

The stoloniferous octocoral, *Hanabira yukibana*, gen. nov., sp. nov., of the southern Ryukyus has morphological and symbiont variation

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Supplementary material



FIGURE S1 Maximum likelihood phylogenetic reconstruction of gene region 28S rDNA of *Hanabira yukibana*, gen. nov., sp. nov., specimens from Okinawa and Iriomote Islands and octocoral references from 120 genera, including outgroup *Cornularia* spp.

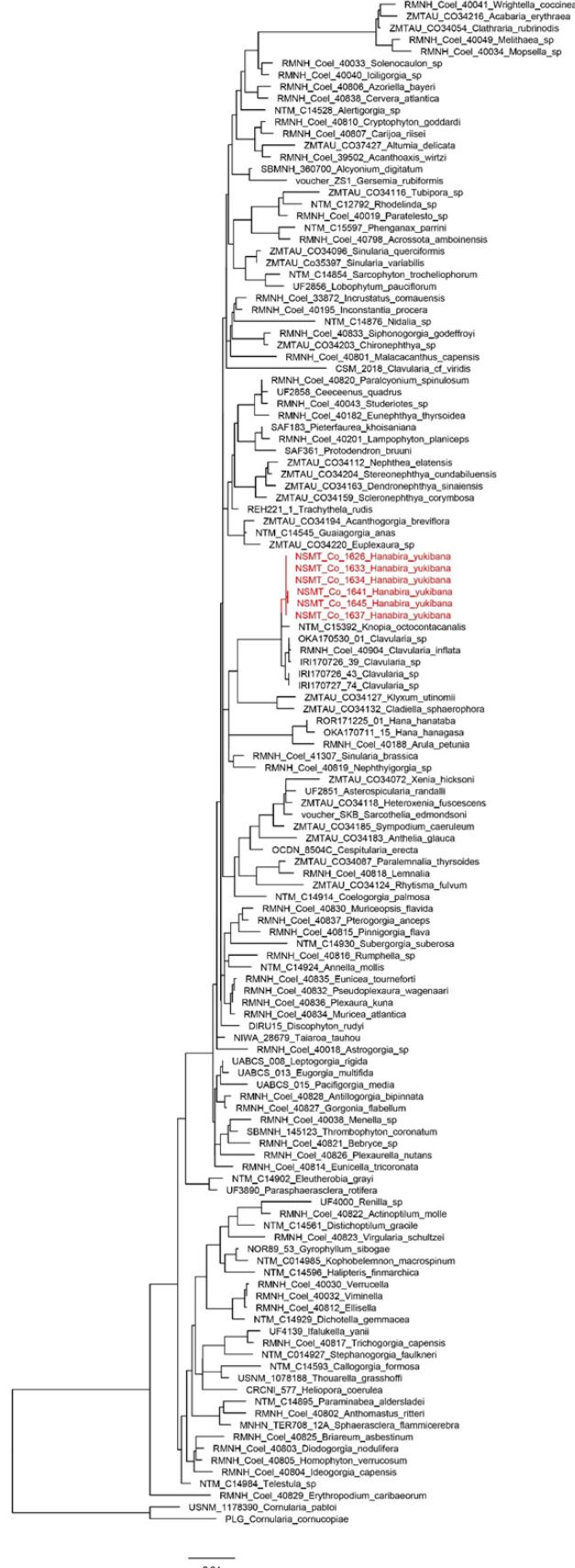


FIGURE S2 Maximum likelihood phylogenetic reconstruction of gene region COI of *Hanabira yukibana*, gen. nov., sp. nov., specimens from Okinawa and Iriomote Islands and octocoral references from 120 genera, including outgroup *Cornularia* spp.

