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

J. Cameron Thrash[1*], Kiley W. Seitz[2], Brett J. Baker[2*], Ben Temperton[3], Lauren E. Gillies[4], Nancy N. Rabalais[5,6], Bernard Henrissat[7,8,9], and Olivia U. Mason[4]

1. Department of Biological Sciences, Louisiana State University, Baton Rouge, LA, USA
2. Department of Marine Science, Marine Science Institute, University of Texas at Austin, Port Aransas, TX, USA
3. School of Biosciences, University of Exeter, Exeter, UK
4. Department of Earth, Ocean, and Atmospheric Science, Florida State University, Tallahassee, FL, USA
5. Department of Oceanography and Coastal Sciences, Louisiana State University, Baton Rouge, LA, USA
6. Louisiana Universities Marine Consortium, Chauvin, LA USA
7. Architecture et Fonction des Macromolécules Biologiques, CNRS, Aix-Marseille Université, 13288 Marseille, France
8. INRA, USC 1408 AFMB, F-13288 Marseille, France
9. Department of Biological Sciences, King Abdulaziz University, Jeddah, Saudi Arabia

*Correspondence:
JCT thrashc@lsu.edu
BJB acidophile@gmail.com

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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**

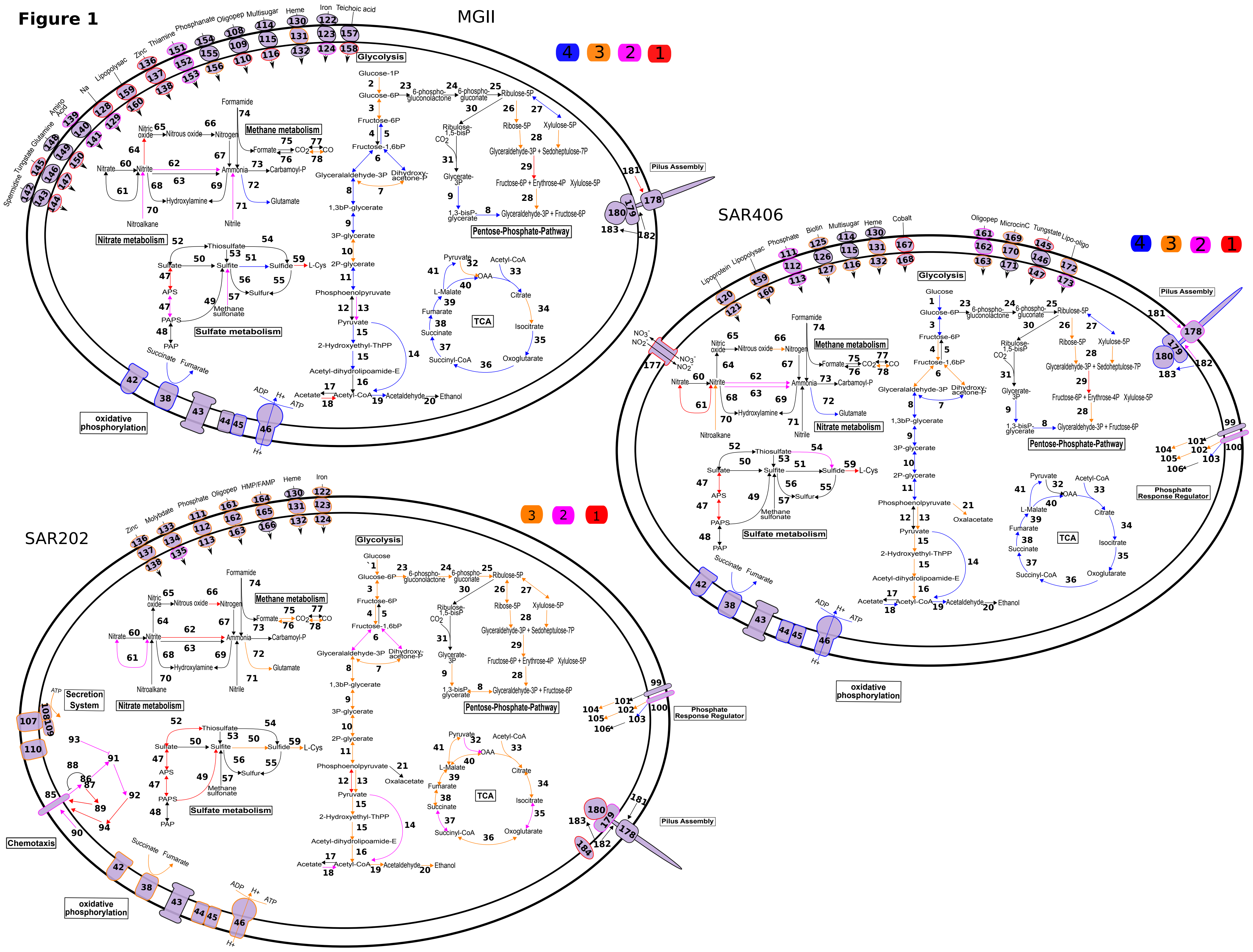
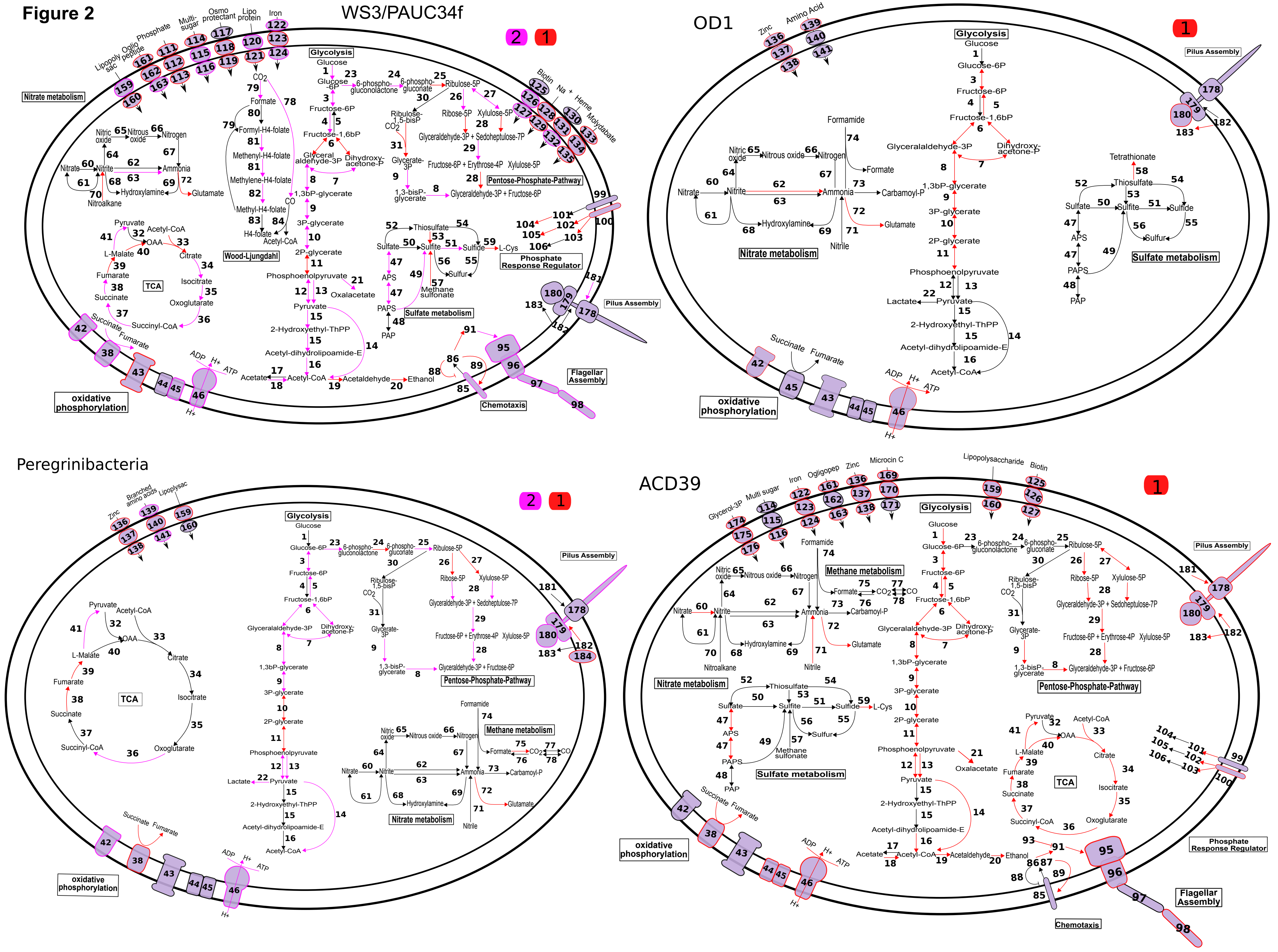

MGII
4
3
2
1
Glycolysis
Glucose-1P
Glucose-6P
6-phospho-gluconolactone
6-phospho-gluconate
Ribulose-5P
Fructose-6P
Fructose-1,6bP
Glyceralaldehyde-3P
Dihydroxy-acetone-P
1,3bP-glycerate
3P-glycerate
2P-glycerate
Phosphoenolpyruvate
Pyruvate
2-Hydroxyethyl-ThPP
Acetyl-dihydrolipoamide-E
Acetate
Acetyl-CoA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

**Figure 2**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Fructose-6P
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Glyceraldehyde-3P
Dihydroxy-acetone-P
1,3bP-glycerate
3P-glycerate
2P-glycerate
Phosphoenolpyruvate
Oxalacetate
Pyruvate
Lactate
2-Hydroxyethyl-ThPP
Acetyl-dihydrolipoamide-E
Acetyl-CoA
Acetate
Acetaldehyde
Ethanol
6-phospho-gluconolactone
6-phospho-gluconate
Ribulose-5P
Ribulose-1,5-bisP
CO2
Glycerate-3P
1,3-bisP-glycerate
Ribose-5P
Xylulose-5P
Glyceraldehyde-3P + Sedoheptulose-7P
Fructose-6P + Erythrose-4P
Glyceraldehyde-3P + Fructose-6P
Pentose-Phosphate-Pathway
Wood-Ljungdahl
Formate
Formyl-H4-folate
Methenyl-H4-folate
Methylene-H4-folate
Methyl-H4-folate
H4-folate
Nitrate metabolism
Nitrate
Nitrite
Nitric oxide
Nitrous oxide
Nitrogen
Ammonia
Hydroxylamine
Glutamate
Nitroalkane
Nitrile
Formamide
Carbamoyl-P
Methane metabolism
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TCA
OAA
Citrate
Isocitrate
Oxoglutarate
Succinyl-CoA
Succinate
Fumarate
L-Malate
Sulfate metabolism
Sulfate
Thiosulfate
Tetrathionate
Sulfite
Sulfide
Sulfur
L-Cys
APS
PAPS
PAP
Methane sulfonate
Phosphate Response Regulator
Pilus Assembly
Flagellar Assembly
Chemotaxis
oxidative phosphorylation
ADP
H+
ATP
Lipopoly sac
Oglio peptide
Phosphate
Multi-sugar
Osmo protectant
Lipo protein
Iron
Biotin
Na +
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Branched amino acids
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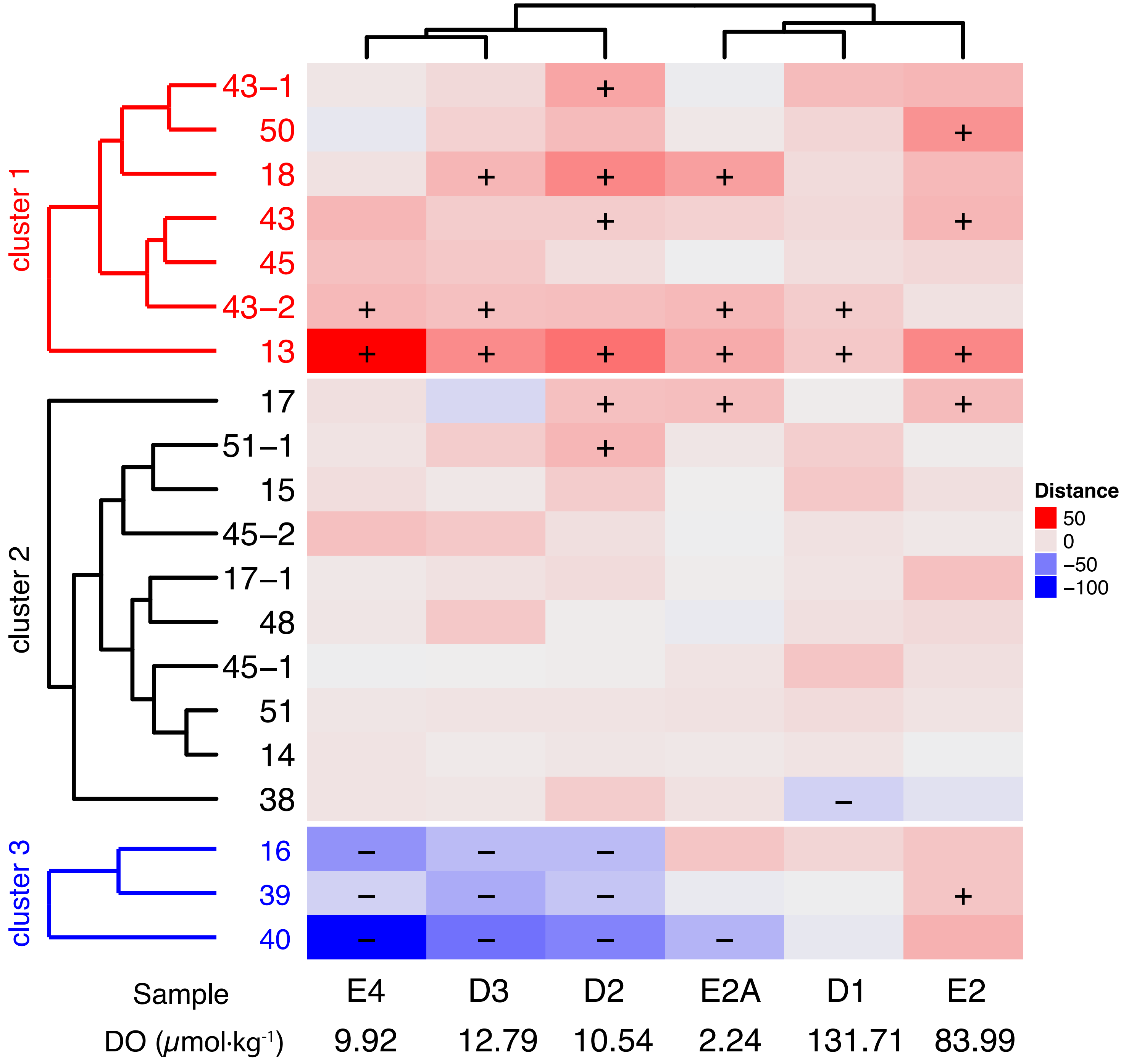
Oligopep
Microcin C
Lipopolysaccharide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14
38
cluster 3
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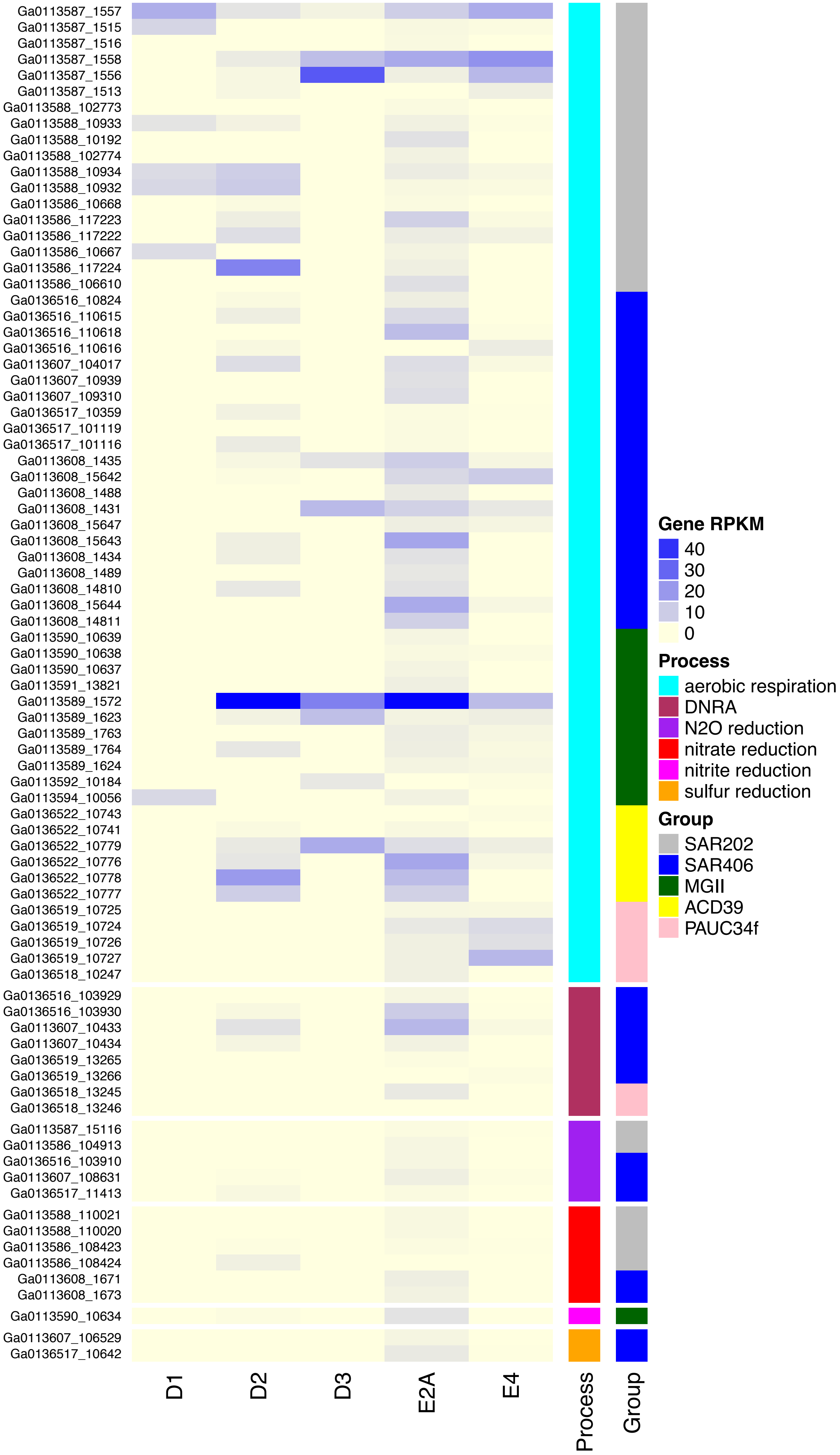
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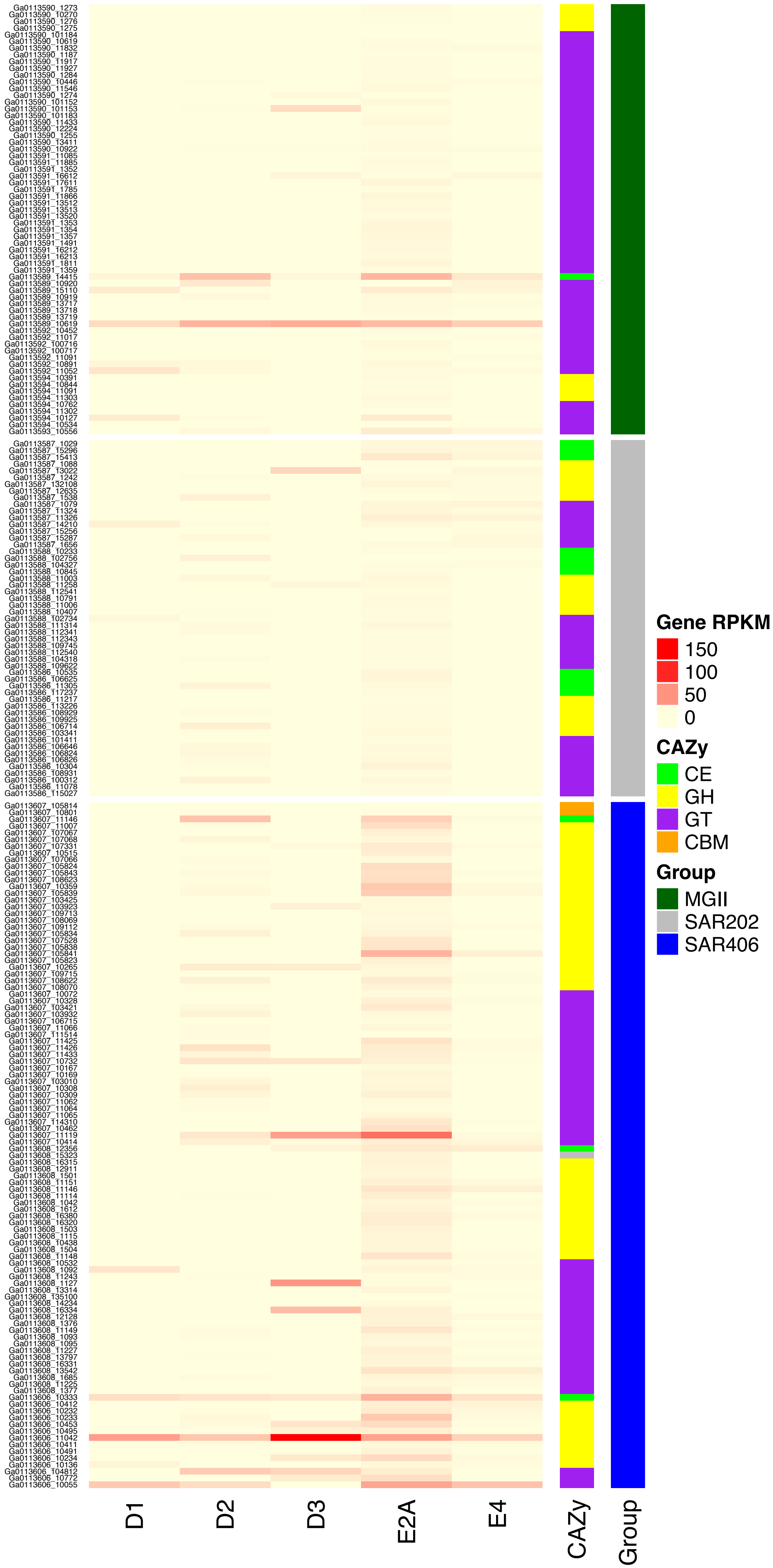
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Group
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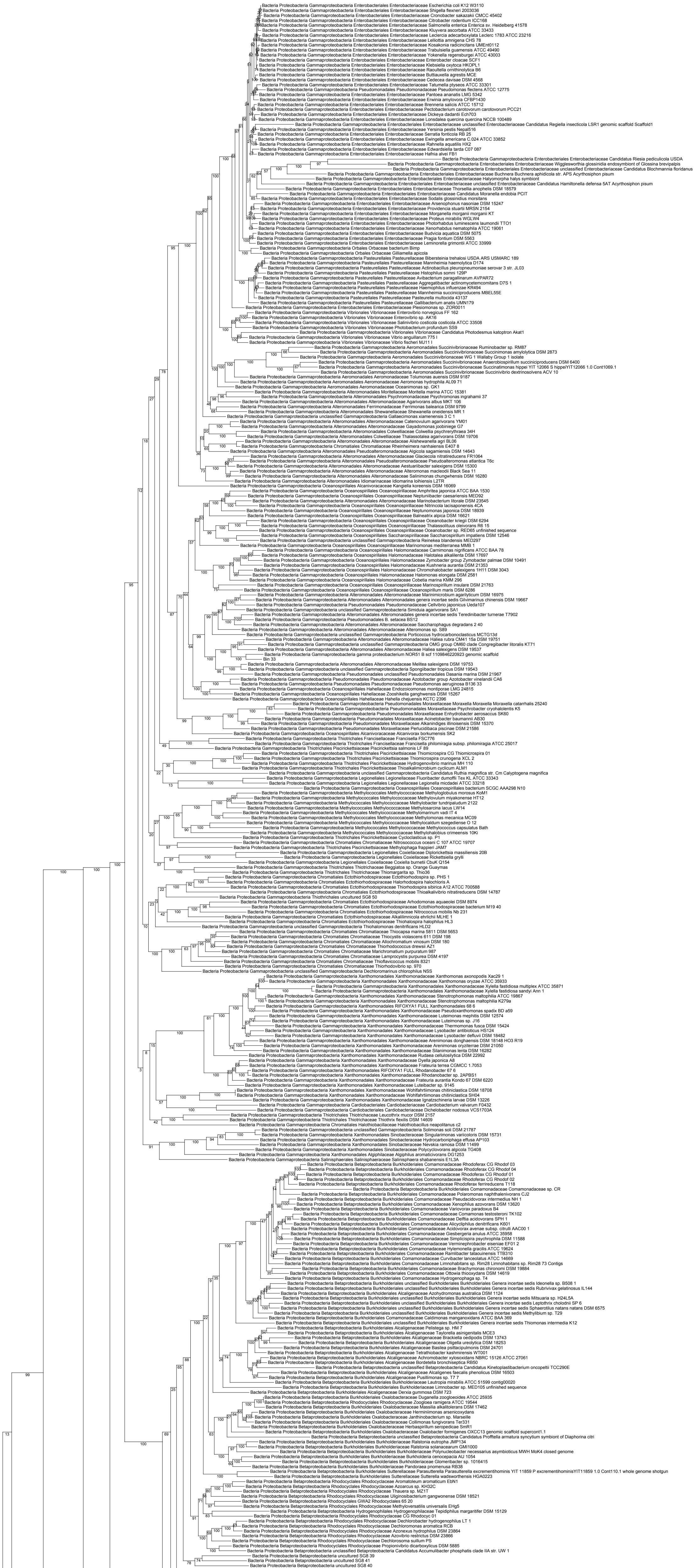
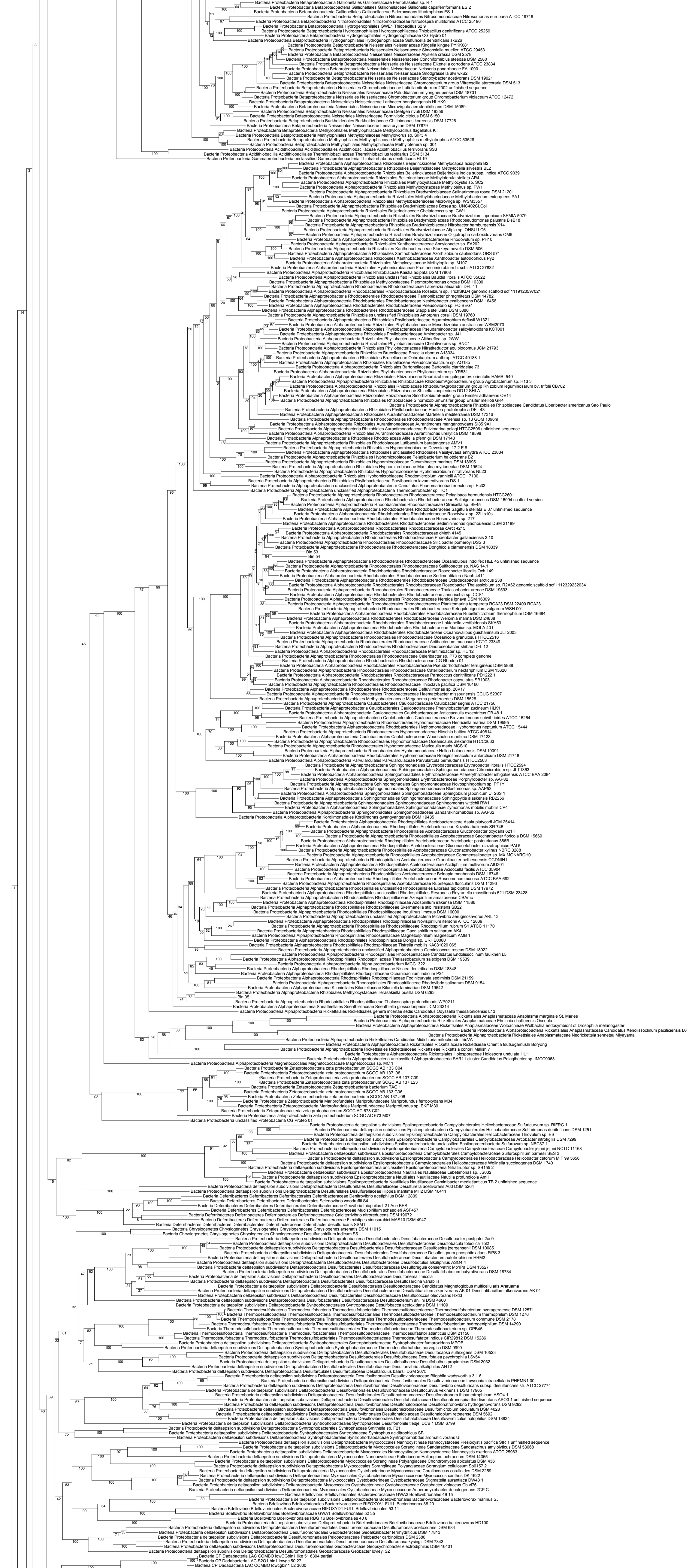
SAR406

