

Supplementary materials

TABLE S1. Database used to map the spatial distribution of SARS-CoV-2 natural infection.

Country	Species
Argentina ¹	<i>Canis familiaris</i>
	<i>Felis catus</i>
	<i>Puma concolor</i>
	<i>Panthera tigris</i>
Belgium ¹	<i>Hippopotamus amphibius</i>
	<i>Felis catus</i>
Bosnia and Herzegovina ¹	<i>Canis familiaris</i>
Brazil ¹	<i>Felis catus</i>
	<i>Canis familiaris</i>
Canada ¹	<i>Neovison vison</i>
	<i>Odocoileus virginianus</i>
	<i>Felis catus</i>
	<i>Canis familiaris</i>
Czech Rep	<i>Gorilla gorilla</i>
	<i>Panthera leo</i>
Chile ¹	<i>Felis catus</i>
Colombia ¹	<i>Panthera leo</i>
	<i>Panthera leo</i>
Croatia ¹	<i>Felis lynx</i>
	<i>Canis familiaris</i>
	<i>Felis catus</i>
	<i>Panthera tigris</i>
Denmark ¹	<i>Neovison vison</i>
	<i>Felis catus</i>
Ecuador	<i>Canis familiaris</i>
	<i>Felis catus</i>
Estonia ¹	<i>Panthera leo</i>
	<i>Felis catus</i>
Finland ¹	<i>Felis catus</i>
France ¹	<i>Neovison vison</i>
	<i>Felis catus</i>
Germany ¹	<i>Felis catus</i>
	<i>Canis familiaris</i>
Greece ¹	<i>Neovison vison</i>
	<i>Felis catus</i>
China ¹	<i>Felis catus</i>
	<i>Canis familiaris</i>
	<i>Mesocricetus auratus</i>
India ^{2,3}	<i>Panthera pardus</i>
	<i>Panthera leo</i>
Indonesia ¹	<i>Panthera tigris</i>
	<i>Neovison vison</i>
Italy ¹	<i>Felis catus</i>
	<i>Canis familiaris</i>
Japan ¹	<i>Felis catus</i>
	<i>Felis catus</i>
Korea	<i>Felis catus</i>
Latvia ¹	<i>Neovison vison</i>
	<i>Felis catus</i>
Lithuania ¹	<i>Neovison vison</i>

Mongolia	<i>Castor fiber birulai</i>
	<i>Felis catus</i>
Mexico ¹	<i>Canis familiaris</i>
Myanmar ¹	<i>Canis familiaris</i>
Netherlands	<i>Gorilla gorilla</i>
	<i>Panthera leo</i>
Pakistan	<i>Panthera tigris</i>
Poland ¹	<i>Neovison vison</i>
Russia ¹	<i>Felis catus</i>
Singapore ¹	<i>Panthera leo</i>
Slovenia ¹	<i>Mustela furo</i>
	<i>Neovison vison</i>
South Africa ¹	<i>Panthera leo</i>
	<i>Puma concolor</i>
Spain ¹	<i>Neovison vison</i>
	<i>Panthera leo</i>
	<i>Felis catus</i>
	<i>Mustela furo</i>
Sri Lanka	<i>Canis familiaris</i>
	<i>Pan troglodytes</i>
Sweden ¹	<i>Pongo sp</i>
	<i>Neovison vison</i>
Switzerland ¹	<i>Panthera leo</i>
	<i>Panthera tigris</i>
	<i>Canis familiaris</i>
Thailand ¹	<i>Canis familiaris</i>
	<i>Felis catus</i>
United Kingdom ¹	<i>Felis catus</i>
	<i>Canis familiaris</i>
	<i>Panthera tigris</i>
	<i>Panthera tigris</i>
United States of America ¹	<i>Felis catus</i>
	<i>Canis familiaris</i>
	<i>Panthera leo</i>
	<i>Lynx canadensis</i>
	<i>Crocuta crocuta</i>
	<i>Panthera uncia</i>
	<i>Prionailurus viverrinus</i>
	<i>Arctictis binturong</i>
	<i>Nasua nasua</i>
	<i>Gorilla gorilla</i>
	<i>Neovison vison</i>
	<i>Aonyx cinereus</i>
	<i>Odocoileus virginianus</i>
<i>Puma concolor</i>	
Uruguay ¹	<i>Canis familiaris</i>
	<i>Felis catus</i>

TABLE S2. Breakdown of the genome sequences obtained from GISAID from animal infections in country and lineage/variant.

