SI Appendix

Supplementing Results and Discussion

Laboratory Experiments

Our laboratory experiments simulated the conditions of the Deepwater Horizon (DWH) deepwater plume very realistically. The dispersant dilutions were 1:60,000 (v/v) in Corexit 9500 ('dispersant-only') treatments and 1:30,000 (v/v) in the chemically enhanced water-accommodated fraction (CEWAF) treatments (*SI Appendix* Fig. S1 and S2). These dilutions resulted in dispersant concentrations (~19 µg/L) that were comparable to concentrations observed in the DWH plume *in situ* (below detection to 12 µg/L) (1). Similarly, the concentration of TPH in the deepwater plume ranged from 2 to ~440 µg/L (2) and in the water-accommodated fraction (WAF) and CEWAF microcosms, the TPH concentration were in a similar range, from 30 to 300 µg/L. We aimed to expose microbial communities to the same amount of dissolved organic carbon (DOC), while varying the composition of the added DOC. To achieve this, we quantified the DOC concentration in the different water-accommodated fractions and added aliquots to obtain comparable DOC concentrations (~150 µM DOC) across treatments, which were similar to the concentration of bulk DOC observed in the deepwater plume (3).

Marine oil snow formation

Many hydrocarbon-degrading bacteria produce copious amounts of exopolymeric substances that emulsify oil and increase oil availability to these microorganisms (for general review see Ref. 4). As a result, hydrocarbon addition to a water sample may lead to formation of microbial aggregates, so-called marine "oil" snow, which was documented in the field (5) and in the laboratory (6-9) after the DWH spill. The different types of macroscopical particles formed in these microcosms, resembled the marine snow observed *in situ* during the DWH oil spill.

In the microcosms, the most rapid oil snow formation was observed in CEWAF+nutrients treatments (Fig. S13e). Here, roundish, fractal-looking aggregates were visible after 5 days of incubation and increased significantly in size and number (approaching 2 cm diameter; Fig. S13f, g) during the first 2 weeks of incubation. Thereafter, average aggregate sizes appeared to be unchanged. WAF treatments revealed visible oil snow, that consisted of stringy mucus with attached small particles after about 2 weeks of

incubation (Fig. S13a). These aggregate sizes were much smaller (up to 0.5 cm) than those produced in CEWAF+nutrients with aggregate numbers increasing throughout the experiment (Fig. S13b after 6 weeks of incubation). Compared to CEWAF+nutrients and WAF microcosms, macroscopical particles in the dispersant-only microcosms differed (Fig. S13c). Here, white filaments, ranging in sizes from a few mm up to ~5 cm, were first detected after 10 days and were then visible in most dispersant-only treatments. Similar but smaller filaments as well as small round fluffy aggregates (<0.5 cm; Fig. S13d) were detected after 10 days in CEWAF microcosms.

The formation of micro-aggregates consisting of microbial cells was examined in all treatments using fluorescence microscopy. Fluorescence *in situ* hybridization in combination with catalyzed reporter deposition (CARD-FISH) revealed, that microbial communities grown in CEWAF+nutrients treatments were dominated by Bacteria (green; Fig. S13m-o). Within the Bacteria, different groups contributed to these micro-aggregates, of which the *Gammaproteobacteria* and *Alteromonadales,* including *Colwellia,* were specifically identified using CARD-FISH (red = *Alteromonadales* including *Colwellia*; Fig. S13p-r). These findings support the results of the microbial community composition observed by 16S rRNA gene amplicon sequencing, indicating that *Colwellia* enriched in all dispersant-amended treatments were likely involved in marine oil snow formation when dispersants were present.

Nitrogen-containing compounds and phosphate

Substantial variations in the inorganic nitrogen-containing compounds were observed throughout the experiment. Nitrite concentrations increased from below detection limit to 0.6 µM (*SI Appendix* Table S1) while nitrate concentrations decreased significantly in the WAF (from 23 µM to 2 µM; $p < 0.0001$) and dispersant-only (from 23 µM to 14 µM; $p = 0.002$) microcosms (*SI Appendix* Table S1), implying active nitrate uptake and potentially incomplete denitrification. While denitrification is generally considered to occur under anoxic or suboxic conditions, *Marinobacter hydrocarbonoclasticus* is classified as an aerobic denitrifier and may have denitrified in the presence of oxygen (10) in the WAF treatments. Likewise, *Colwellia psychrerythraea* has the genetic potential to denitrify. Genes for hydrocarbon degradation under nitrate-reducing conditions (*bbs*) as well as genes for denitrification (*narG, nirS, nirK and nosZ*) were observed *in situ* in the DWH deep-water plume (11). The presence of mucus-rich, microbial aggregates could further promote denitrification through formation of anoxic microzones (12). Microbial communities,

especially in WAF treatments, assimilated phosphate but were never phosphate limited (*SI Appendix* Table S1).

Validation of deepwater results in oil-polluted surface waters

To validate the deepwater radiotracer dispersant results, we evaluated rates of hydrocarbon turnover in surface water samples that were impacted by a persistent anthropogenic discharge at the Taylor Energy platform in the Gulf of Mexico. At this site, surface waters exhibited tremendously high concentrations of total petroleum hydrocarbons; TPH, at the source was ~ 38,886 µg/g sample. For this experiment, a transect of oil-contaminated surface water samples was obtained from the Taylor Energy oil platform to the river plume of the Mississippi in the Gulf of Mexico. Four sites were sampled; the source of oil contamination (site 1; 38,886 µg/g sample TPH), the intersection of the oil slick with the Mississippi river plume (site 2; 16,376 µg/g sample TPH) and intermediate sites (site 3; 14 µg/g sample TPH, site 4; 30 µg/g sample TPH) between the source and river.

Supplementing Material and Methods

Sample collection at a natural hydrocarbon seep site

During *R/V* Pelican cruise PE13-21 (March 7th 2013), 160 L of seawater were collected from an oil vent at an active natural hydrocarbon seep (27.3614˚ N, -90.6018˚ W, depth = 1178 m) located at Green Canyon block 600 (GC600). The GC600 site hosts one of the most active natural oil seeps in the Gulf of Mexico (13-15). Indigenous pelagic microbial communities at GC600 seep sites are adapted to natural oil input into the sea. For collection of seawater, an instrumented CTD rosette equipped with twelve 10 L Niskin bottles was lowered into the plume using chirp sonar as guidance. After recovery, water samples were transferred into pre-cleaned (HCl-soaked, Milli-Q rinsed and dried) and sample water rinsed (3×) 20 L carboys. Carboys were transported at 4°C to the laboratory at the University of Georgia where the experiment and sampling was conducted in an 8°C cold room. Water was stored for one month at 8°C prior to the experiment.

Water-accommodated fractions

To produce the WAF, the dispersant-only solution, and CEWAFs, seawater was 0.2 µm-filtered and pasteurized (2 h at 65°C). WAF was prepared with 0.85 L of sterile seawater amended with 0.15 L Louisiana sweet crude oil (Macondo surrogate oil from the Marlin

Platform Dorado provided by BP). Dispersant-only solutions were comprised of 0.85 L of sterile seawater and 0.015 L of Corexit 9500. CEWAFs were prepared with 0.85 L of sterile seawater amended with 0.15 L Macondo surrogate oil and 0.015 L of Corexit 9500. Sterile seawater amended with oil and/or dispersant was mixed at 600 rpm (magnetic stirrer, Fisher Scientific Isotemp; Thermo Fisher Scientific Inc., Waltham, MA, USA) for 48 h at RT in the dark in clean 1 L glass bottles (furnace heat-treated; 500°C for 4 h) with teflon-lined caps (acid-rinsed, Milli-Q rinsed, and dried). The fluid mixture was allowed to settle for 1 h and the aqueous phase was sub-sampled into clean glass bottles (combusted at 500°C for 4 h), avoiding inclusion of the oil or dispersant phases. WAF, CEWAF and dispersant-only solution were prepared 3-5 days before initiation of the experiment, examined for potential cell contamination via DAPI staining, and stored at 4°C until usage. Nutrient treatments were amended with trace metals (1/1000 vol/vol of 1000× trace metal solution; 16) and nutrients (10 µM ammonium chloride, 10 µM potassium nitrate and 1 µM potassium phosphate, final concentrations, respectively). The effective dilution of the dispersant in seawater (dispersant to seawater ratio, v/v) was 1:60,000 in the dispersant only treatment, while the dispersant to seawater ratio was 1:30,000 v/v in the CEWAF (±nutrients) setups.

Setup and sampling of microcosms

Establishment and sampling of microcosms was carried out at 8°C. First, the entire volume (160 L) of seawater was mixed carefully in a clean (soaked in 10% HCl for 24 h, Milli-Q rinsed, and dried) 200 L HDPE-tank and then dispensed into clean, combusted (500ºC for 4 h) 2 L glass bottles with teflon-lined caps (acid-rinsed, Milli-Q rinsed, and dried). Next, 0.4 L of sterile WAF, dispersant-only, or CEWAF (±nutrients) was added to 1.4 L seawater. To achieve comparable addition of dissolved organic carbon across treatments, the prepared solutions were diluted with an appropriate volume of sterile seawater (0.2 µm-filtered and pasteurized for 2 h at 65°C). Dispersant was much more soluble in water than oil; to generate 0.4 L of diluted solutions, only 1.56 ml of original dispersant-only solution or 3.26 ml of CEWAF (±nutrients) was added. For WAF, 0.4 L of undiluted WAF was added. The biotic control (no addition) and abiotic control (0.2 µm-filtered and pasteurized for 2 h at 65°C) were prepared contemporaneously and were comprised of 1.4 L seawater plus 0.4 L of sterile seawater (0.2 µm-filtered and pasteurized for 2 h at 65°C).

Microcosms were established in triplicates and maintained at 8°C on a roller table (Fig. S2) in the dark at a rotation speed of 15 rpm. All treatments except CEWAF+nutrients were sampled at five different points: T_0 after 0 days, T_1 after 1 week, T_2 after 2 ½ weeks,

T_3 after 4 weeks and T_4 after 6 weeks. The CEWAF+nutrients treatment was sampled at T_0, T_1 and T_4 only. Three replicates were sacrificed at each sampling point for WAF, dispersant-only, and CEWAF (±nutrients) microcosms, respectively. For the abiotic and biotic controls, three replicates were sacrificed at T_0 and T_4. For intermediate time points (T_1 to T_3) the same biological triplicate bottles were sub-sampled. At each time point, sampling of the microcosms was performed by removing aliquots for each analysis described below in the following order: (DNA, oxygen, pH, salinity, DIC, NH_4, nutrients [NO_2/NO_3, PO_4, DOC, TDN, TDP], total cell counts, Corexit surfactant, ^{3}H-leucine incorporation, ^{14}C-hydrocarbon oxidation, enzyme activities, hydrocarbons, DOM), summarized in Supplementary Table 3 and Supplementary Table 4. Upon sampling, each bottle was gently inverted several times to distribute particles evenly (macroscopically visible particles were disrupted) and subsamples taken for the analysis described below.

Total cell counts

Samples for total cell counts were fixed with 3.7% formaldehyde for 1 h at RT and stored at -20°C. The volume filtered was optimized for each time point and treatment, resulting in 30-100 cells per grid. Counts were performed with an epifluorescence microscope (Olympus BX40) after staining with 4′,6-Diamidin-2-phenylindol (DAPI; 1 µg/ml). For each filter, a minimum of 10 grids was randomly counted.

CARD-FISH

In situ hybridization with horseradish peroxidase (HRP)-labeled probes followed by fluorescently labeled tyramide signal amplification (catalyzed reporter deposition) was carried out (17) with modifications described previously (18). Hybridized samples were analyzed with an epifluorescence microscope (Axioplan Imager 2; Carl Zeiss, Jena, Germany) and a confocal laser-scanning microscope (LSM 700; Carl Zeiss, Jena, Germany). Dual CARD-FISH hybridization was applied using two different tyramides (Alexa488, Aexa594) (18). Probes (biomers.net; Ulm, Germany), coverage, and formamide concentrations are given in Supplementary Table 5 (19-22).

Extraction of genomic DNA

DNA was extracted according to (23) with the following modifications. Cut sterivex filters were placed in 2 ml tubes. 1.8 ml extraction buffer was added to the filter strips and the tube was vortexed for 2 min at high speed before freeze-thaw cycles. Then, 60 µl Sodium

dodecyl sulfate (SDS; 20%), 20 µl proteinase K (10 mg/ml) and 200 µl lysozyme (50 mg/ml) were added to each sample. Samples were incubated, centrifuged and re-extracted according to (23). An equal volume of phenol-chloroform-isoamyl alcohol (25:24:1) was added to each tube of supernatant, the tubes were mixed gently and centrifuged at room temperature (3,000× g; 10 min). DNA was precipitated overnight at room temperature by addition of 0.6× volume of isopropanol to the aqueous phase. The precipitated DNA was centrifuged at room temperature (13,000× g; 45 min) and the supernatant was replaced with 1 ml of 70% cold ethanol. After a final centrifugation (13,000× g; 30 min), the ethanol was removed and the DNA was dried for 15 min in a laminar flow hood. Genomic DNA was resuspended in 60 µl of TE buffer (23) and stored at -80°C.

PCR and 16S rRNA gene amplicon sequencing

We sequenced the 16S rRNA V4-V5 regions on the Illumina MiSeq platform. The 16S V4 and V5 primer information is located in http://1.usa.gov/1wrFncs. We amplified samples in triplicate 33 µL reactions, each composed of 3.3 U Platinum HiFi Taq Polymerase (Invitrogen), 0.2 mM each Purepeak dNTPs (Thermo Fisher Scientific), 3 mM Mg^{2+}, 1× HiFi Buffer, 0.3 µM each fusion primer, and up to 5 ng of genomic DNA. Thermocycling conditions were an initial denaturation of 94°C for 3 min, 30 cycles of 94°C 30 sec, 57˚C 45 sec, and 72°C 1 min, and a final extension at 72°C for 2 min. Triplicate reactions were pooled, visualized on the Caliper LabChip 5K assay (Perkin Elmer), purified with Agencourt AMPure XP beads (Beckman Coulter), and quantitated with a Picogreen assay (Invitrogen). Samples were pooled in equimolar concentration, quantitated (KAPA Biosystems), and sequenced using a 500 cycle V2 chemistry kit on an Illumina MiSeq at the Marine Biological Laboratory in Woods Hole, Massachusetts (Bioproject accession PRJNA253405).

Quality filtering and clustering of the sequences

Samples were demultiplexed on the instrument and using custom Python scripts (https://github.com/meren/illumina-utils). We retained pairs that merged with 3 or fewer mismatches with the higher quality base recovered. We discarded de novo and reference chimeric reads based on the SILVA GOLD database, and clustered OTUs at 97% similarity using UCLUST. We used GAST against a curated SILVA database version 108 for taxonomy assignment (24, 25). We used the ARB software package (26) with the database SSURef111 from ARB SILVA (24) for phylogenetic analysis. Phylogenetic trees of 16S rRNA gene sequences were calculated by the distance-based neighbor-joining method.

Oligotyping analysis

Sequences from OTUs assigned to *Marinobacter* (309 OTUs), *Oceaniserpentilla* (231), *Cycloclasticus* (311), and *Colwellia* (600) were oligotyped. (27) We incorporated components from previous oligotyping of *Oceaniserpentilla*, *Cycloclasticus*, and *Colwellia* (3), to separate oligotypes here. For *Marinobacter*, we oligotyped de novo. All sequences within the taxon of interest were aligned to full-length 16S rRNA gene sequences of the same taxon in the Greengenes database, and were trimmed to consistent start and end positions. Oligotypes were retained: if they appeared in 3 samples in which the taxon was observed, if the oligotype had 2 or more sequences across all samples, if the oligotype was at least 0.1% of all sequences in that taxon in a sample, and if the most abundant unique sequence in the oligotype was at least 0.05% of all sequences in that taxon. These filters assured exclusion of oligotypes from PCR, sequencing, or misalignment errors.

For *Marinobacter*, 227,231 sequences resolved into 2,731 oligotypes using 17 high entropy positions; after filtering, 24 oligotypes representing 206,284 (89.6%) sequences remained. These oligotypes had over 99% identity and 100% coverage to entries in NCBI's nr/nt database.

For *Oceaniserpentilla*, 278,765 sequences were categorized into 30 oligotypes representing 250,262 (89.8%) sequences after filtering. In the overlap between this study's data and the previous oligotyping (3), 3 high-entropy positions were mutual to both oligotyping efforts. These oligotypes had over 99% identity and 100% coverage to entries in NCBI's nr/nt database.

For *Colwellia*, 356,354 sequences resolved into 24 oligotypes representing 316,206 (88.7%) sequences after filtering. Two high-entropy positions from the previous oligotyping were also used in this effort. These oligotypes had over 99% identity and 100% coverage to entries in NCBI's nr/nt database.

For *Cycloclasticus*, 328,913 sequences resolved into 31 oligotypes representing 298,008 (90.6% of original input) sequences. Four high-entropy positions carried over from the earlier study. These oligotypes had over 98% identity and 100% coverage to entries in NCBI's nr/nt database.

DOC, DIC and nutrient analysis

Ammonium (NH_4^+) samples were filtered (0.2 µm), stored at 4ºC, and analyzed after 1-2 days using the indo-phenol colorimetric method (28). Nutrient samples (NO_x^- = nitrate (NO_3^-) + nitrite (NO_2^-), NO_2^-, phosphate (HPO_4^{3-})), dissolved organic carbon (DOC), and

total dissolved nitrogen (TDN) were collected, 0.2 µm-filtered, stored frozen, and analyzed as described previously (29). Dissolved inorganic carbon (DIC) samples were 0.2 µm-filtered, injected with syringes into He-purged headspace vials, which were capped with rubber septa and crimp sealed prior to sampling. Overpressure was released with a second syringe while injecting the sample. Dissolved inorganic carbon was quantified using gas chromatography (methanizer followed by flame ionization detection). Dissolved organic nitrogen (DON) was calculated as DON = total dissolved nitrogen (TDN) – NO_x^- + NH_4^+.

Hydrocarbon analysis using GC-MS

To determine hydrocarbon concentrations, 200 ml of hexane:dichloromethane (1:1, v/v) was added to a pre-cleaned separation funnel containing 500 ml sample and extracted by vigourous shaking for ~10 min. The organic phase was removed and the aqueous phase re-extracted twice. Combined extracts were first concentrated in a RapidVap (Caliper) to about 5 ml, then further to 1 ml using a stream of high purity nitrogen. Hydrocarbons (*n*-alkanes, naphthalene, phenanthrene) were identified and quantified using a Gas Chromatography/Mass Selective Detector (GC/MSD; Agilent 7890GC/5975MSD) as described previously (30). Briefly, a capillary column coated with DB-5 (J & W Scientific, 30 m x 0.25 mm, 0.25 µm film thickness) was used and helium was the carrier gas. Compound identification was based on individual mass spectra and retention times in comparison to library data and to authentic standards that were injected and analyzed under the same conditions. Compound quantification was made by calibration curves of external standards: *n*-octadecane (for < C_{20} *n*-alkanes), *n*-octacosane (for ≥ C_{21} *n*-alkanes), phenanthrene (for naphthalene and phenanthrene). A procedural blank was run in sequence and no significant background interferences were noted. TPH were quantified as resolved peaks plus UCM, minus resolved peaks not found in the Marlin crude oil such as LMW fatty acids.

Excitation – Emission Spectra

A Perkin Elmer LS50 spectrofluorometer was used to measure the excitation emission matrix spectroscopic analysis (EEMS) of the total hydrocarbon extracts using a pre-cleaned quartz cuvette. Spectra were recorded by scanning emission wavelengths from 300-400 nm for each excitation wavelength from 200-240 nm at 5-nm increments. The excitation-emission wavelengths were selected based on the EEMS spectra of a Louisiana sweet crude oil standard (Macondo surrogate oil) and of a naphthalene standard. The spectra of

the oil and naphthalene were obtained by scanning emission wavelengths from 250-550 nm for each excitation wavelength from 200-500 nm at 5-nm increments. Estimates of total oil equivalents and naphthalene content were based on the EEMs maximum intensity peak measured at the optimal excitation-emission wavelength combination for oil and naphthalene standards, respectively.

Dissolved organic matter analysis

Aliquots of each bottle (ca. 200 ml) were filtered (pre-combusted Whatman GF/F) and the filtrates were acidified to pH 2 with HCl. Dissolved organic matter (DOM) was solid phase extracted (SPE) (31) using PPL cartridges (Agilent Bond Elut, 200 mg) and eluted with methanol. Extraction efficiencies (based on organic carbon yield) were 20-30% in the dispersant-amended treatments and 65-70%, in the oil-only and seawater-only treatments. The SPE-DOM molecular composition was analyzed using a 15 Tesla Solarix Fourier-transform ion cyclotron resonance mass spectrometer (FT-ICR-MS) (Bruker Daltonics) with an electrospray ionization (ESI) source run in negative mode (32). Negative ionization was chosen because DOSS and EHSS are anionic compounds that are readily analyzable in this mode (1, 33, 34). The detected compounds had molecular masses <850 Da. Instrument settings and DOM molecular formulae assignment procedures were described previously (32). Molecular formulae were unambiguously assigned to peaks with signal-to-noise ratios >4 as described by Koch et al. (35) with a mass tolerance <0.5 ppm and using stable carbon isotope confirmation. Normalized peak heights (relative to the sum of peak heights of all identified molecular formulae per sample) were used to assess changes in the DOM molecular composition in the incubations with changes being considered significant if p <0.01 (two-sided paired Student's t-test, comparing triplicates, n = 3) of T_0 with T_4. For statistical testing we only considered the common 1205 molecular formulae that were detected in all T_0 samples of the oil-only and oil-dispersants treatments. Applying this approach to the abiotic control samples proved that it was robust as no significant changes in the molecular DOM composition were detected when comparing T_0 to T_4. A second approach was applied to address how dispersant amendment changed the relative proportion of S-containing compounds in the DOM. In this analysis, a compound was considered to be produced (degraded) when it was absent (present) at the initial time point (T_0) but present (absent) after six weeks (T_4) of incubation. Molecular formulae were considered only when they were detected in at least two of the three replicates of the treatments.

Corexit analysis

Liquid chromatography tandem mass spectrometry (LC–MS/MS) enabled quantitative detection of distinct dispersant compounds: the anionic surfactant DOSS and the nonionic surfactants Span 80, Tween 80, Tween 85, as well as, α/β-ethyhexylsulfosuccinate (EHSS), the hydrolysis products of DOSS (34, 36). Microcosm chambers were sampled and immediately diluted to 75 percent with isopropanol (seawater:isopropanol, 75:25), and stored at -20°C. Bottles were then decanted and rinsed with 20 ml MeOH. The MeOH rinsate was collected and saved (at -20°C) for Corexit surfactant analysis. Samples were shipped overnight on dry ice to Oregon State University and stored at -20°C until analysis. Samples were diluted 0 to 100-fold and quantitative analysis of the surfactant components of Corexit was performed (34) with minor modification.

Calibration curves consisted of at least 5 standards and required a correlation coefficient of 0.99 or greater to be used for quantification. All calibration curves were 1 /× weighted, and standards whose calculated concentrations were beyond 20% of the intended concentration were removed from the calibration curve calculation. Calibration curves spanned from the lower limit of quantification (LLOQ) to the upper limit of quantification (ULOQ): for DOSS (0.2-25 μg L^{-1}), α-/β-EHSS (0.2-23 μg L^{-1}), Span 80 (60-300 μg L^{-1}), Tween 80 (60-300 μg L^{-1}), and Tween 85 (60-300 μg L^{-1}). Each calibration standard was spiked to give a final concentration of 500 ng L^{-1} $^{13}C_4$–DOSS and 500 ng L^{-1} $^{13}C_4$–α-EHSS. Blank and check standards (34) were used for quality control purposes. Standards for DOSS and EHSS fell within 20% of the spiked concentration and the non-ionic Corexit surfactants fell within 35% of the spiked concentration. All blank QC fell below the limit of detection.

A robust whole method error term (37) was calculated using the following method: 250 ml of instant ocean IPA was spiked with standards to yield a concentration of 500 ng L^{-1} DOSS and EHSS and 80,000 ng L^{-1} non-ionics. This solution was divided between 50 ml aliquots and stored at -20°C until analysis. These aliquots were analyzed (5 ml, n = 4) on 4 different days to calculate an accuracy term that accounts for in day and between day variability. On each day of analysis, standards (all analytes) and internal standards (ionics only) were made fresh and used to calibrate the instrument. The whole method error was: DOSS (±7.3%), EHSS (±11.2%), Tween 80 (±24.0%), Tween 85 (±23.3%), and Span 80 (±76%).

