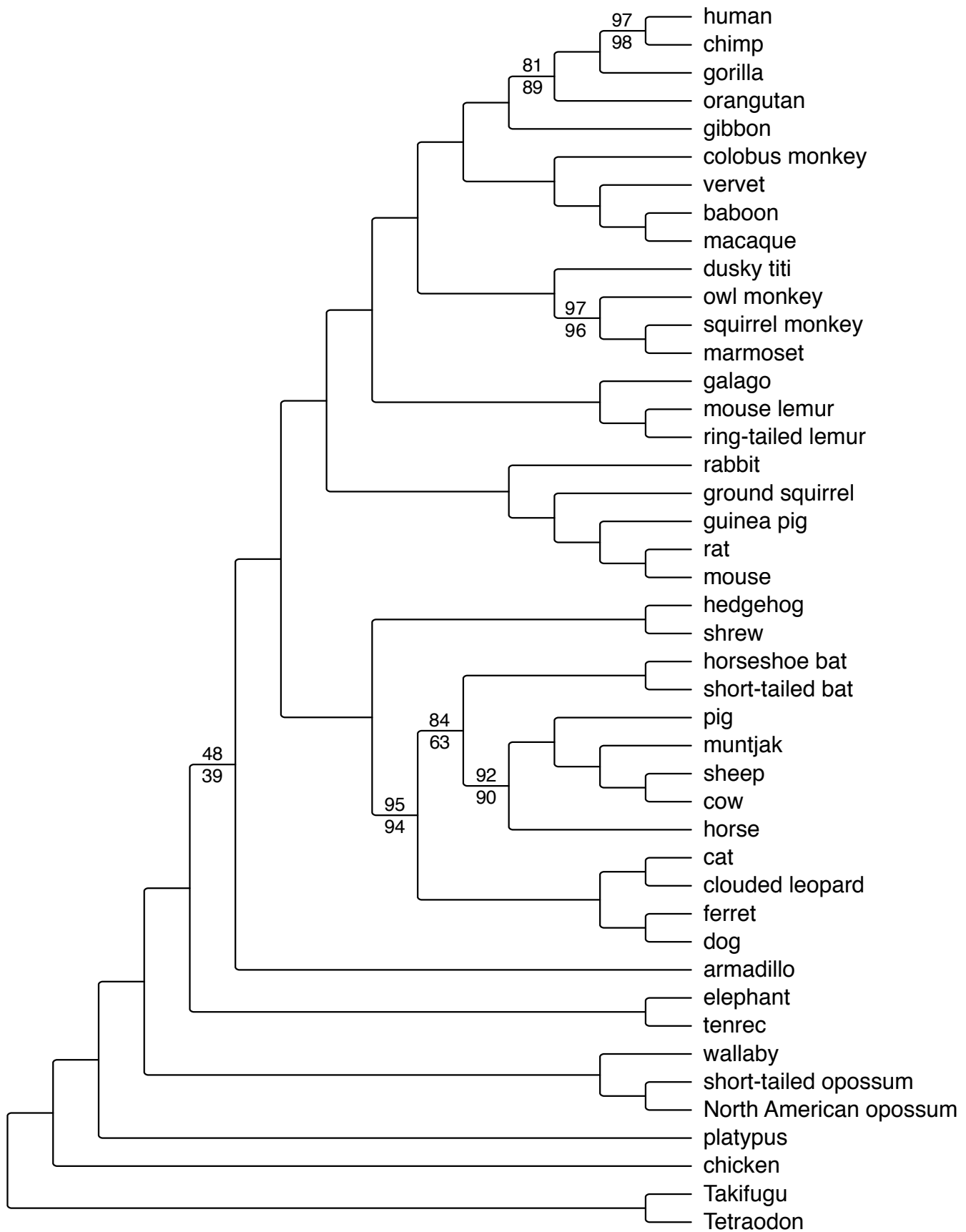
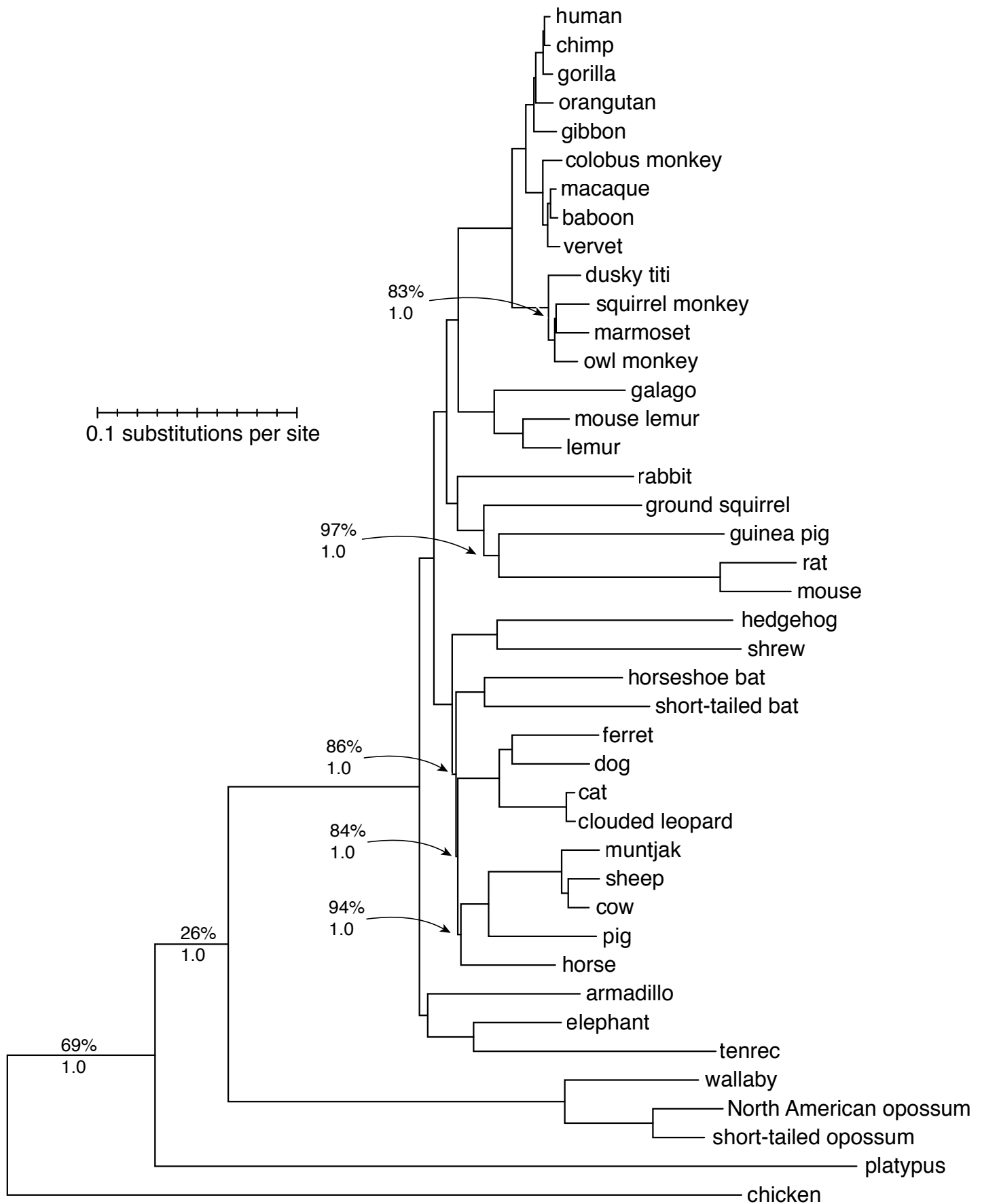


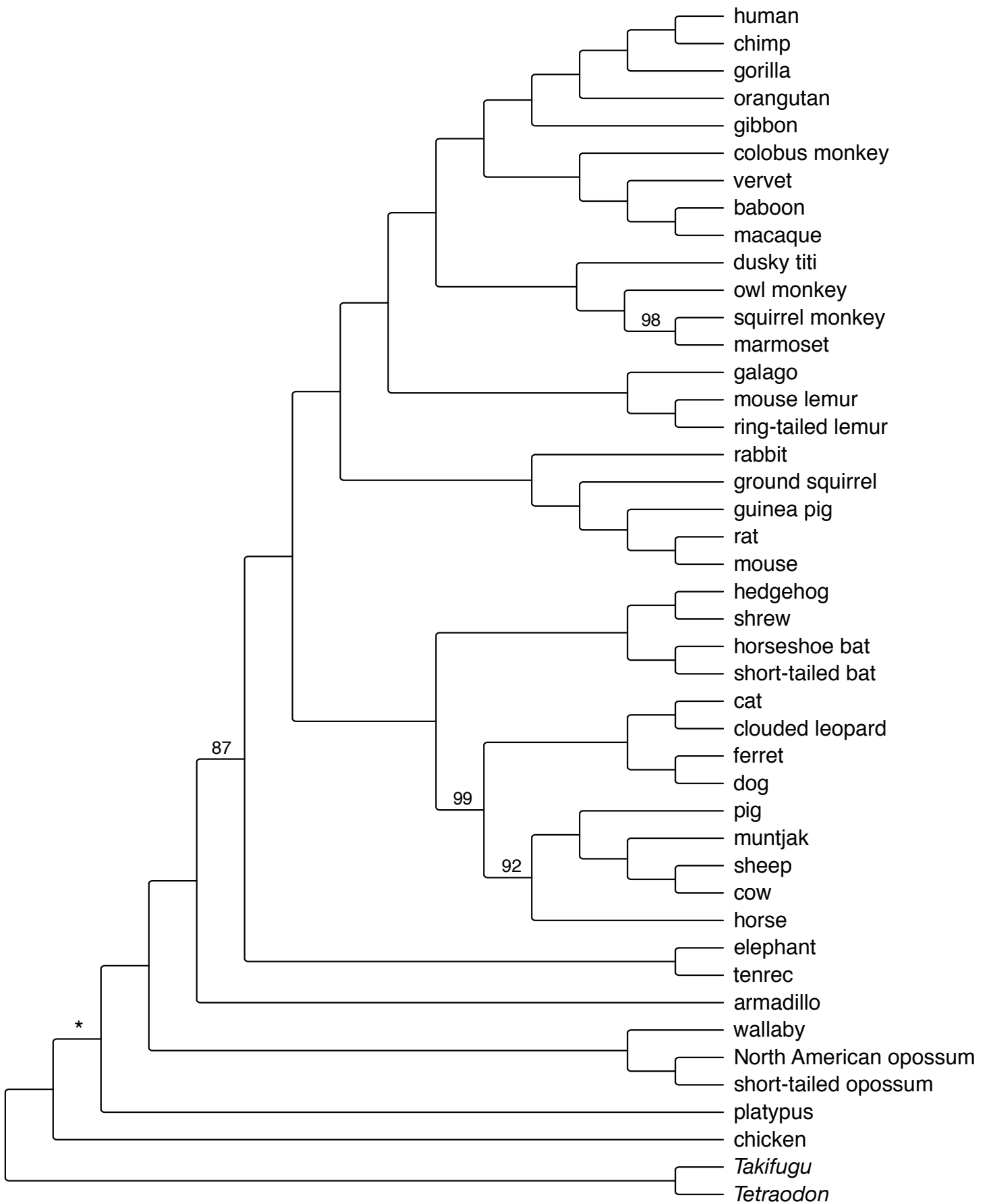
Supplementary Figure 1: Coding sequence maximum likelihood tree. Tree was produced using a GTR + gamma codon partitioned model of sequence evolution. Bootstrap support and Bayesian posterior probabilities for all branches are 100% and 1.0, respectively, unless noted with an arrow and a number. Numbers ending with '%' are maximum likelihood bootstrap proportions, and numbers containing a decimal (e.g. 1.0) are Bayesian posterior probabilities. The branch constraining platypus to the mammals is marked with an asterisk (*) to reflect the fact that it was constrained during analysis and thus has no support figures associated with it.



