

Supplementary Material

Biogeosciences

Identify the core bacterial microbiome of hydrocarbon degradation and a shift of dominant methanogenesis pathways in oil and aqueous phases of petroleum reservoirs with different temperatures from China

Zhichao Zhou¹, Bo Liang², Li-Ying Wang², Jin-Feng Liu², Bo-Zhong Mu², Hojae Shim³, and Ji-Dong Gu^{1,*}

¹ Laboratory of Environmental Microbiology and Toxicology, School of Biological Sciences, The University of Hong Kong, Pokfulam Road, Hong Kong SAR, Hong Kong, People's Republic of China

² State Key Laboratory of Bioreactor Engineering and Institute of Applied Chemistry, East China University of Science and Technology, Shanghai 200237, People's Republic of China

³ Faculty of Science and Technology, University of Macau, Macau, People's Republic of China

*Correspondence to: Ji-Dong Gu (jdgu@hku.hk)

1 Supplementary Data

1.1 Characterization of geographic properties of sampling reservoirs

Petroleum fluids samples were collected from eight sampling sites across China covering oilfields of different geological properties. The reservoir and crude oil properties together with the aqueous phase chemical concentration characteristics were listed in Table 1. P1 represents the sample collected from Zhan3-26 well located in Shengli Oilfield. Zhan3 block region in Shengli Oilfield is located in the coastal area from the Yellow River Estuary to the Bohai Sea. It is a medium-high temperature reservoir of fluvial face, made of a thin layer of crossed sand-mudstones, pebbled sandstones and fine sandstones. P2 represents the sample collected from Ba-51 well, which is located in Bayindulan reservoir layer of Erlian Basin, east Inner Mongolia Autonomous Region. It is a reservoir with highly heterogeneous layers, high crude oil viscosity and low formation fluid temperature. It was dedicated to water-flooding, however, due to low permeability and high viscosity of crude oil, displacement efficiency of water-flooding driving process was slowed down along the increase of water-cut rate. P3 and P4 represents samples which were collected from Liuzhong and Qixi blocks from Karamay Oilfield which located about 30 km to the east of Karamay City. Liuzhong reservoir is located in a piedmont diluvial fan deposit area mainly consisted of conglomerates and uneven gravel bearing sandstones, and is characterized as a reservoir of moderate porosity, high permeability, high crude oil viscosity and high heterogeneity. The reservoir region is distributed in a triangle fault block surrounded by Karamay-Wuerhe fracture belt and northern Baijiantan fracture belt. Qixi reservoir is located at footwall of Baijiantan fracture belt and is characterized as a heterogeneous conglomerate reservoir containing complex pore structures with low porosity and permeability. Both reservoirs from Karamay Oilfield were relatively low temperature reservoirs. P5 represents the sample collected from Wei5 block reservoir located in Gaoyou depression area of Subei Basin (Jiangsu Oilfield). It is a thin sand-mud interbed towards the front margin of a delta region, containing viscous crude oil. Due to its small volume, irregular reserve layers and relatively thin oil-bearing structure, it is difficult to further exploit using commonly applied methods. Many approaches have been carried out on this reservoir, such as cyclic steam stimulation, microorganism and water flood stimulation, etc. P6 represents the sample collected from Gao6 block reservoir located in the middle region of the western slope of Jinhu depression area of Subei Basin. This is a small and thin interbedded reservoir with moderate porosity, low permeability and high inter- and intralayer heterogeneity. P7 represents the sample collected from Xing4 block from Xingbei Oilfield, located in Daqing City. The main reservoir layer is made of lake sedimentary clastic rocks, composed of feldspars and quartz sandstones. The sandstones consist of over half fine sands, second by silty sands, and then medium fine sands. This reservoir is a reservoir comprised of multiple and thin layers, characterized with high porosity and low permeability property. P8 represents the sample collected from Qinying area located in Yangcun fault block. This sampling reservoir is from south part of Jinhu depression area of Subei Basin, and is a newly developed reservoir subjected to production test since 2012. P6 and P8 were both collected from Jinhu depression area from Jiangsu Oilfield and the *in situ* temperatures were higher than rest samples.

1.2 Reservoir geophysical properties and physicochemical properties

Reservoir geophysical properties and ion concentrations of aqueous phase samples were shown in Table 1. The physicochemical properties from P1-P4 aqueous phase samples were derived from the previous work (Wang et al. 2012). P1-P6 samples consist of aqueous and oil phases, while P7 only contains aqueous phase sample and P8 only contains oil phase. P3 and P4 are grouped into low temperature samples; P1, P2, P5 and P7 are grouped into moderate temperature samples; P6 and P8 are characterized as high temperature samples. Meanwhile, P1-P4 samples were pH neutral, P5-P8

samples were slightly alkaline. The reservoir general properties, including depth, temperature, pH, effective porosity, average permeability, and crude oil viscosity, were measured by local oilfield management agencies while sampling. All the reservoirs were operated by water flooding for years, aiming to enhance oil recovery efficiency, except for P8, located at Qinying block, Jiangsu Oilfield, a newly exploited site; so that no aqueous phase sample could be extracted from P8 oil-water fluids. Due to very less oil phase sample extracted from oil-water fluids from Xing4 block, Daqing (Xingbei) Oilfield, P7 sample also only contains aqueous phase. The effective porosity indicates percentage of effective interconnected pore space (excluding the porosity which could not benefit connections between pores) in the total volume of rocks, which could facilitate fluids flowing through rocks or sediments. It is an important parameter indicating pore property of reservoirs, reflecting the formation degree and connectivity of a certain reservoir. Average permeability is a measure of general ability of fluids flowing through reservoir layers to the oilwell. Oil viscosity reflects property and composition of crude oil. In general, crude oil with higher oil viscosity means higher content of asphaltenes and resins, and also higher content of long carbon chain hydrocarbons.

1.3 Diversity of microbial 16S rRNA gene through MiSeq sequencing

To obtain microbial composition structure from 14 aqueous and oil phase samples, we separately amplified prokaryotic and archaeal 16S rRNA gene from DNA samples. Although, archaeal 16S rRNA gene products could also be amplified from the prokaryotic 16S rRNA gene targeting primer pair, quantities of obtained sequences were limited and biased primers pairs could underestimate certain groups of archaea. Hence, in this study, we firstly sequenced the prokaryotic 16S rRNA gene, and then screened out the archaeal 16S rRNA gene and retained the bacterial 16S rRNA gene library. Finally, after subsampling to make all the library acquire even sequencing depth, each bacterial 16S rRNA gene library consisted of 6100 unique, dereplicated sequences, which through the analysis of QIIME pipeline could achieve good coverage (Good's coverage value within 89.6 to 94.1%). Nevertheless, it might be for the reason that low specificity of archaeal 16S rRNA gene primer pair introduced erroneous amplification of non-archaeal sequence and microbial composition was dominated by bacteria, archaeal 16S rRNA gene profile reflected that the majorities of libraries were not archaeal sequences. Consequently, screening out non-archaeal sequences from each library was also conducted, and after sub-sampling, each archaeal 16S rRNA gene library consisted of 760 unique, dereplicated sequences, which through the analysis of QIIME pipeline could achieve Good's coverage values ranging from 93.8 to 98.4% (Table S1). To analyze composition of methanogens, archaeal 16S rRNA gene libraries were further screened to obtain methanogenic libraries with sequencing depth of 240 for each library, and Good's coverage values ranging from 90.5 to 98.4%. Alpha diversity pattern of bacterial, archaeal, methanogenic 16S rRNA gene libraries were summarized into Table S1. From Good's coverage values and rarefaction curves of observed species which have been analyzed through QIIME pipeline for the individual library, it was observed that the majority (generally over 90%) of underlying species were estimated to be covered. According to the alpha diversity values from bacterial, archaeal and methanogenic libraries, bacterial communities had the largest average Chao1, Shannon and Simpson index value (2043, 5.8, 0.9) while archaeal communities had the second largest average Chao1 value (109.9), methanogenic communities had the smallest average Chao1 value (56.2). Archaeal communities had the same level of average Shannon and Simpson values as methanogenic communities (2.6, 0.6; 2.3, 0.6). Whereas, in terms of coefficient of variation of the above three indices (standard deviation over average value), the bacterial community acquired lower variation level of the three indices (2.4%, 13.5%, 5.3%), while, the archaeal and methanogenic communities acquired higher variation level of the three indices (51.5%, 38.1%, 33%; 65.9%, 43.3%, 40.5%). It is indicative that even though archaeal/methanogenic communities of 14 aqueous and oil samples show lower diverse patterns than bacterial communities, their intra-sample variations are larger than those of bacterial communities.

1.4 Taxonomic and compositional profiles of microbial 16S rRNA gene through MiSeq sequencing

The open-reference OTU picking method implemented in QIIME assures that all sequences are divided into genus level OTUs with the guidance of genus level reference sequences, thus offers an exhaustive OTU classification (Rideout et al. 2014). Average bacterial sequences unclassified into known genera could account for 31.91%; and average archaeal sequences unclassified into known genera could account for 9.59%, while the percentage of average methanogenic sequences unclassified into known genera was even as low as 0.38% (Table S2). Taxonomic compositional profiles of 14 aqueous and oil phase samples revealed that on the genus level, 931 bacterial genera and 56 archaeal genera were obtained among all the samples. There were 36 bacterial genera with average abundance percentage over 0.5% amongst all the bacterial communities, and there were 14 archaeal genera with the average abundance percentage over 0.5% amongst all the archaeal communities. The most abundant five genera among bacterial communities were *Pseudomonas* (16.12%), *Acinetobacter* (9.94%), uncultured genus within *Hydrogenophilaceae* (5.44%), *Proteiniphilum* (3.06%) and *Marinobacter* (2.91%). The most abundant five genera among archaeal communities were *Methanosaeta* (42.3%), *Methanothermobacter* (9.69%), *Methanlobus* (9.07%), *Methanocalculus* (8.05%) and *Methanoculleus* (5.01%) (Table S3).

1.5 Quantitation of *mcrA* gene abundance

Quantity units of *mcrA* gene abundance of aqueous and oil samples were gene copy numbers per microliter water sample and gene copy numbers per gram oil sample, respectively (Figure S1). The *mcrA* gene copies of all samples from this study varied substantially from 2.5×10^2 copies/g in P8O to 2.9×10^7 copies/g in P3O sample. The *mcrA* gene abundances in low temperature samples (P3 and P4) were the highest among all the samples in terms of both aqueous and oil phases, ranging from 2.8×10^5 to 4.3×10^5 copies/ml in aqueous phase, and 6.4×10^6 to 2.9×10^7 copies/g in oil phase. For moderate temperature samples (P1, P2, P5 and P7), the *mcrA* gene abundance among aqueous samples was ranging from 1.2×10^3 copies/ml in P5A to 3.3×10^5 copies/ml in P1A, while the highest *mcrA* gene abundance among oil samples was ranging from 1.7×10^3 copies/g in P5O to 1.1×10^6 copies/g in P1O. For high temperature samples (P6 and P8), the *mcrA* gene abundance of aqueous sample was 9.2×10^3 copies/ml in P6A, and the *mcrA* gene abundance of oil samples was ranging from 2.5×10^2 copies/g in P8O to 2.8×10^4 copies/g in P6O. Within aqueous and oil phases of one individual sample, the numerical value of *mcrA* gene copy number in oil phase was generally one to two orders of magnitude larger than that in aqueous phase.

