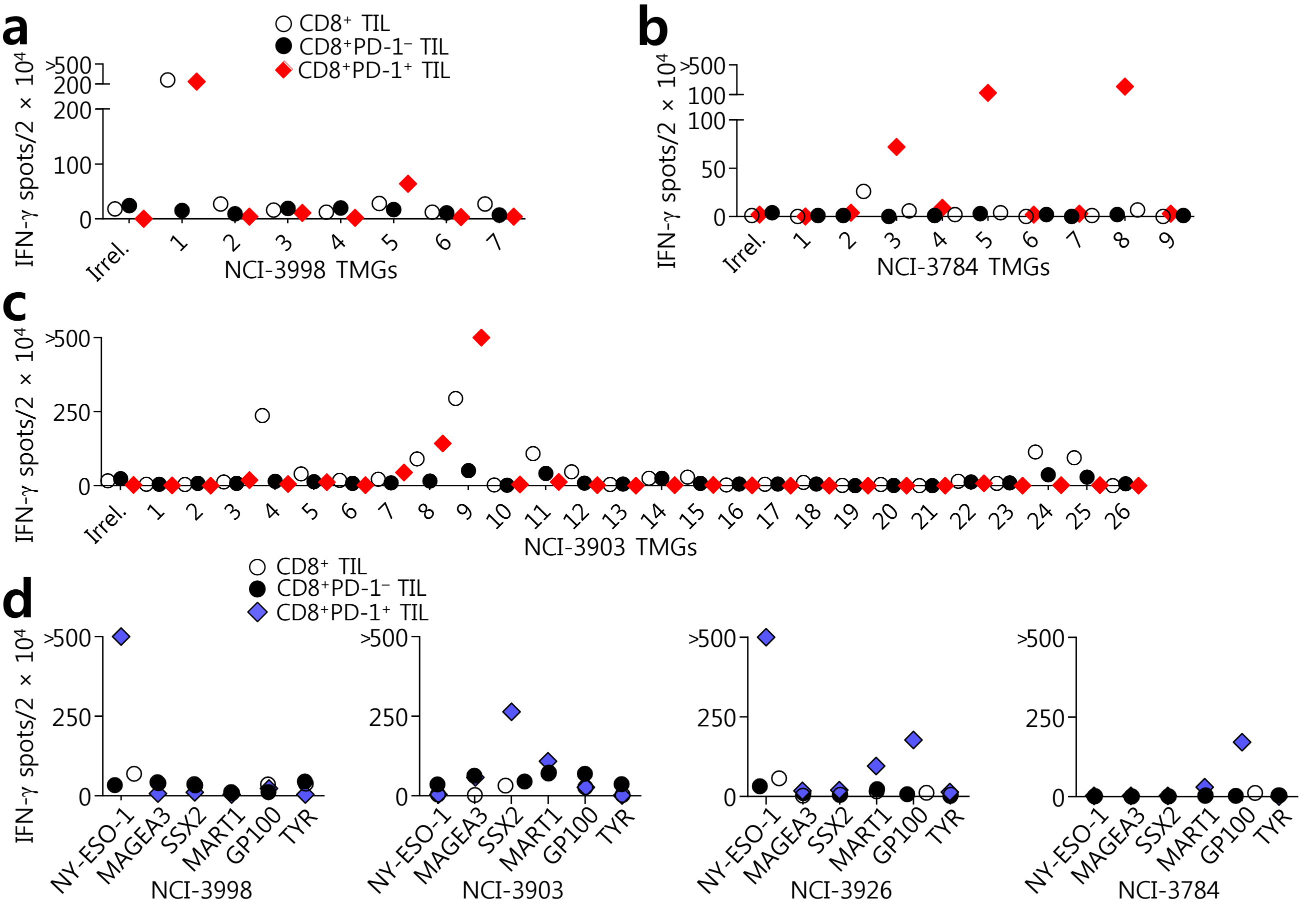
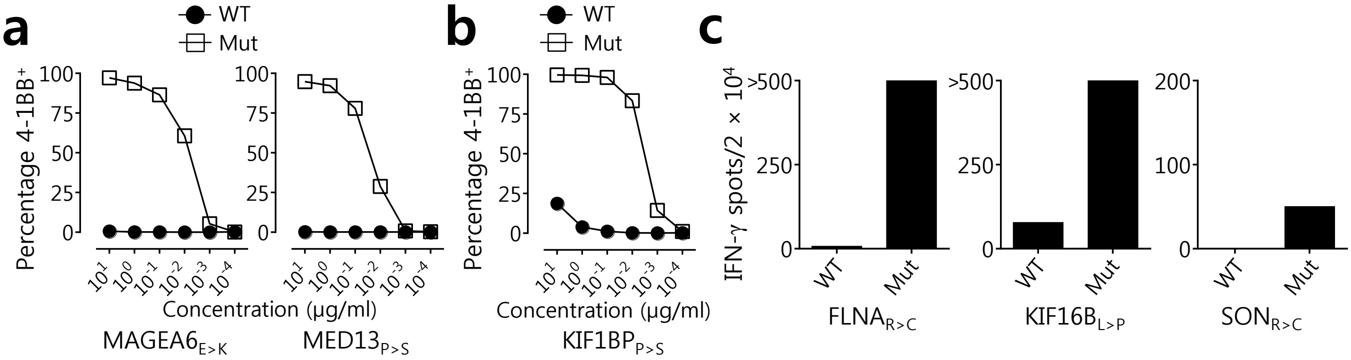
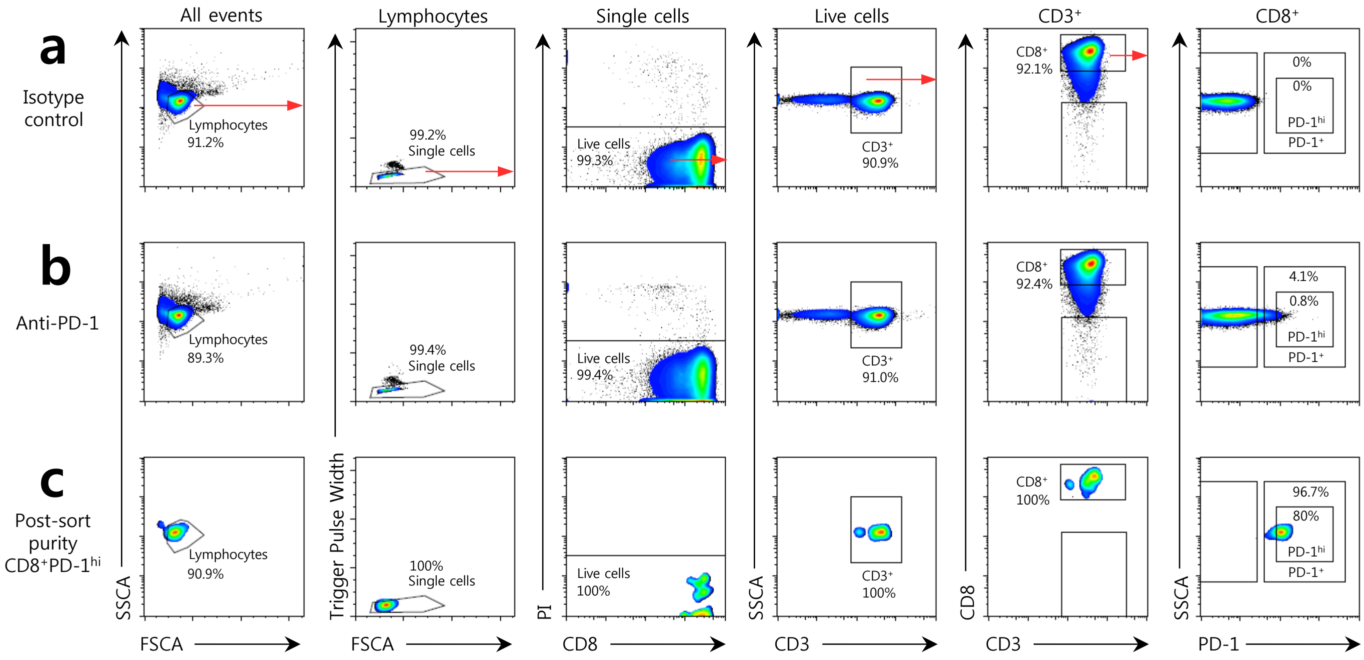


Supplementary Figure 4 Immunological screening of tumor-derived lymphocytes for recognition of mutated neoantigens and shared tumor antigens. (**a–d**) NCI-3998, 3784 and 3903 CD8$^+$ lymphocytes were separated from fresh tumor single cell suspensions based on PD-1 expression, and expanded *in vitro*. Tumor-infiltrating lymphocyte (TIL) subsets from NCI-3998 (**a**), NCI-3784 (**b**), and NCI-3903 (**c**) were cocultured with autologous dendritic cells (DCs) transfected with an irrelevant TMG (Irrel.) or the indicated TMG constructs. IFN-γ spots/2 × 10^4 cells is shown. (**d**) TIL subsets from subjects (indicated below each graph) were cocultured with autologous DCs transfected with full-length RNA encoding for NY-ESO-1, MAGEA3, MART1, GP100, and TYR. IFN-γ spots/2 × 10^4 cells at 20 h is shown. ">" denotes greater than 500 spots /2 × 10^4 cells. Data are representative of at least two independent experiments.



Supplementary Figure 5 Recognition of neoantigens by enriched populations of TMG-reactive cells isolated from the tumor-derived CD8$^+$PD-1$^+$ subsets from subjects NCI-3998, 3903, and 3784. (**a**) NCI-3998 TMG1- (left) and TMG5-reactive TIL (right) were cocultured with DCs pulsed with WT and Mut MAGEA6$_{E>K}$ or MED13P>S minimal epitopes. TMG9-reactive TIL isolated from the tumor of NCI-3903 were cocultured with DCs pulsed with WT or Mut KIF1BP$_{P>S}$ minimal epitopes (**b**), and NCI-3784 TMG3- (left), TMG5- (middle) and TMG8-reactive TIL (right) were cocultured with autologous DCs pulsed with the WT or Mut 25-mers indicated (**c**). Percentage of 4-1BB expression or IFN-γ spots/2 × 10^4 cells at 20 h is shown. ">" denotes greater than 500 spots per 2 × 10^4 cells. All data are representative of at least two independent experiments.



Supplementary Figure 6 Example of the gating strategy used for sorting circulating CD8$^+$ lymphocytes based on PD-1 expression. Flow cytometry analysis of one representative melanoma patient is shown. CD8$^+$ cells were positively selected from a pre-treatment leukapheresis product using CD8 microbeads, and then stained with fluorochrome-labeled anti-CD3, CD8, and either isotype control (IgG4-AF647) or anti-PD-1 (AMP-514 AF647) antibody. Dot plots of the CD8-enriched cells stained with isotype control (**a**), and anti-PD-1 (**b**) are displayed. The hierarchy of the gating strategy is depicted from left to right. The gate used to sort for CD8$^+$PD-1$^+$ cells was set based on the isotype control. (**c**) The post-sort purity for the CD8$^+$PD-1^{hi} sorted cells is shown.

Supplementary Table 1. Patient characteristics

Patient ID	Cancer type	Prior therapy	Months from end of last therapy to leukapheresis (mo)	%PD-1$^+$ (of CD8$^+$) PBMC	# putative mutations[d]	Mutations evaluated[e]
NCI-3713	Mel[a]	IL-2, anti-CTLA-4	7 mo	4.1%	4359	7 minimal epitopes
NCI-3998	Mel	No treatment	-	1.9%	279	115 (TMG#1-7)
NCI-3784	Mel	Surgery, IFN	14 mo	2.1%	440	140 (TMG1-9)
NCI-3903	Mel	Surgery, MART-F5 TCR[b]	55 mo	3.4%	414	308 (TMG#1-26)
NCI-3926	Mel	IL-2, surgery, chemo.[c]	8 mo	7.4%	346	128 (TMG#1-11)
NCI-3759*	Mel	Surgery, IFN	1 mo	1.0%	n.d.[f]	n.e.[g]
NCI-3992*	Mel	Anti-PD-1, anti-CTLA-4	5 mo	8%	n.d.	n.e.

[a] Melanoma; [b] Adoptive transfer of autologous T cells that were gene-engineered to express a MART1 HLA-A*0201-restricted T cell receptor (TCR). [c] Chemotherapy NCI- 3926: dacarbazine and vinblastine. [d] Putative non-synonymous mutations were defined by: >2 exome variant reads, ≥ 10% variant frequency in the exome, ≥10 normal reads, and tumor/normal variant frequency ≥5. Common single nucleotide polymorphisms were filtered. [e] Mutations screened were selected based on whole-exome and transcriptome analysis. [f] Not deteremined. [g] Not evaluated.*NCI-3759 and 3992 were only included in Fig.4i

Supplementary Table 2. Mutated tandem minigenes (TMGs) screened for subjects NCI-3998, 3784, 3903, and 3926

Patient ID	TMG#	Mutation type	Gene	Transcript ID	WT AA	Mut AA	AA position	Wild-type 25-mer	Mutated 25-mer
NCI-3998	**TMG1**	SNV	AMER1	uc022byb.1	P	L	686	SQISHRGITSAFPTTASSEPDWRDF	SQISHRGITSAFLTTASSEPDWRDF
		SNV	LOC100133957	uc011mlt.1	A	V	141	RACEQGPSGNKPANGGLQKRRLEPM	RACEQGPSGNKPVNGGLQKRRLEPM
		SNV	CXorf22	uc004ddj.3	M	I	865	SNELVLRPRGFFMKTCFRGTVRLYN	SNELVLRPRGFFIKTCFRGTVRLYN
		SNV	MAGEA6	uc022chf.1	E	K	168	DSLQLVFGIELMEVDPIGHVYIFAT	DSLQLVFGIELMKVDPIGHVYIFAT
		SNV	GPR112	uc010nsb.1	P	S	2870	EISFPNDDFDKDPYCSSP	EISFPNDDFDKDSYCSSP
		SNV	RBMXL3	uc011mte.1	D	N	577	GGCSADAYSGGHDSSSQSNRYGGGG	GGCSADAYSGGHNSSSQSNRYGGGG
		SNV	CHRDL1	uc011mss.2	R	Q	226	TKQECKKIHCPNRYPCKYPQKIDGK	TKQECKKIHCPNQYPCKYPQKIDGK
		SNV	CDKN2B	uc022beo.1	E	K	3	MREENKGMPSGGGSDEGLASAAARG	MRKENKGMPSGGGSD
		SNV	CDKN2B	uc022beo.1	G	R	17	NKGMPSGGGSDEGLASAAARGLVEK	NKGMPSGGGSDERLASAAARGLVEK
		SNV	UBAC1	uc004cgt.3	E	K	276	SATDEEARDELTEIFKKIRRKREFR	SATDEEARDELTKIFKKIRRKREFR
		SNV	GOLGA2	uc011maw.2	A	V	785	ASAQKEPEAAAPAPGTGGDSVCGET	ASAQKEPEAAAPVPGTGGDSVCGET
		SNV	PAPPA	uc004bjn.3	R	Q	151	GLYDKCSYISRDRGWVVGIHTISDQ	GLYDKCSYISRDQGWVVGIHTISDQ
		SNV	OR13C5	uc011lvp.2	H	Y	176	VQLPFCRNNIINHFTCEILAVMKLA	VQLPFCRNNIINYFTCEILAVMKLA
		SNV	PSD3	uc003wza.3	H	Y	796	AVYKSGFLARKIHADMDGKKTPRGK	AVYKSGFLARKIYADMDGKKTPRGK
		SNV	CSMD3	uc011lhx.2	E	K	1460	FQCDPGYELQGEERITCIQVENRYF	FQCDPGYELQGEKRITCIQVENRYF
		SNV	PVRIG	uc003uuf.1	I	V	114	PARQARWETQSSISLILEGSGASSP	PARQARWETQSSVSLILEGSGASSP
NCI-3998	**TMG2**	SNV	CYP3A43	uc003urz.1	E	K	144	LLSPAFTSVKFKEMVPIISQCGDML	LLSPAFTSVKFKKMVPIISQCGDML
		SNV	ENSG00000021461	ENST00000433277	E	K	93	LLSPAFTSVKFKEVRK	LLSPAFTSVKFKKVRK
		SNV	SAMD9L	uc022ahh.1	R	Q	1188	ETENWSPQKSQRRYDMYNTACFLGE	ETENWSPQKSQRQYDMYNTACFLGE

		SNV	NPC1L1	uc011kbw.2	P	L	459	LQERLRHLQVWSPEAQRNISLQDIC	LQERLRHLQVWSLEAQRNISLQDIC
		SNV	FAM20C	uc003sip.3	P	L	224	FLSPGEAAVDSYPNWLKFHIGINRY	FLSPGEAAVDSYLNWLKFHIGINRY
		SNV	TCRBV22S1A2N1T	uc022amx.2	E	K	39	QKVEFLVSFYNNEISEKSEIFDDQF	QKVEFLVSFYNNKISEKSEIFDDQF
		SNV	BRAF	uc003vwc.4	V	E	600	LTVKIGDFGLATVKSRWSGSHQFEQ	LTVKIGDFGLATEKSRWSGSHQFEQ
		SNV	PRRT4	uc022aky.1	P	S	706	CRGFEGAAANPAPSPASSPCSDYTV	CRGFEGAAANPASSPASSPCSDYTV
		SNV	POP7	uc022ais.1	V	A	108	LQVAANTSTVELVDELEPETDTREP	LQVAANTSTVELADELEPETDTREP
		SNV	PRIM2	uc003pdx.3	R	W	79	TEQYQSKLESELRKLKFSYRENLED	TEQYQSKLESELWKLKFSYRENLED
		SNV	TCTE1	uc003oxi.2	D	N	115	EHQQKVLNHLSPDLPLAVTANLIDS	EHQQKVLNHLSPNLPLAVTANLIDS
		SNV	SERAC1	uc031sqr.1	I	M	34	KSGTHWRDIRNIIKFTGSLILGGSL	KSGTHWRDIRNIMKFTGSLILGGSL
		SNV	AK9	uc003ptr.4	P	L	381	EEALKPFLLNPRPYLLPPMPGPPCK	EEALKPFLLNPRLYLLPPMPGPPCK
		SNV	CDH18	uc003jgd.3	M	I	569	SRTVQDVYYLPIMISDGGIPSLSSS	SRTVQDVYYLPIIISDGGIPSLSSS
		SNV	ZFP62	uc021yjo.1	L	F	794	CECGKSFNYRSVLDQHKRIHTGKKP	CECGKSFNYRSVFDQHKRIHTGKKP
NCI-3998	**TMG3**	SNV	SH3PXD2B	uc003mbr.3	N	S	278	KEGWAPASYLKKNSGEPLPPKPGPG	KEGWAPASYLKKSSGEPLPPKPGPG
		SNV	PPM1K	uc003hrm.5	A	V	181	KAFSSHARLSADATLLTSGTTATVA	KAFSSHARLSADVTLLTSGTTATVA
		SNV	PDS5A	uc003guv.4	Y	F	1000	MATEKLLSLLPEYVVPYMIHLLAHDPDFTRSQ	MATEKLLSLLPEFVVPYMIYLLAHDPDFTRSQ
		SNV			H	Y	1007		
		SNV	FAT1	uc003izf.3	S	L	2713	PKFSEPFYTFTVSEDVPIGTEIDLI	PKFSEPFYTFTVLEDVPIGTEIDLI
		SNV	TENM3	uc003ive.1	G	E	538	HVLDVQNGILYKGNGENQFISQQPP	HVLDVQNGILYKENGENQFISQQPP
		SNV	CNOT10	uc011axj.2	S	L	511	SIQNTVYNDGQSSAIPVASMEFAAI	SIQNTVYNDGQSLAIPVASMEFAAI
		SNV	DLG1	uc011bue.2	S	L	481	LSGELRKGDRIISVNSVDLRAASHE	LSGELRKGDRIILVNSVDLRAASHE
		SNV	ZBTB21	uc021wjo.1	L	F	682	YICTYCGKAYRFLSQFKQHIKMHPG	YICTYCGKAYRFFSQFKQHIKMHPG