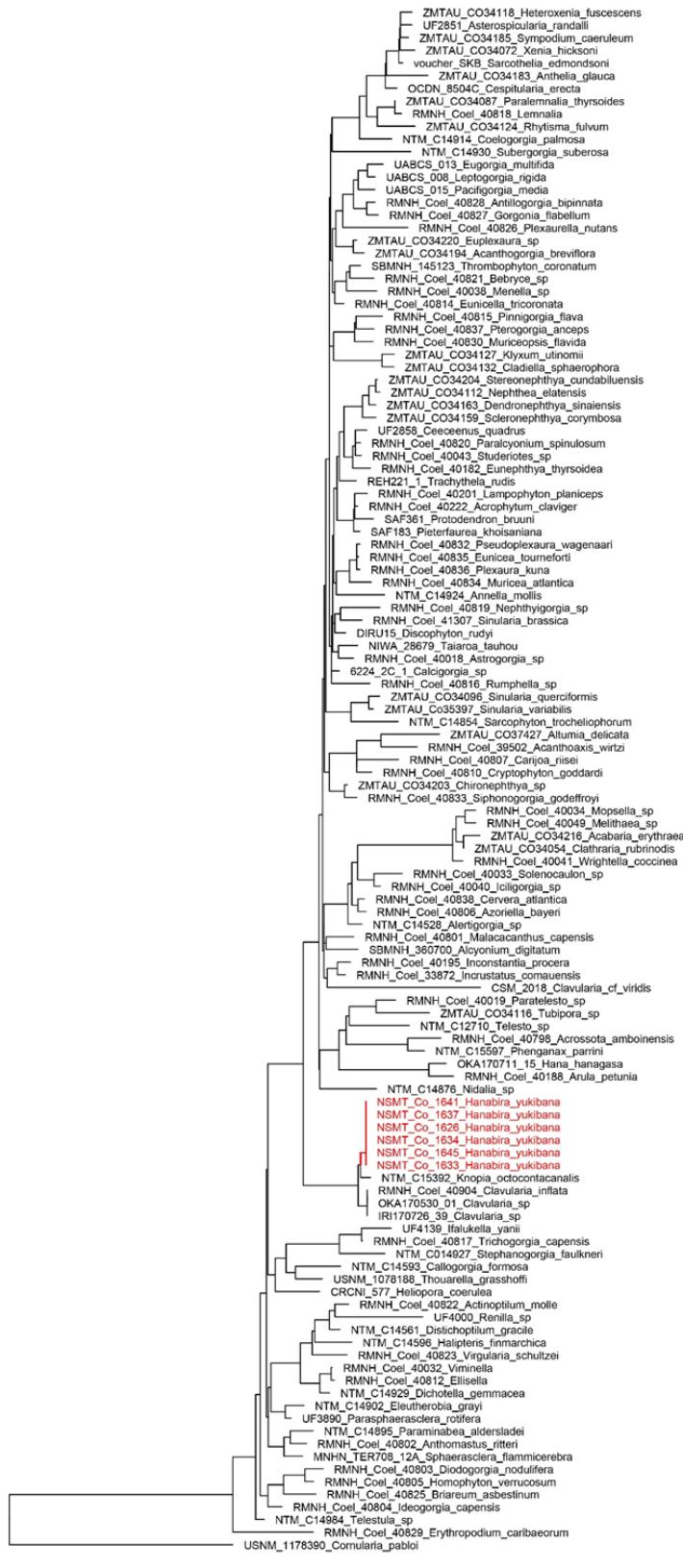


FIGURE S3 Maximum likelihood phylogenetic reconstruction of gene region mtMutS of *Hanabira yukibana*, gen. nov., sp. nov., specimens from Okinawa and Iriomote Islands and octocoral references from 120 genera, including outgroup *Cornularia paboi*.

