Supplementary Figures

- **Figure S1**
- **Figure S2**
- **Figure S3**

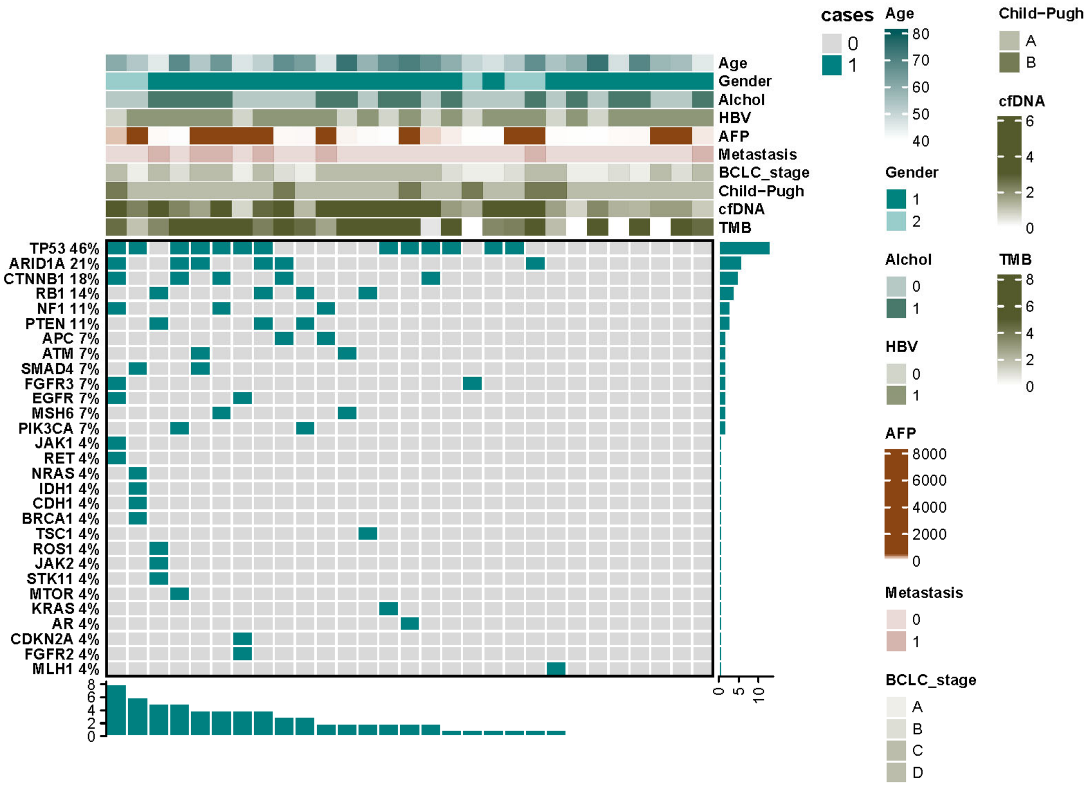
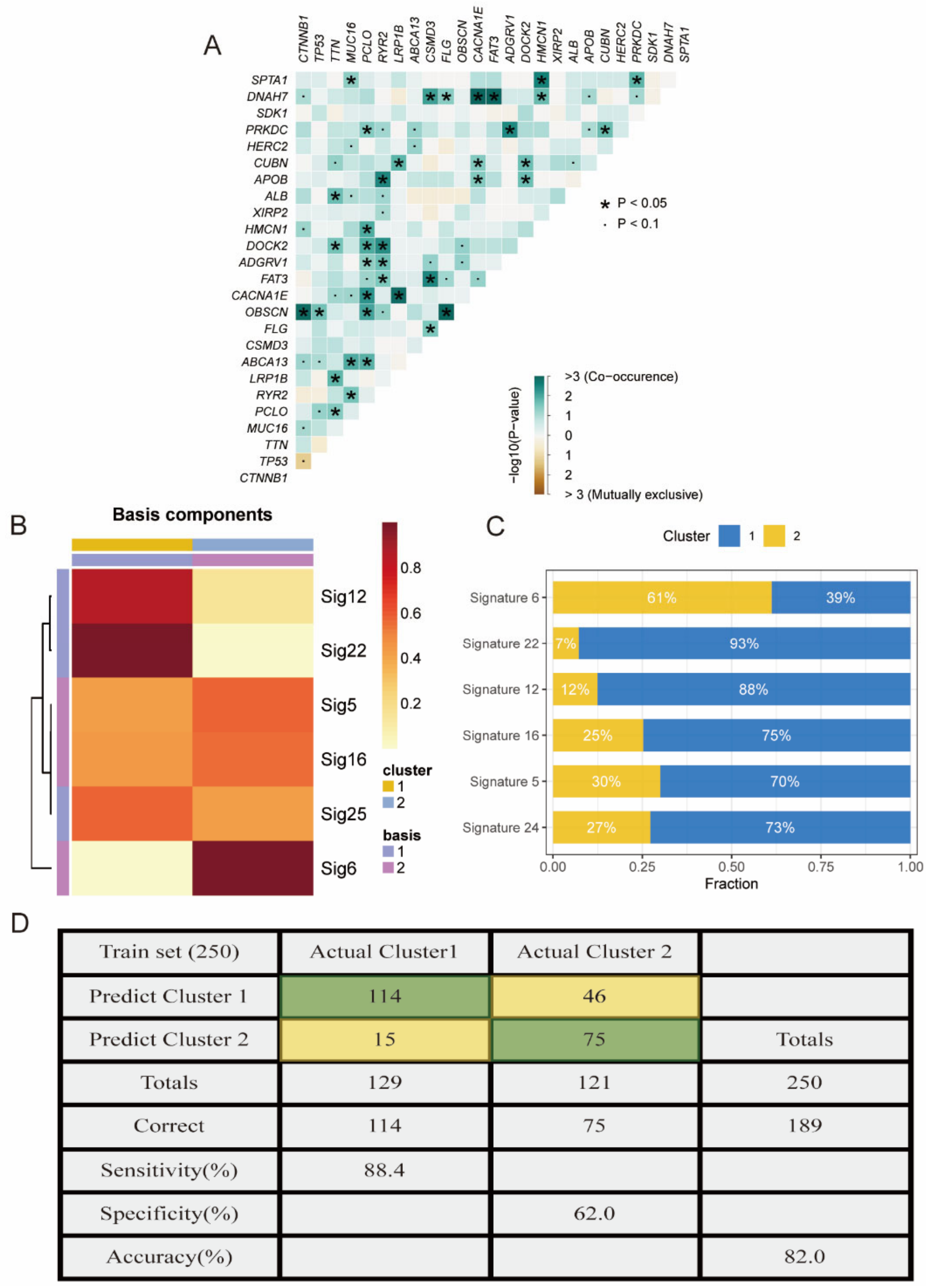
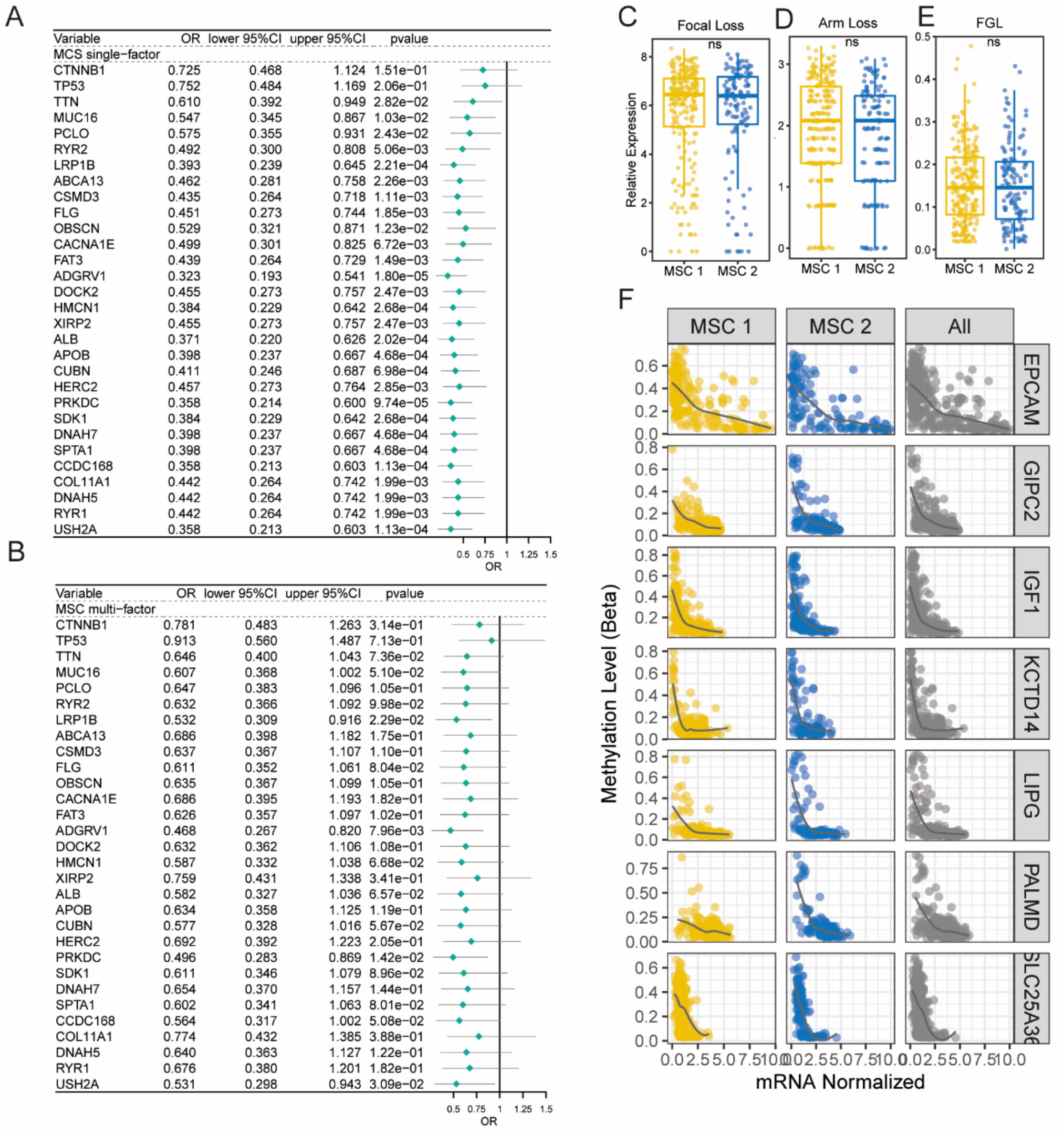


Figure S1. The gene mutation landscape of 30 patients from the in-house cohort.



Train set (250)	Actual Cluster1	Actual Cluster 2	
Predict Cluster 1	114	46	
Predict Cluster 2	15	75	Totals
Totals	129	121	250
Correct	114	75	189
Sensitivity(%)	88.4		
Specificity(%)		62.0	
Accuracy(%)			82.0

Figure S2. Mutation signature landscape in two MSCs. **A** Co-occurrence and mutually exclusive in the top 25 genes. **B** Basis components of NMF with rank =2 in TCGA LIHC cohort. **C** The fraction of six extracted mutation signatures in two MSCs. **D** The confusion matrix of the MSC predictor in the TCGA train set. **P* <0.05.



Variable	OR	lower 95%CI	upper 95%CI	pvalue
MCS single−factor				
CTNNB1	0.725	0.468	1.124	1.51e−01
TP53	0.752	0.484	1.169	2.06e−01
TTN	0.610	0.392	0.949	2.82e−02
MUC16	0.547	0.345	0.867	1.03e−02
PCLO	0.575	0.355	0.931	2.43e−02
RYR2	0.492	0.300	0.808	5.06e−03
LRP1B	0.393	0.239	0.645	2.21e−04
ABCA13	0.462	0.281	0.758	2.26e−03
CSMD3	0.435	0.264	0.718	1.11e−03
FLG	0.451	0.273	0.744	1.85e−03
OBSCN	0.529	0.321	0.871	1.23e−02
CACNA1E	0.499	0.301	0.825	6.72e−03
FAT3	0.439	0.264	0.729	1.49e−03
ADGRV1	0.323	0.193	0.541	1.80e−05
DOCK2	0.455	0.273	0.757	2.47e−03
HMCN1	0.384	0.229	0.642	2.68e−04
XIRP2	0.455	0.273	0.757	2.47e−03
ALB	0.371	0.220	0.626	2.02e−04
APOB	0.398	0.237	0.667	4.68e−04
CUBN	0.411	0.246	0.687	6.98e−04
HERC2	0.457	0.273	0.764	2.85e−03
PRKDC	0.358	0.214	0.600	9.74e−05
SDK1	0.384	0.229	0.642	2.68e−04
DNAH7	0.398	0.237	0.667	4.68e−04
SPTA1	0.398	0.237	0.667	4.68e−04
CCDC168	0.358	0.213	0.603	1.13e−04
COL11A1	0.442	0.264	0.742	1.99e−03
DNAH5	0.442	0.264	0.742	1.99e−03
RYR1	0.442	0.264	0.742	1.99e−03
USH2A	0.358	0.213	0.603	1.13e−04

Variable	OR	lower 95%CI	upper 95%CI	pvalue
MSC multi−factor				
CTNNB1	0.781	0.483	1.263	3.14e−01
TP53	0.913	0.560	1.487	7.13e−01
TTN	0.646	0.400	1.043	7.36e−02
MUC16	0.607	0.368	1.002	5.10e−02
PCLO	0.647	0.383	1.096	1.05e−01
RYR2	0.632	0.366	1.092	9.98e−02
LRP1B	0.532	0.309	0.916	2.29e−02
ABCA13	0.686	0.398	1.182	1.75e−01
CSMD3	0.637	0.367	1.107	1.10e−01
FLG	0.611	0.352	1.061	8.04e−02
OBSCN	0.635	0.367	1.099	1.05e−01
CACNA1E	0.686	0.395	1.193	1.82e−01
FAT3	0.626	0.357	1.097	1.02e−01
ADGRV1	0.468	0.267	0.820	7.96e−03
DOCK2	0.632	0.362	1.106	1.08e−01
HMCN1	0.587	0.332	1.038	6.68e−02
XIRP2	0.759	0.431	1.338	3.41e−01
ALB	0.582	0.327	1.036	6.57e−02
APOB	0.634	0.358	1.125	1.19e−01
CUBN	0.577	0.328	1.016	5.67e−02
HERC2	0.692	0.392	1.223	2.05e−01
PRKDC	0.496	0.283	0.869	1.42e−02
SDK1	0.611	0.346	1.079	8.96e−02
DNAH7	0.654	0.370	1.157	1.44e−01
SPTA1	0.602	0.341	1.063	8.01e−02
CCDC168	0.564	0.317	1.002	5.08e−02
COL11A1	0.774	0.432	1.385	3.88e−01
DNAH5	0.640	0.363	1.127	1.22e−01
RYR1	0.676	0.380	1.201	1.82e−01
USH2A	0.531	0.298	0.943	3.09e−02

Figure S3. The multi-omics landscape of the MSCs. **A-B** Univariant Cox regression analysis of the top 30 FMGs (**A**), FHGs (**B**). **C-E** Differences in focal loss (**C**), arm loss (**D**), and FGL (**E**) between two CMSs. **F** The relationship of methylation levels and expression levels of methylation drive genes in CMS1, CMS2, and all samples.

Supplementary tables

- **Table S1**
- **Table S2**
- **Table S3**
- **Table S4**
- **Table S5**
- **Table S6**
- **Table S7**
- **Table S8**
- **Table S9**
- **Table S10**
- **Table S11**

Table S1. Univariate Cox regression analysis of OS in somatic mutations.

Gene	P value	HR
APC	0.439428	2.292542
NF1	0.001735	13.788627
ARID1A	0.497208	1.575452
ATM	0.073950	4.166601
TP53	0.319357	1.777155
SMAD4	0.687872	0.656918
JAK1	0.022030	25.495098
CTNNB1	0.343957	1.888524
FGFR3	0.994624	1.007093
EGFR	0.389205	2.519012
RET	0.022030	25.495098
MSH6	0.007903	10.128582
TSC1	0.069218	8.153897
RB1	0.214493	2.833713
ROS1	0.111709	5.924447
JAK2	0.111709	5.924447
PTEN	0.724548	1.462041
STK11	0.111709	5.924447
MTOR	0.790929	1.322531
PIK3CA	0.941664	1.079797
KRAS	0.655849	1.602118
AR	0.294009	3.074113

Table S2. Clinical characteristics of two MSC in TCGA cohort and Cox regression analysis for predictors of OS and RFS.

	MSC 1	**MSC 2**	***P***
n	226	130	
Age (mean (SD))	59.58 (12.10)	58.33 (15.68)	0.403
Gender = Male (%)	167 (73.9)	72 (55.4)	**0.001**
pT = T 3|4 (%)	136 (60.2)	71 (54.6)	0.361
Stage = Stage III|IV (%)	137 (60.6)	72 (55.4)	0.393
Child_pugh = C (%)	117 (51.8)	59 (45.4)	0.294
AFP (mean (SD))	5090.78 (21823.13)	24781.15 (181981.16)	0.109
Bilirubin (mean (SD))	0.87 (0.71)	1.20 (2.07)	0.028
Creatinine (mean (SD))	2.28 (10.15)	3.97 (16.04)	0.224
Grade = G3|4 (%)	150 (66.4)	82 (63.1)	0.608
Height (mean (SD))	167.38 (10.94)	167.02 (9.83)	0.758
Mutation Count (mean (SD))	108.87 (121.19)	81.10 (109.37)	**0.032**
PB (mean (SD))	4.04 (4.73)	4.53 (5.42)	0.374
Vascular invasion (%)	81 (35.8)	42 (32.3)	0.576

Multivariate Cox regression in OS

	Coef	HR(95%CI)	*P*
Mutation Count	0.001660	1.001662(1.000683,1.002642)	**0.000874**
Vascular invasion	0.131261	1.140265(0.779594,1.667797)	0.498670
MSC 1	0.499388	1.647712(1.103966,2.459274)	**0.014524**
Stage III|IV	0.687760	1.989255(1.330359,2.974487)	**0.000806**

Multivariate Cox regression in RFS

	Coef	HR	*P*
Mutation Count	0.001507	1.001508(1.000515,1.002502)	**0.002910**
Vascular invasion	0.355531	1.426939(1.075433,1.893334)	**0.013741**
MSC 1	0.218395	1.244078(0.933572,1.657857)	0.136023
Stage III|IV	0.303575	1.354693(1.018065,1.802627)	**0.037269**

Notes: The P-values less than 0.05 are in bold.

Abbreviations: MSC, mutation signature cluster; OS, overall survival; RFS, relapse-free survival.

Table S3. Common genes in all cohort with AUC > 0.60.

ABI3BP
ABR
ACSM1
ACTA2
ACTR5
ADAM7
ADAMTS1
ADAMTS12
ADAMTS2
ADAMTS20
ADAMTSL2
ADARB2
ADCY3
AEBP1
AK2
AKAP10
AKAP11
AKR1A1
AKR7A2
AKT3
ALDH1A3
ALKBH4
ALOX5
AMBP
AMOTL2
AMPH
ANGPT4
ANKHD1
ANTXR1
ANXA3
ANXA4
AP1G2
APBA2
APOC1
APOC4
APOM
APP
ARHGEF10
ARHGEF17
ARHGEF4
ARL5A
ARMCX2
ARMCX3
ARMCX6
ARSA
ASPN
ASTE1
ATP10A
ATP2C2
ATPIF1
AXL
B3GNT2
BASP1
BGN
BMPER
BMPR2
BNC1
BSN
BTG1
BTG2
FLII
FLRT2
FMNL2
FMOD
FOXD2
FOXF1
FOXF2
FSCN1
FSTL3
FUT8
FZD1
FZD7
FZD8
GABBR1
GABRA3
GABRP
GAL
GALE
GALNT3
GALNT7
GAS1
GAS2
GCG
GDAP1
GDF10
GEM
GFPT2
GJB3
GLI2
GLMN
GLP2R
GLT8D2
GNA11
GNL2
GPATCH1
GPATCH3
GPC4
GPR27
GPRASP1
GRIN2A
GRIN2C
GSPT2
GSTK1
GTF2B
GUCY1A3
GUCY1B3
HAND2
HAS2
HCN4
HEPH
HEXA
HEYL
HHLA3
HIF1A
HIRIP3
HIST1H1B
HIST1H2AB
HIST1H2BL
HIST1H3C
HMGN3
PDGFRB
PDZRN3
PDZRN4
PEF1
PELI2
PFDN6
PFKFB4
PGR
PHF7
PHKG1
PHLDB1
PICALM
PIGH
PITPNA
PITPNM3
PKDREJ
PKNOX2
PLA2R1
PLAT
PLD2
PLEKHA2
PLN
PLOD1
PMF1
PMP22
PNMA2
PODNL1
POLE2
POLR3G
POMGNT1
POP5
POSTN
PPFIA3
PPFIBP1
PPIE
PPIF
PPM1H
PPP1R8
PRDM16
PRELP
PRIM1
PRKAR2A
PRKG1
PRMT2
PROM1
PRPSAP1
PRSS23
PRSS8
PSMB2
PSMC2
PSMC3
PSME2
PTBP2
PTGIR
PTGIS
PTGS2
PTK7
PTPN13
PTPRS
PXDN
UNC5C
UQCRC1
USP13
USP48
UTY
VAMP1
VCL
VCX
VGLL1
VPS16
VPS33A
VSNL1
WDFY3
WDR1
WFDC1
WNT2
XYLT1
YARS
YTHDC1
ZBTB17
ZBTB3
ZBTB44
ZFHX4
ZFYVE26
ZMIZ1
ZMYM6
ZMYND10
ZNF174
ZNF212
ZNF214
ZNF324
ZNF365
ZNF544
ZNF592
ZNF76
ZNF764
ZSCAN2

C1orf50
C1QTNF1
CACNA1H
CACNA2D1
CADPS
CAMTA2
CAP2
CASP6
CASP9
CBL
CCDC106
CCDC134
CCDC40
CCHCR1
CCL8
CCNA1
CCNG2
CCNI
CCNJL
CD207
CD28
CDCP1
CDH1
CDH9
CDK2AP1
CDK5RAP1
CDK5RAP2
CDKAL1
CDKN2A
CDKN2C
CELSR3
CETN1
CGRRF1
CHGA
CHODL
CHST3
CLEC11A
CLN8
CLSTN2
CNOT4
COL10A1
COL14A1
COL16A1
COL1A1
COL1A2
COL3A1
COL4A2
COL5A1
COL6A1
COL6A2
COL6A3
COMMD3
COMMD4
COMMD9
COMP
COPS6
CPNE7
CPZ
CRISPLD2
CRMP1
CSPG5
CSTF2
HOXB2
HOXB3
HSPBAP1
HUNK
ID4
IFNGR2
IGF2
IGFALS
IGFBP5
IGFBP7
IKZF2
IL12RB2
IL20RA
IPO13
IQCC
ISLR
ISYNA1
ITGB3BP
ITIH5
JAG1
JPH2
KCND1
KCNIP1
KCNJ16
KCTD12
KIAA0753
KIAA1644
KIF26B
KIRREL
KLF7
KLF8
KLHL3
KLHL9
KLK2
LAMA1
LAMA2
LAMA5
LAMB1
LAS1L
LBH
LDOC1
LHFP
LIFR
LIN7B
LOXL1
LRFN4
LRRC17
LRRC32
LRRK1
LTBP1
LTBP2
LTBP4
LTK
LUM
LY6E
MAGEA12
MAGEA4
MAGEA6
MAGEA8
MAGEB1
MAGEB2
MAGOH
PYGO1
RAB20
RAB28
RAB36
RAB6A
RAI1
RAI2
RANBP2
RARG
RASL11B
RBM23
RBMS3
RBP4
RET
RGS11
RING1
RPP40
RPUSD2
RUSC2
S100PBP
SAMD14
SCD5
SCML2
SCTR
SDCCAG8
SDK1
SDK2
SEC13
SEC14L4
SEMA3C
SEMA4C
11-Sep
2-Sep
7-Sep
SF3A3
SFMBT1
SFRP1
SFRP5
SFTPC
SH3YL1
SIRT4
SIRT7
SLC12A5
SLC17A3
SLC22A17
SLC24A3
SLC25A36
SLC26A10
SLC28A3
SLC34A2
SLC38A6
SLC6A6
SLC7A9
SLC9A6
SLCO3A1
SLCO4A1
SLIT2
SNIP1
SNRPC
SNX11
SNX19
SOD3

CTAG2
CTBP2
CTNNBL1
CTR9
CTSK
CUTA
CUZD1
CXCL12
CXCL14
CYB561
CYP1B1
CYP2J2
DAPK2
DARS
DAXX
DCN
DCTD
DDR2
DDX3X
DENND3
DHDDS
DHRS3
DHX57
DIO3
DKK2
DMRTB1
DNAJA4
DPH2
DTX4
DYNC1I2
E4F1
EAF2
EBNA1BP2
ECHDC3
ECM1
EDC3
EDNRA
EFEMP2
EFNB3
EFS
EHD3
EIF1AX
EIF2B3
EIF2B4
EIF2B5
EIF2S3
ELF1
ELMO3
ELN
ELP4
EMILIN1
ENDOD1
ENTPD1
EPB41L4A
EPHA3
ERCC8
EVC
EXOSC10
F2R
F3
FABP7
FAF1
MAP2K1
MAP3K13
MAP9
MAPK10
MBOAT2
MCM5
MECR
MED18
MED8
MFAP4
MGP
MKNK1
MMP28
MN1
MORN1
MPI
MRC2
MRPS22
MTMR14
MUTYH
MXRA5
MXRA8
MYB
MYH11
MYL9
MYO10
MYO1C
MYO1D
NAT6
NBEA
NCAPH2
NCK2
NCKIPSD
NCOR1
NDST4
NEDD4L
NFKB1
NFYC
NGDN
NGFR
NINJ2
NIT1
NME5
NME7
NOTCH1
NOTCH3
NPTX1
NPTX2
NPTXR
NPY5R
NQO2
NRL
NSDHL
NSFL1C
NSMCE2
NTRK2
NUDC
NXN
OGFRL1
OGG1
OGN
OLFML3
SPEG
SPG20
SPINK5
SPINT2
SRPX
SRPX2
SSPN
SST
SSX1
SSX2
ST7L
STOM
STON1
SUSD4
SUSD5
SUV39H1
SVEP1
SVIL
SYDE1
SYNPO
TAF12
TAF9
TAGLN
TANC2
TBX2
TBXA2R
TCAP
TCF21
TCF7
TF
TGFA
TGFB1
TGFB3
TGFBRAP1
TGM3
THAP3
THBD
THBS1
THBS2
TIGD6
TIMP2
TINAGL1
TIPIN
TM6SF1
TM9SF3
TMEM158
TMEM39B
TMEM51
TNC
TNNT2
TNS1
TNS3
TOE1
TP73
TPBG
TPM4
TRAIP
TRAPPC3
TRERF1
TRIM17
TRIT1
TRPM1

FAM102A
FAM57A
FAM65A
FANCA
FARS2
FBLN2
FBN1
FBXO42
FCHSD2
FCN3
FEZ1
FGF16
FGFR1
FHOD3
FKBP9

PAFAH1B2
PAGE1
PALM
PARP2
PBX1
PCBP3
PCDH7
PCDHGA12
PCDHGC3
PCGF3
PDE1A
PDE3A
PDE5A
PDE9A
PDGFB

TRPV4
TSPAN2
TTC19
TTC23
TTC4
TTYH1
TUBB3
TUBB6
TUT1
TWSG1
UBE2G1
UBE2O
UFD1L
ULK2
UMOD

Table S4. Selected gene pairs and the corresponding coefficient.