# Figure S1

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Bacteria Proteobacteria Alphaproteobacteria Rhodobacterales Rhodobacteraceae cArct 4215
Bacteria Proteobacteria Alphaproteobacteria Rhodobacterales Rhodobacteraceae cMeth 4145
Bacteria Proteobacteria Alphaproteobacteria Rhodobacterales Rhodobacteraceae Phaeobacter gallaeciensis 2.10
Bacteria Proteobacteria Alphaproteobacteria Rhodobacterales Rhodobacteraceae Silicibacter pomeroyi DSS 3
Bacteria Proteobacteria Alphaproteobacteria Rhodobacterales Rhodobacteraceae Donghicola xiamenensis DSM 18339
Bin 53
Bin 54
Bacteria Proteobacteria Alphaproteobacteria Rhodobacterales Rhodobacteraceae Oceanibulbus indolifex HEL 45 unfinished sequence
Bacteria Proteobacteria Alphaproteobacteria Rhodobacterales Rhodobacteraceae Sulfitobacter sp. NAS 14.1
Bacteria Proteobacteria Alphaproteobacteria Rhodobacterales Rhodobacteraceae Roseobacter litoralis Och 149
Bacteria Proteobacteria Alphaproteobacteria Rhodobacterales Rhodobacteraceae Sedimentitalea cNanh 4411
Bacteria Proteobacteria Alphaproteobacteria Rhodobacterales Rhodobacteraceae Octadecabacter arcticus 238
Bacteria Proteobacteria Alphaproteobacteria Rhodobacterales Rhodobacteraceae Roseobacter Thalassiobium sp. R2A62 genomic scaffold scf 1112329232034
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Bacteria Proteobacteria Alphaproteobacteria Rhodobacterales Rhodobacteraceae Jannaschia sp. CCS1
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Bacteria Proteobacteria Alphaproteobacteria Rhodobacterales Hyphomonadaceae Hyphomonas neptunium ATCC 15444
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Bacteria Proteobacteria Alphaproteobacteria Sphingomonadales Erythrobacteraceae Erythrobacter litoralis HTCC2594
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Bacteria Proteobacteria Alphaproteobacteria Rhodospirillales Acetobacteraceae Rubritepida flocculans DSM 14296
Bacteria Proteobacteria Alphaproteobacteria Rhodospirillales unclassified Rhodospirillales Elioraea tepidiphila DSM 17972
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Bacteria Proteobacteria Alphaproteobacteria Rickettsiales Anaplasmataceae Anaplasma marginale St. Maries
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Bacteria Proteobacteria Alphaproteobacteria Rickettsiales Anaplasmataceae Wolbachieae Wolbachia endosymbiont of Drosophila melanogaster
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Bacteria Proteobacteria unclassified Proteobacteria CG Proteo 01
Bacteria Proteobacteria deltaepsilon subdivisions Epsilonproteobacteria Campylobacterales Helicobacteraceae Sulfuricurvum sp. RIFRC 1
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Bacteria Proteobacteria deltaepsilon subdivisions Epsilonproteobacteria Campylobacterales Campylobacteraceae Campylobacter jejuni jejuni NCTC 11168
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Bacteria Proteobacteria deltaepsilon subdivisions Epsilonproteobacteria Campylobacterales Helicobacteraceae Wolinella succinogenes DSM 1740
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Bacteria Deferribacteres Deferribacteres Deferribacterales Deferribacteraceae Denitrovibrio acetiphilus DSM 12809
Bacteria Deferribacteres Deferribacteres Deferribacterales Deferribacteraceae Selenovibrio woodruffii S4
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Bacteria Chrysiogenetes Chrysiogenetes Chrysiogenales Chrysiogenaceae Chrysiogenes arsenatis DSM 11915
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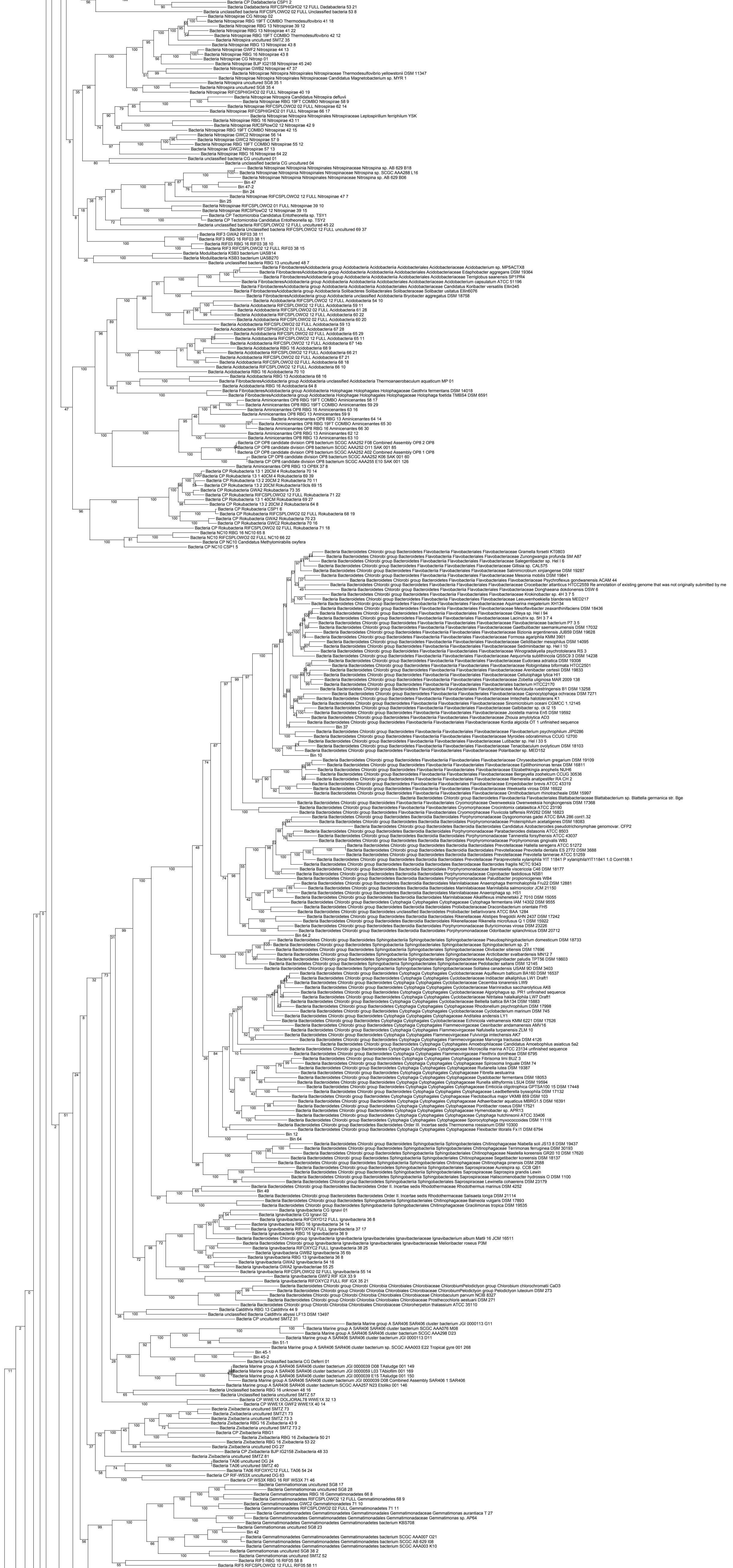
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Bacteria unclassified bacteria RIFCSPLOWO2 02 FULL Unclassified bacteria 53 8
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Bacteria Nitrospirae RBG 19FT COMBO Thermodesulfovibrio 41 18
Bacteria Nitrospirae RBG 13 Nitrospirae 39 12
Bacteria Nitrospirae RBG 13 Nitrospirae 41 22
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Bacteria Nitrospira uncultured SMTZ 35
Bacteria Nitrospirae RBG 13 Nitrospirae 43 8
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Bin 47
Bin 47-2
Bin 24
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Bin 25
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Bacteria CP Tectomicrobia Candidatus Entotheonella sp. TSY2
Bacteria unclassified bacteria RIFCSPLOWO2 12 FULL uncultured 45 22
Bacteria Unclassified bacteria RIFCSPLOWO2 12 FULL uncultured 69 37
Bacteria RIF3 GWA2 RIF03 38 11
Bacteria RIF3 RBG 16 RIF03 38 11
Bacteria RIF03 RBG 16 RIF03 38 10
Bacteria RIF3 RIFCSPLOWO2 12 FULL RIF03 38 15
Bacteria Modulibacteria KSB3 bacterium UASB14
Bacteria Modulibacteria KSB3 bacterium UASB270
Bacteria unclassified bacteria RBG 13 uncultured 48 7
Bacteria FibrobacteresAcidobacteria group Acidobacteria Acidobacteriia Acidobacteriales Acidobacteriaceae Acidobacterium sp. MP5ACTX8
Bacteria FibrobacteresAcidobacteria group Acidobacteria Acidobacteriia Acidobacteriales Acidobacteriaceae Edaphobacter aggregans DSM 19364
Bacteria FibrobacteresAcidobacteria group Acidobacteria Acidobacteriia Acidobacteriales Acidobacteriaceae Terriglobus saanensis SP1PR4
Bacteria FibrobacteresAcidobacteria group Acidobacteria Acidobacteriia Acidobacteriales Acidobacteriaceae Acidobacterium capsulatum ATCC 51196
Bacteria FibrobacteresAcidobacteria group Acidobacteria Acidobacteriia Acidobacteriales Acidobacteriaceae Candidatus Koribacter versatilis Ellin345
Bacteria FibrobacteresAcidobacteria group Acidobacteria Solibacteres Solibacterales Solibacteraceae Solibacter usitatus Ellin6076
Bacteria FibrobacteresAcidobacteria group Acidobacteria unclassified Acidobacteria Bryobacter aggregatus DSM 18758
Bacteria Acidobacteria RIFCSPLOWO2 12 FULL Acidobacteria 54 10
Bacteria Acidobacteria RIFCSPLOWO2 12 FULL Acidobacteria 59 11
Bacteria Acidobacteria RIFCSPLOWO2 12 FULL Acidobacteria 61 28
Bacteria Acidobacteria RIFCSPLOWO2 12 FULL Acidobacteria 60 22
Bacteria Acidobacteria RIFCSPLOWO2 02 FULL Acidobacteria 60 20
Bacteria Acidobacteria RIFCSPLOWO2 02 FULL Acidobacteria 59 13
Bacteria Acidobacteria RIFCSPHIGHO2 01 FULL Acidobacteria 67 28
Bacteria Acidobacteria RIFCSPLOWO2 02 FULL Acidobacteria 65 29
Bacteria Acidobacteria RIFCSPLOWO2 12 FULL Acidobacteria 65 11
Bacteria Acidobacteria RIFCSPLOWO2 12 FULL Acidobacteria 67 14b
Bacteria Acidobacteria RBG 16 Acidobacteria 68 9
Bacteria Acidobacteria RIFCSPLOWO2 12 FULL Acidobacteria 66 21
Bacteria Acidobacteria RIFCSPLOWO2 02 FULL Acidobacteria 67 21
Bacteria Acidobacteria RIFCSPLOWO2 02 FULL Acidobacteria 68 18
Bacteria Acidobacteria RIFCSPLOWO2 12 FULL Acidobacteria 66 10
Bacteria Acidobacteria RBG 16 Acidobacteria 70 10
Bacteria Acidobacteria RBG 13 Acidobacteria 68 16
Bacteria FibrobacteresAcidobacteria group Acidobacteria unclassified Acidobacteria Thermoanaerobaculum aquaticum MP 01
Bacteria Acidobacteria RBG 16 Acidobacteria 64 8
Bacteria FibrobacteresAcidobacteria group Acidobacteria Holophagae Holophagales Holophagaceae Geothrix fermentans DSM 14018
Bacteria FibrobacteresAcidobacteria group Acidobacteria Holophagae Holophagales Holophagaceae Holophaga foetida TMBS4 DSM 6591
Bacteria Aminicenantes OP8 RBG 19FT COMBO Aminicenantes 58 17
Bacteria Aminicenantes OP8 RBG 19FT COMBO Aminicenantes 59 29
Bacteria Aminicenantes OP8 RBG 16 Aminicenantes 63 16
Bacteria Aminicenantes OP8 RBG 13 Aminicenantes 59 9
Bacteria Aminicenantes OP8 RBG 13 Aminicenantes 64 14
Bacteria Aminicenantes OP8 RBG 19FT COMBO Aminicenantes 65 30
Bacteria Aminicenantes OP8 RBG 16 Aminicenantes 66 30
Bacteria Aminicenantes OP8 RBG 13 Aminicenantes 62 12
Bacteria Aminicenantes OP8 RBG 13 Aminicenantes 63 10
Bacteria CP OP8 candidate division OP8 bacterium SCGC AAA252 F08 Combined Assembly OP8 2 OP8
Bacteria CP OP8 candidate division OP8 bacterium SCGC AAA252 O11 SAK 001 85
Bacteria CP OP8 candidate division OP8 bacterium SCGC AAA252 A02 Combined Assembly OP8 1 OP8
Bacteria CP OP8 candidate division OP8 bacterium SCGC AAA252 K06 SAK 001 60
Bacteria CP OP8 candidate division OP8 bacterium SCGC AAA255 E10 SAK 001 126
Bacteria Aminicenantes OP8 RBG 13 OP8X 37 8
Bacteria CP Rokubacteria 13 1 20CM 4 Rokubacteria 70 14
Bacteria CP Rokubacteria 13 1 40CM 4 Rokubacteria 69 39
Bacteria CP Rokubacteria 13 2 20CM 2 Rokubacteria 70 11
Bacteria CP Rokubacteria 13 2 20CM Rokubacteria19cls 69 15
Bacteria CP Rokubacteria GWA2 Rokubacteria 73 35
Bacteria CP Rokubacteria RIFCSPLOWO2 12 FULL Rokubacteria 71 22
Bacteria CP Rokubacteria 13 1 40CM Rokubacteria 69 27
Bacteria CP Rokubacteria 13 2 20CM 2 Rokubacteria 64 8
Bacteria CP Rokubacteria CSP1 6
Bacteria CP Rokubacteria RIFCSPLOWO2 02 FULL Rokubacteria 68 19
Bacteria CP Rokubacteria GWA2 Rokubacteria 70 23
Bacteria CP Rokubacteria GWC2 Rokubacteria 70 16
Bacteria CP Rokubacteria RIFCSPLOWO2 02 FULL Rokubacteria 71 18
Bacteria NC10 RBG 16 NC10 65 8
Bacteria NC10 RIFCSPLOWO2 02 FULL NC10 66 22
Bacteria CP NC10 Candidatus Methylomirabilis oxyfera
Bacteria CP NC10 CSP1 5
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Flavobacteriia Flavobacteriales Flavobacteriaceae Gramella forsetii KT0803
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Flavobacteriia Flavobacteriales Flavobacteriaceae Zunongwangia profunda SM A87
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Flavobacteriia Flavobacteriales Flavobacteriaceae Salegentibacter sp. Hel I 6
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Flavobacteriia Flavobacteriales Flavobacteriaceae Gillisia sp. CAL575
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Flavobacteriia Flavobacteriales Flavobacteriaceae Salinimicrobium xinjiangense DSM 19287
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Flavobacteriia Flavobacteriales Flavobacteriaceae Mesonia mobilis DSM 19841
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Flavobacteriia Flavobacteriales Flavobacteriaceae Psychroflexus gondwanensis ACAM 44
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Flavobacteriia Flavobacteriales Flavobacteriaceae Croceibacter atlanticus HTCC2559 Re annotation of existing genome that was not originally submitted by me
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Flavobacteriia Flavobacteriales Flavobacteriaceae Donghaeana dokdonensis DSW 6
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Flavobacteriia Flavobacteriales Flavobacteriaceae Krokinobacter sp. 4H 3 7 5
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Flavobacteriia Flavobacteriales Flavobacteriaceae Leeuwenhoekiella blandensis MED217
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Flavobacteriia Flavobacteriales Flavobacteriaceae Aquimarina megaterium XH134
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Flavobacteriia Flavobacteriales Flavobacteriaceae Mesoflavibacter zeaxanthinifaciens DSM 18436
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Flavobacteriia Flavobacteriales Flavobacteriaceae Olleya sp. Hel I 94
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Flavobacteriia Flavobacteriales Flavobacteriaceae Lacinutrix sp. 5H 3 7 4
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Flavobacteriia Flavobacteriales Flavobacteriaceae Flavobacteriaceae bacterium P7 3 5
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Flavobacteriia Flavobacteriales Flavobacteriaceae Gaetbulibacter saemankumensis DSM 17032
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Flavobacteriia Flavobacteriales Flavobacteriaceae Bizionia argentinensis JUB59 DSM 19628
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Flavobacteriia Flavobacteriales Flavobacteriaceae Formosa agariphila KMM 3901
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 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
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Flavobacteriia Flavobacteriales Flavobacteriaceae Empedobacter brevis ATCC 43319
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
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Flavobacteriia Flavobacteriales Cryomorphaceae Fluviicola taffensis RW262 DSM 16823
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Bacteroidia Bacteroidales Porphyromonadaceae Dysgonomonas gadei ATCC BAA 286 cont1.32
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Bacteroidia Bacteroidales Porphyromonadaceae Proteiniphilum acetatigenes DSM 18083
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Bacteroidia Bacteroidales Candidatus Azobacteroides pseudotrichonymphae genomovar. CFP2
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Bacteroidia Bacteroidales Porphyromonadaceae Barnesiella sp. 21
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Bacteroidia Bacteroidales Porphyromonadaceae Parabacteroides distasonis ATCC 8503
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Bacteroidia Bacteroidales Porphyromonadaceae Tannerella forsythensis ATCC 43037
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Bacteroidia Bacteroidales Porphyromonadaceae Porphyromonas gingivalis W83
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
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Bacteroidia Bacteroidales Prevotellaceae Prevotella tannerae ATCC 51259
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
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Bacteroidia Bacteroidales Porphyromonadaceae Coprobacter fastidiosus NSB1
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
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Bacteroidia Bacteroidales Prolixibacteraceae Draconibacterium orientale FH5
Bacteria Bacteroidetes Chlorobi group Bacteroidetes unclassified Bacteroidetes Prolixibacter bellariivorans ATCC BAA 1284
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Bacteroidia Bacteroidales Rikenellaceae Alistipes finegoldii AHN 2437 DSM 17242
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Bacteroidia Bacteroidales Rikenellaceae Rikenella microfusus Q 1 DSM 15922
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Bacteroidia Bacteroidales Porphyromonadaceae Butyricimonas virosa DSM 23226
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Bacteroidia Bacteroidales Porphyromonadaceae Odoribacter splanchnicus DSM 20712
Bin 64 2
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Sphingobacteriia Sphingobacteriales Sphingobacteriaceae Pseudosphingobacterium domesticum DSM 18733
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Sphingobacteriia Sphingobacteriales Sphingobacteriaceae Sphingobacterium sp. 21
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Sphingobacteriia Sphingobacteriales Sphingobacteriaceae Olivibacter sitiensis DSM 17696
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Sphingobacteriia Sphingobacteriales Sphingobacteriaceae Arcticibacter svalbardensis MN12 7
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
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Cytophagia Cytophagales Cyclobacteriaceae Aquiflexum balticum BA160 DSM 16537
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 Mariniradius saccharolyticus AK6
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Cytophagia Cytophagales Cyclobacteriaceae Algoriphagus sp. PR1 unfinished sequence
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Cytophagia Cytophagales Cyclobacteriaceae Nitritalea halalkaliphila LW7 Draft1
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Cytophagia Cytophagales Cyclobacteriaceae Belliella baltica BA134 DSM 15883
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Cytophagia Cytophagales Cyclobacteriaceae Rhodonellum psychrophilum DSM 17998
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Cytophagia Cytophagales Cyclobacteriaceae Cyclobacterium marinum DSM 745
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Cytophagia Cytophagales Cyclobacteriaceae Anditalea andensis LY1
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Cytophagia Cytophagales Cyclobacteriaceae Echinicola vietnamensis KMM 6221 DSM 17526
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Cytophagia Cytophagales Flammeovirgaceae Cesiribacter andamanensis AMV16
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Cytophagia Cytophagales Flammeovirgaceae Nafulsella turpanensis ZLM 10
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Cytophagia Cytophagales Flammeovirgaceae Fulvivirga imtechensis AK7
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Cytophagia Cytophagales Flammeovirgaceae Marivirga tractuosa DSM 4126
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Cytophagia Cytophagales Amoebophilaceae Candidatus Amoebophilus asiaticus 5a2
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Cytophagia Cytophagales Flammeovirgaceae Microscilla marina ATCC 23134 unfinished sequence
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Cytophagia Cytophagales Flammeovirgaceae Flexithrix dorotheae DSM 6795
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Cytophagia Cytophagales Cytophagaceae Fibrisoma limi BUZ 3
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Cytophagia Cytophagales Cytophagaceae Spirosoma linguale DSM 74
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Cytophagia Cytophagales Cytophagaceae Rudanella lutea DSM 19387
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
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Cytophagia Cytophagales Cytophagaceae Hymenobacter sp. APR13
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Cytophagia Cytophagales Cytophagaceae Cytophaga hutchinsonii ATCC 33406
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Cytophagia Cytophagales Cytophagaceae Sporocytophaga myxococcoides DSM 11118
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
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Sphingobacteriia Sphingobacteriales Chitinophagaceae Segetibacter koreensis DSM 18137
Bacteria Bacteroidetes Chlorobi group Bacteroidetes Sphingobacteriia Sphingobacteriales Chitinophagaceae Chitinophaga pinensis DSM 2588
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
Bacteria Bacteroidetes Chlorobi group Chlorobi Chlorobia Chlorobiales Chlorobiaceae ChlorobiumPelodictyon group Pelodictyon luteolum DSM 273
Bacteria Bacteroidetes Chlorobi group Chlorobi Chlorobia Chlorobiales Chlorobiaceae Chlorobaculum parvum NCIB 8327
Bacteria Bacteroidetes Chlorobi group Chlorobi Chlorobia Chlorobiales Chlorobiaceae Prosthecochloris aestuarii DSM 271
Bacteria Bacteroidetes Chlorobi group Chlorobi Chlorobia Chlorobiales Chlorobiaceae Chloroherpeton thalassium ATCC 35110
Bacteria Caldithrix RBG 13 Caldithrix 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 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
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Bacteria Gemmatimonas uncultured SG8 23
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Bacteria Gemmatimonadetes Gemmatimonadetes bacterium SCGC AAA003 K10
Bacteria Gemmatimonas uncultured SG8 38 2
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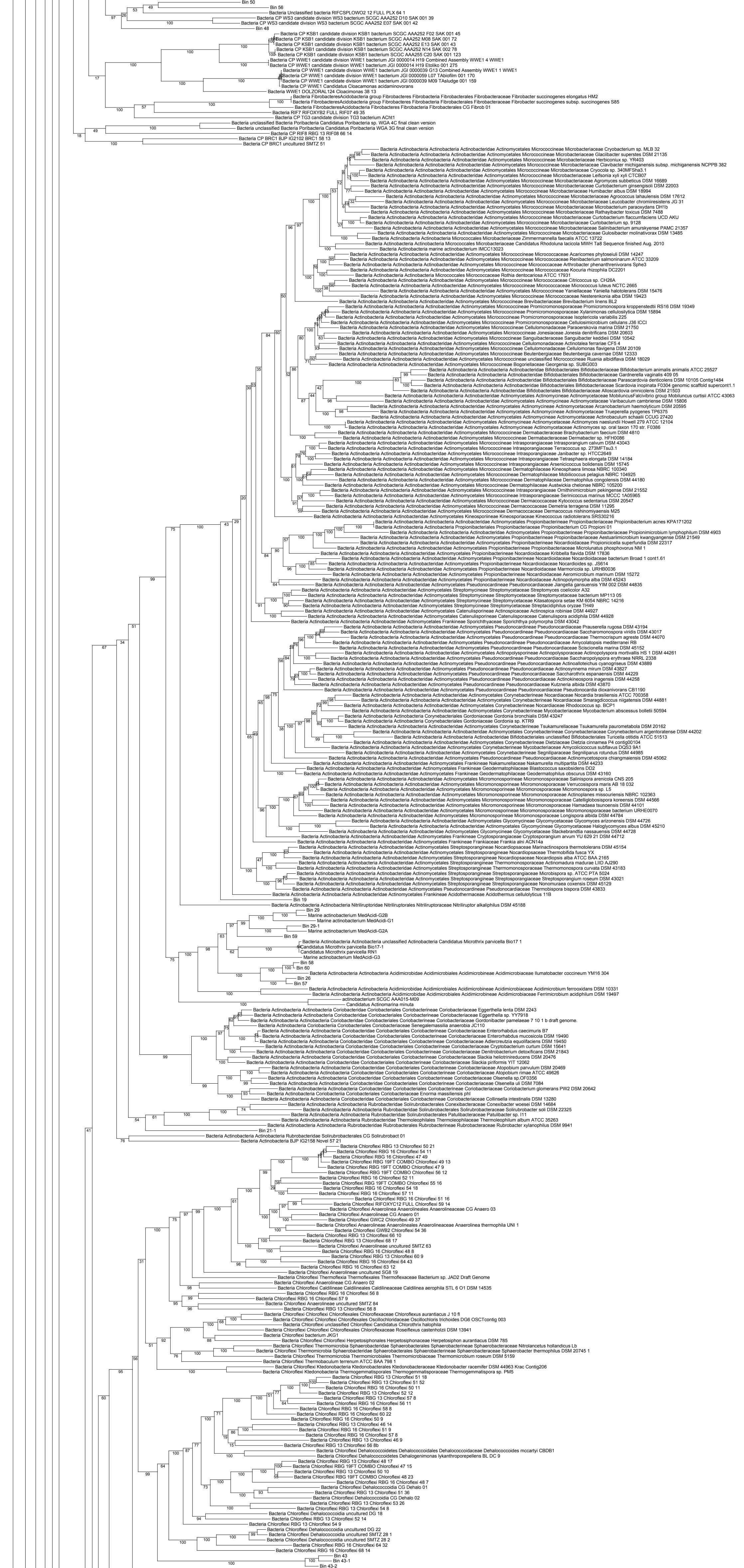
Bacteria RIF5 RIFCSPLOWO2 12 FULL RIF05 58 11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Bacteria WWE1 DOLZORAL124 Cloacimonas 38 13
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Bacteria CP TG3 candidate division TG3 bacterium ACht1
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Bin 19
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Marine actinobacterium MedAcidi-G1
Bin 29-1
Marine actinobacterium MedAcidi-G2A
Bin 59
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Bin 60
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Bacteria Chloroflexi RBG 13 Chloroflexi 68 17
Bacteria Chloroflexi Anaerolineae uncultured SMTZ 63
Bacteria Chloroflexi RBG 16 Chloroflexi 48 8
Bacteria Chloroflexi RBG 13 Chloroflexi 60 9
Bacteria Chloroflexi RBG 16 Chloroflexi 64 43
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Bacteria Chloroflexi RBG 16 Chloroflexi 57 9
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Bacteria Chloroflexi RBG 13 Chloroflexi 56 8
Bacteria Chloroflexi Chloroflexi Chloroflexales Chloroflexaceae Chloroflexus aurantiacus J 10 fl
Bacteria Chloroflexi Chloroflexi Chloroflexales Oscillochloridaceae Oscillochloris trichoides DG6 OSCTcontig 003
Bacteria Chloroflexi unclassified Chloroflexi Candidatus Chlorothrix halophila
Bacteria Chloroflexi Chloroflexi Chloroflexales Chloroflexaceae Roseiflexus castenholzii DSM 13941
Bacteria Chloroflexi bacterium JKG1
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Bacteria Chloroflexi Thermomicrobia Sphaerobacteridae Sphaerobacterales Sphaerobacterineae Sphaerobacteraceae Nitrolancetus hollandicus Lb
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Bacteria Chloroflexi RBG 13 Chloroflexi 51 52
Bacteria Chloroflexi RBG 16 Chloroflexi 50 11
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Bacteria Chloroflexi Dehalococcoidetes Dehalogenimonas lykanthroporepellens BL DC 9
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Bacteria Chloroflexi RBG 19FT COMBO Chloroflexi 47 15
Bacteria Chloroflexi RBG 13 Chloroflexi 50 10
Bacteria Chloroflexi RBG 19FT COMBO Chloroflexi 48 23
Bacteria Chloroflexi RBG 16 Chloroflexi 48 7
Bacteria Chloroflexi Dehalococcoidia CG Dehalo 01
Bacteria Chloroflexi RBG 13 Chloroflexi 51 36
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Bacteria Chloroflexi Dehalococcoidia uncultured DG 22
Bacteria Chloroflexi Dehalococcoidia uncultured SMTZ 28 1
Bacteria Chloroflexi Dehalococcoidia uncultured SMTZ 28 2
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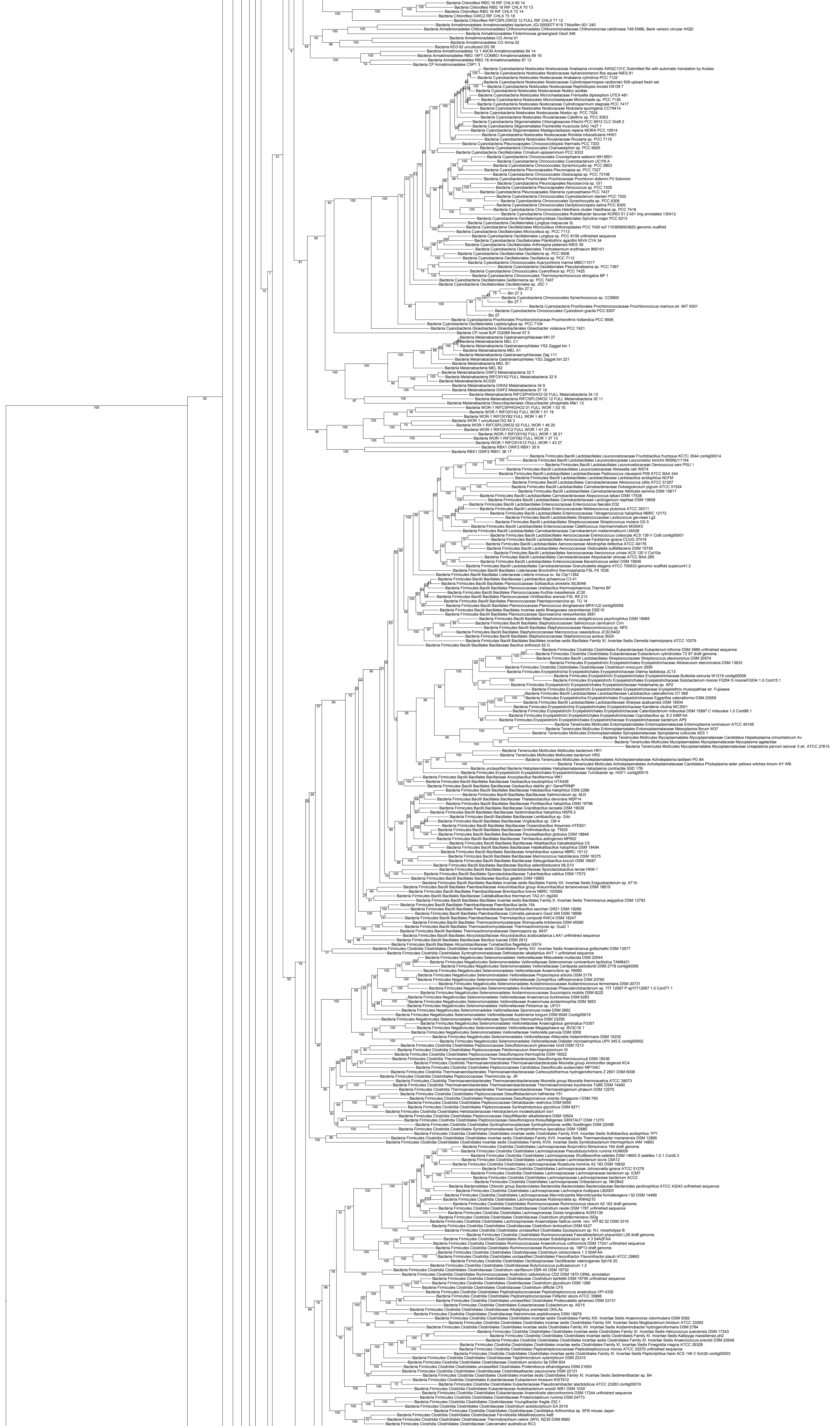
Bacteria Chloroflexi RBG 16 Chloroflexi 68 14
Bin 43
Bin 43-1
Bin 43-2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Bacteria Chloroflexi RIFCSPLOWO2 12 FULL RIF CHLX 71 12
Bacteria Armatimonadetes Armatimonadetes bacterium JGI 0000077 K19 TAbiofilm 001 240
Bacteria Armatimonadetes Chthonomonadetes 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
Bacteria Armatimonadetes 13 1 40CM Armatimonadetes 64 14
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Bacteria Armatimonadetes RBG 16 Armatimonadetes 67 12
Bacteria CP Armatimonadetes CSP1 3
Bacteria Cyanobacteria Nostocales Nostocaceae Anabaena circinalis AWQC131C Submitted file with automatic translation by Kostas
Bacteria Cyanobacteria Nostocales Nostocaceae Aphanizomenon flos aquae NIES 81
Bacteria Cyanobacteria Nostocales Nostocaceae Anabaena cylindrica PCC 7122
Bacteria Cyanobacteria Nostocales Nostocaceae Cylindrospermopsis raciborskii 509 upload fresh set
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Bacteria Cyanobacteria Nostocales Rivulariaceae Rivularia sp. PCC 7116
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Bacteria Cyanobacteria Oscillatoriales Crinalium epipsammum PCC 9333
Bacteria Cyanobacteria Chroococcales Crocosphaera watsonii WH 8501
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Bacteria Cyanobacteria Chroococcales Synechocystis sp. PCC 6803
