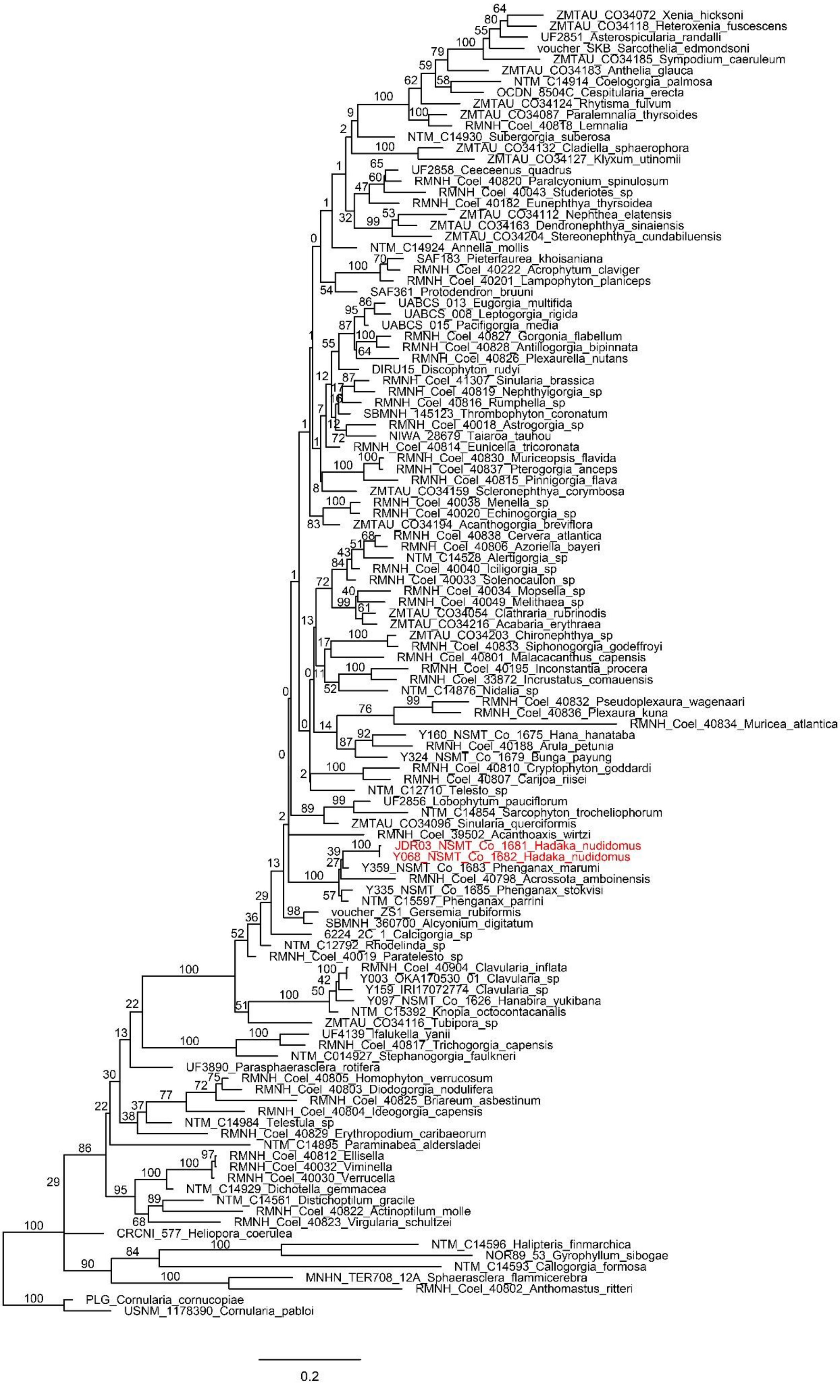

Figure S1. Maximum Likelihood phylogeny reconstruction of 28S rDNA gene region of *Hadaka nudidomus* gen. nov. et sp. nov. from Okinawa and Iriomote Islands (Japan) and octocoral references from 123 genera, including outgroup *Cornularia* spp.

Figure S2. Maximum Likelihood phylogeny reconstruction of COI gene region of *Hadaka nudidomus* gen. nov. et sp. nov. from Okinawa and Iriomote Islands (Japan) and octocoral references from 123 genera, including outgroup *Cornularia* spp.

