# Supplementary Figures



Figure S1: Comparison between the Asian and European cohort in the TCGA dataset. Ethnic comparison in A) Stage, B) Vascular invasion, C) AFP as well as D) purity between Asians and Europeans in the TCGA cohort.

## Multivariate linear model for TMB

| Variable | | N | Estimate | Confidence interval | p−value |
|---|---|---|---|---|---|
| **Race** | ASIAN | 140 | | ref | |
| | EUROPEAN | 158 | | −0.34 (−0.58, −0.11) | 0.00458 |
| **Age** | | 298 | | 0.02 (0.01, 0.03) | < 0.001 |
| **Gender** | FEMALE | 99 | | ref | |
| | MALE | 199 | | 0.33 (0.13, 0.53) | 0.00117 |
| **Stage** | I | 149 | | ref | |
| | II | 67 | | 0.22 (−0.00, 0.45) | 0.05491 |
| | III | 77 | | −0.02 (−0.25, 0.22) | 0.86999 |
| | IV | 5 | | 0.62 (−0.10, 1.34) | 0.09228 |
| **Viral Status** | HBV+ | 89 | | ref | |
| | HCV+ | 35 | | 0.29 (−0.06, 0.64) | 0.10664 |
| | HEPB−C | 6 | | 0.47 (−0.19, 1.13) | 0.16339 |
| | NBNC | 168 | | 0.09 (−0.17, 0.36) | 0.48478 |
| **Purity** | | 298 | | 0.72 (0.25, 1.19) | 0.00253 |
| **(Intercept)** | | | | 0.05 (−0.50, 0.61) | 0.84948 |

Figure S2: Multivariate linear model comparing TMB across cohorts. Multivariate analysis between TMB and the ethnic background controlling for a collection of clinical variables. TMB difference in ethnicity was still significant after controlling for tumor purity and other clinical variables.
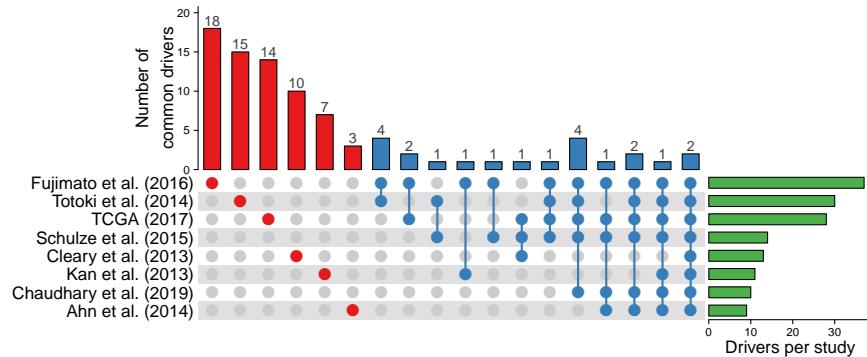


Figure S3: Driver genes identified in a few large cohorts. Summary of driver genes across cohorts. Right bars indicate the number of driver genes identified in each study are summarized. Top bars indicate the number of genes shared by all possible combination of studies. Blue bars denote the number of genes identified by at least two studies and red bars indicate the number of genes identified by only one of the studies.
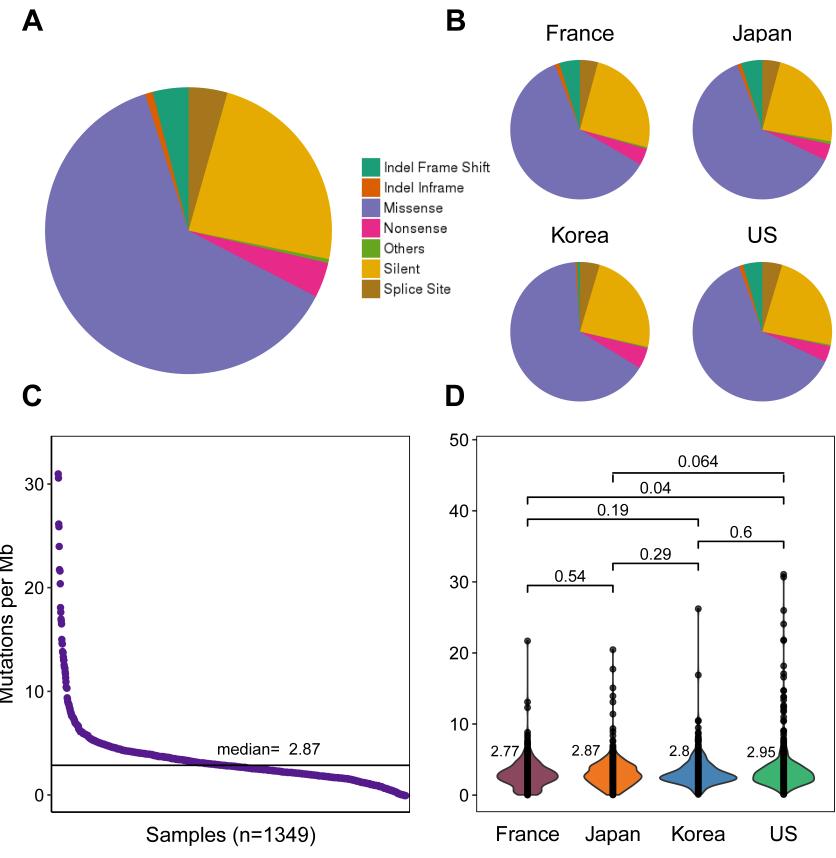
Figure S4: Summary of mutation profile across cohorts. A) Distribution of mutation types across all 1349 patients, B) Distribution of mutation types in different individuals, C) Distribution of mutation rates (i.e. number of mutations per megabase) across all 1349 patients, D) Mutation rate distributions in different cohorts. Median mutation rates are shown for each cohort. P-values from the Wilcoxon signed-rank test across cohorts were listed for each comparison.
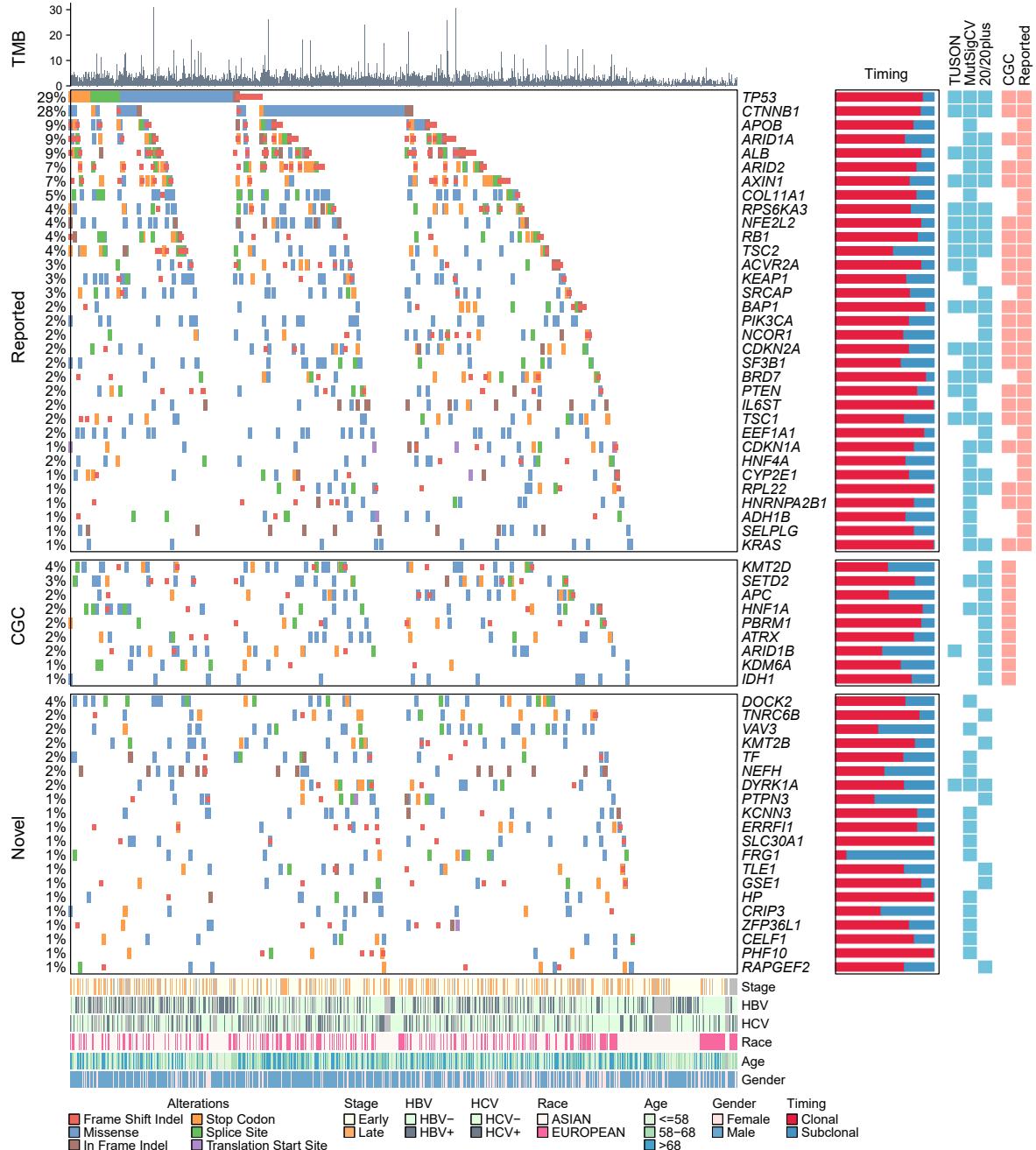
Figure S5: The landscape of 62 HCC drivers across 1349 patients. Each column represents a patient. In each row, somatic alterations (represented by different colors) and mutation frequencies for each driver were given. The timing barplot on the right side indicates proportions of early (red) and late (blue) mutation proportions in the driver across the cohort. Heatmap on the right side indicates whether the driver gene is detected by different methods (MutSigCV, TUSON Explorer and 20/20+) or whether the gene was reported previously by other studies or in the cancer gene census list (Reported or CGC). The barplot on the top indicates the mutation burden of patients. Clinical phenotypes of patients were shown at the bottom of the figure.
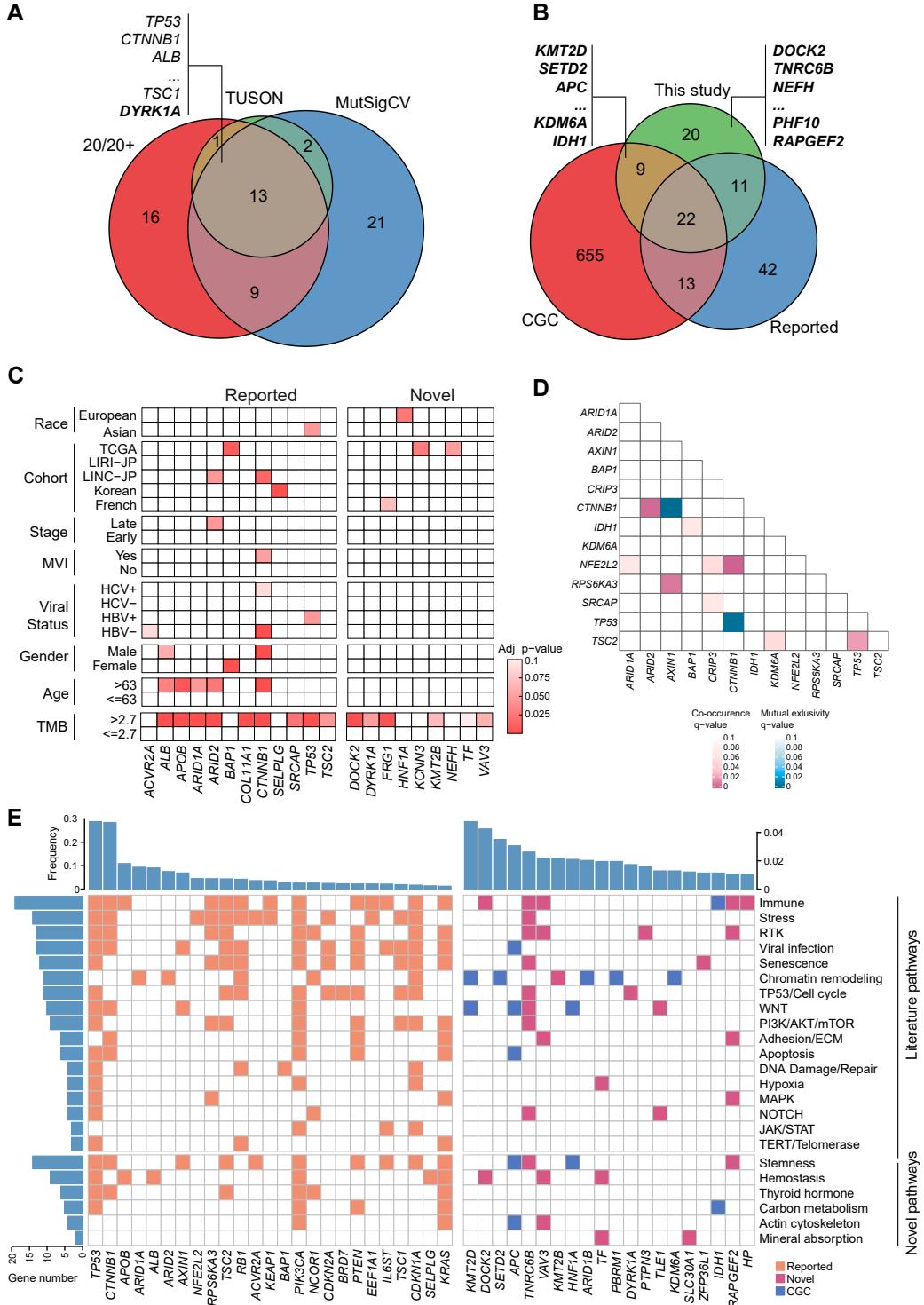
Figure S6: Driver genes identified in different methods. A) Venn diagram of drivers identified by three different methods, B) Venn diagram of overlapping and unique drivers identified in this work, previous studies (Reported) and the Cancer Gene Census (CGC) database. Novel genes were shown in bold font, C) Correlation of drivers with clinical phenotypes. The color scale represents the adjusted p-value after Benjamini-Hochberg multiple test correction, D) Mutual exclusivity and co-occurrence status of drivers. Pairs with a q-value < 0.1 were kept. The q-value for each significant mutually exclusive or co-occurrent pair are shown as gradients of pink (co-occurring) and blue (mutually exclusive),E) Driver genes and their associated pathways . Both literature and novel pathways are shown. The upper panel bar chart shows the mutational frequency of the corresponding driver gene. The left panel bar chart shows the number of genes assigned to corresponding pathways. Heatmaps on the left show pathways for previously reported driver genes and heatmaps on the right show pathways for novel drivers. CGC genes among novel drivers are shown in blue color.
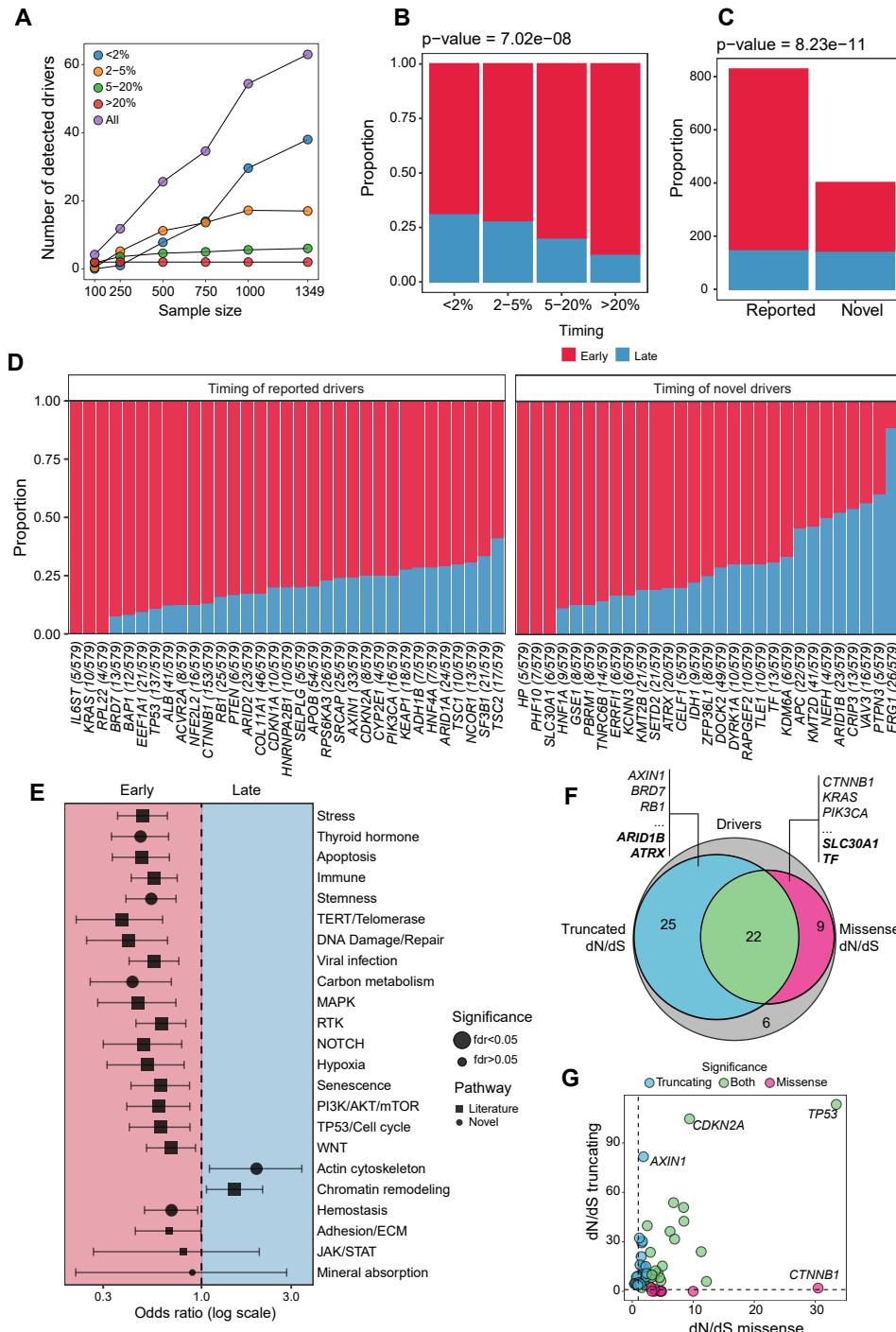
Figure S7: Saturation analysis and the timing of drivers. A) Number of drivers detected with different sample sizes. The relationship between the number of identified driver genes and the sample size (Purple dots). Lines are connecting the median number of detected drivers for that subsample size (5 replicates per sample size). Drivers in different frequency categories across samples are shown with different colors. B) Timing of mutations in driver genes in different frequency groups, C) Subclonal (blue) and clonal (red) fractions of mutations in reported and novel drivers across all patients in the TCGA and Korean cohorts, D)Subclonal (blue) and clonal (red) fractions of mutations in individual drivers across patients in the TCGA and Korean cohorts, E) boxplot for timing of driver genes in different pathways, F)Venn diagram of drivers with significant truncating or missense dN/dS value, G) Truncating versus missense dN/dS values for all the driver genes.
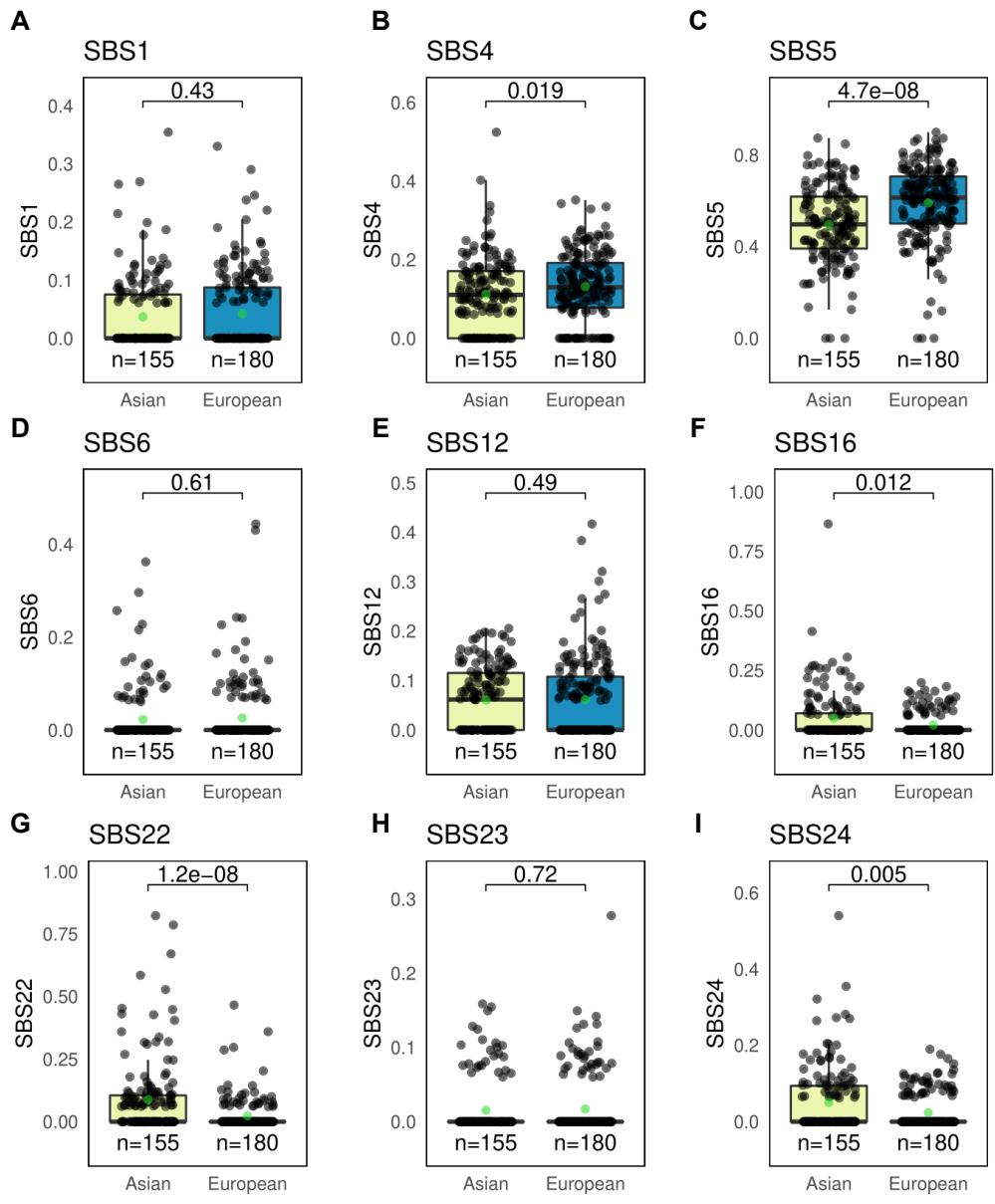
Figure S8: Comparison of mutational signature proportions between Asian and Europeans. A) SBS1 (aging), B) SBS4 (smoking), C) SBS5 (aging), D) SBS6 (MSI), E) SBS12 (liver related signature), F) SBS16 (liver related signature), G) SBS22 (aristolochic acid), H) SBS23 (unknown etiology), I) SBS24 (aflatoxin B1)
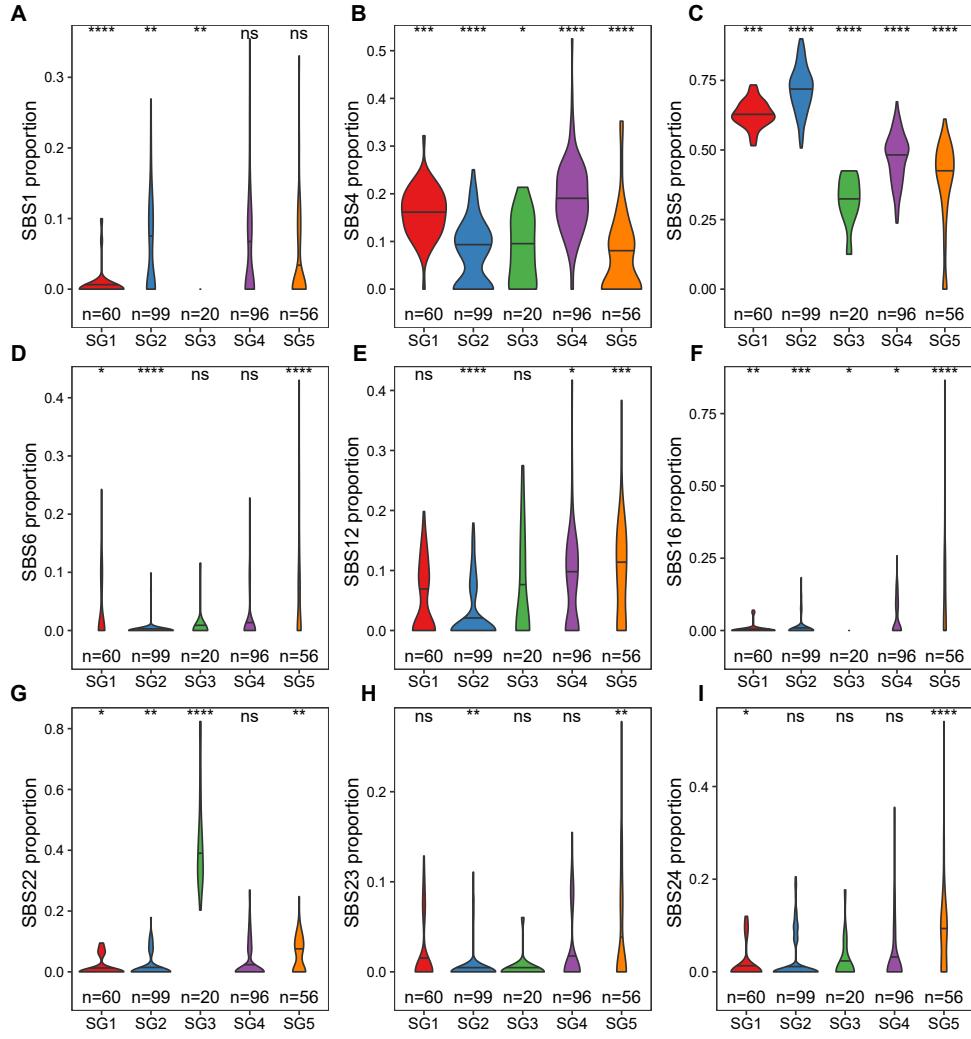
Figure S9: Comparison of mutational signature proportion across signature groups for A) SBS1 (aging), B) SBS4 (smoking), C) SBS5 (aging), D) SBS6 (MSI), E) SBS12 (liver related signature), F) SBS16 (liver related signature), G) SBS22 (aristolochic acid), H) SBS23 (unknown etiology), I) SBS24 (aflatoxin B1). In these comparisons, median value of the signature group was taken as the reference and stars indicates that the signature is significantly different from the median signature proportion across the cohort.
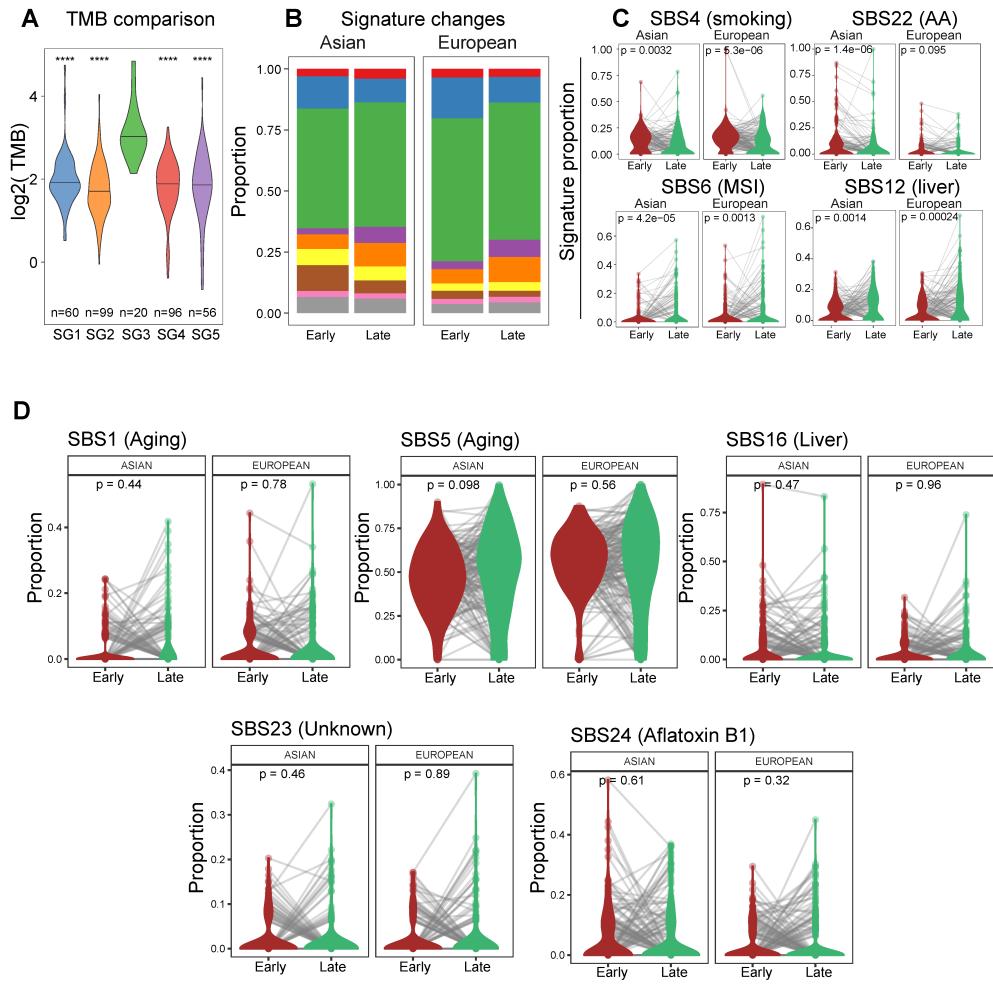
Figure S10: Summary of the signature subgroups. A) Comparison of TMB across signature groups. SG3 is the reference group in the Wilcoxon test and p-value $<= 0.001$ were labelled as "****", B) Proportions of mutational signatures in early (CCF>0.8) and late (CCF<0.8) mutations in the Asian (left) and European (right) cohorts, C) Violin plots for signatures with significant differences in their proportions between early and late mutations, D)Signatures with similar timing between the Asian and European cohorts.

Multivariate linear model for arm SCNA

| Variable | | N | Estimate | Confidence interval | p–value |
|---|---|---|---|---|---|
| **Race** | ASIAN | 140 | | ref | |
| | EUROPEAN | 155 | | −0.10 (−0.18, −0.02) | 0.0203 |
| **Age** | | 295 | | 0.00 (−0.00, 0.00) | 0.1510 |
| **Gender** | FEMALE | 99 | | ref | |
| | MALE | 196 | | −0.03 (−0.10, 0.04) | 0.3577 |
| **Stage** | I | 148 | | ref | |
| | II | 65 | | 0.08 (−0.00, 0.16) | 0.0565 |
| | III | 77 | | 0.07 (−0.01, 0.15) | 0.0866 |
| | IV | 5 | | 0.22 (−0.03, 0.46) | 0.0874 |
| **Viral Status** | HBV+ | 89 | | ref | |
| | HCV+ | 35 | | 0.00 (−0.12, 0.12) | 0.9975 |
| | HEPB−C | 6 | | −0.03 (−0.26, 0.19) | 0.7632 |
| | NBNC | 165 | | 0.01 (−0.08, 0.10) | 0.8687 |
| **Purity** | | 295 | | 0.28 (0.12, 0.45) | <0.001 |
| *TP53* | wt | 211 | | ref | |
| | mut | 84 | | 0.17 (0.10, 0.24) | <0.001 |

Estimate axis: −0.2 −0.1 −0.0 0.1 0.2 0.3 0.4

Figure S11: Multivariate linear model comparing arm level SCNA between Asians and Europeans. Multivariate analysis between arm level SCNA and the ethnic background controlling for a collection of clinical variables and driver genes.

