

Microbial community dynamics during biodegradation of crude oil and its response to biostimulation in Svalbard seawater at low temperature

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Section S1: Prokaryotic Community Structure in Different Treatments According to Kaiju.

Table S1. The means and standard deviations (in parenthesis, $n = 2$) of physicochemical characteristics of the seawater (SW), oil contaminated seawater (SWO) and biostimulated oil contaminated seawater (SWOB). The numbers in sample codes denote time in months. TOC – total organic carbon, N_{tot} – total nitrogen, P_{tot} – total phosphorous, NA – not analysed.

Sample	T (°C)	Salinity (ppt)	pH	O ₂ (mg/L)	TOC (mg/L)	N_{tot} (mg/L)	NH ₄ -N (mg/L)	NO ₃ -N (mg/L)	P_{tot} (mg/L)
SW0	2.0 (0.2)	35.2 (0.3)	7.91 (0.04)	NA	2.20 (0.17)	<0.5	0.064 (0.014)	0.40 (0.10)	0.14 (0.02)
SW4	4.0 (0.1)	34.6 (1.5)	7.96 (0.20)	10.5 (0.5)	NA	<1.0	0.036 (0.002)	0.67 (0.03)	<0.1
SWO4	4.0 (0.1)	33.8 (1.4)	8.00 (0.20)	10.5 (0.5)	NA	<1.0	0.018 (0.001)	0.66 (0.03)	<0.1
SWOB4	4.0 (0.1)	35.2 (1.7)	6.82 (0.02)	8.3 (0.4)	18.3 (1.0)	445 (2.0)	255 (1.00)	42.8 (2.00)	152 (5.0)
SW8	4.0 (0.1)	35.0 (1.5)	8.23 (0.20)	11.8 (0.6)	NA	<0.5	0.033 (0.002)	<0.3	<0.1
SWO8	4.0 (0.1)	34.6 (1.5)	8.16 (0.20)	NA	NA	<0.5	0.010 (0.001)	<0.3	<0.1
SWOB8	4.0 (0.1)	36.0 (1.7)	6.85 (0.02)	10.6 (0.5)	18.0 (0.9)	487 (3.0)	262 (2.00)	22.0 (1.00)	105 (3.0)

Table S2. The characteristics of primer pairs and programs used in qPCR. LOQ – limit of quantification.

Target gene	Primers	Primer sequence 5'-3'	Amplicon size (bp)	Primer concentration (μM)	Amplification program	LOQ (copies/mL water)	Primer reference
Bacterial 16S rRNA	Bact517F	GCCAGCAGCCGCGGTAA	530	0.6	95°C 10 min; 35 cycles: 95°C 30 s; 60°C 45 s; 72°C 45 s ^M	50	[1]
	Bact1028R	CGACARCCATGCASCACCT					[2]
Archaeal 16S rRNA	Arc519F	CAGYCGCCRCGGTAA	393	0.6	95°C 10 min; 35 cycles: 95°C 15 s; 56°C 30 s; 72°C 30 s ^M	50	[3]
	Arch910R	GCYCCCCCGCCWATTC					
<i>Colwellia</i> 16S rRNA	Col134F	CCTTATGGTGGGGGACAACA	96	0.6	95°C 10 min; 35 cycles: 95°C 15 s; 56°C 30 s; 72°C 30 s ^M	25	Modified from [4]
	Col209Rm	AATCAAATGGCGARAGGTCC					
<i>Cycloclasticus</i> 16S rRNA	Cyc467F	AACCTTAGGCCCTGACGT	128	0.6	95°C 10 min; 40 cycles: 95°C 15 s; 54°C 30 s; 72°C 30 s ^M	25	[5]
	Cyc577R	TGTTTAACCGCCTACGCG					
<i>Pseudomonas</i> 16S rRNA	Ps-for	GGTCTGAGAGGATGATCAGT	990	0.6	95°C 10 min; 40 cycles: 95°C 30 s; 55°C 45 s; 72°C 45 s ^M	25	[6]
	Ps-rev	TTAGCTCCACCTCGCGGC					

^M Immediately after the qPCR assay melting curve analysis was performed by increasing the temperature from 70 °C to 90 °C (0.35 °C/3 s) with continuous fluorescence recording.

Table S3. The number of total reads, reads after quality trimming, coverage and diversity metrics, the proportions of classified reads according to different taxonomic assignment methods (%), and the numbers of contigs in the metagenomes of seawater (SW), oil contaminated seawater (SWO) and biostimulated oil contaminated seawater (SWOB). The numbers in sample codes denote time in months.

Sample	Number of total reads	Number of reads after quality trimming	Coverage	Diversity	Kaiju	Classified reads (%)			Contigs
						Kaiju/MAR	Kraken2	Bracken	
SW0	61252004	60751670	0.774	18.85	67.6	74.5	18.0	18.0	215103 (453660249 bp)
SW4	58800661	58762069	0.968	17.55	72.7	71.3	25.1	25.0	78017 (232006212 bp)
SWO4	62447105	62411054	0.990	17.87	88.3	85.3	46.6	42.6	66796 (217880730 bp)
SWOB4	55743647	54954391	0.998	17.26	92.2	87.2	62.1	62.1	23475 (113304343 bp)
SW8	61429147	60960320	0.968	18.29	78.2	72.1	27.0	27.0	104532 (377477043 bp)
SWO8	57527324	57467303	0.992	17.50	77.6	79.3	37.6	37.6	67393 (205560027 bp)
SWOB8	60566394	60529898	1.000	16.37	91.0	84.4	39.1	39.1	19588 (97474974 bp)

Table S4. The number of obtained good quality total, bacterial (Bact) and archaeal (Arch) 16S rRNA gene sequences of amplicon-based sequencing, as well as the coverage estimates, number of operational taxonomic units (OTUs) and diversity indices (1/S - Inverse Simpson index, SH – Shannon diversity index) of bacterial community in the seawater (SW), oil contaminated seawater (SWO) and biostimulated oil contaminated seawater (SWOB). The first number in sample codes denotes time in months and the second number denotes treatment parallel.

Sample	No of sequences			Coverage	No of OTUs	Diversity indices	
	Total	Bact	Arch	Bact	Bact	1/S Bact	SH Bact
SW0.1	42827	41033	1794	0.981	1365	12.38	4.27
SW0.2	43248	41105	2143	0.982	1312	12.52	4.27
SW4.1	45895	45837	58	0.979	1280	19.48	4.21
SW4.2	25449	25375	74	0.976	1603	30.93	4.52

Sample	No of sequences			Coverage	No of OTUs	Diversity indices	
	Total	Bact	Arch	Bact	Bact	1/S Bact	SH Bact
SWO4.1	30636	30527	109	0.974	1654	9.97	4.01
SWO4.2	74275	74156	119	0.980	1078	2.86	2.53
SWOB4.1	43632	43549	83	0.976	1520	10.38	3.81
SWOB4.2	37753	37691	62	0.977	1391	11.62	3.78
SW8.1	53601	53551	50	0.977	1501	3.69	3.20
SW8.2	54580	54539	41	0.977	1596	17.23	4.32
SWO8.1	80806	80680	126	0.977	1468	8.67	3.58
SWO8.2	106585	106443	142	0.978	1345	4.57	2.96
SWOB8.1	101981	101889	92	0.976	1701	15.37	4.16
SWOB8.2	54652	54617	35	0.977	1656	8.78	3.77

Table S5. The mean and standard deviations (in parenthesis, $n = 2$) of n -C17/Pristane and n -C18/Phytane ratios and concentrations ($\mu\text{g/L}$) of polyaromatic hydrocarbons (PAH) in sterilized oil contaminated seawater (SWOs), oil contaminated seawater (SWO) and biostimulated oil contaminated seawater (SWOB). The numbers in sample codes denote time in months.

		SWOs/SWO/ SWOB 0	SWOs4	SWOs8	SWO4	SWO8	SWOB4	SWOB8
		Ratios						
	n -C17/Pristane	0.25 (0.07)	0.25 (0.07)	0.20 (0.06)	0.25 (0.07)	0.20 (0.02)	0.20 (0.04)	0.10 (0.01)
	n -C18/Phytane	0.40 (0.14)	0.40 (0.14)	0.30 (0.10)	0.40 (0.14)	0.30 (0.10)	0.10 (0.02)	0 (0)
		PAH concentrations						
2- ring	Naphthalene	6465 (582)	2346.92 (211)	1092.98 (98)	1845.32 (166)	927.14 (83)	26.21 (2.4)	19.80 (2)
3- ring	Acenaphthylene	4.55 (0.4)	3.42 (0.3)	5.60 (0.5)	3.53 (0.3)	1.49 (0.1)	3.13 (0.3)	3.94 (0.4)
	Acenaphthene	355 (32)	132.53 (12)	163.85 (15)	137.96 (12)	174.47 (16)	150.72 (14)	96.78 (9)
	Fluorene	1169 (105)	528.19 (47.5)	525.85 (47)	544.00 (49)	602.74 (54)	584.28 (53)	276.08 (25)
	Phenanthrene	1745 (105)	1383.49 (83)	1062.98 (64)	1333.38 (80)	1284.70 (77)	1644.95 (99)	675.81 (41)
	Anthracene	19.2 (1.2)	34.15 (2.0)	16.59 (1)	52.61 (3)	23.34 (1.4)	37.61 (2)	9.23 (0.6)
\geq 4- ring	Fluoranthene	152 (9.1)	135.87 (8.2)	103.86 (6)	150.62 (9)	110.05 (7)	143.58 (9)	106.17 (6)
	Pyrene	161 (6.4)	132.53 (5.3)	112.52 (4.5)	150.37 (6)	122.08 (5)	134.48 (5.4)	110.81 (4)
	Benzo(a)anthracene	30 (1.2)	14.46 (0.6)	14.29 (0.5)	11.82 (0.5)	24.39 (1)	28.23 (1)	24.87 (1)
	Chrysene	174 (7.0)	83.15 (3.3)	109.14 (4.4)	87.65 (3.5)	174.17 (7)	128.65 (5)	138.16 (5.5)

	SWO _s /SWO/ SWOB 0	SWO _s 4	SWO _s 8	SWO4	SWO8	SWOB4	SWOB8
Benzo(b)fluoranthene	50.9 (2.0)	34.14 (1.4)	30.83 (1)	31.39 (1.3)	45.85 (2)	43.31 (2)	48.05 (2)
Benzo(k)fluoranthene	8.35 (0.3)	6.06 (0.2)	6.96 (0.3)	5.40 (0.2)	10.04 (0.4)	6.96 (0.3)	6.35 (0.3)
Benzo(a)pyrene	30.2 (1.2)	20.29 (0.8)	17.88 (0.7)	19.75 (0.8)	21.23 (0.8)	26.10 (1)	19.55 (0.8)
Indeno(1,2,3-cd)pyrene	8.01 (0.3)	6.67 (0.3)	5.12 (0.2)	6.19 (0.2)	7.77 (0.3)	8.17 0.3)	8.48 (0.3)
Benzo(ghi)perylene	24.2 (1.0)	15.20 (0.6)	14.76 (0.6)	14.16 (0.6)	20.36 (0.8)	19.70 (0.8)	19.86 (0.8)
Dibenzo(a,h)anthracene	5.99 (0.2)	4.26 (0.2)	4.02 (0.2)	3.03 (0.1)	6.31 (0.2)	4.39 (0.2)	6.01 (0.2)

Table S6. The mean abundances and standard deviations (in parenthesis, $n = 2$) of 16S rRNA genes specific to bacteria (B16S), archaea (A16S), *Colwellia*, *Cycloclasticus*, and *Pseudomonas* in the seawater (SW), oil contaminated seawater (SWO) and biostimulated oil contaminated seawater (SWOB). The numbers in sample codes denote time in months. NA – not analysed.

Target gene	SW0	SW4	SW8	SWO4	SWO8	SWOB4	SWOB8
B16S	1.02×10^6 (0.05×10^6)	3.72×10^6 (1.05×10^6)	5.23×10^6 (3.52×10^6)	2.90×10^6 (1.49×10^6)	4.59×10^6 (1.18×10^6)	8.28×10^7 (1.04×10^7)	1.24×10^8 (0.24×10^8)
A16S	1.83×10^5 (0.71×10^5)	1.89×10^4 (0.77×10^4)	3.37×10^4 (4.14×10^4)	5.46×10^4 (0.59×10^4)	1.01×10^5 (0.38×10^5)	2.63×10^4 (1.99×10^4)	3.35×10^4 (1.58×10^4)
<i>Colwellia</i> 16S rRNA	NA	NA	5.26×10^5 (6.79×10^5)	NA	6.01×10^5 (9.59×10^4)	6.68×10^5 (5.25×10^5)	4.53×10^5 (3.58×10^5)
<i>Cycloclasticus</i> 16S rRNA	NA	NA	9.51×10^3 (1.37×10^3)	NA	4.74×10^2 (1.07×10^2)	1.25×10^5 (1.75×10^5)	9.35×10^6 (1.07×10^6)
<i>Pseudomonas</i> 16S rRNA	NA	NA	1.64×10^5 (1.74×10^5)	NA	2.25×10^5 (3.29×10^3)	7.95×10^6 (2.10×10^6)	1.17×10^7 (4.27×10^6)

Table S7. Major (the 20 most abundant in each sample) bacterial phyla proportions (%) based on taxonomic classification using Kaiju with the NCBI-nr database in the seawater (SW), oil contaminated seawater (SWO) and biostimulated oil contaminated seawater (SWOB). The numbers in sample codes denote time in months.

Phylum	Class	SW0	SW4	SW8	SWO4	SWO8	SWOB4	SWOB8
<i>Proteobacteria</i>		82.33	79.08	69.84	73.33	76.82	90.30	94.52
	<i>Alphaproteobacteria</i>	19.82	11.15	14.20	36.06	18.57	6.75	16.72
	<i>Betaproteobacteria</i>	3.87	3.53	3.96	1.16	1.28	1.41	1.82

Phylum	Class	SW0	SW4	SW8	SW04	SW08	SW0B4	SW0B8
	<i>Gammaproteobacteria</i>	52.94	60.54	48.20	34.94	55.41	80.58	74.46
	<i>Deltaproteobacteria</i>	2.14	2.11	1.32	0.28	0.46	0.13	0.27
	<i>Epsilonproteobacteria</i>	0.19	0.22	0.19	0.08	0.26	0.06	0.11
<i>Bacteroidetes</i>		3.23	13.63	22.47	23.31	15.26	7.35	3.88
<i>Planctomycetes</i>		1.79	1.71	3.12	0.86	4.32	0.049	0.08
<i>Firmicutes</i>		1.98	2.38	1.22	1.20	0.97	1.76	0.71
<i>Actinobacteria</i>		2.90	1.35	1.06	0.56	0.99	0.31	0.40
<i>Verrucomicrobia</i>		2.13	0.18	0.49	0.10	0.21	0.02	0.03
<i>Chloroflexi</i>		1.75	0.19	0.19	0.07	0.13	0.02	0.05
<i>Cyanobacteria</i>		0.40	0.30	0.36	0.14	0.52	0.06	0.09
<i>Acidobacteria</i>		0.45	0.23	0.26	0.11	0.16	0.02	0.04
<i>Gemmatimonadetes</i>		0.51	0.06	0.06	0.02	0.05	<0.01	0.01
<i>Nitrospinae</i>		0.55	0.01	0.04	0.03	0.02	<0.01	0.01
<i>Ca. Marinimicrobia</i>		0.56	0.02	0.03	0.01	0.03	<0.01	<0.01
<i>Spirochaetes</i>		0.15	0.09	0.08	0.03	0.05	0.01	0.02
<i>Nitrospirae</i>		0.11	0.08	0.07	0.03	0.04	0.01	0.02
<i>Balneolaeota</i>		0.05	0.02	0.10	0.02	0.05	<0.01	0.01
<i>Ca. Rokubacteria</i>		0.08	0.04	0.04	0.01	0.01	<0.01	0.01
<i>Ignavibacteriae</i>		0.04	0.03	0.03	0.01	0.02	<0.01	0.01
<i>Deinococcus-Thermus</i>		0.04	0.03	0.03	0.01	0.02	<0.01	0.01
<i>Calditrichaeota</i>		0.06	0.03	0.03	0.01	0.02	<0.01	<0.01
<i>Chlorobi</i>		0.03	0.03	0.03	0.01	0.01	<0.01	0.01
<i>Lentisphaerae</i>		0.06	0.02	0.02	0.01	0.02	<0.01	<0.01
<i>Chlamydiae</i>		0.03	0.05	0.01	0.01	0.01	<0.01	<0.01
<i>Ca. Omnitrophica</i>		0.04	0.02	0.03	0.01	0.01	<0.01	<0.01
<i>Ca. Tectomicrobia</i>		0.06	0.01	0.02	0.01	0.01	<0.01	<0.01
<i>Armatimonadetes</i>		0.03	0.02	0.02	0.01	0.02	<0.01	<0.01
<i>Tenericutes</i>		0.02	0.06	0.02	<0.01	0.01	<0.01	<0.01
<i>Ca. Dadabacteria</i>		0.05	0.01	0.01	<0.01	0.01	<0.01	<0.01
<i>Ca. Poribacteria</i>		0.06	<0.01	<0.01	<0.01	<0.01	<0.01	<0.01
<i>Aquificae</i>		0.02	0.01	0.01	<0.01	0.01	<0.01	<0.01
<i>Thermotogae</i>		0.02	<0.01	<0.01	<0.01	0.01	<0.01	<0.01

Phylum	Class	SW0	SW4	SW8	SW04	SW08	SW0B4	SW0B8
<i>Ca. Melainabacteria</i>		0.01	0.01	0.01	<0.01	0.01	<0.01	<0.01
<i>Deferribacteres</i>		<0.01	<0.01	<0.01	<0.01	0.01	<0.01	<0.01

Table S8. Major (the 20 most abundant in each sample) bacterial phyla proportions (%) based on taxonomic classification using Kaiju with the MAR_{DB} database in the seawater (SW), oil contaminated seawater (SWO) and biostimulated oil contaminated seawater (SWOB). The numbers in sample codes denote time in months.

