Rarefaction curve and principal coordinate analysis (PCoA)
Statistical analyses of alpha and beta diversity were conducted in the Quantitative Insights into Microbial Ecology Version 2 (QIIME2) by using the build-in core metric phylogenetic method (Bolyen et al. 2019). To include all samples, we set the rarefied sequence depth to 2000 after observed ASVs plateau with increasing sequence depth. To illustrate the dissimilarity between microbial communities, principal coordinate analysis (PCoA) using the unweighted UniFrac distances was performed in QIIME2 (Lozupone & Knight 2005, Bolyen et al. 2019). The PCoA plot was further processed and visualized in EMPeror (Vázquez-Baeza et al. 2013). Rarefied samples were only used to calculate alpha and beta diversity.

Similarity analyses
The similarities in the relative abundances of bacterial communities in sediment and Upogebia/Neaeromya samples were accessed. We selected 16 phyla that were majorly abundant for the similarity analysis. Every one of the 16 selected phyla comprised more than 1% of the total fractions in their respective samples. These 16 phyla together were comprised the 90% of the ASV's found in the bacterial communities of all samples. Microsoft Excel was used to generate a correlation matrix of bacteria communities in *Upogebia* and *Neaeromya* samples relative to sediment types. The absence of replication among samples precluded tests of interaction between *Upogebia/Neaeromya* and sediment types. We therefore compared the correlations among the UGM, UHG and NDO samples relative to UB-U, UB-I, UB-Nex, UB-Bel, and UB-Sur samples using the two-way analysis of variation (ANOVA) without replicates.

Phylogenetic tree of the *Desulfobulbaceae* family
The 5 most abundant amplicon sequence variants (ASVs) in the family of *Desulfobulbaceae*, and the 5 most abundant ASVs of *Electrothrix* were extracted and compared between samples. These ASVs were placed in a taxonomic framework of CB (Trojan et al. 2016), against partial 16s rRNA genes of CB from Yaquina Bay (Li et al. 2020), and in relation to family members in *Desulfobulbaceae* that are not recognized CB. A phylogenetic tree was constructed using RaxML with 1,000 bootstraps (Stamatakis 2014).

