# Metabolic roles of uncultivated bacterioplankton lineages in the northern Gulf of Mexico "Dead Zone"

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## Abstract

Marine regions that have seasonal to long-term low dissolved oxygen (DO) concentrations, sometimes called ‘dead zones,’ are increasing in number and severity around the globe with deleterious effects on ecology and economics. One of the largest of these coastal dead zones occurs on the continental shelf of the northern Gulf of Mexico (nGOM), which results from eutrophication-enhanced bacterioplankton respiration and strong seasonal stratification. Previous research in this dead zone revealed the presence of multiple cosmopolitan bacterioplankton lineages that have eluded cultivation, and thus their metabolic roles in this ecosystem remain unknown. We used a coupled shotgun metagenomic and metatranscriptomic approach to determine the metabolic potential of Marine Group II Euryarchaeota, SAR406, and SAR202. We recovered multiple high-quality, nearly complete genomes from all three groups as well as near-complete genomes belonging to Candidate Phyla usually associated with anoxic environments-Parcubacteria (OD1) and Peregrinibacteria. Two additional groups with putative assignments to ACD39 and PAUC34f supplement the metabolic contributions by uncultivated taxa. Our results indicate active metabolism in all groups, including prevalent aerobic respiration, with concurrent expression of genes for nitrate reduction in SAR406 and SAR202, and dissimilatory nitrite reduction to ammonia and sulfur reduction by SAR406. We also report a variety of active heterotrophic carbon processing mechanisms, including degradation of complex carbohydrate compounds by SAR406, SAR202, ACD39, and PAUC34f. Together, these data help constrain the metabolic contributions from uncultivated groups in the nGOM during periods of low DO and suggest roles for these organisms in the breakdown of recalcitrant organic matter.

## Importance

Dead zones receive their name primarily from the reduction of eukaryotic macrobiota (demersal fish, shrimp, etc.) that are also key coastal fisheries. Excess nutrients contributed from anthropogenic activity such as fertilizer runoff result in algal blooms and therefore ample new carbon for aerobic microbial metabolism. Combined with strong stratification, microbial respiration reduces oxygen in shelf bottom waters to levels unfit for many animals (termed hypoxia). The nGOM shelf remains one of the largest eutrophication-driven hypoxic zones in the world, yet despite its potential as a model study system, the microbial metabolisms underlying and resulting from this phenomenon—many of which occur in bacterioplankton from poorly understood lineages—have received only preliminary study. Our work details the metabolic potential and gene expression activity for uncultivated lineages across several low DO sites in the nGOM, improving our understanding of the active biogeochemical cycling mediated by these “microbial dark matter” taxa during hypoxia.

## Introduction

Hypoxia (dissolved oxygen [DO] below 2 mg·L$^{-1}$/~62.5 μmol·kg$^{-1}$) becomes dangerous or lethal to a wide variety of marine life, including organisms of economic importance (1). Hypoxia results from oxygen consumption by aerobic microbial metabolism combined with strong stratification that prevents reoxygeneation of bottom waters. These taxa are fueled primarily by autochthonous organic matter generated from phytoplankton responding to nitrogen input (1). Hypoxic zones have become more widespread globally through the proliferation of nitrogen-based fertilizers and the resulting increases in transport to coastal oceans via runoff (2). In the nGOM, nitrogen runoff from the Mississippi and Atchafalaya Rivers leads to one of the world's largest seasonal regions of coastal hypoxia, with bottom water hypoxia that can extend over 20,000 km$^2$ (1). Action plans to mitigate nGOM hypoxia have stressed that removing continued uncertainties and increasing our "understanding of nutrient cycling and transformations" remain vital for plan implementation (3). These needs motivated our current study of the engines of hypoxic zone nutrient transformation: microorganisms.

Much of our current knowledge regarding microbial contributions to regions of low DO comes from numerous studies investigating naturally occurring, deep-water oxygen minimum zones (OMZs), such as those in the Eastern Tropical North and South Pacific, the Saanich Inlet, and the Arabian, Baltic, and Black Seas (4-11). In many of these systems, continual nutrient supply generates permanent or semi-permanent decreases in oxygen, sometimes to the point of complete anoxia (4). During these conditions, anaerobic metabolisms, such as nitrate and sulfate reduction and anaerobic ammonia oxidation, become prevalent (5, 9, 11-13). In contrast, nGOM hypoxia is distinguished by a seasonal pattern of formation, persistence, and dissolution (1); benthic contributions to bottom water oxygen consumption (14, 15); and a shallow shelf that places much of the water column within the euphotic zone (16). While parts of the nGOM hypoxic zone can become anoxic (1, 17), many areas maintain low oxygen concentrations even during peak hypoxia while the upper water column remains oxygenated (18-20).

The first studies of bacterioplankton assemblages during nGOM hypoxia showed nitrifying Thaumarchaea dominated (21) and could be highly active (22), suggesting a major role for these taxa in nGOM nitrogen cycling. However, many more poorly understood organisms from cosmopolitan, but still uncultivated lineages, such as Marine Group II Euryarchaeota (MGII), SAR406, and SAR202, also occurred in abundance (21, 22). While the likely functions of some of these groups have become clearer recently, all of them contain multiple sublineages that may have distinct metabolic roles. For example, the SAR202 lineage of Chloroflexi contains at least five subclades with distinct ecological profiles (23, 24), and the best understood examples have been examined in the context of complex carbon degradation in the deep ocean (24). Likewise, SAR406 represents a distinct phylum with numerous sublineages, and the bulk of metabolic inference comes from taxa in deep water OMZs (25-28).

None of these groups have been studied in detail in the shallow coastal waters, particularly in the context of seasonal hypoxia. Thus, we pursued a combined metagenomic/metatranscriptomic approach to i) elucidate the specific contributions of these uncultivated lineages to biogeochemical cycling in the nGOM during hypoxia, ii) evaluate the relative similarity of these organisms to their counterparts elsewhere, and iii) determine if other uncultivated lineages had eluded previous microbial characterization in the region due to primer bias (29),16S rRNA gene introns (30), or low abundance. Metagenomic binning recovered 20 genomes across seven uncultivated lineages including MGII, SAR406, and SAR202, and also from Candidate Phyla previously uncharacterized in the nGOM: Parcubacteria (28), Peregrinibacteria (31), and possibly PAUC34f (32) and ACD39 (33). Our results provide the first information on the likely potential function and activity of these taxa during hypoxia in the shallow nGOM and suggest novel roles for some of these groups that possibly reflect sublineage-specific adaptations.

## Results

### *Study area*

Our previous work used 16S rRNA gene amplicon data and qPCR to examine correlations between whole microbial communities, nutrients, and DO across the geographic range of the 2013 seasonal hypoxia (21). Here we selected six of those samples from offshore of the region between Atchafalaya Bay and Terrebonne Bay (D', D, and E transects). These sites ranged considerably in DO concentration (~2.2 – 132 $\mu mol \cdot kg^{-1}$), and we chose them to facilitate a detailed investigation of the metabolic repertoire of individual taxa across the span of suboxic (1-20 $\mu mol \cdot kg^{-1}$ DO) to oxic (> 90 $\mu mol \cdot kg^{-1}$ DO) (5) water. Microbial samples from these sites were collected at the oxygen minimum near the bottom. Site depth ranged from 8 – 30 m, with the hypoxic (< 2 $mg \cdot L^{-1}$/62.5 $\mu mol \cdot kg^{-1}$) layer (at sites D2, D3, E2A, and E4) extending up to ~5 m off the bottom (Table S1).

### *Metagenomic assembly yielded high quality genomes from multiple uncultivated lineages*

Our initial assembly and binning efforts recovered 76 genomes. Using a concatenated ribosomal protein tree that included members of the Candidate Phylum Radiation (CPR)(34) (Fig. S1), CheckM (35) (Fig. S2), 16S rRNA genes and other single copy markers where available, and analyses of individual gene taxonomy (Fig. S3), we assigned 20 genomes to uncultivated "microbial dark matter" groups. These were six Marine Group II Euryarchaeota (MGII), five Marinimicrobia (SAR406), three in the SAR202 clade of Chloroflexi, and within Candidate Phyla (CP), one Parcubacteria (OD1), two Peregrinibacteria, and putatively, one ACD39 and two PAUC34f (Table 1). All genomes, with the exception of the Parcubacteria Bin 40, had estimated contamination of less than 6%, and in the majority of cases, less than 2%. Four of the six MGII genomes had estimated completeness (via CheckM) of greater than 61%, four of the five SAR406 greater than 73%, and all three SAR202 genomes were estimated to be greater than 83% complete. All CP lineages had at least one genome estimated to be greater than 71% complete (Table 1).

The six MGII genomes spanned a range of GC content from 41-62%, which may indicate the presence of sublineages, although their clustering within the ribosomal protein tree did not correspond with GC content (Fig. S1). Average amino acid identity (AAI) supported a close relationship between Bins 14, 17-1, and 18, congruent with the ribosomal phylogeny (Table S1). Expected complete genome sizes, based on estimated completion percentages, were between 1.7 and 3.2 Mbp (Table 1). Within SAR406, GC content groupings did correspond to phylogenetic inference. A low GC group (Group A) made up of Bins 51-1, and 51 with 39% and 41% GC, respectively, and a higher GC group (Group B) with Bins 45-2, 45, and 45-1 having 46%, 47%, and 49% GC, respectively. This pattern matched the ribosomal protein tree phylogeny where Bins 45-1 and 45-2 were sister and separated by large branch lengths from Bin 51-1 (Fig. S1). Bins 45 and 51 could not be included in the tree because of missing ribosomal proteins, but they were grouped with SAR406 through 16S rRNA genes, markers on other contigs like the RNA polymerase in Bin 45, similar patterns of protein family expansions (see below), based on their bin of origin, and via AAI calculations (Table S1). During quality control, Bin 51-1 was separated out of Bin 51, and Bins 45-1 and 45-2 out of Bin 45. The pairwise identities of the 16S rRNA genes between bins also support the 45/45-1 and 51/51-1 groupings, as does AAI, where Group A were more similar to each other than Group B, and vice versa (Table S1). The aggregate data therefore supported Bins 45 and 51 as SAR406. Based on 16S rRNA gene phylogeny (Fig. S4), Group A are sister to the Arctic96B-7 clade, and Group B form a monophyletic group with the early diverging SHBH1141 clade identified by Wright and colleagues (26). Expected genome sizes for SAR406 Group A were 2.6-2.7 Mbp and for Group B, 2.8-3.5 Mbp (Table 1). The three SAR202 genomes had very similar GC content (52-53%), were tightly grouped on the ribosomal protein tree on their own branch as early diverging members of the Chloroflexi (Fig. S1), and closely related- possibly at the level of Genus- based on AAI (36) (Table S1). We classified these genomes as subclade I based on 16S rRNA gene phylogeny (Fig. S5), which distinguishes them from the subclade III and V genomes recently reported (24). Estimated complete genome sizes were between 2.2-3.0 Mbp (Table 1). These genomes also had the lowest coding density of all the groups: 88-91% (Table S1).

CP lineages had fewer representative genomes. A single genome from Parcubacteria had a GC content of 52% and the two Perigrinibacteria genomes had 39 and 45% GC content. Both of these groups had well-supported positions in the ribosomal protein tree (Fig. S1) that were corroborated by BLASTP-derived annotation of encoded proteins against the NCBI nr database (Fig. S3). We estimated complete genome sizes for Parcubacteria and Perigrinibacteria at near 1.5 Mbp (Table 1). Bins 50 and 48 grouped with WS3 bacteria in the ribosomal protein tree, although their relative positions inside the clade were poorly supported at the internal nodes. AAI generally supports the designation of these two bins in the same phylum (37) (Table S1), as does their relationship in the ribosomal protein tree. However, the nearly complete Bin 50 16S rRNA gene sequence had best blast hits to the PAUC34f CP in the GreenGenes database. 16S rRNA gene phylogenetic inference grouped Bin 50 with other PAUC34f sequences sister to the entire WS3 clade (Fig. S6), in conflict with the ribosomal protein phylogeny. The lack of

PAUC34f genomes makes it possible that the ribosomal protein tree grouping of Bins 50 and 48 occurred simply due to inadequate taxon selection, as these are nearby clades in the 16S rRNA gene tree. Although a rare group, PAUC34f was more abundant than WS3 in the amplicon dataset and we detected 18 PAUC34f operational taxonomic units (OTUs) compared to three assigned to WS3 (21), so reconstruction of PAUC34f genomes was more likely than WS3. Bin 13 grouped with genomes designated as ACD39, a group previously identified in an aquifer (33), however Bin 13 was on a long branch and the relationship was poorly supported (Fig. S1). For the Bin 13 and PAUC34f genomes, blast-based identification via best hit annotation did not return clear results- hit annotations included a wide variety of taxa. These results are consistent with what we would expect from novel genomes that have few or no members in the database, however this analysis did not directly corroborate either the ribosomal protein tree phylogeny for all three bins, or the 16S rRNA gene phylogeny for Bin 50. We therefore consider the designation of Bins 50/48 as PAUC34f, and Bin 13 as ACD39, putative. Bins 50 and 48 had 58 and 55% GC content, and larger estimated complete genomes than the others at 6.3 and 4.9 Mbp, respectively. Bin 13 also had a large expected genome size at 4.8 Mbp, and GC content of 47%.

### *Unique roles for the ubiquitous MGII, SAR406, and SAR202 lineages in nGOM hypoxia*

Marine group II (MGII) is a broadly distributed archaeal clade, with members found in different marine (38, 39), and sedimentary (40), environments. Previous work during 2012 and 2013 hypoxia indicated a proliferation of archaeal taxa in both the Thaumarchaea and MGII phyla (21, 22). MGII comprised over 10% of the total community in some samples from 2013, and one MGII OTU also had a strong negative correlation with DO during 2013 hypoxia (21). Within the metagenomics dataset herein, MGII were more abundant in lower oxygen samples than in fully oxic ones, and the most abundant of the lineages reported here (Fig. S7). The majority encoded for aerobic, chemoheterotrophic metabolism, with no predicted genes for nitrogen or sulfur respiration except for a putative nitrite reductase (*nirK*) in a single genome- Bin 15 (Fig.1, Table S1). Abundance of MGII genomic abundance correlated well with transcriptional abundance in most samples (Fig. 3), and we specifically found MGII cytochrome c oxidase expression throughout, though the levels and patterns differed depending on the gene and the source genome (Fig. 4, Table S1). Expression of the *nirK* gene occurred in the D2 and E2A samples- both suboxic. All but the most incomplete genome encoded for ammonia assimilation, making this a likely nitrogen source. Aggregate metabolic construction also indicated a complete TCA cycle, glycolysis via the pentose phosphate pathway, and gluconeogenesis (Fig. 1). Carbohydrate active enzyme (CAZy) genes can provide critical information on the relationships between microbes and possible carbon sources (41). We found few and these were largely restricted to glycosyltransferases (GT) in families 2 and 4, with activities related to cellular synthesis. In general, CAZy expression occurred for at least one gene in every genome and we detected expression of GT cellular synthesis genes in the E2A sample (Fig. 5), likely indicating actively growing cells.

Another cosmopolitan group found in our samples was SAR406 or Marine Group A. These organisms were discovered over 20 years ago (27, 42), and the clade has recently been proposed as the phylum "Marinimicrobia" (28). SAR406 occur in numerous marine (5, 25, 27, 28, 43), sedimentary (28), and even oil reservoir (44) environments. They are prevalent in deeper ocean waters (27, 43, 45) and prefer lower oxygen concentrations in OMZs (5, 25, 46). SAR406 represented over 5% of the population in some locations during hypoxia in 2013, and one abundant OTU was negatively correlated with DO (21). Metagenomic read recruitment to the SAR406 bins confirmed this trend, with greater recruitment in the suboxic samples relative to dysoxic or oxic (Fig. S7). Total RNA recruitment was strongest to Bins 45 and 51-1, though most bins showed a positive RNA to DNA recruitment ratio in at least one sample, indicating these taxa were likely active (Fig. 3).

Despite their affinity for low oxygen environments, the SAR406 genomes encoded a predicted capacity for aerobic respiration (Fig. 1), and we found expression of cytochrome c oxidases in even the lowest oxygen samples (Fig. 4). The Group B genomes encoded both high and low-affinity cytochrome c oxidases (47), whereas the high affinity ($cbb_3$-type) oxidases were not recovered in the Group A genomes (Table S1), which may indicate sublineage-specific optimization for different oxygen regimes. Sublineage variation also appeared in genes for the nitrogen and sulfur cycles. Group B genomes all contained predicted nitrous oxide reductases (*nosZ*) and *nrfAH* genes for dissimilatory nitrite reduction to ammonium (defined here as DNRA, although this acronym frequently refers to nitrate, even though that is a misnomer (48)). The *nrfA* genes formed a monophyletic group with *Anaeromyxobacter dehalogenans* 2CP-1, an organism with demonstrated DNRA activity (48) (Fig. S8). The genes also contained conserved motifs diagnostic of the *nrfA* gene (48) (Fig. S9). We observed expression of *nrfAH* and *nosZ* at the sites with the lowest DO concentrations (D2, E2A, and E4) and expression appeared to have a negative relationship with DO concentration (Fig. 4). The Bin 51-1 Group A genome contained predicted *narHI* genes for dissimilatory nitrate reduction, which we did not find in the Group B genomes. We observed expression of SAR406 *narHI* only in the lowest DO sample from station E2A (Fig. 4). Two Group B SAR406 genomes had predicted *phsA* genes for thiosulfate reduction to sulfide (and/or polysulfide reduction (49)), as previously described from fosmid sequences (26). We detected transcripts for these genes only in samples E2A and E4, the two lowest DO samples (Fig. 4). Interestingly, many of the anaerobic respiratory genes were co-expressed with cytochrome c oxidases, indicating a potential for either co-reduction of these alternative terminal electron acceptors or poising of these organisms for rapid switching between aerobic and anaerobic metabolism (50).

All SAR406 genomes had numerous genes for heterotrophy. We found CAZy genes in all major categories except polysaccharide lyases, and expression for most of these genes in both Group A and Group B genomes in one or more samples (Fig. 5). Notable carbohydrate compounds for which degradation capacity was predicted include cellulose (glycoside hydrolase (GH) families GH3, GH5; carbohydrate binding module (CBM) family CBM6), starch (GH13), agar and other sulfated galactans (GH2, GH16), chitin (GH18), xylan (GH30, CBM9), and peptidoglycan (GH23, GH103, CBM50). The genomes contained putative transporters for a variety of dissolved organic matter (DOM) components including nucleosides, amino and fatty acids, and oligopeptides (Table S1). We also found numerous outer membrane transporters, including cation symporters; Outer Membrane Receptors (OMR- TonB-dependent), which play important roles in transport of metals, vitamins, colicins, and other compounds; Outer Membrane Factors (OMF); and most genomes also had large numbers of duplicated genes (24 in Bin 45-2), identified via hidden Markov model searches against the SFam database (51), annotated as "Por secretion system C-terminal sorting domain-containing protein," some of which were associated with GH16. These genes likely play a role in sorting C-terminal tags of proteins targeted for secretion via the Por system, which is essential for gliding motility and chitinase secretion in some Bacteroidetes (52). The extensive gene duplication may indicate expanded and/or specialized sorting functionality, and suggests an emphasis on protein secretion in this group. Expression of a membrane-bound lytic murein transglycosylase D (GH23) involved in membrane remodeling, also supports the idea of active and growing cells from Group A in all samples (Table S1). Thus, SAR406 likely perform chemoorganoheterotrophic metabolism, possibly degrading extracellular material, with flexibility in terminal electron accepting processes that implicate them in nitrogen and sulfur cycling in the lowest suboxic DO samples.

Members of the SAR202 clade of Chloroflexi also inhabit a wide variety of marine environments (23), frequently in deeper waters (23, 43, 45, 53, 54), and remain functionally understudied, although recent work on subclades III and V has suggested roles in degrading recalcitrant DOM in the mesopelagic (24). We detected Chloroflexi 16S rRNA gene sequences during 2013 hypoxia at up to 5% of the community (21). In contrast to the single-cell genomes examined by Landry et al. (24), the three SAR202 genomes that we recovered belong to subclade I (23) (Fig. S5). Although present at lower abundance than MGII and SAR406 (Fig. S7), these genomes showed relatively high activity in some samples (Fig. 3). Like subclade III and V, subclade I organisms likely respire oxygen, however we also found *napAB* and *nosZ* genes for nitrate and nitrous oxide reduction, respectively (Fig. 1). As in SAR406, we detected concurrent expression of these genes with cytochrome c oxidases in the lowest DO samples (Fig. 4) (Fig. 4, Table S1).

The SAR202 genomes have numerous transporters with predicted roles in organic matter transport, which supports previous observations of DOM uptake (53). In particular, SAR202 genomes also had considerably more Major Facilitator Superfamily (MFS) transporters than the other genomes in this study (Table S1) and those of the subclade III genomes (24), and SFam searches revealed a the majority of these shared annotation as a "Predicted arabinose efflux permease" (SFam 346742). MFS genes transport numerous diverse substrates, such as sugars and amino acids, through coupling with an ion gradient, and can be associated with either uptake or export of compounds (55). SAR202 genomes also had between 53 and 66 predicted ABC transporters. The largest gene family expansion that we observed in SAR202 was associated with SFam 6706, with between 46 and 48 genes in this family encoded in each genome. Most of these (121/142) were annotated as either a "galactonate dehydratase" or a "L-alanine-DL-glutamate epimerase." Galactonate dehydratase catalyzes the first step of the pathway to utilize D-galactonate in central carbon metabolism via the pentose phosphate pathway. The large number of genes in these categories likely indicate some divergence for alternative roles as this group belongs broadly to the COG4948 "L-alanine-DL-glutamate epimerase or related enzyme of enolase superfamily." All genomes also had numerous dehydrogenases as reported for the subclade III genomes (24). Specifically, SFams 346640 and 1639 were the third and fourth most abundant, with 16-18 and 13-15 genes in each family, respectively, across the three genomes. Genes in these families were annotated as "short-chain alcohol dehydrogenase family," "3-alpha (or 20-beta)-hydroxysteroid dehydrogenase," "meso-butanediol dehydrogenase," and others. These match the annotations of the subclade III genomes, and suggest a similar role in conversion of alcohols to ketones (24). The SAR202 genomes have comparatively few CAZy genes relative to the other genomes. GH15 and GH63 suggest starch degradation, and GH105 pectin degradation, and we detected expression of multiple genes in these categories across samples (Fig. 5, Table S1).

### *Other Candidate Phyla organisms in nGOM hypoxia*

In contrast to the abundant and cosmopolitan MGII, SAR406, and SAR202 clades, we also recovered genomes from several groups that were either previously undetected in the nGOM or very rare. Although these taxa likely do not contribute the biomass of more populous clades, their genomes provide important insight into their functional potential during hypoxia. The Bin 13 genome (possibly ACD39) also had the highest relative activity compared to all the other genomes in our study (Fig. 3), underlining the point that low abundance does not automatically equate to low metabolic impact. Bin 13 had predicted aerobic respiration with both high and low-affinity cytochrome c oxidases (Fig. 2), however, the low affinity oxidases contributed more reads in the samples where we could detect expression (Table S1). The genome contained numerous predicted CAZy genes in the glycosyltransferase and glycoside hydrolase categories, spread across numerous families in each (Table S1). Notable degradation capacity included starch (GH13) and peptidoglycan (GH23, GH103, GH104).

Bin 13 had ~ 80 ABC transporter genes, and similarly to the SAR406 genomes, numerous outer membrane transporters, including the OMR and OMF families. We predict complete glycolysis/gluconeogenesis pathways and a TCA cycle. We recovered paralogous pilus subunit genes, chemotaxis genes, and a partial flagellar assembly. Furthermore we detected relatively high expression of the *flgLN* flagellin genes in samples D2, D3, E2A, and E4 (Table S1) suggesting active motility in these environments. Several other Bin 13 genes were among the most highly expressed in all samples, but could only be classified as hypothetical (Table S1). Similarly, the three most populous SFams in Bin 13, according to number of genes (n=16, 15, and 13) also linked to genes annotated as hypothetical proteins with either tetratricopeptide, HEAT, TPR, or Sel1 repeats. Although currently obscure, these and the highly expressed hypothetical genes represent important targets for future research into the function of this group. The organism likely leads an aerobic heterotrophic lifestyle, with substantial capacity for interacting with the environment through numerous transporters and possible surface attachment via multiple motility genes.

Bins 50 and 48 were lower in abundance than SAR202 genomes, with no observable trend associated with oxygen levels (Fig. S7). These genomes encoded flagellar motility, aerobic respiration, glycolysis via the pentose-phosphate pathway, gluconeogenesis, assimilatory sulfate reduction, and DNRA (Fig. 2). The *nrfA* subunit from both genomes grouped in the same monophyletic clade as those from SAR406 (Fig. S8), and had similar conserved motifs (Fig. S9). However, we note that the *nrfAH* gene sets for Bins 50 and 48 occurred on relatively short contigs (5650 and 5890 bp, respectively), so the metabolic assignment cannot be corroborated as definitively as that for SAR406. The Bin 50 genome was among the more active in our analysis (Fig. 3), and we detected highest expression of cytochrome c oxidase components in samples E2A and E4 (Fig. 4). DNRA gene expression was low but observable in the same samples. We also recovered a partial gene for the ribulose-bisphosphate carboxylase (RuBisCO) large subunit, however this fragment was on a very short contig (3954 bp), and we did not detect expression in any of our samples, so we cannot rule out that this gene occurred on a contaminating contig.

These genomes had abundant CAZy genes in all categories, suggesting a highly flexible metabolic repertoire for carbon acquisition. They contain possible capacity for breakdown of starch (GH13, CBM48), peptidoglycan (GH23, CBM50), fructose-based oligosaccharides (GH32), and hemicellulose (GH2, GH3, GH43). Notably these genomes were the only ones with predicted polysaccharide lyases (PL) among those compared (with the exception of a single predicted PL gene in SAR406- Table S1). PL genes cleave uronic-acid containing polysaccharides (56). These organisms seem particularly adapted for pectin (PL1, PL2, PL9, PL10, PL11, PL22, GH78) and alginate (PL15, PL17) degradation- both compounds are common cell wall components of green and brown algae, respectively. In line with the algal cell wall degradation ability, we detected a large expansion (102 genes in Bin 50) of sulfatase genes in SFam 1534, annotated predominantly as either “arylsulfatase A” or “choline-sulfatase.” Arylsulfatases cleave sulfate esters, usually to supply microbes with a source of sulfur, and can be located intracellularly or in membranes (57). Choline-sulfatases cleave choline sulfate to choline and sulfate, with downstream use for the former as a carbon source or osmoprotectant and the latter as a sulfur source (58). Given the predicted assimilatory sulfate reduction pathway in Bins 50 and 48, this is a logical means to obtain sulfur for the group. We observed large expansions in galactonate and other dehydratases (as in SAR202, above- SFam 6706 n=42 in Bin 50), as well as numerous ABC transporter permeases (SFam 4442), which match the transporter prediction via IMG: 117 predicted genes for ABC transporters in all. These genomes also had numerous OMF and OMR transporter genes (Table S1). The large number of transporters and protein family expansions correspond to the relatively large expected genome sizes (between 5 and 6 Mbp). Thus, we expect these organisms to have an aerobic, potentially facultatively anaerobic, multifaceted chemoorganoheterotrophic metabolism with roles in complex carbon compound degradation (like that of algal cell walls) and the nitrogen cycle.

We also recovered genomes associated with CPR taxa usually associated with anoxic environments: two Peregrinibacteria and one from the Uhrbacteria subclade of the Parcubacteria (formerly OD1). All three genomes could be assigned taxonomically with high confidence based on their positions in the ribosomal protein tree (Fig. S1) and via gene annotations (Fig. S3). We note that although the Peregrinibacteria bins (16 and 39) had very low predicted contamination, the Parcubacteria Bin 40 has 15% predicted contamination (75% of which we attribute to strain heterogeneity in the bin) (Table 1). Recovery of Parcubacteria from a coastal marine system is unusual, but not unprecedented. Parcubacteria single-cell genomes have been identified in marine and brackish sources (28), and we previously identified 26 rare OTUs assigned to the phylum in nGOM hypoxia (21). That number of low abundance OTUs may explain why we have 20 single copy marker genes present in two copies in Bin 40 (Table S1). In contrast to Parcubacteria, Peregrinibacteria have thus far only been found in terrestrial subsurface aquifers (31, 33, 59, 60), and remained undetected in our amplicon survey (21). Both groups occurred in low relative abundance to the other taxa in this study, and showed the lowest activity (Fig. 3). Consistent with previous reports of obligate fermentative metabolism by Parcubacteria and Peregrinibacteria (28, 30, 31, 59), we identified no respiratory pathways for these taxa (Fig. 2) and they trended towards greater abundances in the lowest DO samples (Fig. S7). In spite of relatively high predicted genome completion, we found very few CAZy genes, and those were mostly restricted to glycosyltransferases (Table S1), hence probably involved in capsular polysaccharide synthesis. While these organisms had low relative abundance to the other groups (Fig. S7), we did observe activity in some samples (E2, E2A, D1), suggesting these organisms are either insensitive to oxygen or occupy microanoxic niches (Fig. 3).

## Discussion

This work provides the first reconstruction of multiple nearly complete genomes from uncultivated bacterioplankton during nGOM hypoxia. Although we define roles for MGII, SAR406, SAR202, Bin 13 and Bins 50/48 as aerobic heterotrophs, we also observed concurrent expression of genes associated with anaerobic metabolism in SAR406 (nitrate reduction, DNRA, nitrous oxide reduction, and sulfur reduction), SAR202 (nitrate and nitrous oxide reduction), MGII (nitrite reduction), and Bins 50/48 (DNRA) in suboxic samples with the lowest measured DO concentrations. Simultaneous utilization of multiple electron acceptors with different redox potentials likely indicates an abundant supply of electron donors (61), may denote niche partitioning within group sublineages at a finer level of taxonomic resolution than we observed, or indicate poising of taxa for rapidly changing chemical gradients (50). An organism's set of carbohydrate active enzyme (CAZy) genes often gives insights into its biology, in particular into nutrient sensing and acquisition. All taxa examined in this study had predicted chemoorganoheterotrophic metabolism, and the CAZy genes found in these genomes suggest that SAR406, SAR202, Bin 13, and Bins 50/48 participate in the degradation of complex organic matter resulting from the detritus of larger organisms. This matches the general model of hypoxic zone oxygen consumption resulting from sinking organic matter provided by algal blooms in surface waters (1). The observed activity of obligate fermentative groups Parcubacteria and Peregrinibacteria also suggests that anoxic pockets occur in the water column where these organisms can thrive.

The prevalence of MGII among lower oxygen samples in the hypoxic zone is somewhat surprising, considering that they are commonly associated with aerobic environments (39). However, oxygen was still present in even the lowest DO samples, and MGII success likely had more to do with the carbon content than oxygen levels. These nGOM MGII appear to be metabolically similar to those described in previous work: MGII have been shown to be dominant in water column environments associated with blooms in productivity, for example at deep-sea hydrothermal plumes (38). Thus, the increased availability of organic matter (proteins and carbohydrates), thought to be preferred substrates for MGII (62, 63), probably explains their abundance.

Members of the SAR406 clade have frequently been observed in OMZs (5, 25), and our data now define roles for them in the eutrophication-driven hypoxia of the nGOM. Our genomes had larger estimated genome sizes- 2.6-2.7 Mbp (Group A) and 2.8-3.5 Mbp (Group B)- compared to 1.1-2.4 Mbp from single-cell genomes (28). Overall GC content, however, was in the range of the 30-48% reported for fosmids (26) and single-cell genomes (28). The lower GC Group A genomes specifically had a similar GC content to the Arctic96B-7 fosmids, matching their predicted phylogenetic affiliation (see below) (26). Previous metabolic reconstructions of SAR406 predicted aerobic metabolism (28) and sulfur reduction (26), which our data confirm, although the sulfur reduction genes were only found in Group B organisms (Table S1). Our genomes now also suggest multiple nitrogen cycling roles that appear to be organized by sublineages within the phylum, and sublineage specific presence of both high and low affinity cytochrome c oxidases. Specifically, Group B organisms contained both types of cytochrome c oxidases, *nosZ* and *nrfAH* genes, whereas Group A organisms contained the low affinity cytochrome c oxidases only, and additionally *narHI* genes not found in Group B. The unique roles predicted for these taxa is not surprising given the diversity of the SAR406 clade and the genetic distances between Group A and B (Fig. S4). Group A organisms were sister to the Arctic96B-7 clade. Previous fosmids associated with this clade contained genes for oxidative stress and sulfur reduction, although we only found sulfur reduction genes in the distantly related Group B genomes. The ArcticB96-7 clade may be diverse enough to encompass differing metabolic strategies, however the variable presence of *phsA* genes in this group may simply be due to incomplete genomes (herein) and fosmids (26). The Group B organisms group with the early diverging SBH1141 clade (26), for which no previous genome data exist. In addition to sublineage-specific respiratory characteristics, our results also generate specific hypotheses about organic matter metabolism in SAR406: likely degradation capacity for cellulose, starch, agar, xylan, and peptidoglycan; transport of nucleosides, amino and fatty acids, and oligopeptides; and substantial gene duplication associated with protein secretion for possible extracellular metabolism. Together these data suggest that during nGOM hypoxia SAR406 members degrade complex carbohydrates fueled by aerobic respiration, and supplemented with facultative anaerobic respiration of nitrate, nitrite, or sulfur compounds.

Genome data for SAR202 have been lacking until recently. Landry and colleagues have recently described the properties for several single-cell genomes representing subclades III and V of SAR202 recovered from the mesopelagic (24). Our genomes have generally higher GC content and much lower expected genome sizes than those predicted by Landry et al., although these calculations are likely complicated by the relative incompleteness of the genomes (8-47%). Their genomes indicated a role for SAR202 in the oxidation of recalcitrant dissolved organic matter, and specifically cyclic alkanes, via flavin mononucleotide monooxygenases (FMNOs) and different dehydrogenases that occurred in paralogous groups (24). We observed many of the same gene expansions, namely that of MFS transporters and short-chain dehydrogenases (and related genes), but we did not recover any FMNOs of SFams 4832 or 4965, suggesting subclade and/or niche-specific adaptations. Furthermore, we observed *napAB* and *nosZ* genes for nitrate and nitrous oxide reduction (and expression of these genes), which were not reported for subclade III or V. The nGOM hypoxia SAR202 genomes had CAZy genes implicating them in degradation of complex compounds such as chitin and pectin. The emerging picture of these taxa from both shallow hypoxic waters and the mesopelagic is one of recalcitrant carbon degraders, with overlapping suites of paralogous genes, but that may be specialized for specific compounds more commonly available in their respective habitats.

This study has also developed roles for CP taxa in a shallow marine water column during hypoxia. The most active organism in our survey based on the ratio of RNA to DNA reads recruited, Bin 13, putatively belongs to a group with little genomic data- ACD39. The original ACD39 genome was reconstructed from an aquifer community (33). Although this was only a partial genome, it shared some features with our putative ACD39 member, namely pilin and chemotaxis genes, those containing TPR and tetratricopeptide repeats, and CAZy genes for degradation of complex compounds such as starch (33). Our study provides evidence that these taxa have relatively large genomes (~4.8 Mbp), are active aerobes in nGOM hypoxia, and have chemotaxis and motility genes that could facilitate scavenging and surface attachment. However, most of the highly expressed genes in this organism were annotated as hypothetical proteins, so much of the function of these organisms remains to be uncovered.

Bins 50 and 48 provide novel genome data for bacterioplankton in nGOM hypoxia, although the exact taxonomic position of these bins remains in conflict. The ribosomal protein tree provides evidence that these taxa belong to the Latescibacteria (WS3) (Fig. S1), but 16S rRNA genes (Fig. S6) and our amplicon data point toward membership in the more poorly understood PAUC34f clade. Since no previous genome data exist for PAUC34f, we cannot rule out erroneous assignment in the ribosomal protein tree due to insufficient taxon selection. Bins 50 and 48 represented the largest genomes of the study, with estimated complete sizes of ~5-6 Mbp, and numerous genes suggesting degradation of a wider suite of complex organic matter than any of the other genomes examined. For example, they were the only genomes with numerous polysaccharide lyase genes, and these likely facilitate breakdown of algal cell wall components like pectin and alginate. The Bin 50 genome was among the most active across all samples (Fig. 3), and we detected expression of cytochrome c oxidase genes, and those for DNRA, in both the Bin 50 and 48 genomes. Thus we expect these organisms to play a role in the breakdown of algal detritus through respiration of oxygen, with nitrite as an alternative electron sink.

If these bins belong to PAUC34f, they represent the first genomic data for the group. Although originally discovered, and commonly found, in marine sponges (32, 64-66), this putative bacterial phylum (via GreenGenes/SILVA) has been detected as a rare group in other marine invertebrates (67) and stream sediment (68), and we identified 18 distinct but rare PAUC34f OTUs in nGOM hypoxia, compared to just three from WS3 (21). Although the majority of studies suggest an endosymbiotic lifestyle for PAUC34f, our representative genome data point towards a free-living existence with multiple terminal electron accepting processes, motility genes for seeking more favorable conditions, and a large metabolic repertoire for degradation of complex compounds. On the other hand, if these genomes represent WS3, the sister clade to PAUC34f (Fig. S6), they have many similarities to the lifestyles inferred from recent metagenomic investigations (69, 70). Specifically, while this group was previously considered anaerobic (69), new data have supported an aerobic lifestyle for some members (59), and revealed complete electron transport chains and both high and low affinity cytochrome c oxidases (70). The Bin 50 and 48 genomes predict aerobic metabolism as well, although only with low affinity cytochrome c oxidases. Farag et al. also found little evidence of these taxa in host-associated environments, contrary to PAUC34f sequence data (70). The enrichment of PL family genes in Bins 50 and 48, polysaccharide degradation capability in general, and specific genes for degradation of cell wall components, all corroborate previous findings on WS3 as well (70). Bin 50 had 78 annotated peptidases, nearly double that in all other genomes in the study (Bin 48 had 46), which also concurs with metagenomic predictions for WS3 (70). Our genomes differed from WS3 metagenomes principally in the predicted DNRA metabolism and the dramatic expansion of sulfatases. Although sulfatases were observed in WS3 metagenomes (70), they were not present in the numbers associated with Bin 50 (n=102). A large cadre of sulfatases has been previously reported for *Lentisphaera* (n=267) and *Pirellula* (n=110) genomes (71, 72) and suggests specialization for degradation of sulfate-esters to satisfy carbon and/or sulfur requirements.

Although Parcubacteria and Peregrinibacteria occurred in low abundance and we detected activity in only a few samples, their recovery in the hypoxic zone is notable because these organisms have generally been associated with anoxic environments. Our predicted genome sizes (~1.5 Mbp) corroborate previous reports of these organisms having small genomes (31, 59). We did not observe any genes associated with nitrogen or sulfur redox transitions, although we cannot rule these capabilities entirely due to incomplete genomes. Regardless, we can hypothesize that Parcubacteria and Peregrinibacteria persist as members of the rare biosphere until they can take advantage of microanoxic niches in the water column where they participate in carbon cycling as obligately fermentative organisms.

## *Conclusions*

Our study helps define the metabolism for many of the most enigmatic organisms observed in cultivation-independent studies during nGOM hypoxia. We also provide new information about sublineage specific attributes for the important cosmopolitan marine clades SAR406 and SAR202, for which previous metabolic information has been limited. Notably, although Parcubacteria and Peregrinibacteria likely subsist via an obligate anaerobic lifestyle, the remaining uncultivated groups in the nGOM hypoxic zone had one or more genomes that encoded cytochrome c oxidases (and other electron transport chain components) for respiring oxygen, making these taxa likely only facultative anaerobes. Pervasive aerobic metabolism in an oxygen-depleted water column may seem counterintuitive, yet despite DO being as low as 2.2 $\mu$mol kg$^{-1}$ in the E2A sample, oxygen probably remained high enough to sustain aerobic microbes. As little as ~0.3 $\mu$mol kg$^{-1}$ oxygen inhibited denitrification in OMZ populations by 50% (73), and even *Eschericia coli* K-12 could grow aerobically at oxygen concentrations as low as 3 nM (74). Thus, for many organisms, active aerobic respiration likely persists even in suboxic waters. Nevertheless, our data also suggests pervasive co-reduction of alternative terminal electron acceptors (oxygen, nitrate, nitrite, nitrous oxide, and sulfur), sometimes within the same organism (Fig. 4). Co-reduction of electron acceptors with different redox potentials across a community could indicate microniches and/or aggregates in the water column where DO concentrations drop below bulk values (50). Alternatively this can occur with an abundance of electron donor, and overlapping redox processes have been reported in multiple environments, including aquatic ones (61, 75). Concurrent expression of genes for multiple terminal electron accepting processes within a single organism has been proposed as a means of improved readiness for dynamic conditions, albeit at the cost of lower productivity (50). Given that many uncultivated taxa likely perform multiple terminal electron accepting processes (and possibly do so simultaneously), and we found a comparative cornucopia of genes for degradation of chemoorganohetrotrophic energy sources, we hypothesize that niche differentiation within uncultivated hypoxic zone bacterioplankton occurs predominantly via specialization for different oxidizable substrates rather than for distinct roles in the canonical redox cascade (4, 5). Importantly, many of the active uncultivated taxa also appeared adapted for degradation of complex carbon substrates. Such compounds might comprise the bulk of available organic matter during the later stages of hypoxia after initial oxygen depletion by microorganisms feeding on more labile carbon sources. Selection for chemoorganotrophic microbes adapted to utilize recalcitrant organic matter could also explain why organisms that do not require an exogenous carbon source, such as the chemolithoautotrophic *Nitrosopumilus*, proliferate during hypoxia (21, 22) compared to their levels during spring before DO decreases (76, 77). Temporal data on the relative abundance and activity of these organisms, and of organic matter composition in the water column, will be critical to more fully understand the relationship of bacterioplankton to the creation, maintenance, and dissolution of nGOM hypoxia.

## Materials and Methods

*Sample selection and nucleic acid processing.* Six samples representing hypoxic (n=4) and oxic (n=2) DO concentrations were picked from among those previously reported (21) at stations D1, D2, D3, E2, E2A, and E4 (Table S1). DO, and nutrient collection information is detailed in Gillies et al., 2015. Nucleic acids were collected as follows: At these six stations 10 L of seawater was collected and filtered with a peristaltic pump. A 2.7 μM Whatman GF/D pre-filter was used and samples were concentrated on 0.22 μM Sterivex filters (EMD Millipore). Sterivex filters were immediately sparged, filled with RNAlater, and placed at -20˚C, at which they were maintained until extraction. DNA and RNA were extracted directly off of the filter by placing half of the Sterivex filter in a Lysing matrix E (LME) glass/zirconia/silica beads Tube (MP Biomedicals, Santa Ana, CA) using the protocol described in Gillies *et al.* (2015) which combines phenol:chloroform:isoamyalcohol (25:24:1) and bead beating. Genomic DNA and RNA were stored at -80°C until purified. DNA and RNA were purified using QIAGEN (Valencia, CA) AllPrep DNA/RNA Kit. DNA quantity was determined using a Qubit2.0 Fluorometer (Life Technologies, Grand Island, NY). RNA with an RNA integrity number (RIN) (16S/23S rRNA ratio determined with the Agilent TapeStation) ≥ 8 (on a scale of 1-10, with 1 being degraded and 10 being undegraded RNA) was selected for metatranscriptomic sequencing. Using a Ribo-Zero kit (Illumina) rRNA was subtracted from total RNA. Subsequently, mRNA was reverse transcribed to cDNA as described in Mason *et al.* (2012) (78).

*Sequencing, assembly, and binning.* DNA and RNA were sequenced separately, six samples per lane, with Illumina HiSeq 2000 chemistry to generate 100 bp, paired-end reads (180 bp insert size) at the Argonne National Laboratory Next Generation Sequencing facility. The data are available at the NCBI SRA repository under the BioSample accession numbers SAMN05791315-SAMN05791320 (DNA) and SAMN05791321-SAMN05791326 (RNA). DNA sequencing resulted in a total of 416,924,120 reads that were quality trimmed to 413,094,662 reads after adaptors were removed using Scythe (https://github.com/vsbuffalo/scythe), and low-quality reads (Q < 30) were trimmed with Sickle (https://github.com/najoshi/sickle). Reads with three or more Ns or with average quality score of less than Q20 and a length < 50 bps were removed. Genomes were reconstructed using two rounds of assembly. Metagenomic reads from all six samples were pooled, assembled, and binned using previously described methods (79, 80). Briefly, quality filtered reads were assembled with IDBA-UD (81) on a 1TB RAM, 40-core node at the LSU High Performance Computing cluster SuperMikeII, using the following settings: -mink 65 –maxk 105 –step 10 –pre_correction –seed_kmer 55. Initial binning of the assembled fragments was performed using tetra-nucleotide frequency signatures using 5 kbp fragments of the contigs. Emergent self-organizing maps (ESOM) were manually delineated and curated based on clusters within the map (Fig. S8, S9). The primary assembly utilized all reads and produced 28,080 contigs ≥ 3 kb totaling 217,715,956 bp. Of these, 303 contigs were over 50 kb, 72 over 100 kb, and the largest contig was just under 495 kb. Binning produced 76 genomes, of which 20 genomes were assigned to lineages with uncultivated representatives using CheckM, ribosomal protein trees, and 16S rRNA gene sequences (below).

*DNA and RNA mapping.* Metagenomic and metatranscriptomic sequencing reads from each sample were separately mapped to binned contigs using BWA (82) to compare bin abundance across samples and facilitate bin cleanup (below). Contigs within each bin were concatenated into a single fasta sequence and BWA was used to map the reads from each sample to all bins. All commands used for these steps are available in supplementary information.

*Bin QC.* Bins were examined for contamination and completeness with CheckM (35), and we attempted to clean bins with > 10% estimated contamination using a combination of methods. First, the CheckM modify command removed contigs determined to be outliers by GC content, coding density, and tetranucleotide frequency. Next, in bins that still showed > 10% contamination, contigs were separated according to comparative relative abundance of mean DNA read coverage by sample. Final bins were evaluated with CheckM again to generate the statistics in Table S1 and final bin placements in the CheckM concatenated gene tree (Fig. S2).

*Ribosomal protein tree.* The concatenated ribosomal protein tree was generated using 16 syntenic genes that have been shown to undergo limited lateral gene transfer (rpL2, 3, 4, 5, 6, 14, 15, 16, 18, 22, 24 and rpS3, 8, 10, 17, 19) (83). Ribosomal proteins for each bin were identified with Phylosift (84). Amino acid alignments of the individual ribosomal proteins were generated using MUSCLE (85) and trimmed using BMGE (86) (with the following settings: -m BLOSUM30 –g 0.5). The curated alignments were then concatenated for phylogenetic analyses and phylogeny inferred via RAxML v 8.2.8 (87) with 100 bootstrap runs (with the following settings: mpirun -np 4 -npernode 1 raxmlHPC-HYBRID-AVX -f a -m PROTCATLG -T 16 -p 12345 -x 12345 -# 100). Note this is similar to the number utilized in a previous publication for this tree with automated bootstrapping (88), and required just over 56 hours of wall clock time. The alignment is available in SI.

*Average amino acid identity.* AAI was calculated with Get Homologues (89) v. 02032017, with the following settings: –M –t 0 –n 16 –A.

*Taxonomic assignment.* Taxonomy for each bin was assigned primarily using the ribosomal protein tree. However, for bins that did not have enough ribosomal proteins to be included in the tree, or for which the placement within the tree was poorly supported, assignments were made based on the concatenated marker gene tree as part of the CheckM analysis (Fig. S2), or via 16S rRNA gene sequences, when available. 16S rRNA genes were identified via CheckM, and these sequences were aligned against the NCBI nr database using BLASTN to corroborate CheckM assignments. In the case of the SAR202 genomes, which did not have representative genomes in either the ribosomal protein tree or the CheckM tree, the 16S rRNA gene sequences for two of the three bins (43-1, 43-2) were available and aligned with the sequences used to define the SAR202 clade (23) (Fig. S5). Alignment, culling, and inference were completed with MUSCLE (85), Gblocks (90), and FastTree2 (91), respectively, with the FT_pipe script. The script is provided in SI. The 16S rRNA gene tree for subclade assignment of SAR406 (Fig. S4) was assembled by blasting the four 16S sequences predicted by CheckM against a local GenBank nt database using blastn (v. 2.2.28+) (92), selected the top 100 non-redundant hits to each sequence, and manually removing all hits to genome sequences. These were combined with previously defined SAR406 subclade reference sequences (25), fosmid 16S sequences (26), single-cell genome sequences (28), and run through alignment, culling, and inference with FT_pipe. Taxa with identical alignments were removed with RAxML v 8.2.8 (87) using default settings, and the final tree was inferred using FastTree2 (91). For putative CP genomes, taxonomy was also evaluated by examining the taxonomic identification for each of the predicted protein sequences after a BLASTP search against the NCBI nr database. Post-blast, the number of assignments to the dominant one or two taxonomic names, along with the number of assignments to "uncultured bacterium," was plotted for each genome according to the bit score quartile (Fig. S3). Quartiles were determined in R using the summary function. Bin 56 has two ribosomal protein operons on scaffold_2719/Ga0113622_1153 and scaffold_21777/Ga0113622_1009. In the ribosomal protein tree, the former placed the organism in the *Planctomycetaceae*, while the latter (which was much smaller) placed the organism in CP WS3. The majority of BLASTP annotations to the nr database matched *Planctomycetaceae* taxa, as did the 16S rRNA gene sequences found in the genome, so Bin 56 organism was designated a Planctomycetes and not WS3, and excluded from this study. The 16S rRNA gene from Bin 50 was also used to infer taxonomic identity using and established phylogeny for the WS3 clade (70) and relevant outgroups. The Bin 50 sequence was blasted against the greengenes database (Dec. 2013) with megablast, and since many of the top hits belonged to the PAUC34f clade, these were included with the sequences from Farag et al. 2017. Alignment, culling, and inference was completed with FT_pipe. Node labels were constructed with the newick utilities (93) script nw_rename.

*Metabolic reconstruction*. Post-binning, genomes were submitted individually to IMG (94) for annotation. Genome accession numbers are in Table S1, and all are publically available. Metabolic reconstruction found in Table S1 and Figs S5-7/ S11-13, came from these annotations and inspection with IMG's analysis tools, including KEGG pathway assignments and transporter predictions. Transporters highlighted for DOM uptake were identified based on information at the Transporter Classification Database (95). Carbohydrate-active enzymes (CAZymes) were predicted using the same routines as those in operation for the updates of the carbohydrate-active enzymes database (www.cazy.org) (96).

*RPKM abundance of taxa and genes.* Abundance of taxa within the sample was quantified by evaluating mapped reads using Reads-Per-Kilobase-Per-Million (RPKM) normalization (97) according to $A_{ij} = (N_{ij}/L_i) \times (1/T_j)$, where $A_{ij}$ is the abundance of bin $i$ in sample $j$, $N_{ij}$ is the number of reads that map to bin from sample $j$, $L_i$ is the length of bin $i$ in kilobases, and $T_j$ is the total number of reads in sample $j$ divided by $10^6$. These values were generated for all bins, with only the data for the 20 uncultivated bins reported here. All contigs within a given bin were artificially concatenated into "supercontigs" prior to mapping. $N_{ij}$ was generated using the samtools (82) idxstats function after mapping with BWA. The data in Fig. S7 were created by summing $(N_{ij}/L_i)$ for groups of taxa defined in Table S1 prior to multiplying by $(1/T_j)$. RNA coverage was used to evaluate both bin and gene activity for all bins. Mean coverage for each supercontig was calculated using bedtools (98) and bins were assigned a rank from lowest mean recruitment (1) to highest mean recruitment (2). Bins with particularly high or low activity (transcript abundance) relative to their abundance (genome abundance) were identified using rank-residuals, calculated as follows: On a plot of DNA coverage rank vs. RNA coverage rank, residuals for each bin or gene were calculated from the identity. As the rank-residuals followed a Gaussian distribution, bins with a residual that was > 1 s.d. from the rank-residual mean were classified as having higher-than-expected transcriptional activity; bins with a residual that was < 1 s.d. from the mean were classified as having lower-than-expected transcriptional activity. RPKM values were also calculated for every gene in every bin analogously to that for bins, using RNA mapping values extracted with the bedtools multicov function. Sample E2 was omitted from gene-specific calculations as only 4588 transcriptomic reads mapped successfully from this sample, compared to >100,000 from other samples. 17,827 of 140,347 genes had no evidence of expression in any sample and so were removed from further analysis. 3,840 genes recruited reads in all remaining samples. All calculations are available in Table S1 or the R markdown document Per.gene.RPKM.Rmd in Supplemental Information. Table S1 includes only analyzed data for the uncultivated bins reported in this study. Note that RPKM values indicate abundance measurements across a small number of samples. While we can evaluate the relative expression of genes for those samples, our dataset lacks sufficient power to evaluate estimates of significance in differential expression.

*nrfA sequence assessment.* Initial annotation of our bins identified putative homologs to the *nrfAH* genes associated with dissimilatory nitrite reduction to ammonia. Since *nrfA*-type nitrite reductases can be misannotated due to homology with other nitrite reductases, annotation for these genes was curated with phylogenetic analysis using known *nrfA* genes (48) (Fig. 3) obtained via Dr. Welsh (personal communication). Alignment, culling, and inference were completed with the FT_pipe script. The tree was rooted on the designated outgroup octaheme nitrite reductase sequence from *Thioalkalivibrio nitratireducens* ONR. Node labels were constructed with the newick utilities (93) script nw_rename. Visualization of the alignment (Fig. S9) to confirm the presence of the first CXXCK/CXXCH and highly conserved KXQH/KXRH catalytic site was completed with the MSAViewer (99) online using the un-culled *nrfA* alignment as input.

*SFam homology searches.* To identify group specific expansions in particular gene families, we performed a homology search of all predicted protein coding sequences in each bin against the Sifted Families (SFam) database (51) using hmmsearch (HMMER 3.1b (100)) with default settings except for the utilization of 16 cpus per search.

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## Author contributions

JCT and OUM designed the study. LEG, NNR, and JCT collected samples. NNR provided processed oceanographic data. LEG and OUM extracted, quantified, and determined quality of nucleic acids. JCT, KWS, and BJB reconstructed the genomes. KWS, BJB, BT, BH, and JCT conducted downstream analyses. JCT led manuscript writing and all co-authors evaluated and contributed edits.

