

YMTHE, Volume 26

Supplemental Information

An Efficient Single-Cell RNA-Seq Approach to Identify Neoantigen-Specific T Cell Receptors

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Supplementary Table 1. 4090 tandem minigene (TMG) library

TMG ID	Minigene ID	Gene name	Position and change of mutated amino acid	Mutated amino acid sequence
1	1	KCNB2	S421Y	IALPIPIVNNFYEFYKEQKRQEKA
1	2	ABR	P804L	AQVQVLLYYLQHLPISFaelKRNTL
1	3	MAG	V81A	YPPVVFKSRTQVAHESFQGRSRLLG
1	4	ZNF483	S536L	KCKDCGRPFSDSLSLIQHQRIHTGE
1	5	FSCB	Q659P	QPPPAEEAPAEVPPPAEEAPAEVQ
1	6	MST1R	V188 frameshift	DCVASPLGTRVTG
1	7	MMP1	W13S	MHSFPPLLLLLFSGVVSHSFPATLE
1	8	PRR35	E488K	GPQALGEAWGRPKLGPVLTGGTPEP
1	9	KARS	S160 frameshift	RGEGVKLQVMANSEIINQKKNLFLITNCVGET
1	10	UGT2A3	P342 frameshift	PQKVLWRYKGGKKTIIHRSQYSAV
1	11	SLC17A2	D391E	LLILIPGTSNLCESGFIINTLDIAP
1	12	TMX4	R102C	KVDVIQEPGLSGCFFVTTLPaffHA
2	13	OLFML2A	R355W	DLSVHRETTWKTWLRNRNSYGNCFV
2	14	TLR5	R224K	VSVDWGKCMNPFKNMVLELDVSGN
2	15	SETD1B	P1268L	PERAPEHDLEVELEPPMMLPLPLQP
2	16	PCDHA13	A642T	EISTTRPLDEVDTPHHRLLVLVKDH
2	17	HYOU1	R925W	KPRPRPKDKNGTWAEPPLNASASDQ
2	18	SRRM2	P1171L	LETAESKEKMALLPQEDATASPPRQ
2	19	CDRT15L2	G53R	VRRRTQVPQDSPROALAGQATPEIP
2	20	PCNT	R2543H	THLQNQEKLQHLHTALTSAEARGSQ
2	21	RYR2	D1621Y	ISERQGWLVQCLYPLQFMSLHIPEE
2	22	PRSS12	R630W	VCGLRLLHRRQKWIIGGKNSLRGGW
2	23	TP53	V272M	SSGNLLGRNSFEMRVCACPRDRRT
2	24	MAP2	A172V	EFHDQDELTPSTVEPSDQKEKESEK
3	25	KCND2	P358S	EKGSSASKFTSISAAFVYTIIVTMTT
3	26	MED12	T1546M	KLRLNLVGGMFDMVQRSTQQTTEWA
3	27	ADAM28	I184T	DGVLWAHDLQNTALPATKLVKDKD
3	28	ZNF843	A92V	APASPLGRSHSVGVVQGFSGQLCC
3	29	GIMAP6	G62S	GSGKSATGNSILSRDVFESKLSTRP
3	30	SDK1	P772 frameshift	RLMLPEPPSAPPKYSYGQWAD
3	31	PTCHD1	K619E	KNFTDMLRNSFLEAPQFSHFQEDII
3	32	KRAS	G12V	MTEYKLVVVGAVGVGKSALTIQLI
3	33	OR5H1	M136T	VAICKPLLYPAITTNGLCIRLLILS
3	34	KMT2E	I960 frameshift	FENISSPESSPEIETHL
3	35	PKD1L1	F164I	ASCSMMRHSPLRIFVAGLVGALML
3	36	MAOA	S2649R	PPGIMTQYGRVIHQPVGRIFFAGTE
4	37	HRNR	R424H	GSGSGRSSSSGQQGSGLGESSGFH
4	38	FGD5	H2567Q	ETDEDYIVVPRVLLREDEPKDEGSV
4	39	ATF6	P72L	ELGYFTDTDELQMEANETAYENNFD
4	40	CDH7	F164S	FKRLADMYGTGQGSLSYS
4	41	C5orf42	N19T	LRWSQLPVKENKGFSGAAKSHFECCG
4	42	KIF5B	A406T	KDITLTNDKPATTIGVIGNFTDAER
4	43	ISL2	G269E	QQQOHSDKTSLQELTGTPLVAGSPI
4	44	R3HDM4	E12V	MVALENPECGPVAAEGTPGGRLL
4	45	ATG101	R209L	TDALGTSVTTTMLRLIKDTLAL
4	46	PAPOLA	A414D	VGSLEKNEFITLDHVNQSPAPKE
4	47	MPRIP	L786V	DAESKHSMSMFTVRGRYEEIEIRCVV
4	48	HIST1H1E	E42D	AAKRKASGPPVSDLITKAVAASKER
5	49	RC3H1	Y890C	RFGAISRTSKTICQGAGPMQAMAPQ
5	50	ZBTB33	R510Q	VCKRSYVCLTSLQRHFNIHSWEKKY
5	51	OR52E8	R178C	VFLLLRPFPCGHCIIPHTYCEHMG
5	52	PRB3	K235Q	GKPEGPPSQGGNQPGPPHPGKPKQ
5	53	C2CD2L	R212C	GEGLLISWAFDPCDLSLTVLPKLQ
5	54	EVC2	294-294 deletion	DQMIDILSSEDPSMLQALELEIAT
5	55	USP8	R667H	WAKFLDPITGTFHYHSPNTVHMY
5	56	MYO19	P550S	YHTAGLVEKNKDSIPPELTRLLOQS
5	57	MRPL39-1	L189V	VRAPEVPVLDSKVDEWMPKLENLRS
5	58	MRPL39-2	L189V	GAFICYDVVLDSKVDEWMPKLENLRS
5	59	PRDM15	E580K	CSATFLELQLLNKHLGHLEQAKSL
5	60	C4B	S1242W	WGSVGTGSQSNVWPTPAPRNPSPDPM
6	61	TMEM255B	C151Y	QTEVTCBSLDGKYQLKVRSNTCYCC
6	62	PCDHGA3	E523K	TGVLYALRSFDYKQFRDLKLLVTAS
6	63	PRAMEF11	D67V	PRRWKLQVLDLQVVCENFWMVWSEA
6	64	FIGNL2	Q474P	AAPGAAEGARLLPAAFAAACRPPS
6	65	PRR36	L760Q	ASAPLTPPLENQPSLAPPPLQTAS
6	66	OLIG2	S88A	KSSSSSTSSSTSAAAASSTKDKKQ
6	67	NUTM2F	P559H	VETSPPTAAQDHQGGQGRVRTGMAR

