

Chromosome	Start	Stop	Reference	Variant	Transcript	Ensembl Gene ID	Variant Type
3	48641756	48641757	T	A	ENST00000203407	ENSG00000010256	missense
4	1843381	1843382	C	T	ENST00000302787	ENSG00000168924	missense
4	1843381	1843382	C	T	ENST00000302787	ENSG00000168924	missense
4	1843381	1843382	C	T	ENST00000302787	ENSG00000168924	missense
19	21476655	21476656	T	C	ENST00000356929	ENSG00000182141	missense
19	21476655	21476656	T	C	ENST00000356929	ENSG00000182141	missense
22	19865625	19865626	C	G	ENST00000400521	ENSG00000184470	missense

Mutation	Protein Position	Gene Name	HLA Allele	Peptide Length	Sub-peptide Position	Mutation Position
M/L	179	UQCRC1	HLA-B*40:02	10	2	10
V/M	96	LETM1	HLA-A*26:01	9	3	9
V/M	96	LETM1	HLA-C*12:03	9	3	9
V/M	96	LETM1	HLA-C*12:03	9	5	7
K/R	371	ZNF708	HLA-C*03:05	9	11	1
K/R	371	ZNF708	HLA-C*12:03	9	11	1
A/P	478	TXNRD2	HLA-B*40:02	9	4	8

MT Epitope Seq	WT Epitope Seq	Tumor DNA Depth	Tumor DNA VAF	Tumor RNA Depth	Tumor RNA VAF
REMQENDASL	REMQENDASM	746	42.84	251	37.85
WTSTSVGFM	WTSTSVGFV	778	37.02	70	47.14
WTSTSVGFM	WTSTSVGFV	778	37.02	70	47.14
STSVGFMAV	STSVGFVAV	778	37.02	70	47.14
RAFNRSSHL	KAFNRSSHL	4309	40.91	104	39.42
RAFNRSSHL	KAFNRSSHL	4309	40.91	104	39.42
GEVTQGFPL	GEVTQGFAL	533	40.07	28	46.43

Normal Depth	Normal VAF	Gene Expression	Median MT Score	Median WT Score	Median Fold Change
2084	0	22.9386	49.79	115.66	2.323
2113	0.09	7.29694	348.45	2040	5.854
2113	0.09	7.29694	116.26	229.3	1.972
2113	0.09	7.29694	193.7	338.8	1.749
4524	0.2	8.98713	183.42	203.045	1.107
4524	0.2	8.98713	16.4	27.1	1.652
1143	0.09	4.6209	49.53	52.34	1.057

NetMHC WT Score	NetMHC MT Score	NetMHCpan WT Score	NetMHCpan MT Score	PickPocket WT Score
115.66	49.79	61.2	41	158.17
2040	223.09	2692.2	145	711.66
1068.75	2117.25	229.3	106.6	6978.43
4333.92	5344.18	338.8	193.7	11857.88
NA	NA	22	14.6	384.09
37	25.86	27.1	16.4	605.05
22.76	17.22	8.7	6	83.54

PickPocket MT Score	SMM WT Score	SMM MT Score	SMMPMBEC WT Score	SMMPMBEC MT Score
138.91	73.77	49.3	131.17	81.25
348.45	2492.36	451.45	1976.1	381.78
5267.25	22.92	45.31	46.28	116.26
9047.59	25.95	26.07	41.25	42.31
352.24	NA	NA	NA	NA
548.91	12.06	12.45	12.54	13.41
85.36	57.53	55.7	52.34	49.53

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Chromosome	Start	Stop	Reference	Variant	Transcript	Ensembl Gene ID	Variant Type
3	48641756	48641757	T	A	ENST00000203407	ENSG00000010256	missense
19	21476655	21476656	T	C	ENST00000356929	ENSG00000182141	missense
19	21476655	21476656	T	C	ENST00000356929	ENSG00000182141	missense

Mutation	Protein Position	Gene Name	HLA Allele	Peptide Length	Sub-peptide Position	Mutation Position
M/L	179	UQCRC1	HLA-B*40:02	10	2	10
K/R	371	ZNF708	HLA-C*03:05	9	11	1
K/R	371	ZNF708	HLA-C*12:03	9	11	1

MT Epitope Seq	WT Epitope Seq	Tumor DNA Depth	Tumor DNA VAF	Tumor RNA Depth	Tumor RNA VAF
REMQENDASL	REMQENDASM	834	46.89	220	0.91
RAFNRSSHL	KAFNRSSHL	4845	45.88	81	3.7
RAFNRSSHL	KAFNRSSHL	4845	45.88	81	3.7

Normal Depth	Normal VAF	Gene Expression	Median MT Score	Median WT Score	Median Fold Change
2084	0	20.5851	49.79	115.66	2.323
4524	0.2	5.94178	183.42	203.045	1.107
4524	0.2	5.94178	16.4	27.1	1.652

NetMHC WT Score	NetMHC MT Score	NetMHCpan WT Score	NetMHCpan MT Score	PickPocket WT Score
115.66	49.79	61.2	41	158.17
NA	NA	22	14.6	384.09
37	25.86	27.1	16.4	605.05

PickPocket MT Score	SMM WT Score	SMM MT Score	SMMPMBEC WT Score	SMMPMBEC MT Score
138.91	73.77	49.3	131.17	81.25
352.24	NA	NA	NA	NA
548.91	12.06	12.45	12.54	13.41

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[illegible]

19	21476655	21476656	T	C	ENST00000356929	ENSG00000182141
20	2841206	2841207	A	G	ENST00000380445	ENSG00000215305
20	2841206	2841207	A	G	ENST00000380445	ENSG00000215305
22	19865625	19865626	C	G	ENST00000400521	ENSG00000184470