Phylum	Class	SW0	SW4	SW8	SW04	SW08	SW0B4	SW0B8
<i>Proteobacteria</i>		84.94	82.15	73.64	74.21	75.20	91.20	94.17
	<i>Alphaproteobacteria</i>	12.58	11.94	15.47	37.17	17.38	8.90	19.61
	<i>Betaproteobacteria</i>	0.53	1.31	2.45	0.31	0.30	0.70	1.30
	<i>Gammaproteobacteria</i>	67.20	64.65	51.17	35.19	55.77	79.54	70.35
	<i>Deltaproteobacteria</i>	2.01	2.16	1.11	0.30	0.34	0.29	0.54
	<i>Epsilonproteobacteria</i>	0.05	0.14	0.13	0.15	0.25	0.08	0.14
<i>Bacteroidetes</i>		2.51	13.30	19.95	22.67	14.46	7.90	4.27
<i>Planctomycetes</i>		1.96	1.74	3.77	1.58	8.70	0.09	0.18
<i>Actinobacteria</i>		1.59	0.96	0.50	0.42	0.36	0.33	0.51
<i>Verrucomicrobia</i>		2.26	0.36	0.62	0.11	0.21	0.05	0.09
<i>Chloroflexi</i>		2.22	0.19	0.17	0.07	0.10	0.04	0.08
<i>Cyanobacteria</i>		0.26	0.31	0.28	0.41	0.31	0.11	0.18
<i>Ca. Marinimicrobia</i>		1.42	0.09	0.11	0.04	0.10	0.02	0.04
<i>Gemmatimonadetes</i>		1.39	0.10	0.13	0.04	0.08	0.01	0.03
<i>Firmicutes</i>		0.15	0.28	0.22	0.10	0.13	0.12	0.20
<i>Nitrospinae</i>		0.69	0.03	0.05	0.04	0.03	0.01	0.01
<i>Acidobacteria</i>		0.20	0.07	0.07	0.13	0.06	0.01	0.02
<i>Nitrospirae</i>		0.04	0.06	0.06	0.02	0.02	0.01	0.04
<i>Aquificae</i>		0.04	0.02	0.04	0.03	0.05	0.03	0.03
<i>Spirochaetes</i>		0.06	0.05	0.05	0.02	0.02	0.01	0.02
<i>Balneolaeota</i>		0.01	0.02	0.07	0.01	0.04	0.01	0.01
<i>Ca. Poribacteria</i>		0.05	0.02	0.03	0.01	0.02	<0.01	<0.01
<i>Ca. Tectomicrobia</i>		0.02	0.02	0.02	0.01	0.01	0.01	0.01

Phylum	Class	SW0	SW4	SW8	SW04	SW08	SW0B4	SW0B8
<i>Ignavibacteriae</i>		0.01	0.02	0.03	0.01	0.01	<0.01	0.01
<i>Lentisphaerae</i>		0.02	0.02	0.02	0.01	0.01	<0.01	0.01
<i>Kiritimatiellaeota</i>		0.02	0.02	0.02	0.01	0.01	<0.01	0.01
<i>Chlorobi</i>		0.01	0.02	0.02	0.01	0.01	0.01	0.01
<i>Thermodesulfobacteria</i>		<0.01	0.01	0.01	0.01	0.02	0.01	0.01
<i>Ca. Kaiserbacteria</i>		0.01	0.01	0.01	0.01	0.01	<0.01	<0.01
<i>Thermotogae</i>		0.01	0.01	0.01	<0.01	0.01	<0.01	0.01

Table S9. Major (the 20 most abundant in each sample) bacterial phyla proportions (%) based on taxonomic classification using Kraken2 with the Standard Kraken2 database in the seawater (SW), oil contaminated seawater (SWO) and biostimulated oil contaminated seawater (SWOB). The numbers in sample codes denote time in months.

Phylum	Class	SW0	SW4	SW8	SW04	SW08	SW0B4	SW0B8
<i>Proteobacteria</i>		83.67	75.31	57.52	67.27	80.49	92.69	93.33
	<i>Alphaproteobacteria</i>	15.35	12.71	14.85	23.08	10.69	5.25	18.65
	<i>Betaproteobacteria</i>	3.39	4.21	3.21	2.14	4.69	1.21	3.89
	<i>Gammaproteobacteria</i>	61.06	54.69	36.42	39.85	63.18	85.12	67.87
	<i>Deltaproteobacteria</i>	0.46	0.62	0.44	0.24	0.16	0.08	0.28
	<i>Epsilonproteobacteria</i>	0.60	0.30	0.37	0.14	0.28	0.07	0.16
<i>Bacteroidetes</i>		4.31	15.64	33.66	28.10	15.91	4.43	3.87
<i>Firmicutes</i>		7.20	6.12	5.56	2.75	2.19	2.29	1.47
<i>Actinobacteria</i>		2.42	1.70	1.60	1.35	0.69	0.40	0.87
<i>Cyanobacteria</i>		0.92	0.50	0.40	0.18	0.24	0.09	0.19
<i>Planctomycetes</i>		0.50	0.23	0.76	0.14	0.26	0.02	0.07
<i>Tenericutes</i>		0.22	0.06	0.09	0.02	0.04	0.01	0.02
<i>Spirochaetes</i>		0.10	0.08	0.06	0.03	0.03	0.01	0.03
<i>Verrucomicrobia</i>		0.10	0.04	0.05	0.03	0.02	0.01	0.02
<i>Fusobacteria</i>		0.08	0.05	0.07	0.01	0.02	<0.01	0.01
<i>Deinococcus-Thermus</i>		0.04	0.06	0.04	0.03	0.01	0.01	0.02
<i>Chloroflexi</i>		0.07	0.05	0.03	0.01	0.02	0.01	0.02
<i>Acidobacteria</i>		0.07	0.03	0.03	0.02	0.01	0.01	0.02
<i>Thermotogae</i>		0.05	0.02	0.02	0.01	0.01	<0.01	0.01

Phylum	Class	SW0	SW4	SW8	SW04	SW08	SW0B4	SW0B8
<i>Chlorobi</i>		0.03	0.02	0.02	0.01	0.01	<0.01	0.02
<i>Aquificae</i>		0.05	0.01	0.01	<0.01	0.01	<0.01	<0.01
<i>Chlamydiae</i>		0.03	0.01	0.01	<0.01	0.01	<0.01	0.01
<i>Gemmatimonadetes</i>		0.02	0.01	0.01	0.01	<0.01	<0.01	<0.01
<i>Thermodesulfobacteria</i>		0.03	0.01	0.01	<0.01	0.01	<0.01	<0.01
<i>Nitrospirae</i>		0.01	0.01	0.01	0.01	0.01	<0.01	<0.01
<i>Deferribacteres</i>		0.01	0.01	0.01	<0.01	<0.01	<0.01	<0.01
<i>Synergistetes</i>		0.01	<0.01	<0.01	<0.01	<0.01	<0.01	<0.01
<i>Chrysiogenetes</i>		<0.01	<0.01	<0.01	<0.01	<0.01	<0.01	<0.01

Table S10. Major (the 20 most abundant in each sample) bacterial phyla proportions (%) based on taxonomic classification using Bracken with the Standard Kraken2 database in the seawater (SW), oil contaminated seawater (SWO) and biostimulated oil contaminated seawater (SWOB). The numbers in sample codes denote time in months.

Phylum	Class	SW0	SW4	SW8	SW04	SW08	SW0B4	SW0B8
<i>Proteobacteria</i>		81.90	75.88	57.04	67.21	79.90	92.40	93.18
	<i>Alphaproteobacteria</i>	14.44	12.08	14.41	22.53	10.55	5.16	18.41
	<i>Betaproteobacteria</i>	3.58	4.11	3.45	2.36	4.82	1.25	3.90
	<i>Gammaproteobacteria</i>	62.77	58.72	38.24	41.92	64.06	85.84	70.38
	<i>Deltaproteobacteria</i>	0.43	0.59	0.43	0.23	0.16	0.08	0.28
	<i>Epsilonproteobacteria</i>	0.57	0.29	0.37	0.14	0.28	0.07	0.16
<i>Bacteroidetes</i>		4.06	14.88	32.66	27.33	15.60	4.35	3.82
<i>Firmicutes</i>		9.36	6.41	7.08	3.60	3.10	2.66	1.70
<i>Actinobacteria</i>		2.34	1.64	1.57	1.32	0.69	0.40	0.87
<i>Cyanobacteria</i>		0.90	0.49	0.40	0.19	0.24	0.10	0.19
<i>Planctomycetes</i>		0.47	0.22	0.74	0.13	0.26	0.02	0.07
<i>Tenericutes</i>		0.21	0.06	0.08	0.02	0.04	0.01	0.02
<i>Spirochaetes</i>		0.09	0.07	0.06	0.03	0.03	0.01	0.02
<i>Acidobacteria</i>		0.13	0.03	0.03	0.02	0.02	0.01	0.02
<i>Verrucomicrobia</i>		0.09	0.03	0.05	0.03	0.02	0.01	0.02
<i>Fusobacteria</i>		0.08	0.05	0.06	0.01	0.02	<0.01	0.01
<i>Deinococcus-Thermus</i>		0.04	0.06	0.04	0.03	0.01	0.01	0.02

Phylum	Class	SW0	SW4	SW8	SW04	SW08	SW0B4	SW0B8
<i>Chloroflexi</i>		0.07	0.04	0.03	0.01	0.01	<0.01	0.02
<i>Thermotogae</i>		0.05	0.03	0.04	0.01	0.01	<0.01	0.01
<i>Chlorobi</i>		0.02	0.02	0.02	0.01	0.01	<0.01	0.02
<i>Aquificae</i>		0.05	0.01	0.01	<0.01	0.01	<0.01	<0.01
<i>Chlamydiae</i>		0.03	0.01	0.01	<0.01	0.01	<0.01	0.01
<i>Gemmatimonadetes</i>		0.02	0.01	0.01	0.01	<0.01	<0.01	<0.01
<i>Thermodesulfobacteria</i>		0.02	0.01	0.01	<0.01	0.01	<0.01	<0.01
<i>Nitrospirae</i>		0.01	0.01	0.01	0.01	0.01	<0.01	<0.01
<i>Deferribacteres</i>		0.01	0.01	0.01	<0.01	<0.01	<0.01	<0.01
<i>Synergistetes</i>		0.01	<0.01	<0.01	<0.01	<0.01	<0.01	<0.01
<i>Chrysiogenetes</i>		<0.01	<0.01	<0.01	<0.01	<0.01	<0.01	<0.01

Table S11. The mean proportions and standard deviations (in parenthesis, $n = 2$) of major (the 20 most abundant in each sample) bacterial phyla based on taxonomic classification using amplicon-based sequencing with the SILVA database in the seawater (SW), oil contaminated seawater (SWO) and biostimulated oil contaminated seawater (SWOB). The numbers in sample codes denote time in months.

Phylum	Class	SW0	SW4	SW8	SWO4	SWO8	SWOB4	SWOB8
<i>Proteobacteria</i>		61.02 (0.88)	53.27 (8.10)	43.64 (30.00)	29.71 (12.31)	32.43 (6.41)	59.89 (7.65)	62.16 (1.58)
	<i>Alphaproteobacteria</i>	13.48 (0.37)	24.10 (11.29)	20.24 (21.09)	15.33 (4.30)	7.56 (1.36)	13.38 (0.26)	15.88 (6.28)
	<i>Gammaproteobacteria</i>	45.97 (0.61)	23.00 (12.00)	20.13 (7.88)	13.82 (7.76)	24.25 (7.63)	45.68 (7.76)	45.02 (7.89)
	<i>Deltaproteobacteria</i>	1.27 (0.07)	5.85 (7.21)	2.82 (0.80)	0.34 (0.14)	0.38 (0.11)	0.43 (0.03)	0.78 (0.02)
<i>Bacteroidetes</i>		13.30 (1.58)	35.02 (12.55)	38.63 (39.52)	62.72 (16.69)	53.84 (3.39)	33.48 (7.31)	27.13 (1.60)
<i>Cyanobacteria</i>		14.68 (2.51)	3.88 (1.14)	0.58 (0.23)	2.28 (1.41)	0.16 (0.11)	2.59 (0.25)	0.17 (0.03)
<i>Chloroflexi</i>		1.54 (0.12)	0.36 (0.22)	0.51 (0.08)	0.34 (0.23)	0.32 (0.05)	0.28 (0.03)	0.59 (0.01)
<i>Marinimicrobia</i>		1.62	0.11	0.02	0.08	0.04	0.09	0.02

Phylum	Class	SW0	SW4	SW8	SWO4	SWO8	SWOB4	SWOB8
		(0.02)	(0.05)	(0.02)	(0.05)	(0.02)	(<0.01)	(<0.01)
<i>Verrucomicrobia</i>		1.56	0.86	1.74	0.57	0.67	0.62	1.24
		(0.02)	(0.36)	(1.06)	(0.33)	(0.15)	(0.07)	(0.01)
<i>Planctomycetes</i>		1.47	2.95	9.60	1.69	9.14	0.57	1.91
		(0.12)	(0.73)	(7.78)	(0.67)	(10.89)	(0.06)	(<0.00)
<i>Acidobacteria</i>		1.10	1.32	2.88	1.07	1.85	1.21	2.92
		(0.23)	(0.80)	(0.38)	(0.69)	(0.40)	(0.03)	(0.03)
<i>Nitrospinae</i>		1.01	0.09	0.02	0.08	0.02	0.05	0.01
		(0.01)	(0.06)	(0.02)	(<0.01)	(<0.01)	(<0.01)	(<0.01)
<i>Actinobacteria</i>		0.61	0.67	0.83	0.47	0.52	0.46	1.15
		(0.05)	(0.22)	(0.07)	(0.22)	(0.12)	(0.11)	(0.03)
<i>Dadabacteria</i>		0.42	0.02	<0.01	0.02	0.01	0.01	<0.01
		(0.06)	(0.01)	(<0.01)	(0.01)	(<0.01)	(<0.01)	(<0.01)
<i>Gemmatimonadetes</i>		0.42	0.28	0.32	0.20	0.21	0.18	0.46
		(<0.01)	(0.18)	(0.04)	(0.14)	(0.03)	(0.02)	(<0.01)
<i>Firmicutes</i>		0.66	0.70	0.41	0.43	0.24	0.23	1.34
		(0.48)	(0.47)	(0.10)	(0.46)	(0.09)	(0.04)	(0.01)
<i>PAUC34f</i>		0.15	0.02	0.00	0.01	<0.01	0.01	<0.01
		(0.04)	(<0.01)	(0.00)	(<0.01)	(<0.01)	(<0.01)	(<0.01)
<i>Lentisphaerae</i>		0.07	0.02	<0.01	0.02	0.01	0.01	<0.01
		(<0.01)	(0.01)	(<0.01)	(<0.01)	(0.01)	(0.01)	(<0.01)
<i>Margulisbacteria</i>		0.05	0.01	0.00	<0.01	<0.01	0.00	<0.01
		(<0.01)	(<0.01)	(0.00)	(<0.01)	(<0.01)	(0.00)	(<0.01)
<i>AncK6</i>		0.04	0.00	0.00	<0.01	0.00	<0.01	0.00
		(<0.01)	(0.00)	(0.00)	(<0.01)	(0.00)	(<0.01)	(0.00)
<i>Latescibacteria</i>		0.03	0.07	0.14	0.05	0.08	0.05	0.18
		(0.01)	(0.04)	(<0.01)	(0.01)	(0.03)	(0.01)	(0.01)
<i>Rokubacteria</i>		0.02	0.04	0.09	0.05	0.06	0.04	0.13
		(0.01)	(0.02)	(0.02)	(0.03)	(<0.01)	(0.01)	(0.01)
<i>Spirochaetes</i>		0.04	0.02	0.06	0.02	0.04	0.01	0.09
		(0.01)	(0.01)	(0.01)	(0.02)	(<0.01)	(0.01)	(0.01)
<i>Armatimonadetes</i>		0.02	0.03	0.06	0.01	0.03	0.04	0.07

Phylum	Class	SW0	SW4	SW8	SWO4	SWO8	SWOB4	SWOB8
		(0.01)	(0.01)	(0.01)	(0.01)	(0.01)	(0.01)	(<0.01)
<i>Patescibacteria</i>		0.01	0.02	0.01	0.02	0.01	0.01	0.02
		(0.01)	(<0.01)	(<0.01)	(0.02)	(<0.01)	(0.01)	(<0.01)
<i>Nitrospirae</i>		0.02	0.04	0.08	0.02	0.04	0.03	0.08
		(0.01)	(0.03)	(0.01)	(0.00)	(0.01)	(0.01)	(0.02)
<i>Elusimicrobia</i>		0.02	0.04	0.05	0.03	0.04	0.03	0.07
		(0.01)	(0.03)	(0.01)	(0.02)	(0.02)	(0.01)	(<0.01)
<i>Epsilonbacteraeota</i>		0.01	0.02	0.01	0.03	0.11	0.03	0.03
		(<0.01)	(<0.01)	(0.01)	(0.01)	(0.03)	(0.01)	(<0.01)
<i>Omnitrophicaeota</i>		0.02	0.02	0.03	0.02	0.01	0.01	0.02
		(0.01)	(0.01)	(<0.01)	(0.01)	(0.01)	(0.01)	(<0.01)
<i>Synergistetes</i>		0.01	0.01	0.02	0.01	0.02	0.01	0.02
		(<0.01)	(0.01)	(<0.01)	(0.01)	(0.01)	(0.01)	(<0.01)
<i>Fibrobacteres</i>		0.01	<0.01	0.02	0.01	0.01	0.01	0.02
		(<0.01)	(0.01)	(<0.01)	(<0.01)	(0.01)	(0.01)	(<0.01)
<i>Thermotogae</i>		0.01	0.01	0.02	0.01	0.02	0.01	0.02
		(0.01)	(<0.01)	(0.01)	(0.01)	(<0.01)	(<0.01)	(<0.01)
<i>WPS-2</i>		0.01	<0.01	0.12	<0.01	0.01	0.01	0.01
		(<0.01)	(<0.01)	(0.15)	(<0.01)	(0.01)	(<0.01)	(<0.01)
<i>Entotheonellaeota</i>		0.00	0.01	0.01	0.01	0.01	0.01	0.02
		(0.00)	(<0.01)	(<0.01)	(0.01)	(<0.01)	(<0.01)	(<0.01)

Table S12. The proportions (%) of the 50 predominant bacterial genera across all samples in seawater (SW), oil contaminated seawater (SWO), and biostimulated oil contaminated seawater (SWOB) according to taxonomic classification using Kaiju with the NCBI-nr database. The numbers in sample codes denote time in months.

