

Supplemental Material

Table S1: Taxonomy of indicator OTUs, alphabetically ordered from phylum to species level.

OTU	Phylum	Class	Order	Family	Genus	Species
152	Actinobacteria	Actinobacteria	Actinomycetales	Corynebacteriaceae	<i>Corynebacterium</i>	<i>variabile</i>
46	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	<i>Candidatus Aquiluna</i>	<i>rubra</i>
34	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	<i>Microbacterium</i>	<i>maritypicum</i>
24	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	<i>Salinibacterium</i>	<i>amurskyense</i>
23	Actinobacteria	Actinobacteria	Actinomycetales	Nocardiaceae	<i>Rhodococcus</i>	<i>fascians</i>
112	Actinobacteria	Actinobacteria	Actinomycetales	Propionibacteriaceae	<i>Propionibacterium</i>	<i>acnes</i>
12	Bacteroidetes	Flavobacteriia	Flavobacteriales	Cryomorphaceae	unclassified	unclassified
7	Bacteroidetes	Flavobacteriia	Flavobacteriales	Flavobacteriaceae	<i>Lacinutrix</i>	unclassified
45	Bacteroidetes	Flavobacteriia	Flavobacteriales	Flavobacteriaceae	<i>Lacinutrix</i>	unclassified
16	Bacteroidetes	Flavobacteriia	Flavobacteriales	Flavobacteriaceae	unclassified	unclassified
28	Bacteroidetes	Flavobacteriia	Flavobacteriales	Flavobacteriaceae	unclassified	unclassified
11	Bacteroidetes	Flavobacteriia	Flavobacteriales	Flavobacteriaceae	<i>Zhouia</i>	unclassified
17	Bacteroidetes	Saprospirae	Saprospirales	Saprospiraceae	unclassified	unclassified
61	Bacteroidetes	Saprospirae	Saprospirales	Saprospiraceae	unclassified	unclassified
37	Bacteroidetes	unclassified	unclassified	unclassified	unclassified	unclassified
74	Firmicutes	Bacilli	Bacillales	Staphylococcaceae	<i>Staphylococcus</i>	<i>epidermidis</i>
35	Nitrospinae	Nitrospina	Nitrospinales	Nitrospinaceae	<i>Nitrospina</i>	unclassified
18	Planctomycetes	Phycisphaerae	Phycisphaerales	unclassified	unclassified	unclassified
32	Proteobacteria	Alphaproteobacteria	Kiloniellales	unclassified	unclassified	unclassified
126	Proteobacteria	Alphaproteobacteria	Rhizobiales	Bradyrhizobiaceae	<i>Bradyrhizobium</i>	unclassified
33	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae	unclassified	unclassified
21	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	<i>Loktanella</i>	unclassified
13	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	<i>Marivita</i>	unclassified
29	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	<i>Octadecabacter</i>	unclassified
22	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	<i>Phaeobacter</i>	<i>gallaeciensis</i>
58	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	<i>Rhodobacter</i>	unclassified
20	Proteobacteria	Alphaproteobacteria	Rhodobacterales	unclassified	unclassified	unclassified
6	Proteobacteria	Alphaproteobacteria	Rickettsiales	Pelagibacteraceae	unclassified	unclassified
40	Proteobacteria	Alphaproteobacteria	Rickettsiales	Pelagibacteraceae	unclassified	unclassified

