Supplementary Tables and Figures

Table S1.

HMCL Name	IL-6 dependence[1]	Disease[2]	Patient sample[3]	t(14q32 or 22q11 ;)	Target genes	Available EBV control	TP53 bi-allelic event	FAM46C bi-allelic event
HMCL[serum+IL-6]								
XG1	++	MM	PB	t(11;14)	CCND1	x		
XG2	++	MM	PE	t(12;14)	CD40			
XG5	++	MM	PB	t(11;14)	CCND1	x	x	
XG6	++	MM	PB	t(16;22)	c-MAF			
XG7	+	MM	PB	t(4;14)	MMSET			x
XG11	++	PCL	PB	t(11;14)	CCND1		x	
XG12	++	PCL	PB	t(14;16)	c-MAF			
XG13	++	PCL	PB	t(14;16)	c-MAF	x	x	
XG16	++	PCL	PB	NA	NA	x	x	
XG19	++	PCL	PB	t(14;16)	c-MAF	x	x	
XG20	++	PCL	PB	t(4;14)	MMSET			x
XG23	++	MM	PE	t(11;14)	CCND1			
XG24	++	PCL	PB	t(4;14)	MMSET/FGFR3			
XG25	++	PCL	PB	t(11;14)	CCND1			x
XG26	++	MM	BM	t(4;14)	MMSET			
XG27	++	MM	BM	NA	NA			
XG28	++	MM	BM	t(4;14)	MMSET			
XG29	++	PCL	PB	t(11;14)	CCND1			
XG30	++	PCL	PB	t(14;16)	c-MAF		x	
Lopra	+	MM	AF	NA	NA			

HMCL[serum]							
AMO1	-	PCT	AF	t(12;14)	NA		
JJN3	-	MM	PE	t(14;16)	c-Maf		
L363	-	PCL	PE	t(20;22)	MafB	x	
LP1	-	MM	PB	t(4;14)	MMSET/FGFR3		
MM1S	-	PCL	PB	t(14;16)	c-Maf		x
OPM2	-	MM	PB	t(4;14)	MMSET	x	x
RPMI8226	-	MM	PB	t(14;16)	c-Maf	x	
SKMM2	-	PCL	PB	t(11;14)	CCND1	x	
MOLP2	-	MM	PB	t(4;14)	MMSET/FGFR3		
MOLP8	-	MM	PB	t(11;14)	CCND1		

Table S1. Characteristics of the HMCL cohort. HMCLs were obtained culturing primary myeloma cells with culture medium supplemented with Fetal Calf Serum alone or with recombinant IL-6.

1. ++ if the growth is strictly dependent on adding exogenous IL-6, + if dependent on adding exogenous IL-6, - if not.
2. Disease at diagnosis: MM multiple myeloma, PCL plasma cell leukemia, PCT plasmacytoma.
3. Origin of the sample: AF ascitic fluid, BM bone marrow, PE pleural effusion, PB peripheral blood, SC subcutaneous.

NA : Not Available

Table S2.

Patient	MM/PCL	Relpase	Ig	Kappa/Lambda	Treatment
E14186	MM	First Relapse	IgG	Lambda	VRD + HDT + HSCT
E15012	MM	First Relapse	IgG	Lambda	VRD + HDT + HSCT
E15008	MM	First Relapse	IgG	Kappa	VRD + HDT + HSCT
E15168	MM	First Relapse	IgG	Lambda	VTD + HDT + HSCT
E13067	MM	First Relapse	IgA	Lambda	VRD + HDT + HSCT
E13098	MM	First Relapse	IgA	Lambda	VD + HDT + HSCT
E13187	MM	First Relapse	IgG	Kappa	VRD + HDT + HSCT
E13093	MM	First Relapse	IgA	Lambda	VD + HDT + HSCT
E14182	MM	First Relapse	IgG	Kappa	RD + HDT + HSCT
E15177	MM	First Relapse	BJ	Kappa	RD + Daratumumab
E14144	MM	First Relapse	IgG	Lambda	VD + HDT + HSCT
E14005	MM	First Relapse	IgG	Kappa	VTD + HDT + HSCT
E11158	MM	First Relapse	IgG	Lambda	VD + HDT + HSCT
E11248	MM	First Relapse	BJ	Kappa	VD + HDT + HSCT
E11221	MM	First Relapse	IgG	Lambda	VRD + HDT + HSCT
E15030	MM	First Relapse	BJ	Lambda	VTD + HDT + HSCT

Table S2. Clinical characteristics of the cohort of patients at relapse

V = Velcade, R = Revlimid, D = Dexamethasone, HDT = High Dose Melphalan, HSCT = Hematopoietic Stem Cell Transplantation

Table S3.

HMCL	Melphalan (µM)	Lenalidomide (µM)	Pomalidomide (nM)	Bortezomib (nM)	Dexamethasone (µM)	CDK1.2.4.5.6.9i (µM)	TSA (nM)	Panobinostat (nM)	SAHA (nM)	IKK2i (µM)
AMO1	3.3	100	NA	2	NA	248	NA	3.2	695	NA
JJN3	1.5	NA	NA	NA	NA	NA	NA	2.7	897	NA
L363	NA	2.1	NA	NA	NA	NA	NA	NA	NA	NA
Lopra	NA	NA	NA	NA	NA	NA	37.7	NA	NA	NA
LP1	2	25.82	NA	8.6	NA	206	NA	2.6	728	NA
MM1S	NA	NA	54.78	NA	NA	NA	23.8	14.266	549.198	NA
MOLP2	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
MOLP8	NA	NA	NA	NA	NA	NA	19.318	2.279	NA	NA
OPM2	1.87	0.8	51	2	60	335	97.221	2.23	613.5	NA
RPMI	3.1	8.3	231	NA	NA	294	NA	NA	NA	NA
SKMM2	0.4	NA	622	NA	NA	NA	NA	NA	NA	NA
XG1	2.76	75	170	4.8	52	619	NA	NA	NA	2.8
XG11	2.6	100	NA	3.9	66	NA	NA	NA	NA	4.2
XG12	2.2	NA	15	4	24	NA	7.5	NA	NA	1.3
XG13	2.9	NA	373	NA	NA	579	NA	0.5	462	3.3
XG16	1.6	3	220	4.5	NA	482	NA	1.2	528	NA
XG19	1.2	79	841	2.5	36	NA	57.8	NA	NA	2.4
XG2	1.2	50	NA	4.5	66	NA	NA	NA	NA	3
XG20	6.2	100	16	3.3	62	NA	6.3	3.5	1070	6.4
XG23	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
XG24	NA	NA	NA	2.5	170	NA	NA	NA	NA	NA
XG25	2.5	100	NA	NA	NA	194	32.9	10.2	653.7	NA
XG26	0.96	NA	NA	NA	NA	NA	NA	NA	NA	NA
XG27	2.2	50	NA	NA	NA	NA	NA	NA	NA	NA

XG28	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
XG29	0.2	NA	NA	NA	NA	NA	NA	11.259	233.248	NA
XG30	NA	50	NA	NA	NA	NA	54.2	NA	NA	NA
XG5	4.8	100	27	NA	50	NA	11	2	548	NA
XG6	1.2	70	220	NA	NA	334	16.3	2.5	805	2.3
XG7	2.1	100	131	3.4	17	205	52.3	5	1154	6.7

Table S3. IC50 of drugs tested on HMCLs

NA : Not Available

Table S4.

Sample	Gene	Chromosome	Start_Position	End_Position	Variant_Classification	Variant_Type	Amino_Acid_Change	Nucleotide_Change
AMO1	ERBB3	chr12	56487560	56487560	Missense_Mutation	SNP	p.K498I	c.A1493T
L363	CARM1	chr19	10982400	10982400	In_Frame_Ins	INS	p.V8delinsAV	c.22_23insCGG
L363	CALR	chr19	13051094	13051094	Missense_Mutation	SNP	p.R177Q	c.G530A
L363	CRTC1	chr19	18887981	18887981	Missense_Mutation	SNP	p.V581G	c.T1742G
L363	CNOT3	chr19	54656620	54656620	Missense_Mutation	SNP	p.N641D	c.A1921G
L363	CNOT3	chr19	54656621	54656621	Missense_Mutation	SNP	p.N641S	c.A1922G
Lopra	NRAS	chr1	115258747	115258747	Missense_Mutation	SNP	p.G12A	c.G35C
Lopra	USP6	chr17	5042837	5042837	Missense_Mutation	SNP	p.R456W	c.C1366T
Lopra	IKZF1	chr7	50444480	50444480	Missense_Mutation	SNP	p.R137I	c.G410T
AMO1	USP6	chr17	5042837	5042837	Missense_Mutation	SNP	p.R456W	c.C1366T
Lopra	KIF5B	chr10	32311107	32311107	Missense_Mutation	SNP	p.D665N	c.G1993A
Lopra	ERBB3	chr12	56494892	56494892	Frame_Shift_Ins	INS	p.S1083fs	c.3249dupT
Lopra	TBX3	chr12	115118874	115118874	Missense_Mutation	SNP	p.I156T	c.T467C
Lopra	FANCA	chr16	89806435	89806435	Missense_Mutation	SNP	p.S1301T	c.T3901A
Lopra	COL1A1	chr17	48271499	48271499	Frame_Shift_Ins	INS	p.G554fs	c.1659_1660insGGGGG
Lopra	ELL	chr19	18572606	18572606	Missense_Mutation	SNP	p.R176W	c.C526T