		SNV	TSHZ2	uc021wex.1	E	K	468	ELKKESKKERPEETSKDEKVVKSED	ELKKESKKERPEKTSKDEKVVKSED
		SNV	ADNP	uc002xvu.1	S	F	1032	QGDREQLKWKNSSYGKVEGFWSKDQ	QGDREQLKWKNSFYGKVEGFWSKDQ
		SNV	CST9	uc002wtl.3	G	S	20	KAMPWALSLLLMGFQLLVTYAWCSE	KAMPWALSLLLMSFQLLVTYAWCSE
		SNV	PCBP1-AS1	uc002sga.3	L	F	9	MVSVDGGFLWTLDINQLLFDSSAEP	MVSVDGGFFWTLDINQLLFDS
		SNV	SRBD1	uc010yoc.2	P	L	54	RNLRQLLLTSPVPGRTLMGVDPGYK	RNLRQLLLTSPVLGRTLMGVDPGYK
		SNV	CAD	uc010eyw.3	S	F	1947	TSSVQKGESLADSVQTMSCYADVVV	TSSVQKGESLADFVQTMSCYADVVV
		SNV	ENSG00000168918	ENST00000455936	E	K	375	YADLLSHDQLLTERREQKVFLHFEE	YADLLSHDQLLTKRREQKVFLHFEE
NCI-3998	**TMG4**	SNV	ZDBF2	uc031rqy.1	P	S	301	RMGTKGSLRVKSPSKLAVNPNKTDM	RMGTKGSLRVKSSSKLAVNPNKTDM
		SNV	TTN	uc031rqd.1	D	N	16446	TDIKAESCYLTWDAPLDNGGSEITH	TDIKAESCYLTWNAPLDNGGSEITH
		SNV	ZNF586	uc010euh.3	T	I	186	YTSSLIKHRRIHTGERPYECSECGR	YTSSLIKHRRIHIGERPYECSECGR
		SNV	NLRP2	uc021vbq.1	G	E	139	FKTEAQAFTETKGNVICLGKEVFKG	FKTEAQAFTETKENVICLGKEVFKG
		SNV	NLRP2	uc010eso.3	G	E	136	LERFKTEAQETKGNVICLGKEVFKG	LERFKTEAQETKENVICLGKEVFKG
		SNV	NLRP2	uc010esn.3	G	E	115	RKPLSLAFTETKGNVICLGKEVFKG	RKPLSLAFTETKENVICLGKEVFKG
		SNV	ENSG00000022556	ENST00000588619	G	E	139	FKTEAQAFTETKGN	FKTEAQAFTETKEN
		SNV	FAM90A27P	uc031rmv.1	E	K	7	MQEAWKEPAEDCLFLRHPTMPLPVH	MQEAWKKPAEDCLFLRHPT
		SNV	C19orf73	uc002pmq.4	G	E	10	MRLKVGFQGGGCFRKDALCLEGGVS	MRLKVGFQGEGCFRKDALCLEG
		SNV	RELB	uc021uvq.1	L	F	153	RYECEGRSAGSILGESSTEASKTLP	RYECEGRSAGSIFGESSTEASKTLP
		FS insertion	HNRNPL	uc021uui.1			291	VKFMKSKPGAAMVEMADGYAVDRAI	VKFMKSKPGAAMVGDG
		SNV	RYR1	uc002oiu.3	H	Y	821	PCHEAVLPRERLHLEPIKEYRREGP	PCHEAVLPRERLYLEPIKEYRREGP
		SNV	NFIC	uc010xhj.2	R	W	122	DQKGKMRRIDCLRQADKVWRLDLVM	DQKGKMRRIDCLWQADKVWRLDLVM
		SNV	LRP3	uc010edh.3	S	F	756	PLGVCRNPPPPCSPMLEASDDEALL	PLGVCRNPPPPCFPMLEASDDEALL

		SNV	CSNK1G2	uc010dsu.3	P	S	328	LNSTNGELNADDPTAGHSNAPITAP	LNSTNGELNADDSTAGHSNAPITAP
NCI-3998	**TMG5**	SNV	ARRDC2	uc002nhv.3	P	L	202	IDRKGYTPGEVIPVFAEIDNGSTRP	IDRKGYTPGEVILVFAEIDNGSTRP
		SNV	CTDP1	uc021ult.1	G	R	660	PGPEVRIYDSNTGKLIRTGARGPPA	PGPEVRIYDSNTRKLIRTGARGPPA
		SNV	SERPINB3	uc002lji.3	E	K	250	GKDLSMIVLLPNEIDGLQKLEEKLT	GKDLSMIVLLPNKIDGLQKLEEKLT
		SNV	HEXDC	uc002kew.3	A	V	63	YEGPLRLLRAKYAYSPSEIKEILHL	YEGPLRLLRAKYVYSPSEIKEILHL
		SNV	ENSG00000169660	ENST00000578775	A	V	24	YEGPLRLLRAKYAYRLECSGAILAH	YEGPLRLLRAKYVYRLECSGAILAH
		SNV	EVPL	uc010wst.1	E	K	59	QSLGTEKETAQKECEAFLSTRPVGP	QSLGTEKETAQKKCEAFLSTRPVGP
		SNV	MED13	uc002izo.3	P	S	1691	PHIKSTVSVQIIPCQYLLQPVKHED	PHIKSTVSVQIISCQYLLQPVKHED
		SNV	HEATR6	uc010ddk.1	P	S	265	GEVICKCMGEADPSIQLHGAKLLEE	GEVICKCMGEADSSIQLHGAKLLEE
		SNV	ABCC3	uc002isl.3	E	K	209	FSAKNVDPNPYPETSAGFLSRLFFW	FSAKNVDPNPYPKTSAGFLSRLFFW
		SNV	PLEKHM1	uc010wjn.1	R	C	530	EEHTCVENCSLLRCESVGPAHSDGR	EEHTCVENCSLLCCESVGPAHSDGR
		SNV	SLFN14	uc010ctu.1	R	C	827	IAILCRRGEDRGRYRLALLKAMELI	IAILCRRGEDRGCYRLALLKAMELI
		SNV	TVP23B	uc002gum.2	S	F	148	VLWVIFAFSALFSFRVKWLAVVIMG	VLWVIFAFSALFFFRVKWLAVVIMG
		SNV	KCNG4	uc010voc.2	R	W	257	DLRAEEDQGECSRKCYYIFIVETIC	DLRAEEDQGECSWKCYYIFIVETIC
		SNV	ADAMTS18	uc002ffc.4	P	S	265	FCGRRKKYAPKPPTEDTYLRFDEYG	FCGRRKKYAPKPSTEDTYLRFDEYG
		SNV	ENSG00000140873	ENST00000449265	S	F	266	CGRRKKCICSQASHRGHLSKV	CGRRKKCICSQAFHRGHLSKV
NCI-3998	**TMG6**	SNV	TIGD7	uc021tcc.1	R	Q	130	DFKASTGWLFRFRNRHAIGNRKGCG	DFKASTGWLFRFQNRHAIGNRKGCG
		SNV	CIITA	uc010bup.1	G	E	225	SSSSLSCLNLPEGPIQFVPTISTLP	SSSSLSCLNLPEEPIQFVPTISTLP
		SNV	EFTUD1	uc002bgu.1	E	D	427	QDGSAIETCPKGEEPRGDEQQVESM	QDGSAIETCPKGDEPRGDEQQVESM
		SNV	FAH	uc010unl.2	R	Q	159	RLLFLSAACYQRRNHVQGQGECVDA	RLLFLSAACYQRQNHVQGQGECVDA
		SNV	FAH	uc002bfn.2	G	R	68	DFYSSRQHATNVGIMFRDKENALMP	DFYSSRQHATNVRIMFRDKENALMP

		SNV	NOP10	uc001zie.1	T	I	47	FSPDDKYSRHRITIKKRFKVLMTQQ	FSPDDKYSRHRIIIKKRFKVLMTQQ
		SNV	ENSG00000182117	ENST00000557912	P	S	28	TLKMTNTLDTESPSRNASRCS	TLKMTNTLDTESSSRNASRCS
		SNV	STON2	uc010tvu.3	P	S	724	GFSANRDPLTQVPCENVMIRYPVPS	GFSANRDPLTQVSCENVMIRYPVPS
		SNV	SLC8A3	uc001xlz.3	R	C	889	RRPHLGGELGGPRGCKLATTWLFVS	RRPHLGGELGGPCGCKLATTWLFVS
		SNV	OR4K1	uc001vwj.2	A	V	150	RRLCVIFVSISWAVGVLHSVSHLAF	RRLCVIFVSISWVVGVLHSVSHLAF
		SNV	AHNAK2	uc010axc.1	M	V	2187	SVDVSPPKVEADMSLPSMQGDLKTT	SVDVSPPKVEADVSLPSMQGDLKTT
		SNV	HTR2A	uc010acr.4	P	S	405	RYIQCQYKENKKPLQLILVNTIPAL	RYIQCQYKENKKSLQLILVNTIPAL
		SNV	NBEA	uc021rid.1	P	L	2468	REDEVVVNDVDLPPWAKKPEDFVRI	REDEVVVNDVDLLPWAKKPEDFVRI
		SNV	KMT2D	uc001rta.4	S	F	654	SPMSPPPEVSRLSPLPVVSRLSPPP	SPMSPPPEVSRLFPLPVVSRLSPPP
		SNV	LRRK2	uc009zjw.3	P	L	689	LLVNPDQPRLTIPISQIAPDLILAD	LLVNPDQPRLTILISQIAPDLILAD
		SNV	EP400	uc010tbo.2	P	S	61	RKGGKISFCAHTPLNCMFGFFCFVK	RKGGKISFCAHTSLNCMFGFFCFVK
		SNV	HECTD4	uc021reb.1	P	S	2876	ISESKVNMDVNFPGAAFVVVSCKES	ISESKVNMDVNFSGAAFVVVSCKES
NCI-3998	**TMG7**	FS insertion	SWAP70	uc001mhw.3			99	KIEFNRMCWTLCVKKNLTKNPLLIT	KIEFNRMCWTLCVKKKPHKESPAHYRRRCI
		FS insertion	ENSG00000133789	ENST00000526358			117	RLNSIGCVGPSVSKKTSQRIPCSLQ	RLNSIGCVGPSVSKKNLTKNPLLITEEDAFKIWVIFNFLSEDKYPLA
		SNV	ZFP91	uc001nmy.4	T	I	233	EEIPFKDDPRDETYKPHLERETPKP	EEIPFKDDPRDEIYKPHLERETPKP
		SNV	PRDM11	uc031qab.1	R	W	216	SERIYFRACRDIRPGEWLRVWYSED	SERIYFRACRDIWPGEWLRVWYSED
		SNV	MOB2	uc001ltp.1	S	F	176	LLWGWGLLSQRPSFPLTPPLPASPG	LLWGWGLLSQRPFFPLTPPLPASPG
		SNV	LGI1	uc021pwk.1	E	I	84	LSFVRSGFTEISEGSFLFTPSLQLL	LSFVRSGFTEISIGSFLFTPSLQLL
		SNV	MYOF	uc001kio.3	E	D	1477	LKIYNCELENVAEFEGLTDFSDTFK	LKIYNCELENVADFEGLTDFSDTFK
		SNV	POLR3A	uc001jzn.3	G	A	1066	HFAGVASMNITLGVPRIKEIINASK	HFAGVASMNITLAVPRIKEIINASK
		SNV	C10orf120	uc001lgn.3	H	Y	334	IWKERMRKATPYHY	IWKERMRKATPYYY

		SNV	ACSL5	uc009xxz.3	S	F	148	GIFAQNRPEWIISELACYTYSMVAV	GIFAQNRPEWIIFELACYTYSMVAV
		SNV	PRKAA2	uc031pms.1	M	I	239	FYLASSPPSGSFMDDSAMHIPPGLK	FYLASSPPSGSFIDDSAMHIPPGLK
		SNV	ZBTB41	uc001gtx.1	P	L	425	NETEFHKKEHKCPYCNKLHASKKTL	NETEFHKKEHKCLYCNKLHASKKTL
		SNV	KCNT2	uc009wyu.3	G	E	129	FETILLGYLSYKGNIWEQILRIPFI	FETILLGYLSYKENIWEQILRIPFI
		SNV	INSRR	uc010pht.2	D	N	669	CHRGLRLPTSNNDPRFDGEDGDPEA	CHRGLRLPTSNNNPRFDGEDGDPEA
		SNV	PDE4DIP	uc021ouh.1	R	Q	2291	LLELRTKVSKQERLLQSTTEHLKNA	LLELRTKVSKQEQLLQSTTEHLKNA
		SNV	AP4B1	uc010owp.2	P	S	548	WLSLKVAHQQVLPWRGEFHPDTLQM	WLSLKVAHQQVLSWRGEFHPDTLQM

Patient ID	TMG#	Mutation type	Gene	Transcript ID	WT AA	Mut AA	AA position	Wild-type 25-mer	Mutated 25-mer
NCI-3784	**TMG1**	SNV	ABHD16A	NM_021160	P	S	322	WNHPGFAGSTGVPFPQNEANAMDVV	WNHPGFAGSTGVSFPQNEANAMDVV
		SNV	ALMS1	NM_015120	P	F	892	HLTEEALKVSIVPGPGDQKTGIPSA	HLTEEALKVSIVFGPGDQKTGIPSA
		SNV	ANKHD1-EIF4EBP3	NM_020690	P	S	1555	RKNKKNKTKETPPTAHLILPEQHMS	RKNKKNKTKETPSTAHLILPEQHMS
		SNV	ATP8B1	NM_005603	R	K	946	RLLLVHGRWSYIRMCKFLRYFFYKN	RLLLVHGRWSYIKMCKFLRYFFYKN
		SNV	ATR	NM_001184	L	F	1405	AYGLLMELTRAYLAYADNSRAQDSA	AYGLLMELTRAYFAYADNSRAQDSA
		SNV	ATXN7	NM_000333	P	L	780	VNVRHDQSGRGPPTGSPAESIKRMS	VNVRHDQSGRGPLTGSPAESIKRMS
		SNV	B4GALT5	NM_004776	S	F	326	VSRPEGDTGKYKSIPHHHRGEVQFL	VSRPEGDTGKYKFIPHHHRGEVQFL
		SNV	BLM	NM_000057	A	V	1351	MPASQRSKRRKTASSGSKAKGGSAT	MPASQRSKRRKTVSSGSKAKGGSAT
		SNV	BRAF	NM_004333	V	E	600	LTVKIGDFGLATVKSRWSGSHQFEQ	LTVKIGDFGLATEKSRWSGSHQFEQ
		SNV	BRAT1	NM_152743	T	I	418	APASSVGGHLCGTLAGCVRVQRAAL	APASSVGGHLCGILAGCVRVQRAAL
		SNV	BRD9	NM_023924	S	F	554	GGSRPSSNLSSLSNASERDQHHLGS	GGSRPSSNLSSLFNASERDQHHLGS
		SNV	BRF1	NM_001519	T	I	109	GNQLQLNQHCLDTAFNFFKMAVSRH	GNQLQLNQHCLDIAFNFFKMAVSRH
		SNV	C11orf30	NM_020193	P	L	992	IHLQADQLQHKLPQMPQLSIRHQKL	IHLQADQLQHKLLQMPQLSIRHQKL
		SNV	C2CD3	NM_015531	S	L	486	SKKISQSTALARSSKVLESSDHKLK	SKKISQSTALARLSKVLESSDHKLK
		SNV	CAMKK2	NM_172226	P	L	124	GGSLDMNGRCICPSLPYSPVSSPQS	GGSLDMNGRCICLSLPYSPVSSPQS
		SNV	CD164	NM_006016	L	P	50	PISNVTSAPVTSLPLVTTPAPETCE	PISNVTSAPVTSPPLVTTPAPETCE
NCI-3784	**TMG2**	SNV	CDCA3	NM_031299	P	S	145	EEQMPPWNQTEFPSKQVFSKEEARQ	EEQMPPWNQTEFSSKQVFSKEEARQ

		SNV	CDK13	NM_031267	R	W	757	FPITAIREIKILRQLTHQSIINMKE	FPITAIREIKILWQLTHQSIINMKE
		SNV	CHPF	NM_024536	R	C	629	DTVLTPDFLNRCRMHAISGWQAFFP	DTVLTPDFLNRCCMHAISGWQAFFP
		SNV	CLEC4F	NM_173535	P	S	19	RFCTDNQCVSLHPQEVDSVAMAPAA	RFCTDNQCVSLHSQEVDSVAMAPAA
		SNV	COL5A2	NM_000393	G	E	1110	GQRGDPGSRGPIGPPGRAGKRGLPG	GQRGDPGSRGPIEPPGRAGKRGLPG
		SNV	COL7A1	NM_000094	G	E	1412	GDKGDRGERGPPGPGEGGIAPGEPG	GDKGDRGERGPPEPGEGGIAPGEPG
		FS deletion	CTSC	NM_148170			42	CTYLDLLGTWVFQVGSSGSQRDVNC	CTYLDLLGTWVFRWAPAVPSAMSTARLWDHKKKK
		SNV	CTTN	NM_005231	S	F	261	GWDHQEKLQLHESQKDYKTGFGGKF	GWDHQEKLQLHEFQKDYKTGFGGKF
		SNV	CTTN	NM_138565	S	F	261	GWDHQEKLQLHESQKDYSKGFGGKY	GWDHQEKLQLHEFQKDYSKGFGGKY
		SNV	DBF4	uc011khf.1	P	L	16	KELVVVHKKQEKPCSPFDVDKPSSM	KELVVVHKKQEKLCSPFDVDKPSSM
		SNV	DBF4	NM_006716	P	L	249	TNMPFINYSIQKPCSPFDVDKPSSM	TNMPFINYSIQKLCSPFDVDKPSSM
		SNV	DCLRE1A	NM_001271816	P	H	1009	YLEMKRFVQWLKPQKIIPTVNVGTW	YLEMKRFVQWLKHQKIIPTVNVGTW
		SNV	DDX42	NM_007372	P	L	565	VATDVAARGLDIPSIKTVINYDVAR	VATDVAARGLDILSIKTVINYDVAR
		SNV	DHX16	NM_003587	P	S	573	STFFDDAPVFRIPGRRFPVDIFYTK	STFFDDAPVFRISGRRFPVDIFYTK
		SNV	DOLPP1	NM_020438	S	F	111	MPSSHSQFMWFFSVYSFLFLYLRMH	MPSSHSQFMWFFFVYSFLFLYLRMH
		SNV	DTNA	NM_032979	T	I	87	ELNVSRLEAVLSTIFYQLNKRMPTT	ELNVSRLEAVLSIIFYQLNKRMPTT
NCI-3784	**TMG3**	SNV	DTNB	NM_183361	L	F	110	STHQISVEQSISLLLNFMIAAYDSE	STHQISVEQSISFLLNFMIAAYDSE
		SNV	ENSG00000006634	ENST00000413643	P	S	229	KPFVKVEDMSQSPAVHLM	KPFVKVEDMSQSSAVHLM
		SNV	ENSG00000089902	ENST00000560472	T	M	35	SGNMAEIFRQSQT	SGNMAEIFRQSQM
		SNV	ENSG00000099995	ENST00000411423	S	F	32	KQPLVRRSVRRRSRSQRKR	KQPLVRRSVRRRFRSQRKR
		SNV	ENSG00000163738	ENST00000433372	P	L	3	MDPRVSGILVQLPLPDHVDERTICN	MDLRVSGILVQLPLP
		SNV	ENSG00000164124	ENST00000511532	P	L	160	EIPNNTCSMDTTPLITEHGLQSCSD	EIPNNTCSMDTTLLITEHGLQSCSD
		SNV	ENSG00000164124	ENST00000514558	P	L	160	EIPNNTCSMDTTPLITEHVSIV	EIPNNTCSMDTTLLITEHVSIV
		SNV	ENSG00000187098	ENST00000478490	P	L	103	KFEEQNRAESECPDG	KFEEQNRAESECLDG
		SNV	EPHA2	NM_004431	V	M	643	MLKTSSGKKEVPVAIKTLKAGYTEK	MLKTSSGKKEVPMAIKTLKAGYTEK
		SNV	ESPL1	NM_012291	A	V	1380	VCPTESKPEVPQAPRVQQRVQTRLK	VCPTESKPEVPQVPRVQQRVQTRLK
		SNV	EXOC3	NM_007277	A	V	49	ARKKASVEARLKAAIQSQLDGVRTG	ARKKASVEARLKVAIQSQLDGVRTG

