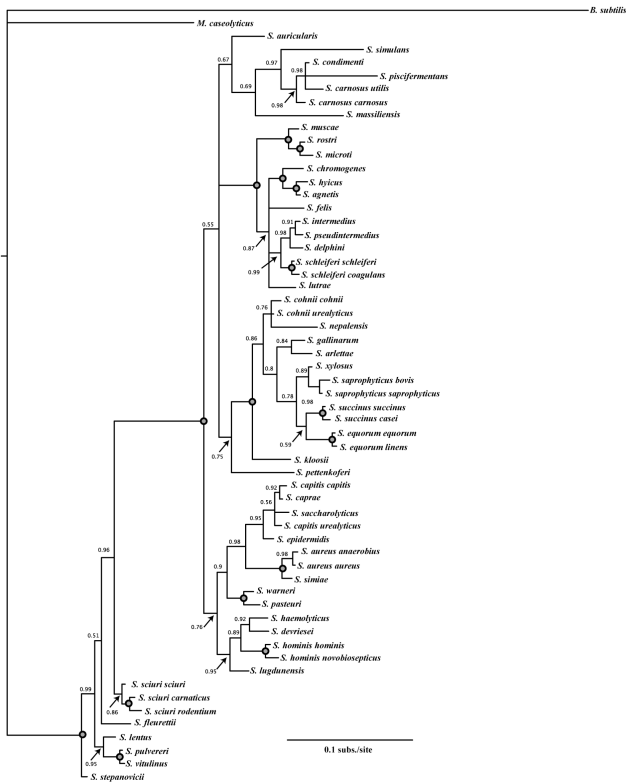
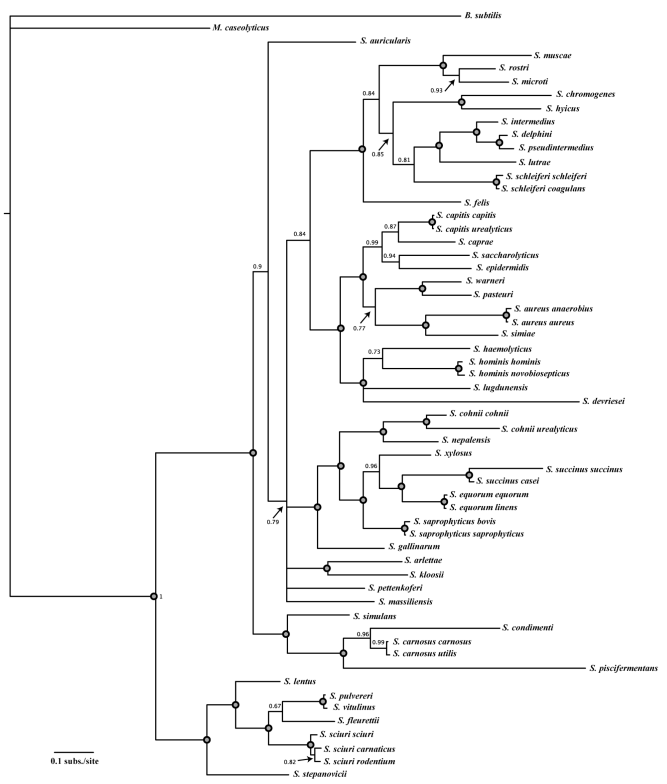
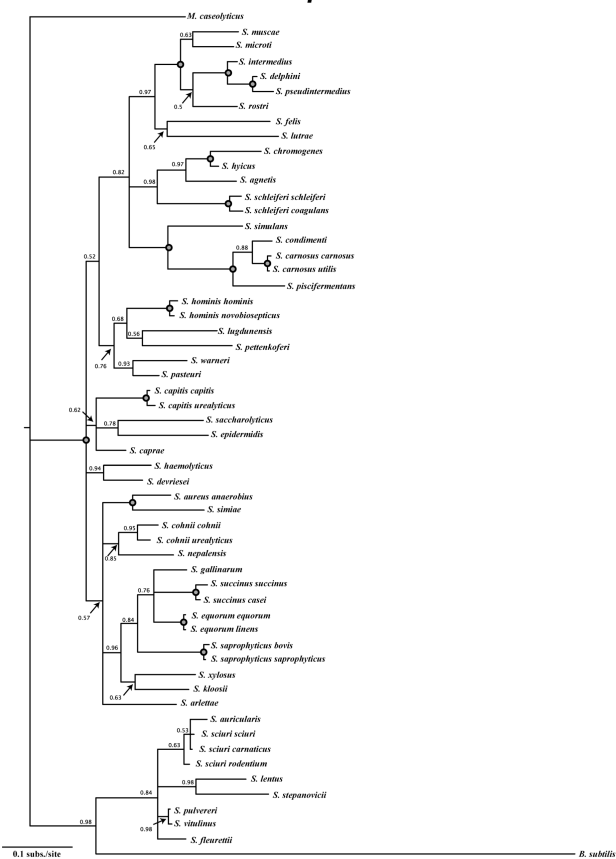
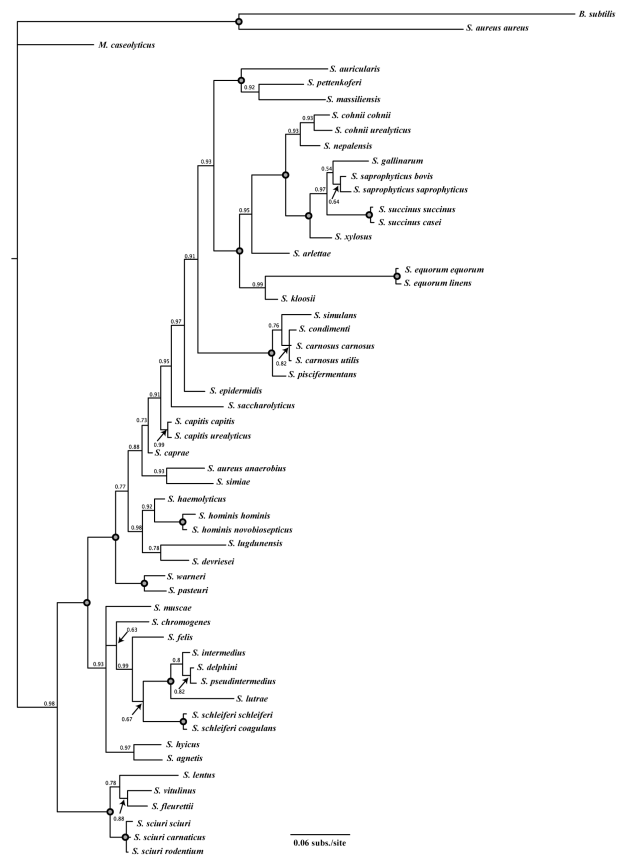


A**16S rRNA****B****dnaJ****C****rpoB****D****tuf**

Supplementary Figure S1. Gene trees for individual loci assessed in this study. Shown are Bayesian 50% majority rule phylograms for A) the 16S rRNA, B) *dnaJ*, C) *rpoB*, and D) *tuf* gene fragments. MrBayes was run under the same conditions as those used for concatenated analyses with evolutionary model specified for whole gene fragments in Supplementary Table S2. Numbers represent posterior probabilities with grey-filled circles representing a posterior support of 1.00.