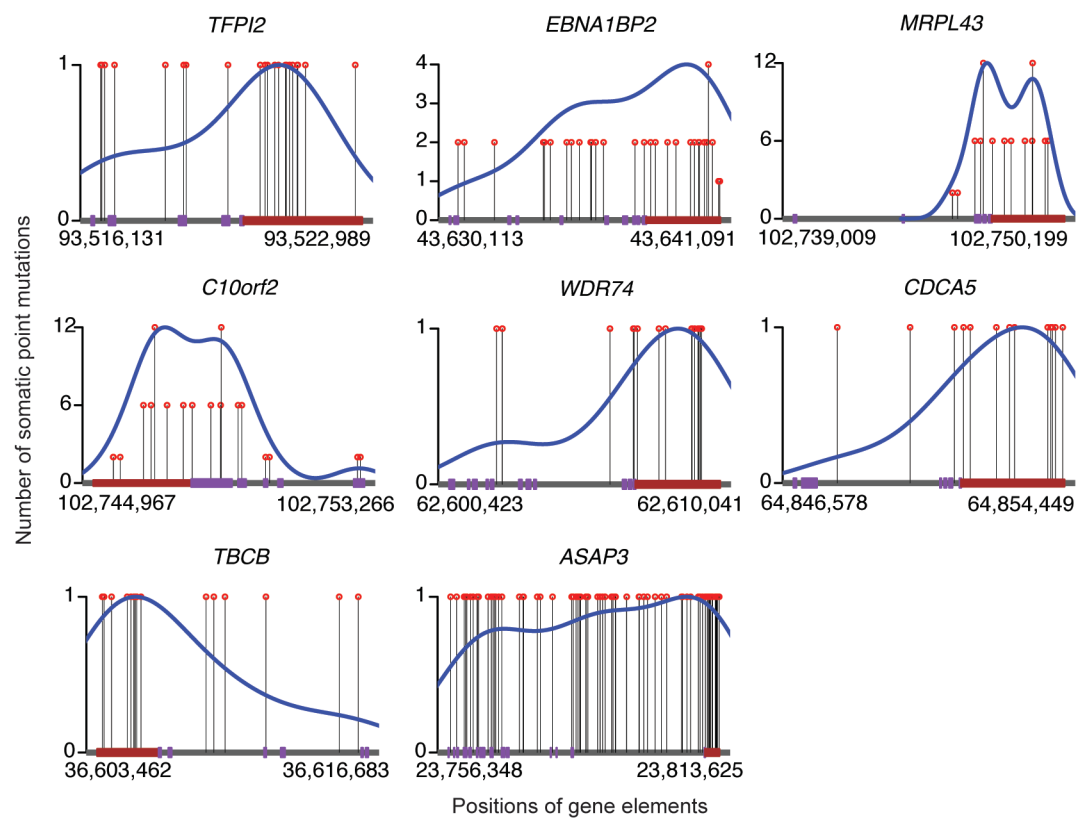


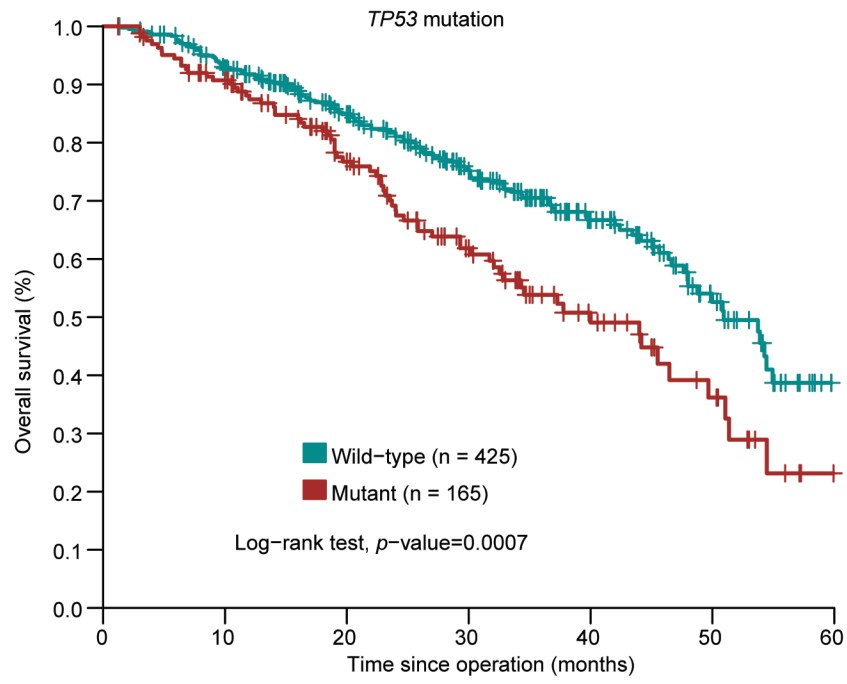
Title: Genomic analysis of liver cancer unveils novel driver genes and distinct prognostic features

Author(s): Xiangchun Li, Weqi Xu, Wei Kang, Sunny H. Wong, Mengyao Wang, Yong Zhou, Xiaodong Fang, Xiuqing Zhang, Huanming Yang, Chi H. Wong, Ka F. To, Stephen L. Chan, Matthew T.V. Chan, Joseph J.Y. Sung, William K.K. Wu, Jun Yu

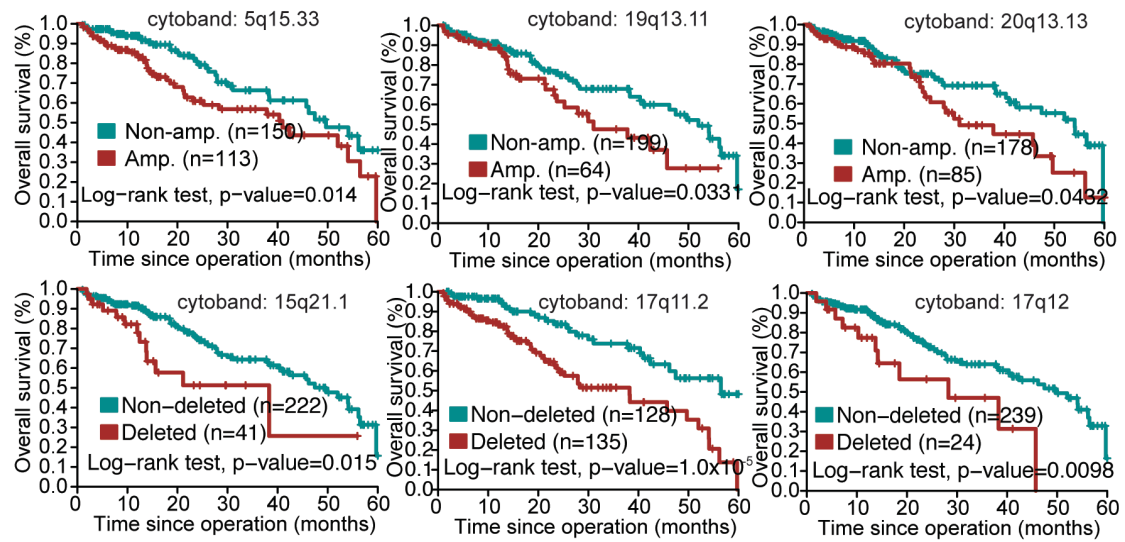
Supplementary Materials



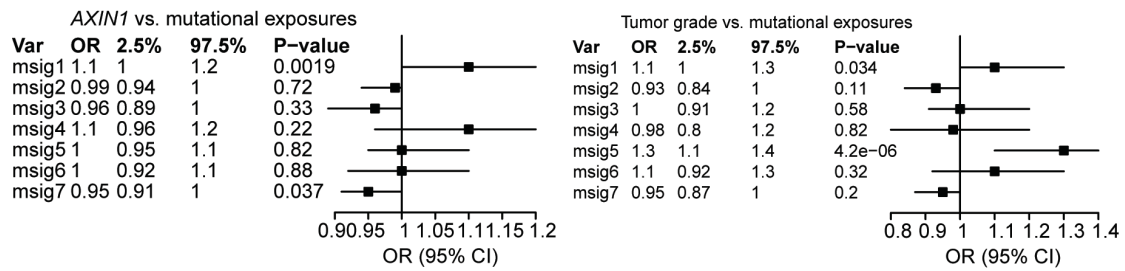
Supplementary Figure 1 Genes enriched for promoter mutations.



