

Supplementary Material

Methods – additional details

Clean up and Assembly

Additional trimming of front and end sequence reads were as follows; for forward reads 5 bp were removed from the beginning and end; for reverse reads 5 bp were removed from the beginning and 35 bp from the end. These were removed to improve the quality score statistics and address sequence quality issues indicated by the FastQC reports. Final cleaned reads were visualised in FastQC and accepted if all elements of the report were passed or showed minor warnings based on the FastQC traffic light system.

Default settings were implemented in MITObim except for raising the kbait from 31 to 35 to implement a more restrictive assembly.

Full genomes were recovered in MITObim, however the circularisation process failed for the majority of samples. The linear contigs were transferred to Geneious and edited manually by aligning the front and end sections of the genomes. The presence of overlapping front and end nucleotide sequences suggested circular genomes. The overlapping sequences were removed from the end section of each contig.

Table S1 | Gblock alignment parameters.

Region	Number of sequences analysed	Minimum number of sequences for a conserved position	Minimum number of sequences for a flanking position	Maximum number of contiguous non-conserved positions	Minimum length of a block	Allowed gap positions	New number of positions	% of original positions
COX1	33	17	17	8	5	With half	1593	96
COX2	32	17	17	8	5	With half	747	97
COX3	32	17	17	8	5	With half	789	96
ND1	32	17	17	8	5	With half	984	91
ND2	33	17	17	8	5	With half	1508	86
ND3	32	17	17	8	5	With half	357	87
ND4	33	16	16	8	5	With half	1476	98
ND5	33	17	17	8	5	With half	1851	93
ND6	33	17	17	8	5	With half	570	83
ND4L	32	17	17	8	5	With half	300	100
CYTB	31	16	16	8	5	With half	1143	85
ATP6	32	17	17	8	5	With half	699	94
ATP8	32	17	17	8	5	With half	210	87
5.8S rRNA	31	16	16	8	5	With half	170	94
18SrRNA	30	16	16	8	5	With half	166	44
28sRNA	30	16	16	8	5	With half	267	99
ITS1	31	16	16	8	5	With half	211	61
ITS2	31	16	16	8	5	With half	214	70

Table S2 Models of evolution implemented in Mr Bayes (Jmodeltest2 results) and IQ tree (ModelFinder). IQ tree parameters implemented: -spp which allows each partition to have its own rate of evolution; -m TESTNEWMERGE ModelFinder performs a strategy that calculates the best model for each partition and subsequently merges two partitions until the model fit does not increase any further.

Alignments	Jmodeltest2	ModelFinder	ModelFinder combined
ATP6	GTR+I+G	TPM3u+F+I+G4	TPM3u+F+I+G4
ATP8	GTR+G	K3Pu+F+G4	K3Pu+F+G4
COX1	GTR+I+G	TPM2+F+I+G4	TPM2+F+I+G4
COX2	GTR+I+G	TPM3u+F+I+G4	TPM3u+F+I+G4
COX3	GTR+I+G	TIM3+F+I+G4	TIM3+F+I+G4
CYTB	GTR+I+G	TPM3u+F+I+G4	TPM3u+F+I+G4
ND1	GTR+I+G	TPM3u+F+I+G4	TPM3u+F+I+G4
ND2	GTR+G	GTR+F+G4	TVM+F+G4
ND3	HKY+G	HKY+F+G4	HKY+F+G4
ND4	GTR+I+G	TPM3u+F+I+G4	TPM3u+F+I+G4
ND4L	GTR+I+G	HKY+F+G4	HKY+F+G4
ND5	GTR+I+G	TVM+F+I+G4	HKY+F+I+G4
ND6	GTR+G	TVM+F+G4	TVM+F+G4
18S rRNA	K80+G	K2P+I+G4	K2P+I
5.8S rRNA	SYM+I+G	K2P+I+G4	TNe+G4
28S rRNA	K80+I+G	K2P+I+G4	K2P+I+G4
ITS1	SYM+G	TNe+G4	TNe+G4
ITS2	GTR+G	TNe+G4	TNe+G4

Table S3 | GenBank accession numbers for all samples included in this study. White cells are newly sequenced samples from the current study. Blue cells are Antipatharia samples available prior to this study. Green cells are hexacoral outgroups. Blank cells represent regions not present on GenBank.

