**Supplementary Materials**
*Biogeosciences*

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

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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 $2.5\times10^2$ copies/g in P8O to $2.9\times10^7$ 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 $2.8\times10^5$ to $4.3\times10^5$ copies/ml in aqueous phase, and $6.4\times10^6$ to $2.9\times10^7$ copies/g in oil phase. For moderate temperature samples (P1, P2, P5 and P7), the *mcrA* gene abundance among aqueous samples was ranging from $1.2\times10^3$ copies/ml in P5A to $3.3\times10^5$ copies/ml in P1A, while the highest *mcrA* gene abundance among oil samples was ranging from $1.7\times10^3$ copies/g in P5O to $1.1\times10^6$ copies/g in P1O. For high temperature samples (P6 and P8), the *mcrA* gene abundance of aqueous sample was $9.2\times10^3$ copies/ml in P6A, and the *mcrA* gene abundance of oil samples was ranging from $2.5\times10^2$ copies/g in P8O to $2.8\times10^4$ 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

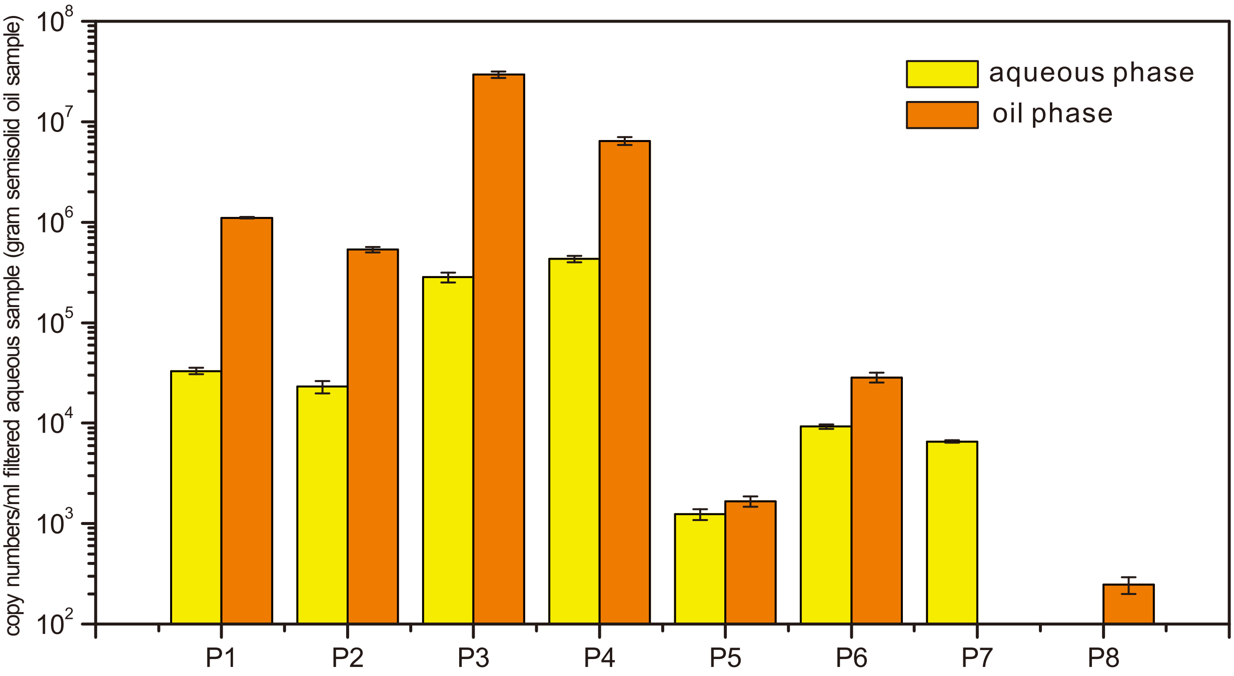


**Figure S1**. *mcrA* gene abundance of 14 aqueous and oil phase samples. Vertical coordinate was drawn in log-normalized label. The aqueous samples *mcrA* gene quantities were gene copy numbers/ml filtered aqueous sample; the oil samples *mcrA* gene quantities were gene copy numbers/gram semisolid oil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

