

## Supplementary tables

Table SI. Synthetic guide RNA for genome editing.

Knock out/in gene	Synthetic guide RNA
<i>TAP2</i> KO	5'-GGGGGCUGCUAAAGCUAAGA-3'
<i>HLA-A*24:02:01:01</i> KO	5'-GAGUAUUGGGACGAGGAGAC-3'
<i>HLA-B*35:08:01</i> KO	5'-GCUGUCGAACCUCACGAACU-3'
<i>HLA-C*04:01:01:06</i> KO	5'-GACACAGAAGUACAAGCGCC-3'
<i>HLA allele</i> cDNA knock-in	5'-CCCUCGUCCUGCUACUCUCG-3'
	5'-CCUGGGCACUGUCACUGCCU-3'

Table SII. Synthetic primers for PCR and gene sequencing.

Sequencing target	Primer for PCR and Sequencing	Amplicon size, bp	T <sub>m</sub> , °C <sup>a</sup>
<i>TAP2</i> KO	Forward: 5'-GATTTCTCATCTCGTATCCGTTGACA-3'		64.6
	Reverse: 5'-CTCAGAACAGCCCACAGTGA-3'	390	61.3
<i>HLA-A</i> KO	Forward: 5'-GGGACTCAGATTCTCCCCAGA-3' <sup>b</sup>		62.3
	Reverse: 5'-GATCTCGGACCCGGAGACTGT-3'	589	64.8
<i>HLA-B</i> KO	Forward: 5'-GGGAGGGAAATGGCCTCTGT-3'		61.8
	Reverse: 5'-TCAACTGAAAATGAAACCGGGTAAAC-3'	556	63.7
<i>HLA-C</i> KO	Forward: 5'-GGGACTCAGATTCTCCCCAGA-3' <sup>c</sup>		62.3
	Reverse: 5'-GATCTCAGACGGGGAGACTCG-3'	591	62.8
Each <i>HLA-allele</i> knock-in	Forward: 5'-TTCTCCCTCTCCCAACCTATGTAG-3'		62.3
	Reverse: 5'-CATGAACAACCTTCATATCTGTACAGTGAG-3'	3,055 (wild)	63.2
		1,419 (cDNA knock-in)	
		<0.5k(locus deleted)	
	Reverse: 5'-CGCGGCTCCATCCTCTG-3' <sup>d</sup>	519 (wild),	61.7

389 (cDNA knock-in)

None (locus deleted)

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<sup>a</sup>The melting temperatures were predicted using Tm calculator tool at Thermo Scientific website. <sup>bc</sup>HLA-A, -C shared primer. <sup>d</sup>Reverse primer for short PCR products to confirm that the HLA-A\*24:02:01:01 locus is not remaining. Tm, melting temperature.

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Table SIII. Synthesized peptides

Gene	AAS position	Peptide sequence <sup>a</sup>	Length
<i>KRAS</i>	A146T	ETST <u>K</u> TRQR	9
		GIPFIETST <u>K</u>	10
	G12A	KLVVVGA <u>A</u> GV	10
		LVVVGA <u>A</u> GV	9
		TEYKLVVVGA <u>A</u>	11
		VVGA <u>A</u> GVGK	9
		G12C	KLVVVGAC <u>G</u> V
	G12C	LVVVGAC <u>G</u> V	9
		VVGAC <u>G</u> VGK	9
		VVVGAC <u>G</u> VGK	10
		G12D	KLVVVGAD <u>G</u> V
	G12D	VVGAD <u>G</u> VGK	9
		VVVGAD <u>G</u> VGK	10
		G12R	EYKLVVVGAR <u>R</u>
	G12R	GAR <u>R</u> GVGKSAL	10
		KLVVVGAR <u>R</u> GV	10
		VVGAR <u>R</u> GVGK	9
		VVVGAR <u>R</u> GVGK	10
	G12S	KLVVVGA <u>S</u> GV	10
		LVVVGA <u>S</u> GV	9
		VVGA <u>S</u> GVGK	9