Figure. S1

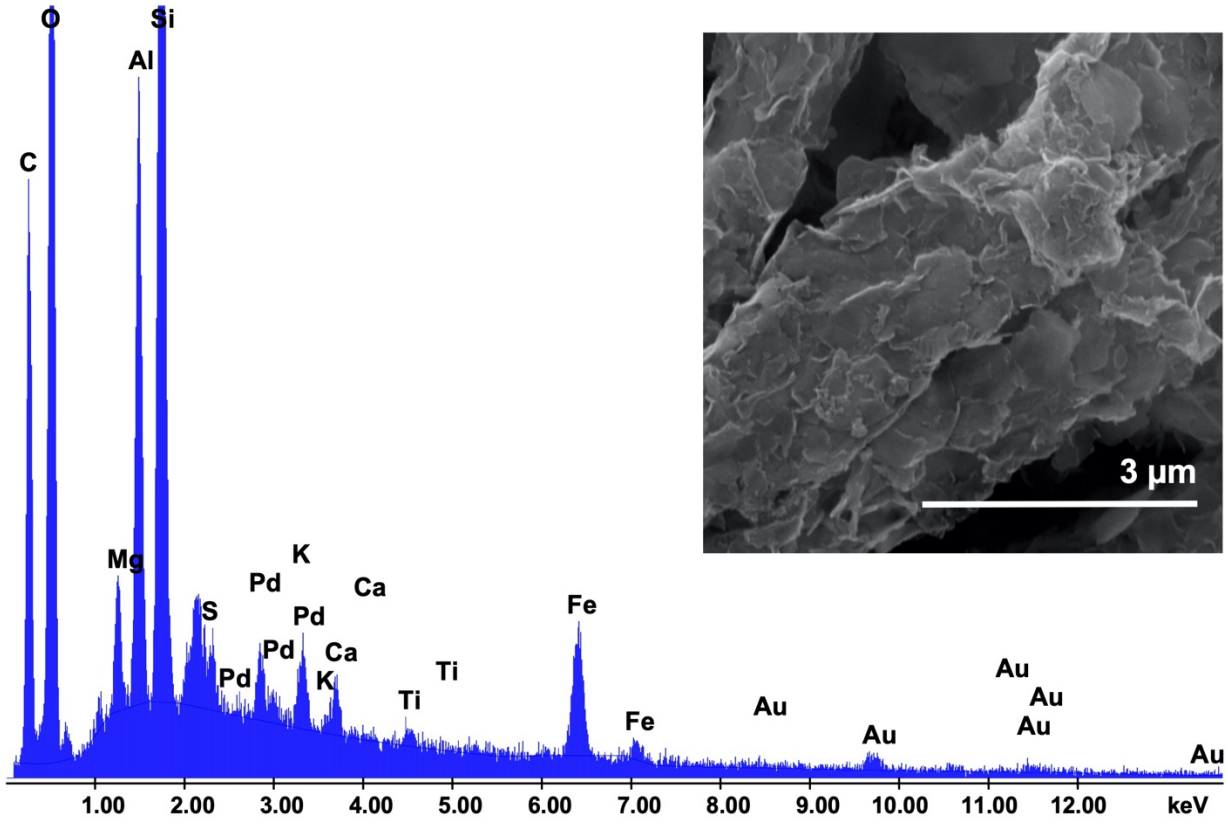

Figure S1. X-Ray Energy Dispersive Spectrometry (EDS) of a section of the cable bacteria filament, showing the enrichment of silicon (Si), aluminum (Al), magnesium (Mg), and iron (Fe). Insert: a scanning electron microscopy (SEM) image of the sampling area. Samples were then coated with gold (Au) and palladium (Pd) prior to visualization.

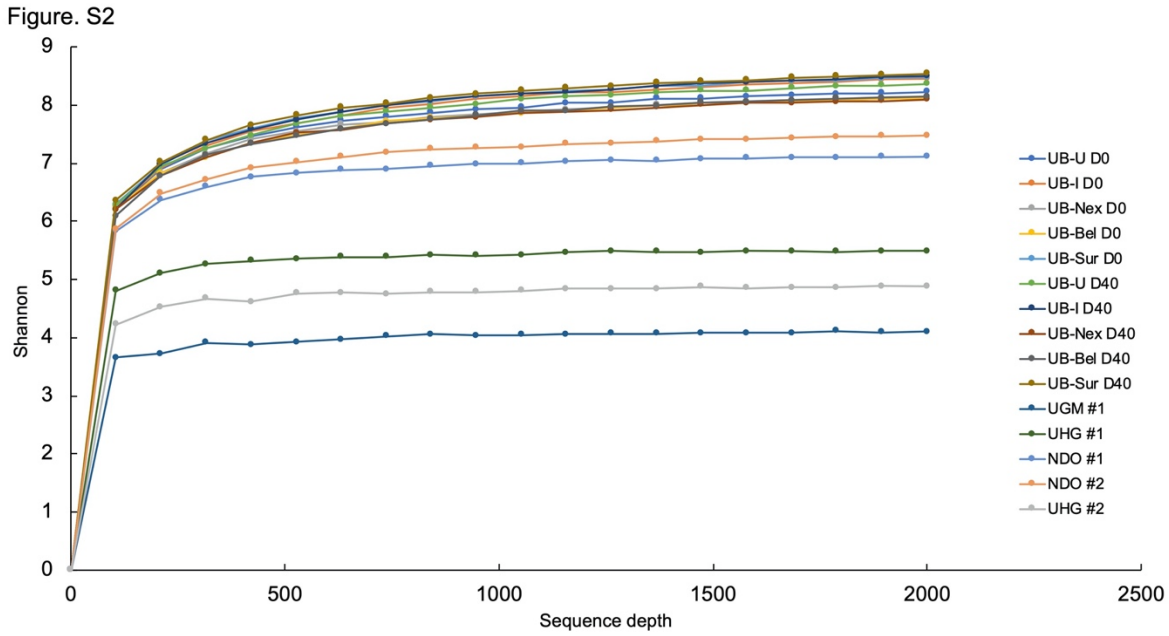

Figure S2. Rarefaction curve illustrating the Shannon index of all samples.