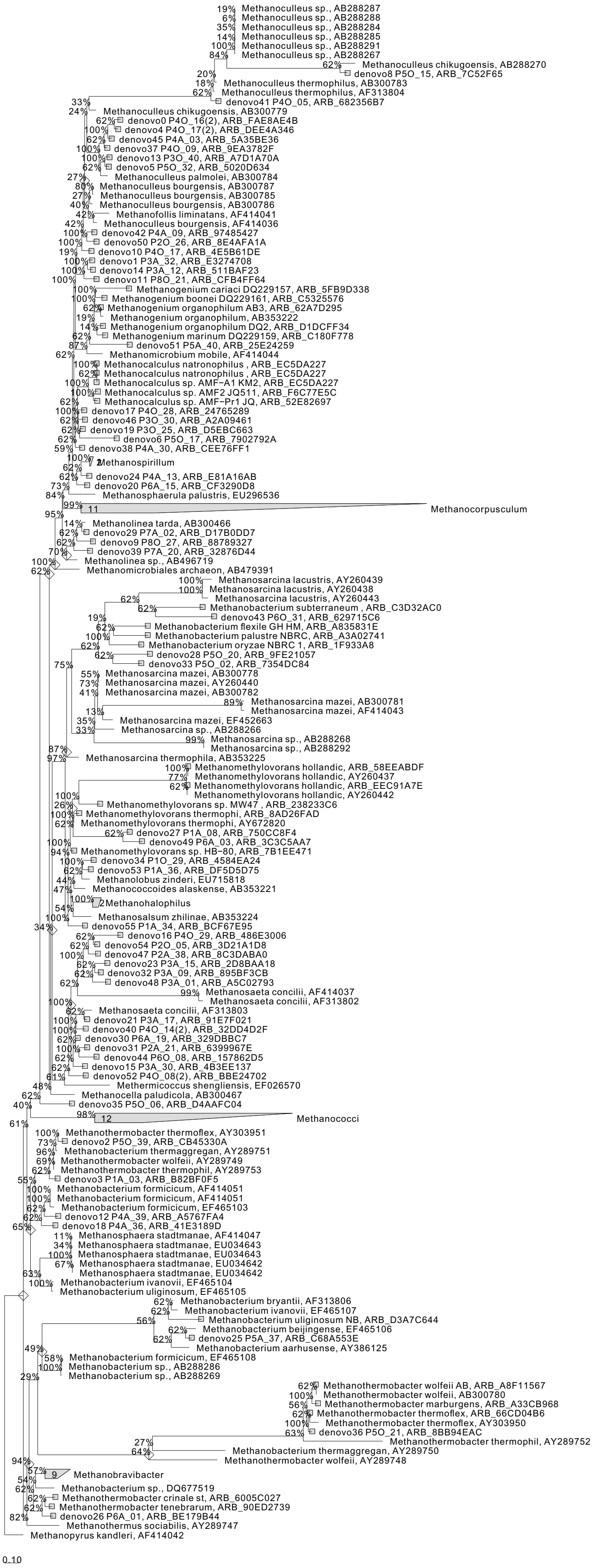


**Figure S2**. Phylogenetic tree based on clone library *mcrA* gene and reference gene sequences. The OTU representative *mcrA* gene clone sequences were obtained by 0.05 cutoff on nucleotide level, and then inserted into *mcrA* gene ARB database by maximum parsimony method without changing the initial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

