

Supplementary Table 3: Conservancy analysis of the HPV45 CD8⁺ T cell epitopes against 15 high-risk HPV strains

S.No	Epitopes	Positions	Protein sub sequences	Identity (%)	Name of the Strain
1	MLAVFKDIY	200-208	MLAVFKDIY	100.00	HPV45
		214-222	MLAVFKDTY	88.89	HPV18
		207-215	MLAKFKELY	66.67	HPV16
		187-195	MLGKFKELY	55.56	HPV31
		193-201	MLAKFKELF	55.56	HPV35
		204-212	MLTQFKETY	55.56	HPV39
		201-209	MYAKFKELY	55.56	HPV59
		197-205	MLTEFKKVY	55.56	HPV68
		208-216	LLAKFKEVY	55.55	HPV37
2	FKDIYGLSF	204-212	FKDIYGLSF	100.00%	HPV45
		218-226	FKDTYGLSF	88.89%	HPV18
		208-216	FKETYGLSF	77.78%	HPV39
		205-213	FKELYGLSF	77.78%	HPV59
		201-209	FKKVYGLSF	77.78%	HPV68
		211-219	FKELYGVSF	66.67%	HPV16
		191-199	FKELYGVSF	66.67%	HPV31
		204-212	FKEAYGISF	66.67%	HPV33
		207-215	FKETYGVSF	66.67%	HPV52
		204-212	FKEAYGVSF	66.67%	HPV58
		212-220	FKEVYGLSY	66.67%	HPV73
		197-205	FKELYGISY	55.56%	HPV51
		197-205	FKELFGISF	55.56%	HPV35
		198-206	FKEVYGIPF	55.56%	HPV56
		197-205	FKTVYGVSY	55.56%	HPV69
		205-213	FKELYGVSY	55.56%	HPV82
3	FTDLVRNFK	212-220	FTDLVRNFK	100.00%	HPV45
		226-234	FTDLVRNFK	100.00%	HPV18
		216-224	FTDLVRTFK	88.89%	HPV39
		213-221	FQDLVRTFK	77.78%	HPV59
		209-217	FNDLVRTFK	77.78%	HPV68
		219-227	FSELVRPFK	66.67%	HPV16
		212-220	FMELVRPFK	66.67%	HPV33
		205-213	FTELIRPFK	66.67%	HPV35
		215-223	FMELVRPFK	66.67%	HPV52
		206-214	FSELVRTFK	66.67%	HPV56
		212-220	FMELVRPFK	66.67%	HPV58
205-213	YTELVRVFK	66.67%	HPV69		

		205-213	YNELVRVFK	55.56%	HPV51
		213-221	YNELVRVFK	55.56%	HPV82
4	CTDWVMAIF	226-234	CTDWVMAIF	100.00%	HPV45
		240-248	CTDWVTAIF	88.89%	HPV18
		230-238	CTDWVAAIF	88.89%	HPV39
		223-231	CTDWVAAIF	88.89%	HPV68
		227-235	CSDWVTAIF	77.78%	HPV59
		227-235	CTDWVCALF	77.78%	HPV82
		219-227	CIDWVCALF	66.67%	HPV51
		220-228	CNDWICAF	66.67%	HPV56
		213-221	CTDWCVAAF	66.67%	HPV31
		219-227	CTDWCVAAF	66.67%	HPV35
		219-227	CSDWVCAAF	66.67%	HPV69
		234-242	CQDWVCAVF	66.67%	HPV73
		233-241	CCDWCIAAF	55.56%	HPV16
5	VLILALLRY	266-274	VLILALLRY	100.00%	HPV45
		280-288	VLILALLRY	100.00%	HPV18
		267-275	VVILALLRY	88.89%	HPV59
		270-278	VLILMLRY	77.78%	HPV39
		263-271	ILILMLRY	66.67%	HPV68
		269-277	VLILLIRF	66.67%	HPV52
		259-267	MVILALLRF	66.67%	HPV35
		259-267	VLPLMLIRF	55.56%	HPV69
		433-441	RPIVQLLRY	55.56%	HPV33
6	SSLAALYWY	307-315	SSLAALYWY	100.00%	45
		321-329	SSVAALYWY	88.89%	18
		314-322	STAAALYWY	77.78%	16
		294-302	STAAALYWY	77.78%	31
		311-319	SPVAALYWY	77.78%	HPV39
		308-316	SPVAALYWY	77.78%	HPV59
		304-312	SPVAALYWY	77.78%	HPV68
		300-308	STPAALYWF	66.67%	HPV35
		310-318	SATCALYWY	66.67%	HPV52
		315-323	STPCALYWY	66.67%	HPV73
		307-315	SQTCALYWF	55.56%	HPV33
		300-308	STPVALYFY	55.56%	HPV51
		301-309	SPAVALYFY	55.56%	HPV56
		307-315	SQACALYWF	55.56%	HPV58
		300-308	STAVALYFY	55.56%	HPV69
		308-316	STAVALYFY	55.56%	HPV82