Genus	SW0	SW4	SW8	SWO4	SWO8	SWOB4	SWOB8
<i>Pseudomonas</i>	1.96	1.23	1.97	9.64	6.42	38.41	25.39
<i>Cycloclasticus</i>	0.13	10.05	8.81	1.10	2.12	1.82	13.36
<i>Marinomonas</i>	1.10	1.71	0.25	5.77	11.68	12.82	4.29
<i>Colwellia</i>	3.96	4.94	3.86	4.57	10.87	1.73	0.60
<i>Paraperlucidibaca</i>	0.02	0.01	0.01	<0.01	<0.01	3.38	14.57

Genus	SW0	SW4	SW8	SWO4	SWO8	SWOB4	SWOB8
<i>Hyphomonas</i>	0.03	0.10	0.17	16.33	4.96	0.02	0.08
<i>Sphingorhabdus</i>	0.02	0.65	0.28	0.27	0.03	2.12	5.05
<i>Polaribacter</i>	0.26	1.38	4.55	1.51	1.30	0.68	0.06
<i>Pacificibacter</i>	0.03	0.87	0.83	4.51	2.32	0.06	0.19
<i>Paraglaciecola</i>	0.18	0.47	1.05	0.65	2.35	1.66	0.94
<i>Ulvibacter</i>	0.02	0.33	0.32	1.50	1.02	3.43	1.05
<i>Methylophaga</i>	0.14	1.31	2.81	0.89	0.62	0.14	0.17
<i>Maribacter</i>	0.03	1.16	0.71	3.21	1.13	0.06	0.05
<i>Ca Thioglobus</i>	4.14	0.05	0.09	0.03	0.33	0.01	0.02
<i>Marinobacter</i>	0.68	0.42	0.27	0.41	0.23	1.97	0.56
<i>Clostridioides</i>	0.53	1.32	0.35	0.36	0.26	1.16	0.31
<i>Oleispira</i>	0.17	0.09	0.18	0.02	0.10	4.35	0.03
<i>Halomonas</i>	0.82	0.32	0.19	0.17	1.67	0.24	0.25
<i>Perlucidibaca</i>	0.05	0.02	0.01	0.00	0.01	0.51	2.15
<i>Neptunomonas</i>	0.87	0.16	0.11	0.60	0.17	2.04	0.09
<i>Ca Pelagibacter</i>	1.70	0.10	1.22	0.01	0.16	0.01	<0.01
<i>Tenacibaculum</i>	0.04	0.60	2.26	0.28	0.14	0.08	0.02
<i>Aequorivita</i>	0.01	0.13	0.19	0.19	0.47	1.03	0.92
<i>Winogradskyella</i>	0.02	0.65	0.56	1.26	0.45	0.07	0.13
<i>Nisaea</i>	0.02	0.01	2.74	0.01	0.01	0.01	0.04
<i>Amphritea</i>	0.62	0.11	0.06	0.73	0.17	1.22	0.17
<i>Lacinutrix</i>	0.01	0.15	0.29	1.26	1.12	0.04	0.06
<i>Sphingopyxis</i>	0.03	0.13	0.07	0.19	0.04	0.48	1.11
<i>Marinobacterium</i>	1.09	0.21	0.12	0.06	0.18	0.08	0.06
<i>Parvibaculum</i>	0.01	0.01	0.01	1.35	0.84	<0.01	<0.01
<i>Marinirhabdus</i>	<0.01	0.03	0.10	0.09	1.84	0.01	0.01
<i>Flavobacterium</i>	0.09	0.38	0.88	0.56	0.37	0.14	0.08
<i>Pseudoalteromonas</i>	0.47	0.51	0.30	0.19	0.42	0.20	0.13
<i>Shewanella</i>	0.46	0.32	0.26	0.14	0.28	0.83	0.12
<i>Hoeflea</i>	0.04	0.11	0.19	0.64	0.28	0.04	0.31
<i>Doktonia</i>	<0.01	0.36	0.90	0.06	0.09	0.02	0.01
<i>Lutibacter</i>	0.02	0.24	0.82	0.18	0.08	0.08	0.03
<i>Streptomyces</i>	0.31	0.31	0.19	0.09	0.39	0.06	0.05

Genus	SW0	SW4	SW8	SW04	SW08	SWOB4	SWOB8
<i>Neptuniibacter</i>	0.34	0.14	0.10	0.04	0.08	0.07	0.37
<i>Photobacterium</i>	0.24	0.10	0.08	0.04	0.64	0.05	0.09
<i>Ralstonia</i>	0.20	0.34	0.06	0.19	0.04	0.47	0.03
<i>Motiliproteus</i>	0.75	0.07	0.04	0.03	0.11	0.04	0.02
<i>Maricaulis</i>	0.01	0.37	0.26	0.55	0.02	<0.01	0.01
<i>Acinetobacter</i>	0.27	0.17	0.10	0.05	0.09	0.09	0.25
<i>Microbulbifer</i>	0.22	0.44	0.19	0.04	0.07	0.03	0.06
<i>Thalassotalea</i>	0.35	0.12	0.15	0.09	0.26	0.04	0.02
<i>Sphingomonas</i>	0.13	0.10	0.09	0.13	0.09	0.09	0.27

Table S13. The proportions (%) of the 50 predominant bacterial genera across all samples in seawater (SW), oil contaminated seawater (SWO), and biostimulated oil contaminated seawater (SWOB) according to taxonomic classification using Kaiju with the MAR_{DB} database. The numbers in sample codes denote time in months.

Genus	SW0	SW4	SW8	SW04	SW08	SWOB4	SWOB8
<i>Cycloclasticus</i>	0.25	23.20	16.69	1.75	3.99	2.66	25.33
<i>Pseudomonas</i>	0.48	0.94	2.24	8.59	9.44	39.03	13.88
<i>Marinomonas</i>	0.91	3.37	0.40	7.90	18.88	16.11	8.05
<i>Colwellia</i>	17.78	8.46	5.18	4.90	13.63	1.86	1.08
<i>Hyphomonas</i>	0.33	0.22	0.29	21.67	8.46	0.05	0.19
<i>Flavobacterium</i>	0.36	5.92	18.51	0.50	0.28	0.13	0.13
<i>Sphingorhabdus</i>	0.05	1.01	0.36	0.30	0.04	2.04	6.98
<i>Paraglaciecola</i>	0.83	1.11	1.90	0.98	4.12	2.20	1.89
<i>Pacificibacter</i>	0.05	1.64	1.26	6.55	4.01	0.08	0.38
<i>Methylophaga</i>	0.34	3.41	6.01	1.62	1.33	0.28	0.53
<i>Ulvibacter</i>	0.04	0.42	0.29	2.05	0.62	4.55	2.07
<i>Ca. Pelagibacter</i>	7.95	0.19	2.05	0.02	0.19	0.01	0.01
<i>Marinobacter</i>	0.85	1.00	0.52	0.71	0.39	2.87	1.94
<i>Maribacter</i>	0.14	2.18	1.00	4.31	1.85	0.10	0.11
<i>Vibrio</i>	2.95	1.08	0.88	0.54	1.01	0.74	0.81
<i>Polaribacter</i>	1.67	0.83	1.31	1.92	1.96	0.84	0.12
<i>Sphingopyxis</i>	0.06	0.32	0.16	0.37	0.07	0.99	3.19

Genus	SW0	SW4	SW8	SW04	SW08	SW0B4	SW0B8
<i>Oleispira</i>	0.29	0.24	0.32	0.04	0.17	5.57	0.13
<i>Halomonas</i>	0.34	0.41	0.22	0.25	2.73	0.53	0.76
<i>Neptunomonas</i>	0.40	0.41	0.23	0.98	0.26	2.99	0.36
<i>Pseudoalteromonas</i>	1.51	1.24	0.66	0.38	0.85	0.39	0.47
<i>Sneathiella</i>	0.09	0.08	0.06	0.67	0.62	0.82	1.68
<i>Nisaea</i>	0.19	0.03	5.14	0.03	0.04	0.02	0.10
<i>Lacinutrix</i>	0.08	0.31	0.33	2.25	2.14	0.09	0.19
<i>Alcanivorax</i>	0.21	0.60	0.26	0.16	0.12	0.42	1.60
<i>Stappia</i>	0.09	0.08	0.12	0.78	0.09	0.81	1.49
<i>Sulfitobacter</i>	0.54	1.11	1.02	0.55	0.60	0.08	0.13
<i>Nitrospina</i>	4.43	0.04	0.06	0.05	0.04	0.01	0.02
<i>Shewanella</i>	0.86	0.65	0.47	0.24	0.45	1.11	0.40
<i>Aequorivita</i>	0.05	0.21	0.22	0.22	0.40	1.11	1.36
<i>Zhongshania</i>	0.03	0.21	3.21	0.02	0.02	0.03	0.11
<i>Hoeflea</i>	0.15	0.31	0.36	0.97	0.50	0.06	0.64
<i>Winogradskyella</i>	0.06	0.80	0.34	1.03	0.43	0.06	0.16
<i>Amphritea</i>	0.20	0.18	0.08	0.77	0.13	1.15	0.26
<i>Donghicola</i>	1.20	0.47	0.26	0.20	0.55	0.10	0.04
<i>Parvibaculum</i>	0.16	0.03	0.07	1.39	1.03	0.00	0.02
<i>Microbulbifer</i>	0.28	1.00	0.34	0.09	0.11	0.11	0.33
<i>Marinobacterium</i>	0.38	0.45	0.22	0.18	0.15	0.30	0.40
<i>Porticoccus</i>	1.11	0.76	0.45	0.02	0.03	0.02	0.05
<i>Loktanella</i>	1.35	0.22	0.14	0.09	0.11	0.06	0.25
<i>Neptuniibacter</i>	0.18	0.33	0.19	0.08	0.08	0.14	0.74
<i>Maricaulis</i>	0.18	0.80	0.48	0.85	0.07	0.01	0.03
<i>Halobacteriovorax</i>	0.08	0.10	2.22	0.01	0.01	0.00	0.01
<i>Ca. Thioglobus</i>	2.27	0.03	0.03	0.01	0.05	0.00	0.01
<i>Thalassotalea</i>	1.05	0.25	0.24	0.15	0.45	0.06	0.07
<i>Psychromonas</i>	0.65	0.40	0.28	0.16	0.35	0.15	0.15
<i>Acinetobacter</i>	0.12	0.06	0.04	0.02	0.03	0.20	0.88
<i>Endozoicomonas</i>	0.60	0.46	0.21	0.07	0.13	0.14	0.29
<i>Alteromonas</i>	0.53	0.37	0.23	0.10	0.20	0.11	0.30
<i>Streptomyces</i>	0.43	1.00	0.16	0.08	0.07	0.10	0.15

Table S14. The proportions (%) of the 50 predominant bacterial genera across all samples in seawater (SW), oil contaminated seawater (SWO), and biostimulated oil contaminated seawater (SWOB) according to taxonomic classification using Kraken2 with the Standard Kraken2 database. The numbers in sample codes denote time in months.

Genus	SW0	SW4	SW8	SW04	SW08	SW0B4	SW0B8
<i>Pseudomonas</i>	3.02	5.68	5.37	13.63	13.06	50.54	34.31
<i>Marinomonas</i>	2.24	5.49	0.62	13.10	25.14	19.14	10.36
<i>Colwellia</i>	8.32	9.97	6.26	4.95	10.82	1.39	0.61
<i>Sphingorhabdus</i>	0.04	2.68	0.96	0.76	0.09	3.53	12.40
<i>Polaribacter</i>	1.36	5.13	15.15	5.14	3.35	1.32	0.34
<i>Staphylococcus</i>	4.46	5.20	4.46	2.26	1.42	2.03	0.89
<i>Cycloclasticus</i>	0.18	1.90	1.47	0.14	0.23	0.21	4.96
<i>Ca. Pelagibacter</i>	7.83	0.23	4.15	0.02	0.20	0.01	0.01
<i>Shewanella</i>	3.14	1.80	1.45	0.59	1.06	1.56	0.93
<i>Klebsiella</i>	0.66	3.01	0.32	0.31	0.16	3.90	1.98
<i>Pseudoalteromonas</i>	3.36	1.94	1.42	0.70	1.47	0.47	0.67
<i>Halomonas</i>	1.19	1.14	0.62	0.93	3.80	0.71	1.40
<i>Acinetobacter</i>	2.96	1.10	1.06	0.31	0.51	0.35	1.88
<i>Lacinutrix</i>	0.06	0.56	1.22	3.67	3.09	0.14	0.21
<i>Vibrio</i>	3.15	1.48	1.24	0.57	0.92	0.41	0.97
<i>Winogradskyella</i>	0.09	1.52	1.59	2.53	1.03	0.15	0.26
<i>Flavobacterium</i>	0.38	1.09	2.07	1.99	0.88	0.37	0.33
<i>Sulfitobacter</i>	0.71	1.28	1.25	1.57	1.34	0.12	0.26
<i>Paraglaciecola</i>	0.61	0.64	1.17	0.53	1.63	0.60	0.60
<i>Ca. Thioglobus</i>	6.31	0.08	0.11	0.03	0.23	0.01	0.03
<i>Marinobacter</i>	0.55	0.87	0.44	0.40	0.16	1.58	0.88
<i>Hyphomonas</i>	0.02	0.06	0.09	4.26	1.11	0.01	0.05
<i>Tenacibaculum</i>	0.15	0.96	3.04	0.79	0.32	0.12	0.09
<i>Neptunomonas</i>	1.25	0.24	0.16	0.95	0.12	2.14	0.17
<i>Maribacter</i>	0.07	0.56	0.68	2.33	0.74	0.06	0.05
<i>Ralstonia</i>	0.06	0.06	0.05	0.07	3.89	0.03	0.09
<i>Formosa</i>	0.09	0.53	1.11	1.71	0.59	0.11	0.18
<i>Alteromonas</i>	1.09	0.50	0.44	0.18	0.36	0.14	0.34
<i>Zhongshania</i>	0.12	0.90	2.01	0.01	0.02	0.01	0.09

Genus	SW0	SW4	SW8	SW04	SW08	SW0B4	SW0B8
<i>Cellulophaga</i>	0.07	0.47	0.80	1.09	0.31	0.11	0.09
<i>Aequorivita</i>	0.02	0.11	0.19	0.22	0.35	0.47	0.70
<i>Algibacter</i>	0.04	0.27	0.48	1.22	0.40	0.11	0.13
<i>Sphingomonas</i>	0.13	0.22	0.21	0.58	0.22	0.14	0.61
<i>Salmonella</i>	0.63	0.74	0.21	0.33	0.15	0.23	0.22
<i>Rhizobium</i>	0.26	0.24	0.34	0.76	0.38	0.07	0.30
<i>Bradyrhizobium</i>	0.26	0.25	0.33	0.70	0.31	0.05	0.25
<i>Microbulbifer</i>	0.38	1.01	0.38	0.10	0.08	0.06	0.21
<i>Legionella</i>	0.78	0.45	0.37	0.08	0.14	0.04	0.22
<i>Celeribacter</i>	0.15	0.48	0.43	0.62	0.29	0.02	0.08
<i>Mesorhizobium</i>	0.21	0.19	0.29	0.62	0.30	0.04	0.23
<i>Haemophilus</i>	0.77	0.43	0.21	0.20	0.18	0.12	0.12
<i>Streptomyces</i>	0.56	0.37	0.38	0.31	0.11	0.09	0.14
<i>Octadecabacter</i>	0.74	0.41	0.32	0.33	0.17	0.01	0.07
<i>Thalassotalea</i>	0.60	0.28	0.29	0.19	0.43	0.05	0.11
<i>Psychrobacter</i>	0.67	0.28	0.19	0.05	0.09	0.07	0.34
<i>Olleya</i>	0.02	0.15	0.28	0.92	0.29	0.04	0.08
<i>Xanthomonas</i>	0.31	0.43	0.19	0.23	0.09	0.20	0.22
<i>Cellvibrio</i>	0.29	0.72	0.29	0.05	0.07	0.05	0.21
<i>Aquimarina</i>	0.06	0.33	0.70	0.37	0.18	0.08	0.06
<i>Burkholderia</i>	0.32	0.37	0.20	0.28	0.10	0.14	0.22

Table S15. The proportions (%) of the 50 predominant bacterial genera across all samples in seawater (SW), oil contaminated seawater (SWO), and biostimulated oil contaminated seawater (SWOB) according to taxonomic classification using Bracken with the Standard Kraken 2 database. The numbers in sample codes denote time in months.

Genus	SW0	SW4	SW8	SW04	SW08	SW0B4	SW0B8
<i>Pseudomonas</i>	2.71	4.74	4.83	12.21	11.97	48.14	31.65
<i>Marinomonas</i>	1.94	4.51	0.54	11.32	22.82	18.07	9.26
<i>Colwellia</i>	6.73	8.16	5.34	4.33	10.05	1.33	0.54
<i>Klebsiella</i>	0.80	11.87	0.51	0.38	0.24	5.58	6.71
<i>Sphingorhabdus</i>	0.03	2.19	0.81	0.65	0.08	3.35	11.23

Genus	SW0	SW4	SW8	SW04	SW08	SW0B4	SW0B8
<i>Polaribacter</i>	1.15	4.48	13.76	4.71	3.25	1.34	0.33
<i>Salmonella</i>	8.57	2.66	3.95	3.44	2.46	1.36	1.30
<i>Staphylococcus</i>	5.00	4.96	5.22	2.76	1.91	2.30	1.01
<i>Pseudoalteromonas</i>	4.81	2.29	2.05	1.27	1.97	0.67	0.85
<i>Cyclocasticus</i>	0.14	1.55	1.25	0.12	0.21	0.20	4.34
<i>Halomonas</i>	1.02	0.94	0.55	0.81	3.57	0.68	1.25
<i>Ca. Pelagibacter</i>	6.16	0.19	3.44	0.02	0.18	0.01	0.00
<i>Shewanella</i>	2.54	1.49	1.30	0.52	1.01	1.48	0.83
<i>Acinetobacter</i>	2.55	0.93	1.00	0.28	0.50	0.35	1.69
<i>Lacinutrix</i>	0.06	0.54	1.23	3.50	3.04	0.16	0.22
<i>Vibrio</i>	2.82	1.22	1.12	0.50	0.88	0.40	0.87
<i>Winogradskyella</i>	0.08	1.46	1.63	2.47	1.05	0.17	0.28
<i>Flavobacterium</i>	0.34	0.99	1.97	1.86	0.86	0.39	0.33
<i>Sulfitobacter</i>	0.66	1.20	1.18	1.47	1.30	0.12	0.26
<i>Paraglaciecola</i>	0.49	0.53	1.00	0.46	1.52	0.58	0.55
<i>Ca. Thioglobus</i>	4.98	0.07	0.15	0.03	0.21	0.01	0.03
<i>Hyphomonas</i>	0.02	0.05	0.08	4.08	1.11	0.01	0.05
<i>Tenacibaculum</i>	0.14	0.88	2.91	0.75	0.31	0.13	0.09
<i>Marinobacter</i>	0.44	0.71	0.38	0.35	0.14	1.49	0.78
<i>Neptunomonas</i>	1.07	0.20	0.14	0.82	0.11	2.02	0.14
<i>Formosa</i>	0.08	0.49	1.09	1.61	0.58	0.12	0.18
<i>Maribacter</i>	0.06	0.51	0.64	2.14	0.72	0.06	0.06
<i>Burkholderia</i>	0.77	0.70	0.61	0.62	0.25	0.27	0.42
<i>Ralstonia</i>	0.05	0.05	0.05	0.06	3.62	0.02	0.09
<i>Aeromonas</i>	0.87	0.39	0.55	0.29	0.27	0.16	0.36
<i>Alteromonas</i>	0.92	0.43	0.42	0.17	0.36	0.14	0.32
<i>Paenibacillus</i>	1.47	0.12	0.36	0.24	0.44	0.10	0.13
<i>Rhizobium</i>	0.26	0.25	0.38	0.89	0.45	0.07	0.33
<i>Algibacter</i>	0.04	0.27	0.51	1.24	0.43	0.13	0.14
<i>Olleya</i>	0.03	0.24	0.47	1.35	0.44	0.07	0.14
<i>Cellulophaga</i>	0.06	0.42	0.76	1.01	0.30	0.11	0.09
<i>Sphingomonas</i>	0.12	0.21	0.21	0.58	0.23	0.16	0.65
<i>Xanthomonas</i>	0.55	0.48	0.39	0.36	0.19	0.25	0.29

Genus	SW0	SW4	SW8	SW04	SW08	SW0B4	SW0B8
<i>Zhongshania</i>	0.10	0.76	1.74	0.01	0.02	0.01	0.08
<i>Sphingobium</i>	0.13	0.16	0.20	0.46	0.20	0.15	0.70
<i>Aequorivita</i>	0.02	0.10	0.16	0.19	0.32	0.46	0.64
<i>Celeribacter</i>	0.17	0.52	0.48	0.70	0.33	0.02	0.09
<i>Bradyrhizobium</i>	0.23	0.22	0.30	0.68	0.32	0.05	0.25
<i>Streptomyces</i>	0.59	0.40	0.38	0.32	0.12	0.10	0.14
<i>Mesorhizobium</i>	0.19	0.17	0.28	0.62	0.32	0.04	0.23
<i>Microbulbifer</i>	0.31	0.85	0.32	0.09	0.08	0.06	0.18
<i>Parvibaculum</i>	0.01	0.01	0.02	1.19	0.72	0.00	0.02
<i>Legionella</i>	0.63	0.38	0.32	0.07	0.13	0.04	0.20
<i>Phaeobacter</i>	0.22	0.71	0.49	0.22	0.12	0.01	0.08
<i>Haemophilus</i>	0.64	0.36	0.19	0.18	0.18	0.12	0.11

Table S16. The mean proportions (%) and standard deviations (in parenthesis, $n = 2$) of the 50 predominant bacterial genera across all samples in seawater (SW), oil contaminated seawater (SWO), and biostimulated oil contaminated seawater (SWOB) according to taxonomic classification based on amplicon-sequencing and the SILVA database. The numbers in sample codes denote time in months.

