

Supplementary Table 1. Candidate HLA-A*0201-binding epitopes indentified from 2098 mel.

No.	Mutated peptide	WT Peptide	Protein change	cDNA change	Predicted HLA-A*0201 binding affinity (nM)		Gene	Gene ID	Expressed gene	IFN- γ (pg/ml)
					Mutated	WT				
1	<u>FLLGKTSSV</u> ^a	FLQGKTSSV	p.Q136L ^b	c.299A>T ^c	4	9	ZNF559	uc002mle.2	WT ^d	130
2	YMFSDC <u>STSL</u>	YMFSDRSTSL	p.R91C	c.271G>A	4	8	TRPC6	uc001pgk.2	NA	<30
3	SLLSLLYAL	SSL S LLYAL	p.S32L	c.95C>T	4	374	SERPINB11	uc002ljk.2	NA	172
4	LMMPFSIVYI	LYMPFSIVYI	p.V76M	c.226G>A	4	20	HTR1F	uc003dqr.2	NA	75
5	GLFGDIYLA	G S FGDIYLA	p.S27L	c.80_81CC>TA	6	1312	CSNK1A1	uc003lqw.1	Mut/WT	41,925
6	<u>FQLNQSF</u> EI	SQLNQSFEI	p.S1281F	c.3842G>A	6	53	UNC13A	uc002nhd.1	Mut/WT	117
7	FILDAVQRV	SILDAVQRV	p.S613F	c.1838G>A	6	44	PXDNL	uc003xqu.2	NA	<30
8	<u>HLFCV</u> FYGL	RLFCVFYGL	p.R112H	c.335C>T	6	5	KCNK5	uc003oon.1	WT	67
9	FLLGKTSSV	FLQGKTSSV	p.Q136L	c.299A>T	7	9	ZNF559	uc002mlh.1	WT	NT ^d
10	MMPF S IVYIV	VMPF S IVYIV	p.V76M	c.226G>A	7	17	HTR1F	uc003dqr.2	NA	NT
11	SLAPLSPRV	SLAPLSPRA	p.A310V	c.929C>T	7	79	CNKSR1	uc001blm.2	NA	39
12	LLIASVTWLL	FLIASVTWLL	p.F254L	c.762G>A	7	3	MAR11	uc003jfo.2	NA	<30
13	RMLDKNPEV	RMLDKNPES	p.S433V	c.1297-1298TC>GT	7	1722	CAMKK2	uc001txt.1	Mut/WT	<30
14	MMPF S IVYI	VMPF S IVYI	p.V76M	c.226G>A	8	29	HTR1F	uc003dqr.2	NA	NT
15	HLMDGDLGL	NLMDGDLGL	p.N558H	c.1672C>A	10	11	C1S	uc001qsj.1	Mut/WT	222
16	LLGDPGWRV	LLGDPGRRV	p.R72W	c.214T>C	11	1081	KCNA6	uc001qnf.1	NA	<30
17	FSFSLDFLV	FSFPLDFLV	p.P251S	c.751T>C	11	17	GPR174	uc004edg.1	NA	<30
18	GLFGDIYLAI	G S FGDIYLAI	p.S27L	c.80_81CC>TA	12	2394	CSNK1A1	uc003lqw.1	Mut/WT	31,538
19	SLADEAEVYL	SLADEAEVHL	p.H225Y	c.673C>T	12	39	GAS7	uc002gmi.1	Mut/WT	57,938
20	MLFLRFCYI	MLFLRFRI	p.R55C	c.247G>A	12	116	WDR47	uc001dww.1	Mut/WT	<30
21	FLQKYTVKL	FLQEYTVKL	p.E183 K	c.547C>T	13	3	GSTA4	uc003pbc.1	NA	32
22	CLFLEIYTV	CLFLGIYTV	p.G33E	c.98G>A	13	10	OR8D4	uc001pzj.1	NA	185
23	MSFSLFYFL	MSSSHLFYFL	p.S13F	c.86G>A	14	151	IGF1	uc001tjn.2	NA	NT
24	LLIASVTWL	FLIASVTWL	p.F254L	c.762C>C	15	4	MAR11	uc003jfo.2	NA	NT
25	TMSFSLFYFL	TMSSSHLFYFL	p.S13F	c.86G>A	16	14	IGF1	uc001tjm.2	NA	<30
26	FLEIYTVTV	FLGIYTVTV	p.G33E	c.98G>A	17	6	OR8D4	uc001pzj.1	NA	<30
27	YLTSLACVEI	YPTSLACVEI	p.P1039L	c.3116C>T	17	21684	BRCA2	uc001uub.1	Mut/WT	<30
28	LLADQNFKFI	LLADQNLKFI	p.L190F	c.568C>T	20	30	RRP1B	uc002zdk.1	Mut/WT	<30
29	SLSTSLSSV	SLSTSSSV	p.S1084L	c.3251G>A	21	189	CNTN5	uc001pga.1	NA	72
30	AMIAKISNEL	AMITKISNEL	p.T160A	c.478T>C	22	33	HAUS3	uc003ges.1	Mut/WT	<30
31	HLMDGDLGLI	NLMDGDLGLI	p.N558H	c.1672A>C	22	20	C1S	uc001qsj.1	Mut/WT	NT
32	ALGTLHTNV	ALGTLHTNL	p.L1577V	c.4729C>G	23	143	NOTCH2	uc001eik.1	Mut/WT	<30
33	TLLGDPGWRV	TLLGDPGRRV	p.R to W	c.214C>T	23	835	KCNA6	uc001qnf.1	NA	NT
34	SVVDVFEQL	SVVDVFSQL	p.S1281F	c.3842G>A	28	323	UNC13A	uc002nhd.1	Mut/WT	<30
35	LLQAYRLISV	PLQAYRLISV	p.P819L	c.2456_2457CT>TG	28	1091	USP29	uc002qny.1	NA	<30
36	MLSILALVRV	MLSILALVGV	p.G65R	c.193G>A	31	19	C15orf32	uc002brc.1	NA	<30
37	VLMMPFSIV	VLYMPFSIV	p.V76M	c.226G>A	33	189	HTR1F	uc003dqr.2	NA	NT
38	ILNAMI AKI	ILNAMITKI	p.T160A	c.478T>C	34	36	HAUS3	uc003ges.1	Mut/WT	4,180
39	GLNETIAKL	GLDETIAKL	p.D990N	c.2968C>T	35	34	MYH4	uc002gmn.1	NA	44
40	YTAPYPHPA	YTAPHPHPA	p.H45Y	c.133C>T	36	182	A2BP1	uc002cyr.1	NA	<30
41	ALVGAISSI	ALVGAIPSI	p.P1333S	c.3997G>A	39	12	SCN3A	uc002ucx.1	NA	36
42	FLEIYTVTV	FLGIYTVTV	p.G33E	c.98G>A	39	6	OR8D4	uc001pzj.1	NA	56
43	RLAVCHFPCL	HLAVCHFPCL	p.H79R	c.236T>C	42	84	GALNT14	uc002rms.1	NA	98
44	SLSSVTLLL	SSSVTLLL	p.S1084L	c.3251C>T	48	7240	CNTN5	uc001pga.1	NA	<30
45	SLFKGLHHKA	SLSKGLHHKA	p.S17F	c.50G>A	48	488	AASS	uc003vka.1	NA	<30
46	YTSEHAASV	YTPEHAASV	p.P16S	c.46C>T	50	95	AK310432	uc009vll.1	NA	<30
47	AICKPLHYV	AICKPLHYM	p.M131V	c.406C>G	50	2504	OR6C68	uc001shb.1	NA	<30
48	ALLMCLLPL	ALLMCPLPL	p.P789L	c.2366C>T	52	75	C1orf175	uc001cxp.1	NA	<30
49	VIIGITIDSV	VIIGITIASV	p.A1107D	c.3320G>T	52	24	IMPG2	uc003duq.1	NA	<30
50	AIPAMVVPNV	AIPAMVVPNA	p.A29V	c.86C>T	52	894	CRISPLD1	uc003yan.1	Mut/WT	<30
51	MQANS S HYARV	MQANPHYARV	p.P427S	c.1279C>T	55	70	CRISPLD1	uc003yan.1	Mut/WT	<30
52	GLPFMCHAEV	GLPFMCHAGV	p.G319E	c.956G>A	58	101	IL1RL2	uc002tbs.1	NA	<30
53	YLDELIRNT	YLDELIKNT	p.K1410R	c.4229A>G	58	78	A2ML1	uc001quz.2	NA	<30
54	WMSDSGTRL	WMSDSGTGL	p.G211R	c.631C>T	60	29	MPHOSPH9	uc001uel.1	NA	<30
55	LLIASVTWL	LFLIASVTWL	p.F254L	c.762G>C	63	7369	MAR11	uc003jfo.2	NA	<30
56	<u>KLYFDEK</u> YSI	<u>ELYFDEK</u> YSI	p.E81K	c.241C>T	64	3189	NETO1	uc002lkw.2	NA	<30
57	KLLPTNTNI	KLLPTNTDI	p.D98N	c.292G>A	64	210	C20orf70	uc002wyo.1	NA	<30
58	SLDLPLNPL	SLDLPLDPL	p.D457N	c.1369G>A	66	101	FGFR4	uc003mfl.1	NA	100
59	CMQANSHYA	CMQANPHYA	p.P427S	c.1279C>T	68	77	CRISPLD1	uc003yan.1	Mut/WT	15
60	GLDGYREYSL	GLDGYRGYSL	p.G 109E	c.326G>A	71	136	SPACA3	uc002hhs.1	NA	<30
61	SLQDHCCRAV	SLQDLCCRAV	p.L195H	c.584A>T	71	66	RAB40B	uc002kft.1	Mut/WT	30
62	MLAVFKLYPT	MLAVSKLYPT	p.S226F	c.677G>A	74	148	GPLD1	uc003ned.1	WT	<30

a. Mutated residues are underlined, and peptides recognized by TIL 2098 are bolded.

