

**Table S1.** Conservancy of predicted CTL epitopes among the SARS-CoV-2 variants. Row 1 contain information about the name of the variants according to the WHO, the pangolin lineage of the variants, and the number of retrieved sequences in the bracket. The duplicated sequences were removed prior to the analysis and the percentage of the conservation was calculated based on the number of the unique sequences only, in which the proportion was shown in the bracket.

Start	Epitope sequence	Alpha B.1.1.7 (158)	Beta B.1.351 (374)	Delta B.1.617.2 (1157)	Eta B.1.525 (436)	Gamma P.1 (9)	Iota B.1.526 (24)	Kappa B.1.617.1 (148)	Lambda C.7 (286)	Mu B.1.621 (18)
295	FMGRIRSVY	100.00% (111/111)	99.32% (145/146)	98.69% (452/458)	100.00% (174/174)	100.00% (8/8)	100.00% (19/19)	100.00% (95/95)	100.00% (113/113)	100.00% (17/17)
541	RVVRSIFSR	100.00% (111/111)	100.00% (146/146)	99.56% (456/458)	100.00% (174/174)	100.00% (8/8)	100.00% (19/19)	100.00% (95/95)	100.00% (113/113)	100.00% (17/17)
611	WLTNIFGTV	100.00% (111/111)	100.00% (146/146)	99.78% (457/458)	100.00% (174/174)	100.00% (8/8)	100.00% (19/19)	100.00% (95/95)	100.00% (113/113)	100.00% (17/17)
806	MVTNNTFTL	100.00% (111/111)	100.00% (146/146)	100.00% (458/458)	100.00% (174/174)	100.00% (8/8)	100.00% (19/19)	100.00% (95/95)	100.00% (113/113)	100.00% (17/17)
899	WSMATYYLF	100.00% (111/111)	97.95% (143/146)	99.56% (456/458)	100.00% (174/174)	100.00% (8/8)	94.74% (18/19)	100.00% (95/95)	100.00% (113/113)	100.00% (17/17)
1055	VVVNAANVY	100.00% (111/111)	99.32% (145/146)	99.13% (454/458)	99.43% (173/174)	100.00% (8/8)	100.00% (19/19)	100.00% (95/95)	99.12% (112/113)	100.00% (17/17)
1140	HEVLLAPLL	100.00% (111/111)	100.00% (146/146)	100.00% (458/458)	100.00% (174/174)	100.00% (8/8)	100.00% (19/19)	100.00% (95/95)	100.00% (113/113)	100.00% (17/17)
1247	FLTENLLLY	100.00% (111/111)	100.00% (146/146)	98.69% (452/458)	100.00% (174/174)	100.00% (8/8)	100.00% (19/19)	98.95% (94/95)	100.00% (113/113)	100.00% (17/17)
1254	LYIDINGNL	100.00% (111/111)	100.00% (146/146)	99.78% (457/458)	100.00% (174/174)	100.00% (8/8)	100.00% (19/19)	100.00% (95/95)	100.00% (113/113)	100.00% (17/17)
1269	LVSDIDITF	100.00% (111/111)	100.00% (146/146)	99.34% (455/458)	100.00% (174/174)	100.00% (8/8)	100.00% (19/19)	100.00% (95/95)	95.58% (108/113)	100.00% (17/17)
1366	ILGTVSWNL	100.00% (111/111)	100.00% (146/146)	100.00% (458/458)	100.00% (174/174)	100.00% (8/8)	100.00% (19/19)	100.00% (95/95)	100.00% (113/113)	100.00% (17/17)
1674	YLATALLTL	99.10% (110/111)	100.00% (146/146)	99.34% (455/458)	100.00% (174/174)	100.00% (8/8)	100.00% (19/19)	100.00% (95/95)	98.23% (111/113)	100.00% (17/17)
2175	LLQLCTFTR	100.00% (111/111)	99.32% (145/146)	99.78% (457/458)	99.43% (173/174)	100.00% (8/8)	100.00% (19/19)	100.00% (95/95)	97.35% (110/113)	100.00% (17/17)
2327	FLAYILFTR	98.20% (109/111)	100.00% (146/146)	100.00% (458/458)	100.00% (174/174)	100.00% (8/8)	100.00% (19/19)	100.00% (95/95)	100.00% (113/113)	100.00% (17/17)
2331	ILFTRFFYV	98.20% (109/111)	100.00% (146/146)	100.00% (458/458)	100.00% (174/174)	100.00% (8/8)	100.00% (19/19)	100.00% (95/95)	100.00% (113/113)	100.00% (17/17)
2350	FSYFAVHFI	100.00% (111/111)	100.00% (146/146)	99.34% (455/458)	100.00% (174/174)	100.00% (8/8)	100.00% (19/19)	100.00% (95/95)	100.00% (113/113)	100.00% (17/17)
2597	FSSTFNVPM	100.00% (111/111)	100.00% (146/146)	99.56% (456/458)	99.43% (173/174)	100.00% (8/8)	100.00% (19/19)	100.00% (95/95)	99.12% (112/113)	100.00% (17/17)
2629	LSTFISAAR	100.00% (111/111)	100.00% (146/146)	100.00% (458/458)	100.00% (174/174)	100.00% (8/8)	100.00% (19/19)	100.00% (95/95)	100.00% (113/113)	100.00% (17/17)
2784	AIFYLITPV	100.00% (111/111)	100.00% (146/146)	99.78% (457/458)	100.00% (174/174)	87.50% (7/8)	100.00% (19/19)	100.00% (95/95)	100.00% (113/113)	100.00% (17/17)
2786	FYLITPVHV	100.00% (111/111)	100.00% (146/146)	99.78% (457/458)	100.00% (174/174)	100.00% (8/8)	100.00% (19/19)	100.00% (95/95)	100.00% (113/113)	100.00% (17/17)
2787	YLITPVHVM	100.00% (111/111)	100.00% (146/146)	99.78% (457/458)	100.00% (174/174)	100.00% (8/8)	100.00% (19/19)	100.00% (95/95)	100.00% (113/113)	100.00% (17/17)
2883	FLPRVFSAV	100.00% (111/111)	97.95% (143/146)	100.00% (458/458)	100.00% (174/174)	100.00% (8/8)	100.00% (19/19)	98.95% (94/95)	99.12% (112/113)	100.00% (17/17)
3059	LAYYFMRFR	100.00% (111/111)	100.00% (146/146)	99.56% (456/458)	100.00% (174/174)	100.00% (8/8)	100.00% (19/19)	100.00% (95/95)	100.00% (113/113)	94.12% (16/17)

3060	AYYFMRFR	100.00% (111/111)	100.00% (146/146)	99.56% (456/458)	100.00% (174/174)	100.00% (8/8)	100.00% (19/19)	100.00% (95/95)	100.00% (113/113)	94.12% (16/17)
3076	VVAFNTLLF	100.00% (111/111)	100.00% (146/146)	100.00% (458/458)	100.00% (174/174)	100.00% (8/8)	100.00% (19/19)	100.00% (95/95)	100.00% (113/113)	100.00% (17/17)
3121	FLAHIQWMV	100.00% (111/111)	100.00% (146/146)	99.78% (457/458)	100.00% (174/174)	100.00% (8/8)	100.00% (19/19)	100.00% (95/95)	100.00% (113/113)	100.00% (17/17)
3137	FWITIAYII	100.00% (111/111)	98.63% (144/146)	9.61% (44/458)	99.43% (173/174)	100.00% (8/8)	100.00% (19/19)	98.95% (94/95)	100.00% (113/113)	100.00% (17/17)
3152	FYWFFSNYL	99.10% (110/111)	100.00% (146/146)	100.00% (458/458)	100.00% (174/174)	100.00% (8/8)	100.00% (19/19)	100.00% (95/95)	100.00% (113/113)	100.00% (17/17)
3466	VLAWLYAAV	100.00% (111/111)	100.00% (146/146)	100.00% (458/458)	100.00% (174/174)	100.00% (8/8)	100.00% (19/19)	100.00% (95/95)	100.00% (113/113)	100.00% (17/17)
3481	FLNRFTTTL	100.00% (111/111)	100.00% (146/146)	99.78% (457/458)	100.00% (174/174)	100.00% (8/8)	100.00% (19/19)	100.00% (95/95)	100.00% (113/113)	100.00% (17/17)
3582	LLLILTSL	100.00% (111/111)	100.00% (146/146)	100.00% (458/458)	100.00% (174/174)	100.00% (8/8)	100.00% (19/19)	100.00% (95/95)	100.00% (113/113)	100.00% (17/17)
3605	LYENAFLPF	99.10% (110/111)	95.89% (140/146)	98.03% (449/458)	97.13% (169/174)	100.00% (8/8)	100.00% (19/19)	90.53% (86/95)	94.69% (107/113)	94.12% (16/17)
3652	VYMPASWVM	100.00% (111/111)	99.32% (145/146)	99.78% (457/458)	100.00% (174/174)	100.00% (8/8)	100.00% (19/19)	100.00% (95/95)	99.12% (112/113)	100.00% (17/17)
3684	YASAVVLLI	100.00% (111/111)	100.00% (146/146)	100.00% (458/458)	100.00% (174/174)	100.00% (8/8)	100.00% (19/19)	100.00% (95/95)	99.12% (112/113)	100.00% (17/17)
3692	ILMTARTVY	100.00% (111/111)	100.00% (146/146)	99.34% (455/458)	100.00% (174/174)	100.00% (8/8)	100.00% (19/19)	100.00% (95/95)	100.00% (113/113)	100.00% (17/17)
3752	FLARGIVFM	100.00% (111/111)	99.32% (145/146)	100.00% (458/458)	100.00% (174/174)	100.00% (8/8)	100.00% (19/19)	98.95% (94/95)	100.00% (113/113)	100.00% (17/17)
4030	TMLFTMLRK	100.00% (111/111)	100.00% (146/146)	100.00% (458/458)	100.00% (174/174)	100.00% (8/8)	100.00% (19/19)	100.00% (95/95)	100.00% (113/113)	100.00% (17/17)
4265	VLSFCAFAV	100.00% (111/111)	100.00% (146/146)	99.78% (457/458)	100.00% (174/174)	100.00% (8/8)	100.00% (19/19)	100.00% (95/95)	100.00% (113/113)	100.00% (17/17)
4513	YTMADLVYA	100.00% (111/111)	100.00% (146/146)	100.00% (458/458)	99.43% (173/174)	100.00% (8/8)	94.74% (18/19)	100.00% (95/95)	100.00% (113/113)	100.00% (17/17)
4656	YIKWDLK	100.00% (111/111)	100.00% (146/146)	100.00% (458/458)	100.00% (174/174)	100.00% (8/8)	100.00% (19/19)	100.00% (95/95)	100.00% (113/113)	100.00% (17/17)
4698	ILHCANFNV	100.00% (111/111)	100.00% (146/146)	100.00% (458/458)	100.00% (174/174)	100.00% (8/8)	100.00% (19/19)	100.00% (95/95)	100.00% (113/113)	100.00% (17/17)
4723	KIFVDGVPF	100.00% (111/111)	100.00% (146/146)	100.00% (458/458)	100.00% (174/174)	100.00% (8/8)	100.00% (19/19)	100.00% (95/95)	100.00% (113/113)	100.00% (17/17)
4846	YYRYNLPTM	100.00% (111/111)	98.63% (144/146)	100.00% (458/458)	100.00% (174/174)	100.00% (8/8)	100.00% (19/19)	100.00% (95/95)	100.00% (113/113)	100.00% (17/17)
4862	FVVEVVDKY	100.00% (111/111)	100.00% (146/146)	100.00% (458/458)	100.00% (174/174)	100.00% (8/8)	100.00% (19/19)	87.37% (83/95)	100.00% (113/113)	100.00% (17/17)
5024	MASLVLARK	100.00% (111/111)	100.00% (146/146)	100.00% (458/458)	100.00% (174/174)	100.00% (8/8)	100.00% (19/19)	100.00% (95/95)	100.00% (113/113)	100.00% (17/17)
5132	FVNEFYAYL	99.10% (110/111)	100.00% (146/146)	100.00% (458/458)	100.00% (174/174)	100.00% (8/8)	100.00% (19/19)	100.00% (95/95)	100.00% (113/113)	100.00% (17/17)
5245	LMIERFVSL	100.00% (111/111)	100.00% (146/146)	100.00% (458/458)	100.00% (174/174)	100.00% (8/8)	100.00% (19/19)	100.00% (95/95)	100.00% (113/113)	100.00% (17/17)
5247	IERFVSLAI	100.00% (111/111)	100.00% (146/146)	100.00% (458/458)	100.00% (174/174)	100.00% (8/8)	100.00% (19/19)	100.00% (95/95)	100.00% (113/113)	100.00% (17/17)
5250	FVSLAIDAY	100.00% (111/111)	100.00% (146/146)	100.00% (458/458)	100.00% (174/174)	100.00% (8/8)	100.00% (19/19)	100.00% (95/95)	100.00% (113/113)	100.00% (17/17)
5273	HLYLQYIRK	100.00% (111/111)	100.00% (146/146)	100.00% (458/458)	100.00% (174/174)	100.00% (8/8)	100.00% (19/19)	100.00% (95/95)	100.00% (113/113)	100.00% (17/17)