AMO1	MAP2K2	chr19	4117541	4117541	Missense_Mutation	SNP	p.Q60P	c.A179C
Lopra	RUNX1	chr21	36206790	36206790	Missense_Mutation	SNP	p.H241P	c.A722C
Lopra	MN1	chr22	28194944	28194944	In_Frame_Ins	INS	p.Q530delinsHQ	c.1587_1588insCAT
Lopra	KDM5C	chrX	53239962	53239962	Frame_Shift_Ins	INS	p.D493fs	c.1478_1479insCAGGG
Lopra	STAG2	chrX	123195624	123195624	Missense_Mutation	SNP	p.L513Q	c.T1538A
Lopra	STAG2	chrX	123195627	123195627	Missense_Mutation	SNP	p.T514K	c.C1541A
LP1	STIL	chr1	47753284	47753284	Missense_Mutation	SNP	p.E311K	c.G931A
LP1	FLT4	chr5	180047894	180047894	Missense_Mutation	SNP	p.A761T	c.G2281A
LP1	ARID1B	chr6	157522211	157522211	Missense_Mutation	SNP	p.R1495C	c.C4483T
AMO1	CBLC	chr19	45296848	45296848	Frame_Shift_Ins	INS	p.Q419fs	c.1255dupC
LP1	TP53	chr17	7577082	7577082	Missense_Mutation	SNP	p.E247K	c.G739A
LP1	PTPRT	chr20	40713407	40713407	Missense_Mutation	SNP	p.R1370C	c.C4108T
LP1	KDM6A	chrX	44922760	44922760	Nonsense_Mutation	SNP	p.Q593X	c.C1777T
LP1	LRP1B	chr2	141643868	141643868	Missense_Mutation	SNP	p.H1268R	c.A3803G
LP1	MAP3K1	chr5	56177848	56177850	In_Frame_Del	DEL	p.941_941del	c.2821_2823del
AMO1	EP300	chr22	41527628	41527628	Missense_Mutation	SNP	p.S507G	c.A1519G
AMO1	ARAF	chrX	47430355	47430355	Missense_Mutation	SNP	p.R544C	c.C1630T
LP1	TRRAP	chr7	98557015	98557015	Missense_Mutation	SNP	p.R2124C	c.C6370T
LP1	KMT2D	chr12	49426645	49426645	Missense_Mutation	SNP	p.L3948H	c.T11843A
AMO1	SPEN	chr1	16174597	16174597	Missense_Mutation	SNP	p.N12S	c.A35G
LP1	KNSTRN	chr15	40678601	40678601	Missense_Mutation	SNP	p.V115I	c.G343A
LP1	PML	chr15	74328011	74328011	Missense_Mutation	SNP	p.R737W	c.C2209T
AMO1	LRP1B	chr2	141081590	141081590	Missense_Mutation	SNP	p.Y4129C	c.A12386G
LP1	ZFHX3	chr16	72831992	72831992	Missense_Mutation	SNP	p.G1530V	c.G4589T
LP1	CNOT3	chr19	54656620	54656620	Missense_Mutation	SNP	p.N641D	c.A1921G
LP1	CNOT3	chr19	54656621	54656621	Missense_Mutation	SNP	p.N641S	c.A1922G
LP1	CNOT3	chr19	54656628	54656628	Missense_Mutation	SNP	p.C643W	c.T1929G
MM1S	FAM46C	chr1	118166298	118166298	Missense_Mutation	SNP	p.M270V	c.A808G

AMO1	LRP1B	chr2	141215159	141215159	Missense_Mutation	SNP	p.W3229C	c.G9687T
MM1S	PBRM1	chr3	52588770	52588770	Missense_Mutation	SNP	p.V1420M	c.G4258A
MM1S	EGFR	chr7	55266457	55266457	Missense_Mutation	SNP	p.G917R	c.G2749C
MM1S	PTCH1	chr9	98211572	98211572	Missense_Mutation	SNP	p.T1044S	c.A3130T
MM1S	PTEN	chr10	89692892	89692892	Missense_Mutation	SNP	p.A299S	c.G895T
MM1S	ATM	chr11	108159732	108159732	Missense_Mutation	SNP	p.H1380Y	c.C4138T
MM1S	KMT2A	chr11	118376934	118376934	Missense_Mutation	SNP	p.A3440T	c.G10318A
MM1S	KRAS	chr12	25398284	25398284	Missense_Mutation	SNP	p.G12A	c.G35C
MM1S	NUP93	chr16	56875738	56875738	Missense_Mutation	SNP	p.R781H	c.G2342A
MM1S	BRCA1	chr17	41244130	41244130	Missense_Mutation	SNP	p.S1140G	c.A3418G
MM1S	PBX1	chr1	164815893	164815893	Missense_Mutation	SNP	p.H425D	c.C1273G
MM1S	MITF	chr3	70001015	70001015	Missense_Mutation	SNP	p.Q289H	c.G867T
MM1S	FIP1L1	chr4	54257205	54257205	Missense_Mutation	SNP	p.G179R	c.G535A
MM1S	MSH3	chr5	79950730	79950730	Missense_Mutation	SNP	p.A62S	c.G184T
MM1S	PTPRD	chr9	8331582	8331582	Frame_Shift_Ins	INS	p.S1845fs	c.5533_5534insAGAAT
MM1S	XPA	chr9	100456006	100456006	Missense_Mutation	SNP	p.D70H	c.G208C
MM1S	MGA	chr15	42046714	42046714	Missense_Mutation	SNP	p.N2363S	c.A7088G
MM1S	FUS	chr16	31195715	31195720	In_Frame_Del	DEL	p.174_175del	c.521_523del
MM1S	MAF	chr16	79632985	79632985	Missense_Mutation	SNP	p.R272H	c.G815A
AMO1	TET2	chr4	106162585	106162585	Missense_Mutation	SNP	p.R1167W	c.A3499T
MM1S	MN1	chr22	28194667	28194667	In_Frame_Ins	INS	p.A622delinsAP	c.1864_1865insCGC
MM1S	MN1	chr22	28194664	28194664	In_Frame_Ins	INS	p.P623delinsPS	c.1867_1868insCGT
MM1S	MYH9	chr22	36710303	36710303	Missense_Mutation	SNP	p.N481D	c.A1441G
MM1S	MKL1	chr22	40814747	40814752	In_Frame_Del	DEL	p.564_565del	c.1690_1695del
MOLP2	AFF3	chr2	100623769	100623769	Missense_Mutation	SNP	p.E110K	c.G328A
MOLP2	SETD2	chr3	47162886	47162886	Missense_Mutation	SNP	p.M1080I	c.G3240A
MOLP2	EZH2	chr7	148525904	148525904	Missense_Mutation	SNP	p.D185H	c.G553C
MOLP2	FGFR1	chr8	38287238	38287238	Missense_Mutation	SNP	p.S140L	c.C419T

MOLP2	BLM	chr15	91295110	91295110	Missense_Mutation	SNP	p.T298M	c.C893T
MOLP2	TP53	chr17	7578454	7578454	Missense_Mutation	SNP	p.A120V	c.C359T
MOLP2	CIC	chr19	42796852	42796852	Missense_Mutation	SNP	p.S2013T	c.T6037A
MOLP2	CLTCL1	chr22	19220971	19220971	Missense_Mutation	SNP	p.L448I	c.C1342A
MOLP2	RAP1GDS1	chr4	99273651	99273651	Missense_Mutation	SNP	p.D88G	c.A263G
MOLP2	ROS1	chr6	117715781	117715781	Missense_Mutation	SNP	p.T326R	c.C977G
MOLP2	PTPRD	chr9	8331583	8331583	Missense_Mutation	SNP	p.S1845C	c.A5533T
MOLP2	PTPRD	chr9	8331585	8331585	Missense_Mutation	SNP	p.C1844Y	c.G5531A
MOLP2	CREB3L1	chr11	46342261	46342261	Frame_Shift_Ins	INS	p.D509fs	c.1525_1526insC
MOLP2	BIRC3	chr11	102196052	102196052	Missense_Mutation	SNP	p.V271G	c.T812G
MOLP2	KDM5A	chr12	416960	416960	Missense_Mutation	SNP	p.Q1197P	c.A3590C
MOLP2	IGF1R	chr15	99434839	99434839	Missense_Mutation	SNP	p.S309L	c.C926T
MOLP2	CREBBP	chr16	3828783	3828783	Missense_Mutation	SNP	p.A620V	c.C1859T
MOLP2	ZNF521	chr18	22805903	22805903	Missense_Mutation	SNP	p.V660A	c.T1979C
MOLP2	TCF3	chr19	1632402	1632402	Missense_Mutation	SNP	p.L50F	c.C148T
MOLP2	CRTC1	chr19	18856712	18856712	Missense_Mutation	SNP	p.R124H	c.G371A
MOLP2	PTPRT	chr20	40743933	40743933	Missense_Mutation	SNP	p.P1021Q	c.C3062A
MOLP8	NRAS	chr1	115256529	115256529	Missense_Mutation	SNP	p.Q61L	c.A182T
MOLP8	SETD2	chr3	47162886	47162886	Missense_Mutation	SNP	p.M1080I	c.G3240A
MOLP8	TNFAIP3	chr6	138196066	138196066	Missense_Mutation	SNP	p.F127C	c.T380G
MOLP8	EZH2	chr7	148525904	148525904	Missense_Mutation	SNP	p.D185H	c.G553C
MOLP8	MAML2	chr11	95825930	95825930	Missense_Mutation	SNP	p.R422Q	c.G1265A
AMO1	PTPRD	chr9	8331582	8331582	Frame_Shift_Ins	INS	p.S1845fs	c.5533_5534insGGAAT
MOLP8	FAM46C	chr1	118166083	118166083	Frame_Shift_Ins	INS	p.S198fs	c.593_594insTATGACTGTTC
MOLP8	FAM46C	chr1	118166083	118166083	Frame_Shift_Ins	INS	p.S198fs	c.593_594insTATGCCTGTTC
MOLP8	FAM46C	chr1	118166113	118166117	Frame_Shift_Del	DEL	p.P208fs	c.623_627del
MOLP8	EPAS1	chr2	46605215	46605217	In_Frame_Del	DEL	p.478_478del	c.1432_1434del
MOLP8	MAP3K1	chr5	56177848	56177850	In_Frame_Del	DEL	p.941_941del	c.2821_2823del

