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

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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 pidemont 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%), *Methanolobus* (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

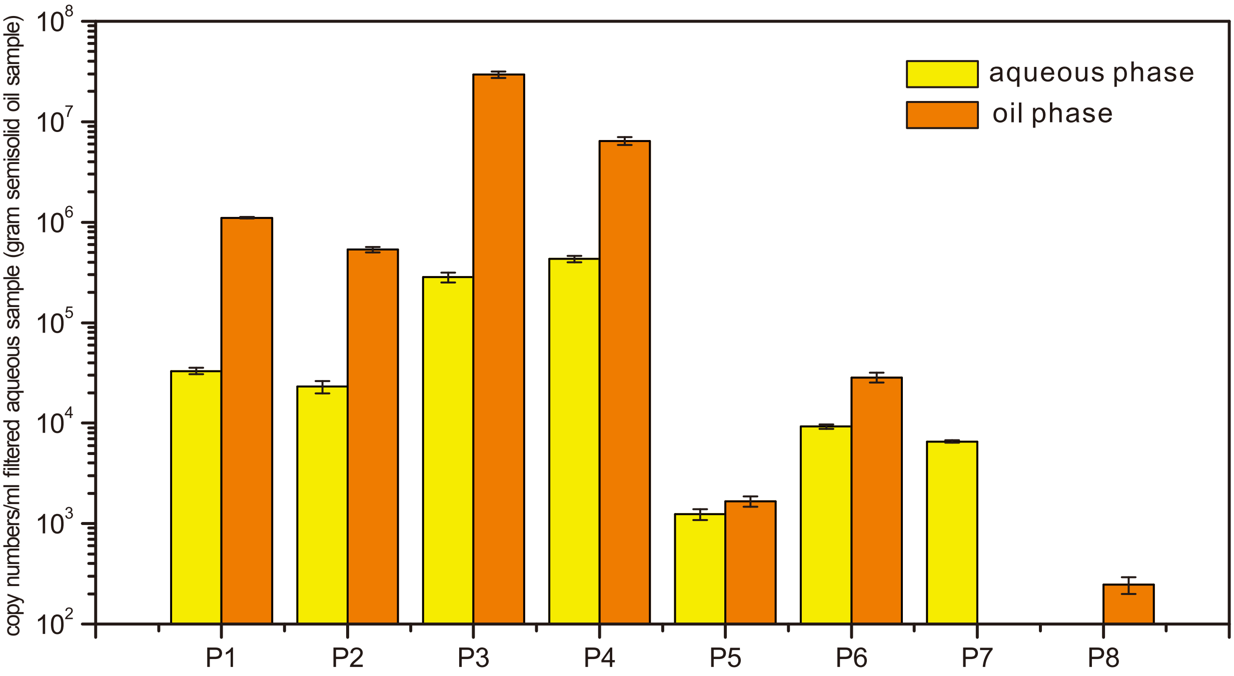


Figure S1. *mcrA* gene abundance of 14 aqueous and oil phase samples. Vertical coordinate was drawn in log-normalized label. The aqueous samples *mcrA* gene quantities were gene copy numbers/ml filtered aqueous sample; the oil samples *mcrA* gene quantities were gene copy numbers/gram semisolid oil sample.

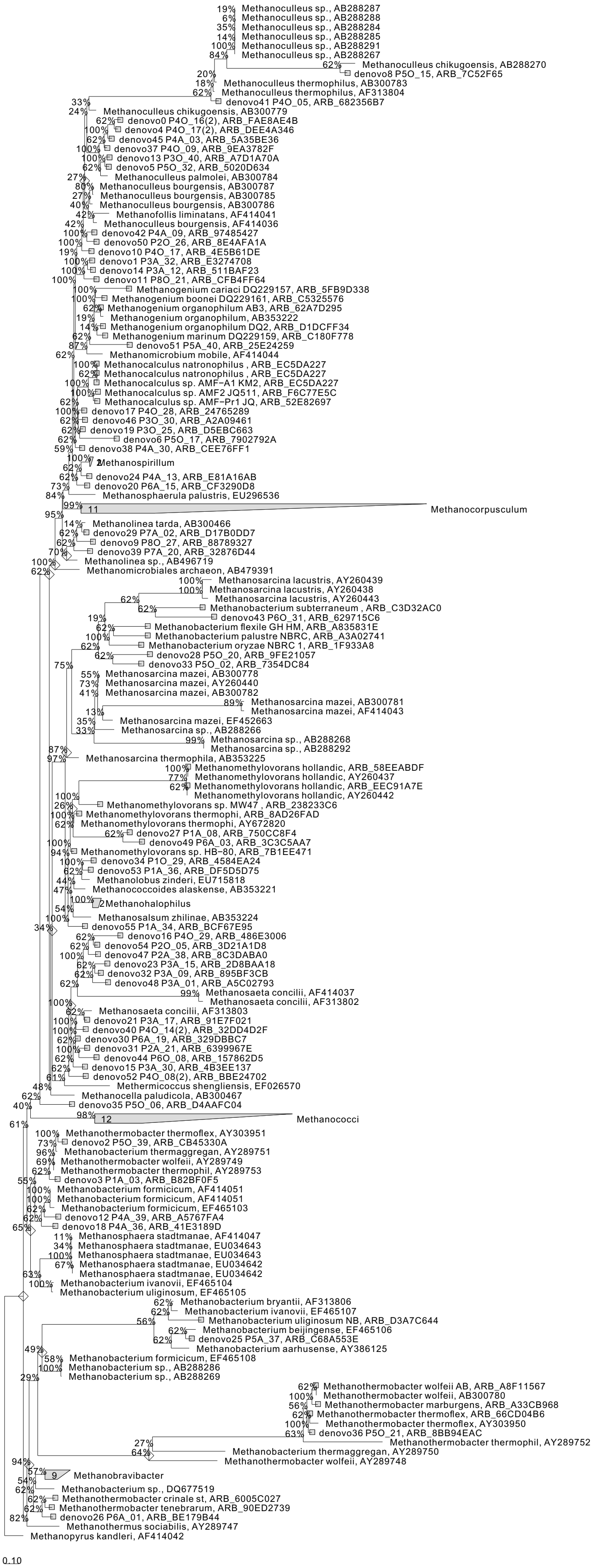


Figure S2. Phylogenetic tree based on clone library *mcrA* gene and reference gene sequences. The OTU representative *mcrA* gene clone sequences were obtained by 0.05 cutoff on nucleotide level, and then inserted into *mcrA* gene ARB database by maximum parsimony method without changing the initial tree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

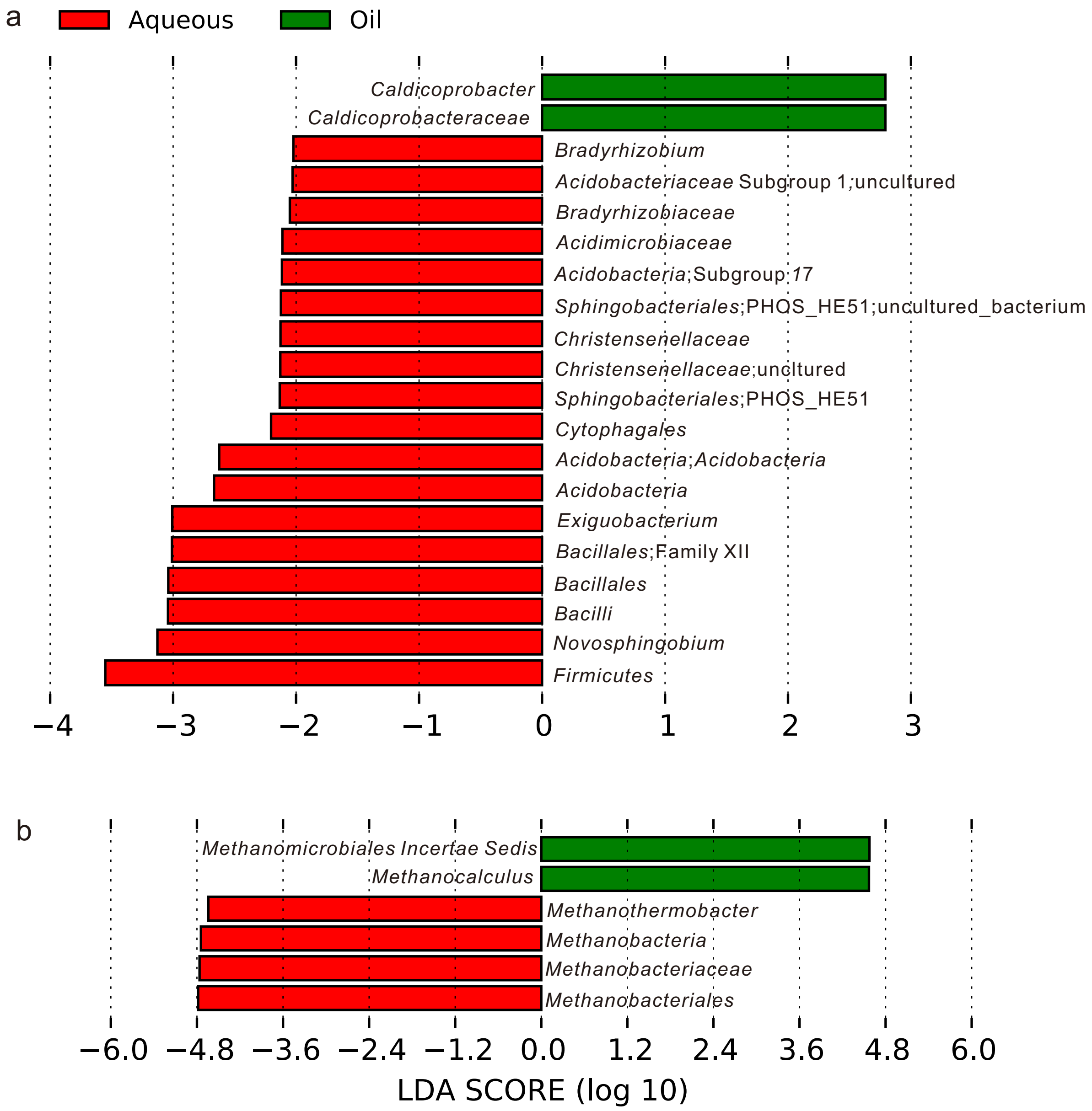


Figure S3. Differentially distributed features of microbial taxon abundance in aqueous and oil phases. LEfSe analysis with LDA effect score was applied. (a) bacterial community feature; (b) archaeal community feature.

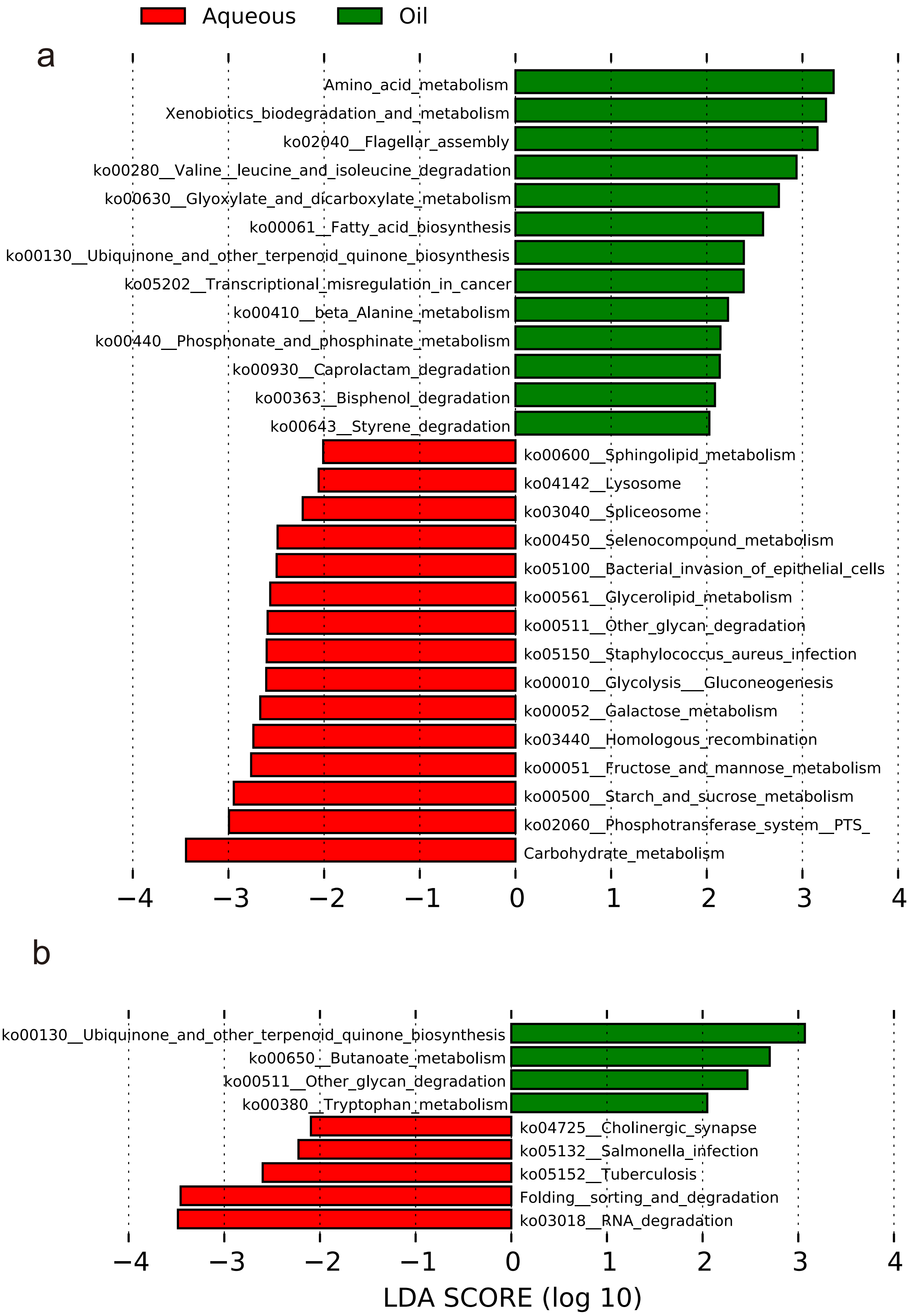


Figure S4. Differentially distributed feature of functional profiles in aqueous and oil phases. LEfSe analysis results based on the predicted functional profiles by Tax4Fun. (a) bacterial community feature; (b) archaeal community feature.

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

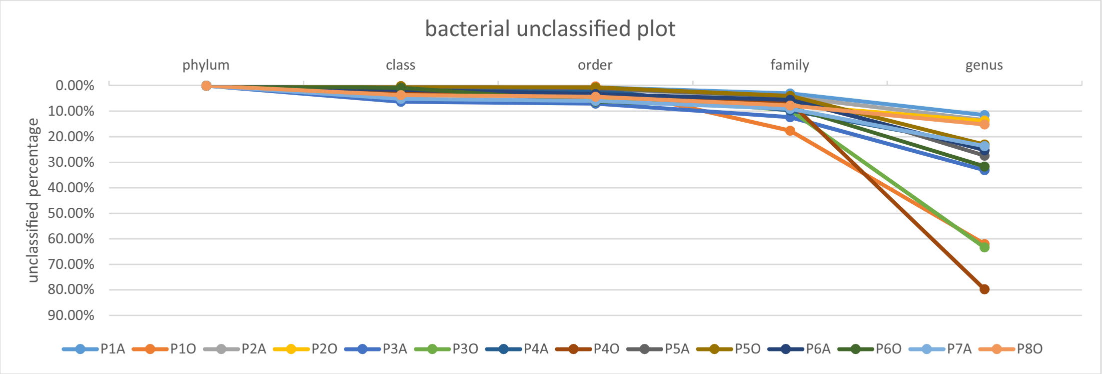
Methanogen (*mcrA* gene clone library)

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.

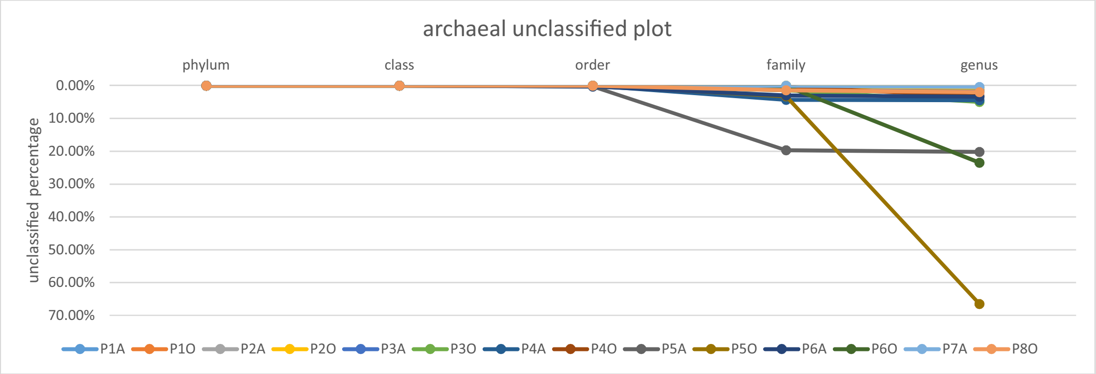
a

	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%

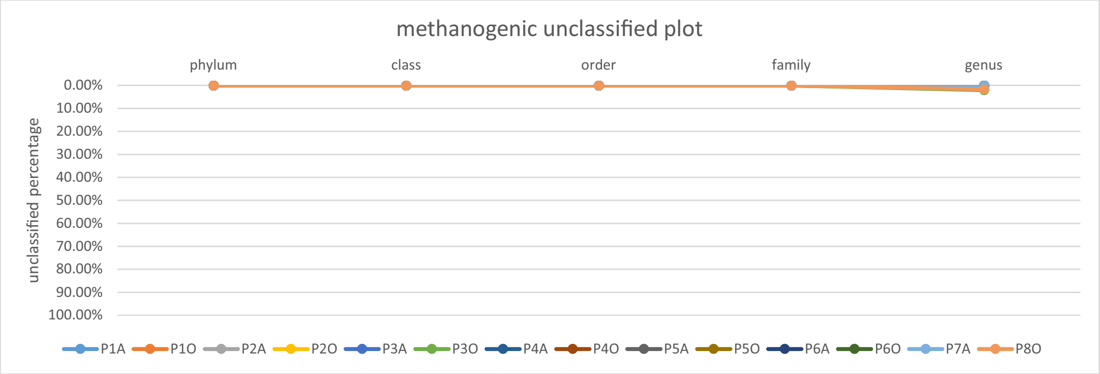


Table S3. Taxonomic composition of aqueous and oil phase samples based on MiSeq 16S rRNA gene sequencing. a) bacterial community composition in genus level; b) archaeal community composition in genus level.