Genus	SW0	SW4	SW8	SWO4	SWO8	SWOB4	SWOB8
<i>Colwellia</i>	6.45 (0.20)	4.63 (5.15)	3.53 (0.72)	2.75 (0.19)	9.91 (4.16)	1.07 (0.57)	1.80 (0.03)
<i>Marinomonas</i>	0.51 (0.01)	2.19 (2.23)	0.36 (0.11)	2.87 (0.37)	5.28 (0.97)	14.70 (6.71)	4.59 (2.25)
<i>SM1A02</i>	0.20 (0.18)	1.43 (0.84)	6.83 (7.40)	0.70 (0.71)	8.36 (10.87)	0.05 (0.01)	0.56 (0.02)
<i>Paraperlucidibaca</i>	0.07 (0.00)	0.15 (0.00)	0.39 (0.03)	0.08 (0.06)	0.24 (0.05)	2.97 (3.94)	16.56 (13.59)
<i>Jejudonia</i>	0.04 (0.01)	0.06 (0.02)	0.49 (0.21)	0.21 (0.22)	13.85 (19.01)	0.02 (0.00)	0.41 (0.02)
<i>Ulvibacter</i>	0.63 (0.05)	3.72 (1.19)	0.52 (0.43)	3.21 (2.66)	0.26 (0.19)	14.16 (18.75)	2.54 (3.13)
<i>Pacificibacter</i>	0.25 (0.09)	1.90 (1.58)	8.05 (10.77)	4.48 (1.16)	2.23 (2.84)	0.58 (0.43)	0.91 (0.38)
<i>Aequorivita</i>	0.09 (0.04)	0.07 (0.04)	0.24 (0.02)	0.16 (0.17)	0.17 (0.04)	3.20 (0.08)	11.55 (8.54)
<i>Sphingorhabdus</i>	0.17 (0.07)	0.67 (0.35)	0.83 (0.68)	0.32 (0.18)	0.18 (0.00)	5.95 (2.70)	5.93 (7.40)
<i>Pseudomonas</i>	0.26 (0.05)	0.20 (0.08)	0.25 (0.09)	0.78 (0.93)	0.24 (0.10)	10.76 (10.51)	3.70 (3.53)
<i>Cycloclasticus</i>	0.05 (0.01)	2.13 (0.21)	1.90 (0.91)	0.25 (0.15)	0.46 (0.36)	0.59 (0.74)	7.74 (4.46)
<i>Sneathiella</i>	0.13 (0.01)	0.33 (0.15)	0.35 (0.23)	0.69 (0.30)	0.52 (0.44)	3.35 (3.00)	3.95 (4.53)
<i>Aurantivirga</i>	0.24 (0.01)	2.55 (2.14)	6.88 (9.09)	0.28 (0.22)	0.13 (0.02)	0.18 (0.05)	0.21 (0.00)
<i>Lacinutrix</i>	0.27 (0.30)	0.10 (0.05)	0.15 (0.09)	1.08 (1.37)	3.13 (4.31)	0.03 (0.00)	0.07 (0.01)

Genus	SW0	SW4	SW8	SWO4	SWO8	SWOB4	SWOB8
<i>Hyphomonas</i>	0.11 (0.01)	0.16 (0.01)	0.06 (0.00)	3.20 (2.25)	1.56 (1.83)	0.10 (0.03)	0.11 (0.03)
<i>Sulfitobacter</i>	0.59 (0.02)	5.36 (4.76)	0.90 (1.14)	0.48 (0.47)	0.03 (0.01)	0.25 (0.01)	0.08 (0.00)
<i>OM43_clade genus</i>	0.64 (0.09)	0.74 (0.90)	3.84 (5.19)	0.03 (0.02)	0.07 (0.02)	0.04 (0.02)	0.12 (0.01)
<i>Maribacter</i>	0.07 (0.01)	0.61 (0.66)	0.22 (0.26)	1.71 (0.15)	0.98 (1.03)	0.08 (0.01)	0.11 (0.01)
<i>Polaribacter</i>	2.29 (0.15)	0.19 (0.03)	0.13 (0.07)	0.23 (0.03)	0.95 (1.19)	0.13 (0.03)	0.07 (0.04)
<i>C1-B045</i>	0.05 (0.01)	4.31 (1.83)	0.76 (0.38)	0.07 (0.05)	0.04 (0.03)	0.04 (0.01)	0.02 (0.00)
<i>Dokdonia</i>	0.12 (0.02)	2.51 (2.20)	1.78 (0.32)	0.11 (0.07)	0.03 (0.00)	0.08 (0.00)	0.05 (0.00)
<i>Clade_Ia genus</i>	4.10 (0.02)	0.14 (0.06)	0.06 (0.03)	0.11 (0.05)	0.06 (0.03)	0.10 (0.03)	0.02 (0.02)
<i>Tenacibaculum</i>	0.18 (0.00)	2.56 (2.93)	0.36 (0.47)	0.32 (0.31)	0.01 (0.01)	0.15 (0.01)	0.08 (0.04)
<i>Paraglaciecola</i>	0.06 (0.02)	0.18 (0.06)	0.21 (0.02)	0.18 (0.12)	0.64 (0.55)	0.89 (1.09)	0.36 (0.08)
<i>SUP05_cluster</i>	3.08 (0.10)	0.10 (0.06)	0.02 (0.01)	0.09 (0.02)	0.08 (0.02)	0.08 (0.02)	0.02 (0.02)
<i>Loktanella</i>	0.41 (0.02)	1.72 (2.00)	0.03 (0.01)	0.23 (0.23)	0.03 (0.01)	0.20 (0.03)	0.42 (0.42)
<i>Parvibaculum</i>	0.05 (0.01)	0.04 (0.03)	0.03 (0.01)	2.13 (2.88)	0.59 (0.81)	0.04 (0.01)	0.03 (0.00)
<i>Oleispira</i>	0.08 (0.02)	0.11 (0.07)	0.10 (0.08)	0.16 (0.18)	0.04 (0.02)	2.21 (2.90)	0.05 (0.01)
<i>Pseudophaeobacter</i>	0.01 (0.00)	1.72 (1.99)	0.82 (1.11)	0.03 (0.02)	0.01 (0.01)	0.02 (0.01)	0.02 (0.00)
<i>Arcticiflavibacter</i>	0.13 (0.03)	0.11 (0.00)	0.08 (0.03)	0.81 (0.34)	0.51 (0.40)	0.09 (0.05)	0.30 (0.29)
<i>Winogradskyella</i>	0.07 (0.01)	1.44 (1.57)	0.25 (0.32)	0.34 (0.29)	0.05 (0.05)	0.03 (0.02)	0.01 (0.00)
<i>Cocleimonas</i>	0.07 (0.02)	1.11 (1.38)	0.01 (0.01)	0.12 (0.10)	0.01 (0.00)	0.07 (0.00)	0.58 (0.52)
<i>Zhongshania</i>	<0.01 (0.00)	0.05 (0.06)	1.79 (1.92)	0.01 (0.01)	0.02 (0.00)	<0.01 (0.00)	0.04 (0.02)
<i>Porticoccus</i>	0.38 (0.01)	0.79 (0.23)	0.63 (0.83)	0.02 (0.00)	0.02 (0.00)	0.05 (0.03)	0.07 (0.01)
<i>Flavobacterium</i>	0.12 (0.01)	0.22 (0.08)	0.22 (0.06)	0.10 (0.04)	0.16 (0.03)	0.45 (0.29)	0.28 (0.00)
<i>Hoeflea</i>	0.01 (0.01)	0.12 (0.05)	0.07 (0.07)	0.21(0.10)	0.10 (0.00)	0.04 (0.01)	0.84 (0.51)
<i>Amphritea</i>	0.02 (0.01)	0.03 (0.03)	<0.01 (0.00)	0.24 (0.01)	0.01 (0.01)	0.94 (0.75)	0.11 (0.07)
<i>Pseudohongiella</i>	0.27 (0.01)	0.22 (0.25)	0.07 (0.01)	0.48 (0.63)	0.24 (0.03)	0.08 (0.08)	0.02 (0.02)
<i>Neptunomonas</i>	0.03 (0.00)	0.05 (0.02)	<0.01 (0.00)	0.24 (0.19)	<0.01 (0.00)	0.88 (1.01)	0.02 (0.01)
<i>Cellulophaga</i>	0.04 (0.01)	0.04 (0.02)	0.01 (0.01)	1.01 (0.84)	0.05 (0.04)	0.04 (0.00)	<0.01 (0.00)
<i>Algimonas</i>	0.01 (0.01)	0.10 (0.10)	0.81 (0.54)	0.13 (0.02)	0.02 (0.01)	0.01 (0.00)	0.02 (0.01)
<i>Sedimentitalea</i>	0.01 (0.01)	0.62 (0.30)	0.39 (0.52)	0.05 (0.02)	0.01 (0.00)	0.01 (0.00)	0.01 (0.00)
<i>Nisaea</i>	<0.01 (0.00)	<0.01 (0.00)	0.87 (1.18)	<0.01 (0.00)	0.02 (0.00)	<0.01 (0.00)	0.01 (0.01)
<i>Lentilitoribacter</i>	0.02 (0.01)	0.67 (0.13)	0.12 (0.17)	0.05 (0.04)	<0.01 (0.00)	0.02 (0.00)	0.01 (0.01)
<i>Bryobacter</i>	0.12 (0.06)	0.08 (0.06)	0.15 (0.02)	0.07 (0.04)	0.13 (0.02)	0.06 (0.00)	0.19 (0.00)
<i>LS-NOB</i>	0.69 (0.02)	0.05 (0.02)	0.01 (0.01)	0.04 (0.00)	0.01 (0.00)	0.03 (0.00)	0.01 (0.00)
<i>Sphingomonas</i>	0.06 (0.00)	0.09 (0.06)	0.13 (0.02)	0.06 (0.03)	0.09 (0.03)	0.08 (0.00)	0.15 (0.02)

Genus	SW0	SW4	SW8	SWO4	SWO8	SWOB4	SWOB8
<i>Ca. Solibacter</i>	0.06 (0.00)	0.07 (0.04)	0.16 (0.03)	0.04 (0.02)	0.09 (0.03)	0.06 (0.02)	0.15 (0.00)
<i>Roseobacter</i>	0.02 (0.00)	0.05 (0.00)	0.04 (0.02)	0.19 (0.09)	0.27 (0.22)	0.09 (0.11)	0.02 (0.02)
<i>RB41</i>	0.04 (0.00)	0.07 (0.05)	0.16 (0.02)	0.06 (0.05)	0.08 (0.01)	0.05 (0.00)	0.15 (0.03)

Table S17. The correlation (multivariate generalization of the Pearson correlation coefficient (RV)) between datasets of proportions of the 50 predominant bacterial genera (white background in table) and proportions of bacterial genera containing hydrocarbon degraders (yellow background in table) acquired with five different taxonomic classification methods (Kaiju with the NCBI-nr database, Kaiju with the MAR_{DB} database, Kraken2 with the Standard Kraken 2 database, Bracken with the Standard Kraken 2 database, and amplicon based sequencing with the SILVA database).

Classification method	Kaiju	Kaiju/MAR	Kraken2	Bracken	Amplicon
Kaiju		0.95	0.92	0.92	0.85
Kaiju/MAR	0.92		0.91	0.90	0.85
Kraken2	0.89	0.90		0.99	0.83
Bracken	0.88	0.89	0.99		0.81
Amplicon	0.58	0.61	0.74	0.76	

Table S18. The proportions (%) of the most abundant bacterial species (>1% of bacterial community in at least one treatment) in seawater (SW), oil contaminated seawater (SWO), and biostimulated oil contaminated seawater (SWOB) according to classification using Kaiju with the NCBI-nr database. The numbers in sample codes denote time in months.

Species	SW0	SW4	SW8	SWO4	SWO8	SWOB4	SWOB8
<i>Clostridioides difficile</i>	0.53	1.32	0.35	0.36	0.26	1.16	0.31
<i>Ca Colwellia aromaticivorans</i>	1.15	0.99	1.13	1.63	4.07	0.43	0.07
<i>Cycloclasticus sp 44_32_T64</i>	0.01	1.52	1.33	0.16	0.32	0.24	1.36
<i>Cycloclasticus sp symbiont of Bathymodiolus heckeriae</i>	0.05	1.10	1.02	0.13	0.25	0.18	0.79
<i>Cycloclasticus sp Phe_18</i>	0.01	1.03	0.84	0.10	0.20	0.35	5.43
<i>Hyphomonas sp BRH_c22</i>	<0.01	0.02	0.02	3.25	0.23	<0.01	<0.01
<i>Hyphomonas chukchiensis</i>	<0.01	0.01	0.03	2.88	1.44	<0.01	0.02
<i>Hyphomonas johnsonii</i>	<0.01	0.01	0.01	2.15	0.15	<0.01	0.01
<i>Hyphomonas oceanitis</i>	<0.01	0.01	0.03	2.83	1.38	<0.01	0.02
<i>Marinirhabdus gelatinilytica</i>	<0.01	0.03	0.10	0.09	1.84	0.01	0.01

Species	SW0	SW4	SW8	SWO4	SWO8	SWOB4	SWOB8
<i>Marinomonas primoryensis</i>	0.01	0.81	0.05	3.08	6.22	6.79	2.27
<i>Neptunomonas japonica</i>	0.11	0.02	0.01	0.43	0.02	1.56	0.02
<i>Nisaea denitrificans</i>	0.02	0.01	2.74	0.01	0.01	0.01	0.04
<i>Oleispira antarctica</i>	0.17	0.09	0.18	0.02	0.10	4.35	0.03
<i>Pacificibacter marinus</i>	0.02	0.59	0.53	4.27	2.22	0.05	0.16
<i>Paraglaciecola polaris</i>	0.01	0.07	0.19	0.13	0.09	1.45	0.77
<i>Paraperlucidibaca beakdonensis</i>	0.02	0.01	0.01	<0.01	<0.01	3.38	14.57
<i>Ca Pelagibacter sp IMCC9063</i>	0.05	0.05	1.08	<0.01	<0.01	<0.01	<0.01
<i>Ca Pelagibacter ubique</i>	1.09	<0.01	0.07	<0.01	0.06	<0.01	<0.01
<i>Pseudomonas fluorescens</i>	0.04	0.02	0.02	0.02	0.02	1.42	0.12
<i>Pseudomonas pelagia</i>	0.01	0.01	0.31	0.61	1.49	0.72	0.70
<i>Pseudomonas sabulinigri</i>	0.01	0.01	0.01	0.12	0.07	0.75	5.61
<i>Pseudomonas salina</i>	0.02	0.02	0.32	5.17	0.03	5.49	3.65
<i>Pseudomonas sp Y22</i>	<0.01	<0.01	0.07	0.14	1.14	0.16	0.17
<i>Sphingorhabdus sp M41</i>	<0.01	0.21	0.09	0.09	0.01	0.72	1.70
<i>Sphingorhabdus sp YGSM121</i>	<0.01	0.19	0.07	0.06	<0.01	0.53	1.17
<i>Ca Thioglobus singularis</i>	1.44	<0.01	0.02	0.01	0.12	<0.01	<0.01
<i>Thioglobus sp NP1</i>	1.33	<0.01	0.02	0.01	0.11	<0.01	<0.01
<i>Ulvibacter litoralis</i>	<0.01	0.09	0.06	1.23	0.24	3.05	0.92

Table S19. The number of detected genera, proportions (%) and estimated abundances (copies/mL) of bacterial genera containing petroleum hydrocarbon degraders ($n = 350$) in seawater (SW), oil contaminated seawater (SWO), and biostimulated oil contaminated seawater (SWOB) based on five taxonomic assignment methods (Kaiju with the NCBI-nr database, Kaiju with the MAR_{DB} database, Kraken2 with the Standard Kraken 2 database, Bracken with the Standard Kraken 2 database, and amplicon-based sequencing with the SILVA database). The numbers in sample codes denote time in months.

	SW0	SW4	SW8	SWO4	SWO8	SWOB4	SWOB8
Genera							
Kaiju	338	338	338	338	338	338	338
Kaiju/MAR	226	226	226	226	226	226	226
Kraken2	279	279	279	279	279	279	279
Bracken	279	279	279	279	279	279	279

	SW0	SW4	SW8	SWO4	SWO8	SWOB4	SWOB8
Amplicon	105	111	126	120	127	117	134
Proportions							
Kaiju	26.56	36.69	36.46	58.94	54.75	83.92	78.13
Kaiju/MAR	49.19	71.52	67.16	73.22	79.54	94.33	87.61
Kraken2	55.84	72.03	67.84	76.79	83.21	95.44	87.65
Bracken	54.81	73.33	66.49	74.36	80.93	94.22	87.17
Amplicon	13.60	29.39	14.49	21.98	24.15	65.11	62.77
Estimated abundances							
Kaiju	2.71×10 ⁵	1.37×10 ⁶	1.91×10 ⁶	1.71×10 ⁶	2.51×10 ⁶	6.95×10 ⁷	9.69×10 ⁷
Kaiju/MAR	5.02×10 ⁵	2.66×10 ⁶	3.51×10 ⁶	2.13×10 ⁶	3.65×10 ⁶	7.81×10 ⁷	1.09×10 ⁸
Kraken2	5.70×10 ⁵	2.68×10 ⁶	3.55×10 ⁶	2.23×10 ⁶	3.82×10 ⁶	7.90×10 ⁷	1.09×10 ⁸
Bracken	5.59×10 ⁵	2.73×10 ⁶	3.48×10 ⁶	2.16×10 ⁶	3.71×10 ⁶	7.80×10 ⁷	1.08×10 ⁸
Amplicon	1.39×10 ⁵	1.09×10 ⁶	7.58×10 ⁵	6.38×10 ⁵	1.11×10 ⁶	5.39×10 ⁷	7.78×10 ⁷

Table S20. Normalized hydrocarbon degradation related gene abundances presented as gene-specific reads per kilobase per genome equivalent (RPKG) in seawater (SW), oil-contaminated seawater (SWO), and biostimulated oil-contaminated seawater (SWOB). Numbers in sample codes denote time in months. Genes related to aliphatic, monoaromatic, polyaromatic, and various types of hydrocarbon compounds degradation are presented on pink, blue, yellow, and green background, respectively. Genes with abbreviations given in this study are supplemented with their KEGG code.