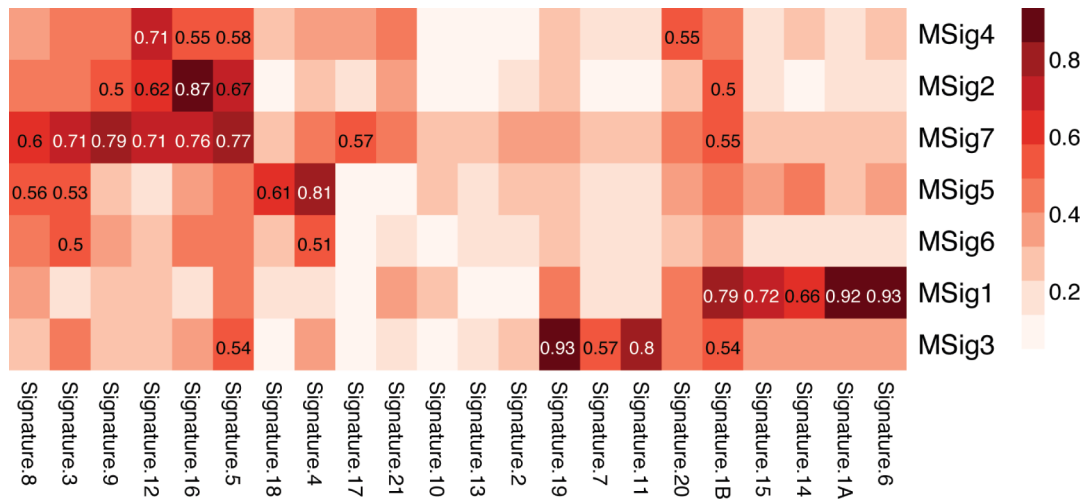
Supplementary Figure 2 Kaplan-Meier survival analysis of *TP53* mutations.



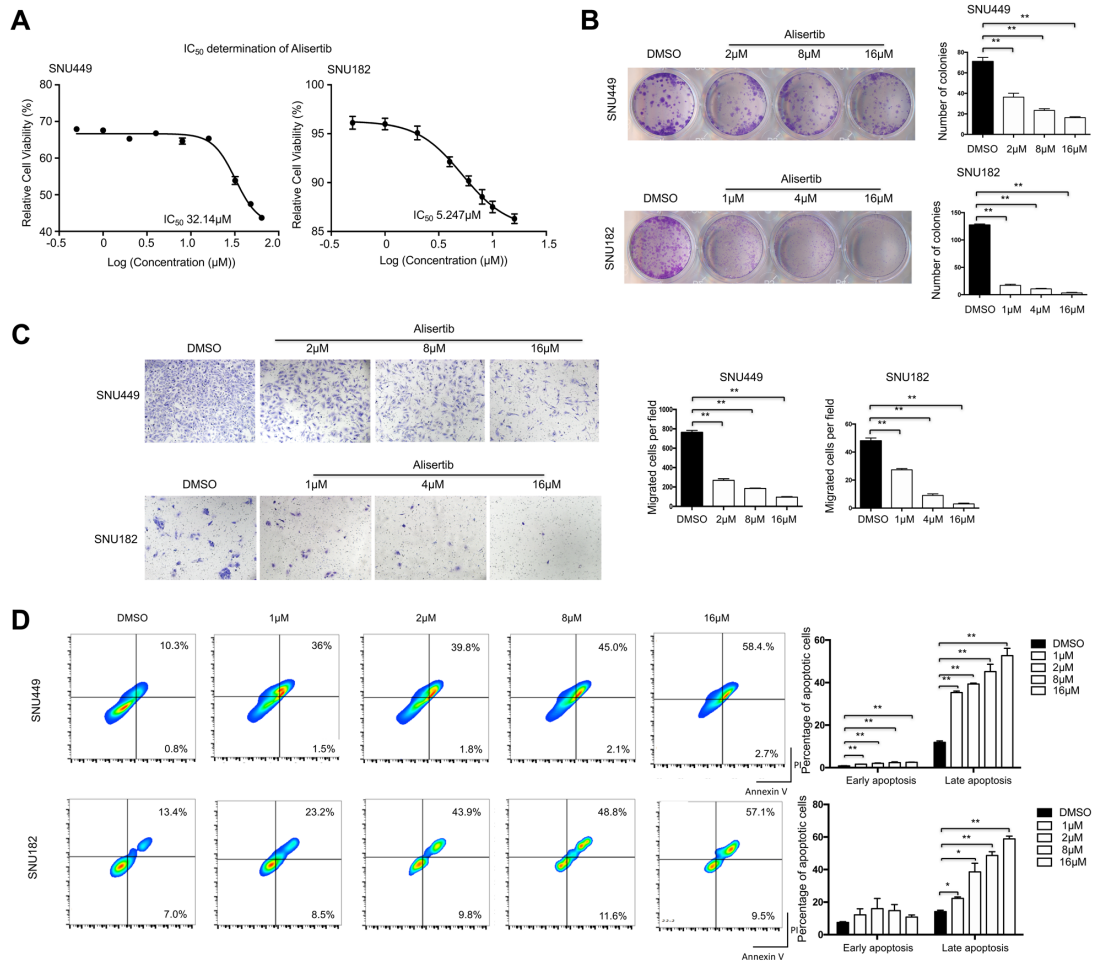
Supplementary Figure 3 Kaplan-Meier survival analysis of focal amplification and deletion peaks.



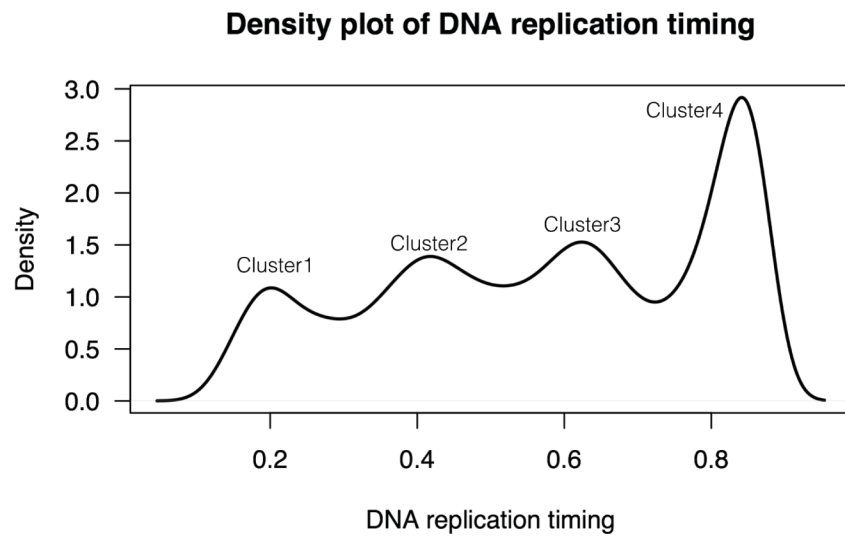
Supplementary Figure 4 Correlation analysis of mutation signatures with tumor grade and *AXIN1* mutations.



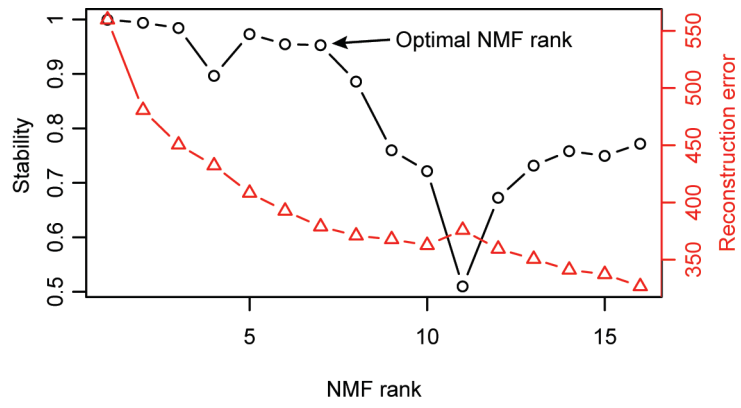
Supplementary Figure 5 Cosine similarities among mutational signatures obtained from our study and COMSIC.