102	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	<i>Sphingomonas</i>	unclassified
9	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	unclassified	unclassified
47	Proteobacteria	Betaproteobacteria	Methylophilales	Methylophilaceae	unclassified	unclassified
5	Proteobacteria	Gammaproteobacteria	Alteromonadales	Alteromonadaceae	<i>Alteromonas</i>	unclassified
8	Proteobacteria	Gammaproteobacteria	Alteromonadales	Alteromonadaceae	<i>Alteromonas</i>	unclassified
15	Proteobacteria	Gammaproteobacteria	Alteromonadales	Alteromonadaceae	<i>Alteromonas</i>	unclassified
44	Proteobacteria	Gammaproteobacteria	Alteromonadales	HTCC2188	HTCC	unclassified
69	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	unclassified	unclassified
19	Proteobacteria	Gammaproteobacteria	Legionellales	Coxiellaceae	unclassified	unclassified
2	Proteobacteria	Gammaproteobacteria	Methylococcales	Crenotrichaceae	<i>Crenothrix</i>	unclassified
53	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	<i>Candidatus Portiera</i>	unclassified
10	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Oceanospirillaceae	unclassified	unclassified
38	Proteobacteria	Gammaproteobacteria	Vibrionales	Pseudoalteromonadaceae	<i>Pseudoalteromonas</i>	<i>porphyrae</i>
14	Proteobacteria	Gammaproteobacteria	Vibrionales	Pseudoalteromonadaceae	<i>Pseudoalteromonas</i>	unclassified
26	Proteobacteria	Gammaproteobacteria	Vibrionales	Pseudoalteromonadaceae	<i>Pseudoalteromonas</i>	unclassified
4	Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	<i>Vibrio</i>	<i>fortis</i>
59	Tenericutes	Mollicutes	Acholeplasmatales	Acholeplasmataceae	<i>Acholeplasma</i>	unclassified
1	Tenericutes	Mollicutes	Mycoplasmatales	Mycoplasmataceae	<i>Mycoplasma</i>	unclassified
3	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
43	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified

Table S2: Oligonucleotide probes used for FISH.

Probe	Target group	Target rRNA	Sequence (5' → 3')	Target site	Hybridisation temperature [°C]	Formamide concentration [%]	Reference
NONEUB338	none (control)	16S	ACTCCTACGGGAGGCAGC	-	55	20	(4)
EUB338	most bacteria	16S	GCTGCCTCCCGTAGGAGT	338-355	55	20	(1)
GAM42a	γ -Proteobacteria	23S	GCCTTCCCACATCGTTT	1027-1043	47	35	(3)
LGC0354a	Firmicutes	16S	TGGAAGATTCCTACTGC	354-371	50	35	(2)
LGC0354b	Firmicutes	16S	CGGAAGATTCCTACTGC	354-371	50	35	(2)
LGC0354c	Firmicutes	16S	CCGAAGATTCCTACTGC	354-371	50	35	(2)

Table S3: Primer used for FLX sequencing.

