

Supplemental Materials

Figure S1. The UF RBD and MassBiologic (MB) RBD sequences. The information on the additional tags is shown with the complete RBD sequence (A). The MB-RBD is longer by 12 aa on the carboxyl-end. This 12 aa sequence is highly conserved among many human and animal coronaviruses, including FCoV and CCoV. The SCoV2 RBD has two strongly predicted O-glycosylation sites (bolded blue threonine **T** or serine **S**) and two N-glycosylation sites with low prediction (bold red asparagine **N**) on the amino-end on both UF and MB RBDs. MB-RBD has an additional O-glycosylation site on the first two aa residues (**S** and **T**) of the 12 aa addition on the carboxyl-end. The glycosylation prediction was based on a NetNGlyc 1.0 Server (<https://services.healthtech.dtu.dk/service.php?NetNGlyc-1.0>) for an N-glycosylation and NetOGlyc 4.1 Server (<https://services.healthtech.dtu.dk/service.php?NetMHCpan-4.1>) for O-glycosylation. Next, the sera from the same time-points as Figure 1E for the three toms were tested for anti-BSA antibodies before the assay for Figures 1D/1E (B). Serum from SPF HOE serves as the negative control and serum from SPF cat DU1, which was vaccinated with FIV vaccine with residual BSA, serves as the anti-BSA Ab positive control.

Figure S2. The comparison of the aa residue numbers and aa sequence identity/similarity of the SCoV2 Wuhan (NC045512.1), FCoV1 UCD-1, and FCoV2 79-1146 (DQ010921.1) structural proteins. The aa residue numbers are provided to estimate the MW of these proteins without glycosylation and to determine the aa sequence identity and similarity between the viruses (A). FCoV1 UCD-1 S (AB088222.1), NC (BAC1157.1) and M (BAC1156.1) were available but its Env sequence was unavailable and, therefore, FCoV1 Dutch Cat1 Env (KX722530.1) was used in its place. The total aa identity or similarity value divided by the total aa residues including gaps x100 provides the percentage. The two values for S1 and S2 are provided, based on where the SCoV2 S is processed into S1 and S2 at the S1/S2 cleavage site and where the FCoV1 S and FCoV2 S are processed into S1 and S2 [47,48]. Under the % aa identity and % aa similarity for S1 and S2 proteins, the first value is for SCoV2, followed by the value for FCoV1 in row-1 and FCoV2 in row-2. The first value is for FCoV1, followed by the value for FCoV2 in row-3. The MW without glycan (B) is determined by using Peptide Analyzing Tool (<https://www.thermofisher.com/us/en/home/life-science/protein-biology/peptides-proteins/custom-peptide-synthesis-services/peptide-analyzing-tool.html>). The predicted N- and O-glycosylation numbers are determined by NetNGlyc 1.0 server and NetOGlyc 4.1 Server, respectively (B), and their network addresses are first described in Figure S1 legend.

Figure S3. Sequence alignment of SCoV2 Wuhan and FCoV2 79-1146 spike glycoproteins. Clustal Omega 1.2.1 of JustBio Server (<https://justbio.com/>) was used for all sequence alignment analyses (A). Signal peptides for all sequences were determined by SignalP – 6.0 server of DTU Health Tech (<https://services.healthtech.dtu.dk/service.php?SignalP>). The abbreviations used include: amino-terminal domain (NTD), receptor binding domain (RBD), receptor binding motif (RBM), carboxyl-terminal domain (CTD), spike glycoprotein-1 (S1), and spike glycoprotein-2 (S2). RBM (underlined bold) has the aa residues that contact the cell receptor (e.g., species-specific ACE2 and APN). S1/S2 cleavage sites are found with cleavage motif (bold red) at the usual site for SCoV2, but the cleavage motif at the usual site is not found for FCoV2 [47,48]. The S1/S2 cleavage site for FCoV2 and CCoV2 is reported to be amino-end adjacent to the fusion peptide, which is the S2' cleavage site for other strains. The FCoV2 79-1146 sequence is shown in magenta. Identical and similar aa residues are shown with an asterisk (*) for complete identity, strong similarity with a colon (:), and modest similarity with a single dot (.). The gaps are shown with a dash (-). The summary table (B) shows the total number of aa with gaps, number of aa with identity, number of aa with similarity, % aa identity, and % aa similarity. Two values for CTD, S1, and S2 are shown in the summary table (B), due to the major difference in the location of the S1/S2 cleavage site. In addition, the values for the proposed RBD sequence are also shown. The bolded % aa sequence similarities are the two lowest values and the two highest values.

Figure S4. Sequence alignment of SCoV2 Wuhan and FCoV2 UCD1 spike glycoproteins. The sequences were aligned using the Clustal Omega 1.2.1 of JustBio Server (A), as described in Figure S2. The aa identity, similarity, gap, abbreviations, cleavage site, and table summary format are the same as those described in Figure S2. The FCoV1 UCD-1 sequence is shown in magenta. Two values for CTD, S1, and S2 are shown in the summary table (B), due to the major difference in the location of the S1/S2

cleavage site for these viruses. In addition, the values for the proposed RBD sequence are also shown. The bolded % aa sequence similarities are the two lowest values and the two highest values.

Figure S5. Anti-CoV analyses of group-housed laboratory and pet cats. The analyses were performed using the FCoV2-WV and SCoV2 RBD ELISA (A) and the immunoblot strips (B,C) with SCoV2 UF-RBD (B1,C2 last row), proposed FCoV2 RBD (B2,C2 second row), FCoV2-WV (B3,C1), and the proposed FCoV1 RBD (B4,C2 first row). The eight group-housed laboratory cats (A,B) were unrelated to our UGA queens and UF toms, but the animal vendor was the same as the UGA queens and had different breeding lineages. Additionally, three group-housed pet cats from a household of five cats were similarly tested as a preliminary study (C1-C4), to determine whether FCoV-infected pet cats develop cross-reactive antibodies to SCoV2 RBD. Pet cat sera KY1 and KY2 are from the same cat, collected first (KY1) at the same time as the other two cats (KM1 and KN1), and again 2.5 months later (KY2). The owner indicated that she has not been infected with SCoV2 and had no signs of COVID-19 (IRB202002902). However, her pet cats are allowed to roam outdoors and, therefore, there is a remote possibility that they have been exposed to SCoV2-infected cat(s) outdoors. We have not tested her cats by SCoV2 RT-PCR or SCoV2 NAb assay. The serum from UGAQ4 was the FCoV1⁺ control for FCoV2-WV (A,B3,C1) and FCoV1 RBD (B4,C2 first row) ELISA or immunoblot. The plasma or serum from cats J2a and UGA4.4 were FCoV2⁺ (B2,C2 second row) and SCoV2⁺ (B1,C2 last row) controls, respectively. The serum from cat UGAQ4 and UGA1.4 also served as weak positive controls for FCoV1 and FCoV2 RBD immunoblots, respectively, (C2 rows 1 & 2, B2 row 1) whereas serum from SPF cats HOF and HOE served as a negative control from all immunoblots and ELISA, respectively. The results for SCoV2 RBD (B1, lower panel; C2, third panel) are shown below each immunoblot strip, with the final result of either a positive (+) or negative (-). Those summary results with a subscript “a”, as shown as (+^a) or (-^a), are supported by results performed at 1:25 dilution (data not shown). All immunoblot photographs were adjusted to 10% brightness and 5% contrast for consistency.

Figure S6. Sequence alignment of SCoV2 Wuhan and SCoV1 Tor2 spike glycoproteins. The sequences were aligned using the Clustal Omega 1.2.1 of JustBio Server as described in Figure S2 (A). The aa identity, similarity, gap, abbreviations, cleavage site, and table summary format are the same as those described in Figure S2. The RBD for each virus is shown in bold blue aa residues and the underlined section represents the RBM (A). These two sequences are highly conserved, with a minimal number of gaps observed predominantly in NTD of S1 glycoprotein. The demarcation sites of the NTD, RBD, and CTD are identical between these viruses. The summary table (B) shows an additional column for the whole spike sequence. The bolded % aa sequence similarities are the one lowest value and the one highest value.

Figure S7. The SCoV2 UF2-RBD sequence with aa extensions. The aa sequence extensions in blue aa residues were selected based on the sequence with aa conservation between SCoV2 and FCoV2 (Figure S3) and SCoV2 Wuhan and SCoV1 Tor2 (Figure S6) (A). The extensions were also based on the number of SCoV2-specific cytotoxic T lymphocyte (CTL) and T-helper (T_H) epitopes increased by the aa extensions as shown in Table S1. Additionally, the aa residue number of UF2-RBD (269 aa) was increased to the residue number. This is similar to our FCoV2 RBD (268 aa) that blocked *in vitro* FCoV2 infection more potently than the short SCoV2 UF-RBD. Our goal is to increase the CTL epitopes, which will eradicate the SCoV2 infected cells, without increasing the T_H epitopes, which has the potential to elevate the inflammatory responses. In our preliminary study (B), the sera from COVID-19 vaccinated humans (Y3, Y6) with no prior SCoV2 exposure were tested with either SCoV2 UF2-RBD or a UF-RBD immunoblot strip. Subject Y3 received three vaccinations with Pfizer S mRNA vaccine. Subject HY6 received two vaccinations with Astra-Zeneca ChAsOX1-S recombinant vaccine, followed by vaccination with the Pfizer S mRNA vaccine. The serum collected in 2017 from Y3 was used as a negative human control. The sera from SCoV2-inoculated cat UGA4.1 and SPF cat HOF also served as positive and negative cat controls, respectively.

Figure S8. Multi-sequence alignment of 10 CCoV2 spike versus four FCoV2 spike sequences. The sequences were aligned using the Clustal Omega 1.2.1 of JustBio Server (A) as described in Figure S2. The aa identity, similarity, gap, abbreviations, cleavage site, and table summary format are the same as those described in Figure S2. The FCoV2 79-1146 sequence is shown in magenta. The RBD for FCoV2 79-1146 is shown with yellow highlight. Two values for CTD, S1, and S2 are shown in the summary table

(B), due to the slight difference in the S1/S2 cleavage site motif among the CCoV2 and FCoV2 strains and are depicted with the cleavage motif. The bolded % aa sequence similarities are the one lowest value and the two highest values.

Figure S9. Multi-sequence alignment of two CCoV1 spike versus 10 FCoV1 spike sequences. The sequences were aligned using the Clustal Omega 1.2.1 of JustBio Server (A), as described in Figure S2. The aa identity, similarity, gap, abbreviations, cleavage site, and table summary format are the same as those described in Figure S2. The FCoV1 UCD-1 sequence is shown in magenta. The RBD for FCoV1 UCD-1 is shown with yellow highlight. Two values for CTD, S1, and S2 are shown in the summary table (B), due to the two aa residues difference in the S1/S2 cleavage site of the CCoV1 and FCoV1 and are designated by the virus. The bolded % aa sequence similarities are the one lowest value and the two highest values.

Figure S10. Titration of sera from the last collection date from all toms and three UGA queens. The last sera collected from the toms (5HQ, HOG, HOJ) were titrated at dilutions of 1:50, 1:100, and 1:1000 using SCoV2 RBD immunoblot strips (A1) and FCoV1 RBD immunoblot strips (A2). Toms 5HQ, HOG, and HOJ are the abbreviation of 5HQT1, HOGT3, and HOJT2. The last sera collected from UGA queens UGAQ2, UGAQ3, and UGAQ4 were also titrated at the same dilutions as the toms using the SCoV2 RBD immunoblot strips (B1) and FCoV1 RBD strips (B2). One set of immunoblot batch at 1:50 was different from those of 1:100 and 1:1000, due to each batch containing not more than 22 strips. However, the SCoV2 RBD and FCoV1 RBD immunoblot strip batches used at 1:50 dilution were the same between the Toms and the queens. The serum from UGA queen UGAQ1 was not included in this analysis, due to her abnormal antibody (Ab) profile, most likely caused by her illness. The last serum from UGAQ3 was negative for Abs to both SCoV2 and FCoV1 RBDs at all dilutions. This was expected because her serum at post-8 mo upon UF arrival had detectable and extremely weak reactivities to FCoV1 RBD at 1:25 and 1:50 dilutions, respectively, but no reactivity to SCoV2 RBD at either dilutions (Figure 3D). The sera from SCoV2-infected cat UGA4.4, FCoV1-infected cat J1A3 (serum from 2 mo post-FCoV1 UK-2 inoculation), and SPF cat HOF served as SCoV2 positive control, FCoV1 positive control, and negative cat control, respectively. All immunoblot photographs were adjusted for consistency to 10% brightness and 5% contrast. SCoV2 control cat UGA4.4 was euthanized at two weeks post-SCoV2 inoculation (1-mL intranasal inoculation with SCoV2 Wuhan at 10^6 TCID₅₀) and may not have had enough time or inoculation dose to develop strong Abs to SCoV2. In contrast, FCoV1 control J1A3, with 1-mL of oral/intranasal inoculation with FCoV1 UK-2 at 10^5 TCID₅₀, developed strong Ab titer to FCoV1 RBD, even at 1:1000 dilution. It is also possible that the immune system of the FCoV1-control J1A3 was more responsive than the SCoV2-control UGA4.4 to their respective virus inoculation.

The virus antigen amounts of SCoV2 and FCoV1 RBDs on the immunoblot strips were identical (5 µg per strip). Hence, the titration of the last sera from the toms shows loss of reactivities to SCoV2 RBD, starting at 1:100 dilution, but not to FCoV1 RBD. The last sera from all toms maintained Ab titers to FCoV1 RBD, even at 1:1000 dilution. The same sera from these toms titrated on FCoV2-WV show strong reactivity to NC, even at 1:1000 dilution by all three toms (Figure 3E). The last sera from two of the three queens (UGAQ2, UGAQ4) had strong reactivity to FCoV1 RBD at all dilutions, whereas, same two queens had no Ab titer to SCoV2 RBD, even at the highest concentration of 1:50 dilution. This suggests that cross-reacting Abs to SCoV2 RBD are lost before Abs to FCoV1 RBD. Our results, shown in this figure, indicate that both the toms and UGA queens were infected with FCoV1, instead of SCoV2.

Figure S11. Another pet cat household with FCoV1-infected cats. An internal medicine veterinarian from the UF CVM hospital contacted the Laboratories of Comparative Immunology & Virology for Companion Animals (LCIV-CA) Program for a consultation. They requested testing of a 7-month-old, female pet cat (AP), suspected of FIPV infection with a severe lung lesion. Her sibling from the same litter of three died from FIPV infection, and her brother is still alive in the same household of three indoor cats. The third cat in this household is unrelated to the patient. The lung lesion biopsy was negative by FCoV RT-PCR, and her serum was negative by FCoV ELISA. The LCIV-CA immediately performed, free of charge, immunoblot analyses with the following antigens: FCoV1 RBD, FCoV2 RBD, and SCoV2 RBD (A), as well as FCoV2-WV and feline immunodeficiency virus (FIV)-WV (B). The FCoV2-WV immunoblot bands show a full-length spike (S), spike-2 (S2), nucleocapsid (NC) and membrane (M) glycoproteins/proteins (B). The feline immunodeficiency virus (FIV) immunoblot bands show surface

envelope (SU), transmembrane envelope (TM), capsid p24 (CA), and matrix (MA) glycoproteins/proteins. The S and S2 bands of the FCoV2-WV immunoblot strips are shown with a white arrow, and the remaining key FCoV protein bands are shown with a white arrow-head. Similarly, the SU and TM bands of FIV-WV immunoblot strips are shown with a white arrow and other key bands are shown with an arrow-head. The BSA band at 67-70 kDa is shown with a small “b” alone or next to the bracket. LCIV-CA provided Figures S11A and S11B to the veterinarian and the owner. The owners of this household were negative for SCoV2 infection. The patient’s code (AP) is in red, and her summary results on the bottom of the strips are also in red. The immunoblot photographs were adjusted for consistency to 10% brightness and 5% contrast.