Order	Species	Mitogenome GenBank accession number	Nuclear region GenBank accession number
Antipatharia	<i>Antipathes</i> cf. <i>dichotoma</i>	MT318841	MT318863
Antipatharia	<i>Bathypathes</i> n. sp. 2	MT318842	MT318864
Antipatharia	<i>Bathypathes</i> n. sp. 3	MT318843	MT318865
Antipatharia	<i>Bathypathes</i> sp. 1	MT318844	MT318866
Antipatharia	<i>Chrysopathes</i> cf. <i>micracantha</i>	MT318860	MT318867
Antipatharia	<i>Cladopathes</i> cf. <i>plumosa</i>	MT318861	MT318868
Antipatharia	<i>Dendrobathypathes</i> n. sp.	MT318845	MT318869
Antipatharia	<i>Leiopathes</i> cf. <i>glaberrima</i>	MT318846	MT318870
Antipatharia	<i>Leiopathes expansa</i>	MT318847	MT318871
Antipatharia	<i>Leiopathes montana</i>	MT318848	MT318872
Antipatharia	<i>Parantipathes</i> cf. <i>hirondelle</i>	MT318849	MT318873
Antipatharia	<i>Parantipathes hirondelle</i>	MT318850	MT318875
Antipatharia	<i>Parantipathes</i> sp.	MT318851	MT318874
Antipatharia	<i>Phanopathes</i> sp.	MT318852	MT318876
Antipatharia	<i>Sibopathes</i> cf. <i>macrospina</i>	MT318853	MT318877
Antipatharia	<i>Stauropathes</i> cf. <i>punctata</i>	MT318855	MT318878
Antipatharia	<i>Stauropathes arctica</i>	MT318854	MT318879
Antipatharia	<i>Stichopathes abyssicola</i>	MT318856	MT318880
Antipatharia	<i>Stichopathes</i> n. sp.	MT318857	MT318881
Antipatharia	<i>Telopathes</i> sp.	MT318858	MT318882
Antipatharia	<i>Trissopathes</i> cf. <i>tetracrada</i>	MT318840	MT318883
Antipatharia	<i>Trissopathes grasshoffi</i>	MT318862	MT318884
Antipatharia	<i>Tylopathes</i> n. sp.	MT318859	MT318885
Antipatharia	<i>Chrysopathes formosa</i>	NC_008411.1	MG023168.1
Antipatharia	<i>Myriopathes japonica</i>	NC_027667.1	
Antipatharia	<i>Myriopathes myriophylla</i>		AM404328.1
Antipatharia	<i>Stichopathes lutkeni</i>	JX023266.1	
Antipatharia	<i>Tanacetipathes thamnea</i>	MN265369	
Actiniaria	<i>Edwardsia timida</i>		KT852241.1 & GU473315.1
Actiniaria	<i>Nematostella</i> sp.	NC_008164	
Actiniaria	<i>Metridium senile</i>	NC_000933.1	KT852218.1
Actiniaria	<i>Isosicyonis striata</i>	NC_027613	KY789422
Corallimorpharia	<i>Discosoma nummiforme</i>	KP938434	AB441417.1
Scleractinia	<i>Acropora tenuis</i>	AF338425.1	AF538477
Zoantharia	<i>Palythoa heliodiscus</i>	NC_035579.1	DQ997883.1
Zoantharia	<i>Savalia savaglia</i>	DQ825686.1	EU591548.1
Zoantharia	<i>Zoanthus sansibaricus</i>	NC_035578.1	AB214155.1

Table S4a Antipatharian gene lengths (bp), intergenic regions (italicised) (bp), intron regions (bold) (bp) and gene variation from Gblock alignments (identical site and pairwise identity percentage). Blank cells in species columns are due to the lack of the *COX1* intron. Note that total IGR does not include intron regions.

	<i>Antipathes</i> cf. <i>dichotoma</i>	<i>Bathypathes</i> sp. 1	<i>Bathypathes</i> n. sp. 2	<i>Bathypathes</i> n. sp. 3	<i>Chrysopathes</i> <i>formosa</i>	<i>Dendrobathy-</i> <i>pathes</i> n. sp.	<i>Leiopathes</i> <i>expansa</i>	<i>Leiopathes</i> cf. <i>glaberrima</i>
COX1	1593	1590	1590	1590	1593	1590	1593	1593
COX1(5')-HEG	357						378	378
HEG	981						996	996
HEG-COX1(3')	91						213	213
<i>COX1-ND4L</i>	122	92	92	92	138	92	169	169
ND4L	300	300	300	300	300	300	300	300
<i>ND4L-COX2</i>	340	70	70	70	128	70	157	157
COX2	750	750	750	750	750	750	750	750
<i>COX2-ND4</i>	98	60	60	60	60	61	110	110
ND4	1476	1476	1476	1476	1476	1476	1476	1476
<i>ND4-ND6</i>	186	104	104	104	66	112	174	174
ND6	579	564	564	564	633	564	579	579
<i>ND6-ATP8</i>	71	21	21	21	61	24	64	64
ATP8	213	216	216	216	213	213	213	213
<i>ATP8-ATP6</i>	69	72	72	72	92	82	233	233
ATP6	699	699	699	699	714	699	699	699
<i>ATP6-ND5</i>	97	110	110	110	164	65	186	186
ND5	1866	1839	1839	1839	1851	1839	1851	1851
ND5(5')-ND1	453	355	355	355	407	365	572	572
ND1	984	984	984	984	984	984	984	984
<i>ND1-ND3</i>	30	48	48	48	48	32	49	49
ND3	357	357	357	357	357	357	408	408
ND3-ND5(3')	106	115	115	115	136	115	221	221
<i>ND5-tRNA^{Trp}</i>	39	27	27	27	39	27	39	39
tRNA ^{Trp}	70	70	70	70	70	70	70	70
<i>tRNA^{Trp}-ND2</i>	78	19	19	19	19	19	518	534
ND2	1542	1509	1509	1509	1575	1518	1584	1584
<i>ND2-12S</i>	244	197	197	197	238	197	431	431
12S	1140	1141	1141	1141	1168	1141	1164	1164
<i>12S-CYTB</i>	70	81	81	81	122	110	106	106
CYTB	1143	1143	1143	1143	1143	1134	1143	1143
<i>CYTB-tRNA^{Met}</i>	75	49	49	49	75	49	68	68
tRNA ^{Met}	71	71	71	71	71	71	71	71
<i>tRNA^{Met}-16S</i>	74	64	64	64	83	74	202	202
16S	2618	2569	2569	2569	2588	2590	2673	2673
<i>16S-COX3</i>	154	115	155	115	217	74	277	277
COX3	789	789	789	789	750	789	819	819
<i>COX3-COX1</i>	44	34	34	34	69	34	113	113
Total IGR	1791	1163	1203	1163	1619	1122	2896	2912
Mitogenome size	19969	17700	17700	17700	18398	17687	21653	21669