		SNV	EXOC4	NM_021807	R	Q	423	EPSAQLSYASTGREFAAFFAKKKPQ	EPSAQLSYASTGQEFAAFFAKKKPQ
		SNV	FKTN	NM_001198963	G	E	359	GKVEDSLELSFQGKDDVKLDVFFFY	GKVEDSLELSFQEKDDVKLDVFFFY
		SNV	FLNA	NM_001110556	R	C	2049	VVISQSEIGDASRVRVSGQGLHEGH	VVISQSEIGDASCVRVSGQGLHEGH
		SNV	FLNC	NM_001458	P	S	2595	IVGSPFKAKVTGPRLSGGHSLHETS	IVGSPFKAKVTGSRLSGGHSLHETS
		SNV	FREM1	NM_144966	G	E	1200	TQKPRHGLLIDRGFSKDFSENKQPA	TQKPRHGLLIDREFSKDFSENKQPA
NCI-3784	**TMG4**	SNV	FSCN1	NM_003088	T	A	484	GDHAGVLKASAETVDPASLWEY	GDHAGVLKASAEAVDPASLWEY
		SNV	GAA	NM_001079803	S	F	144	SYPSYKLENLSSSEMGYTATLTRTT	SYPSYKLENLSSFEMGYTATLTRTT
		SNV	GNB5	uc031qrz.1	P	S	84	DMKTALALYEFPPMGLLSALDHGII	DMKTALALYEFPSMGLLSALDHGII
		SNV	GNB5	NM_016194	P	L	377	GHENRVSTLRVSPDGTAFCSGSWDH	GHENRVSTLRVSLDGTAFCSGSWDH
		SNV	GPATCH8	NM_001002909	S	F	865	RSRSGRRHSSHRSSRRSYSSSSDAS	RSRSGRRHSSHRFSRRSYSSSSDAS
		SNV	GPR98	NM_032119	R	Q	6009	YVLVMNDEHTERRYLLFFLLSWGLP	YVLVMNDEHTERQYLLFFLLSWGLP
		SNV	GPRIN1	NM_052899	P	L	887	PMTPQAAAPPAFPEVRVRPGSALAA	PMTPQAAAPPAFLEVRVRPGSALAA
		SNV	GSE1	NM_014615	R	Q	718	LKPGSPYRPPVPRAPDPAYIYDEFL	LKPGSPYRPPVPQAPDPAYIYDEFL
		SNV	HIF3A	NM_152795	E	K	17	LQRARSTTELRKEKSRDAARSRRSQ	LQRARSTTELRKKKSRDAARSRRSQ
		SNV	HIF3A	NM_152794	E	K	15	WQDHRSTTELRKEKSRDAARSRRSQ	WQDHRSTTELRKKKSRDAARSRRSQ
		SNV	IFIT5	NM_012420	G	E	98	SDKEEVRSLVTWGNYAWVYYHMDQL	SDKEEVRSLVTWENYAWVYYHMDQL
		SNV	IFT140	NM_014714	R	K	1141	CSDFFIEHSQYERAVELLLAARKYQ	CSDFFIEHSQYEKAVELLLAARKYQ
		SNV	IK	uc003lgq.3	P	L	555	KKMEADGVEVKRPKY	KKMEADGVEVKRLKY
		SNV	INF2	NM_032714	T	I	196	ELSGSDNVPYVVTLLSVINAVILGP	ELSGSDNVPYVVILLSVINAVILGP
		SNV	IRF2BP1	NM_015649	S	F	7	MASVQASRRQWCYLCDLPKMPWAMV	MASVQAFRRQWCYLCDLPK
		SNV	ITCH	NM_001257137	V	I	831	IDNEKRMRLLQFVTGTCRLPVGGFA	IDNEKRMRLLQFITGTCRLPVGGFA
NCI-3784	**TMG5**	SNV	ITPR3	NM_002224	H	N	290	SSNALWEVEVVHHDPCRGGAGHWNG	SSNALWEVEVVHNDPCRGGAGHWNG
		SNV	KAZN	NM_015209	T	I	409	QRKSLDPGLFDGTAPDYYIEEDADW	QRKSLDPGLFDGIAPDYYIEEDADW
		SNV	KDM7A	NM_030647	D	N	758	YSTCLQRQIQSTDCSGERNSLQDPS	YSTCLQRQIQSTNCSGERNSLQDPS
		SNV	KIF16B	NM_024704	L	P	1009	REKQQREALERALARLERRHSALQR	REKQQREALERAPARLERRHSALQR
		SNV	KRT10	NM_000421	S	Y	547	SGGGGGGYGGGSSGGGSSSGGGYGG	SGGGGGGYGGGSYGGGSSSGGGYGG
		SNV	LPHN2	NM_012302	R	Q	803	TQGCKLVDTNKTRTTCACSHLTNFA	TQGCKLVDTNKTQTTCACSHLTNFA
		SNV	LTBP4	uc002ooj.1	P	L	281	DDFEALCNVLRPPAYSPPRPGGFGL	DDFEALCNVLRPLAYSPPRPGGFGL

		SNV	MBNL2	NM_207304	G	S	119	GTPLHPVPTFPVGPAIGTNTAISFA	GTPLHPVPTFPVSPAIGTNTAISFA
		SNV	MED4	NM_014166	R	W	173	VCAPLTWVPGDPRRPYPTDLEMRSG	VCAPLTWVPGDPWRPYPTDLEMRSG
		SNV	MFI2	NM_033316	R	K	190	ETSYSESLCRLCRGDSSGEGVCDKS	ETSYSESLCRLCKGDSSGEGVCDKS
		SNV	MITF	NM_198177	P	L	194	KFEEQNRAESECPGMNTHSRASCMQ	KFEEQNRAESECLGMNTHSRASCMQ
		SNV	MOSPD3	NM_001040098	P	L	141	KDITSILRAPAYPLELQGQPDPAPR	KDITSILRAPAYLLELQGQPDPAPR
		SNV	MTHFD2L	NM_001144978	P	L	138	ELLDVTDQLNMDPRVSGILVQLPLP	ELLDVTDQLNMDLRVSGILVQLPLP
		SNV	MYH9	NM_002473	R	Q	1576	AMKAQFERDLQGRDEQSEEKKKQLV	AMKAQFERDLQGQDEQSEEKKKQLV
		SNV	NBPF9	uc010oye.3	M	I	217	VSAGPLSSEKAEMNILEINEKLHPQ	VSAGPLSSEKAEINILEINEKLHPQ
		SNV	NCLN	NM_020170	A	V	202	GVQSKAVSDWLIASVEGRLTGLGGE	GVQSKAVSDWLIVSVEGRLTGLGGE
NCI-3784	**TMG6**	SNV	NCOA2	NM_006540	S	F	593	DSKDCFGLYGEPSEGTTGQAESSCH	DSKDCFGLYGEPFEGTTGQAESSCH
		SNV	NELL1	NM_201551	E	K	433	GYISVQGDSAYCEDIDECAAKMHYC	GYISVQGDSAYCKDIDECAAKMHYC
		SNV	NFKB1	NM_003998	S	F	618	GADLSLLDRLGNSVLHLAAKEGHDK	GADLSLLDRLGNFVLHLAAKEGHDK
		SNV	NOL6	NM_139235	Q	L	380	TMSGYQVLRSVLQFLATTDLTVNGI	TMSGYQVLRSVLLFLATTDLTVNGI
		SNV	NOL6	uc010mjv.3	Q	L	380	TMSGYQVLRSVLQFLDLTVNGISLC	TMSGYQVLRSVLLFLDLTVNGISLC
		SNV	NOL8	NM_001256394	R	C	291	KLHSLIGLGIKNRVSCHDSDDDIMR	KLHSLIGLGIKNCVSCHDSDDDIMR
		SNV	NPIPB5	NM_001135865	P	L	388	PLPPSADDNLKTPSERQLTPLPPSA	PLPPSADDNLKTLSERQLTPLPPSA
		SNV	NQO2	NM_000904	P	S	103	KVREADLVIFQFPLYWFSVPAILKG	KVREADLVIFQFSLYWFSVPAILKG
		SNV	PABPC5	NM_080832	P	L	183	NNRQVYVGRFKFPEERAAEVRTRDR	NNRQVYVGRFKFLEERAAEVRTRDR
		SNV	PAM	NM_001177306	G	D	861	KMQEKQKLIKEPGSGVPVVLITTLL	KMQEKQKLIKEPDSGVPVVLITTLL
		SNV	PARP10	NM_032789	P	L	1015	TCEHVPRASPDDPSGLPGRSPDT	TCEHVPRASPDDLSGLPGRSPDT
		SNV	PCDH18	NM_019035	D	N	886	GRGDSEAGDSDYDLGRDSPIDRLLG	GRGDSEAGDSDYNLGRDSPIDRLLG
		SNV	PCSK7	NM_004716	P	L	14	PKGRQKVPHLDAPLGLPTCLWLELA	PKGRQKVPHLDALLGLPTCLWLELA
		SNV	PHIP	NM_017934	P	L	166	KLNGKYRLERLVPTAVYQHMKMHKR	KLNGKYRLERLVLTAVYQHMKMHKR
		SNV	PHOSPHO2-KLHL23	NM_001199290	S	F	268	IYNALNPMHKEISQRSTATMYIIGG	IYNALNPMHKEIFQRSTATMYIIGG
		SNV	PI4K2A	NM_018425	L	F	162	VFKPKNEEPYGHLNPKWTKWLQKLC	VFKPKNEEPYGHFNPKWTKWLQKLC
NCI-3784	**TMG7**	SNV	PRR14L	NM_173566	P	S	2020	KKVSQIRIRKTIPRPDPNLTPMGLP	KKVSQIRIRKTISRPDPNLTPMGLP
		SNV	PRRC2A	NM_080686	P	S	1098	ETRSEGSEYEEIPKRRRQRGSETGS	ETRSEGSEYEEISKRRRQRGSETGS

		SNV	PTPN11	NM_080601	H	Y	426	TVWQYHFRTWPDHGVPSDPGGVLDF	TVWQYHFRTWPDYGVPSDPGGVLDF
		SNV	RALGDS	uc004ccv.1	H	Y	629	AALQPAGGRLLYHPRQPGRGQWQHV	AALQPAGGRLLYYPRQPGRGQWQHV
		SNV	RAP1GDS1	NM_021159	E	K	571	ICALMGSECLHKEVQDLAFLDVVSK	ICALMGSECLHKKVQDLAFLDVVSK
		SNV	RNF145	NM_144726	P	S	256	ALGMSLWNQLVVPVLFMVFWLVLFA	ALGMSLWNQLVVSVLFMVFWLVLFA
		NFS deletion	RPL11	NM_001199802			97	GLKVREYELRKNNFSDTGNFGFGIQ	GLKVREYELRKNNSDTGNFGFGIQE
		SNV	RRBP1	uc021waw.1	Q	P	436	GAQNQGKKAEGAQNQGKKAEGAQNQ	GAQNQGKKAEGAPNQGKKAEGAQNQ
		SNV	SCRIB	NM_182706	S	F	1561	TPVEDLGPQTSTSPGRLPLSGKKFD	TPVEDLGPQTSTFPGRLPLSGKKFD
		SNV	SCRIB	NM_015356	S	F	1561	TPVEDLGPQTSTSPGRLSPDFAEEL	TPVEDLGPQTSTFPGRLSPDFAEEL
		SNV	SEC31A	NM_016211	E	K	435	QQHHVFISQVVTEKEFLSRSDQLQQ	QQHHVFISQVVTKKEFLSRSDQLQQ
		SNV	SENP5	NM_152699	L	F	503	ASPVDDEQLSVCLSGFLDEVMKKYG	ASPVDDEQLSVCFSGFLDEVMKKYG
		SNV	SERINC2	uc009vtw.1	L	F	143	GLVLLRRRGLLPLHPHPAGAAHRLC	GLVLLRRRGLLPFHPHPAGAAHRLC
		SNV	SETD2	NM_014159	C	Y	1501	KSHRDIKRMQCECTPLSKDERAQGE	KSHRDIKRMQCEYTPLSKDERAQGE
		SNV	SH3TC2	NM_024577	H	Y	243	LVSALEPLPLPFHQWFLKNYPGSCG	LVSALEPLPLPFYQWFLKNYPGSCG
		SNV	SLC30A5	NM_022902	L	P	594	GGGMNANMRGVFLHVLADTLGSIGV	GGGMNANMRGVFPHVLADTLGSIGV
NCI-3784	**TMG8**	SNV	SLIT2	NM_004787	G	E	715	QDVAIQDFTCDDGNDDNSCSPLSRC	QDVAIQDFTCDDENDDNSCSPLSRC
		SNV	SNW1	NM_012245	F	L	499	GREGPVQFEEDPFGLDKFLEEAKQH	GREGPVQFEEDPLGLDKFLEEAKQH
		SNV	SON	NM_138927	R	C	1927	RKTVRARSRTPSRRSRSHTPSRRRR	RKTVRARSRTPSCRSRSHTPSRRRR
		SNV	SPATA20	NM_022827	P	S	285	EEYGGFAEAPKFPTPVILSFLFSYW	EEYGGFAEAPKFSTPVILSFLFSYW
		SNV	ST6GALNAC3	NM_152996	P	L	252	DTYCKTEGYRKVPYHYYEQGRDECD	DTYCKTEGYRKVLYHYYEQGRDECD
		SNV	ST6GALNAC3	uc010orh.1	P	L	151	TGKDRTEGYRKVPYHYYEQGRDECD	TGKDRTEGYRKVLYHYYEQGRDECD
		SNV	STS	NM_000351	E	K	532	EPRFYEILKVMQEAADRHTQTLPEV	EPRFYEILKVMQKAADRHTQTLPEV
		SNV	SZT2	NM_015284	S	L	1576	LTLPLEVELPTASDPQHHRSTSESS	LTLPLEVELPTALDPQHHRSTSESS
		SNV	TAF8	NM_138572	P	L	277	AEKENTSVLQQNPSLSGSRNGEENI	AEKENTSVLQQNLSLSGSRNGEENI
		SNV	TAF8	uc003oru.1	P	S	318	PRRRTPLSCSRTPPCRVAGMGRRTS	PRRRTPLSCSRTSPCRVAGMGRRTS
		SNV	TBL1XR1	NM_024665	P	L	305	WDAHTGEAKQQFPFHSAPALDVDWQ	WDAHTGEAKQQFLFHSAPALDVDWQ
		SNV	TMEM144	NM_018342	P	L	160	EIPNNTCSMDTTPLITEHVINTTQD	EIPNNTCSMDTTLLITEHVINTTQD
		SNV	TRIM24	NM_015905	P	L	750	VIVKQESDEESRPQNANYPRSILTS	VIVKQESDEESRLQNANYPRSILTS
		SNV	TRIM35	NM_171982	D	N	115	LHRGQLSLFCLEDKELLCCSCQADP	LHRGQLSLFCLENKELLCCSCQADP
		SNV	TRIM51	NM_032681	H	Y	346	QAFTSGKYYWEVHM	QAFTSGKYYWEVYMGDS

								GDSWNWAFGVC	WNWAFGVC
		SNV	TTLL5	NM_015072	Y	F	279	LTNYSVNKKSGDYVSCDDPEVEDYG	LTNYSVNKKSGDFVSCDDPEVEDYG
NCI-3784	**TMG9**	SNV	WDFY3	NM_014991	S	T	3352	LDEKDGFIFVNYSEGQTRAHLQGPL	LDEKDGFIFVNYTEGQTRAHLQGPL
		SNV	WDR20	NM_001242417	P	S	459	NSVTTPGNSVPPPLPRSNSLPHSAV	NSVTTPGNSVPPSLPRSNSLPHSAV
		SNV	ZBTB4	NM_020899	R	Q	691	AGGASVGGSGLPRGRRPPRWRQKLE	AGGASVGGSGLPQGRRPPRWRQKLE
		SNV	ZBTB9	NM_152735	R	W	409	KRDRHIMLTFSLRPFGCGICNKRFK	KRDRHIMLTFSLWPFGCGICNKRFK
		SNV	ZC3H13	NM_015070	P	S	1102	PGSTPSPLSSLLPPPPPVATATATT	PGSTPSPLSSLLSPPPPVATATATT
		SNV	ZFAT	NM_001029939	E	K	1214	GGEASEFIVYVQEAMQPVEEQAVEQ	GGEASEFIVYVQKAMQPVEEQAVEQ
		SNV	ZNF25	NM_145011	P	S	215	ECNQCEKSFYQKPHLTEHQKTHTGE	ECNQCEKSFYQKSHLTEHQKTHTGE
		SNV	ZNF32	NM_006973	S	F	85	RQRVYECQECGKSFRQKGSLTLHER	RQRVYECQECGKFFRQKGSLTLHER
		SNV	ZNF346	NM_012279	H	Y	108	KHANKVKRYLAIHGMETLKGETKKL	KHANKVKRYLAIYGMETLKGETKKL
		SNV	ZNF703	NM_025069	S	F	182	SGSSSVSSTSSSSSSSPGDKAGFRV	SGSSSVSSTSSSFSSSPGDKAGFRV
		SNV	ZNF714	uc002npl.3	K	E	382	RSGVQDQPGQHGKTPSLLKIQKFAG	RSGVQDQPGQHGETPSLLKIQKFAG
		SNV	ZNF761	NM_001008401	T	I	342	ECGKTFRQKSILTRHHRLHTGEKPY	ECGKTFRQKSILIRHHRLHTGEKPY

Patient ID	**TMG#**	**Mutation type**	**Gene**	**Transcript ID**	**WT AA**	**Mut AA**	**AA position**	**Wild-type 25-mer**	**Mutated 25-mer**
NCI-3903	**TMG1**	SNV	ANKDD1B	NM_001276713	L	P	221	AAERGHVEMIEKLTFLNLHTSEKDK	AAERGHVEMIEKPTFLNLHTSEKDK
		SNV	C12orf28	uc010stn.1	P	L	71	LQVPEITFCEILPCQETYCCPIRGM	LQVPEITFCEILLCQETYCCPIRGM
		SNV	C3orf56	NM_001007534	E	K	171	WTPASSAPRAAVEGPSRGAPYLKTC	WTPASSAPRAAVKGPSRGAPYLKTC
		SNV	MRDS1	uc003myh.1	G	A	125	NLLEEDDELHSQGDSLTDHSVKGKS	NLLEEDDELHSQADSLTDHSVKGKS
		SNV	MUC3A	uc003uxl.1	S	F	18	MTLRITENTPISSFSTSIVVIPETP	MTLRITENTPISFFSTSIVVIPETP
		SNV	ZNF487	ENST00000431662	R	Q	8	LIRHQRIHTGEKPYTCHECGDSFSH	MASRPRPQTPSRGPSDLRFR
		SNV	ZNF891	NM_001277291	P	S	108	RFSNRSHLLQHRLVHTGERPYRCLQ	DQEEIRNMKKRISQAICPDQKIQPK
		SNV	CALU	uc003vns.3	W	S	96	KDGFVTVDELKDWIKFAQKRWIYED	KDGFVTVDELKDSIKFAQKRWIYED
		SNV	RPL5	NM_000969	E	K	70	RDIICQIAYARIEGDMIVCAAYAHE	RDIICQIAYARIKGDMIVCAAYAHE
		SNV	EIF3A	NM_003750	R	Q	794	RLAEERHNRLEERKRQRKEERRITY	RLAEERHNRLEEQKRQRKEERRITY
		SNV	LAMA1	NM_005559	E	K	78	CRICDGNSANPRERHPISHAIDGTN	CRICDGNSANPRKRHPISHAIDGTN