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Bacteria Cyanobacteria Oscillatoriales Microcoleus chthonoplastes PCC 7420 scf 1103659003820 genomic scaffold
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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
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Bacteria Melainabacteria MEL B1
Bacteria Melainabacteria MEL B2
Bacteria Melainabacteria GWF2 Melainabacteria 32 7
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Bacteria Melainabacteria ACD20
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Bacteria Melainabacteria Obscuribacterales Obscuribacter phosphatis Mle1 12
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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
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Bacteria Firmicutes Bacilli Bacillales Planococcaceae Kurthia massiliensis JC30
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Bacteria Firmicutes Clostridia Thermoanaerobacterales Thermoanaerobacteraceae Desulfovirgula thermocuniculi DSM 16036
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Bacteria Firmicutes Clostridia Clostridiales Clostridiaceae Clostridium lentocellum DSM 5427
Bacteria Firmicutes Clostridia Clostridiales unclassified Clostridiales Epulopiscium sp. N.t. morphotype B
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Bacteria Firmicutes Clostridia Clostridiales Clostridiaceae Thermobrachium celere JW/YL NZ35 DSM 8682
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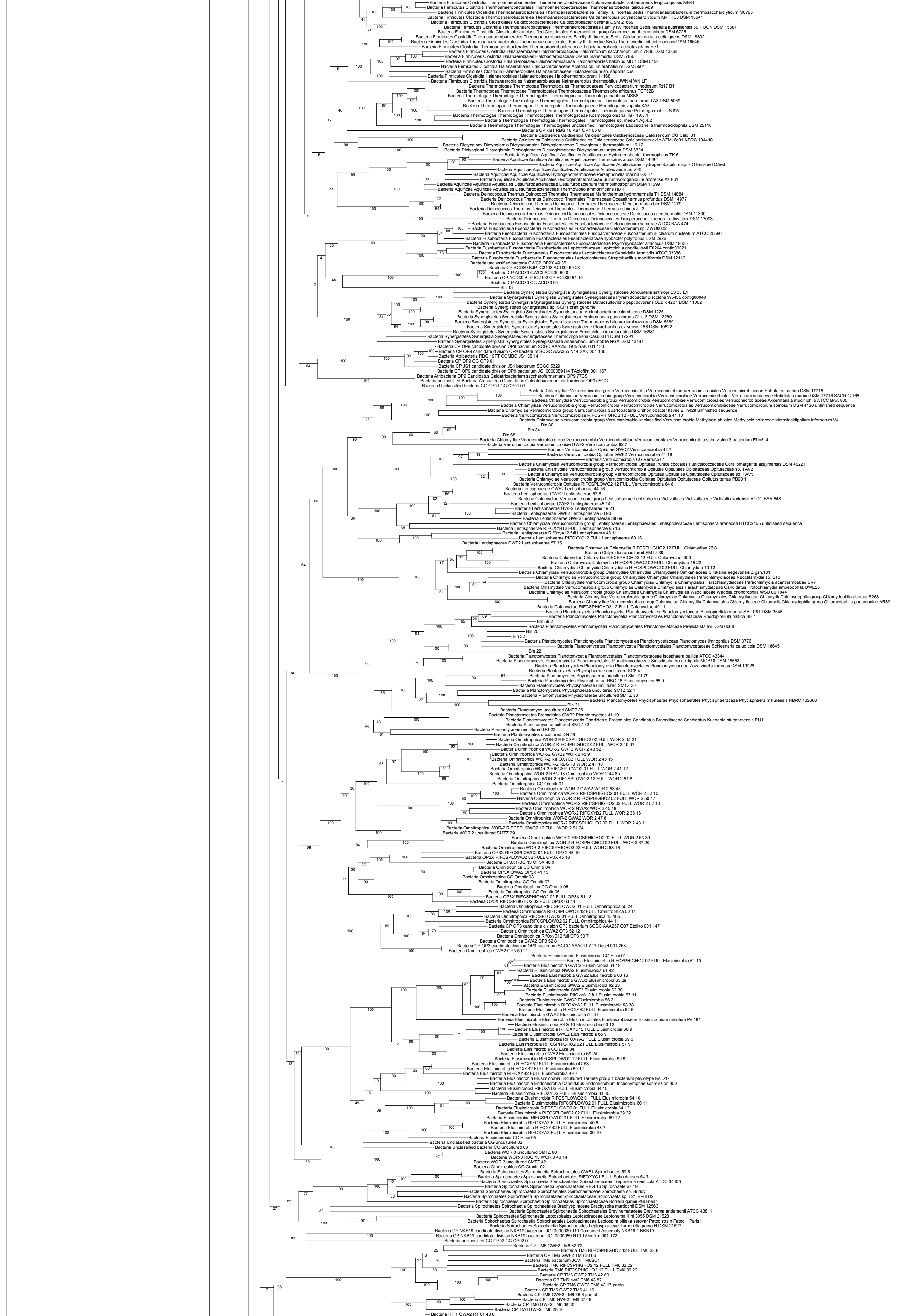
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Bacteria Aquificae Aquificae Aquificales Aquificaceae Hydrogenobacter thermophilus TK 6
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Bacteria Deinococcus Thermus Deinococci Thermales Thermaceae Thermus oshimai JL 2
Bacteria Deinococcus Thermus Deinococci Deinococcales Deinococcaceae Deinococcus geothermalis DSM 11300
Bacteria Deinococcus Thermus Deinococci Deinococcales Trueperaceae Truepera radiovictrix DSM 17093
Bacteria Fusobacteria Fusobacteriia Fusobacteriales Fusobacteriaceae Cetobacterium somerae ATCC BAA 474
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Bacteria Fusobacteria Fusobacteriia Fusobacteriales Fusobacteriaceae Psychrilyobacter atlanticus DSM 19335
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Bacteria unclassified bacteria GWC2 OP9X 49 35
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Bacteria CP ACD39 GWC2 ACD39 50 8
Bacteria CP ACD39 BJP IG2102 CP ACD39 51 10
Bacteria CP ACD39 CG ACD39 01
Bin 13
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Bacteria Synergistetes Synergistia Synergistales Synergistaceae Anaerobaculum mobile NGA DSM 13181
Bacteria CP OP9 candidate division OP9 bacterium SCGC AAA255 G05 SAK 001 130
Bacteria CP OP9 candidate division OP9 bacterium SCGC AAA255 N14 SAK 001 136
Bacteria Atribacteria RBG 19FT COMBO JS1 35 14
Bacteria CP OP9 CG OP9 01
Bacteria CP JS1 candidate division JS1 bacterium SCGC 5329
Bacteria CP OP9 candidate division OP9 bacterium JGI 0000059 I14 TAbiofilm 001 167
Bacteria Atribacteria OP9 Candidatus Caldatribacterium saccharofermentans OP9 77CS
Bacteria unclassified Bacteria Atribacteria Candidatus Caldatribacterium californiense OP9 cSCG
Bacteria Unclassified bacteria CG CP01 CG CP01 01
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Bin 34
Bin 65
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Bacteria Omnitrophica WOR-2 RIFCSPHIGHO2 02 FULL WOR 2 68 15
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Bacteria OP3X RIFCSPLOWO2 02 FULL OP3X 45 16
Bacteria OP3X RBG 13 OP3X 46 9
Bacteria Omnitrophica CG Omnitr 04
Bacteria OP3X GWA2 OP3X 41 15
Bacteria Omnitrophica CG Omnitr 03
Bacteria Omnitrophica CG Omnitr 07
Bacteria Omnitrophica CG Omnitr 05
Bacteria Omnitrophica CG Omnitr 06
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Bacteria Omnitrophica RIFCSPLOWO2 01 FULL Omnitrophica 50 24
Bacteria Omnitrophica RIFCSPLOWO2 12 FULL Omnitrophica 50 11
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Bacteria Omnitrophica RIFCSPLOWO2 02 FULL Omnitrophica 44 11
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Bacteria Omnitrophica GWA2 OP3 52 12
Bacteria Omnitrophica RifOxyB12 full OP3 50 7
Bacteria Omnitrophica GWA2 OP3 52 8
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Bacteria Omnitrophica GWA2 OP3 50 21
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Bacteria Elusimicrobia RIFCSPHIGHO2 02 FULL Elusimicrobia 61 10
Bacteria Elusimicrobia GWC2 Elusimicrobia 61 19
Bacteria Elusimicrobia GWA2 Elusimicrobia 61 42
Bacteria Elusimicrobia GWB2 Elusimicrobia 63 16
Bacteria Elusimicrobia GWD2 Elusimicrobia 63 28
Bacteria Elusimicrobia GWA2 Elusimicrobia 62 23
Bacteria Elusimicrobia GWF2 Elusimicrobia 62 30
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Bacteria Elusimicrobia GWC2 Elusimicrobia 56 31
Bacteria Elusimicrobia RIFOXYA2 FULL Elusimicrobia 53 38
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Bacteria Elusimicrobia GWA2 Elusimicrobia 51 34
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Bacteria Elusimicrobia Elusimicrobia uncultured Termite group 1 bacterium phylotype Rs D17
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Bacteria TM6 bacterium JCVI TM6SC1
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Bacteria CP TM6 GWE2 TM6 41 16
Bacteria CP TM6 GWF2 TM6 36 6 partial
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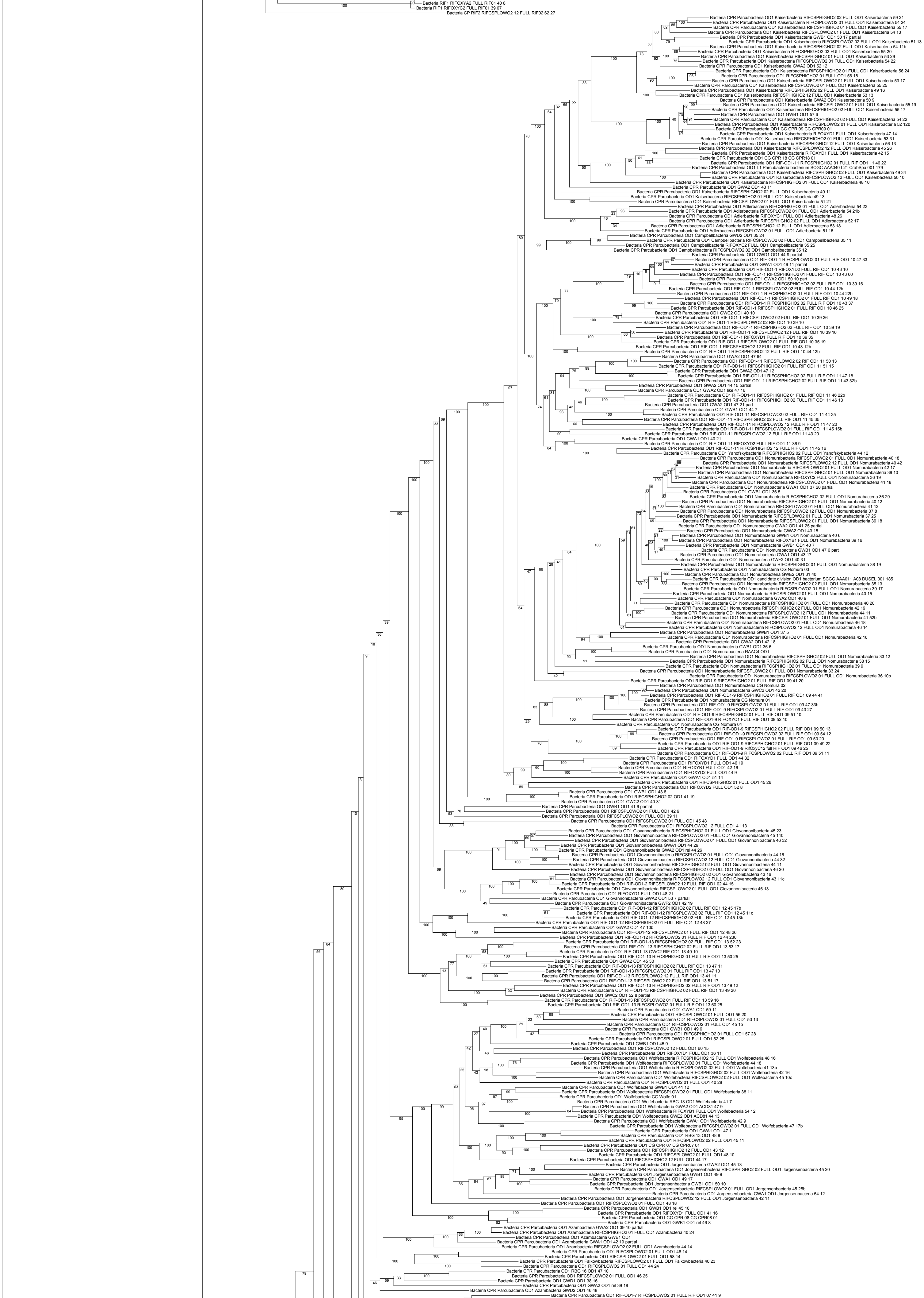
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Bacteria CPR Parcubacteria OD1 Kaiserbacteria RIFCSPLOWO2 01 FULL OD1 Kaiserbacteria 54 24
Bacteria CPR Parcubacteria OD1 Kaiserbacteria RIFCSPHIGHO2 01 FULL OD1 Kaiserbacteria 55 17
Bacteria CPR Parcubacteria OD1 Kaiserbacteria RIFCSPLOWO2 01 FULL OD1 Kaiserbacteria 54 13
Bacteria CPR Parcubacteria OD1 Kaiserbacteria GWB1 OD1 50 17 partial
Bacteria CPR Parcubacteria OD1 Kaiserbacteria RIFCSPLOWO2 02 FULL OD1 Kaiserbacteria 51 13
Bacteria CPR Parcubacteria OD1 Kaiserbacteria RIFCSPHIGHO2 02 FULL OD1 Kaiserbacteria 54 11b
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Bacteria CPR Parcubacteria OD1 Kaiserbacteria GWA2 OD1 52 12
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Bacteria CPR Parcubacteria OD1 Kaiserbacteria RIFCSPHIGHO2 01 FULL OD1 Kaiserbacteria 49 13
Bacteria CPR Parcubacteria OD1 Kaiserbacteria RIFCSPLOWO2 01 FULL OD1 Kaiserbacteria 51 21
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Bacteria CPR Parcubacteria OD1 Campbellbacteria GWD2 OD1 35 24
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Bacteria CPR Parcubacteria OD1 Campbellbacteria RIFCSPLOWO2 02 OD1 Campbellbacteria 35 12
Bacteria CPR Parcubacteria OD1 GWD1 OD1 44 9 partial
Bacteria CPR Parcubacteria OD1 RIF-OD1-1 RIFCSPLOWO2 01 FULL RIF OD1 10 47 33
Bacteria CPR Parcubacteria OD1 GWA1 OD1 49 11 partial
Bacteria CPR Parcubacteria OD1 RIF-OD1-1 RIFOXYD2 FULL RIF OD1 10 43 10
Bacteria CPR Parcubacteria OD1 RIF-OD1-1 RIFCSPHIGHO2 01 FULL RIF OD1 10 43 60
Bacteria CPR Parcubacteria OD1 GWA2 OD1 50 10 part
Bacteria CPR Parcubacteria OD1 RIF-OD1-1 RIFCSPHIGHO2 02 FULL RIF OD1 10 39 16
Bacteria CPR Parcubacteria OD1 RIF-OD1-1 RIFCSPLOWO2 02 FULL RIF OD1 10 44 12b
Bacteria CPR Parcubacteria OD1 RIF-OD1-1 RIFCSPHIGHO2 01 FULL RIF OD1 10 44 22b
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Bacteria CPR Parcubacteria OD1 RIFOXYD1 FULL OD1 48 21
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Bacteria CPR Parcubacteria OD1 Wolfebacteria RIFCSPLOWO2 01 FULL OD1 Wolfebacteria 44 18
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Bacteria CPR Parcubacteria OD1 Wolfebacteria RIFCSPHIGHO2 02 FULL OD1 Wolfebacteria 42 16
Bacteria CPR Parcubacteria OD1 Wolfebacteria RIFCSPLOWO2 02 FULL OD1 Wolfebacteria 45 10c
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Bacteria CPR Parcubacteria OD1 Wolfebacteria GWB1 OD1 41 12
Bacteria CPR Parcubacteria OD1 Wolfebacteria RIFCSPLOWO2 01 FULL OD1 Wolfebacteria 38 11
Bacteria CPR Parcubacteria OD1 Wolfebacteria CG Wolfe 01
Bacteria CPR Parcubacteria OD1 Wolfebacteria RBG 13 OD1 Wolfebacteria 41 7
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Bacteria CPR Parcubacteria OD1 Wolfebacteria RIFCSPLOWO2 01 FULL OD1 Wolfebacteria 47 17b
Bacteria CPR Parcubacteria OD1 GWA1 OD1 47 11
Bacteria CPR Parcubacteria OD1 RBG 13 OD1 48 8
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Bacteria CPR Parcubacteria OD1 RIFCSPLOWO2 01 FULL OD1 48 18
Bacteria CPR Parcubacteria OD1 GWB1 OD1 rel 45 10
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Bacteria CPR Parcubacteria OD1 CG CPR 08 CG CPR08 01
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Bacteria CPR Parcubacteria OD1 Azambacteria GWA1 OD1 42 19 partial
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Bacteria CPR Parcubacteria OD1 RIFCSPLOWO2 01 FULL OD1 46 25
Bacteria CPR Parcubacteria OD1 GWD1 OD1 38 16
Bacteria CPR Parcubacteria OD1 GWA2 OD1 rel 39 18
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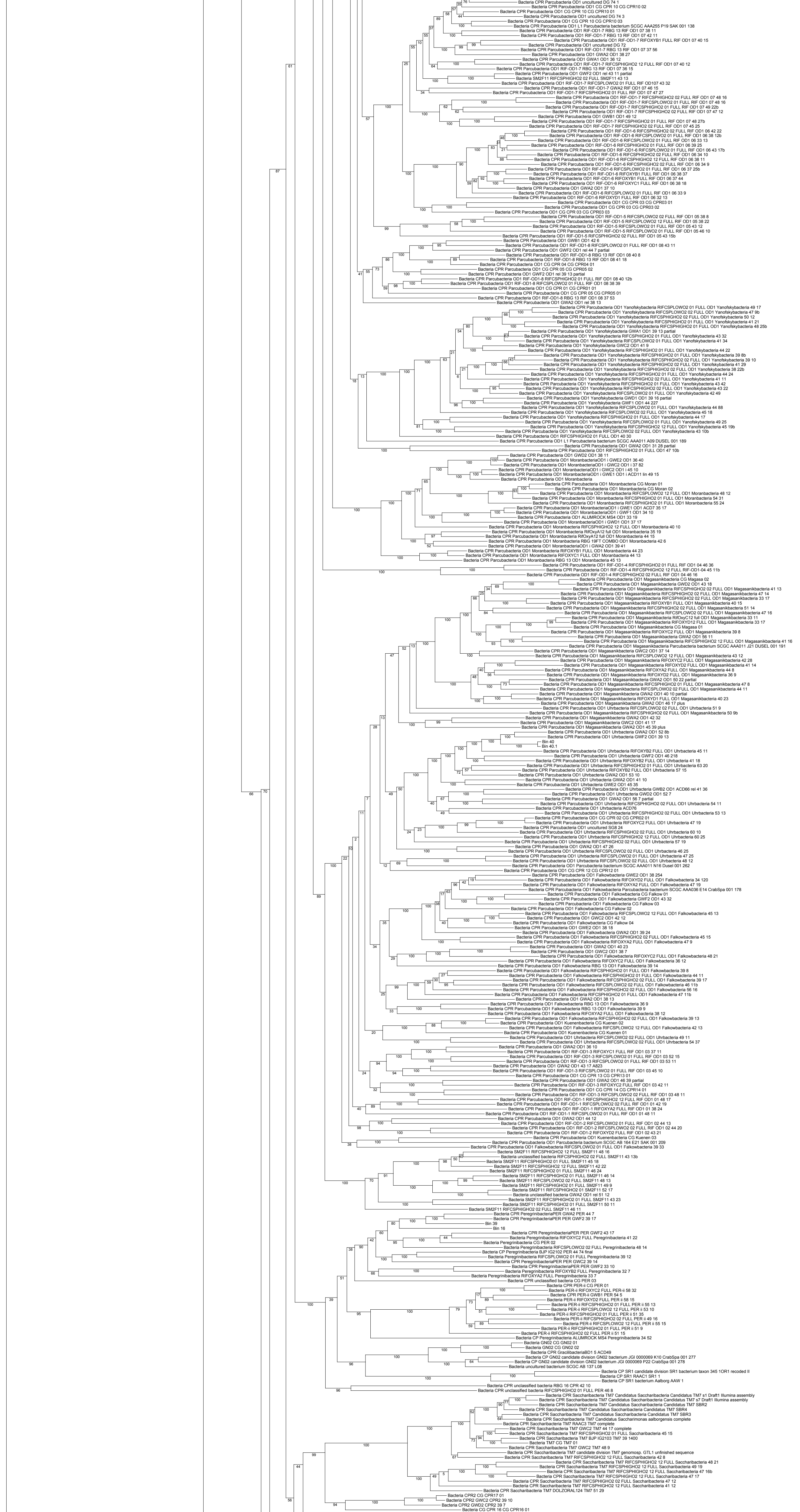
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Bacteria CPR Parcubacteria OD1 CG CPR 10 CG CPR10 03
Bacteria CPR Parcubacteria OD1 L1 Parcubacteria bacterium SCGC AAA255 P19 SAK 001 138
Bacteria CPR Parcubacteria OD1 RIF-OD1-7 RBG 13 RIF OD1 07 38 11
Bacteria CPR Parcubacteria OD1 RIF-OD1-7 RBG 13 RIF OD1 07 42 11
Bacteria CPR Parcubacteria OD1 RIF-OD1-7 RIFOXYB1 FULL RIF OD1 07 40 15
Bacteria CPR Parcubacteria OD1 uncultured DG 72
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Bacteria CPR Parcubacteria OD1 GWA2 OD1 38 27
Bacteria CPR Parcubacteria OD1 GWA1 OD1 36 12
Bacteria CPR Parcubacteria OD1 RIF-OD1-7 RIFCSPHIGHO2 12 FULL RIF OD1 07 40 12
Bacteria CPR Parcubacteria OD1 RIF-OD1-7 RBG 13 RIF OD1 07 36 15
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Bacteria SM2F11 RIFCSPHIGHO2 02 FULL SM2F11 43 13
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Bacteria CPR Parcubacteria OD1 CG CPR 05 CG CPR05 02
Bacteria CPR Parcubacteria OD1 GWF2 OD1 rel 39 13 partial
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Bacteria CPR Parcubacteria OD1 Yanofskybacteria RIFCSPHIGHO2 02 FULL OD1 Yanofskybacteria 38 22b
Bacteria CPR Parcubacteria OD1 Yanofskybacteria RIFCSPHIGHO2 01 FULL OD1 Yanofskybacteria 44 24
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Bin 40
Bin 40.1
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Bacteria CPR Parcubacteria OD1 Falkowbacteria RIFCSPHIGHO2 01 FULL OD1 Falkowbacteria 44 11
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Bacteria CPR Parcubacteria OD1 GWA2 OD1 36 10
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Bacteria CPR Parcubacteria OD1 RIF-OD1-2 RIFCSPLOWO2 02 FULL RIF OD1 02 44 20
Bacteria CPR Parcubacteria OD1 RIF-OD1-2 RIFOXYD2 FULL RIF OD1 02 43 21
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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
Bacteria SM2F11 RIFCSPHIGHO2 01 FULL SM2F11 45 18
Bacteria SM2F11 RIFCSPHIGHO2 12 FULL SM2F11 42 22
Bacteria SM2F11 RIFCSPHIGHO2 01 FULL SM2F11 46 24
Bacteria SM2F11 RIFCSPHIGHO2 01 FULL SM2F11 46 14
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Bacteria SM2F11 RIFCSPHIGHO2 01 FULL SM2F11 49 9
Bacteria SM2F11 RIFCSPHIGHO2 01 SM2F11 52 17
Bacteria unclassified bacteria GWA2 OD1 rel 51 12
Bacteria SM2F11 RIFCSPHIGHO2 01 FULL SM2F11 43 23
Bacteria SM2F11 RIFCSPHIGHO2 01 FULL SM2F11 50 11
Bacteria SM2F11 RIFCSPHIGHO2 02 FULL SM2F11 46 11
Bacteria CPR PeregrinibacteriaPER GWA2 PER 44 7
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 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
Bacteria CPR PeregrinibacteriaPER PER GWC2 39 14
Bacteria CPR PeregrinibacteriaPER PER GWF2 33 10
Bacteria Peregrinibacteria RIFOXYB2 FULL Peregrinibacteria 32 7
Bacteria Peregrinibacteria RIFOXYA2 FULL Peregrinibacteria 33 7
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 02 FULL PER ii 49 16
Bacteria PER-ii RIFCSPLOWO2 12 FULL PER ii 55 15
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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
Bacteria CPR unclassified bacteria RIFCSPHIGHO2 01 FULL PER 46 8
Bacteria CPR Saccharibacteria TM7 Candidatus Saccharibacteria Candidatus TM7 s1 Draft1 Illumina assembly
Bacteria CPR Saccharibacteria TM7 Candidatus Saccharibacteria Candidatus TM7 s7 Draft1 Illumina assembly
Bacteria CPR Saccharibacteria TM7 Candidatus Saccharibacteria Candidatus TM7 SBR2
Bacteria CPR Saccharibacteria TM7 Candidatus Saccharibacteria Candidatus TM7 SBR4
Bacteria CPR Saccharibacteria TM7 Candidatus Saccharibacteria Candidatus TM7 SBR3
Bacteria CPR Saccharibacteria TM7 Candidatus Saccharimonas aalborgensis complete
Bacteria CPR Saccharibacteria TM7 RAAC3 TM7 complete
Bacteria CPR Saccharibacteria TM7 GWC2 TM7 44 17 complete
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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
Bacteria CPR Saccharibacteria TM7 RIFCSPHIGHO2 12 FULL Saccharibacteria 42 8
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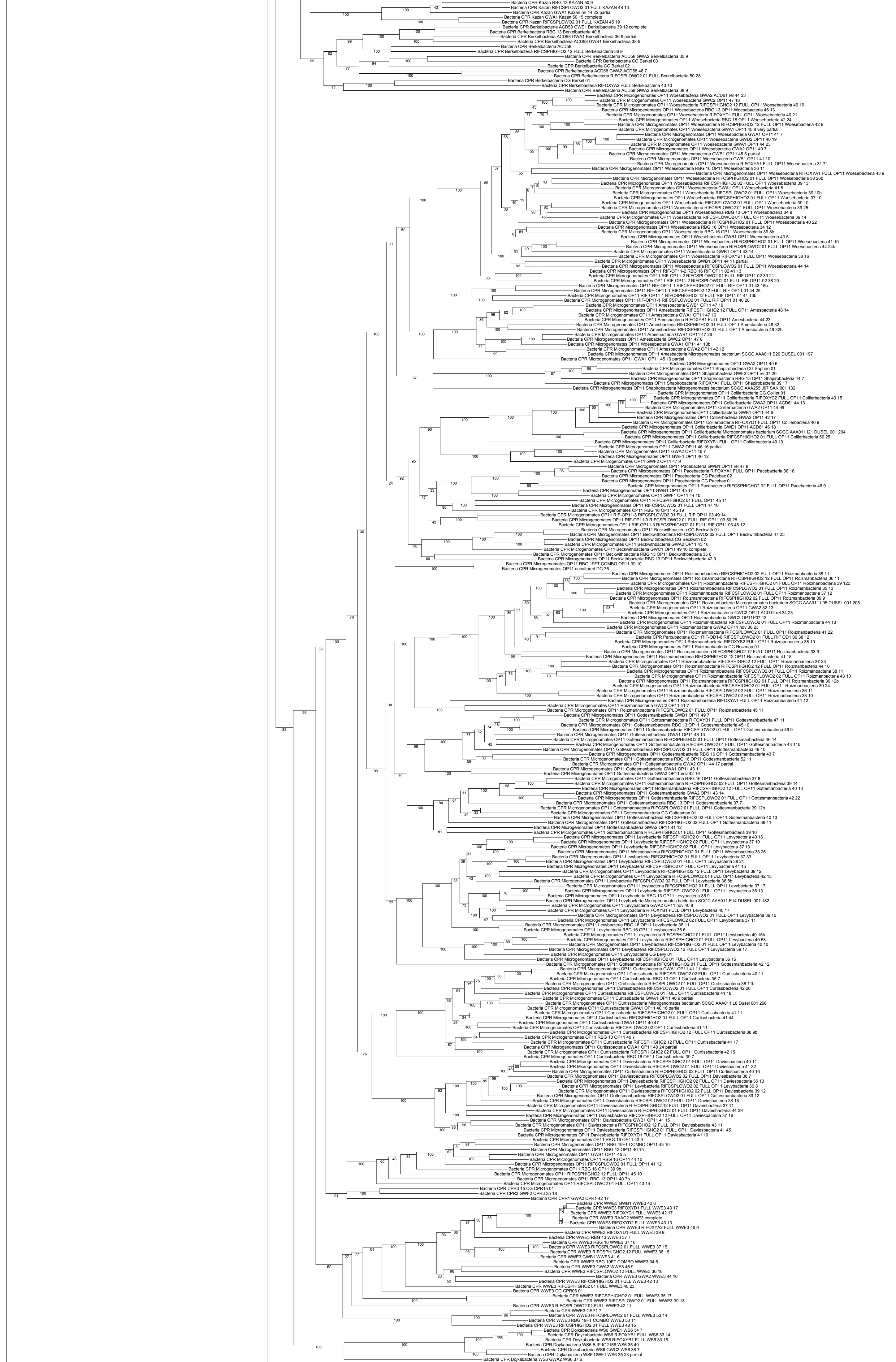
Bacteria CPR Saccharibacteria TM7 RIFCSPHIGHO2 12 FULL Saccharibacteria 47 16b
Bacteria CPR Saccharibacteria TM7 RIFCSPHIGHO2 12 FULL Saccharibacteria 47 17
Bacteria CPR Saccharibacteria TM7 RIFCSPHIGHO2 02 FULL Saccharibacteria 47 12
Bacteria CPR Saccharibacteria TM7 RIFCSPHIGHO2 12 FULL Saccharibacteria 41 12
Bacteria CPR Saccharibacteria TM7 DOLZORAL124 TM7 51 29
Bacteria CPR2 CG CPR17 01
Bacteria CPR2 GWC2 CPR2 39 10
Bacteria CPR2 GWD2 CPR2 39 7
Bacteria CG CPR 16 CG CPR16 01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Bacteria CPR Kazan RIFCSPLOWO2 01 FULL KAZAN 48 13
Bacteria CPR Kazan GWA1 Kazan rel 44 22 partial
Bacteria CPR Kazan GWA1 Kazan 50 15 complete
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
Bacteria CPR Microgenomates OP11 Woesebacteria GWA2 ACD61 rel 44 33
Bacteria CPR Microgenomates OP11 Woesebacteria GWC2 OP11 47 16
Bacteria CPR Microgenomates OP11 Woesebacteria RIFCSPHIGHO2 12 FULL OP11 Woesebacteria 46 16
Bacteria CPR Microgenomates OP11 Woesebacteria RBG 13 OP11 Woesebacteria 46 13
Bacteria CPR Microgenomates OP11 Woesebacteria RIFOXYD1 FULL OP11 Woesebacteria 40 21
Bacteria CPR Microgenomates OP11 Woesebacteria RBG 16 OP11 Woesebacteria 42 24
Bacteria CPR Microgenomates OP11 Woesebacteria RIFCSPHIGHO2 12 FULL OP11 Woesebacteria 42 9
Bacteria CPR Microgenomates OP11 Woesebacteria GWA1 OP11 45 8 very partial
Bacteria CPR Microgenomates OP11 Woesebacteria GWA1 OP11 41 7
Bacteria CPR Microgenomates OP11 Woesebacteria GWD2 OP11 40 19
Bacteria CPR Microgenomates OP11 Woesebacteria GWA1 OP11 44 23
Bacteria CPR Microgenomates OP11 Woesebacteria GWA2 OP11 40 7
Bacteria CPR Microgenomates OP11 Woesebacteria GWB1 OP11 45 5 partial
Bacteria CPR Microgenomates OP11 Woesebacteria GWB1 OP11 41 10
Bacteria CPR Microgenomates OP11 Woesebacteria RIFOXYA1 FULL OP11 Woesebacteria 31 71
Bacteria CPR Microgenomates OP11 Woesebacteria RBG 16 OP11 Woesebacteria 36 11
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Bacteria CPR Microgenomates OP11 Woesebacteria RIFCSPHIGHO2 01 FULL OP11 Woesebacteria 38 26b
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Bacteria CPR Microgenomates OP11 Woesebacteria GWA1 OP11 Woesebacteria 41 8
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Bacteria CPR Microgenomates OP11 Woesebacteria RIFCSPLOWO2 01 FULL OP11 Woesebacteria 39 25
Bacteria CPR Microgenomates OP11 Woesebacteria RBG 13 OP11 Woesebacteria 34 9
Bacteria CPR Microgenomates OP11 Woesebacteria RIFCSPLOWO2 01 FULL OP11 Woesebacteria 39 14
Bacteria CPR Microgenomates OP11 Woesebacteria RIFCSPHIGHO2 01 FULL OP11 Woesebacteria 40 22
Bacteria CPR Microgenomates OP11 Woesebacteria RBG 16 OP11 Woesebacteria 34 12
Bacteria CPR Microgenomates OP11 Woesebacteria RBG 16 OP11 Woesebacteria 39 8b
Bacteria CPR Microgenomates OP11 Woesebacteria GWB1 OP11 Woesebacteria 43 5
Bacteria CPR Microgenomates OP11 Woesebacteria RIFCSPHIGHO2 01 FULL OP11 Woesebacteria 41 10
Bacteria CPR Microgenomates OP11 Woesebacteria RIFCSPLOWO2 01 FULL OP11 Woesebacteria 44 24b
Bacteria CPR Microgenomates OP11 Woesebacteria GWB1 OP11 43 14
Bacteria CPR Microgenomates OP11 Woesebacteria RIFOXYB1 FULL OP11 Woesebacteria 38 16
Bacteria CPR Microgenomates OP11 Woesebacteria GWB1 OP11 44 11 partial
Bacteria CPR Microgenomates OP11 Woesebacteria RIFCSPLOWO2 01 FULL OP11 Woesebacteria 44 14
Bacteria CPR Microgenomates OP11 RIF-OP11-2 RBG 16 RIF OP11 02 41 13
Bacteria CPR Microgenomates OP11 RIF-OP11-2 RIFCSPLOWO2 01 FULL RIF OP11 02 39 21
Bacteria CPR Microgenomates OP11 RIF-OP11-2 RIFCSPLOWO2 01 FULL RIF OP11 02 38 20
Bacteria CPR Microgenomates OP11 RIF-OP11-1 RIFCSPHIGHO2 01 FULL RIF OP11 01 43 15b
Bacteria CPR Microgenomates OP11 RIF-OP11-1 RIFCSPHIGHO2 12 FULL RIF OP11 01 44 25
Bacteria CPR Microgenomates OP11 RIF-OP11-1 RIFCSPHIGHO2 12 FULL RIF OP11 01 41 13b
Bacteria CPR Microgenomates OP11 RIF-OP11-1 RIFCSPLOWO2 01 FULL RIF OP11 01 40 20
Bacteria CPR Microgenomates OP11 Amesbacteria GWB1 OP11 47 19
Bacteria CPR Microgenomates OP11 Amesbacteria RIFCSPHIGHO2 12 FULL OP11 Amesbacteria 48 14
Bacteria CPR Microgenomates OP11 Amesbacteria GWA1 OP11 47 16
Bacteria CPR Microgenomates OP11 Amesbacteria RIFOXYB1 FULL OP11 Amesbacteria 44 23
Bacteria CPR Microgenomates OP11 Amesbacteria RIFCSPHIGHO2 01 FULL OP11 Amesbacteria 48 32
Bacteria CPR Microgenomates OP11 Amesbacteria RIFCSPHIGHO2 01 FULL OP11 Amesbacteria 48 32b
Bacteria CPR Microgenomates OP11 Amesbacteria GWB1 OP11 47 26
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Bacteria CPR Microgenomates OP11 Collierbacteria GWB1 OP11 44 6
Bacteria CPR Microgenomates OP11 Collierbacteria GWA2 OP11 42 17
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Bacteria CPR Microgenomates OP11 Collierbacteria GWE1 OP11 ACD61 46 18
Bacteria CPR Microgenomates OP11 Collierbacteria Microgenomates bacterium SCGC AAA011 I21 DUSEL 001 204
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Bacteria CPR Microgenomates OP11 GWA2 OP11 46 16 partial
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Bacteria CPR Microgenomates OP11 GWF2 OP11 47 9
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Bacteria CPR Microgenomates OP11 GWF1 OP11 44 10
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Bacteria CPR Microgenomates OP11 RBG 16 OP11 45 19
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Bacteria CPR Microgenomates OP11 Roizmanbacteria RIFCSPHIGHO2 12 FULL OP11 Roizmanbacteria 37 23
Bacteria CPR Microgenomates OP11 Roizmanbacteria RIFCSPHIGHO2 12 FULL OP11 Roizmanbacteria 44 10
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Bacteria CPR Microgenomates OP11 Roizmanbacteria RIFCSPHIGHO2 01 FULL OP11 Roizmanbacteria 39 24
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Bacteria CPR Microgenomates OP11 Roizmanbacteria RIFOXYA1 FULL OP11 Roizmanbacteria 41 12
Bacteria CPR Microgenomates OP11 Roizmanbacteria GWC2 OP11 41 7
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Bacteria CPR Microgenomates OP11 Gottesmanbacteria GWB1 OP11 49 7
Bacteria CPR Microgenomates OP11 Gottesmanbacteria RIFOXYB1 FULL OP11 Gottesmanbacteria 47 11
Bacteria CPR Microgenomates OP11 Gottesmanbacteria RBG 13 OP11 Gottesmanbacteria 45 10
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Bacteria CPR Microgenomates OP11 Gottesmanbacteria GWA1 OP11 43 11
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Bacteria CPR Microgenomates OP11 Levybacteria RIFCSPHIGHO2 01 FULL OP11 Levybacteria 37 17
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Bacteria CPR Microgenomates OP11 Levybacteria RIFOXYB1 FULL OP11 Levybacteria 40 17
Bacteria CPR Microgenomates OP11 Levybacteria RIFCSPLOWO2 01 FULL OP11 Levybacteria 39 10
Bacteria CPR Microgenomates OP11 Levybacteria RIFCSPLOWO2 02 FULL OP11 Levybacteria 37 11
Bacteria CPR Microgenomates OP11 Levybacteria RBG 16 OP11 Levybacteria 35 11
Bacteria CPR Microgenomates OP11 Levybacteria RBG 16 OP11 Levybacteria 35 6
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Bacteria CPR Microgenomates OP11 Levybacteria RIFCSPLOWO2 12 FULL OP11 Levybacteria 39 17
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Bacteria CPR Microgenomates OP11 Levybacteria RIFCSPLOWO2 02 FULL OP11 Levybacteria 36 8
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Bacteria CPR Microgenomates OP11 Daviesbacteria RIFCSPHIGHO2 12 FULL OP11 Daviesbacteria 37 11
Bacteria CPR Microgenomates OP11 Daviesbacteria RIFCSPHIGHO2 01 FULL OP11 Daviesbacteria 44 29
Bacteria CPR Microgenomates OP11 Daviesbacteria RIFCSPHIGHO2 12 FULL OP11 Daviesbacteria 37 16
Bacteria CPR Microgenomates OP11 Daviesbacteria GWB1 OP11 41 15
Bacteria CPR Microgenomates OP11 Daviesbacteria RIFCSPHIGHO2 12 FULL OP11 Daviesbacteria 43 11
Bacteria CPR Microgenomates OP11 Daviesbacteria RIFCSPHIGHO2 01 FULL OP11 Daviesbacteria 41 45
Bacteria CPR Microgenomates OP11 Daviesbacteria RIFOXYD1 FULL OP11 Daviesbacteria 41 10
Bacteria CPR Microgenomates OP11 RBG 16 OP11 43 9
Bacteria CPR Microgenomates OP11 RBG 19FT COMBO OP11 43 10
Bacteria CPR Microgenomates OP11 RBG 13 OP11 40 15
Bacteria CPR Microgenomates OP11 GWB1 OP11 45 5
Bacteria CPR Microgenomates OP11 RBG 16 OP11 44 10
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Bacteria CPR Microgenomates OP11 RBG 13 OP11 40 7b
Bacteria CPR Microgenomates OP11 RIFCSPLOWO2 01 FULL OP11 43 14
Bacteria CPR CPR3 15 CG CPR15 01
Bacteria CPR CPR3 GWF2 CPR3 35 18
Bacteria CPR CPR1 GWA2 CPR1 42 17
Bacteria CPR WWE3 GWB1 WWE3 42 6
Bacteria CPR WWE3 RIFOXYD1 FULL WWE3 43 17
Bacteria CPR WWE3 RIFOXYC1 FULL WWE3 42 17
Bacteria CPR WWE3 RAAC2 WWE3 complete
Bacteria CPR WWE3 RIFOXYD2 FULL WWE3 43 10
Bacteria CPR WWE3 RIFOXYA2 FULL WWE3 46 9
Bacteria CPR WWE3 RIFOXYD1 FULL WWE3 39 9
Bacteria CPR WWE3 RBG 13 WWE3 37 7
Bacteria CPR WWE3 RBG 16 WWE3 37 10
Bacteria CPR WWE3 RIFCSPLOWO2 01 FULL WWE3 37 15
Bacteria CPR WWE3 RIFCSPHIGHO2 12 FULL WWE3 38 15
Bacteria CPR WWE3 GWB1 WWE3 41 6
Bacteria CPR WWE3 RBG 19FT COMBO WWE3 34 6
Bacteria CPR WWE3 GWA2 WWE3 46 9
Bacteria CPR WWE3 RIFCSPLOWO2 12 FULL WWE3 36 10
Bacteria CPR WWE3 GWA2 WWE3 44 16
Bacteria CPR WWE3 RIFCSPHIGHO2 01 FULL WWE3 42 13
Bacteria CPR WWE3 RIFCSPHIGHO2 01 FULL WWE3 40 23
Bacteria CPR WWE3 CG CPR06 01
Bacteria CPR WWE3 RIFCSPHIGHO2 01 FULL WWE3 35 17
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Bacteria CPR WWE3 CSP1 7
Bacteria CPR WWE3 RIFCSPLOWO2 01 FULL WWE3 53 14
Bacteria CPR WWE3 RBG 19FT COMBO WWE3 53 11
Bacteria CPR WWE3 RIFCSPHIGHO2 01 FULL WWE3 48 15
Bacteria CPR Dojkabacteria WS6 GWE1 WS6 34 7
Bacteria CPR Dojkabacteria WS6 RIFOXYB1 FULL WS6 33 14
Bacteria CPR Dojkabacteria WS6 RIFOXYB1 FULL WS6 33 15
Bacteria CPR Dojkabacteria WS6 BJP IG2158 WS6 35 49
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Bacteria CPR Dojkabacteria WS6 GWF1 WS6 35 23 partial
Bacteria CPR Dojkabacteria WS6 GWA2 WS6 37 6

