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Supplemental Information

Genome Composition and Divergence of the Novel Coronavirus (2019-nCoV) Originating in China

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Figure S1

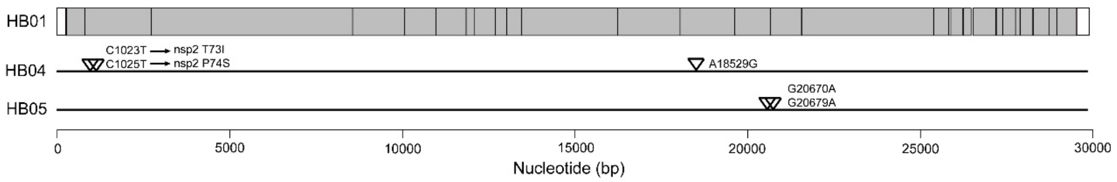

Figure S1. The nucleotide differences (labeled as triangles) of HB04 (short for Wuhan/IVDC-HB-04/2019) and HB05 (Wuhan/IVDC-HB-05/2019) relative to HB01 (Wuhan/IVDC-HB-01/2019) across the viral genomes. Two amino acid substitutions on nsp2 protein were observed between the HB04 and HB01.

Figure S2.

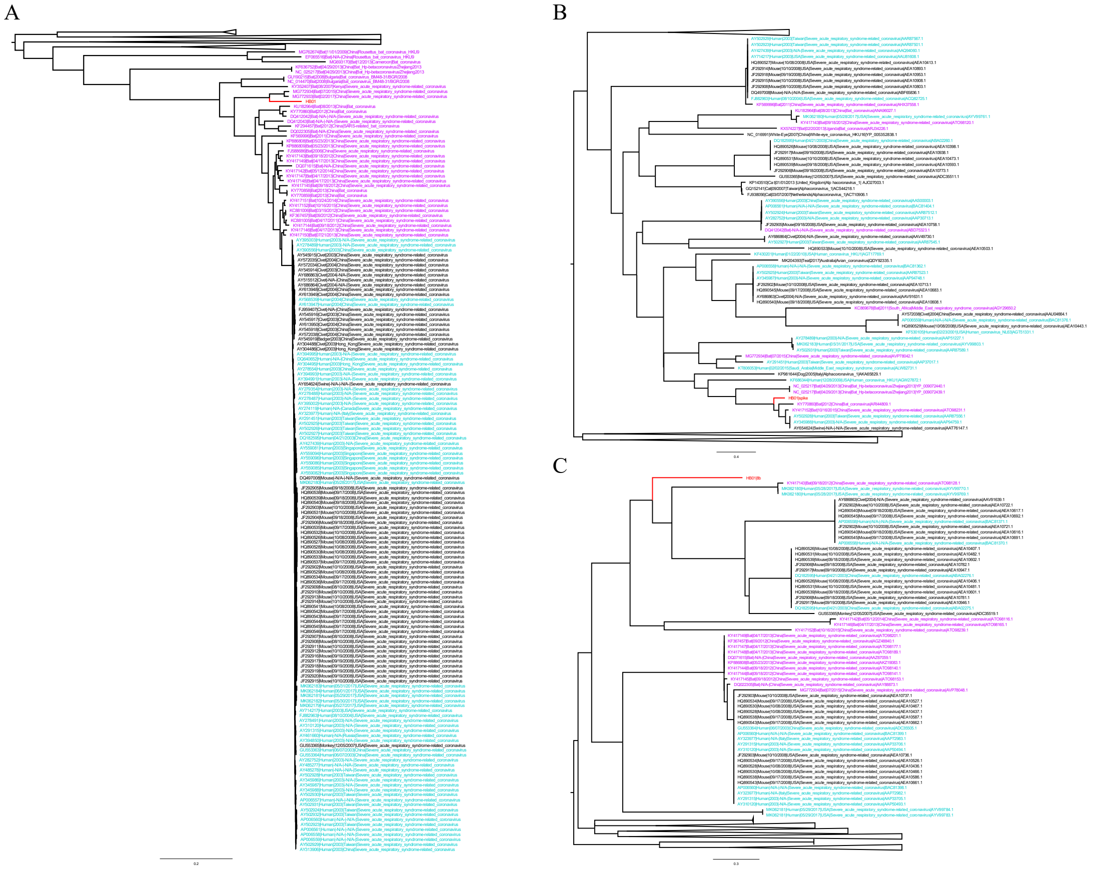

Figure S2. Phylogenetic trees for the whole genome, spike and 8b proteins of 2019-nCoV and related coronaviruses. The coronavirus species were colored in the same way as figure 1B. The phylogenetic tree for the whole genome was constructed using the Molecular Evolutionary Genetics Analysis (MEGA) by the maximum likelihood method under the General Time Reversible (GTR) nucleotide substitution model with the bootstrap tests (500 replicates), while the phylogenetic trees for the individual genes were constructed by the Fasttree software with the GTR nucleotide substitution model as well.