only the topology of gene trees based on summary statistics, whereas fully parametric methods use all aspects of the data to infer phylogenies (4, 21). Because partially parametric methods use only part of the information contained in the data, they usually require more loci than fully parametric methods to achieve a certain level of confidence in the results (4, 21). However, partially parametric methods have computational advantages because these methods can quickly infer phylogenies from large-scale genomic data. In contrast, it is difficult to apply fully parametric methods to such data sets due to their extensive

computational demands. Additionally, MP-EST and STAR are robust to violation of the assumptions that underpin many coalescent analyses. Because both methods are based on summary statistics calculated across all gene trees, a small number of outlier genes that significantly deviate from the coalescent model have little effect on the ability of either method to accurately reconstruct species trees. We compared the results from both coalescent methods with those from concatenation analyses implemented in two popular phylogenetic algorithms, MrBayes (Bayesian) (22) and RAxML (maximum likelihood) (23).
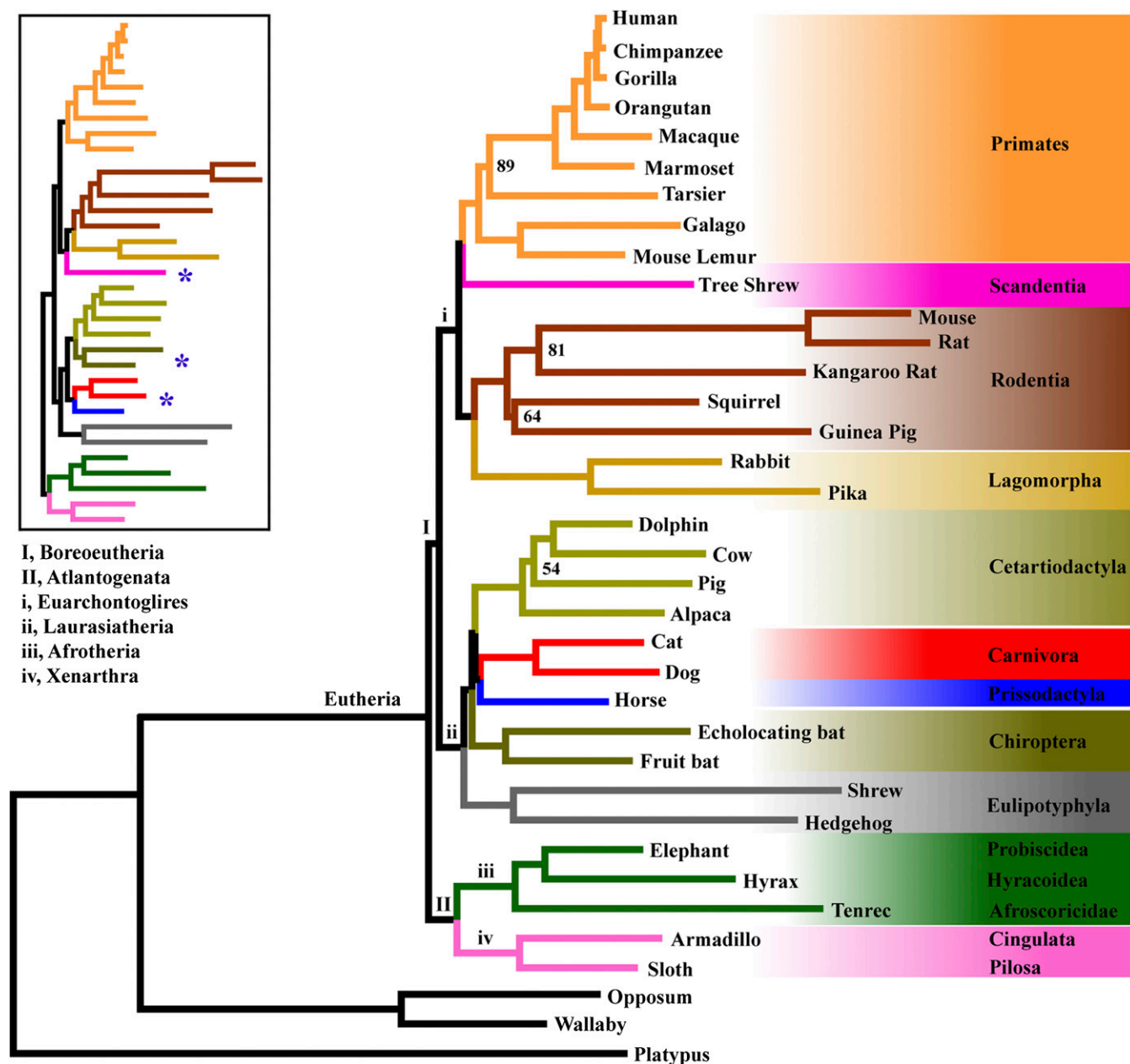

Fig. 1. Evolutionary relationships of eutherian mammals. The phylogeny was estimated using the maximum-pseudolikelihood coalescent method MP-EST with multilocus bootstrapping (8, 40). The numbers on the tree indicate bootstrap support values, and nodes with bootstrap support >90% are not shown. Branch lengths were estimated by fitting the concatenated sequence data for all 447 loci to the MP-EST topology using standard ML and an appropriate substitution model in PAUP* v.4.0 (45). (*Inset*) The eutherian phylogeny estimated using the Bayesian concatenation method implemented in MrBayes (22). The ML concatenation tree built by RAxML (23) is identical to the Bayesian concatenation tree in topology. Branches of the concatenation tree are coded by the same colors as in the MP-EST tree. The blue asterisks indicate the position of Scandentia (tree shrews), Chiroptera (bats), Perissodactyla (odd-toed ungulates), and Carnivora (carnivores), whose placement differs from the coalescent tree. The Bayesian concatenation tree received a posterior probability support of 1.0 for all nodes. In *SI Appendix*, Fig. S2, the concatenation tree with taxon names is shown.

EVOLUTION