Supplementary Figure 6 Effects of alisertib on (A) viability, (B) colony-forming ability, (C) migration and (D) apoptosis of SNU449 and SNU182 cells.



Supplementary Figure 7 **Density plot of DNA replication time data obtained from Chen et al.**



Supplementary Figure 8 The stability and reconstruction error in extracting mutational signatures. Optimal rank was selected with high stability and low reconstruction error.

Supplementary Table 2. Mutually exclusive SMGs.

Gene1	Gene2	CntGene1	CntGene2	AndCnt	XorCnt	Perm_CntGe	Perm_CntGe	Perm_AndCr	Perm_XorCn	Pvalue_And	Pvalue_Xor	Qvalue_And	Qvalue_Xor
ARID1A	KEAP1	100	30	0	130	100	30	3.3101	123.3798	1	0.0261	1	1
ARID1A	TSC2	100	45	1	143	100	45	4.9727	135.0546	0.9959	0.0304	1	1
ARID2	AXIN1	72	62	1	132	72	62	4.9234	124.1532	0.9959	0.031	1	1
AXIN1	CTNNB1	62	249	5	301	62	249	16.5826	277.8348	1	3.00E-04	1	0.13545
BAP1	CTNNB1	26	249	3	269	26	249	6.9778	261.0444	0.9849	0.0495	1	1
BAP1	TERT	26	224	1	248	26	224	6.2717	237.4566	0.9993	0.005	1	0.7525
BAP1	TP53	26	296	3	316	26	296	8.251	305.498	0.9958	0.0163	1	1
CDKN1A	TP53	15	296	1	309	15	296	4.7674	301.4652	0.9973	0.0269	1	1
CTNNB1	HNF4A	249	16	1	263	249	16	4.3166	256.3668	0.9946	0.0442	1	1
CTNNB1	PTEN	249	21	1	268	249	21	5.5988	258.8024	0.9992	0.0094	1	1
CTNNB1	RB1	249	40	2	285	249	40	10.694	267.612	0.9999	5.00E-04	1	0.1505
CTNNB1	TP53	249	296	54	437	249	296	77.3903	390.2194	1	0	1	0
DYRK1A	TP53	14	296	1	308	14	296	4.426	301.148	0.9955	0.0349	1	1
IL6ST	TERT	30	224	2	250	30	224	7.2638	239.4724	0.9987	0.0108	1	1
IL6ST	TP53	30	296	3	320	30	296	9.5007	306.9986	0.9988	0.0043	1	0.7525
RPL22	TP53	15	296	0	311	15	296	4.7476	301.5048	1	0.0023	1	0.519225

Supplementary Table 3.

Module ID	Genes	Total Percent Altered	Total Altered Samples	Multiple Alterations	p-value	adjusted p-value
M1	CDKN1A [12], CTN	41.19%	437	71	0	0.01
M2	CDKN1A [12], CTN	41.19%	437	69	0	0.01
M3	AXIN1 [53], CTNNE	41.38%	439	65	0	0.01
M4	AXIN1 [53], CTNNE	25.54%	271	9	0.004	0.07
M5	AXIN1 [53], CTNNE	27.14%	288	19	0.008	0.15
M6	CTNNB1 [214], HNF	25.54%	271	14	0.016	0.23
M7	CDKN1A [12], JAK	39.87%	423	78	0.036	0.49
M8	IL6ST [24], MTOR [6.97%	74	0	0.042	0.59
M9	CDKN1A [12], CTN	26.11%	277	20	0.059	0.64
M10	CTNNB1 [214], HNF	28.09%	298	27	0.065	0.64
M11	PTEN [17], RPS6K	8.67%	92	1	0.078	0.69
M12	PTEN [17], RPS6K	6.97%	74	0	0.086	0.74
M13	MTOR [13], PIK3C	6.31%	67	0	0.097	0.77
M14	CTNNB1 [214], HNF	28.46%	302	29	0.109	0.79
M15	CDKN1A [12], CTN	28.65%	304	32	0.118	0.79
M16	DYRK1A [12], RPS	8.20%	87	1	0.149	0.95
M17	JAK1 [11], MTOR [7.26%	77	1	0.162	0.95
M18	CDKN1A [12], CDK	26.48%	281	16	0.181	0.95
M19	IL6ST [24], JAK1 [1	7.82%	83	2	0.239	0.97
M20	CDKN1A [12], JAK	24.79%	263	14	0.243	0.97
M21	CDKN1A [12], MTC	8.95%	95	3	0.255	0.97
M22	CDKN1A [12], JAK	26.96%	286	19	0.256	0.98
M23	CDKN1A [12], JAK	25.73%	273	18	0.261	0.98
M24	HNF4A [16], PTEN	9.90%	105	4	0.278	0.98
M25	CTNNB1 [214], PIK	25.82%	274	23	0.303	0.98
M26	CDKN1A [12], IL6S	6.03%	64	1	0.36	0.99
M27	CDKN1A [12], CTN	26.48%	281	28	0.382	1
M28	DYRK1A [12], TSC	6.31%	67	1	0.471	1
M29	CDKN1A [12], JAK	6.31%	67	2	0.501	1
M30	AXIN1 [53], GPAM	7.63%	81	2	0.551	1
M31	CDKN1A [12], HNF	7.73%	82	3	0.562	1
M32	CDKN1A [12], IL6S	6.88%	73	3	0.614	1
M33	HNF1A [30], RPS6I	7.54%	80	3	0.635	1
M34	CTNNB1 [214], RP	23.85%	253	18	0.659	1
M35	ERRFI1 [12], MTOF	4.24%	45	1	0.742	1
M36	CDKN1A [12], MTC	26.11%	277	28	0.754	1
M37	CDKN1A [12], MTC	26.11%	277	27	0.768	1
M38	AXIN1 [53], TERT [26.86%	285	32	0.789	1
M39	CTNNB1 [214], PIK	22.43%	238	13	0.796	1
M40	AXIN1 [53], GPAM	27.80%	295	39	0.805	1
M41	HNF1A [30], HNF4	8.77%	93	6	0.807	1
M42	CDKN1A [12], CDK	24.69%	262	20	0.812	1
M43	DYRK1A [12], PTPN	3.68%	39	1	0.839	1
M44	CDKN1A [12], PIK3	26.86%	285	34	0.843	1
M45	CDKN1A [12], CTN	22.53%	239	14	0.852	1
M46	CTNNB1 [214], JAK	23.00%	244	18	0.896	1
M47	CDKN1A [12], HNF	28.28%	300	44	0.938	1
M48	AXIN1 [53], CTNNE	36.85%	391	98	0.971	1
M49	CTNNB1 [214], HNF	36.85%	391	98	0.977	1
M50	CDKN1A [12], CTN	35.82%	380	95	0.996	1
M51	CDKN1A [12], CTN	36.48%	387	104	0.997	1
M52	CDKN1A [12], CTN	34.68%	368	92	0.999	1
M53	CDKN1A [12], PTE	3.58%	38	4	1	1

Supplementary Table 4.