a

Taxon	average	P1A	P1O	P2A	P2O	P3A	P3O	P4A	P4O	P5A	P5O	P6A	P6O	P7A	P8O
D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Pseudomonadales;D_4__Pseudomonadaceae;D_5__Pseudomonas	16.12%	27.57%	1.93%	38.14%	20.10%	4.39%	4.70%	2.28%	1.85%	6.42%	6.08%	31.21%	23.75%	22.90%	34.39%
D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Pseudomonadales;D_4__Moraxellaceae;D_5__Acinetobacter	9.94%	2.06%	1.41%	28.00%	39.38%	2.54%	1.75%	52.47%	0.87%	1.51%	1.49%	1.21%	1.67%	3.11%	1.72%
D_0__Bacteria;D_1__Proteobacteria;D_2__Betaproteobacteria;D_3__Hydrogenophilales;D_4__Hydrogenophilaceae;D_5__uncultured	5.44%	0.79%	0.95%	0.62%	0.77%	0.54%	21.61%	0.67%	45.12%	0.90%	0.75%	0.79%	0.84%	1.21%	0.62%
D_0__Bacteria;D_1__Bacteroidetes;D_2__Bacteroidia;D_3__Bacteroidales;D_4__Porphyromonadaceae;D_5__Proteiniphilum	3.06%	4.47%	3.39%	6.32%	9.08%	0.57%	1.43%	0.87%	0.54%	5.59%	0.95%	2.16%	1.97%	4.05%	1.49%
D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Alteromonadales;D_4__Alteromonadaceae;D_5__Marinobacter	2.91%	0.43%	0.38%	0.36%	0.52%	0.29%	1.49%	0.28%	0.20%	10.19%	22.35%	0.25%	0.39%	0.28%	3.41%
D_0__Bacteria;D_1__Deferribacteres;D_2__Deferribacteres;D_3__Deferribacterales;D_4__Deferribacteraceae;D_5__uncultured	2.74%	0.59%	0.46%	0.31%	0.34%	1.20%	3.96%	0.75%	1.93%	7.22%	10.32%	0.67%	10.11%	0.34%	0.16%
D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Oceanospirillales;D_4__Oceanospirillaceae;D_5__Nitrincola	2.69%	0.28%	0.62%	0.79%	3.03%	0.26%	0.38%	0.28%	0.20%	12.45%	17.60%	0.33%	0.46%	0.59%	0.34%
D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Pseudomonadales;D_4__Moraxellaceae;D_5__Psychrobacter	2.60%	32.96%	0.13%	0.29%	0.29%	0.13%	0.29%	0.31%	0.18%	0.31%	0.20%	0.29%	0.33%	0.52%	0.21%
D_0__Bacteria;D_1__Deinococcus-Thermus;D_2__Deinococci;D_3__Thermales;D_4__Thermaceae;D_5__uncultured bacterium	2.48%	0.26%	28.26%	0.57%	0.61%	0.34%	0.57%	0.52%	0.28%	0.75%	1.11%	0.18%	0.54%	0.36%	0.33%
D_0__Bacteria;D_1__Proteobacteria;D_2__Betaproteobacteria;D_3__Rhodocyclales;D_4__Rhodocyclaceae;D_5__Thauera	2.46%	0.56%	0.29%	0.48%	0.48%	0.31%	0.59%	0.56%	0.75%	0.44%	0.43%	3.83%	15.24%	10.14%	0.38%
D_0__Bacteria;D_1__Proteobacteria;D_2__Deltaproteobacteria;D_3__Bdellovibrionales;D_4__Bacteriovoracaceae;D_5__uncultured	2.34%	0.33%	0.25%	0.28%	0.28%	0.56%	12.12%	0.21%	16.94%	0.38%	0.20%	0.23%	0.33%	0.36%	0.25%
D_0__Bacteria;D_1__Proteobacteria;D_2__Epsilonproteobacteria;D_3__Campylobacterales;D_4__Helicobacteraceae;D_5__Sulfurovum	1.72%	0.25%	0.15%	0.25%	0.11%	21.33%	0.39%	0.25%	0.39%	0.20%	0.20%	0.11%	0.13%	0.18%	0.18%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhodobacterales;D_4__Rhodobacteraceae;D_5__Defluviimonas	1.72%	1.46%	15.56%	0.33%	0.25%	0.13%	0.29%	0.23%	0.23%	1.92%	0.72%	0.23%	0.34%	0.98%	1.38%
D_0__Bacteria;D_1__Proteobacteria;D_2__Deltaproteobacteria;D_3__Syntrophobacterales;D_4__Syntrophaceae;D_5__Smithella	1.55%	0.20%	0.02%	0.18%	0.13%	4.95%	5.42%	0.66%	9.06%	0.23%	0.16%	0.18%	0.20%	0.20%	0.11%
D_0__Bacteria;D_1__Chloroflexi;D_2__Anaerolineae;D_3__Anaerolineales;D_4__Anaerolineaceae;D_5__uncultured	1.35%	0.23%	0.52%	0.38%	0.36%	4.85%	3.80%	1.15%	1.38%	0.52%	0.26%	3.15%	1.13%	0.98%	0.16%
D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Oceanospirillales;D_4__Halomonadaceae;D_5__Halomonas	1.32%	0.33%	0.29%	0.54%	1.26%	0.11%	0.36%	0.11%	0.08%	8.40%	5.96%	0.38%	0.26%	0.18%	0.20%
D_0__Bacteria;D_1__Bacteroidetes;D_2__Cytophagia;D_3__Order III;D_4__Unknown Family;D_5__Balneola	1.27%	0.08%	15.83%	0.15%	0.11%	0.07%	0.15%	0.20%	0.05%	0.26%	0.56%	0.03%	0.13%	0.11%	0.10%
D_0__Bacteria;D_1__Bacteroidetes;D_2__VC2.1 Bac22;D_3__uncultured bacterium;D_4__uncultured bacterium;D_5__uncultured bacterium	0.96%	0.03%	0.07%	0.66%	5.08%	0.13%	0.38%	0.05%	0.02%	0.15%	0.20%	1.44%	4.90%	0.25%	0.05%
D_0__Bacteria;D_1__Spirochaetae;D_2__Spirochaetes;D_3__Spirochaetales;D_4__Spirochaetaceae;D_5__uncultured	0.95%	0.07%	0.11%	0.18%	0.08%	0.18%	0.48%	5.96%	2.62%	0.21%	0.08%	1.06%	0.74%	1.47%	0.10%
D_0__Bacteria;D_1__Proteobacteria;D_2__Betaproteobacteria;D_3__Burkholderiales;D_4__Comamonadaceae;D_5__Simplicispira	0.93%	0.23%	0.10%	3.47%	1.79%	0.26%	0.21%	0.10%	0.11%	0.49%	0.33%	2.87%	1.29%	1.65%	0.15%
D_0__Bacteria;D_1__Thermotogae;D_2__Thermotogae;D_3__Thermotogales;D_4__Thermotogaceae;D_5__Mesotoga	0.92%	2.31%	0.18%	0.05%	0.08%	6.21%	3.19%	0.15%	0.10%	0.08%	0.11%	0.16%	0.20%	0.03%	0.05%
D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Family XI;D_5__uncultured	0.84%	1.77%	0.13%	0.11%	0.05%	0.08%	0.34%	0.03%	0.08%	4.49%	0.20%	3.82%	0.23%	0.31%	0.11%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhodobacterales;D_4__Rhodobacteraceae;D_5__Stappia	0.76%	0.11%	0.08%	0.10%	0.07%	0.05%	0.03%	0.07%	0.05%	0.13%	0.18%	0.92%	0.38%	0.10%	8.37%
D_0__Bacteria;D_1__Candidate division JS1;D_2__Atribacteria bacterium SCGC AB-164-M20;D_3__Atribacteria bacterium SCGC AB-164-M20;D_4__Atribacteria bacterium SCGC AB-164-M20;D_5__Atribacteria bacterium SCGC AB-164-M20	0.75%	0.02%	0.05%	0.02%	0.02%	9.57%	0.18%	0.10%	0.05%	0.07%	0.07%	0.10%	0.07%	0.10%	0.07%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Sphingomonadales;D_4__Sphingomonadaceae;D_5__Novosphingobium	0.74%	0.13%	0.08%	0.15%	0.15%	0.18%	0.16%	4.78%	0.13%	0.11%	0.03%	1.08%	0.07%	3.24%	0.10%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Caulobacterales;D_4__Hyphomonadaceae;D_5__Glycocaulis	0.72%	0.08%	0.07%	0.07%	0.03%	0.08%	0.10%	0.07%	0.10%	0.20%	0.93%	0.10%	0.05%	0.11%	8.06%
D_0__Bacteria;D_1__Bacteroidetes;D_2__Sphingobacteriia;D_3__Sphingobacteriales;D_4__WCHB1-69;D_5__uncultured bacterium	0.65%	0.03%	0.87%	2.00%	0.23%	0.15%	2.51%	0.20%	0.20%	0.07%	0.08%	0.44%	1.56%	0.70%	0.08%
D_0__Bacteria;D_1__Bacteroidetes;D_2__Bacteroidia;D_3__Bacteroidales;D_4__ML635J-40 aquatic group;D_5__uncultured bacterium	0.64%	0.03%	0.02%	0.67%	0.34%	0.07%	0.08%	0.07%	0.02%	2.42%	2.79%	0.23%	2.13%	0.03%	0.13%
D_0__Bacteria;D_1__Proteobacteria;D_2__Epsilonproteobacteria;D_3__Campylobacterales;D_4__Helicobacteraceae;D_5__Wolinella	0.62%	0.07%	0.03%	0.07%	0.00%	0.08%	0.08%	0.05%	0.02%	0.10%	0.05%	6.34%	0.95%	0.82%	0.05%
D_0__Bacteria;D_1__Firmicutes;D_2__Bacilli;D_3__Bacillales;D_4__Family XII;D_5__Exiguobacterium	0.61%	0.20%	0.02%	0.07%	0.02%	0.05%	0.03%	3.41%	0.05%	0.03%	0.00%	4.18%	0.05%	0.38%	0.08%
D_0__Bacteria;D_1__Actinobacteria;D_2__Coriobacteriia;D_3__Coriobacteriales;D_4__Coriobacteriaceae;D_5__uncultured	0.60%	0.10%	0.05%	0.02%	0.03%	6.78%	0.64%	0.11%	0.07%	0.16%	0.07%	0.13%	0.13%	0.05%	0.13%
D_0__Bacteria;D_1__Bacteroidetes;D_2__Cytophagia;D_3__Order III;D_4__BIgi5;D_5__uncultured bacterium	0.58%	0.05%	6.91%	0.07%	0.16%	0.07%	0.05%	0.07%	0.05%	0.13%	0.28%	0.07%	0.08%	0.03%	0.05%
D_0__Bacteria;D_1__Candidate division JS1;D_2__uncultured bacterium;D_3__uncultured bacterium;D_4__uncultured bacterium;D_5__uncultured bacterium	0.55%	0.08%	0.02%	0.08%	0.10%	2.29%	0.10%	0.21%	0.15%	0.08%	0.02%	0.07%	0.07%	4.37%	0.11%
D_0__Bacteria;D_1__Proteobacteria;D_2__Epsilonproteobacteria;D_3__Campylobacterales;D_4__Campylobacteraceae;D_5__Arcobacter	0.55%	2.11%	0.15%	0.15%	0.03%	0.05%	0.08%	0.02%	0.05%	0.48%	2.82%	0.02%	0.08%	1.61%	0.07%
D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Peptococcaceae;D_5__Desulfosporosinus	0.54%	0.07%	0.08%	0.00%	0.02%	6.90%	0.15%	0.03%	0.02%	0.02%	0.00%	0.18%	0.03%	0.03%	0.03%
D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Gammaproteobacteria Incertae Sedis;D_4__Unknown Family;D_5__Thiohalomonas	0.50%	0.07%	0.08%	0.05%	0.07%	0.31%	0.48%	5.16%	0.34%	0.08%	0.05%	0.05%	0.08%	0.10%	0.03%
D_0__Bacteria;D_1__Bacteroidetes;D_2__Bacteroidia;D_3__Bacteroidales;D_4__Rikenellaceae;D_5__Blvii28 wastewater-sludge group	0.49%	0.08%	0.03%	0.02%	0.07%	0.64%	0.88%	0.03%	0.34%	3.87%	0.52%	0.05%	0.08%	0.03%	0.15%
D_0__Bacteria;D_1__Acidobacteria;D_2__Acidobacteria;D_3__Subgroup 4;D_4__RB41;D_5__uncultured bacterium	0.48%	0.52%	0.44%	0.57%	0.23%	0.56%	0.67%	0.38%	0.28%	0.49%	0.46%	0.38%	0.41%	0.72%	0.54%
D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Xanthomonadales;D_4__Xanthomonadaceae;D_5__Silanimonas	0.45%	0.07%	4.83%	0.05%	0.13%	0.05%	0.10%	0.13%	0.10%	0.23%	0.31%	0.03%	0.18%	0.03%	0.05%
D_0__Bacteria;D_1__Bacteroidetes;D_2__Sphingobacteriia;D_3__Sphingobacteriales;D_4__Chitinophagaceae;D_5__uncultured	0.45%	0.34%	0.43%	0.62%	0.25%	0.44%	0.52%	0.36%	0.23%	0.61%	0.38%	0.54%	0.52%	0.61%	0.39%
D_0__Bacteria;D_1__Proteobacteria;D_2__Epsilonproteobacteria;D_3__Campylobacterales;D_4__Campylobacteraceae;D_5__Sulfurospirillum	0.44%	0.03%	0.07%	0.02%	0.49%	0.05%	0.03%	0.08%	0.00%	1.18%	3.96%	0.05%	0.03%	0.03%	0.07%
D_0__Bacteria;D_1__Proteobacteria;D_2__Betaproteobacteria;D_3__Hydrogenophilales;D_4__Hydrogenophilaceae;D_5__Tepidiphilus	0.41%	0.20%	0.10%	1.21%	0.56%	0.11%	0.25%	0.03%	0.08%	0.75%	1.11%	0.05%	0.07%	1.26%	0.02%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhodobacterales;D_4__Rhodobacteraceae;D_5__Pannonibacter	0.41%	0.02%	0.07%	0.05%	0.08%	0.07%	0.03%	0.07%	0.02%	0.11%	2.41%	0.82%	1.98%	0.05%	0.03%
D_0__Bacteria;D_1__Proteobacteria;D_2__Betaproteobacteria;D_3__Rhodocyclales;D_4__Rhodocyclaceae;D_5__Azoarcus	0.40%	0.07%	0.05%	0.08%	0.08%	0.07%	0.10%	0.03%	0.02%	0.05%	0.07%	0.23%	2.20%	2.51%	0.07%
D_0__Bacteria;D_1__Acidobacteria;D_2__Acidobacteria;D_3__Subgroup 6;D_4__uncultured bacterium;D_5__uncultured bacterium	0.36%	0.34%	0.28%	0.33%	0.31%	0.28%	0.41%	0.41%	0.38%	0.36%	0.20%	0.44%	0.41%	0.49%	0.39%
D_0__Bacteria;D_1__Proteobacteria;D_2__Deltaproteobacteria;D_3__Syntrophobacterales;D_4__Syntrophaceae;D_5__uncultured	0.34%	0.05%	0.00%	0.05%	0.07%	0.82%	2.05%	0.16%	1.34%	0.05%	0.08%	0.05%	0.03%	0.03%	0.00%
D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Syntrophomonadaceae;D_5__Thermosyntropha	0.33%	0.03%	0.00%	0.05%	0.00%	0.00%	0.07%	0.05%	0.05%	0.10%	0.07%	0.02%	0.13%	0.02%	4.11%
D_0__Bacteria;D_1__Firmicutes;D_2__Erysipelotrichia;D_3__Erysipelotrichales;D_4__Erysipelotrichaceae;D_5__Erysipelothrix	0.33%	0.07%	0.05%	0.49%	2.13%	0.03%	0.05%	0.02%	0.00%	0.03%	0.05%	0.25%	0.08%	1.31%	0.05%
D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Family XI;D_5__Soehngenia	0.32%	0.02%	0.05%	0.02%	0.02%	0.03%	0.00%	0.07%	0.00%	2.00%	0.25%	1.57%	0.29%	0.08%	0.10%
D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Caldicoprobacteraceae;D_5__Caldicoprobacter	0.31%	0.02%	0.07%	0.02%	0.05%	0.00%	0.05%	0.03%	0.05%	0.02%	0.02%	0.43%	0.15%	0.02%	3.49%
D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Clostridiales Incertae Sedis;D_5__Dethiosulfatibacter	0.30%	0.05%	0.00%	0.05%	0.03%	0.08%	0.15%	0.05%	0.02%	0.97%	0.02%	2.56%	0.25%	0.00%	0.05%
D_0__Bacteria;D_1__Proteobacteria;D_2__Deltaproteobacteria;D_3__Desulfobacterales;D_4__Desulfobulbaceae;D_5__Desulfobulbus	0.28%	0.20%	0.00%	0.02%	0.03%	0.02%	0.08%	0.05%	0.02%	1.16%	0.03%	1.16%	0.80%	0.05%	0.36%
D_0__Bacteria;D_1__Spirochaetae;D_2__Spirochaetes;D_3__Spirochaetales;D_4__Spirochaetaceae;D_5__Spirochaeta	0.28%	0.13%	0.05%	0.03%	0.03%	0.70%	1.06%	0.11%	0.23%	0.69%	0.29%	0.29%	0.08%	0.08%	0.16%
D_0__Bacteria;D_1__Proteobacteria;D_2__Betaproteobacteria;D_3__Nitrosomonadales;D_4__Nitrosomonadaceae;D_5__uncultured	0.28%	0.25%	0.20%	0.21%	0.23%	0.23%	0.31%	0.23%	0.36%	0.41%	0.31%	0.31%	0.29%	0.39%	0.15%
D_0__Bacteria;D_1__Bacteroidetes;D_2__Flavobacteriia;D_3__Flavobacteriales;D_4__Flavobacteriaceae;D_5__Salinimicrobium	0.27%	3.46%	0.03%	0.02%	0.03%	0.03%	0.02%	0.02%	0.00%	0.05%	0.02%	0.02%	0.02%	0.05%	0.02%
D_0__Bacteria;D_1__Synergistetes;D_2__Synergistia;D_3__Synergistales;D_4__Synergistaceae;D_5__Thermovirga	0.26%	0.57%	0.00%	0.03%	0.07%	1.08%	0.34%	1.10%	0.08%	0.03%	0.10%	0.20%	0.02%	0.02%	0.03%
D_0__Bacteria;D_1__Proteobacteria;D_2__Betaproteobacteria;D_3__Burkholderiales;D_4__Comamonadaceae;D_5__Variovorax	0.26%	0.05%	0.05%	0.03%	0.05%	0.03%	0.13%	0.20%	0.05%	0.03%	0.07%	0.02%	0.54%	2.29%	0.10%
D_0__Bacteria;D_1__Chloroflexi;D_2__Anaerolineae;D_3__Anaerolineales;D_4__Anaerolineaceae;D_5__Ornatilinea	0.26%	0.07%	0.02%	0.05%	0.05%	0.02%	0.15%	0.88%	0.64%	0.00%	0.00%	1.06%	0.51%	0.11%	0.02%
D_0__Bacteria;D_1__Proteobacteria;D_2__Betaproteobacteria;D_3__Burkholderiales;D_4__Comamonadaceae;D_5__Acidovorax	0.25%	0.08%	0.00%	0.08%	0.03%	0.03%	0.02%	0.02%	0.00%	0.05%	0.07%	1.74%	0.56%	0.84%	0.02%
D_0__Bacteria;D_1__Acidobacteria;D_2__Acidobacteria;D_3__Acidobacteriales;D_4__Acidobacteriaceae (Subgroup 1);D_5__uncultured	0.23%	0.23%	0.23%	0.26%	0.15%	0.29%	0.18%	0.23%	0.15%	0.29%	0.20%	0.20%	0.16%	0.43%	0.23%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhizobiales;D_4__Bradyrhizobiaceae;D_5__Bradyrhizobium	0.22%	0.33%	0.16%	0.25%	0.15%	0.10%	0.18%	0.21%	0.25%	0.33%	0.20%	0.28%	0.18%	0.39%	0.15%
D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Oceanospirillales;D_4__Oceanospirillaceae;D_5__Marinobacterium	0.22%	0.10%	0.02%	0.00%	0.07%	0.05%	0.03%	0.02%	0.00%	1.13%	1.64%	0.00%	0.03%	0.00%	0.03%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Sphingomonadales;D_4__Erythrobacteraceae;D_5__Altererythrobacter	0.21%	0.05%	1.20%	0.03%	0.05%	0.08%	0.08%	0.05%	0.02%	0.07%	0.10%	0.03%	0.03%	1.10%	0.03%
D_0__Bacteria;D_1__Candidate division BRC1;D_2__uncultured organism;D_3__uncultured organism;D_4__uncultured organism;D_5__uncultured organism	0.21%	0.03%	0.03%	0.03%	0.02%	0.02%	0.13%	0.02%	0.02%	0.03%	0.02%	0.02%	0.03%	0.02%	2.49%
D_0__Bacteria;D_1__Proteobacteria;D_2__Betaproteobacteria;D_3__Hydrogenophilales;D_4__Hydrogenophilaceae;D_5__Thiobacillus	0.19%	0.05%	0.00%	0.02%	0.03%	0.03%	2.51%	0.00%	0.05%	0.00%	0.00%	0.02%	0.02%	0.00%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Caulobacterales;D_4__Hyphomonadaceae;D_5__Hyphomonas	0.19%	0.07%	0.07%	0.00%	0.03%	0.00%	0.10%	0.00%	0.03%	0.07%	0.36%	0.02%	0.38%	0.39%	1.15%
D_0__Bacteria;D_1__Bacteroidetes;D_2__Sphingobacteriia;D_3__Sphingobacteriales;D_4__Chitinophagaceae;D_5__Terrimonas	0.18%	0.11%	0.11%	0.15%	0.25%	0.20%	0.23%	0.20%	0.15%	0.31%	0.13%	0.11%	0.18%	0.23%	0.21%
D_0__Bacteria;D_1__Synergistetes;D_2__Synergistia;D_3__Synergistales;D_4__Synergistaceae;D_5__uncultured bacterium	0.18%	0.02%	0.02%	0.00%	0.02%	0.00%	0.03%	0.02%	0.02%	0.07%	0.00%	2.00%	0.28%	0.08%	0.02%
D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Xanthomonadales;D_4__uncultured;D_5__uncultured bacterium	0.18%	0.16%	0.15%	0.25%	0.26%	0.11%	0.07%	0.13%	0.26%	0.20%	0.23%	0.11%	0.16%	0.29%	0.15%
D_0__Bacteria;D_1__Chloroflexi;D_2__uncultured;D_3__uncultured bacterium;D_4__uncultured bacterium;D_5__uncultured bacterium	0.18%	0.07%	0.00%	0.00%	0.00%	0.25%	0.08%	0.08%	0.02%	0.02%	0.02%	1.28%	0.33%	0.15%	0.25%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhizobiales;D_4__Xanthobacteraceae;D_5__uncultured	0.18%	0.23%	0.07%	0.26%	0.16%	0.16%	0.29%	0.13%	0.23%	0.13%	0.13%	0.16%	0.18%	0.16%	0.16%
D_0__Bacteria;D_1__Proteobacteria;D_2__Deltaproteobacteria;D_3__GR-WP33-30;D_4__uncultured bacterium;D_5__uncultured bacterium	0.18%	0.23%	0.03%	0.16%	0.11%	0.18%	0.25%	0.20%	0.07%	0.13%	0.31%	0.20%	0.16%	0.23%	0.21%
D_0__Bacteria;D_1__Candidate division OP3;D_2__uncultured bacterium;D_3__uncultured bacterium;D_4__uncultured bacterium;D_5__uncultured bacterium	0.17%	0.00%	0.02%	0.00%	0.00%	0.18%	0.49%	0.25%	1.36%	0.02%	0.00%	0.02%	0.05%	0.03%	0.02%
D_0__Bacteria;D_1__Proteobacteria;D_2__Betaproteobacteria;D_3__Burkholderiales;D_4__Comamonadaceae;D_5__Tepidicella	0.17%	0.05%	0.02%	0.02%	0.02%	0.05%	0.00%	0.02%	0.00%	0.02%	0.03%	0.02%	0.05%	2.13%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhodobacterales;D_4__Rhodobacteraceae;D_5__Donghicola	0.16%	0.52%	0.07%	0.00%	0.00%	0.05%	0.67%	0.00%	0.02%	0.05%	0.00%	0.02%	0.02%	0.74%	0.10%
D_0__Bacteria;D_1__Planctomycetes;D_2__Planctomycetacia;D_3__Planctomycetales;D_4__Planctomycetaceae;D_5__uncultured	0.16%	0.10%	0.07%	0.10%	0.03%	0.08%	0.07%	0.10%	0.02%	0.13%	0.07%	0.05%	0.13%	0.11%	1.20%
D_0__Bacteria;D_1__Acidobacteria;D_2__Acidobacteria;D_3__Subgroup 6;D_4__uncultured Acidobacteria bacterium;D_5__uncultured Acidobacteria bacterium	0.15%	0.21%	0.15%	0.20%	0.15%	0.08%	0.20%	0.20%	0.15%	0.28%	0.13%	0.07%	0.05%	0.18%	0.11%
D_0__Bacteria;D_1__Spirochaetae;D_2__Spirochaetes;D_3__Spirochaetes Incertae Sedis;D_4__Unknown Family;D_5__Candidatus Cloacamonas	0.15%	0.00%	0.00%	0.00%	0.03%	1.69%	0.33%	0.03%	0.02%	0.00%	0.00%	0.02%	0.00%	0.02%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Deltaproteobacteria;D_3__Desulfovibrionales;D_4__Desulfovibrionaceae;D_5__Desulfovibrio	0.15%	0.00%	0.02%	0.03%	0.11%	0.03%	0.05%	0.08%	0.03%	0.18%	0.25%	0.05%	1.16%	0.03%	0.03%
D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Clostridiaceae 1;D_5__Proteiniclasticum	0.15%	0.00%	0.00%	0.02%	0.07%	0.03%	0.07%	0.00%	0.00%	1.72%	0.02%	0.02%	0.03%	0.03%	0.03%
D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Thermoanaerobacterales;D_4__Thermoanaerobacteraceae;D_5__Caldanaerobacter	0.14%	0.02%	0.02%	0.03%	0.00%	0.03%	0.02%	0.05%	0.00%	0.00%	0.00%	0.00%	0.02%	0.02%	1.82%
D_0__Bacteria;D_1__Bacteroidetes;D_2__Bacteroidia;D_3__Bacteroidales;D_4__Marinilabiaceae;D_5__uncultured	0.14%	0.02%	0.00%	0.00%	0.00%	0.00%	0.05%	0.02%	0.00%	0.02%	0.00%	1.16%	0.72%	0.03%	0.00%
D_0__Bacteria;D_1__Candidate division OD1;D_2__uncultured bacterium;D_3__uncultured bacterium;D_4__uncultured bacterium;D_5__uncultured bacterium	0.14%	0.03%	0.02%	0.03%	0.02%	0.75%	0.23%	0.33%	0.36%	0.02%	0.00%	0.00%	0.02%	0.13%	0.02%
D_0__Bacteria;D_1__Spirochaetae;D_2__Spirochaetes;D_3__NK-L14;D_4__uncultured bacterium;D_5__uncultured bacterium	0.14%	0.02%	0.00%	0.02%	0.02%	0.25%	1.46%	0.02%	0.02%	0.02%	0.11%	0.00%	0.00%	0.00%	0.02%
D_0__Bacteria;D_1__Synergistetes;D_2__Synergistia;D_3__Synergistales;D_4__Synergistaceae;D_5__uncultured	0.13%	0.57%	0.02%	0.03%	0.03%	0.02%	0.11%	0.25%	0.03%	0.26%	0.07%	0.07%	0.07%	0.25%	0.11%
D_0__Bacteria;D_1__SHA-109;D_2__uncultured bacterium;D_3__uncultured bacterium;D_4__uncultured bacterium;D_5__uncultured bacterium	0.13%	0.02%	0.00%	0.03%	0.00%	1.46%	0.00%	0.03%	0.02%	0.05%	0.07%	0.00%	0.10%	0.02%	0.02%
D_0__Bacteria;D_1__Proteobacteria;D_2__Betaproteobacteria;D_3__Burkholderiales;D_4__Burkholderiaceae;D_5__Burkholderia	0.13%	0.00%	0.02%	0.02%	0.00%	0.02%	0.05%	1.10%	0.00%	0.05%	0.03%	0.07%	0.10%	0.31%	0.03%
D_0__Bacteria;D_1__Proteobacteria;D_2__Betaproteobacteria;D_3__Burkholderiales;D_4__Comamonadaceae;D_5__uncultured	0.13%	0.02%	0.03%	0.08%	0.05%	0.11%	0.13%	0.07%	0.05%	0.05%	0.05%	0.00%	0.31%	0.75%	0.07%
D_0__Bacteria;D_1__Chloroflexi;D_2__Anaerolineae;D_3__Anaerolineales;D_4__Anaerolineaceae;D_5__Leptolinea	0.13%	0.00%	0.02%	0.02%	0.00%	0.52%	0.20%	0.20%	0.25%	0.07%	0.00%	0.03%	0.00%	0.48%	0.00%
D_0__Bacteria;D_1__Planctomycetes;D_2__Phycisphaerae;D_3__WD2101 soil group;D_4__uncultured bacterium;D_5__uncultured bacterium	0.13%	0.11%	0.11%	0.21%	0.11%	0.08%	0.20%	0.20%	0.18%	0.10%	0.05%	0.13%	0.10%	0.03%	0.13%
D_0__Bacteria;D_1__Nitrospirae;D_2__Nitrospira;D_3__Nitrospirales;D_4__Nitrospiraceae;D_5__Nitrospira	0.12%	0.16%	0.28%	0.16%	0.11%	0.10%	0.03%	0.07%	0.11%	0.13%	0.05%	0.10%	0.16%	0.13%	0.11%
D_0__Bacteria;D_1__Planctomycetes;D_2__Planctomycetacia;D_3__Planctomycetales;D_4__Planctomycetaceae;D_5__Pir4 lineage	0.12%	0.05%	0.02%	0.05%	0.11%	0.52%	0.36%	0.10%	0.03%	0.10%	0.03%	0.08%	0.05%	0.08%	0.11%
D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Xanthomonadales;D_4__Nevskiaceae;D_5__uncultured	0.12%	0.02%	1.36%	0.03%	0.05%	0.02%	0.02%	0.03%	0.00%	0.07%	0.02%	0.00%	0.02%	0.03%	0.02%
D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Acidithiobacillales;D_4__KCM-B-112;D_5__uncultured bacterium	0.12%	0.00%	1.41%	0.00%	0.05%	0.00%	0.00%	0.00%	0.02%	0.03%	0.02%	0.00%	0.00%	0.07%	0.03%
D_0__Bacteria;D_1__Proteobacteria;D_2__Betaproteobacteria;D_3__Burkholderiales;D_4__Alcaligenaceae;D_5__Achromobacter	0.11%	0.07%	0.00%	0.05%	0.07%	0.03%	0.08%	0.00%	0.02%	0.92%	0.05%	0.03%	0.03%	0.11%	0.13%
D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Xanthomonadales;D_4__Xanthomonadales Incertae Sedis;D_5__uncultured	0.11%	0.11%	0.10%	0.21%	0.07%	0.11%	0.02%	0.16%	0.10%	0.13%	0.13%	0.08%	0.10%	0.11%	0.10%
D_0__Bacteria;D_1__Gemmatimonadetes;D_2__Gemmatimonadetes;D_3__Gemmatimonadales;D_4__Gemmatimonadaceae;D_5__uncultured	0.11%	0.07%	0.03%	0.29%	0.10%	0.05%	0.05%	0.05%	0.15%	0.25%	0.07%	0.11%	0.15%	0.11%	0.07%
D_0__Bacteria;D_1__Proteobacteria;D_2__Deltaproteobacteria;D_3__Desulfobacterales;D_4__Desulfobacteraceae;D_5__Desulfotignum	0.11%	0.10%	0.03%	0.00%	0.00%	0.15%	0.20%	0.00%	0.00%	0.84%	0.21%	0.02%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Deltaproteobacteria;D_3__Desulfuromonadales;D_4__Desulfuromonadaceae;D_5__Desulfuromonas	0.11%	0.02%	0.02%	0.00%	0.00%	0.03%	0.46%	0.00%	0.00%	0.25%	0.02%	0.07%	0.64%	0.03%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Betaproteobacteria;D_3__Rhodocyclales;D_4__Rhodocyclaceae;D_5__uncultured	0.11%	0.03%	0.02%	0.07%	0.03%	0.07%	0.13%	0.26%	0.15%	0.02%	0.05%	0.08%	0.20%	0.38%	0.03%
D_0__Bacteria;D_1__Actinobacteria;D_2__Thermoleophilia;D_3__Gaiellales;D_4__uncultured;D_5__uncultured bacterium	0.11%	0.05%	0.08%	0.05%	0.15%	0.11%	0.16%	0.08%	0.03%	0.10%	0.10%	0.10%	0.16%	0.16%	0.13%
D_0__Bacteria;D_1__Thermodesulfobacteria;D_2__Thermodesulfobacteria;D_3__Thermodesulfobacteriales;D_4__Thermodesulfobacteriaceae;D_5__Thermodesulfobacterium	0.11%	0.02%	0.00%	0.00%	0.02%	0.00%	0.02%	0.00%	0.02%	0.02%	0.03%	0.15%	0.16%	0.00%	1.05%
D_0__Bacteria;D_1__Proteobacteria;D_2__Deltaproteobacteria;D_3__Desulfuromonadales;D_4__Geobacteraceae;D_5__Geobacter	0.10%	0.00%	0.00%	0.02%	0.02%	0.08%	0.34%	0.07%	0.08%	0.00%	0.02%	0.02%	0.03%	0.74%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhodospirillales;D_4__Rhodospirillaceae;D_5__uncultured	0.10%	0.07%	0.03%	0.05%	0.07%	0.15%	0.18%	0.05%	0.07%	0.13%	0.07%	0.10%	0.10%	0.25%	0.10%
D_0__Bacteria;D_1__Bacteroidetes;D_2__Cytophagia;D_3__Cytophagales;D_4__Cytophagaceae;D_5__uncultured	0.10%	0.05%	0.07%	0.07%	0.11%	0.16%	0.08%	0.07%	0.03%	0.18%	0.10%	0.16%	0.08%	0.18%	0.03%
D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Lachnospiraceae;D_5__uncultured	0.10%	0.03%	0.02%	0.02%	0.00%	0.00%	0.02%	0.02%	0.00%	0.88%	0.05%	0.23%	0.03%	0.05%	0.00%
D_0__Bacteria;D_1__Acidobacteria;D_2__Acidobacteria;D_3__Subgroup 4;D_4__RB41;D_5__uncultured Acidobacteria bacterium	0.09%	0.13%	0.11%	0.05%	0.03%	0.05%	0.08%	0.07%	0.13%	0.16%	0.08%	0.11%	0.08%	0.15%	0.08%
D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Clostridiaceae 2;D_5__Anoxynatronum	0.09%	0.02%	0.07%	0.10%	0.18%	0.02%	0.00%	0.02%	0.00%	0.87%	0.02%	0.00%	0.03%	0.00%	0.00%
D_0__Bacteria;D_1__Acidobacteria;D_2__Acidobacteria;D_3__Subgroup 3;D_4__Unknown Family;D_5__Bryobacter	0.09%	0.07%	0.03%	0.10%	0.05%	0.03%	0.15%	0.05%	0.10%	0.07%	0.07%	0.20%	0.08%	0.23%	0.05%
D_0__Bacteria;D_1__Proteobacteria;D_2__Deltaproteobacteria;D_3__Desulfuromonadales;D_4__Geobacteraceae;D_5__Geoalkalibacter	0.09%	0.05%	0.00%	0.00%	0.00%	0.00%	0.02%	0.02%	0.00%	0.02%	0.10%	0.03%	1.02%	0.02%	0.00%
D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Christensenellaceae;D_5__uncultured	0.09%	0.00%	0.00%	0.05%	0.00%	0.03%	0.05%	0.05%	0.00%	0.05%	0.00%	0.66%	0.02%	0.31%	0.03%
D_0__Bacteria;D_1__Deferribacteres;D_2__Deferribacteres;D_3__Deferribacterales;D_4__Deferribacteraceae;D_5__Geovibrio	0.09%	0.00%	0.02%	0.00%	0.02%	0.00%	0.03%	0.00%	0.00%	0.00%	0.02%	0.05%	1.08%	0.00%	0.00%
D_0__Bacteria;D_1__Acidobacteria;D_2__Acidobacteria;D_3__Subgroup 3;D_4__Unknown Family;D_5__Candidatus Solibacter	0.09%	0.13%	0.03%	0.15%	0.10%	0.07%	0.08%	0.07%	0.08%	0.10%	0.05%	0.08%	0.08%	0.10%	0.08%
D_0__Bacteria;D_1__Spirochaetae;D_2__Spirochaetes;D_3__LNR A2-18;D_4__uncultured bacterium;D_5__uncultured bacterium	0.09%	0.02%	0.00%	0.00%	0.00%	0.26%	0.10%	0.29%	0.26%	0.05%	0.16%	0.00%	0.00%	0.03%	0.02%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhizobiales;D_4__Hyphomicrobiaceae;D_5__Rhodoplanes	0.08%	0.07%	0.03%	0.08%	0.10%	0.10%	0.05%	0.08%	0.11%	0.10%	0.08%	0.05%	0.07%	0.15%	0.11%
D_0__Bacteria;D_1__Planctomycetes;D_2__Phycisphaerae;D_3__Phycisphaerales;D_4__Phycisphaeraceae;D_5__SM1A02	0.08%	0.00%	0.02%	0.02%	0.00%	0.00%	0.02%	0.03%	0.00%	0.05%	0.02%	0.02%	0.05%	0.00%	0.95%
D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Legionellales;D_4__Coxiellaceae;D_5__Aquicella	0.08%	0.13%	0.02%	0.10%	0.08%	0.10%	0.10%	0.13%	0.05%	0.08%	0.02%	0.10%	0.08%	0.11%	0.05%
D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Xanthomonadales;D_4__uncultured;D_5__uncultured proteobacterium	0.08%	0.11%	0.03%	0.15%	0.07%	0.02%	0.07%	0.07%	0.08%	0.16%	0.05%	0.07%	0.11%	0.07%	0.10%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Sphingomonadales;D_4__Sphingomonadaceae;D_5__Sphingopyxis	0.08%	0.02%	0.00%	0.03%	0.00%	0.03%	0.02%	0.03%	0.02%	0.02%	0.00%	0.00%	0.02%	0.88%	0.05%
D_0__Bacteria;D_1__Planctomycetes;D_2__Planctomycetacia;D_3__Planctomycetales;D_4__Planctomycetaceae;D_5__Pirellula	0.08%	0.10%	0.07%	0.11%	0.10%	0.10%	0.07%	0.05%	0.03%	0.11%	0.00%	0.08%	0.03%	0.08%	0.16%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhodospirillales;D_4__Rhodospirillaceae;D_5__Thalassospira	0.08%	0.00%	0.13%	0.02%	0.00%	0.02%	0.00%	0.03%	0.00%	0.02%	0.02%	0.00%	0.02%	0.00%	0.84%
D_0__Bacteria;D_1__Proteobacteria;D_2__Deltaproteobacteria;D_3__Syntrophobacterales;D_4__Syntrophobacteraceae;D_5__Desulforhabdus	0.08%	0.00%	0.00%	0.05%	0.05%	0.03%	0.02%	0.11%	0.02%	0.00%	0.02%	0.07%	0.70%	0.02%	0.00%
D_0__Bacteria;D_1__Spirochaetae;D_2__Spirochaetes;D_3__LNR A2-18;D_4__uncultured planctomycete;D_5__uncultured planctomycete	0.08%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.03%	0.02%	0.23%	0.44%	0.00%	0.00%	0.00%	0.36%
D_0__Bacteria;D_1__Spirochaetae;D_2__Spirochaetes;D_3__Spirochaetales;D_4__PL-11B10;D_5__uncultured bacterium	0.08%	0.00%	0.02%	0.03%	0.02%	0.00%	0.02%	0.02%	0.02%	0.20%	0.00%	0.61%	0.10%	0.02%	0.03%
D_0__Bacteria;D_1__GOUTA4;D_2__uncultured Bacteroidetes/Chlorobi group bacterium;D_3__uncultured Bacteroidetes/Chlorobi group bacterium;D_4__uncultured Bacteroidetes/Chlorobi group bacterium;D_5__uncultured Bacteroidetes/Chlorobi group bacterium	0.08%	0.02%	0.00%	0.00%	0.02%	0.21%	0.23%	0.11%	0.44%	0.00%	0.00%	0.02%	0.00%	0.02%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhizobiales;D_4__Phyllobacteriaceae;D_5__Phyllobacterium	0.08%	0.03%	0.69%	0.02%	0.03%	0.02%	0.05%	0.03%	0.00%	0.03%	0.02%	0.05%	0.02%	0.02%	0.07%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhodobacterales;D_4__Rhodobacteraceae;D_5__Poseidonocella	0.07%	0.00%	0.00%	0.02%	0.02%	0.02%	0.00%	0.00%	0.02%	0.03%	0.00%	0.03%	0.02%	0.02%	0.88%
D_0__Bacteria;D_1__Bacteroidetes;D_2__Sphingobacteriia;D_3__Sphingobacteriales;D_4__Chitinophagaceae;D_5__Niastella	0.07%	0.11%	0.05%	0.08%	0.16%	0.03%	0.10%	0.05%	0.02%	0.07%	0.08%	0.05%	0.08%	0.08%	0.08%
D_0__Bacteria;D_1__Thermotogae;D_2__Thermotogae;D_3__Thermotogales;D_4__Thermotogaceae;D_5__Thermotoga	0.07%	0.02%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.02%	0.05%	0.10%	0.13%	0.00%	0.69%
D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Alteromonadales;D_4__Alteromonadaceae;D_5__Alishewanella	0.07%	0.00%	0.00%	0.02%	0.20%	0.02%	0.02%	0.02%	0.00%	0.02%	0.02%	0.51%	0.07%	0.13%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Alteromonadales;D_4__Shewanellaceae;D_5__Shewanella	0.07%	0.00%	0.00%	0.07%	0.77%	0.02%	0.05%	0.02%	0.02%	0.00%	0.02%	0.00%	0.05%	0.00%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Chromatiales;D_4__Ectothiorhodospiraceae;D_5__Thioalkalispira	0.07%	0.00%	0.00%	0.00%	0.00%	0.00%	0.98%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__Bacteroidetes;D_2__SB-1;D_3__uncultured bacterium;D_4__uncultured bacterium;D_5__uncultured bacterium	0.07%	0.00%	0.00%	0.02%	0.00%	0.07%	0.10%	0.00%	0.00%	0.10%	0.15%	0.00%	0.02%	0.13%	0.41%
D_0__Bacteria;D_1__Acidobacteria;D_2__Acidobacteria;D_3__Subgroup 2;D_4__uncultured bacterium;D_5__uncultured bacterium	0.07%	0.05%	0.10%	0.05%	0.03%	0.05%	0.11%	0.10%	0.03%	0.11%	0.03%	0.05%	0.08%	0.10%	0.07%
D_0__Bacteria;D_1__Proteobacteria;D_2__Betaproteobacteria;D_3__Rhodocyclales;D_4__Rhodocyclaceae;D_5__Azonexus	0.07%	0.00%	0.00%	0.03%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.10%	0.77%	0.03%	0.02%
D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Clostridiaceae 4;D_5__Geosporobacter	0.07%	0.02%	0.02%	0.02%	0.03%	0.02%	0.00%	0.02%	0.00%	0.00%	0.00%	0.75%	0.07%	0.02%	0.02%
D_0__Bacteria;D_1__Actinobacteria;D_2__Actinobacteria;D_3__Micrococcales;D_4__Micrococcaceae;D_5__Arthrobacter	0.07%	0.02%	0.48%	0.00%	0.03%	0.02%	0.03%	0.02%	0.03%	0.25%	0.02%	0.02%	0.03%	0.02%	0.02%
D_0__Bacteria;D_1__Planctomycetes;D_2__Planctomycetacia;D_3__Planctomycetales;D_4__Planctomycetaceae;D_5__Planctomyces	0.07%	0.00%	0.23%	0.07%	0.08%	0.02%	0.03%	0.03%	0.03%	0.11%	0.05%	0.10%	0.07%	0.07%	0.07%
D_0__Bacteria;D_1__Spirochaetae;D_2__Spirochaetes;D_3__MSBL8;D_4__uncultured bacterium;D_5__uncultured bacterium	0.07%	0.02%	0.00%	0.00%	0.00%	0.54%	0.38%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhizobiales;D_4__Hyphomicrobiaceae;D_5__Pedomicrobium	0.07%	0.03%	0.10%	0.03%	0.05%	0.11%	0.03%	0.08%	0.02%	0.07%	0.07%	0.08%	0.07%	0.18%	0.03%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhizobiales;D_4__Rhodobiaceae;D_5__Parvibaculum	0.07%	0.02%	0.03%	0.00%	0.02%	0.00%	0.62%	0.07%	0.00%	0.03%	0.00%	0.02%	0.00%	0.00%	0.15%
D_0__Bacteria;D_1__Thermotogae;D_2__Thermotogae;D_3__Thermotogales;D_4__Thermotogaceae;D_5__Petrotoga	0.07%	0.18%	0.00%	0.00%	0.00%	0.03%	0.00%	0.00%	0.00%	0.10%	0.59%	0.00%	0.03%	0.00%	0.02%
D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Xanthomonadales;D_4__Xanthomonadaceae;D_5__Pseudoxanthomonas	0.07%	0.08%	0.67%	0.00%	0.02%	0.02%	0.02%	0.03%	0.00%	0.02%	0.00%	0.00%	0.03%	0.05%	0.00%
D_0__Bacteria;D_1__Verrucomicrobia;D_2__Spartobacteria;D_3__Chthoniobacterales;D_4__DA101 soil group;D_5__uncultured bacterium	0.07%	0.03%	0.08%	0.05%	0.03%	0.03%	0.10%	0.10%	0.10%	0.05%	0.02%	0.07%	0.07%	0.08%	0.11%
D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Ruminococcaceae;D_5__Incertae Sedis	0.07%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.02%	0.02%	0.00%	0.00%	0.84%	0.03%	0.00%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhodospirillales;D_4__Rhodospirillaceae;D_5__Tistrella	0.07%	0.00%	0.23%	0.02%	0.02%	0.03%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.20%	0.02%	0.39%
D_0__Bacteria;D_1__Chloroflexi;D_2__Anaerolineae;D_3__Anaerolineales;D_4__Anaerolineaceae;D_5__Bellilinea	0.06%	0.00%	0.00%	0.03%	0.20%	0.02%	0.02%	0.02%	0.00%	0.00%	0.00%	0.03%	0.57%	0.00%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhizobiales;D_4__Phyllobacteriaceae;D_5__Nitratireductor	0.06%	0.05%	0.02%	0.07%	0.05%	0.00%	0.03%	0.03%	0.02%	0.08%	0.16%	0.03%	0.00%	0.03%	0.31%
D_0__Bacteria;D_1__TA06;D_2__uncultured bacterium;D_3__uncultured bacterium;D_4__uncultured bacterium;D_5__uncultured bacterium	0.06%	0.00%	0.00%	0.00%	0.00%	0.03%	0.75%	0.03%	0.05%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Deltaproteobacteria;D_3__Desulfovibrionales;D_4__Desulfomicrobiaceae;D_5__Desulfomicrobium	0.06%	0.66%	0.00%	0.00%	0.02%	0.02%	0.00%	0.00%	0.00%	0.02%	0.02%	0.02%	0.08%	0.03%	0.02%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhizobiales;D_4__Rhizobiales Incertae Sedis;D_5__Rhizomicrobium	0.06%	0.03%	0.03%	0.08%	0.10%	0.10%	0.07%	0.07%	0.03%	0.03%	0.05%	0.05%	0.07%	0.07%	0.10%
D_0__Bacteria;D_1__Synergistetes;D_2__Synergistia;D_3__Synergistales;D_4__Synergistaceae;D_5__Anaerobaculum	0.06%	0.77%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.03%	0.00%	0.00%	0.00%	0.02%	0.02%	0.02%
D_0__Bacteria;D_1__Bacteroidetes;D_2__Sphingobacteriia;D_3__Sphingobacteriales;D_4__Chitinophagaceae;D_5__Ferruginibacter	0.06%	0.07%	0.05%	0.13%	0.02%	0.07%	0.08%	0.05%	0.02%	0.07%	0.05%	0.02%	0.10%	0.11%	0.02%
D_0__Bacteria;D_1__Candidate division KB1;D_2__uncultured bacterium;D_3__uncultured bacterium;D_4__uncultured bacterium;D_5__uncultured bacterium	0.06%	0.02%	0.00%	0.02%	0.00%	0.03%	0.02%	0.02%	0.02%	0.02%	0.07%	0.13%	0.10%	0.00%	0.38%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhizobiales;D_4__KF-JG30-B3;D_5__uncultured bacterium	0.06%	0.13%	0.07%	0.05%	0.02%	0.05%	0.10%	0.02%	0.07%	0.07%	0.02%	0.10%	0.02%	0.07%	0.03%
D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridia Incertae Sedis;D_4__Unknown Family;D_5__Candidatus Desulforudis	0.06%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.03%	0.00%	0.02%	0.03%	0.00%	0.69%
D_0__Bacteria;D_1__Deferribacteres;D_2__Deferribacteres;D_3__Deferribacterales;D_4__SAR406 clade(Marine group A);D_5__uncultured eubacterium AB16	0.05%	0.00%	0.00%	0.00%	0.02%	0.34%	0.10%	0.13%	0.10%	0.00%	0.00%	0.00%	0.00%	0.00%	0.07%
D_0__Bacteria;D_1__Bacteroidetes;D_2__Bacteroidia;D_3__Bacteroidales;D_4__Rikenellaceae;D_5__vadinBC27 wastewater-sludge group	0.05%	0.00%	0.02%	0.07%	0.00%	0.00%	0.34%	0.20%	0.02%	0.00%	0.02%	0.07%	0.03%	0.00%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Caulobacterales;D_4__Caulobacteraceae;D_5__uncultured	0.05%	0.03%	0.00%	0.00%	0.03%	0.00%	0.02%	0.02%	0.00%	0.00%	0.00%	0.03%	0.18%	0.43%	0.02%
D_0__Bacteria;D_1__Acidobacteria;D_2__Acidobacteria;D_3__Subgroup 4;D_4__Unknown Family;D_5__Blastocatella	0.05%	0.11%	0.05%	0.03%	0.02%	0.07%	0.08%	0.10%	0.08%	0.05%	0.03%	0.05%	0.02%	0.05%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhodobacterales;D_4__Rhodobacteraceae;D_5__uncultured bacterium	0.05%	0.15%	0.49%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.03%	0.00%	0.00%	0.02%	0.02%	0.02%
D_0__Bacteria;D_1__Bacteroidetes;D_2__Cytophagia;D_3__Cytophagales;D_4__Cytophagaceae;D_5__Chryseolinea	0.05%	0.00%	0.05%	0.07%	0.03%	0.10%	0.03%	0.11%	0.11%	0.03%	0.03%	0.03%	0.05%	0.03%	0.03%
D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Ruminococcaceae;D_5__Fastidiosipila	0.05%	0.00%	0.00%	0.00%	0.02%	0.00%	0.02%	0.00%	0.00%	0.23%	0.00%	0.13%	0.20%	0.10%	0.03%
D_0__Bacteria;D_1__Candidate division WS3;D_2__uncultured bacterium;D_3__uncultured bacterium;D_4__uncultured bacterium;D_5__uncultured bacterium	0.05%	0.07%	0.02%	0.05%	0.07%	0.05%	0.08%	0.00%	0.16%	0.05%	0.00%	0.02%	0.05%	0.05%	0.03%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhizobiales;D_4__Bradyrhizobiaceae;D_5__uncultured	0.05%	0.02%	0.03%	0.07%	0.00%	0.03%	0.05%	0.05%	0.10%	0.03%	0.07%	0.00%	0.07%	0.11%	0.05%
D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Xanthomonadales;D_4__Xanthomonadaceae;D_5__Stenotrophomonas	0.05%	0.02%	0.03%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.15%	0.00%	0.34%	0.07%	0.05%
D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Peptococcaceae;D_5__uncultured	0.05%	0.00%	0.00%	0.02%	0.00%	0.38%	0.02%	0.03%	0.00%	0.02%	0.00%	0.10%	0.00%	0.10%	0.00%
D_0__Bacteria;D_1__Firmicutes;D_2__Bacilli;D_3__Bacillales;D_4__Bacillaceae;D_5__Bacillus	0.05%	0.00%	0.00%	0.05%	0.03%	0.02%	0.02%	0.21%	0.00%	0.03%	0.02%	0.10%	0.05%	0.02%	0.11%
D_0__Bacteria;D_1__Bacteroidetes;D_2__Cytophagia;D_3__Cytophagales;D_4__Cyclobacteriaceae;D_5__Fontibacter	0.05%	0.00%	0.02%	0.00%	0.02%	0.00%	0.00%	0.02%	0.02%	0.39%	0.03%	0.00%	0.00%	0.15%	0.00%
D_0__Bacteria;D_1__Chloroflexi;D_2__Dehalococcoidia;D_3__vadinBA26;D_4__uncultured bacterium;D_5__uncultured bacterium	0.04%	0.02%	0.00%	0.02%	0.00%	0.02%	0.16%	0.00%	0.38%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%
D_0__Bacteria;D_1__Chloroflexi;D_2__KD4-96;D_3__uncultured bacterium;D_4__uncultured bacterium;D_5__uncultured bacterium	0.04%	0.03%	0.03%	0.00%	0.05%	0.07%	0.05%	0.05%	0.00%	0.13%	0.00%	0.02%	0.07%	0.07%	0.03%
D_0__Bacteria;D_1__Deferribacteres;D_2__Deferribacteres;D_3__Deferribacterales;D_4__SAR406 clade(Marine group A);D_5__uncultured bacterium	0.04%	0.00%	0.00%	0.00%	0.00%	0.08%	0.33%	0.02%	0.00%	0.11%	0.02%	0.00%	0.02%	0.00%	0.02%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhizobiales;D_4__Rhodobiaceae;D_5__Rhodobium	0.04%	0.03%	0.05%	0.05%	0.05%	0.02%	0.07%	0.05%	0.03%	0.05%	0.05%	0.08%	0.03%	0.00%	0.03%
D_0__Bacteria;D_1__Bacteroidetes;D_2__Flavobacteriia;D_3__Flavobacteriales;D_4__Flavobacteriaceae;D_5__Gillisia	0.04%	0.54%	0.02%	0.00%	0.00%	0.02%	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__Betaproteobacteria;D_3__Rhodocyclales;D_4__Rhodocyclaceae;D_5__Sulfuritalea	0.04%	0.00%	0.00%	0.05%	0.05%	0.00%	0.26%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.21%	0.00%
D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Eubacteriaceae;D_5__Alkalibacter	0.04%	0.03%	0.02%	0.00%	0.02%	0.00%	0.00%	0.02%	0.00%	0.02%	0.00%	0.08%	0.05%	0.20%	0.16%
D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Thermoanaerobacterales;D_4__Thermoanaerobacteraceae;D_5__Thermanaeromonas	0.04%	0.00%	0.00%	0.00%	0.00%	0.02%	0.02%	0.02%	0.00%	0.02%	0.00%	0.00%	0.02%	0.03%	0.46%
D_0__Bacteria;D_1__Proteobacteria;D_2__Deltaproteobacteria;D_3__Desulfobacterales;D_4__Desulfobacteraceae;D_5__Desulfatitalea	0.04%	0.02%	0.00%	0.02%	0.02%	0.00%	0.15%	0.02%	0.00%	0.05%	0.29%	0.00%	0.00%	0.00%	0.02%
D_0__Bacteria;D_1__Proteobacteria;D_2__Betaproteobacteria;D_3__Burkholderiales;D_4__Alcaligenaceae;D_5__Pusillimonas	0.04%	0.00%	0.48%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.03%	0.02%	0.00%	0.02%	0.00%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Caulobacterales;D_4__Caulobacteraceae;D_5__Phenylobacterium	0.04%	0.02%	0.02%	0.03%	0.02%	0.07%	0.05%	0.00%	0.02%	0.03%	0.03%	0.07%	0.00%	0.18%	0.03%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Caulobacterales;D_4__Caulobacteraceae;D_5__Brevundimonas	0.04%	0.02%	0.00%	0.02%	0.13%	0.02%	0.00%	0.00%	0.00%	0.02%	0.02%	0.00%	0.05%	0.02%	0.26%
D_0__Bacteria;D_1__Proteobacteria;D_2__Deltaproteobacteria;D_3__Myxococcales;D_4__Haliangiaceae;D_5__Haliangium	0.04%	0.00%	0.03%	0.02%	0.05%	0.03%	0.07%	0.03%	0.00%	0.05%	0.05%	0.08%	0.03%	0.08%	0.02%
D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Alteromonadales;D_4__Idiomarinaceae;D_5__Idiomarina	0.04%	0.49%	0.00%	0.02%	0.02%	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__Bacteroidetes;D_2__Sphingobacteriia;D_3__Sphingobacteriales;D_4__Chitinophagaceae;D_5__Flavisolibacter	0.04%	0.05%	0.00%	0.02%	0.05%	0.03%	0.05%	0.05%	0.02%	0.05%	0.05%	0.03%	0.03%	0.03%	0.07%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhodospirillales;D_4__Rhodospirillaceae;D_5__Oceanibaculum	0.04%	0.00%	0.20%	0.00%	0.02%	0.00%	0.02%	0.00%	0.00%	0.05%	0.05%	0.05%	0.02%	0.07%	0.07%
D_0__Bacteria;D_1__Caldiserica;D_2__Caldisericia;D_3__Caldisericales;D_4__TTA-B15;D_5__uncultured bacterium	0.04%	0.00%	0.00%	0.00%	0.03%	0.00%	0.00%	0.02%	0.00%	0.02%	0.02%	0.00%	0.00%	0.44%	0.00%
D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Family XII;D_5__Fusibacter	0.04%	0.00%	0.00%	0.31%	0.00%	0.03%	0.00%	0.00%	0.00%	0.11%	0.02%	0.00%	0.02%	0.02%	0.00%
D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Clostridiaceae 1;D_5__Youngiibacter	0.04%	0.00%	0.00%	0.00%	0.00%	0.02%	0.05%	0.02%	0.03%	0.00%	0.00%	0.00%	0.02%	0.38%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Betaproteobacteria;D_3__Burkholderiales;D_4__Oxalobacteraceae;D_5__Massilia	0.04%	0.02%	0.00%	0.00%	0.02%	0.03%	0.05%	0.25%	0.05%	0.00%	0.03%	0.02%	0.00%	0.02%	0.03%
D_0__Bacteria;D_1__Proteobacteria;D_2__Deltaproteobacteria;D_3__Desulfovibrionales;D_4__Desulfovibrionaceae;D_5__uncultured	0.04%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.02%	0.00%	0.41%	0.07%	0.00%	0.00%
D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Peptococcaceae;D_5__Desulfotomaculum	0.04%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.05%	0.02%	0.00%	0.39%
D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__P. palm C-A 51;D_5__uncultured bacterium	0.04%	0.00%	0.00%	0.03%	0.00%	0.03%	0.00%	0.00%	0.00%	0.00%	0.00%	0.10%	0.03%	0.29%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhizobiales;D_4__Rhizobiaceae;D_5__Rhizobium	0.04%	0.03%	0.03%	0.05%	0.05%	0.03%	0.03%	0.03%	0.00%	0.02%	0.02%	0.00%	0.02%	0.18%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Deltaproteobacteria;D_3__Desulfobacterales;D_4__Desulfobacteraceae;D_5__uncultured	0.03%	0.00%	0.02%	0.02%	0.02%	0.05%	0.34%	0.03%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__Bacteroidetes;D_2__Bacteroidia;D_3__Bacteroidales;D_4__Porphyromonadaceae;D_5__Petrimonas	0.03%	0.00%	0.00%	0.00%	0.00%	0.00%	0.05%	0.00%	0.02%	0.08%	0.00%	0.02%	0.00%	0.29%	0.02%
D_0__Bacteria;D_1__Spirochaetae;D_2__Spirochaetes;D_3__SHA-4;D_4__uncultured bacterium;D_5__uncultured bacterium	0.03%	0.00%	0.00%	0.44%	0.02%	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__Bacteroidetes;D_2__vadinHA17;D_3__uncultured microorganism;D_4__uncultured microorganism;D_5__uncultured microorganism	0.03%	0.00%	0.00%	0.02%	0.00%	0.13%	0.28%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%
D_0__Bacteria;D_1__Chlorobi;D_2__Ignavibacteria;D_3__Ignavibacteriales;D_4__Ignavibacteriales Incertae Sedis;D_5__Melioribacter	0.03%	0.00%	0.05%	0.00%	0.00%	0.03%	0.29%	0.02%	0.03%	0.00%	0.03%	0.00%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__Actinobacteria;D_2__Actinobacteria;D_3__Corynebacteriales;D_4__Mycobacteriaceae;D_5__Mycobacterium	0.03%	0.03%	0.00%	0.03%	0.02%	0.03%	0.03%	0.05%	0.03%	0.05%	0.02%	0.00%	0.00%	0.00%	0.16%
D_0__Bacteria;D_1__Firmicutes;D_2__Bacilli;D_3__Bacillales;D_4__Planococcaceae;D_5__Planomicrobium	0.03%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.39%	0.00%	0.02%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhodospirillales;D_4__Rhodospirillales Incertae Sedis;D_5__Candidatus Alysiosphaera	0.03%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.05%	0.02%	0.33%
D_0__Bacteria;D_1__Bacteroidetes;D_2__Sphingobacteriia;D_3__Sphingobacteriales;D_4__Chitinophagaceae;D_5__Flavitalea	0.03%	0.07%	0.02%	0.05%	0.02%	0.05%	0.03%	0.02%	0.00%	0.00%	0.03%	0.03%	0.03%	0.05%	0.03%