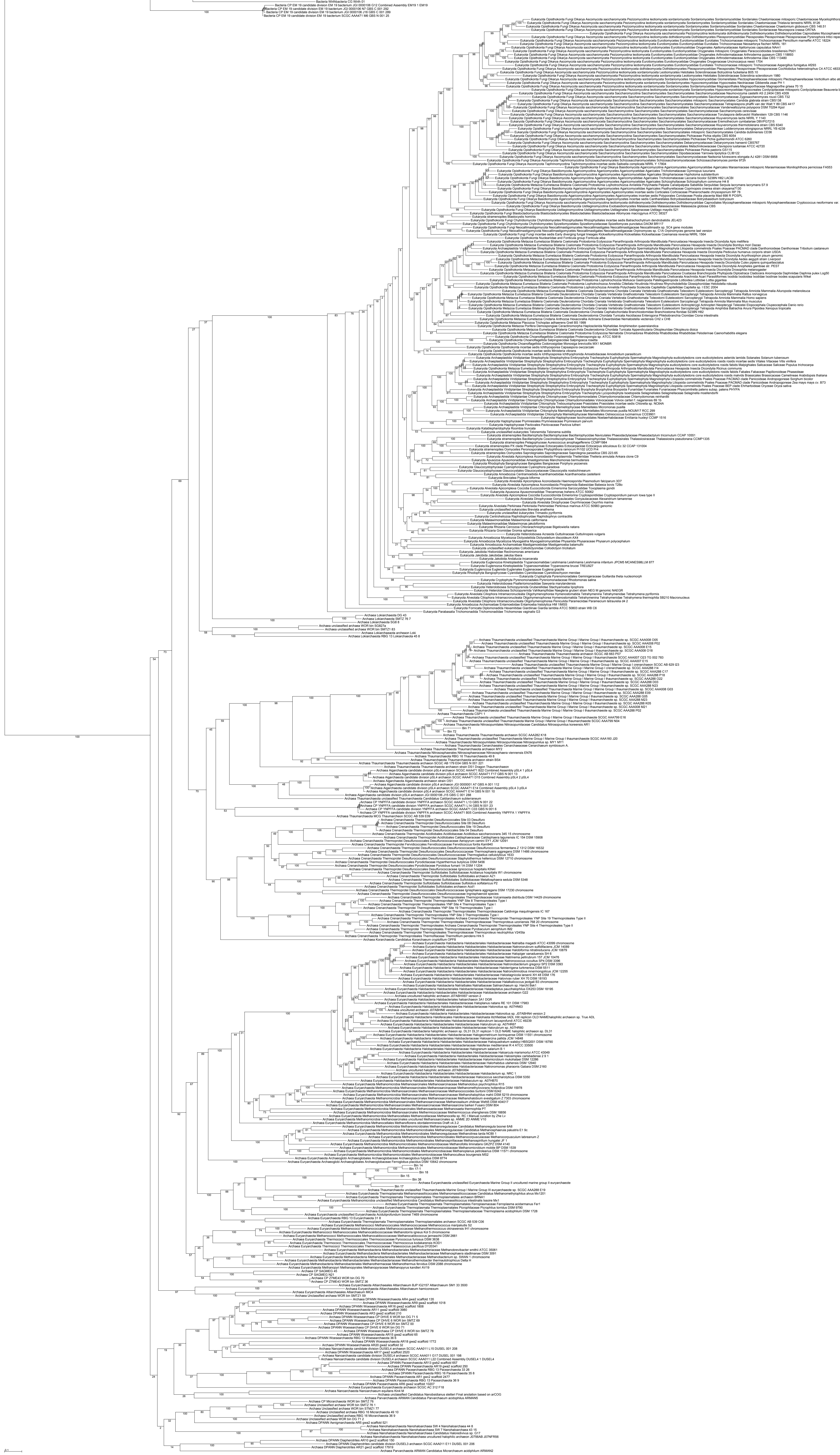
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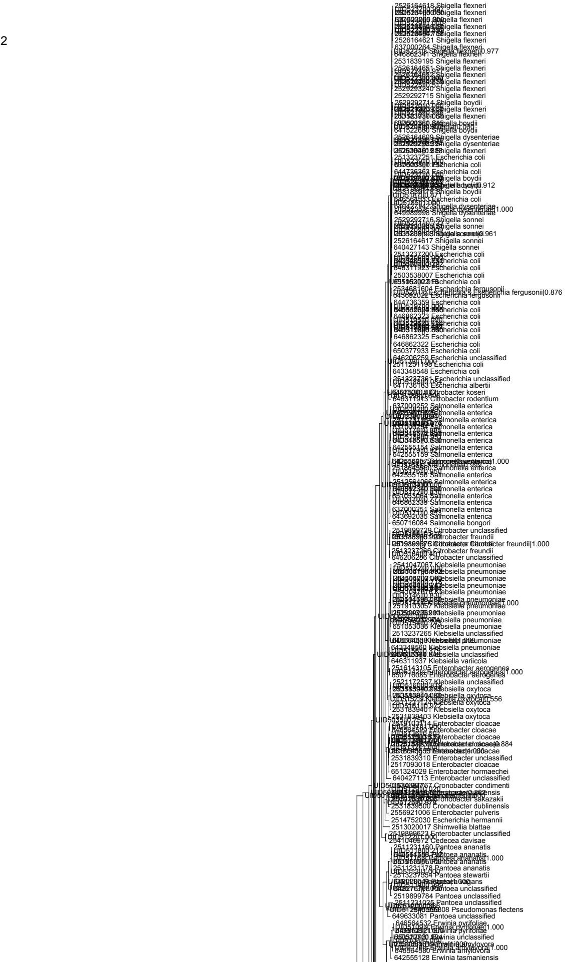
Figure S2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641522656 Shigella boydii
2526164609 Shigella dysenteriae
2513237251 Escherichia coli
644736363 Escherichia coli
649989906 Shigella dysenteriae
2529292716 Shigella sonnei
2526164617 Shigella sonnei
640427143 Shigella sonnei
2513237200 Escherichia coli
646311923 Escherichia coli
2503538007 Escherichia coli
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644736359 Escherichia coli
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646206259 Escherichia unclassified
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646311913 Citrobacter rodentium
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2521172537 Klebsiella unclassified
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Cronobacter condimenti
Cronobacter sakazakii
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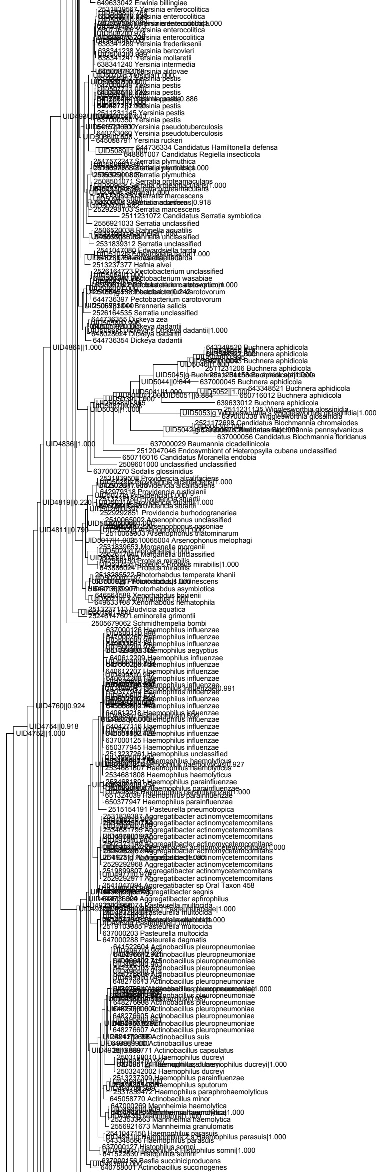
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Yersinia aldovae
Yersinia pestis
Yersinia pestis
Yersinia pestis
Yersinia pestis
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637000350 Yersinia pestis
Yersinia pseudotuberculosis
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648861007 Candidatus Regiella insecticola
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Serratia plymuthica
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Serratia marcescens
2529293103 Serratia marcescens
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Rahnella unclassified
2531839312 Serratia unclassified
2541047080 Edwardsiella tarda
2513237377 Hafnia alvei
2526164723 Pectobacterium unclassified
Pectobacterium wasabiae
Pectobacterium carotovorum
644736397 Pectobacterium carotovorum
Brenneria salicis
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Dickeya dadantii|1.000
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644736354 Dickeya dadantii
UID4864||1.000
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Buchnera aphidicola
Buchnera aphidicola
2511231206 Buchnera aphidicola
UID5045|g Buchnera
UID5044||0.844
637000045 Buchnera aphidicola
UID5041||1.000
UID5052||1.000
643348521 Buchnera aphidicola
650716012 Buchnera aphidicola
639633012 Buchnera aphidicola
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UID5053|g Wigglesworthia|s Wigglesworthia glossinidia|1.000
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Candidatus Blochmannia pennsylvanicus
637000056 Candidatus Blochmannia floridanus
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UID4836||1.000
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Providencia alcalifaciens
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Providencia stuartii
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Morganella unclassified
Proteus mirabilis
Proteus mirabilis|1.000
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Photorhabdus luminescens
Photorhabdus asymbiotica
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649633108 Xenorhabdus nematophila
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2524614760 Leminorella grimontii
2505679062 Schmidhempelia bombi
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Haemophilus influenzae
Haemophilus influenzae
Haemophilus aegyptius
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Haemophilus influenzae
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Haemophilus influenzae
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Haemophilus influenzae
Haemophilus influenzae
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Haemophilus influenzae
640427116 Haemophilus influenzae
Haemophilus influenzae
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Haemophilus haemolyticus
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Haemophilus parainfluenzae|1.000
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650377947 Haemophilus parainfluenzae
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Aggregatibacter actinomycetemcomitans
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Aggregatibacter actinomycetemcomitans
Aggregatibacter actinomycetemcomitans|1.000
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Actinobacillus pleuropneumoniae
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Actinobacillus pleuropneumoniae
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Actinobacillus pleuropneumoniae
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Haemophilus sputorum
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Mannheimia haemolytica|1.000
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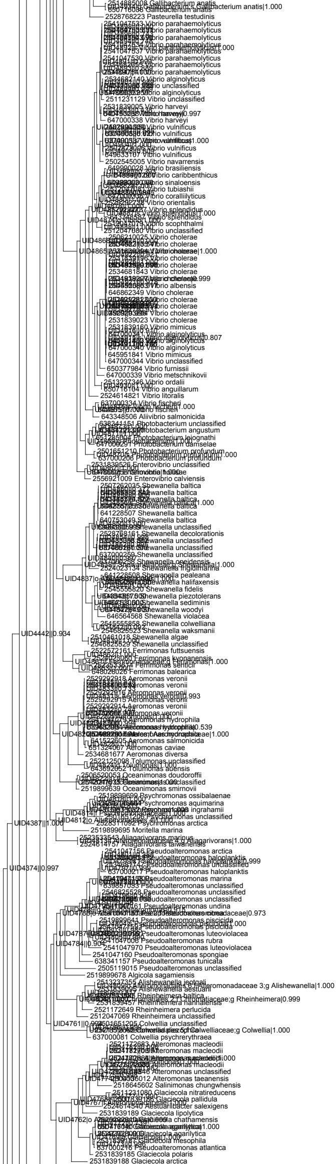
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Vibrio parahaemolyticus
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Vibrio parahaemolyticus|1.000
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Vibrio parahaemolyticus
Vibrio parahaemolyticus
2534682140 Vibrio alginolyticus
Vibrio unclassified
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Vibrio scophthalmi
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Vibrio cholerae
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Photobacterium profundum|1.000
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Shewanella baltica
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Psychromonas aquimarina
Psychromonas ingrahamii
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UID4787
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Alteromonas unclassified
Alteromonas taeanensis
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Glaciecola pallidula
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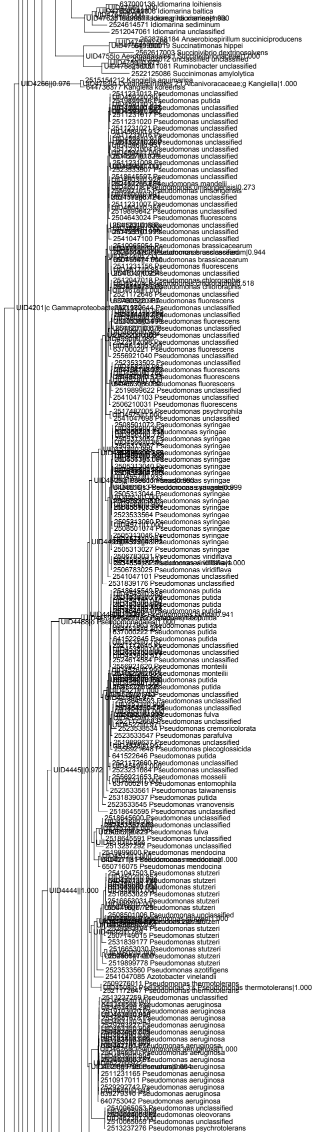
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Pseudomonas umsongensis
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Pseudomonas thermotolerans|1.000
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Pseudomonas aeruginosa
Pseudomonas aeruginosa|1.000
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2510917011 Pseudomonas aeruginosa
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Pseudomonas oleovorans
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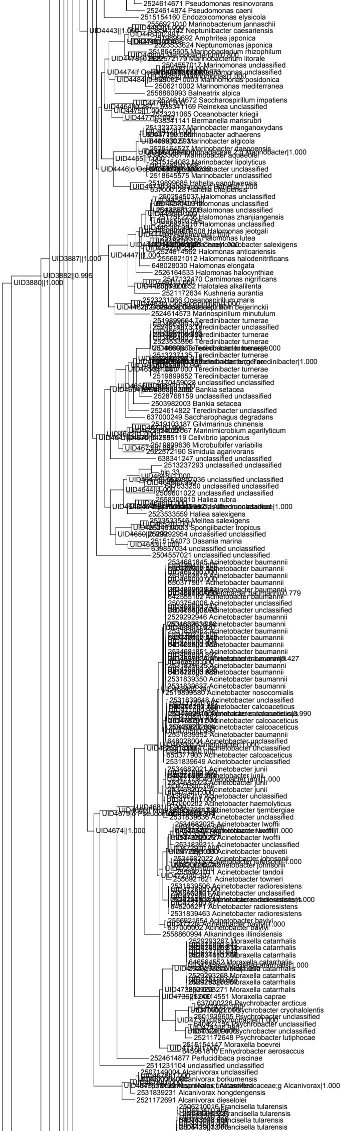
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UID4464||0.287
UID4475||1.000
2523231065 Oceanobacter kriegii
UID4477||0.950
638341141 Bermanella marisrubri
2513237337 Marinobacter manganoxydans
Marinobacter adhaerens
Marinobacter algicola
2526164527 Marinobacter daepoensis
Marinobacter aquaeolei
Marinobacter|1.000
UID4465||1.000
2513154082 Marinobacter lipolyticus
UID4446|o Oceanospirillales
Marinobacter unclassified
2518645575 Marinobacter unclassified
2519899685 Hahella ganghwensis
Hahella|1.000
637000126 Hahella chejuensis
2502545037 Halomonas unclassified
Halomonas unclassified
Halomonas unclassified
2517572236 Halomonas zhanjiangensis
Halomonas unclassified
Halomonas jeotgali
Halomonas lutea
Chromohalobacter salexigens
2524614562 Halomonas anticariensis
UID4447||1.000
2556921012 Halomonas halodenitrificans
648028030 Halomonas elongata
2526164533 Halomonas halocynthiae
2547132470 Carnimonas nigrificans
Halotalea alkalilenta
2521172634 Kushneria aurantia
2523231066 Oceanospirillum maris
Oceanospirillum beijerinckii
UID4462
2524614573 Marinospirillum minutulum
UID3887||1.000
UID3882||0.995
UID3880||1.000
2519899664 Teredinibacter turnerae
2524614873 Teredinibacter unclassified
Teredinibacter turnerae
2523533596 Teredinibacter turnerae
Teredinibacter turnerae|1.000
2513237135 Teredinibacter turnerae
Teredinibacter|1.000
Teredinibacter unclassified
2519899652 Teredinibacter turnerae
2170459028 unclassified unclassified
Bankia setacea
2528768159 unclassified unclassified
2503982003 Bankia setacea
2524614822 Teredinibacter unclassified
637000249 Saccharophagus degradans
2519103187 Gilvimarinus chinensis
Marinimicrobium agarilyticum
Cellvibrio japonicus
2519899636 Microbulbifer variabilis
2522572190 Simiduia agarivorans
638341247 unclassified unclassified
2513237293 unclassified unclassified
bin 33
unclassified unclassified
unclassified unclassified
UID4644||1.000
2509601022 unclassified unclassified
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Alteromonadales|1.000
2523533559 Haliea salexigens
2523533546 Melitea salexigens
Spongiibacter tropicus
UID4650||0.992
unclassified unclassified
2515154073 Dasania marina
639857034 unclassified unclassified
2504557021 unclassified unclassified
2534681845 Acinetobacter baumannii
Acinetobacter baumannii
Acinetobacter baumannii
650377901 Acinetobacter baumannii
Acinetobacter baumannii
Acinetobacter baumannii|0.779
642555102 Acinetobacter baumannii
2503754006 Acinetobacter unclassified
Acinetobacter unclassified
2529292946 Acinetobacter baumannii
Acinetobacter baumannii
Acinetobacter baumannii
Acinetobacter baumannii
Acinetobacter baumannii
Acinetobacter baumannii
Acinetobacter baumannii|0.427
Acinetobacter baumannii
Acinetobacter baumannii
2531839350 Acinetobacter baumannii
2531839637 Acinetobacter baumannii
2519899580 Acinetobacter nosocomialis
2531839648 Acinetobacter unclassified
Acinetobacter calcoaceticus
Acinetobacter calcoaceticus|0.990
Acinetobacter calcoaceticus
Acinetobacter calcoaceticus
2531839552 Acinetobacter baumannii
648028004 Acinetobacter unclassified
Acinetobacter|1.000
Acinetobacter unclassified
650377903 Acinetobacter calcoaceticus
2531839649 Acinetobacter unclassified
2534682021 Acinetobacter junii
Acinetobacter junii
Acinetobacter junii|1.000
Acinetobacter junii
Acinetobacter junii
Acinetobacter unclassified
647000202 Acinetobacter haemolyticus
Acinetobacter tjernbergiae
UID4679|o Pseudomonadales
2531839536 Acinetobacter unclassified
UID4674||1.000
2534682025 Acinetobacter lwoffii
Acinetobacter lwoffii|1.000
Acinetobacter lwoffii
2531839311 Acinetobacter unclassified
Acinetobacter bouvetii
2534682022 Acinetobacter johnsonii
Acinetobacter johnsonii|1.000
Acinetobacter johnsonii
2556921011 Acinetobacter tandoii
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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
646564552 Moraxella catarrhalis
Moraxella catarrhalis|1.000
2529293268 Moraxella catarrhalis
Moraxella catarrhalis
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2524614551 Moraxella caprae
637000226 Psychrobacter arcticus
Psychrobacter cryohalolentis
2501939605 Psychrobacter unclassified
Psychrobacter|1.000
Psychrobacter unclassified
Psychrobacter unclassified
2521172648 Psychrobacter lutiphocae
2515154147 Moraxella boevrei
643581810 Enhydrobacter aerosaccus
2524614877 Perlucidibaca piscinae
2511231104 unclassified unclassified
2507149004 Alcanivorax unclassified
Alcanivorax borkumensis
Alcanivoracaceae;g Alcanivorax|1.000
2531839231 Alcanivorax hongdengensis
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2506210016 Francisella tularensis
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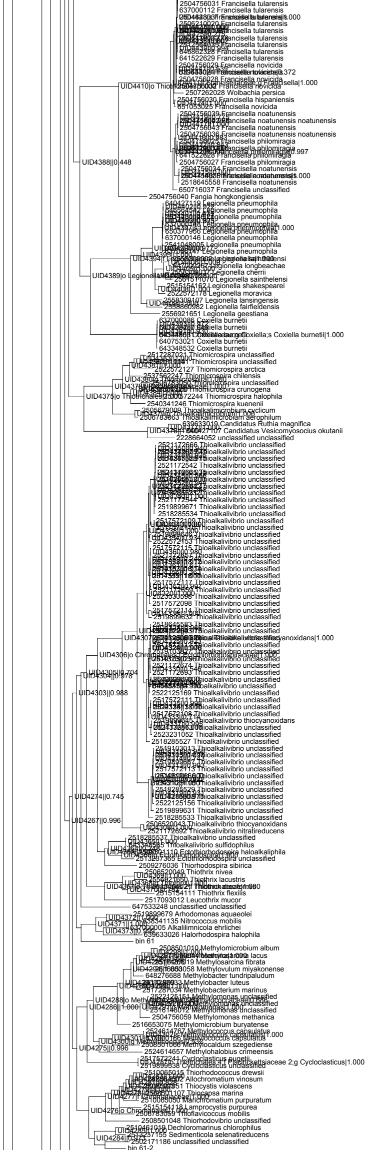
Francisella tularensis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2504756028 Francisella novicida
UID4410|o Thiotrichales
2507262028 Wolbachia persica
2504756030 Francisella hispaniensis
651053025 Francisella novicida
2504756039 Francisella noatunensis
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Francisella 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
UID4394
Legionella longbeachae
Legionella cherrii
2561511070 Legionella sainthelensi
2515154162 Legionella shakespearei
UID4389|o Legionellales
2522572178 Legionella moravica
2558309107 Legionella lansingensis
2558860982 Legionella fairfieldensis
2556921651 Legionella geestiana
637000086 Coxiella burnetii
Coxiella burnetii
Coxiella;s Coxiella burnetii|1.000
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
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2521172542 Thioalkalivibrio unclassified
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2519899671 Thioalkalivibrio unclassified
2518285534 Thioalkalivibrio unclassified
2517572109 Thioalkalivibrio unclassified
2522572153 Thioalkalivibrio unclassified
2517572115 Thioalkalivibrio unclassified
2517572117 Thioalkalivibrio unclassified
2523533598 Thioalkalivibrio unclassified
2517572098 Thioalkalivibrio unclassified
2517572114 Thioalkalivibrio unclassified
2519899632 Thioalkalivibrio unclassified
2518645583 Thioalkalivibrio unclassified
UID4307
Thioalkalivibrio thiocyanoxidans|1.000
UID4306|o Chromatiales
2521172674 Thioalkalivibrio unclassified
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UID4305||0.704
UID4304||0.978
UID4303||0.988
2522125169 Thioalkalivibrio unclassified
2517572111 Thioalkalivibrio unclassified
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Thioalkalivibrio thiocyanoxidans
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2519103013 Thioalkalivibrio unclassified
2517572113 Thioalkalivibrio unclassified
2518285529 Thioalkalivibrio unclassified
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2519899631 Thioalkalivibrio unclassified
2518285533 Thioalkalivibrio unclassified
UID4267||0.996
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2521172692 Thioalkalivibrio nitratireducens
2518285537 Thioalkalivibrio unclassified
Thioalkalivibrio sulfidophilus
Ectothiorhodospira haloalkaliphila
Ectothiorhodospira unclassified
2509276036 Thiorhodospira sibirica
2506520049 Thiothrix nivea
2556921650 Thiothrix lacustris
2515154111 Thiothrix flexilis
2517093012 Leucothrix mucor
647533248 unclassified unclassified
2519899679 Arhodomonas aquaeolei
638341135 Nitrococcus mobilis
UID4371||1.000
637000005 Alkalilimnicola ehrlichei
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
2522125151 Methylomonas unclassified
Methylomonas unclassified
2518148012 Methylomonas unclassified
UID4288|o Methylococcales
UID4286||1.000
2504756059 Methylomonas methanica
2516653075 Methylomicrobium buryatense
2524614767 Methylococcus capsulatus
Methylococcus capsulatus
Methylococcus capsulatus|1.000
UID4300|o Methylococcales
2508501066 Methylocaldum szegediense
UID4275||0.996
2524614657 Methylohalobius crimeensis
2517572241 Cycloclasticus pugetii
Piscirickettsiaceae 2;g Cycloclasticus|1.000
2519899538 Cycloclasticus unclassified
2510065015 Thiorhodococcus drewsii
Allochromatium vinosum
Thiocystis violascens
Thiocapsa marina
UID4277|f Chromatiaceae|1.000
2510065050 Marichromatium purpuratum
2515154118 Lamprocystis purpurea
UID4276|o Chromatiales|1.000
2508783059 Thioflavicoccus mobilis
2508501048 Thiorhodovibrio unclassified
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UID4284||0.975
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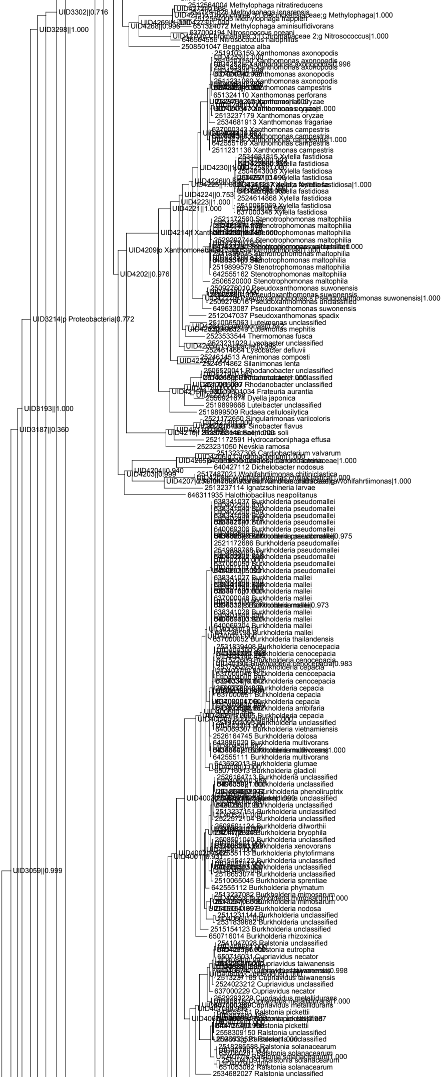
bin 61-2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646564556 Nitrosococcus halophilus
2508501047 Beggiatoa alba
2519103159 Xanthomonas axonopodis
Xanthomonas axonopodis
Xanthomonas axonopodis|0.996
Xanthomonas axonopodis
Xanthomonas axonopodis
2511231060 Xanthomonas axonopodis
Xanthomonas campestris
651324110 Xanthomonas perforans
Xanthomonas oryzae
Xanthomonas oryzae|1.000
2513237179 Xanthomonas oryzae
2534681913 Xanthomonas fragariae
637000343 Xanthomonas campestris
Xanthomonas campestris
Xanthomonas campestris|1.000
642555169 Xanthomonas campestris
2511231136 Xanthomonas campestris
2534681815 Xylella fastidiosa
Xylella fastidiosa
2504643008 Xylella fastidiosa
UID4230||1.000
Xylella fastidiosa
UID4226||0.835
UID4225||1.000
Xylella fastidiosa|1.000
Xylella fastidiosa
UID4224||0.753
UID4223||1.000
2524614868 Xylella fastidiosa
UID4221||1.000
2510065069 Xylella fastidiosa
637000348 Xylella fastidiosa
2521172560 Stenotrophomonas maltophilia
Stenotrophomonas maltophilia
UID4214|f Xanthomonadaceae|1.000
Stenotrophomonas maltophilia
2529292744 Stenotrophomonas maltophilia
UID4209|o Xanthomonadales
Stenotrophomonas maltophilia|1.000
Stenotrophomonas maltophilia
Stenotrophomonas maltophilia
2519899579 Stenotrophomonas maltophilia
UID4202||0.976
642555162 Stenotrophomonas maltophilia
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2509276010 Pseudoxanthomonas suwonensis
Pseudoxanthomonas suwonensis
Pseudoxanthomonas suwonensis|1.000
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649633087 Pseudoxanthomonas suwonensis
2512047037 Pseudoxanthomonas spadix
UID3214|p Proteobacteria|0.772
2510065063 Luteimonas unclassified
Luteimonas mephitis
2523533544 Thermomonas fusca
2523231029 Lysobacter unclassified
2524614664 Lysobacter defluvii
2524614513 Arenimonas composti
2524614862 Silanimonas lenta
2506520041 Rhodanobacter unclassified
Rhodanobacter|1.000
Rhodanobacter unclassified
2509601034 Frateuria aurantia
2556921674 Dyella japonica
2519899668 Luteibacter unclassified
UID3193||1.000
2519899509 Rudaea cellulosilytica
2521172650 Singularimonas variicoloris
Sinobacter flavus
UID3187||0.360
Solimonas soli
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2523231050 Nevskia ramosa
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Cardiobacteriaceae|1.000
640427112 Dichelobacter nodosus
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Wohlfahrtiimonas|1.000
UID4207
2513237114 Ignatzschineria larvae
646311935 Halothiobacillus neapolitanus
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Burkholderia pseudomallei
Burkholderia pseudomallei
Burkholderia pseudomallei
640069306 Burkholderia pseudomallei
Burkholderia pseudomallei|0.975
2521172686 Burkholderia pseudomallei
2519899768 Burkholderia pseudomallei
Burkholderia pseudomallei
637000050 Burkholderia pseudomallei
Burkholderia pseudomallei
638341027 Burkholderia mallei
Burkholderia mallei
Burkholderia mallei
637000048 Burkholderia mallei
Burkholderia mallei|0.973
638341028 Burkholderia mallei
Burkholderia mallei
640069304 Burkholderia mallei
Burkholderia mallei
637000052 Burkholderia thailandensis
2531839408 Burkholderia cenocepacia
Burkholderia cenocepacia
Burkholderia cenocepacia
Burkholderia cenocepacia|0.983
Burkholderia cepacia
637000046 Burkholderia cenocepacia
Burkholderia cenocepacia
Burkholderia cepacia
637000051 Burkholderia cepacia
Burkholderia cepacia
Burkholderia ambifaria
Burkholderia cepacia
Burkholderia unclassified
640069307 Burkholderia vietnamiensis
2526164745 Burkholderia dolosa
643886020 Burkholderia multivorans
Burkholderia multivorans|1.000
642555111 Burkholderia multivorans
643692013 Burkholderia glumae
650716013 Burkholderia gladioli
2526164713 Burkholderia unclassified
Burkholderia unclassified
Burkholderia phenoliruptrix
Burkholderia unclassified
Burkholderia unclassified
2513237151 Burkholderia unclassified
2522572104 Burkholderia unclassified
2508501124 Burkholderia dilworthii
Burkholderia bryophila
2508501040 Burkholderia unclassified
Burkholderia xenovorans
Burkholderia phytofirmans
UID4001||0.931
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UID3059||0.999
Burkholderia unclassified
2516653074 Burkholderia unclassified
2510065045 Burkholderia sprentiae
642555112 Burkholderia phymatum
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Burkholderia mimosarum|1.000
Burkholderia mimosarum
Burkholderia nodosa
2511231144 Burkholderia unclassified
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650716014 Burkholderia rhizoxinica
2541047028 Ralstonia unclassified
Ralstonia eutropha
650716031 Cupriavidus necator
Cupriavidus taiwanensis
Cupriavidus taiwanensis|0.998
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2524023212 Cupriavidus unclassified
637000229 Cupriavidus necator
2529293220 Cupriavidus metallidurans
Cupriavidus metallidurans|1.000
Ralstonia pickettii
Ralstonia pickettii|0.987
Ralstonia pickettii
2558309150 Ralstonia unclassified
Ralstonia|1.000
2518285588 Ralstonia solanacearum
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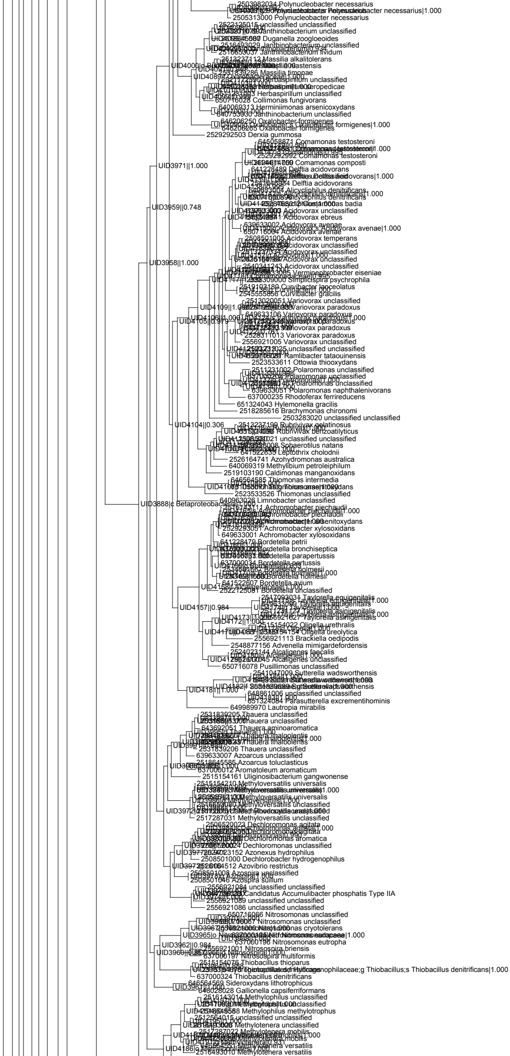
Ralstonia solanacearum
651053062 Ralstonia solanacearum
2534682027 Ralstonia unclassified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Polynucleobacter necessarius|1.000
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2516653037 Janthinobacterium lividum
2513237112 Massilia alkalitolerans
UID4000|o Burkholderiales
2531839286 Massilia timonae
Herbaspirillum unclassified
Herbaspirillum seropedicae
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640753030 Janthinobacterium unclassified
646206250 Oxalobacter formigenes
Oxalobacter formigenes|1.000
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Comamonas testosteroni|1.000
2529292992 Comamonas testosteroni
Comamonas composti
641228489 Delftia acidovorans
Delftia acidovorans|1.000
Delftia acidovorans
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
Acidovorax unclassified
Acidovorax unclassified
2540341243 Acidovorax unclassified
Verminephrobacter eiseniae
Simplicispira psychrophila
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2545555856 Curvibacter gracilis
UID3971||1.000
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649633106 Variovorax paradoxus
Variovorax paradoxus|1.000
Variovorax paradoxus
2528311013 Variovorax paradoxus
2556921005 Variovorax unclassified
UID4109||1.000
UID4106||1.000
UID4105||0.979
unclassified unclassified
Ramlibacter tataouinensis
2523533611 Ottowia thiooxydans
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Polaromonas unclassified
Polaromonas unclassified
639633051 Polaromonas naphthalenivorans
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Rubrivivax benzoatilyticus
unclassified unclassified
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Thiomonas arsenitoxydans
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UID3888|c Betaproteobacteria|1.000
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Achromobacter piechaudii|1.000
Achromobacter piechaudii
Achromobacter arsenitoxydans
2529293051 Achromobacter xylosoxidans
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
UID4157||0.984
2517093031 Taylorella equigenitalis
Taylorella equigenitalis|1.000
Taylorella equigenitalis
Taylorella asinigenitalis
Taylorella asinigenitalis|1.000
2556921627 Taylorella asinigenitalis
UID4173
UID4172||1.000
2515154022 Oligella urethralis
Oligella ureolytica
UID4170
2556921113 Brackiella oedipodis
2548877156 Advenella mimigardefordensis
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
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Methyloversatilis universalis|1.000
Methyloversatilis universalis
Methyloversatilis universalis
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UID3972
Rhodocyclaceae
2517287031 Methyloversatilis unclassified
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Dechloromonas agitata|1.000
Dechloromonas agitata
Dechloromonas aromatica
Dechloromonas unclassified
2524023152 Azonexus hydrophilus
2508501000 Dechlorobacter hydrogenophilus
2526164512 Azovibrio restrictus
2508501008 Azospira unclassified
2508501046 Azospira suillum
2556921084 unclassified unclassified
Candidatus Accumulibacter phosphatis Type IIA
2556921089 unclassified unclassified
2556921086 unclassified unclassified
650716066 Nitrosomonas unclassified
Nitrosomonas unclassified
Nitrosomonas cryotolerans
UID3965|o Nitrosomonadales
Nitrosomonas eutropha|1.000
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UID3962||0.984
2556921001 Nitrosospira briensis
UID3960
637000197 Nitrosospira multiformis
2515154076 Thiobacillus thioparus
Hydrogenophilaceae;g Thiobacillus;s Thiobacillus denitrificans|1.000
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2516143014 Methylophilus unclassified
Methylophilus unclassified
Methylophilus methylotrophus
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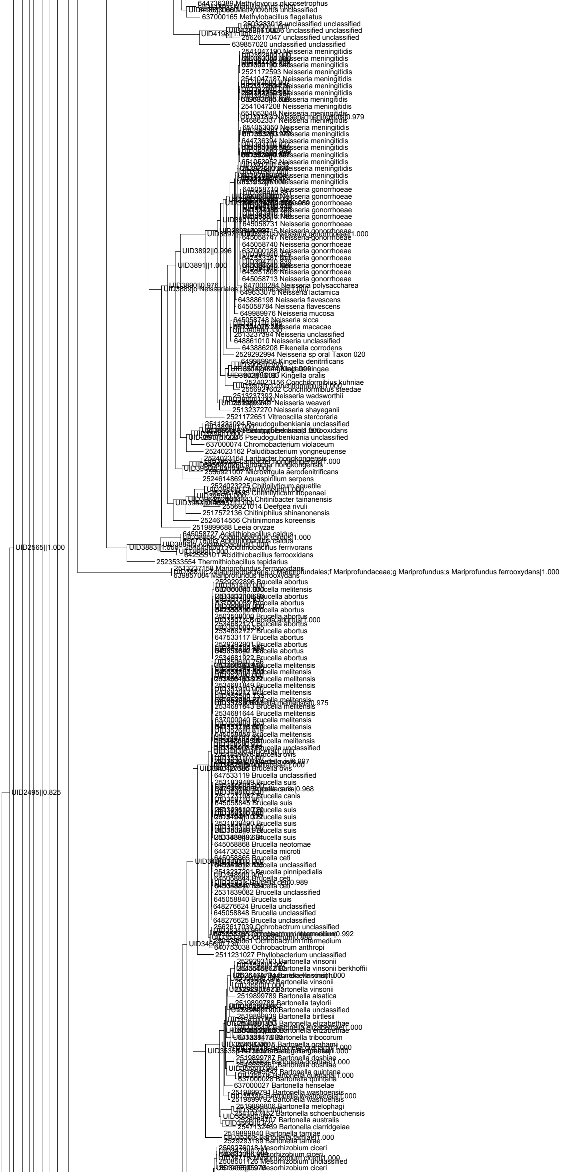
Methylotenera unclassified
2517287022 Methylotenera mobilis
Methylotenera mobilis|1.000
Methylotenera mobilis
UID4186|o Methylophilales
Methylotenera versatilis
2516493010 Methylotenera versatilis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Methylovorus unclassified
637000165 Methylobacillus flagellatus
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unclassified unclassified
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639857020 unclassified unclassified
2541047190 Neisseria meningitidis
Neisseria meningitidis
Neisseria meningitidis
2521172593 Neisseria meningitidis
2541047187 Neisseria meningitidis
Neisseria meningitidis
Neisseria meningitidis
Neisseria meningitidis
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651053048 Neisseria meningitidis
Neisseria meningitidis|0.979
646862337 Neisseria meningitidis
651053050 Neisseria meningitidis
Neisseria meningitidis
644736394 Neisseria meningitidis
Neisseria meningitidis
Neisseria meningitidis
651053052 Neisseria meningitidis
Neisseria meningitidis
Neisseria meningitidis
Neisseria meningitidis
645058710 Neisseria gonorrhoeae
Neisseria gonorrhoeae
Neisseria gonorrhoeae
Neisseria gonorrhoeae
Neisseria gonorrhoeae
645058731 Neisseria gonorrhoeae
Neisseria gonorrhoeae
Neisseria gonorrhoeae|1.000
645058747 Neisseria gonorrhoeae
645058740 Neisseria gonorrhoeae
637000188 Neisseria gonorrhoeae
Neisseria gonorrhoeae
Neisseria gonorrhoeae
645951609 Neisseria gonorrhoeae
645058713 Neisseria gonorrhoeae
UID3892||0.996
UID3891||1.000
UID3890||0.976
647000284 Neisseria polysaccharea
UID3889|o Neisseriales;f Neisseriaceae|1.000
649633075 Neisseria lactamica
643886198 Neisseria flavescens
645058784 Neisseria flavescens
649989976 Neisseria mucosa
645058748 Neisseria sicca
Neisseria macacae
2513237394 Neisseria unclassified
648861010 Neisseria unclassified
643886208 Eikenella corrodens
2529292994 Neisseria sp oral Taxon 020
649989956 Kingella denitrificans
Kingella kingae
Kingella oralis
2524023156 Conchiformibius kuhniae
2556921602 Conchiformibius steedae
2513237392 Neisseria wadsworthii
Neisseria weaveri
2513237270 Neisseria shayeganii
2521172651 Vitreoscilla stercoraria