2 Supplementary Figures and Tables

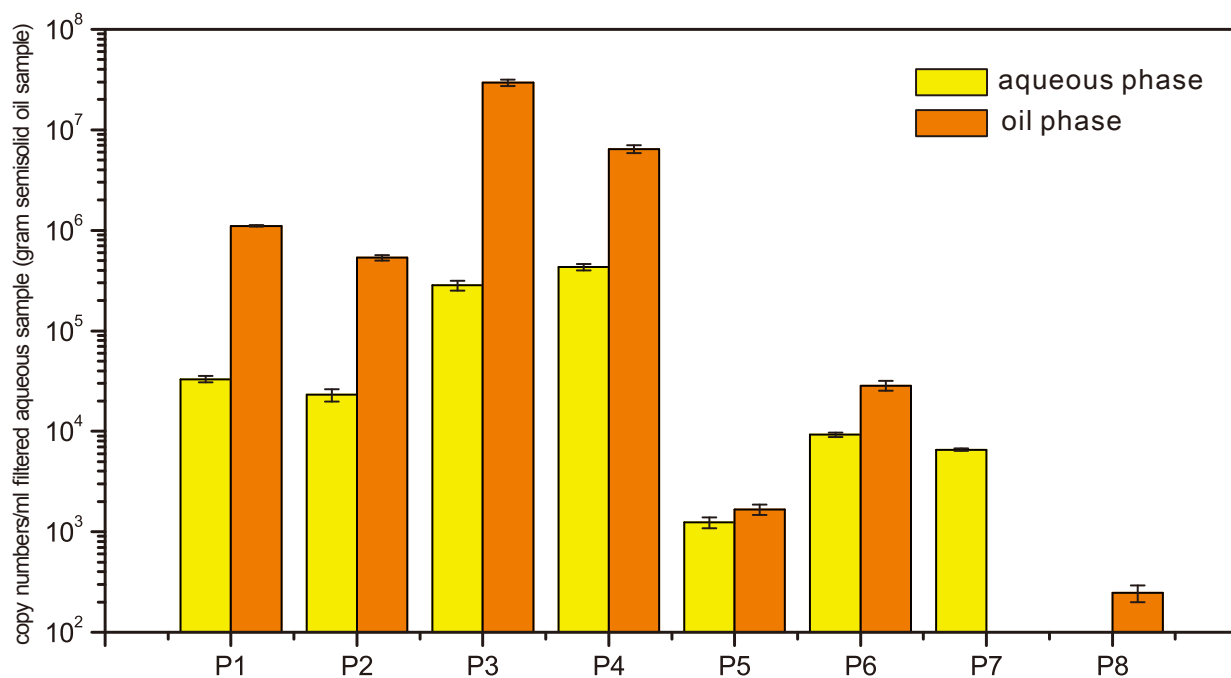
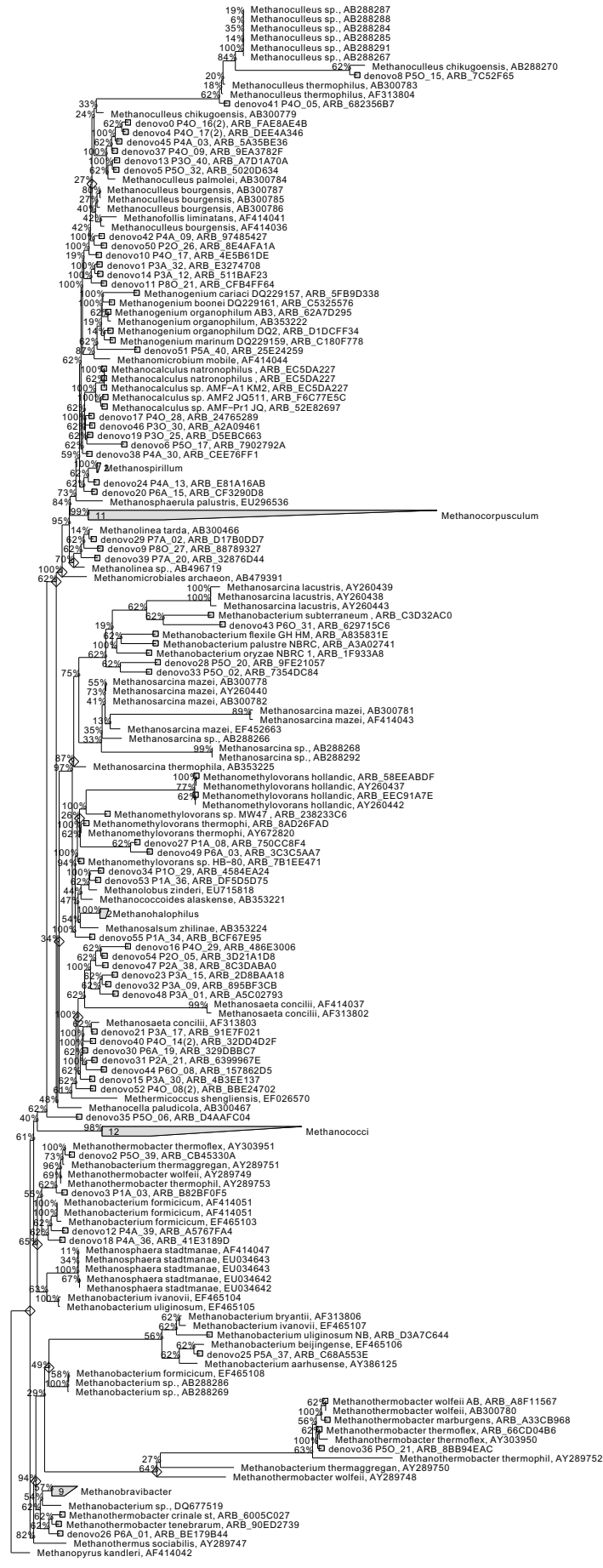


Figure S1. *mcrA* gene abundance of 14 aqueous and oil phase samples. Vertical coordinate was drawn in log-normalized label. The aqueous samples *mcrA* gene quantities were gene copy numbers/ml filtered aqueous sample; the oil samples *mcrA* gene quantities were gene copy numbers/gram semisolid oil sample.



Q-10

Figure S2. Phylogenetic tree based on clone library *mcrA* gene and reference gene sequences. The OTU representative *mcrA* gene clone sequences were obtained by 0.05 cutoff on nucleotide level, and then inserted into *mcrA* gene ARB database by maximum parsimony method without changing the initial tree topology. (*mcrA* gene ARB database: <http://www.mpi-marburg.mpg.de/downloads/conrad/>)

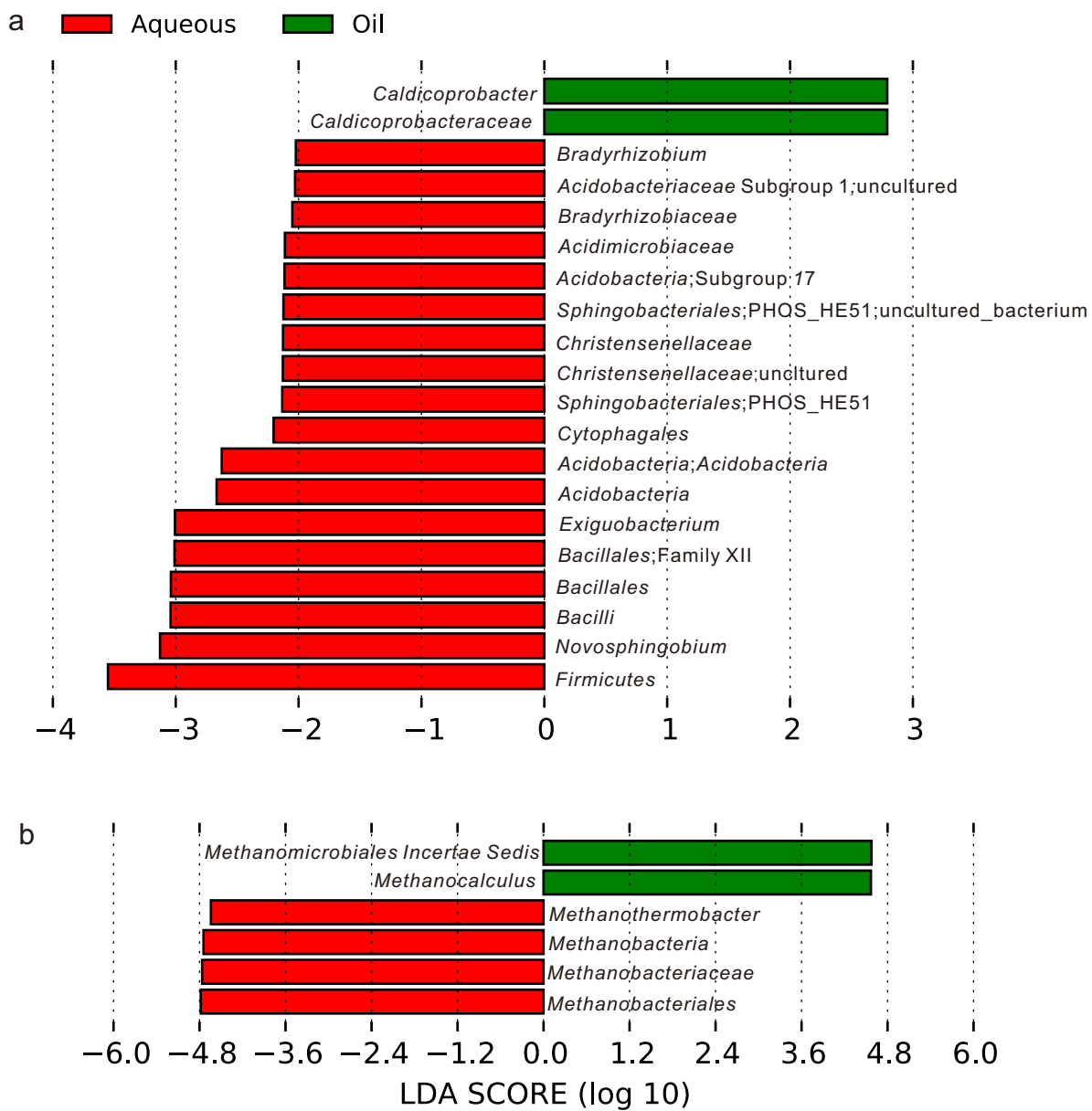


Figure S3. Differentially distributed features of microbial taxon abundance in aqueous and oil phases. LEfSe analysis with LDA effect score was applied. (a) bacterial community feature; (b) archaeal community feature.

