<center>**Supporting information**</center>

Supplementary Materials and Methods

Microcosm Experiment

The Ria de Aveiro is a shallow estuarine coastal lagoon with a mean depth of ≈ 1 m but with a deeper central channel that accesses the port infrastructures. It is influenced by freshwater, through the various rivers that drain there, and by the ocean with which it communicates through a single artificial channel. Collected sediment cores were immediately placed into individual glass microcosms (glass tanks of 25, 28, and 12.4 cm in height, length, and width, respectively, and with a headspace volume of ≈ 3 L) and transferred directly to the Experimental Life Support System (ELSS). A semidiurnal tidal regime emptied the microcosms in ≈ 1 min and filled them with recently prepared synthetic seawater at a renewal rate of about 50% of the total water volume. The diurnal light cycle was programmed with light intensity varying between 50 and 100%. The temperature of the sediment cores was maintained at 19 ºC by immersion in a refrigerated water bath (Seachill TR10, Teco S.R.L., Italy). Synthetic seawater was prepared by dissolving a commercial salt mixture (Tropic Marin Pro Reef salt – Tropic Marine, Germany) in freshwater purified by a four-stage reverse-osmosis unit (Aqua-win RO-6080 - Aqua-win, Taiwan), and salinity was adjusted to ≈ 32 ppt as measured through a refractometer (V2 Refractometer - Tropic Marine, Germany).

Seven and twenty organisms (all adult and at the same stage of development) of *Hediste diversicolor* and *Peringia ulvae*, respectively, were collected from the field (on the same date and location) and added to the sediment natural populations of each microcosm to increase the number of individuals for DNA and biochemical marker analyses (see below). Collected organisms were immediately transported to the laboratory and transferred to the ELSS. Dead organisms registered during the acclimatization period were discarded, and replaced by new individuals which were collected from the same sampling location. Organisms that died during the experimental period were neither collected nor replaced.

Biochemical Markers Assay

The activity of acetylcholinesterase (AChE) was assessed by using acetylthiocholine iodide as a substrate and, according to Ellman et al., (1961), adapted to microplate by monitoring the absorbance (414 nm) of the

5,5′-dithiobis(2-nitrobenzoic acid) reaction with thiocholine every 20 s over 5 min ($\varepsilon_{412} = 1.36 \times 10^4$ M^{-1} cm^{-1}). The AChE activity is expressed as nmol of substrate hydrolysed per min per protein.

The activity of lactate dehydrogenase (LDH) was evaluated by monitoring at 340 nm (every 20 s, during 5 min) the decrease of NADH ($\varepsilon_{340} = 6.3$ mM^{-1} cm^{-1}) due to its oxidation. This was conducted as per the Vassault (1983) protocol adapted to a microplate (Diamantino et al., 2001) and was expressed as nmol of substrate hydrolysed per min per mg of protein.

The activity of catalase (CAT) was monitored by following the decrease in absorbance at 240 nm derived from the consumption of H_2O_2 ($\varepsilon_{240} = 40$ M^{-1} cm^{-1}) and recorded every 10 s for 2 min (Clairborne, 1985). The CAT activity is expressed as µmol of hydrolysed H_2O_2 per min per mg protein.

The activity of glutathione S-transferase (GST) was measured according to Habig et al. (1974) and monitored every 20 s for 5 min at 340 nm. The GST activity is expressed as nmol of the conjugated substrate (GSH plus 2,4-dinitrochlorobenzene) per min per mg protein ($\varepsilon_{340} = 9.6 \times 10^3$ M^{-1} cm^{-1}).

The quantification of lipid peroxidation (LPO) was carried out according to Ohkawa et al. (1979) with adjustments, being expressed as pmol of thiobarbituric acid-reactive substances (TBARS) hydrolysed per mg of soft tissue fresh weight (FW) ($\varepsilon_{535} = 1.56 \times 10^5$ M^{-1} cm^{-1}).

All of the above enzymatic activity analyses and LPO quantifications were determined spectrophotometrically in a microplate reader (Multiskan Spectrum, Thermo Fisher Scientific, USA). For LPO quantification and each enzymatic activity monitoring, all determinations were, respectively, done in triplicate and quadruplicate in 96-well microplates at 25 ºC. After thawing on ice, all samples were homogenized through sonication (Sonifier S-250A, Branson Ultrasonics, USA); pulse intensity and duration were adjusted to each particular species— *H. diversicolor* and *P. ulvae*) in an ice-water bath, and specific homogenization buffers were used for the respective assayed enzymes (AChE: 0.1 M K-phosphate, pH 7.2; LDH: 0.1 M Tris-NaCl, pH 7.2; CAT: 0.05 M K-phosphate, pH 7.0; GST: 0.1 M K-phosphate, pH 6.5).

Except for LPO, all the measurements described above were normalized to protein concentration, which was determined at 595 nm according to Bradford (1976), with the Bio-Rad® dye-binding micro-assay adapted for 96-well microplates. Bovine γ-globulin was used as standard.

The protocols for the determination of energy-related parameters were adapted from De Coen and Janssen (2003), with slight modifications for the microplate reader. Briefly, soft tissue samples of *H. diversicolor* or *P. ulvae* were kept on ice and homogenized (Sonifier S-150A, Branson Ultrasonics) in ultrapure water (50 mg soft tissue: 1 mL^{-1} ultrapure water). Three aliquots of 300 µL were taken from each replicate for the analysis of total lipids, total carbohydrates, total proteins, and electron transport system (ETS) activity. Total

lipids were extracted by centrifugation of the aliquots with a mixture of 500 µL of chloroform (119.38 M; ACS spectrophotometric grade, ≥ 99.8%) and 500 µL of methanol (32.04 M; ACS spectrophotometric grade, ≥ 99.8%). The organic phase of each sample was transferred to clean glass tubes and acidified with 500 µL of H_2SO_4. The absorbance was measured at 345 nm and tripalmitin was used as a standard. In the second aliquot of homogenized samples, proteins were precipitated with 100 µL of 15% trichloroacetic acid, followed by 10 min of incubation at -20 ºC. After centrifugation (1000 ×g for 10 min at 4 ºC), the supernatant was collected and used for total carbohydrate quantification. For this purpose, all samples and standards of glucose were incubated (20 ºC, 30 min) with 5% phenol plus H_2SO_4, and the absorbance was monitored at 492 nm. The pellets were then resuspended in 500 µL of NaOH, incubated (60 ºC, 30 min), and neutralized with 280 µL of HCl. Total protein content was quantified according to Bradford (1976) (Bradford, 1976) at 592 nm by using bovine serum albumin as standard. To convert the energy available (E_a; as per sum of total lipids, carbohydrates, and proteins) into the respective energetic equivalent values, the corresponding energy of combustion (39,500 mJ g^{-1} lipid; 17,500 mJ g^{-1} glycogen; 24,000 mJ g^{-1} protein) was used (De Coen and Janssen, 2003). Total lipids, total carbohydrates, total protein contents, and E_a were expressed as mJ mg^{-1} FW.

The homogenate for the determination of energy consumption (E_c; measured as ETS activity) was processed by adding 150 µL of homogenization buffer [0.3 M Tris base, 0.45% (w/v) polyvinylpyrrolidone, 459 µM $MgSO_4$, 0.6% (v/v) Triton X-100, pH 8.5], and centrifuged (1000 ×g, 10 min 4 ºC). The resulting supernatant was transferred to a 96-well microplate, and 150 µL of a buffered solution [0.13 M Tris base, 0.27% (v/v) Triton X-100, 1.7 mM NADH, 274 µM NADPH, 100 µL of INT (*p*-iodonitrotetrazolium; 8 mM)] was added before measurement (absorbance kinetically monitored at 490 nm, for 3 min). The conversion of the oxygen consumption rate was based on the stoichiometric relationship, whereby 1 µmol of oxygen is consumed for every 2 µmol of formed formazan. The quantity of oxygen consumed was determined by the formula of Lambert–Beer (A = ε × l × c, where A = absorbance; ε for INT-formazan = 15,900 M cm^{-1}; l = 0.9 cm; and c = oxygen consumed in M). The E_c values were obtained by converting to energetic values by using the specific oxyenthalpic equivalent for an average lipid, carbohydrate, and protein mixture of 480 kJ mol^{-1} O_2. The obtained values were divided by the FW of organisms and the results were expressed as mJ mg^{-1} FW h^{-1}. The sum of total lipids, total carbohydrates, and total proteins constitutes the E_a, and the correspondent cellular energy allocation (CEA) ratio was computed as CEA = E_a/E_c (Verslycke et al., 2003).

