Supplementary Table 2: *Details of variants.*

Patient number	Gene	Type of gene	Pathway	Chromosome	Start	End	Reference	Alteration	Location	Type	C_point	P_point	P_point	Closest_exon	Depth_of_coverage_S1	Allelic_ratio_S1
1	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7578406	7578406	C	T	exonic	nonsynonymous_SNV	c.524G>A	p.(Arg175His)	R175H	5	3213	32.84
2	*NFE2L2*	ONCOGENE	OXYDATIVE STRESS	chr2	178098945	178098945	G	C	exonic	nonsynonymous_SNV	c.100C>G	p.(Arg34Gly)	R34G	2	70	25.71
2	*PIK3CA*	ONCOGENE	PI3K	chr3	178916929	178916929	G	A	exonic	nonsynonymous_SNV	c.316G>A	p.(Gly106Ser)	G106S	2	48	16.67
2	*TERT*	ONCOGENE	SENESCENCE	chr5	1295228	1295228	G	A	upstream	NA	NA	NA	NA	1	499	14.23
3	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7577058	7577058	C	A	exonic	stopgain	c.880G>T	p.(Glu294Ter)	E294X	8	2618	52.41
4	*CDKN2A*	TUMOR SUPRESSOR	CELL CYCLE	chr9	21971191	21971191	GC	G	exonic	frameshift_deletion	c.167del	p.(Ser56ThrfsTer90)	S56TfsX90	2	3651	25.42
4	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7578439	7578440	T	TTGTAGATGGCC	exonic	frameshift_insertion	c.480_490dup	p.(Lys164ArgfsTer10)	K164RfsX10	5	5765	8.05
4	*U2AF1*	ONCOGENE	OTHER	chr21	44524486	44524486	A	G	exonic	nonsynonymous_SNV	c.71T>C	p.(Ile24Thr)	I24T	2	83	25.3
4	*TERT*	ONCOGENE	SENESCENCE	chr5	1295250	1295250	G	A	upstream	NA	NA	NA	NA	1	494	68.83
5	*KMT2B*	TUMOR SUPRESSOR	EPIGENETIC	chr19	36213970	36213971	T	TG	exonic	frameshift_insertion	c.2801dup	p.(Glu935ArgfsTer60)	E935RfsX60	6	3043	12.39
5	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7578508	7578508	C	T	exonic	nonsynonymous_SNV	c.422G>A	p.(Cys141Tyr)	C141Y	5	2181	16.74
5	*TERT*	ONCOGENE	SENESCENCE	chr5	1295228	1295228	G	A	upstream	NA	NA	NA	NA	1	544	25.74
6	*TET2*	TUMOR SUPRESSOR	EPIGENETIC	chr4	106164076	106164076	TG	T	konic;splicir	frameshift_deletion	c.3586del	p.(Ala1196LeufsTer30)	A1196LfsX30	5	245	5.71
6	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7577538	7577538	C	T	exonic	nonsynonymous_SNV	c.743G>A	p.(Arg248Gln)	R248Q	7	2558	11.85
6	*NCKAP1*	TUMOR SUPRESSOR	OTHER	chr2	183822240	183822240	TC	T	exonic	frameshift_deletion	c.1984del	p.(Glu662LysfsTer10)	E662KfsX10	20	202	5.94
7	*NOTCH1*	BOTH	DEVELOPMENT	chr9	139393364	139393370	CATATCTT	C	exonic	frameshift_deletion	c.6161_6167del	p.(Lys2054SerfsTer55)	K2054SfsX55	33	3655	12.34
7	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7577106	7577106	G	T	exonic	nonsynonymous_SNV	c.832C>A	p.(Pro278Thr)	P278T	8	1136	5.11
8	*NOTCH1*	BOTH	DEVELOPMENT	chr9	139413214	139413214	C	T	exonic	nonsynonymous_SNV	c.928G>A	p.(Gly310Arg)	G310R	6	3513	18.47
8	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7578263	7578263	G	A	exonic	stopgain	c.586C>T	p.(Arg196Ter)	R196X	6	3490	14.27
8	*ZRSR2*	TUMOR SUPRESSOR	OTHER	chrX	15841230	NA	C	CAGCCGGAGCCGG	exonic	nonframeshift_insertion	c.1314_1315insAGCCGGAGCCGG	p.G438delinsGSRSR	G438delinsGSRSR	NA	696	29
8	*TERT*	ONCOGENE	SENESCENCE	chr5	1295228	1295228	G	A	upstream	NA	NA	NA	NA	1	349	6.88
9	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7576855	7576855	G	A	konic;splicir	stopgain	c.991C>T	p.(Gln331Ter)	Q331X	9	1216	19.49
9	*TERT*	ONCOGENE	SENESCENCE	chr5	1295228	1295228	G	A	upstream	NA	NA	NA	NA	1	165	11.52
10	*KMT2D*	TUMOR SUPRESSOR	EPIGENETIC	chr12	49423021	49423021	T	A	splicing	NA	c.14076-2A>T	p.?	?	44	1007	40.02
10	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7579341	7579341	GA	G	exonic	frameshift_deletion	c.346del	p.(Ser116LeufsTer7)	S116LfsX7	4	882	66.78
10	*DICER1*	TUMOR SUPRESSOR	OTHER	chr14	95557703	95557703	C	G	splicing	NA	c.5365-1G>C	p.?	?	25	217	5.07
11	*FAT1*	TUMOR SUPRESSOR	DIFFERENCIATION CELL	chr4	187540375	187540376	G	GGGGC	exonic	frameshift_insertion	c.7364_7365insGGCC	p.(His2455GlnfsTer11)	H2455QfsX11	10	1718	10.71
11	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7578394	7578394	T	C	exonic	nonsynonymous_SNV	c.536A>G	p.(His179Arg)	H179R	5	3439	29.54
11	*TERT*	ONCOGENE	SENESCENCE	chr5	1295228	1295228	G	A	upstream	NA	NA	NA	NA	1	185	9.19
12	*CDKN2A*	TUMOR SUPRESSOR	CELL CYCLE	chr9	21971208	21971208	C	T	splicing	NA	c.151-1G>A	p.?	?	2	2500	28.56
12	*FAT2*	TUMOR SUPRESSOR	DIFFERENCIATION CELL	chr5	150887151	150887161	AACCCCTCGCCT	A	exonic	frameshift_deletion	c.12071_12081del	p.(Glu4024ValfsTer67)	E4024VfsX67	22	692	12.72
12	*NOTCH1*	BOTH	DEVELOPMENT	chr9	139390923	139390923	G	C	exonic	stopgain	c.7268C>G	p.(Ser2423Ter)	S2423X	34	2589	14.29
12	*NOTCH1*	BOTH	DEVELOPMENT	chr9	139396523	139396523	G	C	exonic	stopgain	c.5402C>G	p.(Ser1801Ter)	S1801X	29	2258	16.25
12	*BCOR*	TUMOR SUPRESSOR	EPIGENETIC	chrX	39922984	39922984	G	A	exonic	stopgain	c.3724C>T	p.(Gln1242Ter)	Q1242X	8	1336	25.82
12	*PIK3CA*	ONCOGENE	PI3K	chr3	178936091	178936091	G	A	exonic	nonsynonymous_SNV	c.1633G>A	p.(Glu545Lys)	E545K	10	25	48
12	*TERT*	ONCOGENE	SENESCENCE	chr5	1295228	1295228	G	A	upstream	NA	NA	NA	NA	1	257	15.56
13	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7577609	7577609	C	T	splicing	NA	c.673-1G>A	p.?	?	7	1166	8.23
13	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7579591	7579591	C	A	splicing	NA	c.97-1G>T	p.?	?	4	3253	6.27
13	*CUX1*	TUMOR SUPRESSOR	OTHER	chr7	101840058	101840058	T	G	exonic	stopgain	c.1400T>G	p.(Leu467Ter)	L467X	15	1574	5.08
13	*PXDNL*	TUMOR SUPRESSOR	OTHER	chr8	52320883	52320884	G	GA	exonic	frameshift_insertion	c.3300dup	p.(Leu1101SerfsTer10)	L1101SfsX10	17	983	6.82
13	*TERT*	ONCOGENE	SENESCENCE	chr5	1295250	1295250	G	A	upstream	NA	NA	NA	NA	1	146	8.22
14	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7578212	7578212	G	A	exonic	stopgain	c.637C>T	p.(Arg213Ter)	R213X	6	2580	11.67
14	*ZFHX3*	TUMOR SUPRESSOR	CRIPTION FACTOR-REGUL	chr16	72821593	NA	.	<DEL>	exonic	frameshift_deletion	c.10570_10582del	p.G3524fs	G3524fs	NA	2357	30
14	*TERT*	ONCOGENE	SENESCENCE	chr5	1295228	1295228	G	A	upstream	NA	NA	NA	NA	1	318	7.86
15	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7578176	7578176	C	A	splicing	NA	c.672+1G>T	p.?	?	6	1877	27.65
15	*AJUBA*	TUMOR SUPRESSOR	OTHER	chr14	23445728	23445728	C	T	splicing	NA	c.1177-1G>A	p.?	?	4	1026	33.33
16	*CHD1*	TUMOR SUPRESSOR	EPIGENETIC	chr5	98228389	98228389	C	A	exonic	stopgain	c.2020G>T	p.(Glu674Ter)	E674X	14	300	5
16	*KMT2C*	TUMOR SUPRESSOR	EPIGENETIC	chr7	151864441	151864441	A	T	exonic	stopgain	c.9540T>A	p.(Tyr3180Ter)	Y3180X	42	658	27.66
16	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7578175	7578175	A	G	splicing	NA	c.672+2T>C	p.?	?	6	1219	28.3
16	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7578406	7578406	C	T	exonic	nonsynonymous_SNV	c.524G>A	p.(Arg175His)	R175H	5	2799	16.65
16	*ZFP36L2*	TUMOR SUPRESSOR	CRIPTION FACTOR-REGUL	chr2	43452637	43452638	C	CT	exonic	frameshift_insertion	c.305dup	p.(Glu103GlyfsTer23)	E103GfsX23	2	1062	5.56
16	*TERT*	ONCOGENE	SENESCENCE	chr5	1295228	1295228	G	A	upstream	NA	NA	NA	NA	1	249	63.45
17	*CDKN2A*	TUMOR SUPRESSOR	CELL CYCLE	chr9	21971120	21971120	G	A	exonic	stopgain	c.238C>T	p.(Arg80Ter)	R80X	2	2284	66.07
17	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7573982	7573982	C	A	exonic	stopgain	c.1045G>T	p.(Glu349Ter)	E349X	10	922	44.79
17	*ZFHX3*	TUMOR SUPRESSOR	CRIPTION FACTOR-REGUL	chr16	72991696	NA	.	<DEL>	exonic	frameshift_deletion	c.2322_2349del	p.A774fs	A774fs	NA	1828	20
17	*PTEN*	TUMOR SUPRESSOR	PI3K	chr10	89692904	89692904	C	G	exonic	nonsynonymous_SNV	c.388C>G	p.(Arg130Gly)	R130G	5	23	43.48
17	*TERT*	ONCOGENE	SENESCENCE	chr5	1295228	1295228	G	A	upstream	NA	NA	NA	NA	1	154	20.13
18	*CDKN2A*	TUMOR SUPRESSOR	CELL CYCLE	chr9	21971028	21971028	C	T	exonic	stopgain	c.330G>A	p.(Trp110Ter)	W110X	2	2811	38.14
18	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7577538	7577538	C	T	exonic	nonsynonymous_SNV	c.743G>A	p.(Arg248Gln)	R248Q	7	1261	26.41
19	*HIST1H3C*	ONCOGENE	EPIGENETIC	chr6	26045748	26045748	A	T	exonic	nonsynonymous_SNV	c.110A>T	p.(Lys37Met)	K37M	1	1118	9.93
19	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7577081	7577081	T	C	exonic	nonsynonymous_SNV	c.857A>G	p.(Glu286Gly)	E286G	8	1018	17.39
20	*CDKN2A*	TUMOR SUPRESSOR	CELL CYCLE	chr9	21971120	21971120	G	A	exonic	stopgain	c.238C>T	p.(Arg80Ter)	R80X	2	2372	41.78
20	*NOTCH2*	BOTH	DEVELOPMENT	chr1	120512357	120512357	G	T	exonic	stopgain	c.885C>A	p.(Cys295Ter)	C295X	6	265	29.81
20	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7577532	7577532	G	A	exonic	nonsynonymous_SNV	c.749C>T	p.(Pro250Leu)	P250L	7	996	33.43
20	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7577538	7577538	C	T	exonic	nonsynonymous_SNV	c.743G>A	p.(Arg248Gln)	R248Q	7	1064	17.01
21	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7577130	7577130	A	G	exonic	nonsynonymous_SNV	c.808T>C	p.(Phe270Leu)	F270L	8	485	15.88
21	*NFE2L2*	ONCOGENE	OXYDATIVE STRESS	chr2	178098944	178098944	C	A	exonic	nonsynonymous_SNV	c.101G>T	p.(Arg34Leu)	R34L	2	93	9.68
21	*TERT*	ONCOGENE	SENESCENCE	chr5	1295228	1295228	G	A	upstream	NA	NA	NA	NA	1	280	13.57
22	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7579414	7579414	GC	G	exonic	frameshift_deletion	c.273del	p.(Trp91CysfsTer32)	W91CfsX32	4	1450	18.28
22	*TERT*	ONCOGENE	SENESCENCE	chr5	1295250	1295250	G	A	upstream	NA	NA	NA	NA	1	110	18.18
