

Table S1. Epitope Candidates to SARS-CoV

Epitope	Length	Position	Epitope score	Surface Accessibility
VOAPNYTQHTSS	12	25-36	0.582	2.177
ATEKSN	6	91-96	0.501	1.723
PMGTQT	6	143-148	0.574	1.670
VSEKSGN	7	172-178	0.543	1.736
PAQDTW	6	240-245	0.547	1.610
AWERKK	6	339-344	0.546	2.855
DYNYKLP	7	407-413	0.519	2.542
TSTGNYNKYRYLR	14	431-444	0.529	3.149
GKLRPFERD	9	446-454	0.572	1.998
PSSKRFQPF	9	540-548	0.537	2.396
HVDTSY	6	641-646	0.537	1.369
EQDRNTR	7	755-761	0.504	4.431
QVKQMYKTPTL	11	766-776	0.551	2.246
DPLKPTKRFS	10	790-799	0.528	2.636
TQRNFF	6	1087-1092	0.520	1.336
DPLOPELDSFKEELDKYFKNHTSP	24	1121-1144	0.558	2.244
FDEDDS	6	1238-1243	0.569	3.157

Table S2. Epitope Candidates to SARS-CoV-2

Epitope	Length	Position	Epitope score	Surface Accessibility
LTTTRTQLPPAYTNSF	15	18-32	0.613	1.766
TNGTKRFD	8	73-80	0.541	2.352
YYHKNNKSWM	10	144-153	0.585	2.934
LEGKQGN	7	179-185	0.558	1.825
TPGDSS	6	250-255	0.589	1.290
QTSNFRVQPT	10	314-323	0.547	1.664
AWNRRK	6	352-357	0.586	2.592
ADYNYKLPDD	10	419-428	0.510	2.153
NSNNLD	6	437-442	0.510	1.682
LFRKSNLKPFERDI	14	455-468	0.550	2.078
YGFQPT	6	495-500	0.519	1.328
GTNTSN	6	601-606	0.523	1.925
DQLTPTWRVY	10	627-636	0.518	1.353
HVNNSY	6	655-660	0.561	1.448
YQTQTNSPRRAR	12	674-685	0.661	3.343
EQDKNTQ	7	773-779	0.512	3.868
KQIYKTPPI	9	786-794	0.560	1.960
DPSKPSKRSF	10	808-817	0.544	3.233
TQRNFYE	7	1105-1111	0.521	2.216
DPLQPELDSFKEELDKYFKNHTSP	24	1139-1162	0.559	2.198
FDEDDS	6	1256-1261	0.574	3.093

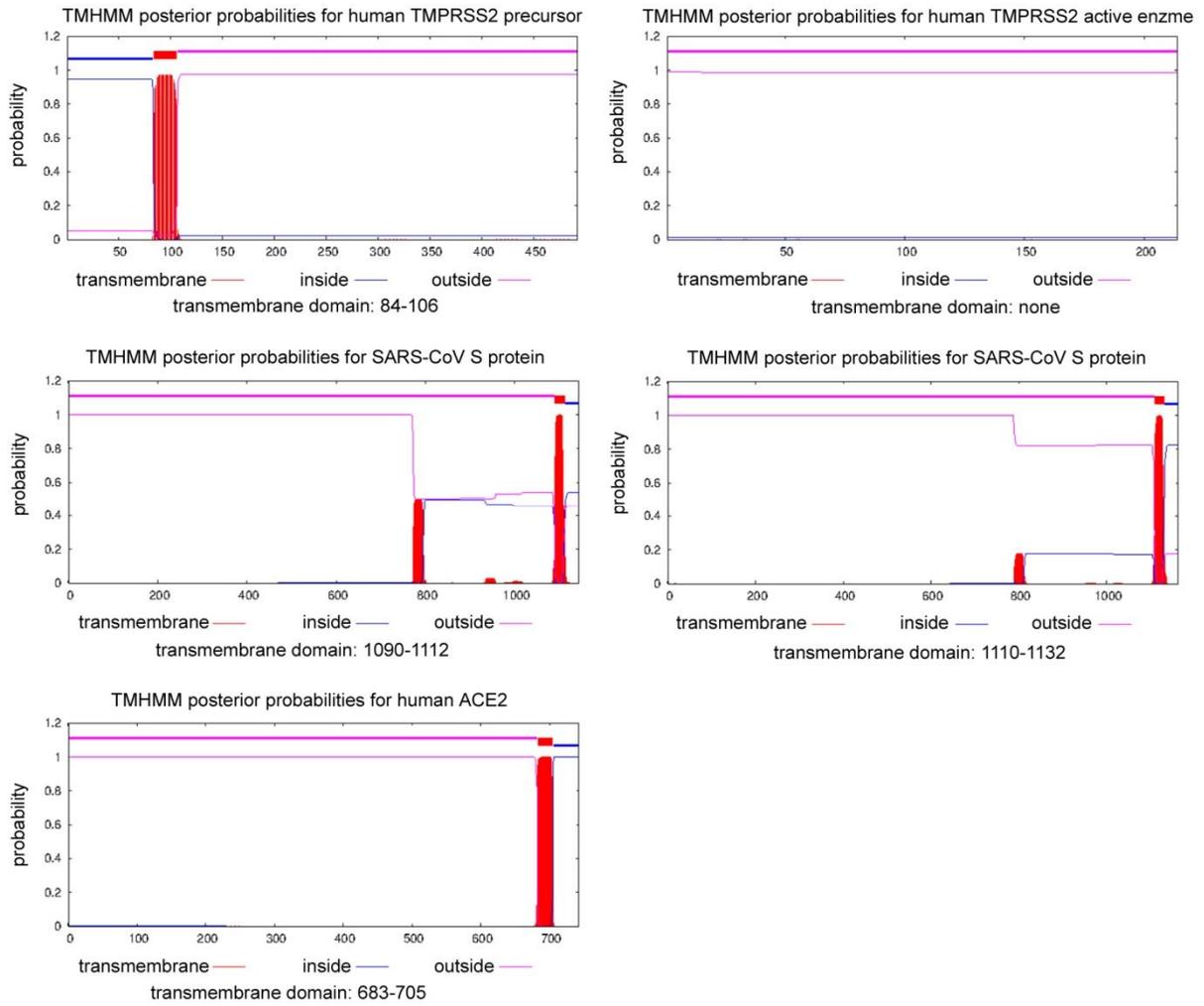


Figure S1. Transmembrane Domain Prediction

Full-length sequences of human TMPRSS2 precursor, TMPRSS2 active enzyme, ACE2, SARS-CoV S protein and SARS-CoV-2 S protein were subject to transmembrane domain prediction by using TMHMM Server v. 2.0 bioinformatic tool.

Epitope with SA 1.0-2.0  
   Epitope with SA 2.0-3.0  