^{3}H-leucine incorporation

Rates of bacterial protein synthesis were determined using ^{3}H-leucine incorporation (38) in the triplicate samples for each treatment. For each triplicate series, a killed control (mixed sample of triplicates) and a replicate (n = 2; random sample) were analyzed. Subsamples were stored overnight at 4°C before the ^{3}H-leucine incorporation assays were conducted at 8ºC. A final concentration of 6-9 nmol L^{-1} (T_0-T_3: 6 nmol L^{-1}, T_4: 9 nmol L^{-1}) ^{3}H-leucine (specific activity of 60 Ci $mmol^{-1}$) was achieved. 1.5 ml of sample were incubated for 1-6 h (T_0: 6 h, T_1: 1.5 h, T_2-T_4: 1 h) at 8°C. Killed controls were amended with trichloroacetic acid (TCA; final concentration of 6.25% v/v TCA) prior to incubations and the incubations were terminated using the same procedure (final concentration of 6.25% v/v TCA). Subsequently, the samples were washed with 5% w/v TCA and then with 80% ethanol, according to Ref. 39 with minor modifications: centrifugation of 30 min for first pelleting and the pellet was not resuspended afterwards. Finally, the dried pellets were resuspended in 1 ml Scintillation Cocktail (Scintisafe Gel; Fisher) and analyzed immediately using a Beckman LS 6500 multi-purpose scintillation counter. Rates of bacterial production were calculated according to Kirchman (39).

^{14}C-hydrocarbon oxidation rates

We selected two hydrocarbon classes, alkanes and PAHs, for direct determination of biodegradation rates because alkanes and PAHs are chemically distinct and PAHs are inherently toxic and mutagenic (40). Rates of ^{14}C-hydrocarbon oxidation were determined in triplicates. For each series, a killed control (mixed sample of triplicates) and a replicate (n = 2; random sample) were analyzed. Subsamples were stored overnight at 4°C before the ^{14}C-hydrocarbon oxidation assays were conducted. 8 ml of sample was incubated in headspace free scintillation vials with teflon-coated stoppers and caps. [1-^{14}C]-hexadecane (American Radiolabel Chemicals; ARC) and [1-^{14}C]-naphthalene (ARC) were diluted in ethanol. Hexane was evaporated from the [1-^{14}C]-hexadecane prior to ethanol dissolution using a slow argon stream. Tracer volumes per 8 ml samples were 10-20 µl to prevent ethanol inhibition (final ethanol concentration ≤ 0.2%; units of radioactivity per sample = 1.4×10^{3} Bq). Killed controls were transferred to a 15 ml tube and amended with 1 M NaOH solution (final concentration of 0.2 mM NaOH) prior to tracer addition and activity was halted with the same procedure (final concentration of 0.2 mM NaOH). Samples were incubated for 12-24 h (T_0 and T_1: 24 h, T_2-T_4: 12 h) at 8°C.

To remove tracer [1-^{14}C]-hydrocarbons, 1 g of activated carbon (Sigma Aldrich) was added to the samples in the 15 ml tubes and the samples were mixed (shaker table, 100 rpm) horizontally for 5 h to allow absorption of the hydrocarbons to the activated carbon. Afterwards, microbial [1-^{14}C]-hydrocarbon degradation was measured via the accumulation of oxidation product (^{14}C-DIC), which was released by acid digestion: samples and activated carbon were transferred to a 250-ml flask. Sample tubes were rinsed with Milli-Q to remove residual sample and activated carbon. The rinse water was transferred to the flask of the appropriate sample, respectively. Each flask was sealed with a black rubber stopper fitted with a holder for 7-ml glass scintillation vials. Scintillation vials contained ¼ of a glass fiber filter (Whatman) and 2 ml of Carbo-Sorb (Perkin Elmer). Samples (~50 ml including rinse water) were acidified to pH 1 by the addition of 5 ml phosphoric acid (H_3PO_4 ≥85 wt. % in H_2O). Then, samples were shaken at room temperature for 6 h (100 rpm) to release and trap ^{14}C-CO_2. After sample distillation, 4.5 ml of Scintillation Cocktail (Scintisafe Gel; Fisher) was added to the scintillation vial and radioactivity was quantified using a Beckman 6500 liquid scintillation counter. The rate of hydrocarbon oxidation was calculated using: hydrocarbon oxidation rate = rate constant (per hour) × µg/L concentration × fractionation factor.

Enzyme activities

Potential enzyme activities were measured using fluorogenic substrate analogs for lipase (4-MUF-butyrate; final concentration: 100 µM), β-glucosidase (4-MUF-β-D-glucopyranoside; 200 µM), and peptidase (L-leucine-MCA hydrochloride; 400 µM; all from Sigma-Aldrich) to determine enzymatic degradation of lipids, carbohydrates, and peptides, respectively (41). Shortly after sampling, water was added to disposable methacrylate cuvettes containing individual fluorogenic substrate analogs at saturation levels (total incubation volume: 3 ml). Fluorescence was measured immediately afterwards in a clean cuvette, containing 1 ml of the water-substrate solution and 1 ml of borate buffer (20 nM; pH 9.2), using a Turner Biosystems TBS-380 fluorometer, with excitation/emission channels set to “UV” (365 nm excitation, 440-470 nm emission). All cuvettes were incubated in the dark at 8°C, and fluorescence was measured two more times over the course of 24 hours. Fluorescence changes were calibrated using standard solutions of 4-methylumbelliferone and 4-methylcoumarin in pasteurized control water, and used to calculate hydrolysis rates (expressed in nmol L^{-1} h^{-1}). Changes in fluorescence measured in abiotic controls were always minimal for β-glucosidase and peptidase. Abiotic hydrolysis of MUF-butyrate in AC-

bottles was detectable at every sampling time, but was considerably lower compared to the live treatments.

Transparent exopolymeric particle analysis and documentation of macroscopic particles

Transparent exopolymeric particles (TEPs) were quantified colorimetrically in 3 replicates per bottle by filtration onto 0.4 µm PC filters (Poretics) and subsequent staining with Alcian Blue (42). TEP was only measured in bottles without Corexit, because Corexit interferes with the stain. Values in samples with oil were corrected for interference from oil. The dye solution was calibrated using Gum Xanthan and TEP are expressed as Gum Xanthan equivalents per liter (GXeq L^{-1}). TEP determinations are semi-quantitative as the chemical composition of TEP varies, is complex and unknown, and variation between replicate measurements are high. The methodological coefficient of variation (standard deviation divided by average) between replicate measurements within each container in our experiments was usually ≤10% and was always ≤20%. Standard deviations were calculated from replicate containers.

Macroscopically visible particles were monitored every 2-3 days. Pictures of marine snow formations were taken with an SLR camera (Canon 500 EOS equipped with a 18-55 mm lens).

Statistical analysis

Correspondence analysis (CA), a multivariate ordination method, was used to determine whether the observed patterns of microbial taxa were associated with specific treatments. The ordination was performed using the vegan package (43) within the R statistical platform (44). Distances between sample and species points in a CA plot indicate the probability of the occurrence of the species in the respective sample (e.g. Ref. 45). CA is useful if the analyzed species show an unimodal relationship within the samples (46).

We evaluated relationships between measured microbiological and geochemical parameters, microbial activity, and oligotype abundances using R (44), and packages vegan (43) and qvalue (47). Spearman's rank correlation coefficient ρ was calculated for each oligotype distribution and environmental parameter. Storey's FDR correction for multiple tests at $q < 0.01$ was used to retain significant ($p < 0.02$) correlations. Student's t-test was used to determine the significance of the differences of cell counts, nitrate,

bacterial production as well as hexadecane and naphthalene oxidation rates between the different treatments.

Hydrocarbon turnover in oil-contaminated surface seawater samples

Surface seawater samples were collected on 9 Oct 2014 near the site where the Taylor Energy Production Platform sank in 2004 following Hurricane Ivan. A chartered vessel was used to sample at four sites: site 1, near the source of the leaking sunken platform, 28.9371˚ N, 88.982˚ W; site 2, at confluence of oil slick and Mississippi river plume (i.e., the mousse site; 28.91834˚ N, 89.0184˚ W) and site 3 (28.93319˚ N, 88.9969˚ W) and site 4 (28.93243˚ N, 89.0093˚ W), which were in between the source and plume confluence sites. Water samples were collected in 10 L cubitainers and kept at 4˚C until arrival in the laboratory. From sites 2 and 4, sufficient water was available to test effects of dispersant addition on hydrocarbon turnover; at sites 1 and 3, we were only able to determine biodegradation rates in the absence of dispersant. For the dispersant amendments, Corexit 9500 was diluted 1:10 into filter-sterilized seawater. Then 100 µL of the dispersant-seawater mixture was added to 1 L of surface seawater into a 2 L combusted glass bottle (with teflon lined cap), leading to a final concentration of 10 µL Corexit per 1 L seawater, or a 1 in 100,000 dilution. Samples were incubated for 24 hours at 20˚C (or RT). Then, hydrocarbon turnover was determined applying the improved radiotracer assays (see above). Hydrocarbons were extracted and concentrations determined as described in the hydrocarbon analysis section (GC-MS).

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Supplementing Figures and Tables

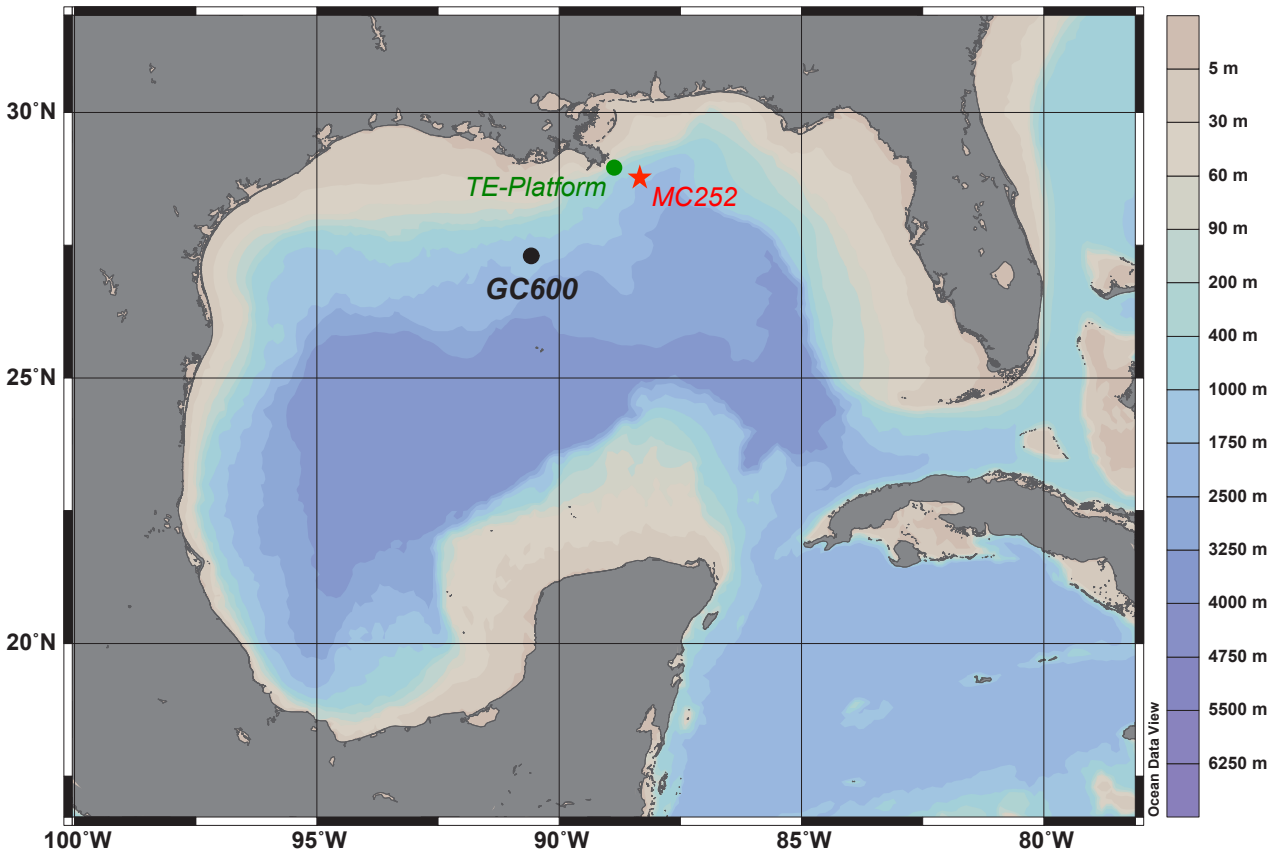


Fig. S1. Location of sampling sites at GC600 (black circle) and the Taylor Energy platform (green circle). Green Canyon block 600 (GC600) in the northern Gulf of Mexico is a natural gas and oil seepage. The GC600 area is 260 kilometers to the southwest of the DWH spill site MC252 (red star) and was therefore not directly impacted by the DWH oil spill. Deepwater samples obtained from GC600 represent natural pelagic seep communities including microorganisms with hydrocarbon-degrading abilities and, hence, are perfectly suitable to survey the impact of dispersants on hydrocarbon-degrading microbial populations. Surface seawater samples were obtained from the sunken Taylor Energy platform, which has been discharging hydrocarbons into the Gulf since the platform sank in 2004.

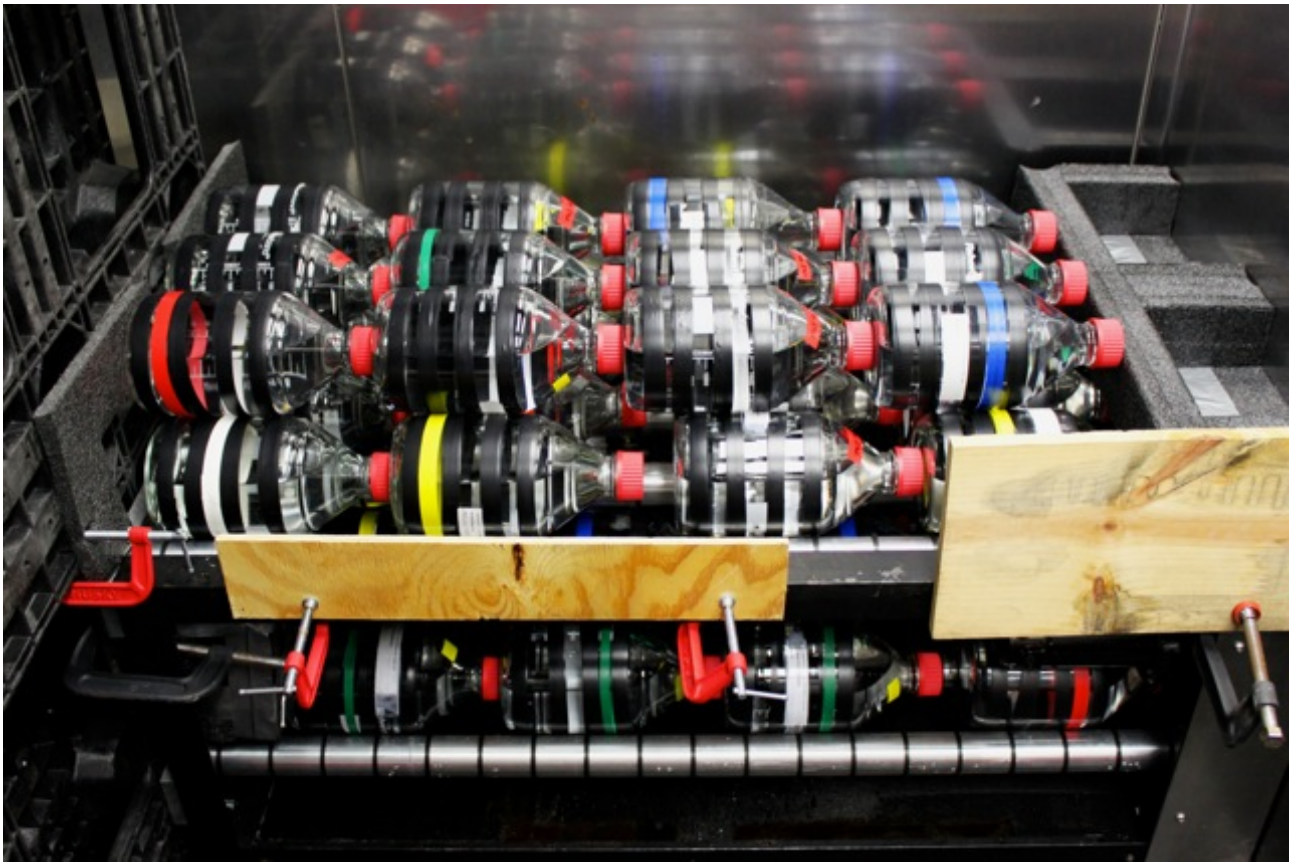


Fig. S2. Photograph of microcosm with deep-seawater incubated on a roller table. Before the microcosm setups, 2-L glass bottles were wrapped with teflon tape to assure better rolling abilities. For the time course of the experiment, bottles were stacked in two layers on the two rolling units of the table and permanently rotated at the same speed (15 rpm).

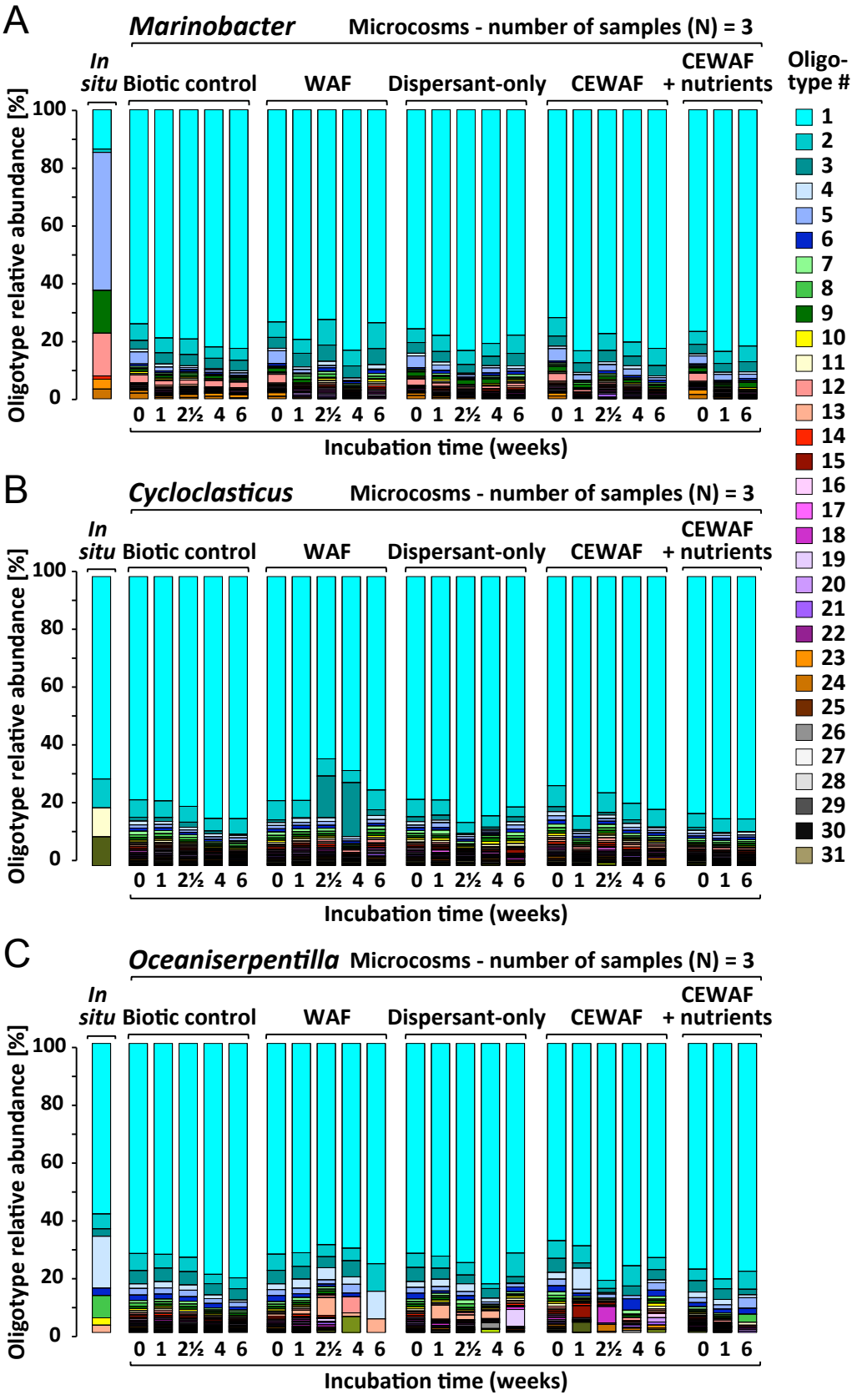
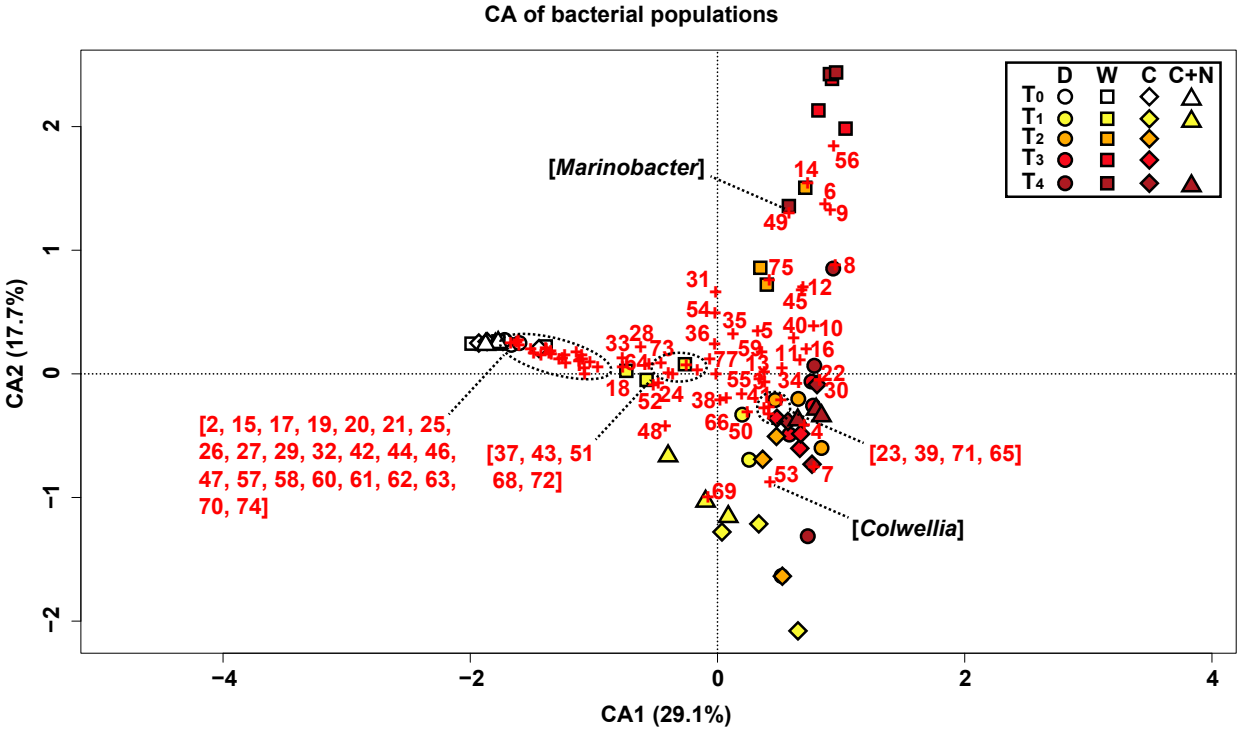


Fig. S3. Different microbial oligotypes respond to dispersants or oil (WAF). Oligotyping enabled the interpretation of 16S rRNA gene sequence diversity at the level of

specific oligotypes. Relative abundance (averaged across biological triplicates) of (A) *Marinobacter*, (B) *Cycloclasticus*, and (C) *Oceanisperpentilla* oligotypes in microcosms, simulating DWH spill-like plumes.