## Competing financial interests

The authors declare no competing financial interests.

**Table 1.** Genome characteristics for the 20 bins associated with uncultivated lineages.

| IMG Genome ID | Bin Id | Taxonomy | Compl % | Contam % | Strain het. | Scaff. | Longest scaff. (bp) | Size (bp) | Genes | GC (fract.) | Coding density (fract.) | Estim. Compl. Size (Mbp) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **2651870035** | **43-1** | Chloroflexi (SAR202) | 90.3 | 0 | 0 | 69 | 161242 | 1972793 | 1882 | 0.52 | 0.88 | 2.2 |
| **2651870036** | **43-2** | Chloroflexi (SAR202) | 88.6 | 4.1 | 15.4 | 134 | 157345 | 2402386 | 2373 | 0.52 | 0.91 | 2.7 |
| **2651870034** | **43** | Chloroflexi (SAR202) | 83.2 | 0.1 | 100 | 179 | 90503 | 2475308 | 2392 | 0.53 | 0.89 | 3.0 |
| **2693429801** | **45** | Marinimicrobia (SAR406) –B | 89.8 | 5.5 | 71.4 | 124 | 105140 | 2811623 | 2487 | 0.47 | 0.93 | 3.1 |
| **2651870052** | **45-1** | Marinimicrobia (SAR406) –B | 85.2 | 0.1 | 100 | 144 | 100582 | 2410233 | 2235 | 0.49 | 0.93 | 2.8 |
| **2693429802** | **45-2** | Marinimicrobia (SAR406) –B | 79.3 | 1.8 | 12.5 | 287 | 61408 | 2811444 | 2554 | 0.46 | 0.94 | 3.5 |
| **2651870053** | **51-1** | Marinimicrobia (SAR406) –A | 73.6 | 1.7 | 50 | 75 | 191525 | 1901306 | 1835 | 0.39 | 0.95 | 2.6 |
| **2651870051** | **51** | Marinimicrobia (SAR406) –A | 21.3 | 0 | 0 | 115 | 16923 | 578802 | 686 | 0.41 | 0.95 | 2.7 |
| **2651870038** | **15** | Euryarchaeota (MGII) | 83.2 | 1.6 | 0 | 43 | 255599 | 1885130 | 1614 | 0.62 | 0.95 | 2.3 |
| **2651870039** | **17** | Euryarchaeota (MGII) | 81.9 | 0.1 | 50 | 88 | 137319 | 1803861 | 1564 | 0.43 | 0.96 | 2.2 |
| **2651870037** | **14** | Euryarchaeota (MGII) | 71.2 | 0.8 | 100 | 80 | 90069 | 1389909 | 1305 | 0.54 | 0.94 | 2.0 |
| **2651870040** | **18** | Euryarchaeota (MGII) | 61.1 | 0.8 | 100 | 155 | 20633 | 1033226 | 1025 | 0.50 | 0.96 | 1.7 |
| **2651870042** | **38** | Euryarchaeota (MGII) | 27.1 | 0 | 0 | 138 | 12893 | 615290 | 610 | 0.55 | 0.96 | 2.3 |
| **2651870041** | **17-1** | Euryarchaeota (MGII) | 16.6 | 2.8 | 33.3 | 123 | 16952 | 538052 | 566 | 0.41 | 0.95 | 3.2 |
| **2693429807** | **13** | Unclassified (ACD39) | 89.8 | 5.1 | 20 | 401 | 75104 | 4269849 | 3686 | 0.47 | 0.93 | 4.8 |
| **2693429799** | **40** | Parcubacteria (OD1) | 71.9 | 15.1 | 75 | 97 | 65104 | 1086283 | 1208 | 0.52 | 0.92 | 1.5 |
| **2693429797** | **16** | Peregrinibacteria | 83.2 | 0.3 | 100 | 67 | 59308 | 1384712 | 1318 | 0.39 | 0.93 | 1.7 |
| **2693429798** | **39** | Peregrinibacteria | 49.9 | 0.3 | 100 | 131 | 18806 | 747520 | 809 | 0.45 | 0.95 | 1.5 |
| **2693429804** | **50** | Unclassified (PAUC34f) | 84.8 | 1.4 | 0 | 455 | 76269 | 5346994 | 5484 | 0.58 | 0.92 | 6.3 |
| **2693429803** | **48** | Unclassified (PAUC34f) | 51.9 | 2.2 | 0 | 470 | 20176 | 2566149 | 2596 | 0.55 | 0.94 | 4.9 |

**Figure 1.** Metabolic reconstruction of Marine Group II Euryarchaeota, SAR406, and SAR202, based on the top three or four most complete genomes. Colors indicate pathway elements based on the number of genomes in which they were recovered, according to the key. Black outlines and/or arrows indicate genes that were not observed. Numbers correspond to annotations supplied in Table S2.

**Figure 2.** Metabolic reconstruction of the Candidate Phylum members PAUC34f, Parcubacteria (OD1), Peregrinibacteria, and ACD39 (Bin 13). Colors indicate pathway elements based on the number of genomes in which they were recovered, according to the key. Black outlines and/or arrows indicate genes that were not observed. Numbers correspond to annotations supplied in Table S2.

**Figure 3.** Relative DNA to RNA recruitment rank for each genome, by sample. Colors indicate the relative difference in the ratio of rank based on total RNA and DNA mapping. Red indicates a higher RNA recruitment rank compared to DNA recruitment rank, and vice-versa for blue. + and - symbols indicate bins where the rank-residual from the identity in RNA vs. DNA read mapping was more or less than one standard deviation beyond 0, respectively. Dendrograms were calculated using an Unweighted Pair Group Method with Arithmetic Mean (UPGMA) from Euclidian distances of rank residuals across all samples and bins.

**Figure 4.** Expression of predicted respiratory genes. RPKM values of RNA recruitment for each gene, by sample, are depicted with colors according to the key (yellow to blue follows increasing intensity). Genes are grouped by bin, taxonomic affiliation, and specific respiratory process. DNRA- dissimilatory nitrite reduction to ammonia.

**Figure 5.** Expression of predicted CAZy genes. RPKM values or RNA recruitment for each gene, by sample, are depicted with colors according to the key (yellow to red follows increasing intensity). Genes are grouped by bin, taxonomic affiliation, and general CAZy categories. CE- carbohydrate esterase; GH- glycoside hydrolase; GT- glycosyltransferase; CBM- carbohydrate binding module.

Supplemental Information

**Table S1.** Spreadsheet (Table_S1.xlsx) containing information on taxonomy, CheckM results, IMG statistics, partial metabolic reconstruction, transporter classifications, CAZy predictions, sample chemical data, RPKM values and gene neighborhoods for WS3 cytochrome c oxidases and *nrfA* genes from SAR406 and WS3.

**Table S2.** Gene annotations associated with Figures 1 and 2. Numbers correspond to those in the figures.

**Figure S1.** Maximum likelihood tree of concatenated ribosomal protein coding genes. Values at internal nodes indicate bootstrap support (n=100). Scale bar indicates changes per position.

**Figure S2.** Phylogenetic placement of bins based on CheckM.

**Figure S3.** Annotations of protein-coding gene sequence best blastp hits in the nr database, divided into quartiles by bit score, for CP bacteria.

**Figure S4.** SAR406 16S rRNA gene phylogeny. Genes recovered from assembled bins have 45* or 51* designations. Values at nodes indicate Shimodaira-Hasegawa "like" values (91). Scale bar indicates changes per position.

**Figure S5.** SAR202 16S rRNA gene phylogeny. Genes recovered from assembled bins are indicated as 43-*. Subclades are designated according to Morris et al. 2004, and the tree is rooted according to Figure 1 in that publication. Values at nodes indicate Shimodaira-Hasegawa "like" values (91). Scale bar indicates changes per position.

**Figure S6.** 16S rRNA gene phylogeny of the WS3 clade (70) with added PAUC34f sequences from the GreenGenes database and the Bin 50 sequence. Tree is rooted on the Archaea according to Fig. S1 in Farag et al. 2017. Values at nodes indicate Shimodaira-Hasegawa "like" values (91). Scale bar indicates changes per position.

**Figure S7.** Metagenomic RPKM values for each group, comprised of aggregated values for each bin within the group. Values are plotted according to sample and colored according to the dissolved oxygen (DO) concentration from where the sample was taken.

**Figure S8.** Phylogenetic tree of predicted *nrfA* genes in SAR406 and WS3. Additional taxa are from Figure 3 in Welch et al., 2014. The tree was rooted at the midpoint. Values at nodes indicate Shimodaira-Hasegawa "like" values (91). Scale bar indicates changes per position.

**Figure S9.** Conserved catalytic motifs within the *nrfA* gene. A- black square surrounds the first heme-binding CXXCK/CXXCH motif. B- black square surrounds the catalytic KXQH/KXRH motif. The alignment follows highlighting found in Welsh *et al.*, 2014 (48). All genes numbers from this study are indicated as 26536*, corresponding to rows 64 and 66-68.

**Additional Supplemental Information** such as scripts, workflows, and key files, including fasta files for each tree, are provided as a link hosted at the Thrash Lab website: http://thethrashlab.com/publications.

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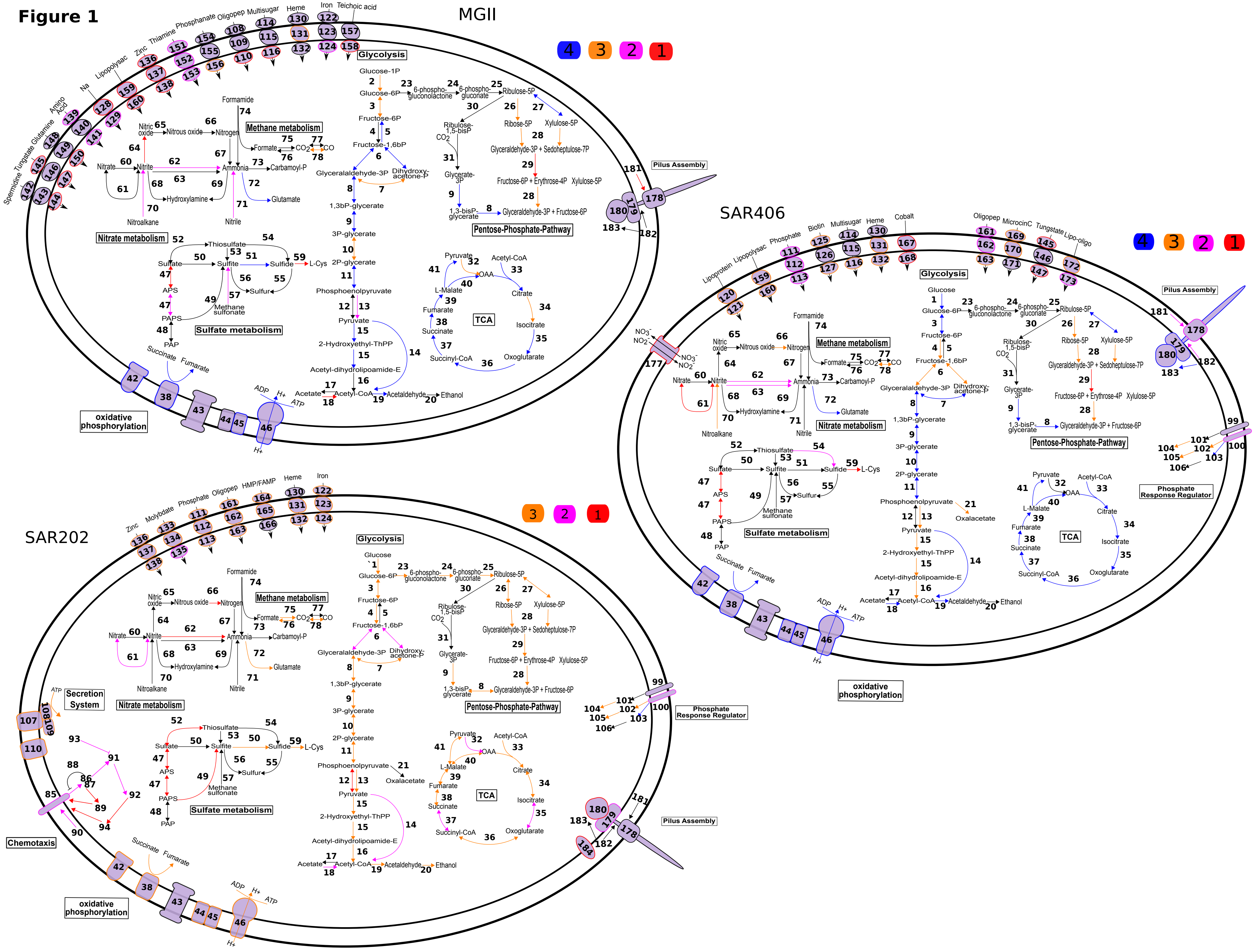
**Figure 1**


MGII
SAR406
SAR202
4
3
2
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Glycolysis
Pentose-Phosphate-Pathway
Methane metabolism
Nitrate metabolism
Sulfate metabolism
TCA
oxidative phosphorylation
Pilus Assembly
Phosphate Response Regulator
Secretion System
Chemotaxis
Spermidine
Tungstate
Glutamine
Amino Acid
Na
Lipopolysac
Zinc
Thiamine
Phosphanate
Oligopep
Multisugar
Heme
Iron
Teichoic acid
Lipoprotein
Phosphate
Biotin
Cobalt
MicrocinC
Tungstate
Lipo-oligo
Molybdate
HMP/FAMP
Glucose-1P
Glucose
Glucose-6P
6-phospho-gluconolactone
6-phospho-gluconate
Ribulose-5P
Ribose-5P
Xylulose-5P
Ribulose-1,5-bisP
CO2
Glycerate-3P
1,3-bisP-glycerate
Glyceraldehyde-3P + Sedoheptulose-7P
Fructose-6P + Erythrose-4P
Glyceraldehyde-3P + Fructose-6P
Fructose-6P
Fructose-1,6bP
Glyceralaldehyde-3P
Dihydroxy-acetone-P
1,3bP-glycerate
3P-glycerate
2P-glycerate
Phosphoenolpyruvate
Oxalacetate
Pyruvate
2-Hydroxyethyl-ThPP
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Acetaldehyde
Ethanol
OAA
Citrate
Isocitrate
Oxoglutarate
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Succinate
Fumarate
L-Malate
Formamide
Formate
CO
Carbamoyl-P
Nitric oxide
Nitrous oxide
Nitrogen
Nitrate
Nitrite
Ammonia
Hydroxylamine
Glutamate
Nitroalkane
Nitrile
NO3-
NO2-
Thiosulfate
Sulfate
Sulfite
Sulfide
L-Cys
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PAPS
PAP
Methane sulfonate
ADP
H+
ATP
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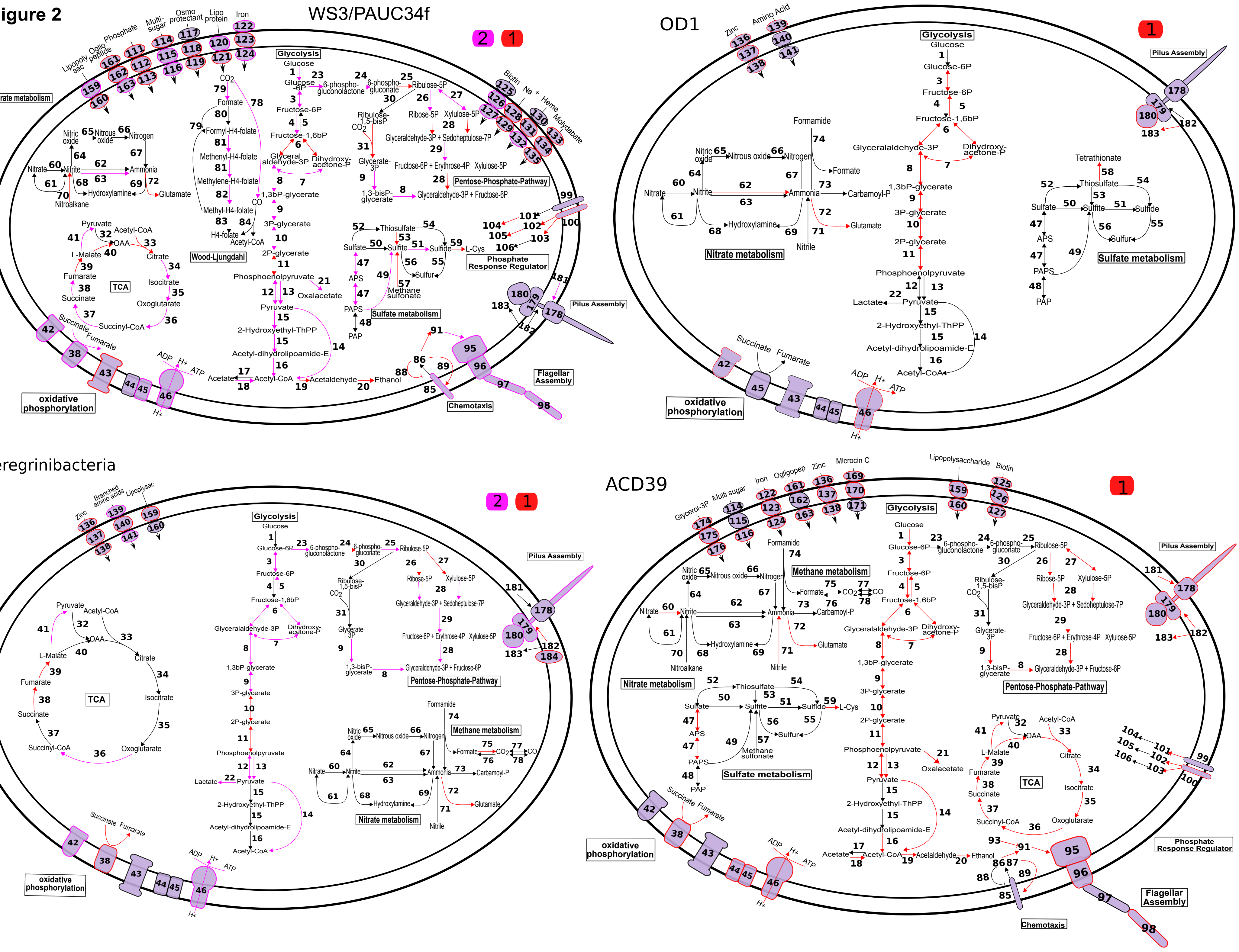
**Figure 2**



WS3/PAUC34f

OD1

Peregrinibacteria

ACD39

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TCA
Sulfate metabolism
Methane metabolism
Phosphate Response Regulator
Pilus Assembly
Flagellar Assembly
Chemotaxis
oxidative phosphorylation
Lipopoly sac
Oglio peptide
Phosphate
Multi-sugar
Osmo protectant
Lipo protein
Iron
Biotin
Na +
Heme
Molydabate
Zinc
Amino Acid
Branched amino acids
Lipoplysac
Glycerol-3P
Multi sugar
Oligopep
Microcin C
Lipopolysaccharide
Glucose
Glucose-6P
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6-phospho-gluconate
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Ribulose-1,5-bisP
Ribose-5P
Xylulose-5P
Fructose-6P
Fructose-1,6bP
Glyceraldehyde-3P
Dihydroxy-acetone-P
Glyceraldehyde-3P + Sedoheptulose-7P
Fructose-6P + Erythrose-4P
Glyceraldehyde-3P + Fructose-6P
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Oxalacetate
Pyruvate
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Acetate
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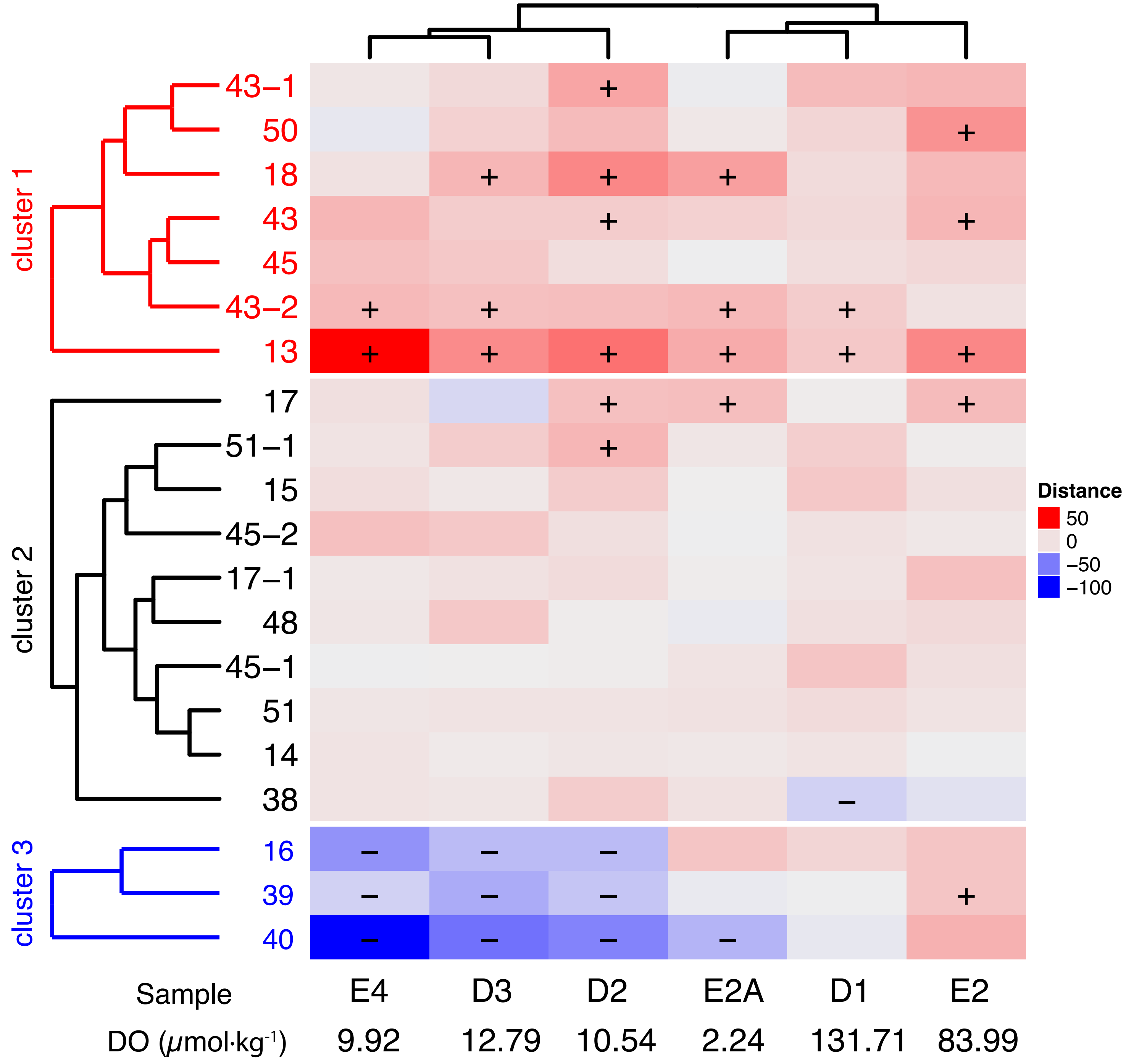
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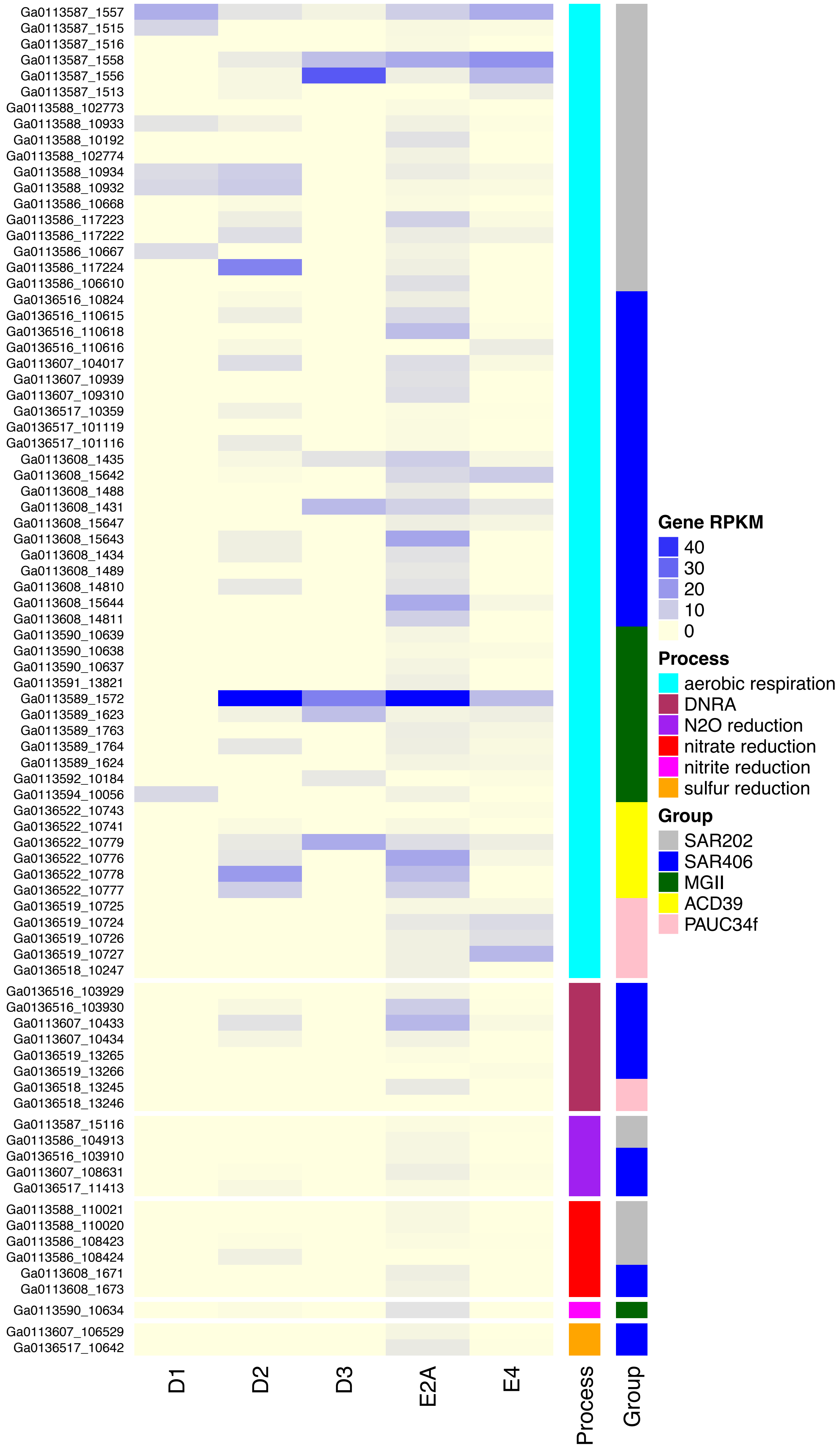

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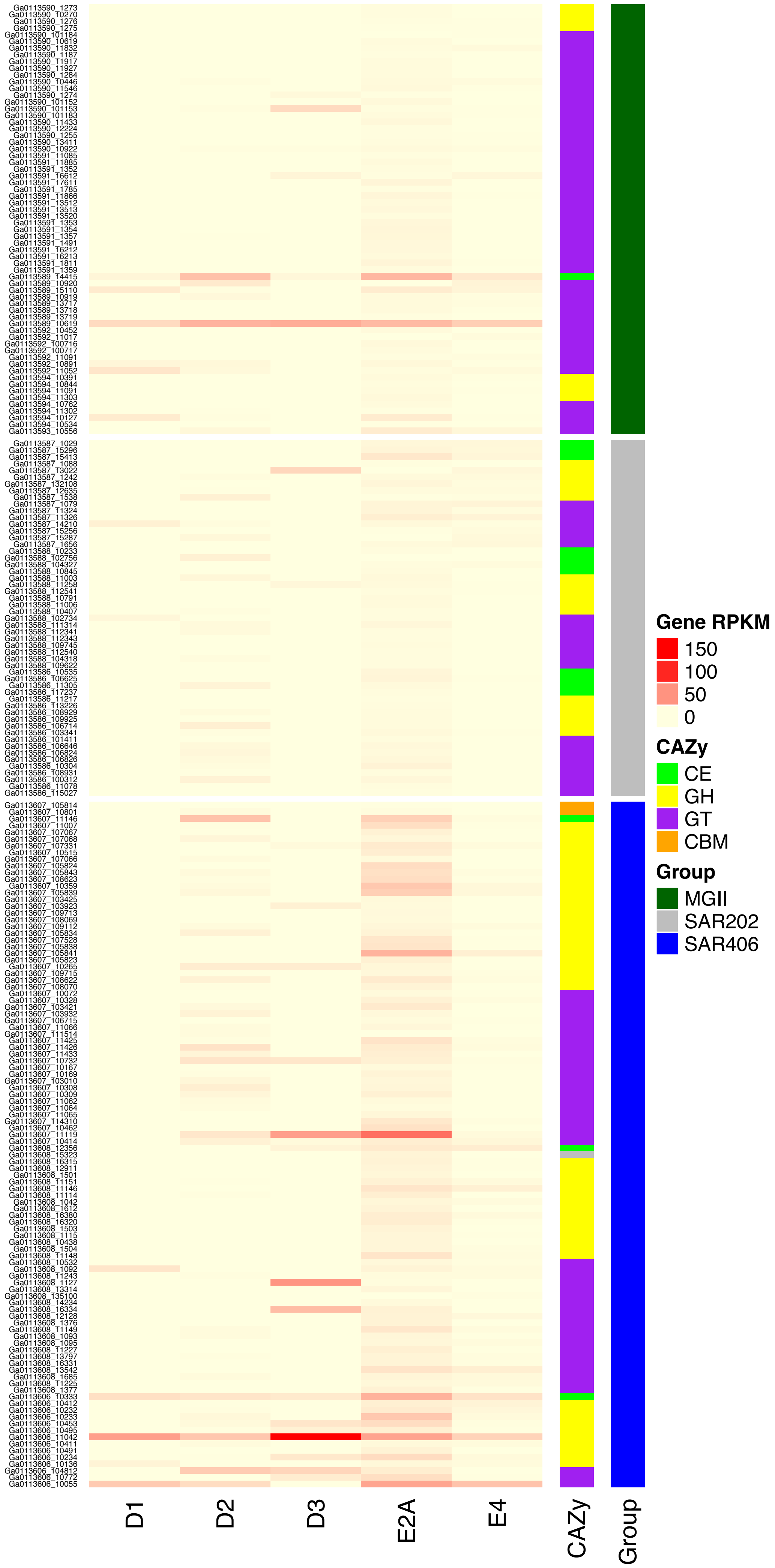
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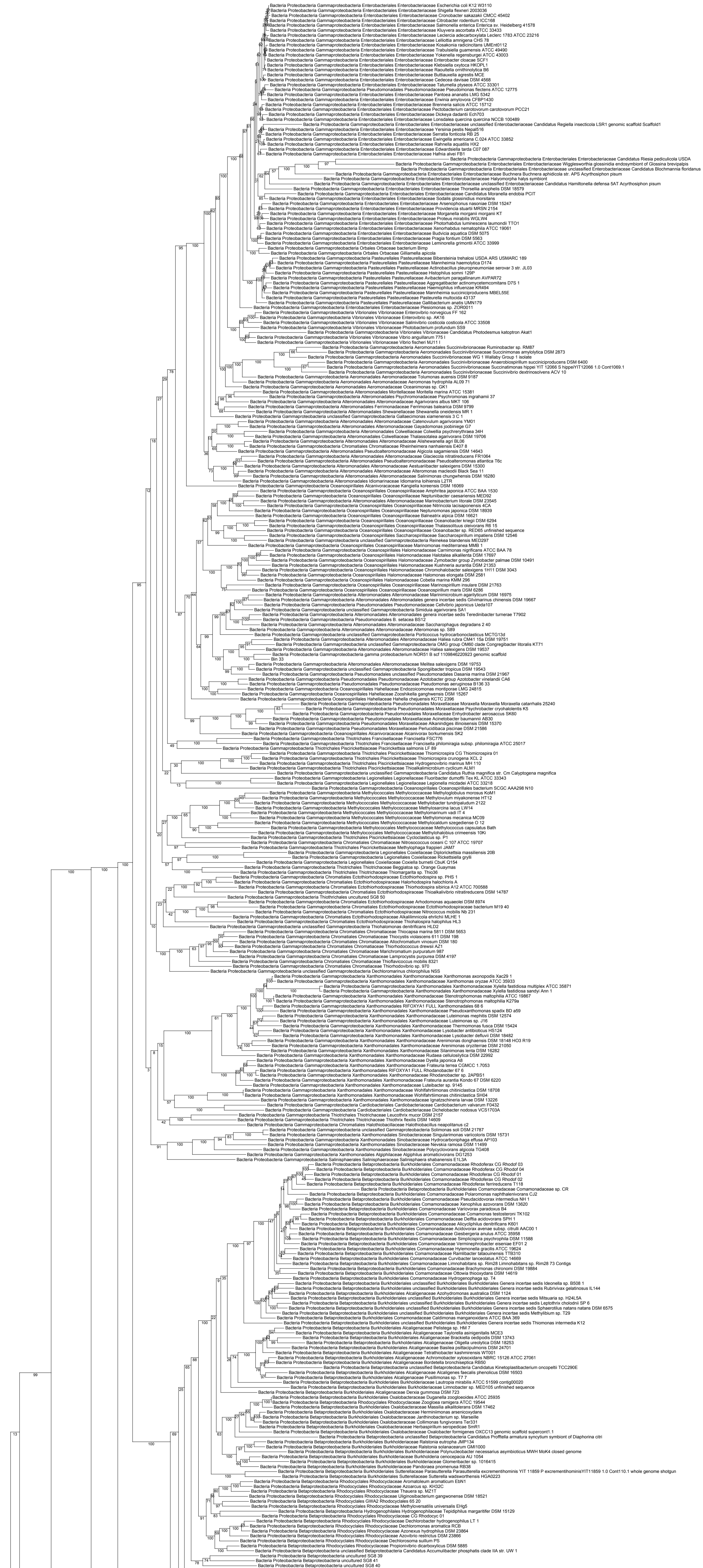
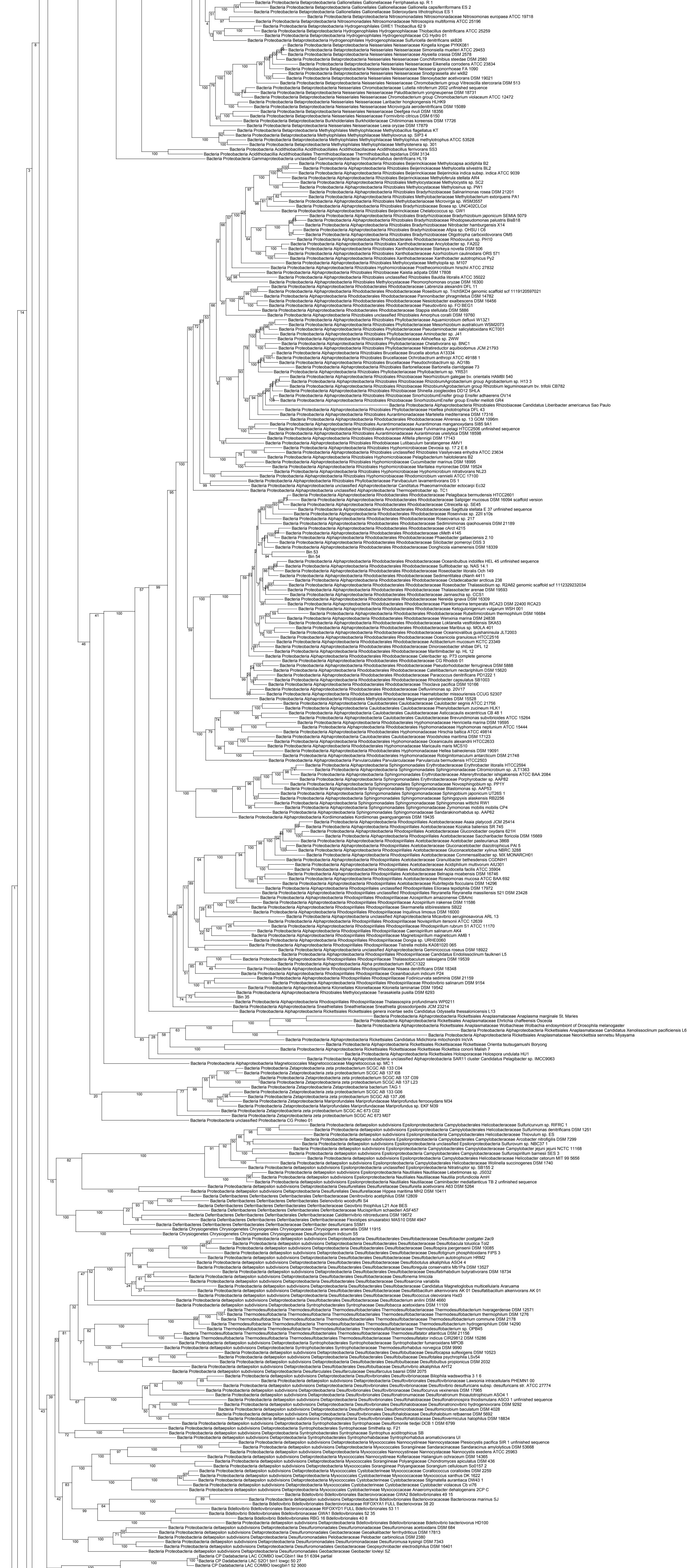
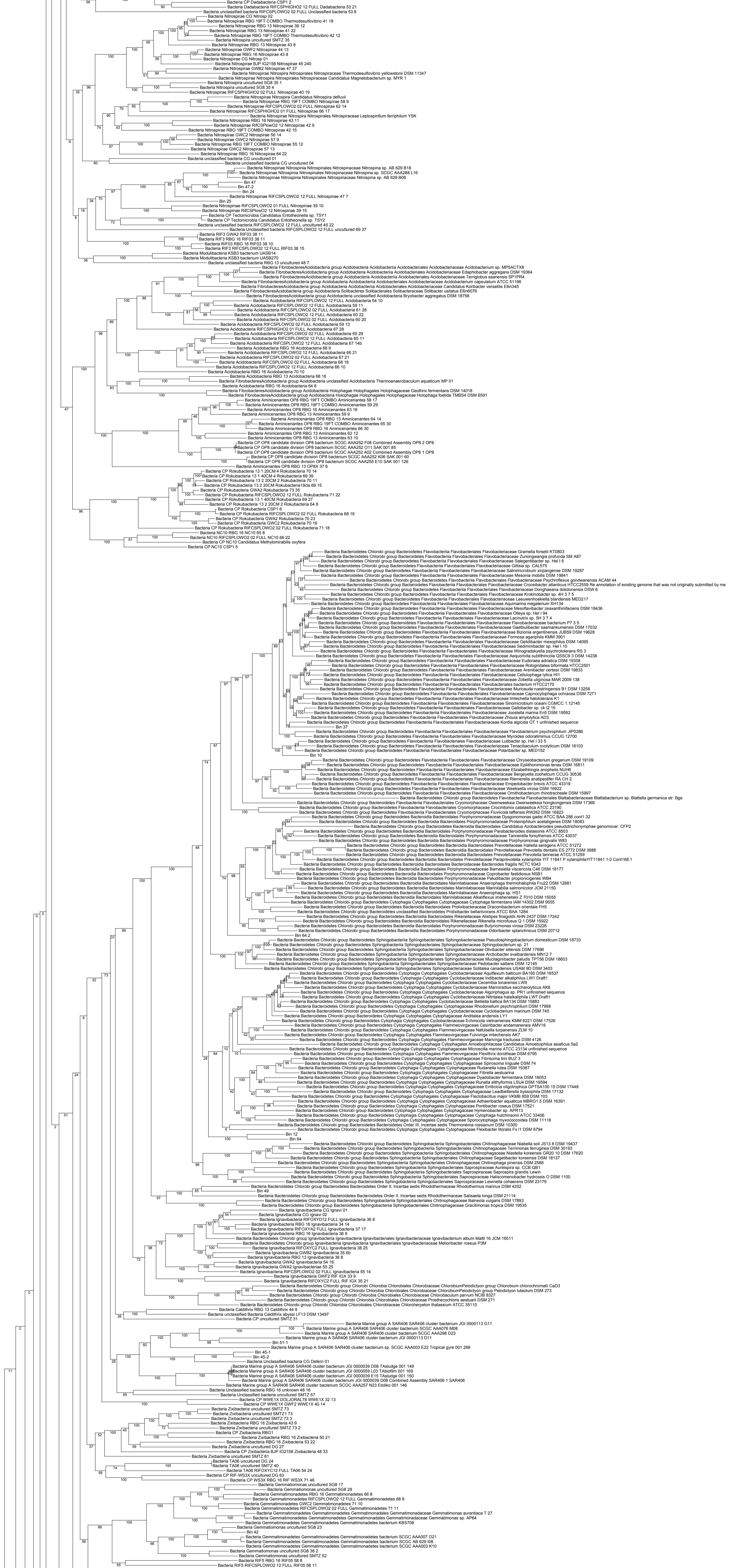
Figure S1