   Glycosylation sequons  
   Receptor binding motif  
  Epitope with SA 3.0-3.8  
  Epitope with SA >3.8  
  Heparin-binding site  
  S1/S2 cleavage site

		Section 1																																																														
		(1)	1	10	20	30	40	50	62																																																							
SARS-CoV	(1)	M	F	I	F	L	L	F	L	T	L	S	G	S	D	L	R	C	T	F	D	V	Q	A	P	N	Y	T	Q	H	T	S	S	M	R	G	V	Y	P	D	E	I	F	R	S	D	T	L	Y	L	T	Q	D	L	F	L	P	F						
SARS	SNU01	(1)	M	F	V	F	L	V	L	L	P	L	V	S	---	S	Q	C	V	N	L	T	T	R	T	Q	L	P	P	A	Y	T	N	S	F	T	R	G	V	Y	P	D	K	V	F	R	S	S	V	L	H	S	T	Q	D	L	F	L	P	F				
-CoV-2	WA1	(1)	M	F	V	F	L	V	L	L	P	L	V	S	---	S	Q	C	V	N	L	T	T	R	T	Q	L	P	P	A	Y	T	N	S	F	T	R	G	V	Y	P	D	K	V	F	R	S	S	V	L	H	S	T	Q	D	L	F	L	P	F				
	WHU01	(1)	M	F	V	F	L	V	L	L	P	L	V	S	---	S	Q	C	V	N	L	T	T	R	T	Q	L	P	P	A	Y	T	N	S	F	T	R	G	V	Y	P	D	K	V	F	R	S	S	V	L	H	S	T	Q	D	L	F	L	P	F				
	Consensus	(1)	M	F	V	F	L	V	L	L	P	L	V	S	---	S	Q	C	V	N	L	T	T	R	T	Q	L	P	P	A	Y	T	N	S	F	T	R	G	V	Y	P	D	K	V	F	R	S	S	V	L	H	S	T	Q	D	L	F	L	P	F				
		Section 2																																																														
		(63)	63	70	80	90	100	110	124																																																							
SARS-CoV	(63)	Y	S	N	V	T	W	F	H	A	I	H	V	S	G	T	N	G	T	K	R	F	D	N	P	V	L	P	F	N	D	G	V	F	A	S	T	E	K	S	N	I	R	G	W	I	F	G	T	T	L	D	S	K	T	Q	S	L	L	I	V			
SARS	SNU01	(59)	F	S	N	V	T	W	F	H	A	I	H	V	S	G	T	N	G	T	K	R	F	D	N	P	V	L	P	F	N	D	G	V	F	A	S	T	E	K	S	N	I	R	G	W	I	F	G	T	T	L	D	S	K	T	Q	S	L	L	I	V		
-CoV-2	WA1	(59)	F	S	N	V	T	W	F	H	A	I	H	V	S	G	T	N	G	T	K	R	F	D	N	P	V	L	P	F	N	D	G	V	F	A	S	T	E	K	S	N	I	R	G	W	I	F	G	T	T	L	D	S	K	T	Q	S	L	L	I	V		
	WHU01	(59)	F	S	N	V	T	W	F	H	A	I	H	V	S	G	T	N	G	T	K	R	F	D	N	P	V	L	P	F	N	D	G	V	F	A	S	T	E	K	S	N	I	R	G	W	I	F	G	T	T	L	D	S	K	T	Q	S	L	L	I	V		
	Consensus	(63)	F	S	N	V	T	W	F	H	A	I	H	V	S	G	T	N	G	T	K	R	F	D	N	P	V	L	P	F	N	D	G	V	F	A	S	T	E	K	S	N	I	R	G	W	I	F	G	T	T	L	D	S	K	T	Q	S	L	L	I	V		