Data analysis

Evenness (Pielou's J) index was calculated by dividing Shannon's H' by the number of ASVs in each sample. Significant differences in community diversity were tested with an analysis of deviance using the glm() function in 'stats' (R Core Team, 2020). A number of these variables included an excess of zero counts in the samples, and, therefore, we set the family argument to 'tweedie' (Dunn, 2017) using the tweedie() function in 'tweedie' with var.power=1.5 and link.power=0 (a compound Poisson–gamma distribution). Using the generalized-linear model (GLM), significant variations among factors and their interaction (pH*Oil) were tested for significance using the anova() function. The relative abundance of selected prokaryotic higher taxa and most abundant ASVs (50 most abundant) were tested for significant differences among factors and their interaction (pH*Oil) with an analysis of deviance, using the glm() function with the family argument set to quasibinomial.

For compositional analyses, the ASV table in the present report was transformed using the ordinate() function in 'phyloseq' (McMurdie and Holmes, 2013). First, a phyloseq object was generated using the phyloseq() function; the input for the function included the ASV table, taxonomic metadata for the ASV table, and metadata for each sample. The ordinate() function in 'phyloseq' was subsequently used with the phyloseq object as input, the method argument set to 'PCoA', and the distance argument set to 'bray'. A biplot was then produced using the plot_ordination() function with the type argument set to 'biplot'. In addition to producing PCoA ordinations for the full dataset, separate ordinations were also produced for samples from each organism (gastropod, polychaete). The BLAST search tool (http://www.ncbi.nlm.nih.gov/) was used to compare representative sequences of the top 50 most abundant ASVs of each organism with sequences in the NCBI nucleotide collection (nr/nt) database using standard parameter settings (Altschul et al., 1990). Sequences that exhibited the highest levels of similarity to our data were considered to be the closest related organisms.

Variations among factors were tested for significance for each biochemical marker in each model organism dataset through a permutational multivariate analysis of variance (PERMANOVA) using the adonis() function in the vegan package in R. The number of permutations was set at 999; all other arguments used the default values set in the function.

Supporting tables

Table S1 – Description of the factorial treatments in the microcosm experiment.

Acronym	Treatment	Oil added?	pH altered?	Description	Observations
Cont	Control	No	No	No oil added and no acidification of seawater pH	None
OnpH	Only pH	No	Yes	No oil added and seawater pH was acidified with CO_2	None
OnOi	Only Oi	Yes	No	Oil added and no acidification of seawater pH	None
pHOi	pH and Oil	Yes	Yes	Oil added and seawater was acidified with CO_2	For *P. ulvae*, this treatment was removed because it lacked organisms from at least three tank-replicates.

Table S2 – Results of analysis of variance (ANOVA) of evenness, richness, Shannon, and Fisher diversity indices of the *Peringia ulvae* (gastropod)-associated bacterial communities. Coef: coefficient; Df: degrees of freedom; Resid.Df: residual degrees of freedom; Resid.Dev: residual deviance; F: f-value; P: p-value; Sig: significance. Note the absence of the pHOi treatment.

Model	Coef	Df	Deviance	Resid.Df	Resid.Dev	F	P	Sig
	NULL			8	0.008			
Evenness	pH	1	0.000	7	0.008	0.064	0.809	
	Oil	1	0.003	6	0.006	2.756	0.148	
	NULL			8	11.074			
Richness	pH	1	0.795	7	10.279	0.657	0.449	
	Oil	1	2.853	6	7.426	2.357	0.176	
	NULL			8	0.060			
Shannon	pH	1	0.005	7	0.055	1.279	0.301	
	Oil	1	0.032	6	0.023	8.457	0.027	*
	NULL			8	5.933			
Fisher	pH	1	0.254	7	5.679	0.353	0.574	
	Oil	1	1.309	6	4.371	1.822	0.226	

Note: * p < 0.05.

Table S3 – Results of analysis of variance (ANOVA) for evenness, richness, Shannon, and Fisher diversity indices of the *Hediste diversicolor* (polychaete)-associated bacterial communities. Coef: coefficient; Df: degrees of freedom; Resid.Df: residual degrees of freedom; Resid.Dev: residual deviance; F: *f*-value; P: *p*-value; Sig: significance.

Model	Coef	Df	Deviance	Resid.Df	Resid.Dev	F	P	Sig
Evenness	NULL			11	0.606			
	pH	1	0.088	10	0.518	1.777	0.219	
	Oil	1	0.018	9	0.499	0.371	0.559	
	pH:Oil	1	0.085	8	0.415	1.712	0.227	
Richness	NULL			11	35.283			
	pH	1	4.236	10	31.047	1.293	0.288	
	Oil	1	3.033	9	28.014	0.926	0.364	
	pH:Oil	1	1.056	8	26.958	0.322	0.586	
Shannon	NULL			11	1.662			
	pH	1	0.334	10	1.328	2.987	0.122	
	Oil	1	0.101	9	1.227	0.901	0.370	
	pH:Oil	1	0.272	8	0.955	2.430	0.158	
Fisher	NULL			11	19.578			
	pH	1	2.951	10	16.626	1.663	0.233	
	Oil	1	1.311	9	15.315	0.738	0.415	
	pH:Oil	1	0.571	8	14.744	0.322	0.586	

Table S4: Results of the PERMANOVA for polychaete (*Hediste diversicolor*)- and gastropod (*Peringia ulvae*)-associated bacterial communities. Coef: coefficient; Df: degrees of freedom; SumsOfSqs: sum of squares; MeanSqs: mean squares; F: *f*-value; P: *p*-value; Sig: significance.

Model	Coef	Df	SumsOfSqs	MeanSqs	F	R^2	P	Sig
	pH	1	0.238	0.238	0.863	0.078	0.720	
	Oil	1	0.348	0.348	1.261	0.114	0.089	
Polychaete	pH:Oil	1	0.255	0.255	0.925	0.084	0.574	
	Residuals	8	2.206	0.276		0.724		
	Total	11	3.047			1.000		
	pH	1	0.276	0.276	1.616	0.160	0.053	
Gastropod	Oil	1	0.419	0.419	2.459	0.244	0.001	***
	Residuals	6	1.023	0.170		0.596		
	Total	8	1.718			1.000		

Note: *** p < 0.001.

Table S5: Mean relative abundance and standard deviation of the four most abundant phyla and orders in the dataset. Control: control treatment, i.e., without oil and with normal pH; OnpH: only pH treatment, i.e., without oil and with reduced seawater pH; OnOi: only oil treatment, i.e., with oil and with normal seawater pH; pHOi: pH and oil treatment, i.e., with oil and with reduced seawater pH.

Rank	Taxa	Gastropod (*Peringia ulvae*)				Polychaete (*Hediste diversicolor*)			
		Cont	**OnpH**	**OnOi**	**OipH**	**Cont**	**OnpH**	**OnOi**	**OipH**
Phylum	*Proteobacteria*	48.39 ± 6.63	54.2 ± 6.14	69.16 ± 4.28	31.46 ± 38.79	42.98 ± 7.71	38.28 ± 25.39	44.16 ± 17.33	46.34 ± 18.12
	Cyanobacteria	1.08 ± 0.12	2.35 ± 2.97	0.44 ± 0.69	0.54 ± 0.76	2.32 ± 3.93	30.48 ± 36.82	0.15 ± 0.17	0.64 ± 1.03
	Planctomycetota	12.11 ± 3.95	14.24 ± 1.23	8.98 ± 1.89	8.32 ± 10.64	11.59 ± 1.72	5.13 ± 2.79	15.24 ± 8.33	9.91 ± 4.44
	Bacteroidota	31.20 ± 5.29	25.05 ± 2.71	12.63 ± 4.88	25.73 ± 9.27	0.75 ± 0.58	0.39 ± 0.3	0.23 ± 0.02	0.94 ± 1.37
Order	*Rhodobacterales*	34.28 ± 5.35	35.4 ± 7.62	35.19 ± 7.6	16.13 ± 21.08	4.84 ± 0.82	2.34 ± 1.15	11.76 ± 7.34	5.14 ± 2.15
	Cyanobacteriales	0.6 ± 0.43	0.32 ± 0.39	0.4 ± 0.62	0.03 ± 0.04	2.3 ± 3.92	30.42 ± 36.86	0.05 ± 0.05	0.59 ± 1.02
	Pirellulales	7.38 ± 2.24	8.73 ± 1.93	4.19 ± 1.65	4.41 ± 6.08	10.23 ± 1.39	4.34 ± 2.25	11.67 ± 7.44	8.23 ± 3.30
	Chitinophagales	27.26 ± 5.89	18.19 ± 1.33	7.06 ± 2.51	4.87 ± 6.56	0.08 ± 0.07	0.01 ± 0.01	0.04 ± 0.02	0.03 ± 0.05

Table S6: Results of the ANOVA of Proteobacteria, Cyanobacteria, Planctomycetota, and Bacteroidota abundances of the polychaete (*Hediste diversicolor*)-associated bacterial communities. Coef: coefficient; Df: degrees of freedom; Resid.Df: residual degrees of freedom; Resid.Dev: residual deviance; F: *f*-value; P: *p*-value; Sig: significance.

