



**Fig 1. Species-level relationships and tempo of diversification across mammals.** The node-dated molecular phylogeny of 5,911 extant and recently extinct species shows branches colored with tip-level speciation rates (tip DR metric; interior branches reconstructed using Brownian motion for visual purposes only). Zoom in to the branch tips to see species labels (gray branches of 1,813 species are included via taxonomic constraints rather than DNA). The maximum clade credibility topology of 10,000 trees is shown, and numbered clade labels correspond to orders and subclades listed in the plot periphery; scale in Ma. Dryad data: <https://doi.org/10.5061/dryad.tb03d03>; phylogeny subsets: <http://vertlife.org/phylousubsets>. Afro, Afrotheria; Euar, Euarchontoglires; Lago, Lagomorpha; Laur, Laurasiatheria; Ma, millions of years; Mars, Marsupialia; tip DR, tip-level pure-birth diversification rate; X, Xenarthra. Artwork from phylopic.org and open source fonts (see S1 Text, section 9 for detailed credits).

<https://doi.org/10.1371/journal.pbio.3000494.g001>

random variation in the placement of unresolved branches [87]. Versions of the MRP super-tree have been widely applied to questions of species diversification (e.g., [1,9,88,89]) and conservation (e.g., [25,29,90,91]) despite the initially unresolved species and consequent potential for artifacts in downstream analyses, in part because it contained the only estimates of evolutionary branch lengths across most of Mammalia.

