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Distribution of PAHs and the PAH-degrading bacteria in the deep-sea sediments of the high-latitude Arctic Ocean

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Supplemental Material

Supplemental script

The script (combine.bipes.pl) is posted below.

During the IHTS data analysis process, all clean reads of each sample were stored in an independent “fasta” format file. Before executing this script, user should build a file named “fa.list” for storing the file paths of all these “fasta” format files. Then, the user can use the command “perl combine.bipes.pl fa.list outprefix” to execute the script. Finally, clean reads of each sample were combined into a file named “outprefix.combined.fa”.

```
#!/usr/bin/perl -w
use strict;

if ($#ARGV ne 1)
{
  print "perl $0 <fa.list> <outprefix>\n";
  die;
}

open I,"$ARGV[0]" || die "can not find I:$!";
my $out = "$ARGV[1].combined.fa";
open OUT,">$out" || die "can not open OUT:$!";


while(<I>)
{
```

```
 chomp;
 open II,"$_" || die "can not find II:$!";
 #my @m = split/\./;
 #pop @m;
 my $sample = $_;
 my $n = 0;
 while(<II>)
 {
   my $seq = <II>;
   chomp $seq;
   $n++;
   print OUT ">$sample\_$n\n$seq\n";
   }
 }
---------------------------------------------------------------------------------------------------------------------------
```

Supplemental Tables

Table S1 Sampling sites and deep-sea sediments in the Arctic Ocean

Site	**Location**	**Sample**[a]	**Layer (cm)**	**Longitude (W)**	**Latitude (N)**	**Water depth (m)**	**Date**
BN03	Chukchi Plateau	BN03U	0-4	158°53.99′	78°29.96′	-2790	31/7/2010
		BN03M	8-12				
		BN03L	16-20				
BN06	Canada Basin	BN06U	0-2	164°56.37′	81°27.69′	-3566	2/8/2010
		BN06M	6-10				
		BN06L	26-30				
BN09	Alpha Ridge	BN09U	0-2	167°07.61′	84°11.21′	-2500	5/8/2010
		BN09M	6-10				
		BN09L	22-24				
BN12	Makarov Basin	BN12U	0-4	170°29.31′	87°04.27′	-4000	17/8/2010
		BN12M	8-12				
		BN12L	36-38				

a: U, M, and L, refer to the upper, middle, and lower layer of each sediment core, respectively.

Table S2 The concentrations (ng g^{-1} dw) of 16 priority-control PAHs in the sediments of the western Arctic Ocean.

	BN03U[a]	BN03M	BN03L	BN06U	BN06M	BN06L	BN09U	BN09M	BN09L	BN12U	BN12M	BN12L
Naphthalene	2.92	4.64	4.84	5.65	2.68	1.80	3.51	0.69	1.54	2.73	0.76	0.86
Acenaphthylene	nd[b]	nd	nd	nd	nd	nd	nd	nd	nd	nd	nd	nd
Acenaphthene	nd	nd	nd	nd	nd	nd	nd	nd	nd	nd	nd	nd
Fluorene	0.46	1.09	0.64	1.49	0.87	0.37	2.69	nd	nd	0.54	nd	0.87
Phenanthrene	4.31	8.34	6.45	7.16	4.53	1.35	14.61	2.50	0.74	3.58	0.67	4.09
Anthracene	nd	nd	nd	nd	nd	nd	nd	nd	nd	nd	nd	nd
Fluoranthene	0.62	1.13	1.25	0.53	0.27	0.20	0.75	0.20	0.15	0.31	0.15	0.24
Pyrene	0.77	1.58	1.81	0.64	0.34	0.16	1.18	0.25	0.13	0.39	0.13	0.29
Benz[a]anthracene	0.36	0.77	0.92	0.20	nd	nd	nd	nd	nd	nd	nd	nd
Chrysene	1.80	3.37	3.83	1.48	0.21	0.14	0.69	nd	nd	0.57	nd	nd
Benzo[b]fluoranthene	2.99	8.14	10.46	2.53	0.86	0.44	0.98	0.60	0.23	1.08	0.31	0.19
Benzo[k]fluoranthene	0.44	1.12	1.02	0.38	nd	nd	nd	nd	nd	nd	nd	nd
Benzo[a]pyrene	0.37	0.76	0.96	0.23	nd	nd	nd	0.37	nd	nd	nd	nd
Indeno[1,2,3-c,d]pyrene	1.08	3.31	3.13	1.04	nd	0.40	nd	nd	nd	nd	nd	nd
Dibenz[a,h]anthracene	0.42	1.17	1.13	0.42	nd	nd	nd	nd	nd	nd	nd	nd
Benzo[g,h,i]perylene	2.27	6.09	5.19	2.08	nd	nd	0.42	nd	nd	nd	nd	nd
Total	18.81	41.51	41.63	23.83	9.76	4.86	24.83	4.61	2.79	9.20	2.02	6.54

a: The mean of U, M and L within the sample names refer to the note of Table S1.

b: nd indicates the concentration of this kind of PAH is below the detection limit.

Table S3 Illumina sequencing efforts and bacterial diversity indexes of the *in situ* sediment samples and PAH-degrading consortia from the Arctic Ocean

Sample type	Sample ID	Location	Layer (cm)	Tags	Unique	OTUs[a, b]	Chao1[b]	Shannon[b]
Sediment	sBN03U	Chukchi Plateau	0-4	76840	11628	1643	4025	8.85
	sBN03M		8-12	35538	3419	726	1496	7.12
	sBN03L		16-20	41552	5067	975	2007	7.58
	sBN06U	Canada Basin	0-2	70641	10071	1422	3294	8.46
	sBN06M		6-10	131903	8074	557	1005	6.46
	sBN06L		26-30	108680	8734	610	1720	6.64
	sBN09U	Alpha Ridge	0-2	79766	12226	1621	3654	8.89
	sBN09M		6-10	108001	9133	786	1400	7.44
	sBN09L		22-24	123022	10631	889	1583	7.58
	sBN12U	Makarov Basin	0-4	55880	8673	1476	3603	8.47
	sBN12M		8-12	126324	7543	552	1334	6.37
	sBN12L		36-38	93831	9174	941	1516	7.87
4 ℃	4BN03U	Chukchi Plateau	0-4	106319	3494	249	627	3.36
	4BN03M		8-12	48430	1544	209	644	1.96
	4BN03L		16-20	45224	1722	239	711	2.55
	4BN06U	Canada Basin	0-2	36857	1745	238	802	2.66
	4BN06M		6-10	50991	1983	237	836	2.19
	4BN06L		26-30	35709	2330	391	1170	3.24
	4BN09U	Alpha Ridge	0-2	65282	2763	253	724	3.67
	4BN09M		6-10	45457	1507	207	614	1.47
	4BN09L		22-24	54201	2509	251	661	3.35
	4BN12U	Makarov Basin	0-4	34816	2150	319	829	4.23
	4BN12M		8-12	38878	2401	315	673	4.46