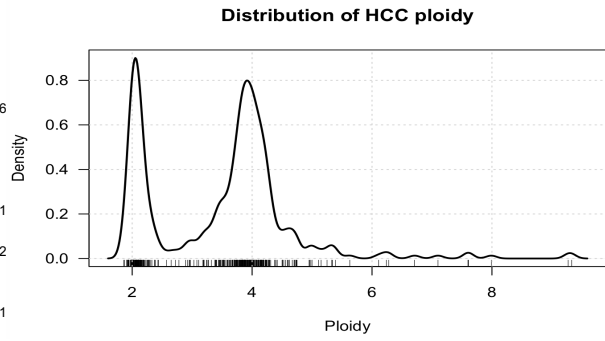
gene	pathway	transit	C->A	flip	A->C	null+indel	obs.total.mut.num	exp.total.mut.num	p	q	Genes
beta-catenin signal	Wnt/beta-catenin si	139	50	70	51	36	347	71.7689786	6.19E-121	1.98E-119	APC, CTNBB1, AXIN2, TBL1XR1, SOX17
CellFate	APC	195	66	87	58	125	532	194.3248602	9.09E-89	1.45E-87	FAM123B, AXIN1, GNAS, RNF43, CTNBB1, HNF1A, NF2, CDH1, APC, EP300, SOX9, KLF4
CellSurvival	Cell Cycle/Apoptosi	164	87	78	38	165	534	245.191824	1.20E-87	1.28E-86	DAXX, CDKN2A, TP53, CDC73, NFE2L2, CARD11, FUBP1, CASP8, PPP2R1A, TNFAIP3, MED12, CYLD, RB1, ABL1, MYD88, NPM1, BCL2, TRAF7
GenomeMaintenance	DNA Damage Cont	161	77	69	32	151	491	229.7693391	5.20E-81	4.21E-80	BRC1, BRCA2, TP53, STAG2, MSH2, ATM, MLL1, MSH6, BAP1
NFE2L	NFE2L	28	4	10	15	11	69	15.0720966	8.94E-25	5.72E-24	NFE2L2, NFE2L3
Genome integrity	Genome integrity	189	82	76	35	154	537	353.0869553	3.99E-20	2.13E-19	TP53, ATM, ATRX, BRCA2, ATR, STAG2, BAP1, BRCA1, SMC1A, SMC3, CHEK2, RAD21, ERCC2
Cell cycle	Cell cycle	25	12	13	7	66	126	62.9459902	8.78E-13	4.02E-12	CDKN2A, RB1, CDK12, CDKN1B, CCND1, CDKN1A, CDKN2C
Histone	Histone	15	3	8	1	2	29	7.376354481	3.35E-10	1.34E-09	HIST1H1C, H3F3C, HIST1H2BD
TGF-beta signalling	TGF-beta signalling	28	13	11	9	30	91	49.46511579	4.19E-08	1.49E-07	SMAD4, TGFBR2, ACVR1B, SMAD2, ACVR2A
PI3K signalling	PI3K signalling	54	10	15	11	19	113	77.95541598	7.71E-05	0.00024668	PIK3CA, PTEN, PIK3R1, TLR4, PIK3CG, AKT1
Proteolysis	Proteolysis	26	9	6	1	9	51	30.5440448	0.000253856	0.00073849	FBXW7, KEAP1, SPOP
Ribosome	Ribosome	4	4	5	0	10	23	10.74791539	0.000336601	0.000697603	RPL22, RPL5
Metabolism	Metabolism	13	5	5	1	2	26	16.96539691	0.014823838	0.036501766	IDH1, IDH2
DNA methylation	DNA methylation	14	5	5	3	10	39	38.09729461	0.400209938	0.914765572	DNMT3A, TET2
CellSurvival	STAT	73	25	10	5	14	127	165.3287477	0.99886126	0.999999998	CRLF2, MPL, FLT3, VHL, JAK2, JAK3, JAK1, SOCS1, KIT, FGFR2, FGFR3
CellFate	Chromatin Modifica	228	71	75	38	275	691	758.2330846	0.992941177	0.999999998	MEN1, MLL3, MLL2, EZH2, SETBP1, SMARCA4, NCOR1, DAXX, SETD2, ASXL1, DNMT1, KDM6A, H3F3A, ARID2, WT1, DNMT3A, SMARCB1, SPOP, IDH2, IDH1, TET2, PAX5, ATRX, EP300, HIST1H3B, ARID1B, ARID1A, PRDM1, PBRM1, CREBBP, KDM5C, SETBP1
CellSurvival	PI3K	173	58	45	17	51	349	410.0290919	0.998890502	0.999999998	PDGFRA, EGFR, RET, AKT1, B2M, TSHR, FLT3, TSC1, CE2PA, PTEN, PIK3CA, CSF1R, PIK3R1, ERBB2, VHL, FGFR2, FGFR3, GNAQ, ALK, GNAS, CBL, KIT, MET, GNA11, STK11
CellSurvival	MAPK	27	8	9	1	4	49	74.18295569	0.998782336	0.999999998	CEBPA, GNAQ, MAP3K1, TNFAIP3, B2M, GNA11, TSHR
CellFate	Transcriptional Reg	57	12	14	6	10	99	134.1947503	0.999111677	0.999999998	RUNX1, SRSF2, U2AF1, SF3B1, KLF4, AR, BCOR, PHF6, GATA3, CREBBP
CellFate	HH	13	5	9	0	4	31	48.47567444	0.995070604	0.999999998	SMO, SPOP, PTCH1
CellSurvival	RAS	187	53	45	29	39	353	463.9147826	0.999999995	0.999999998	CIC, PDGFRA, NRAS, HRAS, EGFR, RET, VHL, MAP2K1, FLT3, CE2PA, MAP3K1, CSF1R, NF1, ERBB2, GNAQ, FGF2, FGF3, KRAS, ALK, GNAS, PTPN11, B2M, CBL, KIT, MET, BRAF, GNA11
CellFate	NOTCH	38	10	12	6	8	75	136.9294207	0.999999995	0.999999998	FBXW7, NOTCH1, NOTCH2, EP300, GATA2, GATA1
CellSurvival	TGF-beta	49	16	18	6	13	102	140.9486307	0.999651564	0.999999998	GNAS, SMAD4, ACVR1B, SMAD2, MED12, FOXL2, EP300, GATA2, GATA1
regulator	Transcription factor	121	28	45	18	231	254.2103965	0.924471173	0.999999998	0.924471173	VHL, GATA3, TSHZ3, EP300, CTCF, TAF1, TSHZ2, RUNX1, MECOM, TBX3, SIN3A, WT1, EIF4A2, FOXA1, PHF6, CBF5, SOX9, ELF3, VEZF1, CE2PA, FOXA2
Histone modifier	Histone modifier	118	34	37	29	165	383	433.3381644	0.992537745	0.999999998	MLL3, MLL2, ARID1A, PBRM1, SETD2, NSD1, SETBP1, KDM5C, KDM6A, MLL4, ARID5B, ASXL1, EZH2
RTK signalling	RTK signalling	93	44	30	4	19	191	191.5013737	0.495231966	0.999999998	EGFR, FLT3, EPHA3, ERBB4, PDGFRA, EPHB6, FGFR2, KIT, FGFR3
MAPK signalling	MAPK signalling	51	5	12	18	18	104	130.1828191	0.989738738	0.999999998	KRAS, NF1, MAP3K1, BRAF, NRAS, MAP2K4, MAPK8IP1
Splicing	Splicing	18	2	3	4	4	31	35.11277542	0.723034372	0.999999998	SF3B1, U2AF1, PCBP1
HPPD signalling	HPPD signalling	6	1	1	1	1	10	16.71609572	0.943952406	0.999999998	CDH1, AJUBA
Protein phosphatase	Protein phosphatase	9	1	1	2	0	13	25.96039298	0.996082606	0.999999998	PPP2R1A, PTPN11
TOR signalling	TOR signalling	14	2	8	2	1	27	68.04981184	0.999999987	0.999999998	MTOR, STK11
Other	Other	106	44	41	16	44	251	356.319529	0.999999998	0.999999998	NAV3, NOTCH1, LRRK2, MALAT1, ARHGAP35, POLO, NCOR1, USP9X, NPM1, HGF, EPPK1, AR, LIFR, PRX, CRIPAK, EGR3, B4GALT3, MIR142

Supplementary Table 5.