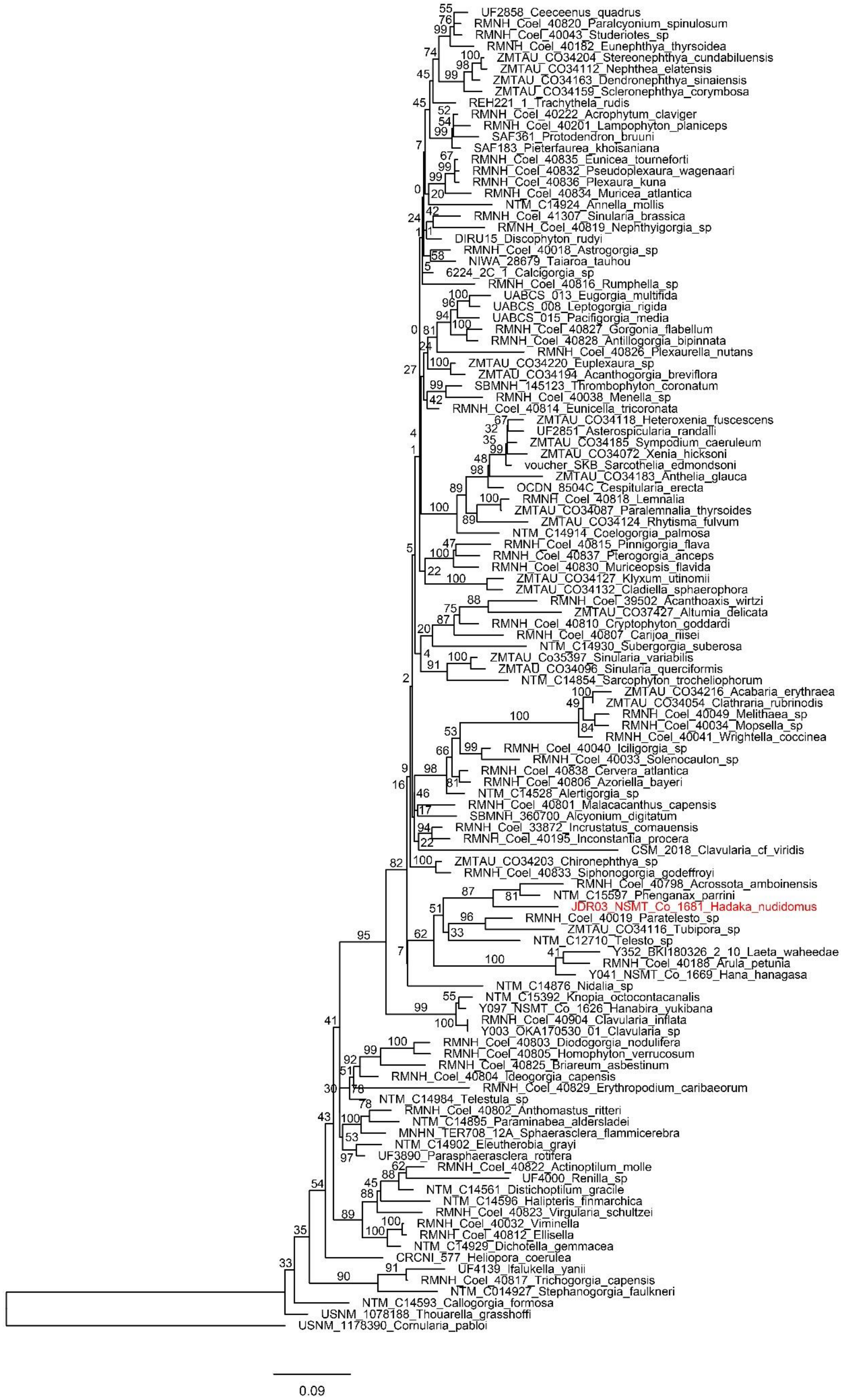

Figure S3. Maximum Likelihood phylogeny reconstruction of mtMutS gene region of *Hadaka nudidomus* gen. nov. et sp. nov. from Okinawa and Iriomote Islands (Japan) and octocoral references from 123 genera, including outgroup *Cornularia* spp.

