

Table S1 Patient clinical information

Patient ID	Age	Gender	Clinicopathologic diagnosis	Drinking history	history of hepatitis	Microvascular invasion	Macrovascular invasion	lymphatic metastasis	Extrahepatic metastasis	BCLC staging	CNLC staging	therapy method	Analysis of group
P1_T1	61	M	HCC	Yes	Other	No	No	No	No	B	Ila	excision	Avascular invasion
P2_T1	44	M	HCC	No	HBV	No	No	No	No	A	Ia	excision	Avascular invasion
P3_T1	56	M	HCC	Yes	HBV	No	No	No	No	A	Ib	excision	Avascular invasion
P4_T1	55	M	HCC	Yes	HBV	Yes	No	No	No	A	Ia	excision	Microvascular invasion
P5_T1	74	M	HCC	Yes	HBV	Yes	No	No	No	A	Ia	excision	Microvascular invasion
P6_T1	53	M	HCC	No	HBV	Yes	No	No	No	B	IIb	excision	Microvascular invasion
P7_T1	57	M	HCC	Yes	Other	Yes	No	No	No	A	Ia	excision	Microvascular invasion
P8_T1	61	M	HCC	Yes	Other	Yes	No	No	No	B	Ila	excision	Microvascular invasion
P9_T1	40	M	HCC	Yes	Other	No	No	No	No	A	Ia	excision	Avascular invasion
P10_T1	41	F	HCC	No	HBV	No	No	No	No	A	Ib	excision	Avascular invasion
P11_T1	55	M	HCC	Yes	HBV	No	No	No	No	A	Ia	excision	Avascular invasion
P12_T1	61	M	HCC	Yes	HBV	Yes	No	No	No	A	Ib	excision	Microvascular invasion
P13_T1	54	M	HCC	No	HBV	Yes	No	Yes	No	B	Ila	excision	Microvascular invasion
P14_T1	50	M	HCC	Yes	Other	Yes	No	No	No	C	IIla	excision	Microvascular invasion
P15_T1	25	M	HCC	No	HBV	No	No	Yes	No	C	IIla	excision	Avascular invasion
P16_T1	34	M	HCC	Yes	HBV	Yes	No	No	No	A	Ib	excision	Microvascular invasion
P17_T1	40	M	HCC	Yes	HBV	Yes	Yes	Yes	No	C	IIla	excision	Macrovascular invasion
P18_T1	64	M	HCC	No	Other	Yes	Yes	No	No	C	IIla	medication	Macrovascular invasion
P19_T1	55	M	HCC	Yes	HBV	Yes	Yes	No	Yes	C	IIIb	medication	Macrovascular invasion
P20_T1	54	M	HCC	No	HBV	Yes	No	No	No	A	Ib	excision	Microvascular invasion
P21_T1	56	F	HCC	No	HBV	No	No	No	No	A	Ib	excision	Avascular invasion
P22_T1	44	M	HCC	No	HBV	Yes	Yes	Yes	No	C	IIla	medication	Macrovascular invasion
P23_T1	45	M	HCC	No	HBV	Yes	No	Yes	Yes	C	IIIb	medication	Microvascular invasion
P24_T1	71	M	HCC	Yes	Other	Yes	Yes	No	No	C	IIla	medication	Macrovascular invasion
P25_T1	35	M	HCC	No	HBV	Yes	No	No	Yes	C	IIIb	medication	Microvascular invasion
P26_T1	27	M	HCC	Yes	HBV	Yes	Yes	Yes	No	C	IIIb	medication	Macrovascular invasion
P27_T1	60	M	HCC	Yes	HBV	Yes	No	No	No	A	Ib	excision	Microvascular invasion
P28_T1	40	M	HCC	No	HBV	No	No	No	No	A	Ia	excision	Avascular invasion
P29_T1	46	M	HCC	No	HBV	Yes	Yes	No	No	C	IIla	medication	Macrovascular invasion
P30_T1	80	M	HCC	No	HBV	No	No	No	No	A	Ib	excision	Avascular invasion
P31_T1	63	M	HCC	No	HBV	Yes	Yes	No	No	C	IIla	medication	Macrovascular invasion
P32_T1	55	F	HCC	No	HBV	Yes	Yes	No	No	C	IIla	excision	Macrovascular invasion
P33_T1	64	M	HCC	No	HBV	No	No	No	No	A	Ib	excision	Avascular invasion
P34_T1	60	M	HCC	No	HBV	Yes	Yes	No	No	C	IIla	medication	Macrovascular invasion
P35_T1	67	M	HCC	No	HBV	Yes	No	No	No	B	IIb	excision	Microvascular invasion
P36_T1	51	M	HCC	No	HBV	No	No	No	No	A	Ib	excision	Avascular invasion
P37_T1	46	M	HCC	No	HBV	Yes	Yes	Yes	Yes	C	IIIb	medication	Macrovascular invasion
P38_T1	41	M	HCC	No	HBV	No	No	No	No	A	Ia	excision	Avascular invasion
P39_T1	50	M	HCC	Yes	HBV	No	No	No	No	B	IIb	medication	Avascular invasion
P40_T1	54	M	HCC	Yes	HBV	Yes	Yes	No	No	C	IIla	excision	Macrovascular invasion
P41_T1	45	M	HCC	No	HBV	Yes	Yes	No	No	C	IIla	medication	Macrovascular invasion
P42_T1	46	M	HCC	No	HBV	No	No	No	No	A	Ia	excision	Avascular invasion
P43_T1	71	F	HCC	No	Other	Yes	No	No	Yes	C	IIIb	medication	Microvascular invasion
P44_T1	41	M	HCC	No	HBV	Yes	Yes	No	No	C	IIla	excision	Macrovascular invasion
P45_T1	35	M	HCC	No	HBV	Yes	No	No	No	B	IIb	excision	Microvascular invasion
P46_T1	63	M	HCC	No	HBV	Yes	Yes	Yes	Yes	C	IIIb	medication	Macrovascular invasion
P47_T1	48	M	HCC	No	HBV	Yes	Yes	No	No	C	IIla	medication	Macrovascular invasion
P48_T1	47	M	HCC	Yes	HBV	Yes	Yes	No	No	B	IIb	medication	Macrovascular invasion
P49_T1	49	M	HCC	No	HBV	Yes	Yes	No	No	C	IIla	medication	Macrovascular invasion
P50_T1	52	M	HCC	No	HBV	Yes	Yes	No	No	C	IIla	medication	Macrovascular invasion

M, male; F, female; HCC, hepatocellular carcinoma; HBV, hepatitis B; BCLC, Barcelona Clinic Liver Cancer; CNLC staging, China liver cancer staging.

Table S2 Single nucleotide variants detected in all tumor samples.

