The following supplement accompanies the article

Different microbiomes associated with the copepods *Acartia tonsa* and *Temora longicornis* from the same marine environment

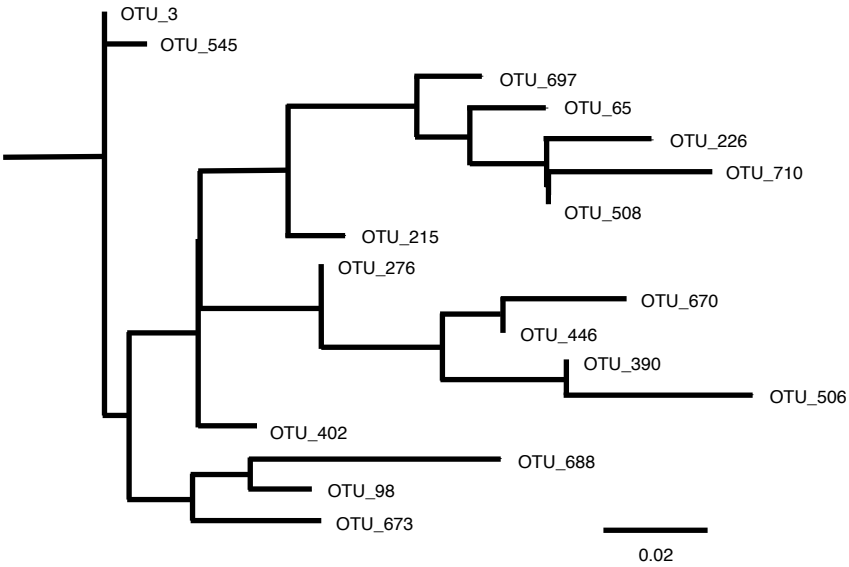
Julia N. A. Dorosz, Josue L. Castro-Mejia, Lars Hestbjerg Hansen, Dennis Sandris Nielsen, Alf Skovgaard*

*Corresponding author: dr.alf.skovgaard@gmail.com

Aquatic Microbial Ecology 78: 1–9 (2016)

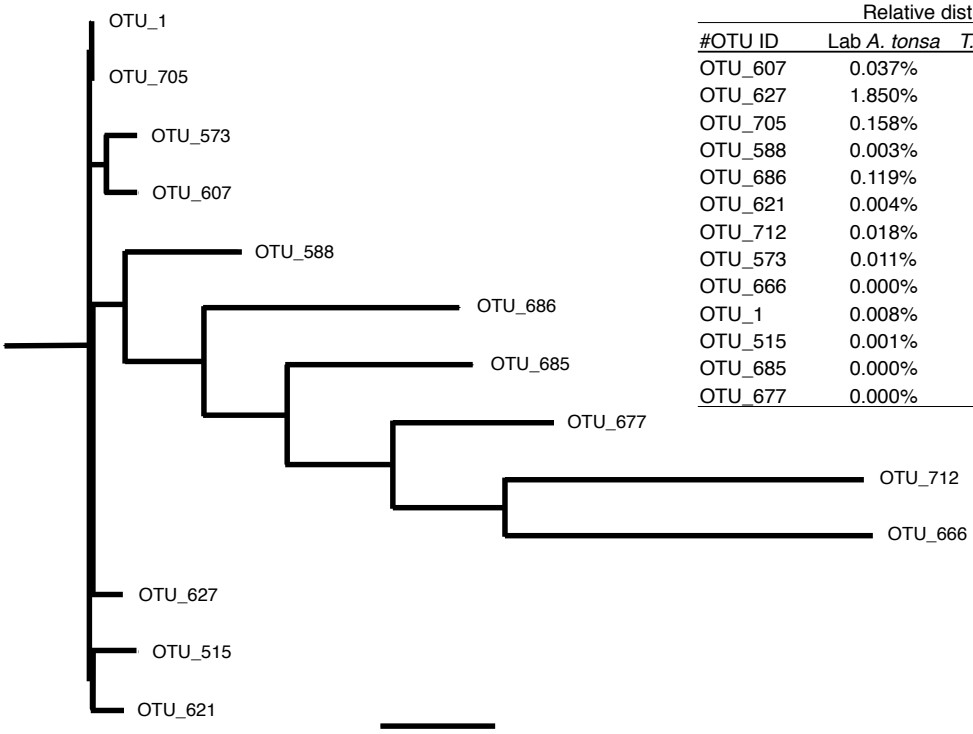
Table S1. Samples information. Mapping file

SampleID	Species
ALF..01	Lab_A_tonsa
ALF..02	Lab_A_tonsa
ALF..03	Lab_A_tonsa
ALF..04	Lab_A_tonsa
ALF..41	Wild_A_tonsa
ALF..42	Wild_A_tonsa
ALF..43	Wild_A_tonsa
ALF..44	Wild_A_tonsa
ALF..45	Wild_A_tonsa
ALF..46	Wild_T_longicornis
ALF..47	Wild_T_longicornis
ALF..48	Wild_T_longicornis
ALF..49	Wild_T_longicornis
ALF..50	Wild_T_longicornis



	Relative distribution	
#OTU ID	Lab *A. tonsa*	*A. tonsa*
OTU_545	47.050%	0.295%
OTU_3	5.803%	0.092%
OTU_673	0.252%	0.359%
OTU_98	0.167%	0.000%
OTU_215	0.033%	0.326%
OTU_688	0.002%	0.000%
OTU_697	0.001%	0.105%
OTU_710	0.000%	0.011%
OTU_276	0.010%	0.005%
OTU_670	0.001%	0.005%
OTU_402	0.004%	0.005%
OTU_508	0.001%	0.123%
OTU_446	0.000%	0.005%
OTU_65	0.021%	0.019%
OTU_390	0.000%	0.004%
OTU_506	0.000%	0.003%
OTU_226	0.000%	0.028%

Figure S1. Phylogenetic distance and relative distribution of OTUs belonging to unclassified members of the Rhodobacteraceae family. Percentages represent their relative distribution based on 53,000 sequences per sample.



	Relative distribution	
#OTU ID	Lab *A. tonsa*	*T. longicornis*
OTU_607	0.037%	0.786%
OTU_627	1.850%	36.280%
OTU_705	0.158%	3.732%
OTU_588	0.003%	0.073%
OTU_686	0.119%	1.857%
OTU_621	0.004%	0.118%
OTU_712	0.018%	0.292%
OTU_573	0.011%	0.151%
OTU_666	0.000%	0.011%
OTU_1	0.008%	0.107%
OTU_515	0.001%	0.021%
OTU_685	0.000%	0.006%
OTU_677	0.000%	0.019%

Figure S2. Phylogenetic distance and relative distribution of OTUs belonging to unclassified members of the Sinobacteraceae family. Percentages represent their relative distribution based on 53,000 sequences per sample.