Table S4b

	<i>Leiopathes montana</i>	<i>Myriopathes japonica</i>	<i>Parantipathes sp.</i>	<i>Parantipathes cf. hirondelle</i>	<i>Parantipathes hirondelle</i>	<i>Phanopathes sp.</i>	<i>Sibopathes cf. macrospina</i>	<i>Stauroopathes arctica</i>
COX1	1593	1581	1590	1590	1590	1593	1590	1590
COX1(5')-HEG	378	206				344		
HEG	996	657				918		
HEG-COX1(3')	213	61				103		
<i>COX1-ND4L</i>	169	83	92	92	92	106	92	92
ND4L	300	300	300	300	300	300	300	300
<i>ND4L-COX2</i>	157	30	82	82	82	134	82	70
COX2	750	750	750	750	750	750	750	750
<i>COX2-ND4</i>	110	10	61	61	61	82	61	60
ND4	1476	1476	1476	1476	1476	1476	1476	1476
<i>ND4-ND6</i>	174	77	104	104	104	597	104	104
ND6	579	570	564	564	564	579	564	564
<i>ND6-ATP8</i>	64	4	24	24	24	113	24	21
ATP8	213	213	213	213	213	213	213	216
<i>ATP8-ATP6</i>	233	9	82	82	82	19	82	72
ATP6	699	699	699	699	699	699	699	699
<i>ATP6-ND5</i>	186	25	108	108	108	116	108	110
ND5	1851	1851	1839	1839	1839	1866	1839	1839
ND5(5')-ND1	572	253	367	367	367	441	367	355
ND1	984	984	984	984	984	984	984	984
<i>ND1-ND3</i>	49	5	48	48	48	109	48	48
ND3	408	360	357	357	357	357	357	357
ND3-ND5(3')	221	97	115	115	115	106	115	115
<i>ND5-tRNA_{Trp}</i>	39	33	27	27	27	39	27	27
tRNA _{Trp}	70	70	70	70	70	70	70	70
<i>tRNA_{Trp}-ND2</i>	534	17	19	19	19	81	19	19
ND2	1587	1488	1518	1518	1518	1575	1518	1509
<i>ND2-12S</i>	431	120	197	197	197	258	197	197
12S	1164	1148	1141	1141	1141	1171	1141	1141
<i>12S -CYTB</i>	106	65	100	100	100	61	100	80
CYTB	1143	1137	1143	1143	1143	1143	1143	1143
<i>CYTB-tRNA_{Met}</i>	68	59	49	49	49	39	49	49
tRNA _{Met}	71	71	71	71	71	71	71	71
<i>tRNA_{Met}-16S</i>	202	48	64	64	64	141	64	64
16S	2673	2255	2561	2561	2561	2662	2569	2569
<i>16S-COX3</i>	277	101	96	96	96	57	96	115
COX3	819	789	789	789	789	789	789	789
<i>COX3-COX1</i>	113	30	34	34	34	79	34	34
Total IGR	2912	716	1187	1187	1187	2031	1187	1162
Mitogenome size	21672	17733	17734	17734	17734	20304	17734	17700

Table S4c

	<i>Stauropathes</i> cf. <i>punctata</i>	<i>Stichopathes</i> n. sp.	<i>Stichopathes</i> <i>abyssicola</i>	<i>Stichopathes</i> <i>luetkeni</i>	<i>Tanacetipathes</i> <i>thamnea</i>	<i>Telopathes</i> sp.	<i>Trissopathes</i> cf. <i>tetracrada</i>	<i>Tylopathes</i> n. sp.
COX1	1590	1593	1593	1593	1581	1590	1629	1581
COX1(5')-HEG		373	357	272	184			184
HEG			981	1062	657			657
HEG-COX1(3')		97	91	105	61			61
<i>COX1-ND4L</i>	92	35	122	148	83	92	138	83
ND4L	300	300	300	300	300	300	300	300
<i>ND4L-COX2</i>	70	178	340	107	30	70	128	30
COX2	750	750	750	750	750	750	750	750
<i>COX2-ND4</i>	60	82	98	56	10	60	60	10
ND4	1476	1476	1476	1503	1476	1476	1476	1476
<i>ND4-ND6</i>	104	165	186	205	77	104	121	77
ND6	564	579	579	591	570	564	579	570
<i>ND6-ATP8</i>	21	114	71	74	4	21	61	4
ATP8	216	213	213	213	213	216	213	213
<i>ATP8-ATP6</i>	72	19	69	156	9	72	92	9
ATP6	699	699	699	720	699	699	699	699
<i>ATP6-ND5</i>	110	28	97	138	25	110	175	25
ND5	1839	1962	1866	1851	1851	1839	1851	1851
ND5(5')-ND1	355	426	453	350	253	355	406	253
ND1	984	984	984	1050	984	984	984	984
<i>ND1-ND3</i>	48	12	30	137	5	48	48	5
ND3	357	357	357	357	360	357	357	360
ND3-ND5(3')	115	107	106	168	97	115	135	97
<i>ND5-tRNA_{Trp}</i>	27	38	39	44	33	27	39	33
tRNA _{Trp}	70	70	70	70	70	70	70	70
<i>tRNA_{Trp}-ND2</i>	19	109	78	119	17	19	19	17
ND2	1509	1557	1542	1518	1488	1509	1575	1488
<i>ND2-12S</i>	197	277	244	229	120	197	238	154
12S	1141	1170	1139	1149	1148	1141	1168	1089
<i>12S-CYTB</i>	71	69	70	105	66	71	122	66
CYTB	1143	1143	1143	1143	1137	1143	1143	1137
<i>CYTB-tRNA_{Met}</i>	49	51	75	76	59	49	75	59
tRNA _{Met}	71	71	71	71	71	71	71	71
<i>tRNA_{Met}-16S</i>	64	66	74	104	48	64	82	42
16S	2569	2641	2618	2663	2255	2560	2588	2252
<i>16S-COX3</i>	115	187	154	166	101	115	224	101
COX3	789	789	789	789	789	789	789	789
<i>COX3-COX1</i>	34	56	44	296	30	34	64	30
Total IGR	1153	1486	1791	2160	717	1153	1686	745
Mitogenome size	17690	19839	19968	20448	17712	17681	18469	17679

Table S5 | Open read frames (ORFs) found in intergenic regions (IGRs). Numbers represent length of ORF in base pairs. < designates an ORF on the opposite strand.

