Supplementary Materials for

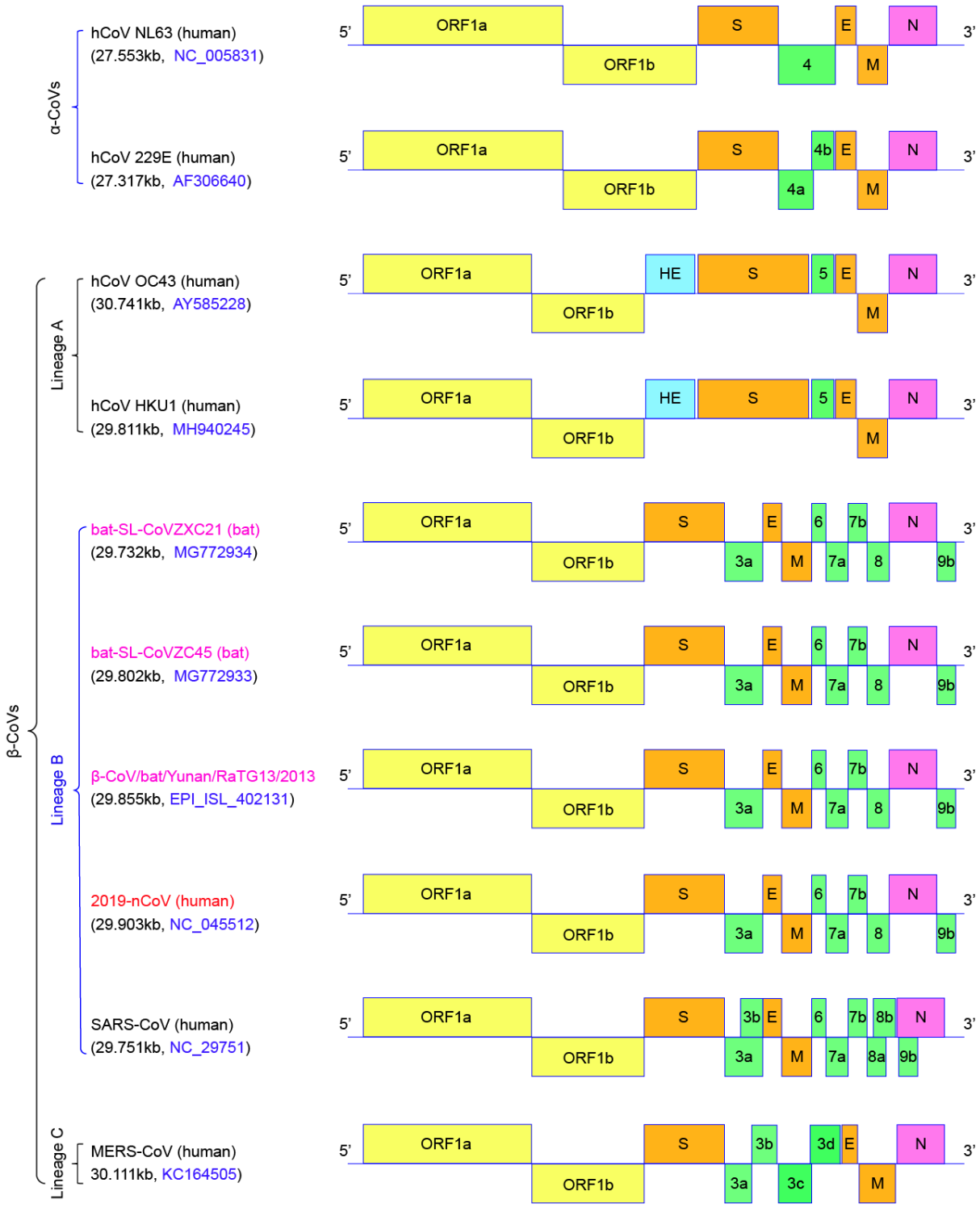

Figure S1 Genomic context of 2019-nCoV and other viral relatives

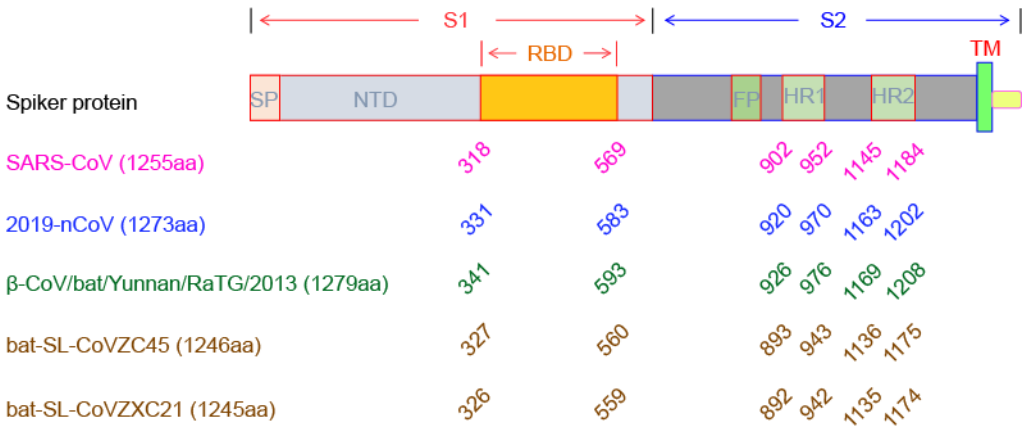

Figure S2 Linear scheme for distinct domains/motifs in spike protein of different coronaviruses