		Section 3																																																														
		(125)	125	130	140	150	160	170	186																																																							
SARS-CoV	(118)	N	N	A	T	N	V	V	I	R	A	C	N	F	E	L	C	D	N	P	F	F	A	V	S	K	P	M	G	---	T	Q	T	H	T	M	I	F	D	N	A	F	N	C	T	F	E	Y	I	S	D	A	F	S	L	E	V	S	E	K				
SARS	SNU01	(121)	N	N	A	T	N	V	V	I	K	V	C	F	Q	F	C	N	D	P	F	L	G	V	Y	H	K	N	K	S	W	M	E	S	E	F	R	V	Y	S	S	A	N	N	C	T	F	E	Y	V	S	Q	P	F	L	M	D	L	E	G	K			
-CoV-2	WA1	(121)	N	N	A	T	N	V	V	I	K	V	C	F	Q	F	C	N	D	P	F	L	G	V	Y	H	K	N	K	S	W	M	E	S	E	F	R	V	Y	S	S	A	N	N	C	T	F	E	Y	V	S	Q	P	F	L	M	D	L	E	G	K			
	WHU01	(121)	N	N	A	T	N	V	V	I	K	V	C	F	Q	F	C	N	D	P	F	L	G	V	Y	H	K	N	K	S	W	M	E	S	E	F	R	V	Y	S	S	A	N	N	C	T	F	E	Y	V	S	Q	P	F	L	M	D	L	E	G	K			
	Consensus	(125)	N	N	A	T	N	V	V	I	K	V	C	F	Q	F	C	N	D	P	F	L	G	V	Y	H	K	N	K	S	W	M	E	S	E	F	R	V	Y	S	S	A	N	N	C	T	F	E	Y	V	S	Q	P	F	L	M	D	L	E	G	K			
		Section 4																																																														
		(187)	187	200	210	220	230	248																																																								
SARS-CoV	(176)	S	G	N	F	K	H	L	R	E	F	V	F	K	N	K	D	G	F	L	V	Y	V	K	G	Y	Q	P	I	D	V	V	R	D	L	P	S	G	F	N	T	L	K	P	I	F	K	L	P	L	G	I	N	I	T	N	F	R	A	I	L	T	A	
SARS	SNU01	(183)	Q	G	N	F	K	N	L	R	E	F	V	F	K	N	I	D	G	Y	F	K	I	Y	S	K	H	T	P	I	N	L	V	R	D	L	P	Q	G	F	W	A	L	E	P	L	V	D	L	P	I	G	I	N	I	T	R	F	Q	T	L	L	A	L
-CoV-2	WA1	(183)	Q	G	N	F	K	N	L	R	E	F	V	F	K	N	I	D	G	Y	F	K	I	Y	S	K	H	T	P	I	N	L	V	R	D	L	P	Q	G	F	S	A	L	E	P	L	V	D	L	P	I	G	I	N	I	T	R	F	Q	T	L	L	A	L
	WHU01	(183)	Q	G	N	F	K	N	L	R	E	F	V	F	K	N	I	D	G	Y	F	K	I	Y	S	K	H	T	P	I	N	L	V	R	D	L	P	Q	G	F	S	A	L	E	P	L	V	D	L	P	I	G	I	N	I	T	R	F	Q	T	L	L	A	L
	Consensus	(187)	Q	G	N	F	K	N	L	R	E	F	V	F	K	N	I	D	G	Y	F	K	I	Y	S	K	H	T	P	I	N	L	V	R	D	L	P	Q	G	F	S	A	L	E	P	L	V	D	L	P	I	G	I	N	I	T	R	F	Q	T	L	L	A	L