b. The wild type amino acid is followed by the mutated residue along with its position.

c. The wild type base is followed by the mutated base along with its position in the coding sequence.

d. Oligonucleotide primers flanking the regions that encode the candidate epitopes detailed in Supplementary Methods Primer list were used to amplify the indicated transcripts as described in the Online Methods. Mut - mutated WT-wild type NA- A product corresponding to the appropriate gene product was not amplified from tumor cell RNA.

e. NT - The indicated peptides were not tested, as they overlapped extensively with additional peptides that were evaluated in this assay for T cell recognition.

Supplementary Table 2. Candidate HLA-A*0101-binding epitopes identified from 2369 mel.

No.	<u>Mutated Peptide</u>	<u>WT Peptide</u>	<u>Protein change</u>	<u>cDNA change</u>	Predicted HLA-A*0101 binding affinity (nM)		<u>Gene</u>	<u>Gene ID</u>	<u>Expressed gene</u>	<u>IFN-γ (pg/ml)</u>
					<u>Mutated</u>	<u>WT</u>				
1	FSDYYDLSY ^a	FSDYYDLGY	p.G117S ^b	c.349C>T ^c	2	2	C22orf33	uc003aqe.1	NA ^d	<30
2	LTDDR^uLF^uTCY	LTDDR ^u LF ^u TC ^u H	p.H1005Y	c.3013C>T	3	97	PLEKHM2	uc001axa.2	Mut	8,655
3	YSSALDLCY	YSSALNLCY	p.N621D	c.861A>G	5	4	GRIN3B	uc002lqo.1	NA	<30
4	FSDK^uKVGT^uY	LSDK^uKVGT^uY	p.L688F	c.2062C>T	5	8	PLCB1	uc002wna.1	Mut/WT	<30
5	HSEYSSFF ^u Y	HSEYSSFF ^u H	p.H603Y	c.1807G>A	6	867	HEG1	uc003ehs.2	Mut/WT	<30
6	CSNFLLLAY	CSNF ^u SLLAY	p.S84L	c.251C>T	7	7	BAI3	uc003pev.2	Mut/WT	<30
7	ESDK ^u EELVGY	ESDK ^u EELVGY	p.F332L	c.994A>G	7	8	MPP4	uc002uyj.2	NA	<30
8	CTDTY ^u MLELF	CTDT ^u HMLELF	p.H191Y	c.571C>T	8	9	OR4C46	uc001nhj.1	NA	<30
9	FTGTIS ^u VMY	FTGTIP ^u VMY	p.P60S	c.178G>A	12	11	UEVLD	uc001mot.1	Mut/WT	<30
10	QTQSVVFLY	QTQSVVFS ^u Y	p.S156L	c.467G>A	13	62	COL9A1	uc003pfg.2	NA	<30
11	MSSYIASFTY	MSSYIASLTY	p.L356F	c.1066C>T	14	9	LST-3TM12	uc001ren.1	NA	<30
12	ATALLEYLEY	ATALLEYPEY	p.P466L	c.1397_1398CC>TT	20	81	TBRG4	uc003tmv.1	Mut/WT	<30
13	CTDTY ^u MLEL	CTDT ^u HMLEL	p.H191Y	c.571C>T	22	30	OR4C46	uc001nhj.1	NA	<30
14	LLDLMAYDRY	LLGLMAYDRY	p.G117D	c.350G>A	22	1558	OR2T2	uc001iek.1	NA	<30
15	SSDSQEENY	SSDSQEGNY	p.G117E	c.530C>T	23	16	MEOX2	uc003stc.1	NA	<30
16	LTSMA ^u YDCY	LTSMA ^u YDRY	p.R122C	c.364G>A	31	25	OR8B3	uc001qac.1	NA	<30
17	YTDF^uHCQYV	YTDF ^u PCQYV	p.P176H	c.527G>T	49	72	PPP1R3B	uc003wsn.2	Mut/WT	14,678
18	WADWGHRTY	WADWGHRA ^u Y	p.A3344T	c.10030C>T	51	47	LRP2	uc002ues.1	Mut/WT	<30
19	FTMVILYVVY	FTMVISYVVY	p.S219L	c.656C>T	54	44	LRR3B	uc003cdp.1	NA	<30
20	CVDSPPPLFF	CVDSPPPLS ^u F	p.S528F	c.1583C>T	71	210	C15orf2	uc001ywo.1	NA	<30
21	VSDGFTAVM	VPDGFTAVM	p.P198S	c.592C>T	85	5735	RNPEP	uc001gxd.1	Mut/WT	<30
22	WSCLGHLGY	RSCLGHLGY	p.R267W	c.799C>T	86	699	MIRO-2	uc002ciq.1	NA	<30
23	YTDF^uHCQYVK	YTDF ^u PCQYVK	p.P176H	c.527G>T	100	136	PPP1R3B	uc003wsn.2	Mut/WT	8,835
24	YTFLIESDY	YTFLISSDY	p.S849F	c.2546C>T	104	72	BCR	uc002zww.1	Mut/WT	<30
25	ISANSPYISY	ISANSPYIPY	p.P86 S	c.257C>T	124	84	ABCA12	uc002vev.1	NA	<30
26	SSFLVPSLPY	PSFLVPSLPY	p.P796S	c.2386C>T	125	479	KIAA1211	uc003hbk.2	Mut/WT	<30
27	VTLGIFFFFY	VTLGIF ^u SFFY	p.S125F	c.374C>T	127	103	SYPL2	uc001dxo.2	Mut	<30
28	FSDK^uKVGT^uYV	LSDK^uKVGT^uYV	p.L688F	c.2062C>T	134	262	PLCB1	uc002wna.1	Mut/WT	<30
29	HLEK ^u LCHGLY	HLG ^u LCHGLY	p.G318E	c.953G>A	165	884	PPP4R4	uc001yca.1	Mut/WT	<30
30	LSEFTVMAY	LSLFTVMAY	p.L444F	c.1330C>T	168	229	FLRT2	uc001xvr.1	Mut/WT	<30
31	KSGTFFVLAY	KSGTFSVLAY	p.S269F	c.806C>T	172	209	HHLA2	uc003dwy.2	NA	<30
32	GTFFVLAYY	GTF ^u SVLAYY	p.S269F	c.806C>T	173	126	HHLA2	uc003dwy.2	NA	<30
33	ITDVDELPIF	ITDVDEPIF	p.P369L	c.1106C>T	180	377	CDH5	uc002eom.2	NA	<30
34	ISISSEQTFY	IPISSEQTFY	p.P2632S	c.5806C>T	191	8595	PCLO	uc003uhv.2	Mut/WT	<30
35	CVDSPPPLF	CVDSPPPLS ^u	p.S528F	c.1583C>T	193	3644	C15orf2	uc001ywo.1	NA	NT ^e
36	CTAGASSLLV	CTAGAGSLLV	p.G307S	c.919G>A	196	227	EDEM1	uc003bqh.1	Mut/WT	<30
37	NSDLSPYLCH	NSDLSPY ^u PCH	p.P592L	c.1775C>T	224	1041	NCAPH	uc002svz.1	WT	<30
38	L ^u VVLAPLLY	PVVLAPLLY	p.P220L	c.659G>A	253	942	CNOT1	uc002enu.2	Mut/WT	<30
39	ITDVDELPI	ITDVDEPI	p.P369L	c.1106C>T	233	1833	CDH5	uc002eom.2	NA	NT
40	YSSEENLIF	YSSEG ^u NLIF	p.G1158E	c.3473G>A	272	233	RIMS2	uc003yjp.2	NA	<30
41	SSYIASFTY	SSYIASLTY	p.L356F	c.1066C>T	273	104	LST-3TM12	uc001ren.1	NA	<30
42	SISSEQTFY	PISSEQTFY	p.P2632S	c.5806C>T	278	886	PCLO	uc003uhv.2	Mut/WT	<30
43	LTDTSLTAL	PTDTSLTAL	p.P199L	c.596G>A	287	1447	OC90	uc003ytg.1	NA	<30
44	LTDTSLTALS	PTDTSLTALS	p.P199L	c.596G>A	304	2147	OC90	uc003ytg.1	NA	NT
45	SCSNFLLLAY	SCSNF ^u SLLAY	p.S84L	c.251C>T	305	309	BAI3	uc003pev.2	Mut/WT	<30
46	ELDEETNLKF	ELDGETNLKF	p.G233E	c.698C>T	312	457	ATP8B1	uc002lgw.1	Mut/WT	<30
47	WLSFTVMAY	WLSLFTVMAY	p.L444F	c.1330C>T	328	520	FLRT2	uc001xvr.1	Mut/WT	<30
48	SSDFTYLQEI	SSDFTILQEI	p.I201V	c.601A>G	398	359	SAFB	uc002mce.2	Mut	<30
49	KAERSY ^u IFY	KAERSY ^u HIFY	p.H287Y	c.859G>A	410	360	MYH2	uc002gmp.2	NA	<30
50	YVDVTY ^u NFI	YVDVTY ^u DFI	p.D225N	c.673C>T	411	539	CHRN4	uc002bed.1	NA	<30
51	HLSHQAHRY	HPSHQAHRY	p.P495L	c.1484G>A	413	6199	CDC2L6	uc003puh.1	NA	<30
52	FSDYERA^uEW	SSDYERA^uEW	p.S849F	c.2546C>T	414	1751	BCR	uc002zww.1	Mut/WT	<30
53	VVNPII ^u FY	VVNPII ^u SY	p.S294F	c.881G>A	431	1382	LPAR3	uc001dkl.2	Mut	<30
54	FGYEHWALY	LGYEHWALY	p.L19F	c.55C>T	439	944	RARRES3	uc001nxf.2	Mut/WT	<30
55	ISV ^u MYQGNTY	IPV ^u MYQGNTY	p.P60S	c.178G>A	475	14715	UEVLD	uc001mot.1	Mut/WT	<30
56	YVDVTY ^u NFII	YVDVTY ^u DFII	p.D225N	c.673C>T	476	545	CHRN4	uc002bed.1	NA	<30