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Bacteria Bacteroidetes Chlorobi group Bacteroidetes Flavobacteriia Flavobacteriales Flavobacteriaceae Gelidibacter mesophilus DSM 14095
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Flavobacteriia Flavobacteriales Flavobacteriaceae Sediminibacter sp. Hel I 10
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Flavobacteriia Flavobacteriales Flavobacteriaceae Winogradskyella psychrotolerans RS 3
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Flavobacteriia Flavobacteriales Flavobacteriaceae Aequorivita sublithincola QSSC9 3 DSM 14238
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Flavobacteriia Flavobacteriales Flavobacteriaceae Eudoraea adriatica DSM 19308
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Flavobacteriia Flavobacteriales Flavobacteriaceae Robiginitalea biformata HTCC2501
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Flavobacteriia Flavobacteriales Flavobacteriaceae Arenibacter certesii DSM 19833
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Flavobacteriia Flavobacteriales Flavobacteriaceae Cellulophaga lytica HI1
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Flavobacteriia Flavobacteriales Flavobacteriaceae Zobellia uliginosa MAR 2009 138
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Flavobacteriia Flavobacteriales Flavobacteriaceae bacterium HTCC2170
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Flavobacteriia Flavobacteriales Flavobacteriaceae Muricauda ruestringensis B1 DSM 13258
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Flavobacteriia Flavobacteriales Flavobacteriaceae Capnocytophaga ochracea DSM 7271
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Flavobacteriia Flavobacteriales Flavobacteriaceae Imtechella halotolerans K1
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Flavobacteriia Flavobacteriales Flavobacteriaceae Sinomicrobium oceani CGMCC 1.12145
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Flavobacteriia Flavobacteriales Flavobacteriaceae Galbibacter sp. ck I2 15
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Flavobacteriia Flavobacteriales Flavobacteriaceae Joostella marina En5 DSM 19592
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Flavobacteriia Flavobacteriales Flavobacteriaceae Zhouia amylolytica AD3
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Flavobacteriia Flavobacteriales Flavobacteriaceae Kordia algicida OT 1 unfinished sequence
Bin 37
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Flavobacteriia Flavobacteriales Flavobacteriaceae Flavobacterium psychrophilum JIP0286
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Flavobacteriia Flavobacteriales Flavobacteriaceae Myroides odoratimimus CCUG 12700
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Flavobacteriia Flavobacteriales Flavobacteriaceae Lutibacter sp. Hel I 33 5
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Flavobacteriia Flavobacteriales Flavobacteriaceae Tenacibaculum ovolyticum DSM 18103
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Flavobacteriia Flavobacteriales Flavobacteriaceae Polaribacter sp. MED152
Bin 10
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Flavobacteriia Flavobacteriales Flavobacteriaceae Chryseobacterium gregarium DSM 19109
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Flavobacteriia Flavobacteriales Flavobacteriaceae Epilithonimonas tenax DSM 16811
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Flavobacteriia Flavobacteriales Flavobacteriaceae Elizabethkingia anophelis NUHP1
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Flavobacteriia Flavobacteriales Flavobacteriaceae Bergeyella zoohelcum CCUG 30536
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Flavobacteriia Flavobacteriales Flavobacteriaceae Riemerella anatipestifer RA CH 2
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Bacteria Bacteroidetes Chlorobi group Bacteroidetes Flavobacteriia Flavobacteriales Flavobacteriaceae Weeksella virosa DSM 16922
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Flavobacteriia Flavobacteriales Flavobacteriaceae Ornithobacterium rhinotracheale DSM 15997
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Flavobacteriia Flavobacteriales Blattabacteriaceae Blattabacterium sp. Blattella germanica str. Bge
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Flavobacteriia Flavobacteriales Cryomorphaceae Owenweeksia hongkongensis DSM 17368
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Flavobacteriia Flavobacteriales Cryomorphaceae Crocinitomix catalasitica ATCC 23190
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Bacteria Bacteroidetes Chlorobi group Bacteroidetes Bacteroidia Bacteroidales Porphyromonadaceae Dysgonomonas gadei ATCC BAA 286 cont1.32
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Bacteria Bacteroidetes Chlorobi group Bacteroidetes Bacteroidia Bacteroidales Candidatus Azobacteroides pseudotrichonymphae genomovar. CFP2
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Bacteroidia Bacteroidales Porphyromonadaceae Parabacteroides distasonis ATCC 8503
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Bacteroidia Bacteroidales Porphyromonadaceae Tannerella forsythensis ATCC 43037
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Bacteria Bacteroidetes Chlorobi group Bacteroidetes Bacteroidia Bacteroidales Prevotellaceae Hallella seregens ATCC 51272
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Bacteroidia Bacteroidales Prevotellaceae Prevotella dentalis ES 2772 DSM 3688
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Bacteria Bacteroidetes Chlorobi group Bacteroidetes Bacteroidia Bacteroidales Prevotellaceae Paraprevotella xylaniphila YIT 11841 P xylaniphilaYIT11841 1.0 Cont168.1
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Bacteroidia Bacteroidales Bacteroidaceae Bacteroides fragilis NCTC 9343
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Bacteroidia Bacteroidales Porphyromonadaceae Barnesiella viscericola C46 DSM 18177
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Bacteria Bacteroidetes Chlorobi group Bacteroidetes Bacteroidia Bacteroidales Porphyromonadaceae Paludibacter propionicigenes WB4
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Bacteroidia Bacteroidales Marinilabiaceae Anaerophaga thermohalophila Fru22 DSM 12881
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Bacteroidia Bacteroidales Marinilabiaceae Marinilabilia salmonicolor JCM 21150
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Bacteroidia Bacteroidales Marinilabiaceae Anaerophaga sp. HS1
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Bacteroidia Bacteroidales Marinilabiaceae Alkaliflexus imshenetskii Z 7010 DSM 15055
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Cytophagia Cytophagales Cytophagaceae Cytophaga fermentans IAM 14302 DSM 9555
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Bacteria Bacteroidetes Chlorobi group Bacteroidetes Bacteroidia Bacteroidales Rikenellaceae Alistipes finegoldii AHN 2437 DSM 17242
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Bin 64 2
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Bacteria Bacteroidetes Chlorobi group Bacteroidetes Sphingobacteriia Sphingobacteriales Sphingobacteriaceae Mucilaginibacter paludis TPT56 DSM 18603
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Sphingobacteriia Sphingobacteriales Sphingobacteriaceae Pedobacter saltans DSM 12145
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Sphingobacteriia Sphingobacteriales Sphingobacteriaceae Solitalea canadensis USAM 9D DSM 3403
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Bacteria Bacteroidetes Chlorobi group Bacteroidetes Cytophagia Cytophagales Cyclobacteriaceae Indibacter alkaliphilus LW1 Draft1
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Cytophagia Cytophagales Cyclobacteriaceae Cecembia lonarensis LW9
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Cytophagia Cytophagales Cyclobacteriaceae Marinilradius saccharolyticus AK6
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Cytophagia Cytophagales Cyclobacteriaceae Algoriphagus sp. PR1 unfinished sequence
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Bacteria Bacteroidetes Chlorobi group Bacteroidetes Cytophagia Cytophagales Flammeovirgaceae Flexithrix dorotheae DSM 6795
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Cytophagia Cytophagales Cytophagaceae Fibrisoma limi BUZ 3
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Bacteria Bacteroidetes Chlorobi group Bacteroidetes Cytophagia Cytophagales Cytophagaceae Fibrella aestuarina
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Cytophagia Cytophagales Cytophagaceae Dyadobacter fermentans DSM 18053
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Cytophagia Cytophagales Cytophagaceae Runella slithyformis LSU4 DSM 19594
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Cytophagia Cytophagales Cytophagaceae Emticicia oligotrophica GPTSA100 15 DSM 17448
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Cytophagia Cytophagales Cytophagaceae Leadbetterella byssophila DSM 17132
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Cytophagia Cytophagales Cytophagaceae Flectobacillus major VKMB 859 DSM 103
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Cytophagia Cytophagales Cytophagaceae Adhaeribacter aquaticus MBRG1.5 DSM 16391
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Cytophagia Cytophagales Cytophagaceae Pontibacter roseus DSM 17521
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Bacteria Bacteroidetes Chlorobi group Bacteroidetes Bacteroidetes Order III. Incertae sedis Thermonema rossianum DSM 10300
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Cytophagia Cytophagales Cytophagaceae Flexibacter litoralis Fx l1 DSM 6794
Bin 12
Bin 64
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Sphingobacteriia Sphingobacteriales Chitinophagaceae Niabella soli JS13 8 DSM 19437
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Sphingobacteriia Sphingobacteriales Chitinophagaceae Terrimonas ferruginea DSM 30193
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Sphingobacteriia Sphingobacteriales Chitinophagaceae Niastella koreensis GR20 10 DSM 17620
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Bacteria Bacteroidetes Chlorobi group Bacteroidetes Sphingobacteriia Sphingobacteriales Saprospiraceae Aureispira sp. CCB QB1
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Sphingobacteriia Sphingobacteriales Saprospiraceae Saprospira grandis Lewin
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Sphingobacteriia Sphingobacteriales Saprospiraceae Haliscomenobacter hydrossis O DSM 1100
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Sphingobacteriia Sphingobacteriales Saprospiraceae Lewinella cohaerens DSM 23179
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Bacteroidetes Order II. Incertae sedis Rhodothermaceae Rhodothermus marinus DSM 4252
Bin 49
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Bacteroidetes Order II. Incertae sedis Rhodothermaceae Salisaeta longa DSM 21114
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Sphingobacteriia Sphingobacteriales Chitinophagaceae Balneola vulgaris DSM 17893
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Sphingobacteriia Sphingobacteriales Chitinophagaceae Gracilimonas tropica DSM 19535
Bacteria Ignavibacteria CG Ignavi 01
Bacteria Ignavibacteria CG Ignavi 02
Bacteria Ignavibacteria RIFOXYD12 FULL Ignavibacteria 36 8
Bacteria Ignavibacteria RBG 16 Ignavibacteria 34 14
Bacteria Ignavibacteria RIFOXYA2 FULL Ignavibacteria 37 17
Bacteria Ignavibacteria RBG 16 Ignavibacteria 36 9
Bacteria Bacteroidetes Chlorobi group Ignavibacteriae Ignavibacteria Ignavibacteriales Ignavibacteriaceae Ignavibacterium album Mat9 16 JCM 16511
Bacteria Bacteroidetes Chlorobi group Ignavibacteriae Ignavibacteria Ignavibacteriales Ignavibacteriaceae Melioribacter roseus P3M
Bacteria Ignavibacteria RIFOXYC2 FULL Ignavibacteria 38 25
Bacteria Ignavibacteria GWB2 Ignavibacteria 35 6b
Bacteria Ignavibacteria RBG 13 Ignavibacteria 36 8
Bacteria Ignavibacteria GWA2 Ignavibacteria 54 16
Bacteria Ignavibacteria GWA2 Ignavibacteriae 55 25
Bacteria Ignavibacteria RIFCSPLOWO2 02 FULL Ignavibacteria 55 14
Bacteria Ignavibacteria GWF2 RIF IGX 33 9
Bacteria Ignavibacteria RIFOXYC2 FULL RIF IGX 35 21
Bacteria Bacteroidetes Chlorobi group Chlorobi Chlorobia Chlorobiales Chlorobiaceae ChlorobiumPelodictyon group Chlorobium chlorochromatii CaD3
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Bacteria Bacteroidetes Chlorobi group Chlorobi Chlorobia Chlorobiales Chlorobiaceae Chloroherpeton thalassium ATCC 35110
Bacteria Calditrhix RBG 13 Calditrhix 44 9
Bacteria unclassified Bacteria Caldithrix abyssi LF13 DSM 13497
Bacteria CP uncultured SMTZ 31
Bacteria Marine group A SAR406 SAR406 cluster bacterium JGI 0000113 G11
Bacteria Marine group A SAR406 SAR406 cluster bacterium SCGC AAA076 M08
Bacteria Marine group A SAR406 SAR406 cluster bacterium SCGC AAA298 D23
Bacteria Marine group A SAR406 SAR406 cluster bacterium JGI 0000113 D11
Bin 51-1
Bacteria Marine group A SAR406 SAR406 cluster bacterium sp. SCGC AAA003 E22 Tropical gyre 001 268
Bin 45-1
Bin 45-2
Bacteria Unclassified bacteria CG Deferri 01
Bacteria Marine group A SAR406 SAR406 cluster bacterium JGI 0000039 D08 TAsludge 001 149
Bacteria Marine group A SAR406 SAR406 cluster bacterium JGI 0000059 L03 TAbiofilm 001 169
Bacteria Marine group A SAR406 SAR406 cluster bacterium JGI 0000039 E15 TAsludge 001 150
Bacteria Marine group A SAR406 SAR406 cluster bacterium JGI 0000039 D08 Combined Assembly SAR406 1 SAR406
Bacteria Marine group A SAR406 SAR406 cluster bacterium SCGC AAA257 N23 Etoliko 001 146
Bacteria Unclassified bacteria RBG 16 unknown 48 16
Bacteria Unclassified bacteria uncultured SMTZ 57
Bacteria CP WWE1X DOLJORAL78 WWE1X 32 13
Bacteria CP WWE1X GWF2 WWE1X 40 14
Bacteria Zixibacteria uncultured SMTZ 73
Bacteria Zixibacteria uncultured SMTZ1 73
Bacteria Zixibacteria uncultured SMTZ 73 3
Bacteria Zixibacteria RBG 16 Zixibacteria 43 9
Bacteria Zixibacteria uncultured SMTZ 73 2
Bacteria CP Zixibacteria RBG1
Bacteria Zixibacteria RBG 16 Zixibacteria 50 21
Bacteria Zixibacteria RBG 16 Zixibacteria 53 22
Bacteria Zixibacteria uncultured DG 27
Bacteria CP Zixibacteria BJP IG2158 Zixibacteria 48 33
Bacteria Zixibacteria uncultured SMTZ 81
Bacteria TA06 uncultured DG 24
Bacteria TA06 uncultured SMTZ 40
Bacteria TA06 RIFOXYC12 FULL TA06 54 24
Bacteria TA06 uncultured DG 63
Bacteria CP RIF-WS3X uncultured DG 63
Bacteria CP WS3X RBG 16 RIF WS3X 71 46
Bacteria Gemmatimonas uncultured SG8 17
Bacteria Gemmatimonas uncultured SG8 28
Bacteria Gemmatimonadetes RBG 16 Gemmatimonadetes 66 8
Bacteria Gemmatimonadetes RIFCSPLOWO2 12 FULL Gemmatimonadetes 68 9
Bacteria Gemmatimonadetes GWC2 Gemmatimonadetes 71 10
Bacteria Gemmatimonadetes RIFCSPLOWO2 02 FULL Gemmatimonadetes 71 11
Bacteria Gemmatimonadetes Gemmatimonadetes Gemmatimonadales Gemmatimonadaceae Gemmatimonas aurantiaca T 27
Bacteria Gemmatimonadetes Gemmatimonadetes Gemmatimonadales Gemmatimonadaceae Gemmatimonas sp. AP64
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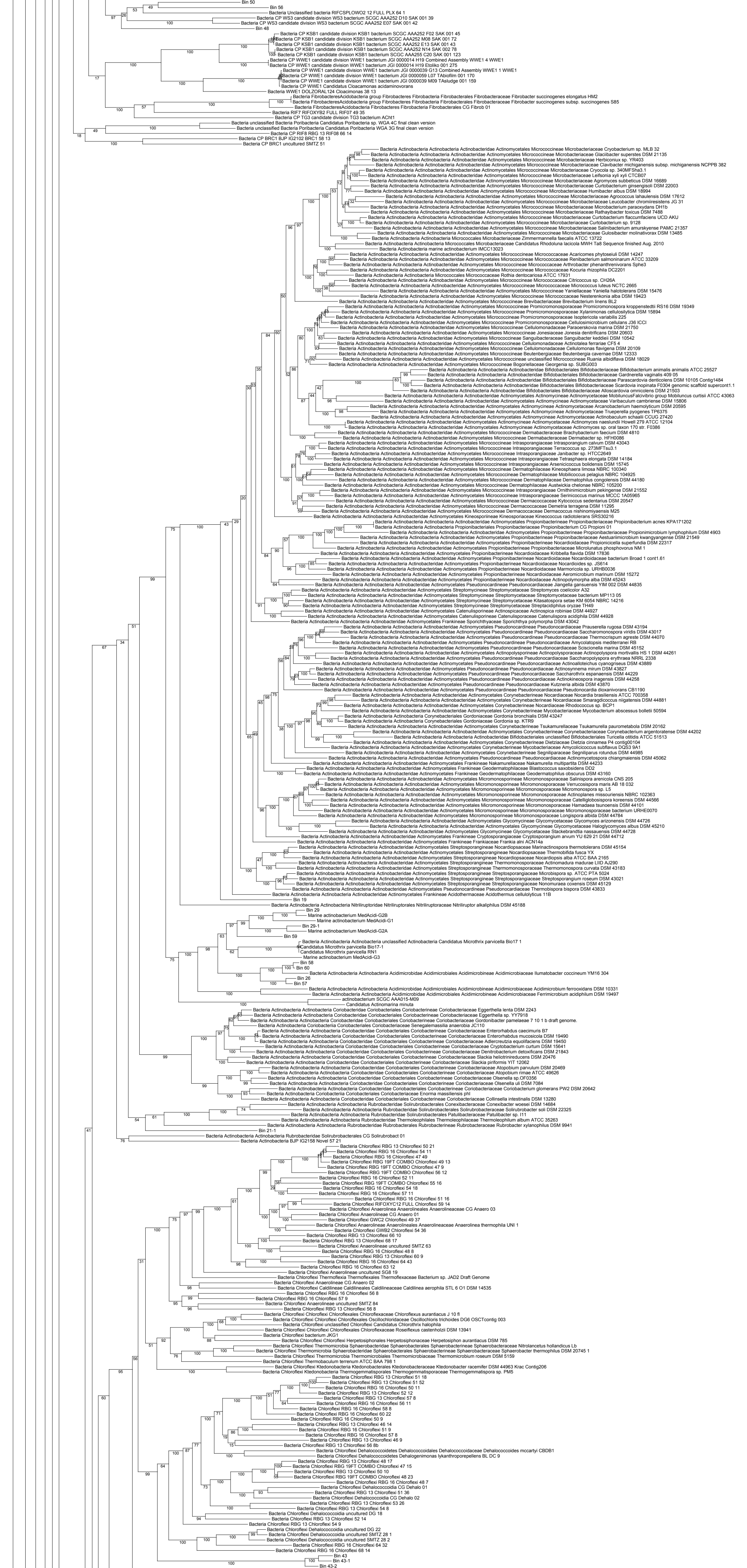
Bacteria Gemmatimonas uncultured SG8 23
Bin 42
Bacteria Gemmatimonadetes Gemmatimonadetes Gemmatimonadetes bacterium SCGC AAA007 O21
Bacteria Gemmatimonadetes Gemmatimonadetes Gemmatimonadetes bacterium SCGC AB 629 I08
Bacteria Gemmatimonadetes Gemmatimonadetes Gemmatimonadetes bacterium SCGC AAA003 K10
Bacteria Gemmatimonas uncultured SG8 38 2
Bacteria Gemmatimonas uncultured SMTZ 52
Bacteria RIF5 RBG 16 RIF05 58 8
Bacteria RIF5 RIFCSPLOWO2 12 FULL RIF05 58 11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Bin 48
Bacteria CP KSB1 candidate division KSB1 bacterium SCGC AAA252 F02 SAK 001 45
Bacteria CP KSB1 candidate division KSB1 bacterium SCGC AAA252 M08 SAK 001 72
Bacteria CP KSB1 candidate division KSB1 bacterium SCGC AAA252 E13 SAK 001 43
Bacteria CP KSB1 candidate division KSB1 bacterium SCGC AAA252 N14 SAK 002 78
Bacteria CP KSB1 candidate division KSB1 bacterium SCGC AAA255 C20 SAK 001 123
Bacteria CP WWE1 candidate division WWE1 bacterium JGI 0000014 H19 Combined Assembly WWE1 4 WWE1
Bacteria CP WWE1 candidate division WWE1 bacterium JGI 0000014 H19 Etoliko 001 275
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Bacteria CP WWE1 candidate division WWE1 bacterium JGI 0000059 L07 TAbiofilm 001 170
Bacteria CP WWE1 candidate division WWE1 bacterium JGI 0000039 M09 TAsludge 001 159
Bacteria CP WWE1 Candidatus Cloacamonas acidaminovorans
Bacteria WWE1 DOLZORAL124 Cloacimonas 38 13
Bacteria FibrobacteresAcidobacteria group Fibrobacteres Fibrobacteria Fibrobacterales Fibrobacteraceae Fibrobacter succinogenes elongatus HM2
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Bacteria RIF7 RIFOXYB2 FULL RIF07 49 35
Bacteria CP TG3 candidate division TG3 bacterium ACht1
Bacteria unclassified Bacteria Poribacteria Candidatus Poribacteria sp. WGA 4C final clean version
Bacteria unclassified Bacteria Poribacteria Candidatus Poribacteria WGA 3G final clean version
Bacteria CP RIF8 RBG 13 RIF08 66 14
Bacteria CP BRC1 BJP IG2102 BRC1 58 13
Bacteria CP BRC1 uncultured SMTZ 51
Bacteria Actinobacteria Actinobacteria Actinobacteridae Actinomycetales Micrococcineae Microbacteriaceae Cryobacterium sp. MLB 32
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Bacteria Actinobacteria marine actinobacterium IMCC13023
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Bacteria Actinobacteria Actinobacteria Actinobacteridae Actinomycetales Micrococcineae Micrococcaceae Arthrobacter phenanthrenivorans Sphe3
Bacteria Actinobacteria Actinobacteria Actinobacteridae Actinomycetales Micrococcineae Micrococcaceae Kocuria rhizophila DC2201
Bacteria Actinobacteria Actinobacteria Micrococcales Micrococcaceae Rothia dentocariosa ATCC 17931
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Bacteria Actinobacteria Actinobacteria Actinobacteridae Actinomycetales Micrococcineae Promicromonosporaceae Promicromonospora kroppenstedtii RS16 DSM 19349
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Bacteria Actinobacteria Actinobacteria Actinobacteridae Bifidobacteriales Bifidobacteriaceae Bifidobacterium animalis animalis ATCC 25527
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Bin 19
Bacteria Actinobacteria Actinobacteria Nitriliruptoridae Nitriliruptorales Nitriliruptoraceae Nitriliruptor alkaliphilus DSM 45188
Bin 29
Marine actinobacterium MedAcidi-G2B
Marine actinobacterium MedAcidi-G1
Bin 29-1
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Bin 59
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Bin 21-1
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Bacteria Chloroflexi Anaerolineae uncultured SMTZ 63
Bacteria Chloroflexi RBG 16 Chloroflexi 48 8
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Bacteria Chloroflexi RBG 13 Chloroflexi 54 9
Bacteria Chloroflexi Dehalococcoidia uncultured DG 22
Bacteria Chloroflexi Dehalococcoidia uncultured SMTZ 28 1
Bacteria Chloroflexi Dehalococcoidia uncultured SMTZ 28 2
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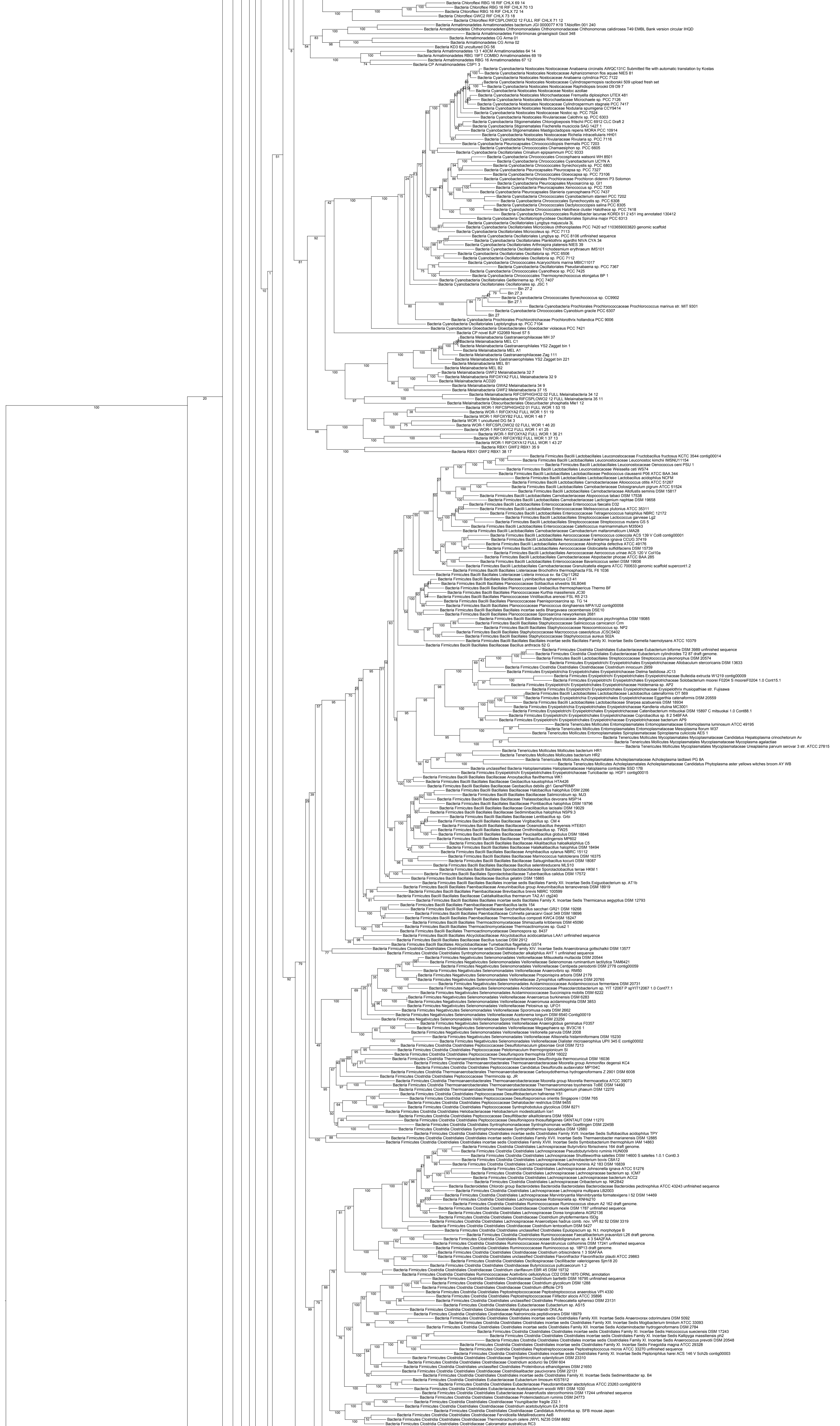
Bin 43-1
Bin 43-2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Bacteria Armatimonadetes Chthonomonadetes Chthonomonadales Chthonomonadaceae Chthonomonas calidirosea T49 EMBL Bank version circular IHQD
Bacteria Armatimonadetes Fimbriimonas ginsengisoli Gsoil 348
Bacteria Armatimonadetes CG Arma 01
Bacteria Armatimonadetes CG Arma 02
Bacteria KD3 62 uncultured DG 56
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Bacteria Cyanobacteria Nostocales Nostocaceae Anabaena circinalis AWQC131C Submitted file with automatic translation by Kostas
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Bacteria Cyanobacteria Nostocales Rivulariaceae Calothrix sp. PCC 6303
Bacteria Cyanobacteria Stigonematales Chlorogloeopsis fritschii PCC 6912 CLC Draft 2
Bacteria Cyanobacteria Stigonematales Fischerella muscicola SAG 1427 1
Bacteria Cyanobacteria Stigonematales Mastigocladopsis repens MORA PCC 10914
Bacteria Cyanobacteria Nostocales Nostocaceae Richelia intracellularis HH01
Bacteria Cyanobacteria Nostocales Rivulariaceae Rivularia sp. PCC 7116
Bacteria Cyanobacteria Pleurocapsales Chroococcidiopsis thermalis PCC 7203
Bacteria Cyanobacteria Chroococcales Chamaesiphon sp. PCC 6605
Bacteria Cyanobacteria Oscillatoriales Crinalium epipsammum PCC 9333
Bacteria Cyanobacteria Chroococcales Crocosphaera watsonii WH 8501
Bacteria Cyanobacteria Chroococcales Cyanobacterium UCYN A
Bacteria Cyanobacteria Chroococcales Synechocystis sp. PCC 6803
Bacteria Cyanobacteria Pleurocapsales Pleurocapsa sp. PCC 7327
Bacteria Cyanobacteria Chroococcales Gloeocapsa sp. PCC 73106
Bacteria Cyanobacteria Prochlorales Prochloron didemni P3 Solomon
Bacteria Cyanobacteria Pleurocapsales Myxosarcina sp. GI1
Bacteria Cyanobacteria Pleurocapsales Xenococcus sp. PCC 7305
Bacteria Cyanobacteria Pleurocapsales Stanieria cyanosphaera PCC 7437
Bacteria Cyanobacteria Chroococcales Cyanobacterium stanieri PCC 7202
Bacteria Cyanobacteria Chroococcales Synechocystis sp. PCC 6308
Bacteria Cyanobacteria Chroococcales Dactylococcopsis salina PCC 8305
Bacteria Cyanobacteria Chroococcales Halothece cluster Halothece sp. PCC 7418
Bacteria Cyanobacteria Chroococcales Rubidibacter lacunae KORDI 51 2 k51 img annotated 130412
Bacteria Cyanobacteria Oscillatoriophycideae Oscillatoriales Spirulina major PCC 6313
Bacteria Cyanobacteria Oscillatoriales Lyngbya majuscula 3L
Bacteria Cyanobacteria Oscillatoriales Microcoleus chthonoplastes PCC 7420 scf 1103659003820 genomic scaffold
Bacteria Cyanobacteria Oscillatoriales Microcoleus sp. PCC 7113
Bacteria Cyanobacteria Oscillatoriales Lyngbya sp. PCC 8106 unfinished sequence
Bacteria Cyanobacteria Oscillatoriales Planktothrix agardhii NIVA CYA 34
Bacteria Cyanobacteria Oscillatoriales Arthrospira platensis NIES 39
Bacteria Cyanobacteria Oscillatoriales Trichodesmium erythraeum IMS101
Bacteria Cyanobacteria Oscillatoriales Oscillatoria sp. PCC 6506
Bacteria Cyanobacteria Oscillatoriales Oscillatoria sp. PCC 7112
Bacteria Cyanobacteria Chroococcales Acaryochloris marina MBIC11017
Bacteria Cyanobacteria Oscillatoriales Pseudanabaena sp. PCC 7367
Bacteria Cyanobacteria Chroococcales Cyanothece sp. PCC 7425
Bacteria Cyanobacteria Chroococcales Thermosynechococcus elongatus BP 1
Bacteria Cyanobacteria Oscillatoriales Geitlerinema sp. PCC 7407
Bacteria Cyanobacteria Oscillatoriales Oscillatoriales sp. JSC 1
Bin 27.2
Bin 27.3
Bacteria Cyanobacteria Chroococcales Synechococcus sp. CC9902
Bin 27.1
Bacteria Cyanobacteria Prochlorales Prochlorococcaceae Prochlorococcus marinus str. MIT 9301
Bacteria Cyanobacteria Chroococcales Cyanobium gracile PCC 6307
Bin 27
Bacteria Cyanobacteria Prochlorales Prochlorotrichaceae Prochlorothrix hollandica PCC 9006
Bacteria Cyanobacteria Oscillatoriales Leptolyngbya sp. PCC 7104
Bacteria Cyanobacteria Gloeobacterales Gloeobacteraceae Gloeobacter violaceus PCC 7421
Bacteria CP novel BJP IG2069 Novel 57 5
Bacteria Melainabacteria Gastranaerophilaceae MH 37
Bacteria Melainabacteria MEL C1
Bacteria Melainabacteria Gastranaerophilales YS2 Zagget bin 1
Bacteria Melainabacteria MEL A1
Bacteria Melainabacteria Gastranaerophilaceae Zag 111
Bacteria Melainabacteria Gastranaerophilales YS2 Zagget bin 221
Bacteria Melainabacteria MEL B1
Bacteria Melainabacteria MEL B2
Bacteria Melainabacteria GWF2 Melainabacteria 32 7
Bacteria Melainabacteria RIFOXYA2 FULL Melainabacteria 32 9
Bacteria Melainabacteria ACD20
Bacteria Melainabacteria GWA2 Melainabacteria 34 9
Bacteria Melainabacteria GWF2 Melainabacteria 37 15
Bacteria Melainabacteria RIFCSPHIGHO2 02 FULL Melainabacteria 34 12
Bacteria Melainabacteria RIFCSPLOWO2 12 FULL Melainabacteria 35 11
Bacteria Melainabacteria Obscuribacterales Obscuribacter phosphatis Mle1 12
Bacteria WOR-1 RIFCSPHIGHO2 01 FULL WOR 1 53 15
Bacteria WOR-1 RIFOXYA2 FULL WOR 1 51 19
Bacteria WOR-1 RIFOXYB2 FULL WOR 1 48 7
Bacteria WOR 1 uncultured DG 54 3
Bacteria WOR-1 RIFCSPLOWO2 02 FULL WOR 1 46 20
Bacteria WOR-1 RIFOXYC2 FULL WOR 1 41 25
Bacteria WOR-1 RIFOXYA2 FULL WOR 1 36 21
Bacteria WOR-1 RIFOXYB2 FULL WOR 1 37 13
Bacteria WOR-1 RIFOXYA12 FULL WOR 1 43 27
Bacteria RBX1 GWF2 RBX1 35 9
Bacteria RBX1 GWF2 RBX1 38 17
Bacteria Firmicutes Bacilli Lactobacillales Leuconostocaceae Fructobacillus fructosus KCTC 3544 contig00014
Bacteria Firmicutes Bacilli Lactobacillales Leuconostocaceae Leuconostoc kimchii IMSNU11154
Bacteria Firmicutes Bacilli Lactobacillales Leuconostocaceae Oenococcus oeni PSU 1
Bacteria Firmicutes Bacilli Lactobacillales Leuconostocaceae Weissella ceti WS74
Bacteria Firmicutes Bacilli Lactobacillales Lactobacillaceae Pediococcus claussenii P06 ATCC BAA 344
Bacteria Firmicutes Bacilli Lactobacillales Lactobacillaceae Lactobacillus acidophilus NCFM
Bacteria Firmicutes Bacilli Lactobacillales Carnobacteriaceae Alloiococcus otitis ATCC 51267
Bacteria Firmicutes Bacilli Lactobacillales Carnobacteriaceae Dolosigranulum pigrum ATCC 51524
Bacteria Firmicutes Bacilli Lactobacillales Carnobacteriaceae Allofustis seminis DSM 15817
Bacteria Firmicutes Bacilli Lactobacillales Carnobacteriaceae Atopococcus tabaci DSM 17538
Bacteria Firmicutes Bacilli Lactobacillales Carnobacteriaceae Lacticigenium naphtae DSM 19658
Bacteria Firmicutes Bacilli Lactobacillales Enterococcaceae Enterococcus faecalis D32
Bacteria Firmicutes Bacilli Lactobacillales Enterococcaceae Melissococcus plutonius ATCC 35311
Bacteria Firmicutes Bacilli Lactobacillales Enterococcaceae Tetragenococcus halophilus NBRC 12172
Bacteria Firmicutes Bacilli Lactobacillales Streptococcaceae Lactococcus garvieae Lg2
Bacteria Firmicutes Bacilli Lactobacillales Streptococcaceae Streptococcus mutans GS 5
Bacteria Firmicutes Bacilli Lactobacillales Enterococcaceae Catellicoccus marimammalium M35043
Bacteria Firmicutes Bacilli Lactobacillales Carnobacteriaceae Carnobacterium maltaromaticum LMA28
Bacteria Firmicutes Bacilli Lactobacillales Aerococcaceae Eremococcus coleocola ACS 139 V Col8 contig00001
Bacteria Firmicutes Bacilli Lactobacillales Aerococcaceae Facklamia ignava CCUG 37419
Bacteria Firmicutes Bacilli Lactobacillales Aerococcaceae Abiotrophia defectiva ATCC 49176
Bacteria Firmicutes Bacilli Lactobacillales Aerococcaceae Globicatella sulfidifaciens DSM 15739
Bacteria Firmicutes Bacilli Lactobacillales Aerococcaceae Aerococcus urinae ACS 120 V Col10a
Bacteria Firmicutes Bacilli Lactobacillales Carnobacteriaceae Atopobacter phocae ATCC BAA 285
Bacteria Firmicutes Bacilli Lactobacillales Enterococcaceae Bavariicoccus seileri DSM 19936
Bacteria Firmicutes Bacilli Lactobacillales Carnobacteriaceae Granulicatella elegans ATCC 700633 genomic scaffold supercont1.2
Bacteria Firmicutes Bacilli Bacillales Listeriaceae Brochothrix thermosphacta FSL F6 1036
Bacteria Firmicutes Bacilli Bacillales Listeriaceae Listeria innocua sv. 6a Clip11262
Bacteria Firmicutes Bacilli Bacillales Bacillaceae Lysinibacillus sphaericus C3 41
Bacteria Firmicutes Bacilli Bacillales Planococcaceae Solibacillus silvestris StLB046
Bacteria Firmicutes Bacilli Bacillales Planococcaceae Ureibacillus thermosphaericus Thermo BF
Bacteria Firmicutes Bacilli Bacillales Planococcaceae Kurthia massiliensis JC30
Bacteria Firmicutes Bacilli Bacillales Planococcaceae Viridibacillus arenosi FSL R5 213
Bacteria Firmicutes Bacilli Bacillales Planococcaceae Paenisporosarcina sp. TG 14
Bacteria Firmicutes Bacilli Bacillales Planococcaceae Planococcus donghaensis MPA1U2 contig00058
Bacteria Firmicutes Bacilli Bacillales Bacillales incertae sedis Bhargavaea cecembensis DSE10
Bacteria Firmicutes Bacilli Bacillales Planococcaceae Sporosarcina newyorkensis 2681
Bacteria Firmicutes Bacilli Bacillales Staphylococcaceae Jeotgalicoccus psychrophilus DSM 19085
Bacteria Firmicutes Bacilli Bacillales Staphylococcaceae Salinicoccus carnicancri Crm
Bacteria Firmicutes Bacilli Bacillales Staphylococcaceae Nosocomiicoccus sp. NP2
Bacteria Firmicutes Bacilli Bacillales Staphylococcaceae Macrococcus caseolyticus JCSC5402
Bacteria Firmicutes Bacilli Bacillales Staphylococcaceae Staphylococcus aureus 502A
Bacteria Firmicutes Bacilli Bacillales Bacillales incertae sedis Bacillales Family XI. Incertae Sedis Gemella haemolysans ATCC 10379
Bacteria Firmicutes Bacilli Bacillales Bacillaceae Bacillus anthracis 52 G
Bacteria Firmicutes Clostridia Clostridiales Eubacteriaceae Eubacterium biforme DSM 3989 unfinished sequence
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Bacteria Firmicutes Bacilli Lactobacillales Streptococcaceae Streptococcus pleomorphus DSM 20574
Bacteria Firmicutes Erysipelotrichi Erysipelotrichales Erysipelotrichaceae Allobaculum stercoricanis DSM 13633
Bacteria Firmicutes Clostridia Clostridiales Clostridiaceae Clostridium innocuum 2959
Bacteria Firmicutes Erysipelotrichia Erysipelotrichales Erysipelotrichaceae Dielma fastidiosa JC13
Bacteria Firmicutes Erysipelotrichi Erysipelotrichales Erysipelotrichaceae Bulleidia extructa W1219 contig00009
Bacteria Firmicutes Erysipelotrichi Erysipelotrichales Erysipelotrichaceae Solobacterium moorei F0204 S mooreiF0204 1.0 Cont15.1
Bacteria Firmicutes Erysipelotrichi Erysipelotrichales Erysipelotrichaceae Holdemania sp. AP2
Bacteria Firmicutes Erysipelotrichi Erysipelotrichales Erysipelotrichaceae Erysipelothrix rhusiopathiae str. Fujisawa
Bacteria Firmicutes Bacilli Lactobacillales Lactobacillaceae Lactobacillus catenaformis OT 569
Bacteria Firmicutes Erysipelotrichi Erysipelotrichales Erysipelotrichaceae Eggerthia catenaformis DSM 20559
Bacteria Firmicutes Bacilli Lactobacillales Lactobacillaceae Sharpea azabuensis DSM 18934
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Bacteria Firmicutes Erysipelotrichi Erysipelotrichales Erysipelotrichaceae Catenibacterium mitsuokai DSM 15897 C mitsuokai 1.0 Cont88.1
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Bacteria Firmicutes Erysipelotrichi Erysipelotrichales Erysipelotrichaceae Erysipelotrichaceae bacterium AP9
Bacteria Tenericutes Mollicutes Entomoplasmatales Entomoplasmataceae Entomoplasma luminosum ATCC 49195
Bacteria Tenericutes Mollicutes Entomoplasmatales Entomoplasmataceae Mesoplasma florum W37
Bacteria Tenericutes Mollicutes Entomoplasmatales Spiroplasmataceae Spiroplasma culicicola AES 1
Bacteria Tenericutes Mollicutes Mycoplasmatales Mycoplasmataceae Candidatus Hepatoplasma crinochetorum Av
Bacteria Tenericutes Mollicutes Mycoplasmatales Mycoplasmataceae Mycoplasma agalactiae
Bacteria Tenericutes Mollicutes Mycoplasmatales Mycoplasmataceae Ureaplasma parvum serovar 3 str. ATCC 27815
Bacteria Tenericutes Mollicutes Mollicutes bacterium HR1
Bacteria Tenericutes Mollicutes Mollicutes bacterium HR2
Bacteria Tenericutes Mollicutes Acholeplasmatales Acholeplasmataceae Acholeplasma laidlawii PG 8A
Bacteria Tenericutes Mollicutes Acholeplasmatales Acholeplasmataceae Candidatus Phytoplasma aster yellows witches broom AY WB
Bacteria unclassified Bacteria Haloplasmatales Haloplasmataceae Haloplasma contractile SSD 17B
Bacteria Firmicutes Erysipelotrichi Erysipelotrichales Erysipelotrichaceae Turicibacter sp. HGF1 contig00015
Bacteria Firmicutes Bacilli Bacillales Bacillaceae Anoxybacillus flavithermus WK1
Bacteria Firmicutes Bacilli Bacillales Bacillaceae Geobacillus kaustophilus HTA426
Bacteria Firmicutes Bacilli Bacillales Bacillaceae Geobacillus debilis gb1 GenePRIMP
Bacteria Firmicutes Bacilli Bacillales Bacillaceae Halobacillus halophilus DSM 2266
Bacteria Firmicutes Bacilli Bacillales Bacillaceae Salimicrobium sp. MJ3
Bacteria Firmicutes Bacilli Bacillales Bacillaceae Thalassobacillus devorans MSP14
Bacteria Firmicutes Bacilli Bacillales Bacillaceae Pontibacillus halophilus DSM 19796
Bacteria Firmicutes Bacilli Bacillales Bacillaceae Gracilibacillus lacisalsi DSM 19029
Bacteria Firmicutes Bacilli Bacillales Bacillaceae Sediminibacillus halophilus NSP9.3
Bacteria Firmicutes Bacilli Bacillales Bacillaceae Lentibacillus sp. Grbi
Bacteria Firmicutes Bacilli Bacillales Bacillaceae Virgibacillus sp. CM 4
Bacteria Firmicutes Bacilli Bacillales Bacillaceae Oceanobacillus iheyensis HTE831
Bacteria Firmicutes Bacilli Bacillales Bacillaceae Ornithinibacillus sp. TW25
Bacteria Firmicutes Bacilli Bacillales Bacillaceae Paucisalibacillus globulus DSM 18846
Bacteria Firmicutes Bacilli Bacillales Bacillaceae Terribacillus aidingensis MP602
Bacteria Firmicutes Bacilli Bacillales Bacillaceae Alkalibacillus haloalkaliphilus C5
Bacteria Firmicutes Bacilli Bacillales Bacillaceae Halalkalibacillus halophilus DSM 18494
Bacteria Firmicutes Bacilli Bacillales Bacillaceae Amphibacillus xylanus NBRC 15112
Bacteria Firmicutes Bacilli Bacillales Bacillaceae Marinococcus halotolerans DSM 16375
Bacteria Firmicutes Bacilli Bacillales Bacillaceae Salsuginibacillus kocurii DSM 18087
Bacteria Firmicutes Bacilli Bacillales Bacillaceae Bacillus selenitireducens MLS10
Bacteria Firmicutes Bacilli Bacillales Sporolactobacillaceae Sporolactobacillus terrae HKM 1
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Bacteria Firmicutes Bacilli Bacillales Bacillaceae Bacillus gelatini DSM 15865
Bacteria Firmicutes Bacilli Bacillales Bacillales incertae sedis Bacillales Family XII. Incertae Sedis Exiguobacterium sp. AT1b
Bacteria Firmicutes Bacilli Bacillales Paenibacillaceae Aneurinibacillus group Aneurinibacillus terranovensis DSM 18919
Bacteria Firmicutes Bacilli Bacillales Paenibacillaceae Brevibacillus brevis NBRC 100599
Bacteria Firmicutes Bacilli Bacillales Bacillaceae Caldalkalibacillus thermarum TA2.A1 ctg240
Bacteria Firmicutes Bacilli Bacillales Bacillales incertae sedis Bacillales Family X. Incertae Sedis Thermicanus aegyptius DSM 12793
Bacteria Firmicutes Bacilli Bacillales Paenibacillaceae Paenibacillus lactis 154
Bacteria Firmicutes Bacilli Bacillales Paenibacillaceae Saccharibacillus sacchari GR21 DSM 19268
Bacteria Firmicutes Bacilli Bacillales Paenibacillaceae Cohnella panacarvi Gsoil 349 DSM 18696
Bacteria Firmicutes Bacilli Bacillales Paenibacillaceae Thermobacillus composti KWC4 DSM 18247
Bacteria Firmicutes Bacilli Bacillales Thermoactinomycetaceae Shimazuella kribbensis DSM 45090
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Bacteria Firmicutes Bacilli Bacillales Thermoactinomycetaceae Desmospora sp. 8437
Bacteria Firmicutes Bacilli Bacillales Alicyclobacillaceae Alicyclobacillus acidocaldarius LAA1 unfinished sequence
Bacteria Firmicutes Bacilli Bacillales Bacillaceae Bacillus tusciae DSM 2912
Bacteria Firmicutes Bacilli Bacillales Alicyclobacillaceae Tumebacillus flagellatus GST4
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Bacteria Firmicutes Clostridia Clostridiales Syntrophomonadaceae Dethiobacter alkaliphilus AHT 1 unfinished sequence
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Bacteria Firmicutes Negativicutes Selenomonadales Veillonellaceae Anaerovibrio sp. RM50
Bacteria Firmicutes Negativicutes Selenomonadales Veillonellaceae Propionispira arboris DSM 2179
Bacteria Firmicutes Negativicutes Selenomonadales Veillonellaceae Zymophilus raffinosivorans DSM 20765
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Bacteria Firmicutes Negativicutes Selenomonadales Veillonellaceae Anaeromusa acidaminophila DSM 3853
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Bacteria Firmicutes Negativicutes Selenomonadales Veillonellaceae Sporomusa ovata DSM 2662
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Bacteria Firmicutes Negativicutes Selenomonadales Sporolituus thermophilus DSM 23256
Bacteria Firmicutes Negativicutes Selenomonadales Veillonellaceae Anaeroglobus geminatus F0357
Bacteria Firmicutes Negativicutes Selenomonadales Veillonellaceae Megasphaera sp. BV3C16 1
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Bacteria Firmicutes Negativicutes Selenomonadales Veillonellaceae Allisonella histaminiformans DSM 15230
Bacteria Firmicutes Negativicutes Selenomonadales Veillonellaceae Dialister micraerophilus UPII 345 E contig00002
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Bacteria Firmicutes Clostridia Thermoanaerobacterales Thermoanaerobacteraceae Desulfovirgula thermocuniculi DSM 16036
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Bacteria Firmicutes Clostridia Clostridiales Peptococcaceae Candidatus Desulforudis audaxviator MP104C
Bacteria Firmicutes Clostridia Thermoanaerobacterales Thermoanaerobacteraceae Carboxydothermus hydrogenoformans Z 2901 DSM 6008
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Bacteria Firmicutes Clostridia Thermoanaerobacterales Thermoanaerobacteraceae Thermanaeromonas toyohensis ToBE DSM 14490
Bacteria Firmicutes Clostridia Thermoanaerobacterales Thermoanaerobacteraceae Thermacetogenium phaeum DSM 12270
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Bacteria Firmicutes Clostridia Clostridiales Peptococcaceae Dehalobacter restrictus DSM 9455
Bacteria Firmicutes Clostridia Clostridiales Peptococcaceae Syntrophobotulus glycolicus DSM 8271
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Bacteria Firmicutes Clostridia Clostridiales Lachnospiraceae Pseudobutyrivibrio ruminis HUN009
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Bacteria Firmicutes Clostridia Clostridiales Lachnospiraceae Lachnospiraceae bacterium sp. ICM7
Bacteria Firmicutes Clostridia Clostridiales Lachnospiraceae Lachnospiraceae bacterium ACC2
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Bacteria Bacteroidetes Bacteroidia Bacteroidales Bacteroidaceae Bacteroides pectinophilus ATCC 43243 unfinished sequence
Bacteria Firmicutes Chlorobi group Clostridia Clostridiales Lachnospiraceae Lachnospira pectinoschiza LB2003
Bacteria Firmicutes Clostridia Clostridiales Lachnospiraceae Marvinbryantia Marvinbryantia formatexigens I 52 DSM 14469
Bacteria Firmicutes Clostridia Clostridiales Lachnospiraceae Robinsoniella sp. KNHs210
Bacteria Firmicutes Clostridia Clostridiales Ruminococcaceae Ruminococcus obeum A2 162 draft genome.
Bacteria Firmicutes Clostridia Clostridiales Clostridiaceae Clostridium nexile DSM 1787 unfinished sequence
Bacteria Firmicutes Clostridia Clostridiales Lachnospiraceae Dorea longicatena AGR2136
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Bacteria Firmicutes Clostridia Clostridiales Lachnospiraceae Anaerostipes hadrus comb. nov. VPI 82 52 DSM 3319
Bacteria Firmicutes Clostridia Clostridiales Clostridiaceae Clostridium lentocellum DSM 5427
Bacteria Firmicutes Clostridia Clostridiales unclassified Clostridiales Epulopiscium sp. N.t. morphotype B
Bacteria Firmicutes Clostridia Clostridiales Ruminococcaceae Faecalibacterium prausnitzii L2 6 draft genome.
Bacteria Firmicutes Clostridia Clostridiales Ruminococcaceae Subdoligranulum sp. 4 3 54A2FAA
Bacteria Firmicutes Clostridia Clostridiales Ruminococcaceae Anaerotruncus colihominis DSM 17241 unfinished sequence
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Bacteria Firmicutes Clostridia Clostridiales Clostridiaceae Clostridium orbiscindens 1 3 50AFAA
Bacteria Firmicutes Clostridia Clostridiales unclassified Clostridiales Flavonifractor Flavonifractor plautii ATCC 29863
Bacteria Firmicutes Clostridia Clostridiales Oscillospiraceae Oscillibacter valericigenes Sjm18 20
Bacteria Firmicutes Clostridia Clostridiales Clostridiaceae Butyricicoccus pullicaecorum 1.2
Bacteria Firmicutes Clostridia Clostridiales Clostridiaceae Clostridium clariflavum EBR 45 DSM 19732
Bacteria Firmicutes Clostridia Clostridiales Ruminococcaceae Acetivibrio cellulolyticus CD2 DSM 1870 ORNL annotation
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Bacteria Firmicutes Clostridia Clostridiales Clostridiaceae Clostridium glycolicum DSM 1288
Bacteria Firmicutes Clostridia Clostridiales Clostridiaceae Clostridium difficile CF5
Bacteria Firmicutes Clostridia Clostridiales Peptostreptococcaceae Peptostreptococcus anaerobius VPI 4330
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Bacteria Firmicutes Clostridia Clostridiales unclassified Clostridiales Proteocatella sphenisci DSM 23131
Bacteria Firmicutes Clostridia Clostridiales Eubacteriaceae Eubacterium sp. AS15
Bacteria Firmicutes Clostridia Clostridiales Clostridiaceae Alkaliphilus oremlandii OhILAs
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Bacteria Firmicutes Clostridia Clostridiales Clostridiaceae Clostridium acidurici 9a DSM 604
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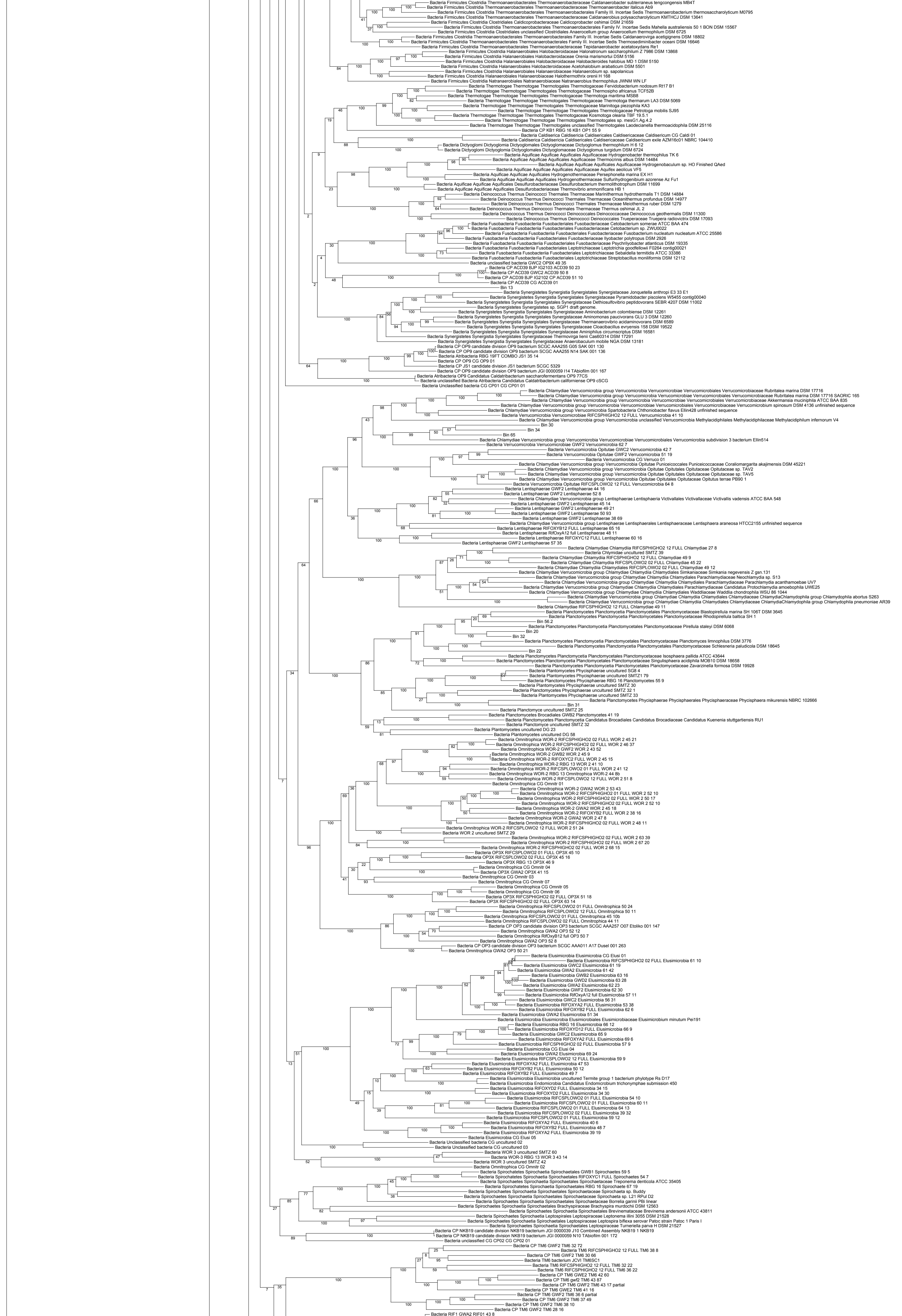
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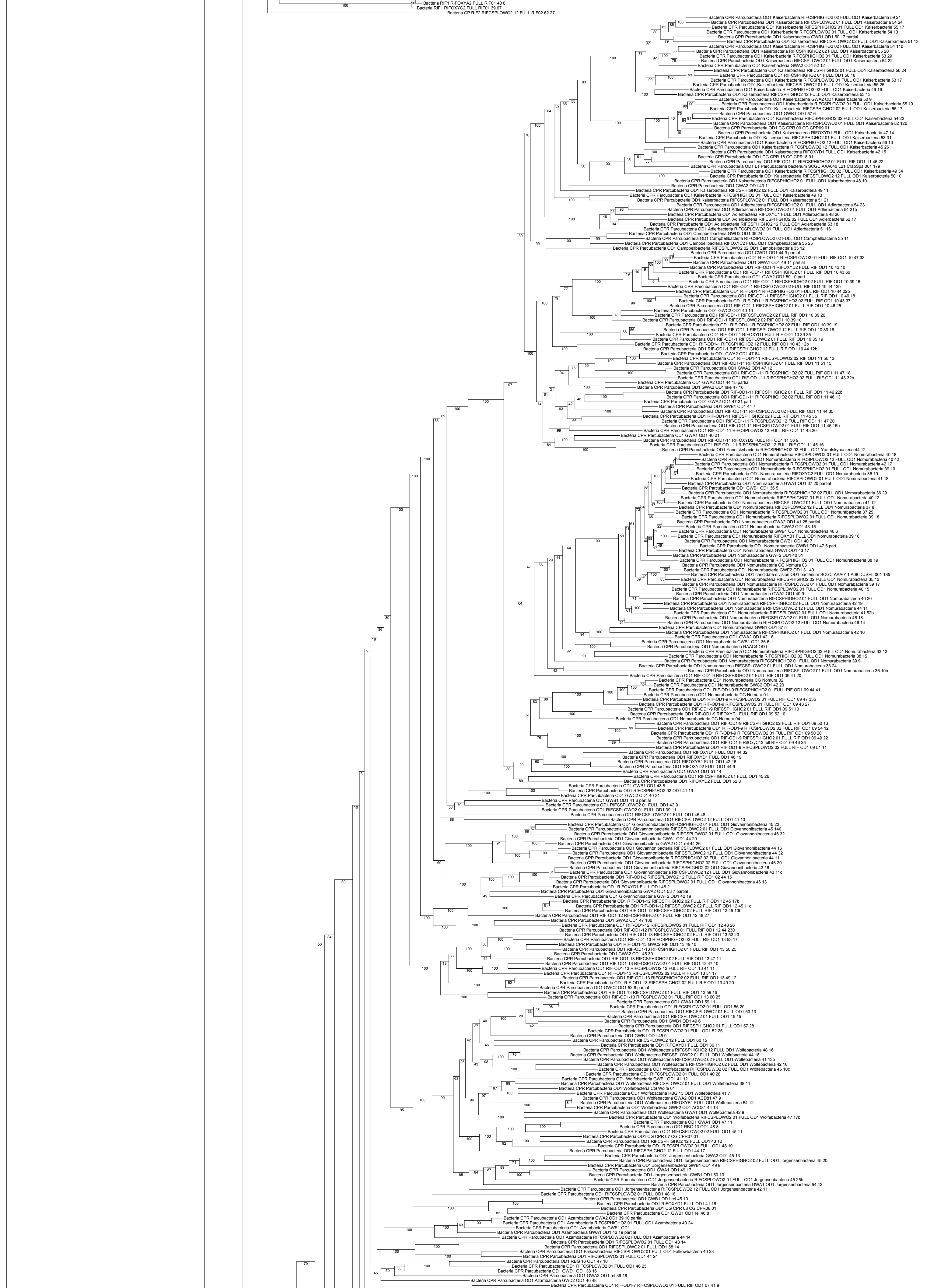
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Bacteria CPR Parcubacteria OD1 Kaiserbacteria RIFCSPLOWO2 01 FULL OD1 Kaiserbacteria 53 17
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Bacteria CPR Parcubacteria OD1 Kaiserbacteria RIFCSPHIGHO2 02 FULL OD1 Kaiserbacteria 49 16
Bacteria CPR Parcubacteria OD1 Kaiserbacteria RIFCSPHIGHO2 12 FULL OD1 Kaiserbacteria 53 13
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Bacteria CPR Parcubacteria OD1 Kaiserbacteria RIFCSPLOWO2 01 FULL OD1 Kaiserbacteria 55 19
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Bacteria CPR Parcubacteria OD1 GWB1 OD1 57 6
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Bacteria CPR Parcubacteria OD1 CG CPR 09 CG CPR09 01
Bacteria CPR Parcubacteria OD1 Kaiserbacteria RIFOXYD1 FULL OD1 Kaiserbacteria 47 14
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Bacteria CPR Parcubacteria OD1 Kaiserbacteria RIFCSPLOWO2 12 FULL OD1 Kaiserbacteria 45 26
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Bacteria CPR Parcubacteria OD1 Kaiserbacteria RIFCSPHIGHO2 01 FULL OD1 Kaiserbacteria 48 10
Bacteria CPR Parcubacteria OD1 GWA2 OD1 43 11
Bacteria CPR Parcubacteria OD1 Kaiserbacteria RIFCSPHIGHO2 02 FULL OD1 Kaiserbacteria 49 11
Bacteria CPR Parcubacteria OD1 Kaiserbacteria RIFCSPHIGHO2 01 FULL OD1 Kaiserbacteria 49 13
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Bacteria CPR Parcubacteria OD1 GWA1 OD1 49 11 partial
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Bacteria CPR Parcubacteria OD1 RIF-OD1-1 RIFCSPLOWO2 12 FULL RIF OD1 10 39 16
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Bacteria CPR Parcubacteria OD1 GWA2 OD1 47 12
Bacteria CPR Parcubacteria OD1 RIF-OD1-11 RIFCSPHIGHO2 12 FULL RIF OD1 11 47 18
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Bacteria CPR Parcubacteria OD1 GWA2 OD1 44 15 partial
Bacteria CPR Parcubacteria OD1 GWA2 OD1 like 47 16
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Bacteria CPR Parcubacteria OD1 RIF-OD1-11 RIFCSPLOWO2 12 FULL RIF OD1 11 47 20
Bacteria CPR Parcubacteria OD1 RIF-OD1-11 RIFCSPLOWO2 01 FULL RIF OD1 11 45 15b
Bacteria CPR Parcubacteria OD1 RIF-OD1-11 RIFCSPLOWO2 12 FULL RIF OD1 11 43 20
Bacteria CPR Parcubacteria OD1 GWA1 OD1 40 21
Bacteria CPR Parcubacteria OD1 RIF-OD1-11 RIFOXYD2 FULL RIF OD1 11 36 9
Bacteria CPR Parcubacteria OD1 RIF-OD1-11 RIFCSPHIGHO2 12 FULL RIF OD1 11 45 16
Bacteria CPR Parcubacteria OD1 Yanofskybacteria RIFCSPHIGHO2 02 FULL OD1 Yanofskybacteria 44 12
Bacteria CPR Parcubacteria OD1 Nomurabacteria RIFCSPLOWO2 01 FULL OD1 Nomurabacteria 40 18
Bacteria CPR Parcubacteria OD1 Nomurabacteria RIFCSPLOWO2 12 FULL OD1 Nomurabacteria 40 42
Bacteria CPR Parcubacteria OD1 Nomurabacteria RIFCSPLOWO2 01 FULL OD1 Nomurabacteria 42 17
Bacteria CPR Parcubacteria OD1 Nomurabacteria RIFCSPHIGHO2 01 FULL OD1 Nomurabacteria 39 10
Bacteria CPR Parcubacteria OD1 Nomurabacteria RIFOXYC2 FULL OD1 Nomurabacteria 36 19
Bacteria CPR Parcubacteria OD1 Nomurabacteria RIFCSPLOWO2 01 FULL OD1 Nomurabacteria 41 18
Bacteria CPR Parcubacteria OD1 Nomurabacteria GWA1 OD1 37 20 partial
Bacteria CPR Parcubacteria OD1 GWB1 OD1 36 5
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Bacteria CPR Parcubacteria OD1 Nomurabacteria RIFCSPHIGHO2 02 FULL OD1 Nomurabacteria 40 12
Bacteria CPR Parcubacteria OD1 Nomurabacteria RIFCSPLOWO2 01 FULL OD1 Nomurabacteria 41 12
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Bacteria CPR Parcubacteria OD1 Nomurabacteria RIFCSPLOWO2 01 FULL OD1 Nomurabacteria 37 25
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Bacteria CPR Parcubacteria OD1 Nomurabacteria GWA2 OD1 40 9
Bacteria CPR Parcubacteria OD1 Nomurabacteria RIFCSPHIGHO2 01 FULL OD1 Nomurabacteria 40 20