23	*MSH6*	TUMOR SUPRESSOR	DNA REPAIR	chr2	48026605	48026606	C	CGA	exonic	frameshift_insertion	c.1484_1485dup	p.(Cys496AspfsTer15)	C496DfsX15	4	1221	32.68
23	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7578189	7578189	A	T	exonic	stopgain	c.660T>A	p.(Tyr220Ter)	Y220X	6	1425	63.16
23	*TBL1XR1*	TUMOR SUPRESSOR	OTHER	chr3	176768269	176768269	G	C	konic;splicir	stopgain	c.557C>G	p.(Ser186Ter)	S186X	6	441	26.3
24	*CDKN2A*	TUMOR SUPRESSOR	CELL CYCLE	chr9	21968242	21968242	C	T	splicing	NA	c.458-1G>A	p.?	?	3	392	19.39
24	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7579311	7579311	C	T	splicing	NA	c.375+1G>A	p.?	?	4	497	11.87
24	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7577538	7577538	C	A	exonic	nonsynonymous_SNV	c.743G>T	p.(Arg248Leu)	R248L	7	626	9.27
25	*TET2*	TUMOR SUPRESSOR	EPIGENETIC	chr4	106156282	106156285	CACTA	C	exonic	frameshift_deletion	c.1183_1186del	p.(Thr395ProfsTer31)	T395PfsX31	3	210	7.14
25	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7574003	7574003	G	A	exonic	stopgain	c.1024C>T	p.(Arg342Ter)	R342X	10	1362	25.99
25	*PIK3CA*	ONCOGENE	PI3K	chr3	178916946	178916946	G	T	exonic	nonsynonymous_SNV	c.333G>T	p.(Lys111Asn)	K111N	2	69	20.29
25	*TERT*	ONCOGENE	SENESCENCE	chr5	1295228	1295228	G	A	upstream	NA	NA	NA	NA	1	507	21.3
26	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7577022	7577022	G	A	konic;splicir	stopgain	c.916C>T	p.(Arg306Ter)	R306X	8	1584	11.55
26	*PIK3CA*	ONCOGENE	PI3K	chr3	178922321	178922321	G	C	exonic	nonsynonymous_SNV	c.1090G>C	p.(Gly364Arg)	G364R	6	56	14.29

26	*TERT*	ONCOGENE	SENESCENCE	chr5	1295228	1295228	G	A	upstream	NA	NA	NA	NA	1	629	17.01
27	*NOTCH1*	BOTH	DEVELOPMENT	chr9	139440194	139440194	CG	C	exonic	frameshift_deletion	c.45del	p.(Ala16ArgfsTer17)	A16RfsX17	1	5014	17.11
27	*KMT2B*	TUMOR SUPRESSOR	EPIGENETIC	chr19	36223997	36223997	GC	G	exonic	frameshift_deletion	c.6552del	p.(Lys2185AsnfsTer18)	K2185NfsX18	28	2034	6.83
27	*BRAF*	ONCOGENE	RTK/RAS	chr7	140453155	140453155	C	T	exonic	nonsynonymous_SNV	c.1780G>A	p.(Asp594Asn)	D594N	15	74	12.16
27	*TERT*	ONCOGENE	SENESCENCE	chr5	1295228	1295228	G	A	upstream	NA	NA	NA	NA	1	796	7.66
28	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7577105	7577105	G	C	exonic	nonsynonymous_SNV	c.833C>G	p.(Pro278Arg)	P278R	8	220	34.55
28	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7577539	7577539	G	A	exonic	nonsynonymous_SNV	c.742C>T	p.(Arg248Trp)	R248W	7	655	12.67
30	*PIK3CA*	ONCOGENE	PI3K	chr3	178916891	178916891	G	T	exonic	nonsynonymous_SNV	c.278G>T	p.(Arg93Leu)	R93L	2	188	5.85
31	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7577110	7577110	AG	A	exonic	frameshift_deletion	c.828del	p.(Cys277ValfsTer68)	C277VfsX68	8	236	16.95
32	*PTPRB*	TUMOR SUPRESSOR	OTHER	chr12	70970327	70970327	C	A	exonic	stopgain	c.2023G>T	p.(Glu675Ter)	E675X	9	209	7.18
32	*TERT*	ONCOGENE	SENESCENCE	chr5	1295228	1295228	G	A	upstream	NA	NA	NA	NA	1	621	9.18
32	*SMAD4*	TUMOR SUPRESSOR	TGFβ	chr18	48591925	48591925	G	A	exonic	nonsynonymous_SNV	c.1088G>A	p.(Cys363Tyr)	C363Y	9	64	26.56
33	*BRCA1*	TUMOR SUPRESSOR	DNA REPAIR	chr17	41209086	41209086	C	A	exonic	stopgain	c.5260G>T	p.(Glu1754Ter)	E1754X	19	201	6.47
33	*NCOR1*	TUMOR SUPRESSOR	CRIPTION FACTOR-REGUL	chr17	15989715	15989715	C	A	exonic	stopgain	c.3058G>T	p.(Glu1020Ter)	E1020X	23	238	5.88
33	*HIST1H3C*	ONCOGENE	EPIGENETIC	chr6	26045748	26045748	A	T	exonic	nonsynonymous_SNV	c.110A>T	p.(Lys37Met)	K37M	1	2490	10.44
33	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7578266	7578266	T	A	exonic	nonsynonymous_SNV	c.583A>T	p.(Ile195Phe)	I195F	6	4747	12.85
33	*SPOP*	TUMOR SUPRESSOR	OTHER	chr17	47696642	47696642	G	T	exonic	nonsynonymous_SNV	c.306C>A	p.(Phe102Leu)	F102L	6	62	12.9
33	*THSD7B*	TUMOR SUPRESSOR	OTHER	chr2	137988684	137988684	C	A	exonic	stopgain	c.1701C>A	p.(Cys567Ter)	C567X	7	237	9.28
33	*PIK3CA*	ONCOGENE	PI3K	chr3	178916946	178916946	G	C	exonic	nonsynonymous_SNV	c.333G>C	p.(Lys111Asn)	K111N	2	19	63.16
33	*KRAS*	ONCOGENE	RTK/RAS	chr12	25398284	25398284	C	A	exonic	nonsynonymous_SNV	c.35G>T	p.(Gly12Val)	G12V	2	62	19.35
33	*TERT*	ONCOGENE	SENESCENCE	chr5	1295228	1295228	G	A	upstream	NA	NA	NA	NA	1	586	2.39
34	*FAT1*	TUMOR SUPRESSOR	DIFFERENCIATION CELL	chr4	187542410	187542410	G	C	exonic	stopgain	c.5330C>G	p.(Ser1777Ter)	S1777X	10	234	29.91
34	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7577108	7577108	C	A	exonic	nonsynonymous_SNV	c.830G>T	p.(Cys277Phe)	C277F	8	1557	36.54
34	*TERT*	ONCOGENE	SENESCENCE	chr5	1295228	1295228	G	A	upstream	NA	NA	NA	NA	1	308	40.26
35	*KMT2D*	TUMOR SUPRESSOR	EPIGENETIC	chr12	49434618	49434618	G	C	exonic	stopgain	c.6935C>G	p.(Ser2312Ter)	S2312X	31	3185	10.68
35	*SMARCA4*	TUMOR SUPRESSOR	EPIGENETIC	chr19	11150225	11150225	C	G	konic;splicir	stopgain	c.4262C>G	p.(Ser1421Ter)	S1421X	30	1022	15.26
35	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7579345	7579352	GCAAGAAGC	G	exonic	frameshift_deletion	c.335_342del	p.(Gly112AlafsTer34)	G112AfsX34	4	966	11.08
36	*FAT2*	TUMOR SUPRESSOR	DIFFERENCIATION CELL	chr5	150934236	150934236	T	A	splicing	NA	c.3634-2A>T	p.?	?	4	241	67.63
36	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7576928	7576928	T	C	splicing	NA	c.920-2A>G	p.?	?	9	414	70.29
37	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7577105	7577105	G	C	exonic	nonsynonymous_SNV	c.833C>G	p.(Pro278Arg)	P278R	8	1287	19.97
37	*ZFHX3*	TUMOR SUPRESSOR	CRIPTION FACTOR-REGUL	chr16	72821988	NA	.	<DEL>	exonic	frameshift_deletion	c.10166_10187del	p.Q3389fs	Q3389fs	NA	2766	22
38	*KMT2D*	TUMOR SUPRESSOR	EPIGENETIC	chr12	49438044	49438045	TGC	T	exonic	frameshift_deletion	c.5126_5127del	p.(Arg1709HisfsTer25)	R1709HfsX25	21	3034	9.62
38	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7578526	7578526	C	A	exonic	nonsynonymous_SNV	c.404G>T	p.(Cys135Phe)	C135F	5	1360	39.56
38	*ZFHX3*	TUMOR SUPRESSOR	CRIPTION FACTOR-REGUL	chr16	72822548	NA	.	<DEL>	exonic	frameshift_deletion	c.9612_9627del	p.Q3204fs	Q3204fs	NA	1531	24
38	*TERT*	ONCOGENE	SENESCENCE	chr5	1295228	1295228	G	A	upstream	NA	NA	NA	NA	1	385	15.58
39	*SMARCC1*	TUMOR SUPRESSOR	EPIGENETIC	chr3	47730885	47730885	C	A	konic;splicir	stopgain	c.1255G>T	p.(Gly419Ter)	G419X	13	282	5.67
39	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7573010	7573010	T	A	splicing	NA	c.1101-2A>T	p.?	?	11	2135	6.18
39	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7578406	7578406	C	T	exonic	nonsynonymous_SNV	c.524G>A	p.(Arg175His)	R175H	5	4325	6.98
39	*TERT*	ONCOGENE	SENESCENCE	chr5	1295228	1295228	G	A	upstream	NA	NA	NA	NA	1	213	6.57
40	*RAD50*	TUMOR SUPRESSOR	DNA REPAIR	chr5	131977928	131977928	G	T	exonic	stopgain	c.3811G>T	p.(Glu1271Ter)	E1271X	25	240	5
40	*KMT2D*	TUMOR SUPRESSOR	EPIGENETIC	chr12	49443873	49443874	C	CA	exonic	frameshift_insertion	c.3497dup	p.(Met1166IlefsTer18)	M1166IfsX18	11	3044	34.3
40	*NSD1*	BOTH	EPIGENETIC	chr5	176638690	176638690	T	A	exonic	stopgain	c.3290T>A	p.(Leu1097Ter)	L1097X	5	2648	50.57
40	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7577082	7577082	C	T	exonic	nonsynonymous_SNV	c.856G>A	p.(Glu286Lys)	E286K	8	2166	59.51
40	*RASA1*	TUMOR SUPRESSOR	RTK/RAS	chr5	86672209	86672209	G	T	splicing	NA	c.2012-1G>T	p.?	?	16	200	5
41	*CDKN2A*	TUMOR SUPRESSOR	CELL CYCLE	chr9	21974782	21974782	C	T	exonic	stopgain	c.45G>A	p.(Trp15Ter)	W15X	1	4121	15
41	*NFE2L2*	ONCOGENE	OXYDATIVE STRESS	chr2	178098806	178098806	G	A	exonic	nonsynonymous_SNV	c.239C>T	p.(Thr80Ile)	T80I	2	134	5.97
41	*NFE2L2*	ONCOGENE	OXYDATIVE STRESS	chr2	178098944	178098944	C	A	exonic	nonsynonymous_SNV	c.101G>T	p.(Arg34Leu)	R34L	2	148	8.11
41	*GNAQ*	ONCOGENE	OTHER	chr9	80409488	80409488	T	A	exonic	nonsynonymous_SNV	c.626A>T	p.(Gln209Leu)	Q209L	5	92	8.7
41	*PIK3CA*	ONCOGENE	PI3K	chr3	178916930	178916930	G	T	exonic	nonsynonymous_SNV	c.317G>T	p.(Gly106Val)	G106V	2	95	8.42
41	*TERT*	ONCOGENE	SENESCENCE	chr5	1295250	1295250	G	T	upstream	NA	NA	NA	NA	1	521	1.34
42	*FBXW7*	BOTH	DEVELOPMENT	chr4	153244092	153244092	G	A	exonic	nonsynonymous_SNV	c.1825C>T	p.(Arg609Trp)	R609W	11	1545	22.27
42	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7578263	7578263	G	A	exonic	stopgain	c.586C>T	p.(Arg196Ter)	R196X	6	3626	41.92
42	*AJUBA*	TUMOR SUPRESSOR	OTHER	chr14	23450522	NA	.	<DEL>	exonic	frameshift_deletion	c.908_954del	p.G303fs	G303fs	NA	4266	23
43	*BCL7C*	TUMOR SUPRESSOR	APOPTOSIS	chr16	30903934	30903934	G	A	exonic	stopgain	c.415C>T	p.(Gln139Ter)	Q139X	4	969	14.96
43	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7578524	7578524	G	A	exonic	stopgain	c.406C>T	p.(Gln136Ter)	Q136X	5	1084	23.89
43	*DICER1*	TUMOR SUPRESSOR	OTHER	chr14	95557629	95557629	T	C	exonic	nonsynonymous_SNV	c.5438A>G	p.(Glu1813Gly)	E1813G	25	117	6.84
44	*KMT2D*	TUMOR SUPRESSOR	EPIGENETIC	chr12	49432297	49432298	G	GA	exonic	frameshift_insertion	c.8841dup	p.(Pro2948SerfsTer25)	P2948SfsX25	34	2611	26.5
44	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7577547	7577547	C	T	exonic	nonsynonymous_SNV	c.734G>A	p.(Gly245Asp)	G245D	7	1271	45.95
44	*KEAP1*	TUMOR SUPRESSOR	OXYDATIVE STRESS	chr19	10602620	10602620	G	A	exonic	nonsynonymous_SNV	c.958C>T	p.(Arg320Trp)	R320W	3	5097	60.66