Model	Coef	Df	Deviance	Resid.Df	Resid.Dev	F	P	Sig
Proteobacteria	NULL			11	34564.889			
	pH	1	613.964	10	33950.924	0.172	0.689	
	Oil	1	3184.485	9	30766.439	0.892	0.372	
	pH:Oil	1	1744.169	8	29022.271	0.489	0.504	
Cyanobacteria	NULL			11	174885.422			
	pH	1	66618.802	10	108266.620	15.338	0.004	*
	Oil	1	67544.386	9	40722.234	15.551	0.004	*
	pH:Oil	1	32.810	8	40689.424	0.008	0.933	
Planctomycetota	NULL			11	19166.883			
	pH	1	7649.737	10	11517.146	10.193	0.013	
	Oil	1	3841.560	9	7675.586	5.119	0.054	
	pH:Oil	1	1192.557	8	6483.029	1.589	0.243	
Bacteroidota	NULL			11	2000.308			
	pH	1	17.162	10	1983.147	0.063	0.807	
	Oil	1	10.583	9	1972.564	0.039	0.848	
	pH:Oil	1	275.057	8	1697.507	1.017	0.343	

Note: $*P < 0.0125$ (Bonferroni-corrected α value).

Table S7: Results of the permutational analysis of variance (PERMANOVA) for Proteobacteria, Cyanobacteria, Planctomycetota, and Bacteroidota abundances of the gastropod (*Peringia ulvae*)-associated bacterial communities. Coef: coefficient; Df: degrees of freedom; Resid.Df: residual degrees of freedom; Resid.Dev: residual deviance; F: *f*-value; P: *p*-value; Sig: significance.

Model	Coef	Df	Deviance	Resid.Df	Resid.Dev	F	P	Sig
	NULL			8	3602.381			
Proteobacteria	pH	1	600.587	7	3001.794	4.017	0.092	
	Oil	1	2104.263	6	897.531	14.073	0.009	*
	NULL			8	6251.024			
Cyanobacteria	pH	1	2954.086	7	3296.939	6.745	0.041	
	Oil	1	361.985	6	2934.954	0.827	0.398	
	NULL			8	2212.046			
Planctomycetota	pH	1	728.009	7	1484.037	4.817	0.071	
	Oil	1	584.399	6	899.637	3.867	0.097	
	NULL			8	9503.683			
Bacteroidota	pH	1	912.356	7	8591.327	2.715	0.151	
	Oil	1	6601.033	6	1990.294	19.642	0.004	*

Note: *P < 0.0125 (Bonferroni-corrected α value).

Table S8: Results of analysis of variance (ANOVA) of Rhodobacterales, Cyanobacteriales, Pirellulales, and Chitinophagales abundances of the polychaete (*Hediste diversicolor*)-associated bacterial communities. Coef: coefficient; Df: degrees of freedom; Resid.Df: residual degrees of freedom; Resid.Dev: residual deviance; F: *f*-value; P: *p*-value; Sig: significance.

Model	Coef	Df	Deviance	Resid.Df	Resid.Dev	F	P	Sig
Rhodobacterales	NULL			11	16670.869			
	pH	1	6174.364	10	10496.505	12.053	0.008	*
	Oil	1	5805.465	9	4691.040	11.333	0.010	*
	pH:Oil	1	32.499	8	4658.541	0.063	0.807	
Cyanobacteriales	NULL			11	176412.217			
	pH	1	66992.289	10	109419.928	15.375	0.004	*
	Oil	1	68315.927	9	41104.000	15.679	0.004	*
	pH:Oil	1	2.591	8	41101.409	0.001	0.981	
Pirellulales	NULL			11	15798.006			
	pH	1	5861.830	10	9936.176	8.445	0.020	
	Oil	1	2316.263	9	7619.913	3.337	0.105	*
	pH:Oil	1	1311.876	8	6308.037	1.890	0.206	
Chitinophagales	NULL			11	138.911			
	pH	1	26.875	10	112.036	1.802	0.216	
	Oil	1	4.717	9	107.319	0.316	0.589	
	pH:Oil	1	4.828	8	102.491	0.324	0.585	

Note: *P < 0.0125 (Bonferroni-corrected α value).

Table S9: Results of analysis of variance (ANOVA) of Rhodobacterales, Cyanobacteriales, Pirellulales, and Chitinophagales abundances of the gastropod (*Peringia ulvae*)-associated bacterial communities. Coef: coefficient; Df: degrees of freedom; Resid.Df: residual degrees of freedom; Resid.Dev: residual deviance; F: *f*-value; P: *p*-value; Sig: significance.

Model	Coef	Df	Deviance	Resid.Df	Resid.Dev	F	P	Sig
	NULL			8	2660.193			
Rhodobacterales	pH	1	110.776	7	2549.417	0.264	0.626	
	Oil	1	2.907	6	2546.510	0.007	0.936	
	NULL			8	1421.375			
Cyanobacteriales	pH	1	11.355	7	1410.020	0.048	0.834	
	Oil	1	33.845	6	1376.174	0.144	0.718	
	NULL			8	3186.633			
Pirellulales	pH	1	983.070	7	2203.564	5.301	0.061	
	Oil	1	1094.173	6	1109.391	5.900	0.051	
	NULL			8	13194.793			
Chitinophagales	pH	1	497.394	7	12697.399	2.096	0.198	
	Oil	1	11226.659	6	1470.740	47.311	0.0004	*

Note: *P < 0.0125 (Bonferroni-corrected α value).

Table S10: List of the 50 most abundant bacterial amplicon sequence variants (ASVs) associated with the polychaete *Hediste diversicolor*. The table includes the ASV numbers (ASV), and the taxonomic assignment at the family and genus levels was performed by using the SILVA database (https://www.arb-silva.de). Seq. ID: BLAST sequence ID of a close match with our ASV sequence; Seq. sim: sequence similarity; Source/Context: source of these organisms.

ASV	Family	Genus	Seq. ID	Seq. sim	Source/Context
1	Cyanobacteriaceae	Unclassified	KF624242.1	100%	Suboxic pyrite-particle colonization experiment; Janssand tidal flat at Wadden Sea
2	Endozoicomonadaceae	*Endozoicomonas*	AY494615.1	100%	Salmonid gill
3	Unclassified	Unclassified	KU353777.1	88.80%	*Galaxea fascicularis*
4	Clostridiaceae	*Clostridium sensu stricto 2*	NR 115712.1	98.80%	*Clostridium hydrogeniformans* - Contaminated groundwater by chloroethanes and other solvents
7	Thiotrichaceae	*Thiothrix*	KP948979.1	99.20%	*Penaeus vannamei*
8	Rhodobacteraceae	Unclassified	CP054599.1	100%	Shallow sea; symbiosis with algae
11	Desulfocapsaceae	Uncultured	HE803922.1	100%	Marine seabed sediments
12	Burkholderiaceae	*Ralstonia*	MT565488.1	100%	Biodegradation of diethyl-phthalate by halotolerant bacteria in estuarine sediment
13	Clostridiaceae	*Clostridium sensu stricto* 2	NR 115712.1	99.20%	*Clostridium hydrogeniformans* - Contaminated groundwater by chloroethanes and other solvents
17	Clostridiaceae	*Clostridium sensu stricto 2*	KX967682.1	97.19%	Tropical urban freshwater
18	Pirellulaceae	*Rhodopirellula*	MK554582.1	100%	*Stieleria varia*
19	Desulfosarcinaceae	Sva0081 sediment group	JQ199040.1	100%	Seawater
21	Endozoicomonadaceae	*Endozoicomonas*	AY494615.1	99.60%	Salmonid gill
22	Cyanobacteriaceae	Unclassified	MF508061.1	100%	Intertidal microbial mats/sediment
23	Endozoicomonadaceae	*Endozoicomonas*	AY494615.1	99.60%	Salmonid gill
24	Uncultured	uncultured *Thioalkalivibrio*	MG637622.1	100%	Near-surface sediments
25	Rhizobiales Incertae Sedis	*Anderseniella*	KP948621.1	100%	Shrimp/Intestinal flora
28	Chromatiaceae	*Candidatus* Thiobios	MF581677.1	100%	Hydrocarbon contaminated sites
31	Desulfocapsaceae	Uncultured	MG638511.1	100%	Marine Sediment
34	Unclassified	Uncultured bacterium	KY891873.1	100%	Soil
39	Desulfovibrionaceae	*Halodesulfovibrio*	LC490621.1	100%	Deep-sea methane seep sediment
41	Pirellulaceae	*Rubripirellula*	MK559976.1	100%	*Planctomycetes* bacterium
42	Chromatiaceae	*Candidatus* Thiobios	JF344427.1	100%	Hydrocarbon polluted marine sediments
44	Methyloligellaceae	*Methyloceanibacter*	MH091214.1	100%	Mangrove sediments

