



Figure S1. ML trees and genomic mutations of 624 SARS-CoV-2 genomes

The ML trees of 624 SARS-CoV-2 genomes (**A**), *S* gene region (**B**) and RBD-encoding region (**C**) are shown. In ML trees, a red or blue circle in the internal node is shown if the bootstrap value (1000 times ultrafast bootstrap test) is $\geq 80\%$ or $\geq 50\%$, respectively. In (**B**), the two numbers in the internal nodes indicate the bootstrap value. In (**B**) and (**C**), ML trees are shown in the left, and the mutations of in the corresponding sequence are shown as dot in right.