2511231094 Pseudogulbenkiania unclassified
Pseudogulbenkiania ferrooxidans
Pseudogulbenkiania unclassified
637000074 Chromobacterium violaceum
2524023162 Paludibacterium yongneupense
2524023164 Laribacter hongkongensis
Laribacter hongkongensis|1.000
Laribacter hongkongensis
2556921007 Microvirgula aerodenitrificans
2524614869 Aquaspirillum serpens
2524023225 Chitiniliyticum aquatile
Chitiniliyticum litopenaei
Chitinibacter tainanensis
UID3953
2556921014 Deefgea rivuli
2517572136 Chitiniphilus shinanonensis
2524614556 Chitinimonas koreensis
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Acidithiobacillus caldus|1.000
Acidithiobacillus caldus
UID3883||1.000
Acidithiobacillus ferrivorans
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2523533554 Thermithiobacillus tepidarius
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o Mariprofundales;f Mariprofundaceae;g Mariprofundus;s Mariprofundus ferrooxydans|1.000
639857004 Mariprofundus ferrooxydans
2529292896 Brucella abortus
Brucella melitensis
Brucella abortus
637000039 Brucella abortus
Brucella abortus
2503508000 Brucella abortus
Brucella abortus|1.000
2534682121 Brucella abortus
2534682127 Brucella abortus
647533117 Brucella abortus
2529292901 Brucella abortus
Brucella abortus
2534681922 Brucella abortus
Brucella melitensis
Brucella melitensis
Brucella melitensis
2534681849 Brucella melitensis
Brucella melitensis
Brucella melitensis
Brucella melitensis|0.975
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637000040 Brucella melitensis
Brucella melitensis
Brucella melitensis
Brucella melitensis
Brucella unclassified
Brucella|1.000
2531839078 Brucella ovis
Brucella ovis|0.997
Brucellaceae|1.000
Brucella ovis
647533119 Brucella unclassified
2531839489 Brucella suis
Brucella canis|0.968
Brucella canis
645058845 Brucella suis
Brucella suis
Brucella suis
2531839490 Brucella suis
Brucella suis
Brucella suis
645058868 Brucella neotomae
644736332 Brucella microti
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Brucella unclassified
2513237201 Brucella pinnipedialis
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Brucella ceti|0.989
Brucella ceti
2531839082 Brucella unclassified
645058840 Brucella suis
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2562617039 Ochrobactrum unclassified
Ochrobactrum intermedium|0.992
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640753038 Ochrobactrum anthropi
2511231027 Phyllobacterium unclassified
UID2495||0.825
2529293193 Bartonella vinsonii
Bartonella vinsonii berkhoffii
Bartonella vinsonii|1.000
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Bartonella vinsonii
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Bartonella unclassified
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Bartonella elizabethae
Bartonella elizabethae|1.000
Bartonella elizabethae
Bartonella tribocorum
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Bartonella grahamii|1.000
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Bartonella doshiae
Bartonella quintana
Bartonella quintana|1.000
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2519899791 Bartonella washoensis
Bartonella washoensis|1.000
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Bartonella schoenbuchensis
Bartonella australis
2547132469 Bartonella clarridgeiae
2519899840 Bartonella tamiae
Bartonella tamiae|1.000
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2509276018 Mesorhizobium ciceri
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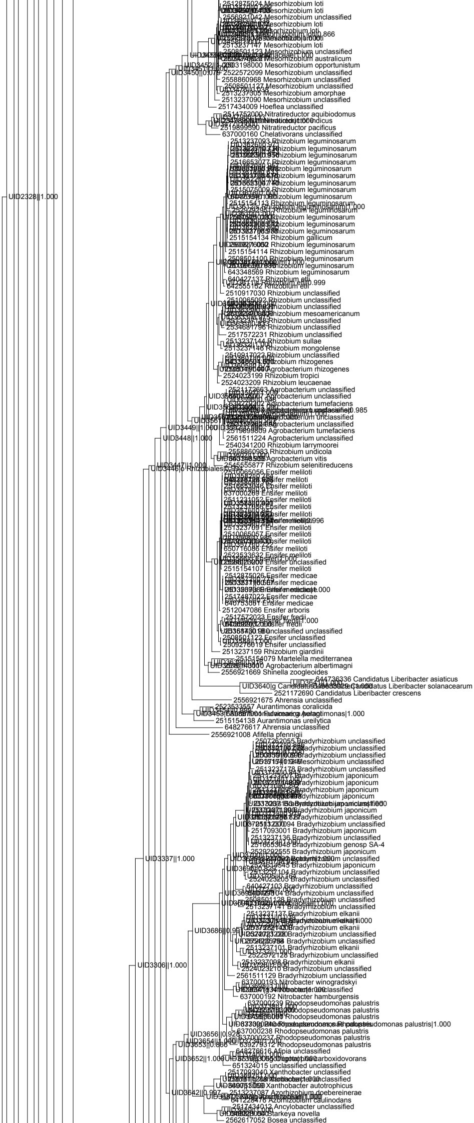
Mesorhizobium ciceri|1.000
2508501126 Mesorhizobium unclassified
Mesorhizobium ciceri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Mesorhizobium australicum
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2513237305 Mesorhizobium amorphae
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2517434009 Hoeflea unclassified
2514752000 Nitratireductor aquibiodomus
2516899590 Nitratireductor pacificus
637000160 Chelativorans unclassified
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Rhizobium leguminosarum
Rhizobium leguminosarum
2516653077 Rhizobium leguminosarum
Rhizobium leguminosarum
Rhizobium leguminosarum
Rhizobium leguminosarum
2515075009 Rhizobium leguminosarum
Rhizobium leguminosarum
2515154113 Rhizobium leguminosarum
Rhizobium leguminosarum
Rhizobium leguminosarum
Rhizobium leguminosarum
Rhizobium leguminosarum
2515154134 Rhizobium gallicum
Rhizobium leguminosarum
2515154114 Rhizobium leguminosarum
2508501100 Rhizobium leguminosarum
Rhizobium leguminosarum
643348569 Rhizobium leguminosarum
640427137 Rhizobium etli
642555152 Rhizobium etli
2510917030 Rhizobium unclassified
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Rhizobium mesoamericanum
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Rhizobium rhizogenes
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Agrobacterium vitis
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UID3447||1.000
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Ensifer meliloti
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Ensifer meliloti
Ensifer meliloti
Ensifer meliloti
Ensifer meliloti|0.996
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Ensifer medicae
Ensifer medicae|1.000
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2517572023 Ensifer fredii
Ensifer fredii|1.000
Ensifer fredii
unclassified unclassified
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2509276019 Ensifer unclassified
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2515154079 Martelella mediterranea
Agrobacterium albertimagni
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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
Aurantimonas|1.000
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648276617 Ahrensia unclassified
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Bradyrhizobium unclassified
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Mesorhizobium unclassified
2513237178 Bradyrhizobium unclassified
Bradyrhizobium japonicum
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Bradyrhizobium japonicum
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2516653048 Bradyrhizobium genosp SA-4
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Bradyrhizobium unclassified
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2513237137 Bradyrhizobium elkanii
Bradyrhizobium elkanii|1.000
Bradyrhizobium elkanii
Bradyrhizobium unclassified
Bradyrhizobium unclassified
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2522572128 Bradyrhizobium unclassified
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637000193 Nitrobacter winogradskyi
Nitrobacter|1.000
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Rhodopseudomonas palustris
Rhodopseudomonas palustris
Rhodopseudomonas palustris|1.000
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637000237 Rhodopseudomonas palustris
639279312 Rhodopseudomonas palustris
648276616 Afipia unclassified
carboxidovorans
651324015 unclassified unclassified
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Xanthobacter unclassified
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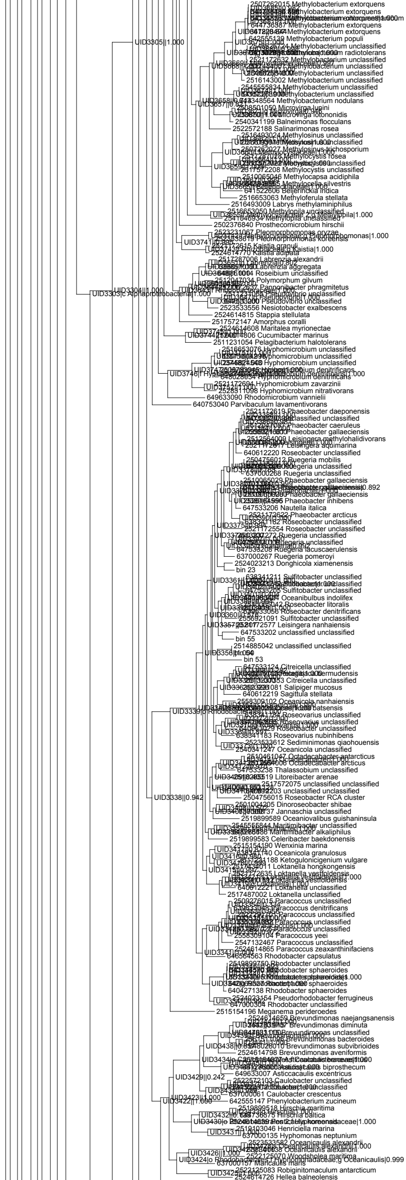
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radiotolerans
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Methylobacterium unclassified
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Methylobacterium unclassified
Methylobacterium unclassified
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Microvirga lotononidis
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2522572188 Salinarimonas rosea
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Methylosinus unclassified
2507262027 Methylosinus trichosporium
Methylocystis rosea
Methylocystis unclassified
2517572208 Methylocystis unclassified
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2516493009 Labrys methylaminiphilus
2516653050 Methylopila unclassified
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Pleomorphomonas koreensis
2521172615 Kaistia granuli
2524614770 Kaistia adipata
2517287006 Labrenzia alexandrii
Labrenzia aggregata
Roseibium unclassified
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Pannonibacter phragmitetus
Pseudovibrio unclassified
Pseudovibrio unclassified
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2517572147 Amorphus coralli
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Hyphomicrobium unclassified
Hyphomicrobium unclassified
Hyphomicrobium denitrificans
Hyphomicrobium denitrificans
2521172694 Hyphomicrobium zavarzinii
2528311098 Hyphomicrobium nitrativorans
649633090 Rhodomicrobium vannielii
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2521172619 Phaeobacter daeponensis
unclassified unclassified
Phaeobacter caeruleus
Phaeobacter gallaeciensis
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2521172617 Leisingera aquimarina
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Ruegeria unclassified
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Phaeobacter gallaeciensis
Phaeobacter inhibens
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2521172622 Phaeobacter arcticus
Roseobacter unclassified
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Ruegeria unclassified
Ruegeria unclassified
647533208 Ruegeria lacuscaerulensis
637000267 Ruegeria pomeroyi
2524023213 Donghicola xiamenensis
bin 23
638341211 Sulfitobacter unclassified
Sulfitobacter unclassified
Sulfitobacter unclassified
Oceanibulbus indolifex
Roseobacter litoralis
Roseobacter denitrificans
2556921091 Sulfitobacter unclassified
Leisingera nanhaiensis
647533202 unclassified unclassified
bin 55
2514885042 unclassified unclassified
bin 53
647533124 Citreicella unclassified
bermudensis
Citreicella unclassified
Salipiger mucosus
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2558309102 Oceanicola nanhaiensis
batsensis
Roseovarius unclassified
Roseovarius unclassified
Roseobacter unclassified
638341183 Roseovarius nubinhibens
2523533612 Sediminimonas qiaohouensis
2540341247 Oceanicola unclassified
2510461047 Octadecabacter antarcticus
Octadecabacter arcticus
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Litoreibacter arenae
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unclassified unclassified
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2501004205 Dinoroseobacter shibae
Jannaschia unclassified
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Maritimibacter alkaliphilus
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Oceanicola granulosus
Ketogulonicigenium vulgare
Loktanella hongkongensis
2521172635 Loktanella vestfoldensis
Loktanella vestfoldensis
640612221 Loktanella unclassified
2517487002 Loktanella unclassified
2509276015 Paracoccus unclassified
Paracoccus denitrificans
Paracoccus unclassified
Paracoccus unclassified
Paracoccus unclassified
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2547132467 Paracoccus unclassified
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Rhodobacter sphaeroides
Rhodobacter sphaeroides
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Brevundimonas diminuta
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2524614798 Brevundimonas aveniformis
Asticcacaulis biprosthecum
649633007 Asticcacaulis excentricus
2522572103 Caulobacter unclassified
Caulobacter unclassified
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Oceanicaulis alexandrii
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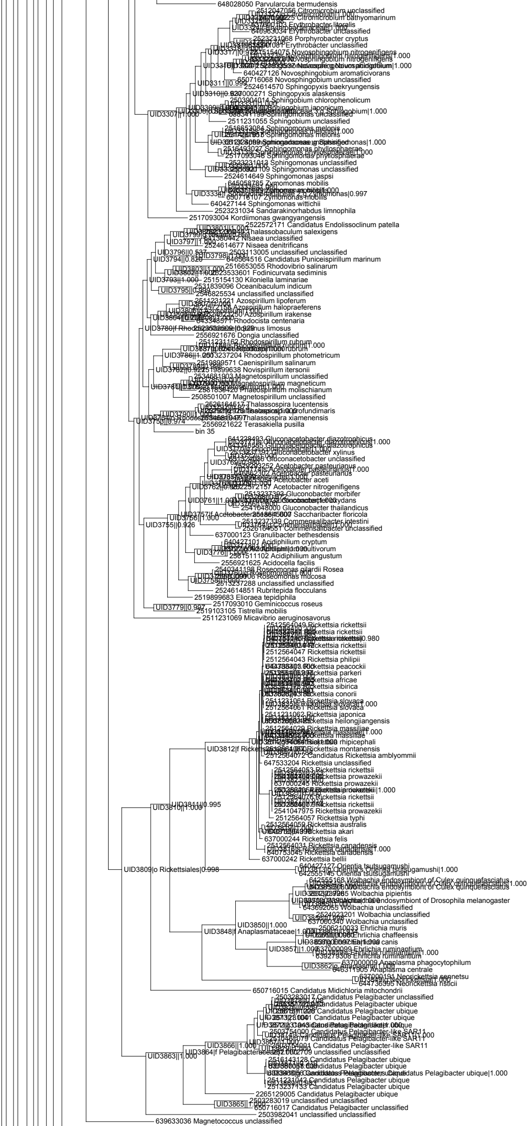
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2523231068 Porphyrobacter cryptus
Erythrobacter unclassified
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2524614570 Sphingopyxis baekryungensis
UID3310||0.927
637000271 Sphingopyxis alaskensis
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Sphingobium japonicum
UID3307||1.000
638341199 Sphingomonas unclassified
2511231055 Sphingobium unclassified
2546653084 Sphingomonas melonis
Sphingomonas melonis
2516493027 Sphingomonas phyllosphaerae
2517093046 Sphingomonas phyllosphaerae
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Sphingomonas unclassified
2524614649 Sphingomonas jaspsi
645058785 Zymomonas mobilis
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640427144 Sphingomonas wittichii
2523231034 Sandarakinorhabdus limnophila
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Thalassobaculum salexigens
Nisaea unclassified
UID3797||1.000
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UID3796||0.537
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646564516 Candidatus Puniceispirillum marinum
UID3803||1.000
2516653055 Rhodovibrio salinarum
UID3802||1.000
2523533601 Fodinicurvata sediminis
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2515154130 Kiloniella laminariae
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2511231221 Azospirillum lipoferum
Azospirillum halopraeferens
Azospirillum irakense
643348571 Rhodocista centenaria
UID3780|f Rhodospirillaceae
2556921676 Dongia unclassified
2511231162 Rhodospirillum rubrum
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2556921622 Terasakiella pusilla
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Gluconacetobacter diazotrophicus
Gluconacetobacter xylinus
Gluconacetobacter unclassified
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2522203252 Acetobacter pasteurianus
Acetobacter pasteurianus
Acetobacter aceti
UID3762||0.987
2522572157 Acetobacter nitrogenifigens
2513237393 Gluconobacter morbifer
UID3761||1.000
Gluconobacter oxydans
2541048000 Gluconobacter thailandicus
UID3757|f Acetobacteraceae
Saccharibacter floricola
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2513237339 Commensalibacter intestini
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640427101 Acidiphilium cryptum
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Acidiphilium multivorum
2561511102 Acidiphilium angustum
2556921625 Acidocella facilis
2540341198 Roseomonas gilardii Rosea
Roseomonas mucosa
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2513237288 unclassified unclassified
2524614851 Rubritepida flocculans
2519899683 Elioraea tepidiphila
UID3779||0.997
2517093010 Geminicoccus roseus
2519103105 Tistrella mobilis
2511231069 Micavibrio aeruginosavorus
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
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647533204 Rickettsia unclassified
2512564053 Rickettsia rickettsii
Rickettsia prowazekii
637000245 Rickettsia prowazekii
Rickettsia prowazekii|1.000
2512564076 Rickettsia rickettsii
Rickettsia rickettsii
2541047975 Rickettsia prowazekii
UID3811||0.995
UID3810||1.000
2512564057 Rickettsia typhi
2512564059 Rickettsia australis
Rickettsia akari
637000244 Rickettsia felis
2512564031 Rickettsia canadensis
Rickettsia canadensis|1.000
640753045 Rickettsia canadensis
637000242 Rickettsia bellii
640427127 Orientia tsutsugamushi
UID3809|o Rickettsiales|0.998
Orientia tsutsugamushi|1.000
642555145 Orientia tsutsugamushi
642555168 Wolbachia endosymbiont of Culex quinquefasciatus
Wolbachia endosymbiont of Culex quinquefasciatus|1.000
Wolbachia endosymbiont of Culex quinquefasciatus
Wolbachia pipientis
Wolbachia endosymbiont of Drosophila melanogaster
643692055 Wolbachia unclassified
2524023201 Wolbachia unclassified
637000340 Wolbachia unclassified
UID3850||1.000
2506210033 Ehrlichia muris
UID3848|f Anaplasmataceae|1.000
Ehrlichia chaffeensis
Ehrlichia canis
UID3857||1.000
637000099 Ehrlichia ruminantium
Ehrlichia ruminantium|1.000
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|1.000
Candidatus Pelagibacter-like SAR11
Candidatus Pelagibacter-like SAR11
UID3866||1.000
unclassified unclassified
UID3864|f Pelagibacteraceae
UID3863||1.000
2516143128 Candidatus Pelagibacter ubique
Candidatus Pelagibacter ubique
Candidatus Pelagibacter ubique|1.000
2511231042 Candidatus Pelagibacter ubique
2513237133 Candidatus Pelagibacter ubique
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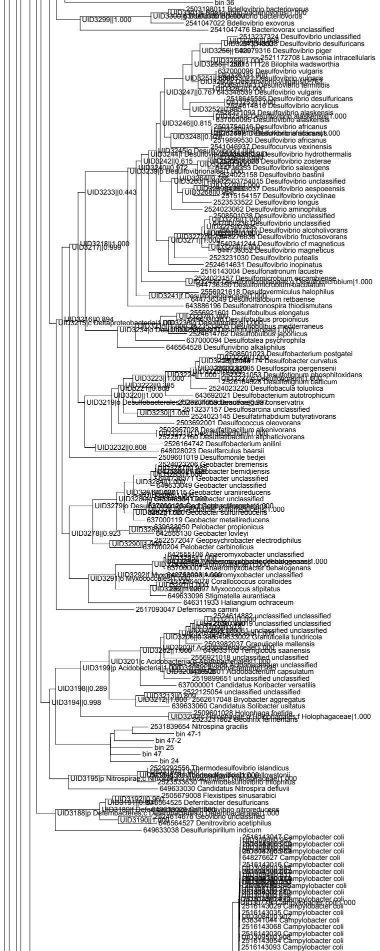
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Desulfovibrio piger
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Bilophila wadsworthia
637000096 Desulfovibrio vulgaris
Desulfovibrio vulgaris
Desulfovibrio termitidis
UID3247||0.767
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2518645586 Desulfovibrio desulfuricans
Desulfovibrio acrylicus
UID3252||0.995
Desulfovibrio alaskensis
637000095 Desulfovibrio alaskensis
UID3246||0.815
Desulfovibrio africanus
UID3248
2519899530 Desulfovibrio africanus
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Desulfovibrio hydrothermalis
UID3242||0.615
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Desulfovibrio salexigens
2524023158 Desulfovibrio bastinii
Desulfovibrio unclassified
Desulfovibrio aespoeensis
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2523533522 Desulfovibrio longus
2524023062 Desulfovibrio aminophilus
UID3233||0.443
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Desulfovibrio fructosovorans
UID3271||1.000
Desulfovibrio cf magneticus
Desulfovibrio magneticus
2523231030 Desulfovibrio putealis
2524614631 Desulfovibrio inopinatus
2516143004 Desulfonatronum lacustre
UID3218||1.000
UID3217||0.999
2524023157 Desulfomicrobium escambiense
Desulfomicrobium baculatum
2556921618 Desulfovermiculus halophilus
UID3241|f Desulfohalobiaceae|1.000
644736349 Desulfohalobium retbaense
643886196 Desulfonatronospira thiodismutans
UID3216||0.894
UID3215|c Deltaproteobacteria|1.000
2556921601 Desulfobulbus elongatus
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Desulfobulbus mediterraneus
UID3234|o Desulfobulbales
2524614762 Desulfobulbus japonicus
637000094 Desulfotalea psychrophila
646564528 Desulfurivibrio alkaliphilus
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Desulfobacter curvatus
Desulfospira joergensenii
2523231053 Desulfotignum phosphitoxidans
UID3223||1.000
UID3224||1.000
Desulfotignum balticum
UID3222||0.385
2524023220 Desulfobacula toluolica
UID3221||0.808
UID3220||1.000
643692021 Desulfobacterium autotrophicum
UID3219|o Desulfobacterales
Desulfococcus conservatrix
2513237157 Desulfosarcina unclassified
UID3230||1.000
2524023145 Desulfatirhabdium butyrativorans
2503692001 Desulfococcus oleovorans
2502957028 Desulfatibacillum alkenivorans
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
UID3279|o Desulfuromonadales
Geobacter sulfurreducens
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Acidobacterium unclassified
Acidobacterium capsulatum
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bin 24
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2523533630 Thermodesulfovibrio thiophilus
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Denitrovibrio nitroreducens
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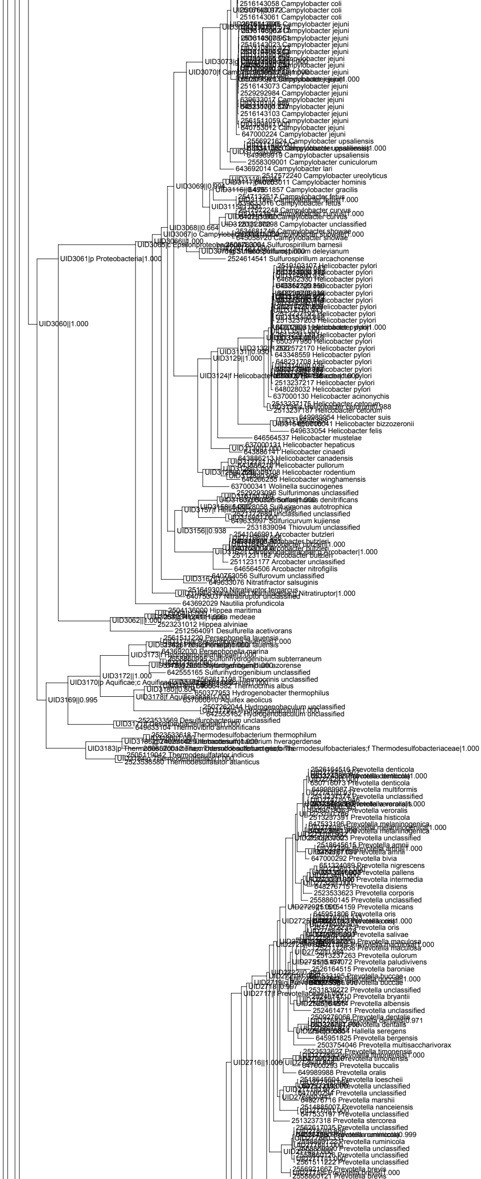
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2561511059 Campylobacter jejuni
640753012 Campylobacter jejuni
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2556921624 Campylobacter upsaliensis
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2558309001 Campylobacter cuniculorum
643692014 Campylobacter lari
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UID3073|g Campylobacter
UID3070|f Campylobacteraceae
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UID3067|o Campylobacterales
UID3066||1.000
UID3065|c Epsilonproteobacteria
UID3061|p Proteobacteria|1.000
UID3060||1.000
Campylobacter hominis
2551857 Campylobacter gracilis
2547132517 Campylobacter fetus
639633016 Campylobacter fetus
2512572248 Campylobacter curvus
Campylobacter curvus
2503230298 Campylobacter unclassified
2534681746 Campylobacter showae
645058720 Campylobacter showae
Sulfurospirillum barnesii
Sulfurospirillum deleyianum
2524614541 Sulfurospirillum arcachonense
2519103107 Helicobacter pylori
646862330 Helicobacter pylori
2513237203 Helicobacter pylori
2502572170 Helicobacter pylori
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648231708 Helicobacter pylori
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648028032 Helicobacter pylori
637000130 Helicobacter acinonychis
2513237175 Helicobacter cetorum
2513237187 Helicobacter cetorum
UID3131||0.930
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UID3124|f Helicobacteraceae
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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
Sulfurimonas autotrophica
Sulfurovum unclassified
649633097 Sulfuricurvum kujiense
2531839094 Thiovulum unclassified
UID3157|f Helicobacteraceae
UID3156||0.938
2541046991 Arcobacter butzleri
Arcobacter butzleri
2511231182 Arcobacter butzleri
2511231177 Arcobacter unclassified
646564506 Arcobacter nitrofigilis
640753056 Sulfurovum unclassified
649633076 Nitratifractor salsuginis
2516493030 Nitratiruptor tergarcus
640753037 Nitratiruptor unclassified
643692029 Nautilia profundicola
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Hippea medeae
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Thermocrinis albus
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650377953 Hydrogenobacter thermophilus
UID3178|f Aquificaceae
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2507262044 Hydrogenobaculum unclassified
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649633104 Thermovibrio ammonificans
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Thermodesulfobacterium hveragerdense
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2505119042 Thermodesulfatator indicus
2523533580 Thermodesulfatator atlanticus
2526164516 Prevotella denticola
650716073 Prevotella denticola
649989987 Prevotella multiformis
2513237374 Prevotella unclassified
Prevotella veroralis
645951836 Prevotella veroralis
2513237391 Prevotella histicola
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Prevotella melaninogenica
Prevotella unclassified
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647000292 Prevotella bivia
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2558860145 Prevotella unclassified
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645951806 Prevotella oris
Prevotella oris
Prevotella oris
Prevotella salivae
Prevotella maculosa
Prevotella maculosa
2513237263 Prevotella oulorum
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Prevotella bryantii
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Hallella seregens
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Prevotella timonensis
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Prevotella unclassified
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Prevotella unclassified
Prevotella unclassified
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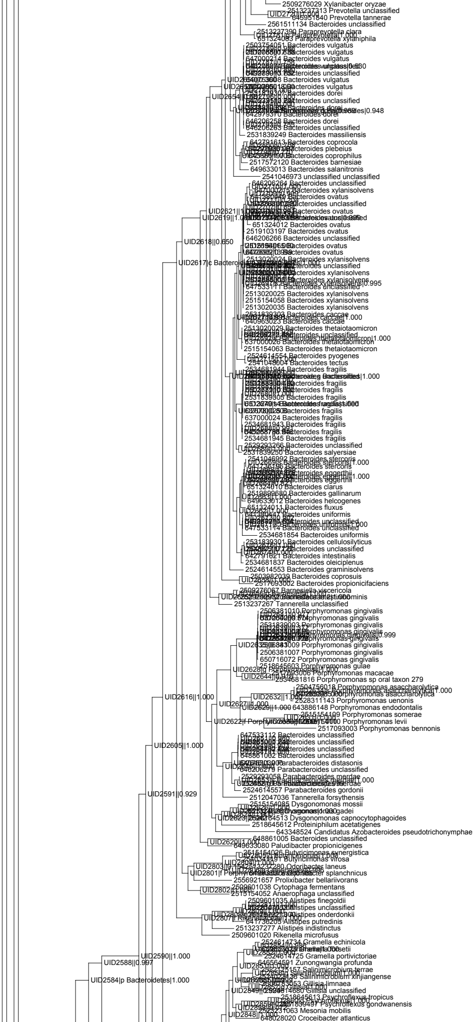
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2503754051 Bacteroides vulgatus
Bacteroides vulgatus
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Bacteroides vulgatus
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2531839307 Bacteroides dorei
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Bacteroides plebeius
Bacteroides coprophilus
2517572120 Bacteroides barnesiae
649633013 Bacteroides salanitronis
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Bacteroides ovatus
Bacteroides unclassified
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646206266 Bacteroides unclassified
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Bacteroides ovatus
Bacteroides ovatus
UID2617|c Bacteroidia
2513020024 Bacteroides xylanisolvens
Bacteroides unclassified
Bacteroides xylanisolvens
Bacteroides xylanisolvens
647533111 Bacteroides unclassified
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Bacteroides stercoris
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Porphyromonas macacae
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Bacteroides unclassified
Bacteroides unclassified
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Dysgonomonas gadei
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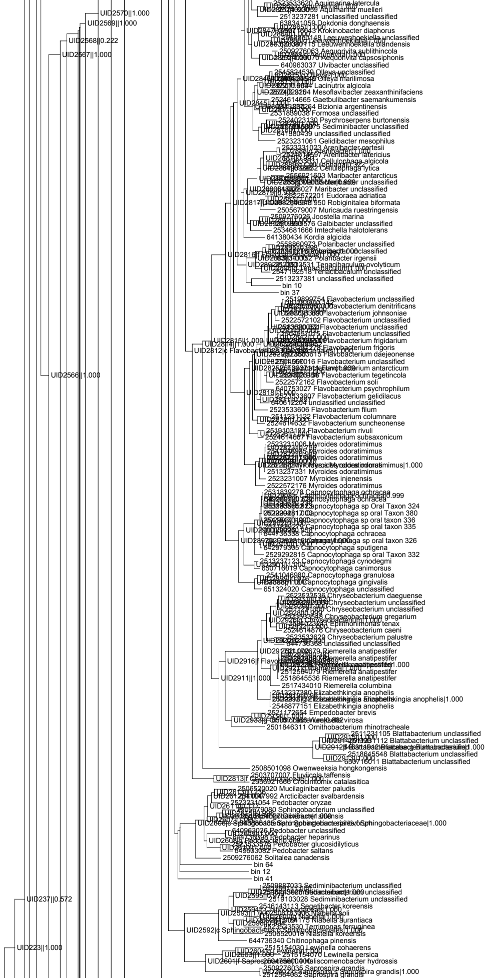
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Maribacter unclassified
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Robiginitalea biformata
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Flavobacterium tegetincola
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Riemerella anatipestifer
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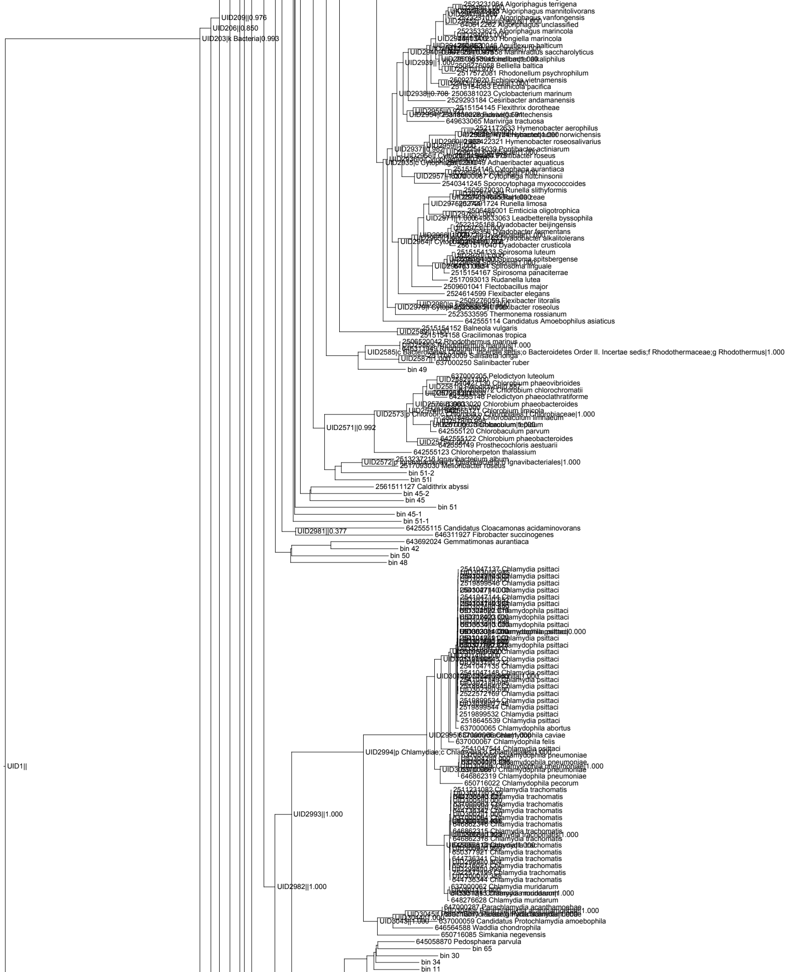
2548877151 Elizabethkingia anophelis
2521172654 Empedobacter brevis
Weeksella virosa
2501846311 Ornithobacterium rhinotracheale
UID2916|f Flavobacteriaceae
UID2911||1.000
UID2933|g
2511231105 Blattabacterium unclassified
Blattabacterium unclassified
Blattabacterium unclassified|1.000
2518645548 Blattabacterium unclassified
650716011 Blattabacterium unclassified
2508501098 Owenweeksia hongkongensis
2503707007 Fluviicola taffensis
2556921666 Crocinitomix catalasitica
UID2813|f Cryomorphaceae|1.000
2506520020 Mucilaginibacter paludis
Arcticibacter svalbardensis
2523231054 Pedobacter oryzae
2505679080 Sphingobacterium unclassified
Sphingobacteriales|Sphingobacteriaceae|1.000
640963036 Pedobacter unclassified
Pedobacter heparinus
Pedobacter glucosidilyticus
649633082 Pedobacter saltans
2509276062 Solitalea canadensis
bin 64
bin 12
bin 41
2509887033 Sediminibacterium unclassified
Sediminibacterium unclassified
2519103028 Sediminibacterium unclassified
2516143113 Segetibacter koreensis
Niabella soli
Niabella aurantiaca
2523533530 Terrimonas ferruginea
2506520019 Niastella koreensis
644736340 Chitinophaga pinensis
UID2592|c Sphingobacteriia
UID2593||1.000
2515154030 Lewinella cohaerens
2515154070 Lewinella persica
UID2603||1.000
Haliscomenobacter hydrossis
UID2601|f Saprospiraceae
Saprospira grandis|1.000
2509276035 Saprospira grandis
2512564062 Saprospira grandis