	4BN12L		36-38	35464	3003	587	1558	4.24
15 ℃	15BN03U		0-4	66023	2528	272	647	2.14
	15BN03M	Chukchi Plateau	8-12	54412	1369	179	587	0.93
	15BN03L		16-20	44293	1597	247	700	2.18
	15BN06U		0-2	82040	2812	247	748	3.00
	15BN06M	Canada Basin	6-10	115973	3031	224	628	2.35
	15BN06L		26-30	69534	5153	602	1522	4.00
	15BN09U		0-2	162190	3339	214	626	2.02
	15BN09M	Alpha Ridge	6-10	48740	3231	478	1803	3.24
	15BN09L		22-24	58217	3874	531	1501	3.73
	15BN12U		0-4	123498	3564	214	529	2.60
	15BN12M	Makarov Basin	8-12	207256	5079	261	847	2.78
	15BN12L		36-38	123324	3854	260	673	2.66
25 ℃	25BN03U		0-4	10194	1141	411	1978	2.64
	25BN03M	Chukchi Plateau	8-12	12372	1194	309	2255	2.54
	25BN03L		16-20	12677	1079	329	2054	2.26
	25BN06U		0-2	12561	1492	372	1338	3.14
	25BN06M	Canada Basin	6-10	11071	1184	440	1403	2.31
	25BN06L		26-30	10927	927	277	2829	2.39
	25BN09U		0-2	7047	1224	469	1408	4.49
	25BN09M	Alpha Ridge	6-10	8513	1087	396	2335	2.77
	25BN09L		22-24	10101	1321	327	1705	3.53
	25BN12U		0-4	9985	1458	379	2032	4.05
	25BN12M	Makarov Basin	8-12	9718	1328	389	1331	3.88
	25BN12L		36-38	12741	1810	459	2223	4.05

a: Sequences with similarities ≥ 97%; b: These diversity estimators were calculated using the normalized tags data, and the resampling tag number is 7,047.

Table S4 The most abundant bacteria[a, b] from the *in situ* sediments of the Arctic Ocean

Sediment

	sBN03U	sBN03M	sBN03L	sBN06U	sBN06M	sBN06L	sBN09U	sBN09M	sBN09L	sBN12U	sBN12M	sBN12L
Acinetobacter[c]	0.03	0.31	0.04	0.02	**1.33**	**2.42**	0.01	0.60	0.39	0.03	**1.55**	**1.62**
Bacillus	0.01	0.01	0.02	0.01	0.34	0.21	0.01	0.32	0.05	0.01	0.47	**2.66**
Caldithrix	**1.12**	0.18	**4.58**	0.86	0.41	0.13	0.82	0.14	0.68	0.87	0.18	0.33
Colwellia	0.13	0.09	0.21	0.34	0.09	0.04	**1.94**	0.17	**1.63**	0.16	0.14	0.18
Corynebacterium	0.02	0.09	0.03	0.01	0.09	0.15	0.01	0.23	0.33	0.00	0.16	**1.12**
Dietzia	0.09	**1.65**	0.62	0.13	**5.38**	**6.66**	0.07	**3.04**	**1.97**	0.08	**7.82**	**3.41**
Gemmatimonas	**2.66**	**1.70**	**1.05**	**5.34**	**5.25**	**3.12**	**3.09**	**4.76**	**4.67**	**3.93**	**6.80**	**1.82**
Gp10	**1.60**	0.31	0.59	**1.00**	0.18	0.06	**1.11**	0.20	0.73	0.51	0.20	0.19
Gp22	**1.92**	0.23	0.15	**1.62**	0.25	0.01	**2.08**	0.40	0.41	**1.16**	0.01	0.25
Gp6	**1.38**	**7.10**	**2.74**	0.91	0.67	**1.07**	**1.40**	0.33	**1.05**	0.76	0.09	0.62
Halomonas	0.06	0.11	0.11	0.05	0.37	**1.00**	0.06	0.28	0.14	0.05	0.42	**1.39**
Marinomonas	0.03	0.19	0.20	0.04	0.45	0.31	0.05	0.36	0.14	0.03	0.41	**2.34**
Nitrospina	**1.91**	**1.92**	**2.02**	**1.20**	0.39	0.04	**1.33**	0.77	0.44	**1.38**	**1.20**	0.37
Nitrospira	**1.69**	0.07	0.28	**1.54**	0.75	0.75	**1.94**	**1.06**	0.91	**1.70**	0.17	0.45
Opitutus	**1.06**	0.14	0.13	0.62	0.01	0.01	0.91	0.12	0.29	0.53	0.01	0.33
Propionibacterium	0.00	0.14	0.02	0.01	0.50	0.89	0.00	0.51	0.23	0.01	0.78	**2.87**
Pseudoalteromonas	0.18	0.40	0.29	0.23	0.81	0.29	0.27	0.51	0.51	0.11	0.71	**1.56**
Pseudomonas	0.24	0.68	0.53	0.26	**1.56**	**1.52**	0.25	0.80	0.60	0.17	0.89	**1.83**
Rhodovibrio	0.08	**1.57**	0.55	0.12	0.20	0.16	0.33	0.46	0.37	0.17	0.09	0.01
Salinibacter	**1.23**	0.05	0.07	0.41	0.00	0.01	0.48	0.00	0.26	0.46	0.00	0.16
Salinisphaera	0.06	0.78	0.09	0.07	**1.80**	**1.34**	0.06	0.78	0.59	0.05	**2.05**	**4.02**
Shewanella	0.26	0.18	0.10	0.20	0.67	**2.22**	0.35	0.28	0.41	0.14	0.37	**2.82**
Staphylococcus	0.00	**1.02**	0.09	0.01	0.49	0.70	0.00	0.79	0.23	0.01	0.50	**3.23**

Cycloclasticus	0.36	0.23	0.34	0.17	0.26	0.39	0.28	0.41	0.40	0.21	0.39	0.53
Alcanivorax	0.18	0.41	0.38	0.19	0.41	0.31	0.19	0.27	0.27	0.20	0.43	0.49
Others [d]	7.67	5.42	5.75	7.17	7.64	10.02	8.58	7.14	6.94	6.55	10.05	18.30
Unclassified	76.57	75.67	79.75	77.86	70.36	66.87	74.85	75.96	76.02	81.16	64.96	48.12

a: Relative abundance (%) was calculated using the total tag numbers for each sample;

b: The numbers in bold indicate that the abundance of that bacterium occupied more than 1% of the total tags in that consortium; red bold indicated that that bacterium was the most abundant group in that consortium;

c: The bacteria in bold indicate they were previously described oil hydrocarbon-degraders;

d: “Others” refer to the bacteria constituting less than 1% of the total tags of a consortium for all consortia.