Gene		RPKG						
		SW0	SW4	SW8	SWO4	SWO8	SWOB4	SWOB8
Aliphatic compounds	<i>alkB1_2</i>	0.36	0.79	0.62	0.53	0.52	0.85	0.87
	<i>alkT/rubB</i>	4.12	7.39	6.62	7.92	8.15	9.37	8.98
	<i>almA</i>	2.33	1.68	1.55	1.77	1.63	1.99	2.08
	<i>bmoB</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	<i>bmoC</i>	0.74	1.40	1.57	1.61	1.52	2.91	2.28
	<i>bmoD</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	<i>bmoX</i>	0.04	0.16	0.08	0.06	0.05	0.21	0.22
	<i>bmoY</i>	0.00	0.00	0.01	0.00	0.00	0.00	0.00
	<i>bmoZ</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	<i>ladA</i>	1.81	0.17	0.25	0.18	0.24	0.16	0.35
	<i>MAH1</i>	0.27	0.54	0.46	0.43	0.28	0.23	0.40

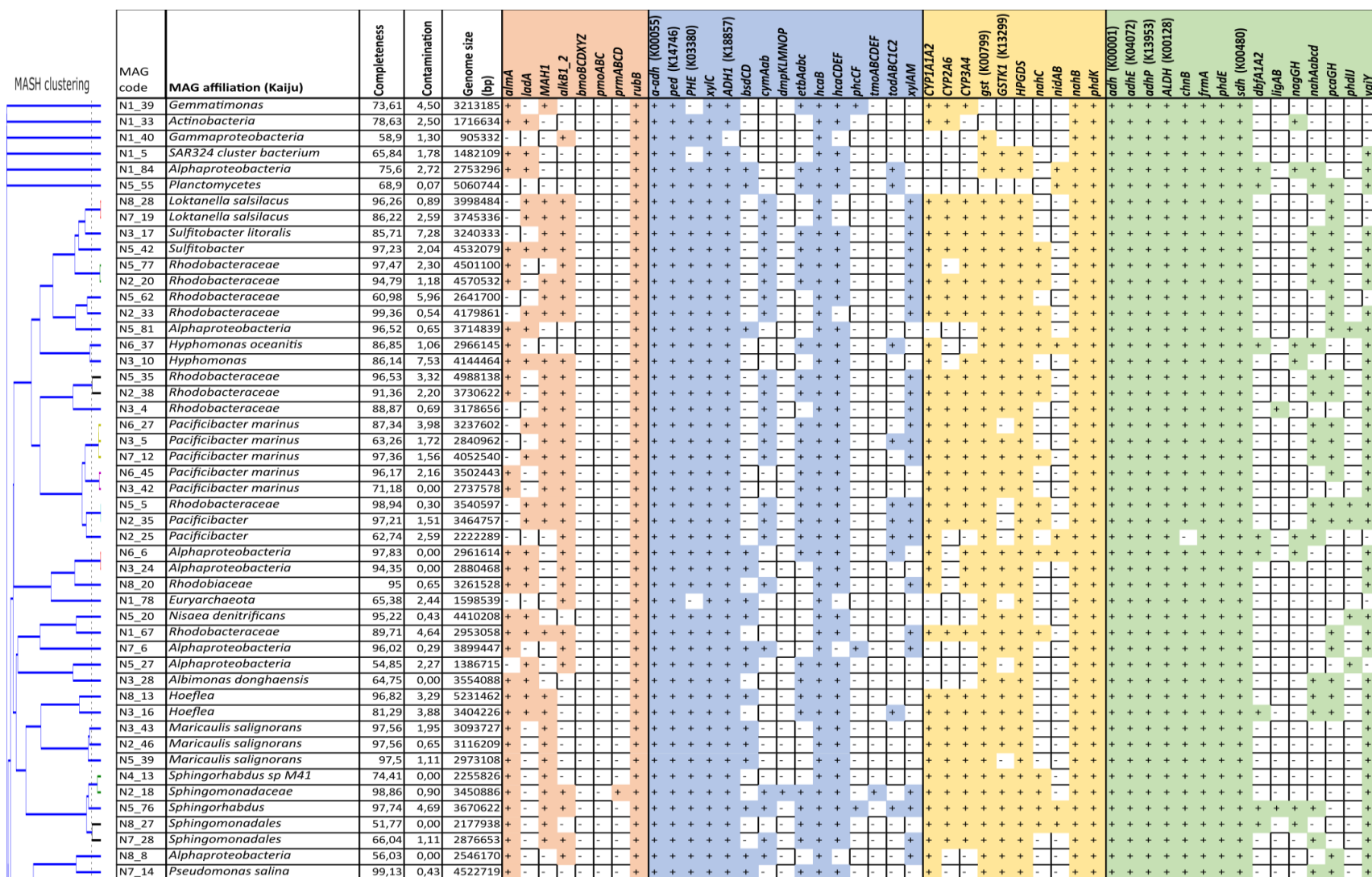
Gene		RPKG						
	SW0	SW4	SW8	SWO4	SWO8	SWOB4	SWOB8	
	<i>pmoA-amoA</i>	0.05	0.24	0.12	0.13	0.08	0.05	0.19
	<i>pmoB-amoB</i>	0.04	0.18	0.05	0.05	0.07	0.06	0.08
	<i>pmoC-amoC</i>	0.06	0.30	0.18	0.14	0.24	0.10	0.26
	<i>prmA</i>	0.04	0.16	0.08	0.07	0.05	0.21	0.23
	<i>prmB</i>	2.44	4.83	4.34	4.91	5.31	7.75	5.82
	<i>prmC</i>	0.08	0.34	0.18	0.14	0.14	0.46	0.43
	<i>prmD</i>	0.00	0.25	0.09	0.11	0.12	0.54	0.41
	Sum	12.37	18.45	16.22	18.04	18.39	24.89	22.60
Monoaromatic compounds	<i>a-adh</i> (K00055)	8.59	7.57	6.72	8.02	8.75	7.85	7.91
	<i>ADH1</i> (K18857)	3.54	3.36	2.96	3.77	3.96	3.68	3.95
	<i>bsdC1</i>	1.24	0.61	0.72	0.50	0.62	0.56	0.52
	<i>bsdC2</i>	0.77	0.44	0.55	0.40	0.48	0.44	0.40
	<i>bsdD</i>	0.00	0.27	0.19	0.14	0.10	0.28	0.36
	<i>cymAa</i>	0.29	0.89	0.71	0.49	0.46	0.81	0.94
	<i>cymAb</i>	1.21	2.69	2.46	2.72	2.70	4.52	3.35
	<i>dmpK</i>	0.04	0.32	0.16	0.22	0.25	0.66	0.42
	<i>dmpL</i>	0.06	0.26	0.17	0.15	0.15	0.30	0.36
	<i>dmpM</i>	0.11	0.97	0.49	0.42	0.31	1.12	1.37
	<i>dmpN</i>	0.05	0.22	0.10	0.11	0.06	0.22	0.30
	<i>dmpO</i>	0.06	0.37	0.21	0.26	0.23	0.85	0.45
	<i>dmpP</i>	2.44	4.62	4.15	4.70	4.91	7.68	5.40
	<i>etbAa</i>	2.68	2.95	2.20	1.89	1.88	2.88	3.25
	<i>etbAb</i>	0.52	3.43	2.31	1.70	2.05	3.62	4.16
	<i>etbAc</i>	2.51	3.34	2.48	1.73	1.99	2.08	2.25
	<i>hcaB</i>	35.21	31.47	29.13	32.78	36.36	33.12	36.03
	<i>hcaC</i>	8.62	8.11	6.97	6.48	6.65	6.57	6.57
	<i>hcaD</i>	5.19	8.77	7.59	9.17	9.12	10.01	9.60
	<i>hcaE</i>	2.93	3.26	2.48	2.03	2.06	3.05	3.48
	<i>hcaF</i>	0.34	2.99	2.05	1.42	1.37	3.21	3.76
	<i>pchC</i>	0.07	0.07	0.10	0.11	0.25	0.11	0.19
	<i>pchF</i>	1.63	1.74	1.38	1.69	2.03	1.37	1.50

Gene		RPKG						
		SW0	SW4	SW8	SWO4	SWO8	SWOB4	SWOB8
	<i>ped</i> (K14746)	35.03	31.15	28.20	32.01	35.41	32.57	36.23
	<i>phe</i> (K03380)	0.89	1.15	0.84	0.99	1.23	1.33	1.35
	<i>tmoA</i>	0.05	0.22	0.10	0.10	0.06	0.23	0.30
	<i>tmoB</i>	0.08	0.38	0.11	0.13	0.07	0.13	0.49
	<i>tmoC</i>	7.43	9.96	7.27	7.25	7.43	7.84	7.85
	<i>tmoD</i>	0.10	0.84	0.39	0.42	0.27	0.97	1.19
	<i>tmoE</i>	0.09	0.42	0.22	0.17	0.15	0.57	0.53
	<i>tmoF</i>	2.72	5.06	4.44	5.17	5.41	8.06	5.89
	<i>todA</i>	1.36	3.19	2.58	3.42	3.17	4.40	4.06
	<i>todB</i>	1.54	1.22	0.75	0.59	0.91	1.30	1.50
	<i>todC1</i>	2.31	2.76	2.02	1.82	1.71	2.72	3.10
	<i>todC2</i>	0.28	2.49	1.44	1.08	1.12	2.29	2.95
	<i>xylA</i>	1.84	3.62	3.27	3.73	3.98	6.34	4.55
	<i>xylC</i>	8.04	9.87	7.45	10.27	11.31	11.86	9.96
	<i>xylM</i>	0.33	1.03	0.76	0.55	0.51	0.89	0.99
	Sum	140.20	162.06	136.13	148.63	159.47	176.51	177.46
Polyaromatic compounds	<i>CYP1A1</i>	1.03	0.85	0.79	1.05	0.75	0.55	1.01
	<i>CYP1A2</i>	0.71	0.81	0.72	0.78	0.53	0.45	0.82
	<i>CYP2A6</i>	0.19	0.43	0.37	0.36	0.27	0.20	0.30
	<i>CYP3A4</i>	0.32	0.62	0.54	0.48	0.32	0.25	0.57
	<i>gst</i> (K00799)	7.10	9.61	8.40	9.61	10.72	10.33	10.47
	<i>GSTK1</i> (K13299)	0.71	0.74	0.82	0.83	1.16	1.42	1.28
	<i>HPGSD</i> (K04097)	1.16	2.05	1.49	1.91	2.24	2.58	2.45
	<i>nahB</i>	28.44	25.95	23.78	27.40	30.24	29.27	30.65
	<i>nahC</i>	0.21	0.89	0.58	0.65	0.56	0.96	1.06
	<i>nidA</i>	2.22	2.62	1.91	1.76	1.64	2.66	3.06
	<i>nidB</i>	0.34	3.06	1.84	1.41	1.41	3.36	3.85
	<i>phdK</i>	7.33	9.02	6.81	9.59	10.18	11.10	9.32
	Sum	49.77	56.66	48.05	55.83	60.02	63.12	64.85
V	<i>adh</i> (K00001)	10.12	9.44	8.27	10.33	11.11	10.75	10.22

Gene	RPKG						
	SW0	SW4	SW8	SW04	SW08	SWOB4	SWOB8
<i>adhE</i> (K04072)	2.81	3.15	2.65	4.24	4.35	5.78	4.45
<i>adhP</i> (K13953)	8.88	7.83	6.91	8.51	9.16	8.61	8.48
<i>ALDH</i> (K00128)	4.92	5.94	4.50	6.19	6.82	6.93	5.96
<i>chnB</i>	2.30	2.00	1.66	1.90	2.04	2.18	2.24
<i>dbfA1</i>	2.47	2.97	2.19	1.96	1.82	2.87	3.25
<i>dbfA2</i>	0.56	3.66	2.47	1.85	2.22	3.85	4.36
<i>frmA</i>	4.37	3.91	3.43	4.21	4.69	4.11	4.23
<i>ligA</i>	0.46	0.28	0.28	0.24	0.37	0.48	0.51
<i>ligB</i>	0.47	0.29	0.27	0.25	0.33	0.60	0.48
<i>nagG</i>	2.76	3.03	2.33	2.01	1.85	3.15	3.41
<i>nagH</i>	0.69	2.36	1.47	1.16	1.11	2.17	2.92
<i>nahAa</i>	2.60	4.99	4.42	5.04	5.35	8.23	5.93
<i>nahAb</i>	3.78	6.24	4.10	3.54	3.73	3.96	3.15
<i>nahAc</i>	2.28	2.75	2.08	1.84	1.70	2.70	3.06
<i>nahAd</i>	0.14	1.91	1.04	0.78	0.86	1.89	2.50
<i>nmsA</i>	0.00	0.00	0.00	0.01	0.00	0.04	0.00
<i>nmsB</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<i>nmsC</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<i>pcaG</i>	0.76	1.09	0.64	0.68	1.36	0.74	0.76
<i>pcaH</i>	0.36	0.60	0.37	0.30	0.59	0.32	0.37
<i>phdE</i>	18.38	16.31	14.81	17.43	19.41	18.44	20.79
<i>phdI</i>	0.33	0.06	0.23	0.02	0.06	0.10	0.12
<i>phdJ</i>	1.11	1.47	1.20	1.21	1.30	1.52	1.43
<i>sdh</i> (K00480)	2.90	4.13	2.96	4.07	4.20	4.36	3.97
<i>yiaY</i>	1.20	1.35	1.24	2.20	1.90	2.76	1.83
Sum	74.67	85.75	69.53	79.97	86.33	96.56	94.40

Table S21. The clustering of good quality (completeness >50%, contamination <10%) metagenome assembled genomes (MAGs) based on their average nucleotide identity (ANI) score along with their oil hydrocarbon degradation gene profiles. MAG affiliations are based on Kaiju with the NCBI-nr database.

Genes related to aliphatic, monoaromatic, polyaromatic, and various types of hydrocarbon compounds degradation are presented on pink, blue, yellow, and green background, respectively.