Designation	Sequence (5' → 3')
V2_A_Pyro_27F	CGTATCGCCTCCCTCGCGCCATCAGTCAGAGTTTGATCCTGGCTCAG
V2_B_Pyro_27F	CTATGCGCCTTGCCAGCCCGCTCAGTCAGAGTTTGATCCTGGCTCAG
V2_A_338R_tMID1	CGTATCGCCTCCCTCGCGCCATCAGACGAGTGCATGCTGCCTCCCGTAGGAGT
V2_A_338R_tMID2	CGTATCGCCTCCCTCGCGCCATCAGACGCTCGACACATGCTGCCTCCCGTAGGAGT
V2_A_338R_tMID3	CGTATCGCCTCCCTCGCGCCATCAGAGACGCACTCCATGCTGCCTCCCGTAGGAGT
V2_A_338R_tMID4	CGTATCGCCTCCCTCGCGCCATCAGAGCACTGTAGCATGCTGCCTCCCGTAGGAGT
V2_A_338R_tMID5	CGTATCGCCTCCCTCGCGCCATCAGATCAGACACGCATGCTGCCTCCCGTAGGAGT
V2_A_338R_tMID6	CGTATCGCCTCCCTCGCGCCATCAGATATCGCGAGCATGCTGCCTCCCGTAGGAGT
V2_A_338R_tMID7	CGTATCGCCTCCCTCGCGCCATCAGCGTGTCTCTACATGCTGCCTCCCGTAGGAGT
V2_A_338R_tMID8	CGTATCGCCTCCCTCGCGCCATCAGCTCGCGTGTCCATGCTGCCTCCCGTAGGAGT
V2_B_338R_tMID1	CTATGCGCCTTGCCAGCCCGCTCAGACGAGTGCATGCTGCCTCCCGTAGGAGT
V2_B_338R_tMID2	CTATGCGCCTTGCCAGCCCGCTCAGACGCTCGACACATGCTGCCTCCCGTAGGAGT
V2_B_338R_tMID3	CTATGCGCCTTGCCAGCCCGCTCAGAGACGCACTCCATGCTGCCTCCCGTAGGAGT
V2_B_338R_tMID4	CTATGCGCCTTGCCAGCCCGCTCAGAGCACTGTAGCATGCTGCCTCCCGTAGGAGT
V2_B_338R_tMID5	CTATGCGCCTTGCCAGCCCGCTCAGATCAGACACGCATGCTGCCTCCCGTAGGAGT
V2_B_338R_tMID6	CTATGCGCCTTGCCAGCCCGCTCAGATATCGCGAGCATGCTGCCTCCCGTAGGAGT
V2_B_338R_tMID7	CTATGCGCCTTGCCAGCCCGCTCAGCGTGTCTCTACATGCTGCCTCCCGTAGGAGT
V2_B_338R_tMID8	CTATGCGCCTTGCCAGCCCGCTCAGCTCGCGTGTCCATGCTGCCTCCCGTAGGAGT
V2_B_338R_tMID9	CTATGCGCCTTGCCAGCCCGCTCAGTCTCTATGCGCATGCTGCCTCCCGTAGGAGT
V2_B_338R_tMID10	CTATGCGCCTTGCCAGCCCGCTCAGTGTACTACTCCATGCTGCCTCCCGTAGGAGT
V2_B_338R_tMID11	CTATGCGCCTTGCCAGCCCGCTCAGCATAGTAGTGCATGCTGCCTCCCGTAGGAGT
V2_B_338R_tMID12	CTATGCGCCTTGCCAGCCCGCTCAGCGAGAGATACCATGCTGCCTCCCGTAGGAGT
V2_B_338R_tMID13	CTATGCGCCTTGCCAGCCCGCTCAGATACGACGTACATGCTGCCTCCCGTAGGAGT
V2_B_338R_tMID14	CTATGCGCCTTGCCAGCCCGCTCAGTACGTAATACATGCTGCCTCCCGTAGGAGT
V2_B_338R_tMID15	CTATGCGCCTTGCCAGCCCGCTCAGCGTCTAGTACCATGCTGCCTCCCGTAGGAGT
V2_B_338R_tMID16	CTATGCGCCTTGCCAGCCCGCTCAGTCTACGTAGCCATGCTGCCTCCCGTAGGAGT
V2_B_338R_tMID17	CTATGCGCCTTGCCAGCCCGCTCAGTGTACTACTCCATGCTGCCTCCCGTAGGAGT
V2_B_338R_tMID18	CTATGCGCCTTGCCAGCCCGCTCAGACGACTACAGCATGCTGCCTCCCGTAGGAGT
V2_B_338R_tMID19	CTATGCGCCTTGCCAGCCCGCTCAGCGTAGACTAGCATGCTGCCTCCCGTAGGAGT
V2_B_338R_tMID20	CTATGCGCCTTGCCAGCCCGCTCAGTACGAGTATGCATGCTGCCTCCCGTAGGAGT
V2_B_338R_tMID21	CTATGCGCCTTGCCAGCCCGCTCAGTACTCTCGTGCATGCTGCCTCCCGTAGGAGT
V2_B_338R_tMID22	CTATGCGCCTTGCCAGCCCGCTCAGTAGAGACGAGCATGCTGCCTCCCGTAGGAGT
V2_B_338R_tMID23	CTATGCGCCTTGCCAGCCCGCTCAGTCGTCGCTCGCATGCTGCCTCCCGTAGGAGT
V2_B_338R_tMID26	CTATGCGCCTTGCCAGCCCGCTCAGACTACTATGTCATGCTGCCTCCCGTAGGAGT
V2_B_338R_tMID27	CTATGCGCCTTGCCAGCCCGCTCAGACTGTACAGTCATGCTGCCTCCCGTAGGAGT
V2_B_338R_tMID28	CTATGCGCCTTGCCAGCCCGCTCAGAGACTATACTCATGCTGCCTCCCGTAGGAGT
V2_B_338R_tMID29	CTATGCGCCTTGCCAGCCCGCTCAGAGCGTCGTCTCATGCTGCCTCCCGTAGGAGT
V2_B_338R_tMID30	CTATGCGCCTTGCCAGCCCGCTCAGAGTACGCTATCATGCTGCCTCCCGTAGGAGT
V2_B_338R_tMID31	CTATGCGCCTTGCCAGCCCGCTCAGATAGAGTACTCATGCTGCCTCCCGTAGGAGT
V2_B_338R_tMID32	CTATGCGCCTTGCCAGCCCGCTCAGCACGCTACGTCATGCTGCCTCCCGTAGGAGT
V2_B_338R_tMID33	CTATGCGCCTTGCCAGCCCGCTCAGCAGTAGACGTCATGCTGCCTCCCGTAGGAGT

