34.3	9	1.39E+08	1.39E+08	DEL	0.123731	2.155392
9q34.3	9	1.39E+08	1.39E+08	DEL	0.123731	2.155392
9q34.3	9	1.39E+08	1.39E+08	DEL	0.13987	2.89204
9q34.3	9	1.39E+08	1.39E+08	AMP	0.453961	3.82849
9q34.3	9	1.39E+08	1.39E+08	DEL	0.164751	4.015656
9q34.3	9	1.4E+08	1.4E+08	AMP	0.370512	2.184987

9q34.3	9	1.4E+08	1.4E+08	DEL	0.149285	3.290679
9q34.3	9	1.4E+08	1.4E+08	DEL	0.136508	2.706517
9q34.3	9	1.4E+08	1.4E+08	DEL	0.136508	2.706517
9q34.3	9	1.4E+08	1.4E+08	DEL	0.121714	2.011432
9q34.3	9	1.4E+08	1.4E+08	DEL	0.121714	2.011432
9q34.3	9	1.4E+08	1.4E+08	AMP	0.378118	2.31574
9q34.3	9	1.4E+08	1.4E+08	DEL	0.18358	5.060463
9q34.3	9	1.4E+08	1.4E+08	DEL	0.15063	3.337087
9q34.3	9	1.4E+08	1.4E+08	DEL	0.15063	3.337087
9q34.3	9	1.4E+08	1.4E+08	DEL	0.151302	3.368047
9q34.3	9	1.4E+08	1.4E+08	DEL	0.152647	3.497781
9q34.3	9	1.4E+08	1.4E+08	DEL	0.148612	3.230372
9q34.3	9	1.4E+08	1.4E+08	DEL	0.151302	3.368047
9q34.3	9	1.4E+08	1.4E+08	AMP	0.399095	2.715132
9q34.3	9	1.4E+08	1.4E+08	DEL	0.15063	3.337087
9q34.3	9	1.4E+08	1.4E+08	DEL	0.164751	4.033126
9q34.3	9	1.4E+08	1.4E+08	DEL	0.164751	4.033126
9q34.3	9	1.4E+08	1.4E+08	DEL	0.162734	3.927376
9q34.3	9	1.4E+08	1.4E+08	DEL	0.164751	4.033126
9q34.3	9	1.4E+08	1.4E+08	DEL	0.165424	4.051105
9q34.3	9	1.4E+08	1.4E+08	DEL	0.165424	4.051105
9q34.3	9	1.4E+08	1.4E+08	DEL	0.165424	4.051105
9q34.3	9	1.4E+08	1.4E+08	DEL	0.162734	3.895528
9q34.3	9	1.4E+08	1.4E+08	DEL	0.162734	3.895528
9q34.3	9	1.4E+08	1.4E+08	DEL	0.162734	3.895528
9q34.3	9	1.4E+08	1.4E+08	DEL	0.160716	3.770443
9q34.3	9	1.4E+08	1.4E+08	DEL	0.152647	3.497237
9q34.3	9	1.4E+08	1.4E+08	DEL	0.17551	4.560824
9q34.3	9	1.4E+08	1.4E+08	DEL	0.178873	4.764506
9q34.3	9	1.4E+08	1.4E+08	DEL	0.178873	4.764506
9q34.3	9	1.4E+08	1.4E+08	DEL	0.171476	4.342449
9q34.3	9	1.4E+08	1.4E+08	DEL	0.171476	4.342449
9q34.3	9	1.4E+08	1.4E+08	DEL	0.165424	4.045394
9q34.3	9	1.4E+08	1.4E+08	DEL	0.165424	4.045394
9q34.3	9	1.4E+08	1.4E+08	AMP	0.373598	2.242657
9q34.3	9	1.4E+08	1.4E+08	DEL	0.165424	4.045394
9q34.3	9	1.4E+08	1.4E+08	AMP	0.373598	2.242657
9q34.3	9	1.4E+08	1.4E+08	DEL	0.165424	4.082226
9q34.3	9	1.4E+08	1.4E+08	AMP	0.373598	2.242657
9q34.3	9	1.4E+08	1.4E+08	DEL	0.164751	4.00892
9q34.3	9	1.4E+08	1.4E+08	AMP	0.373598	2.242657
9q34.3	9	1.4E+08	1.4E+08	DEL	0.164751	4.00892
9q34.3	9	1.4E+08	1.4E+08	AMP	0.373598	2.242657
9q34.3	9	1.4E+08	1.4E+08	DEL	0.161389	3.812373
9q34.3	9	1.4E+08	1.4E+08	DEL	0.162734	3.93972
9q34.3	9	1.4E+08	1.4E+08	DEL	0.162734	3.93972
9q34.3	9	1.4E+08	1.4E+08	DEL	0.164079	3.97492
9q34.3	9	1.4E+08	1.4E+08	DEL	0.179545	4.867394
9q34.3	9	1.4E+08	1.4E+08	DEL	0.196356	5.783785
9q34.3	9	1.4E+08	1.4E+08	DEL	0.196356	5.783785
9q34.3	9	1.4E+08	1.4E+08	DEL	0.177528	4.700895
9q34.3	9	1.4E+08	1.4E+08	DEL	0.14794	3.136594
9q34.3	9	1.4E+08	1.4E+08	DEL	0.14794	3.136594
10p11.21	10	35894338	35897863	AMP	0.369013	2.170574
10p11.21	10	35927177	35930362	AMP	0.369013	2.170574
10q21.2	10	63942794	64028466	AMP	0.36409	2.083496
10q21.3	10	69990386	69991871	DEL	0.121714	2.031388
10q21.3	10	70480769	70552134	DEL	0.121714	2.052321
10q26.13	10	1.25E+08	1.25E+08	AMP	0.410508	2.910503
11p15.5	11	616565	626078	DEL	0.201736	6.068688
11p15.5	11	626431	627143	DEL	0.201736	6.068688
11p15.5	11	637293	640706	DEL	0.201064	6.008153
11p15.5	11	1012821	1036706	AMP	0.585983	7.135663
11p15.5	11	1244296	1283406	AMP	0.378049	2.31574
11p11.2	11	47487496	47587121	DEL	0.123059	2.151848
11p11.2	11	47586888	47606114	DEL	0.121714	2.041508
11p11.2	11	47608198	47610746	DEL	0.134491	2.535942
11p11.2	11	47611216	47616211	DEL	0.165424	4.046452
11p11.2	11	47638867	47664175	DEL	0.165424	4.046452
11p11.2	11	47681143	47736941	DEL	0.162734	3.895263
11p11.2	11	47738072	47788995	DEL	0.165424	4.076559
11p11.2	11	47799639	47870107	DEL	0.155337	3.570747
11p11.2	11	48002113	48189670	DEL	0.128439	2.347644
11q12.1	11	56949221	56959191	DEL	0.136508	2.707604
11q12.1	11	57001051	57004709	DEL	0.13718	2.720618
11q13.1	11	64126620	64139687	AMP	0.449408	3.722135
11q13.3	11	69061605	69182494	AMP	0.378533	2.31574
11q13.3	11	69455855	69469242	AMP	0.378533	2.31574
11q13.3	11	69467844	69490184	AMP	0.378533	2.31574

