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## Tables

HLA Allele	Gene	Mutation	Peptide Sequence	Length
HLA-A*31:01	AKT1	E17K	KYIK <u>T</u> WRPR	9
HLA-C*07:02	CTNNB1	S37F	QSYLD <u>S</u> GIH <u>F</u>	10
HLA-A*24:02	CTNNB1	S37F	YLDSGIH <u>F</u>	8
HLA-A*24:02	CTNNB1	S37F	SYLD <u>S</u> GIH <u>F</u>	9
HLA-A*03:01	CTNNB1	S45F	TTAP <u>F</u> LSGK	9
HLA-A*03:01	CTNNB1	S45F	TTTAP <u>F</u> LSGK	10
HLA-A*03:01	CTNNB1	S45F	ATTTAP <u>F</u> LSGK	11
HLA-A*03:01	CTNNB1	T41A	AT <u>A</u> PSLSGK	9
HLA-C*03:04	EGFR	T790M	STVQLIM <u>Q</u> L	9
HLA-A*33:03	EGFR	L858R	HVKITDF <u>G</u> R	9
HLA-C*12:03	EGFR	T790M	STVQLIM <u>Q</u> L	9
HLA-A*31:01	EGFR	L858R	HVKITDF <u>G</u> R	9
HLA-A*24:02	ESR1	D538G	LY <u>G</u> LLLEML	9
HLA-A*11:01	KRAS	G12A	VVVGA <u>A</u> GVGK	10
HLA-A*11:01	KRAS	G12S	VVVGA <u>S</u> GVGK	10
HLA-A*11:01	KRAS	G12V	VVGA <u>V</u> GVGK	9
HLA-A*11:01	KRAS	G12V	VVVGA <u>V</u> GVGK	10
HLA-A*03:01	KRAS	G12R	VVVGA <u>R</u> GVGK	10
HLA-C*08:02	KRAS	G12D	GAD <u>G</u> VGKSAL	10
HLA-A*11:01	KRAS	G12C	VVVGA <u>C</u> GVGK	10
HLA-A*11:01	KRAS	G12D	VVGAD <u>D</u> GVGK	9
HLA-A*11:01	KRAS	G12D	VVVGAD <u>D</u> GVGK	10
HLA-B*15:01	MUTYH	Y165C	QLWAGLG <u>C</u> Y	9
HLA-A*02:01	NOTCH1	V1575L	RLAAGTL <u>L</u> VVV	11
HLA-A*33:01	PIK3CA	H1047R	DAR <u>H</u> HGGWTTK	10
HLA-B*08:01	PIK3CA	H1047L	FMKQMND <u>A</u> L	9
HLA-A*02:01	TP53	H193Y	GLAPPQY <u>L</u> IRV	11
HLA-A*02:01	TP53	P190L	ALPQH <u>L</u> IRV	9
HLA-A*02:01	TP53	P190L	GLA <u>L</u> PQH <u>L</u> IRV	11
HLA-A*02:01	TP53	P250L	RL <u>L</u> ILTI <u>T</u> L	9
HLA-A*24:02	TP53	S241F	HYNYMCN <u>S</u> F	9
HLA-A*02:01	TP53	R213L	YLDDRNT <u>F</u> L	9
HLA-A*33:03	TP53	R282W	D <u>W</u> RTEENLR	10
HLA-A*03:01	AKR1A1	D63N	ALKEN <u>N</u> VGPGK	10
HLA-A*01:01	CDO1	E41K	<u>K</u> SDPTEWAMY	10
HLA-A*01:01	PRSS23	E300D	DVKD <u>D</u> TYDLLY	11
HLA-A*02:01	RADIL	T550M	<u>L</u> MASEEAMAVL	11

HLA-A*01:01	SDK1	D644N	Q <b>T</b> W <b>S</b> G <b>D</b> I <b>G</b> N <b>Y</b>	10
HLA-A*03:01	SYT7	T133M	R <b>M</b> VQ <b>S</b> H <b>L</b> AAGK	11
HLA-A*03:01	SYT8	T133M	<b>M</b> VQ <b>S</b> H <b>L</b> AAGK	10
HLA-B*07:02	TAS2R43	L5R	<b>R</b> PIIFSSL	8
HLA-A*02:01	TP53	C135Y	<b>Y</b> QLAKTCPV	9
HLA-A*01:01	TP53	I232F	SDCT <b>T</b> FHY	8
HLA-B*08:01	UBE2G2	E12A	TALKRLMA <b>A</b>	9
HLA-B*08:01	UBE2G2	E12A	ALKRLMA <b>A</b>	8

**Table S1: Summary table listing the peptide sequences detected by immunopeptidomics.** Peptides of different lengths, derived from various genomically altered driver genes and passenger mutations, are presented across different HLA alleles. Underscored letters indicate mutated amino acids.

HLA Allele	Gene	Mutation	COS-7 (Monkey)	K562 (Human, Baseline)	K562 (Human, + IFN- $\gamma$ )	Match Status
<b>I. Positive Set (N=5)</b>						
HLA-A*02:01	TP53	H193Y	Detected	Detected	N/A	Match
HLA-A*03:01	KRAS	G12R	Detected	Detected	N/A	Match
HLA-A*24:02	ESR1	D538G	Detected	Detected	N/A	Match
HLA-A*03:01	CTNNB1	T41A	Detected	Detected	N/A	Match
HLA-A*02:01	TP53	R213L	Detected	Detected	N/A	Match
<b>II. Negative Set (N = 9; 5 tested under IFN-<math>\gamma</math>)</b>						
HLA-A*02:01	SF3B1	K700E	Not detected	Not detected	N/A	Match
HLA-A*02:01	CDKN2A	P114L	Not detected	Not detected	Not detected	Match
HLA-B*58:01	TP53	R248W	Not detected	Not detected	Not detected	Match
HLA-B*07:02	PIK3CA	E453K	Not detected	Not detected	Not detected	Match
HLA-B*07:02	TP53	R158L	Not detected	Not detected	Not detected	Match
HLA-C*07:01	PPP2R1A	R183W	Not detected	Not detected	Not detected	Match
HLA-A*03:01	PPP2R1A	R183W	Not detected	Not detected	N/A	Match
HLA-B*07:02	TP53	P152L	Not detected	Not detected	N/A	Match
HLA-B*07:02	TP53	R249S	Not detected	Not detected	N/A	Match

**Table S2: Summary table comparing neoepitope presentation across monkey and human cell lines under baseline and IFN- $\gamma$ -stimulated conditions.** Neoepitope–HLA allele combinations analyzed by mass spectrometry are listed for COS-7 (monkey) and K562 (human) cell lines. Presentation outcomes are shown as Detected or Not detected under baseline and IFN- $\gamma$  (100 IU/mL, 24 h) treatment. The “Match Status” column indicates concordance between the COS-7 and K562 systems. The positive set includes neoepitopes detected in the COS-7 system, while the negative set contains neoepitopes not detected in COS-7; five of these were re-screened under IFN- $\gamma$  treatment to evaluate presentation stability. N/A indicates conditions that were not assessed. All combinations selected for K562 validation were predicted as strong binders (NetMHC EL Rank < 0.5). N/A indicates conditions not assessed.