Bacterial populations associated with numbers in CA plot

1	*Acidobacteria*
2	*Actinobacteria*
3	BRC1
4	*Flavobacteriales/Cryomorphaceae/Crocinitomix*
5	*Flavobacteriales/Cryomorphaceae/Owenweeksia*
6	*Flavobacteriales/Flavobacteriaceae/Bizionia*
7	*Flavobacteriales/Flavobacteriaceae/Kordia*
8	*Flavobacteriales/Flavobacteriaceae/Pibocella*
9	*Flavobacteriales/Flavobacteriaceae/Psychroserpens*
10	*Flavobacteriales/Flavobacteriaceae/Ulvibacter*
11	*Flavobacteriales/*Other *Flavobacteriaceae*
12	*Sphingobacteria/Sphingobacteriales/Chitinophagaceae/Balneola*
13	Other *Bacteroidetes*
14	*Caldiserica*
15	*Chlamydiae*
16	*Chlorobi*
17	*Chloroflexi/SAR202*
18	Other *Chloroflexi*
19	*Cyanobacteria*
20	*Deferribacteres/Deferribacteres/Deferribacterales/SAR406*
21	*Other Deferribacteres*
22	*Deinococcus-Thermus*
23	*Fibrobacteres*
24	*Firmicutes*
25	*Fusobacteria*
26	*Gemmatimonadetes*
27	*Lentisphaerae*
28	*Nitrospirae*
29	OD1
30	OP1
31	OP10
32	OP11
33	OP3
34	OP8
35	OP9
36	*Planctomycetes*
37	*Rhizobiales/Phyllobacteriaceae*
38	Other *Rhizobiales*
39	*Rhodobacterales/Rhodobacteraceae/Marinosulfomonas*
40	*Rhodobacterales/Rhodobacteraceae/Phaeobacter*
41	*Rhodobacterales/*Other *Rhodobacteraceae*
42	*Rickettsiales/SAR11/Pelagibacter*
43	*Proteobacteria/*Other *Alphaproteobacteria*
44	*Betaproteobacteria*
45	*Bdellovibrionales/Bdellovibrionaceae*
46	SAR324
47	Other *Deltaproteobacteria*
48	*Epsilonproteobacteria*
49	*Alteromonadales/Alteromonadaceae/Marinobacter*
50	*Alteromonadales/Alteromonadaceae/SAR92*
51	*Alteromonadales/Alteromonadaceae/Teredinibacter*
52	*Alteromonadales/*Other *Alteromonadaceae*
53	*Alteromonadales/Colwelliaceae/Colwellia*
54	*Oceanospirillales/Alcanivoracaceae/Alcanivorax*
55	*Oceanospirillales/Alcanivoracaceae/Kangiella*
56	*Oceanospirillales/Oceanospirillaceae/Amphritea*
57	*Oceanospirillales/Oceanospirillaceae/Balneatrix*
58	*Oceanospirillales/Oceanospirillaceae/Oceaniserpentilla*
59	*Oceanospirillales/Oceanospirillaceae/Pseudospirillum*
60	*Oceanospirillales/*Other *Oceanospirillaceae*
61	*Oceanospirillales/Oleiphilaceae/Oleiphilus*
62	Other *Oceanospirillales*
63	*Salinisphaerales/Salinisphaeraceae*
64	*Thiotrichales/Piscirickettsiaceae/Cycloclasticus*
65	*Thiotrichales/Piscirickettsiaceae/Methylophaga*
66	Other *Gammaproteobacteria*
67	Other *Proteobacteria*
68	*Spirochaetes*
69	TA06
70	TG-1
71	TM6
72	TM7
73	*Tenericutes*
74	*Verrucomicrobia*
75	WS1
76	WS3
77	Other Bacteria

Fig. S4. **Statistical analysis of bacterial populations**. Correspondence Analysis (CA) plot of bacterial populations and microcosm samples of oil and dispersant treatments

[D (dispersant-only) = circle, W (WAF) = square, C (CEWAF) = diamond, C + N (CEWAF+nutrients) = triangle] explaining 46.6% of the data on two axes. The time points when samples were collected are color-coded (T_0 = white, T_1 = yellow, T_2 = orange, T_3 = red, T_4 = dark-red) and the numbers referring to specific bacterial populations are listed below the plot. CA maximizes the correspondence between species scores and sample scores to address whether certain species are abundant in specific samples or treatments, as a measure of their ecological preferences. Bacterial populations located close to each other correspond to populations occurring together in microcosm samples. The distance between a bacterial population point and a sample point approximates the probability of that specific population to be abundant in that particular sample. Numbers of bacterial populations with too-close proximity in the CA plot are listed in parenthesis for better readability. *Marinobacter* and *Colwellia*, which correlated with oil-only or dispersant-amended samples, respectively, are pointed out.

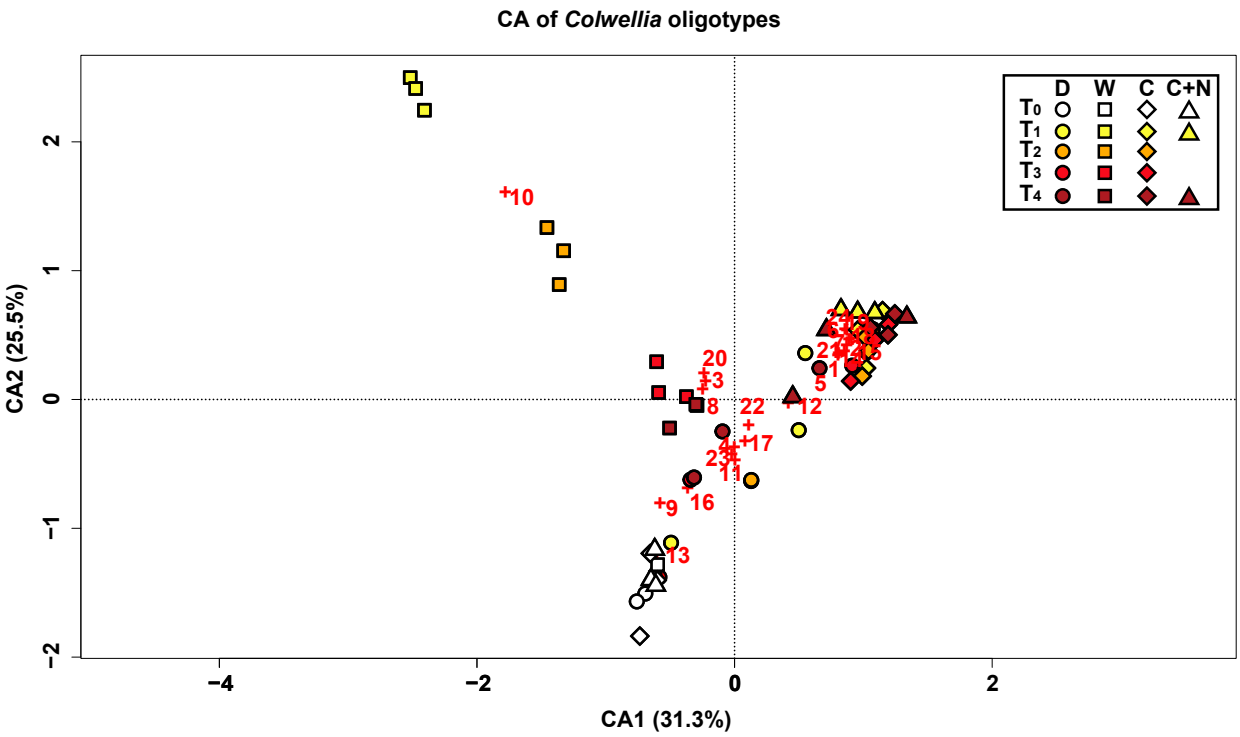


Fig. S5. **Statistical analysis of *Colwellia* populations**. Correspondence Analysis (CA) plot of *Colwellia* oligotypes and microcosm samples of all oil and dispersant treatments [D (dispersant-only) = circle, W (WAF) = square, C (CEWAF) = diamond, C + N (CEWAF+nutrients) = triangle] explaining 56.8% of the data on two axes. The time points of microcosm samples are color-coded (T_0 = white, T_1 = yellow, T_2 = orange, T_3 = red, T_4 = dark-red). CA maximizes the correspondence between species scores and sample scores to address whether certain species are abundant in specific samples or treatments, as a measure of their ecological preferences. Oligotypes located close to each other correspond to oligotypes occurring together in microcosm samples. The distance between an oligotype point and a sample point approximates the probability of that specific oligotype to be abundant in that particular sample.

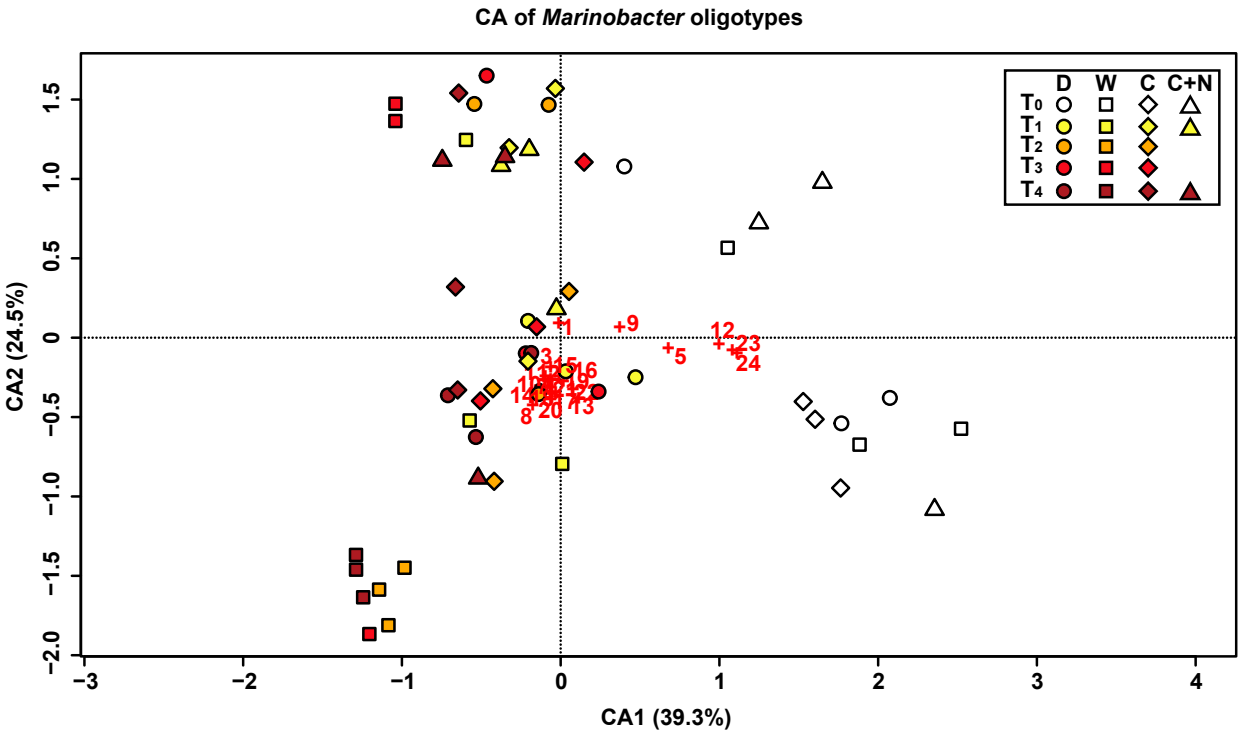


Fig. S6. **Statistical analysis of *Marinobacter* populations**. Correspondence Analysis (CA) plot of *Marinobacter* oligotypes and microcosm samples of all oil and dispersant treatments [D (dispersant-only) = circle, W (WAF) = square, C (CEWAF) = diamond, C + N (CEWAF+nutrients) = triangle] explaining 63.8% of the data on two axes. The time points of microcosm samples are color-coded (T_0 = white, T_1 = yellow, T_2 = orange, T_3 = red, T_4 = dark-red). CA maximizes the correspondence between species scores and sample scores to address whether certain species are abundant in specific samples or treatments, as a measure of their ecological preferences. Oligotypes located close to each other correspond to oligotypes occurring together in microcosm samples. The distance between an oligotype point and a sample point approximates the probability of that specific oligotype to be abundant in that particular sample.

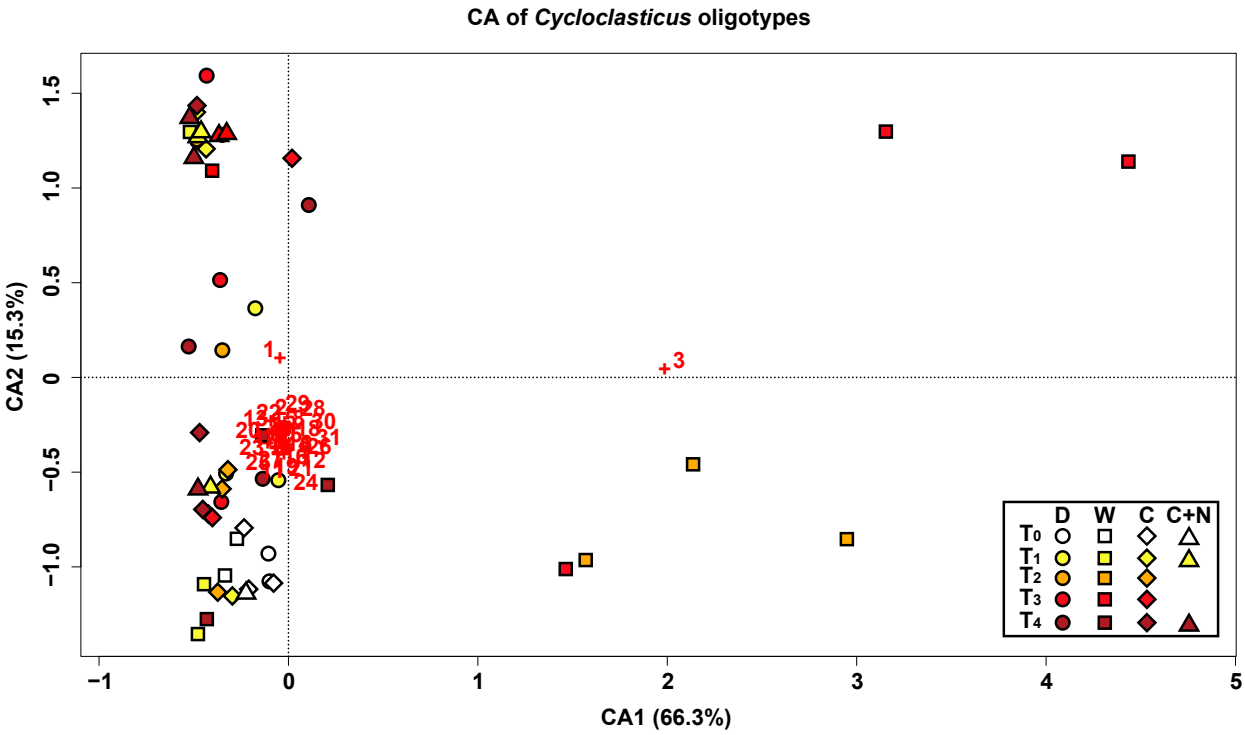


Fig. S7. **Statistical analysis of *Cycloclasticus* populations.** Correspondence Analysis (CA) plot of *Cycloclasticus* oligotypes and microcosm samples of all oil and dispersant treatments [D (dispersant-only) = circle, W (WAF) = square, C (CEWAF) = diamond, C + N (CEWAF+nutrients) = triangle] explaining 63.8% of the data on two axes. The time points of microcosm samples are color-coded (T_0 = white, T_1 = yellow, T_2 = orange, T_3 = red, T_4 = dark-red). CA maximizes the correspondence between species scores and sample scores to address whether certain species are abundant in specific samples or treatments, as a measure of their ecological preferences. Oligotypes located close to each other correspond to oligotypes occurring together in microcosm samples. The distance between an oligotype point and a sample point approximates the probability of that specific oligotype to be abundant in that particular sample.

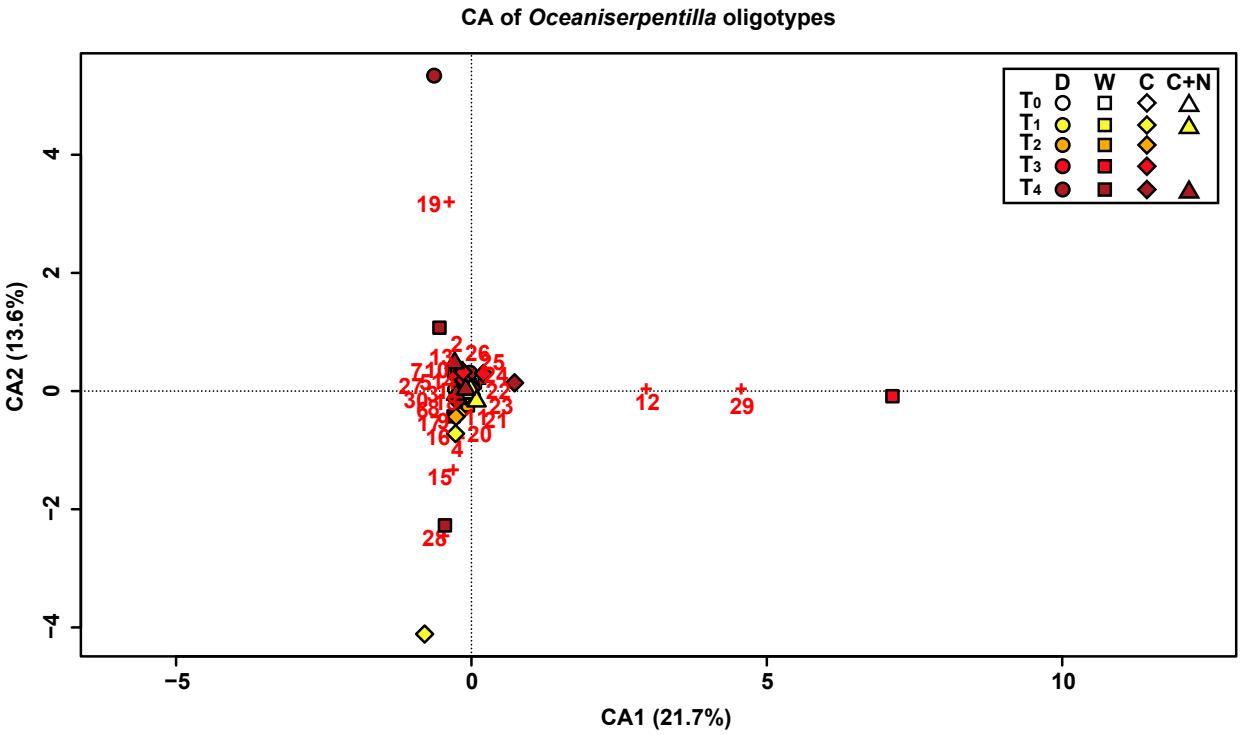


Fig. S8. **Statistical analysis of *Oceaniserpentilla* populations.** Correspondence Analysis (CA) plot of *Oceaniserpentilla* oligotypes and microcosm samples of all oil and dispersant treatments [D (dispersant-only) = circle, W (WAF) = square, C (CEWAF) = diamond, C + N (CEWAF+nutrients) = triangle] explaining 63.8% of the data on two axes. The time points of microcosm samples are color-coded (T_0 = white, T_1 = yellow, T_2 = orange, T_3 = red, T_4 = dark-red). CA maximizes the correspondence between species scores and sample scores to address whether certain species are abundant in specific samples or treatments, as a measure of their ecological preferences. Oligotypes located close to each other correspond to oligotypes occurring together in microcosm samples. The distance between an oligotype point and a sample point approximates the probability of that specific oligotype to be abundant in that particular sample.

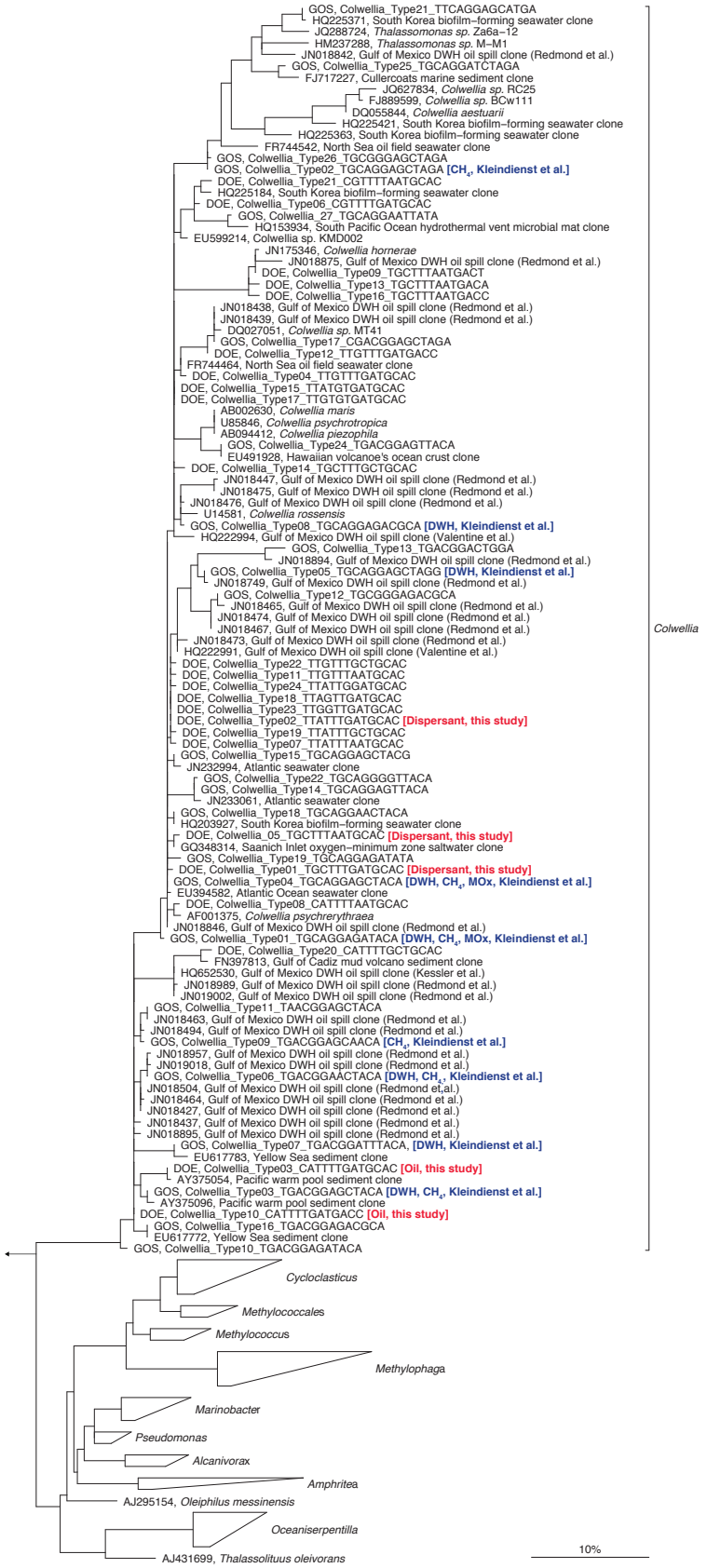


Fig. S9. Phylogenetic relationships of *Colwellia* oligotypes from the microcosms with closely related organisms including spp. detected during the DWH oil spill. The tree

was calculated by the distance-based neighbor-joining method and the bar represents 10% estimated sequence divergence. Oligotypes from the microcosms (dispersant-oil experiments; DOE) are shown in bold font. Furthermore, DOE-oligotypes that significantly correlated with dispersant and/or oil samples are shown in red font and labeled with [Dispersant] and/or [Oil]. Oligotypes detected before, during and/or after the DWH oil spill in Gulf of Mexico deep-sea waters *in situ* (Gulf of Mexico survey; GOS) are illustrated in blue font (3). Dominant GOS-oligotypes are shown in bold and increased GOS-oligotype abundance during the spill [DWH] as well as correlations with methane [CH_4] and methane oxidation [MOx] are indicated.