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Bacteria CPR Parcubacteria OD1 Nomurabacteria RIFCSPLOWO2 12 FULL OD1 Nomurabacteria 44 11
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Bacteria CPR Parcubacteria OD1 Nomurabacteria RIFCSPLOWO2 01 FULL OD1 Nomurabacteria 46 18
Bacteria CPR Parcubacteria OD1 Nomurabacteria RIFCSPLOWO2 12 FULL OD1 Nomurabacteria 46 14
Bacteria CPR Parcubacteria OD1 Nomurabacteria GWB1 OD1 37 5
Bacteria CPR Parcubacteria OD1 Nomurabacteria RIFCSPHIGHO2 01 FULL OD1 Nomurabacteria 42 16
Bacteria CPR Parcubacteria OD1 GWA2 OD1 42 18
Bacteria CPR Parcubacteria OD1 Nomurabacteria GWB1 OD1 36 6
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Bacteria CPR Parcubacteria OD1 RIF-OD1-9 RIFCSPHIGHO2 01 FULL RIF OD1 09 41 20
Bacteria CPR Parcubacteria OD1 Nomurabacteria CG Nomura 02
Bacteria CPR Parcubacteria OD1 Nomurabacteria GWC2 OD1 42 20
Bacteria CPR Parcubacteria OD1 RIF-OD1-9 RIFCSPHIGHO2 01 FULL RIF OD1 09 44 41
Bacteria CPR Parcubacteria OD1 Nomurabacteria CG Nomura 01
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Bacteria CPR Parcubacteria OD1 RIF-OD1-9 RIFCSPHIGHO2 01 FULL RIF OD1 09 51 10
Bacteria CPR Parcubacteria OD1 RIF-OD1-9 RIFOXYC1 FULL RIF OD1 09 52 10
Bacteria CPR Parcubacteria OD1 Nomurabacteria CG Nomura 04
Bacteria CPR Parcubacteria OD1 RIF-OD1-9 RIFCSPHIGHO2 02 FULL RIF OD1 09 50 13
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Bacteria CPR Parcubacteria OD1 RIF-OD1-9 RIFCSPLOWO2 01 FULL RIF OD1 09 50 20
Bacteria CPR Parcubacteria OD1 RIF-OD1-9 RIFCSPHIGHO2 01 FULL RIF OD1 09 49 22
Bacteria CPR Parcubacteria OD1 RIF-OD1-9 RifOxyC12 full RIF OD1 09 46 25
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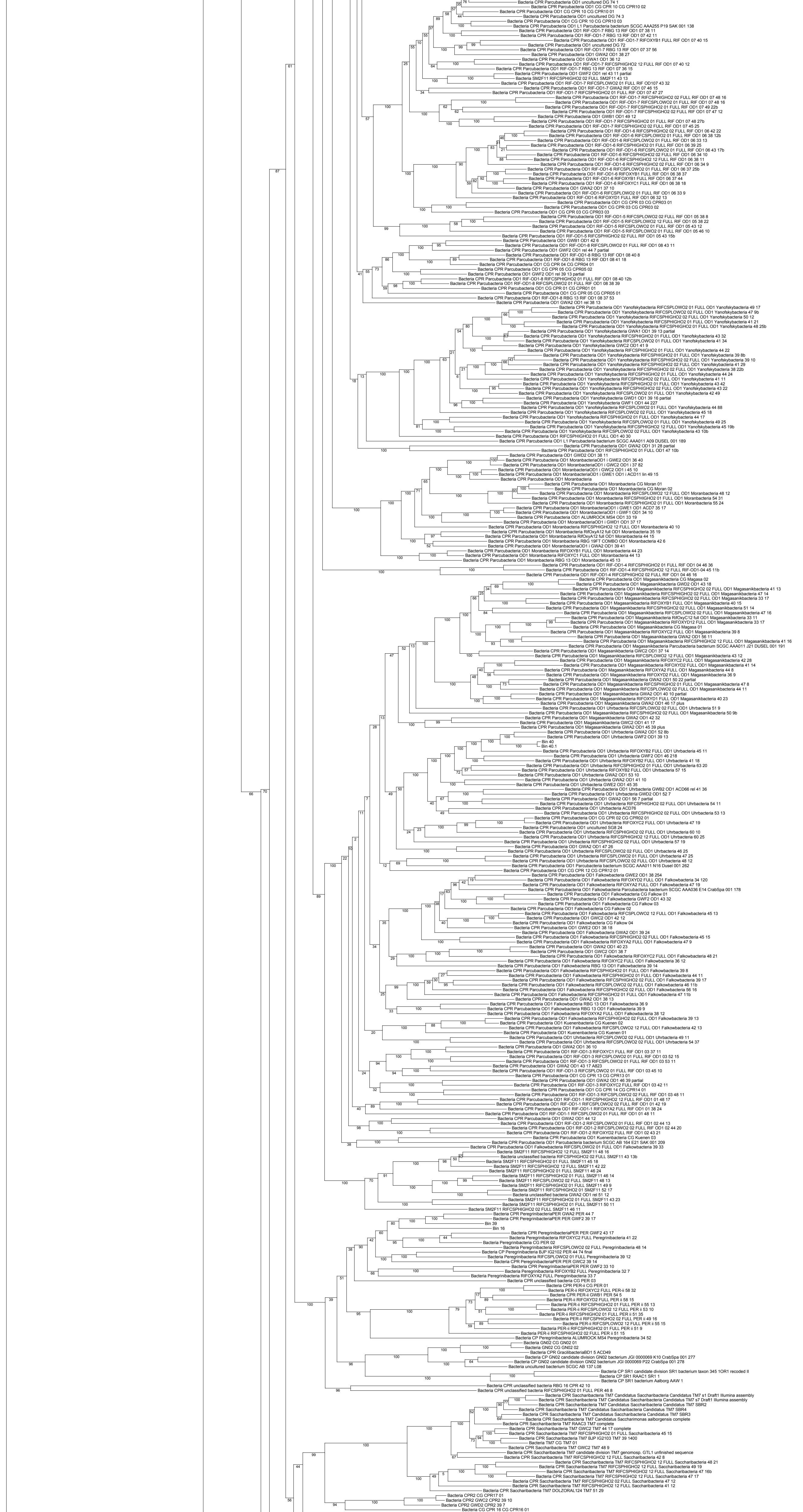
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Bacteria CPR Parcubacteria OD1 GWA2 OD1 38 27
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Bacteria CPR Parcubacteria OD1 RIF-OD1-6 RIFCSPHIGHO2 01 FULL RIF OD1 06 39 25
Bacteria CPR Parcubacteria OD1 RIF-OD1-6 RIFCSPLOWO2 01 FULL RIF OD1 06 43 17b
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Bacteria CPR Parcubacteria OD1 RIF-OD1-6 RIFCSPHIGHO2 12 FULL RIF OD1 06 38 11
Bacteria CPR Parcubacteria OD1 RIF-OD1-6 RIFCSPHIGHO2 02 FULL RIF OD1 06 34 9
Bacteria CPR Parcubacteria OD1 RIF-OD1-6 RIFCSPLOWO2 01 FULL RIF OD1 06 37 25b
Bacteria CPR Parcubacteria OD1 RIF-OD1-6 RIFOXYB1 FULL RIF OD1 06 38 37
Bacteria CPR Parcubacteria OD1 RIF-OD1-6 RIFOXYB1 FULL RIF OD1 06 37 44
Bacteria CPR Parcubacteria OD1 RIF-OD1-6 RIFOXYC1 FULL RIF OD1 06 38 18
Bacteria CPR Parcubacteria OD1 GWA2 OD1 37 10
Bacteria CPR Parcubacteria OD1 RIF-OD1-6 RIFCSPLOWO2 01 FULL RIF OD1 06 33 9
Bacteria CPR Parcubacteria OD1 RIF-OD1-6 RIFOXYD1 FULL RIF OD1 06 32 13
Bacteria CPR Parcubacteria OD1 CG CPR 03 CG CPR03 01
Bacteria CPR Parcubacteria OD1 CG CPR 03 CG CPR03 02
Bacteria CPR Parcubacteria OD1 CG CPR 03 CG CPR03 03
Bacteria CPR Parcubacteria OD1 RIF-OD1-5 RIFCSPLOWO2 02 FULL RIF OD1 05 38 8
Bacteria CPR Parcubacteria OD1 RIF-OD1-5 RIFCSPLOWO2 12 FULL RIF OD1 05 38 22
Bacteria CPR Parcubacteria OD1 RIF-OD1-5 RIFCSPLOWO2 01 FULL RIF OD1 05 43 12
Bacteria CPR Parcubacteria OD1 RIF-OD1-5 RIFCSPLOWO2 01 FULL RIF OD1 05 46 10
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Bacteria CPR Parcubacteria OD1 GWB1 OD1 42 6
Bacteria CPR Parcubacteria OD1 RIF-OD1-8 RIFCSPLOWO2 01 FULL RIF OD1 08 43 11
Bacteria CPR Parcubacteria OD1 GWF2 OD1 rel 44 7 partial
Bacteria CPR Parcubacteria OD1 RIF-OD1-8 RBG 13 RIF OD1 08 40 8
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Bacteria CPR Parcubacteria OD1 CG CPR 04 CG CPR04 01
Bacteria CPR Parcubacteria OD1 CG CPR 05 CG CPR05 02
Bacteria CPR Parcubacteria OD1 GWF2 OD1 rel 39 13 partial
Bacteria CPR Parcubacteria OD1 RIF-OD1-8 RIFCSPHIGHO2 01 FULL RIF OD1 08 40 12b
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Bacteria CPR Parcubacteria OD1 CG CPR 01 CG CPR01 01
Bacteria CPR Parcubacteria OD1 CG CPR 05 CG CPR05 01
Bacteria CPR Parcubacteria OD1 RIF-OD1-8 RBG 13 RIF OD1 08 37 53
Bacteria CPR Parcubacteria OD1 GWA2 OD1 rel 38 13
Bacteria CPR Parcubacteria OD1 Yanofskybacteria RIFCSPLOWO2 01 FULL OD1 Yanofskybacteria 49 17
Bacteria CPR Parcubacteria OD1 Yanofskybacteria RIFCSPLOWO2 02 FULL OD1 Yanofskybacteria 47 9b
Bacteria CPR Parcubacteria OD1 Yanofskybacteria RIFCSPHIGHO2 02 FULL OD1 Yanofskybacteria 50 12
Bacteria CPR Parcubacteria OD1 Yanofskybacteria RIFCSPHIGHO2 01 FULL OD1 Yanofskybacteria 41 21
Bacteria CPR Parcubacteria OD1 Yanofskybacteria RIFCSPHIGHO2 01 FULL OD1 Yanofskybacteria 48 25b
Bacteria CPR Parcubacteria OD1 Yanofskybacteria GWA1 OD1 39 13 partial
Bacteria CPR Parcubacteria OD1 Yanofskybacteria RIFCSPHIGHO2 01 FULL OD1 Yanofskybacteria 43 32
Bacteria CPR Parcubacteria OD1 Yanofskybacteria RIFCSPLOWO2 01 FULL OD1 Yanofskybacteria 41 34
Bacteria CPR Parcubacteria OD1 Yanofskybacteria GWC2 OD1 41 9
Bacteria CPR Parcubacteria OD1 Yanofskybacteria RIFCSPHIGHO2 01 FULL OD1 Yanofskybacteria 44 22
Bacteria CPR Parcubacteria OD1 Yanofskybacteria RIFCSPHIGHO2 01 FULL OD1 Yanofskybacteria 39 8b
Bacteria CPR Parcubacteria OD1 Yanofskybacteria RIFCSPHIGHO2 02 FULL OD1 Yanofskybacteria 39 10
Bacteria CPR Parcubacteria OD1 Yanofskybacteria RIFCSPHIGHO2 02 FULL OD1 Yanofskybacteria 41 29
Bacteria CPR Parcubacteria OD1 Yanofskybacteria RIFCSPHIGHO2 01 FULL OD1 Yanofskybacteria 38 22b
Bacteria CPR Parcubacteria OD1 Yanofskybacteria RIFCSPHIGHO2 01 FULL OD1 Yanofskybacteria 44 24
Bacteria CPR Parcubacteria OD1 Yanofskybacteria RIFCSPHIGHO2 02 FULL OD1 Yanofskybacteria 41 11
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Bacteria CPR Parcubacteria OD1 Yanofskybacteria RIFCSPHIGHO2 02 FULL OD1 Yanofskybacteria 43 22
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Bacteria CPR Parcubacteria OD1 Yanofskybacteria GWD1 OD1 39 16 partial
Bacteria CPR Parcubacteria OD1 Yanofskybacteria GWF1 OD1 44 227
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Bacteria CPR Parcubacteria OD1 Yanofskybacteria RIFCSPLOWO2 02 FULL OD1 Yanofskybacteria 45 18
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Bacteria CPR Parcubacteria OD1 Yanofskybacteria RIFCSPLOWO2 01 FULL OD1 Yanofskybacteria 49 25
Bacteria CPR Parcubacteria OD1 Yanofskybacteria RIFCSPHIGHO2 12 FULL OD1 Yanofskybacteria 45 19b
Bacteria CPR Parcubacteria OD1 Yanofskybacteria RIFCSPLOWO2 02 FULL OD1 Yanofskybacteria 43 10b
Bacteria CPR Parcubacteria OD1 RIFCSPHIGHO2 01 FULL OD1 40 30
Bacteria CPR Parcubacteria OD1 L1 Parcubacteria bacterium SCGC AAA011 A09 DUSEL 001 189
Bacteria CPR Parcubacteria OD1 GWA2 OD1 31 28 partial
Bacteria CPR Parcubacteria OD1 RIFCSPHIGHO2 01 FULL OD1 47 10b
Bacteria CPR Parcubacteria OD1 GWD2 OD1 38 11
Bacteria CPR Parcubacteria OD1 MoranbacteriaOD1 i GWE2 OD1 36 40
Bacteria CPR Parcubacteria OD1 MoranbacteriaOD1 i GWC2 OD1 i 37 82
Bacteria CPR Parcubacteria OD1 MoranbacteriaOD1 i GWC2 OD1 i 45 10
Bacteria CPR Parcubacteria OD1 MoranbacteriaOD1 i GWE1 OD1 i ACD11 lin 49 15
Bacteria CPR Parcubacteria OD1 Moranbacteria
Bacteria CPR Parcubacteria OD1 Moranbacteria CG Moran 01
Bacteria CPR Parcubacteria OD1 Moranbacteria CG Moran 02
Bacteria CPR Parcubacteria OD1 Moranbacteria RIFCSPLOWO2 12 FULL OD1 Moranbacteria 48 12
Bacteria CPR Parcubacteria OD1 Moranbacteria RIFCSPHIGHO2 01 FULL OD1 Moranbacteria 54 31
Bacteria CPR Parcubacteria OD1 Moranbacteria RIFCSPHIGHO2 01 FULL OD1 Moranbacteria 55 24
Bacteria CPR Parcubacteria OD1 MoranbacteriaOD1 i GWE1 OD1 ACD7 35 17
Bacteria CPR Parcubacteria OD1 MoranbacteriaOD1 i GWF1 OD1 34 10
Bacteria CPR Parcubacteria OD1 ALUMROCK MS4 OD1 33 19
Bacteria CPR Parcubacteria OD1 MoranbacteriaOD1 i GWD1 OD1 37 17
Bacteria CPR Parcubacteria OD1 Moranbacteria RIFCSPHIGHO2 12 FULL OD1 Moranbacteria 40 10
Bacteria CPR Parcubacteria OD1 Moranbacteria RifOxyA12 full OD1 Moranbacteria 35 19
Bacteria CPR Parcubacteria OD1 Moranbacteria RifOxyA12 full OD1 Moranbacteria 44 15
Bacteria CPR Parcubacteria OD1 Moranbacteria RBG 19FT COMBO OD1 Moranbacteria 42 6
Bacteria CPR Parcubacteria OD1 MoranbacteriaOD1 i GWA2 OD1 39 41
Bacteria CPR Parcubacteria OD1 Moranbacteria RIFOXYB1 FULL OD1 Moranbacteria 44 23
Bacteria CPR Parcubacteria OD1 Moranbacteria RIFOXYC1 FULL OD1 Moranbacteria 44 13
Bacteria CPR Parcubacteria OD1 Moranbacteria RBG 13 OD1 Moranbacteria 45 13
Bacteria CPR Parcubacteria OD1 RIF-OD1-4 RIFCSPHIGHO2 01 FULL RIF OD1 04 46 36
Bacteria CPR Parcubacteria OD1 RIF-OD1-4 RIFCSPHIGHO2 12 FULL RIF OD1 04 45 11b
Bacteria CPR Parcubacteria OD1 RIF-OD1-4 RIFCSPHIGHO2 02 FULL RIF OD1 04 46 16
Bacteria CPR Parcubacteria OD1 Magasanikbacteria CG Magasa 02
Bacteria CPR Parcubacteria OD1 Magasanikbacteria GWD2 OD1 43 18
Bacteria CPR Parcubacteria OD1 Magasanikbacteria RIFCSPHIGHO2 02 FULL OD1 Magasanikbacteria 41 13
Bacteria CPR Parcubacteria OD1 Magasanikbacteria RIFCSPHIGHO2 02 FULL OD1 Magasanikbacteria 47 14
Bacteria CPR Parcubacteria OD1 Magasanikbacteria RIFCSPHIGHO2 02 FULL OD1 Magasanikbacteria 33 17
Bacteria CPR Parcubacteria OD1 Magasanikbacteria RIFOXYB1 FULL OD1 Magasanikbacteria 40 15
Bacteria CPR Parcubacteria OD1 Magasanikbacteria RIFCSPHIGHO2 02 FULL OD1 Magasanikbacteria 51 14
Bacteria CPR Parcubacteria OD1 Magasanikbacteria RIFCSPHIGHO2 02 FULL OD1 Magasanikbacteria 47 16
Bacteria CPR Parcubacteria OD1 Magasanikbacteria RifOxyC12 full OD1 Magasanikbacteria 33 11
Bacteria CPR Parcubacteria OD1 Magasanikbacteria RIFOXYD12 FULL OD1 Magasanikbacteria 33 17
Bacteria CPR Parcubacteria OD1 Magasanikbacteria CG Magasa 01
Bacteria CPR Parcubacteria OD1 Magasanikbacteria RIFOXYC2 FULL OD1 Magasanikbacteria 39 8
Bacteria CPR Parcubacteria OD1 Magasanikbacteria GWA2 OD1 56 11
Bacteria CPR Parcubacteria OD1 Magasanikbacteria RIFCSPHIGHO2 12 FULL OD1 Magasanikbacteria 41 16
Bacteria CPR Parcubacteria OD1 Magasanikbacteria Parcubacteria bacterium SCGC AAA011 J21 DUSEL 001 191
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Bacteria CPR Parcubacteria OD1 Magasanikbacteria RIFOXYC2 FULL OD1 Magasanikbacteria 42 28
Bacteria CPR Parcubacteria OD1 Magasanikbacteria RIFOXYD2 FULL OD1 Magasanikbacteria 41 14
Bacteria CPR Parcubacteria OD1 Magasanikbacteria RIFOXYA2 FULL OD1 Magasanikbacteria 44 8
Bacteria CPR Parcubacteria OD1 Magasanikbacteria RIFOXYD2 FULL OD1 Magasanikbacteria 36 9
Bacteria CPR Parcubacteria OD1 Magasanikbacteria GWA2 OD1 50 22 partial
Bacteria CPR Parcubacteria OD1 Magasanikbacteria RIFCSPHIGHO2 01 FULL OD1 Magasanikbacteria 47 8
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Bacteria CPR Parcubacteria OD1 Magasanikbacteria GWA2 OD1 40 10 partial
Bacteria CPR Parcubacteria OD1 Magasanikbacteria RIFOXYD1 FULL OD1 Magasanikbacteria 40 23
Bacteria CPR Parcubacteria OD1 Magasanikbacteria GWA2 OD1 46 17 plus
Bacteria CPR Parcubacteria OD1 Uhrbacteria RIFCSPLOWO2 02 FULL OD1 Uhrbacteria 51 9
Bacteria CPR Parcubacteria OD1 Magasanikbacteria RIFCSPHIGHO2 02 FULL OD1 Magasanikbacteria 50 9b
Bacteria CPR Parcubacteria OD1 Magasanikbacteria GWA2 OD1 42 32
Bacteria CPR Parcubacteria OD1 Magasanikbacteria GWC2 OD1 41 17
Bacteria CPR Parcubacteria OD1 Magasanikbacteria GWA2 OD1 45 39 plus
Bacteria CPR Parcubacteria OD1 Uhrbacteria GWA2 OD1 52 8b
Bacteria CPR Parcubacteria OD1 Uhrbacteria GWF2 OD1 39 13
Bin 40
Bin 40 1
Bacteria CPR Parcubacteria OD1 Uhrbacteria RIFOXYB2 FULL OD1 Uhrbacteria 45 11
Bacteria CPR Parcubacteria OD1 Uhrbacteria GWF2 OD1 46 218
Bacteria CPR Parcubacteria OD1 Uhrbacteria RIFOXYB2 FULL OD1 Uhrbacteria 41 18
Bacteria CPR Parcubacteria OD1 Uhrbacteria RIFCSPHIGHO2 01 FULL OD1 Uhrbacteria 63 20
Bacteria CPR Parcubacteria OD1 Uhrbacteria RIFOXYB2 FULL OD1 Uhrbacteria 57 15
Bacteria CPR Parcubacteria OD1 Uhrbacteria GWA2 OD1 53 10
Bacteria CPR Parcubacteria OD1 Uhrbacteria GWA2 OD1 41 10
Bacteria CPR Parcubacteria OD1 Uhrbacteria GWE2 OD1 45 35
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Bacteria CPR Parcubacteria OD1 Uhrbacteria ACD76
Bacteria CPR Parcubacteria OD1 Uhrbacteria RIFCSPHIGHO2 02 FULL OD1 Uhrbacteria 53 13
Bacteria CPR Parcubacteria OD1 CG CPR 02 CG CPR02 01
Bacteria CPR Parcubacteria OD1 Uhrbacteria RIFOXYC2 FULL OD1 Uhrbacteria 47 19
Bacteria CPR Parcubacteria OD1 uncultured SG8 24
Bacteria CPR Parcubacteria OD1 Uhrbacteria RIFCSPHIGHO2 02 FULL OD1 Uhrbacteria 60 10
Bacteria CPR Parcubacteria OD1 Uhrbacteria RIFCSPHIGHO2 12 FULL OD1 Uhrbacteria 60 25
Bacteria CPR Parcubacteria OD1 Uhrbacteria RIFCSPHIGHO2 02 FULL OD1 Uhrbacteria 57 19
Bacteria CPR Parcubacteria OD1 GWA2 OD1 47 26
Bacteria CPR Parcubacteria OD1 Uhrbacteria RIFCSPLOWO2 02 FULL OD1 Uhrbacteria 46 25
Bacteria CPR Parcubacteria OD1 Uhrbacteria RIFCSPLOWO2 01 FULL OD1 Uhrbacteria 47 25
Bacteria CPR Parcubacteria OD1 Uhrbacteria RIFCSPLOWO2 01 FULL OD1 Uhrbacteria 48 12
Bacteria CPR Parcubacteria OD1 Parcubacteria bacterium SCGC AAA011 N16 Dusel 001 262
Bacteria CPR Parcubacteria OD1 CG CPR 12 CG CPR12 01
Bacteria CPR Parcubacteria OD1 Falkowbacteria GWE2 OD1 38 254
Bacteria CPR Parcubacteria OD1 Falkowbacteria RIFOXYD2 FULL OD1 Falkowbacteria 34 120
Bacteria CPR Parcubacteria OD1 Falkowbacteria RIFOXYA2 FULL OD1 Falkowbacteria 47 19
Bacteria CPR Parcubacteria OD1 Falkowbacteria Parcubacteria bacterium SCGC AAA036 E14 CrabSpa 001 178
Bacteria CPR Parcubacteria OD1 Falkowbacteria CG Falkow 01
Bacteria CPR Parcubacteria OD1 Falkowbacteria GWF2 OD1 43 32
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Bacteria CPR Parcubacteria OD1 Falkowbacteria CG Falkow 02
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Bacteria CPR Parcubacteria OD1 GWE2 OD1 38 18
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Bacteria CPR Parcubacteria OD1 GWA2 OD1 40 23
Bacteria CPR Parcubacteria OD1 GWC2 OD1 38 7
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Bacteria CPR Parcubacteria OD1 Falkowbacteria RIFOXYC2 FULL OD1 Falkowbacteria 36 12
Bacteria CPR Parcubacteria OD1 Falkowbacteria RBG 13 OD1 Falkowbacteria 39 14
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Bacteria CPR Parcubacteria OD1 Falkowbacteria RIFCSPHIGHO2 01 FULL OD1 Falkowbacteria 44 11
Bacteria CPR Parcubacteria OD1 Falkowbacteria RIFCSPHIGHO2 02 FULL OD1 Falkowbacteria 39 17
Bacteria CPR Parcubacteria OD1 Falkowbacteria RIFCSPLOWO2 02 FULL OD1 Falkowbacteria 46 11b
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Bacteria CPR Parcubacteria OD1 Falkowbacteria RIFCSPHIGHO2 01 FULL OD1 Falkowbacteria 47 11b
Bacteria CPR Parcubacteria OD1 GWA2 OD1 38 13
Bacteria CPR Parcubacteria OD1 Falkowbacteria RBG 13 OD1 Falkowbacteria 36 9
Bacteria CPR Parcubacteria OD1 Falkowbacteria RBG 13 OD1 Falkowbacteria 39 9
Bacteria CPR Parcubacteria OD1 Falkowbacteria RifOXYA2 FULL OD1 Falkowbacteria 38 12
Bacteria CPR Parcubacteria OD1 Falkowbacteria RIFCSPHIGHO2 02 FULL OD1 Falkowbacteria 39 13
Bacteria CPR Parcubacteria OD1 Kuenenbacteria CG Kuenen 02
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Bacteria CPR Parcubacteria OD1 Uhrbacteria RIFCSPHIGHO2 02 FULL OD1 Uhrbacteria 49 11
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Bacteria CPR Parcubacteria OD1 RIF-OD1-1 RIFCSPLOWO2 02 FULL RIF OD1 01 42 19
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Bacteria CPR Parcubacteria OD1 GWA2 OD1 44 12
Bacteria CPR Parcubacteria OD1 RIF-OD1-2 RIFCSPLOWO2 01 FULL RIF OD1 02 44 13
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Bacteria CPR Parcubacteria OD1 RIF-OD1-2 RIFOXYD2 FULL RIF OD1 02 43 21
Bacteria CPR Parcubacteria OD1 Kuenenbacteria CG Kuenen 03
Bacteria CPR Parcubacteria OD1 Parcubacteria bacterium SCGC AB 164 E21 SAK 001 209
Bacteria CPR Parcubacteria OD1 Falkowbacteria RIFCSPLOWO2 01 FULL OD1 Falkowbacteria 39 33
Bacteria SM2F11 RIFCSPHIGHO2 12 FULL SM2F11 48 16
Bacteria unclassified bacteria RIFCSPHIGHO2 02 FULL SM2F11 43 13b
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Bacteria unclassified bacteria GWA2 OD1 rel 51 12
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Bacteria CPR PeregrinibacteriaPER PER GWF2 39 17
Bin 39
Bin 16
Bacteria CPR PeregrinibacteriaPER PER GWF2 43 17
Bacteria Peregrinibacteria RIFOXYC2 FULL Peregrinibacteria 41 22
Bacteria CPR Peregrinibacteria CG PER 02
Bacteria Peregrinibacteria RIFCSPLOWO2 02 FULL Peregrinibacteria 48 14
Bacteria CP Peregrinibacteria BJP IG2102 PER 44 74 final
Bacteria Peregrinibacteria RIFCSPLOWO2 01 FULL Peregrinibacteria 39 12
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Bacteria CPR unclassified bacteria CG PER 03
Bacteria CPR PER-ii CG PER 01
Bacteria PER-ii RIFOXYC2 FULL PER ii 58 32
Bacteria CPR PER-ii GWB1 PER 54 5
Bacteria PER-ii RIFOXYD2 FULL PER ii 58 15
Bacteria PER-ii RIFCSPHIGHO2 01 FULL PER ii 55 13
Bacteria PER-ii RIFCSPLOWO2 12 FULL PER ii 53 10
Bacteria PER-ii RIFCSPHIGHO2 01 FULL PER ii 51 35
Bacteria PER-ii RIFCSPHIGHO2 01 FULL PER ii 49 16
Bacteria PER-ii RIFCSPLOWO2 12 FULL PER ii 55 15
Bacteria PER-ii RIFCSPHIGHO2 01 FULL PER ii 51 9
Bacteria PER-ii RIFCSPHIGHO2 02 FULL PER ii 51 15
Bacteria CP Peregrinibacteria ALUMROCK MS4 Peregrinibacteria 34 52
Bacteria GN02 CG GN02 01
Bacteria GN02 CG GN02 02
Bacteria CPR GracilibacteriaBD1 5 ACD49
Bacteria CP GN02 candidate division GN02 bacterium JGI 0000069 K10 CrabSpa 001 277
Bacteria CP GN02 candidate division GN02 bacterium JGI 0000069 P22 CrabSpa 001 278
Bacteria uncultured bacterium SCGC AB 137 L08
Bacteria CP SR1 candidate division SR1 bacterium taxon 345 1OR1 recoded II
Bacteria CP SR1 RAAC1 SR1 1
Bacteria CP SR1 bacterium Aalborg AAW 1
Bacteria CPR unclassified bacteria RBG 16 CPR 42 10
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Bacteria CPR Saccharibacteria TM7 BJP IG2103 TM7 39 1400
Bacteria TM7 CG TM7 01
Bacteria CPR Saccharibacteria TM7 GWC2 TM7 48 9
Bacteria CPR Saccharibacteria TM7 candidate division TM7 genomosp. GTL1 unfinished sequence
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Bacteria CPR Saccharibacteria TM7 RIFCSPHIGHO2 12 FULL Saccharibacteria 47 16b
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Bacteria CPR Saccharibacteria TM7 RIFCSPHIGHO2 02 FULL Saccharibacteria 47 12
Bacteria CPR Saccharibacteria TM7 RIFCSPHIGHO2 12 FULL Saccharibacteria 41 12
Bacteria CPR Saccharibacteria TM7 DOLZORAL124 TM7 51 29
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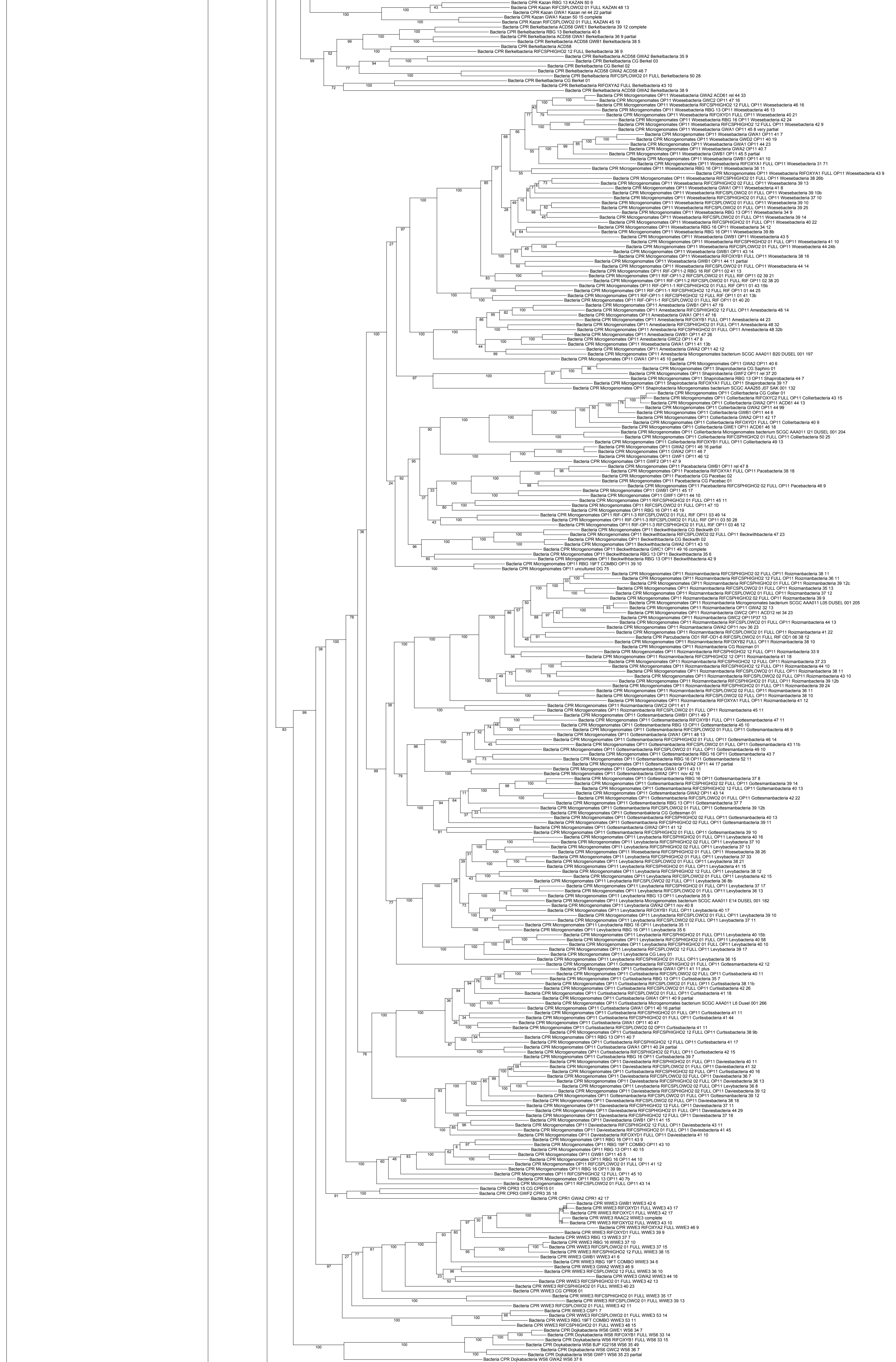
Bacteria CPR2 GWD2 CPR2 39 7
Bacteria CG CPR 16 CG CPR16 01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Bacteria CPR Kazan GWA1 Kazan rel 44 22 partial
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Bacteria CPR Kazan RIFCSPLOWO2 01 FULL KAZAN 45 19
Bacteria CPR Berkelbacteria ACD58 GWE1 Berkelbacteria 39 12 complete
Bacteria CPR Berkelbacteria RBG 13 Berkelbacteria 40 8
Bacteria CPR Berkelbacteria ACD58 GWA1 Berkelbacteria 36 9 partial
Bacteria CPR Berkelbacteria ACD58 GWB1 Berkelbacteria 38 5
Bacteria CPR Berkelbacteria ACD58
Bacteria CPR Berkelbacteria RIFCSPHIGHO2 12 FULL Berkelbacteria 36 9
Bacteria CPR Berkelbacteria ACD58 GWA2 Berkelbacteria 35 9
Bacteria CPR Berkelbacteria CG Berkel 03
Bacteria CPR Berkelbacteria CG Berkel 02
Bacteria CPR Berkelbacteria ACD58 GWA2 ACD58 46 7
Bacteria CPR Berkelbacteria RIFCSPLOWO2 01 FULL Berkelbacteria 50 28
Bacteria CPR Berkelbacteria CG Berkel 01
Bacteria CPR Berkelbacteria RIFOXYA2 FULL Berkelbacteria 43 10
Bacteria CPR Berkelbacteria ACD58 GWA2 Berkelbacteria 38 9
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Bacteria CPR Microgenomates OP11 Woesebacteria GWC2 OP11 47 16
Bacteria CPR Microgenomates OP11 Woesebacteria RIFCSPHIGHO2 12 FULL OP11 Woesebacteria 46 16
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Bacteria CPR Microgenomates OP11 Woesebacteria RIFOXYB1 FULL OP11 Woesebacteria 38 16
Bacteria CPR Microgenomates OP11 Woesebacteria GWB1 OP11 44 11 partial
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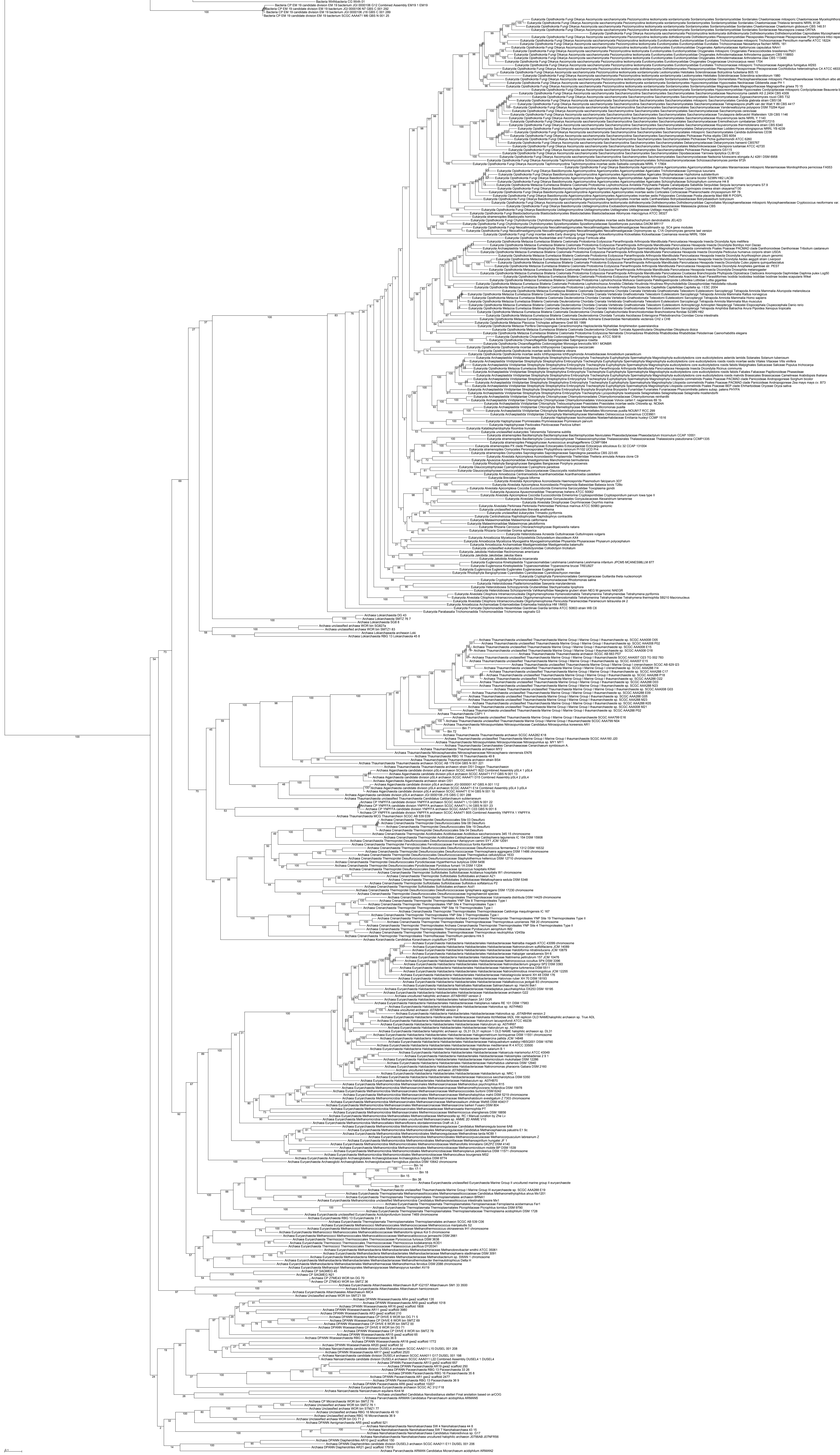
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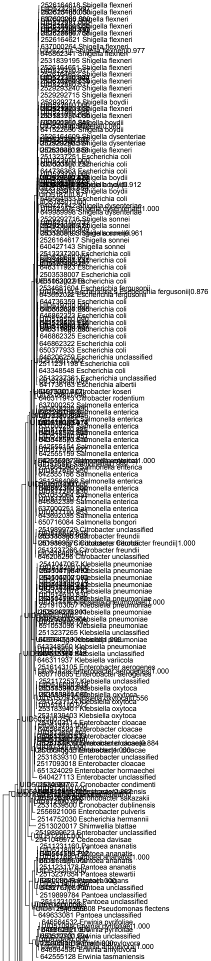
Figure S2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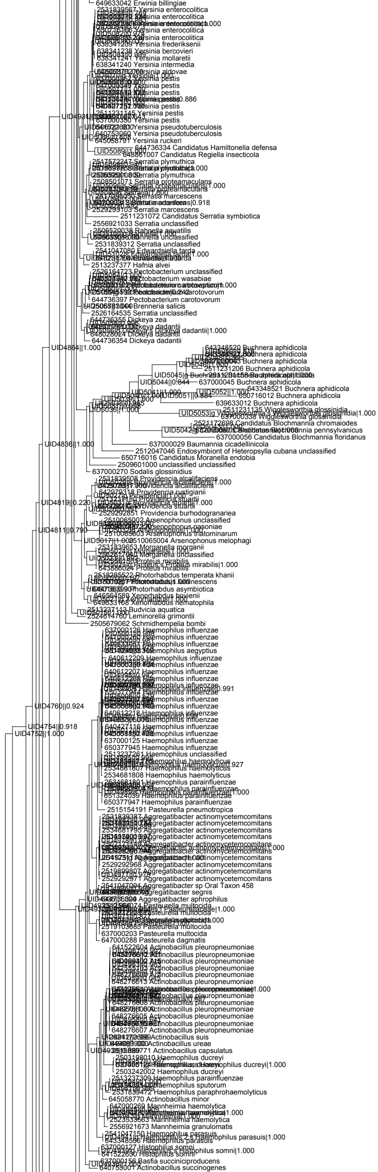
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2531839567 Yersinia enterocolitica
Yersinia enterocolitica
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638341241 Yersinia mollaretii
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Yersinia aldovae
Yersinia pestis
Yersinia pestis
Yersinia pestis
Yersinia pestis
2511231145 Yersinia pestis
637000350 Yersinia pestis
Yersinia pseudotuberculosis
640753060 Yersinia pseudotuberculosis
645058791 Yersinia ruckeri
644736334 Candidatus Hamiltonella defensa
648861007 Candidatus Regiella insecticola
2517572247 Serratia plymuthica
Serratia plymuthica
2508501071 Serratia proteamaculans
Serratia marcescens
2529293103 Serratia marcescens
2511231072 Candidatus Serratia symbiotica
2556921033 Serratia unclassified
2506520038 Rahnella aquatilis
Rahnella unclassified
2531839312 Serratia unclassified
2541047080 Edwardsiella tarda
2513237377 Hafnia alvei
2526164723 Pectobacterium unclassified
Pectobacterium wasabiae
644736397 Pectobacterium carotovorum
Brenneria salicis
2526164535 Serratia unclassified
644736355 Dickeya zea
648028024 Dickeya dadantii
644736354 Dickeya dadantii
UID4931
UID4864||1.000
643348520 Buchnera aphidicola
Buchnera aphidicola
Buchnera aphidicola
2511231206 Buchnera aphidicola
UID5045
UID5044||0.844
637000045 Buchnera aphidicola
UID5041||1.000
UID5052||1.000
643348521 Buchnera aphidicola
UID5051||0.884
650716012 Buchnera aphidicola
639633012 Buchnera aphidicola
2511231135 Wigglesworthia glossinidia
637000338 Wigglesworthia glossinidia
UID5053|g Wigglesworthia|s Wigglesworthia glossinidia|1.000
2521172698 Candidatus Blochmannia chromaiodes
UID5042
Candidatus Blochmannia pennsylvanicus
637000056 Candidatus Blochmannia floridanus
637000029 Baumannia cicadellinicola
2512047046 Endosymbiont of Heteropsylla cubana unclassified
650716016 Candidatus Moranella endobia
2509601000 unclassified unclassified
637000270 Sodalis glossinidius
UID5036||1.000
UID4836||1.000
2531839508 Providencia alcalifaciens
Providencia alcalifaciens
642979318 Providencia rustigianii
Providencia stuartii
Providencia stuartii
2529292851 Providencia burhodogranariea
2510065002 Arsenophonus unclassified
Arsenophonus nasoniae
2510065003 Arsenophonus triatominarum
UID5017||1.000
2510065004 Arsenophonus melophagi
UID4819||0.220
UID4811||0.790
2531839653 Morganella morganii
Morganella unclassified
Proteus mirabilis
643886024 Proteus mirabilis
2518285522 Photorhabdus temperata khanii
Photorhabdus luminescens
Photorhabdus asymbiotica
646564589 Xenorhabdus bovienii
649633106 Xenorhabdus nematophila
2513237113 Budvicia aquatica
2524614760 Leminorella grimontii
2505679062 Schmidhempelia bombi
637000126 Haemophilus influenzae
Haemophilus influenzae
Haemophilus influenzae
Haemophilus aegyptius
640612209 Haemophilus influenzae
Haemophilus influenzae
640612207 Haemophilus influenzae
Haemophilus influenzae
Haemophilus influenzae
Haemophilus influenzae
640612218 Haemophilus influenzae
Haemophilus influenzae
640427116 Haemophilus influenzae
Haemophilus influenzae
637000125 Haemophilus influenzae
650377945 Haemophilus influenzae
UID4760||0.924
UID4754||0.918
UID4752||1.000
2513237261 Haemophilus unclassified
Haemophilus haemolyticus
2534681807 Haemophilus haemolyticus
2534681808 Haemophilus haemolyticus
Haemophilus parainfluenzae
Haemophilus parainfluenzae
651324039 Haemophilus parainfluenzae
650377947 Haemophilus parainfluenzae
2515154191 Pasteurella pneumotropica
2531839387 Aggregatibacter actinomycetemcomitans
Aggregatibacter actinomycetemcomitans
Aggregatibacter actinomycetemcomitans
Aggregatibacter actinomycetemcomitans
Aggregatibacter actinomycetemcomitans
Aggregatibacter actinomycetemcomitans
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2541047094 Aggregatibacter sp Oral Taxon 458
Aggregatibacter segnis
Aggregatibacter aphrophilus
Pasteurella multocida
Pasteurella multocida
2519103085 Pasteurella multocida
637000203 Pasteurella multocida
647000288 Pasteurella dagmatis
641522604 Actinobacillus pleuropneumoniae
Actinobacillus pleuropneumoniae
Actinobacillus pleuropneumoniae
Actinobacillus pleuropneumoniae
648276613 Actinobacillus pleuropneumoniae
Actinobacillus pleuropneumoniae
648276608 Actinobacillus pleuropneumoniae
648276605 Actinobacillus pleuropneumoniae
Actinobacillus pleuropneumoniae
648276607 Actinobacillus pleuropneumoniae
Actinobacillus suis
Actinobacillus ureae
2519899771 Actinobacillus capsulatus
2503198010 Haemophilus ducreyi
Haemophilus ducreyi|1.000
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Haemophilus sputorum
2531839472 Haemophilus paraphrohaemolyticus
645058770 Actinobacillus minor
647000269 Mannheimia haemolytica
Mannheimia haemolytica
2523533563 Mannheimia haemolytica
2556921673 Mannheimia granulomatis
2541047150 Haemophilus parasuis
Haemophilus parasuis|1.000
643348556 Haemophilus parasuis
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Histophilus somni|1.000
641522650 Histophilus somni
637000156 Basfia succiniciproducens
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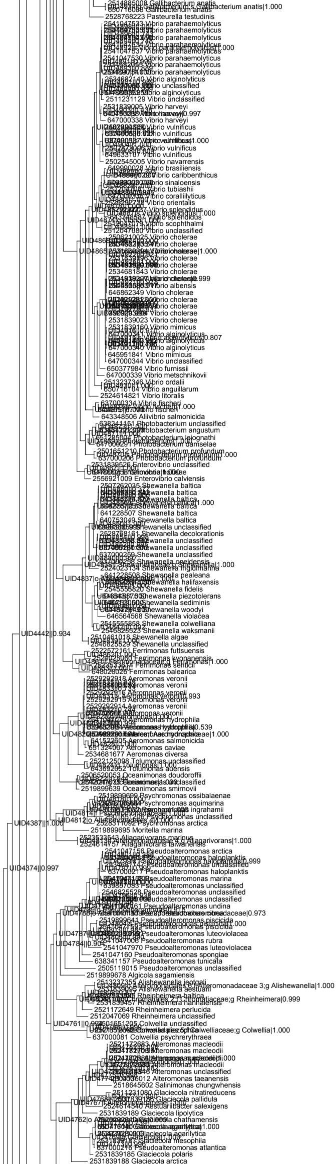
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Gallibacterium anatis|1.000
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Vibrio parahaemolyticus
Vibrio parahaemolyticus
Vibrio parahaemolyticus|1.000
2541047537 Vibrio parahaemolyticus
2541047530 Vibrio parahaemolyticus
Vibrio parahaemolyticus
Vibrio parahaemolyticus
2534682140 Vibrio alginolyticus
Vibrio unclassified
Vibrio alginolyticus
2511231129 Vibrio unclassified
2531839005 Vibrio harveyi
Vibrio harveyi|0.997
647000338 Vibrio harveyi
Vibrio vulnificus
Vibrio vulnificus
Vibrio vulnificus|1.000
Vibrio vulnificus
645533107 Vibrio vulnificus
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649990028 Vibrio brasiliensis
Vibrio caribbenthicus
Vibrio sinaloensis
Vibrio tubiashii
Vibrio coralliilyticus
Vibrio orientalis
Vibrio splendidus
Vibrio splendidus|1.000
Vibrio splendidus
Vibrio scophthalmi
2512047080 Vibrio unclassified
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Vibrio cholerae
Vibrio cholerae|1.000
Vibrio cholerae
Vibrio cholerae
2534681843 Vibrio cholerae
Vibrio cholerae|0.999
Vibrio albensis
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Vibrio cholerae
Vibrio cholerae
Vibrio cholerae
2531839023 Vibrio cholerae
2531839160 Vibrio mimicus
Vibrio alginolyticus
Vibrio alginolyticus|0.807
647000340 Vibrio alginolyticus
645951841 Vibrio mimicus
647000344 Vibrio unclassified
650377984 Vibrio furnissii
647000339 Vibrio metschnikovii
2513237346 Vibrio ordalii
650716104 Vibrio anguillarum
2524614821 Vibrio litoralis
637000334 Vibrio fischeri
Vibrio fischeri|1.000
Vibrio fischeri
643348506 Aliivibrio salmonicida
638341151 Photobacterium unclassified
Photobacterium angustum
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647000251 Photobacterium damselae
2501651210 Photobacterium profundum
Photobacterium profundum|1.000
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Enterovibrio|1.000
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Shewanella baltica
641228507 Shewanella baltica
640753049 Shewanella baltica
Shewanella unclassified
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Shewanella unclassified
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637000259 Shewanella unclassified
Shewanella oneidensis
Shewanella|1.000
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UID4837|o
641228508 Shewanella pealeana
Shewanella halifaxensis
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Shewanella piezotolerans
Shewanella sediminis
Shewanella woodyi
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Ferrimonas kyonanensis
Ferrimonadaceae;g Ferrimonas|1.000
Ferrimonas sediminum
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Aeromonas veronii
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2529292915 Aeromonas veronii
2529292914 Aeromonas veronii
Aeromonas veronii
Aeromonas hydrophila
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2534681677 Aeromonas diversa
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Oceanimonas|1.000
Oceanimonas unclassified
2519899639 Oceanimonas smirnovii
2519899699 Psychromonas ossibalaenae
Psychromonas aquimarina
Psychromonas ingrahamii
2501651206 Psychromonas unclassified
UID4814
UID4812|o
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UID4387||1.000
2519899695 Moritella marina
2523533543 Aliagarivorans marinus
Aliagarivorans|1.000
2524614757 Aliagarivorans taiwanensis
UID4374||0.997
2541047156 Pseudoalteromonas arctica
Pseudoalteromonas haloplanktis
Pseudoalteromonas haloplanktis|0.999
Pseudoalteromonas unclassified
637000217 Pseudoalteromonas haloplanktis
Pseudoalteromonas marina
639857033 Pseudoalteromonas unclassified
2546825528 Pseudoalteromonas unclassified
Pseudoalteromonas unclassified
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UID4788|o
Pseudoalteromonadaceae|0.973
Pseudoalteromonas citrea
2519899641 Pseudoalteromonas piscicida
Pseudoalteromonas piscicida
Pseudoalteromonas|1.000
UID4787
Pseudoalteromonas luteoviolacea
2541047006 Pseudoalteromonas rubra
UID4784||0.904
2541047970 Pseudoalteromonas luteoviolacea
2541047160 Pseudoalteromonas spongiae
638341157 Pseudoalteromonas tunicata
2505119015 Pseudoalteromonas unclassified
2519899678 Algicola sagamiensis
2513237355 Alishewanella jeotgali
Alteromonadales 6;f Alteromonadaceae 3;g Alishewanella|1.000
Alishewanella aestuarii
Rheinheimera baltica
Chromatiales 2;f Chromatiaceae;g Rheinheimera|0.999
2531839457 Rheinheimera nanhaiensis
2521172649 Rheinheimera perlucida
2512047069 Rheinheimera unclassified
UID4761||0.99
2501651205 Colwellia unclassified
Colwellia piezophila
Colwelliaceae;g Colwellia|1.000
637000081 Colwellia psychrerythraea
2521172683 Alteromonas macleodii
Alteromonas macleodii
Alteromonas macleodii|1.000
Alteromonas macleodii
Alteromonas unclassified
2509036012 Alteromonas taeanensis
2518645602 Salinimonas chungwhensis
2511231080 Glaciecola nitratireducens
Glaciecola pallidula
2524614540 Aestuariibacter salexigens
2531839189 Glaciecola lipolytica
UID4762|o
Glaciecola chathamensis
Glaciecola agarilytica
Glaciecola agarilytica|1.000
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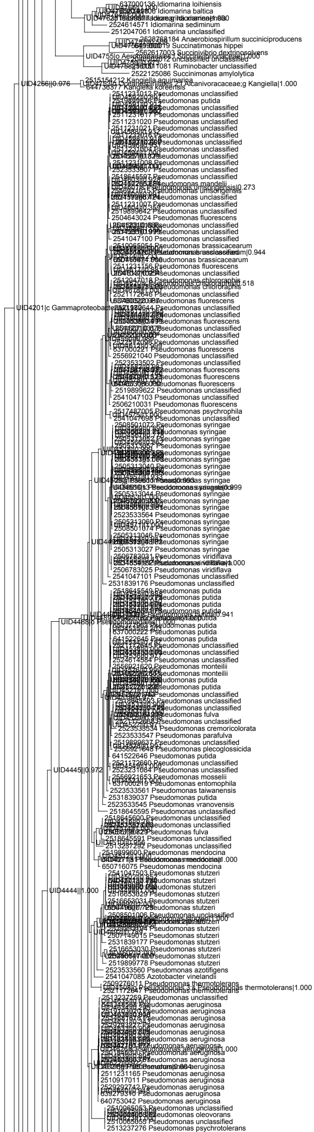
Glaciecola mesophila
637000215 Pseudoalteromonas atlantica
2531839185 Glaciecola polaris
2531839188 Glaciecola arctica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Idiomarina baltica
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Succinatimonas hippei
2562617003 Succinivibrio dextrinosolvens
UID4755|o Aeromonadales
Ruminobacter unclassified
2522125086 Succinimonas amylolytica
UID4266||0.976
2515154212 Kangiella aquimarina
Alcanivoracaceae;g Kangiella|1.000
644736377 Kangiella koreensis
2511231012 Pseudomonas unclassified
Pseudomonas putida
Pseudomonas unclassified
2511231017 Pseudomonas unclassified
2511231020 Pseudomonas unclassified
2511231021 Pseudomonas unclassified
Pseudomonas unclassified
Pseudomonas unclassified
2511231004 Pseudomonas unclassified
Pseudomonas unclassified
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2523533507 Pseudomonas unclassified
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Pseudomonas mandelii
Pseudomonas umsongensis|0.273
Pseudomonas umsongensis
Pseudomonas unclassified
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2519899642 Pseudomonas unclassified
2504643024 Pseudomonas fluorescens
Pseudomonas unclassified
Pseudomonas unclassified
2541047100 Pseudomonas unclassified
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Pseudomonas brassicacearum|0.944
Pseudomonas brassicacearum
2511231156 Pseudomonas fluorescens
Pseudomonas unclassified
2512047018 Pseudomonas chlororaphis
Pseudomonas chlororaphis|0.518
Pseudomonas chlororaphis
2521172646 Pseudomonas unclassified
Pseudomonas fluorescens
UID4201|c Gammaproteobacteria
Pseudomonas unclassified
Pseudomonas unclassified
Pseudomonas fluorescens
Pseudomonas unclassified
Pseudomonas unclassified
2523533066 Pseudomonas unclassified
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Pseudomonas fluorescens
Pseudomonas fluorescens
Pseudomonas fluorescens
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Pseudomonas syringae
Pseudomonas syringae
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Pseudomonas syringae
Pseudomonas syringae
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Pseudomonas syringae
Pseudomonas syringae|0.999
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Pseudomonas syringae
Pseudomonas syringae
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Pseudomonas syringae
2505313027 Pseudomonas syringae
2506783031 Pseudomonas viridiflava
Pseudomonas viridiflava|1.000
2506783025 Pseudomonas viridiflava
2541047101 Pseudomonas unclassified
2531839176 Pseudomonas unclassified
2518645549 Pseudomonas putida
Pseudomonas putida
Pseudomonas putida
Pseudomonas putida
Pseudomonas putida|0.941
UID4488|o Pseudomonadales|1.000
Pseudomonas putida
637000222 Pseudomonas putida
641522645 Pseudomonas putida
Pseudomonas unclassified
Pseudomonas unclassified
2524614584 Pseudomonas unclassified
2556921620 Pseudomonas monteilii
Pseudomonas monteilii
Pseudomonas putida
Pseudomonas putida
Pseudomonas unclassified
Pseudomonas unclassified
Pseudomonas unclassified
Pseudomonas fulva
Pseudomonas unclassified
2523533534 Pseudomonas cremoricolorata
2523533547 Pseudomonas parafulva
2519899637 Pseudomonas unclassified
Pseudomonas plecoglossicida
641522646 Pseudomonas putida
2521172660 Pseudomonas unclassified
2523231084 Pseudomonas unclassified
2556921653 Pseudomonas mosselii
637000219 Pseudomonas entomophila
2523533561 Pseudomonas taiwanensis
UID4445||0.972
2531839037 Pseudomonas putida
2523533545 Pseudomonas vranovensis
2518645595 Pseudomonas unclassified
2518645600 Pseudomonas unclassified
Pseudomonas unclassified
Pseudomonas fulva
2518645591 Pseudomonas unclassified
2513237292 Pseudomonas unclassified
2519899600 Pseudomonas mendocina
Pseudomonas mendocina|1.000
650716075 Pseudomonas mendocina
2541047503 Pseudomonas stutzeri
Pseudomonas stutzeri
Pseudomonas stutzeri
UID4444||1.000
2516653029 Pseudomonas stutzeri
2516653031 Pseudomonas stutzeri
Pseudomonas stutzeri
2508501006 Pseudomonas unclassified
Pseudomonas stutzeri
Pseudomonas stutzeri
2507149015 Pseudomonas stutzeri
2531839177 Pseudomonas stutzeri
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Pseudomonas stutzeri
2519899778 Pseudomonas stutzeri
2523533560 Pseudomonas azotifigens
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2509276011 Pseudomonas thermotolerans
Pseudomonas thermotolerans|1.000
2521172647 Pseudomonas thermotolerans
2513237259 Pseudomonas unclassified
Pseudomonas aeruginosa
Pseudomonas aeruginosa
Pseudomonas aeruginosa
Pseudomonas aeruginosa
Pseudomonas aeruginosa
Pseudomonas aeruginosa
Pseudomonas aeruginosa|1.000
Pseudomonas aeruginosa
Pseudomonas aeruginosa
Pseudomonas aeruginosa
2511231165 Pseudomonas aeruginosa
2510917011 Pseudomonas aeruginosa
2529292742 Pseudomonas aeruginosa
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2510065053 Pseudomonas unclassified
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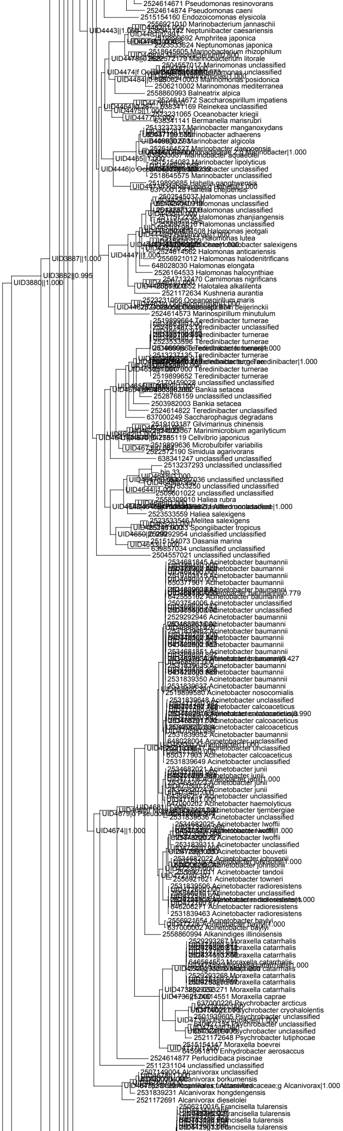
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2519899692 Amphritea japonica
2523533624 Neptunomonas japonica
2518645605 Marinobacterium rhizophilum
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UID4478||0.982
2504557017 Marinomonas unclassified
Marinomonas unclassified
UID4474|f Oceanospirillaceae
UID4484||0.508
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UID4464||0.287
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UID4475||1.000
2523231065 Oceanobacter kriegii
UID4477||1.000
638341141 Bermanella marisrubri
2513237337 Marinobacter manganoxydans
Marinobacter adhaerens
Marinobacter algicola
2526164527 Marinobacter daepoensis
Marinobacter aquaeolei
Marinobacter|1.000
UID4465||1.000
2513154082 Marinobacter lipolyticus
UID4446|o Oceanospirillales
Marinobacter unclassified
2518645575 Marinobacter unclassified
2519899685 Hahella ganghwensis
637000126 Hahella chejuensis
Hahella|1.000
UID3887||1.000
UID3882||0.995
UID3880||1.000
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Halomonas unclassified
Halomonas unclassified
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Halomonas unclassified
508 Halomonas jeotgali
Halomonas lutea
Chromohalobacter salexigens
UID4447||1.000
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Halotalea alkalilenta
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Oceanospirillum beijerinckii
UID4462
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Teredinibacter unclassified
Teredinibacter turnerae
2523533596 Teredinibacter turnerae
Teredinibacter turnerae|1.000
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Teredinibacter|1.000
Teredinibacter turnerae
2519899652 Teredinibacter turnerae
2170459028 unclassified unclassified
Bankia setacea
2528768159 unclassified unclassified
2503982003 Bankia setacea
2524614822 Teredinibacter unclassified
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Marinimicrobium agarilyticum
Cellvibrio japonicus
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638341247 unclassified unclassified
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bin 33
unclassified unclassified
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UID4644||1.000
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Alteromonadales|1.000
2523533559 Haliea salexigens
2523533546 Melitea salexigens
Spongiibacter tropicus
UID4650
unclassified unclassified
2515154073 Dasania marina
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2504557021 unclassified unclassified
2534681845 Acinetobacter baumannii
Acinetobacter baumannii
Acinetobacter baumannii
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Acinetobacter baumannii
Acinetobacter baumannii|0.779
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Acinetobacter unclassified
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Acinetobacter baumannii
Acinetobacter baumannii
Acinetobacter baumannii
Acinetobacter baumannii
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Acinetobacter baumannii
Acinetobacter baumannii
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Acinetobacter calcoaceticus
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Acinetobacter|1.000
Acinetobacter unclassified
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2531839649 Acinetobacter unclassified
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Acinetobacter junii
Acinetobacter junii|1.000
Acinetobacter junii
Acinetobacter junii
Acinetobacter unclassified
647000202 Acinetobacter haemolyticus
Acinetobacter tjernbergiae
UID4681||1.000
UID4679|o Pseudomonadales
2531839536 Acinetobacter unclassified
2534682025 Acinetobacter lwoffii
Acinetobacter lwoffii|1.000
Acinetobacter lwoffii
UID4674||1.000
2531839311 Acinetobacter unclassified
Acinetobacter bouvetii
2534682022 Acinetobacter johnsonii
Acinetobacter johnsonii|1.000
Acinetobacter johnsonii
2556921011 Acinetobacter tandoii
2556921621 Acinetobacter towneri
2531839506 Acinetobacter radioresistens
Acinetobacter unclassified
Acinetobacter radioresistens|1.000
646206271 Acinetobacter radioresistens
2531839463 Acinetobacter radioresistens
2556921654 Acinetobacter baylyi
Acinetobacter baylyi|1.000
637000002 Acinetobacter baylyi
2558860994 Alkanindiges illinoisensis
2529293267 Moraxella catarrhalis
Moraxella catarrhalis
Moraxella catarrhalis
Moraxella catarrhalis
646564552 Moraxella catarrhalis
Moraxella catarrhalis|1.000
Moraxella catarrhalis
2529293268 Moraxella catarrhalis
Moraxella catarrhalis
Moraxella catarrhalis
2529293271 Moraxella catarrhalis
2524614551 Moraxella caprae
637000226 Psychrobacter arcticus
Psychrobacter cryohalolentis
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Psychrobacter|1.000
Psychrobacter unclassified
Psychrobacter unclassified
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2515154147 Moraxella boevrei
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2507149004 Alcanivorax unclassified
Alcanivorax borkumensis
Alcanivoracaceae;g Alcanivorax|1.000
2531839231 Alcanivorax hongdengensis
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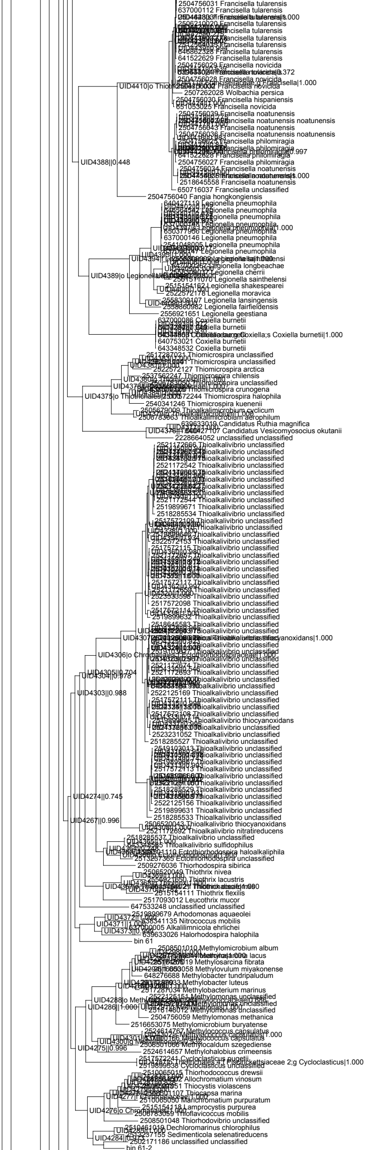
2506210016 Francisella tularensis
Francisella tularensis
Francisella tularensis
Francisella tularensis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2506210020 Francisella tularensis
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2504756028 Francisella novicida
UID4410|o Thiotr
2507262028 Wolbachia persica
2504756030 Francisella hispaniensis
651053025 Francisella novicida
2504756039 Francisella noatunensis
Francisella noatunensis noatunensis
2504756043 Francisella noatunensis
2504756036 Francisella noatunensis noatunensis
Francisella philomiragia
641522628 Francisella philomiragia
2504756027 Francisella philomiragia
2504756034 Francisella noatunensis
2518645558 Francisella noatunensis
650716037 Francisella unclassified
UID4388||0.448
2504756040 Fangia hongkongiensis
640427119 Legionella pneumophila
650377956 Legionella pneumophila
637000146 Legionella pneumophila
2541948005 Legionella pneumophila
Legionella pneumophila
Legionella longbeachae
Legionella cherrii
UID4389|o Legionell
2561511070 Legionella sainthelensi
2515154162 Legionella shakespearei
2522572178 Legionella moravica
2558309107 Legionella lansingensis
2558860082 Legionella fairfieldensis
2556921651 Legionella geestiana
637000086 Coxiella burnetii
Coxiella burnetii
640753021 Coxiella burnetii
643348532 Coxiella burnetii
2517287021 Thiomicrospira unclassified
Thiomicrospira unclassified
2522572127 Thiomicrospira arctica
2537562247 Thiomicrospira chilensis
Thiomicrospira unclassified
Thiomicrospira crunogena
UID4375|o Thiotrichales
Thiomicrospira halophila
2540341246 Thiomicrospira kuenenii
2505679009 Thioalkalimicrobium cyclicum
2506783063 Thioalkalimicrobium aerophilum
639633019 Candidatus Ruthia magnifica
640427107 Candidatus Vesicomyosocius okutanii
2228664052 unclassified unclassified
2521172666 Thioalkalivibrio unclassified
2521172542 Thioalkalivibrio unclassified
2521172544 Thioalkalivibrio unclassified
2519899671 Thioalkalivibrio unclassified
2518285534 Thioalkalivibrio unclassified
2517572109 Thioalkalivibrio unclassified
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2523533598 Thioalkalivibrio unclassified
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UID4305||0.704
UID4304||0.978
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2517572111 Thioalkalivibrio unclassified
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Thioalkalivibrio thiocyanoxidans
2523231052 Thioalkalivibrio unclassified
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2521172692 Thioalkalivibrio nitratireducens
2518285537 Thioalkalivibrio unclassified
Thioalkalivibrio sulfidophilus
Ectothiorhodospira haloalkaliphila
2513237365 Ectothiorhodospira unclassified
2509276036 Thiorhodospira sibirica
2506520049 Thiothrix nivea
2556921650 Thiothrix lacustris
2515154111 Thiothrix flexilis
2517093012 Leucothrix mucor
647533248 unclassified unclassified
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UID4372||1.000
UID4371||1.000
638341135 Nitrococcus mobilis
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UID4373||0.999
639633026 Halorhodospira halophila
bin 61
2508501010 Methylomicrobium album
Methylosarcina lacus
Methylosarcina fibrata
Methylovulum miyakonense
648276688 Methylobacter tundripaludum
Methylobacter luteus
2517287034 Methylobacterium marinus
Methylomonas unclassified
UID4288|o Meth
UID4286||1.000
Methylomonas unclassified
2504756059 Methylomonas methanica
2516653075 Methylomicrobium buryatense
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Methylococcus capsulatus
UID4300|o Me
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2517572241 Cycloclasticus pugetii
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Cycloclasticus unclassified
2510065015 Thiorhodococcus drewsii
Allochromatium vinosum
Thiocystis violascens
Thiocapsa marina
2510065050 Marichromatium purpuratum
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UID4276|o Chromatiales|1.000
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2508501048 Thiorhodovibrio unclassified
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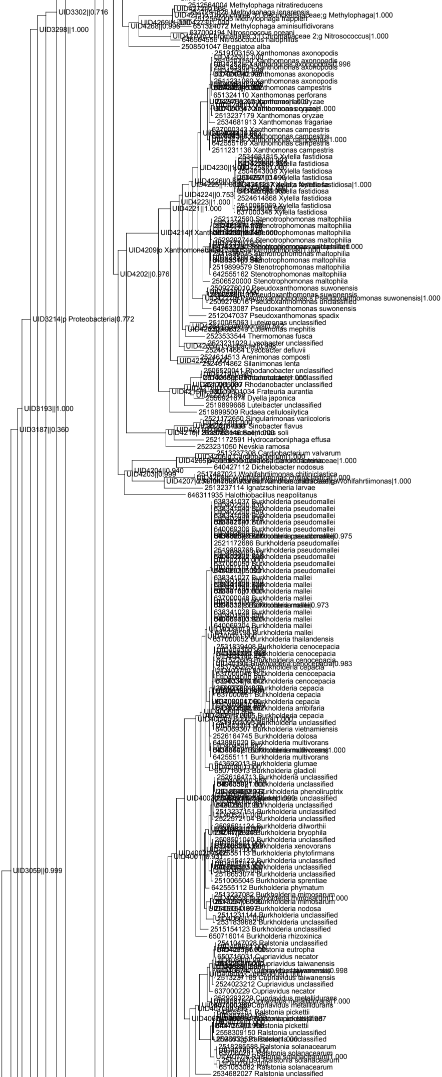