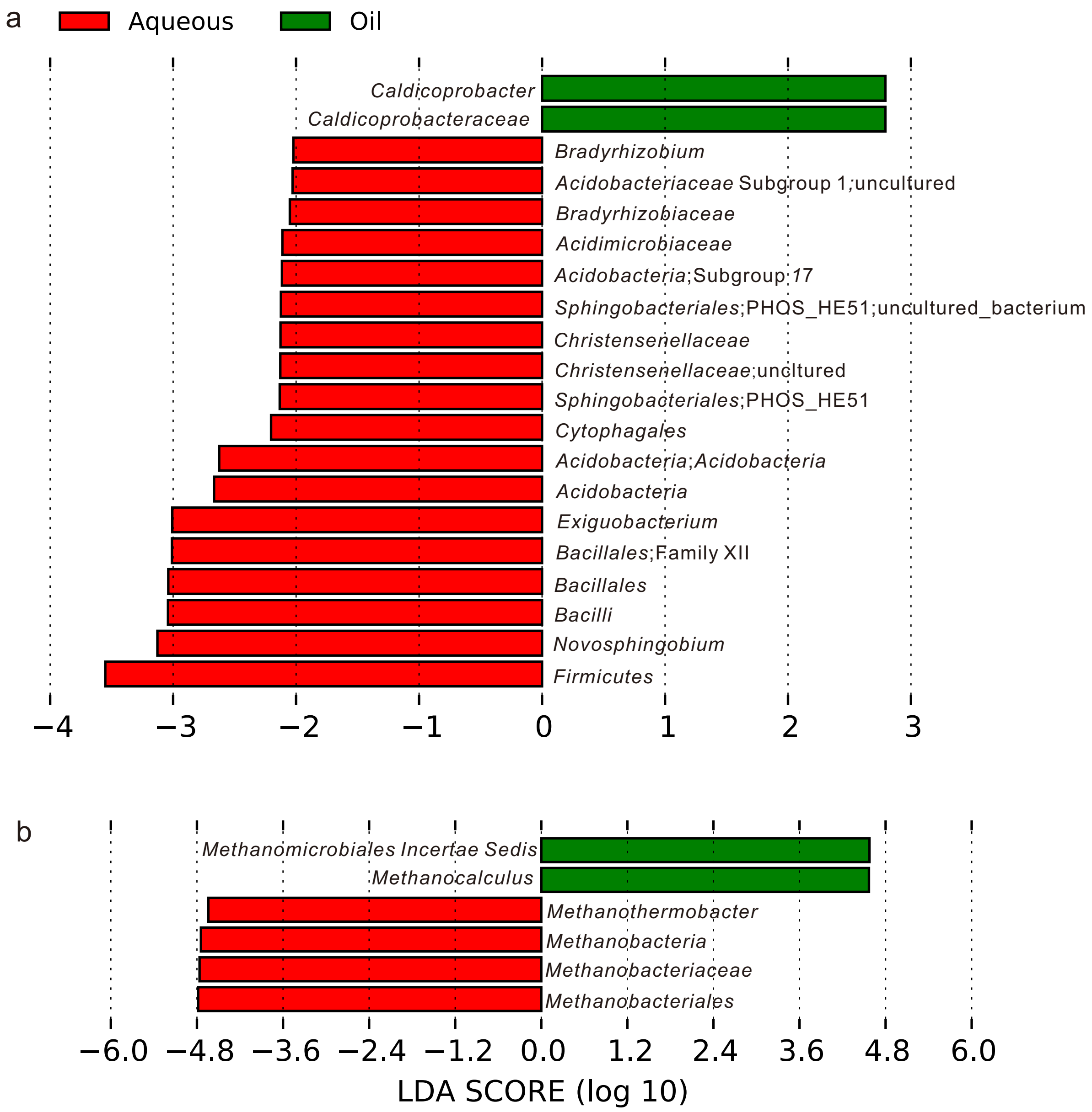


**Figure S3**. Differentially distributed features of microbial taxon abundance in aqueous and oil phases. LEfSe analysis with LDA effect score was applied. (a) bacterial community feature; (b) archaeal community feature.