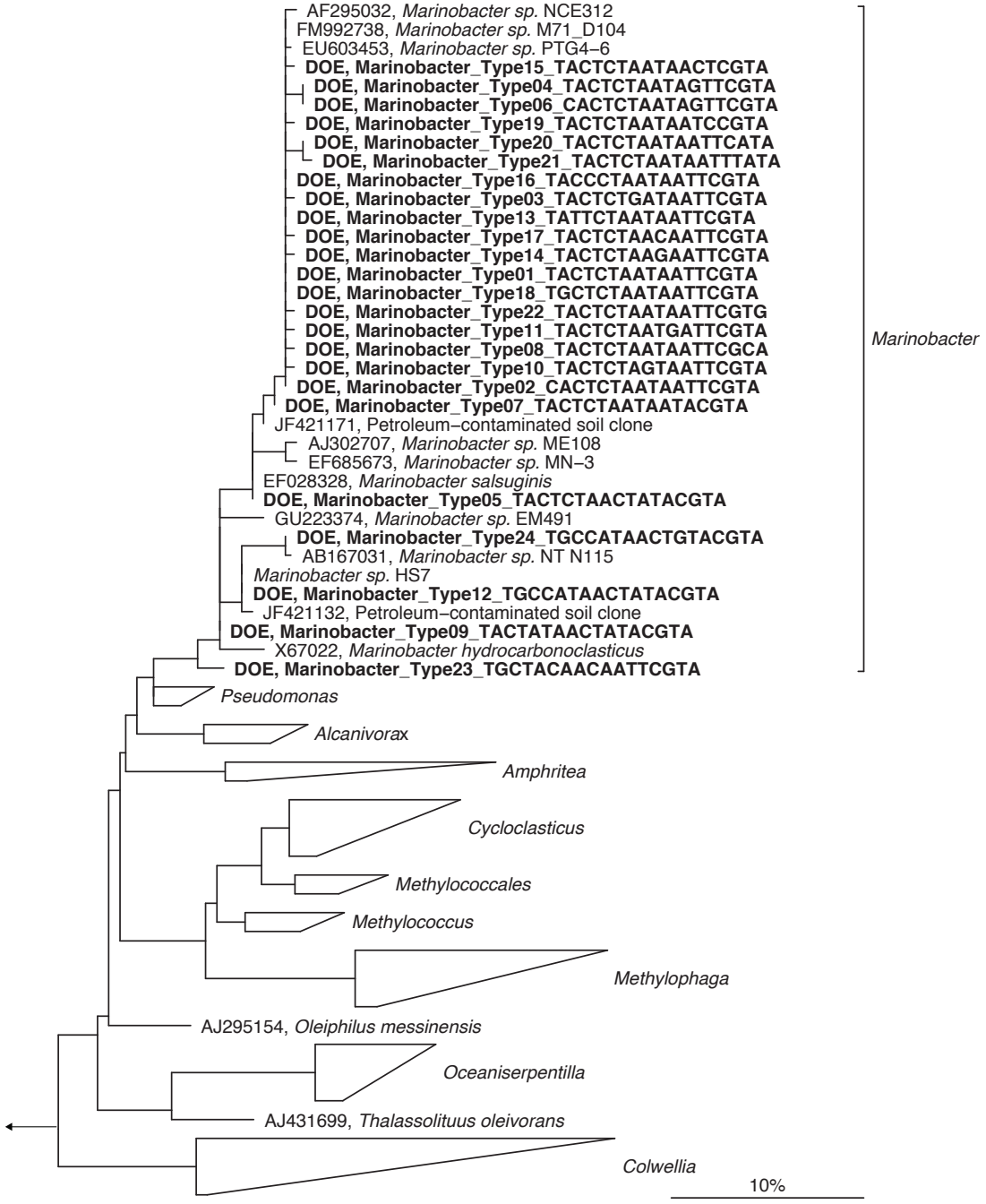


Fig. S10. Phylogenetic relationships of *Marinobaccter* oligotypes from the microcosms with closely related organisms. The tree was calculated by the distance-based neighbor-joining method and the bar represents 10% estimated sequence divergence. Oligotypes from the microcosms (dispersant-oil experiments; DOE) are shown in bold font. *Marinobacter* were not found to be abundant before, during and/or after the DWH oil spill in Gulf of Mexico deep-sea waters *in situ* and, hence, potential spill oligotypes remained undetected (3).

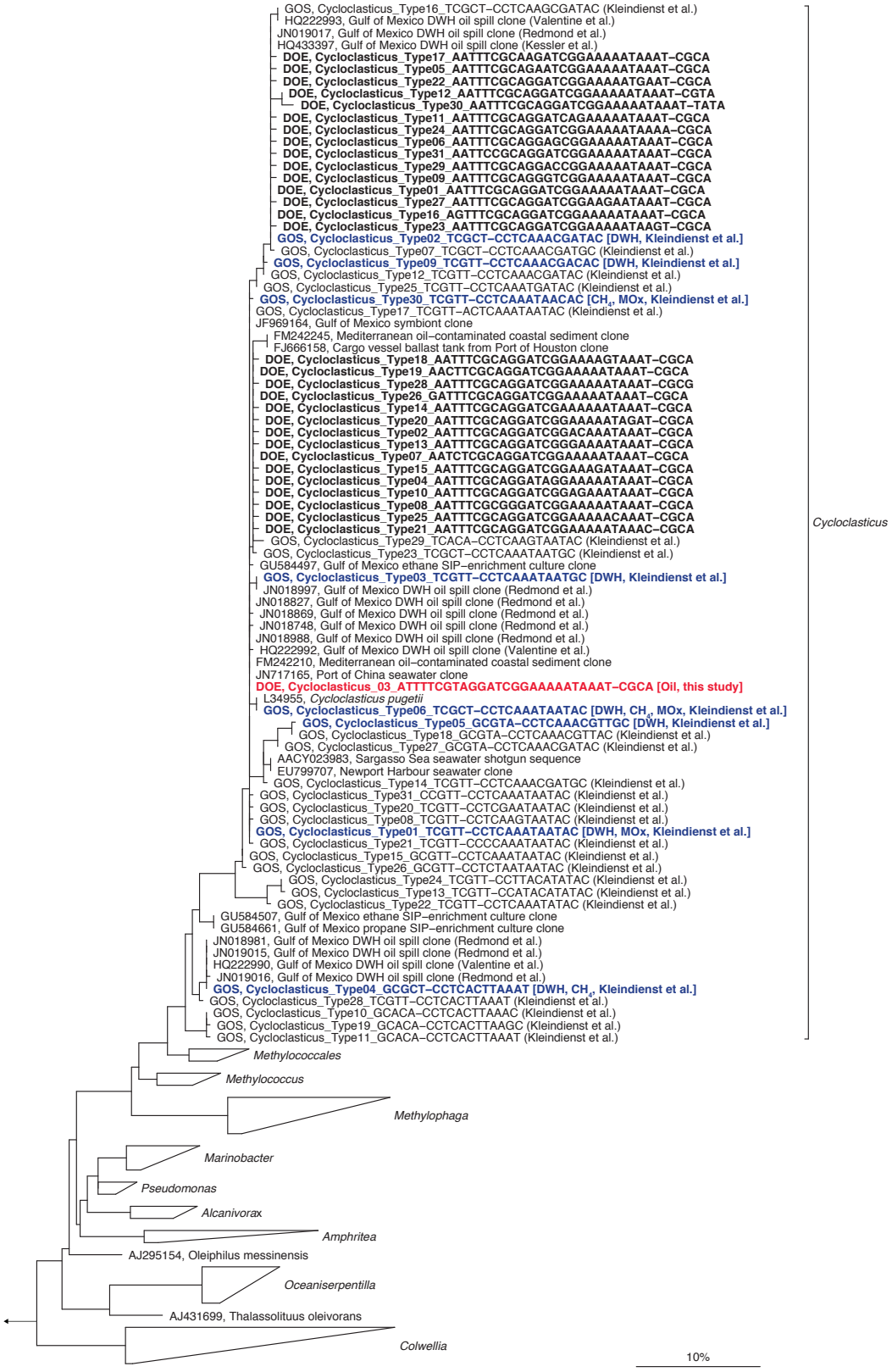


Fig. S11. Phylogenetic relationships of *Cycloclasticus* oligotypes from the microcosms with closely related organisms including spp. detected during the DWH

oil spill. The tree was calculated by the distance-based neighbor-joining method and the bar represents 10% estimated sequence divergence. Oligotypes from the microcosms (dispersant-oil experiments; DOE) are shown in bold font. Furthermore, a DOE-oligotype that significantly correlated with oil samples is shown in red font and labeled with [Oil]. Oligotypes detected before, during and/or after the DWH oil spill in Gulf of Mexico deep-sea waters *in situ* (Gulf of Mexico survey; GOS) are illustrated in blue font (3). Dominant GOS-oligotypes are shown in bold and increased GOS-oligotype abundance during the spill [DWH] as well as correlations with methane [CH_4] and methane oxidation [MOx] are indicated.

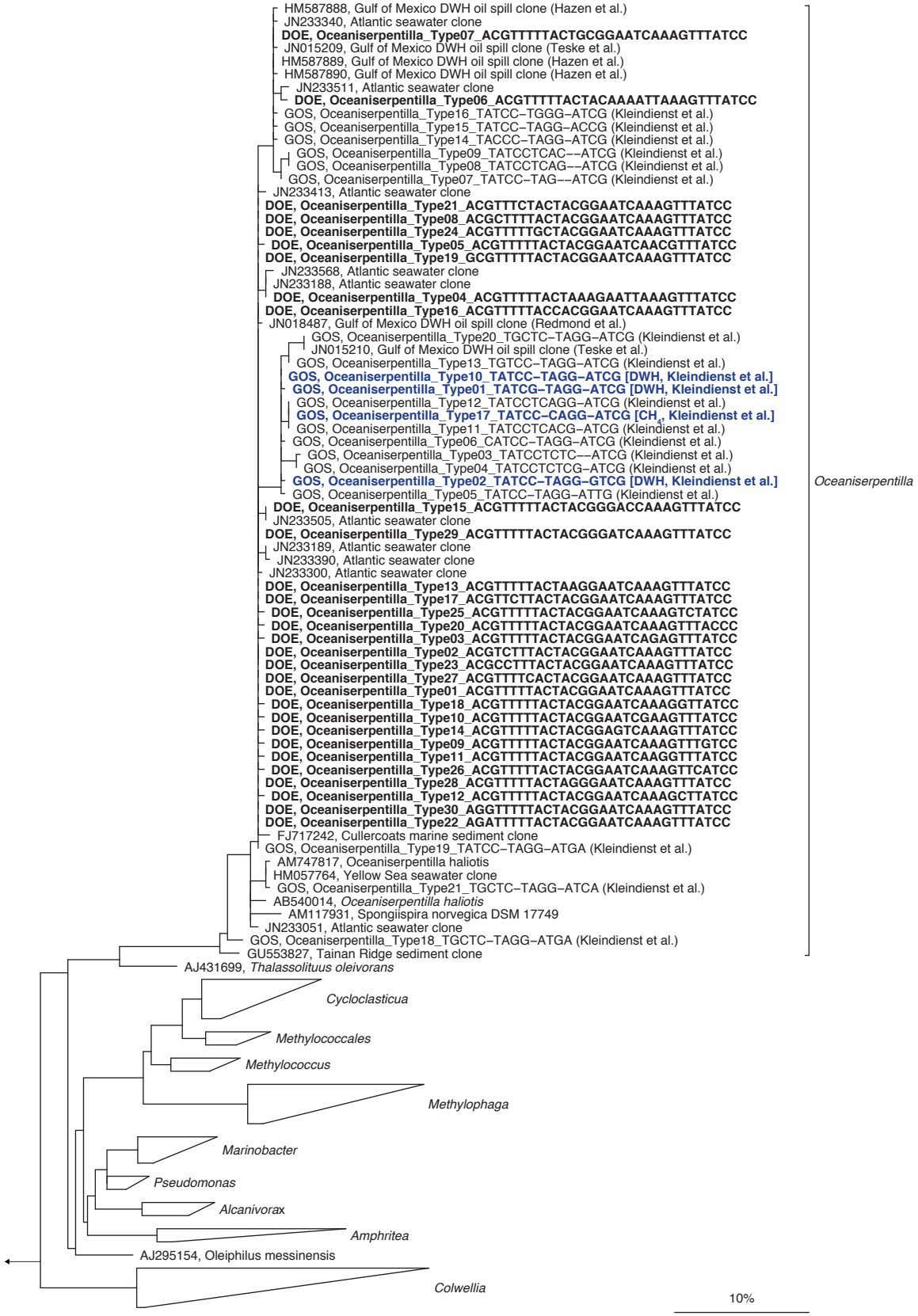


Fig. S12. Phylogenetic relationships of *Oceaniserpentilla* oligotypes from the microcosms with closely related organisms including spp. detected during the DWH

oil spill. The tree was calculated by the distance-based neighbor-joining method and the bar represents 10% estimated sequence divergence. Oligotypes from the microcosms (dispersant-oil experiments; DOE) are shown in bold font. Oligotypes detected before, during and/or after the DWH oil spill in Gulf of Mexico deep-sea waters *in situ* (Gulf of Mexico survey; GOS) are illustrated in blue font (3). Dominant GOS-oligotypes are shown in bold and increased GOS-oligotype abundance during the spill [DWH] as well as correlations with methane [CH_4] are indicated.

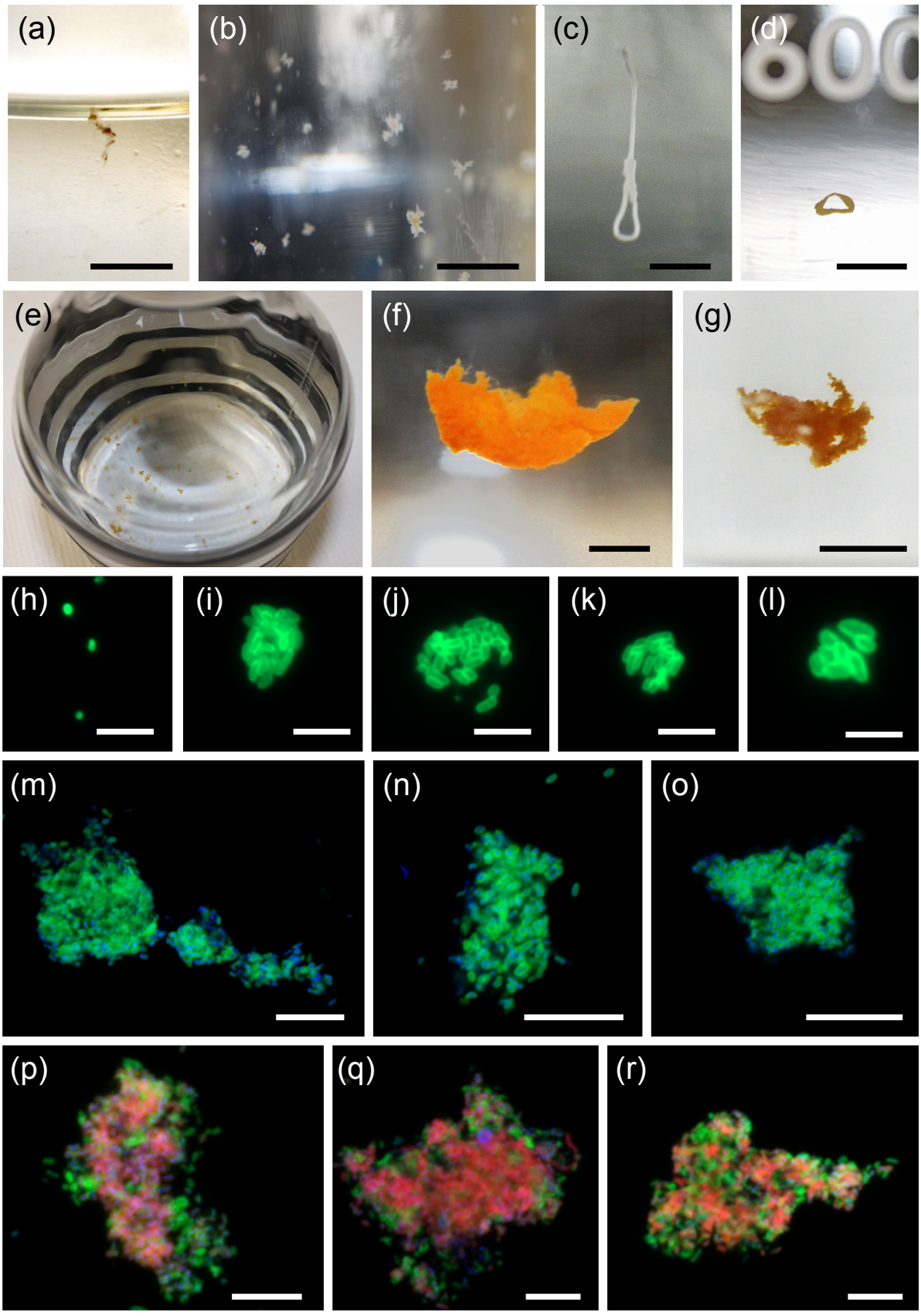


Fig. S13. Photographs of representative macroscopically visible particles (>0.5 mm) that formed during the experiment in the different treatments (a-g) and

epifluorescence micrographs (h-l) as well as confocal laser scanning micrographs (m-r) of bacterial micro-aggregates (<500 µm) visualized by CARD-FISH. Scale bars = 0.5 cm in photographs (a-d, f, g), 5 µm in epifluorescence micrographs (h-l), and 10 µm in confocal laser scanning micrographs (m-r).

In contrast to controls, where no macroscopical aggregates formed during the experiment, stringy, mucus-rich and fractal looking, colored macroscopical particles formed abundantly in WAF treatments (a; after 15 days), with their abundance increasing continuously over time (b; after 8 weeks). A few white long (cm) filaments formed in dispersant-only treatments (c after 15 days of incubation). Macroscopic particles in the CEWAF treatment were rare, small, colored. Formation of macroscopic particles was fastest and particles largest in the CEWAF+nutrients treatment: bird eye view of the whole bottle of the CEWAF+nutrients treatment, showing numerous macroscopic particles (after 9 days; e) and close-up of large, single particles from the same treatment (CEWAF+nutrients) after 11 days (f) and 15 days (g). During the six-week experiment the number of aggregates increased in all three treatments containing oil (WAF, CEWAF ±nutrients) but comparably the particles formed slower and remained smaller in both treatments without added nutrients (WAF, CEWAF).

Fluorescence microscopy demonstrated the formation of microbial aggregates or clusters in all treatments that contained macroscopical particles (k = WAF, l = dispersant-only, m = CEWAF, n-t = CEWAF+nutrients each after 2½ weeks,). Only individual cells were observed in the controls (j; biotic control after 2½ weeks). Single CARD-FISH hybridizations were performed using a probe targeting all *Gammaproteobacteria* (j-n), while dual CARD-FISH hybridizations were performed using probes targeting all Bacteria (green; o-t) and *Alteromonadales* including *Colwellia* (red; o-t). Counter-staining with 4′,6-Diamidin-2-phenylindol (DAPI; blue) is visualized in confocal laser scanning micrographs (o-t).

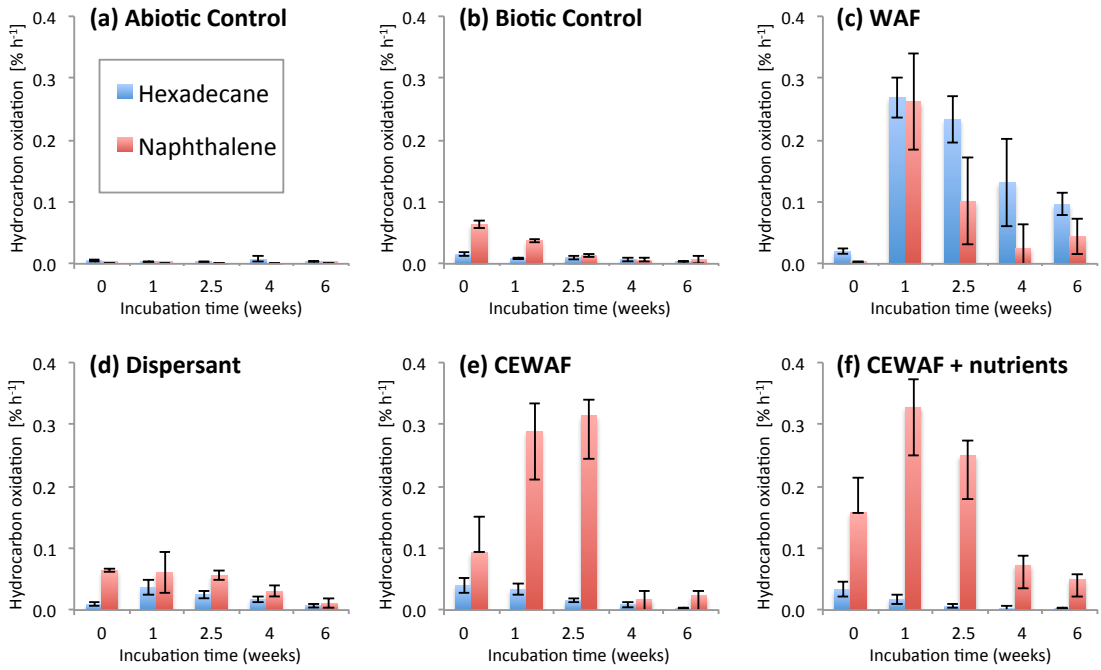


Fig. S14. Hydrocarbon turnover of ^{14}C-hexadecane and ^{14}C-naphthalene per hour in the different microcosms (a-f) over time. Standard deviations represent variations among triplicate setups.

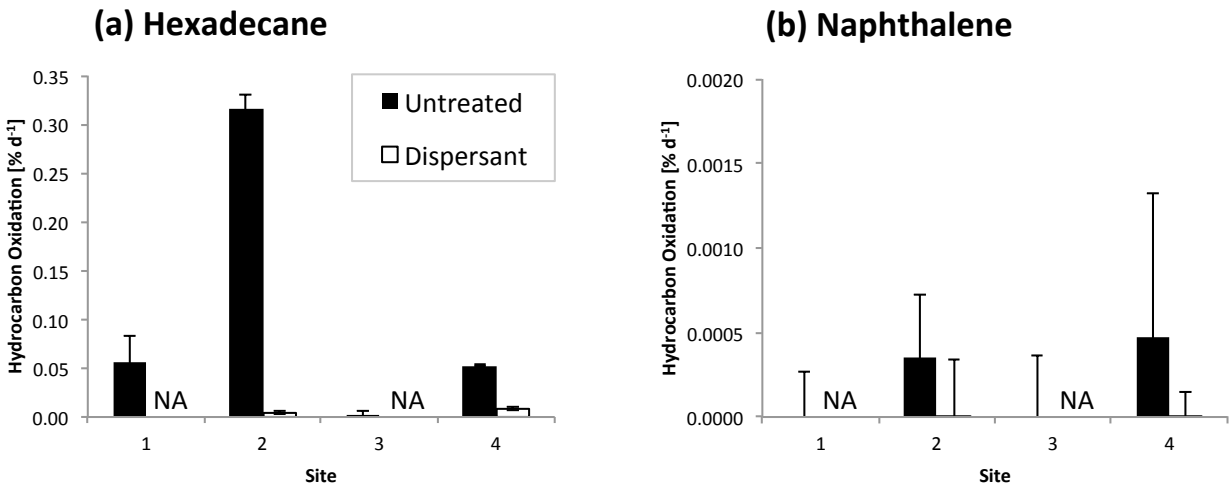


Fig. S15. Hydrocarbon turnover of ^{14}C-hexadecane (a) and ^{14}C-naphthalene (b) in oil-contaminated seawater samples. Samples remained untreated (■) or were amended with 10 µl dispersant per L seawater (□) prior to the application of radiotracer. Oil-contaminated samples were collected in the Gulf of Mexico along a transect from the Taylor Energy Platform to the Mississippi plume; site 1: source of oil (strong fumes), site 2: slick meets Mississippi plume (i.e., the mousse site), sites 3 and 4: intermediate transect. Due to sample volume limitations, sites 1 and 3 were not assayed with dispersants (NA).

