

## Electronic Supplementary Material

### Genomic Characterization of a New Coronavirus from Migratory Birds in Jiangxi Province of China

Wentao Zhu<sup>1</sup> • Wentao Song<sup>2</sup> • Guoyin Fan<sup>2</sup> • Jing Yang<sup>1,3,4</sup> • Shan Lu<sup>1,3,4</sup> • Dong Jin<sup>1,3,4</sup> • Xue-lian Luo<sup>1</sup> • Ji Pu<sup>1</sup> • Haiying Chen<sup>2✉</sup> • Jianguo Xu<sup>1,3,4✉</sup>

1. State Key Laboratory of Infectious Disease Prevention and Control, National Institute for Communicable Disease Control and Prevention, Chinese Center for Disease Control and Prevention, Beijing 102206, China;
2. The Collaboration Unit for Field Epidemiology of State Key Laboratory of Infectious Disease Prevention and Control, Jiangxi Provincial Key Laboratory of Animal-origin and Vector-borne Diseases, Nanchang Center for Disease Control and Prevention, Nanchang 330038, China;
3. Shanghai Public Health Clinical Center, Fudan University, Shanghai 201508, China;
4. Research Units of Discovery of Unknown Bacteria and Function, Chinese Academy of Medical Sciences, Beijing 100730, China;

Supporting information to DOI: 10.1007/s12250-021-00402-x

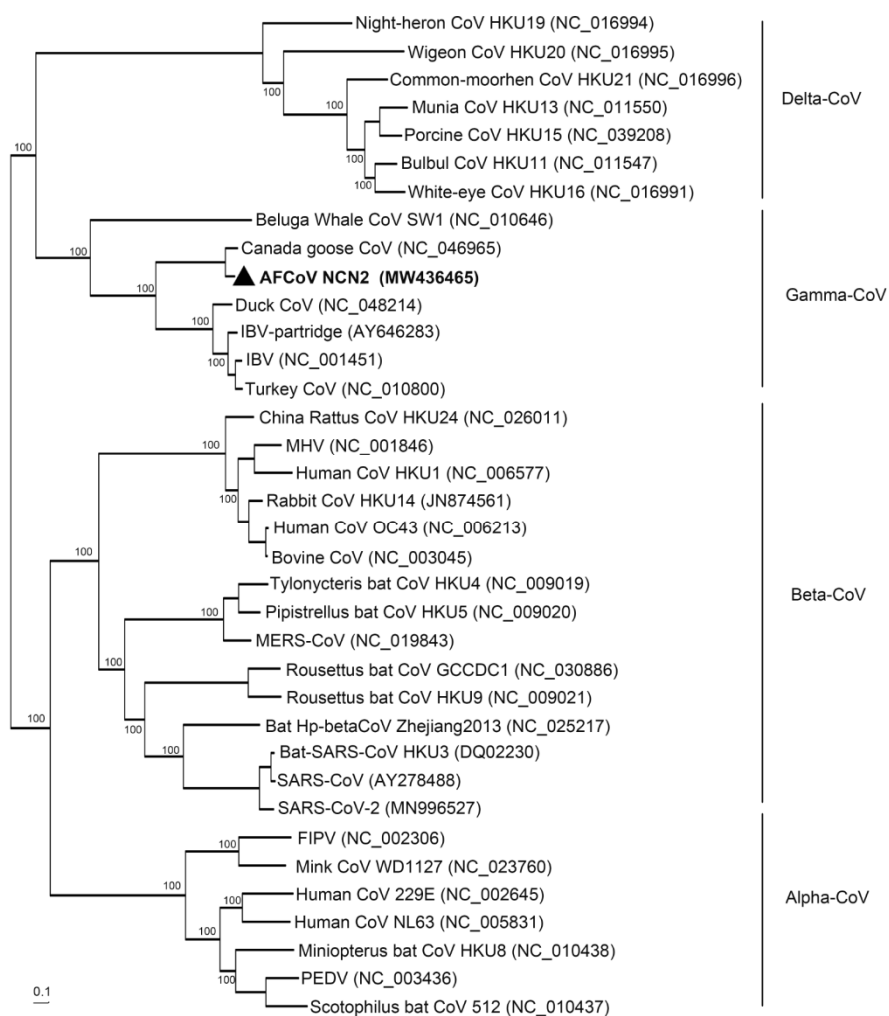
**Table S1** Comparison of cleavage sites and non-structural protein sizes of AFCoV and CGCoV

