Supplementary: Table 2 List of somatic mutations tested by Sanger sequencing.

Case ID	Type	Gene Symbol	Chr	Start	End	Ref	Alt	Function	Effect	VAF	Sanger Validation	Pathogenicity	Missense Pathogenic Predictions	MutationTaster missense	Polyphen2 missense	Provean missense	SIFT missense	In-frame indel Pathogenic Predictions	FATHMM in-frame indel	Provean in-frame indel	SIFT in-frame indel	VEST in-frame indel
1	SNV	HIST1H1B	chr6	27855933	27855933	T	C	missense	c.592N	1	verified	tolerated missense	1/4	D	T	T	T					
1	SNV	PRKCA	chr17	64492379	64492379	C	T	missense	c.A49E	1	verified	pathogenic missense	2/4	D	T	D	T					
3	SNV	ATP2C1	chr3	32650927	32650927	G	A	stoncoding	c.W60X	0.17	verified	stoncoding										
3	SNV	ATR4	chr3	76907801	76907801	C	A	stoncoding	c.E1416X	0.72	verified	stoncoding										
3	SNV	CDK5	chr5	180416687	180416687	G	A	missense	c.A31T	0.29	verified	tolerated missense	0/4	D	T	T	T					
3	SNV	HIST1H2BA	chr6	25727177	25727177	G	A	missense	c.R14M	0.16	verified	pathogenic missense	2/4	D	D	D	T					
3	SNV	HDC3	chr8	42805579	42805579	C	A	missense	c.V150	0.11	verified	pathogenic missense	2/4	D	D	T	T					
3	SNV	MCM5	chr22	35851884	35851884	G	A	missense	c.G1732	0.3	verified	tolerated missense	2/4	D	D	D	T					
3	SNV	MYO10	chr17	12651402	12651402	G	A	missense	c.C407Y	0.31	verified	pathogenic missense	2/4	D	D	D	T					
3	SNV	PKD2L	chr5	178921149	178921149	T	G	missense	c.V346G	0.11	verified	pathogenic missense	2/4	D	D	T	T					
3	SNV	PPM1G	chr17	58740227	58740227	C	T	missense	c.P426L	0.12	verified	tolerated missense	1/4	D	D	T	T					
3	SNV	TEX15	chr8	103701242	103701242	G	A	missense	c.D1764E	0.12	verified	tolerated missense	1/4	D	D	T	T					
4	DEL	ATR4	chr6	76909621	76909621	A	-	framesift	c.I1390fs	0.71	verified	frameshift										
4	SNV	CEP290	chr11	88451607	88451607	G	A	missense	c.G1177V	0.12	verified	tolerated missense	1/4	D	T	T	D					
4	SNV	COL4A1	chr13	111108887	111108887	G	C	missense	c.G1510Q	0.43	verified	tolerated missense	1/4	D	T	T	T					
4	SNV	EGFR	chr7	55174197	55174197	G	A	missense	c.A887T	0.67	verified	pathogenic missense	4/4	D	D	D	D					
4	SNV	HNF4G	chr8	76470822	76470822	A	T	missense	c.E239V	0.47	verified	pathogenic missense	4/4	D	D	D	D					
4	SNV	KIAA1468	chr18	59052850	59052850	G	G	missense	c.Y17X	0.39	verified	pathogenic missense	3/4	D	D	D	D					
4	SNV	MYO9A	chr9	70116655	70116655	G	A	missense	c.T259I	0.45	verified	pathogenic missense	4/4	D	D	T	D					
4	SNV	SOX17	chr8	55400801	55400801	C	T	stoncoding	c.Q239X	0.42	verified	stoncoding										
5	DEL	ACL	chr2	39924688	39924688	T	-	missense	c.W663R	0.14	verified	pathogenic missense	4/4	D	D	D	D					
5	INS	ACLB	chr1	147062888	147062888	C	C	framesift	c.S807fs	0.19	verified	frameshift										