11q22.3	11	1.07E+08	1.08E+08	DEL	0.174838	4.520314
11q22.3	11	1.08E+08	1.08E+08	DEL	0.174838	4.520314
11q22.3	11	1.08E+08	1.08E+08	DEL	0.151302	3.383729
11q25	11	1.34E+08	1.34E+08	DEL	1.917165	264.33266
11q25	11	1.34E+08	1.34E+08	DEL	1.917165	264.33266
12p13.31	12	7965108	8043744	DEL	0.125076	2.234504
12p13.31	12	8071826	8088871	DEL	0.125076	2.234504
12p13.1	12	14765576	14849519	AMP	0.374592	2.260728
12p12.3	12	14920933	14924065	AMP	0.39021	2.542309
12p12.3	12	14927270	14930936	AMP	0.39021	2.542309
12p12.3	12	14939410	14956474	AMP	0.39021	2.542309
12p12.1	12	25562241	25801513	AMP	0.369386	2.181486
12p12.1	12	26111962	26232825	AMP	0.385004	2.461837
12p12.1	12	26272959	26278060	AMP	0.385004	2.461837
12p12.1	12	26274924	26452223	AMP	0.385004	2.461837
12p12.1	12	26490342	26986131	AMP	0.400622	2.743536
12p11.23	12	27058114	27091259	AMP	0.410881	2.92897
12p11.23	12	27091316	27119583	AMP	0.410881	2.92897
12p11.23	12	27126128	27167367	AMP	0.410881	2.92897
12p11.23	12	27175479	27219276	AMP	0.400622	2.743536
12p11.23	12	27233991	27235447	AMP	0.400622	2.743536
12p11.23	12	27396901	27478892	AMP	0.400622	2.743536
12p11.23	12	27485787	27576241	AMP	0.385004	2.461837
12p11.23	12	27676364	27848497	AMP	0.369386	2.181486
12p11.22	12	27849428	27850566	AMP	0.369386	2.181486
12p11.22	12	27863706	27909228	AMP	0.369386	2.181486
12p11.22	12	27915671	27924209	AMP	0.385004	2.461837
12p11.22	12	28111017	28125638	AMP	0.385004	2.461837
12p11.22	12	28286182	28732883	AMP	0.395263	2.638263
12p11.22	12	29653773	29937692	DEL	0.121714	2.032497
12p11.21	12	30781922	30848920	DEL	0.122387	2.090575
12q14.3	12	66741211	67197966	AMP	0.388731	2.504901
12q15	12	69139886	69187508	AMP	0.379732	2.36057
12q15	12	69201956	69239214	AMP	0.379732	2.36057
12q15	12	69235977	69365350	AMP	0.389991	2.542309
12q15	12	69633317	69668138	AMP	0.421275	3.130086
12q15	12	69742121	69748014	AMP	0.476096	4.340779
12q15	12	69753483	69784576	AMP	0.476096	4.340779
12q15	12	69864129	69973562	AMP	0.436893	3.454418
12q15	12	69979114	69995350	AMP	0.436893	3.454418
12q15	12	70002351	70004942	AMP	0.421275	3.130086
12q15	12	70037140	70093256	AMP	0.436893	3.454418
12q15	12	70132461	70216984	AMP	0.452511	3.805317
12q15	12	70636774	70748773	AMP	0.442252	3.578278
12q15	12	70760056	70828072	AMP	0.442252	3.578278
12q15	12	70910630	71031220	AMP	0.442252	3.578278
12q15	12	71031853	71314623	AMP	0.369522	2.181486
12q21.1	12	72233487	72320629	AMP	0.370881	2.184987
12q21.1	12	72332626	72580398	AMP	0.386439	2.465016
12q21.1	12	72481046	73059422	AMP	0.402057	2.743536
12q22	12	93115281	93166231	DEL	0.195684	5.758041
12q22	12	93164413	93323107	DEL	0.195684	5.758041
12q22	12	93771659	93797024	DEL	0.196356	5.778809
12q22	12	93799449	93836038	DEL	0.195684	5.723229
12q24.23	12	1.21E+08	1.21E+08	DEL	0.124404	2.184922
12q24.23	12	1.21E+08	1.21E+08	DEL	0.128439	2.34737
12q24.31	12	1.21E+08	1.21E+08	DEL	0.126421	2.320768
12q24.31	12	1.21E+08	1.21E+08	DEL	0.127094	2.330713
12q24.31	12	1.21E+08	1.21E+08	DEL	0.121714	2.031388
12q24.31	12	1.21E+08	1.21E+08	DEL	0.126421	2.320768
12q24.31	12	1.21E+08	1.21E+08	DEL	0.129111	2.364859
12q24.31	12	1.21E+08	1.21E+08	DEL	0.176183	4.631612
12q24.31	12	1.21E+08	1.21E+08	DEL	0.176183	4.631612
12q24.31	12	1.21E+08	1.21E+08	DEL	0.179545	4.885026
12q24.31	12	1.21E+08	1.21E+08	DEL	0.125076	2.214025
12q24.31	12	1.21E+08	1.21E+08	DEL	0.127094	2.330713
12q24.31	12	1.21E+08	1.21E+08	DEL	0.125076	2.232978
12q24.31	12	1.21E+08	1.21E+08	DEL	0.122387	2.119755
12q24.31	12	1.21E+08	1.21E+08	DEL	0.129784	2.385885
12q24.31	12	1.21E+08	1.21E+08	DEL	0.160716	3.760161
12q24.31	12	1.21E+08	1.21E+08	DEL	0.151974	3.421698
12q24.31	12	1.21E+08	1.21E+08	DEL	0.129784	2.385885
12q24.31	12	1.21E+08	1.21E+08	DEL	0.129784	2.385885
12q24.31	12	1.21E+08	1.21E+08	DEL	0.125749	2.262617
12q24.31	12	1.21E+08	1.21E+08	DEL	0.125749	2.262617
12q24.31	12	1.22E+08	1.22E+08	DEL	0.123731	2.165303
12q24.31	12	1.22E+08	1.22E+08	DEL	0.123731	2.165303
12q24.31	12	1.22E+08	1.22E+08	DEL	0.121714	2.006608
12q24.31	12	1.22E+08	1.22E+08	DEL	0.121714	2.006608

12q24.31	12	1.22E+08	1.22E+08	DEL	0.125076	2.204345
12q24.31	12	1.22E+08	1.22E+08	DEL	0.127094	2.330713
12q24.31	12	1.22E+08	1.22E+08	DEL	0.125749	2.27244
12q24.31	12	1.22E+08	1.22E+08	DEL	0.125076	2.223409
12q24.31	12	1.22E+08	1.22E+08	DEL	0.128439	2.34737
12q24.31	12	1.22E+08	1.22E+08	DEL	0.14794	3.144529
12q24.31	12	1.22E+08	1.22E+08	DEL	0.136508	2.712055
12q24.31	12	1.22E+08	1.22E+08	DEL	0.138525	2.802539
12q24.31	12	1.22E+08	1.22E+08	DEL	0.138525	2.802539
12q24.31	12	1.22E+08	1.22E+08	DEL	0.137853	2.745425
12q24.31	12	1.23E+08	1.23E+08	DEL	0.141215	2.918892
12q24.31	12	1.23E+08	1.23E+08	DEL	0.141215	2.918892
12q24.31	12	1.23E+08	1.23E+08	DEL	0.141215	2.918892
12q24.31	12	1.23E+08	1.23E+08	DEL	0.139198	2.887017
12q24.31	12	1.23E+08	1.23E+08	DEL	0.127766	2.339664
12q24.31	12	1.23E+08	1.23E+08	DEL	0.127766	2.339664
12q24.31	12	1.23E+08	1.23E+08	DEL	0.133818	2.507933
12q24.31	12	1.23E+08	1.23E+08	DEL	0.125076	2.244507
12q24.31	12	1.23E+08	1.23E+08	DEL	0.125076	2.244507
12q24.31	12	1.23E+08	1.23E+08	DEL	0.131128	2.438127
12q24.31	12	1.23E+08	1.23E+08	DEL	0.131128	2.438127
12q24.31	12	1.23E+08	1.23E+08	DEL	0.131128	2.438127
12q24.31	12	1.23E+08	1.23E+08	DEL	0.126421	2.320971
12q24.31	12	1.23E+08	1.23E+08	DEL	0.126421	2.320971
12q24.31	12	1.23E+08	1.23E+08	DEL	0.125076	2.234718
12q24.31	12	1.23E+08	1.23E+08	DEL	0.127094	2.330968
12q24.31	12	1.25E+08	1.25E+08	AMP	0.38434	2.452057
12q24.31	12	1.25E+08	1.25E+08	DEL	0.138525	2.818235
12q24.31	12	1.25E+08	1.26E+08	DEL	0.138525	2.818235
12q24.31	12	1.26E+08	1.26E+08	DEL	0.122387	2.057859
12q24.33	12	1.32E+08	1.32E+08	DEL	0.122387	2.072507
12q24.33	12	1.33E+08	1.33E+08	DEL	0.124404	2.196719
12q24.33	12	1.33E+08	1.33E+08	DEL	0.135836	2.700735
12q24.33	12	1.33E+08	1.33E+08	DEL	0.148612	3.230081
12q24.33	12	1.33E+08	1.33E+08	DEL	0.131801	2.459903
12q24.33	12	1.33E+08	1.33E+08	DEL	0.131801	2.459903
12q24.33	12	1.33E+08	1.33E+08	DEL	0.131801	2.459903
13q12.11	13	21727734	21750741	DEL	0.155337	3.563007
13q12.11	13	21750784	21753223	DEL	0.155337	3.563007
13q12.11	13	21950263	22033509	DEL	0.148612	3.174608
13q12.11	13	22245522	22278637	DEL	0.124404	2.172245
13q13.3	13	38923986	38937140	DEL	0.319415	13.931005
13q13.3	13	39261266	39460074	DEL	0.298569	12.314731
13q13.3	13	39540062	39565203	DEL	0.298569	12.314731
13q14.3	13	53418109	53422775	DEL	0.248808	8.861627
13q32.3	13	99853028	1E+08	AMP	0.425361	3.193544
13q32.3	13	1E+08	1E+08	AMP	0.425361	3.193544
13q33.1	13	1.02E+08	1.03E+08	AMP	0.378236	2.31574
13q33.1	13	1.03E+08	1.03E+08	AMP	0.378236	2.31574
13q33.1	13	1.04E+08	1.04E+08	AMP	0.368294	2.15155
13q33.2	13	1.06E+08	1.06E+08	AMP	0.39953	2.715132
13q33.2	13	1.06E+08	1.06E+08	AMP	0.39953	2.715132
13q33.3	13	1.07E+08	1.07E+08	AMP	0.39953	2.715132
13q33.3	13	1.07E+08	1.07E+08	AMP	0.368294	2.15155
13q33.3	13	1.08E+08	1.09E+08	AMP	0.368294	2.15155
13q33.3	13	1.09E+08	1.09E+08	AMP	0.368294	2.15155
13q33.3	13	1.09E+08	1.09E+08	AMP	0.368071	2.15155
13q33.3	13	1.09E+08	1.1E+08	AMP	0.368071	2.15155
13q33.3	13	1.09E+08	1.1E+08	DEL	0.36716	18.022142
13q34	13	1.1E+08	1.1E+08	DEL	0.36716	18.022142
13q34	13	1.11E+08	1.11E+08	DEL	0.231324	7.769851
13q34	13	1.11E+08	1.11E+08	DEL	0.231324	7.769851
13q34	13	1.11E+08	1.11E+08	AMP	0.610279	7.822429
13q34	13	1.11E+08	1.11E+08	AMP	0.610279	7.822429
13q34	13	1.12E+08	1.12E+08	AMP	0.372914	2.22297
13q34	13	1.12E+08	1.12E+08	AMP	0.372914	2.22297
13q34	13	1.14E+08	1.14E+08	AMP	0.362216	2.021001
13q34	13	1.14E+08	1.14E+08	AMP	0.362216	2.021001
13q34	13	1.14E+08	1.14E+08	AMP	0.362216	2.021001
14q13.1	14	34393437	34931980	DEL	0.32076	14.043662
14q13.1	14	34901995	34931562	DEL	0.32076	14.043662
14q13.1	14	34985135	35008916	DEL	0.138525	2.793954
14q13.1	14	35030300	35099389	DEL	0.132473	2.474561
14q13.1	14	35179593	35184029	DEL	0.138525	2.805256
14q13.1	14	35221937	35344853	DEL	0.13718	2.722638
14q21.3	14	50110273	50155140	DEL	0.124404	2.197617
14q21.3	14	50159823	50219870	DEL	0.123059	2.15278
14q21.3	14	50234326	50249909	DEL	0.123059	2.15278
14q24.2	14	73704205	73741348	DEL	0.148612	3.216095