2523231064 Algoriphagus terrigena
Algoriphagus mannitolivorans
Algoriphagus vanfongensis
640612202 Algoriphagus unclassified
2523533625 Algoriphagus marincola
Hongiella marincola
Aquiflexum balticum
Mariniradius saccharolyticus
Indibacter alkaliphilus
2509276058 Belliella baltica
2517572081 Rhodonellum psychrophilum
2509276020 Echinicola vietnamensis
2515154083 Echinicola pacifica
UID2939||1.000
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2506381023 Cyclobacterium marinum
2529293184 Cesiribacter andamanensis
2515154145 Flexithrix dorotheae
Fabibacter pacificus
649633065 Marivirga tractuosa
2521172633 Hymenobacter aerophilus
Hymenobacter norwichensis
2522422321 Hymenobacter roseosalivarius
UID2937||0.982
2522545039 Pontibacter actiniarum
Pontibacter roseus
Adhaeribacter aquaticus
2515154146 Cytophaga aurantiaca
Cytophaga hutchinsonii
2540341245 Sporocytophaga myxococcoides
2505679030 Runella slithyformis
Runella zeae
Runella limosa
2506485001 Emticicia oligotrophica
649633063 Leadbetterella byssophila
2522125168 Dyadobacter beijingensis
Dyadobacter fermentans
Dyadobacter alkalitolerans
2561511040 Dyadobacter crusticola
2515154133 Spirosoma luteum
Spirosoma spitsbergense
Spirosoma linguale
2515154167 Spirosoma panaciterrae
2517093013 Rudanella lutea
2509601041 Flectobacillus major
2524614599 Flexibacter elegans
2509276059 Flexibacter litoralis
Flexibacter roseolus
2523533595 Thermonema rossianum
642555114 Candidatus Amoebophilus asiaticus
2515154152 Balneola vulgaris
UID2589||1.000
2515154158 Gracilimonas tropica
2506520042 Rhodothermus marinus
Rhodothermus marinus|1.000
UID2585|c Bacteroidetes Order II. Incertae sedis;o Bacteroidetes Order II. Incertae sedis;f Rhodothermaceae;g Rhodothermus|1.000
Salisaeta longa
UID2587||1.000
637000250 Salinibacter ruber
bin 49
637000205 Pelodictyon luteolum
Chlorobium phaeovibrioides
Chlorobium chlorochromatii
642555146 Pelodictyon phaeoclathratiforme
Chlorobium phaeobacteroides
Chlorobium limicola
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Chlorobaculum limnaeum
642555120 Chlorobaculum parvum
642555122 Chlorobium phaeobacteroides
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642555123 Chloroherpeton thalassium
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2513237218 Ignavibacterium album
UID2572|p Ignavibacteriae;c Ignavibacteria;o Ignavibacteriales|1.000
2517093030 Melioribacter roseus
bin 51-2
bin 51I
2561511127 Caldithrix abyssi
bin 45-2
bin 45
bin 51
bin 45-1
bin 51-1
UID2981||0.377
642555115 Candidatus Cloacamonas acidaminovorans
646311927 Fibrobacter succinogenes
643692024 Gemmatimonas aurantiaca
bin 42
bin 50
bin 48
2541047137 Chlamydia psittaci
Chlamydia psittaci
2519899546 Chlamydia psittaci
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Chlamydophila psittaci
2541047135 Chlamydia psittaci
2541047148 Chlamydia psittaci
2522572169 Chlamydia psittaci
2519899534 Chlamydia psittaci
2519899544 Chlamydia psittaci
2519899532 Chlamydia psittaci
2518645539 Chlamydia psittaci
637000065 Chlamydophila abortus
Chlamydophila caviae
637000067 Chlamydophila felis
2541047544 Chlamydia psittaci
UID2994|p Chlamydiae;c Chlamydiia
Chlamydophila pneumoniae
Chlamydophila pneumoniae|1.000
646862319 Chlamydophila pneumoniae
650716022 Chlamydophila pecorum
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Chlamydia trachomatis
646862315 Chlamydia trachomatis
Chlamydia trachomatis|1.000
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650377921 Chlamydia trachomatis
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637000062 Chlamydia muridarum
Chlamydia muridarum|1.000
648276628 Chlamydia muridarum
647000287 Parachlamydia acanthamoebae
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UID2982||1.000
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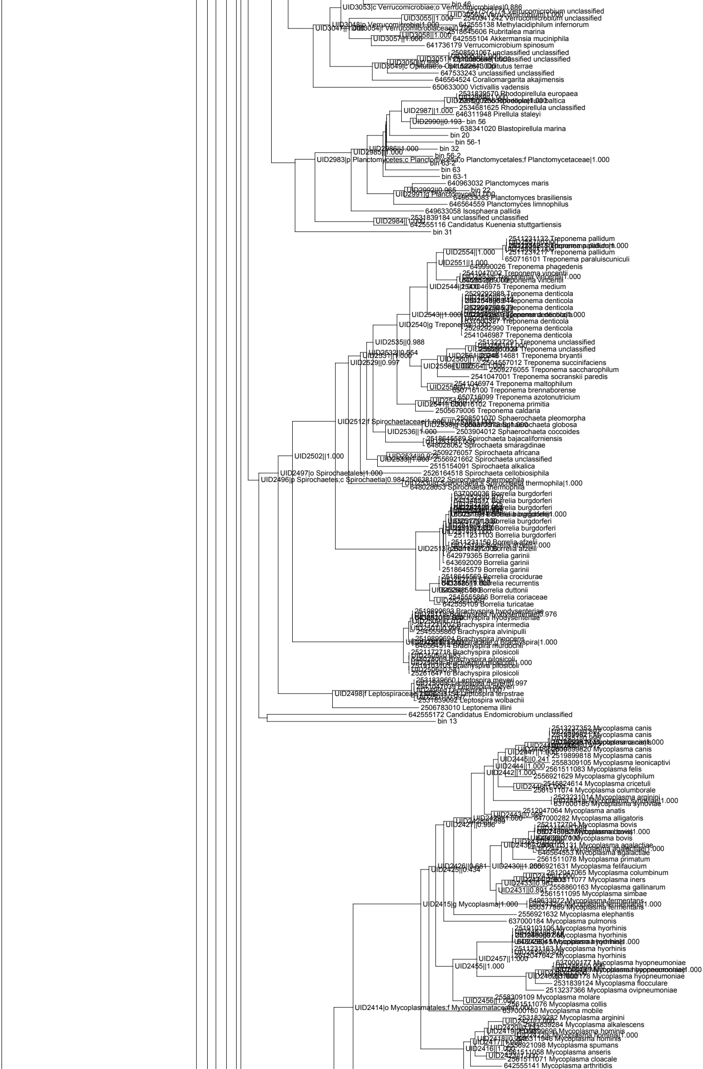
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UID3053|c Verrucomicrobiae;o Verrucomicrobiales|0.886
Verrucomicrobium unclassified
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UID3048|o Verrucomicrobiales|1.000
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UID3054|f Verrucomicrobiaceae|0.796
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641736179 Verrucomicrobium spinosum
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unclassified unclassified
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Opitutus terrae
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646564524 Coraliomargarita akajimensis
650633000 Victivallis vadensis
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Rhodopirellula baltica
UID2987||1.000
2534681625 Rhodopirellula unclassified
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bin 56
638341020 Blastopirellula marina
bin 20
bin 56-1
UID2986||1.000
bin 32
UID2985||1.000
bin 56-2
bin 63-2
UID2983|p Planctomycetes;c Planctomycetia;o Planctomycetales;f Planctomycetaceae|1.000
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
2531839184 unclassified unclassified
UID2984||1.000
642555116 Candidatus Kuenenia stuttgartiensis
bin 31
2511231132 Treponema pallidum
Treponema pallidum|1.000
2511231217 Treponema pallidum
UID2554||1.000
650716101 Treponema paraluiscuniculi
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649990026 Treponema phagedenis
2541047002 Treponema vincentii
Treponema vincentii|1.000
Treponema vincentii
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2541046975 Treponema medium
2529292988 Treponema denticola
Treponema denticola
Treponema denticola
Treponema denticola
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Treponema denticola|1.000
637000327 Treponema denticola
UID2540|g Treponema|1.000
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Treponema unclassified
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UID2558
UID2564
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UID2559
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650716099 Treponema azotonutricium
UID2541||1.000
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Sphaerochaeta globosa
UID2536||1.000
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2518645589 Spirochaeta bajacaliforniensis
648028052 Spirochaeta smaragdinae
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UID2533||1.000
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UID2496|p Spirochaetes;c Spirochaetia|0.984
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637000036 Borrelia burgdorferi
643348517 Borrelia burgdorferi
Borrelia burgdorferi|1.000
Borrelia burgdorferi
Borrelia burgdorferi
2511231103 Borrelia burgdorferi
2511231150 Borrelia afzelii
Borrelia afzelii|1.000
UID2513|g Borrelia
Borrelia afzelii
642979365 Borrelia garinii
643692009 Borrelia garinii
2518645579 Borrelia garinii
2518645569 Borrelia crocidurae
Borrelia recurrentis
Borrelia duttonii
2545555866 Borrelia coriaceae
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2519899693 Brachyspira hyodysenteriae
Brachyspira hyodysenteriae|0.976
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2531839660 Leptospira meyeri
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Leptospira meyeri
UID2498|f Leptospiraceae
Leptospira|1.000
Leptospira terpstrae
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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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UID2445||0.241
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UID2442||1.000
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UID2446
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2523231014 Mycoplasma arginini
637000185 Mycoplasma synoviae
Mycoplasma synoviae|1.000
2512047064 Mycoplasma anatis
UID2443||0.998
UID2428||0.999
647000282 Mycoplasma alligatoris
UID2427||0.996
2521172704 Mycoplasma bovis
Mycoplasma bovis|1.000
Mycoplasma bovis
2563103131 Mycoplasma agalactiae
Mycoplasma agalactiae|1.000
646564553 Mycoplasma agalactiae
2561511078 Mycoplasma primatum
UID2426||0.681
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UID2425||0.434
2512047065 Mycoplasma columbinum
2561511077 Mycoplasma iners
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
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637000184 Mycoplasma pulmonis
2519103106 Mycoplasma hyorhinis
Mycoplasma hyorhinis
Mycoplasma hyorhinis|1.000
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2512047042 Mycoplasma hyorhinis
UID2455||1.000
637000177 Mycoplasma hyopneumoniae
Mycoplasma hyopneumoniae|1.000
637000178 Mycoplasma hyopneumoniae
2531839124 Mycoplasma flocculare
2513237366 Mycoplasma ovipneumoniae
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UID2414|o Mycoplasmatales;f Mycoplasmataceae|1.000
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UID2419
2519899696 Mycoplasma hominis
Mycoplasma hominis|1.000
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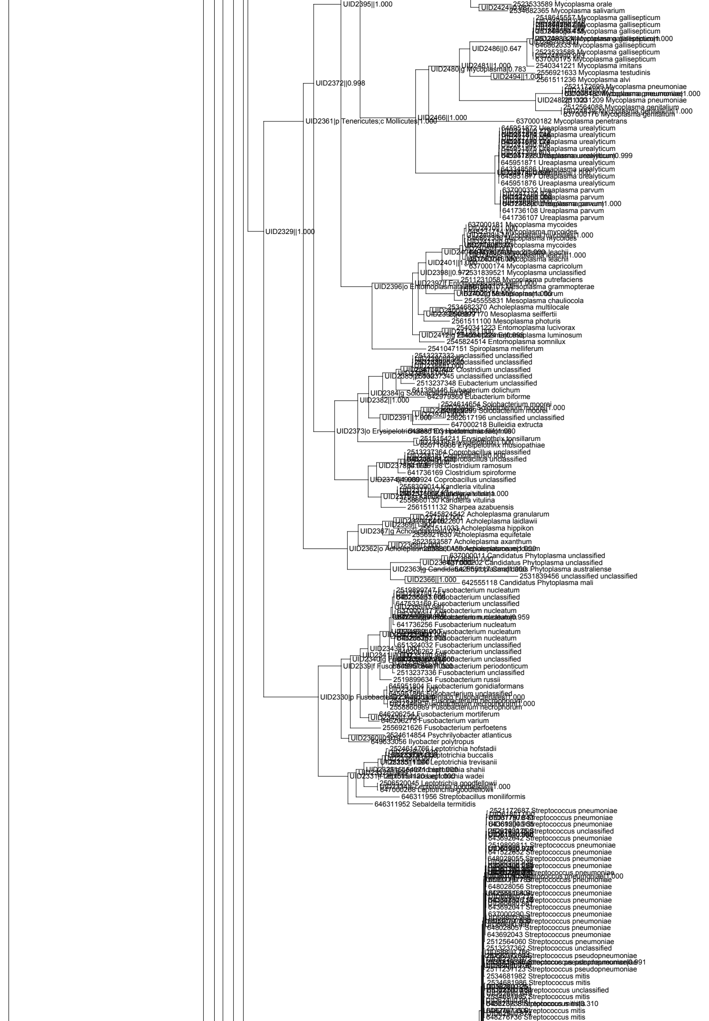
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UID2494||1.000
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2512564088 Mycoplasma genitalium
637000176 Mycoplasma genitalium
UID2466||1.000
UID2361|p Tenericutes;c Mollicutes|1.000
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645951871 Ureaplasma urealyticum
645951877 Ureaplasma urealyticum
645951876 Ureaplasma urealyticum
637000332 Ureaplasma parvum
641736108 Ureaplasma parvum
641736107 Ureaplasma parvum
UID2329||1.000
637000181 Mycoplasma mycoides
Mycoplasma mycoides
Mycoplasma leachii
UID2401||1.000
637000174 Mycoplasma capricolum
UID2398||0.972
2531839521 Mycoplasma unclassified
2511231058 Mycoplasma putrefaciens
UID2396|o Entomoplasmatales
Mesoplasma grammopterae
Mesoplasma florum
2545555831 Mesoplasma chauliocola
2534682370 Acholeplasma multilocale
Mesoplasma seiffertii
2561511100 Mesoplasma photuris
2540341223 Entomoplasma lucivorax
Entomoplasma luminosum
2545824514 Entomoplasma somnilux
2541047151 Spiroplasma melliferum
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Clostridium unclassified
2513237345 unclassified unclassified
2513237348 Eubacterium unclassified
641380446 Eubacterium dolichum
642979360 Eubacterium biforme
UID2382||1.000
UID2384|g Solobacterium
2524614654 Solobacterium moorei
Solobacterium moorei
UID2391||1.000
2562617196 unclassified unclassified
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
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Acholeplasma laidlawii
2561511033 Acholeplasma hippikon
UID2367|g Acholeplasma
2556921630 Acholeplasma equifetale
2523533587 Acholeplasma axanthum
UID2362|o Acholeplasmatales
637000011 Candidatus Phytoplasma unclassified
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
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637000117 Fusobacterium nucleatum
641736256 Fusobacterium nucleatum
Fusobacterium nucleatum
Fusobacterium nucleatum
651324032 Fusobacterium unclassified
Fusobacterium unclassified
Fusobacterium unclassified
UID2339|f Fusobacteriaceae
Fusobacterium periodonticum
2513237336 Fusobacterium unclassified
2519899634 Fusobacterium russii
645951804 Fusobacterium gonidiaformans
Fusobacterium unclassified
Fusobacterium necrophorum
2558860969 Fusobacterium necrophorum
UID2330|p Fusobacteria
646206254 Fusobacterium mortiferum
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2524614854 Psychrilyobacter atlanticus
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Leptotrichia buccalis
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Leptotrichia shahii
Leptotrichia wadei
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647000268 Leptotrichia goodfellowii
646311956 Streptobacillus moniliformis
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2521172687 Streptococcus pneumoniae
Streptococcus pneumoniae
Streptococcus pneumoniae
Streptococcus unclassified
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Streptococcus pneumoniae
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2512564060 Streptococcus pneumoniae
2513237362 Streptococcus unclassified
Streptococcus pseudopneumoniae
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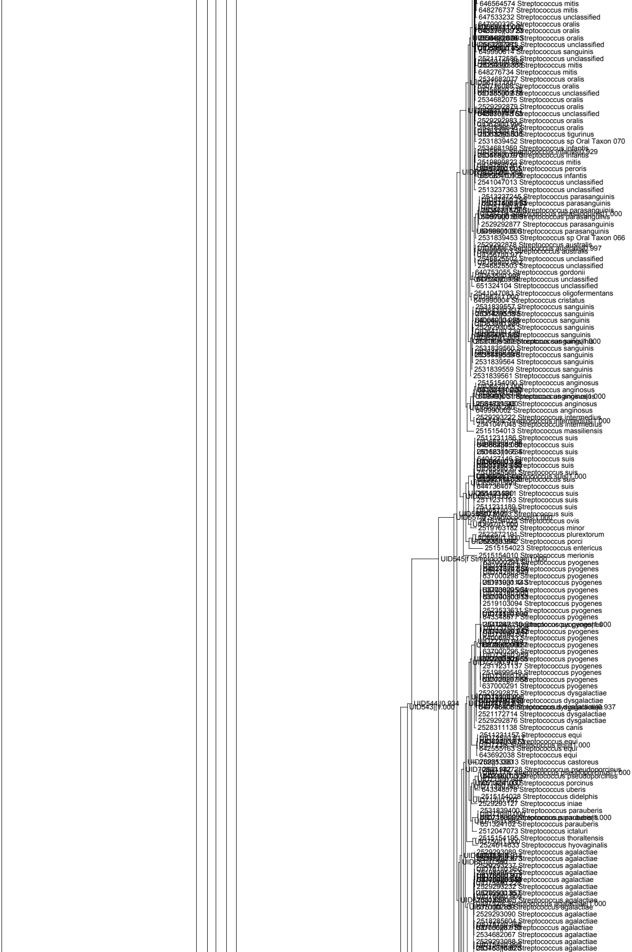
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640427146 Streptococcus suis
644736407 Streptococcus suis
2511231193 Streptococcus suis
2511231189 Streptococcus suis
2515154025 Streptococcus ovis
2519103182 Streptococcus minor
2522572191 Streptococcus plurextorum
2515154023 Streptococcus entericus
2515154010 Streptococcus merionis
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2523533631 Streptococcus pyogenes
643348577 Streptococcus pyogenes
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2511231137 Streptococcus pyogenes
2519899549 Streptococcus pyogenes
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2529292875 Streptococcus dysgalactiae
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643692038 Streptococcus equi
643348578 Streptococcus uberis
2515154028 Streptococcus didelphis
2529293127 Streptococcus iniae
2531839400 Streptococcus parauberis
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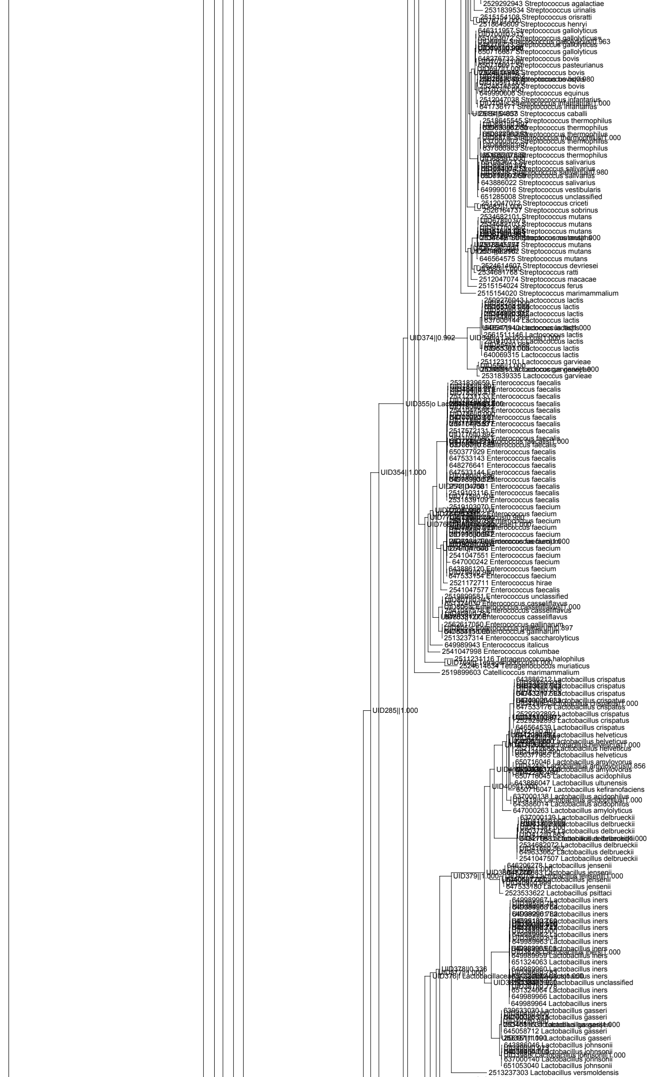
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648276732 Streptococcus bovis
650716091 Streptococcus pasteurianus
2524614859 Streptococcus bovis
649990006 Streptococcus equinus
2512047038 Streptococcus infantarius
641736171 Streptococcus infantarius
Streptococcus caballi
2518645545 Streptococcus thermophilus
Streptococcus thermophilus
637000302 Streptococcus thermophilus
637000303 Streptococcus thermophilus
Streptococcus thermophilus
Streptococcus salivarius
Streptococcus salivarius
Streptococcus salivarius
643886022 Streptococcus salivarius
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Streptococcus mutans
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Streptococcus mutans
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2515154020 Streptococcus marimammalium
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Lactococcus lactis
Lactococcus lactis
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2561511146 Lactococcus lactis
Lactococcus lactis
Lactococcus lactis
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2531839659 Enterococcus faecalis
Enterococcus faecalis
Enterococcus faecalis
UID355|o Lac
Enterococcus faecalis
Enterococcus faecalis
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Enterococcus faecalis
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Enterococcus faecalis
UID354||1.000
Enterococcus faecalis
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Enterococcus gallinarum
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649989943 Enterococcus italicus
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Lactobacillus helveticus
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650716046 Lactobacillus amylovorus
Lactobacillus amylovorus
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Lactobacillus delbrueckii
Lactobacillus delbrueckii
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646206278 Lactobacillus jensenii
UID379||1.000
Lactobacillus jensenii
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Lactobacillus iners
Lactobacillus iners
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UID378||0.336
UID376|f Lactobacillaceae
Lactobacillus unclassified
651324064 Lactobacillus iners
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639633030 Lactobacillus gasseri
Lactobacillus gasseri
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Lactobacillus gasseri
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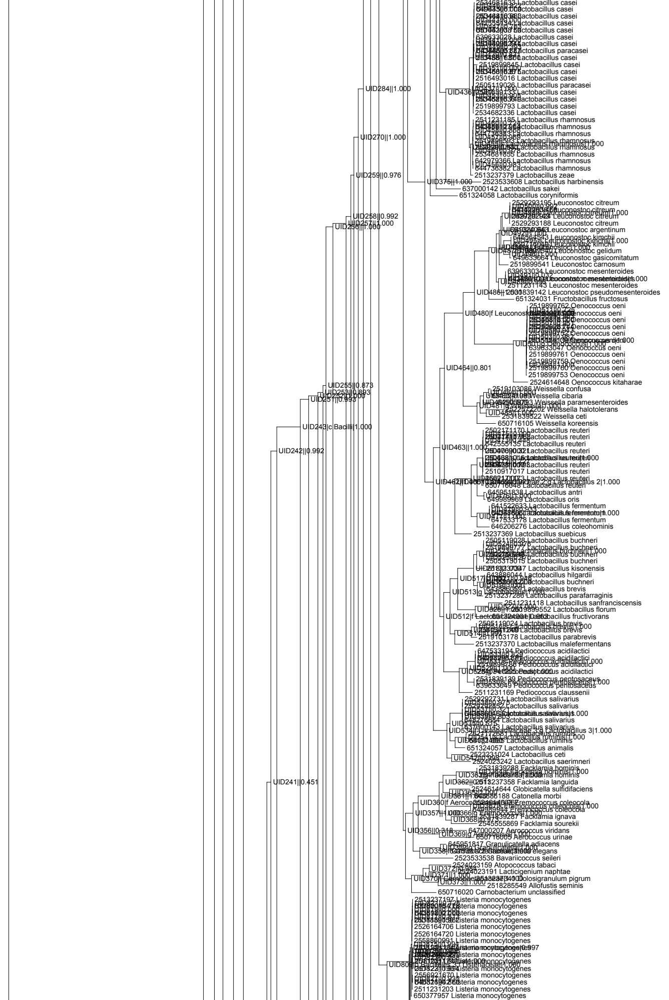
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Lactobacillus casei
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UID436
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Lactobacillus casei
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Lactobacillus rhamnosus
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642979366 Lactobacillus rhamnosus
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Leuconostoc argentinum
Leuconostoc kimchii
Leuconostoc gelidum
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UID486
2501839142 Leuconostoc pseudomesenteroides
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Oenococcus oeni
Oenococcus oeni
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Lactobacillus reuteri
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Lactobacillus hilgardii
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Lactobacillus buchneri
Lactobacillus brevis
UID513|g
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Lactobacillus fructivorans
2505119024 Lactobacillus brevis
Lactobacillus brevis
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Pediococcus acidilactici
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2511231169 Pediococcus claussenii
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Lactobacillus salivarius
Lactobacillus salivarius
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Lactobacillus ruminis
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Facklamia hominis
UID241||0.451
UID362
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Catonella morbi
UID360|f Aeroco
Eremococcus coleocola
Eremococcus coleocola
UID357
Facklamia ignava
2545555869 Facklamia sourekii
UID356||0.318
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Granulicatella elegans
2523533538 Bavariicoccus seileri
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2524023191 Lacticigenium naphtae
UID370
Dolosigranulum pigrum
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650716020 Carnobacterium unclassified
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Listeria monocytogenes
Listeria monocytogenes
Listeria monocytogenes
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UID80
Listeria monocytogenes
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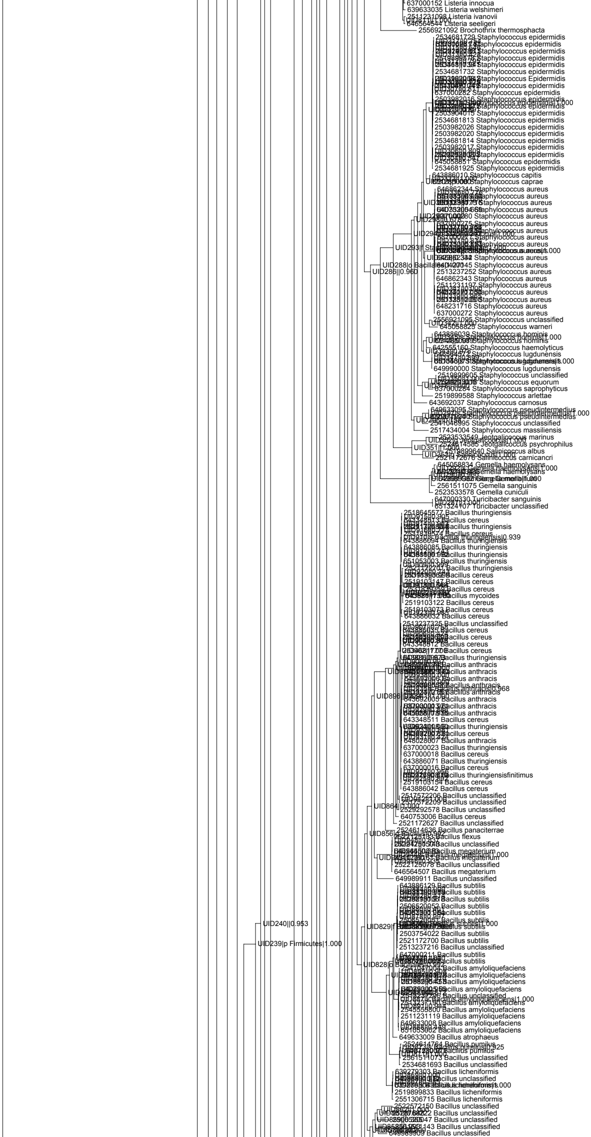
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Staphylococcus caprae
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Staphylococcus equorum
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2519899640 Salinicoccus albus
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Gemella haemolysans
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648028007 Bacillus anthracis
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Bacillus thuringiensisfinitimus
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Bacillus flexus
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Bacillus amyloliquefaciens
Bacillus unclassified
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Bacillus amyloliquefaciens
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Bacillus pumilus
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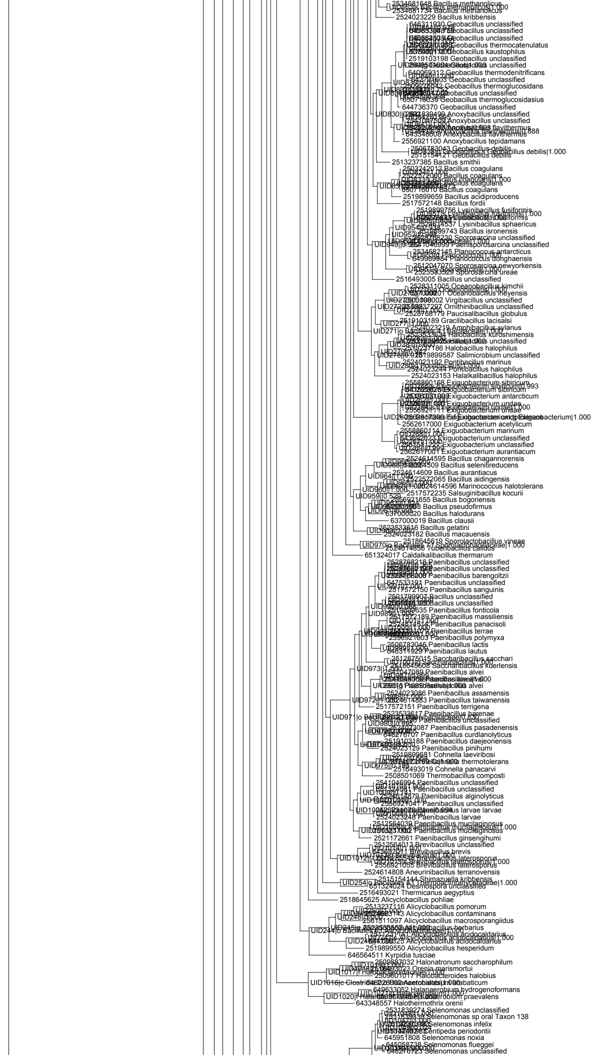
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Anoxybacillus flavithermus
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Bacillus coagulans
Bacillus coagulans
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Lysinibacillus fusiformis
Lysinibacillus sphaericus
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Paenisporosarcina unclassified
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Oceanobacillus iheyensis
Virgibacillus unclassified
Ornithinibacillus unclassified
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Bacillus unclassified
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Paenibacillus larvae larvae
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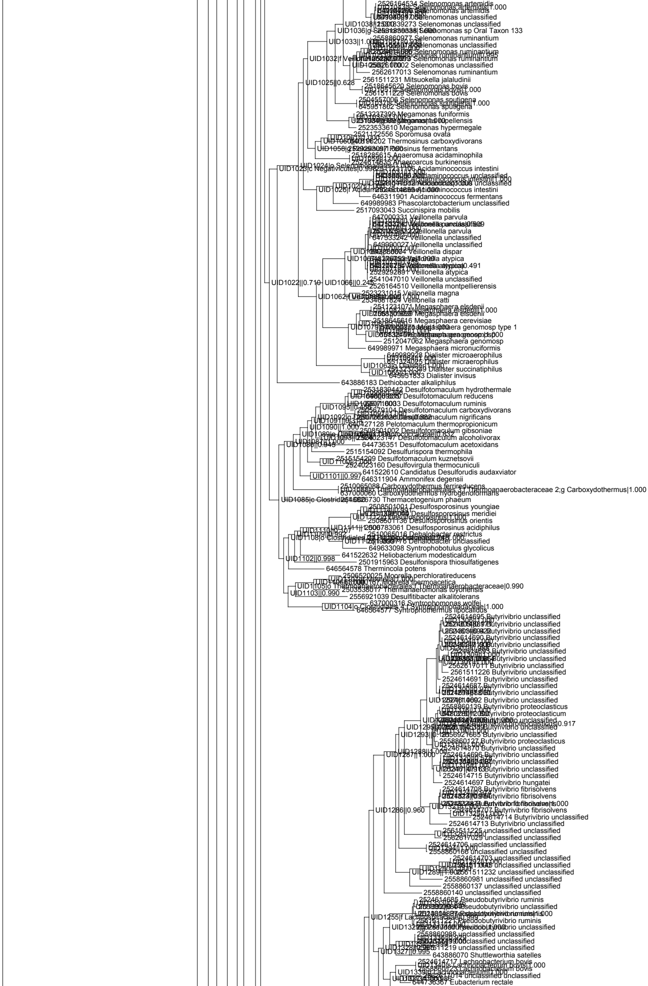
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Selenomonas sp Oral Taxon 133
UID1033||1.000
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Selenomonas unclassified
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Selenomonas ruminantium
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Selenomonas ruminantium
2562617002 Selenomonas unclassified
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2518645620 Selenomonas bovis
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Megamonas|1.000
Megamonas rupellensis
2523533610 Megamonas hypermegale
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Thermosinus carboxydivorans
UID1058
Thermosinus fermentans
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2524614635 Anaeroarcus burkinensis
UID1024|o Selenomonadales
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Acidaminococcus intestini
Acidaminococcus unclassified
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Veillonella parvula|0.509
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Megasphaera elsdenii
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UID1295
UID1293
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unclassified unclassified
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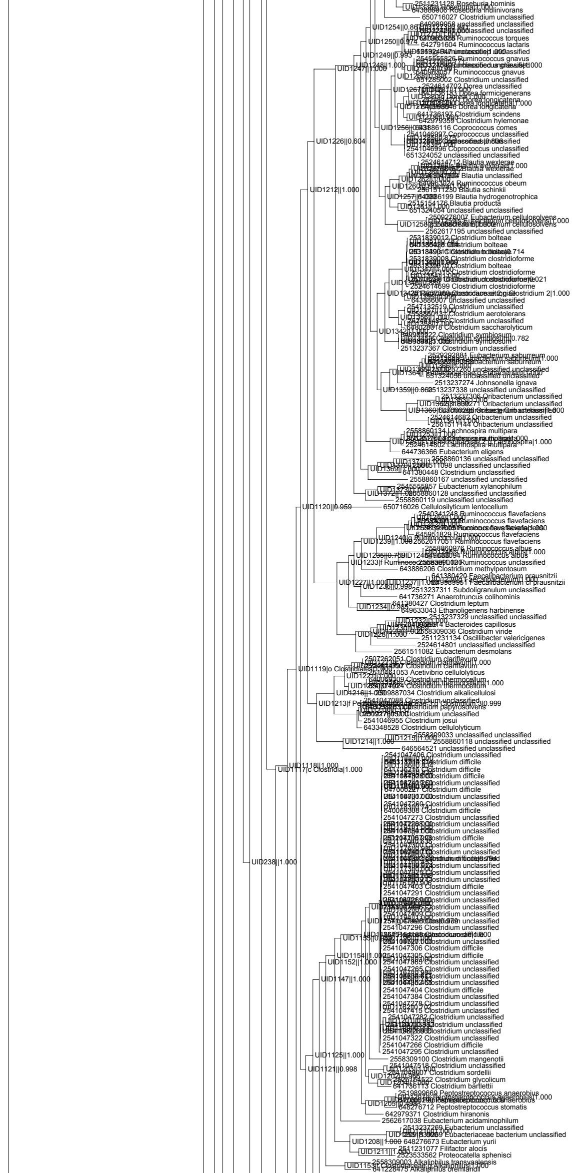
Lachnobacterium bovis|1.000
Lachnobacterium bovis
UID1339
unclassified unclassified
644736367 Eubacterium rectale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643886006 Roseburia inulinivorans
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642791604 Ruminococcus lactaris
Ruminococcus torques
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2545555826 Ruminococcus gnavus
Ruminococcus gnavus
651285002 Clostridium unclassified
2524614702 Dorea unclassified
Dorea formicigenerans
Dorea longicatena
641736197 Clostridium scindens
642979359 Clostridium hylemonae
UID1256||0.931
643886116 Coprococcus comes
2541046997 Coprococcus unclassified
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651324052 unclassified unclassified
UID1226||0.604
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Blautia wexlerae
Blautia unclassified
UID1260
Ruminococcus obeum
2561511230 Blautia schinkii
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UID1257||
643886199 Blautia hydrogenotrophica
2515154176 Blautia producta