D_0__Bacteria;D_1__Actinobacteria;D_2__Acidimicrobiia;D_3__Acidimicrobiales;D_4__uncultured;D_5__uncultured bacterium	0.03%	0.03%	0.03%	0.02%	0.03%	0.05%	0.00%	0.03%	0.02%	0.03%	0.02%	0.10%	0.02%	0.02%	0.03%
D_0__Bacteria;D_1__Thermotogae;D_2__Thermotogae;D_3__Thermotogales;D_4__Thermotogaceae;D_5__uncultured	0.03%	0.00%	0.00%	0.00%	0.00%	0.21%	0.18%	0.00%	0.00%	0.00%	0.02%	0.00%	0.02%	0.00%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhodobacterales;D_4__Rhodobacteraceae;D_5__Roseovarius	0.03%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.02%	0.02%	0.00%	0.00%	0.03%	0.31%	0.00%	0.02%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhodospirillales;D_4__Rhodospirillaceae;D_5__Dongia	0.03%	0.03%	0.00%	0.10%	0.03%	0.03%	0.02%	0.00%	0.05%	0.05%	0.02%	0.00%	0.02%	0.07%	0.00%
D_0__Bacteria;D_1__Acidobacteria;D_2__Acidobacteria;D_3__Subgroup 4;D_4__Elev-16S-573;D_5__uncultured bacterium	0.03%	0.03%	0.02%	0.02%	0.05%	0.03%	0.03%	0.03%	0.03%	0.05%	0.00%	0.03%	0.02%	0.02%	0.05%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhizobiales;D_4__Hyphomicrobiaceae;D_5__Rhodomicrobium	0.03%	0.00%	0.05%	0.02%	0.05%	0.03%	0.02%	0.02%	0.02%	0.02%	0.03%	0.03%	0.07%	0.02%	0.05%
D_0__Bacteria;D_1__Thermotogae;D_2__Thermotogae;D_3__Thermotogales;D_4__Thermotogaceae;D_5__Thermosipho	0.03%	0.36%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.02%
D_0__Bacteria;D_1__Candidate division OP11;D_2__uncultured bacterium;D_3__uncultured bacterium;D_4__uncultured bacterium;D_5__uncultured bacterium	0.03%	0.00%	0.00%	0.03%	0.00%	0.11%	0.03%	0.16%	0.00%	0.02%	0.02%	0.00%	0.02%	0.00%	0.00%
D_0__Bacteria;D_1__Hyd24-12;D_2__uncultured bacterium;D_3__uncultured bacterium;D_4__uncultured bacterium;D_5__uncultured bacterium	0.03%	0.02%	0.02%	0.00%	0.00%	0.03%	0.25%	0.00%	0.08%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhodobacterales;D_4__Rhodobacteraceae;D_5__uncultured	0.03%	0.03%	0.10%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.02%	0.02%	0.21%
D_0__Bacteria;D_1__Acidobacteria;D_2__Holophagae;D_3__Subgroup 7;D_4__uncultured bacterium;D_5__uncultured bacterium	0.03%	0.00%	0.00%	0.07%	0.00%	0.03%	0.02%	0.00%	0.02%	0.03%	0.05%	0.03%	0.05%	0.03%	0.05%
D_0__Bacteria;D_1__Nitrospirae;D_2__Nitrospira;D_3__Nitrospirales;D_4__0319-6A21;D_5__uncultured bacterium	0.03%	0.02%	0.03%	0.02%	0.02%	0.05%	0.03%	0.03%	0.03%	0.07%	0.00%	0.00%	0.03%	0.02%	0.03%
D_0__Bacteria;D_1__Actinobacteria;D_2__Thermoleophilia;D_3__Solirubrobacterales;D_4__Solirubrobacteraceae;D_5__Solirubrobacter	0.03%	0.00%	0.03%	0.03%	0.02%	0.02%	0.05%	0.03%	0.02%	0.03%	0.02%	0.03%	0.05%	0.03%	0.02%
D_0__Bacteria;D_1__Synergistetes;D_2__Synergistia;D_3__Synergistales;D_4__Synergistaceae;D_5__Aminiphilus	0.03%	0.02%	0.00%	0.03%	0.02%	0.00%	0.02%	0.05%	0.02%	0.00%	0.00%	0.23%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhizobiales;D_4__MNG7;D_5__uncultured bacterium	0.03%	0.03%	0.00%	0.00%	0.05%	0.03%	0.00%	0.07%	0.03%	0.07%	0.03%	0.02%	0.03%	0.00%	0.00%
D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Thermoanaerobacterales;D_4__Family III;D_5__uncultured Thermovenabulum sp.	0.03%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.02%	0.00%	0.00%	0.02%	0.00%	0.31%
D_0__Bacteria;D_1__Proteobacteria;D_2__Deltaproteobacteria;D_3__Desulfurellales;D_4__Desulfurellaceae;D_5__uncultured	0.03%	0.05%	0.00%	0.02%	0.03%	0.00%	0.00%	0.03%	0.05%	0.05%	0.03%	0.03%	0.03%	0.03%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhodospirillales;D_4__Rhodospirillales Incertae Sedis;D_5__Reyranella	0.03%	0.02%	0.00%	0.05%	0.00%	0.03%	0.02%	0.00%	0.05%	0.00%	0.03%	0.07%	0.07%	0.02%	0.02%
D_0__Bacteria;D_1__Proteobacteria;D_2__Deltaproteobacteria;D_3__Sh765B-TzT-29;D_4__uncultured bacterium;D_5__uncultured bacterium	0.03%	0.07%	0.00%	0.03%	0.03%	0.00%	0.02%	0.02%	0.05%	0.08%	0.02%	0.00%	0.00%	0.02%	0.03%
D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Thiotrichales;D_4__Piscirickettsiaceae;D_5__Thiomicrospira	0.03%	0.02%	0.26%	0.02%	0.00%	0.00%	0.00%	0.03%	0.00%	0.00%	0.02%	0.00%	0.02%	0.00%	0.00%
D_0__Bacteria;D_1__Acidobacteria;D_2__Acidobacteria;D_3__Acidobacteriales;D_4__Acidobacteriaceae (Subgroup 1);D_5__Telmatobacter	0.03%	0.00%	0.00%	0.00%	0.02%	0.03%	0.05%	0.02%	0.05%	0.02%	0.05%	0.00%	0.05%	0.07%	0.02%
D_0__Bacteria;D_1__Actinobacteria;D_2__Thermoleophilia;D_3__Gaiellales;D_4__Gaiellaceae;D_5__Gaiella	0.03%	0.00%	0.03%	0.05%	0.02%	0.08%	0.00%	0.02%	0.02%	0.02%	0.03%	0.05%	0.03%	0.02%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhizobiales;D_4__A0839;D_5__uncultured bacterium	0.03%	0.02%	0.02%	0.05%	0.02%	0.05%	0.00%	0.02%	0.02%	0.03%	0.02%	0.03%	0.07%	0.02%	0.02%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhizobiales;D_4__Hyphomicrobiaceae;D_5__Devosia	0.03%	0.02%	0.02%	0.02%	0.03%	0.05%	0.00%	0.02%	0.02%	0.02%	0.00%	0.02%	0.03%	0.05%	0.08%
D_0__Bacteria;D_1__Proteobacteria;D_2__Betaproteobacteria;D_3__SC-I-84;D_4__uncultured bacterium;D_5__uncultured bacterium	0.03%	0.02%	0.00%	0.00%	0.08%	0.02%	0.02%	0.02%	0.02%	0.05%	0.05%	0.07%	0.02%	0.02%	0.00%
D_0__Bacteria;D_1__Armatimonadetes;D_2__uncultured bacterium;D_3__uncultured bacterium;D_4__uncultured bacterium;D_5__uncultured bacterium	0.02%	0.00%	0.00%	0.02%	0.02%	0.03%	0.08%	0.00%	0.00%	0.02%	0.00%	0.02%	0.03%	0.11%	0.02%
D_0__Bacteria;D_1__Proteobacteria;D_2__Deltaproteobacteria;D_3__Myxococcales;D_4__uncultured;D_5__uncultured bacterium	0.02%	0.02%	0.03%	0.05%	0.02%	0.07%	0.05%	0.00%	0.05%	0.00%	0.03%	0.02%	0.00%	0.02%	0.00%
D_0__Bacteria;D_1__Candidate division OP3;D_2__uncultured Clostridiales bacterium;D_3__uncultured Clostridiales bacterium;D_4__uncultured Clostridiales bacterium;D_5__uncultured Clostridiales bacterium	0.02%	0.00%	0.00%	0.00%	0.00%	0.02%	0.23%	0.05%	0.03%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%
D_0__Bacteria;D_1__Acidobacteria;D_2__Holophagae;D_3__Subgroup 10;D_4__ABS-19;D_5__uncultured bacterium	0.02%	0.02%	0.00%	0.02%	0.02%	0.03%	0.00%	0.05%	0.05%	0.05%	0.02%	0.02%	0.02%	0.05%	0.02%
D_0__Bacteria;D_1__Candidate division BRC1;D_2__uncultured bacterium;D_3__uncultured bacterium;D_4__uncultured bacterium;D_5__uncultured bacterium	0.02%	0.02%	0.00%	0.00%	0.00%	0.10%	0.00%	0.00%	0.02%	0.02%	0.00%	0.03%	0.00%	0.02%	0.15%
D_0__Bacteria;D_1__Proteobacteria;D_2__Betaproteobacteria;D_3__TRA3-20;D_4__uncultured bacterium;D_5__uncultured bacterium	0.02%	0.03%	0.03%	0.05%	0.00%	0.00%	0.03%	0.03%	0.03%	0.02%	0.00%	0.00%	0.05%	0.03%	0.02%
D_0__Bacteria;D_1__Proteobacteria;D_2__Deltaproteobacteria;D_3__Desulfobacterales;D_4__Nitrospinaceae;D_5__Candidatus Entotheonella	0.02%	0.02%	0.00%	0.00%	0.07%	0.05%	0.02%	0.03%	0.00%	0.02%	0.03%	0.03%	0.00%	0.03%	0.03%
D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Xanthomonadales;D_4__Xanthomonadaceae;D_5__Lysobacter	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.03%	0.05%	0.03%	0.02%	0.03%	0.07%	0.08%
D_0__Bacteria;D_1__Chloroflexi;D_2__Anaerolineae;D_3__Anaerolineales;D_4__Anaerolineaceae;D_5__Longilinea	0.02%	0.00%	0.02%	0.00%	0.05%	0.05%	0.00%	0.05%	0.10%	0.00%	0.00%	0.00%	0.00%	0.07%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Deltaproteobacteria;D_3__Desulfobacterales;D_4__Nitrospinaceae;D_5__uncultured	0.02%	0.03%	0.00%	0.07%	0.00%	0.00%	0.02%	0.02%	0.00%	0.03%	0.02%	0.03%	0.02%	0.05%	0.05%
D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Thermoanaerobacterales;D_4__Thermodesulfobiaceae;D_5__Coprothermobacter	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.02%	0.02%	0.03%	0.00%	0.25%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhodobacterales;D_4__Rhodobacteraceae;D_5__Rhodovulum	0.02%	0.00%	0.05%	0.02%	0.02%	0.00%	0.00%	0.00%	0.00%	0.18%	0.05%	0.00%	0.02%	0.00%	0.00%
D_0__Bacteria;D_1__Acidobacteria;D_2__Acidobacteria;D_3__Subgroup 4;D_4__11-24;D_5__uncultured Acidobacteria bacterium	0.02%	0.02%	0.00%	0.00%	0.00%	0.05%	0.03%	0.00%	0.07%	0.03%	0.03%	0.00%	0.03%	0.02%	0.03%
D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Thermoanaerobacterales;D_4__Thermoanaerobacteraceae;D_5__Thermacetogenium	0.02%	0.00%	0.00%	0.00%	0.03%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.28%
D_0__Bacteria;D_1__Proteobacteria;D_2__Betaproteobacteria;D_3__Rhodocyclales;D_4__Rhodocyclaceae;D_5__Dechloromonas	0.02%	0.00%	0.00%	0.00%	0.02%	0.00%	0.28%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhizobiales;D_4__Rhizobiales Incertae Sedis;D_5__Nordella	0.02%	0.00%	0.03%	0.02%	0.02%	0.07%	0.02%	0.02%	0.07%	0.05%	0.00%	0.00%	0.02%	0.02%	0.00%
D_0__Bacteria;D_1__Bacteroidetes;D_2__Sphingobacteriia;D_3__Sphingobacteriales;D_4__Saprospiraceae;D_5__uncultured	0.02%	0.05%	0.00%	0.02%	0.02%	0.02%	0.02%	0.02%	0.00%	0.03%	0.00%	0.03%	0.03%	0.02%	0.07%
D_0__Bacteria;D_1__Cyanobacteria;D_2__Chloroplast;D_3__Pisum sativum (pea);D_4__Pisum sativum (pea);D_5__Pisum sativum (pea)	0.02%	0.02%	0.02%	0.10%	0.05%	0.02%	0.03%	0.00%	0.00%	0.02%	0.00%	0.02%	0.00%	0.05%	0.00%
D_0__Bacteria;D_1__Chloroflexi;D_2__Dehalococcoidia;D_3__GIF9;D_4__uncultured bacterium;D_5__uncultured bacterium	0.02%	0.00%	0.00%	0.00%	0.00%	0.21%	0.03%	0.03%	0.00%	0.00%	0.00%	0.00%	0.02%	0.02%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Betaproteobacteria;D_3__Burkholderiales;D_4__Comamonadaceae;D_5__Chlorochromatium	0.02%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.02%	0.00%	0.00%	0.23%	0.03%
D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Family XIII;D_5__uncultured	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.16%	0.07%	0.05%	0.02%
D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Family XIII;D_5__Anaerovorax	0.02%	0.03%	0.00%	0.00%	0.00%	0.02%	0.00%	0.07%	0.00%	0.02%	0.00%	0.15%	0.02%	0.00%	0.02%
D_0__Bacteria;D_1__Thermotogae;D_2__Thermotogae;D_3__Thermotogales;D_4__Thermotogaceae;D_5__Fervidobacterium	0.02%	0.05%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.02%	0.07%	0.15%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Sphingomonadales;D_4__Sphingomonadaceae;D_5__Sphingomonas	0.02%	0.02%	0.00%	0.00%	0.00%	0.02%	0.00%	0.02%	0.03%	0.00%	0.00%	0.00%	0.07%	0.11%	0.03%
D_0__Bacteria;D_1__Proteobacteria;D_2__Betaproteobacteria;D_3__Rhodocyclales;D_4__Rhodocyclaceae;D_5__Azospira	0.02%	0.02%	0.02%	0.05%	0.00%	0.00%	0.03%	0.02%	0.00%	0.02%	0.00%	0.00%	0.11%	0.02%	0.02%
D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Xanthomonadales;D_4__Xanthomonadaceae;D_5__Arenimonas	0.02%	0.05%	0.03%	0.03%	0.02%	0.00%	0.00%	0.03%	0.00%	0.07%	0.00%	0.00%	0.05%	0.00%	0.02%
D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Xanthomonadales;D_4__Xanthomonadaceae;D_5__Thermomonas	0.02%	0.02%	0.00%	0.00%	0.00%	0.00%	0.03%	0.00%	0.05%	0.02%	0.03%	0.03%	0.03%	0.03%	0.05%
D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Chromatiales;D_4__Chromatiaceae;D_5__Nitrosococcus	0.02%	0.00%	0.02%	0.03%	0.00%	0.00%	0.02%	0.03%	0.03%	0.02%	0.00%	0.02%	0.05%	0.03%	0.05%
D_0__Bacteria;D_1__Acidobacteria;D_2__Acidobacteria;D_3__Subgroup 17;D_4__uncultured bacterium;D_5__uncultured bacterium	0.02%	0.05%	0.02%	0.00%	0.02%	0.02%	0.00%	0.05%	0.00%	0.03%	0.00%	0.02%	0.03%	0.05%	0.02%
D_0__Bacteria;D_1__Acidobacteria;D_2__Acidobacteria;D_3__Subgroup 4;D_4__11-24;D_5__uncultured bacterium	0.02%	0.00%	0.02%	0.00%	0.02%	0.05%	0.05%	0.03%	0.02%	0.02%	0.03%	0.00%	0.00%	0.05%	0.02%
D_0__Bacteria;D_1__Acidobacteria;D_2__Acidobacteria;D_3__Subgroup 6;D_4__uncultured Acidobacteriales bacterium;D_5__uncultured Acidobacteriales bacterium	0.02%	0.05%	0.02%	0.00%	0.05%	0.03%	0.02%	0.00%	0.00%	0.05%	0.02%	0.02%	0.00%	0.03%	0.02%
D_0__Bacteria;D_1__Proteobacteria;D_2__Epsilonproteobacteria;D_3__Campylobacterales;D_4__Helicobacteraceae;D_5__Sulfuricurvum	0.02%	0.00%	0.00%	0.02%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.25%	0.00%
D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Syntrophomonadaceae;D_5__Pelospora	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.20%	0.10%	0.00%	0.00%
D_0__Bacteria;D_1__Acidobacteria;D_2__Acidobacteria;D_3__Subgroup 6;D_4__uncultured soil bacterium;D_5__uncultured soil bacterium	0.02%	0.02%	0.02%	0.02%	0.02%	0.02%	0.00%	0.02%	0.05%	0.05%	0.02%	0.03%	0.00%	0.02%	0.03%
D_0__Bacteria;D_1__Proteobacteria;D_2__Betaproteobacteria;D_3__Hot Creek 32;D_4__uncultured bacterium;D_5__uncultured bacterium	0.02%	0.00%	0.02%	0.02%	0.00%	0.03%	0.02%	0.11%	0.00%	0.00%	0.02%	0.02%	0.02%	0.03%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Betaproteobacteria;D_3__TRA3-20;D_4__uncultured beta proteobacterium;D_5__uncultured beta proteobacterium	0.02%	0.02%	0.02%	0.00%	0.02%	0.00%	0.00%	0.00%	0.03%	0.03%	0.02%	0.03%	0.03%	0.03%	0.05%
D_0__Bacteria;D_1__Chloroflexi;D_2__Chloroflexia;D_3__Chloroflexales;D_4__Roseiflexaceae;D_5__Roseiflexus	0.02%	0.02%	0.03%	0.02%	0.02%	0.03%	0.00%	0.02%	0.00%	0.05%	0.00%	0.00%	0.03%	0.03%	0.03%
D_0__Bacteria;D_1__Actinobacteria;D_2__Thermoleophilia;D_3__Solirubrobacterales;D_4__288-2;D_5__uncultured bacterium	0.02%	0.02%	0.00%	0.00%	0.02%	0.05%	0.05%	0.00%	0.02%	0.02%	0.02%	0.03%	0.02%	0.03%	0.02%
D_0__Bacteria;D_1__Elusimicrobia;D_2__Elusimicrobia;D_3__Lineage I (Endomicrobia);D_4__uncultured bacterium;D_5__uncultured bacterium	0.02%	0.00%	0.00%	0.00%	0.00%	0.15%	0.00%	0.03%	0.08%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__Tenericutes;D_2__Mollicutes;D_3__EUB33-2;D_4__uncultured bacterium;D_5__uncultured bacterium	0.02%	0.00%	0.00%	0.08%	0.02%	0.00%	0.00%	0.07%	0.08%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%
D_0__Bacteria;D_1__Bacteroidetes;D_2__Bacteroidia;D_3__Bacteroidales;D_4__S24-7;D_5__uncultured bacterium	0.02%	0.00%	0.00%	0.00%	0.00%	0.02%	0.03%	0.00%	0.03%	0.05%	0.02%	0.03%	0.05%	0.03%	0.00%
D_0__Bacteria;D_1__Elusimicrobia;D_2__Elusimicrobia;D_3__Lineage IIa;D_4__uncultured bacterium;D_5__uncultured bacterium	0.02%	0.02%	0.00%	0.00%	0.00%	0.03%	0.00%	0.02%	0.05%	0.00%	0.05%	0.03%	0.03%	0.03%	0.00%
D_0__Bacteria;D_1__Firmicutes;D_2__Erysipelotrichia;D_3__Erysipelotrichales;D_4__Erysipelotrichaceae;D_5__Allobaculum	0.02%	0.05%	0.00%	0.00%	0.03%	0.02%	0.03%	0.02%	0.05%	0.00%	0.00%	0.05%	0.00%	0.02%	0.00%
D_0__Bacteria;D_1__Acidobacteria;D_2__Subgroup 22;D_3__uncultured bacterium;D_4__uncultured bacterium;D_5__uncultured bacterium	0.02%	0.02%	0.00%	0.03%	0.05%	0.02%	0.03%	0.00%	0.00%	0.02%	0.02%	0.00%	0.02%	0.03%	0.03%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhodospirillales;D_4__JG37-AG-20;D_5__uncultured bacterium	0.02%	0.05%	0.02%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.03%	0.02%	0.03%	0.00%	0.05%	0.05%
D_0__Bacteria;D_1__Actinobacteria;D_2__Actinobacteria;D_3__Micromonosporales;D_4__Micromonosporaceae;D_5__Actinoplanes	0.02%	0.05%	0.00%	0.00%	0.00%	0.02%	0.02%	0.00%	0.05%	0.03%	0.02%	0.00%	0.02%	0.05%	0.02%
D_0__Bacteria;D_1__Gemmatimonadetes;D_2__Gemmatimonadetes;D_3__Gemmatimonadales;D_4__Gemmatimonadaceae;D_5__Gemmatimonas	0.02%	0.02%	0.02%	0.00%	0.02%	0.02%	0.02%	0.03%	0.03%	0.03%	0.02%	0.02%	0.02%	0.02%	0.02%
D_0__Bacteria;D_1__Bacteroidetes;D_2__Flavobacteriia;D_3__Flavobacteriales;D_4__Flavobacteriaceae;D_5__Flavobacterium	0.02%	0.00%	0.02%	0.02%	0.02%	0.03%	0.00%	0.00%	0.02%	0.00%	0.00%	0.02%	0.00%	0.15%	0.00%
D_0__Bacteria;D_1__Actinobacteria;D_2__Actinobacteria;D_3__Propionibacteriales;D_4__Propionibacteriaceae;D_5__uncultured	0.02%	0.00%	0.00%	0.00%	0.00%	0.02%	0.11%	0.10%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhizobiales;D_4__JG34-KF-361;D_5__uncultured bacterium	0.02%	0.00%	0.02%	0.00%	0.00%	0.03%	0.03%	0.03%	0.00%	0.03%	0.00%	0.02%	0.02%	0.07%	0.00%
D_0__Bacteria;D_1__Bacteroidetes;D_2__vadinHA17;D_3__uncultured bacterium;D_4__uncultured bacterium;D_5__uncultured bacterium	0.02%	0.00%	0.00%	0.00%	0.00%	0.02%	0.05%	0.02%	0.10%	0.00%	0.00%	0.00%	0.00%	0.07%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Betaproteobacteria;D_3__Burkholderiales;D_4__Comamonadaceae;D_5__Comamonas	0.02%	0.03%	0.00%	0.03%	0.02%	0.00%	0.02%	0.00%	0.00%	0.03%	0.02%	0.02%	0.03%	0.05%	0.00%
D_0__Bacteria;D_1__Tenericutes;D_2__Mollicutes;D_3__Acholeplasmatales;D_4__Acholeplasmataceae;D_5__Acholeplasma	0.02%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.03%	0.10%	0.02%	0.00%	0.08%	0.00%	0.00%
D_0__Bacteria;D_1__Cyanobacteria;D_2__Chloroplast;D_3__uncultured bacterium;D_4__uncultured bacterium;D_5__uncultured bacterium	0.02%	0.00%	0.00%	0.00%	0.02%	0.03%	0.00%	0.02%	0.00%	0.00%	0.03%	0.02%	0.10%	0.03%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Xanthomonadales;D_4__Xanthomonadaceae;D_5__Dokdonella	0.02%	0.00%	0.02%	0.02%	0.00%	0.03%	0.00%	0.02%	0.00%	0.03%	0.02%	0.02%	0.03%	0.02%	0.05%
D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Chromatiales;D_4__Halothiobacillaceae;D_5__Thiofaba	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.02%	0.21%	0.00%
D_0__Bacteria;D_1__Firmicutes;D_2__Negativicutes;D_3__Selenomonadales;D_4__Veillonellaceae;D_5__uncultured	0.02%	0.00%	0.00%	0.00%	0.02%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.20%	0.02%	0.00%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Deltaproteobacteria;D_3__Desulfobacterales;D_4__Desulfobacteraceae;D_5__Desulfobotulus	0.02%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.20%	0.02%	0.00%
D_0__Bacteria;D_1__Bacteroidetes;D_2__Bacteroidia;D_3__Bacteroidales;D_4__Porphyromonadaceae;D_5__Paludibacter	0.02%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.11%	0.00%	0.00%	0.00%	0.08%	0.02%	0.00%
D_0__Bacteria;D_1__Bacteroidetes;D_2__Sphingobacteriia;D_3__Sphingobacteriales;D_4__AKYH767;D_5__uncultured bacterium	0.02%	0.02%	0.02%	0.03%	0.00%	0.03%	0.00%	0.05%	0.03%	0.00%	0.00%	0.02%	0.02%	0.02%	0.00%
D_0__Bacteria;D_1__Firmicutes;D_2__Bacilli;D_3__Bacillales;D_4__Family XII;D_5__Incertae Sedis	0.02%	0.00%	0.02%	0.02%	0.00%	0.02%	0.00%	0.05%	0.00%	0.02%	0.07%	0.00%	0.00%	0.03%	0.02%
D_0__Bacteria;D_1__Planctomycetes;D_2__OM190;D_3__uncultured bacterium;D_4__uncultured bacterium;D_5__uncultured bacterium	0.02%	0.02%	0.02%	0.00%	0.03%	0.00%	0.03%	0.05%	0.03%	0.00%	0.00%	0.00%	0.02%	0.02%	0.02%
D_0__Bacteria;D_1__Proteobacteria;D_2__Betaproteobacteria;D_3__Burkholderiales;D_4__Comamonadaceae;D_5__Tepidimonas	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%	0.23%	0.00%
D_0__Bacteria;D_1__Actinobacteria;D_2__Thermoleophilia;D_3__Solirubrobacterales;D_4__480-2;D_5__uncultured bacterium	0.02%	0.03%	0.02%	0.00%	0.00%	0.00%	0.02%	0.02%	0.02%	0.02%	0.00%	0.03%	0.00%	0.07%	0.02%
D_0__Bacteria;D_1__Candidate division OD1;D_2__uncultured organism;D_3__uncultured organism;D_4__uncultured organism;D_5__uncultured organism	0.02%	0.00%	0.00%	0.00%	0.00%	0.21%	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__Alphaproteobacteria;D_3__Rhodospirillales;D_4__Acetobacteraceae;D_5__Roseomonas	0.02%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.03%	0.00%	0.18%	0.00%
D_0__Bacteria;D_1__Bacteroidetes;D_2__Sphingobacteriia;D_3__Sphingobacteriales;D_4__PHOS-HE51;D_5__uncultured bacterium	0.02%	0.03%	0.00%	0.02%	0.02%	0.03%	0.00%	0.02%	0.00%	0.05%	0.00%	0.00%	0.03%	0.02%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhizobiales;D_4__Phyllobacteriaceae;D_5__Mesorhizobium	0.02%	0.00%	0.00%	0.03%	0.03%	0.02%	0.00%	0.03%	0.02%	0.02%	0.00%	0.03%	0.00%	0.02%	0.02%
D_0__Bacteria;D_1__Actinobacteria;D_2__Actinobacteria;D_3__Pseudonocardiales;D_4__Pseudonocardiaceae;D_5__Pseudonocardia	0.02%	0.02%	0.02%	0.00%	0.03%	0.05%	0.02%	0.00%	0.00%	0.00%	0.03%	0.02%	0.02%	0.02%	0.00%
D_0__Bacteria;D_1__Bacteroidetes;D_2__Flavobacteriia;D_3__Flavobacteriales;D_4__Flavobacteriaceae;D_5__Wautersiella	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.21%	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__SC-I-84;D_4__uncultured beta proteobacterium;D_5__uncultured beta proteobacterium	0.02%	0.00%	0.00%	0.02%	0.00%	0.00%	0.05%	0.00%	0.00%	0.02%	0.05%	0.02%	0.02%	0.02%	0.03%
D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Peptococcaceae;D_5__Dehalobacter	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.18%	0.00%	0.03%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhodospirillales;D_4__MND8;D_5__uncultured bacterium	0.02%	0.02%	0.02%	0.00%	0.02%	0.03%	0.00%	0.00%	0.02%	0.05%	0.00%	0.02%	0.02%	0.02%	0.02%
D_0__Bacteria;D_1__Proteobacteria;D_2__Deltaproteobacteria;D_3__Desulfobacterales;D_4__Desulfobacteraceae;D_5__Desulfatirhabdium	0.02%	0.02%	0.00%	0.00%	0.00%	0.02%	0.03%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.15%	0.00%
D_0__Bacteria;D_1__Caldiserica;D_2__Caldisericia;D_3__Caldisericales;D_4__WCHB1-02;D_5__uncultured bacterium	0.01%	0.02%	0.00%	0.00%	0.00%	0.11%	0.02%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.03%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Betaproteobacteria;D_3__Burkholderiales;D_4__Comamonadaceae;D_5__Hydrogenophaga	0.01%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.02%	0.00%	0.03%	0.11%	0.00%
D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Ruminococcaceae;D_5__uncultured	0.01%	0.00%	0.00%	0.00%	0.02%	0.02%	0.00%	0.00%	0.02%	0.00%	0.00%	0.11%	0.02%	0.00%	0.02%
D_0__Bacteria;D_1__Chloroflexi;D_2__TK10;D_3__uncultured bacterium;D_4__uncultured bacterium;D_5__uncultured bacterium	0.01%	0.02%	0.00%	0.03%	0.00%	0.00%	0.05%	0.00%	0.00%	0.03%	0.03%	0.02%	0.00%	0.02%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhizobiales;D_4__Xanthobacteraceae;D_5__Pseudolabrys	0.01%	0.02%	0.02%	0.03%	0.05%	0.00%	0.00%	0.00%	0.00%	0.03%	0.00%	0.00%	0.03%	0.02%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Betaproteobacteria;D_3__Burkholderiales;D_4__Burkholderiaceae;D_5__Cupriavidus	0.01%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.07%	0.02%	0.03%	0.00%	0.02%	0.00%	0.03%	0.02%
D_0__Bacteria;D_1__Acidobacteria;D_2__Acidobacteria;D_3__Acidobacteriales;D_4__Acidobacteriaceae (Subgroup 1);D_5__Edaphobacter	0.01%	0.00%	0.02%	0.02%	0.00%	0.02%	0.03%	0.00%	0.02%	0.00%	0.00%	0.02%	0.08%	0.00%	0.00%
D_0__Bacteria;D_1__Acidobacteria;D_2__Acidobacteria;D_3__Subgroup 4;D_4__RB41;D_5__uncultured Acidobacterium sp.	0.01%	0.02%	0.02%	0.00%	0.03%	0.02%	0.02%	0.02%	0.00%	0.03%	0.00%	0.00%	0.02%	0.03%	0.00%
D_0__Bacteria;D_1__Actinobacteria;D_2__Actinobacteria;D_3__Propionibacteriales;D_4__Nocardioidaceae;D_5__Nocardioides	0.01%	0.02%	0.02%	0.00%	0.02%	0.03%	0.00%	0.00%	0.02%	0.03%	0.02%	0.02%	0.00%	0.03%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Xanthomonadales;D_4__Xanthomonadales Incertae Sedis;D_5__Steroidobacter	0.01%	0.00%	0.00%	0.02%	0.02%	0.02%	0.00%	0.02%	0.02%	0.00%	0.03%	0.00%	0.00%	0.03%	0.05%
D_0__Bacteria;D_1__Proteobacteria;D_2__Betaproteobacteria;D_3__Burkholderiales;D_4__Comamonadaceae;D_5__Ramlibacter	0.01%	0.00%	0.00%	0.02%	0.02%	0.02%	0.00%	0.00%	0.00%	0.02%	0.02%	0.05%	0.02%	0.03%	0.02%
D_0__Bacteria;D_1__Proteobacteria;D_2__Deltaproteobacteria;D_3__Myxococcales;D_4__Sandaracinaceae;D_5__uncultured bacterium	0.01%	0.02%	0.02%	0.03%	0.02%	0.02%	0.02%	0.05%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.02%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Caulobacterales;D_4__Caulobacteraceae;D_5__Caulobacter	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.18%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Deltaproteobacteria;D_3__Syntrophobacterales;D_4__Syntrophaceae;D_5__Syntrophus	0.01%	0.00%	0.00%	0.00%	0.00%	0.11%	0.00%	0.05%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Deltaproteobacteria;D_3__Desulfarculales;D_4__Desulfarculaceae;D_5__uncultured	0.01%	0.00%	0.00%	0.00%	0.00%	0.05%	0.08%	0.03%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Family XII;D_5__Acidaminobacter	0.01%	0.02%	0.00%	0.02%	0.02%	0.00%	0.00%	0.00%	0.00%	0.02%	0.02%	0.05%	0.00%	0.05%	0.00%
D_0__Bacteria;D_1__Planctomycetes;D_2__Planctomycetacia;D_3__Planctomycetales;D_4__Planctomycetaceae;D_5__Gemmata	0.01%	0.02%	0.00%	0.00%	0.03%	0.02%	0.02%	0.00%	0.00%	0.00%	0.00%	0.02%	0.02%	0.05%	0.02%
D_0__Bacteria;D_1__Planctomycetes;D_2__Phycisphaerae;D_3__WD2101 soil group;D_4__uncultured soil bacterium;D_5__uncultured soil bacterium	0.01%	0.02%	0.00%	0.03%	0.00%	0.03%	0.02%	0.00%	0.00%	0.02%	0.02%	0.00%	0.02%	0.02%	0.02%
D_0__Bacteria;D_1__Candidate division OP9;D_2__Unknown Class;D_3__Unknown Order;D_4__Unknown Family;D_5__Candidatus Caldatribacterium	0.01%	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%	0.16%
D_0__Bacteria;D_1__Lentisphaerae;D_2__Lentisphaeria;D_3__Victivallales;D_4__Victivallaceae;D_5__Victivallis	0.01%	0.00%	0.00%	0.00%	0.00%	0.03%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.15%	0.00%
D_0__Bacteria;D_1__Spirochaetae;D_2__Spirochaetes;D_3__C-2;D_4__uncultured bacterium;D_5__uncultured bacterium	0.01%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.16%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__Chlorobi;D_2__Ignavibacteria;D_3__Ignavibacteriales;D_4__SR-FBR-L83;D_5__uncultured bacterium	0.01%	0.00%	0.00%	0.00%	0.00%	0.02%	0.15%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhizobiales;D_4__Hyphomicrobiaceae;D_5__Pelagibacterium	0.01%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.15%
D_0__Bacteria;D_1__BD1-5;D_2__uncultured bacterium;D_3__uncultured bacterium;D_4__uncultured bacterium;D_5__uncultured bacterium	0.01%	0.00%	0.00%	0.11%	0.00%	0.03%	0.00%	0.02%	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__Legionellales;D_4__Legionellaceae;D_5__Legionella	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.02%	0.00%	0.13%
D_0__Bacteria;D_1__Actinobacteria;D_2__Actinobacteria;D_3__Micrococcales;D_4__Dermabacteraceae;D_5__Brachybacterium	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.02%	0.02%	0.11%
D_0__Bacteria;D_1__Lentisphaerae;D_2__PBS-III-20;D_3__uncultured soil bacterium PBS-III-20;D_4__uncultured soil bacterium PBS-III-20;D_5__uncultured soil bacterium PBS-III-20	0.01%	0.00%	0.00%	0.02%	0.00%	0.03%	0.02%	0.03%	0.07%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Betaproteobacteria;D_3__Rhodocyclales;D_4__Rhodocyclaceae;D_5__Denitratisoma	0.01%	0.00%	0.00%	0.08%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.07%	0.00%
D_0__Bacteria;D_1__Acidobacteria;D_2__Holophagae;D_3__Subgroup 7;D_4__uncultured Acidobacteria bacterium;D_5__uncultured Acidobacteria bacterium	0.01%	0.00%	0.03%	0.00%	0.03%	0.00%	0.03%	0.03%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.02%
D_0__Bacteria;D_1__Bacteroidetes;D_2__Cytophagia;D_3__Cytophagales;D_4__Cytophagaceae;D_5__Ohtaekwangia	0.01%	0.00%	0.00%	0.03%	0.00%	0.03%	0.00%	0.00%	0.00%	0.02%	0.02%	0.03%	0.03%	0.00%	0.00%
D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Syntrophomonadaceae;D_5__uncultured	0.01%	0.00%	0.00%	0.02%	0.02%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.02%	0.00%	0.03%	0.07%
D_0__Bacteria;D_1__Proteobacteria;D_2__Betaproteobacteria;D_3__Burkholderiales;D_4__Burkholderiaceae;D_5__Pandoraea	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.02%	0.00%	0.05%	0.08%
D_0__Bacteria;D_1__Proteobacteria;D_2__Betaproteobacteria;D_3__Burkholderiales;D_4__Comamonadaceae;D_5__Delftia	0.01%	0.02%	0.00%	0.00%	0.02%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.03%	0.08%
D_0__Bacteria;D_1__Planctomycetes;D_2__Phycisphaerae;D_3__Phycisphaerales;D_4__Phycisphaeraceae;D_5__AKYG587	0.01%	0.00%	0.00%	0.02%	0.00%	0.00%	0.02%	0.02%	0.03%	0.00%	0.00%	0.03%	0.00%	0.03%	0.02%
D_0__Bacteria;D_1__Planctomycetes;D_2__Planctomycetacia;D_3__Planctomycetales;D_4__Planctomycetaceae;D_5__Singulisphaera	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.03%	0.03%	0.03%	0.02%	0.00%	0.02%	0.02%	0.00%	0.02%
D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__KI89A clade;D_4__uncultured bacterium;D_5__uncultured bacterium	0.01%	0.00%	0.00%	0.02%	0.03%	0.00%	0.02%	0.00%	0.02%	0.00%	0.02%	0.03%	0.00%	0.03%	0.00%
D_0__Bacteria;D_1__Chloroflexi;D_2__Ktedonobacteria;D_3__C0119;D_4__uncultured bacterium;D_5__uncultured bacterium	0.01%	0.02%	0.00%	0.02%	0.02%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.05%	0.02%	0.00%	0.03%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhizobiales;D_4__DUNssu371;D_5__uncultured bacterium	0.01%	0.00%	0.00%	0.02%	0.02%	0.00%	0.02%	0.02%	0.00%	0.03%	0.02%	0.03%	0.00%	0.02%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhizobiales;D_4__Bradyrhizobiaceae;D_5__Afipia	0.01%	0.02%	0.00%	0.02%	0.00%	0.02%	0.00%	0.03%	0.00%	0.02%	0.02%	0.02%	0.02%	0.00%	0.02%
D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Thermoanaerobacterales;D_4__Thermoanaerobacteraceae;D_5__Ammonifex	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.15%	0.02%	0.00%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__Spirochaetae;D_2__Spirochaetes;D_3__Spirochaetales;D_4__PL-11B10;D_5__uncultured Firmicutes bacterium	0.01%	0.13%	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__Alphaproteobacteria;D_3__Rhodobacterales;D_4__Rhodobacteraceae;D_5__Roseicitreum	0.01%	0.11%	0.02%	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__Tenericutes;D_2__Mollicutes;D_3__NB1-n;D_4__bacterium enrichment culture clone R4-81B;D_5__bacterium enrichment culture clone R4-81B	0.01%	0.00%	0.00%	0.00%	0.00%	0.11%	0.02%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__Tenericutes;D_2__Mollicutes;D_3__NB1-n;D_4__uncultured bacterium;D_5__uncultured bacterium	0.01%	0.02%	0.00%	0.00%	0.00%	0.00%	0.03%	0.00%	0.00%	0.07%	0.03%	0.00%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__Chloroflexi;D_2__S085;D_3__uncultured bacterium;D_4__uncultured bacterium;D_5__uncultured bacterium	0.01%	0.00%	0.00%	0.02%	0.03%	0.00%	0.03%	0.00%	0.03%	0.02%	0.00%	0.00%	0.00%	0.00%	0.02%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Parvularculales;D_4__Parvularculaceae;D_5__Parvularcula	0.01%	0.00%	0.08%	0.00%	0.02%	0.00%	0.03%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhizobiales;D_4__Methylobacteriaceae;D_5__Microvirga	0.01%	0.03%	0.03%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.02%	0.03%	0.00%	0.00%	0.02%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Betaproteobacteria;D_3__Burkholderiales;D_4__Burkholderiaceae;D_5__Ralstonia	0.01%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.08%	0.00%	0.00%	0.00%	0.00%	0.00%	0.05%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Enterobacteriales;D_4__Enterobacteriaceae;D_5__Escherichia-Shigella	0.01%	0.00%	0.00%	0.02%	0.00%	0.00%	0.08%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.05%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhizobiales;D_4__Hyphomicrobiaceae;D_5__uncultured	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.02%	0.02%	0.00%	0.05%	0.00%	0.05%	0.00%
D_0__Bacteria;D_1__Actinobacteria;D_2__Actinobacteria;D_3__Micrococcales;D_4__Microbacteriaceae;D_5__Leifsonia	0.01%	0.00%	0.10%	0.02%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%
D_0__Bacteria;D_1__Actinobacteria;D_2__Actinobacteria;D_3__Micromonosporales;D_4__Micromonosporaceae;D_5__Catelliglobosispora	0.01%	0.00%	0.00%	0.02%	0.02%	0.02%	0.03%	0.03%	0.00%	0.02%	0.00%	0.00%	0.02%	0.00%	0.00%
D_0__Bacteria;D_1__Cyanobacteria;D_2__Cyanobacteria;D_3__SubsectionIII;D_4__FamilyI;D_5__Microcoleus	0.01%	0.02%	0.00%	0.00%	0.03%	0.02%	0.00%	0.00%	0.02%	0.02%	0.00%	0.00%	0.00%	0.03%	0.02%
D_0__Bacteria;D_1__Chlorobi;D_2__Chlorobia;D_3__Chlorobiales;D_4__OPB56;D_5__uncultured bacterium	0.01%	0.00%	0.00%	0.00%	0.15%	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__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__TTA-B61;D_5__uncultured bacterium	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%	0.15%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rickettsiales;D_4__Rickettsiaceae;D_5__Rickettsia	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%	0.15%
D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Peptococcaceae;D_5__Desulfitibacter	0.01%	0.00%	0.00%	0.00%	0.03%	0.00%	0.03%	0.00%	0.03%	0.00%	0.00%	0.03%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Thermoanaerobacterales;D_4__Thermoanaerobacteraceae;D_5__Gelria	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.03%	0.00%	0.03%	0.07%
D_0__Bacteria;D_1__Candidate division OP8;D_2__uncultured bacterium;D_3__uncultured bacterium;D_4__uncultured bacterium;D_5__uncultured bacterium	0.01%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.03%	0.02%	0.07%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Deltaproteobacteria;D_3__Deltaproteobacteria Incertae Sedis;D_4__Syntrophorhabdaceae;D_5__Syntrophorhabdus	0.01%	0.00%	0.00%	0.02%	0.00%	0.03%	0.02%	0.07%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__Bacteroidetes;D_2__Bacteroidia;D_3__Bacteroidales;D_4__Prevotellaceae;D_5__Prevotella	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.03%	0.00%	0.05%	0.00%	0.00%	0.00%	0.02%	0.03%
D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__D8A-2;D_4__uncultured bacterium;D_5__uncultured bacterium	0.01%	0.00%	0.00%	0.00%	0.02%	0.03%	0.00%	0.00%	0.00%	0.07%	0.00%	0.00%	0.00%	0.00%	0.02%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhizobiales;D_4__DUNssu371;D_5__uncultured Gemmatimonadetes bacterium	0.01%	0.00%	0.00%	0.00%	0.00%	0.07%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.03%
D_0__Bacteria;D_1__Proteobacteria;D_2__Deltaproteobacteria;D_3__Myxococcales;D_4__0319-6G20;D_5__uncultured bacterium	0.01%	0.02%	0.02%	0.00%	0.00%	0.03%	0.00%	0.00%	0.03%	0.00%	0.00%	0.00%	0.00%	0.00%	0.03%
D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Alteromonadales;D_4__Idiomarinaceae;D_5__Aliidiomarina	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.03%	0.08%	0.00%	0.00%	0.02%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Oceanospirillales;D_4__Oceanospirillaceae;D_5__Thalassolituus	0.01%	0.03%	0.00%	0.00%	0.00%	0.00%	0.08%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%
D_0__Bacteria;D_1__Chloroflexi;D_2__Anaerolineae;D_3__Anaerolineales;D_4__Anaerolineaceae;D_5__Anaerolinea	0.01%	0.00%	0.02%	0.02%	0.10%	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__Burkholderiales;D_4__Alcaligenaceae;D_5__Parapusillimonas	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.10%	0.00%
D_0__Bacteria;D_1__Actinobacteria;D_2__MB-A2-108;D_3__uncultured bacterium;D_4__uncultured bacterium;D_5__uncultured bacterium	0.01%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.05%	0.02%	0.03%
D_0__Bacteria;D_1__Proteobacteria;D_2__Deltaproteobacteria;D_3__Desulfobacterales;D_4__Desulfobulbaceae;D_5__Desulfurivibrio	0.01%	0.00%	0.00%	0.00%	0.02%	0.03%	0.03%	0.02%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.02%
D_0__Bacteria;D_1__Thermotogae;D_2__Thermotogae;D_3__Thermotogales;D_4__Thermotogaceae;D_5__EM3	0.01%	0.03%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.02%	0.05%	0.02%	0.00%
D_0__Bacteria;D_1__Actinobacteria;D_2__Actinobacteria;D_3__Propionibacteriales;D_4__Nocardioidaceae;D_5__Kribbella	0.01%	0.02%	0.00%	0.00%	0.02%	0.00%	0.00%	0.02%	0.00%	0.02%	0.02%	0.02%	0.00%	0.03%	0.00%
D_0__Bacteria;D_1__Firmicutes;D_2__Bacilli;D_3__Bacillales;D_4__Planococcaceae;D_5__Paenisporosarcina	0.01%	0.02%	0.02%	0.00%	0.00%	0.02%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.03%	0.02%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhizobiales;D_4__Rhizobiales Incertae Sedis;D_5__Bauldia	0.01%	0.02%	0.00%	0.02%	0.02%	0.00%	0.00%	0.02%	0.00%	0.02%	0.00%	0.03%	0.00%	0.00%	0.02%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhodospirillales;D_4__DA111;D_5__uncultured bacterium	0.01%	0.02%	0.00%	0.00%	0.00%	0.02%	0.00%	0.02%	0.02%	0.02%	0.02%	0.00%	0.02%	0.02%	0.02%
D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Thermoanaerobacterales;D_4__Thermoanaerobacteraceae;D_5__Moorella	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%	0.11%	0.00%
D_0__Bacteria;D_1__Chrysiogenetes;D_2__Chrysiogenetes;D_3__Chrysiogenales;D_4__Chrysiogenaceae;D_5__Desulfurispirillum	0.01%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.07%	0.03%	0.00%	0.00%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__Acidobacteria;D_2__Holophagae;D_3__Subgroup 7;D_4__uncultured Acidobacterium sp.;D_5__uncultured Acidobacterium sp.	0.01%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.03%	0.02%	0.00%	0.03%	0.00%	0.02%
D_0__Bacteria;D_1__Bacteroidetes;D_2__Sphingobacteriia;D_3__Sphingobacteriales;D_4__Sphingobacteriaceae;D_5__Solitalea	0.01%	0.00%	0.05%	0.00%	0.00%	0.00%	0.02%	0.02%	0.00%	0.03%	0.00%	0.00%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__Chloroflexi;D_2__Anaerolineae;D_3__Anaerolineales;D_4__Anaerolineaceae;D_5__Levilinea	0.01%	0.00%	0.00%	0.00%	0.00%	0.02%	0.02%	0.00%	0.03%	0.00%	0.00%	0.00%	0.00%	0.05%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhodobacterales;D_4__Rhodobacteraceae;D_5__Rhodobacter	0.01%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.08%
D_0__Bacteria;D_1__Proteobacteria;D_2__Betaproteobacteria;D_3__Burkholderiales;D_4__Comamonadaceae;D_5__Limnohabitans	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.08%	0.02%
D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Xanthomonadales;D_4__Xanthomonadaceae;D_5__uncultured	0.01%	0.02%	0.03%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.03%	0.02%	0.00%
D_0__Bacteria;D_1__Acidobacteria;D_2__Acidobacteria;D_3__Subgroup 25;D_4__uncultured bacterium;D_5__uncultured bacterium	0.01%	0.00%	0.00%	0.02%	0.00%	0.02%	0.00%	0.02%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.05%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhodospirillales;D_4__I-10;D_5__uncultured bacterium	0.01%	0.03%	0.00%	0.00%	0.00%	0.02%	0.02%	0.02%	0.00%	0.02%	0.00%	0.00%	0.02%	0.00%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Betaproteobacteria;D_3__Burkholderiales;D_4__Alcaligenaceae;D_5__uncultured	0.01%	0.02%	0.00%	0.02%	0.00%	0.00%	0.02%	0.02%	0.02%	0.00%	0.00%	0.03%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__TA18;D_3__uncultured proteobacterium;D_4__uncultured proteobacterium;D_5__uncultured proteobacterium	0.01%	0.02%	0.00%	0.00%	0.02%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.03%	0.02%	0.00%	0.02%
D_0__Bacteria;D_1__Proteobacteria;D_2__Betaproteobacteria;D_3__Burkholderiales;D_4__Comamonadaceae;D_5__Rhizobacter	0.01%	0.02%	0.00%	0.00%	0.02%	0.00%	0.02%	0.02%	0.02%	0.00%	0.00%	0.02%	0.02%	0.00%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Betaproteobacteria;D_3__SC-I-84;D_4__uncultured Nitrosomonadaceae bacterium;D_5__uncultured Nitrosomonadaceae bacterium	0.01%	0.00%	0.00%	0.02%	0.00%	0.02%	0.00%	0.02%	0.00%	0.00%	0.00%	0.02%	0.02%	0.02%	0.02%
D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Alteromonadales;D_4__Alteromonadaceae;D_5__OM60(NOR5) clade	0.01%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.02%	0.02%	0.02%	0.02%	0.02%	0.00%	0.00%
D_0__Bacteria;D_1__Planctomycetes;D_2__Phycisphaerae;D_3__MSBL9;D_4__uncultured microorganism;D_5__uncultured microorganism	0.01%	0.00%	0.00%	0.00%	0.00%	0.03%	0.07%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__Actinobacteria;D_2__Actinobacteria;D_3__Micromonosporales;D_4__Micromonosporaceae;D_5__Plantactinospora	0.01%	0.00%	0.00%	0.00%	0.02%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.03%	0.00%	0.00%	0.03%
D_0__Bacteria;D_1__Bacteroidetes;D_2__Sphingobacteriia;D_3__Sphingobacteriales;D_4__Chitinophagaceae;D_5__Sediminibacterium	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.08%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__Bacteroidetes;D_2__Sphingobacteriia;D_3__Sphingobacteriales;D_4__ST-12K33;D_5__uncultured Cytophagales bacterium	0.01%	0.00%	0.00%	0.00%	0.00%	0.03%	0.05%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__Chlorobi;D_2__Ignavibacteria;D_3__Ignavibacteriales;D_4__Ignavibacteriaceae;D_5__Ignavibacterium	0.01%	0.00%	0.00%	0.03%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.05%	0.00%
D_0__Bacteria;D_1__Chloroflexi;D_2__Thermomicrobia;D_3__JG30-KF-CM45;D_4__uncultured bacterium;D_5__uncultured bacterium	0.01%	0.02%	0.00%	0.03%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.03%	0.00%
D_0__Bacteria;D_1__Chloroflexi;D_2__uncultured;D_3__uncultured Chloroflexi bacterium;D_4__uncultured Chloroflexi bacterium;D_5__uncultured Chloroflexi bacterium	0.01%	0.00%	0.00%	0.00%	0.00%	0.08%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__Elusimicrobia;D_2__Elusimicrobia;D_3__Lineage IIb;D_4__uncultured bacterium;D_5__uncultured bacterium	0.01%	0.00%	0.00%	0.03%	0.00%	0.00%	0.02%	0.00%	0.00%	0.03%	0.00%	0.00%	0.02%	0.00%	0.00%
D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Clostridiaceae 1;D_5__uncultured	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.03%	0.00%	0.05%
D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Clostridiaceae 2;D_5__Anaerovirgula	0.01%	0.00%	0.00%	0.03%	0.05%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhizobiales;D_4__Aurantimonadaceae;D_5__Martelella	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%	0.10%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhodobacterales;D_4__Rhodobacteraceae;D_5__Labrenzia	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.05%	0.00%	0.00%	0.00%	0.03%
D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Aeromonadales;D_4__Aeromonadaceae;D_5__Aeromonas	0.01%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.07%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%
D_0__Bacteria;D_1__TM6;D_2__uncultured organism;D_3__uncultured organism;D_4__uncultured organism;D_5__uncultured organism	0.01%	0.00%	0.00%	0.00%	0.00%	0.10%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__Verrucomicrobia;D_2__Spartobacteria;D_3__Chthoniobacterales;D_4__DA101 soil group;D_5__uncultured Spartobacteria bacterium	0.01%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.03%	0.00%	0.02%	0.00%	0.00%	0.00%	0.03%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhodobacterales;D_4__Rhodobacteraceae;D_5__Gemmobacter	0.01%	0.02%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.05%	0.00%