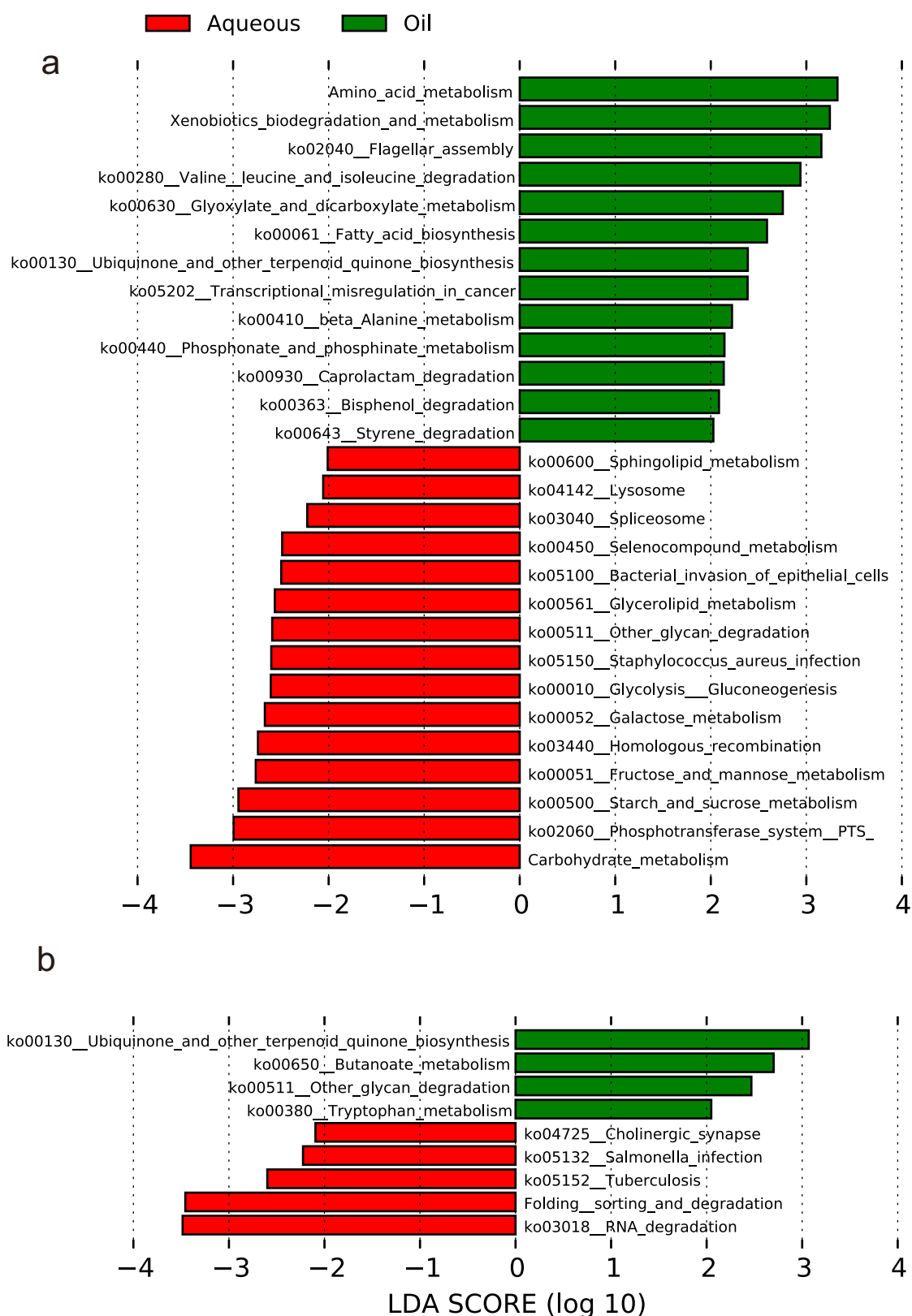


Figure S4. Differentially distributed feature of functional profiles in aqueous and oil phases. LefSe analysis results based on the predicted functional profiles by Tax4Fun. (a) bacterial community feature; (b) archaeal community feature.

Table S1. Alpha diversity values of aqueous and oil phase samples including bacterial, archaeal, methanogenic microorganism communities based on MiSeq archaeal 16S rRNA gene sequencing, methanogenic 16S rRNA gene clone library and *mcrA* gene clone library construction.

Bacteria (MiSeq)

SampleID	Seqs/Sample	PD whole tree	Chao1	Good's coverage	observed species	Shannon	Simpson
P1A	6100	39.222	1951.164	0.918	742.2	5.868	0.939
P1O	6100	32.782	1378.172	0.941	552.6	4.727	0.873
P2A	6100	39.311	2137.544	0.915	720.4	4.886	0.872
P2O	6100	36.549	1869.683	0.923	669.6	5.003	0.875
P3A	6100	50.028	2183.686	0.903	921.3	6.194	0.932
P3O	6100	48.894	2098.391	0.903	972.5	6.653	0.941
P4A	6100	43.85	2081.336	0.913	794.5	5.475	0.876
P4O	6100	45.632	2156.457	0.906	843.4	4.765	0.794
P5A	6100	45.792	2468.217	0.9	891.2	6.499	0.961
P5O	6100	36.263	2112.554	0.923	669.7	5.396	0.915
P6A	6100	39.937	2006.069	0.916	769.7	6.157	0.941
P6O	6100	40.756	2196.376	0.91	826.6	6.5	0.959
P7A	6100	49.66	2195.145	0.896	1032.6	7.2	0.969
P8O	6100	39.205	1767.685	0.924	726.8	5.73	0.924

Archaea (MiSeq)

SampleID	Seqs/Sample	PD whole tree	Chao1	Good's coverage	observed species	Shannon	Simpson
P1A	760	3.089	262.751	0.938	77.4	3.747	0.86
P1O	760	2.265	39.79	0.984	26.7	1.774	0.512
P2A	760	2.7	66.741	0.977	42.5	2.297	0.557
P2O	760	2.697	102.594	0.958	51.7	1.529	0.327
P3A	760	2.615	96.15	0.966	63	4.121	0.896
P3O	760	4.15	144.067	0.948	58.7	2.263	0.584
P4A	760	2.733	125.857	0.952	65.4	2.791	0.668
P4O	760	3.542	147.413	0.94	84.2	3.862	0.843
P5A	760	2.732	130.623	0.958	56.3	3.262	0.829
P5O	760	2.714	99.733	0.96	61.7	3.861	0.886
P6A	760	2.105	108.36	0.968	35.8	1.282	0.306
P6O	760	2.288	100.186	0.962	50	2.75	0.746
P7A	760	2.569	91.164	0.962	50.7	1.735	0.393
P8O	760	1.682	23.15	0.992	15.9	1.494	0.518

Methanogen (MiSeq)

SampleID	Seqs/Sample	PD whole tree	Chao1	Good's coverage	observed species	Shannon	Simpson
P1A	240	1.135	71.814	0.911	36.2	3.391	0.846
P1O	240	0.3	15.65	0.984	12.9	1.695	0.508
P2A	240	1.16	32.463	0.951	21.5	1.492	0.361
P2O	240	0.98	60.625	0.928	25.3	1.506	0.349
P3A	240	0.918	63.343	0.926	39.6	3.932	0.881
P3O	240	1.288	107.15	0.926	24.6	2.1	0.602
P4A	240	1.156	144.65	0.905	31.9	2.435	0.621
P4O	240	1.356	62.492	0.926	32.6	3.336	0.823
P5A	240	1.242	37.325	0.942	25.7	2.72	0.756
P5O	240	1.393	83.467	0.916	34	3.559	0.874
P6A	240	0.986	23.1	0.971	12.9	1.049	0.277
P6O	240	1.228	37.39	0.95	24	2.649	0.733
P7A	240	0.865	31.808	0.954	21.8	1.547	0.375
P8O	240	0.825	15.1	0.98	9.8	0.798	0.218

Methanogen (Methanogenic 16S rRNA gene clone library)

SampleID	Seqs/Sample	PD whole tree	Chao1	Good's coverage	observed species	Shannon	Simpson
P1A	28	1.167	8.5	0.893	7	2.132	0.689
P1O	28	1.101	10	0.857	7	1.84	0.589
P2A	28	0.997	7.5	0.929	7	2.277	0.724
P2O	28	0.415	6.333	0.929	6	1.698	0.554
P3A	28	0.337	8.333	0.929	8	2.564	0.781
P3O	28	0.305	3	0.964	3	1.139	0.503
P4A	28	0.519	12.5	0.821	10	2.52	0.717
P4O	28	0.472	6	1	6	2.296	0.758
P5A	28	1.314	13.333	0.821	10	2.846	0.827
P5O	28	0.472	4	1	4	1.662	0.64
P6A	28	1.078	5	0.964	5	1.67	0.582
P6O	28	1.051	13	0.857	7	2.032	0.671
P7A	28	0.238	2	1	2	0.592	0.245
P8O	28	1.267	8	0.929	7	2.503	0.801

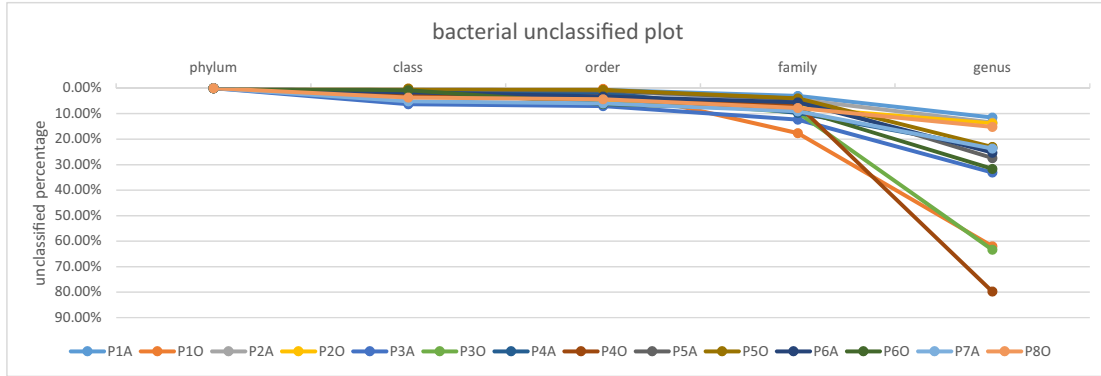
Methanogen (*mcrA* gene clone library)

SampleID	Seqs/Sample	PD whole tree	Chao1	Good's coverage	observed species	Shannon	Simpson
P1A	23	10	0.826	8	2.435	0.756	0.756
P1O	23	5	0.957	5	1.684	0.582	0.582
P2A	23	8	0.87	5	1.578	0.582	0.582
P2O	23	6	0.913	5	1.808	0.658	0.658
P3A	23	9.6	0.87	9	2.729	0.794	0.794
P3O	23	17	0.783	7	2.036	0.681	0.681
P4A	23	57	0.565	12	2.975	0.813	0.813
P4O	23	26	0.739	11	3.208	0.877	0.877
P5A	23	9	0.87	8	2.595	0.794	0.794
P5O	23	19	0.696	12	3.262	0.87	0.87
P6A	23	8	0.87	7	2.255	0.733	0.733
P6O	23	6.5	0.913	6	2.086	0.699	0.699
P7A	23	7.333	0.913	7	2.351	0.745	0.745
P8O	23	6.5	0.87	5	1.173	0.374	0.374

Table S2. Unclassified sequences percentage in each taxon level based on QIIME software applying SILVA compatible 119 release SSURef database as reference. a) bacterial community table and chart; b) archaeal community table and chart.