45	Hyphomicrobiaceae	*Filomicrobium*	MH091208.1	100%	Mangrove. sediment during anaerobic debromination of PBDEs
46	Desulfosarcinaceae	Sva0081 sediment group	KY276786.1	100%	Southern Korean coastal waters
48	Ectothiorhodospiraceae	*Thiogranum*	KX422144.1	100%	Hydrothermal sulphur vent microbial mats
52	Chromatiaceae	Unclassified	KF512938.1	100%	Pink berry consortia / microscale sulphur cycling
55	Rhodobacteraceae	*Sulfitobacter*	MK660323.1	100%	Antarctic sponge
56	Rhodobacteraceae	Unclassified	MF992419.1	100%	Lake water
61	Run-SP154	Run-SP154	JF774695.1	100%	Impact of oil on bacterial community structure in bioturbated sediments
62	Desulfocapsaceae	Uncultured	MF968105.1	100%	Paddy soil
64	Milano-WF1B-44	Milano-WF1B-44	KY277845.1	100%	Dinoflagellate *Cochlodinium*
72	Rhizobiaceae	Unclassified	KY277500.1	100%	Dinoflagellate *Cochlodinium*
74	Peptostreptococcaceae	*Romboutsia*	MN646982.1	100%	Sediment
77	Methyloligellaceae	*Methyloceanibacter*	AB806486.1	100%	Ocean drilling core sample
80	Arenicellaceae	Unclassified	JF774699.1	100%	Impact of oil on bacterial community structure in bioturbated sediments
81	Sedimenticolaceae	Uncultured	GU197440.1	100%	*Tubificoides benedii*
82	HOC36	HOC36	MG638519.1	100%	Marine sediment
89	Thiotrichaceae	*Thiothrix*	KP948979.1	100%	*Penaeus vannamei*
92	Pirellulaceae	*Ilumatobacter*	KT880452.1	97.61%	Hymeniacidon heliophila
93	B2M28	B2M28	KT017836.1	100%	Heavy metal contaminated soil
98	Sedimenticolaceae	Uncultured	HQ191099.1	100%	Dangast muddy intertidal sediment
102	Sedimenticolaceae	Uncultured	KU676710.1	100%	Surface coastal water
105	Desulfocapsaceae	Unclassified	KU675538.1	100%	Surface coastal water
107	Rhodobacteraceae	Unclassified	LR722717.1	100%	Coastal marine surface water
110	Desulfosarcinaceae	*Desulfosarcina*	NR 044680.2	100%	*Desulfosarcina variabilis*
113	Unclassified	Unclassified	HM032657.1	100%	*Trichodesmium erythraeum*
116	Desulfosarcinaceae	Sva0081 sediment group	AY374976.1	100%	Salt marsh sediment
121	Desulfocapsaceae	Uncultured	KY276689.1	100%	Southern Korean coastal waters

Table S11: List of the 50 most abundant bacterial amplicon sequence variants (ASVs) associated with the gastropod *Peringia ulvae*. The table includes the ASV numbers (ASV), and the taxonomic assignment at the family and genus levels was performed by using the SILVA database (https://www.arb-silva.de). Seq. ID: BLAST sequence ID of a close match with our ASV sequence; Seq. sim: sequence similarity; Source/Context: source of these organisms.

ASV	Family	Species/organism	Seq. ID	Seq. sim	Source/Context
5	*Porticoccaceae*	*Porticoccus*	KU382363.1	100%	Bay Pomme d'Or Louisiana
6	*Saprospiraceae*	Uncultured	JQ236019.1	100%	*Cladocora caespitosa* skeleton naturally exposed to pH 8.1
8	*Rhodobacteraceae*	Unclassified	CP054599.1	100%	Shallow sea symbiosis with algae
10	*Rhodobacteraceae*	Unclassified	MH061217.1	100%	Carapace of *Cancer pagurus*
14	*Rhodobacteraceae*	Unclassified	LR722720.1	100%	Coastal marine surface water
15	*Rhodobacteraceae*	Unclassified	MF195218.1	100%	Shrimp intestine
16	*Rubinisphaeraceae*	*Fuerstia*	HM437309.1	100%	Surface of thriving-algae collected at peak-bloom period
18	*Pirellulaceae*	*Rhodopirellula*	KX213868.1	100%	Macroalgae
20	*Rhodobacteraceae*	Unclassified	MK967063.1	100%	*Aurita medusa* Baltic Sea husbandry
26	*Granulosicoccaceae*	*Granulosicoccus*	JQ579712.1	99.60%	Oil-polluted subtidal sediments
27	*Saprospiraceae*	*Lewinella*	KT979445.1	100%	Marine intertidal outcrops/endolithic community of Mono Island
29	*Rhodobacteraceae*	Unclassified	JN232290.1	100%	Seagrass epiphytic biofilm
30	*Rhodobacteraceae*	Unclassified	EU346516.1	99.60%	Marine sponge
32	*Saprospiraceae*	*Phaeodactylibacter*	KP945312.1	98.40%	Shrimp intestine
33	*Alcalinovoracaceae*	*Alcanivorax*	MN186614.1	100%	*Alcanivorax borkumensis*
			MH595649.1	100%	*Lessonia trabeculata*
36	*Rhodobacteraceae*	Unclassified	HQ441219.1	99.60%	*Fucus vesiculosus*
38	*Rhodobacteraceae*	Unclassified	AJ968650.1	100%	Intertidal sediment
40	*Rhodobacteraceae*	Unclassified	NR 163664.1	100%	Tidal flat sediment
43	*Rhodobacteraceae*	Unclassified	MT484146.1	100%	*Hymeniacidon perlevis* (Marine sponge)
49	*Saprospiraceae*	Uncultured	KY277423	98.40%	Dinoflagellate *Cochlodinium polykrikoides* blooms
50	*Rhodobacteraceae*	Unclassified	JX984082.1	100%	Biofilm age on settlement of *Mytilus edulis*
51	*Saprospiraceae*	Uncultured	MK175881.1	100%	Coral tissue mucus and skeleton
53	*Rhodobacteraceae*	Unclassified	MF581839.1	100%	*Holothuria arguinensis* (sea cucumber)
54	*Rhodobacteraceae*	Unclassified	MK967052.1	100%	*Aurita medusa* Baltic Sea husbandry
57	*Rhodobacteraceae*	Unclassified	HM171150.1	100%	Marine bacterial community in the presence of Prestige fuel oil