Figure. S3

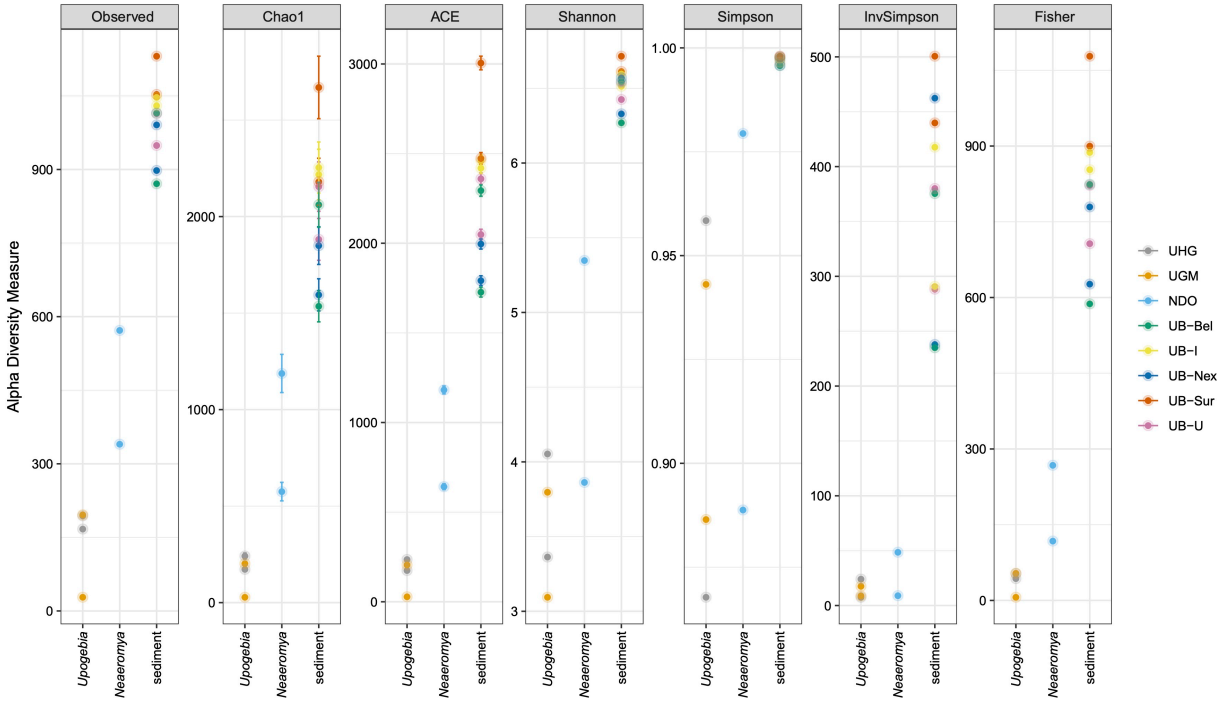

Figure S3. Alpha diversity measures of observed ASVs, Chao1, ACE, Shannon, Simpson, InvSimpson, and Fisher indexes across sample types and locations. UHG: *Upogebia* hind gut, UGM: *Upogebia* gastric mill, NDO: *Neaeromya* digestive organ, UB-U: sediment linings in U part of the burrow, UB-I: sediment linings in I part of the burrow, UB-Nex: anoxic sediment next to the burrow, UB-Bel: anoxic sediment below the burrow, and UB-Sur, surface sediment avoiding the burrow openings; D0 = day 0 and D40 = day 40.

