

Supplement Table (1): Concentration and purity for extracted DNA from tissue samples L=Non-HCC, T=HCC using Qubit and Nanodrop

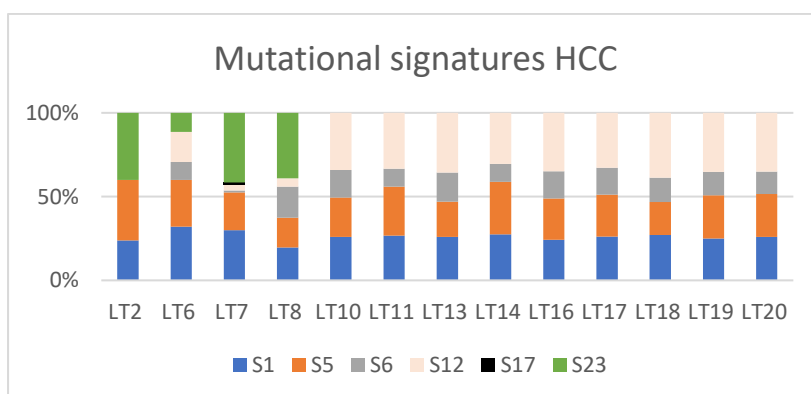
Sample ID (Extracted DNA)	Sample Type	Concentration (ng/uL) Qubit	Purity NanoDrop
LT2 117T HCC	FFPE	33.8	2.09
LT2 117L Non-HCC	FFPE	69.8	1.93
LT6 1807 T HCC	FFPE	116	2.03
LT6 1807 L Non-HCC	FFPE	120	2.07
LT7 1617 T HCC	FFPE	21	2.2
LT7 1617 L Non-HCC	FFPE	26	1.98
LT8 2158T HCC	FFPE	47.4	2
LT8 2158L Non-HCC	FFPE	52.2	2
LT9 HCC HBV	Fresh Tissue	55.8	1.91
LT9 Non HCC HBV	Fresh Tissue	35.5	1.9
LT10 HCC	Fresh Tissue	75.2	1.75
LT10 Non HCC	Fresh Tissue	49.8	1.72
LT11 Budd-Chiari HCC	Fresh Tissue	72.4	1.77
LT11 Budd-Chiari Non HCC	Fresh Tissue	42.4	1.9
LT12 HCC	Fresh Tissue	11.3	1.7
LT12 Non HCC	Fresh Tissue	26.4	1.89
LT13 HCC HBV	Fresh Tissue	32.6	1.6
LT13 NonHCC HBV	Fresh Tissue	35	1.5
LT14 HCC	Fresh Tissue	68.2	1.91
LT14 Non HCC	Fresh Tissue	52	1.8
LT15 HCC	Fresh Tissue	0.23*	1.66
LT15 Non HCC	Fresh Tissue	100	1.8
LT16 HCC	Fresh Tissue	95.2	1.99
LT16 Non HCC	Fresh Tissue	56	2.1
LT17 HCC	Fresh Tissue	80.2	2
LT17 Non HCC	Fresh Tissue	28.8	1.94
LT18 HCC	Fresh Tissue	22.8	2.1
LT18 Non HCC	Fresh Tissue	14.8	1.9
LT19 HCC	Fresh Tissue	100.4	2.0
LT19 Non HCC	Fresh Tissue	56.4	1.87
LT20 HCC	Fresh Tissue	127.6	1.89
LT20 Non HCC	Fresh Tissue	74.4	1.95

Supplement Table (2): Variants number with pathogenic, synonymous, and intron variants in HCC samples

	HCC	Variants no	Missense	frameshift truncation	Stop-gained	splice site	Synonymous	Other
1	LT2	187	61	3	7	1	53	62
2	LT6	9328	2195	169	98	34	2276	4556
3	LT7	17884	4816	193	281	103	4432	8059
4	LT8	3007	989	71	47	9	867	1024
5	LT10	28788	4091	507	43	66	4970	19111
6	LT11	44275	6863	689	63	80	7809	28771
7	LT13	34846	5624	1972	59	35	6797	20359
8	LT14	37328	5400	919	67	97	6251	24594
9	LT16	37467	6138	766	63	65	7200	23235
10	LT17	27847	4564	723	39	48	5562	16911
11	LT18	12352	2086	211	13	25	2401	7616
12	LT19	32876	5612	495	74	70	6263	20362
13	LT20	32910	5349	560	57	52	6159	20733

Supplement Table (3): Percentage of pathogenic variants in HCC samples FFPE and fresh tissue

Sample/% of variants		Missense %	frameshift %	Stop-gained %	Splice site %	Synonymous %	Other %
FFPE	Median	29.8	1.7	1.6	0.4	26.6	39.6
	Q1	26.1	1.5	1.4	0.3	24.7	33.8
	Q3	32.7	1.9	2.1	0.5	28.5	46.0
Fresh Tissue	Median	29.8	1.7	1.6	0.4	26.6	39.6
	Q1	27.9	1.6	1.5	0.4	25.6	36.7
	Q3	31.2	1.8	1.8	0.5	27.5	42.8