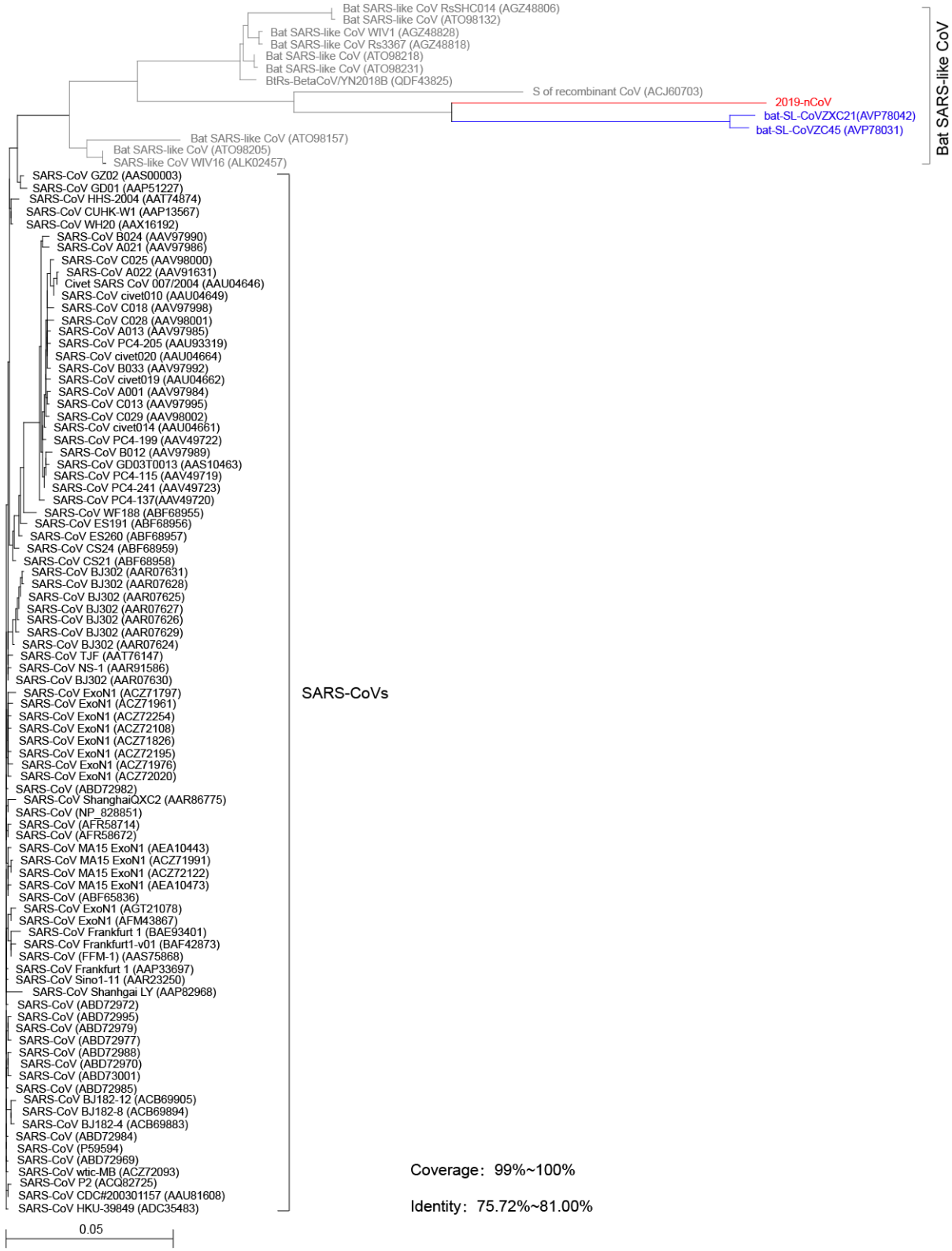

Figure S3 Phylogeny of 2019-nCoV surface spike protein

Multiple sequence alignment of spike protein was conducted with Clustal Omega (https://www.ebi.ac.uk/Tools/msa/clustalo/), and the phylogenic analysis was given with TreeView.