Gene pair	coefficient
ACSM1|IGFALS	-0.086619064
ALKBH4|TTC19	-0.049502986
C1orf50|PRMT2	-0.088819868
CCL8|FEZ1	-0.063474111
CDK5RAP2|CYB561	-0.050336217
CDK5RAP2|SEPT11	-0.013964313
CDKAL1|ZBTB44	-0.016344191
CDKN2C|IGFALS	-0.012260936
CGRRF1|CLN8	-0.007150271
CHGA|GAL	-0.019547761
CTR9|TNS3	-0.081773192
CUZD1|NME5	-0.00414488
GPATCH1|LTBP1	-0.008672178
GPATCH3|MYO1D	-0.050406826
GTF2B|PITPNA	-0.024163817
IKZF2|PDZRN3	-0.056021814
IQCC|KLF7	-0.040442964
MAGOH|RAB20	-0.006572587
MYB|SUSD5	-0.011397993
NINJ2|SEC14L4	-0.042866993
OGG1|SDCCAG8	-0.013044519
PKDREJ|WNT2	-0.002710877

Table S5. Enrichment terms of GO, KEGG and Hallmark.

GO

Description	enrichmentScore	*P* adjust
GOBP_AMEBOIDAL_TYPE_CELL_MIGRATION	-0.503046098	1.22E-08
GOBP_AXON_DEVELOPMENT	-0.507281281	1.22E-08
GOBP_CARTILAGE_DEVELOPMENT	-0.601449435	1.22E-08
GOBP_CELLULAR_AMINO_ACID_METABOLIC_PROCESS	0.509027038	1.22E-08
GOBP_CELL_CELL_JUNCTION_ORGANIZATION	-0.578959587	1.22E-08
GOBP_CELL_CELL_SIGNALING_BY_WNT	-0.461491932	1.22E-08
GOBP_CELL_JUNCTION_ASSEMBLY	-0.497825523	1.22E-08
GOBP_CELL_SUBSTRATE_ADHESION	-0.542398535	1.22E-08
GOBP_CHROMOSOME_SEGREGATION	0.496803881	1.22E-08
GOBP_COLLAGEN_FIBRIL_ORGANIZATION	-0.781316571	1.22E-08
GOBP_CONNECTIVE_TISSUE_DEVELOPMENT	-0.589174973	1.22E-08
GOBP_DNA_REPAIR	0.432095266	1.22E-08
GOBP_EMBRYONIC_ORGAN_DEVELOPMENT	-0.459761924	1.22E-08
GOBP_EPITHELIAL_CELL_PROLIFERATION	-0.477255752	1.22E-08
GOBP_EPITHELIAL_TUBE_MORPHOGENESIS	-0.517641992	1.22E-08
P_EXTERNAL_ENCAPSULATING_STRUCTURE_ORGANIZA	-0.674635546	1.22E-08
GOBP_EXTRACELLULAR_MATRIX_ASSEMBLY	-0.842303167	1.22E-08
GOBP_FATTY_ACID_METABOLIC_PROCESS	0.454364173	1.22E-08
GOBP_HEART_MORPHOGENESIS	-0.547887242	1.22E-08
GOBP_MITOTIC_SISTER_CHROMATID_SEGREGATION	0.565495878	1.22E-08

KEGG

Description	**NES**	***P* adjust**
KEGG_ECM_RECEPTOR_INTERACTION	-2.304902728	9.20E-09
KEGG_FOCAL_ADHESION	-2.313824754	9.20E-09
KEGG_PATHWAYS_IN_CANCER	-1.818197456	3.87E-07
KEGG_PEROXISOME	2.192461811	1.31E-06
KEGG_PPAR_SIGNALING_PATHWAY	2.144661288	1.24E-05
KEGG_CYTOKINE_CYTOKINE_RECEPTOR_INTERACTION	-1.766853983	1.91E-05
KEGG_REGULATION_OF_ACTIN_CYTOSKELETON	-1.776692188	5.40E-05
KEGG_RETINOL_METABOLISM	2.08809515	9.29E-05
KEGG_BUTANOATE_METABOLISM	2.127994978	9.65E-05
KEGG_DNA_REPLICATION	2.068685514	0.000155373
KEGG_TGF_BETA_SIGNALING_PATHWAY	-1.942495927	0.000180395
KEGG_LEISHMANIA_INFECTION	-1.979199335	0.000269263
KEGG_DILATED_CARDIOMYOPATHY	-1.910398095	0.000309267
KEGG_PROTEASOME	1.963707471	0.00035496
KEGG_DRUG_METABOLISM_OTHER_ENZYMES	1.957944033	0.00035496
KEGG_COMPLEMENT_AND_COAGULATION_CASCADES	1.909366646	0.000478584
KEGG_LEUKOCYTE_TRANSENDOTHELIAL_MIGRATION	-1.808717976	0.000508974
KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME_P450	1.904170587	0.0005112
KEGG_DRUG_METABOLISM_CYTOCHROME_P450	1.898651803	0.000650177
KEGG_GLYCINE_SERINE_AND_THREONINE_METABOLISM	1.958615491	0.000677703
KEGG_FC_GAMMA_R_MEDIATED_PHAGOCYTOSIS	-1.814071463	0.000729739
KEGG_STEROID_HORMONE_BIOSYNTHESIS	1.880101541	0.001117503
KEGG_AXON_GUIDANCE	-1.72437545	0.001734274
KEGG_MAPK_SIGNALING_PATHWAY	-1.537630321	0.001821479
KEGG_PRIMARY_BILE_ACID_BIOSYNTHESIS	1.949093767	0.001859876
KEGG_HYPERTROPHIC_CARDIOMYOPATHY_HCM	-1.74479628	0.002043853
KEGG_GNRH_SIGNALING_PATHWAY	-1.732495862	0.002228053
KEGG_WNT_SIGNALING_PATHWAY	-1.611401353	0.002526688
KEGG_RENAL_CELL_CARCINOMA	-1.777920183	0.002576971
KEGG_NEUROTROPHIN_SIGNALING_PATHWAY	-1.681540652	0.002576971
KEGG_JAK_STAT_SIGNALING_PATHWAY	-1.598128587	0.002598794
KEGG_VASCULAR_SMOOTH_MUSCLE_CONTRACTION	-1.6271728	0.002965363
KEGG_BASE_EXCISION_REPAIR	1.828184669	0.003326792
KEGG_TERPENOID_BACKBONE_BIOSYNTHESIS	1.933651561	0.00368829
KEGG_STEROID_BIOSYNTHESIS	1.862849313	0.003746076
KEGG_NOTCH_SIGNALING_PATHWAY	-1.773213585	0.003746076
KEGG_SMALL_CELL_LUNG_CANCER	-1.705416099	0.003746076
KEGG_PENTOSE_AND_GLUCURONATE_INTERCONVERSIONS	1.781557396	0.004761062

KEGG_NUCLEOTIDE_EXCISION_REPAIR	1.747510609	0.009593394
KEGG_CELL_CYCLE	1.550237826	0.009741113
KEGG_PYRIMIDINE_METABOLISM	1.600149928	0.009741113
KEGG_CALCIUM_SIGNALING_PATHWAY	-1.503438408	0.010029393
KEGG_MELANOGENESIS	-1.601732	0.010029393
KEGG_PORPHYRIN_AND_CHLOROPHYLL_METABOLISM	1.689670117	0.010029393
KEGG_HEDGEHOG_SIGNALING_PATHWAY	-1.638121655	0.012732949
KEGG_VALINE_LEUCINE_AND_ISOLEUCINE_DEGRADATION	1.620719286	0.013123614
KEGG_CHRONIC_MYELOID_LEUKEMIA	-1.634483296	0.013127912
KEGG_ABC_TRANSPORTERS	1.690079969	0.013185188
KEGG_LYSINE_DEGRADATION	1.684482095	0.01407195
KEGG_O_GLYCAN_BIOSYNTHESIS	-1.65480244	0.015422931
KEGG_LINOLEIC_ACID_METABOLISM	1.664981314	0.020506959
KEGG_FATTY_ACID_METABOLISM	1.541041691	0.020847281
KEGG_PROSTATE_CANCER	-1.572627739	0.022469818
KEGG_HOMOLOGOUS_RECOMBINATION	1.689369125	0.023783131
KEGG_NEUROACTIVE_LIGAND_RECEPTOR_INTERACTION	-1.397859073	0.024913939
KEGG_MISMATCH_REPAIR	1.679435772	0.026991437
KEGG_ERBB_SIGNALING_PATHWAY	-1.515727305	0.032368354
KEGG_STARCH_AND_SUCROSE_METABOLISM	1.519082997	0.033747188
KEGG_ASCORBATE_AND_ALDARATE_METABOLISM	1.564310193	0.033747188
KEGG_GAP_JUNCTION	-1.480574831	0.040118419
KEGG_BLADDER_CANCER	-1.518337022	0.040544145
KEGG_APOPTOSIS	-1.469066035	0.040922831
KEGG_CELL_ADHESION_MOLECULES_CAMS	-1.412476157	0.041289619
KEGG_VIRAL_MYOCARDITIS	-1.492299994	0.041882287
KEGG_CHEMOKINE_SIGNALING_PATHWAY	-1.398771771	0.045211802
KEGG_TRYPTOPHAN_METABOLISM	1.531312202	0.045329303
ARRHYTHMOGENIC_RIGHT_VENTRICULAR_CARDIOMYOPATHY	-1.489727085	0.047160046

HALLmarker

Description	**logFC**	***P* adjust**
HALLMARK_DNA_REPAIR	-0.07830454	0.000967533
HALLMARK_PANCREAS_BETA_CELLS	0.054968678	0.016160203
HALLMARK_UNFOLDED_PROTEIN_RESPONSE	-0.05145596	0.016160203
HALLMARK_KRAS_SIGNALING_DN	0.031547678	0.019834245
HALLMARK_MYOGENESIS	0.060279429	0.032832973
HALLMARK_REACTIVE_OXYGEN_SPECIES_PATHWAY	-0.04856825	0.12475714
HALLMARK_APICAL_SURFACE	0.042593552	0.130448724
HALLMARK_G2M_CHECKPOINT	-0.05924452	0.136601447
HALLMARK_HEDGEHOG_SIGNALING	0.058644294	0.136601447
HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION	0.065961104	0.136601447
HALLMARK_PI3K_AKT_MTOR_SIGNALING	-0.02975136	0.136601447
HALLMARK_E2F_TARGETS	-0.06848715	0.168763283
HALLMARK_NOTCH_SIGNALING	0.048934244	0.196594049
HALLMARK_IL6_JAK_STAT3_SIGNALING	0.047372562	0.201709351
HALLMARK_MTORC1_SIGNALING	-0.03954396	0.208819571
HALLMARK_HYPOXIA	0.030816205	0.228835408
HALLMARK_OXIDATIVE_PHOSPHORYLATION	-0.0387152	0.325836944
HALLMARK_APICAL_JUNCTION	0.026776646	0.325836944
HALLMARK_GLYCOLYSIS	-0.02012059	0.408440178
HALLMARK_MYC_TARGETS_V2	-0.04461324	0.408440178
HALLMARK_XENOBIOTIC_METABOLISM	-0.03459357	0.408440178
HALLMARK_INTERFERON_ALPHA_RESPONSE	-0.04080852	0.444493612
HALLMARK_ANDROGEN_RESPONSE	-0.02051407	0.444493612
HALLMARK_MYC_TARGETS_V1	-0.03631286	0.444493612
HALLMARK_BILE_ACID_METABOLISM	-0.03701625	0.444493612
HALLMARK_WNT_BETA_CATENIN_SIGNALING	-0.02777501	0.444493612
HALLMARK_MITOTIC_SPINDLE	-0.02121296	0.444493612
HALLMARK_INFLAMMATORY_RESPONSE	0.029770492	0.444493612
HALLMARK_ESTROGEN_RESPONSE_LATE	0.015485091	0.500371772
HALLMARK_P53_PATHWAY	-0.01322749	0.500371772
HALLMARK_INTERFERON_GAMMA_RESPONSE	-0.0290946	0.521283016
HALLMARK_PEROXISOME	0.015389527	0.534596497
HALLMARK_COAGULATION	-0.02137661	0.634756862
HALLMARK_PROTEIN_SECRETION	-0.01666487	0.640024096
HALLMARK_TNFA_SIGNALING_VIA_NFKB	0.019149046	0.646871118
HALLMARK_ADIPOGENESIS	-0.01297881	0.651416008
HALLMARK_KRAS_SIGNALING_UP	0.008773754	0.762715106
HALLMARK_HEME_METABOLISM	-0.00710641	0.787861434

HALLMARK_TGF_BETA_SIGNALING	0.011600528	0.787861434
HALLMARK_CHOLESTEROL_HOMEOSTASIS	-0.00860181	0.787861434
HALLMARK_FATTY_ACID_METABOLISM	-0.01002188	0.787861434
HALLMARK_APOPTOSIS	-0.0075566	0.787861434
HALLMARK_ESTROGEN_RESPONSE_EARLY	-0.00453947	0.886414215
HALLMARK_ALLOGRAFT_REJECTION	-0.00663172	0.900062956
HALLMARK_SPERMATOGENESIS	0.002845838	0.900062956
HALLMARK_UV_RESPONSE_UP	-0.00260639	0.900062956
HALLMARK_ANGIOGENESIS	0.005780802	0.900062956
HALLMARK_COMPLEMENT	-0.00317775	0.900062956
HALLMARK_UV_RESPONSE_DN	-0.00204315	0.944395154
HALLMARK_IL2_STAT5_SIGNALING	0.000235854	0.99017797

Table S6. Immune related indicators in TCHA-LIHC patients.

	SNV.Neoantigens	Indel.Neoantigens	CTA.Score	Intratumor.Heterogeneity	Number.of.Segments	Fraction.Altered
TCGA-2V-A95S	36	85	NA	0.07	84	0.245784405
TCGA-2Y-A9GS	43	34	3.955155741	0.16	109	0.719476541
TCGA-2Y-A9GT	35	17	1.171609984	0.01	83	0.062187446
TCGA-2Y-A9GU	59	53	1.031207748	0.05	120	0.317505909
TCGA-2Y-A9GV	35	5	0.863332684	0.01	85	0.092790726
TCGA-2Y-A9GW	42	74	1.197767759	0.11	81	0.776233756
TCGA-2Y-A9GX	23	120	1.397903253	0.07	40	0.174674088
TCGA-2Y-A9GY	23	5	3.511003074	0.4	203	0.696873558
TCGA-2Y-A9GZ	39	38	3.957740143	0.15	353	0.890420828
TCGA-2Y-A9H0	33	121	2.729933332	0.02	620	0.206101593
TCGA-2Y-A9H1	74	132	1.473894746	0.08	93	0.390791077
TCGA-2Y-A9H2	22	5	1.538601674	0.14	142	0.80131409
TCGA-2Y-A9H3	103	56	1.466532555	0.18	158	0.591576833
TCGA-2Y-A9H4	28	87	3.81712324	0.04	186	0.281848534
TCGA-2Y-A9H5	37	45	0.491726271	0.14	88	0.525677253
TCGA-2Y-A9H6	28	5	0.839067552	0.08	239	0.260411914
TCGA-2Y-A9H7	44	61	1.310943063	0.05	101	0.160754987
TCGA-2Y-A9H8	28	13	0.54417858	0.1	176	0.545865574
TCGA-2Y-A9H9	65	171	2.540084653	0.18	348	0.26326484
TCGA-2Y-A9HA	42	10	5.291869039	0.18	215	0.36492941
TCGA-2Y-A9HB	34	1	1.129425241	0.09	78	0.158512707
TCGA-3K-AAZ8	48	12	0.976951912	0.05	77	0.947535184
TCGA-4R-AA8I	460	1081	5.196854549	0.02	164	0.181902114
TCGA-5C-A9VG	62	2	0.911305108	0.12	83	0.65215662
TCGA-5C-A9VH	54	44	0.616695303	0.33	82	0.34193756
TCGA-5C-AAPD	27	1	4.413602347	0.1	146	0.816782584
TCGA-5R-AA1C	27	10	1.839524276	0.02	106	0.820182385
TCGA-5R-AA1D	8	NA	0.651140546	0.14	45	0.109028563
TCGA-5R-AAAM	32	15	1.120688503	0.11	105	0.16448549
TCGA-BC-4073	35	20	5.116809194	0	617	0.074757118
TCGA-BC-A10Q	12	1	NA	0.05	100	0.624196332
TCGA-BC-A10R	32	0	3.102672333	0.1	533	0.703043656
TCGA-BC-A10T	37	70	2.958244423	0.04	558	0.262749604
TCGA-BC-A10U	52	167	2.979286993	0.07	121	0.354116055
TCGA-BC-A10W	42	17	1.288064522	0.06	132	0.276109502
TCGA-BC-A10Y	25	NA	3.202137678	0.12	767	0.280578723
TCGA-BC-A10Z	58	252	3.524981579	0	786	0.201206881
TCGA-BC-A216	28	1	2.230385874	0.07	567	0.209204918
TCGA-BC-A217	45	10	4.254714142	0.27	574	0.79188261

TCGA-BC-A3KF	35	4	0.799379475	0.05	157	0.700815539
TCGA-BC-A5W4	30	8	1.171903764	0.01	249	0.944510971
TCGA-BC-A69H	47	32	3.068849164	0.27	142	0.541832319
TCGA-BC-A8YO	22	90	2.204916882	0.01	506	0.146138485
TCGA-BD-A2L6	28	16	2.724587864	0.98	170	0.153524309
TCGA-BD-A3EP	69	178	4.755113373	0.32	120	0.518902218
TCGA-BW-A5NO	52	16	3.982604753	0.55	469	0.671669915
TCGA-BW-A5NQ	42	53	NA	0.01	57	0.880727287
TCGA-CC-5258	75	264	0.982148489	0.03	191	0.445875657
TCGA-CC-5260	31	9	2.10814455	0.1	164	0.317378982
TCGA-CC-5262	59	9	2.747798436	0	79	0.145817735
TCGA-CC-5263	70	3	3.64102167	0.14	515	0.390039904
TCGA-CC-5264	49	18	3.741782895	0.23	160	0.817639981
TCGA-CC-A1HT	52	49	5.444076292	0.2	120	0.210070667
TCGA-CC-A3M9	56	48	3.602366015	0.44	188	0.598569729
TCGA-CC-A3MA	23	53	1.204244069	0.08	167	0.891430677
TCGA-CC-A3MB	42	39	0.809002304	0.19	157	0.573792051
TCGA-CC-A3MC	33	37	1.162453765	0.42	114	0.571369497
TCGA-CC-A5UC	24	59	0.851047715	0.03	79	0.508275929
TCGA-CC-A5UD	62	14	1.374561976	0.01	96	0.946347609
TCGA-CC-A5UE	65	112	3.723518721	0.51	85	0.791883927
TCGA-CC-A7IE	79	98	1.55542874	0.08	146	0.855115209
TCGA-CC-A7IF	50	24	0.909085541	0.1	122	0.333608632
TCGA-CC-A7IG	66	10	0.848094794	0.44	143	0.749752041
TCGA-CC-A7IH	315	58	1.427574104	0.07	152	0.839505377
TCGA-CC-A7II	52	26	5.35136583	0.11	168	0.737283745
TCGA-CC-A7IJ	73	117	2.240673615	0.24	316	0.826713353
TCGA-CC-A7IK	137	17	4.538172747	0.11	151	0.775304309
TCGA-CC-A7IL	38	163	1.994545111	0.2	103	0.797315614
TCGA-CC-A8HT	99	95	4.945920921	0	161	0.207523994
TCGA-CC-A8HU	19	1	2.236721691	0.18	163	0.489821363
TCGA-CC-A8HV	65	191	1.066687815	0.2	400	0.814793975
TCGA-CC-A9FS	58	0	1.337351131	0.07	81	0.724439084
TCGA-CC-A9FU	27	52	NA	0.14	161	0.920025443
TCGA-CC-A9FV	6	6	NA	0	50	3.20E-05
TCGA-CC-A9FW	78	58	4.015373347	0.01	129	0.709235875
TCGA-DD-A113	69	7	1.1586694	0.36	165	0.839269482
TCGA-DD-A114	52	42	2.082359655	0.42	97	0.362153554
TCGA-DD-A115	18	5	3.40980134	0.13	457	0.64092608
TCGA-DD-A116	55	20	1.27360476	0.19	165	0.470111838
TCGA-DD-A118	52	97	0.771426274	0.02	172	0.531631097

TCGA-DD-A119	35	1	0.711570906	0.51	97	0.41681225
TCGA-DD-A11A	71	30	3.704801488	0.21	386	0.931801192
TCGA-DD-A11B	20	29	0.782270983	0.02	78	0.91141736
TCGA-DD-A11C	47	97	3.258529678	0.25	752	0.537351065
TCGA-DD-A11D	54	247	2.197154729	0	552	0.178802896
TCGA-DD-A1E9	NA	NA	NA	0.32	95	0.484428971
TCGA-DD-A1EA	NA	NA	1.595668994	NA	79	0.124734683
TCGA-DD-A1EB	91	78	0.90801145	0.01	394	0.111754884
TCGA-DD-A1EC	7	NA	0.452772998	0	137	0.216544888
TCGA-DD-A1ED	8	99	1.410412607	0	41	3.54E-05
TCGA-DD-A1EE	366	411	0.793815766	0.13	60	0.198865442
TCGA-DD-A1EF	61	4	0.730751522	0.25	152	0.710027715
TCGA-DD-A1EH	17	5	1.016812433	0.28	53	0.46399297
TCGA-DD-A1EI	27	198	1.017196608	0.13	155	0.401671215
TCGA-DD-A1EJ	38	54	4.175529439	0.56	145	0.541367944
TCGA-DD-A1EK	36	0	4.040711223	0.02	451	0.175893672
TCGA-DD-A1EL	29	9	4.416595403	0.21	136	0.684494886
TCGA-DD-A39V	38	2	3.364082523	0	89	0.859646421
TCGA-DD-A39W	21	10	0.765068532	0	71	0.094734832
TCGA-DD-A39X	36	0	0.866549068	0.51	104	0.612417565
TCGA-DD-A39Z	40	8	1.012828769	0.03	50	0.277823016
TCGA-DD-A3A2	42	222	1.315489106	0	47	0.057240338
TCGA-DD-A3A3	1	0	0.655656556	0	118	0.582229505
TCGA-DD-A3A4	17	42	0.267091809	0.01	64	0.056447788
TCGA-DD-A3A5	23	4	3.5945011	0.1	437	0.220138922
TCGA-DD-A3A6	14	8	NA	0.04	47	0.04678589
TCGA-DD-A3A7	40	34	1.26666082	0.06	239	0.94638928
TCGA-DD-A3A8	77	19	0.99751525	0.11	88	0.224231448
TCGA-DD-A3A9	170	242	0.55456373	0.11	166	0.633520634
TCGA-DD-A4NA	13	53	2.681533996	NA	240	0.804146036
TCGA-DD-A4NB	15	64	0.678027566	0.13	85	0.16607032
TCGA-DD-A4ND	26	13	1.510707319	0.01	84	0.398497913
TCGA-DD-A4NF	79	6	1.103598369	0.08	57	0.118854169
TCGA-DD-A4NH	19	24	1.215642445	0.03	72	0.374766062
TCGA-DD-A4NI	57	27	1.084725719	0.3	59	0.655262355
TCGA-DD-A4NK	36	23	0.962882463	0	60	0.344123014
TCGA-DD-A4NL	14	17	0.754385705	0	53	2.06E-05
TCGA-DD-A4NN	28	140	0.891235018	0.23	108	0.445138447
TCGA-DD-A4NO	25	3	0.692076134	0.17	117	0.792238222
TCGA-DD-A4NP	15	4	0.765682258	0	55	0.038904472
TCGA-DD-A4NQ	19	12	2.148968385	0.13	63	0.35427729

