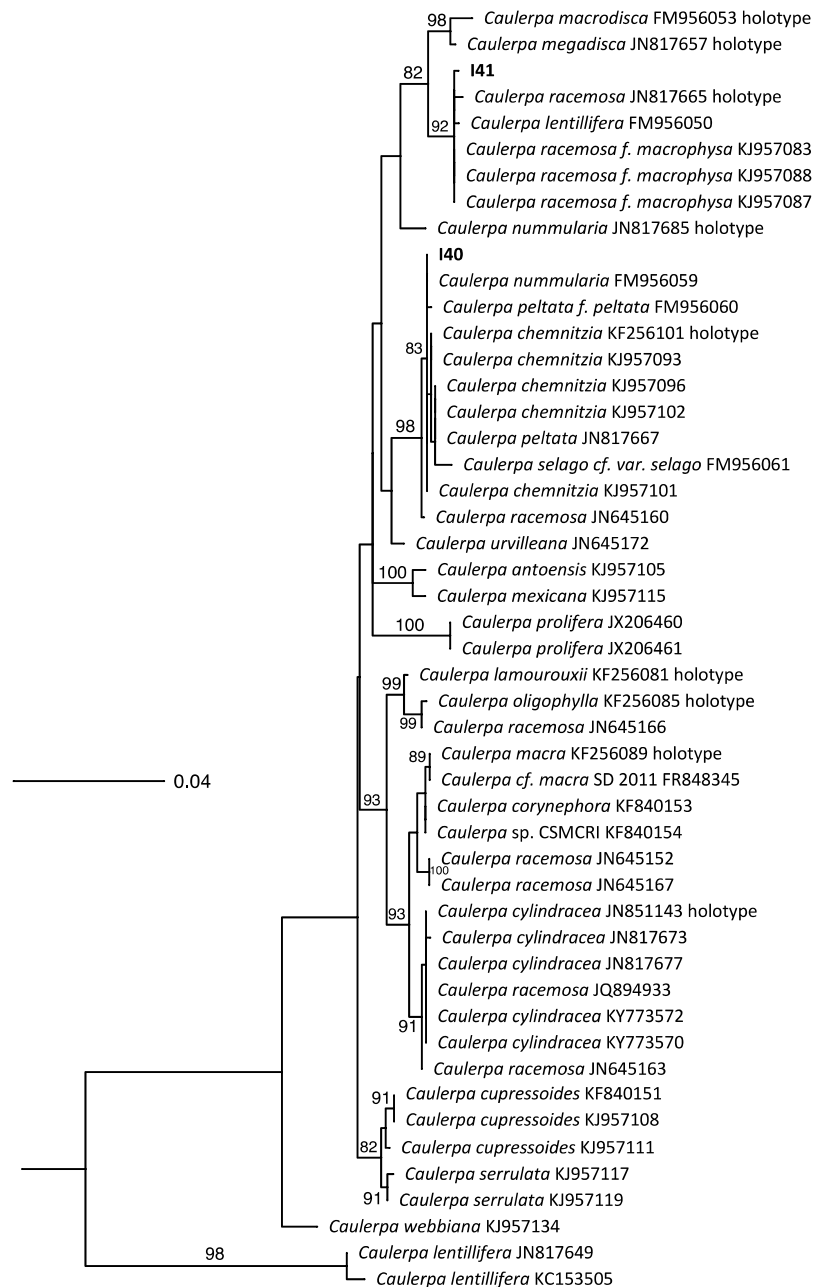


Supplementary File S1

A



B

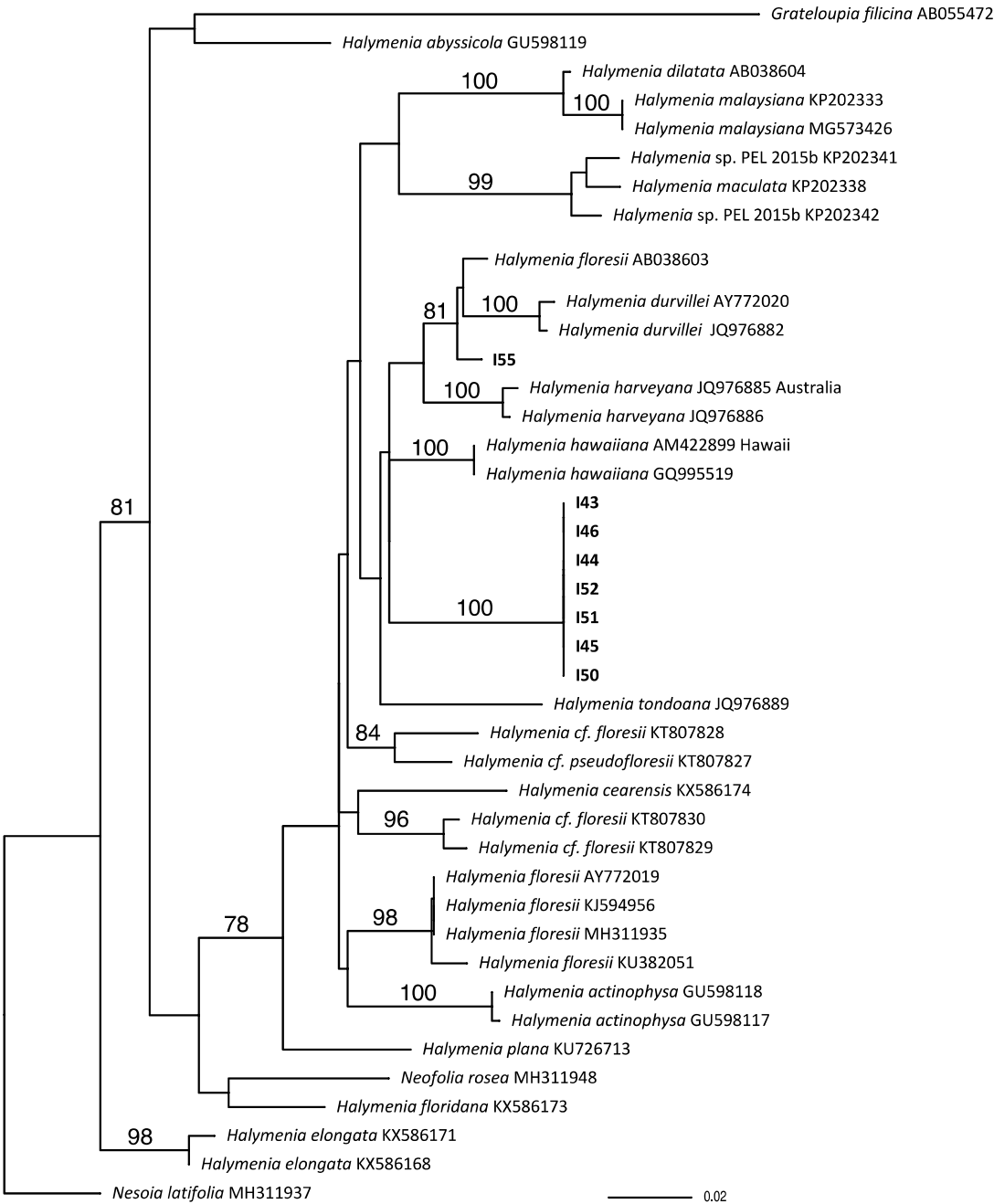


Figure S1. Phylogenetic analyses of *Caulerpa* and *Halymenia* from Samoa. The following samples were used: two *Caulerpa* samples **I40** from Siufaga (29/2/20) on Savai'i Island and **I41** from Apolima (13/2/20) on Upolu Island; and eight *Halymenia* samples (**I43** from Apia (1/2/19), **I44** from Savaia (13/12/19), **I45** from Savaia (5/12/18), **I46** from Apia (17/12/18), **I50** from Metafele (12/2/20), **I51** from Metafele (11/12/19), **I55** from Satapuala (6/3/19) from Upolu Island, and, **I52** from Sapini (29/2/20) on Savai'i Island). Phylogenetic analyses were run by Professor Giuseppe Zuccarello at Victoria University Wellington, New Zealand (see Zuccarello & Paul, 2019). Maximum Likelihood (ML) analyses were implemented using IQTREE 2.1.3. Genes were partitioned by codon. Model selection and partitioning to select the best partitions were implemented in IQTREE. Branch support was determined using non-parametric bootstrapping (500 replicates). For Fig. S1A, ML phylogeny based on *tufA* sequences of *Caulerpa* species downloaded from Genbank (903 basepair alignment), plus samples from Samoa (in bold). Sample I41 groups with *Caulerpa chemnitzia* (including the holotype KF256101) while sample I41 groups with *Caulerpa racemosa* (including the holotype JN817665). *Caulerpa flexilis* AJ417970 used as an outgroup (removed for clarity). Bootstrap values below 70% removed. Scale bar = substitutions per site. For Fig. S1B, ML phylogeny based on *rbcL* sequences of *Halymenia* species downloaded from Genbank (600 basepair alignment), plus samples from Samoa (in bold). Sample I55 groups with *Halymenia durvillei*; all other samples (I43-I46, I50-I52) identical and in a strongly supported clade distinct from all other sequenced *Halymenia* species. *Nesioia latifolia* used as an outgroup. Bootstrap values below 70% removed. Scale bar = substitutions per site.