The owner wanted to purchase anti-CoV polymerase inhibitor, Remdesivir, from China to treat cat AP [91]. FCoVs and their mutated FIPVs are highly contagious in a multi-cat household. Therefore, LCIV-CA suggested to the owner that she should make sure the remaining two cats are FCoV negative and, if positive, they should be treated at the same time. The patient’s brother (HP) and her 2-year-old male friend (MP) were bled 1.5 months later at the UF CVM Hospital. The original serum from AP, stored in refrigeration, was also included in the testing of the household cats. All of the immunoblot strips were different batches from those used in the initial clinical tests in Figure S11, to demonstrate reproducibility in our analyses. These immunoblot photographs are shown without any adjustments. All three cats were positive for Abs to FCoV1 RBD (C1) and NC protein (43 kDa band) (D). Patient AP and her brother HP were positive for Abs to SCoV2 RBD (C3), but negative for Abs to FCoV2 (C2). Cat MP had extremely weak bands for S, S2, and M glycoproteins. Both AP and HP had no S2 Abs, which was somewhat of a rare observation. The only other cat, G-3, (Figure S5B3, first bleeding) also had no S2 Abs, but developed S2 Abs by the second bleeding. In summary, all three pet cats were exposed to FCoV1 infection and not to FCoV2 infection. Patient AP and her brother HP had cross-reacting Abs to SCoV2 RBD, whereas cat MP was negative for SCoV2 RBD Abs, suggesting that MP may be clearing FCoV1 infection based on the results from Figure S10.

Table S1. CD8⁺ CTL and CD4⁺ T_H Epitopes on SCoV2 UF-RBD and UF2-RBD.

Figure S1

A MB-RBD (MassBiologics Wuhan RBD residue 319 to 541) glycoprotein kindly provided by MassBiologics with attached Tags: c-Myc Peptide; 6xHis Tag

UF-RBD from a plasmid with Wuhan RBD residue 319-529 sequence (MN975262.1) with attached Tags: HRV 3C Cleavage Site; 8xHis Tag; Streptavidin-Binding Peptide (SBP) Tag

MB-RBD	319-RVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLYNSASFSTFK-378
UF-RBD	319-RVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLYNSASFSTFK-378

MB-RBD	379-CYGVSPTKLNDLCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNS-438
UF-RBD	379-CYGVSPTKLNDLCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNS-438

MB-RBD	439-NNLDSKVGGNYNLYRLFRKSNLKPFERDISTEIQAGSTPCNGVEGFNCYFPLQSYGFQ-498
UF-RBD	439-NNLDSKVGGNYNLYRLFRKSNLKPFERDISTEIQAGSTPCNGVEGFNCYFPLQSYGFQ-498

MB-RBD	499-PTNGVGYPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNF – c-Myc Peptide - 6xHis Tag
UF-RBD	499-PTNGVGYPYRVVLSFELLHAPATVCGPKK- HRV 3C Cleavage Site - 8xHis Tag - SBP Tag

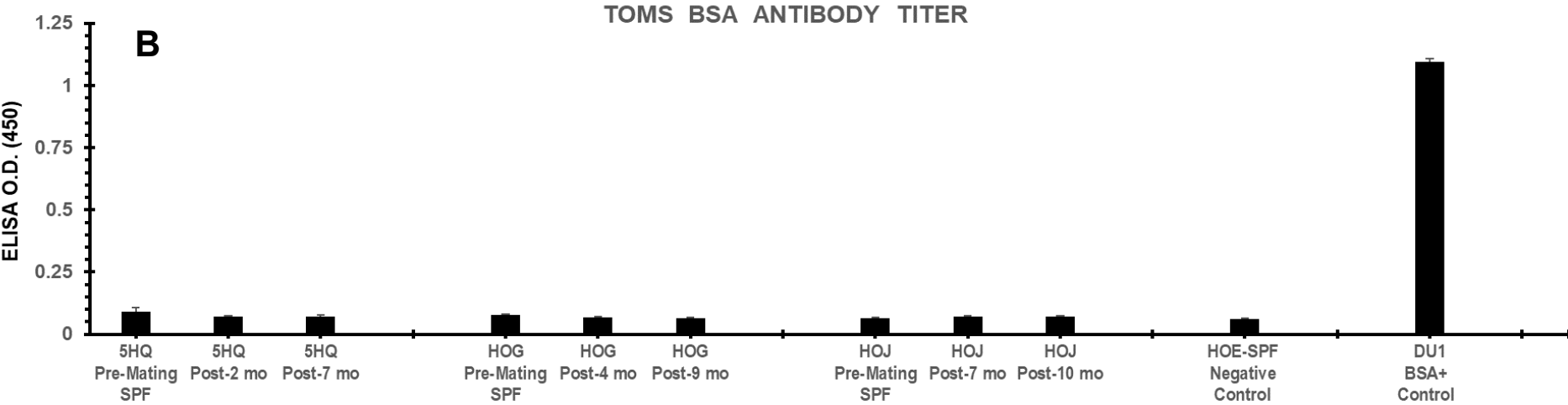


Figure S2

A Summary of SCoV2 versus FCoV1/FCoV2 Structural Proteins

SCoV2 vs. FCoV1 FCoV1 vs. FCoV2	Structural Protein *	Number of AA	AA Identity (%)	AA Similarity (%)
SCoV2 vs. FCoV1	Spike (S1+S2)	1273 vs. 1457	20.7%	50.1%
SCoV2 vs. FCoV2	Spike (S1+S2)	1273 vs. 1452	22.0%	50.4%
FCoV1 vs. FCoV2	Spike (S1+S2)	1457 vs. 1452	43.7%	72.6%
SCoV2 vs. FCoV1	S1	685 vs. 790	12.9% / 13.0%	39.4% / 40.0%
SCoV2 vs. FCoV2	S1	685 vs. 959	14.5% / 16.3%	41.4% / 43.4%
FCoV1 vs. FCoV2	S1	790 vs. 959	29.5% / 31.6%	62.9% / 64.5%
SCoV2 vs. FCoV1	S2	588 vs. 667	31.6% / 30.1%	65.1% / 62.2%
SCoV2 vs. FCoV2	S2	588 vs. 493	32.0% / 33.5%	62.2% / 64.5%
FCoV1 vs. FCoV2	S2	667 vs. 493	60.6% / 68.7%	84.0% / 89.9%
SCoV2 vs. FCoV1	Env	75 vs. 82	25.6%	68.3%
SCoV2 vs. FCoV2	Env	75 vs. 82	23.2%	67.1%
FCoV1 vs. FCoV2	Env	82 vs. 82	96.3%	97.6%
SCoV2 vs. FCoV1	NC	419 vs. 377	25.3%	59.2%
SCoV2 vs. FCoV2	NC	419 vs. 377	25.7%	58.0%
FCoV1 vs. FCoV2	NC	377 vs. 377	92.8%	97.6%
SCoV2 vs. FCoV1	M	222 vs. 262	26.3%	55.0%
SCoV2 vs. FCoV2	M	222 vs. 262	25.6%	54.2%
FCoV1 vs. FCoV2	M	262 vs. 262	95.4%	98.5%

* Spike 1 (S1), Spike 2 (S2), Envelope (Env), Nucleocapsid (NC) and Membrane (M) proteins.

B Structural Proteins Based on Total AA Number and the Predicted N- and O-Glycosylation(s)

Structural Protein	FCoV1 (Da)*	FCoV1 Glycan N / O†	FCoV2 (Da)*	FCoV2 Glycan N / O†
S (S1+S2)	163,727	3 / 3	160,473	4 / 1
S1	89,666	3 / 1	106,185	4 / 1
S2	74,080	1 / 2	54,307‡	1 / 0
Env	9,379	0 / 0	9,371	0 / 0
NC	42,663	0 / 0	42,703	0 / 4
M	29,920	1 / 0	29,832	1 / 0

* The MW of FCoV is determined by the total aa residue number using the Peptide Analyzing Tool server.

† The number of N-glycosylation (N) with high or medium potential and O-glycosylation (O) with strong potential are shown as (N / O).

‡ The predicted FCoV2 S2 shown in Fig. 2B matches the MW of FCoV1 S2 with glycan(s). Hence, the predicted FCoV2 S1/S2 cleavage site may be more closer to that of FCoV1, and FCoV2 S2 with glycan may be closer in size to the FCoV1 S2 with glycan(s).

A

YP009724390.1_SCoV2_Wuhan
AA32596.1_FCoV2_WSU79-1146

Signal Peptide → **NTD / S1**

MFVF-----**LVLLPLVSS**QCQVNLTRT-----QLPP-----AYTNSFTRGVVY
MIVLVTCLLLLCSYHTVLST**TNNECIQVNV**TQLAGNENLIRDFLSNFKEEGSSVVVGGYY
*::: .: * . . . *::: .: * * . . *
↓ **NTD**

PDKVFRRSSVLHSTQDLFLPFFSNVTFWFA-IH-VSGTNGTKRFDNPVLPFNDGV-----
PTEVWYNCSRTARTTAF-QYFNNIHAFYFVMEAMENSTGNAR-GKPLLHVHGEFVSVII
*::: .: * :*: *: :. :. :*. * :*: . *

--YFASTEKSNII-----RGWIFGTTLDSKTQSL--LIVNNATNV
SAYRDDVQQRPLLKHGLVCITKNRHINYEQFTSNQWNSTCTGADRKIPFSVPTDNGTKI
* .::: : : . * * . . : : :*: *: :

VIKVFCEQFCNDPFLGVYYH-KNNKSWMESEFRVYSSANNCTFEYVSQPFMLDLEG----
YGLEWNDFVTAYISGRSYHLNINTNWFNNVTLTLYSRSSATATWEYSAAAYAQGVSNFTYY
: : * : * ** : * .*: .: ** : . . : :

KQGNFKNLREFV---FKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP-IGINIT
KLNNTNGLKTYELCEDYEHCTGYATNVFAP---TSGGYIPDGFSSFNNWFLLTNSSTFVSG
* * : * : : :. * . . :*: ** : : :

RFQTLALHRSYLTPG---DSSSGWTA-----GAAAYVGYL---Q-
RFVTNQPLLINCLWPVPSFGVAAQEFCEFGAQFSQCNGVSLNNTVDVIRFNLNFTADVQS
** * . * * :. : . : : : *

↓ **NTD** ← **RBD / S1**

-PRTFLLKYNENGTITDAVDCALDPLSETKCTLKSFSTVEKGIYQTSNFRVQPTESIVREF
GMGATVFSLNTTGGVILEISCYSDTVSESSSY-GEIPFGITDGPY-----CYVLY-
: :. * . * : : * * :*: .: * * : : . * :

↓ **NTD**

NITNLCPFGEVFNATRFASVYAWNKRIS-----NCVA-----
NGTALKYLGTLPSPVKEIAISKWGHFYINGYNFFSTFPIGICISFNLTGTGVS GAFWTIAYT
* * * : * : :. : : * : * . *::
↓ **Proposed RBD / S1**

-----DYSVLYNASASFSTFKCYGVSP-----KLNLCFTN--VYADS
SYTEALVQVENTAIKNVTYCNSHINNIKCSQLTANLNGGFYPVASSEVGFVNKSVLLPS
. * * .: :. :*: :. . :. : * . * *

FVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAW**NSNNLDSKVG**GNYNLYRLFRKS
FFTYTA--VNITIDLGMKLSGYGQPIASTLSNITLPMQDNN**TDVY**CIRS--NQFSVYVHS
* . :*: * : :. :. :. :. :*: *

NLK-----PFERDI-----STEIYQAGSTPC-----N--GVEGFNCYFP
TCKSSLWDNIFNQDCTDVLEATAVIKTGTCPFSFDKLNLYLTNKFCLSLSPVGANCKED
. * :*: : : : * . * * *

↓ **RBD** ← **CTD / S1**

LQSYGFQPTNGVGYPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNFNGLTGTGV
VAARTR-NEQVVRSLYVIYEEDNIVGVPSDNSGLHDLVLHLD**SCTD**YNIYGR**TGVGI**
: : .: * . * : : :. : * :. : * : * : * : *

↓ **Proposed RBD** ← **CTD**

LTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVL
IRRTNSTLLSGLYTSLSG-DLLGFKNVSDGVIYSVTPCDVSVQAVIDGAIVGAMTS--
: .*: . * : . . :. : * :*: . : :

YQDVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIG---A
---INSE---LLGLTHWTTT**PNFY**YSIYNYT**SERT**RGTAI---DSNDVDCEPVITYSNI
: * : :. : * :. : * * . : * * . * : : *

↓ **CTD** ← **S1/S2** →

GICASYQTQTN**SPRRAR**SVASQSIAYTMSLGAENSVAYSNNNSIAIPTNFTISVTTEILP
GVCKN-----GALVFINVTHSDGDVQPISTGNVTIPTNFTISVQVEYMQ
* * : : : : : * : : : : : * : : : : *

VSMTKTSVDCTMYICGDSTEC SNLLLQYGSFCTQLNRALTGIAVEQDKNTQE-VF-----
 VYTPVPSIDCARYVCNGNPRCNKLLTQYVSACQTIEQALAMGARLENMEVDSMLFVSENA
 *

YP009724390.1_SCoV2_Wuhan
AA32596.1_FCoV2_WSU79-1146

[illegible]

YP009724390.1_SCoV2_Wuhan
 AAY32596.1_FCoV2_WSU79-1146

TLADAGFI-KQYGDCLGDIAARDLICAQKFNGLTVLPPLLTDEMQYTSALLAGTITSG
 VTSGLGTVDEDYKRCTGGYDIADLVCAQYNGIMVLPGVANADKMTMYTASLAGGI-TLG
 . : * : : * * * * * : : : * * : : : * * *

YP009724390.1_SCoV2_Wuhan
 AAY32596.1_FCoV2_WSU79-1146

WTFTGAGAALQIPFAMQMAYFRNGIGVTVQNVLNYENQKLIANQFNSAIGKIQDSL-----
A--LGGGAVAIPFAVAVQARLNLYVALQTDVLNKNQQIILANAFNQAGNIQTAFGKVNDAI
* * : ***** : *.* : : ** **:*** :** ** **.* :

YP009724390.1_SCoV2_Wuhan
 AAY32596.1_FCoV2_WSU79-1146

-----SSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDKVEAEV
HQT SQGLATVAKALAKVQDVVNTQGQALSHLTVQLQNNFQAISSSIDY NRLDELSADA
: * * * * : * * * * * : * * * * * : * * * * * : * * * * * : * * * * * : * * * * * : * * * * * : * * * * *

YP009724390.1_SCoV2_Wuhan
 AAY32596.1_FCoV2_WSU79-1146

QIDRLITGRLQSLQTIVTQQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGHYHLS
QVDRLLTGRLTALNAFVSQTLTRQAEVRASRQLAKDKVNECVRSQSQRFGFCGNTHLFS
*.***** .*:.*.* * * *.***** :** *:*** **:*. ****.* **.*

YP009724390.1_SCoV2_Wuhan
 AAY32596.1_FCoV2_WSU79-1146

FPQSAPHG VVFLHVTYVPAQEKNFTTAPAICHDGKA-HFP-----REGV FVSNGTHW FV
LANAAPNGMIFFHTVLLPTAYETVTAWSGICASDGDRTFGLVVKDVQLTLFRNLDDKFYL
: : : * * : : * : : * : : * : : * : : * : : * : : * : : *

YP009724390.1_SCoV2_Wuhan
 AAY32596.1_FCoV2_WSU79-1146

Stem Helix (SH)

SH Core

TQRNFYEPQIIITDNTFVSGNCDVVIGIVNNTVYDPLQPE---LDSFKEELDKYFKNHT
TPRTMYQPVRVATSSDFVQIEGCDVLVFVNATVIDLPSTIPDYIDINQTVDILENYEFPNW
* * * * * : * * * * : * * * * : * * * * : * * * * : *

YP009724390.1_SCoV2_Wuhan
AA32596.1_FCoV2_WSU79-1146

SPVDVLGDISGINASVVNIQKEI-----DRLNEVAKNLNESLIDLQELGKY
VPEFTLDIF---NATYLNLTGEIDDLEFRSEKLHNTTVELAILIDNINNTLVNLEWLNRI
* : * : ** : * : ** : * : * : * : * : * : *

YP009724390.1_SCoV2_Wuhan
 AAY32596.1_FCoV2_WSU79-1146

EQYIKWPWYIWLGFIAGLIAIVMVTIMLCM-TSCCCLK--GCCSCGSCCKFDEDDSE
ETVYKWPWYVWLLIGLVVFC-IPLLLFCCFSTGCCGIGCLGSCCH-SICSRQFENYE
* * * * * * * * * * ** * . . . *

