Supplementary data

Table S1 Detailed information of recent SARS-CoV-2 variants.

PANGO lineages	Nextstrain clade	Other names	Featured mutations	Distribution	Sequences in GISAID*
B.1.1.7	20I/501Y.V1	VOC-202012/01	NSP3:T183I,A890D,I1412T NSP6: Δ106-108 NSP12:P323L S:N501Y,A570D,D614G,P681H,T716I,S982A,D1118H,Δ69-70,Δ144/145 ORF8:Q27stop,R52I,Y73C N:D3L,R203K,G204R,S253F	Africa, Asia, Europe, North America, South America	161760
B.1.351	20H/501Y.V2	VOC-202012/02	NSP2:T85I NSP3:K837N NSP5:K90R NSP6:Δ106-108 NSP12:P323L S:D80A,D215G,K417N,E484K,N501Y,D614G,A701V,Δ242-244 ORF3a:Q57H,S171L E:P71L N:T205I	Africa, Asia, Europe, North America, South America	3885
P.1	20J/501Y.V3	VOC-202101/02	NSP3:S370L,K977Q NSP6: Δ106-108 NSP12:P323L NSP13:E341D S:L18F,T20N,P26S,D138Y,R190S,K417T,E484K,N501Y,D614G,H655Y,T1027I,V1176F ORF3a:S253P ORF8:E92K N:P80R,R203K,G204R	Asia, Europe, North America, South America	760
B.1.1.207	-	-	NSP6:A2V NSP12:P323L S:E484K,D614G,P681H M:V70F ORF3a:A143S N:R203K,G204R	Asia, Europe, North America, South America	638
B.1.429	20C	CAL.20C	NSP2:T85I NSP9:I65V NSP12:P323L NSP13:D260Y S:W152C,L452R ORF3a:Q57H N:T205I	Asia, Europe, North America, South America	8600
B.1.525	-	VUI-202102/03	NSP3:T1189I NSP6:Δ106-108 NSP12:P323F S:Q52R,A67V,E484K,D614G,Q677H,F888L,Δ69-70,Δ144/145 E:L21F M:I82T N:A12G,T205I	Africa, Asia, Europe, North America	558
-	-	COH.20G/677H	NSP2:T85I NSP3:M1788I NSP5:L89F NSP12:P323L NSP14:N129D NSP16:R216C S:Q677H,D614G ORF3a:Q57H,G172V M:A85S ORF8:S24L N:P67S,P199L,D377Y	North America	722
-	-	COH.20G/501Y	NSP2:T85I NSP3:T181I,A256V NSP5:L89F NSP12:P323L NSP14:N129D NSP16:R216C S:N501Y,D614G ORF3a:Q57H,G172V ORF8:S24L,R52I N:P67S,P199L	North America	5
-	-	Mink Cluster 5	NSP1:Δ85 NSP3: Δ1263 NSP12:P323L,T739I NSP15:T112I S:Y453F,I692V,M1229I,Δ69-70 ORF3a:H182Y N:S194L,R203K,G204R	Europe	11

*The data updated until 17th Mar. 2021, mutations identified in different variants were colored red.

Figure S1

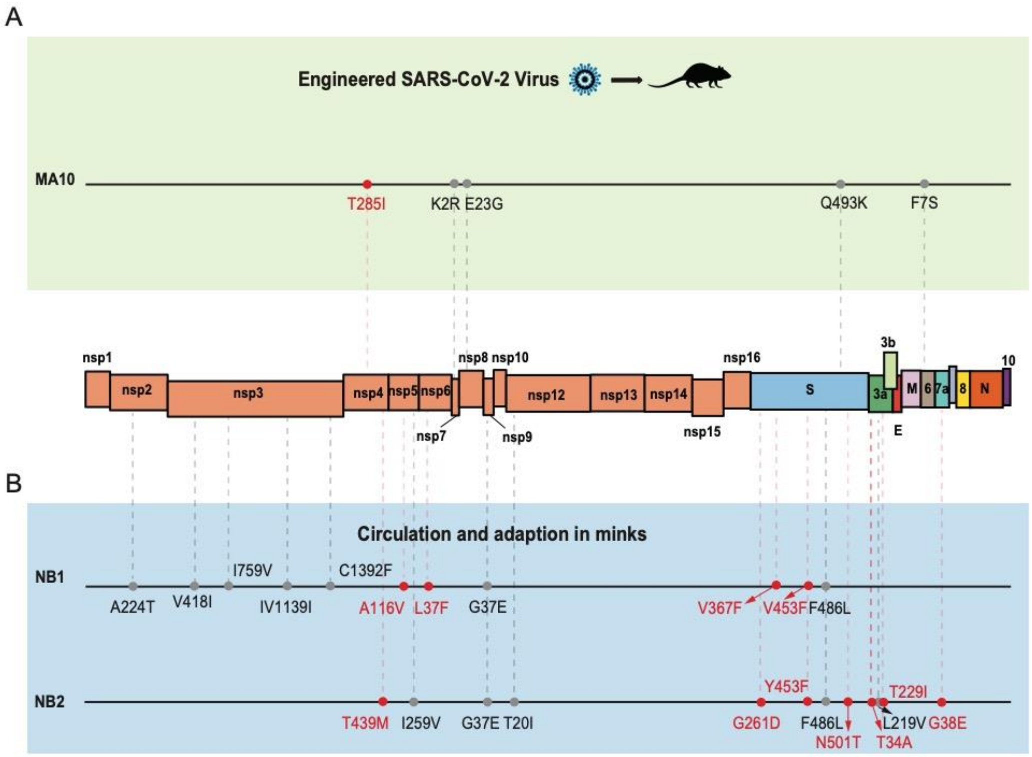

Figure S1 Mutations of SARS-CoV-2 strains during their adaption in mice and minks. (A) In the research conducted by Baric and colleagues, after 10 serial passage of an engineered SARS-CoV-2 virus (with Q493H mutation in S protein) in mice for 10 passages, 4 mutations including T285I in nsp4, K2R in nsp7, E23G in nsp8 and F7S in orf6 could be detected. Of the 4 mutations, the T285I mutation could be detected in human as well. (B) In the research conducted by Munnink et al., 20 mutations could be detected in minks isolated from NB1 and NB2 farms, in which 10 of them could also be found in human-infecting strains. The V453F could be detected both in NB1 and NB2 farms and could also be found in 916 viral strains circulated in human. Besides, T439M in nsp4, A116V in nsp5, L37F in nsp6, G261D, V367F, N501T in S, T34A, T229I in orf3a and G38E in orf7a were detected in human population as well.