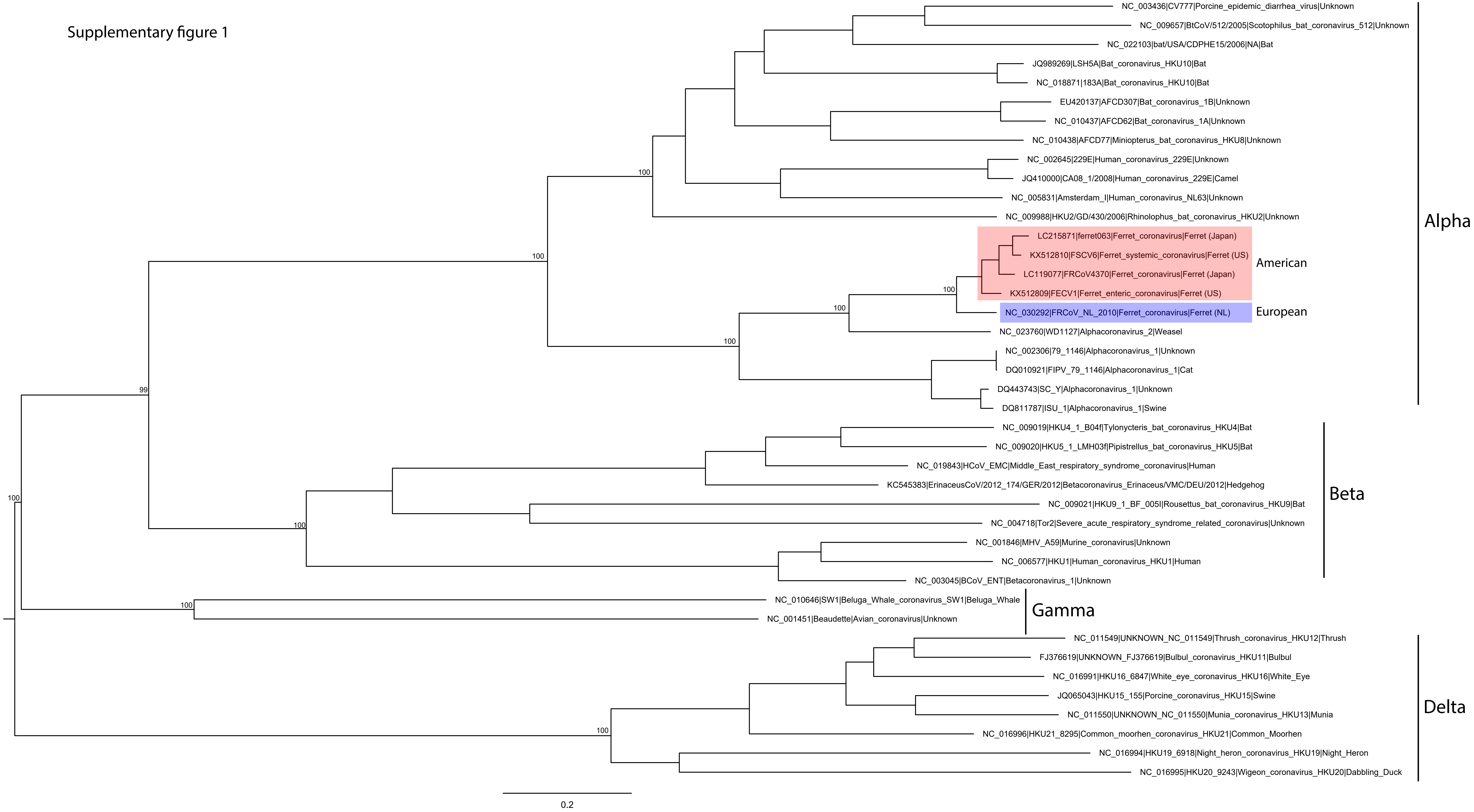
Supplementary figure 1. Phylogenetic analyses for complete genome of FRCoVs and a collection of coronaviruses from other hosts. Four genetic genera of coronavirus are indicated by bars to the right of tree. FRCoVs from America and Europe are indicated by red and blue boxes, respectively. Numbers at the nodes indicate bootstrap support evaluated by 500 replicates.