YP009724390.1_SCoV2_Wuhan
AA32596.1_FCoV2_WSU79-1146

PVLKGVKLHYT
PI-EKVHVH--
* : : * : : *

B

Summary of Amino Acid (AA) Sequence Identity and Similarity between SCoV2 and FCoV2

	NTD	RBD	RBD (Proposed)	CTD (SCoV2)	CTD (FCoV2)	S1 (SCoV2)	S1 (FCoV2)	S2 (SCoV2)	S2 (FCoV2)
Total No. of AA	370	290	273	147	297	834	984	654	504
No. of AA with Identity	55	38	36	24	64	121	161	210	170
No. of AA with Similarity	155	107	100	69	151	345	427	410	327
% Identity	14.9%	13.1%	13.2%	16.8%	21.5%	14.5%	16.4%	32.1%	33.7%
% Similarity	41.9%	36.9%	36.6%	54.7%	50.8%	41.4%	43.4%	62.7%	64.9%

A

YP009724390.1_ScCoV2_Wuhan
AB088222.1_FCoV1_UCD-1

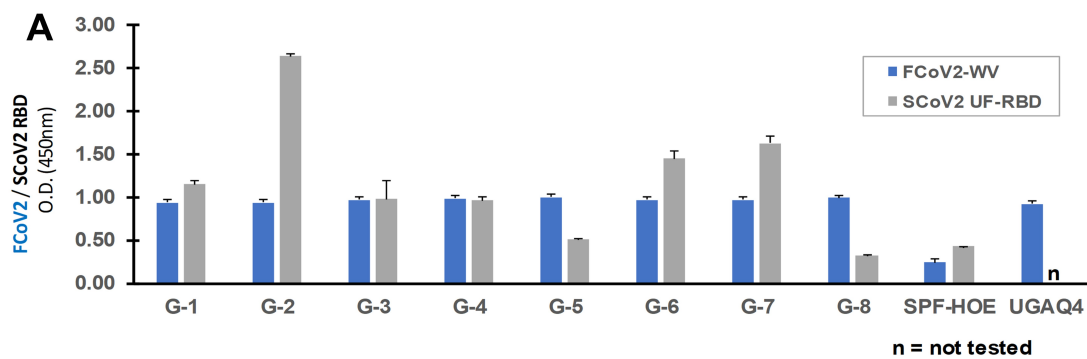
TRWRVYSTGSN----VFQTRAGCLIGAEHVNSYECDIPIGAGICASYQTQTNSP**RR**RS↓
T**HSRRSR**GSTSTSVTTYTMPQFYITKWNNDTSTNCTSVITYSS-----FA
* * ** : * : * : * *

Proposed RBD ←

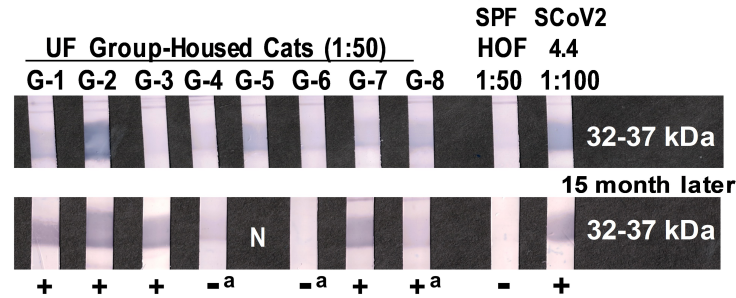
← S1/S2 →
CTD ←

CTD ← S1/S2 →

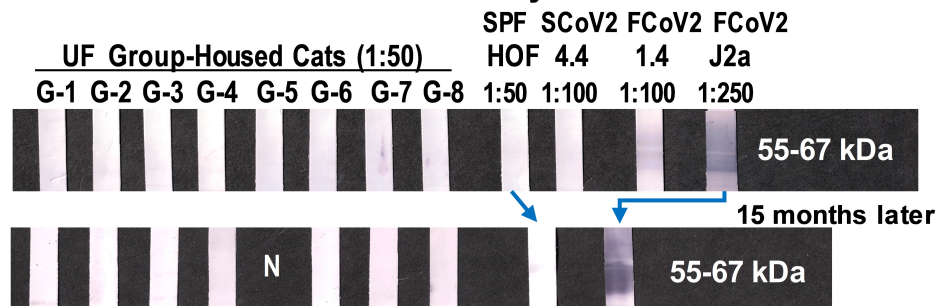
Fig. S5



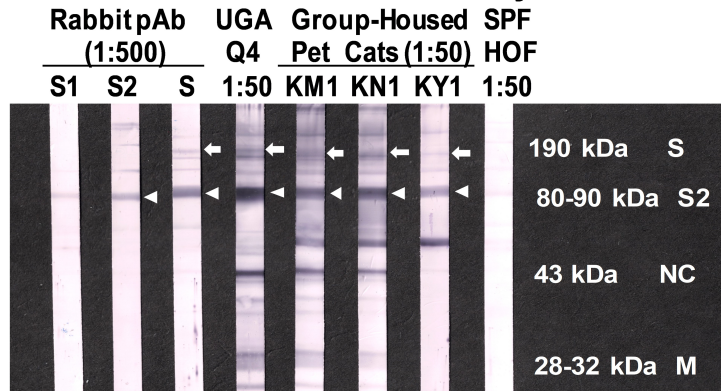
B1 SCoV2 RBD Immunoblot Analyses



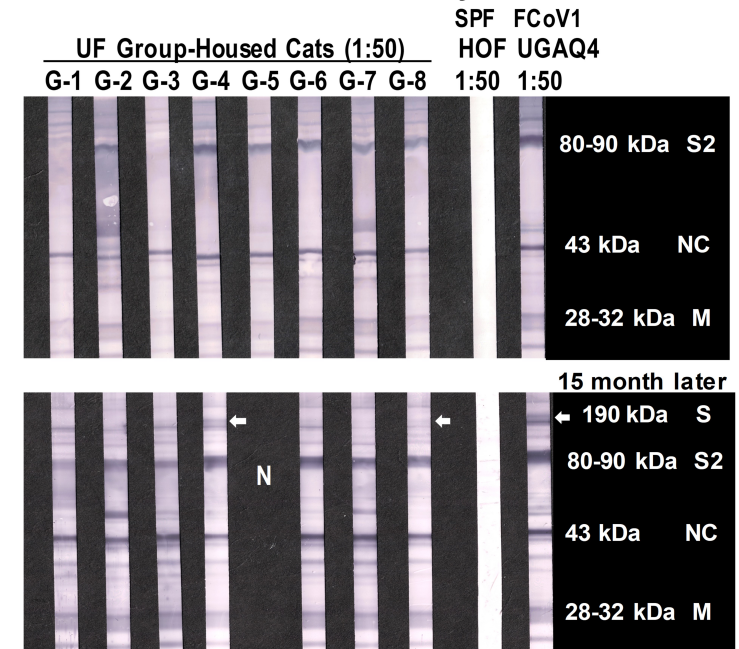
B2 FCoV2 RBD Immunoblot Analyses



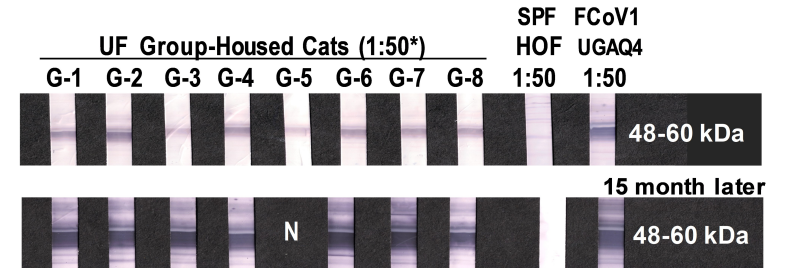
C1 FCoV2-WV Immunoblot Analysis



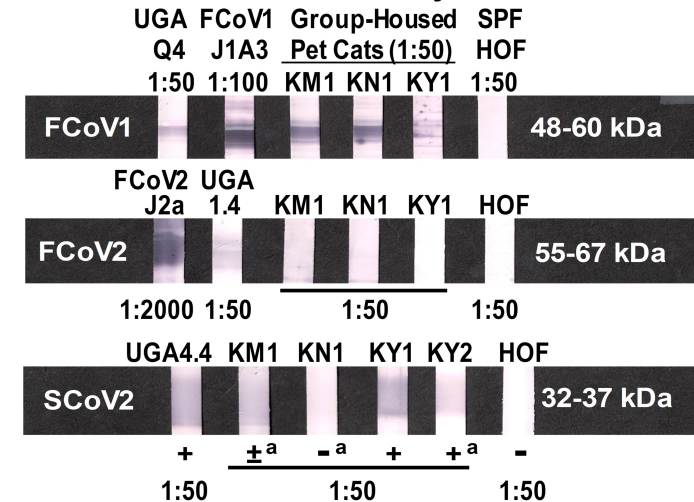
B3 FCoV2-WV Immunoblot Analyses



B4 FCoV1 RBD Immunoblot Analyses



C2 RBD Immunoblot Analyses



A

Signal Peptide → **NTD / S1**
 YP_009724390.1_SCoV2_Wuhan MFVFLVLLPLVSSQCVNLTT--RTQLPPAY--TNSFTRGVYYPDKVFRSSSVLHSTQDLFL
 YP_009825051.1_SCoV1_Tor2 MFIFLLFLTLTSGSDLDRCTTFDDVQAPNYTQHTSSMRGVYYPDEIFRSDTLYLTDLFL
 :*::* *.*.. :: * * * * *:***.:*: *****

 YP_009724390.1_SCoV2_Wuhan PFFSNVTWFHAIHVSGTNGTKRFDNPVLPFNDGVYFASTEKSNIRGWIFGTTLDSKTQS
 YP_009825051.1_SCoV1_Tor2 PFYSNVTGFHTIN-----HTFGNPVPIPKDGIYFAATEKSNVVRGWVFGSTMNKSQS
 :* **:* : * ***:**:*:***:*****:***:***:*.:.:***

 YP_009724390.1_SCoV2_Wuhan LLIVNNATNVVIKVCFFQFCNDPFLGVYYHKNKNSWMESEFRVYSSANNCTFEYVSQPFL
 YP_009825051.1_SCoV1_Tor2 VIIINNSTNVVIRACNFELCDNPFFAVSKPMGT---QTHMTIFDNAFNCTFEYISDAFS
 :*:***:*****.:*:*:*:*:***.* . :.. :...* *****:*.

 YP_009724390.1_SCoV2_Wuhan MDLEGKQGNFKNLREFVFKNIDGYFKIYSKHPTINLVRDLPGGFSALEPLVDLPIGINIT
 YP_009825051.1_SCoV1_Tor2 LDVSEKSGNFKHLREFVFKNKDGLYVYKGYQPIDVVRDLPSGFNTLKPFIKPLGINIT
 :*:. *.****.***** **:: :*. : **::****.***:***:..*:*:*****

 YP_009724390.1_SCoV2_Wuhan RFQTLALHRSYLTPGDSSSGWTAGAAAYVGYLQPRFTLLKYNENGTITDAVDCALDPL
 YP_009825051.1_SCoV1_Tor2 NFRAILTAFS-----PAQDIWGTSAAYFVGYLKPTTFMLKYDENGITDAVDCSQNPL
 .*:***: . :.. * :.****:****:* **:*:***:*****:***: :**

NTD ← **RBD / S1**
 YP_009724390.1_SCoV2_Wuhan SETKCTLKSFTEVEKGIYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRR
 YP_009825051.1_SCoV1_Tor2 AELKCSVKSEFIDKGIYQTSNFRVVPSPGDVVRFPNITNLCPFGEVFNATKFPSVYAWERK
 :* **::*** :*:***** ** :. :*****:***:***:*****:***:***

 YP_009724390.1_SCoV2_Wuhan RISNCVADYSVLYNSASFSTFKCYGVSPTKLNLDLCTNVYADSFVIRGDEVQRQIAPGQTG
 YP_009825051.1_SCoV1_Tor2 KISNCVADYSVLYNSTFFSTFKCYGVSATKLNLDLCSNVYADSFVVKGDDEVQRQIAPGQTG
 :*****: ***** *****:*****:***:*****

 YP_009724390.1_SCoV2_Wuhan KIADYNYKLPPDFTGCVIAWNSNNLDSKVGNGYNYLYRLFRKSNLKPFERDISTEIQAG
 YP_009825051.1_SCoV1_Tor2 VIADYNYKLPPDFMGCVLAWNTRNIDATSTGNYNKYRYLRHGKLRPFERDISNVFPSPD
 ***** ***:***:*.*:.. ***** ** :*:..:*****. :.

RBD ←
 YP_009724390.1_SCoV2_Wuhan STPCNGVEGFNCYFPLQSYGFGPTNGVGYQPYRVVVLSEFELHAPATVCGPKKSTNLVKN
 YP_009825051.1_SCoV1_Tor2 GKPCPTP-PALNCYWPLNDYGFYTTTGIGYQPYRVVVLSEFELNAPATVCGPKLSTDLIKN
 ..** .:***:***:*** *.*:*****:*****:***** ***:***

CTD / S1
 YP_009724390.1_SCoV2_Wuhan KCVNFFNFNGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVS
 YP_009825051.1_SCoV1_Tor2 QCVNFFNFNGLTGTGVLTPSSKRFQFPQQFGRDVSDFTDSVRDPKTSEILDISPACFAGGVS
 :***** **:* * *****:*. ***:***:***:*****:***:***

 YP_009724390.1_SCoV2_Wuhan VITPGTNTSNQVAVLYQDVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHV
 YP_009825051.1_SCoV1_Tor2 VITPGTNASSEVAVLYQDVNCTDVSTAIHADQLTPAWRIYSTGNNVVFQTAGCLIGAEHV
 *****:*. :*****:*. *****:***:***. *****:*****

CTD ← **S1/S2** →
 YP_009724390.1_SCoV2_Wuhan NNSYECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTMSLGAENSVAYSNNNSIAIPT
 YP_009825051.1_SCoV1_Tor2 DTSYECDIPIGAGICASYHTVSL---LRSTSQKSIVAYTMSLGADSSIAYSNNNTIAIPT
 :.*****:*. : ***:..:***:*****:*.*:***:*****

 YP_009724390.1_SCoV2_Wuhan NFTISVTTEILPVSMKTSTVDCTMYICGDSTECNLLLQYGSFCTQLNRLTGLIAVEQDK
 YP_009825051.1_SCoV1_Tor2 NFSISITTEVMPVSMAKTSVDCNMYICGDSTECANLLLQYGSFCTQLNRLSGIAAEQDR
 :*:***:****:*****:*****.*****:*****:*****:***:***:

S2' **Fusion Peptide (FP)**
 YP_009724390.1_SCoV2_Wuhan NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLDAGFIKQ
 YP_009825051.1_SCoV1_Tor2 NTREVFQAQVKQMYKTPPTLKYFGGFNFSQILPDPLKPTKRSFIEDLLFNKVTLDAGFMKQ
 *****:***:***.*****:*****.*****:*****:*****:*****:***:***:

