Supporting Information

Protein structure and sequence re-analysis of 2019nCoV genome refutes snakes as its intermediate host or the unique similarity between its spike protein insertions and HIV-1

Chengxin Zhang, Wei Zheng, Xiaoqiang Huang, Eric W. Bell, Xiaogen Zhou, Yang Zhang

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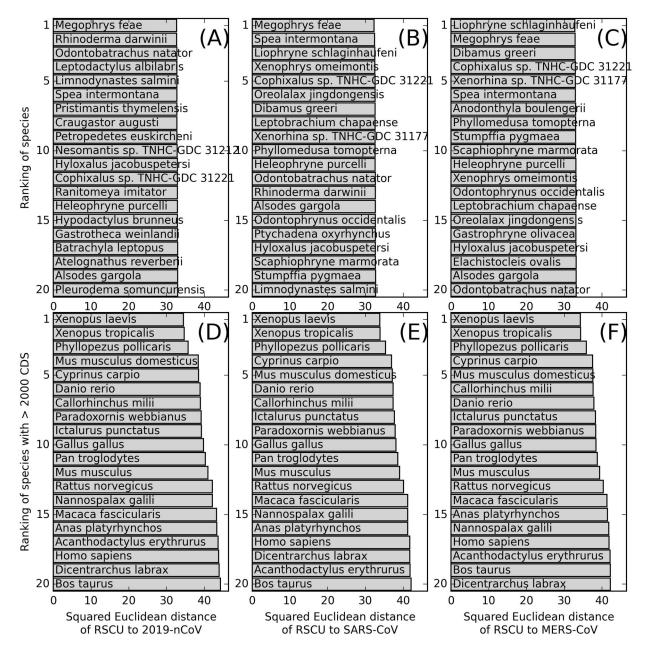


Figure S1. Top 20 vertebrate species ranked in ascending order of squared Euclidean distance of RSCU to 2019-nCoV (**A**, **D**), SARS-CoV (**B**, **E**), and MERS-CoV (**C**, **F**). The upper panels (**A-C**) are for all vertebrates with known codon usage in CoCoPUTS database, while the lower panel (**D-F**) is for the subset of species where more than 2000 CDSs are available for codon usage calculation.

Table S1. Squared Euclidean distances of RSCU among coronaviruses and representative vertebrate species, sorted in ascending order of RSCU distances to 2019-nCoV. Unrelated species such as frogs (*Megophrys feae* and *Liophryne schlaginhaufeni*) have smaller RSCU distances to the coronaviruses than snakes (*Naja atra and Bungarus multicinctus*), which in turn have smaller RSCU distances to known hosts of all three coronaviruses. These data suggest that the closeness of RSCU between a virus and an animal is not indicative of potential pathogen-host relation.

Species	2019- nCoV	SARS- CoV	MERS -CoV	Comment	
2019-nCoV	0	0.28	0.40		
SARS-CoV	0.28	0	0.12	Coronaviruses	
MERS-CoV	0.40	0.12	0		
Megophrys feae	32.64	32.28	32.86	Vertebrates with the closest RSCU to the coronaviruses	
Liophryne schlaginhaufeni	33.07	32.50	32.80		
Naja atra	34.44	33.98	34.39	Proposed intermediate hosts of 2019- nCoV by Ji et al.	
Bungarus multicinctus	34.48	34.36	34.84		
Rhinolophus sinicus	37.55	36.25	36.49	Natural host of SARS-CoV	
Rhinolophus affinis	37.58	36.47	36.50	Natural host of 2019-nCoV	
Manis javanica	38.64	38.98	39.58	Potential intermediate host of 2019- nCoV according to metagenomics evidence	
Homo sapiens	43.81	41.71	41.84	Eventual host	
Camelus dromedarius	46.47	44.28	44.63	Intermediate host of MERS-CoV	
Paguma larvata	47.34	45.08	45.04	Intermediate host of SARS-CoV	