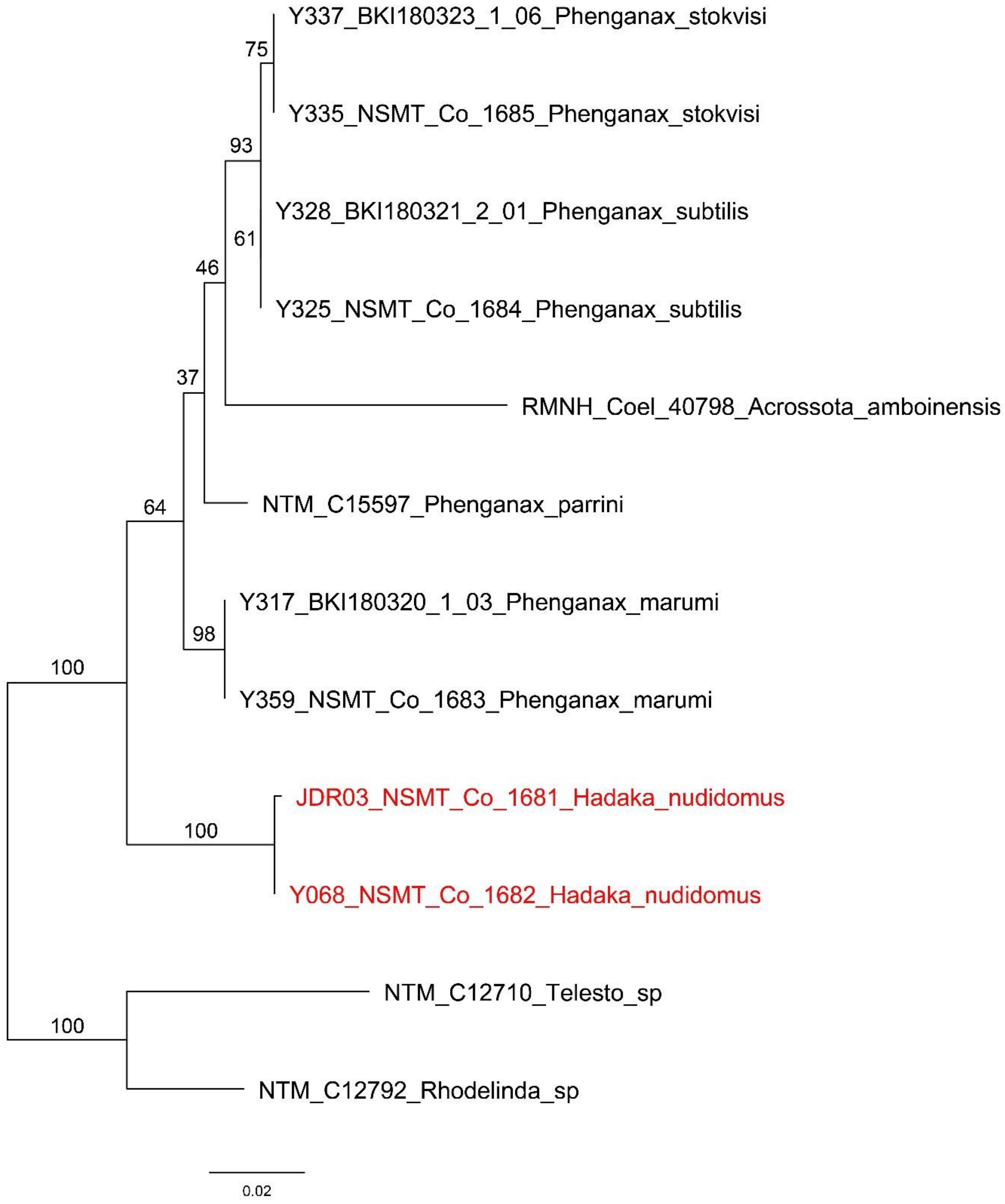

Figure S4. Maximum Likelihood phylogeny reconstruction of 28S rDNA gene region of *Hadaka nudidomus* gen. nov. et sp. nov. from Okinawa and Iriomote Islands (Japan) and five octocoral references (*Phenganax* spp., *Acrossota amboinensis*), and outgroup (*Telesto* sp., *Rhodelinda* sp.).