5	INS	CDH17	chr3	111272867	111272867	T	-	framesift	c.A289fs	0.27	verified	frameshift										
5	SNV	CDN3	chr5	54527228	54527228	C	T	missense	c.C242Y	0.2	verified	pathogenic missense	3/4	D	T	D	D					
5	SNV	ELF1	chr1	145151136	145151136	A	G	missense	c.E82V	0.34	verified	pathogenic missense	3/4	D	D	D	D					
5	SNV	REF17	chr1	210443466	210443466	C	G	missense	c.F52L	0.28	verified	pathogenic missense	4/4	D	D	D	D					
5	SNV	REF1A	chr2	241685166	241685166	G	T	missense	c.R1020L	0.16	verified	pathogenic missense	4/4	D	D	D	D					
5	INS	MAMSTR	chr19	49218101	49218101	-	G	framesift	c.P59fs	0.28	verified	frameshift										
5	SNV	MAPBP1	chr17	61765956	61765956	T	C	splicing	c.T79+2T>C	0.18	verified	splicing										
5	SNV	MTMR6	chr13	25828014	25828014	G	A	missense	c.P412S	0.1	verified	pathogenic missense	3/4	D	D	D	T					
5	SNV	NTATS	chr16	69681293	69681293	A	G	missense	c.T138A	0.33	verified	pathogenic missense	2/4	D	T	T	D					
5	SNV	PAKP2	chr3	51977488	51977488	C	G	missense	c.H6M	0.2	verified	tolerated missense	1/4	D	T	D	T					
5	SNV	PRJCB	chr3	138417857	138417857	T	C	missense	c.D68V	0.19	verified	pathogenic missense	4/4	D	D	D	D					
5	SNV	PRC8FL	chr17	8794207	8794207	T	T	missense	c.V160M	0.39	verified	tolerated missense	1/4	D	D	T	T					
5	SNV	PTEN	chr10	89711869	89711869	C	T	missense	c.R173C	0.36	verified	pathogenic missense	4/4	D	D	D	D					
5	DEL	TOP2B	chr3	25666236	25666253	ACGTTTATCATTCCTCT	-	framesift	c.K751fs	0.24	verified	frameshift										
6	DEL	RF1	chr7	26667527	26667527	-	T	framesift	c.S238fs	0.06	verified	frameshift										
7	SNV	ACF1	chr4	88035511	88035511	G	A	missense	c.T149I	0.35	verified	tolerated missense	1/4	T	T	T	D					
7	INS	ATR4	chr3	76939529	76939529	C	AA	stoncoding	c.E1459FX	0.4	verified	stoncoding										
7	DEL	CDKN2C	chr1	51434169	51434169	T	-	framesift	c.S23fs	0.42	verified	frameshift										
7	SNV	TEX15	chr8	103764425	103764425	T	C	missense	c.H342	0.46	verified	tolerated missense	1/4				T					
7	SNV	TP53	chr17	7579262	7579262	G	A	stoncoding	c.R64X	0.48	verified	stoncoding										
9	INS	ATR4	chr4	76908934	76908934	-	A	framesift	c.G547fs	0.16	verified	frameshift										
9	SNV	GPT	chr1	168675912	168675912	G	A	missense	c.S142T	0.19	verified	tolerated missense	1/4	D	T	T	T					
9	SNV	HDAC8	chr9	88675776	88675776	C	G	missense	c.A412G	0.1	verified	pathogenic missense	4/4	D	D	D	D					
9	SNV	NOTCH4	chr6	32187483	32187483	G	A	missense	c.C462S	0.26	verified	pathogenic missense	4/4	D	D	D	D					
9	SNV	PDE1A	chr2	181604949	181604949	A	T	stoncoding	c.L60X	0.2	verified	stoncoding										
9	SNV	PRJDA	chr3	178952084	178952084	T	A	missense	c.M1060K	0.23	verified	tolerated missense	1/4	D	T	T	T					
9	SNV	PLEKHA7	chr11	16821268	16821268	G	A	missense	c.S78I0	0.23	verified	pathogenic missense	4/4	D	D	D	D					