gene_num	genes	weight	sig_level	aggregated_mutation_frequency
2	TP53,CTNNB1	1.61E+02	0.05	0.531429
3	TP53,CDKN2A,RPL22	1.59E+02	0.05	0.571429
4	TP53,CTNNB1,AXIN1,TNRC6B	1.69E+02	0	0.634286
5	TP53,IL6ST,CDKN2A,RPL22,CELF1	1.57E+02	0	0.608571
6	CTNNB1,AXIN1,HNF1A,BAP1,TNRC6B,PLEKHA5	1.73E+02	0	0.591429
7	TP53,ARID2,BAP1,VAV3,LAMA3,CDKN2A,BRD7	1.63E+02	0	0.611429
8	CTNNB1,AXIN1,HNF1A,TNRC6B,MACC1,HNF4A,CELF1,PLEKHA5	1.77E+02	0	0.605714
9	CTNNB1,AXIN1,HNF1A,TNRC6B,MACC1,HNF4A,DYRK1A,PLEKHA5,HNRNPA2B1	1.74E+02	0	0.62
10	CTNNB1,AXIN1,HNF1A,BAP1,PTEN,MACC1,PCF11,HNF4A,CELF1,KRAS	1.64E+02	0	0.648571
11	CTNNB1,AXIN1,HNF1A,IL6ST,PIK3CA,MACC1,PCF11,HNF4A,CELF1,KRAS,MORC3	1.61E+02	0	0.654286
12	CTNNB1,AXIN1,HNF1A,IL6ST,TNRC6B,MACC1,PCF11,HNF4A,BRD7,CELF1,PLEKHA5,MORC3	1.56E+02	0	0.651429
13	CTNNB1,TSC2,ACVR2A,HNF1A,IL6ST,KEAP1,PIK3CA,MACC1,HNF4A,CELF1,KRAS,MORC3,HNRNPA2B1	1.44E+02	0	0.714286
14	CTNNB1,AXIN1,HNF1A,IL6ST,TNRC6B,MACC1,PCF11,HNF4A,DYRK1A,CELF1,KRAS,PLEKHA5,MORC3,HNRNPA2B1	1.45E+02	0	0.668571
15	ARID2,TSC2,ACVR2A,IL6ST,KEAP1,PTEN,MACC1,LAMA3,SRAP,CDKN2A,DYRK1A,BRD7,CELF1,PLEKHA5,HNRNPA2B1	1.21E+02	0.23	0.637143
16	CTNNB1,AXIN1,IL6ST,TNRC6B,PTEN,MACC1,LAMA3,PCF11,HNF4A,PTPN3,BRD7,CELF1,KRAS,PLEKHA5,MORC3,HNRNPA2B1	1.25E+02	0.05	0.66

Supplementary Table 6.

sample	call status	purity	ploidy	Cancer DNA fraction	Subclonal genome fraction
TCGA-G3-A7M8-0	low purity	NA	NA	NA	NA
TCGA-UB-AA0V-0	low purity	NA	NA	NA	NA
TCGA-DD-A73C-0	called	0.66	2.02	0.66	0
TCGA-G3-A3CI-0	called	0.44	1.98	0.44	0
TCGA-DD-A3A6-0	low purity	NA	NA	NA	NA
TCGA-DD-A1ED-0	low purity	NA	NA	NA	NA
TCGA-2Y-A9GT-0	called	0.41	3.99	0.58	0.06
TCGA-ED-A627-0	low purity	NA	NA	NA	NA
TCGA-DD-AACX-0	called	0.91	4.01	0.95	0
TCGA-CC-A8HT-0	called	0.5	1.98	0.49	0
TCGA-BD-A2L6-0	called	0.61	4.13	0.76	0
TCGA-DD-A3A4-0	called	0.52	3.93	0.68	0.01
TCGA-K7-A5RF-0	high non-clonal	0.91	2	0.91	0.2
TCGA-G3-A7M7-0	called	0.62	2.12	0.64	0.02
TCGA-FV-A3R2-0	called	0.76	2.09	0.77	0
TCGA-DD-A39W-0	called	0.72	4.16	0.84	0
TCGA-DD-A3A2-0	called	0.39	2.1	0.4	0.11
TCGA-DD-AAEB-0	called	0.82	2.1	0.83	0
TCGA-DD-A3A1-0	called	0.68	2.11	0.7	0
TCGA-2Y-A9GV-0	called	0.71	1.95	0.7	0
TCGA-DD-A4NI-0	called	0.26	3.83	0.4	0
TCGA-EP-A26S-0	called	0.88	2.05	0.88	0
TCGA-G3-AAV3-0	called	0.8	4.01	0.89	0.08
TCGA-DD-A1EB-0	called	0.75	2.03	0.75	0
TCGA-WX-AA47-0	called	0.9	4.15	0.95	0.01
TCGA-2Y-A9H7-0	called	0.84	1.94	0.83	0
TCGA-DD-A1EC-0	called	0.73	4.23	0.85	0.05
TCGA-CC-A9FV-0	low purity	NA	NA	NA	NA
TCGA-2Y-A9GX-0	high non-clonal	0.74	2	0.74	0.24
TCGA-FV-A495-0	called	0.34	4.11	0.51	0
TCGA-DD-A4NB-0	called	0.3	3.74	0.44	0
TCGA-G3-A5SJ-0	called	0.73	2.08	0.74	0.04
TCGA-G3-A25V-0	low purity	NA	NA	NA	NA
TCGA-DD-A73A-0	called	0.65	2.05	0.65	0
TCGA-MI-A75H-0	called	0.65	2.1	0.66	0
TCGA-MI-A75E-0	called	0.52	4.04	0.68	0.07
TCGA-FV-A23B-0	called	0.82	1.98	0.81	0.02
TCGA-BC-4073-0	called	0.54	1.94	0.53	0
TCGA-CC-5262-0	called	0.57	3.96	0.72	0.04
TCGA-ED-A4XI-0	called	0.45	3.97	0.62	0.16
TCGA-CC-5260-0	called	0.27	4.62	0.46	0
TCGA-G3-AAV2-0	called	0.84	2.1	0.84	0.09
TCGA-XR-A8TD-0	called	0.45	2.02	0.45	0.01
TCGA-DD-AACM-0	called	0.66	2.07	0.66	0.04
TCGA-DD-AAW3-0	called	0.83	2.12	0.84	0.15
TCGA-LG-A9QD-0	called	0.56	2.14	0.58	0.02
TCGA-BC-A10X-0	low purity	NA	NA	NA	NA
TCGA-G3-A7M5-0	called	0.67	3.52	0.78	0.05
TCGA-HP-A5N0-0	called	0.64	2	0.64	0.06
TCGA-UB-A7MD-0	called	0.6	2.08	0.61	0.07
TCGA-ED-A8O5-0	called	0.88	1.98	0.87	0.02
TCGA-DD-AAW0-0	called	0.92	4.02	0.96	0.05
TCGA-DD-AAE7-0	called	0.62	2.01	0.62	0.07
TCGA-5R-AAAM-0	called	0.38	3.99	0.55	0
TCGA-DD-AAACH-0	called	0.65	4.01	0.79	0.02
TCGA-FV-A3R3-0	called	0.46	2.01	0.46	0.06
TCGA-DD-AAE4-0	called	0.22	3.87	0.35	0
TCGA-DD-AAEH-0	called	0.72	2.06	0.72	0.06
TCGA-GJ-A6C0-0	called	0.35	3.95	0.51	0
TCGA-BD-A3ER-0	called	0.48	2.09	0.49	0
TCGA-K7-AAU7-0	called	0.51	2.14	0.53	0.02
TCGA-RC-A7S9-0	called	0.27	4.4	0.45	0.13
TCGA-G3-A3CJ-0	called	0.68	2.17	0.69	0.07
TCGA-ES-A2HT-0	called	0.88	4.22	0.94	0
TCGA-BC-A10T-0	called	0.47	4.06	0.64	0.01
TCGA-G3-A3CH-0	called	0.48	3.86	0.64	0
TCGA-DD-AADK-0	called	0.7	3.94	0.82	0.05
TCGA-G3-AAV0-0	called	0.82	2.07	0.82	0.07
TCGA-EP-A12J-0	called	0.81	2.03	0.81	0.03
TCGA-DD-AAEI-0	called	0.75	2.11	0.76	0.04
TCGA-CC-A9FW-0	called	0.85	4.06	0.92	0.03
TCGA-G3-AAV5-0	called	0.81	2.29	0.83	0.06
TCGA-DD-A3A0-0	called	0.27	3.91	0.42	0
TCGA-DD-A11B-0	called	0.7	3.73	0.81	0.06
TCGA-DD-A4NH-0	called	0.54	3.89	0.69	0.04
TCGA-DD-AACL-0	called	0.3	3.84	0.45	0
TCGA-DD-A118-0	called	0.55	3.03	0.65	0.03
TCGA-DD-AAVP-0	called	0.85	2.01	0.85	0.08
TCGA-CC-A9FS-0	called	0.63	3.85	0.77	0.09
TCGA-BC-A216-0	called	0.25	4.22	0.41	0
TCGA-DD-A3A8-0	called	0.73	2.07	0.73	0.18
TCGA-DD-A11D-0	low purity	NA	NA	NA	NA
TCGA-DD-A1EK-0	called	0.31	3.79	0.47	0.01
TCGA-ED-A7PY-0	called	0.72	4	0.83	0.04
TCGA-DD-AAC9-0	called	0.56	2.11	0.57	0.08
TCGA-DD-AACT-0	called	0.56	2.37	0.6	0.09
TCGA-DD-AADA-0	called	0.51	4.11	0.68	0.01
TCGA-MI-A75C-0	called	0.67	2.19	0.69	0.11
TCGA-CC-5261-0	called	0.51	4.19	0.68	0
TCGA-WX-AA46-0	low purity	NA	NA	NA	NA
TCGA-DD-AACK-0	called	0.63	4.03	0.77	0.02
TCGA-RC-A7SB-0	called	0.67	3.67	0.79	0.08
TCGA-ZP-A9CV-0	called	0.65	2.06	0.65	0.07