		SNV	GADD45GIP1	NM_052850	R	C	23	LLGVAATLAPGSRGYRARPPPRRRP	LLGVAATLAPGSCGYRARPPPRRRP
NCI-3903	**TMG2**	SNV	C19orf2	NM_001252641	R	K	386	GSGHSAQELPTIRTPADIYRAFVDV	GSGHSAQELPTIKTPADIYRAFVDV
		SNV	RUVBL1	NM_003707	G	E	421	LLTPANLLAKINGKDSIEKEHVEEI	LLTPANLLAKINEKDSIEKEHVEEI
		SNV	RND3	NM_001254738	A	D	44	SQCGKTALLHVFAKDCFPENYVPTV	SQCGKTALLHVFDKDCFPENYVPTV
		SNV	MATN2	uc003yid.3	E	K	421	NKPGCEHECVNMEESYYCRCHRGYT	NKPGCEHECVNMKESYYCRCHRGYT
		SNV	EPB41L2	NM_001135554	R	C	516	PKAKFLTLGSKFRYSGRTQAQTRQA	PKAKFLTLGSKFCYSGRTQAQTRQA
		SNV	DIP2B	NM_173602	D	N	401	LGTKNEPVLKPGDRVALVYPNNDPV	LGTKNEPVLKPGNRVALVYPNNDPV
		SNV	CMTM6	NM_017801	E	K	162	LDFITMLYEKRQESQLRKPENTTRA	LDFITMLYEKRQKSQLRKPENTTRA
		SNV	RNF10	NM_014868	D	N	747	ENSLVPPAPVDSDGESDNSDRVPVP	ENSLVPPAPVDSNGESDNSDRVPVP
		SNV	SSFA2	NM_001287504	R	Q	288	QPVSRASSVSKQSSCESITDEFSRF	SNKETDPPPPLTQSNTANRLMKTLS
		SNV	MARK3	NM_001128921	S	R	443	AYPKRSQTSTADSDLKEDGISSRKS	AYPKRSQTSTADRDLKEDGISSRKS
		SNV	PSMF1	NM_006814	P	L	224	PLRSGFPRALIDPSSGLPNRLPPGA	PLRSGFPRALIDLSSGLPNRLPPGA
		SNV	C12orf49	NM_024738	R	C	70	PWKVQFNLGNSSRPSNQCRNSIQGK	PWKVQFNLGNSSCPSNQCRNSIQGK
NCI-3903	**TMG3**	SNV	STK25	NM_001271978	P	L	214	SNKETDPPPPLTRSNTANRLMKTLS	GITAIELAKGEPLNSDLHPMRVLFL
		SNV	CSNK1E	NM_001894	Y	H	201	EQSRRDDLESLGYVLMYFNLGSLPW	EQSRRDDLESLGHVLMYFNLGSLPW
		SNV	VKORC1L1	NM_001284342	E	K	45	LSVSASPEKSYSRPSPLVLPSSRIE	AYHVEREKERDPKHRALCDLGPWVK
		SNV	CRELD1	NM_015513	R	Q	220	HLVCSACFGPCARCSGPEESNCLQC	HLVCSACFGPCAQCSGPEESNCLQC
		SNV	PLXND1	NM_015103	P	S	134	DLTKELNRSQGIPFLEYKHFVTRTF	DLTKELNRSQGISFLEYKHFVTRTF
		SNV	KIAA1967	NM_021174	H	Y	227	KKPRHDLPPYRVHLTPYTVDSPICD	KKPRHDLPPYRVYLTPYTVDSPICD
		SNV	NUP107	NM_020401	G	E	392	GWKLYHDPNVNGGTELEPVEGNPYR	GWKLYHDPNVNGETELEPVEGNPYR
		SNV	RCC1	NM_001269	G	E	407	QLENRVVLSVSSGGQHTVLLVKDKE	QLENRVVLSVSSEGQHTVLLVKDKE
		SNV	DHX38	NM_014003	S	L	305	GRGRREEGEEGISFDTEEERQQWED	GRGRREEGEEGILFDTEEERQQWED
		SNV	UBTF	NM_001076683	P	S	202	TLECTVAGTPELSTKWFKDGKELTS	AKKSDIPEKPKTSQQLWYTHEKKVY
		SNV	LSG1	NM_018385	L	F	433	TKHFQTLYVEPGLCLCDCPGLVMPS	TKHFQTLYVEPGFCLCDCPGLVMPS
		SNV	NUP98	NM_005387	P	L	381	KLTTFGSSTTSAPSFGTTSGGLFGN	KLTTFGSSTTSALSFGTTSGGLFGN
NCI-3903	**TMG4**	SNV	RBM6	NM_001167582	P	S	884	APAEDVFKKPLPPTVKKEESPPPPK	APAEDVFKKPLPSTVKKEESPPPPK
		SNV	CPSF2	NM_017437	I	V	523	MDQDLSDVPTKCISTTESIEIKARV	MDQDLSDVPTKCVSTTESIEIKARV
		SNV	TNS3	NM_022748	P	L	711	IEQLNRLILELDPTFEPIPTHMNAL	IEQLNRLILELDLTFEPIPTHMNAL
		SNV	BLVRB	uc002onw.2	S	F	88	GTRNDLSPTTVMSEGARNIVAAMKA	GTRNDLSPTTVMFEGARNIVAAMKA

		SNV	CLDN1	uc003fsh.3	T	Y	80	DSLLNLSSTLQATRALMVVGILLGV	DSLLNLSSTLQAYRALMVVGILLGV
		SNV	LMBR1	uc010lqn.3	G	E	259	LQRRLNVGMLCAGNPEVATGRQVPE	LQRRLNVGMLCAENPEVATGRQVPE
		SNV	TJP1	uc010azl.3	P	L	364	VSTPVKHADDHTPKTVEEVTVERNE	VSTPVKHADDHTLKTVEEVTVERNE
		SNV	GPD1L	uc003cew.3	E	K	126	KALGITLIKGIDEGPEGLKLISDII	KALGITLIKGIDKGPEGLKLISDII
		SNV	FAM176A	uc002snk.1	E	K	125	TSAEELERAQRLEERERIIREIWMN	TSAEELERAQRLKERERIIREIWMN
		SNV	TDRD7	uc004axj.3	V	G	59	PTLEAYLRSVPAVVRIETSRSGEIT	PTLEAYLRSVPAGVRIETSRSGEIT
		SNV	TBC1D15	uc010stt.2	G	R	368	NVDNMKQMIFRGGLSHALRKQAWKF	NVDNMKQMIFRGRLSHALRKQAWKF
		SNV	NFATC3	uc010vlb.2	A	T	1024	IKPEPEDREPNFATIGLQDITLDDV	IKPEPEDREPNFTTIGLQDITLDDV
NCI-3903	**TMG5**	SNV	KRT18	uc009zmn.2	R	K	325	MRNLKASLENSLREVEARYALQMEQ	MRNLKASLENSLKEVEARYALQMEQ
		SNV	CSGALNACT1	uc011kyp.2	P	S	404	PGIIYGHHDAVPPLEQQLVIKKETG	PGIIYGHHDAVPSLEQQLVIKKETG
		SNV	PCYT2	uc031rex.1	P	L	321	KTEIIPDRDGSDPYQEPKRRGIFRQ	KTEIIPDRDGSDLYQEPKRRGIFRQ
		SNV	SEC24B	uc011cfq.2	P	L	371	EYVNNQASSAPTPLSSTSDDEEEEE	EYVNNQASSAPTLLSSTSDDEEEEE
		SNV	CARKD	uc001vrc.3	P	L	342	TPTSPHLLLSPSPQVQPSPGGRVWR	TPTSPHLLLSPSLQVQPSPGGRVWR
		SNV	PIGN	uc021ulb.1	T	K	916	FLVFLNGLAQLLTTKKLRLCGKPKS	FLVFLNGLAQLLKTKKLRLCGKPKS
		SNV	SUMF1	uc003bpz.2	G	N	17	ALGLVCGRCPELGLVLLLLLLSLLC	ALGLVCGRCPELNLVLLLLLLSLLC
		NFS deletion	LARP7	uc003iay.4			22	KVMEEESTEKKKEVEKKKRSRVKQV	KVMEEESTEKKKVEKKKRSRVKQV
		SNV	FAM120B	uc003qxp.3	E	K	178	YGLQHNCLGILGEDTDYLIYDTCPY	YGLQHNCLGILGKDTDYLIYDTCPY
		SNV	TRPM7	uc010bew.2	S	F	103	AYGVINFQGGSHSYRAKYVRLSYDT	AYGVINFQGGSHFYRAKYVRLSYDT
		SNV	USP6NL	uc001ikt.3	R	H	687	LSVSASPEKSYSRPSPLVLPSSRIE	LSVSASPEKSYSHPSPLVLPSSRIE
		SNV	LIG3	uc010cth.1	E	K	464	ERVLHNAQEVEKEPGQRRALSVQAS	ERVLHNAQEVEKKPGQRRALSVQAS
NCI-3903	**TMG6**	SNV	CAPN7	uc003bzn.3	P	S	806	EGPFFLDFNSIIPIKITQLQ	EGPFFLDFNSIISIKITQLQ
		SNV	DBR1	uc003erv.3	H	Y	182	IFLSHDWPRSIYHYGNKKQLLKTKS	IFLSHDWPRSIYYYGNKKQLLKTKS
		SNV	UNC119B	uc001tyz.4	EH	DP	180	SNFRMIERHYFREHLLKNFDFDFGFC	SNFRMIERHYFRDPLLKNFDFDFGFC
		SNV	UNC119B	uc001tyz.4	E	D	180	SNFRMIERHYFREHLLKNFDFDFGF	SNFRMIERHYFRDHLLKNFDFDFGF
		SNV	PMS2CL	uc011jxb.1	P	L	84	TSDAISDKGVLRPQKEAVSSSQGPS	TSDAISDKGVLRLQKEAVSSSQGPS
		SNV	RNF213	uc021uen.2	P	L	837	VFMMVVCIELKIPLFLVGKPGSSKS	VFMMVVCIELKILLFLVGKPGSSKS
		SNV	TCF20	uc003bck.1	P	L	467	SLSALSTQVANLPNTVQHMLLSDAL	SLSALSTQVANLLNTVQHMLLSDAL
		SNV	AGAP1	uc002vvt.3	P	S	632	GNSHCVDCETQNPNWASLNLGALMC	GNSHCVDCETQNSNWASLNLGALMC

		SNV	TMEM2	uc011lsa.1	N	S	122	DENCPDQNPRLRNWDPGQDSAKQVV	DENCPDQNPRLRSWDPGQDSAKQVV
		SNV	SORCS1	uc021pxw.1	E	K	301	AYSQDQKLYSSAEFGRRWQLIQEGV	AYSQDQKLYSSAKFGRRWQLIQEGV
		SNV	CHST14	uc001zlw.3	E	V	270	VTFPEFLRYLVDEDPERMNEHWMPV	VTFPEFLRYLVDVDPERMNEHWMPV
		SNV	VPS13C	uc002ahc.2	L	F	74	IDKLTLKIPWKNLYGEAVVATLEGL	IDKLTLKIPWKNFYGEAVVATLEGL
NCI-3903	**TMG7**	SNV	NDRG2	uc010tll.2	S	F	338	SRSRTASLTSAASVDGNRSRSRTLS	SRSRTASLTSAAFVDGNRSRSRTLS
		SNV	SLC25A22	uc009yci.3	P	S	281	LDCARKILRHEGPSAFLKGAYCRAL	LDCARKILRHEGSSAFLKGAYCRAL
		SNV	SLC27A4	uc004but.3	G	S	180	CLTTSRARALVFGSEMASAICEVHA	CLTTSRARALVFSSEMASAICEVHA
		SNV	IFNGR1	uc011edm.1	P	S	328	LEKEVVCEEPLSPATVPGMHTEDNP	LEKEVVCEEPLSSATVPGMHTEDNP
		SNV	CPS1	uc010fus.3	G	S	731	LSRSSALASKATGYPLAFIAAKIAL	LSRSSALASKATSYPLAFIAAKIAL
		SNV	CSGALNACT2	uc001jan.4	H	Y	304	FRDVCIHQDKKIHLTVVYFGKEGLS	FRDVCIHQDKKIYLTVVYFGKEGLS
		SNV	ZNF263	uc010uww.2	P	S	630	LIRHQRIHTGEKPYTCHECGDSFSH	LIRHQRIHTGEKSYTCHECGDSFSH
		SNV	ANKRD27	uc002ntn.1	E	K	412	CLFKHIASGNQKEVERLLSQEDHDK	CLFKHIASGNQKKVERLLSQEDHDK
		SNV	BCL9L	uc009zal.3	P	S	963	NLKSPQTPSQMVPLPSANPPGPLKS	NLKSPQTPSQMVSLPSANPPGPLKS
		SNV	ADCY9	uc002cvx.3	H	Y	292	ELLSRGLLHGCIHAIGVHLFVMSQV	ELLSRGLLHGCIYAIGVHLFVMSQV
		SNV	LONRF2	uc002tal.4	R	K	566	LHVFEPRYRLMIRRCMETGTKRFGM	LHVFEPRYRLMIKRCMETGTKRFGM
		SNV	LONRF2	uc002tal.4	N	I	323	EVLFSATANVHENLTSSIQSRLKAQ	EVLFSATANVHEILTSSIQSRLKAQ
NCI-3903	**TMG8**	SNV	DNAH14	uc001how.2	L	F	3052	QKKPNWATAKLLLSETGFLKKLINL	QKKPNWATAKLLFSETGFLKKLINL
		SNV	VPS13B	uc003yiv.4	IP	MS	3284	KDIPKFEVYCKKIPSECSIHHELYH	KDIPKFEVYCKKMSSECSIHHELYH
		SNV	PIAS4	uc002lzg.3	S	F	222	PNIAVKVNHSYCSVPGYYPSNKPGV	PNIAVKVNHSYCFVPGYYPSNKPGV
		SNV	SLC5A4	uc003ami.3	E	K	139	TMPEYLKKRFGGERLQVYLSILSLF	TMPEYLKKRFGGKRLQVYLSILSLF
		SNV	LRRC42	uc001cwk.2	G	D	132	SAAEARQKFTEPGAGLRALQKFTEA	SAAEARQKFTEPDAGLRALQKFTEA
		SNV	PHKA1	uc011mqi.2	P	L	34	ILCHQNPVTGLLPASYDQKDAWVRD	ILCHQNPVTGLLLASYDQKDAWVRD
		SNV	GPSM2	uc010ove.1	A	T	682	ALLEFKNSGKKSADH	ALLEFKNSGKKSTDH
		SNV	N4BP1	uc002efp.3	P	S	522	GASSHQPRVPLFPENGLHQQPEPLL	GASSHQPRVPLFSENGLHQQPEPLL
		SNV	FASTKD3	uc011cmp.2	P	L	598	DIHKRIALCIDGPKRFCSNSKHLLG	DIHKRIALCIDGLKRFCSNSKHLLG
		SNV	ARAP3	uc003llo.1	S	F	280	TSDDLISPYASFSFTADRLTPLLSG	TSDDLISPYASFFFTADRLTPLLSG
		SNV	ASH1L	uc009wqr.1	M	I	534	QPPVYCTSPDFKMGGASDVSTAKSP	QPPVYCTSPDFKIGGASDVSTAKSP
		SNV	ZXDC	uc003eix.2	P	L	494	LLPQLEAPSSLTPSSELSSPGQSEL	LLPQLEAPSSLTLSSELSSPGQSEL
NCI-3903	**TMG9**	SNV	CABIN1	uc021wnc.1	R	C	1783	SDLERTPPLLPGRPARDRGPESRPT	SDLERTPPLLPGCPARDRGPESRPT

		SNV	KIF1BP	uc001joy.3	P	S	246	TLKRQLEHNAYHPIEWAINAATLSQ	TLKRQLEHNAYHSIEWAINAATLSQ
		SNV	CASD1	uc003unj.4	S	L	647	FSNKISNFLLFISVVSFLTYSIWAS	FSNKISNFLLFILVVSFLTYSIWAS
		SNV	RAPGEF6	uc010jdk.3	S	G	94	VLVKGSMVLPPCSFGKQFGGKRGCD	VLVKGSMVLPPCGFGKQFGGKRGCD
		SNV	FMN2	uc010pyf.1	K	Q	1417	NRAQSDELEKIEKHGRSSKDKENAK	NRAQSDELEKIEQHGRSSKDKENAK
		SNV	EXOC6	uc010qnr.2	S	F	284	EEILTVQDLVDFSPVYRCLHIYSVL	EEILTVQDLVDFFPVYRCLHIYSVL
		SNV	DOCK9	uc021rlw.1	P	S	1824	GKEYIYKEPKLTPLSEISQRLLKLY	GKEYIYKEPKLTSLSEISQRLLKLY
		SNV	HEG1	uc011bke.2	S	F	400	TGNPGDEEFIEPSTENEFGLTSLRW	TGNPGDEEFIEPFTENEFGLTSLRW
		SNV	HDAC4	uc010fyy.3	S	F	861	QAFYSDPSVLYMSLHRYDDGNFFPG	QAFYSDPSVLYMFLHRYDDGNFFPG
		SNV	BRAF	uc003vwc.4	V	E	600	LTVKIGDFGLATVKSRWSGSHQFEQ	LTVKIGDFGLATEKSRWSGSHQFEQ
		SNV	LINS1	uc002bwi.3	S	F	46	PAVSDQDCSTATSLEWANTCGIQGR	PAVSDQDCSTATFLEWANTCGIQGR
		SNV	ZNF550	uc031rnf.1	A	V	9	DAAQMLVTFKDVAVTFTREEWRQLD	DAAQMLVTFKDVVVTFTREEWRQLD
NCI-3903	**TMG10**	SNV	KLHL36	uc002fig.3	A	V	363	GGSFSRDNGGDAASNLLYRYDPRCK	GGSFSRDNGGDAVSNLLYRYDPRCK
		SNV	ALKBH4	uc003uzl.3	E	K	37	ICERQRGSDPPWELPPAKTYRFIYC	ICERQRGSDPPWKLPPAKTYRFIYC
		SNV	BCAR3	uc001dqb.4	S	F	32	PLASSMDLLSSRSPLAEHRPDAYQD	PLASSMDLLSSRFPLAEHRPDAYQD
		SNV	KATNAL1	uc001ust.4	R	W	56	RDPAIKGKWQQVRQELLEEYEQVKS	RDPAIKGKWQQVWQELLEEYEQVKS
		SNV	CP110	uc002dgl.4	G	R	765	FVSANEAPFYLWGSSTSGLTKLSVT	FVSANEAPFYLWRSSTSGLTKLSVT
		SNV	C6orf70	uc011ehb.1	R	C	502	MPENRCVLKDLDRLPTETWPQLLRE	MPENRCVLKDLDCLPTETWPQLLRE
		SNV	LMF1	uc021tae.1	E	K	356	LQMQRDIRGARPEPRFGSVVRRAAN	LQMQRDIRGARPKPRFGSVVRRAAN
		SNV	DEPDC6	uc003yow.4	H	Y	99	KLMQKLADRGIIHHVCDEHKEFKDV	KLMQKLADRGIIYHVCDEHKEFKDV
		SNV	GMEB1	uc001brb.3	G	R	79	AVETHTIHKIEEGIDTGTIEANEDM	AVETHTIHKIEERIDTGTIEANEDM
		SNV	VPS13A	uc004aks.3	P	L	2313	SSFNITRIVTFTPFYMIKNKSKYHI	SSFNITRIVTFTLFYMIKNKSKYHI
		SNV	ZNF142	uc010fvt.4	H	Y	185	KKRTHLVEHLHLHFPDPSLQCPNCQ	KKRTHLVEHLHLYFPDPSLQCPNCQ
		SNV	PALLD	uc011cjx.2	E	K	941	HFLQAPGDLTVQEGKLCRMDCKVSG	HFLQAPGDLTVQKGKLCRMDCKVSG
NCI-3903	**TMG11**	SNV	SH3TC1	uc003gkw.4	P	S	762	LVLQNAPQPHSLPAQTSHYLRQALA	LVLQNAPQPHSLSAQTSHYLRQALA
		SNV	TMEM132A	uc001nqj.3	R	G	1018	LKDPEELRNYMERIRGSS	LKDPEELRNYMEGIRGSS
		SNV	TNRC6C	uc002juf.2	P	S	1298	SVKDPSQSQSRLPQWTHPNSMDNLP	SVKDPSQSQSRLSQWTHPNSMDNLP
		SNV	RING1	uc003odl.3	G	S	322	QQEAGEPGGPGGGASDTGGPDGCGG	QQEAGEPGGPGGSASDTGGPDGCGG
		SNV	OPTN	uc001ily.1	H	Y	3	MSHQPLSCLTEKEDS	MSYQPLSCLTEKEDS
		SNV	ERCC4	uc010bva.3	P	S	85	INQLKIEGVEHLPRRVTNEITSNSR	INQLKIEGVEHLSRRVTNEITSNSR
		SNV	NICN1	uc011bcr.2	R	C	63	KNYYTAFLSIRVRQYTS	KNYYTAFLSIRVCQYTSAH