YP_009724390.1_SCoV2_Wuhan	YGDCLGDIARDLICAQKFNGLTVLPPLLTDemiaQYTSALLAGTITSGWTFGAGAALQI
YP_009825051.1_SCoV1_Tor2	YGECLGDINARDLICAQKFNGLTVLPPLLTDMMIAAYTAALVSGTATAGWTFGAGAALQI *:*****:*** **:::* *:*****
YP_009724390.1_SCoV2_Wuhan	PFAMQMAYRFNGIGVTQNVLYENQKLIANQFNsaIGKIQDSLSTASALGKLQDVVNQNA
YP_009825051.1_SCoV1_Tor2	PFAMQMAYRFNGIGVTQNVLYENQKQIANQFNKAISQIQESLTtTSTALGKLQDVVNQNA *****.***.***:***:***:*****
YP_009724390.1_SCoV2_Wuhan	QALNTLVKQLSSNFGAISSVLNDILSRldKVEAEVQIDRLITGRLQSLQTYVTQQLIRAA
YP_009825051.1_SCoV1_Tor2	QALNTLVKQLSSNFGAISSVLNDILSRldKVEAEVQIDRLITGRLQSLQTYVTQQLIRAA *****
YP_009724390.1_SCoV2_Wuhan	EIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSFPQSAPHGVVFLHVTYVPAQEKNFT
YP_009825051.1_SCoV1_Tor2	EIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSFPQAAPHGVVFLHVTYVPSQERNFT *****:*****:***:***
YP_009724390.1_SCoV2_Wuhan	TAPAICHdGKAHFPREGVfVSNgTHWfVTQRNFYEPQIITDNTfVSGNCDVVIGIVNNT
YP_009825051.1_SCoV1_Tor2	TAPAICHEGKAYFPREGVfVNGTSWfITQRNFSPQIITDNTfVSGNCDVVIGIINNT *****:***:***** ** *:***: . *****:***
	<div style="border: 1px dashed red; padding: 2px; display: inline-block;"> Stem Helix (SH) SH Core </div>
YP_009724390.1_SCoV2_Wuhan	VYDPLQPELDSFKEELDKYfKNHTSPDVLGDISGINASVVNIQKEIDRLNEVAKNLNEs
YP_009825051.1_SCoV1_Tor2	VYDPLQPELDSFKEELDKYfKNHTSPDVLGDISGINASVVNIQKEIDRLNEVAKNLNEs *****
YP_009724390.1_SCoV2_Wuhan	LIDLQELGKYEQYIKWPWYIwLGFIAGLIAIVMTIMLCCMTSCCScLKGCCScGSCCKF
YP_009825051.1_SCoV1_Tor2	LIDLQELGKYEQYIKWPWYVwLGFIAGLIAIVMTILCCMTSCCScLKGAcsGScGSCCKF *****:*****:*****.*****
YP_009724390.1_SCoV2_Wuhan	DEDDSEPVLKGvKLHYT
YP_009825051.1_SCoV1_Tor2	DEDDSEPVLKGvKLHYT *****

B

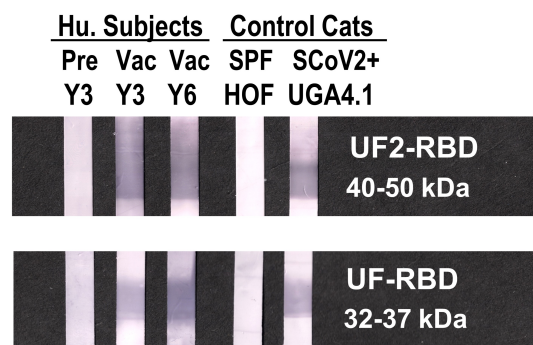
Summary of Amino Acid (AA) Sequence Identity and Similarity between SCoV2 and SCoV1

	NTD	RBD	CTD	S1	S2	Spike
Total No. of AA	322	211	144	676	588	1277
No. of AA with Identity	164	154	111	438	529	967
No. of AA with Similarity	259	190	132	594	579	1173
% Identity	50.9%	73.0%	77.1%	64.8%	90.0%	75.7%
% Similarity	80.4%	90.0%	91.7%	87.9%	98.5%	91.9%

Figure S7. SCoV2 UF2-RBD Sequence with AA Extensions

A **RTFLLKYNENGTITDAVDCALDPLSETKCTLKSFTVEKGIYQTSNFRVQPTESIVRFPNITNLCPFGGEVFNAT**
RFASVYAWNRRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLNDLCFTNVYADSFVIRGDEVQRQIAPGQTGKI
ADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYYLYRLFRKSNLKPFERDISTEIIYQAGSTPCNGVEGFNCYFP
LQSYGFQPTNGVGYQPYRVVVLVSFELLHAPATVCGPKKSTNLVKNKCVNF

B SCoV2 RBD Immunoblot Analysis



C Description of Human Subjects* and Laboratory Cats

Subject or Cat	Age (yr) Gender	Vac Freq	Vaccination Types	SCoV2 Infection
Y3 Pre	63F	-	-	-
Y3 Vac	68F	3	Pfizer S mRNA	-
Y6 Vac	38F	3	Astra-Zeneca-S Pfizer S mRNA	-
UGA4.1	1F	-	-	+
SPF HOF	1F	-	-	-

* Blood from the subjects collected using UF IRB202002902.

** Abbreviations: year (yr), Vaccinated/Vaccination (Vac), frequency (Freq), Pre-vaccination (Pre), female (F), human (Hu), specific pathogen free (SPF)

A

KP981644_CCoV2a_Italy_CB/05
KC175339_CCoV2_Germany_171
KC175340_CCoV2_US,NY_K378
KC175341_CCoV2_US,NY_S378
JQ404410_CCoV2_US,GA_UGA-TN449
JQ404409_CCoV2_US,GA_UGA-1-71
KY063616_CCoV2_China_HLJ071
KY063617_CCoV2_China_HLJ072
KY063618_CCoV2_China_HLJ073
GQ477367_CCoV2_Taiwan_NTU336
GQ152141_FCoV2_Taiwan_NTU156
JQ408981_FCoV2_Hungary_DF2
JN634064_FCoV2_WSU79-1683
DQ010921_FCoV2_WSU79-1146

[illegible]

KP981644_CCoV2a_Italy_CB/05
KC175339_CCoV2_Germany_171
KC175340_CCoV2_US,NY_K378
KC175341_CCoV2_US,NY_S378
JQ404410_CCoV2_US,GA_UGA-TN449
JQ404409_CCoV2_US,GA_UGA-1-71
KY063616_CCoV2_China_HLJ071
KY063617_CCoV2_China_HLJ072
KY063618_CCoV2_China_HLJ073
GQ477367_CCoV2_Taiwan_NTU336
GQ152141_FCoV2_Taiwan_NTU156
JN408981_FCoV2_Hungary_DF2
JN634064_FCoV2_WSU79-1683
DQ010921_FCoV2_WSU79-1146

R Y C Y A L Y N G T A L K Y L G T L P P S V K E I A I S K W G H F Y I N G Y N F F S T F P I D C I S F N L T T G T S G A
R Y C Y V L Y N G T A L K Y L G T L P P S V K E I A I S K W G H F Y I N G Y N F F S T F P I G C I S F N L T T G V S G A
R Y C F A L Y N G T A L K Y L G T L P P S V K E I A I S K W G H F Y I N G Y N F F S T F P I D C I S F N L T T G D S G A
R Y C F A L Y N G T A L K Y L G T L P P S V K E I A I S K W G H F Y I N G Y N F F S T F P I D C I S F N L T T G D S G A
R Y C Y V L Y N G T A L K Y L G T L P P S V K E I A I S K W G H F Y I N G Y N F F S T F P I D C I S F N L T T G A S G A
R Y C Y A L Y N G T A L K Y L G T L P P S V K E I A I S K W G H F Y I N G Y N F F S T F P I D C I S F N L T T G D S G A
R Y C Y V L Y N G T A L K Y L G T L P P S V K E I A I S K W G H F Y I N G Y N F F S T F P I D C I S F N L T T G A S G A
R Y C Y V L Y N G T A L K Y L G T L P P S V K E I A I S K W G H F Y I N G Y N F F S T F P I D C I S F N L T T G A S G A
R Y C Y V L Y N G T A L K Y L G T L P P S V K E I A I S K W G H F Y I N G Y N F F S T F P I D C I S F N L T T G A S G A
R Y C Y V L Y N G T A L K Y L G T L P P S V K E I A I S K W G H F Y I N G Y N F F S T F P I D C I S F N L T T G A S G A
R Y C Y V L Y N G T A L K Y L G T L P P S V K E I A I S K W G H F Y I N G Y N F F S T F P I G C I S F N L T T G A S G A
R Y C Y V L Y N G T A L K Y L G T L P P S V K E I A I S K W G H F Y I N G Y N F F S T F P I D C I S F N L T T G D S G A
R Y C Y V L Y N G T A L K Y L G T L P P S V K E I A I S K W G H F Y I N G Y N F F S T F P I G C I S F N L T T G V S G A
. **.*****.*****.*****.*****.*****.*****.*****.*****.*****.*****.*****.*****.

Proposed RBD / S1

RBD
53T
51I
51S

KP981644_CCoV2a_Italy_CB/05
KC175339_CCoV2_Germany_171
KC175340_CCoV2_US,NY_K378
KC175341_CCoV2_US,NY_S378
JQ404410_CCoV2_US,GA_UGA-TN449
JQ404409_CCoV2_US,GA_UGA-1-71
KY063616_CCoV2_China_HLJ071
KY063617_CCoV2_China_HLJ072
KY063618_CCoV2_China_HLJ073
GQ477367_CCoV2_Taiwan_NTU336
GQ152141_FCoV2_Taiwan_NTU156
JN408981_FCoV2_Hungary_DF2
JN634064_FCoV2_WSU79-1683
DQ010921_FCoV2_WSU79-1146

[illegible]

Proposed RBD ←

RBD Total (T): 268 aa
RBD Identity (I): 235 / 268 = 87.7%
RBD Similarity (S): 257 / 268 = 95.9 %

KP981644_CCov2a_Italy_CB/05
KC175339_CCov2_Germany_171
KC175340_CCov2_US,NY_K378
KC175341_CCov2_US,NY_S378
JQ404410_CCov2_US,GA_UGA-TN449
JQ404409_CCov2_US,GA_UGA-1-71
KY063616_CCov2_China_HLJ071
KY063617_CCov2_China_HLJ072
KY063618_CCov2_China_HLJ073
GQ477367_CCov2_Taiwan_NTU336
GQ152141_FCoV2_Taiwan_NTU156
JQ408981_FCoV2_Hungary_DF2
JN634064_FCoV2_WSU79-1683
DQ010921_FCoV2_WSU79-1146

KP981644_CCov2a_Italy_CB/05
KC175339_CCov2_Germany_171
KC175340_CCov2_US,NY_K378
KC175341_CCov2_US,NY_S378
JQ404410_CCov2_US,GA_UGA-TN449
JQ404409_CCov2_US,GA_UGA-1-71
KY063616_CCov2_China_HLJ071
KY063617_CCov2_China_HLJ072
KY063618_CCov2_China_HLJ073
GQ477367_CCov2_Taiwan_NTU336
GQ152141_FCoV2_Taiwan_NTU156
JQ408981_FCoV2_Hungary_DF2
JN634064_FCoV2_WSU79-1683
DQ010921_FCoV2_WSU79-1146

KP981644_CCov2a_Italy_CB/05
KC175339_CCov2_Germany_171
KC175340_CCov2_US,NY_K378
KC175341_CCov2_US,NY_S378
JQ404410_CCov2_US,GA_UGA-TN449
JQ404409_CCov2_US,GA_UGA-1-71
KY063616_CCov2_China_HLJ071
KY063617_CCov2_China_HLJ072
KY063618_CCov2_China_HLJ073
GQ477367_CCov2_Taiwan_NTU336
GQ152141_FCoV2_Taiwan_NTU156
JQ408981_FCoV2_Hungary_DF2
JN634064_FCoV2_WSU79-1683
DQ010921_FCoV2_WSU79-1146

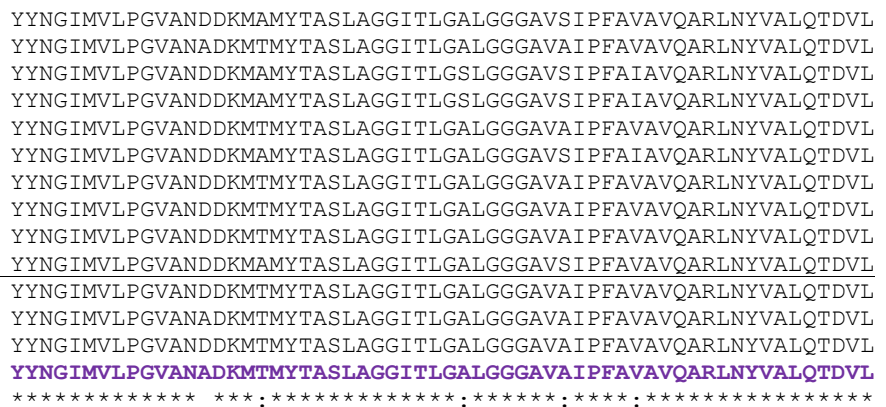
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KC175341_CCov2_US,NY_S378
JQ404410_CCov2_US,GA_UGA-TN449
JQ404409_CCov2_US,GA_UGA-1-71
KY063616_CCov2_China_HLJ071
KY063617_CCov2_China_HLJ072
KY063618_CCov2_China_HLJ073
GQ477367_CCov2_Taiwan_NTU336
GQ152141_FCoV2_Taiwan_NTU156
JQ408981_FCoV2_Hungary_DF2
JN634064_FCoV2_WSU79-1683
DQ010921_FCoV2_WSU79-1146

GIIRQTNSTLLSGLYYTSLSGDLLGFKNVSDGVVYSVTPCDVSAQAVIDGAIVGAMTSI
GIIRRTNSTLLSGLYYTSLSGDLLGFKNVSDGVVYSVTPCDVSAQAVIDGAIVGAMTSI
GIIRQTNSTLLSGLYYTSLSGDLLGFKNVSDGVVYSVTPCDVSAHAVIDGAIVGAMTSI
GIIRQTNSTLLSGLYYTSLSGDLLGFKNVSDGVVYSVTPCDVSAQAVIDGAIVGAMTSI
GIIRQTNSTLLSGLYYTSLSGDLLGFKNVSDGVVYSVTPCDVSAQAVIDGAIVGAMTSI
GIIRQTNSTLLSGLYYTSLSGDLLGFKNVSDGVVYSVTPCDVSAQAVIDGAIVGAMTSI
GIIRQTNSTLLSGLYYTSLSGDLLGFKNVSDGVVYSVTPCDVSAQAVIDGAIVGAMTSI
GIIRQTNSTLLSGLYYTSLSGDLLGFKNVSDGVVYSVTPCDVSAQAVIDGAIVGAMTSI
GIIRQTNSTLLSGLYYTSLSGDLLGFKNVSDGVVYSVTPCDVSAQAVIDGAIVGAMTSI
GIIRQTNSTLLSGLYYTSLSGDLLGFKNVSDGVVYSVTPCDVSAQAVIDGAIVGAMTSI
GIIRQTNSTLLSGLYYTSLSGDLLGFKNVSDGVVYSVTPCDVSAQAVIDGAIVGAMTSI
GIIRQTNSTLLSGLYYTSLSGDLLGFKNVSDGVVYSVTPCDVSAQAVIDGAIVGAMTSI
GIIRQTNSTLLSGLYYTSLSGDLLGFKNVSDGVVYSVTPCDVSAQAVIDGAIVGAMTSI
GIIRQTNSTLLSGLYYTSLSGDLLGFKNVSDGVVYSVTPCDVSAQAVIDGAIVGAMTSI
GIIRRTNSTLLSGLYYTSLSGDLLGFKNVSDGVVYSVTPCDVSVQAVIDGAIVGAMTSI
****.****.*****.***.*****.:.*****

