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	SVQII**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

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