14q24.3	14	74424713	74486102	DEL	0.131128	2.437254
14q24.3	14	74523553	74551196	DEL	0.127766	2.340967
14q24.3	14	74551499	74667936	DEL	0.132473	2.468121
14q24.3	14	74872596	74892805	DEL	0.139198	2.8608
14q24.3	14	74942895	74960880	DEL	0.139198	2.8608
14q32.31	14	1.02E+08	1.02E+08	DEL	0.196356	5.776284
14q32.31	14	1.03E+08	1.03E+08	DEL	0.137853	2.768292
14q32.31	14	1.03E+08	1.03E+08	DEL	0.140543	2.903804
14q32.31	14	1.03E+08	1.03E+08	DEL	0.138525	2.819258
14q32.31	14	1.03E+08	1.03E+08	DEL	0.138525	2.819258
14q32.31	14	1.03E+08	1.03E+08	DEL	0.14256	2.94858
14q32.31	14	1.03E+08	1.03E+08	DEL	0.14256	2.94858
14q32.31	14	1.03E+08	1.03E+08	DEL	0.131128	2.438127
14q32.31	14	1.03E+08	1.03E+08	DEL	0.141888	2.934814
14q32.32	14	1.03E+08	1.03E+08	DEL	0.190304	5.425609
14q32.32	14	1.03E+08	1.03E+08	DEL	0.192322	5.583183
14q32.32	14	1.03E+08	1.04E+08	DEL	0.133818	2.502405
14q32.32	14	1.04E+08	1.04E+08	DEL	0.151974	3.431321
14q32.32	14	1.04E+08	1.04E+08	DEL	0.151974	3.431321
14q32.32	14	1.04E+08	1.04E+08	DEL	0.122387	2.115322
14q32.32	14	1.04E+08	1.04E+08	DEL	0.130456	2.412268
14q32.33	14	1.05E+08	1.05E+08	DEL	0.135836	2.653936
14q32.33	14	1.05E+08	1.05E+08	DEL	0.152647	3.470879
14q32.33	14	1.05E+08	1.05E+08	DEL	0.157354	3.671591
14q32.33	14	1.05E+08	1.05E+08	DEL	0.157354	3.671591
14q32.33	14	1.05E+08	1.05E+08	DEL	0.161389	3.802445
14q32.33	14	1.06E+08	1.06E+08	DEL	0.125076	2.209655
14q32.33	14	1.06E+08	1.06E+08	DEL	0.125076	2.209655
14q32.33	14	1.06E+08	1.06E+08	DEL	0.125076	2.209655
14q32.33	14	1.06E+08	1.06E+08	DEL	0.200391	5.970401
14q32.33	14	1.06E+08	1.06E+08	DEL	0.184252	5.073363
14q32.33	14	1.06E+08	1.06E+08	DEL	0.164751	3.991166
14q32.33	14	1.06E+08	1.06E+08	DEL	0.192994	5.641509
15q15.1	15	40820882	40857256	DEL	0.131128	2.432982
15q15.1	15	40861499	40866659	DEL	0.131801	2.460518
15q15.1	15	40886218	40956540	DEL	0.131801	2.460518
15q15.1	15	40986972	41024354	DEL	0.134491	2.556606
15q15.1	15	41271078	41408552	DEL	0.15063	3.344077
15q15.1	15	41474923	41522941	DEL	0.164751	4.033791
15q15.1	15	41601466	41624819	DEL	0.174838	4.515783
15q15.1	15	41624892	41673248	DEL	0.169458	4.26039
15q15.1	15	41679551	41694717	DEL	0.168786	4.212351
15q15.1	15	41700606	41775761	DEL	0.161389	3.815215
15q15.1	15	41785591	41795747	DEL	0.143233	2.977349
15q15.1	15	41795836	41806085	DEL	0.138525	2.81499
15q15.1	15	41809374	41836467	DEL	0.184925	5.107698
15q15.1	15	41913422	42062141	DEL	0.134491	2.556606
15q21.1	15	47476298	48066420	DEL	0.172148	4.382789
15q26.1	15	91643180	91844539	DEL	0.136508	2.716244
16p13.3	16	96407	103628	AMP	0.369413	2.181486
16p13.3	16	446725	460367	DEL	0.125749	2.303842
16p13.3	16	451826	462487	DEL	0.125749	2.303842
16p13.3	16	475619	573011	DEL	0.156682	3.63321
16p13.3	16	765115	769655	DEL	0.131801	2.458754
16p13.3	16	770581	772601	DEL	0.131801	2.458754
16p13.3	16	772582	776954	DEL	0.162061	3.845669
16p13.3	16	776936	785525	DEL	0.173493	4.407251
16p13.3	16	779753	791329	DEL	0.173493	4.407251
16p13.3	16	810762	818865	DEL	0.139198	2.854971
16p13.3	16	819428	833370	DEL	0.151974	3.440019
16p13.3	16	834974	838397	DEL	0.151974	3.440019
16p13.3	16	838046	850737	DEL	0.164751	3.996077
16p13.3	16	848041	850733	DEL	0.164751	3.996077
16p13.3	16	855443	863861	DEL	0.13987	2.89204
16p13.3	16	903634	1031318	DEL	0.193667	5.651835
16p13.3	16	1031808	1036979	DEL	0.193667	5.651835
16p13.3	16	1122756	1131454	DEL	0.140543	2.903804
16p13.3	16	1140005	1146244	DEL	0.139198	2.839188
16p13.3	16	1203241	1271771	DEL	0.152647	3.512728
16p13.3	16	1271651	1275257	DEL	0.152647	3.512728
16p13.3	16	1290697	1292555	DEL	0.191649	5.492872
16p13.3	16	1306060	1308532	DEL	0.189632	5.386025
16p13.3	16	1355548	1377019	DEL	0.283775	11.255068
16p13.3	16	1383602	1399439	DEL	0.139198	2.849992
16p13.3	16	1401924	1413352	DEL	0.139198	2.849992
16p13.3	16	1413206	1464752	DEL	0.125076	2.238732
16p13.3	16	1469745	1479345	DEL	0.125749	2.29674
16p13.3	16	1484384	1494557	DEL	0.124404	2.18159
16p13.3	16	2047655	2059824	DEL	0.124404	2.191295