58	*Rhodobacteraceae*	Unclassified	KP949962.1	99.2%	*Penaeus vannamei*
59	*Rhodobacteraceae*	Unclassified	MN267475.1	100%	*Loktanella* sp.
60	*Rhodobacteraceae*	Unclassified	KX602047.1	98.80%	Surface sea water
63	*Saprospiraceae*	Uncultured	KY277107.1	100%	Dinoflagellate *Cochlodinium polykrikoides* blooms
65	*Saprospiraceae*	*Lewinella*	MK588934.1	100%	Gut microbiome of *Litopenaeus vannamei*
66	*Pirellulaceae*	*Blastopirellula*	KF185446.1	98.80%	Uncultured marine bacterium
67	OM190	OM190	MK559991.1	100%	*Planctomycetes* bacterium
68	*Saprospiraceae*	*Lewinella*	EU371935.1	100%	*Lewinella persica*
70	*Saprospiraceae*	*Lewinella*	EU371937.1	100%	*Lewinella cohaerens*
75	*Saprospiraceae*	Uncultured	MN890266.1	100%	Marine recirculation aquaculture system
76	*Saprospiraceae*	*Lewinella*	KY276469.1	100%	Dinoflagellate *Cochlodinium*
78	*Rhodobacteraceae*	Unclassified	KY770426.1	100%	Phycosphere *Synechococcus*-bacteria interactions
79	*Rhodobacteraceae*	*Marivita*	MN746209.1	100%	Isolates in the coastal dinoflagellate bloom
83	*Rhodobacteraceae*	Unclassified	MH773428.1	100%	*Roseobacter* sp.
84	*Myxococcaceae*	P3OB-42	MN890217.1	98.80%	Marine recirculation aquaculture system
85	*Arenicellaceae*	HTCC5015	JX391735.1	99.20%	Marine sediment
86	*Rhodobacteraceae*	Unclassified	KP262766.1	100%	Surface seawater
87	*Rhizobiaceae*	Unclassified	MT112371.1	100%	*Salaquimonas pukyongi*
88	*Pirellulaceae*	*Blastopirellula*	KF364638.1	99.60%	Surface of macroalgae / *Sargassum muticum*
90	*Rhodobacteraceae*	*Sulfitobacter*	LR722698.1	100%	Coastal marine surface water
91	*Pirellulaceae*	*Blastopirellula*	KY278739.1	98.80%	Dinoflagellate *Cochlodinium*
95	*Rhodobacteraceae*	Unclassified	MK100380.1	100%	*Thalassobius* sp.
96	*Pirellulaceae*	*Blastopirellula*	KF185573.1	99.20%	Northern Adriatic Sea: Gulf of Trieste; marine snow sample
97	*Rhodobacteraceae*	*Sulfitobacter*	MT012050.1	100%	Phycosphere of *Prorocentrum donghaiense*
99	*Rhodobacteraceae*	Unclassified	GU451554.1	100%	Macroalgal surface

Table S12: Results of analysis of variance (ANOVA) for the 50 most abundant amplicon sequence variants (ASV) of the *Hediste diversicolor* bacterial communities. Significant results ($p<0.01$) are highlighted. Resid.Dev: residual deviance; F: *f*-value; Pr(>F): *p*-value.

ASV	Factor	Resid. Dev	F	Pr(>F)
1	Oil	92957.26	20.21	0.002
	pH	41984.87	11.66	0.009
	Oil*pH	41977.42	0.00	0.968
2	Oil	32321.79	3.06	0.118
	pH	26711.93	1.66	0.234
	Oil*pH	26364.60	0.10	0.757
3	Oil	37776.61	6.71	0.032
	pH	36972.36	0.20	0.663
	Oil*pH	36558.09	0.11	0.754
4	Oil	12131.35	0.11	0.748
	pH	11969.47	0.10	0.763
	Oil*pH	11928.30	0.02	0.879
7	Oil	31771.64	9.88	0.014
	pH	16317.80	9.98	0.013
	Oil*pH	16317.80	0.00	1.000
8	Oil	1158.30	11.63	0.009
	pH	1147.18	0.12	0.743
	Oil*pH	1072.87	0.77	0.405
11	Oil	6236.23	0.29	0.606
	pH	6141.82	0.11	0.748
	Oil*pH	5264.27	1.03	0.341
12	Oil	5915.10	4.08	0.078
	pH	5758.42	0.20	0.668
	Oil*pH	5757.26	0.00	0.970
13	Oil	11739.75	2.28	0.170
	pH	11711.72	0.02	0.897
	Oil*pH	11707.05	0.00	0.958
17	Oil	7338.19	3.36	0.104
	pH	7300.26	0.04	0.855
	Oil*pH	7298.77	0.00	0.971
18	Oil	776.43	15.69	0.004
	pH	463.21	7.35	0.027
	Oil*pH	392.20	1.67	0.233
19	Oil	1874.02	1.04	0.338
	pH	1595.58	10.75	0.011
	Oil*pH	232.66	52.60	<0.001
21	Oil	9939.49	1.86	0.210
	pH	8260.51	1.62	0.239
	Oil*pH	8175.62	0.08	0.782
22	Oil	6611.09	8.71	0.018
	pH	5484.00	1.90	0.206
	Oil*pH	5484.00	0.00	1.000

	Oil	9206.48	1.62	0.238
23	pH	8296.36	0.90	0.370
	Oil*pH	8241.22	0.05	0.821
	Oil	1143.23	0.02	0.879
24	pH	1096.69	0.40	0.547
	Oil*pH	789.92	2.61	0.145
	Oil	1286.28	0.03	0.856
25	pH	840.51	3.96	0.082
	Oil*pH	832.21	0.07	0.793
	Oil	1464.29	2.30	0.168
28	pH	1397.15	0.67	0.435
	Oil*pH	853.09	5.47	0.048
	Oil	2170.89	0.93	0.363
31	pH	2169.63	0.00	0.956
	Oil*pH	2085.56	0.21	0.657
	Oil	341.19	1.28	0.292
34	pH	340.88	0.01	0.926
	Oil*pH	281.11	1.79	0.217
	Oil	4286.94	3.61	0.094
39	pH	4084.57	0.52	0.491
	Oil*pH	2915.36	3.01	0.121
	Oil	1149.24	1.20	0.306
41	pH	869.73	2.90	0.127
	Oil*pH	851.89	0.19	0.678
	Oil	1401.55	0.93	0.362
42	pH	1390.68	0.10	0.758
	Oil*pH	772.69	5.78	0.043
	Oil	1032.39	0.87	0.379
44	pH	778.21	4.64	0.063
	Oil*pH	482.84	5.39	0.049
	Oil	680.22	2.95	0.124
45	pH	161.73	32.48	<0.001
	Oil*pH	136.50	1.58	0.244
	Oil	1617.82	0.58	0.467
46	pH	1422.30	2.42	0.159
	Oil*pH	924.02	6.16	0.038
	Oil	968.63	0.39	0.550
48	pH	605.09	10.33	0.012
	Oil*pH	355.91	7.08	0.029
	Oil	946.38	4.21	0.074
52	pH	743.80	3.89	0.084
	Oil*pH	492.52	4.82	0.059
	Oil	520.79	4.29	0.072
55	pH	314.43	6.22	0.037
	Oil*pH	279.86	1.04	0.337
56	Oil	1004.95	1.38	0.273

	pH	980.32	0.27	0.616
	Oil*pH	698.75	3.12	0.115
	Oil	1074.35	0.00	0.982
61	pH	1027.32	0.29	0.604
	Oil*pH	979.05	0.30	0.599
	Oil	1972.71	1.10	0.324
62	pH	1911.68	0.32	0.586
	Oil*pH	1296.83	3.24	0.110
	Oil	1985.05	0.07	0.791
64	pH	1979.66	0.02	0.902
	Oil*pH	1904.81	0.22	0.649
	Oil	727.76	6.27	0.037
72	pH	201.75	26.14	0.001
	Oil*pH	168.28	1.66	0.233
	Oil	739.61	1.58	0.244
74	pH	640.14	1.32	0.284
	Oil*pH	595.69	0.59	0.465
	Oil	703.79	0.55	0.479
77	pH	488.98	5.32	0.050
	Oil*pH	316.56	4.27	0.073
	Oil	818.70	2.21	0.175
80	pH	622.28	3.01	0.121
	Oil*pH	592.14	0.46	0.516
	Oil	1792.48	0.10	0.760
81	pH	1769.72	0.32	0.585
	Oil*pH	486.43	18.20	0.003
	Oil	1154.19	0.17	0.695
82	pH	977.69	1.16	0.314
	Oil*pH	949.99	0.18	0.681
	Oil	6086.47	9.19	0.016
89	pH	3170.80	9.40	0.015
	Oil*pH	3170.80	0.00	1.000
	Oil	671.69	4.54	0.066
92	pH	428.17	5.48	0.047
	Oil*pH	402.04	0.59	0.465
	Oil	1517.30	0.27	0.620
93	pH	1474.76	0.89	0.373
	Oil*pH	621.94	17.88	0.003
	Oil	1004.50	0.43	0.532
98	pH	914.55	2.08	0.188
	Oil*pH	362.45	12.75	0.007
	Oil	741.06	0.16	0.696
102	pH	684.25	2.06	0.189
	Oil*pH	213.05	17.12	0.003
	Oil	1172.53	5.00	0.056
105	pH	1006.42	1.09	0.328

