

Fig. S2. The Bayesian tree for the Ycf16 obtained in PhyloBayes under the LG+ Γ model. Eukaryotic taxa are placed in colored rectangles. Sequences encoded in the nuclear genome are underlined. The nucleomorph-encoded sequence of the chlorarachniophyte *Bigelowiella natans* is double-underlined. Sequences of unknown localization are indicated by the asterisk “*”. Numbers at nodes, in the order shown, correspond to: posterior probabilities estimated in Phylobayes for LG+ Γ model (PP-LG) and CAT+ Γ model (PP-CAT), as well as support values resulting from bootstrap analysis in PhyML (B-Ph) and TreeFinder (B-TF). Additionally, the minimum of support values calculated in PhyML by χ^2 and Shimodaira-Hasegawa-like procedure (χ^2 -SH) and support values obtained by Local Rearrangements-Expected Likelihood Weights method in TreeFinder (LR-EWL) are shown for selected nodes relating to the position of the dinoflagellate *Ceratium horridum* sequence. Values of the posterior probabilities and bootstrap percentages lower or equal to 0.50 and 50%, respectively, were omitted or indicated by a dash “-”.

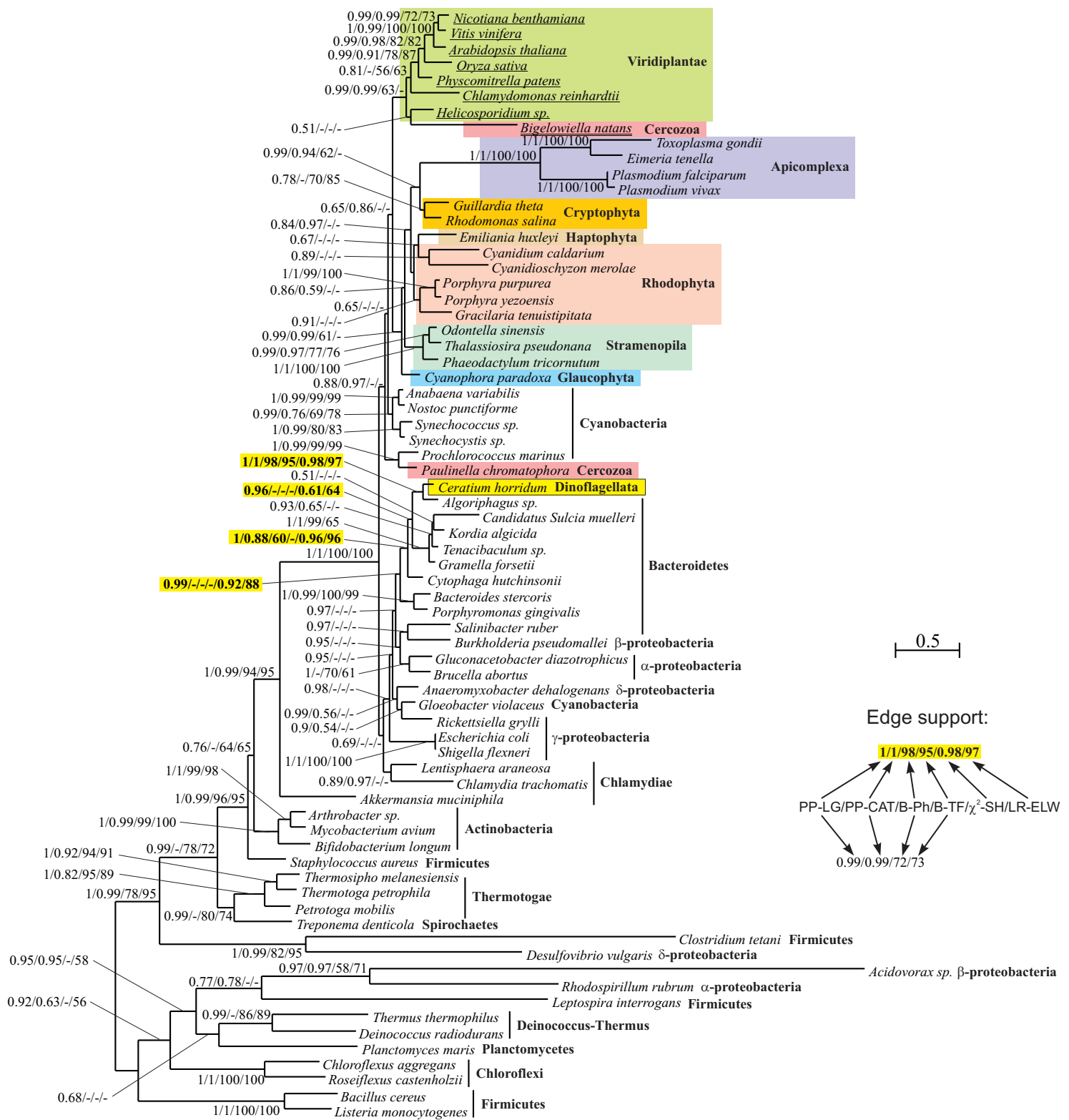


Fig. S3. The Bayesian tree for the Ycf24 obtained in PhyloBayes under the LG+ Γ model. Selected nodes refer to the position of the dinoflagellate *Ceratium horridum* sequence. Other explanations as in Fig. S2.