	G12V	GAVGVGKSAL	10
		KLVVVGAVGV	10
		LVVVGAVGV	9
		TEYKLVVVGA <u>V</u>	11
		VVGAVGVGK	9
		VVVGA <u>V</u> GVGK	10
	G13D	KLVVVGAGD <u>V</u>	10
		VVGAGD <u>V</u> GK	9
		VVVGAGD <u>V</u> GK	10
<i>KRAS, NRAS, HRAS</i>	Q61H	AG <u>H</u> EEYSAM	9
		DTAG <u>H</u> EEYSAM	11
	Q61L	DILDTAG <u>L</u> EEY	11
		DTAG <u>L</u> EEYSAM	11
		LLDILDTAG <u>L</u>	10
	Q61R	AG <u>R</u> EEYSAMR	10
		DTAG <u>R</u> EEYSAM	11
<i>TP53</i>	C135F	ALNKMFF <u>Q</u> L	9
		<u>F</u> QLAKTCPV	9
		KMFF <u>Q</u> LAK	8
		KMFF <u>Q</u> LAKT	9
		LNKMFF <u>Q</u> LAK	10
		SPALNKMFF <u>Q</u>	9
		SPALNKMFF <u>Q</u> L	11
		TYSPALNKMFF <u>Q</u>	11

	YSPALNKMF <u>E</u>	10
C176F	EVVRR <u>F</u> PHH	9
	HMTEVVRR <u>E</u>	9
	VVRR <u>F</u> PHHER	10
G245D	NSSCMG <u>D</u> MNR	10
	SSCMG <u>D</u> MNR	9
G245S	G <u>S</u> MNRRPIL	9
	SCMG <u>S</u> MNRR	9
	SSCMG <u>S</u> MNR	9
	SSCMG <u>S</u> MNRR	10
H179R	EVVRRCP <u>H</u> R	9
	<u>R</u> ERCSDSDGL	10
	VVRRCP <u>H</u> RER	10
H193R	<u>R</u> LIRVEGNLR	10
M237I	NY <u>I</u> CNSSCM	9
	YNY <u>I</u> CNSSCM	10
R110L	SYGF <u>L</u> LGFL	8
	SYGF <u>L</u> LGFL	9
	TYQGSYG <u>F</u> L	9
	TYQGSYG <u>F</u> LL	10
R158L	GTRV <u>L</u> AMAIY	10
	RV <u>L</u> AMAIYK	9
	TPPPGTRV <u>L</u>	9
R175H	EVVR <u>H</u> CPHHER	11

	VVR <u>H</u> CPHHER	10
R248Q	MNQR <u>P</u> ILTII	10
	NQR <u>P</u> ILTII	9
	NSSCMGGMN <u>Q</u> R	11
	<u>Q</u> RPILTIITL	10
	SCMGGMN <u>Q</u> R	9
	SSCMGGMN <u>Q</u> R	10
R248W	GMN <u>W</u> RPILTI	10
	MN <u>W</u> RPILTI	9
	N <u>W</u> RPILTII	9
	SSCMGGMN <u>W</u> R	10
	<u>W</u> RPILTIITL	10
R249S	NR <u>S</u> PILTII	9
	R <u>S</u> PILTIITL	10
	<u>S</u> PILTIITL	9
R273C	EV <u>C</u> VCACPGR	10
	LLGRNSFEV <u>C</u> V	11
R273H	EV <u>H</u> VCACPGR	10
	LLGRNSFEV <u>H</u> V	11
	NSFEV <u>H</u> VCA	9
R282W	CACPGRD <u>W</u> R	9
	RVCACPGRD <u>W</u> R	11
Y163C	RVRAMA <u>C</u> ICK	9
	TRVRAMA <u>C</u> ICK	10