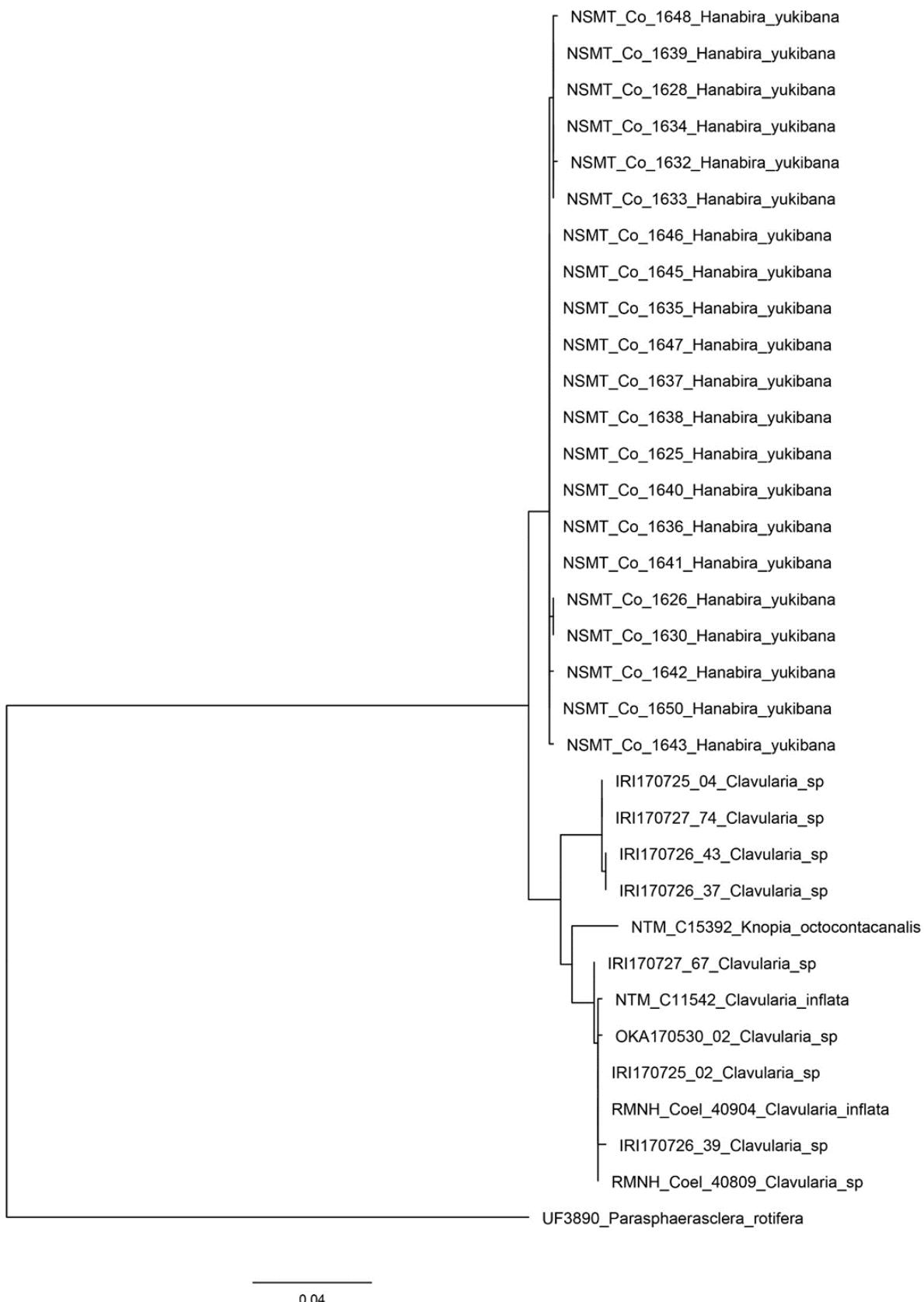


FIGURE S4 Maximum likelihood phylogenetic reconstruction of gene region 28S rDNA of *Hanabira yukibana*, gen. nov., sp. nov. specimens from Okinawa and Iriomote Islands, *Clavularia* spp., *Knopia octocontacanalisis* and outgroup taxa *Paraspheasclera rotifera*.

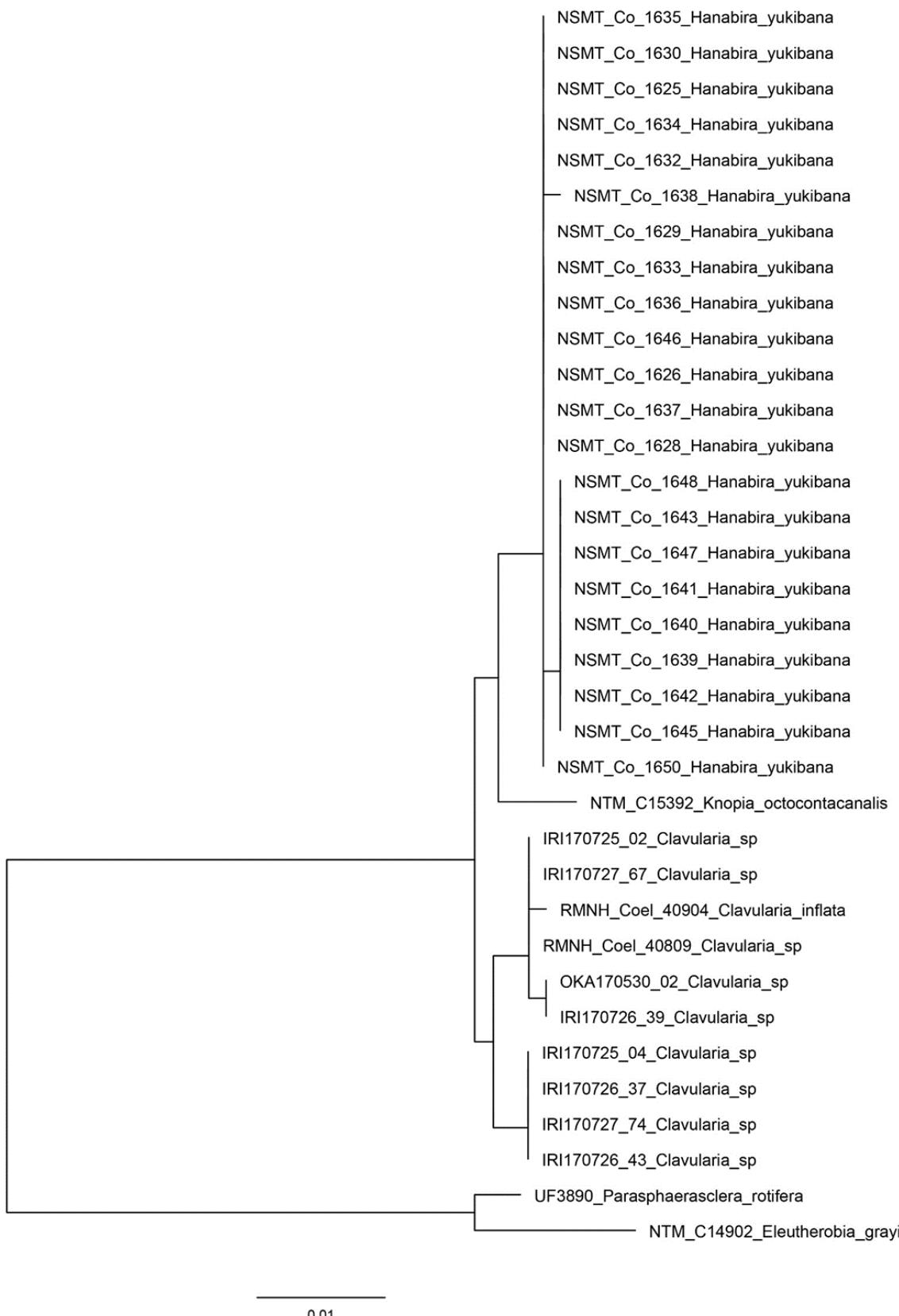


FIGURE S5 Maximum likelihood phylogenetic reconstruction of gene region COI of *Hanabira yukibana*, gen. nov., sp. nov. specimens from Okinawa and Iriomote Islands, *Clavularia* spp., *Knopia octocontacanalisis* and outgroup taxa *Eleutherobia grayi* and *Parasphaerasclera rotifera*.

