Decoding bacterioplankton metabolism 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], 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: thrashc@lsu.edu

Short title: Decoding microbes of the Dead Zone

Abstract

Marine regions that experience low dissolved oxygen (DO) from seasonal to long-term time scales, a.k.a. dead zones, are increasing in number and severity around the globe with deleterious effects on ecology and economics. One of the largest of these occurs on the continental shelf of the northern Gulf of Mexico (nGOM) as a result of eutrophication-enhanced bacterioplankton respiration and strong stratification. The effects of this perturbation on microbial assemblages, and therefore the underlying potential for biogeochemical cycling, have only begun to be explored. Here we present predicted roles for multiple organisms in various phases of nitrogen, carbon, and sulfur cycling and evidence for electron donor-based niche partitioning based on more than 70 high-quality genomes (33 of which are > 70% complete) reconstructed from whole community metagenomic data in the 2013 nGOM dead zone and metatranscriptomic expression data. All but two genomes could be classified into 17 named bacterial and archaeal phyla, and many represented the most abundant organisms in the dead zone (e.g. Thaumarchaeota, *Synechococcus*), some of which include members of the uncultivated "microbial dark matter" (e.g. Marine group II Euryarchaeota, SAR406). Surprisingly, we also recovered near complete genomes belonging to Candidate Phyla that are usually associated with anoxic environments: Parcubacteria (OD1), Peregrinibacteria, Latescibacteria (WS3), and ACD39. This work provides an important biogeochemical map for multiple phyla that will help to resolve the impacts of hypoxia on nutrient flow in the dead zone.

Introduction

Dissolved oxygen (DO) below 2 mg L^{-1} (~62.5 µM- "hypoxia") becomes dangerous or lethal to a wide variety of marine life, including organisms of economic importance[1]. Hypoxia results from 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]. Dead zones are increasing in number and frequency as use of nitrogen-based fertilizers increases with a concomitant increase in transport to coastal oceans via runoff [2]. In the nGOM, nitrogen deposition from the Mississippi and Atchafalaya Rivers leads to one of the world's largest seasonal dead zones, with bottom water hypoxia that can extend over 20,000 km^2 [1]. Action plans to mitigate the nGOM dead zone 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 dead zone nutrient transformation: microorganisms.

Much of our current knowledge regarding microbial contributions to regions of low DO comes from numerous reports describing 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, the nGOM dead zone 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 dead 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 in the dead zone showed Thaumarchaea dominated[21] in low DO waters and could be highly active[22]. Of the thousands of operational taxonomic units (OTUs), only 15 OTU abundances correlated with DO (either positively or negatively), and many of the most abundant taxa were expected aerobes based on taxonomic affiliation[21]. Further, *amoA* and Thaumarchaeal 16S rRNA gene copy per L of seawater inversely correlated with DO. Consistently, aerobic ammonia oxidation, not nitrate reduction, was the dominant source of nitrite in the 2012 dead zone[22]. Nitrite accumulation in waters even with low DO was unusually high and possibly due to a decoupling of ammonia- and nitrite-oxidation[22]. Thus the nGOM dead zone has unique microbiological features that echo its physico-chemical distinctions.

However, despite being one of the largest zones of eutrophication-based hypoxia in the world and its relevance to comparisons with global oxygen minimum zones, we still know comparatively little about the microbial ecology and physiology within the nGOM dead zone. To improve our understanding of the metabolic roles played by dead zone taxa, we reconstructed nearly 80 bacterioplankton genomes from metagenomic sequences across six sampling sites spanning DO concentrations of 2.2 - 128.8 μM[21], and mapped metatranscriptomic sequences to measure gene and genome activity. We confirm that many of the most dominant and active taxa have predicted aerobic metabolism, implicate many organisms in the nitrogen, sulfur, and carbon cycles, recover members of Candidate Phyla (CP) that have gone previously unreported in the system, and provide evidence for electron donor-based niche partitioning.

Results

Metagenomic assembly yielded high quality genomes from a wide range of taxa

We recovered a total of 77 bacterioplankton genomes from two separate assemblies (Table 1). 33 had predicted completeness > 70%, and only six had predicted contamination > 6% (Table S1). The genomes belonged to 17 bacterial and archaeal phyla, and in some cases, multiple subclades within a phylum (Table 1). Multiple genomes represented dominant taxa previously observed with 16S rRNA gene surveys[21]: two Thaumarchaeota genomes that grouped closely with *Nitrosopumilus* taxa, six Marine Group II Euryarchaeota (MGII), three *Synechococcus*, five *Nitrospina* and SAR406 (Marinimicrobia) genomes, and several species from the *Alpha*- and *Gammaproteobacteria* (Figs S1, S2). Actinobacteria, Proteobacteria, and Planctomycetes were represented by the largest number of genomes, although most in the latter two phyla had low predicted completion percentages (Table S1). None of the Planctomycetes genomes grouped with known anammox bacteria in the *Brocadiaceae* that play important roles in some OMZs[9,11], but instead grouped with either the *Planctomycetaceae* or *Phycisphaerae* (Fig. S1). In general, all of the most abundant phyla detected with 16S rRNA gene analysis in Gillies *et al.* (2015) were represented by at least three genomes, and there were many from less abundant phyla, including *Gemmatimonadetes* and *Ignavibacteriae* (Table 1). Notably, we recovered genomes from several uncultivated microbial “dark matter” clades. In addition to the uncultivated SAR406s and MGIIs, we reconstructed three SAR202 genomes and six genomes from three different Candidate Phyla (CP): Parcubacteria (formerly OD1- specifically *Candidatus* Uhrbacteria), Peregrinibacteria, Latescibacteria (WS3), and one putatively assigned to ACD39 (Fig. S1, S3).

