Bacteria of the genus *Endozoicomonas* dominate the microbiome of the Mediterranean gorgonian coral *Eunicella cavolini*

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Supplement. Data supplementing the alpha and beta diversity measurements, as well as details of the sample-group to OTU associations
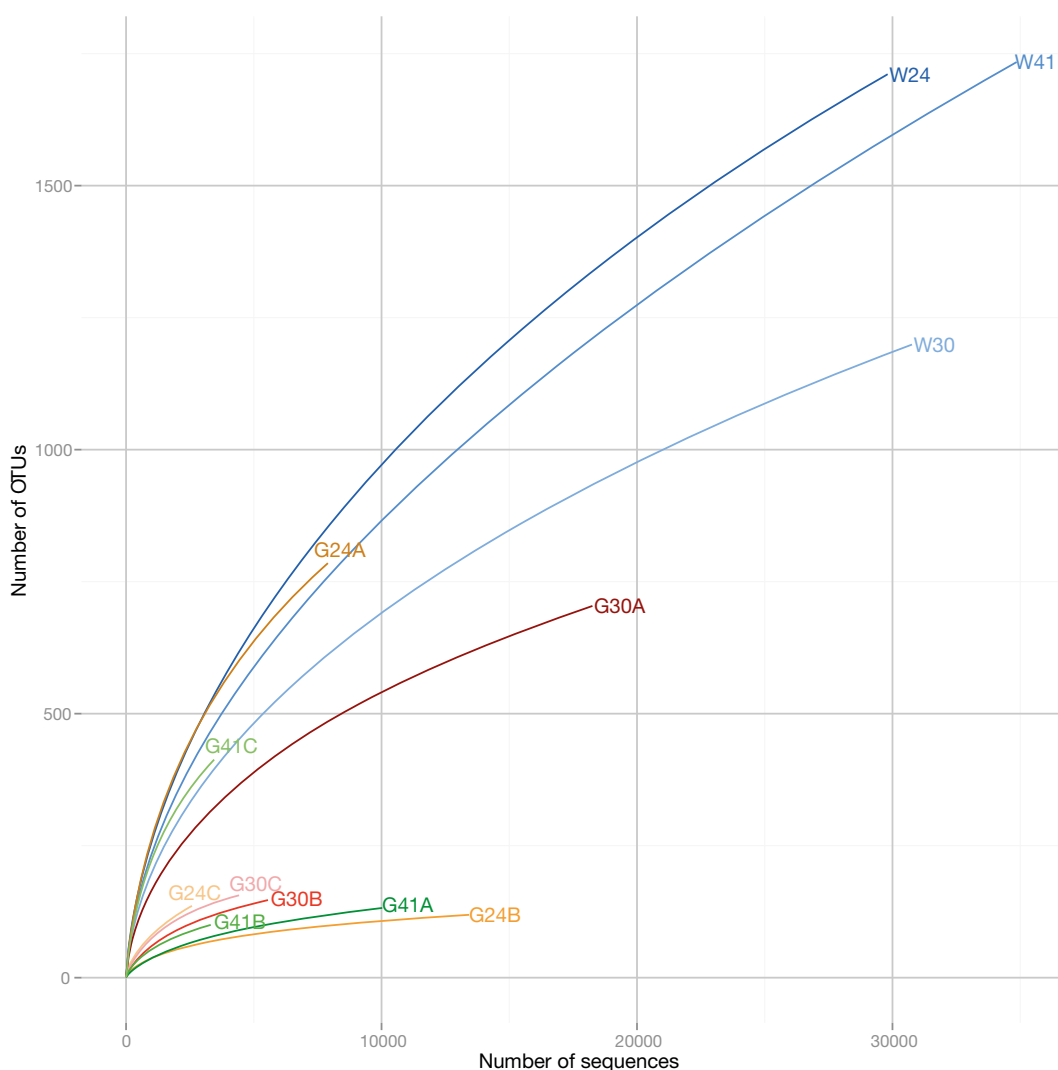

