

THE LANCET

Supplementary appendix

This appendix formed part of the original submission and has been peer reviewed.
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Supplement to: Chen N, Zhou M, Dong X, et al. Genomic characterisation and epidemiology of 2019 novel coronavirus: implications for virus origins and receptor binding. *Lancet* 2020; published online Jan 29. [http://dx.doi.org/10.1016/S0140-6736\(20\)30251-8](http://dx.doi.org/10.1016/S0140-6736(20)30251-8).

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Table S1. Primers used for 5' and 3' end sequencing of the 2019-nCoV.

Primer name	Primer sequence(5'-3')
5'raceR1	CCATTGAAGGTGTCAAATTC
5'raceR2	GACCATGAGGTGCAGTTCGA
3'raceF1	GCTGGTTCCTATAAAGATTGG
3'raceF2	CAGCAAAGTGTGACTCTTCTTC

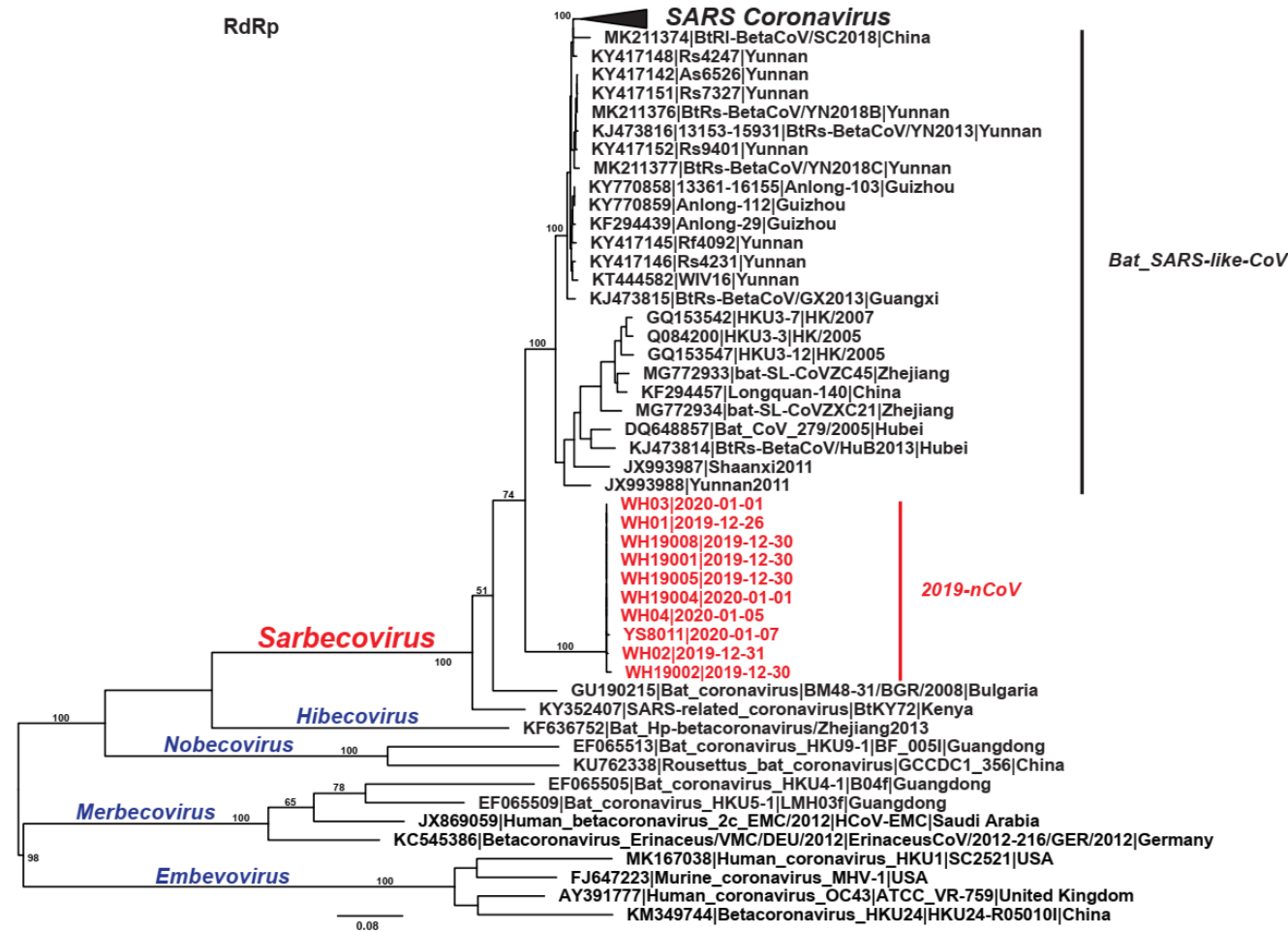


Figure S1. Phylogenetic analysis of the complete RdRp gene of 2019-nCoV and representative viruses of the subgenus *Sarbecoronavirus*.