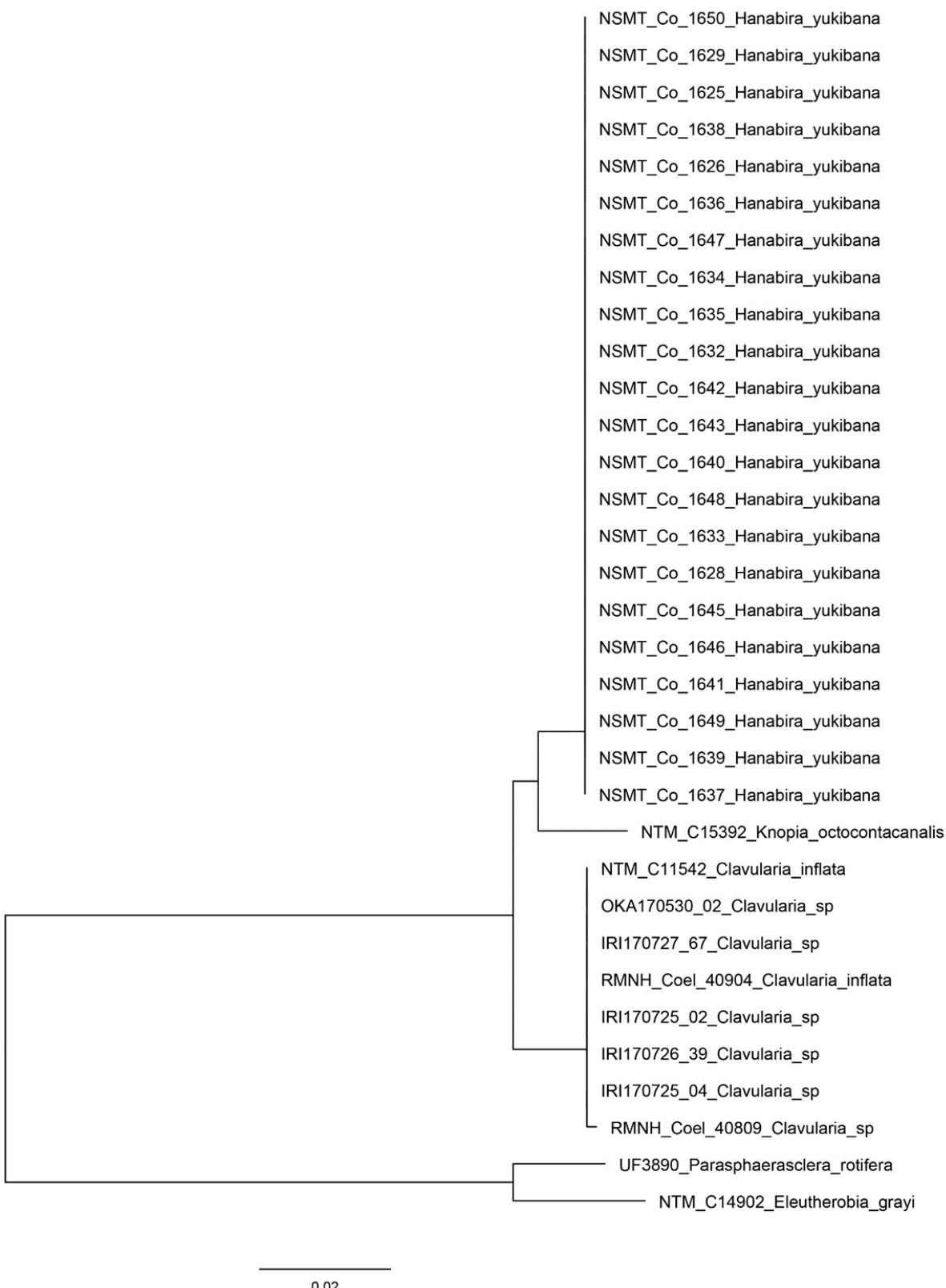


FIGURE S6 Maximum likelihood phylogenetic reconstruction of gene region mtMutS of *Hanabira yukibana*, gen. nov., sp. nov. specimens from Okinawa and Iriomote Islands, *Clavularia* spp., *Knopia octocontacanalis* and outgroup taxa *Eleutherobia grayi* and *Paraspheasclera rotifera*.