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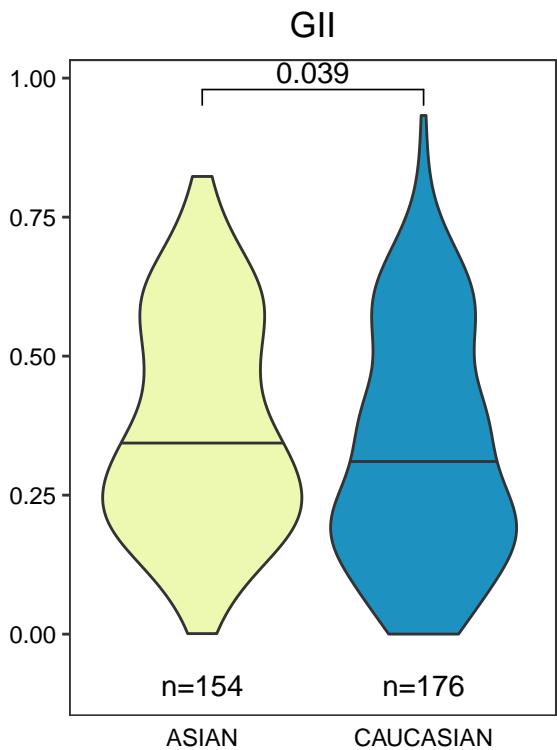
Figure S12: Genomic instability index (GII) differences between Asians and Europeans. Violin plots for GII values between the two cohorts

Multivariate linear model for GII

| Variable | | N | Estimate | Confidence interval | p−value |
|---|---|---|---|---|---|
| **Race** | ASIAN | 140 | | ref | |
| | EUROPEAN | 155 | | −0.05 (−0.11, 0.01) | 0.1121 |
| **Age** | | 295 | | 0.00 (−0.00, 0.00) | 0.5589 |
| **Gender** | FEMALE | 99 | | ref | |
| | MALE | 196 | | −0.02 (−0.07, 0.03) | 0.4526 |
| **Stage** | I | 148 | | ref | |
| | II | 65 | | 0.06 (0.01, 0.12) | 0.0316 |
| | III | 77 | | 0.05 (−0.01, 0.11) | 0.0837 |
| | IV | 5 | | 0.23 (0.05, 0.41) | 0.0125 |
| **Viral status** | HBV+ | 89 | | ref | |
| | HCV+ | 35 | | −0.01 (−0.09, 0.08) | 0.8752 |
| | HEPB−C | 6 | | −0.01 (−0.17, 0.16) | 0.9198 |
| | NBNC | 165 | | 0.04 (−0.03, 0.10) | 0.2773 |
| **purity** | | 295 | | −0.09 (−0.21, 0.03) | 0.1234 |
| *TP53* | wt | 211 | | ref | |
| | mut | 84 | | 0.11 (0.06, 0.16) | <0.001 |

Figure S13: Multivariate linear model comparing GII between Asians and Europeans. Regression analysis between GII and the ethnic background controlling for a collection of clinical variables and driver genes.

Figure S14: Focal SCNA comparison between Asian and European cohorts. Violin plots for focal SCNA values between the two cohorts

**A**

ASIAN

EUROPEAN

Cophenetic correlation

Consensus silhouette

rank (number of subtypes)

**B**

Consensus matrix for subtypes 2:4

rank = 2    rank = 3    rank = 4

rank = 2    rank = 3    rank = 4

1  0.8  0.6  0.4  0.2  0

**C**

Heatmap of overlapping top variable genes in both cohort (n= 2450)

Subtypes
Race

matrix_2
4
2
0
-2
-4

**Subtypes**
P1
P2
M1
M2

**Race**
ASIAN
EUROPEAN
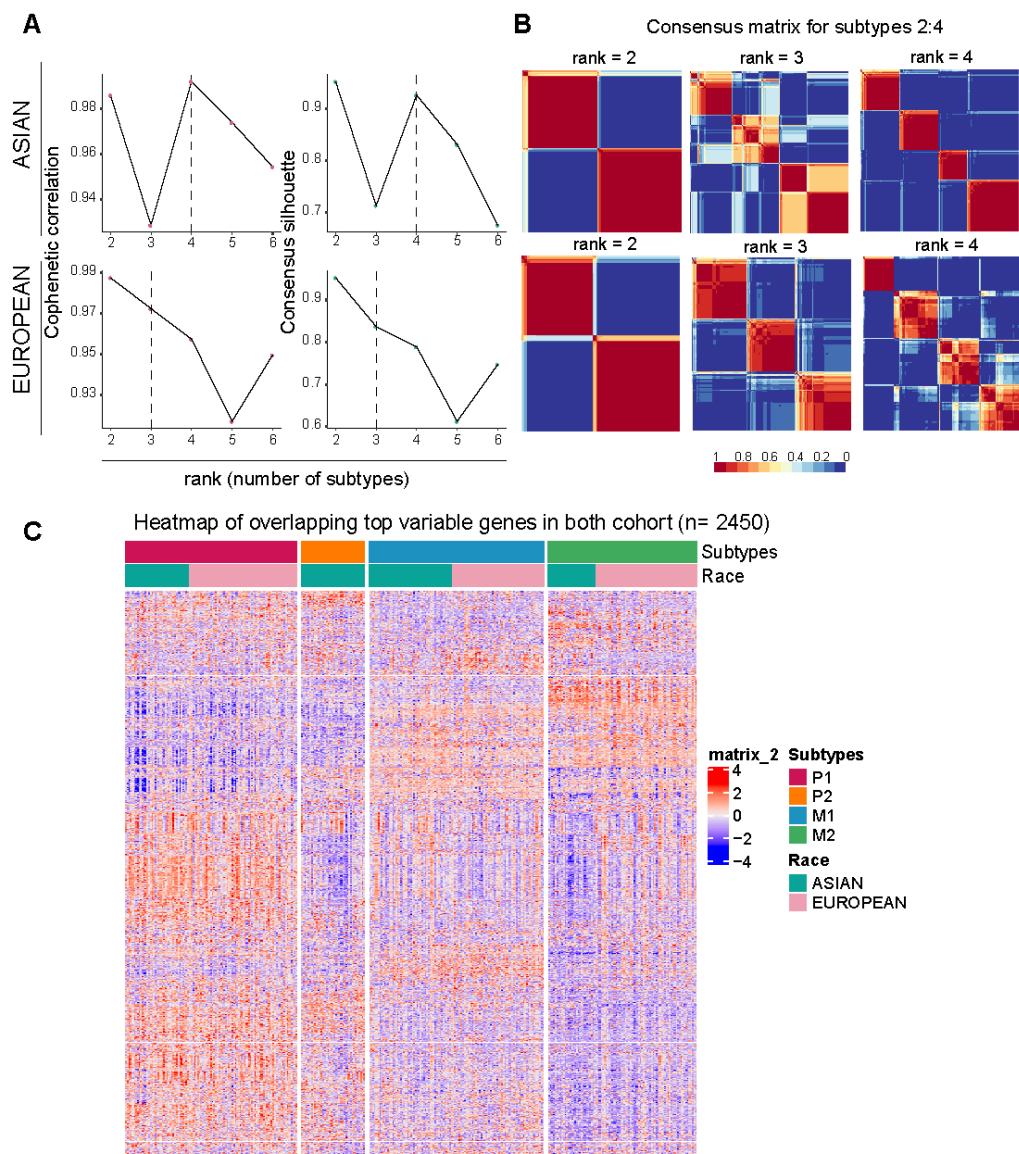
Figure S15: Clustering stability analysis for the two cohorts. A) Cophenetic correlation and silhouette values across the ranks (number of clusters, n=2-4) for Asians (top) and Europeans (bottom), B) Consensus matrix that that shows robustness of subtypes. When patients were assigned to the same subtype across multiple runs of NMF (n=200), they were plotted with a red color (coefficient =1). Top panels are for the Asian cohort and the bottom panels are for the European cohort. C) Heatmap for normalized expression of top most variable genes across identified subtypes. Overlapping genes between Asian and European top 3000 most variable genes are shown (n=2450).
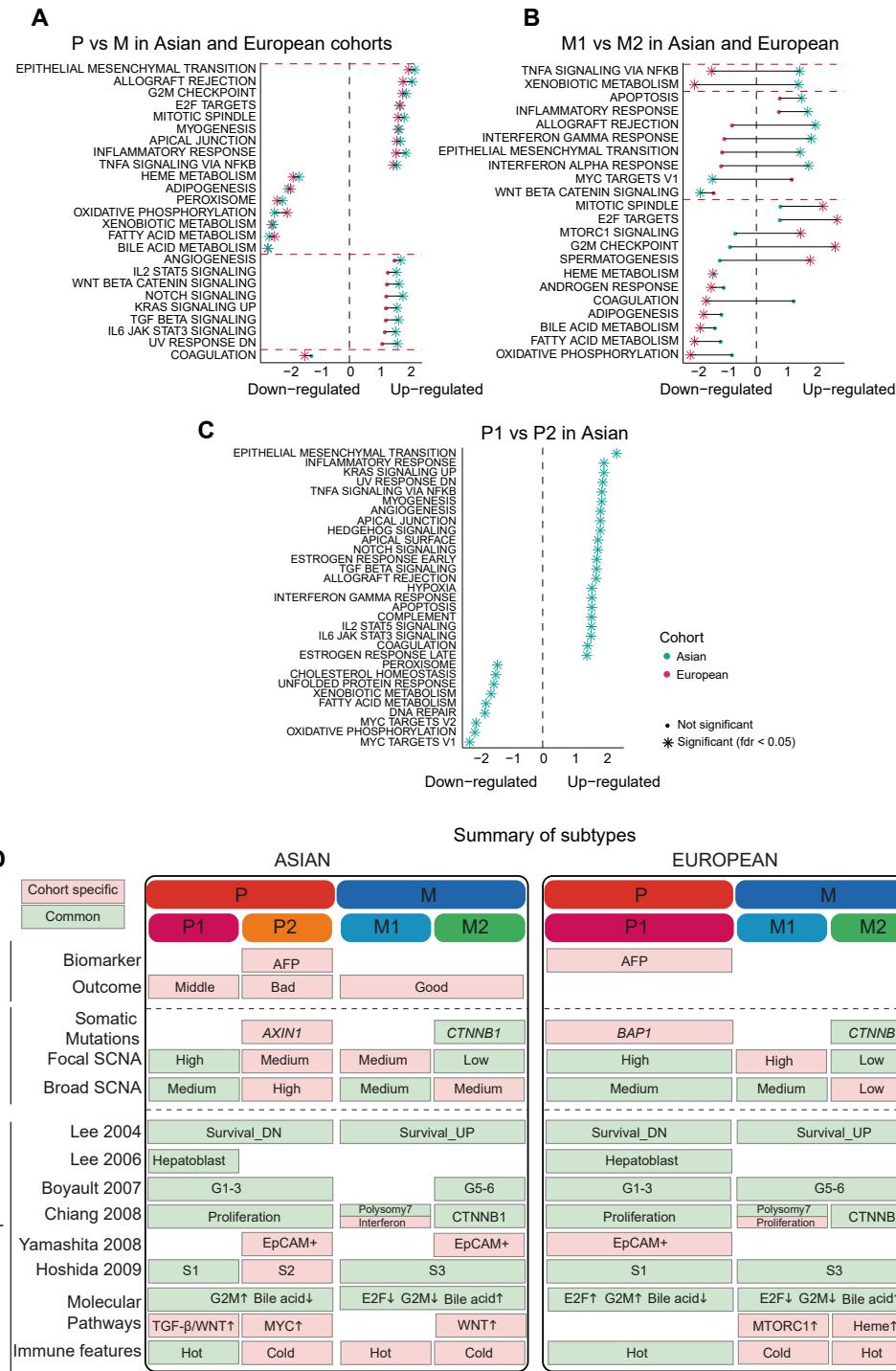
Figure S16: Pathway enrichment analysis for different subtypes in the Asian and European cohorts. A) Comparison between P and M in both Asian and European cohorts, significant pathways were marked with a *, green color represents Asians and pink color is used for Europeans, B) Comparison between M1 and M2 in both Asian and European cohorts, significant pathways were marked with a *, green color represents Asians and pink color is Europeans, C) Comparison between P1 and P2 in the Asian cohort, D) Summary of molecular subtypes and comparison of subtype features. Similar features between two cohorts are shown with a green color while cohort specific features are shown in pink blocks. Corresponding transcriptomic subtypes from the literature are shown in the "transcriptomic" section.
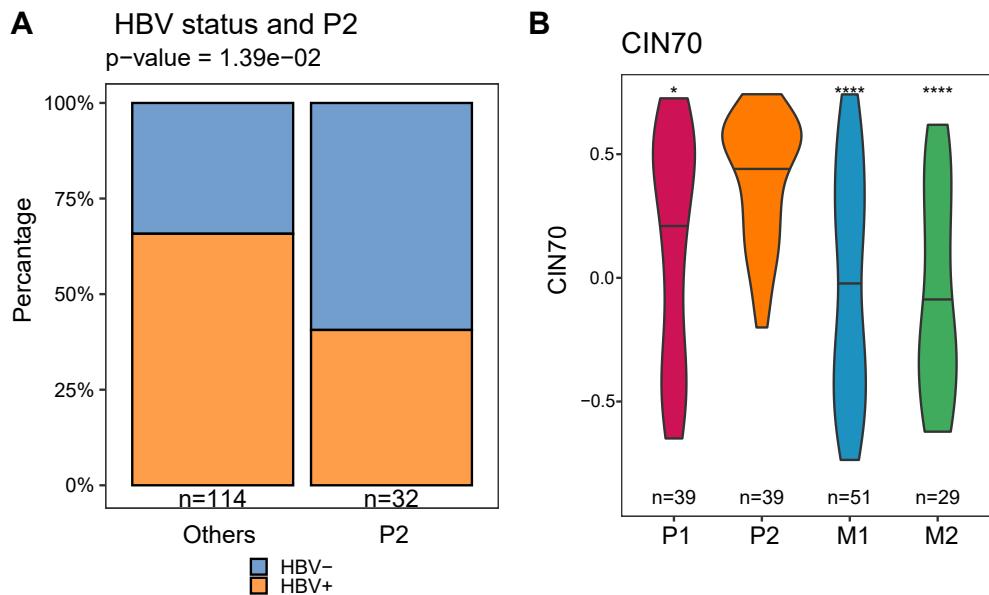
Figure S17: A) Comparison of HBV status between P2 and the rest of the subtypes. B) CIN70 signature gene expression across RNA subtypes. Vioin plot for the CIN70 score across the subtypes. P2 was used as the reference group in the Wilcoxon's rank sum test. * and **** represent p-value < 0.05 and 0.0001.
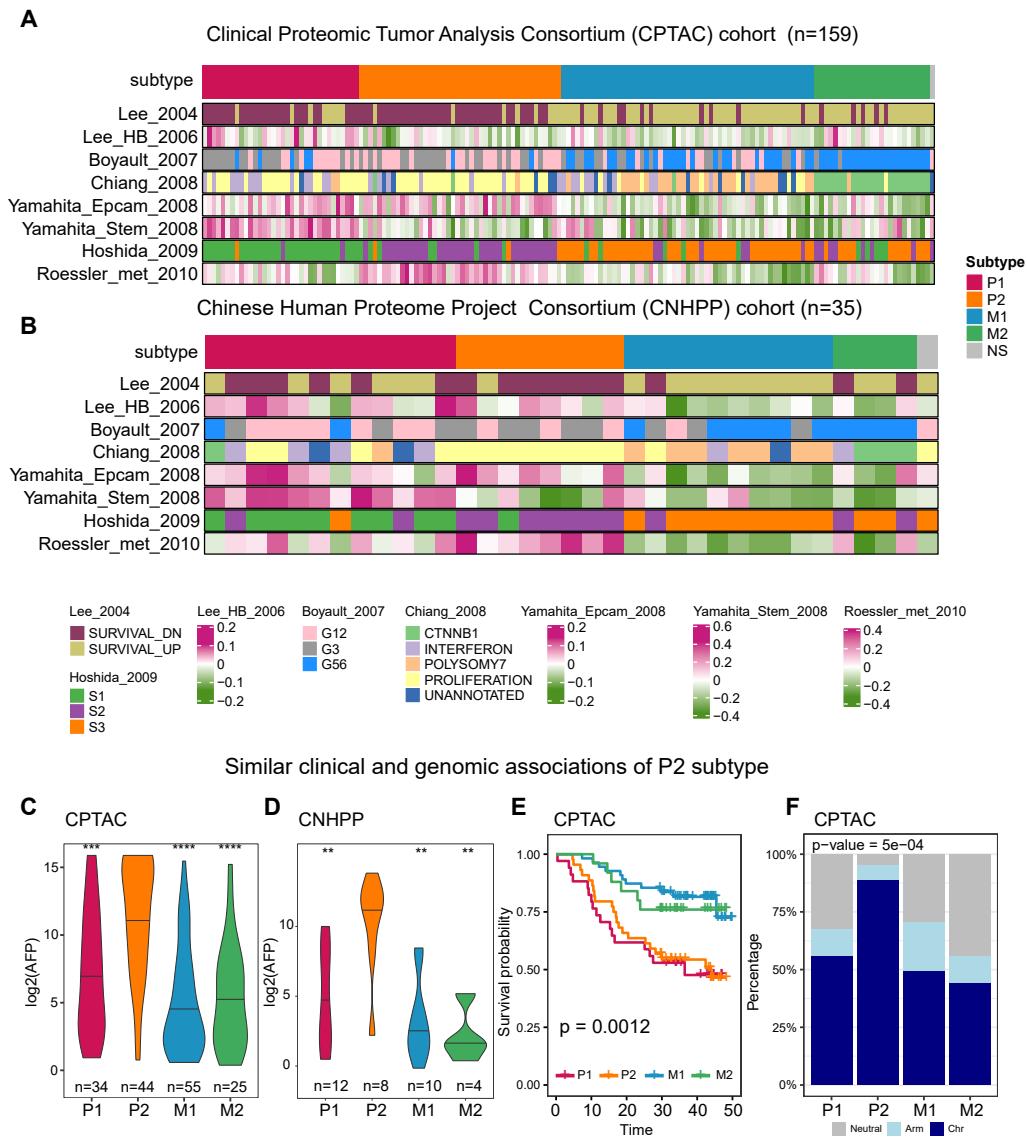
Figure S18: Assignment of patients from the external Chinese cohorts Clinical Proteomic Tumor Analysis Consortium (CPTAC) and the Chinese Human Proteome Project Consortium (CNHPP) to the Asian subtypes (P1, P2, M1 and M2). Similarity of assigned subtypes to literature subtype for A) CPTAC cohort and B) CNHPP cohort. Comparison of AFP levels between subtypes for C) CPTAC cohort and D) CNHPP cohort. P2 was used as the reference group in the Wilcoxon's rank sum test. * and **** represent p-value $< 0.05$ and 0.0001. E) Survival comparison between subtypes in the CPTAC cohort. F) Comparison of chromosome 16 deletion frequencies across assigned subtypes in CPTAC cohort.
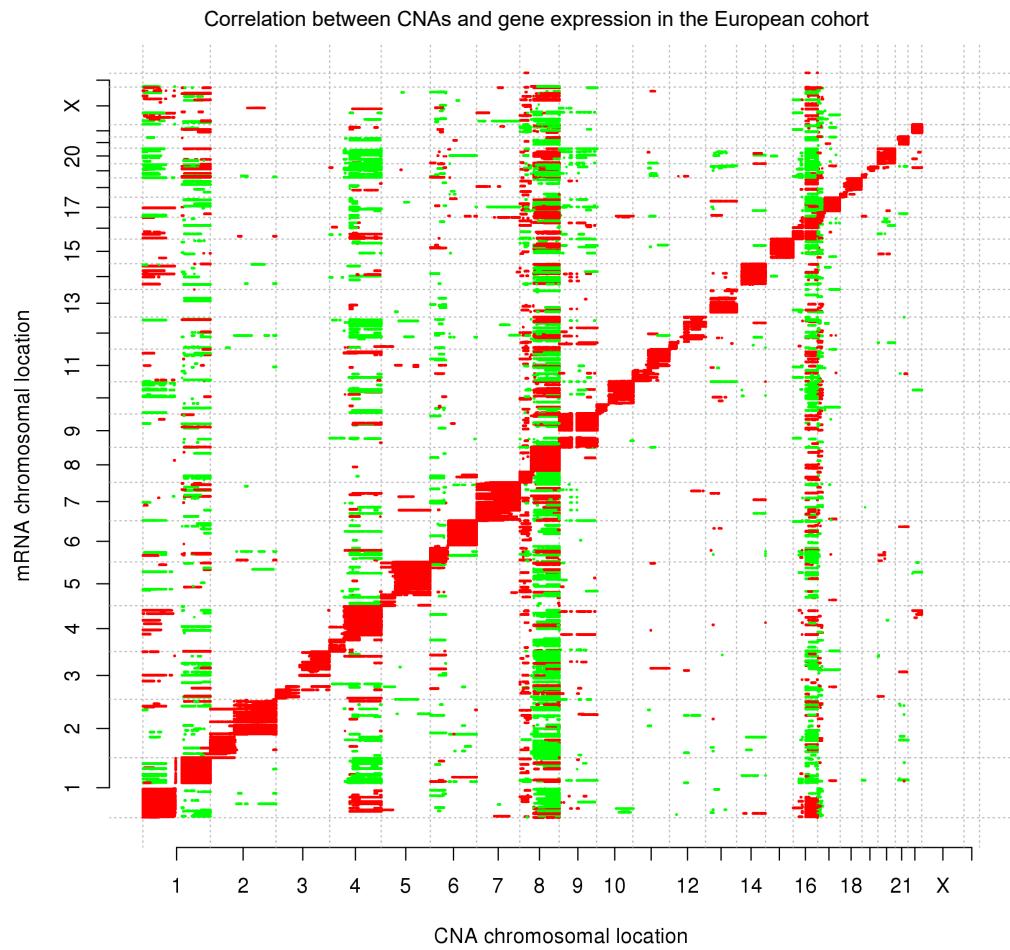
Figure S19: Correlation between copy number alterations (x axis) and mRNA expression (y axis) across the genome in the European cohort. Red color represents a significant positive correlation and green color indicates a significant negative correlation.
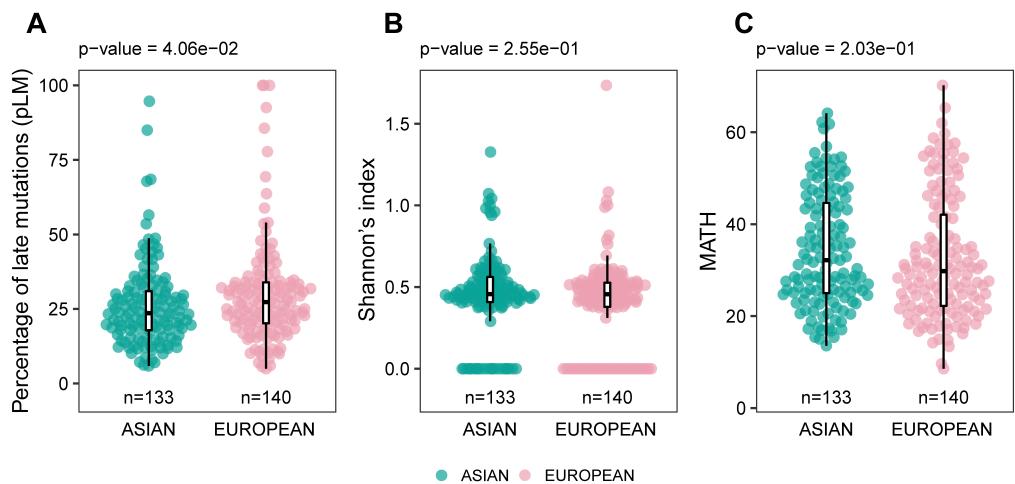
Figure S20: Comparison of multiple ITH features between Asian and European cohorts. A) Violin plot for the percentage of late mutations (pLM) between Asian and European cohorts. B) Violin plot for the Shannon's index between Asian and European cohorts. C) Violin plot for the MATH score between Asian and European cohorts.
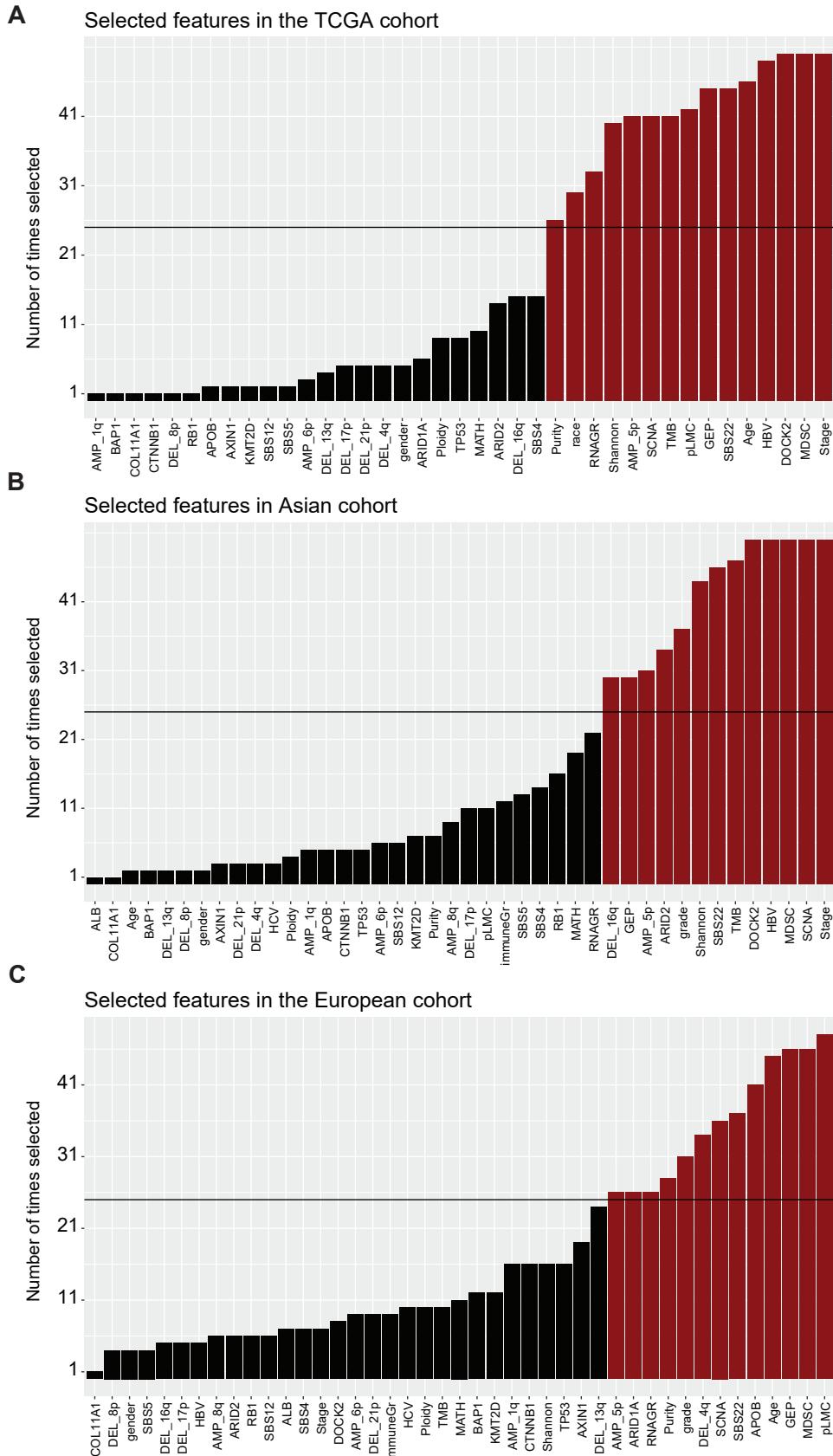
Figure S21: Importance of selected features from the random forest model. Ranking of different features in the A) TCGA, B) the Asian Cohort, C) the European cohorts. Red color represents selected features which have been selected in least 25 times across all runs (n=50)
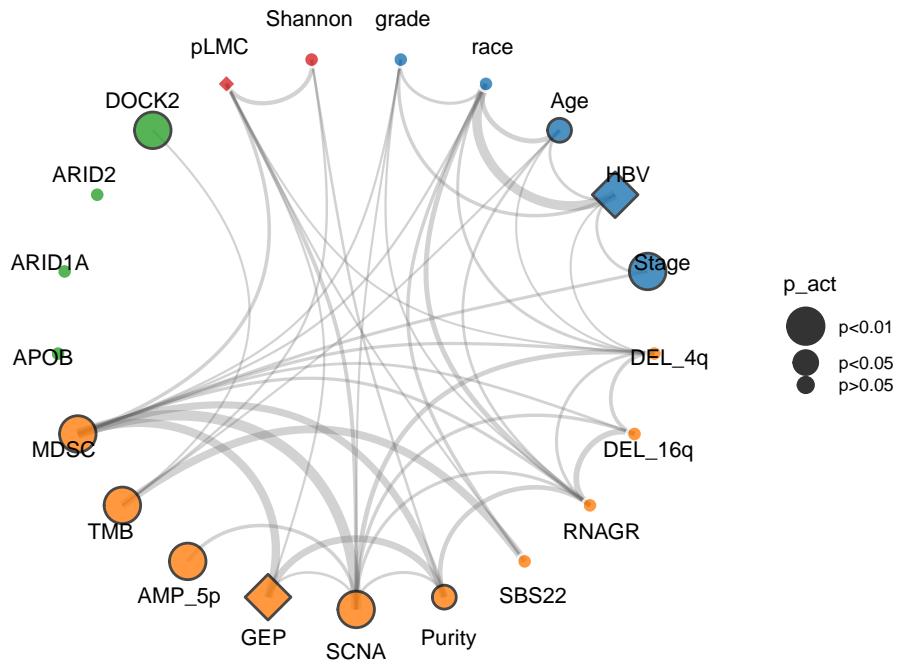
Figure S22: Correlation networkfor the variables that can stratify patients in the combined TCGA cohort. Edges of the network indicate the significance of correlation between features with the width of edges proportional to the re-scaled p-values (-log10(p)). Diamonds represent hazard ratios (HR) less than 1 (good prognosis) and circles represent HRs greater than 1 (poor prognosis). For features with multiple levels such as stage, HR of the most significant level was chosen. The black border around the nodes and size indicates its significance of the variable in the univariate Cox model.
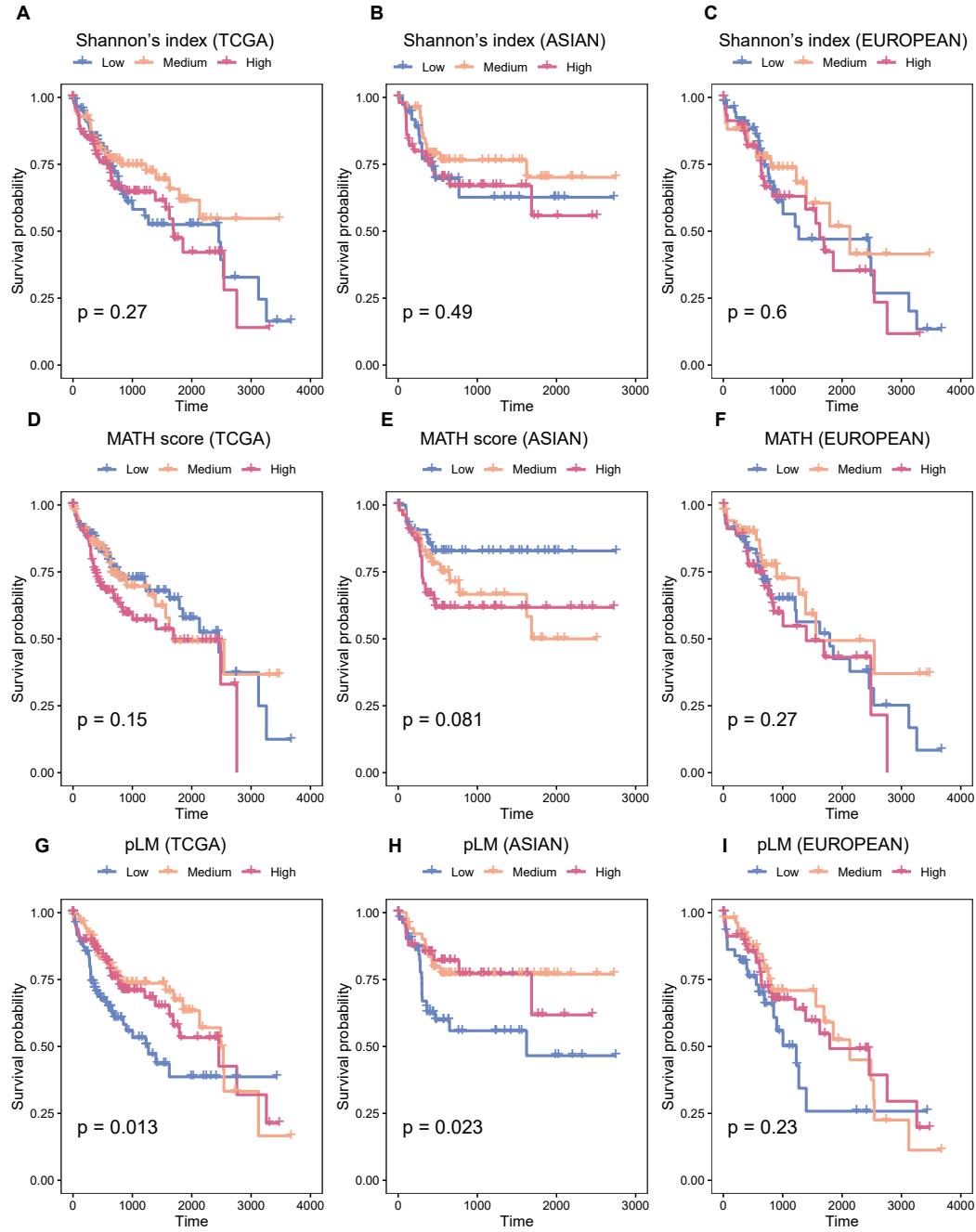
Figure S23: Survival analysis using ITH metrics in the TCGA cohort. Survival curves using the Shannon's index in A) the combined TCGA cohort, B) the Asian cohort, C) the European cohort, Survival curves for MATH score in D) the combined TCGA cohort, E) the Asian cohort, F) the European cohort. Survival curves for percentage of late mutations (pLM) in G) the combined TCGA cohort, H) the Asian cohort, I) the European cohort.