Hugo_Symbol	NCBI_Build	Chromosome	Start_Position	End_Position	Strand	Variant_Classification	Reference_Allele	Tumor_Seq_Allele2	dbSNP_RS	Tumor_Sample_Barcode	HGVSc	HGVSp	t_depth	t_ref_count	t_alt_count	n_depth	n_ref_count	n_alt_count	BIOTYPE	CANONICAL	IMPACT	VARIANT_CLASS
RRAGC	GRCh38	chr1	38859556	38859556	+	Nonsense_Mutation	C	A	novel	P1_T1	c.91G>T	p.Glu31Ter	34	30	4	62	62	0	protein_coding	YES	HIGH	SNV
MSH6	GRCh38	chr2	47801150	47801150	+	Missense_Mutation	T	C	novel	P1_T1	c.3167T>C	p.Val1056Ala	177	169	8	70	70	0	protein_coding	YES	MODERATE	SNV
CTNNB1	GRCh38	chr2	41224622	41224622	+	Missense_Mutation	C	T	rs121913403	P1_T1	c.110C>T	p.Ser37Phe	198	192	6	102	102	0	protein_coding	YES	MODERATE	SNV
SETD2	GRCh38	chr3	47123876	47123905	+	In_Frame_Del	TATCTGCTCTAAAGATTCTGGACAATTA	-	novel	P1_T1	c.731_760del	p.Ile244_Asp253del	140	124	16	118	118	0	protein_coding	YES	MODERATE	deletion
EPHA3	GRCh38	chr3	89210158	89210158	+	Missense_Mutation	G	A	novel	P1_T1	c.452G>A	p.Ser151Asn	256	213	43	139	139	0	protein_coding	YES	MODERATE	SNV
FGFR4	GRCh38	chr5	1.77E+08	1.77E+08	+	Missense_Mutation	C	T	rs72098218	P1_T1	c.160C>T	p.Arg54Cys	139	134	5	26	26	0	protein_coding	YES	MODERATE	SNV
VEGFA	GRCh38	chr6	43771229	43771229	+	Missense_Mutation	G	A	rs761101895	P1_T1	c.523G>A	p.Gly175Ser	31	26	5	25	25	0	protein_coding	YES	MODERATE	SNV
GRM3	GRCh38	chr7	86838886	86838886	+	Missense_Mutation	A	G	novel	P1_T1	c.1372A>G	p.Thr458Ala	273	264	9	102	102	0	protein_coding	YES	MODERATE	SNV
PPP2R2A	GRCh38	chr8	26361017	26361017	+	Missense_Mutation	C	G	novel	P1_T1	c.533C>G	p.Pro176Arg	263	233	30	75	75	0	protein_coding	YES	MODERATE	SNV
CDH1	GRCh38	chr16	68738376	68738376	+	Missense_Mutation	G	C	novel	P1_T1	c.128G>C	p.Arg43Pro	96	58	38	30	30	0	protein_coding	YES	MODERATE	SNV
CD22	GRCh38	chr19	35337931	35337931	+	Missense_Mutation	G	A	novel	P1_T1	c.895G>A	p.Val299Met	91	87	4	53	53	0	protein_coding	YES	MODERATE	SNV
KMT2B	GRCh38	chr19	35718232	35718253	+	Frame_Shift_Del	GGGCTCCGGCCGGGCTGGCC	-	novel	P1_T1	c.216_237del	p.Leu73SerfsTer87	11	8	3	16	16	0	protein_coding	YES	HIGH	deletion
CIC	GRCh38	chr19	42291409	42291409	+	Missense_Mutation	G	A	novel	P1_T1	c.2641G>A	p.Ala881Thr	167	161	6	65	65	0	protein_coding	YES	MODERATE	SNV
ERCC2	GRCh38	chr19	45368955	45368955	+	Missense_Mutation	G	A	novel	P1_T1	c.221C>T	p.Ser74Leu	139	119	20	40	40	0	protein_coding	YES	MODERATE	SNV
ERCC1	GRCh38	chr19	45421188	45421188	+	Missense_Mutation	C	T	novel	P1_T1	c.311G>A	p.Ser104Asn	190	141	49	101	101	0	protein_coding	YES	MODERATE	SNV
NF2	GRCh38	chr22	29678269	29678269	+	Missense_Mutation	T	A	novel	P1_T1	c.1520T>A	p.Phe507Tyr	118	100	18	27	27	0	protein_coding	YES	MODERATE	SNV
NF2	GRCh38	chr22	29678270	29678270	+	Missense_Mutation	C	A	novel	P1_T1	c.1521C>A	p.Phe507Leu	118	100	18	27	27	0	protein_coding	YES	MODERATE	SNV
STAG2	GRCh38	chrX	1.24E+08	1.24E+08	+	Missense_Mutation	G	A	novel	P1_T1	c.1510G>A	p.Glu504Lys	148	144	4	32	32	0	protein_coding	YES	MODERATE	SNV
PTPRS	GRCh38	chr19	5238990	5238990	+	Missense_Mutation	C	T	rs771916005	P1_T1	c.1778G>A	p.Arg593His	68	64	4	43	43	0	protein_coding	YES	MODERATE	SNV
ARID1A	GRCh38	chr1	26732713	26732713	+	Nonsense_Mutation	C	G	novel	P10_T1	c.1841C>G	p.Ser614Ter	274	223	51	51	51	0	protein_coding	YES	HIGH	SNV
NRAS	GRCh38	chr1	1.15E+08	1.15E+08	+	Missense_Mutation	T	C	rs11554290	P10_T1	c.182A>G	p.Gln61Arg	560	436	124	111	111	0	protein_coding	YES	MODERATE	SNV
MGA	GRCh38	chr15	41729294	41729294	+	Nonsense_Mutation	C	A	novel	P10_T1	c.3788G>A	p.Ser1263Ter	574	531	43	122	122	0	protein_coding	YES	HIGH	SNV
MGA	GRCh38	chr15	41729306	41729306	+	Missense_Mutation	A	T	novel	P10_T1	c.3800A>T	p.Gln1267Leu	574	531	43	124	124	0	protein_coding	YES	MODERATE	SNV
AXIN1	GRCh38	chr16	314671	314671	+	Nonsense_Mutation	C	C	novel	P10_T1	c.891G>A	p.Trp297Ter	174	115	59	35	35	0	protein_coding	YES	HIGH	SNV
CDH1	GRCh38	chr16	68819423	68819423	+	Missense_Mutation	A	G	rs1555516592	P10_T1	c.1709A>G	p.Asn570Ser	246	185	61	72	72	0	protein_coding	YES	MODERATE	SNV
ZFXH3	GRCh38	chr16	72950509	72950509	+	Missense_Mutation	G	T	novel	P10_T1	c.3176C>A	p.Thr1059Lys	266	213	53	58	58	0	protein_coding	YES	MODERATE	SNV
PTPRS	GRCh38	chr19	5244314	5244314	+	Missense_Mutation	C	C	novel	P10_T1	c.1157G>A	p.Arg386His	341	232	109	97	97	0	protein_coding	YES	MODERATE	SNV
AXL	GRCh38	chr19	41222011	41222011	+	Missense_Mutation	G	A	novel	P10_T1	c.541G>A	p.Ala181Thr	202	196	6	30	30	0	protein_coding	YES	MODERATE	SNV
AR	GRCh38	chrX	67545197	67545197	+	Missense_Mutation	G	T	rs370971743	P10_T1	c.51G>T	p.Lys17Asn	724	708	16	103	103	0	protein_coding	YES	MODERATE	SNV
JAK1	GRCh38	chr1	64844820	64844820	+	Missense_Mutation	T	A	novel	P11_T1	c.2185A>T	p.Ser729Cys	476	245	231	404	404	0	protein_coding	YES	MODERATE	SNV
TENT5C	GRCh38	chr1	1.18E+08	1.18E+08	+	Missense_Mutation	A	T	novel	P11_T1	c.476A>T	p.Asn159Ile	1206	927	279	738	738	0	protein_coding	YES	MODERATE	SNV
DNMT3A	GRCh38	chr2	25282476	25282476	+	Missense_Mutation	G	A	rs1310158529	P11_T1	c.413C>T	p.Thr138Ile	198	193	5	245	245	0	protein_coding	YES	MODERATE	SNV
XPO1	GRCh38	chr2	61522626	61522626	+	Missense_Mutation	T	C	novel	P11_T1	c.286A>G	p.Arg96Gly	792	671	121	325	325	0	protein_coding	YES	MODERATE	SNV
NFE2L2	GRCh38	chr2	1.77E+08	1.77E+08	+	Missense_Mutation	T	C	novel	P11_T1	c.1751A>G	p.Gln584Arg	2022	1990	32	819	819	0	protein_coding	YES	MODERATE	SNV
CTNNB1	GRCh38	chr3	41224607	41224607	+	Missense_Mutation	A	G	rs121913396	P11_T1	c.95A>G	p.Asp32Gly	1124	1099	25	518	518	0	protein_coding	YES	MODERATE	SNV
CTNNB1	GRCh38	chr3	41224610	41224610	+	Missense_Mutation	G	G	rs121913400	P11_T1	c.98C>G	p.Ser33Cys	1106	930	176	508	508	0	protein_coding	YES	MODERATE	SNV
NSD1	GRCh38	chr5	1.77E+08	1.77E+08	+	Missense_Mutation	G	A	novel	P11_T1	c.3856G>A	p.Glu1286Lys	554	536	18	280	280	0	protein_coding	YES	MODERATE	SNV
TE11	GRCh38	chr10	68646235	68646235	+	Missense_Mutation	A	G	rs756422497	P11_T1	c.3506A>G	p.Gln1169Arg	1266	1046	220	643	643	0	protein_coding	YES	MODERATE	SNV
IRS2	GRCh38	chr13	1.1E+08	1.1E+08	+	Missense_Mutation	C	T	rs1200134173	P11_T1	c.1598G>A	p.Gly533Asp	326	320	6	364	364	0	protein_coding	YES	MODERATE	SNV
NF1	GRCh38	chr17	31169938	31169938	+	Missense_Mutation	A	T	novel	P11_T1	c.527A>T	p.Asp176Val	1126	1096	30	396	396	0	protein_coding	YES	MODERATE	SNV
STAT3	GRCh38	chr17	42338773	42338773	+	Missense_Mutation	C	G	novel	P11_T1	c.508G>C	p.Asp171His	633	334	299	231	231	0	protein_coding	YES	MODERATE	SNV
ZNF217	GRCh38	chr20	53575936	53575936	+	Missense_Mutation	G	C	novel	P11_T1	c.2828C>G	p.Pro943Arg	1201	759	442	832	832	0	protein_coding	YES	MODERATE	SNV
RTEL1	GRCh38	chr20	63689613	63689613	+	Missense_Mutation	G	A	novel	P11_T1	c.1990G>A	p.Asp664Asn	131	126	5	220	220	0	protein_coding	YES	MODERATE	SNV
SPEN	GRCh38	chr1	15919477	15919477	+	Missense_Mutation	A	G	novel	P12_T1	c.1595A>G	p.Tyr532Cys	1000	818	182	138	138	0	protein_coding	YES	MODERATE	SNV
MKNK1	GRCh38	chr1	46558591	46558591	+	Missense_Mutation	G	A	rs373002774	P12_T1	c.1382C>T	p.Pro461Leu	312	308	4	29	29	0	protein_coding	YES	MODERATE	SNV
IRS1	GRCh38	chr2	2.27E+08	2.27E+08	+	Missense_Mutation	A	T	novel	P12_T1	c.845T>C	p.Val282Ala	482	474	8	62	62	0	protein_coding	YES	MODERATE	SNV
PIK3CA	GRCh38	chr3	1.79E+08	1.79E+08	+	Missense_Mutation	A	T	rs121913279	P12_T1	c.3140A>T	p.His1047Leu	589	575	14	122	122	0	protein_coding	YES	MODERATE	SNV
KLHL6	GRCh38	chr3	1.84E+08	1.84E+08	+	Missense_Mutation	A	T	novel	P12_T1	c.437T>A	p.Leu146Gln	736	593	143	80	80	0	protein_coding	YES	MODERATE	SNV
GFRR3	GRCh38	chr4	1804450	1804450	+	Missense_Mutation	G	A	rs761896295	P12_T1	c.1202G>A	p.Arg401His	360	355	5	60	60	0	protein_coding	YES	MODERATE	SNV
KIT	GRCh38	chr4	54725909	54725909	+	Missense_Mutation	C	A	novel	P12_T1	c.1399C>A	p.Pro467Thr	726	500	226	99	99	0	protein_coding	YES	MODERATE	SNV
APC	GRCh38	chr5	1.13E+08	1.13E+08	+	Nonsense_Mutation	G	T	novel	P12_T1	c.2752G>T	p.Glu918Ter	1053	950	103	176	176	0	protein_coding	YES	HIGH	SNV
FLT4	GRCh38	chr5	1.81E+08	1.81E+08	+	Missense_Mutation	C	T	novel	P12_T1	c.3374G>A	p.Cys1125Tyr	229	225	4	33	33	0	protein_coding	YES	MODERATE	SNV
GRM3	GRCh38	chr7	86839787	86839787	+	Missense_Mutation	C	A	rs141671463	P12_T1	c.2273C>A	p.Thr758Lys	1326	665	661	209	209	0	protein_coding	YES	MODERATE	SNV
PTEN	GRCh38	chr10	87933154	87933154	+	Missense_Mutation	A	G	rs121909241	P12_T1	c.395G>A	p.Gly132Asp	788	626	162	192	192	0	protein_coding	YES	MODERATE	SNV
HNF1A	GRCh38	chr12	1.21E+08	1.21E+08	+	Missense_Mutation	G	T	novel	P12_T1	c.1576G>T	p.Asp526Tyr	354	180	174	51	50	1	protein_coding	YES	MOD	

Table S2 (continued)