D_0__Bacteria;D_1__Acidobacteria;D_2__Holophagae;D_3__Subgroup 7;D_4__uncultured candidate division OS-K bacterium;D_5__uncultured candidate division OS-K bacterium	0.01%	0.02%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.02%	0.03%
D_0__Bacteria;D_1__Actinobacteria;D_2__Actinobacteria;D_3__Micromonosporales;D_4__Micromonosporaceae;D_5__Luedemannella	0.01%	0.02%	0.00%	0.03%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.02%	0.00%	0.00%	0.02%
D_0__Bacteria;D_1__Chloroflexi;D_2__JG37-AG-4;D_3__uncultured bacterium;D_4__uncultured bacterium;D_5__uncultured bacterium	0.01%	0.00%	0.00%	0.00%	0.03%	0.00%	0.00%	0.00%	0.02%	0.02%	0.00%	0.00%	0.02%	0.02%	0.00%
D_0__Bacteria;D_1__Nitrospirae;D_2__Nitrospira;D_3__Nitrospirales;D_4__0319-6A21;D_5__uncultured candidate division SPAM bacterium	0.01%	0.02%	0.00%	0.03%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.02%
D_0__Bacteria;D_1__Planctomycetes;D_2__Phycisphaerae;D_3__Pla1 lineage;D_4__uncultured bacterium;D_5__uncultured bacterium	0.01%	0.00%	0.00%	0.02%	0.02%	0.05%	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__Syntrophobacterales;D_4__Syntrophobacteraceae;D_5__Syntrophobacter	0.01%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.05%	0.00%	0.00%	0.00%	0.02%	0.02%	0.00%
D_0__Bacteria;D_1__Actinobacteria;D_2__Actinobacteria;D_3__Frankiales;D_4__Geodermatophilaceae;D_5__Blastococcus	0.01%	0.00%	0.00%	0.00%	0.00%	0.02%	0.02%	0.02%	0.00%	0.02%	0.02%	0.00%	0.02%	0.00%	0.00%
D_0__Bacteria;D_1__Actinobacteria;D_2__Actinobacteria;D_3__Micromonosporales;D_4__Micromonosporaceae;D_5__Asanoa	0.01%	0.02%	0.02%	0.00%	0.00%	0.00%	0.00%	0.02%	0.02%	0.00%	0.00%	0.02%	0.00%	0.00%	0.02%
D_0__Bacteria;D_1__Bacteroidetes;D_2__Cytophagia;D_3__Cytophagales;D_4__Cytophagaceae;D_5__Adhaeribacter	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.02%	0.02%	0.00%	0.00%	0.02%	0.00%	0.02%	0.02%
D_0__Bacteria;D_1__Bacteroidetes;D_2__Flavobacteriia;D_3__Flavobacteriales;D_4__NS9 marine group;D_5__uncultured bacterium	0.01%	0.00%	0.02%	0.00%	0.02%	0.00%	0.02%	0.00%	0.00%	0.02%	0.00%	0.00%	0.02%	0.02%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhizobiales;D_4__DUNssu371;D_5__uncultured proteobacterium	0.01%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.02%	0.02%	0.00%	0.00%	0.02%	0.02%	0.00%	0.02%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhizobiales;D_4__Hyphomicrobiaceae;D_5__Hyphomicrobium	0.01%	0.02%	0.00%	0.02%	0.00%	0.00%	0.00%	0.02%	0.02%	0.02%	0.00%	0.02%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Betaproteobacteria;D_3__SC-I-84;D_4__beta proteobacterium JGI 0001003-N18;D_5__beta proteobacterium JGI 0001003-N18	0.01%	0.00%	0.00%	0.02%	0.02%	0.00%	0.02%	0.02%	0.00%	0.02%	0.00%	0.00%	0.00%	0.02%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Deltaproteobacteria;D_3__Myxococcales;D_4__Phaselicystidaceae;D_5__Phaselicystis	0.01%	0.00%	0.00%	0.00%	0.02%	0.00%	0.02%	0.02%	0.02%	0.00%	0.00%	0.00%	0.02%	0.02%	0.00%
D_0__Bacteria;D_1__Actinobacteria;D_2__Actinobacteria;D_3__Micrococcales;D_4__Microbacteriaceae;D_5__Microbacterium	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.07%	0.00%	0.02%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__Bacteroidetes;D_2__Bacteroidia;D_3__Bacteroidales;D_4__ML635J-40 aquatic group;D_5__uncultured Sphingobacteria bacterium	0.01%	0.00%	0.00%	0.00%	0.03%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.03%	0.00%	0.00%
D_0__Bacteria;D_1__Bacteroidetes;D_2__Flavobacteriia;D_3__Flavobacteriales;D_4__Flavobacteriaceae;D_5__Lutibacter	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.08%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__Bacteroidetes;D_2__SB-1;D_3__uncultured Bacteroidetes bacterium;D_4__uncultured Bacteroidetes bacterium;D_5__uncultured Bacteroidetes bacterium	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.07%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%
D_0__Bacteria;D_1__Bacteroidetes;D_2__Sphingobacteriia;D_3__Sphingobacteriales;D_4__B01R012;D_5__uncultured bacterium	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.08%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__Bacteroidetes;D_2__Sphingobacteriia;D_3__Sphingobacteriales;D_4__WCHB1-69;D_5__bacterium enrichment culture clone R4-78B	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.07%	0.00%
D_0__Bacteria;D_1__Caldiserica;D_2__Caldisericia;D_3__Caldisericales;D_4__WCHB1-02;D_5__uncultured Firmicutes bacterium	0.01%	0.00%	0.00%	0.00%	0.00%	0.07%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__Candidate division OD1;D_2__uncultured Microgenomates bacterium;D_3__uncultured Microgenomates bacterium;D_4__uncultured Microgenomates bacterium;D_5__uncultured Microgenomates bacterium	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.07%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__Candidate division OP9;D_2__uncultured bacterium;D_3__uncultured bacterium;D_4__uncultured bacterium;D_5__uncultured bacterium	0.01%	0.00%	0.00%	0.00%	0.00%	0.03%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.03%	0.00%
D_0__Bacteria;D_1__Chlorobi;D_2__Chlorobia;D_3__Chlorobiales;D_4__OPB56;D_5__uncultured anaerobic bacterium	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.08%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__Chloroflexi;D_2__P2-11E;D_3__uncultured bacterium;D_4__uncultured bacterium;D_5__uncultured bacterium	0.01%	0.00%	0.00%	0.00%	0.03%	0.00%	0.00%	0.00%	0.00%	0.02%	0.03%	0.00%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__Deferribacteres;D_2__Deferribacteres;D_3__Deferribacterales;D_4__SAR406 clade(Marine group A);D_5__Marinimicrobia bacterium JGI 0000039-D08	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%	0.08%	0.00%
D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Peptococcaceae;D_5__Cryptanaerobacter	0.01%	0.00%	0.00%	0.00%	0.00%	0.08%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Peptococcaceae;D_5__Pelotomaculum	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.07%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%
D_0__Bacteria;D_1__Planctomycetes;D_2__Phycisphaerae;D_3__MSBL9;D_4__uncultured bacterium;D_5__uncultured bacterium	0.01%	0.00%	0.00%	0.00%	0.00%	0.03%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.03%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__DB1-14;D_4__uncultured bacterium;D_5__uncultured bacterium	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%	0.08%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhizobiales;D_4__FFCH5858;D_5__uncultured bacterium	0.01%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.03%	0.00%	0.00%	0.00%	0.03%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Betaproteobacteria;D_3__Burkholderiales;D_4__Comamonadaceae;D_5__Albidiferax	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.07%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__TA18;D_3__uncultured bacterium;D_4__uncultured bacterium;D_5__uncultured bacterium	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.07%
D_0__Bacteria;D_1__Acidobacteria;D_2__Acidobacteria;D_3__Subgroup 3;D_4__SJA-149;D_5__uncultured bacterium	0.01%	0.02%	0.00%	0.03%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__Acidobacteria;D_2__Holophagae;D_3__Subgroup 10;D_4__ABS-19;D_5__uncultured soil bacterium	0.01%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.02%	0.00%	0.03%	0.00%
D_0__Bacteria;D_1__Acidobacteria;D_2__Subgroup 22;D_3__uncultured proteobacterium;D_4__uncultured proteobacterium;D_5__uncultured proteobacterium	0.01%	0.02%	0.00%	0.03%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%
D_0__Bacteria;D_1__Actinobacteria;D_2__Acidimicrobiia;D_3__Acidimicrobiales;D_4__Acidimicrobiaceae;D_5__uncultured	0.01%	0.02%	0.00%	0.02%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.03%	0.00%
D_0__Bacteria;D_1__Actinobacteria;D_2__Actinobacteria;D_3__Micrococcales;D_4__Cellulomonadaceae;D_5__Actinotalea	0.01%	0.00%	0.00%	0.02%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.03%	0.00%	0.02%	0.00%
D_0__Bacteria;D_1__Chloroflexi;D_2__Caldilineae;D_3__Caldilineales;D_4__Caldilineaceae;D_5__uncultured	0.01%	0.02%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.03%	0.02%	0.00%	0.00%
D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__MAT-CR-H4-C10;D_5__uncultured bacterium	0.01%	0.05%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Syntrophomonadaceae;D_5__Dethiobacter	0.01%	0.00%	0.00%	0.00%	0.00%	0.03%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.02%
D_0__Bacteria;D_1__Lentisphaerae;D_2__PBS-III-20;D_3__uncultured bacterium;D_4__uncultured bacterium;D_5__uncultured bacterium	0.01%	0.00%	0.00%	0.00%	0.00%	0.03%	0.00%	0.02%	0.00%	0.02%	0.00%	0.00%	0.00%	0.02%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Sphingomonadales;D_4__Erythrobacteraceae;D_5__Porphyrobacter	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.02%	0.00%	0.05%	0.00%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Betaproteobacteria;D_3__Burkholderiales;D_4__Comamonadaceae;D_5__Ideonella	0.01%	0.02%	0.00%	0.03%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Deltaproteobacteria;D_3__Myxococcales;D_4__uncultured;D_5__uncultured delta proteobacterium	0.01%	0.02%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.03%	0.00%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Xanthomonadales;D_4__Xanthomonadaceae;D_5__Rhodanobacter	0.01%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.03%	0.00%	0.02%	0.00%	0.00%	0.02%	0.00%
D_0__Bacteria;D_1__Verrucomicrobia;D_2__Spartobacteria;D_3__Chthoniobacterales;D_4__Xiphinematobacteraceae;D_5__Candidatus Xiphinematobacter	0.01%	0.02%	0.00%	0.00%	0.02%	0.03%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%
D_0__Bacteria;D_1__WCHB1-60;D_2__uncultured bacterium;D_3__uncultured bacterium;D_4__uncultured bacterium;D_5__uncultured bacterium	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.02%	0.00%	0.02%	0.00%	0.03%	0.00%
D_0__Bacteria;D_1__Actinobacteria;D_2__Actinobacteria;D_3__Streptomycetales;D_4__Streptomycetaceae;D_5__Streptomyces	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.02%	0.02%	0.00%	0.00%	0.00%	0.00%	0.02%	0.02%
D_0__Bacteria;D_1__Actinobacteria;D_2__Thermoleophilia;D_3__Solirubrobacterales;D_4__0319-6M6;D_5__uncultured bacterium	0.01%	0.00%	0.00%	0.02%	0.02%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.02%	0.02%
D_0__Bacteria;D_1__Bacteroidetes;D_2__Sphingobacteriia;D_3__Sphingobacteriales;D_4__env.OPS 17;D_5__uncultured bacterium	0.01%	0.02%	0.00%	0.00%	0.02%	0.02%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.02%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhizobiales;D_4__Bradyrhizobiaceae;D_5__Nitrobacter	0.01%	0.00%	0.00%	0.00%	0.02%	0.02%	0.00%	0.00%	0.00%	0.02%	0.00%	0.02%	0.00%	0.00%	0.02%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhizobiales;D_4__Xanthobacteraceae;D_5__Labrys	0.01%	0.00%	0.02%	0.02%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.02%
D_0__Bacteria;D_1__Proteobacteria;D_2__Betaproteobacteria;D_3__Methylophilales;D_4__Methylophilaceae;D_5__Methylotenera	0.01%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.02%	0.02%	0.00%	0.02%	0.00%	0.02%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Deltaproteobacteria;D_3__GR-WP33-30;D_4__uncultured proteobacterium;D_5__uncultured proteobacterium	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.02%	0.00%	0.02%	0.00%	0.00%	0.02%	0.02%
D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Pseudomonadales;D_4__Moraxellaceae;D_5__uncultured	0.01%	0.00%	0.00%	0.00%	0.02%	0.00%	0.02%	0.02%	0.00%	0.00%	0.02%	0.00%	0.00%	0.02%	0.00%
D_0__Bacteria;D_1__Verrucomicrobia;D_2__Spartobacteria;D_3__Chthoniobacterales;D_4__DA101 soil group;D_5__uncultured Verrucomicrobia bacterium	0.01%	0.02%	0.00%	0.00%	0.00%	0.00%	0.02%	0.02%	0.00%	0.00%	0.00%	0.02%	0.00%	0.02%	0.00%
D_0__Bacteria;D_1__Bacteroidetes;D_2__Bacteroidia;D_3__Bacteroidales;D_4__LKC2.127-25;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%	0.07%	0.00%
D_0__Bacteria;D_1__Bacteroidetes;D_2__Flavobacteriia;D_3__Flavobacteriales;D_4__Flavobacteriaceae;D_5__Psychroflexus	0.00%	0.00%	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%
D_0__Bacteria;D_1__Candidate division SR1;D_2__uncultured candidate division SR1 bacterium;D_3__uncultured candidate division SR1 bacterium;D_4__uncultured candidate division SR1 bacterium;D_5__uncultured candidate division SR1 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%	0.07%	0.00%
D_0__Bacteria;D_1__Chlorobi;D_2__Chlorobia;D_3__Chlorobiales;D_4__OPB56;D_5__uncultured Chlorobi bacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.07%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Family XIII;D_5__Mogibacterium	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%	0.07%	0.00%
D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Ruminococcaceae;D_5__Papillibacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.07%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__Lentisphaerae;D_2__BS5;D_3__uncultured bacterium;D_4__uncultured bacterium;D_5__uncultured bacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.07%	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__Alphaproteobacteria;D_3__Rhodospirillales;D_4__Rhodospirillaceae;D_5__Ferrovibrio	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%	0.07%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Betaproteobacteria;D_3__B1-7BS;D_4__uncultured bacterium;D_5__uncultured bacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.07%	0.00%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Gammaproteobacteria Incertae Sedis;D_4__Unknown Family;D_5__Alkalimonas	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.07%	0.00%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Xanthomonadales;D_4__Xanthomonadaceae;D_5__Tahibacter	0.00%	0.00%	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%
D_0__Bacteria;D_1__SBYG-2791;D_2__uncultured organism;D_3__uncultured organism;D_4__uncultured organism;D_5__uncultured organism	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.03%	0.00%	0.00%	0.03%	0.00%	0.00%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__WCHB1-60;D_2__uncultured microorganism;D_3__uncultured microorganism;D_4__uncultured microorganism;D_5__uncultured microorganism	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.07%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__Acidobacteria;D_2__Acidobacteria;D_3__Subgroup 5;D_4__uncultured bacterium;D_5__uncultured bacterium	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.03%	0.00%
D_0__Bacteria;D_1__Acidobacteria;D_2__Acidobacteria;D_3__Subgroup 6;D_4__uncultured proteobacterium;D_5__uncultured proteobacterium	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.03%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%
D_0__Bacteria;D_1__Actinobacteria;D_2__Actinobacteria;D_3__Corynebacteriales;D_4__Dietziaceae;D_5__Dietzia	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.05%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%
D_0__Bacteria;D_1__Actinobacteria;D_2__Actinobacteria;D_3__Micromonosporales;D_4__Micromonosporaceae;D_5__uncultured	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.03%	0.00%
D_0__Bacteria;D_1__Bacteroidetes;D_2__BD2-2;D_3__uncultured sediment bacterium;D_4__uncultured sediment bacterium;D_5__uncultured sediment bacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.05%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__Bacteroidetes;D_2__Sphingobacteriia;D_3__Sphingobacteriales;D_4__Chitinophagaceae;D_5__Parasegetibacter	0.00%	0.00%	0.00%	0.00%	0.05%	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__Candidate division OP11;D_2__uncultured Chloroflexi bacterium;D_3__uncultured Chloroflexi bacterium;D_4__uncultured Chloroflexi bacterium;D_5__uncultured Chloroflexi bacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.05%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__Chloroflexi;D_2__Ardenticatenia;D_3__uncultured;D_4__uncultured bacterium;D_5__uncultured bacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.02%	0.03%	0.00%	0.00%
D_0__Bacteria;D_1__Firmicutes;D_2__Bacilli;D_3__Lactobacillales;D_4__Lactobacillaceae;D_5__Lactobacillus	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.03%	0.00%
D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Syntrophomonadaceae;D_5__Syntrophomonas	0.00%	0.00%	0.00%	0.02%	0.05%	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__Lentisphaerae;D_2__Oligosphaeria;D_3__Oligosphaerales;D_4__uncultured bacterium;D_5__uncultured bacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.03%	0.00%
D_0__Bacteria;D_1__Nitrospirae;D_2__Nitrospira;D_3__Nitrospirales;D_4__Nitrospiraceae;D_5__Thermodesulfovibrio	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.05%	0.00%	0.00%
D_0__Bacteria;D_1__Planctomycetes;D_2__Phycisphaerae;D_3__Phycisphaerales;D_4__Sva0503;D_5__uncultured planctomycete	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%	0.05%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhizobiales;D_4__DUNssu044;D_5__uncultured bacterium	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.03%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Sphingomonadales;D_4__Erythrobacteraceae;D_5__Erythrobacter	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%	0.05%
D_0__Bacteria;D_1__Proteobacteria;D_2__Betaproteobacteria;D_3__Burkholderiales;D_4__Comamonadaceae;D_5__Aquabacterium	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%	0.05%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Betaproteobacteria;D_3__Burkholderiales;D_4__Comamonadaceae;D_5__Pelomonas	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.05%	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__Desulfobacterales;D_4__Desulfobacteraceae;D_5__Desulfocella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.05%	0.02%	0.00%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Deltaproteobacteria;D_3__Sh765B-TzT-29;D_4__uncultured soil bacterium;D_5__uncultured soil bacterium	0.00%	0.00%	0.03%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Chromatiales;D_4__Chromatiaceae;D_5__Rheinheimera	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.05%	0.02%	0.00%	0.00%
D_0__Bacteria;D_1__Spirochaetae;D_2__Spirochaetes;D_3__uncultured bacterium;D_4__uncultured bacterium;D_5__uncultured bacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.03%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%
D_0__Bacteria;D_1__Thermotogae;D_2__Thermotogae;D_3__Thermotogales;D_4__Thermotogaceae;D_5__060F05-B-SD-P93	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.02%	0.00%	0.00%	0.03%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__Verrucomicrobia;D_2__Opitutae;D_3__Opitutales;D_4__Opitutaceae;D_5__Opitutus	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.03%
D_0__Bacteria;D_1__Verrucomicrobia;D_2__Spartobacteria;D_3__Chthoniobacterales;D_4__Chthoniobacteraceae;D_5__Chthoniobacter	0.00%	0.03%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__Acidobacteria;D_2__Acidobacteria;D_3__Subgroup 3;D_4__PAUC26f;D_5__uncultured Solibacteraceae bacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.02%	0.00%	0.02%
D_0__Bacteria;D_1__Acidobacteria;D_2__Acidobacteria;D_3__Subgroup 4;D_4__11-24;D_5__uncultured Acidobacteriales bacterium	0.00%	0.00%	0.02%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.02%	0.00%
D_0__Bacteria;D_1__Acidobacteria;D_2__Acidobacteria;D_3__Subgroup 5;D_4__uncultured Acidobacteria bacterium;D_5__uncultured Acidobacteria bacterium	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.02%	0.00%	0.02%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__Actinobacteria;D_2__Acidimicrobiia;D_3__Acidimicrobiales;D_4__Acidimicrobiaceae;D_5__CL500-29 marine group	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.02%	0.00%	0.02%	0.02%	0.00%	0.00%
D_0__Bacteria;D_1__Actinobacteria;D_2__Actinobacteria;D_3__Frankiales;D_4__Acidothermaceae;D_5__Acidothermus	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.02%	0.02%	0.00%
D_0__Bacteria;D_1__Chloroflexi;D_2__Gitt-GS-136;D_3__uncultured Anaerolineae bacterium;D_4__uncultured Anaerolineae bacterium;D_5__uncultured Anaerolineae bacterium	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.02%	0.00%	0.02%	0.00%	0.00%
D_0__Bacteria;D_1__Chloroflexi;D_2__KD4-96;D_3__uncultured Chloroflexi bacterium;D_4__uncultured Chloroflexi bacterium;D_5__uncultured Chloroflexi bacterium	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.02%	0.00%	0.00%	0.00%	0.00%	0.02%
D_0__Bacteria;D_1__Chloroflexi;D_2__Thermomicrobia;D_3__JG30-KF-CM45;D_4__uncultured Chloroflexi bacterium;D_5__uncultured Chloroflexi bacterium	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.02%	0.02%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rickettsiales;D_4__EF100-94H03;D_5__uncultured bacterium	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.02%	0.02%	0.00%	0.00%	0.02%	0.00%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Betaproteobacteria;D_3__Nitrosomonadales;D_4__Nitrosomonadaceae;D_5__Nitrosospira	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.02%	0.02%	0.02%	0.00%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Betaproteobacteria;D_3__Rhodocyclales;D_4__Rhodocyclaceae;D_5__Azovibrio	0.00%	0.02%	0.00%	0.02%	0.00%	0.00%	0.02%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Betaproteobacteria;D_3__TRA3-20;D_4__uncultured bacterium CSL142;D_5__uncultured bacterium CSL142	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.02%	0.00%	0.02%	0.00%	0.00%	0.00%	0.02%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Deltaproteobacteria;D_3__Myxococcales;D_4__Nannocystaceae;D_5__Nannocystis	0.00%	0.00%	0.02%	0.02%	0.00%	0.02%	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__Gammaproteobacteria;D_3__NKB5;D_4__uncultured bacterium;D_5__uncultured bacterium	0.00%	0.00%	0.02%	0.00%	0.02%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%
D_0__Bacteria;D_1__Verrucomicrobia;D_2__OPB35 soil group;D_3__uncultured bacterium;D_4__uncultured bacterium;D_5__uncultured bacterium	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.02%	0.00%	0.00%	0.02%	0.00%
D_0__Bacteria;D_1__Actinobacteria;D_2__Actinobacteria;D_3__Micrococcales;D_4__Jonesiaceae;D_5__Jonesia	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.05%	0.00%	0.00%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__Actinobacteria;D_2__Actinobacteria;D_3__Micromonosporales;D_4__Micromonosporaceae;D_5__Dactylosporangium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.03%	0.00%	0.02%	0.00%	0.00%
D_0__Bacteria;D_1__Bacteroidetes;D_2__Sphingobacteriia;D_3__Sphingobacteriales;D_4__CMW-169;D_5__uncultured bacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.03%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__Candidate division JS1;D_2__uncultured organism;D_3__uncultured organism;D_4__uncultured organism;D_5__uncultured organism	0.00%	0.00%	0.00%	0.00%	0.00%	0.03%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__Candidate division OP8;D_2__uncultured microorganism;D_3__uncultured microorganism;D_4__uncultured microorganism;D_5__uncultured microorganism	0.00%	0.00%	0.00%	0.00%	0.00%	0.03%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Peptostreptococcaceae;D_5__Incertae Sedis	0.00%	0.00%	0.00%	0.02%	0.03%	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__Alphaproteobacteria;D_3__DB1-14;D_4__uncultured organism;D_5__uncultured organism	0.00%	0.00%	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%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhizobiales;D_4__Bradyrhizobiaceae;D_5__Rhodopseudomonas	0.00%	0.00%	0.03%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhizobiales;D_4__Methylobacteriaceae;D_5__Methylobacterium	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%	0.03%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhodospirillales;D_4__Rhodospirillaceae;D_5__Magnetospirillum	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.03%	0.00%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Betaproteobacteria;D_3__Burkholderiales;D_4__Comamonadaceae;D_5__Curvibacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.05%	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__Desulfobacterales;D_4__Desulfobulbaceae;D_5__MSBL7	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.05%	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__Desulfuromonadales;D_4__Desulfuromonadaceae;D_5__Desulfuromusa	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.05%	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__Desulfuromonadales;D_4__GR-WP33-58;D_5__uncultured delta proteobacterium	0.00%	0.00%	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%
D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Chromatiales;D_4__Ectothiorhodospiraceae;D_5__uncultured bacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.05%	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__Enterobacteriales;D_4__Enterobacteriaceae;D_5__Enterobacter	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%	0.03%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Xanthomonadales;D_4__Algiphilaceae;D_5__Algiphilus	0.00%	0.00%	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%
D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Xanthomonadales;D_4__Xanthomonadaceae;D_5__Xanthomonas	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.03%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__Acidobacteria;D_2__Acidobacteria;D_3__Subgroup 11;D_4__uncultured bacterium;D_5__uncultured bacterium	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%
D_0__Bacteria;D_1__Acidobacteria;D_2__Acidobacteria;D_3__Subgroup 17;D_4__uncultured Acidobacteria bacterium;D_5__uncultured Acidobacteria bacterium	0.00%	0.00%	0.00%	0.02%	0.02%	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__Acidobacteria;D_2__Acidobacteria;D_3__Subgroup 18;D_4__uncultured bacterium;D_5__uncultured bacterium	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.02%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__Acidobacteria;D_2__Acidobacteria;D_3__Subgroup 4;D_4__Elev-16S-573;D_5__uncultured Acidobacteria bacterium	0.00%	0.02%	0.00%	0.02%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__Acidobacteria;D_2__Holophagae;D_3__Subgroup 10;D_4__ABS-19;D_5__uncultured Acidobacteria bacterium	0.00%	0.00%	0.00%	0.02%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%
D_0__Bacteria;D_1__Acidobacteria;D_2__Holophagae;D_3__Subgroup 7;D_4__uncultured proteobacterium;D_5__uncultured proteobacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.02%
D_0__Bacteria;D_1__Actinobacteria;D_2__Acidimicrobiia;D_3__Acidimicrobiales;D_4__Iamiaceae;D_5__Iamia	0.00%	0.02%	0.00%	0.02%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__Actinobacteria;D_2__Actinobacteria;D_3__Micrococcales;D_4__Microbacteriaceae;D_5__Agromyces	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.02%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__Actinobacteria;D_2__Actinobacteria;D_3__Propionibacteriales;D_4__Nocardioidaceae;D_5__Marmoricola	0.00%	0.02%	0.00%	0.00%	0.00%	0.02%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__Actinobacteria;D_2__Actinobacteria;D_3__Streptosporangiales;D_4__Streptosporangiaceae;D_5__Streptosporangium	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.02%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__Actinobacteria;D_2__Thermoleophilia;D_3__Gaiellales;D_4__uncultured;D_5__uncultured microorganism	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.02%
D_0__Bacteria;D_1__Actinobacteria;D_2__Thermoleophilia;D_3__Solirubrobacterales;D_4__Patulibacteraceae;D_5__Patulibacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.02%	0.00%
D_0__Bacteria;D_1__Actinobacteria;D_2__Thermoleophilia;D_3__Solirubrobacterales;D_4__TM146;D_5__freshwater sediment metagenome	0.00%	0.02%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__Bacteroidetes;D_2__Flavobacteriia;D_3__Flavobacteriales;D_4__Flavobacteriaceae;D_5__uncultured	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%
D_0__Bacteria;D_1__Bacteroidetes;D_2__Sphingobacteriia;D_3__Sphingobacteriales;D_4__Chitinophagaceae;D_5__Chitinophaga	0.00%	0.00%	0.02%	0.02%	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__Bacteroidetes;D_2__Sphingobacteriia;D_3__Sphingobacteriales;D_4__Sphingobacteriaceae;D_5__Sphingobacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.02%
D_0__Bacteria;D_1__Bacteroidetes;D_2__VC2.1 Bac22;D_3__unidentified;D_4__unidentified;D_5__unidentified	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.02%	0.02%	0.00%	0.00%
D_0__Bacteria;D_1__Bacteroidetes;D_2__WCHB1-32;D_3__uncultured bacterium;D_4__uncultured bacterium;D_5__uncultured bacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.02%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__Chlorobi;D_2__Ignavibacteria;D_3__Ignavibacteriales;D_4__IheB3-7;D_5__uncultured bacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.02%	0.00%
D_0__Bacteria;D_1__Chloroflexi;D_2__Chloroflexia;D_3__AKIW781;D_4__uncultured bacterium;D_5__uncultured bacterium	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.02%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__Chloroflexi;D_2__KD4-96;D_3__uncultured Anaerolineae bacterium;D_4__uncultured Anaerolineae bacterium;D_5__uncultured Anaerolineae bacterium	0.00%	0.02%	0.00%	0.00%	0.02%	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__Chloroflexi;D_2__TK10;D_3__uncultured Chloroflexi bacterium;D_4__uncultured Chloroflexi bacterium;D_5__uncultured Chloroflexi bacterium	0.00%	0.02%	0.00%	0.02%	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__Cyanobacteria;D_2__Chloroplast;D_3__Athetis lepigone;D_4__Athetis lepigone;D_5__Athetis lepigone	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%
D_0__Bacteria;D_1__Gemmatimonadetes;D_2__Gemmatimonadetes;D_3__BD2-11 terrestrial group;D_4__uncultured bacterium;D_5__uncultured bacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.02%	0.00%	0.02%
D_0__Bacteria;D_1__Planctomycetes;D_2__Planctomycetacia;D_3__Planctomycetales;D_4__Planctomycetaceae;D_5__Isosphaera	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.02%	0.02%	0.00%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Caulobacterales;D_4__Hyphomonadaceae;D_5__Hirschia	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.02%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhizobiales;D_4__Methylobacteriaceae;D_5__uncultured	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%	0.02%	0.02%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhodobacterales;D_4__Rhodobacteraceae;D_5__Salinihabitans	0.00%	0.02%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhodospirillales;D_4__Rhodospirillaceae;D_5__Skermanella	0.00%	0.02%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Sphingomonadales;D_4__Sphingomonadaceae;D_5__Blastomonas	0.00%	0.00%	0.00%	0.00%	0.02%	0.02%	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__Burkholderiales;D_4__Comamonadaceae;D_5__Aquincola	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.02%	0.00%	0.00%	0.02%
D_0__Bacteria;D_1__Proteobacteria;D_2__Betaproteobacteria;D_3__TRA3-20;D_4__uncultured Rhodocyclaceae bacterium;D_5__uncultured Rhodocyclaceae bacterium	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.02%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Betaproteobacteria;D_3__TRA3-20;D_4__uncultured gamma proteobacterium;D_5__uncultured gamma proteobacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.02%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Xanthomonadales;D_4__uncultured;D_5__uncultured gamma proteobacterium	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%
D_0__Bacteria;D_1__Spirochaetae;D_2__Spirochaetes;D_3__W5;D_4__uncultured Spirochaetes bacterium;D_5__uncultured Spirochaetes bacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.02%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%
D_0__Bacteria;D_1__Synergistetes;D_2__Synergistia;D_3__Synergistales;D_4__Synergistaceae;D_5__Aminivibrio	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.02%	0.00%	0.02%	0.00%
D_0__Bacteria;D_1__Acidobacteria;D_2__Holophagae;D_3__Holophagales;D_4__Holophagaceae;D_5__uncultured	0.00%	0.00%	0.00%	0.00%	0.00%	0.03%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__Actinobacteria;D_2__Actinobacteria;D_3__Frankiales;D_4__Cryptosporangiaceae;D_5__Cryptosporangium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.03%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__Actinobacteria;D_2__Actinobacteria;D_3__Micrococcales;D_4__Intrasporangiaceae;D_5__Lapillicoccus	0.00%	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%
D_0__Bacteria;D_1__Candidate division BRC1;D_2__uncultured Fusobacteria bacterium;D_3__uncultured Fusobacteria bacterium;D_4__uncultured Fusobacteria bacterium;D_5__uncultured Fusobacteria bacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.03%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__Candidate division JS1;D_2__uncultured bacterium UASB_TL94;D_3__uncultured bacterium UASB_TL94;D_4__uncultured bacterium UASB_TL94;D_5__uncultured bacterium UASB_TL94	0.00%	0.00%	0.00%	0.03%	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__Candidate division KB1;D_2__uncultured Acetothermia bacterium;D_3__uncultured Acetothermia bacterium;D_4__uncultured Acetothermia bacterium;D_5__uncultured Acetothermia 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%	0.03%	0.00%
D_0__Bacteria;D_1__Chloroflexi;D_2__Dehalococcoidia;D_3__GIF9;D_4__uncultured Chloroflexi bacterium;D_5__uncultured Chloroflexi 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%	0.03%	0.00%
D_0__Bacteria;D_1__Chloroflexi;D_2__uncultured;D_3__uncultured organism;D_4__uncultured organism;D_5__uncultured organism	0.00%	0.00%	0.00%	0.00%	0.00%	0.03%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__Chloroflexi;D_2__uncultured;D_3__uncultured soil bacterium;D_4__uncultured soil bacterium;D_5__uncultured soil bacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.03%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__Deferribacteres;D_2__Deferribacteres;D_3__Deferribacterales;D_4__PAUC34f;D_5__uncultured bacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.03%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Clostridiaceae 1;D_5__Clostridium sensu stricto 1	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.03%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Lachnospiraceae;D_5__Acetitomaculum	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%	0.03%	0.00%
D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Peptococcaceae;D_5__Desulfitobacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.03%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Thermoanaerobacterales;D_4__Thermoanaerobacteraceae;D_5__Thermoanaerobacter	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%	0.03%
D_0__Bacteria;D_1__Firmicutes;D_2__Erysipelotrichia;D_3__Erysipelotrichales;D_4__Erysipelotrichaceae;D_5__uncultured	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.03%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__Firmicutes;D_2__Negativicutes;D_3__Selenomonadales;D_4__uncultured;D_5__uncultured bacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.03%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__Fusobacteria;D_2__Fusobacteriia;D_3__Fusobacteriales;D_4__Leptotrichiaceae;D_5__uncultured	0.00%	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%
D_0__Bacteria;D_1__NPL-UPA2;D_2__uncultured bacterium;D_3__uncultured bacterium;D_4__uncultured bacterium;D_5__uncultured bacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.03%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__Planctomycetes;D_2__Phycisphaerae;D_3__KCLunmb-38-53;D_4__uncultured bacterium;D_5__uncultured bacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.03%	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__Alphaproteobacteria;D_3__Caulobacterales;D_4__Hyphomonadaceae;D_5__Woodsholea	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%	0.03%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhizobiales;D_4__Xanthobacteraceae;D_5__Aquabacter	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%	0.03%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhodobacterales;D_4__Rhodobacteraceae;D_5__Thalassobius	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%	0.03%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhodospirillales;D_4__Rhodospirillaceae;D_5__Novispirillum	0.00%	0.00%	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%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rickettsiales;D_4__Rickettsiales Incertae Sedis;D_5__Candidatus Captivus	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%	0.03%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Betaproteobacteria;D_3__Burkholderiales;D_4__Alcaligenaceae;D_5__Castellaniella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.03%	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__Burkholderiales;D_4__Comamonadaceae;D_5__Brachymonas	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%	0.03%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Deltaproteobacteria;D_3__Desulfobacterales;D_4__Desulfobacteraceae;D_5__Desulfococcus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.03%	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__Desulfuromonadales;D_4__uncultured;D_5__uncultured bacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.03%	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__1013-28-CG33;D_4__uncultured bacterium;D_5__uncultured bacterium	0.00%	0.00%	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%
D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Xanthomonadales;D_4__uncultured;D_5__gamma proteobacterium CH43	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%	0.03%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__SPOTSOCT00m83;D_3__uncultured bacterium;D_4__uncultured bacterium;D_5__uncultured bacterium	0.00%	0.00%	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%
D_0__Bacteria;D_1__Tenericutes;D_2__Mollicutes;D_3__NB1-n;D_4__uncultured organism;D_5__uncultured organism	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.03%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__Acidobacteria;D_2__Acidobacteria;D_3__Subgroup 3;D_4__Elev-16S-1166;D_5__uncultured soil bacterium	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__Acidobacteria;D_2__Acidobacteria;D_3__Subgroup 4;D_4__DS-100;D_5__uncultured bacterium	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%	0.02%	0.00%
D_0__Bacteria;D_1__Acidobacteria;D_2__Acidobacteria;D_3__Subgroup 5;D_4__uncultured Acidobacteriales bacterium;D_5__uncultured Acidobacteriales bacterium	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%	0.00%	0.02%
D_0__Bacteria;D_1__Acidobacteria;D_2__Acidobacteria;D_3__Subgroup 6;D_4__Acidobacteria bacterium IGE-003;D_5__Acidobacteria bacterium IGE-003	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%	0.02%	0.00%
D_0__Bacteria;D_1__Acidobacteria;D_2__Acidobacteria;D_3__Subgroup 6;D_4__uncultured Acidobacteriaceae bacterium;D_5__uncultured Acidobacteriaceae bacterium	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%

D_0__Bacteria;D_1__Acidobacteria;D_2__Holophagae;D_3__Subgroup 7;D_4__uncultured soil bacterium;D_5__uncultured soil bacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__Actinobacteria;D_2__Acidimicrobiia;D_3__Acidimicrobiales;D_4__uncultured;D_5__uncultured actinobacterium	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%	0.02%	0.00%
D_0__Bacteria;D_1__Actinobacteria;D_2__Actinobacteria;D_3__Frankiales;D_4__Cryptosporangiaceae;D_5__Fodinicola	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__Actinobacteria;D_2__Actinobacteria;D_3__Frankiales;D_4__Geodermatophilaceae;D_5__Modestobacter	0.00%	0.00%	0.00%	0.02%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__Actinobacteria;D_2__Actinobacteria;D_3__Frankiales;D_4__Nakamurellaceae;D_5__Nakamurella	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__Actinobacteria;D_2__Actinobacteria;D_3__Frankiales;D_4__Sporichthyaceae;D_5__uncultured	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%	0.02%	0.00%
D_0__Bacteria;D_1__Actinobacteria;D_2__Actinobacteria;D_3__Micrococcales;D_4__Microbacteriaceae;D_5__Frigoribacterium	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%	0.02%
D_0__Bacteria;D_1__Actinobacteria;D_2__Actinobacteria;D_3__Micrococcales;D_4__Microbacteriaceae;D_5__Salinibacterium	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%	0.02%
D_0__Bacteria;D_1__Actinobacteria;D_2__Actinobacteria;D_3__Propionibacteriales;D_4__Propionibacteriaceae;D_5__Microlunatus	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%
D_0__Bacteria;D_1__Actinobacteria;D_2__Actinobacteria;D_3__Pseudonocardiales;D_4__Pseudonocardiaceae;D_5__Actinophytocola	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__Actinobacteria;D_2__Actinobacteria;D_3__Pseudonocardiales;D_4__Pseudonocardiaceae;D_5__Crossiella	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%	0.02%	0.00%
D_0__Bacteria;D_1__Actinobacteria;D_2__MB-A2-108;D_3__uncultured actinobacterium;D_4__uncultured actinobacterium;D_5__uncultured actinobacterium	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%	0.02%	0.00%
D_0__Bacteria;D_1__Actinobacteria;D_2__Thermoleophilia;D_3__Solirubrobacterales;D_4__0319-6M6;D_5__uncultured Rubrobacteraceae bacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__Actinobacteria;D_2__Thermoleophilia;D_3__Solirubrobacterales;D_4__480-2;D_5__uncultured actinobacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.02%	0.00%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__Actinobacteria;D_2__Thermoleophilia;D_3__Solirubrobacterales;D_4__TM146;D_5__uncultured bacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%
D_0__Bacteria;D_1__Bacteroidetes;D_2__Cytophagia;D_3__Cytophagales;D_4__Cytophagaceae;D_5__Meniscus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__Bacteroidetes;D_2__Flavobacteriia;D_3__Flavobacteriales;D_4__NS9 marine group;D_5__uncultured soil 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%	0.02%
D_0__Bacteria;D_1__Bacteroidetes;D_2__Sphingobacteriia;D_3__Sphingobacteriales;D_4__Sphingobacteriaceae;D_5__uncultured	0.00%	0.02%	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__Candidate division BRC1;D_2__uncultured candidate division BRC1 bacterium;D_3__uncultured candidate division BRC1 bacterium;D_4__uncultured candidate division BRC1 bacterium;D_5__uncultured candidate division BRC1 bacterium	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%	0.02%	0.00%
D_0__Bacteria;D_1__Candidate division OP11;D_2__uncultured anaerobic bacterium;D_3__uncultured anaerobic bacterium;D_4__uncultured anaerobic bacterium;D_5__uncultured anaerobic bacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__Candidate division OP11;D_2__uncultured eubacterium WCHB1-56;D_3__uncultured eubacterium WCHB1-56;D_4__uncultured eubacterium WCHB1-56;D_5__uncultured eubacterium WCHB1-56	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__Chloroflexi;D_2__Ktedonobacteria;D_3__Ktedonobacterales;D_4__HSB OF53-F07;D_5__uncultured Ktedonobacter sp.	0.00%	0.00%	0.00%	0.02%	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__Cyanobacteria;D_2__Chloroplast;D_3__Fraxinus excelsior (European ash);D_4__Fraxinus excelsior (European ash);D_5__Fraxinus excelsior (European ash)	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%	0.02%	0.00%
D_0__Bacteria;D_1__Cyanobacteria;D_2__Melainabacteria;D_3__Obscuribacterales;D_4__uncultured bacterium;D_5__uncultured bacterium	0.00%	0.02%	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%
D_0__Bacteria;D_1__Dictyoglomi;D_2__Dictyoglomia;D_3__Dictyoglomales;D_4__Dictyoglomaceae;D_5__Dictyoglomus	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__Elusimicrobia;D_2__Elusimicrobia;D_3__12-31;D_4__uncultured bacterium;D_5__uncultured bacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%
D_0__Bacteria;D_1__Elusimicrobia;D_2__Elusimicrobia;D_3__Lineage IIa;D_4__uncultured Elusimicrobia bacterium;D_5__uncultured Elusimicrobia bacterium	0.00%	0.02%	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__Firmicutes;D_2__Bacilli;D_3__Bacillales;D_4__Planococcaceae;D_5__Incertae Sedis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__Firmicutes;D_2__Bacilli;D_3__Bacillales;D_4__Planococcaceae;D_5__Lysinibacillus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__Firmicutes;D_2__Bacilli;D_3__Bacillales;D_4__Planococcaceae;D_5__Sporosarcina	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%	0.02%	0.00%
D_0__Bacteria;D_1__Firmicutes;D_2__Bacilli;D_3__Lactobacillales;D_4__Enterococcaceae;D_5__Enterococcus	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%	0.02%	0.00%
D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Family XI;D_5__Sedimentibacter	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%	0.02%
D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Gracilibacteraceae;D_5__uncultured	0.00%	0.00%	0.00%	0.02%	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__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Lachnospiraceae;D_5__Blautia	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__TSAC18;D_5__uncultured bacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%
D_0__Bacteria;D_1__Firmicutes;D_2__OPB54;D_3__uncultured bacterium;D_4__uncultured bacterium;D_5__uncultured bacterium	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__Lentisphaerae;D_2__Oligosphaeria;D_3__Oligosphaerales;D_4__uncultured Lentisphaerae bacterium;D_5__uncultured Lentisphaerae bacterium	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%	0.02%	0.00%
D_0__Bacteria;D_1__Planctomycetes;D_2__Phycisphaerae;D_3__CCM11a;D_4__uncultured bacterium;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%	0.02%	0.00%	0.02%
D_0__Bacteria;D_1__Planctomycetes;D_2__Phycisphaerae;D_3__S-70;D_4__uncultured bacterium;D_5__uncultured bacterium	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%	0.02%	0.00%
D_0__Bacteria;D_1__Planctomycetes;D_2__Phycisphaerae;D_3__WD2101 soil group;D_4__uncultured planctomycete;D_5__uncultured planctomycete	0.00%	0.02%	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%
D_0__Bacteria;D_1__Planctomycetes;D_2__Planctomycetacia;D_3__Planctomycetales;D_4__Planctomycetaceae;D_5__Schlesneria	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%	0.02%	0.00%
D_0__Bacteria;D_1__Planctomycetes;D_2__vadinHA49;D_3__uncultured bacterium;D_4__uncultured bacterium;D_5__uncultured bacterium	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%	0.02%	0.00%
D_0__Bacteria;D_1__Planctomycetes;D_2__vadinHA49;D_3__uncultured sediment bacterium;D_4__uncultured sediment bacterium;D_5__uncultured sediment bacterium	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%	0.02%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhizobiales;D_4__DUNssu371;D_5__uncultured Hyphomicrobiaceae bacterium	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhizobiales;D_4__Elev-16S-1546;D_5__uncultured Methylocystaceae bacterium	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%	0.02%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhizobiales;D_4__MNG7;D_5__uncultured Rhizobiales bacterium	0.00%	0.00%	0.00%	0.02%	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__Alphaproteobacteria;D_3__Rhizobiales;D_4__Methylocystaceae;D_5__Methylocystis	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhizobiales;D_4__Rhizobiales Incertae Sedis;D_5__Agaricicola	0.00%	0.02%	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__Alphaproteobacteria;D_3__Rhodobacterales;D_4__Rhodobacteraceae;D_5__Amaricoccus	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%	0.02%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhodospirillales;D_4__Acetobacteraceae;D_5__uncultured	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhodospirillales;D_4__DA111;D_5__uncultured alpha proteobacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rickettsiales;D_4__AKIW1012;D_5__uncultured bacterium	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%	0.02%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rickettsiales;D_4__mitochondria;D_5__Populus euphratica	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Sphingomonadales;D_4__Ellin6055;D_5__uncultured bacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	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__Comamonadaceae;D_5__Piscinibacter	0.00%	0.00%	0.02%	0.00%	0.00%	0.02%	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__Burkholderiales;D_4__Oxalobacteraceae;D_5__Paucimonas	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Betaproteobacteria;D_3__Burkholderiales;D_4__Oxalobacteraceae;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%	0.02%
D_0__Bacteria;D_1__Proteobacteria;D_2__Betaproteobacteria;D_3__Rhodocyclales;D_4__Rhodocyclaceae;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%	0.02%	0.02%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Betaproteobacteria;D_3__SC-I-84;D_4__uncultured Rhodocyclaceae bacterium;D_5__uncultured Rhodocyclaceae bacterium	0.00%	0.00%	0.00%	0.02%	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__Deltaproteobacteria;D_3__Desulfovibrionales;D_4__Desulfovibrionaceae;D_5__uncultured bacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.02%	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__GR-WP33-30;D_4__uncultured Gemmatimonadetes bacterium;D_5__uncultured Gemmatimonadetes bacterium	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%	0.02%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Deltaproteobacteria;D_3__GR-WP33-30;D_4__uncultured delta proteobacterium;D_5__uncultured delta proteobacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%
D_0__Bacteria;D_1__Proteobacteria;D_2__Deltaproteobacteria;D_3__Myxococcales;D_4__0319-6G20;D_5__uncultured delta proteobacterium	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.02%	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__Myxococcales;D_4__Sandaracinaceae;D_5__uncultured delta proteobacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Deltaproteobacteria;D_3__Syntrophobacterales;D_4__Syntrophobacteraceae;D_5__Thermodesulforhabdus	0.00%	0.02%	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__Alteromonadales;D_4__Alteromonadaceae;D_5__BD1-7 clade	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%	0.02%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Alteromonadales;D_4__Alteromonadaceae;D_5__Haliea	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%	0.00%	0.02%
D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Legionellales;D_4__Coxiellaceae;D_5__Coxiella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Legionellales;D_4__Coxiellaceae;D_5__uncultured	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__NKB5;D_4__Legionella-like amoebal pathogen HT99;D_5__Legionella-like amoebal pathogen HT99	0.00%	0.00%	0.00%	0.02%	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__WN-HWB-116;D_4__uncultured gamma proteobacterium;D_5__uncultured gamma proteobacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	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__Xanthomonadales;D_4__Xanthomonadaceae;D_5__Luteimonas	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Xanthomonadales;D_4__Xanthomonadaceae;D_5__uncultured bacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.02%	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 Incertae Sedis;D_5__compost metagenome	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__SHA-109;D_2__uncultured soil bacterium;D_3__uncultured soil bacterium;D_4__uncultured soil bacterium;D_5__uncultured soil bacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__SM2F11;D_2__uncultured bacterium;D_3__uncultured bacterium;D_4__uncultured bacterium;D_5__uncultured bacterium	0.00%	0.00%	0.02%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__TM6;D_2__uncultured bacterium;D_3__uncultured bacterium;D_4__uncultured bacterium;D_5__uncultured bacterium	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__Verrucomicrobia;D_2__OPB35 soil group;D_3__uncultured Verrucomicrobia bacterium;D_4__uncultured Verrucomicrobia bacterium;D_5__uncultured Verrucomicrobia bacterium	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%
D_0__Bacteria;D_1__Acidobacteria;D_2__Acidobacteria;D_3__Acidobacteriales;D_4__Acidobacteriaceae (Subgroup 1);D_5__Acidobacterium	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%	0.00%
D_0__Bacteria;D_1__Acidobacteria;D_2__Acidobacteria;D_3__Subgroup 17;D_4__uncultured Acidobacteriaceae bacterium;D_5__uncultured Acidobacteriaceae bacterium	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%	0.00%
D_0__Bacteria;D_1__Acidobacteria;D_2__Acidobacteria;D_3__Subgroup 3;D_4__Elev-16S-1166;D_5__uncultured bacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__Acidobacteria;D_2__Acidobacteria;D_3__Subgroup 3;D_4__PAUC26f;D_5__uncultured bacterium	0.00%	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__Acidobacteria;D_2__Acidobacteria;D_3__Subgroup 3;D_4__SJA-149;D_5__uncultured Acidobacteria bacterium	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%	0.00%
D_0__Bacteria;D_1__Acidobacteria;D_2__Acidobacteria;D_3__Subgroup 4;D_4__RB41;D_5__uncultured bacterium gp4	0.00%	0.00%	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%
D_0__Bacteria;D_1__Acidobacteria;D_2__Acidobacteria;D_3__Subgroup 4;D_4__RB41;D_5__uncultured soil bacterium	0.00%	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__Acidobacteria;D_2__Acidobacteria;D_3__Subgroup 6;D_4__uncultured Acidobacterium sp.;D_5__uncultured Acidobacterium sp.	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%	0.00%	0.00%
D_0__Bacteria;D_1__Acidobacteria;D_2__Holophagae;D_3__Subgroup 10;D_4__ABS-19;D_5__Acidobacteria bacterium WY67	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%	0.02%
D_0__Bacteria;D_1__Acidobacteria;D_2__Holophagae;D_3__Subgroup 10;D_4__Sva0725;D_5__uncultured bacterium	0.00%	0.00%	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%
D_0__Bacteria;D_1__Actinobacteria;D_2__Actinobacteria;D_3__Micrococcales;D_4__Microbacteriaceae;D_5__Pseudoclavibacter	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%	0.00%
D_0__Bacteria;D_1__Actinobacteria;D_2__Actinobacteria;D_3__Micromonosporales;D_4__Micromonosporaceae;D_5__Catellatospora	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%	0.00%
D_0__Bacteria;D_1__Actinobacteria;D_2__Actinobacteria;D_3__Micromonosporales;D_4__Micromonosporaceae;D_5__Hamadaea	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%	0.00%	0.00%
D_0__Bacteria;D_1__Actinobacteria;D_2__Actinobacteria;D_3__Micromonosporales;D_4__Micromonosporaceae;D_5__Micromonospora	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%	0.00%
D_0__Bacteria;D_1__Actinobacteria;D_2__Actinobacteria;D_3__Micromonosporales;D_4__Micromonosporaceae;D_5__Planosporangium	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%	0.00%
D_0__Bacteria;D_1__Actinobacteria;D_2__Actinobacteria;D_3__Pseudonocardiales;D_4__Pseudonocardiaceae;D_5__Actinomycetospora	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%	0.00%	0.00%
D_0__Bacteria;D_1__Actinobacteria;D_2__Actinobacteria;D_3__Streptosporangiales;D_4__Thermomonosporaceae;D_5__Actinocorallia	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%	0.00%
D_0__Bacteria;D_1__Actinobacteria;D_2__OPB41;D_3__uncultured bacterium;D_4__uncultured bacterium;D_5__uncultured bacterium	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%	0.00%
D_0__Bacteria;D_1__Actinobacteria;D_2__Thermoleophilia;D_3__Solirubrobacterales;D_4__0319-6M6;D_5__uncultured Rubrobacteridae bacterium	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%	0.00%	0.00%
D_0__Bacteria;D_1__Actinobacteria;D_2__Thermoleophilia;D_3__Solirubrobacterales;D_4__0319-6M6;D_5__uncultured actinobacterium	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%	0.00%
D_0__Bacteria;D_1__Actinobacteria;D_2__Thermoleophilia;D_3__Solirubrobacterales;D_4__Conexibacteraceae;D_5__Conexibacter	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%	0.00%	0.00%
D_0__Bacteria;D_1__Actinobacteria;D_2__Thermoleophilia;D_3__Solirubrobacterales;D_4__Elev-16S-1332;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%	0.00%	0.02%
D_0__Bacteria;D_1__Armatimonadetes;D_2__Chthonomonadetes;D_3__Chthonomonadales;D_4__Chthonomonadaceae;D_5__Chthonomonas	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%	0.00%	0.00%
D_0__Bacteria;D_1__Armatimonadetes;D_2__uncultured Armatimonadetes bacterium;D_3__uncultured Armatimonadetes bacterium;D_4__uncultured Armatimonadetes bacterium;D_5__uncultured Armatimonadetes 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%	0.00%
D_0__Bacteria;D_1__Bacteroidetes;D_2__BD2-2;D_3__uncultured Cytophagales bacterium;D_4__uncultured Cytophagales bacterium;D_5__uncultured Cytophagales bacterium	0.00%	0.00%	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%
D_0__Bacteria;D_1__Bacteroidetes;D_2__Bacteroidia;D_3__Bacteroidales;D_4__Bacteroidaceae;D_5__Bacteroides	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%	0.00%
D_0__Bacteria;D_1__Bacteroidetes;D_2__Bacteroidia;D_3__Bacteroidales;D_4__Marinilabiaceae;D_5__Anaerophaga	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%	0.00%
D_0__Bacteria;D_1__Bacteroidetes;D_2__Bacteroidia;D_3__Bacteroidales;D_4__Marinilabiaceae;D_5__Thermophagus	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%	0.00%
D_0__Bacteria;D_1__Bacteroidetes;D_2__Bacteroidia;D_3__Bacteroidales;D_4__Rikenellaceae;D_5__RC9 gut group	0.00%	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__Bacteroidetes;D_2__Cytophagia;D_3__Cytophagales;D_4__Cytophagaceae;D_5__Sporocytophaga	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%	0.00%
D_0__Bacteria;D_1__Bacteroidetes;D_2__Sphingobacteriia;D_3__Sphingobacteriales;D_4__Chitinophagaceae;D_5__Flavihumibacter	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%	0.00%
D_0__Bacteria;D_1__Bacteroidetes;D_2__Sphingobacteriia;D_3__Sphingobacteriales;D_4__KD3-93;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%	0.00%
D_0__Bacteria;D_1__Bacteroidetes;D_2__Sphingobacteriia;D_3__Sphingobacteriales;D_4__S15-21;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%	0.00%
D_0__Bacteria;D_1__Bacteroidetes;D_2__Sphingobacteriia;D_3__Sphingobacteriales;D_4__WCHB1-69;D_5__uncultured Cytophagales bacterium	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%	0.00%	0.00%
D_0__Bacteria;D_1__Candidate division OP11;D_2__uncultured Microgenomates bacterium;D_3__uncultured Microgenomates bacterium;D_4__uncultured Microgenomates bacterium;D_5__uncultured Microgenomates bacterium	0.00%	0.00%	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%
D_0__Bacteria;D_1__Candidate division OP11;D_2__uncultured soil bacterium;D_3__uncultured soil bacterium;D_4__uncultured soil bacterium;D_5__uncultured soil bacterium	0.00%	0.00%	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%
D_0__Bacteria;D_1__Candidate division OP3;D_2__uncultured Omnitrophica bacterium;D_3__uncultured Omnitrophica bacterium;D_4__uncultured Omnitrophica bacterium;D_5__uncultured Omnitrophica 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%	0.00%
D_0__Bacteria;D_1__Candidate division OP3;D_2__uncultured Verrucomicrobia bacterium;D_3__uncultured Verrucomicrobia bacterium;D_4__uncultured Verrucomicrobia bacterium;D_5__uncultured Verrucomicrobia 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%	0.00%
D_0__Bacteria;D_1__Candidate division WS3;D_2__uncultured Latescibacteria bacterium;D_3__uncultured Latescibacteria bacterium;D_4__uncultured Latescibacteria bacterium;D_5__uncultured Latescibacteria bacterium	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%	0.00%	0.00%
D_0__Bacteria;D_1__Candidate division WS3;D_2__uncultured delta proteobacterium;D_3__uncultured delta proteobacterium;D_4__uncultured delta proteobacterium;D_5__uncultured delta proteobacterium	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%	0.00%	0.00%
D_0__Bacteria;D_1__Chlamydiae;D_2__Chlamydiae;D_3__Chlamydiales;D_4__Simkaniaceae;D_5__Candidatus Rhabdochlamydia	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%	0.02%
D_0__Bacteria;D_1__Chlorobi;D_2__Chlorobia;D_3__Chlorobiales;D_4__OPB56;D_5__uncultured Desulfuromonadales 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%	0.00%
D_0__Bacteria;D_1__Chlorobi;D_2__Chlorobia;D_3__Chlorobiales;D_4__OPB56;D_5__uncultured organism	0.00%	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__Chlorobi;D_2__Chlorobia;D_3__Chlorobiales;D_4__SJA-28;D_5__uncultured bacterium	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%	0.00%
D_0__Bacteria;D_1__Chloroflexi;D_2__Caldilineae;D_3__Caldilineales;D_4__Caldilineaceae;D_5__Litorilinea	0.00%	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__Chloroflexi;D_2__Dehalococcoidia;D_3__FW22;D_4__uncultured organism;D_5__uncultured organism	0.00%	0.00%	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%
D_0__Bacteria;D_1__Chloroflexi;D_2__Gitt-GS-136;D_3__uncultured Caldilinea sp.;D_4__uncultured Caldilinea sp.;D_5__uncultured Caldilinea 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%	0.02%	0.00%	0.00%
D_0__Bacteria;D_1__Chloroflexi;D_2__Gitt-GS-136;D_3__uncultured bacterium;D_4__uncultured bacterium;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%	0.02%	0.00%	0.00%
D_0__Bacteria;D_1__Chloroflexi;D_2__Ktedonobacteria;D_3__JG30-KF-AS9;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%	0.00%
D_0__Bacteria;D_1__Chloroflexi;D_2__Ktedonobacteria;D_3__Ktedonobacterales;D_4__FCPS473;D_5__uncultured Ktedonobacter sp.	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%	0.00%
D_0__Bacteria;D_1__Chloroflexi;D_2__Ktedonobacteria;D_3__Ktedonobacterales;D_4__Ktedonobacteraceae;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%	0.00%
D_0__Bacteria;D_1__Chloroflexi;D_2__Thermomicrobia;D_3__AKYG1722;D_4__uncultured bacterium;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%	0.02%	0.00%	0.00%
D_0__Bacteria;D_1__Cyanobacteria;D_2__Chloroplast;D_3__Lotus corniculatus;D_4__Lotus corniculatus;D_5__Lotus corniculatus	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%	0.00%
D_0__Bacteria;D_1__Elusimicrobia;D_2__Elusimicrobia;D_3__Lineage IV;D_4__uncultured microorganism;D_5__uncultured microorganism	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%	0.00%	0.00%
D_0__Bacteria;D_1__Firmicutes;D_2__Bacilli;D_3__Bacillales;D_4__Paenibacillaceae;D_5__Paenibacillus	0.00%	0.00%	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%
D_0__Bacteria;D_1__Firmicutes;D_2__Bacilli;D_3__Bacillales;D_4__Planococcaceae;D_5__uncultured	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%	0.00%	0.00%
D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Clostridiaceae 2;D_5__Alkaliphilus	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%	0.00%
D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Clostridiaceae 4;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%	0.02%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Defluviitaleaceae;D_5__Defluviitalea	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%	0.00%
D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Family XI;D_5__Tissierella	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%	0.00%	0.00%
D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Lachnospiraceae;D_5__Marvinbryantia	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%	0.00%
D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__MAT-CR-H4-C10;D_5__uncultured Synergistetes 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%	0.00%
D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__P. palm C-A 51;D_5__uncultured organism	0.00%	0.00%	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%
D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Peptostreptococcaceae;D_5__uncultured	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%	0.00%
D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Syntrophomonadaceae;D_5__Candidatus Contubernalis	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%	0.02%
D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Syntrophomonadaceae;D_5__Syntrophothermus	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%	0.00%
D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__bacterium enrichment culture clone ecb10;D_5__bacterium enrichment culture clone ecb10	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%	0.00%
D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__NRB23;D_4__uncultured Clostridia bacterium;D_5__uncultured Clostridia bacterium	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%	0.00%	0.00%
D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Thermoanaerobacterales;D_4__Family III;D_5__Caldanaerovirga	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%	0.02%
D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Thermoanaerobacterales;D_4__Family IV;D_5__Mahella	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%	0.00%
D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Thermoanaerobacterales;D_4__Thermoanaerobacteraceae;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%	0.00%
D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Thermolithobacterales;D_4__Thermolithobacteraceae;D_5__Thermolithobacter	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%	0.00%
D_0__Bacteria;D_1__GOUTA4;D_2__uncultured bacterium;D_3__uncultured bacterium;D_4__uncultured bacterium;D_5__uncultured bacterium	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%	0.00%
D_0__Bacteria;D_1__Gemmatimonadetes;D_2__Gemmatimonadetes;D_3__BD2-11 terrestrial group;D_4__uncultured Gemmatimonadetes bacterium;D_5__uncultured Gemmatimonadetes bacterium	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%	0.00%
D_0__Bacteria;D_1__Gemmatimonadetes;D_2__Gemmatimonadetes;D_3__Gemmatimonadales;D_4__Gemmatimonadaceae;D_5__uncultured bacterium	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%	0.00%	0.00%
D_0__Bacteria;D_1__Gemmatimonadetes;D_2__Gemmatimonadetes;D_3__S0134 terrestrial group;D_4__uncultured bacterium;D_5__uncultured bacterium	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%	0.00%
D_0__Bacteria;D_1__Lentisphaerae;D_2__Oligosphaeria;D_3__Oligosphaerales;D_4__uncultured organism;D_5__uncultured organism	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%	0.00%
D_0__Bacteria;D_1__NPL-UPA2;D_2__uncultured organism;D_3__uncultured organism;D_4__uncultured organism;D_5__uncultured organism	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%	0.00%	0.00%
D_0__Bacteria;D_1__Planctomycetes;D_2__Phycisphaerae;D_3__CPla-3 termite group;D_4__uncultured planctomycete;D_5__uncultured planctomycete	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%	0.00%	0.00%
D_0__Bacteria;D_1__Planctomycetes;D_2__Phycisphaerae;D_3__Phycisphaerales;D_4__AKAU3564 sediment group;D_5__uncultured planctomycete	0.00%	0.00%	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%
D_0__Bacteria;D_1__Planctomycetes;D_2__Phycisphaerae;D_3__mle1-8;D_4__uncultured bacterium;D_5__uncultured bacterium	0.00%	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__Planctomycetes;D_2__Pla4 lineage;D_3__uncultured bacterium;D_4__uncultured bacterium;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%	0.02%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__Planctomycetes;D_2__Pla4 lineage;D_3__uncultured planctomycete;D_4__uncultured planctomycete;D_5__uncultured planctomycete	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%	0.00%
D_0__Bacteria;D_1__Planctomycetes;D_2__vadinHA49;D_3__uncultured organism;D_4__uncultured organism;D_5__uncultured organism	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%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__ARKICE-90;D_3__uncultured gamma proteobacterium;D_4__uncultured gamma proteobacterium;D_5__uncultured gamma proteobacterium	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%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Caulobacterales;D_4__Caulobacteraceae;D_5__Amorphus	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%	0.02%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Caulobacterales;D_4__Caulobacteraceae;D_5__uncultured bacterium	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%	0.00%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__DB1-14;D_4__uncultured marine bacterium;D_5__uncultured marine bacterium	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%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhizobiales;D_4__Aurantimonadaceae;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%	0.00%	0.02%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhizobiales;D_4__BCf3-20;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%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhizobiales;D_4__Brucellaceae;D_5__Ochrobactrum	0.00%	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__Alphaproteobacteria;D_3__Rhizobiales;D_4__D05-2;D_5__uncultured bacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhizobiales;D_4__Elev-16S-1546;D_5__uncultured proteobacterium	0.00%	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__Alphaproteobacteria;D_3__Rhizobiales;D_4__Hyphomicrobiaceae;D_5__Prosthecomicrobium	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%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhizobiales;D_4__Methylocystaceae;D_5__Pleomorphomonas	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%	0.00%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhizobiales;D_4__Phyllobacteriaceae;D_5__Aquamicrobium	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%	0.00%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhizobiales;D_4__Phyllobacteriaceae;D_5__Pseudaminobacter	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%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhizobiales;D_4__Rhizobiaceae;D_5__Shinella	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%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhizobiales;D_4__Rhodobiaceae;D_5__Tepidamorphus	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%	0.02%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhizobiales;D_4__Xanthobacteraceae;D_5__Ancylobacter	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%	0.02%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhodobacterales;D_4__Rhodobacteraceae;D_5__Celeribacter	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%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhodobacterales;D_4__Rhodobacteraceae;D_5__Citreicella	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%	0.02%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhodobacterales;D_4__Rhodobacteraceae;D_5__Falsirhodobacter	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%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhodobacterales;D_4__Rhodobacteraceae;D_5__Paracoccus	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%	0.02%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhodobacterales;D_4__Rhodobacteraceae;D_5__Ruegeria	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%	0.00%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhodobacterales;D_4__Rhodobacteraceae;D_5__Seohaeicola	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%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhodobacterales;D_4__Rhodobacteraceae;D_5__Tabrizicola	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%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhodobacterales;D_4__Rhodobacteraceae;D_5__Thioclava	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%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhodospirillales;D_4__MNC12;D_5__uncultured Rhodospirillales bacterium	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%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhodospirillales;D_4__Rhodospirillaceae;D_5__Defluviicoccus	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%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rickettsiales;D_4__RB446;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%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rickettsiales;D_4__Rickettsiaceae;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%	0.00%	0.02%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rickettsiales;D_4__Rickettsiales Incertae Sedis;D_5__Candidatus Odyssella	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%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rickettsiales;D_4__mitochondria;D_5__Jakoba libera	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%	0.02%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rickettsiales;D_4__mitochondria;D_5__Polypodium aureum	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%	0.00%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rickettsiales;D_4__mitochondria;D_5__Vermamoeba vermiformis	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%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Sphingomonadales;D_4__Sphingomonadaceae;D_5__Sphingobium	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%	0.00%