Supplement Figure (1): Mutational signatures % in HCC samples

Supplement Table (4) : Percentage of mutational signatures in HCC samples

Samples	S1	S5	S6	S12	S17	S23
LT2 HCC	23.9%	36.1%				40%
LT6 HCC	25.7%	22.2%	8.6%	14.4		9.1%
LT7 HCC	30%	22.5%	1.1%	3.4%	1.4%	41.5%
LT8 HCC	19.7%	17.8%	18.5%	4.9%		39.1%
LT10 HCC	26%	23.4%	16.5%	34.1%		
LT11 HCC	26.6%	29.2%	10.7%	33.4%		
LT13 HCC	26%	20.9%	17.4%	35.6%		
LT14 HCC	27.4%	31.5%	10.7%	30.4%		
LT16 HCC	24.3%	24.5%	16.3%	34.9%		
LT17 HCC	26.1%	25.2%	15.9%	32.9%		
LT18 HCC	27.2%	19.7%	14.5%	38.7%		
LT19 HCC	24.9%	25.9%	14%	35.2%		
LT20 HCC	26%	25.5%	13.4%	35.1%		
Median	26%	24.5%	14.2%	34.5%	1.4%	39.5%
1 st quartile	24.9	22.2	10.7	32.3		31.6
3 rd quartile	0.266	0.259	16.3	35.3		40.4

Supplement Table (5): Pathogenic variants in highly mutated genes in HCC

High mutated	complex_substitution	frameshift_truncation	missense	splice_site	stop_gained	Grand Total
AHNAK2	31	6	131			168
MUC6	25	1	91		1	118
MUC16	1	10	95			106
TTN	4	22	72	2		100
ZNF717	12	4	71		3	90
FLG	10	2	77			89
MUC12	3	2	80		1	86
OBSCN	2	4	55	1	1	63
PDE4DIP	1	7	45		5	58
MUC5B	3	8	46			57
HYDIN	1	4	38	1	1	45
Total	93	70	801	4	12	980

Supplement Table (6): Pathogenic variants in highly mutated genes in Non-HCC

Genes Non-HCC	complex_substitution	frameshift_truncation	missense	stop_gained	Grand Total
AHNAK2	23	2	114	1	140
MUC6	28	1	94		123
MUC16	4	3	97		104
FLG	11		72		83
MUC12	3	3	65	1	72
ZNF717	13	2	56	1	72
MUC17	7	1	54		62
OBSCN	2	4	51		57
PDE4DIP	1	4	39	6	50
TTN	1	10	35		46
Grand Total	93	30	677	9	809

Supplement Table (7): Unique Pathogenic mutations in oncogenes and tumor suppressor genes in HCC samples.

Row Labels	Oncogene	TSG	Grand Total	
Frameshift_truncation	31	49	80	37%
Missense	48	84	132	60%
Splice_site_variant		1	1	0.3%
Stop_gained	2	4	6	2.7%
Grand Total	81	138	219	
	37%	63%		

Supplement Table (8): Unique pathogenic variants medium to high confidence (Franklin), missense sorted according to CHASMPplus LIHC (Hepatocellular carcinoma) score in HCC samples, with Tier 1&2 genes & variants shown in red.

Chr	Pos	Ref	Alt	Gene	Sequence_ontology	cDNA	Protein	Sample	Class/ACMG category	CHASMPplus Score	CHASMPplus LIHC Score	Target Recommended_Therapy	Phred	Zygotity /VAF
chr17	7578508	C	T	TP53	missense	c.422G>A	p.Cys141Tyr	LT19	TSG/ Tier 1	0.78	0.716	Weel inhibitors, Chk1 inhibitors, kevetrin, APR-246, nutlins, gene therapy/	101.81	het/22.95%
chr5	112176756	T	A	APC	missense	c.5465T>A	p.Val1822Asp	LT16	TSG/ Tier 3	0.489	0.378	WNT inhibitors	1099.3	het/
chr9	21974732	A	T	CDKN2A	missense	c.95T>A	p.Leu32Gln	LT14	TSG/ Tier 1	0.551	0.37	CDK4/6 inhibitors	25.12	het/7.14%
chr17	41222975	C	T	BRCA1	missense	c.4956G>A	p.Met1652Ile	LT13	TSG/ Tier 3	0.432	0.111	PARP Inhibitor	345.35	het
chr12	49446736	G	C	KMT2D	missense	c.1074C>G	p.Ile358Met	LT13	TSG/ Tier 3	0.222	0.107		1100.7	het
chr17	41244524	C	T	BRCA1	missense	c.3024G>A	p.Met1008Ile	LT20	TSG/ Tier 3	0.391	0.095	PARP Inhibitor	417.04	het
chr11	108143456	C	G	ATM	missense	c.3161C>G	p.Pro1054Arg	LT16	TSG/ Tier 3	0.277	0.093	PARP Inhibitors	252.03	het
chr12	49445173	C	G	KMT2D	missense	c.2293G>C	p.Ala765Pro	LT6	TSG/ Tier 3	0.166	0.084		190.62	het
chr18	42529996	G	C	SETBP1	missense	c.691G>C	p.Val231Leu	LT17	Oncogene/Tier 3	0.085	0.061		805.6	het
chr6	138202173	G	A	TNFAIP3	missense	c.2090G>A	p.Arg697Lys	LT14	TSG/Tier 3	0.119	0.058		427.33	het
chr4	55139771	T	C	PDGFR A	missense	c.1432T>C	p.Ser478Pro	LT11	Oncogene/Tier 3	0.044	0.052	Imatininb	1653.6	het
chr9	98278940	C	G	PTCH1	missense	c.163G>C	p.Asp55His	LT17	TSG/ Tier 3	0.12	0.051	Vismodegib, hedgehog inhibitors	1045.1	hom
chr21	36164866	G	A	RUNX1	missense	c.1009C>T	p.Pro337Ser	LT8	TSG/Tier 3	0.268	0.031		35.98	het
chr2	29416757	A	G	ALK	missense	c.4196T>C	p.Ile1399Thr	LT14	Oncogene/Tier 3	0.083	0.03	Crizotinib, ALK inhibitor	1047.1	het
chr4	55604655	G	T	KIT	missense	c.2863G>T	p.Val1955Leu	LT20	Oncogene/Tier 3	0.072	0.03	Imatinib, Sunitinib, Novel	331.09	het

