

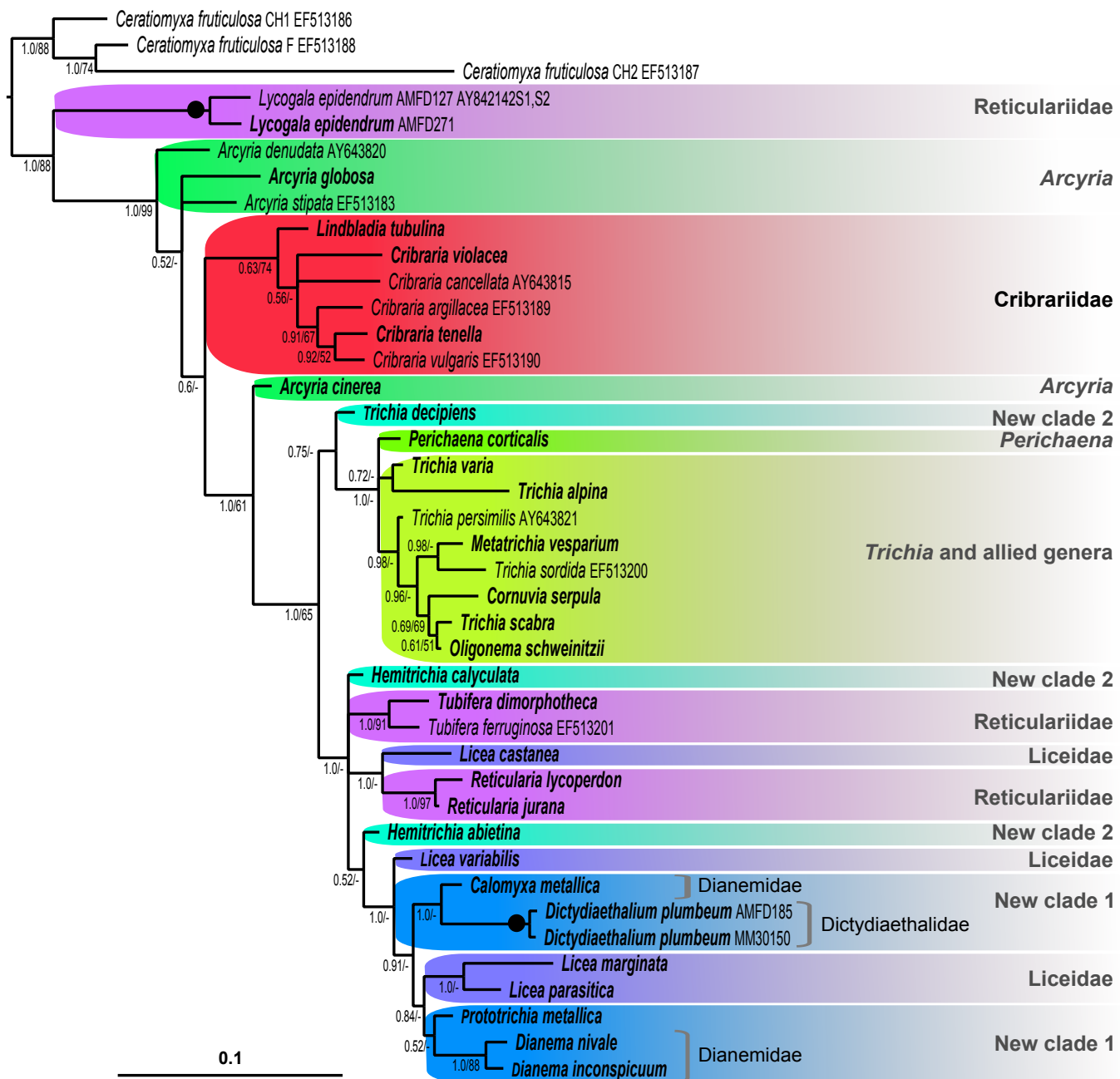


Figure S2. EF-1alpha gene tree of Lucisporidia derived by Bayesian inference of 380 amino-acid positions of 38 taxa, with *Ceratiomyxa fruticulosa* as outgroup. Species names are followed by GenBank accession number, except for sequences obtained during this study (in bold), whose accession numbers and collection sites are in Table S1; Groups are labelled and highlighted as in Fig. 1, with labels in grey if appearing as polyphyletic, in black if monophyletic. Bayesian posterior probabilities (BPP)/ML bootstrap replicates (MLB) are shown for each branch; dashes indicate a conflicting topology in the ML tree; a dot on the line indicates maximum support in both analyses. The scale bar indicates the fraction of substitutions per site.