	Y220C	VVP <u>C</u> EPPEV	9
		VVVP <u>C</u> EPPEV	10
<i>PIK3CA</i>	C420R	AKEEHR <u>P</u> LAW	10
		GAKEEHR <u>P</u> L	9
		<u>R</u> PLAWGNINL	10
	E542K	AISTRDPL <u>S</u> K	10
		ISTRDPL <u>S</u> K	9
		KAISTRDPL <u>S</u> K	11
		STRDPL <u>S</u> KI	9
		STRDPL <u>S</u> EITK	11
	H1047L	AL <u>H</u> GGWTTK	9
		AL <u>H</u> GGWTTKM	10
		FMKQMNDAL <u>L</u>	9
		<u>L</u> HGGWTTKM	9
	H1047R	EYFMKQMNDAR <u>R</u>	11
		FMKQMNDAR <u>R</u>	9
		YFMKQMNDAR <u>R</u>	10
	R88Q	EFFDETR <u>Q</u> L	9
		ETR <u>Q</u> LCDLR	9
		ETR <u>Q</u> LCDLRLF	11
		FFDETR <u>Q</u> L	8
		REEFFDETR <u>Q</u> L	11
		R <u>Q</u> LCDLRLF	9
<i>EGFR</i>	E746_A750.del	IPVA <u>I</u> K <u>T</u> SP	9

		IPVAIK <u>T</u> SPKA	11
		AIK <u>T</u> SPKANK	10
		IPVAIK <u>T</u> SPK	10
	L858R	HVKITDFG <u>R</u>	9
		ITDFG <u>R</u> AKL	9
		KITDFG <u>R</u> AK	9
		QHVKITDFG <u>R</u>	10
	T790M	LTSTVQL <u>I</u> M	9
		<u>M</u> QLMPFGCLL	10
		QL <u>I</u> MQLMPF	9
		STVQL <u>I</u> MQL	9
		TVQL <u>I</u> MQLM	9
		VQL <u>I</u> MQLMPF	10
<i>BRAF</i>	D594G	DLTVKIG <u>G</u> F	9
		<u>G</u> FGLATVKSR	10
		<u>G</u> GFGLATVK	9
		KIG <u>G</u> FGLATV	10
		KIG <u>G</u> FGLATVK	11
		TVKIG <u>G</u> FGLA	10
	V600E	DFGLATE <u>E</u> KSR	10
		KIGDFGLATE <u>E</u> K	11
CMV- <i>UL83</i> (A02)	-	NLVPMVATV	9
CMV- <i>UL83</i> (A24)	-	QYDPVAALF	9

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<sup>a</sup>Underlined letters mean AAS positions. AAS, amino acid substitution.

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Table SIV. Mutation frequencies of major five cancer driver genes in the HOPE cohort and TCGA.

Gene symbol	AAS position	HOPE, /5,143 cases	TCGA, /24,592 cases	%HOPE/%TCGA ratio
<i>KRAS</i>	G12D	336	757	2.12
	G12V	204	657	1.48
	G13D	162	214	3.55
	G12C	82	384	1.02
	G12A	55	134	1.96
	G12S	55	68	3.87
	A146T	46	65	3.38
	Q61H	36	108	1.59
	G12R	16	166	0.46
	Q61L	16	21	3.64
	K117N	14	17	3.94
	Q61R	14	37	1.68
	G13C	11	32	1.64
<i>TP53</i>	R175H	159	386	1.97
	R273H	106	251	2.02
	R282W	106	201	2.50
	R273C	93	283	1.57
	R248Q	85	292	1.39
	G245S	67	128	2.50

	R248W	60	222	1.29
	Y220C	55	127	2.07
	M237I	17	55	1.48
	C176F	16	54	1.42
	I195T	16	42	1.82
	H179R	15	63	1.14
	G245D	15	50	1.43
	H193R	14	54	1.24
	Y234C	13	42	1.48
	P152L	13	28	2.22
	R158L	12	42	1.37
	R249S	12	45	1.28
	R158H	12	36	1.59
	V157F	11	67	0.79
	Y163C	11	54	0.97
	R110L	11	25	2.10
	C135F	11	24	2.19
<i>PIK3CA</i>	H1047R	127	537	1.13
	E545K	102	575	0.85
	E542K	74	356	0.99
	R88Q	34	75	2.17
	H1047L	22	85	1.24
	C420R	20	46	2.08
	Q546K	13	35	1.78