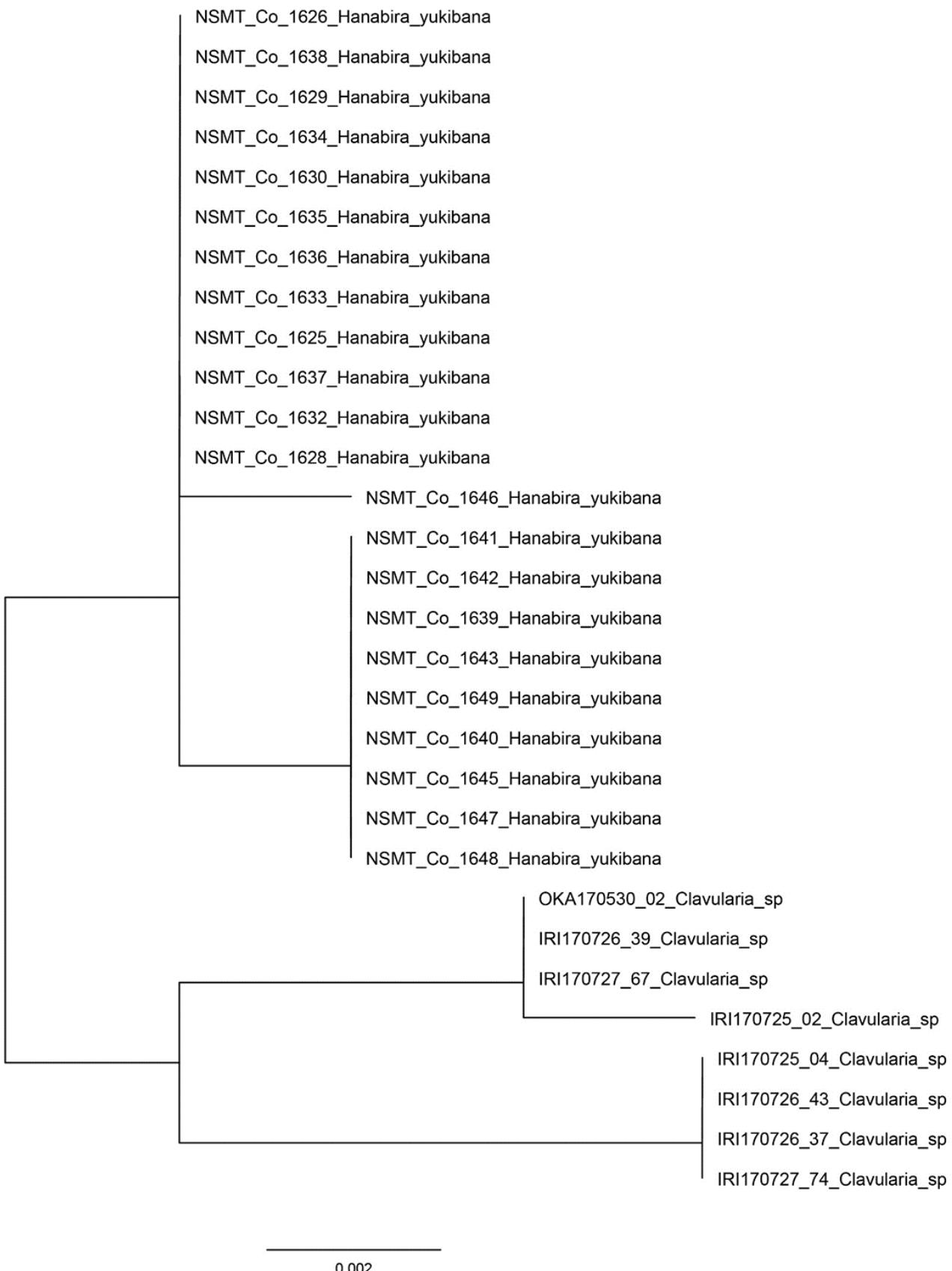


FIGURE S7 Maximum likelihood phylogenetic reconstruction of gene region ND6 of *Hanabira yukibana*, gen. nov., sp. nov. specimens from Okinawa and Iriomote Islands and outgroup taxa *Clavularia* spp.