Figure. S4

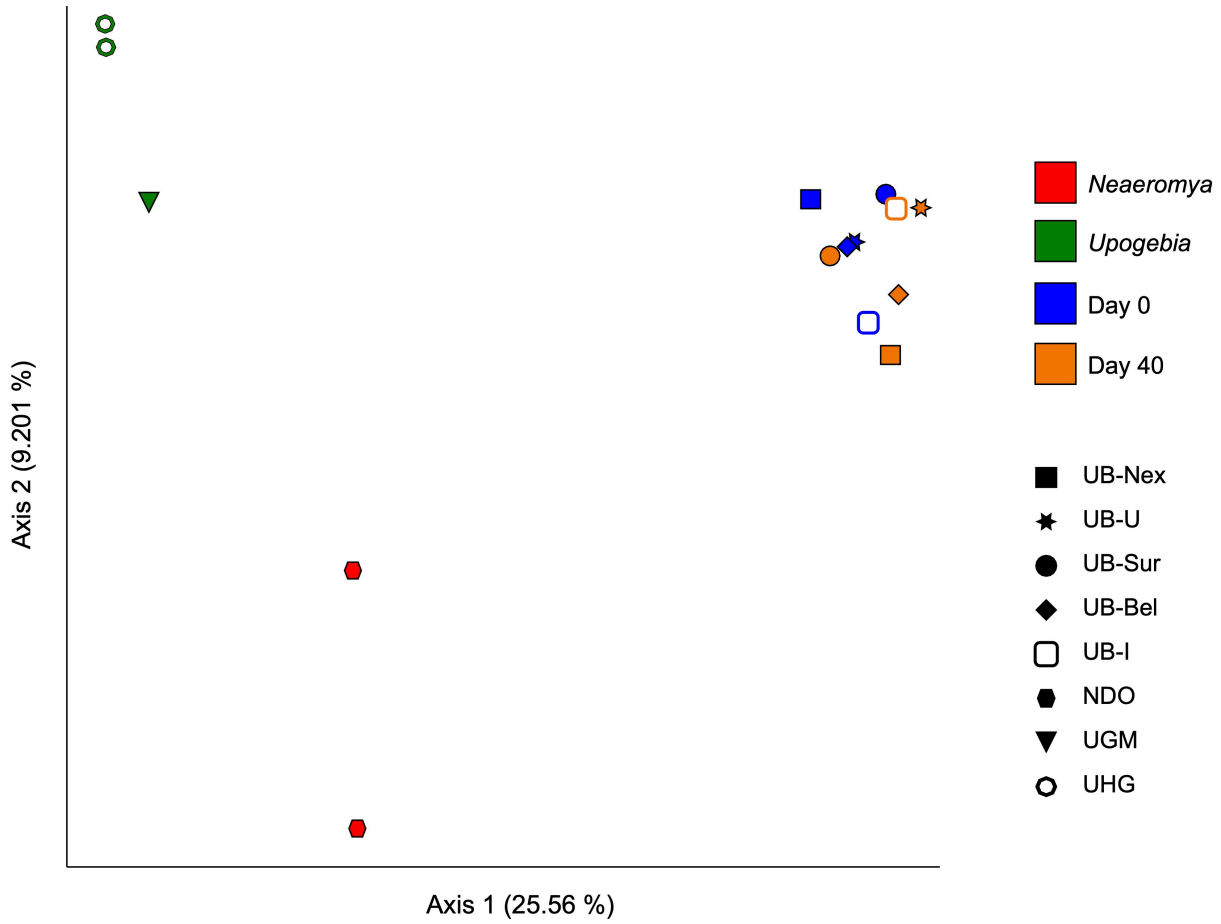

Figure S4. Principal coordinate analysis based on unweighted Unifrac distance for all samples.