5614	FAIGLALYY	100.00% (111/111)	100.00% (146/146)	99.34% (455/458)	99.43% (173/174)	100.00% (8/8)	100.00% (19/19)	100.00% (95/95)	100.00% (113/113)	100.00% (17/17)
5678	YVFCTVNAL	100.00% (111/111)	100.00% (146/146)	99.13% (454/458)	100.00% (174/174)	100.00% (8/8)	100.00% (19/19)	100.00% (95/95)	100.00% (113/113)	100.00% (17/17)
6070	FKHLIPLMY	100.00% (111/111)	100.00% (146/146)	99.13% (454/458)	100.00% (174/174)	100.00% (8/8)	100.00% (19/19)	100.00% (95/95)	100.00% (113/113)	100.00% (17/17)
6108	VLWAHGFEL	100.00% (111/111)	100.00% (146/146)	100.00% (458/458)	98.85% (172/174)	100.00% (8/8)	100.00% (19/19)	100.00% (95/95)	100.00% (113/113)	100.00% (17/17)
6506	FELWAKRNI	100.00% (111/111)	100.00% (146/146)	100.00% (458/458)	100.00% (174/174)	100.00% (8/8)	100.00% (19/19)	100.00% (95/95)	100.00% (113/113)	100.00% (17/17)
6585	FRNARNGVL	100.00% (111/111)	100.00% (146/146)	100.00% (458/458)	100.00% (174/174)	100.00% (8/8)	100.00% (19/19)	100.00% (95/95)	100.00% (113/113)	100.00% (17/17)
6700	HLLIGLAKR	100.00% (111/111)	100.00% (146/146)	99.78% (457/458)	100.00% (174/174)	100.00% (8/8)	100.00% (19/19)	100.00% (95/95)	100.00% (113/113)	100.00% (17/17)
6714	FELEDFIPM	98.20% (109/111)	100.00% (146/146)	99.34% (455/458)	100.00% (174/174)	100.00% (8/8)	100.00% (19/19)	100.00% (95/95)	100.00% (113/113)	100.00% (17/17)
6748	LLDDFVEI	100.00% (111/111)	100.00% (146/146)	100.00% (458/458)	100.00% (174/174)	100.00% (8/8)	100.00% (19/19)	100.00% (95/95)	100.00% (113/113)	100.00% (17/17)
6848	CQYLNTLTL	100.00% (111/111)	100.00% (146/146)	100.00% (458/458)	100.00% (174/174)	100.00% (8/8)	100.00% (19/19)	100.00% (95/95)	100.00% (113/113)	100.00% (17/17)
6850	YLNTLTLAV	100.00% (111/111)	100.00% (146/146)	100.00% (458/458)	100.00% (174/174)	100.00% (8/8)	100.00% (19/19)	100.00% (95/95)	100.00% (113/113)	100.00% (17/17)
6885	WLPTGTLLV	100.00% (111/111)	100.00% (146/146)	100.00% (458/458)	98.28% (171/174)	100.00% (8/8)	100.00% (19/19)	97.89% (93/95)	100.00% (113/113)	100.00% (17/17)
6978	YKLMGHFAW	100.00% (111/111)	100.00% (146/146)	100.00% (458/458)	100.00% (174/174)	100.00% (8/8)	100.00% (19/19)	100.00% (95/95)	100.00% (113/113)	100.00% (17/17)
7019	YVMHANYIF	100.00% (111/111)	100.00% (146/146)	100.00% (458/458)	100.00% (174/174)	100.00% (8/8)	100.00% (19/19)	100.00% (95/95)	100.00% (113/113)	100.00% (17/17)
7026	IFWRNTNPI	100.00% (111/111)	100.00% (146/146)	100.00% (458/458)	99.43% (173/174)	100.00% (8/8)	100.00% (19/19)	100.00% (95/95)	100.00% (113/113)	100.00% (17/17)

**Table S2.** Conservancy of predicted HTL epitopes among the SARS-CoV-2 variants. Row 1 contain information about the name of the variants according to the WHO, the pangolin lineage of the variants, and the number of retrieved sequences in the bracket. The duplicated sequences were removed prior to the analysis and the percentage of the conservation was calculated based on the number of the unique sequences only, in which the proportion was shown in the bracket.

Start	Epitope sequence	Alpha B.1.1.7 (158)	Beta B.1.351 (374)	Delta B.1.617.2 (1157)	Eta B.1.525 (436)	Gamma P.1 (9)	Iota B.1.526 (24)	Kappa B.1.617.1 (148)	Lambda C.7 (286)	Mu B.1.621 (18)
447	NDNLEILQKEKVNI	99.10% (110/111)	100.00% (146/146)	100.00% (458/458)	100.00% (174/174)	100.00% (8/8)	100.00% (19/19)	100.00% (95/95)	99.12% (112/113)	100.00% (17/17)
448	DNLLEILQKEKVNIN	99.10% (110/111)	100.00% (146/146)	100.00% (458/458)	100.00% (174/174)	100.00% (8/8)	100.00% (19/19)	100.00% (95/95)	99.12% (112/113)	100.00% (17/17)
554	TAQNSVRVLQKAAIT	100.00% (111/111)	99.32% (145/146)	98.91% (453/458)	95.98% (167/174)	100.00% (8/8)	100.00% (19/19)	98.95% (94/95)	100.00% (113/113)	100.00% (17/17)
736	PKEIIFLEGETLPTE	100.00% (111/111)	100.00% (146/146)	99.56% (456/458)	100.00% (174/174)	100.00% (8/8)	100.00% (19/19)	100.00% (95/95)	100.00% (113/113)	100.00% (17/17)
1054	PTVVVNAANVYLKHG	99.10% (110/111)	99.32% (145/146)	98.69% (452/458)	98.85% (172/174)	100.00% (8/8)	100.00% (19/19)	100.00% (95/95)	98.23% (111/113)	0.00% (0/17)
1187	VSSFLEMKSEKQVEQ	100.00% (111/111)	98.63% (144/146)	99.78% (457/458)	100.00% (174/174)	0.00% (0/8)	100.00% (19/19)	100.00% (95/95)	99.12% (112/113)	100.00% (17/17)
1211	VKPFITESKPSVEQR	94.59% (105/111)	100.00% (146/146)	98.91% (453/458)	100.00% (174/174)	87.50% (7/8)	100.00% (19/19)	100.00% (95/95)	100.00% (113/113)	100.00% (17/17)
1349	CKSAFYILPSIISNE	100.00% (111/111)	100.00% (146/146)	99.56% (456/458)	98.85% (172/174)	100.00% (8/8)	100.00% (19/19)	100.00% (95/95)	99.12% (112/113)	100.00% (17/17)
1350	KSAFYILPSIISNEK	100.00% (111/111)	100.00% (146/146)	99.56% (456/458)	98.85% (172/174)	100.00% (8/8)	100.00% (19/19)	100.00% (95/95)	99.12% (112/113)	100.00% (17/17)
1355	ILPSIISNEKQEILG	100.00% (111/111)	100.00% (146/146)	100.00% (458/458)	99.43% (173/174)	100.00% (8/8)	100.00% (19/19)	100.00% (95/95)	100.00% (113/113)	100.00% (17/17)
1356	LPSIISNEKQEILGT	100.00% (111/111)	100.00% (146/146)	100.00% (458/458)	99.43% (173/174)	100.00% (8/8)	100.00% (19/19)	100.00% (95/95)	100.00% (113/113)	100.00% (17/17)
1357	PSIISNEKQEILGTV	100.00% (111/111)	100.00% (146/146)	100.00% (458/458)	99.43% (173/174)	100.00% (8/8)	100.00% (19/19)	100.00% (95/95)	100.00% (113/113)	100.00% (17/17)
2944	AYESLRPDTRYVLMD	100.00% (111/111)	99.32% (145/146)	99.78% (457/458)	100.00% (174/174)	87.50% (7/8)	100.00% (19/19)	100.00% (95/95)	100.00% (113/113)	94.12% (16/17)
2945	YESLRPDTRYVLM DG	100.00% (111/111)	100.00% (146/146)	99.78% (457/458)	100.00% (174/174)	87.50% (7/8)	100.00% (19/19)	100.00% (95/95)	100.00% (113/113)	88.24% (15/17)
2958	DGSHIQFPNTYLEGS	100.00% (111/111)	98.63% (144/146)	99.13% (454/458)	100.00% (174/174)	100.00% (8/8)	100.00% (19/19)	100.00% (95/95)	99.12% (112/113)	94.12% (16/17)
3815	VSTQEFYRMNSQG LL	97.30% (108/111)	96.58% (141/146)	99.13% (454/458)	98.85% (172/174)	100.00% (8/8)	100.00% (19/19)	97.89% (93/95)	99.12% (112/113)	100.00% (17/17)
3944	IASEFSSLPSYA AFA	100.00% (111/111)	95.89% (140/146)	99.78% (457/458)	100.00% (174/174)	100.00% (8/8)	100.00% (19/19)	98.95% (94/95)	100.00% (113/113)	100.00% (17/17)
3945	ASEFSSLPSYAA FAT	99.10% (110/111)	95.89% (140/146)	99.78% (457/458)	100.00% (174/174)	100.00% (8/8)	100.00% (19/19)	100.00% (95/95)	100.00% (113/113)	100.00% (17/17)
3951	LPSYAAFATAQEAYE	99.10% (110/111)	94.52% (138/146)	99.56% (456/458)	98.85% (172/174)	100.00% (8/8)	100.00% (19/19)	100.00% (95/95)	100.00% (113/113)	100.00% (17/17)
4457	LIDSYFVVKRHTFSN	100.00% (111/111)	99.32% (145/146)	100.00% (458/458)	100.00% (174/174)	100.00% (8/8)	100.00% (19/19)	100.00% (95/95)	100.00% (113/113)	100.00% (17/17)
4458	IDSYFVVKRHTFSNY	100.00% (111/111)	99.32% (145/146)	100.00% (458/458)	100.00% (174/174)	100.00% (8/8)	100.00% (19/19)	100.00% (95/95)	100.00% (113/113)	100.00% (17/17)
4560	NPDILRVYANLGERV	100.00% (111/111)	100.00% (146/146)	95.63% (438/458)	100.00% (174/174)	100.00% (8/8)	100.00% (19/19)	100.00% (95/95)	100.00% (113/113)	100.00% (17/17)
4561	PDILRVYANLGERVR	100.00% (111/111)	100.00% (146/146)	95.63% (438/458)	100.00% (174/174)	100.00% (8/8)	100.00% (19/19)	100.00% (95/95)	100.00% (113/113)	100.00% (17/17)