MOLP8	MSH3	chr5	79950735	79950735	In_Frame_Ins	INS	p.P63delinsPAAP	c.189_190insGCAGCGCCC
AMO1	PPP6C	chr9	127951850	127951850	Frame_Shift_Ins	INS	p.P50fs	c.148dupC
MOLP8	RAC1	chr7	6441557	6441557	Missense_Mutation	SNP	p.K135T	c.A404C
MOLP8	TSC1	chr9	135796762	135796762	Missense_Mutation	SNP	p.L242P	c.T725C
MOLP8	BMPR1A	chr10	88659883	88659883	Missense_Mutation	SNP	p.K177I	c.A530T
MOLP8	PTEN	chr10	89692859	89692859	Missense_Mutation	SNP	p.D288Y	c.G862T
MOLP8	DDX10	chr11	108788660	108788660	In_Frame_Ins	INS	p.G789delinsDDG	c.2365_2366insATGATG
MOLP8	KMT2A	chr11	118376140	118376140	Missense_Mutation	SNP	p.P3175L	c.C9524T
MOLP8	BCL9L	chr11	118769935	118769935	Missense_Mutation	SNP	p.P1230L	c.C3689T
MOLP8	ZNF384	chr12	6777108	6777113	In_Frame_Del	DEL	p.501_502del	c.1501_1506del
MOLP8	PER1	chr17	8048261	8048261	Missense_Mutation	SNP	p.S757R	c.A2269C
MOLP8	CEBPA	chr19	33792752	33792752	In_Frame_Ins	INS	p.S190delinsSHP	c.568_569insCGCACC
MOLP8	CIC	chr19	42794583	42794583	Missense_Mutation	SNP	p.G1464R	c.G4390C
MOLP8	CIC	chr19	42796793	42796793	Missense_Mutation	SNP	p.C1993S	c.G5978C
MOLP8	CNOT3	chr19	54656620	54656620	Missense_Mutation	SNP	p.N641D	c.A1921G
MOLP8	GNAS	chr20	57466852	57466852	Missense_Mutation	SNP	p.K24T	c.A71C
MOLP8	OLIG2	chr21	34399702	34399702	Missense_Mutation	SNP	p.G178R	c.G532A
MOLP8	MKL1	chr22	40814748	40814748	Frame_Shift_Ins	INS	p.A565fs	c.1693_1694insGGGGC
MOLP8	AR	chrX	66766441	66766441	Missense_Mutation	SNP	p.R485W	c.C1453T
OPM2	CAMTA1	chr1	7731097	7731097	Missense_Mutation	SNP	p.A927S	c.G2779T
OPM2	FAM46C	chr1	118166023	118166023	Missense_Mutation	SNP	p.E178A	c.A533C
OPM2	LRP1B	chr2	141113924	141113924	Missense_Mutation	SNP	p.N3839K	c.C11517A
OPM2	LRP1B	chr2	141113930	141113930	Missense_Mutation	SNP	p.M3837I	c.G11511A
OPM2	LRP1B	chr2	141115674	141115674	Missense_Mutation	SNP	p.Y3757H	c.T11269C
OPM2	FGFR3	chr4	1807889	1807889	Missense_Mutation	SNP	p.K652E	c.A1954G
AMO1	FGF3	chr11	69625305	69625305	Missense_Mutation	SNP	p.P163L	c.C488T
OPM2	FGFR1	chr8	38287238	38287238	Missense_Mutation	SNP	p.S140L	c.C419T
OPM2	CDKN2A	chr9	21971111	21971111	Missense_Mutation	SNP	p.A97V	c.C290T

OPM2	EXT2	chr11	44129528	44129528	Missense_Mutation	SNP	p.T89M	c.C266T
OPM2	DIS3	chr13	73355008	73355008	Missense_Mutation	SNP	p.Y121S	c.A362C
OPM2	TP53	chr17	7578406	7578406	Missense_Mutation	SNP	p.R136H	c.G407A
OPM2	NCOR1	chr17	16049706	16049706	Missense_Mutation	SNP	p.Q356E	c.C1066G
OPM2	SETBP1	chr18	42531184	42531184	Missense_Mutation	SNP	p.R627C	c.C1879T
OPM2	ASXL1	chr20	31022469	31022469	Missense_Mutation	SNP	p.G652S	c.G1954A
OPM2	BCORL1	chrX	129150080	129150080	Missense_Mutation	SNP	p.T1111M	c.C3332T
OPM2	ARID1A	chr1	27088658	27088658	Missense_Mutation	SNP	p.N756S	c.A2267G
OPM2	ASXL2	chr2	25965806	25965806	Missense_Mutation	SNP	p.G1134S	c.G3400A
OPM2	PMS1	chr2	190670550	190670550	Frame_Shift_Ins	INS	p.K163fs	c.488dupA
OPM2	NUP98	chr11	3723971	3723971	Missense_Mutation	SNP	p.F1078L	c.C3234G
OPM2	CHD4	chr12	6682392	6682392	Missense_Mutation	SNP	p.A1802D	c.C5405A
OPM2	CDKN1B	chr12	12870972	12870972	Missense_Mutation	SNP	p.H67Y	c.C199T
OPM2	CDKN1B	chr12	12871831	12871831	Missense_Mutation	SNP	p.S183F	c.C548T
OPM2	KMT2D	chr12	49440169	49440169	Missense_Mutation	SNP	p.G1486D	c.G4457A
OPM2	HMGA2	chr12	66219066	66219066	Missense_Mutation	SNP	p.E6Q	c.G16C
OPM2	ZFHX3	chr16	72821633	72821635	In_Frame_Del	DEL	p.3514_3514del	c.10540_10542del
OPM2	SMAD2	chr18	45396912	45396912	Missense_Mutation	SNP	p.L87R	c.T260G
OPM2	BRD4	chr19	15364461	15364461	Missense_Mutation	SNP	p.H764Q	c.T2292A
OPM2	CEBPA	chr19	33792752	33792752	In_Frame_Ins	INS	p.S190delinsSHP	c.568_569insCGCACC
OPM2	CNOT3	chr19	54656620	54656620	Missense_Mutation	SNP	p.N641D	c.A1921G
OPM2	CNOT3	chr19	54656621	54656621	Missense_Mutation	SNP	p.N641S	c.A1922G
OPM2	EIF1AX	chrX	20153876	20153876	Missense_Mutation	SNP	p.R62G	c.A184G
RPMI	SPEN	chr1	16255925	16255925	Missense_Mutation	SNP	p.K1064E	c.A3190G
RPMI	MUTYH	chr1	45797105	45797105	Missense_Mutation	SNP	p.R409Q	c.G1226A
RPMI	IDH1	chr2	209113296	209113296	Missense_Mutation	SNP	p.V71I	c.G211A
RPMI	EGFR	chr7	55242482	55242482	Missense_Mutation	SNP	p.T751I	c.C2252T
RPMI	ATM	chr11	108106443	108106443	Missense_Mutation	SNP	p.D126E	c.T378A

RPMI	CCND2	chr12	4409098	4409098	Nonsense_Mutation	SNP	p.Q265X	c.C793T
RPMI	KRAS	chr12	25398284	25398284	Missense_Mutation	SNP	p.G12A	c.G35C
RPMI	CDX2	chr13	28539092	28539092	Missense_Mutation	SNP	p.L201Q	c.T602A
RPMI	CDH1	chr16	68867203	68867203	Missense_Mutation	SNP	p.A817V	c.C2450T
RPMI	ZFHX3	chr16	72830446	72830454	In_Frame_Del	DEL	p.2043_2045del	c.6127_6135del
RPMI	TP53	chr17	7577085	7577085	Missense_Mutation	SNP	p.E246K	c.G736A
AMO1	ZFHX3	chr16	72821633	72821635	In_Frame_Del	DEL	p.3514_3514del	c.10540_10542del
RPMI	JAK3	chr19	17954215	17954215	Missense_Mutation	SNP	p.P132T	c.C394A
RPMI	CBLC	chr19	45296848	45296848	Frame_Shift_Ins	INS	p.Q419fs	c.1255dupC
RPMI	ASXL1	chr20	31022737	31022737	Missense_Mutation	SNP	p.D741V	c.A2222T
RPMI	MUC1	chr1	155159847	155159847	Missense_Mutation	SNP	p.V412F	c.G1234T
AMO1	PER1	chr17	8048261	8048261	Missense_Mutation	SNP	p.S757R	c.A2269C
RPMI	ARID1B	chr6	157099196	157099204	In_Frame_Del	DEL	p.45_47del	c.133_141del
RPMI	ARID1B	chr6	157099417	157099417	In_Frame_Ins	INS	p.Q118delinsQKQ	c.354_355insAAGCAG
RPMI	PTCH1	chr9	98278974	98278974	In_Frame_Ins	INS	p.G43delinsGE	c.128_129insAGA
RPMI	NUP214	chr9	134014667	134014668	Frame_Shift_Del	DEL	p.I336fs	c.1006_1006del
AMO1	STAT3	chr17	40469209	40469209	Missense_Mutation	SNP	p.C712Y	c.G2135A
RPMI	SUFU	chr10	104263940	104263941	Frame_Shift_Del	DEL	p.G11fs	c.31_32del
RPMI	PAFAH1B2	chr11	117031947	117031947	Missense_Mutation	SNP	p.K86N	c.G258C
RPMI	KMT2D	chr12	49432706	49432706	Missense_Mutation	SNP	p.Q2811H	c.G8433T
RPMI	MN1	chr22	28194667	28194667	In_Frame_Ins	INS	p.A622delinsAP	c.1864_1865insCGC
RPMI	MN1	chr22	28194665	28194665	In_Frame_Ins	INS	p.P623delinsPP	c.1866_1867insCCT
RPMI	KDM6A	chrX	44920663	44920663	Missense_Mutation	SNP	p.Q527P	c.A1580C
SKMM2	TCF12	chr15	57545488	57545488	Missense_Mutation	SNP	p.R372T	c.G1115C
SKMM2	TP53	chr17	7578534	7578534	Missense_Mutation	SNP	p.K93N	c.G279T
SKMM2	PAX7	chr1	19029760	19029760	Missense_Mutation	SNP	p.M373I	c.G1119A
SKMM2	LRP1B	chr2	141625823	141625823	Missense_Mutation	SNP	p.F1393L	c.C4179G
SKMM2	PMS1	chr2	190738363	190738363	Missense_Mutation	SNP	p.K872R	c.A2615G

SKMM2	HIP1	chr7	75210555	75210555	Missense_Mutation	SNP	p.T201I	c.C602T
SKMM2	CUX1	chr7	101740766	101740766	Missense_Mutation	SNP	p.E131K	c.G391A
SKMM2	NUP98	chr11	3742050	3742050	Missense_Mutation	SNP	p.I718F	c.A2152T
SKMM2	AXIN1	chr16	343581	343581	Missense_Mutation	SNP	p.H698P	c.A2093C
SKMM2	TSC2	chr16	2136781	2136781	Missense_Mutation	SNP	p.H1633P	c.A4898C
SKMM2	ZFHX3	chr16	72821964	72821964	Missense_Mutation	SNP	p.P3404R	c.C10211G
SKMM2	NCOR1	chr17	15968292	15968292	Missense_Mutation	SNP	p.P1665T	c.C4993A
SKMM2	CDK12	chr17	37686892	37686892	Missense_Mutation	SNP	p.P1266A	c.C3796G
SKMM2	PIK3R2	chr19	18279295	18279295	Missense_Mutation	SNP	p.Q583K	c.C1747A
SKMM2	CNOT3	chr19	54650344	54650344	Missense_Mutation	SNP	p.S282F	c.C845T
SKMM2	CNOT3	chr19	54656620	54656620	Missense_Mutation	SNP	p.N641D	c.A1921G
SKMM2	CNOT3	chr19	54656621	54656621	Missense_Mutation	SNP	p.N641S	c.A1922G
SKMM2	ZRSR2	chrX	15840962	15840962	Missense_Mutation	SNP	p.S349Y	c.C1046A
XG1	NRAS	chr1	115258748	115258748	Missense_Mutation	SNP	p.G12R	c.G34C
XG1	DNMT3A	chr2	25457191	25457191	Missense_Mutation	SNP	p.R899H	c.G2696A
XG1	TP53	chr17	7578554	7578554	Missense_Mutation	SNP	p.Y87N	c.T259A
XG1	PBX1	chr1	164776790	164776790	Missense_Mutation	SNP	p.R238Q	c.G713A
XG1	MECOM	chr3	168834380	168834380	Missense_Mutation	SNP	p.C427F	c.G1280T
XG1	IKZF1	chr7	50450282	50450282	Missense_Mutation	SNP	p.Q156K	c.C466A
XG1	TRRAP	chr7	98506508	98506508	Missense_Mutation	SNP	p.N425H	c.A1273C
XG1	CNOT3	chr19	54656620	54656620	Missense_Mutation	SNP	p.N641D	c.A1921G
XG11	MLH1	chr3	37089130	37089130	Missense_Mutation	SNP	p.K377E	c.A1129G
XG11	MLH1	chr3	37089131	37089131	Missense_Mutation	SNP	p.K377T	c.A1130C
XG11	KIT	chr4	55593464	55593464	Missense_Mutation	SNP	p.M537L	c.A1609C
XG11	ARID1B	chr6	157099402	157099402	In_Frame_Ins	INS	p.F113delinsFQ	c.339_340insCAG
XG11	EXT2	chr11	44254000	44254000	Missense_Mutation	SNP	p.T597M	c.C1790T
XG11	ATM	chr11	108119823	108119823	Missense_Mutation	SNP	p.V410A	c.T1229C
XG11	KRAS	chr12	25378647	25378647	Missense_Mutation	SNP	p.K117N	c.A351C