a. Mutated residues are underlined, and peptides recognized by TIL 2369 are bolded.

b. The wild type amino acid is followed by the mutated residue along with its position.

c. The wild type base is followed by the mutated base along with its position in the coding sequence.

d. Oligonucleotide primers flanking the regions that encode the candidate epitopes detailed in Supplementary Table 7 were used to amplify the indicated transcripts as described in the Online Methods. Mut - mutated WT-wild type NA- A product corresponding to the appropriate gene product was not amplified from tumor cell RNA.

e. NT - The indicated peptides were not tested, as they overlapped extensively with additional peptides that were evaluated in this assay for T cell recognition.

Supplementary Table 3. Candidate HLA-A*2601-binding epitopes identified from 2369 mel.

				Predicted		HLA-A*2601 binding			
				affinity (nM)					
No.	<u>Mutated Peptide</u>	<u>WT Peptide</u>	<u>Protein change</u>	<u>cDNA change</u>	<u>Mutated</u>	<u>WT</u>	<u>Gene</u>	<u>Gene ID</u>	<u>IFN-γ (pg/ml)</u>
1	EVSDGFTAVM ^a	EVPDGFTAVM	p.P198S ^b	c.592C>T ^c	4	4	RNPEP	uc001gxd.1	<30
2	EVYFGPCSLY	EVYFGPCSPY	p.P468L	c.1403C>T	7	7	FMO3	uc001ghh.1	<30
3	EVMKKLPLF	EVMKKLPLS	p.S488F	c.1463C>T	10	2300	KIF6	uc010jxb.1	<30
4	SIPGIMGALY	SIPGIMGALY	p.T162I	c.485C>T	19	19	CLP1	uc001nkw.1	<30
5	ETADTKVHF	GTADTKVHF	p.G724E	c.2171G>A	21	7247	DPP10	uc002tla.1	<30
6	FSKEDLAAM	SSKEDLAAM	p.S297F	c.890C>T	25	82	RALGPS1	uc004bqp.2	<30
7	YTIEEFMEL	YTMEEFMEL	p.M249I	c.747G>A	25	80	ACSBG1	uc002bdh.1	<30
8	DLIEIFRFGY	DLIEIFRLGY	p.L19F	c.55C>T	26	26	RARRES3	uc001nxf.2	<30
9	EINPSLHTPM	GINPSLHTPM	p.G50E	c.149G>A	27	27	OR8B4	uc001qad.1	<30
10	ETLSPTPSY	ETPSPTPSY	p.P1142L	c.3425C>T	27	12	ROBO3	uc001qbc.1	<30
11	EVSDGFTAV	EVPDGFTAV	p.P198S	c.592C>T	28	32	RNPEP	uc001gxd.1	<30
12	ESFFWLEEM	ESFSWLEEM	p.S123F	c.368C>T	29	28	DONSON	uc002ysi.1	<30
13	HLIAIFCAY	HLIAILCAY	p.L269F	c.805C>T	34	25	OR10D3	uc0000318666	<30
14	SVVNPIIFY	SVVNPIIYSY	p.S294F	c.881C>T	34	29	LPAR3	uc001dkl.2	<30
15	FTMVILYVVY	FTMVISYVVY	p.S219L	c.656C>T	43	39	LRRC3B	uc003cdp.1	<30
16	YLIGVIGNF	YLIGVIGNS	p.S45F	c.134C>T	49	9253	OR52A5	uc001mab.1	<30
17	ETWRETGIF	ETWRETGIS	p.S1169F	c.3506C>T	52	9327	DOCK3	uc003dbb.1	NT ^d
18	ELSFHPSGNY	GLSFHPSGNY	p.G196E	c.587G>A	52	5842	DKFZp434C2	uc003dev.1	<30
19	YTFLIFSDY	YTFLISSDY	p.S849F	c.2546C>T	60	58	BCR	uc002zww.1	<30
20	MVILYVVYY	MVISYVVYY	p.S219L	c.656C>T	62	14	LRRC3B	uc002zww.1	<30
21	ETWRETGIF	ETWRETGIS	p.S1169F	c.3506C>T	75	72	DOCK3	uc003dbb.1	<30
22	NTASSSLAF	DTASSSLAF	p.D48N	c.142G>A	81	10	MAGEB4	uc004dcb.1	<30
23	EATNPYMY	GATNPYMY	p.G103E	c.308G>A	86	9589	MAS1L	uc003nmm.1	<30
24	SVMYQGNTY	PVMYQGNTY	p.P60S	c.178C>T	87	4455	UEVLD	uc001mot.1	<30
25	ETAPSTNSV	GTAPSTNSV	p.G428E	c.1283G>A	88	10172	LLRN4	uc002wmo.2	<30
26	EIKKDG VGF	EIKEDG VGF	p.E1176K	c.3526G>A	90	52	KIF21B	uc001gvr.1	<30
27	FAHFHSGEM	FAHFHSGGM	p.G286E	c.857G>A	98	54	CXorf64	uc010nra.1	<30
28	ELPIFQQPFY	EPPIFQQPFY	p.P369L	c.1106C>T	101	2510	CDH5	uc002eom.2	<30
29	EIPLIGLIPF	EIPLIGLIPS	p.S138F	c.413C>T	104	8911	CXorf22	uc004ddj.1	<30
30	FLFINTSSY	SLFINTSSY	p.S169F	c.506C>T	118	642	KIAA0922	uc003inm.2	<30
31	DMIFFSIDRY	DMISFSIDRY	p.S211F	c.632C>T	122	148	IGSF10	uc003eyz.1	<30
32	ESVINQGPM	GSVINQGPM	p.G653E	c.1958G>A	133	11694	RFX6	uc003pxm.1	<30
33	ESVTSCEAY	EPVTSCEAY	p.P144S	c.430C>T	162	1402	AFP	uc003hgz.1	<30
34	YVKLANLSY	YVKLANLPY	p.P123S	c.367C>T	173	144	TRYX3	uc003vxb.1	<30
35	ELVGYGQKF	EFVGYGQKF	p.F360L	c.1078T>C	173	1634	MPP4	uc010ftj.1	NT
36	FGYEHWALY	LYGYEHWALY	p.L19F	c.55C>T	176	2666	RARRES3	uc001nxf.2	<30
37	YVVTISSLL	HVVTISSLL	p.H776Y	c.2326C>T	181	141	PTPRO	uc001rev.1	<30
38	SVVNPIIYF	SVVNPIIYS	p.S294F	c.881C>T	190	13358	LPAR3	uc001dkl.2	NT
39	TTATISGLV	TTATVSGLV	p.V901I	c.2701G>A	209	370	UBA6	uc003hdg.2	<30
40	GTFEVLAYY	GTFSVLAYY	p.S269F	c.806C>T	213	182	HHLA2	uc003dwy.2	<30
41	ELKHILYAF	ELKHILYHAF	p.H142Y	c.424C>T	214	103	CALN1	uc003twa.2	<30
42	HMSSYIASF	HMSSYIASL	p.L356F	c.1066C>T	225	2654	LST-3TM12	uc001ren.1	<30
43	ETCTAGASSL	ETCTAGAGSL	p.G307S	c.919G>A	235	176	EDEM1	uc003bqh.1	<30
44	ELVGYGQKFF	EFVGYGQKFF	p.F360L	c.1078T>C	247	1681	MPP4	uc010ftj.1	<30
45	EVLVEYSFF	EVLVEYPPF	p.P649S	c.1945C>T	254	821	ATXN1	uc003nbt.1	<30
46	TTTATISGL	TTTATVSGL	p.V901I	c.2701G>A	258	405	UBA6	uc003hdg.2	<30
47	MIFFSIDRY	MISFSIDRY	p.S211F	c.632C>T	274	406	IGSF10	uc003eyz.1	NT
48	YMAELFSFI	YMAELFPFI	p.P334S	c.1000C>T	339	762	CLCN4	uc004csy.2	<30
49	HMIVISIAIY	HMIVVSIAY	p.V246I	c.736G>A	350	464	OR6C2	uc001sgz.1	<30
50	FTGTISVMY	FTGTIPVMY	p.P60S	c.178G>A	359	1043	UEVLD	uc001mot.1	<30