Roles in nitrogen and sulfur cycling

We identified potential bacterioplankton contributions to every phase of inorganic nitrogen cycling except nitrogen fixation (Fig. 1). *Nitrosopumilus* and *Nitrospina* spp. exclusively occupied roles in ammonia and nitrite oxidation, respectively, consistent with previous observations in the dead zone[21,22]. The Bin 71 *Nitrosopumilus* genome has predicted *amoABC* genes in a syntenic arrangement to that of *Nitrosopumilus maritimus* SCM1 (Walker, 2010), and we observed transcripts from these genes in all samples, supporting the view of active nitrification. *Nitrosopumilus* spp. dominated the lowest DO sites (Fig. 2), and showed proportionate activity, based on rank-residuals (see methods) for RNA vs. DNA recruitment rank (Fig. 3, Rows 21 & 28). In contrast, *Nitrospina* spp. displayed much lower abundances (Fig. 2), but one genome (Bin 25) demonstrated high activity relative to other taxa across all samples

(Fig. 3, Row 75). Bin 25 was also the only genome with a nitrite oxidase *nxrA*[23], and we observed expression across all samples with reliable data (Table S1). Active, but low abundance *Nitrospina* corroborate Bristow *et al.* (2015), who found low overall expression of *nxrA*, with all transcripts predicted to belong to *Nitrospina* spp.. Nitrite levels and temperatures in our samples also support their suggestion that *Nitrospina* spp. may have been nitrite and/or temperature limited[22,24], thus leading to low rates of nitrite- relative to ammonia-oxidation and an accumulation of nitrite to micromolar concentrations- an unusual phenomenon in a system not fully anoxic.

The 2013 dead zone data show a similar nitrite accumulation to micromolar concentrations (Table S1). Abundant nitrite may have been reduced along two different paths. Two each of Bacteriodetes, Latescibacteria, and SAR406 genomes had predicted *nrfAH* genes for nitrite reduction to ammonia (Table S1). We observed activity for these taxa (Fig. 3) and the *nrfAH* genes (Fig. 4), indicating a possible nitrite/ammonia metabolic loop in three of the four hypoxic sites. Alternatively, multiple genomes contained predicted *nirK* and *nirS* genes for reduction of nitrite to nitric oxide. Aggregate expression of *nirK* genes, found primarily in the *Nitrospina* and *Nitrosopumilus* genomes, but also in one *Flavobacteriaceae* and one MGII genome, exceeded that of all other reductive nitrogen cycle genes (Fig. 4). The presence of *nirK* in the absence of other denitrification genes may indicate a nitrite detoxification method[25,26], or simply an alternative terminal electron accepting process during low DO[27].

We observed roles for many organisms in other parts of the nitrogen cycle as well. Although multiple genomes contained genes for nitrate reduction, and we observed expression of *narGH* in most samples (Fig. 4), complete denitrification capability was only predicted for one *Flavobacteriaceae* genome (Bin 10, *Polaribacter* sp.) (Fig. 1). Also, we only observed expression of all required genes (*nar*, *nap*, *nir*, *nor*, *nos*) in the lowest DO sample (E2A- Fig. 4). However, our findings suggest denitrification can occur via multiple taxa in concert, and many organisms appeared poised to reduce nitrous oxide via *nosZ* genes (Fig. 1). The pervasive *nosZ* genes in the absence of other parts of the denitrification pathway suggest that these taxa have evolved to reduce nitrous oxide as a terminal electron acceptor. Given the paucity of genomes with nitric oxide reductases, production of nitrous oxide via *Nitrosopumilus*[28,29] seems plausible as the dominant source. We detected *nosZ* transcripts in nearly all samples (Fig. 4). A number of genomes also had predicted capacities to convert organic nitrogen compounds to inorganic sources of nitrogen (Fig. 1). Importantly, *Synechococcus* and one *Rhodobacteraceae* genome, closely related to *Donghicola* spp., encoded cyanate lyases corroborating previous reports of similar organisms using cyanate as a nitrogen source[30,31].

Fewer organisms had putative pathways for sulfur cycling (Fig. 1). *Chromatiales*, *Rhodobacteraceae*, and *Rhodospirillales* genomes contained *dsrAB* genes (Table S1), predicted by phylogenetic analysis[32] to operate oxidatively (Fig. S4). Genomes in these same clades also contained *aprAB* and *sat* genes for sulfate/sulfite conversion, although based on the *dsrAB* data, *aprAB* likely function in reverse as well. We observed putative thiosulfate oxidation genes in the same groups and the *Gemmatimonadaceae*. Thus, sulfur oxidation was phylogenetically restricted. *Chromatiales* taxa were abundant in hypoxic samples (Fig. 2) similarly to reports in the ETNP OMZ[33]. However, these taxa contributed fewer transcripts than would be expected based on DNA abundance (Fig. 3) suggesting a limited influence. Two SAR406 genomes had predicted genes for thiosulfate reduction to sulfide (and/or polysulfide reduction[34])- we detected transcripts for these genes only in samples E2A and E4 (Table S1).

Illuminating metabolism within microbial dark matter

Several recovered genomes belonged to clades with no cultured representatives: Marinimicrobia, MGII, SAR202, and the CP Parcubacteria (OD1), Peregrinibacteria, and Latescibacteria (WS3). Marinimicrobia (a.k.a. SAR406 and Marine Group A) are widely distributed[35,36] and frequently observed in oxygen minimum zones[5,37], but nevertheless remain poorly understood from a functional perspective. Four Marinimicrobia genomes (estimated at > 73% complete) informed our metabolic reconstruction of this group (Figs. 5, S5). SAR406 genomes have both high and low-affinity cytochrome c oxidases[38] (Table S1) extending previous observations of adaptive traits for a range of DO concentrations[37]. This is consistent with their predominance in lower DO samples from the dead zone (Fig. 2). The genomes also encode potential for thiosulfate/polysulfide reduction to sulfide as previously observed[37], however we additionally predict capabilities in nitrate reduction, nitrous oxide reduction, and nitrite reduction to ammonia (Fig. 1, Table S1). The genomes contain putative transporters for a variety of dissolved organic matter (DOM) components including nucleosides, amino and fatty acids, and oligopeptides. They also contain an enrichment of both glycoside hydrolases (GH) and carbohydrate binding modules (CBM) (Table S1), the majority of which have secretion signals indicating they target external carbohydrate nutrients. This supports previous predictions for organic matter degradation by these taxa[39]. Thus, Marinimicrobia likely perform chemoorganoheterotrophic metabolism with flexibility in terminal electron accepting processes that implicate them in nitrogen and sulfur cycling.