4761	KELLYAADPAMHAA	99.10% (110/111)	100.00% (146/146)	99.78% (457/458)	100.00% (174/174)	100.00% (8/8)	100.00% (19/19)	100.00% (95/95)	100.00% (113/113)	100.00% (17/17)
4830	KHFFFAQDGNAAISD	100.00% (111/111)	100.00% (146/146)	99.78% (457/458)	99.43% (173/174)	100.00% (8/8)	100.00% (19/19)	100.00% (95/95)	100.00% (113/113)	94.12% (16/17)
4933	QMNLKYAISAKNRAR	100.00% (111/111)	100.00% (146/146)	99.78% (457/458)	100.00% (174/174)	100.00% (8/8)	100.00% (19/19)	100.00% (95/95)	100.00% (113/113)	100.00% (17/17)
4934	MNLKYAISAKNRART	100.00% (111/111)	100.00% (146/146)	99.78% (457/458)	100.00% (174/174)	100.00% (8/8)	100.00% (19/19)	100.00% (95/95)	100.00% (113/113)	100.00% (17/17)
4935	NLKYAISAKNRARTV	100.00% (111/111)	100.00% (146/146)	99.78% (457/458)	100.00% (174/174)	100.00% (8/8)	100.00% (19/19)	100.00% (95/95)	100.00% (113/113)	100.00% (17/17)
5019	PNMLRIMASLVLARK	100.00% (111/111)	100.00% (146/146)	100.00% (458/458)	100.00% (174/174)	100.00% (8/8)	100.00% (19/19)	100.00% (95/95)	100.00% (113/113)	88.24% (15/17)
5717	AKHYVYIGDPAQLPA	100.00% (111/111)	100.00% (146/146)	100.00% (458/458)	99.43% (173/174)	100.00% (8/8)	100.00% (19/19)	100.00% (95/95)	100.00% (113/113)	100.00% (17/17)
5775	TVSALVYDNKLKAHK	82.88% (92/111)	100.00% (146/146)	100.00% (458/458)	100.00% (174/174)	100.00% (8/8)	100.00% (19/19)	100.00% (95/95)	100.00% (113/113)	100.00% (17/17)
5776	VSALVYDNKLKAHKD	82.88% (92/111)	100.00% (146/146)	100.00% (458/458)	100.00% (174/174)	100.00% (8/8)	100.00% (19/19)	100.00% (95/95)	100.00% (113/113)	100.00% (17/17)
5777	SALVYDNKLKAHKDK	82.88% (92/111)	100.00% (146/146)	100.00% (458/458)	100.00% (174/174)	100.00% (8/8)	100.00% (19/19)	100.00% (95/95)	100.00% (113/113)	100.00% (17/17)
5834	VFISPYNSQNAVASK	100.00% (111/111)	100.00% (146/146)	99.78% (457/458)	99.43% (173/174)	100.00% (8/8)	100.00% (19/19)	100.00% (95/95)	100.00% (113/113)	100.00% (17/17)
6046	PTGYVDTPNNTDFSR	100.00% (111/111)	100.00% (146/146)	100.00% (458/458)	100.00% (174/174)	100.00% (8/8)	100.00% (19/19)	100.00% (95/95)	100.00% (113/113)	94.12% (16/17)
6454	LENVAFNVVNKGHFD	100.00% (111/111)	99.32% (145/146)	100.00% (458/458)	100.00% (174/174)	100.00% (8/8)	100.00% (19/19)	100.00% (95/95)	100.00% (113/113)	100.00% (17/17)
6726	TVKNYFITDAQTGSS	99.10% (110/111)	100.00% (146/146)	99.34% (455/458)	100.00% (174/174)	100.00% (8/8)	94.74% (18/19)	100.00% (95/95)	100.00% (113/113)	100.00% (17/17)
7075	KGRLIIRENNRVVIS	100.00% (111/111)	100.00% (146/146)	100.00% (458/458)	100.00% (174/174)	100.00% (8/8)	100.00% (19/19)	100.00% (95/95)	100.00% (113/113)	100.00% (17/17)
7076	GRLIIRENNRVVISS	100.00% (111/111)	100.00% (146/146)	100.00% (458/458)	100.00% (174/174)	100.00% (8/8)	100.00% (19/19)	100.00% (95/95)	100.00% (113/113)	100.00% (17/17)
7077	RLIIRENNRVVISSD	100.00% (111/111)	100.00% (146/146)	100.00% (458/458)	100.00% (174/174)	100.00% (8/8)	100.00% (19/19)	100.00% (95/95)	100.00% (113/113)	100.00% (17/17)

**Table S3.** Five out of 7 SARS-CoV-2 peptides that match with the human peptides were reported in IEDB as experimentally confirmed by T-cell assay. However, 4 peptides were recognized by T-cells from healthy individuals who have not infected by SARS-CoV-2. This table showing the comparison of the degree of homology of SARS-CoV-2 peptides versus peptides from human proteomes and versus peptides from human common cold coronaviruses (229E, HKU, NL63, and OC43). For homology with HCC, only homology of > 60% was considered.

SARS-CoV-2 Epitope	Immunization	Assay Antigen	MHC Restriction	Assay Description	Homology with human peptides (%)	Homology with human common cold coronavirus (%)
2784 AIFYLITPV <sup>2792</sup>	Infectious disease via exposure to SARS-CoV2 (Source Organism)	AIFYLITPV	HLA-A*02:01	biological activity activation Positive	<u>AIFYLITLV</u> (77.8 %)	n.a.
5614 FAIGLALYY <sup>5622</sup>	Infectious disease via exposure to SARS-CoV2 (Source Organism)	FAIGLALYY	HLA-C*07:02	multimer/tetramer qualitative binding Positive	SYIGLALYY (77.8%)	HKU <u>LAIGLAVYY</u> (77.8%)
	Exposure to endemic/ubiquitous agent Coronavirus (Taxonomic Parent) without evidence for disease	FAIGLALYY	HLA-C*07:02	multimer/tetramer qualitative binding Positive		NL63 <u>CSIGLGLYY</u> (66.7%) OC43 <u>LAIGLAVFY</u> (66.7%)
3684 YASAVVLLI <sup>3692</sup>	Exposure to endemic/ubiquitous agent Coronavirus (Taxonomic Parent) without evidence for disease	YASAVVLLI	HLA-C*06:02	multimer/tetramer qualitative binding Positive	<u>VASAVVLLG</u> (77.8%)	229E <u>YESAVVNGI</u> (66.7%)
6748 LLLDDFVEI <sup>6756</sup>	Exposure to endemic/ubiquitous agent Coronavirus (Taxonomic Parent) without evidence for disease	LLLDDFVEI	HLA-A*02:01	ELISPOT IFN $\gamma$ release Positive-High	<u>IALDDFVEI</u> (77.8%)	229E <u>LLLDDFVSV</u> (77.8%) HKU <u>LLLDDFVSI</u> (88.9%) NL63 <u>LLLDDFVTI</u> (88.9%)
	Infectious disease via exposure to SARS-CoV2 (Source Organism)	LLLDDFVEI	HLA-A*02:01	ELISPOT IFN $\gamma$ release Positive-High		OC43 <u>ILLDDFVAL</u> (66.7%)
3752 FLARGIVFM <sup>3760</sup>	Infectious disease via exposure to SARS-CoV2 (Source Organism)	FLARGIVFM	HLA-A*02:01	multimer/tetramer qualitative binding Positive	XCARGIVFM (77.8%)	HKU <u>FLQSGIVKM</u> (66.7%)
	Exposure to endemic/ubiquitous agent Coronavirus (Taxonomic Parent) without evidence for disease	FLARGIVFM	HLA-A*02:01	multimer/tetramer qualitative binding Positive		OC43 <u>FLQSGIVKM</u> (66.7%)

**Table S4.** SARS-CoV-2 peptides that do not have homology match with the human peptides were reported in IEDB as experimentally confirmed by T-cell assay. Majority of these peptides were recognized by T-cells from individuals who were infected by SARS-CoV-2.