7	DATHTCWTY	516-524	DATHTCWTY	100.00%	HPV45		
		530-538	DATTCWTY	88.89%	HPV18		
		520-528	DATGTCWSY	77.78%	HPV39		
		509-517	DATYGCWTY	77.78%	HPV51		
		517-525	DATDSCWTY	77.78%	HPV59		
		513-521	DATGTCWSY	77.78%	68		
		524-532	DATPGCWTY	77.78%	73		
		517-525	DATYGCWTY	77.78%	82		
		523-531	DATVPCWNY	66.67%	16		
		503-511	DATTPCWHY	66.67%	31		
		509-517	DATSPCWAY	66.67%	35		
		519-527	DVTPICWTY	66.67%	52		
		510-518	DATEICWKY	66.67%	56		
		509-517	DATYGCWLY	66.67%	69		
		516-524	DVTPISTWY	55.56%	33		
		516-524	DVTAISWY	55.56%	58		
		8	ATHTCWTYF	517-525	ATHTCWTYF	100.00%	45
				531-539	ATTCWTYF	88.89%	18
				521-529	ATGTCWSYF	77.78%	39
518-526	ATDSCWTYF			77.78%	59		
514-522	ATGTCWSYF			77.78%	68		
510-518	ATYGCWTYI			66.67%	51		
525-533	ATPGCWTYI			66.67%	73		
518-526	ATYGCWTYI			66.67%	82		
524-532	ATVPCWNYI			55.56%	16		
504-512	ATTPCWHYI			55.56%	31		
510-518	ATSPCWAYI			55.56%	35		
520-528	VTPICWTYI			55.56%	52		
511-519	ATEICWKYI			55.56%	56		
510-518	ATYGCWLYI			55.56%	69		
9	YLESRVTVF			571-579	YLESRVTVF	100.00%	45
		585-593	YLESRITVF	88.89%	18		
		572-580	YLHSRVTVF	88.89%	82		
		571-579	YLHSRLTVF	77.78%	33		
		564-572	YLHSRVVVF	77.78%	35		
		575-583	YLSRSLTVF	77.78%	39		
		571-579	YLHSRLTVF	77.78%	58		
		568-576	YLHSRLTVF	77.78%	68		
		564-572	YLHSRVTVI	77.78%	69		
		558-566	YLHSRLVVF	66.67%	31		
		564-572	YLHTRVTVL	66.67%	51		
		574-582	YLHSRLVVF	66.67%	52		
		565-573	YLHSRMLVF	66.67%	56		
		572-580	YLSRMLMVF	66.67%	59		
		579-587	YLHSRIKVF	66.67%	73		
		578-586	YLHNRLVVF	55.56%	16		

10	FTFPHAFPF	579-587	FTFPHAFPF	100.00%	45
		586-594	FTFPNEFPF	77.78%	16
		593-601	FEFPNAFPF	77.78%	18
		566-574	FTFPNPFPF	77.78%	31
		583-591	FKFPNAFPF	77.78%	39
		576-584	FKFPNAFPF	77.78%	68
		572-580	FTFHNEFPF	66.67%	35
		587-595	FTFLNPFPF	66.67%	73
		580-588	FQFLNAFPF	66.67%	82
		579-587	FEFKNPFPF	55.56%	33
		582-590	FHFKNPFPF	55.56%	52
		579-587	FEFNPFPF	55.56%	58
		580-588	FKFPNKLPF	55.56%	59
		572-580	IPFPNTEFPF	55.56%	69
11	YVWVDSIYY	77-85	YVWVDSIYY	100.00%	45
		135-143	YVAWDSVYY	77.78%	18
		136-144	YVLWGAIYY	66.67%	39
		131-139	YVAWKYIYY	66.67%	56
		136-144	YVWVGTIYF	66.67%	68
		135-143	YTSWTFIYY	55.56%	59
		131-139	YIRWTSVYY	55.56%	69
		132-140	YVFWTHIYC	55.56%	73
12	MTETGIWEK	144-152	MTDAGTWDK	55.56%	18
		146-154	MTETGIWEK	100.00%	45
13	CVSYWGVYY	158-166	CVSYWGVYY	100.00%	45
		157-165	CVDYWGVYY	88.89%	68
		157-165	CVDYWGIYY	77.78%	39
		156-164	CVSHRGLYY	66.67%	18
		151-159	QVDYYGLYY	55.56%	16
		151-159	KVDYIGMY	55.56%	33
		152-160	LVNYKGIYY	55.56%	35
		151-159	NVDYTGIIY	55.56%	51
		151-159	QVDYYGLYY	55.56%	52
		151-159	GVDYRGIYY	55.56%	56
		151-159	EVDYVGLYY	55.56%	58
		156-164	NVDFWGLYY	55.56%	59
		151-159	EVDYKGIYY	55.56%	69
		151-159	NVDYTGIIY	55.56%	82
14	YIKDGDTTY	166-174	YIKDGDTTY	100.00%	45
		159-167	YVHDGHKTY	55.56%	56
15	NSNTWEVQY	187-195	NSNTWEVQY	100.00%	45
		185-193	NTGTWEVHF	55.56%	18
		186-194	TSGKWEVHY	55.56%	39
16	NTGILTVTY	332-340	NTGILTVTY	100.00%	45
		334-342	NTGILTVTY	100.00%	68