	R108H	12	25	2.30
<i>EGFR</i>	L858R	122	144	4.05
	E746_A750 deletion	74	123	2.88
	L747_P753 deletion	12	8	7.17
	insertion S			
	G719A	11	18	2.92
	T790M	1	59	0.08
<i>BRAF</i>	V600E	105	833	0.60
	D594G	12	21	2.73

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AAS, amino acid substitution; HOPE, High-tech Omics-based Patient Evaluation project in Shizuoka Cancer Center; TCGA, The Cancer Genome Atlas.

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Table SV. MHC-stabilization assay with the synthesized peptides.

A, HLA-A*02:01								
Peptide ID	Gene	AAS position	Freq. <sup>a</sup>	Sequence <sup>b</sup>	BA_model	EL_model	$\Delta$ HLA <sup>c</sup>	
					IC <sub>50</sub> , nM	%Rank	Aver., %	$\pm$ SD, %
1	<i>KRAS</i>	G12D	336	KLVVVGAD <u>G</u> V	280	3.80	24.1	3.7
2				VVGAD <u>G</u> VGK	35,485	29.00	5.6	3.4
5		G12V	204	KLVVVGAV <u>G</u> V	175	2.10	34.8	7.6
6				LVVVGAV <u>G</u> V	553	2.30	2.4	4.1
7				VVGAV <u>G</u> VGK	30,145	21.00	-0.3	1.0
9		G13D	159	KLVVVGAG <u>D</u> V	348	4.50	9.6	3.0
12		G12C	82	KLVVVGAC <u>G</u> V	167	4.00	32.6	4.6
13				LVVVGAC <u>G</u> V	596	5.10	1.8	2.2
14				VVGAC <u>G</u> VGK	30,282	32.00	3.4	0.7
16		G12A	55	TEYKLVVVGAA <u>A</u>	36,323	43.00	1.1	4.4
17				KLVVVGAA <u>G</u> V	180	3.20	22.8	5.3

18				L <u>V</u> V <u>V</u> G <u>A</u> <u>A</u> GV	559	3.30	1.6	3.9
20		G12S	55	KL <u>V</u> V <u>V</u> G <u>A</u> <u>S</u> GV	258	3.20	26.4	6.8
21				L <u>V</u> V <u>V</u> G <u>A</u> <u>S</u> GV	1532	4.20	-8.9	1.3
26		G12R	16	KL <u>V</u> V <u>V</u> G <u>A</u> <u>R</u> GV	343	4.00	4.0	1.0
29				G <u>A</u> <u>R</u> <u>G</u> <u>V</u> G <u>K</u> SAL	32,222	22.00	2.4	3.0
30	<i>KRAS,</i> <i>NRAS, HRAS</i>	Q61L	16	LLDILDTAG <u>L</u>	113	1.80	7.3	7.7
33	<i>TP53</i>	R273H	106	LLGRNSFEV <u>H</u> V	199	1.40	4.5	6.4
37		R273C	93	LLGRNSFEV <u>C</u> V	385	4.00	9.1	4.8
40		R248Q	85	MN <u>Q</u> RPILTII	9,443	17.00	2.3	5.3
47		R248W	60	GMN <u>W</u> RPILTI	125	1.50	12.4	2.8
48				MN <u>W</u> RPILTI	4,792	5.30	2.0	5.1
50		Y220C	55	V <u>V</u> P <u>C</u> EPPEV	564	0.55	25.9	6.8
53		C176F	16	HMTEV <u>V</u> RR <u>F</u>	9,077	1.90	-0.5	3.2
60		H193R	14	<u>R</u> LIRVEGNLR	9,876	18.00	3.2	2.3

