Supplementary Table S2. 79 deleterious SAAVs predicted by the AssVar server. The information for each SAAV is shown including protein name, gene name, UniProt accession number, mutation position, wild amino acid, mutant amino acid, impact score and prediction results. The default cut-off impact score was set at 0.57 which means that if the value of the impact score for SAAVs is greater than 0.57, the variant will be assigned as a "driver" mutation.

Protein Name	Gene name	Accession Number	Mutation Position	Wild-type AA	Mutant-type AA	Impact Score	Prediction Results
HLA class I histocompatibility antigen	HLA-C	A2BF26	137	Y	H	0.67	1*
Transcriptional regulator ATRX	ATRX	P46100	929	E	Q	0.62	1
Canalicular multispecific organic anion transporter 2	ABCC3	O15438	718	K	M	0.66	1
Glucose-6-phosphate exchanger SLC37A4	SLC37A4	O43826	88	G	D	0.91	1
Isocitrate dehydrogenase [NADP] cytoplasmic	IDH1	O75874	19	T	P	0.67	1
ATP synthase subunit d, mitochondrial	ATP5PD	O75947	135	D	N	0.76	1
Extracellular matrix protein 2	ECM2	O94769	213	S	Y	0.61	1
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 3	NDUFA3	O95167	62	N	D	0.57	1
Mitogen-activated protein kinase kinase kinase 6	MAP3K6	O95382	673	R	L	0.59	1
L-lactate dehydrogenase A chain	LDHA	P00338	144	T	I	0.75	1
Phosphoglycerate kinase 1	PGK1	P00558	315	D	N	0.85	1
GTPase Hras	HRAS	P01112	61	Q	E	0.88	1
GTPase Kras	KRAS	P01116	22	Q	E	0.87	1
GTPase Kras	KRAS	P01116	12	G	D	0.95	1
GTPase Kras	KARS	P01116	12	G	R	0.94	1
Insulin	INS	P01308	90	G	C	0.82	1
Prelamin-A/C	LMNA	P02545	465	G	D	0.78	1
Serum albumin	ALB	P02768	300	K	N	0.71	1
HLA class I histocompatibility antigen, A-3 alpha chain	HLA-A	P04439	176	E	V	0.69	1
Receptor tyrosine-protein kinase erbB-2	ERBB2	P04626	776	G	V	0.70	1
Calpain small subunit 1	CAPNS1	P04632	120	L	F	0.68	1

Cellular tumor antigen p53	TP53	P04637	273	R	H	0.87	1
Fructose-bisphosphate aldolase B	ALDOB	P05062	335	N	K	0.77	1
Aldehyde dehydrogenase, mitochondrial	ALDH2	P05091	287	G	A	0.91	1
Intercellular adhesion molecule 1	ICAM1	P05362	397	R	Q	0.68	1
Insulin receptor	INSR	P06213	1055	A	V	0.86	1
Alpha-galactosidase A	GLA	P06280	321	Q	E	0.64	1
Heat shock 70 kDa protein 1A	HSPA1A	P0DMV8	467	A	V	0.72	1
Glycogen phosphorylase, muscle form	PYGM	P11217	666	Q	E	0.74	1
Myosin-7	MYH7	P12883	953	D	H	0.56	1
Small nuclear ribonucleoprotein-associated proteins B and B'	SNRPB	P14678	79	S	P	0.77	1
Ankyrin-1	ANK1	P16157	276	L	R	0.95	1
Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-3	GNB3	P16520	76	D	N	0.83	1
Heat shock 70 kDa protein 6	HSPA6	P17066	375	A	S	0.75	1
Protein kinase C alpha type	PRKCA	P17252	467	D	N	0.65	1
Filamin-A	FLNA	P21333	207	P	L	0.74	1
Filamin-A	FLNA	P21333	605	D	N	0.62	1
Integrin alpha-6	ITGA6	P23229	419	A	T	0.58	1
HLA class I histocompatibility antigen, B-8 alpha chain	HLA-B	P30460	140	Y	D	0.83	1
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	P40939	510	E	Q	0.77	1
Leukemia inhibitory factor receptor	LIFR	P42702	1068	F	L	0.61	1
DNA mismatch repair protein Msh2	MSH2	P43246	331	N	D	0.57	1
Olfactory receptor 3A1	OR3A1	P47881	78	S	G	0.75	1
Annexin A11	ANXA11	P50995	230	R	C	0.69	1
Anthrax toxin receptor 2	ANTXR2	P58335	105	G	D	0.67	1
Actin, cytoplasmic 1	ACTB	P60709	243	P	L	0.75	1
Ubiquitin-40S ribosomal protein S27a	RPS27A	P62979	57	S	P	0.74	1
Actin, alpha skeletal muscle	ACTA1	P68133	45	V	F	0.72	1
Hemoglobin subunit beta	HBB	P68871	37	P	T	0.60	1
HLA class II	HLA-	P79483	100	K	T	0.57	1