Country	20E (EU1)	A	Alpha	B	B.1	B.1.1	B.1.1.298	B.1.1.464	B.1.2	B.1.22	B.1.234	B.1.311	B.1.536	B.1.8	B.11	Delta	Omicron (BA.1)	Other
Argentina	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3
Austria	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Belarus	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0
Belgium	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	2	0	0
Bosnia_and_Herzegovina	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2
Botswana	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
Brazil	0	14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2
Canada	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	5
China	0	1	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Colombia	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2
Croatia	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1
Czech_Republic	0	0	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Denmark	0	0	0	0	5	0	437	0	3	0	0	0	11	0	0	0	0	15
Egypt	0	7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
England	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0

France	0	1	1	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	5
Germany	0	0	1	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Greece	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
Hong_Kong	0	3	0	0	1	1	0	0	0	0	0	0	0	0	0	0	12	0	1
India	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	5	12	0
Iran	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Italy	2	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Japan	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	2
Latvia	62	0	1	0	0	0	0	3	0	0	0	0	0	0	0	0	1	0	2
Lithuania	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0	0	3
Netherlands	1	0	0	2	5	0	0	0	0	68	0	0	0	167	44	4	0	0	2
Peru	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3
Poland	0	0	0	0	0	12	0	4	0	0	0	0	0	0	0	8	0	0	0
Portugal	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Puerto_Rico	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0
Russia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4
Singapore	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
Slovenia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1

South_Africa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0
Spain	12	5	0	0	5	0	0	0	0	0	0	0	0	0	0	0	1	0	0
Sri_Lanka	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Sweden	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Switzerland	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	5
Thailand	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0
United_Kingdom	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
USA	0	2	14	8	158	2	0	0	78	0	12	21	0	0	0	126	4	47	

TABLE S3. *Host distribution across continents.*

Host	America	Africa	Europe	Asia
binturong	1	0	0	0
cat	66	5	35	10
coati	1	0	0	0
deer	138	0	0	0
dog	47	3	18	5
ferret	1	0	0	0
fishing cat	1	0	0	0
gorilla	9	0	6	0
hamster	0	0	0	29
hippo	0	0	1	0
hyena	1	0	0	0
leopard	0	0	1	0
lion	38	3	22	10
mink	144	0	862	0
monkey	4	0	0	0
mouse	1	0	1	3
otter	8	0	0	0
puma	1	0	0	0
snow leopard	11	0	0	0
tiger	39	0	2	0

TABLE S4. *Summary of trait data used for ancestral character mapping.*

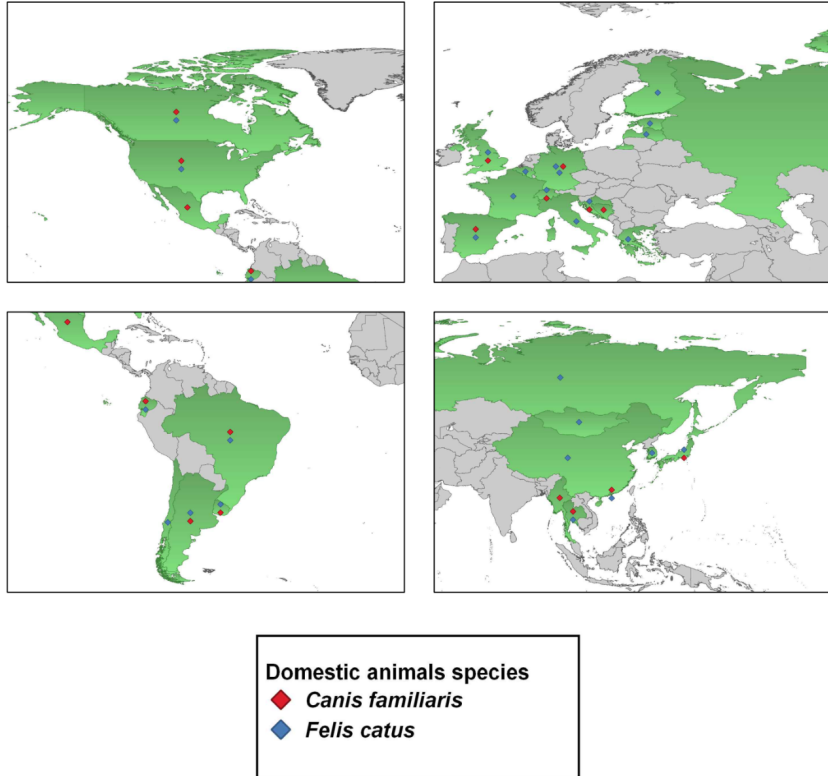
Infection	Species Count	Family Count
Experimental	26	11
Natural	22	8
Both Experimental + Natural	NA	3