6	68	C1orf21	T75S	LEKSSASSNVRLKSNKEVPLVHQPR
6	69	PTGS2	Q39H	QNRGVCMSVGFHDHYKCDCTRTRTFYGY
6	70	CKAP4	Q57P	PPPAPHPPQHPQHPQNPQAHGKGGH
6	71	WDHD1	R369H	DEDEDLMMASGHPRQRSHILEDDE
6	72	ITGAM-1	T486P	LVLIGAPHYYEQPRGGQVSVCLPR
7	73	ITGAM-2	T486P	PGPHRGPPLLRAAPRPGVVRVPLAQ
7	74	RAVER1-1	G65S	PESLPEPTQPAPSSQPPGGSSKAFQL
7	75	RAVER1-2	G65S	PESLPEPTQPAPSSQPPGGPWRWQQQ
7	76	EYA2	S100I	PPPAQAYGIPSYIIKTEDSLNHSPG
7	77	TRANK1	V257L	LHVVAAHSPGYLLKRQTEDVQMLLR
7	78	ZKSCAN7-1	G195R	PPYDPGTHHLPSRDFGYCGI
7	79	ZKSCAN7-2	G195R	PPYDPGTHHLPSRDFQAQCTSPVPTL
7	80	DUX4L4	Q378L	QGSPWWGWRGPLVAGAWEPPQAGE
7	81	TNXB	R1081H	TVTDRTSDSLHLLHWTVPPEGEFDSFV
7	82	MUC12	E2160D	SPGSTTALSFGQDSTTFHSSPSTH
7	83	KCNQ4	A348V	EKRMPAANLIQVAWRLYSTDMSRA
7	84	MTERFD3	Q192 frameshift	PVEKNKQMVRLRELSRRCRWL
8	85	DMXL2	T1644M	AMGIGWVVRNINMLRRCIEKVAKAS
8	86	OR2C1	Y252C	TCLSHLLVVFLLFCGSASYGYLLPAK
8	87	UNC13D	G1035S	REVPGLSGSEEPSEVPQTRPLPTY
8	88	SAMSN1	R235H	DDDGYPYSGPFCGHARVHTDFTPSPY
8	89	AF035281	T192M	TPTTARTSGRSPMSAPSSLAACPRC
8	90	FBXL18	T546M	RHLTLAQLPSVLMGSLVNLIGLQCQ
8	91	OCRL	G147E	KLDTKDKPSVFSSELLGFEDNFSSMN
8	92	ZNF182	A6E	MTPASESGEDSGSFYSWQ
8	93	DTX3	P2L	MLILSSSGSKMAAC
8	94	MAG	A404T	CVAENQYQGRATTFNLSVEFAPVLL
8	95	PCDHGC5-1	R816W	EPDAIRSRNTLWERSQQAPPNTDW
8	96	PCDHGC5-2	R816W	EPDAIRSRNTLWERSQVRGSAPPR
9	97	RXFP3	T179M	YASVFFLTAMSVMRVHVSASALKSH
9	98	KCNA10	G49R	PKGRPGGSSFSNRKILISESTNHET
9	99	TRH	R226W	DDLRSRQGAEEKWQHPGRRAAWVRE
9	100	C4orf48	V85A	GARARAEPAGSAAPAQSRPCVDCHA
9	101	FPGS	E429K	CLEHQHWNHLDKEQASPDLSWAPS
9	102	FXN	C50S	GRRGLRTDIDATSTPRRASSNORGL
9	103	HPSE2-1	E262D	QFSNTYSNLLTDPNNYRTMHGRAV
9	104	HPSE2-2	E262D	PGPDYLLKNYEDDPNNYRTMHGRAV
9	105	HPSE2-3	E262D	SKKYNISWELGNDPNNYRTMHGRAV
9	106	RAD9A-1	T93M	GQDLLRCKILMKMVEKCCISLNGRS
9	107	RAD9A-2	T93M	LSVFRSLAMLEKMVEKCCISLNGRS
9	108	OGFOD1-1	V39L	SDAVTEETLKKQLAEAWSRRTPFKV
10	109	OGFOD1-2	V39L	SDAVTEETLKKQLAEAWSRRTPFVSH
10	110	MUC12	T1035A	TTSHSSPGSTDTALLPASTTTSGPS
10	111	NRK	Q1252H	DITKLIRRRPFRHIQVLEPLNLLIT
10	112	ITIH6	R523C	PGKQELGIHLAACGPKDQLLVAHHS
10	113	TFAP2E	Q97P	GGLAPLAQPQPPAAWAAPRAAARA
10	114	ATPAF1	D84G	VRPGSGRPEGGAGSSGVGAELQA
10	115	MUC5B	T2445P	PGTTWILTELTPATTTESTGSTAT
10	116	POU5F1P3	G59R	IGPGFPGSEEWRIIPCPPPYFCG
10	117	FAM71E2	R480L	PSQKAPAIPAPSLKASAASASPRKA
10	118	FAM134A	L67R	TLWLRLRGWEAVRAAAQRLLVWEKP
10	119	KCNIP3	A210T	MGRHTYPILREDTPAEHVERFFEKM
10	120	PCDH10	R230H	GGGAGLPPQQOHTGTALLTIRVLD
11	121	ATPAF1	E93A	GGADSSGVGAEEAALQANPFYDRYRD
11	122	SERPING1	D30A	AGSEAGWLRSAAVAAQMASRLTLL
11	123	LEPREL2	L60R	YAAGAWAPAVALRREALRSQAALGR
11	124	SLC25A35	V114G	PARSAAAGAMAGGMGAYLGSPIYMV
11	125	HIPK4	R603P	LPPRRSHQHGGPPPGATSFLQHVTHG
11	126	IQCJ	K146T	QLARPTGFIHTLTPQIERLGFLLTL
11	127	CIZ1	Q578L	FCYICKASCSSQLEFQDHMSEPPHQH
11	128	VCX	M180K	SQVEEPPSQESEKEELPSV
11	129	CROCC	L1066Q	LLAESEKQALSQKSEKTLALSEKL
11	130	GJB4	D142V	TYLLSLIFKAAVVAGFLYIFHRLYK
11	131	TNNT3-1	V26A	EEEEEAQEEAAEAHEEEKPRPKLT
11	132	TNNT3-2	V26A	EEEEEAQEEAAEAHEEDTAEEDAEE
12	133	TNNT3-3	V26A	EEEEEAQEEAAEAHEEGMRTQDFHH
12	134	HOXA3	L90Q	PPSQPPSLGEPHQHPPPPQAAPPAP
12	135	FEM1A	D257A	AGGEAQPGLPQEAPESTSQGCAQPGG
12	136	DMD-1	I106R	GNHKLTLGLIWNRLHWQVKNVMKN
12	137	DEAF1	A388V	NQAQQLKTLFEQVKHASTYREAAATN

12	138	ZNF705E	F271Y	DNSGKAFSQSSGYRGNKIHTGKPK
12	139	CABP1	H88P	AAAASGGSRAPRPGPARDPGLPSRR
12	140	CCER1	D10A	MTQTLDTREAPLNLGGGGGGGC
12	141	SMARCE1	M103L	LKLWEIGKIIGGLWRDLTDDEEKQEY
12	142	UBE2Z	D107G	RTAPQCLLRIRKRGIMSIYKEPPPGM
12	143	ARHGAP15	I159N	AKEKSSRKNVFQNTTVSGNEFLLQS
12	144	PCNT	S2667R	LESEQKGRALQRQLEEEQLRHLLQR
13	145	ZNF451	S853T	ERKLLKQAINYSKTLDMKGVENDLS
13	146	TNNT3-4	V26A	EEEEEAQEEAAEAHEEVHEPEEVQE
13	147	GLI3	P942A	KAKYAAATGGPPATPLPNMERMSLK
13	148	TNRC18	E60A	GLYPSYLHLNHLAPPSSGSPLLSQL
13	149	DISP1	E473D	GESMMNIYLDNFDNWNSSDGVTTIT
13	150	PRR35	S358P	LPKASPSLTRFCPRSSLPTGSSVML
13	151	ADAT1	A354 frameshift	QRALIGRCQNVSLLYQKASEFKN
13	152	RSAD1	N26T	AARAAQRRRRVETAGGSPSPPEAGR
13	153	TEX14	L105F	VHAAAFSGNQWIFSKLLDAGGLRL
13	154	KCNH6	V110G	YYRKDASSFRCLGDVVPVKNEGDGAV
13	155	USP36	P234A	KACLNGCAKCVLAHPPSQGFHLY
13	156	CTDP1	V43G	RLEWRV AAGAAGRIGSVLAVFEAA
14	157	RPS15	R16Q	EQLMQLYSARQRQLNRGLRRKQHS
14	158	TNNT3-5	V26A	EEEEEAQEEAAEAHEEVHEPEEKPR
14	159	SFT2D3	L153R	APSRPALLYMAARGATLFAALGLRS
14	160	CCM2L	G210A	ICSLDWRMGWGGAAAEARAGGGGGG
14	161	PKDREJ	L139Q	TWSVRLPRSPGRQAWAFRLRLGPG
14	162	RPL34	Q114L	IVVKVLKAAQASLKAK
14	163	TRAPPC3L	K92 frameshift	IGITFLKKRDEKNI
14	164	AKAP12	E24A	PEQPPEGSSTPAAPEPSGGGPSAEA
14	165	PEX6	L81R	PGPPQLVSRALRRLLALGSGAWVR
14	166	WDR86	Q407P	AAGLIPRGPCRRPPRHPAAPRAPRP
14	167	TNNT3-6	V26A	EEEEEAQEEAAEAHEEVHEPEDDLK
14	168	DMD-2	I106R	GNHKLTLGLIWNRLHWQVLGDRWA
15	169	GDPD2	L441Q	DLPLLDIKDRFLQPAQAGLKLLASS
15	170	AIM1L	Q562L	KGPGAPAASSPTLKEVVQSGGAPAA
15	171	SERINC2	D343A	LLCTLFISLRSSAHRQVNSLMQTEE
15	172	C11orf65	K110M	ANSPRNYAKLPAMHTSHNKNDHLQE
15	173	UHRF1BP1L	D844V	ESLILLSENLRKVVEAVTGSPASQT
15	174	PKP2	D26G	RTVLGQQILGQLGSSSLALPSEAKL
15	175	SMARCD1	Q46H	PGPPVRMGPAAGHGLYRSPMPGAAY
15	176	KCNK13	D384H	NGCPHQTSTLARHNEFSGGVGAFAI
15	177	SLC12A1	L553P	NNEPLRGYILTFPIAMAFILIAELN
15	178	SMAD6	F2L	MLRSKRSGLVRRLLW
15	179	SSTR5-AS1	P39T	MRLRTPKPRPRTRPHAAADPRPRP
15	180	YBX3P1	Q41P	PATKSRVGGGAPPAAPAPAALVAG
16	181	MSLNL	L326Q	GANLWASANCSLQQGFWCQPASQLP
16	182	SARM1	C518S	TAAREMLHSPLPSTGGKPSGDTDPV
16	183	RUNDC3A-1	F73L	FAAILEQILSHRLKACAPAGVSWF
16	184	RUNDC3A-2	F73L	FAAILEQILSHRLKGPVSWFSSDQG
16	185	HID1	S675R	WREQRRPSTSSARGQWSPTPEWVLS
16	186	OSBPL1A	A216D	LKNKNDQKPLDLDDQGAEMKHILVGN
16	187	NLRP13	C270Y	FQQRFSYVFYLSYHKIRYMKETTFA
16	188	KANK3	L224R	EQVRALRAEKARRLAGRAQPEPDGE
16	189	GRB14	R48Q	AHDLAPAPWLHAQALLPLPDGTRGC
16	190	SPEG	L2525Q	AQAGATTPSAESQSEASATSGSSA
16	191	TRPC4AP	Q56L	GQLTGRGLVRAVLFETFLTERDKQ
16	192	MPST	S9P	MAEPGSREPETRARSPSVAAM
17	193	ZNF662	E17A	ALASGTRLGLVLALLPGQPALPRAR
17	194	ADAMTS2	23-24 deletion	LLCPALLLLLLPPPLPPPPPPAN
17	195	AMZ1	E287A	LRCLMQGALSLDAALRRPLDLCPIC
17	196	PDLIM2	H284P	PASRALATPPKLPCEKCEKSTSIANQ
17	197	NKX3-1	E61A	QRORDPEPEPEPAPEGGRSAGAQN
17	198	CEBPD	S191R	EKSAGKRGPRDRPEYRQRRENNI
17	199	SGK223	L1188H	PCSSAAPPAGGTHSPAAGPASPEGP
17	200	ZNF462	P582T	PPHQVPPQPQTQTPTQPQPPTQA
17	201	ARID1A	L1051 frameshift	TNLPAVGRKPLDLLSPLCVCEGDWWIDSGQQEQ KMAGTCNQPCGHIKQCCOLLEKAVYPSLCL