Other well-known, but still as yet uncultivated, taxa include SAR202 and MGII. Members of the SAR202 clade of Chloroflexi also inhabit a wide variety of marine environments[40], frequently in deeper waters[40-42], but remain functionally obscure. We recovered three SAR202 genomes (estimated > 83% complete) that, although present at low abundance (Fig. 2), nevertheless showed relatively high activity in some samples (Fig. 3). These organisms likely respire oxygen, however nitrate and nitrous oxide reductases were recovered in two genomes, indicating a potential for utilization of alternative terminal electron acceptors (Table S1). While transporter predictions support previous observations of DOM uptake[41], the SAR202 genomes also contained predicted copies of 2-oxogluterate synthase and citryl-CoA lyase, suggesting a possible C-fixation route via the reductive TCA cycle. Our MGII reconstructions largely corroborate previous descriptions[43,44] of these organisms as aerobic chemoorganoheterotrophs with transporters for a variety of DOM compounds (Table S1).

Recovery of Parcubacteria from a coastal marine system is unusual, but not unprecedented. Parcubacteria SAGs have been identified from marine and brackish sources[39].

However, Peregrinibacteria have thus far only been found in terrestrial subsurface aquifers[45-48]. Consistent with previous reports of obligate fermentative metabolism by Parcubacteria and Peregrinibacteria[39,45,47,49], we identified no respiratory pathways for these taxa and they trended towards greater abundances in the lowest DO samples (Fig. 2). Furthermore, we found no genes linking them to substantial roles in nitrogen or sulfur cycling.

Latescibacteria have been proposed to have a particle-associated, strictly anaerobic lifestyle, with many genes available for the breakdown of complex algal cell wall components and utilization of the resultant monomers[39,50]. While our carbon substrate predictions and flagellar gene identification largely substantiate these findings, the dead zone Latescibacteria encode cytochrome c oxidases and other elements of aerobic electron transport chains (Table S1). The discrepancy in predicted physiological roles between these and previously identified Latescibacteria may be due to the incompleteness of the single-cell genomes[39] or perhaps horizontal gene transfer causing differentiation within the phylum. Indeed, the best BLASTP hits to the cytochrome c oxidase subunits in the Bin 50 genome matched an *Acidobacteria* strain (Table S1). While the possibility also exists that the entire contig was inappropriately binned, the remaining genes on the contig do not support its assignment to another specific taxon (Table S1). The even distribution of the dead zone Latescibacteria across varied DO concentrations also supports their predicted aerobic capability (Fig. 2), but this hypothesis needs further investigation.

One of the genomes with the highest transcriptional activity across samples was Bin 13 (Fig. 3), which grouped with CP ACD39 taxa (Fig. S1). However, the phylogenetic position was poorly supported, so we consider this designation putative. The genome for this organism encodes a predicted obligate aerobic chemoheterotrophic metabolism, with no designated roles in the nitrogen or sulfur cycles (Fig. S7). Its high activity indicated the importance of a DO consuming, organic carbon-based lifestyle even in low DO waters.

Evidence for electron donor-based niche partitioning

Although some of the recovered CP taxa likely subsist via an obligate anaerobic lifestyle, the majority of groups in the dead zone had one or more genomes that encoded cytochrome c oxidases (and other electron transport chain components) for respiring oxygen (Table S1). Pervasive aerobic metabolism in an area of depleted oxygen seems counterintuitive, yet despite DO being as low as 0.2 μM in the E2A sample, oxygen likely remained prevalent enough to sustain aerobic microbes. As little as 0.2-0.3 μM oxygen inhibited denitrification in OMZ populations by 50%[51], and Bristow *et al.* (2015) experimentally verified that at levels as low as 20 μM DO, aerobic ammonia oxidation by marine Thaumarchaea, rather than nitrate reduction, led to nitrite accumulation in 2012 nGOM dead zone bottom waters. Most of the taxa responsible for the largest number of transcripts (proportionally- Fig. 3, stars) were from groups of predicted aerobes, and the only groups that could be assigned dissimilatory nitrate reduction genes (e.g. Bin 10 (Flavobacteriaceae), Bin 51-1 (Marinimicrobia), etc.) also had cytochrome c oxidases (Table S1), making these taxa likely only facultative anaerobes. Based on overall pathway reconstruction and gene expression, the likely options for external terminal electron acceptors appeared limited to oxygen, nitrate, nitrite, or nitrous oxide. Indeed, we observed expression of cytochrome c oxidase genes at similar or greater levels than nitrate reductases (Fig. 4), indicating active aerobic respiration in dead zone bacterioplankton, even in dysoxic (1-20 μM DO[5]) water. Although we also observed *nirK* transcripts at higher levels than any of these other gene sets, concurrent expression of all genes indicates possible co-reduction of multiple compounds, which can occur in non-limiting electron donor circumstances[52].

In contrast to the limited number of terminal electron-accepting processes available, electron-donating processes occurred in much greater variety, spanning different forms of both lithotrophy and organotrophy. The dominant Thaumarchaea were predicted ammonia-oxidizing chemolithotrophs and one of the most active genomes, Bin 25, represented nitrite-oxidizing *Nitrospina* spp. We identified the potential for sulfur chemolithotrophy in both *Gamma-* (*Chromatiales*) and *Alphaproteobacteria* (*Rhodobacteraceae* and *Rhodospirillales*) genomes. Furthermore, these genomes encoded a multitude of chemoorganoheterotrophic options. We identified transporters for import of many different DOM components, from sugars to amino and carboxylic acids, differentially distributed throughout the various taxonomic groups (e.g., oligopeptide transporter family vs. p-aminobenzoyl-glutamate transporter family- Table S1). Within carbohydrate metabolism, CAZy profiles indicated other differential preferences. For example, while as expected the chemolithotrophic *Nitrosopumilus* genomes contained no predicted GH or polysaccharide lyases (PL) (e.g., see the CAZy database), Marinimicrobia genomes were enriched in the former, and Latescibacteria genomes showed evidence for enrichment in both (similarly to previous observations[50]). SAR202 genomes contained similar numbers of GH and carbohydrate esterases. The comparative cornucopia of metabolic pathways for electron-donating relative to electron-accepting processes strongly supports the hypothesis that niche differentiation within dead zone bacterioplankton occurs predominantly via specialization for different oxidizable substrates rather than for different roles in the important redox cascade in OMZs[4,5]. Indeed, the diversity of compounds within DOM supplies myriad opportunities for microbial differentiation in the chemoorganoheterotrophic space[53-56].