63		R249S	12	R <u>S</u> PILTIITL	5,043	7.90	2.6	8.8
66		C135F	11	SPALNKMFF <u>Q</u> L	903	3.70	22.1	3.5
67				ALNKMFF <u>Q</u> L	16	0.10	15.7	10.4
69				KMFF <u>Q</u> LAKT	196	1.30	4.3	3.7
71				<u>F</u> QLAKTCPV	7	0.58	43.9	2.2
75		R110L	11	TYQGSYG <u>F</u> LL	1,895	11.00	2.6	2.7
82	<i>PIK3CA</i>	E545K	102	SEIT <u>K</u> QEKDF	42,566	40.00	3.8	1.6
88		R88Q	34	R <u>Q</u> LCDLRLF	6,147	9.30	9.3	4.6
89		H1047L	22	FMKQMND <u>A</u> L	89	0.58	2.5	5.2
90			22	AL <u>H</u> GGWTTKM	3,156	2.10	4.0	4.5
92		C420R	20	AKEE <u>H</u> RPLAW	44,117	42.00	1.9	1.1
93				<u>R</u> PLAWGNINL	270	1.30	6.1	4.0
97	<i>EGFR</i>	L858R	122	ITDFG <u>R</u> AKL	7,344	2.80	0.1	4.0
100		T790M	1	LTSTV <u>Q</u> LIM	8,044	8.30	3.5	7.7
102				V <u>Q</u> LIM <u>Q</u> LMPF	5,635	25.00	8.7	6.1

103				QLIMQLMPF	2,774	7.00	5.1	8.4
104				MQLMPFGCLL	26	2.20	45.7	8.1
107	<i>BRAF</i>	D594G	12	TVKIGGFGLA	5,356	9.10	-2.9	2.2
108				KIGGFGLATVK	4,026	12.00	-1.4	1.2
109				KIGGFGLATV	44	0.77	42.6	21.3
CMVpp65A02	CMV- <i>UL83</i>	-	-	NLVPMVATV	18	0.06	56.6	7.9
CMVpp65A24	CMV- <i>UL83</i>	-	-	QYDPVAALF	17,364	3.30	3.1	2.2

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B, HLA-A\*11:01

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Peptide ID	Gene	AAS position	Freq.	Sequence	BA_model	EL_model	$\Delta$ HLA	
					IC <sub>50</sub> , nM	%Rank	Aver., %	$\pm$ SD, %
1	<i>KRAS</i>	G12D	336	KLVVVGADGV	33,137	53.00	15.5	5.0
2				VVGADGVGK	172	0.35	202.8	61.8
3				VVVGADGVGK	194	0.59	236.3	69.0
7		G12V	204	VVGAVGVGK	39	0.10	230.5	77.1
8				VVVGAVGVGK	69	0.35	228.1	69.2

10		G13D	159	VVVGAG <u>D</u> VGK	213	0.59	195.4	58.6
11				VVGAG <u>D</u> VGK	314	0.60	181.2	43.4
14		G12C	82	VVGAC <u>G</u> VGK	73	0.52	234.3	72.6
15				VVVGAC <u>G</u> VGK	122	0.59	123.4	30.1
19		G12A	55	VVGA <u>A</u> GVGK	60	0.18	218.5	65.1
22		G12S	55	VVGAS <u>G</u> VGK	51	0.15	219.1	66.6
23		A146T	46	GIPFIETS <u>T</u> K	167	0.81	73.0	12.1
27		G12R	16	VVVGAR <u>G</u> VGK	162	0.55	198.4	60.9
28				VVGAR <u>G</u> VGK	107	0.33	156.5	35.5
29				GAR <u>G</u> VGKSAL	38,444	34.00	11.2	5.1
31	<i>TP53</i>	R175H	159	VVRH <u>C</u> PHHER	2,073	3.10	68.9	12.2
35		R282W	105	RVCACPGRD <u>W</u> R	4,937	4.30	102.1	2.7
36				CACPGRD <u>W</u> R	7,086	7.20	21.8	3.3
38		R273C	93	EVC <u>V</u> CACPGR	8,971	19.00	11.5	3.8
39		R248Q	85	SSCMGGMN <u>Q</u> R	171	0.49	88.7	9.5