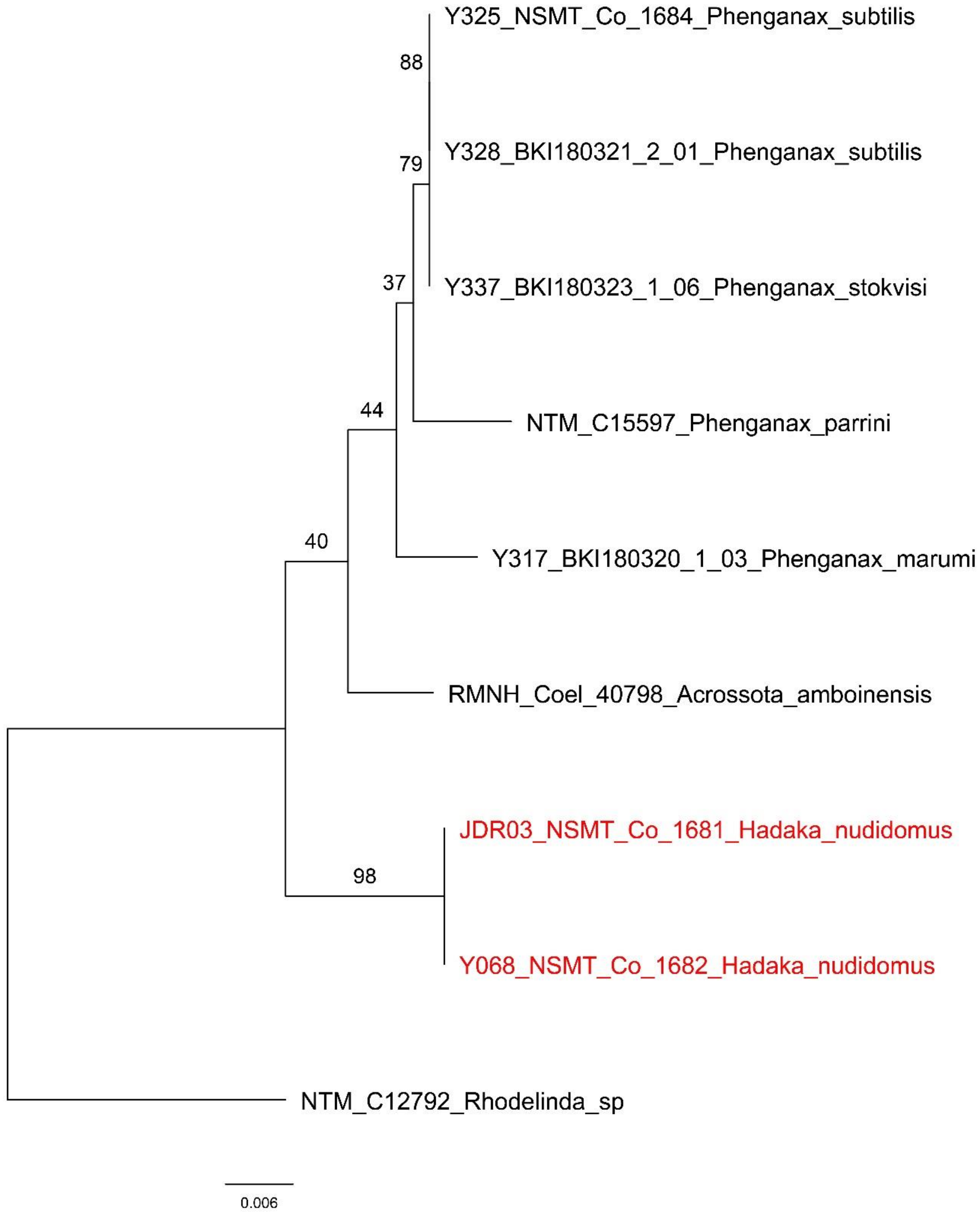

Figure S5. Maximum Likelihood phylogeny reconstruction of COI gene region of *Hadaka nudidomus* gen. nov. et sp. nov. from Okinawa and Iriomote Islands (Japan) and five octocoral references (*Phenganax* spp., *Acrossota amboinensis*), and outgroup (*Rhodelinda* sp.).