Discussion

Our results provide the first system-level genomic, and some of the most comprehensive metabolic, reconstructions and assessment of active functions to date for bacterioplankton in the nGOM dead zone. These genomes comprise the most abundant and/or active taxa observed throughout the region in both 2012[22] and 2013[21] and CP taxa that had gone previously undetected. The pervasiveness of aerobic respiration pathways and the limited number of alternative terminal electron accepting processes supports a view that bacterioplankton likely occupy different niches based on specialized oxidation of different electron donors, including various DOM components.

This has distinct implications for dead zone creation, maintenance, and dissolution because the amount of oxygen consumed by a given taxon will depend greatly on the kinetics of the terminal oxidase(s), the reducing equivalents available from the electron donor of choice, and in the case of organic compounds, the relative use of that substrate for growth vs. energy (bacterial growth efficiency[57]). How changing electron donor affects the relative abundance and DO consumption rates of these organisms will be an important area of future research. Unfortunately, the relative oxygen consumption rates for different taxa across different substrates has been cataloged for only a small number of taxa[58] and many important to the dead zone remain uncultured. Customized cultivation strategies for nGOM bacterioplankton are showing some success in this area[59], and can provide valuable additional data on respiration rates for individual organisms. We also know little about the seasonal variations in bacterioplankton assemblages in the nGOM, or how these relate to electron donor availability. Previous work indicates, for example, that Thaumarchaea occur in lower abundances during spring[60,61], before DO decreases, than they did during the 2013 dead zone. This means that these taxa become competitive at a later seasonal stage, but whether that is caused by low DO, changes in competitiveness based on electron donor availability, or some other factor is unknown. Indeed, the lack of microbial time series data in the nGOM leaves many additional open questions for these and other taxa. Which taxa respire the most oxygen? Are they abundant year round, or, if not, when do they become important and what selects for this? How do changing DOM sources and components affect respiration rates at the individual taxon and whole community scale? What is the role of particle-associated taxa in DO consumption? Answers will provide greater understanding of the dynamics resulting in low DO and deoxygenation trends in the world's oceans, as well as provide context for comparative studies between dead zones and oxygen minimum zones around the globe.

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). 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 sparged and filled with RNAlater. 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)[62]. RNA (as cDNA) and DNA libraries (six samples/lane) were linker barcoded and pooled for high-throughput Illumina HiSeq 2000 paired-end sequencing at Argonne National Laboratory.

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 at the Argonne National Laboratory Next Generation Sequencing facility. The data are available at the NCBI SRA repository under the BioSample accession numbers SAMN05791315, SAMN05791316, SAMN05791317, SAMN05791318, SAMN05791319, SAMN05791320, SAMN05791321, SAMN05791322, SAMN05791323, SAMN05791324, SAMN05791325, SAMN05791326 (the first six refer to DNA samples, the latter six, RNA). DNA sequencing resulted in a total of 416,924,120 reads that were quality trimmed to 413,094,662 reads. Prior to assembly, 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[63,64]. Briefly, quality filtered reads were assembled with IDBA-UD[65] 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, but the Thaumarchaeota bin was very large and predicted to have high contamination from other taxa. Assuming expected genome sizes of ~1.6 Mb and average relative abundances within the community of 20% or greater, our initial sequencing run would have produced at least 5000x coverage for a hypothetical Thaumarchaeota genome. To reduce this burden on the assembly algorithm, a second round of assembly using a 5% random sub-selection of the pooled DNA reads was completed using the same settings. The subset of reads was generated randomly using the split command to create sub-files that were 1/20th the size of the original the metagenomic file. A sub-file was chosen at random and was assembled using the parameters previously stated. The subassembly resulted in a mixed Thaumarcheaota bin (Fig. S9) that could be separated in two based on comparative read mapping from different samples (below). The final genomes were nearly complete (96 and 79%, respectively), and grouped with other *Nitrosopumilus* genomes (Table 1, Figs. S1, S2).

DNA and RNA mapping. Metagenomic and metatranscriptomic sequencing reads from each sample were separately mapped to binned contigs using BWA[66] 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[67], 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. In one case (Bin 51_l), the outlying contigs were sufficiently similar to be formed into a separate bin. Next, in bins that still showed > 10% contamination, contigs were separated according to comparative relative abundance of mean DNA read coverage by sample. In three cases (Bins 33, 40, 62), this was insufficient to reduce contamination. 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)[68]. Ribosomal proteins for each bin were identified with Phylosift[69]. Amino acid alignments of the individual ribosomal proteins were generated using MUSCLE[70] and trimmed using BMGE[71] (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[72] 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[73], and required just over 56 hours of wall clock time. The alignment is available in SI.

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 blasted against the NCBI nr database to corroborate CheckM assignments. Several of the most abundant OTUs in Gillies *et al.* (2015) matched the elusive and important OM1 clade of marine Actinobacteria[74], so we explicitly included genome sequences in our ribosomal protein tree from taxa that have been placed near this clade previously[75,76]. While several of our genomes group with Illumatobacter or the MedAcidi sequences, these are not expected to be true OM1 organisms, and 16S rRNA gene blast results from bins 29-1, 58, and 60 did not support classifying these taxa as OM1. However, their proximity to a close relative of the OM1 clade, *Candidatus* Actinomarina minuta, make them useful contributions to future studies of the group. 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[40] (Fig. S10). Alignment, culling, and inference were completed with MUSCLE[70], Gblocks[77], and FastTree2[78], respectively, with the FT_pipe script. The script is provided in SI. 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. Quartiles were determined in R using the summary function. In the case of the Parcubacteria and Peregrinibacteria genomes, the majority of high quality blast hits were consistent with the ribosomal protein tree taxonomy (Figs. S1, S3). For the Bin 13 and WS3 genomes, blast hit identification did not return clear results- hits included a wide variety of taxa. This is consistent with what would be expected from novel genomes that have few or no members in the database, however this analysis did not directly corroborate the ribosomal protein tree phylogeny. 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 this organism was designated a Planctomycetes.

Metabolic reconstruction. Post-binning, genomes were submitted individually to IMG[79] 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[80]. 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)[81].