Epitope	Immunization	Assay Antigen	MHC Restriction	Assay Description	Homology with human common cold coronavirus (%)
5678YVFCTVNAL <sup>5686</sup>	No immunization was performed	YVFCTVNAL	HLA class I	biological activity activation Positive	229E <u>YVFSTVNAL</u> (88.9%)
	Infectious disease via exposure to SARS-CoV2 (Source Organism)	YVFCTVNAL	HLA class I	biological activity activation Positive	HKU <u>YVFTTNAL</u> (77.8%) NL63 <u>YFSTVNAL</u> (77.8%) OC43 <u>YVFTTNAL</u> (77.8%)
	No immunization was performed	LMIERFVSL	HLA class I	biological activity activation Positive	
	Exposure to endemic/ubiquitous agent Coronavirus (Taxonomic Parent) without evidence for disease	LMIERFVSL	HLA-A*02:01	multimer/tetramer qualitative binding Positive	HKU <u>LLIERFVSL</u> (88.9%) OC43 <u>LLIERFVSL</u> (88.9%)
2787YLITPVHVM <sup>2795</sup>	Exposure to endemic/ubiquitous agent Coronavirus (Taxonomic Parent) without evidence for disease	YLITPVHVM	HLA-C*07:01	multimer/tetramer qualitative binding Positive	
	Exposure to endemic/ubiquitous agent Coronavirus (Taxonomic Parent) without evidence for disease	YLITPVHVM	HLA-A*02:01	multimer/tetramer qualitative binding Positive	n.a.
	Infectious disease via exposure to SARS-CoV2 (Source Organism)	YLITPVHVM	HLA-B*15:01	multimer/tetramer qualitative binding Positive	
	Infectious disease via exposure to SARS-CoV2 (Source Organism)	YLITPVHVM	HLA-A*02:01	biological activity activation Positive	
	Infectious disease via exposure to SARS-CoV2 (Source Organism)	LVSDIDITF	HLA-B*35:01	biological activity activation Positive	n.a.
1269LVSDIDITF <sup>1277</sup>	Infectious disease via exposure to SARS-CoV2 (Source Organism)	YVMHANYIF	HLA-A*32:01	biological activity activation Positive	HKU <u>NVMHANYLF</u> (77.8%) NL63 <u>NTVHANYIF</u> (66.7%) OC43 <u>NVMHANYLF</u> (77.8%)
7019YVMHANYIF <sup>7027</sup>	Infectious disease via exposure to SARS-CoV2 (Source Organism)	ILMTARTVY	HLA-B*15:01	multimer/tetramer qualitative binding Positive-Low	
3692ILMTARTVY <sup>3700</sup>	Infectious disease via exposure to SARS-CoV2 (Source Organism)	ILMTARTVY	HLA-B*15:01	multimer/tetramer qualitative binding Positive	n.a.
1055VVVNAANVY <sup>1063</sup>	No immunization was performed	ILMTARTVY	HLA-B*15:01	multimer/tetramer qualitative binding Positive	
	Infectious disease via exposure to SARS-CoV2 (Source Organism)	VVVNAANVY	HLA-B*35:01	biological activity activation Positive	NL63 <u>FVVNAANEN</u> (66.7%) OC43 <u>VVVNPANGH</u> (66.7%)

5024MASLVLARK <sup>5032</sup>	Infectious disease via exposure to SARS-CoV2 (Source Organism)	MASLVLARK	HLA-A*68:01	biological activity activation Positive	HKU <u>VSSLVLARK</u> (77.8%) OC43 <u>VSSLVLARK</u> (77.8%)
5132FVNEFYAYL <sup>5140</sup>	Exposure to endemic/ubiquitous agent Coronavirus (Taxonomic Parent) without evidence for disease	FVNEFYAYL	HLA-A*02:01	multimer/tetramer qualitative binding positive	229E <u>FVDDFYGYL</u> (44.4%) HKU <u>FVNEYEFL</u> (66.7%)
4862FVVEVVDKY <sup>4870</sup>	Infectious disease via exposure to SARS-CoV2 (Source Organism)	FVVEVVDKY	HLA-B*15:01	multimer/tetramer qualitative binding positive	HKU <u>FVLEVVKY</u> (77.8%) OC43 <u>FVLEVVKY</u> (77.8%)
2331ILFTRFFYV <sup>2339</sup>	Infectious disease via exposure to SARS-CoV2 (Source Organism)	ILFTRFFYV	HLA-A*02:01	biological activity activation Positive	n.a.
	Infectious disease via exposure to SARS-CoV2 (Source Organism)	ILFTRFFYV	HLA-A*02:01	ICS IFN $\gamma$ release Positive-Low	
	Infectious disease via exposure to SARS-CoV2 (Source Organism)	ILFTRFFYV	HLA-A*02:01	ICS IFN $\gamma$ release Positive-Low	
3481FLNRFTTTL <sup>3489</sup>	No immunization was performed	FLNRFTTTL	HLA class I	biological activity activation Positive	n.a.
	Infectious disease via exposure to SARS-CoV2 (Source Organism)	FLNRFTTTL	HLA class I	biological activity activation Positive	
	Infectious disease via exposure to SARS-CoV2 (Source Organism)	FLNRFTTTL	HLA class I	biological activity activation Positive	
1674YLATALLTL <sup>1682</sup>	Infectious disease via exposure to SARS-CoV2 (Source Organism)	YLATALLTL	HLA-A*02:01	biological activity activation Positive	n.a.
	Infectious disease via exposure to SARS-CoV2 (Source Organism)	YLATALLTL	HLA-A*02:01	ELISPOT IFN $\gamma$ release Positive-High	
	Exposure to endemic/ubiquitous agent Coronavirus (Taxonomic Parent) without evidence for disease	YLATALLTL	HLA-A*02:01	ELISPOT IFN $\gamma$ release Positive-High	
	Infectious disease via exposure to SARS-CoV2 (Source Organism)	YLATALLTL	HLA-A*02:01	multimer/tetramer qualitative binding positive	
	Exposure to endemic/ubiquitous agent Coronavirus (Taxonomic Parent) without evidence for disease	YLATALLTL	HLA-A*02:01	multimer/tetramer qualitative binding positive	
2883FLPRVFS <sup>2891</sup>	Infectious disease via exposure to SARS-CoV2 (Source Organism)	FLPRVFS	HLA class I	biological activity activation Positive	OC43 <u>FLRVFSQV</u> (66.7%)



	Documented exposure to SARS-CoV2 (Source Organism) without evidence for disease	FLPRVFSAV	HLA class I	biological activity activation Positive	
	Infectious disease via exposure to SARS-CoV2 (Source Organism)	FLPRVFSAV	HLA-A*02:01	biological activity activation Positive	
	No immunization was performed	FLPRVFSAV	HLA class I	biological activity activation Positive	
	Infectious disease via exposure to SARS-CoV2 (Source Organism)	FLPRVFSAV	HLA class I	biological activity activation Positive	
	Exposure to endemic/ubiquitous agent Coronavirus (Taxonomic Parent) without evidence for disease	FLPRVFSAV	HLA-A*02:01	multimer/tetramer qualitative binding positive	
3466VLAWLYAAV <sup>3474</sup>	No immunization was performed	VLAWLYAAV	HLA class I	biological activity activation Positive	229E <u>VVAFLYAAI</u> (66.7%) HKU <u>VIAWLYAAI</u> (77.8%)
	Infectious disease via exposure to SARS-CoV2 (Source Organism)	VLAWLYAAV	HLA class I	biological activity activation Positive	NL63 <u>VVAFLYAAL</u> (66.7%) OC43 <u>FVAWLYAAI</u> (66.7%)
4698ILHCANFNV <sup>4707</sup>	Infectious disease via exposure to SARS-CoV2 (Source Organism)	ILHCANFNV	HLA class I	biological activity activation Positive	229E <u>ILHCSNFNT</u> (77.8%) HKU <u>IILHCANFNI</u> (77.8%)
	No immunization was performed	ILHCANFNV	HLA class I	biological activity activation Positive	NL63 <u>VIHCANFNT</u> (77.8%) OC43 <u>IILHCANFNI</u> (77.8%)
6850YLNTLTLAV <sup>6858</sup>	No immunization was performed	YLNTLTLAV	HLA class I	biological activity activation Positive	HKU <u>YLNTTTLAV</u> (88.9%)
	Infectious disease via exposure to SARS-CoV2 (Source Organism)	YLNTLTLAV	HLA class I	biological activity activation Positive	OC43 <u>YLNTTTLAV</u> (88.9%)
3121FLAHIQWMV <sup>3129</sup>	Infectious disease via exposure to SARS-CoV2 (Source Organism)	FLAHIQWMV	HLA-A*02:06	biological activity activation Positive	
	Infectious disease via exposure to SARS-CoV2 (Source Organism)	FLAHIQWMV	HLA-A*02:01	multimer/tetramer qualitative binding positive	n.a.
	Exposure to endemic/ubiquitous agent Coronavirus (Taxonomic Parent) without evidence for disease	FLAHIQWMV	HLA-A*02:01	multimer/tetramer qualitative binding positive	
2786FYLITPVHV <sup>2794</sup>	Exposure to endemic/ubiquitous agent Coronavirus (Taxonomic Parent) without evidence for disease	FYLITPVHV	HLA-C*07:02	multimer/tetramer qualitative binding positive	n.a.
6108VLWAHGFEL <sup>6116</sup>	Infectious disease via exposure to SARS-	VLWAHGFEL	HLA class I	biological activity activation Positive	229E <u>VLWAGGLEL</u> (77.8%)

	CoV2 (Source Organism)				NL63 <u>VLWAGSLEL</u> (66.7%)
	Infectious disease via exposure to SARS-CoV2 (Source Organism)	VLWAHGFEL	HLA class I	biological activity activation Positive	OC43 <u>VTWAAANFEL</u> (66.7%)
	No immunization was performed	VLWAHGFEL	HLA class I	biological activity activation Positive	
3652VYMPASWVM3660	Infectious disease via exposure to SARS-CoV2 (Source Organism)	VYMPASWVM	HLA-A*24:02	biological activity activation Positive	n.a.
	Infectious disease via exposure to SARS-CoV2 (Source Organism)	VYMPASWVM	HLA-A*24:02	multimer/tetramer qualitative binding positive	
3059LAYYFMRFR3067	Infectious disease via exposure to SARS-CoV2 (Source Organism)	LAYYFMRFR	HLA-A*31:01	biological activity activation Positive	n.a.
4862FVVEVVVDKY4870	Infectious disease via exposure to SARS-CoV2 (Source Organism)	FVVEVVVDKY	HLA-B*15:01	multimer/tetramer qualitative binding positive	HKU <u>FVLEVVYKY</u> (77.8%) OC43 <u>FVLEVVYKY</u> (77.8%)

**Table S5.** Toxicity of VC. Toxinpred scan for fragments of 10 amino acid length and predict their toxicity. Only residue 29-48 which is part of the beta defensin adjuvant that contain toxic fragments of 10 mer peptides.