		Section 5																																																														
		(249)	249	260	270	280	290	310																																																								
SARS-CoV	(238)	F	S	---	P	---	A	Q	D	T	W	G	T	S	A	A	A	F	V	G	Y	L	K	P	T	F	M	L	K	Y	D	E	N	G	T	I	T	D	A	V	D	C	S	Q	N	P	L	A	E	L	K	C	S	V	K	S	F							
SARS	SNU01	(245)	H	R	S	Y	L	T	P	G	D	S	S	G	W	T	A	G	A	A	Y	V	G	Y	L	Q	P	R	T	F	L	L	K	Y	N	E	N	G	T	I	T	D	A	V	D	C	A	L	D	P	L	S	E	T	K	C	T	L	K	S	F			
-CoV-2	WA1	(245)	H	R	S	Y	L	T	P	G	D	S	S	G	W	T	A	G	A	A	Y	V	G	Y	L	Q	P	R	T	F	L	L	K	Y	N	E	N	G	T	I	T	D	A	V	D	C	A	L	D	P	L	S	E	T	K	C	T	L	K	S	F			
	WHU01	(245)	H	R	S	Y	L	T	P	G	D	S	S	G	W	T	A	G	A	A	Y	V	G	Y	L	Q	P	R	T	F	L	L	K	Y	N	E	N	G	T	I	T	D	A	V	D	C	A	L	D	P	L	S	E	T	K	C	T	L	K	S	F			
	Consensus	(249)	H	R	S	Y	L	T	P	G	D	S	S	G	W	T	A	G	A	A	Y	V	G	Y	L	Q	P	R	T	F	L	L	K	Y	N	E	N	G	T	I	T	D	A	V	D	C	A	L	D	P	L	S	E	T	K	C	T	L	K	S	F			
		Section 6																																																														
		(311)	311	320	330	340	350	360	372																																																							
SARS-CoV	(294)	E	I	D	K	G	I	Y	Q	T	S	N	F	R	V	P	S	G	D	V	V	R	F	F	N	I	T	N	L	C	P	F	G	E	V	F	N	A	T	R	F	A	S	V	Y	A	W	N	R	K	R	I	S	N	C	V	A	D	Y	S	V	L		
SARS	SNU01	(307)	T	V	E	K	G	I	Y	Q	T	S	N	F	R	V	Q	P	T	E	S	I	V	R	F	F	N	I	T	N	L	C	P	F	G	E	V	F	N	A	T	R	F	A	S	V	Y	A	W	N	R	K	R	I	S	N	C	V	A	D	Y	S	V	L
-CoV-2	WA1	(307)	T	V	E	K	G	I	Y	Q	T	S	N	F	R	V	Q	P	T	E	S	I	V	R	F	F	N	I	T	N	L	C	P	F	G	E	V	F	N	A	T	R	F	A	S	V	Y	A	W	N	R	K	R	I	S	N	C	V	A	D	Y	S	V	L
	WHU01	(307)	T	V	E	K	G	I	Y	Q	T	S	N	F	R	V	Q	P	T	E	S	I	V	R	F	F	N	I	T	N	L	C	P	F	G	E	V	F	N	A	T	R	F	A	S	V	Y	A	W	N	R	K	R	I	S	N	C	V	A	D	Y	S	V	L
	Consensus	(311)	T	V	E	K	G	I	Y	Q	T	S	N	F	R	V	Q	P	T	E	S	I	V	R	F	F	N	I	T	N	L	C	P	F	G	E	V	F	N	A	T	R	F	A	S	V	Y	A	W	N	R	K	R	I	S	N	C	V	A	D	Y	S	V	L
		Section 7																																																														
		(373)	373	380	390	400	410	420	434																																																							
