Supplementary material:

Table 1: *Turritopsis nutricula* with its most related individuals *T. Dohnrnii, T. Rubra, Hydractinia sp., Podocoryna borealis, Symplectoscyphus tricuspidatus, Halecium delicatulum, Eucheilota menoni, Bimeria vestita* and *Salacia desmoides* arranged according to their E-Value and Max Ident based on gene relative study.

Relative Species	**Max score**	**Total score**	**Query coverage**	**E value**	**Max Ident**
Turritopsis nutricula isolate WHOI_1 16S ribosomal RNA gene, partial sequence; mitochondrial	1081	1081	100%	0	100%
Turritopsis sp. 1 MPM-2008 isolate Bocas_2 16S ribosomal RNA gene, partial sequence; mitochondrial	1037	1037	100%	0	99%
Turritopsis dohrnii isolate Fort Pierce_2 16S ribosomal RNA gene, partial sequence; mitochondrial	961	961	100%	0	96%
Turritopsis rubra isolate Japan_1 16S ribosomal RNA gene, partial sequence; mitochondrial	778	778	100%	0	91%
Hydractinia sp. 1 MPM-2009 isolate 078 16S ribosomal RNA gene, partial sequence; mitochondrial	614	614	99%	3.00E-172	86%
Podocoryna borealis isolate 152 16S ribosomal RNA gene, partial sequence; mitochondrial	601	601	99%	2.00E-168	85%
Symplectoscyphus tricuspidatus voucher MNHN INVE29953 16S ribosomal RNA gene, partial sequence; mitochondrial	599	599	99%	8.00E-168	85%
Halecium delicatulum mitochondrial partial 16S rRNA gene, isolated from Antarctica, Ross Sea	595	595	99%	1.00E-166	85%
Eucheilota menoni voucher MHNG INVE33457 16S ribosomal RNA gene, partial sequence; mitochondrial	590	590	100%	5.00E-165	85%
Bimeria vestita mitochondrial partial 16S rRNA gene	590	590	99%	5.00E-165	85%
Salacia desmoides 16S ribosomal RNA gene, partial sequence; mitochondrial	588	588	100%	2.00E-164	85%

Table 2: *Turritopsis nutricula* with its most related individuals *Clytia sp, Eirene ceylonensis, Nemopsis bachei, Clytia folleata, Clytia elsaeoswaldae, Obelia bidentata, Clytia gracilis, Eirene brevistylus* and *Turritopsis lata* arranged according to their E-Value and Max Indent based on 16s rRNA relative study.

Relative Species	**Max score**	**Total score**	**Query coverage**	**E value**	**Max ident**
Turritopsis nutricula isolate 1 cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial	1147	1147	100%	0	100%
Clytia sp. KC JRH-2012 isolate 1 cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial	625	625	98%	1.00E-175	85%
Eirene ceylonensis isolate 3 cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial	625	625	99%	1.00E-175	85%
Nemopsis bachei mitochondrion, partial genome	625	625	99%	1.00E-175	85%
Clytia folleata cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial	619	619	99%	7.00E-174	85%
Clytia elsaeoswaldae cytochrome oxidase subunit I gene, partial cds; mitochondrial	619	619	97%	7.00E-174	85%
Obelia bidentata voucher 76NC cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial	619	619	95%	7.00E-174	85%
Clytia gracilis voucher Brazil.5 cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial	617	617	98%	2.00E-173	85%
Eirene brevistylus isolate 4 cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial	614	614	99%	3.00E-172	85%
Turritopsis lata cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial	593	593	100%	4.00E-166	84%

Table 3: *Turritopsis nutricula* with its most related individuals *Turritopsis lata, Didiscus sp., Tiaricodon coeruleus, Amphinema dinema, Laodicea undulata, Bougainvillia muscus, Clytia sp., Eirene ceylonensis, Eutima levuka, Eucheilota menoni* and *Helgicirrha malayensis* arranged according to their E-Value and Max Indent based on protein relative study.

Description	**Max score**	**Total score**	**Query coverage**	**E value**	**Max ident**
cytochrome oxidase subunit I, partial (mitochondrion) [Turritopsis nutricula]	407	407	100%	1.00E-142	100%
cytochrome oxidase subunit I, partial (mitochondrion) [Turritopsis lata]	362	362	100%	6.00E-125	97%
cytochrome oxidase subunit I [Didiscus sp. UCMPWC1040]	363	363	100%	6.00E-125	87%
cytochrome oxidase subunit I, partial (mitochondrion) [Tiaricodon coeruleus]	359	359	100%	9.00E-124	96%
cytochrome oxidase subunit I, partial (mitochondrion) [Amphinema dinema]	353	353	100%	3.00E-121	97%
cytochrome oxidase subunit I, partial (mitochondrion) [Laodicea undulata]	350	350	100%	4.00E-120	97%
cytochrome oxidase subunit I, partial (mitochondrion) [Bougainvillia muscus]	350	350	100%	5.00E-120	94%
cytochrome oxidase subunit I, partial (mitochondrion) [Clytia sp. KC JRH-2012]	349	349	100%	7.00E-120	97%
cytochrome oxidase subunit I, partial (mitochondrion) [Eirene ceylonensis]	349	349	100%	8.00E-120	97%
cytochrome oxidase subunit I, partial (mitochondrion) [Eutima levuka]	349	349	100%	9.00E-120	97%
cytochrome oxidase subunit I, partial (mitochondrion) [Eucheilota menoni]	349	349	100%	9.00E-120	97%
cytochrome oxidase subunit I, partial (mitochondrion) [Helgicirrha malayensis]	349	349	100%	1.00E-119	97%