TCGA-DD-A4NR	29	107	3.151227682	0	71	0.187091196
TCGA-DD-A4NS	32	4	1.548720581	0.14	45	0.108337192
TCGA-DD-A4NV	71	0	2.694032629	0.11	61	0.953563018
TCGA-DD-A73A	47	130	0.858565187	0	149	0.090767085
TCGA-DD-A73B	NA	NA	0.519929362	0.02	123	0.946304169
TCGA-DD-A73C	38	NA	1.064303479	0	71	0.046721974
TCGA-DD-A73D	44	15	0.736727628	0	128	0.946951756
TCGA-DD-A73E	59	14	0.837142144	0	80	0.385325965
TCGA-DD-A73F	34	0	3.208107048	0.07	543	0.180820917
TCGA-DD-A73G	53	2	0.478731417	0.12	640	0.852126266
TCGA-DD-AA3A	15	21	1.501600592	0.01	152	0.389367013
TCGA-DD-AAC8	298	24	1.917933749	0.02	120	0.463744462
TCGA-DD-AAC9	31	0	0.203421572	0.03	89	0.099997109
TCGA-DD-AACA	26	NA	1.825668453	0.04	148	0.166047475
TCGA-DD-AACB	47	64	4.376988673	0.16	160	0.618129086
TCGA-DD-AACC	46	49	0.874129855	0.04	120	0.206777751
TCGA-DD-AACD	49	52	1.247627694	0.13	303	0.227483714
TCGA-DD-AACE	48	12	1.276033291	0.09	87	0.718387906
TCGA-DD-AACF	66	209	0.518413756	0.01	128	0.311144072
TCGA-DD-AACG	50	96	3.519895191	0.06	237	0.868524409
TCGA-DD-AACH	42	71	5.028528303	0.05	214	0.328589335
TCGA-DD-AACI	180	297	1.130884396	0.15	288	0.912972618
TCGA-DD-AACJ	27	19	2.370799049	0.02	146	0.914746442
TCGA-DD-AACK	44	1	2.26665724	0.01	106	0.042724456
TCGA-DD-AACL	124	13	2.844276337	0.04	170	0.233344085
TCGA-DD-AACM	NA	NA	NA	0.01	158	0.262960133
TCGA-DD-AACN	22	75	0.702085281	0	133	0.540430301
TCGA-DD-AACO	23	9	0.153092585	0.24	156	0.623129067
TCGA-DD-AACP	92	15	5.470918676	0.15	119	0.76186438
TCGA-DD-AACQ	98	242	0.761155987	0	133	0.175150339
TCGA-DD-AACS	30	2	0.47151304	0.04	159	0.426018736
TCGA-DD-AACT	51	48	1.136716944	0.12	122	0.923036369
TCGA-DD-AACU	72	8	1.806103345	0.14	137	0.810807004
TCGA-DD-AACV	42	91	4.3516642	0.05	269	0.928686653
TCGA-DD-AACW	26	11	1.368117516	0	96	0.653212043
TCGA-DD-AACX	65	18	0.703622528	0	142	0.111572383
TCGA-DD-AACY	31	16	0.885670464	0.03	160	0.282726672
TCGA-DD-AACZ	73	15	3.538895786	0.31	219	0.646860071
TCGA-DD-AAD0	57	24	1.104762718	0	143	0.166355609
TCGA-DD-AAD1	59	35	1.043052565	0.15	104	0.235099248
TCGA-DD-AAD2	36	2	1.30713488	0.02	111	0.157049894

TCGA-DD-AAD3	35	1	1.424615009	0.05	165	0.248645527
TCGA-DD-AAD5	27	60	4.907398221	0.19	227	0.527708617
TCGA-DD-AAD6	53	3	0.86262	0.08	140	0.292250766
TCGA-DD-AAD8	61	0	3.668861832	0.1	132	0.909828627
TCGA-DD-AADA	62	4	1.155295034	0.04	133	0.245465581
TCGA-DD-AADB	55	NA	1.427769621	0.16	149	0.775953937
TCGA-DD-AADC	29	8	4.269844661	0.02	318	0.454738245
TCGA-DD-AADD	38	9	4.183625383	0.43	148	0.544769663
TCGA-DD-AADE	NA	NA	NA	0	151	0.072830013
TCGA-DD-AADF	88	127	3.220068012	0.11	665	0.386137512
TCGA-DD-AADG	85	67	3.378323504	0.03	154	0.179586804
TCGA-DD-AADI	61	113	0.907978057	0.17	116	0.267465773
TCGA-DD-AADJ	31	126	2.121639635	0.03	447	0.206082974
TCGA-DD-AADK	34	139	1.475330127	0.04	86	0.312155772
TCGA-DD-AADL	59	157	3.555900115	0.34	189	0.839490306
TCGA-DD-AADM	74	80	1.408596591	0.07	171	0.280164941
TCGA-DD-AADN	56	21	0.756785702	0.23	233	0.467553713
TCGA-DD-AADO	88	110	1.045906724	0.01	230	0.849190666
TCGA-DD-AADP	45	0	0.775192565	0.01	165	0.85360047
TCGA-DD-AADQ	56	84	1.550291511	0.11	154	0.20735583
TCGA-DD-AADS	71	27	0.759753967	0	102	0.087955199
TCGA-DD-AADU	43	11	0.823091175	0	90	0.947385412
TCGA-DD-AADV	60	48	4.053027519	0.26	243	0.772779883
TCGA-DD-AADW	27	11	1.17805685	0.22	165	0.436569007
TCGA-DD-AADY	21	0	0.483937233	0.02	175	0.94630988
TCGA-DD-AAE0	27	28	0.906105569	0.19	143	0.497886472
TCGA-DD-AAE1	18	1	1.180215397	0.03	95	0.258263302
TCGA-DD-AAE2	47	32	4.044217532	0.04	515	0.622050666
TCGA-DD-AAE3	60	117	2.758816682	0.06	203	0.693285256
TCGA-DD-AAE4	30	0	2.745472904	0.01	408	0.117051239
TCGA-DD-AAE6	31	71	1.189011101	0.04	152	0.451558343
TCGA-DD-AAE7	122	166	0.819075087	0.04	84	0.047470074
TCGA-DD-AAE8	NA	NA	NA	0.22	98	0.471489113
TCGA-DD-AAE9	49	8	2.721312253	0.05	134	0.947220615
TCGA-DD-AAEA	41	83	1.216231847	0.09	153	0.287688062
TCGA-DD-AAEB	56	70	1.768861626	0.01	125	0.144637823
TCGA-DD-AAED	35	134	0.366707445	0.02	188	0.894990001
TCGA-DD-AAEE	39	21	2.183695105	0.11	172	0.403343652
TCGA-DD-AAEG	61	109	1.322676324	0.18	214	0.312938935
TCGA-DD-AAEH	40	57	0.259326611	0.02	129	0.221412035
TCGA-DD-AAEI	15	28	0.771179729	0.01	192	0.152868884

TCGA-DD-AAEK	32	1	1.214055724	0.08	120	0.59751123
TCGA-DD-AAVP	42	9	0.53670631	0.03	146	0.237494003
TCGA-DD-AAVQ	27	0	0.747606921	0.01	83	0.530730082
TCGA-DD-AAVR	27	6	0.418729601	0.04	215	0.155698308
TCGA-DD-AAVS	15	24	0.474640633	0.04	90	0.345224467
TCGA-DD-AAVU	24	55	1.018386053	0.04	153	0.916926684
TCGA-DD-AAVV	56	36	1.030071817	0.25	163	0.722307972
TCGA-DD-AAVW	18	1	2.291516681	0.04	182	0.35499112
TCGA-DD-AAVX	22	0	0.539434886	0.02	83	0.124224639
TCGA-DD-AAVY	41	166	0.475508602	0.04	147	0.301235656
TCGA-DD-AAVZ	21	5	0.834397669	0.04	138	0.335366663
TCGA-DD-AAW0	42	6	1.740915826	0.04	137	0.286027287
TCGA-DD-AAW1	59	7	1.045223779	0.01	36	0.196435123
TCGA-DD-AAW2	59	6	0.849569113	0.08	143	0.823366008
TCGA-DD-AAW3	35	99	0.579637819	0.01	69	0.224825927
TCGA-ED-A459	126	179	1.405517021	0.34	348	0.882000088
TCGA-ED-A4XI	91	12	0.866217867	0.04	81	0.103810866
TCGA-ED-A5KG	14	0	2.027296377	0.4	53	0.020974725
TCGA-ED-A66X	20	0	0.889349714	0.07	83	0.526991573
TCGA-ED-A66Y	39	1	1.5165608	0.15	121	0.843368879
TCGA-ED-A7PX	17	1	1.272248141	0.13	280	0.800077731
TCGA-ED-A7PY	18	NA	0.754013572	0.09	78	0.365116766
TCGA-ED-A7PZ	86	7	5.036493828	0.26	187	0.846310603
TCGA-ED-A7XO	36	36	2.050811733	0.32	203	0.530831931
TCGA-ED-A7XP	36	5	1.666509758	0.13	109	0.288964002
TCGA-ED-A82E	13	0	0.551009623	0.06	184	0.66757037
TCGA-ED-A8O5	31	0	0.753780552	0	110	0.257510208
TCGA-ED-A8O6	30	87	0.967732395	0.33	129	0.589619068
TCGA-ED-A97K	24	28	2.351003199	0.1	182	0.827746078
TCGA-EP-A12J	27	94	0.863901327	0.04	123	0.198122767
TCGA-EP-A26S	51	65	1.538424489	0	97	0.08447616
TCGA-EP-A2KA	41	123	1.085873813	0.06	1020	0.68986212
TCGA-EP-A2KB	33	5	0.854650992	0.35	58	0.642665892
TCGA-EP-A2KC	42	59	1.86987415	0.5	84	0.511203646
TCGA-EP-A3JL	46	26	1.990131118	0.33	47	0.656296256
TCGA-EP-A3RK	39	0	2.628646258	0.04	58	0.233153193
TCGA-ES-A2HS	28	68	0.350067097	0.14	117	0.711757518
TCGA-ES-A2HT	44	NA	0.716874708	0.1	81	0.14887616
TCGA-FV-A23B	36	7	2.616364459	0.13	130	0.201889241
TCGA-FV-A2QQ	66	162	3.430954521	0.14	95	0.36967814
TCGA-FV-A2QR	46	22	3.085092859	0.01	159	0.26057102

TCGA-FV-A3I0	30	0	NA	0.06	149	0.868953451
TCGA-FV-A3I1	11	1	2.944539602	0.25	141	0.312949874
TCGA-FV-A3R2	37	67	0.356562862	0	103	0.401820246
TCGA-FV-A3R3	30	5	1.039473919	0	43	0.096857797
TCGA-FV-A495	67	13	2.830754316	0.07	339	0.194120596
TCGA-FV-A496	65	1	1.810699312	0.26	517	0.973318299
TCGA-FV-A4ZP	56	119	0.734133064	0.07	217	0.543737063
TCGA-FV-A4ZQ	34	0	1.097625065	0.05	120	0.947679586
TCGA-G3-A25S	88	102	4.190898775	0.26	228	0.935356301
TCGA-G3-A25T	35	14	1.137952736	0.17	63	0.530182168
TCGA-G3-A25U	34	2	1.061295647	0.07	157	0.366826554
TCGA-G3-A25V	33	47	2.937659063	0.11	45	0.027641482
TCGA-G3-A25W	NA	NA	NA	0.01	109	0.303750295
TCGA-G3-A25Y	57	1	0.888238324	0.11	128	0.302606967
TCGA-G3-A25Z	35	113	2.343183285	0.24	149	0.317708085
TCGA-G3-A3CH	19	7	0.661755434	0.07	83	0.230354032
TCGA-G3-A3CI	4	NA	0.400832166	0	61	0.016386815
TCGA-G3-A3CK	69	18	0.940604006	0.03	62	0.078143499
TCGA-G3-A5SI	18	6	0.402644341	0.07	105	0.320955831
TCGA-G3-A5SJ	56	154	3.702932773	0.01	91	0.205197545
TCGA-G3-A5SL	59	45	1.158982883	0.18	100	0.378621624
TCGA-G3-A5SM	58	7	2.385185172	0.35	58	0.496995615
TCGA-G3-A6UC	58	33	0.548643581	0.08	148	0.250360781
TCGA-G3-A7M5	94	297	3.425515038	0	95	0.95231933
TCGA-G3-A7M6	48	12	4.770797158	0.07	124	0.277581559
TCGA-G3-A7M7	34	NA	0.882019448	0.04	122	0.069826545
TCGA-G3-A7M8	10	0	0.690477419	0	55	3.06E-05
TCGA-G3-A7M9	67	165	7.074107932	0.45	154	0.662035592
TCGA-G3-AAUZ	31	25	0.948954688	0.1	277	0.202495387
TCGA-G3-AAV0	91	254	0.916458349	0	103	0.176762485
TCGA-G3-AAV1	31	87	0.707950794	0.29	127	0.817803243
TCGA-G3-AAV2	26	2	1.234963415	0	78	0.213284132
TCGA-G3-AAV3	40	6	1.627544873	0	69	0.210608873
TCGA-G3-AAV4	44	2	0.832349764	0.09	73	0.808168524
TCGA-G3-AAV5	47	1	1.373914371	0	80	0.940868885
TCGA-G3-AAV6	30	18	2.680829812	0.22	104	0.778334353
TCGA-G3-AAV7	39	16	1.3576436	0.15	107	0.932475978
TCGA-GJ-A3OU	26	20	0.577153649	0.23	69	0.276433255
TCGA-GJ-A6C0	21	NA	NA	0.03	687	0.158393799
TCGA-GJ-A9DB	42	1	3.769248092	0.06	140	0.258772407
TCGA-HP-A5MZ	18	22	0.973319966	0.21	43	0.155189954

TCGA-HP-A5N0	86	159	0.988282332	0.01	89	0.201970664
TCGA-K7-A5RG	62	3	5.513777398	0.16	50	0.226656785
TCGA-K7-A6G5	32	2	0.997027504	0.04	92	0.148176195
TCGA-K7-AAU7	28	6	3.723482173	0.01	114	0.130997344
TCGA-KR-A7K0	41	130	1.331042633	0	54	0.040319225
TCGA-KR-A7K2	16	54	NA	0.12	66	0.854130603
TCGA-KR-A7K7	35	13	2.319317143	0.15	69	0.92668846
TCGA-KR-A7K8	15	11	3.641997071	0.28	493	0.253729351
TCGA-LG-A6GG	58	0	3.744184358	0.05	209	0.931309487
TCGA-LG-A9QC	NA	NA	0.496644865	0	108	0.27444726
TCGA-LG-A9QD	29	96	0.735483742	0.07	80	0.099519949
TCGA-MI-A75C	32	85	1.010798468	0.03	82	0.138489028
TCGA-MI-A75E	60	128	0.878981158	0.02	91	0.228896616
TCGA-MI-A75G	121	176	2.207605588	0.48	140	0.743827618
TCGA-MI-A75H	74	87	1.070384867	0	63	0.15879958
TCGA-MI-A75I	69	14	3.99190686	0.14	99	0.37067283
TCGA-MR-A520	12	NA	0.826079258	0	51	9.55E-06
TCGA-MR-A8JO	15	4	0.563079375	0.51	69	0.205883122
TCGA-NI-A4U2	59	61	1.443601926	0.02	167	0.126869285
TCGA-NI-A8LF	37	5	1.467012563	0.04	426	0.606479431
TCGA-O8-A75V	33	15	1.129572685	0.01	88	0.351968195
TCGA-PD-A5DF	18	12	2.839622832	0.07	390	0.241804371
TCGA-QA-A7B7	39	5	3.147028924	0	231	0.907176757
TCGA-RC-A6M3	31	3	NA	0.2	251	0.63121644
TCGA-RC-A6M4	65	14	0.631591413	0.04	156	0.945852531
TCGA-RC-A6M5	14	45	0.221115222	0.13	65	0.097886502
TCGA-RC-A6M6	77	65	4.986838674	0.11	346	0.329539709
TCGA-RC-A7S9	32	5	0.41730917	0.02	116	0.164602659
TCGA-RC-A7SB	34	8	5.024041415	0.03	142	0.941311587
TCGA-RC-A7SF	30	60	1.195284132	0.12	105	0.262884638
TCGA-RC-A7SH	27	4	0.816046677	0.22	132	0.761882041
TCGA-RC-A7SK	75	6	3.404704543	0.15	179	0.944359023
TCGA-RG-A7D4	58	35	3.1634587	0.54	100	0.697743016
TCGA-UB-A7MA	31	14	NA	0.03	235	0.504427017
TCGA-UB-A7MB	683	233	1.082875488	0.17	239	0.663267486
TCGA-UB-A7MC	18	47	1.263471974	0.04	133	0.456182163
TCGA-UB-A7MD	55	45	4.0082537	0.04	73	0.221256595
TCGA-UB-A7ME	40	10	1.38415543	0.34	143	0.659514773
TCGA-UB-A7MF	NA	NA	0.428388582	0.09	109	0.795925356
TCGA-UB-AA0U	32	3	1.065470796	0.12	91	0.515385969
TCGA-UB-AA0V	18	NA	0.485328553	0	41	4.17E-05

TCGA-WJ-A86L	55	171	5.652270248	0.02	429	0.160200074
TCGA-WQ-A9G7	161	395	1.378439541	0.14	124	0.621239825
TCGA-WQ-AB4B	35	39	0.64667538	0.15	74	0.669896868
TCGA-WX-AA44	37	152	0.851083613	0.47	132	0.365176964
TCGA-WX-AA46	25	32	0.748254583	0.04	75	0.054333669
TCGA-WX-AA47	20	31	0.559568001	0.06	101	0.230020096
TCGA-XR-A8TD	28	3	3.612429263	0.02	387	0.239283252
TCGA-XR-A8TE	7	3	0.667381396	0	88	0.298920884
TCGA-XR-A8TF	61	15	2.359388145	0.08	167	0.516488993
TCGA-XR-A8TG	28	48	2.014879901	0.11	794	0.232144823
TCGA-YA-A8S7	33	7	1.837259364	0.16	99	0.498175048
TCGA-ZP-A9CV	38	8	1.16989053	0.02	62	0.153011252
TCGA-ZP-A9CY	41	2	1.962678404	0.01	75	0.030374178
TCGA-ZP-A9CZ	27	7	0.36140762	0.12	91	0.25159121
TCGA-ZP-A9D0	26	54	0.51879669	0.26	128	0.17480344
TCGA-ZP-A9D1	75	NA	1.849006617	0.25	56	0.551938644
TCGA-ZP-A9D2	17	3	1.730759459	0.04	144	0.587142158
TCGA-ZP-A9D4	39	124	1.113792781	0.03	201	0.141389666
TCGA-ZS-A9CD	NA	NA	0.844210708	0.1	77	0.159314668
TCGA-ZS-A9CE	21	19	2.041709942	0	118	0.773321833
TCGA-ZS-A9CF	44	NA	2.07661762	0.25	863	0.85047738
TCGA-ZS-A9CG	28	49	1.075059622	0.08	57	0.235737127

LOH_n_seg	LOH_frac_altered	Homologous.Recombination.Defects	Aneuploidy.Score	TCR.Richness	TCR.Shannon
18	0.0353	14	4	31	3.315039415
72	0.242	9	9	5	1.609437912
15	0.00833	2	1	27	3.23823154
13	0.0427	17	10	4	1.386294361
25	0.0751	19	2	9	2.197224577
29	0.0216	12	5	18	2.815204927
29	0.0625	18	3	43	3.721032164
77	0.186	24	23	34	3.436238682
38	0.071	22	13	0	NA
83	0.104	16	7	18	2.508834101
18	0.0338	9	5	3	1.039720771
55	0.141	34	22	4	1.33217904
49	0.0718	22	18	8	2.043191871
49	0.116	19	4	3	1.098612289
52	0.173	25	7	11	2.397895273
69	0.171	18	6	14	2.63905733
51	0.112	10	5	14	2.615630577
119	0.354	40	12	24	2.947248859
45	0.0498	11	3	2	0.693147181
75	0.138	21	5	3	1.098612289
23	0.041	6	5	17	2.813355405
11	0.0159	7	18	4	1.386294361
53	0.107	16	1	1	0
9	0.0258	13	17	3	1.098612289
37	0.118	12	6	9	2.197224577
88	0.345	28	12	21	3.01494688
32	0.0602	7	10	4	1.33217904
12	0.0524	1	4	10	2.271868513
33	0.0728	12	4	8	2.079441542
162	0.0678	12	1	62	4.097187614
9	0.126	15	18	NA	NA
68	0.229	26	20	2	0.636514168
44	0.147	33	3	4	1.351783994
15	0.11	13	8	1	0
11	0.13	24	4	6	1.732867951
51	0.113	29	2	1	0
63	0.0661	19	2	0	NA
93	0.0841	20	5	21	2.867687639
16	0.0704	34	21	6	1.791759469

47	0.257	34	7	5	1.609437912
104	0.228	30	13	0	NA
55	0.215	23	15	2	0.693147181
96	0.0945	19	2	33	3.476131241
18	0.0457	13	5	4	1.386294361
17	0.17	18	22	16	2.725550396
41	0.083	25	17	2	0.693147181
11	0.021	3	29	27	2.913089005
42	0.223	26	9	26	3.24449263
29	0.187	17	5	12	2.45831133
9	0.0969	14	3	13	2.51265853
72	0.182	34	8	4	1.386294361
33	0.371	26	19	20	2.995732274
17	0.175	26	11	72	4.201724105
49	0.278	37	21	52	3.268608548
46	0.275	35	6	0	NA
29	0.249	27	18	5	1.609437912
12	0.0854	25	6	1	0
33	0.103	19	15	0	NA
58	0.228	23	16	4	1.386294361
45	0.169	34	20	3	1.098612289
69	0.1	28	17	28	3.299829686
41	0.0797	23	11	1	0
91	0.317	63	17	0	NA
40	0.042	11	7	0	NA
21	0.027	25	23	2	0.693147181
173	0.357	31	8	43	3.625809829
18	0.0357	14	22	1	0
42	0.101	19	20	1	0
48	0.122	13	7	4	1.33217904
78	0.307	34	16	2	0.693147181
128	0.245	39	24	2	0.636514168
67	0.251	23	8	5	1.609437912
75	0.218	31	16	6	1.791759469
4	0.000186	0	0	22	3.031590576
64	0.337	21	21	9	2.163955657
36	0.201	31	19	14	2.615630577
14	0.232	11	7	24	3.134162459
40	0.117	26	7	4	1.386294361
33	0.208	16	8	5	1.560710409
14	0.151	19	16	9	2.163955657

8	0.0738	17	5	4	1.33217904
32	0.036	46	13	0	NA
13	0.188	7	9	4	1.386294361
119	0.178	40	5	4	1.386294361
32	0.016	5	6	2	0.693147181
2	0.0156	4	27	NA	NA
4	0.00769	3	5	15	2.708050201
42	0.0635	22	3	5	1.609437912
17	0.0406	11	8	103	4.558934303
19	3.04E-05	0	0	7	1.69878299
6	0.0537	7	6	2	0.693147181
17	0.192	24	24	22	3.052520502
8	0.153	9	6	15	2.685945325
39	0.146	18	11	14	2.63905733
16	0.0907	16	11	4	1.386294361
44	0.12	15	5	6	1.791759469
28	0.226	33	8	1	0
16	0.0361	6	11	3	1.098612289
6	0.00715	7	1	4	1.386294361
33	0.112	16	1	2	0.693147181
15	0.103	11	9	2	0.693147181
5	0.00344	1	2	0	NA
7	0.0308	8	8	0	NA
9	0.0691	8	2	0	NA
48	0.0895	17	4	2	0.693147181
3	0.0116	0	0	NA	NA
46	0.136	32	26	0	NA
15	0.0865	14	5	1	0
64	0.154	20	19	4	1.351783994
93	0.213	24	11	4	1.329661349
12	0.00218	0	0	13	2.540036304
36	0.141	14	13	19	2.902002313
5	0.00528	4	2	0	NA
52	0.264	23	9	3	1.098612289
13	0.0124	8	4	17	2.770973881
27	0.0557	8	9	0	NA
8	0.00127	0	0	5	1.560710409
60	0.221	34	8	0	NA
35	0.0568	11	16	3	1.098612289
2	6.66E-05	0	2	2	0.636514168
64	0.248	14	8	2	0.636514168

28	0.0392	14	7	32	3.201249638
19	0.0367	8	3	27	3.183922422
37	0.144	8	15	9	2.197224577
37	0.0328	12	1	11	2.397895273
93	0.333	38	5	1	0
15	0.0157	2	2	2	0.636514168
22	0.0138	10	9	0	NA
26	0.0796	17	13	0	NA
120	0.0968	20	1	27	3.23823154
120	0.0912	29	16	0	NA
76	0.211	17	8	2	0.693147181
26	0.0466	11	14	1	0
22	0.0495	9	2	6	1.747868097
26	0.0688	19	4	3	1.098612289
52	0.173	19	16	10	2.166084939
53	0.128	28	5	54	3.657358179
90	0.069	13	7	2	0.636514168
19	0.024	6	19	2	0.693147181
53	0.131	14	10	1	0
72	0.126	26	14	2	0.693147181
98	0.239	52	6	4	1.33217904
29	0.0624	25	20	6	1.676987774
31	0.0408	8	9	0	NA
14	0.0161	6	1	12	2.403640411
65	0.165	14	4	7	1.831020481
70	0.169	24	6	NA	NA
77	0.203	20	12	9	2.197224577
43	0.0985	17	10	1	0
34	0.166	10	18	10	2.271868513
34	0.0954	26	4	0	NA
69	0.171	33	5	0	NA
13	0.0131	8	12	6	1.791759469
96	0.236	21	23	11	2.338371705
96	0.203	25	8	1	0
52	0.148	15	5	5	1.609437912
27	0.0589	12	5	2	0.693147181
27	0.0954	22	5	2	0.693147181
109	0.196	29	20	32	3.429486232
47	0.0838	23	4	5	1.609437912
34	0.0812	20	7	40	3.626656184
26	0.0206	8	5	12	2.48490665