Variant Type	Mutation	Protein Position	Gene Name	HLA Allele	Peptide Length	Sub-peptide Position
missense	N/D	819	GON4L	HLA-C*12:03	9	8
missense	Y/C	412	KCNF1	HLA-C*12:03	9	10
FS	NA	430	TSGA10	HLA-B*40:02	8	221
FS	NA	430	TSGA10	HLA-B*40:02	8	102
FS	NA	430	TSGA10	HLA-B*40:02	8	168
FS	NA	430	TSGA10	HLA-B*40:02	9	157
FS	NA	430	TSGA10	HLA-B*40:02	9	44
FS	NA	430	TSGA10	HLA-B*40:02	9	102
FS	NA	430	TSGA10	HLA-B*40:02	9	8
FS	NA	430	TSGA10	HLA-B*40:02	9	176
FS	NA	430	TSGA10	HLA-B*40:02	9	52
FS	NA	430	TSGA10	HLA-B*40:02	9	139
FS	NA	430	TSGA10	HLA-B*40:02	9	128
FS	NA	430	TSGA10	HLA-B*40:02	10	79
FS	NA	430	TSGA10	HLA-B*40:02	10	170
FS	NA	430	TSGA10	HLA-B*40:02	10	128
FS	NA	430	TSGA10	HLA-B*40:02	10	219
FS	NA	430	TSGA10	HLA-B*40:02	10	114
FS	NA	430	TSGA10	HLA-B*40:02	10	102
FS	NA	430	TSGA10	HLA-B*40:02	11	176
FS	NA	430	TSGA10	HLA-C*03:05	9	236
FS	NA	430	TSGA10	HLA-C*03:05	9	142
FS	NA	430	TSGA10	HLA-C*12:03	9	236
FS	NA	430	TSGA10	HLA-C*12:03	9	142
FS	NA	430	TSGA10	HLA-C*12:03	9	77
FS	NA	430	TSGA10	HLA-C*12:03	9	192
FS	NA	430	TSGA10	HLA-C*12:03	9	125
FS	NA	430	TSGA10	HLA-C*12:03	9	151
missense	K/I	19	CIR1	HLA-C*12:03	9	9
missense	K/I	19	CIR1	HLA-C*12:03	9	6
missense	M/L	179	UQCRC1	HLA-B*40:02	10	2
FS	NA	1514	ADAMTS9	HLA-C*12:03	9	29
missense	V/M	96	LETM1	HLA-A*26:01	9	3
missense	V/M	96	LETM1	HLA-C*12:03	9	3
missense	V/M	96	LETM1	HLA-C*12:03	9	5
missense	H/R	339	ALDH7A1	HLA-B*40:02	9	11
missense	Q/H	230	PPARD	HLA-A*26:01	9	11
missense	Q/H	230	PPARD	HLA-C*12:03	9	11
FS	NA	223	TRMT11	HLA-B*40:02	10	2
FS	NA	223	TRMT11	HLA-B*40:02	11	2
missense	D/N	370	ZCCHC7	HLA-A*24:02	10	9
missense	D/N	370	ZCCHC7	HLA-B*40:02	9	7
missense	D/N	370	ZCCHC7	HLA-C*12:03	9	10
missense	D/N	370	ZCCHC7	HLA-C*12:03	9	7
missense	D/V	370	ZCCHC7	HLA-A*26:01	9	10
missense	D/V	370	ZCCHC7	HLA-B*40:02	9	7
missense	D/V	370	ZCCHC7	HLA-B*40:02	10	7
missense	D/V	370	ZCCHC7	HLA-C*12:03	9	10
missense	S/T	243	ST6GALNAC6	HLA-B*38:01	9	6
missense	S/T	243	ST6GALNAC6	HLA-B*40:02	9	3
missense	K/R	371	ZNF708	HLA-C*03:05	9	11

missense	K/R	371	ZNF708	HLA-C*12:03	9	11
missense	D/G	161	VPS16	HLA-C*03:05	9	6
missense	D/G	161	VPS16	HLA-C*12:03	9	6
missense	A/P	478	TXNRD2	HLA-B*40:02	9	4

Mutation Position	MT Epitope Seq	WT Epitope Seq	Tumor DNA Depth	Tumor DNA VAF	Tumor RNA Depth
4	KAKDPQDKI	KAKNPQDKI	669	23.43	78
2	RCYNKQRVL	RYYNKQRVL	971	6.08	52
0	RERAVQEL	NA	861	40.3	3
0	KELLNRQL	NA	861	40.3	3
0	KESEIQLL	NA	861	40.3	3
0	KEYQSQIAL	NA	861	40.3	3
0	REVEQHLNA	NA	861	40.3	3
0	KELLNRQLV	NA	861	40.3	3
4	WENARQSEA	NA	861	40.3	3
0	KEHLCLAEN	NA	861	40.3	3
0	AERSYKSQI	NA	861	40.3	3
0	NERISMQNL	NA	861	40.3	3
0	SEIELLRSQ	NA	861	40.3	3
0	FEKVSALADL	NA	861	40.3	3
0	SEIQLLKEHL	NA	861	40.3	3
0	SEIELLRSQM	NA	861	40.3	3
0	FERERAVQEL	NA	861	40.3	3
0	QEIEMRENEL	NA	861	40.3	3
0	KELLNRQLVA	NA	861	40.3	3
0	KEHLCLAENKM	NA	861	40.3	3
0	NAYHMSSTM	NA	861	40.3	3
0	ISMQNLEAL	NA	861	40.3	3
0	NAYHMSSTM	NA	861	40.3	3
0	ISMQNLEAL	NA	861	40.3	3
0	VQFEKVSAL	NA	861	40.3	3
0	DVAQFRNVV	NA	861	40.3	3
0	SAHSEIELL	NA	861	40.3	3
0	LVANRDKEY	NA	861	40.3	3
3	ASISNIKKV	ASKSNIKKV	542	5.52	62
6	FHPASISNI	FHPASKSNI	542	5.52	62
10	REMQENDASL	REMQENDASM	577	58.93	190
0	SQRDRVQPI	NA	803	40.22	107
9	WTSTSVGFM	WTSTSVGFV	783	39.19	61
9	WTSTSVGFM	WTSTSVGFV	783	39.19	61
7	STSVGFMAV	STSVGFVAV	783	39.19	61
1	RESIHDEVV	HESIHDEVV	348	3.74	180
1	HLVNGLPPY	QLVNGLPPY	892	3.36	28
1	HLVNGLPPY	QLVNGLPPY	892	3.36	28
10	KENDIVFDPL	KENDIVFDPF	409	43.28	70
10	KENDIVFDPLL	KENDIVFDPFV	409	43.28	70
3	VYNPSPVSPF	VYDPSPVSPF	351	27.35	31
5	REVYNPSPV	REYDPSPV	351	27.35	31
2	YNPSPVSPF	YDPSPVSPF	351	27.35	31
5	REVYNPSPV	REYDPSPV	351	27.35	31
2	YVPSPVSPF	YDPSPVSPF	347	27.35	30
5	REYVVPSPV	REYDPSPV	347	27.35	30
5	REYVVPSPVS	REYDPSPVS	347	27.35	30
2	YVPSPVSPF	YDPSPVSPF	347	27.35	30
6	SHSWLTTGW	SHSWLSTGW	694	41.01	63
9	REKSHSWLT	REKSHSWLS	694	41.01	63
1	RAFNRSSHL	KAFNRSSHL	4047	42.52	118

