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Supplementary material

Cyphastrea (Cnidaria : Scleractinia : Merulinidae) in the Red Sea: phylogeny and a new reef coral species

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Fig. S1. Phylogenetic tree inferred from the nuclear histone H3 gene. Bayesian topology is shown. Numbers associated with branches indicate BI posterior probabilities (>0.7), ML bootstrap (>70) support, and ML bootstrap (>70) support, respectively.

Fig. S2. Phylogenetic tree inferred from the partial 28S gene of nuclear ribosomal DNA (28S). Bayesian topology is shown. Numbers associated with branches indicate BI posterior probabilities (>0.7), ML bootstrap (>70) support, and ML bootstrap (>70) support, respectively.

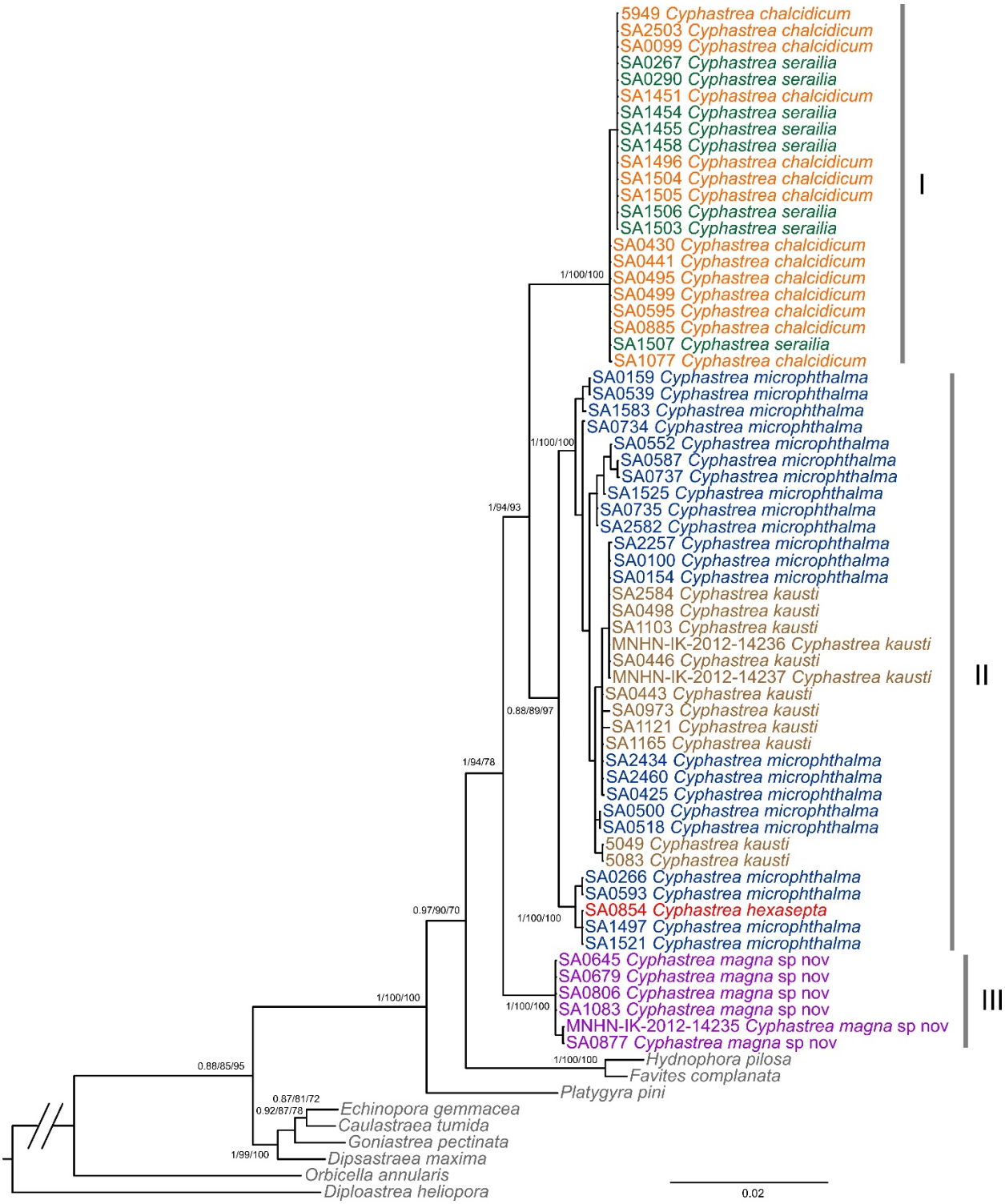

Fig. S3. Phylogenetic tree inferred from the mitochondrial intergenic spacer between COI and l-rRNA (IGR). Bayesian topology is shown. Numbers associated with branches indicate BI posterior probabilities (>0.7), ML bootstrap (>70) support, and ML bootstrap (>70) support, respectively.