NSELLGLTHWTTTPNFYYYSIYNYTNARTRGTAIDSNDVDCEPIITYSNIGVCKNGALVF
NSELLGLTHWTTTPNFYYYSIYNYTSERTRGTAIDSNDVDCEPVITYSNIGVCKNGALVF
NSELLGLTHWTTTPNFYYYSIYNYTNERTRGTAIDSNDVDCEPIITYSNIGVCKNGALVF
NSELLGLTHWTTTPNFYYYSIYNYTNERTRGTAIDSNDVDCEPIITYSNIGVCKNGALVF
NSELLGLTHWTTTPNFYYYSIYNYTNERTRGTAIDSNDVDCEPIITYANIGVCKNGALVF
NSELLGLTHWTTTPNFYYYSIYNYTNERTRGTAIDSNDVDCEPIITYSNIGVCKNGALVF
NSELLGLTHWTTTPNFYYYSIYNYTNERTRGTAIDSNDVDCEPIITYANIGVCKNGALVF
NSELLGLTHWTTTPNFYYYSIYNYTNERTRGTAIDSNDVDCEPIITYANIGVCKNGALVF
NSELLGLTHWTTTPNFYYYSIYNYTNERTRGTAIDSNDVDCEPIITYANIGVCKNGALVF
NSELLGLTHWTTTPNFYYYSIYNYTNERTRGTAIDSNDVDCEPIITYSNIGVCKNGALVF
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NSELLGLTHWTTTPNFYYYSIYNYTSERTRGTAIDSNDVDCEPVITYSNIGVCKNGALVF
NSELLGLKHWTTTPNFYYYSIYNYTNERTRGTAIDSNDVDCEPIITYSNIGVCKNGALVF
NSELLGLTHWTTTPNFYYYSIYNYTSERTRGTAIDSNDVDCEPVITYSNIGVCKNGALVF
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INVTHSDGDVQPISTGNVTIPTNFTISVQVEYIQVYTPVPSIDCSRYVCNGNPRCNKLLT
INVTHSDGDVQPISTGNVTIPTNFTISVQVEYMQVYTPVPSIDCARYVCNGNPRCNKLLT
INVTHSDGDVQPISTGNVTIPTNFTISVQVEYIQVYTPVPSIDCSRYVCNGNPRCNKLLT
INVTHSDGDVQPISTGNVTIPTNFTISVQVEYIQVYTPVPSIDCSRYVCNGNPRCNKLLT
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INVTHSDGDVQPISTGNVTIPTNFTISVQVEYIQVYTPVPSIDCSRYVCNGNPRCNKLLT
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INVTHSDGDVQPISTGNVTIPTNFTISVQVEYMQVYTPVPSIDCARYVCNGNPRCNKLLT
INVTHSDGDVQPISTGTVTIPTNFTISVQVEYIQVYTPVPSIDCARYVCNGNPRCNKLLT
INVTHSDGDVQPISTGNVTIPTNFTISVQVEYMQVYTPVPSIDCARYVCNGNPRCNKLLT
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QYVSACQTIEQALAMGARLENMEVDSMLFVSENALKLASVEAFNSTETLDPIYKEWPNIG
QYVSACQTIEQALAMGARLENMEVDSMLFVSENALKLASVEAFNSTENLDPIYKEWPSIG
QYVSACQTIEQALAMGARLENMEIDSMLFVSENALKLASVEAFNSTETLDPIYKEWPNIG
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QYVSACQTIEQALAMGARLENMEVDSMLFVSENALKLASVEAFNSTENLDPIYKEWPNIG
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QYVSACQTIEQALAMGARLENMEVDSMLFVSENALKLASVEAFNSTENLDPIYKEWPSIG
*****.*****.*****.*****.*****

[illegible]

NKNQQILANAFNQAIGNITQAFGKVNDIAIHQTSKGLATVAKALAKVDVVNTQGQALSHL
NKNQQILANAFNQAIGNITQAFGKVNDIAIHQTSQGLATVAKALAKVDVVNTQGQALSHL
NKNQQILANAFNQAIGNITQAFGKVNDIAIHQTSQGLATVAKVLAKVDVVNTQGQALSHL
NKNQQILANAFNQAIGNITQAFGKVNDIAIHQTSQGLATVAKVLAKVDVVNTQGQALSHL
NKNQQILANAFNQAIGNITQAFGKVNDIAIHQTSQGLATVAKALAKVDVVNTQGQALSHL
NKNQQILANAFNQAIGNITQAFGKVNDIAIHQTSQGLATVAKALAKVDVVNTQGQALSHL
NKNQQILANAFNQAIGNITQAFGKVNDIAIHQTSQGLATVAKALAKVDVVNTQGQALSHL
NKNQQILANAFNQAIGNITQAFGKVNDIAIHQTSQGLATVAKALAKVDVVNTQGQALSHL
NKNQQILANAFNQAIGNITQAFGKVNDIAIHQTSQGLATVAKALAKVDVVNTQGQALSHL
NKNQQILANAFNQAIGNITQAFGKVNDIAIHQTSQGLATVAKALAKVDVVNTQGQALSHL
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NKNQQILANAFNQAIGNITQAFGKVNDIAIHQTSQGLATVAKALAKVDVVNTQGQALSHL
NKNQQILANAFNQAIGNITQAFGKVNDIAIHQTSQGLATVAKALAKVDVVNTQGQALSHL
NKNQQILANAFNQAIGNITQAFGKVNDIAIHQTSQGLATVAKALAKVDVVNTQGQALSHL
NKNQQILANAFNQAIGNITQAFGKVNDIAIHQTSQGLATVAKALAKVDVVNTQGQALSHL
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[illegible]

KP981644_CCoV2a_Italy_CB/05
KC175339_CCoV2_Germany_171
KC175340_CCoV2_US,NY_K378
KC175341_CCoV2_US,NY_S378
JQ404410_CCoV2_US,GA_UGA-TN449
JQ404409_CCoV2_US,GA_UGA-1-71
KY063616_CCoV2_China_HLJ071
KY063617_CCoV2_China_HLJ072
KY063618_CCoV2_China_HLJ073
GQ477367_CCoV2_Taiwan_NTU336

GQ152141_FCoV2_Taiwan_NTU156
JQ408981_FCoV2_Hungary_DF2
JN634064_FCoV2_WSU79-1683
DQ010921_FCoV2_WSU79-1146

KP981644_CCoV2a_Italy_CB/05
KC175339_CCoV2_Germany_171
KC175340_CCoV2_US,NY_K378
KC175341_CCoV2_US,NY_S378
JQ404410_CCoV2_US,GA_UGA-TN449
JQ404409_CCoV2_US,GA_UGA-1-71
KY063616_CCoV2_China_HLJ071
KY063617_CCoV2_China_HLJ072
KY063618_CCoV2_China_HLJ073
GQ477367_CCoV2_Taiwan_NTU336
GQ152141_FCoV2_Taiwan_NTU156
JQ408981_FCoV2_Hungary_DF2
JN634064_FCoV2_WSU79-1683
DQ010921_FCoV2_WSU79-1146

[illegible]

Stem Helix (SH)

SH Core

IELPSIIPDYIDINQTVQDILENYPNPWTVPELTLDIFNATYLNLTGEINDLEFRSEKLH
IDLPSIIPDYIDINQTVQDILENYPNPWTVPEFTLDIFNATYLNLTGEIDDLEFRSEKLH
IDLPSIIPDYIDINQTVQDILENFRPNWTVPELPLDIFNATYLNLTGEINDLEFRSEKLH
IDLPSIIPDYIDINQTVQDILENFRPNWTVPELPLDIFNATYLNLTGEINDLEFRSEKLH
IDLPSIIPDYIDINQTVQDILENYPNPWTVPELTLDIFNATYLNLTGEIDDLEFRSEKLH
IDLPSIIPDYIDINQTVQDILENFRPNWTVPELPLDIFNATYLNLTGEINDLEFRSEKLH
IDLPSIIPDYIDINQTVQDILENYPNPWTVPELTLDIFNATYLNLTGEIDDLEFRSEKLH
IDLPSIIPDYIDINQTVQDILENYPNPWTVPELTLDIFNATYLNLTGEIDDLEFRSEKLH
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IDLPSIIPDYIDINQTVQDILENYPNPWTVPELTLDIFNATYLNLTGEIDDLEFRSEKLH
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IDLPSIIPDYIDINQTVQDILENYPNPWTVPELTLDIFNATYLNLTGEIDDLEFRSEKLH
IDLPSIIPDYIDINQTVQDILENYPNPWTVPELTLDIFNATYLNLTGEIDDLEFRSEKLH
IDLPSIIPDYIDINQTVQDILENYEPNPWTVPEFTLDIFNATYLNLTGEIDDLEFRSEKLH
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[illegible]

KP981644_CCoV2a_Italy_CB/05	CGCIGCLGSCCHSICSRRQFENYEPIEKVHVH
KC175339_CCoV2_Germany_171	CGCIGCLGSCCHSICSRRQFENYEPIEKVHVH
KC175340_CCoV2_US,NY_K378	CGCIGCLGSCCHSICSRRQFESYEPIEKVHVH
KC175341_CCoV2_US,NY_S378	CGCIGCLGSCCHSICSRRQFESYEPIEKVHVH
JQ404410_CCoV2_US,GA_UGA-TN449	CGCIGCLGSCCHSICSRRQFENYEPIEKVHVH
JQ404409_CCoV2_US,GA_UGA-1-71	CGCIGCLGSCCHSICSRRQFESYEPIEKVHVH
KY063616_CCoV2_China_HLJ071	CGCIGCLGSCCHSICSRRQFENYEPIEKVHVH
KY063617_CCoV2_China_HLJ072	CGCIGCLGSCCHSICSRRQFENYEPIEKVHVH
KY063618_CCoV2_China_HLJ073	CGCIGCLGSCCHSICSRRQFENYEPIEKVHVH
GQ477367_CCoV2_Taiwan_NTU336	CGCIGCLGSCCHSICSRRQFENYEPIEKVHVH
GQ152141_FCoV2_Taiwan_NTU156	CGCIGCLGSCCHSICSRRQFENYEPIEKVHVH
JQ408981_FCoV2_Hungary_DF2	CGCIGCLGSCCHSICSRRQFYYEPIEKVHVH
JN634064_FCoV2_WSU79-1683	CGCIGCLGSCCHSMCSRRQFENYEPIEKVHVH
DQ010921_FCoV2_WSU79-1146	CGCIGCLGSCCHSICSRRQFENYEPIEKVHVH
	*****: ** **** *****

B

Summary of Amino Acid (AA) Sequence Identity and Similarity between CCoV2 and FCoV2

	NTD	RBD	CTD (KRK)	CTD (KRKYR)	S1 (KRK)	S1 (KRKYR)	S2 (KRK)	S2 (KRKYR)
Total No. of AA	390	268	267	269	960	962	493	491
No. of AA with Identity	127	235	246	247	637	638	464	463
No. of AA with Similarity	229	257	264	265	782	783	485	484
% Identity	32.6%	87.7%	92.1%	91.8%	66.3 %	66.3%	94.1%	94.3%
% Similarity	58.7%	95.9%	98.9%	98.5%	81.6%	81.4%	98.4 %	98.6%

Figure S9. Two CCoV1 Spike Sequences *versus* 10 FCoV1 Spike Sequences

A

	Signal Peptide
KP849472.1_CCoV1_Italy-23/03	MKIVLFITLLSVVSC DEESYEAPNDNPAKFNIS-SNSRFEANMYNFLQTWDIPPGETETS
AY307020.1_CCoV1_Elmo/02	MKIFLLSALLAIANCKDE ---AGPFDDPQHFNSTFSNQRFASMYNFLKSWNIPPDTETI
AAB47503_FCoV1_KU-2	-- MIFIILTLTLLSVAKS EDA----PHGVTLPQFNSTSHNNERFELNFYNFLQTWDIPPNTETI
KX722530_FCoV1_Dutch_cat2	-- MILLILALLSTAKS EDA----PHGVTLPYFNSTSYDNKFKELNFYNFLQTWDIPPNTETI
KX722529_FCoV1_Belgium_UG-FH8	-- MILLLLAILLSIAK CDDA----PNGAILPHFNSTSYNNAKFELNFYNFLQTWNIPPNTETI
KP143512_FCoV1_UK26M	-- MILLLVLF SVVGAHDA----PHGVTLPQFNSTSYNNDKFELNFYNFLQTWDIPPNTETI
MG893511_FCoV1_Germany_Felix	-- MIVLIFAILLSTALS EDA----PQGVTLPPQFNSTSYDNKFKELSFYNFLQTWDIPPNTETI
KY566209_FCoV1_China10	-- MILLLLAFFSVVKS QDA----PHGVTLPQFNSTSHNNDKFELNLFNFLTWDIPPGETETI
FJ938054_FCoV1_Utrecht_UU4	-- MILLLALLS IASSEDA----PHGVTLPHFNTSHNNSKFELNFYNFLQTWDIPPNTETI
DQ848678_FCoV1_C1Je_Kitten_FIP	-- MILLLLAFSVVSS SRDT----PYRVTLPPQFNSTSHNNDKFELNLFNFLTWDIPPSTETI
EU186072_FCoV1_Black	-- MIVLIFALLSTARS EDA----PHGVTLPQFNSTSSNNQKFELNFYNFLQTWDIPPNTETI
AB088222_FCoV1_UCD1	-- MILLIFALFSVVRSEDA ---- PHGVTLPHFNTSYNNPKFELNFYNFLQTWDIPPNTETI
	: : : : . : : : * * * . * : * * : : * * : : * * * * * *
	NTD / S1
KP849472.1_CCoV1_Italy-23/03	FGRVIYHYCQGSVNSNTDCAWYNLRWQPG---SGFKEKFLSSAGLGITNVHGIFYFDVREH
AY307020.1_CCoV1_Elmo/02	LGGYL-PYCGS----SQRCGWINLLGSDKPNANNKKIQYFDSVSMGITDVHGVYFDVREH
AAB47503_FCoV1_KU-2	LGGYL-PYCGA----GVNCGWYNFS--QSVG-QNGKYAYINTQNLNIPNVHGVYFDVREH
KX722530_FCoV1_Dutch_cat2	LGGYL-PYCGN----GVNCGWYNFVYGRPVG-SNGKYAYINTQNLNIPNVHGVYFDVREH
KX722529_FCoV1_Belgium_UG-FH8	LGGYL-PYCGR----GDNCGWYNFVYQSQQG-TYAKYKINTEY-LIPNVHGVYFDVREY
KP143512_FCoV1_UK26M	LGGYL-PYCGT----GANCGWYNFVYQQNVG-SNGKYSYINTQNLNIPNVHGVYFDVREH
MG893511_FCoV1_Germany_Felix	LGGYL-PYCGK----GLNCGWYNFVYQQPVT--DAKYSYINTQNLNIPNVHGVYFDVREH
KY566209_FCoV1_China10	LGGYL-PYCGV----GNNCGWYNFVFSQNVG-SNGKYSYINTQNLNIPNVHGVYFDVREH
FJ938054_FCoV1_Utrecht_UU4	LGGYL-PYCDH----EDNCGWYNFVYNKVG-PNAKYSYINTQNLNIPNVHGVYFDVREH
DQ848678_FCoV1_C1Je_Kitten_FIP	LGGYL-PYCGI----GDNCGWYNFVYKQHDD-IEAKYSYINTQNLNIPNVHGVYFDVREH
EU186072_FCoV1_Black	LGGYL-PYCGD----GPNCGWYNFVYSQNVG-QNGRHSYINTKLNIPNVHGVYFDVREH
AB088222_FCoV1_UCD1	LGGYL-PYCRT ---- GQNCGWYNFVYNHAV -- QNAKYSYINTQNLNIPNVHGVYFDVREH
	: * : * * * * . * . * : : : : * : * * . * * * * :
KP849472.1_CCoV1_Italy-23/03	D-ENNRWETWDRVGLAVTIYGYSSYDLFMILEDGFSDDSLSIIVKICHWTSGNST---SL
AY307020.1_CCoV1_Elmo/02	AADNNQWDDQERVGLAIVYGYSSWYDLYMLHGNNVESGSLSVSVKICHWTHGSINDTKWY
AAB47503_FCoV1_KU-2	--NNDGEWDDRDKVGLLLIAIHGNSKYSLLMVLQDAVEANQPHVAVKICHWK--PGNI---S
KX722530_FCoV1_Dutch_cat2	--NSDGVWDTDRVGLLLIAIHGSAHYSLLMVLQDSVEENQPHFAVKICHWK--PGNI---S
KX722529_FCoV1_Belgium_UG-FH8	GNSDGAWTDMDKVGLLLIAIHGTSHYSLLMVLQDRVEENKPHVAVKICHWK--PGNI---S
KP143512_FCoV1_UK26M	--NSDGVWDPDRVGLLLIAIHGKSQYSLLMVLQDNVEENQPHVAVKICHWK--PGNI---S
MG893511_FCoV1_Germany_Felix	--DADGVWETDRVGLLLIAIHGTSHYSLLMVLQDGVEENQPHVAVKICHWK--PGNI---S
KY566209_FCoV1_China10	--NSDGLWDERDRVGLLLSVHGHKSHYSLLMVLQDAVEANAPDVAVKICNWOHLTGNI---S
FJ938054_FCoV1_Utrecht_UU4	--NSDGVWDQIDRVGLLLIAIHGTSHYSLLMVLQDGVEASQPHVAVKICHWN--PGNI---S
DQ848678_FCoV1_C1Je_Kitten_FIP	--DSDGVWDQDKVGLLLIAIHGNSHYSLLMVLQDGVEDNQPHVAVKICHWK--PSNI---S
EU186072_FCoV1_Black	--NSDGLWDARDRVGLLLIAIYGTSYYSLLMVLQDKVEENQPHVAVKICHWK--PGNI---S
AB088222_FCoV1_UCD1	-- NSDGVWDTDRVGLLLIAIHGESHSYLLMVLQDNVEENQPHVAVKICHWQ -- LGNI ---S
	: * : : * * : : * : * . * : : . : : * * . *
KP849472.1_CCoV1_Italy-23/03	GGNRYNLHIGDTSDCVFNHRFALDSKLITTDIYGFQWTETYINIYLGGTISRVIDNTWD
AY307020.1_CCoV1_Elmo/02	ESNRWDLSQLGTVDPCKFNHQFALDTKLITSDFYGFQWTNTYVNIYLGGTISRVIENTWD
AAB47503_FCoV1_KU-2	SYHAFSVNLGDGGQCQVFNQRFSLDTVLTNDYFGFQWTDYVDIYLGGTITKVWVDNDWS
KX722530_FCoV1_Dutch_cat2	SYHQFNVVEFGDGGQCQVFNRRFSLDTVLTNDYFGFQWTDYVDIYLGGTITKVWIANDWS
KX722529_FCoV1_Belgium_UG-FH8	SYHQFGVDLGDGGQCQVFNRRFSLDTKLITNDYFGFQWTDYVDIYLGGTITKVWIDNDWS
KP143512_FCoV1_UK26M	SIHQFSVNLGDGGQCQVFNQRFSLDTILTNDYFGFQWTNNYVNIYLGGTITKVWVENDWS
MG893511_FCoV1_Germany_Felix	SYHSFTIDFGDGGQCQVFNQRFSLDTKLITNDYFGFQWTNTYVDIYLGGTITKVWVANDWS
KY566209_FCoV1_China10	IYHKWSASLGDGGQCQVFNRRFSLDTVLTANDYFGFQWTDYVDIYLSGTVTKVWIENDWN
FJ938054_FCoV1_Utrecht_UU4	TYHQFDVNLGDGGQCQVFNQRFSLDTVLTANDYFGFQWTDYVDIYLGGTITKVWVNDWS
DQ848678_FCoV1_C1Je_Kitten_FIP	SYHQFNVNLGDVGVCVFNRRFSLDTVLTNDYFGFQWTDYVDIYLGGTITKVWVIGNDWS
EU186072_FCoV1_Black	SYHQFVSNLEDGGQCQVFNQRF--DVTLTANDYFGFQWTDYVDIYLGGTITKVWVNDWS
AB088222_FCoV1_UCD1	SYHQFNLLNLGDGGQCQVFNQRFSLDTVLTANDYFGFQWTDYVDIYLGGTITKVWVDNDWS
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KP849472.1_CCoV1_Italy-23/03
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AAB47503_FCoV1_KU-2
KX722530_FCoV1_Dutch_cat2
KX722529_FCoV1_Belgium_UG-FH8
KP143512_FCoV1_UK26M
MG893511_FCoV1_Germany_Felix
KY566209_FCoV1_China10
FJ938054_FCoV1_Utrecht_UU4
DQ848678_FCoV1_C1Je_Kitten_FIP
EU186072_FCoV1_Black
AB088222_FCoV1_UCD1