41			SCMGGMN <u>Q</u> R	5,475	2.00	275.5	89.6
42			NSSCMGGMN <u>Q</u> R	5,441	3.40	16.3	12.5
43	G245S	67	SSCMG <u>S</u> MNRR	145	0.78	27.7	5.5
44			SCMG <u>S</u> MNRR	5,603	2.70	224.0	100.7
45			SSCMG <u>S</u> MNR	95	0.54	107.4	30.9
46	R248W	60	SSCMGGMN <u>W</u> R	158	1.10	47.9	6.3
55	C176F	16	VVRR <u>F</u> PHHER	3,614	3.90	25.6	17.8
56	G245D	15	NSSCMG <u>D</u> MNR	2,611	6.60	18.8	10.4
57			SSCMG <u>D</u> MNR	464	1.40	71.5	7.2
59	H179R	15	VVRR <u>C</u> PHRER	9,157	7.70	28.6	6.8
60	H193R	14	<u>R</u> LIRVEGNLR	1,956	3.30	10.6	4.7
61	R158L	12	GTRV <u>L</u> AMAIY	2,509	5.20	8.6	1.9
62			RV <u>L</u> AMAIYK	5	0.01	177.2	97.6
68	C135F	11	LNKM <u>F</u> QLAK	257	4.20	20.5	7.6
70			KM <u>F</u> QLAK	239	1.50	12.6	3.3

76		Y163C	11	TRVRAMA <u>I</u> CK	454	3.30	22.3	1.2
77				RVRAMA <u>I</u> CK	72	0.44	111.4	11.4
81	<i>PIK3CA</i>	E545K	102	STRDPLSEIT <u>K</u>	92	0.04	80.0	32.7
82				SEIT <u>K</u> QEKDF	40,671	32.00	7.5	3.2
84		E542K	74	AISTRDPL <u>S</u> K	99	0.25	79.9	9.1
85				ISTRDPL <u>S</u> K	333	0.48	124.3	30.1
86				KAISTRDPL <u>S</u> K	256	0.22	127.1	28.7
90		H1047L	22	AL <u>H</u> GGWTTKM	7,767	5.00	14.1	11.7
91				AL <u>H</u> GGWTTK	121	0.19	76.2	15.7
92		C420R	20	AKEEHR <u>P</u> LAW	41,444	26.00	12.0	4.8
95	<i>EGFR</i>	L858R	122	HVKITDF <u>G</u> R	4,596	3.00	109.0	17.6
96				KITDF <u>G</u> RAK	101	0.19	51.8	10.6
98		E746_A750del	74	IPVAI <u>K</u> TSPK	173	1.60	28.0	2.3
99				AI <u>K</u> TSPKANK	423	0.54	73.1	12.7
105	<i>BRAF</i>	V600E	105	KIGDFGLATE <u>E</u> K	108	0.28	97.7	4.4

108		D594G	12	KIG <u>G</u> FGLATVK	212	0.67	32.3	4.7
110				GG <u>F</u> GGLATVK	522	0.92	28.0	1.5
CMVpp65A02	CMV-UL83	-	-	NLVPMVATV	31,807	25.00	8.3	2.3
CMVpp65A24	CMV-UL83	-	-	QYDPVAALF	26,028	6.70	3.1	7.3

C, HLA-A\*24:02

Peptide ID	Gene	AAS position	Freq.	Sequence	BA_model	EL_model	ΔHLA	
					IC <sub>50</sub> , nM	%Rank	Aver., %	±SD, %
29	<i>KRAS</i>	G12R	16	G <u>A</u> R <u>G</u> VGKSAL	41,217	30.00	-3.5	2.2
48	<i>TP53</i>	R248W	60	M <u>N</u> W <u>R</u> PILTI	5,038	2.80	25.6	11.6
49				N <u>W</u> R <u>P</u> ILTI	945	0.53	31.9	6.0
51		M237I	17	Y <u>N</u> Y <u>I</u> CNSSCM	953	3.60	48.1	9.6
52				NY <u>I</u> CNSSCM	1,054	1.80	65.4	12.5
53		C176F	16	HMTEV <u>V</u> RR <u>F</u>	3,646	0.40	37.6	10.4
63		R249S	12	R <u>S</u> PILTIITL	7,939	3.00	7.7	6.0
64		C135F	11	TYSPAL <u>N</u> KM <u>F</u>	39	0.01	69.9	15.0