Fig. S1. Rarefaction curves for all samples. Curves show the number of OTUs at different sampling depths.
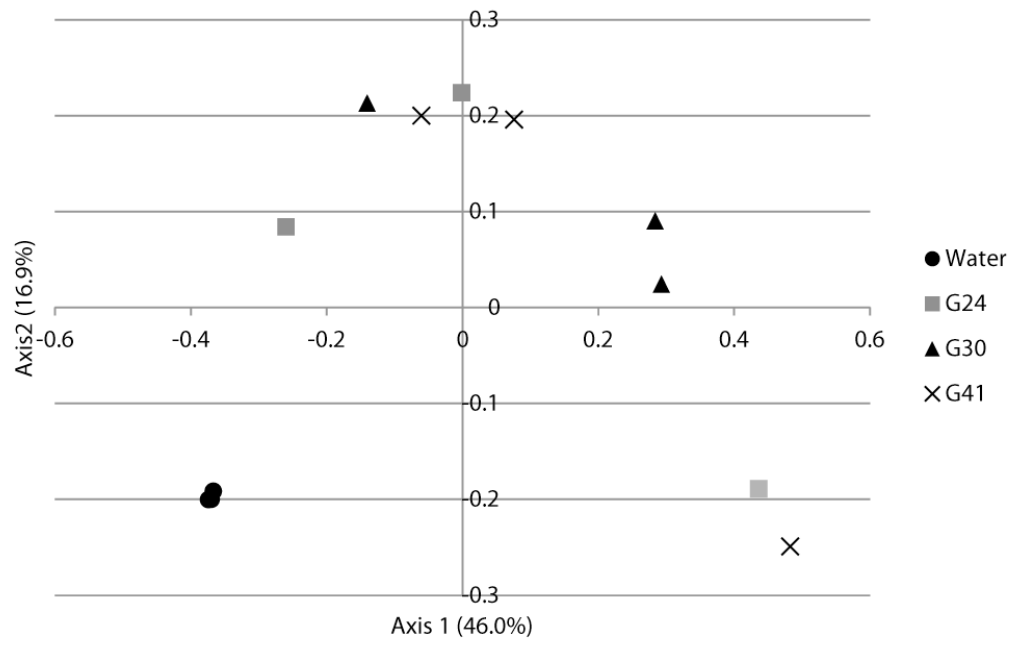
Fig. S2. Principal coordinate analysis of weighted UniFrac distances. The percentages of variability explained by each axis are given in parentheses.
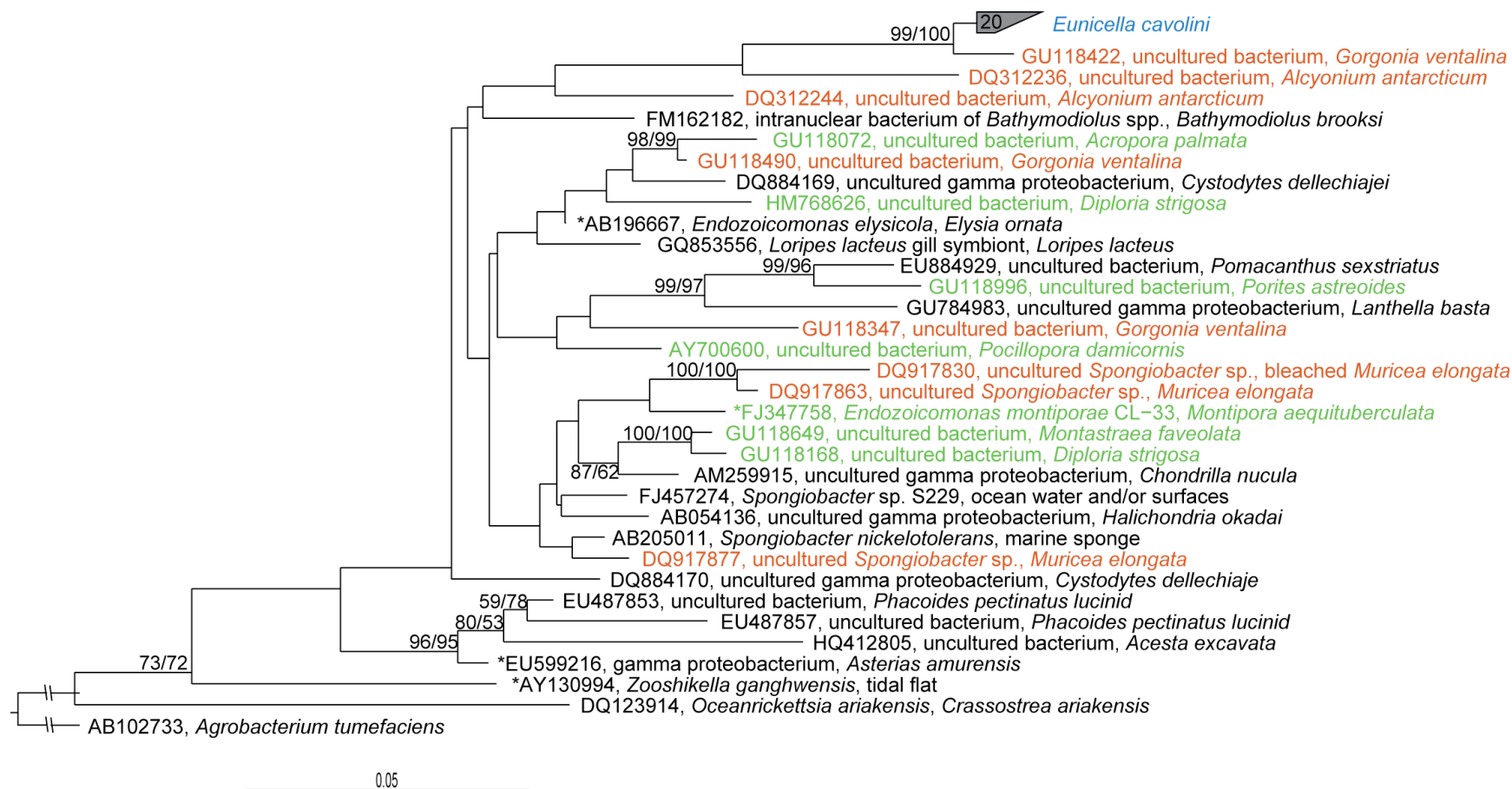
20 *Eunicella cavolini*