XG11	CDK8	chr13	26967566	26967566	Nonsense_Mutation	SNP	p.R237X	c.C709T
XG11	TP53	chr17	7578526	7578526	Missense_Mutation	SNP	p.C96Y	c.G287A
AMO1	MKL1	chr22	40807753	40807753	Missense_Mutation	SNP	p.R813C	c.C2437T
AMO1	BCOR	chrX	39933660	39933662	In_Frame_Del	DEL	p.313_313del	c.937_939del
AMO1	BCOR	chrX	39933665	39933667	In_Frame_Del	DEL	p.311_312del	c.932_934del
XG11	TRRAP	chr7	98582616	98582616	Missense_Mutation	SNP	p.M3117K	c.T9350A
XG11	NUP214	chr9	134026118	134026118	Missense_Mutation	SNP	p.H748R	c.A2243G
XG11	KIF5B	chr10	32306071	32306071	Missense_Mutation	SNP	p.A921S	c.G2761T
XG11	BMPR1A	chr10	88651898	88651898	Missense_Mutation	SNP	p.C82Y	c.G245A
XG11	KMT2D	chr12	49426645	49426645	Missense_Mutation	SNP	p.L3948H	c.T11843A
XG11	ASXL1	chr20	31022608	31022608	Missense_Mutation	SNP	p.P698L	c.C2093T
JJN3	CTNNB1	chr3	41277329	41277329	Missense_Mutation	SNP	p.V593L	c.G1777T
XG11	GNAS	chr20	57415244	57415244	Frame_Shift_Ins	INS	p.A28fs	c.83_84insGGCCGCCGGGC
XG11	MKL1	chr22	40814749	40814749	In_Frame_Ins	INS	p.A565delinsGA	c.1692_1693insGGG
XG12	NRAS	chr1	115256530	115256530	Missense_Mutation	SNP	p.Q61K	c.C181A
XG12	MET	chr7	116339642	116339642	Missense_Mutation	SNP	p.E168D	c.G504T
XG12	BMPR1A	chr10	88681437	88681437	Missense_Mutation	SNP	p.R443C	c.C1327T
JJN3	IL6ST	chr5	55265588	55265588	Missense_Mutation	SNP	p.C54S	c.T160A
XG12	SFPQ	chr1	35650073	35650073	Missense_Mutation	SNP	p.K703R	c.A2108G
JJN3	IRF4	chr6	405075	405075	Missense_Mutation	SNP	p.C386Y	c.G1157A
XG12	BRD3	chr9	136918541	136918541	Missense_Mutation	SNP	p.N20S	c.A59G
XG12	ERBB3	chr12	56482642	56482642	Missense_Mutation	SNP	p.G367S	c.G1099A
XG12	MYO5A	chr15	52609295	52609295	Missense_Mutation	SNP	p.D1762N	c.G5284A
XG12	AXIN1	chr16	338240	338240	Missense_Mutation	SNP	p.F824Y	c.T2471A
XG12	MAP2K2	chr19	4101118	4101118	Missense_Mutation	SNP	p.V202M	c.G604A
JJN3	EZH2	chr7	148525904	148525904	Missense_Mutation	SNP	p.D185H	c.G553C
XG12	CNOT3	chr19	54656628	54656628	Missense_Mutation	SNP	p.C643W	c.T1929G
XG12	MKL1	chr22	40814748	40814748	Frame_Shift_Ins	INS	p.A565fs	c.1693_1694insGGCC

JJN3	NCOA2	chr8	71036930	71036930	Missense_Mutation	SNP	p.G1363R	c.G4087A
XG13	BRAF	chr7	140453155	140453155	Missense_Mutation	SNP	p.D594N	c.G1780A
XG13	WRN	chr8	30948045	30948045	Missense_Mutation	SNP	p.T573A	c.A1717G
XG13	NOTCH1	chr9	139401233	139401233	Missense_Mutation	SNP	p.R1279H	c.G3836A
XG13	TP53	chr17	7577538	7577538	Missense_Mutation	SNP	p.R209Q	c.G626A
XG13	HLF	chr17	53392779	53392779	Missense_Mutation	SNP	p.R215C	c.C643T
XG13	TRIM33	chr1	114945396	114945396	Missense_Mutation	SNP	p.P960S	c.C2878T
XG13	NTRK1	chr1	156848969	156848969	Missense_Mutation	SNP	p.P621S	c.C1861T
XG13	FBXO11	chr2	48132713	48132713	In_Frame_Ins	INS	p.P49delinsPQ	c.146_147insGCA
XG13	FBXO11	chr2	48132724	48132724	In_Frame_Ins	INS	p.P46delinsPP	c.135_136insCCG
XG13	SF3B1	chr2	198274497	198274497	In_Frame_Ins	INS	p.R301delinsRR	c.900_901insAGA
XG13	SETD2	chr3	47161937	47161937	Missense_Mutation	SNP	p.D1397N	c.G4189A
XG13	MSH3	chr5	79950735	79950735	In_Frame_Ins	INS	p.P63delinsPAAP	c.189_190insGCAGCGCCC
XG13	PTPRD	chr9	8521292	8521292	Missense_Mutation	SNP	p.Q316E	c.C946G
XG13	TGFBR1	chr9	101867557	101867565	In_Frame_Del	DEL	p.24_26del	c.70_78del
XG13	NUP214	chr9	134025795	134025795	Missense_Mutation	SNP	p.E709K	c.G2125A
XG13	PICALM	chr11	85725989	85725989	Missense_Mutation	SNP	p.R157K	c.G470A
XG13	DIS3	chr13	73345958	73345958	Missense_Mutation	SNP	p.G365E	c.G1094A
XG13	MYO5A	chr15	52656792	52656792	Missense_Mutation	SNP	p.E1090K	c.G3268A
XG13	MYO5A	chr15	52664530	52664530	Missense_Mutation	SNP	p.Q870E	c.C2608G
XG13	MAF	chr16	79632985	79632985	Missense_Mutation	SNP	p.R272H	c.G815A
XG13	STAT3	chr17	40478160	40478160	Missense_Mutation	SNP	p.H447Y	c.C1339T
XG13	COL1A1	chr17	48271499	48271499	Frame_Shift_Ins	INS	p.G554fs	c.1659_1660insGGGGGGGGGG
AMO1	EGFR	chr7	55219054	55219054	Missense_Mutation	SNP	p.K209N	c.A627C
JJN3	SOCS1	chr16	11348706	11348706	Missense_Mutation	SNP	p.Q210H	c.G630C
XG13	KEAP1	chr19	10610444	10610444	Missense_Mutation	SNP	p.P89L	c.C266T
XG13	CNOT3	chr19	54656620	54656620	Missense_Mutation	SNP	p.N641D	c.A1921G
JJN3	USP6	chr17	5042837	5042837	Missense_Mutation	SNP	p.R456W	c.C1366T

XG13	MKL1	chr22	40827457	40827457	Missense_Mutation	SNP	p.R31C	c.C91T
XG16	NRAS	chr1	115256528	115256528	Missense_Mutation	SNP	p.Q61H	c.A183C
XG16	SOCS1	chr16	11348706	11348706	Missense_Mutation	SNP	p.Q210H	c.G630C
XG16	TP53	chr17	7578190	7578190	Missense_Mutation	SNP	p.Y181C	c.A542G
JJN3	H3F3B	chr17	73775024	73775024	Missense_Mutation	SNP	p.R50P	c.G149C
XG16	ASXL2	chr2	25967177	25967177	In_Frame_Ins	INS	p.A677delinsAAA	c.2028_2029insGCCGCC
JJN3	KMT2B	chr19	36211742	36211742	Missense_Mutation	SNP	p.T498N	c.C1493A
XG16	NUP98	chr11	3765835	3765835	Missense_Mutation	SNP	p.K438E	c.A1312G
XG16	CYLD	chr16	50784063	50784064	Frame_Shift_Del	DEL	p.L152fs	c.454_455del
XG16	CNOT3	chr19	54656621	54656621	Missense_Mutation	SNP	p.N641S	c.A1922G
XG16	TOP1	chr20	39708777	39708777	Missense_Mutation	SNP	p.K130E	c.A388G
XG19	FEV	chr2	219846841	219846841	Missense_Mutation	SNP	p.E89K	c.G265A
XG19	BRAF	chr7	140453132	140453132	Missense_Mutation	SNP	p.K601N	c.A1803C
XG19	ATM	chr11	108160488	108160488	Nonsense_Mutation	SNP	p.R1466X	c.C4396T
XG19	TP53	chr17	7577139	7577139	Missense_Mutation	SNP	p.R228W	c.C682T
XG19	ARID1A	chr1	27105826	27105826	Missense_Mutation	SNP	p.P1596A	c.C4786G
XG19	PMS1	chr2	190719748	190719748	Missense_Mutation	SNP	p.D584H	c.G1750C
XG19	EZR	chr6	159206414	159206414	Missense_Mutation	SNP	p.A132T	c.G394A
XG19	IKZF1	chr7	50467931	50467931	Missense_Mutation	SNP	p.S389Y	c.C1166A
XG19	CNTRL	chr9	123852642	123852642	Missense_Mutation	SNP	p.L103V	c.C307G
XG19	MLLT10	chr10	22015197	22015197	Missense_Mutation	SNP	p.L390V	c.C1168G
XG19	ATM	chr11	108218052	108218052	Missense_Mutation	SNP	p.L2877F	c.G8631C
XG19	ARHGEF12	chr11	120346129	120346129	Missense_Mutation	SNP	p.K1064E	c.A3190G
XG19	ARHGEF12	chr11	120346174	120346174	Missense_Mutation	SNP	p.V1079L	c.G3235C
XG19	KTN1	chr14	56079026	56079026	Missense_Mutation	SNP	p.S87L	c.C260T
XG19	GRIN2A	chr16	9934855	9934855	Missense_Mutation	SNP	p.L479V	c.C1435G
XG19	MAF	chr16	79632974	79632974	Missense_Mutation	SNP	p.R276W	c.C826T
XG19	PLCG2	chr16	81973601	81973601	Missense_Mutation	SNP	p.D1140N	c.G3418A

