Supplementary Information

Raman fingerprints of SARS-CoV-2 Omicron subvariants: molecular roots of virological characteristics and evolutionary directions

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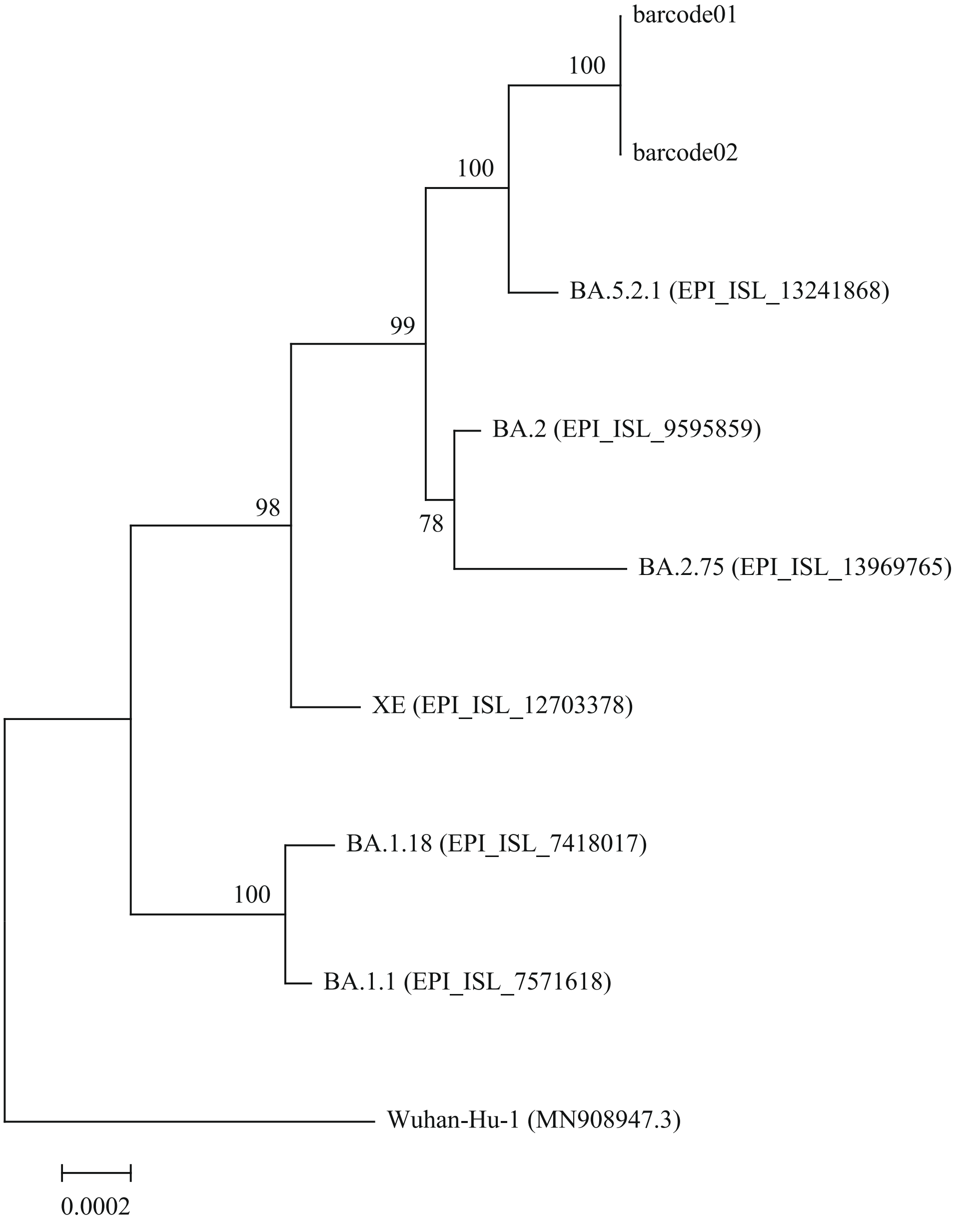

Figure S1: The maximum likelihood (ML) tree of SARS-CoV-2 whole genome sequences. Numbers in parentheses are GISAD or GenBank accession numbers. The Hasegawa-Kishino-Yano model with gamma-distributed rate variation across site was used as a distance measure. The internal node number represents boostrap values (1000 replications). A SARS-CoV-2 reference genome sequence (Wuhan-Hu-1) was used as an outgroup. The ML tree analysis indicating that the genome sequences of the swab samples can be classified into BA.5.2.