9	SNV	RTTN	chr18	67733104	67733104	G	T	missense	c.L570I	0.25	verified	tolerated missense	0/4	T	T	T	T					
9	SNV	SLC9C1	chr3	111995506	111995506	G	A	missense	c.T67M	0.13	verified	tolerated missense	1/4	D	T	T	T					
10	SNV	ERG	chr21	39775633	39775633	C	G	missense	c.D38G	0.07	verified	pathogenic missense	4/4	D	D	D	D					
10	SNV	GJA4	chr1	147266359	147266359	C	T	missense	c.D228N	0.43	verified	pathogenic missense	3/4	D	D	T	D					
11	SNV	MRAP	chr21	45854339	45854339	G	T	missense	c.V90M	0.25	verified	pathogenic missense	3/4	D	D	D	D					
11	SNV	CEP152	chr15	40854769	40854769	C	G	missense	c.Q794R	0.23	verified	pathogenic missense	3/4	D	D	T	D					
11	SNV	COL10A1	chr6	70812867	70812867	C	T	stoncoding	c.R411X	0.24	verified	stoncoding										
12	SNV	KIUPM	chr11	3761781	3761781	T	C	missense	c.T475A	0.32	verified	tolerated missense	1/4	T	T	T	D					
13	SNV	SLC6A5	chr3	112208614	112208614	G	T	missense	c.G257V	0.36	verified	tolerated missense	0/4	D	T	T	T					
13	SNV	SUFN12L	chr17	33806387	33806387	T	C	missense	c.V281E	0.34	verified	tolerated missense	0/4	T	T	T	T					
13	SNV	CCDC154	chr16	14851122	14851122	G	A	stoncoding	c.Q154X	0.29	verified	stoncoding										
13	SNV	SST	chr3	187288923	187288923	G	A	missense	c.P94L	0.54	verified	pathogenic missense	4/4	D	D	D	D					
14	DEL	ATR4	chr4	76908897	76908897	TCTT	-	framesift	c.Q845fs	0.4	verified	frameshift										
14	SNV	BEST2	chr19	12864077	12864077	T	G	missense	c.F52L	0.45	verified	tolerated missense	1/4	D	T	T	T					
14	SNV	Esterf12	chr10	98743827	98743827	G	A	missense	c.R390N	0.47	verified	pathogenic missense	4/4	D	D	D	D					
14	SNV	DGAZ	chr11	66397362	66397362	G	A	missense	c.A608T	0.36	verified	tolerated missense	1/4	D	T	T	T					
14	SNV	EL1L	chr7	42007366	42007366	G	A	missense	c.V977N	0.2	verified	tolerated missense	0/4	D	T	T	T					
14	SNV	KIAE23	chr2	170592000	170592000	C	T	missense	c.R159P	0.48	verified	pathogenic missense	3/4		D	D	D					
14	SNV	MAPK11	chr19	39087771	39087771	C	T	missense	c.G63S	0.54	verified	tolerated missense	1/4	D	T	D	D					
14	SNV	RF1	chr17	29550462	29550462	G	A	missense	c.S176R	0.27	verified	pathogenic missense	4/4	D	D	D	D					
14	SNV	PAK1	chr19	39860564	39860564	C	T	missense	c.H60Y	0.23	verified	tolerated missense	1/4	D	T	D	D					
14	SNV	PDE1A	chr2	181909493	181909493	T	G	missense	c.A513T	0.48	verified	tolerated missense	0/4	D	T	T	T					
14	SNV	PRKCA	chr17	64770511	64770511	G	T	missense	c.H526C	0.67	verified	pathogenic missense	4/4	D	D	D	D					
14	DEL	RAG1	chr11	36597939	36597939	T	-	stoncoding	c.L1029X	0.42	verified	stoncoding										
14	SNV	RCBB8	chr14	64065509	64065509	T	A	stoncoding	c.W244R	0.39	verified	stoncoding										
15	SNV	RAPRA2	chr1	174748812	174748812	G	A	missense	c.D146BN	0.27	verified	pathogenic missense	2/4	D	D	D	T					