												KIT Inhibitor s		
chr10 8100506	C	G	GATA3	missense	c.480C>Gg	p.Asp160Glu	LT10	TSG/Tier 3	0.082	0.03			708. 35	het
chr11 64575505	C	T	MEN1	missense	c.512G>A	p.Arg171Gln	LT17	TSG/Tier 4	0.094	0.029			406. 55	het
chr13 28608473	C	T	FLT3	missense	c.1669G>A	p.Val557Ile	LT17	Oncogene/ Tier 4	0.061	0.026	Sunitinib , FLT3 inhibitor s		319. 57	het
chr7 151859683	G	A	KMT2C	missense	c.10979C>T	p.Ser3660Leu	LT17	TSG/Tier 4	0.169	0.025			364. 98	het
chr7 128843411	G	A	SMO	missense	c.518G>A	p.Arg173His	LT17	Oncogene/Ti er3	0.034	0.024	Vismodegi b, hedgehog inhibitor s		869. 81	het
chr4 106155751	G	A	TET2	missense	c.715G>A	p.Val239Met	LT13	TSG/Tier3	0.073	0.012			1058 .8	het
chr4 106196951	A	G	TET2	missense	c.5347A>G	p.Ile1783Val	LT18	TSG/Tier3	0.06	0.012			603. 05	het
chr4 106197000	A	G	TET2	missense	c.5396A>G	p.His1799Arg	LT19	TSG/Tier3	0.054	0.011			312. 12	het
chr3 138665029	G	C	FOXL2	missense	c.536C>G	p.Ala179Gly	LT11	Oncogene/ Tier4	0.02	0.003			314. 8	het
chr2 16082320	CG	-	MYCN	frameshif t	c.134_135del	p.Pro45ArgfsTer9	LT11	Oncogene/ Tier 3					53.2 23	het
chr2 47630385	T	-	MSH2	frameshif t	c.56del	p.Phe19SerfsTer4 5	LT13	TSG /Tier 2					37.5 58	het/18.1 8%
chr9 37020775	C	-	PAX5	frameshif t	c.76del	p.Val26PhefsTer3	LT13	TSG /Tier 3					50.7 09	het
chr16 3778897	GC	-	CREBB P	frameshif t	c.6150_6151del	p.Arg2052AspfsTe r288	LT13	TSG/ Tier 3					251. 17	het
chr16 68856088	CG	T	CDH1	frameshif t	c.1896_1897del insT	p.Ala634ArgfsTer 19	LT13	TSG/Tier 3					801. 03	het
chr2 48033792	TAA C	-	MSH6	splice_si te	c.4001+12_4001+15del		LT19	TSG /Tier 4					973. 56	het

Supplement Table (9): Unique pathogenic variants sorted with medium to high confidence (Franklin), missense sorted according to CHASMplus LIHC (Hepatocellular carcinoma) score in Non-HCC samples

Chro	Pos	Ref	Alt	Gene	Sequence_Ontology	cDNA_change	Protein_Change	Sample	Class/ACMG category	CHASM plus Score	LIHC Score	Recommended_Therapy	Phred	Zygotity
chr12	121416864	C	T	HNF1A	missense	c.293C>T	p.Ala98Val	LT19N	TSG/ Tier3	0.149	0.324		435.99	het
chr17	29653218	T	C	NF1	missense	c.5216T>C	p.Val1739Ala	LT14N	TSG/ Tier3	0.562	0.275	PI3K/AKT/MTOR inhibitors, RAF inhibitors, MEK inhibitors	379.39	het
chr22	41573602	G	T	EP300	missense	c.5887G>T	p.Ala1963Ser	LT10N	TSG/ Tier3	0.44	0.184		428.47	het
chr2	25467077	C	A	DNMT3A	missense	c.1798G>T	p.Asp600Tyr	LT13N	Oncogene/ Tier3	0.505	0.159	DNAMT inhibitors	61.321	het
chr16	68835680	T	C	CDH1	missense	c.271T>C	p.Phe91Leu	LT20N	TSG/ Tier3	0.247	0.124		27.86	het
chr17	41244492	A	G	BRCA1	missense	c.3056T>C	p.Ile1019Thr	LT18N	TSG/ Tier3	0.375	0.114	PARP Inhibitor	51.21	het
chr4	1806131	T	C	FGFR3	missense	c.1156T>C	p.Phe386Leu	LT10N	Oncogene/ Tier3	0.334	0.107	FGFR Inhibitors	327.25	het
chr17	41245449	A	G	BRCA1	missense	c.2099T>C	p.Leu700Pro	LT20N	TSG/ Tier3	0.361	0.107	PARP Inhibitor	26.79	het
chr17	41244435	T	C	BRCA1	missense	c.3113A>G	p.Glu1038Gly	LT10N	TSG/ Tier4	0.389	0.103	PARP Inhibitor	219.6	het
chr13	32914236	C	T	BRCA2	missense	c.5744C>T	p.Thr1915Met	LT20N	TSG/ Tier4	0.177	0.09	PARP Inhibitor	50.386	het
chr10	123353264	G	T	FGFR2	missense	c.68C>A	p.Pro23His	LT19N	Oncogene/ Tier3	0.509	0.08	FGFR Inhibitors	338.06	het
chr7	55268896	C	A	EGFR	missense	c.2962C>A	p.His988Asn	LT19N	Oncogene/ Tier3	0.228	0.077	Erlotinib, Gefitinib, EGFR Inhibitors	384.98	het
chr11	108128247	A	G	ATM	missense	c.2290A>G	p.Lys764Glu	LT18N	TSG/ Tier3	0.206	0.065	PARP Inhibitors	27.487	het
chr4	1801029	G	C	FGFR3	missense	c.158G>C	p.Ser53Thr	LT20N	Oncogene/ Tier3	0.191	0.065	FGFR Inhibitors	326.43	het
chr11	108160516	A	G	ATM	missense	c.4424A>G	p.Tyr1475Cys	LT18N	TSG/ Tier3	0.184	0.06	PARP Inhibitors	345.71	het
chr2	202149589	G	C	CASP8	missense	c.853G>C	p.Asp285His	LT20N	TSG/ Tier4	0.4	0.055		519.13	het
chr11	108098404	A	G	ATM	missense	c.53A>G	p.Asp18Gly	LT18N	TSG/ Tier3	0.161	0.049	PARP Inhibitors	20.21	het
chr11	108115522	A	G	ATM	missense	c.670A>G	p.Lys224Glu	LT20N	TSG/ Tier3	0.11	0.047	PARP Inhibitors	22.725	het
chr6	106553096	G	A	PRDM1	missense	c.1061G>A	p.Ser354Asn	LT11N	TSG/ Tier4	0.071	0.043		1232.1	het
chr6	106536253	G	A	PRDM1	missense	c.220G>A	p.Gly74Ser	LT10N	TSG/ Tier4	0.082	0.039		400.34	het
chr8	128751016	G	A	MYC	missense	c.553G>A	p.Val185Ile	LT16N	Oncogene/ Tier4	0.039	0.013		473.5	het