1	RAFNRSSHL	KAFNRSSHL	4047	42.52	118
6	SANVGGLKL	SANVGDLKL	1280	3.82	74
6	SANVGGLKL	SANVGDLKL	1280	3.82	74
8	GEVTQGFPL	GEVTQGFAL	564	44.15	37

Tumor RNA VAF	Normal Depth	Normal VAF	Gene Expression	Median MT Score	Median WT Score
24.36	1544	0.06	9.17449	227.09	513.97
3.85	1760	0	4.98073	471.82	866.4
66.67	520	0	2.36219	287.56	NA
66.67	520	0	2.36219	443.2	NA
66.67	520	0	2.36219	476.88	NA
66.67	520	0	2.36219	13.89	NA
66.67	520	0	2.36219	81.9	NA
66.67	520	0	2.36219	98.37	NA
66.67	520	0	2.36219	184.02	NA
66.67	520	0	2.36219	185.34	NA
66.67	520	0	2.36219	372.8	NA
66.67	520	0	2.36219	375.72	NA
66.67	520	0	2.36219	448.48	NA
66.67	520	0	2.36219	81.63	NA
66.67	520	0	2.36219	140.89	NA
66.67	520	0	2.36219	144.52	NA
66.67	520	0	2.36219	167.4	NA
66.67	520	0	2.36219	169.9	NA
66.67	520	0	2.36219	373.96	NA
66.67	520	0	2.36219	471.75	NA
66.67	520	0	2.36219	186.875	NA
66.67	520	0	2.36219	303.05	NA
66.67	520	0	2.36219	12.1	NA
66.67	520	0	2.36219	56	NA
66.67	520	0	2.36219	60.69	NA
66.67	520	0	2.36219	241.04	NA
66.67	520	0	2.36219	247.6	NA
66.67	520	0	2.36219	442	NA
4.84	622	0	5.1225	412.5	925.2
4.84	622	0	5.1225	449.59	1960.77
59.47	2084	0	24.5351	49.79	115.66
25.23	782	0	18.2563	278.2	NA
37.7	2113	0.09	10.2637	348.45	2040
37.7	2113	0.09	10.2637	116.26	229.3
37.7	2113	0.09	10.2637	193.7	338.8
0.56	603	0	16.611	203.64	281.8
3.57	1855	0.05	2.73924	344.99	618.28
3.57	1855	0.05	2.73924	325.4	1556.6
22.86	166	0	7.48474	27.47	81.63
22.86	166	0	7.48474	330.1	883.6
74.19	335	0.3	4.66855	47.5	53.54
74.19	335	0.3	4.66855	96.35	146.51
74.19	335	0.3	4.66855	49.2	103.27
74.19	335	0.3	4.66855	179.9	852.53
76.67	336	0.3	4.66855	314.49	8294.88
76.67	336	0.3	4.66855	66.05	146.51
76.67	336	0.3	4.66855	263	989.7
76.67	336	0.3	4.66855	31	103.27
38.1	1601	0.25	8.36518	312.82	326.81
38.1	1601	0.25	8.36518	277.25	953.12
62.71	4524	0.2	9.40023	183.42	203.045

62.71	4524	0.2	9.40023	16.4	27.1
8.11	2574	0	9.36587	477.27	811.445
8.11	2574	0	9.36587	462.9	1342.2
48.65	1143	0.09	5.87289	49.53	52.34

Median Fold Change	NetMHC WT Score	NetMHC MT Score	NetMHCpan WT Score	NetMHCpan MT Score
2.263	513.97	227.09	6557.2	5507.5
1.836	934.63	471.82	866.4	3438.7
NA	NA	287.56	NA	222.9
NA	NA	379.83	NA	443.2
NA	NA	297.4	NA	208
NA	NA	13.89	NA	9.2
NA	NA	92.85	NA	81.9
NA	NA	134.99	NA	57.5
NA	NA	89.66	NA	824.1
NA	NA	185.34	NA	1176
NA	NA	1239.18	NA	372.8
NA	NA	871.57	NA	259.5
NA	NA	448.48	NA	1743.2
NA	NA	246.63	NA	80.6
NA	NA	86.8	NA	81.8
NA	NA	144.52	NA	40.8
NA	NA	321.09	NA	167.4
NA	NA	93.35	NA	169.9
NA	NA	196.14	NA	366.9
NA	NA	418.9	NA	420.8
NA	NA	NA	NA	47.2
NA	NA	NA	NA	14
NA	NA	12.1	NA	19.1
NA	NA	628.82	NA	31.2
NA	NA	60.69	NA	37.4
NA	NA	241.04	NA	4755.5
NA	NA	9297.37	NA	247.6
NA	NA	5694.67	NA	442
2.243	925.2	1291.23	4204.4	412.5
4.361	1960.77	449.59	7115.6	911.1
2.323	115.66	49.79	61.2	41
NA	NA	1161.97	NA	278.2
5.854	2040	223.09	2692.2	145
1.972	1068.75	2117.25	229.3	106.6
1.749	4333.92	5344.18	338.8	193.7
1.384	411.78	204.4	281.8	84.8
1.792	190.15	46.63	434.8	177.2
4.784	6718.66	1896.77	1556.6	325.4
2.972	30.38	14.49	47.1	15.1
2.677	258.63	104.35	469.5	114.9
1.127	43.38	43.38	68.9	36.6
1.521	134.44	51.29	43.4	25.2
2.099	103.27	49.2	7259	509.6
4.739	852.53	179.9	13387	6985.8
26.376	8495.79	37.05	8649.6	43.2
2.218	134.44	55.49	43.4	14.7
3.763	1068.7	392.37	989.7	263
3.331	103.27	19.38	7259	31
1.045	535.5	752.4	350.7	402.2
3.438	1295.1	330.14	335.6	162.3
1.107	NA	NA	22	14.6