								AHTPAKWV	TPAKWV
		SNV	SGEF	uc021xgc.1	P	S	648	INSQLEFKIKPFPLVSSSRWLVKRG	INSQLEFKIKPFSLVSSSRWLVKRG
		SNV	KIFC2	uc003zcz.3	E	K	163	RPPSPDGSTSQEESPSHFTAVPGEP	RPPSPDGSTSQEKSPSHFTAVPGEP
		SNV	C4orf23	uc003glg.2	R	K	159	EGHPGRGIDVRRRKIWDMYGPQTQL	EGHPGRGIDVRRKKIWDMYGPQTQL
		SNV	CUL9	uc010jyk.3	H	Y	2069	VHQAQAVPVRPDHCPVCVSPLGCDD	VHQAQAVPVRPDYCPVCVSPLGCDD
		SNV	HOXA3	uc011jzl.2	P	L	322	ASYPASLPSCAPPPPPQKRYTAAGA	ASYPASLPSCAPLPPPQKRYTAAGA
NCI-3903	**TMG12**	SNV	FREM2	uc001uwv.3	P	S	1185	FSERQFFPIVIIPTNDEQPEMFMRE	FSERQFFPIVIISTNDEQPEMFMRE
		SNV	FANCC	uc022bkl.1	A	T	226	ILQPEFFEAVNEAILLKKISLPMSA	ILQPEFFEAVNETILLKKISLPMSA
		SNV	CACNA2D1	uc003uhr.1	D	N	662	APRDYCNDLKISDNNTEFLLNFNEF	APRDYCNDLKISNNNTEFLLNFNEF
		SNV	HEYL	uc010oiw.2	R	Q	67	RRDRINSSLSELRRLVPTAFEKQGS	RRDRINSSLSELQRLVPTAFEKQGS
		SNV	ZFP62	uc021yjo.1	L	F	744	VECGKSFSYSSLLSQHKRIHTGEKP	VECGKSFSYSSLFSQHKRIHTGEKP
		SNV	ANKMY1	uc010fzd.1	P	L	201	ELDARIFLNEIPPFVEDGEPWFIIN	ELDARIFLNEIPLFVEDGEPWFIIN
		SNV	C16orf55	uc031qxq.1	S	F	103	TRASNETLVSCSSSGSDQQRTIREP	TRASNETLVSCSFSGSDQQRTIREP
		SNV	ARHGAP39	uc011llk.1	M	I	1032	VFVQPANVAVTKMDVSNLAMVMAPN	VFVQPANVAVTKIDVSNLAMVMAPN
		SNV	HIVEP1	uc003nac.3	R	Q	2608	RTESPQGLPTVQRENAKKVLNPPAP	RTESPQGLPTVQQENAKKVLNPPAP
		SNV	ZNF653	uc002mrz.2	P	F	501	NLVHRKGKTKVCPHPGCGKKFYLSN	NLVHRKGKTKVCFHPGCGKKFYLSN
		SNV	PCDHGB6	uc003lkj.2	L	F	338	GLSTQCKVIIEILDENDNSPEIIIT	GLSTQCKVIIEIFDENDNSPEIIIT
		SNV	AKD1	uc003ptr.4	R	K	229	QMVAEILHHLVQRPEDYLENVENIV	QMVAEILHHLVQKPEDYLENVENIV
NCI-3903	**TMG13**	SNV	TNFAIP2	uc001ymm.1	E	K	24	PLEAGAAPYREEEEAAKKKKEKKKK	PLEAGAAPYREEKEAAKKKKEKKKK
		SNV	CEBPA	uc002nun.3	R	H	264	ALKGLGAAHPDLRASGGSGAGKAKK	ALKGLGAAHPDLHASGGSGAGKAKK
		SNV	ANKDD1A	uc010bha.3	M	V	205	NTALHLAAGRGHMAVLQRLVDIGLD	NTALHLAAGRGHVAVLQRLVDIGLD
		SNV	C14orf79	uc001ypy.1	A	S	66	ISMPREGGSTCTARCPDPGEHSSTW	ISMPREGGSTCTSRCPDPGEHSSTW
		SNV	PRICKLE1	uc010skw.2	E	K	276	QMTYDGQHWHATEACFSCAQCKASL	QMTYDGQHWHATKACFSCAQCKASL
		SNV	DNAH2	uc002giu.1	D	N	2632	SKVFQGMLRANKDFHDTKSSITRLW	SKVFQGMLRANKNFHDTKSSITRLW
		SNV	CLSTN3	uc001qss.3	T	I	313	SERALRKLCGAATGEVDLLPMPGPN	SERALRKLCGAAIGEVDLLPMPGPN
		SNV	ANKRD5	uc010gbz.3	S	L	514	AGDLASLKKAFESGIPVDMKDNYYK	AGDLASLKKAFELGIPVDMKDNYYK
		SNV	CLIC6	uc010gmt.1	K	E	514	VIFNVTTVDLKRKPADLQNLAPGTN	VIFNVTTVDLKREPADLQNLAPGTN
		SNV	FRY	uc001utx.3	R	C	1143	AGPFSIMFTPLDRYSDRNHQITRYQ	AGPFSIMFTPLDCYSDRNHQITRYQ
		SNV	ANK3	uc001jky.3	P	S	2141	GFETRSEKTPSAPQSAESTGPKPLF	GFETRSEKTPSASQSAESTGPKPLF

		SNV	TBX19	uc001gfl.3	S	F	141	PNFGAHWMKAPISFSKVKLTNKLNG	PNFGAHWMKAPIFFSKVKLTNKLNG
NCI-3903	**TMG14**	SNV	BTC	uc003hig.2	E	K	159	KRRKRKKKEEEMETLGKDITPINED	KRRKRKKKEEEMKTLGKDITPINED
		SNV	SAMD9L	uc022ahh.1	T	A	1255	LLEYLNPNYKDATTMESIVNEYAFL	LLEYLNPNYKDAATMESIVNEYAFL
		SNV	KIAA0895	uc003tfd.2	G	R	37	RWKRWFKFRKRKGEKRPRPNHKAVA	RWKRWFKFRKRKREKRPRPNHKAVA
		SNV	GPR158	uc001isk.3	D	N	713	NSAWSEHSLDPEDIRDELKKLYAQL	NSAWSEHSLDPENIRDELKKLYAQL
		SNV	PCDHGA1	uc011dan.2	R	C	293	FHNVDHRVAQIFRLDSYTGEISNKE	FHNVDHRVAQIFCLDSYTGEISNKE
		SNV	SLC12A5	uc010zxl.1	P	L	305	IYAGVIKSAFDPPNFPICLLGNRTL	IYAGVIKSAFDPLNFPICLLGNRTL
		SNV	PCLO	uc003uhx.2	P	S	4870	GIFPDPSKDMQVPTIEKSHSSPGSS	GIFPDPSKDMQVSTIEKSHSSPGSS
		SNV	RDH12	uc001xjz.4	R	Q	95	IRVDTKNSQVLVRKLDLSDTKSIRA	IRVDTKNSQVLVQKLDLSDTKSIRA
		SNV	PCDH18	uc003ihg.4	S	L	777	INGTLPIRSHHRSSPSSSPTLERGQ	INGTLPIRSHHRLSPSSSPTLERGQ
		SNV	CETP	uc002eki.2	D	N	297	RVFHSLAKVAFQDGRLMLSLMGDEF	RVFHSLAKVAFQNGRLMLSLMGDEF
		SNV	LGI2	uc003grf.2	E	K	337	KPNDIELFQIDDETFFVIADSSKAG	KPNDIELFQIDDKTFFVIADSSKAG
		SNV	MRAP2	uc003pkg.4	E	K	26	QSASNSDYTWEYEYYEIGPVSFEGL	QSASNSDYTWEYKYYEIGPVSFEGL
NCI-3903	**TMG15**	SNV	TTN	uc031rqd.1	S	N	7616	TLECTVAGTPELSTKWFKDGKELTS	TLECTVAGTPELNTKWFKDGKELTS
		SNV	OLIG2	uc021wil.1	D	G	97	STSSAAASSTKKDKKQMTEPELQQL	STSSAAASSTKKGKKQMTEPELQQL
		SNV	SAMD14	uc002iqg.4	T	N	254	TDSGKGSASSGSTTSPTCSPKHEGF	TDSGKGSASSGSNTSPTCSPKHEGF
		SNV	ILDR2	uc001gdx.2	G	E	239	DSCCCPQALYEAGKAAKAGYPPSVS	DSCCCPQALYEAEKAAKAGYPPSVS
		SNV	EFCAB5	uc010wbj.2	G	R	325	LQEFFQNPDFKLGSHCKQLDITDST	LQEFFQNPDFKLRSHCKQLDITDST
		SNV	LRRC36	uc010vjk.2	E	K	621	LVRVLEENLILSEKIQQLEEGAAIS	LVRVLEENLILSKKIQQLEEGAAIS
		SNV	GPC5	uc010tif.2	A	T	137	LFCSTYRNMALEAAASVQEFFTDVG	LFCSTYRNMALETAASVQEFFTDVG
		SNV	RP1	uc003xsd.1	E	K	490	KMIGQFSYSEERESGENKSEYHMFT	KMIGQFSYSEERKSGENKSEYHMFT
		SNV	DNAH10	uc001uft.4	G	E	2881	GFLELINNMLTSGIVPALFSEEEKE	GFLELINNMLTSEIVPALFSEEEKE
		SNV	APOB48R	uc002dqb.2	A	T	331	AETASGGEEAGTASGGEEAGIASGG	AETASGGEEAGTTSGGEEAGIASGG
		SNV	DNAH1	uc011bef.2	M	V	1484	DLVALVRGKLSRMQRAVLSALIVIE	DLVALVRGKLSRVQRAVLSALIVIE
		SNV	CFI	uc011cft.2	H	Y	95	PTYCQQKSLECLHPGTKFLNNGTCT	PTYCQQKSLECLYPGTKFLNNGTCT
NCI-3903	**TMG16**	SNV	IL2RB	uc003aqv.1	R	H	131	MAIQDFKPFENLRLMAPISLQVVHV	MAIQDFKPFENLHLMAPISLQVVHV
		SNV	RYR3	uc010bar.3	G	R	4338	QAAEMKAANEAEGKVESEKADMEDG	QAAEMKAANEAERKVESEKADMEDG
		SNV	FILIP1L	uc021xbr.1	V	I	417	RETLQSKDFKLEVEKLSKRIMALEK	RETLQSKDFKLEIEKLSKRIMALEK
		SNV	NXPH3	uc002ipa.3	R	H	85	GEAWGILGQPPNRPNHSPPPSAKVK	GEAWGILGQPPNHPNHSPPPSAKVK

		SNV	FAM171A1	uc001iob.3	H	Y	398	EAPGTKELMSGVHLEMMSPGGEGDL	EAPGTKELMSGVYLEMMSPGGEGDL
		SNV	MXRA5	uc004crg.4	S	F	1260	VSSRASGSKPSPSPENKHRNIVTPS	VSSRASGSKPSPFPENKHRNIVTPS
		SNV	CCDC116	uc002zve.3	D	N	437	SHFSNRLYEELADFLTQQAASLVIR	SHFSNRLYEELANFLTQQAASLVIR
		SNV	CA9	uc003zxo.4	E	K	302	EQLLSRLEEIAEEGSETQVPGLDIS	EQLLSRLEEIAEKGSETQVPGLDIS
		SNV	GRM8	uc003vlt.2	P	S	573	RPNMNRTGCQLIPIIKLEWHSPWAV	RPNMNRTGCQLISIIKLEWHSPWAV
		SNV	OLFML2B	uc010pkq.2	D	N	525	NEGAWMKDPLAKDERIYVTNYYYGN	NEGAWMKDPLAKNERIYVTNYYYGN
		SNV	FGD3	uc004ata.3	R	Q	256	LKMYGEYVKNFDRAVGLVSTWTQRS	LKMYGEYVKNFDQAVGLVSTWTQRS
		SNV	TAS2R3	uc003vwp.1	P	S	277	AKMIGEVMTMFYPAGHSFILILGNS	AKMIGEVMTMFYSAGHSFILILGNS
NCI-3903	**TMG17**	SNV	C12orf56	uc021qzu.1	D	N	96	LIDDYPEFLSSPDREISQHIRIIYS	LIDDYPEFLSSPNREISQHIRIIYS
		SNV	GPR98	uc003kju.3	G	R	1589	FTGACIPEIAEEGSTISCVVERTRG	FTGACIPEIAEERSTISCVVERTRG
		SNV	KIAA1543	uc002mgv.4	R	Q	762	TGPKAASPSPARRVPATRRSPGPGP	TGPKAASPSPARQVPATRRSPGPGP
		SNV	KIAA1543	uc002mgw.3	A	T	1072	HNNLGVKRPTSRAPSPSGLMSPSRL	HNNLGVKRPTSRTPSPSGLMSPSRL
		SNV	ARHGEF4	uc010fmw.1	G	R	570	RPSAQRMGLHYPGRGSAISMVSLGS	RPSAQRMGLHYPRRGSAISMVSLGS
		SNV	CNGA1	uc003gxu.3	R	Q	629	GSDPKDLEEKVTRMEGSVDLLQTRF	GSDPKDLEEKVTQMEGSVDLLQTRF
		SNV	CNGA1	uc003gxu.3	I	S	297	FQRTETRTNYPNIFRISNLVMYIVI	FQRTETRTNYPNSFRISNLVMYIVI
		SNV	GRIN3A	uc004bbq.1	R	K	730	SALNICYALLFGRTVAIKPPKCWTG	SALNICYALLFGKTVAIKPPKCWTG
		SNV	PREX2	uc011lez.1	M	R	218	AVCSNINEAKRQMEKLEVLEEWQSH	AVCSNINEAKRQREKLEVLEEWQSH
		SNV	PREX2	uc003xxu.1	S	F	954	EFLLLPPPLLGISQDGRQHCIPEDL	EFLLLPPPLLGIFQDGRQHCIPEDL
		SNV	TRIML2	uc011cle.1	G	R	365	ALRPVFSLCIPNGDTSPDSLTILQH	ALRPVFSLCIPNRDTSPDSLTILQH
		SNV	COL28A1	uc003src.1	P	S	259	PGDPGPPGTHGNPGIKGERGPKGNP	PGDPGPPGTHGNSGIKGERGPKGNP
NCI-3903	**TMG18**	SNV	SAMD12	uc010mda.1	G	R	123	LLRLTDKKLERMGIAQENLRQHILQ	LLRLTDKKLERMRIAQENLRQHILQ
		SNV	VWDE	uc003ssj.2	D	N	411	VNEDFLWNNYIPDSIQIKVKDVPTA	VNEDFLWNNYIPNSIQIKVKDVPTA
		SNV	ABCA12	uc010zjn.2	E	K	1883	SQVIYNLTGQRVENYLISTANEFVQ	SQVIYNLTGQRVKNYLISTANEFVQ
		SNV	COL4A6	uc011msn.2	P	L	548	LGPSGPKGKKGEPILSTIQGMPGDR	LGPSGPKGKKGELILSTIQGMPGDR
		SNV	IL22RA1	uc010oeg.1	P	L	512	SSVQIEGHPMSLPLQPPSRPCSPSD	SSVQIEGHPMSLLLQPPSRPCSPSD
		SNV	ALPK3	uc002ble.3	P	S	1073	GLSQEVPTMPSLPGTGLTASPKAGP	GLSQEVPTMPSLSGTGLTASPKAGP
		SNV	GJB7	uc021zcj.1	D	N	167	IKCDLKPCPNTVDCFISKPTEKTIF	IKCDLKPCPNTVNCFISKPTEKTIF
		SNV	ISL1	uc003jor.3	G	R	5	MGDMGDPPKKKRLISLC	MGDMRDPPKKKRLISLC
		SNV	KIAA1324	uc021orb.1	P	L	643	QPYGVQACVPCGPGTKNNKIHSLCY	QPYGVQACVPCGLGTKNNKIHSLCY
		SNV	COL11A2	uc003ocz.1	P	L	1440	KGDRGLPGPQGSPGQ	KGDRGLPGPQGSLGQKG

								KGEMGIPGAS	EMGIPGAS
		SNV	C3orf15	uc011bje.2	P	S	255	RAREKRAWEASLPALSDTSQFEKRR	RAREKRAWEASLSALSDTSQFEKRR
		SNV	NEFL	uc003xee.4	S	L	63	LSVRRSYSSSSGSLMPSLENLDLSQ	LSVRRSYSSSSGLLMPSLENLDLSQ
NCI-3903	**TMG19**	SNV	MMEL1	uc001ajy.2	R	K	393	QNLENIIDTYSARTIQNYLVWRLVL	QNLENIIDTYSAKTIQNYLVWRLVL
		SNV	DNAH5	uc003jfd.2	E	K	1279	QISIDFQVGPIEESYALLNRYGLLI	QISIDFQVGPIEKSYALLNRYGLLI
		SNV	MYO15A	uc021trm.1	G	S	2147	VWHNHNAHNAERGWLLLAACLSGFA	VWHNHNAHNAERSWLLLAACLSGFA
		SNV	FPR1	uc021uyo.1	G	R	172	VIIRVTTVPGKTGTVACTFNFSPWT	VIIRVTTVPGKTRTVACTFNFSPWT
		SNV	DLEC1	uc010hgv.1	R	Q	1125	TRQLILTNRSPIRTRFSLKFEYFGS	TRQLILTNRSPIQTRFSLKFEYFGS
		SNV	KIAA1409	ENST00000555664	M	I	1	LNDDVLSTLPYTMISTLATFPPFLH	LNDDILSTLPYTIISTLATFPPFLH
		SNV	CD3E	uc010rya.2	G	S	29	VGVWGQDGNEEMGGITQTPYKVSIS	VGVWGQDGNEEMSGITQTPYKVSIS
		SNV	DCC	uc010xdr.1	S	F	868	THDAVRVSWADNSVPKNQKTSEVRL	THDAVRVSWADNFVPKNQKTSEVRL
		SNV	SCN2A	uc021vry.1	S	N	1930	RYLLKQKVKKVSSIYKKDKGKECDG	RYLLKQKVKKVSNIYKKDKGKECDG
		SNV	MAPT	uc010dau.3	G	E	385	QLKARMVSKSKDGTGSDDKKAKTST	QLKARMVSKSKDETGSDDKKAKTST
		SNV	CXCR7	uc021vys.1	N	S	62	IYIFIFVIGMIANSVVVWVNIQAKT	IYIFIFVIGMIASSVVVWVNIQAKT
		SNV	CDH6	uc003jhe.2	D	N	294	PPGTPIGRIKASDADVGENAEIEYS	PPGTPIGRIKASNADVGENAEIEYS
NCI-3903	**TMG20**	SNV	FAM133A	uc022bzx.1	G	E	128	SSSDSEDEEKKQGKRRKKKKNRSYK	SSSDSEDEEKKQEKRRKKKKNRSYK
		SNV	DNAH7	uc002utj.4	S	F	3327	PYANLCTWLPQKSWDEICRLDDLPA	PYANLCTWLPQKFWDEICRLDDLPA
		SNV	DMBX1	uc001cpx.3	P	L	338	AAAAAHQGVWGSPLLPAPPAGLAPA	AAAAAHQGVWGSLLLPAPPAGLAPA
		SNV	SLC4A10	uc010zcs.2	R	Q	135	EICWREGEDAEWRETARWLKFEEDV	EICWREGEDAEWQETARWLKFEEDV
		SNV	LRRIQ1	uc021rbo.1	D	N	1269	EPDSPDIPEKWMDSVSSHSPLSKSA	EPDSPDIPEKWMNSVSSHSPLSKSA
		SNV	KNDC1	uc001llz.1	P	S	1600	LSGLEHLAVRQSPAWRILPAKIAEV	LSGLEHLAVRQSSAWRILPAKIAEV
		SNV	HYDIN	uc031qwy.1	D	N	4151	EGWIPPLSRFPIDIFFTPKQEGDVN	EGWIPPLSRFPINIFFTPKQEGDVN
		SNV	MYH6	uc001wjv.3	E	K	1529	QLGEGGKNVHELEKVRKQLEVEKLE	QLGEGGKNVHELKKVRKQLEVEKLE
		SNV	COL29A1	uc021xdz.1	E	K	2225	LNSGRESPFVKTEDNGSDYLVYLPS	LNSGRESPFVKTKDNGSDYLVYLPS
		SNV	CSMD3	uc011lhx.2	K	E	2209	TSLYFHSDYSQNKQGFHIVYQAYQL	TSLYFHSDYSQNEQGFHIVYQAYQL
		SNV	PKHD1	uc003pah.1	P	S	3449	FVDVFSSVNANIPCSTSGSVSTFYS	FVDVFSSVNANISCSTSGSVSTFYS
		SNV	LRP1B	uc010fnl.1	S	F	1102	GTIRLCDHKTKFSCWSTGRCINKAW	GTIRLCDHKTKFFCWSTGRCINKAW
NCI-3903	**TMG21**	SNV	ZNF711	uc011mqy.1	P	S	517	HVCVECGKGFRHPSELKKHMRTHTG	HVCVECGKGFRHSSELKKHMRTHTG
		SNV	PRSS54	uc002eng.3	S	F	36	LYSSTSCGVQKASVFYGPDPKEGLV	LYSSTSCGVQKAFVFYGPDPKEGLV