XG19	NF1	chr17	29701100	29701100	Missense_Mutation	SNP	p.G2816E	c.G8447A
XG19	KMT2B	chr19	36210770	36210770	Frame_Shift_Del	DEL	p.P174fs	c.521delC
XG2	EZH2	chr7	148525904	148525904	Missense_Mutation	SNP	p.D185H	c.G553C
XG2	PTPRD	chr9	8375990	8375990	Missense_Mutation	SNP	p.R1536L	c.G4607T
XG2	KRAS	chr12	25398284	25398284	Missense_Mutation	SNP	p.G12A	c.G35C
XG2	TP53	chr17	7578212	7578212	Nonsense_Mutation	SNP	p.R174X	c.C520T
XG2	TP53	chr17	7578403	7578403	Missense_Mutation	SNP	p.C137Y	c.G410A
XG2	RNF213	chr17	78265440	78265440	Missense_Mutation	SNP	p.D429H	c.G1285C
XG2	NF2	chr22	30035154	30035154	Nonsense_Mutation	SNP	p.E106X	c.G316T
JJN3	PAX3	chr2	223066678	223066678	Missense_Mutation	SNP	p.G469R	c.G1405A
XG2	PPARG	chr3	12458404	12458404	Missense_Mutation	SNP	p.D313N	c.G937A
XG2	PIK3CB	chr3	138461446	138461446	Missense_Mutation	SNP	p.L192P	c.T575C
XG2	RAP1GDS1	chr4	99300171	99300171	Missense_Mutation	SNP	p.E123G	c.A368G
XG2	NRG1	chr8	32616905	32616905	Missense_Mutation	SNP	p.T343A	c.A1027G
XG2	BRD3	chr9	136918518	136918518	Missense_Mutation	SNP	p.N28H	c.A82C
XG2	KMT2D	chr12	49426641	49426641	Missense_Mutation	SNP	p.Q3949H	c.A11847T
XG2	NUTM1	chr15	34649217	34649217	Missense_Mutation	SNP	p.P975L	c.C2924T
XG2	TAF15	chr17	34171918	34171918	Missense_Mutation	SNP	p.S539C	c.A1615T
XG2	KMT2B	chr19	36228965	36228965	Missense_Mutation	SNP	p.S2582L	c.C7745T
XG20	PTPN13	chr4	87685866	87685866	Missense_Mutation	SNP	p.I1380L	c.A4138T
XG20	IKBKB	chr8	42171902	42171902	Missense_Mutation	SNP	p.T252M	c.C755T
XG20	PTCH1	chr9	98231110	98231110	Missense_Mutation	SNP	p.P574S	c.C1720T
XG20	KRAS	chr12	25380276	25380276	Missense_Mutation	SNP	p.Q61R	c.A182G
XG20	DIS3	chr13	73346905	73346905	Missense_Mutation	SNP	p.D276N	c.G826A
XG20	FAM46C	chr1	118165742	118165742	Frame_Shift_Ins	INS	p.N84fs	c.252_253insAAGCCAAT
XG20	FAM46C	chr1	118165743	118165743	Missense_Mutation	SNP	p.G85R	c.G253C
XG20	FAM46C	chr1	118165744	118165744	Missense_Mutation	SNP	p.G85V	c.G254T
XG20	FAM46C	chr1	118165761	118165761	Missense_Mutation	SNP	p.L91M	c.C271A

XG20	FAM46C	chr1	118165762	118165762	Missense_Mutation	SNP	p.L91Q	c.T272A
XG20	FAM46C	chr1	118165764	118165764	Missense_Mutation	SNP	p.D92N	c.G274A
XG20	FAM46C	chr1	118165766	118165766	Missense_Mutation	SNP	p.D92E	c.C276G
XG20	FAM46C	chr1	118165768	118165768	Missense_Mutation	SNP	p.L93P	c.T278C
XG20	PTPRC	chr1	198701675	198701675	Missense_Mutation	SNP	p.S711I	c.G2132T
XG20	MSH3	chr5	79950732	79950732	In_Frame_Ins	INS	p.A62delinsAAAA	c.186_187insGCCGCAGCG
XG20	ARID1B	chr6	157100007	157100007	In_Frame_Ins	INS	p.G315delinsGG	c.944_945insCGG
XG20	NCOA2	chr8	71128967	71128967	Missense_Mutation	SNP	p.G5E	c.G14A
XG20	TGFBR1	chr9	101867557	101867565	In_Frame_Del	DEL	p.24_26del	c.70_78del
XG20	FGFR2	chr10	123279565	123279565	Missense_Mutation	SNP	p.Q289H	c.G867C
XG20	CREB3L1	chr11	46342261	46342261	Frame_Shift_Ins	INS	p.D509fs	c.1525_1526insT
XG20	NUMA1	chr11	71715786	71715786	Missense_Mutation	SNP	p.S1969T	c.G5906C
XG20	ATM	chr11	108172391	108172391	Missense_Mutation	SNP	p.A1732T	c.G5194A
XG20	TBX3	chr12	115120747	115120747	Missense_Mutation	SNP	p.L87V	c.C259G
XG20	CREBBP	chr16	3779250	3779250	Missense_Mutation	SNP	p.V1933G	c.T5798G
JJN3	EZH2	chr7	148523651	148523651	Missense_Mutation	SNP	p.N268D	c.A802G
JJN3	EZH2	chr7	148524314	148524314	Missense_Mutation	SNP	p.F224V	c.T670G
XG20	NF2	chr22	30064383	30064383	Missense_Mutation	SNP	p.L316W	c.T947G
XG23	NRAS	chr1	115258745	115258745	Missense_Mutation	SNP	p.G13R	c.G37C
XG23	NOTCH1	chr9	139399132	139399132	Missense_Mutation	SNP	p.V1671I	c.G5011A
JJN3	NCOA2	chr8	71036261	71036261	Missense_Mutation	SNP	p.Y1384F	c.A4151T
XG23	KMT2D	chr12	49433883	49433883	Missense_Mutation	SNP	p.P2557L	c.C7670T
XG23	TP53BP1	chr15	43767874	43767874	Missense_Mutation	SNP	p.S320C	c.C959G
XG23	NOTCH2	chr1	120464916	120464916	Missense_Mutation	SNP	p.R1719Q	c.G5156A
XG23	LRP1B	chr2	141643746	141643746	Missense_Mutation	SNP	p.E1309K	c.G3925A
XG23	ETV5	chr3	185769905	185769905	Frame_Shift_Ins	INS	p.G409fs	c.1224_1225insGGCATCCA
XG23	PRDM1	chr6	106553798	106553798	Missense_Mutation	SNP	p.S588C	c.C1763G
XG23	PREX2	chr8	68995622	68995622	Missense_Mutation	SNP	p.E676K	c.G2026A

XG23	HEY1	chr8	80678497	80678497	In_Frame_Ins	INS	p.M1delinsML	c.1_2insTGC
XG23	PTPRD	chr9	8331582	8331582	Frame_Shift_Ins	INS	p.S1845fs	c.5533_5534insAGAAT
XG23	SUFU	chr10	104263939	104263939	Frame_Shift_Ins	INS	p.P10fs	c.30_31insCC
XG23	CCND1	chr11	69458687	69458687	Missense_Mutation	SNP	p.M168V	c.A502G
XG23	ZNF384	chr12	6777108	6777113	In_Frame_Del	DEL	p.501_502del	c.1501_1506del
XG23	PTPRB	chr12	71029597	71029597	Missense_Mutation	SNP	p.L102R	c.T305G
XG23	PER1	chr17	8045191	8045191	Missense_Mutation	SNP	p.R1178W	c.C3532T
XG23	MED12	chrX	70361150	70361150	In_Frame_Ins	INS	p.Q2113delinsHQ	c.6338_6339insCCA
XG24	NRAS	chr1	115258745	115258745	Missense_Mutation	SNP	p.G13R	c.G37C
JJN3	ZNF384	chr12	6777108	6777113	In_Frame_Del	DEL	p.501_502del	c.1501_1506del
XG24	NOTCH1	chr9	139399132	139399132	Missense_Mutation	SNP	p.V1671I	c.G5011A
XG24	KMT2D	chr12	49433883	49433883	Missense_Mutation	SNP	p.P2557L	c.C7670T
XG24	TP53BP1	chr15	43767874	43767874	Missense_Mutation	SNP	p.S320C	c.C959G
XG24	NOTCH2	chr1	120464916	120464916	Missense_Mutation	SNP	p.R1719Q	c.G5156A
XG24	EPAS1	chr2	46574062	46574062	Missense_Mutation	SNP	p.R26L	c.G77T
XG24	AFF3	chr2	100218031	100218033	In_Frame_Del	DEL	p.412_413del	c.1235_1237del
XG24	LRP1B	chr2	141643746	141643746	Missense_Mutation	SNP	p.E1309K	c.G3925A
XG24	ETV5	chr3	185769905	185769905	Frame_Shift_Ins	INS	p.G409fs	c.1224_1225insGGCATCCA
XG24	PRDM1	chr6	106553798	106553798	Missense_Mutation	SNP	p.S588C	c.C1763G
JJN3	CTCF	chr16	67645489	67645489	Missense_Mutation	SNP	p.P252S	c.C754T
XG24	PREX2	chr8	68995622	68995622	Missense_Mutation	SNP	p.E676K	c.G2026A
XG24	PTPRD	chr9	8331582	8331582	Frame_Shift_Ins	INS	p.S1845fs	c.5533_5534insAGAAT
JJN3	ZFHX3	chr16	72821964	72821964	Missense_Mutation	SNP	p.P3404R	c.C10211G
XG24	CCND1	chr11	69458687	69458687	Missense_Mutation	SNP	p.M168V	c.A502G
XG24	BCL9L	chr11	118773113	118773113	Frame_Shift_Ins	INS	p.A447fs	c.1338_1339insGGGG
XG24	PTPRB	chr12	71029597	71029597	Missense_Mutation	SNP	p.L102R	c.T305G
XG24	PER1	chr17	8045191	8045191	Missense_Mutation	SNP	p.R1178W	c.C3532T
XG24	CIC	chr19	42799293	42799293	In_Frame_Ins	INS	p.Q2502delinsPE	c.7504_7505insCCG