65				YSPALNKMF <u>F</u>	1,256	1.70	37.0	11.0
67				ALNKMF <u>F</u> QL	4,538	2.00	18.5	5.7
72		R110L	11	SYG <u>F</u> LLGF	460	0.40	31.5	16.3
73				SYG <u>F</u> LLGFL	174	0.45	20.8	6.1
74				TYQGSYG <u>F</u> L	116	0.18	28.5	14.9
75				TYQGSYG <u>F</u> LL	22	0.15	22.9	12.0
82	<i>PIK3CA</i>	E545K	102	SEIT <u>K</u> QEKDF	34,856	6.80	2.0	6.5
88		R88Q	34	R <u>Q</u> LCDLRLF	496	0.96	26.3	13.4
92		C420R	20	AKEE <u>H</u> RPLAW	37,377	13.00	4.9	4.0
94	<i>EGFR</i>	L858R	122	QHVKITDF <u>G</u> R	34,358	19.00	2.2	5.2
95				HVKITDF <u>G</u> R	39,532	31.00	4.9	4.8
102		T790M	1	V <u>Q</u> LIMQLMPF	2,408	4.10	25.3	7.8
103				Q <u>L</u> IMQLMPF	3,623	3.00	30.7	15.8
104			1	<u>M</u> QLMPFGCLL	3,423	7.10	21.4	2.9
CMVpp65A02	CMV-UL83	-	-	NLVPMVATV	23,900	9.10	5.3	3.5

CMVpp65A24 CMV-UL83 - - QYDPVAALF 67 0.01 60.8 7.3

D, HLA-A\*33:03

Peptide ID	Gene	AAS position	Freq.	Sequence	BA_model	EL_model	ΔHLA	
					IC <sub>50</sub> , nM	%Rank	Aver., %	±SD, %
1	<i>KRAS</i>	G12D	336	KLVVVGAD <u>G</u> V	33,428	61.00	1.1	2.4
4		G12V	204	TEYKLVVVGA <u>V</u>	32,760	48.00	0.3	1.2
7				VVGA <u>V</u> GVGK	5,218	3.80	1.5	6.6
8				VVVGA <u>V</u> GVGK	7,734	5.20	2.6	5.5
9		G13D	159	KLVVVGAG <u>D</u> V	34,655	64.00	-2.7	3.3
14		G12C	82	VVGAC <u>C</u> GVGK	7,482	7.50	1.9	6.2
15				VVVGAC <u>C</u> GVGK	7,066	7.20	3.3	3.1
19		G12A	55	VVGA <u>A</u> GVGK	9,264	5.90	-3.9	7.3
22		G12S	55	VVGAS <u>S</u> GVGK	9,492	5.70	2.1	1.2
24		A146T	46	ETS <u>T</u> KTRQR	124	0.05	11.4	7.3
25		G12R	16	EYKLVVVGAR <u>R</u>	35	0.11	67.0	13.9