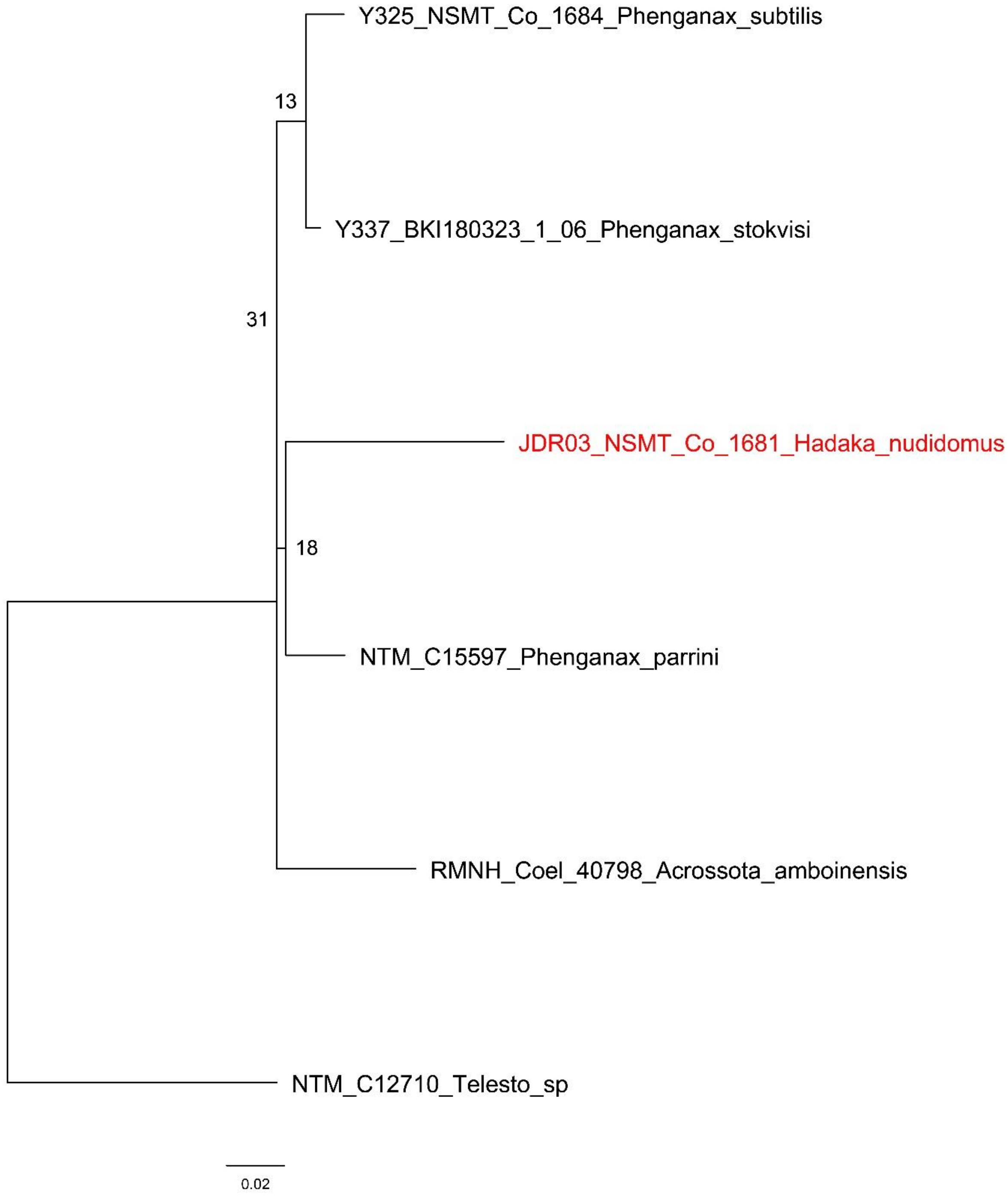

Figure S6. Maximum Likelihood phylogeny reconstruction of mtMutS gene region of *Hadaka nudidomus* gen. nov. et sp. nov. from Okinawa and Iriomote Islands (Japan) and four octocoral references (*Phenganax* spp., *Acrossota amboinensis*), and outgroup (*Telesto* sp.).