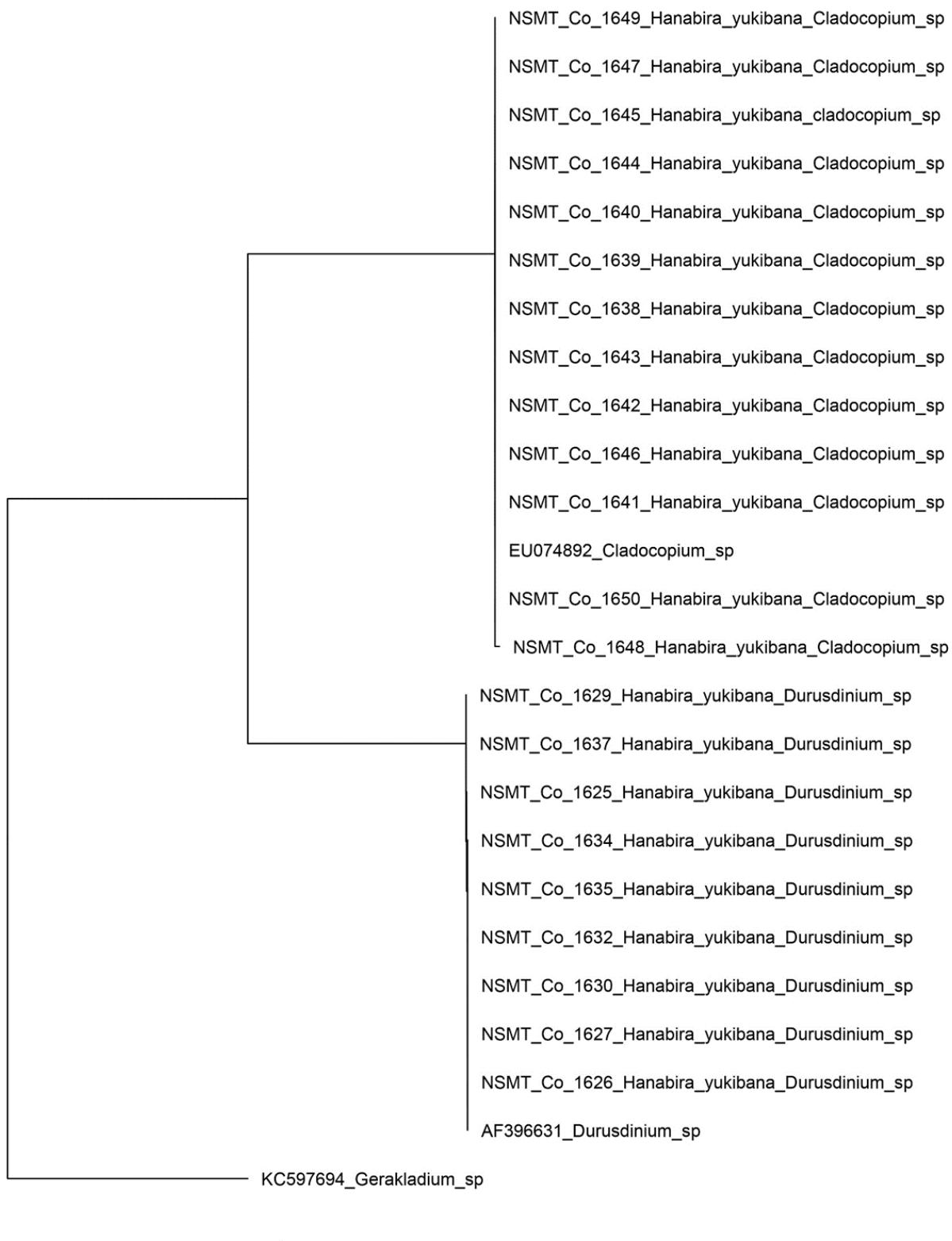


FIGURE S8 Maximum likelihood phylogenetic reconstruction of gene region ITS of Symbiodiniaceae hosted by *Hanabira yukibana*, gen. nov., sp. nov. specimens from Okinawa and Iriomote Islands and reference taxa obtained from GenBank; *Durusdinium* sp. and *Cladocopium* sp. (accession numbers: AF396631 and EU074892, respectively) and outgroup sister taxa, *Gerakladium* sp. (=former *Symbiodinium* 'Clade G', accession number: KC597694).



FIGURE S9 Phylogenetic relationships among 134 species of octocorals, including *Hanabira yukibana*, gen. nov., sp. nov. specimens, using the combined 28S rDNA+COI+mtMutS dataset. The best maximum likelihood tree is shown, with all values at branches representing bootstrap probabilities and Bayesian posterior probabilities, respectively. Values are not shown when 100%/1.00. Stoloniferous species are highlighted in grey boxes. *Cornularia* spp. were used as outgroup.