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Methylophaga lonarensis
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Methylophaga frappieri
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637000194 Nitrosococcus oceani
Chromatiales 3 Chromatiaceae 2;g Nitrosococcus|1.000
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Xanthomonas axonopodis
Xanthomonas axonopodis|0.996
Xanthomonas axonopodis
2511231060 Xanthomonas axonopodis
Xanthomonas campestris
651324110 Xanthomonas perforans
Xanthomonas oryzae
Xanthomonas|1.000
Xanthomonas oryzae|1.000
2513237179 Xanthomonas oryzae
2534681913 Xanthomonas fragariae
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Xanthomonas campestris
Xanthomonas campestris|1.000
642555169 Xanthomonas campestris
2511231136 Xanthomonas campestris
2534681815 Xylella fastidiosa
Xylella fastidiosa
2504643008 Xylella fastidiosa
Xylella fastidiosa
Xylella fastidiosa|1.000
Xylella fastidiosa
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637000348 Xylella fastidiosa
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UID4225||1.000
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UID4223||1.000
UID4221||1.000
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2521172560 Stenotrophomonas maltophilia
Stenotrophomonas maltophilia
Stenotrophomonas maltophilia
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Stenotrophomonas maltophilia|1.000
Stenotrophomonas maltophilia
Stenotrophomonas maltophilia
2519899579 Stenotrophomonas maltophilia
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Pseudoxanthomonas suwonensis|1.000
2509276016 Pseudoxanthomonas unclassified
649633087 Pseudoxanthomonas suwonensis
2512047037 Pseudoxanthomonas spadix
2510065063 Luteimonas unclassified
Luteimonas mephitis
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Rhodanobacter|1.000
Rhodanobacter unclassified
Frateuria aurantia
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2519899668 Luteibacter unclassified
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UID3193||1.000
2521172650 Singularimonas variicoloris
Sinobacter flavus
UID3187||0.360
Steroidobacter soli
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Cardiobacteriaceae|1.000
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Wohlfahrtiimonas chitiniclastica|1.000
Wohlfahrtiimonas|1.000
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638341037 Burkholderia pseudomallei
Burkholderia pseudomallei
Burkholderia pseudomallei
Burkholderia pseudomallei
640069306 Burkholderia pseudomallei
Burkholderia pseudomallei|0.975
2521172686 Burkholderia pseudomallei
2519899768 Burkholderia pseudomallei
Burkholderia pseudomallei
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Burkholderia pseudomallei
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Burkholderia mallei
Burkholderia mallei
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Burkholderia mallei|0.973
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Burkholderia mallei
640069304 Burkholderia mallei
641736199 Burkholderia mallei
637000052 Burkholderia thailandensis
2531839408 Burkholderia cenocepacia
Burkholderia cenocepacia
Burkholderia cenocepacia
Burkholderia cenocepacia|0.983
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637000046 Burkholderia cenocepacia
Burkholderia cenocepacia
Burkholderia cepacia
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Burkholderia unclassified
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2526164745 Burkholderia dolosa
643886020 Burkholderia multivorans
Burkholderia multivorans|1.000
642555111 Burkholderia multivorans
643692013 Burkholderia glumae
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Burkholderia unclassified
Burkholderia phenoliruptrix
Burkholderia unclassified
Burkholderia unclassified
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Burkholderia bryophila
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Burkholderia xenovorans
Burkholderia phytofirmans
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Burkholderia unclassified
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Burkholderia nodosa
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650716031 Cupriavidus necator
Cupriavidus taiwanensis
Cupriavidus taiwanensis|0.998
2513237165 Cupriavidus taiwanensis
2524023212 Cupriavidus unclassified
637000229 Cupriavidus necator
2529293220 Cupriavidus metallidurans
Cupriavidus metallidurans|1.000
Cupriavidus metallidurans
Ralstonia pickettii
Ralstonia pickettii|0.987
Ralstonia pickettii
2558309150 Ralstonia unclassified
Ralstonia|1.000
Ralstonia unclassified
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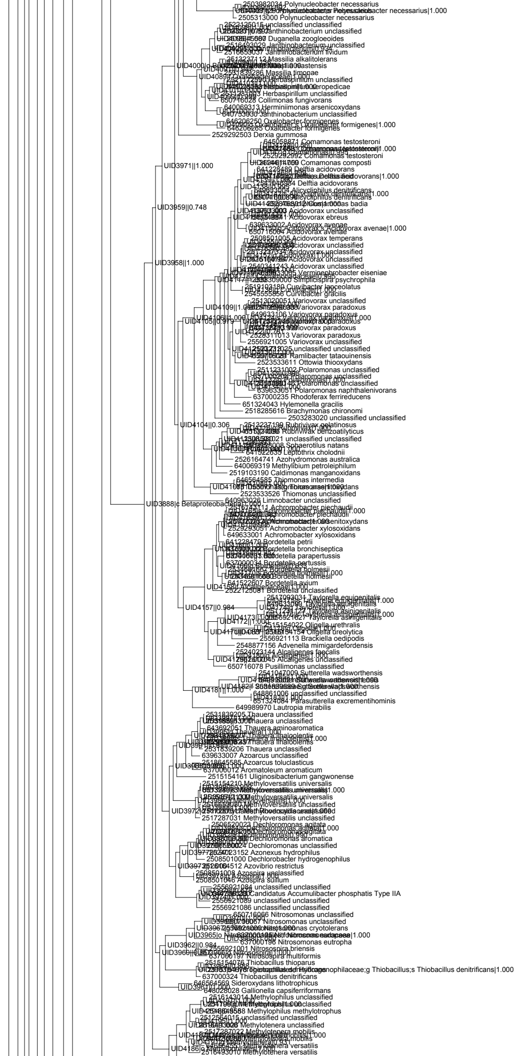
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UID4000
2531839286 Massilia timonae
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Herbaspirillum unclassified
Herbaspirillum seropedicae
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646206250 Oxalobacter formigenes
Oxalobacter formigenes|1.000
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645058871 Comamonas testosteroni
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UID3971||1.000
Comamonas composti
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Delftia acidovorans|1.000
Delftia acidovorans
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Alicycliphilus denitrificans
Alicycliphilus denitrificans|1.000
Alicycliphilus denitrificans
Comamonas badia
Acidovorax unclassified
Acidovorax ebreus
639633002 Acidovorax avenae
Acidovorax avenae|1.000
650716004 Acidovorax avenae
2508501005 Acidovorax temperans
Acidovorax unclassified
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Acidovorax unclassified
Acidovorax unclassified
2540341243 Acidovorax unclassified
Verminephrobacter eiseniae
2530309000 Simplicispira psychrophila
2519103180 Curvibacter lanceolatus
2545555856 Curvibacter gracilis
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Variovorax paradoxus
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649633106 Variovorax paradoxus
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Variovorax paradoxus|1.000
Variovorax paradoxus
2528311013 Variovorax paradoxus
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unclassified unclassified
Ramlibacter tataouinensis
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Polaromonas unclassified
Polaromonas unclassified
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651324043 Hylemonella gracilis
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Rubrivivax benzoatilyticus
unclassified unclassified
Sphaerotilus natans
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640069319 Methylibium petroleiphilum
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Thiomonas arsenitoxydans
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Achromobacter piechaudii
Achromobacter piechaudii|1.000
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Achromobacter arsenitoxydans
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649633001 Achromobacter xylosoxidans
641228479 Bordetella petrii
Bordetella bronchiseptica
Bordetella parapertussis
637000034 Bordetella pertussis
Bordetella holmesii
Bordetella holmesii|1.000
Bordetella holmesii
641522607 Bordetella avium
2522125081 Bordetella unclassified
2517093031 Taylorella equigenitalis
Taylorella equigenitalis|1.000
Taylorella equigenitalis
UID4157||0.984
Taylorella asinigenitalis
Taylorella asinigenitalis|1.000
2556921627 Taylorella asinigenitalis
2515154022 Oligella urethralis
Oligella ureolytica
2556921113 Brackiella oedipodis
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2524023144 Alcaligenes faecalis
Alcaligenes unclassified
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Sutterella wadsworthensis
UID4181||1.000
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651324084 Parasutterella excrementihominis
649989970 Lautropia mirabilis
2531839205 Thauera unclassified
Thauera unclassified
643692051 Thauera aminoaromatica
Thauera linaloolentis
Thauera linaloolentis|1.000
Thauera linaloolentis
2531839206 Thauera unclassified
639633007 Azoarcus unclassified
2518645585 Azoarcus toluclasticus
637000012 Aromatoleum aromaticum
2515154161 Uliginosibacterium gangwonense
2515154210 Methyloversatilis universalis
Methyloversatilis universalis|1.000
Methyloversatilis universalis
Methyloversatilis universalis
Methyloversatilis unclassified
UID3972
2517287031 Methyloversatilis unclassified
2506520023 Dechloromonas agitata
Dechloromonas agitata|1.000
Dechloromonas agitata
Dechloromonas aromatica
Dechloromonas unclassified
Azonexus hydrophilus
2508501000 Dechlorobacter hydrogenophilus
Azovibrio restrictus
2508501008 Azospira unclassified
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Candidatus Accumulibacter phosphatis Type IIA
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2556921086 unclassified unclassified
650716066 Nitrosomonas unclassified
Nitrosomonas unclassified
Nitrosomonas cryotolerans
Nitrosomonas europaea|1.000
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UID3962||0.984
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Thiobacillus;s Thiobacillus denitrificans|1.000
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646564569 Sideroxydans lithotrophicus
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2516143014 Methylophilus unclassified
Methylophilus unclassified
Methylophilus methylotrophus
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Methylotenera unclassified
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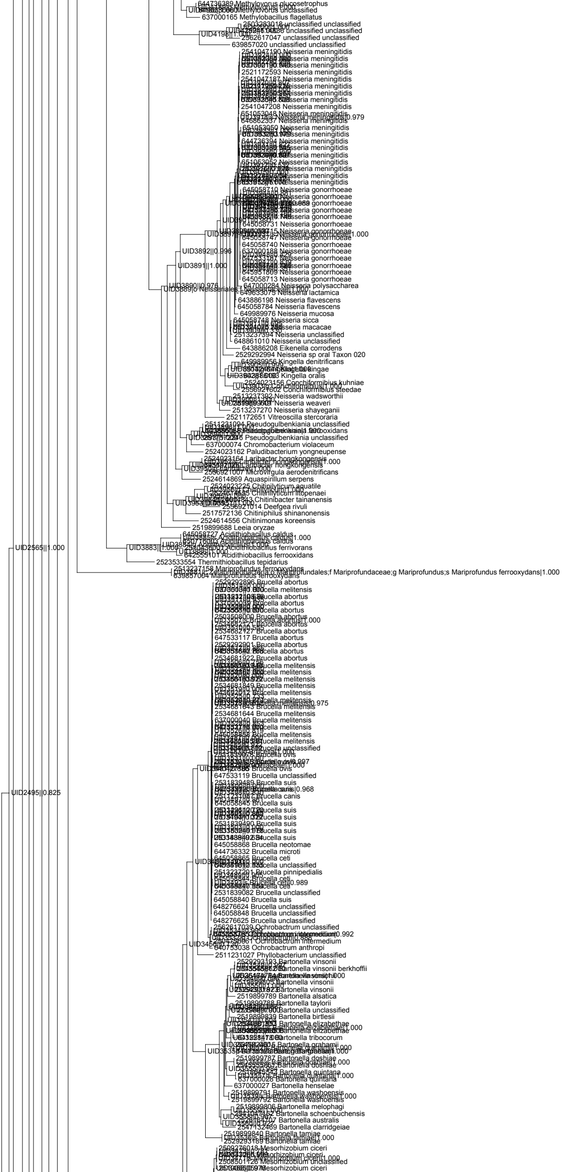
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2541047187 Neisseria meningitidis
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644736394 Neisseria meningitidis
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645058710 Neisseria gonorrhoeae
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645058747 Neisseria gonorrhoeae
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637000188 Neisseria gonorrhoeae
645951609 Neisseria gonorrhoeae
645058713 Neisseria gonorrhoeae
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UID3891||1.000
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649633075 Neisseria lactamica
643886198 Neisseria flavescens
645058784 Neisseria flavescens
649989976 Neisseria mucosa
645058748 Neisseria sicca
Neisseria macacae
2513237394 Neisseria unclassified
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643886208 Eikenella corrodens
2529292994 Neisseria sp oral Taxon 020
649989956 Kingella denitrificans
Kingella oralis
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2556921602 Conchiformibius steedae
2513237392 Neisseria wadsworthii
Neisseria weaveri
2513237270 Neisseria shayeganii
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2511231094 Pseudogulbenkiania unclassified
Pseudogulbenkiania unclassified
637000074 Chromobacterium violaceum
2524023162 Paludibacterium yongneupense
2524023164 Laribacter hongkongensis
2556921007 Microvirgula aerodenitrificans
2524614869 Aquaspirillum serpens
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Chitinilyticum litopenaei
Chitinibacter tainanensis
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Acidithiobacillus ferrivorans
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UID3883||1.000
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o Mariprofundales;f Mariprofundaceae;g Mariprofundus;s Mariprofundus ferrooxydans|1.000
639857004 Mariprofundus ferrooxydans
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2534682127 Brucella abortus
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2534681849 Brucella melitensis
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UID2495||0.825
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644736332 Brucella microti
645058865 Brucella ceti
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Ochrobactrum intermedium
640753038 Ochrobactrum anthropi
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Bartonella vinsonii berkhoffii
Bartonella vinsonii
2519899789 Bartonella alsatica
2519899788 Bartonella taylorii
Bartonella unclassified
2519899839 Bartonella birtlesii
Bartonella elizabethae
Bartonella tribocorum
2519899787 Bartonella doshiae
Bartonella quintana
637000028 Bartonella quintana
637000027 Bartonella henselae
2519899791 Bartonella washoensis
2519899792 Bartonella washoensis
2519899806 Bartonella melophagi
Bartonella schoenbuchensis
Bartonella australis
2547132469 Bartonella clarridgeiae
2519899840 Bartonella tamiae
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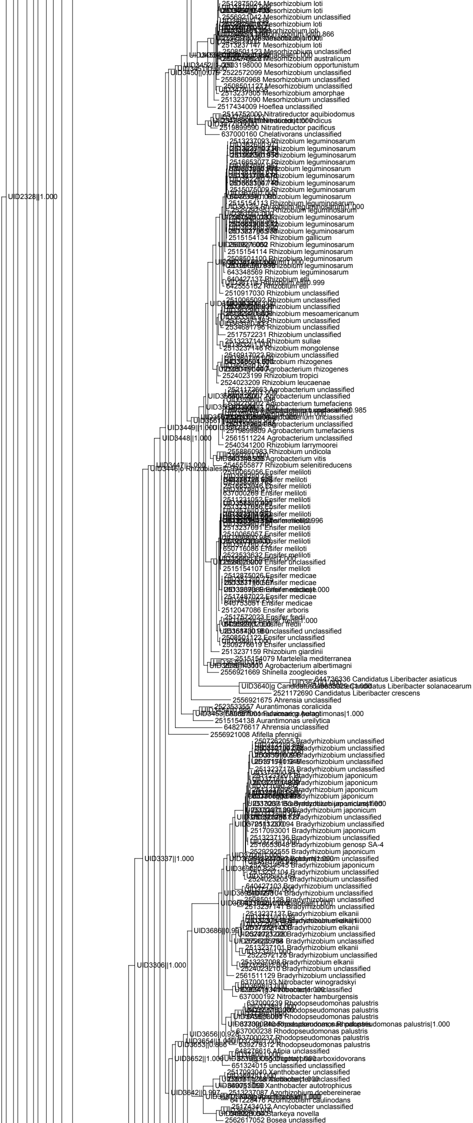
Mesorhizobium ciceri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2513237090 Mesorhizobium unclassified
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2514752000 Nitratireductor aquibiodomus
2516899590 Nitratireductor pacificus
637000160 Chelativorans unclassified
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UID3450||0.079
UID2328||1.000
2513237093 Rhizobium leguminosarum
Rhizobium leguminosarum
2516653077 Rhizobium leguminosarum
2515075009 Rhizobium leguminosarum
2515154113 Rhizobium leguminosarum
2515154134 Rhizobium gallicum
2515154114 Rhizobium leguminosarum
2508501100 Rhizobium leguminosarum
643348569 Rhizobium leguminosarum
640427137 Rhizobium etli
642555152 Rhizobium etli
2510917030 Rhizobium unclassified
2510065092 Rhizobium unclassified
Rhizobium unclassified
Rhizobium mesoamericanum
Rhizobium unclassified
2534681796 Rhizobium unclassified
2517572231 Rhizobium unclassified
2513237144 Rhizobium sullae
2513237148 Rhizobium mongolense
2510917022 Rhizobium unclassified
Rhizobium rhizogenes
Agrobacterium rhizogenes
2524023199 Rhizobium tropici
2524023209 Rhizobium leucaenae
2521172663 Agrobacterium unclassified
Agrobacterium unclassified
Agrobacterium tumefaciens
Agrobacterium unclassified
2516653009 Agrobacterium tumefaciens
2561511224 Agrobacterium unclassified
2540341200 Rhizobium larrymoorei
2558860983 Rhizobium undicola
Agrobacterium vitis
2545555877 Rhizobium selenitireducens
UID3449||1.000
UID3448||1.000
UID3447||1.000
UID3446|o Rhizobiales|0.994
2510065056 Ensifer meliloti
Ensifer meliloti
Ensifer meliloti
637000269 Ensifer meliloti
2511231052 Ensifer meliloti
Ensifer meliloti
Ensifer meliloti
2513237091 Ensifer meliloti
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Ensifer meliloti
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Ensifer unclassified
2515154107 Ensifer meliloti
2512875026 Ensifer medicae
Ensifer medicae
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2512047086 Ensifer arboris
2517572023 Ensifer fredii
Ensifer fredii
unclassified unclassified
2508501122 Ensifer unclassified
2509276019 Ensifer unclassified
2513237159 Rhizobium giardinii
2515154079 Martelella mediterranea
Agrobacterium albertimagni
2556921669 Shinella zoogleoides
644736336 Candidatus Liberibacter asiaticus
UID3640|g Candidatus Liberibacter|1.000
Candidatus Liberibacter solanacearum
2521172690 Candidatus Liberibacter crescens
2556921675 Ahrensia unclassified
2523533557 Aurantimonas coralicida
Fulvimarina pelagi
2515154138 Aurantimonas ureilytica
648276617 Ahrensia unclassified
2556921008 Afifella pfennigii
2507262055 Bradyrhizobium unclassified
Bradyrhizobium unclassified
Bradyrhizobium unclassified
Mesorhizobium unclassified
2513237178 Bradyrhizobium unclassified
Bradyrhizobium japonicum
Bradyrhizobium japonicum
Bradyrhizobium japonicum
Bradyrhizobium japonicum
Bradyrhizobium japonicum
Bradyrhizobium unclassified
Bradyrhizobium unclassified
2517093001 Bradyrhizobium japonicum
2513237136 Bradyrhizobium unclassified
2516653048 Bradyrhizobium genosp SA-4
2529292555 Bradyrhizobium japonicum
Bradyrhizobium unclassified
Bradyrhizobium japonicum
2513237104 Bradyrhizobium unclassified
2524023205 Bradyrhizobium unclassified
640427103 Bradyrhizobium unclassified
Bradyrhizobium unclassified
2508501128 Bradyrhizobium unclassified
2513237141 Bradyrhizobium unclassified
2513237137 Bradyrhizobium elkanii
Bradyrhizobium elkanii
Bradyrhizobium elkanii
Bradyrhizobium unclassified
Bradyrhizobium unclassified
2513237101 Bradyrhizobium elkanii
2522572128 Bradyrhizobium unclassified
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2524023210 Bradyrhizobium unclassified
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637000193 Nitrobacter winogradskyi
Nitrobacter unclassified
637000192 Nitrobacter hamburgensis
UID3337||1.000
UID3686||0.951
UID3306||1.000
637000239 Rhodopseudomonas palustris
Rhodopseudomonas palustris
Rhodopseudomonas palustris
Rhodopseudomonas palustris|1.000
637000238 Rhodopseudomonas palustris
637000237 Rhodopseudomonas palustris
639279312 Rhodopseudomonas palustris
648276616 Afipia unclassified
carboxidovorans
651324015 unclassified unclassified
2517093040 Xanthobacter unclassified
Xanthobacter unclassified
Xanthobacter autotrophicus
2513237087 Azorhizobium doebereinerae
641228476 Azorhizobium caulinodans
2517434012 Ancylobacter unclassified
Starkeya novella
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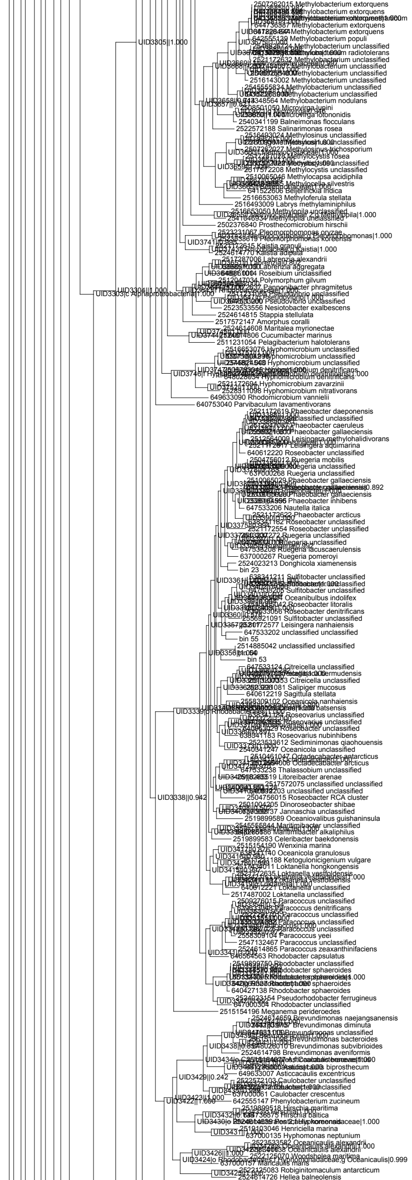
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2546826724 Methylobacterium unclassified
Methylobacterium radiotolerans
2521172632 Methylobacterium unclassified
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2516143002 Methylobacterium unclassified
2545555834 Methylobacterium unclassified
Methylobacterium unclassified
Methylobacterium nodulans
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2508501050 Microvirga lupini
Microvirga lotononidis
2540341199 Balneimonas flocculans
2522572188 Salinarimonas rosea
2516493024 Methylosinus unclassified
Methylosinus unclassified
2507262027 Methylosinus trichosporium
UID3660|f Methylocystaceae|1.000
Methylocystis rosea
Methylocystis unclassified
UID3659||1.000
2517572208 Methylocystis unclassified
2510065046 Methylocapsa acidiphila
Methylocella silvestris
UID3665|f Beijerinckiaceae|1.000
641522606 Beijerinckia indica
2516653063 Methyloferula stellata
2516493009 Labrys methylaminiphilus
2516653050 Methylopila unclassified
UID3655|f Methylocystaceae 2;g Methylopila|1.000
2541046934 Methylopila unclassified
2502376840 Prosthecomicrobium hirschii
2523231067 Pleomorphomonas oryzae
Methylocystaceae;g Pleomorphomonas|1.000
2523533619 Pleomorphomonas koreensis
UID3741||0.995
2521172615 Kaistia granuli
Rhizobiaceae;g Kaistia|1.000
2524614770 Kaistia adipata
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UID3651|g Labrenzia|0.802
Labrenzia aggregata
Roseibium unclassified
2512047034 Polymorphum gilvum
Pannonibacter phragmitetus
Rhodobacteraceae|1.000
2511231065 Pseudovibrio unclassified
Pseudovibrio|1.000
Pseudovibrio unclassified
2523533556 Nesiotobacter exalbescens
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2517572147 Amorphus coralli
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Cucumibacter marinus
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Hyphomicrobium unclassified
Hyphomicrobium unclassified
Hyphomicrobium denitrificans
Hyphomicrobium denitrificans|1.000
648028034 Hyphomicrobium denitrificans
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649633090 Rhodomicrobium vannielii
640753040 Parvibaculum lavamentivorans
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UID3304||1.000
UID3303|c Alphaproteobacteria|1.000
2521172619 Phaeobacter daeponensis
unclassified unclassified
2512047087 Phaeobacter caeruleus
Phaeobacter gallaeciensis
2512564009 Leisingera methylohalidivorans
Leisingera|1.000
2521172617 Leisingera aquimarina
640612220 Roseobacter unclassified
2504756012 Ruegeria mobilis
Ruegeria unclassified
637000268 Ruegeria unclassified
2510065029 Phaeobacter gallaeciensis
Phaeobacter gallaeciensis|0.892
Phaeobacter gallaeciensis
Phaeobacter inhibens
647533206 Nautella italica
2521172622 Phaeobacter arcticus
UID3390||1.000
Roseobacter unclassified
UID3375||0.994
2521172554 Roseobacter unclassified
Ruegeria unclassified
Ruegeria unclassified
UID3395|g Ruegeria|0.992
647533208 Ruegeria lacuscaerulensis
637000267 Ruegeria pomeroyi
2524023213 Donghicola xiamenensis
bin 23
638341211 Sulfitobacter unclassified
Sulfitobacter unclassified
647533205 Sulfitobacter unclassified
UID3401||0.404
Oceanibulbus indolifex
Roseobacter litoralis
Roseobacter denitrificans
2556921091 Sulfitobacter unclassified
Leisingera nanhaiensis
647533202 unclassified unclassified
bin 55
2514885042 unclassified unclassified
bin 53
647533124 Citreicella unclassified
Citreicella unclassified
Salipiger mucosus
640612219 Sagittula stellata
2558309102 Oceanicola nanhaiensis
Oceanicola batsensis
UID3339|o Rhodobacterales|1.000
Roseovarius unclassified
UID3372||1.000
Roseovarius unclassified
Roseovarius|1.000
Roseobacter unclassified
UID3369||0.897
638341183 Roseovarius nubinhibens
2523533612 Sediminimonas qiaohouensis
UID3373||1.000
2540341247 Oceanicola unclassified
2510461047 Octadecabacter antarcticus
Octadecabacter|1.000
Octadecabacter arcticus
UID3412||0.970
647533238 Thalassobium unclassified
Litoreibacter arenae
2517572075 unclassified unclassified
unclassified unclassified
2504756015 Roseobacter RCA cluster
2501004205 Dinoroseobacter shibae
Jannaschia unclassified
2519899589 Oceaniovalibus guishaninsula
2545555844 Maritimibacter unclassified
Maritimibacter|1.000
Maritimibacter alkaliphilus
2519899583 Celeribacter baekdonensis
2515154190 Wenxinia marina
UID3417||0.876
Oceanicola granulosus
UID3416||0.980
Ketogulonicigenium vulgare
UID3418||0.999
2517434011 Loktanella hongkongensis
UID3415||0.997
2521172635 Loktanella vestfoldensis
Loktanella vestfoldensis|1.000
Loktanella vestfoldensis
Loktanella|1.000
640612221 Loktanella unclassified
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UID3338||0.942
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UID3354||0.334
Paracoccus denitrificans
UID3353||0.956
Paracoccus unclassified
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2558309104 Paracoccus yeei
2547132467 Paracoccus unclassified
2524614865 Paracoccus zeaxanthinifaciens
UID3341||1.000
646564563 Rhodobacter capsulatus
2519899750 Rhodobacter unclassified
Rhodobacter sphaeroides
Rhodobacter sphaeroides|1.000
Rhodobacter sphaeroides
640427138 Rhodobacter sphaeroides
2524023154 Pseudorhodobacter ferrugineus
UID3347||0.992
647000304 Rhodobacter unclassified
2515154196 Meganema perideroedes
2524614659 Brevundimonas naejangsanensis
UID3443||1.000
Brevundimonas diminuta
Brevundimonas unclassified
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Brevundimonas bacteroides
UID3441||1.000
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2524614798 Brevundimonas aveniformis
UID3434|o Caulobacterales|1.000
UID3445||1.000
Asticcacaulis biprosthecum
649633007 Asticcacaulis excentricus
UID3429||0.242
2522572103 Caulobacter unclassified
Caulobacter unclassified
Caulobacter|1.000
637000061 Caulobacter crescentus
UID3423||1.000
UID3422||1.000
642555147 Phenylobacterium zucineum
2519899518 Hirschia maritima
Hirschia|1.000
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Hyphomonadaceae|1.000
2519103046 Henriciella marina
UID3431||1.000
637000135 Hyphomonas neptunium
2523533582 Oceanicaulis alexandrii
Oceanicaulis alexandrii|1.000
Oceanicaulis alexandrii
UID3426||1.000
2522125070 Woodsholea maritima
UID3424|o Rhodobacterales;f Hyphomonadaceae;g Oceanicaulis|0.999
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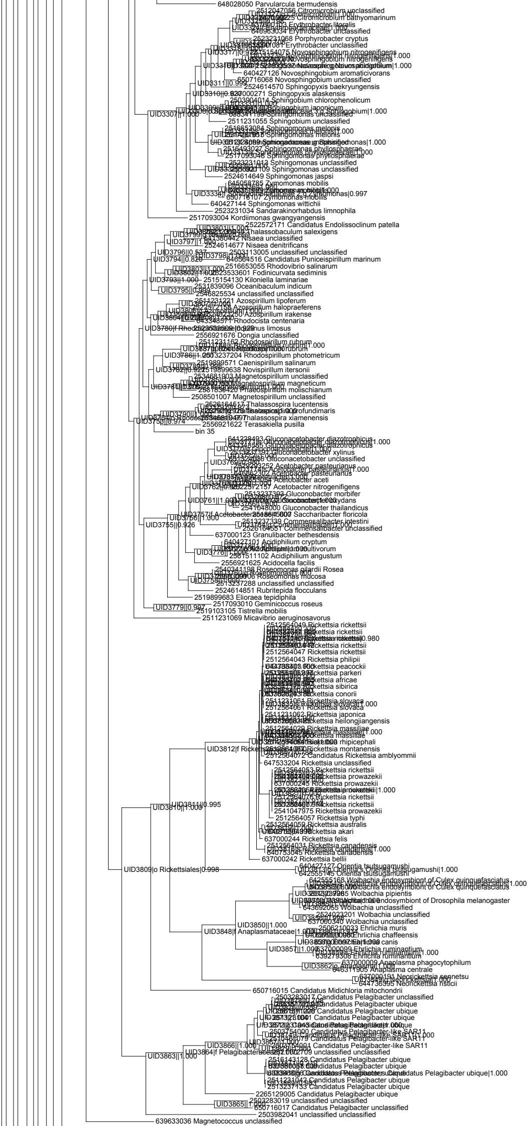
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Erythrobacter unclassified
2515154075 Novosphingobium nitrogenifigens
Novosphingobium nitrogenifigens
640427126 Novosphingobium aromaticivorans
650716068 Novosphingobium unclassified
2524614570 Sphingopyxis baekryungensis
UID3311||0.999
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637000271 Sphingopyxis alaskensis
2503904014 Sphingobium chlorophenolicum
Sphingobium japonicum
Sphingomonas unclassified
UID3307||1.000
2511231055 Sphingobium unclassified
2546653084 Sphingomonas melonis
Sphingomonas melonis
2516493027 Sphingomonas phyllosphaerae
Sphingomonas phyllosphaerae
2523231013 Sphingomonas unclassified
Sphingomonas unclassified
2524614649 Sphingomonas jaspsi
645058785 Zymomonas mobilis
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640427144 Sphingomonas wittichii
2523231034 Sandarakinorhabdus limnophila
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2522572171 Candidatus Endolissoclinum patella
Thalassobaculum salexigens
Nisaea unclassified
2524614677 Nisaea denitrificans
UID3796||0.537
UID3794||0.826
2503113005 unclassified unclassified
646564516 Candidatus Puniceispirillum marinum
2516653055 Rhodovibrio salinarum
2523533601 Fodinicurvata sediminis
UID3793||1.000
2515154130 Kiloniella laminariae
2531839096 Oceanibaculum indicum
2546825534 unclassified unclassified
2511231221 Azospirillum lipoferum
Azospirillum halopraeferens
Azospirillum irakense
643348571 Rhodocista centenaria
Inquilinus limosus
2556921676 Dongia unclassified
2511231162 Rhodospirillum rubrum
Rhodospirillum rubrum
2503237204 Rhodospirillum photometricum
2519899571 Caenispirillum salinarum
2519899638 Novispirillum itersonii
2534681903 Magnetospirillum unclassified
Magnetospirillum magneticum
Phaeospirillum molischianum
2508501007 Magnetospirillum unclassified
2526164517 Thalassospira lucentensis
Thalassospira profundimaris
Thalassospira xiamenensis
2556921622 Terasakiella pusilla
bin 35
641228493 Gluconacetobacter diazotrophicus
Gluconacetobacter diazotrophicus
Gluconacetobacter xylinus
Gluconacetobacter unclassified
2529293252 Acetobacter pasteurianus
Acetobacter pasteurianus
Acetobacter aceti
2522572157 Acetobacter nitrogenifigens
2513237393 Gluconobacter morbifer
Gluconobacter oxydans
2541048000 Gluconobacter thailandicus
Saccharibacter floricola
UID3756||1.000
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2513237339 Commensalibacter intestini
2526164551 Commensalibacter unclassified
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640427101 Acidiphilium cryptum
Acidiphilium multivorum
2561511102 Acidiphilium angustum
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2540341198 Roseomonas gilardii Rosea
Roseomonas mucosa
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2524614851 Rubritepida flocculans
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2512564049 Rickettsia rickettsii
Rickettsia rickettsii
Rickettsia rickettsii|0.980
Rickettsia rickettsii
2512564047 Rickettsia rickettsii
2512564043 Rickettsia philipii
Rickettsia peacockii
Rickettsia parkeri
Rickettsia africae
Rickettsia sibirica
Rickettsia conorii
2511231061 Rickettsia slovaca
2512564061 Rickettsia slovaca
2511231062 Rickettsia japonica
Rickettsia heilongjiangensis
2512564029 Rickettsia massiliae
Rickettsia massiliae
Rickettsia rhipicephali
UID3812|f Rickettsiaceae
Rickettsia montanensis
2512564072 Candidatus Rickettsia amblyommii
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Rickettsia prowazekii
637000245 Rickettsia prowazekii
Rickettsia prowazekii|1.000
2512564076 Rickettsia rickettsii
Rickettsia rickettsii
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2512564057 Rickettsia typhi
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Rickettsia akari
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2512564031 Rickettsia canadensis
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UID3809|o Rickettsiales|0.998
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Orientia tsutsugamushi|1.000
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642555168 Wolbachia endosymbiont of Culex quinquefasciatus
Wolbachia endosymbiont of Culex quinquefasciatus
Wolbachia pipientis
Wolbachia endosymbiont of Drosophila melanogaster
643692055 Wolbachia unclassified
2524023201 Wolbachia unclassified
637000340 Wolbachia unclassified
UID3850||1.000
UID3848|f Anaplasmataceae|1.000
2506210033 Ehrlichia muris
Ehrlichia chaffeensis
Ehrlichia canis
UID3857||1.000
637000099 Ehrlichia ruminantium
639279308 Ehrlichia ruminantium
637000009 Anaplasma phagocytophilum
646311905 Anaplasma centrale
637000191 Neorickettsia sennetsu
644736395 Neorickettsia risticii
650716015 Candidatus Midichloria mitochondrii
2503283017 Candidatus Pelagibacter unclassified
Candidatus Pelagibacter ubique
Candidatus Pelagibacter ubique
Candidatus Pelagibacter ubique
2503754000 Candidatus Pelagibacter-like SAR11
Candidatus Pelagibacter-like SAR11
Candidatus Pelagibacter-like SAR11
UID3866||1.000
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unclassified unclassified
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Candidatus Pelagibacter ubique
Candidatus Pelagibacter ubique|1.000
2511231042 Candidatus Pelagibacter ubique
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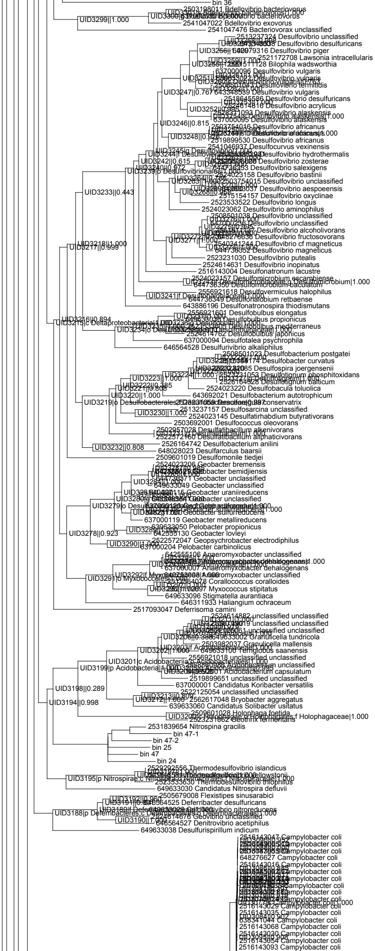
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2503198011 Bdellovibrio bacteriovorus
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2541047022 Bdellovibrio exovorus
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Desulfovibrio desulfuricans
UID3256||1.000
Desulfovibrio piger
2521172708 Lawsonia intracellularis
Bilophila wadsworthia
637000096 Desulfovibrio vulgaris
Desulfovibrio vulgaris
Desulfovibrio termitidis
UID3247||0.767
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2519899530 Desulfovibrio africanus
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Desulfovibrio hydrothermalis
UID3242||0.615
Desulfovibrio zosterae
Desulfovibrio salexigens
2524023158 Desulfovibrio bastinii
Desulfovibrio unclassified
Desulfovibrio aespoeensis
2515154157 Desulfovibrio oxyclinae
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2523533522 Desulfovibrio longus
2524023062 Desulfovibrio aminophilus
2508501038 Desulfovibrio unclassified
Desulfovibrio unclassified
Desulfovibrio alcoholivorans
Desulfovibrio fructosovorans
UID3271||1.000
2540341244 Desulfovibrio cf magneticus
644736352 Desulfovibrio magneticus
UID3218||1.000
UID3217||0.999
2523231030 Desulfovibrio putealis
2524614631 Desulfovibrio inopinatus
2516143004 Desulfonatronum lacustre
2524023157 Desulfomicrobium escambiense
Desulfomicrobium baculatum
2556921618 Desulfovermiculus halophilus
UID3241|f Desulfohalobiaceae|1.000
644736349 Desulfohalobium retbaense
643886196 Desulfonatronospira thiodismutans
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UID3216||0.894
Desulfobulbus propionicus
UID3215|c Deltaproteobacteria|1.000
Desulfobulbus mediterraneus
2524614762 Desulfobulbus japonicus
637000094 Desulfotalea psychrophila
646564528 Desulfurivibrio alkaliphilus
2508501023 Desulfobacterium postgatei
Desulfobacter curvatus
Desulfospira joergensenii
UID3224||1.000
Desulfotignum phosphitoxidans
UID3223||1.000
Desulfotignum balticum
2524023220 Desulfobacula toluolica
UID3220||1.000
643692021 Desulfobacterium autotrophicum
conservatrix
2513237157 Desulfosarcina unclassified
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2524023145 Desulfatirhabdium butyrativorans
2503692001 Desulfococcus oleovorans
2502957028 Desulfatibacillum alkenivorans
2522572160 Desulfatibacillum aliphaticivorans
UID3232||0.808
2526164742 Desulfobacterium anilini
648028023 Desulfarculus baarsii
2509601019 Desulfomonile tiedjei
2524023206 Geobacter bremensis
Geobacter bemidjiensis
644736371 Geobacter unclassified
649633049 Geobacter unclassified
Geobacter uraniireducens
Geobacter unclassified
Geobacter sulfurreducens
637000119 Geobacter metallireducens
639633050 Pelobacter propionicus
UID3278||0.923
642555130 Geobacter lovleyi
2522572047 Geopsychrobacter electrodiphilus
UID3290||1.000
637000204 Pelobacter carbinolicus
642555106 Anaeromyxobacter unclassified
637000007 Anaeromyxobacter dehalogenans
Anaeromyxobacter unclassified
Corallococcus coralloides
Myxococcus stipitatus
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646311933 Haliangium ochraceum
2517093047 Deferrisoma camini
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unclassified unclassified
unclassified unclassified
Granulicella tundricola
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2556921018 unclassified unclassified
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Acidobacterium unclassified
Acidobacterium capsulatum
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2509601028 Holophaga foetida
Holophagales;f Holophagaceae|1.000
2523231062 Geothrix fermentans
2531839654 Nitrospina gracilis
bin 47-1
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bin 25
bin 47
bin 24
2529292556 Thermodesulfovibrio islandicus
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2523533630 Thermodesulfovibrio thiophilus
649633030 Candidatus Nitrospira defluvii
2505679008 Flexistipes sinusarabici
646564525 Deferribacter desulfuricans
Denitrovibrio nitroreducens
UID3188|p Deferribacteres;c Deferribacteres;o Deferribacterales|1.000
2524614676 Geovibrio unclassified
UID3190||1.000
646564527 Denitrovibrio acetiphilus
649633038 Desulfurispirillum indicum
2516143047 Campylobacter coli
Campylobacter coli
Campylobacter coli
Campylobacter coli
648276627 Campylobacter coli
2516143016 Campylobacter coli
Campylobacter coli
Campylobacter coli
Campylobacter coli
Campylobacter coli
Campylobacter coli
2516143029 Campylobacter coli
2516143035 Campylobacter coli
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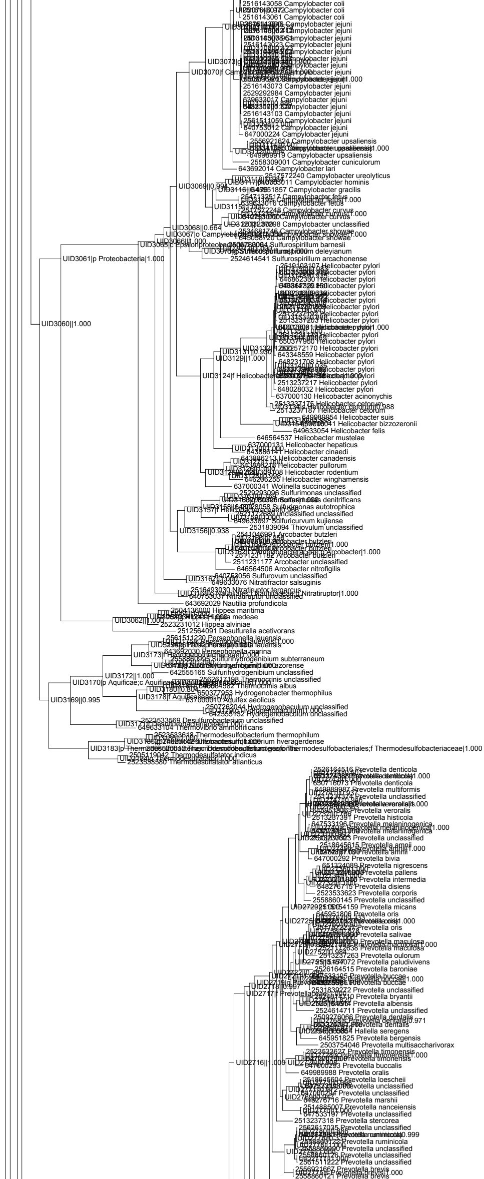
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2556921624 Campylobacter upsaliensis
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2558309001 Campylobacter cuniculorum
643692014 Campylobacter lari
2517572240 Campylobacter ureolyticus
UID3073|g
UID3070|f
UID3069||0.994
UID3116||0.455
2551857 Campylobacter gracilis
2547132517 Campylobacter fetus
639633016 Campylobacter fetus
2512572248 Campylobacter curvus
2513237298 Campylobacter unclassified
2534681746 Campylobacter showae
645058720 Campylobacter showae
UID3068||0.664
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UID3065|c Epsilonproteobacteria
Sulfurospirillum barnesii
Sulfurospirillum deleyianum
2524614541 Sulfurospirillum arcachonense
UID3061|p Proteobacteria|1.000
UID3060||1.000
2519103107 Helicobacter pylori
646862330 Helicobacter pylori
2513237203 Helicobacter pylori
2522572170 Helicobacter pylori
650377960 Helicobacter pylori
643348559 Helicobacter pylori
648231708 Helicobacter pylori
2513237217 Helicobacter pylori
648028032 Helicobacter pylori
637000130 Helicobacter acinonychis
2513237175 Helicobacter cetorum
2513237187 Helicobacter cetorum
UID3131||0.930
UID3129||1.000
UID3124|f Helicobacteraceae
649989954 Helicobacter suis
Helicobacter bizzozeronii
649633054 Helicobacter felis
646564537 Helicobacter mustelae
637000131 Helicobacter hepaticus
643886141 Helicobacter cinaedi
643886213 Helicobacter canadensis
Helicobacter pullorum
Helicobacter rodentium
646206255 Helicobacter winghamensis
637000341 Wolinella succinogenes
2529293096 Sulfurimonas unclassified
Sulfurimonas denitrificans
UID3157|f Helicobacteraceae
648028058 Sulfurimonas autotrophica
Sulfuricurvum unclassified
649633097 Sulfuricurvum kujiense
UID3156||0.938
2531839094 Thiovulum unclassified
2541046991 Arcobacter butzleri
Arcobacter butzleri
Arcobacter|1.000
2511231182 Arcobacter butzleri
2511231177 Arcobacter unclassified
646564506 Arcobacter nitrofigilis
640753056 Sulfurovum unclassified
649633076 Nitratifractor salsuginis
2516493030 Nitratiruptor tergarcus
640753037 Nitratiruptor unclassified
Nitratiruptor|1.000
643692029 Nautilia profundicola
2504136000 Hippea maritima
Hippea medeae
UID3062||1.000
2523231012 Hippea alviniae
2512564091 Desulfurella acetivorans
2561511220 Persephonella lauensis
Persephonella lauensis
643692030 Persephonella marina
UID3173|f Hydrogenothermaceae
Sulfurihydrogenibium subterraneum
Sulfurihydrogenibium azorense
642555165 Sulfurihydrogenibium unclassified
UID3172||1.000
UID3170|p Aquificae;c Aquificae
2562617198 Thermocrinis unclassified
Thermocrinis albus
UID3180||0.804
650377953 Hydrogenobacter thermophilus
UID3178|f Aquificaceae
637000010 Aquifex aeolicus
UID3169||0.995
2507262044 Hydrogenobaculum unclassified
642555132 Hydrogenobaculum unclassified
2523533569 Desulfurobacterium unclassified
649633104 Thermovibrio ammonificans
2523533618 Thermodesulfobacterium thermophilum
Thermodesulfobacterium hveragerdense
UID3183|p Thermodesulfobacteria;c Thermodesulfobacteria;o Thermodesulfobacteriales;f Thermodesulfobacteriaceae|1.000
2505119042 Thermodesulfatator indicus
2523533580 Thermodesulfatator atlanticus
2526164516 Prevotella denticola
650716073 Prevotella denticola
649989987 Prevotella multiformis
Prevotella unclassified
Prevotella veroralis
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Prevotella melaninogenica
Prevotella unclassified
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Prevotella amnii
647000292 Prevotella bivia
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Prevotella pallens
Prevotella intermedia
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Prevotella micans
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Prevotella oris
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UID2719
UID2717|f Prevotellaceae
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Prevotella bryantii
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2509276066 Prevotella dentalis
Prevotella dentalis
Prevotella dentalis
Hallella seregens
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Prevotella timonensis
Prevotella timonensis
UID2716||1.000
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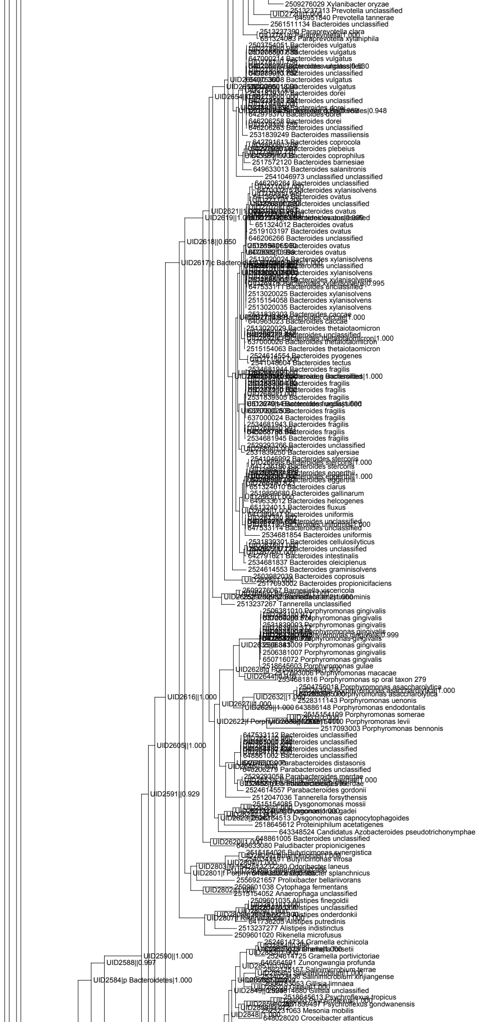
Prevotella brevis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651324083 Paraprevotella xylaniphila
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2531839307 Bacteroides dorei
642979370 Bacteroides dorei
646206258 Bacteroides dorei
646206263 Bacteroides unclassified
2531839249 Bacteroides massiliensis
642791613 Bacteroides coprocola
Bacteroides plebeius
Bacteroides coprophilus
2517572120 Bacteroides barnesiae
649633013 Bacteroides salanitronis
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Bacteroides ovatus
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646206266 Bacteroides unclassified
Bacteroides ovatus
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UID2617|c Bacteroidia
Bacteroides unclassified
Bacteroides xylanisolvens
Bacteroides xylanisolvens|0.995
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2531839303 Bacteroides caccae
Bacteroides caccae|1.000
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Bacteroides thetaiotaomicron|1.000
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Bacteroides fragilis|1.000
Bacteroides fragilis
Bacteroides fragilis
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Bacteroides fragilis
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Bacteroides stercoris|1.000
Bacteroides stercoris
Bacteroides eggerthii
Bacteroides eggerthii|1.000
Bacteroides eggerthii
651324010 Bacteroides clarus
2519899680 Bacteroides gallinarum
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Bacteroides uniformis
Bacteroides unclassified
Bacteroides uniformis|1.000
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Barnesiella intestinihominis
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Porphyromonas gingivalis
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Porphyromonas gingivalis|0.999
Porphyromonas gingivalis
Porphyromonas gingivalis
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Porphyromonas macacae
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Porphyromonas asaccharolytica|1.000
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Porphyromonas levii
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Bacteroides unclassified
Bacteroides unclassified
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646206279 Parabacteroides unclassified
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Parabacteroides merdae|1.000
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Dysgonomonas|1.000
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Gramella|1.000
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UID2590||1.000
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Salinimicrobium terrae
Salinimicrobium|1.000
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Gillisia limnaea
UID2849||
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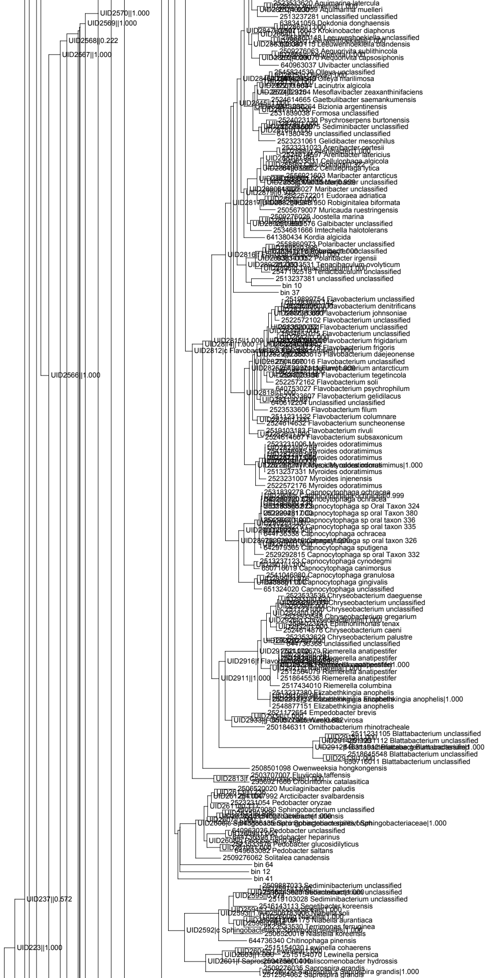
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Leeuwenhoekiella blandensis
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Aequorivita capsosiphonis
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2545824539 Olleya unclassified
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Lacinutrix algicola
Mesoflavibacter zeaxanthinifaciens
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Cellulophaga algicola
Cellulophaga lytica
2556921603 Maribacter antarcticus
Maribacter unclassified
Maribacter unclassified
2522572201 Eudoraea adriatica
Robiginitalea biformata
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Galbibacter unclassified
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Tenacibaculum ovolyticum
2547132518 Tenacibaculum unclassified
2513237381 unclassified unclassified
bin 10
bin 37
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UID2817
UID2816|f Flavobacteriaceae
2519899754 Flavobacterium unclassified
Flavobacterium denitrificans
Flavobacterium johnsoniae
2522572102 Flavobacterium unclassified
Flavobacterium unclassified
Flavobacterium frigidarium
Flavobacterium frigoris
Flavobacterium daejeonense
Flavobacterium unclassified
Flavobacterium antarcticum
Flavobacterium tegetincola
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640753027 Flavobacterium psychrophilum
Flavobacterium gelidilacus
640612204 unclassified unclassified
2523533606 Flavobacterium filum
2511231122 Flavobacterium columnare
2524614632 Flavobacterium suncheonense
2519103183 Flavobacterium rivuli
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UID2814||1.000
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UID2818||1.000
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Myroides odoratimimus
Myroides odoratimimus|1.000
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Capnocytophaga gingivalis
651324020 Capnocytophaga unclassified
2523533536 Chryseobacterium daeguense
Chryseobacterium unclassified
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Epilithonimonas tenax
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Riemerella anatipestifer
Riemerella anatipestifer
Riemerella anatipestifer|1.000
2512564079 Riemerella anatipestifer
2518645536 Riemerella anatipestifer
2517434010 Riemerella columbina
2513237380 Elizabethkingia anophelis
Elizabethkingia anophelis|1.000
2548877151 Elizabethkingia anophelis
2521172654 Empedobacter brevis
Weeksella virosa
2501846311 Ornithobacterium rhinotracheale
UID2916|f Flavobacteriaceae
UID2911||1.000
UID2933|g
2511231105 Blattabacterium unclassified
Blattabacterium unclassified
Blattabacterium unclassified
Blattabacterium unclassified|1.000
2518645548 Blattabacterium unclassified
650716011 Blattabacterium unclassified
2508501098 Owenweeksia hongkongensis
2503707007 Fluviicola taffensis
2556921606 Crocinitomix catalasitica
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2506520020 Mucilaginibacter paludis
Arcticibacter svalbardensis
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2505679080 Sphingobacterium unclassified
Sphingobacteriaceae|1.000
UID2606|c Sphingobacteriia
640963036 Pedobacter unclassified
Pedobacter heparinus
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649633082 Pedobacter saltans
2509276062 Solitalea canadensis
bin 64
bin 12
bin 41
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Sediminibacterium unclassified
2519103028 Sediminibacterium unclassified
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Niastella soli
Niabella aurantiaca
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2506520016 Niastella koreensis
644736340 Chitinophaga pinensis
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UID2603||1.000
Haliscomenobacter hydrossis
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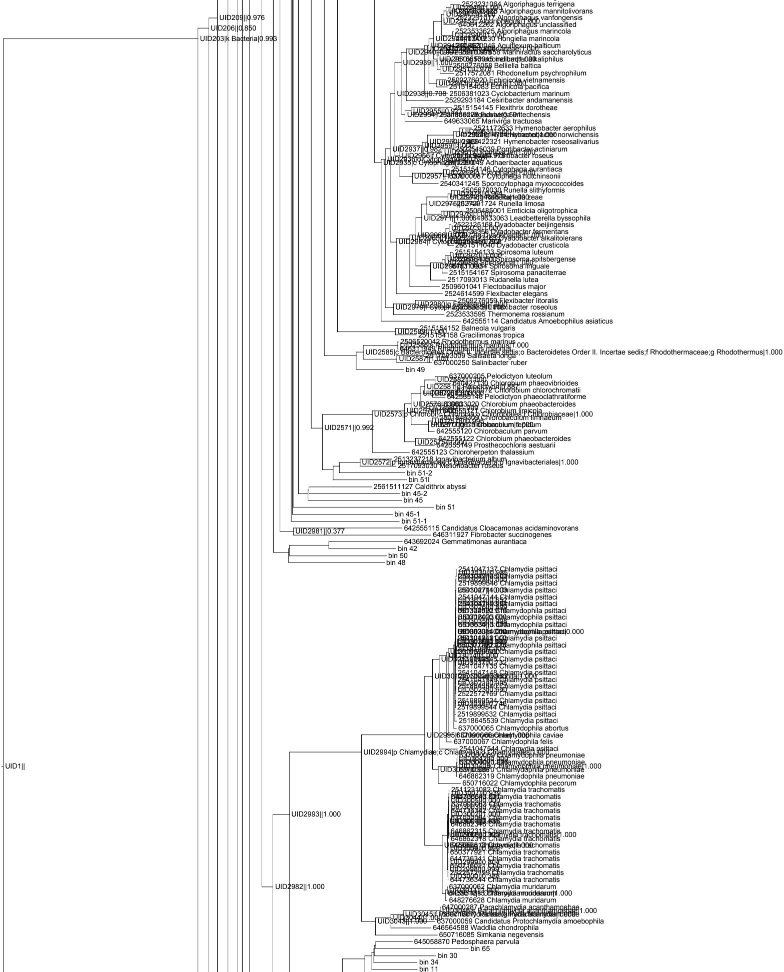
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640612202 Algoriphagus unclassified
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649633065 Marivirga tractuosa
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Hymenobacter norwichensis
UID2960
2522422321 Hymenobacter roseosalivarius
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Adhaeribacter aquaticus
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2540341245 Sporocytophaga myxococcoides
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2515154133 Spirosoma luteum
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UID2586
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Salisaeta longa
UID2587||1.000
637000250 Salinibacter ruber
bin 49
637000205 Pelodictyon luteolum
Chlorobium phaeovibrioides
UID2581
Chlorobium chlorochromatii
642555146 Pelodictyon phaeoclathratiforme
UID2576
Chlorobium phaeobacteroides
Chlorobium limicola
UID2573|p Chlorobi;c Chlorobia;o Chlorobiales;f Chlorobiaceae|1.000
Chlorobaculum limnaeum
UID2571||0.992
642555120 Chlorobaculum parvum
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UID2575
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bin 51-2
bin 51I
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bin 45-2
bin 45
bin 51
bin 45-1
bin 51-1
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643692024 Gemmatimonas aurantiaca
bin 42
bin 50
bin 48
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Chlamydia psittaci
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Chlamydia psittaci
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Chlamydophila psittaci
Chlamydophila psittaci
Chlamydophila psittaci
Chlamydophila psittaci|0.000
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2541047135 Chlamydia psittaci
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UID301
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Chlamydia psittaci
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637000065 Chlamydophila abortus
UID2995
Chlamydophila caviae
637000067 Chlamydophila felis
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2541047544 Chlamydia psittaci
Chlamydophila pneumoniae
Chlamydophila pneumoniae
Chlamydophila pneumoniae|1.000
Chlamydophila pneumoniae
646862319 Chlamydophila pneumoniae
650716022 Chlamydophila pecorum
2511231082 Chlamydia trachomatis
Chlamydia trachomatis
Chlamydia trachomatis
Chlamydia trachomatis
Chlamydia trachomatis
UID2993||1.000
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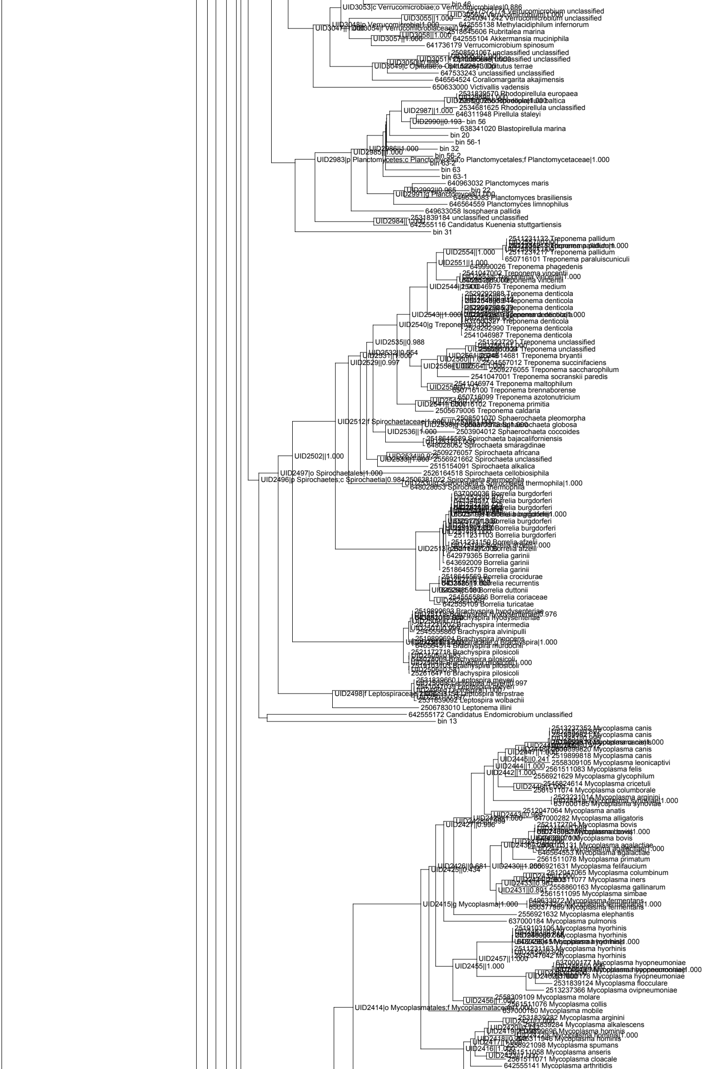
Chlamydia trachomatis
646862315 Chlamydia trachomatis
Chlamydia trachomatis|1.000
646862318 Chlamydia trachomatis
Chlamydia trachomatis
650377921 Chlamydia trachomatis
644736341 Chlamydia trachomatis
Chlamydia trachomatis
Chlamydia trachomatis
644736344 Chlamydia trachomatis
UID2982||1.000
637000062 Chlamydia muridarum
Chlamydia muridarum|1.000
648276628 Chlamydia muridarum
647000287 Parachlamydia acanthamoebae
UID3045
Parachlamydia acanthamoebae|1.000
UID3043||1.000
637000059 Candidatus Protochlamydia amoebophila
646564588 Waddlia chondrophila
650716085 Simkania negevensis
645058870 Pedosphaera parvula
bin 65
bin 30
bin 34
bin 11