SARS-CoV	(356)	Y	N	S	T	F	F	S	T	F	F	K	C	Y	G	V	S	A	T	K	L	N	D	L	C	F	S	N	V	Y	A	D	S	F	V	I	R	G	D	E	V	R	Q	I	A	P	Q	T	G	V	I	A	D	Y	N	K	L	E	D	D	F	M		
SARS	SNU01	(369)	Y	N	S	A	S	F	S	T	F	F	K	C	Y	G	V	S	P	T	K	L	N	D	L	C	F	T	N	V	Y	A	D	S	F	V	I	R	G	D	E	V	R	Q	I	A	P	Q	T	G	K	I	A	D	Y	N	K	L	P	D	D	F	T	
-CoV-2	WA1	(369)	Y	N	S	A	S	F	S	T	F	F	K	C	Y	G	V	S	P	T	K	L	N	D	L	C	F	T	N	V	Y	A	D	S	F	V	I	R	G	D	E	V	R	Q	I	A	P	Q	T	G	K	I	A	D	Y	N	K	L	P	D	D	F	T	
	WHU01	(369)	Y	N	S	A	S	F	S	T	F	F	K	C	Y	G	V	S	P	T	K	L	N																																									

		Section 11																			
		(621)	621	630	640	650	660	670	682												
SARS-CoV	(603)		CTD	VSTAIHADQLTPAWRI	YSTGNNVFQ	TQAGCLIGAE	HVDTSE	YECDIP	IGAGICASYHTVS												
SARS	SNU01	(617)	CTE	VPVAIHADQLTPTTRVRY	YSTGNSVVFQ	TRAGCLIGAE	HVNNSY	ECEDIP	IGAGICASYQTQT												
-CoV-2	WA1	(617)	CTE	VPVAIHADQLTPTTRVRY	YSTGNSVVFQ	TRAGCLIGAE	HVNNSY	ECEDIP	IGAGICASYQTQT												
-CoV-2	WHU01	(617)	CTE	VPVAIHADQLTPTTRVRY	YSTGNSVVFQ	TRAGCLIGAE	HVNNSY	ECEDIP	IGAGICASYQTQT												
	Consensus	(621)	CTE	VPVAIHADQLTPTTRVRY	YSTGNSVVFQ	TRAGCLIGAE	HVNNSY	ECEDIP	IGAGICASYQTQT												
		Section 12																			
		(683)	683	690	700	710	720	730	744												
SARS-CoV	(665)		---	LLRSTSQKSI	VAYTMSLGADSS	IAYSNN	TAIPTN	FSISITTE	VMPVSMAKT	SVDCNMM											
SARS	SNU01	(679)	NSP	RRAARSVASQ	SI IAYTMSLGA	ENSVAYS	NNSIAI	PTNFTI	SVTTEIL	PVSMKT	KTSDVCTM										
SARS	WA1	(679)	NSP	RRAARSVASQ	SI IAYTMSLGA	ENSVAYS	NNSIAI	PTNFTI	SVTTEIL	PVSMKT	KTSDVCTM										
-CoV-2	WHU01	(679)	NSP	RRAARSVASQ	SI IAYTMSLGA	ENSVAYS	NNSIAI	PTNFTI	SVTTEIL	PVSMKT	KTSDVCTM										
	Consensus	(683)	NSP	RRAARSVASQ	SI IAYTMSLGA	ENSVAYS	NNSIAI	PTNFTI	SVTTEIL	PVSMKT	KTSDVCTM										
		Section 13																			
		(745)	745	750	760	770	780	790	806												