Supplementary Table 2. 4095 tandem minigene (TMG) library

TMG ID	Minigene ID	Gene name	Position and change of mutated amino acid	Mutated amino acid sequence
1	1	KLF5	P309A	ATYFPPSPSSSEAGSPDRQAEMLQN
1	2	ZC3H3	T840P	HGPRKPSASQRPPRQTPSSAALTA
1	3	WRNIP1	L12I	MEVSGPEDDPFISQLHQVQCPVCQ
1	4	SENP2	G262R	LKTKGWGEEQNHRVKTTOFVPKQYR
1	5	UGT8	K128N	LMVGNHALIQGLNKEKFDLLLVDPN
1	6	WWC1	K671N	ATRIQIALKYDENNKQFALIIQLS
1	7	PEX1	Q79E	SDQGENVAEINREVQKLGLSNGGQ
1	8	KRAS	G12D	MTEYKLVVVGADGVGKSALTIQLI
1	9	ROBO2	P929T	GDPSYPWLADSWTATSLPVNNSNSG
1	10	PGBD1	E656K	VRATGTIRENRTKKCPLMNVEHMKK
1	11	PLEC	L3602M	KGLVLRQHGIIRLMEAQIATGGIIDP
1	12	ESRRA	P173L	YKRRPEVDPLPFLGPPFAGPLAVAG
2	13	LIX1L	G121W	QMKQSRGADLKNWALVYEMVPSNS
2	14	TACC2	A677T	EEDPVLPPVPDGTGEPTVPEGAIWE
2	15	KDM2A	A507S	LLEELANSDPKLSLTGVPIVQWPKR
2	16	KCNH2	E435D	VFTPYSAAFLLKDTTEGPPATECGY
2	17	PCSK5	R1302H	FFFLLRSKGECHEHSCPDHYVEQST
2	18	KCNN3	D711Y	SVAVGTTHTPISYSPIGVSSTSFPT
2	19	DNAJB6	N248T	DALAEERMRRGQTALPAQAPGLRPP
2	20	FAM109A	Q151P	QSHPCLLPQPRSPPCPCPAGVPVSR
2	21	DDX60	L101I	DAEYAYFNPELISLRTALILHLQK
2	22	DUOX2	K529N	YWFENTRNGLFSNKEIEDIRNTTLR
2	23	COL17A1	W455G	GAGGGPWGPAPAGCPCGSCCSWWKW
2	24	WISP1	M32K	VLATALSPAPTTKDFTAPLEDTSS
3	25	AGAP3	H576P	SSSPKLDPPSPSPSNRKKHRRKKST
3	26	ZC3H3	T493P	ALRGKSSPVLKPPNKGLVQVTTHR
3	27	C8orf82	V165G	RLYHPAPERAGGGGLVRSALAFELS
3	28	LINC00115	L16H	VFHRPHRPSWPHRAALGFGRQSS
3	29	TRIM11	H123L	CAACERSGEHWALRVRPLQDAAEDL
3	30	CPEB3	R544L	DRPKTIFVGGVPLPLRAVELAMIMD
3	31	PRB1	R558L	POGPPPOGGNRPLGPPPGKPOGPP
3	32	PRG4	L1016F	AGGAEGETPHMLFRPHVFMPEVTPD
3	33	HLA-DQB1	S229R	TVEWRAQSESAQRKMLSGVGGFVLG
3	34	ZNF717	V114L	GICHRSLVELQEL
3	35	MUC4	D1125Y	VSTGHTTPLPVTYTSSASTGHATS
3	36	MCHR2	N116T	PLCTIITSLDCTQFACSAIMTVMS
3	37	OBSCN	R4668W	WHKGMERIQGGWFEVVSQGRQOQML
4	38	DSPP	S845R	SNSSDSSDSSNSRSDSSDSSDSDGS
4	39	ADAMTSL2	R420W	EQAGGGACEGPPWKGFRDRNVTGT
4	40	RSAD2	F248L	QIKALNPVRWVKVLQCLLIEGENCGE
4	41	AEBP1	P387R	EEWTPTEKVKCPRIGMESHRIEDNQ
4	42	AKAP6	D1033Y	EALKKGGVLLPNYLLEKVDSENEKW
4	43	TMEM132D	T394M	SSSMGLMEGRGTMTRDRILOKQKKGQ
4	44	DPY19L2	S598P	FEKVIFGILTVMPIQGYANLRNQWS
4	45	ARL14EPL	A65S	DFNPETRQKKKSRMSKMNEYFSTK
4	46	SPTB	V445M	MRETWLTSENQRLMAQDNFGYDLAAV
4	47	PPM1K	V194M	NCAWSAALDLEPMDTICGASVEREI
4	48	TTN	D4157E	SWFKDGGKEIAASERYRIAFVEGTAS
4	49	IL17F	R72H	GIINENQRVSMHNIERSRSTSPWNY
5	50	FRMPD1	T1562M	SVKLLARQCTALMAAVFCLTQKFRA
5	51	LRFN5	R516H	GCIQFTTEQDYVHCHFMQSQFLGGT
5	52	ANKRD18B	S397L	NEEMITKKVAQYLQQLNDLKAENAR
5	53	NPC1L1	R242C	GSGIQPLNEGVACCNESQGGDVATC
5	54	PCDHB3	E320K	NFEAINSYEVDIAKADGGGLSGKST
5	55	LRRC4	S147Y	LTVIPSGAFEYLKRELWLRNPNPI
5	56	MAGI2	R136C	ELQIIRDNLVLCVPCPTRPHKEG
5	57	LMOD1	P521T	PKPSPQSPKSTKNSPKKGGAPAA
5	58	ZNF853	V457M	ELMVLPAVAAPAMVAIPGPAGSAAL
5	59	TENM3	V17F	APDPGNLAAALGFSFPHGHSEGAPROE
5	60	MYO1G	D488V	GTITDRIFLQTLVMHHRHHLHYTSR
5	61	SYT7	M256L	TTSQSLGQLQAHLASAPGNPRAYG

