



Supplementary Fig. S4. SSU Ulvophyceae phylogenies built without and with *Symbiochlorum* gene sequences. (A) Tree built without *Symbiochlorum* gene sequences including 22 Ulvophyceae members (1,780 aligned nucleotide positions, 651 parsimony-informative). Bootstrap support values (>70) are shown at nodes. (B) Tree built with *Symbiochlorum* gene sequences including 24 Ulvophyceae members (1,787 aligned nucleotide positions, 672 parsimony-informative). All nodes were recovered by both Maximum likelihood (ML) and Bayesian inference methods. Bayesian posterior probabilities and ML bootstrap support values (>70) are shown at nodes. Collapsed branch hosts the sequences of the two *Symbiochlorum* members. The minor phylogenetic insertion within the *Symbiochlorum* branch demonstrates that both *Symbiochlorum hainanense* strains from the Indo-Pacific region group together, while CCMR0224 occupies the outermost branch. Scale bars represent the expected number of substitutions per site.