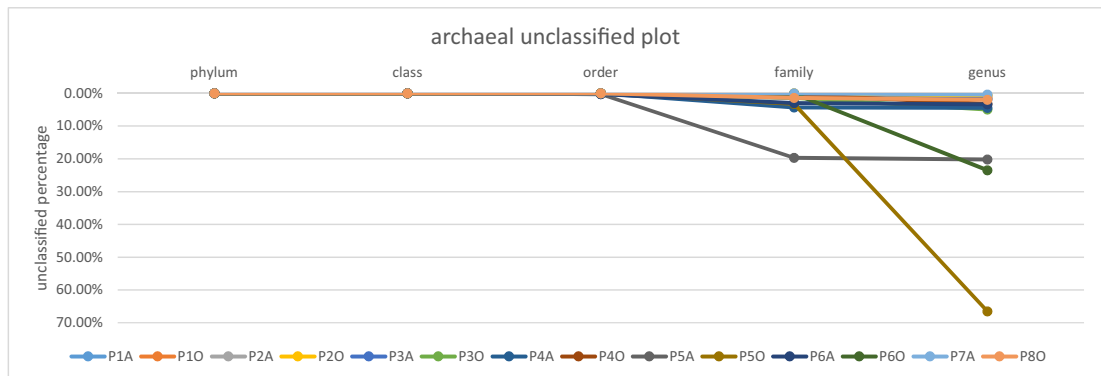
a

	P1A	P1O	P2A	P2O	P3A	P3O	P4A	P4O	P5A	P5O	P6A	P6O	P7A	P8O	average
phylum	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
class	0.38%	0.15%	0.44%	0.23%	6.32%	2.85%	1.43%	2.92%	0.41%	0.20%	1.67%	0.84%	5.18%	3.65%	1.90%
order	0.69%	0.29%	1.28%	5.59%	7.01%	4.05%	1.77%	3.24%	0.95%	0.70%	3.26%	6.19%	5.96%	4.34%	3.24%
family	3.06%	17.66%	4.39%	7.72%	12.37%	9.52%	9.71%	6.62%	4.16%	3.98%	5.52%	8.40%	9.11%	7.75%	7.86%
genus	11.53%	61.99%	13.50%	13.76%	33.08%	63.37%	23.53%	79.77%	27.42%	23.05%	25.29%	31.65%	23.69%	15.17%	31.91%

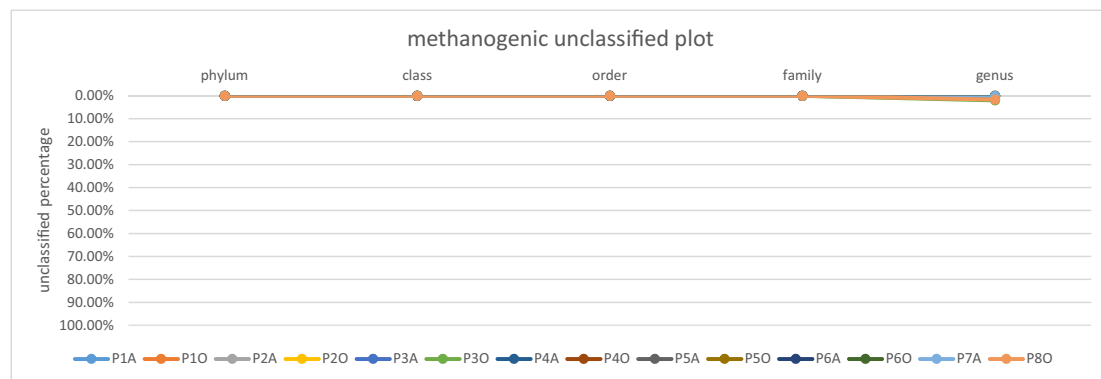


b

	P1A	P1O	P2A	P2O	P3A	P3O	P4A	P4O	P5A	P5O	P6A	P6O	P7A	P8O	average
phylum	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
class	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
order	0.13%	0.13%	0.00%	0.00%	0.13%	0.00%	0.00%	0.00%	0.26%	0.00%	0.26%	0.00%	0.00%	0.00%	0.07%
family	0.39%	0.91%	0.39%	0.00%	1.43%	1.43%	4.30%	0.39%	19.69%	3.26%	3.00%	0.13%	0.00%	1.43%	2.63%
genus	1.56%	1.17%	0.52%	0.65%	1.83%	4.95%	4.43%	3.26%	20.21%	66.49%	3.39%	23.47%	0.39%	1.96%	9.59%



	P1A	P1O	P2A	P2O	P3A	P3O	P4A	P4O	P5A	P5O	P6A	P6O	P7A	P8O	average
phylum	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
class	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
order	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
family	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
genus	1.22%	0.00%	0.00%	0.00%	0.00%	2.04%	0.00%	0.00%	0.00%	0.00%	0.41%	0.00%	0.00%	1.63%	0.38%



D_0_Bacteria_D_1_Proteobacteria_D_2_Betaproteobacteria_D_3_Burkholderiales_D_4_Burkholderiaceae_D_5_Lutimpa	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%
D_0_Bacteria_D_1_Proteobacteria_D_2_Betaproteobacteria_D_3_Burkholderiales_D_4_Burkholderia_incertae_sedis_D_5_Thiomonas	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%
D_0_Bacteria_D_1_Proteobacteria_D_2_Betaproteobacteria_D_3_Hydrogenisphaerales_D_4_Hydrogenisphaerales_D_5_Hydrogenisphaera	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
D_0_Bacteria_D_1_Proteobacteria_D_2_Betaproteobacteria_D_3_Nitrospirales_D_4_Nitrospirales_D_5_Nitrospira	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
D_0_Bacteria_D_1_Proteobacteria_D_2_Betaproteobacteria_D_3_Nitrospirales_D_4_Nitrospirales_D_5_uncultured_bacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%
D_0_Bacteria_D_1_Proteobacteria_D_2_Betaproteobacteria_D_3_Rhodocyclales_D_4_Rhodocyclales_D_5_Georgiella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%
D_0_Bacteria_D_1_Proteobacteria_D_2_Betaproteobacteria_D_3_Rhodocyclales_D_4_Rhodocyclales_D_5_uncultured_soil_bacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%
D_0_Bacteria_D_1_Proteobacteria_D_2_Deltaproteobacteria_D_3_Desulfobacteriales_D_4_Desulfobacteriales_D_5_Desulfotomaculum	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
D_0_Bacteria_D_1_Proteobacteria_D_2_Deltaproteobacteria_D_3_Desulfobacteriales_D_4_Desulfobacteriales_D_5_Desulfocapsa	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
D_0_Bacteria_D_1_Proteobacteria_D_2_Deltaproteobacteria_D_3_Mycosphaeriales_D_4_Her-168-1158-D_5_uncultured_bacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%
D_0_Bacteria_D_1_Proteobacteria_D_2_Deltaproteobacteria_D_3_Mycosphaeriales_D_4_Mycosphaeriales_D_5_Caulobacterium_equisetum	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%
D_0_Bacteria_D_1_Proteobacteria_D_2_Deltaproteobacteria_D_3_Mycosphaeriales_D_4_Polyunguicaceae_D_5_Bysoviox	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%
D_0_Bacteria_D_1_Proteobacteria_D_2_Deltaproteobacteria_D_3_Mycosphaeriales_D_4_uncultured_Cytophactaceae_bacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%
D_0_Bacteria_D_1_Proteobacteria_D_2_Deltaproteobacteria_D_3_Syntrophobacteriales_D_4_Syntrophobacteriales_D_5_Desulfotomaculum	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%
D_0_Bacteria_D_1_Proteobacteria_D_2_Epsilonproteobacteria_D_3_Epsilonproteobacteria_D_4_uncultured_Mariprofundum_sp_D_5_uncultured_Mariprofundum_sp	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
D_0_Bacteria_D_1_Proteobacteria_D_2_Gammaproteobacteria_D_3_EC-D_4_uncultured_bacterium_D_5_uncultured_bacterium	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
D_0_Bacteria_D_1_Proteobacteria_D_2_Gammaproteobacteria_D_3_Methylospirales_D_4_Methylospirales_D_5_Methylospirillum	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%
D_0_Bacteria_D_1_Proteobacteria_D_2_Gammaproteobacteria_D_3_PVR10-D_4_uncultured_gamma_proteobacterium_D_5_uncultured_gamma_proteobacterium	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
D_0_Bacteria_D_1_Proteobacteria_D_2_Gammaproteobacteria_D_3_PVR10-D_4_uncultured_gamma_proteobacterium_D_5_uncultured_gamma_proteobacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%
D_0_Bacteria_D_1_Proteobacteria_D_2_Gammaproteobacteria_D_3_Pseudomonadales_D_4_Pseudomonadales_D_5_uncultured	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
D_0_Bacteria_D_1_Proteobacteria_D_2_Gammaproteobacteria_D_3_Thiorhodales_D_4_Piscirickettsiaceae_D_5_Cycloclasticus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%
D_0_Bacteria_D_1_Proteobacteria_D_2_Gammaproteobacteria_D_3_Thiorhodales_D_4_Piscirickettsiaceae_D_5_Methylophilus	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
D_0_Bacteria_D_1_Proteobacteria_D_2_Gammaproteobacteria_D_3_Xanthomonadales_D_4_Xanthomonadales_D_5_uncultured	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%
D_0_Bacteria_D_1_Proteobacteria_D_2_Gammaproteobacteria_D_3_Xanthomonadales_D_4_Xanthomonadales_D_5_Dyella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%
D_0_Bacteria_D_1_Proteobacteria_D_2_Gammaproteobacteria_D_3_Xanthomonadales_D_4_Xanthomonadales_D_5_Metallibacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
D_0_Bacteria_D_1_Proteobacteria_D_2_Gammaproteobacteria_D_3_Xanthomonadales_D_4_Xanthomonadales_D_5_Xanthomonadales_bacterium_K-1-9	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%
D_0_Bacteria_D_1_Verrucomicrobia_D_2_Spirillum_D_3_Citrobacteriales_D_4_DNAII soil group_D_5_uncultured_soil_bacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%