ACE2 conservation	Species Count	Family Count
Very High	19	2
High	27	12
Medium	56	17
Low	47	19
Very Low	99	41
Mixed State	NA	10

TABLE S5. *AIC scores for model selection for ancestral state reconstructions. Bold numbers indicate the model used for analyses. The same model was used for both simmap and ace methods of reconstruction.*

Analysis	Equal Rates (ER)	Symmetric (SYM)	All-rates- different (ARD)
Species level	2944.304	2932.392	2600.044
Family level	599.6598	769.4932	764.2774
Felidae only	42.85952	42.85952	41.22131

A



B

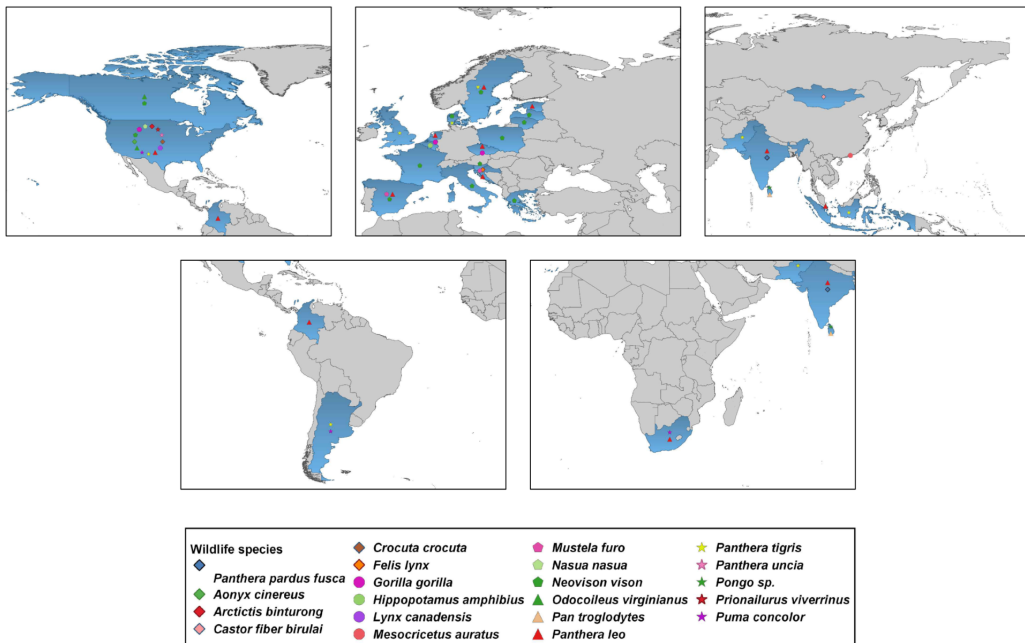


Figure S1: Spatial distribution of SARS-CoV-2 of A) natural infection in domestic animals and B) natural infection in wildlife.

ACE2 Receptor
■ Very High
■ High
■ Medium
■ Low
■ Very Low
■ No Data

Infection
○ Natural
○ Experimental - Susceptible
○ Experimental - Not Susceptible



Figure S2: Stochastic character mapping of ACE2 receptor conservation with SARS-CoV-2 infection secondarily mapped at tips. Phylogeny limited to just mammal species with DNA and time-scaled using node dating (TopoFree_ND; Upham et al. 2019).