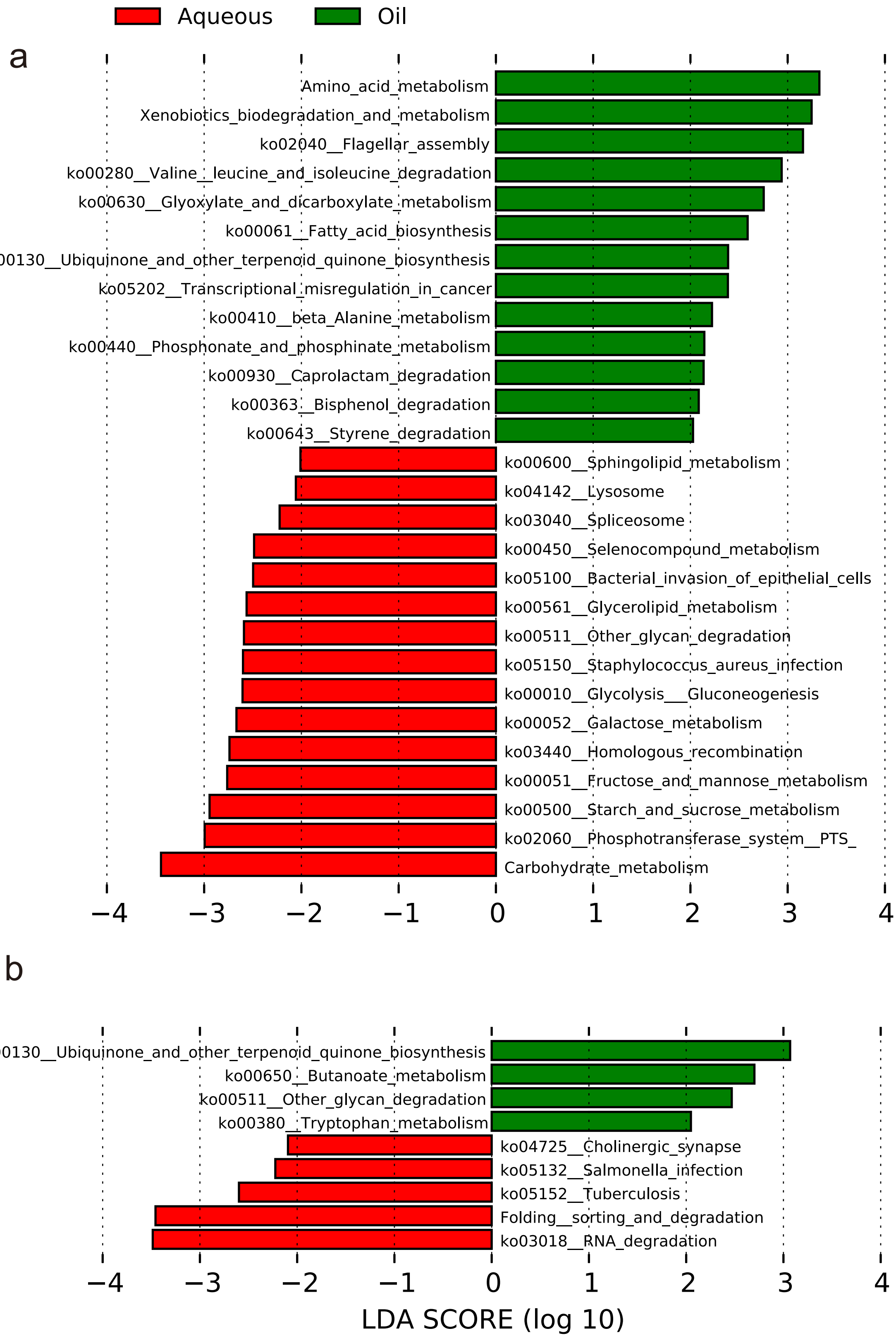


**Figure S4**. Differentially distributed feature of functional profiles in aqueous and oil phases. LEfSe analysis results based on the predicted functional profiles by Tax4Fun. (a) bacterial community feature; (b) archaeal community feature.

**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 |

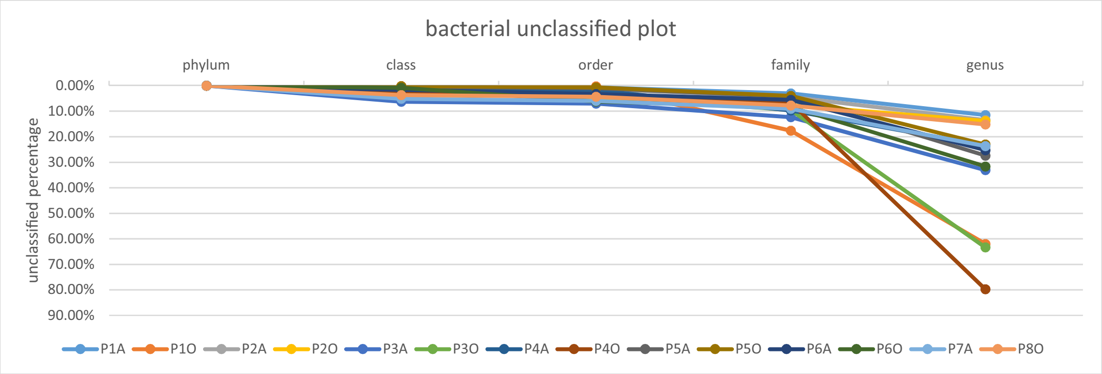
### Methanogen ( *mcrA* gene clone library)

| 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.