MAG code	MAG affiliation (Kaiju)	Completeness	Contamination	Genome size (bp)	almA	lcaA	MAH1	alkB1_2	bmoBCDXYZ	pmoABC	prmA	prnA	prnB	prnD	prnE	prnF	prnG	prnH	prnI	prnJ	prnK	prnL	prnM	prnN	prnO	prnP	prnQ	prnR	prnS	prnT	prnU	prnV	prnW	prnX	prnY	prnZ	prnAA	prnAB	prnAC	prnAD	prnAE	prnAF	prnAG	prnAH	prnAI	prnAJ	prnAK	prnAL	prnAM	prnAN	prnAO	prnAP	prnAQ	prnAR	prnAS	prnAT	prnAU	prnAV	prnAW	prnAX	prnAY	prnAZ	prnBA	prnBB	prnBC	prnBD	prnBE	prnBF	prnBG	prnBH	prnBI	prnBJ	prnBK	prnBL	prnBM	prnBN	prnBO	prnBP	prnBQ	prnBR	prnBS	prnBT	prnBU	prnBV	prnBW	prnBX	prnBY	prnBZ	prnC	prnD	prnE	prnF	prnG	prnH	prnI	prnJ	prnK	prnL	prnM	prnN	prnO	prnP	prnQ	prnR	prnS	prnT	prnU	prnV	prnW	prnX	prnY	prnZ	prnAA	prnAB	prnAC	prnAD	prnAE	prnAF	prnAG	prnAH	prnAI	prnAJ	prnAK	prnAL	prnAM	prnAN	prnAO	prnAP	prnAQ	prnAR	prnAS	prnAT	prnAU	prnAV	prnAW	prnAX	prnAY	prnAZ	prnBA	prnBB	prnBC	prnBD	prnBE	prnBF	prnBG	prnBH	prnBI	prnBJ	prnBK	prnBL	prnBM	prnBN	prnBO	prnBP	prnBQ	prnBR	prnBS	prnBT	prnBU	prnBV	prnBW	prnBX	prnBY	prnBZ	prnC	prnD	prnE	prnF	prnG	prnH	prnI	prnJ	prnK	prnL	prnM	prnN	prnO	prnP	prnQ	prnR	prnS	prnT	prnU	prnV	prnW	prnX	prnY	prnZ	prnAA	prnAB	prnAC	prnAD	prnAE	prnAF	prnAG	prnAH	prnAI	prnAJ	prnAK	prnAL	prnAM	prnAN	prnAO	prnAP	prnAQ	prnAR	prnAS	prnAT	prnAU	prnAV	prnAW	prnAX	prnAY	prnAZ	prnBA	prnBB	prnBC	prnBD	prnBE	prnBF	prnBG	prnBH	prnBI	prnBJ	prnBK	prnBL	prnBM	prnBN	prnBO	prnBP	prnBQ	prnBR	prnBS	prnBT	prnBU	prnBV	prnBW	prnBX	prnBY	prnBZ	prnC	prnD	prnE	prnF	prnG	prnH	prnI	prnJ	prnK	prnL	prnM	prnN	prnO	prnP	prnQ	prnR	prnS	prnT	prnU	prnV	prnW	prnX	prnY	prnZ	prnAA	prnAB	prnAC	prnAD	prnAE	prnAF	prnAG	prnAH	prnAI	prnAJ	prnAK	prnAL	prnAM	prnAN	prnAO	prnAP	prnAQ	prnAR	prnAS	prnAT	prnAU	prnAV	prnAW	prnAX	prnAY	prnAZ	prnBA	prnBB	prnBC	prnBD	prnBE	prnBF	prnBG	prnBH	prnBI	prnBJ	prnBK	prnBL	prnBM	prnBN	prnBO	prnBP	prnBQ	prnBR	prnBS	prnBT	prnBU	prnBV	prnBW	prnBX	prnBY	prnBZ	prnC	prnD	prnE	prnF	prnG	prnH	prnI	prnJ	prnK	prnL	prnM	prnN	prnO	prnP	prnQ	prnR	prnS	prnT	prnU	prnV	prnW	prnX	prnY	prnZ	prnAA	prnAB	prnAC	prnAD	prnAE	prnAF	prnAG	prnAH	prnAI	prnAJ	prnAK	prnAL	prnAM	prnAN	prnAO	prnAP	prnAQ	prnAR	prnAS	prnAT	prnAU	prnAV	prnAW	prnAX	prnAY	prnAZ	prnBA	prnBB	prnBC	prnBD	prnBE	prnBF	prnBG	prnBH	prnBI	prnBJ	prnBK	prnBL	prnBM	prnBN	prnBO	prnBP	prnBQ	prnBR	prnBS	prnBT	prnBU	prnBV	prnBW	prnBX	prnBY	prnBZ	prnC	prnD	prnE	prnF	prnG	prnH	prnI	prnJ	prnK	prnL	prnM	prnN	prnO	prnP	prnQ	prnR	prnS	prnT	prnU	prnV	prnW	prnX	prnY	prnZ	prnAA	prnAB	prnAC	prnAD	prnAE	prnAF	prnAG	prnAH	prnAI	prnAJ	prnAK	prnAL	prnAM	prnAN	prnAO	prnAP	prnAQ	prnAR	prnAS	prnAT	prnAU	prnAV	prnAW	prnAX	prnAY	prnAZ	prnBA	prnBB	prnBC	prnBD	prnBE	prnBF	prnBG	prnBH	prnBI	prnBJ	prnBK	prnBL	prnBM	prnBN	prnBO	prnBP	prnBQ	prnBR	prnBS	prnBT	prnBU	prnBV	prnBW	prnBX	prnBY	prnBZ	prnC	prnD	prnE	prnF	prnG	prnH	prnI	prnJ	prnK	prnL	prnM	prnN	prnO	prnP	prnQ	prnR	prnS	prnT	prnU	prnV	prnW	prnX	prnY	prnZ	prnAA	prnAB	prnAC	prnAD	prnAE	prnAF	prnAG	prnAH	prnAI	prnAJ	prnAK	prnAL	prnAM	prnAN	prnAO	prnAP	prnAQ	prnAR	prnAS	prnAT	prnAU	prnAV	prnAW	prnAX	prnAY	prnAZ	prnBA	prnBB	prnBC	prnBD	prnBE	prnBF	prnBG	prnBH	prnBI	prnBJ	prnBK	prnBL	prnBM	prnBN	prnBO	prnBP	prnBQ	prnBR	prnBS	prnBT	prnBU	prnBV	prnBW	prnBX	prnBY	prnBZ	prnC	prnD	prnE	prnF	prnG	prnH	prnI	prnJ	prnK	prnL	prnM	prnN	prnO	prnP	prnQ	prnR	prnS	prnT	prnU	prnV	prnW	prnX	prnY	prnZ	prnAA	prnAB	prnAC	prnAD	prnAE	prnAF	prnAG	prnAH	prnAI	prnAJ	prnAK	prnAL	prnAM	prnAN	prnAO	prnAP	prnAQ	prnAR	prnAS	prnAT	prnAU	prnAV	prnAW	prnAX	prnAY	prnAZ	prnBA	prnBB	prnBC	prnBD	prnBE	prnBF	prnBG	prnBH	prnBI	prnBJ	prnBK	prnBL	prnBM	prnBN	prnBO	prnBP	prnBQ	prnBR	prnBS	prnBT	prnBU	prnBV	prnBW	prnBX	prnBY	prnBZ	prnC	prnD	prnE	prnF	prnG	prnH	prnI	prnJ	prnK	prnL	prnM	prnN	prnO	prnP	prnQ	prnR	prnS	prnT	prnU	prnV	prnW	prnX	prnY	prnZ	prnAA	prnAB	prnAC	prnAD	prnAE	prnAF	prnAG	prnAH	prnAI	prnAJ	prnAK	prnAL	prnAM	prnAN	prnAO	prnAP	prnAQ	prnAR	prnAS	prnAT	prnAU	prnAV	prnAW	prnAX	prnAY	prnAZ	prnBA	prnBB	prnBC	prnBD	prnBE	prnBF	prnBG	prnBH	prnBI	prnBJ	prnBK	prnBL	prnBM	prnBN	prnBO	prnBP	prnBQ	prnBR	prnBS	prnBT	prnBU	prnBV	prnBW	prnBX	prnBY	prnBZ	prnC	prnD	prnE	prnF	prnG	prnH	prnI	prnJ	prnK	prnL	prnM	prnN	prnO	prnP	prnQ	prnR	prnS	prnT	prnU	prnV	prnW	prnX	prnY	prnZ	prnAA	prnAB	prnAC	prnAD	prnAE	prnAF	prnAG	prnAH	prnAI	prnAJ	prnAK	prnAL	prnAM	prnAN	prnAO	prnAP	prnAQ	prnAR	prnAS	prnAT	prnAU	prnAV	prnAW	prnAX	prnAY	prnAZ	prnBA	prnBB	prnBC	prnBD	prnBE	prnBF	prnBG	prnBH	prnBI	prnBJ	prnBK	prnBL	prnBM	prnBN	prnBO	prnBP	prnBQ	prnBR	prnBS	prnBT	prnBU	prnBV	prnBW	prnBX	prnBY	prnBZ	prnC	prnD	prnE	prnF	prnG	prnH	prnI	prnJ	prnK	prnL	prnM	prnN	prnO	prnP	prnQ	prnR	prnS	prnT	prnU	prnV	prnW	prnX	prnY	prnZ	prnAA	prnAB	prnAC	prnAD	prnAE	prnAF	prnAG	prnAH	prnAI	prnAJ	prnAK	prnAL	prnAM	prnAN	prnAO	prnAP	prnAQ	prnAR	prnAS	prnAT	prnAU	prnAV	prnAW	prnAX	prnAY	prnAZ	prnBA	prnBB	prnBC	prnBD	prnBE	prnBF	prnBG	prnBH	prnBI	prnBJ	prnBK	prnBL	prnBM	prnBN	prnBO	prnBP	prnBQ	prnBR	prnBS	prnBT	prnBU	prnBV	prnBW	prnBX	prnBY	prnBZ	prnC	prnD	prnE	prnF	prnG	prnH	prnI	prnJ	prnK	prnL	prnM	prnN	prnO	prnP	prnQ	prnR	prnS	prnT	prnU	prnV	prnW	prnX	prnY	prnZ	prnAA	prnAB	prnAC	prnAD	prnAE	prnAF	prnAG	prnAH	prnAI	prnAJ	prnAK	prnAL	prnAM	prnAN	prnAO	prnAP	prnAQ	prnAR	prnAS	prnAT	prnAU	prnAV	prnAW	prnAX	prnAY	prnAZ	prnBA	prnBB	prnBC	prnBD	prnBE	prnBF	prnBG	prnBH	prnBI	prnBJ	prnBK	prnBL	prnBM	prnBN	prnBO	prnBP	prnBQ	prnBR	prnBS	prnBT	prnBU	prnBV	prnBW	prnBX	prnBY	prnBZ	prnC	prnD	prnE	prnF	prnG	prnH	prnI	prnJ	prnK	prnL	prnM	prnN	prnO	prnP	prnQ	prnR	prnS	prnT	prnU	prnV	prnW	prnX	prnY	prnZ	prnAA	prnAB	prnAC	prnAD	prnAE	prnAF	prnAG	prnAH	prnAI	prnAJ	prnAK	prnAL	prnAM	prnAN	prnAO	prnAP	prnAQ	prnAR	prnAS	prnAT	prnAU	prnAV	prnAW	prnAX	prnAY	prnAZ	prnBA	prnBB	prnBC	prnBD	prnBE	prnBF	prnBG	prnBH	prnBI	prnBJ	prnBK	prnBL	prnBM	prnBN	prnBO	prnBP	prnBQ	prnBR	prnBS	prnBT	prnBU	prnBV	prnBW	prnBX	prnBY	prnBZ	prnC	prnD	prnE	prnF	prnG	prnH	prnI	prnJ	prnK	prnL	prnM	prnN	prnO	prnP	prnQ	prnR	prnS	prnT	prnU	prnV	prnW	prnX	prnY	prnZ	prnAA	prnAB	prnAC	prnAD	prnAE	prnAF	prnAG	prnAH	prnAI	prnAJ	prnAK	prnAL	prnAM	prnAN	prnAO	prnAP	prnAQ	prnAR	prnAS	prnAT	prnAU	prnAV	prnAW	prnAX	prnAY	prnAZ	prnBA	prnBB	prnBC	prnBD	prnBE	prnBF	prnBG	prnBH	prnBI	prnBJ	prnBK	prnBL	prnBM	prnBN	prnBO	prnBP	prnBQ	prnBR	prnBS	prnBT	prnBU	prnBV	prnBW	prnBX	prnBY	prnBZ	prnC	prnD	prnE	prnF	prnG	prnH	prnI	prnJ	prnK	prnL	prnM	prnN	prnO	prnP	prnQ	prnR	prnS	prnT	prnU	prnV	prnW	prnX	prnY	prnZ	prnAA	prnAB	prnAC	prnAD	prnAE	prnAF	prnAG	prnAH	prnAI	prnAJ	prnAK	prnAL	prnAM	prnAN	prnAO	prnAP	prnAQ	prnAR	prnAS	prnAT	prnAU	prnAV	prnAW	prnAX	prnAY	prnAZ	prnBA	prnBB	prnBC	prnBD	prnBE	prnBF	prnBG	prnBH	prnBI	prnBJ	prnBK	prnBL	prnBM	prnBN	prnBO	prnBP	prnBQ	prnBR	prnBS	prnBT	prnBU	prnBV	prnBW	prnBX	prnBY	prnBZ	prnC	prnD	prnE	prnF	prnG	prnH	prnI	prnJ	prnK	prnL	prnM	prnN	prnO	prnP	prnQ	prnR	prnS	prnT	prnU	prnV	prnW	prnX	prnY	prnZ	prnAA	prnAB	prnAC	prnAD	prnAE	prnAF	prnAG	prnAH	prnAI	prnAJ	prnAK	prnAL	prnAM	prnAN	prnAO	prnAP	prnAQ	prnAR	prnAS	prnAT	prnAU	prnAV	prnAW	prnAX	prnAY	prnAZ	prnBA	prnBB	prnBC	prnBD	prnBE	prnBF	prnBG	prnBH	prnBI	prnBJ	prnBK	prnBL	prnBM	prnBN	prnBO	prnBP	prnBQ	prnBR	prnBS	prnBT	prnBU	prnBV	prnBW	prnBX	prnBY	prnBZ	prnC	prnD	prnE	prnF	prnG	prnH	prnI	prnJ	prnK	prnL	prnM	prnN	prnO	prnP	prnQ	prnR	prnS	prnT	prnU	prnV	prnW	prnX	prnY	prnZ	prnAA	prnAB	prnAC	prnAD	prnAE	prnAF	prnAG	prnAH	prnAI	prnAJ	prnAK	prnAL	prnAM	prnAN	prnAO	prnAP	prnAQ	prnAR	prnAS	prnAT	prnAU	prnAV	prnAW	prnAX	prnAY	prnAZ	prnBA	prnBB	prnBC	prnBD	prnBE	prnBF	prnBG	prnBH	prnBI	prnBJ	prnBK	prnBL	prnBM	prnBN	prnBO	prnBP	prnBQ	prnBR	prnBS	prnBT	prnBU	prnBV	prnBW	prnBX	prnBY	prnBZ	prnC	prnD	prnE	prnF	prnG	prnH	prnI	prnJ	prnK	prnL	prnM	prnN	prnO	prnP	prnQ	prnR	prnS	prnT	prnU	prnV	prnW	prnX	prnY	prnZ	prnAA	prnAB	prnAC	prnAD	prnAE	prnAF	prnAG	prnAH	prnAI	prnAJ	prnAK	prnAL	prnAM	prnAN	prnAO	prnAP	prnAQ	prnAR	prnAS	prnAT	prnAU	prnAV	prnAW	prnAX	prnAY	prnAZ	prnBA	prnBB	prnBC	prnBD	prnBE	prnBF	prnBG	prnBH	prnBI	prnBJ	prnBK	prnBL	prnBM	prnBN	prnBO	prnBP	prnBQ	prnBR	prnBS	prnBT	prnBU	prnBV	prnBW	prnBX	prnBY	prnBZ	prnC	prnD	prnE	prnF	prnG	prnH	prnI	prnJ	prnK	prnL	prnM	prnN	prnO	prnP	prnQ	prnR	prnS	prnT	prnU	prnV	prnW	prnX	prnY	prnZ	prnAA	prnAB	prnAC	prnAD	prnAE	prnAF	prnAG	prnAH	prnAI	prnAJ	prnAK	prnAL	prnAM	prnAN	prnAO	prnAP	prnAQ	prnAR	prnAS	prnAT	prnAU	prnAV	prnAW	prnAX	prnAY	prnAZ	prnBA	prnBB	prnBC	prnBD	prnBE	prnBF	prnBG	prnBH	prnBI	prnBJ	prnBK	prnBL	prnBM	prnBN	prnBO	prnBP	prnBQ	prnBR	prnBS	prnBT	prnBU	prnBV	prnBW	prnBX	prnBY	prnBZ	prnC	prnD	prnE	prnF	prnG	prnH	prnI	prnJ	prnK	prnL	prnM	prnN	prnO	prnP	prnQ	prnR	prnS	prnT	prnU	prnV	prnW	prnX	prnY	prnZ	prnAA	prnAB	prnAC	prnAD	prnAE	prnAF	prnAG	prnAH	prnAI	prnAJ	prnAK	prnAL	prnAM	prnAN	prnAO	prnAP	prnAQ	prnAR	prnAS	prnAT	prnAU	prnAV	prnAW	prnAX	prnAY	prnAZ	prnBA	prnBB	prnBC	prnBD	prnBE	prnBF	prnBG	prnBH	prnBI	prnBJ	prnBK	prnBL	prnBM	prnBN	prnBO	prnBP	prnBQ	prnBR	prnBS	prnBT	prnBU	prnBV	prnBW	prnBX	prnBY	prnBZ	prnC	prnD	prnE	prnF	prnG	prnH	prnI	prnJ	prnK	prnL	prnM	prnN	prnO	prnP	
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[illegible]

ASH Average Nucleotide Identity (ANI)

Table S22. Major operational taxonomic units (OTUs) of bacterial and archaeal genera found in seawater (SW), oil contaminated seawater (SWO), and biostimulated oil contaminated seawater (SWOB) after four and eight months of incubation according to amplicon-based sequencing. Multiple hits within the same genera are indicated in brackets after the genera name.

Treat-ment type	Phylum	Class	Order	Family	Genus	4 months	8 months
SW	Bacteroidetes	Bacteroidia	Flavobacteriales	Crocinitomicaceae	Unclassified Crocinitomicaceae	+	-
				Flavobacteriaceae	Doktonia	+	+
					Ulvibacter	+	-
					Unclassified Flavobacteriaceae	+	+
				NS9 marine group	NS9 marine group genus	+	-
			Sphingobacteriales	NS11-12 marine group	NS11-12 marine group genus	+	+
	Firmicutes	Clostridia	Clostridiales	Clostridiaceae	Clostridium (sensu stricto)	+	-
	Planctomycetes	OM190			OM190 genus	+	+
		Phycisphaerae	Phycisphaerales	Phycisphaeraceae	SMIA02	+	+
	Proteobacteria	α -proteobacteria	Kordiimonadales	Uncultured Kordiimonadales		+	-
			Rhizobiales	Rhizobiaceae	Lentilitoribacter	+	+
			Rhodobacterales	Rhodobacteraceae	Planktomarina	+	-
					Pseudophaeobacter	+	+
					Unclassified Rhodobacteraceae (2)	+	+
					Sedimentitaleae	+	+
			Rhodospirillales	Magnetospiraceae	Uncultured Magnetospiraceae	+	+
			SAR11 clade	Clade III	Clade III genus	+	+
		γ -proteobacteria	Betaproteobacteriales	Methylophilaceae	OM43_clade	+	+
			Cellvibrionales	Porticoccaceae	Porticoccus	+	+
				Spongiibacteraceae	Zhongshania	+	+
				Unclassified Cellvibrionales		+	+
		δ -proteobacteria	Bdellovibrionales	Bdellovibrionaceae	OM27_clade	+	-
			Myxococcales	Sandaracinaceae	Uncultured Sandaracinaceae	+	-
SWO	Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	Cellulophaga	+	-
					Maribacter (2)	+	+

Treat-ment type	Phylum	Class	Order	Family	Genus	4 months	8 months	
	Proteobacteria	α -proteobacteria	Parvibaculales	Parvibaculaceae	Ulvibacter	+	-	
					Unclassified Flavobacteriaceae (2)	+	+	
					Parvibaculum	+	+	
					Pacificibacter	+	+	
					Pelagibius	-	+	
					Colwellia	-	+	
					Pseudohongiella	+	+	
					Ca. Nitrosopumilus	+	-	
Thaumarchaeota	Nitrososphaeria	Nitrosopumilales	Nitrosopumiliaceae					
SWOB	Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	Aequorivita	+	+	
	Proteobacteria	α -proteobacteria	Rhodobacterales	Rhodobacteriaceae	Unclassified Rhodobacteraceae	+	+	
			Sphingomonadales	Sphingomonadaceae	Unclassified Sphingomonadaceae	+	+	
			Alteromonadales	Alteromonadaceae	Paraglaciecola	+	+	
		γ -proteobacteria	Moraxellaceae	Paraperlucidibaca	+	+		
				Pseudomonadaceae	Pseudomonas (2)	+	+	
			SW & SWO	Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	Tenacibaculum
	Ulvibacter (2)	+						+
Unclassified Flavobacteriaceae (2)	+	+						
Planctomycetes	OM190			OM190 genus	+	+		
Proteobacteria	α -proteobacteria	Caulobacterales		Hyphomonadaceae	Algimonas	+	+	
					Hyphomonas	+	+	
					Maricaulis	+	+	
		Rhodobacterales		Rhodobacteriaceae	Unclassified Rhodobacteraceae (2)	+	-	
		Rhodospirillales		Terasakiellaceae	Uncultured Terasakiellaceae	+	+	
		SAR11 clade		Clade I	Clade Ia genus	+	-	
		γ -proteobacteria		Alteromonadales	Alteromonadaceae	Paraglaciecola	+	+
	Colwelliaceae				Colwellia	+	+	
				Uncultured Colwelliaceae	-	+		
	Nitrosococcales	Methylophagaceae		Uncultured Methylophagaceae	+	+		
S W &	Acidobacteria	Subgroup 6			Subgroup 6 genus (2)	+	+	
	Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	Flavobacterium	+	+	

Treat-ment type	Phylum	Class	Order	Family	Genus	4 months	8 months
SWO & SWOB	Proteobacteria	α -proteobacteria	Unclassified α -proteobacteria			-	+
		γ -proteobacteria	Methylococcales	Cycloclasticaceae	Cycloclasticus	+	+
	Proteobacteria	α -proteobacteria	Sneathiellales	Sneathiellaceae	Sneathiella	+	+
		γ -proteobacteria	Oceanospirillales	Marinomonadaceae	Marinomonas	+	+
				Nitrincolaceae	Amphritea	+	+(SWOB)
SW & SWO & SWOB	Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	Aequorivita	+(SWO. SWOB)	+
					Aurantivirga	+	+
					Jejudonia	+(SWO)	+
					Ulvibacter	+	+
					Unclassified Flavobacteriaceae (3)	+	+
	Planctomycetes	Phycisphaerae	Phycisphaerales	Phycisphaeraceae	SM1A02	+(SW. SWO)	+
	Proteobacteria	α -proteobacteria	Rhizobiales	Rhizobiaceae	Hoeflea	+(SW. SWO)	+
			Rhodobacterales	Rhodobacteraceae	Pacificibacter	+	+
					Unclassified Rhodobacteraceae	+	+
			Sneathiellales	Sneathiellaceae	Sneathiella	+	+
			Sphingomonadales	Sphingomonadaceae	Sphingorhabdus	+	+
		γ -proteobacteria	Alteromonadales	Colwelliaceae	Colwellia (2)	+	+
			Enterobacteriales	Enterobacteraceae	Unclassified Enterobacteraceae	-	+
			Methylococcales	Cycloclasticaceae	Cycloclasticus	+	+
			Oceanospirillales	Marinomonadaceae	Marinomonas	+	+
				Nitrincolaceae	Uncultured Nitrincolaceae	+	+
				Saccharospirillaceae	Oleispira	+	-
			Pseudomonadales	Moraxellaceae	Paraperlucidibaca	+(SW. SWOB)	+
			Unclassified Gammaproteobacteria			+	+

Supplementary figures

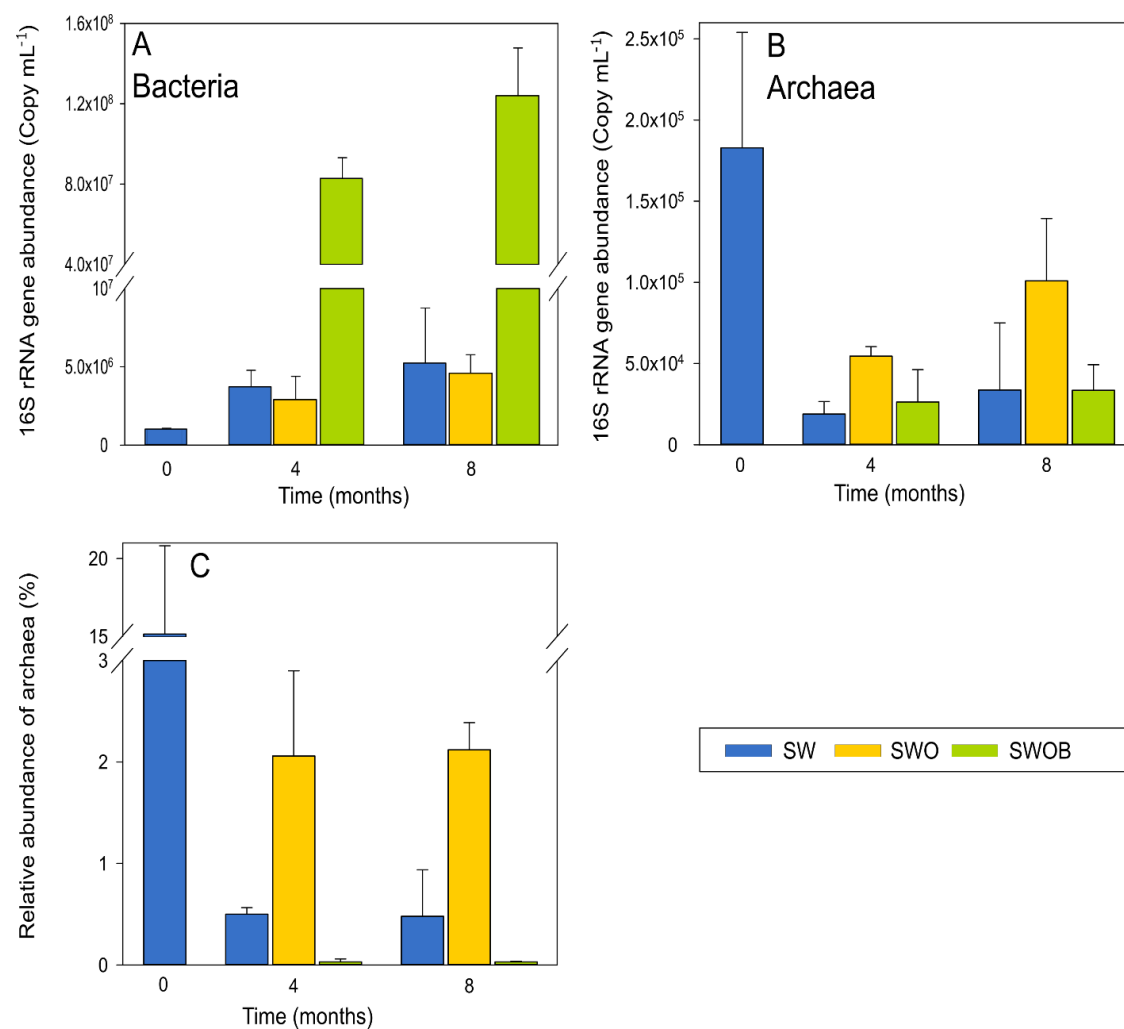


Fig. S1. The abundances of bacterial (A) and archaeal (B) communities, as well as the relative abundance of the archaeal community (C) in seawater (SW), oil contaminated seawater (SWO) and biostimulated oil contaminated seawater (SWOB), $n = 2$.