	Oil*pH	924.53	0.54	0.485
	Oil	969.34	11.67	0.009
107	pH	366.82	17.75	0.003
	Oil*pH	361.59	0.15	0.705
	Oil	923.54	0.11	0.747
110	pH	802.18	3.60	0.094
	Oil*pH	326.88	14.10	0.006
	Oil	4649.10	3.92	0.083
113	pH	3819.64	1.72	0.226
	Oil*pH	3819.64	0.00	1.000
	Oil	546.84	0.01	0.933
116	pH	434.52	10.80	0.011
	Oil*pH	118.72	30.36	0.001
	Oil	682.70	1.31	0.286
121	pH	632.36	1.52	0.253
	Oil*pH	304.69	9.88	0.014

Table S13: Results of analysis of variance for the 50 most abundant amplicon sequence variants (ASVs) of the *Peringia ulvae* bacterial communities. Significant results ($p<0.01$) are highlighted. Resid.Dev: residual deviance; F: *f*-value; Pr(>F): *p*-value.

ASV	Factor	Resid. Dev	F	Pr(>F)
5	Oil	1353.02	0.26	0.628
	pH	803.71	3.94	0.094
6	Oil	559.34	31.02	0.001
	pH	477.75	1.01	0.353
8	Oil	1890.16	1.31	0.295
	pH	1824.74	0.18	0.684
10	Oil	3062.76	19.66	0.004
	pH	972.73	13.00	0.011
14	Oil	1864.91	0.24	0.644
	pH	1772.16	0.32	0.590
15	Oil	847.14	0.22	0.655
	pH	449.65	5.98	0.050
16	Oil	1325.18	3.36	0.117
	pH	1322.80	0.01	0.923
18	Oil	464.30	0.64	0.454
	pH	447.33	0.23	0.650
20	Oil	1510.39	1.89	0.219
	pH	1133.82	2.33	0.177
26	Oil	1986.59	0.10	0.768
	pH	1942.10	0.16	0.705
27	Oil	4553.31	6.63	0.042
	pH	1861.64	10.23	0.019
29	Oil	642.25	13.49	0.010
	pH	490.15	2.14	0.194
30	Oil	792.17	0.53	0.496
	pH	755.80	0.26	0.627
32	Oil	2127.24	12.28	0.013
	pH	1306.95	3.50	0.111
33	Oil	1021.64	38.21	0.001
	pH	1021.64	0.00	1.000
36	Oil	4171.00	0.77	0.414
	pH	2861.86	3.04	0.132
38	Oil	181.42	0.44	0.533
	pH	163.48	0.72	0.430
40	Oil	332.46	1.24	0.308
	pH	305.13	0.49	0.509
43	Oil	711.98	12.38	0.013
	pH	571.84	1.64	0.247
49	Oil	6379.47	7.50	0.034
	pH	2702.64	10.48	0.018
50	Oil	1079.83	0.13	0.731
	pH	1074.12	0.03	0.870

51	Oil	981.12	10.61	0.017
	pH	579.19	4.22	0.086
53	Oil	2480.65	0.70	0.434
	pH	1126.44	8.58	0.026
54	Oil	980.90	0.88	0.385
	pH	875.13	0.83	0.397
57	Oil	2076.00	19.53	0.004
	pH	2076.00	0.00	1.000
58	Oil	788.65	2.17	0.191
	pH	264.79	11.59	0.014
59	Oil	1604.22	3.26	0.121
	pH	985.07	4.49	0.078
60	Oil	1300.91	0.16	0.700
	pH	978.86	2.15	0.193
63	Oil	796.26	22.28	0.003
	pH	691.22	1.02	0.352
65	Oil	4284.73	3.29	0.120
	pH	3167.40	2.48	0.166
66	Oil	851.32	18.79	0.005
	pH	622.46	2.94	0.137
67	Oil	253.07	1.33	0.293
	pH	243.68	0.27	0.620
68	Oil	784.42	23.24	0.003
	pH	394.89	6.23	0.047
70	Oil	837.25	3.82	0.099
	pH	836.45	0.01	0.935
75	Oil	2353.24	0.00	0.966
	pH	1461.81	5.06	0.065
76	Oil	1352.55	0.65	0.451
	pH	1352.29	0.00	0.972
78	Oil	1202.14	7.37	0.035
	pH	1173.05	0.15	0.711
79	Oil	708.57	0.38	0.560
	pH	606.05	1.09	0.337
83	Oil	4180.05	6.95	0.039
	pH	1475.52	14.76	0.009
84	Oil	350.54	14.67	0.009
	pH	350.40	0.00	0.963
85	Oil	859.11	4.21	0.086
	pH	758.72	0.87	0.387
86	Oil	2167.65	12.16	0.013
	pH	2167.65	0.00	1.000
87	Oil	567.74	35.00	0.001
	pH	172.27	15.88	0.007
88	Oil	242.36	20.12	0.004
	pH	241.50	0.02	0.883

90	Oil	750.71	0.00	0.964
	pH	437.44	4.45	0.079
91	Oil	546.93	15.54	0.008
	pH	546.85	0.00	0.975
95	Oil	3630.68	0.60	0.467
	pH	3215.73	0.85	0.393
96	Oil	696.91	25.81	0.002
	pH	360.42	6.44	0.044
97	Oil	1443.60	3.12	0.128
	pH	490.97	14.21	0.009
99	Oil	634.10	23.00	0.003
	pH	399.85	3.66	0.104

Table S14: Results of the permutational analysis of variance (PERMANOVA) for the polychaete (*Hediste diversicolor*) biochemical markers. Coef: coefficient; Df: degrees of freedom; SumsOfSqs: sum of squares; MeanSqs: mean squares; F: *f*-value; P: *p*-value; AChE: acetylcholinesterase; LDH: lactate dehydrogenase; CAT: catalase; GST: glutathione *S*-transferase; LPO: lipid peroxidation; E_a: Energy available; E_c: Energy consumption; CEA: cellular energy allocation.

Model	Coef	Df	SumsOfSqs	MeanSqs	F	R^2	P	Sig
	pH	1	0.012	0.012	0.233	0.037	0.658	
AChE	Residuals	6	0.311	0.0519		0.963		
	Total	7	0.323			1.000		
	pH	1	0.002	0.002	0.021	0.003	0.879	
LDH	Residuals	6	0.463	0.077		0.997		
	Total	7	0.46445			1.000		
	pH	1	0.008	0.008	0.0721	0.012	0.848	
CAT	Residuals	6	0.669	0.112		0.988		
	Total	7	0.677			1.000		
	pH	1	0.004	0.004	0.075	0.012	0.717	
GST	Residuals	6	0.324	0.054		0.988		
	Total	7	0.328			1.000		
	pH	1	0.002	0.002	0.050	0.008	0.866	
LPO	Residuals	6	0.257	0.043		0.992		
	Total	7	0.259			1.000		
	pH	1	0.068	0.068	0.461	0.072	0.575	
Lipids	Residuals	6	0.886	0.148		0.929		

	Source	df					
	Total	7	0.954			1.000	
Carbohydrates	pH	1	0.115	0.115	0.629	0.095	0.436
	Residuals	6	1.099	0.183		0.905	
	Total	7	1.215			1.000	
Proteins	pH	1	0.001	0.001	0.004	0.001	0.981
	Residuals	6	0.909	0.151		0.999	
	Total	7	0.909			1.000	
E_a	pH	1	0.005	0.005	0.038	0.006	0.829
	Residuals	6	0.807	0.135		0.994	
	Total	7	0.813			1.000	
E_c	pH	1	0.022	0.022	0.219	0.035	0.636
	Residuals	6	0.603	0.101		0.965	
	Total	7	0.625			1.000	
CEA	pH	1	0.164	0.164	0.764	0.113	0.454
	Residuals	6	1.290	0.215		0.887	
	Total	7	1.455			1.000	

Table S15: Results of permutational multivariate analysis of variance (PERMANOVA) for the gastropod (*Peringia ulvae*) biochemical parameters. Coef: coefficient; Df: degrees of freedom; SumsOfSqs: sum of squares; MeanSqs: mean squares; F: *f*-value; P: *p*-value; AChE: acetylcholinesterase; LDH: lactate dehydrogenase; CAT: catalase; GST: glutathione *S*-transferase; LPO: lipid peroxidation; E_a: Energy available; E_c: Energy consumption; CEA: cellular energy allocation.