Supplementary Table 3. 4112 tandem minigene (TMG) library

TMG ID	Minigene ID	Gene name	Position and change of mutated amino acid	Mutated amino acid sequence
1	1	STS	V215 frameshift	LNCLGLLHVPLGVFFQPSLPPSSPNPDPFLGLPSLLP APELLHDEELRDHSAAHVL
1	2	HEPH	S881R	TLFTVFSRTEHLRPLTVITKETEKA
1	3	POLA1	D105Y	EIFDDDDLEDDALYADEKGKDGKARN
1	4	COL4A5	G902R	GFPGTKGEMGMMRPPGPPGLGIPG
1	5	SEC23B	Q152 frameshift	EEDDLQALKESLRCP
1	6	USP34	Q1495K	SWSCKFVAAGGLKQLEIFNSGILE
1	7	RBM41	G210D	MKKRLEEFQLMRDEPFASHLSVSAT
1	8	NAA35	D139Y	QTVFTCLYIHNPYFIEDPAMKAFAL
1	9	VPS13A	G1333V	SGVTTNASHHSGVATVVTAAVVEVH
1	10	TJP2	G904V	DSRLISDFEDTDVEGGAYTDNELDE
1	11	KIAA2026	V1464A	TRSEATAATNGDAISGTPVQKMLLV
1	12	SETX	G2567R	LWDPQPSSPQHPRATPPTGEPGFPV
1	13	DNM1	P756L	DINTTTVSTPMLPVDSDWLQVQSV
2	14	C5	G836R	FLEMNIPYSVVRREQIQLKGTVYNY
2	15	STK3	V220L	TVIGTPFWMAPELIQEIGNYCVADI
2	16	CRISPLD1	T12S	MKCTAREWLRVSTVLFMARAIAPAM
2	17	PRKDC	A1942S	NQLLERRRLYHCSAYNCAISVICCV
2	18	OPLAH	P869S	ADIGGITPGSMPSHSTMLQQEGAVF
2	19	OPLAH	P143L	RRHRGHHTRLHALPLHHAATGGCRL
2	20	PLEC	E4084K	AQIATGGIIDPEKSHRLPVEVAYKR
2	21	RIMS2	R479T	RKTREKREMETMLTNDLSSDQSESV
2	22	DCAF13	E192G	YDPALHPFEVPRGYRALNATKLER
2	23	PTCD1	I625N	MKQNRVPVNEVVNRQLEFAAQYPPT
2	24	ARPC1A	S201I	MPFQQLMSEFGGIGTGGVWHGVSEFS
2	25	TRRAP	A2809T	MDKAKKEHERSNTSPAIFPEYQLWE
2	26	DLX5	E204Q	IKKIMKNGEMPPQHSPPSSDFMACN
3	27	CALCR	R454P	QFKIQWNQRWGRPPSNRSARAAAAA
3	28	AKAP9	V1990D	RQKEAMKAEAGPDEQQLQETEKLM
3	29	STEAP2	P260T	YKIPIEIVNKTLTIVAITLLSLVYL
3	30	DMTF1	R569K	TSDNVTVQCHTPKVIIQTVATEDIT
3	31	SUMF2	K308N	SAIPSSRASASGNNFPFVSHPSVA
3	32	ADCY1	Q1019H	SRMDSTGVQGRIVTEEVHRLLRRC
3	33	TAX1BP1	M527T	DFDIVTKGQVCETTKEIADKTEKYN
3	34	CDC47L	A216T	MPDFFPVRTPTSTSRKKTVRRAFSE
3	35	REPIN1	G285V	PRGRPAVTAPRPVGDVDRPFQCAC
3	36	ZNF282	WD339-340CY	LSRIKQEEHQVCVYQQDLADRDIPDT
3	37	KIAA1244	C1357F	QVFANAATSYMFLMKFVKGLGEVD
3	38	MET	G643V	NKHFNMSIIISNVHGTQYSTFSYV
3	39	TRIP6	G210V	PHFPLPGRGEVWVPGYRSQREPGPG
4	40	ORC3	G477D	YYLKNEALKSEEDCIPNIAPDICIA
4	41	SYNCRIP	R412T	RGGRGARGAAPSTGRGAAPPRGRAG
4	42	DST	D31A	LQAYEDVLERYKAERDKVQKKTFTK
4	43	ZNF445	G491 frameshift	HTVGVSVFKSCDCEGLSVIAPILRIIRDFTLKRKHLN VGCVKGKPSGGVPTVRGMRKFTLE
4	44	PSTPIP2	S330C	PDDPNYSLVDDYCLLYQ
4	45	DST	L1606F	DTSATHREVQRKFDHATDRFRSLYS
4	46	GCLC	R128L	EFNTVEANMRKRLKEATSILEENQA
4	47	TMEM63B	N186Y	LPVNFSGDLLENYAYSFGRTTIANL
4	48	CNPY3	V55L	VRLPSKCEVCKYLAVELKSAFEETG
4	49	ULBP3	A223S	PPTMAPGLAQPKSIATTLSPWSFLI
4	50	HIVEP2	D20N	LGQKATSRSGETNKASGRWRQEQSA
4	51	SLC37A3	R9I	MAWPNVFQIGSLLSQFSHHHV
4	52	SLC39A1	T130A	MGFFLVLVMEQIALAYKEQSGSPSL
5	53	PAK1IP1	D304H	TNARLTCLGVWLHKVADMKESLPPA
5	54	AIM1	E1034G	GKVVIIYSEPDVSGKCIEVFSIDIQC
5	55	ZFYVE16	F1118L	NEDTIPKDIFRLLITIIYKDALKGKY
5	56	SKP2	H171L	DGTLQLLKEALPLLQINCSHFTTIA
5	57	RAI14	G402C	TQTDLGPPLGKPCETSPDPSKSSPS
5	58	TARS	V587L	YVSHDGGDDKRPLIVHRAILGVSER
5	59	GOLPH3	G32V	RNAADKERAAGGVAGSSEDDAQRR
5	60	KDM3B	G334V	GPWKGGNASGEPVLDQRAKQPPSTF
5	61	SNX2	F369L	EVGRFEKERVKDLKTVIIKYLESLV
5	62	DMXL1	R1069K	LAVAYKQPASNSKSSQDFVMHVSIF
5	63	MARCH6	R690S	AACGLYVCWLTISAVTVMVAWMPQG
5	64	NFXL1	C486F	RDCQKHQCRKCFPGNCPDQNCG
5	65	ATP10D	E853A	TLCIAKKVMSDTAYAEWLRNHFLAE