D_0__Bacteria;D_1__Proteobacteria;D_2__Betaproteobacteria;D_3__Burkholderiales;D_4__Burkholderiaceae;D_5__Lautropia	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%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Betaproteobacteria;D_3__Burkholderiales;D_4__Burkholderiales 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%	0.00%	0.02%
D_0__Bacteria;D_1__Proteobacteria;D_2__Betaproteobacteria;D_3__Hydrogenophilales;D_4__Hydrogenophilaceae;D_5__Hydrogenophilus	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%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Betaproteobacteria;D_3__Nitrosomonadales;D_4__Nitrosomonadaceae;D_5__Nitrosomonas	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%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Betaproteobacteria;D_3__Nitrosomonadales;D_4__Nitrosomonadaceae;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%	0.02%	0.00%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Betaproteobacteria;D_3__Rhodocyclales;D_4__Rhodocyclaceae;D_5__Georgfuchsia	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%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Betaproteobacteria;D_3__Rhodocyclales;D_4__Rhodocyclaceae;D_5__Uliginosibacterium	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%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Betaproteobacteria;D_3__SC-I-84;D_4__uncultured soil bacterium;D_5__uncultured soil 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%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Deltaproteobacteria;D_3__Desulfobacterales;D_4__Desulfobacteraceae;D_5__Desulfosarcina	0.00%	0.00%	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%
D_0__Bacteria;D_1__Proteobacteria;D_2__Deltaproteobacteria;D_3__Desulfobacterales;D_4__Desulfobulbaceae;D_5__Desulfocapsa	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%	0.00%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Deltaproteobacteria;D_3__Myxococcales;D_4__Elev-16S-1158;D_5__uncultured bacterium	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%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Deltaproteobacteria;D_3__Myxococcales;D_4__Myxococcaceae;D_5__Corallococcus exiguus	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%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Deltaproteobacteria;D_3__Myxococcales;D_4__Polyangiaceae;D_5__Byssovorax	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%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Deltaproteobacteria;D_3__Myxococcales;D_4__Polyangiaceae;D_5__Sorangium	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%	0.00%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Deltaproteobacteria;D_3__Myxococcales;D_4__uncultured;D_5__uncultured Cystobacteraceae 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%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Deltaproteobacteria;D_3__Syntrophobacterales;D_4__Syntrophobacteraceae;D_5__Desulfovirga	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%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Epsilonproteobacteria;D_3__R103-B63;D_4__uncultured Marinobacterium sp.;D_5__uncultured Marinobacterium sp.	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%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__EC3;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%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Methylococcales;D_4__Methylococcaceae;D_5__Methylomonas	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%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__PYR10d3;D_4__uncultured bacterium;D_5__uncultured bacterium	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%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__PYR10d3;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%	0.02%	0.00%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Pseudomonadales;D_4__Pseudomonadaceae;D_5__uncultured	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%	0.00%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Thiotrichales;D_4__Piscirickettsiaceae;D_5__Cycloclasticus	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%	0.00%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Thiotrichales;D_4__Piscirickettsiaceae;D_5__Methylophaga	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%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Xanthomonadales;D_4__Solimonadaceae;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%	0.02%	0.00%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Xanthomonadales;D_4__Xanthomonadaceae;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%	0.00%
D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Xanthomonadales;D_4__Xanthomonadaceae;D_5__Metallibacterium	0.00%	0.00%	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%
D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Xanthomonadales;D_4__Xanthomonadaceae;D_5__Xanthomonadaceae 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%	0.02%	0.00%	0.00%
D_0__Bacteria;D_1__Verrucomicrobia;D_2__Spartobacteria;D_3__Chthoniobacterales;D_4__DA101 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%	0.02%	0.00%	0.00%	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__Methanomicrobia;D_3__Methanosarcinales;D_4__Methanosaetaceae;D_5__Methanosaeta	42.30%	33.77%	1.30%	74.45%	94.00%	94.26%	1.43%	78.88%	12.13%	46.94%	14.21%	7.69%	46.02%	87.09%	0.00%
D_0__Archaea;D_1__Euryarchaeota;D_2__Methanobacteria;D_3__Methanobacteriales;D_4__Methanobacteriaceae;D_5__Methanothermobacter	9.69%	0.65%	0.13%	2.22%	0.00%	0.00%	0.00%	0.00%	0.00%	9.78%	11.47%	83.31%	26.86%	0.39%	0.91%
D_0__Archaea;D_1__Euryarchaeota;D_2__Methanomicrobia;D_3__Methanosarcinales;D_4__Methanosarcinaceae;D_5__Methanolobus	9.07%	40.55%	79.79%	0.00%	0.00%	0.00%	0.39%	0.00%	0.13%	0.00%	0.52%	4.04%	1.56%	0.00%	0.00%
D_0__Archaea;D_1__Euryarchaeota;D_2__Methanomicrobia;D_3__Methanomicrobiales;D_4__Methanomicrobiales Incertae Sedis;D_5__Methanocalculus	8.05%	0.26%	0.00%	0.39%	0.00%	0.78%	68.06%	9.39%	32.20%	1.30%	0.13%	0.00%	0.00%	0.13%	0.00%
D_0__Archaea;D_1__Euryarchaeota;D_2__Methanomicrobia;D_3__Methanomicrobiales;D_4__Methanomicrobiaceae;D_5__Methanoculleus	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__Thermococci;D_3__Thermococcales;D_4__Thermococcaceae;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__Methanobacteria;D_3__Methanobacteriales;D_4__Methanobacteriaceae;D_5__Methanobacteriaceae archaeon 15aZ	3.59%	0.39%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	19.82%	1.30%	0.13%	0.39%	0.00%	28.16%
D_0__Archaea;D_1__Euryarchaeota;D_2__Archaeoglobi;D_3__Archaeoglobales;D_4__Archaeoglobaceae;D_5__uncultured	3.50%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	32.99%	0.00%	16.04%	0.00%	0.00%
D_0__Archaea;D_1__Euryarchaeota;D_2__Methanomicrobia;D_3__Methanosarcinales;D_4__Methanosarcinaceae;D_5__Methanomethylovorans	3.02%	22.43%	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__Archaeoglobi;D_3__Archaeoglobales;D_4__Archaeoglobaceae;D_5__uncultured archaeon 20b-54	2.33%	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__Thermoplasmata;D_3__Kazan-3A-21;D_4__uncultured euryarchaeote;D_5__uncultured euryarchaeote	2.10%	0.26%	0.39%	0.13%	0.00%	1.30%	1.17%	2.87%	0.26%	19.43%	3.26%	0.26%	0.00%	0.00%	0.13%
D_0__Archaea;D_1__Euryarchaeota;D_2__Methanomicrobia;D_3__Methanomicrobiales;D_4__Methanoregulaceae;D_5__Methanolinea	1.70%	0.26%	0.00%	4.82%	3.26%	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__Halobacteria;D_3__Halobacteriales;D_4__Miscellaneous Euryarchaeotic Group(MEG);D_5__Candidatus Iainarchaeum	1.11%	0.13%	0.00%	15.25%	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__Methanobacteria;D_3__Methanobacteriales;D_4__Methanobacteriaceae;D_5__Methanobacterium	1.04%	0.00%	0.00%	1.04%	0.91%	0.52%	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__Archaeoglobi;D_3__Archaeoglobales;D_4__Archaeoglobaceae;D_5__Archaeoglobus	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__Halobacteria;D_3__Halobacteriales;D_4__Deep Sea Hydrothermal Vent Gp 6(DHVEG-6);D_5__uncultured euryarchaeote	0.30%	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__Thermoplasmata;D_3__Thermoplasmatales;D_4__Terrestrial Miscellaneous Gp(TMEG);D_5__uncultured 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__Thermoplasmata;D_3__WCHA1-57;D_4__uncultured archaeon;D_5__uncultured 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__Methanomicrobia;D_3__Methanomicrobiales;D_4__Methanospirillaceae;D_5__Methanospirillum	0.18%	0.00%	0.00%	0.00%	0.00%	0.13%	0.00%	1.56%	0.00%	0.52%	0.00%	0.26%	0.00%	0.00%	0.00%
D_0__Archaea;D_1__Euryarchaeota;D_2__Halobacteria;D_3__Halobacteriales;D_4__Halobacteriaceae;D_5__Candidatus Halobonum	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__Halobacteria;D_3__Halobacteriales;D_4__Deep Sea Hydrothermal Vent Gp 6(DHVEG-6);D_5__uncultured 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__Methanomicrobia;D_3__Methanomicrobiales;D_4__Methanomicrobiaceae;D_5__Methanomicrobium	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__Crenarchaeota;D_2__Thermoprotei;D_3__Terrestrial Miscellaneous Gp(TMCG);D_4__uncultured Thermoprotei archaeon;D_5__uncultured 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__Methanomicrobia;D_3__Methanosarcinales;D_4__Methanosarcinaceae;D_5__uncultured	0.08%	1.04%	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__Methanobacteria;D_3__Methanobacteriales;D_4__Methanobacteriaceae;D_5__Methanobrevibacter	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__Thermoplasmata;D_3__Thermoplasmatales;D_4__Marine Group II;D_5__uncultured euryarchaeote	0.07%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.91%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
D_0__Archaea;D_1__Euryarchaeota;D_2__Thermoplasmata;D_3__Thermoplasmatales;D_4__20c-4;D_5__uncultured 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%	0.52%	0.00%	0.00%
D_0__Archaea;D_1__Euryarchaeota;D_2__Halobacteria;D_3__Halobacteriales;D_4__Halobacteriaceae;D_5__Halarchaeum	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__Thermoplasmata;D_3__Kazan-3A-21;D_4__uncultured archaeon;D_5__uncultured 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__Methanobacteria;D_3__Methanobacteriales;D_4__Methanobacteriaceae;D_5__uncultured	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__Methanobacteria;D_3__Methanobacteriales;D_4__Methanobacteriaceae;D_5__uncultured Methanobacteriales archaeon	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%	0.52%
D_0__Archaea;D_1__Euryarchaeota;D_2__Methanomicrobia;D_3__Methanomicrobiales;D_4__LR-13;D_5__uncultured archaeon	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__Thermoplasmata;D_3__014H09-A-SD-P15;D_4__uncultured archaeon;D_5__uncultured 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__Thermoplasmata;D_3__059A02-A-SD-P93;D_4__uncultured archaeon;D_5__uncultured 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__Thermoplasmata;D_3__Thermoplasmatales;D_4__Thermoplasmatales Incertae Sedis;D_5__Candidatus Methanomethylophilus	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__Archaeoglobi;D_3__Archaeoglobales;D_4__Archaeoglobaceae;D_5__uncultured Archaeoglobi archaeon	0.03%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.39%	0.00%	0.00%
D_0__Archaea;D_1__Euryarchaeota;D_2__Methanobacteria;D_3__Methanobacteriales;D_4__Methanobacteriaceae;D_5__Methanosphaera	0.03%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.39%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
D_0__Archaea;D_1__Euryarchaeota;D_2__Methanomicrobia;D_3__Methanomicrobiales;D_4__Methanomicrobiaceae;D_5__uncultured	0.03%	0.00%	0.00%	0.00%	0.00%	0.00%	0.39%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
D_0__Archaea;D_1__Euryarchaeota;D_2__Thermoplasmata;D_3__WCHA1-57;D_4__uncultured euryarchaeote;D_5__uncultured euryarchaeote	0.03%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.39%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
D_0__Archaea;D_1__Euryarchaeota;D_2__Halobacteria;D_3__Halobacteriales;D_4__Miscellaneous Euryarchaeotic Group(MEG);D_5__uncultured 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%	0.26%	0.00%
D_0__Archaea;D_1__Euryarchaeota;D_2__Methanobacteria;D_3__Methanobacteriales;D_4__Methanobacteriaceae;D_5__uncultured Methanobacteriaceae 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%	0.13%	0.13%	0.00%
D_0__Archaea;D_1__Euryarchaeota;D_2__Methanomicrobia;D_3__Methanomicrobiales;D_4__Methanoregulaceae;D_5__Methanoregula	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__Euryarchaeota;D_2__Methanomicrobia;D_3__Methanosarcinales;D_4__Methanosarcinaceae;D_5__Methanosarcina	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.13%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.13%	0.00%
D_0__Archaea;D_1__Thaumarchaeota;D_2__Marine Benthic Group B;D_3__uncultured archaeon;D_4__uncultured archaeon;D_5__uncultured archaeon	0.02%	0.13%	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__Thaumarchaeota;D_2__Marine Group I;D_3__Unknown Order;D_4__Unknown Family;D_5__Candidatus Nitrosopumilus	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__Thaumarchaeota;D_2__Terrestrial Hot Spring Gp(THSCG);D_3__Unknown Order;D_4__Unknown Family;D_5__Candidatus Caldiarchaeum	0.02%	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%	0.00%
D_0__Archaea;D_1__Euryarchaeota;D_2__Archaeoglobi;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__Halobacteria;D_3__Halobacteriales;D_4__Deep Sea Hydrothermal Vent Gp 6(DHVEG-6);D_5__uncultured crenarchaeote	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__Halobacteria;D_3__Halobacteriales;D_4__Deep Sea Hydrothermal Vent Gp 6(DHVEG-6);D_5__unidentified archaeon	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.13%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
D_0__Archaea;D_1__Euryarchaeota;D_2__Halobacteria;D_3__Halobacteriales;D_4__Halobacteriaceae;D_5__Haloterrigena	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.13%	0.00%	0.00%
D_0__Archaea;D_1__Euryarchaeota;D_2__Halobacteria;D_3__Halobacteriales;D_4__Halobacteriaceae;D_5__Halovenus	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.13%	0.00%	0.00%
D_0__Archaea;D_1__Euryarchaeota;D_2__Halobacteria;D_3__Halobacteriales;D_4__Halobacteriaceae;D_5__Salarchaeum	0.01%	0.00%	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%
D_0__Archaea;D_1__Euryarchaeota;D_2__Halobacteria;D_3__Halobacteriales;D_4__Miscellaneous Euryarchaeotic Group(MEG);D_5__uncultured crenarchaeote	0.01%	0.00%	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%
D_0__Archaea;D_1__Euryarchaeota;D_2__Thermoplasmata;D_3__Thermoplasmatales;D_4__Terrestrial Miscellaneous Gp(TMEG);D_5__uncultured Thermoplasmata 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%	0.13%	0.00%	0.00%
D_0__Archaea;D_1__Euryarchaeota;D_2__Thermoplasmata;D_3__Thermoplasmatales;D_4__VC2.1 Arc6;D_5__uncultured archaeon VC2.1 Arc6	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__Thaumarchaeota;D_2__Marine Group I;D_3__uncultured archaeon;D_4__uncultured archaeon;D_5__uncultured 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)
Nitrincola (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)
Bacteriovoracaceae UG (Delta.)	2.1%					
Psychrobacter (Gamma.)	1.9%	Aerobic hydrocarbon degrader				(Deppe et al., 2005; Bowman and Deming, 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)
Glycocaulis (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%					

Table S6. The taxonomic summary of shared OTUs of bacterial communities between a) aqueous samples, b) oil samples, c) all samples. Red labeled genera acquired average proportional size over 0.5%.

a

Taxon	average	P1A	P1O	P2A	P2O	P3A	P3O	P4A	P4O	P5A	P5O	P6A	P6O	P7A	P8O
D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Pseudomonadales;D_4__Pseudomonadaceae;D_5__Pseudomonas	14.7%	22.6%	1.6%	37.1%	17.9%	4.1%	3.7%	2.1%	1.7%	6.1%	5.4%	30.4%	18.8%	21.5%	33.4%
D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Pseudomonadales;D_4__Moraxellaceae;D_5__Acinetobacter	8.3%	1.5%	1.3%	26.9%	35.2%	1.4%	1.5%	38.9%	0.6%	1.3%	1.3%	1.1%	1.4%	2.5%	1.5%
D_0__Bacteria;D_1__Proteobacteria;D_2__Betaproteobacteria;D_3__Hydrogenophilales;D_4__Hydrogenophilaceae;D_5__uncultured	5.0%	0.7%	0.7%	0.5%	0.6%	0.4%	20.1%	0.6%	42.0%	0.8%	0.6%	0.7%	0.6%	1.1%	0.5%
D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Alteromonadales;D_4__Alteromonadaceae;D_5__Marinobacter	2.8%	0.3%	0.4%	0.4%	0.5%	0.3%	1.4%	0.3%	0.2%	9.9%	21.6%	0.2%	0.4%	0.3%	3.3%
D_0__Bacteria;D_1__Bacteroidetes;D_2__Bacteroidia;D_3__Bacteroidales;D_4__Porphyromonadaceae;D_5__Proteiniphilum	2.6%	4.2%	2.7%	5.8%	8.3%	0.5%	0.9%	0.5%	0.3%	5.2%	0.8%	2.0%	1.7%	3.3%	0.2%
D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Oceanospirillales;D_4__Oceanospirillaceae;D_5__Nitrincola	2.6%	0.3%	0.6%	0.8%	2.9%	0.2%	0.4%	0.3%	0.2%	11.8%	17.2%	0.3%	0.4%	0.6%	0.3%
D_0__Bacteria;D_1__Deinococcus-Thermus;D_2__Deinococci;D_3__Thermales;D_4__Thermaceae;D_5__uncultured bacterium	2.4%	0.2%	27.7%	0.5%	0.6%	0.3%	0.6%	0.5%	0.3%	0.8%	1.1%	0.2%	0.5%	0.3%	0.3%
D_0__Bacteria;D_1__Deferribacteres;D_2__Deferribacteres;D_3__Deferribacterales;D_4__Deferribacteraceae;D_5__uncultured	2.2%	0.5%	0.4%	0.3%	0.3%	0.2%	0.6%	0.2%	0.4%	6.9%	9.9%	0.6%	9.9%	0.3%	0.1%
D_0__Bacteria;D_1__Proteobacteria;D_2__Betaproteobacteria;D_3__Rhodocyclales;D_4__Rhodocyclaceae;D_5__Thauera	2.1%	0.5%	0.2%	0.4%	0.4%	0.2%	0.5%	0.5%	0.6%	0.4%	0.4%	3.3%	13.4%	8.7%	0.3%
D_0__Bacteria;D_1__Proteobacteria;D_2__Deltaproteobacteria;D_3__Bdellovibrionales;D_4__Bacteriovoracaceae;D_5__uncultured	2.1%	0.3%	0.2%	0.2%	0.2%	0.4%	11.2%	0.2%	15.0%	0.3%	0.2%	0.2%	0.3%	0.3%	0.2%
D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Pseudomonadales;D_4__Moraxellaceae;D_5__Psychrobacter	1.9%	23.9%	0.1%	0.2%	0.2%	0.1%	0.2%	0.2%	0.1%	0.2%	0.2%	0.3%	0.3%	0.2%	0.1%
D_0__Bacteria;D_1__Proteobacteria;D_2__Epsilonproteobacteria;D_3__Campylobacterales;D_4__Helicobacteraceae;D_5__Sulfurovum	1.7%	0.2%	0.1%	0.2%	0.1%	21.2%	0.4%	0.2%	0.4%	0.2%	0.2%	0.1%	0.1%	0.2%	0.2%
D_0__Bacteria;D_1__Proteobacteria;D_2__Deltaproteobacteria;D_3__Syntrophobacterales;D_4__Syntrophaceae;D_5__Smithella	1.4%	0.2%	0.0%	0.2%	0.1%	4.5%	4.4%	0.6%	8.1%	0.2%	0.1%	0.2%	0.2%	0.1%	0.1%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhodobacterales;D_4__Rhodobacteraceae;D_5__Defluviimonas	1.3%	0.3%	14.2%	0.3%	0.2%	0.1%	0.2%	0.2%	0.1%	1.7%	0.6%	0.1%	0.2%	0.1%	0.2%
D_0__Bacteria;D_1__Bacteroidetes;D_2__Cytophagia;D_3__Order III;D_4__Unknown Family;D_5__Balneola	1.2%	0.1%	15.4%	0.1%	0.1%	0.1%	0.1%	0.2%	0.0%	0.2%	0.5%	0.0%	0.1%	0.1%	0.1%
D_0__Bacteria;D_1__Thermotogae;D_2__Thermotogae;D_3__Thermotogales;D_4__Thermotogaceae;D_5__Mesotoga	0.9%	2.2%	0.2%	0.0%	0.1%	5.9%	3.0%	0.1%	0.1%	0.1%	0.1%	0.1%	0.2%	0.0%	0.0%
D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Oceanospirillales;D_4__Halomonadaceae;D_5__Halomonas	0.8%	0.1%	0.2%	0.5%	1.1%	0.1%	0.1%	0.1%	0.0%	5.4%	3.8%	0.1%	0.1%	0.1%	0.0%
D_0__Bacteria;D_1__Bacteroidetes;D_2__VC2.1 Bac22;D_3__uncultured bacterium;D_4__uncultured bacterium;D_5__uncultured bacterium	0.8%	0.0%	0.0%	0.6%	4.5%	0.0%	0.1%	0.0%	0.0%	0.1%	0.2%	1.1%	4.2%	0.1%	0.0%
D_0__Bacteria;D_1__Proteobacteria;D_2__Betaproteobacteria;D_3__Burkholderiales;D_4__Comamonadaceae;D_5__Simplicispira	0.8%	0.2%	0.1%	3.1%	1.6%	0.2%	0.2%	0.1%	0.1%	0.5%	0.3%	2.3%	1.0%	1.2%	0.1%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhodobacterales;D_4__Rhodobacteraceae;D_5__Stappia	0.7%	0.1%	0.1%	0.1%	0.1%	0.0%	0.0%	0.0%	0.0%	0.1%	0.2%	0.9%	0.4%	0.1%	8.1%
D_0__Bacteria;D_1__Candidate division JS1;D_2__Atribacteria bacterium SCGC AB-164-M20;D_3__Atribacteria bacterium SCGC AB-164-M20;D_4__Atribacteria bacterium SCGC AB-164-M20;D_5__Atribacteria bacterium SCGC AB-164-M20	0.7%	0.0%	0.0%	0.0%	0.0%	9.2%	0.2%	0.1%	0.0%	0.1%	0.1%	0.1%	0.0%	0.1%	0.1%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Caulobacterales;D_4__Hyphomonadaceae;D_5__Glycocaulis	0.7%	0.1%	0.1%	0.0%	0.0%	0.1%	0.1%	0.1%	0.1%	0.2%	0.6%	0.1%	0.0%	0.1%	7.8%
D_0__Bacteria;D_1__Bacteroidetes;D_2__Bacteroidia;D_3__Bacteroidales;D_4__ML635J-40 aquatic group;D_5__uncultured bacterium	0.6%	0.0%	0.0%	0.6%	0.3%	0.1%	0.1%	0.1%	0.0%	2.4%	2.7%	0.2%	2.0%	0.0%	0.1%
D_0__Bacteria;D_1__Proteobacteria;D_2__Epsilonproteobacteria;D_3__Campylobacterales;D_4__Helicobacteraceae;D_5__Wolinella	0.6%	0.1%	0.0%	0.1%	0.0%	0.1%	0.1%	0.0%	0.0%	0.1%	0.0%	6.3%	1.0%	0.8%	0.0%
D_0__Bacteria;D_1__Spirochaetae;D_2__Spirochaetes;D_3__Spirochaetales;D_4__Spirochaetaceae;D_5__uncultured	0.6%	0.0%	0.1%	0.1%	0.0%	0.1%	0.1%	5.0%	1.1%	0.1%	0.0%	0.5%	0.3%	0.6%	0.1%
D_0__Bacteria;D_1__Firmicutes;D_2__Bacilli;D_3__Bacillales;D_4__Family XII;D_5__Exiguobacterium	0.6%	0.2%	0.0%	0.1%	0.0%	0.0%	0.0%	3.2%	0.0%	0.0%	0.0%	3.9%	0.0%	0.3%	0.0%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Sphingomonadales;D_4__Sphingomonadaceae;D_5__Novosphingobium	0.6%	0.0%	0.1%	0.1%	0.1%	0.1%	0.1%	4.5%	0.1%	0.1%	0.0%	1.0%	0.1%	1.4%	0.0%
D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Family XI;D_5__uncultured	0.5%	0.8%	0.1%	0.1%	0.0%	0.0%	0.2%	0.0%	0.1%	2.0%	0.1%	3.7%	0.2%	0.2%	0.0%
D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Gammaproteobacteria Incertae Sedis;D_4__Unknown Family;D_5__Thiohalomonas	0.4%	0.1%	0.1%	0.0%	0.1%	0.3%	0.5%	4.6%	0.3%	0.0%	0.0%	0.0%	0.1%	0.1%	0.0%
D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Xanthomonadales;D_4__Xanthomonadaceae;D_5__Silanimonas	0.4%	0.1%	4.7%	0.0%	0.1%	0.0%	0.1%	0.1%	0.1%	0.2%	0.3%	0.0%	0.2%	0.0%	0.0%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhodobacterales;D_4__Rhodobacteraceae;D_5__Pannonibacter	0.4%	0.0%	0.1%	0.0%	0.1%	0.1%	0.0%	0.1%	0.0%	0.1%	2.4%	0.8%	2.0%	0.0%	0.0%
D_0__Bacteria;D_1__Actinobacteria;D_2__Coriobacteriia;D_3__Coriobacteriales;D_4__Coriobacteriaceae;D_5__uncultured	0.4%	0.1%	0.0%	0.0%	0.0%	4.8%	0.1%	0.1%	0.0%	0.1%	0.0%	0.0%	0.0%	0.0%	0.1%
D_0__Bacteria;D_1__Bacteroidetes;D_2__Bacteroidia;D_3__Bacteroidales;D_4__Rikenellaceae;D_5__Blvii28 wastewater-sludge group	0.3%	0.0%	0.0%	0.0%	0.0%	0.0%	0.3%	0.0%	0.0%	3.6%	0.5%	0.0%	0.0%	0.0%	0.1%
D_0__Bacteria;D_1__Proteobacteria;D_2__Betaproteobacteria;D_3__Hydrogenophilales;D_4__Hydrogenophilaceae;D_5__Tepidiphilus	0.3%	0.1%	0.1%	1.2%	0.6%	0.1%	0.1%	0.0%	0.0%	0.5%	0.8%	0.0%	0.0%	1.2%	0.0%
D_0__Bacteria;D_1__Proteobacteria;D_2__Betaproteobacteria;D_3__Rhodocyclales;D_4__Rhodocyclaceae;D_5__Azoarcus	0.3%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.2%	1.9%	1.9%	0.0%
D_0__Bacteria;D_1__Bacteroidetes;D_2__Cytophagia;D_3__Order III;D_4__BIgi5;D_5__uncultured bacterium	0.3%	0.0%	3.4%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.1%	0.0%	0.0%	0.0%	0.0%
D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Family XI;D_5__Soehngenia	0.3%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	1.7%	0.2%	1.3%	0.2%	0.1%	0.1%
D_0__Bacteria;D_1__Proteobacteria;D_2__Betaproteobacteria;D_3__Burkholderiales;D_4__Comamonadaceae;D_5__Acidovorax	0.2%	0.1%	0.0%	0.1%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	1.7%	0.6%	0.1%	0.0%
D_0__Bacteria;D_1__Chloroflexi;D_2__Anaerolineae;D_3__Anaerolineales;D_4__Anaerolineaceae;D_5__uncultured	0.2%	0.0%	0.0%	0.0%	0.1%	0.5%	0.6%	0.2%	0.3%	0.1%	0.0%	0.2%	0.1%	0.3%	0.0%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhizobiales;D_4__Bradyrhizobiaceae;D_5__Bradyrhizobium	0.1%	0.2%	0.1%	0.1%	0.1%	0.1%	0.1%	0.1%	0.2%	0.1%	0.2%	0.2%	0.1%	0.3%	0.1%
D_0__Bacteria;D_1__Acidobacteria;D_2__Acidobacteria;D_3__Subgroup 4;D_4__RB41;D_5__uncultured bacterium	0.1%	0.2%	0.0%	0.1%	0.0%	0.1%	0.1%	0.1%	0.0%	0.1%	0.1%	0.1%	0.2%	0.2%	0.1%
D_0__Bacteria;D_1__Proteobacteria;D_2__Deltaproteobacteria;D_3__GR-WP33-30;D_4__uncultured bacterium;D_5__uncultured bacterium	0.1%	0.1%	0.0%	0.0%	0.1%	0.1%	0.1%	0.1%	0.1%	0.1%	0.2%	0.1%	0.0%	0.1%	0.1%
D_0__Bacteria;D_1__Acidobacteria;D_2__Acidobacteria;D_3__Acidobacteriales;D_4__Acidobacteriaceae (Subgroup 1);D_5__uncultured	0.1%	0.1%	0.1%	0.1%	0.0%	0.1%	0.1%	0.1%	0.0%	0.0%	0.0%	0.1%	0.0%	0.1%	0.1%
D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Xanthomonadales;D_4__uncultured;D_5__uncultured proteobacterium	0.1%	0.1%	0.0%	0.1%	0.0%	0.0%	0.1%	0.1%	0.0%	0.1%	0.0%	0.0%	0.0%	0.1%	0.1%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhodospirillales;D_4__Rhodospirillaceae;D_5__uncultured	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.1%	0.0%	0.0%	0.0%
D_0__Bacteria;D_1__Bacteroidetes;D_2__Sphingobacteriia;D_3__Sphingobacteriales;D_4__Chitinophagaceae;D_5__Terrimonas	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
D_0__Bacteria;D_1__Nitrospirae;D_2__Nitrospira;D_3__Nitrospirales;D_4__Nitrospiraceae;D_5__Nitrospira	0.0%	0.0%	0.0%	0.0%	0.0%	0.1%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
D_0__Bacteria;D_1__Verrucomicrobia;D_2__Spartobacteria;D_3__Chthoniobacterales;D_4__DA101 soil group;D_5__uncultured bacterium	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
D_0__Bacteria;D_1__Acidobacteria;D_2__Acidobacteria;D_3__Subgroup 6;D_4__uncultured Acidobacteria bacterium;D_5__uncultured Acidobacteria bacterium	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
sum	65.5%	61.2%	75.4%	81.6%	77.2%	56.5%	53.0%	64.8%	73.1%	64.2%	73.4%	65.0%	63.6%	49.6%	58.8%

b

Taxon	average	P1A	P1O	P2A	P2O	P3A	P3O	P4A	P4O	P5A	P5O	P6A	P6O	P7A	P8O
D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Pseudomonadales;D_4__Pseudomonadaceae;D_5__Pseudomonas	14.3%	22.5%	1.5%	36.8%	17.8%	4.1%	3.6%	2.0%	1.7%	6.0%	5.5%	30.2%	15.7%	20.1%	33.3%
D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Pseudomonadales;D_4__Moraxellaceae;D_5__Acinetobacter	8.1%	1.4%	1.1%	24.6%	31.8%	1.3%	1.3%	41.6%	0.7%	1.3%	1.3%	1.0%	1.3%	2.6%	1.5%
D_0__Bacteria;D_1__Proteobacteria;D_2__Betaproteobacteria;D_3__Hydrogenophilales;D_4__Hydrogenophilaceae;D_5__uncultured	5.0%	0.7%	0.7%	0.5%	0.6%	0.4%	20.1%	0.6%	42.0%	0.8%	0.6%	0.7%	0.6%	1.1%	0.5%
D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Alteromonadales;D_4__Alteromonadaceae;D_5__Marinobacter	2.8%	0.3%	0.4%	0.4%	0.5%	0.3%	1.4%	0.3%	0.2%	9.9%	21.6%	0.2%	0.4%	0.3%	3.3%
D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Oceanospirillales;D_4__Oceanospirillaceae;D_5__Nitrincola	2.6%	0.3%	0.6%	0.8%	2.9%	0.2%	0.4%	0.3%	0.2%	11.8%	17.2%	0.3%	0.4%	0.6%	0.3%
D_0__Bacteria;D_1__Deinococcus-Thermus;D_2__Deinococci;D_3__Thermales;D_4__Thermaceae;D_5__uncultured bacterium	2.4%	0.2%	27.7%	0.5%	0.6%	0.3%	0.6%	0.5%	0.3%	0.8%	1.1%	0.2%	0.5%	0.3%	0.3%
D_0__Bacteria;D_1__Bacteroidetes;D_2__Bacteroidia;D_3__Bacteroidales;D_4__Porphyromonadaceae;D_5__Proteiniphilum	2.4%	4.2%	2.7%	5.8%	8.3%	0.5%	0.8%	0.4%	0.2%	5.1%	0.8%	1.9%	1.2%	1.1%	0.2%
D_0__Bacteria;D_1__Deferribacteres;D_2__Deferribacteres;D_3__Deferribacterales;D_4__Deferribacteraceae;D_5__uncultured	2.2%	0.5%	0.4%	0.3%	0.3%	0.2%	0.6%	0.2%	0.4%	6.9%	9.9%	0.6%	9.9%	0.3%	0.1%
D_0__Bacteria;D_1__Proteobacteria;D_2__Betaproteobacteria;D_3__Rhodocyclales;D_4__Rhodocyclaceae;D_5__Thauera	2.1%	0.5%	0.2%	0.4%	0.4%	0.2%	0.5%	0.5%	0.6%	0.4%	0.4%	3.3%	13.4%	8.7%	0.3%
D_0__Bacteria;D_1__Proteobacteria;D_2__Deltaproteobacteria;D_3__Bdellovibrionales;D_4__Bacteriovoracaceae;D_5__uncultured	2.1%	0.3%	0.2%	0.2%	0.2%	0.4%	11.2%	0.2%	15.0%	0.3%	0.2%	0.2%	0.3%	0.3%	0.2%
D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Pseudomonadales;D_4__Moraxellaceae;D_5__Psychrobacter	1.9%	23.9%	0.1%	0.2%	0.2%	0.1%	0.2%	0.2%	0.1%	0.2%	0.2%	0.3%	0.3%	0.2%	0.1%
D_0__Bacteria;D_1__Proteobacteria;D_2__Epsilonproteobacteria;D_3__Campylobacterales;D_4__Helicobacteraceae;D_5__Sulfurovum	1.7%	0.2%	0.1%	0.2%	0.1%	21.2%	0.4%	0.2%	0.4%	0.2%	0.2%	0.1%	0.1%	0.2%	0.2%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhodobacterales;D_4__Rhodobacteraceae;D_5__Defluviimonas	1.4%	0.4%	14.4%	0.3%	0.2%	0.1%	0.2%	0.2%	0.1%	1.8%	0.6%	0.2%	0.3%	0.1%	0.3%
D_0__Bacteria;D_1__Bacteroidetes;D_2__Cytophagia;D_3__Order III;D_4__Unknown Family;D_5__Balneola	1.2%	0.1%	15.4%	0.1%	0.1%	0.1%	0.1%	0.2%	0.0%	0.2%	0.5%	0.0%	0.1%	0.1%	0.1%
D_0__Bacteria;D_1__Thermotogae;D_2__Thermotogae;D_3__Thermotogales;D_4__Thermotogaceae;D_5__Mesotoga	0.9%	2.2%	0.2%	0.0%	0.1%	5.9%	3.0%	0.1%	0.1%	0.1%	0.1%	0.1%	0.2%	0.0%	0.0%
D_0__Bacteria;D_1__Bacteroidetes;D_2__VC2.1 Bac22;D_3__uncultured bacterium;D_4__uncultured bacterium;D_5__uncultured bacterium	0.8%	0.0%	0.0%	0.6%	4.5%	0.0%	0.1%	0.0%	0.0%	0.1%	0.2%	1.1%	4.2%	0.1%	0.0%
D_0__Bacteria;D_1__Proteobacteria;D_2__Betaproteobacteria;D_3__Burkholderiales;D_4__Comamonadaceae;D_5__Simplicispira	0.8%	0.2%	0.1%	3.1%	1.6%	0.2%	0.2%	0.1%	0.1%	0.5%	0.3%	2.3%	1.0%	1.2%	0.1%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhodobacterales;D_4__Rhodobacteraceae;D_5__Stappia	0.7%	0.1%	0.1%	0.1%	0.1%	0.0%	0.0%	0.0%	0.0%	0.1%	0.2%	0.9%	0.4%	0.1%	8.1%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Caulobacterales;D_4__Hyphomonadaceae;D_5__Glycocaulis	0.7%	0.1%	0.1%	0.0%	0.0%	0.1%	0.1%	0.1%	0.1%	0.2%	0.6%	0.1%	0.0%	0.1%	7.8%
D_0__Bacteria;D_1__Bacteroidetes;D_2__Bacteroidia;D_3__Bacteroidales;D_4__ML635J-40 aquatic group;D_5__uncultured bacterium	0.6%	0.0%	0.0%	0.6%	0.3%	0.1%	0.1%	0.1%	0.0%	2.4%	2.7%	0.2%	2.0%	0.0%	0.1%
D_0__Bacteria;D_1__Spirochaetae;D_2__Spirochaetes;D_3__Spirochaetales;D_4__Spirochaetaceae;D_5__uncultured	0.6%	0.0%	0.1%	0.1%	0.0%	0.1%	0.1%	5.0%	1.1%	0.1%	0.0%	0.5%	0.3%	0.6%	0.1%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Sphingomonadales;D_4__Sphingomonadaceae;D_5__Novosphingobium	0.6%	0.0%	0.1%	0.1%	0.1%	0.1%	0.1%	4.5%	0.1%	0.1%	0.0%	1.0%	0.1%	1.4%	0.0%
D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Family XI;D_5__uncultured	0.5%	0.8%	0.1%	0.1%	0.0%	0.0%	0.2%	0.0%	0.1%	2.0%	0.1%	3.7%	0.2%	0.2%	0.0%
D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Gammaproteobacteria Incertae Sedis;D_4__Unknown Family;D_5__Thiohalomonas	0.4%	0.1%	0.1%	0.0%	0.1%	0.3%	0.5%	4.6%	0.3%	0.0%	0.0%	0.0%	0.1%	0.1%	0.0%
D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Xanthomonadales;D_4__Xanthomonadaceae;D_5__Silanimonas	0.4%	0.1%	4.7%	0.0%	0.1%	0.0%	0.1%	0.1%	0.1%	0.2%	0.3%	0.0%	0.2%	0.0%	0.0%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhodobacterales;D_4__Rhodobacteraceae;D_5__Pannonibacter	0.4%	0.0%	0.1%	0.0%	0.1%	0.1%	0.0%	0.1%	0.0%	0.1%	2.4%	0.8%	2.0%	0.0%	0.0%
D_0__Bacteria;D_1__Actinobacteria;D_2__Coriobacteriia;D_3__Coriobacteriales;D_4__Coriobacteriaceae;D_5__uncultured	0.4%	0.1%	0.0%	0.0%	0.0%	4.8%	0.1%	0.1%	0.0%	0.1%	0.0%	0.0%	0.0%	0.0%	0.1%
D_0__Bacteria;D_1__Proteobacteria;D_2__Betaproteobacteria;D_3__Hydrogenophilales;D_4__Hydrogenophilaceae;D_5__Tepidiphilus	0.3%	0.1%	0.1%	1.2%	0.6%	0.1%	0.1%	0.0%	0.0%	0.5%	0.8%	0.0%	0.0%	1.2%	0.0%
D_0__Bacteria;D_1__Proteobacteria;D_2__Betaproteobacteria;D_3__Rhodocyclales;D_4__Rhodocyclaceae;D_5__Azoarcus	0.3%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.2%	1.9%	1.9%	0.0%
D_0__Bacteria;D_1__Bacteroidetes;D_2__Cytophagia;D_3__Order III;D_4__BIgi5;D_5__uncultured bacterium	0.3%	0.0%	3.4%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.1%	0.0%	0.0%	0.0%	0.0%
D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Caldicoprobacteraceae;D_5__Caldicoprobacter	0.3%	0.0%	0.1%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.1%	0.0%	0.0%	3.5%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Caulobacterales;D_4__Hyphomonadaceae;D_5__Hyphomonas	0.1%	0.0%	0.0%	0.0%	0.0%	0.0%	0.1%	0.0%	0.0%	0.0%	0.1%	0.0%	0.3%	0.3%	1.0%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhizobiales;D_4__Bradyrhizobiaceae;D_5__Bradyrhizobium	0.1%	0.2%	0.1%	0.1%	0.1%	0.1%	0.1%	0.1%	0.2%	0.1%	0.2%	0.2%	0.1%	0.3%	0.1%
D_0__Bacteria;D_1__Proteobacteria;D_2__Deltaproteobacteria;D_3__Desulfovibrionales;D_4__Desulfovibrionaceae;D_5__Desulfovibrio	0.1%	0.0%	0.0%	0.0%	0.1%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	1.1%	0.0%	0.0%
D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Xanthomonadales;D_4__uncultured;D_5__uncultured proteobacterium	0.1%	0.1%	0.0%	0.1%	0.0%	0.0%	0.1%	0.1%	0.0%	0.1%	0.0%	0.0%	0.0%	0.1%	0.1%
D_0__Bacteria;D_1__Bacteroidetes;D_2__Cytophagia;D_3__Cytophagales;D_4__Cytophagaceae;D_5__uncultured	0.1%	0.0%	0.0%	0.0%	0.1%	0.0%	0.0%	0.0%	0.0%	0.1%	0.0%	0.1%	0.1%	0.1%	0.0%
D_0__Bacteria;D_1__Proteobacteria;D_2__Deltaproteobacteria;D_3__GR-WP33-30;D_4__uncultured bacterium;D_5__uncultured bacterium	0.0%	0.1%	0.0%	0.0%	0.0%	0.1%	0.1%	0.1%	0.0%	0.0%	0.1%	0.0%	0.0%	0.0%	0.0%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhodospirillales;D_4__Rhodospirillaceae;D_5__uncultured	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.1%	0.0%	0.0%	0.0%
D_0__Bacteria;D_1__Nitrospirae;D_2__Nitrospira;D_3__Nitrospirales;D_4__Nitrospiraceae;D_5__Nitrospira	0.0%	0.1%	0.1%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhizobiales;D_4__Rhodobiaceae;D_5__Rhodobium	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.1%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
D_0__Bacteria;D_1__Actinobacteria;D_2__Thermoleophilia;D_3__Gaiellales;D_4__uncultured;D_5__uncultured bacterium	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
sum	59.9%	60.1%	75.0%	77.8%	72.3%	41.6%	46.9%	62.7%	64.4%	52.8%	68.6%	51.0%	59.0%	44.2%	62.5%