45	*FAT2*	TUMOR SUPRESSOR	DIFFERENCIATION CELL	chr5	150947196	150947197	ATG	A	exonic	frameshift_deletion	c.1296_1297del	p.(Ile433GlnfsTer14)	I433QfsX14	1	312	5.13
45	*FANCA*	TUMOR SUPRESSOR	DNA REPAIR	chr16	89874748	89874749	TGC	T	exonic	frameshift_deletion	c.549_550del	p.(Trp183Ter)	W183X	6	226	5.31
45	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7577568	7577568	C	A	exonic	nonsynonymous_SNV	c.713G>T	p.(Cys238Phe)	C238F	7	892	16.14
46	*CDKN2A*	TUMOR SUPRESSOR	CELL CYCLE	chr9	21971120	21971120	G	A	exonic	stopgain	c.238C>T	p.(Arg80Ter)	R80X	2	4627	45.73
46	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7577121	7577121	G	A	exonic	nonsynonymous_SNV	c.817C>T	p.(Arg273Cys)	R273C	8	1353	14.71
46	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7578406	7578406	C	T	exonic	nonsynonymous_SNV	c.524G>A	p.(Arg175His)	R175H	5	5710	28.2
46	*TERT*	ONCOGENE	SENESCENCE	chr5	1295250	1295250	G	A	upstream	NA	NA	NA	NA	1	247	38.06
47	*FAT1*	TUMOR SUPRESSOR	DIFFERENCIATION CELL	chr4	187630258	187630258	T	A	exonic	stopgain	c.724A>T	p.(Lys242Ter)	K242X	2	291	5.15
47	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7577120	7577120	C	T	exonic	nonsynonymous_SNV	c.818G>A	p.(Arg273His)	R273H	8	335	11.64
48	*FANCA*	TUMOR SUPRESSOR	DNA REPAIR	chr16	89851354	89851354	G	A	exonic	stopgain	c.1378C>T	p.(Arg460Ter)	R460X	15	2019	15.06
48	*EP300*	TUMOR SUPRESSOR	EPIGENETIC	chr22	41566457	41566459	GATT	G	exonic	in-frame_deletion	c.4336_4338del	p.(Tyr1446del)	Y1446del	27	204	30.39
48	*FUBP1*	TUMOR SUPRESSOR	OTHER	chr1	78430337	78430337	TC	T	konic;splicir	frameshift_deletion	c.894del	p.(Ile299Ter)	I299X	1	235	5.96
48	*PXDNL*	TUMOR SUPRESSOR	OTHER	chr8	52321534	52321534	G	A	exonic	stopgain	c.2650C>T	p.(Arg884Ter)	R884X	17	6859	22.58
49	*ING1*	TUMOR SUPRESSOR	APOPTOSIS	chr13	111365319	111365319	G	A	splicing	NA	c.-2G>A	p.?	?	1	1587	24.51
49	*FBXW7*	BOTH	DEVELOPMENT	chr4	153251941	153251941	G	T	exonic	stopgain	c.825C>A	p.(Tyr275Ter)	Y275X	6	121	11.57
49	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7577508	7577508	T	C	konic;splicir	nonsynonymous_SNV	c.773A>G	p.(Glu258Gly)	E258G	7	1190	28.4
49	*TERT*	ONCOGENE	SENESCENCE	chr5	1295228	1295228	G	A	upstream	NA	NA	NA	NA	1	428	28.27
50	*CDKN2A*	TUMOR SUPRESSOR	CELL CYCLE	chr9	21971120	21971120	G	A	exonic	stopgain	c.238C>T	p.(Arg80Ter)	R80X	2	5029	22.79
50	*FAT1*	TUMOR SUPRESSOR	DIFFERENCIATION CELL	chr4	187541538	187541539	T	TCACGA	exonic	frameshift_insertion	c.6197_6201dup	p.(Lys2068SerfsTer2)	K2068SfsX2	10	595	12.44
50	*FAT1*	TUMOR SUPRESSOR	DIFFERENCIATION CELL	chr4	187628349	187628355	GTTAACAA	G	exonic	frameshift_deletion	c.2627_2633del	p.(Val876AlafsTer16)	V876AfsX16	2	1080	13.24
50	*KMT2D*	TUMOR SUPRESSOR	EPIGENETIC	chr12	49418413	49418425	TTGATCATGAGTGG	T	exonic	frameshift_deletion	c.15988_16000del	p.(Pro5330ThrfsTer22)	P5330TfsX22	50	2496	6.13
50	*TERT*	ONCOGENE	SENESCENCE	chr5	1295228	1295228	G	A	upstream	NA	NA	NA	NA	1	391	12.53
51	*TCF7L2*	TUMOR SUPRESSOR	DEVELOPMENT	chr10	114910775	114910776	TCC	T	exonic	frameshift_deletion	c.814_815del	p.(Pro272ThrfsTer28)	P272TfsX28	8	320	5
51	*GATA1*	BOTH	CRIPTION FACTOR-REGUL	chrX	48650575	48650575	C	A	exonic	stopgain	c.545C>A	p.(Ser182Ter)	S182X	3	255	5.49
51	*RUNX1*	TUMOR SUPRESSOR	CRIPTION FACTOR-REGUL	chr21	36164600	36164616	GCGGCGAGCGCTCGCCGC	G	exonic	frameshift_deletion	c.1259_1275del	p.(Gly420AlafsTer174)	G420AfsX174	9	4298	22.27

51	*RUNX1*	TUMOR SUPRESSOR	CRIPTION FACTOR-REGUL	chr21	36164599	NA	.	<DEL>	exonic	nonframeshift_deletion	c.1259_1276del	p.420_426del	420_426del	NA	4394	22
52	*KMT2B*	TUMOR SUPRESSOR	EPIGENETIC	chr19	36211000	36211000	G	T	exonic	stopgain	c.751G>T	p.(Glu251Ter)	E251X	3	7299	33.68
52	*NSD1*	BOTH	EPIGENETIC	chr5	176721980	176721980	GA	G	exonic	frameshift_deletion	c.7611del	p.(Arg2537SerfsTer41)	R2537SfsX41	23	170	31.18
52	*PHOX2B*	TUMOR SUPRESSOR	CRIPTION FACTOR-REGUL	chr4	41748031	41748047	CCGCCGCCGCTGCTGCTG	C	exonic	frameshift_deletion	c.722_738del	p.(Ala241GlyfsTer113)	A241GfsX113	3	1248	14.02
53	*KMT2D*	TUMOR SUPRESSOR	EPIGENETIC	chr12	49428051	49428051	C	T	exonic	stopgain	c.10539G>A	p.(Trp3513Ter)	W3513X	38	3090	42.17
53	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7579471	7579472	G	GC	exonic	frameshift_insertion	c.215_216insG	p.(Val73ArgfsTer76)	V73RfsX76	4	3119	49.98
54	*FAT1*	TUMOR SUPRESSOR	DIFFERENCIATION CELL	chr4	187525001	187525001	G	C	exonic	stopgain	c.10679C>G	p.(Ser3560Ter)	S3560X	19	1313	17.21
54	*FAT2*	TUMOR SUPRESSOR	DIFFERENCIATION CELL	chr5	150924174	150924174	G	A	exonic	stopgain	c.6514C>T	p.(Gln2172Ter)	Q2172X	9	789	16.6
54	*FAT2*	TUMOR SUPRESSOR	DIFFERENCIATION CELL	chr5	150925730	150925730	G	C	exonic	stopgain	c.4958C>G	p.(Ser1653Ter)	S1653X	9	246	7.72
54	*MLH1*	TUMOR SUPRESSOR	DNA REPAIR	chr3	37059062	37059062	CA	C	exonic	frameshift_deletion	c.860del	p.(Asn287ThrfsTer10)	N287TfsX10	10	209	5.74
54	*NOTCH1*	BOTH	DEVELOPMENT	chr9	139396305	139396305	G	A	exonic	stopgain	c.5533C>T	p.(Gln1845Ter)	Q1845X	30	4097	18.31
54	*NOTCH2*	BOTH	DEVELOPMENT	chr1	120539688	120539688	G	T	exonic	stopgain	c.683C>A	p.(Ser228Ter)	S228X	4	1962	13.66
54	*CREBBP*	TUMOR SUPRESSOR	EPIGENETIC	chr16	3778807	3778807	G	A	exonic	stopgain	c.6241C>T	p.(Gln2081Ter)	Q2081X	31	9081	16.36
54	*KMT2C*	TUMOR SUPRESSOR	EPIGENETIC	chr7	151859864	151859864	C	A	exonic	stopgain	c.10798G>T	p.(Glu3600Ter)	E3600X	43	293	13.99
54	*KMT2C*	TUMOR SUPRESSOR	EPIGENETIC	chr7	151878464	151878464	G	A	exonic	stopgain	c.6481C>T	p.(Gln2161Ter)	Q2161X	36	1683	16.34
54	*EPHA2*	TUMOR SUPRESSOR	OTHER	chr1	16461651	16461651	C	A	exonic	stopgain	c.1462G>T	p.(Glu488Ter)	E488X	7	2753	34.07
54	*TERT*	ONCOGENE	SENESCENCE	chr5	1295228	1295228	G	A	upstream	NA	NA	NA	NA	1	392	19.39
55	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7577594	7577595	TAC	T	exonic	frameshift_deletion	c.686_687del	p.(Cys229TyrfsTer10)	C229YfsX10	7	1605	34.27
55	*TERT*	ONCOGENE	SENESCENCE	chr5	1295228	1295228	G	A	upstream	NA	NA	NA	NA	1	333	30.03
56	*CDKN2A*	TUMOR SUPRESSOR	CELL CYCLE	chr9	21971108	21971108	C	T	exonic	nonsynonymous_SNV	c.250G>A	p.(Asp84Asn)	D84N	2	5740	33
56	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7577120	7577120	C	T	exonic	nonsynonymous_SNV	c.818G>A	p.(Arg273His)	R273H	8	2301	16.78
56	*TERT*	ONCOGENE	SENESCENCE	chr5	1295250	1295250	G	A	upstream	NA	NA	NA	NA	1	302	24.5
57	*CDKN2A*	TUMOR SUPRESSOR	CELL CYCLE	chr9	21974679	21974679	G	A	konic;splicir	stopgain	c.148C>T	p.(Gln50Ter)	Q50X	1	6501	31.78
57	*FUBP1*	TUMOR SUPRESSOR	OTHER	chr1	78422327	78422328	GAT	G	exonic	frameshift_deletion	c.1697_1698del	p.(Tyr566SerfsTer21)	Y566SfsX21	1	218	6.88
57	*TERT*	ONCOGENE	SENESCENCE	chr5	1295250	1295250	G	A	upstream	NA	NA	NA	NA	1	241	15.77
58	*CDKN2A*	TUMOR SUPRESSOR	CELL CYCLE	chr9	21971096	21971096	C	A	exonic	stopgain	c.262G>T	p.(Glu88Ter)	E88X	2	2555	8.57
58	*NOTCH1*	BOTH	DEVELOPMENT	chr9	139413070	139413072	TAGA	T	exonic	in-frame_deletion	c.1070_1072del	p.(Phe357del)	F357del	6	1460	5.82
58	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7579551	7579551	GA	G	exonic	frameshift_deletion	c.136del	p.(Ser46ProfsTer77)	S46PfsX77	4	2831	6.75
58	*BCL11B*	TUMOR SUPRESSOR	APOPTOSIS	chr14	99640508	99640508	C	A	exonic	stopgain	c.2665G>T	p.(Glu889Ter)	E889X	4	848	52.71
58	*EPHA2*	TUMOR SUPRESSOR	OTHER	chr1	16464561	16464561	C	A	exonic	stopgain	c.1099G>T	p.(Glu367Ter)	E367X	5	2524	20.01
59	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7577547	7577547	C	A	exonic	nonsynonymous_SNV	c.734G>T	p.(Gly245Val)	G245V	7	753	16.33
59	*TERT*	ONCOGENE	SENESCENCE	chr5	1295228	1295228	G	A	upstream	NA	NA	NA	NA	1	485	23.71
60	*TERT*	ONCOGENE	SENESCENCE	chr5	1295228	1295228	G	A	upstream	NA	NA	NA	NA	1	636	22.17
60	*SMAD4*	TUMOR SUPRESSOR	TGFβ	chr18	48591825	48591825	G	A	exonic	nonsynonymous_SNV	c.988G>A	p.(Glu330Lys)	E330K	9	28	28.57
61	*KMT2D*	TUMOR SUPRESSOR	EPIGENETIC	chr12	49418712	49418712	AT	A	exonic	frameshift_deletion	c.15802del	p.(Ile5268LeufsTer7)	I5268LfsX7	49	280	26.43
61	*PIK3CA*	ONCOGENE	PI3K	chr3	178952085	178952085	A	G	exonic	nonsynonymous_SNV	c.3140A>G	p.(His1047Arg)	H1047R	21	78	21.79
62	*CDKN2A*	TUMOR SUPRESSOR	CELL CYCLE	chr9	21970971	21970971	G	C	exonic	stopgain	c.387C>G	p.(Tyr129Ter)	Y129X	2	5832	10.96
62	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7579329	7579329	T	A	exonic	stopgain	c.358A>T	p.(Lys120Ter)	K120X	4	1492	5.5
62	*PTEN*	TUMOR SUPRESSOR	PI3K	chr10	89624297	89624297	A	T	konic;splicir	nonsynonymous_SNV	c.71A>T	p.(Asp24Val)	D24V	1	53	26.42
62	*SMAD4*	TUMOR SUPRESSOR	TGFβ	chr18	48591918	48591918	C	T	exonic	nonsynonymous_SNV	c.1081C>T	p.(Arg361Cys)	R361C	9	87	10.34
63	*CDKN2A*	TUMOR SUPRESSOR	CELL CYCLE	chr9	21971194	21971195	C	CTCATCAT	exonic	frameshift_insertion	c.163_164insATGATGA	p.(Gly55AspfsTer67)	G55DfsX67	2	3038	6.39
64	*KMT2C*	TUMOR SUPRESSOR	EPIGENETIC	chr7	151875096	151875096	C	A	splicing	NA	c.7443-1G>T	p.?	?	38	251	5.18
65	*CASP8*	TUMOR SUPRESSOR	APOPTOSIS	chr2	202131411	202131411	C	T	exonic	stopgain	c.202C>T	p.(Arg68Ter)	R68X	3	671	33.98
65	*CDKN2A*	TUMOR SUPRESSOR	CELL CYCLE	chr9	21971029	21971029	C	T	exonic	stopgain	c.329G>A	p.(Trp110Ter)	W110X	2	3393	71.29
