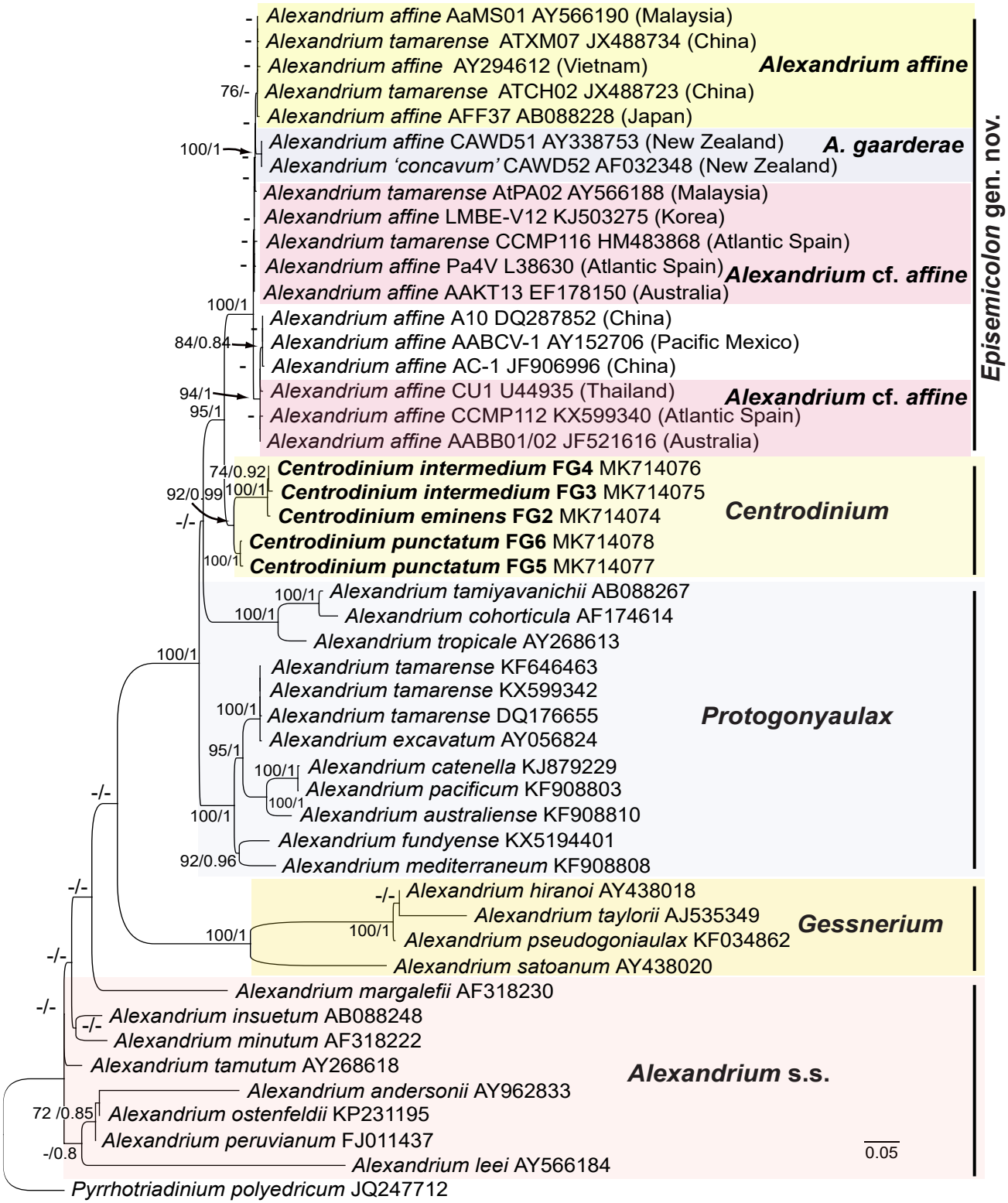

Figure S1. Maximum-likelihood phylogenetic tree of the D1–D2 domains of the LSU rRNA gene of selected species of *Alexandrium* sensu lato and *Centrodinium* spp. Supports at internal nodes are Bootstrap support (BP) >70 and Posterior Probability (PP) >0.8 are shown. *Pyrrhotriadinium polyedricum* was used as outgroup. New sequences are highlighted in bold. The scale bar represents the number of substitutions for a unit branch length.