**Supplementary Note 1: Integrative driver identification and pathway enrichment**

After quality control including removing hyper-mutated samples (greater than 1000 coding mutations, n = 11), the final dataset comprised of 1,349 HCC patients. In the combined driver identification cohort (n = 1,349), 31% of the patients are Europeans (French and TCGA European cohort, n = 179), most of the patients are Asians. Of the disease etiology, 362 (27%) patients are HBV positive and 273 (20%) patients are HCV positive, 13 patients are HBV+HCV infected (1%) and 430 patients are non-viral (non B or C) (32%) (Table S3). Among 129,292 single nucleotide variants (SNV) and 7,242 indels, 62.5% of the SNVs are missense and 23.8% are silent mutations (Figure S4A). While the mutation burden is highly variable across patients, the mutation type and rate (median 2.87/Mb) are similar across cohorts (Figure S4B-D).

Using three different identification tools, we discovered 62 driver genes. Large proportion of these genes (n = 13, 21%) including several classical driver genes such as *TP53*, *CTNNB1* and *DYRK1A* were identified by all three methods. In order to understand the novelty of these drivers. Among these genes, most of them were previously reported as driver gene except for *DYRK1A*. *DYRK1A* phosphorylates a component of DREAM complex (LIN52) which induce quiescence in cells and can be an important driver gene for HCC [1]. In addition to common drivers, a significant amount of driver genes was found in only a subset of methods which can be attributed to distinct features of driver genes captured by different methods (Table S4-S5, Figure S6A). In order to understand the novelty of drivers, a total of 88 literature reported drivers were curated from eight earlier studies (Table S1) and Cancer Gene Census (CGC). 33 genes overlap between literature drivers and our driver list (Figure S6B). Among the novel drivers (n = 29), 9 genes were found in the Cancer Gene Census (CGC) indicated in other cancer types (Figure S5, S6B, Supplementary Table 5). For example, *ATRX* is associated with

alternative lengthening of telomerase (ALT) which can lead to synthesis of telomeres without telomerase in sarcomas [2]. In addition to identification of the driver genes, TUSON Explorer and 20/20+ calculate the probability of oncogene (OG) or tumor suppressor gene (TSG) for each driver. In total, 30 candidate driver genes were classified as TSG and 9 candidate drivers were classified as OG. This list includes known oncogenes such as *CTNNB1*, *PI3KCA*, *NFE2L2*, *KRAS*, *EEF1A1* and *SF3B1* as well as new HCC oncogenes such as *IDH1*, *KCNN3* and *CRIP3* are novel HCC drivers. Among novel oncogenes, *KCNN3* encodes for SK3 protein which is a calcium-dependent potassium channel. The proliferative effect of activation of K channels has been reported by earlier studies and the inhibition of SK3 current can stop invasiveness of breast and colorectal cancer cells [3,4].

In order to explore the correlation between drivers and patient clinical phenotypes, we carried out the association analysis. When correlating driver genes with patient cohorts, only *KCNN3* was significantly enriched in a specific cohort (TCGA, 3.3%) in both univariate and multivariate models (Figure S6C, Fisher's test q value < 0.1). In general, many drivers tend to occur in patients with higher mutational burden and older age (above 63) such as *APOB* and *ALB* (Figure S6C). HBV positive tumors tend to have more *TP53* mutations (Figure S6C). One of the most frequently mutated driver gene *CTNNB1* shows the highest number of correlations. It is found to be correlated with older age, male gender as well as non-HBV etiology. Among novel drivers, *DOCK2* and *DYRK1A* mutations are associated with higher mutation burden and *HNF1A* is enriched in Europeans (Figure S6C).

Since carcinogenesis depends on gaining a full collection of hallmarks associated with cancer, drivers with similar functions from the same pathway may occur exclusively with each other. On the other hand, genetic changes with complementary functional roles might act synergistically and tend to co-occur in the same patient. By testing the association between the driver mutations, we identified 11 pairs of co-occurrence relationship and 2 pairs of mutual

exclusivities after multiple testing correction (Fisher's test q value < 0.1) (Figure S6D). For example, *CTNNB1* and *AXIN1*, activators of the WNT pathway, tend to occur mutually exclusively across patients. On the contrary, multiple driver pairs tends to co-occur. For example, *CTNNB1* and *NFE2L2*, oncogenes of the WNT and the oxidative stress pathways tend to co-occur in many patients, suggesting synergistic effect between these pathways in HCC.

Previous studies have identified several recurrently altered pathways such as WNT signalling, chromatin remodelling, growth factor signalling, TP53/cell cycle [5,6] . In order to identify frequently perturbed pathways, we conducted gene set enrichment analysis of 62 driver genes using g:Profiler [7]  (based on Fisher's Exact test on the ranked gene list) and ConsensusPathDB [8]  (based on the hypergeometric test). After combining pathways with similar function, 23 pathways were identified (13 from g:Profiler and 23 pathways from ConsensusPathDB,  Figure S6E). In order to compare the list of pathways against previously published findings, we compiled a list of significantly perturbed pathways from 7 different studies[5,9–14] and compared with our list. As expected, classical cancer related pathways such as WNT, TP53/cell cycle and hypoxia were among pathways that were previously reported. In addition, we also identified 6 novel pathways including thyroid hormone signalling and hemostasis.

19 of novel HCC drivers were found to be in 17 known pathways (Figure S6E). For example, several novel drivers such as *TLE1, TNRC6B, APC, KMT2D* and *HNF1A* were found in the classical WNT pathway. In addition, 6 novel pathways include genes from both known and new drivers. 14 of previously known HCC drivers were found to be in 6 novel pathways (*e.g.* *PIK3CA* and *ALB*). Finally, 9 novel genes were found to be involved in the novel pathways. For example, *DOCK2*, *VAV3* and *TF* novel driver are involved in hemostasis (Figure S6E).

Similar to the observation in the combined cohort (n = 1349), most of the driver genes have similar frequencies in two cohorts except that *TP53, RB1* and *CDKN2A* have a significantly higher frequency in Asians, but *EEF1A1* occurs more frequently in Europeans (p-value < 0.05, Figure 1F). However, after multiple test correction, only *TP53* and *CDKN2A* remain significant (q-value = 0.016 and 0.08 respectively, Table S7).

**Supplementary Note 2: Saturation analysis of driver genes**

With larger cohort size, we were able to identify many driver genes that are in relative low frequency in the cohorts. In order to understand the relationship between sample size and the number of identified drivers, we down sample the cohort to various subsets and identified driver genes using MutSigCV. Interestingly, we found that the number of driver genes increased linearly with the sample size and has not reach saturation (Figure S7A). Since common drivers are easily detectable using small cohorts, we further break down the drivers according to their frequencies. Drivers above 5% were detected at a sample size around a few hundred samples and drivers in the range of 2-5% will be found around 1,000 samples (Figure S7A). The number of extremely rare drivers (f < 2%) has not yet reached saturation and is still rapidly increasing with sample size. In addition, we showed that these rare drivers tend to be late in the history of tumorigenesis (Fig S7B). Since not all regions of the tumor will have these subclonal rare mutations, it might harder to detect with small sample size. These indicate that there are many extremely rare drivers for HCC not yet found and this might explain the observation that a large proportion (14.6%) of the HCC patients have no driver genes identified.

**Supplementary Note 3: Positive selection in driver genes**

Positively selected driver genes in the history of tumorigenesis tend to have higher nonsynonymous mutation rate with more loss-of-function (*e.g.* truncating mutations) mutations in tumor suppressor genes and gain of function missense mutations in oncogenes. To test the

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existence and type (truncating vs missense) of positive selection, we calculated the somatic rate of non-synonymous to synonymous mutations ($d_N/d_S$) for all the driver genes using dNdScv [15]. As expected, 90% of driver genes were positively selected with a significant $d_N/d_S > 1$ and most of them (45%) have a significant $d_N/d_S$ ratio based only on truncated mutations indicating putative tumor suppressor roles (q value < 0.1, Figure S7D, S7D, Table S6). While 22 of drivers have significant $d_N/d_S$ ratio for both truncating and missense mutations, 9 of them only have significance missense $d_N/d_S$ ratios which implies that those drivers are likely to be oncogenes. When we plot truncated vs missense $d_N/d_S$ values we can see the separation of well-known tumor suppressor genes (*e.g. AXIN1, TP53*) and oncogenes (*e.g. CTNNB1*) (Figure S7G). Interestingly, well known tumor suppressor gene *TP53* is significant in both truncating and missense $d_N/d_S$ values because inactivation for *TP53* can be achieved by truncating mutations, deletions as well as hotspot missense changes in the DNA binding residues such as R249 (Figure S7G). Since oncogenes tend to have nonsynonymous gain-of-function mutations while tumor suppressor genes (TSG) often have truncating mutations spread across functional domains, a significant truncating $d_N/d_S$ value will be a good indicator of TSG while significant missense $d_N/d_S$ values often occur in oncogenes.

**Supplementary Note 4: Collection and timing of mutational signatures**

Several signatures (n = 10) including clock-like signatures (SBS1 and SBS5), smoking (SBS4), DNA mismatch repair (SBS6), aristolochic acid (AA) and aflatoxin B1 exposure (SBS22 and SBS24), liver cancer associated signatures (SBS12 and SBS16) and two signatures with unknown etiology (SBS17 and SBS23) have been identified in HCC [16–18].

To understand the timing of these mutational events along the history of tumorigenesis, we calculated the cancer cell fractions (CCF) for all mutations and deconvoluted signatures separately for early (CCF ≥ 0.8) and late mutations (CCF < 0.8, Figure S10B). Interestingly, the proportion of smoking (SBS4) and AA (SBS22) signatures were significantly lower in the

late stage of tumorigenesis compared to early mutations in both cohorts (Figure 10C). On the other hand, MSI and liver associated signatures SBS6 and SBS12 have higher proportions in the late stages of tumorigenesis, suggesting their active role throughout HCC initiation and progression (Figure S10C). Interestingly other signatures do not show a significant proportion difference between early and late mutations (Figure S10D).

**Supplementary Note 5: RNA subtype comparison across ethnic backgrounds**

A literature review revealed a list of RNA subtypes (n = 7) with varying levels of consistency between multiple cohorts [19–28]. For example, Hoshida et al (2009) described one well-recognized subtyping of HCC, including two subtypes (S1 and S2) with bad prognosis and one with good prognosis (S3) [23]. Boyault *et al.* identified six molecular subtypes (G1-G6) using patients of European descent with different levels of overlap with other RNA subtypes[22] .

Looking across molecular events for all the subtypes, we found that molecular differences between the basal split in P and M are highly similar to subsequent divergence in M1 and M2. This is true in both Asian and European cohorts. For example, *CTNNB1* mutation are highly enriched in subgroup M and M2 in both cohorts. This implies potential connections between genomic events happened in DNA and the transcriptomic changes in RNA. In general, we observed stronger genomic correlations in Europeans as compared with Asians (Figure 3F). For example, both arm and focal level SCNA scores, GII as well as genome doubling (GD) proportions are higher in P and M1 subtypes compared to M and M2 subtypes respectively in the European cohort.

Mapping the literature subtypes together with the molecular events onto the subtype ontology, we found both highly concordant and divergent events across the two cohorts. On one hand, we found good concordance between subtypes identified earlier using different ethnic populations. For example, the basal partition of P and M matches very well with the survival groups found in Lee et al 2004 [24]. Hoshida S1/S2 and S3 match with P1/P2 and M subgroups

in Asians, with S2 (P2) subtype not found in Europeans. The 6 subtypes found in Boyault et al 2007 [22] have a partial overlap in both Asian and European cohorts with G5/G6 subtypes matching well to subtype G in Asians and G2 in Europeans. In addition to molecular convergence, we also found features unique to specific ethnic background. For example, Yamashita EpCAM subtype [20] matches to P2 subtype in Asians, but P subtypes in Europeans. (Figure S16D). The integrative analysis between the two cohorts identified important ethnic similarities and differences between the two cohorts, providing an important base integrating information across multiple studies and ethnic backgrounds.

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**Table S1: Driver genes collected from the literature**

| Driver | Cleary_et_al (2013) | Kan_et_al (2013) | Totoki_et_al (2014) | Ahn_et_al (2014) | Schulze_et_al (2015) | Fujimato_et_al (2016) | TCGA (2017) | Chaudhary_et_al (2019) | #of_studies |
|---|---|---|---|---|---|---|---|---|---|
| TP53 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 8 |
| CTNNB1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 8 |
| AXIN1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 7 |
| RPS6KA3 | 0 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 6 |
| RB1 | 0 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 6 |
| NFE2L2 | 0 | 0 | 1 | 0 | 1 | 1 | 1 | 1 | 5 |
| CDKN2A | 0 | 0 | 1 | 0 | 1 | 1 | 1 | 1 | 5 |
| ARID1A | 0 | 0 | 1 | 0 | 1 | 1 | 1 | 1 | 5 |
| ARID2 | 0 | 0 | 1 | 0 | 1 | 1 | 1 | 0 | 4 |
| ACVR2A | 0 | 0 | 1 | 0 | 1 | 1 | 1 | 1 | 5 |
| ALB | 0 | 0 | 0 | 1 | 1 | 1 | 1 | 1 | 5 |
| KEAP1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 3 |
| BRD7 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 0 | 2 |
| CCND1 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 0 | 2 |
| PTEN | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 0 | 2 |
| CDKN1A | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 2 |
| APOB | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 2 |
| G6PC | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 0 | 2 |
| RPL22 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | 2 |
| LRP1B | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 2 |
| BAP1 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 2 |
| COL11A1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| AHCTF1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 |
| MEN1 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 |
| IL6ST | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 |
| RP1L1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 |
| SETDB1 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 |
| TMEM51 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| CDKN2B | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 |
| PER3 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 |
| EYS | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 |
| BRD9 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| MUC17 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 |
| GPATCH4 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 |
| ERGIC1 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 |
| CACNA2D4 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| KRAS | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 |
| ADRA1A | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 |

| Gene | | | | | | | | | Gene | |
|---|---|---|---|---|---|---|---|---|---|---|
| ADCY2 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | ADCY2 | 1 |
| WDTC1 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | WDTC1 | 1 |
| LZTR1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | LZTR1 | 1 |
| CPS1 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | CPS1 | 1 |
| CDKN1B | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | CDKN1B | 1 |
| CPA2 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | CPA2 | 1 |
| JAK1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | JAK1 | 1 |
| TSC1 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | TSC1 | 1 |
| TMEM170A | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | TMEM170A | 1 |
| TMEM99 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | TMEM99 | 1 |
| GJA1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | GJA1 | 1 |
| HNF4A | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | HNF4A | 1 |
| CYP2E1 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | CYP2E1 | 1 |
| PIK3CA | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | PIK3CA | 1 |
| FAM5C | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | FAM5C | 1 |
| TSC2 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | TSC2 | 1 |
| NCOR1 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | NCOR1 | 1 |
| KRTAP5-11 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | KRTAP5-11 | 1 |
| SLC10A1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | SLC10A1 | 1 |
| FGF19 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | FGF19 | 1 |
| TTC28 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | TTC28 | 1 |
| ASH1L | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | ASH1L | 1 |
| HIST1H1C | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | HIST1H1C | 1 |
| MAP2K3 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | MAP2K3 | 1 |
| TBL1XR1 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | TBL1XR1 | 1 |
| GALNT11 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | GALNT11 | 1 |
| PRKACA | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | PRKACA | 1 |
| NSMCE2 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | NSMCE2 | 1 |
| SRCAP | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | SRCAP | 1 |
| EEF1A1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | EEF1A1 | 1 |
| SF3B1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | SF3B1 | 1 |
| IGSF3 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | IGSF3 | 1 |
| SMARCA4 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | SMARCA4 | 1 |
| EPS15 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | EPS15 | 1 |
| NRAS | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | NRAS | 1 |
| SELPLG | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | SELPLG | 1 |
| HNRNPA2B1 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | HNRNPA2B1 | 1 |
| FCRL1 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | FCRL1 | 1 |
| TERT | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | TERT | 1 |
| ESRRG | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | ESRRG | 1 |

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| PCMTD1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | | 1 |
| ATAD3B | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | | 1 |
| TTLL2 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | | 1 |
| AR | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | AR | 1 |
| VCX | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | VCX | 1 |
| MTAP | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | | 1 |
| AZIN1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | | 1 |
| CREB3L3 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | CREB3L3 | 1 |
| ADH1B | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | ADH1B | 1 |
| MACROD2 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | | 1 |

**Table S2: Study cohorts**

| Data source | Project name | Cohort | N_Samples* | Sequencing approach | Sequencing center | Hypermutated patients |
|---|---|---|---|---|---|---|
| TCGA | LIHC | TCGA | 373 | WES | Broad | 7 |
| ICGC | LIRI-JP | LIRI-JP | 270 | WES/WGS | RIKEN | 1 |
| ICGC | LINC-JP | LINC-JP | 244 | WES/WGS | National Cancer Center | 0 |
| ICGC | LICA-FR | French | 242 | WES | Institut National du Cancer | 1 |
| Ahn et al. 2014 | - | Korean | 231 | WES | Asan Bio-Resource Center, Korea | 2 |

\* Hypermutated patients whose total mutation number in coding regions is greater than 1000 were excluded from this study.

**Table S3: Summary of clinical features across cohorts**

|  | French | Korean | LIRI-JP | LINC-JP | TCGA | Total |
|---|---|---|---|---|---|---|
| **Age** | | | | | | |
| *Median (range)* | 65 (17-90) | 55 (26-80) | 69 (31-89) | 66 (23-85) | 61 (16-90) | 63 (16-90) |
| **Gender** | | | | | | |
| *Male* | 190 | 174 | 201 | 182 | 246 | 993 |
| *Female* | 47 | 55 | 68 | 62 | 120 | 352 |
| *Missing* | 4 | 0 | 0 | 0 | 0 | 4 |
| **Tumor Stage** | | | | | | |
| *Early* | 127 | 229 | 163 | 85 | 254 | 858 |
| *Late* | 55 | 0 | 106 | 110 | 89 | 360 |
| *Missing* | 59 | 0 | 0 | 49 | 23 | 131 |
| **Etiology** | | | | | | |
| *HBV* | 31 | 167 | 66 | NA | 99 | 363 |
| *HCV* | 59 | 21 | 145 | NA | 48 | 273 |
| *HBV+HCV* | 2 | 0 | 4 | NA | 7 | 13 |
| *NBNC* | 143 | 41 | 53 | NA | 193 | 430 |
| *Missing* | 6 | 0 | 1 | 244 | 19 | 270 |
| **Ethnicity** | | | | | | |
| *European* | 241 | 0 | 0 | 0 | 179 | 420 |
| *Asian* | 0 | 229 | 269 | 244 | 159 | 901 |
| *Missing* | 0 | 0 | 0 | 0 | 28 | 28 |

Table S4: Significantly mutated genes from three methods

### MUTSIGCV

| gene | expr | reptime | hic | N_nonsilent | N_silent | N_noncoding | n_nonsilent | n_silent | n_noncoding | nnei | x | X | p | q | Frequency |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| TP53 | 2069567 | 213 | 34 | 4167061 | 1150697 | 0 | 401 | 6 | 0 | 3 | 8 | 3499306 | 1.18E-14 | 5.41E-12 | 0.286879 |
| CTNNB1 | 305811 | 448 | 8 | 7549004 | 2188078 | 0 | 407 | 10 | 0 | 5 | 18 | 6855618 | 5.44E-15 | 2.62E-12 | 0.283173 |
| APOB | 222162 | 698 | -11 | 43727835 | 12136953 | 0 | 147 | 24 | 0 | 6 | 34 | 18056365 | 4.20E-07 | 1.72E-04 | 0.107487 |
| ARID1A | 975965 | 182 | 27 | 21581302 | 6480596 | 0 | 137 | 3 | 0 | 1 | 4 | 9370154 | 1.32E-14 | 5.93E-12 | 0.0919199 |
| ALB | 315782 | 613 | 8 | 6115017 | 1525719 | 0 | 129 | 7 | 0 | 4 | 13 | 5445913 | 0 | 0 | 0.0889548 |
| ARID2 | 820796 | 602 | 10 | 17469550 | 5145086 | 0 | 112 | 8 | 0 | 0 | 8 | 5145086 | 0 | 0 | 0.0733877 |
| AXIN1 | 1444992 | 205 | 40 | 8215410 | 2424153 | 0 | 95 | 3 | 0 | 50 | 109 | 119319050 | 0 | 0 | 0.0674574 |
| COL11A1 | 37620 | 742 | -20 | 18165634 | 5476940 | 0 | 72 | 12 | 0 | 13 | 32 | 19515983 | 9.45E-06 | 3.64E-03 | 0.0622683 |
| NFE2L2 | 372300 | 145 | 36 | 5872197 | 1550001 | 0 | 67 | 2 | 0 | 50 | 65 | 72286165 | 0 | 0 | 0.0437361 |
| RPS6KA3 | 242944 | NaN | 36 | 7418151 | 1918278 | 0 | 65 | 0 | 0 | 8 | 13 | 13123072 | 0 | 0 | 0.0429948 |
| TSC2 | 1722112 | 181 | 44 | 17369724 | 5253006 | 0 | 56 | 5 | 0 | 45 | 55 | 73029464 | 0 | 0 | 0.0422535 |
| DOCK2 | 94542 | 680 | 33 | 18520421 | 4543432 | 0 | 53 | 8 | 0 | 20 | 27 | 32309899 | 5.88E-08 | 2.47E-05 | 0.0422535 |
| RB1 | 349930 | 450 | 41 | 9318892 | 2380985 | 0 | 59 | 1 | 0 | 50 | 72 | 85283780 | 0 | 0 | 0.0407709 |
| SETD2 | 593886 | 365 | 46 | 24742009 | 6731510 | 0 | 42 | 7 | 0 | 50 | 63 | 75418543 | 2.93E-05 | 1.10E-02 | 0.0348406 |
| ACVR2A | 90992 | 951 | -2 | 5100569 | 1301785 | 0 | 49 | 2 | 0 | 50 | 101 | 77648440 | 0 | 0 | 0.0348406 |
| KEAP1 | 1996822 | 207 | 30 | 5949090 | 1719975 | 0 | 44 | 4 | 0 | 13 | 17 | 19011457 | 0 | 0 | 0.0340993 |
| BAP1 | 1078407 | 229 | 62 | 7075505 | 2046433 | 0 | 35 | 3 | 0 | 45 | 46 | 67630766 | 0 | 0 | 0.0252039 |
| CDKN2A | 225405 | 357 | -15 | 3217365 | 837729 | 0 | 30 | 1 | 0 | 38 | 59 | 57654911 | 0 | 0 | 0.02298 |
| SF3B1 | 736523 | 276 | 30 | 12804708 | 3524937 | 0 | 29 | 2 | 0 | 30 | 43 | 59716183 | 9.59E-05 | 3.07E-02 | 0.0222387 |
| NEFH | 723458 | 203 | 35 | 9637256 | 2815363 | 0 | 25 | 9 | 0 | 19 | 30 | 24933567 | 6.27E-05 | 2.19E-02 | 0.0222387 |
| VAV3 | 132139 | 554 | -11 | 8707795 | 2117930 | 0 | 28 | 1 | 0 | 24 | 47 | 45565173 | 7.93E-05 | 2.65E-02 | 0.0214974 |
| BRD7 | 303953 | 520 | 14 | 6612798 | 1582377 | 0 | 29 | 1 | 0 | 16 | 24 | 28903674 | 5.55E-15 | 2.62E-12 | 0.0214974 |
| PTEN | 259678 | 300 | 34 | 4084772 | 949696 | 0 | 28 | 2 | 0 | 10 | 9 | 9917848 | 4.44E-11 | 1.95E-08 | 0.0207561 |
| HNF1A | 1225663 | 380 | 40 | 5947174 | 1879157 | 0 | 35 | 4 | 0 | 50 | 50 | 67672585 | 0 | 0 | 0.0207561 |
| IL6ST | 317374 | 438 | 51 | 9070676 | 2329723 | 0 | 24 | 3 | 0 | 50 | 75 | 88791180 | 0 | 0 | 0.0200148 |
| TF | 489558 | 523 | 26 | 6936558 | 1809009 | 0 | 25 | 2 | 0 | 50 | 73 | 71738471 | 0 | 0 | 0.0192735 |
| TSC1 | 1919560 | 461 | 33 | 11353184 | 3131029 | 0 | 23 | 1 | 0 | 22 | 11 | 28177912 | 2.96E-08 | 1.27E-05 | 0.017791 |
| DYRK1A | 314682 | 366 | 47 | 7767542 | 2038339 | 0 | 23 | 0 | 0 | 13 | 15 | 20894661 | 1.18E-06 | 4.74E-04 | 0.0170497 |
| HNF4A | 769430 | 376 | 16 | 5172066 | 1469061 | 0 | 21 | 2 | 0 | 41 | 60 | 64750651 | 0 | 0 | 0.0163084 |
| CDKN1A | 904665 | 228 | 37 | 1529766 | 505875 | 0 | 20 | 1 | 0 | 11 | 14 | 19271814 | 0 | 0 | 0.0155671 |
| CYP2E1 | 563924 | 525 | -10 | 4822675 | 1312577 | 0 | 18 | 1 | 0 | 50 | 81 | 67346127 | 0 | 0 | 0.0148258 |
| KCNN3 | 1958370 | 559 | 34 | 7021545 | 2059923 | 0 | 19 | 4 | 0 | 32 | 23 | 44179750 | 8.98E-05 | 2.92E-02 | 0.0140845 |
| ERRFI1 | 387339 | 207 | 26 | 4368062 | 1301785 | 0 | 20 | 3 | 0 | 12 | 22 | 16587304 | 5.11E-05 | 1.82E-02 | 0.0140845 |
| RPL22 | 627248 | 240 | 31 | 1317973 | 304874 | 0 | 18 | 0 | 0 | 50 | 52 | 69759488 | 0 | 0 | 0.0133432 |
| HNRNPA2 | 915230 | 445 | 43 | 3581595 | 894387 | 0 | 18 | 2 | 0 | 15 | 25 | 18614851 | 3.18E-05 | 1.18E-02 | 0.0133432 |
| SELPLG | 448698 | 280 | 40 | 3630159 | 1295040 | 0 | 15 | 3 | 0 | 28 | 39 | 39423176 | 0 | 0 | 0.0126019 |
| SLC30A1 | 380154 | 236 | 22 | 4734990 | 1448826 | 0 | 17 | 1 | 0 | 50 | 60 | 76292695 | 0 | 0 | 0.0118606 |
| ZFP36L1 | 543449 | 259 | 46 | 3128331 | 1003656 | 0 | 14 | 2 | 0 | 50 | 65 | 70474458 | 0 | 0 | 0.0111193 |
| KRAS | 259193 | 512 | 16 | 2312186 | 557137 | 0 | 15 | 1 | 0 | 35 | 52 | 48174139 | 9.87E-05 | 3.10E-02 | 0.0111193 |
| FRG1 | 49764 | 1059 | -15 | 2676416 | 605701 | 0 | 18 | 0 | 0 | 50 | 140 | 99007157 | 0 | 0 | 0.0111193 |
| ADH1B | 332785 | 854 | 8 | 3644998 | 1057616 | 0 | 14 | 0 | 0 | 21 | 32 | 28395101 | 7.79E-05 | 2.65E-02 | 0.0111193 |
| PHF10 | 233648 | 447 | 3 | 5004790 | 1247825 | 0 | 12 | 2 | 0 | 27 | 53 | 56342334 | 1.12E-04 | 3.47E-02 | 0.0103781 |
| HP | 438866 | 372 | 19 | 3988993 | 1057616 | 0 | 14 | 0 | 0 | 5 | 11 | 16993353 | 8.02E-05 | 2.65E-02 | 0.0103781 |
| CRIP3 | 1293543 | 363 | 51 | 2073413 | 528808 | 0 | 20 | 0 | 0 | 28 | 46 | 42007860 | 0 | 0 | 0.0103781 |
| CELF1 | 1011926 | 219 | 40 | 5162623 | 1316624 | 0 | 15 | 2 | 0 | 45 | 60 | 76343957 | 0 | 0 | 0.0103781 |
| IRF2 | 207866 | 400 | 55 | 3488514 | 890340 | 0 | 11 | 2 | 0 | 50 | 67 | 77957361 | 0 | 0 | 0.00963677 |
| EFNB2 | 167697 | 1267 | 2 | 3245694 | 882246 | 0 | 12 | 1 | 0 | 50 | 50 | 67141079 | 2.14E-04 | 6.50E-02 | 0.00963677 |
| CDKN1B | 791330 | 136 | 44 | 1920976 | 527459 | 0 | 12 | 2 | 0 | 8 | 10 | 10144480 | 2.41E-06 | 9.49E-04 | 0.00889548 |
| FCN1 | 237562 | 489 | 35 | 3225459 | 882246 | 0 | 12 | 1 | 0 | 11 | 4 | 14751315 | 2.95E-04 | 8.83E-02 | 0.00815419 |
| CELA1 | 504747 | 239 | 33 | 2536120 | 729809 | 0 | 11 | 0 | 0 | 50 | 59 | 72392736 | 0 | 0 | 0.00815419 |
| HMBS | 1390854 | 195 | 58 | 3576199 | 1029287 | 0 | 11 | 0 | 0 | 28 | 25 | 39205987 | 4.25E-05 | 1.54E-02 | 0.0074129 |
| EFNA5 | 78424 | 628 | 21 | 2260924 | 584117 | 0 | 10 | 1 | 0 | 50 | 70 | 80307319 | 0 | 0 | 0.0074129 |
| FUBP1 | 373296 | 256 | 1 | 6359186 | 1787425 | 0 | 9 | 2 | 0 | 50 | 77 | 96649105 | 0 | 0 | 0.00667161 |
| EHD3 | 102236 | 884 | 15 | 5143737 | 1444779 | 0 | 8 | 2 | 0 | 50 | 84 | 77377291 | 0 | 0 | 0.00667161 |
| WDR5B | 416095 | 478 | 34 | 3132378 | 886293 | 0 | 9 | 1 | 0 | 50 | 60 | 61448299 | 0 | 0 | 0.00593032 |
| KRTAP4-1 | 996799 | 468 | -7 | 1246476 | 331854 | 0 | 8 | 0 | 0 | 50 | 74 | 64954350 | 0 | 0 | 0.00593032 |
| KIAA0040 | NaN | NaN | NaN | 967233 | 246867 | 0 | 8 | 0 | 0 | 50 | 173 | 150476903 | 0 | 0 | 0.00444774 |
| BAIAP2L1 | 609918 | 249 | 36 | 5077636 | 1349000 | 0 | 4 | 2 | 0 | 36 | 48 | 50532191 | 0 | 0 | 0.00370645 |
| SPATA3 | NaN | NaN | NaN | 1829244 | 562533 | 0 | 6 | 1 | 0 | 37 | 129 | 106227005 | 0 | 0 | 0.00296516 |
| NSUN3 | 85578 | 1378 | -9 | 3317191 | 903830 | 0 | 3 | 1 | 0 | 25 | 49 | 46324660 | 0 | 0 | 0.00222387 |
| NADK | 1511678 | 243 | 30 | 4380203 | 1224892 | 0 | 3 | 1 | 0 | 50 | 40 | 70571586 | 0 | 0 | 0.00222387 |
| MLF2 | 2816186 | 232 | 48 | 2468670 | 683943 | 0 | 4 | 0 | 0 | 50 | 85 | 95985397 | 0 | 0 | 0.00222387 |
| GNRH1 | 178665 | 515 | 21 | 917320 | 256310 | 0 | 2 | 0 | 0 | 50 | 57 | 78805882 | 0 | 0 | 0.00074129 |