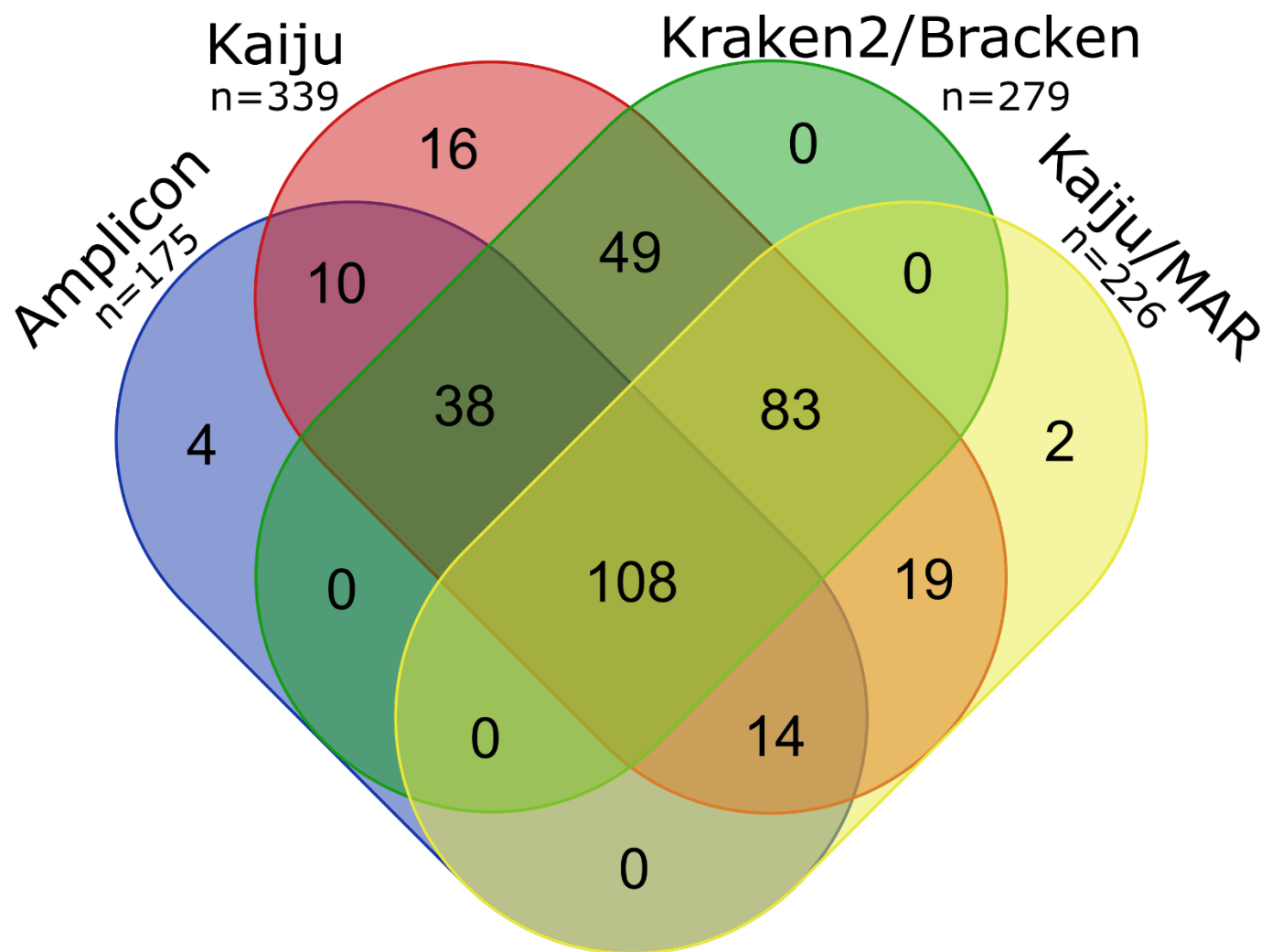
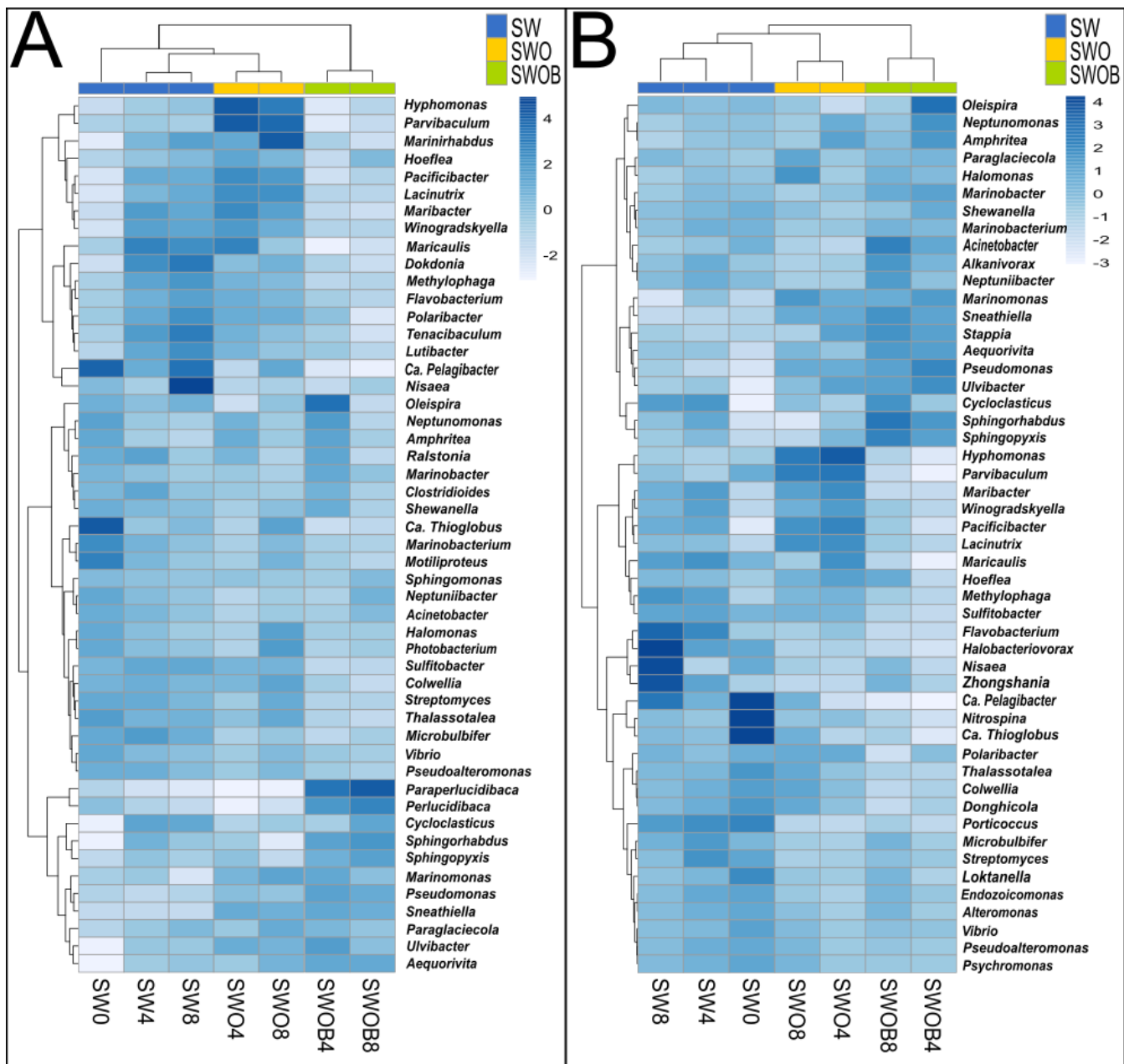
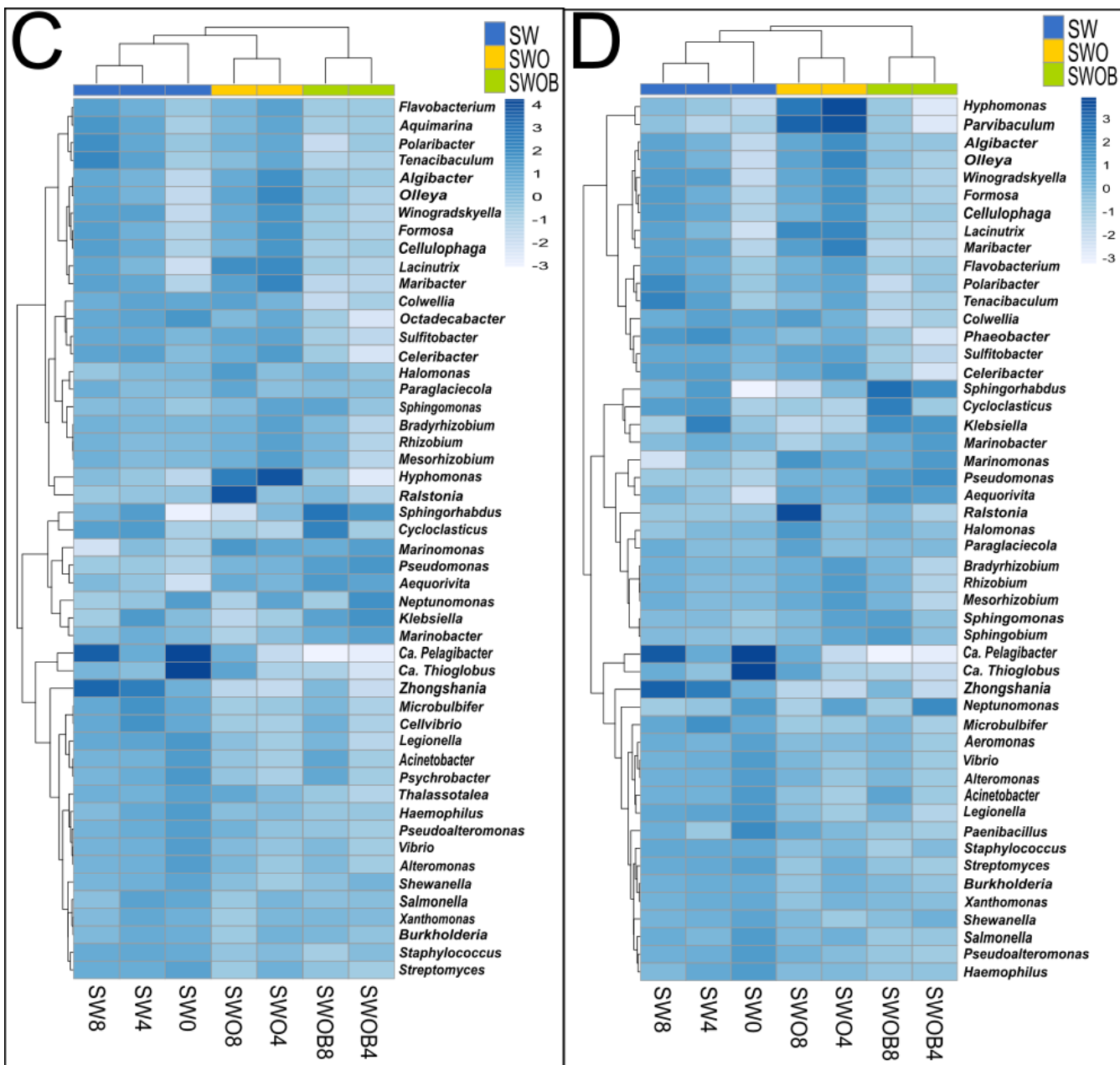


Fig. S2. Venn diagram showing the overlap of detected genera containing oil hydrocarbon degraders between different taxonomic classification methods (Kaiju with the NCBI-nr database, Kaiju with the MAR_{DB} database, Kraken2 with the Standard Kraken 2 database, Bracken with the Standard Kraken 2 database, and amplicon-based sequencing with the SILVA database).





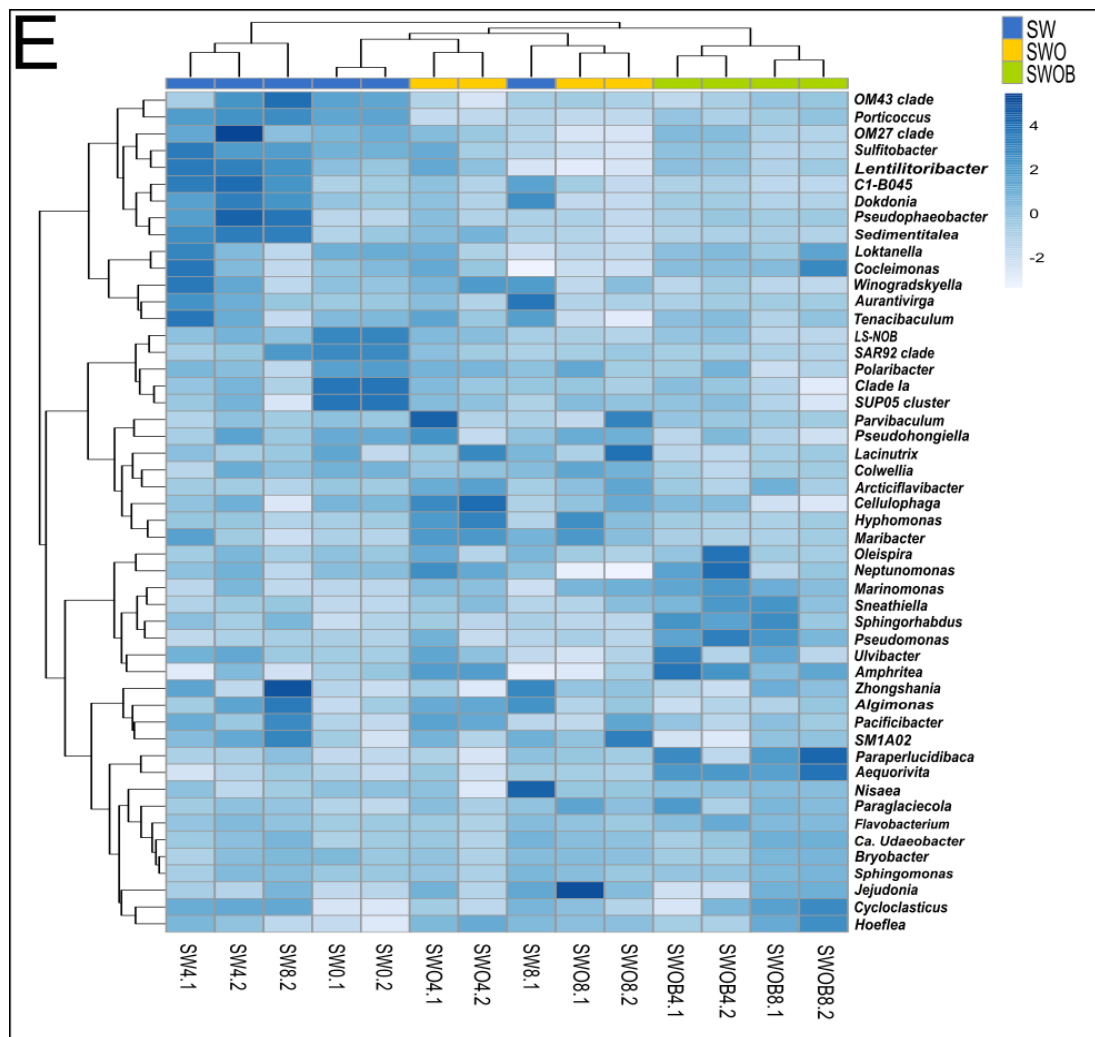


Fig. S3. The clustering of seawater (SW), oil contaminated seawater (SWO) and biostimulated oil contaminated seawater (SWOB) microcosms based on the crl-transformed proportions of the 50 predominant genera of Kaiju (A), Kaiju/MAR (B), Kraken2 (C), Bracken (D), and Amplicon (E) taxonomic classifications. The numbers in sample codes denote time in months, second number in sample code on subplot E denotes the treatment parallel number. The color intensity corresponds to crl-transformed proportion values with dark blue denoting genera with high proportion values in bacterial community.