Table S5 The most abundant bacteria from the enriched consortia in the Arctic Ocean

4 ℃ consortia

	4BN03U	4BN03M	4BN03L	4BN06U	4BN06M	4BN06L	4BN09U	4BN09M	4BN09L	4BN12U	4BN12M	4BN12L
Alcanivorax	0.43	0.41	0.21	0.37	0.61	0.73	0.33	0.20	0.21	**2.15**	0.57	**6.33**
Alteromonas	0.05	0.06	0.09	0.05	0.06	0.08	0.02	0.03	0.10	0.60	0.36	**1.39**
Arcobacter	0.00	0.00	0.00	0.00	0.01	0.02	0.00	0.00	0.00	**1.43**	**4.78**	0.03
Colwellia	0.79	0.05	0.05	0.09	0.10	0.12	**2.03**	7.92	**7.69**	**1.24**	0.32	0.19
Cycloclasticus	0.35	0.57	0.96	0.33	0.47	0.90	0.23	0.31	0.44	27.04	**13.71**	**1.35**
Dietzia	**1.05**	0.03	0.03	0.05	0.05	0.08	0.05	0.05	0.04	0.04	0.04	0.11
Enterovibrio	0.00	0.00	0.00	0.00	0.00	0.01	0.01	0.00	0.00	0.93	**2.83**	0.03
Hahella	0.48	0.38	0.19	0.32	64.96	0.39	0.22	0.09	0.56	0.20	0.23	0.26
Halomonas	0.12	0.15	0.09	0.62	**4.22**	**2.79**	0.11	0.07	0.11	0.12	0.12	0.45
Hyphomonas	0.03	0.02	0.03	**9.01**	0.08	0.06	0.06	0.03	36.26	**2.16**	**1.29**	0.40
Lutibacter	0.00	0.00	0.00	0.00	0.00	0.02	0.32	0.00	0.00	**1.00**	0.83	0.00
Marinobacter	**3.87**	0.33	0.11	**8.33**	**1.82**	0.27	**5.22**	0.05	**23.31**	**2.44**	**5.76**	**2.24**
Marinomonas	0.06	0.04	0.10	0.05	0.14	0.28	30.26	0.15	0.13	**14.72**	19.92	41.23
Methylophaga	0.06	0.02	0.01	0.01	0.03	0.03	0.14	0.01	0.07	0.99	**1.25**	0.06
Oceanobacter	0.00	0.00	0.01	0.01	0.01	0.01	0.00	0.02	0.00	0.03	0.05	**18.53**
Oleispira	0.01	0.01	0.01	0.01	0.01	0.05	0.19	0.01	0.02	**4.22**	**7.18**	0.91
Pseudoalteromonas	**2.79**	**6.46**	71.01	**5.43**	**4.91**	73.03	0.47	0.19	**14.71**	0.77	0.50	**9.44**
Pseudomonas	30.64	70.25	0.31	62.56	**19.06**	0.80	**29.16**	0.18	0.68	**16.93**	**17.32**	**1.99**
Roseovarius	0.31	0.03	0.02	0.15	0.06	0.10	0.09	0.05	0.09	**1.69**	0.46	0.52
Saccharophagus	**9.62**	**2.90**	0.03	**1.63**	0.05	0.04	0.02	0.02	0.04	0.01	0.01	0.11
Salinisphaera	0.11	0.08	0.04	0.10	0.18	**12.29**	0.06	0.05	0.06	0.05	0.08	0.40
Shewanella	0.04	0.05	0.11	0.06	0.11	0.22	**4.27**	0.06	0.28	0.64	0.61	**1.05**
Sphingopyxis	0.47	0.00	0.00	0.02	0.00	0.01	0.30	0.00	0.01	**2.27**	0.12	0.02

Terasakiella	0.00	0.00	0.00	0.00	0.00	0.01	0.42	0.00	**1.34**	0.01	0.45	0.02
Thalassospira	0.02	0.02	0.04	0.02	0.03	0.07	0.02	0.04	0.06	0.14	**1.30**	0.12
Vibrio	0.00	0.00	0.00	0.10	0.02	**1.84**	0.05	0.00	**2.90**	0.10	0.19	0.08
Others	2.28	1.49	0.72	1.55	0.87	1.67	2.03	1.30	1.65	2.50	2.57	3.83
Unclassified	46.42	16.64	25.84	9.13	2.16	4.07	23.93	89.21	9.27	15.56	17.14	8.91

15 ℃ consortia

	15BN03U	15BN03M	15BN03L	15BN06U	15BN06M	15BN06L	15BN09U	15BN09M	15BN09L	15BN12U	15BN12M	15BN12L
Acinetobacter	0.26	0.03	0.05	0.04	0.03	0.16	0.05	**24.34**	0.48	0.03	0.03	0.04
Alcanivorax	0.35	0.20	0.36	0.29	0.59	0.24	0.54	0.94	**2.24**	0.48	0.62	0.48
Bordetella	0.00	0.00	0.01	0.00	0.01	**16.79**	0.00	0.00	0.02	0.01	0.00	0.01
Cobetia	0.00	0.01	0.00	0.00	0.01	0.09	0.01	0.00	0.01	0.03	0.02	**2.00**
Colwellia	0.08	0.03	0.05	0.05	0.04	0.08	0.04	**50.79**	**3.55**	**2.29**	0.04	0.04
Cycloclasticus	0.63	0.70	0.86	0.60	0.48	0.47	0.21	0.37	0.83	**64.52**	**55.12**	**61.63**
Dietzia	**11.25**	0.06	0.06	0.05	0.04	0.06	0.06	0.05	0.14	0.03	0.04	0.04
Hahella	0.31	0.53	0.19	0.81	**7.78**	0.26	0.44	0.36	**1.06**	0.22	0.21	0.27
Halomonas	0.09	0.19	0.16	**12.42**	**39.28**	**2.31**	0.07	**4.40**	**14.60**	0.24	0.16	0.18
Hyphomonas	0.03	0.05	0.05	**2.32**	0.01	0.04	0.03	0.03	0.13	0.04	0.19	0.12
Marinobacter	**2.24**	0.29	0.17	**8.85**	0.59	0.24	**23.26**	0.23	**5.04**	**1.05**	**2.53**	**4.58**
Marinobacterium	0.00	0.01	0.00	0.00	0.00	**2.53**	0.00	0.73	0.03	0.00	0.04	0.00
Methylophaga	0.01	0.00	0.01	0.01	0.02	0.01	0.02	0.02	0.02	**1.41**	**1.83**	**2.75**
Microbacterium	0.00	0.00	0.00	0.00	0.00	0.15	0.00	0.99	0.03	0.00	0.00	0.00
Pseudoalteromonas	**74.33**	**93.02**	**94.75**	**59.68**	**4.17**	0.86	0.37	0.58	**3.98**	**2.47**	**13.96**	**4.54**
Pseudomonas	**1.81**	**1.73**	0.49	**10.60**	**44.78**	0.49	**65.38**	**1.07**	**2.01**	**4.79**	**4.49**	**15.86**
Rhizobium	0.00	0.00	0.00	**1.03**	0.00	0.00	0.00	0.01	0.01	0.00	0.00	0.00
Roseovarius	0.03	0.06	0.05	0.09	0.03	0.58	0.07	0.25	0.36	0.75	0.14	**2.71**
Salinisphaera	0.05	0.08	0.06	0.08	0.08	**10.65**	0.10	**2.26**	**52.57**	0.07	0.06	0.06

Shewanella	0.13	0.14	0.14	0.24	0.07	**44.49**	**6.32**	0.09	0.36	0.10	0.15	0.27
Sphingobium	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	**1.01**
Thalassospira	0.03	0.02	0.02	0.02	0.03	0.06	0.02	0.05	0.07	**9.65**	0.80	0.04
Vibrio	0.00	0.01	0.01	0.02	0.00	**1.22**	0.01	0.00	0.03	0.00	0.00	0.00
Others	3.18	1.12	0.86	1.23	0.75	6.61	1.26	4.03	5.87	1.52	0.95	1.53
Unclassified	5.21	1.73	1.67	1.58	1.22	11.65	1.77	8.40	6.56	10.32	18.61	1.86