15	SNV	FIS1	chr3	180018841	180018841	C	T	missense	c.V64L	0.3	verified	tolerated missense	1/4	T	T	T	T					
17	SNV	GALNT9	chr12	132685869	132685869	C	T	missense	c.G58R	0.11	verified	pathogenic missense	4/4	D	D	D	D					
17	SNV	RABF2	chr4	65212081	65212081	G	C	missense	c.D111Y	0.13	verified	pathogenic missense	4/4	D	D	D	D					
17	INS	RF1	chr17	29554287	29554287	-	A	framesift	c.D88fs	0.28	verified	frameshift										
17	SNV	PTPRZ1	chr14	69967266	69967266	G	A	stoncoding	c.Q229X	0.12	verified	stoncoding										
19	SNV	ATRX	chr6	76939883	76939883	G	A	stoncoding	c.Q251X	0.12	verified	stoncoding										
20	DEL	PTEN	chr10	89624293	89624294	AG	-	framesift	c.L129fs	0.35	verified	frameshift										
20	SNV	RNF31	chr14	24624870	24624870	G	A	missense	c.H670R	0.29	verified	tolerated missense	0/4	T	T	T	T					
20	SNV	SLPG	chr1	156581603	156581603	G	A	missense	c.R94L	0.08	verified	tolerated missense	1/4	D	T	T	T					
20	SNV	SLC02	chr22	24585172	24585172	G	A	missense	c.G1702	0.09	verified	pathogenic missense	4/4	D	D	D	D					
20	SNV	TNN	chr3	170068504	170068504	C	T	missense	c.S1652	0.52	verified	pathogenic missense	4/4	D	D	D	D					
20	SNV	ZFCHH1	chr12	72003349	72003349	A	T	missense	c.M74R	0.38	verified	pathogenic missense	4/4	D	D	T	D					
21	SNV	ADAM1	chr1	155452603	155452603	C	T	missense	c.G601V	0.2	verified	tolerated missense	0/4	T	T	T	T					
21	SNV	ATRX	chr6	76939969	76939969	C	A	stoncoding	c.R861_R862delinsX	0.41	verified	stoncoding										
21	SNV	FKRP	chr9	131007955	131007955	G	A	missense	c.M608I	0.48	verified	tolerated missense	1/4	D	T	T	T					
21	SNV	KIAA0753	chr6	44081693	44081693	G	A	missense	c.G1141V	0.49	verified	tolerated missense	0/4	T	T	T	T					
21	DEL	MPO	chr7	94445808	94445809	TA	-	framesift	c.V604fs	0.44	verified	frameshift										
21	SNV	MAPK15	chr8	144644457	144644457	G	A	missense	c.V391I	0.28	verified	pathogenic missense	1/4	D	D	D	D					
21	SNV	NDUF12	chr5	161180119	161180119	C	A	missense	c.R265Q	0.27	verified	pathogenic missense	2/4	D	D	T	D					
21	SNV	DRC1	chr1	5280922	5280922	G	T	missense	c.D503N	0.43	verified	tolerated missense	0/4	D	T	T	T					
21	SNV	POLR3D	chr8	22105767	22105767	T	G	missense	c.I354M	0.41	verified	pathogenic missense	2/4	D	D	T	T					
23	SNV	AHRR	chr5	434302	434302	G	A	missense	c.V47I	0.31	verified	tolerated missense	1/4	D	T	T	T					
23	SNV	FOXK2	chr17	80521313	80521313	C	G	missense	c.E169D	0.32	verified	pathogenic missense	2/4	D	D	D	D					
23	SNV	RP17	chr1	210113035	210113035	G	A	missense	c.N318N	0.13	verified	pathogenic missense	4/4	D	D	D	D					
23	SNV	PRKX1	chr1	170705317	170705317	G	A	missense	c.T243K	0.22	verified	pathogenic missense	4/4	D	D	D	D					