chr18 60985780	CG	-	BCL2	frameshift	c.119_120del	p.Pro40ArgfsTer112	LT10N	Oncogene/ Tier3			BCL2 inhibitors	296.3	het
chr19 10265311	GT	C	DNMT1	frameshift	c.1782_1783delinsG	p.Cys596AlafsTer5	LT10N	Oncogene/ Tier3				805.93	het
chr3 138665029	G	-	FOXL2	frameshift	c.536del	p.Ala179GlyfsTer92	LT11N	Oncogene/ Tier3				559.19	het
chr12 49432424	ACG	C	KMT2D	frameshift	c.8713_8715delinsG	p.Arg2905ValfsTer6	LT11N	TSG/ Tier2				20.426	het/4.76%
chr12 121432117	G	-	HNF1A	frameshift	c.864del	p.Pro291GlnfsTer51	LT16N	TSG/ Tier3				1165.2	het
chr12 121432118	C	-	HNF1A	frameshift	c.872del	p.Pro291GlnfsTer51	LT16N	TSG/ Tier3				1165.2	het
chr12 49438036	T	-	KMT2D	frameshift	c.5135del	p.Lys1712ArgfsTer10	LT17N	TSG/ Tier2				27.648	het/10.29%
chr1 115251216	T	-	NRAS	frameshift	c.510del	p.Lys170AsnfsTer19	LT18N	Oncogene/ Tier3			Vemurafenib, Dabrafenib, RAF inhibitors, MEK inhibitors	21.275	het
chr11 108190679	A	G	ATM	splice_site	c.6348-2A>G		LT20N	TSG/ Tier1			PARP Inhibitors	23.197	het/4.11%