6	66	ATP8A1	K27N	AEGYEKTDVSENSTLADQEEVRTI
6	67	HTT	D1056Y	GWHCGVPPLSASYESRKSCTVGMAT
6	68	GPR125	G320R	ALTISNIQAGSTRNWGCHVQTKRGN
6	69	FAM198B	K399E	RLDTNCCGFRPREEDACVQNGLRPK
6	70	KIAA0922	P1439L	ENGVPCVIQESALVHNSFIDWSATC
6	71	NAA15	I658V	KLAKVETPLEEAVKFLTPLKNLVKN
6	72	FAT4	S1402P	ITAKDQGRPPRSPTMSVVIHVRDFN
6	73	ALPK1	N1103S	YVTEFNKRLYEQSIPTQIFYIPSTI
6	74	ALPK1	E554D	SDAFRVSLDQDQDVTETEPSDYSNGE
6	75	SETD5	E650K	AQQAELSQLALEKGGNSLVTPTEA
6	76	PPM1M	G128E	RLLGTLAVSRGLEDHQLRVLDTNIIQ
6	77	COL7A1	R185L	VGIKNADPEELKLVASQPTSDFFFF
6	78	DST	D209A	LDPAERAVLRIAAERDKVQKKTFTK
7	79	PARL	S163G	FRKEINKWNNLGDGQRTVTGIIAA
7	80	ITSN1	G783S	GEWVDESQTGEPWSLGGELKGGTGW
7	81	PARL	A284S	GMILGWKFFDHASHLGGALFGIYWV
7	82	TTC14	S134I	DIERGDIVIGRIISIREFGFFMVL
7	83	TBC1D5	G363C	VWDALFADGLSLCLVDYIFVAMLLY
7	84	ZBTB38	Y709F	SNSSENAASVISFSGSAPSIVHSS
7	85	DNAJC13	L877I	PKVNMKCLCLQAIIVYGRCHEEIG
7	86	GOLGB1	V1076L	EIYLKQTISEKELELQHIRKDLEEK
7	87	GOLGB1	V3175M	LRKLEEERDQRMAENALSVAAEQ
7	88	WDR52	E584K	KPHTACVTALAYKRDGEILATGSKD
7	89	RIBC2	T204S	DEAKHLQKLESSTRKAVCASVKDF
7	90	MKL1	S318F	PPVHSLSTTNSFSSGAPGPCGLAR
7	91	SF3A1	A771S	YEGIFIKDSNLSYYNMANGAVIHL
8	92	MTMR3	R728S	EGKEDPILLEKESRKTPEASAIGLH
8	93	GUCD1	L118M	DSEFERALQKLQMTRSIWTIDLAYL
8	94	BCR	K293T	SIYVGGMMEGEGTGPLLRSQSTSEQ
8	95	TRPM2	V1477L	HACDSGASIRWQLVDRRIPLYANHK
8	96	C2CD2	G43W	PEMAVNIQPKALWEDQVAETSAMSD
8	97	PARL	S163G	FRKEINKWNNLGDGQRTVTGLC
8	98	ITSN1	G741S	IVMVDESQTGEPWSLGGELKGGTGW
8	99	ATP5J	F17L	GGISMILQRLFRLSSVIRSAVSVHL
8	100	CSE1L	L340M	PHYKNLFEDQNTMTSICEKVIIVNM
8	101	SAMHD1	D435Y	TDNIFLEILYSTYPKLDAREILKQ
8	102	NDRG3	G128V	SLKSIIGIGVGAAYILSRFALNHP
8	103	AAR2	S187C	GQNLPRCGIECKCYQEGLARLPKMK
8	104	RBM12	H325Y	FSAMENDVRDFFYGLRVDVAHLLKD
9	105	CEP250	L1519P	EENHHKMECQKPIKELEGQRETQR
9	106	PSMD10	Stop loss	IQDTEGNTPLDTPVPMRREWKKQNCWCPKEQV FTLRIKKKRHPCKWPKVAWV
9	107	PTCD3	G213V	QEPSTDYHFQQTQVQSEALEEENDET
9	108	CDTN1	A419T	QQRERLQEELSQTTESTIDELKEQVD
9	109	EHBP1	T165P	SLSCIFLREGKAPDEDMQSLASLMS
9	110	MID2	C734S	PQESPYVSGMKTSH
9	111	BIRC6	M2155I	DNLLSPLQPQLPIHRRTEGVLDIPM
9	112	LRRFIP1	T437A	EAAVTQVEEQAGAVASCPLGHSDDT
9	113	USP40	G1060E	RTDRQPLREYKLERRIEICLEPLQK
9	114	CHPF	E313K	SHLELSPGEPVQKGDPHFRSALTAH
9	115	TNS1	Y366F	VGHTQGPLDGLSLFAKVKKKDSLHGS
9	116	ABCA12	L1290I	TYGMAAPWYFPIPSYWKERFGCAE
9	117	ZDBF2	G1986W	QDDRKTKKKVKIWTVEFPASCTKVL
10	118	ALS2	M689I	KDSYLALVDKNIIGYIASLHELATT
10	119	TRAK2	R795Q	HSPPSPLPFEPQVHLSNFLASRP
10	120	SPATS2L	T27N	SGTLLWIPRAYSNRSKMAELNTHVN
10	121	WDR75	R228C	DCIASGHMDGKICLWRNFYDDKKYT
10	122	DHRS9	D286G	SLFPKTHYAAGKGAKIFWIPLSHMP
10	123	TTC21B	A1012S	GKLEDVPRFFSMSEKRNSRAKLEPG
10	124	GCA	A62P	AGDSVYTYFSAVPGQDGEVDAEELQ
10	125	NBAS	C144S	KPQWRRVAWSYDSTLLAYAESTGTV
10	126	NBAS	V2177F	ESSHHEAEFQHLFLLQAWPPMKSE
10	127	NEB	D3056G	QLGHHIGARNIEGDPKMMWSMHVAK
10	128	NEB	K6202M	VNSELYKETYEMQKGYLAGKVVIG
10	129	PTPN18	G317L	GRVPADQSPAGSLAYEDVAGGAQTG
10	130	POTEF	WD779-780CY	LKYPMEHGIITNCYDMEKIWHHTFYN
11	131	ZNF584	C244F	HQKVHTGIKPFKFSDCGKTFNRKDA
11	132	ZNF587B	R412G	KGNLILHQHGHTGKRPYMCWECKGL
11	133	PTPRH	S44I	PGRNLTVETQTTISISLSWEVPDGL
11	134	POLD1	L546V	EMARVTGVPLSYVLSRGGQVQVVSQ
11	135	NR1H2	Q164L	PLGLGLPLVDLRLAARAPGKARVSS

11	136	CYTH2	A81S	ENELLQNTPEEISRFLYKGEGLNKT
11	137	ZNF114	Y342N	EECGKVIRESSKNTHIRSHTGEKPY
11	138	KCNN4	G50V	GLMVLHAEMLWFGCSWALYLFLVK
11	139	PALMD	A45T	EDKLLKHQHLKKKTLREKWLLDGISS
11	140	PHLDB3	A232S	QEMREQLDVAQRSYEDLEFQQLERE
11	141	C19orf47	G234V	LQYAGVLKKGGRVPAKASPQPALTV
11	142	ACTN4	G68S	FTAWCNSHLRKASTQIENIDEDFRD
11	143	YIF1B	DP19-20EL	KRRIPVSPQGMaelHQLFDdtSSAQs
12	144	SUGP2	E905D	EEDEDEDEDGGEDAPAPGGAGKSEG
12	145	COLGALT1	M233T	RKRDRRGCFVPTVHSTFLIDLKKA
12	146	ANKRD12	T1727I	KVELEENAEDDKIENQIPQRMTRNK
12	147	RBFA	G232V	LWSTKGGKIKGSVAWCGRGRWLS
12	148	ZNF516	R424L	PVNSYQAWQLATLGKVAEPAEYLKY
12	149	PIGN	P579L	MLTAGLTAFAAWLFLTRLWTRAKMT
12	150	CCDC53	V47A	VHTVQFLNRFSTACEETGSHFVTHA
12	151	PIK3C3	R572K	QRESGNRKKKNEKLQALLGDNEKMN
12	152	ROCK1	E524V	VENEVSTLKDQLVDLKKVSQNSQLA
12	153	RNF213	A1254S	EPLSEPKEDQEASELLEPPEEESER
12	154	EIF4A3	D169Y	QHVVAGTPGRVFMIRRRSLRTRAI
12	155	POLR2A	G816V	HRTLPHFIKDDYVPESRGFVENSYL
12	156	TTYH2	Y297C	TEGQISTEVTRYCLYCSQSGSSPFQ
13	157	WIP1I	R212L	KLASASEKGTVILVFSVPDQKLYE
13	158	RABEP1	K427N	GSLQSKALGYNYNAKSAGNLDESDF
13	159	SRCIN1	V151L	MREQVGGWTVDPCLLSSLCSHLHG
13	160	AP2B1	Q59H	VSSLFPDVVNCMHTDNLELKKLVYL
13	161	ZNF830	W365C	DEGELQDLLSQDCRVKGALL
13	162	SSH2	H487Y	ASKQRHNKLRWSYSDSDLSDHHEPI
13	163	SPECC1	E745D	VVANDIKCEAQQLDRLTVKRKLEEE
13	164	ALDH3A2	K447 insertion KV	ANKLRYPPNSQSKVVDWKGKFLKLR
13	165	FAM83G	A767S	LPDPGSPRLAQNSRPMTDGRATEEH
13	166	FANCA	E1293K	LPKAFHVCAAILKCLEKRKISWLAL
13	167	ZNF778	G641V	SSHLVHIRTHTVEKPYICKECGKA
13	168	NUDT7	V111L	LRPHQVEVVCCLLPCLIDTDLTTP
13	169	DST	D24A	WNAKLVGLMCCMAERDKVQKKTFTK
14	170	NUDT7	V111L	LRPHQVEVVCCLLPCLIDVRVS
14	171	AMFR	V440A	RIASWLPSFSVEAMHTTNILGITQA
14	172	TAOK2	R555P	ARRHQAIKEKEAPAAQAEERKFQQH
14	173	ETFA	D236Y	GLKSGENFKLLYYLADQLHAAVGAS
14	174	UBL7	D352Y	PQLQQLRDMGIQYDELSLRLAQATG
14	175	SPG11	303-304 deletion	QHPGHLLCERILDLPQPKGVDDED
14	176	SPG11	A340T	AKFSFQIDRSWKTQLSSLNETIKNS
14	177	MGA	R2543S	QEFLPKKISGDMSGIQYKWKESER
14	178	ZNF770	C16S	LCKLNPSYLKITSGRKSKQITPTYY
14	179	YLPM1	G1480W	EQKEQLQKMKDFWSEPMADHLPQP
14	180	NUMB	S288P	SFRGFPALSQKMPFPKRQLSLRINE
14	181	SLC39A9	A87S	SETHNVIASDKASEKSVVHEHEHSH
14	182	SYNE2	R3216T	CSIKAVTAIEKQTEENSSEASDVET
15	183	DLGAP5	K156N	KAIPSSVRITRSNAKDQMEQTKIDN
15	184	C1orf43	E80D	YRMKALDAIRTSDFPHSEGRHPRS
15	185	SLC22A15	Q517L	GEEALSLQALDPLQCVDKESSLGSE
15	186	AHNKA2	P588N	TEGQIRMPKFKINSLGWSPSKHTKT
15	187	AHNKA2	G844W	KFKMPKFKMPSFWVSAPGKSMEDSV
15	188	DYNC1H1	V1762A	VVLSAQIAWSENAETALSSMGGGGD
15	189	DYNC1H1	R223L	PMITNVAKQCYELGEKPKVTDGDK
15	190	DIAPH3	E507D	ICIDQAKLEEFEDKASELYKKFEKE
15	191	HSPH1	G204E	DEKPRIVFVDMESAFAQVSACAFN
15	192	CRL1	C78F	LSVEEQLSLISGFPNIEAVEGAMH
15	193	TMTC2	Q634R	YEEALSVYKEAIRKMPRQFAPQSLY
15	194	RAB21	Y89C	GQERFHALGPIYCRDSNGAILVYDI
15	195	CDCA3	P175R	WKPNSSKVLGRSRLTILQDDNSPGT
16	196	PIGV	M227I	HSQCQGFSSLTILNPLRQLFKLMA
16	197	TENC1	P1059H	SQMPWLVASPEPHQSSPTPAFPLAA
16	198	FGD4	Q686L	LYMYGAPQDVRALATIPLLGYVVDE
16	199	ETNK1	F202L	QAHGCAPQLYCTLNGLCYEFIQGE
16	200	ZNF268	L195I	TFGKLCLLSTKYISRQKPHKCGTHG
16	201	RILPL1	G219R	DLRHRVTVVEAQRKALIEQKVELEA
16	202	TCP11L2	G477C	GLAVIQQEALCSQYANIVNLNKQ
16	203	CCDC53	V47A	VHTVQFLNRFSTACEEKLADLSLRI
16	204	NUDT7	V111L	LRPHQVEVVCCLLPCLIDRWGSRVY
16	205	WRAP73	V208L	WDTCLEVRILNHLTWKMITEFGHPA