Hugo_Symbol	NCBI_Build	Chromosome	Start_Position	End_Position	Strand	Variation_Classification	Reference_Allele	Tumor_Seq_Allele2	dbSNP_RS	Tumor_Sample_Barcode	HGVSc	HGVSp	t_depth	t_ref_count	t_alt_count	n_depth	n_ref_count	n_alt_count	BIOTYPE	CANONICAL	IMPACT	VARIANT_CLASS
H3-3A	GRCh38	chr1	2.26E+08	2.26E+08	+	Missense_Mutation	C	G	rs749423281	P19_T1	c.344C>G	p.Ala115Gly	467	434	33	25	25	0	protein_coding	YES	MODERATE	SNV
PARP1	GRCh38	chr1	2.26E+08	2.26E+08	+	Missense_Mutation	A	G	rs1136410	P19_T1	c.2285T>C	p.Val762Ala	1643	1593	50	62	62	0	protein_coding	YES	MODERATE	SNV
FANCL	GRCh38	chr2	58241253	58241253	+	Missense_Mutation	A	C	novel	P19_T1	c.61T>G	p.Ser21Ala	817	395	422	65	65	0	protein_coding	YES	MODERATE	SNV
TEK4	GRCh38	chr2	94871827	94871827	+	Missense_Mutation	C	T	rs4854235	P19_T1	c.248C>T	p.Trh83Met	356	346	10	17	17	0	protein_coding	YES	MODERATE	SNV
TEK4	GRCh38	chr2	94871877	94871877	+	Missense_Mutation	A	G	rs11164112	P19_T1	c.298A>G	p.Ser100Gly	367	350	17	23	23	0	protein_coding	YES	MODERATE	SNV
NFE2L2	GRCh38	chr2	1.77E+08	1.77E+08	+	In_Frame_Del	GTTCCTGACTGGATGCTGGGGCTGGCT GAATGGGAGAAATCACCTGTCTCTCA TCTAGTGTAACTAGCGAAA	-	novel	P19_T1	c.210_287del	p.Phe71_Thr96del	2026	1589	437	285	284	1	protein_coding	YES	MODERATE	deletion
IRS1	GRCh38	chr2	2.27E+08	2.27E+08	+	Missense_Mutation	G	A	rs779584301	P19_T1	c.1360C>T	p.Pro454Ser	1354	1335	19	67	67	0	protein_coding	YES	MODERATE	SNV
VHL	GRCh38	chr3	10146592	10146592	+	Missense_Mutation	T	A	novel	P19_T1	c.419T>A	p.Leu140His	1623	1173	450	85	85	0	protein_coding	YES	MODERATE	SNV
FGFR3	GRCh38	chr4	1801411	1801411	+	Missense_Mutation	C	G	rs577990843	P19_T1	c.490C>G	p.Leu164Val	795	783	12	29	29	0	protein_coding	YES	MODERATE	SNV
FAT1	GRCh38	chr4	1.87E+08	1.87E+08	+	Missense_Mutation	T	C	rs11939575	P19_T1	c.3190A>G	p.Arg1064Gly	1430	1394	36	129	129	0	protein_coding	YES	MODERATE	SNV
FAT1	GRCh38	chr4	1.87E+08	1.87E+08	+	Missense_Mutation	C	G	rs1877731	P19_T1	c.2584G>C	p.Val862Leu	2105	2040	65	217	217	0	protein_coding	YES	MODERATE	SNV
FAT1	GRCh38	chr4	1.87E+08	1.87E+08	+	Missense_Mutation	G	C	rs367863	P19_T1	c.1842C>G	p.Phe614Leu	1330	1293	37	157	157	0	protein_coding	YES	MODERATE	SNV
FAT1	GRCh38	chr4	1.87E+08	1.87E+08	+	Missense_Mutation	C	C	rs3733413	P19_T1	c.1444G>A	p.Val482Ile	2117	2076	41	182	182	0	protein_coding	YES	MODERATE	SNV
FAT1	GRCh38	chr4	1.87E+08	1.87E+08	+	Missense_Mutation	A	C	rs3733414	P19_T1	c.1212T>G	p.Ser404Arg	1568	1522	46	158	158	0	protein_coding	YES	MODERATE	SNV
CCND3	GRCh38	chr6	41941600	41941600	+	Missense_Mutation	G	A	rs1254723551	P19_T1	c.50C>T	p.Pro17Leu	380	283	97	31	31	0	protein_coding	YES	MODERATE	SNV
BRAF	GRCh38	chr7	1.41E+08	1.41E+08	+	Missense_Mutation	T	C	rs121913370	P19_T1	c.1742A>G	p.Asn581Ser	949	721	228	55	55	0	protein_coding	YES	MODERATE	SNV
KMT2C	GRCh38	chr7	1.52E+08	1.52E+08	+	Missense_Mutation	G	A	rs74483926	P19_T1	c.10979C>T	p.Ser360Leu	2714	2667	47	252	252	0	protein_coding	YES	MODERATE	SNV
KMT2C	GRCh38	chr7	1.52E+08	1.52E+08	+	Missense_Mutation	A	G	rs78004519	P19_T1	c.10639T>C	p.Ser3547Pro	1828	1786	42	178	178	0	protein_coding	YES	MODERATE	SNV
PRDM14	GRCh38	chr8	70068503	70068503	+	Missense_Mutation	T	C	rs3750226	P19_T1	c.730A>G	p.Lys244Gln	854	844	10	56	56	0	protein_coding	YES	MODERATE	SNV
RECQL4	GRCh38	chr8	1.45E+08	1.45E+08	+	Missense_Mutation	T	G	rs535692036	P19_T1	c.1345A>C	p.Trh449Pro	1236	1214	22	53	52	1	protein_coding	YES	MODERATE	SNV
TEK	GRCh38	chr9	27197488	27197488	+	Missense_Mutation	T	C	rs35030851	P19_T1	c.1798G>T	p.Val600Leu	1304	1289	15	137	137	0	protein_coding	YES	MODERATE	SNV
TET1	GRCh38	chr10	68572823	68572823	+	Missense_Mutation	A	G	rs10823229	P19_T1	c.485A>G	p.Asp162Gly	1797	1765	32	156	156	0	protein_coding	YES	MODERATE	SNV
FGFR2	GRCh38	chr10	1.22E+08	1.22E+08	+	Missense_Mutation	T	C	novel	P19_T1	c.130A>G	p.Ile44Val	1625	1135	490	144	144	0	protein_coding	YES	MODERATE	SNV
INPPL1	GRCh38	chr11	72232917	72232917	+	Missense_Mutation	C	A	rs61749195	P19_T1	c.1894C>A	p.Leu632Ile	1090	1072	18	61	61	0	protein_coding	YES	MODERATE	SNV
INPPL1	GRCh38	chr11	72237492	72237492	+	Missense_Mutation	C	G	rs11548491	P19_T1	c.3248C>G	p.Ala1083Gly	1335	1316	19	71	71	0	protein_coding	YES	MODERATE	SNV
FGF23	GRCh38	chr12	4370383	4370383	+	Missense_Mutation	G	A	rs7955866	P19_T1	c.716C>T	p.Trh239Met	2161	2093	68	100	100	0	protein_coding	YES	MODERATE	SNV
PIK3C2G	GRCh38	chr12	18496123	18496123	+	Missense_Mutation	C	T	rs12312266	P19_T1	c.2855C>T	p.Pro952Leu	1177	1158	19	85	85	0	protein_coding	YES	MODERATE	SNV
GLI1	GRCh38	chr12	57472038	57472038	+	Missense_Mutation	G	C	rs2228226	P19_T1	c.3298G>C	p.Glu1100Gln	1419	1398	21	80	80	0	protein_coding	YES	MODERATE	SNV
HNF1A	GRCh38	chr12	1.21E+08	1.21E+08	+	Missense_Mutation	A	C	rs1169288	P19_T1	c.79A>C	p.Ile27Leu	892	875	17	29	28	1	protein_coding	YES	MODERATE	SNV
BRCA2	GRCh38	chr13	32376672	32376672	+	Missense_Mutation	A	G	novel	P19_T1	c.8635A>G	p.Asn2879Asp	561	307	254	42	42	0	protein_coding	YES	MODERATE	SNV
TSHR	GRCh38	chr14	81144239	81144239	+	Missense_Mutation	G	C	rs1991517	P19_T1	c.2181G>C	p.Glu727Asp	1755	1729	26	148	148	0	protein_coding	YES	MODERATE	SNV
BLM	GRCh38	chr15	90751928	90751928	+	Missense_Mutation	C	T	rs751438275	P19_T1	c.941C>T	p.Ser314Phe	817	807	10	88	88	0	protein_coding	YES	MODERATE	SNV
MAPK3	GRCh38	chr16	30118437	30118437	+	Missense_Mutation	C	T	novel	P19_T1	c.455G>A	p.Arg152Gln	1456	1384	72	68	68	0	protein_coding	YES	MODERATE	SNV
ANKRD11	GRCh38	chr16	89279644	89279644	+	Missense_Mutation	C	A	novel	P19_T1	c.6898G>T	p.Ala2300Ser	899	537	362	41	41	0	protein_coding	YES	MODERATE	SNV
AURKB	GRCh38	chr17	8205013	8205013	+	Missense_Mutation	A	G	rs1059476	P19_T1	c.896T>G	p.Met299Thr	1055	1006	49	74	74	0	protein_coding	YES	MODERATE	SNV
SPOP	GRCh38	chr17	49622064	49622064	+	Missense_Mutation	T	C	novel	P19_T1	c.82A>G	p.Lys228Glu	1153	1045	108	54	54	0	protein_coding	YES	MODERATE	SNV
DLL3	GRCh38	chr19	39504071	39504071	+	Missense_Mutation	T	C	rs1110627	P19_T1	c.653T>C	p.Leu218Pro	826	810	16	22	22	0	protein_coding	YES	MODERATE	SNV
AURKA	GRCh38	chr20	56386485	56386485	+	Missense_Mutation	A	T	rs2273535	P19_T1	c.91T>A	p.Phe31Ile	2027	1977	50	96	96	0	protein_coding	YES	MODERATE	SNV
EP300	GRCh38	chr22	41131624	41131624	+	Missense_Mutation	A	G	rs146224251	P19_T1	c.1519A>G	p.Ser507Gly	599	592	7	56	56	0	protein_coding	YES	MODERATE	SNV
KDM6A	GRCh38	chrX	45069832	45069832	+	Missense_Mutation	A	G	rs2230018	P19_T1	c.2177G>A	p.Trh726Lys	512	491	21	57	57	0	protein_coding	YES	MODERATE	SNV
ARID1A	GRCh38	chr1	26774401	26774401	+	Missense_Mutation	C	T	rs75876486	P2_T1	c.4174C>T	p.Pro1392Ser	159	154	5	40	40	0	protein_coding	YES	MODERATE	SNV
MUTYH	GRCh38	chr1	45332179	45332179	+	Missense_Mutation	C	T	rs140156029	P2_T1	c.911G>A	p.Arg304Gln	182	178	4	51	51	0	protein_coding	YES	MODERATE	SNV
PIK3CA	GRCh38	chr3	1.79E+08	1.79E+08	+	Missense_Mutation	A	G	novel	P2_T1	c.1579G>A	p.Asp527Asn	455	424	31	51	51	0	protein_coding	YES	MODERATE	SNV
MAP3K13	GRCh38	chr3	1.85E+08	1.85E+08	+	Missense_Mutation	A	T	novel	P2_T1	c.719A>T	p.Gln240Leu	592	558	34	68	68	0	protein_coding	YES	MODERATE	SNV
TET2	GRCh38	chr4	1.05E+08	1.05E+08	+	Missense_Mutation	A	T	novel	P2_T1	c.508T>A	p.Tyr1696Phe	811	794	17	100	100	0	protein_coding	YES	MODERATE	SNV
GABRA6	GRCh38	chr5	1.62E+08	1.62E+08	+	Missense_Mutation	C	T	novel	P2_T1	c.395C>T	p.Pro132Leu	528	504	24	78	78	0	protein_coding	YES	MODERATE	SNV
FGF19	GRCh38	chr11	69703344	69703344	+	Missense_Mutation	C	T	rs747918000	P2_T1	c.253G>A	p.Val85Ile	87	83	4	14	14	0	protein_coding	YES	MODERATE	SNV
TYRO3	GRCh38	chr15	41578071	41578071	+	Missense_Mutation	A	T	novel	P2_T1	c.2468G>A	p.Gly823Asp	129	125	4	44	44	0	protein_coding	YES	MODERATE	SNV
PLCG2	GRCh38	chr16	81919504	81919504	+	Missense_Mutation	A	T	rs370718047	P2_T1	c.2075A>T	p.His692Leu	481	462	19	77	77	0	protein_coding	YES	MODERATE	SNV
ALOX12B	GRCh38	chr17	8077024	8077024	+	Missense_Mutation	A	T	novel	P2_T1	c.1241T>A	p.Leu414Gln	174	141	33	55	55	0	protein_coding	YES	MODERATE	SNV
KEAP1	GRCh38	chr19	10491658	10491658	+	Missense_Mutation	C	T	rs1379189956	P2_T1	c.1244G>A	p.Arg415His	205	201	4	81	81	0	protein_coding	YES	MODERATE	SNV
GNAS	GRCh38	chr20	58853458	58853458	+	Missense_Mutation	A	T	novel	P2_T1	c.193G>A	p.Gly65Ser	261	245	16	114	114	0	protein_coding	YES	MODERATE	SNV
RTEL1	GRCh38	chr20	63690199	63690199	+	Missense_Mutation	G	A	novel	P2_T1	c.2254G>A	p.Ala752Thr	122	118	4	45	45	0	protein_coding	YES	MODERATE	SNV
EP300	GRCh38	chr22	41127698	41127698	+	Missense_Mutation	A	T	novel	P2_T1	c.1118A>T	p.Lys373Met	277	221	56	36	36	0	protein_coding	YES	MODERATE	SNV
EP300																						

Table S2 (continued)