	<i>Anipathes cf. dichotoma</i>	<i>Bathypathes sp. 1</i>	<i>Bathypathes n. sp. 2</i>	<i>Bathypathes n. sp. 3</i>	<i>Chrysopathes formosa</i>	<i>Dendrobathypathes n. sp.</i>	<i>Leiopathes expansa</i>	<i>Leiopathes cf. glaberrima</i>	<i>Leiopathes montana</i>	<i>Myriopathes japonica</i>	<i>Parantipathes cf. hirondelle</i>	<i>Parantipathes hirondelle</i>
COX1 - ND4L							87	87	87			
ND4L - COX2	168						75	75	75			
COX2 - ND4							81	81	81			
ND4 - ND6							60					
ND6 - ATP8												
ATP8 - ATP6							51		81<			
ATP6 - ND5												
ND1 - ND3							49					
ND5 - tRNA Trp												
Trp - ND2							87<		168	168		
Trp - ND2							132<	132<	132<			
ND2 - 12S	72	93	93			93	129	129	129			93
ND2 - 12S			120	93			186	186	186		93	
12S - CYTB												
CYTB - tRNA Met												
Met - 16S												
16S - COX3							147	147	147			
COX3 - COX1							105<	105<				

	<i>Parantipathes sp.</i>	<i>Phanopathes sp.</i>	<i>Sibopathes cf. macrospina</i>	<i>Stauropathes cf. punctata</i>	<i>Stauropathes arctica</i>	<i>Sichopathes abyssicola</i>	<i>Sichopathes luetkeni</i>	<i>Sichopathes n. sp.</i>	<i>Tanacetipathes thamea</i>	<i>Telopathes sp.</i>	<i>Trisopathes cf. tetracrada</i>	<i>Tylopathes n. sp.</i>
COX1 - ND4L												
ND4L - COX2						168						
COX2 - ND4						63						
ND4 - ND6		477										
ND6 - ATP8												
ATP8 - ATP6												
ATP6 - ND5												
ND1 - ND3												
ND5 - tRNA Trp												
Trp - ND2												
Trp - ND2												
ND2 - 12S											84	
ND2 - 12S	93	129	93	93	93	72	84<		93	60	120	
12S - CYTB					120							
CYTB - tRNA Met												
Met - 16S				49								
16S - COX3											87	
COX3 - COX1								102				

Table S6 | Location of inverted repeats identified in six antipatharian species in the study.

Species	ND2 to IGR ND2_12S	ND5 (5') - ND1 to ND3 - ND5 (3')	Beginning of 16S	Middle 16S to IGR COX3- COX1	ND4 to ATP6	IGR ND4L- COX2 to COX2	IGR ND2-12S to IGR 12S- CYTB
<i>Leiopathes</i> cf. <i>glaberrima</i>	37/40 bp 92% match	24/28 bp 85% match	21/24 bp 87% match	34/41 bp 82% match			
<i>Leiopathes</i> <i>expansa</i>	37/40 bp 92% match	24/28 bp 85% match	21/24 bp 87% match	34/41 bp 82% match			
<i>Leiopathes</i> <i>montana</i>	37/40 bp 92% match	24/28 bp 85% match	21/24 bp 87% match	34/41 bp 82% match			
<i>Phanopathes</i> sp.						29/34 bp 85% match	
<i>Stichopathes</i> n. sp.					21/23 bp 91% match		
<i>Trissopathes</i> cf. <i>tetracrada</i>							20/22 bp 90% match