SARS-CoV	(723)		YICGD	STECANLLLQYGS	FCTQLNRALS	GIAAEQ	DRNTR	EVFAQ	VKQMYK	TPTLLKY	FGGFNF										
SARS	SNU01	(741)	YICGD	STECANLLLQYGS	FCTQLNRAL	TGIAVE	QDKNTQ	EVFAQ	VKQIYK	TPPIK	DFGGFNF										
SARS	WA1	(741)	YICGD	STECANLLLQYGS	FCTQLNRAL	TGIAVE	QDKNTQ	EVFAQ	VKQIYK	TPPIK	DFGGFNF										
-CoV-2	WHU01	(741)	YICGD	STECANLLLQYGS	FCTQLNRAL	TGIAVE	QDKNTQ	EVFAQ	VKQIYK	TPPIK	DFGGFNF										
	Consensus	(745)	YICGD	STECANLLLQYGS	FCTQLNRAL	TGIAVE	QDKNTQ	EVFAQ	VKQIYK	TPPIK	DFGGFNF										
		Section 14																			
		(807)	807	820	830	840	850	868													
SARS-CoV	(785)		SQILP	DPLKPTKRSF	I	EDLLFN	KVTLADAG	FMKQYGE	CLGDI	NARDL	ICAQKFN	GLTVL	PLPPL								
SARS	SNU01	(803)	SQILP	DPSKPSKRSF	I	EDLLFN	KVTLADAG	FIKQYGD	CLGDI	AARDL	ICAQKFN	GLTVL	PLPPL								
SARS	WA1	(803)	SQILP	DPSKPSKRSF	I	EDLLFN	KVTLADAG	FIKQYGD	CLGDI	AARDL	ICAQKFN	GLTVL	PLPPL								
-CoV-2	WHU01	(803)	SQILP	DPSKPSKRSF	I	EDLLFN	KVTLADAG	FIKQYGD	CLGDI	AARDL	ICAQKFN	GLTVL	PLPPL								
	Consensus	(807)	SQILP	DPSKPSKRSF	I	EDLLFN	KVTLADAG	FIKQYGD	CLGDI	AARDL	ICAQKFN	GLTVL	PLPPL								
		Section 15																			
		(869)	869	880	890	900	910	920	930												
SARS-CoV	(847)		LTDEM	IAAYTAA	LVSGTATAG	WTFGAGAA	LQIPF	FAMQMAYR	FRNGIG	VTQNVLY	ENQKLI	ANQ									
SARS	SNU01	(865)	LTDEM	IAQYTS	ALLAGT	ITSGWT	FGAGAA	LQIPF	FAMQMAYR	FRNGIG	VTQNVLY	ENQKLI	ANQ								
SARS	WA1	(865)	LTDEM	IAQYTS	ALLAGT	ITSGWT	FGAGAA	LQIPF	FAMQMAYR	FRNGIG	VTQNVLY	ENQKLI	ANQ								
-CoV-2	WHU01	(865)	LTDEM	IAQYTS	ALLAGT	ITSGWT	FGAGAA	LQIPF	FAMQMAYR	FRNGIG	VTQNVLY	ENQKLI	ANQ								
	Consensus	(869)	LTDEM	IAQYTS	ALLAGT	ITSGWT	FGAGAA	LQIPF	FAMQMAYR	FRNGIG	VTQNVLY	ENQKLI	ANQ								
		Section 16																			
		(931)	931	940	950	960	970	980	992												
SARS-CoV	(909)		FNKAI	SQIQESL	TTTSTAL	GKQLQDV	VNQNQA	LNTLVK	QLSSNF	GAISSV	LVNDIL	LSRLDK	VE								