b

Taxon	average	P1A	P1O	P2A	P2O	P3A	P3O	P4A	P4O	P5A	P5O	P6A	P6O	P7A	P8O
D_0_Archaea_D_1_Euryarchaeota_D_2_Methanosarcinibacteria_D_3_Methanosarciniales_D_4_Methanosarcinaceae_D_5_Methanosarcina	42.30%	0.377%	1.30%	74.45%	94.00%	94.26%	1.43%	78.88%	12.13%	46.94%	14.21%	7.61%	46.62%	37.09%	0.00%
D_0_Archaea_D_1_Euryarchaeota_D_2_Methanosarcinibacteria_D_3_Methanosarciniales_D_4_Methanosarcinaceae_D_5_Methanohalobium	7.69%	0.67%	0.13%	2.22%	0.00%	0.00%	0.00%	0.00%	0.00%	0.79%	0.17%	0.13%	26.40%	6.39%	0.91%
D_0_Archaea_D_1_Euryarchaeota_D_2_Methanosarcinibacteria_D_3_Methanosarciniales_D_4_Methanosarcinaceae_D_5_Methanohalobium	9.07%	0.55%	79.79%	0.00%	0.00%	0.00%	0.39%	0.00%	0.13%	0.00%	0.52%	4.64%	1.56%	0.00%	0.00%
D_0_Archaea_D_1_Euryarchaeota_D_2_Methanosarcinibacteria_D_3_Methanosarciniales_D_4_Methanosarcinaceae_D_5_Methanohalobium	8.07%	0.24%	0.00%	0.39%	0.00%	0.78%	48.66%	9.31%	12.20%	1.30%	0.13%	0.00%	0.00%	0.13%	0.00%
D_0_Archaea_D_1_Euryarchaeota_D_2_Methanosarcinibacteria_D_3_Methanosarciniales_D_4_Methanosarcinaceae_D_5_Methanohalobium	5.10%	0.00%	0.00%	0.91%	0.91%	0.39%	19.43%	1.69%	44.20%	0.00%	0.00%	0.00%	0.00%	3.91%	0.00%
D_0_Archaea_D_1_Euryarchaeota_D_2_Thermococcales_D_3_Thermococcales_D_4_Thermococcales_D_5_Thermococcus	4.59%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.26%	0.26%	0.00%	0.00%	0.00%	63.75%
D_0_Archaea_D_1_Euryarchaeota_D_2_Thermococcales_D_3_Thermococcales_D_4_Thermococcales_D_5_Thermococcus	3.59%	0.39%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	19.82%	1.36%	0.13%	0.39%	0.00%	28.16%
D_0_Archaea_D_1_Euryarchaeota_D_2_Archaeoglobales_D_3_Archaeoglobales_D_4_Archaeoglobaceae_D_5_undefined	3.50%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	12.99%	0.00%	16.04%	0.00%	0.00%
D_0_Archaea_D_1_Euryarchaeota_D_2_Methanosarcinibacteria_D_3_Methanosarciniales_D_4_Methanosarcinaceae_D_5_Methanohalobium	1.02%	22.41%	17.47%	0.13%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.13%	0.00%	0.13%	0.00%	1.96%
D_0_Archaea_D_1_Euryarchaeota_D_2_Archaeoglobales_D_3_Archaeoglobales_D_4_Archaeoglobaceae_D_5_undefined	2.31%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.39%	26.08%	0.00%	6.13%	0.00%	0.00%
D_0_Archaea_D_1_Euryarchaeota_D_2_Thermoplasmales_D_3_Kanazaki-DP-4_undefined euryarchaeote_D_5_undefined euryarchaeote	2.10%	0.26%	0.39%	0.13%	0.00%	1.36%	1.17%	2.87%	0.26%	19.43%	1.26%	0.26%	0.00%	0.00%	0.13%
D_0_Archaea_D_1_Euryarchaeota_D_2_Methanosarcinibacteria_D_3_Methanosarciniales_D_4_Methanosarcinaceae_D_5_Methanohalobium	1.70%	0.26%	0.00%	4.82%	2.26%	1.83%	3.91%	0.13%	2.74%	0.00%	0.13%	0.00%	0.00%	6.78%	0.00%
D_0_Archaea_D_1_Euryarchaeota_D_2_Halobacteriales_D_3_Miscellaneous Euryarchaeote Group/MEG/D_5_Candidatus Natronalba	1.11%	0.13%	0.00%	15.22%	0.13%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
D_0_Archaea_D_1_Euryarchaeota_D_2_Methanosarcinibacteria_D_3_Methanosarciniales_D_4_Methanosarcinaceae_D_5_Methanohalobium	1.08%	0.00%	0.00%	1.04%	0.91%	0.82%	0.00%	3.91%	4.17%	1.17%	0.00%	1.17%	0.13%	1.17%	0.39%
D_0_Archaea_D_1_Euryarchaeota_D_2_Archaeoglobales_D_3_Archaeoglobales_D_4_Archaeoglobaceae_D_5_undefined	0.46%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	5.22%	0.00%	1.17%	0.00%	0.00%
D_0_Archaea_D_1_Euryarchaeota_D_2_Halobacteriales_D_3_Halobacteriales_D_4_Deep Sea Hydrothermal Vent (pH 9)/DSV/D_5_undefined euryarchaeote	0.39%	0.00%	0.26%	0.00%	0.00%	0.00%	0.13%	0.00%	0.00%	0.00%	3.78%	0.00%	0.00%	0.00%	0.00%
D_0_Archaea_D_1_Euryarchaeota_D_2_Thermoplasmales_D_3_Thermoplasmales_D_4_Territorial Miscellaneous (pH 7)/TMEG/D_5_undefined archaeon	0.28%	0.00%	0.00%	0.00%	0.39%	0.00%	1.69%	0.00%	1.83%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
D_0_Archaea_D_1_Euryarchaeota_D_2_Thermoplasmales_D_3_WCHA-57/D_4_undefined archaeon_D_5_undefined archaeon	0.23%	0.00%	0.00%	0.26%	0.00%	0.00%	0.13%	0.39%	0.00%	0.00%	0.00%	2.35%	0.13%	0.00%	0.00%
D_0_Archaea_D_1_Euryarchaeota_D_2_Methanosarcinibacteria_D_3_Methanosarciniales_D_4_Methanosarcinaceae_D_5_Methanohalobium	0.18%	0.00%	0.00%	0.00%	0.13%	0.00%	1.54%	0.00%	0.25%	0.00%	0.26%	0.00%	0.00%	0.00%	0.00%
D_0_Archaea_D_1_Euryarchaeota_D_2_Halobacteriales_D_3_Halobacteriales_D_4_Halobacteriales_D_5_Candidatus Halobacterium	0.16%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	2.22%
D_0_Archaea_D_1_Euryarchaeota_D_2_Halobacteriales_D_3_Halobacteriales_D_4_Deep Sea Hydrothermal Vent (pH 9)/DSV/D_5_undefined archaeon	0.11%	0.00%	0.00%	0.13%	0.26%	0.26%	0.91%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
D_0_Archaea_D_1_Euryarchaeota_D_2_Methanosarcinibacteria_D_3_Methanosarciniales_D_4_Methanosarcinaceae_D_5_Methanohalobium	0.10%	0.00%	0.00%	0.00%	0.00%	0.00%	0.78%	0.00%	0.65%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
D_0_Archaea_D_1_Thermoplasmales_D_3_Thermoplasmales_D_4_Territorial Miscellaneous (pH 7)/TMEG/D_5_undefined Thermoprotei archaeon_D_5_undefined Thermoprotei archaeon	0.09%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	1.30%
D_0_Archaea_D_1_Euryarchaeota_D_2_Methanosarcinibacteria_D_3_Methanosarciniales_D_4_Methanosarcinaceae_D_5_undefined	0.08%	1.61%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.13%	0.00%	0.00%	0.00%
D_0_Archaea_D_1_Euryarchaeota_D_2_Methanosarcinibacteria_D_3_Methanosarciniales_D_4_Methanosarcinaceae_D_5_Methanohalobium	0.07%	0.00%	0.00%	0.26%	0.00%	0.00%	0.78%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
D_0_Archaea_D_1_Euryarchaeota_D_2_Thermoplasmales_D_3_Thermoplasmales_D_4_Marine Group/D_5_undefined euryarchaeote	0.07%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
D_0_Archaea_D_1_Euryarchaeota_D_2_Thermoplasmales_D_3_Thermoplasmales_D_4_288-4/D_5_undefined archaeon	0.06%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.26%	0.00%	0.00%	0.00%	0.00%
D_0_Archaea_D_1_Euryarchaeota_D_2_Halobacteriales_D_3_Halobacteriales_D_4_Halobacteriales_D_5_Halobacterium	0.05%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.65%
D_0_Archaea_D_1_Euryarchaeota_D_2_Thermoplasmales_D_3_Kanazaki-DP-4_undefined archaeon_D_5_undefined archaeon	0.05%	0.00%	0.39%	0.00%	0.00%	0.00%	0.13%	0.13%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
D_0_Archaea_D_1_Euryarchaeota_D_2_Methanosarcinibacteria_D_3_Methanosarciniales_D_4_Methanosarcinaceae_D_5_undefined	0.04%	0.00%	0.00%	0.00%	0.00%	0.13%	0.00%	0.00%	0.00%	0.13%	0.00%	0.26%	0.00%	0.00%	0.00%
D_0_Archaea_D_1_Euryarchaeota_D_2_Methanosarcinibacteria_D_3_Methanosarciniales_D_4_Methanosarcinaceae_D_5_undefined	0.04%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.22%
D_0_Archaea_D_1_Euryarchaeota_D_2_Methanosarcinibacteria_D_3_Methanosarciniales_D_4_Methanosarcinaceae_D_5_Methanohalobium	0.03%	0.00%	0.00%	0.00%	0.00%	0.00%	0.26%	0.00%	0.13%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
D_0_Archaea_D_1_Euryarchaeota_D_2_Thermoplasmales_D_3_Thermoplasmales_D_4_014908-A8-DP13/D_5_undefined archaeon	0.03%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.26%	0.13%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
D_0_Archaea_D_1_Euryarchaeota_D_2_Thermoplasmales_D_3_Thermoplasmales_D_4_Marine Group/D_5_undefined archaeon	0.03%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.26%	0.00%	0.00%	0.00%	0.13%	0.00%	0.00%	0.00%
D_0_Archaea_D_1_Euryarchaeota_D_2_Thermoplasmales_D_3_Thermoplasmales_D_4_Incense Sodic/D_5_Candidatus Methanohalobium	0.03%	0.00%	0.00%	0.00%	0.13%	0.00%	0.13%	0.00%	0.13%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
D_0_Archaea_D_1_Euryarchaeota_D_2_Archaeoglobales_D_3_Archaeoglobales_D_4_Archaeoglobaceae_D_5_undefined	0.03%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
D_0_Archaea_D_1_Euryarchaeota_D_2_Methanosarcinibacteria_D_3_Methanosarciniales_D_4_Methanosarcinaceae_D_5_undefined	0.03%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
D_0_Archaea_D_1_Euryarchaeota_D_2_Methanosarcinibacteria_D_3_Methanosarciniales_D_4_Methanosarcinaceae_D_5_Methanohalobium	0.03%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
D_0_Archaea_D_1_Euryarchaeota_D_2_Thermoplasmales_D_3_Thermoplasmales_D_4_WCHA-57/D_4_undefined euryarchaeote_D_5_undefined euryarchaeote	0.03%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
D_0_Archaea_D_1_Euryarchaeota_D_2_Halobacteriales_D_3_Halobacteriales_D_4_Miscellaneous Euryarchaeote Group/MEG/D_5_undefined archaeon	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.24%	0.00%
D_0_Archaea_D_1_Euryarchaeota_D_2_Methanosarcinibacteria_D_3_Methanosarciniales_D_4_Methanosarcinaceae_D_5_undefined	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.22%
D_0_Archaea_D_1_Euryarchaeota_D_2_Methanosarcinibacteria_D_3_Methanosarciniales_D_4_Methanosarcinaceae_D_5_Methanohalobium	0.02%	0.00%	0.00%	0.00%	0.00%	0.26%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
D_0_Archaea_D_1_Thermoplasmales_D_3_Marine Group/D_5_undefined Thermoprotei archaeon_D_5_undefined Thermoprotei archaeon	0.02%	0.11%	0.00%	0.00%	0.00%	0.13%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
D_0_Archaea_D_1_Thermoplasmales_D_3_Marine Group/D_5_undefined Thermoprotei archaeon_D_5_undefined Thermoprotei archaeon	0.02%	0.00%	0.13%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.13%	0.00%	0.00%	0.00%	0.00%	0.00%
D_0_Archaea_D_1_Thermoplasmales_D_3_Territorial Hot Spring (pH 7)/TMS/D_4_Ukawa Family/D_5_Candidatus Caldarchaeum	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.26%	0.00%	0.00%
D_0_Archaea_D_1_Euryarchaeota_D_2_Archaeoglobales_D_3_Archaeoglobales_D_4_Archaeoglobaceae_D_5_Geoglobus	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.13%	0.00%	0.00%	0.00%	0.00%
D_0_Archaea_D_1_Euryarchaeota_D_2_Halobacteriales_D_3_Halobacteriales_D_4_Deep Sea Hydrothermal Vent (pH 6)/DSV/D_5_undefined euryarchaeote	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.13%	0.00%	0.00%	0.00%	0.00%
D_0_Archaea_D_1_Euryarchaeota_D_2_Halobacteriales_D_3_Halobacteriales_D_4_Deep Sea Hydrothermal Vent (pH 6)/DSV/D_5_undefined archaeon	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
D_0_Archaea_D_1_Euryarchaeota_D_2_Halobacteriales_D_3_Halobacteriales_D_4_Halobacteriales_D_5_Halobacterium	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.13%	0.00%
D_0_Archaea_D_1_Euryarchaeota_D_2_Halobacteriales_D_3_Halobacteriales_D_4_Halobacteriales_D_5_Halobacterium	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.13%	0.00%
D_0_Archaea_D_1_Euryarchaeota_D_2_Halobacteriales_D_3_Halobacteriales_D_4_Miscellaneous Euryarchaeote Group/MEG/D_5_undefined	0.01%	0.00%	0.00%	0.00%	0.00%	0.13%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
D_0_Archaea_D_1_Euryarchaeota_D_2_Thermoplasmales_D_3_Thermoplasmales_D_4_Territorial Miscellaneous (pH 7)/TMEG/D_5_undefined Thermoprotei archaeon	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.13%	0.00%
D_0_Archaea_D_1_Euryarchaeota_D_2_Thermoplasmales_D_3_Thermoplasmales_D_4_WC12/AC6/D_5_undefined archaeon WC12/AC6	0.01%	0.13%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
D_0_Archaea_D_1_Thermoplasmales_D_3_Marine Group/D_5_undefined Thermoprotei archaeon_D_5_undefined Thermoprotei archaeon	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.13%	0.00%	0.00%	0.00%	0.00%	0.00%