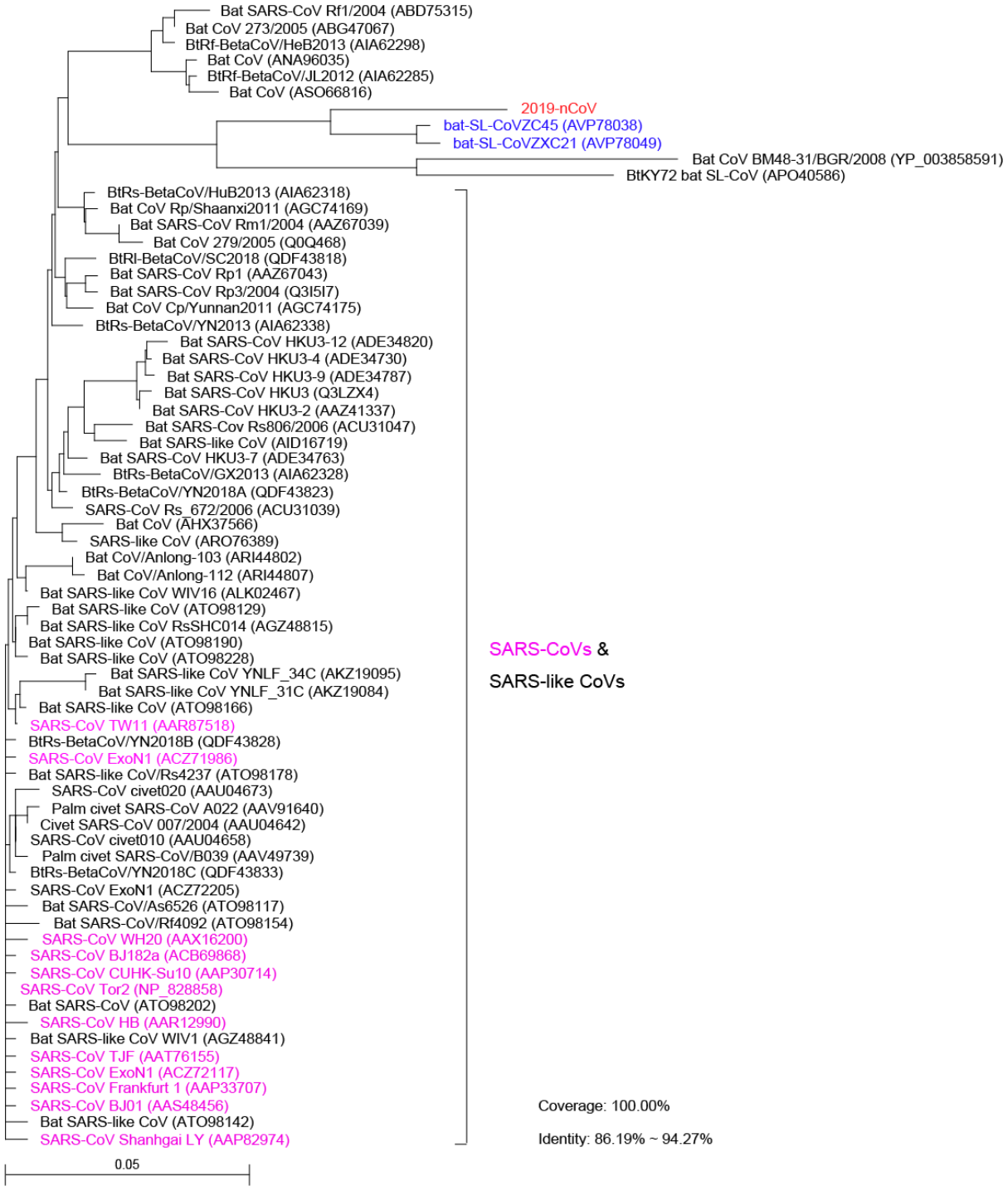

Figure S4 Phylogeny of 2019-nCoV nucleoprotein

Phylogenetic tree of nucleoproteins was generated with TreeView, which follows the multiple sequence alignment with Clustal Omega (https://www.ebi.ac.uk/Tools/msa/clustalo/).

