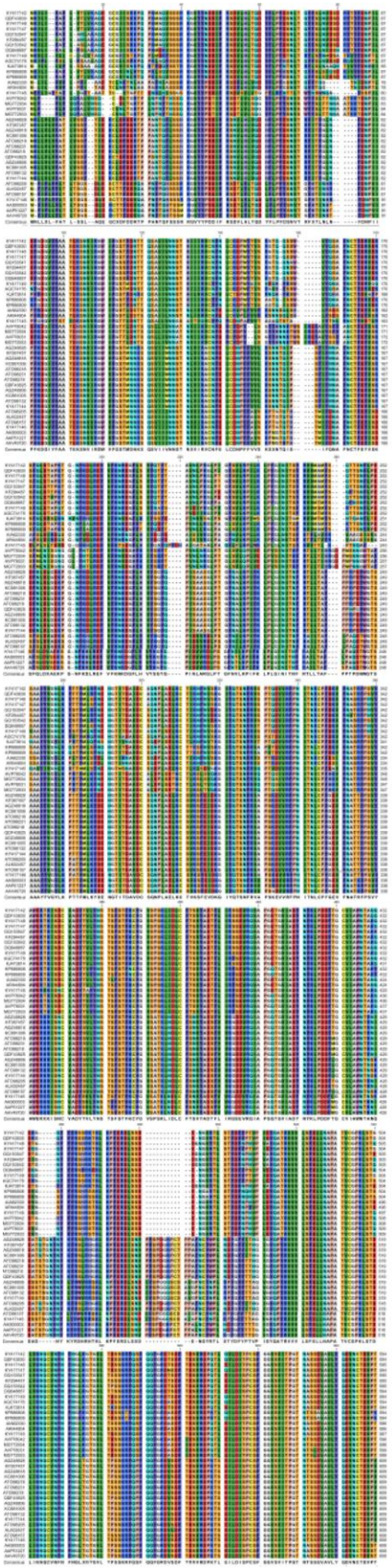
Table S1. All 27 conserved regions observed in SARS-CoV-2, bat SL-CoV and SARS-CoV consensus sequences of spike region.

No	Conserved regions	Positions
1	ENGTITDAVDC	286-296
2	KGIYQTSNFRV	315-325
3	VRFPNITNLCPFGEVFNAT	332-350
4	ISNCVADYSVLYNS	363-376
5	FSTFKCYGVS	379-388
6	VRQIAPGQTG	412-421
7	IADYNYKLPDDF	423-434
8	GYQPYRVVVLSFELL	509-523
9	CVNFNFNGLTGTGVLT	543-558
10	PCSFGGVSVITPGTN	594-608
11	VAVLYQDVNCT	613-623
12	AGCLIGAEHV	652-661
13	SYECDIPIGAGICASY	664-679
14	MYICGDSTEC	745-754
15	NLLLQYGSFCTQLNRAL	756-772
16	FGGFNFSQILPDP	802-814
17	KRSFIEDLLFNKVTLADAGF	819-838
18	ARDLICAQKFNGLTVLPPLLTD	851-872
19	GWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQK	890-926
20	ALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDKVEAEVQIDRLITGRLQSLQTYVTQQLIR AAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSFPQ	949-1059
21	APHGVVFLHVTYVP	1061-1074
22	NFTTAPAICH	1079-1088
23	PQIITTDNTFVSGNCDVVIGI	1117-1137
24	NNTVYDPLQPELDSFKEELDKYFKNHTSPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGK YEQYIKWPWY	1139-1220
25	WLGFIAGLIAIVMVTI	1222-1237
26	LCCMTSCCSCLKG	1239-1251
27	CSCGSCCKFDEDDSEPVLKGVKLHYT	1253-1278

Figure S1. Illustration of generating spike consensus sequences using SARS-CoV-2 and bat SL-CoV as examples.