23	SNV	TP53	chr17	7579363	7579363	C	A	stoncoding	c.S51X	0.49	verified	stoncoding										
27	SNV	PCDHAB	chr5	140222193	140222193	G	T	missense	c.D429Y	0.22	verified	pathogenic missense	4/4	D	D	D	D					
28	SNV	FGFR1	chr8	38273557	38273557	T	G	missense	c.E473A	0.39	verified	pathogenic missense	4/4	D	D	D	D					
29	INS	RF1	chr17	29562813	29562813	-	CTCTGT	in-frame	c.T124SdelinsTLS	0.39	verified	pathogenic in-frame indel						3/4	D		D	
31	DEL	ATR4	chr4	76944365	76944369	TGAT	-	framesift	c.N1437fs	0.29	verified	frameshift										
31	SNV	DMBX1	chr1	46978128	46978128	T	C	missense	c.A360V	0.57	verified	pathogenic missense	3/4	D	D	T	D					
32	SNV	BCL9L	chr11	118773657	118773657	G	T	missense	c.M472I	1	verified	tolerated missense	0/4	D	D	D	D					
32	SNV	GERGE	chr8	133645121	133645121	C	G	missense	c.E175Q	0.67	verified	pathogenic missense	4/4	D	D	D	D					
32	SNV	MCM5	chr22	35795925	35795925	C	T	missense	c.D151N	1	verified	tolerated missense	1/4	D	T	T	T					
34	DEL	ATR4	chr6	76931772	76931772	CCT	-	framesift	c.R1232fs	1	verified	frameshift										
34	DEL	RF1	chr7	29549845	29549845	TG	-	framesift	c.L560fs	0.22	verified	frameshift										
34	SNV	TP53	chr17	7578403	7578403	C	A	missense	c.C44F	1	verified	pathogenic missense	4/4	D	D	D	D					
37	SNV	CDKCR	chr3	180312461	180312461	G	T	missense	c.T307L	1	verified	tolerated missense	0/4	D	T	T	T					
37	SNV	CEP152	chr15	49040392	49040392	C	T	missense	c.R1177R	1	verified	tolerated missense	1/4	D	T	T	T					
37	SNV	DGI4	chr7	107144522	107144522	T	C	missense	c.M892V	0.22	verified	tolerated missense	1/4	D	T	T	T					
38	SNV	BCL9	chr1	147095682	147095682	C	T	stoncoding	c.R1064X	0.86	verified	stoncoding										
38	SNV	RTF17	chr3	107881072	107881072	C	T	missense	c.R441K	1	verified	pathogenic missense	2/4	D	D	T	T					
39_1	SNV	DGR1	chr4	962325	962325	G	A	missense	c.C185Y	0.33	verified	pathogenic missense	4/4	D	D	D	D					
39_1	SNV	DNF36B	chr5	75756504	75756504	C	T	missense	c.V318M	0.17	verified	tolerated missense	0/4	D	T	T	T					
39_2	SNV	DGR1	chr4	962325	962325	G	A	missense	c.C185Y	0.26	verified	pathogenic missense	4/4	D	D	D	D					
39_2	SNV	DNF36B	chr5	75756504	75756504	C	T	missense	c.V318M	0.2	verified	tolerated missense	0/4	D	T	T	T					
39_3	SNV	DGR1	chr4	962325	962325	G	A	missense	c.C185Y	0.15	verified	pathogenic missense	4/4	D	D	D	D					
39_3	SNV	DNF36B	chr5	75756504	75756504	C	T	missense	c.V318M	0.13	verified	tolerated missense	0/4	D	T	T	T					
39_4	SNV	DGR1	chr4	962325	962325	G	A	missense	c.C185Y	0.24	verified	pathogenic missense	4/4	D	D	D	D					
39_4	SNV	DNF36B	chr5	75756504	75756504	C	T	missense	c.V318M	0.19	verified	tolerated missense	0/4	D	T	T	T					
40	SNV	ClpP2B	chr1	244191969	244191969	G	A	missense	c.G157S	0.29	verified	pathogenic missense	4/4	D	D	D	D					
