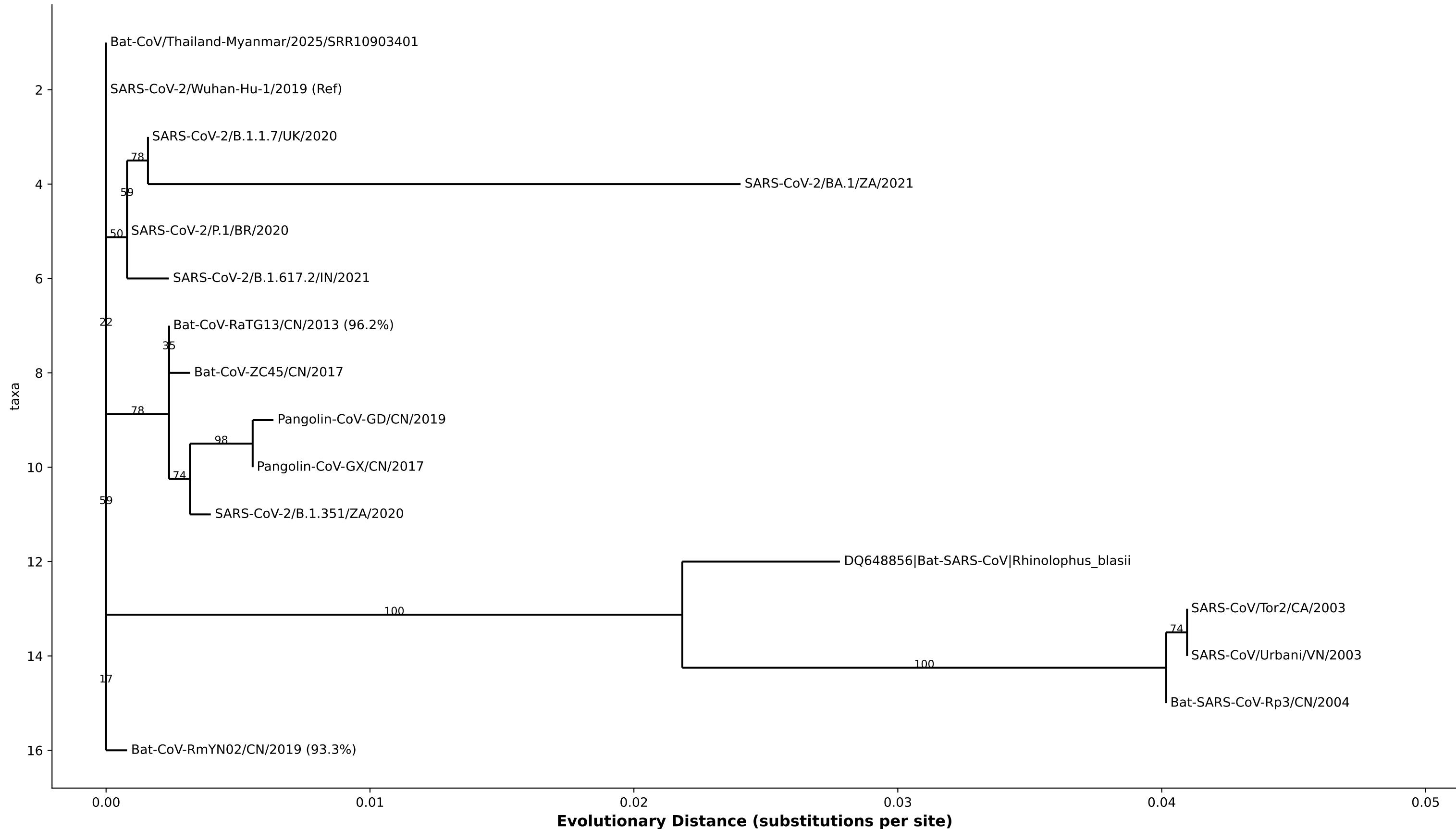


Phylogenetic Analysis of SARS-CoV-2 and Related Coronaviruses

Maximum Likelihood Tree of Spike Protein Sequences (n=16)



Phylogenetic tree constructed using IQ-TREE v2.0 with Blosum62+F+G4 model.
Bootstrap support values (1000 replicates) shown at nodes.
Sequence nomenclature follows WHO/GenBank standards.