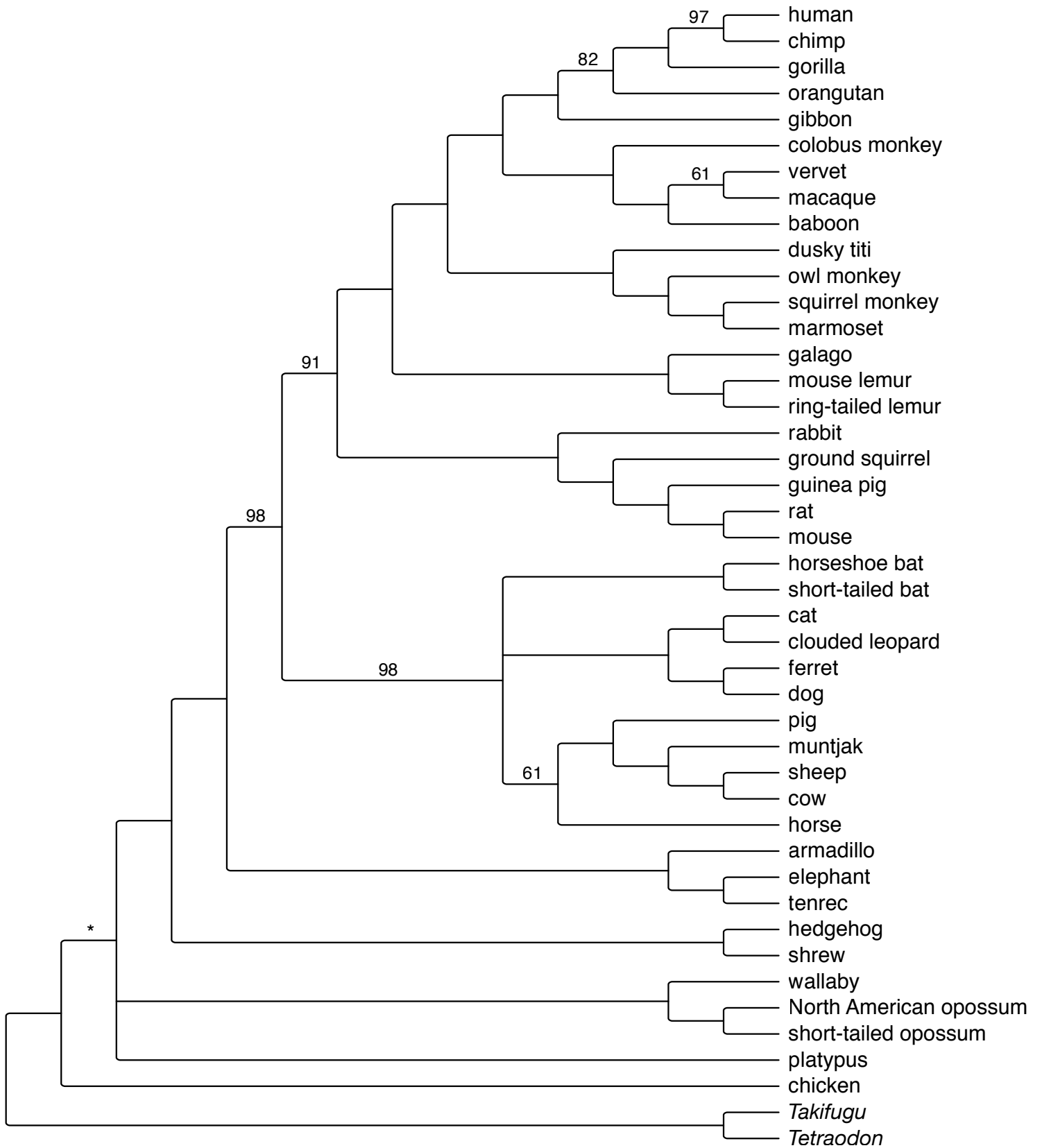
Supplementary Figure 2: Maximum likelihood bootstrap values (in %, above line) compared to majority rules consensus of sampled Bayesian majority rules trees (in %, below line). All nodes without numbers appear in 100% of bootstrap replicates. Maximum likelihood tree was created from bootstrapped nucleotide-coded coding sequence data and a single partitioned GTR + gamma model of sequence evolution with RAxML-HPC. Bayesian results are for bootstrapped nucleotide-coded coding sequence data analyzed with single-partitioned GTR + gamma + I models. The majority rules consensus tree for each run was taken at stationarity (after 166,700 generations). Bootstrap proportions were then taken from the proportion of those trees containing each group.