1.652	37	25.86	27.1	16.4
1.7	NA	NA	583.6	219.4
2.9	21186.99	11360.79	1342.2	462.9
1.057	22.76	17.22	8.7	6

PickPocket WT Score	PickPocket MT Score	SMM WT Score	SMM MT Score	SMPMBEC WT Score
2635.42	2010.83	2.93	2.93	3.72
4151.52	2664.09	54.98	58.64	121.74
NA	367.82	NA	278.37	NA
NA	337.32	NA	3432.65	NA
NA	476.88	NA	1041.43	NA
NA	39.17	NA	14.15	NA
NA	392.49	NA	68.68	NA
NA	497.98	NA	63.95	NA
NA	508.87	NA	74.28	NA
NA	1062.03	NA	51.39	NA
NA	883.6	NA	286.99	NA
NA	659.75	NA	375.72	NA
NA	953.12	NA	106.87	NA
NA	618.28	NA	77.25	NA
NA	759.4	NA	140.89	NA
NA	560.92	NA	143.84	NA
NA	492.62	NA	78.68	NA
NA	751.22	NA	70.13	NA
NA	767.66	NA	463.33	NA
NA	471.75	NA	6105.06	NA
NA	326.55	NA	NA	NA
NA	592.1	NA	NA	NA
NA	1097.07	NA	9.47	NA
NA	2314.53	NA	56	NA
NA	1584.89	NA	39.19	NA
NA	22451.54	NA	25.6	NA
NA	1672.99	NA	47.23	NA
NA	14882.82	NA	42.29	NA
2240.61	4106.84	3.75	16.23	4.55
9346.08	7208.66	23.03	23.03	24.51
158.17	138.91	73.77	49.3	131.17
NA	3454.02	NA	34.69	NA
711.66	348.45	2492.36	451.45	1976.1
6978.43	5267.25	22.92	45.31	46.28
11857.88	9047.59	25.95	26.07	41.25
356.07	251.87	154.48	203.64	168.99
618.28	396.76	733.85	353.68	642.41
25017.04	18082.85	32.98	32.98	48.13
333.69	209.55	194.94	79.78	81.63
883.6	330.1	1226.56	649.67	5289.81
396.76	176.24	40.62	47.5	53.54
194.27	163.39	206	124.41	146.51
4830.5	5044.15	42	39.74	28.02
16404.99	14882.82	18.76	17.03	45.97
4062.65	456.69	6896.2	314.49	8294.88
194.27	148.23	206	98.37	146.51
1332.95	1097.07	313.25	197.19	308.2
4830.5	2873.7	42	46.37	28.02
190.11	196.38	85.92	96.18	326.81
953.12	652.65	1451.64	265.99	935.13
384.09	352.24	NA	NA	NA

605.05	548.91	12.06	12.45	12.54
1039.29	735.14	NA	NA	NA
4936.17	2936.57	30.35	30.35	49.71
83.54	85.36	57.53	55.7	52.34

SMMPMBEC MT Score	
3.26	
92.35	
675.26	
4802.53	
2293.35	
10.96	
80.89	
98.37	
184.02	
167.44	
329.51	
356.34	
181.92	
81.63	
229	
199.45	
153.4	
194.01	
373.96	
12631.07	
NA	
NA	
11.73	
55.26	
68.46	
12.54	
37.71	
63.89	
19.65	
17.92	
81.25	
55.77	
381.78	
116.26	
42.31	
148.89	
344.99	
38.59	
27.47	
5668.13	
52.08	
96.35	
36.76	
36.09	
359.59	
66.05	
245.37	
27	
312.82	
277.25	
NA	

13.41	
NA	
44.61	
49.53	

[illegible]

Variant Type	Mutation	Protein Position	Gene Name	HLA Allele	Peptide Length	Sub-peptide Position
FS	NA	430	TSGA10	HLA-B*40:02	8	221
FS	NA	430	TSGA10	HLA-B*40:02	8	102
FS	NA	430	TSGA10	HLA-B*40:02	8	168
FS	NA	430	TSGA10	HLA-B*40:02	9	157
FS	NA	430	TSGA10	HLA-B*40:02	9	44
FS	NA	430	TSGA10	HLA-B*40:02	9	102
FS	NA	430	TSGA10	HLA-B*40:02	9	8
FS	NA	430	TSGA10	HLA-B*40:02	9	176
FS	NA	430	TSGA10	HLA-B*40:02	9	52
FS	NA	430	TSGA10	HLA-B*40:02	9	139
FS	NA	430	TSGA10	HLA-B*40:02	9	128
FS	NA	430	TSGA10	HLA-B*40:02	10	79
FS	NA	430	TSGA10	HLA-B*40:02	10	170
FS	NA	430	TSGA10	HLA-B*40:02	10	128
FS	NA	430	TSGA10	HLA-B*40:02	10	219
FS	NA	430	TSGA10	HLA-B*40:02	10	114
FS	NA	430	TSGA10	HLA-B*40:02	10	102
FS	NA	430	TSGA10	HLA-B*40:02	11	176
FS	NA	430	TSGA10	HLA-C*03:05	9	236
FS	NA	430	TSGA10	HLA-C*03:05	9	142
FS	NA	430	TSGA10	HLA-C*12:03	9	236
FS	NA	430	TSGA10	HLA-C*12:03	9	142
FS	NA	430	TSGA10	HLA-C*12:03	9	77
FS	NA	430	TSGA10	HLA-C*12:03	9	192
FS	NA	430	TSGA10	HLA-C*12:03	9	125
FS	NA	430	TSGA10	HLA-C*12:03	9	151
missense	M/L	179	UQCRC1	HLA-B*40:02	10	2
FS	NA	1514	ADAMTS9	HLA-C*12:03	9	29
missense	V/M	96	LETM1	HLA-A*26:01	9	3
missense	V/M	96	LETM1	HLA-C*12:03	9	3
missense	V/M	96	LETM1	HLA-C*12:03	9	5
FS	NA	223	TRMT11	HLA-B*40:02	10	2
FS	NA	223	TRMT11	HLA-B*40:02	11	2
missense	D/N	370	ZCCHC7	HLA-A*24:02	10	9
missense	D/N	370	ZCCHC7	HLA-B*40:02	9	7
missense	D/N	370	ZCCHC7	HLA-C*12:03	9	10
missense	D/N	370	ZCCHC7	HLA-C*12:03	9	7
missense	D/V	370	ZCCHC7	HLA-A*26:01	9	10
missense	D/V	370	ZCCHC7	HLA-B*40:02	9	7
missense	D/V	370	ZCCHC7	HLA-B*40:02	10	7
missense	D/V	370	ZCCHC7	HLA-C*12:03	9	10
missense	S/T	243	ST6GALNAC6	HLA-B*38:01	9	6
missense	S/T	243	ST6GALNAC6	HLA-B*40:02	9	3
missense	V/A	552	NAALAD2	HLA-B*40:02	9	11
missense	K/R	371	ZNF708	HLA-C*03:05	9	11
missense	K/R	371	ZNF708	HLA-C*12:03	9	11
missense	A/P	478	TXNRD2	HLA-B*40:02	9	4