Figures

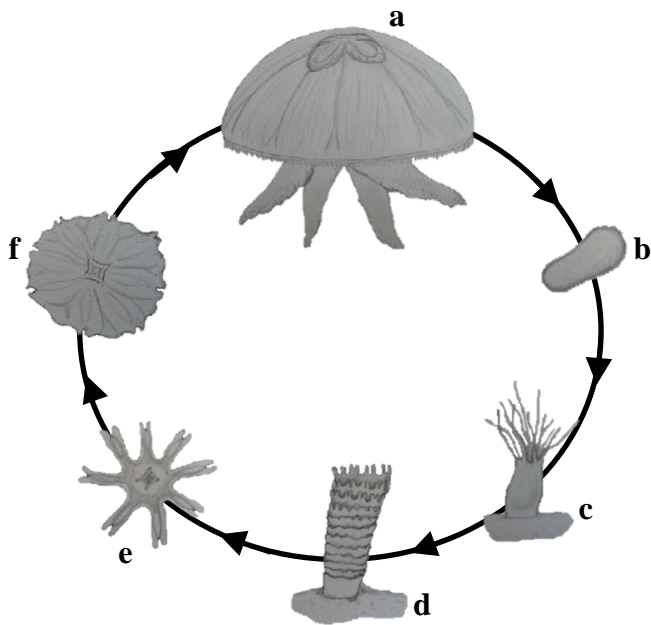


Fig. S1: Life cycle of the moon jellyfish *Aurelia aurita*. The sexual medusa stage (a) releases planula larvae (b) which settle and colonize shallow benthos and develop into the asexual polyp stage (c). The polyp reproduces either by asexual budding or strobilation (d) releasing ephyrae (e). Young medusae (f) develop from this stage and further become the adult medusa.

