

Clade	Taxon	Transcripts	genes	N50	Average contig length	Median contig length	percent G/C	BUSCO % (protein)	BUSCO %
Stichodactylina	<i>C.adhaesivum (body)</i>	634715	423320	1127	724.23	403	39.86	83.5	87.2
	<i>C.adhaesivum (nematocyst)</i>	271167	160450	1574	962.67	571	46.2	87.8	91.1
	<i>S.haddoni</i>	196433	150054	1038	718.72	449	43.48	81.2	83.7
	<i>Ha.hemprichii (A)</i>	131444	116964	605	507.94	339	46.63	50.2	50.1
	<i>Ha.hemprichii (B)</i>	161588	132154	1352	834.03	479	47.14	85.8	86.5
	<i>Ha.hemprichii (C)</i>	140865	123392	870	628.95	401	48.63	60.4	59.7
	<i>Ha.hemprichii (D)</i>	166159	139624	1232	768.72	430	45.9	92.2	92.5
Heteractina	<i>Hs.crispa (combined)</i>	655116	581957	545	459.17	263	45.17	91.8	92.8
	<i>M.doreensis (1)</i>	169310	125063	1280	829.65	518	45.69	81.7	82.6
	<i>M.doreensis (2)</i>	128634	102820	678	633.31	388	45.79	49.8	50.1
	<i>M.doreensis (3)</i>	174026	123083	1609	984.01	587	46.27	85.5	87.2
	<i>M.doreensis (4)</i>	152321	113560	1326	856.41	549	47.49	70.7	75
Entacmaea	<i>E.quadricolor (1)</i>	159879	110724	1398	815.42	433	38.95	95.1	95.8
	<i>E.quadricolor (2)</i>	182027	136593	1001	687.55	407	40.25	89.3	90.1
	<i>E.quadricolor (3)</i>	218132	166239	1051	722.73	438	41.93	90.7	92.4
	<i>E.quadricolor (4)</i>	211617	161980	1058	728.22	448	42.49	93	94
	<i>E.quadricolor (5)</i>	216944	166660	1054	713.1	415	41.54	94.2	94.8
	<i>E.quadricolor (6)</i>	209482	159611	1052	722.63	436	41.8	92.6	93.8

Supplementary table S1. The the table shos individual transcriptomes state for each SRA sample. Results were sourced by using Trinity_stats.pl withinTrinity. BUSCO v5.4.2 was used to retrieve BUSCO scores.