42	SNV	CDK18	chr1	205495571	205495571	T	C	missense	c.A200S	0.13	verified	pathogenic missense	2/4	D	D	T	D					
42	SNV	GJB3	chr1	151145361	151145361	G	A	missense	c.G61R	0.18	verified	pathogenic missense	3/4	D	D	D	D					
43	SNV	HDAC3	chr7	27347898	27347898	G	A	missense	c.P323S	0.11	verified	pathogenic missense	4/4	D	D	D	D					
43	SNV	IRF25	chr6	168458687	168458687	C	T	missense	c.P48L	0.11	verified	pathogenic missense	4/4	D	D	D	D					
43	SNV	TUBGCP2	chr10	135065793	135065793	C	T	missense	c.A671T	0.19	verified	tolerated missense	0/4	D	T	T	T					
44	SNV	SAFT10	chr19	49050357	49050357	G	A	missense	c.V767I	0.09	verified	pathogenic missense	3/4	D	D	D	D					
46	SNV	CQN	chr1	151491162	151491162	G	A	missense	c.R56H	0.08	verified	pathogenic missense	4/4	D	D	D	D					
46	SNV	MTM1	chrX	149822938	149822938	C	A	missense	c.S132N	0.05	verified	pathogenic missense	3/4	D	D	D	D					
51	SNV	ATF2	chrX	148083812	148083812	G	T	missense	c.R494C	0.16	verified	pathogenic missense	4/4	D	D	D	D					
51	SNV	DDX3	chr11	125780355	125780355	G	A	missense	c.G185V	0.1	verified	pathogenic missense	3/4	D	D	D	D					
51	SNV	RTTN4	chr10	3199718	3199718	C	T	missense	c.G387E	0.12	verified	pathogenic missense	4/4	D	D	D	D					
51	SNV	PPARA	chr2	46611148	46611148	G	A	missense	c.G36E	0.13	verified	tolerated missense	1/4	D	T	D	T					
51	SNV	PKDP1	chr5	177421147	177421147	C	A	missense	c.S102I	0.13	verified	pathogenic missense	3/4	D	D	D	D					
51	SNV	TBX15	chr1	119627565	119627565	C	T	missense	c.G447V	0.16	verified	pathogenic missense	2/4	D	D	T	T					
51	SNV	TP53	chr17	7577511	7577511	C	T	missense	c.G132S	0.21	verified	pathogenic missense	4/4	D	D	D	D					
51	DEL	TSC1	chr9	135772660	135772660	TTC	-	in-frame	c.F40_E40del	0.33	verified	pathogenic in-frame indel						3/4	D	T	D	D
52	SNV	RF1	chr7	29528489	29528489	C	T	stoncoding	c.R410X	0.49	verified	stoncoding										
52	SNV	TOP3B	chr22	22311925	22311925	G	T	stoncoding	c.Q71X	0.5	verified	stoncoding										
55	DEL	KIF16B	chr20	16360093	16360094	CT	-	framesift	c.S885fs	0.35	verified	frameshift										
55	SNV	RF27	chr9	86452007	86452007	C	T	stoncoding	c.S127X	0.1	verified	stoncoding										
55	DEL	RF1	chr7	29562888	29562888	-	C	framesift	c.Y1264fs	0.37	verified	frameshift										
55	SNV	PKSCA	chr3	178916019	178916019	C	T	missense	c.G1080S	0.18	verified	pathogenic missense	4/4	D	D	D	D					
55	DEL	RAB14	chr3	27041682	27041682	-	A	framesift	c.P159fs	0.32	verified	frameshift										
56	SNV	ATR4	chr4	76908807	76908807	G	A	stoncoding	c.R782X	0.53	verified	stoncoding										
56	SNV	CCP110	chr16	19547438	19547438	G	T	missense	c.D549Y	0.08	verified	pathogenic missense	2/4	D	D	D	D					
56	SNV	CIAO2	chr8	61614461	61614461	G	T	missense	c.R107S	0.38	verified	pathogenic missense	2/4	D	D	D	T					
