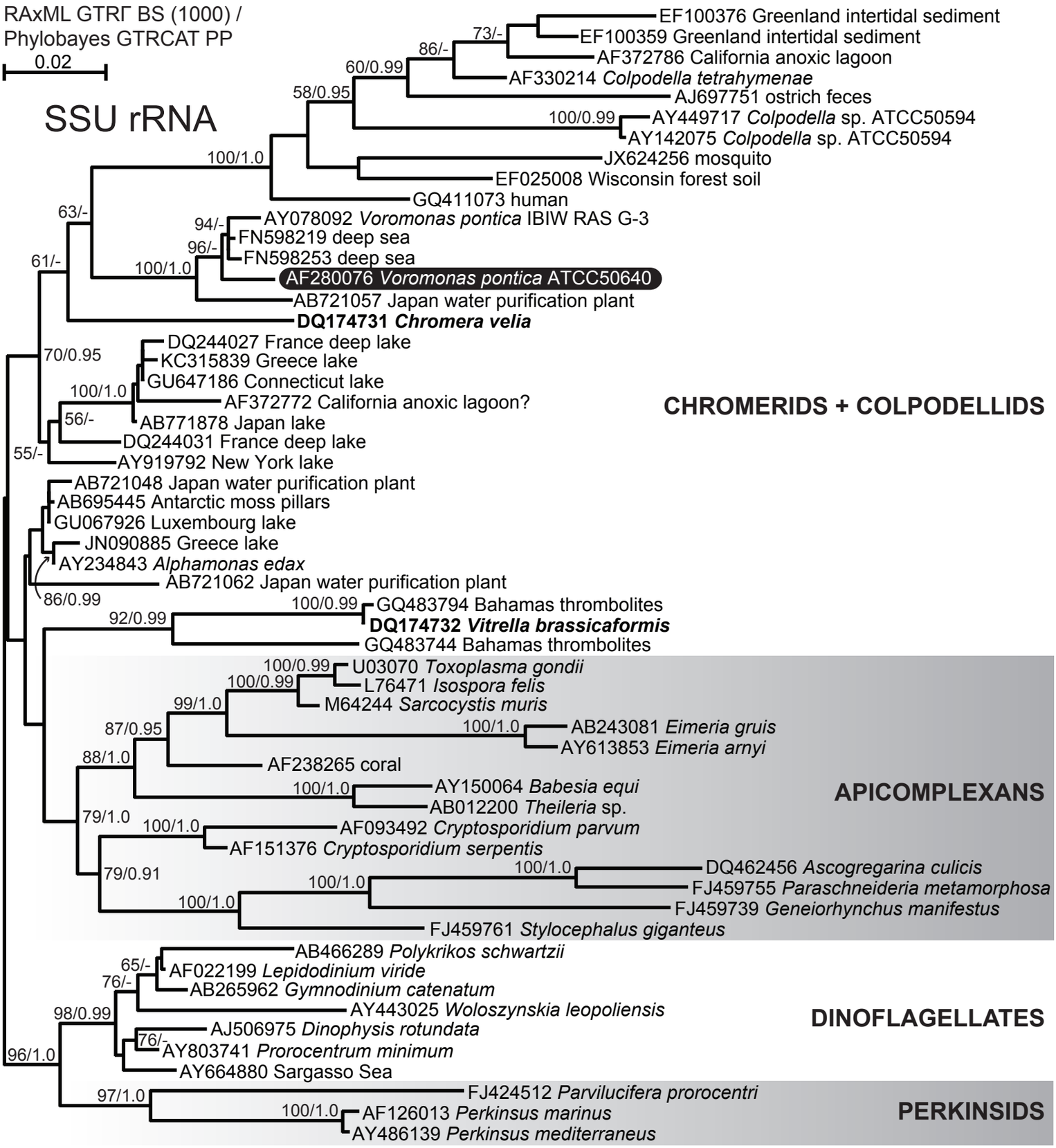

Fig. S1. Maximum likelihood phylogeny of small subunit rRNA sequences from alveolates representing the available diversity of colpodellids, chromerids, and related environmental sequences. Support for nodes is indicated by % bootstrap support (out of 1000) in the ML analysis (RAxML GTRΓ) / Bayesian posterior probability (Phylobayes GTRCAT) where greater than 55 or 0.9. The subject of this study, *Voromonas pontica*, is indicated by white text on a black background. The photosynthetic chromerids *Chromera velia* and *Vitrella brassicaformis* are indicated by bold text. A question mark after accession AF372772 indicates a possible misidentification or chimeric sequence; this study also sampled a lake.