Domains	AFCoV		CGCoV	
	Cleavage sites	Size (aa)	Cleavage sites	Size (aa)
NSP1/2	SG^KK	609	SG^KK	609
NSP3	AG^GR	1523	AG^GH	1532
NSP4	AG^GI	503	AG^GV	503
NSP5	LQ^AG	307	LQ^AG	307
NSP6	LQ^SN	295	LQ^SN	295
NSP7	VQ^SK	83	VQ^SK	83
NSP8	LQ^AV	212	LQ^AV	212
NSP9	LQ^NN	111	LQ^NN	111
NSP10	LQ^GK	101	LQ^GK	101
NSP12	IP^SV	1000	AG^GH	1000
NSP13	LQ^SC	599	LQ^SC	599
NSP14	LQ^SN	522	LQ^SN	522
NSP15	LQ^SI	338	LQ^SI	338
NSP16	LQ^SG	298	LQ^SG	298

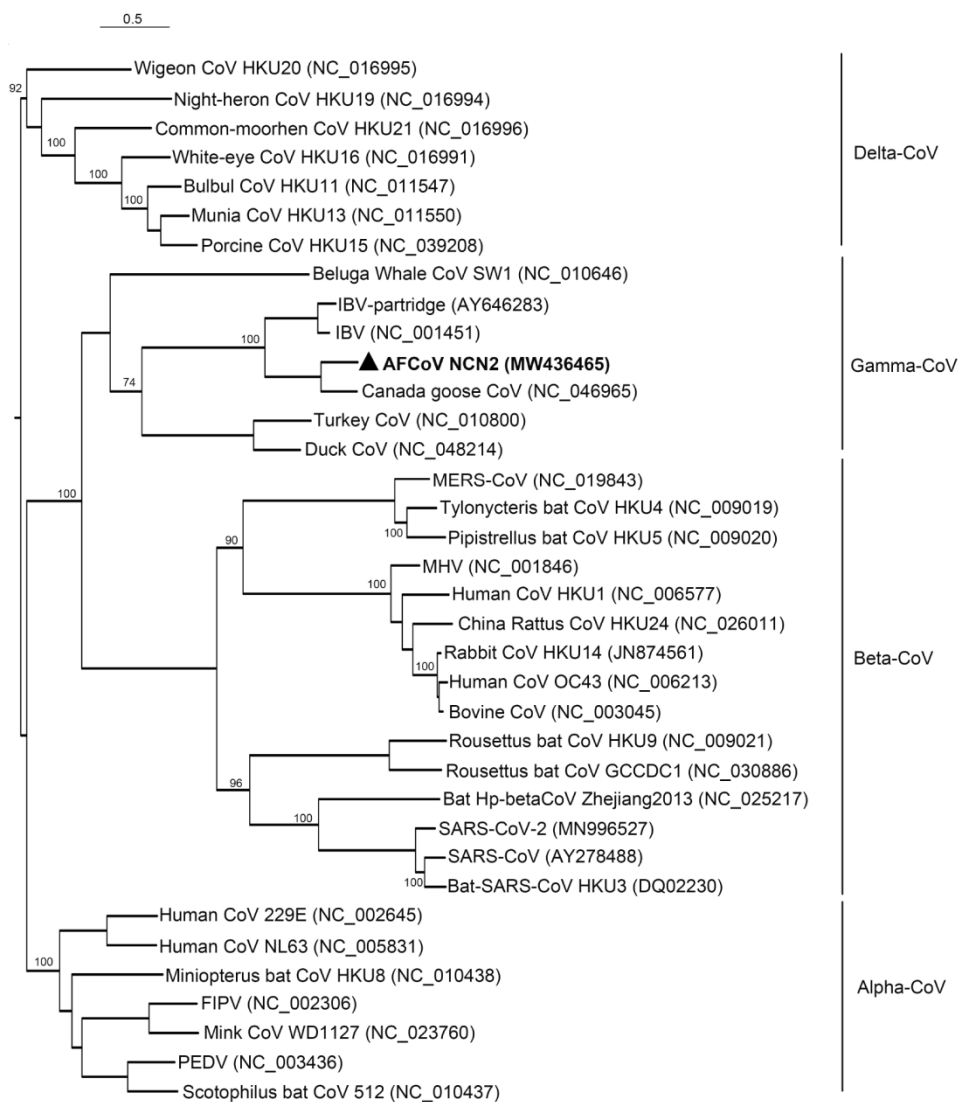
**Table S2** Coding of potential viral proteins of AFCoV