16	206	GAS2L3	C110F	EESGNFPMRKVPFKKDAASGSFFAR
16	207	ANKS1B	K362N	HTISDHYLDNLSNISEEELGKNGSQ
16	208	PCF11	A926S	GLRFEFGHGPGSGAIRFDGPHGQPG
17	209	RSF1	D681N	LKEDSEFTKVMNNLDNAQTSGIEE
17	210	DGAT2	I157M	VKTHNLLTRNYMFGYHPHGIMGLG
17	211	BBS1	A11S	MAAASSSDSDSCGAESNEANSKW
17	212	SF3B2	Q873 frameshift	SDMVAEHAAKQKQKKTSSAPGQPWGQEI
17	213	EIF1AD	E123V	EKHNNRRNRQTQPVLPAEPQLSGEES
17	214	TMEM216	I41T	WYNATYFLELFTFLYKGVLLPYPT
17	215	TMEM109	A191S	VPDPSTRALLLSLLILYALLSRLT
17	216	OSBP	R320T	LEQLAKQHNHLETAFRGATVLPANT
17	217	PTPRJ	G75V	STAESFHKQNGTVTPQVETNTSEDG
17	218	ZNF408	G505V	CGRAFRQRGNLRVHLRLHTGERPYR
17	219	KIF18A	E202Q	HGLTLHQPKSSEQILHLLDNGNKNR
17	220	ARHGAP32	D827N	GASFLDSPGYSKNKPSANKKDAETG
17	221	MUC5B	L1907I	ATPSSTPGTWTIKPTTTATTAS
18	222	DIXDC1	I23F	SPSPIHSAKSESFITQSEEKADFVI
18	223	FDX1	D132H	EDHIYEKLDATHEENDMLDLAYGL
18	224	ADM	H122Q	CRFGTCTVQKLAQQIYQFTDKDKDN
18	225	PFKFB3	V371F	RQENVLVICHQAFRLCLLAYFLDKS
18	226	FAM107B	R43S	QDLHRELLMNQKSGLAPQNKPELQK
18	227	DNTTIP2	A303T	ETKQCNCKDLDEDTNGITDEGKEINE
18	228	LRRC8B	L545F	GFQDLKNLRTLYFKSSLSRIPQVVT
18	229	PKN2	D123Y	DPEDITDCPRTPYTPNNDPRCSTSN
18	230	HS2ST1	E334 frameshift	EQFQFIRAHAVREKRWRPLHPRTKLFL
18	231	NOL9	T343S	DYLECDLQGTEFSPPGCISLLNITE
18	232	INADL	R1506M	RNSSHEEAITALMQTPQKVRLLVYR
18	233	WRAP73	V253L	GSYDGVKVRILNHLTWKMITEFGHPA
18	234	CCDC53	V47A	VHTVQFLNRFSTACEETGSCCITEA
19	235	MFSD5	T549I	VRHDAELRVSPSIEEPIYAPEL
19	236	ASAP3	A244P	AAQSLFPFIEKLPASVHALHQAQED
19	237	HEATR1	M619I	VVINDDTESAEIKIAIYLSKSGIC
19	238	TARBP1	V544L	CYLLQTAMNLLDLEKVSLSDVSTFL
19	239	OBSCN	G4333R	FTQDLKTKEASERATATLQCELSKV
19	240	OBSCN	A2103T	QGTATMEVQLSHTDVGSWTRDGLR
19	241	CCDC42BPA	V1277L	QLVAVISGRNRHLRLFPMSALDGRE
19	242	IARS2	V443F	QNKAVLEEGTDVFKMLQTAKNLLK
19	243	GPATCH2	K416N	QLLRDNRAERGHKNKCSVRTASRQT
19	244	ZBED6	S355I	LSDTLHGEKSTGIQDLTAEDLSDSD
19	245	OTUD3	H146D	AGNDAIVAFARNDQLNVVIHQNLAP
19	246	SWT1	S257Y	QKLVEENVFNIDYNNSTKQOEEREY
19	247	CACNA1E	R1297L	VDHEKNKMEVKGLEWKRHEFHFDNI
19	248	CEP350	R1167L	QHSSGAQSAASSLSTSSKGGKGGK
20	249	CRP	G97V	WSKDIGYSFTVGVSEILFEVPEVTV
20	250	DNAJC16	G93I	SNEEKRSNYDQYIDAGENQGYQKQQ
20	251	ARHGEF2	V500M	KDVLVLLMTDVLMLFQEKDQKYIFP
20	252	ASH1L	E2901K	ATANVSEGEKKTKESSQEPQSTCTP
20	253	UBAP2L	G640V	QLQTTQSVEGATVSAVKSDSPSTSS
20	254	NIN	K1192 frameshift	NPSGTMNPTEQEN
20	255	C1orf43	K62N	ARLLQLETQGNQNPFFHSEGRHPRS
20	256	TPM3	V59L	NLRARVDINCSPLGTFWALINKVSA
20	257	SIRT5	H286Q	PCGTTLPEALACQENETVS
20	258	SLC39A1	H86R	HGLLPGPGDADRGLQGAVRAVTS
20	259	SELENBP1	P188S	IVQTLSLKDGILSLEIRFLHNPDA
20	260	TBX15	P453T	PSNGAFGERQYLTSGMEHSMHMISP
20	261	FKBP3	N158 frameshift	DTNIQTSAKKKKKCQAFKF
20	262	RHOC	G144C	AKMKQEPVRSEECRDMANRISAFGY
20	263	KCNN4	G50V	GLMVLHAEMLWVFGCSTHFG

Supplementary Table 4. Predicted high-affinity peptides from 4112 TMG-9.