Table S4. Shared OTU numbers of all pairs of samples (I). The statistical table of average shared OTU numbers and the percentages of shared OTU numbers in each sample's OTU numbers (II). a) bacterial community tables; b) archaeal community tables.

a	I	P1A	P1O	P2A	P2O	P3A	P3O	P4A	P4O	P5A	P5O	P6A	P6O	P7A	P8O
	P1A	743	205	228	228	241	248	230	208	265	206	243	249	295	232
	P1O	205	553	195	184	183	207	201	168	235	179	188	218	234	202
	P2A	228	195	721	249	235	250	244	202	239	210	247	264	302	225
	P2O	228	184	249	670	226	237	234	203	254	214	239	237	278	216
	P3A	241	183	235	226	922	323	296	228	272	217	238	266	306	230
	P3O	248	207	250	237	323	973	286	338	307	238	269	282	325	240
	P4A	230	201	244	234	296	286	795	260	260	204	253	258	300	236
	P4O	208	168	202	203	228	338	260	844	227	176	220	231	259	194
	P5A	265	235	239	254	272	307	260	227	892	280	273	297	322	269
	P5O	206	179	210	214	217	238	204	176	280	670	213	245	249	220
	P6A	243	188	247	239	238	269	253	220	273	213	770	302	329	257
	P6O	249	218	264	237	266	282	258	231	297	245	302	827	330	259
	P7A	295	234	302	278	306	325	300	259	322	249	329	330	1033	272
	P8O	232	202	225	216	230	240	236	194	269	220	257	259	272	727

II	P1A	P1O	P2A	P2O	P3A	P3O	P4A	P4O	P5A	P5O	P6A	P6O	P7A	P8O
average shared OTU number	236.8	199.9	237.7	230.7	250.8	273.1	250.9	224.2	269.2	219.3	251.6	264.5	292.4	234.8
OTU number	743	553	721	670	922	973	795	844	892	670	770	827	1033	727
percentage	31.9%	36.2%	33.0%	34.4%	27.2%	28.1%	31.6%	26.6%	30.2%	32.7%	32.7%	32.0%	28.3%	32.3%

b	I	P1A	P1O	P2A	P2O	P3A	P3O	P4A	P4O	P5A	P5O	P6A	P6O	P7A	P8O
	P1A	66	14	17	7	16	7	9	8	18	7	14	7	8	4
	P1O	14	26	4	1	1	2	1	3	3	6	4	5	2	2
	P2A	17	4	51	21	25	8	15	12	18	5	12	4	12	2
	P2O	7	1	21	52	12	3	9	6	8	2	5	2	10	0
	P3A	16	1	25	12	76	10	25	9	21	1	10	1	6	0
	P3O	7	2	8	3	10	57	11	20	7	2	4	1	2	0
	P4A	9	1	15	9	25	11	68	18	17	2	10	1	6	0
	P4O	8	3	12	6	9	20	18	72	10	4	5	1	6	0
	P5A	18	3	18	8	21	7	17	10	55	9	15	5	10	4
	P5O	7	6	5	2	1	2	2	4	9	63	5	19	3	5
	P6A	14	4	12	5	10	4	10	5	15	5	37	6	7	2
	P6O	7	5	4	2	1	1	1	1	5	19	6	52	8	3
	P7A	8	2	12	10	6	2	6	6	10	3	7	8	44	1
	P8O	4	2	2	0	0	0	0	0	4	5	2	3	1	16

II	P1A	P1O	P2A	P2O	P3A	P3O	P4A	P4O	P5A	P5O	P6A	P6O	P7A	P8O
average shared OTU number	10.5	3.7	11.9	6.6	10.5	5.9	9.5	7.8	11.2	5.4	7.6	4.8	6.2	1.8
OTU number	66	26	51	52	76	57	68	72	55	63	37	52	44	16
percentage	15.9%	14.2%	23.4%	12.7%	13.9%	10.4%	14.0%	10.9%	20.3%	8.5%	20.6%	9.3%	14.2%	11.1%

Table S5. Functional roles and corresponding reference of core bacterial microbiome in all petroleum samples. Core microbial OTUs (23 OTUs) were affiliated to the most abundant genera.