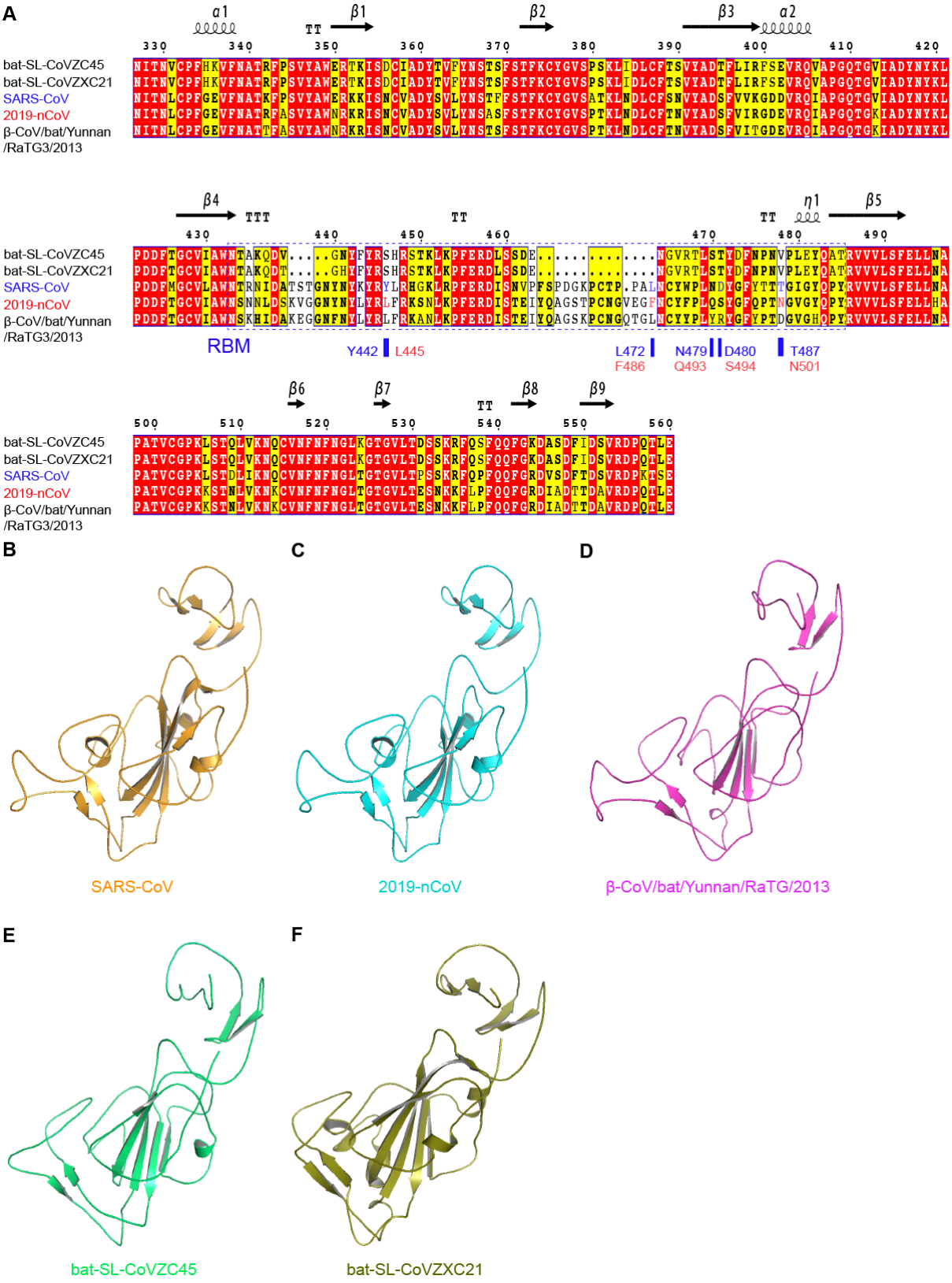

Figure S5 Structural analyses of RBD from 2019-nCoV and four closely-related

CoVs

A. Sequence analyses of RBD from 2019-nCoV and four closely-related CoVs

Putative residues of RBD interacting with ACE2 are highlighted with letters coloring blue for SARS-CoV, and red for 2019-nCoV.