		SNV	ABCC12	uc002efc.1	S	L	631	SDRQLYLLDDPLSAVDAHVGKHVFE	SDRQLYLLDDPLLAVDAHVGKHVFE
		SNV	ALB	uc011cbf.2	E	K	165	DNEETFLKKYLYEIARRHPYFYAPE	DNEETFLKKYLYKIARRHPYFYAPE
		SNV	ASGR2	uc010clw.2	S	N	101	LQAELRSLKEAFSNFSSSTLTEVQA	LQAELRSLKEAFNNFSSSTLTEVQA
		SNV	BANK1	uc010ill.3	P	S	206	TIPLAVVLPTEIPCENPGEIFIILR	TIPLAVVLPTEISCENPGEIFIILR
		SNV	BDKRB1	uc021sbj.1	R	Q	176	VGGLLSIPTFLLRSIQAVPDLNITA	VGGLLSIPTFLLQSIQAVPDLNITA
		SNV	BTBD11	uc001tml.1	A	V	775	SLEEILAEGTDLAETAPPPLCASRN	SLEEILAEGTDLVETAPPPLCASRN
		SNV	C1orf100	uc031psw.1	R	C	13	MTAIRLREFIERRPVIPPSIFIAHQ	MTAIRLREFIERCPVIPPSIFIAHQ
		SNV	C6	uc003jml.2	E	K	651	EADSGCPQPVPPENGFIRNEKQLYL	EADSGCPQPVPPKNGFIRNEKQLYL
		SNV	C9orf79	uc004app.4	G	E	896	RVESVPKVPIFLGKRPQNGPGDNRT	RVESVPKVPIFLEKRPQNGPGDNRT
		SNV	CACNA1E	uc009wxt.3	P	L	2118	TSTPRRSRRQLPPVPPKPRPLLSYS	TSTPRRSRRQLPLVPPKPRPLLSYS
NCI-3903	**TMG22**	SNV	CACNA1I	uc003ayf.3	D	N	250	RCFLEENFTIQGDVALPPYYQPEED	RCFLEENFTIQGNVALPPYYQPEED
		SNV	CAPN9	uc001hua.1	H	Y	132	DQSFGPGYAGIFHFQFWQHSEWLDV	DQSFGPGYAGIFYFQFWQHSEWLDV
		SNV	CATSPERB	uc010aub.1	S	F	1114	SISLSELIHRSKSEE	SISLSELIHRSKFEE
		SNV	CD5L	uc001frk.4	P	S	241	NHDEDTWVECEDPFDLRLVGGDNLC	NHDEDTWVECEDSFDLRLVGGDNLC
		SNV	CDH12	uc011cno.1	A	V	740	PTAPPYDSLATYAYEGSGSVAESLS	PTAPPYDSLATYVYEGSGSVAESLS
		SNV	CHRM2	uc022ame.1	I	K	301	VSAVASNMRDDEITQDENTVSTSLG	VSAVASNMRDDEKTQDENTVSTSLG
		SNV	CNTN5	uc021qpc.1	G	E	1068	ASSQIRVPSYSGGKITSAQSTLHSL	ASSQIRVPSYSGEKITSAQSTLHSL
		SNV	CRP	uc001ftx.1	P	S	30	GQTDMSRKAFVFPKESDTSYVSLKA	GQTDMSRKAFVFSKESDTSYVSLKA
		SNV	CSN3	uc003hfe.4	T	I	133	PPKKIQDKIIIPTINTIATVEPTPA	PPKKIQDKIIIPIINTIATVEPTPA
		SNV	CTNNA2	uc010ysj.2	S	L	939	TRVRRGSQKKHISPVQALSEFKAMD	TRVRRGSQKKHILPVQALSEFKAMD
		SNV	CYP4F2	uc010xou.1	D	N	252	LLHIDFLYYLTPDGQRFRRACRLVH	LLHIDFLYYLTPNGQRFRRACRLVH
		SNV	CYP4F22	uc002nbh.4	G	R	290	VIQERRRALRQQGAEAWLKAKQGKT	VIQERRRALRQQRAEAWLKAKQGKT
NCI-3903	**TMG23**	SNV	GPRIN2	uc021pNCI-1	R	Q	110	VSTMGGSDLCRLRAPSAAAMQRSHS	VSTMGGSDLCRLQAPSAAAMQRSHS
		SNV	DAOA	uc001vqb.3	F	C	28	SRYTLGKIYFIGFQRSILLSKSENS	SRYTLGKIYFIGCQRSILLSKSENS
		SNV	DNAH8	uc021yzh.1	D	N	1019	FQKYKTLWTEDRDVKVKEFLANNPS	FQKYKTLWTEDRNVKVKEFLANNPS
		SNV	DNAH8	uc021yzh.1	E	K	4381	KGWALDTVTIHNEVLRQTKEEITSP	KGWALDTVTIHNKVLRQTKEEITSP
		SNV	FAM170A	uc003ksm.2	H	Y	323	RRSWSQCPGCVFHSPKDRNS	RRSWSQCPGCVFYSPKDRNS
		SNV	FGA	uc003iod.1	G	E	824	CQAANLNGIYYPGGSYDPRNNSPYE	CQAANLNGIYYPEGSYDPRNNSPYE
		SNV	FKSG83		P	S	164	RLTCAILNMIISPCLPHSFLLHQRN	RLTCAILNMIISSCLPHSFLLHQRN
		SNV	GADL1	uc003cep.2	G	R	488	KGSLMLGYQPHRGKVNFFRQVVISP	KGSLMLGYQPHRRKVNFFRQVVISP

		SNV	GLYATL2	uc009ymq.3	D	N	198	ERSLKYIERCLQDFLGFGVLGPEGQ	ERSLKYIERCLQNFLGFGVLGPEGQ
		SNV	GPRIN2	uc021pNCI-1	R	Q	110	VSTMGGSDLCRLRAPSAAAMQRSHS	VSTMGGSDLCRLQAPSAAAMQRSHS
		SNV	GRHL2	uc010mbu.3	H	Y	407	TYSYNNRSNKPIHRAYCQIKVFCDK	TYSYNNRSNKPIYRAYCQIKVFCDK
		FS deletion	GZMA	uc003jpm.3			248	DPRGPGVYILLSKKHLNWIIMTIKG	DPRGPGVYILLSKNTSTG
NCI-3903	**TMG24**	SNV	KANK4	uc001dah.4	A	T	228	GYPELASAIKQPASKLSSIQSQLLS	GYPELASAIKQPTSKLSSIQSQLLS
		SNV	KANK4	uc001dah.4	V	D	228	SSPRASTRIPELVQEGAEPPEGVVK	SSPRASTRIPELDQEGAEPPEGVVK
		SNV	KIAA0748	uc001sgn.4	P	F	389	APSQTLDSNPKVPCCTHSLPIEDPQ	APSQTLDSNPKVFCCTHSLPIEDPQ
		SNV	KIAA2022	uc004eby.3	E	K	1343	QRFMMASIEPLWEPMEHHGDPNIFY	QRFMMASIEPLWKPMEHHGDPNIFY
		SNV	KL	uc001uus.3	E	K	897	QLRVYYMQNYINEALKAHILDGINL	QLRVYYMQNYINKALKAHILDGINL
		SNV	KRT38	uc002hwq.1	R	K	21	SCPLGCTMAPGARNVSVSPIDIGCQ	SCPLGCTMAPGAKNVSVSPIDIGCQ
		SNV	KRT77	uc009zmi.3	A	V	353	QYELIAQRSKDEAEALYQTKYQELQ	QYELIAQRSKDEVEALYQTKYQELQ
		SNV	KRTAP20-2	uc011adg.2	G	R	57	GYGYGCCRPSCYGRYWSCGFY	GYGYGCCRPSCYRRYWSCGFY
		SNV	LALBA	uc001rrt.3	R	K	89	KLWCKSSQVPQSRNICDISCDKFLD	KLWCKSSQVPQSKNICDISCDKFLD
		SNV	MAB21L2		N	T	209	PNRVAEVKAEGFNLLSKECYSLTGK	PNRVAEVKAEGFTLLSKECYSLTGK
		SNV	MAB21L2	uc003ilw.3	E	K	58	EVQEPRFISSLSEIDARYEGLEVIS	EVQEPRFISSLSKIDARYEGLEVIS
		SNV	MGC26647	uc022ahc.1	R	K	235	FMDPATFINMYNRPIHITLDSEVVW	FMDPATFINMYNKPIHITLDSEVVW
NCI-3903	**TMG25**	SNV	MNDA	uc001fsz.1	E	K	282	DYSECKGVMEIKEASSVSDFNQNFE	DYSECKGVMEIKKASSVSDFNQNFE
		SNV	MOV10L1	uc011arq.1	G	R	403	LSRKQMTEPEPGGLVPPGGKTFIVV	LSRKQMTEPEPGRLVPPGGKTFIVV
		SNV	MUC15	uc001mqx.3	R	Q	284	RRLYDDRNEPVLRLDNAPEPYDVSF	RRLYDDRNEPVLQLDNAPEPYDVSF
		SNV	MUC16	uc002mkp.3	S	F	8189	ETSTETITRLPTSSIMTESAEMMIK	ETSTETITRLPTFSIMTESAEMMIK
		SNV	MUC16	uc002mkp.3	P	S	1490	SPSSPMSTFAIFPPMSTPSHELSKS	SPSSPMSTFAIFSPMSTPSHELSKS
		SNV	MUC21	uc021yuf.1	G	E	532	HGLNHGLGPGPGGNHGAPHRPRWSP	HGLNHGLGPGPGENHGAPHRPRWSP
		SNV	MYH8	uc002gmm.2	L	V	1304	RQLDEKDALVSQLSRSKQASTQQIE	RQLDEKDALVSQVSRSKQASTQQIE
		SNV	NEUROD6	uc022abi.1	G	R	269	EGPLSPPPINYNGIFSLKQEETLDY	EGPLSPPPINYNRIFSLKQEETLDY
		SNV	NLRP13	uc010ygg.2	E	K	147	QGCQDPNQEELDELEEETGNVQAQG	QGCQDPNQEELDKLEEETGNVQAQG
		SNV	NWD1	uc002nev.4	G	E	474	VHLILSACSGALGVLDTLQRVLLDP	VHLILSACSGALEVLDTLQRVLLDP
		SNV	OR10J3	uc010piu.2	P	F	80	SISETCYTVAIIPHMLSGLLNPHQP	SISETCYTVAIIFHMLSGLLNPHQP
		SNV	OR51G2	uc001lzr.1	L	F	115	FAQLFFIHCFSFLESSVLLSMAFDR	FAQLFFIHCFSFFESSVLLSMAFDR
NCI-3903	**TMG26**	SNV	OR56B1	uc009yev.1	A	T	173	NGLFVTPVPVLAAQRDYCSKNEIEH	NGLFVTPVPVLATQRDYCSKNEIEH

		SNV	OR5D16	uc010rio.2	A	V	127	ILFAVMAYDHFVAICNPLLYTVAIS	ILFAVMAYDHFVVICNPLLYTVAIS
		SNV	OR9K2	uc010spe.2	S	F	173	MSTRLCTQLVAGSYFCGCISSVIQT	MSTRLCTQLVAGFYFCGCISSVIQT
		SNV	PCDHA6	uc011dab.2	G	R	193	DVKINSDDNKQIGLLLKKSLDREEA	DVKINSDDNKQIRLLLKKSLDREEA
		SNV	PCDHAC1	uc003lih.2	V	A	435	PPLSTRRTITVSVADVNDNTPNFPQ	PPLSTRRTITVSAADVNDNTPNFPQ
		SNV	PDE1A	uc010zfq.2	S	F	403	QGDKEAELGLPFSPLCDRKSTMVAQ	QGDKEAELGLPFFPLCDRKSTMVAQ
		SNV	PDYN	uc021vzu.1	D	N	243	RRQFKVVTRSQEDPNAYSGELFDA	RRQFKVVTRSQENPNAYSGELFDA
		SNV	PEG3	uc010etr.2	S	F	1313	VTVHKNEPYEYGSSYTHTSFLTEPL	VTVHKNEPYEYGFSYTHTSFLTEPL
		SNV	PIK3C2G	uc010sic.2	E	K	703	LPLVLGSAPGWDERTVSEMHTILRR	LPLVLGSAPGWDKRTVSEMHTILRR
		SNV	PLCZ1	ENST00000541695	P	S	402	IKKNGQGNMVIIPA	IKKNGQGNMVIISA
		SNV	PTH2R	uc010zjb.2	E	K	49	QIVLVLKAKVQCELNITAQLQEGEG	QIVLVLKAKVQCKLNITAQLQEGEG
		FS deletion	TMEM132D	uc009zyl.1			577	GRGCTLQYQHAMVRVLTQFVAEAAG	GRGCTLQYQHAMVGS

Patient ID	TMG#	Mutation Type	Gene	Transcript ID	WT AA	Mut AA	AA position	Wild-type 25-mer	Mutated 25-mer
NCI-3926	**TMG1**	SNV	FAM86C1	uc009ysr.3	A	S	7	MAPEENAGSELLLQSFKRR	MAPEENSGSELLLQSFKRR
		SNV	ENSG00000228532	ENST00000449327	I	N	18	PKEGVKTENNDHINLKVAGQDGSVV	PKEGVKTENNDHNNLKVAGQDGSVV
		SNV	ENSG00000153230	ENST00000283225	S	F	237	RISQRQRQSKAFSNCVPHLIVVTVF	RISQRQRQSKAFFNCVPHLIVVTVF
		SNV	FAM5C	uc010pot.1	S	N	159	DYLQERFVQAALSYIACNSEGEFIC	DYLQERFVQAALNYIACNSEGEFIC
		SNV	LOC440295	uc002bhl.2	R	C	204	QEERLREQEERLREQEERLHEQEER	QEERLREQEERLCEQEERLHEQEER
		SNV	MRC1	uc001ipk.4	S	F	1046	GKGYPGGRRSSLSYEDADCVVIIGG	GKGYPGGRRSSLFYEDADCVVIIGG
		SNV	OR11H2	uc021rno.1	L	F	177	VCGFLWFLIPIVLISQKPFCGPNII	VCGFLWFLIPIVFISQKPFCGPNII
		SNV	OR11H2	uc021rno.1	L	F	177	VCGFLWFLIPIVLISQMPFCGPNII	VCGFLWFLIPIVFISQMPFCGPNII
		SNV	TCRBV9S1A1T	uc003vxf.3	A	V	91	VPNRFSPKSPDKAHLNLHINSLELG	VPNRFSPKSPDKVHLNLHINSLELG
		SNV	ENSG00000211941	ENST00000390601	S	N	54	AASGFTFSDYYMSWIRQAPGKGLEW	AASGFTFSDYYMNWIRQAPGKGLEW
		SNV	ENSG00000211941	ENST00000390601	I	V	56	SGFTFSDYYMSWIRQAPGKGLEWVS	SGFTFSDYYMSWVRQAPGKGLEWVS
		SNV	DUX2	uc031sid.1	A	P	240	GVSQPAPARGDFAYAAPAPPDGALS	GVSQPAPARGDFPYAAPAPPDGALS
NCI-3926	**TMG2**	SNV	TRIM49B	uc021qix.1	L	F	49	PCFYLNWKDSPFLVQCSECTKSTGQ	PCFYLNWKDSPFFVQCSECTKSTGQ

		SNV	USP17L17	uc031sdl.1	G	E	86	RPAAVGAGLQNMGNTCYVNASLQCL	RPAAVGAGLQNMENTCYVNASLQCL
		SNV	AK9	uc003ptr.4	S	L	367	YSVSFLGKIYCLSSEEALKPFLLNP	YSVSFLGKIYCLLSEEALKPFLLNP
		SNV	RPL19	uc002hrq.1	A	G	169	DQAEARRSKTKEARKRREERLQAKK	DQAEARRSKTKEGRKRREERLQAKK
		SNV	NES	uc001fpq.3	G	D	205	YQERVAHMETSLGQARERLGRAVQG	YQERVAHMETSLDQARERLGRAVQG
		SNV	COL11A1	uc009weh.3	G	E	1274	GAKGEAGAEGPPGKTGPVGPQGPAG	GAKGEAGAEGPPEKTGPVGPQGPAG
		SNV	PI15	uc003yam.3	N	K	75	SQNDMIAILDYHNQVRGKVFPPAAN	SQNDMIAILDYHKQVRGKVFPPAAN
		SNV	ATF5	uc010enq.2	S	P	126	DFFLDAPPLPPPSPPPLPPPPLPPA	DFFLDAPPLPPPPPPPLPPPPLPPA
		SNV	L1CAM	uc031tks.1	P	S	372	PQPEVTWRINGIPVEELAKDQKYRI	PQPEVTWRINGISVEELAKDQKYRI
		SNV	MSH2	uc002rvz.4	G	E	902	LILLTWKRKLRGGKRSACSRPERQN	LILLTWKRKLRGEKRSACSRPERQN
		SNV	MET	uc011kna.1	P	S	518	TGKKVSCSHREFP	TGKKVSCSHREFS
		SNV	CRELD2	uc031ryb.1	R	P	85	WIDSQDRPLRFLRPSAVRTGLSDSY	WIDSQDRPLRFLPPSAVRTGLSDSY
NCI-3926	**TMG3**	SNV	PAM	uc011cuz.2	V	A	56	PPTRLPKGVGFRVGGETGSKYFVLQ	PPTRLPKGVGFRAGGETGSKYFVLQ
		SNV	DROSHA	uc003jhi.2	P	L	922	NIMSRLGQDDPTPSRINHNERLEFL	NIMSRLGQDDPTLSRINHNERLEFL
		SNV	YTHDF2	uc021okf.1	G	E	360	PTRWVAPRNRGSGFGHNGVDGNGVG	PTRWVAPRNRGSEFGHNGVDGNGVG
		SNV	PARP4	uc001upl.3	Q	R	1059	CSPSCHSVSVKWQQLNPDVPEALQA	CSPSCHSVSVKWRQLNPDVPEALQA
		SNV	GALNT5	uc002tzg.3	H	Y	421	HIKALLPEDSGTHQVLRIDVTLSPR	HIKALLPEDSGTYQVLRIDVTLSPR
		SNV	AKAP6	uc010aml.3	P	L	695	VKKKHTRLGRVSPSSSSDIASSLGE	VKKKHTRLGRVSLSSSSDIASSLGE
		SNV	E2F4	uc002erz.3	S	T	323	SSSSSSSSSNSNSSSSSGPNPSTSF	SSSSSSSSSNSNTSSSSGPNPSTSF
		SNV	ZNF532	uc010xeg.2	T	S	891	FKSAPSTHSHAYTQHPGIKIGEPKI	FKSAPSTHSHAYSQHPGIKIGEPKI
		SNV	COL19A1	uc010kam.2	P	S	25	WFLWQVLNQQNIPQISIVVDGGKKV	WFLWQVLNQQNISQISIVVDGGKKV
		SNV	C1QTNF1	uc002jwt.3	P	S	92	LPNSVPSLCVSFPPGPGRKMGSRGQ	LPNSVPSLCVSFSPGPGRKMGSRGQ
		SNV	LOC150776	uc002tsz.3	E	K	14	DTSGSYTANDLDEMGQDSVRKTDEY	DTSGSYTANDLDKMGQDSVRKTDEY
		FS-insertion	PARP6	uc031qsq.1			236	PSVVDPTDPKTLAFNPKKKNYERLQ	PSVVDPTDPKTLSGL
NCI-3926	**TMG4**	SNV	UBR7	uc010auq.3	K	N	101	VPEQGKDDVREVKVEQNSEPCAGSS	VPEQGKDDVREVNVEQNSEPCAGSS
		SNV	GXYLT1	uc001rmt.4	A	T	91	IQPVEKMHLAVVACGERLEETMTML	IQPVEKMHLAVVTCGERLEETMTML
		SNV	SYVN1	uc009yqc.3	P	R	308	EPADQGPPPAPHPPPLLPQPPNFPQ	EPADQGPPPAPHRPPLLPQPPNFPQ
		SNV	SETX	uc010mzt.3	Y	H	2095	SGFAKTSVAASLYHTPSDSKEITLT	SGFAKTSVAASLHHTPSDSKEITLT
		SNV	NCAPH	uc002svz.1	R	Q	20	LPATMNNSSSETRGHPHSASSPSER	LPATMNNSSSETQGHPHSASSPSER
		SNV	NCAPH	uc010fhv.1	R	Q	9	MGPPGPETRGHPHSASSPSER	MGPPGPETQGHPHSASSPSER