25 ℃ consortia

	25BN03U	**25BN03M**	**25BN03L**	**25BN06U**	**25BN06M**	**25BN06L**	**25BN09U**	**25BN09M**	**25BN09L**	**25BN12U**	**25BN12M**	**25BN12L**
Acinetobacter	0.53	0.00	0.06	0.01	0.08	0.01	**4.06**	0.23	0.07	0.01	0.05	0.11
Alcanivorax	0.26	0.02	0.02	0.01	0.03	0.00	0.23	0.06	0.02	**11.36**	**3.04**	**15.35**
Alteromonas	0.01	0.03	0.02	0.01	0.00	0.01	0.47	0.00	0.01	**1.70**	**1.85**	**1.38**
Aurantimonas	0.00	0.00	0.00	0.00	0.00	0.00	0.04	**7.47**	0.01	0.00	0.00	0.10
Bacillus	0.07	0.01	0.01	**6.70**	0.01	0.00	**4.17**	0.11	0.02	0.03	0.02	0.02
Colwellia	0.26	0.36	0.00	0.00	0.00	0.00	**4.31**	0.09	**25.54**	0.31	0.01	0.00
Cycloclasticus	0.78	0.04	0.00	0.02	0.02	0.01	**9.10**	0.12	0.06	**29.32**	**46.03**	**30.50**
Dietzia	**5.69**	0.01	0.00	0.02	0.00	0.02	0.06	0.01	0.00	0.00	0.00	0.00
Enterovibrio	0.02	0.01	0.01	0.00	0.00	0.00	0.00	0.01	0.00	**1.15**	**2.28**	0.00
Hahella	0.18	**4.90**	0.10	**6.96**	**21.04**	**30.20**	0.28	**19.09**	**9.87**	0.01	0.05	0.11
Halomonas	0.59	**59.23**	**55.59**	**51.98**	**71.03**	**33.39**	0.53	**10.24**	**9.05**	0.02	0.03	0.24
Hyphomonas	0.01	0.01	0.00	**1.18**	0.00	0.00	0.04	0.01	0.27	0.18	0.05	0.13
Marinobacter	0.21	0.06	0.02	0.18	**1.82**	0.81	0.98	0.28	0.11	**1.10**	**5.91**	**6.71**
Marinomonas	0.01	**8.12**	0.00	0.00	0.00	0.00	**41.63**	0.01	0.00	**4.65**	**3.24**	**9.67**
Methylophaga	0.02	0.03	0.00	0.00	0.02	0.00	0.79	0.04	0.05	0.70	**1.45**	0.10
Oceanobacter	0.00	0.15	0.22	0.14	0.23	0.14	0.00	0.05	0.03	0.00	0.00	**1.37**
Olleya	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	**1.80**	**1.32**	0.01
Pseudoalteromonas	**79.65**	**18.57**	**7.60**	**16.93**	**1.32**	**2.98**	**1.04**	**3.01**	**6.65**	0.60	0.91	**5.64**

Pseudomonas	**3.55**	**5.31**	**32.33**	**7.39**	**3.03**	**31.55**	**4.54**	**54.12**	0.26	**21.55**	**6.52**	**4.09**
Rhizobium	0.00	0.00	0.00	**2.37**	0.02	0.00	0.00	0.02	0.00	0.00	0.00	0.00
Roseovarius	0.34	0.02	**1.59**	0.72	0.01	0.01	0.23	0.01	**30.23**	**3.66**	**3.68**	**14.61**
Shewanella	0.59	0.23	0.28	**1.68**	0.32	0.30	**7.44**	0.99	**1.43**	**6.14**	**3.31**	0.35
Sulfitobacter	0.67	0.00	0.00	0.01	0.00	0.00	**1.42**	0.01	0.00	0.03	0.00	**2.36**
Terasakiella	0.00	0.00	0.00	0.00	0.00	0.00	**1.06**	0.00	0.00	0.14	0.09	0.00
Thalassospira	0.34	0.01	0.11	0.00	0.06	0.07	0.23	0.85	0.01	**5.55**	**11.16**	0.00
Vibrio	0.03	0.00	0.01	0.06	0.00	0.03	0.04	0.00	**13.15**	0.03	0.02	0.05
Others	4.31	1.97	1.36	2.54	0.60	0.27	5.36	1.99	1.41	4.49	3.16	2.19
Unclassified	1.88	0.92	0.69	1.12	0.36	0.22	11.95	1.19	1.76	5.47	5.80	4.91

a: Relative abundance (%) was calculated using the total tag numbers for each sample;

b: The numbers in bold indicate that the abundance of that bacterium occupied more than 1% of the total tags in that consortium; red bold indicated that that bacterium was the most abundant group in that consortium;

c: “Others” refer to the bacteria constituting less than 1% of the total tags of a consortium for all consortia.

Table S6 DGGE-band information of 12 PAH-degrading consortia that were enriched at 25 ℃ from the Arctic Ocean

DGGE-Band	Accession No.	Closest strains in GenBank	Similarities % (Diff/Total nt)
25BN03U-1	KC581837	*Pseudoalteromonas undina* NCIMB 2128^{T} (X82140)	98.469 (3/196)
25BN03U-2	KC581838	*Pseudoalteromonas arctica* A 37-1-2^{T} (DQ787199)	98.98 (2/196)
25BN03U-3	KC581839	*Pseudoalteromonas translucida* KMM 520^{T} (AY040230)	96.939 (6/196)
25BN03U-4	KC581840	*Halomonas axialensis* Althf1^{T} (AF212206)	98.469 (5/196)
25BN03M-1	KC581830	*Pseudomonas sabulinigri* J64^{T} (EU143352)	96.939 (6/196)
25BN03M-2	KC581831	*Marinobacter vinifirmus* FB1^{T} (DQ235263)	98.98 (2/196)
25BN03M-3	KC581832	*Halomonas axialensis* Althf1^{T} (AF212206)	98.469 (3/196)
25BN03M-4	KC581833	*Halomonas axialensis* Althf1^{T} (AF212206)	98.469 (3/196)
25BN03M-5	KC581834	*Pseudoalteromonas translucida* KMM 520^{T} (AY040230)	96.939 (6/196)
25BN03M-6	KC581835	*Halomonas axialensis* Althf1^{T} (AF212206)	98.469 (3/196)
25BN03M-7	KC581836	*Halomonas axialensis* Althf1^{T} (AF212206)	98.469 (3/196)
25BN03L-1	KC581825	*Pseudomonas pelagia* CL-AP6^{T} (EU888911)	98.98 (2/196)
25BN03L-2	KC581826	*Pseudomonas pelagia* CL-AP6^{T} (EU888911)	97.449 (8/196)
25BN03L-3	KC581827	*Pseudoalteromonas undina* NCIMB2128^{T} (X82140)	98.98 (2/196)
25BN03L-4	KC581828	*Halomonas axialensis* Althf1^{T} (AF212206)	97.449 (5/196)
25BN03L-5	KC581829	*Halomonas axialensis* Althf1^{T} (AF212206)	97.449 (5/196)
25BN06U-1	KC581847	*Pseudomonas pelagia* CL-AP6^{T} (EU888911)	98.98 (2/196)
25BN06U-2	KC581848	*Pseudoalteromonas undina* NCIMB2128^{T} (X82140)	98.98 (2/196)
25BN06U-3	KC581849	*Pseudoalteromonas arctica* A 37-1-2 ^{T} (DQ787199)	98.98 (2/196)
25BN06U-4	KC581850	*Halomonas axialensis* Althf1^{T} (AF212206)	98.469 (3/196)
25BN06U-5	KC581851	*Halomonas axialensis* Althf1^{T} (AF212206)	98.98 (2/196)
25BN06M-1	KC581844	*Pseudoalteromonas ulvae* UL12^{T} (AF172987)	96.923 (6/195)
25BN06M-2	KC581845	*Halomonas axialensis* Althf1^{T} (AF212206)	98.469 (4/196)