AFCoV	Location (nt)	Length (aa)	Frames(s)	TRS distance bases to AUG
1a	520-11940	3,806	+1	AAACA(167)AUG
1ab	520-20024	6,500	+1, +3	AAACA(167)AUG
S	20008-23568	1,186	+1	AAACA(19)AUG
3	23561-23725	54	+2	
4a	23734-23901	55	+1	
E	23861-24163	100	+2	
M	24160-24843	227	+1	AAACT(15)AUG
5b	24843-25109	88	+3	
6	25106-25297	63	+2	
7	25305-25562	85	+3	
8a	25719-25919	66	+3	
8b	25916-26173	85	+2	
N	26101-27345	414	+1	AAACA(93)AUG
10	27356-27643	95	+2	
11	27655-27840	61	+1	AAACA(138)AUG

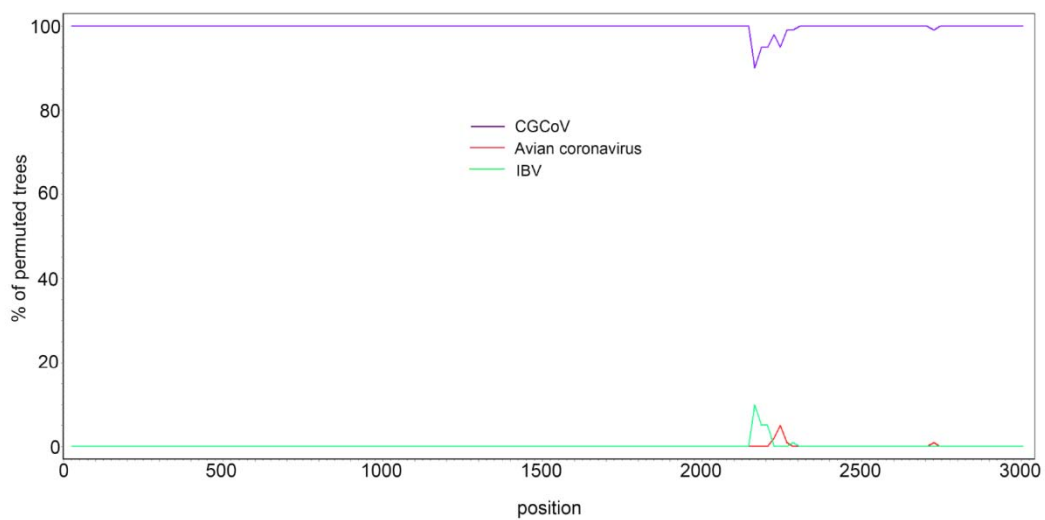
TRS: transcription regulatory sequences.



**Fig. S1** The phylogenetic tree was constructed using amino acid sequences of ORF1ab of different coronaviruses. The maximum-likelihood tree was constructed using PhyML 3.0, and only bootstrap values (>70%) are showed. The viral sequence acquired in this study is marked in bold type.



**Fig. S2** The phylogenetic tree was constructed using amino acid sequences of S protein of different coronaviruses. The maximum-likelihood tree was constructed using PhyML 3.0, and only bootstrap values (>70%) are showed. The viral sequence acquired in this study is marked in bold type.



**Fig. S3** Bootscan analysis (F84 model; window size, 500 bp; step, 200 bp) of Avian coronavirus (MK204411, red line), IBV (NC\_001451, green line) CGCoV (NC\_046965, purple line) and AFCoV (as the query sequence).