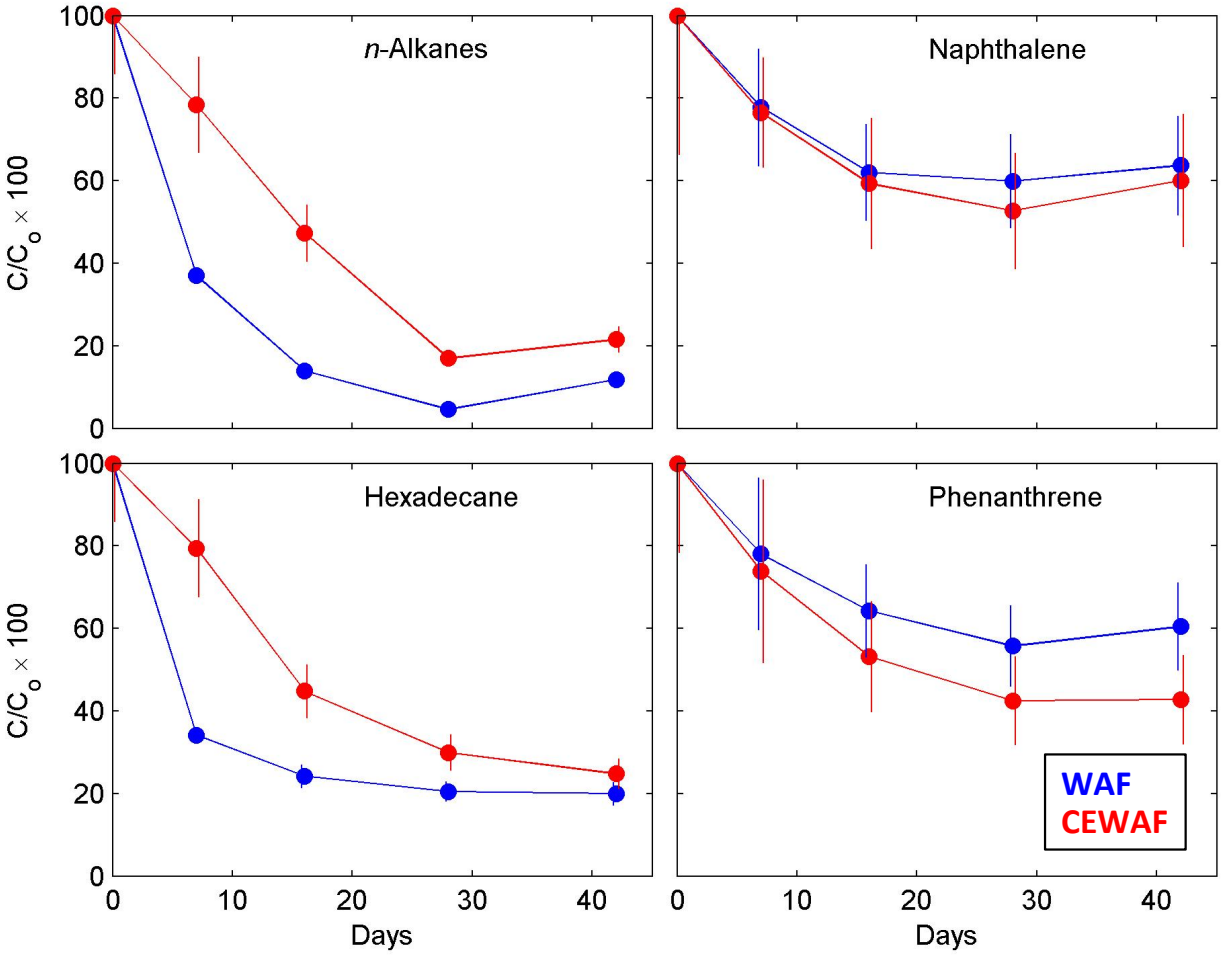


Fig. S16. **Biodegradation of oil-derived compounds.** Time series of normalized concentration of oil-derived compounds in WAF (blue) and CEWAF (red) treatments. Error bars show standard deviation between replicates. In some cases error bars are smaller than the size of the symbols.

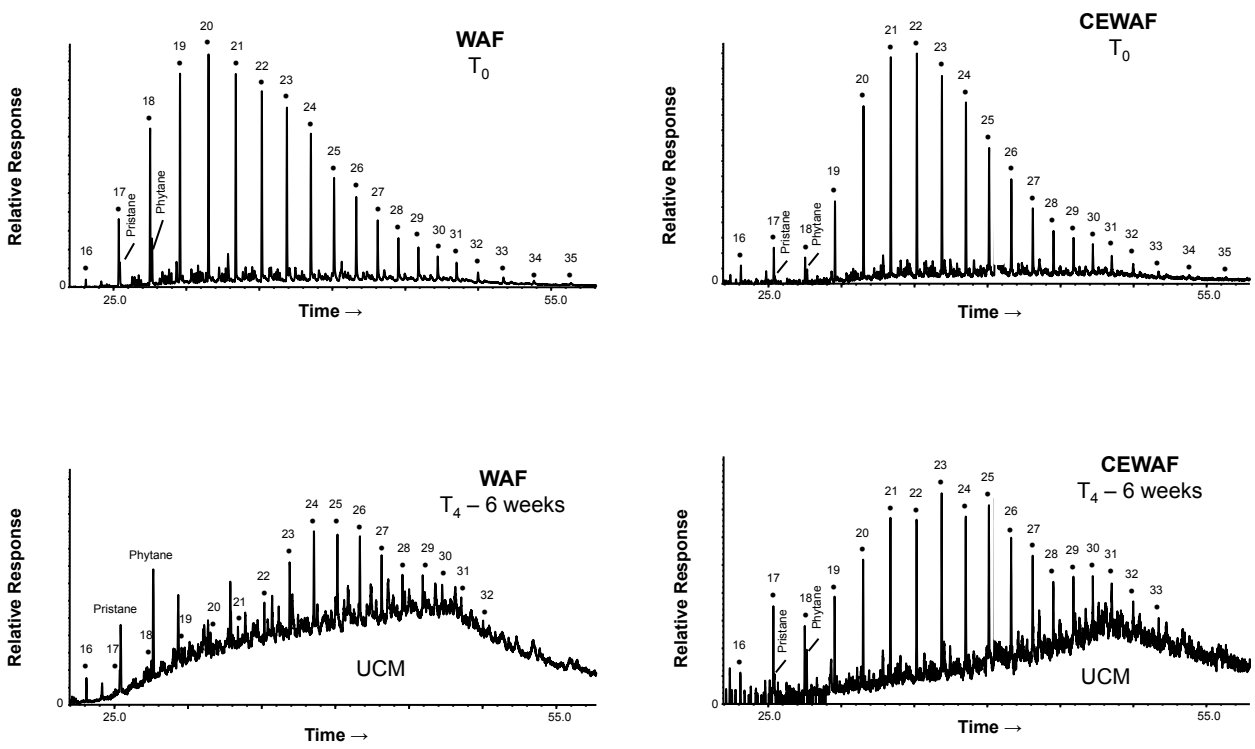


Fig. S17. **Chromatograms of WAF and CEWAF treatments before and after 6 weeks incubation.** Salient features of GC-MS data from different treatments summarized in total ion current (TIC) traces. Numbers refer to carbon chain length of *n*-alkanes. UCM = unresolved complex mixture.

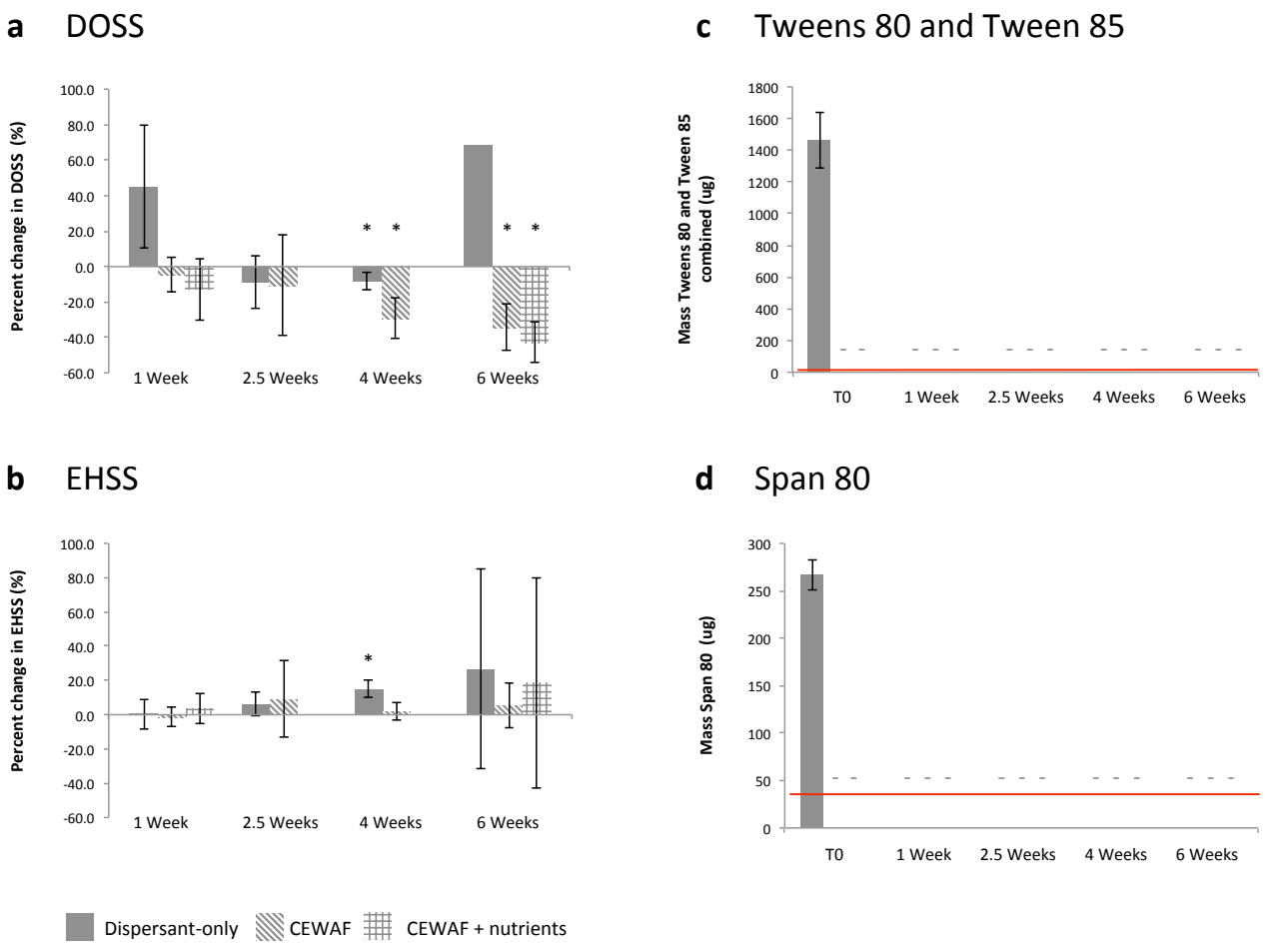


Fig. S18. **Anionic and nonionic surfactants in dispersant-only and CEWAF ± nutrients treatments within 6 weeks incubation.** Mean percent change in DOSS (a) and EHSS (b) relative to time zero samples as well as mean mass of total Tweens (Tween 80 and Tween 85; c) and Span 80 (d) were determined by liquid chromatography tandem mass spectrometry. Error bars represent 95% confidence intervals (*n* = 3). Asterisk (*) indicates a statistically significant change (Student's t-test, α = 0.05) and negative (-) indicates an observation below the limit of detection for the nonionic surfactants (36 µg, 20 µg/L), illustrated as red line.

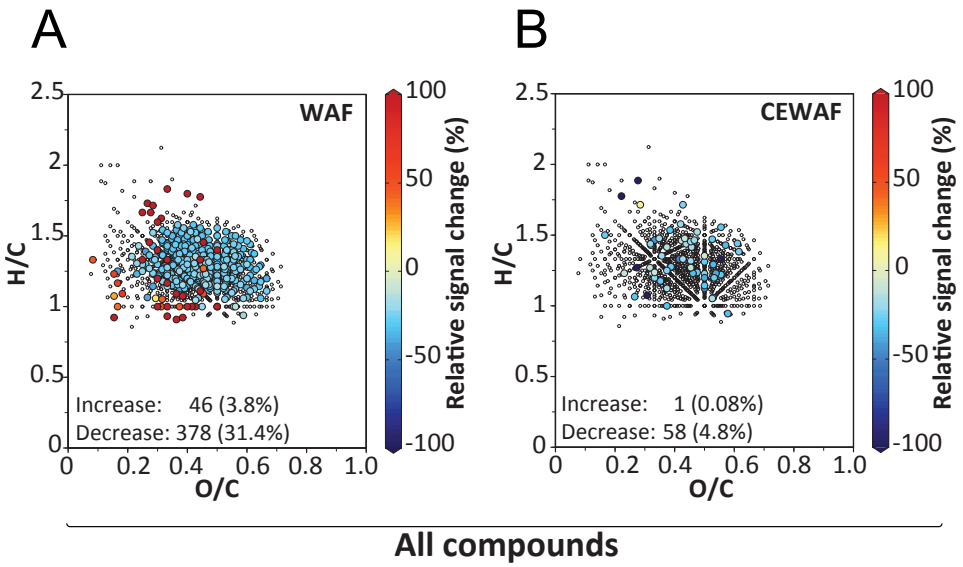


Fig. S19. Dispersants impact microbial turnover of dissolved organic matter. Analysis of molecular-level patterns in Van Krevelen diagrams (hydrogen-to- carbon, H/C, and oxygen-to-carbon, O/C ratios; each circle represents a molecular formula). (A and B) Molecular formulae present in all treatments (n = 1,205) and that significantly changed ($p \leq 0.01$, determined on triplicates using Student's t test) relative signal intensities between the initial and last time points. The color scales represent changes in relative intensities (open circles, no significant change).

Table S1: Analytical data, cell counts, rate measurements and TEP data from the microcosms simulating DWH spill-like plumes (abiotic control, biotic control, WAF, dispersant-only, CEWAF, CEWAF+nutrients) monitored for 6 weeks.

Treat-ment	Time (weeks)	Setup #	Salinity	pH	O_2 (µM)	DOC (µM)	DON (µM)	TDN (µM)	TDP (µM)	NO_2 (µM)	NO_3 (µM)	PO_4 (µM)	NH_4 (µM)	DIC (mM)	Cell counts (ml^{-1})	Bact. Prod. (nM C/day)	Naphth. (µg/L)*	Total Petroleum (µg/L)#	Hydrocarbon ox rates		Hydrolysis rates			TEP (Gxeq/L)
																			^{14}C Hexadec. rate (nM/day)	^{14}C Naphth. rate (nM/day)	Peptidase (nM/day)	Glucosidase (nM/day)	Lipase (nM/day)	
Abiotic Control	0	1	36	7.78	240.41	50.65	9.89	33.80	1.65	<LOD	24.15	1.65	0.24	3.45	6.35E+02	-0.02	NA	NA	NA	NA	-0.2349	-0.0657	2.0427	43.25
		2	36	7.79	236.35	45.84	10.46	34.17	1.70	<LOD	23.71	1.70	0.00	3.26	6.35E+02	-0.03	NA	NA	NA	NA	-0.0599	-0.0609	1.9272	58.98
		3	36.5	7.81	239.78	39.92	9.18	32.97	1.70	<LOD	24.04	1.70	0.24	3.37	0.00E+00	-0.07	NA	NA	NA	NA	-0.0599	-0.0285	1.8893	54.32
		AV	36.17	7.79	238.85	45.47	9.84	33.65	1.69	<LOD	23.97	1.68	0.16	3.36	4.23E+02	-0.04	<LOD	<LOD	7.53E-08	3.76E-09	-0.1182	-0.0517	1.9531	52.18
		SD	0.29	0.02	2.19	5.38	0.64	0.61	0.03	<LOD	0.23	0.03	0.14	0.09	3.66E+02	0.03	NA	NA	2.87E-11	2.42E-12	0.1010	0.0202	0.0799	8.08
	1	1	NA	7.74	235.72	37.40	12.55	35.45	1.70	NA	23.02	1.70	0.12	2.62	1.90E+03	-0.12	NA	NA	NA	NA	0.2039	0.1960	3.1366	NA
		2	NA	7.86	247.91	78.03	14.44	37.72	1.75	<LOD	23.23	1.24	-0.05	2.67	6.35E+02	0.00	NA	NA	NA	NA	0.2982	0.2026	2.4749	NA
		3	NA	7.86	239.78	42.29	12.06	34.31	1.75	<LOD	22.78	1.70	0.52	2.57	9.52E+02	0.31	NA	NA	NA	NA	0.3557	0.1806	2.6188	NA
		AV	NA	7.82	241.14	52.57	13.01	35.83	1.74	<LOD	23.01	1.55	0.20	2.62	1.16E+03	0.07	<LOD	<LOD	9.05E-08	-4.67E-09	0.2859	0.1931	2.7434	NA
		SD	NA	0.07	6.21	22.18	1.26	1.74	0.03	<LOD	0.23	0.26	0.29	0.05	6.61E+02	0.22	NA	NA	4.22E-11	2.13E-12	0.0766	0.0113	0.3480	NA
	2.5	1	NA	7.82	232.91	39.54	12.40	33.77	1.70	<LOD	21.64	1.75	0.26	2.74	3.17E+02	-0.33	NA	NA	NA	NA	-0.3941	0.0538	5.7140	NA
		2	NA	7.77	236.35	37.59	12.72	33.66	1.70	<LOD	21.75	1.70	0.81	2.69	3.17E+02	-0.14	NA	NA	NA	NA	-0.3700	0.0222	3.4673	NA
		3	NA	7.74	266.98	41.46	13.28	33.91	1.70	<LOD	21.20	1.65	0.57	2.37	6.35E+02	0.04	NA	NA	NA	NA	-0.3700	0.0127	4.4681	NA
		AV	NA	7.78	245.41	39.53	12.80	33.78	1.70	<LOD	21.53	1.70	0.55	2.60	4.23E+02	-0.14	<LOD	<LOD	4.58E-08	2.63E-09	-0.3780	0.0296	4.5498	NA
		SD	NA	0.04	18.76	1.93	0.45	0.12	0.00	<LOD	0.29	0.05	0.27	0.20	1.83E+02	0.18	NA	NA	2.70E-11	1.04E-12	0.0139	0.0215	1.1256	NA
	4	1	NA	7.79	235.10	36.55	11.47	33.96	1.90	<LOD	22.55	1.73	0.06	2.41	0.00E+00	0.06	NA	NA	NA	NA	0.7001	0.0930	6.7215	NA
		2	NA	7.81	241.97	38.94	12.55	34.72	1.74	0.02	22.21	1.73	0.06	2.67	0.00E+00	0.27	NA	NA	NA	NA	0.6148	0.0930	5.2604	NA
		3	NA	7.82	256.67	43.76	10.76	34.72	9.98	0.02	23.95	1.59	0.00	2.57	3.17E+02	-0.47	NA	NA	NA	NA	0.4146	0.0930	5.3191	NA
		AV	NA	7.81	244.58	39.75	11.59	34.47	4.54	0.02	22.90	1.68	0.04	2.55	1.06E+02	-0.05	<LOD	<LOD	1.14E-07	-2.62E-09	0.5765	0.0930	5.7670	NA
		SD	NA	0.02	11.02	3.67	0.91	0.44	4.71	0.00	0.92	0.08	0.03	0.13	1.83E+02	0.38	NA	NA	5.79E-11	1.66E-12	0.1466	0.0000	0.8271	NA
	6	1	36	7.9	252.92	38.44	11.78	33.50	1.74	<LOD	22.35	1.96	0.63	2.90	3.17E+02	-0.64	NA	NA	NA	NA	0.8427	0.0000	4.5370	118.34
		2	36	7.93	248.54	39.73	11.92	34.11	1.79	0.02	22.67	1.59	0.49	2.19	0.00E+00	-0.62	NA	NA	NA	NA	0.7881	0.0404	3.2573	50.63
		3	36	7.97	250.73	36.12	11.89	34.16	1.74	0.02	22.46	2.23	0.21	2.30	3.17E+02	-0.08	NA	NA	NA	NA	0.7831	0.0000	4.7704	59.95
		AV	36.00	7.93	250.73	38.10	11.86	33.92	1.76	0.02	22.50	1.93	0.45	2.47	2.12E+02	-0.45	<LOD	<LOD	5.04E-08	-1.15E-08	0.8047	0.0135	4.1882	76.31
		SD	0.00	0.04	2.19	1.83	0.07	0.37	0.03	0.00	0.16	0.32	0.21	0.38	1.83E+02	0.32	NA	NA	7.17E-12	1.40E-12	0.0330	0.0234	0.8146	36.70

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Table S1 (continued)

Treat-ment	Time (weeks)	Setup #	Salinity	pH	O_2 (µM)	DOC (µM)	DON (µM)	TDN (µM)	TDP (µM)	NO_2 (µM)	NO_3 (µM)	PO_4 (µM)	NH_4 (µM)	DIC (mM)	Cell counts (ml^{-1})	Bact. Prod. (nM C/day)	Naphth. (µg/L)*	Total Petroleum (µg/L)#	Hydrocarbon ox rates		Hydrolysis rates			TEP (Gxeq/L)
																			^{14}C Hexadec. rate (nM/day)	^{14}C Naphth. rate (nM/day)	Peptidase (nM/day)	Glucosidase (nM/day)	Lipase (nM/day)	
Biotic Control	0	1	36	7.81	239.16	45.74	10.64	34.66	1.70	<LOD	24.02	1.47	0.00	3.30	2.69E+05	18.23	NA	NA	NA	NA	0.1008	0.0316	2.0912	60.14
		2	36.5	7.8	244.79	39.31	10.35	33.53	1.70	<LOD	23.17	1.70	0.00	3.38	2.72E+05	15.00	NA	NA	NA	NA	0.1344	0.0041	1.6131	53.74
		3	36	7.81	241.35	42.78	11.15	34.33	1.70	<LOD	23.17	1.52	0.00	2.49	2.75E+05	24.65	NA	NA	NA	NA	0.0374	0.0134	1.0853	62.47
		AV	36.17	7.81	241.76	42.61	10.72	34.17	1.70	<LOD	23.45	1.56	0.00	3.06	2.72E+05	19.29	<LOD	<LOD	2.93E-07	2.23E-06	0.0909	0.0164	1.5965	58.78
		SD	0.29	0.01	2.84	3.22	0.40	0.58	0.00	<LOD	0.49	0.12	0.00	0.50	2.71E+03	4.91	NA	NA	9.47E-11	2.28E-10	0.0492	0.0140	0.5031	4.52
	1	1	NA	7.87	239.16	42.56	8.83	32.93	1.81	0.02	23.88	1.70	-0.21	2.51	2.31E+05	111.83	NA	NA	NA	NA	0.4636	0.2508	1.3478	NA
		2	NA	7.83	243.85	37.18	10.44	34.09	1.70	<LOD	23.77	1.70	0.12	2.54	2.74E+05	107.13	NA	NA	NA	NA	0.7525	0.2264	0.9147	NA
		3	NA	7.84	244.79	38.06	11.21	34.49	1.70	<LOD	23.40	1.65	0.12	2.15	2.81E+05	148.24	NA	NA	NA	NA	0.5226	0.2183	0.8670	NA
		AV	NA	7.85	242.60	39.26	10.16	33.84	1.74	0.02	23.68	1.68	0.01	2.40	2.62E+05	122.40	NA	<LOD	2.21E-07	1.14E-06	0.5796	0.2318	1.0432	NA
		SD	NA	0.02	3.01	2.89	1.22	0.81	0.06	<LOD	0.25	0.03	0.19	0.22	2.73E+04	22.50	NA	NA	1.75E-11	2.50E-10	0.1526	0.0169	0.2649	NA
	2.5	1	NA	7.78	248.54	37.74	12.37	33.34	1.75	<LOD	21.55	1.70	0.57	2.71	2.65E+05	25.57	NA	NA	NA	NA	0.0339	0.0222	1.3182	NA
		2	NA	7.78	252.29	37.06	13.49	34.72	1.75	<LOD	21.27	1.75	0.03	2.77	2.58E+05	31.19	NA	NA	NA	NA	0.0563	0.0189	1.1225	NA
		3	NA	7.77	253.85	33.82	13.51	33.97	1.70	<LOD	20.73	1.75	0.26	2.40	2.98E+05	36.29	NA	NA	NA	NA	0.2108	0.0127	0.4910	NA
		AV	NA	7.78	251.56	36.21	13.12	34.01	1.74	<LOD	21.18	1.73	0.29	2.63	2.74E+05	31.02	NA	<LOD	1.38E-07	2.17E-07	0.1003	0.0179	0.9772	NA
		SD	NA	0.01	2.73	2.09	0.65	0.69	0.03	<LOD	0.42	0.03	0.27	0.20	2.13E+04	5.37	NA	NA	2.96E-11	3.63E-11	0.0963	0.0048	0.4323	NA
	4	1	NA	7.8	254.48	33.06	12.70	34.05	1.79	0.02	21.46	1.73	0.12	2.43	2.20E+05	22.60	NA	NA	NA	NA	2.1699	0.1236	0.8441	NA
		2	NA	7.78	258.86	35.98	13.77	34.74	1.74	0.02	21.37	2.51	0.42	2.43	2.81E+05	16.36	NA	NA	NA	NA	2.2613	0.0587	1.2422	NA
		3	NA	7.76	258.54	36.65	13.35	34.08	1.74	0.02	21.19	1.77	0.48	2.57	3.17E+05	24.93	NA	NA	NA	NA	3.3077	0.1193	0.2646	NA
		AV	NA	7.78	257.29	35.23	13.27	34.29	1.76	0.02	21.34	2.00	0.34	2.48	2.72E+05	21.30	NA	<LOD	8.60E-08	8.04E-08	2.5796	0.1005	0.7836	NA
		SD	NA	0.02	2.44	1.91	0.54	0.39	0.03	0.00	0.14	0.44	0.19	0.08	4.87E+04	4.43	NA	NA	5.00E-11	5.07E-11	0.6322	0.0363	0.4916	NA
	6	1	36	7.89	256.35	36.43	12.86	33.93	1.74	<LOD	21.70	1.96	0.63	2.24	2.47E+05	27.18	NA	NA	NA	NA	2.2258	0.0951	1.6314	43.65
		2	36	7.85	259.17	35.41	12.62	33.42	1.69	<LOD	21.37	2.51	0.56	2.41	2.83E+05	26.39	NA	NA	NA	NA	2.8906	0.0376	1.2506	70.42
		3	36	7.84	256.98	35.59	13.96	35.08	1.69	0.02	21.74	2.33	0.63	2.34	2.80E+05	26.57	NA	NA	NA	NA	3.4509	0.0318	2.7051	58.78
		AV	36.00	7.86	257.50	35.81	13.15	34.14	1.71	0.02	21.60	2.27	0.61	2.33	2.70E+05	26.72	<LOD	<LOD	4.82E-08	8.69E-08	2.8557	0.0548	1.8624	57.62
		SD	0.00	0.03	1.48	0.55	0.72	0.85	0.03	<LOD	0.20	0.28	0.04	0.08	2.02E+04	0.41	NA	NA	4.40E-12	7.98E-11	0.6133	0.0350	0.7542	13.42

