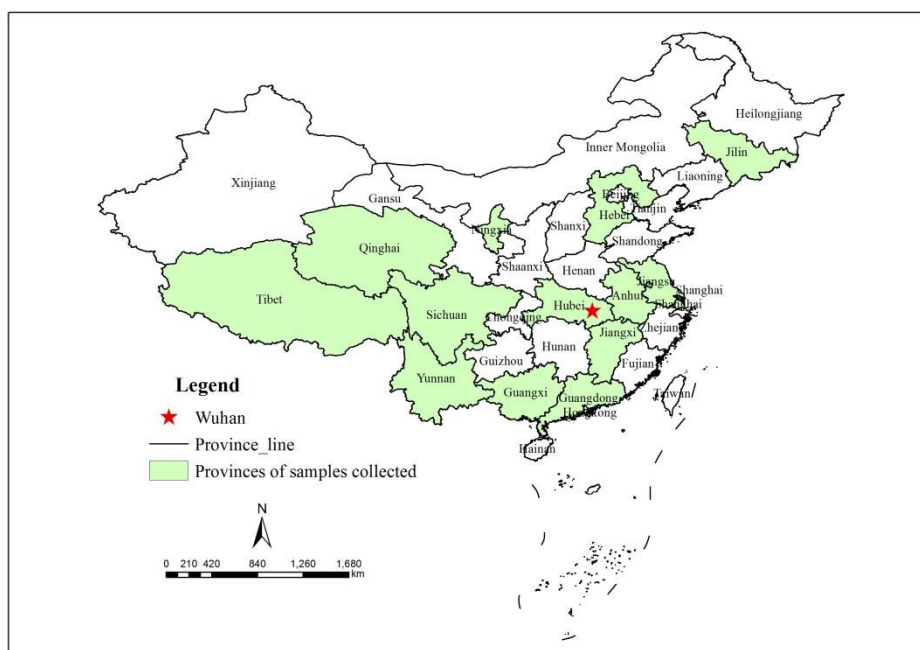


1 **FIGURE 1 Geographical distribution of the samples collected in 2019.**



2

3

4 **FIGURE 2 Phylogenetic trees based on the RdRp gene sequences of**  
5 **coronaviruses.** The trees were constructed using the model with the maximum  
6 likelihood (ML) method, gaps were handled by partial deletion and bootstrap values  
7 were calculated out of 1000 replicates. IBV: avian infectious bronchitis virus; DuCoV:  
8 duck coronavirus; PiCoV: pigeon coronavirus; SARS-CoV-2: severe acute respiratory  
9 syndrome coronavirus 2. Two SARS-CoV-2 representative strains were marked with  
10 black solid circles (●), which belonged to the *Betacoronavirus* of *Coronaviridae*. A  
11 total of 593 avian coronaviruses were detected, including 485 IBVs, 72 DuCoVs and  
12 36 PiCoVs, which all belonged to the *Gammacoronavirus*.

13