65	*NOTCH1*	BOTH	DEVELOPMENT	chr9	139413085	139413085	G	A	exonic	nonsynonymous_SNV	c.1057C>T	p.(Arg353Cys)	R353C	6	1887	34.92
65	*TERT*	ONCOGENE	SENESCENCE	chr5	1295250	1295250	G	A	upstream	NA	NA	NA	NA	1	207	61.84
66	*KMT2B*	TUMOR SUPRESSOR	EPIGENETIC	chr19	36220936	36220936	TC	T	exonic	frameshift_deletion	c.4987del	p.(His1663ThrfsTer33)	H1663TfsX33	23	2882	11.17
66	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7577106	7577106	G	A	exonic	nonsynonymous_SNV	c.832C>T	p.(Pro278Ser)	P278S	8	1417	18.21
66	*TERT*	ONCOGENE	SENESCENCE	chr5	1295228	1295228	G	A	upstream	NA	NA	NA	NA	1	262	9.92
67	*CDKN2A*	TUMOR SUPRESSOR	CELL CYCLE	chr9	21974676	21974676	C	T	konic;splicir	NA	c.150+1G>A	p.?	?	1	3424	19.66
67	*NSD1*	BOTH	EPIGENETIC	chr5	176562850	176562850	GA	G	exonic	frameshift_deletion	c.750del	p.(Ala251GlnfsTer10)	A251QfsX10	2	482	10.37
67	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7574030	7574030	CG	C	konic;splicir	frameshift_deletion	c.997del	p.(Arg333ValfsTer12)	R333VfsX12	10	1181	18.63
67	*TERT*	ONCOGENE	SENESCENCE	chr5	1295228	1295228	G	A	upstream	NA	NA	NA	NA	1	198	6.06
68	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7579552	7579552	AC	A	exonic	frameshift_deletion	c.135del	p.(Ser46ProfsTer77)	S46PfsX77	4	2756	17.6
68	*HNF1A*	TUMOR SUPRESSOR	CRIPTION FACTOR-REGUL	chr12	121426820	121426820	C	T	exonic	stopgain	c.511C>T	p.(Arg171Ter)	R171X	2	1045	8.52
68	*TERT*	ONCOGENE	SENESCENCE	chr5	1295228	1295228	G	A	upstream	NA	NA	NA	NA	1	205	19.51
69	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7578553	7578553	T	C	konic;splicir	nonsynonymous_SNV	c.377A>G	p.(Tyr126Cys)	Y126C	5	665	13.83
69	*TERT*	ONCOGENE	SENESCENCE	chr5	1295250	1295250	G	A	upstream	NA	NA	NA	NA	1	146	18.49
70	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7579528	7579528	C	T	exonic	stopgain	c.159G>A	p.(Trp53Ter)	W53X	4	3930	9.34
70	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7578479	7578479	G	A	exonic	nonsynonymous_SNV	c.451C>T	p.(Pro151Ser)	P151S	5	2355	11.63
71	*PIK3CA*	ONCOGENE	PI3K	chr3	178936082	178936082	G	A	exonic	nonsynonymous_SNV	c.1624G>A	p.(Glu542Lys)	E542K	10	51	15.69
72	*FAT2*	TUMOR SUPRESSOR	DIFFERENCIATION CELL	chr5	150897234	150897234	G	A	exonic	stopgain	c.11410C>T	p.(Gln3804Ter)	Q3804X	19	2492	24.4
72	*FAT2*	TUMOR SUPRESSOR	DIFFERENCIATION CELL	chr5	150947130	150947130	GC	G	exonic	frameshift_deletion	c.1363del	p.(Ala455ProfsTer26)	A455PfsX26	1	2186	25.39
72	*ARID1B*	TUMOR SUPRESSOR	EPIGENETIC	chr6	157100247	157100256	GCCGGCTCGGC	G	exonic	frameshift_deletion	c.1184_1193del	p.(Ala395GlyfsTer32)	A395GfsX32	1	2353	20.95
72	*ARID1B*	TUMOR SUPRESSOR	EPIGENETIC	chr6	157100246	NA	.	<DEL>	exonic	frameshift_deletion	c.1183_1193del	p.A395fs	A395fs	NA	2397	21
72	*ASXL1*	TUMOR SUPRESSOR	EPIGENETIC	chr20	31023474	31023475	G	GGAGA	exonic	frameshift_insertion	c.2960_2963dup	p.(Asp988GlufsTer4)	D988EfsX4	12	1761	21.69
72	*KMT2B*	TUMOR SUPRESSOR	EPIGENETIC	chr19	36209098	36209098	G	T	exonic	stopgain	c.178G>T	p.(Glu60Ter)	E60X	1	1189	38.27
72	*KMT2B*	TUMOR SUPRESSOR	EPIGENETIC	chr19	36210440	36210440	C	T	konic;splicir	stopgain	c.433C>T	p.(Arg145Ter)	R145X	2	2052	22.81
72	*KMT2D*	TUMOR SUPRESSOR	EPIGENETIC	chr12	49420213	49420213	C	T	exonic	nonsynonymous_SNV	c.15536G>A	p.(Arg5179His)	R5179H	48	1869	27.13
72	*AJUBA*	TUMOR SUPRESSOR	OTHER	chr14	23450925	NA	.	<DEL>	exonic	frameshift_deletion	c.121_551del	p.L41fs	L41fs	NA	1963	25
73	*NOTCH1*	BOTH	DEVELOPMENT	chr9	139418191	139418191	G	T	exonic	stopgain	c.381C>A	p.(Cys127Ter)	C127X	3	2650	20.45
73	*KMT2D*	TUMOR SUPRESSOR	EPIGENETIC	chr12	49425839	49425839	G	A	exonic	stopgain	c.12649C>T	p.(Gln4217Ter)	Q4217X	39	3225	10.98
73	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7579434	7579435	G	GA	exonic	frameshift_insertion	c.252_253insT	p.(Pro85SerfsTer64)	P85SfsX64	4	1562	10.82
73	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7577121	7577121	G	A	exonic	nonsynonymous_SNV	c.817C>T	p.(Arg273Cys)	R273C	8	988	6.28
73	*ALPK2*	TUMOR SUPRESSOR	OTHER	chr18	56278985	56278986	T	TA	exonic	frameshift_insertion	c.44dup	p.(Leu15PhefsTer11)	L15FfsX11	2	864	49.07
74	*CDKN2A*	TUMOR SUPRESSOR	CELL CYCLE	chr9	21971191	21971207	GCTGCCCATCATCATGAC	G	exonic	frameshift_deletion	c.151_167del	p.(Val51ArgfsTer63)	V51RfsX63	2	2075	11.04
74	*FAT1*	TUMOR SUPRESSOR	DIFFERENCIATION CELL	chr4	187629360	187629360	G	C	exonic	stopgain	c.1622C>G	p.(Ser541Ter)	S541X	2	2110	15.55
74	*TP53BP1*	TUMOR SUPRESSOR	DNA REPAIR	chr15	43762083	43762083	TA	T	exonic	frameshift_deletion	c.1347del	p.(Ile450SerfsTer36)	I450SfsX36	11	510	5.69
74	*AXIN2*	TUMOR SUPRESSOR	DEVELOPMENT	chr17	63532613	63532613	G	A	exonic	stopgain	c.1966C>T	p.(Arg656Ter)	R656X	8	2051	7.51
74	*NFE2L2*	ONCOGENE	OXYDATIVE STRESS	chr2	178098810	178098810	C	G	exonic	nonsynonymous_SNV	c.235G>C	p.(Glu79Gln)	E79Q	2	1390	7.05
75	*CDKN2A*	TUMOR SUPRESSOR	CELL CYCLE	chr9	21968243	21968243	T	A	splicing	NA	c.458-2A>T	p.?	?	3	526	31.75
75	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7576852	7576852	C	A	splicing	NA	c.993+1G>T	p.?	?	9	243	19.34
76	*ASXL1*	TUMOR SUPRESSOR	EPIGENETIC	chr20	31024709	31024710	C	CT	exonic	frameshift_insertion	c.4196dup	p.(Leu1399PhefsTer25)	L1399FfsX25	12	209	24.88
76	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7578268	7578268	A	T	exonic	nonsynonymous_SNV	c.581T>A	p.(Leu194His)	L194H	6	2243	62.91

76	*SMAD3*	TUMOR SUPRESSOR	TGFβ	chr15	67473669	67473669	GC	G	exonic	frameshift_deletion	c.750del	p.(Ser251ArgfsTer5)	S251RfsX5	6	1807	12.45
77	*ARID1A*	TUMOR SUPRESSOR	EPIGENETIC	chr1	27057633	NA	.	<DEL>	exonic	frameshift_deletion	c.1351delA	p.I451fs	I451fs	NA	1320	23
77	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7574003	7574003	G	A	exonic	stopgain	c.1024C>T	p.(Arg342Ter)	R342X	10	2856	70.13
77	*PIK3CA*	ONCOGENE	PI3K	chr3	178952085	178952085	A	G	exonic	nonsynonymous_SNV	c.3140A>G	p.(His1047Arg)	H1047R	21	344	40.41
78	*KMT2D*	TUMOR SUPRESSOR	EPIGENETIC	chr12	49426007	49426007	C	A	exonic	stopgain	c.12481G>T	p.(Glu4161Ter)	E4161X	39	4937	10.96
78	*TERT*	ONCOGENE	SENESCENCE	chr5	1295228	1295228	G	A	upstream	NA	NA	NA	NA	1	333	2.4
79	*CDKN2A*	TUMOR SUPRESSOR	CELL CYCLE	chr9	21971110	21971110	T	C	exonic	nonsynonymous_SNV	c.248A>G	p.(His83Arg)	H83R	2	1800	47
79	*FAT2*	TUMOR SUPRESSOR	DIFFERENCIATION CELL	chr5	150897328	150897328	T	A	splicing	NA	c.11318-2A>T	p.?	?	19	2664	65.99
79	*NOTCH1*	BOTH	DEVELOPMENT	chr9	139400141	139400151	CAGGTCCCCTGG	C	exonic	frameshift_deletion	c.4197_4207del	p.(Asn1399LysfsTer2)	N1399KfsX2	25	2564	49.38
79	*NOTCH1*	BOTH	DEVELOPMENT	chr9	139400140	NA	.	<DEL>	exonic	nonframeshift_deletion	c.4197_4208del	p.1399_1403del	1399_1403del	NA	2615	49
79	*KMT2D*	TUMOR SUPRESSOR	EPIGENETIC	chr12	49443774	49443775	TGA	T	exonic	frameshift_deletion	c.3596_3597del	p.(Leu1199HisfsTer7)	L1199HfsX7	11	2558	27.56
79	*KMT2D*	TUMOR SUPRESSOR	EPIGENETIC	chr12	49446787	49446799	TCTCAAACCACTCC	T	exonic	frameshift_deletion	c.1011_1023del	p.(Glu338ThrfsTer60)	E338TfsX60	8	1489	19.14
79	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7578395	7578395	G	A	exonic	nonsynonymous_SNV	c.535C>T	p.(His179Tyr)	H179Y	5	2320	41.34
80	*CDKN2A*	TUMOR SUPRESSOR	CELL CYCLE	chr9	21971091	21971092	G	GC	exonic	frameshift_insertion	c.266dup	p.(Phe90LeufsTer30)	F90LfsX30	2	3820	7.7
80	*NOTCH1*	BOTH	DEVELOPMENT	chr9	139409769	139409769	C	A	exonic	stopgain	c.1987G>T	p.(Glu663Ter)	E663X	12	3758	8.22
80	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7577093	7577093	C	T	exonic	nonsynonymous_SNV	c.845G>A	p.(Arg282Gln)	R282Q	8	1869	6.58
80	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7578406	7578406	C	T	exonic	nonsynonymous_SNV	c.524G>A	p.(Arg175His)	R175H	5	4135	15.91
80	*PIK3CA*	ONCOGENE	PI3K	chr3	178952085	178952085	A	G	exonic	nonsynonymous_SNV	c.3140A>G	p.(His1047Arg)	H1047R	21	3154	7.29
80	*TERT*	ONCOGENE	SENESCENCE	chr5	1295228	1295228	G	A	upstream	NA	NA	NA	NA	1	273	10.62
81	*DNMT3A*	TUMOR SUPRESSOR	EPIGENETIC	chr2	25466783	25466784	CAA	C	exonic	frameshift_deletion	c.1919_1920del	p.(Phe640Ter)	F640X	16	1274	6.59
82	*PTCH1*	TUMOR SUPRESSOR	DEVELOPMENT	chr9	98220280	NA	.	<DEL>	exonic	frameshift_deletion	c.3167_3168del	p.I1056fs	I1056fs	NA	2153	41
82	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7577538	7577538	C	T	exonic	nonsynonymous_SNV	c.743G>A	p.(Arg248Gln)	R248Q	7	819	32.11
83	*CDKN2A*	TUMOR SUPRESSOR	CELL CYCLE	chr9	21971120	21971120	G	A	exonic	stopgain	c.238C>T	p.(Arg80Ter)	R80X	2	4373	38.12
83	*FAT1*	TUMOR SUPRESSOR	DIFFERENCIATION CELL	chr4	187524700	187524700	C	T	exonic	stopgain	c.10980G>A	p.(Trp3660Ter)	W3660X	19	3266	35.46
83	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7577114	7577114	C	A	exonic	nonsynonymous_SNV	c.824G>T	p.(Cys275Phe)	C275F	8	1765	32.97
83	*PIK3CA*	ONCOGENE	PI3K	chr3	178936091	178936091	G	A	exonic	nonsynonymous_SNV	c.1633G>A	p.(Glu545Lys)	E545K	10	86	22.09
83	*TERT*	ONCOGENE	SENESCENCE	chr5	1295228	1295228	G	A	upstream	NA	NA	NA	NA	1	296	11.49
83	*TGFBR2*	TUMOR SUPRESSOR	TGFβ	chr3	30648469	30648493	GGTGAGTGGTCCCCAGCCCGGGCT	G	exonic	frameshift_deletion	c.94_94+24del	p.?	?	1	2326	7.74