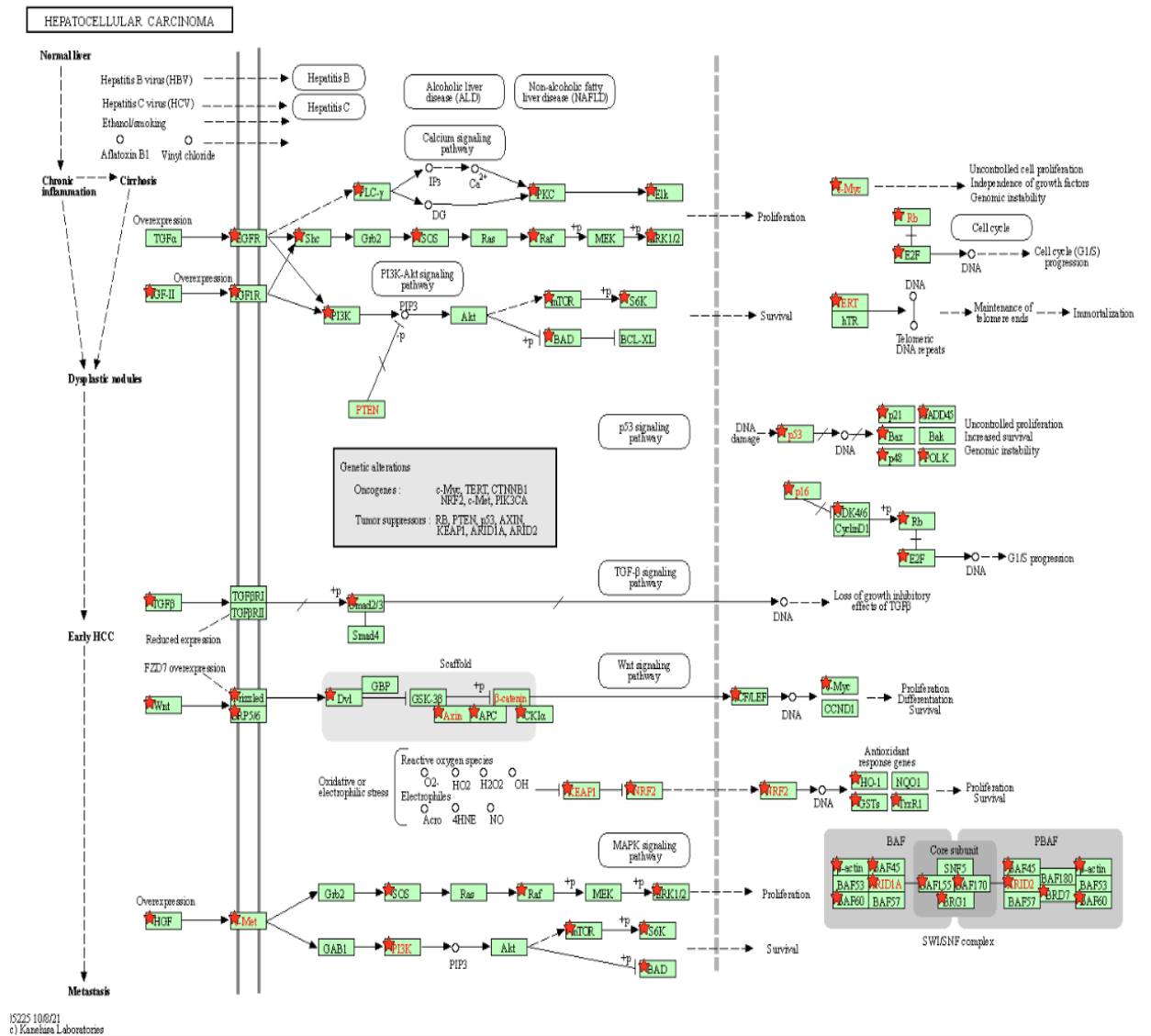


Figure (8): Hepatocellular carcinoma pathway: Genes written in red are disease associated gene variants, red stars are genes having pathogenic mutations in our HCC samples (27)

Sherman, B.T., Hao, M., Qiu, J., Jiao, X., Baseler, M.W., Lane, H.C., Imamichi, T. and Chang W. (2022): DAVID: a web server for functional enrichment analysis and functional annotation of gene lists (2021 update). *Nucleic Acids Research*. 50(W1):W216-W221. doi:10.1093/nar/gkac194.

Supplement Table (10): Tier1 and Tier2 variants in HCC and Non-HCC samples (GRCH37) all heterozygous, population frequency <0.1, HP= homopolymers regions.

	Variant	Position	Sequence ontology/ VAF	ACMG category	HCC LT/Non-HCC LTN (VAF)
1	TP53 c.422G>A NM_000546.6	chr17 7578508	Missense	Tier1	LT19 (22.95%)
2	CDKN2A c.95T>A NM_000077.5	chr9 21974732	Missense	Tier1	LT14 (7.14%)
3	MSH2 c.56del NM_000251.3	chr2 47630385	Frameshift	Tier2	LT13 (18.18%)
4	KMT2D c.8713_8715delinsG NM_003482.4	chr12 49432424	Frameshift	Tier2 HP	LT11N (4.76%)
5	KMT2D c.5135_5136del NM_003482.4	chr12 4943803	Frameshift	Tier2 HP	LT11N (3.86%)
6	KMT2D c.5135del NM_003482.4	chr12 49438036	Frameshift	Tier2 HP	LT17N (10.29%)
7	ATM c.6348-2A>G NM_000051.4	chr11 108190679	Splice site	Tier1	LT20N (4.11%)
8	KIT c.1621A>C p.Met541Leu NM_000222.3	chr4: 55593464	Missense	Tier2	LT11, 18,19 (0.22, 0.43, 0.52%)
9	NOTCH1 c.6472G>A NM_017617.5	Chr9 139391719	Missense	Tier1	LT6 (2.42%)
10	NOTCH1 c.1947del NM_017617.5	Chr9 139409808	Frameshift	Tier1HP	LT6 (5.56%)
11	ARID1A c.4899del NM_006015.6	Chr1 27101612	Frameshift	Tier2 HP	LT06 (2.74%)
12	KIT c.520del NM_000222.3	Chr4 55564628	Frameshift	Tier2 HP	LT6 (3.64%)
13	NOTCH1 c.3146delinsCAG NM_017617.5	Chr9 139403347	Frameshift	Tier1 HP	LT7 3.7%)
14	ARID1A c.4052dup NM_006015.6	Chr1 27100338	Frameshift	Tier2	LT7 (3.49%)
15	KMT2D c.8455C>T NM_003482.4	Chr12 49432684	Stop_gained	Tier2	LT7 (3.33%)
16	KMT2D c.3853dup NM_003482.4	Chr12 49443517	Frameshift	Tier2	LT7 (3.92%)
17	KMT2D c.3553C>T NM_003482.4	Chr12 49443818	Stop_gained	Tier2	LT7 (4.29%)
18	KMT2D c.9594del NM_003482.4	Chr12 49431544	Frameshift	Tier2HP	LT7N (3.92%)
19	PIK3CA c.3140A>G NM_006218.4	Chr3 178952085	Missense	Tier1	LT10 (2.41%)
20	NOTCH1 c.3849_3850insG NM_017617.5	Chr9 139401219	Frameshift	Tier1	LT10 (1.49%)
21	BAP1 c.688_689insG NM_004656.4	Chr3 52440364	Frameshift	Tier2	LT10 (1.69%)
22	KMT2C c.14125dup NM_170606.3	Chr7 151842286	Frameshift	Tier2	LT10 (2.9%)
23	KMT2C c.11293_11294del NM_170606.3	Chr7 151859367	Frameshift	Tier2 HP	LT10 (3.37%)
24	KMT2C c.7241_7242insC	Chr7 151877119	Frameshift	Tier2	LT10 (2.82%)