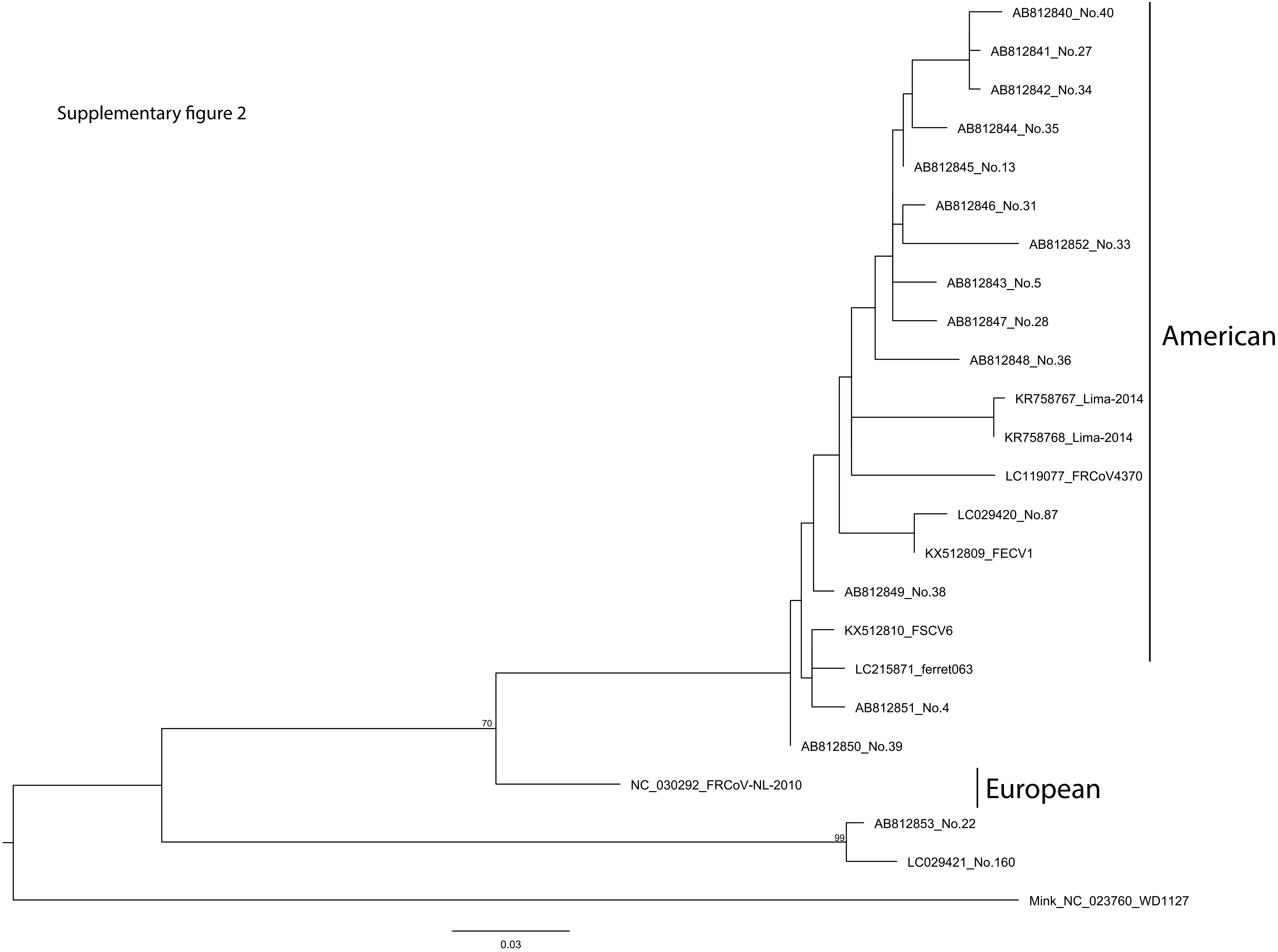
Supplementary figure 2. Phylogenetic analyses for RdRp gene of FRCoVs. FRCoVs from America and Europe are indicated by bars to the right of tree. Numbers at the nodes indicate bootstrap support evaluated by 500 replicates.

Supplementary figure 3. Phylogenetic analyses for the non-recombination and recombination part in the spike gene of FRCoVs. A (non-recombination part) and B (recombination part) include spike gene of the 5 complete FRCoV genomes, C (non-recombination part) and D (recombination part) include spike gene of all available FRCoVs. Two geographically dependent groups (European and American) and two sub-groups (American-I and American-II) are indicated by bars to the right of tree. FRCoV strains in American-II sub-group are clustered together with other strains from America in the non-recombination part but closer to European group in the recombination part, indicated by red. Numbers at the nodes indicate bootstrap support evaluated by 500 replicates.

Supplementary figure 1



Supplementary figure 2



Supplementary figure 3