ACE2 Receptor

- Very High
- High
- Medium
- Low
- Very Low
- No Data

Infection

- Natural
- Experimental - Susceptible
- Experimental - Not Susceptible



Figure S3: Ancestral character estimation of ACE2 receptor conservation with SARS-CoV-2 infection secondarily mapped at tips. Phylogeny limited to just mammal species with DNA and time-scaled using node dating (TopoFree_ND; Upham et al. 2019).

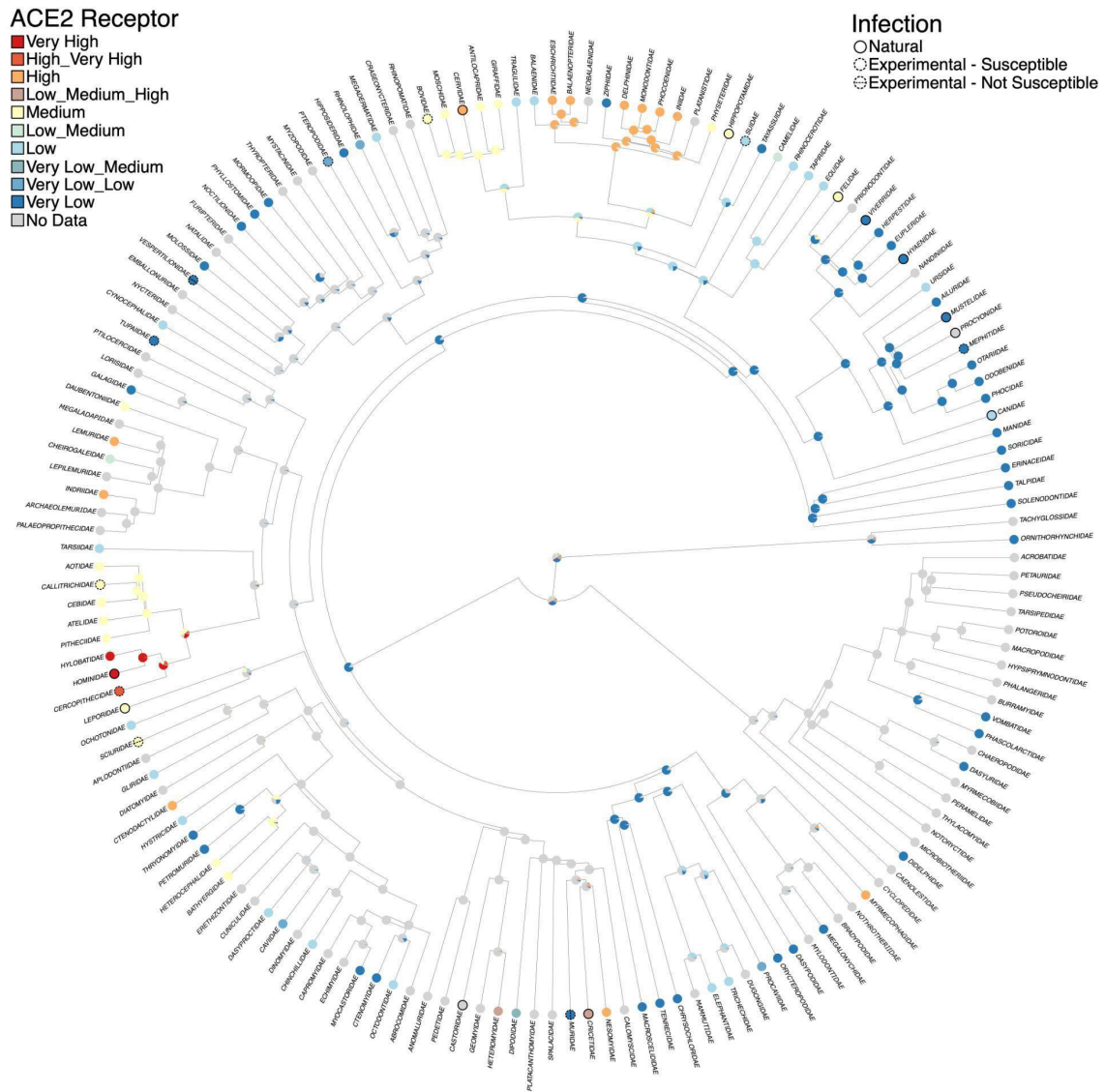


Figure S4: Ancestral character estimation of ACE2 receptor conservation with SARS-CoV-2 infection secondarily mapped at tips. Phylogeny limited to just mammal families with DNA and time-scaled using node dating (TopoFree_ND; Upham et al. 2019).