67	0.173	21	8	8	2.043191871
63	0.0979	34	15	0	NA
37	0.128	15	8	2	0.693147181
48	0.135	14	15	0	NA
24	0.0504	18	8	12	2.48490665
90	0.199	17	7	39	3.626656184
114	0.299	39	8	3	1.098612289
50	0.21	16	14	4	1.386294361
31	0.0219	5	3	NA	NA
98	0.0954	39	10	4	1.386294361
39	0.0446	13	6	0	NA
39	0.109	13	5	30	3.36326707
193	0.117	14	5	3	1.039720771
59	0.258	17	7	13	2.540036304
52	0.186	19	13	4	1.386294361
49	0.113	31	5	7	1.906154747
69	0.148	24	16	12	2.441015278
75	0.159	38	18	8	1.979204517
71	0.206	23	6	6	1.791759469
65	0.132	9	6	4	1.33217904
30	0.014	0	4	5	1.427061043
15	0.0108	13	23	0	NA
117	0.268	23	6	3	1.098612289
95	0.179	37	5	6	1.791759469
106	0.318	30	8	1	0
62	0.149	21	16	2	0.693147181
30	0.138	16	5	5	1.609437912
132	0.175	25	5	19	2.944438979
57	0.195	21	24	1	0
58	0.077	15	2	10	2.13338193
48	0.146	41	9	0	NA
17	0.0206	8	2	5	1.609437912
68	0.274	27	11	NA	NA
56	0.165	9	14	0	NA
34	0.0937	19	8	4	1.386294361
30	0.0402	7	5	1	0
65	0.216	20	7	0	NA
69	0.214	32	6	2	0.693147181
82	0.121	18	6	0	NA
45	0.0826	14	7	36	3.539627567
57	0.0615	16	4	8	2.079441542

57	0.198	29	14	28	3.286462961
48	0.124	28	5	1	0
25	0.118	18	13	79	4.356001161
34	0.0336	13	4	10	2.302585093
54	0.19	20	7	7	1.945910149
70	0.192	16	29	0	NA
51	0.238	29	17	11	2.397895273
85	0.223	29	8	15	2.708050201
21	0.0346	8	2	5	1.609437912
41	0.0601	10	8	1	0
65	0.161	17	6	2	0.693147181
71	0.207	23	8	18	2.890371758
19	0.00638	5	3	2	0.693147181
21	0.0535	8	9	0	NA
25	0.103	13	7	1	0
196	0.282	42	14	2	0.693147181
32	0.0308	12	1	10	2.205598359
14	0.00224	0	0	163	5.057036621
7	0.000874	12	20	8	2.079441542
31	0.0797	15	14	2	0.693147181
121	0.277	36	4	3	1.098612289
40	0.133	18	8	3	1.098612289
67	0.202	25	17	0	NA
121	0.229	25	5	6	1.791759469
74	0.219	27	6	6	1.747868097
65	0.203	29	20	3	1.098612289
47	0.168	14	8	5	1.560710409
63	0.203	23	24	7	1.906154747
99	0.372	46	28	10	2.271868513
8	0.0674	9	4	1	0
3	0.0171	5	3	2	0.693147181
77	0.0652	14	5	31	3.321477718
12	0.236	5	7	5	1.609437912
8	0.0232	5	9	4	1.386294361
3	0.0758	6	26	17	2.780466369
11	0.177	17	5	23	2.956488663
7	0.121	9	21	0	NA
2	0.0154	3	33	1	0
15	0.13	19	5	13	2.293118601
14	0.0745	12	4	8	2.043191871
43	0.133	27	5	0	NA

38	0.194	30	17	NA	NA
43	0.217	15	9	14	2.615630577
17	0.167	12	13	6	1.747868097
3	0.0246	7	1	9	2.197224577
90	0.0778	20	5	6	1.672625446
96	0.104	43	8	0	NA
53	0.0842	18	13	0	NA
55	0.109	15	11	44	3.591699931
26	0.272	26	23	2	0.693147181
6	0.113	13	15	0	NA
22	0.154	19	6	1	0
19	0.00178	1	0	11	2.397895273
12	0.0396	12	9	NA	NA
19	0.189	32	3	13	2.523210953
20	0.0887	12	7	3	1.098612289
15	0.106	12	3	10	2.25385759
5	0.0173	2	0	8	2.079441542
4	0.002	4	1	9	1.745608564
43	0.144	32	4	0	NA
41	0.102	12	7	14	2.55779386
29	0.0609	7	6	3	1.098612289
16	0.0905	9	19	13	2.406159575
50	0.0593	9	6	0	NA
47	0.182	6	16	0	NA
55	0.131	21	8	10	2.302585093
17	0.0157	3	2	1	0
2	6.16E-05	0	0	0	NA
57	0.178	31	15	2	0.693147181
47	0.0731	13	7	2	0.693147181
16	0.0404	16	4	6	1.747868097
32	0.101	27	15	5	1.560710409
21	0.0594	13	4	0	NA
23	0.0712	8	4	26	3.144314011
25	0.0795	12	9	2	0.693147181
19	0.0231	7	11	4	1.386294361
37	0.15	29	20	2	0.693147181
78	0.369	23	9	13	2.540036304
48	0.13	15	6	68	4.083687893
149	0.093	23	3	NA	NA
44	0.0788	9	6	0	NA
9	0.000867	2	5	24	3.122424598

38	0.11	19	4	1	0
3	0.000858	6	3	55	3.811174982
28	0.0275	5	3	5	1.475076311
37	0.0582	11	4	9	2.145841753
15	0.00711	4	2	0	NA
26	0.0328	9	18	NA	NA
27	0.0221	4	17	10	2.25385759
5	9.57E-05	24	4	15	2.625048159
78	0.113	16	15	1	0
47	0.189	13	7	3	1.098612289
25	0.0286	7	3	7	1.945910149
25	0.0636	10	5	9	2.163955657
9	0.00061	6	5	12	2.48490665
44	0.0948	10	12	1	0
23	0.0599	9	5	4	1.33217904
58	0.194	13	10	5	1.560710409
5	0.00115	0	0	3	1.098612289
28	0.127	11	4	17	2.787788119
47	0.0726	17	4	0	NA
115	0.129	51	18	3	1.098612289
29	0.0663	18	8	16	2.772588722
74	0.107	28	3	5	1.609437912
90	0.221	23	7	12	2.45831133
93	0.172	24	20	4	1.386294361
32	0.108	19	15	1	0
5	0.0281	7	12	5	1.560710409
118	0.2	42	4	11	2.397895273
42	0.0523	19	5	3	1.039720771
65	0.181	19	5	0	NA
49	0.139	13	8	5	1.609437912
72	0.224	26	6	2	0.693147181
19	0.0902	20	17	1	0
29	0.066	29	27	16	2.725550396
61	0.121	42	13	NA	NA
110	0.174	29	4	1	0
51	0.156	20	14	2	0.693147181
25	0.0571	9	6	7	1.906154747
61	0.131	36	22	21	2.982965029
36	0.099	29	11	20	2.882937427
48	0.146	41	16	16	2.772588722
6	0.00131	0	0	3	1.098612289

64	0.087	23	4	3	1.098612289
91	0.291	34	18	0	NA
15	0.0334	9	20	1	0
47	0.0581	15	5	2	0.693147181
17	0.0281	5	2	2	0.693147181
33	0.059	6	6	0	NA
107	0.127	29	7	27	3.282693997
20	0.088	4	6	4	1.386294361
72	0.159	14	15	0	NA
122	0.0842	20	5	3	1.098612289
30	0.177	19	19	10	2.302585093
17	0.0335	5	3	7	1.906154747
12	0.00996	6	0	5	1.609437912
45	0.142	30	4	13	2.479955521
41	0.141	23	4	0	NA
37	0.179	14	15	18	2.871476118
122	0.354	12	9	2	0.693147181
43	0.0429	8	5	0	NA
8	0.015	6	3	5	1.609437912
31	0.0741	17	13	0	NA
164	0.17	38	5	3	1.098612289
23	0.116	6	5	3	1.098612289

Table S7. Top 30 mutated genes in TCHA-LIHC patients.

TCGA-BC-A5W4	TCGA-RG-A7D4	TCGA-DD-A1EE	TCGA-DD-AACB	TCGA-BW-A5NQ	TCGA-CC-A5UD	TCGA-G3-A5SJ
CTNNB1	Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation
TP53	Missense_Mutation	Missense_Mutation	Nonsense_Mutation	Missense_Mutation	Nonsense_Mutation	Missense_Mutation
TTN	Missense_Mutation	Missense_Mutation				
MUC16			Missense_Mutation	Missense_Mutation	Missense_Mutation	
PCLO	Missense_Mutation		Missense_Mutation			Missense_Mutation
RYR2						
LRP1B						
ABCA13			Missense_Mutation	Missense_Mutation		
CSMD3				Missense_Mutation	Missense_Mutation	
FLG					Missense_Mutation	
OBSCN			Missense_Mutation			Missense_Mutation
CACNA1E						
FAT3						
ADGRV1		Missense_Mutation			Missense_Mutation	
DOCK2						
HMCN1			Missense_Mutation		Missense_Mutation	
XIRP2						
ALB						
APOB				Nonsense_Mutation		
CUBN						Nonsense_Mutation
HERC2			Missense_Mutation			
PRKDC						
SDK1						Missense_Mutation
DNAH7				Missense_Mutation		
SPTA1			Missense_Mutation			
CCDC168						
COL11A1	Splice_Site					
DNAH5			Missense_Mutation			
RYR1						
USH2A						Missense_Mutation

TCGA-G3-A25Z	TCGA-FV-A4ZQ	TCGA-UB-A7MC	TCGA-DD-A1EL	TCGA-DD-AADD	TCGA-UB-A7MD	TCGA-ED-A7PZ
Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation
Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation	Splice_Site
Nonsense_Mutation						
	Missense_Mutation					
		Missense_Mutation				
			Missense_Mutation	Missense_Mutation		
Missense_Mutation						
			Missense_Mutation		Missense_Mutation	Missense_Mutation
Missense_Mutation						
	Missense_Mutation					
Missense_Mutation					Missense_Mutation	

TCGA-MI-A75H	TCGA-DD-AACK	TCGA-DD-AAW2	TCGA-DD-AACP	TCGA-DD-AAC8	TCGA-DD-AADM	TCGA-4R-AA8I
Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation
Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation
Missense_Mutation	Multi_Hit	Missense_Mutation	Missense_Mutation	Missense_Mutation		
					Missense_Mutation	Missense_Mutation
					Multi_Hit	
Missense_Mutation	Missense_Mutation					
Missense_Mutation					Nonsense_Mutation	
	Missense_Mutation				Missense_Mutation	
		Missense_Mutation				
Missense_Mutation						
					Missense_Mutation	Missense_Mutation
					Missense_Mutation	Missense_Mutation
						Missense_Mutation
		Missense_Mutation	Missense_Mutation			
Missense_Mutation						
				Splice_Site	Splice_Site	Splice_Site
Missense_Mutation		Missense_Mutation				Nonsense_Mutation
	Missense_Mutation	Missense_Mutation				
	Missense_Mutation					
					Missense_Mutation	
					Missense_Mutation	

TCGA-CC-A7IK	TCGA-DD-A73E	TCGA-G3-AAV3	TCGA-FV-A2QQ	TCGA-DD-AAEB	TCGA-NI-A8LF	TCGA-ZP-A9D4
Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation
Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation
Missense_Mutation						
Missense_Mutation	Nonsense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation		
					Missense_Mutation	
	Missense_Mutation					
Missense_Mutation	Missense_Mutation					
Missense_Mutation		Missense_Mutation				
						Missense_Mutation
Missense_Mutation						
Missense_Mutation			Missense_Mutation			
				Missense_Mutation		
Missense_Mutation						
Missense_Mutation		Missense_Mutation				
				Missense_Mutation		
Missense_Mutation						
Splice_Site						Missense_Mutation

TCGA-LG-A9QD	TCGA-K7-A6G5	TCGA-G3-A6UC	TCGA-3K-AAZ8	TCGA-DD-A1EJ	TCGA-DD-AACD	TCGA-DD-AAD0
Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation
Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation
Missense_Mutation	Splice_Site					
		Missense_Mutation				
Missense_Mutation						
			Missense_Mutation			

TCGA-DD-AADU	TCGA-EP-A3JL	TCGA-KR-A7K0	TCGA-G3-AAV4	TCGA-O8-A75V	TCGA-CC-5262	TCGA-DD-A116
Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation
Missense_Mutation						
	Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation	Nonsense_Mutation	Missense_Mutation
	Missense_Mutation					
		Missense_Mutation				
			Missense_Mutation			
				Missense_Mutation	Multi_Hit	
						Missense_Mutation
		Missense_Mutation				
				Missense_Mutation		
			Nonsense_Mutation			
	Missense_Mutation					
				Missense_Mutation		
			Missense_Mutation			

TCGA-DD-A4NF	TCGA-DD-AAVY	TCGA-XR-A8TF	TCGA-DD-AADG	TCGA-DD-AAEH	TCGA-2Y-A9HA	TCGA-DD-AAW1
Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation
Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation			
				Nonsense_Mutation	Missense_Mutation	Missense_Mutation
				Missense_Mutation		
					Missense_Mutation	
					Missense_Mutation	
Missense_Mutation						
						Missense_Mutation
Missense_Mutation						
					Multi_Hit	Missense_Mutation
				Missense_Mutation		
	Missense_Mutation	Splice_Site				
	Missense_Mutation					Missense_Mutation
						Missense_Mutation
	Missense_Mutation					
						Missense_Mutation
Missense_Mutation						
		Missense_Mutation				

TCGA-G3-A5SL	TCGA-DD-AAW3	TCGA-2Y-A9HB	TCGA-CC-A7IL	TCGA-EP-A2KA	TCGA-G3-AAV6	TCGA-2Y-A9H1
Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation
Missense_Mutation	Missense_Mutation					
		Nonsense_Mutation	Missense_Mutation			
		Missense_Mutation		Missense_Mutation	Missense_Mutation	Missense_Mutation
				Missense_Mutation		
					Missense_Mutation	
Missense_Mutation						
				Missense_Mutation		

TCGA-DD-AAE9	TCGA-DD-A4NK	TCGA-G3-AAV5	TCGA-G3-AAV2	TCGA-MI-A75C	TCGA-DD-AACA	TCGA-DD-AADE
Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation
Missense_Mutation	Missense_Mutation	Splice_Site	Missense_Mutation			
				Missense_Mutation	Missense_Mutation	
						Missense_Mutation
						Missense_Mutation
Missense_Mutation						
	Missense_Mutation					
		Missense_Mutation				
	Missense_Mutation					
Missense_Mutation						Missense_Mutation
	Missense_Mutation					
	Missense_Mutation					

TCGA-G3-A3CK	**TCGA-5R-AA1C**	**TCGA-DD-AAVX**	**TCGA-DD-A73A**	**TCGA-EP-A26S**	**TCGA-RC-A6M4**	**TCGA-DD-AAVP**
Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation
Missense_Mutation						
	Missense_Mutation	Missense_Mutation	Missense_Mutation			
	Missense_Mutation			Missense_Mutation		
		Nonsense_Mutation				
					Missense_Mutation	Missense_Mutation
					Missense_Mutation	
					Missense_Mutation	
						Missense_Mutation
	Splice_Site					
		Missense_Mutation				
					Missense_Mutation	

TCGA-DD-AAEE	TCGA-5C-A9VG	TCGA-DD-A4NI	TCGA-DD-A39V	TCGA-G3-AAV1	TCGA-ZS-A9CG	TCGA-CC-A9FW
Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation
Missense_Mutation						
	Missense_Mutation					
Missense_Mutation		Missense_Mutation				
		Missense_Mutation				
			Missense_Mutation	Missense_Mutation		
					Missense_Mutation	
		Missense_Mutation				Missense_Mutation
			Missense_Mutation			

TCGA-BC-A69H	**TCGA-DD-A3A3**	**TCGA-DD-A3A4**	**TCGA-DD-A4NL**	**TCGA-DD-A73D**	**TCGA-DD-AACJ**	**TCGA-DD-AACX**
Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation
Missense_Mutation						
Missense_Mutation						

TCGA-EP-A12J	TCGA-EP-A3RK	TCGA-WX-AA47	TCGA-ZP-A9CV	TCGA-UB-A7MB	TCGA-CC-A8HT	TCGA-DD-A114
Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation		
					Missense_Mutation	Missense_Mutation
					Missense_Mutation	Missense_Mutation
					Missense_Mutation	Missense_Mutation
					Multi_Hit	Missense_Mutation
					Missense_Mutation	
					Missense_Mutation	
					Multi_Hit	
					Missense_Mutation	
					Missense_Mutation	
					Missense_Mutation	
					Multi_Hit	
					Missense_Mutation	Missense_Mutation
						Missense_Mutation
					Missense_Mutation	
					Missense_Mutation	Missense_Mutation
					Missense_Mutation	
						Missense_Mutation
					Missense_Mutation	
					Nonsense_Mutation	
					Missense_Mutation	Missense_Mutation

TCGA-DD-A1EB	TCGA-2Y-A9GS	TCGA-MI-A75I	TCGA-DD-AADL	TCGA-CC-5263	TCGA-DD-AAD8	TCGA-RC-A6M6
Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation	Nonsense_Mutation	Splice_Site
Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation
Missense_Mutation						
	Missense_Mutation					
	Missense_Mutation	Missense_Mutation				
			Missense_Mutation			
				Missense_Mutation		
				Missense_Mutation		
Missense_Mutation						
			Missense_Mutation			
					Nonsense_Mutation	
						Splice_Site
	Missense_Mutation					
				Missense_Mutation		
	Missense_Mutation					

TCGA-2Y-A9H8	TCGA-G3-A5SM	TCGA-DD-AAEA	TCGA-FV-A3R2	TCGA-CC-A8HS	TCGA-ZP-A9D2	TCGA-BC-A10U
Nonsense_Mutation	Missense_Mutation	Splice_Site	Missense_Mutation	Nonsense_Mutation	Missense_Mutation	Missense_Mutation
Missense_Mutation	Nonsense_Mutation	Missense_Mutation				
			Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation
			Splice_Site	Missense_Mutation		
					Missense_Mutation	
						Missense_Mutation
Missense_Mutation						
			Missense_Mutation			

TCGA-WJ-A86L	TCGA-MI-A75G	TCGA-UB-A7MF	TCGA-CC-A3MA	TCGA-G3-A25U	TCGA-K7-A5RG	TCGA-DD-AACL
Missense_Mutation	Nonsense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation	Splice_Site
Nonsense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation
Missense_Mutation						
	Missense_Mutation					
Missense_Mutation						
		Missense_Mutation				
		Missense_Mutation				
		Missense_Mutation				
		Missense_Mutation				
		Missense_Mutation				
			Missense_Mutation			
			Missense_Mutation			
	Missense_Mutation					

TCGA-DD-AADB	TCGA-T1-A6J8	TCGA-DD-AACU	TCGA-DD-AAED	TCGA-CC-A7IG	TCGA-DD-AACV	TCGA-CC-A7II
Missense_Mutation	Missense_Mutation	Splice_Site	Missense_Mutation	Splice_Site	Nonsense_Mutation	Nonsense_Mutation
Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation
Missense_Mutation	Missense_Mutation	Missense_Mutation				
Missense_Mutation			Missense_Mutation			
Missense_Mutation						
Missense_Mutation						
			Missense_Mutation	Missense_Mutation		
			Missense_Mutation		Missense_Mutation	
Missense_Mutation					Missense_Mutation	
					Nonsense_Mutation	
					Missense_Mutation	
Splice_Site						
			Missense_Mutation			
Missense_Mutation						
			Missense_Mutation		Missense_Mutation	

TCGA-G3-A7M6	TCGA-BC-A10R	TCGA-DD-AAE0	TCGA-BC-A216	TCGA-2Y-A9GY	TCGA-CC-A7IJ	TCGA-ED-A7XO
Missense_Mutation	Missense_Mutation	Nonsense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation
Missense_Mutation	Missense_Mutation	Missense_Mutation				
			Missense_Mutation			
				Missense_Mutation	Missense_Mutation	
Missense_Mutation						Missense_Mutation
Missense_Mutation						Missense_Mutation
	Missense_Mutation					
				Splice_Site		
Missense_Mutation						

TCGA-DD-A3A7	TCGA-DD-AADC	TCGA-DD-AAD5	TCGA-DD-AAVV	TCGA-ED-A7XP	TCGA-CC-A8HU	TCGA-YA-A8S7
Missense_Mutation	Nonsense_Mutation	Splice_Site	Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation
Missense_Mutation	Missense_Mutation	Missense_Mutation				
			Missense_Mutation	Missense_Mutation		
					Missense_Mutation	
						Missense_Mutation
			Splice_Site			
Missense_Mutation						
					Missense_Mutation	
					Missense_Mutation	
			Missense_Mutation	Missense_Mutation		

TCGA-WQ-AB4B	TCGA-QA-A7B7	TCGA-BC-A217	TCGA-DD-AACG	TCGA-DD-AADV	TCGA-ED-A459	TCGA-K7-AAU7
Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation	Nonsense_Mutation	Missense_Mutation	Missense_Mutation
Missense_Mutation						
	Missense_Mutation					
		Missense_Mutation				
			Missense_Mutation			
	Missense_Mutation					
				Missense_Mutation		
					Missense_Mutation	Missense_Mutation
		Missense_Mutation	Missense_Mutation			

TCGA-WX-AA44	TCGA-XR-A8TG	TCGA-CC-A8HV	TCGA-DD-AACS	TCGA-GJ-A3OU	TCGA-RC-A7SH	TCGA-DD-A1EI
Missense_Mutation	Splice_Site	Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation
Missense_Mutation						
	Missense_Mutation	Missense_Mutation				
			Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation

TCGA-RC-A7SB	TCGA-FV-A4ZP	TCGA-BD-A3EP	TCGA-CC-A3M9	TCGA-CC-A3MB	TCGA-DD-AAD3	TCGA-DD-AADW
Nonsense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation
Missense_Mutation						
	Missense_Mutation					
		Missense_Mutation				

TCGA-FV-A3I1	TCGA-RC-A7SK	TCGA-CC-A7IH	TCGA-DD-AACI	TCGA-DD-A3A9	TCGA-DD-AACH	TCGA-CC-A1HT
Missense_Mutation	Missense_Mutation	Missense_Mutation				
			Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation
			Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation
			Missense_Mutation	Missense_Mutation		
			Multi_Hit		Missense_Mutation	Missense_Mutation
			Multi_Hit			
			Missense_Mutation			
			Missense_Mutation			
			Missense_Mutation	Splice_Site		
			Missense_Mutation			
					Missense_Mutation	
				Missense_Mutation		
			Missense_Mutation			
					Missense_Mutation	
					Missense_Mutation	
			Missense_Mutation			
			Missense_Mutation			
				Nonsense_Mutation		
					Missense_Mutation	Missense_Mutation
					Missense_Mutation	

TCGA-ZS-A9CE	TCGA-WQ-A9G7	TCGA-G3-AAV0	TCGA-DD-AACZ	TCGA-BD-A3ER	TCGA-DD-A3A8	TCGA-ES-A2HT
Missense_Mutation	Nonsense_Mutation	Missense_Mutation	Missense_Mutation	Multi_Hit	Missense_Mutation	Missense_Mutation
Missense_Mutation	Missense_Mutation					
		Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation
Missense_Mutation		Missense_Mutation				
Missense_Mutation						
			Missense_Mutation			
Missense_Mutation		Multi_Hit				
			Missense_Mutation			
			Missense_Mutation			
		Missense_Mutation				
Missense_Mutation						
				Nonsense_Mutation		
	Missense_Mutation					
			Missense_Mutation			

TCGA-G3-A5SK	**TCGA-2V-A95S**	**TCGA-BC-A10Z**	**TCGA-DD-A118**	**TCGA-DD-A11A**	**TCGA-DD-AACF**	**TCGA-NI-A4U2**
Missense_Mutation	Splice_Site	Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation
Missense_Mutation	Missense_Mutation	Missense_Mutation				
			Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation
			Missense_Mutation			
				Missense_Mutation		
Missense_Mutation						
	Missense_Mutation	Missense_Mutation				
	Missense_Mutation				Nonsense_Mutation	
	Missense_Mutation					

TCGA-CC-A9FS	TCGA-BC-A10Q	TCGA-BW-A5NP	TCGA-2Y-A9H9	TCGA-DD-AAD2	TCGA-CC-A123	TCGA-DD-AACQ
Nonsense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation
Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation Missense_Mutation	Missense_Mutation	Missense_Mutation
Missense_Mutation	Missense_Mutation			Missense_Mutation		
	Missense_Mutation					
	Missense_Mutation				Missense_Mutation	
				Missense_Mutation		
		Missense_Mutation				

TCGA-DD-AAVU	**TCGA-LG-A6GG**	**TCGA-BW-A5NO**	**TCGA-G3-A25W**	**TCGA-DD-AACE**	**TCGA-DD-AAW0**	**TCGA-DD-AACW**
Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation
Missense_Mutation	Missense_Mutation					
		Missense_Mutation				
		Missense_Mutation				
			Missense_Mutation			
				Nonsense_Mutation		
					Missense_Mutation	
Missense_Mutation						Missense_Mutation
					Missense_Mutation	
						Missense_Mutation
	Missense_Mutation					
Missense_Mutation			Missense_Mutation			
Missense_Mutation						

TCGA-BC-A3KF	**TCGA-DD-A4NJ**	**TCGA-5R-AAAM**	**TCGA-DD-A73G**	**TCGA-5C-A9VH**	**TCGA-CC-A9FU**	**TCGA-DD-A11D**
Missense_Mutation	Missense_Mutation	Missense_Mutation	Nonsense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation
Missense_Mutation						
	Missense_Mutation					
		Missense_Mutation				
			Missense_Mutation	Missense_Mutation		

TCGA-DD-A4NG	**TCGA-DD-AADY**	**TCGA-G3-A25T**	**TCGA-ZS-A9CF**	**TCGA-DD-AADF**	**TCGA-UB-A7ME**	**TCGA-DD-AADS**
Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation			
				Nonsense_Mutation	Missense_Mutation	Missense_Mutation
				Missense_Mutation		
					Missense_Mutation	Missense_Mutation
					Missense_Mutation	
					Missense_Mutation	Missense_Mutation
					Missense_Mutation	
						Missense_Mutation

TCGA-DD-AAE7	TCGA-DD-AAVS	TCGA-DD-AACO	TCGA-FV-A23B	TCGA-DD-AADO	TCGA-DD-AAD6	TCGA-UB-A7MA
Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation	Nonsense_Mutation
Missense_Mutation	Missense_Mutation					
		Missense_Mutation				
			Missense_Mutation	Missense_Mutation		
					Missense_Mutation	
						Missense_Mutation
						Missense_Mutation
						Missense_Mutation
					Missense_Mutation	
Missense_Mutation						
					Missense_Mutation	
					Missense_Mutation	