KVDVKISSNWNNAKTNYGYVQFVNKTTYTYNNTGGTGVNQLQLGLCEDDFCAGYVTNVF
KVQVKMSPFWSS-LTYGYYFQLVNRTTYIYNNTGGDDVEQLQLIECKNEFCAGFSKNVF
IVEASISYHWN-INYGYMQFVNRTTYAYNNTGGANYTQLQLSECHTDYCYAGYAKNVF
VVESSISYHWNQ-LNYGYIQQFVNRTTYIYNNTGGSNYTHLRLSECHGAYCAGYAKNVF
VVESSISYHWNQ-LNYGYIQQFVNRTTYAYNSTGGSNYTHLQLSECHSEYCYAGYAKNVF
VVESSISYHWSQ-INYGYMQFVNRTTYVYNNTGGANYTHLQLEECHSEYCYAGYAKNVF
VVEASISYHWN-INYGYIQQFVNRTTYTYNNTGGMNYTHLQLEECTSDYCYAGYAKNVF
VVEASISYHWN-INYGYIQQFVNRTTYAYNSTAGSNYTHLQLKECHSDYCYAGYAKNVF
VVEASISSHWN-LNYGYIQQFVNRTTYAYNSTGGSNYTHLQLTECHTDYCYAGYAKNVF
IVEASISYHWNQ-LNYGYIQQFVNRTTYTYNSTAGSNYTHLQLAECTSEYCYAGYAKNVF
SVEASISYHWNQ-LNYGYIQQFVNRTTYTYNNTGGSNYTHLQLAECTSEYCYAGYAKNVF
VVEASISYHWSR-LNYGYMQFVNRTTYIYNNTGGSNYTHLQLQECHSDYCYAGYAKNVF
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KP849472.1_CCoV1_Italy-23/03
AY307020.1_CCoV1_Elmo/02
AAB47503_FCoV1_KU-2
KX722530_FCoV1_Dutch_cat2
KX722529_FCoV1_Belgium_UG-FH8
KP143512_FCoV1_UK26M
MG893511_FCoV1_Germany_Felix
KY566209_FCoV1_China10
FJ938054_FCoV1_Utrecht_UU4
DQ848678_FCoV1_C1Je_Kitten_FIP
EU186072_FCoV1_Black
AB088222_FCoV1_UCD1

TPVNGKIPGDFSFNWFLSDKSTIVQGRVSSQPVYVECLRPVPSWSNNSAIVSFDNDT
TPVNGKIPEDFSFNWFLSDKSTIVQGRVRSQPVYVECLRPVPSWSNNSAIVSFDNDT
VPIDGKIPEDFSFNWFLSDKSTLVQGRVLSQPVFVQCLRPVPSWSNNTAVVHFKNDA
VPIDGKIPESFSFNWFLSDKSTLVQGRILSKQPVFVQCLRPVPLWSNNSAVVYFKNDA
VPIEGKIPESFSFNWFLSDKSTLVQGRVLSKQPVFVQCLRPVPSWSNNTAVVLFNTDS
VPIDGKIPGDFSFNWFLSDKSTLVQGRVLSKQPVFVQCLRAVPSWSNNSAVVHFSNDD
VPVDGKIPESFSFNWFLSDKSTLVQGRVLSKQPVFVQCLRPVPSWSNNSAVVYFTNDS
VPIDGKIPESFSFNWFLSDKSTLVQGRVLSRQPVFVQCLRPVPTWSNNSAVVYFKNDA
VPIDGKIPGDFSFNWFLSDKSTLVQGRVLSQPVFVQCLRPVPTWSNNTAVVHFKNDA
VPIDGKIPESFSFNWFLSDKSTLVQGRVLSKQPVFVHCLRPVPSWSNNSAVVHFSDDP
VPIDGKIPESFSFNWFLSDKSTLVQGRVLSRQPVLVQCLRPVPTWSNNSAVVHFSNDL
VPIDGKIPESFSFNWFLSDKSTLVQGRVLSQPVFVQCLRPVPTLSNNTAVVHFNDV
.*:**** **.*****:****:****: ** *.* ** ** *.:*: * *

KP849472.1_CCoV1_Italy-23/03
AY307020.1_CCoV1_Elmo/02
AAB47503_FCoV1_KU-2
KX722530_FCoV1_Dutch_cat2
KX722529_FCoV1_Belgium_UG-FH8
KP143512_FCoV1_UK26M
MG893511_FCoV1_Germany_Felix
KY566209_FCoV1_China10
FJ938054_FCoV1_Utrecht_UU4
DQ848678_FCoV1_C1Je_Kitten_FIP
EU186072_FCoV1_Black
AB088222_FCoV1_UCD1

FPCQASADVLRFLNLFSGEVFHPNATADDQIIFTFEDNSTAEISCYNGANVTDPTIGFNT
FPCQASADVLRFLNLFSGEVFHPNATADDQIIFTFEDNSTAEISCYNGANVTDPTVGFNT
FCPNVADVLRFLNLFSDTDVYTDSTNDEQLFFTFEDNTTASIACYSSANVTDQFANN
FCHNVTDVLRFLNLFSDTDIYIESTKDDQLHFTFEDNTTASIACYSSANVTDQFANN
YCPNVADVLRFLNLFSDTDVYTESTNDDQLYFTFEDNTTASIACYSSANVTDQFANN
FCPNVTAELVLRFLNLFSDTDVYVASNSDDRLYFTFEDNTTAGVACYSSANITDYKPNNA
FCPNVADVLRFLNLFSDTDVYTNNSNDEQLYFTFEDNTTASIACYSSANVTDQFANN
FCPNVADVLRFLNLFSDTDVYTESTNDDQLYFTFEDNTTASIACYSSANVTDQFANN
FCPNVADVLRFLNLFSDTDVYTESTNDDQLHFTFEDNTTASITCYSSANVTDNQPASGS
FCPGVTAELVLRFLNLFSDTDVYTESTSDQLHFTFEDNTTASIACYSSANVTDNQPDNT
YCPGVTAELVLRFLNLFSDTDVYTDLTNDQFYFTFEDNTTASIACYSSANVTDQFANN
FCPNVADVLRFLNLFSDTDVYTA-NDQLYFTFEDNTTASIACYSSANVTDNQPANNS
:* .:.*:***** ** .: . :.: *****:.* :*:.* *.*

NTD ←

KP849472.1_CCoV1_Italy-23/03
AY307020.1_CCoV1_Elmo/02
AAB47503_FCoV1_KU-2
KX722530_FCoV1_Dutch_cat2
KX722529_FCoV1_Belgium_UG-FH8
KP143512_FCoV1_UK26M
MG893511_FCoV1_Germany_Felix
KY566209_FCoV1_China10
FJ938054_FCoV1_Utrecht_UU4
DQ848678_FCoV1_C1Je_Kitten_FIP
EU186072_FCoV1_Black
AB088222_FCoV1_UCD1

TSQIPFGGTADPYLCFVNFAALDNQFLGILPPTIREMAFGRDGSIFVNGYKYFSLPPI
TSQIPFGSTDDPYLCFANFSTAALDNQFLGILPPTVREMAFGRDGSIFVNGYKYFSLPPI
VSHIPFGKT--AHFCFANFSSHVSQRQFLGILPPTVREFAFGRDGSIFVNGYKYFSLPAI
VSHIPFGKT--AYFCFATFSSHVSQRQFLGILPPTVREFAFGRDGSIFVNGYKYFSLPPI
ASHIPFGKTMHSYFCFANFSSHVSQRQFLGILPPTVREFAFGRDGSIFVNGYKYFSLPPI
SAQIPFGKTHSYFCFANFSSSHV-TQFLGILPPTVREFAFGRDGSIFVNGYKYFSLPPI
NSHIPFGTTAQSYFCFANFSSNAVARQFLGILPPTVREFAFGRDGSIFVNGYKYFSLPPI
VSHVPFGKTEHSYFCFANFSSHVSQRQFLGILPPTVREFAFGRDGSIFVNGYKYFSLPPI
ISHTPFVS--NSYLCFANFSSHVSQRQFLGILPPTVREFAFGRDGSIFVNGYKYFSLQPI
LSDIPFGKITHSYLCFANFSSNAPVSMQFLGILPPTVREFAFGRDGSIFVNGYKYFSFPPI
VSHIPLGKTRHSYFCFANFSSHVSQRQFLGILPPTVREFAFGRDGSIFVNGYKYFSLPPI
TSHIPFGKTMHSYFCFANFSSNS-MVRQFLGILPPTVREFAFGRDGSIFVNGYKYFSLPPI
.. *: :****.* : : *.***** :*:***:***:*.*****: *

Proposed RBD / S1

KP849472.1_CCoV1_Italy-23/03
AY307020.1_CCoV1_Elmo/02
AAB47503_FCoV1_KU-2
KX722530_FCoV1_Dutch_cat2
KX722529_FCoV1_Belgium_UG-FH8
KP143512_FCoV1_UK26M
MG893511_FCoV1_Germany_Felix
KY566209_FCoV1_China10
FJ938054_FCoV1_Utrecht_UU4
DQ848678_FCoV1_C1Je_Kitten_FIP
EU186072_FCoV1_Black
AB088222_FCoV1_UCD1

KSINFAISAVEYYGFWTIAYTKYTDVMVDVNGTSITRLFYCDSPINRIKCQQLKHELDPG
KSINFAISAVEYYGFWTIAYTKYTDVMVDVNGTSITRLFYCDSPINRIKCQQLKHELDPG
RSVNFSISSVEEYGFWTIAYTNYTDVMVDVNGTAITRLFYCDSPINRIKCQQLKHELDPG
KSVNFSISSVEYQGFWTIAYTNYTDVMVDVNGTGITRLFYCDSPINRIKCQQLKHELDPG
KSVNFSISSVEYQGFWTIAYTNYTDVMVDVNGTVITRLFYCDSPINRIKCQQLKHELDPG
KSVNFSISSVENFGFWTIAYTNYTDVMVDVNGTGITRLFYCDSPINRIKCQQLKHELDPG
KSVNFSISSIQRGFWTIAYTNYTDVMVDVNGTGITRLFYCDSPINRIKCQQLKHELDPG
KSVNFSISSVEYQGFWTIAYTNYTDVMVDVNGTSITRLFYCDSPINRIKCQQLKHELDPG
KSVNFSISSVENYGFWTIAYTNYTDVMVDVNGTVITRLFYCDSPINRIKCQQLKHELDPG
KSVNFSISSVENYGSWTIAYTNYTDVMVDVNGTGITRLFYCDSPINRIKCQQLKHELDPG
KSVNFSISSVEYQGFWTIAYTNYTDVMVDVNGTGISRLFYCDSPINRIKCQQLKHELDPG
KSVNFSIGSVEQHGFWTIAYTNYTDVMVDVNGTGITRLFYCDSPINRIKCQQLKHELDPG
*:***:*.:.: . * *****:*****:*** *.* ** *.* ** *.*

RBD
55T
27I
42S

60T
39I
53S

KP849472.1_CCoV1_Italy-23/03	FYSANSLVKKNLPKTFVTTPOFYNGMNVTLHVILNDTSAGTKVVGFFERYELEQIADILFE	
AY307020.1_CCoV1_Elmo/02	FYSANSLVKKDLPKTFVTTPOFYNNMNVTLHVILNDTEADYKVVGFFERYELEKIADIHFE	
AAB47503_FCoV1_KU-2	FYSASMLVKKDLPKTFVTMPQFYHWMNVTLHVVLNDTEKKYDIIILAKAPELAALADVHFE	
KX722530_FCoV1_Dutch_cat2	FYSASMLVKKDLPKTFVTMPQFYNNMNVTLHVVLNDTEKKPDIIILAKAPELASLADIHFE	
KX722529_FCoV1_Belgium_UG-FH8	FYSASMLVKKDLPKTFVTMPQFYNNMNVTLHVVLNDTEKKQDIIILAKASELASLADIHFE	
KP143512_FCoV1_UK26M	FYSASMLVKKDLPKTFVTMPQFYNNMNVTLHVVLNDTEKKADIIILAKASELASLADVHFE	
MG893511_FCoV1_Germany_Felix	FYSASTLVKKDLPKTFVTMPQFYNNMNVTLHVVLNDTQKGANIIILSKAAELASLADIHFE	
KY566209_FCoV1_China10	FYSASTLVKKDLPKTFVTMPQFYNNMNVTLHVVLNDTEKKEDIIILAKAPELLSLADIHFE	
FJ938054_FCoV1_Utrecht_UU4	FYSASMLVKKDLPKTFVTMPQFYNNMNVTLHVVLNDIEKKADIIILAGAPELASLADIHFE	
DQ848678_FCoV1_C1Je_Kitten_FIP	FYSASALVKKDLPKTFVIMPQFYNNMNVTLHVVLNDTAKGADIIILAKAPELASLADVHFE	RBD
EU186072_FCoV1_Black	FYSASMLVKNLDPKTFVTMPQFYNNMHITLHVVLNDTAKKEDIIILAKAPELASLADVHFE	60T
AB088222_FCoV1_UCD1	FYAASMLVKKDLPKTFVTMPQFYNNMTVTLHVVLNDTEKKADIIILAKAPELASLADIHFE	30I
	.:. ***.:** ****. * :****:*** . : ** :*: **	41S