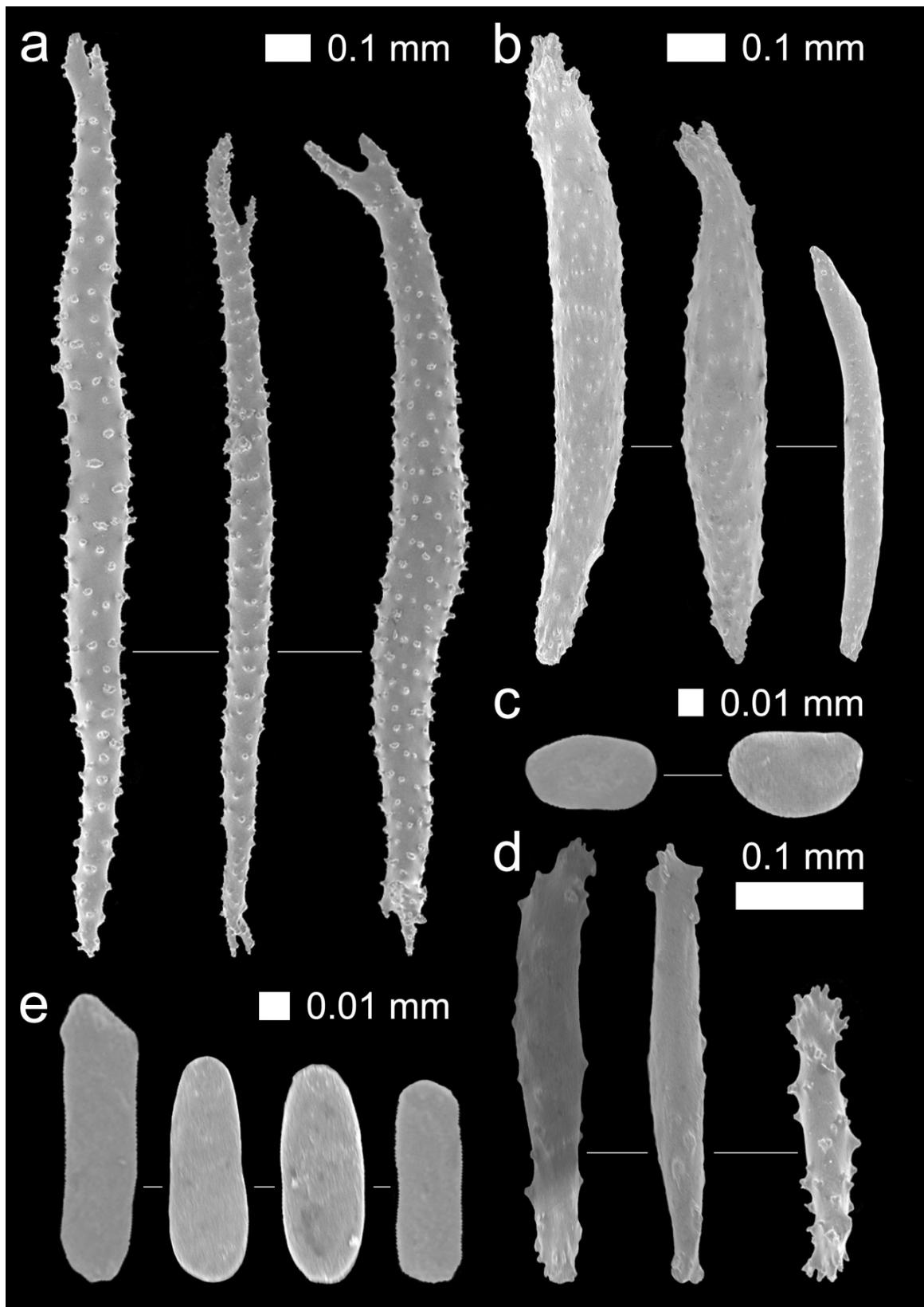


FIGURE S10 Sclerite types seen in *Clavularia inflata*, OKA170530-02; a) spindles of calyx (scale bar 0.1 mm), b) spindles of anthocodiae (scale bar 0.1 mm), c) anthocodial and tentacular platelets (0.01 mm), d) anthocodial and tentacular rodlets (scale bar 0.01 mm), e) anthocodial and tentacular rods (scale bar 0.1 mm).