TCGA-DD-A39Z	TCGA-BC-A10W	TCGA-CC-A7IF	TCGA-DD-A4NA	TCGA-DD-A73F	TCGA-G3-A7M9	TCGA-2Y-A9GZ
Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation	
						Missense_Mutation
						Missense_Mutation
						Nonsense_Mutation
						Missense_Mutation
						Missense_Mutation
Missense_Mutation						
	Missense_Mutation					
	Missense_Mutation					
		Missense_Mutation				
			Missense_Mutation			
						Missense_Mutation
			Missense_Mutation			

TCGA-KR-A7K2	TCGA-EP-A2KC	TCGA-BC-A10Y	TCGA-BD-A2L6	TCGA-DD-A4NV	TCGA-DD-A113	TCGA-CC-A5UE
Nonsense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation	
						Missense_Mutation
Missense_Mutation						
						Missense_Mutation
						Missense_Mutation
Missense_Mutation	Missense_Mutation					
		Missense_Mutation				
			Missense_Mutation	Missense_Mutation		

TCGA-DD-A1E9	TCGA-DD-AAD1	TCGA-BC-4073	TCGA-DD-A3A5	TCGA-RC-A7S9	TCGA-DD-A4NQ	TCGA-RC-A6M3
Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation
Missense_Mutation	Missense_Mutation					
Missense_Mutation						
		Missense_Mutation				
	Missense_Mutation		Missense_Mutation			
				Missense_Mutation	Missense_Mutation	
		Missense_Mutation				
						Missense_Mutation
				Nonsense_Mutation		
Missense_Mutation						
		Missense_Mutation				

TCGA-FV-A496	TCGA-2Y-A9GW	TCGA-FV-A2QR	TCGA-DD-A4NE	TCGA-BC-A10T	TCGA-2Y-A9H5	TCGA-5C-AAPD
Missense_Mutation						
	Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation	Splice_Site
	Missense_Mutation					
	Missense_Mutation	Missense_Mutation				
			Missense_Mutation			
				Missense_Mutation		
		Missense_Mutation				
	Missense_Mutation				Missense_Mutation	

TCGA-CC-5264	TCGA-DD-A11C	TCGA-DD-AAE2	TCGA-G3-A3CG	TCGA-ED-A4XI	TCGA-CC-A7IE	TCGA-2Y-A9GV
Missense_Mutation	Missense_Mutation					
		Missense_Mutation	Missense_Mutation	Missense_Mutation		
					Missense_Mutation	Missense_Mutation
					Missense_Mutation	
						Nonsense_Mutation
		Missense_Mutation				
						Missense_Mutation
			Missense_Mutation			

TCGA-CC-5258	TCGA-DD-AADI	TCGA-DD-AAVZ	TCGA-ED-A8O5	TCGA-2Y-A9H3	TCGA-BC-A8YO	TCGA-DD-A4NH
Missense_Mutation	Missense_Mutation	Nonsense_Mutation	Missense_Mutation			
				Nonsense_Mutation	Missense_Mutation	Missense_Mutation
				Missense_Mutation		
Missense_Mutation	Missense_Mutation					
				Missense_Mutation		
					Missense_Mutation	

TCGA-DD-AADR	TCGA-G3-A7M7	TCGA-LG-A9QC	TCGA-DD-AACT	TCGA-DD-A4NN	TCGA-CC-A5UC	TCGA-G3-A7M5
Missense_Mutation	Missense_Mutation	Missense_Mutation				
			Missense_Mutation			
				Missense_Mutation	Missense_Mutation	Missense_Mutation
				Missense_Mutation		
					Missense_Mutation	
					Missense_Mutation	Splice_Site
					Missense_Mutation	

TCGA-G3-A25Y	TCGA-MR-A520	TCGA-DD-AACN	TCGA-ZP-A9CY	TCGA-2Y-A9GX	TCGA-2Y-A9H2	TCGA-DD-AAEI
Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation
			Splice_Site	Missense_Mutation		

TCGA-ED-A8O6	**TCGA-2Y-A9GT**	**TCGA-DD-A1EF**	**TCGA-ZP-A9D1**	**TCGA-DD-AAE8**	**TCGA-ED-A7PY**	**TCGA-DD-AADJ**
Nonsense_Mutation	Missense_Mutation	Nonsense_Mutation	Missense_Mutation	Missense_Mutation		
Missense_Mutation	Missense_Mutation				Missense_Mutation	Nonsense_Mutation
					Missense_Mutation	
Missense_Mutation						

TCGA-DD-AAVR	TCGA-G3-A25S	TCGA-ES-A2HS	TCGA-CC-5259	TCGA-HP-A5MZ	TCGA-DD-A1EK	TCGA-G3-A3CI
Missense_Mutation	Missense_Mutation	Missense_Mutation				
			Splice_Site			
				Missense_Mutation	Missense_Mutation	Missense_Mutation
				Nonsense_Mutation		
					Missense_Mutation	
				Missense_Mutation		

TCGA-DD-A1ED	TCGA-EP-A2KB	TCGA-G3-AAV7	TCGA-GJ-A9DB	TCGA-DD-A1EA	TCGA-DD-AACM	TCGA-DD-AAVQ
Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation

TCGA-MI-A75E	TCGA-WX-AA46	TCGA-KR-A7K7	TCGA-2Y-A9H0	TCGA-2Y-A9H7	TCGA-DD-AAE6	TCGA-G3-AAUZ
Missense_Mutation						
	Missense_Mutation	Missense_Mutation	Missense_Mutation			
	Missense_Mutation			Missense_Mutation		
					Missense_Mutation	Splice_Site
		Missense_Mutation				
				Missense_Mutation		

TCGA-FV-A3I0	TCGA-UB-AA0V	TCGA-XR-A8TD	TCGA-DD-AADK	TCGA-DD-AAE3	TCGA-G3-A25V	TCGA-DD-A73B
Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation
Missense_Mutation	Multi_Hit					

TCGA-KR-A7K8	**TCGA-DD-AADQ**	**TCGA-DD-AAVW**	**TCGA-DD-AAEG**	**TCGA-2Y-A9GU**
Missense_Mutation	Nonsense_Mutation	Missense_Mutation	Missense_Mutation	Missense_Mutation

Table S8. Tumor mutation burden in TCHA-LIHC patients.

Tumor_Sample_Barcode	total	total_perMB	total_perMB_log
TCGA-ED-A5KG	4	0.08	-1.096910013
TCGA-XR-A8TE	7	0.14	-0.853871964
TCGA-5R-AA1D	8	0.16	-0.795880017
TCGA-DD-A1ED	8	0.16	-0.795880017
TCGA-DD-A3A6	9	0.18	-0.744727495
TCGA-CC-A9FV	11	0.22	-0.657577319
TCGA-G3-A3CI	11	0.22	-0.657577319
TCGA-RC-A6M5	11	0.22	-0.657577319
TCGA-MR-A520	12	0.24	-0.619788758
TCGA-DD-A4NB	13	0.26	-0.585026652
TCGA-DD-A4NP	15	0.3	-0.522878745
TCGA-G3-A7M8	15	0.3	-0.522878745
TCGA-G3-A5SI	16	0.32	-0.494850022
TCGA-DD-A4NL	17	0.34	-0.468521083
TCGA-DD-A1EC	18	0.36	-0.443697499
TCGA-G3-A25V	18	0.36	-0.443697499
TCGA-BC-A10Q	19	0.38	-0.420216403
TCGA-MR-A8JO	19	0.38	-0.420216403
TCGA-ED-A82E	20	0.4	-0.397940009
TCGA-DD-A1EH	21	0.42	-0.37675071
TCGA-DD-A4NS	21	0.42	-0.37675071
TCGA-DD-A4NA	22	0.44	-0.356547324
TCGA-DD-AAVW	22	0.44	-0.356547324
TCGA-ED-A7PX	23	0.46	-0.337242168
TCGA-ED-A7PY	23	0.46	-0.337242168
TCGA-K7-A5RF	23	0.46	-0.337242168
TCGA-UB-AA0V	23	0.46	-0.337242168
TCGA-G3-A3CH	25	0.5	-0.301029996
TCGA-G3-A25T	26	0.52	-0.283996656
TCGA-WX-AA47	26	0.52	-0.283996656
TCGA-DD-AAVZ	27	0.54	-0.26760624
TCGA-DD-A3A4	28	0.56	-0.251811973
TCGA-ED-A66X	28	0.56	-0.251811973
TCGA-DD-A4NR	29	0.58	-0.236572006
TCGA-HP-A5MZ	29	0.58	-0.236572006
TCGA-KR-A7K8	29	0.58	-0.236572006
TCGA-2Y-A9GX	30	0.6	-0.22184875
TCGA-DD-AADW	30	0.6	-0.22184875
TCGA-FV-A3R3	30	0.6	-0.22184875
TCGA-2Y-A9H2	31	0.62	-0.207608311
TCGA-DD-AA3A	31	0.62	-0.207608311
TCGA-LG-A9QC	31	0.62	-0.207608311
TCGA-PD-A5DF	31	0.62	-0.207608311
TCGA-DD-A39W	32	0.64	-0.193820026
TCGA-DD-AACO	32	0.64	-0.193820026
TCGA-CC-5260	33	0.66	-0.180456064
TCGA-CC-A3MA	33	0.66	-0.180456064
TCGA-EP-A12J	33	0.66	-0.180456064
TCGA-WX-AA46	33	0.66	-0.180456064
TCGA-2Y-A9H6	34	0.68	-0.167491087
TCGA-KR-A7K2	34	0.68	-0.167491087
TCGA-DD-AACN	35	0.7	-0.15490196
TCGA-GJ-A6C0	35	0.7	-0.15490196
TCGA-DD-A11B	36	0.72	-0.142667504
TCGA-DD-A4NN	36	0.72	-0.142667504
TCGA-DD-AADY	36	0.72	-0.142667504

TCGA-ED-A97K	36	0.72	-0.142667504
TCGA-EP-A3RK	36	0.72	-0.142667504
TCGA-BD-A3ER	37	0.74	-0.13076828
TCGA-DD-A3A3	37	0.74	-0.13076828
TCGA-DD-A4NH	37	0.74	-0.13076828
TCGA-DD-AAVQ	37	0.74	-0.13076828
TCGA-GJ-A3OU	37	0.74	-0.13076828
TCGA-CC-A9FU	38	0.76	-0.119186408
TCGA-DD-A1EI	38	0.76	-0.119186408
TCGA-DD-A4ND	38	0.76	-0.119186408
TCGA-DD-AAE1	38	0.76	-0.119186408
TCGA-G3-AAV1	38	0.76	-0.119186408
TCGA-CC-A5UC	40	0.8	-0.096910013
TCGA-CC-A8HS	40	0.8	-0.096910013
TCGA-DD-A1E9	40	0.8	-0.096910013
TCGA-DD-AAVS	40	0.8	-0.096910013
TCGA-G3-AAV2	40	0.8	-0.096910013
TCGA-RC-A7SB	40	0.8	-0.096910013
TCGA-ZP-A9CZ	40	0.8	-0.096910013
TCGA-DD-A1EJ	41	0.82	-0.086186148
TCGA-DD-A4NE	41	0.82	-0.086186148
TCGA-DD-AACW	41	0.82	-0.086186148
TCGA-G3-A7M7	41	0.82	-0.086186148
TCGA-DD-A4NO	42	0.84	-0.075720714
TCGA-DD-AACS	42	0.84	-0.075720714
TCGA-DD-AADK	42	0.84	-0.075720714
TCGA-XR-A8TC	42	0.84	-0.075720714
TCGA-ZP-A9D0	42	0.84	-0.075720714
TCGA-DD-A119	43	0.86	-0.065501549
TCGA-WQ-AB4B	43	0.86	-0.065501549
TCGA-RC-A7S9	44	0.88	-0.055517328
TCGA-DD-AACM	45	0.9	-0.045757491
TCGA-DD-AAE8	45	0.9	-0.045757491
TCGA-G3-A25U	45	0.9	-0.045757491
TCGA-YA-A8S7	45	0.9	-0.045757491
TCGA-DD-AAVU	46	0.92	-0.036212173
TCGA-ED-A7XO	46	0.92	-0.036212173
TCGA-G3-AAV6	46	0.92	-0.036212173
TCGA-BC-A10Y	47	0.94	-0.026872146
TCGA-DD-A39X	47	0.94	-0.026872146
TCGA-DD-AAE0	47	0.94	-0.026872146
TCGA-G3-A25Y	47	0.94	-0.026872146
TCGA-XR-A8TD	47	0.94	-0.026872146
TCGA-BC-A216	48	0.96	-0.017728767
TCGA-BC-A8YO	48	0.96	-0.017728767
TCGA-DD-A73F	48	0.96	-0.017728767
TCGA-DD-AAE4	48	0.96	-0.017728767
TCGA-DD-AAVR	48	0.96	-0.017728767
TCGA-ZP-A9D2	48	0.96	-0.017728767
TCGA-ED-A7XP	49	0.98	-0.008773924
TCGA-ES-A2HS	49	0.98	-0.008773924
TCGA-BW-A5NP	50	1	0
TCGA-G3-A25W	50	1	0
TCGA-2Y-A9GV	51	1.02	0.008600172
TCGA-5C-AAPD	51	1.02	0.008600172
TCGA-5R-AAAM	51	1.02	0.008600172
TCGA-CC-A3MB	51	1.02	0.008600172
TCGA-2Y-A9GS	52	1.04	0.017033339
TCGA-DD-A3A5	52	1.04	0.017033339

TCGA-DD-A73C	52	1.04	0.017033339
TCGA-DD-AADJ	52	1.04	0.017033339
TCGA-ED-A8O6	52	1.04	0.017033339
TCGA-ES-A2HT	52	1.04	0.017033339
TCGA-KR-A7K7	52	1.04	0.017033339
TCGA-UB-A7MC	52	1.04	0.017033339
TCGA-2Y-A9H4	53	1.06	0.025305865
TCGA-DD-A1EK	53	1.06	0.025305865
TCGA-DD-A39V	53	1.06	0.025305865
TCGA-DD-AAD3	53	1.06	0.025305865
TCGA-K7-A6G5	53	1.06	0.025305865
TCGA-RC-A7SH	53	1.06	0.025305865
TCGA-ZP-A9D4	53	1.06	0.025305865
TCGA-BC-A5W4	54	1.08	0.033423755
TCGA-DD-A4NG	54	1.08	0.033423755
TCGA-DD-A73D	54	1.08	0.033423755
TCGA-G3-A25Z	54	1.08	0.033423755
TCGA-DD-A3A2	55	1.1	0.041392685
TCGA-DD-AAED	55	1.1	0.041392685
TCGA-K7-AAU7	55	1.1	0.041392685
TCGA-BC-A69H	56	1.12	0.049218023
TCGA-DD-AACC	56	1.12	0.049218023
TCGA-O8-A75V	56	1.12	0.049218023
TCGA-UB-A7MA	56	1.12	0.049218023
TCGA-UB-AA0U	56	1.12	0.049218023
TCGA-2Y-A9GW	57	1.14	0.056904851
TCGA-2Y-A9H8	57	1.14	0.056904851
TCGA-2Y-A9HB	57	1.14	0.056904851
TCGA-DD-A4NK	57	1.14	0.056904851
TCGA-FV-A3I1	57	1.14	0.056904851
TCGA-RC-A7SF	57	1.14	0.056904851
TCGA-2Y-A9H5	58	1.16	0.064457989
TCGA-BC-A10T	58	1.16	0.064457989
TCGA-BD-A2L6	58	1.16	0.064457989
TCGA-DD-A39Z	58	1.16	0.064457989
TCGA-EP-A2KC	58	1.16	0.064457989
TCGA-FV-A23B	58	1.16	0.064457989
TCGA-FV-A4ZQ	58	1.16	0.064457989
TCGA-2Y-A9GY	59	1.18	0.071882007
TCGA-DD-AAEE	59	1.18	0.071882007
TCGA-DD-AAEK	59	1.18	0.071882007
TCGA-DD-AAVP	59	1.18	0.071882007
TCGA-DD-AAVX	59	1.18	0.071882007
TCGA-CC-A123	60	1.2	0.079181246
TCGA-DD-A4NQ	60	1.2	0.079181246
TCGA-DD-AACY	60	1.2	0.079181246
TCGA-DD-AAD2	60	1.2	0.079181246
TCGA-G3-AAV5	60	1.2	0.079181246
TCGA-WX-AA44	60	1.2	0.079181246
TCGA-DD-AACE	61	1.22	0.086359831
TCGA-DD-AAE2	61	1.22	0.086359831
TCGA-FV-A3R2	61	1.22	0.086359831
TCGA-G3-A5SK	61	1.22	0.086359831
TCGA-GJ-A9DB	61	1.22	0.086359831
TCGA-RC-A6M3	61	1.22	0.086359831
TCGA-XR-A8TG	61	1.22	0.086359831
TCGA-DD-A115	62	1.24	0.093421685
TCGA-DD-A4NJ	62	1.24	0.093421685
TCGA-FV-A3I0	62	1.24	0.093421685

TCGA-2Y-A9H0	63	1.26	0.100370545
TCGA-CC-A1HT	63	1.26	0.100370545
TCGA-DD-AAE6	63	1.26	0.100370545
TCGA-G3-AAUZ	63	1.26	0.100370545
TCGA-G3-AAV7	63	1.26	0.100370545
TCGA-DD-AAC9	64	1.28	0.10720997
TCGA-RG-A7D4	64	1.28	0.10720997
TCGA-ZS-A9CG	64	1.28	0.10720997
TCGA-DD-A1EA	65	1.3	0.113943352
TCGA-DD-AADC	65	1.3	0.113943352
TCGA-EP-A26S	66	1.32	0.120573931
TCGA-FV-A4ZP	66	1.32	0.120573931
TCGA-T1-A6J8	66	1.32	0.120573931
TCGA-ZP-A9CY	66	1.32	0.120573931
TCGA-DD-A73B	67	1.34	0.127104798
TCGA-DD-AAEH	67	1.34	0.127104798
TCGA-2Y-A9GZ	68	1.36	0.133538908
TCGA-2Y-A9H7	68	1.36	0.133538908
TCGA-BC-A3KF	68	1.36	0.133538908
TCGA-KR-A7K0	68	1.36	0.133538908
TCGA-UB-A7ME	68	1.36	0.133538908
TCGA-EP-A2KB	69	1.38	0.139879086
TCGA-G3-AAV3	69	1.38	0.139879086
TCGA-2V-A95S	70	1.4	0.146128036
TCGA-BW-A5NQ	70	1.4	0.146128036
TCGA-DD-A11C	70	1.4	0.146128036
TCGA-DD-AACD	70	1.4	0.146128036
TCGA-DD-AADR	70	1.4	0.146128036
TCGA-FV-A495	70	1.4	0.146128036
TCGA-CC-A3MC	71	1.42	0.152288344
TCGA-DD-AACB	71	1.42	0.152288344
TCGA-DD-AAEG	71	1.42	0.152288344
TCGA-DD-AAVV	71	1.42	0.152288344
TCGA-DD-AAW3	71	1.42	0.152288344
TCGA-G3-A7M6	71	1.42	0.152288344
TCGA-QA-A7B7	71	1.42	0.152288344
TCGA-ZS-A9CF	71	1.42	0.152288344
TCGA-CC-A8HU	72	1.44	0.158362492
TCGA-DD-A1EL	72	1.44	0.158362492
TCGA-2Y-A9GT	73	1.46	0.164352856
TCGA-5R-AA1C	73	1.46	0.164352856
TCGA-DD-A1EF	73	1.46	0.164352856
TCGA-DD-AADV	73	1.46	0.164352856
TCGA-DD-AADD	74	1.48	0.170261715
TCGA-ED-A66Y	74	1.48	0.170261715
TCGA-DD-A73G	75	1.5	0.176091259
TCGA-DD-AAVY	75	1.5	0.176091259
TCGA-EP-A3JL	75	1.5	0.176091259
TCGA-DD-AADI	76	1.52	0.181843588
TCGA-CC-5264	77	1.54	0.187520721
TCGA-DD-A114	77	1.54	0.187520721
TCGA-DD-A73A	77	1.54	0.187520721
TCGA-DD-AACH	77	1.54	0.187520721
TCGA-DD-AACJ	77	1.54	0.187520721
TCGA-DD-AAW0	77	1.54	0.187520721
TCGA-ZS-A9CD	77	1.54	0.187520721
TCGA-BW-A5NO	78	1.56	0.193124598
TCGA-DD-A116	78	1.56	0.193124598
TCGA-G3-A3CG	78	1.56	0.193124598

TCGA-LG-A9QD	78	1.56	0.193124598
TCGA-BD-A3EP	79	1.58	0.198657087
TCGA-DD-AADU	79	1.58	0.198657087
TCGA-G3-A25S	79	1.58	0.198657087
TCGA-UB-A7MF	79	1.58	0.198657087
TCGA-5C-A9VH	80	1.6	0.204119983
TCGA-BC-A10W	80	1.6	0.204119983
TCGA-BC-A217	80	1.6	0.204119983
TCGA-DD-AACG	81	1.62	0.209515015
TCGA-G3-A5SJ	81	1.62	0.209515015
TCGA-NI-A8LF	81	1.62	0.209515015
TCGA-UB-A7MD	82	1.64	0.214843848
TCGA-DD-A4NV	83	1.66	0.220108088
TCGA-DD-AADE	83	1.66	0.220108088
TCGA-EP-A2KA	83	1.66	0.220108088
TCGA-FV-A2QR	83	1.66	0.220108088
TCGA-ZP-A9CV	83	1.66	0.220108088
TCGA-DD-AADN	84	1.68	0.225309282
TCGA-FV-A496	84	1.68	0.225309282
TCGA-G3-AAV4	84	1.68	0.225309282
TCGA-NI-A4U2	84	1.68	0.225309282
TCGA-CC-A7IL	85	1.7	0.230448921
TCGA-DD-AAD6	85	1.7	0.230448921
TCGA-DD-AADA	85	1.7	0.230448921
TCGA-G3-A7M9	85	1.7	0.230448921
TCGA-DD-AAD1	86	1.72	0.235528447
TCGA-DD-AAE9	86	1.72	0.235528447
TCGA-MI-A75E	86	1.72	0.235528447
TCGA-CC-A9FS	87	1.74	0.240549248
TCGA-DD-AAW1	87	1.74	0.240549248
TCGA-ED-A4XI	87	1.74	0.240549248
TCGA-G3-A5SM	87	1.74	0.240549248
TCGA-MI-A75C	87	1.74	0.240549248
TCGA-CC-A3M9	88	1.76	0.245512668
TCGA-DD-A11A	88	1.76	0.245512668
TCGA-G3-A5SL	88	1.76	0.245512668
TCGA-BC-A10R	89	1.78	0.250420002
TCGA-K7-A5RG	89	1.78	0.250420002
TCGA-DD-A3A8	90	1.8	0.255272505
TCGA-DD-AACV	90	1.8	0.255272505
TCGA-DD-AADP	90	1.8	0.255272505
TCGA-DD-A11D	91	1.82	0.260071388
TCGA-DD-A73E	91	1.82	0.260071388
TCGA-DD-AACA	91	1.82	0.260071388
TCGA-DD-AAD0	92	1.84	0.264817823
TCGA-5C-A9VG	93	1.86	0.269512944
TCGA-CC-A7IF	93	1.86	0.269512944
TCGA-DD-A3A7	93	1.86	0.269512944
TCGA-DD-AAD5	94	1.88	0.274157849
TCGA-DD-AAD8	94	1.88	0.274157849
TCGA-HP-A5N0	94	1.88	0.274157849
TCGA-ZS-A9CE	95	1.9	0.278753601
TCGA-FV-A2QQ	96	1.92	0.283301229
TCGA-G3-A6UC	96	1.92	0.283301229
TCGA-CC-5263	97	1.94	0.28780173
TCGA-DD-A118	97	1.94	0.28780173
TCGA-DD-A4NF	97	1.94	0.28780173
TCGA-DD-AACU	97	1.94	0.28780173
TCGA-DD-AADQ	97	1.94	0.28780173

TCGA-DD-AAEI	97	1.94	0.28780173
TCGA-DD-AAW2	97	1.94	0.28780173
TCGA-ED-A8O5	97	1.94	0.28780173
TCGA-DD-AACF	98	1.96	0.292256071
TCGA-DD-AADB	98	1.96	0.292256071
TCGA-DD-AAEB	98	1.96	0.292256071
TCGA-2Y-A9H9	100	2	0.301029996
TCGA-DD-AACX	101	2.02	0.305351369
TCGA-BC-4073	102	2.04	0.309630167
TCGA-CC-5258	102	2.04	0.309630167
TCGA-DD-A113	103	2.06	0.31386722
TCGA-DD-A4NI	103	2.06	0.31386722
TCGA-DD-AADL	103	2.06	0.31386722
TCGA-CC-A5UE	105	2.1	0.322219295
TCGA-MI-A75H	105	2.1	0.322219295
TCGA-2Y-A9GU	106	2.12	0.326335861
TCGA-BC-A10U	106	2.12	0.326335861
TCGA-RC-A7SK	106	2.12	0.326335861
TCGA-WJ-A86L	106	2.12	0.326335861
TCGA-CC-5262	107	2.14	0.330413773
TCGA-ZP-A9D1	107	2.14	0.330413773
TCGA-3K-AAZ8	108	2.16	0.334453751
TCGA-2Y-A9H1	109	2.18	0.338456494
TCGA-2Y-A9H3	109	2.18	0.338456494
TCGA-DD-AACK	110	2.2	0.342422681
TCGA-CC-A7IG	111	2.22	0.346352974
TCGA-XR-A8TF	111	2.22	0.346352974
TCGA-2Y-A9HA	112	2.24	0.350248018
TCGA-CC-5259	112	2.24	0.350248018
TCGA-DD-A1EB	112	2.24	0.350248018
TCGA-DD-AAE3	113	2.26	0.354108439
TCGA-CC-A8HV	114	2.28	0.357934847
TCGA-DD-AADS	114	2.28	0.357934847
TCGA-DD-AADG	116	2.32	0.365487985
TCGA-CC-A7IJ	119	2.38	0.376576957
TCGA-DD-AACP	123	2.46	0.390935107
TCGA-CC-A9FW	124	2.48	0.394451681
TCGA-CC-A7II	127	2.54	0.404833717
TCGA-G3-AAV0	129	2.58	0.411619706
TCGA-MI-A75I	133	2.66	0.424881637
TCGA-DD-AADM	134	2.68	0.428134794
TCGA-BC-A10Z	137	2.74	0.437750563
TCGA-CC-A7IE	137	2.74	0.437750563
TCGA-G3-A7M5	139	2.78	0.444044796
TCGA-DD-AACZ	145	2.9	0.462397998
TCGA-RC-A6M4	145	2.9	0.462397998
TCGA-DD-AAEA	147	2.94	0.46834733
TCGA-RC-A6M6	150	3	0.477121255
TCGA-ED-A459	152	3.04	0.482873584
TCGA-DD-AACT	160	3.2	0.505149978
TCGA-DD-AADO	161	3.22	0.507855872
TCGA-CC-A5UD	163	3.26	0.5132176
TCGA-CC-A8HT	164	3.28	0.515873844
TCGA-LG-A6GG	164	3.28	0.515873844
TCGA-G3-A3CK	169	3.38	0.5289167
TCGA-DD-AAE7	175	3.5	0.544068044
TCGA-DD-AACQ	176	3.52	0.546542663
TCGA-DD-AADF	180	3.6	0.556302501
TCGA-MI-A75G	188	3.76	0.575187845

TCGA-ED-A7PZ	221	4.42	0.645422269
TCGA-DD-AACL	251	5.02	0.700703717
TCGA-CC-A7IK	259	5.18	0.71432976
TCGA-DD-A3A9	274	5.48	0.738780558
TCGA-DD-AACI	277	5.54	0.743509765
TCGA-WQ-A9G7	294	5.88	0.769377326
TCGA-DD-A1EE	384	7.68	0.88536122
TCGA-DD-AAC8	480	9.6	0.982271233
TCGA-CC-A7IH	594	11.88	1.074816441
TCGA-4R-AA8I	802	16.04	1.205204364
TCGA-UB-A7MB	1251	25.02	1.398287305

Table S9. Top 30 gain or loss local segments in TCHA-LIHC patients.