99/100

GU118422, uncultured bacterium, *Gorgonia ventalina*

DQ312236, uncultured bacterium, *Alcyonium antarcticum*

DQ312244, uncultured bacterium, *Alcyonium antarcticum*

FM162182, intranuclear bacterium of *Bathymodiolus* spp., *Bathymodiolus brooksi*

98/99 — GU118072, uncultured bacterium, *Acropora palmata*

GU118490, uncultured bacterium, *Gorgonia ventalina*

DQ884169, uncultured gamma proteobacterium, *Cystodytes dellechiajei*

HM768626, uncultured bacterium, *Diploria strigosa*

*AB196667, *Endozoicomonas elysicola*, *Elysia ornata*

GQ853556, *Loripes lacteus* gill symbiont, *Loripes lacteus*

99/96 — EU884929, uncultured bacterium, *Pomacanthus sexstriatus*

99/97 — GU118996, uncultured bacterium, *Porites astreoides*

GU784983, uncultured gamma proteobacterium, *Lanthella basta*

GU118347, uncultured bacterium, *Gorgonia ventalina*

AY700600, uncultured bacterium, *Pocillopora damicornis*

100/100 — DQ917830, uncultured *Spongiobacter* sp., bleached *Muricea elongata*

DQ917863, uncultured *Spongiobacter* sp., *Muricea elongata*

*FJ347758, *Endozoicomonas montiporae* CL−33, *Montipora aequituberculata*

100/100 — GU118649, uncultured bacterium, *Montastraea faveolata*

GU118168, uncultured bacterium, *Diploria strigosa*

87/62

AM259915, uncultured gamma proteobacterium, *Chondrilla nucula*

FJ457274, *Spongiobacter* sp. S229, ocean water and/or surfaces

AB054136, uncultured gamma proteobacterium, *Halichondria okadai*

AB205011, *Spongiobacter nickelotolerans*, marine sponge

DQ917877, uncultured *Spongiobacter* sp., *Muricea elongata*

DQ884170, uncultured gamma proteobacterium, *Cystodytes dellechiaje*

59/78 — EU487853, uncultured bacterium, *Phacoides pectinatus* lucinid

80/53 — EU487857, uncultured bacterium, *Phacoides pectinatus* lucinid

HQ412805, uncultured bacterium, *Acesta excavata*

96/95 — *EU599216, gamma proteobacterium, *Asterias amurensis*

73/72

*AY130994, *Zooshikella ganghwensis*, tidal flat

DQ123914, *Oceanrickettsia ariakensis*, *Crassostrea ariakensis*

AB102733, *Agrobacterium tumefaciens*

0.05

Fig. S3. Phylogenetic tree of the Encozoicomonas from *Eunicella cavolini* (blue) and closely related bacteria. Most bacteria represented originate from marine invertebrates, such as soft corals (*Alcyonacea*, red) or scleractinian corals (green). Others include bivalves, sponges or sea slugs. EU884929 represents a bacterium from a fish, *Pomacanthus sextriatus*. Type strains are marked with *. The tree was calculated using PhyML as implemented in ARB, with a GTR substitution model. Bootstrap values are shown for 1000 bootsraps of PhyML, and 1000 bootstraps of a neighborhood joining tree calculated in MEGA 5. Full length 16S sequences obtained from cloning were used for this tree. The scale bar corresponds to 0.05 substitutions per nucleotide position

Table S1. Sample-group to OTU associations as calculated with the indicspecies package. OTUs with p < 0.05 are shown for two different analyses. The first table shows the results for grouping the samples into water and gorgonians, the second table shows the gorgoninan samples grouped by depth. Rows indicate the OTU with p values and number of reads, columns show the samples and the groups they belong to. The lower table shows the taxonomic assignment of the OTUs.