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[82] 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. N_{ij} was generated using the samtools[66] idxstats function after mapping with BWA. The data in Fig. 2 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. Mean coverage for each supercontig was calculated using bedtools[83] 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. 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.

nxrA and dsrAB phylogeny. Initial annotation of our bins identified putative nitrate reductases, however none with explicit assignment as nxr genes putatively involved in nitrite oxidation, which was unusual considering that *Nitrospina* spp. are nitrite-oxidizing chemolithotrophs. Since *nxrA*-type nitrite oxidases are homologous with *narG*-type nitrate reductases (and polyphyletic)[23], annotation for these genes was curated with phylogenetic analysis using known *nxr* genes. Reference sequences of known *nxrA*/*narG* homologs from Lüke *et al.* (2015) were searched against a database of all the binned scaffolds (makeblastdb –dbtype nucl with default settings except -parse_seqids -hash_index) using tblastn with default settings (except –max_query_seqs 10000). Nine bins had hits to any sequences in the reference file with bit scores > 100. All annotated protein sequences were downloaded for these bins and used to create a blast protein database (makeblastdb –dbtype prot with default settings except -parse_seqids -hash_index); the reference sequences were searched through this database using blastp with default settings (except –max_query_seqs 10000). All blast suite commands used v. 2.2.28+. The eight proteins returning matches with bit scores > 100 were selected for phylogenetic analysis using the original reference sequences. Alignment, culling, and inference were completed with the FT_pipe script. The protein from *Nitrospina* Bin 25 grouped closely with the *nxrA* gene from *N. gracilis* (Fig. S15), providing strong evidence for this being a functional nitrite oxidase. To evaluate whether the predicted *dsrAB* genes in bins 23, 35, and 61-2 functioned most likely as oxidative or reductive, they aligned with a previously established reference dataset[32] that was used for phylogenetic inference also using the FT_pipe script.

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Author contributions

JCT, BJB, 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 lead manuscript writing and all co-authors evaluated and contributed edits.

Competing financial interests

The authors declare no competing financial interests.

Table 1. Summary of recovered genomes.

Domain	Phylum	Bins	Total	Subclades	Completion range	Contamination range
Bacteria	Actinobacteria	19, 21, 21-1, 26, 29, 29-1, 52, 57, 57-1, 58, 59, 60	12	“Near OM1” Rubrobacteridae	15 – 92%	0 – 5.5%
	Bacteroidetes	10, 12, 37, 41, 49, 64	6	Flavobacteriaceae Sphingobacteriales Rhodothermaceae	17 – 96%	0 – 5.3%
	Chloroflexi	43, 43-1, 43-2	3	SAR202	83 – 90%	0 – 4%
	Cyanobacteria	27, 28, 28-1	3	Synechococcus	44 – 89%	0.5 – 3.7%
	Gemmatimonadetes	42	1	Gemmatimonas	86%	2.2%
	Ignavibacteria	51 l, 51-2	2	Ignavibacteria	5 – 57%	0%
	Marinimicrobia (SAR406)	45, 45-1, 45-2, 51, 51-1	5		21 – 90%	0 – 5.5%
	Nitrospinae	24, 25, 47, 47-1, 47-2	5	Nitrospina	11 – 94%	0.3 – 5.2%
	Planctomycetes	20, 22, 31, 32, 56, 56-1, 56-2, 63, 63-1, 63-2	10	Phycisphaerae Planctomycetaceae	9 – 95%	0 – 7.0%
	Proteobacteria	23, 33, 35, 36, 53, 54, 55, 61, 61-2	9	OM50/NOR5 Chromatiales Rhodbacteraceae Rhodospirillales	22 – 93%	0 – 47 %
	Verrucomicrobia	11, 30, 34, 46, 65	5	Verrucomicrobiales	11 – 52%	0 – 1.8%
	CP ACD39*	13	1		90%	5.1%
	CP Parcubacteria (OD1)	40	1	Cand. Uhrbacteria	72%	15%**
	CP Peregrinibacteria	16, 39	2		50 – 83%	0.3%
	CP Latescibacteria (WS3)	48, 50	2		52 – 85%	1.4 – 2.2%
Archaea	Euryarchaeota	14, 15, 17, 17-1, 18, 38	6	Marine Group II	17 – 83%	0 – 1.6%
	Thaumarchaeota	71, 72	2	Nitrosopumilus	79 – 96%	5.2 – 6.3%
Unclassified		61-1, 62	2	N/A	3 – 46%	0 – 25%

*Putative assignment. Placement in the ribosomal protein tree was poorly supported.

** 75% estimated to be due to strain heterogeneity

Figure Legends

Figure 1. N, S, and C cycling by dead zone taxa. Compounds are organized roughly according to oxidation state, with predicted genes and taxa encoding those genes indicated at the arrows between compounds. Conversions with no predicted taxa have red dashed lines. NMO = nitronate monooxygenase.

Figure 2. Read-per-kilobase-per-million (RPKM) abundances of phylogenetically cohesive groups by site. Sites are colored by DO concentration, according to the legend.

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. The heatplot compresses data in Fig. S14 Asterisks and circles 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. RPKM values for predicted cytochrome c oxidase and reductive nitrogen cycle genes and subunits. Boxplots display distribution (median, 1st & 3rd quartile, 1.5 x interquartile range) of RPKM values for genes assigned to a given functional category. Individual gene RPKMs are represented by colored dots for each sample.

Figure 5. Metabolic reconstruction for important uncultivated dead zone taxa. Solid arrows and outlines indicate the presence of a predicted pathway or gene with that function. Dotted lines indicate genes/pathways that were not found.

Supplemental Table Legend

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 WS3 cytochrome c oxidase gene neighborhoods.

Supplemental Figure Legends

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.

Figure S4. Phylogenetic tree of *dsrAB* genes. Genes from our bins are highlighted in pink. Clades are labeled according to (Müller, 2015). Values at nodes indicate Shimodaira-Hasegawa "like" values (Price, 2010). Scale bar indicates changes per position.

Figure S5. Metabolic reconstruction of SAR406 based on the four most complete genomes (Bins 45, 45-1, 45-2, and 51-1). Colors indicate recovered pathways and the number of genomes according to the scale in the upper right corner. Pathways/genes in black were not identified.

Figure S6. Metabolic reconstruction of SAR202 based on three genomes (Bins 43-1, 43-2, and 43). Colors indicate recovered pathways and the number of genomes according to the scale in the upper right corner. Pathways/genes in black were not identified.

Figure S7. Metabolic reconstruction of the putative ACD39 organism based on the Bin 13 genome. Red indicates recovered pathways. Pathways/genes in black were not identified.