	TCGA-2V-A95S	TCGA-2Y-A9GS	TCGA-2Y-A9GT	TCGA-2Y-A9GU	TCGA-2Y-A9GV	TCGA-2Y-A9GW	TCGA-2Y-A9GX
1q21.3-Amp	2	0	0	2	0	2	1
1q42.2-Amp	1	1	0	2	0	2	1
8q24.21-Amp	2	0	0	0	0	2	1
6p21.1-Amp	0	1	0	0	1	0	0
5p15.33-Amp	0	0	0	0	0	1	0
6p25.2-Amp	1	1	0	0	1	0	0
17q25.3-Amp	1	0	0	0	0	0	0
5q35.3-Amp	1	0	0	0	0	1	0
20q13.33-Amp	0	1	0	0	0	0	1
20q13.13-Amp	0	1	0	0	0	0	1
7q31.2-Amp	0	1	0	1	0	1	0
6q12-Amp	1	1	0	0	0	0	0
19q13.11-Amp	0	0	0	1	0	1	0
Xq28-Amp	1	0	1	0	0	1	0
3q26.31-Amp	0	1	0	0	0	0	0
8p23.2-Del	1	1	0	1	0	1	1
8p12-Del	1	1	0	1	0	1	1
17p13.1-Del	0	1	1	0	1	0	0
13q14.2-Del	0	1	0	0	1	0	0
4q21.3-Del	0	1	0	0	1	0	0
4q24-Del	0	1	0	0	0	0	0
4q35.1-Del	0	1	0	0	0	0	0
1p36.31-Del	0	0	0	0	0	0	1
16q23.1-Del	0	0	0	0	0	0	0
9p21.3-Del	0	1	0	1	1	0	0
1p36.11-Del	0	0	0	0	0	0	1
6q27-Del	0	0	0	0	0	0	0
14q32.33-Del	0	1	0	0	0	0	1
14q23.3-Del	0	1	0	0	0	0	1
9q31.3-Del	0	1	0	1	0	0	0

TCGA-2Y-A9GY	TCGA-2Y-A9GZ	TCGA-2Y-A9H0	TCGA-2Y-A9H1	TCGA-2Y-A9H2	TCGA-2Y-A9H3	TCGA-2Y-A9H4	TCGA-2Y-A9H5
1	1	1	1	1	1	0	1
0	1	1	1	1	1	0	1
1	0	0	2	2	0	1	1
1	1	0	0	1	1	0	1
1	1	1	1	1	1	1	0
1	2	0	0	1	1	0	1
2	2	1	2	1	0	0	0
0	1	0	1	0	1	1	0
1	1	0	0	0	0	0	0
1	1	1	0	0	0	0	0
1	1	0	0	1	2	0	0
1	1	0	0	0	1	0	1
1	0	0	0	0	1	0	0
0	1	0	1	1	0	1	0
0	1	2	0	0	0	2	0
1	0	0	1	1	1	1	1
0	1	0	1	1	1	1	1
1	1	1	0	1	0	1	1
1	1	1	0	1	0	1	1
1	0	1	0	1	1	0	0
1	1	1	0	1	1	0	0
1	0	1	0	1	1	0	0
0	0	0	0	1	1	0	1
1	0	0	0	1	1	0	1
1	0	0	0	1	1	0	1
0	0	0	0	1	1	0	1
0	1	1	0	1	0	0	1
1	0	0	1	1	1	1	0
1	0	0	1	1	1	1	0
0	0	0	0	1	1	0	1

TCGA-2Y-A9H6	TCGA-2Y-A9H7	TCGA-2Y-A9H8	TCGA-2Y-A9H9	TCGA-2Y-A9HA	TCGA-2Y-A9HB	TCGA-3K-AAZ8	TCGA-4R-AA8I
2	1	1	2	1	0	1	2
1	1	2	1	0	2	1	0
0	0	0	0	2	0	1	0
0	0	1	1	1	0	2	2
0	0	2	1	1	1	1	0
0	0	1	0	1	0	2	0
0	0	0	1	0	0	1	0
1	0	0	1	1	1	1	0
0	0	0	1	1	0	0	0
0	0	2	1	1	0	0	0
0	0	0	1	0	0	1	0
0	0	1	0	1	0	1	0
0	0	0	0	0	0	1	0
0	0	0	0	0	0	0	0
0	0	1	0	0	0	1	0
1	1	0	1	1	1	1	0
1	1	0	1	1	1	1	0
0	0	1	1	1	0	0	1
0	0	1	0	1	0	1	1
0	0	1	0	0	0	1	0
0	0	1	0	1	0	1	0
0	0	1	0	1	0	1	0
1	1	0	0	0	0	1	0
0	1	1	0	1	0	0	0
1	1	1	0	0	0	1	0
1	1	0	0	0	0	1	0
1	1	1	0	1	0	0	1
1	0	0	1	0	0	0	0
0	0	0	1	0	0	0	0
1	0	1	1	1	0	1	0

TCGA-5C-A9VG	TCGA-5C-A9VH	TCGA-5C-AAPD	TCGA-5R-AA1C	TCGA-5R-AA1D	TCGA-5R-AAAM	TCGA-BC-A10Q	TCGA-BC-A10R
2	2	1	2	0	0	1	1
2	2	1	2	0	0	1	2
1	2	0	1	1	1	0	0
1	0	0	1	0	1	0	0
1	0	0	0	0	0	1	1
0	0	0	1	0	0	0	1
0	0	0	0	0	1	1	0
1	0	0	0	0	0	1	0
1	1	0	0	0	1	1	1
0	1	0	0	0	1	1	1
1	1	0	0	0	0	1	1
1	0	0	0	0	0	1	0
0	0	0	0	0	0	1	1
0	0	0	1	0	0	0	0
0	0	1	1	0	0	0	1
0	1	0	1	0	1	0	1
0	1	0	1	0	1	1	1
0	0	1	0	0	1	0	1
1	1	0	0	0	0	1	1
1	1	1	0	0	0	0	0
1	1	1	0	0	0	0	0
1	1	1	0	0	0	0	1
1	1	0	0	0	0	1	0
1	0	1	0	0	0	0	1
1	1	0	0	0	0	1	1
1	1	0	0	0	0	1	0
0	0	0	1	0	1	1	0
1	0	1	0	0	0	1	1
1	0	1	0	0	0	1	0
1	1	0	0	0	0	1	1

TCGA-BC-A10T	TCGA-BC-A10U	TCGA-BC-A10W	TCGA-BC-A10Y	TCGA-BC-A10Z	TCGA-BC-A216	TCGA-BC-A217	TCGA-BC-A3KF
0	2	2	1	1	1	2	0
2	2	0	1	0	2	2	0
1	1	2	0	0	0	0	1
2	2	0	2	1	2	1	1
0	0	1	0	2	1	1	0
0	2	0	0	0	1	1	0
1	1	1	1	1	1	2	0
1	0	1	0	0	2	1	0
0	0	0	1	0	0	1	1
1	0	0	1	0	0	1	1
0	1	0	0	0	0	0	1
2	0	0	0	0	0	1	1
2	0	0	2	0	0	2	0
0	2	0	0	0	0	0	0
2	0	0	1	2	0	2	0
1	1	0	0	0	1	1	1
1	0	0	0	0	1	1	1
1	1	0	1	1	1	1	1
1	0	1	1	1	0	1	1
1	1	0	1	1	0	1	1
1	1	0	1	1	0	1	1
1	0	1	0	1	0	1	1
1	0	1	1	0	0	1	0
0	0	1	1	1	1	1	0
0	1	0	0	0	0	0	1
1	0	1	0	0	0	0	0
0	0	0	0	0	0	0	1
1	0	0	0	1	0	1	1
0	0	0	0	1	1	0	1
0	1	0	0	0	0	1	0

TCGA-BC-A5W4	TCGA-BC-A69H	TCGA-BC-A8YO	TCGA-BD-A2L6	TCGA-BD-A3EP	TCGA-BD-A3ER	TCGA-BW-A5NO
0	1	2	0	0	1	2
2	1	0	0	0	2	1
0	2	0	0	1	1	0
0	1	0	2	1	0	2
0	0	2	0	1	0	2
0	1	0	1	1	0	1
0	1	0	0	1	0	2
0	0	0	0	0	0	0
0	1	0	1	1	0	2
0	1	0	2	1	0	2
1	2	0	0	1	1	1
0	1	1	1	1	0	1
0	0	0	0	1	0	2
0	0	0	0	0	0	1
1	1	0	0	2	0	2
0	1	0	0	1	0	1
0	1	0	0	1	0	1
1	1	1	1	1	0	1
1	1	1	0	0	0	1
1	1	0	1	1	0	1
1	1	0	0	1	0	1
1	1	0	0	1	0	1
0	1	0	0	0	1	0
0	1	1	0	1	0	1
1	1	0	0	0	0	0
0	1	0	0	0	1	0
1	0	0	0	0	1	0
0	0	0	0	0	0	0
0	0	0	0	1	0	0
1	1	0	0	0	0	0

TCGA-BW-A5NP	TCGA-BW-A5NQ	TCGA-CC-5258	TCGA-CC-5260	TCGA-CC-5262	TCGA-CC-5263	TCGA-CC-5264	TCGA-CC-A1HT
2	1	1	0	1	1	2	1
2	1	0	0	1	0	2	0
1	1	2	0	1	0	1	1
2	1	0	0	0	2	0	0
2	1	1	0	0	1	2	1
2	1	0	0	0	1	0	0
0	1	0	1	0	1	1	0
1	1	0	0	0	0	0	1
2	0	0	0	0	0	1	0
0	0	0	0	0	0	1	1
1	1	0	1	0	0	2	0
0	1	0	0	0	1	0	0
1	1	0	0	0	0	0	0
0	0	0	0	0	0	1	0
0	1	0	0	0	0	0	0
1	0	1	0	1	1	0	1
1	0	1	0	1	1	0	1
1	1	1	1	1	1	1	1
0	1	1	1	1	1	1	1
1	1	1	0	0	1	1	0
1	1	1	0	0	1	1	0
1	1	1	0	0	0	1	1
1	0	0	1	1	1	0	0
1	1	1	1	0	1	1	0
0	1	1	0	0	1	0	1
1	0	1	1	0	0	0	0
1	0	0	1	0	0	0	1
1	1	1	1	0	0	1	1
1	1	1	1	0	0	1	1
0	1	1	1	0	0	0	1

TCGA-CC-A3M9	TCGA-CC-A3MA	TCGA-CC-A3MB	TCGA-CC-A3MC	TCGA-CC-A5UC	TCGA-CC-A5UD	TCGA-CC-A5UE
0	2	1	2	1	1	1
1	1	0	2	1	0	1
1	2	1	2	1	2	2
0	0	1	1	0	0	1
1	0	1	1	1	1	0
0	0	2	1	0	0	1
0	0	1	1	1	0	2
0	0	1	1	1	0	0
1	0	1	1	1	0	1
1	0	1	1	1	0	1
1	0	1	0	0	0	1
0	0	1	1	0	0	1
1	0	0	0	0	0	0
0	2	0	0	0	0	1
0	1	0	0	0	0	0
1	0	0	1	0	0	0
1	1	0	0	0	0	0
0	1	1	1	1	1	1
1	1	0	1	1	0	1
1	0	1	1	0	1	1
1	0	1	1	0	1	1
1	1	1	1	0	1	0
0	1	1	0	1	1	0
1	0	1	1	1	1	1
1	0	1	1	0	1	1
0	1	1	0	1	1	0
1	1	0	1	0	0	0
0	1	1	1	0	0	1
0	1	1	1	0	0	1
1	0	1	1	0	0	1

TCGA-CC-A7IE	TCGA-CC-A7IF	TCGA-CC-A7IG	TCGA-CC-A7IH	TCGA-CC-A7II	TCGA-CC-A7IJ	TCGA-CC-A7IK	TCGA-CC-A7IL
1	1	2	2	0	0	2	2
1	1	2	2	0	0	2	2
2	2	2	2	2	1	2	1
1	0	2	2	1	0	1	2
0	0	1	0	1	1	0	2
2	0	2	2	1	0	1	2
1	2	1	0	0	1	1	2
0	0	1	0	0	0	0	1
1	0	0	0	2	0	0	1
1	0	0	0	2	0	0	1
0	0	0	0	1	1	0	0
1	0	2	0	1	1	1	0
0	0	0	0	2	0	0	0
1	0	1	1	0	0	0	0
1	0	1	0	0	1	1	0
1	1	1	1	1	1	0	1
1	1	1	1	0	1	0	1
0	1	1	0	1	0	1	1
0	1	1	0	1	1	1	1
1	1	1	0	1	1	1	1
1	1	1	0	1	1	1	1
1	1	1	0	1	1	1	1
1	1	1	0	0	1	0	1
1	1	1	0	0	0	0	0
1	1	1	0	0	1	1	1
1	1	1	0	0	1	0	1
0	1	0	0	0	0	0	1
0	0	0	0	1	1	1	0
1	0	1	0	1	1	1	0
0	1	0	0	0	1	0	1

TCGA-CC-A8HT	TCGA-CC-A8HU	TCGA-CC-A8HV	TCGA-CC-A9FS	TCGA-CC-A9FU	TCGA-CC-A9FV	TCGA-CC-A9FW	TCGA-DD-A113
1	2	1	0	2	0	1	2
1	2	1	0	2	0	1	2
1	0	1	2	1	0	1	1
0	1	1	0	1	0	0	0
0	2	0	0	0	0	1	0
0	1	0	0	1	0	0	0
1	1	0	0	1	0	1	0
0	1	0	0	0	0	2	0
0	2	1	0	2	0	1	1
0	2	0	0	2	0	1	0
0	1	0	0	1	0	1	0
0	1	0	0	1	0	0	0
0	1	0	0	1	0	0	1
0	0	0	1	0	0	0	0
0	0	0	0	0	0	0	0
1	1	1	1	1	0	1	1
1	1	1	1	1	0	1	1
1	1	1	1	1	0	0	0
0	1	1	1	1	0	1	1
0	1	1	1	1	0	1	1
0	1	1	1	1	0	1	1
0	1	1	1	1	0	1	1
0	0	0	1	1	0	1	1
1	1	1	1	1	0	1	1
0	1	0	1	1	0	1	1
0	0	1	1	1	0	1	1
0	0	0	1	0	0	1	0
1	1	1	0	1	0	0	1
1	1	1	0	1	0	0	1
0	0	0	0	1	0	1	1

TCGA-DD-A114	TCGA-DD-A115	TCGA-DD-A116	TCGA-DD-A118	TCGA-DD-A119	TCGA-DD-A11A	TCGA-DD-A11B	TCGA-DD-A11C
1	0	0	1	2	0	1	1
1	0	0	1	2	0	1	0
0	0	2	1	2	1	0	1
1	1	0	1	2	1	0	1
0	1	1	1	0	1	0	0
1	0	0	1	2	1	0	1
1	1	1	0	1	1	0	1
0	1	1	1	1	0	0	0
0	0	0	1	1	1	1	2
0	0	0	1	1	1	1	2
0	0	0	1	0	0	0	0
1	1	0	1	2	1	0	1
0	0	0	1	1	0	0	0
1	0	0	0	0	1	0	0
1	1	0	0	0	0	0	2
0	1	1	1	1	0	0	1
0	1	1	1	1	0	0	1
1	1	1	1	1	1	0	1
1	1	1	1	0	1	0	1
1	0	1	0	1	1	0	0
1	0	1	0	1	1	1	1
1	0	1	0	1	1	1	0
0	0	1	1	1	1	1	1
1	0	1	0	0	1	1	0
0	1	1	0	1	1	1	1
0	0	1	1	1	1	1	1
1	1	0	1	1	1	0	1
0	1	0	0	0	1	0	1
0	1	0	1	0	1	0	1
0	0	1	0	1	1	1	1

TCGA-DD-A11D	TCGA-DD-A1EA	TCGA-DD-A1EB	TCGA-DD-A1EC	TCGA-DD-A1ED	TCGA-DD-A1EE	TCGA-DD-A1EF	TCGA-DD-A1EH
1	2	1	0	0	2	1	2
1	2	0	0	0	2	1	2
0	0	0	1	0	2	2	0
2	0	1	0	0	1	1	2
1	1	0	0	0	1	1	0
0	0	0	0	0	1	2	2
0	1	2	0	0	0	0	0
1	1	0	0	0	1	0	0
0	0	0	0	0	0	1	1
0	0	0	0	0	0	1	1
1	0	0	1	0	1	0	0
0	0	0	0	0	1	1	2
0	0	0	1	0	0	1	0
0	0	0	0	0	0	0	0
0	0	0	0	0	0	1	0
0	0	0	0	0	1	1	0
0	0	0	0	0	1	1	0
1	1	1	0	0	0	0	1
0	0	0	0	0	0	1	0
0	0	1	0	0	0	1	1
0	0	1	0	0	0	1	1
0	0	0	0	0	0	1	1
1	0	1	0	0	0	1	1
0	0	0	0	0	0	1	1
0	0	0	0	0	0	1	0
0	0	0	0	0	0	0	1
0	0	0	0	0	1	0	1
0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0
0	0	0	0	0	0	1	0

TCGA-DD-A1EI	TCGA-DD-A1EJ	TCGA-DD-A1EK	TCGA-DD-A1EL	TCGA-DD-A39V	TCGA-DD-A39W	TCGA-DD-A39X	TCGA-DD-A39Z
0	1	1	1	2	1	2	1
0	1	1	1	2	1	0	1
2	0	0	2	2	0	2	1
0	0	0	0	0	0	1	1
2	0	0	1	1	0	1	0
0	1	0	0	0	0	1	1
1	1	0	0	0	0	0	0
0	0	0	0	1	1	1	0
0	1	0	0	1	0	0	0
0	1	0	0	1	0	0	0
0	1	0	0	1	0	0	1
0	1	0	0	0	0	0	1
1	0	0	1	1	0	0	0
0	0	0	0	1	0	0	0
0	1	0	1	0	0	0	0
1	1	1	1	1	0	1	1
1	1	1	1	1	0	0	1
1	1	1	1	0	0	0	0
1	0	1	0	0	0	1	0
1	1	0	1	0	0	1	0
1	1	0	1	0	0	1	0
1	1	0	1	0	1	1	0
0	1	0	0	0	0	1	1
1	1	0	0	0	0	0	1
1	1	0	1	0	0	1	0
0	1	0	0	1	0	1	0
1	1	1	0	0	0	1	1
0	1	0	1	0	0	1	0
1	1	0	1	0	0	1	0
1	1	1	0	0	0	1	0

TCGA-DD-A3A2	TCGA-DD-A3A3	TCGA-DD-A3A4	TCGA-DD-A3A5	TCGA-DD-A3A6	TCGA-DD-A3A7	TCGA-DD-A3A8	TCGA-DD-A3A9
0	2	0	0	0	2	2	2
0	2	0	0	0	2	2	2
0	2	0	0	0	2	2	0
0	0	0	2	0	0	1	1
0	1	0	1	0	2	1	0
0	0	0	1	0	1	1	1
0	1	1	0	0	2	0	1
0	1	0	1	0	2	1	0
0	0	0	1	0	1	0	1
0	0	0	2	0	2	0	1
1	0	0	0	0	0	0	0
0	0	0	1	0	1	1	1
0	0	0	0	0	2	0	1
0	1	0	0	0	1	0	0
0	0	0	2	0	0	0	0
0	1	0	0	0	1	1	1
0	1	0	1	0	1	1	1
0	1	1	1	0	1	0	1
0	0	0	1	0	0	0	1
0	0	0	1	0	0	0	1
0	0	0	1	0	0	0	1
1	0	0	0	0	0	0	1
0	0	0	0	0	0	0	1
0	0	0	0	0	0	1	1
0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	1
0	0	0	0	0	0	1	0
0	0	0	0	0	1	0	1
0	0	0	0	0	1	0	1
0	0	0	0	0	0	0	1

TCGA-DD-A4NA	TCGA-DD-A4NB	TCGA-DD-A4ND	TCGA-DD-A4NF	TCGA-DD-A4NH	TCGA-DD-A4NI	TCGA-DD-A4NJ
0	0	0	2	1	1	1
1	1	0	2	1	1	1
0	0	1	1	0	1	1
0	0	0	0	1	0	0
0	0	1	0	0	0	1
0	0	0	0	1	0	1
0	0	0	0	1	1	1
0	0	1	0	0	0	0
0	0	1	0	0	0	0
0	0	1	0	0	0	0
1	0	0	0	0	1	0
1	0	0	0	1	0	0
0	0	1	0	0	0	0
0	0	0	1	0	0	0
0	0	0	0	0	1	0
1	0	1	1	1	1	1
1	0	1	0	1	0	1
1	1	0	0	1	1	1
1	0	0	0	1	0	1
0	0	1	0	1	1	1
0	0	1	0	1	1	1
0	0	0	0	1	1	1
0	0	0	0	1	1	1
0	0	1	0	1	1	1
0	0	1	0	0	1	0
1	0	0	0	1	1	1
1	0	0	0	1	0	1
0	1	0	0	1	1	1
0	1	0	0	1	1	0
1	0	0	0	0	1	1

TCGA-DD-A4NK	TCGA-DD-A4NL	TCGA-DD-A4NN	TCGA-DD-A4NO	TCGA-DD-A4NP	TCGA-DD-A4NQ	TCGA-DD-A4NR
1	0	2	2	0	0	1
1	0	2	2	0	1	1
1	0	1	2	0	1	2
1	0	1	0	0	0	0
1	0	0	1	0	0	0
1	0	1	0	0	0	0
0	0	0	1	1	0	0
1	0	0	1	0	0	1
0	0	1	2	0	0	1
0	0	1	2	0	0	1
1	0	0	0	0	1	0
1	0	1	0	0	0	0
0	0	1	1	0	1	0
1	0	0	0	0	0	0
0	0	0	0	0	0	0
1	0	1	1	0	0	1
1	0	1	1	0	0	1
0	0	0	1	0	1	0
0	0	1	1	0	1	1
0	0	1	1	0	1	0
0	0	1	1	0	1	0
0	0	1	1	0	0	0
0	0	1	1	0	0	1
0	0	1	1	0	1	0
0	0	0	1	0	0	0
0	0	1	1	0	0	0
1	0	1	0	0	0	0
0	0	0	1	0	1	0
0	0	0	1	0	1	0
0	0	1	1	0	0	0

TCGA-DD-A4NS	TCGA-DD-A4NV	TCGA-DD-A73A	TCGA-DD-A73B	TCGA-DD-A73C	TCGA-DD-A73D	TCGA-DD-A73E	TCGA-DD-A73F
0	2	0	1	0	2	0	1
0	1	0	0	0	2	1	1
1	0	2	0	0	2	0	0
1	0	0	0	0	2	2	1
0	1	0	0	1	0	0	0
1	0	0	0	0	2	2	0
0	0	2	0	0	2	1	2
0	1	1	0	0	0	0	0
0	1	0	0	0	0	0	1
0	1	0	0	0	0	0	0
0	2	0	0	1	0	2	0
1	0	0	0	0	0	1	0
0	1	0	0	0	0	0	1
0	1	0	0	0	1	0	0
0	1	0	0	0	0	1	0
1	1	1	0	1	1	1	1
1	1	1	1	1	1	1	1
0	0	1	1	0	0	1	0
0	0	0	0	0	0	1	1
0	0	0	1	0	0	0	0
0	0	0	1	0	0	0	0
0	0	0	1	0	0	0	0
0	0	1	1	0	0	0	1
0	0	0	1	0	0	0	1
0	0	0	0	0	0	0	1
0	0	0	1	0	0	0	1
1	0	0	0	0	0	1	0
0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0