a. Mutated residues are underlined.

b. The wild type amino acid is followed by the mutated residue along with its position.

c. The wild type base is followed by the mutated base along with its position in the coding sequence.

d. NT -The indicated peptides were not tested, as they overlapped extensively with additional peptides that were evaluated in this assay for T cell recognition.

Supplementary Table 4. Candidate HLA-A*0101-binding epitopes identified from 3309 mel.

No.	<u>Mutated Peptide</u>	<u>WT Peptide</u>	<u>Protein change</u>	<u>cDNA change</u>	Predicted HLA-A*0101 binding affinity (nM)		<u>Gene</u>	<u>Gene ID</u>	IFN- γ (pg/ml)
					<u>Mutated</u>	<u>WT</u>			
1	LTERAN <u>F</u> QY ^a	LTERAD <u>F</u> QY	p.D75N ^b	c.223G>A ^c	10	11	FAM108A1	uc001hkn.1	<30
2	F <u>S</u> SYEPWGY	F <u>P</u> SYEPWGY	p.P506S	c.1516C>T	17	2390	GYS2	uc001rfb.1	<30
3	FTN <u>F</u> WGLLI	FTD <u>F</u> WGLLI	p.D101N	c.301G>A	70	10	PLA2G4E	uc001zov.1	<30
4	<u>L</u> SAKTCNV <u>D</u> Y	<u>P</u> SAKTCNV <u>D</u> Y	p.P212L	c.635C>T	73	823	AEBP1	uc003tkd.1	<30
5	<u>S</u> SYEPWGY	<u>P</u> SYEPWGY	p.P506S	c.1516C>T	79	328	GYS2	uc001rfb.1	NT ^d
6	STEDCL <u>I</u> LLF	STEDCL <u>I</u> PLF	p.P1376L	c.4127C>T	102	421	SMG1	uc002dfm.1	<30
7	S <u>S</u> EMAENEDY	S <u>P</u> EMAENEDY	p.P1645S	c.4933C>T	114	10787	JARID1A	uc001qif.1	<30
8	F <u>S</u> ARVLKSY	F <u>P</u> ARVLKSY	p.P191S	c.571C>T	115	9052	ATP1B1	uc001gfr.1	<30
9	GMD <u>G</u> AYLNGY	GMD <u>V</u> AYLNGY	p.V430G	c.1289T>G	135	131	KBTBD6	uc001uxu.1	<30
10	NSGGY <u>P</u> PLCY	NSGGY <u>P</u> PCY	p.S161L	c.482C>T	148	652	PBX3	uc004bqd.1	<30
11	KTMCEC <u>M</u> SFY	KTMCEC <u>M</u> SSY	p.S319F	c.956C>T	153	523	CUL3	uc002vny.1	<30
12	Q <u>S</u> ARLYIVAY	Q <u>S</u> ARLYIVAY	p.T23I	c.68C>T	153	102	XKR5	uc003wqp.1	<30
13	ASIR <u>N</u> ANLY	ASIR <u>D</u> ANLY	p.D134N	c.400G>A	106	132	ELAVL4	uc001cry.2	NT
14	NT <u>L</u> EQTVPY	NT <u>P</u> EQTVPY	p.P121L	c.362C>T	205	401	EDN3	uc002yar.1	<30
15	MSH <u>N</u> TEMNNY	MSH <u>D</u> TEMNNY	p.D251N	c.751G>A	227	144	CCDC33	uc002axp.2	<30
16	ESDQ <u>P</u> DLS <u>S</u> F	ESDQ <u>P</u> DLS <u>N</u> F	p.N189S	c.566A>G	319	424	CHRNA1	uc002uje.2	<30
17	LVEQAL <u>R</u> FY	LVEQAL <u>R</u> FH	p.H1295Y	c.3883C>T	357	13059	NBAS	uc002rec.1	<30
18	SCD <u>S</u> LCGGY	SCD <u>A</u> LCGGY	p.A394S	c.1180G>T	359	426	KIAA1890	uc003wqc.2	<30
19	SASIR <u>N</u> ANLY	SASIR <u>D</u> ANLY	p.D134N	c.400G>A	378	428	ELAVL4	uc001cry.2	<30
20	G <u>S</u> YECHVGIY	G <u>P</u> YECHVGIY	p.P113S	c.337C>T	429	11910	IGSF21	uc001bau.1	<30
21	LMDD <u>S</u> LMQIF	LMDD <u>S</u> LMQIS	p.S222F	c.665C>T	461	6556	RTTN	uc002lqp.1	<30
22	<u>F</u> VASRTRPDY	<u>S</u> VASRTRPDY	p.S56F	c.167C>T	559	1567	TMC5	uc002dgb.2	<30
23	TMCEC <u>M</u> SFY	TMCEC <u>M</u> SSY	p.S319F	c.956C>T	589	1769	CUL3	uc002vny.1	NT
24	CATCA <u>E</u> NFY	CATCA <u>E</u> NSY	p.S82F	c.245C>T	627	2569	LTBR	uc001qnz.1	<30
25	A <u>L</u> EVLQSIY	A <u>P</u> EVLQSIY	p.P184L	c.551C>T	648	6454	TSSK2	uc002zow.1	<30
26	LGDIYNEK <u>R</u> Y	LGDIYNEK <u>G</u> Y	p.G394R	c.1180G>A	671	795	TTC29	uc003ikx.2	<30
27	VIN <u>L</u> LSCLPY	VID <u>L</u> LSCLPY	p.D238N	c.712G>A	798	19	KCNH5	uc001xga.2	<30
28	FVDEN <u>V</u> DRM	FVDEN <u>L</u> DRM	p.L423V	c.1267T>G	889	561	NOL4	uc010dmi.1	<30
29	VSD <u>M</u> SLSLS	VSD <u>M</u> GLSLS	p.G72S	c.214G>A	828	643	OR51A7	uc001lzq.1	NT
30	VSD <u>M</u> SLSLSS	VSD <u>M</u> GLSLSS	p.G72S	c.214G>A	991	875	OR51A7	uc001lzq.1	<30
31	STEDCL <u>I</u> LL	STEDCL <u>I</u> PL	p.P1376L	c.4127C>T	888	421	SMG1	uc002dfm.1	NT
32	F <u>S</u> QESPLDTF	F <u>P</u> QESPLDTF	p.P404S	c.1210C>T	1030	15956	NOBOX	uc003wen.1	<30
33	TMM <u>F</u> FAEHY	TMM <u>F</u> LAEHY	p.L1354F	c.4060C>T	1052	1272	KIAA1429	uc003ygo.1	<30
34	HLGVF <u>S</u> SY	HLGVF <u>P</u> SY	p.P506S	c.1516C>T	1082	999	GYS2	uc001rfb.1	<30

a. Mutated residues are underlined.

b. The wild type amino acid is followed by the mutated residue along with its position.

c. The wild type base is followed by the mutated base along with its position in the coding sequence.

d. NT - The indicated peptides were not tested, as they overlapped extensively with additional peptides that were evaluated in this assay for T cell recognition.