Hugo_Symbol	NCBI_Build	Chromosome	Start_Position	End_Position	Strand	Variant_Classification	Reference_Allele	Tumor_Seq_Allele2	dbSNP_RS	Tumor_Sample_Barcode	HGVSc	HGVSp	t_depth	t_ref_count	t_alt_count	n_depth	n_ref_count	n_alt_count	BIOTYPE	CANONICAL	IMPACT	VARIANT_CLASS
DNAH5	GRCh38	chr5	13883053	13883053	+	Missense_Mutation	T	C	rs74853358	P24_T1	c.3025A>G	p.Ile1009Val	404	326	76	163	163	0	protein_coding	YES	MODERATE	SNV
TMEM151B	GRCh38	chr6	44270781	44270783	+	In_Frame_Del	CGG	-	rs130796398	P24_T1	c.54_56del	p.Leu1042Phe	145	42	6	42	20	0	protein_coding	YES	MODERATE	deletion
ELAVL2	GRCh38	chr9	23762054	23762054	+	Missense_Mutation	T	C	novel	P24_T1	c.288A>G	p.Ser90Gln	277	265	12	152	152	0	protein_coding	YES	MODERATE	SNV
TUSC1	GRCh38	chr9	25677852	25677852	+	Missense_Mutation	A	A	novel	P24_T1	c.470T>A	p.Leu157Gln	248	241	6	93	93	0	protein_coding	YES	MODERATE	SNV
UNC13B	GRCh38	chr9	35930712	35930712	+	Missense_Mutation	A	G	novel	P24_T1	c.3059A>G	p.Glu1020Gly	144	137	5	57	57	0	protein_coding	YES	MODERATE	SNV
VPS13A	GRCh38	chr9	77353484	77353484	+	Missense_Mutation	A	G	rs751982239	P24_T1	c.7495A>G	p.Ile2499Val	221	205	5	99	99	0	protein_coding	YES	MODERATE	SNV
FKBP15	GRCh38	chr9	1.13E+08	1.13E+08	+	Missense_Mutation	G	T	novel	P24_T1	c.2855C>A	p.Pro952Gln	280	274	6	128	127	1	protein_coding	YES	MODERATE	SNV
VPS51	GRCh38	chr11	65108514	65108514	+	Missense_Mutation	A	G	rs1174287312	P24_T1	c.1043A>G	p.Tyr348Cys	323	276	44	100	99	0	protein_coding	YES	MODERATE	SNV
ATP2A2	GRCh38	chr12	1.1E+08	1.1E+08	+	Missense_Mutation	G	A	rs761676527	P24_T1	c.1841G>A	p.Arg614Gln	395	388	6	141	141	0	protein_coding	YES	MODERATE	SNV
ZC3H13	GRCh38	chr13	45969418	45969418	+	Missense_Mutation	C	A	novel	P24_T1	c.3126G>T	p.Leu1042Phe	309	260	49	114	114	0	protein_coding	YES	MODERATE	SNV
METRN	GRCh38	chr16	715660	715660	+	Missense_Mutation	C	A	rs1304352379	P24_T1	c.181C>A	p.Pro61Thr	165	159	6	30	30	0	protein_coding	YES	MODERATE	SNV
TP53	GRCh38	chr17	7674218	7674218	+	Missense_Mutation	T	C	rs587782082	P24_T1	c.745A>G	p.Arg249Gly	114	80	33	51	51	0	protein_coding	YES	MODERATE	SNV
SHC2	GRCh38	chr19	460588	460588	+	Missense_Mutation	G	T	rs1253640609	P24_T1	c.409C>G	p.His137Asn	178	60	117	29	26	3	protein_coding	YES	MODERATE	SNV
HCM2	GRCh38	chr19	615947	615949	+	In_Frame_Del	CGG	-	rs527536363	P24_T1	c.2162_2164del	p.Pro721del	199	53	9	43	18	0	protein_coding	YES	MODERATE	deletion
RANBP3	GRCh38	chr19	5941696	5941696	+	Missense_Mutation	C	G	novel	P24_T1	c.331G>C	p.Glu111Gln	139	131	8	48	48	0	protein_coding	YES	MODERATE	SNV
ZNF225	GRCh38	chr19	44131381	44131381	+	Missense_Mutation	G	C	novel	P24_T1	c.767G>C	p.Gly256Ala	315	263	52	147	147	0	protein_coding	YES	MODERATE	SNV
KLK6	GRCh38	chr19	50963421	50963421	+	Missense_Mutation	A	G	novel	P24_T1	c.326T>C	p.Leu109Pro	196	176	19	101	101	0	protein_coding	YES	MODERATE	SNV
CHGB	GRCh38	chr20	5923424	5923424	+	Missense_Mutation	G	T	novel	P24_T1	c.1280G>T	p.Arg427Leu	265	232	33	81	81	0	protein_coding	YES	MODERATE	SNV
SEC14L2	GRCh38	chr22	30415801	30415801	+	Missense_Mutation	A	G	novel	P24_T1	c.707A>G	p.Gln236Arg	139	108	31	67	67	0	protein_coding	YES	MODERATE	SNV
TERT	GRCh38	chr5	1294866	1294866	+	Missense_Mutation	C	T	novel	P25_T1	c.124G>A	p.Gly42Arg	297	242	55	41	41	0	protein_coding	YES	MODERATE	SNV
CPLANE1	GRCh38	chr5	37224604	37224604	+	Missense_Mutation	A	G	rs886060581	P25_T1	c.2428T>C	p.Cys810Arg	252	208	42	57	57	0	protein_coding	YES	MODERATE	SNV
ZNF853	GRCh38	chr7	6621815	6621815	+	Missense_Mutation	A	T	novel	P25_T1	c.824A>T	p.Gln275Leu	486	316	166	64	64	0	protein_coding	YES	MODERATE	SNV
PIGO	GRCh38	chr9	35094317	35094317	+	Missense_Mutation	A	G	novel	P25_T1	c.554T>C	p.Leu185Pro	340	334	6	26	26	0	protein_coding	YES	MODERATE	SNV
NUP98	GRCh38	chr11	3744548	3744548	+	Missense_Mutation	A	A	novel	P25_T1	c.1369A>T	p.Thr457Ser	298	254	43	41	41	0	protein_coding	YES	MODERATE	SNV
TP53	GRCh38	chr17	7674254	7674254	+	Missense_Mutation	T	C	rs730882004	P25_T1	c.709A>G	p.Met237Val	80	30	50	29	29	0	protein_coding	YES	MODERATE	SNV
LONP1	GRCh38	chr19	5693299	5693299	+	Missense_Mutation	G	A	rs562878082	P25_T1	c.2702C>T	p.Ala901Val	182	133	49	37	37	0	protein_coding	YES	MODERATE	SNV
SLC45A2	GRCh38	chr5	33963895	33963895	+	Missense_Mutation	C	A	novel	P26_T1	c.684G>T	p.Leu228Phe	327	317	10	105	105	0	protein_coding	YES	MODERATE	SNV
MPDZ	GRCh38	chr9	13188812	13188812	+	Missense_Mutation	A	C	novel	P26_T1	c.2336T>G	p.Val779Gly	260	246	12	108	106	0	protein_coding	YES	MODERATE	SNV
PHKG2	GRCh38	chr16	30753263	30753263	+	Missense_Mutation	A	C	novel	P26_T1	c.358A>C	p.Thr120Pro	133	119	12	55	54	1	protein_coding	YES	MODERATE	SNV
ZBTB32	GRCh38	chr19	35716001	35716001	+	Missense_Mutation	C	A	novel	P26_T1	c.1018C>A	p.His340Asn	207	202	5	77	77	0	protein_coding	YES	MODERATE	SNV
ZNF595	GRCh38	chr4	87282	87282	+	Missense_Mutation	C	A	novel	P27_T1	c.1778C>A	p.Thr593Lys	64	59	5	88	88	0	protein_coding	YES	MODERATE	SNV
SRF	GRCh38	chr6	43171747	43171749	+	In_Frame_Del	GCG	-	rs774568148	P27_T1	c.102_104del	p.Gly35del	71	21	7	65	41	0	protein_coding	YES	MODERATE	deletion
ERMP1	GRCh38	chr9	5825128	5825128	+	Missense_Mutation	T	C	rs144810528	P27_T1	c.732A>G	p.Ile244Met	52	9	42	43	43	0	protein_coding	YES	MODERATE	SNV
ODF3	GRCh38	chr11	197363	197363	+	Missense_Mutation	T	A	novel	P27_T1	c.59T>A	p.Met20Lys	29	11	18	25	25	0	protein_coding	YES	MODERATE	SNV
TAT	GRCh38	chr16	7150779	7150779	+	Missense_Mutation	G	T	novel	P27_T1	c.812C>A	p.Pro271His	112	12	99	92	92	0	protein_coding	YES	MODERATE	SNV
CD300LB	GRCh38	chr17	74525762	74525762	+	Missense_Mutation	A	T	novel	P27_T1	c.356T>A	p.Val119Glu	92	87	5	36	36	0	protein_coding	YES	MODERATE	SNV
LAMA1	GRCh38	chr18	7050914	7050914	+	Missense_Mutation	A	T	novel	P27_T1	c.368T>A	p.Ile123Asn	81	51	30	86	86	0	protein_coding	YES	MODERATE	SNV
PPP4R1	GRCh38	chr18	9570603	9570603	+	Missense_Mutation	C	G	novel	P27_T1	c.1127G>C	p.Ser376Thr	131	61	70	90	90	0	protein_coding	YES	MODERATE	SNV
ZNF519	GRCh38	chr18	14104958	14104958	+	Missense_Mutation	G	C	novel	P27_T1	c.1582C>G	p.Arg528Gly	133	127	6	83	82	0	protein_coding	YES	MODERATE	SNV
SHC2	GRCh38	chr19	425168	425168	+	Missense_Mutation	A	T	rs754244054	P27_T1	c.1238T>A	p.Leu413Gln	33	11	22	32	32	0	protein_coding	YES	MODERATE	SNV
ARID3A	GRCh38	chr19	971934	971936	+	In_Frame_Del	GCG	-	rs753131507	P27_T1	c.1666_1668del	p.Gly556del	125	42	6	64	52	0	protein_coding	YES	MODERATE	deletion
CDH4	GRCh38	chr20	61873886	61873886	+	Missense_Mutation	G	T	novel	P27_T1	c.1036G>T	p.Gly346Cys	68	63	5	36	36	0	protein_coding	YES	MODERATE	SNV
ZNF595	GRCh38	chr4	86247	86247	+	Missense_Mutation	A	T	novel	P28_T1	c.743A>T	p.Lys248Ile	431	415	6	91	91	0	protein_coding	YES	MODERATE	SNV
ZNF736	GRCh38	chr7	64348625	64348625	+	Missense_Mutation	C	G	novel	P28_T1	c.762C>G	p.Asp254Glu	119	112	6	49	49	0	protein_coding	YES	MODERATE	SNV
ZNF736	GRCh38	chr7	64348627	64348627	+	Missense_Mutation	G	A	novel	P28_T1	c.764G>A	p.Arg255Lys	115	108	6	49	49	0	protein_coding	YES	MODERATE	SNV
ZBTB5	GRCh38	chr9	37420008	37420008	+	Missense_Mutation	A	A	rs747980674	P28_T1	c.544C>T	p.Arg172Cys	563	415	147	24	24	0	protein_coding	YES	MODERATE	SNV
ABCA7	GRCh38	chr19	1054636	1054636	+	Missense_Mutation	C	A	novel	P28_T1	c.3793C>A	p.His1265Asn	811	446	364	33	33	0	protein_coding	YES	MODERATE	SNV
TPR	GRCh38	chr1	1.86E+08	1.86E+08	+	Missense_Mutation	T	T	novel	P29_T1	c.4445C>A	p.Thr1482Lys	345	337	5	29	29	0	protein_coding	YES	MODERATE	SNV
SPEF2	GRCh38	chr5	35704586	35704586	+	Missense_Mutation	G	T	novel	P29_T1	c.2431G>T	p.Asp811Tyr	192	177	15	21	21	0	protein_coding	YES	MODERATE	SNV
SPEN	GRCh38	chr1	15928906	15928906	+	Missense_Mutation	A	G	novel	P3_T1	c.2666A>G	p.Lys889Arg	470	453	17	154	154	0	protein_coding	YES	MODERATE	SNV
JAK1	GRCh38	chr1	64844820	64844820	+	Missense_Mutation	T	A	novel	P3_T1	c.2185A>T	p.Ser729Cys	922	654	268	136	136	0	protein_coding	YES	MODERATE	SNV
ELF3	GRCh38	chr1	2.02E+08	2.02E+08	+	Missense_Mutation	G	A	novel	P3_T1	c.1093G>A	p.Glu365Lys	1566	1539	27	118	118	0	protein_coding	YES	MODERATE	SNV
REL	GRCh38	chr2	60922488	60922494	+	Frame_Shift_Del	AATGAGC	-	novel	P3_T1	c.1816_1822del	p.Glu606Ter	231	190	41	122	122	0	protein_coding	YES	HIGH	deletion
CTNNB1	GRCh38	chr3	41233420	41233420	+	Missense_Mutation	T	G	novel	P3_T1	c.1161T>G	p.Asn387Lys	329	260	69	153	152	1	protein_coding	YES	MODERATE	SNV
MST1R	GRCh38	chr3	49896889	49896889	+	Missense_Mutation	C	A	novel	P3_T1	c.2185G>T	p.Val729Phe	532	399	133	38	38	0	protein_coding	YES	MODERATE	SNV
PPP4R2	GRCh38	chr3	73065466	73065466																		