Mutation Position	MT Epitope Seq	WT Epitope Seq	Tumor DNA Depth	Tumor DNA VAF	Tumor RNA Depth
0	RERAVQEL	NA	752	34.97	9
0	KELLNRQL	NA	752	34.97	9
0	KESEIQLL	NA	752	34.97	9
0	KEYQSQIAL	NA	752	34.97	9
0	REVEQHNA	NA	752	34.97	9
0	KELLNRQLV	NA	752	34.97	9
4	WENARQSEA	NA	752	34.97	9
0	KEHLCLAEN	NA	752	34.97	9
0	AERSYKSQI	NA	752	34.97	9
0	NERISMQNL	NA	752	34.97	9
0	SEIELLRSQ	NA	752	34.97	9
0	FEKVSALADL	NA	752	34.97	9
0	SEIQLLKEHL	NA	752	34.97	9
0	SEIELLRSQM	NA	752	34.97	9
0	FERERAVQEL	NA	752	34.97	9
0	QEIEMRENEL	NA	752	34.97	9
0	KELLNRQLVA	NA	752	34.97	9
0	KEHLCLAENKM	NA	752	34.97	9
0	NAYHMSSTM	NA	752	34.97	9
0	ISMQNLEAL	NA	752	34.97	9
0	NAYHMSSTM	NA	752	34.97	9
0	ISMQNLEAL	NA	752	34.97	9
0	VQFEKVSAL	NA	752	34.97	9
0	DVAQFRNVV	NA	752	34.97	9
0	SAHSEIELL	NA	752	34.97	9
0	LVANRDKEY	NA	752	34.97	9
10	REMQENDASL	REMQENDASM	739	32.88	975
0	SQRDRVQPI	NA	755	41.72	383
9	WTSTSVGFV	WTSTSVGFV	773	33.72	205
9	WTSTSVGFV	WTSTSVGFV	773	33.72	205
7	STSVGFMAV	STSVGFVAV	773	33.72	205
10	KENDIVFDPL	KENDIVFDPF	443	37.7	269
10	KENDIVFDPLL	KENDIVFDPFV	443	37.7	269
3	VYNPSPVSPF	VYDPSPVSPF	375	31.2	140
5	REVYNPSPV	REVYDPSPV	375	31.2	140
2	YNPSPVSPF	YDPSPVSPF	375	31.2	140
5	REVYNPSPV	REVYDPSPV	375	31.2	140
2	YVPSPVSPF	YDPSPVSPF	375	31.2	140
5	REVVVPSPV	REVYDPSPV	375	31.2	140
5	REVVVPSPVS	REVYDPSPVS	375	31.2	140
2	YVPSPVSPF	YDPSPVSPF	375	31.2	140
6	SHSWLTTGW	SHSWLSTGW	551	38.41	227
9	REKSHSWLT	REKSHSWLS	551	38.41	227
1	AEKFYDPTF	VEKFYDPTF	899	7.11	155
1	RAFNRSSHL	KAFNRSSHL	4078	37.87	335
1	RAFNRSSHL	KAFNRSSHL	4078	37.87	335
8	GEVTQGFPL	GEVTQGFAL	582	36.71	152

Tumor RNA VAF	Normal Depth	Normal VAF	Gene Expression	Median MT Score	Median WT Score
55.56	520	0	2.7974	287.56	NA
55.56	520	0	2.7974	443.2	NA
55.56	520	0	2.7974	476.88	NA
55.56	520	0	2.7974	13.89	NA
55.56	520	0	2.7974	81.9	NA
55.56	520	0	2.7974	98.37	NA
55.56	520	0	2.7974	184.02	NA
55.56	520	0	2.7974	185.34	NA
55.56	520	0	2.7974	372.8	NA
55.56	520	0	2.7974	375.72	NA
55.56	520	0	2.7974	448.48	NA
55.56	520	0	2.7974	81.63	NA
55.56	520	0	2.7974	140.89	NA
55.56	520	0	2.7974	144.52	NA
55.56	520	0	2.7974	167.4	NA
55.56	520	0	2.7974	169.9	NA
55.56	520	0	2.7974	373.96	NA
55.56	520	0	2.7974	471.75	NA
55.56	520	0	2.7974	186.875	NA
55.56	520	0	2.7974	303.05	NA
55.56	520	0	2.7974	12.1	NA
55.56	520	0	2.7974	56	NA
55.56	520	0	2.7974	60.69	NA
55.56	520	0	2.7974	241.04	NA
55.56	520	0	2.7974	247.6	NA
55.56	520	0	2.7974	442	NA
40.57	2084	0	29.4963	49.79	115.66
22.72	782	0	26.9401	278.2	NA
42.44	2113	0.09	9.71658	348.45	2040
42.44	2113	0.09	9.71658	116.26	229.3
42.44	2113	0.09	9.71658	193.7	338.8
30.11	166	0	8.00036	27.47	81.63
30.11	166	0	8.00036	330.1	883.6
43.26	335	0.3	5.47939	47.5	53.54
43.26	335	0.3	5.47939	96.35	146.51
43.26	335	0.3	5.47939	49.2	103.27
43.26	335	0.3	5.47939	179.9	852.53
42.14	336	0.3	5.47939	314.49	8294.88
42.14	336	0.3	5.47939	66.05	146.51
42.14	336	0.3	5.47939	263	989.7
42.14	336	0.3	5.47939	31	103.27
36.12	1601	0.25	7.7439	312.82	326.81
36.12	1601	0.25	7.7439	277.25	953.12
0.65	269	0	6.53175	185.4	401.08
38.39	4524	0.2	8.71444	183.42	203.045
38.39	4524	0.2	8.71444	16.4	27.1
37.5	1143	0.09	5.53544	49.53	52.34