bin 46
UID3053|c Verrucomicrobiae;o Verrucomicrobiales|0.886
2517572174 Verrucomicrobium unclassified
2540341242 Verrucomicrobium unclassified
UID3055||1.000
UID3048|o Verrucomicrobiales
UID3047||1.000
UID3054|f Verrucomicrobiaceae|0.796
642555138 Methylacidiphilum infernorum
2518645606 Rubritalea marina
UID3058||1.000
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642555104 Akkermansia muciniphila
641736179 Verrucomicrobium spinosum
2508501067 unclassified unclassified
unclassified unclassified
UID3051
UID3050||0.998
UID3049|c Opitutae;o Opitutales
Opitutus terrae
647533243 unclassified unclassified
646564524 Coraliomargarita akajimensis
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2531839570 Rhodopirellula europaea
Rhodopirellula baltica
UID2987||1.000
2534681625 Rhodopirellula unclassified
646311948 Pirellula staleyi
UID2990||0.193
bin 56
638341020 Blastopirellula marina
bin 20
bin 56-1
UID2986||1.000
UID2985||1.000
bin 32
bin 56-2
UID2983|p Planctomycetes;c Planctomycetia;o Planctomycetales;f Planctomycetaceae|1.000
bin 63-2
bin 63
bin 63-1
640963032 Planctomyces maris
UID2992||0.965
bin 22
UID2991|g Planctomyces|1.000
649633083 Planctomyces brasiliensis
646564559 Planctomyces limnophilus
649633058 Isosphaera pallida
UID2984||1.000
2531839184 unclassified unclassified
642555116 Candidatus Kuenenia stuttgartiensis
bin 31
2511231132 Treponema pallidum
Treponema pallidum|1.000
2511231217 Treponema pallidum
UID2554||1.000
UID2551||1.000
650716101 Treponema paraluiscuniculi
649990026 Treponema phagedenis
2541047002 Treponema vincentii
Treponema vincentii|1.000
Treponema vincentii
UID2544||1.000
2541046975 Treponema medium
2529292988 Treponema denticola
Treponema denticola
Treponema denticola
UID2543||1.000
Treponema denticola|1.000
637000327 Treponema denticola
UID2540|g Treponema|1.000
2529292990 Treponema denticola
2541046987 Treponema denticola
2513237291 Treponema unclassified
Treponema unclassified
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UID2532||0.554
UID2531||1.000
UID2529||0.997
UID2561
2524614681 Treponema bryantii
UID2560||1.000
2504557012 Treponema succinifaciens
UID2558
UID2564
2509276055 Treponema saccharophilum
2541047001 Treponema socranskii paredis
2541046974 Treponema maltophilum
650716100 Treponema brennaborense
650716099 Treponema azotonutricium
UID2541
650716102 Treponema primitia
2505679006 Treponema caldaria
2508501070 Sphaerochaeta pleomorpha
UID2512|f Spirochaetaceae|1.000
UID2538|g Sphaerochaeta
Sphaerochaeta globosa
UID2536||1.000
2503904012 Sphaerochaeta coccoides
2518645589 Spirochaeta bajacaliforniensis
648028052 Spirochaeta smaragdinae
UID2502||1.000
2509276057 Spirochaeta africana
UID2534
UID2533||1.000
2556921662 Spirochaeta unclassified
2515154091 Spirochaeta alkalica
UID2497|o Spirochaetales|1.000
2526164518 Spirochaeta cellobiosiphila
UID2496|p Spirochaetes;c Spirochaetia|0.984
2506381022 Spirochaeta thermophila
UID2530|g Spirochaeta;s Spirochaeta thermophila|1.000
648028053 Spirochaeta thermophila
637000036 Borrelia burgdorferi
Borrelia burgdorferi
Borrelia burgdorferi|1.000
Borrelia burgdorferi
Borrelia burgdorferi
2511231103 Borrelia burgdorferi
2511231159 Borrelia afzelii
Borrelia afzelii|1.000
UID2513
Borrelia afzelii
642979365 Borrelia garinii
643692009 Borrelia garinii
2518645579 Borrelia garinii
2518645569 Borrelia crocidurae
Borrelia recurrentis
Borrelia duttonii
2545555866 Borrelia coriaceae
UID2528||0.997
642555109 Borrelia turicatae
2519899693 Brachyspira hyodysenteriae
Brachyspira hyodysenteriae|0.976
Brachyspira hyodysenteriae
2511231202 Brachyspira intermedia
2545555860 Brachyspira alvinipulli
2519899694 Brachyspira innocens
Brachyspiraceae;g Brachyspira|1.000
646564514 Brachyspira murdochii
2521172718 Brachyspira pilosicoli
648028009 Brachyspira pilosicoli
Brachyspira pilosicoli|1.000
Brachyspira pilosicoli
2526164116 Brachyspira pilosicoli
2531839660 Leptospira meyeri
Leptospira meyeri|0.997
Leptospira meyeri
UID2498|f Leptospiraceae
Leptospira terpstrae
2531839092 Leptospira wolbachii
2506783010 Leptonema illini
642555172 Candidatus Endomicrobium unclassified
bin 13
2513237352 Mycoplasma canis
Mycoplasma canis
Mycoplasma canis|1.000
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UID2447||1.000
2519899818 Mycoplasma canis
UID2445||0.241
2558309105 Mycoplasma leonicaptivi
UID2444||1.000
2561511083 Mycoplasma felis
UID2442||1.000
2556921629 Mycoplasma glycophilum
2545824614 Mycoplasma cricetuli
UID2446
2561511074 Mycoplasma columborale
2523231014 Mycoplasma arginini
637000185 Mycoplasma synoviae
Mycoplasma synoviae|1.000
2512047064 Mycoplasma anatis
UID2443||0.998
647000282 Mycoplasma alligatoris
UID2427||0.996
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Mycoplasma bovis|1.000
Mycoplasma bovis
Mycoplasma agalactiae
Mycoplasma agalactiae|1.000
646564553 Mycoplasma agalactiae
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UID2425||0.434
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UID2433||0.981
2558860163 Mycoplasma gallinarum
UID2431||0.891
2561511095 Mycoplasma simbae
649633072 Mycoplasma fermentans
UID2415|g Mycoplasma|1.000
Mycoplasma fermentans|1.000
650377955 Mycoplasma fermentans
2556921632 Mycoplasma elephantis
637000184 Mycoplasma pulmonis
2519103106 Mycoplasma hyorhinis
Mycoplasma hyorhinis
Mycoplasma hyorhinis|1.000
2511231163 Mycoplasma hyorhinis
UID2457||1.000
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637000177 Mycoplasma hyopneumoniae
Mycoplasma hyopneumoniae|1.000
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2531839124 Mycoplasma flocculare
2513237366 Mycoplasma ovipneumoniae
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UID2456||1.000
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Mycoplasma hominis
Mycoplasma hominis|1.000
Mycoplasma hominis
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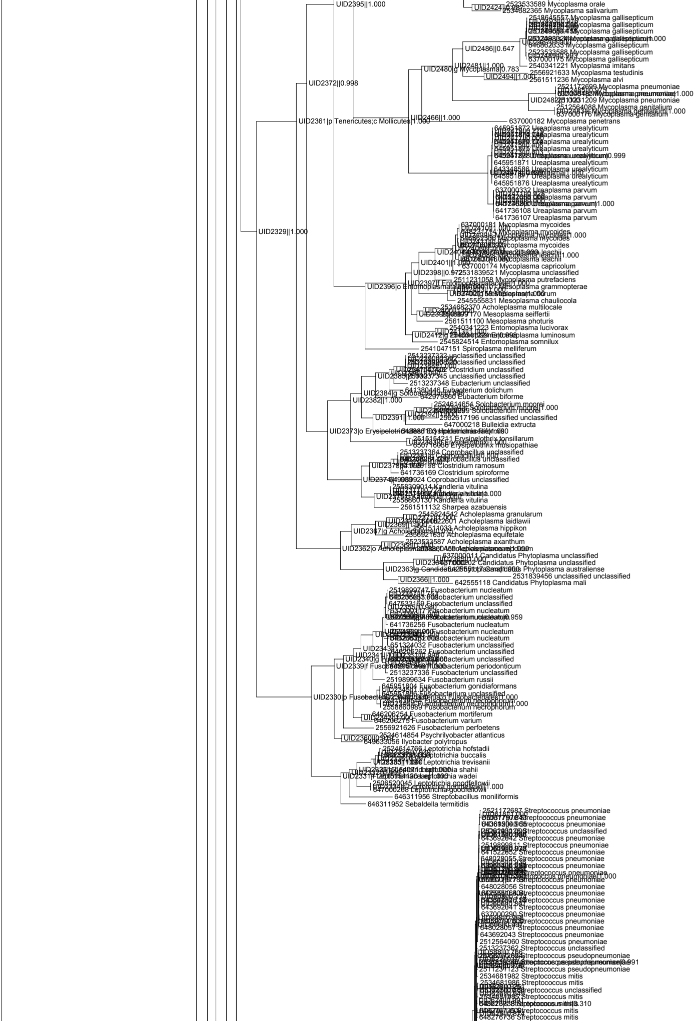
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2534682365 Mycoplasma salivarium
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Mycoplasma gallisepticum
Mycoplasma gallisepticum
Mycoplasma gallisepticum
646862333 Mycoplasma gallisepticum
UID2486||0.647
2523533588 Mycoplasma gallisepticum
637000175 Mycoplasma gallisepticum
UID2481||1.000
2540341221 Mycoplasma imitans
UID2480|g Mycoplasma|0.783
2556921633 Mycoplasma testudinis
UID2494||1.000
2561511236 Mycoplasma alvi
UID2372||0.998
2521172699 Mycoplasma pneumoniae
2511231209 Mycoplasma pneumoniae
2512564088 Mycoplasma genitalium
637000176 Mycoplasma genitalium
UID2466||1.000
637000182 Mycoplasma penetrans
UID2361|p Tenericutes;c Mollicutes|1.000
645951872 Ureaplasma urealyticum
Ureaplasma urealyticum
Ureaplasma urealyticum
Ureaplasma urealyticum
645951873 Ureaplasma urealyticum
645951871 Ureaplasma urealyticum
643348586 Ureaplasma urealyticum
645951877 Ureaplasma urealyticum
645951876 Ureaplasma urealyticum
637000332 Ureaplasma parvum
Ureaplasma parvum
641736108 Ureaplasma parvum
641736107 Ureaplasma parvum
UID2329||1.000
637000181 Mycoplasma mycoides
Mycoplasma mycoides
Mycoplasma mycoides
Mycoplasma mycoides
Mycoplasma leachii
UID2401||1.000
637000174 Mycoplasma capricolum
UID2398||0.972
2531839521 Mycoplasma unclassified
2511231058 Mycoplasma putrefaciens
Mesoplasma grammopterae
UID2396|o Entomoplasmatales
2545555831 Mesoplasma chauliocola
2534682370 Acholeplasma multilocale
Mesoplasma seiffertii
2561511100 Mesoplasma photuris
2540341223 Entomoplasma lucivorax
Entomoplasma luminosum
2545824514 Entomoplasma somnilux
2541047151 Spiroplasma melliferum
2513237332 unclassified unclassified
unclassified unclassified
Clostridium unclassified
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641380446 Eubacterium dolichum
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642979360 Eubacterium biforme
UID2382||1.000
2524614654 Solobacterium moorei
Solobacterium moorei
UID2391||1.000
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647000218 Bulleidia extructa
UID2373|o Erysipelotrichales
2515154211 Erysipelothrix tonsillarum
650716066 Erysipelothrix rhusiopathiae
2513237364 Coprobacillus unclassified
Coprobacillus unclassified
Clostridium ramosum
641736169 Clostridium spiroforme
649989924 Coprobacillus unclassified
2558309014 Kandleria vitulina
2558860130 Kandleria vitulina
2561511132 Sharpea azabuensis
2545824542 Acholeplasma granularum
Acholeplasma laidlawii
UID2367|g Acholeplasma
2561511033 Acholeplasma hippikon
2556921630 Acholeplasma equifetale
2523533587 Acholeplasma axanthum
UID2362|o Acholeplasmatales
637000011 Candidatus Phytoplasma unclassified
637000202 Candidatus Phytoplasma unclassified
UID2363|g Candidatus Phytoplasma
Candidatus Phytoplasma australiense
2531839456 unclassified unclassified
UID2366||1.000
642555118 Candidatus Phytoplasma mali
2519899747 Fusobacterium nucleatum
Fusobacterium unclassified
647533169 Fusobacterium unclassified
637000117 Fusobacterium nucleatum
Fusobacterium nucleatum|0.959
641736256 Fusobacterium nucleatum
Fusobacterium nucleatum
Fusobacterium nucleatum
651324032 Fusobacterium unclassified
Fusobacterium unclassified
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UID2340|g Fusobacterium
Fusobacterium unclassified
UID2339|f Fusobacteriaceae
Fusobacterium periodonticum
2513237336 Fusobacterium unclassified
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645951804 Fusobacterium gonidiaformans
Fusobacterium unclassified
UID2330|p Fusobacteria
Fusobacterium necrophorum
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646206254 Fusobacterium mortiferum
646206273 Fusobacterium varium
2556921626 Fusobacterium perfoetens
UID2360||0.934
2524614854 Psychrilyobacter atlanticus
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2524614766 Leptotrichia hofstadii
Leptotrichia buccalis
Leptotrichia trevisanii
Leptotrichia shahii
UID2331|f Leptotrichiaceae
Leptotrichia wadei
2506520045 Leptotrichia goodfellowii
647000268 Leptotrichia goodfellowii
646311956 Streptobacillus moniliformis
646311952 Sebaldella termitidis
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Streptococcus pneumoniae
Streptococcus pneumoniae
Streptococcus unclassified
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Streptococcus pneumoniae
Streptococcus pneumoniae|1.000
Streptococcus pneumoniae
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Streptococcus pneumoniae
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643692043 Streptococcus pneumoniae
2512564060 Streptococcus pneumoniae
2513237362 Streptococcus unclassified
Streptococcus pseudopneumoniae
Streptococcus pseudopneumoniae|0.991
2511231123 Streptococcus pseudopneumoniae
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2534681986 Streptococcus mitis
Streptococcus unclassified
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Streptococcus mitis|0.310
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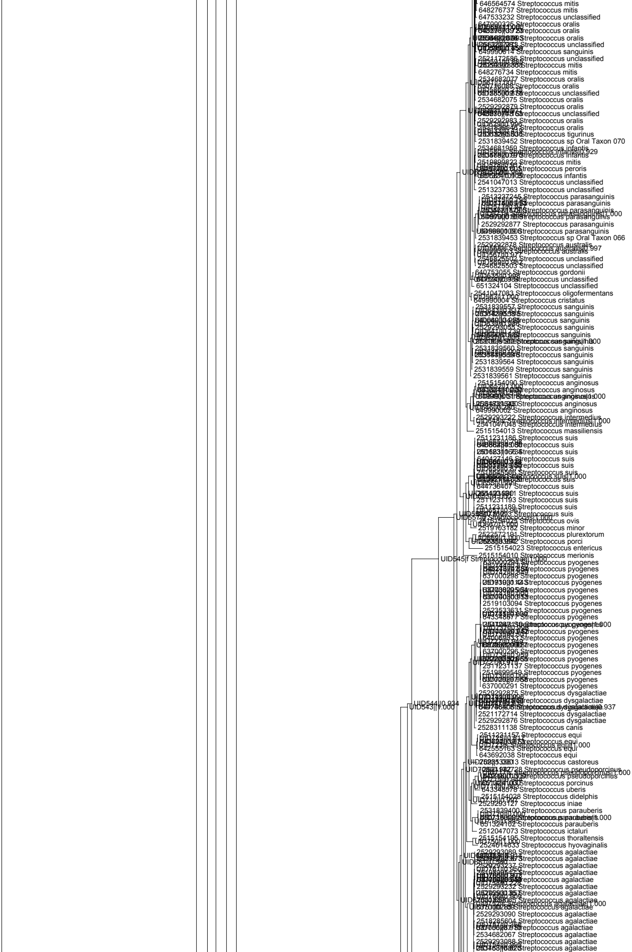
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Streptococcus mitis
648276734 Streptococcus mitis
2534682077 Streptococcus oralis
Streptococcus oralis
Streptococcus unclassified
2534682075 Streptococcus oralis
2529292879 Streptococcus oralis
Streptococcus unclassified
2529292983 Streptococcus oralis
Streptococcus oralis
Streptococcus tigurinus
2531839452 Streptococcus sp Oral Taxon 070
2534681959 Streptococcus infantis
Streptococcus infantis
2518899822 Streptococcus mitis
Streptococcus peroris
Streptococcus infantis
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2513237363 Streptococcus unclassified
2513237245 Streptococcus parasanguinis
Streptococcus parasanguinis
Streptococcus parasanguinis
Streptococcus parasanguinis
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Streptococcus parasanguinis
2531839453 Streptococcus sp Oral Taxon 066
2529292878 Streptococcus australis
Streptococcus australis
2546825502 Streptococcus unclassified
2546825503 Streptococcus unclassified
640753055 Streptococcus gordonii
Streptococcus unclassified
651324104 Streptococcus unclassified
2541047083 Streptococcus oligofermentans
649990004 Streptococcus cristatus
2531839557 Streptococcus sanguinis
Streptococcus sanguinis
Streptococcus sanguinis
Streptococcus sanguinis
Streptococcus sanguinis
2531839560 Streptococcus sanguinis
Streptococcus sanguinis
2531839564 Streptococcus sanguinis
2531839559 Streptococcus sanguinis
2531839561 Streptococcus sanguinis
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Streptococcus anginosus
Streptococcus anginosus
649990002 Streptococcus anginosus
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2541047048 Streptococcus intermedius
2515154013 Streptococcus massiliensis
2511231186 Streptococcus suis
Streptococcus suis
Streptococcus suis
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Streptococcus suis
Streptococcus suis
644736407 Streptococcus suis
Streptococcus suis
2511231193 Streptococcus suis
2511231189 Streptococcus suis
Streptococcus suis
2515154025 Streptococcus ovis
2519103182 Streptococcus minor
2522572191 Streptococcus plurextorum
Streptococcus porci
2515154023 Streptococcus entericus
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Streptococcus pyogenes
Streptococcus pyogenes
637000298 Streptococcus pyogenes
Streptococcus pyogenes
Streptococcus pyogenes
Streptococcus pyogenes
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Streptococcus pyogenes
2511231137 Streptococcus pyogenes
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Streptococcus pyogenes
637000291 Streptococcus pyogenes
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Streptococcus dysgalactiae
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2529292876 Streptococcus dysgalactiae
2528311138 Streptococcus canis
2511231157 Streptococcus equi
Streptococcus equi
642555163 Streptococcus equi
643692038 Streptococcus equi
Streptococcus castoreus
Streptococcus pseudoporcinus
Streptococcus pseudoporcinus
Streptococcus porcinus
643348578 Streptococcus uberis
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2529293089 Streptococcus agalactiae
Streptococcus agalactiae
Streptococcus agalactiae
Streptococcus agalactiae
Streptococcus agalactiae
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Streptococcus agalactiae
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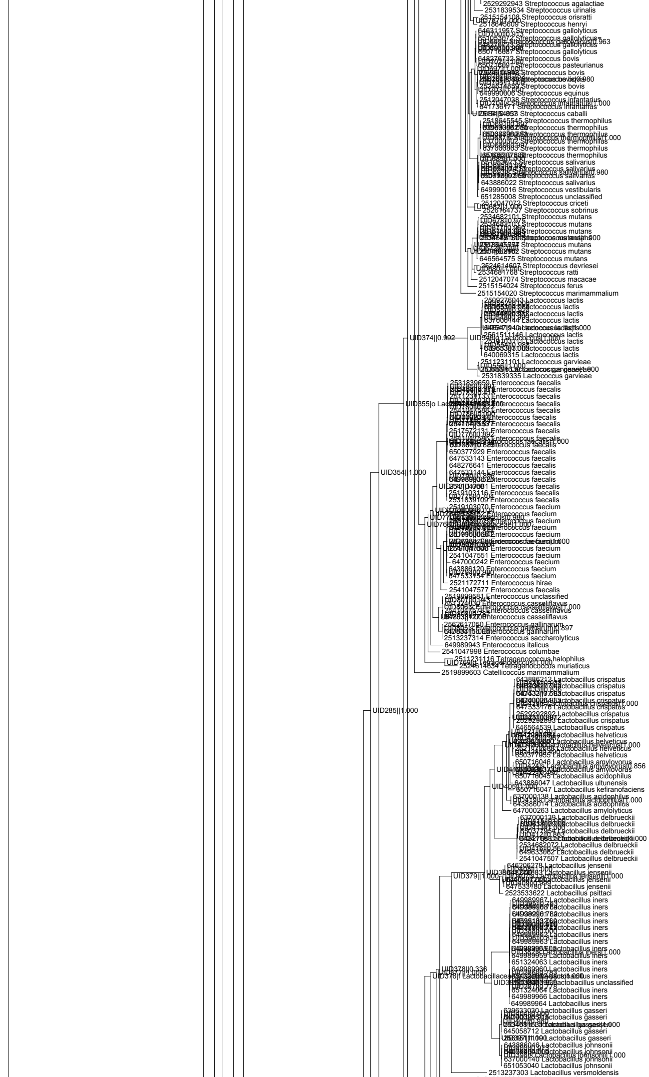
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2524614859 Streptococcus bovis
649990006 Streptococcus equinus
2512047038 Streptococcus infantarius
641736171 Streptococcus infantarius
Streptococcus caballi
2518645545 Streptococcus thermophilus
637000302 Streptococcus thermophilus
637000303 Streptococcus thermophilus
643886022 Streptococcus salivarius
649990016 Streptococcus vestibularis
651285008 Streptococcus unclassified
2512047072 Streptococcus criceti
2526164737 Streptococcus sobrinus
2534682101 Streptococcus mutans
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2512047074 Streptococcus macacae
2515154024 Streptococcus ferus
2515154020 Streptococcus marimammalium
UID374||0.992
2509276043 Lactococcus lactis
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2561511146 Lactococcus lactis
640069315 Lactococcus lactis
2511231101 Lactococcus garvieae
2531839335 Lactococcus garvieae
2531839659 Enterococcus faecalis
UID355|o Lac
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UID354||1.000
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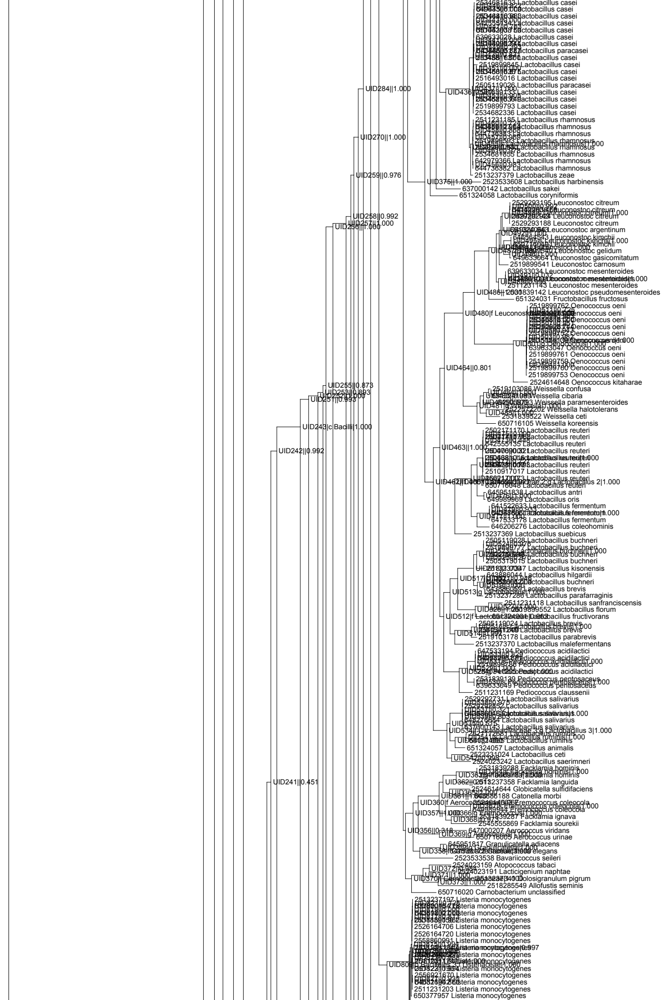
651324030 Enterococcus casseliflavus
2562617050 Enterococcus gallinarum
2513237314 Enterococcus saccharolyticus
649989943 Enterococcus italicus
2541047998 Enterococcus columbae
2511231116 Tetragenococcus halophilus
2524614634 Tetragenococcus muriaticus
2519899603 Catellicoccus marimammalium
UID285||1.000
643886212 Lactobacillus crispatus
647533176 Lactobacillus crispatus
2529292892 Lactobacillus crispatus
646564539 Lactobacillus crispatus
650377955 Lactobacillus helveticus
650716046 Lactobacillus amylovorus
650716045 Lactobacillus acidophilus
643886047 Lactobacillus ultunensis
650716047 Lactobacillus kefiranofaciens
637000138 Lactobacillus acidophilus
643886014 Lactobacillus acidophilus
647000263 Lactobacillus amylolyticus
637000139 Lactobacillus delbrueckii
2534682072 Lactobacillus delbrueckii
649633062 Lactobacillus delbrueckii
2541047507 Lactobacillus delbrueckii
646206278 Lactobacillus jensenii
UID379||1.000
647533180 Lactobacillus jensenii
2523533622 Lactobacillus psittaci
649989967 Lactobacillus iners
649989963 Lactobacillus iners
649989959 Lactobacillus iners
651324063 Lactobacillus iners
649989960 Lactobacillus iners
UID378||0.336
UID376|f Lactobacillaceae
Lactobacillus unclassified
651324064 Lactobacillus iners
649989966 Lactobacillus iners
649989964 Lactobacillus iners
639633030 Lactobacillus gasseri
645058712 Lactobacillus gasseri
643886046 Lactobacillus johnsonii
637000140 Lactobacillus johnsonii
651053040 Lactobacillus johnsonii
2513237303 Lactobacillus versmoldensis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Lactobacillus casei
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Lactobacillus casei
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Lactobacillus paracasei
Lactobacillus casei
2519899845 Lactobacillus casei
Lactobacillus casei
2516493016 Lactobacillus casei
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Lactobacillus casei
Lactobacillus casei
2519899793 Lactobacillus casei
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UID284||1.000
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2511231185 Lactobacillus rhamnosus
Lactobacillus rhamnosus
Lactobacillus rhamnosus
Lactobacillus rhamnosus
2534681855 Lactobacillus rhamnosus
642979366 Lactobacillus rhamnosus
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2513237379 Lactobacillus zeae
UID270||1.000
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UID375||1.000
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Leuconostoc citreum
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Leuconostoc gelidum
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639633034 Leuconostoc mesenteroides
2511231143 Leuconostoc mesenteroides
UID486
2501839142 Leuconostoc pseudomesenteroides
651324031 Fructobacillus fructosus
UID480|f Leuconost
2519899762 Oenococcus oeni
Oenococcus oeni
Oenococcus oeni
Oenococcus oeni
Oenococcus oeni
639633047 Oenococcus oeni
2519899761 Oenococcus oeni
2519899759 Oenococcus oeni
2519899760 Oenococcus oeni
2519899753 Oenococcus oeni
2524614648 Oenococcus kitaharae
UID464||0.801
UID255||0.873
UID253||0.893
UID252||1.000
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2519103086 Weissella confusa
Weissella cibaria
Weissella paramesenteroides
Weissella halotolerans
2531839522 Weissella ceti
650716105 Weissella koreensis
UID243|c Bacilli|1.000
2502171170 Lactobacillus reuteri
Lactobacillus reuteri
642555135 Lactobacillus reuteri
Lactobacillus reuteri
UID463||1.000
UID242||0.992
2510917017 Lactobacillus reuteri
Lactobacillus reuteri
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UID462
Lactobacillus 2|1.000
645951838 Lactobacillus antri
649989969 Lactobacillus oris
641522633 Lactobacillus fermentum
647533178 Lactobacillus fermentum
646206276 Lactobacillus coleohominis
2513237369 Lactobacillus suebicus
2505119028 Lactobacillus buchneri
Lactobacillus buchneri
Lactobacillus buchneri
2505313015 Lactobacillus buchneri
Lactobacillus kisonensis
Lactobacillus hilgardii
Lactobacillus buchneri
UID517
Lactobacillus brevis
UID513
2513237286 Lactobacillus parafarraginis
2511231118 Lactobacillus sanfranciscensis
Lactobacillus florum
UID512|f Lactob
Lactobacillus fructivorans
2505119024 Lactobacillus brevis
Lactobacillus brevis
2519103178 Lactobacillus parabrevis
2513237370 Lactobacillus malefermentans
647533194 Pediococcus acidilactici
Pediococcus acidilactici
Pediococcus acidilactici
Pediococcus acidilactici
2531839139 Pediococcus pentosaceus
639633046 Pediococcus pentosaceus
2511231169 Pediococcus claussenii
2529292731 Lactobacillus salivarius
Lactobacillus salivarius
642791684 Lactobacillus salivarius
637000143 Lactobacillus salivarius
Lactobacillus 3|1.000
Lactobacillus ruminis
651324057 Lactobacillus animalis
2523231024 Lactobacillus ceti
2524023242 Lactobacillus saerimneri
UID241||0.451
2531839288 Facklamia hominis
Facklamia hominis
UID362
2513237358 Facklamia languida
2524614644 Globicatella sulfidifaciens
Catonella morbi
UID360|f Aeroco
Eremococcus coleocola
Eremococcus coleocola
UID357
2513239287 Facklamia ignava
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UID356||0.318
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UID369
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elegans
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UID372
2524023191 Lacticigenium naphtae
UID370
Dolosigranulum pigrum
UID373||1.000
2518285549 Allofustis seminis
650716020 Carnobacterium unclassified
2513237197 Listeria monocytogenes
Listeria monocytogenes
Listeria monocytogenes
Listeria monocytogenes
2526164706 Listeria monocytogenes
2526164720 Listeria monocytogenes
2558860991 Listeria monocytogenes
Listeria monocytogenes
UID809
Listeria monocytogenes
Listeria monocytogenes
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2511231203 Listeria monocytogenes
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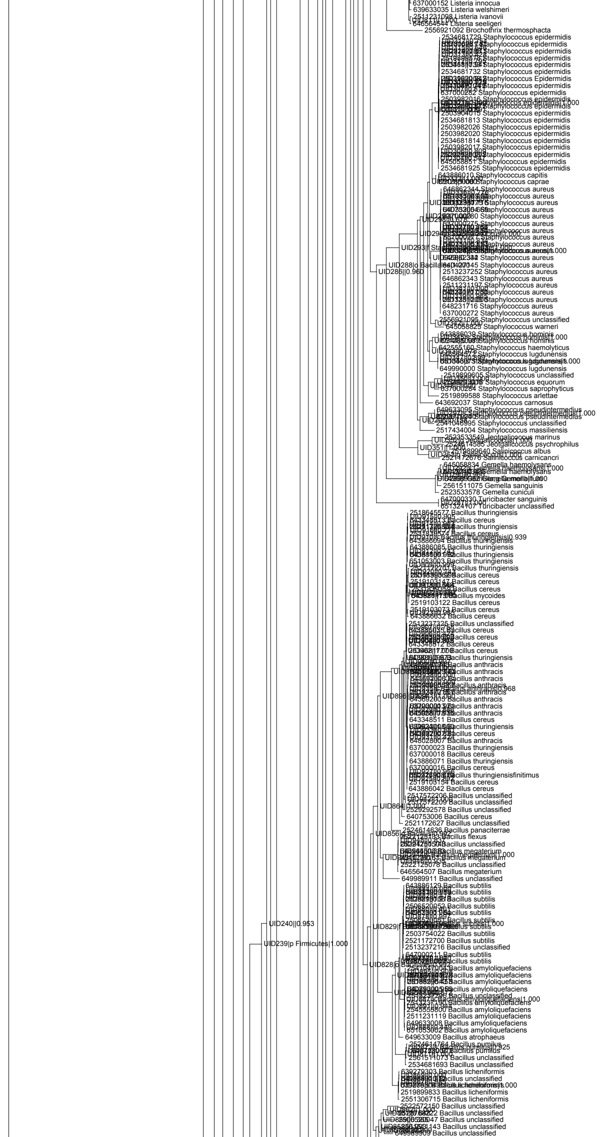
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2534681729 Staphylococcus epidermidis
2534681732 Staphylococcus epidermidis
637000262 Staphylococcus epidermidis
2534681813 Staphylococcus epidermidis
2503982026 Staphylococcus epidermidis
2503982020 Staphylococcus epidermidis
2534681814 Staphylococcus epidermidis
2503982017 Staphylococcus epidermidis
645058851 Staphylococcus epidermidis
2534681925 Staphylococcus epidermidis
643886010 Staphylococcus capitis
Staphylococcus caprae
646862344 Staphylococcus aureus
Staphylococcus aureus
2513237252 Staphylococcus aureus
646862343 Staphylococcus aureus
2511231197 Staphylococcus aureus
648231716 Staphylococcus aureus
637000272 Staphylococcus aureus
UID293|f Sta
UID288|o Bacillales
UID286||0.960
2556921095 Staphylococcus unclassified
645058825 Staphylococcus warneri
643886039 Staphylococcus hominis
642555160 Staphylococcus haemolyticus
Staphylococcus lugdunensis
649990000 Staphylococcus lugdunensis
2519899605 Staphylococcus unclassified
Staphylococcus equorum
637000284 Staphylococcus saprophyticus
2519899588 Staphylococcus arlettae
643692037 Staphylococcus carnosus
649633095 Staphylococcus pseudintermedius
2541046995 Staphylococcus unclassified
2517434004 Staphylococcus massiliensis
2523533549 Jeotgalicoccus marinus
Jeotgalicoccus psychrophilus
UID351||1.000
Salinicoccus albus
2521172676 Salinicoccus carnicancri
645058834 Gemella haemolysans
2561511075 Gemella sanguinis
2523533578 Gemella cuniculi
647000330 Turicibacter sanguinis
651324107 Turicibacter unclassified
2518645577 Bacillus thuringiensis
Bacillus cereus
Bacillus thuringiensis
643886094 Bacillus thuringiensis
643886085 Bacillus thuringiensis
651053003 Bacillus thuringiensis
2519103147 Bacillus cereus
Bacillus mycoides
2519103122 Bacillus cereus
2519103073 Bacillus cereus
643886032 Bacillus cereus
2513237325 Bacillus unclassified
643348512 Bacillus cereus
Bacillus anthracis
643692005 Bacillus anthracis
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648028007 Bacillus anthracis
637000023 Bacillus thuringiensis
637000018 Bacillus cereus
643886071 Bacillus thuringiensis
637000016 Bacillus cereus
Bacillus thuringiensisfinitimus
2519103154 Bacillus cereus
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UID896|
2517572206 Bacillus unclassified
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2521172627 Bacillus unclassified
UID864||1.000
UID856|
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Bacillus flexus
Bacillus unclassified
Bacillus megaterium
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649989911 Bacillus unclassified
643886129 Bacillus subtilis
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2521172700 Bacillus subtilis
2513237216 Bacillus unclassified
647000211 Bacillus subtilis
UID829|
UID828|o Ba
UID240||0.953
UID239|p Firmicutes|1.000
Bacillus amyloliquefaciens
2545555800 Bacillus amyloliquefaciens
2511231119 Bacillus amyloliquefaciens
649633008 Bacillus amyloliquefaciens
651053002 Bacillus amyloliquefaciens
649633009 Bacillus atrophaeus
2524614764 Bacillus pumilus
2561511073 Bacillus unclassified
2534681693 Bacillus unclassified
639279303 Bacillus licheniformis
Bacillus unclassified
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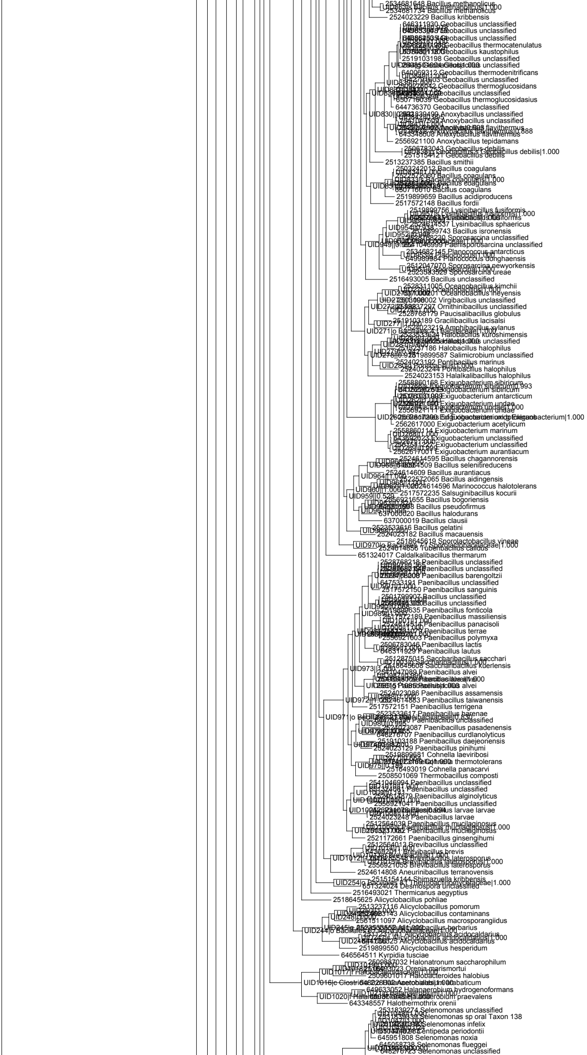