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Eubacterium cellulosolvens
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2531839012 Clostridium bolteae
Clostridium bolteae
2531839008 Clostridium clostridioforme
Clostridium bolteae
Clostridium clostridioforme
2524614699 Clostridium clostridioforme
Clostridium 2|1.000
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2547132519 Clostridium unclassified
Clostridium aerotolerans
Clostridium unclassified
640028018 Clostridium saccharolyticum
UID1342||1.000
Clostridium symbiosum
Clostridium symbiosum
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Eubacterium saburreum
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unclassified unclassified
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Oribacterium unclassified
UID1360
2524614682 Oribacterium unclassified
2561511144 Oribacterium unclassified
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unclassified unclassified
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Ruminococcus flavefaciens
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UID1240
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2562617051 Ruminococcus flavefaciens
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Ruminococcus albus
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UID1233|f Ruminococcaceae
2558309010 Ruminococcus unclassified
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Clostridium clariflavum
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Acetivibrio cellulolyticus
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Clostridium thermocellum
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Clostridium unclassified
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Clostridium unclassified
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Clostridium unclassified
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Clostridium unclassified
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Clostridium unclassified
Clostridium unclassified
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Clostridium sordellii
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Clostridium glycolicum
641736113 Clostridium bartlettii
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Peptostreptococcus anaerobius
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648276712 Peptostreptococcus stomatis
642979371 Clostridium hiranonis
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2513237269 Eubacterium unclassified
Eubacteriaceae bacterium unclassified
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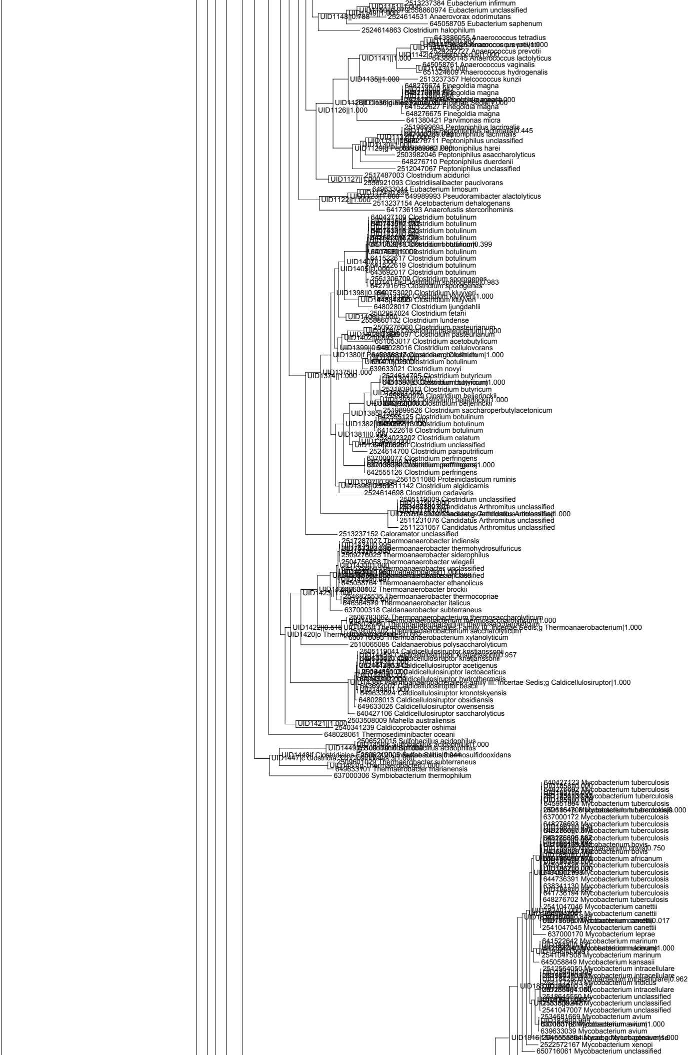
Alkaliphilus oremlandii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Peptoniphilus harei
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Candidatus Arthromitus unclassified
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2517287027 Thermoanaerobacter indiensis
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Thermoanaerobacter unclassified
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646564579 Thermoanaerobacter italicus
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Thermoanaerobacterium thermosaccharolyticum|1.000
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Thermoanaerobacteriaceae Family III. Incertae Sedis;g Thermoanaerobacterium|1.000
Thermoanaerobacterium saccharolyticum
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Caldicellulosiruptor acetigenus
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Caldicellulosiruptor bescii
649633024 Caldicellulosiruptor kronotskyensis
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2503508009 Mahella australiensis
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Sulfobacillus acidophilus
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Mycobacterium bovis|0.750
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637000170 Mycobacterium leprae
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Mycobacterium ulcerans|1.000
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Mycobacterium intracellulare
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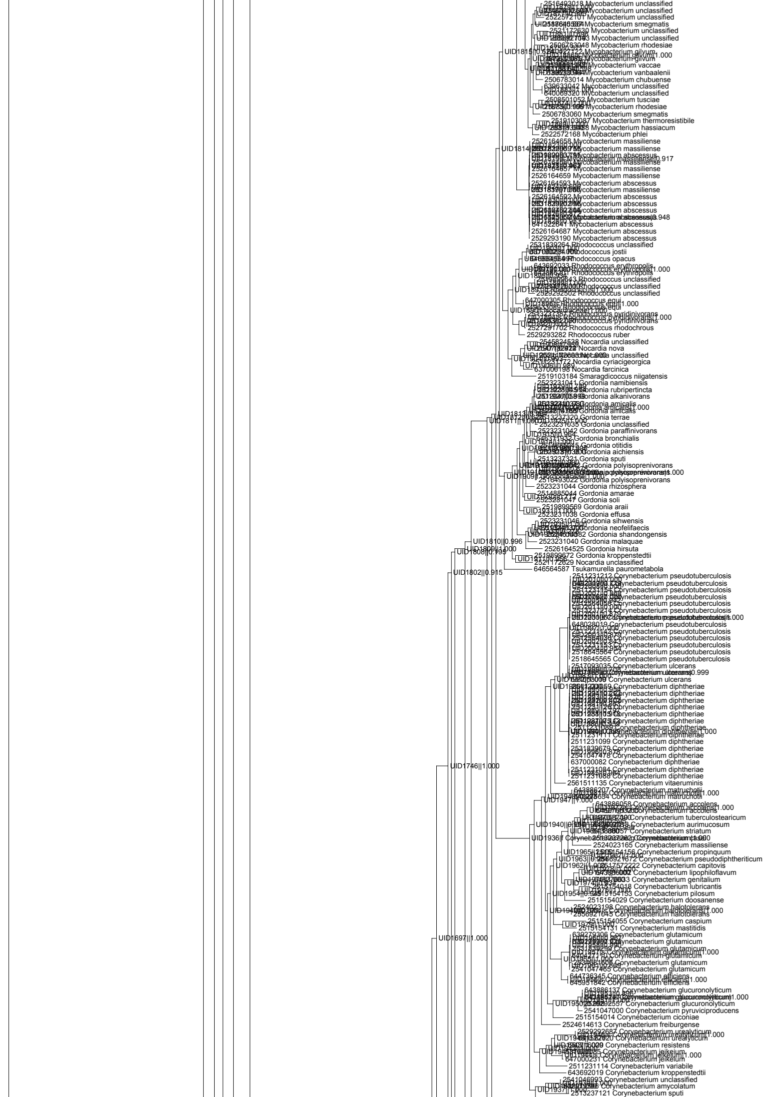
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Mycobacterium gilvum
Mycobacterium vaccae
Mycobacterium vanbaalenii
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639633042 Mycobacterium unclassified
640069320 Mycobacterium unclassified
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Mycobacterium rhodesiae
2506783060 Mycobacterium smegmatis
2519103087 Mycobacterium thermoresistibile
Mycobacterium hassiacum
2522572168 Mycobacterium phlei
2526164658 Mycobacterium massiliense
UID1814
Mycobacterium massiliense
Mycobacterium abscessus
Mycobacterium massiliense
2526164657 Mycobacterium massiliense
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Mycobacterium massiliense
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Mycobacterium abscessus
Mycobacterium abscessus
Mycobacterium abscessus
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2531839264 Rhodococcus unclassified
Rhodococcus jostii
Rhodococcus opacus
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Rhodococcus erythropolis
2519899643 Rhodococcus unclassified
Rhodococcus unclassified
2529292502 Rhodococcus unclassified
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Rhodococcus equi
Rhodococcus pyridinivorans
Rhodococcus pyridinivorans
2527291702 Rhodococcus rhodochrous
2529293282 Rhodococcus ruber
2545824538 Nocardia unclassified
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2511231772 Nocardia cyriacigeorgica
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Gordonia amicalis
Gordonia amicalis
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UID1811
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Gordonia otitidis
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2516493022 Gordonia polyisoprenivorans
2523231044 Gordonia rhizosphera
2514885044 Gordonia amarae
2523231047 Gordonia soli
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Gordonia shandongensis
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646564587 Tsukamurella paurometabola
2511231212 Corynebacterium pseudotuberculosis
Corynebacterium pseudotuberculosis
Corynebacterium pseudotuberculosis
Corynebacterium pseudotuberculosis
Corynebacterium pseudotuberculosis
Corynebacterium pseudotuberculosis
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Corynebacterium pseudotuberculosis
Corynebacterium pseudotuberculosis
Corynebacterium pseudotuberculosis
Corynebacterium pseudotuberculosis
2518645564 Corynebacterium pseudotuberculosis
2518645565 Corynebacterium pseudotuberculosis
2517093035 Corynebacterium ulcerans
Corynebacterium ulcerans
Corynebacterium ulcerans
Corynebacterium diphtheriae
Corynebacterium diphtheriae
Corynebacterium diphtheriae
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Corynebacterium glucuronolyticum
Corynebacterium glucuronolyticum
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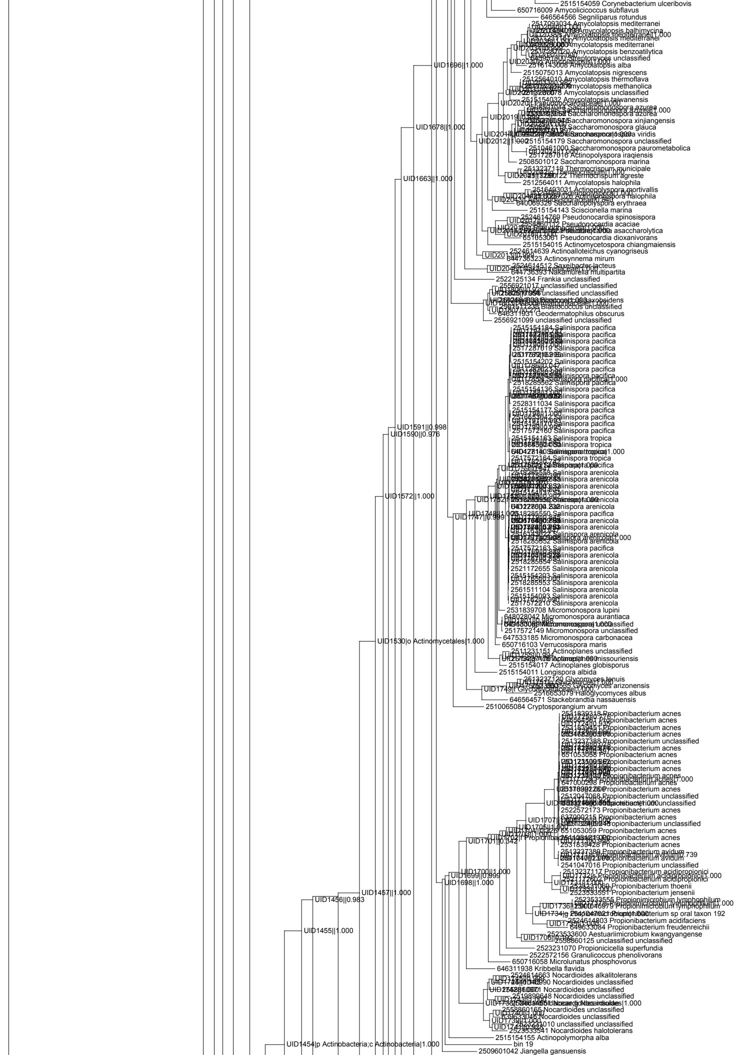
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bin 19
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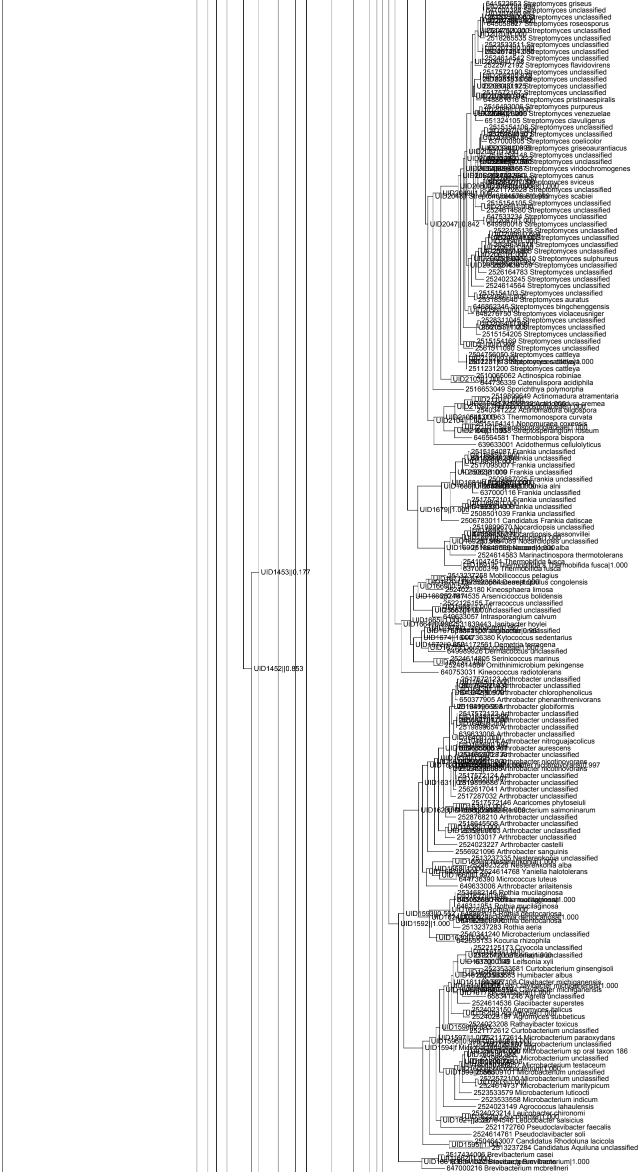
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Streptomyces unclassified
645058827 Streptomyces roseosporus
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2523533511 Streptomyces unclassified
2524614542 Streptomyces unclassified
2522572192 Streptomyces flavidovirens
2517572190 Streptomyces unclassified
648861016 Streptomyces pristinaespiralis
2516493006 Streptomyces purpureus
Streptomyces venezuelae
651324105 Streptomyces clavuligerus
2515154106 Streptomyces unclassified
637000305 Streptomyces coelicolor
Streptomyces griseoaurantiacus
Streptomyces viridochromogenes
Streptomyces canus
Streptomyces sviceus
2521172628 Streptomyces unclassified
UID2049||1.000
UID2048||Streptomyces scabiei
2515154105 Streptomyces unclassified
2524614580 Streptomyces unclassified
647533234 Streptomyces unclassified
UID2047||0.842
649990018 Streptomyces unclassified
2522125135 Streptomyces unclassified
Streptomyces unclassified
Streptomyces unclassified
Streptomyces sulphureus
Streptomyces unclassified
2526164783 Streptomyces unclassified
2524023245 Streptomyces unclassified
2524614564 Streptomyces unclassified
2515154103 Streptomyces unclassified
2531839540 Streptomyces auratus
646862346 Streptomyces bingchenggensis
648276750 Streptomyces violaceusniger
2528311045 Streptomyces unclassified
Streptomyces unclassified
2515154205 Streptomyces unclassified
2515154169 Streptomyces unclassified
2561511090 Streptomyces unclassified
2504756050 Streptomyces cattleya
Streptomyces cattleya|1.000
2511231200 Streptomyces cattleya
2510065062 Actinospica robiniae
644736339 Catenulispora acidiphila
2516653049 Sporichthya polymorpha
2519899649 Actinomadura atramentaria
Actinomadura cremea
2540341222 Actinomadura oligospora
Thermomonospora curvata
2515154141 Nonomuraea coxensis
Streptosporangium roseum
646564581 Thermobispora bispora
639633001 Acidothermus cellulolyticus
2515154087 Frankia unclassified
Frankia unclassified
2517093007 Frankia unclassified
Frankia unclassified
2509887025 Frankia unclassified
Frankia alni
637000116 Frankia unclassified
2517572101 Frankia unclassified
Frankia unclassified
2508501039 Frankia unclassified
UID1679||1.000
2506783011 Candidatus Frankia datiscae
2519899670 Nocardiopsis unclassified
Nocardiopsis dassonvillei
Nocardiopsis unclassified
Nocardiopsis alba
2524614583 Marinactinospora thermotolerans
2541047451 Thermobifida fusca
Thermobifida fusca|1.000
637000319 Thermobifida fusca
UID1453||0.177
2513237258 Mobilicoccus pelagius
Dermatophilus congolensis
2524023180 Kineosphaera limosa
Arsenicicoccus bolidensis
2522125155 Terracoccus unclassified
unclassified
649633057 Intrasporangium calvum
UID1665||1.000
UID1664
2531839443 Janibacter hoylei
Intrasporangiaceae unclassified
644736380 Kytococcus sedentarius
2521172561 Demetria terragena
649989926 Dermacoccus unclassified
2524614805 Serinicoccus marinus
2524614884 Ornithinimicrobium pekingense
UID1452||0.853
640753031 Kineococcus radiotolerans
2517572123 Arthrobacter unclassified
Arthrobacter unclassified
Arthrobacter chlorophenolicus
650377905 Arthrobacter phenanthrenivorans
Arthrobacter globiformis
2517572122 Arthrobacter unclassified
Arthrobacter unclassified
2519899654 Arthrobacter unclassified
639633006 Arthrobacter unclassified
2510461014 Arthrobacter nitroguajacolicus
Arthrobacter aurescens
Arthrobacter unclassified
Arthrobacter nicotinovorans
Arthrobacter nicotinovorans
2517572124 Arthrobacter unclassified
UID1631||0.997
2519899686 Arthrobacter unclassified
2562617041 Arthrobacter unclassified
2517287032 Arthrobacter unclassified
2517572146 Acaricomes phytoseiuli
Renibacterium salmoninarum
2528768210 Arthrobacter unclassified
2518645508 Arthrobacter unclassified
Arthrobacter unclassified
2519103017 Arthrobacter unclassified
2524023227 Arthrobacter castelli
2556921096 Arthrobacter sanguinis
2513237335 Nesterenkonia unclassified
Nesterenkonia alba
2524614768 Yaniella halotolerans
644736390 Micrococcus luteus
649633006 Arthrobacter arilaitensis
2534682146 Rothia mucilaginosa
Rothia mucilaginosa|1.000
646311954 Rothia mucilaginosa
Rothia dentocariosa
Rothia dentocariosa|1.000
Rothia dentocariosa
2513237283 Rothia aeria
UID1593||0.582
UID1592||1.000
2540341240 Microbacterium unclassified
642555133 Kocuria rhizophila
2522125173 Cryocola unclassified
unclassified
Leifsonia xyli
2523533581 Curtobacterium ginsengisoli
Humibacter albus
Clavibacter michiganensis
Clavibacter michiganensis|1.000
Clavibacter michiganensis
658341246 Agreia unclassified
2524614536 Glaciibacter superstes
2524023150 Agromyces italicus
2524023187 Agromyces subbeticus
2524023208 Rathayibacter toxicus
2521172612 Curtobacterium unclassified
2521172614 Microbacterium paraoxydans
Microbacterium unclassified
Microbacterium sp oral taxon 186
Microbacterium unclassified
Microbacterium testaceum
Microbacterium unclassified
2522572100 Microbacterium unclassified
2524614737 Microbacterium maritypicum
2523533579 Microbacterium luticocti
2523533558 Microbacterium indicum
2524023149 Agrococcus lahaulensis
2524023214 Leucobacter chironomi
Leucobacter salsicius
2521172760 Pseudoclavibacter faecalis
2524614761 Pseudoclavibacter soli
2504643007 Candidatus Rhodoluna lacicola
UID1595||1.000
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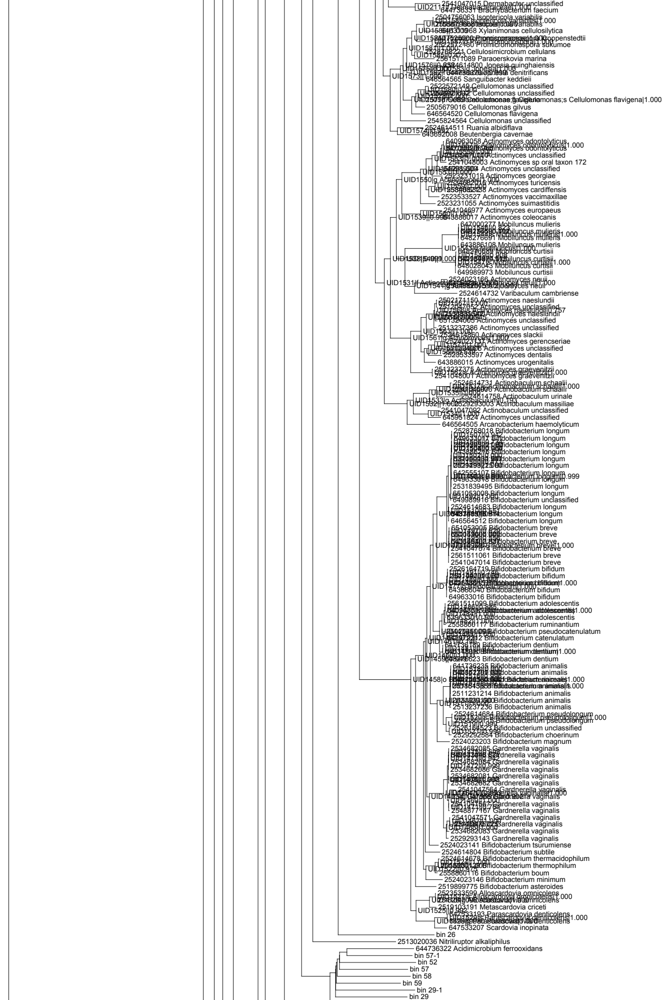
2517434006 Brevibacterium casei
Brevibacterium|1.000
647000216 Brevibacterium mcbrellneri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Xylanimonas cellulosilytica
Promicromonospora kroppenstedtii
2522572180 Promicromonospora sukumoe
2528768221 Cellulosimicrobium cellulans
2561511089 Paraoerskovia marina
2524614800 Jonesia quinghaiensis
Jonesia denitrificans
646564565 Sanguibacter keddieii
2522572149 Cellulomonas unclassified
Cellulomonas unclassified
Cellulomonas flavigena|1.000
2505679016 Cellulomonas gilvus
646564520 Cellulomonas flavigena
2545824564 Cellulomonas unclassified
2524614511 Ruania albidiflava
643692008 Beutenbergia cavernae
640963058 Actinomyces odontolyticus
Actinomyces odontolyticus|1.000
Actinomyces odontolyticus
Actinomyces unclassified
2541048003 Actinomyces sp oral taxon 172
Actinomyces unclassified
UID1550|g Actinomyces|1.000
2523231019 Actinomyces georgiae
Actinomyces turicensis
Actinomyces cardiffensis
2523533527 Actinomyces vaccimaxillae
2523231055 Actinomyces suimastitidis
2541046977 Actinomyces europaeus
UID1539||0.998
643886017 Actinomyces coleocanis
647000277 Mobiluncus mulieris
Mobiluncus mulieris
Mobiluncus mulieris|1.000
Mobiluncus mulieris
643886108 Mobiluncus mulieris
Mobiluncus curtisii
Mobiluncus curtisii
Mobiluncus curtisii|1.000
Mobiluncus curtisii
649989973 Mobiluncus curtisii
UID1531|f Actinomycetaceae
2524023166 Actinomyces neuii
Actinomyces neuii|1.000
2524614732 Varibaculum cambriense
2502171150 Actinomyces naeslundii
2512047052 Actinomyces unclassified
Actinomyces naeslundii|0.757
Actinomyces naeslundii
651324005 Actinomyces unclassified
2513237386 Actinomyces unclassified
2524614860 Actinomyces slackii
UID1561|g Actinomyces|1.000
2524023137 Actinomyces gerencseriae
Actinomyces unclassified
Actinomyces dentalis
643886015 Actinomyces urogenitalis
2513237375 Actinomyces graevenitzii
Actinomyces graevenitzii|1.000
2541046001 Actinomyces graevenitzii
2524614731 Actinobaculum schaalii
Actinobaculum schaalii|1.000
Actinobaculum schaalii
2524614758 Actinobaculum urinale
UID1533|g Actinobaculum|0.193
2529293003 Actinobaculum massiliae
2541047092 Actinobaculum unclassified
645951824 Actinomyces unclassified
646564505 Arcanobacterium haemolyticum
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
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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
UID1458|o Bifidobacteriales
Bifidobacteriaceae|1.000
Bifidobacterium animalis|1.000
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
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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
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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
Parascardovia denticolens
647533207 Scardovia inopinata
bin 26
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bin 57-1
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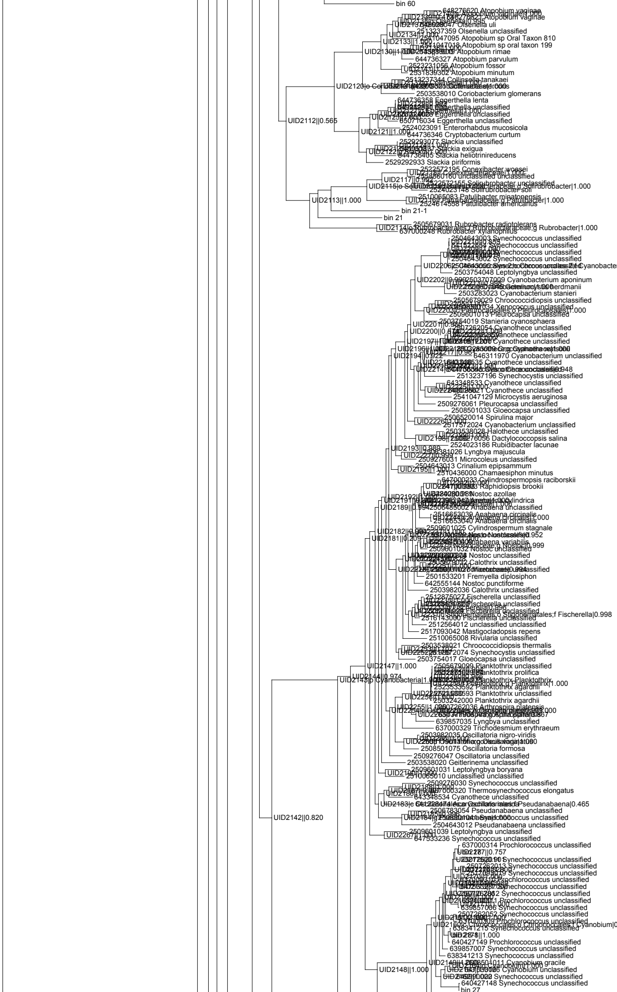
bin 59
bin 29-1
bin 29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Atopobium vaginae
Olsenella uli
2513237359 Olsenella unclassified
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UID2130||1.000
Atopobium rimae
644736327 Atopobium parvulum
2523231056 Atopobium fossor
2531839302 Atopobium minutum
2513237344 Collinsella tanakaei
UID2120|o Coriobacteriales
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Eggerthella unclassified
Eggerthella unclassified
Eggerthella unclassified
650716034 Eggerthella unclassified
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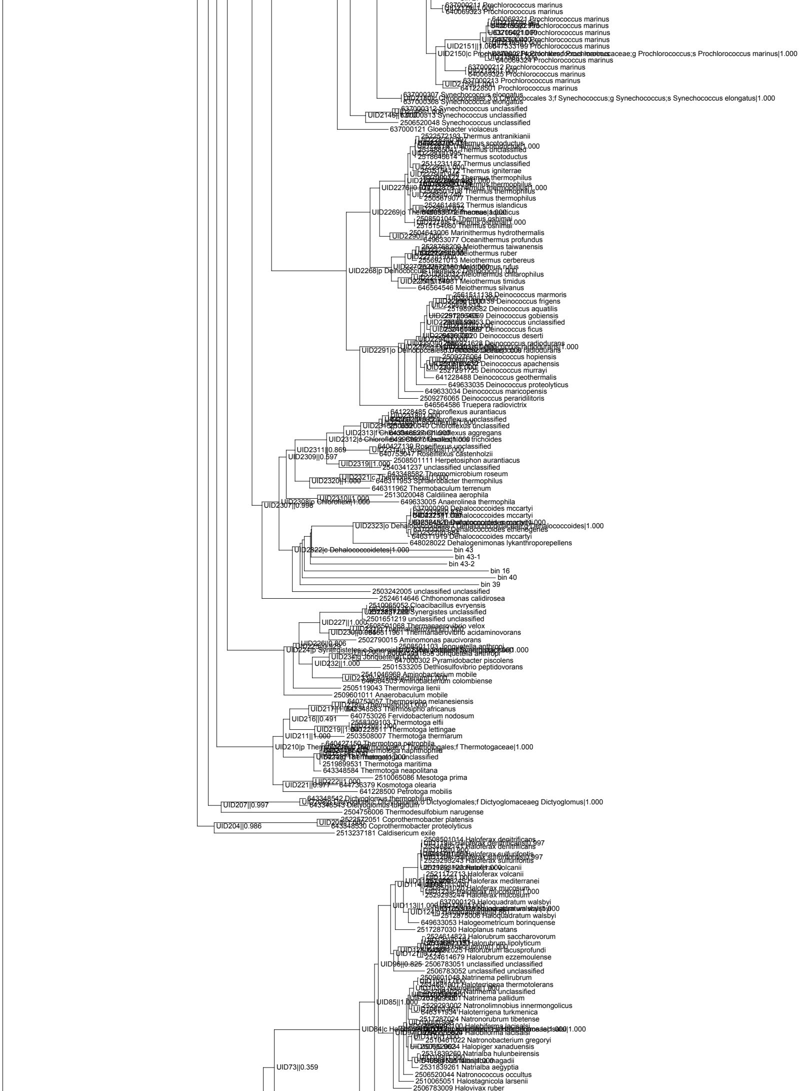
UID2121||1.000
644736346 Cryptobacterium curtum
2529293077 Slackia unclassified
Slackia exigua
644736405 Slackia heliotrinireducens
2529292933 Slackia piriformis
2522572195 Conexibacter woesei
unclassified unclassified
UID2117||0.992
Solirubrobacter unclassified
UID2115|o Solirubrobacterales
Solirubrobacter|1.000
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
Rubrobacteraceae;g 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
Geminocystis herdmanii
2503283023 Cyanobacterium stanieri
2505679029 Chroococcidiopsis unclassified
Xenococcus unclassified
Pleurocapsales|1.000
2509601013 Pleurocapsa unclassified
2503754019 Stanieria cyanosphaera
UID2201||0.986
2507262054 Cyanothece unclassified
UID2200||0.874
Cyanothece unclassified
UID2197
Cyanothece unclassified
UID2196
UID2194||0.922
646311970 Cyanobacterium unclassified
Cyanothece unclassified
UID2214
2513237196 Synechocystis unclassified
643348533 Cyanothece unclassified
UID2224
Cyanothece unclassified
2541047129 Microcystis aeruginosa
2509276061 Pleurocapsa unclassified
2508501033 Gloeocapsa unclassified
2506520014 Spirulina major
UID2226||1.000
2517572024 Cyanobacterium unclassified
2503538028 Halothece unclassified
UID2198
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
2516653040 Anabaena circinalis
2509601025 Cylindrospermum stagnale
UID2182||0.993
UID2181||0.209
Nostoc unclassified
Anabaena variabilis
2509601032 Nostoc unclassified
Nostoc unclassified
2505679032 Calothrix unclassified
UID2228
unclassified
2501533201 Fremyella diplosiphon
642555144 Nostoc punctiforme
2503982036 Calothrix unclassified
2512875027 Fischerella unclassified
Fischerella
Fischerella unclassified
Stigonematales;f Fischerella|0.998
2516143090 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
UID2144||0.974
Planktothrix prolifica
UID2143|p Cyanobacteria|1.000
Planktothrix Planktothrix
Planktothrix|1.000
2523533592 Planktothrix agardhii
2523533593 Planktothrix unclassified
UID2256||1.000
2503242000 Planktothrix agardhii
UID2255||1.000
2507262036 Arthrospira platensis
UID2254
Arthrospira
639857035 Lyngbya unclassified
637000329 Trichodesmium erythraeum
2503982035 Oscillatoria nigro-viridis
Oscillatoria
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
Pseudanabaena|0.465
2506783054 Pseudanabaena unclassified
UID2142||0.820
UID2184
Synechococcus
2504643012 Pseudanabaena unclassified
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
Cyanobium|0.557
638341215 Synechococcus unclassified
UID2278||1.000
640427149 Prochlorococcus unclassified
639857007 Synechococcus unclassified
638341213 Synechococcus unclassified
UID2149||1.000
2508501011 Cyanobium gracile
UID2148||1.000
Cyanobium unclassified
Synechococcus unclassified
640427148 Synechococcus unclassified
bin 27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640069323 Prochlorococcus marinus
640069321 Prochlorococcus marinus
Prochlorococcus marinus
Prochlorococcus marinus
Prochlorococcus marinus
UID2151||1.000
Prochlorococcus marinus
UID2150|c Prochlorophyceae;o Prochlorales;f Prochlorococcaceae;g Prochlorococcus;s Prochlorococcus marinus|1.000
640069324 Prochlorococcus marinus
637000212 Prochlorococcus marinus
640069325 Prochlorococcus marinus
637000213 Prochlorococcus marinus
641228501 Prochlorococcus marinus
637000307 Synechococcus elongatus
o Chroococcales 3;f Synechococcus;g Synechococcus;s Synechococcus elongatus|1.000
637000308 Synechococcus elongatus
637000312 Synechococcus unclassified
UID2146
637000313 Synechococcus unclassified
2506520048 Synechococcus unclassified
637000121 Gloeobacter violaceus
2522572193 Thermus antranikianii
Thermus scotoductus
Thermus scotoductus|1.000
Thermus unclassified
2518645614 Thermus scotoductus
2511231187 Thermus unclassified
Thermus igniterrae
Thermus thermophilus
Thermus thermophilus
Thermus thermophilus|1.000
Thermus thermophilus
2505679077 Thermus thermophilus
2524614852 Thermus islandicus
UID2276
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
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;o Chloroflexales|1.000
Oscillochloris trichoides
640427139 Roseiflexus unclassified
UID2311||0.869
Roseiflexus|1.000
640753047 Roseiflexus castenholzii
UID2309||0.597
UID2319||1.000
2508501111 Herpetosiphon aurantiacus
2540341237 unclassified unclassified
643348582 Thermomicrobium roseum
UID2321|c Thermomicrobia|1.000
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
Dehalococcoides mccartyi
UID2323|o Dehalococcoidales;f 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||0.964
646311961 Thermanaerovibrio acidaminovorans
2502790015 Aminomonas paucivorans
UID226||0.806
2508501103 Jonquetella anthropi
UID224|p Synergistetes;c Synergistia;o Synergistales;f Synergistaceae|1.000
Jonquetella anthropi
UID234|g Jonquetella|1.000
647000302 Pyramidobacter piscolens
UID232||1.000
2501533205 Dethiosulfovibrio peptidovorans
2541046968 Aminobacterium mobile
648564503 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;c Thermotogae;o Thermotogales;f Thermotogaceae|1.000
Thermotoga naphthophila
Thermotoga|1.000
Thermotoga unclassified
2519899531 Thermotoga maritima
643348584 Thermotoga neapolitana
2510065086 Mesotoga prima
UID222||1.000
UID221||0.977
644736379 Kosmotoga olearia
641228500 Petrotoga mobilis
643348542 Dictyoglomus thermophilum
Dictyoglomi;o 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
2523533245 Haloferax sulfurifontis
Haloferax volcanii
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Haloferax mediterranei
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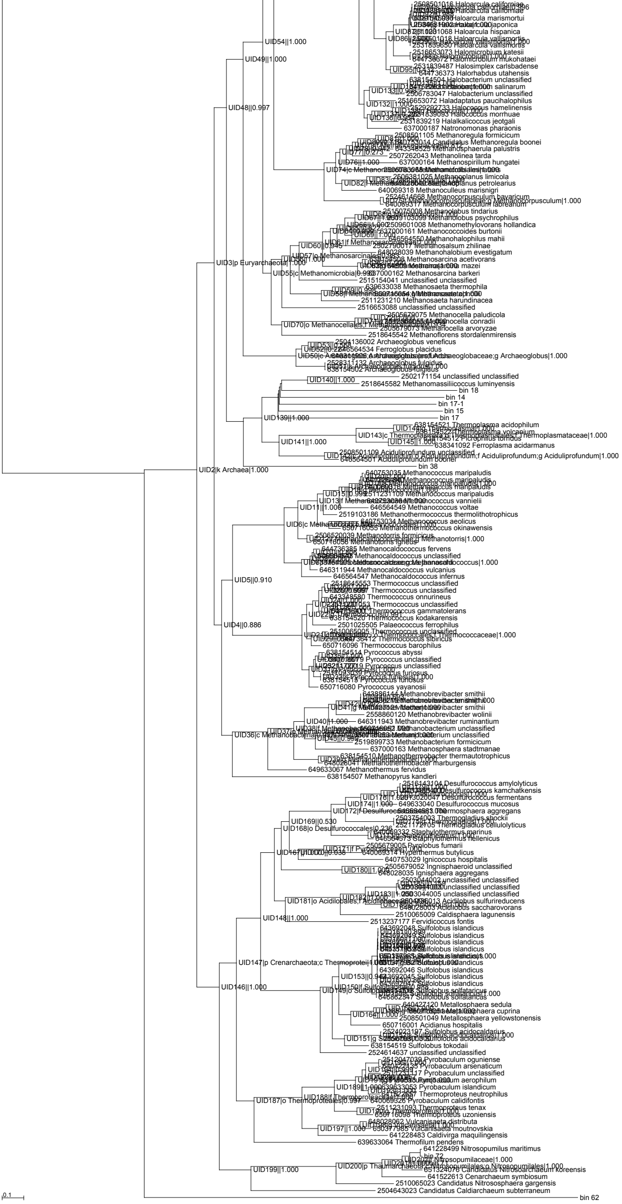
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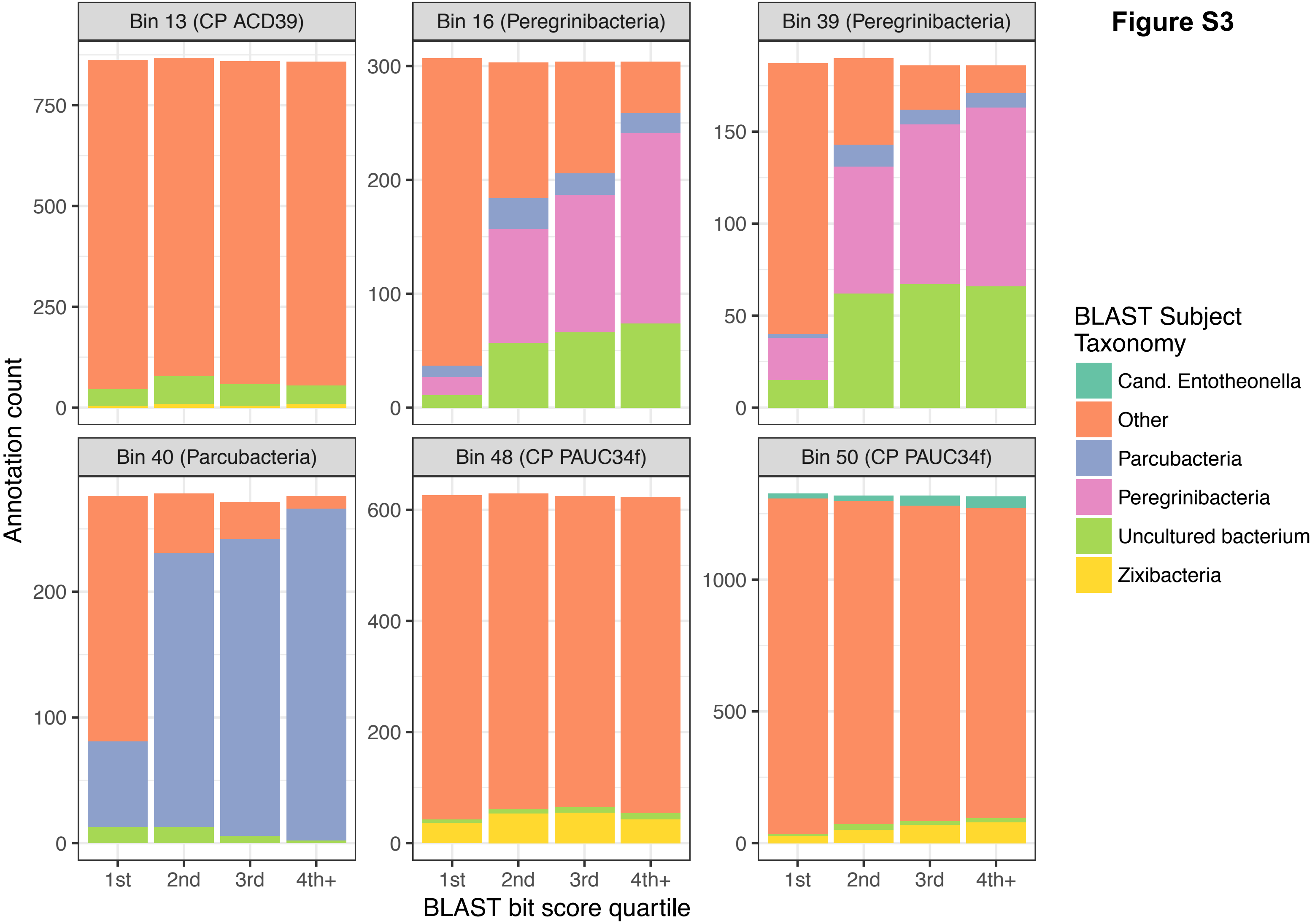
## Figure S3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Peregrinibacteria
Uncultured bacterium
Zixibacteria