TCGA-DD-A4NK-0 called	0.89	2.2	0.9	0.06
TCGA-DD-AADP-0 called	0.62	3.79	0.76	0.06
TCGA-DD-AADY-0 called	0.92	3.48	0.95	0.09
TCGA-DD-A4NF-0 called	0.77	2.1	0.78	0.06
TCGA-DD-AACF-0 called	0.86	2.16	0.87	0.05
TCGA-DD-AAEG-0 called	0.33	4.51	0.52	0
TCGA-DD-A4NL-0 low purity	NA	NA	NA	NA
TCGA-WX-AA44-0 called	0.29	4.14	0.46	0
TCGA-DD-A4NP-0 called	0.79	2.03	0.79	0.03
TCGA-DD-AAC8-0 called	0.81	3.08	0.87	0.05
TCGA-G3-A25W-0 called	0.71	4.24	0.84	0
TCGA-3K-AAZ8-01 called	0.67	3.64	0.79	0.1
TCGA-DD-AAD0-0 called	0.95	2.01	0.95	0.01
TCGA-DD-AAW1-0 called	0.74	2.09	0.75	0.14
TCGA-CC-A5UD-0 called	0.8	2.65	0.85	0.07
TCGA-BC-A69I-01 called	0.81	2.03	0.81	0.03
TCGA-G3-A6UC-0 called	0.88	2.14	0.88	0.08
TCGA-ZS-A9CG-0 called	0.75	2.11	0.76	0.16
TCGA-DD-A39V-01 called	0.65	2.31	0.68	0.07
TCGA-DD-AACQ-0 called	0.93	3.94	0.96	0.01
TCGA-DD-A4NR-0 called	0.35	2.18	0.37	0.06
TCGA-T1-A6J8-01 called	0.64	3.45	0.75	0.2
TCGA-FV-A4ZQ-01 called	0.74	3.38	0.83	0.06
TCGA-G3-AAUZ-0 called	0.37	4.25	0.55	0.01
TCGA-ZP-A9D0-01 called	0.71	1.94	0.71	0.09
TCGA-KR-A7K7-01 called	0.58	2.78	0.66	0.09
TCGA-FV-A2QQ-0 called	0.26	3.82	0.4	0
TCGA-DD-A4ND-0 called	0.65	4.15	0.79	0.04
TCGA-ZP-A9CY-01 called	0.72	2.01	0.72	0.03
TCGA-DD-A3A9-01 called	0.79	4.96	0.9	0.01
TCGA-WJ-A86L-01 called	0.4	4.1	0.58	0.01
TCGA-FV-A2QR-0 called	0.8	2.02	0.81	0.1
TCGA-DD-AAE3-0 called	0.63	4.5	0.79	0.07
TCGA-DD-A73D-0 called	0.82	4.73	0.91	0.08
TCGA-ZP-A9CZ-01 called	0.64	1.97	0.64	0.09
TCGA-BC-A10Z-01 called	0.35	5.11	0.58	0.03
TCGA-DD-AAVR-0 called	0.49	2.13	0.51	0.02
TCGA-DD-A4NS-0 low purity	NA	NA	NA	NA
TCGA-DD-AADU-0 called	0.67	2.57	0.73	0.08
TCGA-2Y-A9H8-01 called	0.83	4.11	0.91	0.04
TCGA-EP-A3RK-0 called	0.41	1.92	0.4	0.03
TCGA-DD-AAVU-0 called	0.92	3.41	0.95	0.1
TCGA-ZS-A9CD-01 called	0.86	4.18	0.93	0.11
TCGA-ED-A66X-01 called	0.31	3.39	0.43	0.15
TCGA-DD-A73B-01 called	0.74	3.54	0.84	0.07
TCGA-DD-A1EE-0 high non-clonal	0.7	2.15	0.71	0.26
TCGA-G3-A5SL-01 high non-clonal	0.78	2.26	0.8	0.35
TCGA-DD-AAD2-0 called	0.57	4.28	0.74	0.01
TCGA-5C-AAPD-0 called	0.39	3.63	0.54	0.1
TCGA-2Y-A9H0-01 called	0.43	4.13	0.61	0.02
TCGA-G3-A5SI-01 called	0.98	4.02	0.99	0.17
TCGA-DD-AADS-0 called	0.51	4.17	0.68	0.04
TCGA-DD-AAE9-0 called	0.66	2.39	0.7	0.16
TCGA-DD-AAD3-0 called	0.66	1.94	0.66	0.11
TCGA-ED-A5KG-0 low purity	NA	NA	NA	NA
TCGA-RC-A6M4-0 called	0.79	3.77	0.88	0.11
TCGA-MR-A520-01 low purity	NA	NA	NA	NA
TCGA-HP-A5MZ-0 called	0.75	2.1	0.76	0.11
TCGA-DD-AADB-0 called	0.34	7.1	0.65	0
TCGA-QA-A7B7-01 called	0.79	1.86	0.78	0.05
TCGA-ED-A7XO-0 called	0.26	3.89	0.4	0
TCGA-UB-A7MF-0 high non-clonal	0.56	3.7	0.71	0.28
TCGA-DD-AADJ-0 called	0.78	3.89	0.87	0.01
TCGA-BC-A5W4-0 called	0.93	3.6	0.96	0.09
TCGA-2Y-A9H4-01 called	0.79	3.9	0.88	0.04
TCGA-DD-A4NV-0 called	0.52	2.44	0.57	0.15
TCGA-DD-A1E9-01 called	0.31	4.29	0.49	0
TCGA-XR-A8TE-01 called	0.7	2.21	0.72	0.08
TCGA-UB-A7MA-0 called	0.66	4.27	0.8	0.05
TCGA-O8-A75V-01 called	0.49	2.37	0.53	0.1
TCGA-DD-AACN-0 called	0.59	3.84	0.73	0.17
TCGA-2Y-A9H6-01 called	0.48	3.81	0.64	0.03
TCGA-DD-AAAC-0 called	0.51	4	0.67	0.08
TCGA-DD-AAVQ-0 called	0.36	3.75	0.51	0.05
TCGA-BW-A5NQ-0 high non-clonal	0.76	3.55	0.85	0.29
TCGA-LG-A9QC-0 called	0.78	1.93	0.77	0.01
TCGA-DD-AACA-0 called	0.89	4.08	0.94	0.03
TCGA-DD-AACV-0 called	1	3.76	1	0.15
TCGA-2Y-A9GZ-01 called	0.87	3.39	0.92	0.06
TCGA-DD-A39Z-01 called	0.76	2.08	0.77	0.15
TCGA-DD-A1EA-0 called	0.71	2.14	0.72	0.14
TCGA-DD-AAEA-0 called	0.53	4.22	0.7	0.03
TCGA-DD-AADG-0 called	0.83	4.18	0.91	0.1
TCGA-WQ-A9G7-0 called	0.4	3.4	0.53	0.01
TCGA-BC-A10W-0 called	0.56	4.38	0.74	0.02
TCGA-LG-A6GG-0 called	0.71	2.43	0.75	0.09
TCGA-RC-A6M5-0 called	0.22	3.59	0.34	0.08
TCGA-BC-A8Y0-0 called	0.4	3.83	0.56	0.03
TCGA-KR-A7K0-01 called	0.56	2.03	0.57	0.06
TCGA-DD-A4NQ-0 called	0.29	6.28	0.56	0
TCGA-DD-AAVZ-0 called	0.75	1.98	0.75	0.08
TCGA-BC-A110-01 low purity	NA	NA	NA	NA
TCGA-DD-A11C-0 called	0.24	3.9	0.39	0.01
TCGA-DD-AAVX-0 called	0.75	2.13	0.76	0.01
TCGA-DD-AAVY-0 called	0.99	2.23	0.99	0.04