Table S2 (continued)

Hugo_Symbol	NCBI_Build	Chromosome	Start_Position	End_Position	Strand	Variant_Classification	Reference_Allele	Tumor_Seq_Allele2	dbSNP_RS	Tumor_Sample_Barcode	HGVSc	HGVSp	t_depth	t_ref_count	t_alt_count	n_depth	n_ref_count	n_alt_count	BIOTYPE	CANONICAL	IMPACT	VARIANT_CLASS
PIGO	GRCh38	chr9	35091452	35091452	+	Nonsense_Mutation	A	C	novel	P33_T1	c.2435T>G	p.Leu812Ter	141	130	10	66	66	0	protein_coding	YES	HIGH	SNV
OR2S2	GRCh38	chr9	35957559	35957559	+	Missense_Mutation	A	C	novel	P33_T1	c.540T>G	p.Cys180Trp	154	135	17	48	48	0	protein_coding	YES	MODERATE	SNV
KDM5A	GRCh38	chr12	310946	310946	+	Missense_Mutation	G	A	rs761933806	P33_T1	c.3155C>T	p.Ala1052Val	230	224	6	40	40	0	protein_coding	YES	MODERATE	SNV
NOP2	GRCh38	chr12	6560535	6560535	+	Missense_Mutation	T	C	novel	P33_T1	c.1571A>G	p.Gln524Arg	70	52	18	34	33	0	protein_coding	YES	MODERATE	SNV
WDR76	GRCh38	chr15	43857051	43857051	+	Missense_Mutation	A	G	novel	P33_T1	c.1297A>G	p.Arg433Gly	205	196	9	41	41	0	protein_coding	YES	MODERATE	SNV
SLC9A5	GRCh38	chr16	67266114	67266116	+	In_Frame_Del	GAG	-	rs770521682	P33_T1	c.2122_2124del	p.Glu708del	78	36	5	22	20	0	protein_coding	YES	MODERATE	deletion
INTS2	GRCh38	chr17	61869771	61869771	+	Missense_Mutation	G	C	novel	P33_T1	c.3020C>G	p.Ala1007Gly	246	194	51	43	42	0	protein_coding	YES	MODERATE	SNV
FCRL2	GRCh38	chr1	1.58E+08	1.58E+08	+	Missense_Mutation	G	T	novel	P34_T1	c.497C>A	p.Ala166Asp	179	152	27	139	138	1	protein_coding	YES	MODERATE	SNV
RASSF1	GRCh38	chr3	50332057	50332057	+	Missense_Mutation	A	C	novel	P34_T1	c.467T>G	p.Met156Arg	90	78	10	85	85	0	protein_coding	YES	MODERATE	SNV
ARMC8	GRCh38	chr3	1.38E+08	1.38E+08	+	Missense_Mutation	A	T	novel	P34_T1	c.34A>T	p.Ser120Cys	147	123	24	82	82	0	protein_coding	YES	MODERATE	SNV
DCKG	GRCh38	chr3	1.86E+08	1.86E+08	+	Missense_Mutation	C	T	novel	P34_T1	c.520G>A	p.Gly174Arg	254	223	31	127	127	0	protein_coding	YES	MODERATE	SNV
BMP2K	GRCh38	chr4	78870931	78870931	+	Missense_Mutation	G	C	rs1367988852	P34_T1	c.1380G>C	p.Gln460His	421	398	11	286	277	1	protein_coding	YES	MODERATE	SNV
CTNND2	GRCh38	chr5	11098612	11098612	+	Missense_Mutation	G	T	novel	P34_T1	c.2600C>A	p.Ala867Glu	214	179	35	90	90	0	protein_coding	YES	MODERATE	SNV
CDH18	GRCh38	chr5	19838844	19838844	+	Missense_Mutation	T	C	rs765370372	P34_T1	c.143A>G	p.His48Arg	239	201	36	117	117	0	protein_coding	YES	MODERATE	SNV
NADK2	GRCh38	chr5	36197579	36197579	+	Missense_Mutation	T	A	novel	P34_T1	c.1152A>T	p.Arg384Ser	324	295	27	145	143	1	protein_coding	YES	MODERATE	SNV
HIVEP1	GRCh38	chr6	12122002	12122002	+	Missense_Mutation	G	T	novel	P34_T1	c.2207G>T	p.Arg736Leu	232	187	35	159	159	0	protein_coding	YES	MODERATE	SNV
KIAA2026	GRCh38	chr9	5920165	5920165	+	Missense_Mutation	G	T	novel	P34_T1	c.5831C>A	p.Thr1944Lys	232	226	6	164	164	0	protein_coding	YES	MODERATE	SNV
FREM1	GRCh38	chr9	14776161	14776161	+	Missense_Mutation	A	C	novel	P34_T1	c.4485T>G	p.Phe1495Leu	165	157	6	137	136	1	protein_coding	YES	MODERATE	SNV
FRMPD1	GRCh38	chr9	37746375	37746375	+	Missense_Mutation	C	A	novel	P34_T1	c.4343C>A	p.Pro1448Gln	100	80	20	81	80	0	protein_coding	YES	MODERATE	SNV
DCAF10	GRCh38	chr9	37801358	37801358	+	Missense_Mutation	C	A	novel	P34_T1	c.492C>A	p.Ser164Arg	203	197	5	139	138	0	protein_coding	YES	MODERATE	SNV
AHNAK	GRCh38	chr11	62533944	62533944	+	Missense_Mutation	A	A	rs752058736	P34_T1	c.473C>T	p.Thr158Met	131	126	5	60	60	0	protein_coding	YES	MODERATE	SNV
NRXN2	GRCh38	chr11	64713663	64713663	+	Missense_Mutation	G	T	novel	P34_T1	c.37C>A	p.Pro13Thr	52	40	12	25	25	0	protein_coding	YES	MODERATE	SNV
KIF26A	GRCh38	chr14	1.04E+08	1.04E+08	+	Missense_Mutation	G	A	novel	P34_T1	c.1856G>A	p.Gly619Asp	52	45	7	34	34	0	protein_coding	YES	MODERATE	SNV
ARIH1	GRCh38	chr15	72580731	72580731	+	Nonsense_Mutation	C	T	novel	P34_T1	c.1216C>T	p.Arg406Ter	218	212	6	122	121	0	protein_coding	YES	HIGH	SNV
SMG1	GRCh38	chr16	18847864	18847864	+	Missense_Mutation	G	T	novel	P34_T1	c.5793C>A	p.Ser1931Arg	212	207	5	105	105	0	protein_coding	YES	MODERATE	SNV
TP53	GRCh38	chr17	7674216	7674216	+	Missense_Mutation	C	C	rs28934571	P34_T1	c.747G>T	p.Arg249Ser	62	48	14	45	43	2	protein_coding	YES	MODERATE	SNV
ATP8B3	GRCh38	chr19	1806116	1806116	+	Missense_Mutation	A	A	novel	P34_T1	c.731G>T	p.Arg244Leu	56	47	9	45	44	0	protein_coding	YES	MODERATE	SNV
LIPE	GRCh38	chr19	42402036	42402036	+	Missense_Mutation	G	C	novel	P34_T1	c.3007C>G	p.Leu1003Val	97	82	13	58	58	0	protein_coding	YES	MODERATE	SNV
SLC4A7	GRCh38	chr3	27385907	27385907	+	Missense_Mutation	G	G	novel	P35_T1	c.3477G>C	p.Lys1159Asn	222	117	99	101	100	0	protein_coding	YES	MODERATE	SNV
ZNF595	GRCh38	chr4	87359	87359	+	Missense_Mutation	T	C	rs998446351	P35_T1	c.1855T>C	p.Ser619Pro	208	199	9	190	185	0	protein_coding	YES	MODERATE	SNV
SPATS1	GRCh38	chr6	44360444	44360444	+	Splice_Site	A	T	novel	P35_T1	c.288-2A>T	-	209	119	88	166	166	0	protein_coding	YES	HIGH	SNV
VWDE	GRCh38	chr7	12373194	12373194	+	Missense_Mutation	C	T	rs1354388896	P35_T1	c.1370C>A	p.Arg457His	186	119	67	146	144	0	protein_coding	YES	MODERATE	SNV
CPSPF1	GRCh38	chr8	1.44E+08	1.44E+08	+	Missense_Mutation	C	T	novel	P35_T1	c.1064G>A	p.Arg355His	169	161	5	101	98	0	protein_coding	YES	MODERATE	SNV
DOCK8	GRCh38	chr9	340255	340255	+	Missense_Mutation	A	A	novel	P35_T1	c.1613G>A	p.Thr538Lys	289	282	6	161	161	0	protein_coding	YES	MODERATE	SNV
TP53	GRCh38	chr17	7674227	7674227	+	Missense_Mutation	T	C	rs483352895	P35_T1	c.736A>G	p.Met246Val	59	18	40	70	69	0	protein_coding	YES	MODERATE	SNV
HIPK4	GRCh38	chr19	40383997	40383997	+	Missense_Mutation	C	G	novel	P35_T1	c.608G>C	p.Cys203Ser	193	125	67	126	126	0	protein_coding	YES	MODERATE	SNV
TEAD2	GRCh38	chr19	49342583	49342583	+	Missense_Mutation	A	A	novel	P35_T1	c.1097G>T	p.Arg366Leu	255	163	91	156	156	0	protein_coding	YES	MODERATE	SNV
MYBPC2	GRCh38	chr19	50455294	50455294	+	Missense_Mutation	T	A	novel	P35_T1	c.2201T>A	p.Ile734Asn	72	43	29	90	89	0	protein_coding	YES	MODERATE	SNV
TRMT2A	GRCh38	chr22	20114600	20114600	+	Missense_Mutation	G	A	rs764530902	P35_T1	c.1207C>T	p.Arg403Trp	115	72	41	81	78	0	protein_coding	YES	MODERATE	SNV
ZNF595	GRCh38	chr4	87359	87359	+	Missense_Mutation	T	C	rs998446351	P36_T1	c.1855T>C	p.Ser619Pro	485	470	8	111	111	0	protein_coding	YES	MODERATE	SNV
PRLR	GRCh38	chr5	35068236	35068236	+	Missense_Mutation	A	C	novel	P36_T1	c.835T>G	p.Phe279Val	215	202	12	41	41	0	protein_coding	YES	MODERATE	SNV
NUP153	GRCh38	chr6	17629102	17629102	+	Missense_Mutation	A	A	rs1359118646	P36_T1	c.3190G>T	p.Pro1064Ser	190	158	32	44	44	0	protein_coding	YES	MODERATE	SNV
TP53	GRCh38	chr17	7674216	7674216	+	Missense_Mutation	A	A	rs28934571	P36_T1	c.747G>T	p.Arg249Ser	77	55	22	20	20	0	protein_coding	YES	MODERATE	SNV
TLE2	GRCh38	chr19	3009566	3009567	+	Frame_Shift_Ins	-	GAGCT	novel	P36_T1	c.1147_1151dup	p.Val385AlafsTer10	148	49	26	44	29	0	protein_coding	YES	HIGH	insertion
S1PR4	GRCh38	chr19	3179522	3179522	+	Missense_Mutation	C	C	rs768125524	P36_T1	c.730C>T	p.Arg244Cys	107	100	7	57	57	0	protein_coding	YES	MODERATE	SNV
TRIP10	GRCh38	chr19	6743089	6743089	+	Missense_Mutation	A	T	novel	P36_T1	c.320A>T	p.Gln107Leu	215	155	60	45	45	0	protein_coding	YES	MODERATE	SNV
FIZ1	GRCh38	chr19	55592740	55592740	+	Missense_Mutation	C	T	novel	P36_T1	c.1201G>A	p.Gly401Arg	170	157	5	35	33	0	protein_coding	YES	MODERATE	SNV
OR2T8	GRCh38	chr1	2.48E+08	2.48E+08	+	Missense_Mutation	C	C	rs61857491	P37_T1	c.479C>T	p.Ala160Val	27	21	6	21	21	0	protein_coding	YES	MODERATE	SNV
VIT	GRCh38	chr2	36808472	36808472	+	Missense_Mutation	A	A	rs129848934	P37_T1	c.1390G>A	p.Ala464Thr	158	151	7	73	73	0	protein_coding	YES	MODERATE	SNV
CCDC71	GRCh38	chr3	49163940	49163940	+	Missense_Mutation	G	G	novel	P37_T1	c.269G>T	p.Ala90Val	116	109	5	72	72	0	protein_coding	YES	MODERATE	SNV
AGTR1	GRCh38	chr3	1.49E+08	1.49E+08	+	Missense_Mutation	T	C	novel	P37_T1	c.944T>C	p.Val315Ala	223	216	6	97	97	0	protein_coding	YES	MODERATE	SNV
DNAJB11	GRCh38	chr3	1.87E+08	1.87E+08	+	Missense_Mutation	C	T	novel	P37_T1	c.97C>T	p.Pro33Ser	179	171	8	59	59	0	protein_coding	YES	MODERATE	SNV
SRD5A1	GRCh38	chr5	6633758	6633758	+	Missense_Mutation	T	C	novel	P37_T1	c.182T>C	p.Leu61Pro	153	145	7	90	89	0	protein_coding	YES	MODERATE	SNV
RANBP9	GRCh38	chr6	13711150	13711150	+	Missense_Mutation	G	A	rs773022063	P37_T1	c.356G>T	p.Pro119Leu	151	145	5	53	50	0	protein_coding	YES	MODERATE	SNV
H1-2	GRCh38	chr6	26056058	26056058	+	Missense_Mutation	C	G	rs121111009	P37_T1	c.371G>C	p.Gly124Ala	193	185	7	93	92	0	protein_coding	YES	MODERATE	SNV
H1-3	GRCh38	chr6	26234891	26234891																		