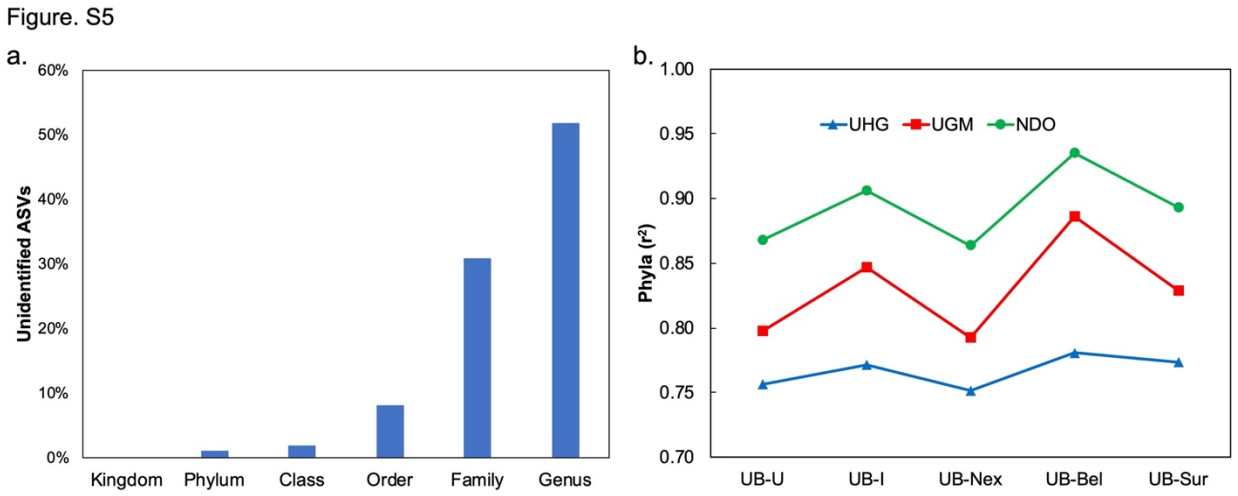

Figure S5. a) Percent of unidentified ASVs with decreasing taxonomic ranks (1-5 = phylum – genus) among combined *Upogebia* gastric mill and hindgut and *Neaeromya* digestive organ samples (% unidentified ASVs = 0.0005* Rank$^{3.8157}$, r^2 = 0.9427). b) Correlations among the 16 dominant phyla* occurring within the *Upogebia* hind gut (UHG) and gastric mill (UGM) and the *Neaermya* digestive organs (NDO), relative to those same phyla in Day 0 sediment samples. (* Note: Phyla by rank - 1 *Proteobacteria*, 2 *Firmicutes*, 3 *Bacteroidetes*, 4 *Tenericutes,* 5 *Actinobacteria*, 7 *Planctomycetes*, 8 *Cyanobacteria,* 9 *Patescibacteria,* 10 *Acidobacteria*, 11 *Verrucomicrobia*, 12 *Gemmatimonadetes,* 13 *Chloroflexi,* 14 *Epsilonbacteraeota,* 15 *Halanaerobiaeota,* 16 *Chlamydiae*)

Figure S6.