16p13.3	16	2059927	2070756	DEL	0.131128	2.431676
16p13.3	16	2075357	2089027	DEL	0.131128	2.431676
16p13.3	16	2089816	2097867	DEL	0.122387	2.137986
16p13.3	16	2097466	2138716	DEL	0.123731	2.163832
16p13.3	16	2138711	2185899	DEL	0.14256	2.95796
16p13.3	16	2190804	2204166	DEL	0.14256	2.95796
16p13.3	16	2205699	2228130	DEL	0.201064	6.020453
16p13.3	16	2227184	2246526	DEL	0.201064	6.020453
16p13.3	16	2254249	2259417	DEL	0.154664	3.549928
16p13.3	16	2261998	2264808	DEL	0.125749	2.278396
16p12.3	16	20791515	20911671	DEL	0.235359	8.013472
16p12.3	16	20866247	20911706	DEL	0.235359	8.013472
16p12.3	16	20911190	20936328	DEL	0.235359	8.013472
16q21	16	58741035	58768261	DEL	0.171476	4.337092
16q21	16	61681146	62070939	DEL	0.181562	4.937829
16q22.1	16	68344877	68392466	DEL	0.174838	4.477707
16q22.1	16	68392231	68482591	DEL	0.188287	5.253572
16q22.1	16	68563993	68609975	DEL	0.188287	5.253572
16q22.1	16	70557691	70608820	DEL	0.139198	2.88659
16q22.1	16	70613798	70694585	DEL	0.139198	2.88659
16q22.1	16	70695107	70719969	DEL	0.122387	2.128951
16q22.2	16	72816784	73093597	DEL	0.177528	4.695441
16q23.1	16	74907468	75034071	DEL	0.121714	2.004754
16q24.2	16	88493879	88507165	DEL	0.143905	3.00626
16q24.2	16	88519725	88603424	DEL	0.161389	3.791495
16q24.3	16	89334038	89556969	DEL	0.138525	2.819401
16q24.3	16	89557325	89624176	DEL	0.135163	2.631589
17p13.3	17	5810	31427	DEL	0.14256	2.957612
17p13.3	17	62293	236045	DEL	0.147267	3.112753
17p13.3	17	260118	273510	DEL	0.144577	3.026321
17p13.3	17	289769	295730	DEL	0.143905	2.98964
17p13.3	17	411908	624957	DEL	0.135836	2.674867
17p13.3	17	635652	646206	DEL	0.14256	2.966619
17p13.3	17	647654	657239	DEL	0.14794	3.149129
17p13.3	17	660337	685581	DEL	0.14794	3.149129
17p13.3	17	685513	695749	DEL	0.144577	3.036554
17p13.3	17	702553	883010	DEL	0.139198	2.835257
17p13.3	17	900357	906911	DEL	0.143905	3.01359
17p13.3	17	906758	1132315	DEL	0.14794	3.162317
17p13.3	17	1173853	1174754	DEL	0.147267	3.112753
17p13.3	17	1182957	1204281	DEL	0.143905	3.01359
17p13.3	17	1247566	1303672	DEL	0.141215	2.910158
17p13.3	17	1323983	1366456	DEL	0.14256	2.966619
17p13.3	17	1367392	1396106	DEL	0.135163	2.614302
17p13.3	17	1397865	1420182	DEL	0.14794	3.149129
17p13.3	17	1421012	1466110	DEL	0.14794	3.149129
17p13.3	17	1472561	1532180	DEL	0.170131	4.280803
17p13.3	17	1537152	1549041	DEL	0.17551	4.577542
17p13.3	17	1549444	1553371	DEL	0.14256	2.966619
17p13.3	17	1553923	1588176	DEL	0.14256	2.966619
17p13.3	17	1611064	1613732	DEL	0.147267	3.112753
17p13.3	17	1619817	1641893	DEL	0.14256	2.957612
17p13.3	17	1646130	1658562	DEL	0.14256	2.957612
17p13.3	17	1665253	1680868	DEL	0.143905	2.98964
17p13.3	17	1682779	1733928	DEL	0.138525	2.793954
17p13.3	17	1732996	1803376	DEL	0.146595	3.077471
17p13.3	17	1837971	1928639	DEL	0.146595	3.077471
17p13.3	17	1933404	1946724	DEL	0.147267	3.112753
17p13.3	17	1945327	1946724	DEL	0.147267	3.112753
17p13.3	17	1957448	1962981	DEL	0.143905	2.98964
17p13.3	17	1963133	2207065	DEL	0.135836	2.653936
17p13.3	17	2206677	2228554	DEL	0.141888	2.921194
17p13.3	17	2225797	2240801	DEL	0.14794	3.162317
17p13.3	17	2232413	2232507	DEL	0.14794	3.162317
17p13.3	17	2233570	2233664	DEL	0.14794	3.162317
17p13.3	17	2240792	2284352	DEL	0.135836	2.6964
17p13.3	17	2287354	2304412	DEL	0.145922	3.063965
17p13.3	17	2308856	2415185	DEL	0.145922	3.063965
17p13.3	17	2496504	2588909	DEL	0.161389	3.778056
17p13.3	17	2680350	2941033	DEL	0.161389	3.778056
17p13.3	17	2965963	2966901	DEL	0.147267	3.112753
17p13.3	17	2995352	2996290	DEL	0.146595	3.08865
17p13.3	17	3029878	3030875	DEL	0.147267	3.112753
17p13.3	17	3100813	3101742	DEL	0.147267	3.112753
17p13.3	17	3118915	3119844	DEL	0.147267	3.112753
17p13.3	17	3181193	3182268	DEL	0.14794	3.136253
17p13.3	17	3194929	3195876	DEL	0.146595	3.08865
17p13.2	17	3300398	3301704	DEL	0.146595	3.08865
17p13.2	17	3323862	3324827	DEL	0.147267	3.112753

17p13.2	17	3336164	3337135	DEL	0.147267	3.112753
17p13.2	17	3413796	3461289	DEL	0.143905	2.98964
17p13.2	17	3468738	3500392	DEL	0.137853	2.749483
17p13.2	17	3511556	3539616	DEL	0.139198	2.888714
17p13.2	17	3539762	3564836	DEL	0.139198	2.888714
17p13.2	17	3566196	3571976	DEL	0.14794	3.162317
17p13.2	17	3566357	3599488	DEL	0.14794	3.162317
17p13.2	17	3575493	3599698	DEL	0.139198	2.867266
17p13.2	17	3617922	3704537	DEL	0.146595	3.08865
17p13.2	17	3627211	3630067	DEL	0.146595	3.08865
17p13.2	17	3714460	3749545	DEL	0.138525	2.805256
17p13.2	17	4613784	4624794	DEL	0.125749	2.274212
17p13.2	17	4634723	4636905	DEL	0.133818	2.491856
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18q21.32	18	56529832	56653712	DEL	0.123731	2.159112
18q21.33	18	59000815	59223006	DEL	0.170803	4.317729
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19q13.42	19	54135310	54140263	DEL	0.157354	3.648456
19q13.42	19	54296857	54327648	DEL	0.166096	4.116113
19q13.42	19	54369477	54379691	DEL	0.170803	4.318734
19q13.42	19	54382444	54410906	DEL	0.149285	3.243916
19q13.42	19	54412589	54447195	DEL	0.155337	3.562504
19q13.42	19	54466294	54493469	DEL	0.200391	5.966618
19q13.42	19	54495542	54515923	DEL	0.190977	5.472646
19q13.42	19	54544079	54567207	DEL	0.151974	3.422902
19q13.42	19	54573149	54584634	DEL	0.153992	3.534099
19q13.42	19	54597933	54606000	DEL	0.152647	3.464248
19q13.42	19	54606036	54612564	DEL	0.152647	3.464248
19q13.42	19	54610320	54619055	DEL	0.125749	2.30046
19q13.42	19	54641444	54659419	AMP	0.378293	2.31574
19q13.42	19	54658899	54663620	AMP	0.393911	2.592212
19q13.42	19	54663846	54676944	AMP	0.362675	2.040765
19q13.42	19	55385704	55401838	DEL	0.131801	2.458568
19q13.42	19	55417508	55427508	DEL	0.144577	3.035237
19q13.42	19	55434877	55477680	DEL	0.138525	2.812701
19q13.42	19	55464498	55512510	DEL	0.144577	3.035237
19q13.42	19	55525073	55549632	DEL	0.144577	3.035237
19q13.42	19	55550476	55582659	DEL	0.143905	2.994954
19q13.42	19	55583388	55599291	DEL	0.14256	2.958026
19q13.42	19	56088899	56092211	AMP	0.442204	3.578278
19q13.42	19	56102746	56113336	AMP	0.514935	5.310901
19q13.42	19	56111388	56114504	AMP	0.514935	5.310901
19q13.42	19	56116771	56128635	AMP	0.457822	3.935663
19q13.42	19	56132108	56135967	AMP	0.39535	2.638263
19q13.42	19	56146382	56154835	AMP	0.39535	2.638263
19q13.42	19	56146825	56156988	AMP	0.39535	2.638263
19q13.42	19	56152428	56164527	AMP	0.39535	2.638263
19q13.42	19	56165512	56186081	AMP	0.364114	2.083496
19q13.43	19	59067079	59070327	AMP	0.370325	2.184987
19q13.43	19	59073298	59084942	AMP	0.385943	2.465016
20q13.32	20	57414773	57486247	AMP	0.391414	2.542309
20q13.33	20	58438618	58508710	AMP	0.385091	2.461837
20q13.33	20	60528525	60640866	AMP	0.39654	2.644987
20q13.33	20	60697517	60710434	AMP	0.412158	2.93218
20q13.33	20	60877149	60883918	AMP	0.422417	3.130086
20q13.33	20	60883011	60942368	AMP	0.649964	8.92057