Median Fold Change	NetMHC WT Score	NetMHC MT Score	NetMHCpan WT Score	NetMHCpan MT Score
NA	NA	287.56	NA	222.9
NA	NA	379.83	NA	443.2
NA	NA	297.4	NA	208
NA	NA	13.89	NA	9.2
NA	NA	92.85	NA	81.9
NA	NA	134.99	NA	57.5
NA	NA	89.66	NA	824.1
NA	NA	185.34	NA	1176
NA	NA	1239.18	NA	372.8
NA	NA	871.57	NA	259.5
NA	NA	448.48	NA	1743.2
NA	NA	246.63	NA	80.6
NA	NA	86.8	NA	81.8
NA	NA	144.52	NA	40.8
NA	NA	321.09	NA	167.4
NA	NA	93.35	NA	169.9
NA	NA	196.14	NA	366.9
NA	NA	418.9	NA	420.8
NA	NA	NA	NA	47.2
NA	NA	NA	NA	14
NA	NA	12.1	NA	19.1
NA	NA	628.82	NA	31.2
NA	NA	60.69	NA	37.4
NA	NA	241.04	NA	4755.5
NA	NA	9297.37	NA	247.6
NA	NA	5694.67	NA	442
2.323	115.66	49.79	61.2	41
NA	NA	1161.97	NA	278.2
5.854	2040	223.09	2692.2	145
1.972	1068.75	2117.25	229.3	106.6
1.749	4333.92	5344.18	338.8	193.7
2.972	30.38	14.49	47.1	15.1
2.677	258.63	104.35	469.5	114.9
1.127	43.38	43.38	68.9	36.6
1.521	134.44	51.29	43.4	25.2
2.099	103.27	49.2	7259	509.6
4.739	852.53	179.9	13387	6985.8
26.376	8495.79	37.05	8649.6	43.2
2.218	134.44	55.49	43.4	14.7
3.763	1068.7	392.37	989.7	263
3.331	103.27	19.38	7259	31
1.045	535.5	752.4	350.7	402.2
3.438	1295.1	330.14	335.6	162.3
2.163	2618.28	818.85	668.1	185.4
1.107	NA	NA	22	14.6
1.652	37	25.86	27.1	16.4
1.057	22.76	17.22	8.7	6

PickPocket WT Score	PickPocket MT Score	SMM WT Score	SMM MT Score	SMMPMBEC WT Score
NA	367.82	NA	278.37	NA
NA	337.32	NA	3432.65	NA
NA	476.88	NA	1041.43	NA
NA	39.17	NA	14.15	NA
NA	392.49	NA	68.68	NA
NA	497.98	NA	63.95	NA
NA	508.87	NA	74.28	NA
NA	1062.03	NA	51.39	NA
NA	883.6	NA	286.99	NA
NA	659.75	NA	375.72	NA
NA	953.12	NA	106.87	NA
NA	618.28	NA	77.25	NA
NA	759.4	NA	140.89	NA
NA	560.92	NA	143.84	NA
NA	492.62	NA	78.68	NA
NA	751.22	NA	70.13	NA
NA	767.66	NA	463.33	NA
NA	471.75	NA	6105.06	NA
NA	326.55	NA	NA	NA
NA	592.1	NA	NA	NA
NA	1097.07	NA	9.47	NA
NA	2314.53	NA	56	NA
NA	1584.89	NA	39.19	NA
NA	22451.54	NA	25.6	NA
NA	1672.99	NA	47.23	NA
NA	14882.82	NA	42.29	NA
158.17	138.91	73.77	49.3	131.17
NA	3454.02	NA	34.69	NA
711.66	348.45	2492.36	451.45	1976.1
6978.43	5267.25	22.92	45.31	46.28
11857.88	9047.59	25.95	26.07	41.25
333.69	209.55	194.94	79.78	81.63
883.6	330.1	1226.56	649.67	5289.81
396.76	176.24	40.62	47.5	53.54
194.27	163.39	206	124.41	146.51
4830.5	5044.15	42	39.74	28.02
16404.99	14882.82	18.76	17.03	45.97
4062.65	456.69	6896.2	314.49	8294.88
194.27	148.23	206	98.37	146.51
1332.95	1097.07	313.25	197.19	308.2
4830.5	2873.7	42	46.37	28.02
190.11	196.38	85.92	96.18	326.81
953.12	652.65	1451.64	265.99	935.13
401.08	312.72	338.73	147.52	258.15
384.09	352.24	NA	NA	NA
605.05	548.91	12.06	12.45	12.54
83.54	85.36	57.53	55.7	52.34

SMMPMBEC MT Score	
675.26	
4802.53	
2293.35	
10.96	
80.89	
98.37	
184.02	
167.44	
329.51	
356.34	
181.92	
81.63	
229	
199.45	
153.4	
194.01	
373.96	
12631.07	
NA	
NA	
11.73	
55.26	
68.46	
12.54	
37.71	
63.89	
81.25	
55.77	
381.78	
116.26	
42.31	
27.47	
5668.13	
52.08	
96.35	
36.76	
36.09	
359.59	
66.05	
245.37	
27	
312.82	
277.25	
125.57	
NA	
13.41	
49.53	

