Supplementary Figure S1A. Bayesian majority-rule consensus trees reconstructed for the ten replicate nuclear concatenated data sets. Trees are presented as phylograms with branch lengths representing the average number of substitutions per site. Filled red circles on branches indicate posterior probability (PP) support of 0.95 or greater. Numbers on branches represent PPs < 0.95.
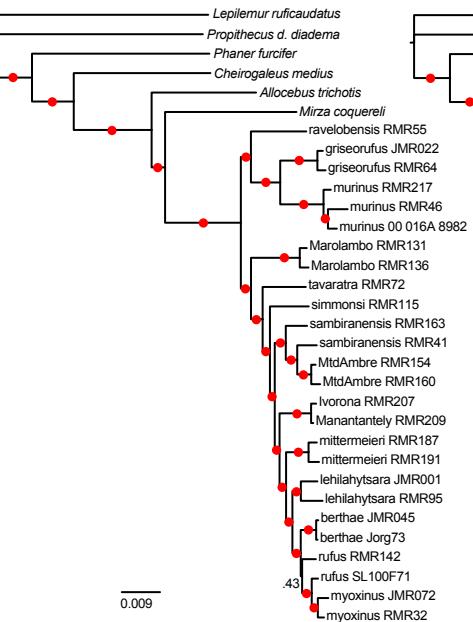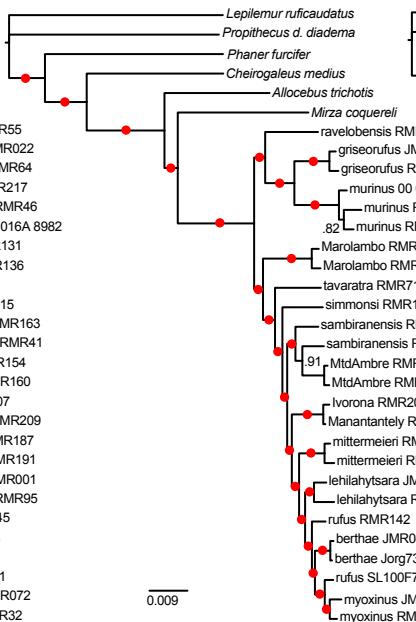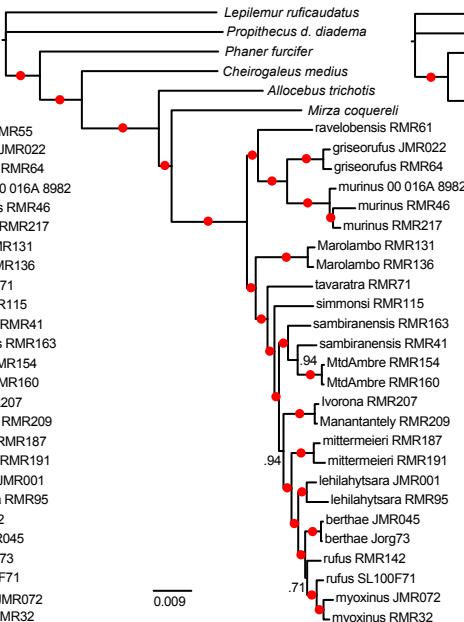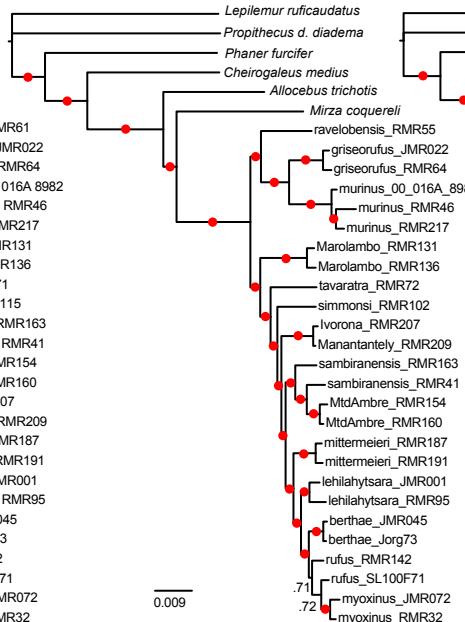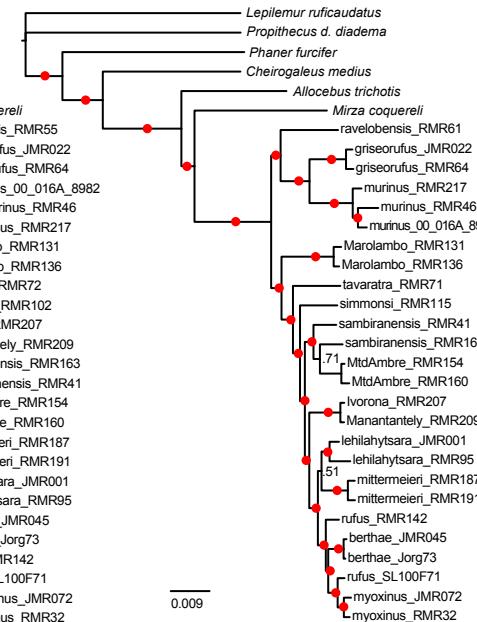