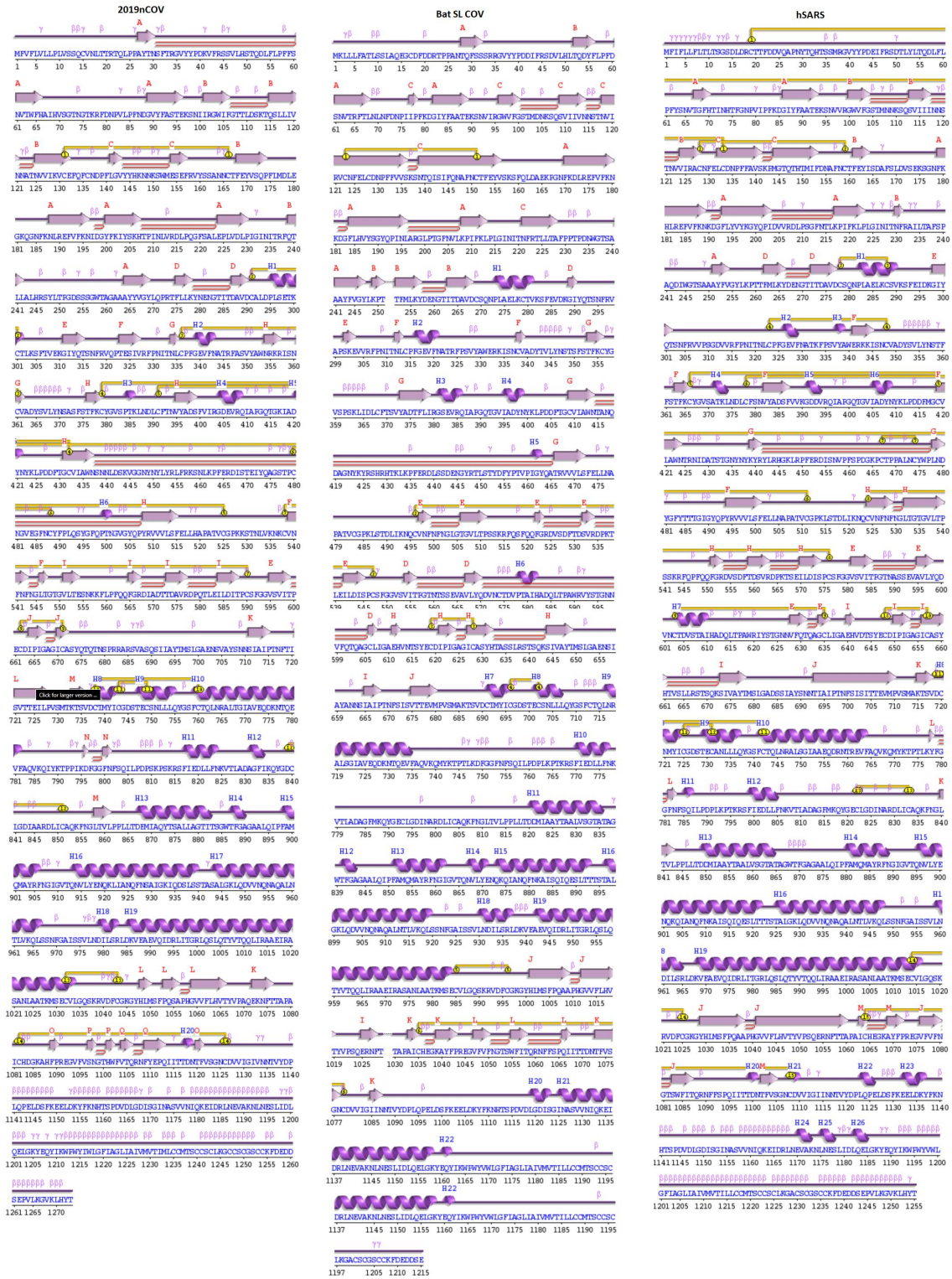

2019nCOV
Bat SL COV
hSARS
Key:
Sec. struc: Helices labelled H1, H2, ... and strands by their sheets A, B, ...
Helix Strand
Motifs: beta turn gamma turn beta hairpin
Disulphides: disulphide bond

Figure S2. Schematic representation of secondary structure prediction of spike of SARS-CoV-2 (left), bat SL-CoV (middle) and SARS-CoV (right) based on the consensus sequences. The secondary structure of SARS-CoV-2 spike contains 17 sheets, 18 beta hair pins, 18 beta bulges, 53 strands, 20 helices, 23 helix-helix nteracts, 209 beta turns, 73 gamma turns and 14 disulphides. Bat SL-CoV spike contains 12 sheets, 1 beta alpha beta unit, 18 beta hair pins, 15 beta bulges, 48 strands, 22 helices, 22 helix-helix interacts, 106 beta turns, 15 gamma turns and 6 disulphides. SARS-CoV spike contains 17 sheets, 18 beta hairpins, 19 beta buldges, 48 strands, 26 helices, 20 helix-helix interacts, 183 beta turns, 60 gamma turns, 14 disulphides.

