Supplementary Figure S1

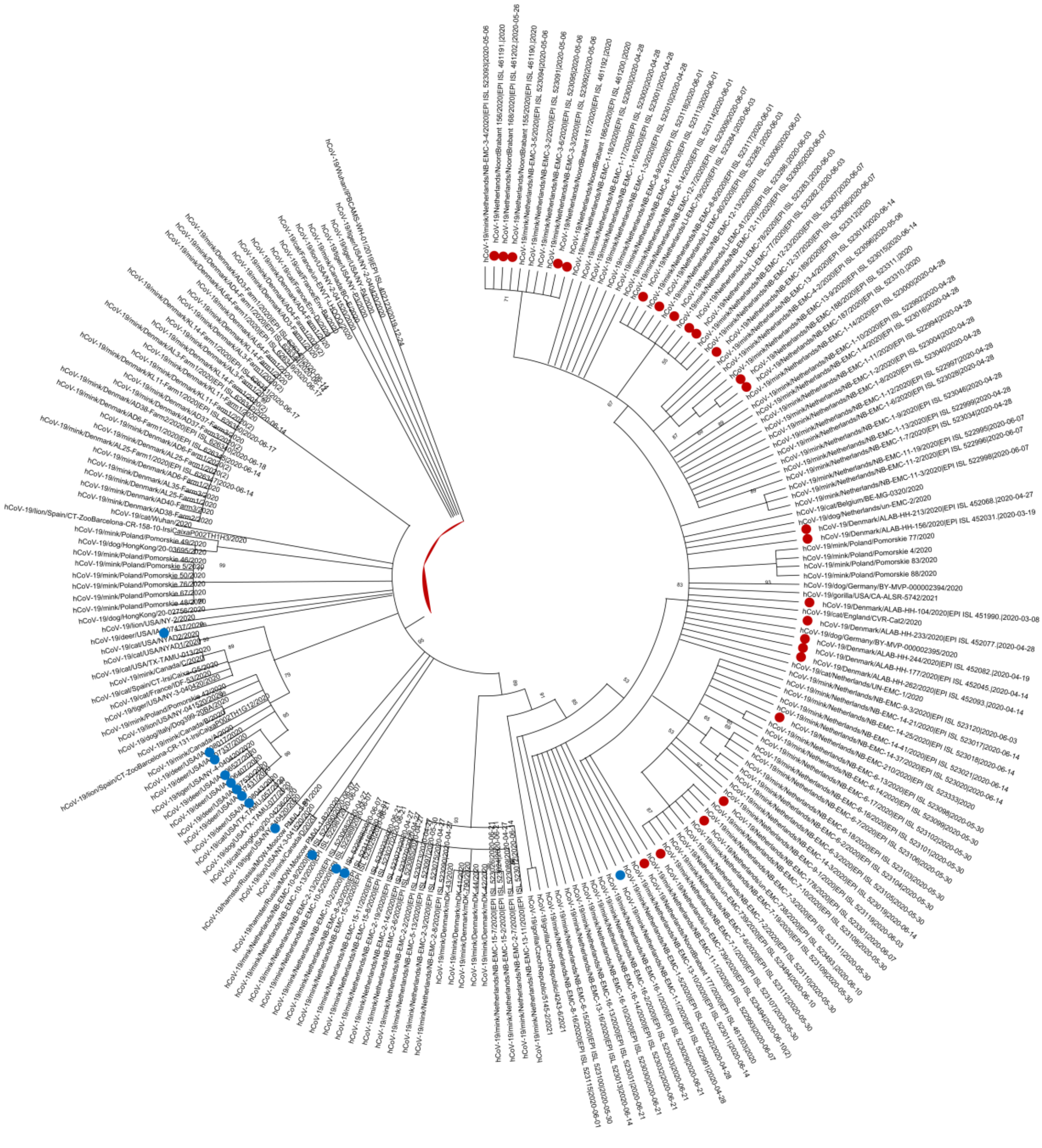
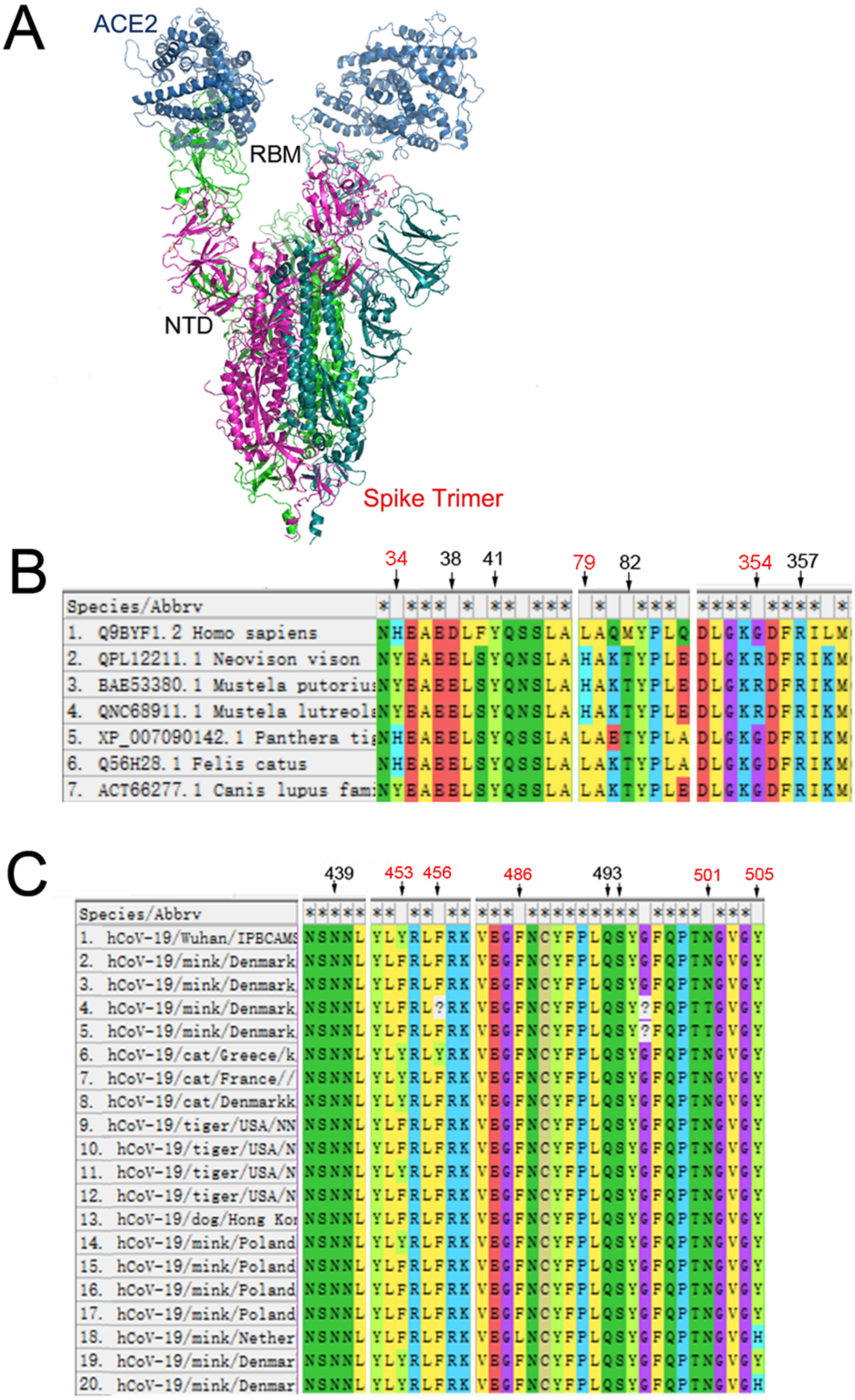


Fig S1. The phylogenetic tree of 258 sequences was analyzed by MEGA-X using the maximum likelihood method and Tamura-Nei model.