Figure S8. ESOM of the first assembly using all assembled contigs. Bins are indicated by different coloration. Squares within bins indicate 5000 bp segments of assembled contigs.

Figure S9. ESOM of the second assembly using 5% of assembled contigs randomly sub-selected. Bins are indicated by different coloration. Squares within bins indicate 5000 bp segments of assembled contigs.

Figure S10. Phylogenetic tree of the SAR202 clade using the 16S rRNA gene. Genes recovered from assembled bins are indicated as 43-*. Values at nodes indicate Shimodaira-Hasegawa "like" values (Price, 2010). Scale bar indicates changes per position.

Figure S11. Metabolic reconstruction of the *Gemmatimonas* organism based on the Bin 42 genome. Red indicates recovered pathways. Pathways/genes in black were not identified.

Figure S12. Metabolic reconstruction of *Nitrosopumilus* based on two genomes (Bins 71 and 72). Colors indicate recovered pathways and the number of genomes according to the scale in the upper right corner. Pathways/genes in black were not identified.

Figure S13. Metabolic reconstruction of *Nitrospina* based on the four most complete genomes (Bins 24, 25, 47-2, and 47). Colors indicate recovered pathways and the number of genomes according to the scale in the upper right corner. Pathways/genes in black were not identified.

Figure S14. RNA vs. DNA coverage rank, according to BWA mapping of reads, for each bin by sample.

Figure S15. Phylogenetic tree of *nxrA* genes and near neighbors from Lüke et al. (2016). Sequences from binned genomes are indicated with *Bin*. Values at nodes indicate Shimodaira-Hasegawa "like" values (Price, 2010). Scale bar indicates changes per position.

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

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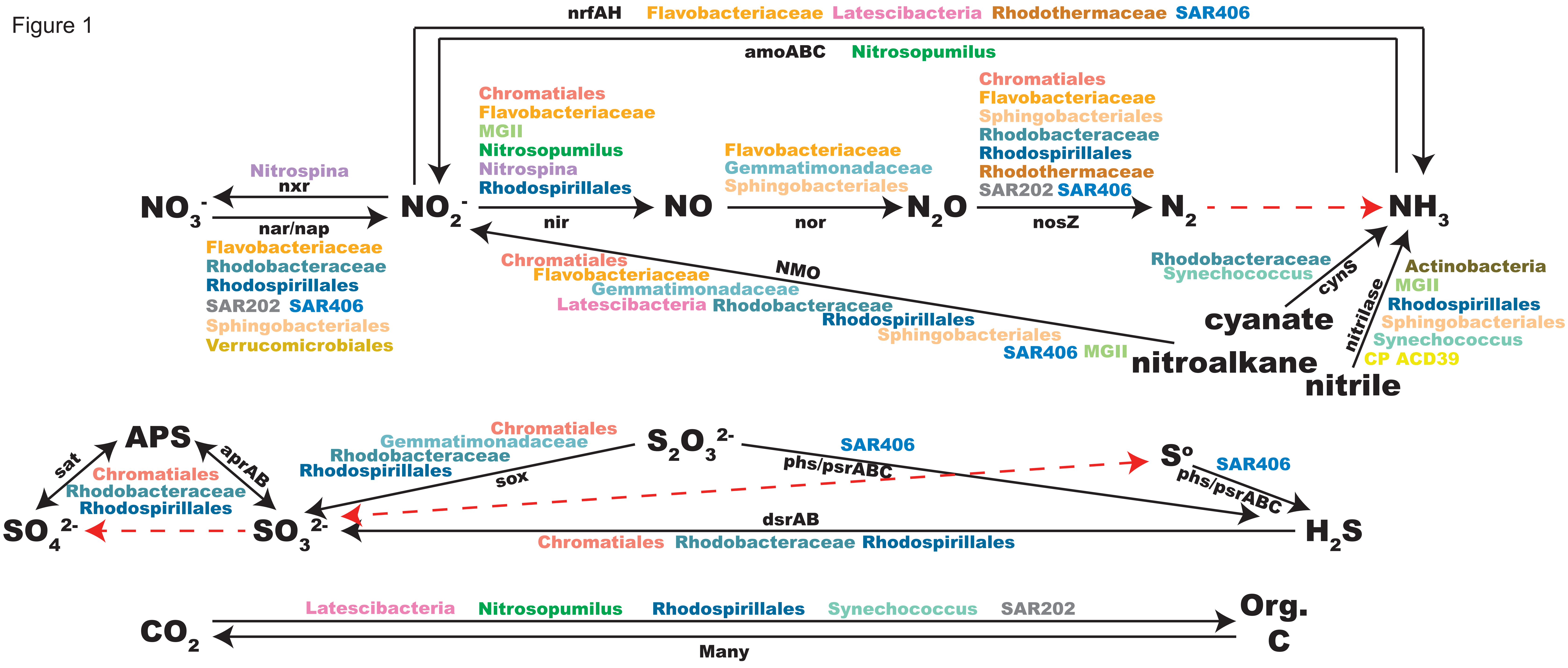
Figure 1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Rhodothermaceae
SAR406
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Nitrospina
nxr
NO_3^-
nar/nap
Flavobacteriaceae
Rhodobacteraceae
Rhodospirillales
SAR202
SAR406
Sphingobacteriales
Verrucomicrobiales
NO_2^-
Chromatiales
Flavobacteriaceae
MGII
Nitrosopumilus
Nitrospina
Rhodospirillales
nir
NO
Flavobacteriaceae
Gemmatimonadaceae
Sphingobacteriales
nor
N_2O
Chromatiales
Flavobacteriaceae
Sphingobacteriales
Rhodobacteraceae
Rhodospirillales
Rhodothermaceae
SAR202
SAR406
nosZ
N_2
NH_3
NMO
Chromatiales
Flavobacteriaceae
Gemmatimonadaceae
Latescibacteria
Rhodobacteraceae
Rhodospirillales
Sphingobacteriales
SAR406
MGII
nitroalkane
Rhodobacteraceae
Synechococcus
cynS
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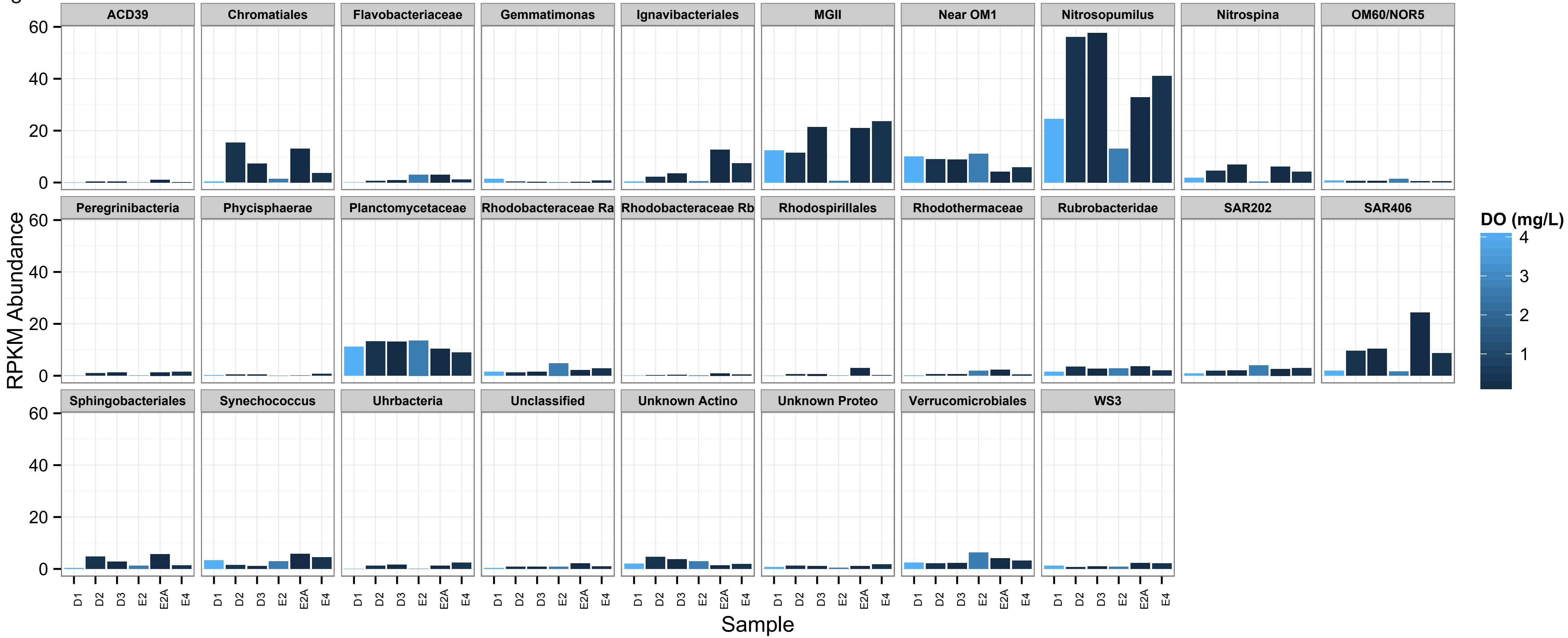
nitrilase
nitrile
Actinobacteria
MGII
Rhodospirillales
Sphingobacteriales
Synechococcus
CP ACD39
APS
sat
aprAB
Chromatiales
Rhodobacteraceae
Rhodospirillales
SO_4^{2-}
SO_3^{2-}
Chromatiales
Gemmatimonadaceae
Rhodobacteraceae
Rhodospirillales
sox
$S_2O_3^{2-}$
SAR406
phs/psrABC
S°
SAR406
phs/psrABC
dsrAB
Chromatiales
Rhodobacteraceae
Rhodospirillales
H_2S
Latescibacteria
Nitrosopumilus
Rhodospirillales
Synechococcus
SAR202
CO_2
Org. C
Many