20q13.33	20	60962172	60963576	AMP	0.427776	3.248187
20q13.33	20	60963688	60982341	AMP	0.412158	2.93218
20q13.33	20	61038553	61051026	AMP	0.412158	2.93218
20q13.33	20	61141550	61148733	AMP	0.412158	2.93218
20q13.33	20	61147660	61167971	AMP	0.443394	3.588251
20q13.33	20	61273797	61317137	AMP	0.459012	3.946275
20q13.33	20	61340189	61394123	AMP	0.38437	2.452057
20q13.33	20	61436187	61445352	AMP	0.38437	2.452057
20q13.33	20	61447596	61472511	AMP	0.38437	2.452057
20q13.33	20	61472467	61493115	AMP	0.368752	2.170574
20q13.33	20	61509090	61569304	AMP	0.38437	2.452057
20q13.33	20	61584052	61599949	AMP	0.415606	3.026232
20q13.33	20	61637331	61638387	AMP	0.368752	2.170574
20q13.33	20	61826781	61847586	AMP	0.415606	3.026232
20q13.33	20	61867235	61871859	AMP	0.472137	4.253406
20q13.33	20	61872136	61904046	AMP	0.38437	2.452057
20q13.33	20	61904137	61921142	AMP	0.472719	4.276863
20q13.33	20	61924538	61966203	AMP	0.472719	4.276863
20q13.33	20	61924538	61966203	DEL	0.139198	2.885998
20q13.33	20	61975420	62009753	AMP	0.441483	3.561562
20q13.33	20	62037542	62103993	AMP	0.415606	3.026232
20q13.33	20	62119366	62130505	AMP	0.431151	3.344587
20q13.33	20	62152077	62153559	AMP	0.431151	3.344587
20q13.33	20	62159778	62168723	AMP	0.743051	11.540928
20q13.33	20	62172163	62178857	AMP	0.743051	11.540928
20q13.33	20	62184373	62188061	AMP	0.685938	9.94931
20q13.33	20	62218955	62258394	AMP	0.59223	7.319424
20q13.33	20	62271061	62284780	AMP	0.415533	3.026232
20q13.33	20	62289163	62328416	AMP	0.446769	3.687345
20q13.33	20	62290653	62330037	AMP	0.446769	3.687345
20q13.33	20	62328021	62330037	AMP	0.446769	3.687345
20q13.33	20	62329996	62339377	AMP	0.431151	3.344587
20q13.33	20	62338817	62367494	AMP	0.431151	3.344587
20q13.33	20	62366815	62370456	AMP	0.431151	3.344587
20q13.33	20	62371214	62374858	AMP	0.51414	5.292904
20q13.33	20	62375019	62462597	AMP	0.51414	5.292904
20q13.33	20	62492566	62494341	AMP	0.415533	3.026232
20q13.33	20	62496596	62522898	AMP	0.415533	3.026232
20q13.33	20	62526518	62567384	AMP	0.415533	3.026232
20q13.33	20	62571186	62587769	AMP	0.415533	3.026232
20q13.33	20	62588055	62680113	AMP	0.415533	3.026232
20q13.33	20	62605466	62611361	AMP	0.399915	2.734703
20q13.33	20	62612488	62664453	AMP	0.399915	2.734703
20q13.33	20	62679076	62680994	AMP	0.399915	2.734703
21q22.12	21	36160098	37376965	DEL	0.122387	2.122123
21q22.12	21	37406839	37451687	DEL	0.191649	5.515544
21q22.12	21	37442239	37445464	DEL	0.191649	5.515544
21q22.12	21	37507210	37518864	DEL	0.247463	8.799352
21q22.12	21	37529080	37666572	DEL	0.291172	11.791899
21q22.12	21	37692487	37758446	DEL	0.295207	12.044869
21q22.12	21	37757676	37791313	DEL	0.280413	11.018657
21q22.13	21	37832919	37948867	DEL	0.314708	13.573096
21q22.13	21	38071433	38122218	DEL	0.227289	7.483855
21q22.13	21	38123189	38362536	DEL	0.227289	7.483855
21q22.13	21	38431470	38445470	DEL	0.182907	4.9946
21q22.13	21	38445526	38575413	AMP	0.362877	2.040765
21q22.13	21	38445526	38575413	DEL	0.184925	5.100398
21q22.3	21	44473301	44497053	DEL	0.156682	3.619834
21q22.3	21	44513066	44527697	DEL	0.162061	3.869288
21q22.3	21	44589118	44592915	DEL	0.129111	2.359344
21q22.3	21	44834395	44847008	DEL	0.123731	2.163832
21q22.3	21	44949072	45079374	DEL	0.123731	2.163832
21q22.3	21	45642874	45660849	DEL	0.130456	2.415823
21q22.3	21	45666222	45682099	DEL	0.123731	2.154251
21q22.3	21	45917775	46131495	AMP	0.410016	2.910503
21q22.3	21	45917775	46131495	DEL	0.143233	2.983733
21q22.3	21	45937099	45945835	DEL	0.135163	2.613197
21q22.3	21	45958864	45960078	AMP	0.410016	2.910503
21q22.3	21	45958864	45960078	DEL	0.135163	2.613197
21q22.3	21	45970240	45971388	AMP	0.410016	2.910503
21q22.3	21	45970240	45971388	DEL	0.135163	2.613197
21q22.3	21	45977673	45978643	DEL	0.143233	2.983733
21q22.3	21	45993606	45994987	DEL	0.135163	2.613197
21q22.3	21	45999332	46000481	DEL	0.135163	2.613197
21q22.3	21	46011149	46012386	DEL	0.135163	2.613197
21q22.3	21	46020497	46022091	DEL	0.135163	2.613197
21q22.3	21	46031996	46032871	DEL	0.135163	2.613197
21q22.3	21	46047040	46048294	DEL	0.135163	2.613197
21q22.3	21	46057273	46058370	DEL	0.135163	2.613197

21q22.3	21	46066331	46067564	AMP	0.384547	2.452057
21q22.3	21	46066331	46067564	DEL	0.135163	2.613197
21q22.3	21	46074130	46074576	AMP	0.384547	2.452057
21q22.3	21	46074130	46074576	DEL	0.135163	2.613197
21q22.3	21	46077849	46078258	DEL	0.135163	2.613197
21q22.3	21	46086106	46086844	DEL	0.135163	2.613197
21q22.3	21	46101491	46102078	DEL	0.135163	2.613197
21q22.3	21	46117087	46117959	DEL	0.135163	2.613197
22q11.21	22	18111621	18213388	DEL	0.122387	2.133385
22q11.21	22	18216906	18257536	DEL	0.122387	2.133385
22q11.21	22	19136089	19137796	DEL	0.141888	2.937082
22q11.21	22	19163095	19166343	DEL	0.141888	2.937082
22q11.21	22	19166986	19279239	DEL	0.129111	2.356487
22q11.21	22	19510547	19515068	DEL	0.121714	2.046182
22q11.21	22	19701987	19712295	DEL	0.121714	2.046182
22q11.21	22	19710468	19712294	DEL	0.121714	2.046182
22q11.21	22	20116979	20135530	DEL	0.180218	4.892021
22q12.2	22	31795509	31924726	DEL	0.125076	2.233321
22q12.2	22	31832963	31892094	DEL	0.121714	2.002318
22q12.2	22	31884674	32014572	DEL	0.140543	2.899398
22q12.2	22	32014477	32058418	DEL	0.140543	2.899398
22q12.2	22	32072242	32146126	DEL	0.140543	2.899398
22q12.2	22	32149944	32303012	DEL	0.135836	2.653936
22q13.33	22	50713408	50746056	AMP	0.362894	2.040765
22q13.33	22	50713408	50746056	DEL	0.139198	2.885998
22q13.33	22	50781733	50883514	DEL	0.190977	5.472646
22q13.33	22	50883429	50913454	AMP	0.406641	2.826772
22q13.33	22	50883429	50913454	DEL	0.190977	5.472646
22q13.33	22	50925213	50929077	DEL	0.121714	2.025749
22q13.33	22	50941376	50946135	DEL	0.121714	2.025749

1 **Supplementary Table S8.** 47 DNA damage repair genes investigated in this study.