SARS	SNU01	(927)	FNSAI	GKIQDSL	SSTASAL	GKQLQDV	VNQNQA	LNTLVK	QLSSNF	GAISSV	LVNDIL	LSRLDK	VE								
SARS	WA1	(927)	FNSAI	GKIQDSL	SSTASAL	GKQLQDV	VNQNQA	LNTLVK	QLSSNF	GAISSV	LVNDIL	LSRLDK	VE								
-CoV-2	WHU01	(927)	FNSAI	GKIQDSL	SSTASAL	GKQLQDV	VNQNQA	LNTLVK	QLSSNF	GAISSV	LVNDIL	LSRLDK	VE								
	Consensus	(931)	FNSAI	GKIQDSL	SSTASAL	GKQLQDV	VNQNQA	LNTLVK	QLSSNF	GAISSV	LVNDIL	LSRLDK	VE								
		Section 17																			
		(993)	993	1000	1010	1020	1030	1040	1054												
SARS-CoV	(971)		AEVQI	DRLLIT	GRQLQSL	QTYV	TQQLIR	AAEIRAS	ANLAAT	KMSECV	LVGQSK	RVDFC	GGYHLM								
SARS	SNU01	(989)	AEVQI	DRLLIT	GRQLQSL	QTYV	TQQLIR	AAEIRAS	ANLAAT	KMSECV	LVGQSK	RVDFC	GGYHLM								
SARS	WA1	(989)	AEVQI	DRLLIT	GRQLQSL	QTYV	TQQLIR	AAEIRAS	ANLAAT	KMSECV	LVGQSK	RVDFC	GGYHLM								
-CoV-2	WHU01	(989)	AEVQI	DRLLIT	GRQLQSL	QTYV	TQQLIR	AAEIRAS	ANLAAT	KMSECV	LVGQSK	RVDFC	GGYHLM								
	Consensus	(993)	AEVQI	DRLLIT	GRQLQSL	QTYV	TQQLIR	AAEIRAS	ANLAAT	KMSECV	LVGQSK	RVDFC	GGYHLM								
		Section 18																			
		(1055)	1055	1060	1070	1080	1090	1100	1116												
SARS-CoV	(1033)		SFPQA	APHGVV	FLHVTY	VP	QER	NFTT	TAPAI	CHGKAY	FPREGV	VVFN	NGT	SWFI	TQRNF	YEP					
SARS	SNU01	(1051)	SFPQS	APHGVV	FLHVTY	VP	QER	NFTT	TAPAI	CHDGKA	HPREGV	VVFN	NGT	HWFV	TQRNF	YEP					
SARS	WA1	(1051)	SFPQS	APHGVV	FLHVTY	VP	QER	NFTT	TAPAI	CHDGKA	HPREGV	VVFN	NGT	HWFV	TQRNF	YEP					
-CoV-2	WHU01	(1051)	SFPQS	APHGVV	FLHVTY	VP	QER	NFTT	TAPAI	CHDGKA	HPREGV	VVFN	NGT	HWFV	TQRNF	YEP					
	Consensus	(1055)	SFPQS	APHGVV	FLHVTY	VP	QER	NFTT	TAPAI	CHDGKA	HPREGV	VVFN	NGT	HWFV	TQRNF	YEP					
		Section 19																			
		(1117)	1117	1130	1140	1150	1160	1178													
SARS-CoV	(1095)		QIITD	NTFV	SGNCDV	VIGI	VNNT	VYD	PLQPE	LDSF	KEELDK	YFKN	NHTSP	DVDL	GD	ISG	INA				