	NM_170606.3				
25	KMT2C c.1084_1085insC NM_170606.3	chr7- 151962222	Frameshift	Tier2	LT10 (3.28%)
26	KMT2D c.6323dup NM_003482.4	Chr12 49435229	Frameshift	Tier2 HP	LT10 (4.62%)
27	KMT2D c.1309_1310insC NM_003482.4	Chr12 49446156	Frameshift	Tier2	LT10 (1.92%)
28	ARID1A c.945_946insG NM_006015.6	Chr1 27023840	Frameshift	Tier2 HP	LT10N (1.79%)
29	CTNNB1 c.727dup NM_001904.4	Chr3 41267054	Frameshift	Tier1	LT10N (3.39%)
30	PIK3CA c.2732_2733del NM_006218.4	Chr3 178947857	Frameshift	Tier1 HP	LT10N (1.92%)
31	ATM c.6984dup NM_000051.4	Chr11 108198377	Frameshift	Tier1 HP	LT10N (3.08%)
32	PIK3CA c.888dup NM_006218.4	Chr3 178921404	Frameshift	Tier1	LT10N (3.92%)
33	KMT2D c.7277dup NM_003482.4	Chr12 49434275	Frameshift	Tier2	LT10N (5.17%)
34	KMT2D c.5015dup NM_003482.4	Chr12 49438253	Frameshift	Tier2 HP	LT10N (3.09%)
35	KMT2D c.3660dup NM_003482.4	Chr12 49443710	Frameshift	Tier2 HP	LT10N (3.77%)
36	KMT2D c.1676_1677insC NM_003482.4	Chr12 49445789	Frameshift	Tier2	LT10N (1.54%)
37	EGFR c.1437dup NM_005228.5	Chr7 55227966	Frameshift	Tier1 HP	LT10N (3.45%)
38	EGFR c.797dup NM_005228.5	Chr7 55221749	Frameshift	Tier1 HP	LT10N (2.33%), LT18N (1.67%)
39	SMARCA4 c.2689_2690insG NM_003072.5	Chr19 11132474	Frameshift	Tier2	LT10N (3.13%)
40	ARID1A c.926delinsCAG NM_006015.6	Chr1 27023820	Frameshift	Tier2 HP	LT10N (1.75%)
41	KMT2C c.3156_3157insG NM_170606.3	Chr7 151921521	Frameshift	Tier2	LT10N (1.69%)
42	KMT2C c.885dup NM_170606.3	Chr7 151970916	Frameshift	Tier2	LT10N (2.86%)
14	PIK3CA c.1325_1326insG NM_006218.4	Chr3 178928048	Frameshift	Tier1	LT11 (3.57%)
43	NOTCH1 c.3153dup NM_017617.5	Chr9 139403339	Frameshift	Tier1	LT11 (3.33%)
44	KMT2C c.4996dup NM_170606.3	Chr7 151884358	Frameshift	Tier2 HP	LT11 (3.13%)
45	KMT2C c.1783dup NM_170606.3	Chr7 151946990	Frameshift	Tier2 HP	LT13 (3.28%)
46	RBI c.2443dup NM_000321.3	Chr13 49039455	Frameshift	Tier2 HP	LT11 (5.97%)
47	SMARCA4 c.153_154insC NM_003072.5	Chr19 11094981	Frameshift	Tier2	LT11 (2.53%)
48	SMARCA4 c.3326_3327insC NM_003072.5	Chr19 11138571	Frameshift	Tier2	LT11 (1.85%)
49	ATM c.1171_1172insG NM_000051.4	Chr11 108119765	Frameshift	Tier1	LT11 (1.59%)
50	ATM c.8668_8669insG NM_000051.4	Chr11 108218089	Frameshift	Tier1	LT11 (1.82%)

51	<i>KIT</i> c.1149dup NM 000222.3	Chr4 55575619	Frameshift	Tier1 HP	LT11N (4.76%)
52	<i>ARID1A</i> c.880delinsCAC NM 006015.6	Chr1 27023774	Frameshift	Tier2 HP	LT11N (2.42%)
53	<i>ARID1A</i> c.1545dup NM 006015.6	Chr1 27057836	Frameshift	Tier2	LT11N (3.28%)
54	<i>KMT2c</i> c.10061dup NM 170606.3	Chr7 151860600	Frameshift	Tier2 HP	LT11N (3.28%)
55	<i>KMT2c</i> c.9267dup NM 170606.3	Chr7 151871322	Frameshift	Tier2 HP	LT11N (2.17%)
56	<i>KMT2D</i> c.9279_9280insG NM 003482.4	Chr12 49431859	Frameshift	Tier2	LT11N (2.2%)
57	<i>KMT2D</i> c.8713_8715delinsG NM 003482.4	Chr12 49432424	Frameshift	Tier2 HP	LT11N (4.76%)
58	<i>KMT2D</i> c.7259_7260insT NM 003482.4	Chr12 49434293	Frameshift	Tier2	LT11N (1.45%)
59	<i>KMT2D</i> c.5135_5136del NM 003482.4	Chr12 49438034	Frameshift	Tier2 HP	LT11N (3.86%)
60	<i>SMARCA4</i> c.3148_3149insC NM 003072.5	Chr19 11136165	Frameshift	Tier2	LT11N (1.85%)
61	<i>KMT2D</i> c.4085dup NM 003482.4	Chr12 49442487	Frameshift	Tier2 HP	LT11N (3.85%)
62	<i>SMARCA4</i> c.3392del NM 003072.5	Chr 19 11141415	Frameshift	Tier2	LT13 (7.73%)
63	<i>TSC1</i> c.2672del NM 000368.5	Chr9 135772951	Frameshift	Tier2 HP	LT13 (9.2%)
64	<i>ARID1A</i> c.3344del NM 006015.6	Chr1 27097751	Frameshift	Tier2 HP	LT13 (2.16%)
65	<i>ARID1A</i> c.4555_4557delinsA NM 006015.6	Chr1 27101273	Frameshift	Tier2 HP	LT13 (1.65%)
66	<i>ARID1A</i> c.4668_4669insG NM 006015.6	Chr1 27101387	Frameshift	Tier2	LT13 (1.59%)
67	<i>KMT2D</i> c.11147del NM 003482.4	Chr12 49427340	Frameshift	Tier2 HP	LT13 (1.59%)
68	<i>KMT2D</i> c.2585dup NM 003482.4	Chr12 49444880	Frameshift	Tier2 HP	LT13 (3.49%)
69	<i>NOTCH1</i> c.6373C>T NM 017617.5	Chr9 139391818	Missense	Tier1	LT13N (2.16%)
70	<i>CTNNB1</i> c.1444dup NM 001904.4	Chr3 41275276	Frameshift	Tier1 HP	LT14 (3.61%)
71	<i>CDKN2A</i> c.64_65del NM 000077.5	chr9 21974762	Frameshift	Tier1 HP	LT14 (2.9%)
72	<i>PIK3CA</i> c.349dup NM_006218.4	Chr3 178916959	Frameshift	Tier1	LT14 (2.25%)
73	<i>NOTCH1</i> c.809del NM 017617.5	Chr9 139413950	Frameshift	Tier1 HP	LT14 (5%)
74	<i>KMT2C</i> c.6836dup NM 170606.3	Chr7 151878108	Frameshift	Tier2 HP	LT14 (2.86%)
75	<i>KMT2D</i> c.15838_15839insC NM 003482.4	Chr12 49418675	Frameshift	Tier2	LT14 (1.75%)
76	<i>RBI</i> c.1848dup NM 000321.3	Chr13 49030367	Frameshift	Tier2 HP	LT14 (5.15%)
77	<i>SMARCA4</i> c.1834_1835insG NM_003072.5	Chr19 11113727	Frameshift	Tier2	LT14 (1.85%)
78	<i>ATM</i> c.3548dup NM 000051.4	Chr11 108151865	Frameshift	Tier1	LT14 (3.85%)