### TUSON

| Gene | TSG q-value | OG q-value | Frequency |
|---|---|---|---|
| ACVR2A | 0.000659841 | 1 | 0.0348406 |
| ALB | 5.95E-16 | 1 | 0.0889548 |
| ARID1B | 8.20E-25 | 1 | 0.0200148 |
| AXIN1 | 7.39E-21 | 1 | 0.0674574 |
| BAP1 | 0.000799981 | 1 | 0.0252039 |
| BRD7 | 0.000118092 | 1 | 0.0214974 |
| CDKN2A | 0.006011515 | 1 | 0.02298 |
| CTNNB1 | 1 | 1.18E-05 | 0.283173 |
| DYRK1A | 0.017590403 | 1 | 0.0170497 |
| NFE2L2 | 1 | 0.025948703 | 0.0437361 |
| PTEN | 0.035324469 | 1 | 0.0207561 |
| RB1 | 4.78E-12 | 1 | 0.0407709 |
| RPS6KA3 | 2.09E-10 | 1 | 0.0429948 |
| TP53 | 1.57E-54 | 1 | 0.286879 |
| TSC1 | 0.07215699 | 1 | 0.017791 |
| TSC2 | 2.18E-06 | 1 | 0.0422535 |

### 20/20+

| Gene | oncogene qval | TSG qval | driver qval | Frequency |
|---|---|---|---|---|
| CTNNB1 | 0 | 1 | 0 | 0.283173 |
| TSC1 | 0.997869962 | 0.007692308 | 0.005263158 | 0.017791 |
| TSC2 | 0.999513824 | 0.007692308 | 0.005263158 | 0.0422535 |
| SETD2 | 0.997869962 | 0.007692308 | 0.005263158 | 0.0348406 |
| TP53 | 0.899661226 | 0.038095238 | 0.005263158 | 0.286879 |
| BAP1 | 0.997869962 | 0.007692308 | 0.005263158 | 0.0252039 |
| PIK3CA | 0 | 1 | 0.005263158 | 0.0244626 |
| KMT2B | 0.997869962 | 0.007692308 | 0.005263158 | 0.0244626 |
| BRD7 | 0.997869962 | 0.007692308 | 0.005263158 | 0.0214974 |
| ARID1A | 0.997869962 | 0.007692308 | 0.005263158 | 0.0919199 |
| RB1 | 0.997869962 | 0.007692308 | 0.005263158 | 0.0407709 |
| IDH1 | 0 | 1 | 0.005263158 | 0.0111193 |
| RPS6KA3 | 0.997869962 | 0.007692308 | 0.005263158 | 0.0429948 |
| NFE2L2 | 0 | 1 | 0.005263158 | 0.0437361 |
| AXIN1 | 0.997869962 | 0.007692308 | 0.005263158 | 0.0674574 |
| DYRK1A | 0.997869962 | 0.007692308 | 0.005263158 | 0.0170497 |
| ARID2 | 0.997869962 | 0.007692308 | 0.005263158 | 0.0733877 |
| KRAS | 0 | 1 | 0.005263158 | 0.0111193 |
| CDKN2A | 0.994321142 | 0.023529412 | 0.01 | 0.02298 |
| APC | 0.913981245 | 0.053571429 | 0.016 | 0.0303929 |
| KDM6A | 0.997869962 | 0.021428571 | 0.016 | 0.0126019 |
| PBRM1 | 0.997869962 | 0.027777778 | 0.016 | 0.0192735 |
| KMT2D | 0.997869962 | 0.023529412 | 0.016 | 0.0474426 |
| CYP2E1 | 0.997869962 | 0.036842105 | 0.023076923 | 0.0148258 |
| ATRX | 0.997732972 | 0.044 | 0.0296963 | 0.0200148 |
| TLE1 | 0.980085898 | 0.061764706 | 0.03030303 | 0.0126019 |
| EEF1A1 | 1 | 1 | 0.03030303 | 0.0207561 |
| ALB | 0.997869962 | 0.044 | 0.03030303 | 0.0889548 |
| CDKN1A | 0.997869962 | 0.038095238 | 0.03030303 | 0.0155671 |
| HNF1A | 0.997869962 | 0.05 | 0.038235294 | 0.0207561 |
| GSE1 | 0.997869962 | 0.044 | 0.042857143 | 0.0148258 |
| SRCAP | 0.990203507 | 0.061764706 | 0.051351351 | 0.0296516 |
| TNRC6B | 0.997869962 | 0.053571429 | 0.051351351 | 0.0259451 |
| RPL22 | 0.997869962 | 0.061764706 | 0.054761905 | 0.0133432 |
| SF3B1 | 0 | 0.999391117 | 0.070212766 | 0.0222387 |
| PTPN3 | 0.997869962 | 0.076315789 | 0.073469388 | 0.0155671 |
| NCOR1 | 0.865929204 | 0.193939394 | 0.073469388 | 0.0244626 |
| RAPGEF2 | 0.984367899 | 0.117307692 | 0.08 | 0.0103781 |
| ARID1B | 0.997869962 | 0.117307692 | 0.098275862 | 0.0200148 |

**Table S5: Concensus driver list and novel status**

| Gene | TUSON | MutSigCV | 2020plus | CGC | Reported | Status |
|------|-------|----------|----------|-----|----------|--------|
| APC | 0 | 0 | 1 | 1 | 0 | Novel |
| ARID1B | 1 | 0 | 1 | 1 | 0 | Novel |
| ATRX | 0 | 0 | 1 | 1 | 0 | Novel |
| CELF1 | 0 | 1 | 0 | 0 | 0 | Novel |
| CRIP3 | 0 | 1 | 0 | 0 | 0 | Novel |
| DOCK2 | 0 | 1 | 0 | 0 | 0 | Novel |
| DYRK1A | 1 | 1 | 1 | 0 | 0 | Novel |
| ERRFI1 | 0 | 1 | 0 | 0 | 0 | Novel |
| FRG1 | 0 | 1 | 0 | 0 | 0 | Novel |
| GSE1 | 0 | 0 | 1 | 0 | 0 | Novel |
| HNF1A | 0 | 1 | 1 | 1 | 0 | Novel |
| HP | 0 | 1 | 0 | 0 | 0 | Novel |
| IDH1 | 0 | 0 | 1 | 1 | 0 | Novel |
| KCNN3 | 0 | 1 | 0 | 0 | 0 | Novel |
| KDM6A | 0 | 0 | 1 | 1 | 0 | Novel |
| KMT2B | 0 | 0 | 1 | 0 | 0 | Novel |
| KMT2D | 0 | 0 | 1 | 1 | 0 | Novel |
| NEFH | 0 | 1 | 0 | 0 | 0 | Novel |
| PBRM1 | 0 | 0 | 1 | 1 | 0 | Novel |
| PHF10 | 0 | 1 | 0 | 0 | 0 | Novel |
| PTPN3 | 0 | 0 | 1 | 0 | 0 | Novel |
| RAPGEF2 | 0 | 0 | 1 | 0 | 0 | Novel |
| SETD2 | 0 | 1 | 1 | 1 | 0 | Novel |
| SLC30A1 | 0 | 1 | 0 | 0 | 0 | Novel |
| TF | 0 | 1 | 0 | 0 | 0 | Novel |
| TLE1 | 0 | 0 | 1 | 0 | 0 | Novel |
| TNRC6B | 0 | 0 | 1 | 0 | 0 | Novel |
| VAV3 | 0 | 1 | 0 | 0 | 0 | Novel |
| ZFP36L1 | 0 | 1 | 0 | 0 | 0 | Novel |
| ACVR2A | 1 | 1 | 0 | 1 | 1 | Reported |
| ADH1B | 0 | 1 | 0 | 0 | 1 | Reported |
| ALB | 1 | 1 | 1 | 0 | 1 | Reported |
| APOB | 0 | 1 | 0 | 0 | 1 | Reported |
| ARID1A | 0 | 1 | 1 | 1 | 1 | Reported |
| ARID2 | 0 | 1 | 1 | 1 | 1 | Reported |
| AXIN1 | 1 | 1 | 1 | 1 | 1 | Reported |
| BAP1 | 1 | 1 | 1 | 1 | 1 | Reported |
| BRD7 | 1 | 1 | 1 | 0 | 1 | Reported |
| CDKN1A | 0 | 1 | 1 | 1 | 1 | Reported |
| CDKN2A | 1 | 1 | 1 | 1 | 1 | Reported |
| COL11A1 | 0 | 1 | 0 | 0 | 1 | Reported |
| CTNNB1 | 1 | 1 | 1 | 1 | 1 | Reported |
| CYP2E1 | 0 | 1 | 1 | 0 | 1 | Reported |
| EEF1A1 | 0 | 0 | 1 | 0 | 1 | Reported |
| HNF4A | 0 | 1 | 0 | 0 | 1 | Reported |
| HNRNPA2B | 0 | 1 | 0 | 1 | 1 | Reported |
| IL6ST | 0 | 1 | 0 | 1 | 1 | Reported |
| KEAP1 | 0 | 1 | 0 | 1 | 1 | Reported |

| | | | | | | |
|---|---|---|---|---|---|---|
| KRAS | 0 | 1 | 1 | 1 | 1 | Reported |
| NCOR1 | 0 | 0 | 1 | 1 | 1 | Reported |
| NFE2L2 | 1 | 1 | 1 | 1 | 1 | Reported |
| PIK3CA | 0 | 0 | 1 | 1 | 1 | Reported |
| PTEN | 1 | 1 | 0 | 1 | 1 | Reported |
| RB1 | 1 | 1 | 1 | 1 | 1 | Reported |
| RPL22 | 0 | 1 | 1 | 1 | 1 | Reported |
| RPS6KA3 | 1 | 1 | 1 | 0 | 1 | Reported |
| SELPLG | 0 | 1 | 0 | 0 | 1 | Reported |
| SF3B1 | 0 | 1 | 1 | 1 | 1 | Reported |
| SRCAP | 0 | 0 | 1 | 0 | 1 | Reported |
| TP53 | 1 | 1 | 1 | 1 | 1 | Reported |
| TSC1 | 1 | 1 | 1 | 1 | 1 | Reported |
| TSC2 | 1 | 1 | 1 | 1 | 1 | Reported |

**Table S6: dNdScv results**

| gene_name | n_syn | n_mis | n_non | n_spl | n_ind | wmis_cv | wnon_cv | wspl_cv | wind_cv | pmis_cv | ptrunc_cv | pallsubs_c | pind_cv | qmis_cv | qtrunc_cv | qallsubs_cv | pglobal_cv | qglobal_cv | issignif_mis | issignif_trunc |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| CTNNB1 | 9 | 390 | 2 | 0 | 13 | 30.45708 | 1.94939 | 1.94939 | 1.817494 | 0 | 0.417982 | 0 | 0.189644 | 0 | 0.470230113 | 0 | 0 | 0 | 1 | 0 |
| KRAS | 1 | 15 | 0 | 0 | 0 | 10.00042 | 0 | 0 | 0 | 8.82E-07 | 0.602203 | 3.71E-06 | 1 | 1.11E-05 | 0.62194719 | 1.11E-05 | 5.01E-05 | 0.000137363 | 1 | 0 |
| PIK3CA | 2 | 34 | 0 | 0 | 0 | 4.826334 | 0 | 0 | 0 | 2.95E-05 | 0.251312 | 2.04E-05 | 1 | 0.000155 | 0.304473661 | 5.36E-05 | 0.000241158 | 0.000607717 | 1 | 0 |
| EEF1A1 | 5 | 27 | 0 | 0 | 0 | 4.531896 | 0 | 0 | 0 | 1.80E-05 | 0.363415 | 3.72E-05 | 1 | 0.000103 | 0.423983791 | 9.02E-05 | 0.000416982 | 0.00101038 | 1 | 0 |
| HNRNPA2B1 | 2 | 12 | 0 | 0 | 6 | 3.68723 | 0 | 0 | 1.853038 | 0.006588 | 0.38388 | 0.01185 | 0.200558 | 0.019598 | 0.439717475 | 0.015883482 | 0.016735751 | 0.025103627 | 1 | 0 |
| IDH1 | 1 | 15 | 0 | 0 | 0 | 4.724699 | 0 | 0 | 0 | 0.001001 | 0.492397 | 0.002495 | 1 | 0.003319 | 0.543467073 | 0.004136292 | 0.017448138 | 0.025563551 | 1 | 0 |
| SF3B1 | 2 | 28 | 0 | 1 | 0 | 3.590315 | 1.390097 | 1.390097 | 0 | 0.001338 | 0.769352 | 0.004817 | 1 | 0.004214 | 0.769351945 | 0.007225211 | 0.030517575 | 0.040906536 | 1 | 0 |
| TF | 2 | 16 | 0 | 1 | 7 | 3.095081 | 2.227982 | 2.227982 | 1.094857 | 0.011781 | 0.500335 | 0.041632 | 0.328446 | 0.030925 | 0.543467073 | 0.047687284 | 0.072365403 | 0.087673469 | 1 | 0 |
| SLC30A1 | 1 | 11 | 0 | 0 | 5 | 3.240331 | 0 | 0 | 1.076075 | 0.022088 | 0.551115 | 0.051822 | 0.34064 | 0.051069 | 0.578670658 | 0.057276801 | 0.088913879 | 0.101846807 | 1 | 0 |
| TP53 | 9 | 260 | 44 | 37 | 57 | 33.43668 | 113.3476 | 113.3476 | 15.81667 | 0 | 0 | 0 | 3.85E-05 | 0 | 0 | 0 | 0 | 0 | 1 | 1 |
| RPS6KA3 | 0 | 26 | 13 | 9 | 17 | 6.775784 | 53.76363 | 53.76363 | 2.508229 | 1.29E-05 | 0 | 0 | 0.116829 | 9.00E-05 | 0 | 0 | 0 | 0 | 1 | 1 |
| ARID1A | 4 | 32 | 28 | 7 | 68 | 2.476697 | 39.80203 | 39.80203 | 3.252139 | 0.012741 | 0 | 0 | 0.065105 | 0.032107 | 0 | 0 | 0 | 0 | 1 | 1 |
| CDKN2A.p16INK4a | 1 | 14 | 6 | 3 | 7 | 9.400846 | 104.5743 | 104.5743 | 4.874553 | 2.78E-06 | 9.91E-14 | 6.33E-15 | 0.038501 | 2.92E-05 | 8.92E-13 | 4.98E-14 | 8.99E-15 | 7.08E-14 | 1 | 1 |
| NFE2L2 | 2 | 57 | 2 | 0 | 8 | 12.16548 | 5.974582 | 5.974582 | 1.443291 | 4.55E-15 | 0.064515 | 4.54E-14 | 0.254311 | 9.56E-14 | 0.086477961 | 3.18E-13 | 3.82E-13 | 2.67E-12 | 1 | 1 |
| ALB | 6 | 31 | 4 | 5 | 67 | 4.207949 | 11.35164 | 11.35164 | 12.0083 | 1.55E-05 | 2.40E-06 | 1.39E-07 | 0.000296 | 9.74E-05 | 9.44E-06 | 6.04E-07 | 1.03E-09 | 5.87E-09 | 1 | 1 |
| CDKN2A.p14arf | 2 | 13 | 1 | 3 | 3 | 8.480843 | 42.48925 | 42.48925 | 2.466074 | 6.10E-06 | 7.36E-06 | 2.71E-08 | 0.168091 | 5.49E-05 | 2.73E-05 | 1.31E-07 | 9.20E-08 | 4.46E-07 | 1 | 1 |
| RPL22 | 0 | 7 | 2 | 3 | 4 | 8.427837 | 50.86905 | 50.86905 | 3.390055 | 0.000605 | 5.29E-07 | 1.44E-07 | 0.098729 | 0.002117 | 3.03E-06 | 6.04E-07 | 2.71E-07 | 1.14E-06 | 1 | 1 |
| CDKN1A | 1 | 11 | 5 | 0 | 7 | 6.205216 | 36.31413 | 36.31413 | 3.845753 | 0.000371 | 1.98E-06 | 4.04E-07 | 0.063681 | 0.001459 | 8.90E-06 | 1.41E-06 | 4.75E-07 | 1.87E-06 | 1 | 1 |
| CRIP3 | 0 | 16 | 3 | 0 | 1 | 11.31012 | 24.01032 | 24.01032 | 0.50151 | 4.59E-07 | 0.000633 | 1.60E-07 | 0.587637 | 7.23E-06 | 0.001534412 | 6.29E-07 | 1.61E-06 | 5.98E-06 | 1 | 1 |
| ACVR2A | 2 | 21 | 4 | 2 | 19 | 4.95619 | 15.3042 | 15.3042 | 4.041354 | 0.000114 | 2.68E-05 | 3.30E-06 | 0.043968 | 0.000512 | 8.88E-05 | 1.07E-05 | 2.43E-06 | 8.50E-06 | 1 | 1 |
| FRG1 | 0 | 11 | 1 | 5 | 1 | 6.961139 | 31.62983 | 31.62983 | 0.422121 | 0.000302 | 9.26E-07 | 3.14E-07 | 0.62016 | 0.001268 | 4.86E-06 | 1.16E-06 | 3.20E-06 | 1.06E-05 | 1 | 1 |
| DYRK1A | 0 | 12 | 5 | 2 | 4 | 2.991107 | 23.65111 | 23.65111 | 0.572405 | 0.040949 | 1.16E-06 | 6.86E-06 | 0.504536 | 0.083219 | 5.64E-06 | 1.96E-05 | 4.70E-05 | 0.000134468 | 1 | 1 |
| KEAP1 | 4 | 33 | 2 | 1 | 8 | 4.716855 | 6.35277 | 6.35277 | 1.399415 | 7.99E-06 | 0.02071 | 2.13E-05 | 0.262155 | 6.29E-05 | 0.031822219 | 5.36E-05 | 7.30E-05 | 0.000191738 | 1 | 1 |
| HNF1A | 5 | 19 | 1 | 4 | 7 | 2.684839 | 9.676925 | 9.676925 | 1.154306 | 0.010978 | 0.000563 | 0.000591 | 0.314608 | 0.03007 | 0.001419458 | 0.001283642 | 0.001782809 | 0.004102132 | 1 | 1 |
| COL11A1 | 11 | 59 | 1 | 7 | 3 | 2.844399 | 2.911227 | 2.911227 | 0.180312 | 7.56E-05 | 0.022916 | 0.00027 | 0.733975 | 0.000366 | 0.033574382 | 0.000630153 | 0.001888283 | 0.004102132 | 1 | 1 |
| PTEN | 2 | 13 | 2 | 1 | 12 | 3.566826 | 9.229142 | 9.229142 | 3.247404 | 0.006844 | 0.008201 | 0.003037 | 0.077003 | 0.019598 | 0.014453288 | 0.004905537 | 0.002188937 | 0.004596768 | 1 | 1 |
| VAV3 | 1 | 23 | 2 | 3 | 0 | 4.497824 | 8.350784 | 8.350784 | 0 | 0.000484 | 0.001911 | 0.000306 | 1 | 0.001792 | 0.00376173 | 0.000689451 | 0.00278555 | 0.005660957 | 1 | 1 |
| DOCK2 | 9 | 41 | 6 | 4 | 0 | 1.954805 | 4.924129 | 4.924129 | 0 | 0.026482 | 0.000448 | 0.001342 | 1 | 0.057529 | 0.001227242 | 0.002641448 | 0.010215378 | 0.017876911 | 1 | 1 |
| HNF4A | 2 | 13 | 2 | 1 | 5 | 3.146097 | 8.386384 | 8.386384 | 1.150834 | 0.014959 | 0.010744 | 0.00677 | 0.32334 | 0.036247 | 0.017812114 | 0.009478527 | 0.015595938 | 0.023964491 | 1 | 1 |
| ADH1B | 0 | 8 | 0 | 2 | 5 | 3.817001 | 12.46681 | 12.46681 | 1.453847 | 0.022697 | 0.016941 | 0.011147 | 0.26418 | 0.051069 | 0.0273657 | 0.015267227 | 0.02010709 | 0.028789697 | 1 | 1 |
| HP | 0 | 8 | 1 | 1 | 3 | 3.241289 | 9.934448 | 9.934448 | 0.740379 | 0.045623 | 0.02668 | 0.026574 | 0.450336 | 0.08982 | 0.036718758 | 0.032195149 | 0.064928696 | 0.081810157 | 1 | 1 |
| APOB | 23 | 89 | 8 | 0 | 45 | 1.565646 | 2.224987 | 2.224987 | 1.077962 | 0.034098 | 0.065916 | 0.050634 | 0.315771 | 0.071605 | 0.086514142 | 0.056963632 | 0.082116559 | 0.095802652 | 1 | 1 |
| ARID2 | 8 | 27 | 35 | 6 | 43 | 1.583567 | 29.37546 | 29.37546 | 2.560544 | 0.17365 | 0 | 0 | 0.106421 | 0.266827 | 0 | 0 | 0 | 0 | 0 | 1 |
| AXIN1 | 3 | 13 | 40 | 8 | 33 | 1.851751 | 81.63297 | 81.63297 | 4.180609 | 0.177991 | 0 | 0 | 0.03723 | 0.266986 | 0 | 0 | 0 | 0 | 0 | 1 |
| RB1 | 2 | 11 | 13 | 9 | 24 | 1.693618 | 30.36129 | 30.36129 | 2.824438 | 0.288705 | 0 | 0 | 0.09209 | 0.413373 | 0 | 0 | 0 | 0 | 0 | 1 |
| BRD7 | 1 | 5 | 12 | 3 | 8 | 1.184904 | 32.29545 | 32.29545 | 1.339409 | 0.788371 | 4.48E-13 | 1.92E-13 | 0.273381 | 0.82779 | 3.53E-12 | 1.21E-12 | 1.66E-12 | 1.05E-11 | 0 | 1 |
| TSC2 | 5 | 23 | 14 | 2 | 16 | 1.751647 | 13.92759 | 13.92759 | 0.967516 | 0.139113 | 3.75E-10 | 1.51E-09 | 0.350529 | 0.230635 | 2.63E-09 | 8.67E-09 | 1.19E-08 | 6.23E-08 | 0 | 1 |
| TSC1 | 1 | 9 | 10 | 1 | 3 | 1.477876 | 21.04405 | 21.04405 | 0.281535 | 0.476179 | 9.08E-09 | 1.74E-08 | 0.659857 | 0.588221 | 5.72E-08 | 9.12E-08 | 2.21E-07 | 9.95E-07 | 0 | 1 |
| TNRC6B | 8 | 13 | 11 | 0 | 5 | 0.715671 | 7.056031 | 7.056031 | 0.298062 | 0.405178 | 1.54E-05 | 3.40E-06 | 0.642145 | 0.554917 | 5.40E-05 | 1.07E-05 | 3.06E-05 | 9.38E-05 | 0 | 1 |
| BAP1 | 3 | 12 | 7 | 1 | 14 | 1.893379 | 14.5863 | 14.5863 | 2.096726 | 0.170471 | 2.34E-06 | 1.43E-05 | 0.156075 | 0.266827 | 9.44E-06 | 3.92E-05 | 3.13E-05 | 9.38E-05 | 0 | 1 |
| ERRFI1 | 3 | 6 | 4 | 0 | 10 | 1.293702 | 16.02889 | 16.02889 | 2.361323 | 0.644753 | 0.000307 | 0.001412 | 0.136185 | 0.72668 | 0.00092094 | 0.002694911 | 0.001837202 | 0.004102132 | 0 | 1 |
| SETD2 | 7 | 24 | 5 | 4 | 9 | 1.180003 | 5.849223 | 5.849223 | 0.383611 | 0.645938 | 0.000292 | 0.000868 | 0.585088 | 0.72668 | 0.000918533 | 0.001764761 | 0.004361764 | 0.008587223 | 0 | 1 |
| KDM6A | 2 | 6 | 3 | 3 | 3 | 0.758659 | 7.91666 | 7.91666 | 0.232781 | 0.632504 | 0.000883 | 0.00085 | 0.693314 | 0.72668 | 0.001989188 | 0.001764761 | 0.00496955 | 0.009487323 | 0 | 1 |
| CYP2E1 | 1 | 8 | 3 | 1 | 4 | 2.221382 | 15.06716 | 15.06716 | 0.885257 | 0.15357 | 0.000551 | 0.002077 | 0.396874 | 0.248075 | 0.001352156 | 0.003701113 | 0.00667784 | 0.012373644 | 0 | 1 |
| TLE1 | 3 | 6 | 4 | 1 | 4 | 0.918869 | 9.19844 | 9.19844 | 0.567208 | 0.878903 | 0.000884 | 0.002115 | 0.506696 | 0.893079 | 0.001989188 | 0.003701113 | 0.008399993 | 0.015119987 | 0 | 1 |
| APC | 8 | 20 | 7 | 1 | 6 | 0.876359 | 4.71889 | 4.71889 | 0.230652 | 0.719151 | 0.001861 | 0.002179 | 0.687425 | 0.781147 | 0.00376173 | 0.003709558 | 0.011238113 | 0.019135165 | 0 | 1 |
| KMT2D | 9 | 41 | 7 | 3 | 8 | 1.584574 | 4.929111 | 4.929111 | 0.157933 | 0.133166 | 0.000445 | 0.002078 | 0.746075 | 0.226742 | 0.001227242 | 0.003701113 | 0.011579227 | 0.01919714 | 0 | 1 |
| PHF10 | 2 | 3 | 4 | 0 | 5 | 0.708046 | 8.725532 | 8.725532 | 1.095484 | 0.619146 | 0.003377 | 0.006139 | 0.336029 | 0.72668 | 0.006446625 | 0.00879 | 0.014819136 | 0.02354283 | 0 | 1 |
| GSE1 | 5 | 4 | 3 | 1 | 7 | 0.367834 | 4.509915 | 4.509915 | 0.628329 | 0.081249 | 0.026314 | 0.004413 | 0.472134 | 0.150549 | 0.036718758 | 0.006807582 | 0.014947828 | 0.02354283 | 0 | 1 |
| PTPN3 | 1 | 12 | 2 | 3 | 4 | 2.23033 | 8.752955 | 8.752955 | 0.478465 | 0.114791 | 0.001561 | 0.005889 | 0.546058 | 0.200884 | 0.003277663 | 0.008628722 | 0.021674482 | 0.029947212 | 0 | 1 |
| CELF1 | 2 | 10 | 3 | 1 | 1 | 2.359675 | 10.77176 | 10.77176 | 0.21229 | 0.089204 | 0.00156 | 0.00443 | 0.733447 | 0.160567 | 0.003277663 | 0.006807582 | 0.021866218 | 0.029947212 | 0 | 1 |
| RAPGEF2 | 3 | 5 | 3 | 1 | 3 | 0.507277 | 4.648782 | 4.648782 | 0.218659 | 0.241522 | 0.026811 | 0.012475 | 0.703727 | 0.353858 | 0.036718758 | 0.016373464 | 0.050351027 | 0.066085723 | 0 | 1 |
| KMT2B | 5 | 17 | 5 | 1 | 3 | 1.122869 | 5.068462 | 5.068462 | 0.120761 | 0.777185 | 0.005045 | 0.014683 | 0.788416 | 0.82779 | 0.0093477 | 0.018877913 | 0.063192106 | 0.081246993 | 0 | 1 |

| | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| PBRM1 | | 3 | 11 | 4 | 1 | 8 | 1.016902 | 5.155611 | 5.155611 | 0.517535 | 0.972298 | 0.01029 | 0.02395 | 0.517867 | 0.972298 | 0.017520935 | 0.029585507 | 0.066849963 | 0.082579366 | 0 | 1 |
| ARID1B | | 7 | 13 | 5 | 0 | 3 | 0.733319 | 4.063142 | 4.063142 | 0.143226 | 0.451492 | 0.019852 | 0.019836 | 0.766589 | 0.586383 | 0.031267531 | 0.024993953 | 0.078861024 | 0.093740463 | 0 | 1 |
| SRCAP | | 7 | 25 | 5 | 1 | 4 | 1.307991 | 4.411561 | 4.411561 | 0.13535 | 0.450375 | 0.008259 | 0.030177 | 0.771522 | 0.586383 | 0.014453288 | 0.035870895 | 0.110825185 | 0.124678333 | 0 | 1 |
| ATRX | | 5 | 16 | 4 | 2 | 2 | 0.936193 | 3.679751 | 3.679751 | 0.087709 | 0.874544 | 0.021227 | 0.037007 | 0.828012 | 0.893079 | 0.031840792 | 0.043175332 | 0.137443233 | 0.151910942 | 0 | 1 |