		SNV	ENSG00000121152	ENST00000455200	R	Q	9	MNNSSSETRGHPHSASSPSER	MNNSSSETQGHPHSASSPSER
		SNV	PCIF1	uc002xqs.3	R	C	265	SNCEPVVSPSMFREIMNDIPIRLSR	SNCEPVVSPSMFCEIMNDIPIRLSR
		SNV	CHEK2	uc010gvh.1	K	E	282	DCLIKITDFGHSKILGETSLMRTLC	DCLIKITDFGHSEILGETSLMRTLC
		SNV	CHEK2	uc003adv.1	K	E	344	LLAVQITDFGHSKILGETSLMRTLC	LLAVQITDFGHSEILGETSLMRTLC
		SNV	TWIST1	uc022aah.1	A	S	195	LSYAFSVWRMEGAWSMSASH	LSYAFSVWRMEGSWSMSASH
		SNV	ENSG00000122691	ENST00000354571	G	V	127	RLSYAFSVWRMEGAWSMSASH	RLSYAFSVWRMEVAWSMSASH
NCI-3926	**TMG5**	SNV	MLLT4	uc021zim.1	T	S	8	MDGVVTVTPRSMDAETYVEG	MDGVVTVSPRSMDAETYVEG
		SNV	MLLT4	uc021zik.1	T	S	421	CDLTNMDGVVTVTPRSMDAETYVEG	CDLTNMDGVVTVSPRSMDAETYVEG
		SNV	FASTKD2	uc002vbx.3	S	L	504	TISSENLLDAVYSFCLMNYFPLAPF	TISSENLLDAVYLFCLMNYFPLAPF
		SNV	UBE3B	uc009zvj.2	P	S	420	ESQEPAHAQPASPQNVLPVKSLLKR	ESQEPAHAQPASSQNVLPVKSLLKR
		SNV	SEC14L1	uc021udx.1	L	F	461	SPFIDDNTRRKFLIYAGNDYQGPGG	SPFIDDNTRRKFFIYAGNDYQGPGG
		SNV	NCOR1	uc010cpb.2	Y	S	20	PNQGAFSTEQSRYPPHSVQYTFPNT	PNQGAFSTEQSRSPPHSVQYTFPNT
		SNV	CRYZ	uc001dgm.3	I	V	51	ILGTAGTEEGQKIVLQNGAHEVFNH	ILGTAGTEEGQKVVLQNGAHEVFNH
		SNV	AKAP9	uc003uli.3	R	C	1570	ERQIQEKTDIIDRLEQELLCASNRL	ERQIQEKTDIIDCLEQELLCASNRL
		SNV	STK39	uc002uea.3	R	Q	406	EEGKAAFSQEKSRRVKEENPEIAVS	EEGKAAFSQEKSQRVKEENPEIAVS
		SNV	MLLT6	uc002hqi.4	K	E	557	SPLLGAGIYTSNKDPISHSGGMLRA	SPLLGAGIYTSNEDPISHSGGMLRA
		SNV	SETDB1	uc009wmf.2	L	P	727	GKGVFINTGPEFLVGCDCKDGCRD	GKGVFINTGPEFPVGCDCKDGCRD
		SNV	SETDB1	uc009wmg.2	L	P	726	GKGVFINTGPEFLVGCDCKDGCRDK	GKGVFINTGPEFPVGCDCKDGCRDK
NCI-3926	**TMG6**	SNV	SORL1	uc001pxx.3	D	N	299	RENQEVILEEVRDFQLRDKYMFATK	RENQEVILEEVRNFQLRDKYMFATK
		SNV	CPEB2	uc003gnn.2	P	S	783	DWPHKAESKSYFPPKGYAFLLFQEE	DWPHKAESKSYFSPKGYAFLLFQEE
		SNV	LAMA5	uc021wfw.1	R	W	2601	ALQGARTQLRDVRAKKDQLEAHIQA	ALQGARTQLRDVWAKKDQLEAHIQA
		SNV	PABPC1L	uc010ggv.1	S	F	399	STMRTLSNPLLGSFQQPSSYFLPAM	STMRTLSNPLLGFFQQPSSYFLPAM
		SNV	ANKHD1-EIF4EBP3	uc011czh.1	M	I	851	SEPAPLTLTSPRMVAADNQDTSNLP	SEPAPLTLTSPRIVAADNQDTSNLP
		SNV	KIAA0556	uc010vco.2	P	L	44	LAMVSHLVGGILPTCEPTVPYHTIL	LAMVSHLVGGILLTCEPTVPYHTIL
		SNV	GOSR1	uc002hff.3	R	K	15	ETMAIEIEQLLARLTGVNDKMAEYT	ETMAIEIEQLLAKLTGVNDKMAEYT
		SNV	CNTNAP4	uc010chb.1	R	W	615	CEQEFTYYCKKSRLVNKQDGTPLSW	CEQEFTYYCKKSWLVNKQDGTPLSW
		SNV	CNTNAP4	uc010chb.1	P	S	435	CPDKSFGSKCKSPLGGFQGCMRLIS	CPDKSFGSKCKSSLGGFQGCMRLIS
		SNV	NAF1	uc010iqw.1	I	V	162	PPVLSDGDDDLQIEKENKNFPLKTK	PPVLSDGDDDLQVEKENKNFPLKTK

		SNV	SDHAP2	uc011btb.1	V	M	196	VWSGMCPEHRRVVQA	VWSGMCPEHRRVMQA
		SNV	SDHAP2	uc003fuu.4	H	Q	104	AKNTIVATGLRAHLLELHVCPHQHQ	AKNTIVATGLRAQLLELHVCPHQHQ
NCI-3926	**TMG7**	SNV	BRAF	uc003vwc.4	V	E	600	LTVKIGDFGLATVKSRWSGSHQFEQ	LTVKIGDFGLATEKSRWSGSHQFEQ
		SNV	ZNF343	uc010gao.1	H	Y	36	ENVETMKKLTQNHKAKGLPSNDTDC	ENVETMKKLTQNYKAKGLPSNDTDC
		SNV	ENSG00000004139	ENST00000457710	A	D	336	LQGKTKVFSDIGAIQSLKRLVSYST	LQGKTKVFSDIGDIQSLKRLVSYST
		SNV	SASS6	uc009wdz.3	K	E	194	QEQKVVLEENGEKNQVQLGKLEATI	QEQKVVLEENGEENQVQLGKLEATI
		SNV	NCOA1	uc010eye.3	I	T	481	LNLNNSPMEGTGISLAQFMSPRRQV	LNLNNSPMEGTGTSLAQFMSPRRQV
		SNV	OGFOD2	uc009zxs.1	S	N	52	LLYPDCGGGRLDSHRAFVVKYAPGQ	LLYPDCGGGRLDNHRAFVVKYAPGQ
		SNV	NBPF1	uc010oce.1	D	E	408	QHLQALLTPDEPDKSQGQDLQEQLA	QHLQALLTPDEPEKSQGQDLQEQLA
		SNV	DOPEY2	uc011aeb.2	P	S	856	NPFFGKLQMVTVPPIAPGILKVIAE	NPFFGKLQMVTVSPIAPGILKVIAE
		SNV	SNAPC4	uc004chh.3	P	S	750	RLLNRRLLLAVTPWVGDVVVPCTQA	RLLNRRLLLAVTSWVGDVVVPCTQA
		SNV	CNTRL	uc004bkx.1	V	L	226	LKPLQDLISLILVENPVVTLPHYLQ	LKPLQDLISLILLENPVVTLPHYLQ
		FS-deletion	KIAA1841	uc002sav.4			375	RCREDKIHTCIFVYIYI	RCREDKIHTCIFVYIYI
		SNV	TRPC1	uc003evc.3	L	R	508	LVAEGLFAFANVLSYLRLFFMYTTS	LVAEGLFAFANVRSYLRLFFMYTTS
NCI-3926	**TMG8**	SNV	ARHGEF17	uc001otu.3	S	L	1570	GLQPRCHREPPPSLRSPPETAPEPA	GLQPRCHREPPPLLRSPPETAPEPA
		SNV	SALL2	uc010tma.1	S	F	701	EMDSNEKTTQQSSLPPPPPPDSLDQ	EMDSNEKTTQQSFLPPPPPPDSLDQ
		SNV	ARMCX5-GPRASP2	uc022cbh.1	S	F	409	ASLEGGASAICESEPGTEEGAIGGS	ASLEGGASAICEFEPGTEEGAIGGS
		SNV	PTPRH	uc010esv.3	N	S	120	SSVGTVTTATAPNPVRNLTVEAQTN	SSVGTVTTATAPSPVRNLTVEAQTN
		SNV	PTPRH	uc002qjs.2	N	S	305	SSVEIVTSATAPNPVRNLTVEAQTN	SSVEIVTSATAPSPVRNLTVEAQTN
		SNV	TCEAL2	uc022car.1	E	K	209	NLQDPFYPRGPREFRGGCRAPRRDT	NLQDPFYPRGPRKFRGGCRAPRRDT
		SNV	SHROOM3	uc011cbx.2	G	S	1650	QSLSHDPVSGTQGLEKKVSPDPQKS	QSLSHDPVSGTQSLEKKVSPDPQKS
		SNV	NLGN3	uc011mps.2	R	Q	696	LAFAALYYRKDKRRQEPLRQPSPQR	LAFAALYYRKDKQRQEPLRQPSPQR
		SNV	AHDC1	uc021ojw.1	E	K	1210	LSSLEKLMMDWNEASSAPGYNWNQS	LSSLEKLMMDWNKASSAPGYNWNQS
		SNV	TMEM44	uc011bsv.2	H	N	24	WDWDYLDRCFARHRVCISFGLWICA	WDWDYLDRCFARNRVCISFGLWICA
		SNV	SNX29	uc002dby.5	S	F	104	EVLNKHELQRFYSLRHIASDVGRGR	EVLNKHELQRFYFLRHIASDVGRGR
		SNV	LAPTM5	uc001bsc.2	D	N	2	MDPRLSTVRQTCCC	MNPRLSTVRQTCCC
NCI-3926	**TMG9**	SNV	MAN1A1	uc003pym.2	A	V	486	LTCFAGGMFALGADAAPEGMAQHYL	LTCFAGGMFALGVDAAPEGMAQHYL
		SNV	MAPK8IP1	uc001nbr.3	S	F	341	ISEEEEGFDCLSSPERAEPPGGGWR	ISEEEEGFDCLSFPERAEPPGGGWR
		SNV	PZP	uc009zgm.1	T	I	101	VAEVGVTVPDTITEWK	VAEVGVTVPDTIIEWKAG

								AGAFCLSED	AFCLSED
		SNV	SLC4A8	uc010snk.2	R	C	454	TFGGLLGEATEGRISAIESLFGASM	TFGGLLGEATEGCISAIESLFGASM
		SNV	PHLDB2	uc003dye.4	P	S	499	AIFLFSPAILLLPISLLIGLFGYLE	AIFLFSPAILLLSISLLIGLFGYLE
		SNV	RYR2	uc001hyl.1	D	N	753	VSSPNQHLLRTDDVISCCLDLSAPS	VSSPNQHLLRTDNVISCCLDLSAPS
		SNV	DPY19L2	uc010sso.1	I	V	94	AVFAGAMPTMASIKLSTLHPIVNHP	AVFAGAMPTMASVKLSTLHPIVNHP
		SNV	FAM115C	uc011ktn.1	R	Q	479	KMLRGSGLPAVSRENPVASDSYEAA	KMLRGSGLPAVSQENPVASDSYEAA
		SNV	NBPF10	uc031poc.1	G	E	2580	CPRLSRELLDEKGPEVLQDSLDRCY	CPRLSRELLDEKEPEVLQDSLDRCY
		SNV	ENSG00000163386	ENST00000369339	G	E	357	GPRLSRELLDEKGPEVLQDSLDRCY	GPRLSRELLDEKEPEVLQDSLDRCY
		FS-deletion	TGFB2	uc001hll.3			216	CCCCCCCCCFRQTLSLSLCHRLEYS	CCCCCCCCCFRQTLSLSLSQARVQWHDHSSLQP
		SNV	PCLO	uc003uhx.2	A	T	2955	VVYKLPFGRSCTAQQPATTLPEDRF	VVYKLPFGRSCTTQQPATTLPEDRF
NCI-3926	**TMG10**	SNV	RGAG1	uc011msr.1	D	A	109	SGALSPLLMPASDSGALSPLLMPAL	SGALSPLLMPASASGALSPLLMPAL
		FS-deletion	CASP5	uc010ruz.1			23	FIFLIEDSGKKKRRKNFEAMFKGIL	FIFLIEDSGKKKGVRILKLCSKVSFRVDWITS
		FS-deletion	CASP5	NM_004347			10	MAEDSGKKKRRKNFEAMFKGIL	MAEDSGKKKGVRILKLCSKVSFRVDWITS
		SNV	CDKL5	uc022btn.1	R	C	234	PSEQMKLFYSNPRFHGLRFPAVNHP	PSEQMKLFYSNPCFHGLRFPAVNHP
		SNV	LRP2	uc002ues.3	I	M	777	IFKQKIDGTGREILAANRVENVESL	IFKQKIDGTGREMLAANRVENVESL
		SNV	LRP2	uc010zdf.1	I	M	640	LDTDERHCIGREILAANRVENVESL	LDTDERHCIGREMLAANRVENVESL
		SNV	TRIL	uc003szt.3	P	L	503	QQPSPSVAAAAGPAPQSLDLHKKPQ	QQPSPSVAAAAGLAPQSLDLHKKPQ
		SNV	MUC5B	uc001lta.3	I	T	2095	PTTRGSTVTPSSIPGTTHTATVLTT	PTTRGSTVTPSSTPGTTHTATVLTT
		SNV	PSG4	uc002owb.4	E	K	264	RSGENLYLSCFAESNPRAQYSWTIN	RSGENLYLSCFAKSNPRAQYSWTIN
		SNV	SPARCL1	uc011cdd.2	D	N	333	ADQQGKPHCVCQDPVTCPPTKPLDQ	ADQQGKPHCVCQNPVTCPPTKPLDQ
		SNV	SLC38A3	NM_006841	G	S	81	GMSVFNLSNAIMGSGILGLAYAMAN	GMSVFNLSNAIMSSGILGLAYAMAN
		SNV	GOLGA6B	uc010uks.1	E	D	421	LWDQEERLWKKEERLQKQEERLALS	LWDQEERLWKKEDRLQKQEERLALS
NCI-3926	**TMG11**	SNV	KRT7	uc001saa.1	Y	N	283	MAKCSRAEAEAWYQTKFETLQAQAG	MAKCSRAEAEAWNQTKFETLQAQAG
		SNV	PCDHB17	uc003lis.3	R	C	461	PAFTQTSYTLFVRENNSPALHIGSV	PAFTQTSYTLFVCENNSPALHIGSV
		SNV	PLEKHA6	uc009xbc.1	S	F	67	PVYYDELDAASSSLRRLSLQPRSHS	PVYYDELDAASSFLRRLSLQPRSHS
		SNV	SLIT2	uc003gps.1	G	S	1022	NNYTCLCPPEYTGELCEEKLDFCAQ	NNYTCLCPPEYTSELCEEKLDFCAQ
		SNV	ENSG00000145147	ENST00000273739	A	T	1034	NNYTCLCPPEYTAANLNEVEKGELC	NNYTCLCPPEYTTANLNEVEKGELC
		SNV	CSMD1	uc022aqr.1	R	K	1407	GMPQNGTRYGDSREAGDTVTFQCDP	GMPQNGTRYGDSKEAGDTVTFQCDP

AA = Amino acid. SNV = non-synonymous single nucleotide variant. FS = frameshift. Green highlight = identified immunogenic; NFS = Non-frameshift

Supplementary Table 3. Binding affinity of candidate immunogenic peptides to the patient-specific HLA-I molecules based on prediction algorithms

Patient ID	Mutated protein	Wild-type epitope	Mutated epitope	Affinity wild-type (nM)	Affinity mutant (nM)	Rank wild-type (%-tile)	Rank mutant (%-tile)	Allele
NCI-3998	MAGEA6$_{E168K}$	EVDPIGHVYI	**K**VDPIGHVYI	12	6	0.4	0.2	C*05:01
		EVDPIGHVYIF	**K**VDPIGHVYIF	9	5	0.3	0.2	C*05:01
		EVDPIGHVY	**K**VDPIGHVY	36	77	0.35	0.3	A*01:01
		LMEVDPIGHVY	LM**K**VDPIGHVY	394	47	2.8	0.5	B*15:01
	PDS5A$_{Y1000F;H1007Y}$	PEYVVPYMIH	PE**F**VVPYMI**Y**	6823	105	4.05	0.25	B*18:01
		YVVPYMIHLL	**F**VVPYMI**Y**LL	6	6	0.4	0.4	C*03:03
		SLLPEYVVPY	SLLPE**F**VVPY	29	23	0.55	0.5	B*15:01
		LSLLPEYVVPY	LSLLPE**F**VVPY	3278	3232	0.7	0.7	A*01:01
		LLPEYVVPY	LLPE**F**VVPY	43	58	0.6	0.5	B*15:01
		YMIHLLAH	YMI**Y**LLAH	93	74	1.1	0.9	B*15:01
	MED13$_{P1691S}$	VQIIPCQY	VQII**S**CQY	253	165	0.75	0.55	A*30:02
		VQIIPCQY	VQII**S**CQY	81	48	0.9	0.6	B*15:01
		VSVQIIPCQY	VSVQII**S**CQY	202	148	0.8	0.65	A*30:02
		SVQIIPCQY	SVQII**S**CQY	605	300	1.35	0.95	A*30:02
		VSVQIIPCQYL	VSVQII**S**CQYL	17	17	1	1	C*03:03
		SVQIIPCQY	VSVQII**S**CQY	5190	5168	1.6	1.6	A*01:01
NCI-3784	FLNA$_{R2049C}$	RVRVSGQGL	**C**VRVSGQGL	17	553	0.5	2	B*07:02
		QSEIGDASRV	QSEIGDAS**C**V	15084	14548	5.85	4.7	A*01:01
	KIB16B$_{L1009P}$	ALARLERRHSA	A**P**ARLERRHSA	6270	33	19.9	1	B*07:02
		ALARLERRHS	A**P**ARLERRHS	25367	1572	32	1.5	B*07:02
	SON$_{R1927C}$ *	RARSRTPSR	RARSRTPS**C**	5568	178	2.4	1.2	B*07:02
		TPSRRSRSH	TPS**C**RSRSH	503	1188	1.2	1.5	B*07:02
		TPSRRSR	TPS**C**RSRS	10901	4212	3.05	1.8	B*07:02
NCI-3903	KIF1BP$_{P246S}$	EHNAYHPIEWAI	EHNAYH**S**IEWAI	333	347	0.3	0.3	B*38:01
		HNAYHPIEWAI	HNAYH**S**IEWAI	12630	12554	5.4	5.4	B*38:01
		NAYHPIEWAI	NAYH**S**IEWAI	16	21	0.5	0.6	C*12:03
		AYHPIEWAI	AYH**S**IEWAI	158	115	0.6	0.6	A*24:02
		YHPIEWAI	YH**S**IEWAI	2742	308	1.1	0.3	B*38:01
		HPIEWAI	H**S**IEWAI	n.d.	n.d.	n.d.	n.d.	n.d.