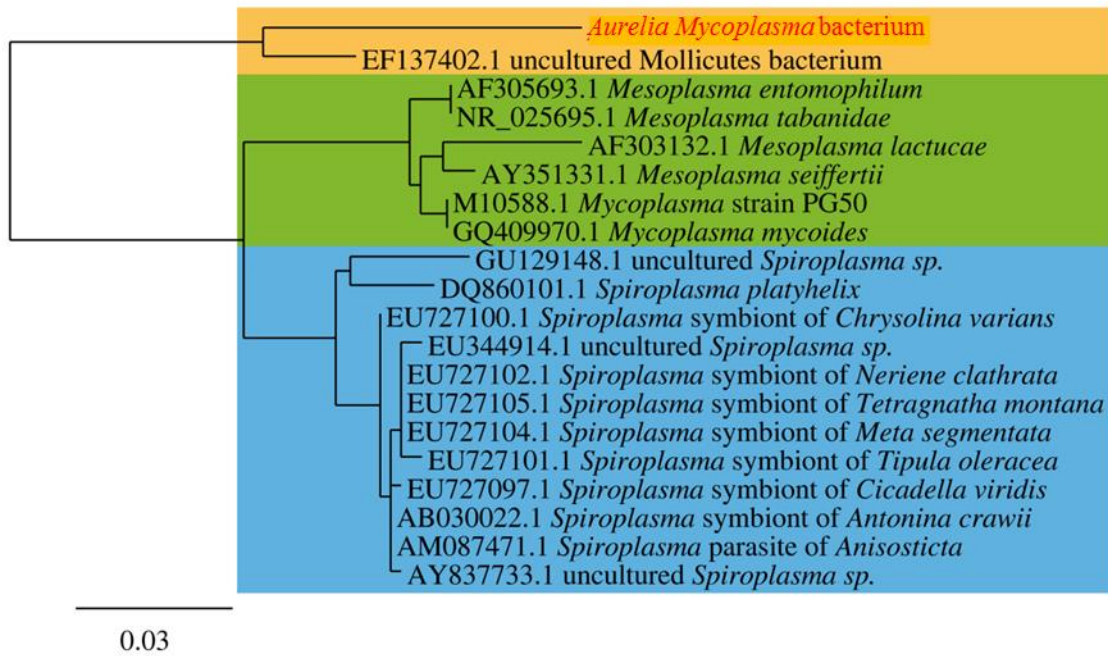


Fig. S2: Phylogenetic position of identified uncultured *A. aurita* specific *Mycoplasma* bacterium. The tree was calculated from full-length 16S rRNA gene sequences by the Maximum-Likelihood method. Nearest relatives to the 16S rRNA sequence of uncultured Mollicutes bacterium (highlighted in orange) were obtained via BLAST search using the NCBI database. Highlighted are clusters (orders) belonging to the class of Mollicutes: order Entomoplasmatales (blue) and Mycoplasmatales (green). The scale bar represents evolutionary distance (substitutions per nucleotide).