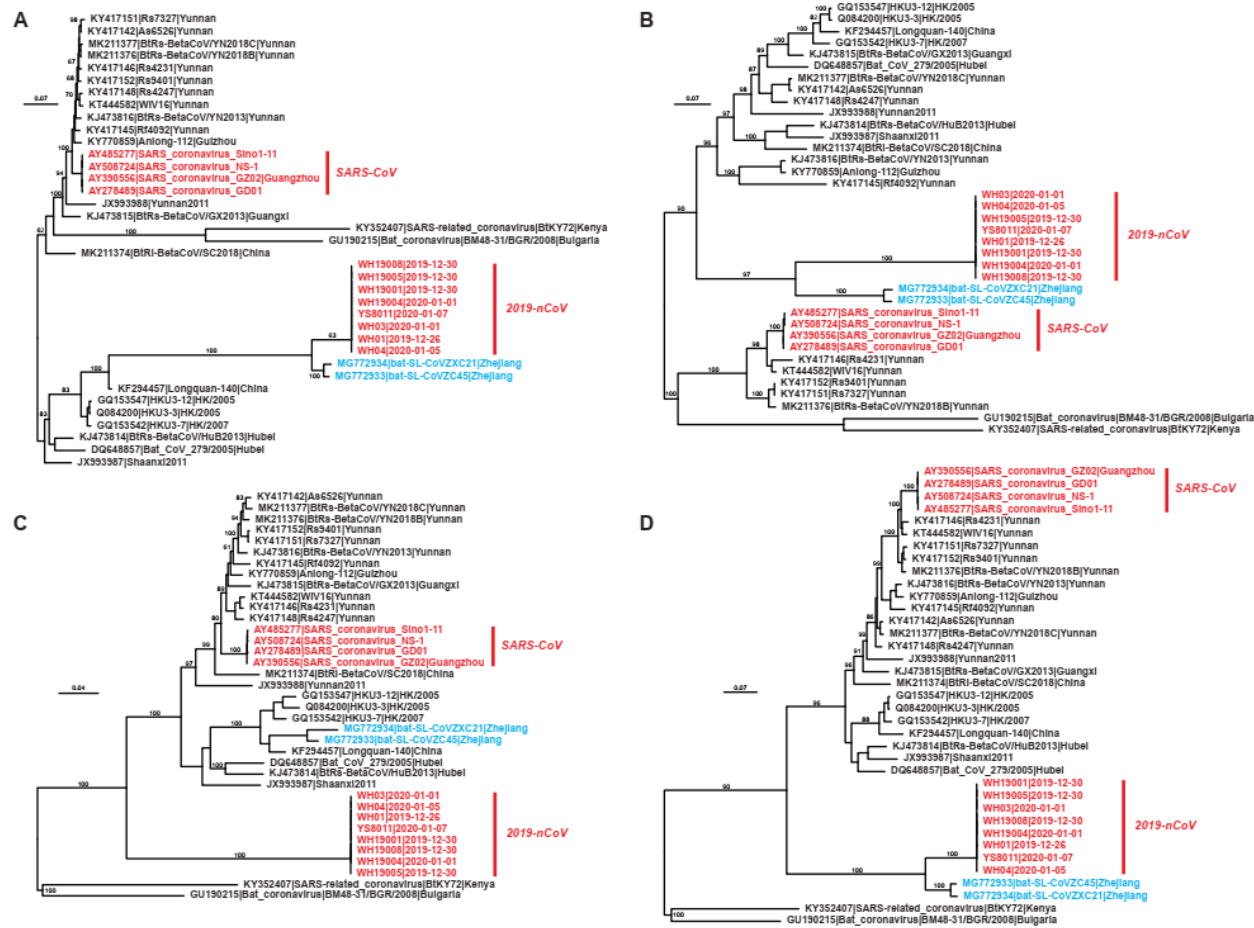


Figure S2. Phylogenetic analysis of separate gene regions of 2019-nCoV and representative viruses of the subgenus *Sarbecoronavirus*.

Panel A: 1a gene; panel B: spike; panel C: 1b gene; panel D: the gene regions excluding 1b. All the trees are midpoint rooted.