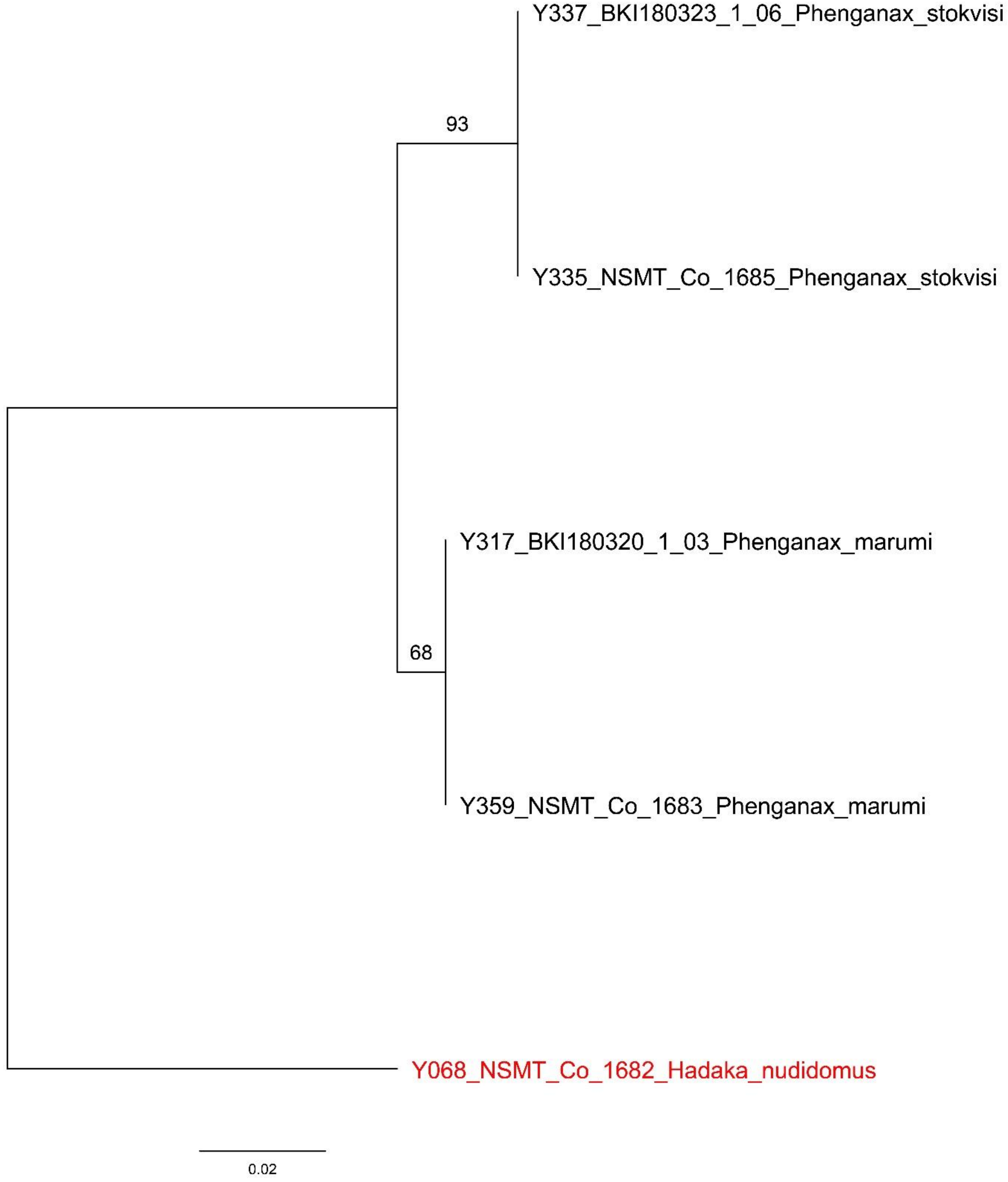

Figure S7. Maximum Likelihood phylogeny reconstruction of ND6 gene region of *Hadaka nudidomus* gen. nov. et sp. nov. from Okinawa and Iriomote Islands (Japan) and two octocoral references (*Phenganax* spp.).