Figure 2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Near OM1
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Peregrinibacteria
Phycisphaerae
Planctomycetaceae
Rhodobacteraceae Ra
Rhodobacteraceae Rb
Rhodospirillales
Rhodothermaceae
Rubrobacteridae
SAR202
SAR406
Sphingobacteriales
Synechococcus
Uhrbacteria
Unclassified
Unknown Actino
Unknown Proteo
Verrucomicrobiales
WS3
RPKM Abundance
0
20
40
60
Sample
D1
D2
D3
E2
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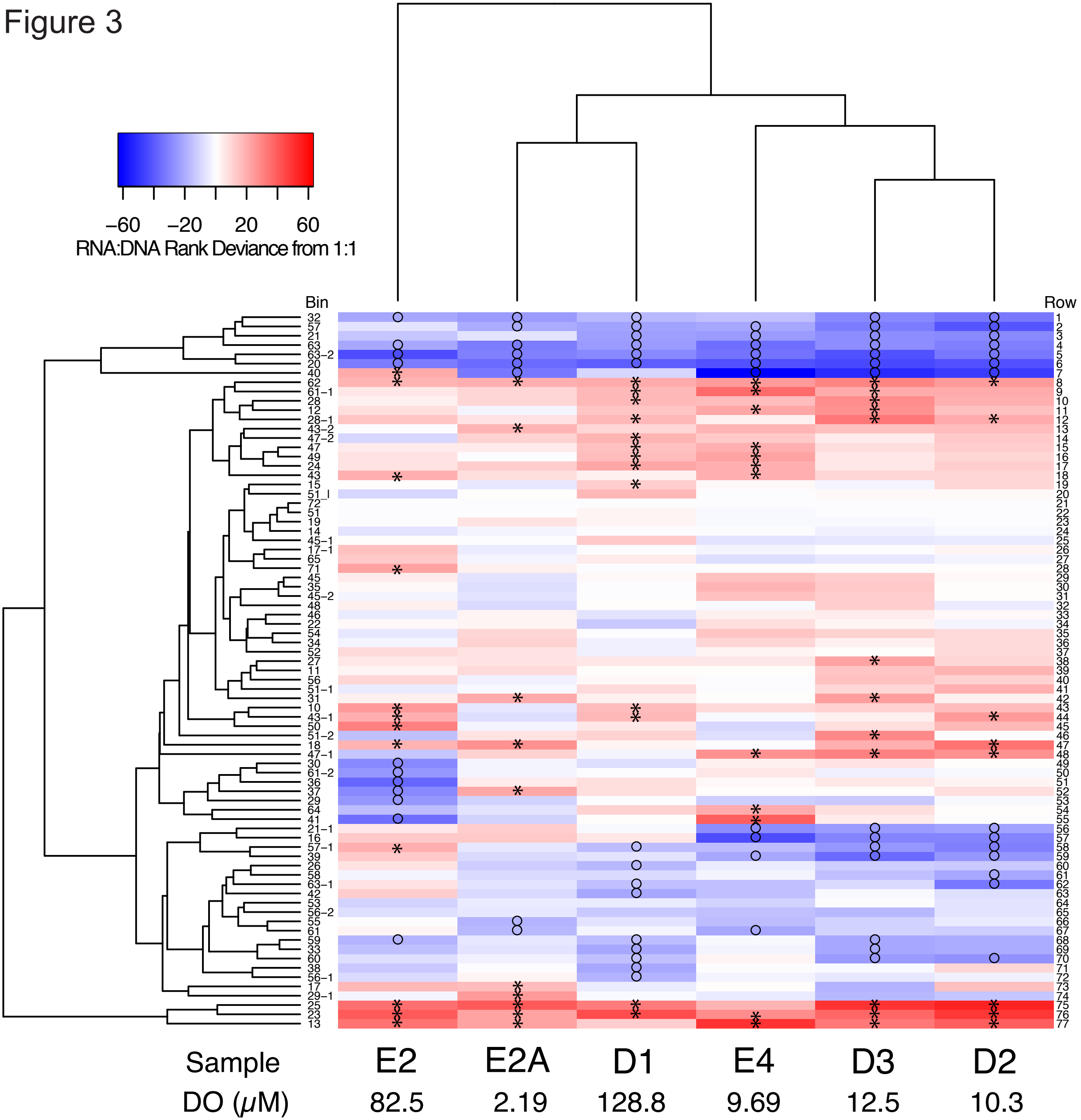
E4
DO (mg/L)
4
3
2
1