Supplementary Table 5. Candidate HLA-A*1101-binding epitopes identified from 3309 mel.

No.	Mutated Peptide	WT Peptide	Protein change	cDNA change	Predicted HLA-A*1101 binding affinity (nM)		Gene	Gene ID	Expressed gene	IFN- γ (pg/ml)
					Mutated	WT				
1	STFFLAHGLK ^a	STFSLAHGLK	p.S6654F ^b	c.19961C>T ^c	4	4	MUC16	uc002mkp.1	Mut ^d	46
2	KT LT S VFQK	ETLTSVFQK	p.E226K	c.676G>A	5	20	MATN2	uc003yid.1	Mut/WT	1263
3	MTFLGGN <u>L</u> VK	MTFLGGN <u>P</u> VK	p.P1210L	c.3629C>T	7	8	SALL1	uc002egt.2	Mut/WT	47
4	KT LT S VFQ KK	ETLTSVFQ KK	p.E226K	c.676G>A	9	133	MATN2	uc003yid.1	Mut/WT	894
5	HTIPQAYWTK	HTIPQAHWTK	p.H36Y	c.106C>T	10	13	NGF	uc001efu.1	NA	38
6	KSSSIYSIV <u>K</u>	KSSSIYSIV <u>N</u>	p.N204K	c.611C>A	15	11154	ZAN	uc003uwj.1	NA	52
7	ITSSAELL <u>K</u>	ITSSAEL <u>F</u> K	p.F414L	c.1240T>C	16	11	LPHN2	uc009wcd.1	NA	69
8	SSSIYSIV <u>K</u>	SSSIYSIV <u>N</u>	p.N204K	c.611C>A	16	14099	ZAN	uc003uwj.1	NA	62
9	MSFYLR E Q G K	MSSYLRE Q G K	p.S319F	c.956C>T	17	64	CUL3	uc002vny.1	Mut/WT	42
10	STGLKMAME <u>K</u>	STGLKMAMER <u>R</u>	p.R2094K	c.6281G>A	17	132	XIRP2	uc002udy.2	NA	53
11	KTMCECM <u>S</u> FY	KTMCECM <u>S</u> SY	p.S319F	c.956C>T	18	25	CUL3	uc002vny.1	Mut/WT	53
12	VVLAVRL <u>S</u> CK	VVLAVRL <u>S</u> RK	p.R337C	c.1106C>T	22	19	SELPLG	uc001tnh.1	Mut/WT	37
13	ASLDGASLEK	ASPDGASLEK	p.P811L	c.2432C>T	24	244	ATP10D	uc003gkx.1	Mut/WT	45
14	QALRFYDYK	QALRFH D YK	p.H1295Y	c.3883C>T	26	25	NBAS	uc002rcc.1	Mut/WT	49
15	KTLKINEV <u>K</u>	KTLKINEV <u>E</u>	p.E103K	c.307G>A	28	18579	AMPH	uc003tgw.1	Mut/WT	48
16	IT S FIERK	IT G FIERK	p.G8733S	c.26197G>A	28	75	TTN	uc010frd.1	NA	49
17	AIANRIK <u>F</u> K	AIANRIK <u>S</u> K	p.S18F	c.53C>T	28	166	Kin17	uc009xip.1	Mut	40
18	QLFNCQAL <u>Q</u> K	QLFNCQAL <u>R</u> K	p.R72Q	c.215G>A	28	26	LRRC7	uc001dep.1	NA	56
19	ITNQMSID <u>K</u>	ITNQMSID <u>E</u>	p.E492K	c.1474G>A	30	19752	PDE1B	uc001sge.1	NA	39
20	HTAKD S FECK	HTAKD P FECK	p.P323S	c.967C>T	30	34	ZNF266	uc010dwq.1	Mut/WT	44
21	KAIANRIK <u>F</u> K	KAIANRIK <u>S</u> K	p.S18F	c.53C>T	31	108	Kin17	uc009xip.1	Mut	46
22	RIHT S A K PYK	RIHT S E K PYK	p.E355A	c.1064A>C	32	54	ZNF667	uc002qne.1	Mut/WT	53
23	TITSSAELL <u>K</u>	TITSSAEL <u>F</u> K	p.F414L	c.1240T>C	33	20	LPHN2	uc009wcd.1	NA	55
24	CILGK L F TK	CILGEL L FTK	p.E928K	c.2782G>A	33	42	CDK12	uc002hrw.2	Mut/WT	6475
25	SLGDHNFLR <u>K</u>	SLGDHNFLR <u>R</u>	p.R29K	c.86G>A	36	285	GRM3	uc010lef.1	NA	58
26	KINEV <u>K</u> TRK	KINEV <u>E</u> TRK	p.E103K	c.307G>A	38	46	AMPH	uc003tgw.1	Mut/WT	47
27	SL S PIEMKK	SP S PIEMKK	p.P87L	c.266C>T	38	5820	BCL11A	uc002sae.1	Mut/WT	61
28	FSLRAC <u>Y</u> HMK	FSLRAR <u>Y</u> HMK	p.R1388C	c.4162C>T	38	35	APOB	uc002red.1	NA	62
29	KMTVVILQK	KMTVVV L QK	p.V840I	c.2518G>A	40	36	ZNF644	uc001dny.1	Mut/WT	37
30	SSIYSIV <u>K</u> IK	SSIYSIV <u>N</u> IK	p.N2037K	c.6111C>A	40	20	ZAN	uc003uwj.1	NA	53
31	SIYSIV <u>K</u> IK	SIYSIV <u>N</u> IK	p.N2037K	c.6111C>A	41	18	ZAN	uc003uwj.1	NA	48
32	DV F KVIAYLK	DV S KVIAYLK	p.S308F	c.923C>T	41	142	SCG2	uc002vnm.1	Mut/WT	55
33	QTACCACRK	QTAR C ACRK	p.R67C	c.199C>T	42	43	AM19A5	uc003bim.2	Mut/WT	73
34	LSYN S HYSR	LSYN S HYSR	p.F586S	c.1757T>C	44	13	TLR8	uc004cvd.1	NA	73
35	<u>L</u> VKFPEMFQK	<u>P</u> VKFPEMFQK	p.P1210L	c.3629C>T	44	716	SALL1	uc002egt.2	Mut/WT	56
36	CILGK L F TK K	CILGEL L FTK K	p.E928K	c.2782G>A	45	50	CDK12	uc002hrw.2	Mut/WT	3622
37	LVANFSQ <u>I</u> K	LVANFSQ <u>E</u>	p.E226K	c.676G>A	47	25904	MATN2	uc003yid.1	Mut/WT	54
38	H I NTVMEVK	H K NTVMEVK	p.K288I	c.863A>T	50	13461	WDR33	uc002tpg.1	WT	64
39	RTMM F EA H	RTMM F LA H	p.L1354F	c.4060C>T	53	81	JAA1429	uc003ygo.1	Mut/WT	43
40	<u>K</u> ANRNLARK	<u>N</u> ANRNLARK	p.N222K	c.664T>G	53	412	RSPO1	uc001cbm.1	NA	52
41	RSNPY F VASR	RSNPY S VASR	p.S56F	c.167C>T	54	99	TMC5	uc002dgb.2	NA	53
42	MVSSNENCRK	MVPSNENCRK	p.P122S	c.364C>T	55	332	JAA1793	uc010llq.1	Mut/WT	52
43	<u>S</u> L F GLSFVR	<u>S</u> P F GLSFVR	p.P141L	c.422C>T	58	4805	XRCC1	uc002owt.2	Mut/WT	56
44	RVR D FIQMK	RV G DFIQMK	p.G173R	c.517G>A	59	26	ATP10B	uc003lym.1	Mut/WT	44
45	TFFLAHGLK	T F SLAHGLK	p.S6654F	c.19961C>T	62	231	MUC16	uc002mkp.1	Mut	45
46	MLNPLIYS <u>R</u>	MLNPLIYS <u>L</u> R	p.L292F	c.874C>T	64	80	OR2T27	uc001iet.1	NA	43

a. Mutated residues are underlined, and peptides recognized by TIL 3309 are bolded.

b. The wild type amino acid is followed by the mutated residue along with its position.

c. The wild type base is followed by the mutated base along with its position in the coding sequence.

d. Oligonucleotide primers flanking the regions that encode the candidate epitopes detailed in Supplementary Table 8 were used to amplify the indicated transcripts as described in the Online Methods. Mut - mutated WT-wild type NA - Not amplified. NA- A product corresponding to the appropriate gene product was not amplified from tumor cell RNA.

