Supplementary Material 8. Bayesian analysis of independent genes 28S rRNA, 12S rRNA, and 16S rRNA, implemented in MrBayes. Putative species names are listed on the right, with corresponding number in parentheses (see Fig. 2; Suppl. Mat. 4). Support values are posterior probabilities (PP); branches with PP < 50% were collapsed, and intraspecific support values were removed for legibility except where relevant (i.e., if there was conflict between delimited ESUs or prior species assignations).