Genus name	Average Abundance	Function role				References
Pseudomonas (Gamma.)	14.3%	Hydrocarbon degrader	Nitrate/Nitrite reducer			(Ma et al., 2006; Wentzel et al., 2007; Mehboob et al., 2009; Zhang et al., 2011)
Acinetobacter (Gamma.)	7.4%	Aerobic hydrocarbon degrader				(Lal and Khanna, 1996; DiCello et al., 1997; Zhang et al., 2014)
Hydrogenophilaceae UG (Beta.)	5.0%	Fermentative bacteria	Nitrate/Nitrite reducer			(Hayashi et al., 1999; Salinas et al., 2004)
Marinobacter (Gamma.)	2.8%	Hydrocarbon degrader	Nitrate/Nitrite reducer			(Gauthier et al., 1992; Takai et al., 2005)
Nitricola (Gamma.)	2.6%	Aerobic hydrocarbon degrader	Nitrate/Nitrite reducer			(Dimitriu et al., 2005; Tiquia, 2010)
Thermaceae UG (D.-T.)	2.4%	Fermentative bacteria	Nitrate/Nitrite reducer			(Miroshnichenko et al., 2003a; Miroshnichenko et al., 2003b)
Proteiniphilum (Bac.)	2.4%	Hydrocarbon degrader				(Chen and Dong, 2005; Gargouri et al., 2014)
Deferribacteraceae UG (Deferri.)	2.2%	Hydrocarbon degrader	Nitrate/Nitrite reducer	Sulfidogenic bacteria (SRB)		(Greene et al., 1997; Takai et al., 2003)
Thauera (Beta.)	2.1%	Hydrocarbon degrader	Nitrate/Nitrite reducer			(Foss and Harder, 1998; Song et al., 2001; Mechichi et al., 2002; Dubbels et al., 2009; Sun and Cupples, 2012)
Bacteriovoraceae UG (Delta.)	2.1%					
Psychrobacter (Gamma.)	1.9%	Aerobic hydrocarbon degrader				(Deppe et al., 2005; Bowman and Denning, 2014)
Sulfurovum (Epsilon.)	1.7%	Sulfur cycling bacteria				(Inagaki et al., 2004; Mino et al., 2014)
Defluviimonas (Alpha.)	1.3%	Nitrate/Nitrite reducer				(Foesel et al., 2011; Pan et al., 2015)
Balneola (Bac.)	1.2%	Aerobic hydrocarbon degrader				(Urios et al., 2006; Urios et al., 2008; Li et al., 2012)
Mesotoga (Thermo.)	0.9%	Hydrocarbon degrader	Fermentative bacteria	Sulfidogenic bacteria (SRB)	Acetogen	(Nesbo et al., 2012; Ben Hania et al., 2013) (Rosenberg et al., 2014)
VC2.1 Bac22 UG (Bac.)	0.8%					
Simplicispira (Beta.)	0.8%					
Stappia (Alpha.)	0.7%	Aerobic hydrocarbon degrader				(Al-Awadhi et al., 2007; Lai et al., 2010)
Glycoaulis (Alpha.)	0.7%	Aerobic hydrocarbon degrader				(Lv et al., 2014; Geng et al., 2015)
ML635J-40 aquatic group UG (Bac.)	0.6%	Fermentative bacteria				(Nolla-Ardevol et al., 2015)
Spirochaetaceae UG (Spiro.)	0.6%	Fermentative bacteria	Acetogen			(Graber and Breznak, 2004; Cheng et al., 2013)
Novosphingobium (Alpha.)	0.6%	Hydrocarbon degrader	Nitrate/Nitrite reducer			(Sohn et al., 2004; Liu et al., 2005; Addison et al., 2007; Niharika et al., 2013)
Clostridiales Family XI UG (Fir.)	0.5%	Fermentative bacteria	Sulfidogenic bacteria (SRB)	Syntrophic acetate oxidizer	Acetogen	(Jones and Vandecasteele, 2008; Müller et al., 2013)
Others	44.4%					

References:

- Addison, S.L., Foote, S.M., Reid, N.M., and Lloyd-Jones, G. (2007). *Novosphingobium nitrogenifigens* sp. nov., a polyhydroxyalkanoate-accumulating diazotroph isolated from a New Zealand pulp and paper wastewater. *Int. J. Syst. Evol. Microbiol.* 57, 2467-2471. doi: doi:10.1099/ijs.0.64627-0.
- Al-Awadhi, H., Sulaiman, R.H.D., Mahmoud, H.M., and Radwan, S.S. (2007). Alkaliphilic and halophilic hydrocarbon-utilizing bacteria from Kuwaiti coasts of the Arabian Gulf. *Appl. Microbiol. Biotechnol.* 77, 183-186. doi: 10.1007/s00253-007-1127-1.
- Ben Hania, W., Postec, A., Auello, T., Ranchou-Peyruse, A., Erauso, G., Brochier-Armanet, C., Hamdi, M., Ollivier, B., Saint-Laurent, S., Magot, M., and Fardeau, M.-L. (2013). *Mesotoga infera* sp nov., a mesophilic member of the order *Thermotogales*, isolated from an underground gas storage aquifer. *Int. J. Syst. Evol. Microbiol.* 63, 3003-3008. doi: 10.1099/ijs.0.047993-0.
- Bowman, J.S., and Deming, J.W. (2014). Alkane hydroxylase genes in psychrophile genomes and the potential for cold active catalysis. *BMC Genomics* 15. doi: 10.1186/1471-2164-15-1120.
- Chen, S.Y., and Dong, X.Z. (2005). *Proteiniphilum acetatigenes* gen. nov., sp nov., from a UASB reactor treating brewery wastewater. *Int. J. Syst. Evol. Microbiol.* 55, 2257-2261. doi: 10.1099/ijs.0.63807-0.
- Cheng, L., Ding, C., Li, Q., He, Q., Dai, L.-R., and Zhang, H. (2013). DNA-SIP Reveals That *Syntrophaceae* Play an Important Role in Methanogenic Hexadecane Degradation. *PLoS One* 8. doi: 10.1371/journal.pone.0066784.
- Deppe, U., Richnow, H.H., Michaelis, W., and Antranikian, G. (2005). Degradation of crude oil by an arctic microbial consortium. *Extremophiles* 9, 461-470. doi: 10.1007/s00792-005-0463-2.
- Dicello, F., Pepi, M., Baldi, F., and Fani, R. (1997). Molecular characterization of an *n*-alkane-degrading bacterial community and identification of a new species, *Acinetobacter venetianus*. *Res. Microbiol.* 148, 237-249. doi: 10.1016/s0923-2508(97)85244-8.
- Dimitriu, P.A., Shukla, S.K., Conradt, J., Marquez, M.C., Ventosa, A., Maglia, A., Peyton, B.M., Pinkart, H.C., and Mormile, M.R. (2005). *Nitrincola lacisaponensis* gen. nov., sp nov., a novel alkaliphilic bacterium isolated from an alkaline, saline lake. *Int. J. Syst. Evol. Microbiol.* 55, 2273-2278. doi: 10.1099/ijs.0.63647-0.
- Dubbels, B.L., Sayavedra-Soto, L.A., Bottomley, P.J., and Arp, D.J. (2009). *Thauera butanivorans* sp nov., a C-2-C-9 alkane-oxidizing bacterium previously referred to as '*Pseudomonas butanovora*'. *Int. J. Syst. Evol. Microbiol.* 59, 1576-1578. doi: 10.1099/ijs.0.000638-0.
- Foesel, B.U., Drake, H.L., and Schramm, A. (2011). *Defluviimonas denitrificans* gen. nov., sp nov., and *Pararhodobacter aggregans* gen. nov., sp nov., non-phototrophic *Rhodobacteraceae* from the biofilter of a marine aquaculture. *Syst. Appl. Microbiol.* 34, 498-502. doi: 10.1016/j.syapm.2011.08.006.
- Foss, S., and Harder, J. (1998). *Thauera linaloolentis* sp. nov. and *Thauera terpenica* sp. nov., isolated on oxygen-containing monoterpenes (linalool, menthol, and eucalyptol) and nitrate. *Syst. Appl. Microbiol.* 21, 365-373.

- Gargouri, B., Karray, F., Mhiri, N., Aloui, F., and Sayadi, S. (2014). Bioremediation of petroleum hydrocarbons-contaminated soil by bacterial consortium isolated from an industrial wastewater treatment plant. *J. Chem. Technol. Biotechnol.* 89, 978-987. doi: 10.1002/jctb.4188.
- Gauthier, M.J., Lafay, B., Christen, R., Fernandez, L., Acquaviva, M., Bonin, P., and Bertrand, J.C. (1992). *Marinobacter hydrocarbonoclasticus* gen. nov., sp. nov., a new, extremely halotolerant, hydrocarbon-degrading marine bacterium. *Int. J. Syst. Bacteriol.* 42, 568-576.
- Geng, S., Pan, X.-C., Mei, R., Wang, Y.-N., Liu, X.-Y., Wang, X.-B., Tang, Y.-Q., and Wu, X.-L. (2015). *Glycocaulis alkaliphilus* sp nov., a dimorphic prosthecate bacterium isolated from crude oil. *Int. J. Syst. Evol. Microbiol.* 65, 838-844. doi: 10.1099/ijs.0.000023.
- Graber, J.R., and Breznak, J.A. (2004). Physiology and nutrition of *Treponema primitia*, an H₂/CO₂ acetogenic *Spirochete* from termite hindguts. *Appl. Environ. Microbiol.* 70, 1307-1314. doi: 10.1128/aem.70.3.1307-1314.2004.
- Greene, A.C., Patel, B.K.C., and Sheehy, A.J. (1997). *Deferribacter thermophilus* gen nov, sp nov, a novel thermophilic manganese- and iron-reducing bacterium isolated from a petroleum reservoir. *Int. J. Syst. Bacteriol.* 47, 505-509.
- Hayashi, N.R., Ishida, T., Yokota, A., Kodama, T., and Igarashi, Y. (1999). *Hydrogenophilus thermoluteolus* gen, nov., sp. nov., a thermophilic, facultatively chemolithoautotrophic, hydrogen-oxidizing bacterium. *Int. J. Syst. Bacteriol.* 49, 783-786.
- Inagaki, F., Takai, K., Nealson, K.H., and Horikoshi, K. (2004). *Sulfurovum lithotrophicum* gen. nov., sp nov., a novel sulfur-oxidizing chemolithoautotroph within the *epsilon-Proteobacteria* isolated from Okinawa Trough hydrothermal sediments. *Int. J. Syst. Evol. Microbiol.* 54, 1477-1482. doi: 10.1099/ijs.0.03042-0.
- Jones, T., and Vandecasteele, J.-P. (2008). *Petroleum Microbiology*. Editions OPHRYS.
- Lai, Q., Qiao, N., Wu, C., Sun, F., Yuan, J., and Shao, Z. (2010). *Stappia indica* sp nov., isolated from deep seawater of the Indian Ocean. *Int. J. Syst. Evol. Microbiol.* 60, 733-736. doi: 10.1099/ijs.0.013417-0.
- Lal, B., and Khanna, S. (1996). Degradation of crude oil by *Acinetobacter calcoaceticus* and *Alcaligenes odorans*. *J. Appl. Bacteriol.* 81, 355-362.
- Li, H., Zhang, Q., Wang, X.-L., Ma, X.-Y., Lin, K.-F., Liu, Y.-D., Gu, J.-D., Lu, S.-G., Shi, L., Lu, Q., and Shen, T.-T. (2012). Biodegradation of benzene homologues in contaminated sediment of the East China Sea. *Bioresour. Technol.* 124, 129-136. doi: 10.1016/j.biortech.2012.08.033.
- Liu, Z.P., Wang, B.J., Liu, Y.H., and Liu, S.J. (2005). *Novosphingobium taihuense* sp nov., a novel aromatic-compound-degrading bacterium isolated from Taihu Lake, China. *Int. J. Syst. Evol. Microbiol.* 55, 1229-1232. doi: 10.1099/ijs.0.63468-0.
- Lv, X.-L., Xie, B.-S., Cai, M., Geng, S., Tang, Y.-Q., Wang, Y.-N., Cui, H.-L., Liu, X.-Y., Ye, S.-Y., and Wu, X.-L. (2014). *Glycocaulis albus* sp nov., a moderately halophilic dimorphic prosthecate bacterium isolated from petroleum-contaminated saline soil. *Int. J. Syst. Evol. Microbiol.* 64, 3181-3187. doi: 10.1099/ijs.0.063537-0.
- Müller, B., Sun, L., and Schnürer, A. (2013). First insights into the syntrophic acetate-oxidizing bacteria – a genetic study. *MicrobiologyOpen* 2, 35-53. doi: 10.1002/mbo3.50.
- Ma, Y.F., Wang, L., and Shao, Z.Z. (2006). *Pseudomonas*, the dominant polycyclic aromatic hydrocarbon-degrading bacteria isolated from Antarctic soils and the role of large