**Supplementary Table 6. Mutated candidate epitopes encoded by expressed genes.
2098 mel**

No.	<u>Mutated Peptide</u>	<u>WT Peptide</u>	<u>Protein change</u>	Predicted HLA-A*0201 binding affinity (nM)		<u>Gene</u>	<u>Gene ID</u>
				<u>Mutated</u>	<u>WT</u>		
1	<u>GLFGDIYLA</u> ^a	G <u>S</u> FGDIYLA	p.S27L ^b	6	1312	CSNK1A1	uc003lqw.1
2	<u>FQLNQSF</u> EI	<u>S</u> QLNQSF <u>E</u> I	p.S1281F	6	53	UNC13A	uc002nhd.1
3	<u>RMLDKNPEV</u>	R <u>M</u> LDKN <u>P</u> ES	p.S433V	7	1722	CAMKK2	uc001txt.1
4	<u>HLMDGDLGL</u>	<u>N</u> LMDGDL <u>G</u> L	p.N558H	10	11	C1S	uc001qsj.1
5	<u>GLFGDIYLAI</u>	G <u>S</u> FGDIYL <u>A</u> I	p.S27L	12	2394	CSNK1A1	uc003lqw.1
6	<u>SLADEAEVYL</u>	SLADEAEV <u>H</u> L	p.H225Y	12	39	GAS7	uc002gmi.1
7	<u>MLFLRF</u> CYI	MLFLRF <u>R</u> YI	p.R55C	12	116	WDR47	uc001dww.1
8	<u>YLTSLACVEI</u>	<u>Y</u> PTSLAC <u>V</u> EI	p.P1039L	17	21684	BRCA2	uc001uub.1
9	<u>LLADQNF</u> KFI	LLADQNL <u>K</u> FI	p.L190F	20	30	RRP1B	uc002zdk.1
10	<u>AMI</u> AKISNEL	AM <u>I</u> TAKISNEL	p.T160A	22	33	HAUS3	uc003ges.1
11	<u>HLMDGDLGLI</u>	<u>N</u> LMDGDL <u>G</u> LI	p.N558H	22	20	C1S	uc001qsj.1
12	<u>ALGTL</u> LHTNV	ALGTL <u>L</u> HNT <u>N</u>	p.L1577V	23	143	NOTCH2	uc001eik.1
13	<u>SVVDV</u> FFQL	SVVDV <u>F</u> S <u>Q</u> L	p.S1281F	28	323	UNC13A	uc002nhd.1
14	<u>ILNAMI</u>AKI	ILNAMI <u>T</u> KI	p.T160A	34	36	HAUS3	uc003ges.1

2369 mel

	<u>Mutated Peptide</u>	<u>WT Peptide</u>	<u>Protein change</u>	Predicted HLA-A*0101 binding affinity (nM)		<u>Gene</u>	<u>Gene ID</u>
				<u>Mutated</u>	<u>WT</u>		
1	<u>LTDDRL</u>FTCY	LTDDRLFT <u>C</u> H	p.H1005Y	3	97	PLEKHM2	uc001axa.2
2	<u>ESDKK</u> VGTY	<u>L</u> SDKK <u>V</u> GTY	p.L688F	5	8	PLCB1	uc002wna.1
3	<u>HSEYSS</u> FFY	HSEYSS <u>F</u> H	p.H603Y	6	867	HEG1	uc003ehs.2
4	<u>CSNFL</u> LLAY	CSNF <u>S</u> LLAY	p.S84L	7	7	BAI3	uc003pev.2
5	<u>FTGTI</u> SVMY	FTGTI <u>P</u> VMY	p.P60S	12	11	UEVLD	uc001mot.1
6	<u>ATALLEY</u> LEY	ATALLEY <u>P</u> EY	p.P466L	20	81	TBRG4	uc003tmv.1
7	<u>YTD</u>FHCQYV	YTD <u>F</u> PCQY <u>V</u>	p.P176H	49	72	PPP1R3B	uc003wsn.2
8	<u>WADWGH</u> RTY	WADWGH <u>R</u> AY	p.A3344T	51	47	LRP2	uc002ues.1
9	<u>VSDG</u> F T A V M	<u>V</u> PDGFT <u>A</u> V <u>M</u>	p.P198S	85	5735	RNPEP	uc001gxd.1
10	<u>YTD</u>FHCQYVK	YTD <u>F</u> PCQY <u>V</u> K	p.P176H	100	136	PPP1R3B	uc003wsn.2

3309 mel

	<u>Mutated Peptide</u>	<u>WT Peptide</u>	<u>Protein change</u>	Predicted HLA-A*1101 binding affinity (nM)		<u>Gene</u>	<u>Gene ID</u>
				<u>Mutated</u>	<u>WT</u>		
1	<u>STF</u> LAHGLK	STF <u>S</u> LAHGLK	p.S6654F	4	4	MUC16	uc002mkp.1
2	<u>KTLT</u>SVFQK	<u>E</u> TLT <u>S</u> VFQK	p.E226K	5	20	MATN2	uc003yid.1
3	<u>MTFLG</u> GNLVK	MTFLG <u>G</u> NP <u>V</u> K	p.P1210L	7	8	SALL1	uc002egt.2
4	<u>KTLT</u>SVFQK	<u>E</u> TLT <u>S</u> VFQ <u>K</u> K	p.E226K	9	133	MATN2	uc003yid.1
5	<u>MSFY</u> LREQGK	M <u>S</u> SYLREQGK	p.S319F	17	64	CUL3	uc002vny.1
6	<u>KTMCE</u> CMSFY	KTMCE <u>C</u> M <u>S</u> SY	p.S319F	18	44	CUL3	uc002vny.1
7	<u>VVLAV</u> RLSCK	VVLAV <u>R</u> LS <u>R</u> K	p.R337C	22	21	SELPLG	uc001tnh.1
8	<u>ASLD</u> GASLEK	AS <u>P</u> DGASLEK	p.P811L	24	374	ATP10D	uc003gsk.1
9	<u>QALRF</u> YDYK	QALRF <u>H</u> DYK	p.H1295Y	26	25	NBAS	uc002rcc.1
10	<u>KTLK</u> INEVK	KTLKINE <u>V</u> E	p.E103K	28	18579	AMPH	uc003tgw.1
11	<u>AIANRI</u> KFK	AIANRI <u>K</u> SK	p.S18F	28	166	Kin17	uc009xip.1
12	<u>HTAKD</u> SFECK	HTAKD <u>P</u> FECK	p.P323S	30	34	ZNF266	uc010dwq.1
13	<u>KAIANRI</u> KFK	KAIANRI <u>K</u> SK	p.S18F	31	108	Kin17	uc009xip.1
14	<u>RIHTS</u> AKPYK	RIHT <u>S</u> EKPYK	p.E355A	32	54	ZNF667	uc002qne.1
15	<u>CILG</u>KLFTK	CIL <u>G</u> ELFTK	p.E928K	33	42	CDK12	uc002hrw.2
16	<u>KINEV</u> KTRK	KINE <u>V</u> ETRK	p.E103K	38	46	AMPH	uc003tgw.1
17	<u>S</u> LSP I EMKK	<u>S</u> PSPIEMKK	p.P87L	38	5820	BCL11A	uc002sae.1
18	<u>KMTV</u> VILQK	KMTV <u>V</u> VLQK	p.V840I	40	36	ZNF644	uc001dny.1
19	<u>DVFK</u> VIAYLK	DV <u>S</u> KVIAYLK	p.S308F	41	142	SCG2	uc002vnm.1
20	<u>QTAC</u> CACRK	QTAR <u>C</u> ACRK	p.R 67C	42	43	FAM19A5	uc003bim.2
21	<u>L</u> VKFP <u>E</u> MFQK	<u>P</u> VKFP <u>E</u> MFQK	p.P1210L	44	716	SALL1	uc002egt.2
22	<u>CILG</u>KLFTK	CIL <u>G</u> ELFT K K	p.E928K	45	50	CDK12	uc002hrw.2

a. Mutated residues are underlined, and peptides recognized by TIL are bolded.

b. The wild type amino acid is followed by the mutated residue along with its position.

Supplementary Methods Primer list.

Primers used to amplify genes encoding candidate HLA-A*0201-binding epitopes from 2098 mel.

