

Supporting Information

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

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Table of Contents

Figure S1. Top 20 vertebrate species ranked in ascending order of squared Euclidean distance of RSCU to 2019-nCoV, SARS-CoV, and MERS-CoV	S1
Table S1. Squared Euclidean distances of RSCU among coronaviruses and representative vertebrate species	S2

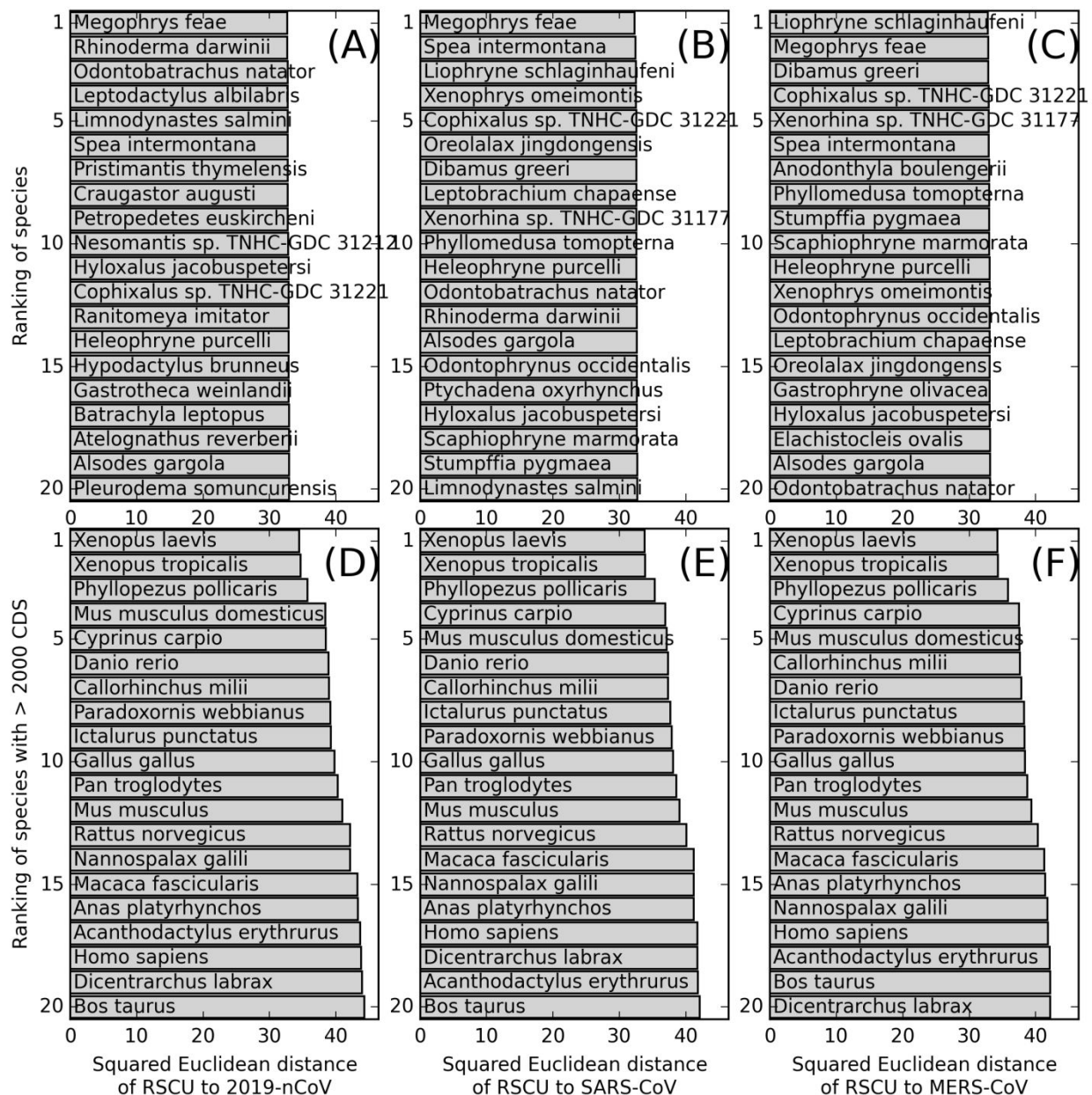


Figure S1. Top 20 vertebrate species ranked in ascending order of squared Euclidean distance of RSCU to 2019-nCoV (A, D), SARS-CoV (B, E), and MERS-CoV (C, F). The upper panels (A-C) are for all vertebrates with known codon usage in CoCoPUTS database, while the lower panel (D-F) is for the subset of species where more than 2000 CDS 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	Coronaviruses
SARS-CoV	0.28	0	0.12	
MERS-CoV	0.40	0.12	0	
<i>Megophrys feae</i>	32.64	32.28	32.86	Vertebrates with the closest RSCU to the coronaviruses
<i>Liophryne schlaginhaufeni</i>	33.07	32.50	32.80	
<i>Naja atra</i>	34.44	33.98	34.39	Proposed intermediate hosts of 2019-nCoV by Ji et al.
<i>Bungarus multicinctus</i>	34.48	34.36	34.84	
<i>Rhinolophus sinicus</i>	37.55	36.25	36.49	Natural host of SARS-CoV
<i>Rhinolophus affinis</i>	37.58	36.47	36.50	Natural host of 2019-nCoV
<i>Manis javanica</i>	38.64	38.98	39.58	Potential intermediate host of 2019-nCoV according to metagenomics evidence
<i>Homo sapiens</i>	43.81	41.71	41.84	Eventual host
<i>Camelus dromedarius</i>	46.47	44.28	44.63	Intermediate host of MERS-CoV
<i>Paguma larvata</i>	47.34	45.08	45.04	Intermediate host of SARS-CoV