histocompatibility antigen, DR beta 3 chain	DRB3						
Neuroblast differentiation-associated protein AHNAK	AHNAK	Q09666	4090	D	G	0.78	1
26S proteasome non-ATPase regulatory subunit 2	PSMD2	Q13200	452	N	D	0.60	1
Peroxisome assembly factor 2	PEX6	Q13608	812	R	W	0.83	1
Pregnancy-specific beta-1-glycoprotein 5	PSG5	Q15238	168	T	I	0.68	1
Protein transport protein Sec23B	SEC23B	Q15437	489	H	Q	0.57	1
Fibronectin type III domain-containing protein 3B	FNDC3B	Q53EP0	927	P	S	0.67	1
Signal-regulatory protein beta-1 isoform 3	SIRPB1	Q5TFQ8	51	T	I	0.72	1
Tetratricopeptide repeat protein 19, mitochondrial	TTC19	Q6DKK2	123	L	I	0.71	1
Cytochrome P450 20A1	CYP20A1	Q6UW02	346	L	F	0.65	1
Mitochondrial Rho GTPase 2	RHOT2	Q8IXI1	425	R	C	0.64	1
Activating signal cointegrator 1 complex subunit 3	ASCC3	Q8N3C0	1995	S	C	0.63	1
Nuclear pore membrane glycoprotein 210	NUP210	Q8TEM1	1052	G	S	0.89	1
ATP-dependent RNA helicase DDX1	DDX1	Q92499	332	Q	E	0.64	1
RNA binding motif protein, X-linked-like-1	RBMXL1	Q96E39	40	I	M	0.60	1
Vacuolar protein-sorting-associated protein 25	VPS25	Q9BRG1	170	G	V	0.57	1
Oxidoreductase HTATIP2	HTATIP2	Q9BUP3	116	A	T	0.59	1
Pantothenate kinase 2, mitochondrial	PANK2	Q9BZ23	322	E	G	0.79	1
Tether containing UBX domain for GLUT4	ASPSCR1	Q9BZE9	252	L	Q	0.79	1
Carbohydrate sulfotransferase 6	CHST6	Q9GZX3	280	P	Q	0.84	1
Cysteine-rich and transmembrane domain-containing protein 1	CYSTM1	Q9H1C7	90	C	S	0.63	1
HEAT repeat-containing protein 1	HEATR1	Q9H583	2017	E	G	0.68	1

ATP-binding cassette sub-family B member 8, mitochondrial	ABCB8	Q9NUT2	321	R	C	0.63	1
7-dehydrocholesterol reductase	DHCR7	Q9UBM7	362	R	C	0.79	1
Protein mono-ADP-ribosyltransferase PARP4	PARP4	Q9UKK3	1108	R	C	0.63	1
NSFL1 cofactor p47	NSFL1C	Q9UNZ2	290	D	N	0.58	1
Bifunctional UDP-N-acetylglucosamine 2-epimerase/N-acetylmannosamine kinase	GNE	Q9Y223	331	V	A	0.76	1
Leucine-rich repeat and calponin homology domain-containing protein 1	LRCH1	Q9Y2L9	234	S	P	0.58	1
ADP-ribosylation factor-like protein 5A	ARL5A	Q9Y689	125	N	S	0.86	1
3-ketoacyl-CoA thiolase, peroxisomal	ACAA1	P09110	387	V	A	0.67	1