XG24	CNOT3	chr19	54656620	54656620	Missense_Mutation	SNP	p.N641D	c.A1921G
XG24	CNOT3	chr19	54656621	54656621	Missense_Mutation	SNP	p.N641S	c.A1922G
XG24	EP300	chr22	41551109	41551109	Nonsense_Mutation	SNP	p.G1085X	c.G3253T
XG24	EP300	chr22	41560133	41560133	Nonsense_Mutation	SNP	p.G1269X	c.G3805T
XG24	MED12	chrX	70361171	70361171	In_Frame_Ins	INS	p.Q2120delinsHQQQQ	c.6359_6360insCCAGCAGCAACA
XG24	BTK	chrX	100608900	100608900	Missense_Mutation	SNP	p.M604L	c.A1810T
XG25	DCTN1	chr2	74597939	74597939	Missense_Mutation	SNP	p.A286V	c.C857T
XG25	SETD2	chr3	47162886	47162886	Missense_Mutation	SNP	p.M1080I	c.G3240A
XG25	KRAS	chr12	25398285	25398285	Missense_Mutation	SNP	p.G12C	c.G34T
XG25	USP6	chr17	5042837	5042837	Missense_Mutation	SNP	p.R456W	c.C1366T
XG25	KMT2B	chr19	36211742	36211742	Missense_Mutation	SNP	p.T498N	c.C1493A
XG25	ARID1A	chr1	27023768	27023768	Missense_Mutation	SNP	p.T292P	c.A874C
XG25	FAM46C	chr1	118166362	118166362	Missense_Mutation	SNP	p.Y291C	c.A872G
XG25	FAM46C	chr1	118166363	118166363	Frame_Shift_Ins	INS	p.Y291fs	c.873_874insTT
XG25	FAM46C	chr1	118166364	118166364	Missense_Mutation	SNP	p.L292F	c.C874T
XG25	FAM46C	chr1	118166365	118166365	Frame_Shift_Ins	INS	p.L292fs	c.875_876insC
XG25	FAM46C	chr1	118166368	118166368	Missense_Mutation	SNP	p.Q293L	c.A878T
XG25	FAM46C	chr1	118166369	118166369	Missense_Mutation	SNP	p.Q293H	c.A879C
XG25	FAM46C	chr1	118166396	118166396	Missense_Mutation	SNP	p.S302R	c.C906G
XG25	FAM46C	chr1	118166398	118166398	Missense_Mutation	SNP	p.K303T	c.A908C
XG25	FAM46C	chr1	118166399	118166399	Missense_Mutation	SNP	p.K303N	c.G909T
XG25	FAM46C	chr1	118166401	118166401	Missense_Mutation	SNP	p.Y304C	c.A911G
XG25	FAM46C	chr1	118166402	118166402	Frame_Shift_Ins	INS	p.Y304fs	c.912_913insTTCTCTC
XG25	ACVR1	chr2	158594109	158594115	Frame_Shift_Del	DEL	p.L486fs	c.1458_1464del
XG25	PMS1	chr2	190670550	190670550	Frame_Shift_Ins	INS	p.K163fs	c.488dupA
XG25	FANCD2	chr3	10116323	10116323	Missense_Mutation	SNP	p.T942M	c.C2825T
XG25	KIT	chr4	55592147	55592147	Missense_Mutation	SNP	p.C491R	c.T1471C
XG25	MSH3	chr5	79950749	79950749	In_Frame_Ins	INS	p.A68delinsAPPA	c.203_204insGCCCCCAGC

XG25	ROS1	chr6	117725519	117725519	Missense_Mutation	SNP	p.S121Y	c.C362A
XG25	FANCG	chr9	35078282	35078282	Missense_Mutation	SNP	p.W122C	c.G366C
XG25	KRAS	chr12	25380268	25380268	Missense_Mutation	SNP	p.Y64N	c.T190A
XG25	RB1	chr13	48954351	48954351	Missense_Mutation	SNP	p.L491P	c.T1472C
XG25	TSC2	chr16	2103427	2103427	Missense_Mutation	SNP	p.L115M	c.C343A
XG25	CDK12	chr17	37686892	37686892	Missense_Mutation	SNP	p.P1266A	c.C3796G
XG25	CNOT3	chr19	54656620	54656620	Missense_Mutation	SNP	p.N641D	c.A1921G
XG25	MN1	chr22	28194937	28194937	In_Frame_Ins	INS	p.Q532delinsQK	c.1594_1595insAGA
XG26	NRAS	chr1	115256530	115256530	Missense_Mutation	SNP	p.Q61K	c.C181A
XG26	RUNX1	chr21	36259324	36259324	Missense_Mutation	SNP	p.L56S	c.T167C
XG26	LRP1B	chr2	141625823	141625823	Missense_Mutation	SNP	p.F1393L	c.C4179G
L363	NRAS	chr1	115256528	115256528	Missense_Mutation	SNP	p.Q61H	c.A183C
XG26	MSH3	chr5	79950735	79950735	In_Frame_Ins	INS	p.P63delinsPAAP	c.189_190insGCAGCGCCC
XG26	TGFBR1	chr9	101867557	101867565	In_Frame_Del	DEL	p.24_26del	c.70_78del
XG26	RET	chr10	43609080	43609086	Frame_Shift_Del	DEL	p.F612fs	c.1836_1842del
XG26	ZNF384	chr12	6777113	6777113	In_Frame_Ins	INS	p.Q501delinsQQQ	c.1500_1501insCAGCAG
XG26	SETBP1	chr18	42456669	42456669	Frame_Shift_Ins	INS	p.L227fs	c.680_681insTTCT
XG26	CIC	chr19	42799293	42799293	In_Frame_Ins	INS	p.Q2502delinsPGQ	c.7504_7505insCGGGCC
XG26	CNOT3	chr19	54656620	54656620	Missense_Mutation	SNP	p.N641D	c.A1921G
XG26	GNAS	chr20	57429350	57429350	Missense_Mutation	SNP	p.D344N	c.G1030A
XG26	EP300	chr22	41568666	41568666	Missense_Mutation	SNP	p.D1539G	c.A4616G
XG27	MSH3	chr5	79950708	79950716	In_Frame_Del	DEL	p.54_57del	c.162_170del
XG27	KRAS	chr12	25380275	25380275	Missense_Mutation	SNP	p.Q61H	c.A183C
XG27	KMT2D	chr12	49446160	49446160	Missense_Mutation	SNP	p.E436K	c.G1306A
L363	MECOM	chr3	168834305	168834305	Missense_Mutation	SNP	p.D452A	c.A1355C
XG27	PAX3	chr2	223096868	223096868	Missense_Mutation	SNP	p.T241S	c.A721T
XG27	BRD3	chr9	136899840	136899840	Missense_Mutation	SNP	p.K683M	c.A2048T
XG27	ZNF384	chr12	6777069	6777071	In_Frame_Del	DEL	p.515_515del	c.1543_1545del

XG27	HOXC11	chr12	54367527	54367527	Missense_Mutation	SNP	p.E168K	c.G502A
XG27	GLI1	chr12	57860072	57860072	Missense_Mutation	SNP	p.H271P	c.A812C
XG27	PTPRB	chr12	70960235	70960235	Missense_Mutation	SNP	p.A1295D	c.C3884A
XG27	SOCS1	chr16	11349328	11349328	Missense_Mutation	SNP	p.A3V	c.C8T
XG27	SMAD4	chr18	48591913	48591913	Missense_Mutation	SNP	p.G359V	c.G1076T
XG27	RUNX1	chr21	36259204	36259204	Missense_Mutation	SNP	p.N96S	c.A287G
XG28	ASXL1	chr20	31023821	31023821	Missense_Mutation	SNP	p.E1102D	c.G3306T
XG28	TGFBR2	chr3	30713749	30713749	Missense_Mutation	SNP	p.I383M	c.T1149G
XG28	FOXL2	chr3	138664756	138664756	Missense_Mutation	SNP	p.V270G	c.T809G
L363	NTRK2	chr9	87338515	87338515	Missense_Mutation	SNP	p.P204H	c.C611A
XG28	PRDM1	chr6	106554958	106554958	Missense_Mutation	SNP	p.C692F	c.G2075T
XG28	PRDM1	chr6	106554966	106554966	Missense_Mutation	SNP	p.N695Y	c.A2083T
XG28	ARID1B	chr6	157099184	157099186	In_Frame_Del	DEL	p.41_41del	c.121_123del
XG28	KMT2D	chr12	49420194	49420194	Missense_Mutation	SNP	p.F5185L	c.C15555G
XG28	KMT2D	chr12	49420820	49420820	Missense_Mutation	SNP	p.P4977S	c.C14929T
XG28	BTG1	chr12	92539304	92539304	Missense_Mutation	SNP	p.P3L	c.C8T
XG28	KMT2B	chr19	36214633	36214633	Frame_Shift_Ins	INS	p.G1020fs	c.3059_3060insT
XG28	CIC	chr19	42799293	42799293	Frame_Shift_Ins	INS	p.Q2502fs	c.7504_7505insCGGG
XG28	GNAS	chr20	57430212	57430212	Missense_Mutation	SNP	p.S631L	c.C1892T
XG28	MN1	chr22	28194939	28194939	In_Frame_Ins	INS	p.Q531delinsQP	c.1592_1593insGCC
XG29	CDKN2A	chr9	21970916	21970916	Missense_Mutation	SNP	p.A148T	c.G442A
XG29	KRAS	chr12	25380275	25380275	Missense_Mutation	SNP	p.Q61H	c.A183C
L363	KMT2D	chr12	49445392	49445392	Missense_Mutation	SNP	p.P692T	c.C2074A
L363	KMT2D	chr12	49448463	49448463	Missense_Mutation	SNP	p.R83Q	c.G248A
XG29	JAK3	chr19	17945696	17945696	Missense_Mutation	SNP	p.V722I	c.G2164A
XG29	CIC	chr19	42796307	42796307	Missense_Mutation	SNP	p.L1895V	c.C5683G
L363	ERBB3	chr12	56487289	56487289	Missense_Mutation	SNP	p.E479K	c.G1435A
XG29	FAM46C	chr1	118165912	118165912	Missense_Mutation	SNP	p.K141T	c.A422C