79	ATM c.3565_3566insCT NM_000051.4	Chr11 108151884	Frameshift	Tier1 HP	LT14 (2%)
80	ATM c.3552_3553insC NM_000051.4	Chr11 108151871	Frameshift	Tier1	LT14N (2.5%)
81	NOTCH1 c.5806dup NM_017617.5	Chr9 139395131	Frameshift	Tier1	LT16 (3.7%)
82	ATM c.6998dup NM_000051.4	Chr11 108198393	Frameshift	Tier1	LT16 (4.29%)
83	KMT2C c.13365_13366insC NM_170606.3	Chr7 151845646	Frameshift	Tier2	LT16 (1.82%)
84	KMT2C c.10405del NM_170606.3	Chr7 151860256	Frameshift	Tier2 HP	LT16 (2.63)
85	KMT2D c.11468dup NM_003482.4	Chr12 49427019	Frameshift	Tier2 HP	LT16 (3.45%)
86	KMT2D c.11386dup NM_003482.4	Chr12 49427101	Frameshift	Tier2 HP	LT16 (4%)
87	EGFR c.1462_1465delinsCC NM_005228.5	Chr7 55227995	Frameshift	Tier1 HP	LT16N (2.08%)
88	ATM c.8682dup NM_000051.4	Chr11 108224499	Frameshift	Tier1 HP	LT16N (3%)
89	ARID1A c.6341del NM_006015.6	Chr1 27106726	Frameshift	Tier2 HP	LT16N (3.64%)
90	KMT2c c.8808dup NM_170606.3	Chr7 151873729	Frameshift	Tier2 HP	LT16N (3.33%)
91	KMT2c c.11602_11605delins GG NM_170606.3	Chr7 151856013	Frameshift	Tier2 HP	LT16N (1.92%)
92	KMT2D c.7306_7308delinsG NM_006015.6	Chr12 49434245	Frameshift	Tier2 HP	LT16N (2.83%)
93	KMT2D c.2803dup NM_006015.6	Chr12 49444567	Frameshift	Tier2 HP	LT16N (3.51)
94	KMT2D c.1473_1474insG NM_006015.6	Chr12 49445992	Frameshift	Tier2	LT16N (1.92%)
95	NOTCH1 c.3763_3764insC NM_017617.5	Chr9 139401305	Frameshift	Tier1	LT17 (2.82%)
96	NOTCH1 c.3587del NM_017617.5	Chr9 139401812	Frameshift	Tier1 HP	LT17 (5%)
97	NOTCH1 c.2812_2813insCG NM_017617.5	Chr9 139404341	Frameshift	Tier1 HP	LT17 (1.92%)
98	NOTCH1 c.2072del NM_017617.5	chr9- 139409096	Frameshift	Tier1 HP	LT17 (7.14%)
99	KMT2c c.14345G>A NM_170606.3	Chr7 151836875	Missense	Tier2 HP	LT17 (2.78%)
100	KMT2D c.7282dup NM_006015.6	Chr12 49434270	Frameshift	Tier2 HP	LT17 (5.36%)
101	KMT2D c.5135del NM_006015.6	Chr12 49438035	Frameshift	Tier2 HP	LT17N (10.29%)
102	KMT2D c.3417_3418insC NM_006015.6	Chr12 49443953	Frameshift	Tier2	LT17N (1.47%)
103	SMARCA4 c.810dup NM_003072.5	Chr19 11097631	Frameshift	Tier2HP	LT11N,18N (3.06%, 7.25%)
104	KMT2c c.574delinsACA NM_170606.3	Chr7 152012239	Frameshift	Tier2	LT18 (2.14%)
105	RBI c.1578del NM_000321.3	Chr13 48955460	Frameshift	Tier2	LT18 (3.85%)
106	ATM c.6885dup NM_000051.4	Chr11 108196860	Frameshift	Tier1	LT18 (3.77%)