84	*CDKN2A*	TUMOR SUPRESSOR	CELL CYCLE	chr9	21971207	21971207	AC	A	xonic;splicir	frameshift_deletion	c.151del	p.(Val51SerfsTer2)	V51SfsX2	2	2750	7.53
84	*TERT*	ONCOGENE	SENESCENCE	chr5	1295250	1295250	G	A	upstream	NA	NA	NA	NA	1	139	17.99
85	*FAT1*	TUMOR SUPRESSOR	DIFFERENCIATION CELL	chr4	187525071	187525071	C	A	exonic	stopgain	c.10609G>T	p.(Glu3537Ter)	E3537X	19	865	29.94
85	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7577018	7577018	C	A	splicing	NA	c.919+1G>T	p.?	?	8	1870	53.37
85	*GRIN2A*	TUMOR SUPRESSOR	OTHER	chr16	10273953	10273953	G	A	exonic	stopgain	c.316C>T	p.(Gln106Ter)	Q106X	3	1727	16.73
85	*TERT*	ONCOGENE	SENESCENCE	chr5	1295228	1295228	G	A	upstream	NA	NA	NA	NA	1	212	34.43
86	*NOTCH1*	BOTH	DEVELOPMENT	chr9	139413070	139413072	TAGA	T	exonic	in-frame_deletion	c.1070_1072del	p.(Phe357del)	F357del	6	876	26.71
86	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7578212	7578212	G	A	exonic	stopgain	c.637C>T	p.(Arg213Ter)	R213X	6	581	45.09
87	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7577535	7577535	C	A	exonic	nonsynonymous_SNV	c.746G>T	p.(Arg249Met)	R249M	7	936	35.26
87	*TERT*	ONCOGENE	SENESCENCE	chr5	1295228	1295228	G	A	upstream	NA	NA	NA	NA	1	136	36.76
88	*CDKN2A*	TUMOR SUPRESSOR	CELL CYCLE	chr9	21974782	21974782	C	T	exonic	stopgain	c.45G>A	p.(Trp15Ter)	W15X	1	1863	10.9
88	*NOTCH1*	BOTH	DEVELOPMENT	chr9	139397771	139397777	GTAGACGA	G	xonic;splicir	frameshift_deletion	c.5024_5030del	p.(Ile1675ThrfsTer121)	I1675TfsX121	27	928	6.57
88	*BCL10*	TUMOR SUPRESSOR	IMMUNITY	chr1	85736385	85736385	G	A	exonic	stopgain	c.262C>T	p.(Arg88Ter)	R88X	2	1437	45.86
89	*CDKN2A*	TUMOR SUPRESSOR	CELL CYCLE	chr9	21974684	21974684	G	A	xonic;splicir	nonsynonymous_SNV	c.143C>T	p.(Pro48Leu)	P48L	1	3519	41.94
89	*FAT2*	TUMOR SUPRESSOR	DIFFERENCIATION CELL	chr5	150923868	150923868	TG	T	exonic	frameshift_deletion	c.6820del	p.(Gln2274AsnfsTer18)	Q2274NfsX18	9	2229	25.3
89	*FAT4*	TUMOR SUPRESSOR	DIFFERENCIATION CELL	chr4	126336204	126336204	TC	T	exonic	frameshift_deletion	c.6087del	p.(Arg2030AspfsTer15)	R2030DfsX15	11	289	5.19
89	*NOTCH1*	BOTH	DEVELOPMENT	chr9	139411737	139411737	G	T	exonic	stopgain	c.1542C>A	p.(Cys514Ter)	C514X	9	2196	59.11
89	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7578392	7578392	C	A	exonic	stopgain	c.538G>T	p.(Glu180Ter)	E180X	5	4289	24.57
89	*PIK3CA*	ONCOGENE	PI3K	chr3	178948100	178948100	C	A	exonic	nonsynonymous_SNV	c.2872C>A	p.(Gln958Lys)	Q958K	20	86	10.47
89	*HRAS*	ONCOGENE	RTK/RAS	chr11	533874	533874	T	A	exonic	nonsynonymous_SNV	c.182A>T	p.(Gln61Leu)	Q61L	3	4635	28.2
89	*TERT*	ONCOGENE	SENESCENCE	chr5	1295250	1295250	G	A	upstream	NA	NA	NA	NA	1	209	44.98
90	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7579377	7579377	G	A	exonic	stopgain	c.310C>T	p.(Gln104Ter)	Q104X	4	2076	8.62
90	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7577121	7577121	G	A	exonic	nonsynonymous_SNV	c.817C>T	p.(Arg273Cys)	R273C	8	1689	9.77
90	*PIK3CA*	ONCOGENE	PI3K	chr3	178936074	178936074	C	G	exonic	nonsynonymous_SNV	c.1616C>G	p.(Pro539Arg)	P539R	10	56	12.5
90	*TERT*	ONCOGENE	SENESCENCE	chr5	1295228	1295228	G	A	upstream	NA	NA	NA	NA	1	252	11.51
91	*MUTYH*	TUMOR SUPRESSOR	DNA REPAIR	chr1	45798768	45798768	C	A	splicing	NA	c.453+1G>T	p.?	?	5	207	6.76
91	*KMT2B*	TUMOR SUPRESSOR	EPIGENETIC	chr19	36211288	36211289	TGG	T	exonic	frameshift_deletion	c.1039_1040del	p.(Gly347ThrfsTer16)	G347TfsX16	3	202	6.93
91	*TERT*	ONCOGENE	SENESCENCE	chr5	1295228	1295228	G	A	upstream	NA	NA	NA	NA	1	384	27.34
92	*RAD51C*	TUMOR SUPRESSOR	DNA REPAIR	chr17	56787296	56787296	T	A	exonic	stopgain	c.782T>A	p.(Leu261Ter)	L261X	5	236	5.93
92	*NOTCH1*	BOTH	DEVELOPMENT	chr9	139401378	139401384	GGGTCAAC	G	exonic	frameshift_deletion	c.3685_3691del	p.(Val1229ProfsTer214)	V1229PfsX214	23	1939	28.88
92	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7574003	7574003	CG	C	exonic	frameshift_deletion	c.1024del	p.(Arg342GlufsTer3)	R342EfsX3	10	1926	19.78
93	*CDKN2A*	TUMOR SUPRESSOR	CELL CYCLE	chr9	21971096	21971096	C	A	exonic	stopgain	c.262G>T	p.(Glu88Ter)	E88X	2	5480	16.15
93	*FAT2*	TUMOR SUPRESSOR	DIFFERENCIATION CELL	chr5	150922822	150922822	G	T	exonic	stopgain	c.7866C>A	p.(Tyr2622Ter)	Y2622X	9	256	8.2
93	*BRCA1*	TUMOR SUPRESSOR	DNA REPAIR	chr17	41245513	41245516	TTGGC	T	exonic	frameshift_deletion	c.2032_2035del	p.(Ala678ArgfsTer22)	A678RfsX22	10	215	6.05
93	*CDK12*	TUMOR SUPRESSOR	DNA REPAIR	chr17	37618447	37618447	AG	A	exonic	frameshift_deletion	c.123del	p.(Lys41AsnfsTer16)	K41NfsX16	1	255	7.06
93	*POLE*	TUMOR SUPRESSOR	DNA REPAIR	chr12	133253184	133253184	G	A	exonic	nonsynonymous_SNV	c.857C>T	p.(Pro286Leu)	P286L	9	155	7.74
93	*FBXW7*	BOTH	DEVELOPMENT	chr4	153247169	153247169	A	G	exonic	nonsynonymous_SNV	c.1393T>C	p.(Tyr465His)	Y465H	9	43	30.23
93	*NOTCH2*	BOTH	DEVELOPMENT	chr1	120512233	120512234	TCA	T	exonic	frameshift_deletion	c.1008_1009del	p.(Ser336ArgfsTer4)	S336RfsX4	6	228	5.26
93	*TCF7L2*	TUMOR SUPRESSOR	DEVELOPMENT	chr10	114710600	114710601	GGA	G	exonic	frameshift_deletion	c.87_88del	p.(Lys30GlufsTer13)	K30EfsX13	1	239	5.44
93	*ARID1B*	TUMOR SUPRESSOR	EPIGENETIC	chr6	157522589	157522589	GA	G	exonic	frameshift_deletion	c.4824del	p.(Lys1608AsnfsTer19)	K1608NfsX19	17	202	6.44
93	*ASXL2*	TUMOR SUPRESSOR	EPIGENETIC	chr2	25965700	25965701	TGC	T	exonic	frameshift_deletion	c.3505_3506del	p.(Ala1169AsnfsTer5)	A1169NfsX5	12	234	5.13
93	*BRD9*	TUMOR SUPRESSOR	EPIGENETIC	chr5	891793	891793	C	A	exonic	stopgain	c.229G>T	p.(Glu77Ter)	E77X	2	265	6.04
93	*KANSL1*	TUMOR SUPRESSOR	EPIGENETIC	chr17	44117182	44117182	AT	A	exonic	frameshift_deletion	c.2089del	p.(Ile697SerfsTer35)	I697SfsX35	8	212	5.66
93	*KMT2C*	TUMOR SUPRESSOR	EPIGENETIC	chr7	151860801	151860802	GCT	G	exonic	frameshift_deletion	c.9860_9861del	p.(Gln3287ProfsTer38)	Q3287PfsX38	43	219	5.94
93	*KMT2C*	TUMOR SUPRESSOR	EPIGENETIC	chr7	151877196	151877196	C	A	exonic	stopgain	c.7165G>T	p.(Glu2389Ter)	E2389X	37	217	9.22
93	*SETD2*	TUMOR SUPRESSOR	EPIGENETIC	chr3	47125539	47125539	G	A	exonic	stopgain	c.5731C>T	p.(Gln1911Ter)	Q1911X	12	239	5.86
93	*SETD2*	TUMOR SUPRESSOR	EPIGENETIC	chr3	47125564	47125564	TG	T	exonic	frameshift_deletion	c.5706del	p.(Lys1903ArgfsTer10)	K1903RfsX10	12	269	7.06
93	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7577099	7577099	C	G	exonic	nonsynonymous_SNV	c.839G>C	p.(Arg280Thr)	R280T	8	128	43.75
93	*CHD6*	TUMOR SUPRESSOR	OTHER	chr20	40162006	40162010	TATGGG	T	exonic	frameshift_deletion	c.233_237del	p.(Ser78Ter)	S78X	3	223	6.28
93	*SDHA*	TUMOR SUPRESSOR	OTHER	chr5	251157	251163	AAGGTTGT	A	exonic	frameshift_deletion	c.1602_1608del	p.(Cys536LysfsTer9)	C536KfsX9	12	287	7.32
93	*SLX4*	TUMOR SUPRESSOR	DNA REPAIR	chr16	3641136	3641137	TTC	T	exonic	frameshift_deletion	c.2502_2503del	p.(Lys835IlefsTer13)	K835IfsX13	12	208	5.77
93	*SLX4*	TUMOR SUPRESSOR	DNA REPAIR	chr16	3658744	3658745	C	CA	exonic	frameshift_insertion	c.221_222insT	p.(Arg74SerfsTer46)	R74SfsX46	2	242	7.02
93	*ZFHX3*	TUMOR SUPRESSOR	CRIPTION FACTOR-REGUL	chr16	72831825	72831825	C	A	exonic	stopgain	c.4756G>T	p.(Glu1586Ter)	E1586X	9	261	6.13
93	*BRAF*	ONCOGENE	RTK/RAS	chr7	140453149	140453149	C	A	exonic	nonsynonymous_SNV	c.1786G>T	p.(Gly596Cys)	G596C	15	149	5.37
93	*NRAS*	ONCOGENE	RTK/RAS	chr1	115256529	115256529	T	G	exonic	nonsynonymous_SNV	c.182A>C	p.(Gln61Pro)	Q61P	3	94	8.51
93	*TERT*	ONCOGENE	SENESCENCE	chr5	1295250	1295250	G	A	upstream	NA	NA	NA	NA	1	346	18.79

94	*CDKN2A*	TUMOR SUPRESSOR	CELL CYCLE	chr9	21971186	21971186	G	A	exonic	stopgain	c.172C>T	p.(Arg58Ter)	R58X	2	2278	55.14
94	*ASXL1*	TUMOR SUPRESSOR	EPIGENETIC	chr20	31022440	31022441	GGA	G	exonic	frameshift_deletion	c.1926_1927del	p.(Gly645TrpfsTer12)	G645WfsX12	12	1518	5.93
94	*ASXL1*	TUMOR SUPRESSOR	EPIGENETIC	chr20	31022441	31022441	GA	G	exonic	frameshift_deletion	c.1926del	p.(Gly645ValfsTer58)	G645VfsX58	12	1517	37.44
94	*SMARCB1*	TUMOR SUPRESSOR	EPIGENETIC	chr22	24176339	24176339	G	A	exonic	nonsynonymous_SNV	c.1130G>A	p.(Arg377His)	R377H	9	3768	30.18
94	*PIK3CA*	ONCOGENE	PI3K	chr3	178936091	178936091	G	A	exonic	nonsynonymous_SNV	c.1633G>A	p.(Glu545Lys)	E545K	10	66	48.48
94	*TERT*	ONCOGENE	SENESCENCE	chr5	1295250	1295250	G	A	upstream	NA	NA	NA	NA	1	305	47.54
95	*FBXW7*	BOTH	DEVELOPMENT	chr4	153247294	153247294	G	C	exonic	nonsynonymous_SNV	c.1268C>G	p.(Ala423Gly)	A423G	9	164	6.1
95	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7578532	7578532	A	T	exonic	nonsynonymous_SNV	c.398T>A	p.(Met133Lys)	M133K	5	1690	9.59
95	*CIITA*	TUMOR SUPRESSOR	IMMUNITY	chr16	11001085	11001085	AT	A	exonic	frameshift_deletion	c.1736del	p.(Met579SerfsTer9)	M579SfsX9	11	8366	8.51
95	*NFE2L2*	ONCOGENE	OXYDATIVE STRESS	chr2	178098809	178098809	T	A	exonic	nonsynonymous_SNV	c.236A>T	p.(Glu79Val)	E79V	2	145	10.34
96	*FAT1*	TUMOR SUPRESSOR	DIFFERENCIATION CELL	chr4	187532849	187532849	G	A	exonic	stopgain	c.9544C>T	p.(Gln3182Ter)	Q3182X	14	1550	12.32
96	*FAT1*	TUMOR SUPRESSOR	DIFFERENCIATION CELL	chr4	187629264	187629264	AT	A	exonic	frameshift_deletion	c.1718del	p.(Asn573IlefsTer10)	N573IfsX10	2	2056	12.35
96	*NOTCH1*	BOTH	DEVELOPMENT	chr9	139397730	139397730	G	A	exonic	stopgain	c.5071C>T	p.(Gln1691Ter)	Q1691X	27	1336	14.15