TCGA-NI-A4U2-01/called	0.68	1.99	0.68	0.03
TCGA-PD-A5DF-01/called	0.74	1.99	0.73	0.08
TCGA-G3-A3CK-01/called	0.53	2.08	0.54	0.04
TCGA-ES-A2HS-01/called	0.46	3.46	0.6	0.05
TCGA-DD-A73E-01high non-clonal	0.77	2.06	0.78	0.29
TCGA-4R-AA8I-01/called	0.84	1.93	0.83	0.04
TCGA-2V-A95S-01 called	0.45	2.23	0.48	0.04
TCGA-XR-A8TF-01 called	0.84	3.11	0.89	0.05
TCGA-DD-A3A5-01called	0.82	2.01	0.82	0.09
TCGA-DD-AACW-Ccalled	0.92	1.93	0.91	0.03
TCGA-ZS-A9CF-01 called	0.89	3.86	0.94	0.05
TCGA-DD-AADE-0 called	0.62	4.14	0.77	0.04
TCGA-DD-AAD1-0 called	0.27	4.24	0.43	0
TCGA-DD-AAEK-0 called	0.45	3.18	0.56	0.2
TCGA-ED-A459-01high non-clonal	0.5	3.58	0.65	0.3
TCGA-DD-A73F-01 called	0.26	3.78	0.4	0
TCGA-DD-AA3A-0' called	0.76	2.06	0.77	0.12
TCGA-ZP-A9D4-01 called	0.41	4.22	0.59	0.03
TCGA-G3-A25U-01 called	0.84	3.97	0.91	0.19
TCGA-5R-AA1D-01low purity	NA	NA	NA	NA
TCGA-2Y-A9HB-01called	0.44	4.23	0.62	0.15
TCGA-BC-A10Q-0' called	0.65	4.16	0.8	0.02
TCGA-BC-A10U-01 called	0.82	2.08	0.82	0.14
TCGA-DD-AAE1-0' called	0.84	2.03	0.85	0.14
TCGA-UB-A7MC-0 called	0.85	2.95	0.89	0.04
TCGA-CC-A7IK-01.called	0.64	6.11	0.85	0.03
TCGA-DD-AAVS-0 called	0.8	2.03	0.81	0.07
TCGA-DD-A73G-0' called	0.26	5	0.46	0
TCGA-DD-A116-01 called	0.71	1.91	0.7	0.16
TCGA-DD-AAD8-0' called	0.95	3.53	0.97	0.13
TCGA-DD-AAE2-0' called	0.24	3.38	0.35	0
TCGA-G3-A25Z-01 called	0.63	4.03	0.77	0.07
TCGA-WQ-AB4B-0 called	0.5	3.87	0.66	0.14
TCGA-DD-AAID-01high non-clonal	0.62	3.88	0.76	0.22
TCGA-DD-AAW2-0called	0.89	2.28	0.9	0.05
TCGA-GJ-A9DB-01high non-clonal	0.73	1.99	0.73	0.23
TCGA-DD-AADM-0called	0.37	4.42	0.56	0.02
TCGA-2Y-A9H9-01 called	0.28	4.29	0.45	0.01
TCGA-BC-A10S-01called	0.54	4.02	0.71	0.05
TCGA-BC-A10R-01called	0.54	3.24	0.66	0.02
TCGA-CC-5258-01 called	0.46	3.8	0.62	0.05
TCGA-ED-A7PX-0' called	0.49	3.47	0.63	0.06
TCGA-ZP-A9D2-01 called	0.56	3.81	0.71	0.06
TCGA-CC-5263-01 called	0.23	3.83	0.37	0
TCGA-DD-AAE6-0' called	1	4.18	1	0.09
TCGA-DD-AAVW-Ccalled	0.43	3.99	0.6	0.04
TCGA-DD-AADD-0 called	0.45	5.39	0.68	0.01
TCGA-CC-A3MB-0 called	0.91	4.04	0.95	0.18
TCGA-EP-A2KA-01called	0.53	2.33	0.57	0.08
TCGA-2Y-A9HA-01called	0.35	4.06	0.52	0.06
TCGA-BC-4072-01 called	0.59	2.18	0.61	0.11
TCGA-DD-AADQ-0 called	0.72	4.28	0.84	0.05
TCGA-CC-A7IL-01high non-clonal	0.88	2.96	0.91	0.31
TCGA-CC-A3MA-0 called	0.75	1.91	0.74	0.12
TCGA-DD-AACS-0 called	0.84	3.97	0.91	0.13
TCGA-DD-AACD-0 called	0.71	2.19	0.72	0.17
TCGA-G3-A3CG-0 high non-clonal	0.4	4.67	0.61	0.24
TCGA-KR-A7K2-01called	0.71	3.8	0.83	0.16
TCGA-CC-A5UE-0 high non-clonal	0.94	3.85	0.97	0.73
TCGA-2Y-A9H1-01 called	0.66	2.27	0.69	0.1
TCGA-DD-AADF-0 called	1	3.25	1	0.13
TCGA-CC-A8HV-0 called	0.51	6.71	0.78	0.01
TCGA-DD-A39Y-01called	0.83	3.71	0.9	0.17
TCGA-BC-A112-01 called	0.56	3.72	0.71	0.09
TCGA-ED-A7XP-0' called	0.53	4.06	0.7	0.1
TCGA-DD-AADW-C high non-clonal	0.76	3.9	0.86	0.38
TCGA-EP-A2KB-01high non-clonal	0.55	4.04	0.71	0.23
TCGA-CC-A7IE-01.called	0.54	4.51	0.72	0.15
TCGA-K7-A6G5-01 called	0.59	2.11	0.6	0.1
TCGA-DD-A115-01 called	0.23	3.51	0.34	0.03
TCGA-2Y-A9H5-01 called	0.56	3.87	0.71	0.08
TCGA-RC-A7SH-0 high non-clonal	0.88	1.87	0.88	0.37
TCGA-DD-A3A7-01called	0.34	5.33	0.58	0.01
TCGA-RC-A7SF-01 called	0.74	2.13	0.75	0.19
TCGA-DD-AACE-0 called	1	3.92	1	0.13
TCGA-DD-A119-01high non-clonal	0.25	4.7	0.44	0.3
TCGA-DD-AACY-0 called	0.75	2.15	0.76	0.12
TCGA-DD-AACI-01 called	0.24	5.33	0.45	0.05
TCGA-G3-A25T-01 called	0.45	3.2	0.56	0.17
TCGA-K7-A5RG-0' called	0.37	3.76	0.52	0.02
TCGA-BC-A3KG-0 called	0.27	3.82	0.41	0.02
TCGA-G3-A25Y-01 called	0.52	3.8	0.68	0.15
TCGA-DD-AAD6-0 called	0.77	4.11	0.87	0.08
TCGA-RC-A6M6-0 called	0.66	2.03	0.66	0.1
TCGA-YA-A8S7-01high non-clonal	0.37	3.71	0.52	0.35
TCGA-FV-A310-01/called	0.48	3.64	0.62	0.2
TCGA-5C-A9VH-01high non-clonal	0.76	2.06	0.77	0.24
TCGA-MI-A75I-01Acalled	0.62	2.01	0.62	0.1
TCGA-DD-A4NQ-0 called	0.71	4.01	0.83	0.19
TCGA-DD-AADC-0 called	0.57	3.96	0.72	0.06
TCGA-DD-AADO-0 called	0.58	3.84	0.73	0.05
TCGA-MI-A75G-01 called	0.3	4.28	0.48	0.01
TCGA-EP-A3JL-01 called	0.25	2.92	0.33	0.01
TCGA-ED-A97K-01called	0.53	4.38	0.71	0.18
TCGA-CC-A7IF-01.called	0.72	3.93	0.84	0.18

