

Supporting Information

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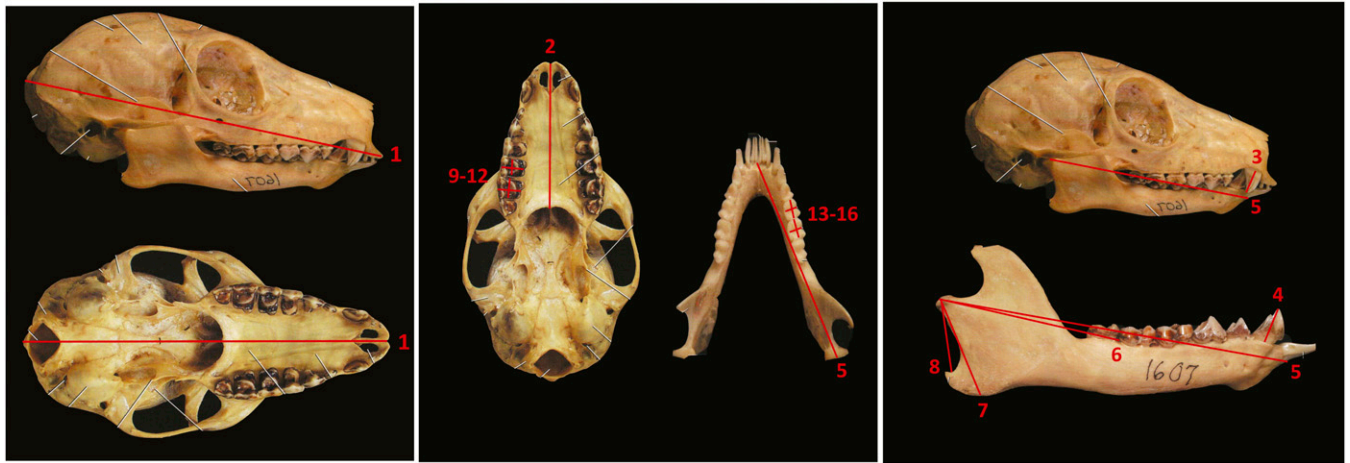


Fig. S1. Schematic of cranial and mandibular measurements. (1) Cranium length: prosthion to inion (i.e., distance from the most anterior point on the maxillary alveolar process, between the central incisors, to the most prominent projection on the occipital bone at the posteroinferior part of the skull). (2) Palate length: prosthion to alveolare (i.e., distance from the most anterior point on the maxillary alveolar process, between the central incisors, to the posterior palatine). (3) Upper canine length: length of the upper canine from gumline to tip. (4) Lower p2 length: length of the lower second (caniniform) premolar from gumline to tip. (5) Mandible length: infradentale to the posterior edge of the mandibular condyle. (6) Superficial masseter origin: measured from the posterior edge of the mandibular condyle to the posterior margin of m2. (7) Mandibular height: measured from the superior edge of the mandibular condyle to the base of the mandibular corpus. (8) Superficial masseter insertion: measured from the superior edge of the mandibular condyle to the superior edge of the angular process. (9) Upper M1 length: length at the longest point on the upper M1. (10) Upper M1 width: width at the broadest point on the upper M1. (11) Upper M2 length: length at the longest point on the upper M2. (12) Upper M2 width: width at the broadest point on the upper M2. (13) Lower m1 length: length at the longest point on the lower m1. (14) Lower m1 width: width at the broadest point on the lower m1. (15) Lower m2 length: length at the longest point on the lower m2. (16) Lower m2 width: width at the broadest point on the lower m2.