107	<i>KMT2c</i> c.10918dup NM 170606.3	Chr7 151859743	Frameshift	Tier2	LT18N (3.77%)
108	<i>KMT2c</i> c.10291_10292insG NM 170606.3	Chr7 151860370	Frameshift	Tier2	LT18N (1.56%)
109	<i>ATM</i> c.5870_5871insC NM 000051.4	Chr11 108180994	Frameshift	Tier1	LT18N (3.17%)
110	<i>ATM</i> c.5883_5884insC NM 000051.4	chr11- 108181007	Frameshift	Tier1	LT18N (1.59%)
111	<i>PTEN</i> c.812T>C NM 000314.8	chr10 89720661	Missense	Tier2	LT18N (2.78%)
112	<i>EGFR</i> c.797del NM 005228.5	Chr7 55221748	Frameshift	Tier1	LT18N (6.67%)
113	<i>PIK3CA</i> c.2196_2197insT NM 006218.4	Chr3 178941878	Frameshift	Tier1	LT19 (1.45%)
114	<i>CTNNB1</i> c.839_840insT NM 001904.4	Chr3 41267256	Frameshift	Tier1	LT19 (1.92%)
115	<i>KMT2D</i> c.3190dup NM 006015.6	Chr12 49444180	Frameshift	Tier2	LT19 (3.57%)
116	<i>MSH2</i> c.577C>T NM 000251.3	Chr2 47637443	Stop_gained	Tier2	LT19 (2.78%)
117	<i>ATM</i> c.5156_5157insG NM 000251.3	Chr11 108170591	Frameshift	Tier1	LT19N (1.85%)
118	<i>BAP1</i> c.201dup NM 004656.4	Chr3 52442545	Frameshift	Tier2	LT19N (3.77%)
119	<i>BAP1</i> c.140_141insG NM 004656.4	Chr3 52442605	Frameshift	Tier2	LT19N (1.79%)
120	<i>KMT2c</i> c.10822dup NM 170606.3	Chr7 151859839	Frameshift	Tier2	LT19N (3.33%)
121	<i>KMT2D</i> c.11858_11859insC NM 006015.6	Chr12 49426629	Frameshift	Tier2	LT19N (1.79%)
123	<i>KMT2c</i> c.7843dup NM 170606.3	Chr7 151874694	Frameshift	Tier2	LT19N (3.7%)
124	<i>KMT2D</i> c.3704del NM 006015.6	Chr12 49443666	Frameshift	Tier2	LT19N (3.31%)
125	<i>RBI</i> c.1237delinsAGA NM 000321.3	Chr13 48951075	Frameshift	Tier2	LT19N (3.23%)
126	<i>ATM</i> c.2831_2832insC NM 000051.4	Chr11 108139329	Frameshift	Tier1	LT20 (1.72%)
127	<i>PTEN</i> c.447_448insC NM 000314.8	Chr10 89692963	Frameshift	Tier1	LT20 (1.85%)
128	<i>KMT2D</i> c.14216dup NM 006015.6	Chr12 49422878	Frameshift	Tier2	LT20 (4.12%)
129	<i>KMT2D</i> c.8262_8263insG NM 006015.6	Chr12 49433108	Frameshift	Tier2	LT20 (1.64%)
130	<i>ATM</i> c.6874C>T NM 000051.4	Chr11 108196851	Stop-gained	Tier1	LT20N (1.80)
131	<i>ATM</i> c.8397dup NM 000051.4	Chr11 108214074	Frameshift	Tier1	LT20N (3.85%)
132	<i>ARID1A</i> c.1732del NM 006015.6	Chr1 27058023	Frameshift	Tier2	LT20N (1.79%)
133	<i>ARID1A</i> c.4060_4061delinsCT TC NM 006015.6	Chr1 27100348	Frameshift	Tier2	LT20N (3.33%)
134	<i>KMT2D</i> c.2658delinsCTG NM 006015.6	Chr12 49444808	Frameshift	Tier2	LT20N (2.91%)
135	<i>PTCH1</i> c.1963C>T NM_000264.5	Chr9 98231320	Stop-gained	Tier1	LT7N (3.23%)

136	<i>PTCH1</i> c.1595_1596del NM_000264.5	Chr9 98239046	Frameshift	Tier1	LT10 (3.19%)
137	<i>PTCH1</i> c.2523_2524insG NM_000264.5	Chr9 98229435	Frameshift	Tier1	LT10N (2.82%)
138	<i>PTCH1</i> c.1898dup NM_000264.5	Chr9 98231385	Frameshift	Tier1	LT11 (3.61%)
139	<i>PTCH1</i> c.2100_2101insC NM_000264.5	Chr9 98231183	Frameshift	Tier1	LT14 (1.89%)
140	<i>PTCH1</i> c.3679dup NM_000264.5	Chr9 98211476	Frameshift	Tier1	LT14N (3.09%)
141	<i>PTCH1</i> c.1469dup NM_000264.5	Chr9 98239863	Frameshift	Tier1	LT16 (2.82%)
142	<i>PTCH1</i> c.4200_4201insG	Chr9 98209338	Frameshift	Tier1	LT17N (1.85%)
143	<i>FLT3</i> c.680C>T p.Thr227Met NM_004119.3 Common in HCC and Non-HCC	chr13 28624294	Missense	Tier2	LT10 (100%); LT11 (81%); LT14 (50%); LT16 (100%); LT20 (46%) LT10N (100%); LT16N (100%)
144	<i>GSTP1</i> c.313A>G p.Ile105Val NM_000852.4 Common in HCC and Non-HCC	chr11: 67352689	Missense	Tier1	HCC and Non-HCC 16 (53, 44%), 18 (54%), 20 (52%), HCC 6 (59%) Non-HCC 17 (57%)