Short peptide pool (SPP) ID	Peptide ID	Peptide sequence	Allele	IEDB		NetMHC	
				% Rank	IC50 (nM)	% Rank	Affinity (nM)
1	1	AVAYKQPASNSK	HLA-A*03:01	0.9	129		
1	2	AWSYDSTLL	HLA-C*04:01	0.4	1862		
1	3	CAPQLYCTL	HLA-C*12:03			1.1	611
1	4	DNIFLEILYSTY	HLA-B*18:01	0.8	362		
1	5	DSYLALVDKNIIGY	HLA-A*25:01/B*18:01	0.5/0.8	1202/318		
1	6	DVLMFLQEKDQKY	HLA-A*25:01	0.2	267		
1	7	DVLVLLMTDVLMF	HLA-A*25:01	0.8	2258		
2	8	DVPRFFSMS	HLA-A*25:01			1.7	11595
2	9	EILYSTYPK	HLA-A*03:01			2	1050
2	10	EILYSTYPKL	HLA-A*25:01	1	4079		
2	11	ETAFRGAT	HLA-A*25:01	0.7	4127		
2	12	ETAFRGATV	HLA-A*25:01			0.5	4192
2	13	FADGLSLCL	HLA-C*04:01			0.7	6237
2	14	FADGLSLCLV	HLA-C*12:03	0.4	12		
3	15	FADGLSLCLVDYI	HLA-C*12:03	0.2	8		
3	16	FFSMSEKRNSRAKL	HLA-C*04:01	0.4	2262		
3	17	FLEILYSTY	HLA-A*25:01/C*12:03			0.8 / 0.7	6350 / 330
3	18	GEGTGPLL	HLA-C*04:01	0.7	3951		
3	19	GEGTGPLL	HLA-C*04:01			1.2	7571
3	20	GMMEGEGTGPLL	HLA-C*04:01	0.6	3228		
3	21	ILYSTYPKL	HLA-C*04:01			0.4	4756
4	22	ILYSTYPKLK	HLA-A*03:01	0.15	12		
4	23	KLEDVPRFF	HLA-C*04:01/C*12:03			1.7 / 1.8	8834 / 1516
4	24	LALVDKNIIGYI	HLA-C*12:03	0.8	34		
4	25	LEILYSTYPKL	HLA-C*04:01	0.9	4417		
4	26	LFADGLSLC	HLA-C*04:01			1.1	7466
4	27	LLMTDVLMF	HLA-C*04:01			0.8	6544
4	28	LLMTDVLMFLQEK	HLA-A*03:01	0.7	78		
5	29	LMTDVLMFL	HLA-C*04:01			1.2	7671
5	30	LVDKNIIGY	HLA-A*25:01/C*04:01			1.4 / 1.1	10282 / 7427
5	31	LWDQPSSPQHPR	HLA-C*04:01	0.8	3948		
5	32	LWDQPSSPQHPR	HLA-C*04:01	0.4	2578		
5	33	LYSTYPKL	HLA-C*04:01	0.8	4171		
5	34	LYSTYPKLK	HLA-C*04:01			1.9	9145
5	35	MEGEGTGPL	HLA-B*18:01/C*04:01			0.3 / 0.25	98 / 4161
6	36	MEGEGTGPLL	HLA-C*04:01	0.4	2251		
6	37	MEGEGTGPLLRSQ	HLA-B*18:01	0.8	207		
6	38	MMEGEGTGPLL	HLA-C*04:01	0.5	2899		
6	39	NIFLEILYSTY	HLA-A*25:01	0.3	613		
6	40	NIIGYIASL	HLA-A*25:01/C*12:03			0.03 / 1.5	270 / 1102
6	41	NIIGYIASLHEL	HLA-A*25:01	0.6	1701		
6	42	QWRRVAWSYDSTLL	HLA-C*04:01	0.2	967		
7	43	RATPPTGEP	HLA-C*12:03			1.8	1571
7	44	RATPPTGEPGFPV	HLA-C*12:03	0.7	24		
7	45	RFFSMSEKR	HLA-C*04:01			0.3	4630
7	46	RFFSMSEKRNSRAK	HLA-A*03:01	1	152		
7	47	RVAWSYDSTLLAY	HLA-A*25:01	0.5	1158		
7	48	SEPDVSGKC	HLA-C*04:01			0.8	6443
7	49	SEPDVSGKCIIEVF	HLA-B*44:03/C*04:01	0.8 / 0.4	461 / 2314		
8	50	STYPKLDAREILK	HLA-A*03:01	0.3	40		
8	51	SYDSTLLAY	HLA-B*18:01			1.9	2617
8	52	TAFRGATV	HLA-C*12:03	0.2	5		
8	53	TAFRGATV	HLA-C*04:01			0.8	6513
8	54	VAWSYDSTL	HLA-C*12:03			0.4	144
8	55	VAYKQPASNSK	HLA-A*03:01	0.9	750		
8	56	VLMFLQEK	HLA-A*03:01	0.9	57		
9	57	VWDALFADGLSLCL	HLA-C*04:01	0.4	2384		
9	58	WRRVAWSYDSTLL	HLA-C*04:01	0.4	1789		
9	59	WSYDSTLL	HLA-C*12:03	0.9	36		
9	60	WSYDSTLLA	HLA-C*12:03			1.3	917
9	61	WSYDSTLLAY	HLA-A*25:01/C*12:03	0.5 / 0.9	1535 / 35		
9	62	YLALVDKNIIGY	HLA-A*25:01	0.8	2969		
9	63	YSEPDVSGK	HLA-C*12:03			1.9	1687
10	64	YSEPDVSGKCI	HLA-C*12:03	0.6	25		
10	65	YSEPDVSGKCIIEVF	HLA-C*12:03	0.7	24		
10	66	YSEPDVSGKCIIEVF	HLA-C*12:03	0.7	30		
10	67	YVGGMMEGEGTGPL	HLA-A*25:01	0.6	1753		

Supplementary Table 5. 4171 peptide library

Peptide pool ID	Peptide ID	Gene name	Position and change of mutated amino acid	Mutated amino acid sequence
1	1	KCNH6	R362H	MVAaipfdllfhtgsdettlligl
1	2	CD226	T157M	GKNVTLTCQPOMMWPVQAVRWEKIQ
1	3	BRCA1	N1384S	LCLPQSIYRSELSVYAFGEHILQIS
1	4	ZNF335	L26H	LAGCPAPYPAAKHFPSLFHAPQEEV
1	5	TP53	R209Q	YMCNSSCMGGMNQRPILTITLEDSE
1	6	MKNK1	G4C	MILCHCSLDLLGSSNP
1	7	ZHX3	R720C	SLEMPSSHILAECKVSPKINLKNL
1	8	POLD1	P815L	EAADWVSGHFPSLRIRLEFEKVYFPY
1	9	KRAS	G12D	MTEYKLVVVGADGVGKSALTIQLI
1	10	PIK3CA	R93W	EFFDETRRLCDLWLFQPFKVIIEPV
1	11	LCE1F	R87H	CCLSHHRRRRSHHHRPQSSDCCSQP
1	12	CTAG2	A60T	AGAARASGPRGGTTPRGPHGGAASAQ
1	13	PDLIM3	A158V	PIGLYSTSNIQDVLHGQLRGLIPSS
1	14	ZNF181	I111N	FHSKSTLSEPPQKNSAEGNSHKYDIL
2	15	TEX13B	R88H	VRFAHRQQQLQNHVRVQWLOGFAKLH
2	16	UGT3A1	R377W	VRVVAKNYGVSIWLNQVTDADTLTLT
2	17	PIK3CA	Q546E	ISTRDPLSEITEEEKDFLWSHRHYC
2	18	TMEM232	L76F	KEELLEARKIIFRCKRKLGLKTLG
2	19	TATDN3	L8F	MRAAGVGFVDCHCHLSAPDF
2	20	CHST11	T88M	VLHQMRDQVTDMCANSATSRKRR
2	21	SYNE1	R471W	LSLSLAQPLRSEWSGRDTPASVDSI
2	22	NME5	M5V	MEISVPPPQIYVEKTLA
2	23	SLAIN1	S292T	SFLQPPKPLSSLTFLRDGNWRDGCY
2	24	SCN5A	R1644H	RILRLIRGAKGIHTLLFALMMSLPA
2	25	PLCD3	R173C	QRWVRGLTKLRACLDAMSQRERLDH
2	26	VCAN	I663T	TEIELFPYSGDKTLVEGISTVYIPS
2	27	NOTCH3	H2227R	PGHGEEYPVAGARSSPPKARFLRVP
2	28	TRIM43	L73S	KMDFKTNILLKNSVTIARKASLWQF
3	29	LRP2	I4371V	FIESTTECDAAVELPINLPPPCRC
3	30	APOB	L1238F	VGSKLIVAMSSWFQKASGSLPYTQT
3	31	NHSL1	R436W	VIAIPTAQSAQWESKSSGSSHARI
3	32	LOR	C103W	SGGGSSGGSGWFSGGGGSGCFS
3	33	SIN3A	N520I	LGKFPPELFNWFKIFLGYKESVHLET
3	34	CPAMD8	R1270H	LTAFVLKSFQAQHSFIVDPRELAA
3	35	APC2	G322D	SGCLPLLQLHDETAAGGRAGAP
3	36	ATP8B3	T1104M	VNFFMTLWISRDMAGPASFSDHQSF
3	37	AMY2A	R267Q	EPIKSSDYFGNGQVTEFKYGAKLGT
3	38	CROT	G565A	FTDPLFSKSGGGANFVLSLTVGYL
3	39	KIF5C	R859C	VHKQLVRDNADLCCLEPKLEKRLRA
3	40	GFRA2	F138V	RTDHLCSRSLADVHANCRASYQTVT
3	41	ARHGAP15	T53I	SKSMILTDVGKVIPIISRHRNRHSQ
3	42	APBB1IP	P270T	LEKEEKYAVFKNTQNFYLDNRGKKE
4	43	UBR7	P39 frameshift	NSKFKNLECKLLLTQR
4	44	UBR7	P115 frameshift	NSKFKNLECKLLLFQMR
4	45	DLGAP4	D944N	KSKPAVSRDKASNASDKQRQEARKR
4	46	GRID2IP	T349M	VVSMLQSGGAMPMLVVEGLVPFAS
4	47	AP4E1	A284T	SPKINKYLGLKTLTYVIQQDPTLA
4	48	ZNF707	R167Q	QRCGRRPGRRRRQKQRAVELSFICG
4	49	SVEP1	G1021R	NLEHFTCESCRIRSYQDEEGQLECK
4	50	ZDBF2	R12H	MQRQGYCSYCHVQYNNLEQHLFS
4	51	VWDE	I68F	DHSLSPGWYRFLFLDRPAEMPTKCV
4	52	PPAPDC2	S21R	EGRPLGVSASSRSPPGSPAHHGGGG
4	53	FAM71A	S519F	KSGRSLWTTSSGFSKGLGRVSSFLR
4	54	TRPC4	L227I	DPFLTAFQLSWEIQELSKVENEFKS
4	55	SERTAD4	G64E	GAGPPLAGSHYREISNPITTSKITIY
4	56	FANCM	A1052 frameshift	SGASCSSSRPHLLGHILLDLRRKE
5	57	FANCM	A1052 frameshift	HLLGHILLDLRRKEKEPVFL
5	58	UNC79	S516T	VQEQALLWLHVLTELDIMVPLQLLI
5	59	SIGLEC8	R68W	WTSDSPVHGYWFWAGDRPYQDAPVA
5	60	GALNT10	R30C	YEISFKVVMCGGCMEDIPCSRVGHI
5	61	GALNT10	R200C	FLLAMQVVMCGGCMEDIPCSRVGHI
5	62	OR2B3	F310L	KEAFKRLMPRIFLCKK
5	63	PTPLA	D142G	PPRPINFCIFGRGRVSPCWPGWSRT
5	64	PRMT3	I380S	SDLEFSSDFTLKSTRTSMCTAIAGY
5	65	MYT1	A359T	SCSSSPGVKSPDTSQRHSSTAPSS
5	66	NADSYN1	I109M	SGGVDSAAATCLMYSMCCQVCEAVR
5	67	ATR	N811I	ETDVKAVLGTLLILMEDPKDVRVA