KP849472.1_CCoV1_Italy-23/03	IPQNQDGEVKNVTNFCVQTRQLAFFFKYTSLQGLYSISNTVWLKNYDCFPSPQQFNYYLQ	
AY307020.1_CCoV1_Elmo/02	IPQDKNGGVKNVTNFCVQTRQLAFFFKYTSLQGLYSISNTVWLKNYDCFPSPQQFNYYLQ	
AAB47503_FCoV1_KU-2	IAQA-NGSVTNVTSLCVQARQLALFYKYTSLQGLYTYSNLVELQNYDCFPSPQQFNYYLQ	
KX722530_FCoV1_Dutch_cat2	VAQS-NGSVTNVTSICVQTRQLALFYKYTSLQGLYTYSNLVELQNYDCFPSPQQFNYYLQ	
KX722529_FCoV1_Belgium_UG-FH8	IAQA-NGSVTNVTSLCIQARQLALFYKYTSLQGLYTYSNLVEVQNHDCFPSPQQFNYYLQ	
KP143512_FCoV1_UK26M	IAQA-NGSVVNATSLCVQTRQLALFYKYTSLQGLYTYSNLVELQNYDCFPSPHQFNYYLQ	
MG893511_FCoV1_Germany_Felix	IDRA-DGSVTNVTSLCVQTRQLALFYKYTSLQGLYTYSNLVELQNYDCFPSPQQFNYYLQ	
KY566209_FCoV1_China10	IAQA-NGSVTNVTSVCVQARQVALFYKYTSLQGLYTYSNLVELQNYDCFPSPQQFNYYLQ	
FJ938054_FCoV1_Utrecht_UU4	IAQA-NGSVVNVTSLCVQARQLALFYKYTSLQGLYTYSNLQNYDCFPSPQQFNYYLQ	
DQ848678_FCoV1_C1Je_Kitten_FIP	IAQA-NGSVANLTSLCVQTRQLALFYKYTSLQGLYTYSNLIELQNYDCFPSPQQFNYYLQ	RBD
EU186072_FCoV1_Black	ILQA-NGSVVNVTSLCVQAKQLALFYKYTSLQGLYTYSNLVELQNYDCFPSPQHFNNYYLQ	60T
AB088222_FCoV1_UCD1	IVQA-NGSVANVTSLCVQTRQIALFYKYTSLSQSLYTYSNLVELQNYDCFPSPQQFNYYLQ	32I
	: : :* * * * ..*:*:*:*:*****.**: * : :*:*****:*****	51S

KP849472.1_CCoV1_Italy-23/03	FETLCFDTNPSVAGCKWAVMHSPWIWNTQFATITVTYKEGAQITTMPK-PQLGFRDVSFKV	
AY307020.1_CCoV1_Elmo/02	FETLCFDTNPSVAGCKWAIMHSPWIWNTQFATITVTYKDGAAQITTMPK-PQLGFRDISFKV	
AAB47503_FCoV1_KU-2	FETLCFDVNPVAVAGCKWSLVHDVQWRTQFATITVSYKHGSMITTHAKGHSWGFGQDTSVLV	
KX722530_FCoV1_Dutch_cat2	FETLCFDVNPVAVAGCKWSLVHDTRWRTQFATITVSYKEGSMITTMPK-SQLGFGDISVLV	
KX722529_FCoV1_Belgium_UG-FH8	FETLCFDVNPVAVAGCKWSLVHDNIWRTQFATITVSYKEGAMITTMPK-AQLGFGDISVLV	
KP143512_FCoV1_UK26M	FETLCFDTSPVAVAGCKWSLVHDVWRWRTQFATITISYKDGAKITTMPK-AKLGFQDISNIV	
MG893511_FCoV1_Germany_Felix	FETLCFDVNPVAVAGCKWSLVHDSIWHRTQFATITVSYKEGARITTMPK-AQIGFGDISNLV	
KY566209_FCoV1_China10	FETLCFDVSPVAVAGCKWSLVHDNKWRTQFATITVSYKEGSMITTMPK-PQLGFGDISNLV	
FJ938054_FCoV1_Utrecht_UU4	FETLCFDVSPVAVAGCKWSLVHDVWKWRTQFATITVSYKDGAMITTMPK-AQLGFGDISNIV	
DQ848678_FCoV1_C1Je_Kitten_FIP	FETLCFDVSPVAVAGCKWALVHDYNWRTQFATITVSYKEGAMITTMPK-AQLGFGDISKL	RBD
EU186072_FCoV1_Black	FETLCFDVNPVAVAGCKWSLVHDVNWRTQFATITVSYKDGAMITTMPK-AQLGFGDISNLV	46T
AB088222_FCoV1_UCD1	FETLCCLDTNPVAVAGCKWALVHDVWKWRTQFATITVSYKDGAMITTMPK-AQLGFGDISNLV	28I
	*****:..* *****:..* .*****:..*.*: * * . **:* * *	40S

Proposed RBD

RBD Total (T): 281 aa

Identity (I): 156 / 281 = 55.5%

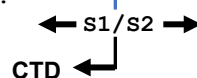
Similarity (S): 227 / 281 = 80.8%

KP849472.1_CCoV1_Italy-23/03	EGECTDYNIIYGFQGTGIIIRKTESKLVAGLFYTSASGDLLAFKNSTTGEIFTVVPCLDLTAQ	
AY307020.1_CCoV1_Elmo/02	EGECTDYNIIYGFQGTGIIIRKTESKLVAGLFYTSASGDLLAFKNSTTGEIFTVVPCLDLTAQ	
AAB47503_FCoV1_KU-2	KDECTDYNIIYGFQGTGIIIRNTTSRLVAGLYYTSISGDLLAFKNSTTGEIFTVVPCLDLTAQ	
KX722530_FCoV1_Dutch_cat2	KDECTDYNIIYGFQGTGIIIRNTTSRLVAGLYYTSISGDLLAFKNSTTGEIFTVVPCLDLTAQ	
KX722529_FCoV1_Belgium_UG-FH8	KDECTDYNIIYGFQGTGIIIRNTTSRLVAGLYYTSISGDLLAFKNSTTGEIFTVVPCLDLTAQ	
KP143512_FCoV1_UK26M	KDECTDYNIIYGFQGTGIIIRNTTTRIVAGLYYTSIIIGDLLAFKNSTTGEIFTVVPCLDLTAQ	
MG893511_FCoV1_Germany_Felix	KDECTDYNIIYGFHGTGIIIRPTTSRLVAGLYYTSISGDLLAFKNSTTGEIFTVVPCLDLTAQ	
KY566209_FCoV1_China10	KDECTDYNIIYGFQGTGIIIRNTTSRLVAGLYYTSISGDLLAFKNSTTGEIFTVVPCLDLTAQ	
FJ938054_FCoV1_Utrecht_UU4	KDECTDYNIIYGFQGTGIIIRNTTSRLVAGLYYTSASGDLLGFKISTTGEIFTVVPCLDLTAQ	
DQ848678_FCoV1_C1Je_Kitten_FIP	KDECTDYNIIYGFQGTGIIIRKTTTSRLVAGLYYTSISGDLLAFKNSTTGEIFTVVPCLDLTAQ	
EU186072_FCoV1_Black	KDECTDYNIIYGFQGTGIIIRSTTSRLVAGLYYTSISGDLLAFKNSTTGEIFTVVPCLDLTVL	
AB088222_FCoV1_UCD1	KDECTDYNIIYGFHGTGIIIRNTTSRLVAGLYYTSISGDLLAFKNSTTGEIFTVVPCLDLTAQ	
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→ CTD / S1

KP849472.1_CCoV1_Italy-23/03
AY307020.1_CCoV1_Elmo/02
AAB47503_FCoV1_KU-2
KX722530_FCoV1_Dutch_cat2
KX722529_FCoV1_Belgium_UG-FH8
KP143512_FCoV1_UK26M
MG893511_FCoV1_Germany_Felix
KY566209_FCoV1_China10
FJ938054_FCoV1_Utrecht_UU4
DQ848678_FCoV1_C1Je_Kitten_FIP
EU186072_FCoV1_Black
AB088222_FCoV1_UCD1

AAVINDEIVGAITSINQTDLFEFVNHTHTV**RRVRR**AVQTGTTITAYSMPQFYYITKWNND
AAVINDEIVGAITSINQTDLFEFVNHTHTV**RRARR**AVQTGTTITAYSMPQFYYITKWNND
VAVINDEIVGAITAVNQTDLFEFVNNTQ**ARRSR**---STPNFVTSYTMPQFYYITKWNND
AAVINDEIVGVITSVNQTDLFEFVNHTST**RRSRI**--AAVPQAATYTMPQFYYITKWNND
AAVINDEIVGAITAVNQTDLFEFVNHTQV**KRLRR**--S-TPETVQTYTMPQFYYITKWNND
AAVINDEIVGVITAVNQTDLFEFVNHTQ**RGARR**--STGSQTVQTYTMPQFYYITKWNND
AAVINDEIVGAITAVNQTDLFEFVNHTSH**RRSRR**--E--VPTVQTYTMPQFYYITKWNND
AAVINDEIVGAITAVNQTDLFEFVNHTHT**RRSRR**--S-PTEAVKTYTMPQFYYITKWNND
AAVINDEIVGAITATNQTDLFEFVNHTWS**RSARG**--SS-PSTVNTYTMPQFYYITKWNNG
AAVINDEIVGVITAVNQTDLFEFVNHTQ**PQRSR**--SANPTTVQTYTMSQFYYITKWNND
AAVINDEIVGAITSVNQTDLFEFFNHTQ**KRSRR**--PT-SHSVTTYNMPQFYYITRWNNND
AAVINDEIVGVITAVNQTDLFEFVNHTS**RRSRG**--ST-STSVTTYTMPQFYYITKWNND
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KP849472.1_CCoV1_Italy-23/03
AY307020.1_CCoV1_Elmo/02
AAB47503_FCoV1_KU-2
KX722530_FCoV1_Dutch_cat2
KX722529_FCoV1_Belgium_UG-FH8
KP143512_FCoV1_UK26M
MG893511_FCoV1_Germany_Felix
KY566209_FCoV1_China10
FJ938054_FCoV1_Utrecht_UU4
DQ848678_FCoV1_C1Je_Kitten_FIP
EU186072_FCoV1_Black
AB088222_FCoV1_UCD1

TSENCTSVITYSSFAICNTGEIKFVNVTKEAVEDGIGTVKPISTGNITIPKNFTVAVQA
TSENCTSVITYSSFAICNTGEIKYVNVTHVEIVDDSIGVIKPVSTGNISIPKNFTVAVQA
TSSNCTSAITYSSFAICNTGEIKYVNVTHVEIVDDSIGVIKPVSTGNISIPKNFTVAVQA
TSTNCTSVITYSSFAICNTGEIKYVNVTHVEV-----VVKPVSTGNITIPKNFTVAVQA
TSTNCTSVITYSSFAICNTGEIKYVNVTKVEIVDDSIGVIKPVSTGNISIPKNFTVAVQA
SSTNCTSVITYSSFAICNTGEIKYVNVTHVEIVDDSIGVIKPISTGNIFIPKNFTVAVQA
TSTNCTSVITYSSFAICNTGEIKYVNVTKVEVDDSIGVIKPISSGNISIPKNFTVAVQA
TSTNCTSVITYSSFAICNTGEIKYVNVTHVETVDDNIGVIRPISTGNISIPKNFTVAVQA
TSSNCTSVITYSSFAICNTGEIKYVNVTHVEIVDDSVGIKPVSTGNITIPKNFTVAVQA
TSTNCTSVITYSSFAICNTGEIKYVNVTHVETVDDSIGVIKPISTGNISIPKNFTVAVQA
TSTNCTSVITYSSFAICNTGEIKYVNVTHVETVDD-IGVIKPISTGNILIPKNFTVAVQA
TSTNCTSVITYSSFAICNTGEIKYV-----DDSIGVIKPISTGNISIPKNFTVAVQA
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KP849472.1_CCoV1_Italy-23/03
AY307020.1_CCoV1_Elmo/02
AAB47503_FCoV1_KU-2
KX722530_FCoV1_Dutch_cat2
KX722529_FCoV1_Belgium_UG-FH8
KP143512_FCoV1_UK26M
MG893511_FCoV1_Germany_Felix
KY566209_FCoV1_China10
FJ938054_FCoV1_Utrecht_UU4
DQ848678_FCoV1_C1Je_Kitten_FIP
EU186072_FCoV1_Black
AB088222_FCoV1_UCD1

EYIQIQVKPVVVDCAKYVCNGNHNHCLNLLTQYTSACQNIENALNLGARLESMLNEMITV
EYIQIQVKPVVVDCAKYVCNGNHNHCLNLLTQYTSACQNIENALNLGARLESMLNEMITV
EYIQIQVKPVVVDCAKYVCNGNTHCLNLLTQYTSACQTIENALNLGARLESMLNEMITV
EYIQIQVKPVVVDCAKYVCNGNTHCLNLLTQYTSACQTIENALNLGARLESMLNEMITV
EYIQIQVKPVVVDCAKYVCNGNTHCLNLLTQYTSACQTIENALNLGARLESMLNEMITV
EYIQIQVKPVVVDCAKYVCNGNTHCLNLLTQYTSACQTIENALNLGARLESMLNEMITV
EYIQIQVKPVVVDCAKYVCNGNTHCLNLLTQYTSACQTIENALNLGARLESMLNEMITV
EYVQIQVKPVVVDCAKYVCNGNTHCLNLLTQYTSACQTIENALNLGARLESMLNEMITV
EYFQIQVKPVVVDCAKYVCNGNTHCLNLLTQYTSACQTIENALNLGARLESMLNEMITV
EYIQIQVKPVVVDCAKYVCNGNTHCLNLLTQYTSACQTIENALNLGARLESMLNEMITV
EYIQIQVKPVVVDCAKYVCNGNTHCLNLLTQYTSACQTIENALNLGARLESMLNEMITV
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Peptide Fusion (FP)

FP Core

KP849472.1_CCoV1_Italy-23/03
AY307020.1_CCoV1_Elmo/02
AAB47503_FCoV1_KU-2
KX722530_FCoV1_Dutch_cat2
KX722529_FCoV1_Belgium_UG-FH8
KP143512_FCoV1_UK26M
MG893511_FCoV1_Germany_Felix
KY566209_FCoV1_China10
FJ938054_FCoV1_Utrecht_UU4
DQ848678_FCoV1_C1Je_Kitten_FIP
EU186072_FCoV1_Black
AB088222_FCoV1_UCD1

SDSSLELATIEKFNTTVVGGEKLGGIYFDGLKDVLPAPGG**RS**AIEDLLFNKVVTSGLGT
SDSSLELATIEKFNTTVVGGEKLGGIYFDGLKDVLPAPGG**RS**AIEDLLFNKVVTSGLGT
SDRGLELATVERFNATALGGEKLGGLYFDGLSSLLPPKIG**KRS**AVEDLLFNKVVTSGLGT
SYRSLELATVEKFNTTVVGGEKLGGLYFDGLRALLPPTIG**KRS**AVEDLLFNKVVTSGLGT
SDRSLELATVEKFNTTVVGGEKLGGLYFDGLSSLLPPKIG**KRS**AVEDLLFNKVVTSGLGT
SDRSLELATVEKFNTTVLGAELGGLYFDGLRELLPPTIG**KRS**AIEDLLFNKVVTSGLGT
SDRSLELATVEKFNTTVLGAELGGLYFDGLSSFLPPRIG**KRS**AIEDLLFNKVVTSGLGT
SDRSLELANVEKFNTTVLGAELGGLYFDGLRELLPPTIG**KRS**AVEDLLFNKVVTSGLGT
SDRSLEFATVDKFNNTALGGEKLGGLYFDGLSSLLPPRVGM**RS**AVEDLLFNKVVTSGLGT
SDRSIQLATVEKFNTTVLGAELGGLYFDGLKSLPPRIG**KRS**AVEDLLFDKVVTSGLGT
SDRSLELATIEKFNTATGGVKLGGLYFDGLSSLLPPKIGV**RS**AVEDLLFNKVVTSGLGT
SSRSLELATVERFNATAPGGEKLGGLYFDGLSSLLPPRVG**QRS**AVEDLLFNKVVTSGLGT
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S2'