Predictions determined by IEDB[1], interrogating 8-11-mer peptides. Candidate minimal mutated epitopes were synthesized based on <500 nM affinity or top 2 percentile (%-tile) rank. Binding affinity and percentile rank for each peptide and HLA allele specified is shown.

The mutated amino acid is bolded in red. Peptides highlighted in grey or yellow were recognized. The most immunogenic minimal neo-epitopes, which showed a greater reactivity either by IFN-γ ELISPOT or percentage 4-1BB upregulation compared to the rest of the peptides tested, are highlighted in yellow. *The SON mutation-specific lymphocytes did not recognize any of the candidate minimal epitopes tested thus far

Supplementary Table 4. Amino acid sequence of the functional mutation-reactive T cell receptors isolated from the peripheral blood CD8^{+}PD-1^{+} subset of NCI-3998

Patient ID	Reactivity	TRA rank/ TRB rank (T cell population of origin)	TRAV /TRAJ	TCR alpha chain V-J amino acid sequence (CDR3 highlighted)	TRBV/TRBJ	TCR beta chain V-D-J amino acid sequence (CDR3 highlighted)
NCI-3998	MAGEA6$_{E168K}$ –specific TCR	A1/B1 (TMG1-enriched)	TRAV21*01/ TRAJ21*01F	METLLGLLILWLQLQWVSSKQEVTQIPAALSVPEGENLVLNCSFTDSAIYNLQWFRQDPGKGLTSLLLIQSSQREQTSGRLNASLDKSSGRSTLYIAASQPGDSATYLCAVDNFNKFYFGSGTKLNVKP	TRBV7-3*01/ TRBJ1-2*01	MGTRLLCWAALCLLGADHTGAGVSQTPSNKVTEKGKYVELRCDPISGHTALYWYRQSLGQGPEFLIYFQGTGAADDSGLPNDRFFAVRPEGSVSTLKIQRTERGDSAVYLCASSSQGGYGYTFGSGTRLTVV
	MAGEA6$_{E168K}$ –specific TCR	A2/B2 (TMG1-enriched)	TRAV39*01/ TRAJ58*01	MKKLLAMILWLQLDRLSGELKVEQNPLFLSMQEGKNYTIYCNYSTTSDRLYWYRQDPGKSLESLFVLLSNGAVKQEGRLMASLDTKARLSTLHITAAVHDLSATYFCAGSGSRLTFGEGTQLTVNP	TRBV7-6*01/ TRBJ1-2*01	MGTSLLCWVVLGFLGTDHTGAGVSQSPRYKVTKRGQDVALRCDPISGHVSLYWYRQALGQGPEFLTYFNYEAQQDKSGLPNDRFSAERPEGSISTLTIQRTEQRDSAMYRCASSFDRGYGYTFGSGTRLTVV
	PDS5A$_{Y1000F;H1007Y}$ –specific TCR	A1/B2 (TMG3-enriched)	TRAV38-1*01/ TRAJ53*01	MTRVSLLWAVVVSTCLESGMAQTVTQSQPEMSVQEAETVTLSCTYDTSENNYYLFWYKQPPSRQMILVIRQEAYKQQNATENRFSVNFQKAAKSFSLKISDSQLGDTAMYFCAFTELNSGGSNYKLTFGKGTLLTVNP	TRBV27*01/ TRBJ2-2*01	MGPQLLGYVVLCLLGAGPLEAQVTQNPRYLITVTGKKLTVTCSQNMNHEYMSWYRQDPGLGLRQIYYSMNVEVTDKGDVPEGYKVSRKEKRNFPLILESPSPNQTSLYFCASSLSGGLLRTGELFFGEGSRLTVL
	MED13$_{P1691S}$ –specific TCR	A1/B1 (TMG5-enriched)	TRAV12-1*01/ TRAJ27*01	MISLRVLLVILWLQLSWVWSQRKEVEQDPGPFNVPEGATVAFNCTYSNSASQSFFWYRQDCRKEPKLLMSVYSSGNEDGRFTAQLNRASQYISLLIRDSKLSDSATYLCVVNTNAGKSTFGDGTTLTVKP	TRBV9*01/ TRBJ2-1*01	MGFRLLCCVAFCLLGAGPVDSGVTQTPKHLITATGQRVTLRCSPRSGDLSVYWYQQSLDQGLQFLIQYYNGEERAKGNILERFSAQQFPDLHSELNLSSLELGDSALYFCASSGRVTGGFYNEQFFGPGTRLTVL
	MED13$_{P1691S}$ –specific TCR	A2/B2 (TMG5-enriched)	TRAV12-2*01/ TRAJ29*01	MKSLRVLLVILWLQLSWVWSQQKEVEQNSGPLSVPEGAIASLNCTYSDRGSQSFFWYRQYSGKSPELIMFIYSNGDKEDGRFTAQLNKASQYVSLLIRDSQPSDSATYLCASSGGNTPLVFGKGTRLSVIA	TRBV27*01/ TRBJ2-7*01	MGPQLLGYVVLCLLGAGPLEAQVTQNPRYLITVTGKKLTVTCSQNMNHEYMSWYRQDPGLGLRQIYYSMNVEVTDKGDVPEGYKVSRKEKRNFPLILESPSPNQTSLYFCASSFGGAYEQYFGPGTRLTVT

The amino acid sequences of the TRAV-TRAJ or the TRBV-TRBD-TRBJ rearrangements, encoding for the hypervariable region of the TRA and TRB genes, used to construct each TCR are shown. The amino acid sequence of the complementarity determining region 3 (CDR3) important for peptide recognition is highlighted in grey.

Supplementary Table 5. Relative frequency of T cell reactivities in the circulating or tumor-infiltrating T cell subsets targeting mutated neoantigens, self-antigens, and the autologous tumor cell lines

		Peripheral blood				Tumor	
		CD8^{+}PD-1^{+}		CD8^{+}PD-1^{hi}		CD8^{+}PD-1^{+}	
Patient ID		**Percentage 4-1BB^{+}**	**Percentage of total reactivities detected**	**Percentage 4-1BB^{+}**	**Percentage of total reactivities detected**	**Percentage 4-1BB^{+}**	**Percentage of total reactivities detected**
NCI-3998	MAGEA6$_{E168K}$ (TMG1)	2.4	10.0	2.9	8.8	3.8	30.1
	PDS5A$_{Y1000F;H1007Y}$ (TMG3)	0.6	2.5	0.5	1.5	0.2	1.6
	MED13$_{P1691S}$ (TMG5)	0.3	1.3	N.D.	N.D.	0.9	7.4
	Mutated antigens	**3.3**	**13.8**	**3.4**	**10.3**	**4.9**	**40.2**
	NY-ESO-1	20.7	86.2	29.7	89.7	7.3	59.8
	Self-antigens	**20.7**	**86.2**	**29.7**	**89.7**	**7.3**	**59.8**
	3998mel	9.5		7.2			11.2
NCI-3784	FLNA$_{R2049C}$ (TMG3)	0.4	16.0	1.4	26.4	0.4	16.0
	KIB16B$_{L1009P}$ (TMG5)	0.4	16.0	0.4	7.5	0.6	24.0
	SON$_{R1927C}$ (TMG8)	1	40.0	0.6	11.3	0.6	24.0
	Mutated antigens	**1.8**	**72.0**	**2.4**	**45.3**	**1.6**	**64.0**
	MAGEA3	N.D.	**N.D.**	0.8	15.1	N.D.	N.D.
	GP100	0.7	28.0	2.1	39.6	0.9	36.0
	Self-antigens	**0.7**	**28.0**	**2.9**	**54.7**	**0.9**	**36.0**
	3784mel	*24.6		*44.9			*45.2
NCI-3903	KIF1BP$_{P246S}$ (TMG9)	1.3	39.4			5.8	75.3
	TMG4 (antigen unknown)	N.D.	N.D.			0.3	3.9
	Mutated antigens	**1.3**	**39.4**			**6.5**	**79.2**
	SSX2	2.0	60.6			1.6	20.8
	Self-antigens	**2.0**	**66.6**			**1.6**	**20.8**
	3903mel	7.8					10.2
NCI-3926	**Mutated antigens**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**
	NY-ESO-1	1.7	100.0	1.4	100.0	3.4	70.8
	MART1	N.D.		N.D.		0.5	10.4
	GP100	N.D.		N.D.		0.9	18.8
	Self-antigens	**1.7**	**100.0**	**1.4**	**100.0**	**4.8**	**100.0**
	3926mel	*6.3		*7.7			*13.3

The absolute and relative frequency of circulating or tumor-infiltrating CD8^{+}PD-1^{+} T cells targeting mutations, self-antigens, and the corresponding autologous tumor cell lines (3998mel, 3784mel, 3903mel, or 3926mel) is shown. Recognition of mutated antigens (TMGs), self-antigens (NY-ESO-1, MAGEA3, SSX2, MART1, GP100, and TYR), and the autologous tumor cell line for each of the patients was evaluated simultaneously in one experiment. IFN-γ ELISPOT and 4-1BB up-regulation were analyzed at 20 h. Only the frequencies from the conditions that demonstrated >40 spots and >twice the background by IFN-γ ELISPOT are shown. For subjects NCI-3998 and 3903 the frequency of T cells recognizing a given antigen was based on the percentage 4-1BB up-regulation at 20 h after coculture. Data are gated on CD3^{+} cells. The frequency of 4-1BB expression against the irrelevant control was subtracted. For subjects NCI-3784 and 3926 the frequency of the reactivities was calculated based on IFN-γ ELISPOT data, as the frequencies were low and sometimes undetectable over background using 4-1BB upregulation. N.D. = Not detected. *The frequency of tumor-reactive cells for subjects NCI-3784 and NCI-3926 using IFN-γ ELISPOT was off-scale. For these, the frequency of autologous tumor-reactive cells was based on the percentage of 4-1BB up-regulation. Data are representative of at least two independent experiments

Supplementary Table 6. Summary of TRB overlap between circulating and tumor-resident CD8^{+} lymphocyte subsets

			PBMC																						
			3903			3926			3998				3992				3713			3759			3784		
			CD8+	CD8+PD-1-	CD8+PD-1+	CD8+	CD8+PD-1-	CD8+PD-1+	CD8+	CD8+PD-1-	CD8+PD-1+	CD8+PD-1hi	CD8+	CD8+PD-1-	CD8+PD-1+	CD8+PD-1hi	CD8+	CD8+PD-1-	CD8+PD-1+	CD8+	CD8+PD-1-	CD8+PD-1+	CD8+	CD8+PD-1-	CD8+PD-1+
Fresh Tumor	3903	CD8+	0.227	0.262	0.597																				
		CD8+PD-1-	0.396	0.382	0.203																				
		CD8+PD-1+	0.097	0.133	0.630																				
	3926	CD8+				0.134	0.119	0.190																	
		CD8+PD-1-				0.134	0.118	0.099																	
		CD8+PD-1+				0.094	0.072	0.316																	
	3998	CD8+							0.123	0.081	0.445	0.307													
		CD8+PD-1-							0.114	0.101	0.140	0.045													
		CD8+PD-1+							0.098	0.060	0.484	0.363													
	3992	CD8+											0.420	0.261	0.525	0.371									
		CD8+PD-1-											0.449	0.307	0.468	0.245									
		CD8+PD-1+											0.211	0.035	0.576	0.710									
	3713	CD8+															0.414	0.352	0.388						
		CD8+PD-1-															0.465	0.438	0.271						
		CD8+PD-1+															0.067	0.041	0.290						
	3759	CD8+																		0.157	0.104	0.467			
		CD8+PD-1-																		0.264	0.256	0.134			
		CD8+PD-1+																		0.055	0.010	0.482			
	3784	CD8+																					0.215	0.200	0.228
		CD8+PD-1-																					0.209	0.206	0.081
		CD8+PD-1+																					0.096	0.083	0.256

Analysis of TRB overlap of nucleotide sequences encoding for the variable V-D-J region of the TRB gene was performed using immunoSEQ (Adaptive Biotechnologies) using the following formula (Sample TCRB overlap between population A and B = [shared sequence reads in A + shared sequence reads in B]/∑sequence reads in A + B). A TRB overlap of 1 represents 100% overlap between two populations. The cells were color coded based on lower (yellow) to greater (blue) TRB overlap

Supplementary Table 7. Relative frequency of the specificities detected in the TIL infusion product of subjects NCI-3998, 3784, 3903, 3926

Patient ID	Clinical outcome in response to TIL therapy	Specificities detected in the infusion bag
NCI-3998	NR	TMG1 (MAGEA6$_{E>K}$), TMG5 (MED13$_{P>S}$), NY-ESO-1
NCI-3784	CR	TMG3 (FLNA$_{R>C}$), TMG4, TMG5 (KIF16B$_{L>P}$), TMG8 (SON$_{R>C}$), GP100
NCI-3903	CR	TMG8, TMG9 (KIF1BP$_{P>S}$), SSX2
NCI-3926	NR	MART1, GP100, TYR, NY-ESO-1

Clinical outcome of the patients following treatment with non-myeloablative preparative regimen, TIL, and high-dose IL-2 was evaluated using RECIST criteria. CR = complete responder; NR = non-responder. The TIL infusion bag was co-incubated with autologous DCs transfected with the autologous TMG RNA encoding for mutated neoantigens identified by exome sequencing, or with RNA encoding for self-antigens MART1, GP100, TYR, NY-ESO-1, MAGEA3, and SSX2. IFN-γ ELISPOT at 20 h was used to evaluate reactivity. Reactivities >40 spots and >than twice the background are shown. The specific antigen recognized encoded by the TMG is shown in parenthesis. TIL infusion products were generated as previously described[2]

Supplementary Table 8. Subjects included in the phenotypic characterization of TIL and circulating lymphocytes

Variable/trait	**Total (%)**
Total no. patients	18
Sex	
Male	14 (78)
Female	4 (22)
Age	
31-40	4 (22)
41-50	3 (17)
51-60	9 (50)
61-70	2 (11)
Prior Treatment	
Surgery	17 (94)
Chemotherapy	2 (11)
Radiotherapy	2 (11)
Immunotherapy	12 (67)
Any 2 or more	13 (72)
Any 3 or more	8 (44)
No treatment	1 (5)

Supplementary Table 9. Reactivity of circulating CD8^{+}PD-1^{+} T cell replicate cultures derived from subjects NCI-3713 or 3784

IFN-γ ELISPOT NCI-3713 circulating T cell subsets after *in vitro* expansion (spots/2 ×10^{4} cells)

		WDR46$_{T>I}$		SRPX$_{P>L}$		AFMID$_{A>V}$		HELZ2$_{D>N}$		CENPL$_{P>L}$		AHNAK$_{S>F}$		PRDX3$_{P>L}$			
T cell subsets	DMSO	WT	MUT	WT	MUT	WT	MUT	WT	MUT	WT	MUT	WT	MUT	WT	MUT	3713mel	Anti-CD3
CD8^{+}PD-1^{-} 3 × 10^{3} /1	1	0	2	3	5	1	3	3	1	2	7	5	3	2	3	2	**1447**
CD8^{+}PD-1^{-} 3 × 10^{3} /2	0	0	0	2	1	4	2	0	2	7	1	0	2	5	3	2	**1428**
CD8^{+}PD-1^{+} 3 × 10^{3} /1	24	12	**142**	8	**266**	5	**52**	109	**466**	5	**74**	3	**49**	79	15	**1156**	**1438**
CD8^{+}PD-1^{+} 3 × 10^{3} /2	1	16	**318**	14	**172**	4	**61**	17	**509**	13	**104**	10	14	10	**176**	**1030**	**1288**
CD8^{+}PD-1^{+} 1 × 10^{3} /3	5	1	**213**	3	**215**	0	4	88	**294**	6	**44**	3	3	7	18	**967**	**1231**
CD8^{+}PD-1^{+} 1 × 10^{3} /4	7	1	18	2	**157**	42	**177**	21	**274**	14	**339**	11	19	15	**331**	**867**	**1406**
CD8^{+}PD-1^{hi} 1 × 10^{3} /1	5	8	**80**	4	**172**	7	1	0	**378**	11	**81**	1	5	4	45	**764**	**601**
CD8^{+}PD-1^{hi} 3 × 10^{3} /2	3	5	**287**	4	**95**	87	164	10	**206**	2	**361**	7	22	8	**138**	**994**	**1205**

IFN-γ ELISPOT NCI-3784 circulating T cell subsets after *in vitro* expansion (spots/2 ×10^{4} cells)

T cell subsets	DC + irrel.	DC+TMG3	DC+TMG5	DC+TMG8	3784 mel	anti-CD3
CD8^{+}PD-1^{-} 3.5 × 10^{3} /1	1	5	2	9	**305**	**1147**
CD8^{+}PD-1^{-} 3.5 × 10^{3} /2	2	3	2	3	**109**	**1478**
CD8^{+}PD-1^{+} 3.5 × 10^{3} /1	10	**178**	**57**	**115**	**1003**	**1243**
CD8^{+}PD-1^{+} 3.5 × 10^{3} /2	7	**297**	**58**	**201**	**1142**	**739**
CD8^{+}PD-1^{+} 1.5 × 10^{3} /3	8	**149**	**314**	**196**	**792**	**932**
CD8^{+}PD-1^{+} 1.5 × 10^{3} /4	50	**280**	**118**	**325**	**1147**	**1277**
CD8^{+}PD-1^{hi} 1.5 × 10^{3} /1	1	**533**	0	**273**	**1545**	**953**
CD8^{+}PD-1^{hi} 1.5 × 10^{3} /2	0	**364**	**48**	**581**	**1324**	**1427**

The specified circulating T cell subsets were sorted from pretreatment PBMC from subjects NCI-3713 or NCI-3784. Replicates of each T cell population, each containing the number of T cells indicated, were expanded independently in separate culture vessels for 15 days and evaluated for recognition of autologous cells pulsed with the minimal mutated neoepitopes (NCI-3713), or with autologous DCs electroporated with NCI-3784 TMG3, 5, and 8, encoding for FLNA$_{R>C}$, KIF16B$_{L>P}$, and SON$_{R>C,}$ respectively (NCI-3784), and the corresponding autologous tumor cell lines. T cells cultured with autologous cells pulsed with DMSO or irrelevant TMG, and stimulated with plate-bound anti-CD3 were used as controls. The number of spots/2 × 10^{4} cells is shown. Reactivities >40 spots, and >than twice the background were considered positive and are shown underlined and bold. >500 spots is off-scale

References

1 Vita, R. *et al.* The immune epitope database (IEDB) 3.0. *Nucleic acids research* **43**, D405-412, doi:10.1093/nar/gku938 (2015).

2 Rosenberg, S. A. *et al.* Durable complete responses in heavily pretreated patients with metastatic melanoma using T cell transfer immunotherapy. *Clinical cancer research : an official journal of the American Association for Cancer Research* **17**, 4550-4557, doi:10.1158/1078-0432.CCR-11-0116 (2011).