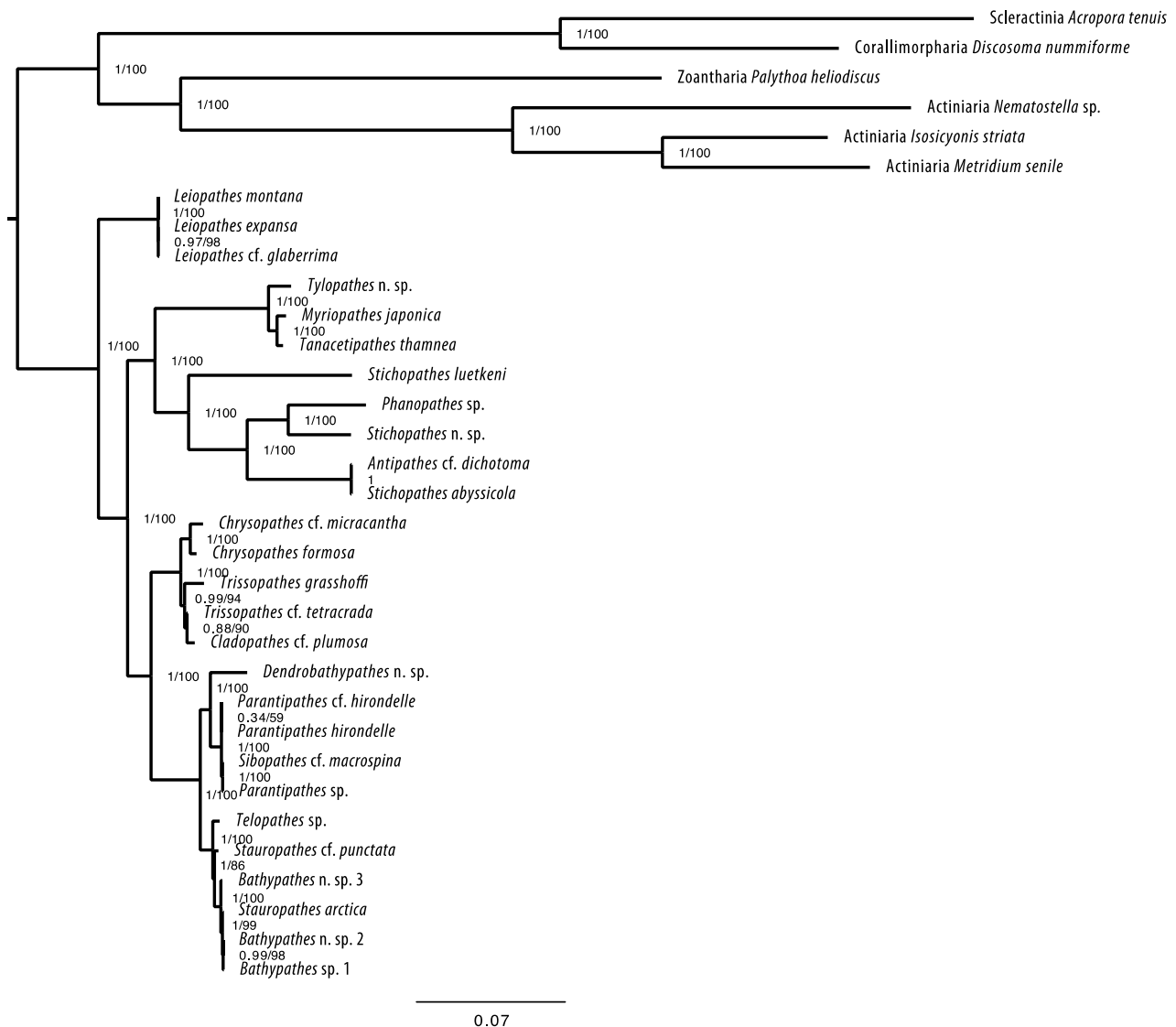


Figure S1| Full hexacoral outgroups. Phylogenetic tree reconstruction based on all available (newly sequenced from this study and GenBank samples) antipatharian mitochondrial genomes using the 13 energy pathway genes based on a Bayesian inference (BI) and maximum likelihood (ML) analysis. The trees are rooted at a midpoint between Antipatharia and the hexacoral outgroups. BI posterior probabilities and ML bootstrap values shown at nodes (BI/ML).

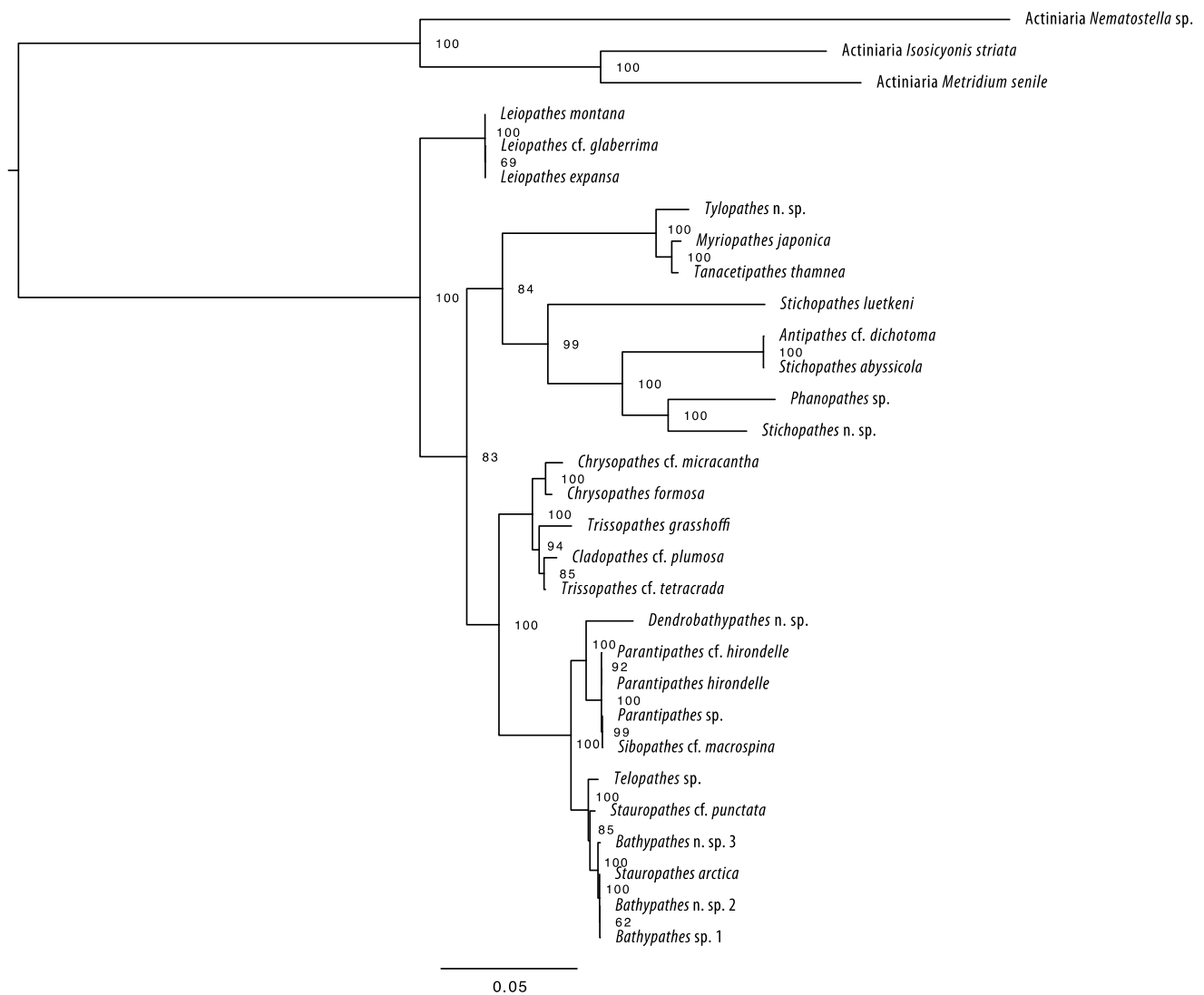


Figure S2| Actiniaria outgroups. Maximum likelihood (ML) phylogenetic tree reconstruction based on 13 mitochondrial protein genes of the antipatharian species used in this study. ML bootstrap values shown at nodes. The trees are rooted at a midpoint between Antipatharia and the Actiniaria outgroups.