Table S2 (continued)

Hugo_Symbol	NCBI_Build	Chromosome	Start_Position	End_Position	Strand	Variant_Classification	Reference_Allele	Tumor_Seq_Allele2	dbSNP_RS	Tumor_Sample_Barcode	HGVSc	HGVSp	t_depth	t_ref_count	t_alt_count	n_ref_count	n_alt_count	BIOTYPE	CANONICAL	IMPACT	VARIANT_CLASS	
ANFX	GRCh38	chr12	1.33E+08	1.33E+08	+	Splice_Site	A	C	novel	P40_T1	c.1053+2T>G		193	184	7	37	37	0	protein_coding	YES	HIGH	SNV
ABCC11	GRCh38	chr16	48210994	48210994	+	Missense_Mutation	T	G	novel	P40_T1	c.1562A>C	p.Asn521Thr	309	297	7	119	119	0	protein_coding	YES	MODERATE	SNV
RNF213	GRCh38	chr17	80273334	80273334	+	Missense_Mutation	T	G	novel	P40_T1	c.191T>G	p.Phe64Cys	306	272	24	69	68	0	protein_coding	YES	MODERATE	SNV
SLC25A23	GRCh38	chr19	6456530	6456530	+	Missense_Mutation	T	A	novel	P40_T1	c.373A>T	p.Met125Leu	88	45	37	38	33	0	protein_coding	YES	MODERATE	SNV
ATP13A1	GRCh38	chr19	19655583	19655583	+	Missense_Mutation	G	T	novel	P40_T1	c.1341C>A	p.Phe447Leu	927	845	80	73	72	0	protein_coding	YES	MODERATE	SNV
ATP13A1	GRCh38	chr19	19656115	19656115	+	Missense_Mutation	G	C	novel	P40_T1	c.1152C>G	p.Ile384Met	953	886	65	66	66	0	protein_coding	YES	MODERATE	SNV
C5AR2	GRCh38	chr19	47341643	47341643	+	Missense_Mutation	G	A	rs200192224	P40_T1	c.844G>A	p.Ala282Thr	256	250	6	46	46	0	protein_coding	YES	MODERATE	SNV
ZNF524	GRCh38	chr19	55602899	55602899	+	Missense_Mutation	C	T	novel	P40_T1	c.787C>T	p.Pro263Ser	289	283	6	82	82	0	protein_coding	YES	MODERATE	SNV
NLRP9	GRCh38	chr19	55711803	55711803	+	Missense_Mutation	A	T	novel	P40_T1	c.2840T>A	p.Leu947Gln	185	121	63	28	28	0	protein_coding	YES	MODERATE	SNV
ZNF543	GRCh38	chr19	57328694	57328694	+	Missense_Mutation	A	A	novel	P40_T1	c.1232A>T	p.Lys411Met	371	262	108	88	86	0	protein_coding	YES	MODERATE	SNV
EIF4G3	GRCh38	chr1	20879466	20879466	+	Missense_Mutation	T	C	novel	P41_T1	c.2419A>G	p.Asn807Asp	354	346	7	61	61	0	protein_coding	YES	MODERATE	SNV
NISCH	GRCh38	chr3	52487998	52487998	+	Missense_Mutation	C	A	novel	P41_T1	c.2506C>A	p.Arg836Ser	172	167	5	48	48	0	protein_coding	YES	MODERATE	SNV
EPHA3	GRCh38	chr3	89449246	89449246	+	Missense_Mutation	T	C	novel	P41_T1	c.2368T>C	p.Trp790Arg	479	460	16	55	55	0	protein_coding	YES	MODERATE	SNV
BMP2K	GRCh38	chr4	78870931	78870931	+	Missense_Mutation	G	C	rs1367988852	P41_T1	c.1380G>C	p.Gln460His	622	602	8	106	105	0	protein_coding	YES	MODERATE	SNV
DNAH5	GRCh38	chr5	13751187	13751187	+	Missense_Mutation	G	A	novel	P41_T1	c.11102G>T	p.Pro3701Leu	400	332	67	36	36	0	protein_coding	YES	MODERATE	SNV
CDH12	GRCh38	chr5	21752076	21752076	+	Missense_Mutation	T	A	novel	P41_T1	c.2046A>T	p.Lys682Asn	437	406	31	48	48	0	protein_coding	YES	MODERATE	SNV
PTGER4	GRCh38	chr5	40681627	40681627	+	Missense_Mutation	C	T	novel	P41_T1	c.634C>T	p.Arg212Cys	402	376	24	68	68	0	protein_coding	YES	MODERATE	SNV
TD2P	GRCh38	chr6	24651015	24651015	+	Missense_Mutation	C	A	novel	P41_T1	c.862G>T	p.Gly288Cys	396	378	7	38	38	0	protein_coding	YES	MODERATE	SNV
HOXA5	GRCh38	chr7	27141888	27141888	+	Missense_Mutation	T	C	novel	P41_T1	c.760A>G	p.Asn254Asp	256	230	26	36	36	0	protein_coding	YES	MODERATE	SNV
DBNL	GRCh38	chr7	44044748	44044748	+	Missense_Mutation	A	G	novel	P41_T1	c.111A>G	p.Asn4Ser	190	158	29	37	37	0	protein_coding	YES	MODERATE	SNV
PLPP6	GRCh38	chr9	4662587	4662587	+	Missense_Mutation	T	C	rs1230036818	P41_T1	c.212T>C	p.Phe71Ser	276	266	5	41	39	0	protein_coding	YES	MODERATE	SNV
KIAA2026	GRCh38	chr9	5968586	5968586	+	Missense_Mutation	G	C	rs1375377845	P41_T1	c.1645C>G	p.Pro549Ala	401	390	10	36	36	0	protein_coding	YES	MODERATE	SNV
TYRP1	GRCh38	chr9	12695648	12695648	+	Missense_Mutation	T	G	novel	P41_T1	c.519T>G	p.Asp173Glu	549	539	10	69	69	0	protein_coding	YES	MODERATE	SNV
FBH1	GRCh38	chr10	5936538	5936538	+	Missense_Mutation	C	T	rs372861811	P41_T1	c.3065C>T	p.Ala102Val	247	231	5	40	40	0	protein_coding	YES	MODERATE	SNV
HBE1	GRCh38	chr11	5269560	5269560	+	Missense_Mutation	G	T	novel	P41_T1	c.209C>A	p.Thr70Asn	245	220	25	37	37	0	protein_coding	YES	MODERATE	SNV
TRIM44	GRCh38	chr11	35685337	35685337	+	Splice_Site	G	C	novel	P41_T1	c.747+1G>C		279	273	6	23	23	0	protein_coding	YES	HIGH	SNV
TJP3	GRCh38	chr19	3746638	3746638	+	Missense_Mutation	C	T	rs571782828	P41_T1	c.2191C>T	p.Arg731Cys	201	147	54	43	43	0	protein_coding	YES	MODERATE	SNV
ZNF578	GRCh38	chr19	52510655	52510655	+	Nonsense_Mutation	A	T	novel	P41_T1	c.274A>T	p.Arg92Ter	655	576	79	94	94	0	protein_coding	YES	HIGH	SNV
UBR3	GRCh38	chr2	1.7E+08	1.7E+08	+	Missense_Mutation	G	C	novel	P42_T1	c.5596G>C	p.Glu1866Gln	232	138	94	21	21	0	protein_coding	YES	MODERATE	SNV
CRIP3	GRCh38	chr6	43306500	43306500	+	Missense_Mutation	T	C	novel	P42_T1	c.346A>G	p.Thr116Ala	89	81	7	20	20	0	protein_coding	YES	MODERATE	SNV
KANK1	GRCh38	chr9	712006	712006	+	Missense_Mutation	G	A	rs776859009	P42_T1	c.1240G>A	p.Val414Met	206	200	6	52	52	0	protein_coding	YES	MODERATE	SNV
PPP4R1	GRCh38	chr18	9550370	9550371	+	Nonsense_Mutation	TA	-	novel	P42_T1	c.2319_2320del		227	67	72	35	20	0	protein_coding	YES	HIGH	deletion
GPX4	GRCh38	chr19	1105695	1105695	+	Missense_Mutation	C	T	rs772822658	P42_T1	c.362C>T	p.Ala121Val	104	86	17	41	39	0	protein_coding	YES	MODERATE	SNV
PLEKHH2	GRCh38	chr2	43712280	43712280	+	Missense_Mutation	A	G	novel	P43_T1	c.2357A>G	p.Glu786Gly	326	319	5	118	118	0	protein_coding	YES	MODERATE	SNV
ALMS1	GRCh38	chr2	73449103	73449103	+	Missense_Mutation	C	A	novel	P43_T1	c.2576C>A	p.Ala859Glu	391	384	6	125	125	0	protein_coding	YES	MODERATE	SNV
DUSP22	GRCh38	chr6	345924	345924	+	Missense_Mutation	C	A	novel	P43_T1	c.259C>A	p.His87Asn	176	170	6	46	46	0	protein_coding	YES	MODERATE	SNV
ZCWPW1	GRCh38	chr7	1E+08	1E+08	+	Missense_Mutation	G	A	novel	P43_T1	c.406C>T	p.Pro136Ser	326	315	6	101	100	0	protein_coding	YES	MODERATE	SNV
PRRC2B	GRCh38	chr9	1.31E+08	1.31E+08	+	Missense_Mutation	C	A	novel	P43_T1	c.3784C>A	p.His1262Asn	169	163	5	61	60	0	protein_coding	YES	MODERATE	SNV
SIRT3	GRCh38	chr11	233128	233128	+	Missense_Mutation	G	T	novel	P43_T1	c.561C>A	p.His187Gln	280	271	6	64	64	0	protein_coding	YES	MODERATE	SNV
ABCC11	GRCh38	chr16	48167523	48167523	+	Missense_Mutation	G	T	novel	P43_T1	c.4029C>A	p.Asp1343Glu	505	478	26	126	126	0	protein_coding	YES	MODERATE	SNV
TRIO	GRCh38	chr5	14497865	14497865	+	Missense_Mutation	A	T	novel	P44_T1	c.8038A>T	p.Ile2680Phe	36	22	14	23	23	0	protein_coding	YES	MODERATE	SNV
FBXL7	GRCh38	chr5	15927947	15927947	+	Missense_Mutation	C	G	novel	P44_T1	c.185C>G	p.Pro62Arg	37	22	13	61	60	0	protein_coding	YES	MODERATE	SNV
RIFK1	GRCh38	chr6	3105907	3105907	+	Missense_Mutation	A	A	rs772895143	P44_T1	c.1432C>A	p.Pro478Thr	25	11	14	54	53	0	protein_coding	YES	MODERATE	SNV
NFX1	GRCh38	chr9	33294796	33294796	+	Missense_Mutation	A	T	novel	P44_T1	c.402A>T	p.Leu134Phe	27	5	22	64	64	0	protein_coding	YES	MODERATE	SNV
TEP1	GRCh38	chr14	20389742	20389742	+	Splice_Site	T	A	novel	P44_T1	c.2335-2A>T		33	23	10	71	71	0	protein_coding	YES	HIGH	SNV
GALK2	GRCh38	chr15	49319737	49319737	+	Missense_Mutation	C	A	novel	P44_T1	c.1101C>A	p.Ser367Arg	32	15	17	70	70	0	protein_coding	YES	MODERATE	SNV
FAM110C	GRCh38	chr2	46181	46181	+	Nonsense_Mutation	T	A	novel	P45_T1	c.205A>T	p.Lys69Ter	42	36	5	72	72	0	protein_coding	YES	HIGH	SNV
ALMS1	GRCh38	chr2	73450719	73450719	+	Missense_Mutation	G	A	rs1445963295	P45_T1	c.4192G>A	p.Gly1398Ser	295	288	7	163	162	0	protein_coding	YES	MODERATE	SNV
ZNF595	GRCh38	chr4	87359	87359	+	Missense_Mutation	T	C	rs998446351	P45_T1	c.1855T>C	p.Ser619Pro	204	196	8	106	106	0	protein_coding	YES	MODERATE	SNV
TMEM129	GRCh38	chr4	1720672	1720672	+	Missense_Mutation	T	G	novel	P45_T1	c.166A>C	p.Thr56Pro	155	147	8	80	80	0	protein_coding	YES	MODERATE	SNV
OXCT1	GRCh38	chr5	41739419	41739419	+	Missense_Mutation	C	T	rs778813276	P45_T1	c.1492G>A	p.Val498Ile	159	154	5	59	59	0	protein_coding	YES	MODERATE	SNV
BAZ1B	GRCh38	chr7	73459553	73459553	+	Missense_Mutation	T	A	novel	P45_T1	c.3415A>T	p.Met1139Leu	219	188	29	75	75	0	protein_coding	YES	MODERATE	SNV
GNB2	GRCh38	chr7	1.01E+08	1.01E+08	+	Missense_Mutation	C	T	rs1193860550	P45_T1	c.746C>T	p.Thr249Met	112	106	6	40	40	0	protein_coding	YES	MODERATE	SNV
TRIM66	GRCh38	chr11	8640870	8640870	+	Missense_Mutation	T	G	novel	P45_T1	c.1505A>C	p.Gln502Pro	163	157	6	129	126	1	protein_coding	YES	MODERATE	SNV
TEP1	GRCh38	chr14	20389638	20389638	+	Missense_Mutation	C	A	novel	P45_T1	c.2437G>T	p.Gly813Cys	131	126	5	111	111	0	protein_coding	YES	MODERATE	SNV
CGNL1	GRCh38	chr15	57545621	57545621	+	Missense_Mutation	G	A	rs1374754801	P45_T1	c.3530C>A	p.Arg1177Gln										