Model	Coef	Df	SumsOfSqs	MeanSqs	F	R^2	P	Sig
AChE	Oil	1	0.024	0.024	0.685	0.064	0.421	
	pH	1	0.037	0.037	1.047	0.098	0.324	
	Residuals	9	0.319	0.035		0.839		
	Total	11	0.380			1.000		
LDH	Oil	1	0.638	0.638	8.664	0.490	0.019	*
	pH	1	0.002	0.002	0.026	0.001	0.863	
	Residuals	9	0.663	0.074		0.509		
	Total	11	1.303			1.000		
CAT	Oil	1	0.012	0.012	1.050	0.064	0.335	
	pH	1	0.073	0.073	6.405	0.389	0.022	*
	Residuals	9	0.103	0.011		0.547		
	Total	11	0.188			1.000		
GST	Oil	1	0.000	0.000	0.019	0.002	0.885	
	pH	1	0.005	0.005	0.634	0.066	0.441	
	Residuals	9	0.074	0.008		0.932		
	Total	11	0.080			1.000		
LPO	Oil	1	0.883	0.883	7.180	0.437	0.026	*
	pH	1	0.029	0.029	0.233	0.014	0.648	
	Residuals	9	1.107	0.123		0.548		
	Total	11	2.018			1.000		
Lipids	Oil	1	0.568	0.568	6.502	0.412	0.011	*

	Source	df						Sig.
	pH	1	0.023	0.023	0.261	0.017	0.646	
	Residuals	9	0.786	0.087		0.571		
	Total	11	1.377			1.000		
Carbohydrates	Oil	1	0.028	0.028	0.811	0.045	0.401	
	pH	1	0.287	0.287	8.338	0.459	0.017	*
	Residuals	9	0.310	0.034		0.496		
	Total	11	0.625			1.000		
Proteins	Oil	1	0.335	0.335	3.494	0.260	0.103	
	pH	1	0.091	0.091	0.947	0.070	0.364	
	Residuals	9	0.862	0.096		0.670		
	Total	11	1.287			1.000		
E_a	Oil	1	0.219	0.219	3.381	0.272	0.093	
	pH	1	0.003	0.003	0.048	0.004	0.873	
	Residuals	9	0.583	0.065		0.724		
	Total	11	0.805			1.000		
E_c	Oil	1	0.050	0.050	2.414	0.211	0.181	
	pH	1	0.000	0.000	0.023	0.002	0.876	
	Residuals	9	0.187	0.021		0.787		
	Total	11	0.238			1.000		
CEA	Oil	1	0.553	0.553	20.353	0.693	0.002	**
	pH	1	0.001	0.001	0.027	0.001	0.878	
	Residuals	9	0.245	0.027		0.306		
	Total	11	0.798			1.000		