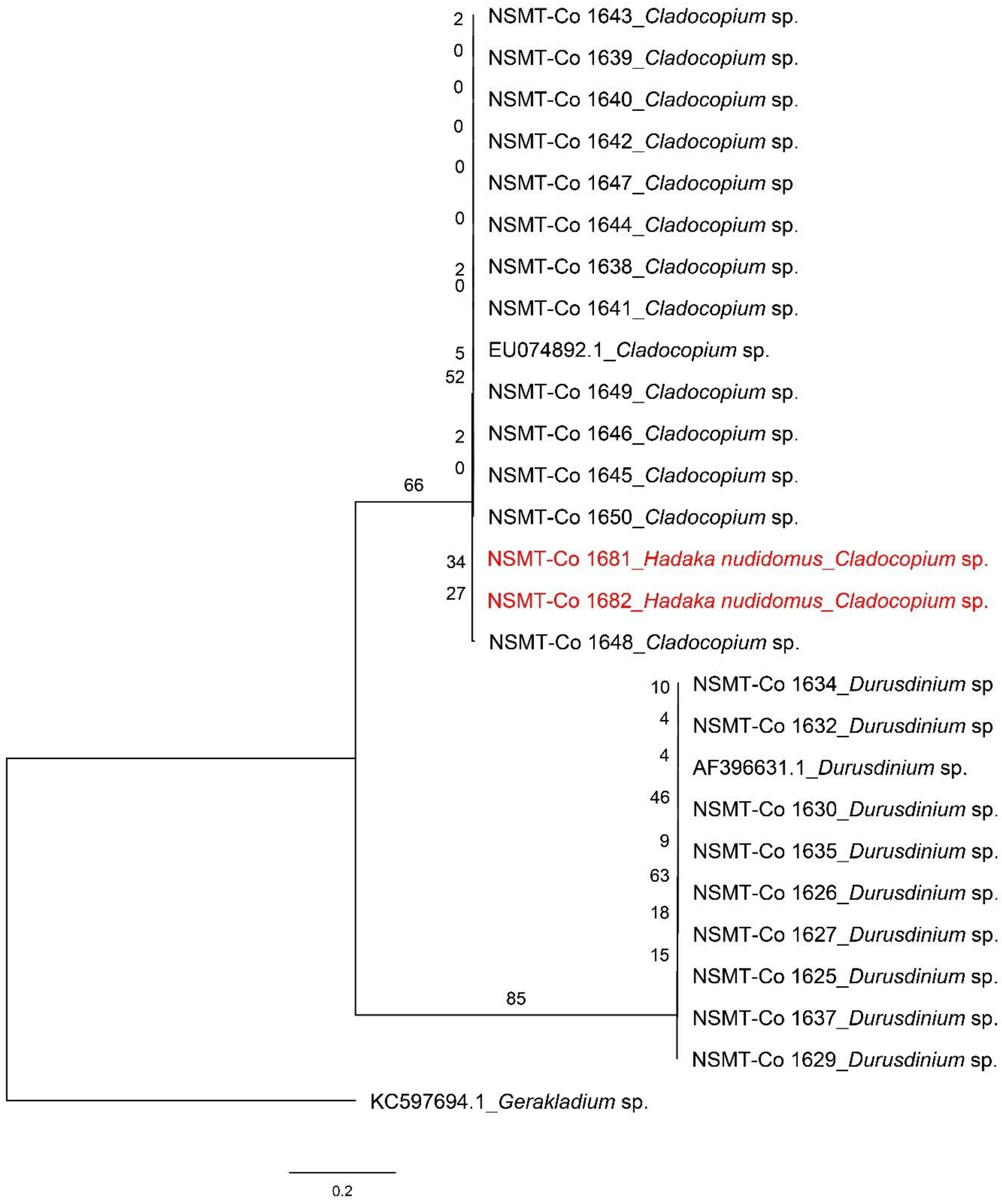

Figure S8. Maximum likelihood phylogenetic reconstruction of gene region ITS of Symbiodiniaceae hosted by *Hadaka nudidomus* gen. nov. et sp. nov. specimens from Okinawa and Iriomote Islands (Japan) and reference taxa *Durusdinium* sp. (= former *Symbiodinium* ‘Clade D’, n = 14) and *Cladocopium* sp. (former *Symbiodinium* ‘Clade C’, n = 10) and outgroup sister taxa, *Gerakladium* sp. (= former *Symbiodinium* ‘Clade G’) as used in Lau et al (2019).

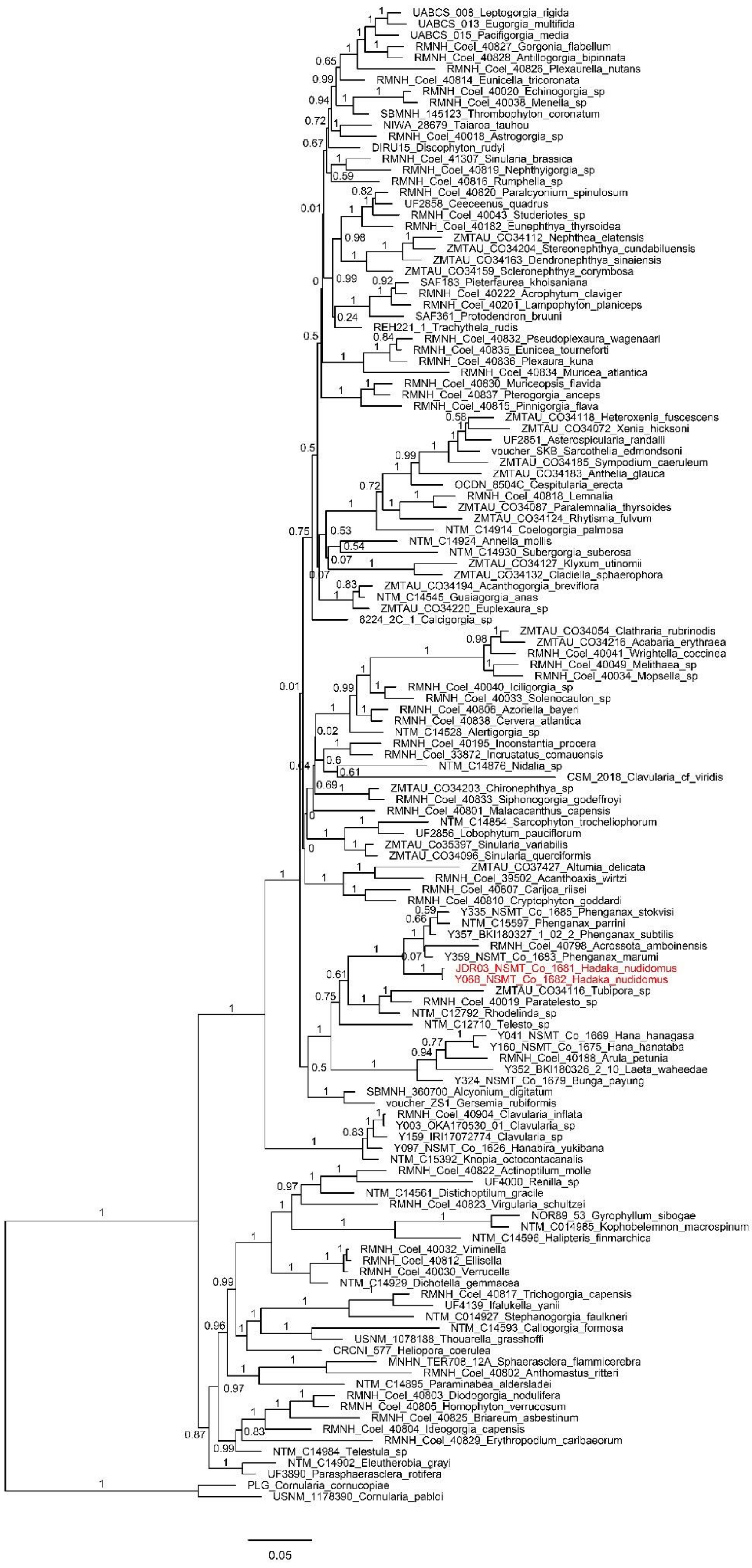

Figure S9. Bayesian inference phylogeny reconstruction of the combined 28S rDNA+COI+mtMutS gene regions of *Hadaka nudidomus* gen. nov. et sp. nov. from Okinawa and Iriomote Islands (Japan) and octocoral references from 123 genera, including outgroup *Cornularia* spp.