Supplementary Figure S2



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Species/Abbrv                        * *** * ** ***   *  ***   **** **** *
1.  Q9BYF1.2 Homo sapiens            NHEAEDLFYQSSLA LAQMYPLQ DLGKGDFRILM
2.  QPL12211.1 Neovison vison        NYEAEELSYQNSLA HAKTYPLE DLGKRDFRIKM
3.  BAE53380.1 Mustela putorius      NYEAEELSYQNSLA HAKTYPLE DLGKRDFRIKM
4.  QNC68911.1 Mustela lutreola      NYEAEELSYQNSLA HAKTYPLE DLGKRDFRIKM
5.  XP_007090142.1 Panthera tig      NHEAEELSYQSSLA LAETYPLA DLGKGDFRIKM
6.  Q56H28.1 Felis catus             NHEAEELSYQSSLA LAKTYPLA DLGKGDFRIKM
7.  ACT66277.1 Canis lupus fam       NYEAEELSYQSSLA LAKTYPLE DLGKGDFRIKM
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Species/Abbrv                   ***** ** ** ** *** ********* **** *** 
1.  hCoV-19/Wuhan/IPBCAMS       NSNNL YLYRLFRK VEGFNCYFPLQSYGFQPTNGVGY
2.  hCoV-19/mink/Denmark        NSNNL YLFRLFRK VEGFNCYFPLQSYGFQPTNGVGY
3.  hCoV-19/mink/Denmark        NSNNL YLFRLFRK VEGFNCYFPLQSYGFQPTNGVGY
4.  hCoV-19/mink/Denmark        NSNNL YLFRL?RK VEGFNCYFPLQSY?FQPTTGVGY
5.  hCoV-19/mink/Denmark        NSNNL YLFRLFRK VEGFNCYFPLQSY?FQPTTGVGY
6.  hCoV-19/cat/Greece/k        NSNNL YLYRLYRK VEGFNCYFPLQSYGFQPTNGVGY
7.  hCoV-19/cat/France//        NSNNL YLYRLFRK VEGFNCYFPLQSYGFQPTNGVGY
8.  hCoV-19/cat/Denmarkk        NSNNL YLYRLFRK VEGFNCYFPLQSYGFQPTNGVGY
9.  hCoV-19/tiger/USA/NN        NSNNL YLFRLFRK VEGFNCYFPLQSYGFQPTNGVGY
10.  hCoV-19/tiger/USA/N        NSNNL YLFRLFRK VEGFNCYFPLQSYGFQPTNGVGY
11.  hCoV-19/tiger/USA/N        NSNNL YLYRLFRK VEGFNCYFPLQSYGFQPTNGVGY
12.  hCoV-19/tiger/USA/N        NSNNL YLFRLFRK VEGFNCYFPLQSYGFQPTNGVGY
13.  hCoV-19/dog/Hong Ko        NSNNL YLFRLFRK VEGFNCYFPLQSYGFQPTNGVGY
14.  hCoV-19/mink/Poland        NSNNL YLYRLFRK VEGFNCYFPLQSYGFQPTNGVGY
15.  hCoV-19/mink/Poland        NSNNL YLFRLFRK VEGFNCYFPLQSYGFQPTNGVGY
16.  hCoV-19/mink/Poland        NSNNL YLFRLFRK VEGFNCYFPLQSYGFQPTNGVGY
17.  hCoV-19/mink/Poland        NSNNL YLFRLFRK VEGFNCYFPLQSYGFQPTNGVGY
18.  hCoV-19/mink/Nether        NSNNL YLFRLFRK VEGLNCYFPLQSYGFQPTNGVGH
19.  hCoV-19/mink/Denmar        NSNNL YLYRLFRK VEGFNCYFPLQSYGFQPTNGVGY
20.  hCoV-19/mink/Denmar        NSNNL YLYRLFRK VEGFNCYFPLQSYGFQPTNGVGH
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Fig S2. Sequences analysis of SARS-CoV-2 spike and receptor ACE2. (A) Receptor ACE2 interacting with the SARS-CoV-2 Spike. (B) Alignment of ACE2 of humans and animals. The positions of the amino acids (aa) that function in the spatial interaction are indicated by arrows. (C) Alignment of the SARS-CoV-2 RBD sequences in humans and in animals reported to have been infected. The residues in contact with ACE2 are indicated.