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Table S1 (continued)

Treat-ment	Time (weeks)	Setup #	Salinity	pH	O_2 (µM)	DOC (µM)	DON (µM)	TDN (µM)	TDP (µM)	NO_2 (µM)	NO_3 (µM)	PO_4 (µM)	NH_4 (µM)	DIC (mM)	Cell counts (ml^{-1})	Bact. Prod. (nM C/day)	Naphth. (µg/L)*	Total Petroleum (µg/L)#	Hydrocarbon ox rates		Hydrolysis rates			TEP (Gxeq/L)
																			^{14}C Hexadec. rate (nM/day)	^{14}C Naphth. rate (nM/day)	Peptidase (nM/day)	Glucosidase (nM/day)	Lipase (nM/day)	
WAF	0	1	36	7.82	244.79	116.47	11.69	35.22	1.65	<LOD	23.53	1.70	0.00	2.35	2.69E+05	15.51	NA	NA	NA	NA	0.0143	0.1527	3.0516	111.36
		2	36.5	7.83	241.97	114.81	12.70	35.82	1.65	<LOD	23.11	1.70	0.00	2.65	2.58E+05	20.71	NA	NA	NA	NA	0.0185	0.1039	2.6514	130.56
		3	36.5	7.82	246.04	114.93	10.20	33.03	1.50	<LOD	22.99	1.52	0.16	2.80	2.72E+05	11.99	NA	NA	NA	NA	0.0562	0.1027	2.8798	96.81
		AV	36.33	7.82	244.27	115.41	11.53	34.69	1.60	<LOD	23.21	1.64	0.05	2.60	2.66E+05	16.07	29.26	144.5768	5.47E-04	1.47E-01	0.0297	0.1198	2.8609	112.91
		SD	0.29	0.01	2.08	0.93	1.26	1.46	0.09	<LOD	0.28	0.11	0.09	0.23	7.68E+03	4.39	NA	NA	2.20E-07	3.91E-05	0.0231	0.0285	0.2008	16.93
	1	1	NA	7.81	244.79	116.04	8.20	24.87	1.15	0.08	16.71	1.10	0.12	2.17	3.17E+06	1172.23	NA	NA	NA	NA	3.5015	0.2790	24.5962	1118.99
		2	NA	7.79	244.79	117.77	8.83	25.80	1.15	0.08	16.92	1.10	0.04	1.95	3.95E+06	1015.92	NA	NA	NA	NA	3.6320	0.3109	22.2411	1043.80
		3	NA	7.77	256.35	120.79	9.84	26.80	1.15	0.10	17.14	1.15	0.28	2.39	4.07E+06	904.97	NA	NA	NA	NA	3.2426	0.1990	21.0067	789.58
		AV	NA	7.79	248.64	118.20	8.96	25.82	1.15	0.08	16.93	1.12	0.14	2.17	3.73E+06	1031.04	97.40	330.1361	5.92E-03	8.16E+01	3.4587	0.2630	22.6147	984.12
		SD	NA	0.02	6.68	2.40	0.83	0.97	0.00	0.01	0.21	0.03	0.12	0.22	4.86E+05	134.27	NA	NA	6.63E-07	3.06E-02	0.1982	0.0576	1.8236	172.62
	2.5	1	NA	7.76	254.48	103.46	11.43	26.70	1.35	0.14	15.78	1.33	0.65	2.41	5.26E+06	1739.87	NA	NA	NA	NA	25.0372	0.2581	37.1217	942.84
		2	NA	7.71	255.10	110.99	8.64	20.40	0.90	0.04	11.91	0.92	0.19	2.25	6.81E+06	2806.81	NA	NA	NA	NA	51.9985	0.4505	41.8060	673.18
		3	NA	7.61	252.60	107.66	6.20	9.47	0.25	0.04	3.81	0.23	0.57	2.46	1.36E+07	4193.74	NA	NA	NA	NA	85.4897	NA	66.1001	5179.80
		AV	NA	7.69	254.06	107.37	8.76	18.86	0.83	0.07	10.50	0.83	0.47	2.37	8.56E+06	2913.47	97.83	362.5801	1.83E-03	1.54E+01	54.1751	0.3543	48.3426	2265.27
		SD	NA	0.08	1.30	3.77	2.62	8.72	0.56	0.06	6.11	0.56	0.25	0.11	4.45E+06	1230.41	NA	NA	2.43E-07	8.11E-03	30.2850	0.1360	15.5558	2527.65
	4	1	NA	7.72	258.54	112.92	10.05	23.82	1.24	0.28	14.20	1.49	0.72	2.64	6.28E+06	1766.63	NA	NA	NA	NA	41.9813	0.3372	43.3329	784.08
		2	NA	7.6	254.48	115.06	7.85	12.18	0.54	0.20	4.31	0.57	0.18	2.80	1.06E+07	2584.77	NA	NA	NA	NA	93.1423	0.5480	44.9155	5231.53
		3	NA	7.69	256.67	106.43	11.40	25.10	1.24	0.28	13.95	1.73	0.54	2.49	5.59E+06	1050.51	NA	NA	NA	NA	34.5729	0.3225	41.4434	1400.68
		AV	NA	7.67	256.56	111.47	9.77	20.37	1.01	0.25	10.82	1.26	0.48	2.64	7.49E+06	1800.64	119.44	204.1767	8.57E-04	2.90E+00	56.5655	0.4026	43.2306	2472.10
		SD	NA	0.06	2.03	4.49	1.80	7.12	0.41	0.05	5.64	0.61	0.27	0.16	2.72E+06	767.70	NA	NA	4.97E-07	4.38E-03	31.8923	0.1261	1.7383	2409.54
	6	1	36	7.49	245.41	109.07	11.88	9.20	0.29	0.02	0.66	0.34	3.36	2.28	1.77E+07	2435.14	NA	NA	NA	NA	47.3926	2.0004	58.8381	5695.84
		2	36	7.45	249.48	110.07	7.02	10.34	0.54	0.77	3.46	0.52	0.91	2.22	1.65E+07	4329.12	NA	NA	NA	NA	72.0829	0.8366	76.9911	2374.88
		3	36	7.42	253.23	108.30	4.96	7.83	0.44	0.87	2.22	0.43	0.21	2.40	1.32E+07	4173.04	NA	NA	NA	NA	63.9006	0.5546	76.1746	3085.41
		AV	36.00	7.45	249.37	109.15	7.96	9.12	0.42	0.55	2.11	0.43	1.50	2.30	1.58E+07	3645.76	216.45	495.2513	7.19E-04	1.24E+01	61.1254	1.1305	70.6680	3718.71
		SD	0.00	0.04	3.91	0.89	3.56	1.25	0.13	0.47	1.40	0.09	1.65	0.09	2.33E+06	1051.33	NA	NA	1.14E-07	6.30E-03	12.5770	0.7664	10.2530	1748.71

Table continued on next page

Table S1 (continued)

Treat-ment	Time (weeks)	Setup #	Salinity	pH	O_2 (µM)	DOC (µM)	DON (µM)	TDN (µM)	TDP (µM)	NO_2 (µM)	NO_3 (µM)	PO_4 (µM)	NH_4 (µM)	DIC (mM)	Cell counts (ml^{-1})	Bact. Prod. (nM C/day)	Naphth. (µg/L)*	Total Petroleum (µg/L)#	Hydrocarbon ox rates		Hydrolysis rates			TEP (Gxeq/L)
																			^{14}C Hexadec. rate (nM/day)	^{14}C Naphth. rate (nM/day)	Peptidase (nM/day)	Glucosidase (nM/day)	Lipase (nM/day)	
Dispersant-only	0	1	36	7.86	241.66	254.71	9.38	32.80	1.70	<LOD	23.42	1.61	0.00	3.03	2.96E+05	16.82	NA	NA	NA	NA	0.6655	0.3663	2.7746	NA
		2	36	7.85	246.35	248.48	10.17	33.82	1.75	0.02	23.63	1.65	0.00	2.81	2.75E+05	17.01	NA	NA	NA	NA	0.1703	0.1602	4.3518	NA
		3	36.5	7.84	254.79	239.18	10.01	32.85	1.75	0.18	22.90	1.61	0.24	3.21	2.55E+05	14.96	NA	NA	NA	NA	0.1597	0.1603	1.9005	NA
		AV	36.17	7.85	247.60	247.46	9.86	33.16	1.74	0.10	23.32	1.62	0.08	3.02	2.75E+05	16.26	<LOD	<LOD	1.51E-07	2.18E-06	0.3318	0.2289	3.0090	NA
		SD	0.29	0.01	6.65	7.82	0.42	0.57	0.03	0.11	0.38	0.03	0.14	0.20	2.06E+04	1.13	NA	NA	4.97E-11	6.09E-11	0.2890	0.1189	1.2423	NA
	1	1	NA	7.81	246.66	276.34	11.59	28.85	1.35	0.36	16.70	1.15	-0.21	2.90	3.05E+06	1645.89	NA	NA	NA	NA	23.9905	0.8174	36.4414	NA
		2	NA	7.81	247.29	263.28	8.88	27.66	1.35	0.20	18.45	1.24	-0.13	2.73	3.44E+06	1027.83	NA	NA	NA	NA	21.3513	0.7154	27.9985	NA
		3	NA	7.81	248.54	291.81	10.08	28.30	1.40	0.20	18.06	1.20	0.04	2.75	3.19E+06	580.50	NA	NA	NA	NA	6.9255	0.7154	32.2631	NA
		AV	NA	7.81	247.50	277.14	10.18	28.27	1.37	0.25	17.74	1.20	-0.10	2.79	3.23E+06	1084.74	<LOD	<LOD	1.01E-06	2.01E-06	17.4224	0.7494	32.2344	NA
		SD	NA	0.00	0.96	14.28	1.36	0.60	0.03	0.09	0.92	0.05	0.12	0.09	2.01E+05	534.97	NA	NA	2.49E-10	8.73E-10	9.1859	0.0589	4.2215	NA
	2.5	1	NA	7.82	247.29	245.46	11.07	27.37	1.39	0.50	16.13	1.22	0.34	2.53	5.71E+06	1934.87	NA	NA	NA	NA	44.9211	0.4628	30.7263	NA
		2	NA	7.81	250.10	248.92	12.75	29.07	1.39	0.18	16.40	1.22	0.26	2.61	9.51E+06	1586.52	NA	NA	NA	NA	42.0186	0.4852	43.1595	NA
		3	NA	7.81	254.17	246.76	10.25	27.24	1.44	0.22	16.87	1.26	0.11	2.69	6.05E+06	1024.90	NA	NA	NA	NA	34.3311	0.4850	35.0384	NA
		AV	NA	7.81	250.52	247.05	11.36	27.89	1.41	0.30	16.47	1.23	0.24	2.61	7.09E+06	1515.43	<LOD	<LOD	3.48E-07	8.92E-07	40.4236	0.4777	36.3081	NA
		SD	NA	0.01	3.46	1.74	1.27	1.02	0.03	0.18	0.38	0.03	0.12	0.08	2.10E+06	459.13	NA	NA	6.47E-11	1.44E-10	5.4722	0.0129	6.3131	NA
	4	1	NA	7.83	260.11	254.52	9.53	26.89	1.29	0.36	17.59	1.45	0.60	2.44	7.79E+06	862.61	NA	NA	NA	NA	94.6429	1.3547	20.9727	NA
		2	NA	7.81	257.92	258.87	8.90	26.02	1.39	0.24	17.54	1.22	0.66	2.25	6.11E+06	1142.06	NA	NA	NA	NA	56.1639	0.8821	23.1232	NA
		3	NA	7.79	255.42	246.46	10.24	26.60	1.34	0.57	16.64	1.45	0.84	2.55	7.75E+06	726.34	NA	NA	NA	NA	91.4419	0.8817	24.3932	NA
		AV	NA	7.81	257.81	253.29	9.55	26.50	1.34	0.39	17.26	1.37	0.70	2.42	7.22E+06	910.34	<LOD	<LOD	1.15E-07	4.13E-07	80.7496	1.0395	22.8297	NA
		SD	NA	0.02	2.35	6.29	0.67	0.44	0.05	0.16	0.54	0.13	0.12	0.15	9.57E+05	211.93	NA	NA	6.57E-11	1.58E-10	21.3519	0.2729	1.7290	NA
	6	1	36	7.7	255.73	367.23	12.37	23.53	1.39	0.40	11.67	0.99	0.91	2.40	8.85E+06	1899.17	NA	NA	NA	NA	67.8496	0.5450	71.4920	NA
		2	36.5	7.67	258.54	314.91	11.68	23.01	1.24	0.40	12.33	0.99	1.40	2.41	1.03E+07	774.12	NA	NA	NA	NA	90.3962	0.9669	42.3501	NA
		3	36	7.73	248.85	228.27	16.39	32.24	1.64	0.48	16.84	1.54	1.47	2.31	4.71E+06	132.40	NA	NA	NA	NA	26.2752	0.9667	12.3098	NA
		AV	36.17	7.70	254.37	303.47	13.48	26.26	1.43	0.43	13.61	1.17	1.26	2.37	7.96E+06	935.23	0.73	<LOD	8.01E-08	2.38E-07	61.5070	0.8262	42.0506	NA
		SD	0.29	0.03	4.99	70.18	2.54	5.18	0.20	0.05	2.81	0.32	0.30	0.06	2.91E+06	894.34	NA	NA	3.75E-11	1.50E-10	32.5276	0.2435	29.5922	NA

Table continued on next page

Table S1 (continued)

Treat-ment	Time (weeks)	Setup #	Salinity	pH	O_2 (µM)	DOC (µM)	DON (µM)	TDN (µM)	TDP (µM)	NO_2 (µM)	NO_3 (µM)	PO_4 (µM)	NH_4 (µM)	DIC (mM)	Cell counts (ml^{-1})	Bact. Prod. (nM C/day)	Naphth. (µg/L)*	Total Petroleum (µg/L)#	Hydrocarbon ox rates		Hydrolysis rates			TEP (Gxeq/L)
																			^{14}C Hexadec. rate (nM/day)	^{14}C Naphth. rate (nM/day)	Peptidase (nM/day)	Glucosidase (nM/day)	Lipase (nM/day)	
CEWAF	0	1	36	7.83	252.60	283.30	9.11	32.67	1.70	<LOD	23.72	1.65	0.16	2.74	2.72E+05	22.47	NA	NA	NA	NA	0.3915	0.1622	2.0371	NA
		2	36	7.83	247.60	293.41	10.03	33.26	1.70	<LOD	23.24	1.65	0.00	2.88	2.63E+05	15.53	NA	NA	NA	NA	0.2391	0.1559	3.4320	NA
		3	36.5	7.84	240.10	272.95	11.28	34.33	1.70	<LOD	23.04	1.47	0.00	3.17	2.98E+05	22.02	NA	NA	NA	NA	0.1751	0.1387	3.0062	NA
		AV	36.17	7.83	246.77	283.22	10.14	33.42	1.70	<LOD	23.33	1.59	0.05	2.93	2.77E+05	20.01	4.06	13.3809	4.33E-04	1.10E+00	0.2686	0.1523	2.8251	NA
		SD	0.29	0.01	6.29	10.23	1.09	0.84	0.00	<LOD	0.35	0.11	0.09	0.22	1.83E+04	3.88	NA	NA	1.51E-07	5.08E-04	0.1112	0.0122	0.7149	NA
	1	1	NA	7.8	251.98	275.85	10.10	31.33	1.55	0.06	21.29	1.56	0.12	2.51	1.11E+06	1470.49	NA	NA	NA	NA	11.8685	0.2565	12.4461	NA
		2	NA	7.85	250.41	257.24	12.47	33.16	1.60	0.18	20.71	1.52	0.20	3.06	1.22E+06	895.73	NA	NA	NA	NA	11.6617	0.2475	9.4389	NA
		3	NA	7.84	241.97	245.34	10.00	29.26	1.50	0.52	18.86	1.42	0.12	2.41	1.79E+06	1603.53	NA	NA	NA	NA	7.7185	0.2695	12.8431	NA
		AV	NA	7.83	248.12	259.47	10.86	31.25	1.55	0.25	20.28	1.50	0.14	2.66	1.38E+06	1323.25	5.39	29.0554	3.70E-04	3.75E+00	10.4163	0.2578	11.5760	NA
		SD	NA	0.03	5.38	15.38	1.40	1.95	0.05	0.24	1.27	0.07	0.05	0.35	3.65E+05	376.17	NA	NA	8.43E-08	8.37E-04	2.3386	0.0110	1.8614	NA
	2.5	1	NA	7.79	254.48	218.66	13.09	29.56	1.59	0.32	17.11	1.45	0.96	2.43	2.99E+06	1838.80	NA	NA	NA	NA	11.8325	0.0818	12.8214	NA
		2	NA	7.83	249.48	238.13	12.89	29.01	1.39	0.65	16.29	1.40	0.81	2.51	2.78E+06	1265.62	NA	NA	NA	NA	11.6748	0.0726	17.4776	NA
		3	NA	7.85	246.04	209.90	11.82	29.17	1.49	0.32	17.52	1.45	0.50	2.63	2.08E+06	1144.99	NA	NA	NA	NA	11.6823	0.2565	11.4883	NA
		AV	NA	7.82	250.00	222.23	12.60	29.25	1.49	0.43	16.97	1.43	0.76	2.52	2.62E+06	1416.47	6.70	31.3638	5.62E-05	2.70E+00	11.7299	0.1370	13.9291	NA
		SD	NA	0.03	4.24	14.45	0.68	0.28	0.10	0.19	0.63	0.03	0.24	0.10	4.72E+05	370.69	NA	NA	1.44E-08	2.62E-04	0.0890	0.1036	3.1446	NA
	4	1	NA	7.8	256.98	248.04	14.89	32.79	1.64	0.54	18.67	2.33	1.31	2.50	6.45E+05	134.91	NA	NA	NA	NA	13.2578	0.1326	5.5864	NA
		2	NA	7.82	255.10	257.04	12.27	30.25	1.59	0.24	19.06	1.82	1.31	2.32	1.37E+06	427.34	NA	NA	NA	NA	9.0568	0.1711	6.6798	NA
		3	NA	7.85	255.10	247.03	12.84	30.45	2.20	0.28	19.00	2.10	1.67	2.30	9.94E+05	453.31	NA	NA	NA	NA	13.0938	0.1563	7.1715	NA
		AV	NA	7.82	255.73	250.70	13.33	31.16	1.81	0.35	18.91	2.08	1.43	2.38	1.00E+06	338.52	4.22	23.7917	2.11E-05	6.65E-02	11.8028	0.1533	6.4792	NA
		SD	NA	0.03	1.08	5.51	1.38	1.41	0.33	0.17	0.21	0.25	0.21	0.11	3.61E+05	176.81	NA	NA	9.91E-09	6.75E-05	2.3795	0.0194	0.8114	NA
	6	1	36.5	7.73	255.10	242.43	15.94	31.41	1.64	0.77	17.35	1.68	2.66	2.39	1.76E+06	352.81	NA	NA	NA	NA	19.5602	0.1840	9.4406	NA
		2	36	7.76	255.73	244.76	14.82	29.87	1.64	0.48	16.66	1.96	2.10	2.60	1.69E+06	449.28	NA	NA	NA	NA	22.7649	0.1516	10.3978	NA
		3	36	7.78	251.98	229.59	17.16	31.11	1.64	0.69	15.86	2.10	2.59	2.76	1.20E+06	232.15	NA	NA	NA	NA	20.4731	0.1615	12.5474	NA
		AV	36.17	7.76	254.27	238.93	15.97	30.80	1.64	0.65	16.63	1.91	2.45	2.58	1.55E+06	344.75	5.74	29.5089	6.83E-06	1.95E-01	20.9327	0.1657	10.7953	NA
		SD	0.29	0.03	2.01	8.17	1.17	0.82	0.00	0.15	0.75	0.21	0.30	0.18	3.06E+05	108.79	NA	NA	2.19E-09	5.87E-05	1.6510	0.0166	1.5911	NA

Table continued on next page

Table S1 (continued)

Treat-ment	Time (weeks)	Setup #	Salinity	pH	O_2 (µM)	DOC (µM)	DON (µM)	TDN (µM)	TDP (µM)	NO_2 (µM)	NO_3 (µM)	PO_4 (µM)	NH_4 (µM)	DIC (mM)	Cell counts (ml^{-1})	Bact. Prod. (nM C/day)	Naphth. (µg/L)*	Total Petroleum (µg/L)#	Hydrocarbon ox rates		Hydrolysis rates			TEP (Gxeq/L)
																			^{14}C Hexadec. rate (nM/day)	^{14}C Naphth. rate (nM/day)	Peptidase (nM/day)	Glucosidase (nM/day)	Lipase (nM/day)	
CEWAF+nutrients	0	1	36	7.61	246.66	267.16	35.32	56.51	1.05	0.02	31.62	1.15	10.45	2.17	2.76E+05	18.08	NA	NA	NA	NA	1.4302	0.1419	2.2470	NA
		2	36	7.59	246.04	268.27	35.58	57.62	1.10	<LOD	32.89	1.15	10.85	2.41	2.85E+05	17.58	NA	NA	NA	NA	0.0387	0.1772	3.6246	NA
		3	36	7.58	248.54	276.22	37.03	57.71	1.10	<LOD	32.02	1.15	11.34	2.32	2.81E+05	13.38	NA	NA	NA	NA	0.1821	0.1322	1.8679	NA
		AV	36.00	7.59	247.08	270.55	35.98	57.28	1.09	0.02	32.18	1.15	10.88	2.30	2.81E+05	16.35	4.84	22.7081	4.87E-04	2.06E+00	0.5503	0.1504	2.5798	NA
		SD	0.00	0.02	1.30	4.94	0.92	0.67	0.03	<LOD	0.65	0.00	0.45	0.12	4.77E+03	2.59	NA	NA	1.18E-07	2.73E-04	0.7653	0.0237	0.9244	NA
	1	1	NA	7.65	247.29	280.16	34.45	56.93	0.95	<LOD	30.66	0.97	8.18	2.53	1.09E+06	963.77	NA	NA	NA	NA	3.9344	0.2268	5.6393	NA
		2	NA	76	248.23	253.72	34.56	56.91	0.95	<LOD	31.02	0.97	8.67	2.18	1.39E+06	653.27	NA	NA	NA	NA	4.2710	0.3311	6.0422	NA
		3	NA	7.55	239.78	262.10	33.40	56.39	0.85	<LOD	30.61	0.87	7.61	2.55	1.67E+06	1217.30	NA	NA	NA	NA	5.7223	0.2882	8.0707	NA
		AV	NA	30.40	245.10	265.33	34.14	56.74	0.92	<LOD	30.76	0.94	8.15	2.42	1.38E+06	944.78	16.55	31.7392	2.84E-04	4.75E+00	4.6426	0.2820	6.5840	NA
		SD	NA	39.49	4.63	13.51	0.64	0.31	0.06	<LOD	0.23	0.05	0.53	0.21	2.93E+05	282.49	NA	NA	5.43E-08	7.63E-04	0.9501	0.0525	1.3031	NA
	2.5	AV	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	22.93	NA	3.58E+06	2351.78	NA	NA	2.65E-04	2.20E+00	18.1345	0.2018	19.8446	NA
		SD	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	5.27E-08	3.15E-05	NA	NA	NA	NA
	4	AV	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	15.82	NA	2.91E+06	803.02	NA	NA	1.12E-04	3.14E-01	NA	NA	NA	NA
		SD	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	9.18E-08	7.39E-05	NA	NA	NA	NA
	6	1	36.5	7.62	250.73	247.53	33.90	54.21	0.89	0.02	29.40	1.22	9.11	2.52	3.31E+06	1076.03	NA	NA	NA	NA	25.2682	0.1940	16.4689	NA
		2	36	7.56	249.16	247.09	38.44	56.77	0.89	0.02	29.53	0.89	11.20	2.60	2.69E+06	99.94	NA	NA	NA	NA	11.3531	0.1198	9.0429	NA
		3	36	7.53	253.54	246.59	31.98	54.62	0.89	0.02	29.99	0.99	7.36	2.58	3.66E+06	189.06	NA	NA	NA	NA	11.9447	0.2124	12.5653	NA
		AV	36.17	7.57	251.14	247.07	34.77	55.20	0.89	0.02	29.64	1.03	9.22	2.57	3.22E+06	455.01	8.65	40.7812	9.49E-06	5.55E-01	16.1887	0.1754	12.6924	NA
		SD	0.29	0.05	2.22	0.47	3.31	1.38	0.00	0.00	0.31	0.17	1.92	0.04	4.94E+05	539.66	NA	NA	6.01E-09	2.25E-04	7.8687	0.0490	3.7146	NA

Abbreviations: average (AV), bact. prod. (bacterial production), hexadecane (hexadec.), limit of detection (LOD), naphthalene (naphth.), not analyzed (NA), oxidation (ox.), phenanthrene (phenanth.), standard deviation (SD).
*: excitation/emission matrix spectra (EEMS); #: gas chromatography-mass spectrometry (GC-MS)

Table S2: Correlation of oligotype abundances with experimental parameters.