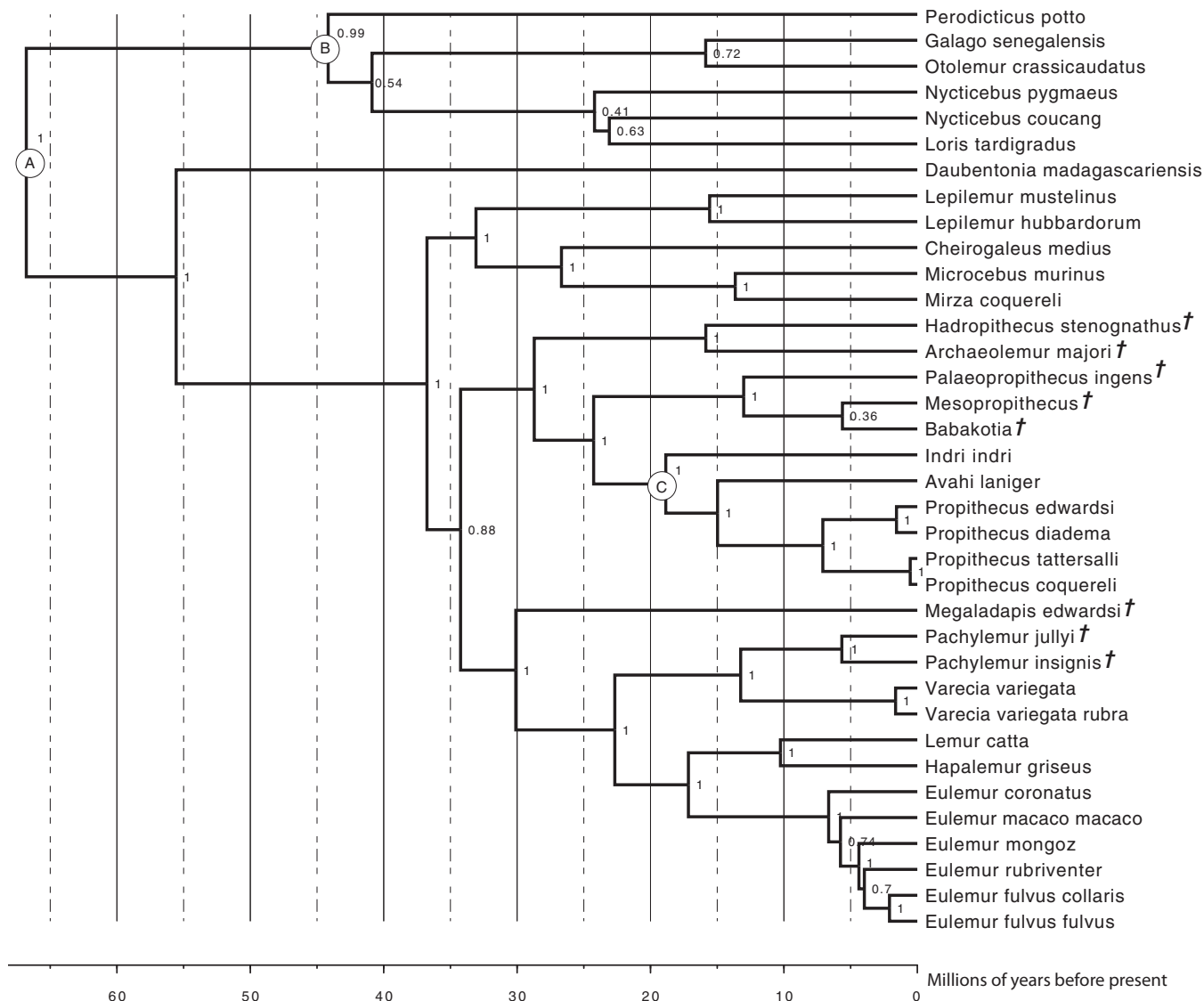


Fig. S2. Lemuriform molecular phylogeny. Maximum clade credibility tree summarizing the results of Bayesian dating analyses (fossil calibration nodes marked with letters A–C) with normal probability priors on nodes B and C and a lognormal probability prior on node A. Numbers at the nodes show Bayesian posterior probabilities (BPPs). Daggers (†) next to species names indicate extinct taxa.

Other Supporting Information Files

- [Dataset S1 \(XLS\)](#)
- [Dataset S2 \(XLSX\)](#)
- [Dataset S3 \(XLSX\)](#)
- [Dataset S4 \(XLSX\)](#)
- [Dataset S5 \(XLSX\)](#)
- [Dataset S6 \(XLSX\)](#)
- [Dataset S7 \(XLSX\)](#)
- [Dataset S8 \(XLSX\)](#)