TP53				
TP53				
Base excision repair (BER)				
MUTYH	APEX1	PARP1	PARP2	PARP3
Mismatch excision repair (MMR)				
MLH1	MSH2	MSH6	PMS2	
Homologous recombination (HR)				
RAD51	RAD51B	RAD51D	XRCC2	XRCC3
RAD52	RAD54L	RAD54B	BRCA1	RAD50
MRE11A	NBN			
Fanconi anemia (FA)				
FANCA	FANCC	BRCA2	FANCD2	FANCE
FANCF	FANCG	BRIP1	FANCL	FANCM
PALB2	RAD51C			
Non-homologous end-joining (NHEJ)				
PRKDC				
DNA polymerases				
POLB	POLD1	POLE		
Checkpoint Factors (CPF)				
BLM	ATM	RECQL	ATR	CHEK1
CHEK2				
Others				
MGMT	FEN1	ERCC1		

2

3

4

Table S9. Germline mutations in DNA damage response (DDR) genes in 803 BTC patients.

Sample.ID	TumorType	Age	Sex	GeneSymbol	RefSeq	DNA_Alter	AA_Alter	VarType
117C0733A1	ECC	49	Male	ATM	NM_000051	c.5853del	p.F1952Lfs*38	Truncation
117H2467A1	ICC	46	Male	FANCA	NM_000135	c.3188G>A	p.W1063*	Truncation
117J3136A1	GBC	57	Female	FANCC	NM_000136	c.339G>A	p.W113*	Truncation
117K3620A1	ICC	51	Male	BRCA1	NM_007294	c.745del	p.T249Lfs*49	Truncation
117K3750A1	ICC	52	Male	MLH1	NM_000249	c.546-1G>A	-	Indel
117L3952A1	ICC	51	Female	BARD1	NM_000465	C.539_540del	P.Y180*	Truncation
117L4139A1	ECC	63	Male	BRCA2	NM_000059	c.9011del	p.K3004Rfs*24	Truncation
118B5044A1	ECC	68	Male	BRCA2	NM_000059	C.3847_3848del	P.V1283Kfs*2	Truncation
118C5506A1	ICC	63	Male	SPINK1	NM_003122	c.194+2T>C	-	Indel
118C5792A1	ICC	65	Male	SDHB	NM_003000	c.689G>A	p.R230H	Indel
118C5833A1	ICC	61	Male	BRCA2	NM_000059	c.5073dup	p.W1692Mfs*3	Truncation
118D6519A1	ECC	46	Male	BRCA1	NM_007294	c.3257T>G	p.L1086*	Truncation
118E7306A1	ICC	63	Male	BRCA1	NM_007294	c.5470_5477del	p.I1824Dfs*3	Truncation
118E7744A1	ECC	61	Male	SPINK1	NM_003122	c.194+2T>C	-	Indel
118E7901A1	ICC	48	Male	SPINK1	NM_003122	c.194+2T>C	-	Indel
118E7940A1	ECC	75	Male	FANCC	NM_000136	c.171_180del	p.N58Lfs*21	Truncation
118E7982A2	ECC	58	Male	MSH6	NM_000179	c.4001+2_4001+26del	-	Indel
118E7982A2	ECC	58	Male	PALB2	NM_024675	c.1684+1G>C	-	Indel
118F8170A1	GBC	55	Female	EPCAM	NM_002354	c.77-2A>G	-	Indel
118F8276A1	ICC	57	Female	EPCAM	NM_002354	c.491+1G>A	-	Indel
118F8372A1	GBC	64	Female	BRCA1	NM_007294	c.3296del	p.P1099Lfs*10	Truncation
118G9391A1	ICC	65	Male	NF1	NM_00112814	c.1742dup	p.L581Ffs*6	Truncation
118G9417A2	ECC	67	Male	BRCA1	NM_007294	c.981_982del	p.C328*	Truncation
118G9448A1	GBC	75	Male	FANCC	NM_000136	c.843+1G>A	-	Indel
118H2149S1	ICC	73	Male	MSH2	NM_000251	c.2444del	p.Y815Ffs*3	Truncation
118H2531A3	GBC	27	Female	MLH1	NM_000249	c.1151T>A	p.V384D	Substitution
118I3426A1	ECC	67	Female	SDHA	NM_004168	c.1A>G	p.M1V	Substitution
118I3426A1	ECC	67	Female	FANCD2	NM_033084	c.3778-1G>A	-	Indel
118I3510A1	ICC	55	Female	MSH2	NM_000251	c.1516del	p.D506Tfs*20	Truncation
118I3592A2	ECC	64	Male	RAD50	NM_005732	c.3806_3807del	p.H1269Rfs*2	Truncation
118I3960A1	GBC	72	Male	SPINK1	NM_003122	c.194+2T>C	-	Indel
118J4299M1	GBC	68	Female	FANCA	NM_000135	-	/FANCA rearrang	Indel
118J4779J1	ECC	49	Male	SPINK1	NM_003122	c.194+2T>C	-	Indel
118J5083M1	ICC	42	Female	PALB2	NM_024675	c.2997-1G>A	-	Indel
118K6186A1	ICC	63	Male	RAD50	NM_005732	c.3715C>T	p.R1239*	Truncation
118K6336A1	ECC	53	Male	BARD1	NM_000465	c.46_68dup	p.A25Gfs*41	Truncation
118K6580A1	GBC	72	Male	MUTYH	NM_00112842	c.857G>A	p.G286E	Substitution
118K6580A1	GBC	72	Male	SPINK1	NM_003122	c.194+2T>C	-	Indel
118L7607A1	ICC	63	Male	MUTYH	NM_00112842	C.1277del	P.R426Lfs*26	Truncation
118L7607A1	ICC	63	Male	MUTYH	NM_00112842	c.616G>T	p.E206*	Truncation
118L7756A1	ICC	47	Male	RAD50	NM_005732	C.3852_3855del	P.E1284Dfs*16	Truncation
118L7895A1	ECC	31	Male	MUTYH	NM_00112842	c.55C>T	p.R19*	Truncation
118L8023M2	ICC	74	Male	SPINK1	NM_003122	c.194+2T>C	-	Indel
118L8367M1	GBC	49	Female	RAD51D	NM_002878	c.270_271dup	p.K911fs*13	Truncation
118L8884A1	ECC	53	Male	FANCC	NM_000136	c.339G>A	p.W113*	Truncation
119A9889A1	ICC	65	Male	ATM	NM_000051	c.1402_1403del	p.K468Efs*18	Truncation
217H2254A1	ICC	57	Male	BRCA2	NM_000059	c.6832dup	p.I2278Nfs*15	Truncation
218E7890A1	ICC	53	Female	RAD51D	NM_002878	c.898C>T	p.R300*	Truncation
218F8298A1	ICC	42	Female	RAD51D	NM_002878	c.860C>G	p.S287*	Truncation
218F8400A1	ICC	52	Male	BRCA1	NM_007294	c.1480C>T	p.Q494*	Truncation
218H2159A1	ECC	61	Male	BRCA1	NM_007294	c.5470_5477del	p.I1824Dfs*3	Truncation
218I3048A1	ECC	60	Male	MUTYH	NM_00112842	c.467G>A	p.W156*	Truncation
218J4308A1	ICC	35	Male	BRCA2	NM_000059	c.3109C>T	p.Q1037*	Truncation
218J4308A1	ICC	35	Male	FANCG	NM_004629	c.688dup	p.S230Kfs*5	Truncation