XG29	PHOX2B	chr4	41748028	41748030	In_Frame_Del	DEL	p.247_247del	c.739_741del
L363	NUTM1	chr15	34649336	34649336	Missense_Mutation	SNP	p.E1015K	c.G3043A
L363	IGF1R	chr15	99482568	99482568	Missense_Mutation	SNP	p.D1145N	c.G3433A
XG29	CBL	chr11	119142477	119142477	Missense_Mutation	SNP	p.S159T	c.G476C
XG29	BUB1B	chr15	40488858	40488860	In_Frame_Del	DEL	p.391_391del	c.1171_1173del
XG29	ERCC4	chr16	14041902	14041902	Missense_Mutation	SNP	p.K817E	c.A2449G
L363	MYH11	chr16	15876295	15876295	Missense_Mutation	SNP	p.L232V	c.C694G
L363	CDH11	chr16	65032507	65032507	Missense_Mutation	SNP	p.H161Y	c.C481T
XG29	KEAP1	chr19	10602254	10602254	Missense_Mutation	SNP	p.R442G	c.A1324G
L363	TP53	chr17	7577499	7577499	Missense_Mutation	SNP	p.S222T	c.G665C
XG29	MN1	chr22	28194941	28194941	In_Frame_Ins	INS	p.Q531delinsHQ	c.1590_1591insCAC
XG30	NOTCH2	chr1	120459251	120459251	Missense_Mutation	SNP	p.H2032N	c.C6094A
XG30	ALK	chr2	29543736	29543736	Missense_Mutation	SNP	p.V476A	c.T1427C
XG30	KIT	chr4	55593464	55593464	Missense_Mutation	SNP	p.M537L	c.A1609C
XG30	KDR	chr4	55984888	55984888	Missense_Mutation	SNP	p.D81N	c.G241A
L363	RNF213	chr17	78351591	78351591	Nonsense_Mutation	SNP	p.G4514X	c.G13540T
XG30	BRAF	chr7	140453193	140453193	Missense_Mutation	SNP	p.N581S	c.A1742G
XG30	EZH2	chr7	148525904	148525904	Missense_Mutation	SNP	p.D185H	c.G553C
L363	RNF213	chr17	78360674	78360674	Missense_Mutation	SNP	p.P4969A	c.C14905G
XG30	ATM	chr11	108170479	108170479	Missense_Mutation	SNP	p.D1682H	c.G5044C
XG30	TP53	chr17	7577538	7577538	Missense_Mutation	SNP	p.R209Q	c.G626A
XG30	TPM3	chr1	154148702	154148702	Missense_Mutation	SNP	p.L89S	c.T266C
XG30	TP63	chr3	189582089	189582089	Missense_Mutation	SNP	p.M216I	c.G648C
XG30	MAP3K1	chr5	56171044	56171044	Missense_Mutation	SNP	p.Q624H	c.G1872C
XG30	PIK3R1	chr5	67569226	67569226	Missense_Mutation	SNP	p.L115F	c.C343T
XG30	SYK	chr9	93607827	93607827	Missense_Mutation	SNP	p.E177K	c.G529A
XG30	PTCH1	chr9	98209627	98209627	In_Frame_Ins	INS	p.R1153delinsRGG	c.3457_3458insGGGGGG
XG30	FANCF	chr11	22646329	22646329	Missense_Mutation	SNP	p.G343A	c.G1028C

XG30	ATM	chr11	108099926	108099926	Missense_Mutation	SNP	p.Q69H	c.G207T
XG30	CYLD	chr16	50816350	50816350	Missense_Mutation	SNP	p.S600F	c.C1799T
XG30	MLLT6	chr17	36873756	36873756	Missense_Mutation	SNP	p.L575V	c.C1723G
XG30	CIC	chr19	42799293	42799293	In_Frame_Ins	INS	p.Q2502delinsPGGE	c.7504_7505insCCGGGGGGG
XG5	ALK	chr2	29543736	29543736	Missense_Mutation	SNP	p.V476A	c.T1427C
XG5	SFRP4	chr7	37951817	37951817	Missense_Mutation	SNP	p.R232Q	c.G695A
L363	ABL2	chr1	179078046	179078046	Missense_Mutation	SNP	p.S786P	c.T2356C
XG5	CCND1	chr11	69456118	69456118	Missense_Mutation	SNP	p.I13F	c.A37T
XG5	TP53	chr17	7577094	7577094	Missense_Mutation	SNP	p.R243W	c.C727T
XG5	ELF3	chr1	201982089	201982089	Missense_Mutation	SNP	p.R205W	c.C613T
XG5	DCTN1	chr2	74595896	74595896	Missense_Mutation	SNP	p.C605G	c.T1813G
XG5	SETD2	chr3	47162639	47162644	In_Frame_Del	DEL	p.1161_1163del	c.3482_3487del
XG5	MAP3K1	chr5	56177873	56177875	In_Frame_Del	DEL	p.949_950del	c.2846_2848del
XG5	NTRK2	chr9	87325610	87325610	Missense_Mutation	SNP	p.Q163K	c.C487A
XG5	CCND1	chr11	69456211	69456211	Missense_Mutation	SNP	p.Y44N	c.T130A
XG5	CCND1	chr11	69456219	69456219	Missense_Mutation	SNP	p.K46N	c.A138T
XG5	PTPN11	chr12	112915494	112915494	Missense_Mutation	SNP	p.N298S	c.A893G
XG5	CRTC3	chr15	91150629	91150629	Missense_Mutation	SNP	p.L166F	c.C496T
XG5	IGF1R	chr15	99478103	99478103	Missense_Mutation	SNP	p.R1002W	c.C3004T
XG5	CYLD	chr16	50830382	50830382	Missense_Mutation	SNP	p.C945Y	c.G2834A
XG5	CYLD	chr16	50830385	50830385	Missense_Mutation	SNP	p.M946K	c.T2837A
XG5	CYLD	chr16	50830386	50830386	Missense_Mutation	SNP	p.M946I	c.G2838A
XG5	CYLD	chr16	50830393	50830393	Missense_Mutation	SNP	p.S949G	c.A2845G
XG5	CYLD	chr16	50830399	50830399	Missense_Mutation	SNP	p.T951S	c.A2851T
L363	RAF1	chr3	12650334	12650334	Missense_Mutation	SNP	p.K171T	c.A512C
XG5	PLCG1	chr20	39802929	39802929	Missense_Mutation	SNP	p.H1270D	c.C3808G
XG6	FHIT	chr3	59999845	59999845	Missense_Mutation	SNP	p.R46H	c.G137A
XG6	TP63	chr3	189612134	189612134	Missense_Mutation	SNP	p.G629D	c.G1886A

XG6	IL7R	chr5	35873648	35873648	Missense_Mutation	SNP	p.E202K	c.G604A
XG6	CDKN2A	chr9	21970916	21970916	Missense_Mutation	SNP	p.A148T	c.G442A
XG6	KRAS	chr12	25380277	25380277	Missense_Mutation	SNP	p.Q61E	c.C181G
XG6	KRAS	chr12	25398262	25398262	Missense_Mutation	SNP	p.L19F	c.G57C
XG6	MAF	chr16	79632847	79632847	Missense_Mutation	SNP	p.S318L	c.C953T
XG6	USP6	chr17	5042837	5042837	Missense_Mutation	SNP	p.R456W	c.C1366T
XG6	STAT3	chr17	40475058	40475058	Missense_Mutation	SNP	p.G618R	c.G1852C
XG6	FUBP1	chr1	78426179	78426179	Missense_Mutation	SNP	p.G470V	c.G1409T
XG6	TRIM33	chr1	115005775	115005775	Missense_Mutation	SNP	p.D292N	c.G874A
XG6	NOTCH2	chr1	120464368	120464368	Missense_Mutation	SNP	p.D1760N	c.G5278A
XG6	FOXL2	chr3	138664779	138664779	Missense_Mutation	SNP	p.Q262H	c.G786C
XG6	MAP3K1	chr5	56111416	56111416	In_Frame_Ins	INS	p.G6delinsAG	c.16_17insCGG
XG6	HSP90AB1	chr6	44218153	44218155	In_Frame_Del	DEL	p.258_259del	c.774_776del
XG6	PMS2	chr7	6035190	6035190	Missense_Mutation	SNP	p.N190S	c.A569G
XG6	KMT2C	chr7	151873726	151873726	In_Frame_Ins	INS	p.P2938delinsPPP	c.8811_8812insCCACCA
XG6	RUNX1T1	chr8	92982979	92982979	Missense_Mutation	SNP	p.E455D	c.G1365C
XG6	PPP6C	chr9	127912015	127912015	Missense_Mutation	SNP	p.F322L	c.C966A
AMO1	ATM	chr11	108115724	108115724	Missense_Mutation	SNP	p.H291R	c.A872G
XG6	TCF7L2	chr10	114710585	114710585	Missense_Mutation	SNP	p.E24Q	c.G70C
XG6	MAML2	chr11	95826272	95826272	Missense_Mutation	SNP	p.E308G	c.A923G
XG6	ATM	chr11	108165715	108165715	Missense_Mutation	SNP	p.G1613A	c.G4838C
XG6	MGA	chr15	42058382	42058382	Missense_Mutation	SNP	p.I2701S	c.T8102G
XG6	CREBBP	chr16	3790422	3790422	Missense_Mutation	SNP	p.V1371F	c.G4111T
XG6	STAT3	chr17	40500521	40500530	Frame_Shift_Del	DEL	p.A2fs	c.5_14del
XG6	ZNF521	chr18	22806245	22806245	Missense_Mutation	SNP	p.S546Y	c.C1637A
XG6	SETBP1	chr18	42531925	42531925	Missense_Mutation	SNP	p.D874N	c.G2620A
XG6	CNOT3	chr19	54656621	54656621	Missense_Mutation	SNP	p.N641S	c.A1922G
XG6	PLCG1	chr20	39794872	39794872	Missense_Mutation	SNP	p.R613Q	c.G1838A

