Fig. S1. The maximum likelihood (ML) phylogenetic trees for yeasts (A) and mammals (B). The ML phylogenies were reconstructed based on the concatenation data sets of 2,832 yeast genes and 2,002 mammalian genes using RAxML, respectively. Internodes without designation in concatenation phylogeny indicate 100% bootstrap support. Thick branches in mammals (B) show conflicts between concatenation phylogeny and eMRC phylogeny (Fig. 1).
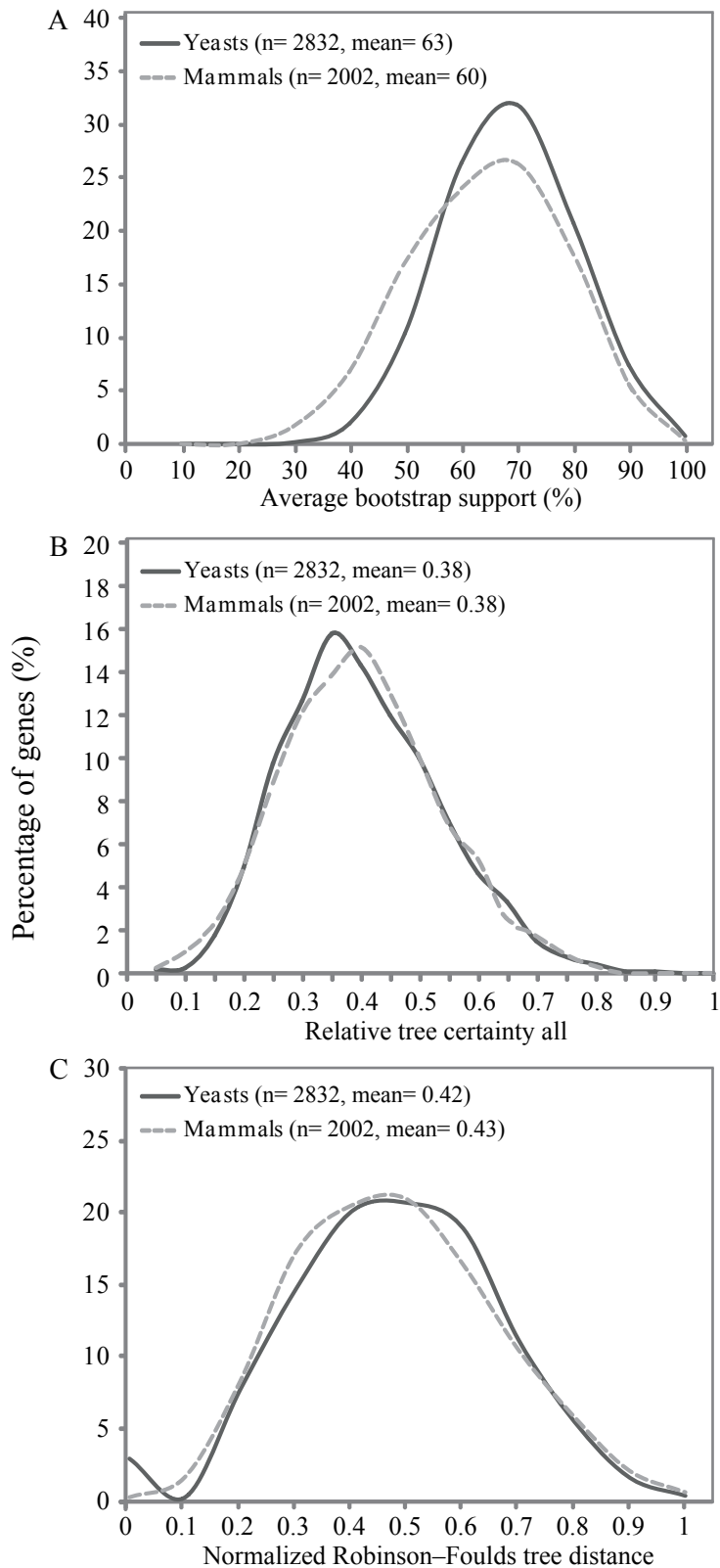
Fig. S2. The distributions of three general properties for full-length data sets in yeast and mammals. For each maximum likelihood tree, average bootstrap support (A), relative tree certainty all (B), and Normalized Robinson–Foulds tree distance in recovering extended majority-rule consensus (eMRC) phylogeny (C) were estimated. Detailed values for the three general properties are provided in supplement tables (see supplementary Table S2 and S3).