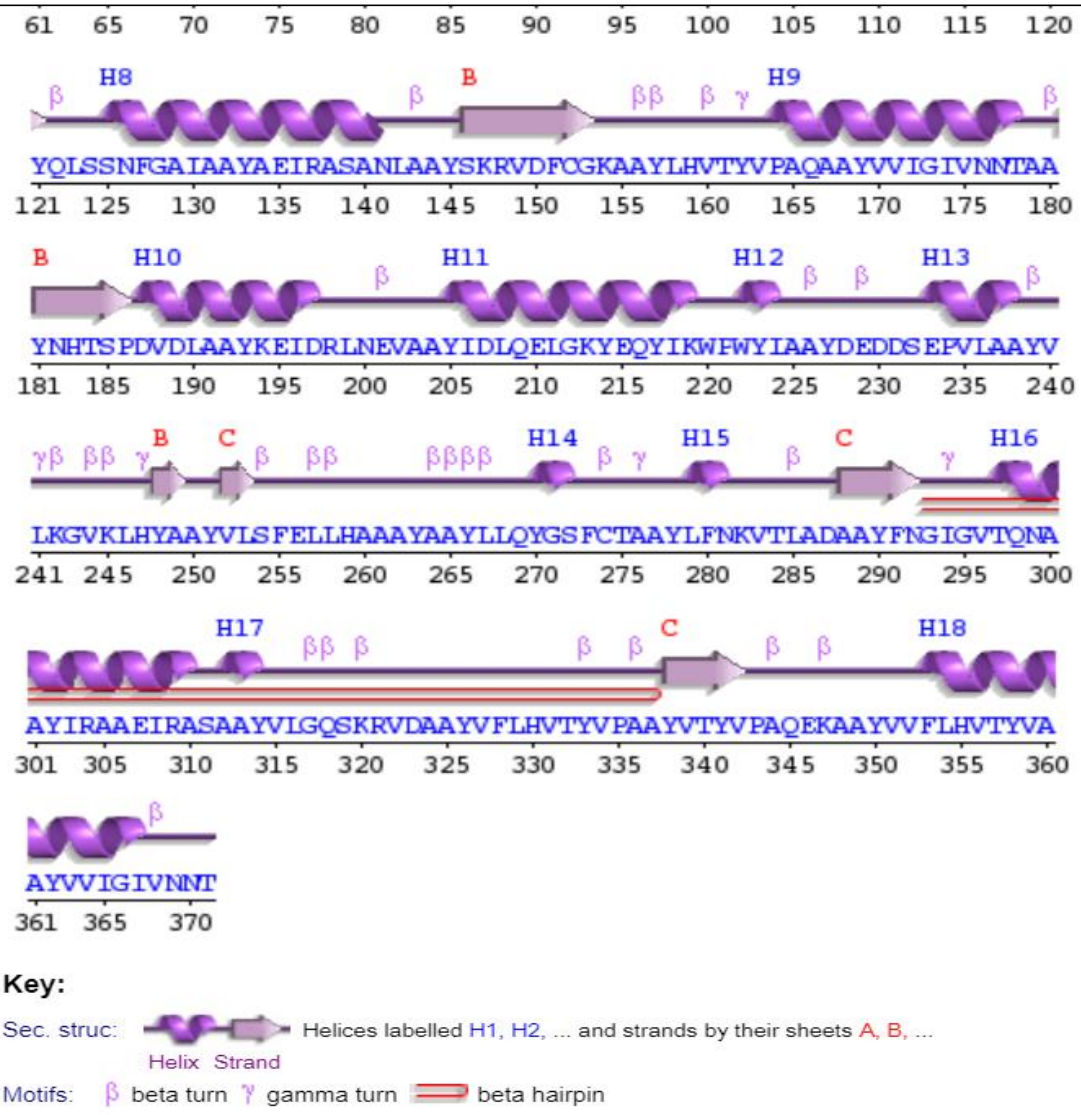


Figure S3. Schematic representation of secondary structure prediction of the multi-epitope vaccine construct. It possesses three sheets, three beta alpha beta units, two beta hairpin, one beta buldge, nine strands, 18 helices, 14 helix-helix interacts, 37 beta turn, 13 gamma turns