B. Ribbon structure of RBD from SARS-CoV

C. Modeled structure of 2019-nCoV RBD

Structural architectures of RBD from β-CoV/bat/Yunnan/RaTG/2013 (**D**), bat-SL-CoVZC45 (**E**), and bat-SL-CoVZC45 (**F**)

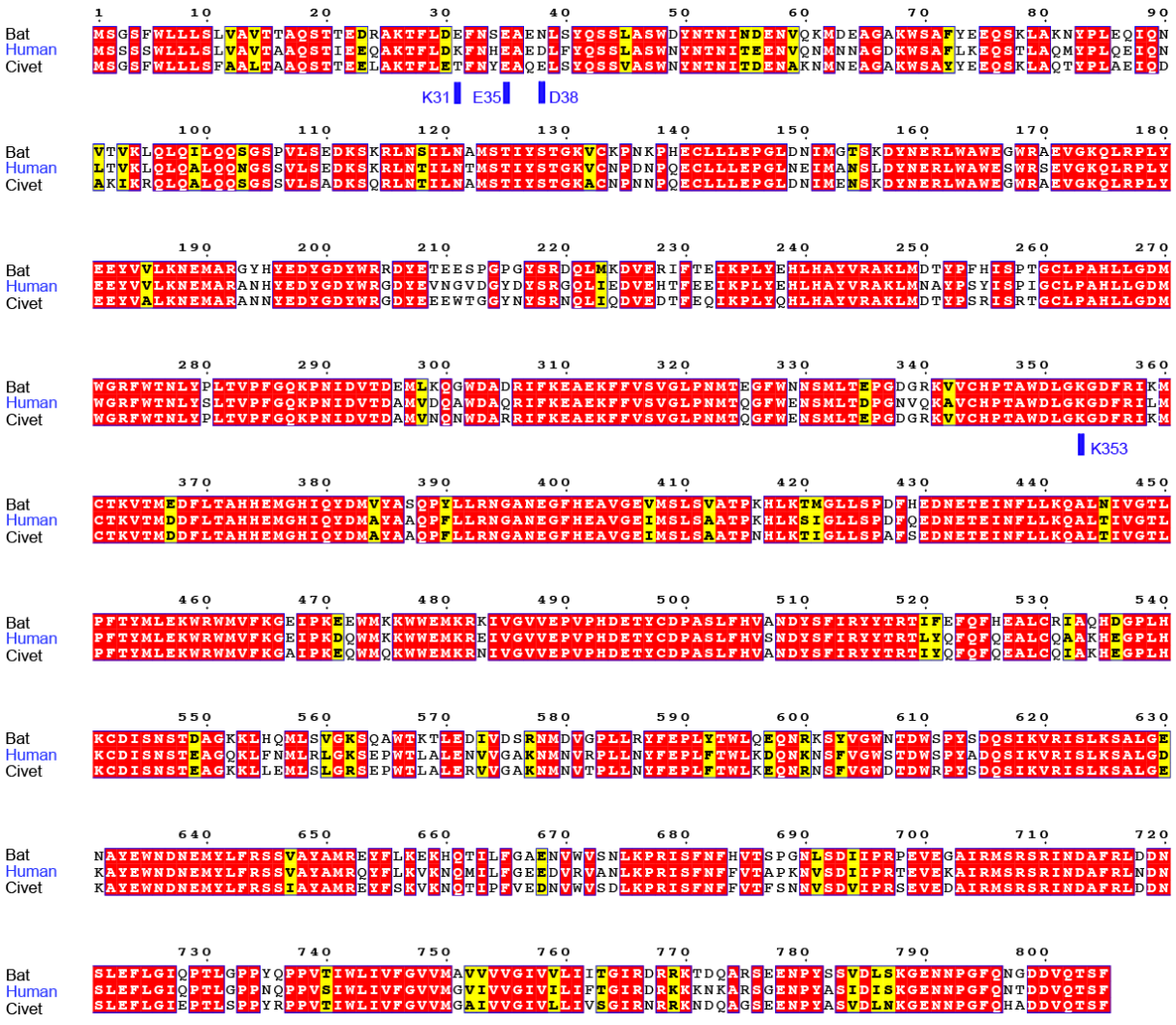

Figure S6 Sequence analysis of the ACE2 receptor

The putative residues of ACE2 indicated with blue letters, are implicated into its RBD binding. Three ACE2 proteins used here are sampled from bats, civets, and humans (homo sapiens).