Table S2 (continued)

Hugo_Symbol	NCBI_Build	Chromosome	Start_Position	End_Position	Strand	Variant_Classification	Reference_Allele	Tumor_Seq_Allele2	dbSNP_RS	Tumor_Sample_Barcode	HGVSc	HGVSp	t_depth	t_ref_count	t_alt_count	n_depth	n_ref_count	n_alt_count	BIOTYPE	CANONICAL	IMPACT	VARIANT_CLASS
OR2S2	GRCh38	chr9	35957457	35957457	+	Missense_Mutation	G	C	novel	P49_T1	c.642C>G	p.Phe214Leu	117	110	5	77	77	0	protein_coding	YES	MODERATE	SNV
OR2S2	GRCh38	chr9	35957877	35957877	+	Missense_Mutation	G	C	novel	P49_T1	c.222C>G	p.Phe74Leu	147	140	5	87	86	0	protein_coding	YES	MODERATE	SNV
OR2S2	GRCh38	chr9	35957930	35957930	+	Missense_Mutation	G	A	rs1194862600	P49_T1	c.168C>T	p.His57Tyr	132	124	8	85	85	0	protein_coding	YES	MODERATE	SNV
OR2S2	GRCh38	chr9	35957991	35957991	+	Nonsense_Mutation	G	C	rs144882847	P49_T1	c.108C>G	p.Tyr96Ter	168	162	6	95	94	1	protein_coding	YES	HIGH	SNV
DIP2C	GRCh38	chr10	327110	327110	+	Missense_Mutation	C	T	rs780701624	P49_T1	c.3820C>A	p.Ala1274Thr	324	315	5	115	112	0	protein_coding	YES	MODERATE	SNV
CRACR2B	GRCh38	chr11	830110	830110	+	Missense_Mutation	G	T	rs557608054	P49_T1	c.583G>T	p.Gly195Cys	123	117	6	78	78	0	protein_coding	YES	MODERATE	SNV
PDHX	GRCh38	chr11	34916702	34916702	+	Missense_Mutation	A	C	rs118136428	P49_T1	c.47A>C	p.Tyr18Ser	141	133	6	89	88	0	protein_coding	YES	MODERATE	SNV
PAFAH1B2	GRCh38	chr11	1.17E+08	1.17E+08	+	Missense_Mutation	C	T	rs75287568	P49_T1	c.554C>T	p.Ala185Val	174	167	7	77	76	0	protein_coding	YES	MODERATE	SNV
KCNJ1	GRCh38	chr11	1.29E+08	1.29E+08	+	Missense_Mutation	A	T	novel	P49_T1	c.692T>A	p.Leu231Gln	178	141	34	84	84	0	protein_coding	YES	MODERATE	SNV
MYO1A	GRCh38	chr12	57038921	57038921	+	Missense_Mutation	T	A	novel	P49_T1	c.1421A>T	p.Gln474Leu	221	101	118	74	73	0	protein_coding	YES	MODERATE	SNV
NDN	GRCh38	chr15	23687132	23687132	+	Nonsense_Mutation	G	T	novel	P49_T1	c.86C>A	p.Ser29Ter	240	231	7	143	143	0	protein_coding	YES	HIGH	SNV
UBE2O	GRCh38	chr17	76399587	76399587	+	Missense_Mutation	G	T	novel	P49_T1	c.1490C>A	p.Ser497Tyr	146	140	6	93	93	0	protein_coding	YES	MODERATE	SNV
L3MBTL4	GRCh38	chr18	6243399	6243399	+	Missense_Mutation	C	T	rs202225184	P49_T1	c.355G>A	p.Asp119Asn	250	242	7	88	86	0	protein_coding	YES	MODERATE	SNV
CEP76	GRCh38	chr18	12699071	12699071	+	Missense_Mutation	C	T	rs202117013	P49_T1	c.428G>A	p.Arg143Gln	320	312	7	77	77	0	protein_coding	YES	MODERATE	SNV
AFID3A	GRCh38	chr19	964859	964859	+	Missense_Mutation	A	T	novel	P49_T1	c.977A>T	p.Glu326Val	89	35	53	57	57	0	protein_coding	YES	MODERATE	SNV
ATP5F1D	GRCh38	chr19	1244417	1244417	+	Missense_Mutation	C	A	rs865966395	P49_T1	c.487C>A	p.Leu163Met	116	109	6	95	95	0	protein_coding	YES	MODERATE	SNV
DUS3L	GRCh38	chr19	5790316	5790316	+	Nonsense_Mutation	G	A	novel	P49_T1	c.118C>T	p.Gln40Ter	121	115	6	50	49	0	protein_coding	YES	HIGH	SNV
TMEM205	GRCh38	chr19	11342865	11342865	+	Missense_Mutation	T	C	novel	P49_T1	c.520A>G	p.Ser174Gly	112	105	6	78	78	0	protein_coding	YES	MODERATE	SNV
PSMC4	GRCh38	chr19	39972540	39972540	+	Missense_Mutation	G	A	novel	P49_T1	c.307G>A	p.Val103Met	140	132	6	67	67	0	protein_coding	YES	MODERATE	SNV
SNX21	GRCh38	chr20	45841242	45841242	+	Nonsense_Mutation	C	T	novel	P49_T1	c.1051C>T	p.Gln351Ter	226	201	7	118	109	0	protein_coding	YES	HIGH	SNV
TAF1	GRCh38	chrX	71401711	71401711	+	Missense_Mutation	A	T	novel	P49_T1	c.4030A>T	p.Ile1344Phe	175	40	134	50	50	0	protein_coding	YES	MODERATE	SNV
CTNNB1	GRCh38	chr3	41224612	41224612	+	Missense_Mutation	G	A	rs121913399	P5_T1	c.100G>A	p.Gly34Arg	323	236	87	195	195	0	protein_coding	YES	MODERATE	SNV
TIPARP	GRCh38	chr3	1.57E+08	1.57E+08	+	Missense_Mutation	C	T	novel	P5_T1	c.380C>T	p.Ser127Phe	407	282	125	225	225	0	protein_coding	YES	MODERATE	SNV
PHOX2B	GRCh38	chr4	41745994	41746011	+	In_Frame_Del	GCCGCGCCCGCTGCCCGG	-	rs771383153	P5_T1	c.741_758del	p.Ala255_Ala260del	41	38	3	31	31	0	protein_coding	YES	MODERATE	deletion
ROS1	GRCh38	chr6	1.17E+08	1.17E+08	+	Missense_Mutation	C	G	novel	P5_T1	c.5854G>C	p.Gly1952Arg	301	116	185	264	264	0	protein_coding	YES	MODERATE	SNV
QKI	GRCh38	chr6	1.64E+08	1.64E+08	+	Missense_Mutation	G	T	novel	P5_T1	c.964G>T	p.Asp322Tyr	329	129	200	181	180	1	protein_coding	YES	MODERATE	SNV
EPHB4	GRCh38	chr7	1.01E+08	1.01E+08	+	Missense_Mutation	A	A	rs759227832	P5_T1	c.950G>T	p.Gly317Val	287	155	132	71	71	0	protein_coding	YES	MODERATE	SNV
BWM-ERCC5	GRCh38	chr13	1.03E+08	1.03E+08	+	Missense_Mutation	T	G	novel	P5_T1	c.3835T>G	p.Phe1279Val	452	330	122	108	108	0	protein_coding	YES	MODERATE	SNV
TRAF7	GRCh38	chr16	2172259	2172259	+	Missense_Mutation	G	C	novel	P5_T1	c.546G>C	p.Gly182Arg	331	300	31	53	53	0	protein_coding	YES	MODERATE	SNV
TP53	GRCh38	chr17	7675206	7675206	+	Frame_Shift_Del	-	-	novel	P5_T1	c.406del	p.Gln136AsnfsTer34	247	60	187	89	89	0	protein_coding	YES	HIGH	deletion
KEAP1	GRCh38	chr19	10499694	10499694	+	Missense_Mutation	C	T	novel	P5_T1	c.340G>A	p.Gly114Arg	314	72	242	93	93	0	protein_coding	YES	MODERATE	SNV
KMT2B	GRCh38	chr19	35727506	35727506	+	Missense_Mutation	G	A	novel	P5_T1	c.4186G>A	p.Ala1396Thr	262	54	208	19	19	0	protein_coding	YES	MODERATE	SNV
SRRM1	GRCh38	chr1	24645985	24645985	+	Missense_Mutation	G	A	novel	P50_T1	c.23G>A	p.Gly9Glu	270	254	15	80	79	0	protein_coding	YES	MODERATE	SNV
PRRC2C	GRCh38	chr1	1.72E+08	1.72E+08	+	Missense_Mutation	A	T	novel	P50_T1	c.2930A>T	p.Glu977Val	213	205	7	129	128	0	protein_coding	YES	MODERATE	SNV
LG66	GRCh38	chr1	2.02E+08	2.02E+08	+	Missense_Mutation	G	G	rs376357186	P50_T1	c.515A>G	p.Asn172Ser	126	120	5	67	67	0	protein_coding	YES	MODERATE	SNV
CNTN2	GRCh38	chr1	2.05E+08	2.05E+08	+	Nonsense_Mutation	C	T	novel	P50_T1	c.124C>T	p.Gln42Ter	175	169	6	73	72	0	protein_coding	YES	HIGH	SNV
TAF5L	GRCh38	chr1	2.3E+08	2.3E+08	+	Missense_Mutation	C	T	rs55655740	P50_T1	c.721G>A	p.Val241Ile	187	275	9	158	156	1	protein_coding	YES	MODERATE	SNV
XPC	GRCh38	chr3	14158112	14158112	+	Missense_Mutation	T	A	rs751819500	P50_T1	c.1771A>T	p.Thr591Ser	329	321	8	149	148	0	protein_coding	YES	MODERATE	SNV
TTC21A	GRCh38	chr3	39133205	39133205	+	Missense_Mutation	A	G	rs199602060	P50_T1	c.2737A>G	p.Lys913Glu	170	165	5	70	70	0	protein_coding	YES	MODERATE	SNV
USP4	GRCh38	chr3	49335472	49335472	+	Missense_Mutation	A	G	novel	P50_T1	c.226T>C	p.Ser76Pro	294	274	16	82	81	0	protein_coding	YES	MODERATE	SNV
YEATS2	GRCh38	chr3	1.84E+08	1.84E+08	+	Missense_Mutation	T	C	rs759145989	P50_T1	c.2165T>C	p.Val722Ala	237	229	5	120	117	0	protein_coding	YES	MODERATE	SNV
SLAIN2	GRCh38	chr4	48422058	48422058	+	Nonsense_Mutation	G	A	novel	P50_T1	c.1727G>A	p.Trp576Ter	179	173	6	84	83	0	protein_coding	YES	HIGH	SNV
SDHA	GRCh38	chr5	228048	228048	+	Splice_Site	A	A	novel	P50_T1	c.621+1G>A	-	154	148	5	86	85	0	protein_coding	YES	HIGH	SNV
ICE1	GRCh38	chr5	5462500	5462500	+	Missense_Mutation	C	T	rs751117948	P50_T1	c.3166C>T	p.Pro1056Ser	152	141	10	111	110	0	protein_coding	YES	MODERATE	SNV
TRIO	GRCh38	chr5	14389321	14389321	+	Missense_Mutation	A	T	novel	P50_T1	c.3981A>T	p.Glu1327Asp	217	208	6	80	80	0	protein_coding	YES	MODERATE	SNV
TRIO	GRCh38	chr5	14507220	14507220	+	Missense_Mutation	A	A	rs182365882	P50_T1	c.8711G>A	p.Arg2904Gln	183	169	13	102	99	0	protein_coding	YES	MODERATE	SNV
PDZD2	GRCh38	chr5	32087307	32087307	+	Missense_Mutation	G	A	rs755562193	P50_T1	c.3859G>A	p.Glu1287Lys	145	122	7	84	80	0	protein_coding	YES	MODERATE	SNV
SPEF2	GRCh38	chr5	35806787	35806787	+	Missense_Mutation	A	T	novel	P50_T1	c.5091A>T	p.Lys1697Asn	340	322	16	127	125	0	protein_coding	YES	MODERATE	SNV
HMGCS1	GRCh38	chr5	43291166	43291166	+	Missense_Mutation	G	T	rs754716585	P50_T1	c.1528C>A	p.Pro510Thr	175	165	6	23	23	0	protein_coding	YES	MODERATE	SNV
EXOC2	GRCh38	chr6	576850	576850	+	Missense_Mutation	G	A	novel	P50_T1	c.1225C>T	p.Leu409Phe	212	205	6	102	102	0	protein_coding	YES	MODERATE	SNV
SLC17A1	GRCh38	chr6	25811758	25811758	+	Missense_Mutation	A	G	novel	P50_T1	c.910T>C	p.Ser304Pro	293	286	6	115	113	0	protein_coding	YES	MODERATE	SNV
PPP1R17	GRCh38	chr7	31695547	31695547	+	Missense_Mutation	T	A	novel	P50_T1	c.161T>A	p.Leu54Gln	167	160	6	102	99	0	protein_coding	YES	MODERATE	SNV
ZAN	GRCh38	chr7	1.01E+08	1.01E+08	+	Missense_Mutation	A	G	rs78193191	P50_T1	c.5765A>G	p.His1922Arg	228	189	13	70	65	0	protein_coding	YES	MODERATE	SNV
ADCK5	GRCh38	chr8	1.44E+08	1.44E+08	+	In_Frame_Ins	-	GCGGGTCAAGGTGA	rs148509143	P50_T1	c.1260_1267+7dup	164	74	12	80	59	0	protein_coding	YES	MODERATE	insertion	
DMRT1	GRCh38	chr9	841965	841965	+	Missense_Mutation	A	T	novel	P50_T1	c.127A>T	p.Ser43Cys	94	89	5	69	67	0	protein_coding	YES	MODERATE	SNV
TPD52L3	GRCh38	chr9																				