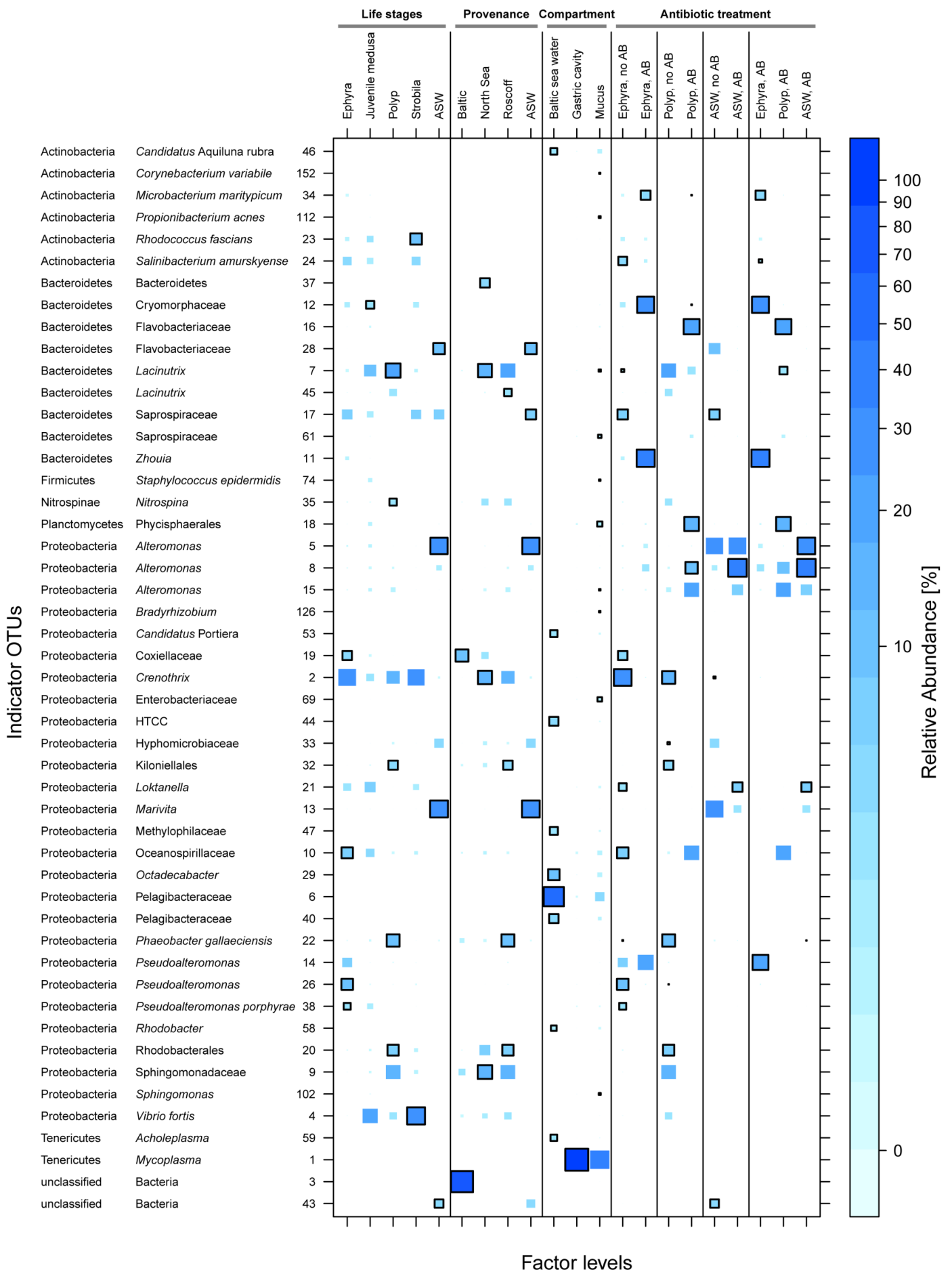


Fig. S3: Distribution of indicator OTUs across experimental factor levels. The matrix visualizes the (log-scaled) average relative abundance of indicator OTUs (rows; sorted at phylum level) across factor levels (columns; sorted by experimental parts) by color code and symbol size. For each OTU, its phylum is stated, followed by its name at the lowest-determinable taxonomic level and the OTU number. The factor level which an OTU is an indicator for is framed in black. Note that an OTU may be an indicator in several experimental parts.

References Supplemental material

1. Amann, R. I., B. J. Binder, R. J. Olson, S. W. Chisholm, R. Devereux, and D. A. Stahl. 1990. Combination of 16S rRNA-targeted oligonucleotide probes with flow cytometry for analyzing mixed microbial populations. *Appl Environ Microbiol* 56:1919-25.
2. Meier, H., R. Amann, W. Ludwig, and K. H. Schleifer. 1999. Specific oligonucleotide probes for in situ detection of a major group of gram-positive bacteria with low DNA G + C content. *Syst Appl Microbiol* 22:186-96.
3. Wagner, M., R. Amann, H. Lemmer, and K. H. Schleifer. 1993. Probing activated sludge with oligonucleotides specific for proteobacteria: inadequacy of culture-dependent methods for describing microbial community structure. *Appl Environ Microbiol* 59:1520-1525.
4. Wallner, G., R. Amann, and W. Beisker. 1993. Optimizing fluorescent in situ hybridization with rRNA-targeted oligonucleotide probes for flow cytometric identification of microorganisms. *Cytometry* 14:136-43.