Peptide Sequence	SVM score	Prediction	Hydrophobicity	Hydropathicity	Hydrophilicity	Charge	Mol wt
GIINTLQKY	-0.66	Non-Toxin	-0.04	-0.18	-0.7	1	1212.57
IINTLQKYC	-0.39	Non-Toxin	-0.05	0.11	-0.8	1	1258.65
INTLQKYCR	-0.4	Non-Toxin	-0.3	-0.79	-0.32	2	1301.67
NTLQKYCRV	-0.48	Non-Toxin	-0.32	-0.82	-0.29	2	1287.64
TLQKYCRVR	-0.56	Non-Toxin	-0.43	-0.92	-0.01	3	1329.72
LQKYCRVRG	-0.54	Non-Toxin	-0.4	-0.89	0.03	3	1285.67
QKYCRVRGG	-0.73	Non-Toxin	-0.44	-1.31	0.21	3	1229.56
KYYCRVRGGR	-0.77	Non-Toxin	-0.54	-1.41	0.49	4	1257.61
YYCRVRGGRC	-0.85	Non-Toxin	-0.43	-0.77	0.09	3	1232.57
YCRVRGGRCA	-0.71	Non-Toxin	-0.41	-0.46	0.27	3	1140.47
CRVRGGRCAV	-0.9	Non-Toxin	-0.35	0.09	0.35	3	1076.43
RVRGGRCAVL	-1.08	Non-Toxin	-0.31	0.22	0.27	3	1086.46
VRGGRCAVLS	-1.01	Non-Toxin	-0.16	0.59	0	2	1017.35
RGGRCAVLSC	-1.02	Non-Toxin	-0.21	0.42	0.05	2	1021.35
GGRC AVL SCL	-0.58	Non-Toxin	0.02	1.25	-0.43	1	978.33
GRC AVL SCLP	-0.6	Non-Toxin	0	1.13	-0.43	1	1018.39
RC AVL SCLPK	-0.63	Non-Toxin	-0.13	0.78	-0.13	2	1089.51
CA VL SCLPKE	-0.68	Non-Toxin	-0.01	0.88	-0.13	0	1062.44
AV L SCLPKEE	-0.71	Non-Toxin	-0.08	0.28	0.27	-1	1088.42
VL SCLPKEEQ	-0.76	Non-Toxin	-0.17	-0.25	0.34	-1	1145.48
LSCLPKEEQI	-0.52	Non-Toxin	-0.15	-0.22	0.31	-1	1159.51
SCLPKEEQIG	-0.43	Non-Toxin	-0.19	-0.64	0.49	-1	1103.4
CLPKEEQIGK	-0.44	Non-Toxin	-0.27	-0.95	0.76	0	1144.5
LPKEEQIGKC	-0.33	Non-Toxin	-0.27	-0.95	0.76	0	1144.5
PKEEQIGKCS	-0.08	Non-Toxin	-0.35	-1.41	0.97	0	1118.41
KEEQIGKCST	-0.16	Non-Toxin	-0.36	-1.32	0.93	0	1122.4
EEQIGKCSTR	-0.07	Non-Toxin	-0.43	-1.38	0.93	0	1150.41
EQIGKCSTRG	-0.13	Non-Toxin	-0.35	-1.07	0.63	1	1078.35
QIGKCSTRGR	0.18	Toxin	-0.47	-1.17	0.63	3	1105.42
IGKCSTRGRK	0.03	Toxin	-0.51	-1.21	0.91	4	1105.46
GKCSTRGRKC	0.19	Toxin	-0.58	-1.41	0.99	4	1095.43
KCSTRGRKCC	1.2	Toxin	-0.59	-1.12	0.89	4	1141.51
CSTRGRKCCR	1.57	Toxin	-0.65	-1.18	0.89	4	1169.52
STRGRKCCRR	1.01	Toxin	-0.83	-1.88	1.29	5	1222.57
TRGRKCCRRK	0.47	Toxin	-0.92	-2.19	1.56	6	1263.67
RGRKCCRRKK	0.18	Toxin	-1.01	-2.51	1.9	7	1290.74
GRKCCRRKKE	0.49	Toxin	-0.9	-2.41	1.9	5	1263.67
RKCCRRKKEA	0.25	Toxin	-0.89	-2.19	1.85	5	1277.69
KCCRRKKEAA	0.66	Toxin	-0.69	-1.56	1.5	4	1192.58
CCRRKKEAAA	-0.02	Non-Toxin	-0.55	-0.99	1.15	3	1135.48
CRRKKEAAAK	-0.97	Non-Toxin	-0.67	-1.63	1.55	4	1160.52
RRKKEAAAKI	-1.29	Non-Toxin	-0.6	-1.43	1.47	4	1170.55
RKKEAAAKIL	-1.34	Non-Toxin	-0.37	-0.6	0.99	3	1127.53

KKEAAAKILM	-1.38	Non-Toxin	-0.17	0.04	0.56	2	1102.54
KEAAAKILMT	-1.5	Non-Toxin	-0.07	0.36	0.22	1	1075.47
EAAAKILMTA	-1.53	Non-Toxin	0.06	0.93	-0.13	0	1018.37
AAAKILMTAR	-1.37	Non-Toxin	-0.05	0.83	-0.13	2	1045.44
AAKILMTART	-1.27	Non-Toxin	-0.1	0.58	-0.12	2	1075.47
AKILMTARTV	-1.12	Non-Toxin	-0.07	0.82	-0.22	2	1103.53
KILMTARTVY	-1.58	Non-Toxin	-0.09	0.51	-0.4	2	1195.63
ILMTARTVYG	-1.31	Non-Toxin	0.04	0.86	-0.7	1	1124.51
LMTARTVYGP	-1.17	Non-Toxin	-0.04	0.25	-0.52	1	1108.46
MTARTVYGPG	-1.18	Non-Toxin	-0.08	-0.17	-0.34	1	1052.35
TARTVYGPGP	-0.81	Non-Toxin	-0.11	-0.52	-0.21	1	1018.27
ARTVYGPGPG	-0.79	Non-Toxin	-0.08	-0.49	-0.17	1	974.22
RTVYGPGPGT	-0.69	Non-Toxin	-0.12	-0.74	-0.16	1	1004.25
TVYGPGPGTM	-0.5	Non-Toxin	0.08	-0.1	-0.59	0	979.26
VYGPGPGTML	-0.66	Non-Toxin	0.15	0.35	-0.73	0	991.32
YGPGP GTMLF	-0.58	Non-Toxin	0.16	0.21	-0.83	0	1039.36
GPGPGT MLFT	-0.62	Non-Toxin	0.14	0.27	-0.64	0	977.29
PGPGT MLFTM	-0.58	Non-Toxin	0.15	0.5	-0.77	0	1051.43
GPGT MLFTML	-0.74	Non-Toxin	0.21	1.04	-0.95	0	1067.48
PGT MLFTMLR	-0.83	Non-Toxin	0.02	0.63	-0.65	1	1166.61
GT MLFTMLRK	-0.77	Non-Toxin	-0.09	0.4	-0.35	2	1197.67
T MLFTMLRKG	-0.71	Non-Toxin	-0.09	0.4	-0.35	2	1197.67
MLFTMLRKGP	-0.94	Non-Toxin	-0.08	0.31	-0.31	2	1193.68
LFTMLRKGP	-0.78	Non-Toxin	-0.09	0.08	-0.18	2	1119.54
FTMLRKGP	-0.63	Non-Toxin	-0.15	-0.46	0	2	1103.49
TMLRKGP	-0.63	Non-Toxin	-0.19	-0.78	0.25	2	1013.37
MLRKGP	-0.84	Non-Toxin	-0.17	-0.84	0.06	2	1075.44
LRKGP	-0.76	Non-Toxin	-0.14	-0.65	0.01	2	1057.41
RKGP	-0.69	Non-Toxin	-0.26	-1.38	0.21	2	1058.35
KGP	-0.68	Non-Toxin	-0.1	-1	-0.13	1	1003.27
GPG	-0.79	Non-Toxin	0.06	-0.23	-0.61	0	988.26
PG	-1.06	Non-Toxin	0.03	-0.26	-0.65	0	1032.31
G	-1.18	Non-Toxin	0.09	0.28	-0.83	0	1048.36
P	-1.33	Non-Toxin	0.1	0.5	-0.88	0	1062.38
G	-1.31	Non-Toxin	0.16	1.08	-1.03	0	1064.4
Y	-1.47	Non-Toxin	0.08	0.77	-0.73	-1	1136.46
L	-1.49	Non-Toxin	0.1	1.08	-0.55	-1	1044.36
N	-1.44	Non-Toxin	0.07	0.88	-0.42	-1	1002.27
T	-1.39	Non-Toxin	0.16	1.41	-0.49	-1	959.24
L	-1.24	Non-Toxin	0.07	1.09	-0.15	0	986.31
T	-1.15	Non-Toxin	0.05	0.62	-0.31	0	1059.36
L	-1.13	Non-Toxin	0.05	0.61	-0.24	0	1045.33
A	-0.98	Non-Toxin	0.02	0.42	-0.19	0	1063.36
V	-0.97	Non-Toxin	0.02	0.42	-0.19	0	1063.36
E	-0.97	Non-Toxin	-0.05	-0.07	-0.08	0	1065.33
A	-0.78	Non-Toxin	0.01	0.15	-0.61	1	1099.39
A	-0.52	Non-Toxin	-0.01	-0.16	-0.79	1	1191.49

AKWSMATYYL	-0.54	Non-Toxin	0.02	0.04	-0.92	1	1233.58
KWSMATYYLF	-0.72	Non-Toxin	0.05	0.14	-1.12	1	1309.68
WSMATYYLFA	-0.98	Non-Toxin	0.19	0.71	-1.47	0	1252.58
SMATYYLFAA	-1.02	Non-Toxin	0.17	0.98	-1.18	0	1137.44
MATYYLFAAG	-1.21	Non-Toxin	0.22	1.02	-1.21	0	1107.42
ATYYLFAAGY	-0.96	Non-Toxin	0.19	0.7	-1.31	0	1139.4
TYYLFAAGYV	-1.07	Non-Toxin	0.22	0.94	-1.41	0	1167.46
YYLFAAGYVF	-1.16	Non-Toxin	0.3	1.29	-1.62	0	1213.53
YLFAAGYVFC	-0.97	Non-Toxin	0.3	1.67	-1.49	0	1153.49
LFAAGYVFCT	-0.8	Non-Toxin	0.28	1.73	-1.3	0	1091.42
FAAGYVFCTV	-0.84	Non-Toxin	0.28	1.77	-1.27	0	1077.39
AAGYVFCTVN	-0.83	Non-Toxin	0.16	1.14	-1	0	1044.32
AGYVFCTVNA	-0.54	Non-Toxin	0.16	1.14	-1	0	1044.32
GYVFCTVNAL	-0.46	Non-Toxin	0.19	1.34	-1.13	0	1086.41
YVFCTVNALA	-0.69	Non-Toxin	0.2	1.56	-1.18	0	1100.43
VFCTVNALAA	-0.7	Non-Toxin	0.22	1.87	-1	0	1008.33
FCTVNALAAAG	-0.68	Non-Toxin	0.18	1.41	-0.85	0	966.25
CTVNALAAAGL	-0.94	Non-Toxin	0.17	1.51	-0.78	0	932.24
TVNALAAAGLM	-1.05	Non-Toxin	0.2	1.45	-0.81	0	960.3
VNALAAAGLMI	-0.98	Non-Toxin	0.29	1.97	-0.95	0	972.36
NALAAAGLMIE	-0.83	Non-Toxin	0.17	1.2	-0.5	-1	1002.34
ALAAGLMIER	-1.32	Non-Toxin	0.06	1.1	-0.22	0	1044.42
LAAGLMIERF	-1.44	Non-Toxin	0.09	1.2	-0.42	0	1120.52
AAGLMIERFV	-1.39	Non-Toxin	0.09	1.24	-0.39	0	1106.49
AGLMIERFVS	-1.39	Non-Toxin	0.04	0.98	-0.31	0	1122.49
GLMIERFVSL	-1.51	Non-Toxin	0.07	1.18	-0.44	0	1164.58
LMIERFVSLA	-1.61	Non-Toxin	0.08	1.4	-0.49	0	1178.6
MIERFVSLAA	-1.63	Non-Toxin	0.05	1.2	-0.36	0	1136.51
IERFVSLAAG	-1.52	Non-Toxin	0.04	0.97	-0.23	0	1062.37
ERFVSLAAGF	-1.64	Non-Toxin	0.03	0.8	-0.3	0	1096.38
RFVSLAAGFE	-1.32	Non-Toxin	0.03	0.8	-0.3	0	1096.38
FVSLAAGFEL	-1.5	Non-Toxin	0.26	1.63	-0.78	-1	1053.36
VSLAAGFELE	-1.46	Non-Toxin	0.14	1	-0.23	-2	1035.3
SLAAGFELED	-1.24	Non-Toxin	0.01	0.23	0.22	-3	1051.25
LAAGFELEDF	-1.48	Non-Toxin	0.1	0.59	-0.06	-3	1111.35
AAGFELEDFI	-1.35	Non-Toxin	0.12	0.66	-0.06	-3	1111.35
AGFELEDFIP	-1.22	Non-Toxin	0.09	0.32	-0.01	-3	1137.39
GFELEDFIPM	-1.04	Non-Toxin	0.09	0.33	-0.09	-3	1197.51
FELEDFIPMA	-1.18	Non-Toxin	0.1	0.55	-0.14	-3	1211.53
ELEDFIPMAA	-1.24	Non-Toxin	0.06	0.45	0.06	-3	1135.43
LEDFIPMAAG	-1.15	Non-Toxin	0.14	0.76	-0.24	-2	1063.37
EDFIPMAAGM	-1.08	Non-Toxin	0.11	0.57	-0.19	-2	1081.4
DFIPMAAGMA	-1.17	Non-Toxin	0.2	1.1	-0.54	-1	1023.36
FIPMAAGMAS	-0.98	Non-Toxin	0.24	1.37	-0.81	0	995.35
IPMAAGMASL	-0.96	Non-Toxin	0.24	1.47	-0.74	0	961.34
PMAAGMASLV	-0.95	Non-Toxin	0.22	1.44	-0.71	0	947.31
MAAGMASLVL	-1.13	Non-Toxin	0.28	1.98	-0.89	0	963.36