**Table S7: Comparison of driver gene frequencies between Asian and European cohorts**

| Gene | Asian_percentage | European_percentage | p_value | q_value |
|---|---|---|---|---|
| CDKN2A | 6.451612903 | 0 | 3.83E-04 | 0.01646234 |
| TP53 | 36.77419355 | 23.49726776 | 0.00378959 | 0.0814762 |
| EEF1A1 | 1.290322581 | 7.650273224 | 0.02454249 | 0.26383182 |
| RB1 | 10.25641026 | 4.395604396 | 0.0225475 | 0.26383182 |
| BRD7 | 5.128205128 | 1.111111111 | 0.08678317 | 0.74633523 |
| AXIN1 | 11.53846154 | 7.142857143 | 0.11764858 | 0.78875208 |
| CDKN1A | 0.64516129 | 4.395604396 | 0.1284015 | 0.78875208 |
| BAP1 | 3.846153846 | 7.182320442 | 0.21224555 | 0.85080444 |
| HNF1A | 0.64516129 | 3.846153846 | 0.22241459 | 0.85080444 |
| PIK3CA | 5.161290323 | 2.222222222 | 0.2374338 | 0.85080444 |
| SETD2 | 5.806451613 | 2.777777778 | 0.18289269 | 0.85080444 |
| TSC1 | 0.64516129 | 2.777777778 | 0.22241459 | 0.85080444 |
| ACVR2A | 2.580645161 | 5 | 0.39578696 | 0.87265752 |
| APOB | 9.032258065 | 13.66120219 | 0.38056823 | 0.87265752 |
| ARID1B | 3.870967742 | 1.666666667 | 0.31187364 | 0.87265752 |
| GSE1 | 2.580645161 | 1.111111111 | 0.4209732 | 0.87265752 |
| KEAP1 | 6.369426752 | 3.333333333 | 0.42618158 | 0.87265752 |
| KRAS | 0.64516129 | 2.222222222 | 0.37826636 | 0.87265752 |
| PTEN | 2.580645161 | 1.111111111 | 0.4209732 | 0.87265752 |
| RAPGEF2 | 0.64516129 | 2.222222222 | 0.37826636 | 0.87265752 |
| TLE1 | 0.64516129 | 2.762430939 | 0.37826636 | 0.87265752 |
| ATRX | 1.290322581 | 3.846153846 | 0.45744733 | 0.88176251 |
| KMT2D | 6.451612903 | 4.972375691 | 0.47164041 | 0.88176251 |
| FRG1 | 4.516129032 | 2.777777778 | 0.557406 | 0.99868575 |
| ALB | 11.46496815 | 13.04347826 | 0.86101931 | 1 |
| APC | 2.580645161 | 3.867403315 | 0.75720162 | 1 |
| ARID1A | 8.974358974 | 7.73480663 | 0.68896113 | 1 |
| ARID2 | 6.451612903 | 6.043956044 | 0.63925841 | 1 |
| COL11A1 | 5.806451613 | 6.593406593 | 1 | 1 |
| CRIP3 | 2.564102564 | 2.197802198 | 0.66565381 | 1 |
| CTNNB1 | 28.125 | 29.12087912 | 0.62414148 | 1 |
| DOCK2 | 7.096774194 | 6.629834254 | 0.82587195 | 1 |
| IDH1 | 2.580645161 | 2.762430939 | 1 | 1 |
| IL6ST | 3.870967742 | 4.419889503 | 1 | 1 |
| KMT2B | 5.128205128 | 3.888888889 | 0.79124424 | 1 |
| NCOR1 | 3.205128205 | 2.209944751 | 0.70810996 | 1 |
| NFE2L2 | 3.225806452 | 3.867403315 | 1 | 1 |
| PBRM1 | 1.935483871 | 2.222222222 | 1 | 1 |
| RPS6KA3 | 5.128205128 | 4.444444444 | 1 | 1 |
| SF3B1 | 3.225806452 | 2.222222222 | 0.73790639 | 1 |
| SRCAP | 3.205128205 | 4.395604396 | 0.75720162 | 1 |
| TSC2 | 3.870967742 | 3.888888889 | 1 | 1 |
| VAV3 | 2.580645161 | 3.314917127 | 1 | 1 |

**Table S8: Proportions of individual signature across patients**

| Patient_ID | SBS1 | SBS4 | SBS5 | SBS6 | SBS12 | SBS16 | SBS22 | SBS23 | SBS24 |
|---|---|---|---|---|---|---|---|---|---|
| TCGA-2V-A95S | 0.06884551 | 0.08394755 | 0.7535272 | 0 | 0 | 0 | 0 | 0 | 0 |
| TCGA-2Y-A9GS | 0 | 0.26283705 | 0.15875992 | 0.24090937 | 0.13529064 | 0 | 0 | 0 | 0.15175082 |
| TCGA-2Y-A9GT | 0.06293926 | 0.09431173 | 0.53174189 | 0 | 0.15396987 | 0 | 0 | 0 | 0.1112014 |
| TCGA-2Y-A9GU | 0.10330835 | 0.1213315 | 0.48344681 | 0 | 0.14803499 | 0 | 0.06661407 | 0.07726428 | 0 |
| TCGA-2Y-A9GV | 0 | 0.15789406 | 0.51106262 | 0 | 0.06971816 | 0.11718115 | 0.14414401 | 0 | 0 |
| TCGA-2Y-A9GW | 0.10112499 | 0.07856702 | 0.37689565 | 0 | 0.18431157 | 0 | 0.07914458 | 0.10175042 | 0.07820578 |
| TCGA-2Y-A9GX | 0 | 0.11481175 | 0.82097358 | 0 | 0 | 0 | 0 | 0 | 0 |
| TCGA-2Y-A9GY | 0 | 0.16941713 | 0.67305343 | 0 | 0 | 0.08830349 | 0 | 0 | 0 |
| TCGA-2Y-A9GZ | 0 | 0.1243169 | 0.76365734 | 0 | 0 | 0 | 0 | 0 | 0.07209035 |
| TCGA-2Y-A9H0 | 0 | 0 | 0.77944958 | 0 | 0 | 0 | 0.07907148 | 0 | 0.09401366 |
| TCGA-2Y-A9H1 | 0 | 0.11632339 | 0.54869583 | 0 | 0.13151178 | 0 | 0 | 0.06395962 | 0 |
| TCGA-2Y-A9H2 | 0.22041058 | 0.09034806 | 0.67157579 | 0 | 0 | 0 | 0 | 0 | 0 |
| TCGA-2Y-A9H3 | 0 | 0.13237951 | 0.75330107 | 0 | 0.0670776 | 0 | 0 | 0 | 0 |
| TCGA-2Y-A9H4 | 0 | 0.20039294 | 0.59029759 | 0 | 0.06740019 | 0 | 0 | 0.1049616 | 0 |
| TCGA-2Y-A9H5 | 0.15169551 | 0 | 0.73259524 | 0 | 0 | 0 | 0 | 0 | 0 |
| TCGA-2Y-A9H6 | 0.12399368 | 0 | 0.59461438 | 0 | 0 | 0.11901193 | 0 | 0 | 0.06819601 |
| TCGA-2Y-A9H7 | 0.10920798 | 0.11053793 | 0.67840564 | 0 | 0 | 0 | 0 | 0 | 0 |
| TCGA-2Y-A9H8 | 0.24598719 | 0.13998166 | 0.42073777 | 0 | 0.08542275 | 0 | 0 | 0.10787062 | 0 |
| TCGA-2Y-A9H9 | 0.10622923 | 0.25963427 | 0.40490766 | 0 | 0.12790462 | 0.08057795 | 0 | 0 | 0 |
| TCGA-2Y-A9HA | 0 | 0.21847051 | 0.4168605 | 0 | 0.08473422 | 0.09979566 | 0 | 0 | 0.09427971 |
| TCGA-2Y-A9HB | 0 | 0.19640076 | 0.49983834 | 0.11791678 | 0.16885468 | 0 | 0 | 0 | 0 |
| TCGA-3K-AAZ8 | 0 | 0 | 0.74314217 | 0 | 0 | 0 | 0.08382008 | 0 | 0 |
| TCGA-4R-AA8I | 0.08696461 | 0.06387857 | 0 | 0.44373453 | 0.32088467 | 0 | 0 | 0 | 0.06927415 |
| TCGA-5C-A9VG | 0.10275184 | 0.189892 | 0.60229308 | 0 | 0 | 0 | 0 | 0.07518087 | 0 |
| TCGA-5C-A9VH | 0 | 0.2165367 | 0.64127714 | 0 | 0 | 0 | 0 | 0 | 0 |
| TCGA-5C-AAPD | 0.07272181 | 0.258348 | 0.51122726 | 0 | 0.08466382 | 0 | 0 | 0.07303911 | 0 |
| TCGA-5R-AA1C | 0 | 0.12494558 | 0.66605899 | 0 | 0 | 0.09541764 | 0.11357778 | 0 | 0 |
| TCGA-5R-AA1D | 0.16045885 | 0 | 0.72678427 | 0 | 0 | 0 | 0.08364165 | 0 | 0 |
| TCGA-5R-AAAM | 0 | 0 | 0.55622139 | 0.12133656 | 0.16711436 | 0.06364002 | 0 | 0 | 0 |
| TCGA-BC-A10R | 0 | 0.16461762 | 0.71319263 | 0.06473447 | 0 | 0 | 0 | 0 | 0 |
| TCGA-BC-A10S | 0.15001405 | 0 | 0.73007824 | 0 | 0.10599982 | 0 | 0 | 0 | 0 |

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| TCGA-BC-A10T | 0 | 0.19180797 | 0.61774448 | 0 | 0.06767611 | 0 | 0.07145711 | 0 | 0 |
| TCGA-BC-A10U | 0 | 0.20950855 | 0.71335906 | 0 | 0 | 0 | 0 | 0 | 0 |
| TCGA-BC-A10W | 0 | 0.18190255 | 0.7168427 | 0 | 0 | 0 | 0 | 0 | 0 |
| TCGA-BC-A10X | 0 | 0.35230783 | 0 | 0.07109885 | 0.38343255 | 0 | 0 | 0.14966062 | 0 |
| TCGA-BC-A10Y | 0 | 0.14230441 | 0.41489998 | 0.19062361 | 0.10390135 | 0.12462568 | 0 | 0 | 0 |
| TCGA-BC-A10Z | 0 | 0.2100818 | 0.62225602 | 0 | 0 | 0 | 0 | 0 | 0.10724681 |
| TCGA-BC-A110 | 0.24219898 | 0.07488548 | 0.65824346 | 0 | 0 | 0 | 0 | 0 | 0 |
| TCGA-BC-A216 | 0.11591656 | 0 | 0.811254 | 0 | 0 | 0 | 0 | 0 | 0 |
| TCGA-BC-A217 | 0 | 0.2510156 | 0.57023703 | 0 | 0.07643377 | 0 | 0 | 0 | 0 |
| TCGA-BC-A3KF | 0 | 0.06085867 | 0.49135121 | 0 | 0.17800193 | 0 | 0.12775039 | 0 | 0.12535679 |
| TCGA-BC-A5W4 | 0.11493741 | 0.1110383 | 0.60515952 | 0 | 0.07444679 | 0 | 0 | 0 | 0 |
| TCGA-BC-A69H | 0 | 0.18956993 | 0.62000824 | 0.09358503 | 0 | 0 | 0 | 0 | 0 |
| TCGA-BC-A69I | 0.13638002 | 0 | 0.71988129 | 0 | 0.13795349 | 0 | 0 | 0 | 0 |
| TCGA-BC-A8YO | 0.09332078 | 0.17684976 | 0.52436128 | 0 | 0.07259578 | 0 | 0.11937019 | 0 | 0 |
| TCGA-BD-A2L6 | 0 | 0.19370367 | 0.67345349 | 0 | 0 | 0 | 0.06347347 | 0 | 0 |
| TCGA-BD-A3EP | 0 | 0.15274008 | 0.73382263 | 0 | 0 | 0 | 0 | 0 | 0 |
| TCGA-BD-A3ER | 0 | 0.16968312 | 0.67055457 | 0 | 0 | 0 | 0 | 0 | 0.11730778 |
| TCGA-BW-A5NO | 0.11039352 | 0.12467543 | 0.63449634 | 0 | 0 | 0 | 0 | 0.07054501 | 0 |
| TCGA-BW-A5NP | 0.14243996 | 0.16108097 | 0.60186973 | 0 | 0 | 0 | 0 | 0.09460934 | 0 |
| TCGA-BW-A5NQ | 0 | 0.15088848 | 0.78910493 | 0 | 0 | 0 | 0 | 0 | 0 |
| TCGA-CC-5258 | 0 | 0 | 0.43947841 | 0.07829714 | 0.08313041 | 0.06577659 | 0 | 0 | 0.28155802 |
| TCGA-CC-5259 | 0.06133934 | 0.1704692 | 0.51236509 | 0 | 0 | 0 | 0.24635785 | 0 | 0 |
| TCGA-CC-5260 | 0.21441376 | 0 | 0.60695595 | 0 | 0 | 0 | 0.17863028 | 0 | 0 |
| TCGA-CC-5261 | 0.26929244 | 0 | 0.65528229 | 0 | 0 | 0 | 0 | 0 | 0 |
| TCGA-CC-5262 | 0 | 0.18237047 | 0.47886756 | 0 | 0 | 0.0688403 | 0.07874599 | 0 | 0.0793955 |
| TCGA-CC-5263 | 0 | 0.33788708 | 0.32850456 | 0 | 0.08614626 | 0 | 0.15589276 | 0 | 0 |
| TCGA-CC-5264 | 0 | 0.2131336 | 0.53948827 | 0 | 0.07020108 | 0 | 0.10188836 | 0 | 0 |
| TCGA-CC-A123 | 0 | 0.32173444 | 0.58485754 | 0 | 0 | 0 | 0 | 0 | 0 |
| TCGA-CC-A1HT | 0 | 0.23563987 | 0.60673283 | 0 | 0 | 0.06061216 | 0 | 0 | 0 |
| TCGA-CC-A3M9 | 0 | 0.11642241 | 0.48557259 | 0 | 0.09845158 | 0.08893487 | 0.11948234 | 0 | 0 |
| TCGA-CC-A3MA | 0.18669627 | 0.11810216 | 0.62505157 | 0 | 0.07015 | 0 | 0 | 0 | 0 |
| TCGA-CC-A3MB | 0.08070509 | 0.20957108 | 0.52339117 | 0 | 0 | 0 | 0 | 0 | 0.11829352 |
| TCGA-CC-A3MC | 0 | 0.18195357 | 0.37435924 | 0 | 0 | 0.10110079 | 0.09921509 | 0 | 0.14204733 |

| | C1 | C2 | C3 | C4 | C5 | C6 | C7 | C8 | C9 |
|---|---|---|---|---|---|---|---|---|---|
| TCGA-CC-A5UC | 0.12497756 | 0.14916798 | 0.50829913 | 0 | 0.11123856 | 0 | 0 | 0.10631678 | 0 |
| TCGA-CC-A5UD | 0 | 0 | 0.30194758 | 0 | 0 | 0 | 0.5283109 | 0 | 0.07047918 |
| TCGA-CC-A5UE | 0 | 0.19031168 | 0.42580342 | 0 | 0 | 0 | 0 | 0 | 0.26482703 |
| TCGA-CC-A7IE | 0 | 0.09813293 | 0.41397951 | 0 | 0.09141605 | 0.06706224 | 0.10547664 | 0 | 0.16158431 |
| TCGA-CC-A7IF | 0 | 0.20684462 | 0.67776813 | 0 | 0 | 0 | 0.0798178 | 0 | 0 |
| TCGA-CC-A7IG | 0 | 0.14533803 | 0.42829565 | 0 | 0 | 0 | 0 | 0 | 0.35505794 |
| TCGA-CC-A7IH | 0 | 0.1733917 | 0.23881599 | 0 | 0.20575154 | 0 | 0.3380071 | 0 | 0 |
| TCGA-CC-A7II | 0 | 0.14666892 | 0 | 0 | 0 | 0.13390527 | 0 | 0 | 0.5402666 |
| TCGA-CC-A7IJ | 0 | 0.18709546 | 0.75399584 | 0 | 0 | 0 | 0 | 0 | 0 |
| TCGA-CC-A7IK | 0 | 0.16002319 | 0.29966053 | 0 | 0.19416925 | 0 | 0.31939074 | 0 | 0 |
| TCGA-CC-A7IL | 0 | 0.10866805 | 0.50528428 | 0 | 0 | 0 | 0 | 0 | 0.32168471 |
| TCGA-CC-A8HS | 0.11168601 | 0.22351139 | 0.41186136 | 0 | 0.12967748 | 0 | 0 | 0.10042477 | 0 |
| TCGA-CC-A8HT | 0 | 0.21912504 | 0.49699743 | 0 | 0 | 0 | 0 | 0 | 0.17981834 |
| TCGA-CC-A8HU | 0 | 0.20777216 | 0.34422249 | 0 | 0.11800822 | 0 | 0 | 0 | 0.20367689 |
| TCGA-CC-A8HV | 0 | 0 | 0.55325996 | 0 | 0 | 0 | 0.06758191 | 0 | 0.20513448 |
| TCGA-CC-A9FS | 0 | 0.06857412 | 0.56331291 | 0 | 0 | 0 | 0 | 0 | 0.27299723 |
| TCGA-CC-A9FU | 0 | 0.10089448 | 0.76744675 | 0 | 0 | 0 | 0 | 0 | 0.09543771 |
| TCGA-CC-A9FV | 0.35450019 | 0 | 0.38684191 | 0 | 0 | 0.25865791 | 0 | 0 | 0 |
| TCGA-CC-A9FW | 0 | 0.10144107 | 0.44210805 | 0 | 0.06091009 | 0.09352373 | 0.0939838 | 0.06660086 | 0.0851509 |
| TCGA-DD-A113 | 0.11208802 | 0.1637431 | 0.52786097 | 0 | 0 | 0 | 0.06448078 | 0.08544677 | 0 |
| TCGA-DD-A114 | 0 | 0.16282862 | 0.38566216 | 0 | 0 | 0 | 0 | 0 | 0.41247226 |
| TCGA-DD-A115 | 0 | 0.25834951 | 0.55092983 | 0 | 0 | 0 | 0 | 0.12630728 | 0.06441337 |
| TCGA-DD-A116 | 0 | 0.24891226 | 0.58372234 | 0 | 0.09713951 | 0 | 0 | 0 | 0 |
| TCGA-DD-A118 | 0.12718171 | 0.07946689 | 0.76053011 | 0 | 0 | 0 | 0 | 0 | 0 |
| TCGA-DD-A119 | 0.11076603 | 0.11428873 | 0.66605843 | 0 | 0.07773783 | 0 | 0 | 0 | 0 |
| TCGA-DD-A11A | 0.13329472 | 0.11520659 | 0.66372967 | 0 | 0 | 0 | 0 | 0 | 0 |
| TCGA-DD-A11B | 0 | 0.12002397 | 0.6424982 | 0 | 0.09651667 | 0 | 0 | 0.08838738 | 0 |
| TCGA-DD-A11C | 0.08622787 | 0.11833239 | 0.68449225 | 0 | 0 | 0 | 0 | 0 | 0 |
| TCGA-DD-A11D | 0 | 0.34277064 | 0.50057137 | 0 | 0.08100088 | 0 | 0 | 0 | 0 |
| TCGA-DD-A1E9 | 0 | 0 | 0.89914007 | 0.06815994 | 0 | 0 | 0 | 0 | 0 |
| TCGA-DD-A1EB | 0 | 0.27569174 | 0.57166051 | 0 | 0 | 0 | 0 | 0 | 0 |
| TCGA-DD-A1EC | 0.23797803 | 0.11350293 | 0.33321244 | 0 | 0.22625413 | 0 | 0 | 0.08905247 | 0 |
| TCGA-DD-A1ED | 0 | 0.24942183 | 0.37202973 | 0 | 0.15044845 | 0.06162539 | 0 | 0.09149637 | 0.07497823 |

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| TCGA-DD-A1EE | 0 | 0.23247329 | 0.62782368 | 0 | 0 | 0 | 0 | 0 | 0.08616202 |
| TCGA-DD-A1EF | 0 | 0 | 0.51327416 | 0.06974707 | 0.17972789 | 0 | 0.07124715 | 0.13171834 | 0 |
| TCGA-DD-A1EH | 0.19035149 | 0 | 0.55472668 | 0.09887129 | 0 | 0 | 0 | 0 | 0.07524727 |
| TCGA-DD-A1EI | 0 | 0.20069797 | 0.4892253 | 0.09592431 | 0.14385444 | 0 | 0 | 0 | 0 |
| TCGA-DD-A1EJ | 0.10437906 | 0.13002318 | 0.69016874 | 0 | 0 | 0 | 0 | 0 | 0 |
| TCGA-DD-A1EK | 0 | 0.19321255 | 0.65454809 | 0 | 0 | 0 | 0 | 0 | 0 |
| TCGA-DD-A1EL | 0.06769234 | 0.19836421 | 0 | 0 | 0.09993753 | 0 | 0 | 0 | 0.57415283 |
| TCGA-DD-A39V | 0 | 0.13500436 | 0.61377976 | 0.10353363 | 0.08354604 | 0 | 0 | 0 | 0 |
| TCGA-DD-A39W | 0.10362946 | 0 | 0.68066486 | 0 | 0 | 0 | 0 | 0 | 0.12659848 |
| TCGA-DD-A39X | 0.09565608 | 0 | 0.73910705 | 0 | 0 | 0 | 0 | 0 | 0.09838304 |
| TCGA-DD-A39Z | 0 | 0.08514558 | 0.55864643 | 0 | 0 | 0 | 0 | 0.17306875 | 0.11147819 |
| TCGA-DD-A3A2 | 0 | 0.07201649 | 0.7308344 | 0.08211675 | 0 | 0 | 0 | 0 | 0.07921639 |
| TCGA-DD-A3A3 | 0.10146705 | 0 | 0.70743101 | 0 | 0 | 0 | 0 | 0 | 0.12022714 |
| TCGA-DD-A3A4 | 0.14167219 | 0.2028298 | 0.37825749 | 0.09792928 | 0.12678342 | 0 | 0 | 0 | 0 |
| TCGA-DD-A3A5 | 0 | 0.12259703 | 0.59531635 | 0.15292267 | 0 | 0 | 0 | 0 | 0 |
| TCGA-DD-A3A6 | 0 | 0.10298309 | 0.46046226 | 0.22657821 | 0.13801596 | 0 | 0 | 0.07196049 | 0 |
| TCGA-DD-A3A7 | 0 | 0.07455084 | 0.504717 | 0 | 0.07283046 | 0.264599 | 0 | 0 | 0 |
| TCGA-DD-A3A8 | 0 | 0.14983454 | 0.66118656 | 0 | 0.08973828 | 0.06134142 | 0 | 0 | 0 |
| TCGA-DD-A3A9 | 0 | 0.07729456 | 0.62221731 | 0 | 0.15241753 | 0 | 0.06166124 | 0.0743273 | 0 |
| TCGA-DD-A4NA | 0.11729429 | 0.09884651 | 0.63938968 | 0 | 0.08596729 | 0 | 0 | 0 | 0 |
| TCGA-DD-A4NB | 0 | 0.13023471 | 0.79127471 | 0 | 0 | 0 | 0 | 0 | 0 |
| TCGA-DD-A4ND | 0 | 0 | 0.82172099 | 0 | 0.06270069 | 0 | 0 | 0 | 0 |
| TCGA-DD-A4NE | 0 | 0 | 0.75864093 | 0 | 0 | 0.18256294 | 0 | 0 | 0 |
| TCGA-DD-A4NF | 0 | 0.19185287 | 0.76498618 | 0 | 0 | 0 | 0 | 0 | 0 |
| TCGA-DD-A4NG | 0 | 0 | 0.82965619 | 0 | 0 | 0 | 0 | 0 | 0 |
| TCGA-DD-A4NH | 0 | 0.10107834 | 0.60767654 | 0.24255892 | 0 | 0 | 0 | 0 | 0 |
| TCGA-DD-A4NI | 0 | 0.18755229 | 0.58428769 | 0 | 0.13537929 | 0 | 0 | 0 | 0 |
| TCGA-DD-A4NJ | 0 | 0.19246365 | 0.67771564 | 0 | 0 | 0 | 0.0625425 | 0 | 0 |
| TCGA-DD-A4NK | 0 | 0.10501092 | 0.73910584 | 0 | 0 | 0 | 0 | 0 | 0 |
| TCGA-DD-A4NL | 0.12872537 | 0 | 0.64104185 | 0 | 0 | 0.11861 | 0 | 0 | 0 |
| TCGA-DD-A4NN | 0.11176701 | 0 | 0.66025609 | 0 | 0.09930473 | 0 | 0.08428237 | 0 | 0 |
| TCGA-DD-A4NO | 0.08903387 | 0.12399055 | 0.55517445 | 0 | 0.14976551 | 0 | 0.07466157 | 0 | 0 |
| TCGA-DD-A4NP | 0.11083196 | 0.09780828 | 0.48652342 | 0 | 0.14980082 | 0.06456535 | 0 | 0 | 0 |

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|---|---|---|---|---|---|---|---|---|---|
| TCGA-DD-A4NQ | 0.12761593 | 0.11685811 | 0.64783971 | 0 | 0.10768625 | 0 | 0 | 0 | 0 |
| TCGA-DD-A4NR | 0 | 0.10734626 | 0.73743961 | 0 | 0.07815206 | 0 | 0 | 0 | 0 |
| TCGA-DD-A4NS | 0.13009913 | 0.3292342 | 0.34162267 | 0 | 0.13605705 | 0 | 0 | 0 | 0 |
| TCGA-DD-A4NV | 0.06811932 | 0.10526917 | 0.66632334 | 0 | 0.07108662 | 0 | 0.08920156 | 0 | 0 |
| TCGA-DD-A73A | 0 | 0.1857384 | 0.33573436 | 0.08208185 | 0.12458379 | 0 | 0.14591267 | 0 | 0.07170067 |
| TCGA-DD-A73B | 0.06333049 | 0.11375315 | 0.44406581 | 0.07567957 | 0.12657244 | 0.08778256 | 0 | 0 | 0 |
| TCGA-DD-A73C | 0 | 0.10605805 | 0.50463639 | 0 | 0 | 0.09561792 | 0.06732134 | 0.13157595 | 0 |
| TCGA-DD-A73D | 0 | 0.11901168 | 0.67739597 | 0 | 0 | 0 | 0 | 0 | 0.09623226 |
| TCGA-DD-A73E | 0 | 0.25039954 | 0.70540333 | 0 | 0 | 0 | 0 | 0 | 0 |
| TCGA-DD-A73F | 0 | 0.12316598 | 0.61531447 | 0.10160606 | 0 | 0 | 0 | 0 | 0.10462287 |
| TCGA-DD-A73G | 0 | 0.06531063 | 0.80634921 | 0 | 0 | 0 | 0 | 0 | 0 |
| TCGA-DD-AA3A | 0.20398724 | 0.26040478 | 0.51602891 | 0 | 0 | 0 | 0 | 0 | 0 |
| TCGA-DD-AAC8 | 0 | 0 | 0.12536594 | 0 | 0 | 0 | 0.7862173 | 0 | 0 |
| TCGA-DD-AAC9 | 0 | 0.22687694 | 0.63304517 | 0.06535672 | 0 | 0 | 0 | 0 | 0 |
| TCGA-DD-AACB | 0 | 0.1162781 | 0.60536103 | 0 | 0 | 0 | 0 | 0.12867773 | 0 |
| TCGA-DD-AACC | 0.07830048 | 0.23266592 | 0.57456768 | 0 | 0.11446592 | 0 | 0 | 0 | 0 |
| TCGA-DD-AACD | 0 | 0.1341619 | 0.50183197 | 0 | 0.12282366 | 0.15236793 | 0 | 0 | 0 |
| TCGA-DD-AACE | 0 | 0.12383896 | 0.44872476 | 0.14728305 | 0.06574486 | 0 | 0.11625208 | 0 | 0.06685405 |
| TCGA-DD-AACF | 0 | 0.14675754 | 0.62816622 | 0 | 0.06163827 | 0 | 0 | 0 | 0 |
| TCGA-DD-AACG | 0 | 0.22209217 | 0.49431653 | 0 | 0.11825813 | 0 | 0.06730268 | 0 | 0 |
| TCGA-DD-AACH | 0 | 0.1170617 | 0.70763812 | 0 | 0.07657543 | 0 | 0.06081916 | 0 | 0 |
| TCGA-DD-AACI | 0 | 0 | 0.41211899 | 0 | 0.14707934 | 0 | 0.31983626 | 0 | 0 |
| TCGA-DD-AACJ | 0.0876239 | 0 | 0.71500743 | 0 | 0.14941645 | 0 | 0 | 0 | 0 |
| TCGA-DD-AACK | 0 | 0 | 0.41863569 | 0 | 0 | 0 | 0.35960568 | 0 | 0.07791428 |
| TCGA-DD-AACL | 0 | 0 | 0.13543076 | 0 | 0 | 0 | 0.82342536 | 0 | 0 |
| TCGA-DD-AACM | 0.1775775 | 0.07652281 | 0.49708405 | 0 | 0.0983297 | 0 | 0.06303285 | 0.0874531 | 0 |
| TCGA-DD-AACN | 0.09340446 | 0.11573153 | 0.38100516 | 0 | 0.08893916 | 0.06644289 | 0.0893619 | 0.12468165 | 0 |
| TCGA-DD-AACO | 0 | 0.10284248 | 0.87343795 | 0 | 0 | 0 | 0 | 0 | 0 |
| TCGA-DD-AACP | 0.13810151 | 0 | 0.28597559 | 0 | 0.10565337 | 0.24925863 | 0.06666792 | 0.06911065 | 0.07877658 |
| TCGA-DD-AACQ | 0 | 0.06164854 | 0.26006954 | 0 | 0 | 0 | 0.67063702 | 0 | 0 |
| TCGA-DD-AACS | 0.08297189 | 0.06361257 | 0.69956347 | 0 | 0 | 0 | 0 | 0 | 0.09696877 |
| TCGA-DD-AACT | 0 | 0.06811881 | 0.36156329 | 0 | 0.11673377 | 0 | 0.40531757 | 0 | 0 |
| TCGA-DD-AACU | 0 | 0.12226781 | 0.60498544 | 0 | 0 | 0 | 0.18535897 | 0 | 0 |

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|---|---|---|---|---|---|---|---|---|---|
| TCGA-DD-AACV | 0.06094514 | 0 | 0.39209277 | 0.0728194 | 0.15961439 | 0.18295231 | 0 | 0 | 0.08186998 |
| TCGA-DD-AACW | 0 | 0.26610029 | 0.34224304 | 0.22781137 | 0 | 0.0773907 | 0 | 0 | 0 |
| TCGA-DD-AACX | 0 | 0.16266337 | 0.63959677 | 0 | 0.09480194 | 0 | 0 | 0 | 0 |
| TCGA-DD-AACY | 0 | 0.122274 | 0.7566861 | 0 | 0 | 0.07135331 | 0 | 0 | 0 |
| TCGA-DD-AACZ | 0 | 0.09846794 | 0.28114041 | 0.11578438 | 0.07743431 | 0 | 0.31699219 | 0 | 0 |
| TCGA-DD-AAD0 | 0 | 0.09061092 | 0.47142499 | 0.08484702 | 0.07587189 | 0 | 0.06122477 | 0 | 0.17732208 |
| TCGA-DD-AAD1 | 0.07741854 | 0.17513438 | 0.44398711 | 0 | 0.08524778 | 0 | 0.10483262 | 0 | 0 |
| TCGA-DD-AAD2 | 0 | 0.13313842 | 0.65439675 | 0.06955659 | 0 | 0 | 0.07834237 | 0 | 0 |
| TCGA-DD-AAD3 | 0 | 0.17957607 | 0.53897988 | 0 | 0.06778139 | 0.12496093 | 0 | 0 | 0 |
| TCGA-DD-AAD5 | 0.0609923 | 0.06760391 | 0.63748158 | 0 | 0 | 0.06193273 | 0.07144694 | 0 | 0 |
| TCGA-DD-AAD6 | 0 | 0.0690116 | 0.50224713 | 0 | 0 | 0.24732138 | 0.06541366 | 0 | 0 |
| TCGA-DD-AAD8 | 0 | 0.06465748 | 0.58386755 | 0 | 0.09774546 | 0 | 0.19412736 | 0 | 0 |
| TCGA-DD-AADA | 0.10712608 | 0.14546008 | 0.52223346 | 0 | 0.07628188 | 0 | 0.11723138 | 0 | 0 |
| TCGA-DD-AADB | 0 | 0.15018451 | 0.61748929 | 0 | 0.15711029 | 0 | 0 | 0 | 0 |
| TCGA-DD-AADC | 0.11144519 | 0 | 0.42973336 | 0 | 0 | 0.18295726 | 0 | 0 | 0.16993496 |
| TCGA-DD-AADD | 0 | 0.09900739 | 0.53017525 | 0 | 0 | 0.27091307 | 0 | 0 | 0 |
| TCGA-DD-AADE | 0 | 0 | 0.53579961 | 0 | 0.07434299 | 0.22220717 | 0 | 0 | 0.09851244 |
| TCGA-DD-AADF | 0 | 0.17115445 | 0.38301105 | 0 | 0 | 0 | 0.42757054 | 0 | 0 |
| TCGA-DD-AADG | 0 | 0.18183339 | 0.49543244 | 0 | 0 | 0.15395891 | 0 | 0 | 0 |
| TCGA-DD-AADI | 0 | 0 | 0.41975609 | 0.06478717 | 0.12026616 | 0 | 0.14296499 | 0.15885133 | 0.06560216 |
| TCGA-DD-AADJ | 0 | 0 | 0.61899068 | 0 | 0 | 0 | 0.07292814 | 0 | 0.1637862 |
| TCGA-DD-AADK | 0 | 0.1602094 | 0.45973304 | 0 | 0.19607367 | 0.0922192 | 0 | 0 | 0 |
| TCGA-DD-AADL | 0 | 0.20036205 | 0.44765071 | 0 | 0.07031269 | 0.16537201 | 0 | 0 | 0 |
| TCGA-DD-AADM | 0 | 0 | 0.41262856 | 0 | 0.10953392 | 0.30556817 | 0.11503811 | 0 | 0 |
| TCGA-DD-AADN | 0.06205142 | 0.21776958 | 0.28956589 | 0 | 0.13045721 | 0.14098573 | 0 | 0.09660351 | 0.06256666 |
| TCGA-DD-AADO | 0 | 0 | 0.68104779 | 0 | 0.10846399 | 0 | 0.1022862 | 0 | 0.06409471 |
| TCGA-DD-AADP | 0.09410388 | 0.11845646 | 0.51879873 | 0 | 0.14285157 | 0.0985354 | 0 | 0 | 0 |
| TCGA-DD-AADQ | 0 | 0.11840027 | 0.70863771 | 0 | 0 | 0 | 0.09678745 | 0 | 0 |
| TCGA-DD-AADR | 0 | 0.12323474 | 0.76720261 | 0 | 0 | 0 | 0 | 0 | 0 |
| TCGA-DD-AADS | 0 | 0.10325178 | 0.42486456 | 0 | 0.0938917 | 0 | 0.30959118 | 0 | 0.06840078 |
| TCGA-DD-AADU | 0 | 0.07932453 | 0.35913811 | 0 | 0.1887349 | 0 | 0.18115696 | 0 | 0.10792406 |
| TCGA-DD-AADV | 0 | 0 | 0.41316581 | 0 | 0.0627933 | 0.28398152 | 0 | 0.07607034 | 0 |
| TCGA-DD-AADW | 0.08643875 | 0.2310982 | 0.28412086 | 0 | 0.12557453 | 0 | 0.11797086 | 0.1547968 | 0 |