Gene	Gene ID	Forward Primer	Reverse Primer
ZNF559	uc002mle.2	GATGCTGGAGAACTATAAGAATCTAGT	ACTGGATGTTTTCCCTGC
CSNK1A1	uc003lqw.1	CACCATGGCGAGTAGCAGCGGCTC	GAAATTGAAGAGGTCTTCGAGGCTAGG
TRPC6	uc001pgk.2	GACTATCTGCTCATGGACTCG	CTTCTAACATCTTCGCACCA
SERPINB11	uc002ljk.2	AGTCTAACTTGCCACTCTGTGAAC	CAAGGAGGACCATGCTTAGAG
HTR1F	uc003dqr.2	AACTCCCTTGATGATCGCTG	ATCTGTGATTGCTCGATACCG
UNC13A	uc002nhd.1	ATGAGTATGTGACGGAACCTCC	AGGCAAAGTCCTTGAGATG
PXDNL	uc003xqu.2	GTGTGGCTCGGAATCTTTTG	CACGCGGTAATGAAATTGAG
KCNK5	uc003oon.1	CATCACAGGAACCAGACC	CTCTTGGTAAGGAACTGCCC
CNKSRI	uc001blm.2	GCTGAAGAAGATCCCATAACC	GAAGACAGGTCAAAGGCAAAG
MAR11	uc003jfo.2	CTGTGCCTGCTAAAATGGATC	CAAATTCACAGCTCGCCAG
C1S	uc001qsj.1	TGGGTGAATGAGGTGCTG	TTAGGAGTGAAAACATAGGCCTC
GPR174	uc004edg.1	AACTCCGCTTCTGATTGTCC	CAAGACACAATGCCACAGAATG
WDR47	uc001dwk.1	AGTGGAGTCATAAATGGCCTG	TCATCTTCTGCTGACATCGC
GAS7	uc010coh.1	CTCTCAGAACTCCTTGCTTC	GAAGGTCCGCAATGTGGT
GSTA4	uc003pbc.1	TGCACACCATTTCCTACAG	TGCCAGGTTCAAGGAATCTC
OR8D4	uc001pzj.1	AACCATTCCACAGTGACTGAG	GGGTAATGACAGAAGAATAGCAGA
IGF1	uc001tjn.2	GTA AACGACGGCCAGAGCAGTCTTCCAACCCAATTA	CTTAGATCACAGCTCCGGAAG
OR8D4	uc001pzj.1	AACCATTCCACAGTGACTGAG	GGGTAATGACAGAAGAATAGCAGA
BRCA2	uc001uub.1	TTTGGAGGTAGCTTCAGAACAG	AGTTCTGTAATTTCTGCCTTTTGG
RRP1B	uc002zdk.1	GATGAACTCTCAAAGTCGGG	CACCCACTTTTGTCTTCTGTTC
CNTN5	uc001pga.1	TTTTATAGGCAAGAGGGTCACAG	GCAGTTTTACCAGGAAGTTG
HAUS3	uc003ges.1	AAGCTGAAGCAGAGTCAAGG	GCATCCAAATTTCTTTGTCCAC
C1S	uc001qsj.1	TGGGTGAATGAGGTGCTG	TTAGGAGTGAAAACATAGGCCTC
NOTCH2	uc001eik.1	GGAGTGTGGTTGGGATGG	TCCGTGTTCTTGAAGCAGTG
KCNA6	uc001qnf.1	GAGGGAGAGCAACAGGATG	AGAAGTACTCGTTCCTCAGGG
UNC13A	uc002nhd.1	ATGAGTATGTGACGGAACCTCC	AGGCAAAGTCCTTGAGATG
MYH4	uc002gmn.1	GAGGTAAGTAAAAGAGCTGAGG	TCACCCTCCAGTTTTCTCTTG
A2BP1	uc002cyr.1	GAGTTCTCCTGCATCCTTATGG	GCTGAGACTTGTTCCTCCGTG
OR8D4	uc001pzj.1	AACCATTCCACAGTGACTGAG	GGGTAATGACAGAAGAATAGCAGA
GALNT14	uc002rns.1	TCAGGAAAAGAAGATAAGAGGTAGC	CTGCAAATGGAAGTGAAGTTC
CNTN5	uc001pga.1	CAGCAACAGCCAAGTTATTG	CAGGAAGTTGAAGGAATCATC
OR6C68	uc001shb.1	TTTCTTAGAAATCTCATTTACAG	CATCTGCTCAATTAATGATGTG
C1orf175	uc001cxp.1	TCGGAGGTCATGCTCAGC	AGCTGTTGACGGACAGGAG
IMPG2	uc003duq.1	TACCTGAGTGTGGAAGAACG	CTTCTCACATCCAGCCCTG
CRISPLD1	uc003yan.1	GTGTACCGCGGGAGTG	AGATCTTTCCAGCTCTACATC
CRISPLD1	uc003yan.1	CATTATTTTCATCAAGTCCAATAG	CCTTTCTCCTGGAGGATTC
IL1RL2	uc002tbs.1	ACCAAGGATAATACAAATCTAC	TCATACAGCTTCCCATCTAC
A2ML1	uc001quz.2	GATCCTTGACTCTCACTATTC	TTCACAGGGATCAGAATACTG
MPHOSPH9	uc001uel.1	CACAAAACTGAAGCAGAACC	GATTCCTCTCAGGTAAGTGC
NETO1	uc002lkw.2	ATCATCCTCCATTTGTCTGG	ATAGATTCAGCTCTCCATC
C20orf70	uc002wyo.1	GTGGATAAGCTGGAACCTG	TCTGGGGATCAGTTCAATTG
FGFR4	uc003mfl.1	AGGGCAGGCGCTCCACG	CCATCTCCGAGACCAGGTC
SPACA3	uc002hhs.1	GTGGTGGCTCCACCTCTG	TTGAGATTAGGATTCACAAAATC
RAB40B	uc002kft.1	CGTTCAAGCGCAGGTGC	CGAGCTTCACTTTGCGGAG
GPLD1	uc003ned.1	GTGATTTTGGAGGAGATGTG	TTTTGCTGGCCGCCACATG
AASS	uc003vka.1	TCGGAGGTCATGCTCAGC	AGCTGTTGACGGACAGGAG
AK310432	uc009vll.1	GATCCTTGACTCTCACTATTC	TTCACAGGGATCAGAATACTG
C15orf32	uc002brc.1	AACACCAAGACTTCCCCAAG	GCTGACTCTCATAAGATGCCTC
CAMKK2	uc001txt.1	GGAAGGCCCTGGATGTTTG	GTTCCCAAAGGAGCGTTTAC
SCN3A	uc002ucx.1	TTCAATGGAGATGCTGGAGG	GATCGCAGTACAGACAATCCC

Primers used to amplify genes encoding candidate HLA-A*0101-binding epitopes from 2369 mel.