AAGMASLVLA	-1.06	Non-Toxin	0.28	1.97	-0.81	0	903.24
AGMASLVLAR	-1.08	Non-Toxin	0.07	1.34	-0.46	1	988.35
GMASVLARK	-1.17	Non-Toxin	-0.06	0.77	-0.11	2	1045.45
MASVLARKA	-1.23	Non-Toxin	-0.05	0.99	-0.16	2	1059.47
ASVLARKAA	-1.11	Non-Toxin	-0.05	0.98	-0.08	2	999.35
SLVLARKAAG	-1.16	Non-Toxin	-0.06	0.76	-0.03	2	985.33
LVLARKAAGC	-0.98	Non-Toxin	-0.03	1.09	-0.16	2	1001.39
VLARKAAGCQ	-0.54	Non-Toxin	-0.15	0.36	0.04	2	1016.36
LARKAAGCQY	-0.5	Non-Toxin	-0.21	-0.19	-0.04	2	1080.4
ARKAAGCQYL	-0.51	Non-Toxin	-0.21	-0.19	-0.04	2	1080.4
RKAAGCQYLN	-0.56	Non-Toxin	-0.29	-0.72	0.03	2	1123.43
KAAGCQYLNT	-0.54	Non-Toxin	-0.14	-0.34	-0.31	1	1068.35
AAGCQYLNTL	-0.72	Non-Toxin	0.03	0.43	-0.79	0	1053.34
AGCQYLNTLT	-0.72	Non-Toxin	-0.02	0.18	-0.78	0	1083.37
GCQYLNTLTL	-0.86	Non-Toxin	0.01	0.38	-0.91	0	1125.46
CQYLNTLTLA	-1.19	Non-Toxin	0.02	0.6	-0.96	0	1139.48
QYLNTLTLAA	-1.46	Non-Toxin	0.04	0.53	-0.91	0	1107.42
YLNTLTLAAG	-1.48	Non-Toxin	0.13	0.84	-0.93	0	1036.34
LNTLTLAAGF	-1.43	Non-Toxin	0.19	1.25	-0.95	0	1020.34
NTLTLAAGFS	-1.42	Non-Toxin	0.11	0.79	-0.74	0	994.25
TLTLAAGFSY	-1.48	Non-Toxin	0.17	1.01	-0.99	0	1043.32
LTLAAGFSYF	-1.44	Non-Toxin	0.25	1.36	-1.2	0	1089.39
TLAAGFSYFA	-1.5	Non-Toxin	0.22	1.16	-1.07	0	1047.3
LAAGFSYFAV	-1.41	Non-Toxin	0.3	1.65	-1.18	0	1045.33
AAGFSYFAVH	-1.29	Non-Toxin	0.2	0.95	-1.05	0.5	1069.31
AGFSYFAVHF	-1.31	Non-Toxin	0.24	1.05	-1.25	0.5	1145.41
GFSYFAVHFI	-1.29	Non-Toxin	0.29	1.32	-1.38	0.5	1187.5

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**Table S6.** VC evaluation for possible CTL epitopes that will be generated and homology of new epitopes with human peptides.

Start	Peptide	HLA alleles	Human proteins	human peptides
0	GIINTLQKY	HLA-A*29:01, HLA-B*15:01, HLA-B*15:12	similar with human beta defensin	<sup>33</sup> GIINTLQKY <sup>41</sup>
1	IINTLQKYY	HLA-A*29:01	similar with human beta defensin	<sup>34</sup> IINTLQKYY <sup>42</sup>
3	NTLQKYYCR	HLA-A*33:03	similar with human beta defensin	<sup>4</sup> NTLQKYYCR <sup>12</sup>
4	TLQKYYCRV	HLA-A*02:03	similar with human beta defensin	<sup>37</sup> TLQKYYCRV <sup>45</sup>
11	RVRGGRCVAV	HLA-A*30:01, HLA-B*07:02, HLA-B*07:05, HLA-B*56:01,	similar with human beta defensin	<sup>44</sup> RVRGGRCVAV <sup>52</sup>
12	VRGGRCVAVL	HLA-B*27:06	similar with human beta defensin	<sup>45</sup> VRGGRCVAVL <sup>53</sup>
15	GRCVAVLSCL	HLA-B*27:06	similar with human beta defensin	<sup>48</sup> GRCVAVLSCL <sup>56</sup>
46	AAAKKSAFY	HLA-A*01:01, HLA-B*15:12,	Mitochondrial ribosomal protein L1	<sup>22</sup> AAAKKSA <sup>28</sup>
47	AAKKSIFY	HLA-A*30:01		
51	SAFYILPSI	HLA-A*32:01, HLA-B*13:02, HLA-B*51:01, HLA-B*51:02, HLA-B*52:01		
52	AFYILPSII	HLA-B*52:01		
56	LPSIISNEK	HLA-B*56:01		
94	SLRPDTRYV	HLA-A*02:03		
95	LRPDTRYVL	HLA-B*27:06		
96	RPDTRYVLM	HLA-B*07:02, HLA-B*07:05,		
103	LMDGPGPGV	HLA-A*02:01	immunoglobulin heavy chain junction region	4DGPDPGV10
110	GVSTQEFY	HLA-A*01:01, HLA-A*29:01,		
116	FRYMNSQGL	HLA-B*15:10, HLA-B*27:06, HLA-B*38:02		
117	RYMNSQGLL	HLA-A*24:02, HLA-A*24:07, HLA-A*24:10		
125	LEAAAKWSM	HLA-B*18:01, HLA-B*18:02, HLA-B*40:01, HLA-B*44:03,		
128	AAKWSMATY	HLA-A*30:01, HLA-B*15:01, HLA-B*15:02, HLA-B*15:12, HLA-B*15:13, HLA-B*15:17, HLA-B*15:21, HLA-B*15:25, HLA-B*15:32, HLA-B*35:05, HLA-B*35:30, HLA-B*46:01, HLA-B*57:01		
130	KWSMATYYL	HLA-A*24:02, HLA-A*24:07, HLA-A*24:10		
131	WSMATYYLF*	HLA-A*24:02, HLA-A*24:07, HLA-A*24:10, HLA-B*15:13, HLA-B*15:17, HLA-B*57:01, HLA-B*58:01		
133	MATYYLFAA	HLA-B*56:01		
135	TYYLFAAGY	HLA-A*29:01		
136	YYLFAAGYV	HLA-A*24:10		
137	YLFAAGYVF	HLA-A*02:01, HLA-A*02:06, HLA-A*02:07, HLA-A*24:02, HLA-A*24:07, HLA-A*29:01, HLA-A*32:01, HLA-B*13:01, HLA-B*15:01, HLA-B*15:02, HLA-B*15:10, HLA-B*15:12, HLA-B*15:13, HLA-B*15:21, HLA-B*15:25, HLA-B*15:32, HLA-B*18:01, HLA-B*18:02, HLA-B*35:01, HLA-B*35:02, HLA-B*35:05, HLA-B*35:30, HLA-B*38:02, HLA-B*46:01, HLA-B*48:01, HLA-B*56:01, HLA-B*56:02	immunoglobulin light chain junction region	8FAAGYVF14
143	YVFCTVNAL*	HLA-A*02:01, HLA-A*02:03, HLA-A*02:06, HLA-A*02:07, HLA-A*26:01, HLA-A*34:01, HLA-B*07:02, HLA-B*07:05, HLA-B*15:02, HLA-B*15:10, HLA-B*15:21, HLA-B*35:01, HLA-B*35:02, HLA-B*35:05, HLA-B*35:30, HLA-B*38:02, HLA-B*46:01, HLA-B*48:01, HLA-B*56:01, HLA-B*56:02,		
155	LMIERFVSL*	HLA-A*02:01, HLA-A*02:03, HLA-A*02:06, HLA-A*02:07, HLA-A*32:01, HLA-B*08:01, HLA-B*15:01, HLA-B*15:02, HLA-B*15:10, HLA-B*15:12, HLA-B*15:21, HLA-B*15:25, HLA-B*15:32, HLA-B*35:02, HLA-B*37:01, HLA-B*38:02, HLA-B*46:01, HLA-B*48:01,		
157	IERFVSLAA	HLA-B*40:06, HLA-B*41:01,		
159	RFVSLAAGF	HLA-A*24:02, HLA-A*24:10,	hCG2019424	52VSLAAGF58
161	VSLAAGFEL	HLA-B*58:01	hCG2019424	52VSLAAGF58