		329-337	KTGILTVTY	88.89%	18
		334-342	NAGILTVTY	88.89%	39
		334-342	KTGILTLY	77.78%	59
		322-330	KVGIVTVTY	66.67%	58
		317-325	KNGIVTVTF	55.56%	33
		332-340	KLGIVTITY	55.56%	52
		332-340	NQGIVTITF	55.56%	69
17	CAVPVTTRY	4-12	CAVPVTTRY	100.00%	45
		4-12	PEVPVTTRY	77.78%	18
		27-35	CAVPVTSKY	77.78%	59
		4-12	REVPVTDY	66.67%	39
		3-11	CEVPAATRY	66.67%	51
		41-44	CLVPVDTTY	66.67%	56
18	RTEVYQFAF	41-49	RTEVYQFAF	100.00%	45
		41-49	RTEVYEFAP	88.89%	68
		46-54	RREVYDFAP	77.78%	16
		39-47	RSEVYDFAP	77.78%	33
		41-49	QTEVYEFAP	77.78%	39
		40-48	RSEVYDFAP	77.78%	73
		41-49	LTEVFEFAP	66.67%	18
		39-47	ETEVLDFAP	66.67%	31
		39-47	RSEVYDFAC	66.67%	35
		39-47	RREVYKFLF	66.67%	52
		42-50	RAEVYNFAC	66.67%	56
		39-47	RSEVYDFVF	66.67%	58
		39-47	RADVYNVAF	55.56%	51
		41-49	EREVFEFAP	55.56%	59
		39-47	RADVYNVAF	55.56%	82
19	YSRIRELRY	72-80	YSRIRELRY	100.00%	45
		72-80	YSRIRELRH	88.89%	18
		72-80	YAKIRELRY	77.78%	39
		72-80	YARVRELRY	77.78%	59
		72-80	YAKIRELRY	77.78%	68
		70-78	YSRIREYRR	77.78%	82
		70-78	YSKIREYRR	66.67%	51
		71-79	YSKIREYRR	66.67%	73
		77-85	YSKISEYRH	55.56%	16
		70-78	YSKISEYRW	55.56%	35
		73-81	YSKVRKYRY	55.56%	56
		70-78	YSKIIEYRR	55.56%	69
20	HVEEYDLQF	428-436	HVEEYDLQF	100.00%	18
		365-373	HVEEYDLQF	100.00%	33
		366-374	HVEEYDLQF	100.00%	39
		51-59	HVEEYDLQF	100.00%	45
		391-399	HVEEYDLQF	100.00%	58