Taxa	Type	Oligotypes	Salinity	pH	O_2	DOC	TDN	TDP	NO_2	NO_3	PO_4	NH_4	DIC
Colwellia	1	TGCTTTGATGCAC	NA	NA	NA	0.36	NA	NA	0.41	NA	NA	0.37	NA
	2	TTATTTGATGCAC	NA	NA	NA	0.38	NA	NA	NA	NA	NA	0.30	NA
	3	CATTTTGATGCAC	NA	-0.29	NA	0.44	-0.33	-0.56	NA	-0.34	-0.46	0.40	NA
	4	TTGTTTGATGCAC	NA	NA	NA	0.45	NA	NA	NA	NA	NA	NA	NA
	5	TGCTTTAATGCAC	NA	NA	NA	0.37	NA	NA	NA	NA	NA	NA	NA
	6	CGTTTTGATGCAC	NA	NA	NA	0.37	NA	-0.33	0.43	NA	NA	0.33	NA
	7	TTATTTAATGCAC	NA	NA	NA	0.41	NA	NA	NA	NA	NA	0.37	NA
	8	CATTTTAATGCAC	NA	-0.32	NA	0.44	-0.34	-0.59	NA	-0.35	-0.49	0.42	NA
	9	TGCTTTAATGACT	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	10	CATTTTGATGACC	NA	NA	NA	0.31	NA	-0.49	NA	NA	-0.56	NA	NA
	11	TTGTTTAATGCAC	NA	NA	NA	0.49	NA	NA	NA	NA	NA	NA	NA
	12	TTGTTTGATGACC	NA	NA	NA	0.49	NA	-0.29	NA	NA	NA	NA	NA
	13	TGCTTTAATGACA	NA	0.30	-0.32	NA	NA	0.38	NA	NA	NA	-0.53	0.31
	14	TGCTTTGCTGCAC	NA	NA	NA	0.38	NA	NA	0.46	NA	NA	0.31	NA
	15	TTATGTGATGCAC	NA	NA	NA	0.44	NA	NA	0.35	NA	NA	0.38	NA
	16	TGCTTTAATGACC	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	17	TTGTGTGATGCAC	NA	NA	NA	0.32	NA	NA	NA	NA	NA	NA	NA
	18	TTAGTTGATGCAC	NA	NA	NA	0.42	NA	NA	NA	NA	NA	0.40	NA
	19	TTATTTGCTGCAC	NA	NA	NA	0.44	NA	NA	0.34	NA	NA	0.38	NA
	20	CATTTTGCTGCAC	NA	NA	NA	0.40	-0.36	-0.50	0.38	-0.39	-0.40	0.35	NA
	21	CGTTTTAATGCAC	NA	NA	NA	0.44	NA	NA	0.43	NA	NA	NA	NA
	22	TTGTTTGCTGCAC	NA	NA	NA	0.43	NA	NA	NA	NA	NA	NA	NA
	23	TTGGTTGATGCAC	NA	NA	NA	0.50	NA	NA	NA	NA	NA	NA	NA
	24	TTATTGGATGCAC	NA	NA	NA	0.46	NA	NA	0.35	NA	NA	0.37	NA
Cycloclasticus	1	AATTTCGCAGGATCGGAAAAATAAAT-CGCA	NA	NA	NA	NA	0.35	NA	-0.46	0.41	NA	NA	NA
	2	AATTTCGCAGGATCGGACAAATAAAT-CGCA	NA	NA	-0.34	NA	0.32	NA	-0.48	0.40	NA	NA	NA
	3	ATTTTCGTAGGATCGGAAAAATAAAT-CGCA	NA	NA	NA	-0.30	NA	NA	NA	NA	NA	-0.28	NA
	4	AATTTCGCAGGATAGGAAAAATAAAT-CGCA	NA	NA	-0.36	NA	0.32	NA	-0.54	0.40	NA	NA	NA
	5	AATTTCGCAGAATCGGAAAAATAAAT-CGCA	NA	NA	-0.38	NA	0.30	NA	-0.54	0.38	NA	NA	NA
	6	AATTTCGCAGGAGCGGAAAAATAAAT-CGCA	NA	NA	-0.39	NA	0.31	NA	-0.47	0.39	NA	NA	NA
	7	AATCTCGCAGGATCGGAAAAATAAAT-CGCA	NA	NA	-0.42	NA	0.30	NA	-0.44	0.41	NA	NA	NA
	8	AATTTCGCGGGATCGGAAAAATAAAT-CGCA	NA	NA	-0.38	NA	0.32	NA	-0.50	0.41	NA	NA	NA
	9	AATTTCGCAGGGTCGGAAAAATAAAT-CGCA	NA	NA	-0.37	NA	0.33	NA	-0.55	0.43	NA	NA	NA
	10	AATTTCGCAGGATCGGAGAAATAAAT-CGCA	NA	NA	-0.43	NA	0.31	NA	-0.52	0.42	NA	NA	NA
	11	AATTTCGCAGGATCAGAAAAATAAAT-CGCA	NA	NA	-0.34	NA	NA	NA	-0.46	0.37	NA	NA	NA
	12	AATTTCGCAGGATCGGAAAAATAAAT-CGTA	NA	NA	-0.35	NA	NA	NA	NA	NA	NA	NA	NA
	13	AATTTCGCAGGATCGGGAAAATAAAT-CGCA	NA	NA	-0.37	NA	0.31	NA	-0.43	0.40	NA	NA	NA
	14	AATTTCGCAGGATCGAAAAAATAAAT-CGCA	NA	NA	-0.43	NA	0.34	NA	-0.53	0.42	NA	NA	NA
	15	AATTTCGCAGGATCGGAAAGATAAAT-CGCA	NA	NA	-0.34	NA	0.31	NA	-0.55	0.41	NA	NA	NA
	16	AGTTTCGCAGGATCGGAAAAATAAAT-CGCA	NA	NA	-0.39	NA	0.31	NA	-0.53	0.40	NA	NA	NA
	17	AATTTCGCAAGATCGGAAAAATAAAT-CGCA	NA	NA	-0.39	NA	NA	NA	-0.49	0.36	NA	NA	NA
	18	AATTTCGCAGGATCGGAAAAGTAAAT-CGCA	NA	NA	-0.38	NA	0.30	NA	-0.55	0.41	NA	NA	NA
	19	AACTTCGCAGGATCGGAAAAATAAAT-CGCA	NA	NA	-0.36	NA	0.32	NA	-0.49	0.42	NA	NA	NA
	20	AATTTCGCAGGATCGGAAAAATAGAT-CGCA	NA	NA	-0.37	NA	0.31	NA	-0.50	0.38	NA	NA	NA
	21	AATTTCGCAGGATCGGAAAAATAAAC-CGCA	NA	NA	-0.33	NA	NA	NA	-0.44	0.37	NA	NA	NA
	22	AATTTCGCAGGATCGGAAAAATGAAT-CGCA	NA	NA	-0.41	NA	0.33	NA	-0.50	0.39	NA	NA	NA
	23	AATTTCGCAGGATCGGAAAAATAAGT-CGCA	NA	NA	-0.45	NA	NA	NA	-0.43	0.37	NA	NA	NA
	24	AATTTCGCAGGATCGGAAAAATAAAA-CGCA	NA	NA	-0.41	NA	0.29	NA	-0.50	0.38	NA	NA	NA
	25	AATTTCGCAGGATCGGAAAAACAAAT-CGCA	NA	NA	-0.37	NA	NA	NA	-0.52	0.38	NA	NA	NA
	26	GATTTCGCAGGATCGGAAAAATAAAT-CGCA	NA	NA	-0.39	NA	0.32	NA	-0.57	0.42	NA	NA	NA
	27	AATTTCGCAGGATCGGAAGAATAAAT-CGCA	NA	NA	-0.38	NA	0.29	NA	-0.52	0.37	NA	NA	NA
	28	AATTTCGCAGGATCGGAAAAATAAAT-CGCG	NA	NA	-0.39	NA	NA	NA	-0.39	0.35	NA	NA	NA
	29	AATTTCGCAGGACCGGAAAAATAAAT-CGCA	NA	NA	-0.30	NA	0.29	NA	-0.52	0.38	NA	NA	NA
	30	AATTTCGCAGGATCGGAAAAATAAAT-TATA	NA	NA	-0.31	NA	NA	NA	-0.47	NA	-0.30	NA	NA
	31	AATTCCGCAGGATCGGAAAAATAAAT-CGCA	NA	NA	-0.41	NA	0.33	NA	-0.53	0.42	NA	NA	NA

Table continued on next page

Table S2 (continued)

Taxa	Type	Cell counts	Bact. Prod.	Naphth. (EEMS)	Hexadec. (GC-MS)	n-Alkanes (GC-MS)	Phenanth. (GC-MS)	Petroleum (GC-MS)	Hexadec. Ox	Naphth. Ox	Total DOSS	Total EHSS	Peptidase	Glucosi-dase	Lipase	TEP
Colwellia	1	0.36	0.48	NA	-0.57	-0.53	-0.64	NA	NA	NA	NA	NA	0.45	0.34	0.34	NA
	2	NA	NA	-0.40	-0.43	-0.41	-0.62	NA	NA	NA	-0.47	NA	NA	NA	NA	NA
	3	0.60	0.67	NA	-0.46	-0.42	-0.40	NA	NA	0.35	NA	NA	0.62	0.52	0.60	0.68
	4	NA	0.35	-0.44	-0.50	-0.49	-0.68	-0.40	NA	NA	NA	NA	0.34	NA	NA	NA
	5	0.40	0.51	NA	-0.62	-0.60	-0.67	NA	NA	NA	NA	NA	0.48	0.34	0.37	NA
	6	0.41	0.47	NA	-0.41	-0.39	-0.47	NA	NA	NA	NA	NA	0.46	0.30	0.37	NA
	7	NA	NA	-0.39	-0.49	-0.43	-0.65	NA	NA	NA	-0.47	NA	NA	NA	NA	NA
	8	0.63	0.68	NA	-0.43	NA	NA	NA	NA	0.34	NA	NA	0.64	0.52	0.61	0.63
	9	NA	NA	NA	0.43	NA	0.40	NA	NA	-0.47	0.62	-0.48	NA	NA	NA	NA
	10	0.48	0.52	NA	NA	NA	NA	0.41	NA	NA	NA	NA	0.38	0.53	0.50	NA
	11	NA	0.33	-0.46	-0.52	-0.51	-0.69	-0.42	NA	NA	NA	NA	0.35	0.30	NA	NA
	12	0.46	0.37	NA	-0.63	-0.57	-0.58	NA	NA	NA	NA	NA	0.53	0.45	0.47	NA
	13	-0.33	-0.37	-0.52	0.54	0.46	NA	-0.49	-0.43	-0.43	0.64	-0.46	-0.42	NA	-0.37	NA
	14	0.36	0.46	NA	-0.61	-0.61	-0.70	NA	NA	NA	-0.38	NA	0.45	NA	0.36	NA
	15	NA	0.28	-0.43	-0.56	-0.51	-0.72	-0.41	NA	NA	-0.49	0.38	0.29	NA	NA	NA
	16	NA	NA	NA	NA	NA	NA	NA	-0.43	-0.50	0.42	-0.45	NA	NA	NA	NA
	17	NA	0.40	NA	-0.53	-0.49	-0.55	NA	NA	NA	NA	NA	0.35	NA	NA	NA
	18	NA	0.36	NA	-0.56	-0.51	-0.70	NA	NA	NA	-0.46	NA	0.35	NA	NA	NA
	19	NA	0.35	NA	-0.55	-0.50	-0.69	NA	NA	0.32	-0.47	NA	0.33	NA	NA	NA
	20	0.58	0.70	NA	-0.40	NA	NA	NA	NA	0.33	NA	NA	0.61	0.49	0.59	0.65
	21	NA	0.33	NA	NA	NA	-0.41	NA	NA	NA	NA	NA	0.29	NA	NA	NA
	22	0.33	0.38	NA	-0.47	-0.47	-0.63	NA	NA	NA	NA	NA	0.38	NA	NA	NA
	23	0.30	0.33	-0.51	-0.56	-0.54	-0.73	-0.46	NA	NA	NA	NA	0.33	NA	NA	NA
	24	NA	0.37	NA	-0.55	-0.50	-0.68	NA	NA	0.33	-0.42	NA	0.34	NA	NA	NA
Cycloclasticus	1	-0.39	-0.29	NA	0.58	0.60	0.47	NA	NA	NA	NA	NA	-0.53	-0.31	-0.43	NA
	2	-0.41	-0.31	NA	0.72	0.72	0.56	NA	0.34	0.30	NA	NA	-0.57	-0.32	-0.43	NA
	3	-0.31	NA	NA	0.58	0.49	0.58	NA	0.31	NA	NA	NA	-0.41	NA	-0.30	NA
	4	-0.38	-0.31	NA	0.74	0.73	0.58	NA	0.36	0.30	NA	NA	-0.57	-0.31	-0.41	NA
	5	-0.36	NA	NA	0.71	0.71	0.55	NA	0.38	0.33	NA	NA	-0.54	NA	-0.38	NA
	6	-0.37	-0.30	NA	0.73	0.70	0.56	NA	0.37	0.31	NA	NA	-0.55	NA	-0.39	NA
	7	-0.41	-0.30	NA	0.79	0.81	0.65	NA	0.36	0.30	NA	NA	-0.60	NA	-0.41	NA
	8	-0.39	-0.29	NA	0.68	0.72	0.54	NA	0.32	0.29	NA	NA	-0.57	-0.31	-0.43	NA
	9	-0.39	-0.29	NA	0.69	0.72	0.54	NA	0.32	0.30	NA	NA	-0.58	-0.30	-0.42	NA
	10	-0.40	-0.31	NA	0.76	0.77	0.59	NA	0.34	0.30	NA	NA	-0.60	NA	-0.41	NA
	11	-0.41	-0.30	NA	0.66	0.65	0.50	NA	0.34	0.32	NA	NA	-0.55	NA	-0.41	NA
	12	NA	NA	NA	0.48	0.49	NA	NA	0.56	0.54	-0.40	0.45	-0.31	NA	NA	0.54
	13	-0.41	-0.29	NA	0.65	0.66	0.46	NA	0.32	0.32	NA	NA	-0.58	-0.31	-0.44	NA
	14	-0.41	-0.31	NA	0.70	0.69	0.50	NA	0.36	0.34	NA	0.40	-0.59	-0.34	-0.43	NA
	15	-0.37	NA	NA	0.73	0.74	0.60	NA	0.30	NA	NA	NA	-0.55	NA	-0.40	NA
	16	-0.41	-0.30	NA	0.74	0.72	0.55	NA	0.32	NA	NA	NA	-0.59	NA	-0.42	NA
	17	-0.32	NA	NA	0.63	0.64	0.46	NA	0.35	0.36	NA	NA	-0.52	NA	-0.36	NA
	18	-0.40	-0.30	NA	0.74	0.73	0.54	NA	0.34	0.32	NA	NA	-0.58	-0.32	-0.40	NA
	19	-0.39	-0.29	NA	0.67	0.70	0.53	NA	0.34	0.32	NA	NA	-0.54	NA	-0.41	NA
	20	-0.40	NA	NA	0.68	0.70	0.52	NA	0.31	0.31	NA	NA	-0.56	-0.30	-0.42	NA
	21	-0.41	-0.30	NA	0.75	0.76	0.60	NA	0.35	NA	NA	NA	-0.57	NA	-0.41	NA
	22	-0.41	-0.34	NA	0.67	0.69	0.51	NA	0.29	NA	NA	NA	-0.60	-0.31	-0.42	NA
	23	-0.35	NA	NA	0.62	0.66	0.49	NA	0.33	0.34	NA	NA	-0.52	NA	-0.34	NA
	24	-0.39	NA	NA	0.67	0.67	0.52	NA	0.36	0.33	NA	NA	-0.58	-0.29	-0.41	NA
	25	-0.34	NA	NA	0.67	0.70	0.54	NA	0.34	0.33	NA	NA	-0.52	NA	-0.36	NA
	26	-0.37	NA	NA	0.71	0.73	0.56	NA	0.36	0.33	NA	NA	-0.55	NA	-0.39	NA
	27	-0.33	NA	NA	0.64	0.66	0.53	NA	0.37	0.31	NA	NA	-0.51	NA	-0.35	NA
	28	-0.34	NA	NA	0.58	0.58	0.40	NA	0.34	0.34	NA	NA	-0.49	NA	-0.35	NA
	29	-0.35	-0.29	NA	0.67	0.67	0.57	NA	0.33	NA	NA	NA	-0.50	NA	-0.35	NA
	30	NA	NA	NA	0.57	0.54	0.43	NA	0.44	0.44	NA	NA	-0.36	NA	NA	NA
	31	-0.37	NA	NA	0.69	0.70	0.52	NA	0.33	0.32	NA	NA	-0.55	NA	-0.37	NA

Table continued on next page

Table S2 (continued)