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|---|---|---|---|---|---|---|---|---|---|
| TCGA-DD-AADY | 0 | 0.09745099 | 0.73339265 | 0.14362102 | 0 | 0 | 0 | 0 | 0 |
| TCGA-DD-AAE0 | 0 | 0 | 0.38360151 | 0.29621431 | 0.15265045 | 0 | 0 | 0.08880336 | 0 |
| TCGA-DD-AAE1 | 0.13434059 | 0.10203451 | 0.61589037 | 0 | 0.09105813 | 0 | 0 | 0 | 0 |
| TCGA-DD-AAE2 | 0 | 0.10864127 | 0.75658973 | 0 | 0 | 0 | 0.1224351 | 0 | 0 |
| TCGA-DD-AAE3 | 0.06223379 | 0 | 0 | 0 | 0 | 0.86557846 | 0 | 0 | 0 |
| TCGA-DD-AAE4 | 0.0931741 | 0.26110017 | 0.36113551 | 0 | 0.11643042 | 0 | 0.06526506 | 0.10289473 | 0 |
| TCGA-DD-AAE6 | 0 | 0 | 0.84770938 | 0 | 0 | 0 | 0 | 0.11064552 | 0 |
| TCGA-DD-AAE8 | 0.09412123 | 0.16968613 | 0.55872665 | 0 | 0 | 0 | 0 | 0 | 0 |
| TCGA-DD-AAE9 | 0 | 0.14058978 | 0.48408223 | 0 | 0.16333575 | 0 | 0.14306603 | 0 | 0 |
| TCGA-DD-AAEA | 0 | 0 | 0.41172093 | 0 | 0 | 0.41422459 | 0 | 0 | 0 |
| TCGA-DD-AAEB | 0 | 0.15999512 | 0.51253522 | 0 | 0 | 0.25154572 | 0 | 0 | 0 |
| TCGA-DD-AAED | 0 | 0.13690967 | 0.7623904 | 0 | 0 | 0 | 0 | 0 | 0 |
| TCGA-DD-AAEE | 0.0783311 | 0 | 0.2743613 | 0 | 0.13743781 | 0.18295371 | 0 | 0 | 0.20126692 |
| TCGA-DD-AAEG | 0.14712278 | 0.15036166 | 0.49225715 | 0 | 0.06306726 | 0.10436198 | 0 | 0 | 0 |
| TCGA-DD-AAEH | 0 | 0.16367415 | 0.47433756 | 0 | 0.14226205 | 0 | 0 | 0 | 0.16199571 |
| TCGA-DD-AAEI | 0 | 0.10914211 | 0.60877701 | 0 | 0 | 0 | 0.15955491 | 0 | 0 |
| TCGA-DD-AAEK | 0 | 0 | 0.52379622 | 0 | 0 | 0.25936102 | 0 | 0 | 0.12776815 |
| TCGA-DD-AAVP | 0 | 0.18174311 | 0.68800587 | 0 | 0.07574488 | 0 | 0 | 0 | 0 |
| TCGA-DD-AAVQ | 0 | 0 | 0.7420196 | 0 | 0 | 0 | 0 | 0 | 0.18334001 |
| TCGA-DD-AAVR | 0.12735199 | 0.07659862 | 0.39078132 | 0.08073742 | 0.06675727 | 0 | 0.0970337 | 0.0653083 | 0.09543136 |
| TCGA-DD-AAVS | 0.07946131 | 0.0706529 | 0.42744413 | 0 | 0 | 0.21883959 | 0 | 0 | 0.16681563 |
| TCGA-DD-AAVU | 0 | 0 | 0.7379547 | 0 | 0.07745764 | 0 | 0.12272272 | 0 | 0 |
| TCGA-DD-AAVV | 0 | 0.1710665 | 0.60117101 | 0 | 0.13082783 | 0 | 0 | 0 | 0 |
| TCGA-DD-AAVX | 0 | 0.15886211 | 0.51535518 | 0.06097144 | 0.11175713 | 0 | 0.06136007 | 0.09169408 | 0 |
| TCGA-DD-AAVY | 0 | 0.16730221 | 0.53961794 | 0 | 0.19825967 | 0 | 0 | 0 | 0 |
| TCGA-DD-AAVZ | 0.07269322 | 0.1107352 | 0.79745893 | 0 | 0 | 0 | 0 | 0 | 0 |
| TCGA-DD-AAW0 | 0.06291071 | 0 | 0.57475633 | 0 | 0 | 0.08967631 | 0.09356689 | 0 | 0.09821923 |
| TCGA-DD-AAW1 | 0 | 0 | 0.36176655 | 0 | 0 | 0 | 0.44809767 | 0.06034383 | 0 |
| TCGA-DD-AAW2 | 0 | 0 | 0.46509111 | 0 | 0.07803585 | 0.11762922 | 0.1360353 | 0 | 0.10217985 |
| TCGA-DD-AAW3 | 0 | 0.06057422 | 0.6988876 | 0 | 0 | 0 | 0.06331461 | 0 | 0 |
| TCGA-ED-A459 | 0 | 0.06424448 | 0.31810953 | 0 | 0 | 0 | 0.58530089 | 0 | 0 |
| TCGA-ED-A4XI | 0 | 0 | 0.48636109 | 0 | 0.16346857 | 0.22044965 | 0.07742879 | 0 | 0 |
| TCGA-ED-A5KG | 0.11930616 | 0.07968089 | 0.66655492 | 0 | 0 | 0 | 0.06586976 | 0 | 0 |

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|---|---|---|---|---|---|---|---|---|---|
| TCGA-ED-A627 | 0 | 0 | 0.46931278 | 0 | 0.417108 | 0 | 0 | 0 | 0 |
| TCGA-ED-A66X | 0.26507452 | 0 | 0.64575504 | 0 | 0 | 0 | 0 | 0 | 0 |
| TCGA-ED-A66Y | 0 | 0 | 0.41357281 | 0.15608517 | 0.1831549 | 0 | 0 | 0.07561819 | 0.11984945 |
| TCGA-ED-A7PX | 0.09983183 | 0.18203707 | 0.62526882 | 0.09286228 | 0 | 0 | 0 | 0 | 0 |
| TCGA-ED-A7PY | 0.1991234 | 0 | 0.30977409 | 0 | 0.19291099 | 0 | 0 | 0 | 0.27034121 |
| TCGA-ED-A7PZ | 0 | 0.14187426 | 0.33525637 | 0 | 0 | 0 | 0.43105129 | 0 | 0 |
| TCGA-ED-A7XO | 0.08233033 | 0.21734423 | 0.29186323 | 0.11220175 | 0.16282553 | 0 | 0 | 0 | 0 |
| TCGA-ED-A7XP | 0 | 0.18603592 | 0.46097971 | 0.1039279 | 0 | 0 | 0 | 0 | 0.15924814 |
| TCGA-ED-A82E | 0.09807428 | 0.17272436 | 0.51904867 | 0.10663569 | 0 | 0 | 0 | 0.103517 | 0 |
| TCGA-ED-A8O5 | 0 | 0.06875389 | 0.18458678 | 0.08982041 | 0.15631473 | 0 | 0.24741226 | 0.14967695 | 0.10343498 |
| TCGA-ED-A8O6 | 0.07400358 | 0.16530628 | 0.23712029 | 0.25714658 | 0.1097008 | 0 | 0.06544666 | 0 | 0 |
| TCGA-ED-A97K | 0.11532718 | 0 | 0 | 0.36190407 | 0 | 0.20327606 | 0.13195156 | 0 | 0.10091929 |
| TCGA-EP-A12J | 0.11953289 | 0.25270398 | 0.58370649 | 0 | 0 | 0 | 0 | 0 | 0 |
| TCGA-EP-A26S | 0 | 0.15473273 | 0.74395255 | 0 | 0 | 0 | 0 | 0 | 0 |
| TCGA-EP-A2KA | 0 | 0.27248269 | 0.49144736 | 0.16547103 | 0 | 0 | 0 | 0 | 0 |
| TCGA-EP-A2KB | 0 | 0.26433538 | 0.54325125 | 0 | 0 | 0.12957405 | 0 | 0 | 0 |
| TCGA-EP-A2KC | 0.08673128 | 0.2128564 | 0.52686417 | 0 | 0.09638892 | 0 | 0 | 0 | 0 |
| TCGA-EP-A3JL | 0 | 0.26223424 | 0.56032828 | 0 | 0.16014105 | 0 | 0 | 0 | 0 |
| TCGA-EP-A3RK | 0 | 0.10765365 | 0.43766606 | 0.08256575 | 0 | 0.10313042 | 0.07878374 | 0.09859931 | 0 |
| TCGA-ES-A2HS | 0 | 0.17971204 | 0.58340101 | 0.10815865 | 0 | 0 | 0 | 0.07778006 | 0 |
| TCGA-ES-A2HT | 0 | 0.16443781 | 0.5700975 | 0 | 0 | 0.10389101 | 0 | 0.06710654 | 0 |
| TCGA-FV-A23B | 0 | 0.10806869 | 0.56882306 | 0.10760946 | 0.13605784 | 0 | 0 | 0.06133 | 0 |
| TCGA-FV-A2QQ | 0 | 0.22947894 | 0.51256162 | 0 | 0.09072486 | 0 | 0 | 0 | 0 |
| TCGA-FV-A2QR | 0 | 0.21380986 | 0.76459025 | 0 | 0 | 0 | 0 | 0 | 0 |
| TCGA-FV-A3I0 | 0.0784331 | 0 | 0.73585404 | 0 | 0 | 0 | 0 | 0.08005433 | 0.10565852 |
| TCGA-FV-A3I1 | 0 | 0.20637391 | 0.62890103 | 0 | 0 | 0 | 0 | 0 | 0 |
| TCGA-FV-A3R2 | 0 | 0.23961544 | 0.60922338 | 0 | 0 | 0 | 0 | 0.06429797 | 0 |
| TCGA-FV-A3R3 | 0.1326944 | 0 | 0.60375478 | 0 | 0.06362698 | 0 | 0 | 0 | 0.12833057 |
| TCGA-FV-A495 | 0 | 0.11889805 | 0.63896143 | 0 | 0.08072319 | 0 | 0 | 0.06924993 | 0 |
| TCGA-FV-A496 | 0.07651968 | 0.18016633 | 0.6753095 | 0 | 0 | 0 | 0 | 0 | 0 |
| TCGA-FV-A4ZP | 0.0829746 | 0.15680061 | 0.62802776 | 0 | 0 | 0 | 0 | 0.09456902 | 0 |
| TCGA-FV-A4ZQ | 0 | 0.2072569 | 0.42329698 | 0 | 0 | 0.08791637 | 0 | 0 | 0.16544924 |
| TCGA-G3-A25S | 0 | 0 | 0.87002071 | 0 | 0 | 0 | 0 | 0 | 0 |

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|---|---|---|---|---|---|---|---|---|---|
| TCGA-G3-A25T | 0.12018497 | 0.07388051 | 0.71511227 | 0 | 0.09082225 | 0 | 0 | 0 | 0 |
| TCGA-G3-A25U | 0 | 0.52486453 | 0.41106395 | 0 | 0 | 0 | 0 | 0 | 0 |
| TCGA-G3-A25V | 0 | 0.23278149 | 0.38885347 | 0 | 0.10860524 | 0.16796546 | 0 | 0 | 0 |
| TCGA-G3-A25W | 0 | 0.16210904 | 0.53031776 | 0 | 0.09671101 | 0.13919125 | 0 | 0 | 0 |
| TCGA-G3-A25Y | 0 | 0.30055887 | 0.55411843 | 0 | 0 | 0 | 0 | 0 | 0.09512794 |
| TCGA-G3-A25Z | 0.07675296 | 0.40284706 | 0.23742788 | 0 | 0.14253433 | 0 | 0 | 0.07588029 | 0 |
| TCGA-G3-A3CG | 0.06876873 | 0.15800018 | 0.52069565 | 0 | 0 | 0.07389126 | 0.09295446 | 0 | 0 |
| TCGA-G3-A3CH | 0.06737785 | 0 | 0.52628449 | 0.13845954 | 0 | 0 | 0.09694791 | 0.07814227 | 0.09278794 |
| TCGA-G3-A3CI | 0 | 0.25186943 | 0.41717575 | 0.07343221 | 0.20154179 | 0 | 0 | 0 | 0 |
| TCGA-G3-A3CK | 0 | 0 | 0.70280104 | 0 | 0.17895094 | 0 | 0 | 0 | 0.06683252 |
| TCGA-G3-A5SI | 0.07103997 | 0.09744762 | 0.5481888 | 0 | 0.1338635 | 0 | 0 | 0 | 0.11003147 |
| TCGA-G3-A5SJ | 0 | 0.13419387 | 0.62543771 | 0 | 0.08787095 | 0.13603183 | 0 | 0 | 0 |
| TCGA-G3-A5SK | 0 | 0.21342926 | 0.71019378 | 0 | 0.07637697 | 0 | 0 | 0 | 0 |
| TCGA-G3-A5SL | 0 | 0.10428358 | 0.69694004 | 0 | 0 | 0.07690947 | 0 | 0 | 0 |
| TCGA-G3-A5SM | 0 | 0.13895373 | 0.64943406 | 0.15088194 | 0 | 0 | 0 | 0 | 0 |
| TCGA-G3-A6UC | 0 | 0.19080825 | 0.60451655 | 0 | 0.06957754 | 0 | 0 | 0 | 0 |
| TCGA-G3-A7M5 | 0 | 0.07272421 | 0.35032434 | 0 | 0 | 0 | 0.45276394 | 0 | 0 |
| TCGA-G3-A7M6 | 0 | 0.0720166 | 0.86563973 | 0 | 0.06234367 | 0 | 0 | 0 | 0 |
| TCGA-G3-A7M7 | 0 | 0.14243657 | 0.79375777 | 0 | 0 | 0 | 0 | 0 | 0 |
| TCGA-G3-A7M8 | 0 | 0 | 0.28935288 | 0.21573979 | 0.18569217 | 0.11459847 | 0.07759347 | 0 | 0.07014808 |
| TCGA-G3-A7M9 | 0 | 0.28512779 | 0.49506971 | 0 | 0.06143314 | 0 | 0 | 0 | 0 |
| TCGA-G3-AAUZ | 0.08176302 | 0.25326583 | 0.31649046 | 0 | 0.20381784 | 0 | 0 | 0 | 0.08970328 |
| TCGA-G3-AAV0 | 0 | 0.08783977 | 0.68119098 | 0 | 0 | 0 | 0.10305393 | 0.0662917 | 0 |
| TCGA-G3-AAV1 | 0 | 0.06078076 | 0.65207184 | 0 | 0 | 0 | 0 | 0 | 0.13816425 |
| TCGA-G3-AAV2 | 0 | 0 | 0.49964234 | 0.1727968 | 0.08025895 | 0 | 0.11753945 | 0 | 0.11654107 |
| TCGA-G3-AAV3 | 0 | 0.17679638 | 0.55879143 | 0.10351475 | 0 | 0 | 0.099818 | 0 | 0 |
| TCGA-G3-AAV4 | 0 | 0.23200766 | 0.35068781 | 0.09987402 | 0 | 0.16283341 | 0 | 0.14212049 | 0 |
| TCGA-G3-AAV5 | 0 | 0.0950545 | 0.59379382 | 0.12368232 | 0 | 0 | 0 | 0 | 0.1199012 |
| TCGA-G3-AAV6 | 0 | 0.21912449 | 0.6398106 | 0.10067195 | 0 | 0 | 0 | 0 | 0 |
| TCGA-G3-AAV7 | 0 | 0.1417963 | 0.62564116 | 0 | 0 | 0 | 0 | 0 | 0.09337492 |
| TCGA-GJ-A3OU | 0.06208102 | 0.07095949 | 0.61352686 | 0 | 0.06759682 | 0 | 0 | 0 | 0.08412142 |
| TCGA-GJ-A6C0 | 0 | 0 | 0.50588401 | 0 | 0 | 0 | 0 | 0.27792843 | 0.12540453 |
| TCGA-GJ-A9DB | 0 | 0.0656052 | 0.70329749 | 0 | 0 | 0 | 0 | 0.06034298 | 0.09143453 |

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|---|---|---|---|---|---|---|---|---|---|
| TCGA-HP-A5MZ | 0 | 0.09325358 | 0.81564765 | 0 | 0 | 0 | 0 | 0 | 0 |
| TCGA-HP-A5N0 | 0 | 0.24745895 | 0.50815482 | 0 | 0.13330396 | 0 | 0 | 0 | 0 |
| TCGA-K7-A5RF | 0.09180831 | 0 | 0.52323407 | 0 | 0.13041676 | 0.12374965 | 0 | 0 | 0.07675336 |
| TCGA-K7-A5RG | 0.07057744 | 0.09894639 | 0.4962278 | 0 | 0.17224688 | 0 | 0.1449706 | 0 | 0 |
| TCGA-K7-A6G5 | 0.07837786 | 0.2211517 | 0.45917103 | 0 | 0 | 0.14806526 | 0 | 0 | 0 |
| TCGA-K7-AAU7 | 0.06104765 | 0 | 0.83038451 | 0 | 0 | 0 | 0 | 0 | 0 |
| TCGA-KR-A7K0 | 0 | 0.24755841 | 0.44895116 | 0 | 0.1040273 | 0 | 0 | 0.0714902 | 0 |
| TCGA-KR-A7K2 | 0 | 0.17332047 | 0.5007188 | 0.06996261 | 0.16322225 | 0 | 0 | 0 | 0 |
| TCGA-KR-A7K7 | 0.16264669 | 0.08964547 | 0.69570537 | 0 | 0 | 0 | 0 | 0 | 0 |
| TCGA-KR-A7K8 | 0.11374872 | 0.21597835 | 0.47455944 | 0 | 0.16515384 | 0 | 0 | 0 | 0 |
| TCGA-LG-A6GG | 0 | 0.14451107 | 0.42170537 | 0 | 0 | 0 | 0.35985078 | 0 | 0 |
| TCGA-LG-A9QC | 0 | 0.09805847 | 0.45724043 | 0 | 0 | 0.15526419 | 0 | 0.07224867 | 0.07803279 |
| TCGA-LG-A9QD | 0 | 0.14408023 | 0.60775918 | 0 | 0.0889251 | 0 | 0 | 0.07871141 | 0 |
| TCGA-MI-A75C | 0 | 0.16267939 | 0.58868096 | 0 | 0 | 0.10242605 | 0 | 0 | 0 |
| TCGA-MI-A75E | 0 | 0.07974121 | 0.58609016 | 0 | 0.1180038 | 0.07031457 | 0.09253276 | 0 | 0 |
| TCGA-MI-A75G | 0 | 0.22682808 | 0.37542219 | 0 | 0.06600465 | 0.16372987 | 0 | 0 | 0.06888679 |
| TCGA-MI-A75H | 0 | 0.2121219 | 0.66677185 | 0 | 0.09514148 | 0 | 0 | 0 | 0 |
| TCGA-MI-A75I | 0 | 0.12528909 | 0.62871529 | 0 | 0.0679188 | 0 | 0.13257125 | 0 | 0 |
| TCGA-MR-A520 | 0 | 0 | 0.61091671 | 0.06901191 | 0 | 0.19906937 | 0 | 0 | 0.09805071 |
| TCGA-MR-A8JO | 0 | 0 | 0.84505712 | 0 | 0 | 0.0732677 | 0 | 0 | 0 |
| TCGA-NI-A4U2 | 0 | 0.08072 | 0.76608904 | 0 | 0 | 0 | 0 | 0 | 0 |
| TCGA-NI-A8LF | 0 | 0.17233431 | 0.73561022 | 0 | 0 | 0 | 0 | 0 | 0 |
| TCGA-O8-A75V | 0 | 0.19701861 | 0.57723748 | 0 | 0 | 0.11979393 | 0 | 0 | 0 |
| TCGA-PD-A5DF | 0.09334693 | 0.06977297 | 0.7363164 | 0 | 0 | 0 | 0.0673877 | 0 | 0 |
| TCGA-QA-A7B7 | 0 | 0.21744197 | 0.55461448 | 0 | 0.10659124 | 0 | 0 | 0 | 0.06930993 |
| TCGA-RC-A6M3 | 0.07752625 | 0 | 0.65105993 | 0 | 0.10896828 | 0.07317978 | 0 | 0 | 0.06614562 |
| TCGA-RC-A6M4 | 0 | 0.21360368 | 0.28064727 | 0 | 0.13148078 | 0 | 0.2869433 | 0 | 0 |
| TCGA-RC-A6M5 | 0.29022457 | 0.08506583 | 0.38893619 | 0 | 0.17466082 | 0.06111259 | 0 | 0 | 0 |
| TCGA-RC-A6M6 | 0 | 0.25407973 | 0.53425056 | 0 | 0 | 0 | 0.07355812 | 0 | 0.09694599 |
| TCGA-RC-A7S9 | 0.08617155 | 0.18974235 | 0.35179805 | 0 | 0.14677827 | 0.07864858 | 0 | 0.08120814 | 0.06565308 |
| TCGA-RC-A7SB | 0 | 0 | 0.45221334 | 0.07387846 | 0.13645878 | 0.09919519 | 0.11405267 | 0 | 0.10757174 |
| TCGA-RC-A7SF | 0 | 0.09165631 | 0.34471911 | 0.12010895 | 0.10655048 | 0.09606579 | 0.10900504 | 0 | 0.11466157 |
| TCGA-RC-A7SH | 0.12769703 | 0.08539329 | 0.52437179 | 0 | 0.13763243 | 0 | 0.0790028 | 0 | 0 |

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|---|---|---|---|---|---|---|---|---|---|
| TCGA-RC-A7SK | 0 | 0.1490753 | 0.35606862 | 0 | 0.13546752 | 0.26941062 | 0.08997793 | 0 | 0 |
| TCGA-RG-A7D4 | 0 | 0.12848425 | 0.78522627 | 0 | 0 | 0 | 0 | 0 | 0 |
| TCGA-T1-A6J8 | 0 | 0.27630342 | 0.40394111 | 0.0913807 | 0 | 0.10744616 | 0 | 0 | 0.11268908 |
| TCGA-UB-A7MA | 0.14572036 | 0 | 0.80517749 | 0 | 0 | 0 | 0 | 0 | 0 |
| TCGA-UB-A7MB | 0 | 0.15024875 | 0.11961636 | 0 | 0.26370188 | 0 | 0.46643301 | 0 | 0 |
| TCGA-UB-A7MC | 0 | 0.09236381 | 0.87283277 | 0 | 0 | 0 | 0 | 0 | 0 |
| TCGA-UB-A7MD | 0.09633676 | 0.18370338 | 0.61226231 | 0 | 0 | 0 | 0 | 0 | 0 |
| TCGA-UB-A7ME | 0.0866608 | 0.11347405 | 0.4485529 | 0 | 0 | 0.08224966 | 0.26906259 | 0 | 0 |
| TCGA-UB-A7MF | 0.10013406 | 0.14963317 | 0.68086273 | 0 | 0.06008704 | 0 | 0 | 0 | 0 |
| TCGA-UB-AA0U | 0.08047357 | 0.10997343 | 0.65818909 | 0 | 0 | 0 | 0 | 0 | 0 |
| TCGA-UB-AA0V | 0.16642293 | 0.24554846 | 0.25712898 | 0 | 0.13884363 | 0 | 0 | 0.08998369 | 0.10207232 |
| TCGA-WJ-A86L | 0 | 0.18722758 | 0.67366519 | 0 | 0 | 0 | 0 | 0 | 0.08075987 |
| TCGA-WQ-A9G7 | 0.10669594 | 0.12319277 | 0.10186982 | 0.43018528 | 0.2380562 | 0 | 0 | 0 | 0 |
| TCGA-WQ-AB4B | 0.06673953 | 0.07166547 | 0.80466084 | 0 | 0 | 0 | 0 | 0 | 0 |
| TCGA-WX-AA44 | 0.06896674 | 0.14991583 | 0.60157227 | 0 | 0.11937491 | 0 | 0.06017024 | 0 | 0 |
| TCGA-WX-AA46 | 0 | 0.14174031 | 0.67477994 | 0 | 0.11819874 | 0 | 0 | 0 | 0 |
| TCGA-WX-AA47 | 0 | 0 | 0.85802466 | 0 | 0 | 0 | 0 | 0 | 0 |
| TCGA-XR-A8TC | 0.1164578 | 0.2476712 | 0.49867453 | 0 | 0 | 0 | 0 | 0 | 0 |
| TCGA-XR-A8TD | 0 | 0.21122674 | 0.73673356 | 0 | 0 | 0 | 0 | 0 | 0 |
| TCGA-XR-A8TE | 0.33036067 | 0.33537549 | 0 | 0 | 0.30136693 | 0 | 0 | 0 | 0 |
| TCGA-XR-A8TF | 0 | 0 | 0.40941996 | 0 | 0 | 0 | 0.29720217 | 0 | 0.17683653 |
| TCGA-XR-A8TG | 0 | 0.21674766 | 0.65274361 | 0 | 0.09473369 | 0 | 0 | 0 | 0 |
| TCGA-YA-A8S7 | 0.09979452 | 0 | 0.61372086 | 0 | 0.15017572 | 0 | 0 | 0 | 0.07756682 |
| TCGA-ZP-A9CV | 0 | 0 | 0.73898573 | 0 | 0.11325467 | 0 | 0 | 0 | 0.06912451 |
| TCGA-ZP-A9CY | 0 | 0.09619573 | 0.48985416 | 0.1136893 | 0.16436517 | 0 | 0 | 0 | 0.13589564 |
| TCGA-ZP-A9CZ | 0.12441455 | 0 | 0.44603259 | 0.06622589 | 0.13924958 | 0 | 0.06558576 | 0 | 0.09459701 |
| TCGA-ZP-A9D0 | 0.06745449 | 0 | 0.7175249 | 0 | 0 | 0 | 0.08884756 | 0 | 0.07558825 |
| TCGA-ZP-A9D1 | 0 | 0.14205 | 0.33124202 | 0 | 0.27476467 | 0 | 0.20289345 | 0 | 0 |
| TCGA-ZP-A9D2 | 0.07330562 | 0.12354847 | 0.44955698 | 0 | 0.2657461 | 0 | 0 | 0 | 0 |
| TCGA-ZP-A9D4 | 0.08458412 | 0 | 0.50721305 | 0 | 0.11330059 | 0 | 0 | 0 | 0.19002424 |
| TCGA-ZS-A9CD | 0 | 0.16032072 | 0.6038868 | 0 | 0 | 0 | 0 | 0.1065871 | 0 |
| TCGA-ZS-A9CE | 0.08054918 | 0.13989916 | 0.72091592 | 0 | 0 | 0 | 0 | 0 | 0 |
| TCGA-ZS-A9CF | 0 | 0.16262114 | 0.64084047 | 0 | 0 | 0 | 0.0948908 | 0 | 0 |

| TCGA-ZS-A9CG | 0 | 0.08654847 | 0.70760864 | 0 | 0 | 0 | 0.10812707 | 0.08001576 | 0 |

**Table S9: GISTIC peaks in Asian and European cohorts**

| Chr | Start | End | Descriptor | Type | Cohort | q.values | Gene.Symbol | Status |
|---|---|---|---|---|---|---|---|---|
| 1 | 121124911 | 145103927 | 1q21.1 | amp | ASIAN | 8.11E-05 | NA | Shared peak |
| 1 | 150460562 | 168519364 | 1q22 | amp | ASIAN | 0.0024811 | NA | Shared peak |
| 2 | 340935968 | 341050597 | 2p11.1 | amp | ASIAN | 4.32E-09 | NA | Shared peak |
| 3 | 659463375 | 690472424 | 3q29 | amp | ASIAN | 0.14801 | BDH1 | Shared peak |
| 4 | 729801527 | 731979093 | 4p14 | amp | ASIAN | 5.00E-04 | NA | Private amp |
| 5 | 882682663 | 882853016 | 5p15.33 | amp | ASIAN | 2.64E-06 | TERT | Shared peak |
| 5 | 1049868532 | 1062541960 | 5q35.2 | amp | ASIAN | 0.088559 | NSD1 | Shared peak |
| 6 | 1062541961 | 1073512967 | 6p25.3 | amp | ASIAN | 0.068883 | NA | Private amp |
| 6 | 1095031630 | 1095039860 | 6p21.32 | amp | ASIAN | 0.18708 | NA | Private amp |
| 6 | 1121319194 | 1132613132 | 6q12 | amp | ASIAN | 0.081582 | EYS | Shared peak |
| 6 | 1121319194 | 1132613132 | 6q12 | amp | ASIAN | 0.081582 | PHF3 | Shared peak |
| 7 | 1391633667 | 1391923977 | 7q36.3 | amp | ASIAN | 0.13082 | PTPRN2 | Shared peak |
| 8 | 1506451443 | 1523546688 | 8q24.13 | amp | ASIAN | 0.016365 | NA | Private amp |
| 11 | 1884963012 | 1885469340 | 11q13.3 | amp | ASIAN | 1.76E-15 | CCND1 | Shared peak |
| 11 | 1884963012 | 1885469340 | 11q13.3 | amp | ASIAN | 1.76E-15 | FGF19 | Shared peak |
| 13 | 2180652651 | 2199936179 | 13q34 | amp | ASIAN | 1.35E-10 | ING1 | Shared peak |
| 14 | 2199936180 | 2219496035 | 14q11.2 | amp | ASIAN | 0.029451 | CHD8 | Private amp |
| 14 | 2199936180 | 2219496035 | 14q11.2 | amp | ASIAN | 0.029451 | PRMT5 | Private amp |
| 16 | 2443236820 | 2457303927 | 16q11.2 | amp | ASIAN | 4.53E-15 | NA | Shared peak |
| 17 | 2520852936 | 2520970982 | 17p11.2 | amp | ASIAN | 0.015886 | NA | Private amp |
| 17 | 2579327271 | 2581367074 | 17q25.3 | amp | ASIAN | 0.052112 | CBX8 | Private amp |
| 17 | 2579327271 | 2581367074 | 17q25.3 | amp | ASIAN | 0.052112 | FOXK2 | Private amp |
| 18 | 2658746978 | 2658824809 | 18q23 | amp | ASIAN | 0.12232 | NA | Private amp |
| 19 | 2673729311 | 2674829948 | 19p13.12 | amp | ASIAN | 0.045401 | NOTCH3 | Private amp |
| 19 | 2673729311 | 2674829948 | 19p13.12 | amp | ASIAN | 0.045401 | BRD4 | Private amp |
| 19 | 2677937514 | 2681264096 | 19p13.11 | amp | ASIAN | 0.071994 | NA | Private amp |
| 19 | 2699132751 | 2701151724 | 19q13.2 | amp | ASIAN | 0.049956 | PAF1 | Private amp |
| 1 | 1 | 8417570 | 1p36.31 | del | ASIAN | 2.71E-17 | RPL22 | Shared peak |
| 2 | 304123567 | 439564226 | 2q31.2 | del | ASIAN | 0.20089 | NFE2L2 | Shared peak |
| 2 | 484020028 | 492449994 | 2q37.3 | del | ASIAN | 0.0077107 | ING5 | Shared peak |
| 4 | 748348736 | 800206972 | 4q13.3 | del | ASIAN | 0.017161 | COX18 | Shared peak |
| 4 | 748348736 | 800206972 | 4q13.3 | del | ASIAN | 0.017161 | ALB | Shared peak |
| 4 | 861470534 | 881626700 | 4q35.1 | del | ASIAN | 1.29E-12 | NA | Shared peak |
| 6 | 1231852223 | 1233657027 | 6q27 | del | ASIAN | 2.39E-06 | PHF10 | Shared peak |
| 8 | 1399548263 | 1400512832 | 8p23.1 | del | ASIAN | 0.017161 | NA | Shared peak |
| 9 | 1558926635 | 1566328026 | 9p21.3 | del | ASIAN | 3.19E-04 | CDKN2A | Shared peak |
| 9 | 1558926635 | 1566328026 | 9p21.3 | del | ASIAN | 3.19E-04 | CDKN2B | Shared peak |
| 9 | 1583334731 | 1605659606 | 9p11.2 | del | ASIAN | 0.13654 | NA | Shared peak |
| 11 | 1881292846 | 1881945346 | 11q13.1 | del | ASIAN | 0.21741 | NA | Private del |
| 11 | 1815907891 | 1950914406 | 11q22.3 | del | ASIAN | 0.18936 | ATM | Shared peak |
| 12 | 2071832920 | 2084766301 | 12q24.32 | del | ASIAN | 0.061234 | NA | Shared peak |
| 13 | 2084766302 | 2126791164 | 13q12.11 | del | ASIAN | 0.024817 | MPHOSPH8 | Private del |
| 13 | 2084766302 | 2126791164 | 13q12.11 | del | ASIAN | 0.024817 | XPO4 | Private del |
| 13 | 2129229282 | 2136253547 | 13q14.2 | del | ASIAN | 8.46E-11 | RB1 | Shared peak |
| 14 | 2306067962 | 2306727184 | 14q32.33 | del | ASIAN | 0.0023367 | TDRD9 | Shared peak |
| 14 | 2306067962 | 2306727184 | 14q32.33 | del | ASIAN | 0.0023367 | AKT1 | Shared peak |
| 15 | 2329403992 | 2329832159 | 15q11.2 | del | ASIAN | 4.89E-05 | NA | Private del |
| 15 | 2393618570 | 2409817111 | 15q26.3 | del | ASIAN | 0.011676 | IGF1R | Shared peak |
| 16 | 2409817112 | 2410241164 | 16p13.3 | del | ASIAN | 0.0054228 | AXIN1 | Shared peak |
| 16 | 2409817112 | 2410241164 | 16p13.3 | del | ASIAN | 0.0054228 | TSC2 | Shared peak |