167	FELEDFIPM*	HLA-B*13:01, HLA-B*13:02, HLA-B*15:10, HLA-B*18:01, HLA-B*18:02, HLA-B*35:02, HLA-B*37:01, HLA-B*38:02, HLA-B*40:01, HLA-B*40:02, HLA-B*40:06, HLA-B*41:01, HLA-B*44:03, HLA-B*48:01,
175	MAAGMASLV	HLA-B*56:01, HLA-B*56:07,
178	GMASLVLAR	HLA-A*74:01
179	MASLVLARK*	HLA-A*03:01, HLA-A*11:01, HLA-A*11:04, HLA-A*30:01, HLA-A*33:03, HLA-A*34:01, HLA-A*74:01
186	RKAAGCQYL	HLA-B*27:06, HLA-B*48:01,
191	CQYLNTLT*	HLA-B*13:01, HLA-B*13:02, HLA-B*15:10, HLA-B*27:06, HLA-B*37:01, HLA-B*38:02, HLA-B*48:01, HLA-B*52:01,
193	YLNTLTAA	HLA-A*02:03
197	LTLAAGFSY	HLA-A*01:01, HLA-A*11:01, HLA-A*29:01, HLA-B*15:01, HLA-B*15:02, HLA-B*15:12, HLA-B*15:13, HLA-B*15:17, HLA-B*15:21, HLA-B*15:25, HLA-B*35:01, HLA-B*35:05, HLA-B*35:30, HLA-B*46:01, HLA-B*57:01, HLA-B*58:01,
198	TLAAGFSYF	HLA-A*26:01, HLA-A*29:01, HLA-A*32:01, HLA-A*34:01, HLA-B*15:01, HLA-B*15:02, HLA-B*15:12, HLA-B*15:13, HLA-B*15:21, HLA-B*15:25, HLA-B*15:32, HLA-B*46:01,
202	GFSYFAVHF	HLA-A*24:02, HLA-A*24:10,
203	FSYFAVHFI*	HLA-B*13:02, HLA-B*51:01, HLA-B*51:02, HLA-B*52:01,

\*CTL epitopes originally put in the vaccine construct



**Table S7.** VC evaluation for possible HTL epitopes that will be generated and possibility of new epitopes homology with human peptides.

Pos	15-mer peptide	Of	Core peptide	HLA alleles
48	AAKSAFYILPSIIS	6	FYILPSIIS	DRB1*04:05, DRB1*10:01, DRB1*16:02
49	AKKSAFYILPSIISN	5	FYILPSIIS	DRB1*01:01, DRB1*04:01, DRB1*04:03, DRB1*04:05, DRB1*04:06, DRB1*08:03, DRB1*10:01, DRB1*11:01, DRB1*12:02, DRB1*14:07, DRB1*15:02, DRB1*16:02,
50	KKSAFYILPSIISNE	4	FYILPSIIS	DRB1*01:01, DRB1*04:01, DRB1*04:02, DRB1*04:03, DRB1*04:05, DRB1*04:06, DRB1*07:01, DRB1*08:03, DRB1*09:01, DRB1*10:01, DRB1*11:01, DRB1*12:02, DRB1*14:07, DRB1*15:01, DRB1*15:02, DRB1*16:02,
51	KSAFYILPSIISNEK*	3	FYILPSIIS	DRB1*01:01, DRB1*04:01, DRB1*04:02, DRB1*04:03, DRB1*04:05, DRB1*04:06, DRB1*07:01, DRB1*08:03, DRB1*09:01, DRB1*10:01, DRB1*11:01, DRB1*12:02, DRB1*13:02, DRB1*14:04, DRB1*14:05, DRB1*14:07, DRB1*15:01, DRB1*15:02, DRB1*16:02
52	SAFYILPSIISNEKG	2	FYILPSIIS	DRB1*01:01, DRB1*04:01, DRB1*04:03, DRB1*04:05, DRB1*04:06, DRB1*08:03, DRB1*10:01, DRB1*11:01, DRB1*12:02, DRB1*14:07, DRB1*15:02, DRB1*16:02,
53	AFYILPSIISNEKGP	1	FYILPSIIS	DRB1*01:01, DRB1*10:01, DRB1*16:02
55	YLPSIISNEKGPGP	5	IISNEKGPG	DRB1*0301, DRB1*11:01, DRB1*13:02, DRB1*1401, DRB1*14:04, DRB1*1405, DRB1*14:07, DRB1*1454,
56	ILPSIISNEKGPGPG	4	IISNEKGPG	DRB1*0301, DRB1*11:01, DRB1*13:02, DRB1*1401, DRB1*14:04, DRB1*1405, DRB1*14:07, DRB1*1454,
57	LPSIISNEKGPGPGG	3	IISNEKGPG	DRB1*0301, DRB1*11:01, DRB1*13:02, DRB1*1401, DRB1*14:04, DRB1*1405, DRB1*14:07, DRB1*1454,
58	PSIISNEKGPGPGGR	2	IISNEKGPG	DRB1*0301, DRB1*11:01, DRB1*13:02, DRB1*1401, DRB1*14:04, DRB1*1405, DRB1*14:07, DRB1*1454,
68	GPGRLIIRENNRVV	5	LIIRENNRV	DRB1*04:02, DRB1*13:02, DRB1*14:04, DRB1*15:01, DRB1*15:02
69	PGGRLIIRENNRVVI	4	LIIRENNRV	DRB1*04:02, DRB1*08:03, DRB1*13:02, DRB1*1401, DRB1*14:04, DRB1*1405, DRB1*1454, DRB1*15:01, DRB1*15:02, DRB1*16:02,
70	GGRLIIRENNRVVIS	5	IRENNRVVI	DRB1*0301, DRB1*04:02, DRB1*08:03, DRB1*12:02, DRB1*13:02, DRB1*1401, DRB1*14:04, DRB1*1405, DRB1*14:07, DRB1*1454, DRB1*15:01, DRB1*15:02, DRB1*16:02
71	GRLIIRENNRVVISS*	4	IRENNRVVI	DRB1*0301, DRB1*04:02, DRB1*12:02, DRB1*13:02, DRB1*1401, DRB1*14:04, DRB1*1405, DRB1*14:07, DRB1*1454, DRB1*15:01, DRB1*15:02, DRB1*16:02,
72	RLIIRENNRVVISSD*	3	IRENNRVVI	DRB1*0301, DRB1*04:02, DRB1*13:02, DRB1*1401, DRB1*14:04, DRB1*1405, DRB1*14:07, DRB1*1454, DRB1*15:01, DRB1*15:02,
73	LIIRENNRVVISSDG	2	IRENNRVVI	DRB1*13:02, DRB1*1401, DRB1*1405, DRB1*14:07, DRB1*1454
74	IIRENNRVVISSDGP	1	IRENNRVVI	DRB1*13:02
76	RENNRVVISSDGP	5	VVISSDGP**	DRB1*04:01, DRB1*04:02, DRB1*04:03, DRB1*04:06,
77	ENNRVVISSDGP	4	VVISSDGP**	DRB1*04:01, DRB1*04:02, DRB1*04:03, DRB1*04:05, DRB1*04:06
78	NNRVVISSDGP	5	ISSDGP	DRB1*0301, DRB1*04:01, DRB1*04:02, DRB1*04:03, DRB1*04:05, DRB1*04:06,
79	NRVVISSDGP	4	ISSDGP	DRB1*0301, DRB1*04:01, DRB1*04:02, DRB1*04:03, DRB1*04:06
80	RVVISSDGP	3	ISSDGP	DRB1*0301, DRB1*04:01,
89	GPGAYESLRPDTRYV	4	YESLRPDTR	DRB1*01:01
90	PGAYESLRPDTRYVL	3	YESLRPDTR	DRB1*01:01, DRB1*0301, DRB1*1401, DRB1*1454,
91	GAYESLRPDTRYVLM	5	LRPDTRYVL	DRB1*0301, DRB1*13:02, DRB1*1401, DRB1*14:04, DRB1*1405, DRB1*14:07, DRB1*1454
92	AYESLRPDTRYVLM	4	LRPDTRYVL	DRB1*0301, DRB1*13:02, DRB1*1401, DRB1*14:04, DRB1*1405, DRB1*14:07, DRB1*1454
93	YESLRPDTRYVLM	3	LRPDTRYVL	DRB1*0301, DRB1*13:02, DRB1*1401, DRB1*14:04, DRB1*1405, DRB1*14:07, DRB1*1454
94	ESLRPDTRYVLM	2	LRPDTRYVL	DRB1*0301, DRB1*13:02, DRB1*1401, DRB1*14:04, DRB1*1405, DRB1*14:07, DRB1*1454
95	SLRPDTRYVLM	1	LRPDTRYVL	DRB1*0301
97	RPDTRYVLM	5	YVLM	DRB1*01:01, DRB1*10:01, DRB1*16:02
98	PDTRYVLM	4	YVLM	DRB1*01:01, DRB1*04:01, DRB1*10:01, DRB1*16:02,
99	DTRYVLM	3	YVLM	DRB1*01:01, DRB1*0301, DRB1*04:01, DRB1*10:01, DRB1*16:02
100	TRYVLM	2	YVLM	DRB1*01:01, DRB1*0301,
111	GVSTQEFYRMNSQGL	6	FRYMNSQGL	DRB1*01:01, DRB1*07:01, DRB1*08:03, DRB1*09:01, DRB1*10:01, DRB1*15:02, DRB1*16:02