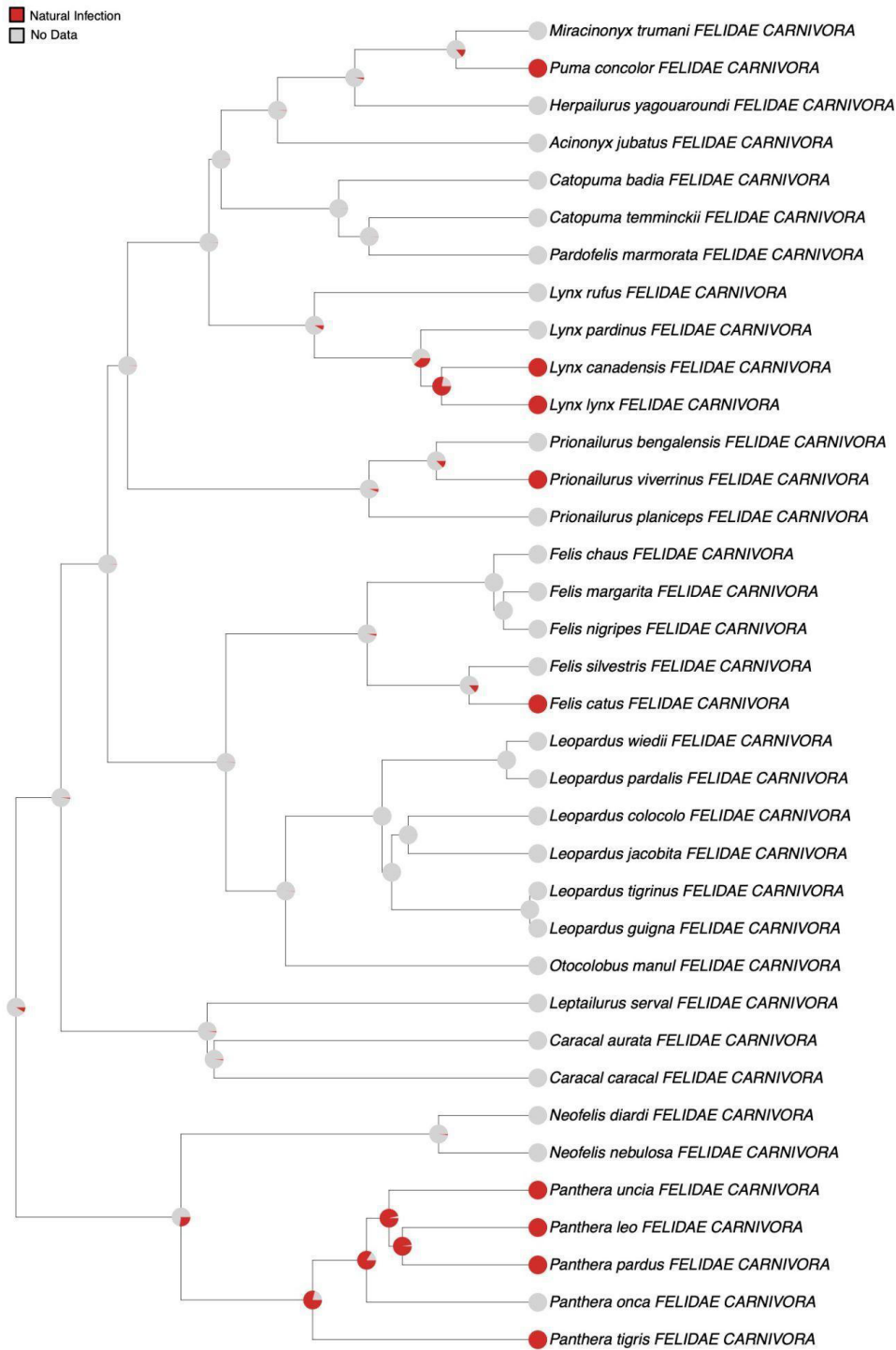


Figure S5: Stochastic character mapping of SARS-CoV-2 infection for the Felidae (cats).