96	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7578453	7578453	TG	T	exonic	frameshift_deletion	c.477del	p.(Met160TrpfsTer10)	M160WfsX10	5	1931	14.71
96	*HRAS*	ONCOGENE	RTK/RAS	chr11	534288	534288	C	T	exonic	nonsynonymous_SNV	c.35G>A	p.(Gly12Asp)	G12D	2	5857	28.21
96	*TERT*	ONCOGENE	SENESCENCE	chr5	1295228	1295228	G	A	upstream	NA	NA	NA	NA	1	191	15.71
97	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7579321	7579322	TCA	T	konic;splicir	frameshift_deletion	c.365_366del	p.(Val122AspfsTer26)	V122DfsX26	4	757	35.27
97	*PIK3CA*	ONCOGENE	PI3K	chr3	178936091	178936091	G	A	exonic	nonsynonymous_SNV	c.1633G>A	p.(Glu545Lys)	E545K	10	72	25
98	*FAT1*	TUMOR SUPRESSOR	DIFFERENCIATION CELL	chr4	187549439	187549439	CG	C	exonic	frameshift_deletion	c.4679del	p.(Pro1560ArgfsTer25)	P1560RfsX25	9	1223	14.55
98	*NOTCH1*	BOTH	DEVELOPMENT	chr9	139412675	139412675	T	C	exonic	nonsynonymous_SNV	c.1169A>G	p.(Asn390Ser)	N390S	7	1747	23.35
98	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7577568	7577569	C	CAACTGCAGTT	exonic	frameshift_insertion	c.712_713insAACTGCAGTT	p.(Cys238Ter)	C238X	7	1364	8.28
98	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7577571	7577572	A	AAC	exonic	frameshift_insertion	c.709_710insGT	p.(Met237SerfsTer11)	M237SfsX11	7	1280	8.75
98	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7577082	7577082	C	T	exonic	nonsynonymous_SNV	c.856G>A	p.(Glu286Lys)	E286K	8	1720	17.73
98	*PDGFRA*	ONCOGENE	RTK/RAS	chr4	55131161	55131161	G	A	exonic	nonsynonymous_SNV	c.704G>A	p.(Cys235Tyr)	C235Y	5	113	9.73
98	*TERT*	ONCOGENE	SENESCENCE	chr5	1295228	1295228	G	A	upstream	NA	NA	NA	NA	1	265	29.81
99	*NOTCH3*	BOTH	DEVELOPMENT	chr19	15288598	15288631	GGTGCCGCGGCGGGCGCCTCGCAC	A	exonic	frameshift_deletion	c.4108_4141del	p.(Pro1370SerfsTer39)	P1370SfsX39	24	1763	22.52
99	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7577569	7577569	A	T	exonic	nonsynonymous_SNV	c.712T>A	p.(Cys238Ser)	C238S	7	1318	79.67
100	*CDKN2A*	TUMOR SUPRESSOR	CELL CYCLE	chr9	21971016	21971016	CG	C	exonic	frameshift_deletion	c.342del	p.(Val115TrpfsTer31)	V115WfsX31	2	1862	19.55
100	*CDKN2A*	TUMOR SUPRESSOR	CELL CYCLE	chr9	21971036	21971037	TCG	T	exonic	frameshift_deletion	c.321_322del	p.(Asp108CysfsTer11)	D108CfsX11	2	1993	19.67
100	*CDKN2A*	TUMOR SUPRESSOR	CELL CYCLE	chr9	21971153	21971153	C	A	exonic	stopgain	c.205G>T	p.(Glu69Ter)	E69X	2	1419	43.55
100	*FANCC*	TUMOR SUPRESSOR	DNA REPAIR	chr9	97864110	97864111	G	GT	exonic	frameshift_insertion	c.1555dup	p.(Thr519AsnfsTer9)	T519NfsX9	15	1566	55.75
100	*NOTCH1*	BOTH	DEVELOPMENT	chr9	139410473	139410473	G	T	exonic	stopgain	c.1629C>A	p.(Cys543Ter)	C543X	10	971	45.83
100	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7577114	7577114	C	A	exonic	nonsynonymous_SNV	c.824G>T	p.(Cys275Phe)	C275F	8	981	75.54
100	*NFE2L2*	ONCOGENE	OXYDATIVE STRESS	chr2	178098957	178098957	G	A	exonic	nonsynonymous_SNV	c.88C>T	p.(Leu30Phe)	L30F	2	4579	33.96
100	*THSD7B*	TUMOR SUPRESSOR	OTHER	chr2	138414418	138414418	C	A	exonic	stopgain	c.4071C>A	p.(Cys1357Ter)	C1357X	22	661	23.6
100	*TERT*	ONCOGENE	SENESCENCE	chr5	1295228	1295228	G	A	upstream	NA	NA	NA	NA	1	161	22.36
101	*FAT1*	TUMOR SUPRESSOR	DIFFERENCIATION CELL	chr4	187524131	187524132	G	GA	exonic	frameshift_insertion	c.11407dup	p.(Ser3803PhefsTer6)	S3803FfsX6	20	1139	19.67
101	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7577121	7577121	G	A	exonic	nonsynonymous_SNV	c.817C>T	p.(Arg273Cys)	R273C	8	1490	9.53
101	*PTEN*	TUMOR SUPRESSOR	PI3K	chr10	89624274	89624274	T	A	exonic	stopgain	c.48T>A	p.(Tyr16Ter)	Y16X	1	1032	20.35
101	*TERT*	ONCOGENE	SENESCENCE	chr5	1295228	1295228	G	A	upstream	NA	NA	NA	NA	1	234	13.68
102	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7579591	7579591	C	G	splicing	NA	c.97-1G>C	p.?	?	4	1739	17.71
102	*TERT*	ONCOGENE	SENESCENCE	chr5	1295228	1295228	G	A	upstream	NA	NA	NA	NA	1	117	6.84
103	*FAT1*	TUMOR SUPRESSOR	DIFFERENCIATION CELL	chr4	187524927	187524927	G	A	exonic	stopgain	c.10753C>T	p.(Gln3585Ter)	Q3585X	19	2205	23.36
103	*ARID1A*	TUMOR SUPRESSOR	EPIGENETIC	chr1	27094328	27094328	T	G	exonic	stopgain	c.3036T>G	p.(Tyr1012Ter)	Y1012X	11	898	5.12
103	*ERBB3*	ONCOGENE	RTK/RAS	chr12	56487277	56487277	C	T	exonic	nonsynonymous_SNV	c.1423C>T	p.(Arg475Trp)	R475W	12	1744	48.91
103	*HRAS*	ONCOGENE	RTK/RAS	chr11	534285	534285	C	A	exonic	nonsynonymous_SNV	c.38G>T	p.(Gly13Val)	G13V	2	3605	20.06
103	*TERT*	ONCOGENE	SENESCENCE	chr5	1295228	1295228	G	A	upstream	NA	NA	NA	NA	1	153	22.22
104	*RB1*	TUMOR SUPRESSOR	CELL CYCLE	chr13	49039340	49039340	G	A	splicing	NA	c.2326-1G>A	p.?	?	23	2940	76.6
104	*AXIN2*	TUMOR SUPRESSOR	DEVELOPMENT	chr17	63554354	63554354	G	A	exonic	stopgain	c.385C>T	p.(Arg129Ter)	R129X	2	2823	5.14
104	*EP300*	TUMOR SUPRESSOR	EPIGENETIC	chr22	41572367	41572368	G	GGCAAGGGACAAG	exonic	in-frame_insertion	c.4901_4918dup	p.(Ala1634_Leu1639dup)	A1634_L1639dup	30	1315	16.81
104	*EP300*	TUMOR SUPRESSOR	EPIGENETIC	chr22	41572367	NA	G	GGCAAGGGACAAG	exonic	nonframeshift_insertion	c.4896_4897insCTGGCAAGGGACAAGCAG	p.T1632delinsTLARDKH	T1632delinsTLARDKH	NA	1353	17
104	*AJUBA*	TUMOR SUPRESSOR	OTHER	chr14	23450639	23450640	C	CAG	exonic	frameshift_insertion	c.836_837insCT	p.(Glu279AspfsTer3)	E279DfsX3	1	3964	36.05
104	*CTCF*	TUMOR SUPRESSOR	CRIPTION FACTOR-REGUL	chr16	67645197	67645198	A	AT	exonic	frameshift_insertion	c.463dup	p.(Cys155LeufsTer8)	C155LfsX8	3	3280	38.23
104	*SRCAP*	TUMOR SUPRESSOR	OTHER	chr16	30747910	30747910	G	T	exonic	stopgain	c.6973G>T	p.(Glu2325Ter)	E2325X	33	1585	24.61
104	*MAPK1*	ONCOGENE	RTK/RAS	chr22	22127164	22127164	C	T	konic;splicir	nonsynonymous_SNV	c.964G>A	p.(Glu322Lys)	E322K	7	1943	38.7
104	*TERT*	ONCOGENE	SENESCENCE	chr5	1295228	1295228	G	A	upstream	NA	NA	NA	NA	1	370	62.43
105	*CASP8*	TUMOR SUPRESSOR	APOPTOSIS	chr2	202136252	202136252	C	T	exonic	stopgain	c.415C>T	p.(Gln139Ter)	Q139X	5	1355	15.87
105	*CDKN2A*	TUMOR SUPRESSOR	CELL CYCLE	chr9	21971120	21971120	G	A	exonic	stopgain	c.238C>T	p.(Arg80Ter)	R80X	2	2205	44.26
105	*FAT1*	TUMOR SUPRESSOR	DIFFERENCIATION CELL	chr4	187539417	187539417	G	A	exonic	stopgain	c.8323C>T	p.(Gln2775Ter)	Q2775X	10	2983	39.69
105	*NSD1*	BOTH	EPIGENETIC	chr5	176638489	176638489	T	A	exonic	stopgain	c.3089T>A	p.(Leu1030Ter)	L1030X	5	3121	25.79
105	*NFE2L2*	ONCOGENE	OXYDATIVE STRESS	chr2	178098960	178098960	C	G	exonic	nonsynonymous_SNV	c.85G>C	p.(Asp29His)	D29H	2	3099	22.14
105	*PIK3CA*	ONCOGENE	PI3K	chr3	178952085	178952085	A	G	exonic	nonsynonymous_SNV	c.3140A>G	p.(His1047Arg)	H1047R	21	2920	21.23
105	*TERT*	ONCOGENE	SENESCENCE	chr5	1295228	1295228	G	A	upstream	NA	NA	NA	NA	1	160	13.12
106	*CDKN2A*	TUMOR SUPRESSOR	CELL CYCLE	chr9	21971050	21971051	CCG	C	exonic	frameshift_deletion	c.307_308del	p.(Arg103AlafsTer16)	R103AfsX16	2	2164	20.24
106	*CDKN2A*	TUMOR SUPRESSOR	CELL CYCLE	chr9	21971120	21971120	G	A	exonic	stopgain	c.238C>T	p.(Arg80Ter)	R80X	2	1580	26.65
106	*CIC*	TUMOR SUPRESSOR	OTHER	chr19	42796490	42796502	CCCCTGGGTACCAG	C	exonic	frameshift_deletion	c.5779_5791del	p.(Gly1927ArgfsTer17)	G1927RfsX17	5	1563	9.15
106	*PXDNL*	TUMOR SUPRESSOR	OTHER	chr8	52721806	52721806	TG	T	exonic	frameshift_deletion	c.99del	p.(Ser33ArgfsTer8)	S33RfsX8	1	1541	64.44
106	*PIK3CA*	ONCOGENE	PI3K	chr3	178952085	178952085	A	G	exonic	nonsynonymous_SNV	c.3140A>G	p.(His1047Arg)	H1047R	21	1033	41.43
106	*TERT*	ONCOGENE	SENESCENCE	chr5	1295228	1295228	G	A	upstream	NA	NA	NA	NA	1	112	16.07
107	*KANSL1*	TUMOR SUPRESSOR	EPIGENETIC	chr17	44116480	44116480	C	A	exonic	stopgain	c.2305G>T	p.(Glu769Ter)	E769X	9	2416	35.6
107	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7577058	7577058	C	A	exonic	stopgain	c.880G>T	p.(Glu294Ter)	E294X	8	2423	40.98
107	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7578176	7578176	C	A	splicing	NA	c.672+1G>T	p.?	?	6	1737	33.39
108	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7577555	7577555	G	T	exonic	stopgain	c.726C>A	p.(Cys242Ter)	C242X	7	1059	48.63
109	*NOTCH1*	BOTH	DEVELOPMENT	chr9	139396486	139396486	C	T	exonic	stopgain	c.5439G>A	p.(Trp1813Ter)	W1813X	29	1360	50.59
109	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7578263	7578263	G	A	exonic	stopgain	c.586C>T	p.(Arg196Ter)	R196X	6	2863	66.57
109	*SF3B1*	ONCOGENE	OTHER	chr2	198265453	198265453	C	T	exonic	nonsynonymous_SNV	c.2704G>A	p.(Glu902Lys)	E902K	18	32	25
110	*FAT1*	TUMOR SUPRESSOR	DIFFERENCIATION CELL	chr4	187539585	187539586	C	CA	exonic	frameshift_insertion	c.8154dup	p.(Gly2719TrpfsTer12)	G2719WfsX12	10	2392	11.29
110	*NOTCH1*	BOTH	DEVELOPMENT	chr9	139401003	139401009	CGCGGGCG	C	exonic	frameshift_deletion	c.3984_3990del	p.(Ala1329GlyfsTer114)	A1329GfsX114	24	1918	16.06
110	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7577156	7577156	C	T	splicing	NA	c.783-1G>A	p.?	?	8	996	16.97
110	*TERT*	ONCOGENE	SENESCENCE	chr5	1295228	1295228	G	A	upstream	NA	NA	NA	NA	1	178	28.65
111	*SMARCA4*	TUMOR SUPRESSOR	EPIGENETIC	chr19	11172458	11172458	A	C	splicing	NA	c.5008-2A>C	p.?	?	36	1193	12.32
111	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7578437	7578437	G	A	exonic	stopgain	c.493C>T	p.(Gln165Ter)	Q165X	5	1632	10.48
111	*TERT*	ONCOGENE	SENESCENCE	chr5	1295228	1295228	G	A	upstream	NA	NA	NA	NA	1	151	5.96