56	SNV	HMGCL1	chr6	55378850	55378850	G	A	stoncoding	c.R149X	0.37	verified	stoncoding										
56	SNV	TP53	chr17	7577572	7577572	C	T	missense	c.M237I	0.66	verified	pathogenic missense	4/4	D	D	D	D					
57	DEL	CD28	chr2	204594840	204594873	GTA	-	in-frame	c.51_53del	0.29	verified	pathogenic in-frame indel						3/4	D	D	T	D
57	DEL	EADH	chr3	138540465	138540465	C	-	framesift	c.Q669fs	0.43	verified	frameshift										
57	SNV	CYS	chr6	64541617	64541617	G	T	missense	c.R245LH	0.24	verified	tolerated missense	1/4	T	D	T	T					
57	DEL	MYO1A	chr10	158067733	158067733	-	A	framesift	c.D435fs	0.21	verified	frameshift										
57	SNV	PARP10	chr8	145055024	145055024	A	T	missense	c.D73L	0.49	verified	tolerated missense	1/4	T	T	T	D					
57	SNV	PHF16	chr9	34971514	34971514	G	A	missense	c.S73R	0.45	verified	tolerated missense	0/4	D	T	T	D					
57	SNV	PTEN	chr10	89711933	89711933	G	A	missense	c.P295S	0.53	verified	pathogenic missense	4/4	D	D	D	D					
57	SNV	RREB1	chr6	7247309	7247309	G	A	missense	c.S1454G	0.39	verified	pathogenic missense	3/4	D	D	D	T					
57	INS	TP53	chr17	7573863	7573863	-	T	framesift	c.L210fs	0.76	verified	frameshift										
66	SNV	RF1	chr17	29528493	29528493	T	-	stoncoding	c.R410X	0.25	verified	stoncoding										
67	SNV	RF1	chr7	29562744	29562744	TC	-	stoncoding	c.E275X	0.34	verified	stoncoding	1/4		D	T	D					
1	SNV	ATR4	chr4	76907808	76907808	T	C	missense	c.R1703G	1	no											
2	SNV	DOK10	chr1	146256948	146256948	G	A	missense	c.A431T	0.12	no											
3	SNV	RGF	chr1	153028832	153028832	G	T	stoncoding	c.G94X	0.07	no											
7	SNV	CCDC12	chr3	42772218	42772218	C	T	stoncoding	c.Q452X	0.06	no											
11	DEL	CD7	chr17	80276142	80276168	CAGGGAGGGCAGAGGCTGCTGGGGGGT	-	in-frame	c.172_181del	0.28	no											
14	SNV	DOK10	chr1	146256948	146256948	G	A	missense	c.S869N	0.17	no											
14	INS	RTTN	chr18	67863852	67863852	CTA	-	in-frame	c.G242delinsVG	0.22	no											
15	INS	ARC	chr3	128245449	128245449	GCGCGCGCGCGCGCGCGCGCTGCC	-	in-frame	c.S10delinsGSGSGSGS	0.41	no											
20	SNV	SMARCA4	chr4	128645993	128645993	G	A	stoncoding	c.R229X	0.09	no											
21	SNV	PTPN12	chr4	87687597	87687597	C	T	missense	c.R129C	0.16	no											
22	SNV	TP53	chr17	7577580	7577580	C	T	missense	c.Y107C	0.08	no											
22	DEL	CD7	chr12	120260722	120260722	T	-	missense	c.I168M	0.07	no											
32	SNV	KIF2C2	chr4	149357147	149357147	T	C	missense	c.N280S	0.08	no											
38	SNV	RF1	chr7	29527401	29527401	T	A	stoncoding	c.R304X	0.14	no											
44	DEL	PAK1	chr20	21686323	21686327	GCG	-	in-frame	c.42_43del	0.07	no											
48	SNV	FTM2	chrX	24602467	24602467	C	A	missense	c.G135D	0.06	no											
52	SNV	GPCP2I	chr20	3548299	3548299	T	A	missense	c.D386V	0.09	no											