25BN06M-3	KC581846	*Halomonas axialensis* Althf1^{T} (AF212206)	98.469 (3/196)
25BN06L-1	KC581841	*Pseudomonas sabulinigri* J64^{T} (EU143352)	96.939 (10/196)
25BN06L-2	KC581842	*Marinobacter vinifirmus* FB1^{T} (DQ235263)	98.98 (2/196)
25BN06L-3	KC581843	*Halomonas axialensis* Althf1^{T} (AF212206)	97.449 (5/196)
25BN09U-1	KC581862	*Cycloclasticus pugetii* PS-1^{T} (U12624)	98.98 (2/196)
25BN09U-2	KC581863	*Alcanivorax borkumensis* SK2^{T} (AM286690)	97.959 (2/196)
25BN09U-3	KC581864	*Halomonas meridiana* DSM 5425^{T} (AJ306891)	98.469 (5/171)
25BN09U-4	KC581865	*Pseudomonas sabulinigri* J64^{T} (EU143352)	96.429 (7/196)
25BN09U-5	KC581866	*Thalassospira tepidiphila* 1-1B^{T} (AB265822)	98.83 (2/171)
25BN09M-1	KC581857	*Pseudomonas sabulinigri* J64^{T} (EU143352)	96.939 (6/196)
25BN09M-2	KC581858	*Marinobacter vinifirmus* FB1^{T} (DQ235263)	98.469 (3/196)
25BN09M-3	KC581859	*Thalassospira tepidiphila* 1-1B^{T} (AB265822)	97.076 (7/171)
25BN09M-4	KC581860	*Halomonas axialensis* Althf1^{T} (AF212206)	97.959 (4/196)
25BN09M-5	KC581861	*Halomonas axialensis* Althf1^{T} (AF212206)	98.98 (2/196)
25BN09L-1	KC581852	*Alcanivorax borkumensis* SK2^{T} (AM286690)	98.469 (3/196)
25BN09L-2	KC581853	*Vibrio splendidus* ATCC 33125^{T} (X74724)	98.98 (2/196)
25BN09L-3	KC581854	*Marinobacter vinifirmus* FB1^{T} (DQ235263)	98.98 (2/196)
25BN09L-4	KC581855	*Colwellia polaris* 537^{T} (DQ007434)	98.462 (3/195)
25BN09L-5	KC581856	*Celeribacter baekdonensis* L-6^{T} (HM997022)	98.83 (2/171)
25BN12U-1	KC581877	*Cycloclasticus pugetii* PS-1^{T} (U12624)	98.98 (2/196)
25BN12U-2	KC581878	*Alcanivorax borkumensis* SK2^{T} (AM286690)	98.469 (3/196)
25BN12U-3	KC581879	*Pseudomonas pelagia* CL-AP6^{T} (EU888911)	98.98 (2/196)
25BN12U-4	KC581880	*Thalassospira tepidiphila* 1-1B^{T} (AB265822)	98.83 (2/171)
25BN12U-5	KC581881	*Marinobacterium georgiense* KW-40^{T} (U58339)	98.969 (2/194)
25BN12M-1	KC581872	*Cycloclasticus pugetii* PS-1^{T} (U12624)	98.98 (2/196)
25BN12M-2	KC581873	*Pseudomonas pelagia* CL-AP6^{T} (EU888911)	98.469 (3/196)

25BN12M-3	KC581874	*Marinobacter guineae* M3B^{T} (AM503093)	98.98 (2/196)
25BN12M-4	KC581875	*Thalassospira tepidiphila* 1-1B^{T} (AB265822)	98.83 (2/196)
25BN12M-5	KC581876	*Marinobacterium georgiense* KW-40^{T} (U58339)	98.969 (2/194)
25BN12L-1	KC581867	*Cycloclasticus pugetii* PS-1^{T} (U12624)	97.959 (2/196)
25BN12L-2	KC581868	*Alcanivorax borkumensis* SK2^{T} (AM286690)	98.98 (2/196)
25BN12L-3	KC581869	*Cycloclasticus pugetii* PS-1^{T} (U12624)	98.469 (3/196)
25BN12L-4	KC581870	*Marinobacter flavimaris* SW-145^{T} (AY517632)	98.98 (2/196)
25BN12L-5	KC581871	*Celeribacter baekdonensis* L-6^{T} (HM997022)	98.83 (2/171)