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|---|---|---|---|---|---|---|---|---|
| 16 | 2409817112 | 2410241164 | 16p13.3 | del | ASIAN | 0.0054228 | RBFOX1 | Shared peak |
| 16 | 2442831013 | 2457303927 | 16q11.2 | del | ASIAN | 1.25E-23 | NA | Shared peak |
| 16 | 2487058908 | 2500171864 | 16q24.3 | del | ASIAN | 0.010288 | NA | Private del |
| 22 | 2829728721 | 2860214161 | 22q11.1 | del | ASIAN | 0.091645 | NA | Shared peak |
| 1 | 16731648 | 16902893 | 1p36.13 | amp | EUROPEAN | 0.017814 | NA | Private amp |
| 1 | 121124363 | 145075207 | 1q21.1 | amp | EUROPEAN | 3.21E-06 | NA | Shared peak |
| 1 | 149726033 | 151740447 | 1q21.3 | amp | EUROPEAN | 1.06E-08 | MCL1 | Shared peak |
| 1 | 149726033 | 151740447 | 1q21.3 | amp | EUROPEAN | 1.06E-08 | ARNT | Shared peak |
| 1 | 149726033 | 151740447 | 1q21.3 | amp | EUROPEAN | 1.06E-08 | KCNN3 | Shared peak |
| 1 | 248722452 | 249250621 | 1q44 | amp | EUROPEAN | 4.11E-04 | SMYD3 | Private amp |
| 2 | 249250622 | 270144360 | 2p24.2 | amp | EUROPEAN | 0.056761 | NA | Private amp |
| 2 | 340928288 | 341059847 | 2p11.1 | amp | EUROPEAN | 3.20E-05 | NA | Shared peak |
| 3 | 663882472 | 666457430 | 3q26.31 | amp | EUROPEAN | 0.10402 | NA | Shared peak |
| 4 | 760260678 | 760473436 | 4q13.2 | amp | EUROPEAN | 0.15697 | NA | Private amp |
| 5 | 882720562 | 882956952 | 5p15.33 | amp | EUROPEAN | 0.0043469 | TERT | Shared peak |
| 5 | 1060689243 | 1062541960 | 5q35.3 | amp | EUROPEAN | 0.10793 | PRELID1 | Shared peak |
| 6 | 1095092059 | 1095151085 | 6p21.32 | amp | EUROPEAN | 0.0041401 | NA | Private amp |
| 6 | 1106141067 | 1106558970 | 6p21.1 | amp | EUROPEAN | 4.85E-04 | CRIP3 | Private amp |
| 6 | 1120014494 | 1127567805 | 6p11.1 | amp | EUROPEAN | 9.46E-05 | NA | Shared peak |
| 7 | 1349797552 | 1354636745 | 7q31.2 | amp | EUROPEAN | 0.0010993 | MET | Private amp |
| 7 | 1391054539 | 1391991961 | 7q36.3 | amp | EUROPEAN | 0.12502 | PTPRN2 | Shared peak |
| 8 | 1478227557 | 1479864810 | 8q21.2 | amp | EUROPEAN | 0.070871 | NA | Private amp |
| 8 | 1535298124 | 1536218523 | 8q24.3 | amp | EUROPEAN | 0.033342 | PARP10 | Private amp |
| 8 | 1535298124 | 1536218523 | 8q24.3 | amp | EUROPEAN | 0.033342 | CYC1 | Private amp |
| 9 | 1678428165 | 1678807797 | 9q34.3 | amp | EUROPEAN | 0.23077 | NOTCH1 | Private amp |
| 11 | 1884646820 | 1885533400 | 11q13.3 | amp | EUROPEAN | 4.54E-09 | CCND1 | Shared peak |
| 11 | 1884646820 | 1885533400 | 11q13.3 | amp | EUROPEAN | 4.54E-09 | FGF19 | Shared peak |
| 12 | 1951579982 | 1953482287 | 12p13.33 | amp | EUROPEAN | 0.22316 | KDM5A | Private amp |
| 12 | 2008914416 | 2010204813 | 12q14.1 | amp | EUROPEAN | 0.056761 | CDK4 | Private amp |
| 13 | 2181296653 | 2199936179 | 13q34 | amp | EUROPEAN | 1.85E-05 | ING1 | Shared peak |
| 15 | 2407179476 | 2409817111 | 15q26.3 | amp | EUROPEAN | 0.024383 | IGF1R | Private amp |
| 16 | 2443242029 | 2462795260 | 16q11.2 | amp | EUROPEAN | 6.36E-34 | NA | Shared peak |
| 17 | 2521492661 | 2526153585 | 17p11.2 | amp | EUROPEAN | 0.070871 | NA | Private amp |
| 17 | 2573089279 | 2573386206 | 17q25.1 | amp | EUROPEAN | 1.17E-04 | NA | Private amp |
| 19 | 2668448072 | 2668532651 | 19p13.2 | amp | EUROPEAN | 0.010132 | MRPL4 | Private amp |
| 19 | 2668448072 | 2668532651 | 19p13.2 | amp | EUROPEAN | 0.010132 | KEAP1 | Private amp |
| 20 | 2718573306 | 2781598825 | 20q13.2 | amp | EUROPEAN | 0.057958 | ZNF217 | Private amp |
| 20 | 2768971655 | 2772985203 | 20q13.2 | amp | EUROPEAN | 0.057958 | ZNF217 | Private amp |
| 22 | 2867215496 | 2868962806 | 22q13.1 | amp | EUROPEAN | 0.099588 | TNRC6B | Private amp |
| 1 | 2309793 | 6654351 | 1p36.31 | del | EUROPEAN | 1.86E-19 | RPL22 | Shared peak |
| 1 | 16950405 | 17007888 | 1p36.13 | del | EUROPEAN | 6.96E-18 | NA | Private del |
| 2 | 388572751 | 407369654 | 2q22.1 | del | EUROPEAN | 3.50E-04 | LRP1B | Shared peak |
| 2 | 482970449 | 492449994 | 2q37.3 | del | EUROPEAN | 0.010525 | ING5 | Shared peak |
| 3 | 538388356 | 558883326 | 3p21.1 | del | EUROPEAN | 0.0017145 | BAP1 | Private del |
| 3 | 538388356 | 558883326 | 3p21.1 | del | EUROPEAN | 0.0017145 | PBRM1 | Private del |
| 3 | 539179193 | 590113645 | 3p13 | del | EUROPEAN | 0.0093281 | NA | Private del |
| 3 | 686762822 | 690472424 | 3q29 | del | EUROPEAN | 0.017818 | BDH1 | Private del |
| 4 | 693948060 | 694251946 | 4p16.3 | del | EUROPEAN | 0.045018 | FGFR3 | Private del |
| 4 | 693948060 | 694251946 | 4p16.3 | del | EUROPEAN | 0.045018 | LETM1 | Private del |
| 4 | 753336394 | 804211969 | 4q21.23 | del | EUROPEAN | 9.84E-07 | NA | Shared peak |
| 4 | 778481941 | 779215159 | 4q22.1 | del | EUROPEAN | 8.22E-08 | FAM190A | Shared peak |
| 4 | 764333152 | 800833263 | 4q23 | del | EUROPEAN | 5.10E-05 | ADH1B | Shared peak |

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|---|---|---|---|---|---|---|---|---|
| 4 | 868750395 | 881626700 | 4q35.2 | del | EUROPEAN | 4.85E-06 | FAT1 | Shared peak |
| 4 | 868750395 | 881626700 | 4q35.2 | del | EUROPEAN | 4.85E-06 | FRG1 | Shared peak |
| 5 | 946616656 | 1019146832 | 5q14.3 | del | EUROPEAN | 0.175 | NA | Private del |
| 6 | 1143291549 | 1173288466 | 6q16.1 | del | EUROPEAN | 0.038251 | NA | Private del |
| 6 | 1231253131 | 1233657027 | 6q27 | del | EUROPEAN | 0.0051302 | PHF10 | Shared peak |
| 7 | 1233657028 | 1240775271 | 7p22.3 | del | EUROPEAN | 0.18864 | NA | Private del |
| 7 | 1384891620 | 1392795690 | 7q36.3 | del | EUROPEAN | 0.12689 | PTPRN2 | Private del |
| 8 | 1394886875 | 1400090031 | 8p23.1 | del | EUROPEAN | 0.0053602 | NA | Shared peak |
| 9 | 1539159713 | 1544330370 | 9p24.2 | del | EUROPEAN | 0.24834 | NA | Private del |
| 9 | 1559780288 | 1566276510 | 9p21.2 | del | EUROPEAN | 0.026514 | NA | Shared peak |
| 9 | 1579913496 | 1605659481 | 9p12 | del | EUROPEAN | 0.0018691 | NA | Shared peak |
| 9 | 1665019423 | 1680373143 | 9q34.3 | del | EUROPEAN | 0.013722 | NOTCH1 | Private del |
| 10 | 1798074294 | 1814293217 | 10q26.11 | del | EUROPEAN | 2.39E-04 | NA | Private del |
| 11 | 1815907891 | 1816555338 | 11p15.5 | del | EUROPEAN | 4.84E-04 | SIRT3 | Shared peak |
| 11 | 1815907891 | 1816555338 | 11p15.5 | del | EUROPEAN | 4.84E-04 | PHRF1 | Shared peak |
| 11 | 1918863697 | 1950914406 | 11q25 | del | EUROPEAN | 0.17979 | NA | Shared peak |
| 12 | 1950914407 | 1965689665 | 12p13.31 | del | EUROPEAN | 0.13301 | NA | Private del |
| 12 | 2072924778 | 2084766301 | 12q24.33 | del | EUROPEAN | 0.030845 | NA | Shared peak |
| 13 | 2131445284 | 2145007261 | 13q14.2 | del | EUROPEAN | 8.96E-09 | RB1 | Shared peak |
| 13 | 2155081109 | 2160627679 | 13q22.2 | del | EUROPEAN | 1.74E-06 | NA | Private del |
| 14 | 2305855341 | 2307285719 | 14q32.33 | del | EUROPEAN | 2.60E-08 | TDRD9 | Shared peak |
| 14 | 2305855341 | 2307285719 | 14q32.33 | del | EUROPEAN | 2.60E-08 | AKT1 | Shared peak |
| 15 | 2392475184 | 2409817111 | 15q26.1 | del | EUROPEAN | 0.18013 | NA | Shared peak |
| 16 | 2409817112 | 2410255666 | 16p13.3 | del | EUROPEAN | 3.07E-04 | AXIN1 | Shared peak |
| 16 | 2409817112 | 2410255666 | 16p13.3 | del | EUROPEAN | 3.07E-04 | TSC2 | Shared peak |
| 16 | 2409817112 | 2410255666 | 16p13.3 | del | EUROPEAN | 3.07E-04 | RBFOX1 | Shared peak |
| 16 | 2442288777 | 2462786552 | 16q11.2 | del | EUROPEAN | 6.91E-22 | NA | Shared peak |
| 17 | 2520620148 | 2526259755 | 17p11.2 | del | EUROPEAN | 0.075925 | NA | Private del |
| 19 | 2659444323 | 2662925142 | 19p13.3 | del | EUROPEAN | 0.034126 | STK11 | Private del |
| 21 | 2811969411 | 2814638523 | 21q21.3 | del | EUROPEAN | 0.06626 | NA | Private del |
| 21 | 2819383192 | 2829728720 | 21q22.3 | del | EUROPEAN | 0.21707 | PTTG1IP | Private del |
| 22 | 2829728721 | 2846178503 | 22q11.1 | del | EUROPEAN | 0.034387 | NA | Shared peak |
| 22 | 2880413370 | 2881033286 | 22q13.33 | del | EUROPEAN | 9.45E-04 | BRD1 | Private del |
| 22 | 2880413370 | 2881033286 | 22q13.33 | del | EUROPEAN | 9.45E-04 | HDAC10 | Private del |

**Table S10: Correlation p-value of each feature pair across TCGA, Asian and European cohorts**

| Feature 1 | Feature 2 | p-value | fdr | Cohort |
|---|---|---|---|---|
| Age | pLMC | 0.059174313 | 0.153414886 | TCGA |
| Age | race | 1.52E-10 | 3.54E-09 | TCGA |
| Age | pLMC | 0.092070849 | 0.312383236 | Asian |
| Age | pLMC | 0.033197698 | 0.157044702 | European |
| AMP_5p | ARID2 | 0.072786516 | 0.184158655 | TCGA |
| AMP_5p | grade | 0.885876141 | 0.973999945 | TCGA |
| AMP_5p | Shannon | 0.200673654 | 0.41315164 | TCGA |
| AMP_5p | SBS22 | 0.11385832 | 0.254364333 | TCGA |
| AMP_5p | TMB | 0.029824207 | 0.097860679 | TCGA |
| AMP_5p | DOCK2 | 1 | 1 | TCGA |
| AMP_5p | HBV | 0.012490644 | 0.048574726 | TCGA |
| AMP_5p | MDSC | 0.006627813 | 0.028996684 | TCGA |
| AMP_5p | SCNA | 3.34E-07 | 4.38E-06 | TCGA |
| AMP_5p | Stage | 0.333382475 | 0.560082558 | TCGA |
| AMP_5p | ARID1A | 0.095309036 | 0.222833524 | TCGA |
| AMP_5p | RNAGR | 0.078497696 | 0.193355187 | TCGA |
| AMP_5p | Purity | 0.927338604 | 0.993577075 | TCGA |
| AMP_5p | DEL_4q | 0.079183553 | 0.193355187 | TCGA |
| AMP_5p | APOB | 1 | 1 | TCGA |
| AMP_5p | Age | 0.903409886 | 0.98370096 | TCGA |
| AMP_5p | pLMC | 0.021362899 | 0.073377643 | TCGA |
| AMP_5p | race | 1 | 1 | TCGA |
| AMP_5p | ARID2 | 0.315829691 | 0.697763271 | Asian |
| AMP_5p | grade | 0.79558803 | 0.998852414 | Asian |
| AMP_5p | Shannon | 0.053744685 | 0.208397756 | Asian |
| AMP_5p | SBS22 | 0.055950621 | 0.21261236 | Asian |
| AMP_5p | TMB | 0.56873869 | 0.834180629 | Asian |
| AMP_5p | DOCK2 | 0.344930602 | 0.712231422 | Asian |
| AMP_5p | HBV | 0.001988622 | 0.01889191 | Asian |
| AMP_5p | MDSC | 0.015351255 | 0.074788165 | Asian |
| AMP_5p | SCNA | 6.07E-04 | 0.006406768 | Asian |
| AMP_5p | Stage | 0.239386338 | 0.590693561 | Asian |
| AMP_5p | ARID1A | 0.195849905 | 0.518662929 | Asian |
| AMP_5p | RNAGR | 0.359864297 | 0.712231422 | Asian |
| AMP_5p | Purity | 0.886675269 | 1 | Asian |
| AMP_5p | DEL_4q | 0.049667726 | 0.200018638 | Asian |
| AMP_5p | APOB | 1 | 1 | Asian |
| AMP_5p | Age | 0.805624085 | 0.998852414 | Asian |
| AMP_5p | pLMC | 0.409406683 | 0.753706474 | Asian |
| AMP_5p | ARID2 | 0.148555064 | 0.409064669 | European |
| AMP_5p | grade | 0.767582572 | 0.925028382 | European |
| AMP_5p | Shannon | 0.945809368 | 0.996687335 | European |
| AMP_5p | SBS22 | 0.943921748 | 0.996687335 | European |
| AMP_5p | TMB | 0.016596667 | 0.092746081 | European |
| AMP_5p | DOCK2 | 0.403571158 | 0.737293462 | European |
| AMP_5p | HBV | 0.739966853 | 0.924958566 | European |
| AMP_5p | MDSC | 0.101818391 | 0.31713925 | European |
| AMP_5p | SCNA | 1.23E-04 | 0.001804124 | European |

| | | | | |
|---|---|---|---|---|
| AMP_5p | Stage | 0.948089224 | 0.996687335 | European |
| AMP_5p | ARID1A | 0.313010182 | 0.631685223 | European |
| AMP_5p | RNAGR | 0.062307046 | 0.236766776 | European |
| AMP_5p | Purity | 0.95475772 | 0.996725092 | European |
| AMP_5p | DEL_4q | 0.574224969 | 0.865894794 | European |
| AMP_5p | APOB | 0.764719727 | 0.925028382 | European |
| AMP_5p | Age | 0.885457639 | 0.980190904 | European |
| AMP_5p | pLMC | 0.011536693 | 0.07306572 | European |
| APOB | Age | 0.041167263 | 0.127134195 | TCGA |
| APOB | pLMC | 0.091111366 | 0.21742485 | TCGA |
| APOB | race | 0.682223591 | 0.864365633 | TCGA |
| APOB | Age | 0.249313965 | 0.599615865 | Asian |
| APOB | pLMC | 0.344258619 | 0.712231422 | Asian |
| APOB | Age | 0.023544266 | 0.120902985 | European |
| APOB | pLMC | 0.211084318 | 0.501325254 | European |
| ARID1A | RNAGR | 0.985317845 | 1 | TCGA |
| ARID1A | Purity | 0.423684299 | 0.649443086 | TCGA |
| ARID1A | DEL_4q | 0.475061723 | 0.711947474 | TCGA |
| ARID1A | APOB | 0.407008571 | 0.634251265 | TCGA |
| ARID1A | Age | 0.775283968 | 0.919828436 | TCGA |
| ARID1A | pLMC | 0.689767834 | 0.864365633 | TCGA |
| ARID1A | race | 0.81465576 | 0.924533162 | TCGA |
| ARID1A | RNAGR | 0.912025737 | 1 | Asian |
| ARID1A | Purity | 0.814424387 | 0.998852414 | Asian |
| ARID1A | DEL_4q | 0.514823503 | 0.794750507 | Asian |
| ARID1A | APOB | 1 | 1 | Asian |
| ARID1A | Age | 0.632490038 | 0.88645336 | Asian |
| ARID1A | pLMC | 0.827753036 | 1 | Asian |
| ARID1A | RNAGR | 0.474911339 | 0.79852349 | European |
| ARID1A | Purity | 0.186904118 | 0.455279263 | European |
| ARID1A | DEL_4q | 1 | 1 | European |
| ARID1A | APOB | 0.177053025 | 0.445556101 | European |
| ARID1A | Age | 0.338185126 | 0.662424473 | European |
| ARID1A | pLMC | 0.736636316 | 0.924958566 | European |
| ARID2 | grade | 0.691492507 | 0.864365633 | TCGA |
| ARID2 | Shannon | 0.332061983 | 0.560082558 | TCGA |
| ARID2 | SBS22 | 0.993846093 | 1 | TCGA |
| ARID2 | TMB | 0.331955061 | 0.560082558 | TCGA |
| ARID2 | DOCK2 | 0.015311548 | 0.055860754 | TCGA |
| ARID2 | HBV | 0.595364803 | 0.80145262 | TCGA |
| ARID2 | MDSC | 0.795437482 | 0.924533162 | TCGA |
| ARID2 | SCNA | 0.662606498 | 0.853664814 | TCGA |
| ARID2 | Stage | 0.756706948 | 0.902888973 | TCGA |
| ARID2 | ARID1A | 0.6176488 | 0.81459206 | TCGA |
| ARID2 | RNAGR | 0.342957108 | 0.563082082 | TCGA |
| ARID2 | Purity | 0.913436606 | 0.98370096 | TCGA |
| ARID2 | DEL_4q | 1 | 1 | TCGA |
| ARID2 | APOB | 0.671326802 | 0.859625783 | TCGA |
| ARID2 | Age | 0.505942464 | 0.73783276 | TCGA |
| ARID2 | pLMC | 0.167811944 | 0.359597022 | TCGA |

| ARID2 | race | 0.805620701 | 0.924533162 | TCGA |
|---|---|---|---|---|
| ARID2 | grade | 0.843509498 | 1 | Asian |
| ARID2 | Shannon | 0.459128146 | 0.778878106 | Asian |
| ARID2 | SBS22 | 0.374165827 | 0.723142858 | Asian |
| ARID2 | TMB | 0.296640089 | 0.679055625 | Asian |
| ARID2 | DOCK2 | 0.027177341 | 0.120085927 | Asian |
| ARID2 | HBV | 1 | 1 | Asian |
| ARID2 | MDSC | 0.939197656 | 1 | Asian |
| ARID2 | SCNA | 0.907292023 | 1 | Asian |
| ARID2 | Stage | 0.813878425 | 0.998852414 | Asian |
| ARID2 | ARID1A | 1 | 1 | Asian |
| ARID2 | RNAGR | 0.774185703 | 0.980635224 | Asian |
| ARID2 | Purity | 0.581576814 | 0.843508357 | Asian |
| ARID2 | DEL_4q | 1 | 1 | Asian |
| ARID2 | APOB | 1 | 1 | Asian |
| ARID2 | Age | 0.530285084 | 0.795908825 | Asian |
| ARID2 | pLMC | 0.871902184 | 1 | Asian |
| ARID2 | grade | 0.356948854 | 0.683439709 | European |
| ARID2 | Shannon | 0.62740634 | 0.899648937 | European |
| ARID2 | SBS22 | 0.164861252 | 0.430733004 | European |
| ARID2 | TMB | 0.732556439 | 0.924958566 | European |
| ARID2 | DOCK2 | 0.305937562 | 0.631685223 | European |
| ARID2 | HBV | 0.461119771 | 0.789304113 | European |
| ARID2 | MDSC | 0.812486009 | 0.964827136 | European |
| ARID2 | SCNA | 0.651985341 | 0.917608999 | European |
| ARID2 | Stage | 0.50392139 | 0.818333882 | European |
| ARID2 | ARID1A | 1 | 1 | European |
| ARID2 | RNAGR | 0.219843624 | 0.515682575 | European |
| ARID2 | Purity | 0.559689692 | 0.864561313 | European |
| ARID2 | DEL_4q | 1 | 1 | European |
| ARID2 | APOB | 0.526623421 | 0.842188639 | European |
| ARID2 | Age | 0.791486484 | 0.945801459 | European |
| ARID2 | pLMC | 0.049592124 | 0.196302156 | European |
| DEL_16q | GEP | 0.05065576 | 0.143888737 | TCGA |
| DEL_16q | AMP_5p | 0.534757145 | 0.751106402 | TCGA |
| DEL_16q | ARID2 | 0.62064157 | 0.81459206 | TCGA |
| DEL_16q | grade | 0.047548168 | 0.140635427 | TCGA |
| DEL_16q | Shannon | 0.839931005 | 0.933256672 | TCGA |
| DEL_16q | SBS22 | 0.856353241 | 0.946495687 | TCGA |
| DEL_16q | TMB | 0.781953764 | 0.922529721 | TCGA |
| DEL_16q | DOCK2 | 0.321034134 | 0.557166678 | TCGA |
| DEL_16q | HBV | 0.300677693 | 0.539677911 | TCGA |
| DEL_16q | MDSC | 2.65E-05 | 1.86E-04 | TCGA |
| DEL_16q | SCNA | 7.17E-07 | 7.92E-06 | TCGA |
| DEL_16q | Stage | 0.264542172 | 0.482994196 | TCGA |
| DEL_16q | ARID1A | 0.343211936 | 0.563082082 | TCGA |
| DEL_16q | RNAGR | 1.75E-12 | 5.25E-11 | TCGA |
| DEL_16q | Purity | 0.479190247 | 0.711947474 | TCGA |
| DEL_16q | DEL_4q | 1.17E-07 | 1.75E-06 | TCGA |
| DEL_16q | APOB | 0.003664109 | 0.016727453 | TCGA |

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|---|---|---|---|---|
| DEL_16q | Age | 0.008967491 | 0.037663463 | TCGA |
| DEL_16q | pLMC | 0.044145735 | 0.134356584 | TCGA |
| DEL_16q | race | 0.068304913 | 0.174927216 | TCGA |
| DEL_16q | GEP | 0.136075049 | 0.417004181 | Asian |
| DEL_16q | AMP_5p | 0.478540776 | 0.784573612 | Asian |
| DEL_16q | ARID2 | 1 | 1 | Asian |
| DEL_16q | grade | 0.918198526 | 1 | Asian |
| DEL_16q | Shannon | 0.840906353 | 1 | Asian |
| DEL_16q | SBS22 | 0.43938432 | 0.765899274 | Asian |
| DEL_16q | TMB | 0.138430433 | 0.417488608 | Asian |
| DEL_16q | DOCK2 | 0.534435875 | 0.795908825 | Asian |
| DEL_16q | HBV | 0.600847752 | 0.858353931 | Asian |
| DEL_16q | MDSC | 0.024664454 | 0.11157729 | Asian |
| DEL_16q | SCNA | 0.207335059 | 0.532346774 | Asian |
| DEL_16q | Stage | 0.195133979 | 0.518662929 | Asian |
| DEL_16q | ARID1A | 0.328241973 | 0.70074129 | Asian |
| DEL_16q | RNAGR | 1.73E-08 | 4.70E-07 | Asian |
| DEL_16q | Purity | 0.645894842 | 0.88645336 | Asian |
| DEL_16q | DEL_4q | 5.61E-05 | 8.89E-04 | Asian |
| DEL_16q | APOB | 0.003688261 | 0.028030786 | Asian |
| DEL_16q | Age | 0.004181116 | 0.029422667 | Asian |
| DEL_16q | pLMC | 0.485175557 | 0.784573612 | Asian |
| DEL_16q | GEP | 0.27075468 | 0.591303325 | European |
| DEL_16q | AMP_5p | 0.078391861 | 0.261306203 | European |
| DEL_16q | ARID2 | 0.714918484 | 0.924958566 | European |
| DEL_16q | grade | 0.009839888 | 0.064468235 | European |
| DEL_16q | Shannon | 0.694872238 | 0.924958566 | European |
| DEL_16q | SBS22 | 0.731446928 | 0.924958566 | European |
| DEL_16q | TMB | 0.127417587 | 0.374367518 | European |
| DEL_16q | DOCK2 | 0.686506056 | 0.924958566 | European |
| DEL_16q | HBV | 0.315842612 | 0.631685223 | European |
| DEL_16q | MDSC | 0.00109381 | 0.010391195 | European |
| DEL_16q | SCNA | 1.22E-07 | 5.81E-06 | European |
| DEL_16q | Stage | 0.542459178 | 0.851795404 | European |
| DEL_16q | ARID1A | 1 | 1 | European |
| DEL_16q | RNAGR | 3.00E-04 | 0.003355061 | European |
| DEL_16q | Purity | 0.266837609 | 0.590610554 | European |
| DEL_16q | DEL_4q | 0.004413236 | 0.03225057 | European |
| DEL_16q | APOB | 0.35970511 | 0.683439709 | European |
| DEL_16q | Age | 0.480798177 | 0.801330295 | European |
| DEL_16q | pLMC | 7.91E-04 | 0.008344684 | European |
| DEL_4q | APOB | 0.407732956 | 0.634251265 | TCGA |
| DEL_4q | Age | 0.001092594 | 0.005306399 | TCGA |
| DEL_4q | pLMC | 0.001337794 | 0.006243041 | TCGA |
| DEL_4q | race | 1.01E-05 | 7.83E-05 | TCGA |
| DEL_4q | APOB | 0.096621855 | 0.322072851 | Asian |
| DEL_4q | Age | 0.029114543 | 0.125721892 | Asian |
| DEL_4q | pLMC | 0.038569979 | 0.162851022 | Asian |
| DEL_4q | APOB | 0.755518997 | 0.925028382 | European |
| DEL_4q | Age | 0.690492523 | 0.924958566 | European |

| DEL_4q | pLMC | 0.042448806 | 0.176218766 | European |
|--------|------|-------------|-------------|----------|
| DOCK2 | HBV | 0.595364803 | 0.80145262 | TCGA |
| DOCK2 | MDSC | 0.317205373 | 0.555109402 | TCGA |
| DOCK2 | SCNA | 0.714368705 | 0.872194349 | TCGA |
| DOCK2 | Stage | 0.60829787 | 0.813646832 | TCGA |
| DOCK2 | ARID1A | 0.6176488 | 0.81459206 | TCGA |
| DOCK2 | RNAGR | 0.110125268 | 0.248669959 | TCGA |
| DOCK2 | Purity | 0.960475719 | 1 | TCGA |
| DOCK2 | DEL_4q | 1 | 1 | TCGA |
| DOCK2 | APOB | 0.215238586 | 0.431736514 | TCGA |
| DOCK2 | Age | 0.713050962 | 0.872194349 | TCGA |
| DOCK2 | pLMC | 0.022192278 | 0.073974261 | TCGA |
| DOCK2 | race | 0.215868257 | 0.431736514 | TCGA |
| DOCK2 | HBV | 0.344930602 | 0.712231422 | Asian |
| DOCK2 | MDSC | 0.376795489 | 0.723142858 | Asian |
| DOCK2 | SCNA | 0.831799141 | 1 | Asian |
| DOCK2 | Stage | 0.404380676 | 0.753258121 | Asian |
| DOCK2 | ARID1A | 1 | 1 | Asian |
| DOCK2 | RNAGR | 0.310207975 | 0.694107744 | Asian |
| DOCK2 | Purity | 0.353689558 | 0.712231422 | Asian |
| DOCK2 | DEL_4q | 1 | 1 | Asian |
| DOCK2 | APOB | 0.325794309 | 0.70074129 | Asian |
| DOCK2 | Age | 0.276878984 | 0.657587586 | Asian |
| DOCK2 | pLMC | 0.428137163 | 0.760243561 | Asian |
| DOCK2 | HBV | 0.060842883 | 0.235921384 | European |
| DOCK2 | MDSC | 0.929185869 | 0.996687335 | European |
| DOCK2 | SCNA | 0.908565541 | 0.992111798 | European |
| DOCK2 | Stage | 0.1786844 | 0.445556101 | European |
| DOCK2 | ARID1A | 1 | 1 | European |
| DOCK2 | RNAGR | 0.874451082 | 0.980190904 | European |
| DOCK2 | Purity | 0.527476042 | 0.842188639 | European |
| DOCK2 | DEL_4q | 0.667109595 | 0.924958566 | European |
| DOCK2 | APOB | 0.426776765 | 0.7578279 | European |
| DOCK2 | Age | 0.859039695 | 0.980190904 | European |
| DOCK2 | pLMC | 0.0177861 | 0.096553112 | European |
| GEP | AMP_5p | 0.22392717 | 0.435413942 | TCGA |
| GEP | ARID2 | 0.219661715 | 0.435178868 | TCGA |
| GEP | grade | 0.560658557 | 0.774594059 | TCGA |
| GEP | Shannon | 0.594909913 | 0.80145262 | TCGA |
| GEP | SBS22 | 0.22271748 | 0.435413942 | TCGA |
| GEP | TMB | 0.152441696 | 0.33346621 | TCGA |
| GEP | DOCK2 | 0.827930087 | 0.926169434 | TCGA |
| GEP | HBV | 0.008837469 | 0.037663463 | TCGA |
| GEP | MDSC | 7.80E-19 | 5.46E-17 | TCGA |
| GEP | SCNA | 8.02E-05 | 5.10E-04 | TCGA |
| GEP | Stage | 0.103252731 | 0.235685582 | TCGA |
| GEP | ARID1A | 0.209966261 | 0.428086551 | TCGA |
| GEP | RNAGR | 0.045130028 | 0.135390084 | TCGA |
| GEP | Purity | 3.33E-15 | 1.16E-13 | TCGA |
| GEP | DEL_4q | 0.077061042 | 0.192652606 | TCGA |