Chromosome	Start	Stop	Reference	Variant	Transcript	Ensembl Gene ID
3	48641756	48641757	T	A	ENST00000203407	ENSG00000010256
4	1843381	1843382	C	T	ENST00000302787	ENSG00000168924
4	1843381	1843382	C	T	ENST00000302787	ENSG00000168924
4	1843381	1843382	C	T	ENST00000302787	ENSG00000168924
5	64875431	64875432	T	A	ENST00000261308	ENSG00000113593
5	64875431	64875432	T	A	ENST00000261308	ENSG00000113593
5	140562249	140562250	C	T	ENST00000361016	ENSG00000196963
5	140562249	140562250	C	T	ENST00000361016	ENSG00000196963
5	141019130	141019131	A	G	ENST00000297164	ENSG00000164620
6	150001238	150001239	C	G	ENST00000543571	ENSG00000131023
9	37354730	37354731	G	A	ENST00000336755	ENSG00000147905
9	37354730	37354731	G	A	ENST00000336755	ENSG00000147905
9	37354730	37354731	G	A	ENST00000336755	ENSG00000147905
9	37354730	37354731	G	A	ENST00000336755	ENSG00000147905
9	37354731	37354732	A	T	ENST00000336755	ENSG00000147905
9	37354731	37354732	A	T	ENST00000336755	ENSG00000147905
9	37354731	37354732	A	T	ENST00000336755	ENSG00000147905
9	37354731	37354732	A	T	ENST00000336755	ENSG00000147905
9	130649846	130649847	C	G	ENST00000373146	ENSG00000160408
9	130649846	130649847	C	G	ENST00000373146	ENSG00000160408
16	3016649	3016650	G	T	ENST00000303746	ENSG00000131650
17	34257197	34257198	T	A	ENST00000293273	ENSG00000187456
17	70845778	70845779	C	A	ENST00000542342	ENSG00000133195
19	21476655	21476656	T	C	ENST00000356929	ENSG00000182141
19	21476655	21476656	T	C	ENST00000356929	ENSG00000182141
22	19865625	19865626	C	G	ENST00000400521	ENSG00000184470
22	31741026	31741027	C	A	ENST00000266269	ENSG00000100105
22	31741026	31741027	C	A	ENST00000266269	ENSG00000100105
22	31741026	31741027	C	A	ENST00000266269	ENSG00000100105

Variant Type	Mutation	Protein Position	Gene Name	HLA Allele	Peptide Length	Sub-peptide Position
missense	M/L	179	UQCRC1	HLA-B*40:02	10	2
missense	V/M	96	LETM1	HLA-A*26:01	9	3
missense	V/M	96	LETM1	HLA-C*12:03	9	3
missense	V/M	96	LETM1	HLA-C*12:03	9	5
missense	F/I	448	PPWD1	HLA-C*12:03	9	6
missense	F/I	448	PPWD1	HLA-C*12:03	9	4
missense	T/M	39	PCDHB16	HLA-B*40:02	10	11
missense	T/M	39	PCDHB16	HLA-C*12:03	9	3
missense	R/G	140	RELL2	HLA-C*03:05	9	6
missense	D/H	789	LATS1	HLA-C*12:03	9	11
missense	D/N	370	ZCCHC7	HLA-A*24:02	10	9
missense	D/N	370	ZCCHC7	HLA-B*40:02	9	7
missense	D/N	370	ZCCHC7	HLA-C*12:03	9	10
missense	D/N	370	ZCCHC7	HLA-C*12:03	9	7
missense	D/V	370	ZCCHC7	HLA-A*26:01	9	10
missense	D/V	370	ZCCHC7	HLA-B*40:02	9	7
missense	D/V	370	ZCCHC7	HLA-B*40:02	10	7
missense	D/V	370	ZCCHC7	HLA-C*12:03	9	10
missense	S/T	243	ST6GALNAC6	HLA-B*38:01	9	6
missense	S/T	243	ST6GALNAC6	HLA-B*40:02	9	3
missense	G/V	165	KREMEN2	HLA-C*12:03	9	3
missense	N/I	53	RDM1	HLA-A*24:02	9	3
missense	V/F	206	SLC39A11	HLA-C*12:03	9	9
missense	K/R	371	ZNF708	HLA-C*03:05	9	11
missense	K/R	371	ZNF708	HLA-C*12:03	9	11
missense	A/P	478	TXNRD2	HLA-B*40:02	9	4
missense	D/Y	188	PATZ1	HLA-A*24:02	9	10
missense	D/Y	188	PATZ1	HLA-C*12:03	9	11
missense	D/Y	188	PATZ1	HLA-C*12:03	9	10

Mutation Position	MT Epitope Seq	WT Epitope Seq	Tumor DNA Depth	Tumor DNA VAF	Tumor RNA Depth
10	REMQENDASL	REMQENDASM	1078	44.86	398
9	WTSTSVGFM	WTSTSVGFV	882	42.71	38
9	WTSTSVGFM	WTSTSVGFV	882	42.71	38
7	STSVGFMAV	STSVGFVAV	882	42.71	38
6	FKKNRIYMF	FKKNRFYMF	354	41.41	20
8	TSFKKNRIY	TSFKKNRFY	354	41.41	20
1	MERGSFVANL	TERGSFVANL	897	18.71	13
9	GSYSVVEEM	GSYSVVEET	897	18.71	13
6	CSRSKGPPL	CSRSKRPPPL	1160	40.4	25
1	HMMSLLIRM	DMMSLLIRM	316	6.6	16
3	VYNPSPVSPF	VYDPSPVSPF	420	38.86	59
5	REVYNPSPV	REVYDPSPV	420	38.86	59
2	YNPSPVSPF	YDPSPVSPF	420	38.86	59
5	REVYNPSPV	REVYDPSPV	420	38.86	59
2	YVPSPVSPF	YDPSPVSPF	426	38.41	59
5	REVYVPSPV	REVYDPSPV	426	38.41	59
5	REVYVPSPVS	REVYDPSPVS	426	38.41	59
2	YVPSPVSPF	YDPSPVSPF	426	38.41	59
6	SHSWLTTGW	SHSWLSTGW	772	40.67	62
9	REKSHSWLT	REKSHSWLS	772	40.67	62
9	RMKGYQLAV	RMKGYQLAG	1228	39.98	5
9	LYSVRVFPI	LYSVRVFPN	957	43.18	10
3	HNPEGLAV	HNPEGLAV	1061	42.2	22
1	RAFNRSSHL	KAFNRSSHL	9320	42.58	48
1	RAFNRSSHL	KAFNRSSHL	9320	42.58	48
8	GEVTQGFPL	GEVTQGFAL	675	45.41	57
2	LYMTNGAAL	LDMTNGAAL	1582	41.54	69
1	YMTNGAALA	DMTNGAALA	1582	41.54	69
2	LYMTNGAAL	LDMTNGAAL	1582	41.54	69