TCGA-2Y-A9GS-01called	0.36	4.15	0.54	0.12
TCGA-DD-AACG-0called	0.71	3.82	0.83	0.07
TCGA-CC-A7IH-01 called	0.43	4.59	0.64	0.08
TCGA-CC-A7IJ-01called	0.32	5.15	0.54	0.01
TCGA-G3-AAV4-01called	0.83	3.74	0.9	0.09
TCGA-UB-AA0U-0 called	0.63	4.25	0.78	0.1
TCGA-G3-A7M6-0 called	0.57	4.29	0.74	0.05
TCGA-BC-A3KF-01called	0.53	3.85	0.68	0.08
TCGA-ZS-A9CE-01called	0.74	3.76	0.84	0.08
TCGA-DD-A1EI-01.high non-clonal	0.31	3.68	0.45	0.32
TCGA-2Y-A9GU-0 called	0.77	4.11	0.87	0.15
TCGA-BC-A10Y-01called	0.39	3.98	0.56	0.04
TCGA-RC-A7SK-0 called	0.59	3.7	0.73	0.12
TCGA-ED-A82E-01called	0.7	3.27	0.79	0.09
TCGA-ZP-A9D1-01called	0.65	3.96	0.78	0.06
TCGA-DD-AADL-0 called	0.27	6.24	0.53	0
TCGA-2Y-A9H3-01high non-clonal	0.38	3.97	0.55	0.21
TCGA-NI-A8LF-01called	0.29	4.73	0.49	0.01
TCGA-DD-AACJ-0 called	0.91	4.71	0.96	0.16
TCGA-KR-A7K8-01called	0.27	5.34	0.49	0.01
TCGA-DD-AACP-0 called	0.8	2.89	0.86	0.12
TCGA-XR-A8TG-0 called	0.23	4.2	0.38	0.01
TCGA-RC-A6M3-0 called	0.56	4.13	0.73	0.09
TCGA-DD-AAVV-0 called	0.36	3.5	0.5	0.19
TCGA-DD-A3A3-01called	0.58	4.56	0.76	0.06
TCGA-5R-AA1C-01called	0.87	2.28	0.88	0.07
TCGA-DD-AAE0-0 called	0.7	3.19	0.79	0.19
TCGA-CC-A3MC-0called	0.42	3.88	0.59	0.05
TCGA-G3-AAV6-01high non-clonal	0.76	4.11	0.86	0.23
TCGA-DD-AACZ-0 called	0.66	9.27	0.9	0.03
TCGA-G3-AAV1-01high non-clonal	0.79	3.7	0.88	0.22
TCGA-DD-AAED-0 called	0.88	3.7	0.93	0.11
TCGA-ED-A66Y-01called	0.81	3.52	0.88	0.15
TCGA-DD-AAE8-0 high non-clonal	0.91	3.87	0.95	0.3
TCGA-CC-A9FU-0 high non-clonal	0.84	3.44	0.9	0.21
TCGA-G3-A5SM-0 called	0.51	4.19	0.68	0.11
TCGA-GJ-A3OU-0 called	0.43	4.01	0.6	0.1
TCGA-2Y-A9H2-01 called	0.52	4.09	0.69	0.17
TCGA-DD-AADN-0 called	0.27	4.53	0.45	0.05
TCGA-CC-A1HT-0 called	0.47	3.93	0.63	0.11
TCGA-DD-A39X-01called	0.34	3.74	0.49	0.19
TCGA-BW-A5NO-0called	0.36	5.63	0.61	0.02
TCGA-5C-A9VG-0 called	0.5	4.75	0.71	0.08
TCGA-BC-A69H-01high non-clonal	0.68	4.07	0.81	0.29
TCGA-BC-A217-01 called	0.26	5.25	0.48	0.05
TCGA-FV-A496-01.called	0.84	3.6	0.9	0.09
TCGA-DD-AACB-0 high non-clonal	0.92	4.38	0.96	0.24
TCGA-DD-A4NA-0 called	0.64	3.68	0.77	0.18
TCGA-BD-A3EP-0 called	0.37	4.31	0.56	0.03
TCGA-DD-A1EJ-01called	0.34	4.6	0.54	0.02
TCGA-CC-5264-01 high non-clonal	0.84	3.19	0.9	0.46
TCGA-2Y-A9GW-0 called	0.44	4.74	0.65	0.06
TCGA-G3-AAV7-01high non-clonal	0.96	2.72	0.97	0.2
TCGA-CC-A7II-01Acalled	0.36	7.99	0.69	0.03
TCGA-DD-AAEE-0 called	0.74	3.92	0.85	0.12
TCGA-ED-A8O6-0 called	0.57	3.98	0.73	0.1
TCGA-FV-A311-01Acalled	0.5	3.88	0.66	0.1
TCGA-DD-AACU-0 called	0.67	3.27	0.77	0.09
TCGA-CC-A8HU-0 high non-clonal	0.78	4.31	0.89	0.23
TCGA-CC-A3M9-0 called	0.21	4.98	0.4	0
TCGA-BW-A5NP-0 high non-clonal	0.95	3.46	0.97	0.42
TCGA-UB-A7MB-0 called	0.41	3.66	0.56	0.08
TCGA-G3-A25S-01called	0.59	3.62	0.72	0.19
TCGA-DD-A4NJ-01called	0.5	3.84	0.66	0.12
TCGA-FV-A4ZP-01called	0.65	4.08	0.79	0.15
TCGA-DD-A1EL-01high non-clonal	0.65	3.74	0.78	0.41
TCGA-DD-A114-01called	0.45	3.84	0.61	0.08
TCGA-CC-A5UC-0 called	0.36	4.19	0.54	0.13
TCGA-DD-AACO-0called	0.75	3.85	0.85	0.18
TCGA-DD-A11A-01called	0.31	7.61	0.63	0.02
TCGA-DD-A4NN-0 called	0.84	2.04	0.84	0.18
TCGA-G3-A7M9-0 called	0.41	9.33	0.76	0.01
TCGA-CC-A7IG-01 called	0.38	4.62	0.59	0.06
TCGA-ED-A7PZ-01high non-clonal	0.73	3.84	0.84	0.24
TCGA-DD-A1EH-0 high non-clonal	0.85	1.99	0.85	0.35
TCGA-DD-A1EG-0 called	0.38	4.08	0.56	0.12
TCGA-UB-A7ME-0 called	0.45	3.44	0.58	0.1
TCGA-DD-A113-01high non-clonal	0.6	3.92	0.75	0.21
TCGA-G3-A25X-01high non-clonal	0.61	2.97	0.7	0.41
TCGA-DD-A1EF-01called	0.22	4.95	0.41	0
TCGA-RG-A7D4-0 high non-clonal	0.48	3.95	0.64	0.22
TCGA-DD-AAD5-0 high non-clonal	0.6	3.99	0.75	0.21
TCGA-DD-AADV-0 called	0.28	7.6	0.6	0
TCGA-EP-A2KC-0 high non-clonal	0.65	2.25	0.68	0.36
TCGA-2Y-A9GY-01high non-clonal	0.6	3.32	0.71	0.28
TCGA-MR-A8JO-0 high non-clonal	0.76	2.03	0.76	0.42
TCGA-DD-AADR-0 high non-clonal	0.62	3.97	0.76	0.42