- plasmids in horizontal gene transfer. *Environ. Microbiol.* 8, 455-465. doi: 10.1111/j.1462-2920.2005.00911.x.
- Mechichi, T., Stackebrandt, E., Gad'on, N., and Fuchs, G. (2002). Phylogenetic and metabolic diversity of bacteria degrading aromatic compounds under denitrifying conditions, and description of *Thauera phenylacetica* sp nov., *Thauera aminoaromatica* sp nov., and *Azoarcus buckelii* sp nov. *Arch. Microbiol.* 178, 26-35. doi: 10.1007/s00203-002-0422-6.
- Mehboob, F., Junca, H., Schraa, G., and Stams, A.J.M. (2009). Growth of *Pseudomonas chloritidismutans* AW-1^T on *n*-alkanes with chlorate as electron acceptor. *Appl. Microbiol. Biotechnol.* 83, 739-747. doi: 10.1007/s00253-009-1985-9.
- Mino, S., Kudo, H., Arai, T., Sawabe, T., Takai, K., and Nakagawa, S. (2014). *Sulfurovum aggregans* sp nov., a hydrogenoxidizing, thiosulfate-reducing chemolithoautotroph within the *Epsilonproteobacteria* isolated from a deep-sea hydrothermal vent chimney, and an emended description of the genus *Sulfurovum*. *Int. J. Syst. Evol. Microbiol.* 64, 3195-3201. doi: 10.1099/ijs.0.065094-0.
- Miroshnichenko, M.L., L'haridon, S., Jeanthon, C., Antipov, A.N., Kostrikina, N.A., Tindall, B.J., Schumann, P., Spring, S., Stackebrandt, E., and Bonch-Osmolovskaya, E.A. (2003a). *Oceanithermus profundus* gen. nov., sp nov., a thermophilic, microaerophilic, facultatively chemolithoheterotrophic bacterium from a deep-sea hydrothermal vent. *Int. J. Syst. Evol. Microbiol.* 53, 747-752. doi: 10.1099/ijs.0.02367-0.
- Miroshnichenko, M.L., L'haridon, S.L., Nercessian, O., Antipov, A.N., Kostrikina, N.A., Tindall, B.J., Schumann, P., Spring, S., Stackebrandt, E., Bonch-Osmolovskaya, E.A., and Jeanthon, C. (2003b). *Vulcanithermus mediatlanticus* gen. nov., sp nov., a novel member of the family Thermaceae from a deep-sea hot vent. *Int. J. Syst. Evol. Microbiol.* 53, 1143-1148. doi: 10.1099/ijs.0.02579-0.
- Nesbo, C.L., Bradnan, D.M., Adebusuyi, A., Dlutek, M., Petrus, A.K., Foght, J., Doolittle, W.F., and Noll, K.M. (2012). *Mesotoga prima* gen. nov., sp nov., the first described mesophilic species of the *Thermotogales*. *Extremophiles* 16, 387-393. doi: 10.1007/s00792-012-0437-0.
- Niharika, N., Moskalikova, H., Kaur, J., Sedlackova, M., Hampl, A., Damborsky, J., Prokop, Z., and Lal, R. (2013). *Novosphingobium barchaimii* sp nov., isolated from hexachlorocyclohexane-contaminated soil. *Int. J. Syst. Evol. Microbiol.* 63, 667-672. doi: 10.1099/ijs.0.039826-0.
- Nolla-Ardevol, V., Strous, M., and Tegetmeyer, H.E. (2015). Anaerobic digestion of the microalga *Spirulina* at extreme alkaline conditions: biogas production, metagenome, and metatranscriptome. *Front. Microbio.* 6. doi: 10.3389/fmicp.2015.00597.
- Pan, X.-C., Geng, S., Lv, X.-L., Mei, R., Jiangyang, J.-H., Wang, Y.-N., Xu, L., Liu, X.-Y., Tang, Y.-Q., Wang, G.-J., and Wu, X.-L. (2015). *Defluviimonas alba* sp nov., isolated from an oilfield. *Int. J. Syst. Evol. Microbiol.* 65, 1805-1811. doi: 10.1099/ijs.0.000181.
- Rosenberg, E., Delong, E.F., Lory, S., Stackebrandt, E., and Thompson, F. (2014). *The Prokaryotes: Other Major Lineages of Bacteria and The Archaea*. Springer Berlin Heidelberg.
- Salinas, M.B., Fardeau, M.L., Cayol, J.L., Casalot, L., Patel, B.K.C., Thomas, P., Garcia, J.L., and Ollivier, B. (2004). *Petrobacter succinatimandens* gen. nov., sp nov., a

- moderately thermophilic, nitrate-reducing bacterium isolated from an Australian oil well. *Int. J. Syst. Evol. Microbiol.* 54, 645-649. doi: 10.1099/ijs.0.02732-0.
- Sohn, J.H., Kwon, K.K., Kang, J.H., Jung, H.B., and Kim, S.J. (2004). *Novosphingobium pentaromativorans* sp nov., a high-molecular-mass polycyclic aromatic hydrocarbon-degrading bacterium isolated from estuarine sediment. *Int. J. Syst. Evol. Microbiol.* 54, 1483-1487. doi: 10.1099/ijs.0.02945-0.
- Song, B.K., Palleroni, N.J., Kerkhof, L.J., and Haggblom, M.M. (2001). Characterization of halobenzoate-degrading, denitrifying *Azoarcus* and *Thauera* isolates and description of *Thauera chlorobenzoica* sp nov. *Int. J. Syst. Evol. Microbiol.* 51, 589-602.
- Sun, W., and Cupples, A.M. (2012). Diversity of Five Anaerobic Toluene-Degrading Microbial Communities Investigated Using Stable Isotope Probing. *Appl. Environ. Microbiol.* 78, 972-980. doi: 10.1128/aem.06770-11.
- Takai, K., Kobayashi, H., Nealson, K.H., and Horikoshi, K. (2003). *Deferribacter desulfuricans* sp nov., a novel sulfur-, nitrate- and arsenate-reducing thermophile isolated from a deep-sea hydrothermal vent. *Int. J. Syst. Evol. Microbiol.* 53, 839-846. doi: 10.1099/ijs.0.02479-0.
- Takai, K., Moyer, C.L., Miyazaki, M., Nogi, Y., Hirayama, H., Nealson, K.H., and Horikoshi, K. (2005). *Marinobacter alkaliphilus* sp nov., a novel alkaliphilic bacterium isolated from seafloor alkaline serpentine mud from Ocean Drilling Program Site 1200 at South Chamorro Seamount, Mariana Forearc. *Extremophiles* 9, 17-27. doi: 10.1007/s00792-004-0416-1.
- Tiquia, S.M. (2010). Salt-adapted bacteria isolated from the Rouge River and potential for degradation of contaminants and biotechnological applications. *Environ. Technol.* 31, 967-978. doi: 10.1080/09593331003706226.
- Urios, L., Agogue, H., Lesongeur, F., Stackebrandt, E., and Lebaron, P. (2006). *Balneola vulgaris* gen. nov., sp nov., a member of the phylum *Bacteroidetes* from the north-western Mediterranean Sea. *Int. J. Syst. Evol. Microbiol.* 56, 1883-1887. doi: 10.1099/ijs.0.64285-0.
- Urios, L., Intertaglia, L., Lesongeur, F., and Lebaron, P. (2008). *Balneola alkaliphila* sp nov, a marine bacterium isolated from the Mediterranean Sea. *Int. J. Syst. Evol. Microbiol.* 58, 1288-1291. doi: 10.1099/ijs.0.65555-0.
- Wentzel, A., Ellingsen, T.E., Kotlar, H.-K., Zotchev, S.B., and Throne-Holst, M. (2007). Bacterial metabolism of long-chain *n*-alkanes. *Appl. Microbiol. Biotechnol.* 76, 1209-1221. doi: 10.1007/s00253-007-1119-1.
- Zhang, Q., Wang, D., Li, M., Xiang, W.-N., and Achal, V. (2014). Isolation and characterization of diesel degrading bacteria, *Sphingomonas* sp and *Acinetobacter junii* from petroleum contaminated soil. *Front. Earth Sci.* 8, 58-63. doi: 10.1007/s11707-013-0415-6.
- Zhang, Z., Hou, Z., Yang, C., Ma, C., Tao, F., and Xu, P. (2011). Degradation of *n*-alkanes and polycyclic aromatic hydrocarbons in petroleum by a newly isolated *Pseudomonas aeruginosa* DQ8. *Bioresour. Technol.* 102, 4111-4116. doi: 10.1016/j.biortech.2010.12.064.

Table S7. Statistical significance test based on unweighted UniFrac distance matrix which obtained from beta diversity analysis

		anosim		adonis	
		<i>R</i> statistic	<i>p</i> -value	<i>R</i> ²	<i>p</i> -value
bacteria	Group	0.5137**	0.007**	0.5773**	0.003**
	pH	0.1531	0.070	0.0949*	0.016*
	Phase	-0.0049	0.493	0.0741	0.625
	Temperature	0.5257**	0.002**	0.2001**	0.001**
archaea	Group	0.3255	0.050	0.5963*	0.024*
	pH	0.2297*	0.029*	0.1107*	0.034*
	Phase	0.2284*	0.020*	0.1142*	0.022*
	Temperature	0.1967	0.101	0.1948*	0.038*
methanogen	Group	0.3176*	0.031*	0.6302*	0.017*
	pH	0.0378	0.280	0.1054	0.090
	Phase	0.0894	0.115	0.0964	0.147
	Temperature	0.3421*	0.016*	0.2430**	0.003**

Scores with *p*-value less than 0.05 were labeled with one star, scores with *p*-value less than 0.01 were labeled with two stars.

Organismal Systems/Digestive system/04973 Carbohydrate digestion and absorption 0.03% 0.03% 0.02% 0.03% 0.04% 0.04% 0.04% 0.04% 0.03% 0.04% 0.03% 0.03% 0.02% 0.02% 0.03%

b

Tables with 16 columns (Samples, average, P2A, P2B, P2C, P2D, P2E, P2F, P2G, P2H, P2I, P2J, P2K, P2L, P2M, P2N) and multiple rows of biological data.