Gene	Gene ID	Forward Primer	Reverse Primer
C22orf33	uc003aqe.1	GTAAAACGACGGCCAGCAGAAAAGGGCAAGCTCATG	ACTGATTTCTCAATGACCTCTGG
PLEKHM2	uc001axa.2	GTAAAACGACGGCCAGCATCTCTGCCAGGCTGTGTC	GAGAACTCCAAGACGCAGTACTC
GRIN3B	uc002lqo.1	GTAAAACGACGGCCAGCTCTTCTCACCCTGTACG	CCCAGAGGTTTCATGAGCAG
PLCB1	uc002wna.1	GTAAAACGACGGCCAGACAATGGACCTGGCTATGC	CTACTTCCACGTAAGTCCCAAC
HEG1	uc003ehs.2	GTAAAACGACGGCCAGACATCTTCTCGGAAAGCTTG	GGACGGAAGGTTGGATGTATG
BAI3	uc003pev.2	GTAAAACGACGGCCAGCTTTACAACTGCCTTGGACG	TTCATGGGAAAAATGATCAAAGTGA
MPP4	uc002uyj.2	GTAAAACGACGGCCAGCTTGTCCCTTCTAACCAC	TGAGACTTCCCTGCGACAAAAG
OR4C46	uc001nhj.1	GTAAAACGACGGCCAGTGCAACCATAACAGATCCTCTTC	CTTAGGGAGCACAAAGATGACC
UEVLD	uc001mot.1	GTAAAACGACGGCCAGCTAACTGTGGAAGAATAAGGAATC	CCATATTTGCAGTTGGCTTC
COL9A1	uc003pfg.2	GTAAAACGACGGCCAGTCCAGCAATACAGCTTTCATCG	GGAGTATCCAATGCTATGCCTAG
LST-3TM12	uc001ren.1	GTAAAACGACGGCCAGTAGCTAATTTGACCAACCGAAG	TCCTGAAAACATGCCAATTG
OR4C46	uc001nhj.1	GTAAAACGACGGCCAGTGCAACCATAACAGATCCTCTTC	CTTAGGGAGCACAAAGATGACC
OR2T2	uc001iek.1	GTAAAACGACGGCCAGCATCTGTATCACTGTCCCAAG	ACCATGAATAAGCAAACCTTG
MEOX2	uc003stc.1	GTAAAACGACGGCCAGTCTGTGCTCCAACCTTCC	CTTTCCTGGGTTTGCTGTTG
OR8B3	uc001qac.1	GTAAAACGACGGCCAGTCCATGTTGGGTGCATGAC	AGAAGGTGAGTCTAAGCATGCAC
PPP1R3B	uc003wsn.2	GTAAAACGACGGCCAGTTTCCAGAACCTCGCATTTGAG	AGTACGTCTGTCCATTGCACTC
LRP2	uc002ues.1	GTAAAACGACGGCCAGTCTTTGTCTCTGACCTCAATGG	ACAGACTTGTGGTTCCATCC
LRRC3B	uc003cdp.1	GTAAAACGACGGCCAGTGATCTGTAAAACGTCCCGTG	CAAGTATTCGAGGTGTCTCCG
C15orf2	uc001ywo.1	GTAAAACGACGGCCAGTCTTAGCTCCACACCCTCC	AGGCTTGCTGGTGATAACTG
RNPEP	uc001gxd.1	GTAAAACGACGGCCAGAGAAGCCCTTCGTGTACACC	ACTTCAGCCGAAACAGATC
MIRO-2	uc002ciq.1	GTAAAACGACGGCCAGATAGCTAATTTGACCAACCGAAG	TCCTGAAAACATGCCAATTG
PPP1R3B	uc003wsn.2	GTAAAACGACGGCCAGTTTCCAGAACCTCGCATTTGAG	AGTACGTCTGTCCATTGCACTC
BCR	uc002zww.1	GTAAAACGACGGCCAGTGTGCGAGCAGGAGTCAC	CACACGAGTTGGTCAGCATC
ABCA12	uc002vev.1	GTAAAACGACGGCCAGCCTTATCTCCAAGCAGTCTGG	ATCGTATTGTGGACTGCAGG
KIAA1211	uc003hbk.2	GTAAAACGACGGCCAGACCCAGCGAAGAGACAGC	CTATCCCCTTTGCAGTCTCG
SYPL2	uc001dxo.2	GACAGGAGCAATGGTTCCG	ATGGCTGCTGTCAAGCTGG
PPP4R4	uc001yes.1	GTGCTCCCTGAATTAATAGAAC	CATGGCCGAAAGTTATAAGC
FLRT2	uc001xvr.1	GACCACTCAGCTCCAC	GAACAAATGGTGTCTTCTACC
HHLA2	uc003dwy.2	GGATCAAATTCATCTTATGAATG	CTACATGCACTGTGTGGATG
CDH5	uc002eom.2	GACGCTTTCACCAATTGAGAC	CTGTCCAGTTCTTCTCATTG
PCLO	uc003uhv.2	CAAGTCTTCACCAAGATTTTCC	AATTGTTATGGAAATGCTGCTG
EDEM1	uc003bqh.1	ATAACTGACTCCAAGCAGCC	ATAGAAGGAGTCCAGCCCCG
NCAPH	uc002svz.1	CAGGCACCAGGTTACTTAAG	GAGCGCTGTCAGCAGACTC
CNOT1	uc002enu.2	CAGATCTTCTGCGTTCTTAC	GACCTCCCGAACACCAAAC
RIMS2	uc003yly.2	GACGAAGGGGCCGACAG	GTTTTACAACAAGGCCACGG
OC90	uc003ytg.1	AGATCATATGTGAGTCCAAGG	CAGCAGGGACAAGGGTTAC
ATP8B1	uc002lgw.1	CATAAAATGGATAAGGAAATCAAC	CCACGTAACAAAATTTTATCAGC
SAFB	uc002mce.2	GATGAAGCAGAAATGATAATGG	GATGGGCGCTGTCAAATAGG
MYH2	uc002gmp.2	GATCAAATCATCAGTGCCAAC	GTAAATGGAGACCTTTTCTTC
CHRN4	uc002bed.1	TCCCTTCGACCAGCAGAAC	ATCGAGGGAGGTGGGTGG
CDC2L6	uc003puh.1	CCTGAACCAGGTGCTCC	GTGGGCTTGGTGGATAGG
LPAR3	uc001dkl.2	CAGCCGCCGGAGGACAC	AGTGCTTTTATGCACTGCTGC
RARRES3	uc001nxf.2	CTTCGCCACACCAAGAGCC	TTGGTACTCATGGTCCAAGC

Primers used to amplify genes encoding candidate HLA-A*1101-binding peptides from 3309 mel.

Gene	Gene ID	Forward primer	Reverse primer
RSPO1	uc001cbl.1	TGGGGGCCCTGCTCCAAGAA	CATCTGCAGGGCCTGCCTAG
LRRC7	uc001dep.1	AAAATCATCGGCCGTCTGGT	ATGGCTTCACACAGCTCCTA
ZNF664	uc001dny.1	CTGTTTTTCATCATCAAGTAA	AGGAGCCTGGAGAAAATGCT
NGF	uc001efu.1	ATGTCCATGTTGTTCTACACT	AAGCTGCAGACACTCAGGAT
OR2T27	uc001iet.1	TATAGGATGAGCGAGGCAGA	CTCAGGAAAGGTAACCACTTTCTAA
PDE1B	uc001sge.1	CCCCTGGCGGATGAGGACTC	CCAGAATGGGAATCTGGATTAG
SELPLG	uc001tnh.1	TCTGTTTCATACCCTTTTCTGTG	CTAAGGGAGGAAGCTGTGC
TMC5	uc002dgc.2	ATGTCTGCCTACTACAGGAAT	ATCCCTACCACCGAGCATCA
SALL1	uc002egt.2	TCCTCATCGAGTGCCCTGCA	GGAACAGCTCACCTGTTAGT
CDK12	uc002hrw.2	TGTTCTAACATTTTGCTGAA	TCATTCCTTCTGCAGCACTT
MUC16	uc002mkp.1	CCTTCCACAAACATAGCAGT	CCACTGAAGTGATCCCCAGC
XRCC1	uc002owt.2	TCAGCTGGAGGCGCTGGGGA	TCACAGCCAGCGACCCAGCA
ZNF667	uc002qne.1	GGCTTCAAAAAGAAATCAGT	TTGAGTGTAAGGAATGTGGG
NBAS	uc002rcc.1	AAGATCCTGCCTTTGCAAGT	CAGCTAGCAGCTCTCTGCAG
APOB	uc002red.1	CACTTCAAGTCTGTGGGATT	TCTCAAAAGGTTTACTAATA
BCL11A	uc002sae.1	CCTCTTGAAGCCATTCTTAC	TAATCCCCACGCCTGGGATG
WDR33	uc002tpg.1	AGCCCAGTGAGGGCCATGAC	AAAACACAGTAATGGAAGTG
XIRP2	uc002udy.2	AATATAAACCTTCAACCAAT	TGTCCACAGAGAAGATAAAG
SCG2	uc002vnm.1	GAAGATGTGGTCTGGGGGAGA	TGCTCAAACTGGGGAGAAG
CUL3	uc002vny.1	GACAAATCAACGGAAGAACC	ACCTCAACTCCAGGTCTCCT
FAM19A5	uc003bim.2	GACAAATCAACGGAAGAACC	ACCTCAACTCCAGGTCTCCT
ATP10D	uc003gxk.1	CGGTCTCGGACACCAGAGCA	GGGAAGAATTACTACTTGAA
ATP10B	uc003lym.1	ATGCCCTCCATGGAAGTCTT	TTTTCCACAATACCATCGTG
AMPH	uc003tgw.1	AAACAGAAGATGGAAGATTC	TAGAAGGCTTTGGAGCCAAA
ZAN	uc003uwj.1	TCGGGTGAAGAGGGCCGCCG	CCAAGAATGCAAGACCTGGG
ZAN	uc003uwj.1	ATCAGTGCCAAGCATGAGAA	GGAAAGATAAGGACATTGAC
KIAA1429	uc003ygo.1	CAGTCTCTCTGTGATCAGGA	GAGATGATAATGGTCTCATG
MATN2	uc003yid.1	AATGTGCCACGGGTCATAAT	AGGACCACAACCTGTGAGCAG
TLR8	uc004cvd.1	GAAAATCTTCTGACATTGC	ACAACAGGTATATCTCCATT
LPHN2	uc009wcd.1	TTAAACCGAGGAGAATATGT	CCAAGGGGATAAAGTGGCCT
Kin17	uc009xip.1	ATGGGGAAGTCGGATTT	AACTTCTCAGGAGACGCTTT
ZNF266	uc010dwq.1	CAGCACAGAAAACTCACAC	AGGAATGTGGAAGGCCTTT
TTN	uc010frd.1	AAGGATGCACTGCGAAAAGA	ATCCACTAGGTCTCCAACA
GRM3	uc010lef.1	ATGTTGACAAGACTGCAAGTT	TGGGTGTTTACATTTTGGAT
KIAA1793	uc010llq.1	GCCCTGCAGGTGATGTATGA	CCTATAAGAAGAGTTACGGC