27				VVVGAR <u>G</u> VGK	5,640	5.30	5.5	3.9
28				VVGAR <u>G</u> VGK	5,068	4.00	1.1	2.7
29				GAR <u>G</u> VGKSAL	37,491	36.00	1.3	1.5
31	<i>TP53</i>	R175H	159	VVRH <u>C</u> PHHER	79	0.29	24.9	7.7
32				EVVRH <u>C</u> PHHER	88	0.16	34.7	3.1
34		R273H	106	EVH <u>V</u> CACPGR	68	1.60	49.6	7.9
35		R282W	105	RVCACPGRD <u>W</u> R	2,472	3.60	0.2	1.9
36				CACPGRD <u>W</u> R	214	1.70	2.4	2.8
38		R273C	93	EV <u>C</u> VCACPGR	87	2.60	26.6	7.2
39		R248Q	85	SSCMGGMN <u>Q</u> R	268	0.51	2.6	2.4
41				SCMGGMN <u>Q</u> R	312	0.35	12.3	5.7
42				NSSCMGGMN <u>Q</u> R	405	0.47	-1.4	5.1
43		G245S	67	SSCMG <u>S</u> MNRR	224	0.77	3.5	1.7
44				SCMG <u>S</u> MNRR	297	0.47	2.6	4.9
45				SSCMG <u>S</u> MNR	191	0.61	14.0	3.8

46		R248W	60	SSCMGGMN <u>WR</u>	151	1.10	1.3	2.7
54		C176F	16	EVVRRF <u>PHH</u>	2,113	1.40	-0.2	3.2
55				VVRRF <u>PHHER</u>	83	0.35	11.1	0.9
56		G245D	15	NSSCMG <u>DMNR</u>	359	2.70	2.1	0.2
57				SSCMG <u>DMNR</u>	376	1.40	1.4	5.3
58		H179R	15	EVVRRCP <u>HR</u>	40	0.11	33.2	8.2
59				VVRRCP <u>HRER</u>	406	1.30	11.8	2.0
60		H193R	14	<u>RLIR</u> VEGNLR	783	2.00	0.8	0.6
62		R158L	12	RV <u>L</u> AMAIYK	1,626	2.60	1.6	4.2
68		C135F	11	LNKMFF <u>QLAK</u>	2,737	7.10	1.0	2.2
70				KMFF <u>QLAK</u>	9,201	8.30	1.5	3.7
75		R110L	11	TYQGSYG <u>FLL</u>	8,375	11.00	2.6	3.7
76		Y163C	11	TRVRAMA <u>ICK</u>	4,680	7.10	4.6	1.8
77				RVRAMA <u>ICK</u>	2,119	3.30	-2.4	1.8
78	<i>PIK3CA</i>	H1047R	127	FMKQMND <u>AR</u>	68	0.54	34.0	12.8

79				YFMKQMNDAR	51	0.51	26.6	10.3
80				EYFMKQMNDAR	64	0.21	60.6	14.9
81		E545K	102	STRDPLSEITK	4,567	1.50	15.4	8.0
82				SEITKQEKDF	43,189	40.00	2.0	1.7
83				KQEKDFLWSHR	7,111	5.50	-0.3	3.3
87		R88Q	34	ETRQLCDLR	47	0.20	33.7	11.8
91		H1047L	22	ALHGGWTTK	6,253	3.30	7.0	1.1
92		C420R	20	AKEEHRPLAW	43,719	45.00	1.3	2.6
94	<i>EGFR</i>	L858R	122	QHVKITDFGR	278	0.98	25.4	6.2
95				HVKITDFGR	17	0.06	54.8	9.7
96				KITDFGRAK	6,302	3.60	0.1	6.5
98		E746_A750del	74	IPVAIKTSPK	4,965	6.50	-2.2	5.3
104		T790M	1	MQLMPFGCLL	6,040	18.00	-0.7	4.6
106	<i>BRAF</i>	V600E	105	DFGLATEKSR	440	0.85	3.1	0.6
111		D594G	12	GFGLATVKSR	1,482	2.30	-0.5	2.3

CMVpp65A02	CMV- <i>UL83</i>	-	-	NLVPMVATV	16,395	6.60	0.8	1.5
CMVpp65A24	CMV- <i>UL83</i>	-	-	QYDPVAALF	18,074	3.80	-0.6	0.2

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<sup>a</sup>Mutation frequency in the HOPE cohort of 5,143 patients.<sup>b</sup>Underlined letters mean AAS positions.<sup>c</sup> $\Delta$ HLA means increasing HLA expression. AAS, amino acid substitution; Freq., frequency; CMV, cytomegalovirus.

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