SARS	SNU01	(1113)	QIITD	NTFV	SGNCDV	VIGI	VNNT	VYD	PLQPE	LDSF	KEELDK	YFKN	NHTSP	DVDL	GD	ISG	INA				
SARS	WA1	(1113)	QIITD	NTFV	SGNCDV	VIGI	VNNT	VYD	PLQPE	LDSF	KEELDK	YFKN	NHTSP	DVDL	GD	ISG	INA				
-CoV-2	WHU01	(1113)	QIITD	NTFV	SGNCDV	VIGI	VNNT	VYD	PLQPE	LDSF	KEELDK	YFKN	NHTSP	DVDL	GD	ISG	INA				
	Consensus	(1117)	QIITD	NTFV	SGNCDV	VIGI	VNNT	VYD	PLQPE	LDSF	KEELDK	YFKN	NHTSP	DVDL	GD	ISG	INA				
		Section 20																			
		(1179)	1179	1190	1200	1210	1220	1230	1240												
SARS-CoV	(1157)		SVVNI	QKEID	RLNE	VAKN	LNES	LIDL	QELG	KYEQ	YIKWP	PWYI	WLG	FIA	GLIA	I	VM	VTI	MLCC		
SARS	SNU01	(1175)	SVVNI	QKEID	RLNE	VAKN	LNES	LIDL	QELG	KYEQ	YIKWP	PWYI	WLG	FIA	GLIA	I	VM	VTI	MLCC		
SARS	WA1	(1175)	SVVNI	QKEID	RLNE	VAKN	LNES	LIDL	QELG	KYEQ	YIKWP	PWYI	WLG	FIA	GLIA	I	VM	VTI	MLCC		
-CoV-2	WHU01	(1175)	SVVNI	QKEID	RLNE	VAKN	LNES	LIDL	QELG	KYEQ	YIKWP	PWYI	WLG	FIA	GLIA	I	VM	VTI	MLCC		
	Consensus	(1179)	SVVNI	QKEID	RLNE	VAKN	LNES	LIDL	QELG	KYEQ	YIKWP	PWYI	WLG	FIA	GLIA	I	VM	VTI	MLCC		
		Section 21																			
		(1241)	1241	1250	1260	1277															
SARS-CoV	(1219)		MTSCC	SCLK	GAC	SCG	SCK	F	DEDD	S	EP	V	L	K	G	V	K	L	H	Y	T
SARS	SNU01	(1237)	MTSCC	SCLK	GAC	SCG	SCK	F	DEDD	S	EP	V	L	K	G	V	K	L	H	Y	T
SARS	WA1	(1237)	MTSCC	SCLK	GAC	SCG	SCK	F	DEDD	S	EP	V	L	K	G	V	K	L	H	Y	T
-CoV-2	WHU01	(1237)	MTSCC	SCLK	GAC	SCG	SCK	F	DEDD	S	EP	V	L	K	G	V	K	L	H	Y	T
	Consensus	(1241)	MTSCC	SCLK	GAC	SCG	SCK	F	DEDD	S	EP	V	L	K	G	V	K	L	H	Y	T

**Figure S2. Alignment of SARS-CoV And SARS-CoV-2 Spike Proteins**

SARS-CoV and SARS-CoV-2 (types A, B and C) amino acid sequences were aligned using the software ClustalX2.1. Putative epitopes with different surface accessibilities (SA), glycosylation sequons, the receptor binding motif (RBM), heparin-binding site and the S1/S2 cleavage site are marked with different colors of boxes.