

## Readme

The deposited data were used in dated BEAST2 analyses and SNAPP analyses implemented in BEAST2.

Data were extracted from whole genomes deposited in GenBank under the following accession numbers.

<i>Otolemur garnettii</i>	#451
<i>Propithecus coquereli</i>	#24390
<i>Microcebus murinus</i>	#777
<i>Tarsius syrichta</i>	#766
<i>Aotus nancymaae</i>	#14430
<i>Callithrix jacchus</i>	#442
<i>Saimiri boliviensis</i>	#6907
<i>Nomascus leucogenys</i>	#480
<i>Pongo abelii</i>	#325
<i>Gorilla gorilla</i>	#2156
<i>Homo sapiens</i>	#51
<i>Pan troglodytes</i>	#202
<i>Pan paniscus</i>	#10729
<i>Colobus angolensis</i>	#36539
<i>Rhinopithecus roxellana</i>	#7996
<i>Nasalis larvatus</i>	#7994
<i>Chlorocebus sabaeus</i>	#13136
<i>Papio anubis</i>	#394
<i>Cercocebus atys</i>	#13303
<i>Mandrillus leucophaeus</i>	#36538
<i>Macaca nemestrina</i>	#13267
<i>Macaca mulatta</i>	#215
<i>Macaca fascicularis</i>	#776

All scripts used to extract these data, generate alignments and perform analyses are deposited at GitHub (<https://github.com/boopsboops/primates-genome-phylo>) and (<https://github.com/legalLab/primates-genome-phylo>).