Sample Group OTU	p value	F24 Water	F30 Water	F41 Water	G24A Gorgonian	G24B Gorgonian	G24C Gorgonian	G30A Gorgonian	G30B Gorgonian	G30C Gorgonian	G41A Gorgonian	G41B Gorgonian	G41C Gorgonian
								No. of reads					
OTU41	0.005	0	0	0	61	48	150	419	17	83	20	2	48
OTU3	0.005	4	0	0	1311	11662	1355	7492	4187	3435	9330	1998	1519
OTU215	0.009	1	0	2	6	23	6	2	6	12	11	10	5
OTU124	0.0093	4	0	2	10	55	7	7	5	7	12	3	6
OTU126	0.0316	0	0	2	0	4	2	20	3	4	5	6	81
OTU707	0.0453	2	0	0	1	20	4	1	4	9	4	4	0
OTU164	0.0462	0	4	0	1	10	6	0	5	10	4	8	5
OTU361	0.0447	0	0	0	2	8	1	8	3	0	0	1	2

Taxonomic assignment of OTU (bootstrap value)

OTU41   *Proteobacteria*(100);*Gammaproteobacteria*(100);*Alteromonadales*(100);*Alteromonadaceae*(99);*Haliea*(98);
OTU3   *Proteobacteria*(100);*Gammaproteobacteria*(100);*Oceanospirillales*(100);*Hahellaceae*(99);*Endozoicomonas*(68);
OTU215   *Bacteroidetes*(100);*Flavobacteria*(100);*Flavobacteriales*(100);*Flavobacteriaceae*(100);*Elizabethkingia*(100);
OTU124   *Actinobacteria*(100);*Actinobacteria*(100);*Actinomycetales*(100);*Micrococcaceae*(100);*Arthrobacter*(100);
OTU126   unclassified(100);unclassified(100);unclassified(100);unclassified(100);unclassified(100);
OTU707   *Proteobacteria*(100);*Gammaproteobacteria*(100);*Xanthomonadales*(100);*Xanthomonadaceae*(100);*Stenotrophomonas*(100);
OTU164   *Proteobacteria*(95);*Deltaproteobacteria*(95);unclassified(95);unclassified(95);unclassified(95);
OTU361   *Proteobacteria*(100);*Betaproteobacteria*(100);*Burkholderiales*(100);*Comamonadaceae*(100);*Acidovorax*(100);

Table S1. (continued)

Sample			G24A	G24B	G24C	G30A	G30B	G30C	G41A	G41B	G41C
Group (sampling depth)			G24	G24	G24	G30	G30	G30	G41	G41	G41
OTU	p value	Group	No. of reads								
OTU66	0.0395	G24	79	1	179	0	0	0	0	0	0
OTU548	0.0395	G24	29	7	3	0	0	0	0	0	0
OTU847	0.0384	G30	0	0	0	2	1	3	0	0	0
OTU309	0.0384	G30	0	0	1	13	5	5	0	0	0
OTU3030	0.0364	G41	0	0	0	0	0	0	1	1	1

Taxonomic assignment of OTU (bootstrap value)

OTU66   *Bacteria*(100);*Bacteroidetes*(100);*Flavobacteria*(100);*Flavobacteriales*(100);*Flavobacteriaceae*(100); *Aquimarina*(100);

OTU548   *Bacteria*(100);*Proteobacteria*(100);*Deltaproteobacteria*(100);*Myxococcales*(100); unclassified_*Myxococcales*(98);unclassified(98);

OTU847   *Bacteria*(100);*Proteobacteria*(100);*Gammaproteobacteria*(100);*Oceanospirillales*(100); *Hahellaceae*(100);*Endozoicomonas*(100);

OTU309   *Bacteria*(100);unclassified(100);unclassified(100);unclassified(100);unclassified(100); unclassified(100);

OTU3030   *Bacteria*(100);unclassified(100);unclassified(100);unclassified(100);unclassified(100); unclassified(100);