Supplemental Figures

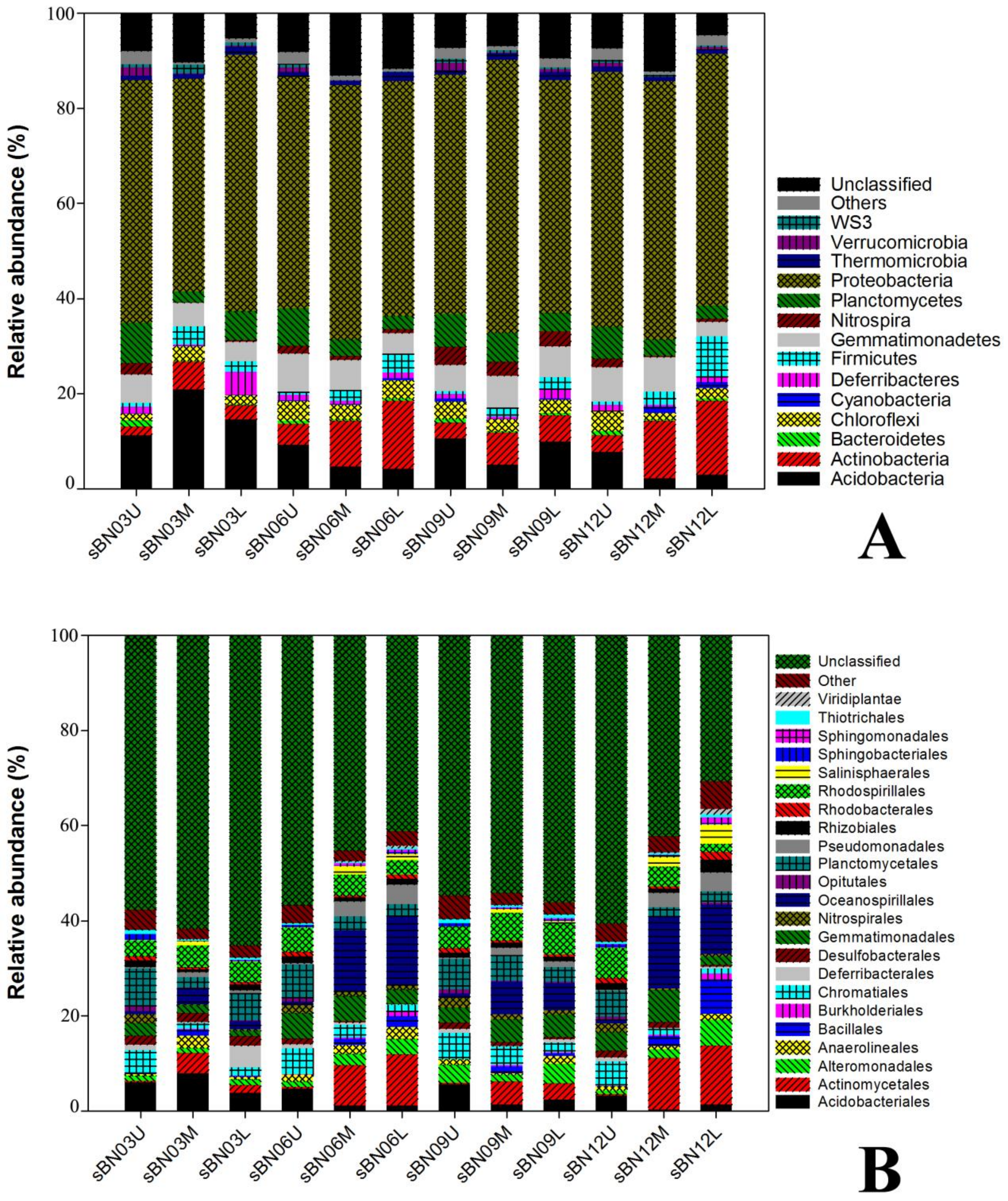


Fig. S1. Relative abundances of bacteria at (A) phylum and (B) order levels in the *in situ* sediments from the Arctic Ocean. The most abundant phyla or orders (abundance more than 1% of the total tags at least in one sediment sample) in the sediment samples are listed in the legend of each plot. “Others” refer to the taxa constituting less than 1% of the total tags of a sample for all samples.

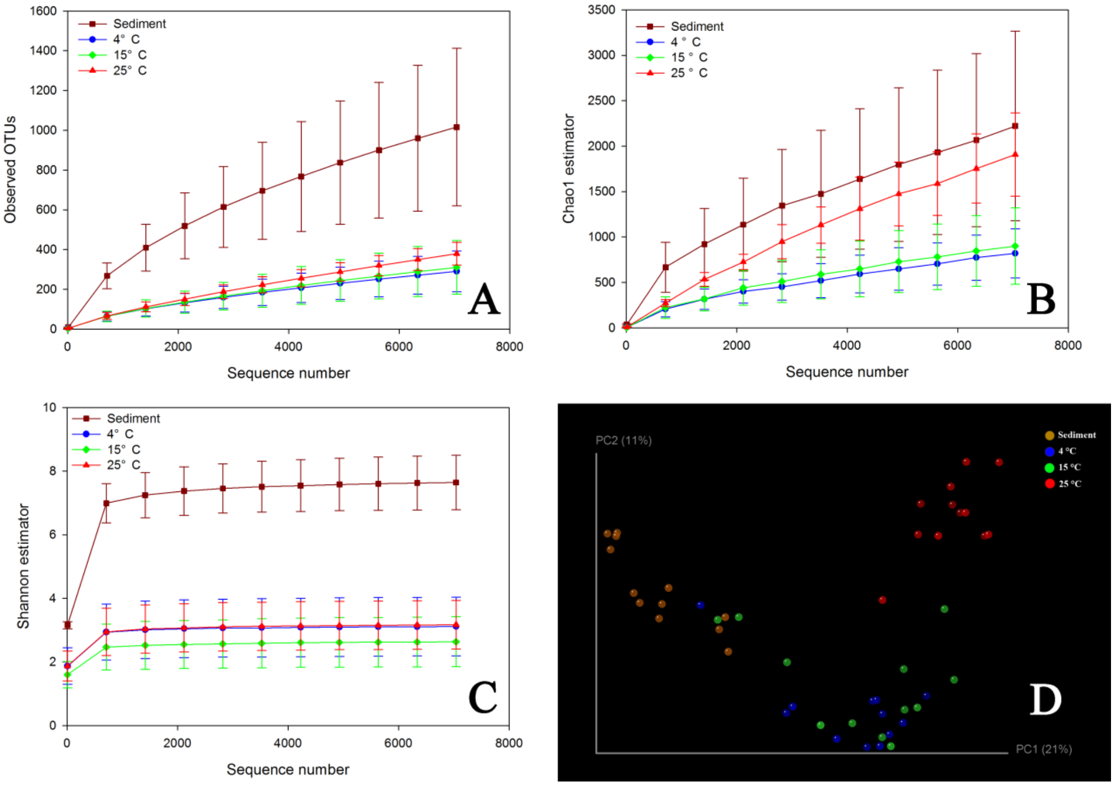


Fig. S2. Comparison of alpha and beta diversity. Rarefaction curves for the Observed OTUs (A), Chao1 (B), and Shannon (C) were calculated using Qiime v1.7 with tags that were normalized to 7,047 for each sample at 0.03 sequence similarity (n = 12). The principal coordinate analysis (D) based on the unweighted UniFrac distances of the bacterial OTUs dataset.