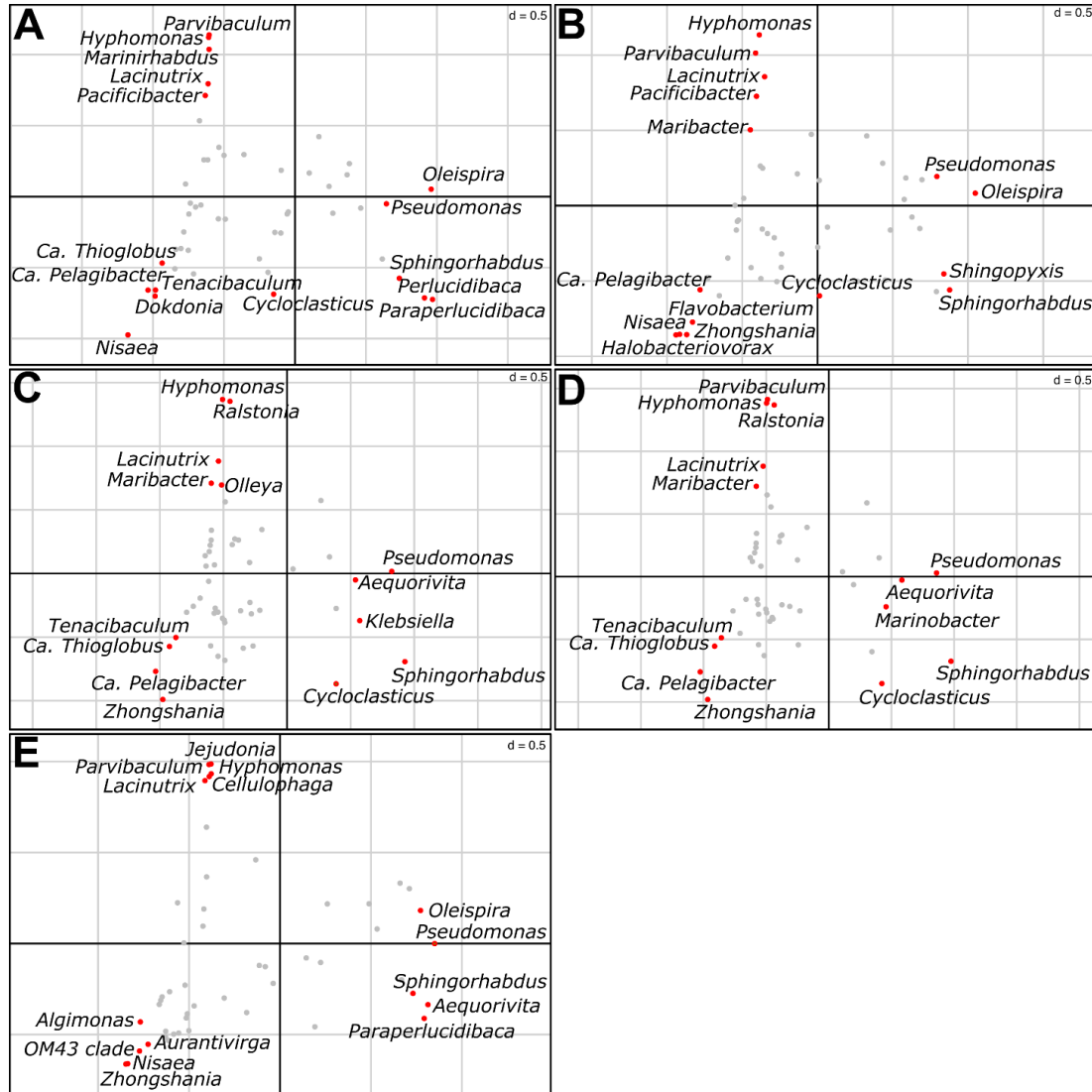


Fig. S4. Multiple co-inertia analysis results based on datasets of the top 50 bacterial genera proportions based on five taxonomic classification methods. Shown are variable spaces for each dataset (Kaiju with the NCBI-nr database (A), Kaiju with the MAR_{DB} database (B), Kraken2 (C) and Bracken (D) with the Standard Kraken2 database, and Amplicon based sequencing with the SILVA database (E)).

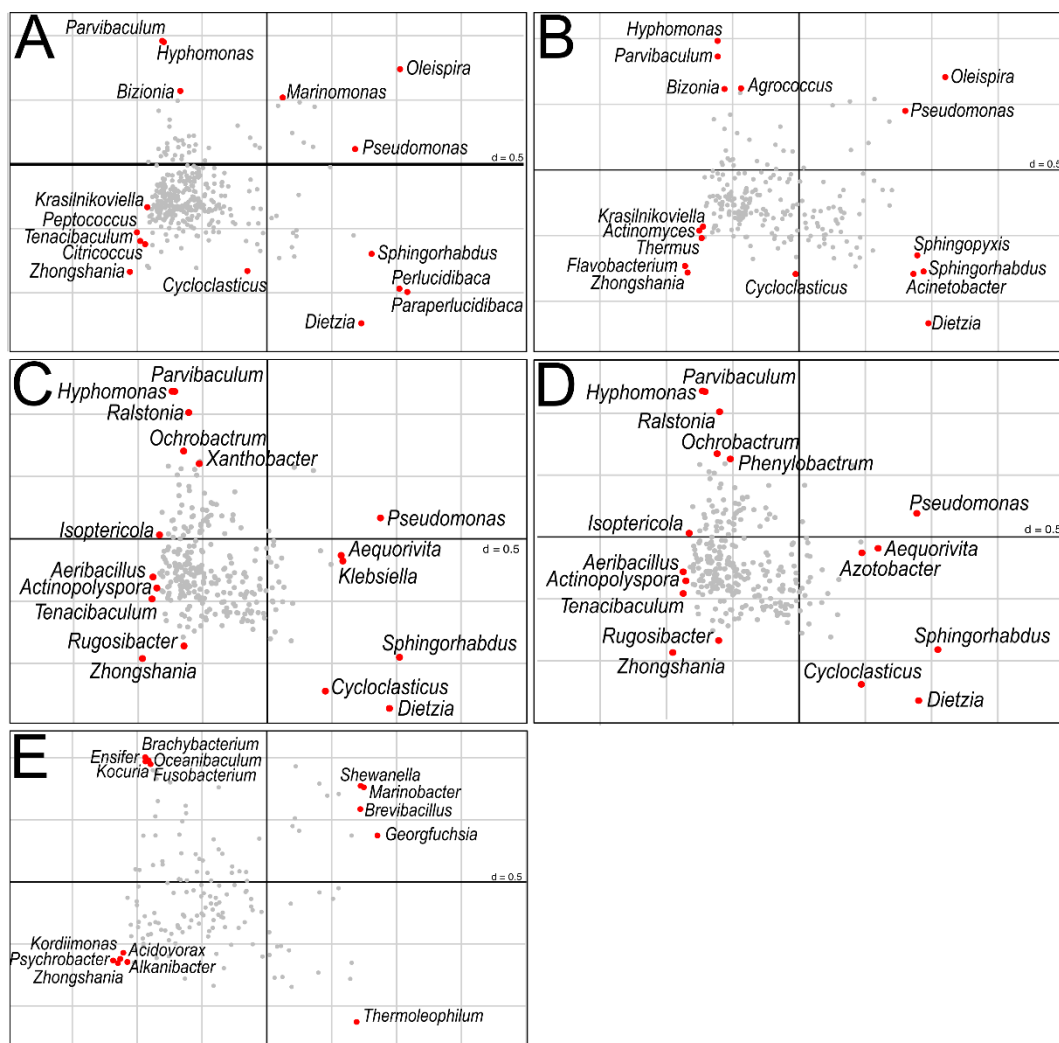


Fig. S5. Multiple co-inertia analysis results based on datasets of proportions of bacterial genera containing oil hydrocarbon degraders based on five taxonomic classification methods. Shown are variable spaces for each data set (Kaiju with the NCBI-nr database (A), Kaiju with the MAR_{DB} database (B), Kraken2 (C) and Bracken (D) with the Standard Kraken2 database, and Amplicon based sequencing with the SILVA database (E)).

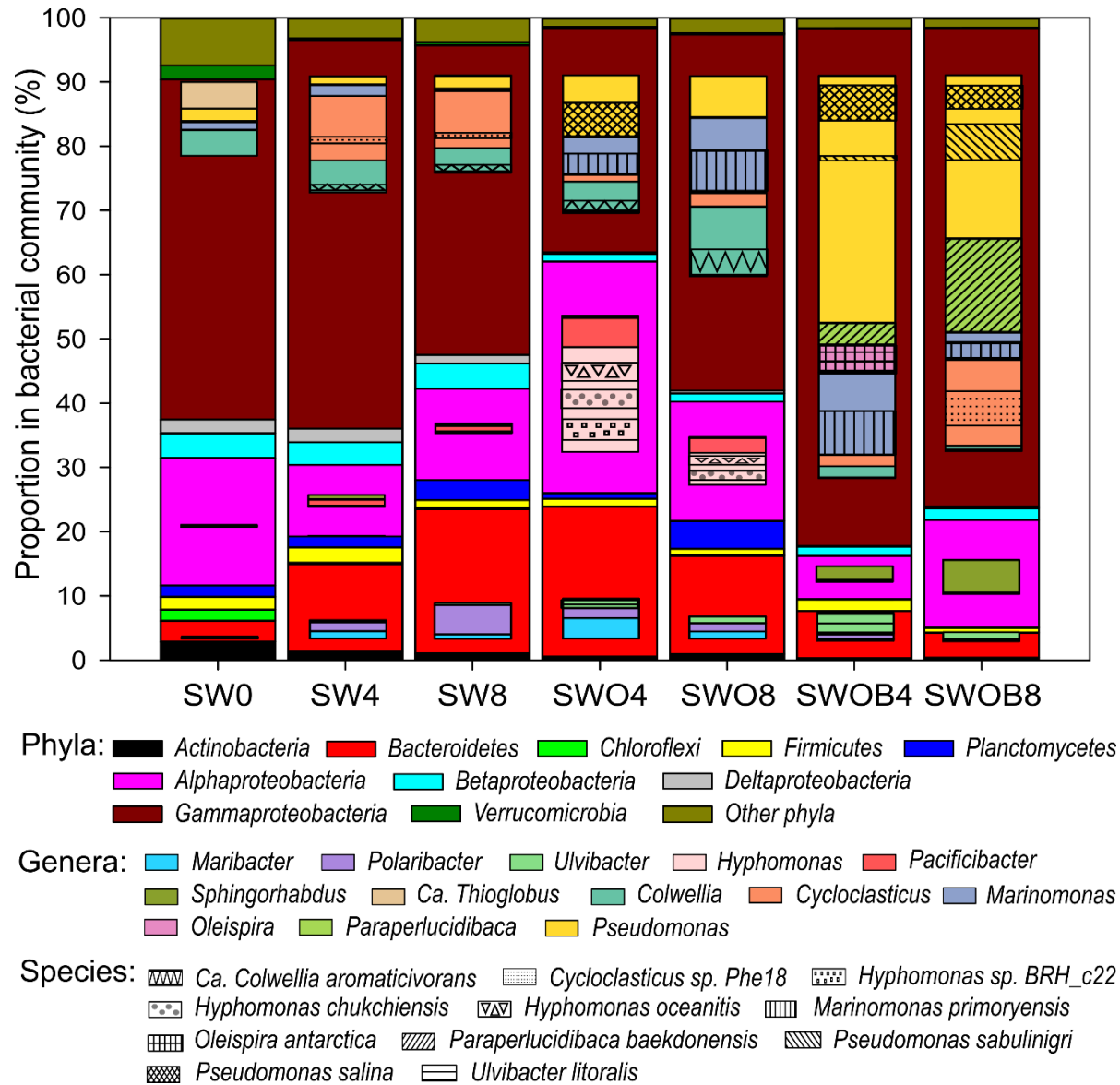


Fig. S6. The bacterial community structure at phylum, genus (>3%), and species (>3%) level in seawater (SW), oil-contaminated seawater (SWO), and biostimulated oil-contaminated seawater (SWOB). The numbers in sample codes denote time in months. Proteobacteria are presented at class level.

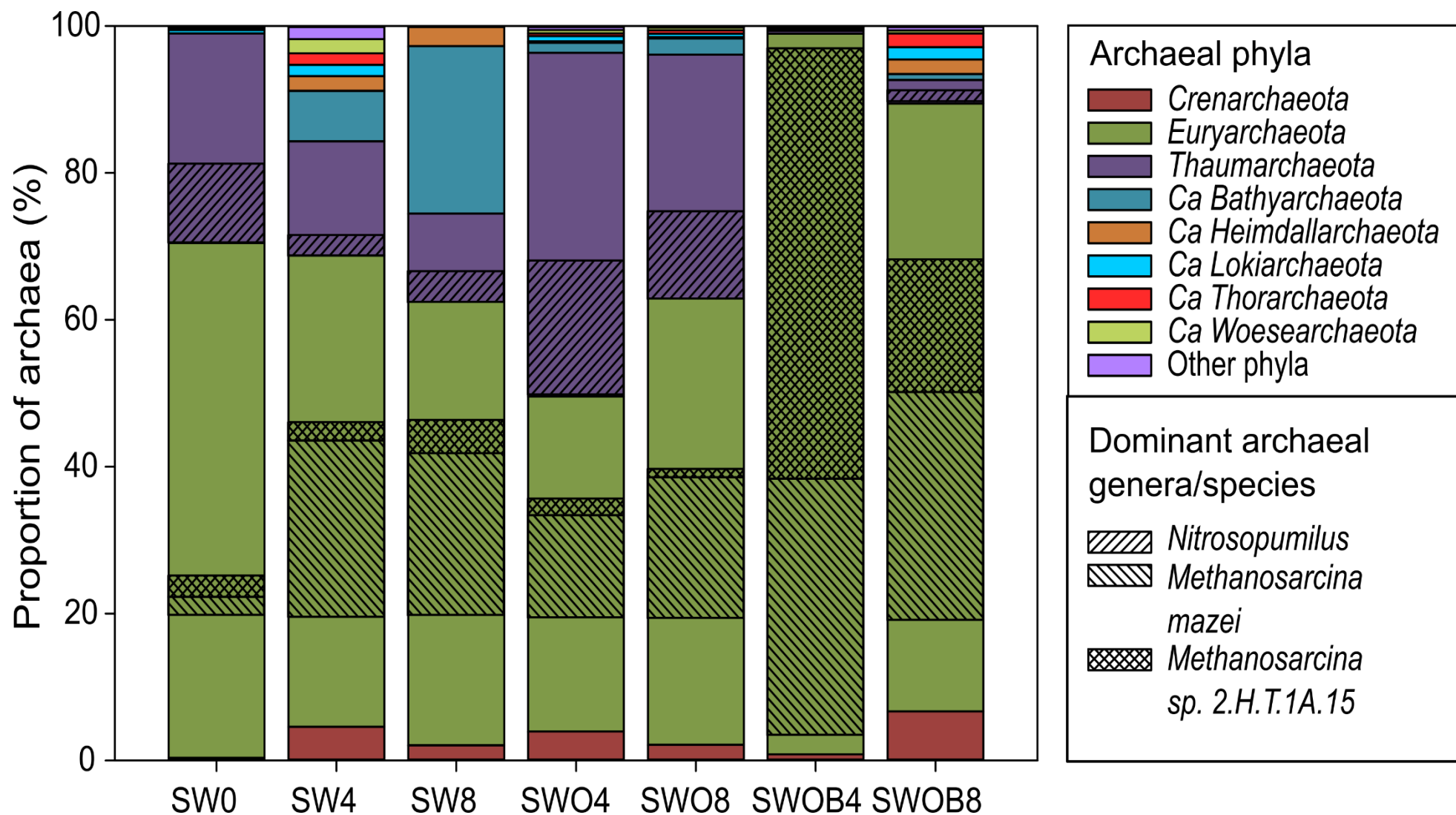


Fig. S7. The proportions of archaeal phyla as well as the most dominant archaeal genera and species in the archaeal community in seawater (SW), oil contaminated seawater (SWO) and biostimulated oil contaminated seawater (SWOB) according to taxonomic classification using Kaiju with the NCBI-nr database. The numbers in sample codes denote time in months.

Section S1: Prokaryotic Community Structure in Different Treatments According to Kaiju

Since Kaiju with the NCBI-nr database generally resulted in the highest number of classified reads (Table S3), the closest rank estimate to the average of all methods on the phylum level (Figure 3), and the highest overlap with other methods when considering the list of 50 most abundant bacterial genera (Figure 4), the prokaryotic community structure in different treatments of the current study is described according to this method.

At the phylum level, the bacterial community in the initial seawater (SW0), used to set up the treatment microcosms, was dominated by Proteobacteria (especially Gamma- and Alphaproteobacteria), which accounted for 79% of the community (Figure S6). Gammaproteobacterial genera *Ca. Thioglobus* and *Colwellia* (4.1% and 4.0%, respectively) were the predominant genera in SW0. In SW, the Bacteroidetes proportion increased over time, from 3.2% in SW0 to 22.5% of the bacterial community in SW8; this increase was mostly at the expense of Alphaproteobacteria in the first half of the experiment and also Gammaproteobacteria during the second half. In this treatment, the proportion of *Colwellia* was quite stable (3.9–4.9%) throughout the experiment, while *Cycloclasticus* became the most predominant genus (8.8–10%) from the fourth month onward.

The addition of Troll B type crude oil markedly changed the seawater bacterial community structure. By the fourth month, the proportions of Gamma-, Beta-, and Deltaproteobacteria, as well as those of less abundant phyla Actinobacteria, Planctomycetes, Chloroflexi, and Verrucomicrobia, were markedly diminished. In SWO4, the proportion of Alphaproteobacteria was almost doubled, and the proportion of Bacteroidetes increased 7-fold compared to SW0. The Alphaproteobacterial genus *Hyphomonas* dominated in SWO4 (16.3%), with four predominant species (Table S18), followed by Gammaproteobacterial genera *Pseudomonas* (especially the species *P. salina*) and *Marinomonas* (9.6% and 5.8%, respectively). At the phylum level, the bacterial community structure in SWO8 became quite similar to that in SW8, but differences were evident at the genus level. In SWO8, *Marinomonas* (especially *M. primoryensis*) and *Colwellia* (especially *Ca. C. aromaticivorans*) replaced *Hyphomonas* in the dominant position (11.7%, 10.9%, and 5.0% of the bacterial community, respectively).

In the SWOB treatment, the proportion of Gammaproteobacteria was increased at the expense of all other phyla (except Bacteroidetes) and Proteobacterial classes compared to SW0. Gammaproteobacteria formed 75–81% of the bacterial community throughout the experiment. *Pseudomonas* strongly dominated in SWOB4 (38%), followed by *Marinomonas*, especially *M. primoryensis* (6.8%), and *Oleispira*, especially *O. antarctica* (4.4%) (Table S18). The proportion of the second most abundant taxon, Alphaproteobacteria, rose from 6.8% in SWOB4 to 17% in SWOB8, largely owing to the increase in the genus *Sphingorhabdus* (5.1%). Although still dominant, the proportions of *Pseudomonas* and *Marinomonas* (25.4% and 4.3%, respectively) decreased over time, and *Paraperlucidibaca* (especially *P. baekdonensis* (14.6%)) and *Cycloclasticus* (13.4%) emerged among community dominants in SWOB8.

Roughly 2/3 of the archaeal community in SW0 was formed by Euryarchaeota, while Thaumarchaeota accounted for 1/3 (Figure S7). In SW, the proportion of Thaumarchaeota decreased over time, and *Ca. Lokiarchaeota* emerged as the second most dominant phylum by the eighth month. In SWO, the proportion of Thaumarchaeota and especially its genus *Nitrosopumilus* initially increased at the expense of Euryarchaeota, while the community structure at the phylum level reverted to that in initial seawater (SW0) by the eighth month. In the SWOB treatment, on the other hand, two Euryarchaeotal *Methanosarcina* species (*M. mazei* and *M. sp. 2HT1A15*) became highly dominant, forming 90% and 45% of the archaeal community in SWOB4 and SWOB8, respectively.

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