Tumor RNA VAF	Normal Depth	Normal VAF	Gene Expression	Median MT Score	Median WT Score
38.19	2084	0	109.673	49.79	115.66
63.16	2113	0.09	9.43348	348.45	2040
63.16	2113	0.09	9.43348	116.26	229.3
63.16	2113	0.09	9.43348	193.7	338.8
55	221	0.45	11.4721	77.88	209.12
55	221	0.45	11.4721	121	132.3
23.08	861	0	2.53072	73.43	121.9
23.08	861	0	2.53072	80.5	2968.51
40	1737	0.17	1.4056	494.455	922.175
12.5	713	0	6.61308	175.6	2785.1
49.15	335	0.3	52.1262	47.5	53.54
49.15	335	0.3	52.1262	96.35	146.51
49.15	335	0.3	52.1262	49.2	103.27
49.15	335	0.3	52.1262	179.9	852.53
49.15	336	0.3	52.1262	314.49	8294.88
49.15	336	0.3	52.1262	66.05	146.51
49.15	336	0.3	52.1262	263	989.7
49.15	336	0.3	52.1262	31	103.27
43.55	1601	0.25	28.8518	312.82	326.81
43.55	1601	0.25	28.8518	277.25	953.12
80	2433	0.21	1.45374	305.6	6399.79
30	1712	0	2.47698	47.5	1085.26
45.45	1618	0.12	13.7829	68.51	672.85
45.83	4524	0.2	121.347	183.42	203.045
45.83	4524	0.2	121.347	16.4	27.1
42.11	1143	0.09	10.0301	49.53	52.34
52.17	2413	0.17	22.7068	246.1	17456.61
52.17	2413	0.17	22.7068	268.9	17441
52.17	2413	0.17	22.7068	408.5	4509.67

Median Fold Change	NetMHC WT Score	NetMHC MT Score	NetMHCpan WT Score	NetMHCpan MT Score
2.323	115.66	49.79	61.2	41
5.854	2040	223.09	2692.2	145
1.972	1068.75	2117.25	229.3	106.6
1.749	4333.92	5344.18	338.8	193.7
2.685	209.12	77.88	2150.1	1070
1.093	1275.72	1279.69	132.3	121
1.66	233.26	130.8	121.9	48.2
36.876	18700.67	2885.32	7282.5	80.5
1.865	NA	NA	496.9	187.3
15.86	18339.39	4515.82	2785.1	175.6
1.127	43.38	43.38	68.9	36.6
1.521	134.44	51.29	43.4	25.2
2.099	103.27	49.2	7259	509.6
4.739	852.53	179.9	13387	6985.8
26.376	8495.79	37.05	8649.6	43.2
2.218	134.44	55.49	43.4	14.7
3.763	1068.7	392.37	989.7	263
3.331	103.27	19.38	7259	31
1.045	535.5	752.4	350.7	402.2
3.438	1295.1	330.14	335.6	162.3
20.942	16490.24	305.6	12504.9	684
22.848	5088.5	53	11400.4	47.5
9.821	672.85	68.51	1573.2	214.1
1.107	NA	NA	22	14.6
1.652	37	25.86	27.1	16.4
1.057	22.76	17.22	8.7	6
70.933	21237.25	148.56	30112.3	246.1
64.861	30790.96	1270.74	17441	268.9
11.04	4509.67	1903.64	6269.8	408.5

PickPocket WT Score	PickPocket MT Score	SMM WT Score	SMM MT Score	SMMPMBEC WT Score
158.17	138.91	73.77	49.3	131.17
711.66	348.45	2492.36	451.45	1976.1
6978.43	5267.25	22.92	45.31	46.28
11857.88	9047.59	25.95	26.07	41.25
13070.67	7208.66	16.87	16.87	21.45
1469.28	1567.83	11.02	13.4	36.68
1017.05	598.54	98.83	73.43	116.37
2968.51	1844.1	24.17	25.89	12.31
1347.45	801.61	NA	NA	NA
24747.82	12653.21	64.3	64.6	124
396.76	176.24	40.62	47.5	53.54
194.27	163.39	206	124.41	146.51
4830.5	5044.15	42	39.74	28.02
16404.99	14882.82	18.76	17.03	45.97
4062.65	456.69	6896.2	314.49	8294.88
194.27	148.23	206	98.37	146.51
1332.95	1097.07	313.25	197.19	308.2
4830.5	2873.7	42	46.37	28.02
190.11	196.38	85.92	96.18	326.81
953.12	652.65	1451.64	265.99	935.13
6399.79	4335.14	15.68	8.5	14.5
1085.26	140.42	777.37	44.43	749.83
17316.93	2579.01	18.42	8.67	28.67
384.09	352.24	NA	NA	NA
605.05	548.91	12.06	12.45	12.54
83.54	85.36	57.53	55.7	52.34
8297.38	211.83	13478.14	301.74	17456.61
50000	17505.31	49.45	48	55.26
7054.34	9759.45	58.24	54.6	71.85

SMMPMBEC MT Score	
81.25	
381.78	
116.26	
42.31	
18.43	
38.32	
68.36	
32.77	
NA	
113.35	
52.08	
96.35	
36.76	
36.09	
359.59	
66.05	
245.37	
27	
312.82	
277.25	
9.99	
47.42	
9.65	
NA	
13.41	
49.53	
366.4	
40.13	
85.79	