c

Taxon	average	P1A	P1O	P2A	P2O	P3A	P3O	P4A	P4O	P5A	P5O	P6A	P6O	P7A	P8O
D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Pseudomonadales;D_4__Pseudomonadaceae;D_5__Pseudomonas	14.3%	22.5%	1.4%	36.8%	17.8%	4.0%	3.6%	2.0%	1.7%	6.0%	5.4%	30.1%	15.0%	20.0%	33.3%
D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Pseudomonadales;D_4__Moraxellaceae;D_5__Acinetobacter	7.4%	1.4%	1.1%	24.5%	31.7%	1.2%	1.2%	33.8%	0.5%	1.2%	1.2%	1.0%	1.2%	2.4%	1.4%
D_0__Bacteria;D_1__Proteobacteria;D_2__Betaproteobacteria;D_3__Hydrogenophilales;D_4__Hydrogenophilaceae;D_5__uncultured	5.0%	0.7%	0.7%	0.5%	0.6%	0.4%	20.1%	0.6%	42.0%	0.8%	0.6%	0.7%	0.6%	1.1%	0.5%
D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Alteromonadales;D_4__Alteromonadaceae;D_5__Marinobacter	2.8%	0.3%	0.4%	0.4%	0.5%	0.3%	1.4%	0.3%	0.2%	9.9%	21.6%	0.2%	0.4%	0.3%	3.3%
D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Oceanospirillales;D_4__Oceanospirillaceae;D_5__Nitrincola	2.6%	0.3%	0.6%	0.8%	2.9%	0.2%	0.4%	0.3%	0.2%	11.8%	17.2%	0.3%	0.4%	0.6%	0.3%
D_0__Bacteria;D_1__Deinococcus-Thermus;D_2__Deinococci;D_3__Thermales;D_4__Thermaceae;D_5__uncultured bacterium	2.4%	0.2%	27.7%	0.5%	0.6%	0.3%	0.6%	0.5%	0.3%	0.8%	1.1%	0.2%	0.5%	0.3%	0.3%
D_0__Bacteria;D_1__Bacteroidetes;D_2__Bacteroidia;D_3__Bacteroidales;D_4__Porphyromonadaceae;D_5__Proteiniphilum	2.4%	4.2%	2.7%	5.8%	8.3%	0.5%	0.8%	0.4%	0.2%	5.1%	0.8%	1.9%	1.2%	1.1%	0.2%
D_0__Bacteria;D_1__Deferribacteres;D_2__Deferribacteres;D_3__Deferribacterales;D_4__Deferribacteraceae;D_5__uncultured	2.2%	0.5%	0.4%	0.3%	0.3%	0.2%	0.6%	0.2%	0.4%	6.9%	9.9%	0.6%	9.9%	0.3%	0.1%
D_0__Bacteria;D_1__Proteobacteria;D_2__Betaproteobacteria;D_3__Rhodocyclales;D_4__Rhodocyclaceae;D_5__Thauera	2.1%	0.5%	0.2%	0.4%	0.4%	0.2%	0.5%	0.5%	0.6%	0.4%	0.4%	3.3%	13.4%	8.7%	0.3%
D_0__Bacteria;D_1__Proteobacteria;D_2__Deltaproteobacteria;D_3__Bdellovibrionales;D_4__Bacteriovoracaceae;D_5__uncultured	2.1%	0.3%	0.2%	0.2%	0.2%	0.4%	11.2%	0.2%	15.0%	0.3%	0.2%	0.2%	0.3%	0.3%	0.2%
D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Pseudomonadales;D_4__Moraxellaceae;D_5__Psychrobacter	1.9%	23.9%	0.1%	0.2%	0.2%	0.1%	0.2%	0.2%	0.1%	0.2%	0.2%	0.3%	0.3%	0.2%	0.1%
D_0__Bacteria;D_1__Proteobacteria;D_2__Epsilonproteobacteria;D_3__Campylobacterales;D_4__Helicobacteraceae;D_5__Sulfurovum	1.7%	0.2%	0.1%	0.2%	0.1%	21.2%	0.4%	0.2%	0.4%	0.2%	0.2%	0.1%	0.1%	0.2%	0.2%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhodobacterales;D_4__Rhodobacteraceae;D_5__Defluviimonas	1.3%	0.3%	14.2%	0.3%	0.2%	0.1%	0.2%	0.2%	0.1%	1.7%	0.6%	0.1%	0.2%	0.1%	0.2%
D_0__Bacteria;D_1__Bacteroidetes;D_2__Cytophagia;D_3__Order III;D_4__Unknown Family;D_5__Balneola	1.2%	0.1%	15.4%	0.1%	0.1%	0.1%	0.1%	0.2%	0.0%	0.2%	0.5%	0.0%	0.1%	0.1%	0.1%
D_0__Bacteria;D_1__Thermotogae;D_2__Thermotogae;D_3__Thermotogales;D_4__Thermotogaceae;D_5__Mesotoga	0.9%	2.2%	0.2%	0.0%	0.1%	5.9%	3.0%	0.1%	0.1%	0.1%	0.1%	0.1%	0.2%	0.0%	0.0%
D_0__Bacteria;D_1__Bacteroidetes;D_2__VC2.1 Bac22;D_3__uncultured bacterium;D_4__uncultured bacterium;D_5__uncultured bacterium	0.8%	0.0%	0.0%	0.6%	4.5%	0.0%	0.1%	0.0%	0.0%	0.1%	0.2%	1.1%	4.2%	0.1%	0.0%
D_0__Bacteria;D_1__Proteobacteria;D_2__Betaproteobacteria;D_3__Burkholderiales;D_4__Comamonadaceae;D_5__Simplicispira	0.8%	0.2%	0.1%	3.1%	1.6%	0.2%	0.2%	0.1%	0.1%	0.5%	0.3%	2.3%	1.0%	1.2%	0.1%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhodobacterales;D_4__Rhodobacteraceae;D_5__Stappia	0.7%	0.1%	0.1%	0.1%	0.1%	0.0%	0.0%	0.0%	0.0%	0.1%	0.2%	0.9%	0.4%	0.1%	8.1%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Caulobacterales;D_4__Hyphomonadaceae;D_5__Glycocaulis	0.7%	0.1%	0.1%	0.0%	0.0%	0.1%	0.1%	0.1%	0.1%	0.2%	0.6%	0.1%	0.0%	0.1%	7.8%
D_0__Bacteria;D_1__Bacteroidetes;D_2__Bacteroidia;D_3__Bacteroidales;D_4__ML635J-40 aquatic group;D_5__uncultured bacterium	0.6%	0.0%	0.0%	0.6%	0.3%	0.1%	0.1%	0.1%	0.0%	2.4%	2.7%	0.2%	2.0%	0.0%	0.1%
D_0__Bacteria;D_1__Spirochaetae;D_2__Spirochaetes;D_3__Spirochaetales;D_4__Spirochaetaceae;D_5__uncultured	0.6%	0.0%	0.1%	0.1%	0.0%	0.1%	0.1%	5.0%	1.1%	0.1%	0.0%	0.5%	0.3%	0.6%	0.1%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Sphingomonadales;D_4__Sphingomonadaceae;D_5__Novosphingobium	0.6%	0.0%	0.1%	0.1%	0.1%	0.1%	0.1%	4.5%	0.1%	0.1%	0.0%	1.0%	0.1%	1.4%	0.0%
D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Family XI;D_5__uncultured	0.5%	0.8%	0.1%	0.1%	0.0%	0.0%	0.2%	0.0%	0.1%	2.0%	0.1%	3.7%	0.2%	0.2%	0.0%
D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Gammaproteobacteria Incertae Sedis;D_4__Unknown Family;D_5__Thiohalomonas	0.4%	0.1%	0.1%	0.0%	0.1%	0.3%	0.5%	4.6%	0.3%	0.0%	0.0%	0.0%	0.1%	0.1%	0.0%
D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Xanthomonadales;D_4__Xanthomonadaceae;D_5__Silanimonas	0.4%	0.1%	4.7%	0.0%	0.1%	0.0%	0.1%	0.1%	0.1%	0.2%	0.3%	0.0%	0.2%	0.0%	0.0%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhodobacterales;D_4__Rhodobacteraceae;D_5__Pannonibacter	0.4%	0.0%	0.1%	0.0%	0.1%	0.1%	0.0%	0.1%	0.0%	0.1%	2.4%	0.8%	2.0%	0.0%	0.0%
D_0__Bacteria;D_1__Actinobacteria;D_2__Coriobacteriia;D_3__Coriobacteriales;D_4__Coriobacteriaceae;D_5__uncultured	0.4%	0.1%	0.0%	0.0%	0.0%	4.8%	0.1%	0.1%	0.0%	0.1%	0.0%	0.0%	0.0%	0.0%	0.1%
D_0__Bacteria;D_1__Proteobacteria;D_2__Betaproteobacteria;D_3__Hydrogenophilales;D_4__Hydrogenophilaceae;D_5__Tepidiphilus	0.3%	0.1%	0.1%	1.2%	0.6%	0.1%	0.1%	0.0%	0.0%	0.5%	0.8%	0.0%	0.0%	1.2%	0.0%
D_0__Bacteria;D_1__Proteobacteria;D_2__Betaproteobacteria;D_3__Rhodocyclales;D_4__Rhodocyclaceae;D_5__Azoarcus	0.3%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.2%	1.9%	1.9%	0.0%
D_0__Bacteria;D_1__Bacteroidetes;D_2__Cytophagia;D_3__Order III;D_4__BIgi5;D_5__uncultured bacterium	0.3%	0.0%	3.4%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.1%	0.0%	0.0%	0.0%	0.0%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhizobiales;D_4__Bradyrhizobiaceae;D_5__Bradyrhizobium	0.1%	0.2%	0.1%	0.1%	0.1%	0.1%	0.1%	0.1%	0.2%	0.1%	0.2%	0.2%	0.1%	0.3%	0.1%
D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Xanthomonadales;D_4__uncultured;D_5__uncultured proteobacterium	0.1%	0.1%	0.0%	0.1%	0.0%	0.0%	0.1%	0.1%	0.0%	0.1%	0.0%	0.0%	0.0%	0.1%	0.1%
D_0__Bacteria;D_1__Proteobacteria;D_2__Deltaproteobacteria;D_3__GR-WP33-30;D_4__uncultured bacterium;D_5__uncultured bacterium	0.0%	0.1%	0.0%	0.0%	0.0%	0.1%	0.1%	0.1%	0.0%	0.0%	0.1%	0.0%	0.0%	0.0%	0.0%
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhodospirillales;D_4__Rhodospirillaceae;D_5__uncultured	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.1%	0.0%	0.0%	0.0%
sum	58.5%	59.8%	74.5%	77.6%	72.0%	41.4%	46.5%	54.8%	64.1%	52.4%	68.2%	50.5%	56.5%	43.4%	57.8%

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

		anosim		adonis	
		R statistic	*p*-value	R^2	*p*-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.

Table S8. Mantel test based on the beta diversity results by unweighted & weighted UniFrac matrix and Bray-Curtis (non-phylogenetic) matrix measurement. The aqueous and oil phase samples were analyzed separately. The physiochemical parameter distance matrices were also separately used according to phase difference. The significant scores (*p*-value<0.05) were highlighted.

	DM1	**DM2**	**Mantel r statistic**	***p*-value**
aqueous phase bacteria	unweighted_unifrac_dm	aqueous phase parameter 1	0.4081	0.176
	unweighted_unifrac_dm	aqueous phase parameter 2	**0.64753**	**0.013**
	unweighted_unifrac_dm	aqueous phase parameter 3	0.28869	0.081
	unweighted_unifrac_dm	aqueous phase parameter 4	-0.27129	0.203
	unweighted_unifrac_dm	aqueous phase parameter 5	-0.16333	0.457
	unweighted_unifrac_dm	aqueous phase parameter 6	0.31944	0.15
	unweighted_unifrac_dm	aqueous phase parameter 7	-0.23419	0.277
	unweighted_unifrac_dm	aqueous phase parameter 8	-0.12684	0.67
	unweighted_unifrac_dm	aqueous phase parameter 9	-0.24162	0.239
	unweighted_unifrac_dm	aqueous phase parameter 10	**0.7289**	**0.018**
	unweighted_unifrac_dm	aqueous phase parameter 11	-0.19852	0.386
	unweighted_unifrac_dm	aqueous phase parameter 12	-0.11009	0.629
	unweighted_unifrac_dm	aqueous phase parameter 13	-0.05797	0.812
	unweighted_unifrac_dm	aqueous phase parameter 14	0.1986	0.317
	unweighted_unifrac_dm	aqueous phase parameter 15	0.25858	0.163
	unweighted_unifrac_dm	aqueous phase parameter 16	0.24449	0.263
	weighted_unifrac_dm	aqueous phase parameter 1	0.34545	0.363
	weighted_unifrac_dm	aqueous phase parameter 2	0.33405	0.352
	weighted_unifrac_dm	aqueous phase parameter 3	-0.01151	0.974
	weighted_unifrac_dm	aqueous phase parameter 4	-0.15934	0.652
	weighted_unifrac_dm	aqueous phase parameter 5	-0.08061	0.751
	weighted_unifrac_dm	aqueous phase parameter 6	0.02407	0.959
	weighted_unifrac_dm	aqueous phase parameter 7	-0.092	0.72
	weighted_unifrac_dm	aqueous phase parameter 8	-0.06287	0.93
	weighted_unifrac_dm	aqueous phase parameter 9	-0.10384	0.795
	weighted_unifrac_dm	aqueous phase parameter 10	**0.94397**	**0.006**
	weighted_unifrac_dm	aqueous phase parameter 11	-0.2112	0.314
	weighted_unifrac_dm	aqueous phase parameter 12	-0.04413	0.899
	weighted_unifrac_dm	aqueous phase parameter 13	-0.05078	0.81
	weighted_unifrac_dm	aqueous phase parameter 14	-0.06254	0.712
	weighted_unifrac_dm	aqueous phase parameter 15	0.00921	0.95
	weighted_unifrac_dm	aqueous phase parameter 16	**0.59095**	**0.044**
	bray_curtis_dm	aqueous phase parameter 1	-0.11603	0.705
	bray_curtis_dm	aqueous phase parameter 2	0.09572	0.75
	bray_curtis_dm	aqueous phase parameter 3	-0.13263	0.438
	bray_curtis_dm	aqueous phase parameter 4	-0.08298	0.797
	bray_curtis_dm	aqueous phase parameter 5	0.15813	0.643
	bray_curtis_dm	aqueous phase parameter 6	0.25085	0.358
	bray_curtis_dm	aqueous phase parameter 7	0.24613	0.609
	bray_curtis_dm	aqueous phase parameter 8	0.25904	0.306
	bray_curtis_dm	aqueous phase parameter 9	0.03822	0.981
	bray_curtis_dm	aqueous phase parameter 10	**0.43431**	**0.011**
	bray_curtis_dm	aqueous phase parameter 11	0.30085	0.276
	bray_curtis_dm	aqueous phase parameter 12	0.34957	0.303
	bray_curtis_dm	aqueous phase parameter 13	0.40306	0.106
	bray_curtis_dm	aqueous phase parameter 14	**0.47986**	**0.044**
	bray_curtis_dm	aqueous phase parameter 15	**0.47202**	**0.028**
	bray_curtis_dm	aqueous phase parameter 16	-0.04687	0.884
oil phase bacteria	unweighted_unifrac_dm	oil phase parameter 1	0.01351	0.97
	unweighted_unifrac_dm	oil phase parameter 2	0.3428	0.153
	unweighted_unifrac_dm	oil phase parameter 3	0.26224	0.198
	unweighted_unifrac_dm	oil phase parameter 4	0.10013	0.789
	unweighted_unifrac_dm	oil phase parameter 5	0.13235	0.763
	unweighted_unifrac_dm	oil phase parameter 6	0.39099	0.109
	weighted_unifrac_dm	oil phase parameter 1	-0.20549	0.561
	weighted_unifrac_dm	oil phase parameter 2	-0.01431	0.973
	weighted_unifrac_dm	oil phase parameter 3	-0.17587	0.434
	weighted_unifrac_dm	oil phase parameter 4	0.60031	0.073
	weighted_unifrac_dm	oil phase parameter 5	0.62552	0.054
	weighted_unifrac_dm	oil phase parameter 6	0.24391	0.348
	bray_curtis_dm	oil phase parameter 1	-0.01036	0.95
	bray_curtis_dm	oil phase parameter 2	0.24591	0.297
	bray_curtis_dm	oil phase parameter 3	0.14685	0.627
	bray_curtis_dm	oil phase parameter 4	0.23029	0.259
	bray_curtis_dm	oil phase parameter 5	0.36859	0.054
	bray_curtis_dm	oil phase parameter 6	**0.50466**	**0.018**

	DM1	**DM2**	**Mantel r statistic**	***p*-value**
aqueous phase archaea	unweighted_unifrac_dm	aqueous phase parameter 1	-0.1562	0.679
	unweighted_unifrac_dm	aqueous phase parameter 2	-0.07316	0.806
	unweighted_unifrac_dm	aqueous phase parameter 3	0.20278	0.273
	unweighted_unifrac_dm	aqueous phase parameter 4	0.4013	0.079
	unweighted_unifrac_dm	aqueous phase parameter 5	0.19431	0.417
	unweighted_unifrac_dm	aqueous phase parameter 6	-0.16588	0.552
	unweighted_unifrac_dm	aqueous phase parameter 7	-0.17779	0.483
	unweighted_unifrac_dm	aqueous phase parameter 8	-0.12593	0.785
	unweighted_unifrac_dm	aqueous phase parameter 9	-0.24737	0.241
	unweighted_unifrac_dm	aqueous phase parameter 10	-0.19016	0.509
	unweighted_unifrac_dm	aqueous phase parameter 11	-0.16362	0.497
	unweighted_unifrac_dm	aqueous phase parameter 12	0.19952	0.436
	unweighted_unifrac_dm	aqueous phase parameter 13	0.13495	0.592
	unweighted_unifrac_dm	aqueous phase parameter 14	-0.00463	0.984
	unweighted_unifrac_dm	aqueous phase parameter 15	0.07193	0.714
	unweighted_unifrac_dm	aqueous phase parameter 16	-0.24024	0.403
	weighted_unifrac_dm	aqueous phase parameter 1	0.51684	0.15
	weighted_unifrac_dm	aqueous phase parameter 2	0.47496	0.117
	weighted_unifrac_dm	aqueous phase parameter 3	**0.38173**	**0.05**
	weighted_unifrac_dm	aqueous phase parameter 4	0.02559	0.931
	weighted_unifrac_dm	aqueous phase parameter 5	0.15647	0.505
	weighted_unifrac_dm	aqueous phase parameter 6	-0.06455	0.881
	weighted_unifrac_dm	aqueous phase parameter 7	-0.08697	0.663
	weighted_unifrac_dm	aqueous phase parameter 8	-0.15358	0.598
	weighted_unifrac_dm	aqueous phase parameter 9	0.03186	0.882
	weighted_unifrac_dm	aqueous phase parameter 10	-0.32541	0.144
	weighted_unifrac_dm	aqueous phase parameter 11	-0.02853	0.895
	weighted_unifrac_dm	aqueous phase parameter 12	-0.03156	0.879
	weighted_unifrac_dm	aqueous phase parameter 13	0.15106	0.558
	weighted_unifrac_dm	aqueous phase parameter 14	0.0783	0.726
	weighted_unifrac_dm	aqueous phase parameter 15	-0.0195	0.92
	weighted_unifrac_dm	aqueous phase parameter 16	0.01354	0.965
	bray_curtis_dm	aqueous phase parameter 1	0.06242	0.79
	bray_curtis_dm	aqueous phase parameter 2	0.10464	0.707
	bray_curtis_dm	aqueous phase parameter 3	-0.08756	0.57
	bray_curtis_dm	aqueous phase parameter 4	0.37502	0.086
	bray_curtis_dm	aqueous phase parameter 5	0.11778	0.705
	bray_curtis_dm	aqueous phase parameter 6	-0.05611	0.84
	bray_curtis_dm	aqueous phase parameter 7	-0.28674	0.316
	bray_curtis_dm	aqueous phase parameter 8	-0.2785	0.256
	bray_curtis_dm	aqueous phase parameter 9	-0.41457	0.115
	bray_curtis_dm	aqueous phase parameter 10	-0.25901	0.504
	bray_curtis_dm	aqueous phase parameter 11	0.13512	0.65
	bray_curtis_dm	aqueous phase parameter 12	0.0084	0.983
	bray_curtis_dm	aqueous phase parameter 13	-0.07579	0.803
	bray_curtis_dm	aqueous phase parameter 14	-0.15899	0.446
	bray_curtis_dm	aqueous phase parameter 15	-0.17954	0.337
	bray_curtis_dm	aqueous phase parameter 16	-0.17079	0.557
oil phase archaea	unweighted_unifrac_dm	oil phase parameter 1	0.00286	0.997
	unweighted_unifrac_dm	oil phase parameter 2	0.38221	0.08
	unweighted_unifrac_dm	oil phase parameter 3	0.35302	0.096
	unweighted_unifrac_dm	oil phase parameter 4	-0.31264	0.106
	unweighted_unifrac_dm	oil phase parameter 5	-0.01977	0.919
	unweighted_unifrac_dm	oil phase parameter 6	0.22681	0.351
	weighted_unifrac_dm	oil phase parameter 1	0.09287	0.596
	weighted_unifrac_dm	oil phase parameter 2	0.38597	0.064
	weighted_unifrac_dm	oil phase parameter 3	**0.56527**	**0.021**
	weighted_unifrac_dm	oil phase parameter 4	-0.15186	0.461
	weighted_unifrac_dm	oil phase parameter 5	0.11992	0.539
	weighted_unifrac_dm	oil phase parameter 6	0.38103	0.065
	bray_curtis_dm	oil phase parameter 1	0.01248	0.945
	bray_curtis_dm	oil phase parameter 2	0.24516	0.303
	bray_curtis_dm	oil phase parameter 3	0.35803	0.103
	bray_curtis_dm	oil phase parameter 4	0.10095	0.622
	bray_curtis_dm	oil phase parameter 5	0.27525	0.165
	bray_curtis_dm	oil phase parameter 6	0.3878	0.055

	DM1	**DM2**	**Mantel r statistic**	***p*-value**
aqueous phase methanogen	unweighted_unifrac_dm	aqueous phase parameter 1	**0.74583**	**0.019**
	unweighted_unifrac_dm	aqueous phase parameter 2	**0.69711**	**0.007**
	unweighted_unifrac_dm	aqueous phase parameter 3	0.14591	0.42
	unweighted_unifrac_dm	aqueous phase parameter 4	0.06402	0.812
	unweighted_unifrac_dm	aqueous phase parameter 5	-0.136	0.651
	unweighted_unifrac_dm	aqueous phase parameter 6	-0.31355	0.228
	unweighted_unifrac_dm	aqueous phase parameter 7	-0.32314	0.366
	unweighted_unifrac_dm	aqueous phase parameter 8	-0.19328	0.549
	unweighted_unifrac_dm	aqueous phase parameter 9	-0.35846	0.529
	unweighted_unifrac_dm	aqueous phase parameter 10	0.55066	0.121
	unweighted_unifrac_dm	aqueous phase parameter 11	-0.24737	0.396
	unweighted_unifrac_dm	aqueous phase parameter 12	0.06981	0.836
	unweighted_unifrac_dm	aqueous phase parameter 13	0.08523	0.78
	unweighted_unifrac_dm	aqueous phase parameter 14	0.10257	0.683
	unweighted_unifrac_dm	aqueous phase parameter 15	0.03119	0.862
	unweighted_unifrac_dm	aqueous phase parameter 16	0.43712	0.074
	weighted_unifrac_dm	aqueous phase parameter 1	0.55591	0.116
	weighted_unifrac_dm	aqueous phase parameter 2	0.44544	0.129
	weighted_unifrac_dm	aqueous phase parameter 3	**0.432**	**0.049**
	weighted_unifrac_dm	aqueous phase parameter 4	0.13816	0.616
	weighted_unifrac_dm	aqueous phase parameter 5	0.11883	0.643
	weighted_unifrac_dm	aqueous phase parameter 6	-0.29356	0.299
	weighted_unifrac_dm	aqueous phase parameter 7	-0.07679	0.74
	weighted_unifrac_dm	aqueous phase parameter 8	-0.10082	0.851
	weighted_unifrac_dm	aqueous phase parameter 9	0.06059	0.713
	weighted_unifrac_dm	aqueous phase parameter 10	-0.28104	0.194
	weighted_unifrac_dm	aqueous phase parameter 11	-0.09072	0.69
	weighted_unifrac_dm	aqueous phase parameter 12	0.05044	0.797
	weighted_unifrac_dm	aqueous phase parameter 13	0.21596	0.389
	weighted_unifrac_dm	aqueous phase parameter 14	0.05518	0.86
	weighted_unifrac_dm	aqueous phase parameter 15	-0.03789	0.868
	weighted_unifrac_dm	aqueous phase parameter 16	0.11778	0.772
	bray_curtis_dm	aqueous phase parameter 1	0.18127	0.562
	bray_curtis_dm	aqueous phase parameter 2	0.17923	0.503
	bray_curtis_dm	aqueous phase parameter 3	-0.05747	0.726
	bray_curtis_dm	aqueous phase parameter 4	0.37654	0.102
	bray_curtis_dm	aqueous phase parameter 5	0.11246	0.683
	bray_curtis_dm	aqueous phase parameter 6	-0.11124	0.668
	bray_curtis_dm	aqueous phase parameter 7	-0.35733	0.169
	bray_curtis_dm	aqueous phase parameter 8	-0.34202	0.23
	bray_curtis_dm	aqueous phase parameter 9	-0.48724	0.106
	bray_curtis_dm	aqueous phase parameter 10	-0.13699	0.75
	bray_curtis_dm	aqueous phase parameter 11	0.07328	0.812
	bray_curtis_dm	aqueous phase parameter 12	-0.02739	0.959
	bray_curtis_dm	aqueous phase parameter 13	-0.10301	0.688
	bray_curtis_dm	aqueous phase parameter 14	-0.15058	0.465
	bray_curtis_dm	aqueous phase parameter 15	-0.18157	0.339
	bray_curtis_dm	aqueous phase parameter 16	-0.02709	0.923
oil phase methanogen	unweighted_unifrac_dm	oil phase parameter 1	0.19509	0.564
	unweighted_unifrac_dm	oil phase parameter 2	0.36776	0.101
	unweighted_unifrac_dm	oil phase parameter 3	-0.10147	0.625
	unweighted_unifrac_dm	oil phase parameter 4	0.46194	0.203
	unweighted_unifrac_dm	oil phase parameter 5	**0.74692**	**0.002**
	unweighted_unifrac_dm	oil phase parameter 6	0.23154	0.374
	weighted_unifrac_dm	oil phase parameter 1	**0.4746**	**0.02**
	weighted_unifrac_dm	oil phase parameter 2	**0.60094**	**0.025**
	weighted_unifrac_dm	oil phase parameter 3	**0.44522**	**0.044**
	weighted_unifrac_dm	oil phase parameter 4	-0.13356	0.66
	weighted_unifrac_dm	oil phase parameter 5	0.1592	0.591
	weighted_unifrac_dm	oil phase parameter 6	**0.57385**	**0.015**
	bray_curtis_dm	oil phase parameter 1	-0.04154	0.878
	bray_curtis_dm	oil phase parameter 2	0.19544	0.399
	bray_curtis_dm	oil phase parameter 3	0.33993	0.146
	bray_curtis_dm	oil phase parameter 4	0.078	0.67
	bray_curtis_dm	oil phase parameter 5	0.30857	0.091
	bray_curtis_dm	oil phase parameter 6	**0.40252**	**0.047**

aqueous phase parameter 1	Depth(m)
aqueous phase parameter 2	Temp(°C)
aqueous phase parameter 3	pH
aqueous phase parameter 4	Effective porosity (%)
aqueous phase parameter 5	Average permeability ($\times 10^{-3} \mu m^2$)
aqueous phase parameter 6	Water flooding operation (years)
aqueous phase parameter 7	Cl^-(mg l^{-1})
aqueous phase parameter 8	SO_4^{2-}(mg l^{-1})
aqueous phase parameter 9	PO_4^{3-}(mg l^{-1})
aqueous phase parameter 10	NO^{3-}(mg l^{-1})
aqueous phase parameter 11	Na^+(mg l^{-1})
aqueous phase parameter 12	K^+(mg l^{-1})
aqueous phase parameter 13	Ca^{2+}(mg l^{-1})
aqueous phase parameter 14	Mg^{2+}(mg l^{-1})
aqueous phase parameter 15	Mn^{2+}(mg l^{-1})
aqueous phase parameter 16	Acetate(mg l^{-1})

oil phase parameter 1	Depth(m)
oil phase parameter 2	Temp(°C)
oil phase parameter 3	pH
oil phase parameter 4	Effective porosity (%)
oil phase parameter 5	Average permeability ($\times 10^{-3} \mu m^2$)
oil phase parameter 6	Water flooding operation (years)

Table S9. Predicted functional profiles based on microbial 16S taxonomic abundance dataset. a) bacterial community functional profiles; b) archaeal community functional profiles. FTU:Fraction of OTUs that could not be mapped to KEGG organisms.