112	VSTQEFYRMNSQGLL*	5	FRYMNSQGL	DRB1*01:01, DRB1*04:01, DRB1*04:05, DRB1*07:01, DRB1*08:03, DRB1*09:01, DRB1*10:01, DRB1*12:02, DRB1*13:02, DRB1*14:07, DRB1*15:01, DRB1*15:02, DRB1*16:02
113	STQEFYRMNSQGLLE	4	FRYMNSQGL	DRB1*01:01, DRB1*04:01, DRB1*04:02, DRB1*04:03, DRB1*04:05, DRB1*04:06, DRB1*07:01, DRB1*08:03, DRB1*09:01, DRB1*10:01, DRB1*11:01, DRB1*12:02, DRB1*13:02, DRB1*14:01, DRB1*14:04, DRB1*14:07, DRB1*14:54, DRB1*15:01, DRB1*15:02, DRB1*16:02
114	TQEFYRMNSQGLLEA	3	FRYMNSQGL	DRB1*01:01, DRB1*04:01, DRB1*04:02, DRB1*04:03, DRB1*04:05, DRB1*04:06, DRB1*07:01, DRB1*08:03, DRB1*09:01, DRB1*10:01, DRB1*11:01, DRB1*12:02, DRB1*13:02, DRB1*14:01, DRB1*14:04, DRB1*14:05, DRB1*14:07, DRB1*14:54, DRB1*15:01, DRB1*15:02, DRB1*16:02
115	QEFYRMNSQGLLEAA	2	FRYMNSQGL	DRB1*01:01, DRB1*04:01, DRB1*04:05, DRB1*07:01, DRB1*08:03, DRB1*09:01, DRB1*10:01, DRB1*12:02, DRB1*13:02, DRB1*14:07, DRB1*15:01, DRB1*15:02, DRB1*16:02
116	EFRYMNSQGLLEAAA	1	FRYMNSQGL	DRB1*01:01, DRB1*07:01, DRB1*09:01, DRB1*10:01, DRB1*15:02, DRB1*16:02
121	NSQGLLEAAAKWSMA	5	LEAAAKWSM	DRB1*14:01, DRB1*14:04, DRB1*14:05, DRB1*14:54,
122	SQGLLEAAAKWSMAT	4	LEAAAKWSM	DRB1*14:01, DRB1*14:04, DRB1*14:05, DRB1*14:54,
123	QGLLEAAAKWSMATY	3	LEAAAKWSM	DRB1*14:01, DRB1*14:04, DRB1*14:05, DRB1*14:54,
139	LFAAGYVFCTVNALA	5	YVFCTVNAL	DRB1*09:01
140	FAAGYVFCTVNALAA	4	YVFCTVNAL	DRB1*01:01, DRB1*07:01, DRB1*09:01, DRB1*10:01, DRB1*14:07
141	AAGYVFCTVNALAAG	3	YVFCTVNAL	DRB1*01:01, DRB1*04:01, DRB1*07:01, DRB1*09:01, DRB1*10:01, DRB1*14:07, DRB1*16:02
142	AGYVFCTVNALAAGL	2	YVFCTVNAL	DRB1*01:01, DRB1*09:01, DRB1*10:01
153	AAGLMIERFVSLAAG	5	IERFVSLAA	DRB1*04:02, DRB1*15:01, DRB1*15:02
154	AGLMIERFVSLAAGF	4	IERFVSLAA	DRB1*04:02, DRB1*15:01, DRB1*15:02
155	GLMIERFVSLAAGFE	3	IERFVSLAA	DRB1*04:02, DRB1*15:01, DRB1*15:02, DRB1*16:02,
156	LMIERFVSLAAGFEL	5	FVSLAAGFE**	DRB1*04:05, DRB1*15:01, DRB1*15:02
157	MIERFVSLAAGFELE	4	FVSLAAGFE**	DRB1*04:05, DRB1*09:01, DRB1*10:01
158	IERFVSLAAGFELED	3	FVSLAAGFE**	DRB1*01:01, DRB1*04:03, DRB1*04:05, DRB1*04:06, DRB1*07:01, DRB1*08:03, DRB1*09:01, DRB1*10:01, DRB1*16:02
159	ERFVSLAAGFELEDF	2	FVSLAAGFE**	DRB1*01:01, DRB1*04:05, DRB1*09:01, DRB1*10:01,
168	FELEDFIPMAAGMAS	5	FIPMAAGMA	DRB1*01:01, DRB1*10:01, DRB1*11:01, DRB1*16:02,
169	ELEDFIPMAAGMASL	4	FIPMAAGMA	DRB1*01:01, DRB1*04:01, DRB1*10:01, DRB1*11:01, DRB1*16:02
170	LEDFIPMAAGMASLV	3	FIPMAAGMA	DRB1*01:01, DRB1*04:01, DRB1*10:01, DRB1*11:01, DRB1*16:02
171	EDFIPMAAGMASLVL	2	FIPMAAGMA	DRB1*01:01, DRB1*10:01,
177	AAGMASLVLARKAAG	6	LVLARKAAG	DRB1*11:01, DRB1*14:05,
178	AGMASLVLARKAAGC	5	LVLARKAAG	DRB1*11:01, DRB1*14:05,
179	GMASLVLARKAAGCQ	4	LVLARKAAG	DRB1*11:01, DRB1*14:01, DRB1*14:05, DRB1*14:54,
180	MASLVLARKAAGCQY	3	LVLARKAAG	DRB1*11:01, DRB1*14:01, DRB1*14:05, DRB1*14:54,
181	ASLVLARKAAGCQYL	2	LVLARKAAG	DRB1*11:01, DRB1*14:05,
190	AGCQYLNTLTLAAGF	4	YLNTLTLAA	DRB1*04:01
191	GCQYLNTLTLAAGFS	3	YLNTLTLAA	DRB1*04:01

\*HTL epitopes originally put in the vaccine construct

\*\*HTL epitopes with core peptides sequence homologous to human peptides. Peptide FVSLAAGFE contain residue that match with heptamer VSLAAGF from human protein hCG2019424 (sequence ID EAX10398.1). Peptide VVISSDGP contain residues that match with heptamer VVISSDG from guanine nucleotide binding protein (G protein) (sequence ID EAW53700.1).

**Table S8.** Non homology analysis of VC peptides against gut microbiota proteomes using PBIT server. All 43 of 9-mer CTL epitopes (left panel) and 17 of 9-mer core peptides of HTL epitopes (right panel) that were generated from VC were input into the PBIT server, which will calculate the similarity of peptide sequences with the sequences from the gut microbiomes.

Non-homology analysis against gut microbiota proteomes			
Number of input sequence/s:43			
Criteria for non-homologous proteins: E-value > 0.005 or % sequence identity < 50			
<input type="checkbox"/>	Query name	No. of hits	BLAST report
<input type="checkbox"/>	1	Undefined	<a href="#">Download</a>
<input type="checkbox"/>	2	Undefined	<a href="#">Download</a>
<input type="checkbox"/>	3	Undefined	<a href="#">Download</a>
<input type="checkbox"/>	4	Undefined	<a href="#">Download</a>
<input type="checkbox"/>	5	Undefined	<a href="#">Download</a>
<input type="checkbox"/>	6	Undefined	<a href="#">Download</a>
<input type="checkbox"/>	7	Undefined	<a href="#">Download</a>
<input type="checkbox"/>	8	Undefined	<a href="#">Download</a>
<input type="checkbox"/>	9	Undefined	<a href="#">Download</a>
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<input type="checkbox"/>	11	Undefined	<a href="#">Download</a>
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<input type="checkbox"/>	19	Undefined	<a href="#">Download</a>
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<input type="checkbox"/>	37	Undefined	<a href="#">Download</a>
<input type="checkbox"/>	38	Undefined	<a href="#">Download</a>
<input type="checkbox"/>	39	Undefined	<a href="#">Download</a>
<input type="checkbox"/>	40	Undefined	<a href="#">Download</a>
<input type="checkbox"/>	41	Undefined	<a href="#">Download</a>
<input type="checkbox"/>	42	Undefined	<a href="#">Download</a>
<input type="checkbox"/>	43	Undefined	<a href="#">Download</a>

43 of the 43 input sequences are non-homologous (highlighted in blue) based on input BLAST parameters.

Non-homology analysis against gut microbiota proteomes			
Number of input sequence/s:17			
Criteria for non-homologous proteins: E-value > 0.005 or % sequence identity < 50			
<input type="checkbox"/>	Query name	No. of hits	BLAST report
<input type="checkbox"/>	1	Undefined	<a href="#">Download</a>
<input type="checkbox"/>	2	Undefined	<a href="#">Download</a>
<input type="checkbox"/>	3	Undefined	<a href="#">Download</a>
<input type="checkbox"/>	4	Undefined	<a href="#">Download</a>
<input type="checkbox"/>	5	Undefined	<a href="#">Download</a>
<input type="checkbox"/>	6	Undefined	<a href="#">Download</a>
<input type="checkbox"/>	7	Undefined	<a href="#">Download</a>
<input type="checkbox"/>	8	Undefined	<a href="#">Download</a>
<input type="checkbox"/>	9	Undefined	<a href="#">Download</a>
<input type="checkbox"/>	10	Undefined	<a href="#">Download</a>
<input type="checkbox"/>	11	Undefined	<a href="#">Download</a>
<input type="checkbox"/>	12	Undefined	<a href="#">Download</a>
<input type="checkbox"/>	13	Undefined	<a href="#">Download</a>
<input type="checkbox"/>	14	Undefined	<a href="#">Download</a>
<input type="checkbox"/>	15	Undefined	<a href="#">Download</a>
<input type="checkbox"/>	16	Undefined	<a href="#">Download</a>
<input type="checkbox"/>	17	Undefined	<a href="#">Download</a>

17 of the 17 input sequences are non-homologous (highlighted in blue) based on input BLAST parameters.

**Table S9.** Summary of the Top 10 models generated by HDOCK for interaction between TLR4 and VC.

Rank	1	2	3	4	5	6	7	8	9	10
Docking Score	-283.87	-247.70	-247.20	-246.91	-246.37	-242.17	-240.76	-239.35	-239.05	-238.82
Ligand rmsd (Å)	50.26	45.64	51.23	53.39	34.65	44.80	43.67	56.62	44.74	29.67
Interface residues	Model 1	Model 2	Model 3	Model 4	Model 5	Model 6	Model 7	Model 8	Model 9	Model 10

**Table S10.** Receptor-ligand interface residues pair for Model 1.

Receptor interface residue(s)	Ligand interface residue(s):	Receptor-ligand interface residue pair(s):
ASN 205A 2.788	GLY 1A 2.593	205A - 21A 2.788
HIS 229A 2.353	ILE 2A 4.741	229A - 20A 4.653
HIS 256A 3.052	ILE 3A 3.178	229A - 21A 2.353
GLU 286A 3.344	THR 5A 3.357	256A - 21A 4.576
GLU 287A 2.934	GLN 7A 2.599	256A - 38A 3.052
ASN 309A 3.135	LYS 8A 1.779	286A - 35A 4.823
VAL 310A 4.100	TYR 9A 2.827	286A - 36A 3.344
SER 311A 3.307	TYR 10A 3.110	287A - 35A 3.486
GLN 333A 2.498	ARG 17A 3.329	287A - 38A 2.934
HIS 334A 3.489	VAL 20A 4.653	309A - 36A 3.135
LYS 354A 4.414	LEU 21A 2.353	310A - 36A 4.100
ARG 355A 2.827	SER 34A 2.498	311A - 34A 4.045
GLU 376A 1.779	THR 35A 3.486	311A - 35A 4.339
PHE 377A 2.840	ARG 36A 3.135	311A - 36A 3.307
LYS 402A 3.318	ARG 38A 2.934	333A - 34A 2.498
TYR 403A 3.591		333A - 35A 4.826
GLU 425A 2.599		333A - 36A 3.871
HIS 426A 3.445		334A - 34A 3.489
ILE 450A 4.142		354A - 9A 4.414
TYR 451A 2.593		355A - 9A 2.827
VAL 475A 4.057		355A - 10A 3.584
LYS 477A 3.743		355A - 17A 3.329
PHE 500A 4.404		355A - 34A 4.369
		376A - 8A 1.779
		376A - 9A 2.931
		377A - 9A 2.840
		377A - 10A 3.110
		377A - 17A 4.836
		402A - 7A 3.318
		402A - 8A 4.316
		402A - 9A 3.657
		403A - 9A 3.908
		403A - 10A 3.591
		425A - 5A 3.357
		425A - 7A 2.599
		426A - 3A 3.445
		426A - 5A 4.930
		450A - 3A 4.142
		450A - 5A 4.837
		451A - 1A 2.593
		451A - 2A 4.741
		451A - 3A 3.178
		475A - 1A 4.554
		475A - 3A 4.057
		477A - 1A 3.743
		477A - 2A 4.797
		500A - 1A 4.404