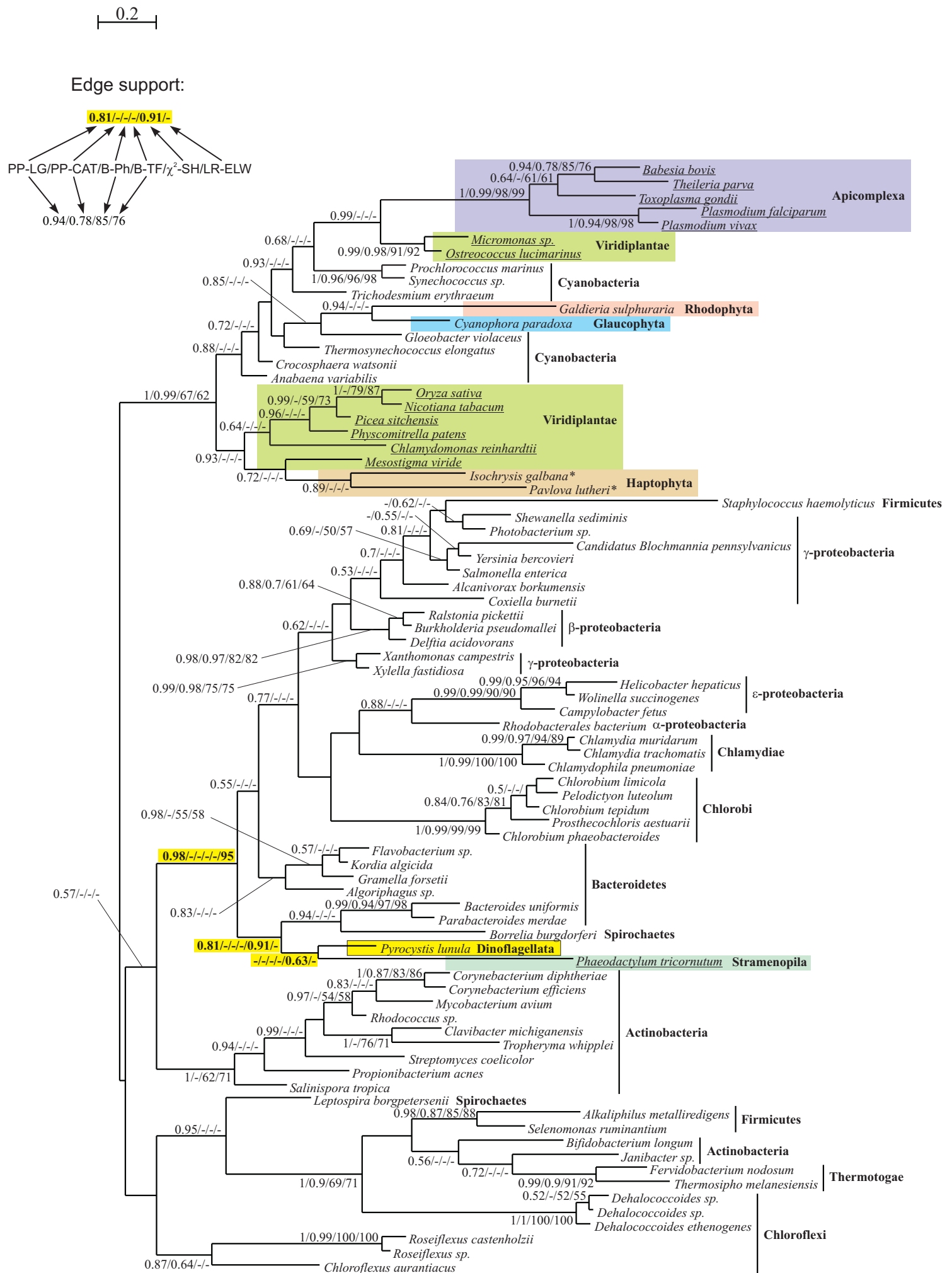


Fig. S5. The Bayesian tree for the Rpl28 obtained in PhyloBayes under the LG+ Γ model. Selected nodes refer to the position of the dinoflagellate *Pyrocystis lunula* sequence. Other explanations as for Fig. S2.