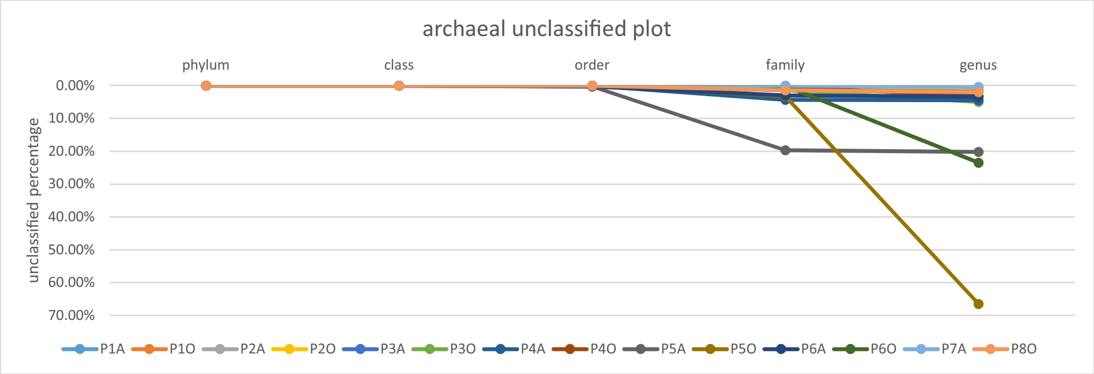
a

| | 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% |

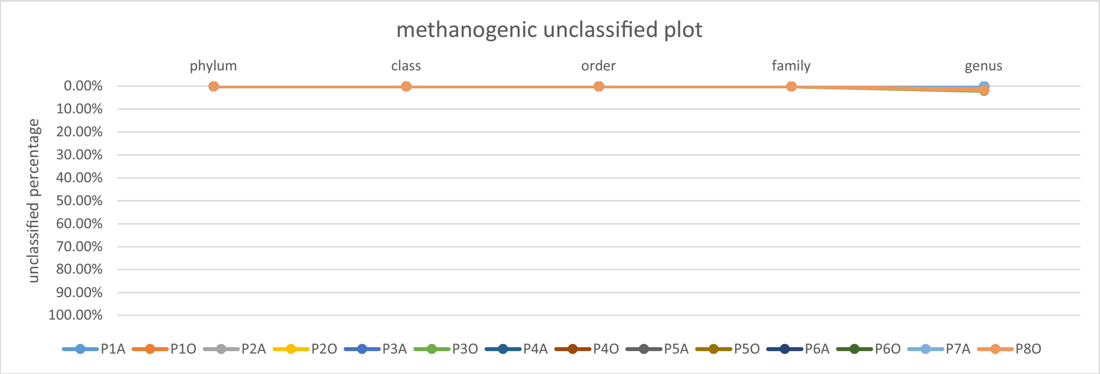


**Table S3**. Taxonomic composition of aqueous and oil phase samples based on MiSeq 16S rRNA gene sequencing. a) bacterial community composition in genus level; b) archaeal community composition in genus level.

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% |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 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% | 0.00% | 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% | 0.02% | 0.00% | 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% | 0.00% | 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% | 0.02% | 0.00% | 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% | 0.02% | 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% | 0.02% | 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% | 0.00% | 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% | 0.00% | 0.07% | 0.03% | 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% |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 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% | 0.00% | 0.02% | 0.00% | 0.02% | 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% | 0.00% | 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% | 0.00% | 0.03% | 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% | 0.00% | 0.02% | 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% | 0.00% | 0.02% | 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% | 0.00% | 0.02% | 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% | 0.02% | 0.00% | 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% | 0.02% | 0.00% | 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% | 0.00% | 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__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% | 0.00% | 0.02% | 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% | 0.00% | 0.02% | 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% | 0.02% | 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__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% |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 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% | | | | | |

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**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__Bacteriovoraceae;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__Bacteriovoraceae;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% |

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| 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__Bacteriovoraceae;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 (× $10^{-3}$μ$m^2$) |
| 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 (× $10^{-3}$μ$m^2$) |
| 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% |

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| 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% |

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| **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% |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 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% | 0.01% | 0.00% | 0.01% | 0.00% | 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% |

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| 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% |