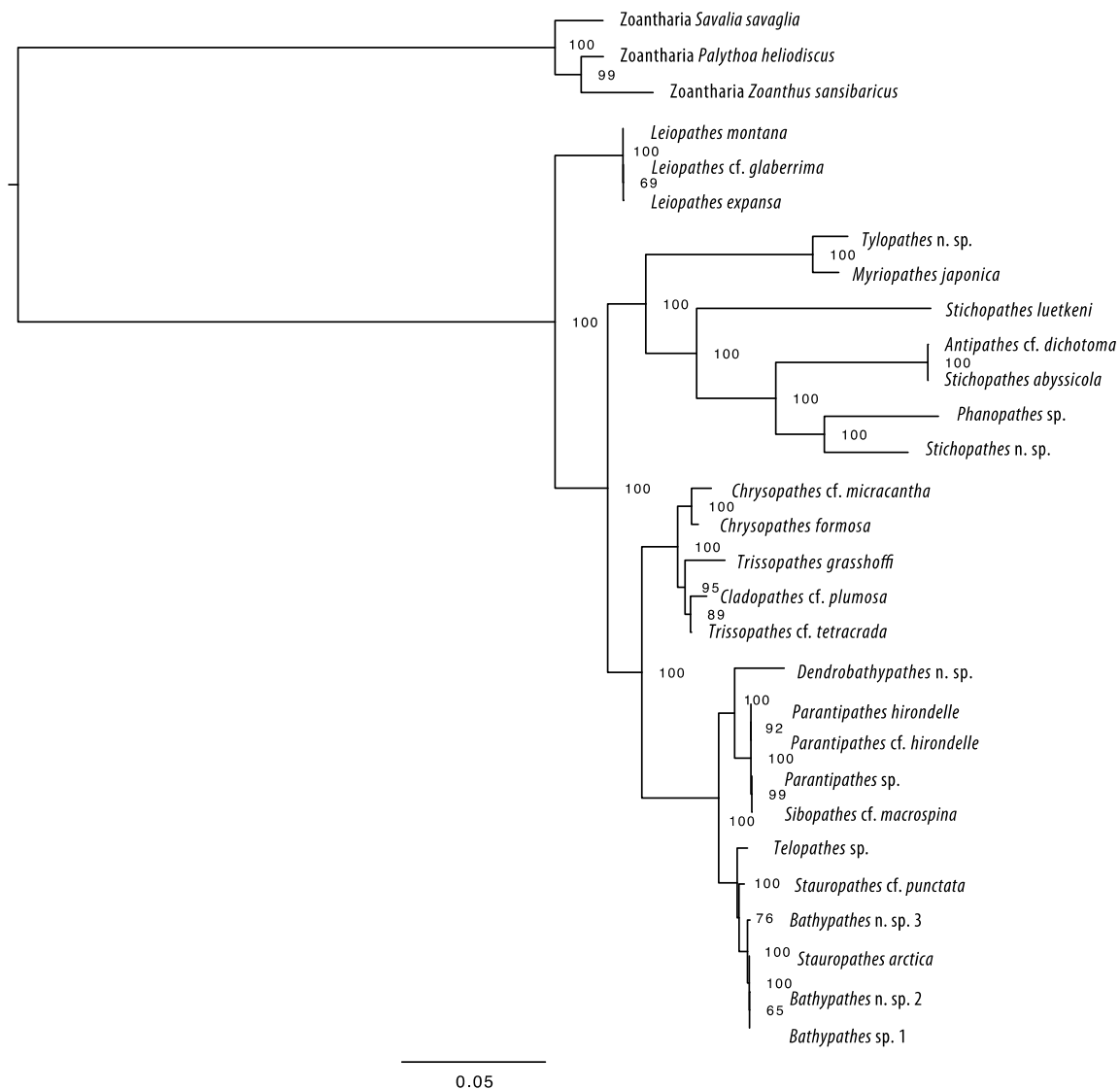


Figure S3| Zoantharia outgroups. Maximum likelihood (ML) phylogenetic tree reconstruction based on 13 mitochondrial protein genes of the antipatharian species used in

this study. ML bootstrap values shown at nodes. The trees are rooted at a midpoint between Antipatharia and the Zoantharia outgroups.