Taxa	Type	Oligotypes	Salinity	pH	O_2	DOC	TDN	TDP	NO_2	NO_3	PO_4	NH_4	DIC
Oceaniserpentilla	1	ACGTTTTTACTACGGAATCAAAGTTTATCC	NA	0.30	-0.28	NA	0.51	0.42	-0.48	0.56	NA	-0.35	NA
	2	ACGTCTTTACTACGGAATCAAAGTTTATCC	NA	NA	-0.37	NA	0.52	0.46	-0.49	0.57	NA	-0.41	NA
	3	ACGTTTTTACTACGGAATCAGAGTTTATCC	NA	NA	-0.31	NA	0.50	0.44	-0.49	0.54	NA	-0.38	NA
	4	ACGTTTTTACTAAAGAATTAAAGTTTATCC	NA	NA	-0.43	NA	0.47	0.36	-0.60	0.55	NA	-0.45	NA
	5	ACGTTTTTACTACGGAATCAACGTTTATCC	NA	NA	-0.34	NA	0.54	0.46	-0.52	0.58	NA	-0.37	NA
	6	ACGTTTTTACTACAAAATTAAAGTTTATCC	NA	NA	-0.37	NA	0.56	0.49	-0.53	0.60	0.30	-0.37	NA
	7	ACGTTTTTACTGCGGAATCAAAGTTTATCC	NA	NA	-0.36	NA	0.46	0.44	-0.43	0.53	NA	-0.39	NA
	8	ACGCTTTTACTACGGAATCAAAGTTTATCC	NA	0.28	-0.43	NA	0.54	0.50	-0.52	0.60	NA	-0.44	NA
	9	ACGTTTTTACTACGGAATCAAAGTTTGTCC	NA	NA	-0.35	NA	0.49	0.48	-0.45	0.54	NA	-0.42	NA
	10	ACGTTTTTACTACGGAATCGAAGTTTATCC	NA	NA	-0.39	NA	0.52	0.47	-0.43	0.56	NA	-0.45	NA
	11	ACGTTTTTACTACGGAATCAAGGTTTATCC	NA	NA	-0.36	NA	0.52	0.45	-0.47	0.57	NA	-0.39	NA
	12	ACGTTTTTACTACGGAATCAAAGCTTATCC	NA	NA	-0.36	NA	0.49	0.44	-0.44	0.54	NA	-0.40	NA
	13	ACGTTTTTACTAAGGAATCAAAGTTTATCC	NA	NA	-0.36	NA	NA	0.29	-0.42	0.37	NA	-0.51	NA
	14	ACGTTTTTACTACGGAGTCAAAGTTTATCC	NA	NA	-0.37	NA	0.48	0.42	-0.54	0.54	NA	-0.41	NA
	15	ACGTTTTTACTACGGGACCAAAGTTTATCC	NA	0.31	-0.37	NA	0.55	0.53	-0.46	0.59	0.33	-0.39	NA
	16	ACGTTTTTACCACGGAATCAAAGTTTATCC	NA	NA	-0.36	NA	0.51	0.46	-0.43	0.57	NA	-0.41	NA
	17	ACGTTCTTACTACGGAATCAAAGTTTATCC	NA	NA	-0.39	NA	0.52	0.40	-0.59	0.59	NA	-0.40	NA
	18	ACGTTTTTACTACGGAATCAAAGGTTATCC	NA	NA	-0.36	NA	0.46	0.46	-0.41	0.51	NA	-0.45	NA
	19	GCGTTTTTACTACGGAATCAAAGTTTATCC	NA	NA	-0.31	-0.31	0.44	0.46	-0.50	0.47	NA	-0.39	NA
	20	ACGTTTTTACTACGGAATCAAAGTTTACCC	NA	NA	-0.32	NA	0.46	0.43	-0.45	0.51	NA	-0.40	NA
	21	ACGTTTCTACTACGGAATCAAAGTTTATCC	NA	NA	-0.38	NA	0.50	0.42	-0.57	0.56	NA	-0.39	NA
	22	AGATTTTTACTACGGAATCAAAGTTTATCC	NA	NA	-0.34	NA	0.39	0.30	-0.55	0.46	NA	-0.35	NA
	23	ACGCCTTTACTACGGAATCAAAGTTTATCC	NA	0.28	-0.41	NA	0.52	0.49	-0.48	0.56	0.30	-0.44	NA
	24	ACGTTTTTGCTACGGAATCAAAGTTTATCC	NA	NA	-0.39	NA	0.48	0.44	-0.50	0.54	NA	-0.42	NA
	25	ACGTTTTTACTACGGAATCAAAGTCTATCC	NA	NA	-0.36	NA	0.49	0.43	-0.47	0.54	NA	-0.40	NA
	26	ACGTTTTTACTACGGAATCAAAGTTCATCC	NA	0.29	-0.36	NA	0.47	0.47	-0.48	0.54	NA	-0.43	NA
	27	ACGTTTTCACTACGGAATCAAAGTTTATCC	NA	NA	-0.36	NA	0.49	0.42	-0.49	0.55	NA	-0.38	NA
	28	ACGTTTTTACTAGGGAATCAAAGTTTATCC	NA	NA	NA	-0.38	0.45	0.46	-0.50	0.46	0.29	-0.37	NA
	29	ACGTTTTTACTACGGGATCAAAGTTTATCC	NA	NA	-0.35	NA	0.49	0.42	-0.40	0.52	NA	-0.35	NA
	30	AGGTTTTTACTACGGAATCAAAGTTTATCC	NA	NA	-0.36	NA	0.52	0.36	-0.45	0.60	NA	-0.31	NA
Marinobacter	1	TACTCTAATAATTCGTA	NA	-0.40	NA	NA	NA	-0.43	NA	NA	-0.31	0.29	NA
	2	CACTCTAATAATTCGTA	NA	-0.43	NA	NA	NA	-0.41	NA	NA	-0.29	NA	NA
	3	TACTCTGATAATTCGTA	NA	-0.42	NA	NA	NA	-0.42	NA	-0.28	-0.31	NA	NA
	4	TACTCTAATAGTTCGTA	NA	-0.31	NA	NA	NA	-0.40	NA	NA	-0.32	NA	NA
	5	TACTCTAACTATACGTA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	6	CACTCTAATAGTTCGTA	NA	-0.46	NA	NA	-0.28	-0.41	NA	-0.36	-0.29	NA	NA
	7	TACTCTAATAATACGTA	NA	-0.55	NA	NA	-0.33	-0.44	NA	-0.31	-0.37	NA	NA
	8	TACTCTAATAATTCGCA	NA	-0.36	NA	NA	NA	-0.43	NA	NA	-0.39	NA	NA
	9	TACTATAACTATACGTA	NA	NA	NA	NA	NA	-0.32	NA	NA	NA	NA	NA
	10	TACTCTAGTAATTCGTA	NA	-0.44	NA	NA	NA	-0.34	NA	NA	NA	NA	NA
	11	TACTCTAATGATTCGTA	NA	-0.40	NA	NA	-0.28	-0.41	NA	-0.33	-0.32	NA	NA
	12	TGCCATAACTATACGTA	NA	0.30	NA	NA	0.48	0.53	NA	0.48	0.36	-0.37	NA
	13	TATTCTAATAATTCGTA	NA	-0.42	NA	NA	NA	-0.41	NA	NA	-0.31	NA	NA
	14	TACTCTAAGAATTCGTA	NA	-0.42	0.32	NA	-0.38	-0.42	NA	-0.38	-0.29	NA	NA
	15	TACTCTAATAACTCGTA	NA	-0.48	NA	NA	-0.31	-0.47	NA	-0.31	-0.37	NA	NA
	16	TACCCTAATAATTCGTA	NA	-0.39	NA	NA	NA	-0.42	NA	NA	-0.37	NA	NA
	17	TACTCTAACAATTCGTA	NA	-0.31	NA	NA	NA	-0.40	NA	NA	-0.28	NA	NA
	18	TGCTCTAATAATTCGTA	NA	-0.49	NA	NA	-0.37	-0.35	NA	-0.38	-0.33	NA	NA
	19	TACTCTAATAATCCGTA	NA	-0.42	NA	NA	NA	-0.35	NA	NA	NA	NA	NA
	20	TACTCTAATAATTCATA	NA	-0.51	NA	NA	-0.30	-0.47	NA	-0.32	-0.37	NA	NA
	21	TACTCTAATAATTTATA	NA	-0.47	NA	NA	-0.40	-0.52	NA	-0.39	-0.48	NA	NA
	22	TACTCTAATAATTCGTG	NA	-0.44	NA	NA	NA	-0.38	NA	NA	NA	NA	NA
	23	TGCTACAACAATTCGTA	NA	NA	NA	-0.34	0.53	0.35	-0.56	0.52	NA	NA	NA
	24	TGCCATAACTGTACGTA	NA	NA	-0.34	NA	0.41	0.42	-0.46	0.45	NA	-0.39	NA

Table continued on next page

Table S2 (continued)

Taxa	Type	Cell counts	Bact. Prod.	Naphth. (EEMS)	Hexadec. (GC-MS)	n-Alkanes (GC-MS)	Phenanth. (GC-MS)	Petroleum (GC-MS)	Hexadec. Ox	Naphth. Ox	Total DOSS	Total EHSS	Peptidase	Glucosi-dase	Lipase	TEP
Oceaniserpentilla	1	-0.63	-0.63	NA	0.69	0.65	NA	NA	NA	NA	NA	NA	-0.73	-0.44	-0.69	-0.60
	2	-0.67	-0.66	NA	0.71	0.67	0.41	NA	NA	NA	NA	NA	-0.78	-0.48	-0.70	-0.61
	3	-0.65	-0.67	NA	0.74	0.69	0.43	NA	NA	NA	NA	NA	-0.76	-0.46	-0.69	-0.60
	4	-0.62	-0.58	NA	0.81	0.80	0.56	NA	NA	NA	NA	NA	-0.75	-0.40	-0.61	NA
	5	-0.66	-0.66	NA	0.69	0.66	0.39	NA	NA	NA	NA	NA	-0.78	-0.50	-0.71	-0.66
	6	-0.70	-0.71	NA	0.69	0.63	NA	NA	NA	NA	NA	NA	-0.80	-0.50	-0.73	-0.63
	7	-0.63	-0.64	NA	0.74	0.69	0.41	NA	NA	NA	NA	NA	-0.77	-0.44	-0.67	-0.54
	8	-0.70	-0.70	NA	0.73	0.69	0.43	NA	NA	-0.29	NA	NA	-0.80	-0.51	-0.71	-0.65
	9	-0.66	-0.65	NA	0.75	0.71	0.45	NA	NA	NA	NA	NA	-0.78	-0.48	-0.69	-0.62
	10	-0.68	-0.69	NA	0.76	0.74	0.46	NA	NA	-0.30	NA	NA	-0.78	-0.44	-0.69	-0.59
	11	-0.66	-0.66	NA	0.72	0.70	0.42	NA	NA	NA	NA	NA	-0.78	-0.48	-0.70	-0.60
	12	-0.65	-0.63	NA	0.77	0.69	0.45	NA	NA	NA	NA	NA	-0.77	-0.46	-0.69	-0.64
	13	-0.48	-0.48	NA	0.83	0.81	0.65	NA	NA	NA	0.46	NA	-0.64	NA	-0.46	NA
	14	-0.61	-0.63	NA	0.78	0.75	0.50	NA	NA	NA	NA	NA	-0.76	-0.43	-0.66	-0.54
	15	-0.72	-0.70	NA	0.68	0.65	NA	-0.38	NA	NA	NA	NA	-0.82	-0.55	-0.76	-0.66
	16	-0.67	-0.67	NA	0.69	0.67	NA	NA	NA	NA	NA	NA	-0.80	-0.49	-0.70	-0.59
	17	-0.65	-0.66	NA	0.75	0.72	0.46	NA	NA	NA	NA	NA	-0.81	-0.48	-0.68	-0.55
	18	-0.62	-0.64	NA	0.68	0.65	0.39	NA	NA	NA	NA	NA	-0.76	-0.45	-0.66	-0.55
	19	-0.63	-0.65	NA	0.79	0.73	0.54	NA	NA	NA	NA	NA	-0.74	-0.48	-0.68	-0.64
	20	-0.62	-0.65	NA	0.65	0.62	0.39	NA	NA	NA	NA	NA	-0.74	-0.48	-0.65	-0.55
	21	-0.66	-0.65	NA	0.74	0.70	0.45	NA	NA	NA	NA	NA	-0.79	-0.49	-0.68	-0.58
	22	-0.52	-0.55	NA	0.81	0.77	0.56	NA	NA	NA	NA	NA	-0.71	-0.41	-0.56	NA
	23	-0.70	-0.69	NA	0.72	0.68	0.42	NA	NA	NA	NA	NA	-0.80	-0.50	-0.72	-0.67
	24	-0.66	-0.65	NA	0.72	0.68	0.40	NA	NA	NA	NA	NA	-0.79	-0.47	-0.69	-0.59
	25	-0.65	-0.63	NA	0.80	0.76	0.49	NA	NA	NA	NA	NA	-0.78	-0.47	-0.68	-0.63
	26	-0.64	-0.69	NA	0.74	0.67	0.44	NA	NA	-0.32	NA	NA	-0.78	-0.45	-0.70	-0.59
	27	-0.64	-0.66	NA	0.79	0.75	0.48	NA	NA	NA	NA	NA	-0.77	-0.45	-0.68	-0.58
	28	-0.62	-0.57	NA	0.77	0.74	0.52	NA	NA	NA	NA	NA	-0.73	-0.50	-0.70	-0.65
	29	-0.62	-0.64	NA	0.77	0.72	0.48	NA	NA	NA	NA	NA	-0.75	-0.43	-0.66	-0.57
	30	-0.62	-0.66	NA	0.76	0.73	0.42	NA	NA	NA	NA	NA	-0.78	-0.44	-0.69	-0.50
Marinobacter	1	0.39	0.41	0.60	NA	NA	NA	0.57	0.29	NA	NA	NA	0.37	NA	0.31	0.69
	2	0.38	0.39	0.60	NA	NA	NA	0.58	0.31	NA	-0.38	NA	0.34	NA	0.31	0.71
	3	0.38	0.39	0.65	NA	NA	NA	0.63	0.34	NA	NA	NA	0.33	NA	0.32	0.77
	4	0.35	0.39	0.63	NA	NA	NA	0.62	0.37	NA	NA	NA	0.30	0.31	0.32	0.74
	5	NA	NA	NA	NA	NA	NA	NA	0.45	0.32	NA	NA	NA	NA	NA	NA
	6	0.42	0.46	0.61	NA	NA	NA	0.59	NA	NA	NA	NA	0.42	0.29	0.38	0.67
	7	0.41	0.37	0.60	NA	NA	NA	0.58	0.33	NA	NA	NA	0.38	0.33	0.38	0.78
	8	0.32	0.39	0.73	NA	NA	0.43	0.71	0.44	0.32	NA	NA	NA	NA	0.30	0.81
	9	NA	NA	NA	NA	NA	NA	0.38	NA	NA	NA	NA	NA	NA	NA	0.74
	10	0.38	0.41	0.61	NA	NA	NA	0.61	NA	NA	NA	NA	0.35	NA	0.32	0.70
	11	0.40	0.46	0.59	NA	NA	NA	0.57	0.33	NA	NA	NA	0.35	NA	0.38	0.68
	12	-0.67	-0.66	NA	0.53	0.51	NA	NA	-0.30	-0.38	0.39	NA	-0.64	-0.41	-0.65	-0.75
	13	0.36	0.33	0.56	NA	NA	NA	0.53	0.32	NA	NA	NA	0.30	0.30	0.33	0.74
	14	0.47	0.43	0.58	NA	NA	NA	0.59	0.29	NA	NA	NA	0.49	0.36	0.47	0.75
	15	0.46	0.42	0.55	NA	NA	NA	0.53	0.38	NA	NA	NA	0.42	0.34	0.41	0.84
	16	0.34	0.43	0.65	NA	NA	NA	0.62	0.34	NA	NA	NA	0.31	NA	0.35	0.60
	17	0.34	0.43	0.66	NA	NA	NA	0.65	0.39	NA	NA	NA	0.32	NA	0.30	0.73
	18	0.43	0.40	0.65	NA	NA	NA	0.66	NA	NA	NA	NA	0.39	NA	0.41	0.80
	19	0.31	0.32	0.58	NA	NA	NA	0.57	0.37	NA	-0.41	NA	NA	NA	NA	0.75
	20	0.45	0.43	0.62	NA	NA	NA	0.62	0.41	NA	NA	NA	0.37	NA	0.40	0.80
	21	0.54	0.50	0.60	NA	NA	NA	0.60	0.42	0.32	NA	NA	0.39	NA	0.52	0.80
	22	0.33	0.32	0.60	NA	NA	NA	0.60	0.37	NA	-0.44	NA	NA	NA	NA	0.71
	23	-0.56	-0.55	NA	0.62	0.54	0.41	NA	NA	NA	NA	NA	-0.64	-0.42	-0.61	-0.58
	24	-0.57	-0.59	NA	0.53	0.50	NA	NA	NA	-0.30	NA	NA	-0.63	-0.39	-0.55	NA

Abbreviations: Bact. prod. (bacterial production), bis-2-(ethylhexyl)sulfosuccinate (DOSS), ethylhexylsulfosuccinate (EHSS), excitation/emission matrix spectra (EEMS), gas chromatography-mass spectrometry (GC-MS), hexadecane (hexadec.), naphthalene (naphth.), not analyzed (NA), oxidation (ox.), phenanthrene (phenanth.)

Table S3: Procedure, treatment and storage of samples for the microcosms simulating DWH spill-like plumes (abiotic control, biotic control, WAF, dispersant-only, CEWAF, CEWAF+nutrients) monitored for 6 weeks. Numbers indicate biological replicates analyzed, respectively.

Analysis	Sample (ml)	Procedure	Preservation	Storage
DIC	5	Transferred sample into a stoppered and crimped 10.8 ml helium-purged headspace vial containing 1 NaOH pellet	NaOH	RT
NH_4	5	Transferred sample into a sterile 15 ml tube containing 100 µl phenol	Phenol	4°C
DOC and nutrients	45	Filtered sample through 0.22 µm-sterivex filter into clean plastic bottle	NA	-20°C
Cell counts	9	Transferred sample into a sterile 20 ml plastic scint vial containing 1 ml of 37% formaldehyde	3.7% formaldehyde	-20°C
DNA	500	Filtered sample through 0.22 µm-sterivex filter and frozen sample immediately	NA	-80°C
DOSS and EHSS	7.5	Transferred sample into a sterile 15 ml tube containing 2.5 ml isopropanol	25% isopropanol	-20°C
DOSS and EHSS rinsate	NA	After sampling was completed, microcosm bottles were rinsed with 20 ml methanol and rinsate collected in sterile 50 ml centrifuge vial	Methanol	-20°C
Hydrocarbons	500	Filtered sample through 0.7 µm-filter into clean glass bottles, kept at 4°C for a few hours and then extracted	NA	4°C
DOM	200	Filtered sample through 0.7 µm-filter into clean glass bottles, kept at -20°C for a few days and then extracted	NA	-20°C
Bacterial Production	10	Transferred sample into a sterile 50 ml tube and stored over night until analysis	NA	8°C
Hexadecane oxidation rates	30	Transferred sample into a sterile 50 ml tube and stored over night	NA	8°C
Naphthalene oxidation rates	30	Transferred sample into a sterile 50 ml tube and stored over night	NA	8°C
Enzyme activity	30	Transferred sample into a sterile 50 ml tube and stored over night	NA	8°C
TEP	500	Transferred sample into a clean plastic bottle	3.7% formaldehyde	4°C

Table S4: Sampling strategy for the microcosms simulating DWH spill-like plumes (abiotic control, biotic control, dispersant-only, CEWAF, oil-only, CEWAF+nutrients) monitored for 6 weeks. Numbers indicate biological replicates analyzed, respectively.

Treat-ment	Time (weeks)	Salinity	pH	O_2 (µM)	DOC (µM)	TD (µM)	TDP (µM)	NO_2 (µM)	NO_3 (µM)	PO_4 (µM)	NH_4 (µM)	DIC (mM)	Cell counts (ml^{-1})	Bact. Prod. (nM C/day)
Abiotic Control	0	3	3	3	3	3	3	3	3	3	3	3	3	3
	1	NA	3	3	3	3	3	3	3	3	3	3	3	3
	2.5	NA	3	3	3	3	3	3	3	3	3	3	3	3
	4	NA	3	3	3	3	3	3	3	3	3	3	3	3
	6	3	3	3	3	3	3	3	3	3	3	3	3	3
Biotic Control	0	3	3	3	3	3	3	3	3	3	3	3	3	3
	1	NA	3	3	3	3	3	3	3	3	3	3	3	3
	2.5	NA	3	3	3	3	3	3	3	3	3	3	3	3
	4	NA	3	3	3	3	3	3	3	3	3	3	3	3
	6	3	3	3	3	3	3	3	3	3	3	3	3	3
Oil	0	3	3	3	3	3	3	3	3	3	3	3	3	3
	1	NA	3	3	3	3	3	3	3	3	3	3	3	3
	2.5	NA	3	3	3	3	3	3	3	3	3	3	3	3
	4	NA	3	3	3	3	3	3	3	3	3	3	3	3
	6	3	3	3	3	3	3	3	3	3	3	3	3	3
Dispersants	0	3	3	3	3	3	3	3	3	3	3	3	3	3
	1	NA	3	3	3	3	3	3	3	3	3	3	3	3
	2.5	NA	3	3	3	3	3	3	3	3	3	3	3	3
	4	NA	3	3	3	3	3	3	3	3	3	3	3	3
	6	3	3	3	3	3	3	3	3	3	3	3	3	3
CEWAF	0	3	3	3	3	3	3	3	3	3	3	3	3	3
	1	NA	3	3	3	3	3	3	3	3	3	3	3	3
	2.5	NA	3	3	3	3	3	3	3	3	3	3	3	3
	4	NA	3	3	3	3	3	3	3	3	3	3	3	3
	6	3	3	3	3	3	3	3	3	3	3	3	3	3
CEWAF+nutrients	0	3	3	3	3	3	3	3	3	3	3	3	3	3
	1	NA	3	3	3	3	3	3	3	3	3	3	3	3
	2.5	NA	NA	NA	NA	NA	NA	NA	NA	NA	1	NA	1	1
	4	NA	NA	NA	NA	NA	NA	NA	NA	NA	1	NA	1	1
	6	3	3	3	3	3	3	3	3	3	3	3	3	3

Table continued on next page

Table S4 (continued)

Treatment	Time (weeks)	EEMS data		GC-MS data					^{14}C Hexadec. rate (nM/day)	^{14}C Naphth. rate (nM/day)
		Oil (µg/L)	Naphth. (µg/L)	Hexadec. (µg/L)	Total n-Alkanes (µg/L)	Naphth. (µg/L)	Phenanth. (µg/L)	Total Petroleum (µg/L)		
Abiotic Control	0	<LOD	<LOD	<LOD	<LOD	<LOD	<LOD	<LOD	3	3
	1	<LOD	<LOD	<LOD	<LOD	<LOD	<LOD	<LOD	3	3
	2.5	<LOD	<LOD	<LOD	<LOD	<LOD	<LOD	<LOD	3	3
	4	<LOD	<LOD	<LOD	<LOD	<LOD	<LOD	<LOD	3	3
	6	<LOD	<LOD	<LOD	<LOD	<LOD	<LOD	<LOD	3	3
Biotic Control	0	<LOD	<LOD	<LOD	<LOD	<LOD	<LOD	<LOD	3	3
	1	NA	NA	<LOD	<LOD	<LOD	<LOD	<LOD	3	3
	2.5	NA	NA	<LOD	<LOD	<LOD	<LOD	<LOD	3	3
	4	NA	NA	<LOD	<LOD	<LOD	<LOD	<LOD	3	3
	6	<LOD	<LOD	<LOD	<LOD	<LOD	<LOD	<LOD	3	3
Oil	0	1	1	1	1	1	1	1	3	3
	1	1	1	1	1	1	1	1	3	3
	2.5	1	1	1	1	1	1	1	3	3
	4	1	1	1	1	1	1	1	3	3
	6	1	1	1	1	1	1	1	3	3
Dispersants	0	1	1	<LOD	<LOD	<LOD	<LOD	<LOD	3	3
	1	1	1	<LOD	<LOD	<LOD	<LOD	<LOD	3	3
	2.5	1	1	<LOD	<LOD	<LOD	<LOD	<LOD	3	3
	4	1	1	<LOD	<LOD	<LOD	<LOD	<LOD	3	3
	6	1	1	<LOD	<LOD	<LOD	<LOD	<LOD	3	3
CEWAF	0	1	1	1	1	1	1	1	3	3
	1	1	1	1	1	1	1	1	3	3
	2.5	1	1	1	1	1	1	1	3	3
	4	1	1	1	1	1	1	1	3	3
	6	1	1	1	1	1	1	1	3	3
CEWAF+nutrients	0	1	1	1	1	1	1	1	3	3
	1	1	1	1	1	1	1	1	3	3
	2.5	NA	NA	NA	NA	NA	NA	NA	1	1
	4	NA	NA	NA	NA	NA	NA	NA	1	1
	6	1	1	1	1	1	1	1	3	3

Table continued on next page

Table S4 (continued)

Treatment	Time (weeks)	Dispersants			Hydrolysis rates			TEP (Gxeq/L)
		Total DOSS (nM)	Total EHSS (nM)	Total T80, T85 and S80 (nM)	Peptidase (nM/day)	Glucosidase (nM/day)	Lipase (nM/day)	
Abiotic Control	0	NA	NA	NA	3	3	3	3
	1	NA	NA	NA	3	3	3	NA
	2.5	NA	NA	NA	3	3	3	NA
	4	NA	NA	NA	3	3	3	NA
	6	NA	NA	NA	3	3	3	3
Biotic Control	0	NA	NA	NA	3	3	3	3
	1	NA	NA	NA	3	3	3	NA
	2.5	NA	NA	NA	3	3	3	NA
	4	NA	NA	NA	3	3	3	NA
	6	NA	NA	NA	3	3	3	3
Oil	0	NA	NA	NA	3	3	3	3
	1	NA	NA	NA	3	3	3	3
	2.5	NA	NA	NA	3	3	3	3
	4	NA	NA	NA	3	3	3	3
	6	NA	NA	NA	3	3	3	3
Dispersants	0	3	3	3	3	3	3	NA
	1	3	3	3	3	3	3	NA
	2.5	3	3	3	3	3	3	NA
	4	3	3	3	3	3	3	NA
	6	3	3	3	3	3	3	NA
CEWAF	0	3	3	3	3	3	3	NA
	1	3	3	3	3	3	3	NA
	2.5	3	3	3	3	3	3	NA
	4	3	3	3	3	3	3	NA
	6	3	3	3	3	3	3	NA
CEWAF+nutrients	0	3	3	3	3	3	3	NA
	1	3	3	3	3	3	3	NA
	2.5	NA	NA	NA	1	1	1	NA
	4	NA	NA	NA	NA	NA	NA	NA
	6	3	3	3	3	3	3	NA

Abbreviations: bacterial production (bact. prod.), EEMS (excitation/emission matrix spectra), gas chromatography-mass spectrometry (GC-MS), hexadecane (hexadec.), limit of detection (LOD), naphthalene (naphth.), not analyzed (NA), oxidation (ox.), phenanthrene (phenanth.).

Table S5: CARD-FISH probes, formamide concentrations, and probe coverage.

Probe name	Specificity	Formamide [%]	Sequence (5' to 3')	Reference
ALT1413	*Alteromonas, Colwellia*	40	TTT GCA TCC CAC TCC CAT	(22)
EUB338	Most Bacteria	35	GCT GCC TCC CGT AGG AGT	(21)
EUB338 II	*Planctomycetales*	35	GCA GCC ACC CGT AGG TGT	(20)
EUB338 III	*Verrucomicrobiales*	35	GCT GCC ACC CGT AGG TGT	(20)
GAM42a	*Gammaproteobacteria*	35	GCC TTC CCA CAT CGT TT	(19)
cBet42a	Competitor against *Betaproteobacteria*	35	GCC TTC CCA CTT CGT TT	(19)