5	68	OR13C8	R122C	TECMILGTMALDCYVAICYPLRYPV
5	69	MAOA	R96W	RKFVGGSGQVSEWIMDLLGDQVKLN
5	70	LILRB4	R188W	RSPMDTFLLIKAWAAHPLLHLRSEH
6	71	OR5B17	A103P	SYSACAAQMFFFCVPVFATVENYLLSS
6	72	KCNS2	R418Q	ITLIFNKFSHFYQRQKQLESAMRSC
6	73	ZFAND4	S539R	NLQHFQEENFRKRSPQLEHTGVFLS
6	74	TMEM132B	A80T	KKGRGCSLQYQHTTVRVLTQFVAES
6	75	NBEAL2	P386L	YPHLQEVLSQSHGLPTHRLLQELNLM
6	76	SLCO6A1	L376F	GLVLIPGGALGQFLGGVIVSTLEMS
6	77	GTF3C1	R777S	KKSDNKMGITPLSNYHPIVVPGLGR
6	78	MAGIX	N102K	HRPQVGDVLVHLIKGESTQGLTHAQA
6	79	MAGIX	N178K	GRLEVGDVLVHLIKGESTQGLTHAQA
6	80	STAT5B	H588N	GVMEVLKHKHLKPNWWDGAILGFVVK
6	81	SPAG17	R225Q	VKKEDTIVPPNLQSRSWETFPVSVEK
6	82	DNAH5	L3563V	KARKIPFGKNLNVSEMLIDAPTISE
6	83	PCDHB2	K74Q	AVRGARVVSXGKQMKMLQFDRQTGDL
6	84	ATP2B2	V194M	LQSRIEQEQKFTMVRAGQVQIPVA
7	85	FBXO11	L87V	LPDEVVLKIFSYVLEQDLCRAACVC
7	86	NUP107	E681D	KFLASKKHEAAKDVFKIPQDSIAE
7	87	BPIFB3	E23D	LLLLWGLATPCQDLETVGTLARID
7	88	PCDHB12	L327R	YSIIIQATDGGGRFGKSTVRIQVMD
7	89	GUCY2F	G434R	YTVDMEMELLRFRGTPHFPGGRPP
7	90	KRT73	K137T	IQKVRAQEREQITVLNKFKASFIDK
7	91	GNAS	R314Q	PLMPRREEKYPLQGTDPPLPGQPQR
7	92	KMT2D	R5500W	FDKEDKIISSWRIPKGEELTYDY
7	93	DCHS2	II155F	DRRLRSLTAQIVFLDVNDHNPTFIS
7	94	ARMC8	W355C	QQLRTSFQDHAVCKPLMKVLQNPAD
7	95	CCDC151	E73A	GAGKPSVHSQVAALHKKIQLEGEDR
7	96	CCDC151	E73A	GAGKPSVHSQVAALHKKIQLLESHS
7	97	OR52N5	F268L	AIITVYPAFFTLFAHRFGGHTIPP
7	98	MICALL2	K439N	LGPDPAFGLGLGNLLSLQGACGQQ
8	99	PLG	N428K	YPNAGLTMNYCRKPDADKGPWCFTT
8	100	C1orf101	I224M	LSDDERRSVAHVMLSRDGVIVFLNG
8	101	DDX21	K2N	HISGATSVDQRSVINSNVGFVTMIL
8	102	PASD1	L561V	MNMRGEKRRDKVNP
8	103	PCDHGA4	L798R	EKSEPLLITQDLRETKGDPNLQVSO
8	104	PCDHGA4	L798R	EKSEPLLITQDLRETKGDPNLQVAP
8	105	ATF7	E345D	KLWVSSLEKKAEDLTSQNIQLSNEV
8	106	SMAD6	S133I	RTRSKIGFGLLIIKEPDGVWAYNRG
8	107	CYFIP1	L253P	MKRLESKYAPLHPVPLIERLGTPOQ
8	108	MED15	Q241P	QQQQQQQALQAPPIQPPMQPQQPQ
8	109	ZKSCAN4	G146S	EDIAQIPTHAEASEQEGRLQRKQKN
8	110	TERF1	Q275H	VVESKRTRTITSHDKPSGNDVEMET
8	111	CYFIP1	K606R	LESLIADKSGSKRTLRSLEGPTIL
8	112	CD40	A17T	PLQCVLWGCLLTTVHPEPPTACREK
8	113	SLC11A1	R206C	SALVKSREIDRACRADIREANMYFL
9	114	PRR34	T53P	RARCPQSAHPAPPRGALTFWAPGSW
9	115	ZNF729	F416Y	YKCEECGKAFSQYSTLKKHKIIHTG
9	116	NRCAM	G612R	HLVVADVSDDDSRITYTCVANITLDS
9	117	KIAA0020	K4N	MEVNGKKQFTGKSTKT
9	118	CILP2	E504G	EPLRFARILLGQGPIGFTAYQGDFT
9	119	ATM	W579C	NRSFSLKESIMKCLLFYQLEGDLEN
9	120	WNK2	H758P	POPVVLPQVPPPLPPYLAPASQVG
9	121	DLGAP2	S848T	QNMDPSAMPRTTQDLAGYWDMLQL
9	122	TCF3	A162S	YPSYSGSSRRRASDGLDTPQPKVR
9	123	OPRM1	S83R	NASNCTDALAYSRCSPAPSPGSVWN
9	124	LEFTY1	F78I	QRSHGDRSRGKRISQSFREVAGRFL
9	125	THSD7B	S993Y	CSSSCGIVRIRYKWLKEKPYNGGR
9	126	CCDC88A	S583C	ERENRKLKKTLDLCKNLTFQLESLE
9	127	KRTAP10-12	G232V	SCQPCSGRLASCVSLLCRPTCSRLA
9	128	SYK	E26K	PPFFGNITREEAKDYLVQGGMSDGL