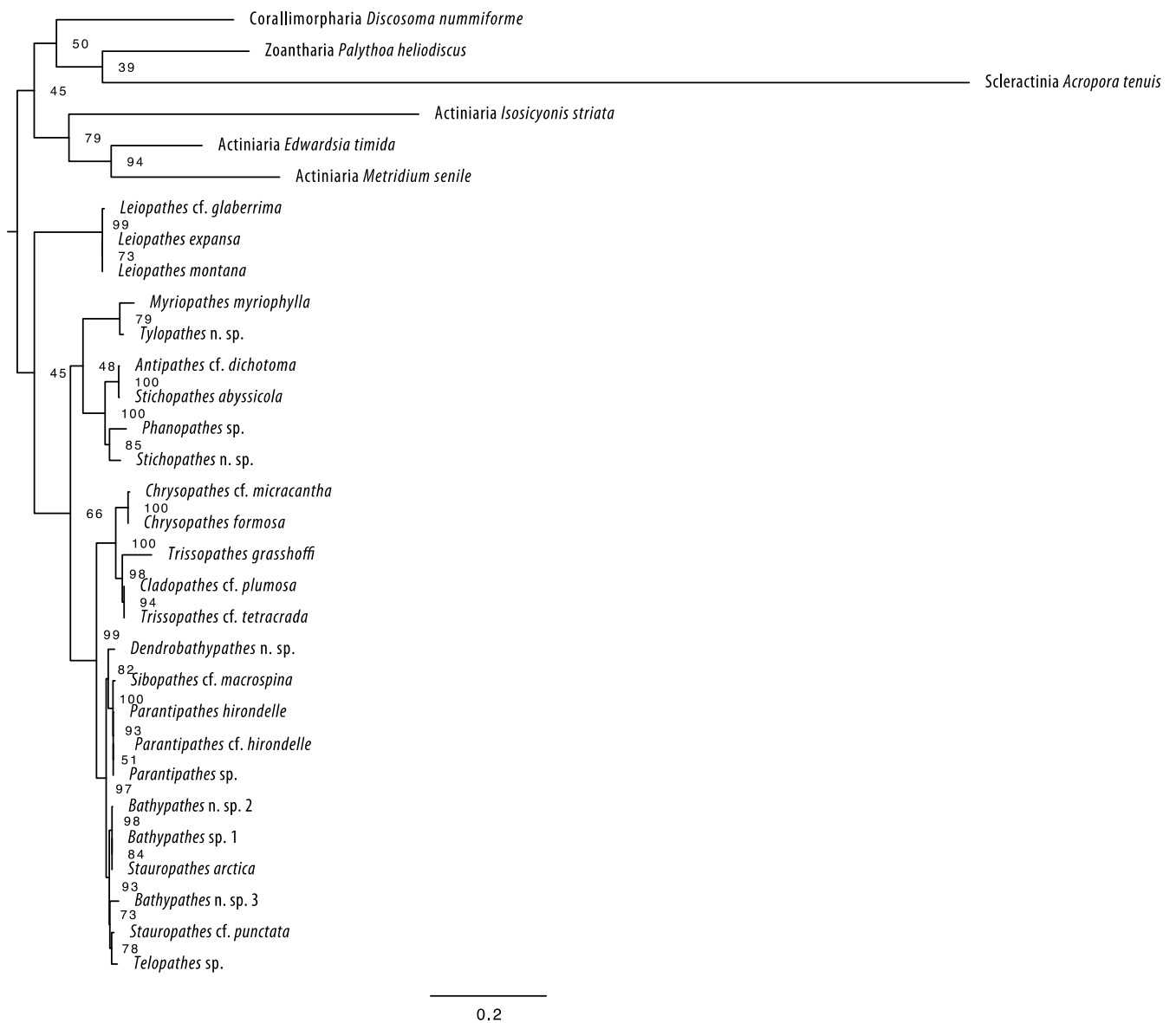


Figure S4| Maximum likelihood (ML) phylogenetic tree reconstruction based on recovered nuclear regions of the antipatharian species used in this study. ML bootstrap values shown at nodes.

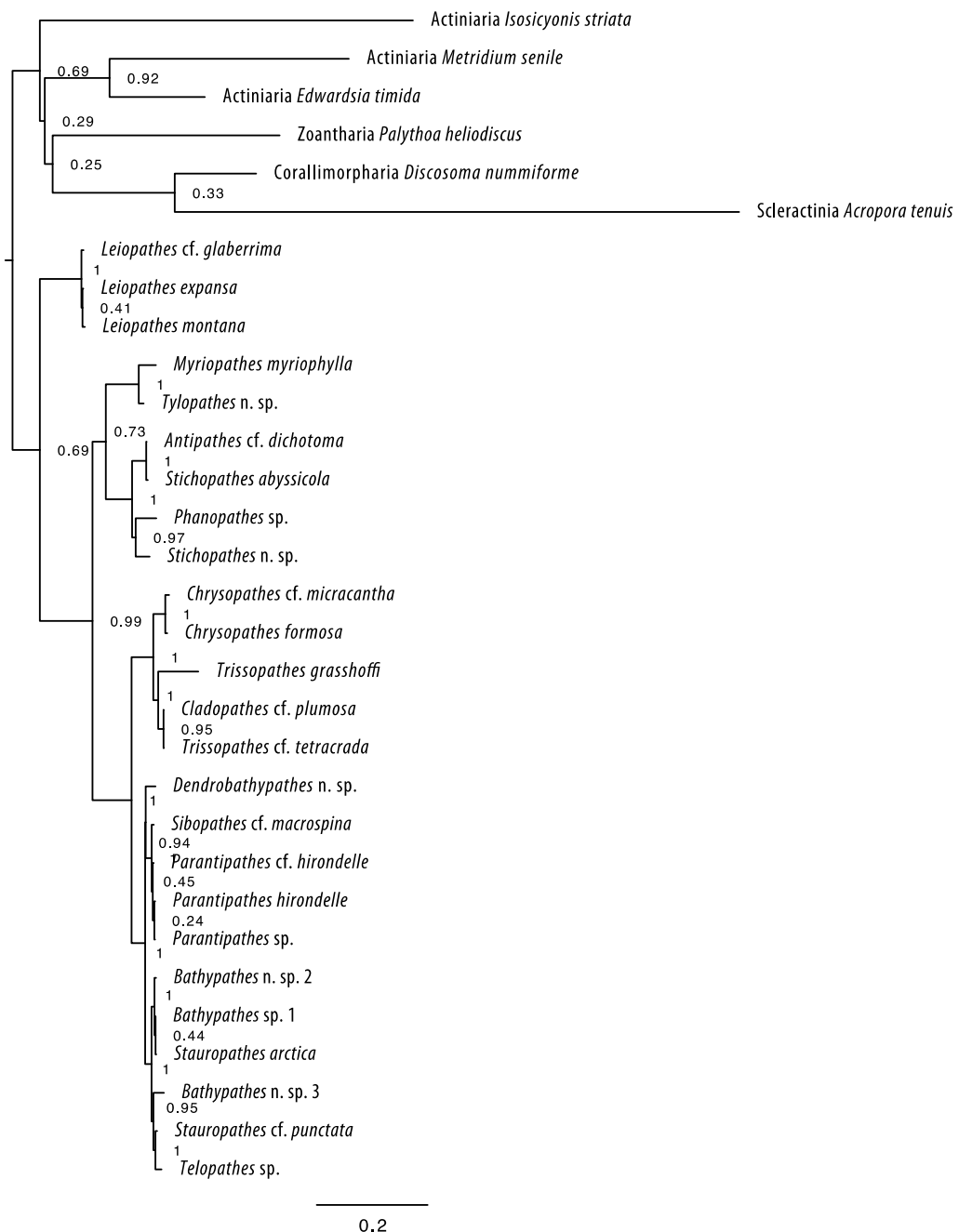


Figure S5| Bayesian inference (BI) phylogenetic tree reconstruction based on recovered nuclear regions of the antipatharian species used in this study. BI posterior probability values shown at nodes.



