



Fig. 1. Phylogenetic time tree of mammalian families (13) created on the basis of an analysis of the amino acid matrix (autocorrelated rates and hard-bounded constraints) of 164 mammals, rooted with five vertebrate outgroups (chicken, zebrafish, green anole, frog, and zebrafish; see SOM for trees with outgroups). All nodes were strongly supported ($BS \geq 90\%$, $BPP \geq 0.95$) in amino acid and DNA analyses except for nodes that are denoted by solid blue circles (conflict between DNA and amino acid trees) or solid black circles (DNA and amino acid trees agree, but with $BS < 90\%$). Strongly supported nodes that disagree with Bininda-Emonds *et al.* (8) are indicated with solid red circles. Several nodes that remain difficult to resolve

(e.g., placental root) have variable support between studies of rare genomic changes (29, 30), as well as genome-scale data sets (31–33), which suggest that diversification was not fully bifurcating or occurred in such rapid succession that phylogenetic signal tracking true species relations may not be recoverable with current methods. The KPg boundary is denoted by the transition from gray background (Mesozoic) to white background (Cenozoic). Color-coded branches in Placentalia correspond to Laurasiatheria (green), Euarchontoglires (blue), Xenarthra (orange), and Afrotheria (pink). See table S11 for ordinal affiliations of mammalian families. [Mammal paintings are by Carl Buell]