Figure S4

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gi 326485776 gb GU940737 1 Uncultured bacterium clone N201B 317
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SAR406 cluster bacterium SCGC AAA160-I06
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gi 260071998 gb GQ350728 1 Uncultured marine bacterium clone SHBH1051
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45-1&&scaffold 922rc
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gi 189909304 gb EU570890 1 Uncultured bacterium clone Nit5A0650 165
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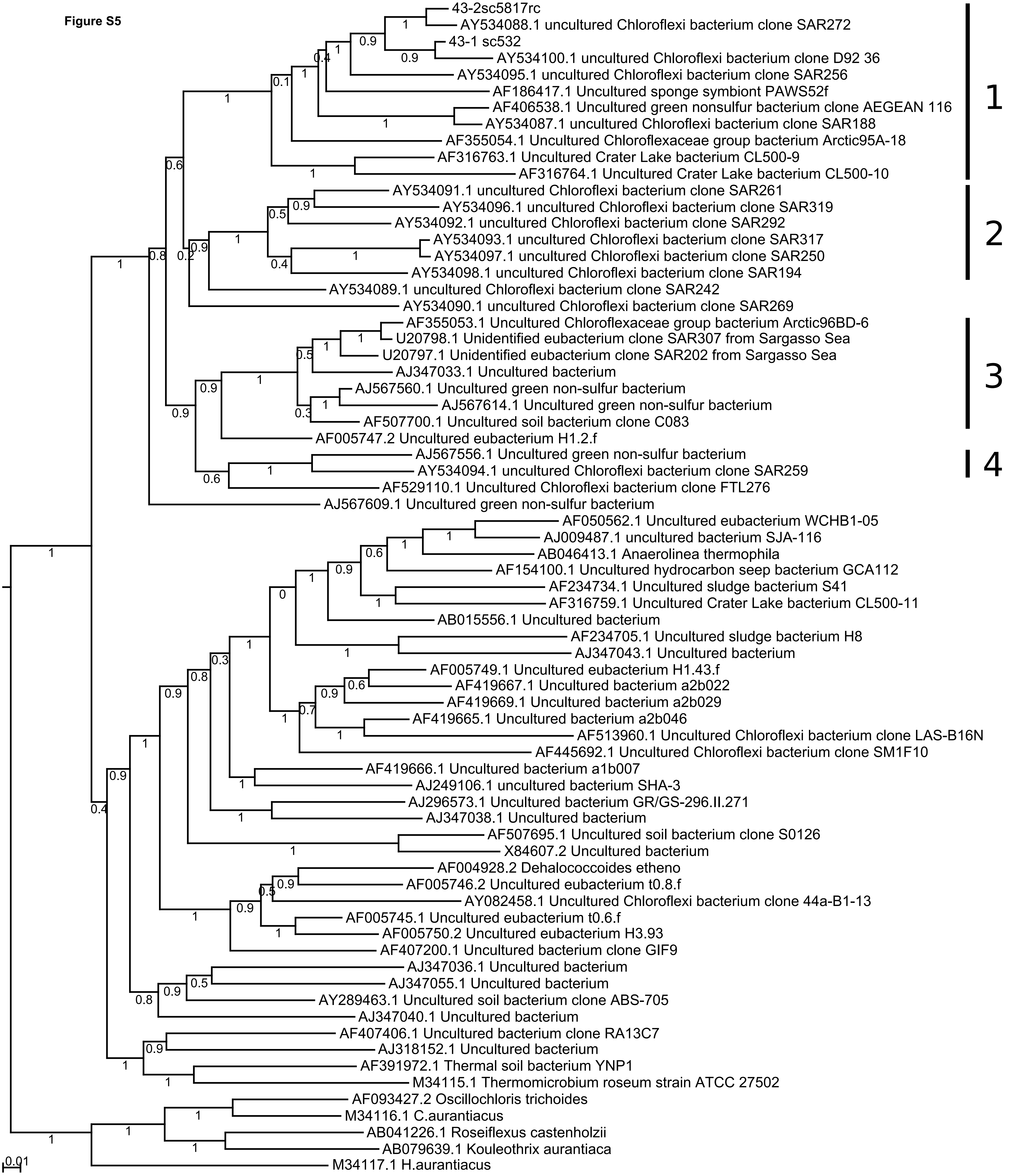
**Figure S5**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AJ567614.1 Uncultured green non-sulfur bacterium
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AF050562.1 Uncultured eubacterium WCHB1-05
AJ009487.1 uncultured bacterium SJA-116
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AF154100.1 Uncultured hydrocarbon seep bacterium GCA112
AF234734.1 Uncultured sludge bacterium S41
AF316759.1 Uncultured Crater Lake bacterium CL500-11
AB015556.1 Uncultured bacterium
AF234705.1 Uncultured sludge bacterium H8
AJ347043.1 Uncultured bacterium
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AB041226.1 Roseiflexus castenholzii
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3
4
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**Figure S6**

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Lactobacillus acidophilus 108734 11429
Clostridium acetobutylicum 129255 11429
Desulfitobacter alkalitolerans 98963 11387
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M62696 2 Fibrobacter succinogenes subsp succinogenes S85
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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
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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
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Caldilinea aerophila 26613 11427
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Kosmotoga 376719 11429
Thermotoga 62474 11429
Aminobacterium 11429
Synergistes 11377
Armatimonas 11429
Chthonomonas 11404
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P limnophilus 2845 11429
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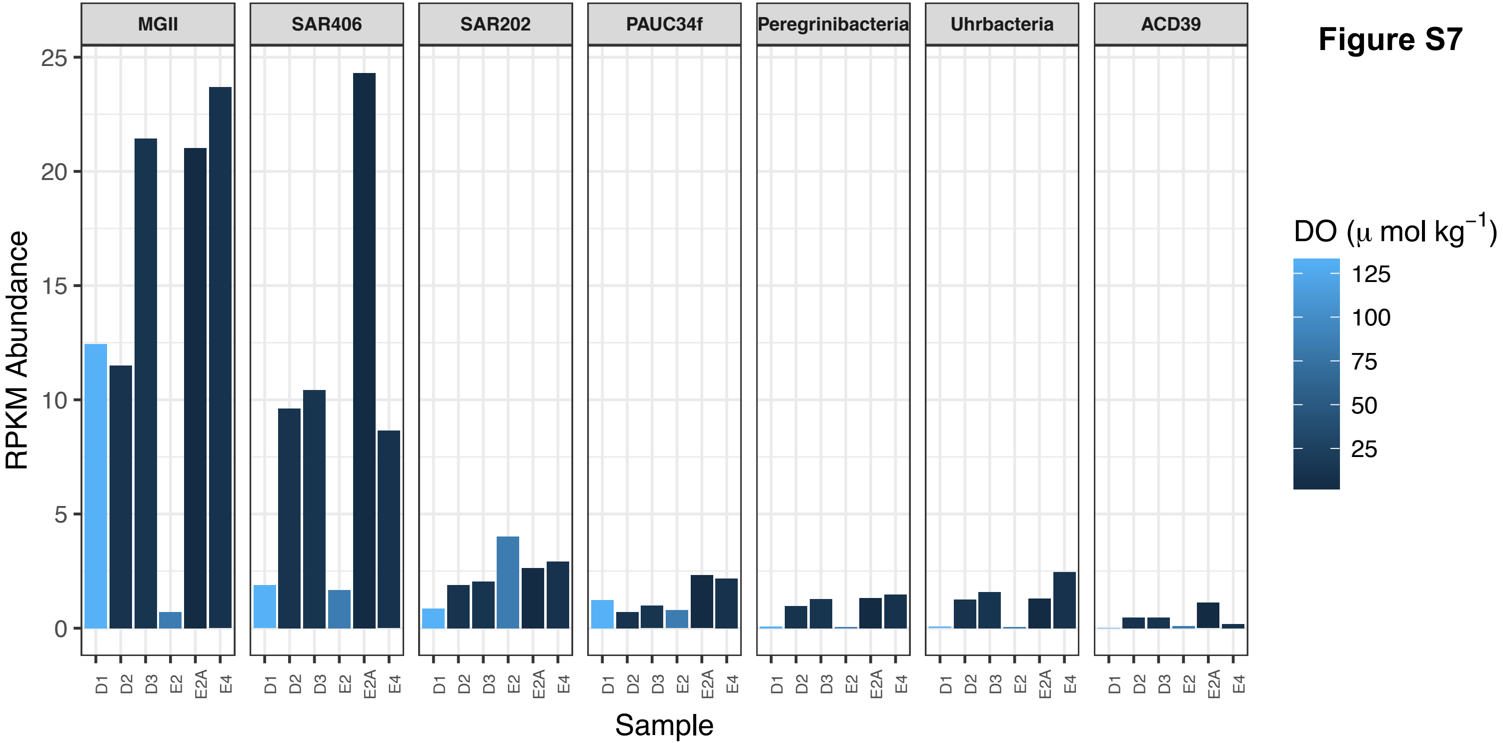
# Figure S7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Peregrinibacteria
Uhrbacteria
ACD39
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5
10
15
20
25
D1
D2
D3
E2
E2A
E4
Sample
DO (μ mol kg$^{-1}$)
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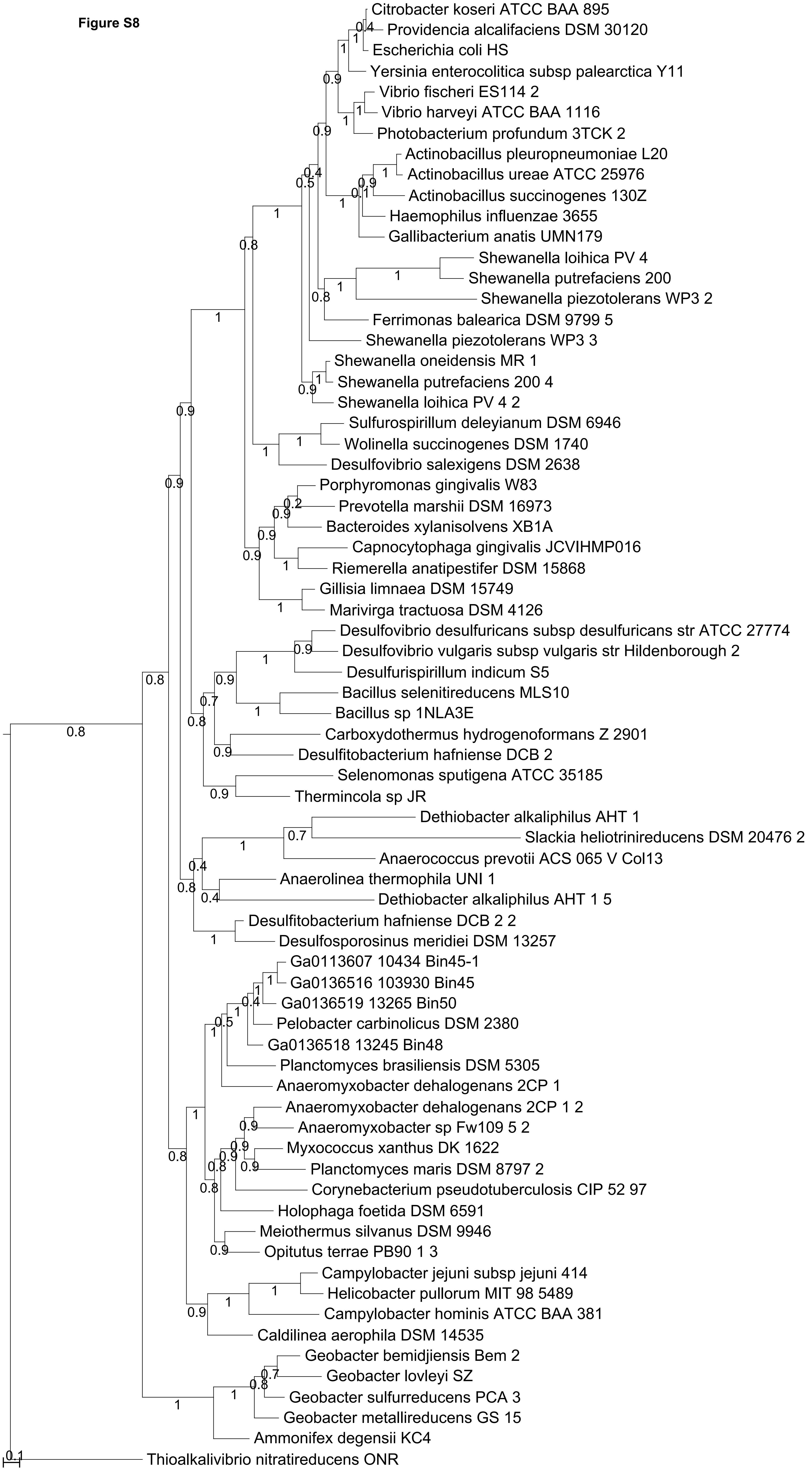
100
75
50
25

**Figure S8**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Vibrio harveyi ATCC BAA 1116
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Photobacterium profundum 3TCK 2
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Actinobacillus pleuropneumoniae L20
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Actinobacillus ureae ATCC 25976
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0.9
0.5
0.1
Actinobacillus succinogenes 130Z
1
Haemophilus influenzae 3655
Gallibacterium anatis UMN179
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Shewanella putrefaciens 200
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1
Ferrimonas balearica DSM 9799 5
Shewanella piezotolerans WP3 3
Shewanella oneidensis MR 1
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Wolinella succinogenes DSM 1740
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Desulfovibrio salexigens DSM 2638
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Porphyromonas gingivalis W83
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Prevotella marshii DSM 16973
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Bacteroides xylanisolvens XB1A
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Capnocytophaga gingivalis JCVIHMP016
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Gillisia limnaea DSM 15749
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Marivirga tractuosa DSM 4126
Desulfovibrio desulfuricans subsp desulfuricans str ATCC 27774
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Thermincola sp JR
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Ga0136516 103930 Bin45
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Ga0136519 13265 Bin50
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Pelobacter carbinolicus DSM 2380
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Ga0136518 13245 Bin48
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Meiothermus silvanus DSM 9946
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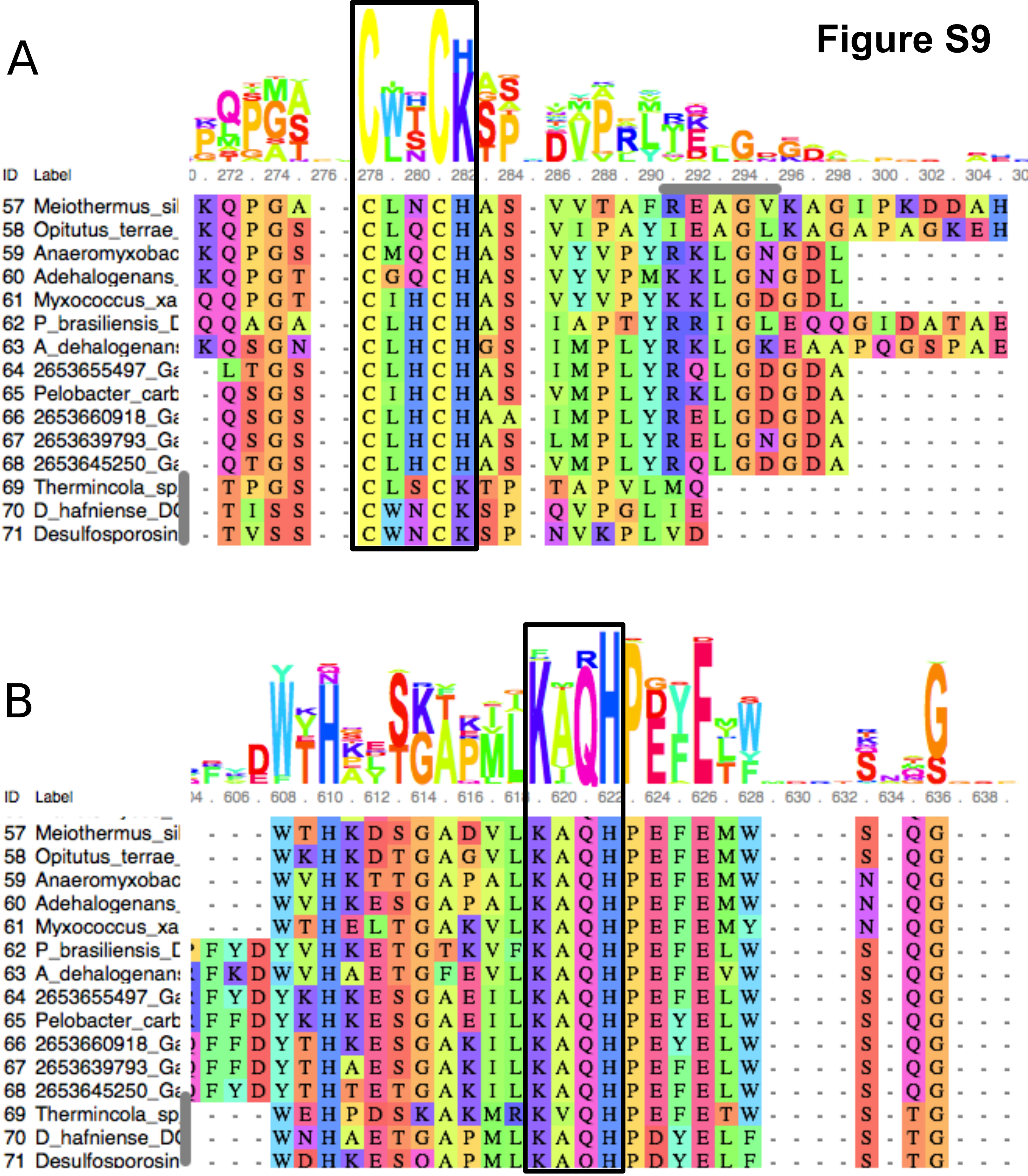
## Figure S9



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60 Adehalogenans_ K Q P G T - - C G Q C H A S - V Y V P M K K L G N G D L - - - - - - -
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B

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62 P_brasiliensis_D F Y D Y V H K E T G T K V F K A Q H P E F E L W - - - - S - Q G - - -
63 A_dehalogenans F K D W V H A E T G F E V L K A Q H P E F E V W - - - - S - Q G - - -
64 2653655497_Ga F Y D Y K H K E S G A E I L K A Q H P E F E L W - - - - S - Q G - - -
65 Pelobacter_carb F F D Y K H K E S G A E I L K A Q H P E Y E L W - - - - S - Q G - - -
66 2653660918_Ga F F D Y T H K E S G A K I L K A Q H P E Y E L W - - - - S - Q G - - -
67 2653639793_Ga F F D Y T H A E S G A K I L K A Q H P E F E L W - - - - S - Q G - - -
68 2653645250_Ga F Y D Y T H T E T G A K I L K A Q H P E F E L W - - - - S - Q G - - -
69 Thermincola_sp - - - W E H P D S K A K M R K V Q H P E F E T W - - - - S - T G - - -
70 D_hafniense_DC - - - W N H A E T G A P M L K A Q H P D Y E L F - - - - S - T G - - -
71 Desulfosporosin - - - W D H K E S Q A P M L K A Q H P D Y E L F - - - - S - T G - - -

**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 |

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|---|---|---|---|
| **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, 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. 14.99.39 |

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|---|---|---|---|
| **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 | |

| | | | |
|---|---|---|---|
| **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 | |