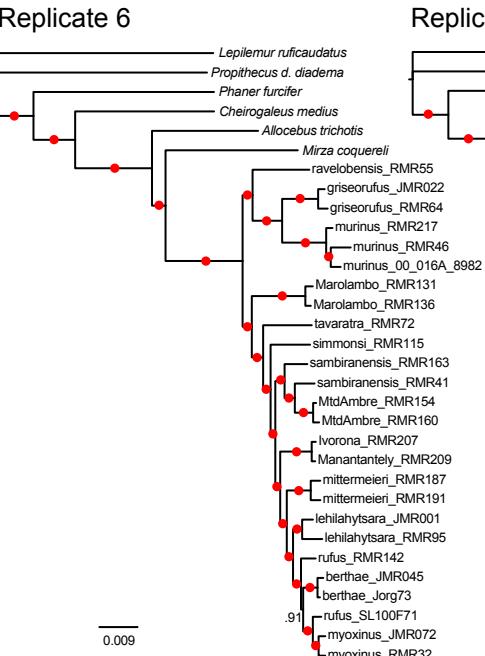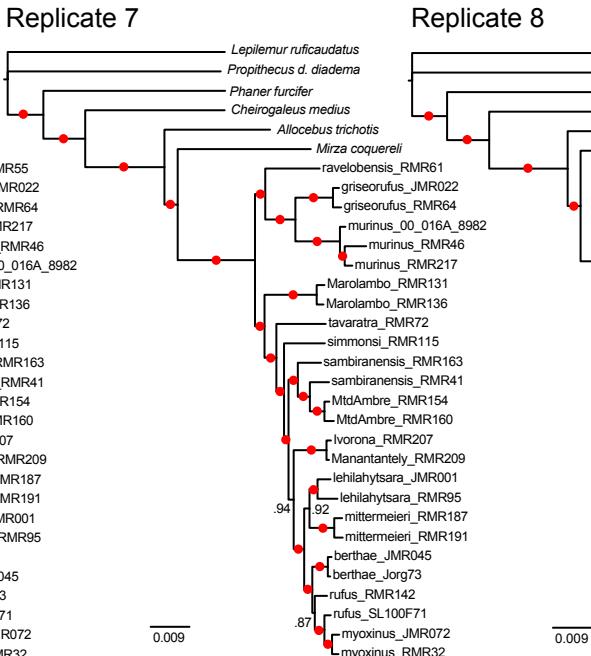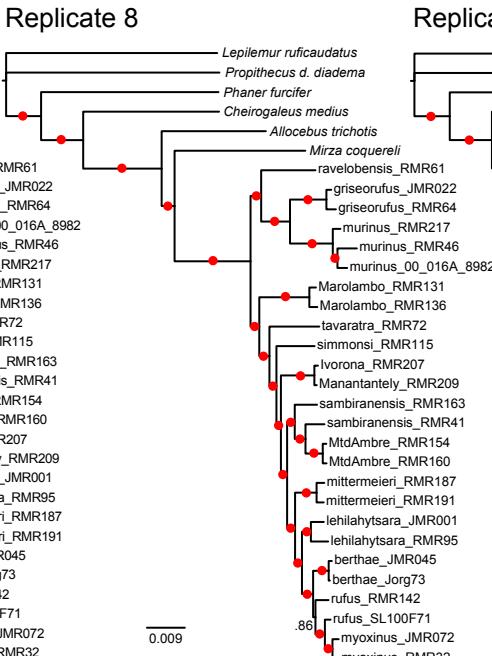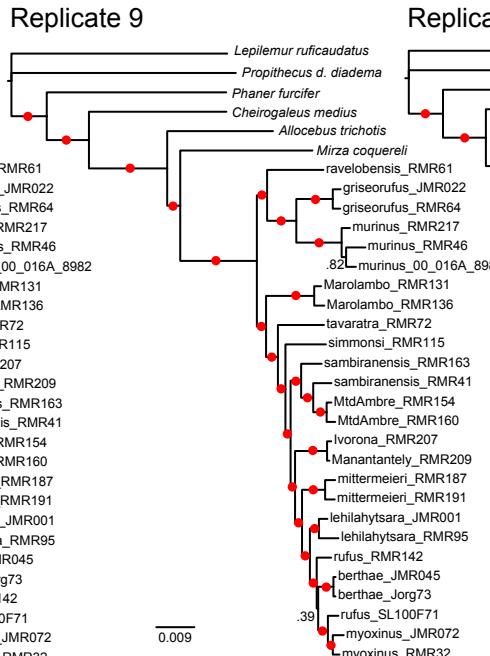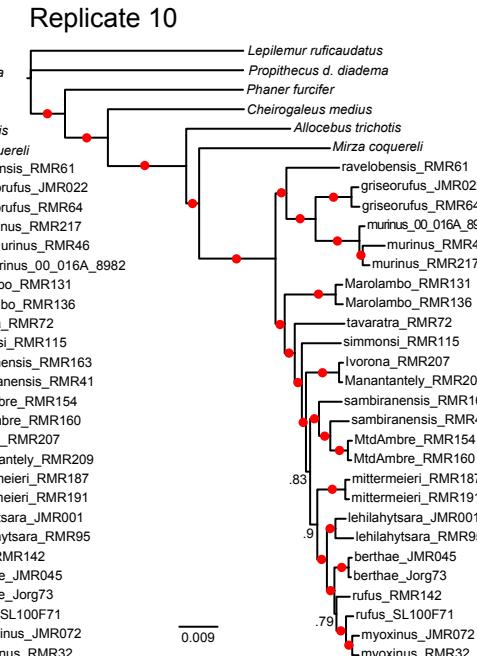
Supplementary Figure S1B. Bayesian majority-rule consensus trees reconstructed for the ten replicate nuclear+mtDNA concatenated data sets. Trees are presented as phylograms with branch lengths representing the average number of substitutions per site. Filled red circles on branches indicate posterior probability (PP) support of 0.95 or greater. Numbers on branches represent PPs < 0.95.