Table S2 (continued)

Hugo_Symbol	NCBI_Build	Chromosome	Start_Position	End_Position	Strand	Variant_Classification	Reference_Allele	Tumor_Seq_Allele2	dbSNP_RS	Tumor_Sample_Barcode	HGVSc	HGVSp	t_depth	t_ref_count	t_alt_count	n_depth	n_ref_count	n_alt_count	BIOTYPE	CANONICAL	IMPACT	VARIANT_CLASS
CD79A	GRCh38	chr19	41880940	41880940	+	Missense_Mutation	G	A	novel	P7_T1	c.641G>A	p.Gly214Asp	209	205	4	18	17	1	protein_coding	YES	MODERATE	SNV
STAG2	GRCh38	chrX	1.24E+08	1.24E+08	+	Missense_Mutation	C	T	rs1375196362	P7_T1	c.899C>T	p.Ala300Val	171	167	4	27	26	1	protein_coding	YES	MODERATE	SNV
BCORL1	GRCh38	chrX	1.3E+08	1.3E+08	+	Missense_Mutation	G	A	novel	P7_T1	c.3233G>A	p.Gly1078Asp	276	271	5	17	17	0	protein_coding	YES	MODERATE	SNV
ARID1A	GRCh38	chr1	26780655	26780656	+	Frame_Shift_Ins	-	TG	novel	P8_T1	c.6759_6760dup	p.Tyr2254CysfsTer14	951	382	569	19	19	0	protein_coding	YES	HIGH	insertion
ALK	GRCh38	chr2	29239753	29239753	+	Missense_Mutation	C	T	novel	P8_T1	c.2282G>A	p.Gly761Asp	1454	915	539	53	53	0	protein_coding	YES	MODERATE	SNV
TEK4	GRCh38	chr2	94871614	94871614	+	Missense_Mutation	G	A	novel	P8_T1	c.35G>A	p.Cys12Tyr	382	376	6	16	16	0	protein_coding	YES	MODERATE	SNV
CTNNB1	GRCh38	chr3	41224609	41224609	+	Missense_Mutation	T	C	rs1057519886	P8_T1	c.97T>C	p.Ser33Pro	1499	874	625	44	44	0	protein_coding	YES	MODERATE	SNV
PLK2	GRCh38	chr5	58459774	58459782	+	In_Frame_Del	ATGGTGGTG	-	rs1561217633	P8_T1	c.178_186del	p.His60_His62del	782	520	262	10	10	0	protein_coding	YES	MODERATE	deletion
KMT2C	GRCh38	chr7	1.52E+08	1.52E+08	+	Missense_Mutation	A	G	rs761007667	P8_T1	c.2882T>C	p.Val961Ala	834	751	83	30	30	0	protein_coding	YES	MODERATE	SNV
TGFBR1	GRCh38	chr9	99137956	99137956	+	Nonsense_Mutation	G	A	rs201021249	P8_T1	c.684G>A	p.Trp228Ter	1853	1211	642	73	73	0	protein_coding	YES	HIGH	SNV
NF1	GRCh38	chr17	31343055	31343055	+	Missense_Mutation	A	T	novel	P8_T1	c.7109A>T	p.His2370Leu	1824	1128	696	62	62	0	protein_coding	YES	MODERATE	SNV
STAT5A	GRCh38	chr17	42301381	42301381	+	Frame_Shift_Del	C	-	rs759027671	P8_T1	c.1102del	p.Gln368ArgfsTer2	1573	1552	21	34	34	0	protein_coding	YES	HIGH	deletion
KEAP1	GRCh38	chr19	10489753	10489753	+	Missense_Mutation	C	A	novel	P8_T1	c.1426G>T	p.Gly476Trp	890	377	513	86	86	0	protein_coding	YES	MODERATE	SNV
CCNE1	GRCh38	chr19	29817491	29817491	+	Missense_Mutation	C	A	novel	P8_T1	c.412C>A	p.Pro138Thr	1934	1233	701	117	117	0	protein_coding	YES	MODERATE	SNV
MST1R	GRCh38	chr3	49902534	49902534	+	Missense_Mutation	C	T	novel	P9_T1	c.1076G>A	p.Gly359Asp	1191	938	253	90	90	0	protein_coding	YES	MODERATE	SNV
FOXL2	GRCh38	chr3	1.39E+08	1.39E+08	+	Frame_Shift_Del	GGGCTCGGGCGGCCCTTCTGGCTCC TTGACTGTGGACCGTCTCTGGGGCCA GCAGGGCCCCCGCGCTCCTC	-	novel	P9_T1	c.25_101del	p.Glu8ArgfsTer61	698	691	7	62	62	0	protein_coding	YES	HIGH	deletion
ARID1B	GRCh38	chr6	1.57E+08	1.57E+08	+	Missense_Mutation	C	G	rs797045270	P9_T1	c.1379C>G	p.Ala460Gly	372	363	9	17	17	0	protein_coding	YES	MODERATE	SNV
FGF4	GRCh38	chr11	69774909	69774909	+	Missense_Mutation	G	A	novel	P9_T1	c.176C>T	p.Pro59Leu	959	913	46	39	39	0	protein_coding	YES	MODERATE	SNV
TP53	GRCh38	chr17	7674216	7674216	+	Missense_Mutation	C	A	rs28934571	P9_T1	c.747G>T	p.Arg249Ser	580	427	153	84	84	0	protein_coding	YES	MODERATE	SNV
NOTCH3	GRCh38	chr19	15186963	15186963	+	Missense_Mutation	G	C	novel	P9_T1	c.1866C>G	p.Asp622Glu	671	530	141	80	80	0	protein_coding	YES	MODERATE	SNV