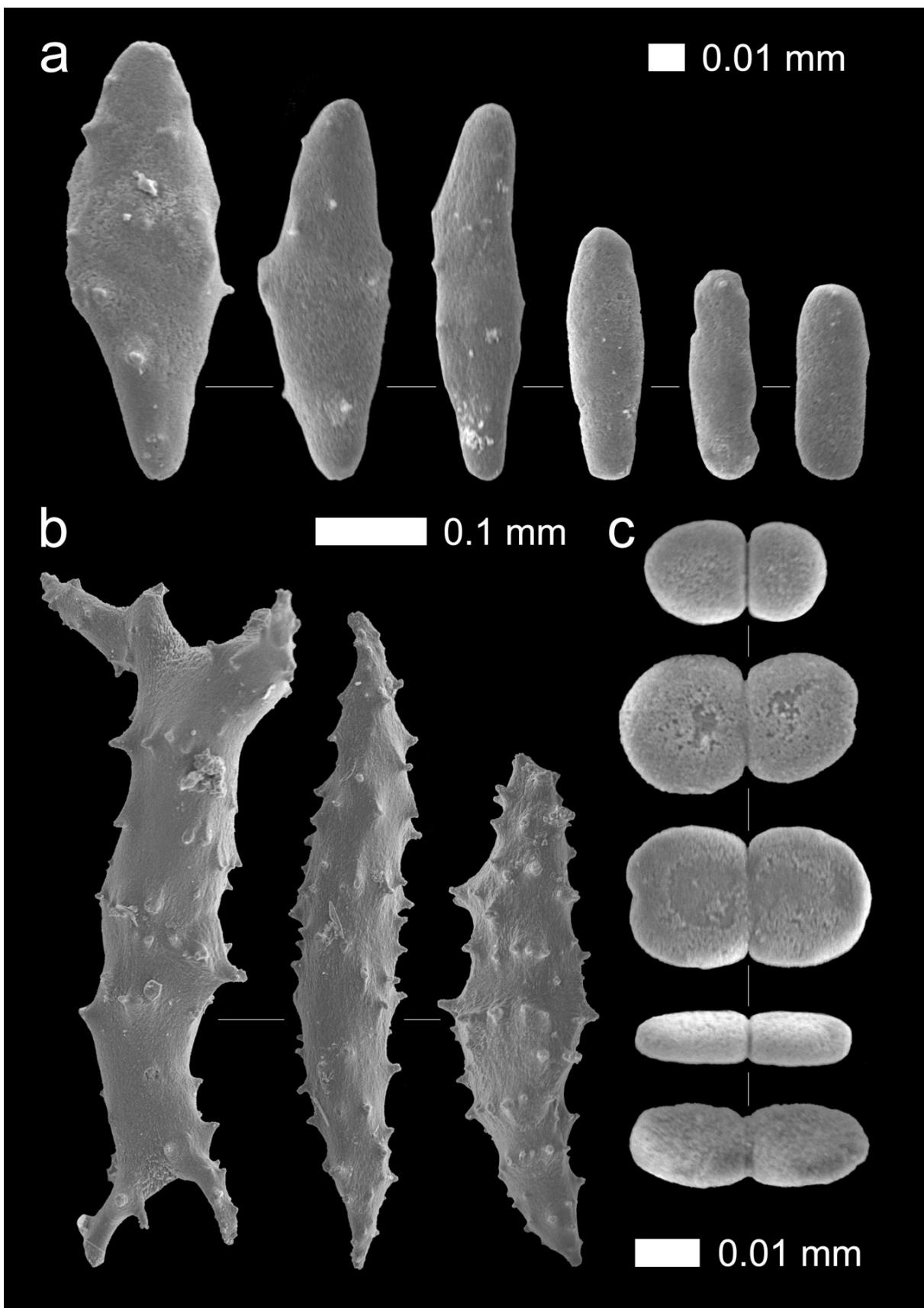


FIGURE S11 Sclerite types seen in *Clavularia* sp., IRI170727-74; a) anthocodial and tentacular rods (scale bar 0.01 mm), b) spindles of stolon (scale bar 0.1 mm), c) anthocodial and tentacular platelets (scale bar 0.01 mm).

TABLE S1 Number of base differences per site from averaging over all sequence pairs between *Hanabira* groups (1-3) is shown (uncorrected p , expressed as percentage) for gene regions COI and mtMutS. Standard error estimates (S.E.) are shown above the diagonal. Analysis involved 22 nucleotide sequences for both COI and mtMutS. All positions containing gaps and missing data were eliminated. There were a total of 638 and 717 positions in the final dataset for COI and mtMutS, respectively. Evolutionary analyses were conducted in MEGA7 (Kumar et al., 2016)

COI	between groups	<i>Hanabira yukibana 1</i>	<i>Hanabira yukibana 2</i>	<i>Hanabira yukibana 3</i>
	<i>Hanabira yukibana 1</i>		0.0133	0.1468
	<i>Hanabira yukibana 2</i>	0.0131		0.1470
	<i>Hanabira yukibana 3</i>	0.1698	0.1567	

mtMutS	between groups	<i>Hanabira yukibana 1</i>	<i>Hanabira yukibana 2</i>	<i>Hanabira yukibana 3</i>
	<i>Hanabira yukibana 1</i>		0.0000	0.0000
	<i>Hanabira yukibana 2</i>	0.0000		0.0000
	<i>Hanabira yukibana 3</i>	0.0000	0.0000	

TABLE S2 Estimates of average evolutionary divergence over sequence pairs within groups for gene regions COI and mtMutS. The numbers of base differences per site from averaging over all sequence pairs within each group (d) are shown (uncorrected p , expressed as percentage). Standard error estimates (S.E.) are shown in the second column and were obtained by a bootstrap procedure (1000 replicates). Analyses involved 22 nucleotide sequences for both COI and mtMutS for *Hanabira yukibana* specimens and nine and six nucleotide sequences for COI and mtMutS, respectively, for *Clavularia* spp. specimens. All positions containing gaps and missing data were eliminated. There were a total of 638 and 717 positions in the final dataset for COI and mtMutS, respectively, for *Hanabira yukibana* specimens and 777 and 541 positions for COI and mtMutS, respectively, for *Clavularia* spp. specimens. Evolutionary analyses were conducted in MEGA7 (Kumar et al., 2016)

	COI		mtMutS	
Within groups	d	S.E.	d	S.E.
<i>Hanabira yukibana</i>	0.09	0.07	0.00	0.00
<i>Clavularia</i> spp.	0.00	0.00	0.00	0.00

TABLE S3 Number of base differences per site from averaging over all sequence pairs between *Clavularia* spp. is shown (uncorrected p , expressed as percentage) for gene regions COI and mtMutS. Standard error estimates (S.E.) are shown above the diagonal. Analysis involved nine and six nucleotide sequences for COI and mtMutS, respectively. All positions containing gaps and missing data were eliminated. There were a total of 777 and 541 positions in the final dataset for COI and mtMutS, respectively. Evolutionary analyses were conducted in MEGA7 (Kumar et al., 2016).

COI	between groups	<i>Clavularia inflata</i>	<i>Clavularia</i> sp.
	<i>Clavularia inflata</i>		0.25
	<i>Clavularia</i> sp.	0.59	

mtMutS	between groups	<i>Clavularia inflata</i>	<i>Clavularia</i> sp.
	<i>Clavularia inflata</i>		0.00
	<i>Clavularia</i> sp.	0.00	