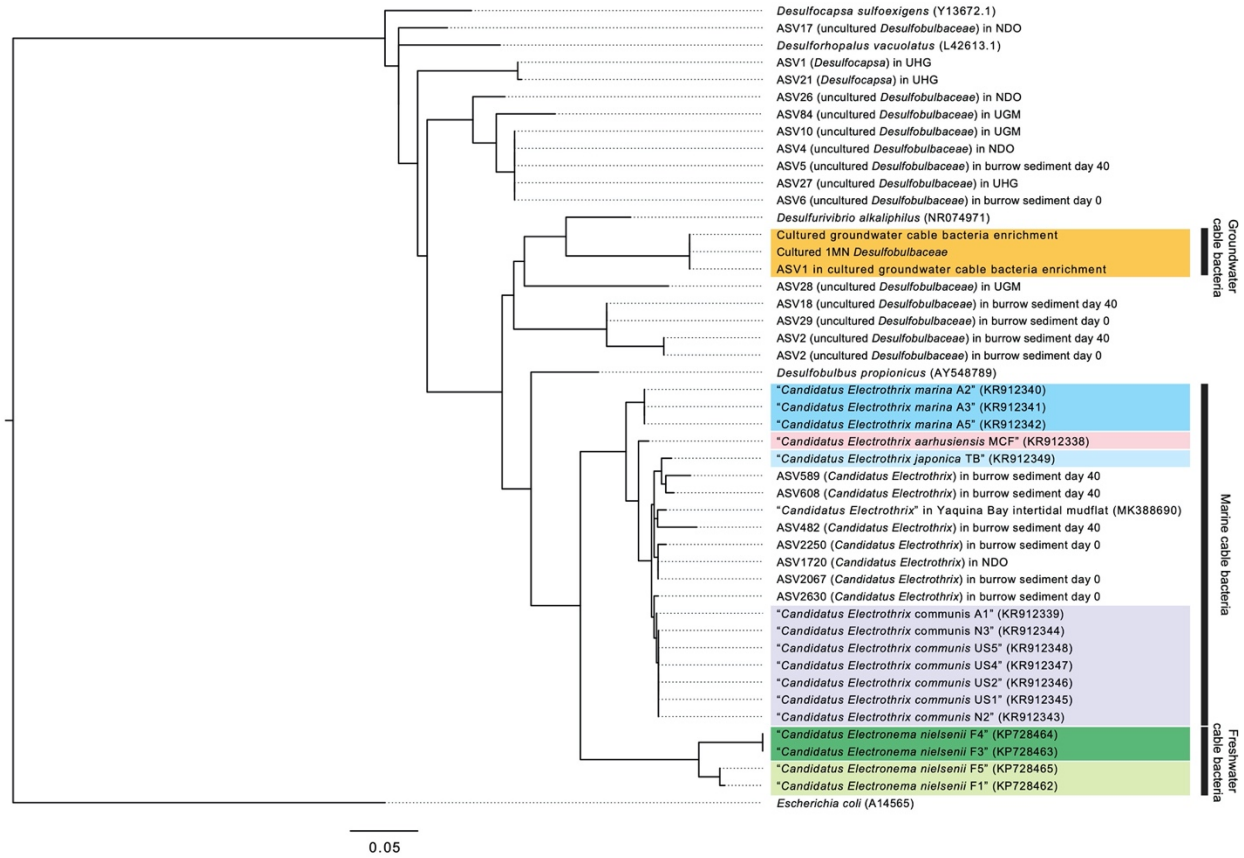

Figure S6. Phylogenetic tree of *Desulfobulbaceae* 16s rRNA gene sequences recovered from the shrimp burrow and surrounding sediments, the *U. pugettensis* gastric mill (UGM) and hind gut (UHG), and the stomach of *N. rugifera* (NDO). Color boxes indicate previously recognized genera of cable bacteria. Scale bar shows 5% sequence divergence.

Table S1. Top 10 most abundant phyla and families in sediment samples before and after lab culture. NA indicates that this phylum or family was absent from the sample.

Phylum	Day	UB-U	UB-I	UB-Nex	UB-Bel	UB-Sur
Acidobacteria		0.050	0.042	0.048	0.055	0.041
Actinobacteria		0.056	0.033	0.047	0.032	0.043
Bacteroidetes		0.253	0.202	0.259	0.150	0.228
Calditrichaeota		NA	NA	NA	0.021	NA
Chloroflexi		0.024	0.033	0.023	0.051	0.025
Cyanobacteria		NA	0.031	0.015	0.019	0.023
Gemmatimonadetes	Day0	0.029	0.025	0.030	0.024	0.027
Kiritimatiellaeota		NA	0.015	NA	NA	NA
Latescibacteria		0.021	0.020	0.017	0.022	0.020
Patescibacteria		0.011	NA	NA	NA	NA
Planctomycetes		0.018	0.026	0.018	0.028	0.024
Proteobacteria		0.444	0.450	0.446	0.475	0.451
Verrucomicrobia		0.020	NA	0.019	NA	0.013
others		0.074	0.121	0.078	0.122	0.105
Acidobacteria		0.044	0.045	0.041	0.052	0.034
Actinobacteria		0.049	0.036	0.042	0.034	0.040
Bacteroidetes		0.197	0.177	0.183	0.104	0.218
Calditrichaeota		NA	0.015	NA	0.016	NA
Chloroflexi		0.034	0.050	0.028	0.047	0.029
Cyanobacteria		0.032	0.025	0.021	NA	NA
Epsilonbacteraeota		NA	NA	NA	0.028	NA
Firmicutes		NA	NA	0.029	NA	0.046
Gemmatimonadetes	Day40	0.027	0.026	0.023	0.026	NA
Kiritimatiellaeota		NA	NA	NA	NA	0.018
Latescibacteria		0.021	0.023	0.019	0.023	0.017
Planctomycetes		0.037	0.031	0.031	0.029	0.026
Proteobacteria		0.446	0.446	0.452	0.555	0.424
Verrucomicrobia		0.014	NA	NA	NA	0.016
others		0.098	0.125	0.131	0.085	0.131