218J4341A1	ICC	40	Male	RAD50	NM_005732	c.2476C>T	p.Q826*	Truncation
R18D6523R1	GBC	74	Female	RAD50	NM_005732	c.2979_2980del	p.H993Qfs*6	Truncation
R18F8364R1	GBC	73	Female	ATM	NM_000051	c.6196C>T	p.Q2066*	Truncation
R18F8385R1	GBC	70	Female	ATM	NM_000051	c.6453-2A>G	-	Indel
R18G9220R1	ICC	38	Female	BRCA2	NM_000059	c.5809_5812del	p.S1937Dfs*25	Truncation
R18G9244R1	ECC	42	Male	BRCA1	NM_007294	c.2138C>G	p.S713*	Truncation
R18G9250R1	ECC	58	Male	MSH6	NM_000179	c.3261dup	p.F1088Lfs*5	Truncation
R18G9255R1	ECC	67	Male	BRIP1	NM_032043	c.2392C>T	p.R798*	Truncation
SH_01	ICC	61	Male	PRSS1	NM_002769	c.C166T	p.Q56X	Truncation
SH_02	ICC	44	Female	MUTYH	NM_012222	c.925-2A>G	-	Indel
SH_06	ICC	48	Male	BARD1	NM_000465	c.1746_1747del	p.Q582fs	Truncation
SH_06	ICC	48	Male	PRSS1	NM_002769	c.C166T	p.Q56X	Truncation
SH_10	ICC	46	Male	CFTR	NM_000492	c.G4056C	p.Q1352H	Substitution
SH_101	ICC	54	Male	PRSS1	NM_002769	c.C166T	p.Q56X	Truncation
SH_107	ICC	65	Male	PRSS1	NM_002769	c.C166T	p.Q56X	Truncation
SH_121	ICC	48	Male	PRSS1	NM_002769	c.C166T	p.Q56X	Truncation
SH_122	ICC	49	Male	PRSS1	NM_002769	c.C166T	p.Q56X	Truncation
SH_129	ICC	68	Female	MUTYH	NM_012222	c.925-2A>G	-	Indel
SH_131	ICC	48	Male	PRSS1	NM_002769	c.C166T	p.Q56X	Truncation
SH_137	ICC	58	Female	PRSS1	NM_002769	c.C166T	p.Q56X	Truncation
SH_144	ICC	62	Male	MSH6	NM_000179	c.181_193del	p.A61Hfs*16	Truncation
SH_144	ICC	62	Male	NF2	NM_000268	AGTGGAAAGGGA	-	Indel
SH_20	ICC	44	Male	FANCA	NM_000135	c.C3613T	p.Q1205*	Truncation
SH_24	ICC	55	Female	PRSS1	NM_002769	c.C166T	p.Q56X	Truncation
SH_29	ICC	74	Female	CHEK2	NM_007194	c.684-1G>A	-	Indel
SH_34	ICC	52	Male	PRSS1	NM_002769	c.C166T	p.Q56X	Truncation
SH_52	ICC	49	Male	MUTYH	NM_012222	c.925-2A>G	-	Indel
SH_56	ICC	38	Male	PRSS1	NM_002769	c.C166T	p.Q56X	Truncation
SH_63	ICC	52	Female	FANCD2	NM_033084	c.1278+1del	-	Indel
SH_63	ICC	52	Female	PRSS1	NM_002769	c.A86T	p.N29I	Substitution
SH_69	ICC	50	Male	PRSS1	NM_002769	c.C166T	p.Q56X	Truncation
SH_70	ICC	54	Female	PRSS1	NM_002769	c.C166T	p.Q56X	Truncation
SH_79	ICC	43	Female	MUTYH	NM_012222	c.925-2A>G	-	Indel
SH_79	ICC	43	Female	PRSS1	NM_002769	c.C166T	p.Q56X	Truncation
SH_85	ICC	57	Female	SPINK1	NM_003122	c.194+2T>C	-	Indel
SH_86	ICC	66	Male	PRSS1	NM_002769	c.C166T	p.Q56X	Truncation
SH_90	ICC	56	Male	PRSS1	NM_002769	c.C166T	p.Q56X	Truncation
XH_P01	ICC	43	Male	PRSS1	NM_002769	c.C166T	p.Q56X	Truncation
XH_P03	ICC	60	Female	PRSS1	NM_002769	c.C166T	p.Q56X	Truncation
XH_P06	ICC	62	Male	PRSS1	NM_002769	c.C166T	p.Q56X	Truncation
XH_P11	ICC	45	Male	PRSS1	NM_002769	c.C166T	p.Q56X	Truncation
XH_P16	ICC	62	Male	MUTYH	NM_012222	c.925-2A>G	-	Indel
XH_P18	ICC	66	Male	PRSS1	NM_002769	c.C166T	p.Q56X	Truncation
XH_P20	ICC	62	Male	FANCG	NM_004629	c.511-2del	-	Indel
XH_P25	ICC	56	Male	PRSS1	NM_002769	c.C166T	p.Q56X	Truncation
XH_P29	ICC	49	Male	CFTR	NM_000492	c.G4056C	p.Q1352H	Substitution
XH_P30	ICC	48	Male	PRSS1	NM_002769	c.C166T	p.Q56X	Truncation
XH_P37	ICC	61	Female	BRCA2	NM_000059	c.1004_1014del	p.E335fs	Truncation
XH_P43	ICC	42	Male	BRCA2	NM_000059	c.C196T	p.Q66*	Truncation
XH_P54	ICC	57	Female	BRCA2	NM_000059	c.4251delT	p.N1417fs	Truncation
XH_P62	ICC	36	Male	BRCA2	NM_000059	c.67+1G>C	-	Indel

1 **Table S10.** Statistically significant outcomes from univariate and multivariate Cox analyses for the
2 effect on DFS or OS.

Variable class	Variable factor	n/N (DFS)	Univariate Cox for DFS		Multivariate Cox for DFS	
			HR, 95% CI (DFS)	P-value (DFS)	HR, 95% CI (DFS)	P-value (DFS)
Clinical	Clinical stage (phase I)	56/160	0.43 (0.28-0.64)	<0.001	0.5 (0.3-0.84)	0.009**
Clinical	Lymphatic metastasis (N1)	41/152	2.24 (1.5-3.35)	<0.001	1.32 (0.81-2.14)	0.268
Clinical	Serum CA19-9 (>200)	48/158	1.75 (1.19-2.55)	0.004	1.56 (0.98-2.49)	0.062
Clinical	Vascular invasion (positive)	27/160	1.78 (1.12-2.81)	0.014	1.47 (0.86-2.52)	0.162
SMGs	KRAS	26/160	1.99 (1.23-3.2)	0.005	1.4 (0.8-2.46)	0.244
SMGs	TP53	61/160	1.51 (1.05-2.19)	0.028	1.33 (0.89-1.99)	0.16
SCNAs	amp7p15.2	24/160	1.85 (1.17-2.93)	0.008	0.99 (0.54-1.81)	0.985
SCNAs	amp7q31.2	22/160	1.86 (1.15-3.03)	0.012	2.23 (1.28-3.86)	0.004**
SCNAs	amp5p15.33	41/160	1.55 (1.05-2.31)	0.029	1.41 (0.87-2.29)	0.164
SCNAs	amp17q21.2	37/160	1.53 (1.02-2.3)	0.041	1.24 (0.76-2.04)	0.391
Variable class	Variable factor	n/N (OS)	Univariate Cox for OS		Multivariate Cox for OS	
			HR, 95% CI (OS)	P-value (OS)	HR, 95% CI (OS)	P-value (OS)
Clinical	Clinical stage (phase I)	56/160	0.48 (0.31-0.74)	0.001	0.68 (0.4-1.2)	0.153
Clinical	Lymphatic metastasis (N1)	41/152	1.96 (1.28-3.0)	0.002	1.41 (0.85-2.3)	0.18
Clinical	Serum CA19-9 (>200)	48/158	1.6 (1.06-2.42)	0.025	1.1 (0.68-1.8)	0.699
Clinical	Vascular invasion (positive)	27/160	1.92 (1.2-3.07)	0.007	1.83 (1.07-3.1)	0.027*
SMGs	KRAS	26/160	1.87 (1.15-3.05)	0.012	1.84 (1.06-3.2)	0.03*
SMGs	TP53	61/160	1.84 (1.25-2.72)	0.002	1.48 (0.98-2.2)	0.062
SMGs	EPHA2	11/160	0.3 (0.11-0.81)	0.018	0.41 (0.14-1.1)	0.086
SMGs	IDH1	19/160	0.48 (0.23-0.98)	0.044	0.53 (0.23-1.2)	0.144
SCNAs	amp7q31.2	22/160	1.88 (1.14-3.1)	0.013	1.7 (0.97-3.0)	0.065

1 **Table S11.** FGFR2/3 fusions identified in 643 patients through the CYCS platform.