a

Samples	average	P1A	P1O	P2A	P2O	P3A	P3O	P4A	P4O	P5A	P5O	P6A	P6O	P7A	P8O
FTU	0.4697	0.3716	0.7009	0.4282	0.5890	0.5215	0.3540	0.7713	0.2426	0.4920	0.5324	0.3486	0.5064	0.3655	0.3519
Environmental Information Processing|Signal transduction|ko02020 Two-component system	8.85%	8.65%	7.20%	9.38%	9.21%	7.50%	9.04%	8.69%	9.11%	9.42%	9.84%	8.93%	9.52%	9.21%	8.19%
Environmental Information Processing|Membrane transport|ko02010 ABC transporters	8.29%	7.90%	9.02%	7.98%	8.15%	7.44%	7.83%	8.64%	7.96%	8.36%	7.73%	8.97%	8.49%	8.72%	8.92%
Metabolism|Nucleotide metabolism|ko00230 Purine metabolism	3.29%	3.20%	3.29%	3.19%	3.25%	3.86%	3.38%	3.28%	3.32%	3.29%	3.17%	3.29%	3.12%	3.16%	3.25%
Genetic Information Processing|Translation|ko00970 Aminoacyl-tRNA biosynthesis	2.78%	2.86%	2.73%	2.58%	2.69%	3.63%	2.81%	2.84%	2.69%	2.75%	2.58%	2.76%	2.56%	2.57%	2.80%
Metabolism|Energy metabolism|ko00910 Nitrogen metabolism	2.15%	2.00%	2.06%	2.13%	2.08%	2.83%	2.10%	2.00%	2.08%	2.09%	2.25%	2.02%	2.20%	2.15%	2.05%
Metabolism|Nucleotide metabolism|ko00240 Pyrimidine metabolism	2.05%	2.07%	2.07%	1.98%	2.06%	2.46%	2.07%	2.10%	2.02%	2.05%	1.91%	2.05%	1.90%	1.94%	2.07%
Environmental Information Processing|Membrane transport|ko03070 Bacterial secretion system	2.00%	1.96%	1.67%	2.22%	2.07%	1.69%	1.97%	1.83%	2.13%	2.02%	2.32%	1.91%	2.17%	2.11%	2.00%
Metabolism|Energy metabolism|ko00190 Oxidative phosphorylation	1.88%	1.74%	1.91%	1.76%	1.76%	2.45%	1.99%	1.91%	1.91%	1.76%	1.74%	1.88%	1.89%	1.85%	1.81%
Metabolism|Amino acid metabolism|ko00330 Arginine and proline metabolism	1.86%	1.93%	2.19%	1.84%	1.80%	1.82%	1.68%	1.81%	1.69%	1.95%	2.13%	1.77%	1.79%	1.82%	1.90%
Metabolism|Metabolism of cofactors and vitamins|ko00860 Porphyrin and chlorophyll metabolism	1.69%	1.52%	1.99%	1.62%	1.62%	1.55%	1.60%	1.64%	1.57%	1.80%	1.77%	1.71%	1.76%	1.71%	1.77%
Metabolism|Carbohydrate metabolism|ko00520 Amino sugar and nucleotide sugar metabolism	1.65%	1.58%	1.46%	1.63%	1.76%	2.03%	1.77%	1.76%	1.64%	1.63%	1.48%	1.70%	1.54%	1.56%	1.58%
Genetic Information Processing|Translation|ko03010 Ribosome	1.62%	1.67%	1.60%	1.51%	1.58%	2.09%	1.68%	1.63%	1.62%	1.62%	1.51%	1.61%	1.46%	1.49%	1.64%
Cellular Processes|Cell growth and death|ko04112 Cell cycle - Caulobacter	1.58%	1.47%	1.55%	1.50%	1.52%	1.75%	1.65%	1.52%	1.59%	1.66%	1.74%	1.54%	1.52%	1.51%	1.64%
Metabolism|Carbohydrate metabolism|ko00500 Starch and sucrose metabolism	1.54%	1.41%	1.35%	1.62%	1.63%	1.59%	1.40%	1.81%	1.15%	1.65%	1.54%	1.71%	1.59%	1.55%	1.61%
Metabolism|Amino acid metabolism|ko00260 Glycine, serine and threonine metabolism	1.47%	1.55%	1.96%	1.41%	1.36%	1.15%	1.40%	1.46%	1.42%	1.49%	1.52%	1.43%	1.41%	1.46%	1.50%
Cellular Processes|Cell motility|ko02030 Bacterial chemotaxis	1.45%	1.33%	1.04%	1.47%	1.50%	1.05%	1.59%	1.38%	1.61%	1.69%	1.84%	1.45%	1.50%	1.44%	1.41%
Metabolism|Glycan biosynthesis and metabolism|ko00550 Peptidoglycan biosynthesis	1.39%	1.37%	1.33%	1.35%	1.40%	1.59%	1.46%	1.41%	1.45%	1.37%	1.24%	1.42%	1.30%	1.32%	1.38%
Metabolism|Energy metabolism|ko00680 Methane metabolism	1.34%	1.16%	1.18%	1.19%	1.24%	1.71%	1.34%	1.48%	1.24%	1.42%	1.27%	1.43%	1.46%	1.29%	1.40%
Cellular Processes|Cell motility|ko02040 Flagellar assembly	1.30%	1.22%	1.16%	1.26%	1.28%	0.52%	1.53%	1.28%	1.67%	1.39%	1.61%	1.19%	1.30%	1.27%	1.45%
Genetic Information Processing|Folding, sorting and degradation|ko03018 RNA degradation	1.29%	1.36%	1.29%	1.28%	1.32%	1.56%	1.27%	1.25%	1.25%	1.31%	1.28%	1.23%	1.22%	1.24%	1.22%
Metabolism|Carbohydrate metabolism|ko00620 Pyruvate metabolism	1.29%	1.31%	1.33%	1.35%	1.32%	1.21%	1.21%	1.28%	1.23%	1.26%	1.29%	1.29%	1.32%	1.33%	1.29%
Metabolism|Carbohydrate metabolism|ko00630 Glyoxylate and dicarboxylate metabolism	1.25%	1.23%	1.44%	1.25%	1.19%	1.06%	1.21%	1.17%	1.29%	1.20%	1.33%	1.17%	1.36%	1.36%	1.27%
Genetic Information Processing|Replication and repair|ko03440 Homologous recombination	1.20%	1.28%	1.08%	1.22%	1.23%	1.40%	1.13%	1.19%	1.05%	1.27%	1.23%	1.24%	1.13%	1.13%	1.18%
Metabolism|Carbohydrate metabolism|ko00051 Fructose and mannose metabolism	1.19%	1.13%	1.15%	1.18%	1.24%	1.50%	1.12%	1.30%	1.03%	1.17%	1.09%	1.22%	1.18%	1.19%	1.18%
Metabolism|Amino acid metabolism|ko00250 Alanine, aspartate and glutamate metabolism	1.07%	1.10%	1.07%	1.06%	1.06%	1.19%	1.08%	1.05%	1.07%	1.05%	1.10%	1.03%	1.04%	1.03%	1.06%
Metabolism|Amino acid metabolism|ko00270 Cysteine and methionine metabolism	1.06%	1.07%	1.07%	1.05%	1.03%	1.22%	1.03%	1.10%	1.00%	1.07%	1.03%	1.09%	1.03%	1.03%	1.05%
Metabolism|Amino acid metabolism|ko00400 Phenylalanine, tyrosine and tryptophan biosynthesis	1.06%	1.13%	1.05%	1.07%	1.03%	1.24%	0.96%	1.05%	0.92%	1.04%	1.09%	1.06%	1.04%	1.01%	1.10%
Genetic Information Processing|Replication and repair|ko03420 Nucleotide excision repair	1.00%	0.96%	0.92%	0.94%	0.98%	1.22%	1.08%	0.99%	1.08%	1.01%	0.94%	1.00%	0.97%	0.97%	1.00%
Metabolism|Lipid metabolism|ko00564 Glycerophospholipid metabolism	0.99%	0.95%	0.93%	1.04%	1.02%	1.06%	1.03%	0.97%	1.04%	0.97%	0.97%	1.00%	0.95%	0.95%	0.94%
Metabolism|Energy metabolism|ko00720 Carbon fixation pathways in prokaryotes	0.98%	0.98%	1.02%	0.93%	0.92%	1.10%	1.03%	0.95%	1.05%	0.93%	0.89%	0.95%	1.01%	0.98%	0.95%
Genetic Information Processing|Replication and repair|ko03430 Mismatch repair	0.96%	0.92%	0.88%	0.93%	0.98%	1.11%	1.00%	0.99%	0.96%	0.99%	0.90%	1.01%	0.90%	0.92%	0.98%
Metabolism|Amino acid metabolism|ko00300 Lysine biosynthesis	0.91%	0.96%	0.89%	0.87%	0.88%	1.09%	0.89%	0.95%	0.89%	0.87%	0.88%	0.89%	0.88%	0.89%	0.91%
Metabolism|Carbohydrate metabolism|ko00030 Pentose phosphate pathway	0.90%	0.91%	0.93%	0.93%	0.95%	0.84%	0.84%	0.99%	0.78%	0.90%	0.89%	0.95%	0.88%	0.90%	0.94%
Metabolism|Glycan biosynthesis and metabolism|ko00540 Lipopolysaccharide biosynthesis	0.89%	0.89%	0.64%	0.94%	0.88%	0.87%	1.07%	0.83%	1.10%	0.80%	1.00%	0.78%	0.91%	0.85%	0.86%
Metabolism|Carbohydrate metabolism|ko00650 Butanoate metabolism	0.88%	0.91%	1.05%	0.89%	0.87%	0.74%	0.84%	0.84%	0.92%	0.83%	0.83%	0.83%	0.94%	0.96%	0.90%
Metabolism|Carbohydrate metabolism|ko00010 Glycolysis / Gluconeogenesis	0.85%	0.86%	0.84%	0.88%	0.90%	0.94%	0.80%	0.96%	0.74%	0.82%	0.77%	0.91%	0.81%	0.83%	0.85%
Metabolism|Amino acid metabolism|ko00340 Histidine metabolism	0.85%	0.93%	0.92%	0.81%	0.79%	0.89%	0.82%	0.87%	0.79%	0.83%	0.87%	0.84%	0.81%	0.81%	0.86%
Metabolism|Metabolism of other amino acids|ko00480 Glutathione metabolism	0.84%	0.92%	1.07%	0.88%	0.84%	0.69%	0.84%	0.74%	0.89%	0.83%	0.84%	0.80%	0.81%	0.85%	0.83%
Metabolism|Metabolism of cofactors and vitamins|ko00760 Nicotinate and nicotinamide metabolism	0.76%	0.79%	0.78%	0.76%	0.76%	0.84%	0.72%	0.73%	0.72%	0.74%	0.75%	0.73%	0.73%	0.74%	0.78%
Metabolism|Metabolism of terpenoids and polyketides|ko00900 Terpenoid backbone biosynthesis	0.75%	0.74%	0.75%	0.71%	0.74%	0.96%	0.75%	0.75%	0.73%	0.72%	0.71%	0.72%	0.70%	0.71%	0.78%
Metabolism|Lipid metabolism|ko00061 Fatty acid biosynthesis	0.74%	0.83%	0.87%	0.73%	0.71%	0.62%	0.80%	0.69%	0.84%	0.72%	0.76%	0.66%	0.71%	0.71%	0.76%
Metabolism|Amino acid metabolism|ko00280 Valine, leucine and isoleucine degradation	0.74%	0.82%	1.03%	0.67%	0.65%	0.45%	0.90%	0.65%	1.00%	0.68%	0.70%	0.62%	0.75%	0.76%	0.71%
Metabolism|Metabolism of cofactors and vitamins|ko00130 Ubiquinone and other terpenoid-quinone biosynthesis	0.74%	0.73%	0.74%	0.78%	0.72%	0.71%	0.81%	0.70%	0.82%	0.66%	0.74%	0.71%	0.74%	0.73%	0.75%
Metabolism|Amino acid metabolism|ko00360 Phenylalanine metabolism	0.70%	0.79%	0.85%	0.68%	0.65%	0.43%	0.80%	0.63%	0.94%	0.61%	0.59%	0.65%	0.80%	0.79%	0.65%
Metabolism|Metabolism of cofactors and vitamins|ko00770 Pantothenate and CoA biosynthesis	0.66%	0.66%	0.63%	0.66%	0.67%	0.76%	0.63%	0.68%	0.62%	0.63%	0.63%	0.67%	0.67%	0.66%	0.68%
Metabolism|Carbohydrate metabolism|ko00020 Citrate cycle (TCA cycle)	0.65%	0.65%	0.65%	0.65%	0.62%	0.78%	0.66%	0.64%	0.65%	0.60%	0.63%	0.62%	0.63%	0.63%	0.62%
Metabolism|Carbohydrate metabolism|ko00640 Propanoate metabolism	0.62%	0.66%	0.68%	0.63%	0.60%	0.50%	0.62%	0.60%	0.65%	0.59%	0.63%	0.59%	0.64%	0.65%	0.59%
Genetic Information Processing|Replication and repair|ko03410 Base excision repair	0.61%	0.59%	0.61%	0.61%	0.62%	0.64%	0.61%	0.60%	0.61%	0.61%	0.59%	0.61%	0.58%	0.59%	0.61%
Metabolism|Xenobiotics biodegradation and metabolism|ko00362 Benzoate degradation	0.59%	0.65%	0.74%	0.58%	0.56%	0.42%	0.58%	0.53%	0.65%	0.57%	0.57%	0.55%	0.66%	0.66%	0.61%
Genetic Information Processing|Folding, sorting and degradation|ko03060 Protein export	0.59%	0.61%	0.58%	0.56%	0.57%	0.74%	0.63%	0.59%	0.61%	0.58%	0.56%	0.58%	0.54%	0.54%	0.59%
Human Diseases|Infectious diseases: Bacterial|ko05111 Vibrio cholerae pathogenic cycle	0.59%	0.65%	0.39%	0.64%	0.59%	0.30%	0.68%	0.51%	0.80%	0.55%	0.66%	0.56%	0.70%	0.67%	0.51%
Metabolism|Metabolism of cofactors and vitamins|ko00790 Folate biosynthesis	0.58%	0.58%	0.56%	0.56%	0.54%	0.72%	0.58%	0.56%	0.58%	0.57%	0.61%	0.55%	0.55%	0.54%	0.59%
Metabolism|Amino acid metabolism|ko00310 Lysine degradation	0.57%	0.67%	0.60%	0.58%	0.55%	0.34%	0.72%	0.54%	0.75%	0.55%	0.56%	0.53%	0.55%	0.55%	0.55%
Metabolism|Metabolism of cofactors and vitamins|ko00730 Thiamine metabolism	0.55%	0.53%	0.54%	0.53%	0.54%	0.66%	0.53%	0.55%	0.53%	0.59%	0.55%	0.56%	0.54%	0.54%	0.55%
Human Diseases|Infectious diseases: Bacterial|ko05133 Pertussis	0.55%	0.73%	0.27%	0.81%	0.69%	0.29%	0.44%	0.51%	0.51%	0.45%	0.56%	0.61%	0.63%	0.62%	0.53%
Metabolism|Metabolism of cofactors and vitamins|ko00780 Biotin metabolism	0.55%	0.63%	0.52%	0.56%	0.55%	0.54%	0.52%	0.54%	0.50%	0.54%	0.57%	0.53%	0.57%	0.55%	0.53%
Metabolism|Amino acid metabolism|ko00350 Tyrosine metabolism	0.54%	0.58%	0.63%	0.54%	0.53%	0.40%	0.54%	0.53%	0.58%	0.52%	0.52%	0.53%	0.58%	0.58%	0.55%
Metabolism|Metabolism of other amino acids|ko00450 Selenocompound metabolism	0.54%	0.51%	0.50%	0.54%	0.54%	0.76%	0.52%	0.57%	0.50%	0.54%	0.50%	0.58%	0.51%	0.52%	0.52%
Genetic Information Processing|Replication and repair|ko03030 DNA replication	0.54%	0.53%	0.53%	0.52%	0.54%	0.67%	0.55%	0.54%	0.53%	0.55%	0.51%	0.54%	0.50%	0.51%	0.54%
Metabolism|Amino acid metabolism|ko00290 Valine, leucine and isoleucine biosynthesis	0.53%	0.56%	0.56%	0.54%	0.52%	0.55%	0.45%	0.53%	0.45%	0.50%	0.53%	0.54%	0.55%	0.54%	0.56%
Metabolism|Energy metabolism|ko00920 Sulfur metabolism	0.51%	0.57%	0.49%	0.55%	0.52%	0.60%	0.39%	0.47%	0.41%	0.50%	0.58%	0.48%	0.52%	0.53%	0.53%
Metabolism|Carbohydrate metabolism|ko00040 Pentose and glucuronate interconversions	0.50%	0.49%	0.57%	0.58%	0.58%	0.38%	0.37%	0.60%	0.32%	0.50%	0.45%	0.57%	0.49%	0.53%	0.59%
Genetic Information Processing|Folding, sorting and degradation|ko04122 Sulfur relay system	0.49%	0.48%	0.40%	0.47%	0.48%	0.57%	0.54%	0.52%	0.51%	0.52%	0.51%	0.51%	0.47%	0.46%	0.47%
Metabolism|Carbohydrate metabolism|ko00052 Galactose metabolism	0.48%	0.42%	0.49%	0.49%	0.55%	0.61%	0.45%	0.61%	0.37%	0.45%	0.35%	0.57%	0.44%	0.48%	0.48%
Metabolism|Xenobiotics biodegradation and metabolism|ko00627 Aminobenzoate degradation	0.48%	0.50%	0.60%	0.48%	0.46%	0.31%	0.47%	0.44%	0.53%	0.44%	0.45%	0.46%	0.53%	0.54%	0.48%
Metabolism|Lipid metabolism|ko00561 Glycerolipid metabolism	0.46%	0.46%	0.41%	0.51%	0.55%	0.40%	0.40%	0.54%	0.37%	0.50%	0.45%	0.54%	0.43%	0.45%	0.43%
Metabolism|Metabolism of cofactors and vitamins|ko00670 One carbon pool by folate	0.44%	0.45%	0.45%	0.42%	0.43%	0.53%	0.44%	0.44%	0.42%	0.45%	0.43%	0.45%	0.41%	0.42%	0.44%
Metabolism|Lipid metabolism|ko00071 Fatty acid degradation	0.43%	0.47%	0.54%	0.44%	0.41%	0.30%	0.44%	0.37%	0.49%	0.41%	0.45%	0.38%	0.46%	0.46%	0.42%
Metabolism|Energy metabolism|ko00710 Carbon fixation in photosynthetic organisms	0.40%	0.39%	0.43%	0.39%	0.39%	0.44%	0.42%	0.41%	0.43%	0.38%	0.36%	0.40%	0.40%	0.40%	0.42%
Environmental Information Processing|Membrane transport|ko02060 Phosphotransferase system (PTS)	0.39%	0.38%	0.26%	0.55%	0.62%	0.56%	0.21%	0.51%	0.17%	0.39%	0.29%	0.50%	0.33%	0.39%	0.38%
Metabolism|Metabolism of terpenoids and polyketides|ko00281 Geraniol degradation	0.39%	0.48%	0.56%	0.37%	0.35%	0.16%	0.39%	0.31%	0.46%	0.37%	0.41%	0.32%	0.41%	0.42%	0.42%
Metabolism|Metabolism of terpenoids and polyketides|ko01054 Nonribosomal peptide structures	0.38%	0.40%	0.22%	0.38%	0.42%	0.19%	0.32%	0.40%	0.34%	0.50%	0.66%	0.36%	0.43%	0.41%	0.31%
Metabolism|Metabolism of cofactors and vitamins|ko00740 Riboflavin metabolism	0.37%	0.41%	0.38%	0.38%	0.37%	0.36%	0.38%	0.33%	0.39%	0.35%	0.39%	0.34%	0.36%	0.36%	0.39%
Metabolism|Metabolism of cofactors and vitamins|ko00750 Vitamin B6 metabolism	0.32%	0.33%	0.32%	0.33%	0.32%	0.31%	0.33%	0.34%	0.31%	0.32%	0.33%	0.35%	0.31%	0.32%	0.33%
Metabolism|Xenobiotics biodegradation and metabolism|ko00625 Chloroalkane and chloroalkene degradation	0.31%	0.28%	0.36%	0.29%	0.30%	0.25%	0.29%	0.31%	0.29%	0.32%	0.30%	0.31%	0.32%	0.32%	0.33%
Metabolism|Carbohydrate metabolism|ko00053 Ascorbate and aldarate metabolism	0.29%	0.31%	0.32%	0.33%	0.32%	0.31%	0.23%	0.28%	0.25%	0.28%	0.29%	0.29%	0.29%	0.31%	0.31%
Metabolism|Amino acid metabolism|ko00380 Tryptophan metabolism	0.28%	0.34%	0.38%	0.29%	0.27%	0.12%	0.31%	0.25%	0.35%	0.25%	0.26%	0.25%	0.28%	0.29%	0.27%
Metabolism|Xenobiotics biodegradation and metabolism|ko00983 Drug metabolism - other enzymes	0.28%	0.26%	0.27%	0.26%	0.27%	0.26%	0.34%	0.30%	0.32%	0.28%	0.24%	0.29%	0.25%	0.26%	0.27%
Human Diseases|Infectious diseases: Bacterial|ko05134 Legionellosis	0.27%	0.26%	0.24%	0.31%	0.29%	0.30%	0.26%	0.24%	0.25%	0.25%	0.25%	0.28%	0.25%	0.25%	0.32%
Organismal Systems|Environmental adaptation|ko04626 Plant-pathogen interaction	0.27%	0.27%	0.24%	0.27%	0.27%	0.25%	0.30%	0.26%	0.31%	0.27%	0.27%	0.27%	0.26%	0.26%	0.25%
Metabolism|Xenobiotics biodegradation and metabolism|ko00363 Bisphenol degradation	0.27%	0.27%	0.34%	0.25%	0.25%	0.21%	0.26%	0.25%	0.28%	0.26%	0.26%	0.25%	0.27%	0.28%	0.27%
Genetic Information Processing|Translation|ko03013 RNA transport	0.26%	0.20%	0.15%	0.26%	0.25%	0.43%	0.27%	0.30%	0.23%	0.24%	0.21%	0.29%	0.26%	0.23%	0.26%
Metabolism|Lipid metabolism|ko01040 Biosynthesis of unsaturated fatty acids	0.26%	0.30%	0.29%	0.27%	0.25%	0.15%	0.26%	0.24%	0.28%	0.25%	0.28%	0.23%	0.26%	0.27%	0.25%
Metabolism|Metabolism of terpenoids and polyketides|ko01053 Biosynthesis of siderophore group nonribosomal peptides	0.25%	0.27%	0.19%	0.27%	0.27%	0.17%	0.22%	0.25%	0.24%	0.27%	0.34%	0.24%	0.26%	0.26%	0.22%
Metabolism|Energy metabolism|ko00195 Photosynthesis	0.24%	0.24%	0.24%	0.22%	0.23%	0.30%	0.26%	0.22%	0.26%	0.22%	0.23%	0.22%	0.23%	0.22%	0.24%
Cellular Processes|Transport and catabolism|ko04146 Peroxisome	0.24%	0.25%	0.27%	0.23%	0.22%	0.22%	0.26%	0.22%	0.28%	0.21%	0.23%	0.21%	0.25%	0.25%	0.21%
Metabolism|Carbohydrate metabolism|ko00562 Inositol phosphate metabolism	0.24%	0.23%	0.30%	0.24%	0.25%	0.16%	0.21%	0.26%	0.21%	0.23%	0.21%	0.24%	0.24%	0.25%	0.26%
Metabolism|Biosynthesis of other secondary metabolites|ko00521 Streptomycin biosynthesis	0.23%	0.20%	0.22%	0.21%	0.23%	0.27%	0.26%	0.24%	0.24%	0.22%	0.21%	0.23%	0.23%	0.22%	0.24%
Metabolism|Xenobiotics biodegradation and metabolism|ko00633 Nitrotoluene degradation	0.23%	0.20%	0.20%	0.22%	0.22%	0.39%	0.20%	0.21%	0.19%	0.22%	0.22%	0.24%	0.24%	0.22%	0.25%
Metabolism|Metabolism of terpenoids and polyketides|ko00903 Limonene and pinene degradation	0.23%	0.26%	0.30%	0.23%	0.23%	0.14%	0.21%	0.21%	0.23%	0.23%	0.25%	0.21%	0.23%	0.24%	0.24%
Metabolism|Metabolism of other amino acids|ko00473 D-Alanine metabolism	0.22%	0.21%	0.27%	0.21%	0.23%	0.25%	0.21%	0.27%	0.17%	0.22%	0.18%	0.25%	0.19%	0.21%	0.23%
Metabolism|Xenobiotics biodegradation and metabolism|ko00624 Polycyclic aromatic hydrocarbon degradation	0.22%	0.22%	0.23%	0.20%	0.20%	0.21%	0.23%	0.22%	0.24%	0.22%	0.20%	0.22%	0.23%	0.22%	0.22%
Metabolism|Xenobiotics biodegradation and metabolism|ko00626 Naphthalene degradation	0.20%	0.23%	0.25%	0.21%	0.20%	0.11%	0.20%	0.18%	0.23%	0.18%	0.18%	0.19%	0.24%	0.24%	0.21%
Metabolism|Metabolism of other amino acids|ko00410 beta-Alanine metabolism	0.20%	0.22%	0.25%	0.19%	0.19%	0.13%	0.21%	0.18%	0.24%	0.19%	0.21%	0.18%	0.21%	0.21%	0.20%
Genetic Information Processing|Transcription|ko03020 RNA polymerase	0.19%	0.20%	0.19%	0.18%	0.19%	0.26%	0.20%	0.19%	0.19%	0.19%	0.19%	0.19%	0.18%	0.18%	0.19%
Metabolism|Metabolism of other amino acids|ko00430 Taurine and hypotaurine metabolism	0.19%	0.22%	0.28%	0.20%	0.19%	0.11%	0.18%	0.18%	0.19%	0.19%	0.20%	0.18%	0.20%	0.20%	0.19%
Metabolism|Biosynthesis of other secondary metabolites|ko00311 Penicillin and cephalosporin biosynthesis	0.19%	0.20%	0.23%	0.16%	0.17%	0.10%	0.28%	0.17%	0.30%	0.18%	0.18%	0.15%	0.17%	0.17%	0.15%
Metabolism|Metabolism of other amino acids|ko00440 Phosphonate and phosphinate metabolism	0.18%	0.19%	0.23%	0.17%	0.17%	0.13%	0.17%	0.16%	0.21%	0.17%	0.19%	0.16%	0.21%	0.21%	0.17%
Metabolism|Carbohydrate metabolism|ko00660 C5-Branched dibasic acid metabolism	0.18%	0.19%	0.19%	0.18%	0.17%	0.23%	0.15%	0.19%	0.15%	0.16%	0.16%	0.18%	0.19%	0.19%	0.18%
Human Diseases|Infectious diseases: Bacterial|ko05132 Salmonella infection	0.18%	0.18%	0.12%	0.20%	0.20%	0.13%	0.19%	0.18%	0.19%	0.19%	0.19%	0.19%	0.18%	0.17%	0.18%
Metabolism|Glycan biosynthesis and metabolism|ko00511 Other glycan degradation	0.18%	0.19%	0.14%	0.20%	0.25%	0.17%	0.12%	0.28%	0.07%	0.19%	0.11%	0.24%	0.16%	0.18%	0.18%
Metabolism|Metabolism of other amino acids|ko00471 D-Glutamine and D-glutamate metabolism	0.18%	0.18%	0.17%	0.16%	0.17%	0.21%	0.21%	0.17%	0.22%	0.17%	0.17%	0.17%	0.16%	0.16%	0.16%
Organismal Systems|Endocrine system|ko03320 PPAR signaling pathway	0.17%	0.18%	0.21%	0.17%	0.16%	0.12%	0.21%	0.16%	0.23%	0.16%	0.17%	0.16%	0.19%	0.19%	0.15%
Human Diseases|Infectious diseases: Bacterial|ko05150 Staphylococcus aureus infection	0.16%	0.16%	0.08%	0.28%	0.24%	0.11%	0.08%	0.20%	0.06%	0.15%	0.12%	0.27%	0.14%	0.16%	0.20%
Metabolism|Xenobiotics biodegradation and metabolism|ko00623 Toluene degradation	0.16%	0.17%	0.16%	0.16%	0.15%	0.18%	0.17%	0.13%	0.19%	0.14%	0.14%	0.14%	0.18%	0.18%	0.15%
Metabolism|Metabolism of other amino acids|ko00460 Cyanoamino acid metabolism	0.16%	0.16%	0.16%	0.16%	0.16%	0.16%	0.15%	0.18%	0.14%	0.16%	0.16%	0.17%	0.15%	0.16%	0.14%
Human Diseases|Infectious diseases: Bacterial|ko05152 Tuberculosis	0.16%	0.15%	0.16%	0.14%	0.15%	0.18%	0.16%	0.17%	0.15%	0.16%	0.15%	0.16%	0.15%	0.15%	0.16%
Human Diseases|Infectious diseases: Bacterial|ko05120 Epithelial cell signaling in Helicobacter pylori infection	0.15%	0.13%	0.09%	0.15%	0.15%	0.16%	0.20%	0.14%	0.20%	0.17%	0.15%	0.16%	0.14%	0.14%	0.14%
Metabolism|Xenobiotics biodegradation and metabolism|ko00361 Chlorocyclohexane and chlorobenzene degradation	0.14%	0.15%	0.18%	0.14%	0.14%	0.07%	0.15%	0.13%	0.18%	0.13%	0.13%	0.13%	0.17%	0.17%	0.14%
Metabolism|Lipid metabolism|ko00591 Linoleic acid metabolism	0.14%	0.16%	0.16%	0.14%	0.14%	0.14%	0.13%	0.15%	0.12%	0.14%	0.14%	0.14%	0.13%	0.14%	0.14%
Metabolism|Metabolism of cofactors and vitamins|ko00785 Lipoic acid metabolism	0.14%	0.16%	0.13%	0.14%	0.14%	0.12%	0.17%	0.14%	0.17%	0.13%	0.11%	0.15%	0.13%	0.13%	0.13%
Metabolism|Metabolism of terpenoids and polyketides|ko01051 Biosynthesis of ansamycins	0.14%	0.12%	0.13%	0.13%	0.14%	0.12%	0.15%	0.15%	0.15%	0.13%	0.13%	0.14%	0.14%	0.14%	0.12%
Metabolism|Metabolism of terpenoids and polyketides|ko00523 Polyketide sugar unit biosynthesis	0.14%	0.12%	0.10%	0.12%	0.13%	0.18%	0.17%	0.14%	0.16%	0.13%	0.13%	0.13%	0.13%	0.12%	0.13%
Metabolism|Xenobiotics biodegradation and metabolism|ko00930 Caprolactam degradation	0.13%	0.16%	0.21%	0.13%	0.12%	0.07%	0.14%	0.11%	0.15%	0.13%	0.14%	0.11%	0.13%	0.14%	0.13%
Metabolism|Glycan biosynthesis and metabolism|ko00510 N-Glycan biosynthesis	0.13%	0.10%	0.09%	0.11%	0.11%	0.18%	0.20%	0.14%	0.18%	0.11%	0.09%	0.14%	0.13%	0.12%	0.12%
Metabolism|Biosynthesis of other secondary metabolites|ko00960 Tropane, piperidine and pyridine alkaloid biosynthesis	0.13%	0.12%	0.18%	0.13%	0.12%	0.10%	0.12%	0.12%	0.14%	0.12%	0.12%	0.12%	0.14%	0.14%	0.14%
Metabolism|Metabolism of terpenoids and polyketides|ko00906 Carotenoid biosynthesis	0.13%	0.11%	0.24%	0.11%	0.12%	0.11%	0.14%	0.15%	0.11%	0.12%	0.09%	0.14%	0.12%	0.13%	0.12%
Cellular Processes|Cell growth and death|ko04113 Meiosis - yeast	0.13%	0.10%	0.10%	0.12%	0.12%	0.13%	0.15%	0.15%	0.14%	0.12%	0.11%	0.14%	0.13%	0.13%	0.15%
Human Diseases|Infectious diseases: Bacterial|ko05100 Bacterial invasion of epithelial cells	0.13%	0.13%	0.05%	0.17%	0.17%	0.11%	0.08%	0.20%	0.05%	0.14%	0.10%	0.20%	0.12%	0.12%	0.13%
Metabolism|Xenobiotics biodegradation and metabolism|ko00791 Atrazine degradation	0.12%	0.11%	0.12%	0.11%	0.11%	0.10%	0.10%	0.12%	0.09%	0.13%	0.14%	0.12%	0.11%	0.12%	0.12%
Metabolism|Lipid metabolism|ko00600 Sphingolipid metabolism	0.11%	0.12%	0.12%	0.11%	0.13%	0.15%	0.11%	0.14%	0.10%	0.11%	0.07%	0.11%	0.10%	0.11%	0.11%
Metabolism|Xenobiotics biodegradation and metabolism|ko00642 Ethylbenzene degradation	0.11%	0.12%	0.13%	0.12%	0.12%	0.07%	0.11%	0.10%	0.11%	0.11%	0.12%	0.11%	0.11%	0.12%	0.11%
Metabolism|Xenobiotics biodegradation and metabolism|ko00982 Drug metabolism - cytochrome P450	0.10%	0.11%	0.17%	0.10%	0.10%	0.04%	0.09%	0.09%	0.10%	0.10%	0.10%	0.09%	0.11%	0.11%	0.12%
Metabolism|Lipid metabolism|ko00140 Steroid hormone biosynthesis	0.10%	0.11%	0.15%	0.10%	0.10%	0.11%	0.08%	0.10%	0.08%	0.10%	0.09%	0.09%	0.10%	0.11%	0.11%
Metabolism|Xenobiotics biodegradation and metabolism|ko00643 Styrene degradation	0.10%	0.12%	0.13%	0.10%	0.09%	0.04%	0.10%	0.08%	0.12%	0.09%	0.10%	0.09%	0.11%	0.11%	0.11%
Metabolism|Xenobiotics biodegradation and metabolism|ko00980 Metabolism of xenobiotics by cytochrome P450	0.10%	0.11%	0.16%	0.10%	0.09%	0.04%	0.09%	0.09%	0.10%	0.09%	0.10%	0.09%	0.10%	0.11%	0.11%
Metabolism|Xenobiotics biodegradation and metabolism|ko00984 Steroid degradation	0.09%	0.11%	0.12%	0.07%	0.07%	0.10%	0.12%	0.07%	0.13%	0.08%	0.08%	0.07%	0.09%	0.09%	0.08%
Metabolism|Biosynthesis of other secondary metabolites|ko00940 Phenylpropanoid biosynthesis	0.09%	0.09%	0.11%	0.09%	0.09%	0.08%	0.09%	0.10%	0.08%	0.09%	0.08%	0.09%	0.08%	0.08%	0.08%
Organismal Systems|Endocrine system|ko04910 Insulin signaling pathway	0.09%	0.07%	0.05%	0.09%	0.09%	0.10%	0.10%	0.09%	0.10%	0.10%	0.08%	0.09%	0.09%	0.08%	0.07%
Genetic Information Processing|Translation|ko03008 Ribosome biogenesis in eukaryotes	0.08%	0.10%	0.06%	0.09%	0.09%	0.07%	0.09%	0.08%	0.09%	0.08%	0.09%	0.08%	0.09%	0.08%	0.08%
Human Diseases|Neurodegenerative diseases|ko05010 Alzheimer's disease	0.08%	0.10%	0.08%	0.09%	0.09%	0.09%	0.06%	0.08%	0.06%	0.09%	0.10%	0.08%	0.07%	0.07%	0.08%
Cellular Processes|Transport and catabolism|ko04142 Lysosome	0.08%	0.12%	0.09%	0.09%	0.10%	0.08%	0.06%	0.10%	0.05%	0.09%	0.05%	0.08%	0.07%	0.08%	0.09%
Genetic Information Processing|Folding, sorting and degradation|ko04141 Protein processing in endoplasmic reticulum	0.08%	0.05%	0.07%	0.07%	0.07%	0.15%	0.09%	0.08%	0.09%	0.07%	0.07%	0.08%	0.09%	0.08%	0.08%
Organismal Systems|Endocrine system|ko04920 Adipocytokine signaling pathway	0.08%	0.08%	0.09%	0.07%	0.07%	0.08%	0.10%	0.08%	0.10%	0.07%	0.07%	0.07%	0.09%	0.09%	0.07%
Metabolism|Lipid metabolism|ko00072 Synthesis and degradation of ketone bodies	0.08%	0.09%	0.10%	0.07%	0.07%	0.04%	0.09%	0.07%	0.10%	0.07%	0.07%	0.07%	0.08%	0.08%	0.08%
Human Diseases|Drug resistance|ko01501 beta-Lactam resistance	0.08%	0.08%	0.10%	0.09%	0.09%	0.04%	0.05%	0.08%	0.05%	0.08%	0.06%	0.09%	0.07%	0.08%	0.08%
Human Diseases|Cancers: Overview|ko05204 Chemical carcinogenesis	0.07%	0.08%	0.13%	0.07%	0.07%	0.03%	0.07%	0.06%	0.08%	0.07%	0.07%	0.06%	0.08%	0.08%	0.08%
Metabolism|Biosynthesis of other secondary metabolites|ko00401 Novobiocin biosynthesis	0.07%	0.07%	0.08%	0.07%	0.07%	0.07%	0.07%	0.07%	0.06%	0.07%	0.08%	0.07%	0.07%	0.07%	0.08%
Environmental Information Processing|Signal transduction|ko04070 Phosphatidylinositol signaling system	0.07%	0.06%	0.08%	0.07%	0.07%	0.07%	0.07%	0.07%	0.07%	0.07%	0.07%	0.07%	0.06%	0.07%	0.07%
Metabolism|Xenobiotics biodegradation and metabolism|ko00622 Xylene degradation	0.06%	0.07%	0.07%	0.07%	0.07%	0.04%	0.06%	0.06%	0.07%	0.06%	0.07%	0.06%	0.08%	0.08%	0.06%
Metabolism|Metabolism of terpenoids and polyketides|ko00908 Zeatin biosynthesis	0.06%	0.07%	0.06%	0.06%	0.06%	0.08%	0.07%	0.06%	0.06%	0.06%	0.06%	0.06%	0.06%	0.06%	0.07%
Metabolism|Lipid metabolism|ko00590 Arachidonic acid metabolism	0.06%	0.07%	0.07%	0.07%	0.06%	0.03%	0.08%	0.06%	0.09%	0.06%	0.07%	0.06%	0.06%	0.06%	0.05%
Organismal Systems|Digestive system|ko04974 Protein digestion and absorption	0.06%	0.08%	0.07%	0.07%	0.07%	0.03%	0.04%	0.07%	0.02%	0.06%	0.05%	0.06%	0.05%	0.05%	0.06%
Metabolism|Xenobiotics biodegradation and metabolism|ko00621 Dioxin degradation	0.05%	0.05%	0.05%	0.06%	0.06%	0.04%	0.05%	0.05%	0.06%	0.05%	0.05%	0.06%	0.07%	0.07%	0.05%
Human Diseases|Neurodegenerative diseases|ko05016 Huntington's disease	0.05%	0.05%	0.06%	0.06%	0.06%	0.04%	0.05%	0.05%	0.05%	0.05%	0.05%	0.05%	0.05%	0.05%	0.05%
Metabolism|Metabolism of terpenoids and polyketides|ko01055 Biosynthesis of vancomycin group antibiotics	0.05%	0.04%	0.04%	0.04%	0.04%	0.06%	0.06%	0.05%	0.06%	0.04%	0.04%	0.05%	0.05%	0.05%	0.04%
Metabolism|Xenobiotics biodegradation and metabolism|ko00364 Fluorobenzoate degradation	0.05%	0.06%	0.06%	0.05%	0.05%	0.02%	0.05%	0.04%	0.06%	0.04%	0.05%	0.04%	0.06%	0.06%	0.05%
Metabolism|Metabolism of terpenoids and polyketides|ko00253 Tetracycline biosynthesis	0.05%	0.05%	0.05%	0.05%	0.05%	0.04%	0.05%	0.04%	0.05%	0.05%	0.05%	0.04%	0.05%	0.05%	0.05%
Human Diseases|Infectious diseases: Parasitic|ko05143 African trypanosomiasis	0.05%	0.06%	0.06%	0.06%	0.08%	0.02%	0.04%	0.04%	0.04%	0.06%	0.05%	0.04%	0.03%	0.04%	0.05%
Environmental Information Processing|Signal transduction|ko04011 MAPK signaling pathway - yeast	0.04%	0.04%	0.07%	0.04%	0.04%	0.03%	0.05%	0.04%	0.05%	0.04%	0.04%	0.04%	0.04%	0.05%	0.04%
Human Diseases|Immune diseases|ko05340 Primary immunodeficiency	0.04%	0.05%	0.04%	0.05%	0.04%	0.04%	0.05%	0.04%	0.04%	0.04%	0.05%	0.05%	0.04%	0.04%	0.03%
Metabolism|Metabolism of cofactors and vitamins|ko00830 Retinol metabolism	0.04%	0.05%	0.06%	0.04%	0.04%	0.02%	0.04%	0.04%	0.04%	0.05%	0.05%	0.04%	0.04%	0.04%	0.05%
Metabolism|Metabolism of terpenoids and polyketides|ko00522 Biosynthesis of 12-, 14- and 16-membered macrolides	0.04%	0.03%	0.04%	0.04%	0.04%	0.02%	0.04%	0.05%	0.04%	0.05%	0.05%	0.05%	0.05%	0.05%	0.04%
Metabolism|Glycan biosynthesis and metabolism|ko00531 Glycosaminoglycan degradation	0.04%	0.07%	0.05%	0.05%	0.06%	0.04%	0.03%	0.05%	0.02%	0.05%	0.03%	0.04%	0.03%	0.04%	0.05%
Organismal Systems|Nervous system|ko04727 GABAergic synapse	0.04%	0.04%	0.05%	0.04%	0.04%	0.06%	0.04%	0.04%	0.04%	0.05%	0.05%	0.04%	0.04%	0.04%	0.04%
Genetic Information Processing|Replication and repair|ko03450 Non-homologous end-joining	0.04%	0.04%	0.06%	0.04%	0.04%	0.02%	0.03%	0.04%	0.04%	0.04%	0.04%	0.04%	0.04%	0.05%	0.07%
Human Diseases|Cancers: Overview|ko05200 Pathways in cancer	0.04%	0.04%	0.03%	0.04%	0.04%	0.04%	0.04%	0.03%	0.04%	0.04%	0.04%	0.03%	0.03%	0.04%	0.03%
Organismal Systems|Nervous system|ko04723 Retrograde endocannabinoid signaling	0.04%	0.03%	0.02%	0.03%	0.03%	0.04%	0.08%	0.03%	0.09%	0.03%	0.03%	0.03%	0.03%	0.03%	0.03%
Human Diseases|Endocrine and metabolic diseases|ko04940 Type I diabetes mellitus	0.03%	0.03%	0.04%	0.03%	0.03%	0.04%	0.03%	0.03%	0.03%	0.03%	0.03%	0.03%	0.03%	0.03%	0.04%
Organismal Systems|Nervous system|ko04724 Glutamatergic synapse	0.03%	0.03%	0.04%	0.03%	0.03%	0.04%	0.03%	0.03%	0.04%	0.04%	0.04%	0.03%	0.03%	0.03%	0.03%
Metabolism|Metabolism of terpenoids and polyketides|ko00909 Sesquiterpenoid and triterpenoid biosynthesis	0.03%	0.02%	0.02%	0.03%	0.03%	0.02%	0.04%	0.04%	0.04%	0.03%	0.03%	0.03%	0.05%	0.04%	0.04%
Cellular Processes|Cell growth and death|ko04210 Apoptosis	0.03%	0.05%	0.04%	0.04%	0.04%	0.02%	0.02%	0.03%	0.02%	0.04%	0.03%	0.03%	0.03%	0.03%	0.03%

Organismal Systems|Digestive system|ko04973 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%
Human Diseases|Infectious diseases: Parasitic|ko05142 Chagas disease (American trypanosomiasis)	0.03%	0.04%	0.05%	0.03%	0.03%	0.01%	0.03%	0.03%	0.03%	0.03%	0.03%	0.02%	0.02%	0.02%	0.04%
Metabolism|Lipid metabolism|ko00565 Ether lipid metabolism	0.03%	0.03%	0.03%	0.03%	0.03%	0.01%	0.03%	0.03%	0.04%	0.03%	0.03%	0.03%	0.04%	0.04%	0.02%
Metabolism|Lipid metabolism|ko00120 Primary bile acid biosynthesis	0.03%	0.03%	0.03%	0.03%	0.03%	0.06%	0.02%	0.02%	0.02%	0.02%	0.02%	0.03%	0.03%	0.03%	0.02%
Human Diseases|Cancers: Overview|ko05203 Viral carcinogenesis	0.03%	0.03%	0.02%	0.03%	0.03%	0.03%	0.03%	0.03%	0.03%	0.03%	0.03%	0.02%	0.02%	0.03%	0.02%
Human Diseases|Infectious diseases: Bacterial|ko05110 Vibrio cholerae infection	0.03%	0.04%	0.01%	0.04%	0.04%	0.01%	0.02%	0.02%	0.01%	0.02%	0.03%	0.03%	0.02%	0.03%	0.03%
Human Diseases|Neurodegenerative diseases|ko05014 Amyotrophic lateral sclerosis (ALS)	0.03%	0.03%	0.02%	0.03%	0.03%	0.02%	0.03%	0.03%	0.03%	0.02%	0.03%	0.03%	0.03%	0.03%	0.02%
Organismal Systems|Digestive system|ko04978 Mineral absorption	0.03%	0.02%	0.02%	0.03%	0.03%	0.02%	0.03%	0.03%	0.03%	0.03%	0.03%	0.03%	0.03%	0.03%	0.02%
Metabolism|Biosynthesis of other secondary metabolites|ko00950 Isoquinoline alkaloid biosynthesis	0.02%	0.03%	0.03%	0.02%	0.02%	0.02%	0.02%	0.02%	0.02%	0.03%	0.02%	0.02%	0.02%	0.03%	0.03%
Metabolism|Lipid metabolism|ko00592 alpha-Linolenic acid metabolism	0.02%	0.03%	0.02%	0.03%	0.03%	0.01%	0.03%	0.02%	0.03%	0.02%	0.03%	0.02%	0.03%	0.03%	0.02%
Metabolism|Metabolism of terpenoids and polyketides|ko01057 Biosynthesis of type II polyketide products	0.02%	0.02%	0.03%	0.02%	0.02%	0.03%	0.02%	0.02%	0.02%	0.02%	0.03%	0.02%	0.03%	0.03%	0.02%
Metabolism|Biosynthesis of other secondary metabolites|ko00945 Stilbenoid, diarylheptanoid and gingerol biosynthesis	0.02%	0.02%	0.04%	0.02%	0.02%	0.01%	0.02%	0.02%	0.02%	0.02%	0.02%	0.02%	0.02%	0.02%	0.02%
Metabolism|Glycan biosynthesis and metabolism|ko00603 Glycosphingolipid biosynthesis - globo series	0.02%	0.02%	0.02%	0.02%	0.03%	0.03%	0.02%	0.03%	0.01%	0.02%	0.02%	0.03%	0.02%	0.02%	0.02%
Human Diseases|Neurodegenerative diseases|ko05012 Parkinson's disease	0.02%	0.02%	0.02%	0.02%	0.02%	0.04%	0.02%	0.02%	0.02%	0.02%	0.03%	0.02%	0.02%	0.02%	0.02%
Metabolism|Xenobiotics biodegradation and metabolism|ko00351 DDT degradation	0.02%	0.02%	0.03%	0.02%	0.02%	0.02%	0.03%	0.02%	0.03%	0.02%	0.02%	0.02%	0.02%	0.02%	0.02%
Human Diseases|Cancers: Specific types|ko05211 Renal cell carcinoma	0.02%	0.02%	0.02%	0.02%	0.02%	0.02%	0.02%	0.02%	0.02%	0.02%	0.03%	0.02%	0.02%	0.02%	0.02%
Metabolism|Glycan biosynthesis and metabolism|ko00563 Glycosylphosphatidylinositol(GPI)-anchor biosynthesis	0.02%	0.01%	0.01%	0.01%	0.01%	0.01%	0.10%	0.01%	0.11%	0.01%	0.00%	0.00%	0.01%	0.01%	0.00%
Human Diseases|Endocrine and metabolic diseases|ko04930 Type II diabetes mellitus	0.02%	0.02%	0.02%	0.02%	0.02%	0.02%	0.02%	0.02%	0.02%	0.02%	0.02%	0.02%	0.02%	0.02%	0.02%
Human Diseases|Substance dependence|ko05032 Morphine addiction	0.02%	0.01%	0.02%	0.02%	0.02%	0.02%	0.03%	0.02%	0.03%	0.02%	0.02%	0.02%	0.02%	0.02%	0.02%
Human Diseases|Infectious diseases: Bacterial|ko05131 Shigellosis	0.02%	0.02%	0.00%	0.04%	0.03%	0.01%	0.01%	0.03%	0.01%	0.01%	0.01%	0.03%	0.02%	0.02%	0.03%
Metabolism|Biosynthesis of other secondary metabolites|ko00524 Butirosin and neomycin biosynthesis	0.02%	0.01%	0.02%	0.02%	0.02%	0.02%	0.01%	0.02%	0.01%	0.02%	0.02%	0.02%	0.02%	0.02%	0.02%
Organismal Systems|Immune system|ko04621 NOD-like receptor signaling pathway	0.02%	0.02%	0.01%	0.02%	0.02%	0.02%	0.02%	0.02%	0.02%	0.02%	0.02%	0.02%	0.02%	0.02%	0.01%
Metabolism|Lipid metabolism|ko00121 Secondary bile acid biosynthesis	0.02%	0.01%	0.02%	0.02%	0.02%	0.05%	0.01%	0.01%	0.01%	0.01%	0.01%	0.02%	0.01%	0.01%	0.02%
Genetic Information Processing|Transcription|ko03022 Basal transcription factors	0.02%	0.01%	0.01%	0.01%	0.01%	0.01%	0.02%	0.02%	0.02%	0.03%	0.02%	0.02%	0.02%	0.02%	0.01%
Organismal Systems|Circulatory system|ko04260 Cardiac muscle contraction	0.02%	0.01%	0.02%	0.02%	0.01%	0.02%	0.01%	0.01%	0.01%	0.01%	0.02%	0.01%	0.02%	0.02%	0.01%
Organismal Systems|Excretory system|ko04964 Proximal tubule bicarbonate reclamation	0.02%	0.02%	0.01%	0.01%	0.01%	0.02%	0.02%	0.02%	0.02%	0.01%	0.01%	0.01%	0.02%	0.02%	0.01%
Organismal Systems|Endocrine system|ko04614 Renin-angiotensin system	0.01%	0.02%	0.02%	0.02%	0.02%	0.00%	0.01%	0.01%	0.01%	0.02%	0.01%	0.02%	0.01%	0.01%	0.02%
Human Diseases|Infectious diseases: Parasitic|ko05146 Amoebiasis	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.02%	0.01%	0.02%	0.02%	0.02%	0.03%
Metabolism|Glycan biosynthesis and metabolism|ko00532 Glycosaminoglycan biosynthesis - chondroitin sulfate / dermatan sulfate	0.01%	0.01%	0.01%	0.01%	0.01%	0.05%	0.02%	0.01%	0.02%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%
Human Diseases|Cancers: Specific types|ko05215 Prostate cancer	0.01%	0.02%	0.00%	0.01%	0.02%	0.02%	0.02%	0.01%	0.02%	0.01%	0.02%	0.01%	0.01%	0.01%	0.01%
Organismal Systems|Endocrine system|ko04914 Progesterone-mediated oocyte maturation	0.01%	0.02%	0.00%	0.01%	0.02%	0.02%	0.02%	0.01%	0.02%	0.01%	0.02%	0.01%	0.01%	0.01%	0.01%
Organismal Systems|Immune system|ko04612 Antigen processing and presentation	0.01%	0.02%	0.00%	0.01%	0.02%	0.02%	0.02%	0.01%	0.02%	0.01%	0.02%	0.01%	0.01%	0.01%	0.01%
Metabolism|Biosynthesis of other secondary metabolites|ko00232 Caffeine metabolism	0.01%	0.01%	0.02%	0.01%	0.01%	0.00%	0.02%	0.01%	0.02%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%
Metabolism|Lipid metabolism|ko00100 Steroid biosynthesis	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.02%	0.01%	0.01%	0.01%	0.02%	0.01%	0.01%	0.01%	0.01%
Organismal Systems|Digestive system|ko04976 Bile secretion	0.01%	0.01%	0.02%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%
Genetic Information Processing|Folding, sorting and degradation|ko03050 Proteasome	0.01%	0.01%	0.01%	0.01%	0.01%	0.02%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%
Human Diseases|Cancers: Specific types|ko05219 Bladder cancer	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%
Human Diseases|Substance dependence|ko05034 Alcoholism	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%
Metabolism|Glycan biosynthesis and metabolism|ko00604 Glycosphingolipid biosynthesis - ganglio series	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.00%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%
Metabolism|Glycan biosynthesis and metabolism|ko00601 Glycosphingolipid biosynthesis - lacto and neolacto series	0.01%	0.01%	0.00%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%
Human Diseases|Infectious diseases: Viral|ko05164 Influenza A	0.01%	0.01%	0.01%	0.00%	0.01%	0.01%	0.02%	0.01%	0.02%	0.01%	0.01%	0.00%	0.01%	0.00%	0.01%
Organismal Systems|Immune system|ko04640 Hematopoietic cell lineage	0.01%	0.01%	0.01%	0.01%	0.01%	0.00%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%
Metabolism|Metabolism of terpenoids and polyketides|ko01056 Biosynthesis of type II polyketide backbone	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%
Human Diseases|Infectious diseases: Bacterial|ko05130 Pathogenic Escherichia coli infection	0.01%	0.01%	0.00%	0.02%	0.01%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.01%	0.01%	0.01%	0.01%
Metabolism|Metabolism of other amino acids|ko00472 D-Arginine and D-ornithine metabolism	0.01%	0.01%	0.01%	0.01%	0.01%	0.00%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%
Organismal Systems|Immune system|ko04622 RIG-I-like receptor signaling pathway	0.01%	0.00%	0.01%	0.01%	0.01%	0.01%	0.00%	0.01%	0.01%	0.01%	0.00%	0.01%	0.01%	0.01%	0.01%
Organismal Systems|Immune system|ko04610 Complement and coagulation cascades	0.01%	0.00%	0.01%	0.00%	0.00%	0.00%	0.02%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Metabolism|Metabolism of terpenoids and polyketides|ko00902 Monoterpenoid biosynthesis	0.01%	0.00%	0.03%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.01%
Organismal Systems|Nervous system|ko04725 Cholinergic synapse	0.01%	0.00%	0.00%	0.01%	0.01%	0.00%	0.01%	0.01%	0.01%	0.00%	0.01%	0.01%	0.01%	0.01%	0.00%
Human Diseases|Neurodegenerative diseases|ko05020 Prion diseases	0.00%	0.01%	0.01%	0.01%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.01%	0.01%	0.01%
Organismal Systems|Excretory system|ko04962 Vasopressin-regulated water reabsorption	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.01%
Organismal Systems|Nervous system|ko04721 Synaptic vesicle cycle	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.01%
Metabolism|Lipid metabolism|ko00062 Fatty acid elongation	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.01%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Metabolism|Glycan biosynthesis and metabolism|ko00513 Various types of N-glycan biosynthesis	0.00%	0.00%	0.00%	0.00%	0.00%	0.03%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.01%
Organismal Systems|Nervous system|ko04726 Serotonergic synapse	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.01%	0.00%	0.00%	0.00%	0.00%
Organismal Systems|Digestive system|ko04972 Pancreatic secretion	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Human Diseases|Cardiovascular diseases|ko05410 Hypertrophic cardiomyopathy (HCM)	0.00%	0.00%	0.01%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Organismal Systems|Immune system|ko04666 Fc gamma R-mediated phagocytosis	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Environmental Information Processing|Signaling molecules and interaction|ko04080 Neuroactive ligand-receptor interaction	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Cellular Processes|Transport and catabolism|ko04144 Endocytosis	0.00%	0.00%	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%
Organismal Systems|Endocrine system|ko04912 GnRH signaling pathway	0.00%	0.00%	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%
Human Diseases|Immune diseases|ko05322 Systemic lupus erythematosus	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%
Metabolism|Biosynthesis of other secondary metabolites|ko00901 Indole alkaloid biosynthesis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.01%	0.00%	0.00%	0.00%	0.00%
Metabolism|Energy metabolism|ko00196 Photosynthesis - antenna proteins	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Cellular Processes|Cell growth and death|ko04115 p53 signaling pathway	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.01%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Organismal Systems|Excretory system|ko04961 Endocrine and other factor-regulated calcium reabsorption	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Organismal Systems|Nervous system|ko04728 Dopaminergic synapse	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%
Human Diseases|Substance dependence|ko05030 Cocaine addiction	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%
Human Diseases|Substance dependence|ko05031 Amphetamine addiction	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%
Human Diseases|Infectious diseases: Parasitic|ko05145 Toxoplasmosis	0.00%	0.00%	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%
Organismal Systems|Digestive system|ko04970 Salivary secretion	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Organismal Systems|Digestive system|ko04971 Gastric acid secretion	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Organismal Systems|Excretory system|ko04960 Aldosterone-regulated sodium reabsorption	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Genetic Information Processing|Translation|ko03015 mRNA surveillance pathway	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%
Metabolism|Biosynthesis of other secondary metabolites|ko00944 Flavone and flavonol biosynthesis	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%
Human Diseases|Cancers: Specific types|ko05222 Small cell lung cancer	0.00%	0.00%	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%
Metabolism|Biosynthesis of other secondary metabolites|ko00943 Isoflavonoid biosynthesis	0.00%	0.00%	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%
Human Diseases|Cardiovascular diseases|ko05416 Viral myocarditis	0.00%	0.00%	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%
Human Diseases|Infectious diseases: Viral|ko05168 Herpes simplex infection	0.00%	0.00%	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%
Metabolism|Biosynthesis of other secondary metabolites|ko00965 Betalain biosynthesis	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%
Human Diseases|Cancers: Specific types|ko05210 Colorectal cancer	0.00%	0.00%	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%
Environmental Information Processing|Signal transduction|ko04020 Calcium signaling pathway	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%
Metabolism|Biosynthesis of other secondary metabolites|ko00941 Flavonoid biosynthesis	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%
Genetic Information Processing|Replication and repair|ko03460 Fanconi anemia pathway	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%
Metabolism|Biosynthesis of other secondary metabolites|ko00331 Clavulanic acid biosynthesis	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%
Organismal Systems|Endocrine system|ko04916 Melanogenesis	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%
Genetic Information Processing|Transcription|ko03040 Spliceosome	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%
Cellular Processes|Cellular community|ko04510 Focal adhesion	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%
Environmental Information Processing|Signaling molecules and interaction|ko04512 ECM-receptor interaction	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%
Human Diseases|Cancers: Overview|ko05202 Transcriptional misregulation in cancer	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%
Human Diseases|Infectious diseases: Viral|ko05169 Epstein-Barr virus infection	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%
Environmental Information Processing|Signal transduction|ko04310 Wnt signaling pathway	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%
Environmental Information Processing|Signal transduction|ko04330 Notch signaling pathway	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%
Human Diseases|Cancers: Specific types|ko05220 Chronic myeloid leukemia	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%
Environmental Information Processing|Signal transduction|ko04370 VEGF signaling pathway	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%
Organismal Systems|Digestive system|ko04975 Fat digestion and absorption	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%
Environmental Information Processing|Signal transduction|ko04064 NF-kappa B signaling pathway	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%
Human Diseases|Infectious diseases: Parasitic|ko05140 Leishmaniasis	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%
Cellular Processes|Cell motility|ko04810 Regulation of actin cytoskeleton	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%
Human Diseases|Cardiovascular diseases|ko05412 Arrhythmogenic right ventricular cardiomyopathy (ARVC)	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%
Human Diseases|Cardiovascular diseases|ko05414 Dilated cardiomyopathy	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%
Environmental Information Processing|Signaling molecules and interaction|ko04514 Cell adhesion molecules (CAMs)	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%
Cellular Processes|Cellular community|ko04520 Adherens junction	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%
Cellular Processes|Cellular community|ko04530 Tight junction	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%
Cellular Processes|Transport and catabolism|ko04145 Phagosome	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%
Organismal Systems|Immune system|ko04670 Leukocyte transendothelial migration	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%
Organismal Systems|Sensory system|ko04745 Phototransduction - fly	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%
Human Diseases|Infectious diseases: Viral|ko05160 Hepatitis C	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%
Human Diseases|Infectious diseases: Viral|ko05162 Measles	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%
Environmental Information Processing|Signaling molecules and interaction|ko04060 Cytokine-cytokine receptor interaction	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%
Cellular Processes|Cell growth and death|ko04114 Oocyte meiosis	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%
Human Diseases|Cancers: Specific types|ko05214 Glioma	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%
Organismal Systems|Circulatory system|ko04270 Vascular smooth muscle contraction	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%
Organismal Systems|Nervous system|ko04720 Long-term potentiation	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%
Organismal Systems|Nervous system|ko04722 Neurotrophin signaling pathway	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%
Organismal Systems|Sensory system|ko04740 Olfactory transduction	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%
Organismal Systems|Sensory system|ko04744 Phototransduction	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%

b

Samples	**average**	**P1A**	**P1O**	**P2A**	**P2O**	**P3A**	**P3O**	**P4A**	**P4O**	**P5A**	**P5O**	**P6A**	**P6O**	**P7A**	**P8O**
FTU	0.5129	0.5137	0.1069	0.2399	0.0613	0.2451	0.6858	0.0952	0.4016	0.5489	0.6636	0.9257	0.8357	0.8957	0.9609
Metabolism|Energy metabolism|ko00680 Methane metabolism	8.39%	9.03%	9.25%	8.35%	8.31%	8.32%	8.77%	8.51%	8.77%	8.36%	7.88%	8.37%	7.84%	8.78%	6.91%
Environmental Information Processing|Membrane transport|ko02010 ABC transporters	7.73%	8.06%	8.09%	7.66%	7.66%	7.65%	8.10%	7.65%	7.93%	7.59%	7.49%	7.45%	7.47%	7.82%	7.67%
Genetic Information Processing|Translation|ko00970 Aminoacyl-tRNA biosynthesis	4.45%	4.16%	4.09%	4.39%	4.40%	4.40%	4.02%	4.37%	4.11%	4.43%	5.21%	4.75%	5.21%	4.15%	4.59%
Environmental Information Processing|Signal transduction|ko02020 Two-component system	4.19%	3.86%	3.85%	4.74%	4.72%	4.70%	5.15%	4.48%	5.09%	4.58%	2.61%	4.05%	2.60%	5.27%	2.99%
Metabolism|Metabolism of cofactors and vitamins|ko00860 Porphyrin and chlorophyll metabolism	4.07%	4.70%	4.86%	4.17%	4.18%	4.19%	3.61%	4.14%	3.75%	4.21%	3.58%	4.12%	3.57%	3.82%	4.06%
Metabolism|Nucleotide metabolism|ko00230 Purine metabolism	3.90%	3.58%	3.43%	3.89%	3.90%	3.90%	3.80%	3.90%	3.83%	3.91%	4.22%	3.98%	4.22%	3.85%	4.14%
Metabolism|Nucleotide metabolism|ko00240 Pyrimidine metabolism	3.13%	2.88%	2.75%	3.09%	3.09%	3.09%	3.01%	3.10%	3.03%	3.11%	3.56%	3.20%	3.57%	3.03%	3.35%
Genetic Information Processing|Translation|ko03010 Ribosome	2.84%	2.56%	2.49%	2.77%	2.77%	2.78%	2.65%	2.78%	2.69%	2.80%	3.36%	3.08%	3.36%	2.71%	2.99%
Metabolism|Energy metabolism|ko00190 Oxidative phosphorylation	2.08%	2.15%	2.18%	2.12%	2.13%	2.13%	1.85%	2.04%	1.90%	2.11%	2.10%	2.11%	2.11%	1.94%	2.26%
Genetic Information Processing|Folding, sorting and degradation|ko03018 RNA degradation	1.78%	2.08%	2.03%	2.13%	2.15%	2.14%	1.79%	2.06%	1.85%	2.13%	0.64%	2.00%	0.64%	1.88%	1.43%
Metabolism|Amino acid metabolism|ko00330 Arginine and proline metabolism	1.74%	1.84%	1.88%	1.72%	1.73%	1.72%	1.69%	1.72%	1.68%	1.72%	1.80%	1.71%	1.80%	1.66%	1.63%
Metabolism|Energy metabolism|ko00910 Nitrogen metabolism	1.61%	1.50%	1.49%	1.54%	1.55%	1.54%	1.39%	1.51%	1.43%	1.55%	2.16%	1.55%	2.17%	1.46%	1.64%
Metabolism|Amino acid metabolism|ko00400 Phenylalanine, tyrosine and tryptophan biosynthesis	1.56%	1.51%	1.46%	1.58%	1.59%	1.59%	1.43%	1.58%	1.46%	1.60%	1.76%	1.53%	1.76%	1.47%	1.55%
Genetic Information Processing|Translation|ko03013 RNA transport	1.43%	1.34%	1.32%	1.39%	1.40%	1.40%	1.28%	1.38%	1.30%	1.40%	1.82%	1.43%	1.82%	1.30%	1.41%
Metabolism|Carbohydrate metabolism|ko00520 Amino sugar and nucleotide sugar metabolism	1.43%	1.32%	1.40%	1.36%	1.34%	1.34%	1.88%	1.44%	1.79%	1.35%	1.02%	1.39%	1.03%	1.76%	1.52%
Cellular Processes|Cell motility|ko02030 Bacterial chemotaxis	1.34%	1.39%	1.49%	1.43%	1.42%	1.41%	1.65%	1.34%	1.61%	1.36%	0.83%	1.18%	0.83%	1.67%	1.12%
Metabolism|Amino acid metabolism|ko00300 Lysine biosynthesis	1.33%	1.28%	1.24%	1.38%	1.38%	1.38%	1.25%	1.36%	1.27%	1.38%	1.54%	1.34%	1.54%	1.29%	1.06%
Metabolism|Carbohydrate metabolism|ko00500 Starch and sucrose metabolism	1.33%	1.39%	1.36%	1.35%	1.34%	1.34%	1.94%	1.50%	1.77%	1.35%	0.63%	1.29%	0.63%	1.59%	1.16%
Metabolism|Amino acid metabolism|ko00270 Cysteine and methionine metabolism	1.28%	1.32%	1.32%	1.36%	1.37%	1.37%	1.05%	1.30%	1.12%	1.37%	1.14%	1.42%	1.14%	1.17%	1.45%
Metabolism|Energy metabolism|ko00720 Carbon fixation pathways in prokaryotes	1.25%	1.03%	0.94%	1.21%	1.21%	1.21%	1.18%	1.21%	1.19%	1.21%	1.76%	1.23%	1.76%	1.19%	1.18%
Metabolism|Amino acid metabolism|ko00250 Alanine, aspartate and glutamate metabolism	1.23%	1.16%	1.12%	1.23%	1.23%	1.24%	1.23%	1.25%	1.24%	1.25%	1.22%	1.23%	1.22%	1.23%	1.33%
Metabolism|Carbohydrate metabolism|ko00620 Pyruvate metabolism	1.17%	1.17%	1.15%	1.18%	1.18%	1.18%	1.09%	1.17%	1.10%	1.18%	1.24%	1.14%	1.24%	1.08%	1.23%
Metabolism|Amino acid metabolism|ko00340 Histidine metabolism	1.12%	1.09%	1.07%	1.14%	1.14%	1.14%	1.13%	1.15%	1.13%	1.14%	1.11%	1.08%	1.11%	1.12%	1.18%
Metabolism|Carbohydrate metabolism|ko00051 Fructose and mannose metabolism	1.06%	1.09%	1.15%	0.98%	0.97%	0.97%	1.23%	1.02%	1.18%	0.97%	1.01%	0.98%	1.01%	1.14%	1.09%
Metabolism|Carbohydrate metabolism|ko00010 Glycolysis / Gluconeogenesis	1.03%	1.00%	1.01%	0.98%	0.99%	0.99%	0.97%	0.99%	0.96%	0.98%	1.26%	1.05%	1.26%	0.94%	1.08%
Metabolism|Metabolism of cofactors and vitamins|ko00730 Thiamine metabolism	1.03%	1.03%	1.02%	1.09%	1.09%	1.09%	1.12%	1.10%	1.11%	1.09%	0.75%	1.09%	0.75%	1.10%	0.94%
Metabolism|Amino acid metabolism|ko00260 Glycine, serine and threonine metabolism	1.02%	0.94%	0.90%	0.99%	1.00%	1.00%	0.82%	0.97%	0.85%	1.00%	1.18%	1.10%	1.18%	0.85%	1.52%
Genetic Information Processing|Translation|ko03008 Ribosome biogenesis in eukaryotes	1.00%	0.88%	0.86%	0.97%	0.97%	0.97%	1.00%	0.98%	0.99%	0.97%	1.23%	1.05%	1.23%	0.98%	1.00%
Genetic Information Processing|Replication and repair|ko03420 Nucleotide excision repair	0.97%	1.11%	1.11%	1.06%	1.06%	1.06%	1.02%	1.07%	1.04%	1.08%	0.31%	1.07%	0.32%	1.05%	1.16%
Genetic Information Processing|Replication and repair|ko03430 Mismatch repair	0.96%	0.99%	0.97%	1.07%	1.07%	1.07%	1.08%	1.07%	1.07%	1.07%	0.50%	0.99%	0.50%	1.05%	0.88%
Metabolism|Metabolism of cofactors and vitamins|ko00760 Nicotinate and nicotinamide metabolism	0.93%	0.84%	0.81%	0.95%	0.95%	0.95%	0.98%	0.94%	0.98%	0.94%	0.84%	0.97%	0.84%	0.98%	0.99%
Cellular Processes|Cell growth and death|ko04112 Cell cycle - Caulobacter	0.90%	0.86%	0.89%	0.88%	0.87%	0.87%	1.21%	0.92%	1.15%	0.87%	0.70%	0.80%	0.70%	1.11%	0.73%
Metabolism|Metabolism of cofactors and vitamins|ko00770 Pantothenate and CoA biosynthesis	0.90%	0.91%	0.93%	0.85%	0.85%	0.85%	0.85%	0.86%	0.85%	0.86%	1.03%	0.90%	1.03%	0.85%	0.94%
Metabolism|Metabolism of terpenoids and polyketides|ko00900 Terpenoid backbone biosynthesis	0.85%	0.85%	0.83%	0.87%	0.88%	0.88%	0.68%	0.85%	0.71%	0.88%	0.96%	0.89%	0.96%	0.72%	0.96%
Metabolism|Metabolism of cofactors and vitamins|ko00130 Ubiquinone and other terpenoid-quinone biosynthesis	0.83%	0.83%	0.89%	0.70%	0.70%	0.70%	0.77%	0.72%	0.76%	0.71%	1.31%	0.72%	1.31%	0.75%	0.84%
Metabolism|Carbohydrate metabolism|ko00630 Glyoxylate and dicarboxylate metabolism	0.82%	0.76%	0.75%	0.73%	0.73%	0.73%	0.81%	0.76%	0.79%	0.74%	1.14%	0.76%	1.14%	0.77%	0.83%
Genetic Information Processing|Folding, sorting and degradation|ko04122 Sulfur relay system	0.80%	0.76%	0.73%	0.84%	0.85%	0.85%	0.66%	0.81%	0.69%	0.84%	0.91%	0.83%	0.91%	0.71%	0.80%
Genetic Information Processing|Folding, sorting and degradation|ko04141 Protein processing in endoplasmic reticulum	0.75%	0.79%	0.75%	0.79%	0.80%	0.80%	0.64%	0.78%	0.65%	0.80%	0.71%	0.79%	0.71%	0.65%	0.82%
Metabolism|Amino acid metabolism|ko00360 Phenylalanine metabolism	0.74%	0.69%	0.70%	0.69%	0.69%	0.69%	0.86%	0.73%	0.82%	0.69%	0.95%	0.63%	0.94%	0.78%	0.55%
Genetic Information Processing|Replication and repair|ko03410 Base excision repair	0.74%	0.69%	0.71%	0.71%	0.70%	0.70%	0.93%	0.75%	0.89%	0.71%	0.58%	0.73%	0.58%	0.87%	0.73%
Metabolism|Amino acid metabolism|ko00290 Valine, leucine and isoleucine biosynthesis	0.72%	0.76%	0.75%	0.77%	0.77%	0.77%	0.63%	0.76%	0.66%	0.78%	0.74%	0.74%	0.75%	0.67%	0.56%
Metabolism|Metabolism of cofactors and vitamins|ko00790 Folate biosynthesis	0.71%	0.75%	0.74%	0.74%	0.75%	0.75%	0.62%	0.72%	0.63%	0.74%	0.71%	0.71%	0.71%	0.64%	0.80%