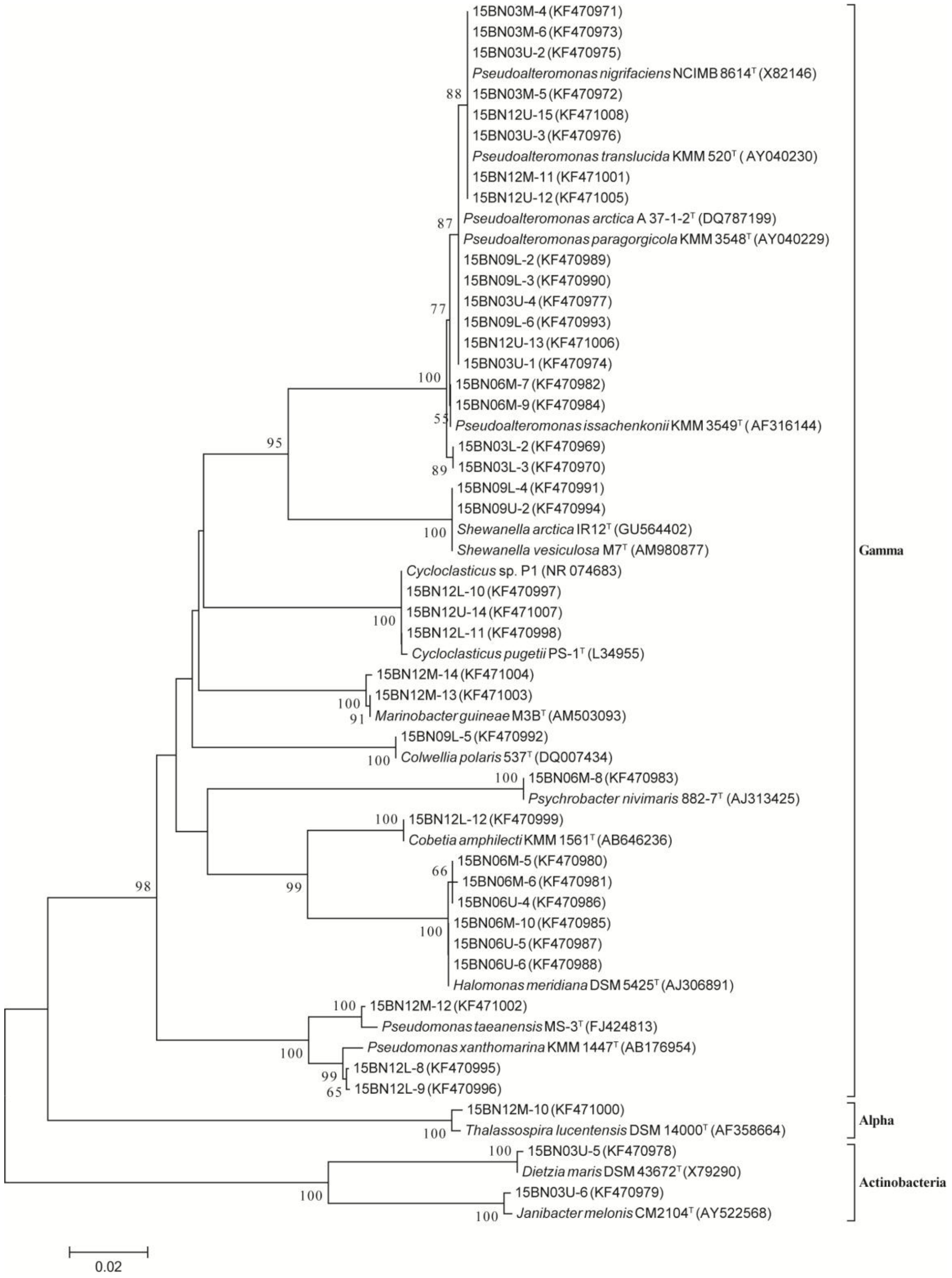
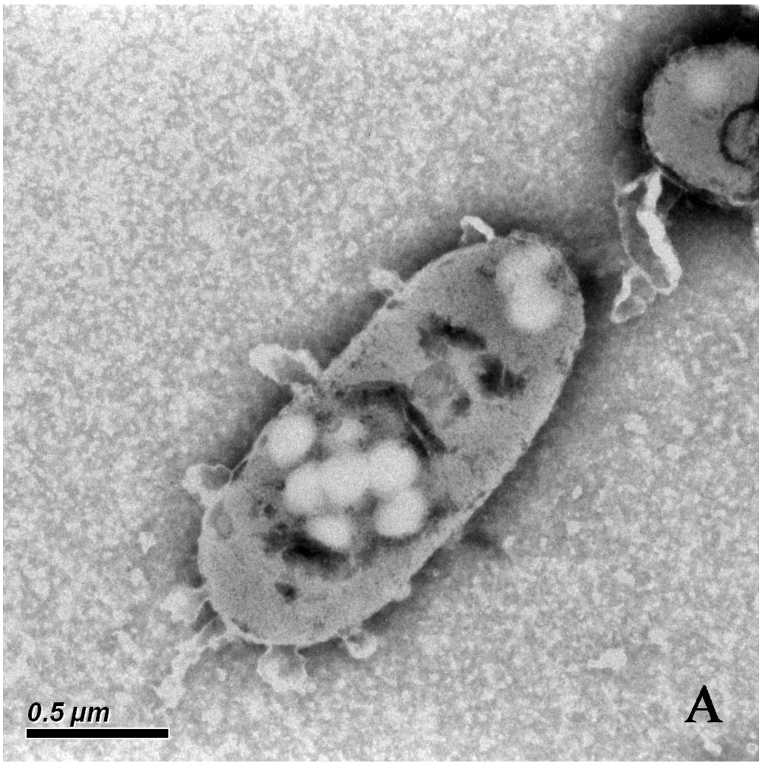
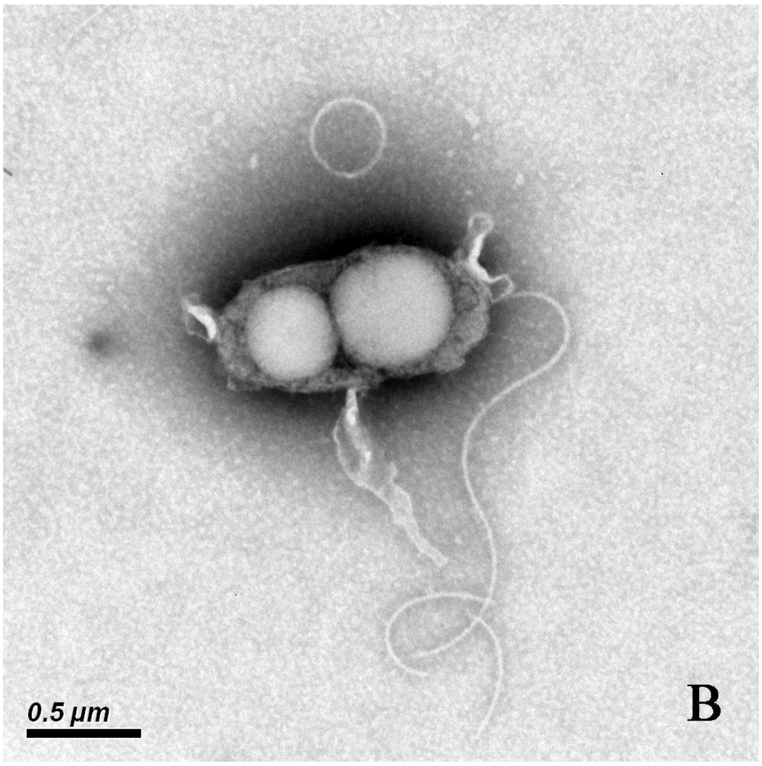


Fig. S3. Phylogenetic tree of the cultivable bacterial strains that were isolated from the PAH-degrading consortia enriched at 15 ℃. The tree was constructed using neighbor joining (NJ) and the Kimura two-parameter model, which is available in the MEGA 5.0 software, based on the partial 16S rRNA gene sequences of the cultivable bacterial strains in this study and their closest type strains. Only bootstrap values ≥ 50% (1,000 replicates) are shown at the nodes. GenBank accession numbers are shown in brackets. The scale bar represents 0.02 nucleotide changes per position.


0.5 µm
A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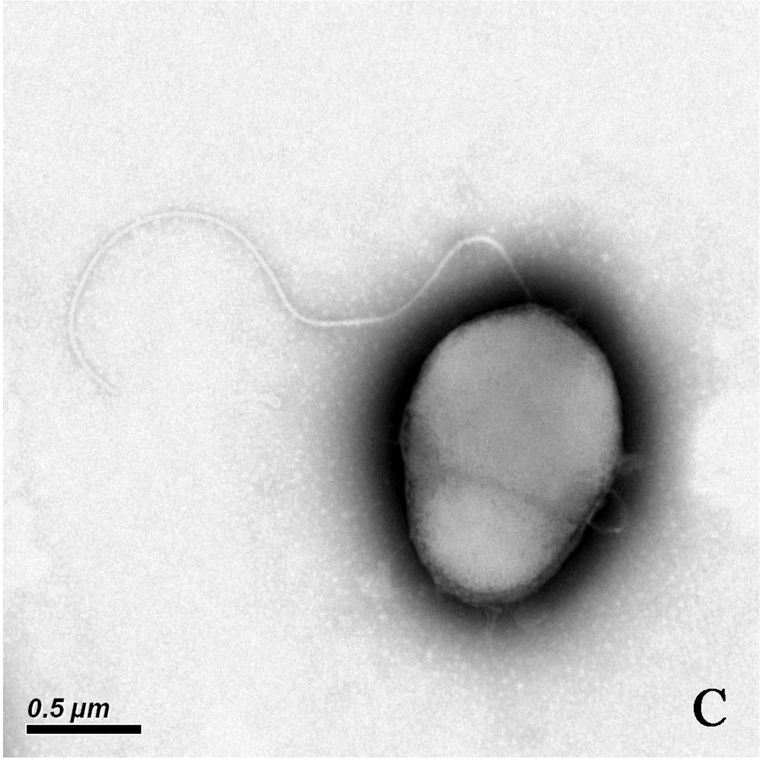

Fig. S4. Transmission electron micrographs of three *Cycloclasticus* isolates that were taken using a JEM-1230 (JEOL) at an operating voltage of 120 kV. A: *Cycloclasticus* sp. 15BN12U-14; B: *Cycloclasticus* sp. 15BN12L-10; **C:** *Cycloclasticus* sp. 15BN12L-11.