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Geobacillus kaustophilus
2519103198 Geobacillus unclassified
Geobacillus unclassified
640069312 Geobacillus thermodenitrificans
Geobacillus unclassified
Geobacillus thermoglucosidans
Geobacillus unclassified
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644736370 Geobacillus unclassified
Anoxybacillus unclassified
Anoxybacillus unclassified
Anoxybacillus flavithermus
643348508 Anoxybacillus flavithermus
2556921100 Anoxybacillus tepidamans
2506783043 Geobacillus debilis
Geobacillus debilis|1.000
2515154121 Geobacillus debilis
2513237385 Bacillus smithii
2503242012 Bacillus coagulans
Bacillus coagulans
Bacillus coagulans|1.000
Bacillus coagulans
650716010 Bacillus coagulans
2519899659 Bacillus acidiproducens
2517572148 Bacillus fordii
2519899756 Lysinibacillus fusiformis
Lysinibacillus fusiformis|1.000
Lysinibacillus fusiformis
Lysinibacillus sphaericus
Bacillus isronensis
Sporosarcina unclassified
2541046995 Paenisporosarcina unclassified
2534682145 Planococcus antarcticus
649989984 Planococcus donghaensis
2512047070 Sporosarcina newyorkensis
2523533529 Sporosarcina ureae
2516493005 Bacillus unclassified
2528311005 Oceanobacillus kimchii
Oceanobacillus iheyensis
Virgibacillus unclassified
Ornithinibacillus unclassified
2528768179 Paucisalibacillus globulus
2519103189 Gracilibacillus lacisalsi
2524023219 Amphibacillus xylanus
UID271|o Bacillales;f Bacillaceae|1.000
Halobacillus kuroshimensis
Halobacillus unclassified
Halobacillus halophilus
2519899587 Salimicrobium unclassified
2524023192 Pontibacillus marinus
2524023244 Pontibacillus halophilus
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2558860168 Exiguobacterium sibiricum
Exiguobacterium sibiricum|0.993
Exiguobacterium sibiricum
Exiguobacterium antarcticum
Exiguobacterium undae
Exiguobacterium undae|1.000
Exiguobacterium undae
Exiguobacterium|1.000
2562617000 Exiguobacterium acetylicum
2558860114 Exiguobacterium marinum
Exiguobacterium unclassified
Exiguobacterium unclassified
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2524614595 Bacillus chagannorensis
Bacillus selenitireducens
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2522572065 Bacillus aidingensis
2524614596 Marinococcus halotolerans
2517572235 Salsuginibacillus kocurii
UID959||0.529
2556921655 Bacillus bogoriensis
Bacillus pseudofirmus
637000020 Bacillus halodurans
637000019 Bacillus clausii
2523533616 Bacillus gelatini
2524023182 Bacillus macauensis
2518645619 Sporolactobacillus vineae
UID970|o Bacillales;f Sporolactobacillaceae|1.000
2524614856 Tuberibacillus calidus
651324017 Caldalkalibacillus thermarum
2528768218 Paenibacillus unclassified
Paenibacillus unclassified
Paenibacillus barengoltzii
647533191 Paenibacillus unclassified
2517572150 Paenibacillus sanguinis
2501799907 Bacillus unclassified
Bacillus unclassified
2519899635 Paenibacillus fonticola
2517572189 Paenibacillus massiliensis
Paenibacillus panacisoli
Paenibacillus terrae
2556921003 Paenibacillus polymyxa
2506783046 Paenibacillus lactis
646311929 Paenibacillus lautus
2512875015 Saccharibacillus sacchari
Saccharibacillus|1.000
Saccharibacillus kuerlensis
UID973||1.000
2524614883 Paenibacillus alvei
Paenibacillus alvei|1.000
Paenibacillus alvei
2524023086 Paenibacillus assamensis
UID972||1.000
2524614883 Paenibacillus taiwanensis
2517572151 Paenibacillus terrigena
2523533617 Paenibacillus barenae
UID971|o Bacillales;f Paenibacillaceae
Paenibacillus unclassified
2524023087 Paenibacillus pasadenensis
646276707 Paenibacillus curdlanolyticus
2519103188 Paenibacillus daejeonensis
2524023129 Paenibacillus pinihumi
2519899681 Cohnella laeviribosi
Cohnella|1.000
Cohnella thermotolerans
2516493019 Cohnella panacarvi
2508501069 Thermobacillus composti
2541046994 Paenibacillus unclassified
Paenibacillus unclassified
Paenibacillus alginolyticus
2556921041 Paenibacillus unclassified
Paenibacillus larvae larvae
2524023248 Paenibacillus larvae
2512564039 Paenibacillus mucilaginosus
Paenibacillus mucilaginosus|1.000
Paenibacillus mucilaginosus
2521172661 Paenibacillus ginsengihumi
2512564013 Brevibacillus unclassified
Brevibacillus brevis
Brevibacillus|1.000
Brevibacillus laterosporus
Brevibacillus laterosporus|1.000
2556921055 Brevibacillus laterosporus
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2518645625 Alicyclobacillus pohliae
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Alicyclobacillus contaminans
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Alicyclobacillus herbarius
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Alicyclobacillus acidocaldarius|1.000
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2519899550 Alicyclobacillus hesperidum
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2509887032 Halonatronum saccharophilum
Orenia marismortui
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UID1016|c Clostridia
Acetohalobium arabaticum
649633052 Halanaerobium hydrogeniformans
UID1020|f Halanaerobiaceae
Halanaerobium praevalens
643348557 Halothermothrix orenii
2531839274 Selenomonas unclassified
2531839039 Selenomonas sp oral Taxon 138
Selenomonas infelix
Centipeda periodontii
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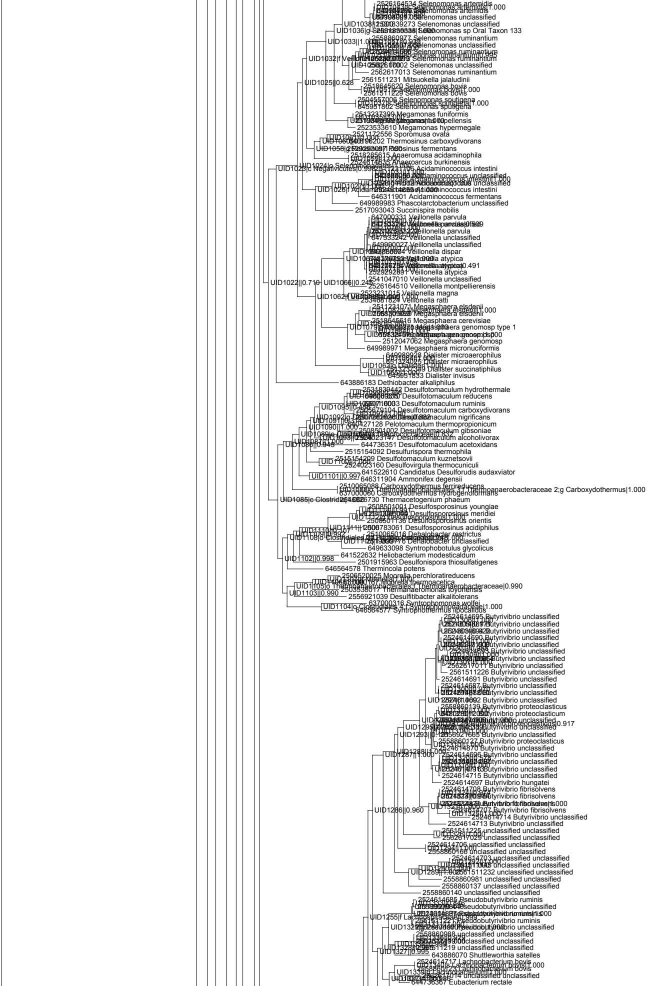
645058738 Selenomonas flueggei
646276723 Selenomonas unclassified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Selenomonas unclassified
Selenomonas ruminantium
UID1032|f Veillonellaceae
Selenomonas unclassified
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2561511231 Mitsuokella jalaludinii
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Megamonas|1.000
Megamonas rupellensis
2523533610 Megamonas hypermegale
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Thermosinus carboxydivorans
UID1058
Thermosinus fermentans
2518285615 Anaeromusa acidaminophila
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UID1024|o Selenomonadales
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Acidaminococcus intestini
Acidaminococcus unclassified
Acidaminococcus intestini|1.000
Acidaminococcus unclassified
UID1026|f Acidaminococcaceae
Acidaminococcus intestini
646311901 Acidaminococcus fermentans
649989983 Phascolarctobacterium unclassified
2517093043 Succinispira mobilis
647000231 Veillonella parvula
Veillonella parvula|0.609
Veillonella parvula
647533242 Veillonella unclassified
649990027 Veillonella unclassified
Veillonella dispar
Veillonella atypica
Veillonella atypica|0.491
2529292891 Veillonella atypica
2541047010 Veillonella unclassified
UID1022||0.710
UID1066||0.245
2526164510 Veillonella montpellierensis
2523231015 Veillonella magna
UID1062
2534681624 Veillonella ratti
2511231071 Megasphaera elsdenii
Megasphaera elsdenii|1.000
2518645616 Megasphaera cerevisiae
Megasphaera genomosp type 1
Megasphaera genomosp|1.000
2512047062 Megasphaera genomosp
649989971 Megasphaera micronuciformis
649989928 Dialister microaerophilus
Dialister micraerophilus
UID1063|g Dialister|1.000
Dialister succinatiphilus
645951833 Dialister invisus
643886183 Dethiobacter alkaliphilus
2531839442 Desulfotomaculum hydrothermale
Desulfotomaculum reducens
Desulfotomaculum ruminis
UID1095
Desulfotomaculum carboxydivorans
UID1092|g Desulfotomaculum|0.882
Desulfotomaculum nigrificans
UID1091
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UID1090||1.000
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UID1089
Desulfotomaculum alcoholivorax
UID1087
UID1086||0.943
644736351 Desulfotomaculum acetoxidans
2515154092 Desulfurispora thermophila
2515154209 Desulfotomaculum kuznetsovii
UID1100||1.000
2524023160 Desulfovirgula thermocuniculi
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2510065088 Carboxydothermus ferrireducens
Thermoanaerobacterales 2;f Thermoanaerobacteraceae 2;g Carboxydothermus|1.000
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UID1085|c Clostridia
2541626730 Thermacetogenium phaeum
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UID1111
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UID1110
UID1109
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2510065016 Dehalobacter restrictus
Dehalobacter unclassified
649633098 Syntrophobotulus glycolicus
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Moorella thermoacetica
UID1105|o Thermoanaerobacterales;f Thermoanaerobacteraceae|0.990
2503538017 Thermanaeromonas toyohensis
UID1103||0.990
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637000316 Syntrophomonas wolfei
UID1104|o Clostridiales 4;f Syntrophomonadaceae|1.000
646564577 Syntrophothermus lipocalidus
2524614695 Butyrivibrio unclassified
Butyrivibrio unclassified
Butyrivibrio unclassified
2524614690 Butyrivibrio unclassified
Butyrivibrio unclassified
Butyrivibrio unclassified
Butyrivibrio unclassified
2562617011 Butyrivibrio unclassified
2561511226 Butyrivibrio unclassified
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Butyrivibrio unclassified
Butyrivibrio unclassified
2558860139 Butyrivibrio proteoclasticus
Butyrivibrio proteoclasticus
Butyrivibrio proteoclasticus|0.917
Butyrivibrio unclassified
UID1295
UID1293
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UID1287||1.000
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Butyrivibrio fibrisolvens
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2524614685 Pseudobutyrivibrio ruminis
Pseudobutyrivibrio unclassified
Pseudobutyrivibrio ruminis|1.000
UID1255|f Lachnospiraceae
Pseudobutyrivibrio ruminis
Pseudobutyrivibrio|1.000
Pseudobutyrivibrio unclassified
2558860988 unclassified unclassified
unclassified unclassified
UID1328
2561511219 unclassified unclassified
UID1327||0.995
643886070 Shuttleworthia satelles
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Lachnobacterium bovis|1.000
UID1339|g Lachnobacterium
Lachnobacterium bovis
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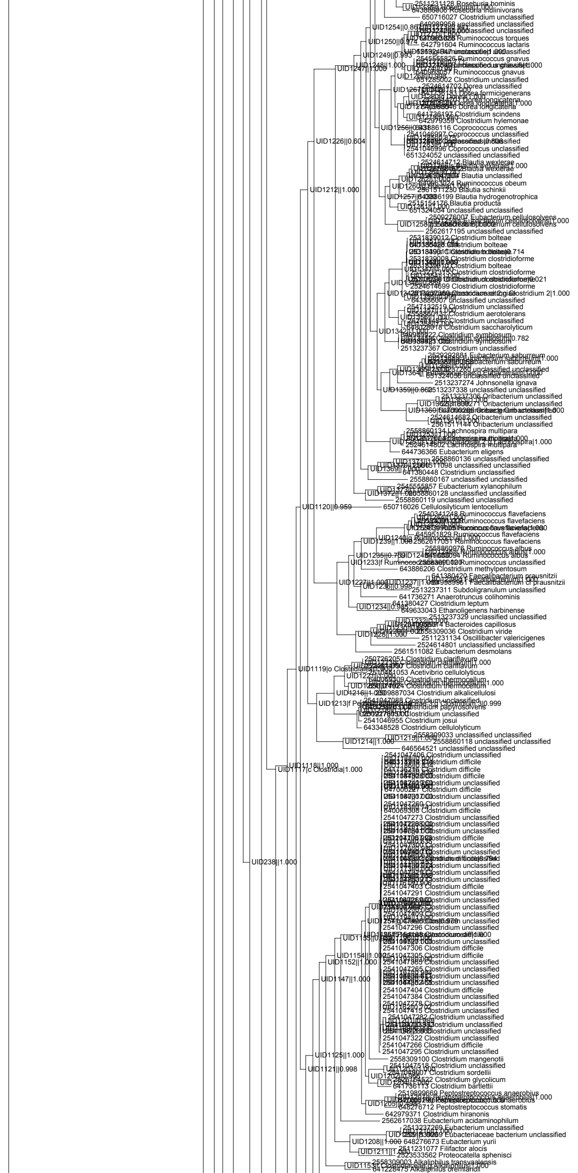
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642791625 Ruminococcus torques
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UID1249||0.993
UID1248||1.000
2545555826 Ruminococcus gnavus
UID1247||1.000
649990047 Ruminococcus gnavus
651285002 Clostridium unclassified
2524614702 Dorea unclassified
643886131 Dorea formicigenerans
Dorea longicatena
642979359 Clostridium hylemonae
641736197 Clostridium scindens
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651324052 unclassified unclassified
UID1226||0.604
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Blautia wexlerae
Blautia unclassified
670953024 Ruminococcus obeum
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643886199 Blautia hydrogenotrophica
2515154176 Blautia producta
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UID1212||1.000
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UID1258
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Clostridium bolteae
2531839008 Clostridium clostridioforme
Clostridium bolteae
Clostridium clostridioforme
2524614699 Clostridium clostridioforme
Clostridium 2|1.000
643886007 unclassified unclassified
2547132519 Clostridium unclassified
Clostridium aerotolerans
Clostridium unclassified
640028018 Clostridium saccharolyticum
UID1342||1.000
649989922 Clostridium symbiosum
Clostridium symbiosum
Clostridium symbiosum|0.782
2513237367 Clostridium unclassified
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Eubacterium saburreum
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Lachnospira|1.000
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UID1369||1.000
unclassified unclassified
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2558860167 unclassified unclassified
2545555857 Eubacterium xylanophilum
UID1372||1.000
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2558860119 unclassified unclassified
UID1120||0.959
650716026 Cellulosilyticum lentocellum
2540341248 Ruminococcus flavefaciens
Ruminococcus flavefaciens
Ruminococcus flavefaciens|1.000
645951829 Ruminococcus flavefaciens
UID1240
UID1239||1.000
2562617051 Ruminococcus flavefaciens
2558860976 Ruminococcus albus
Ruminococcus albus
UID1235||0.759
UID1233|f Ruminococcaceae|1.000
Ruminococcus unclassified
643886206 Clostridium methylpentosum
641380420 Faecalibacterium prausnitzii
UID1227||1.000
UID1237||1.000
Faecalibacterium cf prausnitzii
UID1236||0.998
2513237311 Subdoligranulum unclassified
641736271 Anaerotruncus colihominis
641380427 Clostridium leptum
UID1234||0.985
649633043 Ethanoligenens harbinense
2513237329 unclassified unclassified
UID1232||1.000
Bacteroides capillosus
2558309036 Clostridium viride
UID1228||1.000
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2561511082 Eubacterium desmolans
2507262051 Clostridium clariflavum
Clostridium clariflavum
UID1119|o Clostridiales
2510461053 Acetivibrio cellulolyticus
UID1221||1.000
640069309 Clostridium thermocellum
Clostridium thermocellum
UID1216||1.000
2509887034 Clostridium alkalicellulosi
UID1213|f
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Clostridium 3|0.999
Clostridium papyrosolvens
Clostridium unclassified
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643348528 Clostridium cellulolyticum
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UID1215||1.000
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646564521 unclassified unclassified
UID1118||1.000
UID1117|c Clostridia|1.000
2541047406 Clostridium unclassified
Clostridium difficile
Clostridium difficile
Clostridium difficile
Clostridium unclassified
647000227 Clostridium difficile
Clostridium unclassified
Clostridium unclassified
640069308 Clostridium difficile
2541047273 Clostridium unclassified
Clostridium unclassified
Clostridium unclassified
Clostridium difficile
Clostridium unclassified
Clostridium unclassified
Clostridium unclassified
Clostridium unclassified
Clostridium unclassified
UID238||1.000
Clostridium unclassified
Clostridium unclassified
2541047403 Clostridium difficile
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Clostridium unclassified
Clostridium unclassified
2541047409 Clostridium unclassified
Clostridium unclassified
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Clostridium unclassified
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UID1147||1.000
Clostridium unclassified
Clostridium unclassified
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Clostridium unclassified
Clostridium unclassified
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UID1125||1.000
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UID1121||0.998
Clostridium sordellii
UID1202
2562617122 Clostridium glycolicum
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2519899669 Peptostreptococcus anaerobius
UID1205
Peptostreptococcus anaerobius|1.000
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2562617038 Eubacterium acidaminophilum
2513237269 Eubacterium unclassified
Eubacteriaceae bacterium unclassified
UID1208||1.000
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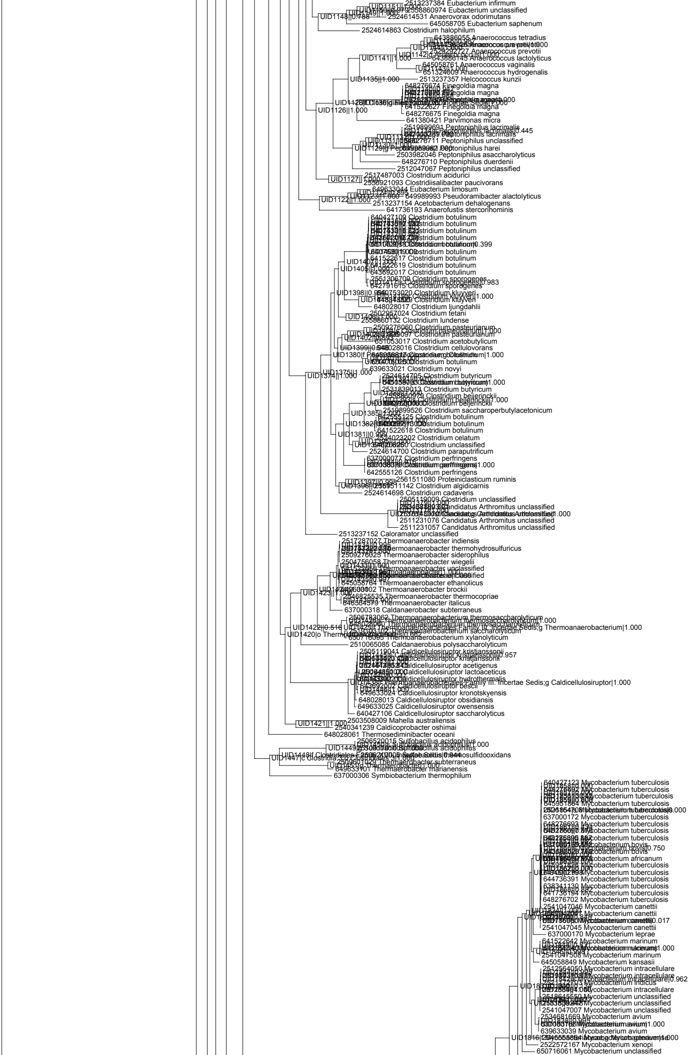
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641736193 Anaerofustis stercorihominis
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2504756058 Thermoanaerobacter wiegelii
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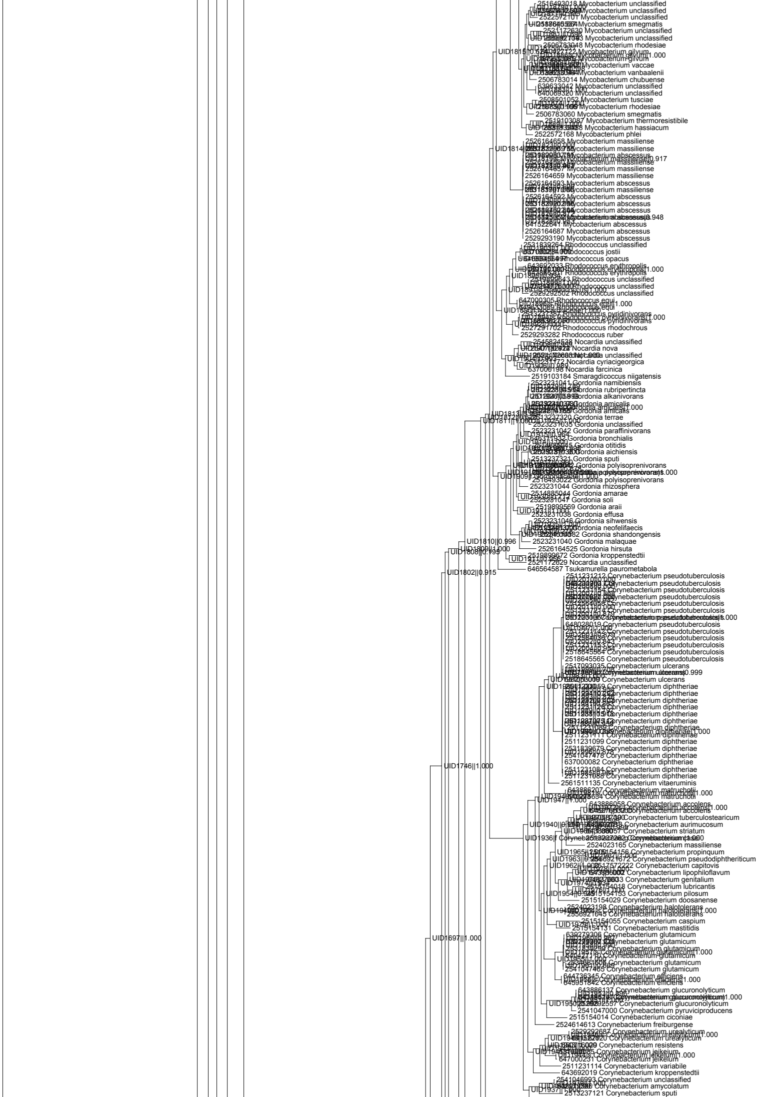
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Mycobacterium gilvum
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Mycobacterium rhodesiae
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Mycobacterium hassiacum
2522572168 Mycobacterium phlei
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UID1814
Mycobacterium massiliense
Mycobacterium abscessus
Mycobacterium massiliense
Mycobacterium massiliense
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Mycobacterium massiliense
2526164592 Mycobacterium abscessus
Mycobacterium abscessus
Mycobacterium abscessus
Mycobacterium abscessus
641522641 Mycobacterium abscessus
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2531839264 Rhodococcus unclassified
Rhodococcus jostii
Rhodococcus opacus
643692033 Rhodococcus erythropolis
Rhodococcus erythropolis
Rhodococcus unclassified
Rhodococcus unclassified
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Rhodococcus equi
Rhodococcus pyridinivorans
Rhodococcus pyridinivorans
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UID1812
UID1811
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Gordonia otitidis
Gordonia aichiensis
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Gordonia polyisoprenivorans
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2514885044 Gordonia amarae
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Gordonia shandongensis
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Corynebacterium urealyticum
Corynebacterium resistens
Corynebacterium jeikeium
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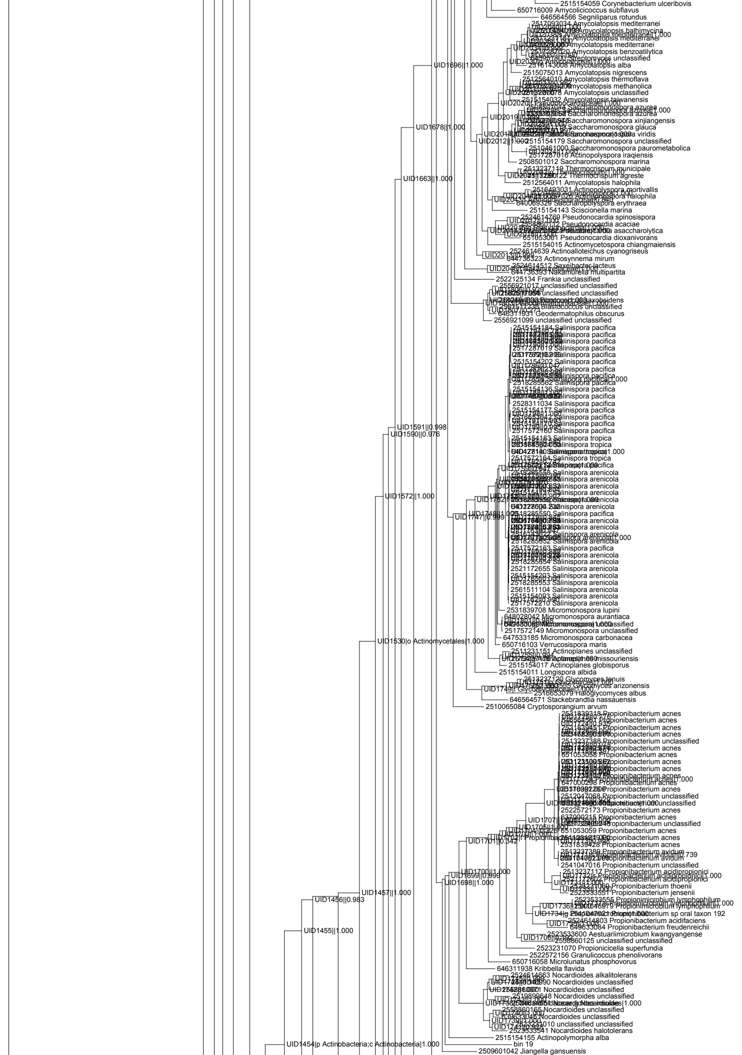
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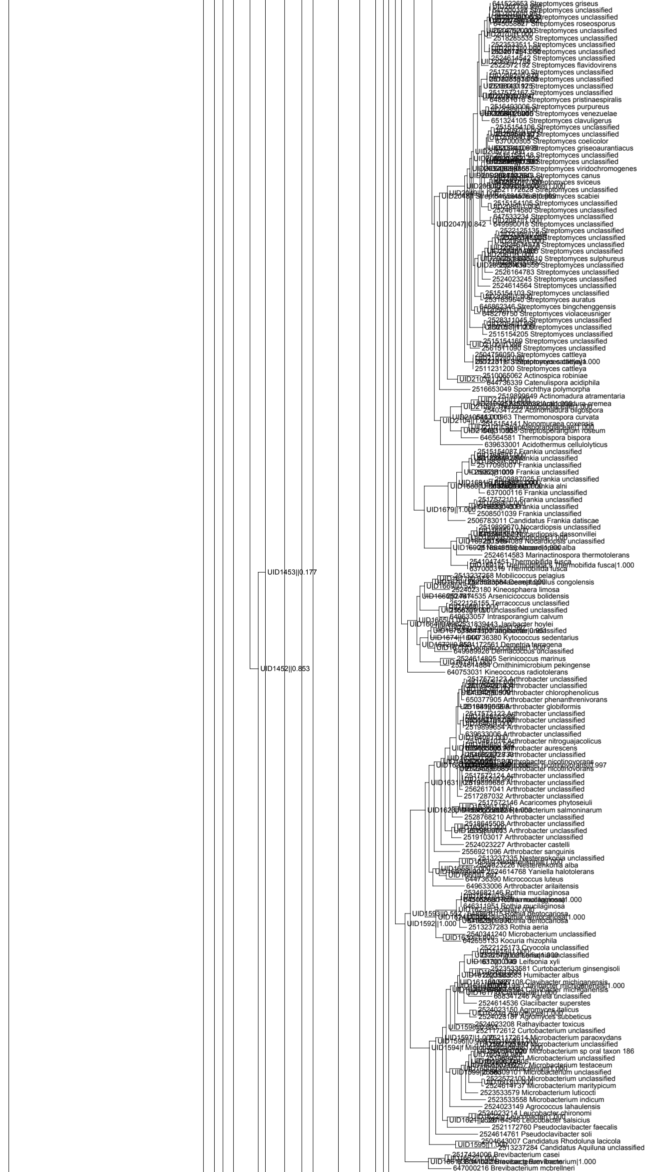
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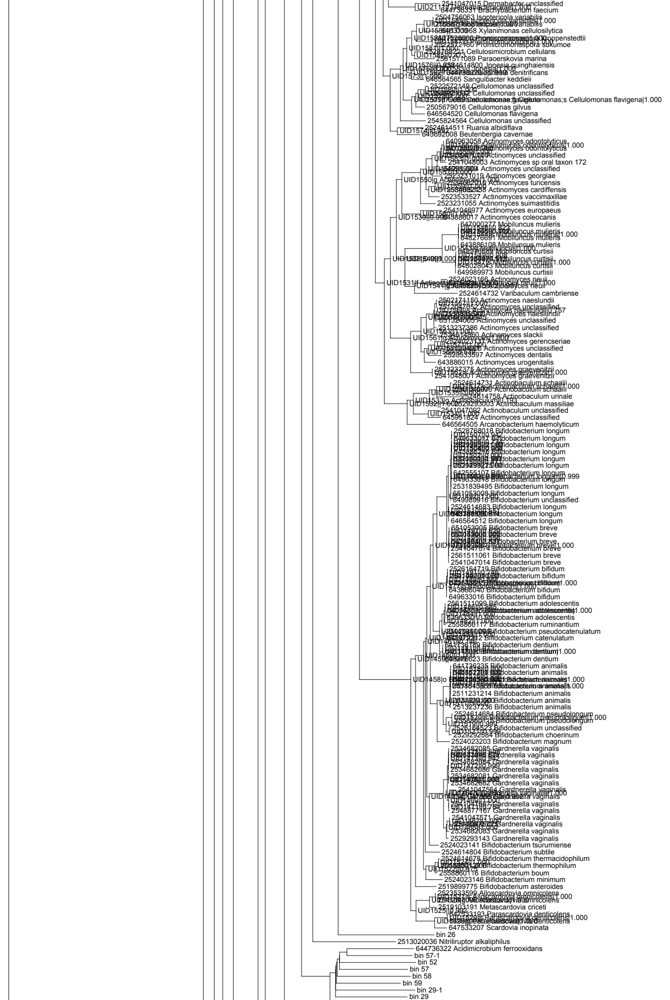
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Cellulomonas unclassified
Cellulomonas flavigena|1.000
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Actinomyces odontolyticus
Actinomyces unclassified
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Actinomyces cardiffensis
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Mobiluncus mulieris
Mobiluncus mulieris|1.000
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643886108 Mobiluncus mulieris
Mobiluncus curtisii
Mobiluncus curtisii|1.000
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Actinomyces unclassified
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Actinomyces naeslundii
651324005 Actinomyces unclassified
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Actinomyces gerencseriae
Actinomyces unclassified
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Actinobaculum schaalii|1.000
Actinobaculum schaalii
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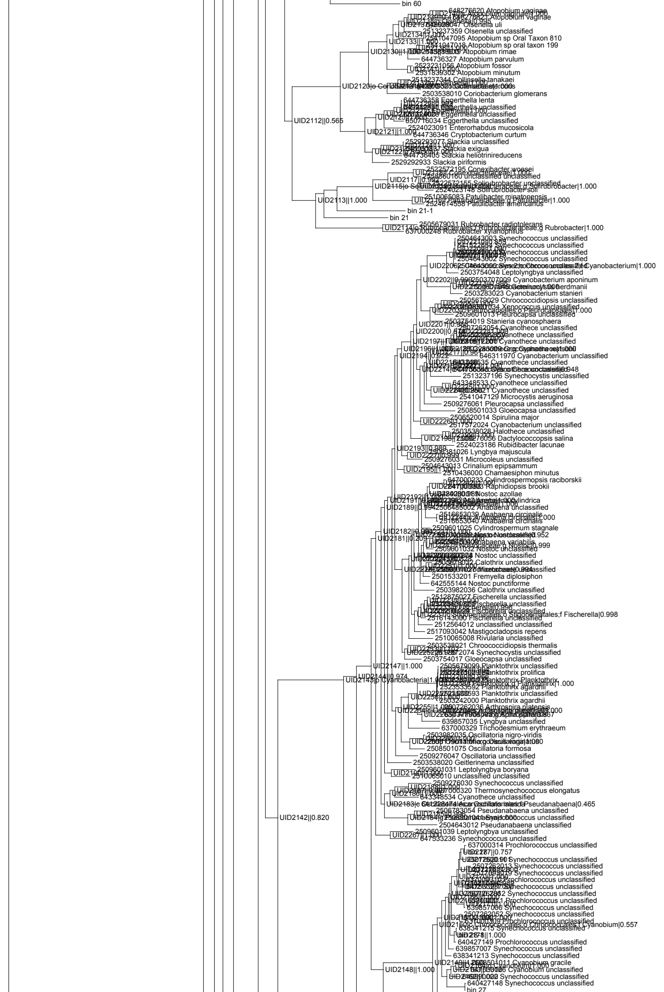
2528768018 Bifidobacterium longum
Bifidobacterium longum
Bifidobacterium longum
Bifidobacterium longum
Bifidobacterium longum
Bifidobacterium longum
642555107 Bifidobacterium longum
Bifidobacterium longum|0.999
Bifidobacterium longum
2531839495 Bifidobacterium longum
651053008 Bifidobacterium longum
649989916 Bifidobacterium unclassified
2524614683 Bifidobacterium longum
Bifidobacterium longum
646564512 Bifidobacterium longum
651053005 Bifidobacterium breve
Bifidobacterium breve
Bifidobacterium breve
Bifidobacterium breve|1.000
2541047074 Bifidobacterium breve
2561511061 Bifidobacterium breve
2541047014 Bifidobacterium breve
2526164719 Bifidobacterium bifidum
Bifidobacterium bifidum
Bifidobacterium bifidum|1.000
643886040 Bifidobacterium bifidum
649633016 Bifidobacterium bifidum
2561511099 Bifidobacterium adolescentis
Bifidobacterium adolescentis|1.000
Bifidobacterium adolescentis
2558860117 Bifidobacterium ruminantium
Bifidobacterium pseudocatenulatum
Bifidobacterium catenulatum
Bifidobacterium dentium
Bifidobacterium dentium|1.000
Bifidobacterium dentium
641736235 Bifidobacterium animalis
Bifidobacterium animalis
Bifidobacteriaceae|1.000
Bifidobacterium animalis|1.000
UID1458|o Bifidobacteriales
2511231214 Bifidobacterium animalis
Bifidobacterium animalis
2513237236 Bifidobacterium animalis
2524614684 Bifidobacterium pseudolongum
Bifidobacterium pseudolongum|1.000
Bifidobacterium pseudolongum
Bifidobacterium unclassified
Bifidobacterium choerinum
2524023203 Bifidobacterium magnum
2534682085 Gardnerella vaginalis
Gardnerella vaginalis
2534682084 Gardnerella vaginalis
2534682086 Gardnerella vaginalis
2534682081 Gardnerella vaginalis
2534682082 Gardnerella vaginalis
2541047564 Gardnerella vaginalis
Gardnerella vaginalis|1.000
Gardnerella vaginalis
Gardnerella vaginalis
2548877167 Gardnerella vaginalis
2541047571 Gardnerella vaginalis
Gardnerella vaginalis
2534682083 Gardnerella vaginalis
2529293143 Gardnerella vaginalis
2524023141 Bifidobacterium tsurumiense
2524614804 Bifidobacterium subtile
2524614678 Bifidobacterium thermacidophilum
Bifidobacterium thermophilum
2558860116 Bifidobacterium boum
2524023146 Bifidobacterium minimum
2519899775 Bifidobacterium asteroides
2523533599 Alloscardovia omnicolens
Alloscardovia omnicolens|1.000
Alloscardovia omnicolens
2519103191 Metascardovia criceti
2523533193 Parascardovia denticolens
Parascardovia denticolens|1.000
647533207 Scardovia inopinata
bin 26
2513020036 Nitriliruptor alkaliphilus
644736322 Acidimicrobium ferrooxidans
bin 57-1
bin 52
bin 57
bin 58
bin 59
bin 29-1
bin 29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648276620 Atopobium vaginae
Atopobium vaginae
Olsenella uli
2513237359 Olsenella unclassified
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UID2133||1.000
2541047018 Atopobium sp oral taxon 199
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Atopobium rimae
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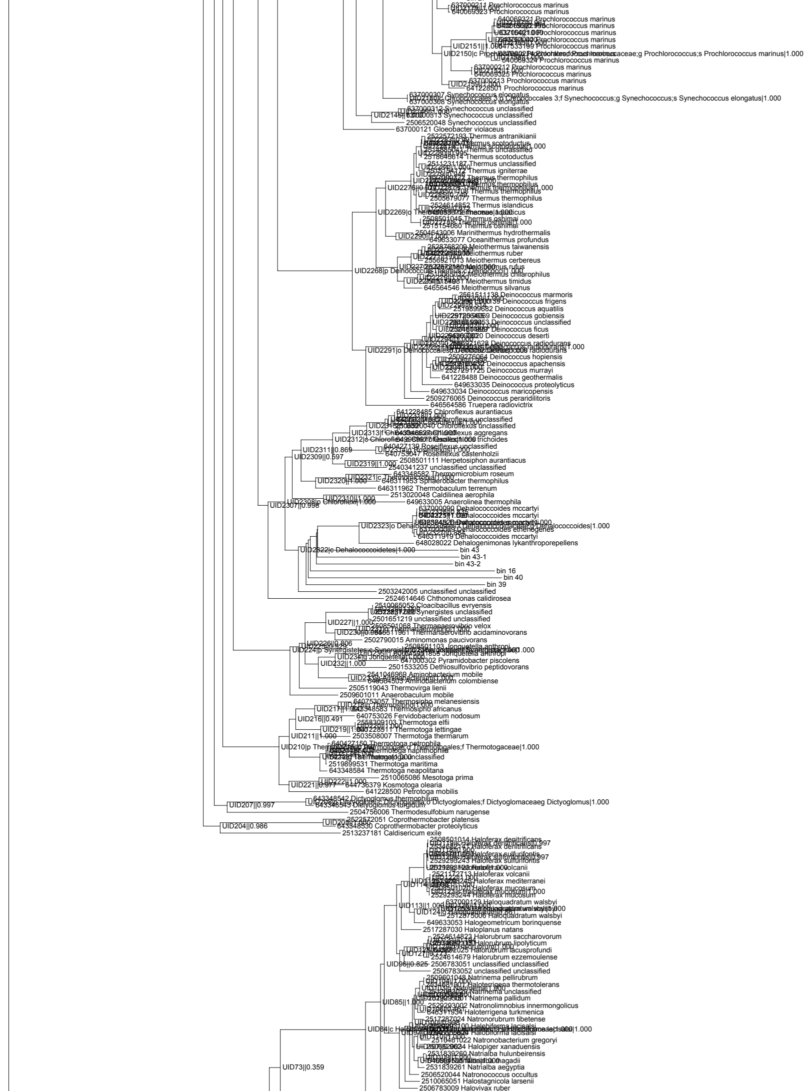
2503538010 Coriobacterium glomerans
644736358 Eggerthella lenta
Eggerthella unclassified
Eggerthella unclassified
650716034 Eggerthella unclassified
UID2112||0.565
2524023091 Enterorhabdus mucosicola
UID2121||1.000
644736346 Cryptobacterium curtum
2529293077 Slackia unclassified
Slackia exigua
644736405 Slackia heliotrinireducens
2529292933 Slackia piriformis
2522572195 Conexibacter woesei
unclassified unclassified
UID2117||0.992
UID2115|o Solirubrobacterales
Solirubrobacter unclassified
Solirubrobacter|1.000
2524023148 Solirubrobacter soli
2510065083 Patulibacter minatonensis
UID2113||1.000
Patulibacter|1.000
2524614558 Patulibacter americanus
bin 21-1
bin 21
2505679031 Rubrobacter radiotolerans
UID2114|o Rubrobacterales
Rubrobacter|1.000
637000248 Rubrobacter xylanophilus
2504643003 Synechococcus unclassified
Synechococcus unclassified
Synechococcus unclassified
2504643002 Synechococcus unclassified
UID2206
Cyanobacterium|1.000
2503754048 Leptolyngbya unclassified
UID2202||0.999
2503707009 Cyanobacterium aponinum
2503283023 Cyanobacterium stanieri
2505679029 Chroococcidiopsis unclassified
Xenococcus unclassified
UID2203|o Pleurocapsales
Pleurocapsales|1.000
2509601013 Pleurocapsa unclassified
2503754019 Stanieria cyanosphaera
UID2201||0.986
2507262054 Cyanothece unclassified
UID2200||0.874
Cyanothece unclassified
UID2197||1.000
Cyanothece unclassified
UID2196||1.000
UID2194||0.922
646311970 Cyanobacterium unclassified
Cyanothece unclassified
UID2214
0.948
2513237196 Synechocystis unclassified
643348533 Cyanothece unclassified
Cyanothece unclassified
2541047129 Microcystis aeruginosa
2509276061 Pleurocapsa unclassified
2508501033 Gloeocapsa unclassified
2506520014 Spirulina major
UID2226||1.000
2517572024 Cyanobacterium unclassified
2503538028 Halothece unclassified
Dactylococcopsis salina
2524023186 Rubidibacter lacunae
UID2193||0.989
2506381026 Lyngbya majuscula
UID2227||0.999
2509276031 Microcoleus unclassified
2504643013 Crinalium epipsammum
UID2195||1.000
2510436000 Chamaesiphon minutus
647000233 Cylindrospermopsis raciborskii
Raphidiopsis brookii
Nostoc azollae
UID2192
UID2191
cylindrica
UID2189||0.994
2506485002 Anabaena unclassified
2516653039 Anabaena circinalis
Anabaena circinalis|1.000
2516653040 Anabaena circinalis
2509601025 Cylindrospermum stagnale
UID2182||0.999
0.952
UID2181||0.209
Anabaena variabilis
Nostoc|0.999
2509601032 Nostoc unclassified
Nostoc unclassified
2505679032 Calothrix unclassified
UID2228
Nostocaceae|0.994
unclassified
2501533201 Fremyella diplosiphon
642555144 Nostoc punctiforme
2503982036 Calothrix unclassified
2512875027 Fischerella unclassified
Fischerella unclassified
Fischerella unclassified
Stigonematales;f Fischerella|0.998
2516143000 Fischerella unclassified
2512564012 unclassified unclassified
2517093042 Mastigocladopsis repens
2510065008 Rivularia unclassified
2503538021 Chroococcidiopsis thermalis
UID2252
2517572074 Synechocystis unclassified
2503754017 Gloeocapsa unclassified
UID2147||1.000
2505679099 Planktothrix unclassified
Planktothrix prolifica
UID2144||0.974
UID2143|p Cyanobacteria|1.000
Planktothrix
Planktothrix|1.000
2523533592 Planktothrix agardhii
2523533593 Planktothrix unclassified
UID2256||1.000
2503242000 Planktothrix agardhii
UID2255||1.000
2507262036 Arthrospira platensis
UID2254
Arthrospira
1.000
0.867
639857035 Lyngbya unclassified
637000329 Trichodesmium erythraeum
2503982035 Oscillatoria nigro-viridis
Oscillatoria|1.000
2508501075 Oscillatoria formosa
2509276047 Oscillatoria unclassified
2503538020 Geitlerinema unclassified
2509601031 Leptolyngbya boryana
UID2190||1.000
2510065010 unclassified unclassified
2509276030 Synechococcus unclassified
637000320 Thermosynechococcus elongatus
UID2186||1.000
643348534 Cyanothece unclassified
UID2183|o
Pseudanabaena|0.465
2506783054 Pseudanabaena unclassified
UID2184
Synechococcus
2504643012 Pseudanabaena unclassified
UID2142||0.820
2509601039 Leptolyngbya unclassified
UID2267||1.000
647533236 Synechococcus unclassified
637000314 Prochlorococcus unclassified
UID2287||0.757
Synechococcus unclassified
2507262013 Synechococcus unclassified
Synechococcus unclassified
Prochlorococcus unclassified
Synechococcus unclassified
Synechococcus unclassified
Prochlorococcus unclassified
639857006 Synechococcus unclassified
2507262052 Synechococcus unclassified
Prochlorococcus unclassified
UID2160
Chroococcales;f Cyanobium|0.557
638341215 Synechococcus unclassified
||1.000
640427149 Prochlorococcus unclassified
639857007 Synechococcus unclassified
638341213 Synechococcus unclassified
UID2148||1.000
UID2149||1.000
2508501011 Cyanobium gracile
Cyanobium unclassified
Synechococcus unclassified
640427148 Synechococcus unclassified
bin 27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Prochlorococcus marinus
Prochlorococcus marinus
Prochlorococcus marinus
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UID2151||1.000
UID2150|c Prochlorococcus marinus|1.000
640069324 Prochlorococcus marinus
637000212 Prochlorococcus marinus
640069325 Prochlorococcus marinus
637000213 Prochlorococcus marinus
UID2159||1.000
641228501 Prochlorococcus marinus
637000307 Synechococcus elongatus
Synechococcales 3;f Synechococcus;g Synechococcus;s Synechococcus elongatus|1.000
637000308 Synechococcus elongatus
637000312 Synechococcus unclassified
UID2146||1.000
637000313 Synechococcus unclassified
2506520048 Synechococcus unclassified
637000121 Gloeobacter violaceus
2522572193 Thermus antranikianii
Thermus scotoductus
2514885041 Thermus unclassified
2518645614 Thermus scotoductus
2511231187 Thermus unclassified
UID2284||1.000
Thermus igniterrae
UID2279||0.946
637000322 Thermus thermophilus
Thermus thermophilus
Thermus thermophilus|1.000
2505001108 Thermus thermophilus
2505679077 Thermus thermophilus
UID2276||0.
2524614852 Thermus islandicus
UID2269|o Thermales;f Thermaceae|1.000
2508501045 Thermus oshimai
Thermus oshimai|1.000
2515154080 Thermus oshimai
2504643006 Marinithermus hydrothermalis
UID2290||1.000
649633077 Oceanithermus profundus
2528768209 Meiothermus taiwanensis
Meiothermus ruber
2556921013 Meiothermus cerbereus
UID2270
Meiothermus rufus
UID2268|p Deinococcus-Thermus;c Deinococci|1.000
Meiothermus chliarophilus
Meiothermus timidus
646564546 Meiothermus silvanus
2561511138 Deinococcus marmoris
Deinococcus frigens
2519899682 Deinococcus aquatilis
Deinococcus gobiensis
Deinococcus unclassified
Deinococcus ficus
Deinococcus deserti
Deinococcus radiodurans
UID2291|o Deinococcales
Deinococcus radiodurans|1.000
2509276064 Deinococcus hopiensis
Deinococcus apachensis
2527291725 Deinococcus murrayi
641228488 Deinococcus geothermalis
649633035 Deinococcus proteolyticus
649633034 Deinococcus maricopensis
2509276065 Deinococcus peraridilitoris
646564586 Truepera radiovictrix
641228485 Chloroflexus aurantiacus
Chloroflexus unclassified
Chloroflexus unclassified
UID2313|f Chloroflexaceae|1.000
Chloroflexus aggregans
UID2312|c Chloroflexi
Oscillochloris trichoides
UID2311||0.869
640427139 Roseiflexus unclassified
Roseiflexus|1.000
640753047 Roseiflexus castenholzii
UID2309||0.597
UID2319||1.000
2508501111 Herpetosiphon aurantiacus
2540341237 unclassified unclassified
UID2321|c Thermomicrobia|1.000
643348582 Thermomicrobium roseum
UID2320||1.000
646311953 Sphaerobacter thermophilus
646311962 Thermobaculum terrenum
2513020048 Caldilinea aerophila
UID2310||1.000
UID2308|p Chloroflexi|1.000
649633005 Anaerolinea thermophila
UID2307||0.998
637000090 Dehalococcoides mccartyi
Dehalococcoides mccartyi
UID2323|o Dehalococcoidales
Dehalococcoidaceae;g Dehalococcoides|1.000
Dehalococcoides ethenogenes
646311919 Dehalococcoides mccartyi
648028022 Dehalogenimonas lykanthroporepellens
UID2322|c Dehalococcoidetes|1.000
bin 43
bin 43-1
bin 43-2
bin 16
bin 40
bin 39
2503242005 unclassified unclassified
2524614646 Chthonomonas calidirosea
2510065052 Cloacibacillus evryensis
Synergistes unclassified
UID227||1.000
2501651219 unclassified unclassified
2508501068 Thermanaerovibrio velox
UID230||0.966
646311961 Thermanaerovibrio acidaminovorans
2502790015 Aminomonas paucivorans
UID226||0.806
2508501103 Jonquetella anthropi
UID224|p Synergistetes
Jonquetella anthropi
UID234|g Jonquetella|1.000
647000302 Pyramidobacter piscolens
UID232||1.000
2501533205 Dethiosulfovibrio peptidovorans
2541046968 Aminobacterium mobile
Aminobacterium|1.000
646564503 Aminobacterium colombiense
2505119043 Thermovirga lienii
2509601011 Anaerobaculum mobile
640753057 Thermosipho melanesiensis
Thermosipho|1.000
UID217||1.000
643348583 Thermosipho africanus
UID216||0.491
640753026 Fervidobacterium nodosum
2558309103 Thermotoga elfii
UID219||1.000
640228511 Thermotoga lettingae
UID211||1.000
2503508007 Thermotoga thermarum
640427150 Thermotoga petrophila
UID210|p Thermotogae
Thermotogales;f Thermotogaceae|1.000
Thermotoga naphthophila
Thermotoga unclassified
2519899531 Thermotoga maritima
643348584 Thermotoga neapolitana
UID222||1.000
2510065086 Mesotoga prima
UID221||0.977
644736379 Kosmotoga olearia
641228500 Petrotoga mobilis
643348542 Dictyoglomus thermophilum
Dictyoglomales;f Dictyoglomaceaeg Dictyoglomus|1.000
UID207||0.997
643348543 Dictyoglomus turgidum
2504756006 Thermodesulfobium narugense
2522572051 Coprothermobacter platensis
UID204||0.986
643348530 Coprothermobacter proteolyticus
2513237181 Caldisericum exile
2508501014 Haloferax denitrificans
Haloferax denitrificans|0.997
Haloferax denitrificans
Haloferax sulfurifontis
Haloferax sulfurifontis|0.997
2523295243 Haloferax sulfurifontis
Haloferax volcanii
2521172713 Haloferax volcanii
Haloferax mediterranei
UID114
2508501020 Haloferax mucosum
Haloferax mucosum|1.000
2529293244 Haloferax mucosum
637000129 Haloquadratum walsbyi
UID113||1.000
Haloquadratum walsbyi|1.000
UID124
2512875006 Haloquadratum walsbyi
649633053 Halogeometricum borinquense
2517287030 Haloplanus natans
2524614823 Halorubrum saccharovorum
Halorubrum lipolyticum
Halorubrum lacusprofundi
UID121
2524614679 Halorubrum ezzemoulense
UID96||0.825
2506783051 unclassified unclassified
2506783052 unclassified unclassified
2509601048 Natrinema pellirubrum
Haloterrigena thermotolerans
Natrinema unclassified
Natrinema pallidum
UID85||1.000
2529293002 Natronolimnobius innermongolicus
646311934 Haloterrigena turkmenica
2517287024 Natronorubrum tibetense
Halobiforma lacisalsi
UID84|c Halo
|1.000
Halobiforma lacisalsi
2510461022 Natronobacterium gregoryi
Halopiger xanaduensis
2531839260 Natrialba hulunbeirensis
Natrialba magadii
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2506520044 Natronococcus occultus
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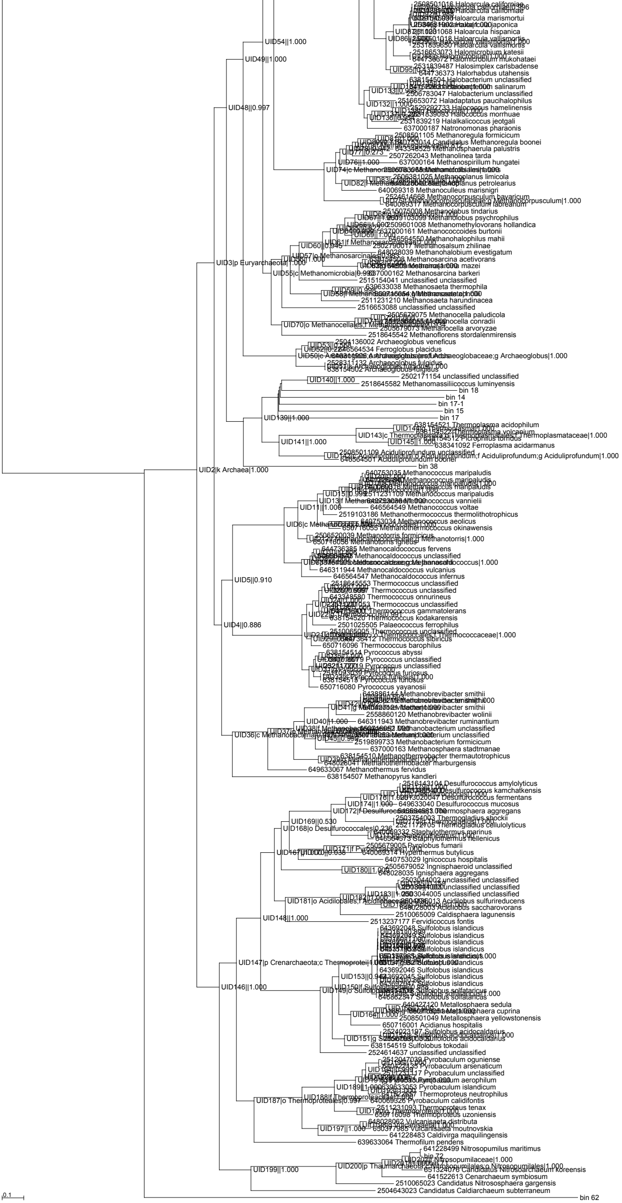
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Haloarcula californiae
Haloarcula marismortui
Haloarcula japonica
UID87
2510201068 Haloarcula hispanica
UID86
Haloarcula vallismortis
2531839650 Haloarcula vallismortis
2516653073 Halomicrobium katesii
644736372 Halomicrobium mukohataei
UID54||1.000
UID49||1.000
2531839487 Halosimplex carlsbadense
UID95
644736373 Halorhabdus utahensis
638154504 Halobacterium unclassified
salinarum
UID133||0.998
2506783047 Halobacterium unclassified
UID132||1.000
2516653072 Haladaptatus paucihalophilus
Halococcus hamelinensis
Halococcus morrhuae
UID136
2531839219 Halalkalicoccus jeotgali
UID48||0.997
637000187 Natronomonas pharaonis
2508501105 Methanoregula formicicum
Candidatus Methanoregula boonei
643348525 Methanosphaerula palustris
UID77||0.273
2507262043 Methanolinea tarda
UID76||1.000
637000164 Methanospirillum hungatei
UID74|c Methanomicrobia;o Methanomicrobiales|1.000
2506381025 Methanoplanus limicola
UID83
UID82
Methanoplanus petrolearius
640069318 Methanoculleus marisnigri
2524614668 Methanocorpusculum bavaricum
UID75|f Methanocorpusculaceae;g Methanocorpusculum|1.000
640069317 Methanocorpusculum labreanum
2515075008 Methanolobus tindarius
UID67
2509103099 Methanolobus psychrophilus
UID66||1.000
2509601008 Methanomethylovorans hollandica
637000161 Methanococcoides burtonii
UID69||1.000
646564550 Methanohalophilus mahii
UID61|f Methanosarcinaceae|1.000
UID60||0.945
2502790017 Methanosalsum zhilinae
648028039 Methanohalobium evestigatum
UID57|o Methanosarcinales|0.988
638154508 Methanosarcina acetivorans
UID56||1.000
Methanosarcina mazei
UID3|p Euryarchaeota|1.000
UID55|c Methanomicrobia|0.993
637000162 Methanosarcina barkeri
2515154041 unclassified unclassified
639633038 Methanosaeta thermophila
UID59||0.998
UID58|f Methanosaetaceae;g Methanosaeta|1.000
2511231210 Methanosaeta harundinacea
2516653088 unclassified unclassified
2505679075 Methanocella paludicola
Methanocella conradii
UID70|o Methanocellales;f Methanocellaceae
2505679073 Methanocella arvoryzae
2518645542 Methanoflorens stordalenmirensis
2504136002 Archaeoglobus veneficus
UID53||0.355
UID52||0.224
646564534 Ferroglobus placidus
UID50|c Archaeoglobi;o Archaeoglobales;f Archaeoglobaceae;g Archaeoglobus|1.000
2528311132 Archaeoglobus fulgidus
638154502 Archaeoglobus fulgidus
UID140||1.000
2502171154 unclassified unclassified
2518645582 Methanomassiliicoccus luminyensis
bin 18
bin 14
bin 17-1
bin 15
UID139||1.000
bin 17
638154521 Thermoplasma acidophilum
Thermoplasma volcanium
UID143|c Thermoplasmata;o Thermoplasmatales;f Thermoplasmataceae|1.000
638154512 Picrophilus torridus
UID145||1.000
UID141||1.000
638341092 Ferroplasma acidarmanus
2508501109 Aciduliprofundum unclassified
g Aciduliprofundum;f Aciduliprofundum;g Aciduliprofundum|1.000
646564501 Aciduliprofundum boonei
bin 38
UID2|k Archaea|1.000
640753035 Methanococcus maripaludis
Methanococcus maripaludis
Methanococcus maripaludis
Methanococcus maripaludis
UID15||0.999
2511231109 Methanococcus maripaludis
UID13|f Methanococcaceae
640753036 Methanococcus vannielii
UID11||1.000
646564549 Methanococcus voltae
2519103186 Methanothermococcus thermolithotrophicus
UID6|c Methanococci;o Methanococcales|1.000
640753034 Methanococcus aeolicus
650716055 Methanothermococcus okinawensis
2506520039 Methanotorris formicicus
Methanotorris|1.000
650716056 Methanotorris igneus
644736385 Methanocaldococcus fervens
Methanocaldococcus unclassified
Methanocaldococcus|1.000
646311944 Methanocaldococcus vulcanius
646564547 Methanocaldococcus infernus
UID5||0.910
2518645553 Thermococcus unclassified
Thermococcus unclassified
643348580 Thermococcus onnurineus
Thermococcus unclassified
Thermococcus gammatolerans
638154520 Thermococcus kodakarensis
2501025505 Palaeococcus ferrophilus
2510065005 Thermococcus unclassified
UID4||0.886
Thermococcaceae|1.000
Thermococcus sibiricus
650716096 Thermococcus barophilus
638154514 Pyrococcus abyssi
Pyrococcus unclassified
Pyrococcus unclassified
Pyrococcus furiosus
Pyrococcus furiosus|1.000
638154513 Pyrococcus furiosus
650716080 Pyrococcus yayanosii
643886144 Methanobrevibacter smithii
Methanobrevibacter smithii
UID41|g
Methanobrevibacter smithii
2558860120 Methanobrevibacter wolinii
UID40||1.000
646311943 Methanobrevibacter ruminantium
Methanobacterium unclassified
UID36|c Methanobacteria
Methanobacterium unclassified
UID45||0.999
2519899733 Methanobacterium formicicum
637000163 Methanosphaera stadtmanae
638154510 Methanothermobacter thermautotrophicus
648028041 Methanothermobacter marburgensis
649633067 Methanothermus fervidus
638154507 Methanopyrus kandleri
2516143104 Desulfurococcus amylolyticus
Desulfurococcus kamchatkensis
UID176||1.000
2513020047 Desulfurococcus fermentans
UID174||1.000
649633040 Desulfurococcus mucosus
UID172|f Desulfurococcaceae
Thermosphaera aggregans
UID169||0.530
2503754003 Thermogladius shockii
UID175|g Thermogladius|1.000
2521172705 Thermogladius cellulolyticus
UID168|o Desulfurococcales|0.236
640069332 Staphylothermus marinus
646564573 Staphylothermus hellenicus
2505679005 Pyrolobus fumarii
UID171|f Pyrodictiaceae
UID167
640069314 Hyperthermus butylicus
640753029 Ignicoccus hospitalis
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UID180||1.000
648028035 Ignisphaera aggregans
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unclassified unclassified
UID183||1.000
2503044005 unclassified unclassified
UID181|o Acidilobales;f Acidilobaceae
Acidilobus sulfurireducens
648028003 Acidilobus saccharovorans
2510065009 Caldisphaera lagunensis
UID148||1.000
2513237177 Fervidicoccus fontis
643692048 Sulfolobus islandicus
Sulfolobus islandicus
Sulfolobus islandicus
Sulfolobus islandicus
Sulfolobus islandicus
Sulfolobus islandicus|1.000
UID147|p Crenarchaeota;c Thermoprotei|1.000
Sulfolobus islandicus
643692046 Sulfolobus islandicus
UID153||0.962
643692045 Sulfolobus islandicus
Sulfolobus islandicus
643692047 Sulfolobus islandicus
UID146||1.000
UID150|f Sulfolobaceae
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Pyrobaculum arsenaticum
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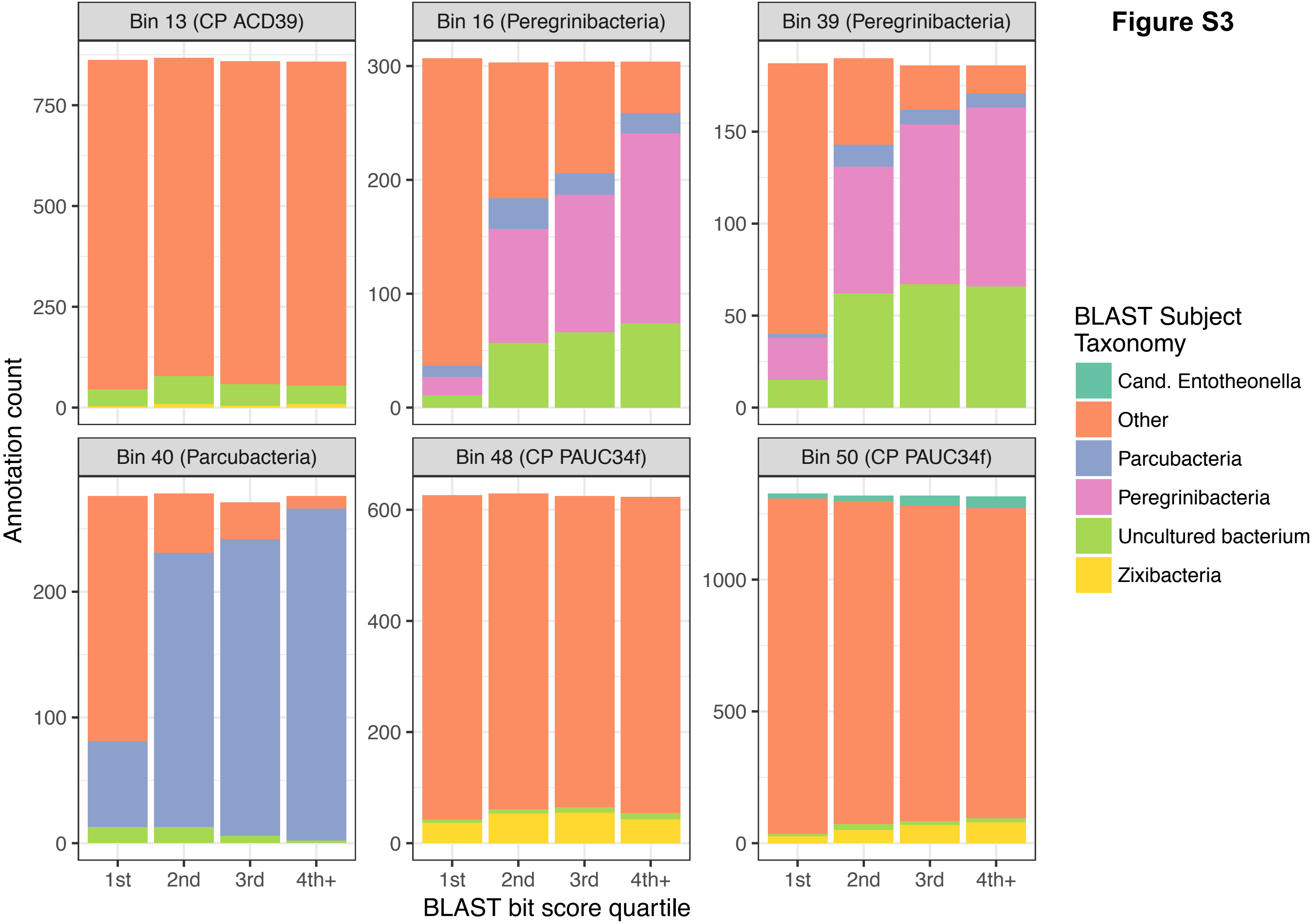
**Figure S3**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Annotation count
BLAST bit score quartile
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2nd
3rd
4th+
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750
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200
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50
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400
600
1000
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Other
Parcubacteria
Peregrinibacteria
Uncultured bacterium
Zixibacteria