Sample.ID	Gene1	Gene2	Gene1_Exon	Gene2_Exon
117L4005A1	FGFR2	MATR3	Exon17	Exon3
119A9340A1	FGFR2	SLC9A1	Exon17	Exon6
218C5588A2	FGFR3	TACC3	Exon17	Exon11
117L3815A1	FGFR3	TACC3	Exon13	Exon3
118L8638M2	FGFR2	INA	Exon17	Exon2
118H2503A1	FGFR3	TACC3	Exon17	Exon9
118F8792A1	FGFR2	MTUS2	Exon17	Exon6
118L7413A1	FGFR2	CTNNA3	Exon17	Exon14
118A4434A1	FGFR2	TRIM15	Exon17	Exon2
118F8201A1	FGFR2	GBE1	Exon17	Exon2
117K3609A1	FGFR2	BICC1	Exon17	Exon3
117L4005A1	FGFR2	CTBP2	Exon17	Exon1
117D0945A1	CASP10	FGFR2	Exon9	Exon17
118F8201A1	MFF	FGFR2	Exon7	Exon17
118G9724A1	FGFR2	LSM11	Exon17	Exon1
217C0745A1	FGFR2	BICC1	Exon17	Exon17
118H1438M1	ITGA9	FGFR2	Exon26	Exon17
218J4612A1	FGFR2	LGSN	Exon17	Exon2
118D6255A1	FGFR2	BICC1	Exon17	Exon3
118H2540A1	FGFR2	PHLDB2	Exon17	Exon6

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3

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Table S12. Actionable targets and molecular-directed treatments in 46 patients with advanced BTCs.

Patient.ID	Types	Targets	Mutation.Levels	Target.Types	Drugs	OncokB.Tier	ESCAT.Tier	Response	PFS2 (months)	PFS2.status (1)	PFS1 (months)	PFS1.status (1)	PFS2/PFS1
MDT001	ECC	BRCA2	SOMATIC	in-PATs	Olaparib	2B	III-A	SD	5	1	6	1	0.833
MDT002	ICC	BRCA2	GERMLINE	in-PATs	Olaparib	2B	III-A	PR	23	1	13	1	1.769
MDT003	GBC	EGFR	SOMATIC	in-PATs	Afatinib	3B	III-A	PR	13	0	4	1	3.250
MDT004	ICC	BRAF V600E	SOMATIC	in-PATs	Dabrafenib	2B	III-A	PD	5	1	2	1	2.500
MDT005	ICC	MET	SOMATIC	in-PATs	Cabozantinib	2B	III-A	SD	2	0	1.5	1	1.333
MDT006	ICC	BRAF V600E	SOMATIC	in-PATs	Trametinib	2B	III-A	PD	3	1	1	1	3.000
MDT007	ICC	MET	SOMATIC	in-PATs	Cabozantinib	2B	III-A	SD	6	1	3.5	1	1.714
MDT008	ICC	MET	SOMATIC	in-PATs	Cabozantinib	2B	III-A	SD	3	1	2	1	1.500
MDT009	GBC	ERBB2	SOMATIC	in-PATs	Trastuzumab	2B	III-A	PD	1	1	3	0	0.333
MDT010	GBC	MET	SOMATIC	in-PATs	Cabozantinib	2B	III-A	SD	7	1	NA	NA	NA
MDT011	ECC	EGFR	SOMATIC	in-PATs	Afatinib	3B	III-A	PD	1.5	1	5	1	0.300
MDT012	ICC	CDKN2A	SOMATIC	off-PATs	Palbociclib	4	III-B	SD	4	1	3.5	1	1.143
MDT013	ICC	FGFR2	SOMATIC	in-PATs	Erfafitinib	3A	I-B	PR	8	0	2	1	4.000
MDT014	ECC	BRCA1	GERMLINE	in-PATs	Olaparib	2B	III-A	PD	4	1	10	1	0.400
MDT015	ICC	CDKN2A	SOMATIC	off-PATs	Palbociclib	4	III-B	PD	3	1	NA	NA	NA
MDT016	ICC	MET	SOMATIC	in-PATs	Cabozantinib	2B	III-A	PR	6	1	1	1	6.000
MDT017	GBC	PIK3CA	SOMATIC	off-PATs	Everolimus	3B	III-B	SD	10	1	NA	NA	NA
MDT018	GBC	EGFR	SOMATIC	in-PATs	Afatinib	3B	III-A	SD	4	1	NA	NA	NA
MDT019	ICC	BRCA2	GERMLINE	in-PATs	Olaparib	2B	III-A	PR	10	1	2	1	5.000
MDT020	ICC	MET	SOMATIC	in-PATs	Cabozantinib	2B	III-A	PD	1.5	1	5	1	0.300
MDT021	ECC	EGFR	SOMATIC	in-PATs	Afatinib	2B	III-A	PR	14	1	1	1	14.000
MDT022	ECC	STK11	SOMATIC	off-PATs	Everolimus	NA	III-B	SD	1	0	2	1	0.500
MDT023	ICC	PIK3CA	SOMATIC	off-PATs	Everolimus	3B	III-B	SD	1	0	1	1	1.000
MDT024	GBC	FBXW7	SOMATIC	off-PATs	Everolimus	NA	III-B	SD	3	1	3	1	1.000
MDT025	GBC	BRCA1	SOMATIC	in-PATs	Olaparib	2B	III-A	SD	5.5	0	8	1	0.688
MDT026	ICC	MET	SOMATIC	in-PATs	Crizotinib	2B	III-A	PD	1	1	1	1	1.000
MDT027	ICC	BRCA1	SOMATIC	in-PATs	Olaparib	2B	III-A	SD	6	0	2	1	3.000
MDT028	ICC	FGFR2	SOMATIC	in-PATs	Erfafitinib	3A	I-B	SD	3	1	NA	NA	NA
MDT029	ICC	BRCA2	GERMLINE	in-PATs	Olaparib	2B	III-A	PR	5	1	2	1	2.500
MDT030	ICC	BRCA2	SOMATIC	in-PATs	Olaparib	2B	III-A	SD	4	1	3	1	1.333
MDT031	ICC	BRCA2	SOMATIC	in-PATs	Olaparib	2B	III-A	PD	2.5	1	6	1	0.417
MDT032	ICC	BRCA2	SOMATIC	in-PATs	Olaparib	2B	III-A	PD	2	1	3	1	0.667
MDT033	ICC	BRCA2	SOMATIC	in-PATs	Olaparib	2B	III-A	PD	2	1	2	1	1.000
MDT034	GBC	BRCA2	GERMLINE	in-PATs	Olaparib	2B	III-A	SD	3	1	2	1	1.500
MDT035	ICC	EGFR	SOMATIC	in-PATs	Afatinib	3B	III-A	SD	4	0	NA	NA	NA
MDT036	ICC	EGFR	SOMATIC	in-PATs	Afatinib	3B	III-A	PR	4	1	1.5	1	2.667
MDT037	GBC	ERBB2	SOMATIC	in-PATs	Pyrotinib	2B	III-A	SD	3	0	3	1	1.000
MDT038	ECC	EGFR	SOMATIC	in-PATs	Afatinib	3B	III-A	SD	3	1	1	1	3.000
MDT039	ICC	MET	SOMATIC	in-PATs	Cabozantinib	2B	III-A	SD	5.5	1	3	1	1.833
MDT040	ICC	ERBB2	SOMATIC	in-PATs	Pyrotinib	2B	III-A	SD	2	0	NA	NA	NA
MDT041	ICC	MSI-H/dMMR	SOMATIC	in-PATs	Pembrolizumab	3B	I-C	PR	6	0	NA	NA	NA
MDT042	ECC	MSI-H/dMMR	SOMATIC	in-PATs	Pembrolizumab	3B	I-C	PR	5	0	2.5	1	2.000
MDT043	ICC	MSI-H/dMMR	SOMATIC	in-PATs	Pembrolizumab	3B	I-C	CR	30	0	2	1	15.000
MDT044	ICC	MSI-H/dMMR	SOMATIC	in-PATs	Pembrolizumab	3B	I-C	SD	6	0	NA	NA	NA
MDT045	GBC	MSI-H/dMMR	SOMATIC	in-PATs	Pembrolizumab	3B	I-C	PD	1	1	2	1	0.500
MDT046	ICC	MSI-H/dMMR	SOMATIC	in-PATs	Pembrolizumab	3B	I-C	PR	12	0	4.5	1	2.667

Table S13. Baseline clinicopathological features of 46 patients who received biomarker-guided personalized targeted therapies.

Clinical parameters	
Age (mean, IQR)	57.3 (51-64)
Sex (Male, n, %)	23 (50%)
Primary tumor (n, %)	
Intrahepatic cholangiocarcinoma (ICC)	29 (63%)
Extrahepatic cholangiocarcinoma (ECC)	7 (15%)
Gallbladder cancer (GBC)	10 (22%)
ECOG performance (n, %)	
0-1	34 (74%)
2	12 (26%)
Extra-hepatobiliary metastasis (n, %)	38 (83%)
Prior surgery of the primary tumor (n, %)	28 (61%)
Prior lines of systematic treatments (n, %)	
1	8 (17%)
2	17 (37%)
≥3	21 (46%)
PFS1 in month (median, 95% CI)	2.0 (1.5-2.5)

Note: PFS1: progression-free survival of the treatment line prior to the MDTs, with 37 patients having assessable PFS1; CI: confidence interval.