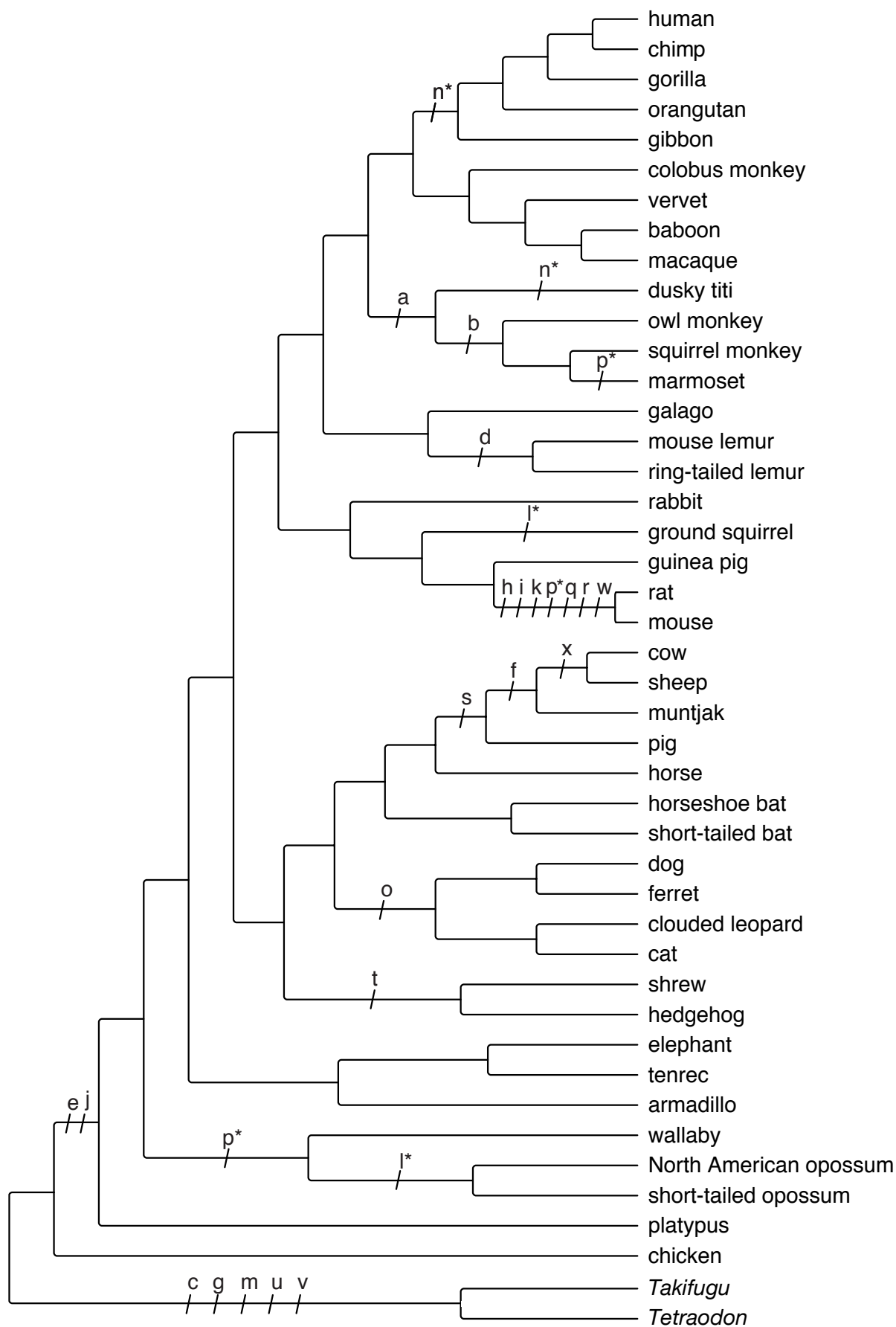
Supplementary Figure 3: Nucleotide-coded maximum likelihood tree for coding plus conserved non-coding matrix. Made with GTR + gamma models with parameters partitioned into three partitions for codon position and one for conserved non-coding positions. Bootstrap support and Bayesian posterior probabilities for all branches are 100% and 1.0, respectively, unless noted with a number. Numbers ending with '%' are maximum likelihood bootstrap proportions, and numbers containing a decimal (e.g. 1.0) are Bayesian posterior probabilities.



Supplementary Figure 4: Maximum parsimony majority rules bootstrap consensus tree for RY-coded coding plus conserved non-coding sequence matrix. 1000 bootstrap replicates with 10 random addition SPR runs with each. Nodes with numbers are bootstrap proportions in %, all others at 100% bootstrap support. Asterisk used to mark the branch constraining the platypus to the mammals which was constrained for this analysis.



Supplementary Figure 5: Neighbor joining majority rules bootstrap tree from coding plus conserved non-coding RY-coded sequence partition. 1000 bootstrap replicates with maximum likelihood distances from unpartitioned CF+G+I models. All branches have 100% bootstrap support unless otherwise noted with a number indicating bootstrap proportion (in percent). The branch constraining the platypus to the mammals indicated with an asterisk to reflect the fact that this branch was constrained for this analysis. Polytomies have less than 50% bootstrap proportion support.



Supplementary Figure 6: Informative coding indels. Maximum likelihood tree from RY-coded protein-coding sequence partition (see Figure 1 in the paper for details). Informative coding indels are marked by crosshatches and labeled with letters a-x. Indels marked with an asterisk appear homoplasic on this tree, and all taxa sharing the implied derived state are marked with the same letter. Indels a&b are from *ASZ1*; c&d are from *CAV1*; e-o from *CFTR*; p-t from *CTTNBP2*; and u-w from *MET*. Sequence alignments for each indel are available in as Supplement S4.