Note: * $P < 0.05$; ** $P < 0.01$
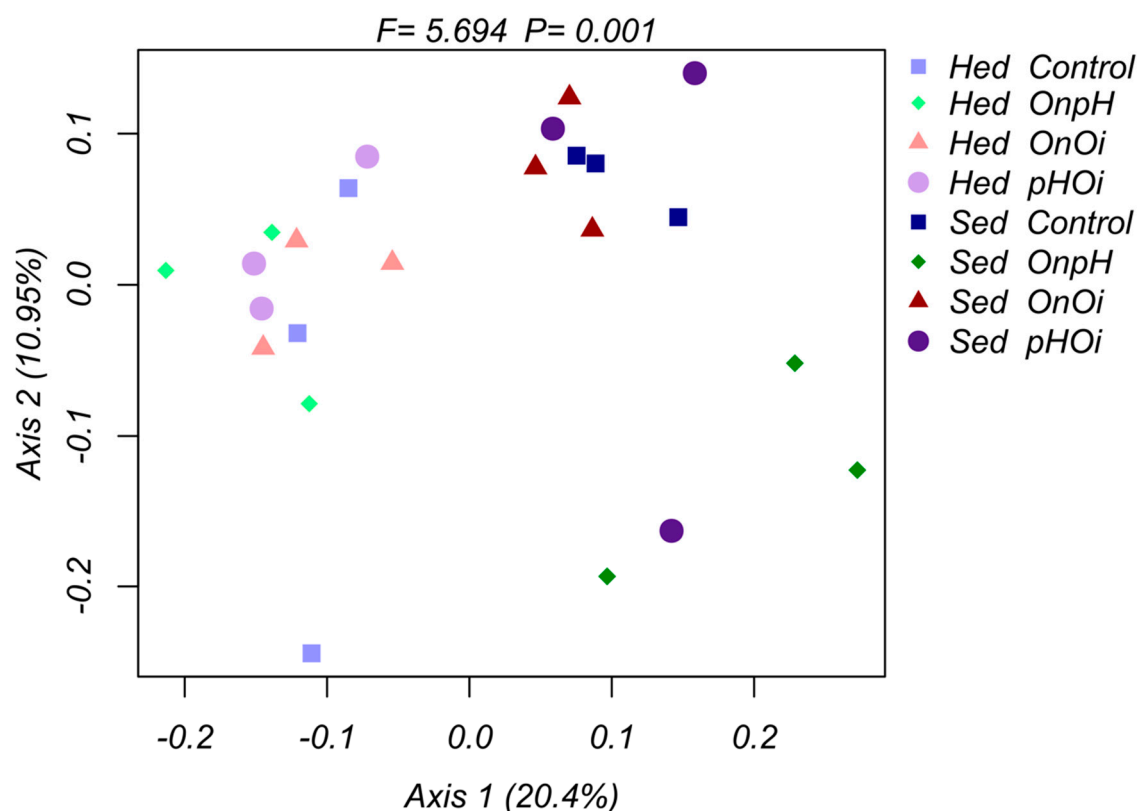
Figure S1. Principal Coordinates Analysis (PCoA) of sediment and polychaete (*Hediste diversicolor*)-associated bacterial DGGE profiles. The first two explanatory axes are shown. Hed: polychaete *H. diversicolor*; Sed: Sediment; Control: control treatment, i.e., without oil and with normal pH; OnpH: only pH treatment, i.e., without oil and with reduced seawater pH; OnOi: on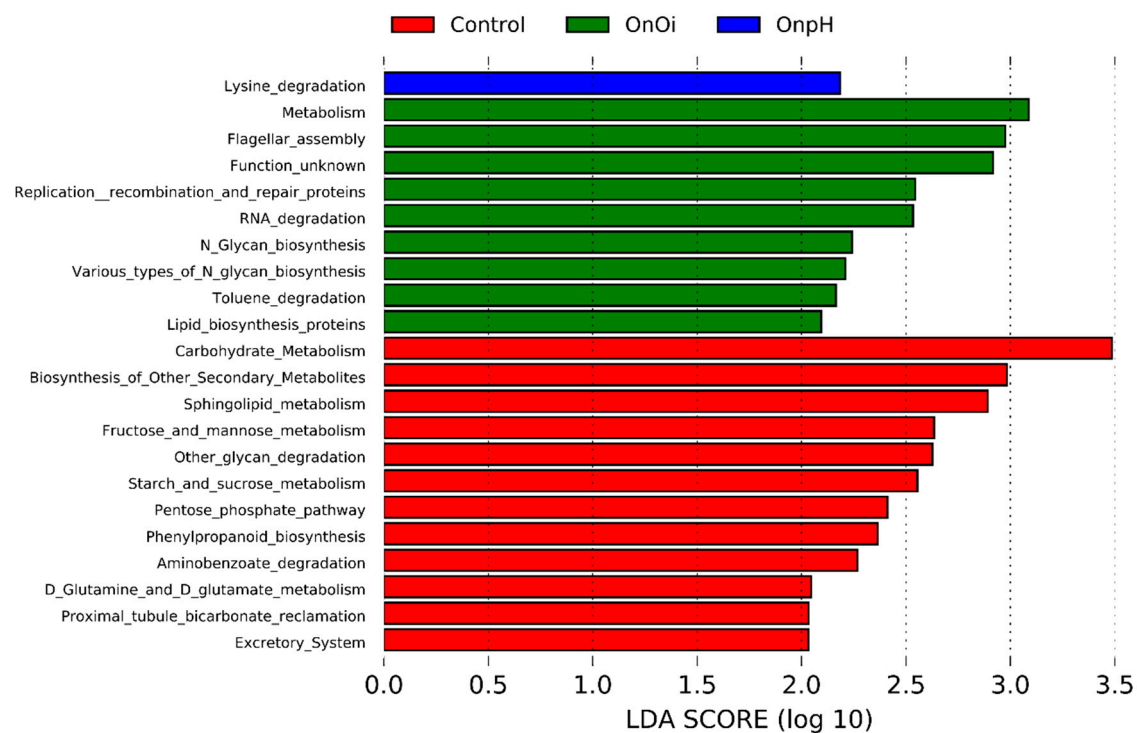ly oil treatment, i.e., with oil and with normal seawater pH; pHOi: pH and oil treatment, i.e., with oil and with reduced seawater pH. The permutational multivariate analysis of variance (PERMANOVA) results of the comparison between sediment and polychaete DGGE profiles are shown above (F: *f*-value; P: *p*-value).
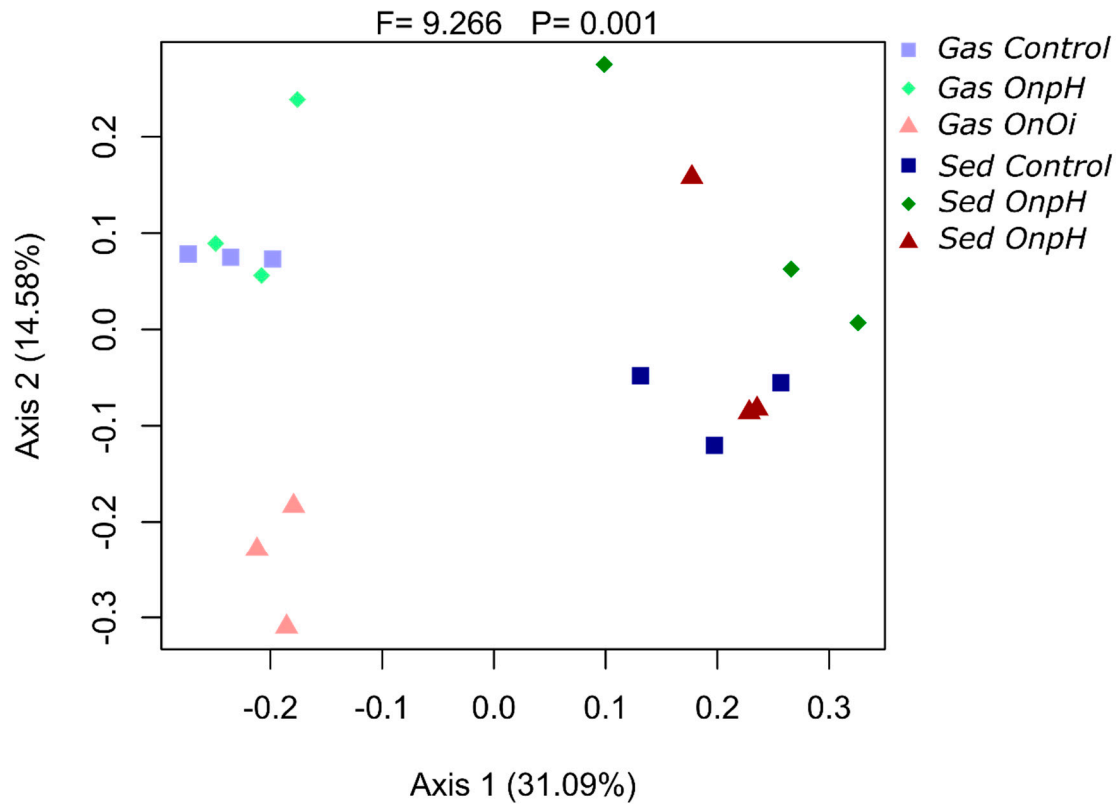
Figure S2. Principal Coordinates Analysis (PCoA) of sediment and gastropod (*Peringia ulvae*)-associated bacterial DGGE profiles. The first two explanatory axes are shown. Gas: gastropod *P. ulvae*; Sed: Sediment; Control: control treatment, i.e., without oil and with normal pH; OnpH: only pH treatment, i.e., without oil and with reduced seawater pH; OnOi: only oil treatment, i.e., with oil and with normal seawater pH; pHOi: pH and oil treatment, i.e., with oil and with reduced seawater pH. The permutational multivariate analysis of variance (PERMANOVA) results of the comparison between sediment and gastropod DGGE profiles are shown above (F: *f*-value; P: *p*-value).
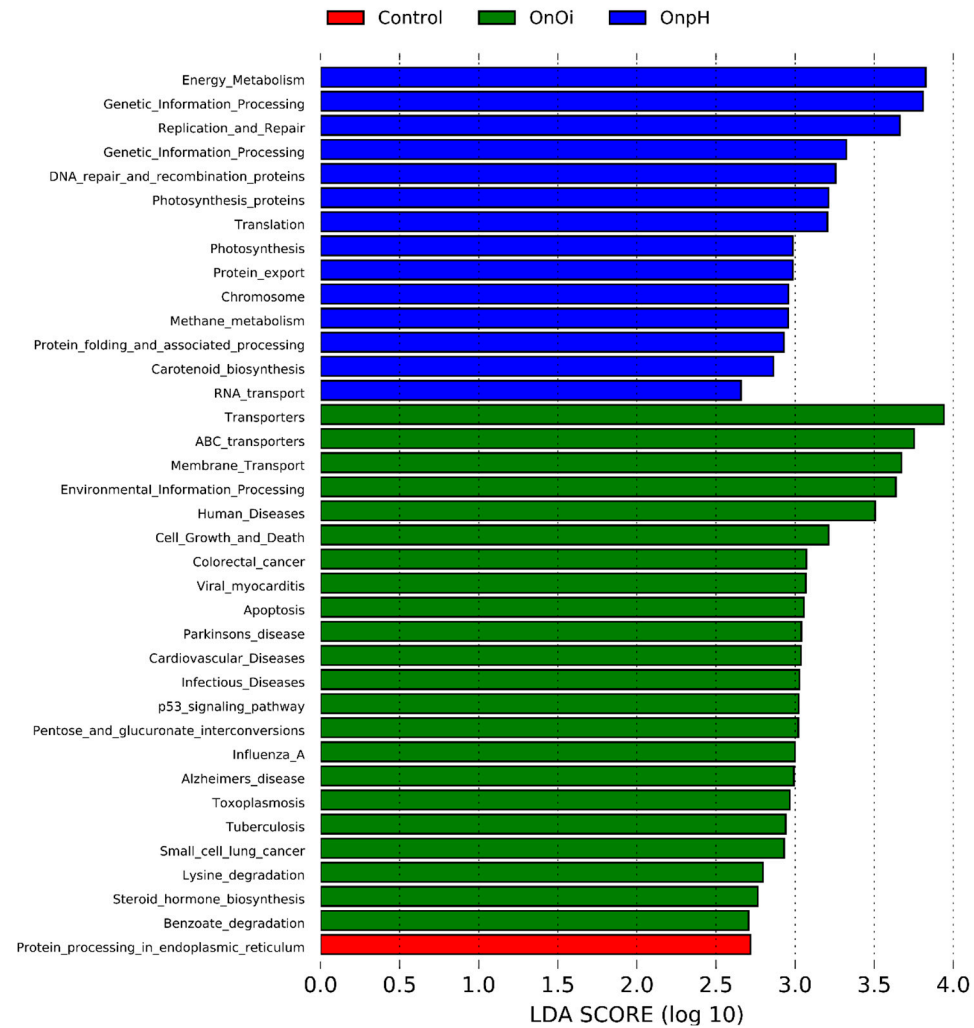
Figure S3. Results from LefSe of predicted metagenome of bacterial communities associated with the polychaete *Hediste diversicolor*. Control: control treatment, i.e., without oil and with normal pH; OnpH: only pH treatment, i.e., without oil and with reduced seawater pH; OnOi: only oil treatment, i.e., with oil and with normal seawater pH.

Figure S4. Results from LefSe of predicted metagenome of bacterial communities associated with the gastropod *Peringia ulvae*. Control: control treatment, i.e., without oil and with normal pH; OnpH: Only pH treatment, i.e., without oil and with reduced seawater pH; OnOi: only oil treatment, i.e., with oil and with normal seawater pH

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Supplementary Dataset S2

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