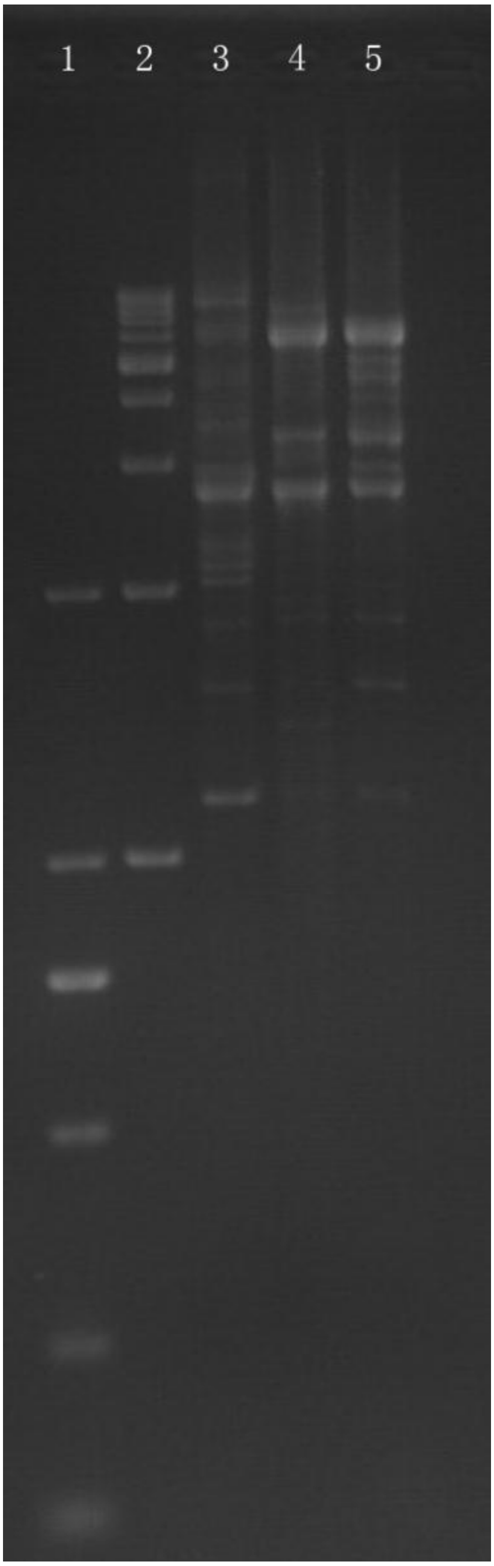

Fig. S5. Rep-PCR comparison of three *Cycloclasticus* isolates. Lane 1, DL2000 marker; lane 2, 100 bp DNA ladder; lane 3, *Cycloclasticus* sp. 15BN12U-14; lane 4, *Cycloclasticus* sp. 15BN12L-10; and lane 5, *Cycloclasticus* sp. 15BN12L-11.

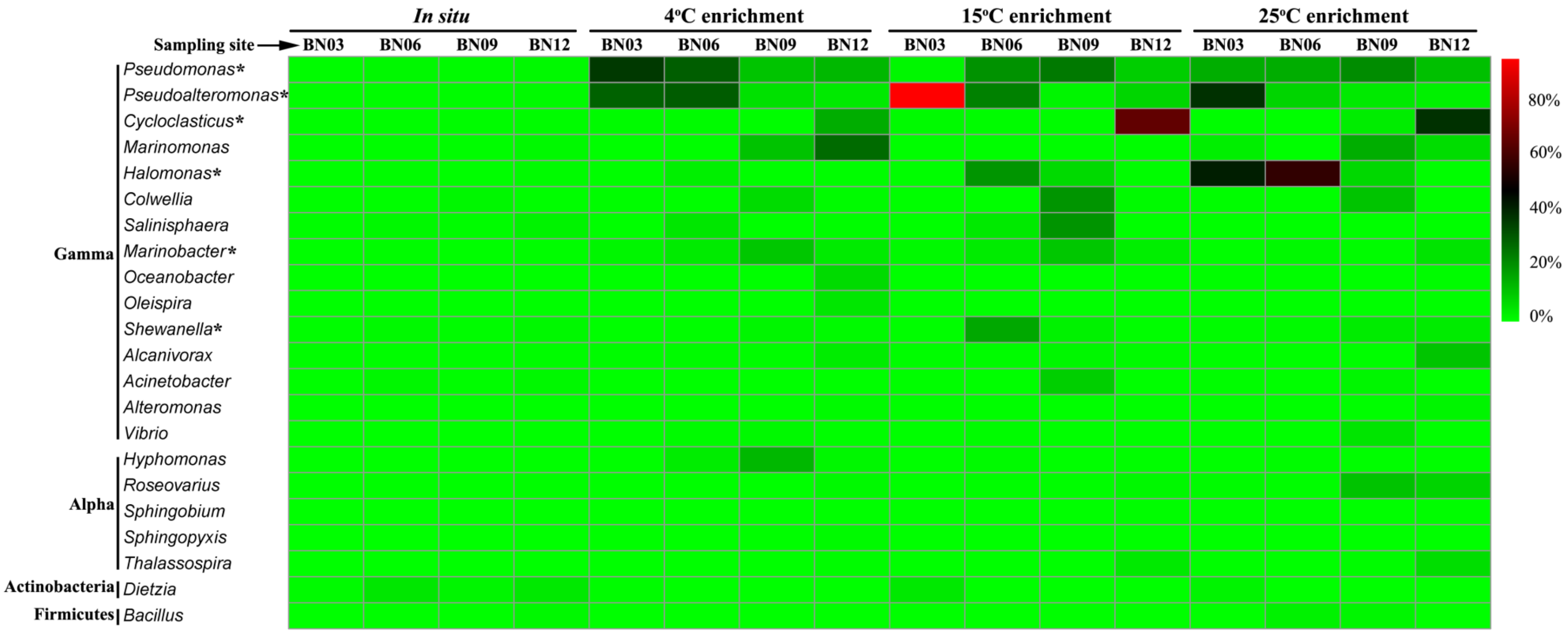

Fig. S6. Heatmap showing the shifts of the bacteria involved in PAH-degrading in the *in situ* sediment and enriched cultures. The abundance for each bacterium was calculated using the total tags of this bacterium retrieved from the three consortia of a same sampling site. The color code indicates relative abundances, ranging from green (low abundance) to black to red (high abundance). The genus marked with an asterisk indicates that a bacterium belonging to this genus has been isolated from the 15 ℃ enriched cultures.