TCGA-DD-A73G	TCGA-DD-AA3A	TCGA-DD-AAC8	TCGA-DD-AAC9	TCGA-DD-AACA	TCGA-DD-AACB	TCGA-DD-AACC
2	2	2	2	0	1	1
2	2	2	2	0	1	1
1	0	2	1	1	2	0
1	1	2	0	2	2	0
1	1	1	0	2	0	0
0	0	2	0	1	2	0
0	0	1	1	2	1	0
1	1	1	0	0	0	1
1	0	1	0	0	1	1
1	0	1	0	0	1	1
1	0	0	1	1	0	0
1	1	0	0	0	2	0
2	0	0	0	0	0	0
1	0	0	0	0	0	0
1	1	0	0	0	0	0
1	0	0	0	0	1	1
1	0	1	0	0	1	1
0	0	0	1	1	1	1
1	1	1	0	0	0	0
1	0	1	0	0	1	1
1	0	1	0	0	1	1
0	0	1	1	0	1	1
1	1	1	0	1	0	1
0	0	0	0	0	0	1
0	1	0	0	1	0	1
1	0	1	0	1	0	1
0	1	1	0	0	1	0
1	1	0	0	1	0	0
0	1	1	0	1	0	0
0	1	0	0	0	1	0

TCGA-DD-AACD	TCGA-DD-AACE	TCGA-DD-AACF	TCGA-DD-AACG	TCGA-DD-AACH	TCGA-DD-AACI	TCGA-DD-AACJ
0	2	2	0	2	2	2
1	2	2	0	2	2	2
2	0	1	1	1	2	2
1	2	1	0	0	1	1
0	0	1	2	0	1	1
1	2	1	0	1	1	1
0	1	0	0	0	1	2
1	0	1	1	1	1	1
0	0	0	0	0	1	0
0	0	0	0	0	1	0
1	1	1	0	0	1	0
1	0	0	0	0	0	1
0	0	0	2	0	0	0
0	0	0	0	0	2	1
0	0	0	1	0	0	0
1	1	0	1	1	0	1
1	1	0	1	1	0	1
0	1	1	1	1	0	1
0	0	1	1	1	1	0
0	1	1	1	0	0	0
0	1	1	1	0	0	0
0	1	1	1	1	1	0
0	0	0	0	1	0	1
0	0	1	1	1	1	0
0	1	0	1	1	0	0
0	0	0	0	0	0	1
1	1	0	0	1	1	0
0	1	0	1	1	1	0
0	1	0	1	1	0	0
1	1	0	0	0	0	0

TCGA-DD-AACK	TCGA-DD-AACL	TCGA-DD-AACN	TCGA-DD-AACO	TCGA-DD-AACP	TCGA-DD-AACQ	TCGA-DD-AACS
0	1	2	1	1	1	2
0	1	2	1	1	1	2
0	0	1	1	1	0	1
0	0	1	0	1	0	0
0	0	0	0	1	0	0
0	0	1	0	1	1	0
0	0	0	0	0	0	1
0	0	0	0	1	0	0
0	0	0	1	1	2	1
0	0	0	1	1	0	1
0	0	0	0	1	0	1
0	0	1	0	0	0	0
0	0	0	1	1	0	0
0	0	0	0	0	0	1
0	1	0	0	0	0	1
0	0	1	1	1	1	1
0	0	1	1	1	1	1
0	1	0	0	0	1	1
0	1	1	1	1	1	1
0	1	1	0	1	0	1
0	1	1	0	1	0	1
0	1	1	0	1	1	1
1	0	1	1	1	0	0
0	1	1	1	1	1	1
0	0	0	1	1	0	1
1	0	1	1	1	0	0
0	0	0	0	1	0	0
0	0	1	1	0	0	1
0	0	1	0	0	0	1
0	0	0	1	1	0	0

TCGA-DD-AACT	TCGA-DD-AACU	TCGA-DD-AACV	TCGA-DD-AACW	TCGA-DD-AACX	TCGA-DD-AACY	TCGA-DD-AACZ
2	1	1	1	1	2	1
2	1	1	1	2	2	1
2	0	0	1	0	2	2
1	0	0	0	0	0	1
1	0	2	0	0	1	1
1	0	0	0	0	0	0
0	0	0	0	1	0	0
2	0	0	0	0	1	1
1	0	1	0	2	0	1
1	0	1	0	0	0	1
1	0	0	0	0	0	0
1	0	0	0	0	0	0
1	0	0	1	0	0	0
1	0	0	0	0	2	0
0	0	2	1	0	0	1
0	1	0	0	0	1	1
0	0	0	0	0	0	1
0	1	1	0	1	0	1
0	1	1	0	0	0	0
0	1	1	1	0	0	1
0	1	1	1	0	0	1
0	1	1	1	0	0	1
0	0	0	1	0	0	0
0	1	1	1	0	0	1
0	1	0	1	0	0	1
0	0	0	1	0	0	0
0	1	0	1	0	1	0
0	1	0	0	1	0	1
0	1	1	0	1	0	1
0	1	0	0	0	0	1

TCGA-DD-AAD0	**TCGA-DD-AAD1**	**TCGA-DD-AAD2**	**TCGA-DD-AAD3**	**TCGA-DD-AAD5**	**TCGA-DD-AAD6**	**TCGA-DD-AAD8**
1	0	1	1	1	0	1
1	1	1	1	2	0	1
1	2	2	0	2	2	0
0	0	0	1	0	0	0
0	0	2	0	1	0	1
0	0	0	1	0	0	0
0	0	0	0	1	2	0
0	1	1	0	0	0	0
2	0	0	0	0	1	0
2	0	0	0	0	1	0
0	0	0	0	0	0	0
0	0	0	1	0	0	0
0	0	0	0	0	0	0
0	0	1	0	0	0	0
0	0	0	0	1	0	0
1	1	1	1	1	0	1
1	1	1	1	1	0	1
1	1	0	1	1	1	1
0	1	0	0	0	0	1
0	0	0	1	1	0	1
0	0	0	1	1	0	1
0	0	1	1	1	0	1
1	1	0	0	1	1	0
1	1	0	1	0	0	0
0	0	0	1	0	0	0
1	1	0	0	1	1	0
1	0	0	1	0	0	1
0	0	0	0	1	1	0
0	0	0	0	1	1	0
0	0	0	1	0	0	1

TCGA-DD-AADA	TCGA-DD-AADB	TCGA-DD-AADC	TCGA-DD-AADD	TCGA-DD-AADF	TCGA-DD-AADG	TCGA-DD-AADI
2	0	1	2	2	1	2
2	0	1	2	2	1	2
1	1	2	2	0	0	1
2	0	0	0	2	1	0
0	0	2	0	2	1	0
2	0	0	0	1	1	0
0	0	2	1	2	1	0
0	0	1	0	2	1	1
1	0	0	2	1	0	0
1	0	0	2	2	0	0
0	0	0	1	0	1	0
0	0	0	0	1	0	0
0	1	2	1	1	0	0
0	0	0	0	0	0	0
0	0	2	1	0	0	0
1	1	1	1	1	1	1
1	1	1	1	1	1	1
0	1	1	1	1	1	0
0	0	1	1	1	0	1
0	1	1	1	0	0	1
0	1	1	1	0	0	1
0	1	1	1	0	0	1
1	1	1	1	1	0	1
1	1	0	0	0	0	1
0	0	1	0	0	0	0
1	1	1	0	0	0	1
0	0	0	0	1	1	0
0	1	0	1	1	0	0
0	1	0	1	1	0	0
0	0	0	0	0	0	0

TCGA-DD-AADJ	TCGA-DD-AADK	TCGA-DD-AADL	TCGA-DD-AADM	TCGA-DD-AADN	TCGA-DD-AADO	TCGA-DD-AADP
1	1	1	2	0	1	1
1	1	1	2	0	1	1
0	2	1	2	2	2	1
0	0	1	0	1	1	0
0	0	0	0	1	0	0
0	0	1	2	1	1	1
0	0	0	0	2	1	0
0	1	0	2	1	0	0
0	0	0	0	1	1	0
0	0	0	0	1	1	0
0	0	1	1	0	0	0
0	0	1	0	1	1	0
0	0	0	2	0	0	0
0	0	0	0	1	1	0
0	0	1	0	1	0	0
0	1	0	1	1	1	1
0	1	0	0	1	1	1
0	0	1	0	1	0	0
0	1	1	1	0	1	0
0	0	1	0	0	1	1
0	0	1	0	0	1	1
0	1	1	1	0	1	1
1	1	0	1	1	1	1
1	1	1	1	0	1	1
1	1	1	0	1	0	1
1	1	0	1	0	1	1
1	0	1	0	1	0	1
0	0	1	1	1	1	0
0	0	1	1	1	1	0
1	1	1	0	0	1	0

TCGA-DD-AADQ	TCGA-DD-AADR	TCGA-DD-AADS	TCGA-DD-AADU	TCGA-DD-AADV	TCGA-DD-AADW	TCGA-DD-AADY
0	1	0	0	1	2	2
0	1	0	2	1	1	2
2	2	0	2	1	0	0
2	0	0	0	1	0	0
2	1	0	1	1	0	0
2	0	0	0	1	1	0
0	1	0	1	0	1	0
2	1	1	2	1	0	0
0	0	2	1	0	1	0
0	0	2	1	0	1	0
0	0	1	0	1	1	0
2	0	0	0	1	0	0
0	0	0	0	0	0	0
0	0	0	1	0	1	0
0	1	0	1	0	0	0
1	1	0	0	1	0	0
1	1	0	0	1	0	0
0	1	0	0	1	1	1
0	1	0	0	1	1	1
0	1	0	0	1	0	1
0	1	0	0	1	0	1
0	1	0	0	1	1	1
0	1	0	0	0	1	1
0	1	0	0	1	1	0
1	0	1	0	1	0	0
0	1	0	0	0	1	1
1	1	0	0	1	1	1
0	1	0	0	1	1	0
0	1	0	0	1	1	0
0	0	0	0	1	0	0

TCGA-DD-AAE0	TCGA-DD-AAE1	TCGA-DD-AAE2	TCGA-DD-AAE3	TCGA-DD-AAE4	TCGA-DD-AAE6	TCGA-DD-AAE7	TCGA-DD-AAE9
2	2	0	1	0	2	1	2
2	2	0	0	0	2	1	2
1	2	0	1	0	1	1	2
1	0	0	2	1	0	2	2
0	0	1	2	0	2	0	0
1	0	1	1	0	0	0	2
1	0	2	1	0	0	0	0
1	1	0	2	0	0	0	0
2	0	0	1	0	2	0	1
2	0	0	1	0	2	0	1
0	0	2	1	0	2	0	1
1	0	0	2	0	0	0	0
1	0	0	0	0	0	1	0
0	0	0	1	0	0	0	1
0	1	0	0	0	1	0	1
1	0	0	0	1	1	1	1
1	0	0	0	1	0	1	1
1	1	1	0	1	1	0	0
1	0	1	1	1	0	0	0
1	1	0	0	0	1	0	0
1	1	0	0	0	1	0	0
1	1	0	0	0	1	0	0
1	1	1	1	0	0	0	0
1	1	0	0	0	1	0	0
0	1	0	1	0	1	0	0
1	1	0	1	0	0	0	0
0	0	1	1	0	0	0	1
1	0	0	0	0	1	0	0
1	0	0	1	0	1	0	0
0	0	0	0	0	0	0	0

TCGA-DD-AAEA	TCGA-DD-AAEB	TCGA-DD-AAED	TCGA-DD-AAEE	TCGA-DD-AAEG	TCGA-DD-AAEH	TCGA-DD-AAEI
1	1	0	0	2	1	0
1	1	2	0	2	1	0
0	1	1	1	2	1	2
0	0	0	0	0	2	0
1	0	0	1	1	0	0
0	0	0	0	1	2	0
1	0	0	1	0	0	0
0	0	0	2	1	0	0
1	0	0	0	1	1	0
1	0	0	0	1	1	0
1	1	0	0	0	0	1
0	0	0	0	2	0	0
1	0	0	0	0	0	0
0	0	0	0	0	2	0
0	0	0	0	0	0	0
0	1	1	1	1	1	1
0	1	1	1	1	1	1
1	1	1	1	0	0	1
1	0	1	1	1	0	1
1	0	1	0	0	0	0
1	0	1	0	0	0	0
0	1	0	1	0	0	0
0	0	0	0	0	1	0
0	0	1	0	1	1	0
0	0	1	1	0	0	0
0	0	0	1	0	0	0
0	0	0	1	1	1	0
0	0	1	1	1	0	0
0	0	1	1	1	0	0
1	0	1	0	0	0	0

TCGA-DD-AAEK	TCGA-DD-AAVP	TCGA-DD-AAVQ	TCGA-DD-AAVR	TCGA-DD-AAVS	TCGA-DD-AAVU	TCGA-DD-AAVV
1	2	2	2	1	0	2
1	2	2	2	1	0	2
2	0	1	1	2	1	1
1	0	0	2	2	0	1
2	0	0	0	0	2	2
1	0	0	1	2	0	1
1	0	0	1	0	0	1
1	1	0	1	0	1	1
1	0	0	1	0	0	2
1	0	0	0	0	0	1
0	0	0	0	0	0	1
1	0	0	0	2	0	1
1	0	0	0	0	0	1
0	2	1	0	0	0	0
1	0	0	0	1	0	1
0	1	1	1	1	1	0
0	1	1	1	1	1	0
1	1	1	1	0	1	1
1	1	1	0	0	0	1
1	0	1	0	1	1	1
1	0	1	0	1	1	1
1	0	1	0	1	1	0
1	0	1	0	1	0	0
1	1	1	0	1	1	1
1	0	1	0	1	1	0
1	0	1	0	1	1	0
1	0	0	0	1	1	0
1	1	0	0	0	1	1
0	1	0	0	0	1	1
1	0	1	0	0	1	0

TCGA-DD-AAVW	TCGA-DD-AAVX	TCGA-DD-AAVY	TCGA-DD-AAVZ	TCGA-DD-AAW0	TCGA-DD-AAW1	TCGA-DD-AAW2
1	0	2	2	2	1	1
1	0	2	2	2	1	1
2	2	2	2	1	2	2
1	0	2	0	0	0	2
0	0	2	0	0	0	1
1	0	2	0	0	0	2
0	0	0	0	0	1	0
0	1	2	0	1	0	1
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	1	0	0	0	0	1
1	0	0	0	0	0	2
0	0	0	0	0	0	0
0	0	2	0	0	1	1
0	0	0	0	1	0	0
0	0	1	1	1	0	1
1	0	1	1	1	0	1
1	0	0	0	0	1	0
0	0	0	0	0	0	0
1	0	0	1	1	0	0
1	0	0	1	1	0	0
1	0	1	0	1	0	0
1	0	0	1	1	0	0
1	0	0	1	1	0	0
1	0	0	1	1	0	0
1	0	0	1	1	0	0
0	0	1	0	1	0	1
0	0	0	0	0	0	0
0	0	0	0	0	0	0
1	0	0	1	1	0	0

TCGA-DD-AAW3	TCGA-ED-A459	TCGA-ED-A4XI	TCGA-ED-A5KG	TCGA-ED-A66X	TCGA-ED-A66Y	TCGA-ED-A7PX	TCGA-ED-A7PY
1	1	1	0	1	1	0	2
1	1	1	1	1	1	0	2
2	1	0	0	2	2	0	1
2	0	0	0	1	0	0	0
0	1	0	0	1	1	0	0
2	0	0	0	1	0	0	1
0	0	0	0	1	1	0	0
0	0	0	0	0	1	0	0
0	0	0	0	1	1	0	0
0	0	0	0	1	1	0	0
1	1	0	0	0	1	0	1
2	0	0	0	1	0	0	0
0	0	0	0	1	1	0	0
0	0	0	0	0	1	0	0
0	0	0	0	0	0	1	0
1	1	0	0	1	0	0	1
1	1	1	0	1	0	0	1
0	1	0	0	0	0	1	0
0	1	1	0	0	1	1	0
0	1	0	0	1	0	1	1
0	1	0	0	1	0	1	1
0	1	0	0	1	0	0	1
0	0	1	0	1	1	1	1
0	1	0	1	1	1	0	1
0	1	1	0	1	0	0	0
0	1	0	0	1	1	0	1
1	1	0	0	0	1	1	0
1	1	0	0	0	0	1	0
1	1	0	0	0	0	1	0
0	1	0	0	1	0	1	0

TCGA-ED-A7PZ	TCGA-ED-A7XO	TCGA-ED-A7XP	TCGA-ED-A82E	TCGA-ED-A8O5	TCGA-ED-A8O6	TCGA-ED-A97K	TCGA-EP-A12J
1	1	2	1	1	1	0	1
1	1	2	1	2	1	0	1
1	0	2	1	0	2	1	2
2	1	0	1	2	1	0	0
0	1	1	1	0	1	0	0
2	0	0	1	2	1	0	0
1	0	1	0	0	1	0	0
0	1	2	0	0	0	0	0
0	1	0	1	1	2	0	0
0	1	0	1	0	2	0	0
0	0	0	0	0	0	0	0
2	0	0	0	1	0	0	0
2	2	0	1	0	0	0	0
1	0	0	0	0	0	0	1
1	0	0	1	0	0	0	0
1	1	0	0	0	1	0	1
1	1	0	0	0	1	0	1
1	1	1	1	0	1	1	0
1	1	1	0	0	0	0	0
1	1	1	0	1	0	1	0
1	1	1	0	1	0	1	0
1	1	1	0	1	0	1	0
0	0	0	1	1	1	1	0
0	0	0	0	1	1	0	0
1	0	1	1	0	1	1	0
0	0	0	1	1	1	1	0
1	0	0	1	1	1	1	1
1	0	1	1	0	1	1	1
1	0	1	1	0	1	1	1
1	0	1	0	0	0	0	0

TCGA-EP-A26S	TCGA-EP-A2KA	TCGA-EP-A2KB	TCGA-EP-A2KC	TCGA-EP-A3JL	TCGA-EP-A3RK	TCGA-ES-A2HS	TCGA-ES-A2HT
1	2	1	2	2	1	0	2
1	1	1	2	2	1	0	2
0	2	1	2	2	1	2	2
0	2	1	1	0	0	2	0
0	0	1	1	2	0	0	1
0	1	1	1	0	0	1	0
0	0	1	1	0	0	1	0
0	0	1	1	1	0	0	1
0	2	1	0	1	0	1	0
0	0	1	0	1	0	1	0
1	2	0	1	1	0	1	0
0	0	1	1	0	0	1	0
0	2	1	1	0	0	1	0
0	2	0	0	1	0	1	0
0	2	0	0	0	0	1	0
1	1	0	1	1	1	1	1
1	1	0	1	1	1	1	1
0	0	0	1	0	0	1	0
0	0	0	0	0	1	0	0
0	0	1	1	0	0	0	0
0	0	1	1	0	0	0	0
0	0	1	1	0	0	0	0
0	0	1	1	0	1	1	0
0	0	1	0	0	0	1	0
0	1	1	1	0	1	0	0
0	0	1	1	0	1	1	0
0	0	0	0	0	1	1	0
0	0	1	0	0	1	0	0
0	0	1	0	0	1	0	0
0	0	0	1	0	1	0	0

TCGA-FV-A23B	TCGA-FV-A2QQ	TCGA-FV-A2QR	TCGA-FV-A3I0	TCGA-FV-A3I1	TCGA-FV-A3R2	TCGA-FV-A3R3	TCGA-FV-A495
1	1	2	0	1	0	1	2
1	1	2	0	1	0	1	1
0	2	0	1	1	1	0	0
2	0	0	1	0	1	0	0
1	1	1	1	0	0	0	2
0	0	0	1	0	1	1	0
0	0	1	0	0	0	0	1
0	0	0	1	0	1	0	1
1	1	0	0	0	1	0	0
1	1	0	0	0	1	0	1
0	0	0	0	1	1	0	0
0	0	0	1	0	0	0	0
0	1	0	1	0	0	0	1
0	0	1	0	0	0	0	0
0	0	0	0	0	1	0	1
0	1	1	1	1	1	0	1
0	1	1	1	1	1	0	1
1	1	1	1	1	1	0	1
0	0	0	1	1	1	0	1
0	1	0	0	1	0	0	0
0	1	0	0	1	0	0	1
0	1	1	0	1	0	0	0
1	1	1	1	0	0	1	1
1	1	0	1	0	1	0	0
1	1	0	1	1	1	0	0
1	1	0	1	0	0	1	0
1	0	1	1	0	1	0	0
0	0	0	1	0	0	0	1
0	0	0	1	0	0	0	0
0	1	0	1	1	1	1	0

TCGA-FV-A496	TCGA-FV-A4ZP	TCGA-FV-A4ZQ	TCGA-G3-A25S	TCGA-G3-A25T	TCGA-G3-A25U	TCGA-G3-A25V	TCGA-G3-A25Y
1	2	0	1	0	1	0	2
1	0	0	1	0	0	0	1
0	2	2	0	1	1	1	0
0	0	2	2	0	1	0	0
0	1	1	1	1	0	0	0
0	0	2	2	0	1	0	2
1	1	0	2	0	1	0	0
0	0	1	1	1	0	0	0
0	0	2	1	0	0	0	0
0	0	2	1	0	0	0	0
0	2	0	0	1	0	1	1
0	0	0	0	0	1	0	0
0	0	1	0	1	0	0	0
1	0	1	0	0	1	0	0
0	0	0	0	0	0	0	0
0	1	1	1	0	0	1	1
0	1	1	1	0	0	1	0
1	1	0	1	0	1	1	1
0	0	0	1	1	0	0	1
1	1	0	1	0	0	0	1
1	1	0	1	0	0	0	1
1	1	0	1	0	0	0	1
1	1	0	1	0	0	1	1
0	0	0	1	0	1	0	1
0	1	0	1	1	0	0	0
1	1	0	1	0	0	0	1
1	1	0	1	1	0	0	1
0	1	0	1	0	0	0	0
0	1	0	1	0	0	0	0
0	1	0	1	1	0	0	0

TCGA-G3-A25Z	TCGA-G3-A3CG	TCGA-G3-A3CH	TCGA-G3-A3CI	TCGA-G3-A3CK	TCGA-G3-A5SI	TCGA-G3-A5SJ	TCGA-G3-A5SL
1	2	0	0	1	2	0	2
1	2	0	0	1	2	0	2
1	1	1	0	0	2	2	2
0	1	0	0	1	0	0	2
0	1	0	0	0	1	0	0
0	1	0	0	1	2	0	2
1	0	0	0	1	2	1	1
0	1	0	0	0	0	0	0
0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0
0	1	0	0	0	0	0	1
0	1	0	0	1	0	0	0
0	0	0	0	0	0	0	0
0	1	0	0	0	1	0	1
0	0	0	0	0	0	0	0
0	1	0	0	0	0	1	1
0	1	0	0	0	0	0	1
1	0	1	0	0	1	1	1
0	0	1	0	0	1	0	0
1	0	0	0	0	1	0	0
1	0	0	0	0	1	0	0
1	0	0	0	0	1	0	0
0	0	0	0	0	1	0	1
1	0	1	0	0	1	0	0
0	0	0	0	0	0	0	0
0	0	0	0	0	1	0	1
0	1	0	0	0	0	0	1
0	0	1	0	0	0	0	0
0	0	1	0	0	0	0	0
0	0	1	0	0	0	0	0

TCGA-G3-A5SM	TCGA-G3-A6UC	TCGA-G3-A7M5	TCGA-G3-A7M6	TCGA-G3-A7M7	TCGA-G3-A7M8	TCGA-G3-A7M9
2	1	0	1	0	0	1
2	1	0	1	0	0	1
0	0	0	2	2	0	0
0	2	0	0	0	0	0
1	0	1	2	0	0	1
0	2	0	0	0	0	0
0	0	0	1	0	0	0
1	0	1	0	0	0	0
1	0	0	1	0	0	1
1	0	0	1	1	0	1
1	1	1	0	0	0	0
0	1	0	0	0	0	0
1	0	0	2	1	0	1
0	2	2	0	0	0	0
0	0	0	0	0	0	1
0	1	1	1	1	0	0
0	1	1	1	1	0	1
1	0	1	1	0	0	1
1	0	1	1	0	0	0
1	0	1	0	0	0	1
1	0	1	0	0	0	1
1	0	1	0	0	0	1
1	0	1	0	0	0	1
0	0	1	0	0	0	1
0	0	1	0	1	0	0
1	0	1	0	0	0	1
0	1	1	0	0	0	1
1	0	0	0	0	0	1
1	0	0	0	0	0	1
0	0	1	0	0	0	0

TCGA-G3-AAUZ	TCGA-G3-AAV0	TCGA-G3-AAV1	TCGA-G3-AAV2	TCGA-G3-AAV3	TCGA-G3-AAV4	TCGA-G3-AAV5	TCGA-G3-AAV6
1	1	1	0	1	1	2	1
0	1	1	2	1	1	2	1
2	0	2	1	1	0	2	1
0	0	2	0	1	2	0	0
2	0	2	1	0	0	1	1
0	0	1	0	1	2	0	1
1	0	2	0	0	0	1	1
0	0	2	0	0	0	1	0
0	0	1	0	0	0	0	1
0	0	1	0	0	0	0	1
0	0	1	0	0	0	1	1
0	0	1	0	0	0	0	0
0	1	0	0	0	0	0	0
0	2	0	1	1	0	1	0
0	0	0	0	0	0	0	0
1	1	0	1	0	1	1	1
1	1	0	1	0	1	1	1
1	0	1	0	0	1	1	0
1	0	0	0	0	1	0	0
0	1	1	1	0	1	0	1
0	0	1	0	0	1	0	1
0	0	1	0	0	1	0	1
0	0	1	0	0	0	0	1
1	0	0	0	0	0	0	1
0	0	1	0	1	0	0	1
0	0	1	0	0	0	0	1
0	0	1	0	1	1	0	1
0	0	1	0	1	0	0	0
0	0	1	0	0	0	0	0