Figure S4

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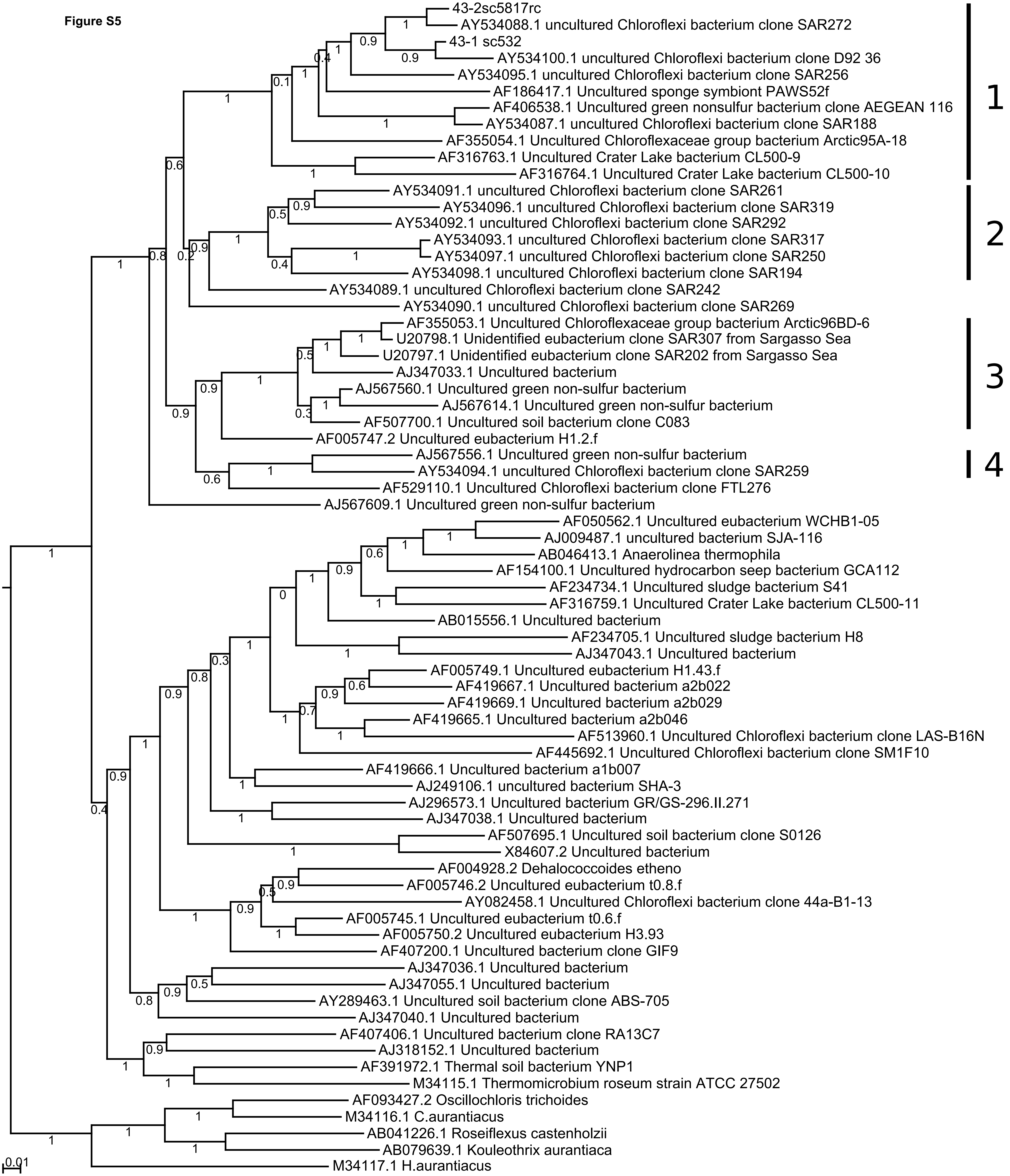
**Figure S5**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1
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AF316764.1 Uncultured Crater Lake bacterium CL500-10
1
0.6
1
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AY534092.1 uncultured Chloroflexi bacterium clone SAR292
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AY534093.1 uncultured Chloroflexi bacterium clone SAR317
AY534097.1 uncultured Chloroflexi bacterium clone SAR250
1
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AY534098.1 uncultured Chloroflexi bacterium clone SAR194
0.9
0.8
0.2
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AY534089.1 uncultured Chloroflexi bacterium clone SAR242
AY534090.1 uncultured Chloroflexi bacterium clone SAR269
2
AF355053.1 Uncultured Chloroflexaceae group bacterium Arctic96BD-6
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U20798.1 Unidentified eubacterium clone SAR307 from Sargasso Sea
1
U20797.1 Unidentified eubacterium clone SAR202 from Sargasso Sea
0.5
AJ347033.1 Uncultured bacterium
1
0.9
AJ567560.1 Uncultured green non-sulfur bacterium
1
AJ567614.1 Uncultured green non-sulfur bacterium
0.3
AF507700.1 Uncultured soil bacterium clone C083
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AF005747.2 Uncultured eubacterium H1.2.f
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AJ567556.1 Uncultured green non-sulfur bacterium
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AY534094.1 uncultured Chloroflexi bacterium clone SAR259
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AF529110.1 Uncultured Chloroflexi bacterium clone FTL276
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AJ567609.1 Uncultured green non-sulfur bacterium
AF050562.1 Uncultured eubacterium WCHB1-05
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AJ009487.1 uncultured bacterium SJA-116
1
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AB046413.1 Anaerolinea thermophila
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AF154100.1 Uncultured hydrocarbon seep bacterium GCA112
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AF234734.1 Uncultured sludge bacterium S41
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1
AF316759.1 Uncultured Crater Lake bacterium CL500-11
AB015556.1 Uncultured bacterium
AF234705.1 Uncultured sludge bacterium H8
1
1
AJ347043.1 Uncultured bacterium
0.3
AF005749.1 Uncultured eubacterium H1.43.f
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0.6
AF419667.1 Uncultured bacterium a2b022
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AF419669.1 Uncultured bacterium a2b029
0.9
0.7
AF419665.1 Uncultured bacterium a2b046
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AF445692.1 Uncultured Chloroflexi bacterium clone SM1F10
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AJ296573.1 Uncultured bacterium GR/GS-296.II.271
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AJ347038.1 Uncultured bacterium
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AF005746.2 Uncultured eubacterium t0.8.f
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AF005750.2 Uncultured eubacterium H3.93
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0.8
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AJ347040.1 Uncultured bacterium
AF407406.1 Uncultured bacterium clone RA13C7
0.9
AJ318152.1 Uncultured bacterium
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AF093427.2 Oscillochloris trichoides
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1
AB041226.1 Roseiflexus castenholzii
1
1
AB079639.1 Kouleothrix aurantiaca
0.01
M34117.1 H.aurantiacus

**Figure S6**

PRR10 4 11429
PRR10 5 11429
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PRR10 11 11429
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PRR12 1 6 1945
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SAW1 B6 6 11395
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PBSIII9 23 11259
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PBSIII9 5 1988
PBSIII9 4 1874
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Planococcus citreus 15025 11429
Lactobacillus acidophilus 108734 11429
Clostridium acetobutylicum 129255 11429
Desulfitobacter alkalitolerans 98963 11387
M62693 1 Fibrobacter succinogenes strain MC1
M62696 2 Fibrobacter succinogenes subsp succinogenes S85
M62691 1 Fibrobacter intestinalis strain LH1
Edaphobacter modestum 160117 11420
Terriglobus roseus 162763 11420
Acidobacterium capsulatum 3704 11422
AJ290824 1 Chlorobium limicola strain DSM246
Y10651 2 Chlorobium phaeobacteroides strain UdG 6047
EU770420 1 Chlorobium sp sy9
NR 119242 1 Chlorobium phaeovibrioides strain DSM 269
C ferrooxidans 171289 11429
NR 119288 2 Chlorobium ferrooxidans strain KofoX
AM086645 1 Pelodictyon clathratiforme strain 4DE
DQ383316 1 Uncultured Chlorobium sp clone i9-10
C tepidum 137177 11429
GQ200196 2 Bacteroidetes bacterium DQHS-15
KP214057 1 Bacteroidetes bacterium FA423
AM179866 1 Sporocytophaga sp A61
Sulcia muelleri 257992 11429
Leptospirillum 11429
Nitro 11426
Nitrospiraes Thermodesulfovibri11429
Chroococcus minutus 570499 11429
Oscillatoria duplisecta 166338 11354
Synechococcus elongatus 110298 11429
Gloeobacter violaceus 108670 11429
Anaerolinea thermophila 44630 11429
Caldilinea aerophila 26613 11427
Dehalococcoides BAV1 76593 11420
Kosmotoga 376719 11429
Thermotoga 62474 11429
Aminobacterium 11429
Synergistes 11377
Armatimonas 11429
Chthonomonas 11404
P brasiliensis 2857 11429
P limnophilus 2845 11429
agg27 OM190 137332 11429
Methylacidiphilum 11429
Verrucomicrobium 11376
OP11 GN01 11354
OP11 WCHB107 11417
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hungatei 11429
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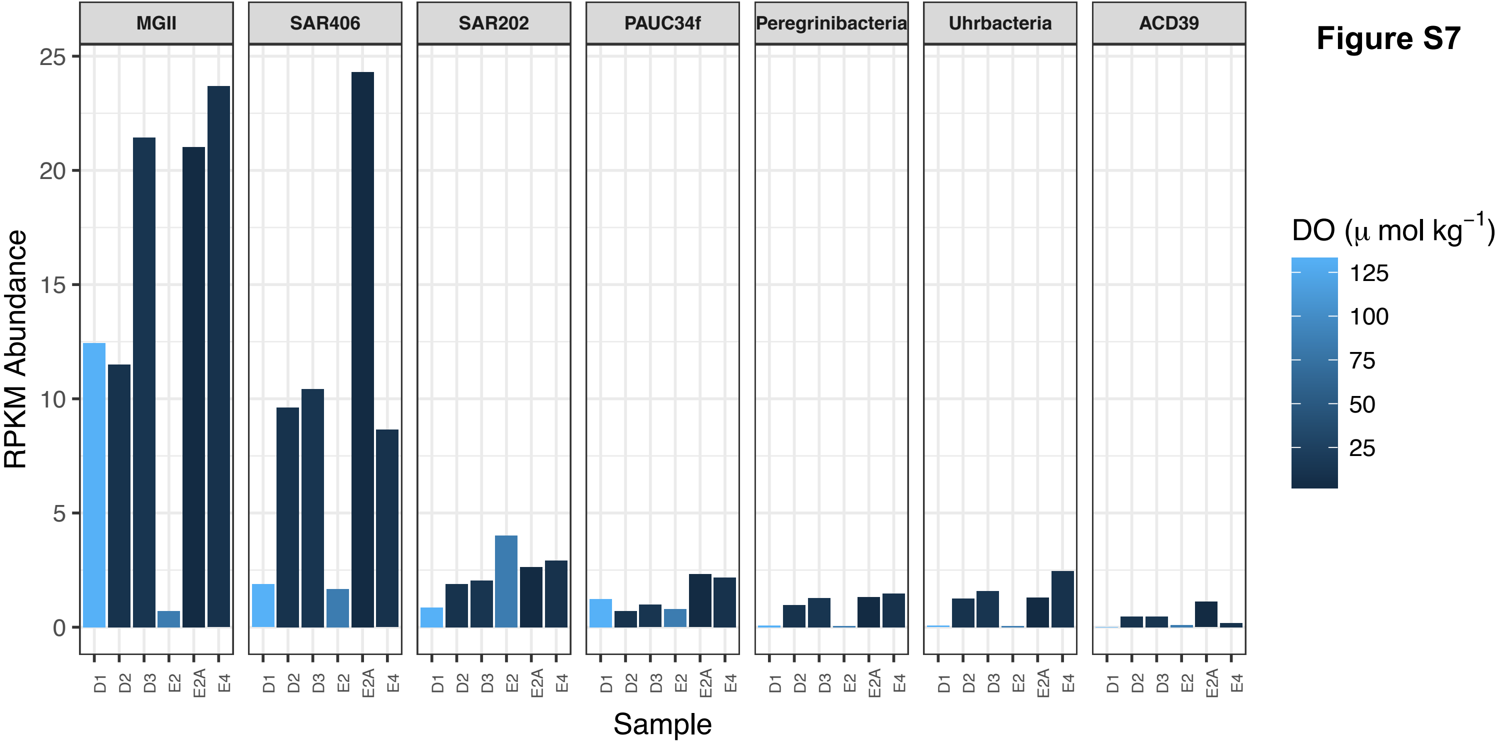
## Figure S7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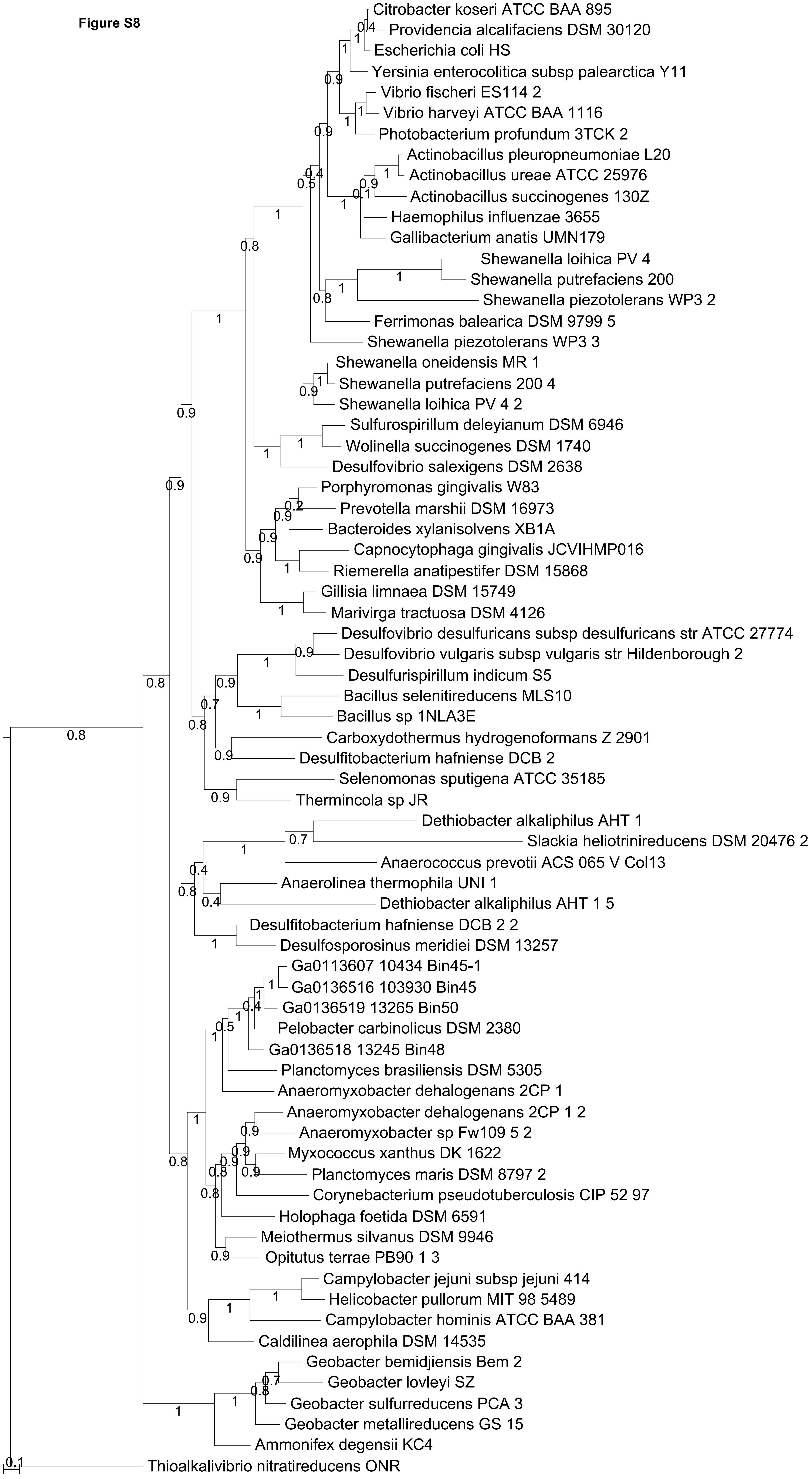
SAR406
SAR202
PAUC34f
Peregrinibacteria
Uhrbacteria
ACD39
RPKM Abundance
0
5
10
15
20
25
D1
D2
D3
E2
E2A
E4
Sample
DO (μ mol kg$^{-1}$)
125
100
75
50
25

**Figure S8**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Escherichia coli HS
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Yersinia enterocolitica subsp palearctica Y11
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Vibrio fischeri ES114 2
1
Vibrio harveyi ATCC BAA 1116
1
0.9
Photobacterium profundum 3TCK 2
Actinobacillus pleuropneumoniae L20
0.4
1
Actinobacillus ureae ATCC 25976
0.5
0.9
0.1
Actinobacillus succinogenes 130Z
1
1
Haemophilus influenzae 3655
Gallibacterium anatis UMN179
0.8
Shewanella loihica PV 4
1
Shewanella putrefaciens 200
1
0.8
Shewanella piezotolerans WP3 2
1
Ferrimonas balearica DSM 9799 5
Shewanella piezotolerans WP3 3
Shewanella oneidensis MR 1
1
Shewanella putrefaciens 200 4
0.9
Shewanella loihica PV 4 2
0.9
Sulfurospirillum deleyianum DSM 6946
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Wolinella succinogenes DSM 1740
1
Desulfovibrio salexigens DSM 2638
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Porphyromonas gingivalis W83
0.2
Prevotella marshii DSM 16973
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Bacteroides xylanisolvens XB1A
0.9
Capnocytophaga gingivalis JCVIHMP016
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Riemerella anatipestifer DSM 15868
Gillisia limnaea DSM 15749
1
Marivirga tractuosa DSM 4126
Desulfovibrio desulfuricans subsp desulfuricans str ATCC 27774
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Desulfovibrio vulgaris subsp vulgaris str Hildenborough 2
1
Desulfurispirillum indicum S5
0.8
0.9
Bacillus selenitireducens MLS10
0.7
1
Bacillus sp 1NLA3E
0.8
0.8
Carboxydothermus hydrogenoformans Z 2901
0.9
Desulfitobacterium hafniense DCB 2
Selenomonas sputigena ATCC 35185
0.9
Thermincola sp JR
Dethiobacter alkaliphilus AHT 1
0.7
Slackia heliotrinireducens DSM 20476 2
1
Anaerococcus prevotii ACS 065 V Col13
0.4
Anaerolinea thermophila UNI 1
0.8
0.4
Dethiobacter alkaliphilus AHT 1 5
Desulfitobacterium hafniense DCB 2 2
1
Desulfosporosinus meridiei DSM 13257
Ga0113607 10434 Bin45-1
1
Ga0136516 103930 Bin45
1
0.4
Ga0136519 13265 Bin50
1
0.5
Pelobacter carbinolicus DSM 2380
1
Ga0136518 13245 Bin48
Planctomyces brasiliensis DSM 5305
Anaeromyxobacter dehalogenans 2CP 1
Anaeromyxobacter dehalogenans 2CP 1 2
1
0.9
Anaeromyxobacter sp Fw109 5 2
0.9
Myxococcus xanthus DK 1622
0.8
0.9
0.8
0.9
Planctomyces maris DSM 8797 2
0.8
Corynebacterium pseudotuberculosis CIP 52 97
Holophaga foetida DSM 6591
Meiothermus silvanus DSM 9946
0.9
Opitutus terrae PB90 1 3
Campylobacter jejuni subsp jejuni 414
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Helicobacter pullorum MIT 98 5489
1
0.9
Campylobacter hominis ATCC BAA 381
Caldilinea aerophila DSM 14535
Geobacter bemidjiensis Bem 2
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Geobacter lovleyi SZ
0.8
1
Geobacter sulfurreducens PCA 3
1
Geobacter metallireducens GS 15
Ammonifex degensii KC4
0.8
0.8
0.1
Thioalkalivibrio nitratireducens ONR

**Table S2.** Gene annotations associated with Figures 1 and 2. Numbers correspond to those in the figures.

| **Enzyme Number** | Gene | Product | EC Number |
|---|---|---|---|
| **Glycolosis** | | | |
| **1** | HK | hexokinase | 2.7.1.1 |
| **2** | pmm-pgm | phosphoglucomutase | 5.4.2.2 |
| **3** | pgi-pmi | glucose-6-phosphate isomerase | 5.3.1.9 |
| **4** | pfkA | 6-phosphofructokinase 1 | 2.7.1.11 |
| **5** | fbp | fructose-1,6-bisphosphatase I | 3.1.3.11 |
| **6** | K01622 | fructose 1,6-bisphosphate aldolase/phosphatase | 4.1.2.13 |
| **7** | tpiA | triosephosphate isomerase | 5.3.1.1 |
| **8** | gapA | glyceraldehyde 3-phosphate dehydrogenase | 1.2.1.12 |
| **9** | pgk | phosphoglycerate kinase | 2.7.2.3 |
| **10** | apgM | 2,3-bisphosphoglycerate-indipendent phosphoglycerate mutase | 5.4.2.12 |
| **11** | eno | enolase | 4.2.1.11 |
| **12** | ppsA | Phosphoenolpyruvate synthase/pyruvate phosphate dikinase | 2.7.9.2 |
| **13** | pyk | pyruvate kinase | 2.7.1.40 |
| **14** | porA | pyruvate ferredoxin oxidoreductase, alpha subunit | 1.2.7.1 |
| **15** | aceE | pyruvate dehydrogenase E1 component alpha subunit | 1.2.4.1 |
| **16** | aceF | pyruvate dehydrogenase E2 component | 2.3.1.12 |
| **17** | E6.2.1.13 | acetyl-CoA synthetase (ADP-forming) | 6.2.1.12 |
| **18** | acs | acetyl-CoA synthetase | 6.2.1.1 |
| **19** | ALDH | aldehyde dehydrogenase | 1.2.1.3 |
| **20** | ADH1 | alcohol dehydrogenase | 1.1.1.1 |
| **21** | pckA | phosphoenolpyruvate carboxykinase | 4.1.1.32 |
| **22** | LDH | lactate dehydrogenase | 1.1.1.27 |
| **23** | G6PD | glucose-6-phosphate 1-dehydrogenase | 1.1.1.49 |
| **24** | PGLS | 6-phosphogluconolactonase | 3.1.1.31 |
| **25** | PGD | 6-phosphogluconate dehydrogenase | 1.1.1.44 |
| **26** | rpiA | ribose 5-phosphate isomerase | 5.3.1.6 |
| **27** | rpe | ribulose-phosphate 3-epimerase | 5.1.3.1 |
| **28** | tktA,tktB | transketolase | 2.2.1.1 |
| **29** | talA,talB | transaldolase | 2.2.1.2 |
| **30** | PRK | phosphoribulokinase | 2.7.1.19 |
| **31** | rbcL | ribulose-bisphosphate carboxylase | 4.1.1.39 |
| **Citrate Acid Cycle** | | | |
| **32** | pyc | pyruvate carboxylase | 6.4.1.1 |
| **33** | CS,gltA | citrate synthase | 2.3.3.1 |
| **34** | acnA | aconitate hydratase | 4.1.2.3 |

| | | | |
|---|---|---|---|
| **35** | icd | isocitrate dehydrogenase | 1.1.1.42 |
| **36** | OGDH,DLST,korA | 2-oxoglutarate synthase | |
| **37** | LSC1 | succinyl-CoA synthetase | 6.2.1.4 |
| **38** | SDHA,SDH1 | succinate dehydrogenase | 1.3.5.1 |
| **39** | fumA, fumb | fumarate hydratase | 4.2.1.2 |
| **40** | MDH1,mgo | malate dehydrogenase | 1.1.1.37,<br>1.1.5.4 |
| **41** | maeB | malic enzyme | 1.1.1.40 |
| **Oxidative phosphorylation** | | | |
| **42** | | NADH dehydrogenase | 1.6.5.3 |
| **38** | SDHA,SDH1 | succinate dehydrogenase | 1.3.5.1 |
| **43** | fbcH | cytochrome c reductase | 1.10.2.2. |
| **44** | cco/cyo | cytochrome c oxidase | 1.9.3.1 |
| **45** | cox | cytochrome c oxidase | |
| **46** | ATP | H+-transporting ATPase | 3.6.3.6 |
| **Sulfur Metabolism** | | | |
| **47** | PAPS/Sat | 3'-phosphoadenosine 5'-phosphosulfate synthase | 2.7.7.4 |
| **48** | | phosphoadenylylsulfatase | 3.6.2.2 |
| **49** | cysH | phosphoadenosine phosphosulfate reductase | |
| **50** | | sulfite dehydrogenase | 1.8.2.1 |
| **51** | | sulfite reductase | |
| **52** | SOX | sulfur-oxidizing protein | |
| **53** | TST | thiosulfate/3-mercaptopyruvate sulfurtransferase | 2.8.1.1 |
| **54** | phsA | thiosulfate reductase | 1.8.5.5 |
| **55** | fccB | sulfide dehydrogenase | 1.8.2.3 |
| **56** | ETHE1 | sulfur dioxygenase | 1.13.11.18 |
| **57** | ssuD | alkanesulfonate monooxygenase | 1.14.14.5 |
| **58** | doxA | thiosulfate dehydrogenase | 1.8.5.2 |
| **59** | cysM | cysteine synthase | 2.5.1.47 |
| **Nitrogen Metabolism** | | | |
| **60** | narB | assimilatory nitrate reductase | 1.7.7.2 |
| **61** | narHI, napAB | dissimilatory nitrate reductase | 1.7.99.4 |
| **62** | nirB/nirD/nirK | assimilatory nitrite reductase | 1.7.7.1 |
| **63** | nrfAH | dissimilatory nitrite reductase | 1.7.2.2 |
| **64** | nirK | nitrite reductase (NO-forming) | 1.7.2.1 |
| **65** | norB | nitric oxide reductase | 1.7.2.5 |
| **66** | nosZ | nitrous-oxide reductase | 1.7.2.4 |
| **67** | nifD | nitrogenase | 1.18.6.1 |
| **68** | hao | hydroxylamine dehydrogenase | 1.7.2.6 |
| **69** | pmoA-amoA | methane/ammonia monooxygenase | 1.14.18.3 1.<br>14.99.39 |

| | | | |
|---|---|---|---|
| **70** | NAO | nitroalkane oxidase | 1.7.3.1 |
| **71** | | nitrilase | 3.5.5.1 |
| **72** | gudB | glutamate dehydrogenase | 1.4.1.2 |
| **73** | CPS1 | carbamoyl-phosphate synthase | 6.3.4.16 |
| **Methane Metabolism** | | | |
| **74** | | formamidase | 3.5.1.49 |
| **75** | FDH | formate dehydrogenase | 1.2.1.2 |
| **76** | fdhA | formate dehydrogenase alpha subunit | 1.2.1.43 |
| **77** | cdhA | acetyl-CoA decarbonylase/synthase complex | 1.2.7.4 |
| **78** | coxMS | carbon-monoxide dehydrogenase | 1.2.7.4 |
| **Wood-Ljungdahl Pathway** | | | |
| **78** | coxMS | carbon-monoxide dehydrogenase | 1.2.7.4 |
| **79** | fdhA | formate dehydrogenase alpha subunit | 1.2.1.43 |
| **80** | fhs | formate--tetrahydrofolate ligase | 6.3.4.3 |
| **81** | folD | methylenetetrahydrofolate dehydrogenase (NADP+) / methenyltetrahydrofolate cyclohydrolase | 1.5.1.5<br>3.5.4.9 |
| **82** | metF | methylenetetrahydrofolate reductase (NADPH) | 1.5.1.20 |
| **83** | acsE | 5-methyltetrahydrofolate corrinoid/iron sulfur protein methyltransferase | 2.1.1.258 |
| **84** | acsB | acetyl-CoA synthase | 2.3.1.169 |
| **Chemotaxis** | | | |
| **85** | mcp | methyl-accepting chemotaxis protein | |
| **86** | cheA | sensor kinase CheA | 2.7.13.3 |
| **87** | chW | purine-binding chemotaxis protein CheW | |
| **88** | cheV | response regulator CheV | |
| **89** | cheB | response regulator CheB | 3.1.1.61 |
| **90** | cheR | chemotaxis protein methyltransferase CheR | 2.1.1.80 |
| **91** | cheY | response regulator CheY | |
| **92** | cheC | chemotaxis protein CheC | |
| **93** | chex | chemotaxis protein CheX | |
| **94** | cheD | chemotaxis protein CheD | 3.5.1.44 |
| **Flagellar assembly** | | | |
| **95** | | Motor/Switch | |
| **96** | | Basal body | |
| **97** | | Hook | |
| **98** | | Filament | |
| **Phosphate response regulator** | | | |
| **99** | SenX3 | sensor histidine kinase SenX3 | 2.7.13.3 |
| **100** | PhoR | phosphate regulon sensor histidine kinase PhoR | 2.7.13.3 |
| **101** | RegX3 | response regulator RegX3 | |

| | | | |
|---|---|---|---|
| **102** | PhoB | phosphate regulon response regulator PhoB | |
| **103** | PhoP | alkaline phosphatase synthesis response regulator PhoP | |
| **104** | PstS | phosphate transport system substrate-binding protein | |
| **105** | PhoA | alkaline phosphatase | 3.1.3.1 |
| **106** | PhoD | alkaline phosphatase D | 3.1.3.1 |
| **Secretion System** | | | |
| **107** | SecDFEGY | protein translocase subunit | |
| **108** | SecA | protein translocase subunit secA | |
| **109** | FtsY | signal recognition particle-docking protein FtsY | |
| **110** | TatAC | sec-independent protein translocase protein | |
| **Transport** | | | |
| **111** | pstS | phosphate transport system substrate-binding protein | |
| **112** | pstC | phosphate transport system permease protein | |
| **113** | pstB | phosphate transport system ATP-binding protein | 3.6.3.27 |
| **114** | | Specific sugar transport system substrate-binding protein | |
| **115** | | specific sugar transport system permease protein | |
| **116** | msmX, msmK, malK, sugC, ggtA, msiK, mtlK, thuK | multiple sugar transport system ATP-binding protein | 3.6.3.- |
| **117** | OpuBC | osmoprotectant transport system substrate-binding protein | |
| **118** | OpuBB | osmoprotectant transport system permease protein | |
| **119** | OpuBA | osmoprotectant transport system ATP-binding protein | |
| **120** | LolC/LolE | lipoprotein-releasing system permease protein | |
| **121** | LolD | lipoprotein-releasing system ATP-binding protein | 3.6.3.- |
| **122** | AfuA | iron(III) transport system substrate-binding protein | |
| **123** | AfuB | iron(III) transport system permease protein | |
| **124** | AfuC | iron(III) transport system ATP-binding protein | 3.6.3.30 |
| **125** | BioY | biotin transport system substrate-specific component | |
| **126** | BioN | biotin transport system permease protein | |
| **127** | BioM | biotin transport system ATP-binding protein | 3.6.3.- |
| **128** | NatB | Sodium transport system permease protein | |
| **129** | NatA | sodium transport system ATP-binding protein | |
| **130** | CcmD | heme exporter protein D | |
| **131** | CcmC/CcmB | heme exporter protein C/B | |
| **132** | CcmA | heme exporter protein A | 3.6.3.41 |
| **133** | modA | molybdate transport system substrate-binding protein | |
| **134** | modB | molybdate transport system permease protein | |
| **135** | modC/modF | molybdate transport system ATP-binding protein | 3.6.3.29 |
| **136** | ZnuA | Zinc transport system substrate-binding protein | |
| **137** | ZnuB | Zinc transport system permease protein | |
| **138** | ZnuC | Zinc transport system ATP-binding protein | |
| **139** | LivK | branched-chain amino acid transport system substrate-binding protein | |

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|---|---|---|---|
| **140** | LivH/LivM | branched-chain amino acid transport system permease protein | |
| **141** | LivG/LivF | branched-chain amino acid transport system ATP-binding protein | |
| **142** | PotD | spermidine/putrescine transport system substrate-binding protein | |
| **143** | potC, potB | spermidine/putrescine transport system permease protein | |
| **144** | PotA | spermidine/putrescine transport system ATP-binding protein | 3.6.3.31 |
| **145** | TupA | tungstate transport system substrate-binding protein | |
| **146** | TupB | tungstate transport system permease protein | |
| **147** | TupC | tungstate transport system ATP-binding protein | 3.6.3.55 |
| **148** | GlnH | glutamine transport system substrate-binding protein | |
| **149** | GlnP | glutamine transport system permease protein | |
| **150** | GlnQ | glutamine transport system ATP-binding protein | 3.6.3.- |
| **151** | tbpA | thiamine transport system substrate-binding protein | |
| **152** | thiP | thiamine transport system permease protein | |
| **153** | thiQ | thiamine transport system ATP-binding protein | |
| **154** | PhnD | phosphonate transport system substrate-binding protein | |
| **155** | PhnE | phosphonate transport system permease protein | |
| **156** | PhnC | phosphonate transport system ATP-binding protein | |
| **157** | TagG | teichoic acid transport system permease protein | |
| **158** | TagH | teichoic acid transport system ATP-binding protein | |
| **159** | RfbA | lipopolysaccharide transport system permease protein | |
| **160** | RfbB | lipopolysaccharide transport system ATP-binding protein | |
| **161** | OppA | oligopeptide transport system substrate-binding protein | |
| **162** | OppB/ OPPC | oligopeptide transport system permease protein | |
| **163** | OppD/ OppF | oligopeptide transport system ATP-binding protein | |
| **164** | thiY | putative hydroxymethylpyrimidine transport system substrate-binding protein | |
| **165** | thiX | putative hydroxymethylpyrimidine transport system permease protein | |
| **166** | thiZ | putative hydroxymethylpyrimidine transport system ATP-binding protein | |
| **167** | cbiN/cbiM/cibQ | cobalt/nickel transport system permease protein | |
| **168** | cbiO | cobalt/nickel transport system permease protein | |
| **169** | YejA | microcin C transport system substrate-binding protein | |
| **170** | YejB/YejE/YejF | microcin C transport system permease protein | |
| **171** | YejF | microcin C transport system ATP-binding protein | |
| **172** | NodJ | lipooligosaccharide transport system permease protein | |
| **173** | NodI | lipooligosaccharide transport system ATP-binding protein | |
| **174** | UgpB | sn-glycerol 3-phosphate transport system substrate-binding protein | |
| **175** | UgpA/UgpE | sn-glycerol 3-phosphate transport system permease protein | |
| **176** | UgpC | sn-glycerol 3-phosphate transport system ATP-binding protein | 3.6.3.20 |

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|---|---|---|---|
| **177** | NNP | MFS transporter, NNP family, nitrate/nitrite transporter |  |
| **Pilus Assembly** |  |  |  |
| **178** | PilQ | type IV pilus assembly protein PilQ |  |
| **179** | PilC | type IV pilus assembly protein PilC |  |
| **180** | PilB/PilT/PilU | type IV pilus assembly protein PilB/PilT/PilU |  |
| **181** | Pil F | type IV pilus assembly protein PilF |  |
| **182** | PilP/PilN/PilO | type IV pilus assembly protein PilP/PilN/PilO |  |
| **183** | PilM | type IV pilus assembly protein PilM |  |
| **184** | PilA/FimV | type IV pilus assembly protein PilA/FimV |  |