112	*CDKN2A*	TUMOR SUPRESSOR	CELL CYCLE	chr9	21971124	21971125	TGA	T	exonic	frameshift_deletion	c.233_234del	p.(Leu78HisfsTer41)	L78HfsX41	2	1676	21.72

112	*CHD3*	TUMOR SUPRESSOR	EPIGENETIC	chr17	7812527	7812527	G	T	exonic	stopgain	c.5359G>T	p.(Glu1787Ter)	E1787X	36	1243	35.08
112	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7577082	7577082	C	T	exonic	nonsynonymous_SNV	c.856G>A	p.(Glu286Lys)	E286K	8	1156	36.25
113	*CDKN2A*	TUMOR SUPRESSOR	CELL CYCLE	chr9	21971029	21971029	C	T	exonic	stopgain	c.329G>A	p.(Trp110Ter)	W110X	2	1949	56.08
113	*FAT1*	TUMOR SUPRESSOR	DIFFERENCIATION CELL	chr4	187540425	187540426	C	CA	exonic	frameshift_insertion	c.7314dup	p.(Val2439CysfsTer3)	V2439CfsX3	10	1799	55.81
113	*BRCA2*	TUMOR SUPRESSOR	DNA REPAIR	chr13	32972744	32972745	T	TGAATTATATC	exonic	frameshift_insertion	c.10094_10095insGAATTATATC	p.(Ser3366AsnfsTer5)	S3366NfsX5	27	1083	45.61
113	*BRCA2*	TUMOR SUPRESSOR	DNA REPAIR	chr13	32972744	NA	T	TGAATTATATC	exonic	frameshift_insertion	c.10094_10095insGAATTATATC	p.V3365fs	V3365fs	NA	1104	46
113	*SMARCA4*	TUMOR SUPRESSOR	EPIGENETIC	chr19	11172458	11172458	A	C	splicing	NA	c.5008-2A>C	p.?	?	36	1747	5.55
113	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7578369	7578369	A	G	splicing	NA	c.559+2T>C	p.?	?	5	2556	69.91
114	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7578411	7578412	TCA	T	exonic	frameshift_deletion	c.518_519del	p.(Val173GlufsTer7)	V173EfsX7	5	2140	64.35
115	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7579414	7579414	GC	G	exonic	frameshift_deletion	c.273del	p.(Trp91CysfsTer32)	W91CfsX32	4	2068	48.94
115	*TERT*	ONCOGENE	SENESCENCE	chr5	1295250	1295250	G	A	upstream	NA	NA	NA	NA	1	202	51.49
116	*CASP8*	TUMOR SUPRESSOR	APOPTOSIS	chr2	202149718	202149718	G	T	exonic	stopgain	c.1033G>T	p.(Gly345Ter)	G345X	9	1517	11.8
116	*CDKN2A*	TUMOR SUPRESSOR	CELL CYCLE	chr9	21971186	21971186	G	A	exonic	stopgain	c.172C>T	p.(Arg58Ter)	R58X	2	1098	14.48
116	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7578212	7578212	G	A	exonic	stopgain	c.637C>T	p.(Arg213Ter)	R213X	6	950	16.11
117	*SUZ12*	TUMOR SUPRESSOR	EPIGENETIC	chr17	30267480	30267480	C	T	exonic	stopgain	c.361C>T	p.(Arg121Ter)	R121X	3	618	8.74
117	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7577082	7577082	C	A	exonic	stopgain	c.856G>T	p.(Glu286Ter)	E286X	8	1035	74.01
117	*RASA1*	TUMOR SUPRESSOR	RTK/RAS	chr5	86645120	86645120	C	T	exonic	stopgain	c.1192C>T	p.(Arg398Ter)	R398X	8	567	50.79
117	*TERT*	ONCOGENE	SENESCENCE	chr5	1295228	1295228	G	A	upstream	NA	NA	NA	NA	1	115	17.39
118	*CDKN2A*	TUMOR SUPRESSOR	CELL CYCLE	chr9	21971147	21971154	TTGGGCTCC	T	exonic	frameshift_deletion	c.204_211del	p.(Glu69LeufsTer48)	E69LfsX48	2	1449	20.77
118	*MEN1*	TUMOR SUPRESSOR	OTHER	chr11	64571895	64571895	G	A	exonic	stopgain	c.1744C>T	p.(Gln582Ter)	Q582X	10	1498	24.17
119	*FAT1*	TUMOR SUPRESSOR	DIFFERENCIATION CELL	chr4	187557883	187557901	TGGCTATGACGTGATAGAGC	T	exonic	frameshift_deletion	c.3810_3828del	p.(Leu1271ProfsTer91)	L1271PfsX91	5	1674	9.8
119	*FAT1*	TUMOR SUPRESSOR	DIFFERENCIATION CELL	chr4	187630588	187630588	G	A	exonic	stopgain	c.394C>T	p.(Arg132Ter)	R132X	2	1161	23
119	*BRIP1*	TUMOR SUPRESSOR	DNA REPAIR	chr17	59886079	59886079	G	A	exonic	stopgain	c.667C>T	p.(Gln223Ter)	Q223X	7	205	5.85
119	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7577139	7577139	G	C	exonic	nonsynonymous_SNV	c.799C>G	p.(Arg267Gly)	R267G	8	728	19.78
119	*BARD1*	TUMOR SUPRESSOR	DNA REPAIR	chr2	215610497	215610497	C	A	exonic	stopgain	c.1759G>T	p.(Glu587Ter)	E587X	8	208	5.29
119	*EPHA2*	TUMOR SUPRESSOR	OTHER	chr1	16451778	16451778	G	A	exonic	stopgain	c.2863C>T	p.(Gln955Ter)	Q955X	17	2196	18.26
119	*TERT*	ONCOGENE	SENESCENCE	chr5	1295228	1295228	G	A	upstream	NA	NA	NA	NA	1	127	23.62
120	*SMARCA4*	TUMOR SUPRESSOR	EPIGENETIC	chr19	11141427	11141427	CG	C	exonic	frameshift_deletion	c.3407del	p.(Gly1136AlafsTer4)	G1136AfsX4	25	1197	12.61
120	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7578290	7578290	C	A	splicing	NA	c.560-1G>T	p.?	?	6	2265	32.32
120	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7578272	7578272	G	T	exonic	nonsynonymous_SNV	c.577C>A	p.(His193Asn)	H193N	6	2083	34.47
120	*FBXO11*	TUMOR SUPRESSOR	OTHER	chr2	48040461	48040461	C	T	exonic	stopgain	c.2139G>A	p.(Trp713Ter)	W713X	18	1199	6.26
121	*CDKN2A*	TUMOR SUPRESSOR	CELL CYCLE	chr9	21968242	21968242	C	T	splicing	NA	c.458-1G>A	p.?	?	3	445	21.35
121	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7577556	7577556	C	T	exonic	nonsynonymous_SNV	c.725G>A	p.(Cys242Tyr)	C242Y	7	846	40.54
121	*MGA*	TUMOR SUPRESSOR	MYC	chr15	41988829	41988829	C	T	exonic	stopgain	c.1621C>T	p.(Gln541Ter)	Q541X	3	635	16.69
122	*CASP8*	TUMOR SUPRESSOR	APOPTOSIS	chr2	202151270	202151270	C	T	exonic	stopgain	c.1444C>T	p.(Gln482Ter)	Q482X	10	752	17.02
122	*TERT*	ONCOGENE	SENESCENCE	chr5	1295228	1295228	G	A	upstream	NA	NA	NA	NA	1	153	12.42
123	*SAMD9*	TUMOR SUPRESSOR	APOPTOSIS	chr7	92735258	92735258	CT	C	exonic	frameshift_deletion	c.153del	p.(Glu52AsnfsTer16)	E52NfsX16	3	2494	12.15
123	*FAT1*	TUMOR SUPRESSOR	DIFFERENCIATION CELL	chr4	187629667	187629668	T	TTG	exonic	frameshift_insertion	c.1314_1315insCA	p.(Thr439GlnfsTer14)	T439QfsX14	2	1587	20.48
123	*MSH6*	TUMOR SUPRESSOR	DNA REPAIR	chr2	48033780	48033780	C	T	exonic	stopgain	c.3991C>T	p.(Arg1331Ter)	R1331X	9	695	18.56
123	*NCOR1*	TUMOR SUPRESSOR	CRIPTION FACTOR-REGUL	chr17	15952262	15952263	C	CCGAAGAGA	exonic	frameshift_insertion	c.6425_6432dup	p.(Glu2145SerfsTer47)	E2145SfsX47	41	1947	13.76
123	*KMT2B*	TUMOR SUPRESSOR	EPIGENETIC	chr19	36211183	36211183	CA	C	exonic	frameshift_deletion	c.939del	p.(Val314Ter)	V314X	3	2485	15.13
123	*SETD2*	TUMOR SUPRESSOR	EPIGENETIC	chr3	47139465	47139465	G	A	exonic	stopgain	c.5122C>T	p.(Arg1708Ter)	R1708X	9	1544	17.1
123	*ATM*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr11	108121536	108121537	T	TG	exonic	frameshift_insertion	c.1348dup	p.(Glu450GlyfsTer37)	E450GfsX37	10	1603	8.05
123	*ALPK2*	TUMOR SUPRESSOR	OTHER	chr18	56278986	56278986	A	T	exonic	stopgain	c.44T>A	p.(Leu15Ter)	L15X	2	946	11.42
123	*EPHA2*	TUMOR SUPRESSOR	OTHER	chr1	16462199	16462199	CG	C	exonic	frameshift_deletion	c.1379del	p.(Pro460ArgfsTer33)	P460RfsX33	6	1356	28.47
123	*FUBP1*	TUMOR SUPRESSOR	OTHER	chr1	78444659	78444659	AG	A	exonic	frameshift_deletion	c.30del	p.(Ser11LeufsTer43)	S11LfsX43	18	1097	8.93
123	*MAPK1*	ONCOGENE	RTK/RAS	chr22	22127164	22127164	C	T	konic;splicir	nonsynonymous_SNV	c.964G>A	p.(Glu322Lys)	E322K	7	1306	16.54
123	*TERT*	ONCOGENE	SENESCENCE	chr5	1295228	1295228	G	A	upstream	NA	NA	NA	NA	1	147	15.65
124	*CASP8*	TUMOR SUPRESSOR	APOPTOSIS	chr2	202150039	202150039	C	T	konic;splicir	stopgain	c.1354C>T	p.(Arg452Ter)	R452X	9	1987	21.19
124	*FAT1*	TUMOR SUPRESSOR	DIFFERENCIATION CELL	chr4	187522440	187522441	C	CA	exonic	frameshift_insertion	c.11622dup	p.(Asp3875Ter)	D3875X	21	1001	20.98
124	*KANSL1*	TUMOR SUPRESSOR	EPIGENETIC	chr17	44248368	44248368	CT	C	exonic	frameshift_deletion	c.1142del	p.(Glu381GlyfsTer8)	E381GfsX8	2	3113	9.44
124	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7579349	7579349	A	G	exonic	nonsynonymous_SNV	c.338T>C	p.(Phe113Ser)	F113S	4	823	42.77
124	*HRAS*	ONCOGENE	RTK/RAS	chr11	534285	534285	C	A	exonic	nonsynonymous_SNV	c.38G>T	p.(Gly13Val)	G13V	2	2862	17.37
126	*NOTCH2*	BOTH	DEVELOPMENT	chr1	120509099	120509100	GCA	G	exonic	frameshift_deletion	c.1466_1467del	p.(Val489AlafsTer3)	V489AfsX3	9	232	5.17
126	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7577535	7577535	C	A	exonic	nonsynonymous_SNV	c.746G>T	p.(Arg249Met)	R249M	7	1025	53.85
127	*CDKN2A*	TUMOR SUPRESSOR	CELL CYCLE	chr9	21971028	21971028	C	T	exonic	stopgain	c.330G>A	p.(Trp110Ter)	W110X	2	2734	73.88
127	*FAT1*	TUMOR SUPRESSOR	DIFFERENCIATION CELL	chr4	187629671	187629684	CTTCAAGTTCAAAAT	C	exonic	frameshift_deletion	c.1298_1311del	p.(His433ArgfsTer5)	H433RfsX5	2	453	19.43
127	*ATR*	TUMOR SUPRESSOR	DNA REPAIR	chr3	142218512	142218512	C	T	exonic	stopgain	c.5337G>A	p.(Trp1779Ter)	W1779X	31	252	5.56
127	*ATR*	TUMOR SUPRESSOR	DNA REPAIR	chr3	142218513	142218513	C	T	exonic	stopgain	c.5336G>A	p.(Trp1779Ter)	W1779X	31	249	5.62
127	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7578437	7578437	G	A	exonic	stopgain	c.493C>T	p.(Gln165Ter)	Q165X	5	2965	80.91
127	*PIK3CA*	ONCOGENE	PI3K	chr3	178916929	178916929	G	A	exonic	nonsynonymous_SNV	c.316G>A	p.(Gly106Ser)	G106S	2	107	8.41
127	*TERT*	ONCOGENE	SENESCENCE	chr5	1295250	1295250	G	A	upstream	NA	NA	NA	NA	1	236	58.05
128	*FAT2*	TUMOR SUPRESSOR	DIFFERENCIATION CELL	chr5	150906800	150906803	ACAGT	A	konic;splicir	frameshift_deletion	c.10300_10303del	p.(Thr3434SerfsTer14)	T3434SfsX14	16	450	46.89
128	*NSD1*	BOTH	EPIGENETIC	chr5	176638911	176638948	CGCATGAACAGATTTAAAGAGAAAG	T	exonic	frameshift_deletion	c.3511_3548del	p.(Arg1171Ter)	R1171X	5	1115	11.84
128	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7579419	7579420	A	ACT	exonic	frameshift_insertion	c.267_268insAG	p.(Trp91ProfsTer33)	W91PfsX33	4	1530	56.86
130	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7579485	7579485	C	A	exonic	stopgain	c.202G>T	p.(Glu68Ter)	E68X	4	1224	24.18