Table S1. Number of base differences per site from averaging over all sequence pairs between stoloniferous octocoral genera (*Hadaka* gen. nov., *Phenganax*, *Acrossota*) is shown (*p* expressed as percentage) for COI and mtMutS gene regions. Standard error estimates (S.E.) are shown above the diagonal. Analysis involved 9 and 6 nucleotide sequences for COI and mtMutS, respectively. All positions containing gaps and missing data were eliminated. There were totals of 708 and 734 positions in the final dataset for COI and mtMutS, respectively. Evolutionary analyses were conducted in MEGA X (Kumar et al. 2018).

COI	**Between groups**	**1.**	**2.**	**3.**	**4.**
	1. *Phenganax*		0.54	0.41	0.98
	2. *Hadaka*	2.52		0.58	0.99
	3. *Acrossota*	1.58	2.54		0.99
	4. *Rhodelinda*	5.72	5.34	5.52	
mtMutS	**Between groups**	**1.**	**2.**	**3.**	**4.**
	1. *Phenganax*		0.94	1.19	1.61
	2. *Acrossota*	5.83		1.55	3.60
	3. *Telesto*	13.22	14.79		2.62
	4. *Hadaka*	7.69	13.33	18.50	

Table S2. Number of base differences per site from averaging over all sequence pairs between stoloniferous octocoral taxa (*Hadaka nudidomus* gen. nov. sp. nov., *Phenganax* spp., *Acrossota amboinensis*) is shown (*p* expressed as percentage) for gene regions COI and mtMutS. Standard error estimates (S.E.) are shown above the diagonal. Analysis involved 7 nucleotide sequences for both COI and mtMutS. All positions containing gaps and missing data were eliminated. There were totals of 717 and 881 positions in the final dataset for COI and mtMutS, respectively. Evolutionary analyses were conducted in MEGA X (Kumar et al. 2018).

COI	**Between groups**	**1.**	**2.**	**3.**	**4.**	**5.**	**6.**	**7.**
	1. *P. marumi*		0.34	0.36	0.47	0.56	0.47	1.00
	2. *P. subtilis*	0.99		0.00	0.36	0.57	0.42	0.96
	3. *P. stokvisi*	0.92	0.00		0.39	0.58	0.43	1.02
	4. *P. parrini*	1.69	0.99	1.08		0.59	0.46	1.02
	5. *H. nudidomus*	2.40	2.54	2.15	2.97		0.57	0.98
	6. *A. amboinensis*	1.84	1.41	1.38	1.84	2.54		0.94
	7. *Rhodelinda* sp.	5.89	5.52	5.57	6.08	5.34	5.52	
mtMutS	**Between groups**	**1.**	**2.**	**3.**	**4.**	**5.**	**6.**	
	1. *P. subtilis*		0.49	0.75	1.01	1.27	1.69	
	2. *P. stokvisi*	1.74		0.71	0.98	1.32	1.80	
	3. *P. parrini*	4.07	3.62		1.02	1.29	1.85	
	4. *A. amboinensis*	5.89	5.49	6.10		1.59	3.56	
	5. *Telesto* sp.	13.27	12.98	13.41	14.79		2.70	
	6. *H. nudidomus*	7.00	7.58	8.50	13.33	18.50		

Table S3. Estimates of average evolutionary divergence over sequence pairs within stoloniferous octocoral genera (*Hadaka* gen. nov., *Phenganax*, *Acrossota*, *Rhodelinda*, *Telesto*) 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 (*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 9 and 6 nucleotide sequences for COI and mtMutS, respectively. All positions containing gaps and missing data were eliminated. There were totals of 708 and 734 positions in the final dataset for COI and mtMutS, respectively. Evolutionary analyses were conducted in MEGA X (Kumar et al. 2018).

	COI			**mtMutS**	
Within groups	**d**	**S.E.**	**Within groups**	**d**	**S.E.**
1. *Phenganax*	0.77	0.20	1. *Phenganax*	3.14	0.54
2. *Hadaka*	0.00	0.00	2. *Acrossota*	n/c	n/c
3. *Acrossota*	n/c	n/c	3. *Telesto*	n/c	n/c
4. *Rhodelinda*	n/c	n/c	4. *Hadaka*	n/c	n/c