

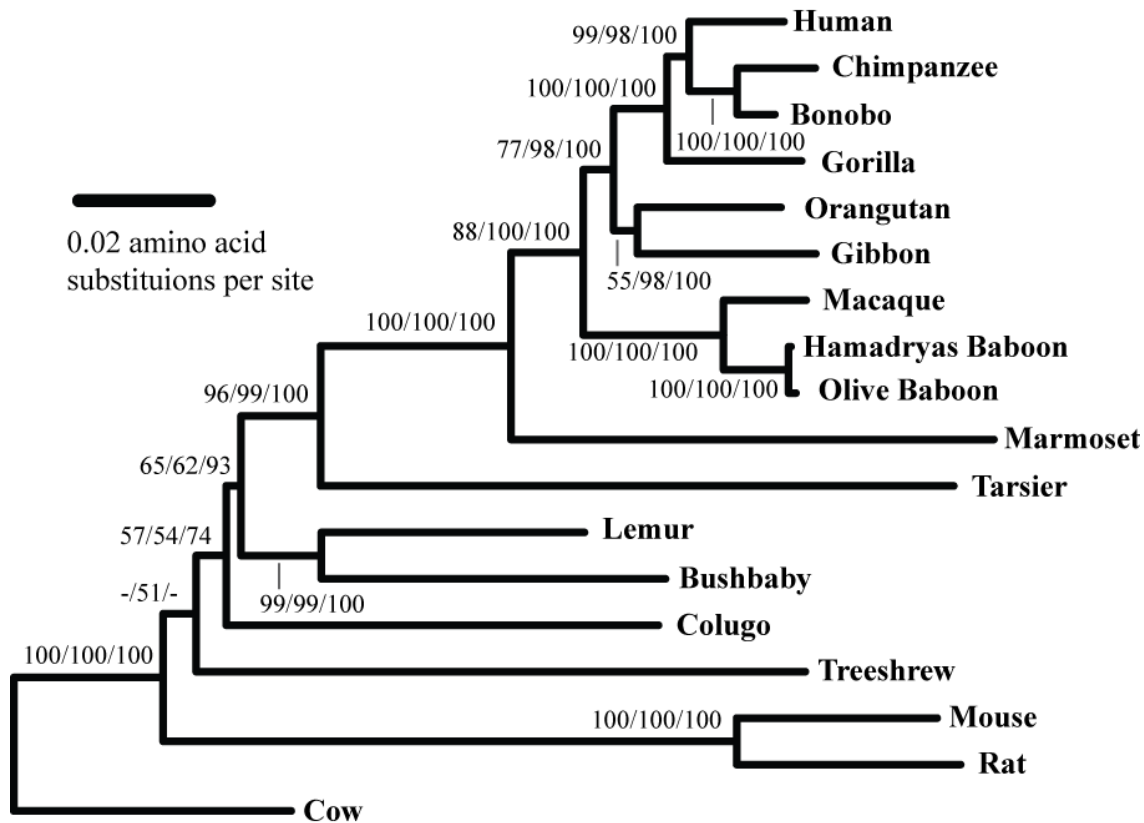


Figure S2. The maximum-likelihood phylogeny inferred from the supermatrix dataset. The sequences are based on concatenated eight orthologous alignments (2810 amino acids). The numbers to the left of the nodes show the bootstrap support values (%) for neighbor-joining and maximum-likelihood reconstructions, and posterior probabilities (%) for the Bayesian analysis, respectively. Note that the codons to have frame-shifts and in-frame stop codons are removed in the alignments. Cow TAAR sequences are used as the outgroup.