XG6	MN1	chr22	28194957	28194957	In_Frame_Ins	INS	p.Q525delinsQR	c.1574_1575insGCG
XG6	ZRSR2	chrX	15809121	15809121	Missense_Mutation	SNP	p.R36G	c.C106G
XG7	DCTN1	chr2	74597939	74597939	Missense_Mutation	SNP	p.A286V	c.C857T
XG7	SETD2	chr3	47162886	47162886	Missense_Mutation	SNP	p.M1080I	c.G3240A
XG7	KRAS	chr12	25398285	25398285	Missense_Mutation	SNP	p.G12C	c.G34T
XG7	USP6	chr17	5042837	5042837	Missense_Mutation	SNP	p.R456W	c.C1366T
XG7	KMT2B	chr19	36211742	36211742	Missense_Mutation	SNP	p.T498N	c.C1493A
XG7	FAM46C	chr1	118166362	118166362	Missense_Mutation	SNP	p.Y291C	c.A872G
XG7	FAM46C	chr1	118166363	118166363	Frame_Shift_Ins	INS	p.Y291fs	c.873_874insTTCT
XG7	FAM46C	chr1	118166367	118166367	Missense_Mutation	SNP	p.Q293E	c.C877G
XG7	FAM46C	chr1	118166399	118166399	Missense_Mutation	SNP	p.K303N	c.G909C
XG7	FAM46C	chr1	118166401	118166401	Missense_Mutation	SNP	p.Y304F	c.A911T
XG7	FAM46C	chr1	118166402	118166402	Frame_Shift_Ins	INS	p.Y304fs	c.912_913insTCTC
XG7	PMS1	chr2	190670550	190670550	Frame_Shift_Ins	INS	p.K163fs	c.488dupA
XG7	MSH3	chr5	79950749	79950749	In_Frame_Ins	INS	p.A68delinsAPPA	c.203_204insGCCCCCAGC
XG7	ROS1	chr6	117725519	117725519	Missense_Mutation	SNP	p.S121Y	c.C362A
XG7	FANCG	chr9	35078282	35078282	Missense_Mutation	SNP	p.W122C	c.G366C
XG7	SUFU	chr10	104263939	104263939	Frame_Shift_Ins	INS	p.P10fs	c.30_31insCC
XG7	KRAS	chr12	25380268	25380268	Missense_Mutation	SNP	p.Y64N	c.T190A
XG7	STAT6	chr12	57490461	57490461	Missense_Mutation	SNP	p.S813W	c.C2438G
XG7	RB1	chr13	48954351	48954351	Missense_Mutation	SNP	p.L491P	c.T1472C
XG7	TSC2	chr16	2103427	2103427	Missense_Mutation	SNP	p.L115M	c.C343A
XG7	MYH11	chr16	15850309	15850309	Missense_Mutation	SNP	p.D553E	c.C1659A
XG7	CIC	chr19	42799293	42799293	In_Frame_Ins	INS	p.Q2502delinsPE	c.7504_7505insCCG
XG7	MN1	chr22	28194962	28194962	In_Frame_Ins	INS	p.Q524delinsHQ	c.1569_1570insCAT
AMO1	KRAS	chr12	25378562	25378562	Missense_Mutation	SNP	p.A146T	c.G436A
L363	TRAF7	chr16	2220636	2220636	Missense_Mutation	SNP	p.R85C	c.C253T
OPM2	NCOR2	chr12	124817000	124817000	Missense_Mutation	SNP	p.K2257E	c.A6769G

XG12	NCOR2	chr12	124857130	124857130	Missense_Mutation	SNP	p.E749K	c.G2245A

Table S4. High confidence list of 236 protein coding genes with somatic mutations affecting the structure of encoded protein. The table shows individual mutations and associated protein coding change among all HMCLs assayed.
DEL = Deletion, SNP = Single Nucleotide Polymorphism, INS = Insertion.

Table S5.

gene	mutated_HMCLs	mutated_primary_tumor_samples
TP53	14	2
CNOT3	13	6
KRAS	11	12
KMT2D	10	1
NRAS	9	9
ATM	8	6
CIC	8	17
MN1	8	3
MSH3	8	8
FAM46C	7	6
LRP1B	7	1
PTPRD	7	1
KMT2B	6	6
MKL1	6	1
SETD2	6	1
USP6	6	NM
ZFHX3	6	7
ARID1B	5	6
EZH2	5	NM
MAP3K1	5	2
PMS1	5	NM
ZNF384	5	3

Table S5. Frequently mutated genes in HMCLs that were also found to be mutated in at least one primary tumor samples from myeloma patients. NM = Not Mutated.

Table S6.
A

HMCL	Number of clones
XG30	4
XG13	3
XG16	3
XG20	3
XG24	3
XG25	3
MM1S	3
SKMM2	3
XG1	2
XG2	2
XG5	2
XG6	2
XG7	2
XG11	2
XG19	2
XG26	2
XG27	2
XG28	2
XG29	2
Lopra	2
AMO1	2
JJN3	2
L363	2
LP1	2

OPM2	2
RPMI8226	2
MOLP2	2
MOLP8	2
XG12	1
XG23	1

B

Patient	Number of clones
E13084	3
E11173	3
E14024	3
E17214	3
E11158	3
E13067	3
E14186	3
E15012	3
E12005	2
E12069	2
E12185	2
E13038	2
E11167	2
E13070	2
E13145	2
E14181	2
E15064	2
E15172	2

E15180	2
E16036	2
E11193	2
E16050	2
E16088	2
E16178	2
E17072	2
E17080	2
E17149	2
E17152	2
E17153	2
E17154	2
E17225	2
E17228	2
E17230	2
E17238	2
E17243	2
E17251	2
E17282	2
E17285	2
E17328	2
E6071	2
E6074	2
E6118	2
E13093	2
E13098	2
E13187	2
E14144	2

E14182	2
E15008	2
E15030	2
E15168	2
E15177	2
E11248	2
E12082	1
E13227	1
E15094	1
E16163	1
E17283	1
E14005	1
E11221	1

Table S6.
A Number of clones for each HMCLs
B Number of clones for each patient

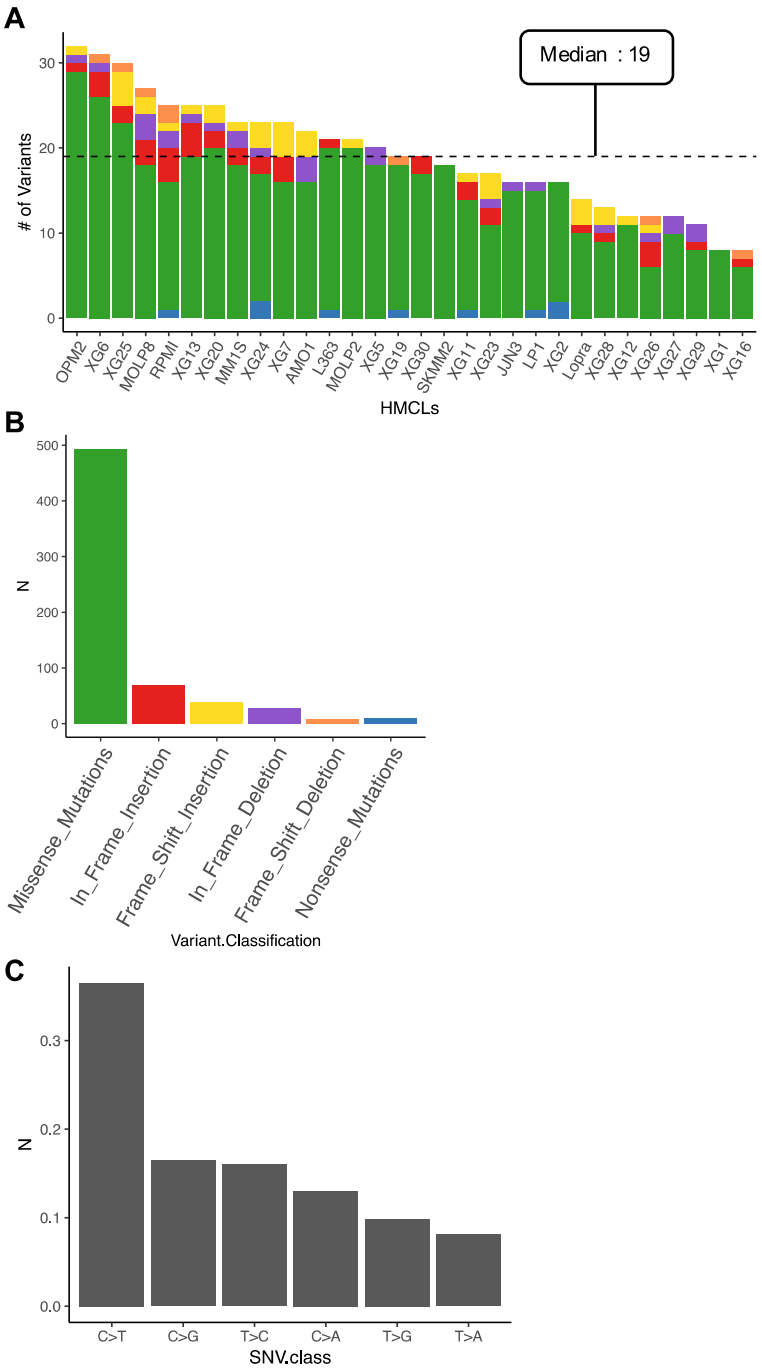
A
Median : 19
# of Variants
30
20
10
0
OPM2
XG6
XG25
MOLP8
RPMI
XG13
XG20
MM1S
XG24
XG7
AMO1
L363
MOLP2
XG5
XG19
XG30
SKMM2
XG11
XG23
JJN3
LP1
XG2
Lopra
XG28
XG12
XG26
XG27
XG29
XG1
XG16
HMCLs
B
N
500
400
300
200
100
0
Missense_Mutations
In_Frame_Insertion
Frame_Shift_Insertion
In_Frame_Deletion
Frame_Shift_Deletion
Nonsense_Mutations
Variant.Classification
C
N
0.3
0.2
0.1
0.0
C>T
C>G
T>C
C>A
T>G
T>A
SNV.class

Figure S1. (A) Rate for each variant in function of the HMCLs for the high confidence list of 236 mutated genes. **(B)** Number of mutations for each type of variant and for all HMCLs among the high confidence list of 236 mutated genes. (**C)** Rate of transition and transversion for all HMCLs and for the high confidence list of 236 mutated genes.

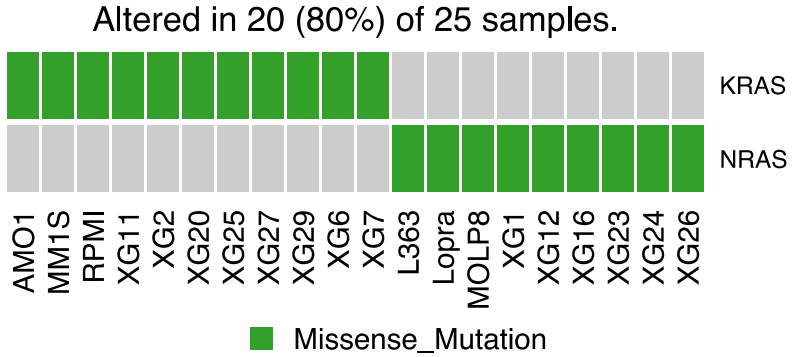

Figure S2. Mutual exclusive mutated genes. Mutual exclusivity between KRAS and NRAS mutations (P value < 0.0005).