130	*TERT*	ONCOGENE	SENESCENCE	chr5	1295228	1295228	G	A	upstream	NA	NA	NA	NA	1	168	23.21
131	*FAT1*	TUMOR SUPRESSOR	DIFFERENCIATION CELL	chr4	187540784	187540784	G	C	exonic	stopgain	c.6956C>G	p.(Ser2319Ter)	S2319X	10	1840	12.99
131	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7578291	7578291	T	A	splicing	NA	c.560-2A>T	p.?	?	6	3500	30.06
131	*CIC*	TUMOR SUPRESSOR	OTHER	chr19	42796616	42796616	C	G	konic;splicir	stopgain	c.5900C>G	p.(Ser1967Ter)	S1967X	5	1964	14.46
131	*HRAS*	ONCOGENE	RTK/RAS	chr11	533874	533874	T	C	exonic	nonsynonymous_SNV	c.182A>G	p.(Gln61Arg)	Q61R	3	4140	15.87
131	*MAPK1*	ONCOGENE	RTK/RAS	chr22	22127164	22127164	C	T	konic;splicir	nonsynonymous_SNV	c.964G>A	p.(Glu322Lys)	E322K	7	1790	29.39
132	*NSD1*	BOTH	EPIGENETIC	chr5	176637649	176637652	GCTCT	G	exonic	frameshift_deletion	c.2254_2257del	p.(Ser752GlnfsTer15)	S752QfsX15	5	3168	16.45
132	*AJUBA*	TUMOR SUPRESSOR	OTHER	chr14	23450492	23450493	T	TGG	exonic	frameshift_insertion	c.982_983dup	p.(Glu329GlnfsTer82)	E329QfsX82	1	2342	13.92
132	*TERT*	ONCOGENE	SENESCENCE	chr5	1295228	1295228	G	A	upstream	NA	NA	NA	NA	1	163	14.11
133	*ARID2*	TUMOR SUPRESSOR	EPIGENETIC	chr12	46246629	46246629	C	T	exonic	stopgain	c.4723C>T	p.(Gln1575Ter)	Q1575X	15	720	13.61
133	*KMT2B*	TUMOR SUPRESSOR	EPIGENETIC	chr19	36209188	36209188	C	T	exonic	stopgain	c.268C>T	p.(Gln90Ter)	Q90X	1	707	18.81
133	*KMT2B*	TUMOR SUPRESSOR	EPIGENETIC	chr19	36218689	36218689	G	T	splicing	NA	c.4392+1G>T	p.?	?	17	2297	16.11
133	*TERT*	ONCOGENE	SENESCENCE	chr5	1295228	1295228	G	A	upstream	NA	NA	NA	NA	1	176	19.89
134	*BCOR*	TUMOR SUPRESSOR	EPIGENETIC	chrX	39923604	39923604	G	A	exonic	stopgain	c.3487C>T	p.(Arg1163Ter)	R1163X	7	1033	37.56
134	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7577096	7577096	T	C	exonic	nonsynonymous_SNV	c.842A>G	p.(Asp281Gly)	D281G	8	1149	77.37
134	*TERT*	ONCOGENE	SENESCENCE	chr5	1295228	1295228	G	A	upstream	NA	NA	NA	NA	1	164	42.07
134	*TGFBR2*	TUMOR SUPRESSOR	TGFβ	chr3	30691870	30691870	AG	A	exonic	frameshift_deletion	c.373del	p.(Glu125LysfsTer38)	E125KfsX38	3	1488	8.2
135	*FAT1*	TUMOR SUPRESSOR	DIFFERENCIATION CELL	chr4	187524079	187524079	CG	C	exonic	frameshift_deletion	c.11460del	p.(Ser3820ArgfsTer13)	S3820RfsX13	20	801	26.59

135	*KMT2C*	TUMOR SUPRESSOR	EPIGENETIC	chr7	151927082	151927082	G	A	exonic	stopgain	c.2902C>T	p.(Gln968Ter)	Q968X	18	244	7.38
135	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7579420	7579420	AG	A	exonic	frameshift_deletion	c.267del	p.(Ser90ProfsTer33)	S90PfsX33	4	2432	25.74
135	*HNF1A*	TUMOR SUPRESSOR	CRIPTION FACTOR-REGUL	chr12	121434361	121434361	GC	G	exonic	frameshift_deletion	c.1129del	p.(Leu377SerfsTer7)	L377SfsX7	6	4955	13.64
135	*TERT*	ONCOGENE	SENESCENCE	chr5	1295250	1295250	G	A	upstream	NA	NA	NA	NA	1	176	18.75
136	*CDKN2A*	TUMOR SUPRESSOR	CELL CYCLE	chr9	21971120	21971120	G	A	exonic	stopgain	c.238C>T	p.(Arg80Ter)	R80X	2	2396	36.81
136	*FAT1*	TUMOR SUPRESSOR	DIFFERENCIATION CELL	chr4	187629184	187629184	G	A	exonic	stopgain	c.1798C>T	p.(Gln600Ter)	Q600X	2	564	17.38
136	*NOTCH1*	BOTH	DEVELOPMENT	chr9	139405231	139405231	C	A	exonic	stopgain	c.2614G>T	p.(Glu872Ter)	E872X	17	3745	17.54
136	*KMT2D*	TUMOR SUPRESSOR	EPIGENETIC	chr12	49436527	49436527	G	A	konic;splicir	stopgain	c.5779C>T	p.(Gln1927Ter)	Q1927X	26	1969	22.35
136	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7578406	7578406	C	T	exonic	nonsynonymous_SNV	c.524G>A	p.(Arg175His)	R175H	5	2990	36.15
136	*TERT*	ONCOGENE	SENESCENCE	chr5	1295228	1295228	G	A	upstream	NA	NA	NA	NA	1	285	16.14
137	*KMT2D*	TUMOR SUPRESSOR	EPIGENETIC	chr12	49437448	49437448	C	A	exonic	stopgain	c.5437G>T	p.(Glu1813Ter)	E1813X	23	900	40
137	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7578213	7578213	GA	G	exonic	frameshift_deletion	c.636del	p.(Arg213AspfsTer34)	R213DfsX34	6	1011	59.94
137	*PTEN*	TUMOR SUPRESSOR	PI3K	chr10	89720808	89720809	TTA	T	exonic	frameshift_deletion	c.959_960del	p.(Leu320TyrfsTer4)	L320YfsX4	8	365	76.44
138	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7578178	7578187	CTCAGGCGGCT	C	konic;splicir	frameshift_deletion	c.662_671del	p.(Glu221GlyfsTer23)	E221GfsX23	7	1274	54.95
138	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7578177	NA	.	<DEL>	exonic	frameshift_deletion	c.662_672del	p.E221fs	E221fs	NA	1309	55
138	*NFE2L2*	ONCOGENE	OXYDATIVE STRESS	chr2	178098944	178098944	C	G	exonic	nonsynonymous_SNV	c.101G>C	p.(Arg34Pro)	R34P	2	200	36.5
139	*CASP8*	TUMOR SUPRESSOR	APOPTOSIS	chr2	202149738	202149738	T	A	exonic	stopgain	c.1053T>A	p.(Tyr351Ter)	Y351X	9	3932	12.13
139	*NOTCH1*	BOTH	DEVELOPMENT	chr9	139438555	139438555	C	A	splicing	NA	c.62-1G>T	p.?	?	2	4086	12.11
139	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7579536	7579536	C	A	exonic	stopgain	c.151G>T	p.(Glu51Ter)	E51X	4	4492	6.1
139	*NFE2L2*	ONCOGENE	OXYDATIVE STRESS	chr2	178098810	178098810	C	G	exonic	nonsynonymous_SNV	c.235G>C	p.(Glu79Gln)	E79Q	2	3777	5.61
139	*TERT*	ONCOGENE	SENESCENCE	chr5	1295250	1295250	G	A	upstream	NA	NA	NA	NA	1	189	6.88
140	*CIITA*	TUMOR SUPRESSOR	IMMUNITY	chr16	11017183	11017183	G	T	splicing	NA	c.*22+1G>T	p.?	?	19	222	5.41
141	*FAT1*	TUMOR SUPRESSOR	DIFFERENCIATION CELL	chr4	187540539	187540539	C	A	exonic	stopgain	c.7201G>T	p.(Glu2401Ter)	E2401X	10	1777	16.66
141	*BRCA2*	TUMOR SUPRESSOR	DNA REPAIR	chr13	32972611	32972611	C	T	exonic	stopgain	c.9961C>T	p.(Gln3321Ter)	Q3321X	27	1183	13.52
141	*NOTCH1*	BOTH	DEVELOPMENT	chr9	139402568	139402568	G	A	exonic	stopgain	c.3349C>T	p.(Gln1117Ter)	Q1117X	21	2903	12.92
141	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7579414	7579414	C	T	exonic	stopgain	c.273G>A	p.(Trp91Ter)	W91X	4	1242	33.82
141	*CIC*	TUMOR SUPRESSOR	OTHER	chr19	42796331	42796331	C	T	exonic	stopgain	c.5707C>T	p.(Gln1903Ter)	Q1903X	5	3055	11.16
141	*LZTR1*	TUMOR SUPRESSOR	OTHER	chr22	21342297	21342297	A	G	splicing	NA	c.401-2A>G	p.?	?	5	1378	51.38
142	*CDKN2A*	TUMOR SUPRESSOR	CELL CYCLE	chr9	21971130	21971130	TG	T	exonic	frameshift_deletion	c.228del	p.(Thr77LeufsTer69)	T77LfsX69	2	3197	11.79
142	*CDKN2A*	TUMOR SUPRESSOR	CELL CYCLE	chr9	21971186	21971186	G	A	exonic	stopgain	c.172C>T	p.(Arg58Ter)	R58X	2	2913	29.93
142	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7577085	7577085	C	T	exonic	nonsynonymous_SNV	c.853G>A	p.(Glu285Lys)	E285K	8	1456	21.91
142	*TERT*	ONCOGENE	SENESCENCE	chr5	1295228	1295228	G	A	upstream	NA	NA	NA	NA	1	231	16.45
144	*TP53BP1*	TUMOR SUPRESSOR	DNA REPAIR	chr15	43712685	43712685	C	T	exonic	stopgain	c.4484G>A	p.(Trp1495Ter)	W1495X	21	1724	5.97
144	*B2M*	TUMOR SUPRESSOR	IMMUNITY	chr15	45003781	45003782	ACT	A	exonic	frameshift_deletion	c.43_44del	p.(Leu15PhefsTer41)	L15FfsX41	1	2584	5.19
144	*TERT*	ONCOGENE	SENESCENCE	chr5	1295228	1295228	G	A	upstream	NA	NA	NA	NA	1	257	10.89
145	*FAT1*	TUMOR SUPRESSOR	DIFFERENCIATION CELL	chr4	187629907	187629907	G	A	exonic	stopgain	c.1075C>T	p.(Gln359Ter)	Q359X	2	1267	67.17
145	*APC2*	TUMOR SUPRESSOR	DEVELOPMENT	chr19	1460220	1460220	T	G	exonic	stopgain	c.1344T>G	p.(Tyr448Ter)	Y448X	11	1515	5.08
145	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7576896	7576897	T	TG	exonic	frameshift_insertion	c.949dup	p.(Gln317ProfsTer20)	Q317PfsX20	9	1320	68.26
145	*PIK3CA*	ONCOGENE	PI3K	chr3	178952085	178952085	A	G	exonic	nonsynonymous_SNV	c.3140A>G	p.(His1047Arg)	H1047R	21	3639	40.86
145	*TERT*	ONCOGENE	SENESCENCE	chr5	1295228	1295228	G	A	upstream	NA	NA	NA	NA	1	104	47.12
146	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7577065	7577065	TC	T	exonic	frameshift_deletion	c.873del	p.(Glu294SerfsTer51)	E294SfsX51	8	1030	36.41
147	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7578275	7578275	G	A	exonic	stopgain	c.574C>T	p.(Gln192Ter)	Q192X	6	2587	27.29
147	*TERT*	ONCOGENE	SENESCENCE	chr5	1295250	1295250	G	A	upstream	NA	NA	NA	NA	1	108	13.89
148	*FAT1*	TUMOR SUPRESSOR	DIFFERENCIATION CELL	chr4	187628687	NA	.	<DEL>	exonic	frameshift_deletion	c.2280_2295del	p.N760fs	N760fs	NA	1280	20
148	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7577580	7577580	T	C	exonic	nonsynonymous_SNV	c.701A>G	p.(Tyr234Cys)	Y234C	7	2999	84.53
148	*TP53*	TUMOR SUPRESSOR	GENOME INTEGRITY	chr17	7578235	7578235	T	C	exonic	nonsynonymous_SNV	c.614A>G	p.(Tyr205Cys)	Y205C	6	5269	7.76
151	*CDKN2A*	TUMOR SUPRESSOR	CELL CYCLE	chr9	21971120	21971120	G	A	exonic	stopgain	c.238C>T	p.(Arg80Ter)	R80X	2	2122	45.38
151	*FAT1*	TUMOR SUPRESSOR	DIFFERENCIATION CELL	chr4	187541913	187541913	G	A	exonic	stopgain	c.5827C>T	p.(Gln1943Ter)	Q1943X	10	1996	16.13
151	*FAT1*	TUMOR SUPRESSOR	DIFFERENCIATION CELL	chr4	187628809	187628809	G	A	exonic	stopgain	c.2173C>T	p.(Gln725Ter)	Q725X	2	1744	16.51
151	*MGA*	TUMOR SUPRESSOR	MYC	chr15	42005562	42005562	C	T	exonic	stopgain	c.3298C>T	p.(Gln1100Ter)	Q1100X	9	1412	17
151	*PIK3CA*	ONCOGENE	PI3K	chr3	178936091	178936091	G	A	exonic	nonsynonymous_SNV	c.1633G>A	p.(Glu545Lys)	E545K	10	512	12.7
151	*HRAS*	ONCOGENE	RTK/RAS	chr11	534288	534288	C	T	exonic	nonsynonymous_SNV	c.35G>A	p.(Gly12Asp)	G12D	2	3213	30.19
151	*TERT*	ONCOGENE	SENESCENCE	chr5	1295228	1295228	G	A	upstream	NA	NA	NA	NA	1	140	14.29