Family	Day	UB-U	UB-I	UB-Nex	UB-Bel	UB-Sur
Bacteroidetes_BD2-2		0.027	0.025	0.023	0.023	0.027
Desulfobacteraceae		0.051	0.061	0.055	0.089	0.047
Desulfobulbaceae		0.062	0.068	0.057	0.080	0.064
Ectothiorhodospiraceae		NA	0.015	0.016	0.016	NA
Flavobacteriaceae		0.152	0.110	0.160	0.079	0.111
Halieaceae		0.031	0.024	0.038	0.011	0.023
Nitrincolaceae		NA	NA	NA	NA	0.020
Sandaracinaceae	Day0	0.017	NA	0.015	0.011	NA
Saprospiraceae		NA	NA	NA	NA	0.013
Thermoanaerobaculaceae		0.024	0.019	0.022	0.023	0.017
Thiohalorhabdaceae		0.015	NA	NA	NA	NA
Thiotrichaceae		NA	0.018	NA	NA	NA
Unknown_Family		0.035	0.029	0.031	0.021	0.031
Woeseiaceae		0.047	0.027	0.043	0.026	0.030
others		0.539	0.602	0.538	0.620	0.618
Anaerolineaceae		NA	0.022	NA	NA	NA
Bacteroidetes_BD2-2		0.028	0.027	0.024	0.016	0.030
Calditrichaceae		NA	0.015	NA	NA	NA
Desulfobacteraceae		0.054	0.066	0.069	0.067	0.095
Desulfobulbaceae		0.069	0.074	0.064	0.081	0.080
Family_XII		NA	NA	0.023	0.000	NA
Flavobacteriaceae		0.098	0.083	0.081	0.052	0.092
Fusobacteriaceae		NA	NA	0.016	0.000	NA
Halieaceae		0.019	NA	NA	NA	NA
Pirellulaceae	Day40	0.017	NA	NA	NA	NA
Prolixibacteraceae		NA	NA	NA	NA	0.022
Sva1033		NA	NA	NA	NA	0.016
Thermoanaerobaculaceae		0.018	0.021	0.020	0.025	0.018
Thiotrichaceae		0.020	0.028	0.022	0.039	0.016
Unknown_Family		0.025	0.018	0.018	0.013	0.016
Woeseiaceae		0.034	0.022	0.031	0.021	0.016
others		0.619	0.626	0.632	0.684	0.600

Table S2. Top 10 most abundant phyla and families in shrimp gastric mill, shrimp gut, and bivalve digestive organ samples. UGM: gastric mill, UHG: shrimp gut, and NDO: bivalve digestive organ. NA indicates that the phylum or family was absent from the sample.

Phylum	UGM	UHG	NDO
Acidobacteria	NA	0.010	0.025
Actinobacteria	0.066	0.042	0.040
Bacteroidetes	NA	0.115	0.061
Chloroflexi	0.012	NA	0.016
Cyanobacteria	0.0401	NA	0.015
Firmicutes	0.117	0.308	0.131
Gemmatimonadetes	NA	0.015	NA
Halanaerobiaeota	0.007	0.003	NA
Patescibacteria	0.014	0.030	NA
Planctomycetes	0.025	0.007	0.039
Proteobacteria	0.528	0.443	0.504
Tenericutes	0.120	NA	0.028
Verrucomicrobia	0.007	0.010	0.021
others	0.062	0.017	0.119

Family	UGM	UHG	NDO
Burkholderiaceae	0.073	0.013	NA
Clostridiaceae_1	0.023	NA	NA
Desulfobacteraceae	NA	NA	0.025
Desulfobulbaceae	0.052	0.249	0.073
Erysipelotrichaceae	NA	0.108	NA
Family_XII	NA	NA	0.040
Flavobacteriaceae	0.012	0.010	0.058
Halieaceae	NA	0.022	NA
Halobacteroidaceae	0.007	NA	NA
Ilumatobacteraceae	NA	0.019	NA
Lachnospiraceae	NA	0.016	NA
Methyloligellaceae	0.006	NA	NA
Moraxellaceae	NA	NA	0.035
Mycoplasmataceae	0.088	NA	0.028
Pirellulaceae	0.025	NA	0.032
Planococcaceae	NA	NA	0.057
Propionibacteriaceae	0.010	NA	NA
Rhodobacteraceae	0.018	0.023	0.021
TC1	NA	0.091	NA
Lentimicrobiaceae	NA	0.008	NA
Pseudoalteromonadaceae	NA	NA	0.189
others	0.685	0.439	0.440

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