Metabolism|Carbohydrate metabolism|ko00030 Pentose phosphate pathway	0.68%	0.66%	0.69%	0.59%	0.59%	0.59%	0.59%	0.60%	0.59%	0.59%	1.01%	0.66%	1.01%	0.59%	0.80%
Metabolism|Carbohydrate metabolism|ko00020 Citrate cycle (TCA cycle)	0.68%	0.64%	0.61%	0.70%	0.70%	0.70%	0.64%	0.69%	0.66%	0.70%	0.64%	0.74%	0.64%	0.67%	0.74%
Genetic Information Processing|Replication and repair|ko03440 Homologous recombination	0.65%	0.59%	0.54%	0.70%	0.69%	0.69%	0.98%	0.75%	0.91%	0.69%	0.32%	0.62%	0.32%	0.85%	0.46%
Metabolism|Xenobiotics biodegradation and metabolism|ko00633 Nitrotoluene degradation	0.58%	0.67%	0.69%	0.58%	0.59%	0.59%	0.33%	0.53%	0.38%	0.58%	0.91%	0.55%	0.91%	0.41%	0.39%
Metabolism|Carbohydrate metabolism|ko00650 Butanoate metabolism	0.55%	0.51%	0.52%	0.49%	0.49%	0.49%	0.57%	0.51%	0.56%	0.49%	0.75%	0.49%	0.75%	0.55%	0.53%
Metabolism|Metabolism of cofactors and vitamins|ko00740 Riboflavin metabolism	0.55%	0.48%	0.46%	0.52%	0.52%	0.52%	0.53%	0.53%	0.54%	0.52%	0.70%	0.54%	0.70%	0.55%	0.58%
Human Diseases|Infectious diseases: Bacterial|ko05134 Legionellosis	0.54%	0.56%	0.53%	0.57%	0.58%	0.58%	0.43%	0.56%	0.45%	0.58%	0.59%	0.57%	0.59%	0.45%	0.57%
Metabolism|Glycan biosynthesis and metabolism|ko00510 N-Glycan biosynthesis	0.54%	0.54%	0.55%	0.51%	0.51%	0.51%	0.64%	0.53%	0.62%	0.51%	0.42%	0.54%	0.42%	0.61%	0.58%
Metabolism|Energy metabolism|ko00920 Sulfur metabolism	0.53%	0.59%	0.64%	0.53%	0.54%	0.54%	0.50%	0.52%	0.50%	0.53%	0.50%	0.54%	0.50%	0.51%	0.50%
Genetic Information Processing|Folding, sorting and degradation|ko03060 Protein export	0.53%	0.49%	0.48%	0.48%	0.48%	0.48%	0.45%	0.48%	0.45%	0.48%	0.79%	0.51%	0.80%	0.45%	0.57%
Metabolism|Amino acid metabolism|ko00350 Tyrosine metabolism	0.48%	0.57%	0.60%	0.46%	0.47%	0.47%	0.40%	0.46%	0.41%	0.46%	0.48%	0.45%	0.48%	0.41%	0.55%
Metabolism|Amino acid metabolism|ko00280 Valine, leucine and isoleucine degradation	0.47%	0.36%	0.34%	0.40%	0.40%	0.40%	0.38%	0.40%	0.39%	0.40%	0.84%	0.44%	0.83%	0.40%	0.57%
Genetic Information Processing|Replication and repair|ko03030 DNA replication	0.46%	0.41%	0.40%	0.44%	0.44%	0.44%	0.40%	0.44%	0.41%	0.45%	0.63%	0.48%	0.63%	0.41%	0.46%
Metabolism|Energy metabolism|ko00710 Carbon fixation in photosynthetic organisms	0.45%	0.46%	0.46%	0.46%	0.46%	0.46%	0.43%	0.45%	0.43%	0.46%	0.46%	0.44%	0.46%	0.43%	0.40%
Metabolism|Lipid metabolism|ko00564 Glycerophospholipid metabolism	0.44%	0.38%	0.38%	0.39%	0.38%	0.38%	0.45%	0.41%	0.44%	0.39%	0.62%	0.37%	0.63%	0.41%	0.58%
Metabolism|Xenobiotics biodegradation and metabolism|ko00983 Drug metabolism - other enzymes	0.44%	0.47%	0.47%	0.44%	0.44%	0.44%	0.41%	0.44%	0.42%	0.45%	0.39%	0.45%	0.39%	0.42%	0.52%
Genetic Information Processing|Folding, sorting and degradation|ko03050 Proteasome	0.44%	0.45%	0.44%	0.46%	0.47%	0.47%	0.38%	0.45%	0.39%	0.47%	0.41%	0.48%	0.41%	0.39%	0.46%
Metabolism|Metabolism of other amino acids|ko00450 Selenocompound metabolism	0.41%	0.41%	0.43%	0.40%	0.40%	0.40%	0.37%	0.39%	0.38%	0.40%	0.44%	0.42%	0.44%	0.39%	0.50%
Metabolism|Metabolism of other amino acids|ko00480 Glutathione metabolism	0.41%	0.68%	0.79%	0.37%	0.38%	0.38%	0.36%	0.38%	0.35%	0.38%	0.24%	0.36%	0.24%	0.33%	0.47%
Metabolism|Xenobiotics biodegradation and metabolism|ko00362 Benzoate degradation	0.40%	0.35%	0.35%	0.37%	0.37%	0.37%	0.35%	0.35%	0.35%	0.36%	0.66%	0.35%	0.66%	0.37%	0.37%
Environmental Information Processing|Membrane transport|ko03070 Bacterial secretion system	0.40%	0.41%	0.43%	0.39%	0.39%	0.39%	0.42%	0.39%	0.41%	0.39%	0.39%	0.37%	0.39%	0.41%	0.44%
Metabolism|Carbohydrate metabolism|ko00640 Propanoate metabolism	0.40%	0.26%	0.23%	0.34%	0.34%	0.34%	0.36%	0.35%	0.36%	0.34%	0.75%	0.36%	0.74%	0.36%	0.45%
Genetic Information Processing|Transcription|ko03020 RNA polymerase	0.38%	0.33%	0.32%	0.36%	0.36%	0.36%	0.41%	0.38%	0.41%	0.36%	0.45%	0.40%	0.45%	0.40%	0.39%
Metabolism|Metabolism of cofactors and vitamins|ko00780 Biotin metabolism	0.37%	0.34%	0.34%	0.34%	0.34%	0.34%	0.34%	0.34%	0.35%	0.35%	0.43%	0.38%	0.43%	0.35%	0.44%
Metabolism|Xenobiotics biodegradation and metabolism|ko00625 Chloroalkane and chloroalkene degradation	0.37%	0.39%	0.41%	0.40%	0.39%	0.39%	0.45%	0.38%	0.46%	0.39%	0.12%	0.39%	0.12%	0.49%	0.34%
Metabolism|Biosynthesis of other secondary metabolites|ko00521 Streptomycin biosynthesis	0.34%	0.30%	0.29%	0.31%	0.31%	0.31%	0.31%	0.32%	0.31%	0.32%	0.45%	0.35%	0.46%	0.31%	0.34%
Metabolism|Metabolism of cofactors and vitamins|ko00670 One carbon pool by folate	0.33%	0.35%	0.35%	0.34%	0.34%	0.34%	0.32%	0.33%	0.32%	0.34%	0.28%	0.33%	0.28%	0.32%	0.34%
Metabolism|Xenobiotics biodegradation and metabolism|ko00627 Aminobenzoate degradation	0.30%	0.31%	0.30%	0.31%	0.32%	0.31%	0.28%	0.31%	0.28%	0.31%	0.32%	0.29%	0.32%	0.28%	0.31%
Genetic Information Processing|Translation|ko03015 mRNA surveillance pathway	0.29%	0.30%	0.29%	0.31%	0.31%	0.31%	0.24%	0.30%	0.25%	0.31%	0.30%	0.33%	0.30%	0.26%	0.31%
Metabolism|Metabolism of cofactors and vitamins|ko00750 Vitamin B6 metabolism	0.28%	0.27%	0.27%	0.26%	0.26%	0.26%	0.24%	0.26%	0.25%	0.27%	0.35%	0.31%	0.36%	0.25%	0.36%
Metabolism|Amino acid metabolism|ko00310 Lysine degradation	0.28%	0.31%	0.30%	0.29%	0.29%	0.29%	0.33%	0.30%	0.31%	0.29%	0.17%	0.25%	0.17%	0.29%	0.38%
Genetic Information Processing|Replication and repair|ko03460 Fanconi anemia pathway	0.27%	0.26%	0.26%	0.26%	0.26%	0.26%	0.24%	0.26%	0.24%	0.26%	0.35%	0.27%	0.35%	0.25%	0.29%
Metabolism|Metabolism of terpenoids and polyketides|ko00906 Carotenoid biosynthesis	0.26%	0.42%	0.48%	0.30%	0.31%	0.31%	0.18%	0.30%	0.19%	0.31%	0.02%	0.28%	0.03%	0.18%	0.36%
Human Diseases|Infectious diseases: Bacterial|ko05120 Epithelial cell signaling in Helicobacter pylori infection	0.25%	0.33%	0.36%	0.28%	0.28%	0.29%	0.23%	0.28%	0.25%	0.29%	0.09%	0.30%	0.09%	0.26%	0.23%
Metabolism|Carbohydrate metabolism|ko00660 C5-Branched dibasic acid metabolism	0.25%	0.25%	0.25%	0.26%	0.26%	0.26%	0.23%	0.25%	0.24%	0.26%	0.27%	0.25%	0.27%	0.24%	0.27%
Metabolism|Xenobiotics biodegradation and metabolism|ko00624 Polycyclic aromatic hydrocarbon degradation	0.25%	0.30%	0.32%	0.25%	0.25%	0.25%	0.26%	0.25%	0.25%	0.24%	0.18%	0.22%	0.18%	0.25%	0.26%
Metabolism|Metabolism of terpenoids and polyketides|ko00523 Polyketide sugar unit biosynthesis	0.24%	0.19%	0.18%	0.24%	0.24%	0.24%	0.23%	0.24%	0.23%	0.24%	0.33%	0.25%	0.33%	0.24%	0.23%
Human Diseases|Infectious diseases: Bacterial|ko05152 Tuberculosis	0.23%	0.26%	0.24%	0.28%	0.28%	0.28%	0.22%	0.27%	0.23%	0.28%	0.09%	0.27%	0.09%	0.24%	0.22%
Metabolism|Carbohydrate metabolism|ko00040 Pentose and glucuronate interconversions	0.22%	0.21%	0.22%	0.21%	0.21%	0.21%	0.18%	0.21%	0.19%	0.21%	0.26%	0.23%	0.27%	0.20%	0.24%
Human Diseases|Infectious diseases: Bacterial|ko05132 Salmonella infection	0.21%	0.20%	0.19%	0.23%	0.23%	0.23%	0.21%	0.23%	0.22%	0.23%	0.17%	0.23%	0.17%	0.22%	0.17%
Genetic Information Processing|Transcription|ko03022 Basal transcription factors	0.20%	0.20%	0.20%	0.20%	0.20%	0.20%	0.19%	0.20%	0.19%	0.20%	0.15%	0.20%	0.16%	0.19%	0.37%
Cellular Processes|Transport and catabolism|ko04146 Peroxisome	0.20%	0.17%	0.18%	0.17%	0.17%	0.17%	0.18%	0.17%	0.18%	0.17%	0.32%	0.17%	0.32%	0.18%	0.20%
Metabolism|Carbohydrate metabolism|ko00052 Galactose metabolism	0.19%	0.18%	0.17%	0.20%	0.20%	0.20%	0.22%	0.21%	0.21%	0.20%	0.11%	0.23%	0.12%	0.21%	0.26%
Metabolism|Lipid metabolism|ko00561 Glycerolipid metabolism	0.18%	0.17%	0.18%	0.16%	0.16%	0.16%	0.19%	0.17%	0.19%	0.16%	0.17%	0.18%	0.17%	0.19%	0.27%
Metabolism|Glycan biosynthesis and metabolism|ko00513 Various types of N-glycan biosynthesis	0.18%	0.18%	0.16%	0.19%	0.19%	0.19%	0.15%	0.18%	0.16%	0.19%	0.16%	0.19%	0.17%	0.16%	0.21%
Human Diseases|Infectious diseases: Bacterial|ko05100 Bacterial invasion of epithelial cells	0.17%	0.12%	0.12%	0.19%	0.18%	0.18%	0.37%	0.22%	0.33%	0.18%	0.01%	0.16%	0.01%	0.30%	0.07%
Metabolism|Lipid metabolism|ko00071 Fatty acid degradation	0.16%	0.08%	0.08%	0.09%	0.09%	0.09%	0.14%	0.10%	0.13%	0.09%	0.47%	0.10%	0.46%	0.13%	0.17%
Metabolism|Glycan biosynthesis and metabolism|ko00540 Lipopolysaccharide biosynthesis	0.16%	0.13%	0.12%	0.16%	0.16%	0.16%	0.20%	0.16%	0.19%	0.16%	0.13%	0.16%	0.13%	0.20%	0.12%
Metabolism|Carbohydrate metabolism|ko00562 Inositol phosphate metabolism	0.15%	0.16%	0.16%	0.14%	0.14%	0.14%	0.15%	0.14%	0.15%	0.14%	0.17%	0.16%	0.17%	0.14%	0.17%
Metabolism|Energy metabolism|ko00196 Photosynthesis - antenna proteins	0.14%	0.16%	0.14%	0.15%	0.15%	0.15%	0.21%	0.16%	0.20%	0.15%	0.02%	0.13%	0.02%	0.18%	0.09%
Human Diseases|Infectious diseases: Parasitic|ko05143 African trypanosomiasis	0.14%	0.17%	0.16%	0.15%	0.15%	0.15%	0.15%	0.15%	0.15%	0.15%	0.08%	0.14%	0.08%	0.15%	0.08%
Metabolism|Glycan biosynthesis and metabolism|ko00550 Peptidoglycan biosynthesis	0.14%	0.13%	0.14%	0.11%	0.10%	0.10%	0.16%	0.14%	0.17%	0.12%	0.06%	0.20%	0.06%	0.18%	0.23%
Metabolism|Biosynthesis of other secondary metabolites|ko00960 Tropane, piperidine and pyridine alkaloid biosynthesis	0.13%	0.13%	0.13%	0.14%	0.14%	0.14%	0.15%	0.14%	0.15%	0.14%	0.13%	0.13%	0.13%	0.15%	0.11%
Metabolism|Metabolism of other amino acids|ko00440 Phosphonate and phosphinate metabolism	0.12%	0.14%	0.14%	0.12%	0.12%	0.12%	0.14%	0.12%	0.13%	0.12%	0.09%	0.11%	0.09%	0.13%	0.10%
Metabolism|Metabolism of other amino acids|ko00410 beta-Alanine metabolism	0.11%	0.19%	0.22%	0.10%	0.10%	0.10%	0.05%	0.09%	0.06%	0.10%	0.12%	0.10%	0.12%	0.06%	0.14%
Human Diseases|Cancers: Overview|ko05203 Viral carcinogenesis	0.11%	0.10%	0.11%	0.10%	0.10%	0.10%	0.11%	0.10%	0.11%	0.10%	0.10%	0.11%	0.11%	0.10%	0.21%
Metabolism|Xenobiotics biodegradation and metabolism|ko00363 Bisphenol degradation	0.11%	0.11%	0.11%	0.11%	0.10%	0.10%	0.17%	0.12%	0.15%	0.10%	0.06%	0.10%	0.06%	0.15%	0.12%
Metabolism|Amino acid metabolism|ko00380 Tryptophan metabolism	0.11%	0.12%	0.12%	0.10%	0.10%	0.10%	0.11%	0.10%	0.11%	0.10%	0.12%	0.09%	0.12%	0.11%	0.16%
Metabolism|Biosynthesis of other secondary metabolites|ko00401 Novobiocin biosynthesis	0.11%	0.11%	0.11%	0.12%	0.12%	0.12%	0.09%	0.11%	0.09%	0.12%	0.09%	0.12%	0.09%	0.10%	0.11%
Metabolism|Lipid metabolism|ko00061 Fatty acid biosynthesis	0.10%	0.08%	0.07%	0.09%	0.09%	0.09%	0.08%	0.09%	0.08%	0.09%	0.15%	0.10%	0.15%	0.08%	0.12%
Metabolism|Xenobiotics biodegradation and metabolism|ko00791 Atrazine degradation	0.10%	0.09%	0.09%	0.09%	0.09%	0.09%	0.07%	0.09%	0.08%	0.09%	0.13%	0.11%	0.13%	0.08%	0.12%
Metabolism|Metabolism of terpenoids and polyketides|ko00281 Geraniol degradation	0.10%	0.05%	0.04%	0.05%	0.05%	0.05%	0.04%	0.05%	0.04%	0.05%	0.35%	0.05%	0.35%	0.04%	0.13%
Human Diseases|Infectious diseases: Viral|ko05169 Epstein-Barr virus infection	0.10%	0.08%	0.08%	0.09%	0.09%	0.09%	0.09%	0.09%	0.09%	0.09%	0.09%	0.10%	0.09%	0.09%	0.19%
Metabolism|Glycan biosynthesis and metabolism|ko00511 Other glycan degradation	0.09%	0.15%	0.18%	0.05%	0.05%	0.05%	0.06%	0.05%	0.06%	0.05%	0.17%	0.05%	0.18%	0.07%	0.12%
Metabolism|Metabolism of terpenoids and polyketides|ko00903 Limonene and pinene degradation	0.09%	0.11%	0.12%	0.09%	0.09%	0.09%	0.09%	0.09%	0.09%	0.09%	0.08%	0.08%	0.08%	0.09%	0.12%
Human Diseases|Infectious diseases: Parasitic|ko05146 Amoebiasis	0.09%	0.09%	0.12%	0.06%	0.05%	0.05%	0.23%	0.09%	0.20%	0.06%	0.02%	0.04%	0.02%	0.17%	0.05%
Organismal Systems|Endocrine system|ko04910 Insulin signaling pathway	0.09%	0.09%	0.06%	0.11%	0.11%	0.11%	0.12%	0.11%	0.11%	0.11%	0.02%	0.11%	0.02%	0.10%	0.09%
Metabolism|Xenobiotics biodegradation and metabolism|ko00623 Toluene degradation	0.09%	0.08%	0.08%	0.07%	0.07%	0.07%	0.06%	0.07%	0.07%	0.07%	0.20%	0.07%	0.20%	0.07%	0.09%
Human Diseases|Infectious diseases: Bacterial|ko05110 Vibrio cholerae infection	0.09%	0.12%	0.14%	0.09%	0.09%	0.09%	0.10%	0.08%	0.10%	0.09%	0.04%	0.08%	0.04%	0.10%	0.07%
Genetic Information Processing|Replication and repair|ko03450 Non-homologous end-joining	0.08%	0.07%	0.07%	0.08%	0.08%	0.08%	0.07%	0.08%	0.07%	0.08%	0.14%	0.08%	0.14%	0.07%	0.07%
Human Diseases|Infectious diseases: Bacterial|ko05150 Staphylococcus aureus infection	0.08%	0.14%	0.16%	0.09%	0.09%	0.09%	0.09%	0.10%	0.09%	0.09%	0.00%	0.08%	0.00%	0.08%	0.07%
Human Diseases|Infectious diseases: Bacterial|ko05111 Vibrio cholerae pathogenic cycle	0.08%	0.12%	0.13%	0.08%	0.08%	0.08%	0.10%	0.08%	0.10%	0.08%	0.02%	0.07%	0.02%	0.10%	0.05%
Metabolism|Xenobiotics biodegradation and metabolism|ko00642 Ethylbenzene degradation	0.08%	0.10%	0.10%	0.07%	0.07%	0.07%	0.05%	0.07%	0.05%	0.07%	0.10%	0.07%	0.10%	0.05%	0.08%
Metabolism|Biosynthesis of other secondary metabolites|ko00950 Isoquinoline alkaloid biosynthesis	0.08%	0.07%	0.07%	0.08%	0.08%	0.08%	0.06%	0.07%	0.06%	0.08%	0.10%	0.08%	0.10%	0.06%	0.08%
Cellular Processes|Cell growth and death|ko04113 Meiosis - yeast	0.08%	0.08%	0.06%	0.10%	0.10%	0.10%	0.09%	0.10%	0.09%	0.10%	0.01%	0.09%	0.01%	0.09%	0.04%
Metabolism|Metabolism of terpenoids and polyketides|ko01055 Biosynthesis of vancomycin group antibiotics	0.07%	0.06%	0.05%	0.07%	0.07%	0.07%	0.09%	0.08%	0.08%	0.08%	0.08%	0.08%	0.08%	0.08%	0.07%
Human Diseases|Endocrine and metabolic diseases|ko04940 Type I diabetes mellitus	0.07%	0.08%	0.09%	0.08%	0.08%	0.08%	0.06%	0.08%	0.07%	0.08%	0.05%	0.08%	0.05%	0.07%	0.06%
Organismal Systems|Endocrine system|ko03320 PPAR signaling pathway	0.07%	0.03%	0.03%	0.03%	0.03%	0.03%	0.04%	0.03%	0.04%	0.03%	0.24%	0.04%	0.23%	0.04%	0.09%
Metabolism|Xenobiotics biodegradation and metabolism|ko00626 Naphthalene degradation	0.07%	0.06%	0.05%	0.06%	0.07%	0.06%	0.04%	0.06%	0.05%	0.06%	0.10%	0.07%	0.10%	0.05%	0.08%
Metabolism|Carbohydrate metabolism|ko00053 Ascorbate and aldarate metabolism	0.06%	0.06%	0.07%	0.06%	0.06%	0.06%	0.07%	0.06%	0.07%	0.06%	0.05%	0.06%	0.05%	0.07%	0.11%
Organismal Systems|Digestive system|ko04973 Carbohydrate digestion and absorption	0.06%	0.10%	0.12%	0.07%	0.07%	0.07%	0.03%	0.07%	0.04%	0.07%	0.03%	0.07%	0.03%	0.04%	0.07%
Human Diseases|Neurodegenerative diseases|ko05016 Huntington's disease	0.06%	0.06%	0.05%	0.07%	0.07%	0.07%	0.07%	0.07%	0.07%	0.07%	0.03%	0.06%	0.03%	0.07%	0.09%
Metabolism|Metabolism of other amino acids|ko00460 Cyanoamino acid metabolism	0.06%	0.05%	0.05%	0.05%	0.05%	0.05%	0.05%	0.05%	0.05%	0.05%	0.08%	0.07%	0.08%	0.05%	0.08%
Organismal Systems|Environmental adaptation|ko04626 Plant-pathogen interaction	0.06%	0.05%	0.05%	0.05%	0.06%	0.06%	0.04%	0.05%	0.04%	0.06%	0.10%	0.06%	0.10%	0.05%	0.08%
Organismal Systems|Digestive system|ko04976 Bile secretion	0.06%	0.07%	0.08%	0.06%	0.06%	0.06%	0.09%	0.06%	0.08%	0.06%	0.01%	0.06%	0.01%	0.08%	0.07%
Metabolism|Biosynthesis of other secondary metabolites|ko00311 Penicillin and cephalosporin biosynthesis	0.06%	0.05%	0.02%	0.06%	0.06%	0.06%	0.04%	0.05%	0.04%	0.06%	0.12%	0.05%	0.12%	0.04%	0.04%
Metabolism|Lipid metabolism|ko00600 Sphingolipid metabolism	0.06%	0.08%	0.07%	0.07%	0.07%	0.07%	0.03%	0.07%	0.03%	0.07%	0.01%	0.07%	0.02%	0.03%	0.10%
Organismal Systems|Endocrine system|ko04920 Adipocytokine signaling pathway	0.05%	0.03%	0.03%	0.03%	0.03%	0.03%	0.04%	0.03%	0.04%	0.03%	0.15%	0.04%	0.15%	0.04%	0.06%
Organismal Systems|Nervous system|ko04727 GABAergic synapse	0.05%	0.05%	0.04%	0.05%	0.05%	0.05%	0.07%	0.06%	0.06%	0.05%	0.05%	0.05%	0.05%	0.06%	0.05%
Metabolism|Lipid metabolism|ko00591 Linoleic acid metabolism	0.05%	0.06%	0.07%	0.04%	0.03%	0.03%	0.10%	0.05%	0.09%	0.04%	0.02%	0.04%	0.02%	0.08%	0.07%
Cellular Processes|Cell motility|ko02040 Flagellar assembly	0.05%	0.03%	0.03%	0.04%	0.04%	0.04%	0.10%	0.05%	0.09%	0.04%	0.05%	0.03%	0.05%	0.08%	0.06%
Metabolism|Lipid metabolism|ko00140 Steroid hormone biosynthesis	0.05%	0.07%	0.06%	0.06%	0.06%	0.06%	0.02%	0.06%	0.03%	0.06%	0.01%	0.06%	0.01%	0.03%	0.08%
Metabolism|Metabolism of other amino acids|ko00430 Taurine and hypotaurine metabolism	0.05%	0.05%	0.06%	0.04%	0.04%	0.04%	0.03%	0.04%	0.03%	0.04%	0.06%	0.05%	0.06%	0.03%	0.08%
Metabolism|Metabolism of other amino acids|ko00471 D-Glutamine and D-glutamate metabolism	0.05%	0.05%	0.05%	0.05%	0.05%	0.05%	0.02%	0.05%	0.04%	0.05%	0.01%	0.08%	0.01%	0.05%	0.09%
Organismal Systems|Digestive system|ko04978 Mineral absorption	0.04%	0.08%	0.10%	0.04%	0.05%	0.05%	0.03%	0.04%	0.03%	0.05%	0.01%	0.05%	0.01%	0.03%	0.06%
Human Diseases|Cancers: Specific types|ko05219 Bladder cancer	0.04%	0.04%	0.04%	0.05%	0.05%	0.05%	0.04%	0.05%	0.04%	0.05%	0.06%	0.04%	0.06%	0.04%	0.03%
Metabolism|Metabolism of cofactors and vitamins|ko00785 Lipoic acid metabolism	0.04%	0.03%	0.03%	0.03%	0.03%	0.03%	0.04%	0.03%	0.03%	0.03%	0.04%	0.05%	0.04%	0.03%	0.12%
Cellular Processes|Cell growth and death|ko04210 Apoptosis	0.04%	0.06%	0.05%	0.05%	0.05%	0.05%	0.03%	0.05%	0.03%	0.05%	0.03%	0.04%	0.03%	0.03%	0.03%
Human Diseases|Infectious diseases: Bacterial|ko05133 Pertussis	0.04%	0.06%	0.07%	0.05%	0.05%	0.05%	0.04%	0.05%	0.04%	0.05%	0.01%	0.04%	0.01%	0.04%	0.03%
Metabolism|Xenobiotics biodegradation and metabolism|ko00361 Chlorocyclohexane and chlorobenzene degradation	0.04%	0.04%	0.04%	0.03%	0.03%	0.03%	0.04%	0.04%	0.04%	0.03%	0.06%	0.03%	0.06%	0.03%	0.06%
Metabolism|Glycan biosynthesis and metabolism|ko00601 Glycosphingolipid biosynthesis - lacto and neolacto series	0.04%	0.04%	0.04%	0.03%	0.03%	0.03%	0.05%	0.03%	0.05%	0.03%	0.07%	0.03%	0.07%	0.04%	0.03%
Human Diseases|Infectious diseases: Viral|ko05164 Influenza A	0.04%	0.04%	0.03%	0.04%	0.04%	0.04%	0.04%	0.04%	0.04%	0.04%	0.03%	0.04%	0.03%	0.04%	0.03%
Metabolism|Lipid metabolism|ko00072 Synthesis and degradation of ketone bodies	0.04%	0.03%	0.02%	0.03%	0.03%	0.03%	0.03%	0.03%	0.03%	0.03%	0.08%	0.03%	0.08%	0.03%	0.04%
Human Diseases|Infectious diseases: Viral|ko05166 HTLV-I infection	0.04%	0.03%	0.03%	0.04%	0.03%	0.03%	0.04%	0.04%	0.04%	0.03%	0.03%	0.04%	0.03%	0.04%	0.06%
Organismal Systems|Nervous system|ko04724 Glutamatergic synapse	0.04%	0.03%	0.03%	0.04%	0.04%	0.04%	0.05%	0.04%	0.04%	0.04%	0.03%	0.04%	0.03%	0.04%	0.03%
Human Diseases|Infectious diseases: Viral|ko05168 Herpes simplex infection	0.04%	0.03%	0.03%	0.04%	0.04%	0.04%	0.04%	0.04%	0.04%	0.04%	0.03%	0.04%	0.03%	0.04%	0.06%
Organismal Systems|Digestive system|ko04974 Protein digestion and absorption	0.04%	0.04%	0.04%	0.04%	0.04%	0.04%	0.04%	0.04%	0.04%	0.04%	0.01%	0.03%	0.01%	0.04%	0.05%
Human Diseases|Neurodegenerative diseases|ko05010 Alzheimer's disease	0.04%	0.03%	0.03%	0.03%	0.03%	0.03%	0.05%	0.03%	0.05%	0.03%	0.04%	0.03%	0.04%	0.05%	0.03%
Metabolism|Metabolism of other amino acids|ko00473 D-Alanine metabolism	0.03%	0.04%	0.04%	0.03%	0.03%	0.03%	0.07%	0.03%	0.06%	0.03%	0.01%	0.02%	0.01%	0.05%	0.03%
Metabolism|Biosynthesis of other secondary metabolites|ko00940 Phenylpropanoid biosynthesis	0.03%	0.02%	0.02%	0.04%	0.04%	0.04%	0.02%	0.03%	0.03%	0.04%	0.04%	0.03%	0.04%	0.03%	0.03%
Metabolism|Lipid metabolism|ko01040 Biosynthesis of unsaturated fatty acids	0.03%	0.02%	0.02%	0.04%	0.04%	0.04%	0.03%	0.04%	0.03%	0.04%	0.02%	0.03%	0.02%	0.03%	0.05%
Environmental Information Processing|Membrane transport|ko02060 Phosphotransferase system (PTS)	0.03%	0.01%	0.01%	0.03%	0.03%	0.03%	0.04%	0.03%	0.04%	0.03%	0.04%	0.03%	0.04%	0.04%	0.04%
Metabolism|Xenobiotics biodegradation and metabolism|ko00930 Caprolactam degradation	0.03%	0.01%	0.01%	0.01%	0.01%	0.01%	0.02%	0.01%	0.02%	0.01%	0.11%	0.01%	0.11%	0.02%	0.04%
Metabolism|Metabolism of terpenoids and polyketides|ko01051 Biosynthesis of ansamycins	0.03%	0.02%	0.03%	0.02%	0.02%	0.02%	0.05%	0.02%	0.04%	0.02%	0.01%	0.02%	0.01%	0.04%	0.03%
Environmental Information Processing|Signal transduction|ko04070 Phosphatidylinositol signaling system	0.03%	0.02%	0.02%	0.02%	0.02%	0.02%	0.02%	0.02%	0.02%	0.03%	0.03%	0.03%	0.03%	0.02%	0.03%
Metabolism|Metabolism of terpenoids and polyketides|ko01054 Nonribosomal peptide structures	0.03%	0.01%	0.00%	0.01%	0.01%	0.01%	0.02%	0.02%	0.02%	0.02%	0.05%	0.04%	0.06%	0.03%	0.05%
Human Diseases|Drug resistance|ko01501 beta-Lactam resistance	0.02%	0.02%	0.01%	0.03%	0.03%	0.03%	0.03%	0.03%	0.03%	0.03%	0.02%	0.03%	0.02%	0.03%	0.02%
Cellular Processes|Transport and catabolism|ko04145 Phagosome	0.02%	0.02%	0.02%	0.02%	0.02%	0.02%	0.02%	0.02%	0.02%	0.02%	0.03%	0.03%	0.03%	0.02%	0.02%
Organismal Systems|Excretory system|ko04964 Proximal tubule bicarbonate reclamation	0.02%	0.03%	0.04%	0.02%	0.02%	0.02%	0.01%	0.02%	0.02%	0.02%	0.01%	0.03%	0.01%	0.02%	0.03%
Metabolism|Xenobiotics biodegradation and metabolism|ko00643 Styrene degradation	0.02%	0.02%	0.02%	0.01%	0.01%	0.01%	0.02%	0.01%	0.02%	0.01%	0.06%	0.01%	0.06%	0.01%	0.02%
Cellular Processes|Transport and catabolism|ko04142 Lysosome	0.02%	0.03%	0.03%	0.02%	0.02%	0.02%	0.01%	0.02%	0.02%	0.02%	0.01%	0.02%	0.01%	0.01%	0.04%
Environmental Information Processing|Signal transduction|ko04150 mTOR signaling pathway	0.02%	0.02%	0.01%	0.02%	0.02%	0.02%	0.02%	0.02%	0.02%	0.02%	0.02%	0.02%	0.02%	0.02%	0.02%
Metabolism|Energy metabolism|ko00195 Photosynthesis	0.02%	0.04%	0.05%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.07%
Metabolism|Metabolism of terpenoids and polyketides|ko01053 Biosynthesis of siderophore group nonribosomal peptides	0.02%	0.01%	0.01%	0.01%	0.01%	0.01%	0.02%	0.01%	0.02%	0.01%	0.03%	0.02%	0.03%	0.02%	0.05%
Metabolism|Xenobiotics biodegradation and metabolism|ko00621 Dioxin degradation	0.02%	0.01%	0.01%	0.01%	0.01%	0.01%	0.02%	0.02%	0.02%	0.01%	0.02%	0.02%	0.02%	0.02%	0.02%
Organismal Systems|Endocrine system|ko04614 Renin-angiotensin system	0.02%	0.01%	0.01%	0.02%	0.02%	0.02%	0.03%	0.02%	0.03%	0.02%	0.00%	0.01%	0.00%	0.03%	0.00%
Metabolism|Lipid metabolism|ko00592 alpha-Linolenic acid metabolism	0.02%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.05%	0.01%	0.05%	0.01%	0.02%
Organismal Systems|Circulatory system|ko04260 Cardiac muscle contraction	0.02%	0.02%	0.02%	0.02%	0.02%	0.02%	0.01%	0.02%	0.01%	0.02%	0.01%	0.02%	0.01%	0.01%	0.01%
Metabolism|Xenobiotics biodegradation and metabolism|ko00622 Xylene degradation	0.02%	0.01%	0.01%	0.02%	0.02%	0.02%	0.02%	0.02%	0.02%	0.02%	0.01%	0.02%	0.01%	0.02%	0.01%
Organismal Systems|Digestive system|ko04970 Salivary secretion	0.01%	0.02%	0.02%	0.02%	0.02%	0.02%	0.01%	0.02%	0.01%	0.02%	0.01%	0.02%	0.01%	0.01%	0.01%
Organismal Systems|Digestive system|ko04971 Gastric acid secretion	0.01%	0.02%	0.02%	0.02%	0.02%	0.02%	0.01%	0.02%	0.01%	0.02%	0.01%	0.02%	0.01%	0.01%	0.01%
Organismal Systems|Digestive system|ko04972 Pancreatic secretion	0.01%	0.02%	0.02%	0.02%	0.02%	0.02%	0.01%	0.02%	0.01%	0.02%	0.01%	0.02%	0.01%	0.01%	0.01%
Organismal Systems|Excretory system|ko04960 Aldosterone-regulated sodium reabsorption	0.01%	0.02%	0.02%	0.02%	0.02%	0.02%	0.01%	0.02%	0.01%	0.02%	0.01%	0.02%	0.01%	0.01%	0.01%
Organismal Systems|Excretory system|ko04961 Endocrine and other factor-regulated calcium reabsorption	0.01%	0.02%	0.02%	0.02%	0.02%	0.02%	0.01%	0.02%	0.01%	0.02%	0.01%	0.02%	0.01%	0.01%	0.01%
Cellular Processes|Cell growth and death|ko04110 Cell cycle	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.02%	0.02%	0.02%	0.01%	0.02%
Human Diseases|Neurodegenerative diseases|ko05014 Amyotrophic lateral sclerosis (ALS)	0.01%	0.03%	0.04%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.00%	0.01%	0.00%	0.01%	0.01%
Human Diseases|Endocrine and metabolic diseases|ko04930 Type II diabetes mellitus	0.01%	0.02%	0.02%	0.01%	0.01%	0.01%	0.02%	0.01%	0.02%	0.01%	0.01%	0.01%	0.01%	0.02%	0.02%
Human Diseases|Neurodegenerative diseases|ko05012 Parkinson's disease	0.01%	0.01%	0.01%	0.02%	0.02%	0.02%	0.01%	0.02%	0.01%	0.02%	0.00%	0.02%	0.00%	0.01%	0.01%
Metabolism|Metabolism of cofactors and vitamins|ko00830 Retinol metabolism	0.01%	0.01%	0.02%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.02%	0.01%	0.01%	0.03%
Metabolism|Glycan biosynthesis and metabolism|ko00532 Glycosaminoglycan biosynthesis - chondroitin sulfate / dermatan sulfate	0.01%	0.01%	0.02%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.02%	0.01%	0.01%	0.02%
Human Diseases|Cancers: Overview|ko05200 Pathways in cancer	0.01%	0.02%	0.02%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.02%
Metabolism|Xenobiotics biodegradation and metabolism|ko00351 DDT degradation	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.02%	0.01%	0.02%	0.01%	0.01%
Human Diseases|Infectious diseases: Viral|ko05160 Hepatitis C	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%
Human Diseases|Infectious diseases: Viral|ko05162 Measles	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%
Metabolism|Xenobiotics biodegradation and metabolism|ko00980 Metabolism of xenobiotics by cytochrome P450	0.01%	0.01%	0.01%	0.01%	0.00%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.02%
Metabolism|Biosynthesis of other secondary metabolites|ko00524 Butirosin and neomycin biosynthesis	0.01%	0.00%	0.00%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%
Environmental Information Processing|Signal transduction|ko04011 MAPK signaling pathway - yeast	0.01%	0.01%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.01%	0.01%	0.00%	0.04%
Metabolism|Xenobiotics biodegradation and metabolism|ko00364 Fluorobenzoate degradation	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.00%	0.01%	0.00%	0.01%	0.01%
Metabolism|Xenobiotics biodegradation and metabolism|ko00984 Steroid degradation	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.02%
Metabolism|Metabolism of terpenoids and polyketides|ko00253 Tetracycline biosynthesis	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%
Metabolism|Metabolism of terpenoids and polyketides|ko00909 Sesquiterpenoid and triterpenoid biosynthesis	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.02%	0.00%	0.03%
Metabolism|Xenobiotics biodegradation and metabolism|ko00982 Drug metabolism - cytochrome P450	0.01%	0.01%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.01%	0.01%	0.01%	0.00%	0.02%
Organismal Systems|Nervous system|ko04725 Cholinergic synapse	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%
Organismal Systems|Immune system|ko04640 Hematopoietic cell lineage	0.01%	0.00%	0.01%	0.00%	0.00%	0.00%	0.02%	0.01%	0.01%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%
Human Diseases|Substance dependence|ko05032 Morphine addiction	0.01%	0.01%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.01%	0.01%	0.00%	0.01%
Human Diseases|Cancers: Specific types|ko05211 Renal cell carcinoma	0.01%	0.01%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%
Genetic Information Processing|Transcription|ko03040 Spliceosome	0.01%	0.00%	0.00%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.00%	0.01%	0.00%	0.01%	0.00%
Metabolism|Metabolism of terpenoids and polyketides|ko01057 Biosynthesis of type II polyketide products	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.03%	0.00%	0.03%	0.00%	0.00%
Metabolism|Glycan biosynthesis and metabolism|ko00603 Glycosphingolipid biosynthesis - globo series	0.01%	0.00%	0.00%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.00%	0.01%	0.00%	0.01%	0.00%
Human Diseases|Substance dependence|ko05034 Alcoholism	0.00%	0.00%	0.00%	0.01%	0.01%	0.01%	0.00%	0.01%	0.00%	0.01%	0.01%	0.01%	0.01%	0.00%	0.00%
Metabolism|Lipid metabolism|ko00120 Primary bile acid biosynthesis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.01%	0.00%	0.01%	0.00%	0.01%	0.01%	0.01%
Metabolism|Lipid metabolism|ko00565 Ether lipid metabolism	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.02%	0.00%	0.00%
Human Diseases|Cancers: Specific types|ko05212 Pancreatic cancer	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.01%	0.00%	0.01%
Metabolism|Metabolism of terpenoids and polyketides|ko00522 Biosynthesis of 12-, 14- and 16-membered macrolides	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%

Metabolism|Lipid metabolism|ko00121 Secondary bile acid biosynthesis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.01%	0.01%
Human Diseases|Immune diseases|ko05340 Primary immunodeficiency	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%	0.01%	0.00%
Human Diseases|Infectious diseases: Parasitic|ko05145 Toxoplasmosis	0.00%	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%
Human Diseases|Cancers: Overview|ko05204 Chemical carcinogenesis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%
Metabolism|Glycan biosynthesis and metabolism|ko00531 Glycosaminoglycan degradation	0.00%	0.01%	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%
Metabolism|Lipid metabolism|ko00062 Fatty acid elongation	0.00%	0.00%	0.00%	0.01%	0.01%	0.01%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%
Organismal Systems|Nervous system|ko04723 Retrograde endocannabinoid signaling	0.00%	0.01%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%
Human Diseases|Cancers: Specific types|ko05222 Small cell lung cancer	0.00%	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%
Cellular Processes|Cell growth and death|ko04115 p53 signaling pathway	0.00%	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%
Human Diseases|Cancers: Specific types|ko05210 Colorectal cancer	0.00%	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%
Human Diseases|Cardiovascular diseases|ko05416 Viral myocarditis	0.00%	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%
Metabolism|Metabolism of other amino acids|ko00472 D-Arginine and D-ornithine metabolism	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%
Metabolism|Glycan biosynthesis and metabolism|ko00563 Glycosylphosphatidylinositol(GPI)-anchor biosynthesis	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%
Organismal Systems|Excretory system|ko04962 Vasopressin-regulated water reabsorption	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%
Organismal Systems|Nervous system|ko04721 Synaptic vesicle cycle	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%
Organismal Systems|Immune system|ko04623 Cytosolic DNA-sensing pathway	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%
Metabolism|Biosynthesis of other secondary metabolites|ko00945 Stilbenoid, diarylheptanoid and gingerol biosynthesis	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%	0.01%
Metabolism|Metabolism of terpenoids and polyketides|ko01056 Biosynthesis of type II polyketide backbone	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%
Cellular Processes|Cellular community|ko04510 Focal adhesion	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%
Metabolism|Lipid metabolism|ko00590 Arachidonic acid metabolism	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%
Human Diseases|Substance dependence|ko05031 Amphetamine addiction	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%
Organismal Systems|Nervous system|ko04728 Dopaminergic synapse	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%
Human Diseases|Infectious diseases: Parasitic|ko05142 Chagas disease (American trypanosomiasis)	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%
Environmental Information Processing|Signaling molecules and interaction|ko04512 ECM-receptor interaction	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%
Human Diseases|Substance dependence|ko05030 Cocaine addiction	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%
Organismal Systems|Nervous system|ko04726 Serotonergic synapse	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%
Metabolism|Biosynthesis of other secondary metabolites|ko00943 Isoflavonoid biosynthesis	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%	0.01%
Human Diseases|Cancers: Specific types|ko05215 Prostate cancer	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%
Organismal Systems|Endocrine system|ko04914 Progesterone-mediated oocyte maturation	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%
Organismal Systems|Immune system|ko04612 Antigen processing and presentation	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%
Organismal Systems|Immune system|ko04621 NOD-like receptor signaling pathway	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%
Metabolism|Biosynthesis of other secondary metabolites|ko00941 Flavonoid biosynthesis	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%
Metabolism|Biosynthesis of other secondary metabolites|ko00901 Indole alkaloid biosynthesis	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%
Metabolism|Biosynthesis of other secondary metabolites|ko00965 Betalain biosynthesis	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%
Human Diseases|Neurodegenerative diseases|ko05020 Prion diseases	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%
Organismal Systems|Immune system|ko04610 Complement and coagulation cascades	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%
Metabolism|Glycan biosynthesis and metabolism|ko00604 Glycosphingolipid biosynthesis - ganglio series	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%
Human Diseases|Cancers: Overview|ko05202 Transcriptional misregulation in cancer	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%
Human Diseases|Infectious diseases: Bacterial|ko05131 Shigellosis	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%
Environmental Information Processing|Signal transduction|ko04020 Calcium signaling pathway	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%
Metabolism|Metabolism of terpenoids and polyketides|ko00908 Zeatin biosynthesis	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%
Cellular Processes|Cell motility|ko04810 Regulation of actin cytoskeleton	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%
Human Diseases|Cardiovascular diseases|ko05410 Hypertrophic cardiomyopathy (HCM)	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%
Cellular Processes|Cell growth and death|ko04114 Oocyte meiosis	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%
Organismal Systems|Circulatory system|ko04270 Vascular smooth muscle contraction	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%
Organismal Systems|Nervous system|ko04720 Long-term potentiation	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%
Metabolism|Lipid metabolism|ko00100 Steroid biosynthesis	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%
Metabolism|Biosynthesis of other secondary metabolites|ko00232 Caffeine metabolism	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%
Environmental Information Processing|Signaling molecules and interaction|ko04080 Neuroactive ligand-receptor interaction	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%
Metabolism|Metabolism of terpenoids and polyketides|ko00902 Monoterpenoid biosynthesis	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%
Environmental Information Processing|Signaling molecules and interaction|ko04514 Cell adhesion molecules (CAMs)	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%
Human Diseases|Cardiovascular diseases|ko05412 Arrhythmogenic right ventricular cardiomyopathy (ARVC)	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%
Human Diseases|Cardiovascular diseases|ko05414 Dilated cardiomyopathy	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%
Environmental Information Processing|Signal transduction|ko04310 Wnt signaling pathway	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%
Environmental Information Processing|Signal transduction|ko04330 Notch signaling pathway	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%
Human Diseases|Cancers: Specific types|ko05220 Chronic myeloid leukemia	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%
Metabolism|Biosynthesis of other secondary metabolites|ko00944 Flavone and flavonol biosynthesis	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%
Cellular Processes|Transport and catabolism|ko04144 Endocytosis	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%
Organismal Systems|Endocrine system|ko04912 GnRH signaling pathway	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%
Organismal Systems|Immune system|ko04666 Fc gamma R-mediated phagocytosis	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%

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