		367-375	HVEEYDLQF	100.00%	68
		366-374	HGEEYDLQF	88.89%	16
		364-372	HGEEYDLQF	88.89%	35
		364-372	HVEEYELQF	88.89%	56
		367-375	HVEEFDLQF	88.89%	59
		367-375	HGEEFDLQF	77.78%	31
		366-374	HGEEYELQF	77.78%	51
		396-404	HGEEFDLQF	77.78%	52
		368-376	HGEEYELQF	77.78%	69
		366-374	HAEEFDLQF	77.78%	73
		398-406	HGEEYELQF	77.78%	82
21	STSFTNPAF	154-162	STSFTNPAF	100.00%	45
		154-162	STSFTNPAF	100.00%	68
		154-162	STSYTNPAF	88.89%	39
		154-162	TTNFTNPAF	77.78%	18
		153-161	SSSFNPAF	77.78%	59
		154-162	STHITNPLF	66.67%	56
		396-404	STGFDPIF	55.56%	31
		133-141, 249-257	SSSTTPAV, FVTFNPAF	55.56%	51
		396-404	STSFDIPIY	55.56%	69
		160-168,4 66-474	VTFKNPTF, SYSFTDVAT	55.56%	73
		133-141,2 50-258	SSSTTPAV,F VTFDNPAF	55.56%	82
22	FSDPSIIEV	162-170	FSDPSIIEV	100.00%	18
		162-170	FSDPSIIEV	100.00%	45
		162-170	FTDPSLIEV	77.78%	39
		161-169	FTDPSVIEV	77.78%	59
		162-170	FTDPTIIEV	77.7%	68
		100-108	PSDPSIVSL	55.56%	16
		163-171	FTEPSIIQP	55.56%	52
		162-170	FIDPPVIEA	55.56%	56
		141-149	NSTPAIDV	55.56%	73
23	LVTFDNPAY	248-256	LVTFDNPAY	100.00%	45
		249-257	LITYDNPAY	77.78%	16
		248-256	LITYDNPAY	77.78%	35
		248-256	FVTFDNPAF	77.78%	39
		249-257	LVTYDNPAF	77.78%	58
		247-255	FVTYDNPAY	77.78%	59
		248-256	FVTFDNPAF	77.78%	68
		249-257	FITFDNPAY	77.78%	69
		254-262	LVTYDNPAF	77.78%	73

		250-258	FVTFDNPAF	77.78%	82
		248-256	LITYDNPAF	66.67%	18
		244-252	LITYENPAY	66.67%	31
		249-257	LITYDNPAF	66.67%	33
		249-257	FVTFNNPAF	66.67%	51
		249-257	LVTYNNPVF	55.56%	52
		248-256	LVSADNPLF	55.56	56
24	HSDFMDIIR	273-281	HSDFMDIIR	100.00%	45
		273-281	DSDFMDIIR	88.89%	18
		277-285	DPDFMDIIA	66.67%	35
		272-280	DPDFMDIVR	66.67%	59
		273-281	DPDFLDIIA	55.56%	31
		278-286	DPDFLDIIA	55.56%	33
		273-281	DPDFLDIVR	55.56%	39
		275-283	DPDFLDIIT	55.56%	51
		278-286	DPDFLDIIA	55.56%	52
		273-281	DPDFLDIVR	55.56%	68
		275-283	DPDFLDIIA	55.56%	69
		282-290	DSDFLDIVK	55.56%	73
		276-284	DPDFLDIIK	55.56%	82
25	QIGGRVHFY	312-320	QIGGRVHFY	100.00%	45
		312-320	QIGARVHFY	88.89%	18
		311-319	QIGARVHFY	88.89%	59
		314-322	QIGARVHYY	77.78%	51
		317-325	QIGARVHYY	77.78%	52
		312-320	QIGARVHYY	77.78%	56
		315-323	QIGARVHYY	77.78%	82
		312-320	TIGARVHYY	66.67%	31
		317-325	QIGARIHYY	66.67%	33
		316-324	AIGARVHYY	66.67%	35
		312-320	QIGAQVHYY	66.67%	39
		317-325	QIGAKVHYY	66.67%	58
		312-320	QIGAQVHYY	66.67%	68
		314-322	QIGAKVHYY	66.67%	69
		321-329	RIGAKVHFY	66.67%	73
		319-327	SIGAKVHYY	55.56%	16
26	TSAWDVPIY	393-401	TSAWDVPIY	100.00%	45
		392-400	TSSWDVPVY	77.78%	18
		404-412	FSGPDVPIE	55.56%	31
		417-425	TSSPFVPIS	55.56%	33
		394-402	ATAWDVPVN	55.56%	59
27	QYYLWPWY Y	435-443	QYYLWPWYY	100.00%	45
		434-442	HYYLWPLY	77.7831%	18

		436-444	NYFLWPIYY	66.67%	59
		438-446	NYYLWPYIY	66.67%	69
		445-453	DYYLWPYTY	66.67%	82
		445-453	DFY LHPSYY	55.56%	16
		438-446	DFY LHPSYY	55.56%	31
		441-449	DFY LHPSYY	55.56%	35
		442-450	NYLLPLY	55.56%	39
		440-448	DYYLWPYTH	55.56%	51

Note: Residues that are different from their corresponding residue in the reference sequence are highlighted in red color. Identity indicates the number (%) of residues in the homologous sequence that are identical to the corresponding residue in the reference sequence