Phylogeny limited to just species with DNA and time-scaled using node dating

(TopoFree_ND; Upham et al. 2019).

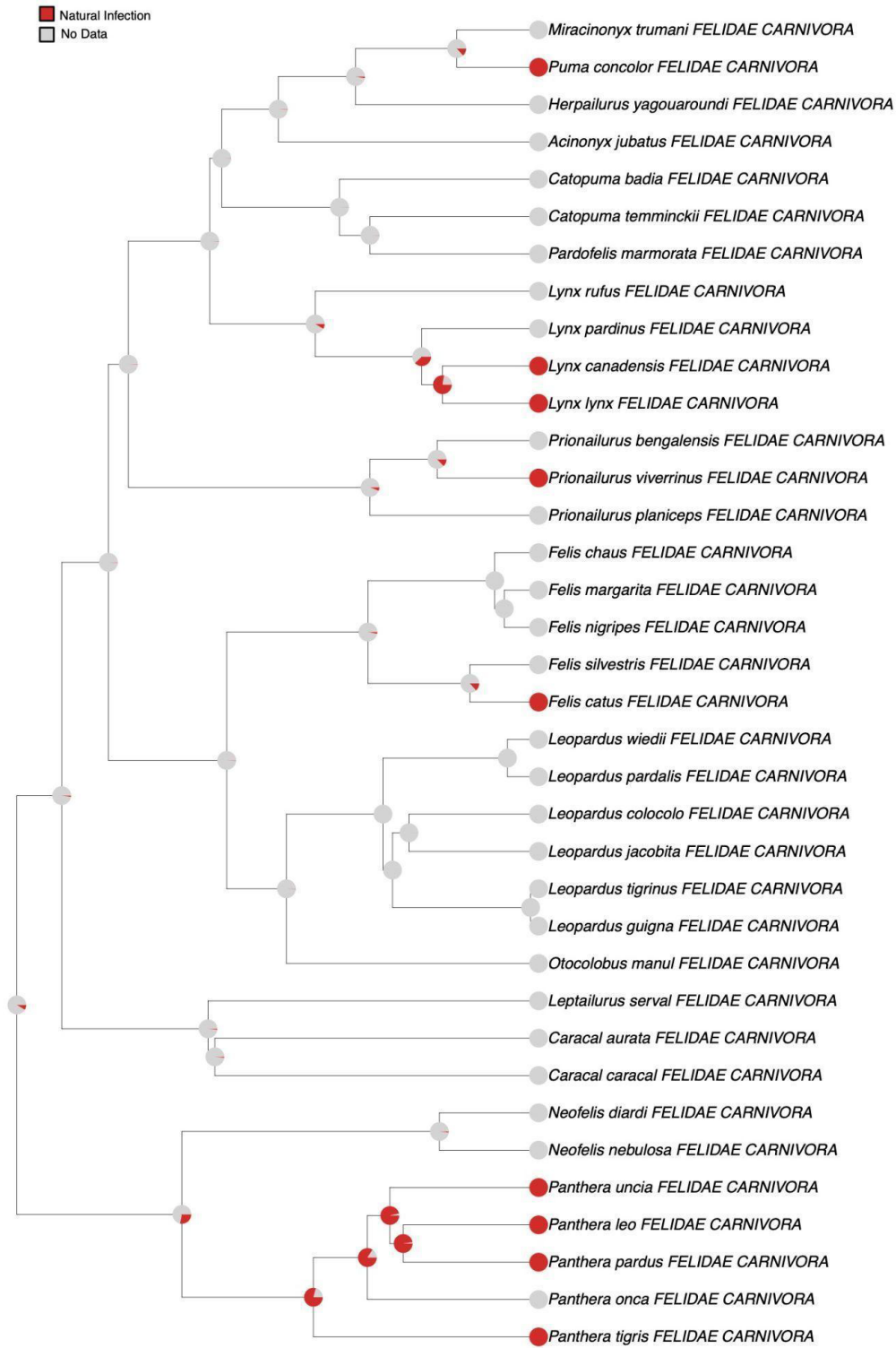


Figure S6: Ancestral character estimation SARS-CoV-2 infection for the Felidae (cats).

Phylogeny limited to just species with DNA and time-scaled using node dating

(TopoFree_ND; Upham et al. 2019).