TCGA-G3-AAV7	TCGA-GJ-A3OU	TCGA-GJ-A6C0	TCGA-GJ-A9DB	TCGA-HP-A5MZ	TCGA-HP-A5N0	TCGA-K7-A5RF	TCGA-K7-A5RG
2	1	2	0	1	1	0	0
2	1	0	0	1	1	0	0
1	2	0	0	2	0	0	0
0	0	0	0	0	2	0	0
2	0	0	1	1	0	0	0
0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0
0	0	0	1	1	0	0	0
0	0	0	0	1	0	0	0
0	0	0	0	1	0	0	0
0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0
0	1	1	0	0	0	0	0
1	0	0	0	1	1	0	0
0	0	2	0	0	0	0	0
1	0	1	1	1	1	0	0
1	0	0	0	1	0	0	0
1	1	1	1	0	1	0	0
1	1	1	1	0	0	0	1
1	1	1	0	0	1	0	1
1	1	0	0	0	1	0	1
1	1	0	0	0	0	0	1
0	1	0	0	0	0	0	0
1	0	0	0	0	0	0	0
1	0	0	1	0	0	0	0
0	1	0	0	0	0	0	0
0	0	0	0	0	1	0	0
1	0	0	0	0	0	0	1
1	0	1	0	0	0	0	1
1	0	1	1	0	0	0	0

TCGA-K7-A6G5	TCGA-K7-AAU7	TCGA-KR-A7K0	TCGA-KR-A7K2	TCGA-KR-A7K7	TCGA-KR-A7K8	TCGA-LG-A6GG	TCGA-LG-A9QC
1	0	1	2	1	1	1	1
1	0	1	2	1	1	2	1
2	2	0	2	2	1	0	0
0	0	0	1	0	2	1	0
0	0	0	1	0	0	1	2
0	0	0	1	0	1	1	0
0	1	0	0	0	1	1	1
0	2	0	1	0	0	2	1
0	0	0	1	1	0	1	0
0	0	0	1	1	0	1	0
0	0	0	1	0	1	1	0
0	0	0	1	0	0	1	0
0	1	0	1	0	0	0	0
1	2	0	0	0	1	1	0
0	0	0	0	0	1	0	0
1	1	0	1	1	0	0	1
1	1	0	1	1	1	0	1
0	1	1	1	0	0	1	0
0	0	0	1	0	1	0	0
0	0	0	1	1	1	1	1
0	0	0	1	1	1	1	1
0	0	0	1	1	0	0	1
0	0	0	1	1	0	0	1
0	0	0	0	1	1	1	0
0	0	0	0	1	1	0	0
0	0	0	1	1	0	1	1
0	0	0	0	0	0	1	0
0	0	0	0	1	1	0	0
0	0	0	0	1	0	0	0
0	0	0	0	0	0	0	0

TCGA-LG-A9QD	TCGA-MI-A75C	TCGA-MI-A75E	TCGA-MI-A75G	TCGA-MI-A75H	TCGA-MI-A75I	TCGA-MR-A520	TCGA-MR-A8JO
0	0	1	1	1	1	0	0
0	2	1	1	1	1	0	1
2	2	1	0	2	2	0	2
0	0	0	1	2	2	0	0
0	0	0	1	0	1	0	0
0	0	0	1	2	2	0	0
0	0	0	1	0	1	0	0
1	2	0	1	0	1	0	0
0	0	0	2	0	0	0	0
0	0	0	2	0	0	0	0
0	0	1	2	0	0	0	0
0	0	0	0	0	0	0	0
0	0	0	1	0	0	0	0
0	1	1	1	0	0	0	0
1	0	0	1	0	0	0	0
1	1	1	0	1	1	0	1
1	1	1	0	1	1	0	1
0	0	1	1	0	1	0	0
0	0	0	1	0	1	0	1
0	0	0	1	0	0	0	0
0	0	0	1	0	0	0	0
0	0	0	1	0	1	0	0
0	0	0	1	1	0	0	0
0	0	0	1	0	1	0	0
0	0	0	1	0	1	0	0
0	0	0	1	0	0	0	0
0	0	1	1	1	1	0	0
0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0
0	0	0	1	0	1	0	0

TCGA-NI-A4U2	TCGA-NI-A8LF	TCGA-O8-A75V	TCGA-PD-A5DF	TCGA-QA-A7B7	TCGA-RC-A6M3	TCGA-RC-A6M4	TCGA-RC-A6M5
0	2	1	0	1	1	0	0
0	0	1	1	1	1	2	0
0	1	2	0	0	2	2	0
0	1	1	0	0	1	1	0
1	0	1	1	0	1	0	0
0	1	2	1	0	1	1	0
1	1	1	2	0	0	0	0
0	1	1	0	0	0	0	0
0	0	0	2	0	0	0	0
0	0	0	1	0	0	0	1
1	1	0	0	0	1	0	0
0	0	1	0	0	1	1	0
0	1	0	1	0	1	0	0
2	0	1	0	0	0	2	0
0	0	0	1	0	0	0	0
1	1	1	1	1	1	1	0
0	1	1	1	1	1	1	0
1	1	1	1	1	1	1	1
0	1	0	1	0	1	1	1
0	0	1	0	0	1	0	0
0	0	1	0	0	1	0	0
1	1	0	0	0	1	0	0
0	0	1	0	0	0	1	0
0	1	1	0	1	0	0	0
0	1	0	0	0	0	1	1
0	0	0	0	0	0	0	0
0	1	0	0	0	0	1	0
0	1	0	0	1	0	0	1
0	1	0	1	0	0	0	1
0	0	0	1	0	0	0	1

TCGA-RC-A6M6	TCGA-RC-A7S9	TCGA-RC-A7SB	TCGA-RC-A7SF	TCGA-RC-A7SH	TCGA-RC-A7SK	TCGA-RG-A7D4	TCGA-T1-A6J8
0	1	0	0	2	1	1	1
0	2	0	1	2	0	1	1
2	0	0	2	1	2	2	0
0	1	0	0	0	1	1	0
0	0	0	2	0	0	1	0
0	1	0	0	0	1	1	0
1	0	0	0	0	0	1	0
0	0	0	1	0	0	1	0
1	0	0	0	0	0	1	0
1	0	0	0	0	0	1	0
2	2	0	0	0	0	0	0
0	0	0	0	0	1	1	1
0	1	0	0	1	0	0	0
0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0
1	1	0	1	0	1	1	1
1	1	0	1	1	1	1	1
1	0	1	0	1	1	1	1
0	1	0	1	1	1	1	0
0	0	1	0	1	1	1	1
0	0	1	0	1	1	1	1
0	0	1	0	1	1	1	1
0	1	0	0	1	1	1	1
0	0	1	1	1	0	1	1
1	1	1	1	1	1	1	1
1	0	0	0	1	1	1	1
1	0	0	0	0	1	0	1
0	0	0	0	1	1	1	0
0	0	0	1	1	1	1	0
1	0	1	0	1	1	1	1

TCGA-UB-A7MA	TCGA-UB-A7MB	TCGA-UB-A7MC	TCGA-UB-A7MD	TCGA-UB-A7ME	TCGA-UB-A7MF	TCGA-UB-AA0U
2	2	2	1	2	1	1
1	0	2	1	2	1	1
1	0	1	1	2	0	2
1	1	1	0	1	1	2
0	0	0	0	2	1	2
1	1	1	0	1	1	2
1	0	1	0	0	0	1
1	0	0	0	0	0	0
1	1	0	0	1	0	1
1	1	0	0	1	0	1
0	0	0	1	0	0	1
2	0	1	0	2	1	1
0	0	0	0	1	0	0
0	0	0	0	1	0	0
0	0	1	1	0	0	0
0	1	0	1	1	1	1
1	1	0	1	1	1	1
0	1	1	1	1	1	1
1	0	1	0	0	1	1
0	1	1	0	1	1	0
0	1	1	0	1	1	0
0	1	1	0	1	1	0
1	0	1	0	1	1	1
1	1	0	0	0	1	1
0	0	0	0	1	1	1
1	0	1	0	0	1	1
0	1	0	0	1	0	1
1	1	1	0	0	1	0
0	0	1	0	0	1	0
0	1	0	0	1	1	1

TCGA-UB-AA0V	TCGA-WJ-A86L	TCGA-WQ-A9G7	TCGA-WQ-AB4B	TCGA-WX-AA44	TCGA-WX-AA46	TCGA-WX-AA47
0	2	1	1	2	0	2
0	1	1	1	2	0	2
0	0	2	2	1	0	0
0	0	1	0	1	0	0
0	0	1	1	0	0	2
0	1	1	0	2	0	0
0	0	0	0	0	0	0
0	0	1	1	0	0	2
0	0	1	1	0	0	0
0	0	1	1	0	0	0
0	0	1	1	0	1	0
0	0	1	0	0	0	0
0	0	0	1	0	0	0
0	0	1	0	0	0	0
0	2	0	0	1	0	0
0	1	1	1	1	0	0
0	1	1	1	1	0	1
0	1	0	1	1	0	0
0	1	0	0	1	0	1
0	0	1	1	1	0	0
0	0	1	1	1	0	0
0	0	1	1	1	0	0
0	0	1	1	0	0	0
0	1	1	0	0	0	0
0	0	1	1	0	0	0
0	0	1	1	0	0	0
0	1	0	0	0	0	0
0	1	1	1	1	0	0
0	0	1	1	1	0	0
0	0	0	1	0	0	0

TCGA-XR-A8TD	TCGA-XR-A8TE	TCGA-XR-A8TF	TCGA-XR-A8TG	TCGA-YA-A8S7	TCGA-ZP-A9CV	TCGA-ZP-A9CY	TCGA-ZP-A9CZ
1	1	2	2	2	2	0	2
1	0	2	1	0	2	1	1
0	0	0	0	2	1	0	0
1	1	1	0	1	0	0	0
0	0	1	1	0	0	0	2
1	1	1	1	1	0	0	0
1	0	0	0	0	0	0	1
0	0	1	0	0	0	0	1
1	0	1	1	1	0	0	0
1	0	1	2	1	0	0	0
0	1	1	0	1	0	0	0
1	1	1	0	1	0	0	0
0	0	0	1	1	0	0	0
0	1	0	0	0	1	0	0
0	0	0	1	0	0	0	0
1	0	0	1	1	1	0	1
1	0	0	1	1	1	0	1
1	0	0	1	1	0	0	0
1	0	1	1	1	0	1	1
0	0	1	1	1	0	0	0
0	0	1	1	1	0	0	0
0	0	1	0	1	0	0	0
0	0	1	0	0	0	1	1
1	0	1	0	0	0	0	1
0	0	1	0	0	0	0	0
0	0	1	0	0	0	0	1
0	0	0	1	0	0	0	0
0	0	0	0	0	0	0	0
0	0	1	1	0	0	0	0
1	0	0	0	0	0	0	1

TCGA-ZP-A9D0	TCGA-ZP-A9D1	TCGA-ZP-A9D2	TCGA-ZP-A9D4	TCGA-ZS-A9CD	TCGA-ZS-A9CE	TCGA-ZS-A9CF	TCGA-ZS-A9CG
2	2	1	1	1	0	0	1
2	2	1	1	1	1	0	1
0	0	0	2	2	0	0	2
0	0	0	0	1	0	2	0
0	1	2	2	0	1	0	0
0	0	0	0	1	0	2	0
0	0	1	2	0	0	2	0
0	1	0	0	0	1	0	0
0	0	0	0	1	0	0	0
0	0	0	0	1	0	0	0
0	1	0	0	0	0	0	0
0	0	0	0	1	0	2	0
0	1	0	0	0	0	2	0
0	0	0	0	1	0	0	1
0	0	0	0	0	0	2	0
1	0	1	1	1	1	1	1
1	0	1	1	1	1	1	1
0	1	1	1	0	1	1	0
1	0	0	0	0	1	0	1
0	0	1	0	0	1	0	0
0	0	1	0	0	1	0	0
0	0	1	0	0	1	0	0
0	1	0	0	0	1	0	0
0	1	0	0	0	0	0	1
1	1	1	0	0	0	0	0
0	1	0	0	0	0	0	0
0	0	0	0	0	1	1	0
1	0	1	0	0	0	0	0
0	0	1	0	0	0	0	0
1	0	1	0	0	1	1	0

Table S10. Methylation drived genes in two MSCs.

ID	Corr	*P*	Corr1	Pval1	Corr2	*P*	Beta-mean1	Beta-mean2	Beta.KW.test.*P*	Beta.Sig
ACSL5	-0.730059	5.75E-59	-0.716798	1.03E-35	-0.755264	1.75E-24	0.171179865	0.215227563	0.034082623	*
APOL3	-0.528918	1.44E-26	-0.518647	1.71E-16	-0.536794	8.54E-11	0.098107227	0.099008422	0.891020799	
C14orf159	-0.406876	1.96E-15	-0.42088	6.77E-11	-0.377634	1.13E-05	0.141350178	0.147255809	0.290214592	
C3orf18	-0.417594	3.13E-16	-0.384522	3.17E-09	-0.455864	9.76E-08	0.083792038	0.102139954	0.070991104	
CA14	-0.75754	1.16E-65	-0.739829	4.74E-39	-0.776303	0	0.159200983	0.185648991	0.064400084	
CCNI2	-0.52886	1.44E-26	-0.551929	6.97E-19	-0.486742	7.05E-09	0.153492254	0.147398733	0.73500905	
CD14	-0.414171	5.56E-16	-0.381111	4.33E-09	-0.460671	4.95E-08	0.135731999	0.161931921	0.132609746	
CDO1	-0.533053	5.27E-27	-0.473817	9.86E-14	-0.630452	2.37E-15	0.123381322	0.186912574	0.003069761	**
DMRTA1	-0.415756	4.27E-16	-0.313563	1.77E-06	-0.575805	0	0.1457733	0.170612492	0.144730478	
EPCAM	-0.686788	7.70E-50	-0.667186	1.28E-29	-0.701726	5.54E-20	0.304099334	0.252561109	0.008918712	**
FAM169A	-0.543559	3.49E-28	-0.489209	1.21E-14	-0.598407	0	0.127249783	0.176367252	0.003146175	**
FXYD1	-0.767535	5.73E-68	-0.75709	1.36E-41	-0.763993	0	0.240630171	0.278691335	0.044463022	*
GALC	-0.695895	1.47E-51	-0.729973	1.36E-37	-0.650049	1.83E-16	0.166726053	0.200328505	0.132609719	
GIPC2	-0.556912	9.77E-30	-0.494036	6.16E-15	-0.630484	0	0.102489623	0.146752951	0.007264424	**
GREB1L	-0.489216	1.73E-22	-0.40307	4.92E-10	-0.639977	0	0.173415348	0.219295727	0.005385291	**
HIST3H2A	-0.531935	6.86E-27	-0.473596	9.91E-14	-0.61503	1.63E-14	0.275267905	0.265181505	0.43516937	
IFITM1	-0.675867	8.78E-48	-0.681928	2.33E-31	-0.652993	1.24E-16	0.290924844	0.315330918	0.276604869	
IGF1	-0.722253	3.35E-57	-0.700606	1.17E-33	-0.738803	0	0.197453054	0.242075453	0.04457785	*
KCNJ8	-0.421965	1.45E-16	-0.387926	2.28E-09	-0.474903	1.77E-08	0.108818095	0.181410631	0.080347857	
KCNT2	-0.386675	5.24E-14	-0.398437	1.11E-09	-0.369438	1.75E-05	0.092701459	0.134464483	0.15928109	
KCTD14	-0.396794	1.02E-14	-0.332559	3.72E-07	-0.487517	1.01E-08	0.120273803	0.173509502	0.010600986	*
LIPG	-0.550283	5.87E-29	-0.530285	0	-0.602227	7.77E-14	0.089414097	0.141119609	0.027707102	*
MCHR1	-0.373244	4.26E-13	-0.374012	8.67E-09	-0.368281	1.84E-05	0.098171937	0.143231396	0.000502404	***
MT1E	-0.692857	5.05E-51	-0.68665	6.93E-32	-0.680389	0	0.136179684	0.169829237	0.003956642	**
NKAPL	-0.54525	2.27E-28	-0.499653	2.76E-15	-0.626376	3.95E-15	0.435454565	0.428489354	0.88075681	
NQO1	-0.658047	1.45E-44	-0.684247	1.29E-31	-0.636009	1.19E-15	0.307334002	0.246056396	0.02824785	*
NSUN7	-0.620528	1.73E-38	-0.602033	4.91E-23	-0.6544	0	0.291197812	0.279628958	0.511940317	
OAS2	-0.482042	8.51E-22	-0.483456	2.69E-14	-0.48771	6.65E-09	0.10432789	0.131441888	0.038217033	*
OSCP1	-0.428749	4.22E-17	-0.468677	1.89E-13	-0.341031	7.90E-05	0.112212946	0.119250233	0.1328889	
P2RX7	-0.433388	1.80E-17	-0.391995	1.55E-09	-0.506928	1.31E-09	0.117667769	0.135343058	0.269026347	
PALMD	-0.399481	6.61E-15	-0.252137	0.000141	-0.61993	8.93E-15	0.118206981	0.169459164	0.01452446	*
PHYHD1	-0.755155	3.82E-65	-0.711767	0	-0.805339	0	0.140061596	0.177186575	0.064556521	
RAB3D	-0.76542	1.14E-67	-0.754347	2.39E-41	-0.78454	1.57E-27	0.341335002	0.282330671	0.067914808	
RANBP3L	-0.537008	1.97E-27	-0.566258	5.52E-20	-0.464997	3.77E-08	0.13089634	0.156253531	0.105979211	
RARRES3	-0.109375	0.0399912	-0.023438	0.727184	-0.228913	0.0091987	0.106325622	0.149493284	0.003339025	**
RTP3	-0.646295	1.42E-42	-0.635043	3.29E-26	-0.643538	0	0.131274506	0.17016959	0.005457638	**
SERPINA3	-0.385886	5.85E-14	-0.390482	1.78E-09	-0.42419	6.23E-07	0.173233206	0.203534747	0.105745442	

SLC16A1	-0.291718	2.40E-08	-0.222468	0.0008119	-0.402763	2.50E-06	0.091233481	0.12568179	0.26996579	
SLC1A4	-0.472756	6.37E-21	-0.434602	1.39E-11	-0.515262	9.10E-10	0.084553031	0.134284728	0.057109471	
SLC25A36	-0.523623	5.40E-26	-0.365617	1.90E-08	-0.726973	6.01E-22	0.273736304	0.228452183	0.007625283	**
SLC2A10	-0.492978	7.83E-23	-0.344624	1.31E-07	-0.712314	8.53E-21	0.107932999	0.152096085	0.040386473	*
SLC46A3	-0.5177	2.28E-25	-0.480877	3.78E-14	-0.577309	0	0.083214251	0.109613277	0.130392827	
SNX7	-0.521105	9.95E-26	-0.507312	8.88E-16	-0.539164	6.94E-11	0.092217516	0.098324028	0.147434933	
SP140L	-0.490291	1.39E-22	-0.445643	3.73E-12	-0.564047	5.56E-12	0.124157672	0.138159655	0.500852448	
SPINT2	-0.556697	9.99E-30	-0.427524	3.18E-11	-0.736319	9.67E-23	0.396263762	0.352012603	0.102972015	
TAT	-0.535487	2.86E-27	-0.50788	8.38E-16	-0.571769	2.48E-12	0.123708004	0.166210787	0.002489887	**
TDRKH	-0.404312	3.00E-15	-0.381183	4.33E-09	-0.432022	3.70E-07	0.10462557	0.149818726	0.010750377	*
TMEM106A	-0.74283	4.99E-62	-0.755947	1.60E-41	-0.719206	2.45E-21	0.351624133	0.298452219	0.141476847	
TRAM1L1	-0.510304	1.38E-24	-0.578803	5.25E-21	-0.372261	1.52E-05	0.122959917	0.118279542	0.683428865	
TRPC1	-0.494871	5.18E-23	-0.515552	2.70E-16	-0.462805	4.37E-08	0.133218722	0.154759596	0.957242986	
XAF1	-0.388637	3.87E-14	-0.440696	6.75E-12	-0.318968	0.000233	0.135598281	0.173432935	0.041347713	*
ZDHHC13	-0.598597	3.01E-35	-0.545091	2.24E-18	-0.668553	1.24E-17	0.119504102	0.131684004	0.719558471	
ZNF300	-0.565117	9.50E-31	-0.530655	2.51E-17	-0.628231	0	0.209469206	0.213658086	0.705025905	
ZNF43	-0.708165	4.18E-54	-0.70708	1.87E-34	-0.719782	2.30E-21	0.188778486	0.199055082	0.440927199	
ZNF433	-0.403165	3.59E-15	-0.367532	1.61E-08	-0.458799	8.05E-08	0.111472149	0.131138166	0.050391311	
ZNF470	-0.667145	3.51E-46	-0.646669	2.41E-27	-0.688635	0	0.11314025	0.135875234	0.286280905	
ZNF471	-0.693863	3.46E-51	-0.706717	1.91E-34	-0.660247	0	0.202376496	0.233647237	0.130668359	
ZNF492	-0.507992	2.37E-24	-0.559769	1.76E-19	-0.439565	2.22E-07	0.244340967	0.278482016	0.026357424	*
ZNF525	-0.651954	1.60E-43	-0.638306	1.67E-26	-0.677559	3.12E-18	0.169188471	0.166709598	0.987469733	
ZNF551	-0.49258	8.39E-23	-0.509609	6.62E-16	-0.461327	4.80E-08	0.087292011	0.089365795	0.586262761	
ZNF665	-0.64121	9.63E-42	-0.63699	2.17E-26	-0.648645	2.16E-16	0.245142044	0.259031198	0.74482332	
ZNF829	-0.684981	1.62E-49	-0.714739	1.79E-35	-0.631839	2.03E-15	0.140319172	0.13623952	0.998703713	
ZNF879	-0.627378	1.62E-39	-0.643792	4.63E-27	-0.595162	1.77E-13	0.155803232	0.172848482	0.194998279	
ZNF93	-0.626315	2.27E-39	-0.614125	3.78E-24	-0.641501	5.74E-16	0.17915586	0.204032103	0.08319797	

Notes: *P <0.05, **P <0.01, ***P <0.001

Zscore-mean1	**Zscore-mean2**	**Zscore.KW.test.*P***
0.072814913	-0.126438299	0.238609184
0.012205338	-0.021193766	0.841961332
-0.006091975	0.010578314	0.893963694
0.092772042	-0.161092538	0.140128268
0.081837074	-0.142104686	0.188985319
-0.020424643	0.035466047	0.753513555
0.043332533	-0.075244088	0.508046103
0.08064034	-0.140026637	0.238609184
0.113197545	-0.196560078	0.084708262
-0.119990975	0.208356422	0.072510539
0.070744098	-0.122842465	0.238609184
0.050328267	-0.087391719	0.41917156
0.040329822	-0.070030078	0.541760827
0.094421574	-0.163956841	0.142654223
0.071166596	-0.123576105	0.238609184
-0.10135449	0.175995393	0.136577327
-0.007536835	0.013087217	0.87557797
0.08144027	-0.141415663	0.188985319
0.057345773	-0.099577156	0.351930186
0.057486722	-0.099821904	0.339981011
0.094842315	-0.164687431	0.140128268
0.105021026	-0.182362092	0.117487357
0.070500213	-0.122418975	0.250450123
0.067490177	-0.117192245	0.238609184
-0.015542287	0.026988157	0.800970457
-0.038309928	0.066522666	0.565105299
-0.063953626	0.111051258	0.309902179
0.017005147	-0.029528317	0.772425159
0.049380955	-0.085746775	0.455095994
0.023666169	-0.041094742	0.753513555
0.118440649	-0.205664383	0.072510539
0.070991423	-0.123271929	0.238609184
-0.095753185	0.166269097	0.142654223
0.021877977	-0.037989665	0.753513555
0.032848606	-0.057039441	0.654971905
0.05763155	-0.100073389	0.339830136
-0.064919332	0.112728142	0.284785265

0.093525282	-0.16240049	0.157791997
0.081112686	-0.140846835	0.218588622
-0.194967334	0.338547929	0.000916023
0.027504334	-0.047759465	0.692600022
0.02863203	-0.049717634	0.692600022
0.036948438	-0.064158528	0.581870347
0.045833409	-0.079586695	0.508046103
-0.131228947	0.22787042	0.072510539
0.070962472	-0.123221656	0.238609184
0.074208576	-0.128858302	0.238609184
-0.026012318	0.045168677	0.692600022
0.021107777	-0.036652264	0.753513555
0.007891494	-0.01370306	0.87557797
0.020477026	-0.035557007	0.753513555
-0.077841053	0.13516586	0.238609184
-0.04409541	0.076568774	0.508046103
-0.027885424	0.048421201	0.692600022
0.061203802	-0.106276369	0.309902179
0.018678028	-0.032433164	0.769383307
0.020178414	-0.035038486	0.753513555
0.01453064	-0.0252315	0.806315744
-0.000668865	0.00116144	0.986994851
-0.042566161	0.073913333	0.508046103
-0.031251043	0.054265377	0.676963576
0.009939732	-0.01725969	0.869309401
-0.00853284	0.014816714	0.87557797
0.029430176	-0.051103561	0.692600022

Table S11. Candidate drugs screened through CTRP, PRISM, Cmap databases for two MSCs.

MSC	CTRP/PRISM	Cmap Score	Targets	Log2FC of mRNA expression	Log2FC of protien expression	Description	Clinical status	Exprimental evidence	PMID	Clinical trail
1	ALL	-10.76	EGFR;ERBB2;ERBB4	0.5991997	0.04054141	EGFR inhibitor	Launched	Present	31432165, 33824166	
1	ALL	-71.43	EGFR;ERBB2	0.5991997	0.04054141	EGFR inhibitor	Phase 3	Present	21982771	
1	CTRP	3.19	EPHA2;KIT;SRC;YES1;ABL1;ABL2;BLK;LYN;FGR;FGK; FYN;HCK;LCK;SRC;SRMS;PDGFRB;STAT5B	0.30189562	0.040219875	BCR-ABL kinase inhibitor	Phase 2	Present	23299860	NCT00459108
1	PRISM	-26.75	JUN;TUBA1A;TUBB;TUBD1;TUBE1;TUBG1	0.30356412	NA	Microtubule inhibitor	Preclinical	Present	22285225	
2	PRISM	NA	ANPEP；LAP3；NPEPPS	0.11119459	NA	bioavailable aminopeptidase inhibitor	Phase 2	Present	33043735, 20733120	
2	CTRP	NA	SRC	0.33680999	0.003098543	Src inhibitor	Phase 2	Present	23361621, 23314737	