Figure S6| Maximum likelihood (ML) phylogenetic tree reconstruction based on the combined 13 mitochondrial protein coding genes and nuclear regions of the antipatharian species used in this study. ML bootstrap values shown at nodes.

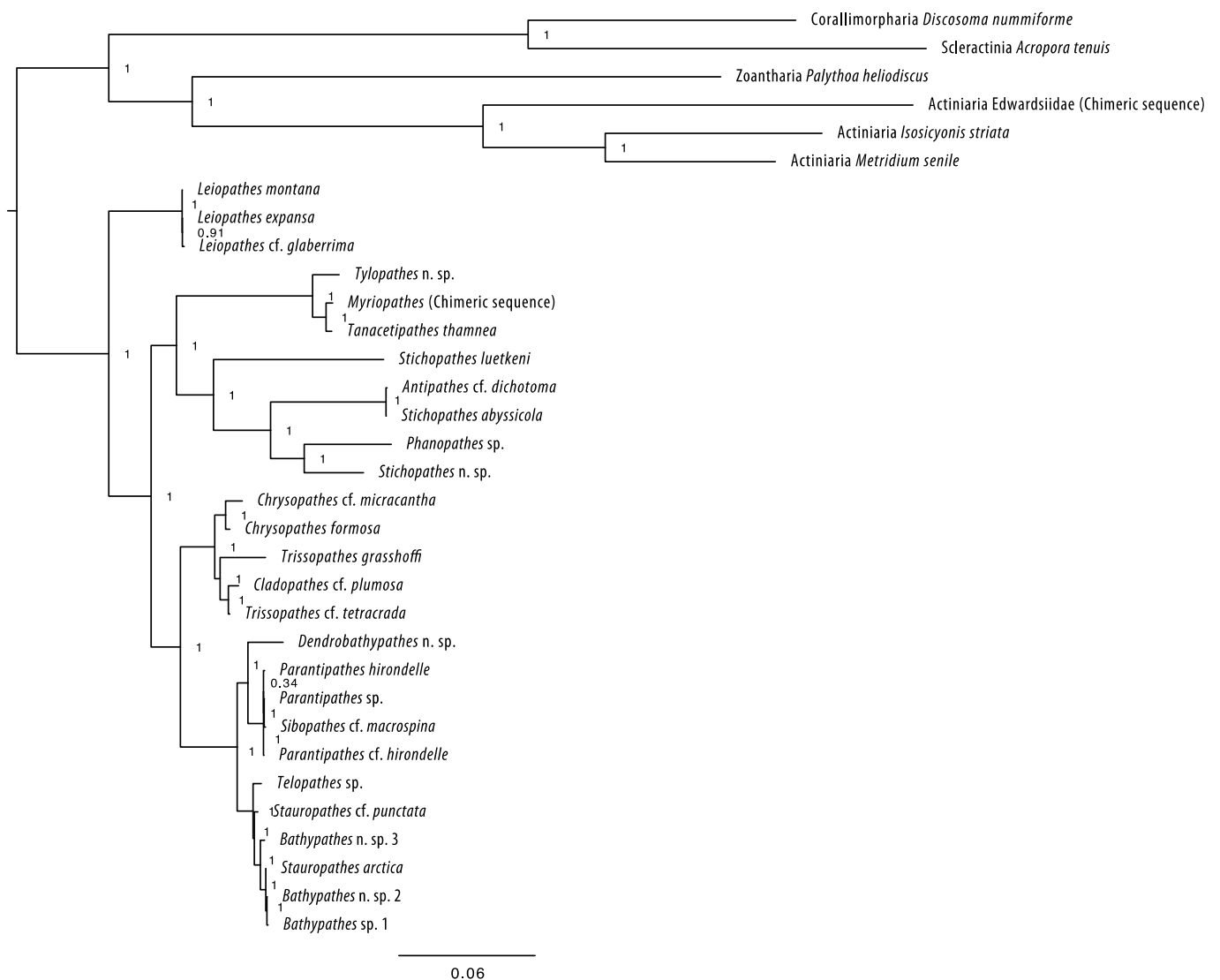


Figure S7 | Bayesian inference (BI) phylogenetic tree reconstruction based on the combined 13 mitochondrial protein coding genes and nuclear regions of the antipatharian species used in this study. BI posterior probability values shown at nodes.

	Tree	<u>logL</u>	<u>deltaL</u>	<u>bp-RELL</u>	p-KH	p-SH	c-ELW	p-AU
1. Unconstrained	1	-81820.37689	0	1 +	<u>0.993</u> +	1 +	1 +	1 +
2. Antipathidae	2	-87235.22449	<u>5414.8</u>	0 -	0 -	0 -	0 -	2.95e-05 -
3. Cladopathidae/Schizopathidae	3	-83107.77428	<u>1287.4</u>	0 -	0 -	0 -	0 -	0.000165 -
4. Bathypathes	4	-81872.72987	<u>52.353</u>	0 -	0.0068 -	0.628 +	7.28e-05 -	1.82e-05 -
5. Parantipathes	5	-81996.56919	<u>176.19</u>	0 -	0 -	0.0783 +	2.53e-37 -	1.35e-06 -
6. Stauropathes	6	-82438.099	<u>617.72</u>	0 -	0 -	0 -	1.1e-163 -	0.00407 -
7. Stichopathes	7	-87246.5991	<u>5426.2</u>	0 -	0 -	0 -	0 -	0.000122 -
8. Trissopathes	8	-82002.29154	<u>181.91</u>	0 -	0 -	0.0836 +	2.36e-40 -	2.82e-08 -

deltaL : logL difference from the maximal logl in the set.
bp-RELL : bootstrap proportion using REll method (Kishino et al. 1990).
p-KH : p-value of one sided Kishino-Hasegawa test (1989).
p-SH : p-value of Shimodaira-Hasegawa test (2000).
c-ELW : Expected Likelihood Weight (Strimmer & Rambaut 2002).
p-AU : p-value of approximately unbiased (AU) test (Shimodaira, 2002).

Figure S8 | Results of approximately unbiased test (AU).