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|---|---|---|---|---|
| GEP | APOB | 0.529364502 | 0.751106402 | TCGA |
| GEP | Age | 0.68465296 | 0.864365633 | TCGA |
| GEP | pLMC | 4.60E-04 | 0.002474921 | TCGA |
| GEP | race | 0.510946167 | 0.739991 | TCGA |
| GEP | AMP_5p | 0.078379361 | 0.275779235 | Asian |
| GEP | ARID2 | 0.156966509 | 0.451873283 | Asian |
| GEP | grade | 0.160083192 | 0.453967261 | Asian |
| GEP | Shannon | 0.008663908 | 0.049883105 | Asian |
| GEP | SBS22 | 0.354699593 | 0.712231422 | Asian |
| GEP | TMB | 0.484862096 | 0.784573612 | Asian |
| GEP | DOCK2 | 0.676961973 | 0.905794189 | Asian |
| GEP | HBV | 2.49E-04 | 0.002788193 | Asian |
| GEP | MDSC | 1.71E-11 | 1.08E-09 | Asian |
| GEP | SCNA | 0.002343086 | 0.019612461 | Asian |
| GEP | Stage | 0.015067188 | 0.074788165 | Asian |
| GEP | ARID1A | 0.533359478 | 0.795908825 | Asian |
| GEP | RNAGR | 0.009883244 | 0.055229891 | Asian |
| GEP | Purity | 2.74E-11 | 1.30E-09 | Asian |
| GEP | DEL_4q | 0.233563662 | 0.583909154 | Asian |
| GEP | APOB | 0.724899467 | 0.949868267 | Asian |
| GEP | Age | 0.293947166 | 0.679055625 | Asian |
| GEP | pLMC | 0.013249208 | 0.068036476 | Asian |
| GEP | AMP_5p | 0.98607726 | 1 | European |
| GEP | ARID2 | 0.736035944 | 0.924958566 | European |
| GEP | grade | 0.468544829 | 0.794852834 | European |
| GEP | Shannon | 0.130043454 | 0.374367518 | European |
| GEP | SBS22 | 0.489417891 | 0.801632752 | European |
| GEP | TMB | 0.194620192 | 0.468073878 | European |
| GEP | DOCK2 | 0.358219763 | 0.683439709 | European |
| GEP | HBV | 0.274714582 | 0.593133757 | European |
| GEP | MDSC | 2.23E-09 | 2.12E-07 | European |
| GEP | SCNA | 0.012315775 | 0.07548378 | European |
| GEP | Stage | 0.949475829 | 0.996687335 | European |
| GEP | ARID1A | 0.283008691 | 0.604175857 | European |
| GEP | RNAGR | 0.413374346 | 0.742460115 | European |
| GEP | Purity | 2.92E-06 | 7.66E-05 | European |
| GEP | DEL_4q | 0.236185134 | 0.540664765 | European |
| GEP | APOB | 0.591616493 | 0.878277788 | European |
| GEP | Age | 0.568604994 | 0.865894794 | European |
| GEP | pLMC | 0.01526891 | 0.090659156 | European |
| grade | Shannon | 0.432255994 | 0.65778086 | TCGA |
| grade | SBS22 | 0.978043374 | 1 | TCGA |
| grade | TMB | 0.191538167 | 0.398247673 | TCGA |
| grade | DOCK2 | 0.657395953 | 0.853664814 | TCGA |
| grade | HBV | 7.04E-07 | 7.92E-06 | TCGA |
| grade | MDSC | 4.31E-04 | 0.002447443 | TCGA |
| grade | SCNA | 7.25E-04 | 0.003681903 | TCGA |
| grade | Stage | 0.310313847 | 0.547612672 | TCGA |
| grade | ARID1A | 0.520369928 | 0.748477293 | TCGA |
| grade | RNAGR | 4.08E-04 | 0.00237907 | TCGA |

| grade | Purity | 0.968980642 | 1 | TCGA |
|---|---|---|---|---|
| grade | DEL_4q | 0.009740545 | 0.039497889 | TCGA |
| grade | APOB | 0.447702619 | 0.676385251 | TCGA |
| grade | Age | 0.04854202 | 0.141580891 | TCGA |
| grade | pLMC | 0.536504573 | 0.751106402 | TCGA |
| grade | race | 5.15E-06 | 4.51E-05 | TCGA |
| grade | Shannon | 0.734536867 | 0.955055652 | Asian |
| grade | SBS22 | 0.48161385 | 0.784573612 | Asian |
| grade | TMB | 0.506141296 | 0.794750507 | Asian |
| grade | DOCK2 | 0.765508441 | 0.976151704 | Asian |
| grade | HBV | 0.002717771 | 0.021515689 | Asian |
| grade | MDSC | 0.310521885 | 0.694107744 | Asian |
| grade | SCNA | 0.184407556 | 0.515256406 | Asian |
| grade | Stage | 0.098332944 | 0.322125161 | Asian |
| grade | ARID1A | 0.907980956 | 1 | Asian |
| grade | RNAGR | 0.936397134 | 1 | Asian |
| grade | Purity | 0.706882992 | 0.932692837 | Asian |
| grade | DEL_4q | 0.570755167 | 0.834180629 | Asian |
| grade | APOB | 0.358229231 | 0.712231422 | Asian |
| grade | Age | 0.457205262 | 0.778878106 | Asian |
| grade | pLMC | 0.425819979 | 0.760243561 | Asian |
| grade | Shannon | 0.629754256 | 0.899648937 | European |
| grade | SBS22 | 0.53899478 | 0.851795404 | European |
| grade | TMB | 0.455708335 | 0.787132578 | European |
| grade | DOCK2 | 0.855731192 | 0.980190904 | European |
| grade | HBV | 0.435958383 | 0.763075229 | European |
| grade | MDSC | 0.003685141 | 0.028007072 | European |
| grade | SCNA | 0.004795106 | 0.033743342 | European |
| grade | Stage | 0.155748066 | 0.42274475 | European |
| grade | ARID1A | 0.136330504 | 0.386608891 | European |
| grade | RNAGR | 5.25E-05 | 9.07E-04 | European |
| grade | Purity | 0.595340911 | 0.878277788 | European |
| grade | DEL_4q | 0.162940861 | 0.430733004 | European |
| grade | APOB | 0.399917579 | 0.737293462 | European |
| grade | Age | 0.180567473 | 0.445556101 | European |
| grade | pLMC | 0.171132789 | 0.439394998 | European |
| HBV | MDSC | 0.732400017 | 0.882204919 | TCGA |
| HBV | SCNA | 0.484802328 | 0.711947474 | TCGA |
| HBV | Stage | 1.87E-05 | 1.35E-04 | TCGA |
| HBV | ARID1A | 0.801702811 | 0.924533162 | TCGA |
| HBV | RNAGR | 0.084542068 | 0.204067062 | TCGA |
| HBV | Purity | 0.158822221 | 0.343841923 | TCGA |
| HBV | DEL_4q | 0.001111817 | 0.005306399 | TCGA |
| HBV | APOB | 0.661823146 | 0.853664814 | TCGA |
| HBV | Age | 1.35E-05 | 1.01E-04 | TCGA |
| HBV | pLMC | 0.527422076 | 0.751106402 | TCGA |
| HBV | race | 8.83E-22 | 9.27E-20 | TCGA |
| HBV | MDSC | 7.51E-05 | 0.001098152 | Asian |
| HBV | SCNA | 0.371381707 | 0.723142858 | Asian |
| HBV | Stage | 4.18E-10 | 1.32E-08 | Asian |

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|---|---|---|---|---|
| HBV | ARID1A | 0.518679278 | 0.794750507 | Asian |
| HBV | RNAGR | 0.070677333 | 0.25337157 | Asian |
| HBV | Purity | 0.738911478 | 0.955055652 | Asian |
| HBV | DEL_4q | 0.593706733 | 0.854577874 | Asian |
| HBV | APOB | 1 | 1 | Asian |
| HBV | Age | 0.904809599 | 1 | Asian |
| HBV | pLMC | 0.433288715 | 0.762267185 | Asian |
| HBV | MDSC | 0.381100865 | 0.716922419 | European |
| HBV | SCNA | 0.596304393 | 0.878277788 | European |
| HBV | Stage | 0.43776421 | 0.763075229 | European |
| HBV | ARID1A | 0.129501169 | 0.374367518 | European |
| HBV | RNAGR | 0.710389066 | 0.924958566 | European |
| HBV | Purity | 0.110986229 | 0.340119089 | European |
| HBV | DEL_4q | 0.001178278 | 0.010660615 | European |
| HBV | APOB | 1 | 1 | European |
| HBV | Age | 0.093662771 | 0.301625873 | European |
| HBV | pLMC | 0.764356626 | 0.925028382 | European |
| MDSC | SCNA | 5.35E-24 | 1.12E-21 | TCGA |
| MDSC | Stage | 4.07E-06 | 3.72E-05 | TCGA |
| MDSC | ARID1A | 0.482595044 | 0.711947474 | TCGA |
| MDSC | RNAGR | 2.33E-06 | 2.45E-05 | TCGA |
| MDSC | Purity | 8.85E-16 | 3.72E-14 | TCGA |
| MDSC | DEL_4q | 2.46E-06 | 2.46E-05 | TCGA |
| MDSC | APOB | 0.244648152 | 0.462847856 | TCGA |
| MDSC | Age | 0.357641108 | 0.573317807 | TCGA |
| MDSC | pLMC | 3.21E-07 | 4.38E-06 | TCGA |
| MDSC | race | 2.18E-04 | 0.001308035 | TCGA |
| MDSC | SCNA | 2.90E-10 | 1.10E-08 | Asian |
| MDSC | Stage | 1.62E-04 | 0.00220197 | Asian |
| MDSC | ARID1A | 0.510414779 | 0.794750507 | Asian |
| MDSC | RNAGR | 1.82E-04 | 0.002300858 | Asian |
| MDSC | Purity | 3.07E-07 | 7.29E-06 | Asian |
| MDSC | DEL_4q | 0.059953393 | 0.223355776 | Asian |
| MDSC | APOB | 0.60715944 | 0.860897714 | Asian |
| MDSC | Age | 0.958499216 | 1 | Asian |
| MDSC | pLMC | 0.019305378 | 0.091700545 | Asian |
| MDSC | SCNA | 5.11E-14 | 9.71E-12 | European |
| MDSC | Stage | 0.001778592 | 0.014692718 | European |
| MDSC | ARID1A | 0.640995306 | 0.908873941 | European |
| MDSC | RNAGR | 9.22E-04 | 0.009217654 | European |
| MDSC | Purity | 5.52E-09 | 3.50E-07 | European |
| MDSC | DEL_4q | 1.58E-04 | 0.001995762 | European |
| MDSC | APOB | 0.334654031 | 0.662336103 | European |
| MDSC | Age | 0.611140665 | 0.886387225 | European |
| MDSC | pLMC | 2.98E-05 | 5.67E-04 | European |
| pLMC | race | 0.033150909 | 0.107102936 | TCGA |
| Purity | DEL_4q | 0.961963561 | 1 | TCGA |
| Purity | APOB | 0.735170766 | 0.882204919 | TCGA |
| Purity | Age | 0.544264842 | 0.756924615 | TCGA |
| Purity | pLMC | 0.058754886 | 0.153414886 | TCGA |

| Purity | race | 0.095500082 | 0.222833524 | TCGA |
|--------|------|-------------|-------------|------|
| Purity | DEL_4q | 0.322559857 | 0.70074129 | Asian |
| Purity | APOB | 0.649322677 | 0.88645336 | Asian |
| Purity | Age | 0.536191209 | 0.795908825 | Asian |
| Purity | pLMC | 0.189930431 | 0.518662929 | Asian |
| Purity | DEL_4q | 0.86765528 | 0.980190904 | European |
| Purity | APOB | 0.48679687 | 0.801632752 | European |
| Purity | Age | 0.234002537 | 0.540664765 | European |
| Purity | pLMC | 0.267328988 | 0.590610554 | European |
| RNAGR | Purity | 1.11E-09 | 2.12E-08 | TCGA |
| RNAGR | DEL_4q | 7.63E-06 | 6.16E-05 | TCGA |
| RNAGR | APOB | 0.340762926 | 0.563082082 | TCGA |
| RNAGR | Age | 3.10E-05 | 2.10E-04 | TCGA |
| RNAGR | pLMC | 0.00978043 | 0.039497889 | TCGA |
| RNAGR | race | 1.26E-10 | 3.32E-09 | TCGA |
| RNAGR | Purity | 3.17E-06 | 6.69E-05 | Asian |
| RNAGR | DEL_4q | 0.126330277 | 0.393487749 | Asian |
| RNAGR | APOB | 0.217948242 | 0.552135547 | Asian |
| RNAGR | Age | 9.95E-04 | 0.009949335 | Asian |
| RNAGR | pLMC | 1.95E-04 | 0.002310517 | Asian |
| RNAGR | Purity | 2.58E-06 | 7.66E-05 | European |
| RNAGR | DEL_4q | 0.001283541 | 0.011085126 | European |
| RNAGR | APOB | 0.932612643 | 0.996687335 | European |
| RNAGR | Age | 0.06599371 | 0.245858919 | European |
| RNAGR | pLMC | 0.024831157 | 0.124155784 | European |
| SBS22 | TMB | 1.04E-17 | 5.44E-16 | TCGA |
| SBS22 | DOCK2 | 0.053350831 | 0.145502268 | TCGA |
| SBS22 | HBV | 0.021663875 | 0.073377643 | TCGA |
| SBS22 | MDSC | 0.18746157 | 0.393669297 | TCGA |
| SBS22 | SCNA | 0.331124586 | 0.560082558 | TCGA |
| SBS22 | Stage | 0.975390294 | 1 | TCGA |
| SBS22 | ARID1A | 0.423592435 | 0.649443086 | TCGA |
| SBS22 | RNAGR | 0.052008294 | 0.145502268 | TCGA |
| SBS22 | Purity | 0.05070365 | 0.143888737 | TCGA |
| SBS22 | DEL_4q | 0.806317889 | 0.924533162 | TCGA |
| SBS22 | APOB | 0.723321532 | 0.878020357 | TCGA |
| SBS22 | Age | 0.251742596 | 0.46373636 | TCGA |
| SBS22 | pLMC | 4.55E-04 | 0.002474921 | TCGA |
| SBS22 | race | 5.57E-07 | 6.88E-06 | TCGA |
| SBS22 | TMB | 3.72E-14 | 7.07E-12 | Asian |
| SBS22 | DOCK2 | 0.688599269 | 0.914922105 | Asian |
| SBS22 | HBV | 0.415547713 | 0.753706474 | Asian |
| SBS22 | MDSC | 0.661596157 | 0.891512552 | Asian |
| SBS22 | SCNA | 0.904499654 | 1 | Asian |
| SBS22 | Stage | 0.987416029 | 1 | Asian |
| SBS22 | ARID1A | 0.641847856 | 0.88645336 | Asian |
| SBS22 | RNAGR | 0.384437657 | 0.723199553 | Asian |
| SBS22 | Purity | 0.416521999 | 0.753706474 | Asian |
| SBS22 | DEL_4q | 0.121382659 | 0.38437842 | Asian |
| SBS22 | APOB | 0.491834736 | 0.785282352 | Asian |

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|---|---|---|---|---|
| SBS22 | Age | 0.002312458 | 0.019612461 | Asian |
| SBS22 | pLMC | 0.005828863 | 0.038189106 | Asian |
| SBS22 | TMB | 0.071340683 | 0.255323224 | European |
| SBS22 | DOCK2 | 0.003466898 | 0.027446273 | European |
| SBS22 | HBV | 0.84726704 | 0.980190904 | European |
| SBS22 | MDSC | 0.895413555 | 0.98340217 | European |
| SBS22 | SCNA | 0.145817739 | 0.407431917 | European |
| SBS22 | Stage | 0.746152108 | 0.925028382 | European |
| SBS22 | ARID1A | 0.667375209 | 0.924958566 | European |
| SBS22 | RNAGR | 0.077759139 | 0.261306203 | European |
| SBS22 | Purity | 0.033920441 | 0.157044702 | European |
| SBS22 | DEL_4q | 0.608590774 | 0.886387225 | European |
| SBS22 | APOB | 0.396822921 | 0.737293462 | European |
| SBS22 | Age | 0.312235489 | 0.631685223 | European |
| SBS22 | pLMC | 0.035651635 | 0.157044702 | European |
| SCNA | Stage | 0.01024373 | 0.040588363 | TCGA |
| SCNA | ARID1A | 0.810480175 | 0.924533162 | TCGA |
| SCNA | RNAGR | 2.73E-06 | 2.61E-05 | TCGA |
| SCNA | Purity | 7.58E-06 | 6.16E-05 | TCGA |
| SCNA | DEL_4q | 4.61E-10 | 9.68E-09 | TCGA |
| SCNA | APOB | 0.82914216 | 0.926169434 | TCGA |
| SCNA | Age | 0.942367127 | 1 | TCGA |
| SCNA | pLMC | 3.90E-08 | 6.30E-07 | TCGA |
| SCNA | race | 0.056120121 | 0.151092632 | TCGA |
| SCNA | Stage | 0.196545952 | 0.518662929 | Asian |
| SCNA | ARID1A | 0.857788677 | 1 | Asian |
| SCNA | RNAGR | 0.050531024 | 0.200018638 | Asian |
| SCNA | Purity | 0.041315556 | 0.170651208 | Asian |
| SCNA | DEL_4q | 9.39E-06 | 1.78E-04 | Asian |
| SCNA | APOB | 0.935720693 | 1 | Asian |
| SCNA | Age | 0.100350485 | 0.323162579 | Asian |
| SCNA | pLMC | 0.011478071 | 0.060578706 | Asian |
| SCNA | Stage | 0.025900017 | 0.12617957 | European |
| SCNA | ARID1A | 0.886854286 | 0.980190904 | European |
| SCNA | RNAGR | 7.58E-06 | 1.60E-04 | European |
| SCNA | Purity | 1.35E-04 | 0.001826437 | European |
| SCNA | DEL_4q | 6.39E-05 | 0.001011262 | European |
| SCNA | APOB | 0.829487598 | 0.972855825 | European |
| SCNA | Age | 0.035782828 | 0.157044702 | European |
| SCNA | pLMC | 3.22E-06 | 7.66E-05 | European |
| Shannon | SBS22 | 0.353462682 | 0.573317807 | TCGA |
| Shannon | TMB | 2.03E-04 | 0.001251608 | TCGA |
| Shannon | DOCK2 | 0.795074198 | 0.924533162 | TCGA |
| Shannon | HBV | 0.053215223 | 0.145502268 | TCGA |
| Shannon | MDSC | 0.174553931 | 0.370265915 | TCGA |
| Shannon | SCNA | 0.121523073 | 0.268629951 | TCGA |
| Shannon | Stage | 0.01479539 | 0.055860754 | TCGA |
| Shannon | ARID1A | 0.711400745 | 0.872194349 | TCGA |
| Shannon | RNAGR | 0.403313856 | 0.634251265 | TCGA |
| Shannon | Purity | 7.50E-05 | 4.92E-04 | TCGA |

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| Shannon | DEL_4q | 0.018779982 | 0.065729938 | TCGA |
| Shannon | APOB | 0.570306504 | 0.782773632 | TCGA |
| Shannon | Age | 0.904546305 | 0.98370096 | TCGA |
| Shannon | pLMC | 7.21E-09 | 1.26E-07 | TCGA |
| Shannon | race | 0.266796794 | 0.482994196 | TCGA |
| Shannon | SBS22 | 0.63507218 | 0.88645336 | Asian |
| Shannon | TMB | 0.487261506 | 0.784573612 | Asian |
| Shannon | DOCK2 | 0.860349456 | 1 | Asian |
| Shannon | HBV | 0.083463198 | 0.288327413 | Asian |
| Shannon | MDSC | 0.006275957 | 0.039747726 | Asian |
| Shannon | SCNA | 0.00237414 | 0.019612461 | Asian |
| Shannon | Stage | 0.02215216 | 0.102656353 | Asian |
| Shannon | ARID1A | 0.901367296 | 1 | Asian |
| Shannon | RNAGR | 0.206962866 | 0.532346774 | Asian |
| Shannon | Purity | 0.149867703 | 0.444919745 | Asian |
| Shannon | DEL_4q | 0.004084594 | 0.029422667 | Asian |
| Shannon | APOB | 0.991210562 | 1 | Asian |
| Shannon | Age | 0.512451133 | 0.794750507 | Asian |
| Shannon | pLMC | 8.03E-12 | 7.62E-10 | Asian |
| Shannon | SBS22 | 0.69662655 | 0.924958566 | European |
| Shannon | TMB | 1.22E-06 | 4.63E-05 | European |
| Shannon | DOCK2 | 0.678484731 | 0.924958566 | European |
| Shannon | HBV | 0.875366661 | 0.980190904 | European |
| Shannon | MDSC | 0.97399729 | 1 | European |
| Shannon | SCNA | 0.82116975 | 0.969082313 | European |
| Shannon | Stage | 0.301621299 | 0.631685223 | European |
| Shannon | ARID1A | 0.732067383 | 0.924958566 | European |
| Shannon | RNAGR | 0.069211677 | 0.252888821 | European |
| Shannon | Purity | 1.73E-04 | 0.002054917 | European |
| Shannon | DEL_4q | 0.312828019 | 0.631685223 | European |
| Shannon | APOB | 0.41421459 | 0.742460115 | European |
| Shannon | Age | 0.769234128 | 0.925028382 | European |
| Shannon | pLMC | 0.009564625 | 0.064468235 | European |
| Stage | ARID1A | 1 | 1 | TCGA |
| Stage | RNAGR | 0.038150754 | 0.120234078 | TCGA |
| Stage | Purity | 0.378073673 | 0.601480844 | TCGA |
| Stage | DEL_4q | 0.908857034 | 0.98370096 | TCGA |
| Stage | APOB | 0.355291023 | 0.573317807 | TCGA |
| Stage | Age | 0.251488938 | 0.46373636 | TCGA |
| Stage | pLMC | 0.818872229 | 0.924533162 | TCGA |
| Stage | race | 0.695847026 | 0.864661985 | TCGA |
| Stage | ARID1A | 0.74681738 | 0.958752041 | Asian |
| Stage | RNAGR | 0.010885911 | 0.059094943 | Asian |
| Stage | Purity | 0.892766769 | 1 | Asian |
| Stage | DEL_4q | 0.65317616 | 0.88645336 | Asian |
| Stage | APOB | 0.866523274 | 1 | Asian |
| Stage | Age | 0.452198835 | 0.778878106 | Asian |
| Stage | pLMC | 0.068625118 | 0.250745624 | Asian |
| Stage | ARID1A | 0.739865628 | 0.924958566 | European |
| Stage | RNAGR | 0.569744855 | 0.865894794 | European |

| Stage | Purity | 0.072565548 | 0.255323224 | European |
|-------|--------|-------------|-------------|----------|
| Stage | DEL_4q | 0.887330713 | 0.980190904 | European |
| Stage | APOB | 0.042663491 | 0.176218766 | European |
| Stage | Age | 0.252025201 | 0.570057003 | European |
| Stage | pLMC | 0.047187362 | 0.190757419 | European |
| TMB | DOCK2 | 7.36E-04 | 0.003681903 | TCGA |
| TMB | HBV | 0.243928575 | 0.462847856 | TCGA |
| TMB | MDSC | 0.014978099 | 0.055860754 | TCGA |
| TMB | SCNA | 0.058896301 | 0.153414886 | TCGA |
| TMB | Stage | 0.250193351 | 0.46373636 | TCGA |
| TMB | ARID1A | 0.228722331 | 0.440657702 | TCGA |
| TMB | RNAGR | 0.015428208 | 0.055860754 | TCGA |
| TMB | Purity | 0.038360396 | 0.120234078 | TCGA |
| TMB | DEL_4q | 0.30658419 | 0.545615932 | TCGA |
| TMB | APOB | 0.102728334 | 0.235685582 | TCGA |
| TMB | Age | 6.62E-04 | 0.003473604 | TCGA |
| TMB | pLMC | 0.017343974 | 0.061732788 | TCGA |
| TMB | race | 0.005268842 | 0.023541633 | TCGA |
| TMB | DOCK2 | 0.004887358 | 0.033164213 | Asian |
| TMB | HBV | 0.381276167 | 0.723199553 | Asian |
| TMB | MDSC | 0.249090771 | 0.599615865 | Asian |
| TMB | SCNA | 0.846328854 | 1 | Asian |
| TMB | Stage | 0.944624387 | 1 | Asian |
| TMB | ARID1A | 0.155378419 | 0.451873283 | Asian |
| TMB | RNAGR | 0.00828092 | 0.049167961 | Asian |
| TMB | Purity | 0.286948741 | 0.67308964 | Asian |
| TMB | DEL_4q | 0.814853285 | 0.998852414 | Asian |
| TMB | APOB | 0.48379099 | 0.784573612 | Asian |
| TMB | Age | 2.77E-05 | 4.79E-04 | Asian |
| TMB | pLMC | 0.007267857 | 0.044544928 | Asian |
| TMB | DOCK2 | 0.097898817 | 0.310012921 | European |
| TMB | HBV | 0.551494819 | 0.858885374 | European |
| TMB | MDSC | 0.092209438 | 0.301625873 | European |
| TMB | SCNA | 0.023105864 | 0.120902985 | European |
| TMB | Stage | 0.036368247 | 0.157044702 | European |
| TMB | ARID1A | 0.927841998 | 0.996687335 | European |
| TMB | RNAGR | 0.077211624 | 0.261306203 | European |
| TMB | Purity | 0.113789304 | 0.343174092 | European |
| TMB | DEL_4q | 0.880438165 | 0.980190904 | European |
| TMB | APOB | 0.165492154 | 0.430733004 | European |
| TMB | Age | 0.016258365 | 0.092746081 | European |
| TMB | pLMC | 0.690952359 | 0.924958566 | European |

**Table S11: Univariate Cox model p-values for selected features**

| Feature | TCGA p-value | Asian p-value | European p-value | TCGA hazard ratio (HR) | Asian HR | European HR |
|---|---|---|---|---|---|---|
| DEL_16q | 0.138852303 | 0.013678165 | 0.944278184 | 1.369969241 | 2.44338328 | 0.980854849 |
| GEP | 0.004972856 | 0.045125428 | 0.049699245 | 0.376435896 | 0.327785639 | 0.400601847 |
| AMP_5p | 0.001684711 | 0.009423369 | 0.127016511 | 1.941098337 | 2.394041284 | 1.52112789 |
| ARID2 | 0.100951073 | 0.021549733 | 0.842230971 | 1.898617213 | 2.904017113 | 1.155734587 |
| grade | 0.933723283 | 0.048943727 | 0.028681825 | 1.446663597 | 0.36809533 | 14.75975762 |
| Shannon | 0.463951822 | 0.456490344 | 0.705370608 | 1.384495382 | 1.775859263 | 1.2316533 |
| SBS22 | 0.097350046 | 0.005695298 | 0.268153591 | 4.605009904 | 12.32816344 | 0.014395778 |
| TMB | 6.27E-04 | 0.007931987 | 0.035615198 | 1.088612816 | 1.084090525 | 1.091857618 |
| DOCK2 | 2.91E-06 | 4.34E-10 | 0.401389969 | 3.894697212 | 7.908068329 | 1.644557134 |
| HBV | 3.44E-04 | 2.90E-06 | 0.823372239 | 0.392817404 | 0.210908639 | 1.111388826 |
| MDSC | 1.29E-06 | 2.69E-06 | 0.012908067 | 10285.79195 | 2911905.649 | 289.4785959 |
| SCNA | 0.006013828 | 0.00858458 | 0.186341882 | 1.851235905 | 2.989302609 | 1.402517578 |
| Stage | 2.37E-05 | 3.21E-07 | 0.47118531 | 2.896326049 | 7.221507673 | 1.451461022 |
| ARID1A | 0.10756669 | 0.81382962 | 0.03295767 | 1.754521841 | 1.152809626 | 2.491580848 |
| RNAGR | 0.133921798 | 0.035666591 | 0.360534077 | 2.115935045 | 2.012747466 | 1.576541171 |
| Purity | 0.034580389 | 0.354047084 | 0.038100819 | 3.476205106 | 2.616649402 | 4.558198786 |
| DEL_4q | 0.198643327 | 0.619572518 | 0.085095733 | 1.313813536 | 1.18956011 | 1.611304186 |
| APOB | 0.281133448 | 0.275742715 | 0.003198091 | 1.434911954 | 0.460820528 | 2.999843187 |
| Age | 0.023641904 | 0.975036795 | 0.010827605 | 1.020235717 | 1.000492908 | 1.031843972 |
| pLMC | 0.539210596 | 0.746872136 | 0.422735079 | 0.995295165 | 0.995357222 | 0.99231304 |
| race | 0.333215593 | NA | NA | 1.236967496 | NA | NA |