KP849472.1_CCoV1_Italy-23/03
AY307020.1_CCoV1_Elmo/02
AAB47503_FCoV1_KU-2
KX722530_FCoV1_Dutch_cat2
KX722529_FCoV1_Belgium_UG-FH8
KP143512_FCoV1_UK26M
MG893511_FCoV1_Germany_Felix
KY566209_FCoV1_China10
FJ938054_FCoV1_Utrecht_UU4
DQ848678_FCoV1_C1Je_Kitten_FIP
EU186072_FCoV1_Black
AB088222_FCoV1_UCD1

VDE DYKKCSAGT DIADLVCAQYYNGVMVLPGVVDDNKMMY TASLIGGMAMGSITS AVAI
VDE DYKKCSAGT DIADLVCAQYYNGVMVLPGVVDDNKMMY TASLIGGMAMGSITS AVAI
VDD DYKKCSSGT DVADLVCAQYYNGIMVLPGVVDGNKMSMY TASLIGGMALGSITS AVAV
VDD DYKKCSSGT DVADLVCAQYYNGIMVLPGVVDGNKMSMY TASLIGGMALGSITS AVAV
VDD DYKKCSAGT DVADLVCAQYYNGIMVLPGVVDDNKMMY TASLIGGMAMGSITS AVAV
VDD DYKKCSAGT DVADLVCAQYYNGIMVLPGVVDQNKMSMY TASLIGGMALGSITS AVAV
VDD DYKKCSSG IDVADLVCAQYYNGIMVLPGVVDDNKMMY TASLIGGMAMGSITS AVAV
VDD DYKKCSSGT DVADLVCAQYYNGIMVLPGVVDQNKMMY TASLIGGMAMGSITS AVAV
VDD DYKKCSAGT DVADLVCAQYYNGIMVLPGVVDQNKMMY TASLIGGMALGSITS AVAV
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VDD DYKKCSAGT DVADLVCAQYYNGIMVLPGIVDGNKMAMY TASLIGGMALGSITS AVAV
VDD DYKKCSAGT DVADLVCAQYYNGIMVLPGVVDGNKMMY TASLIGGMALGSITS AVAV
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KX722530_FCoV1_Dutch_cat2
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MG893511_FCoV1_Germany_Felix
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FJ938054_FCoV1_Utrecht_UU4
DQ848678_FCoV1_C1Je_Kitten_FIP
EU186072_FCoV1_Black
AB088222_FCoV1_UCD1

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KX722529_FCoV1_Belgium_UG-FH8
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MG893511_FCoV1_Germany_Felix
KY566209_FCoV1_China10
FJ938054_FCoV1_Utrecht_UU4
DQ848678_FCoV1_C1Je_Kitten_FIP
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AB088222_FCoV1_UCD1

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SALT KIQSVVNQQGNALSQ L TQQLQNNFQAISSSIAEIYNRLEKVEADAQVDR LITGR L A
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LALT KIQSVVNQQGEALSQ L TSQLQKNFQAISSSIAEIYNRLEKVEADAQVDR LITGR L A
SALT KIQSVVNQQGEALSQ L TSQLQKNFQAISSSIAEIYNRLEKVEADAQVDR LITGR L A
SALT KIQSVVNQQGEALSQ L TSQLQNNFQAISSSIAEIYNRLEKVEADAQVDR LITGR L A
SALT KIQSVVNQQGEALSQ L TSQLQKNFQAISSSIAEIYNRLEKVEADAQVDR LITGR L A
SALT KIQSVVNQQGEALSQ L TSQLQKNFQAISSSIAEIYNRLEKVEADAQVDR LITGR L A
SALT KIQSVVNQQGEALSQ L TSQLQKNFQAISSSIAEIYNRLEKVEADAQVDR LITGR L A
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AAB47503_FCoV1_KU-2
KX722530_FCoV1_Dutch_cat2
KX722529_FCoV1_Belgium_UG-FH8
KP143512_FCoV1_UK26M
MG893511_FCoV1_Germany_Felix
KY566209_FCoV1_China10
FJ938054_FCoV1_Utrecht_UU4
DQ848678_FCoV1_C1Je_Kitten_FIP
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AB088222_FCoV1_UCD1

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ALNAYVAQTLTQYTEVKASRQLAMEKVNCEVKSQSDRYGFCGNGTHLFS LANAAPDGLLF
ALNAYVSQLTQYAEVKASRQIALEKVNCEVKSQSNRYGFCGNGTHLFS LVNSAPDGLLF
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KX722529_FCoV1_Belgium_UG-FH8
KP143512_FCoV1_UK26M
MG893511_FCoV1_Germany_Felix
KY566209_FCoV1_China10
FJ938054_FCoV1_Utrecht_UU4
DQ848678_FCoV1_C1Je_Kitten_FIP
EU186072_FCoV1_Black
AB088222_FCoV1_UCD1

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Stem Helix (SH)
SH Core

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 FJ938054_FCoV1_Utrecht_UU4
 DQ848678_FCoV1_C1Je_Kitten_FIP
 EU186072_FCoV1_Black
 AB088222_FCoV1_UCD1

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 KP143512_FCoV1_UK26M
 MG893511_FCoV1_Germany_Felix
 KY566209_FCoV1_China10
 FJ938054_FCoV1_Utrecht_UU4
 DQ848678_FCoV1_C1Je_Kitten_FIP
 EU186072_FCoV1_Black
 AB088222_FCoV1_UCD1

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 LNLTAEIDELQVRADNLTVIAHNLQEYIDNLNKTLDVLEWLNRIETYVKWPWYVWLLIGL
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 MG893511_FCoV1_Germany_Felix
 KY566209_FCoV1_China10
 FJ938054_FCoV1_Utrecht_UU4
 DQ848678_FCoV1_C1Je_Kitten_FIP
 EU186072_FCoV1_Black
 AB088222_FCoV1_UCD1

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 VVVFICIPLLLFCCCLSTGCCGCGFCGLGSCCHSLCRRQFESYEPIEKVHIH
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B

Summary of Amino Acid (AA) Sequence Identity and Similarity between CCoV1 and FCoV1

	NTD	RBD	CTD (CCoV1)	CTD (FCoV1)	S1 (CCoV1)	S1 (FCoV1)	S2 (CCoV1)	S2 (FCoV1)
Total No. of AA	435	281	88	86	800	798	675	677
No. of AA with Identity	150	156	58	58	375	375	496	496
No. of AA with Similarity	253	227	71	71	567	567	603	603
% Identity	34.5%	55.5%	65.9%	67.4%	46.9%	47.0%	73.5%	73.3%
% Similarity	54.2%	80.8%	80.7%	82.6%	70.9%	71.0%	89.3%	89.1%

Figure S10

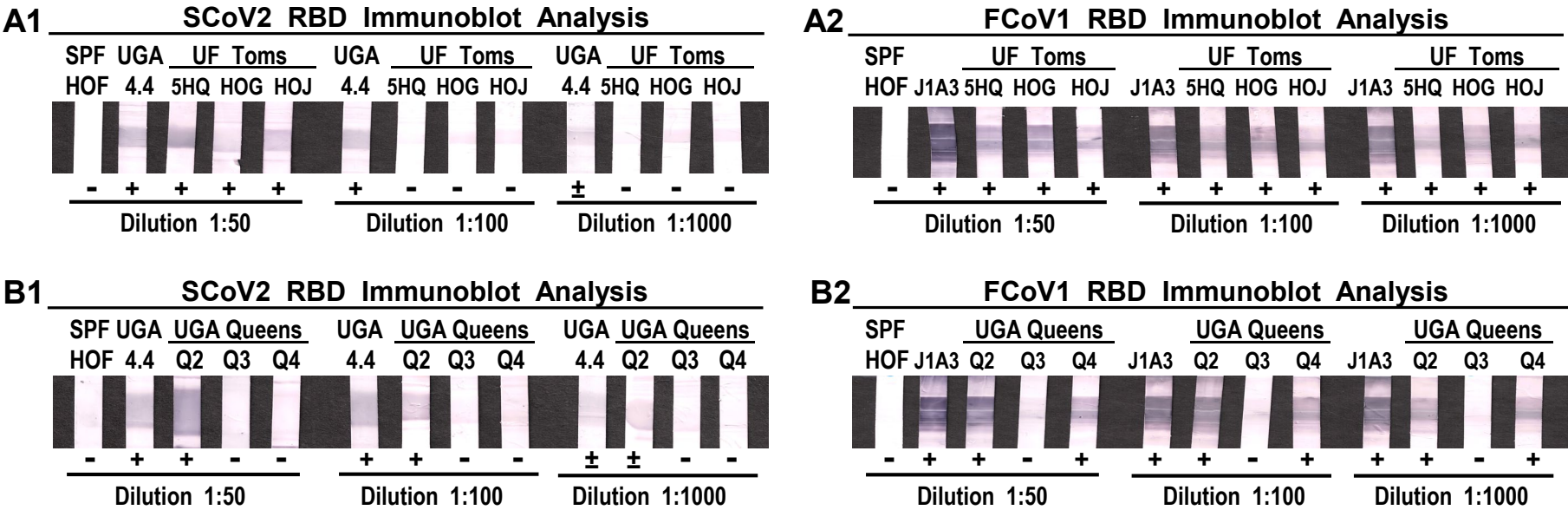


Figure S11

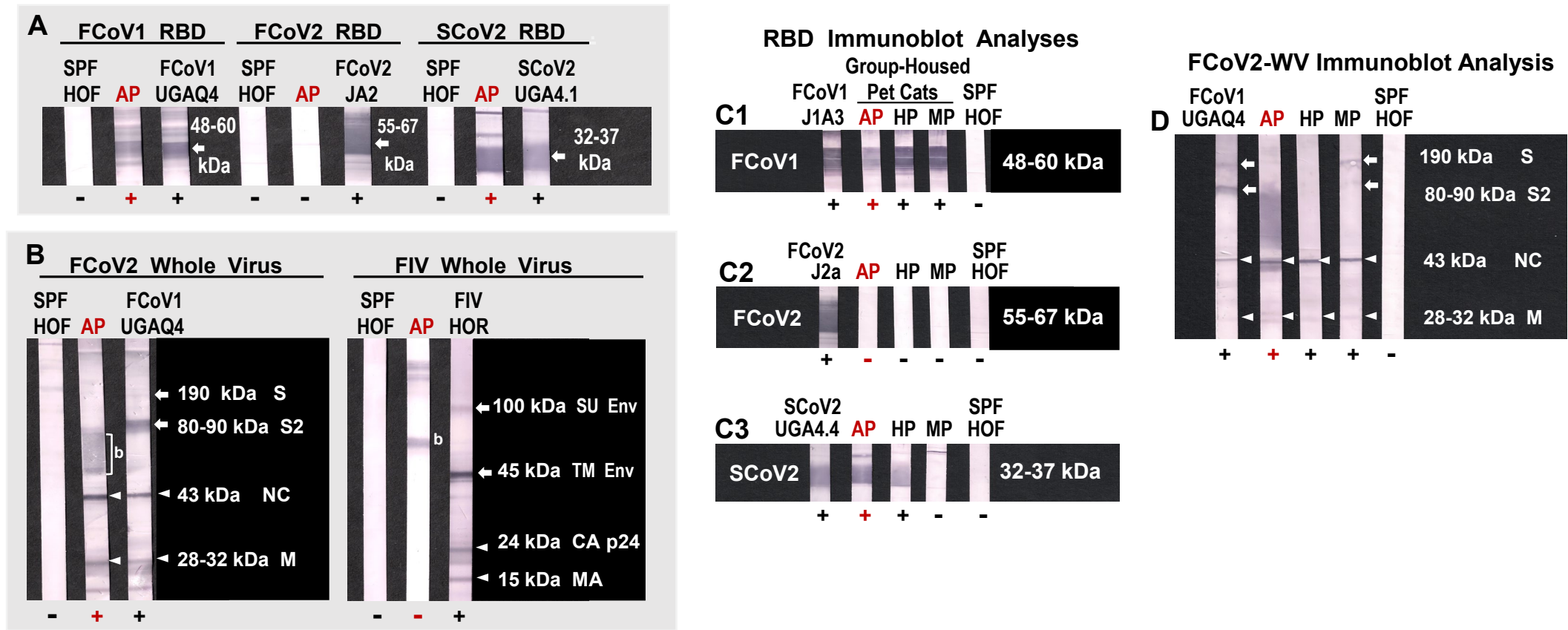


Table S1.
CD8⁺ CTL and CD4⁺ T_H Epitopes on SCoV2 UF-RBD and UF2-RBD *

U.S. Population / Race*	HLA-A/B Supertype / DRB1 Lineage	Allele / Allotype *	UF-RBD	UF2-RBD	
			No. of CTL / T _H Epitope †‡	No. of CTL / T _H Epitope †‡	N/C Extended Seq Epitope §
Both	A1	A*0101	1	1	0
Caucasian	A1	A*3201	3	3	0
Black	A1	A*3001	3	5	1N+1C
Both	A2	A*0201	1	1	0
Caucasian	A2	A*0205	2	2	0
Black	A2	A*6802	3	3	0
Both	A3	A*0301	4	8	3N+1C
Caucasian	A3	A*1101	5	9	3N+1C
Black	A3	A*7401	4	6	2N
HLA-A Subtotal:			26	39	9N+3C
Both	B7	B*0702	1	2	1C
Caucasian	B7	B*5101	1	1	0
Black	B7	B*5301	2	2	0
Caucasian	B44	B*4402	1	1	0
Caucasian	B44	B*4001	2	2	0
Black	B44	B*4501	1	2	1N
Both	B44	B*4403	1	1	0
Caucasian	B27	B*2705	3	4	1N
Both	B27	B*1402	4	5	1N
Black	B27	B*1503	5	5	0
Caucasian	B27	B*3901	2	3	1N
HLA-B Subtotal:			23	28	4N+1C
HLA-A+HLA-B Total:			49	67	13N+4C
Both	DRB1*04	0401	0	0	0
Caucasian	DRB1*04	0404	0	0	0
Caucasian	DRB1*04	0402	1	1	0
Black	DRB1*04	0405	7	7	0
Both	DRB1*15	1501	4	4	0
Both	DRB1*07	0701	1	1	0
Both	DRB1*03	0301	0	0	0
Both	DRB1*13	1301	6	6	0
Both	DRB1*13	1302	0	0	0
Both	DRB1*01	0101	7	7	0
Caucasian	DRB1*01	0103	0	0	0
Both	DRB1*11	1101	13	13	0
Both	DRB1*08	0801	6	6	0
HLA-DRB1 Total:			45	45	0

* Top 2-3 alleles or allotypes for U.S. Caucasian and Black populations according to the survey in the Allele Frequencies in Worldwide Populations database: <http://www.allele-frequencies.net/hla6006a.asp>
Each individual has two HLA-A alleles, two HLA-B alleles, and two HLA-DRB1 alleles. The person will be protected the most if he/she has HLA-A and HLA-B alleles that can express allotypes which recognize many CD8⁺ T-cell (cytotoxic T lymphocyte, CTL) epitopes.

† CD8⁺ T-cell/CTL epitopes derived from NetMHCpan 4.1 server using 9mer peptide as the core.

<https://services.healthtech.dtu.dk/service.php?NetMHCpan-4.1>

CD4⁺ T-cell (T-helper, T_H) epitopes derived from NetMHCII 2.3 server using 15mer peptide as the core.

<https://services.healthtech.dtu.dk/service.php?NetMHCII-2.3>

‡ These epitopes are not conserved epitopes and therefore are susceptible to mutation(s).

§ The number of T-cell epitope(s) present or overlapping with the extended 46-aa sequence (Seq) of the UF2-RBD at the amino-end (N) and with the extended 12-aa sequence at the carboxyl-end (C).