Figure 3


−60
−20
20
60
RNA:DNA Rank Deviance from 1:1
Bin
Row
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21
63
63−2
20
40
62
61−1
28
12
28−1
43−2
47−2
47
49
24
43
15
51_l
72
51
19
14
45−1
17−1
65
71
45
35
45−2
48
46
22
54
34
52
27
11
56
51−1
31
10
43−1
50
51−2
18
47−1
30
61−2
36
37
29
64
41
21−1
16
57−1
39
26
58
63−1
42
53
56−2
55
61
59
33
60
38
56−1
17
29−1
25
23
13
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77
Sample
E2
E2A
D1
E4
D3
D2
DO (μM)
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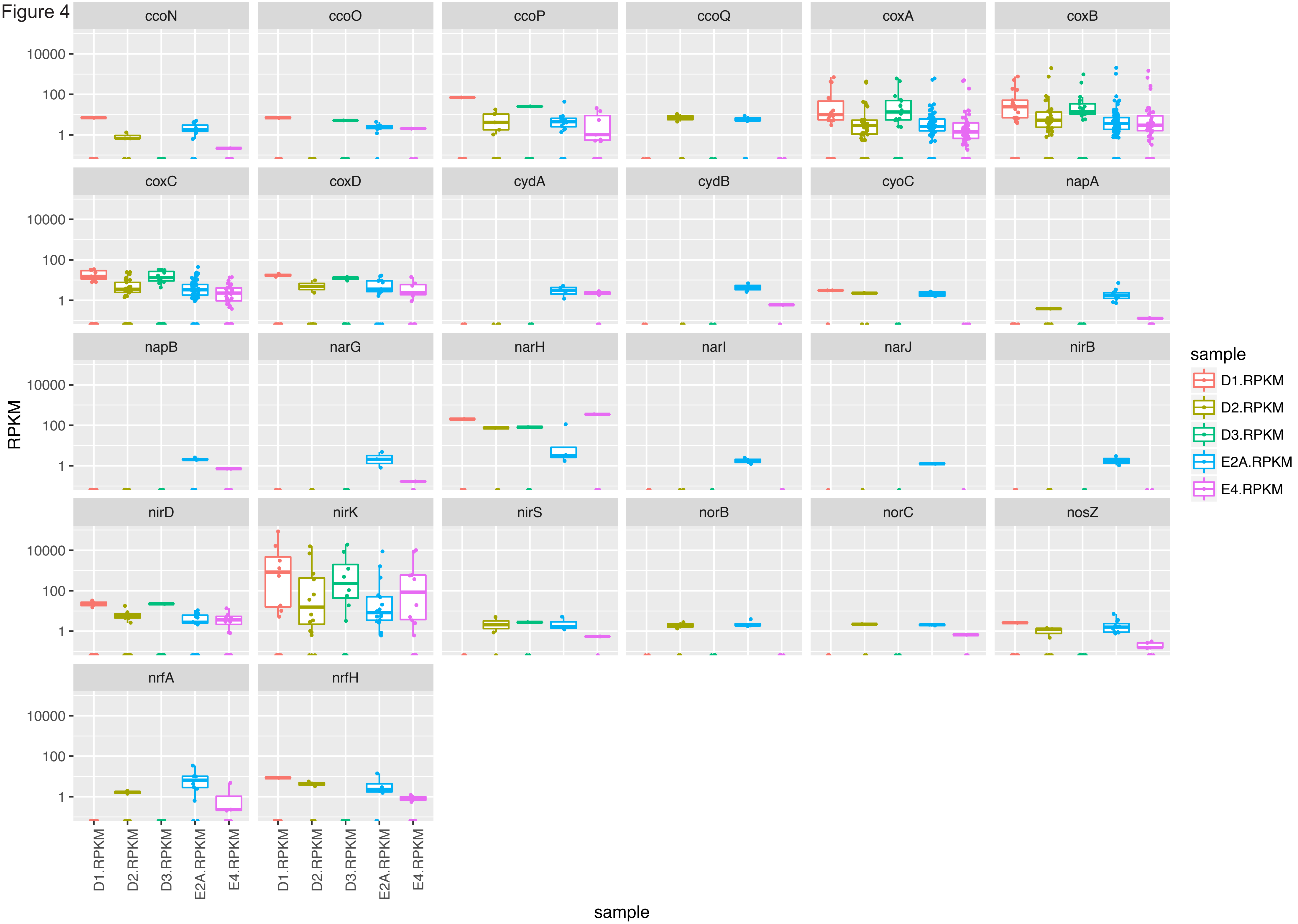
2.19
128.8
9.69
12.5
10.3

Figure 4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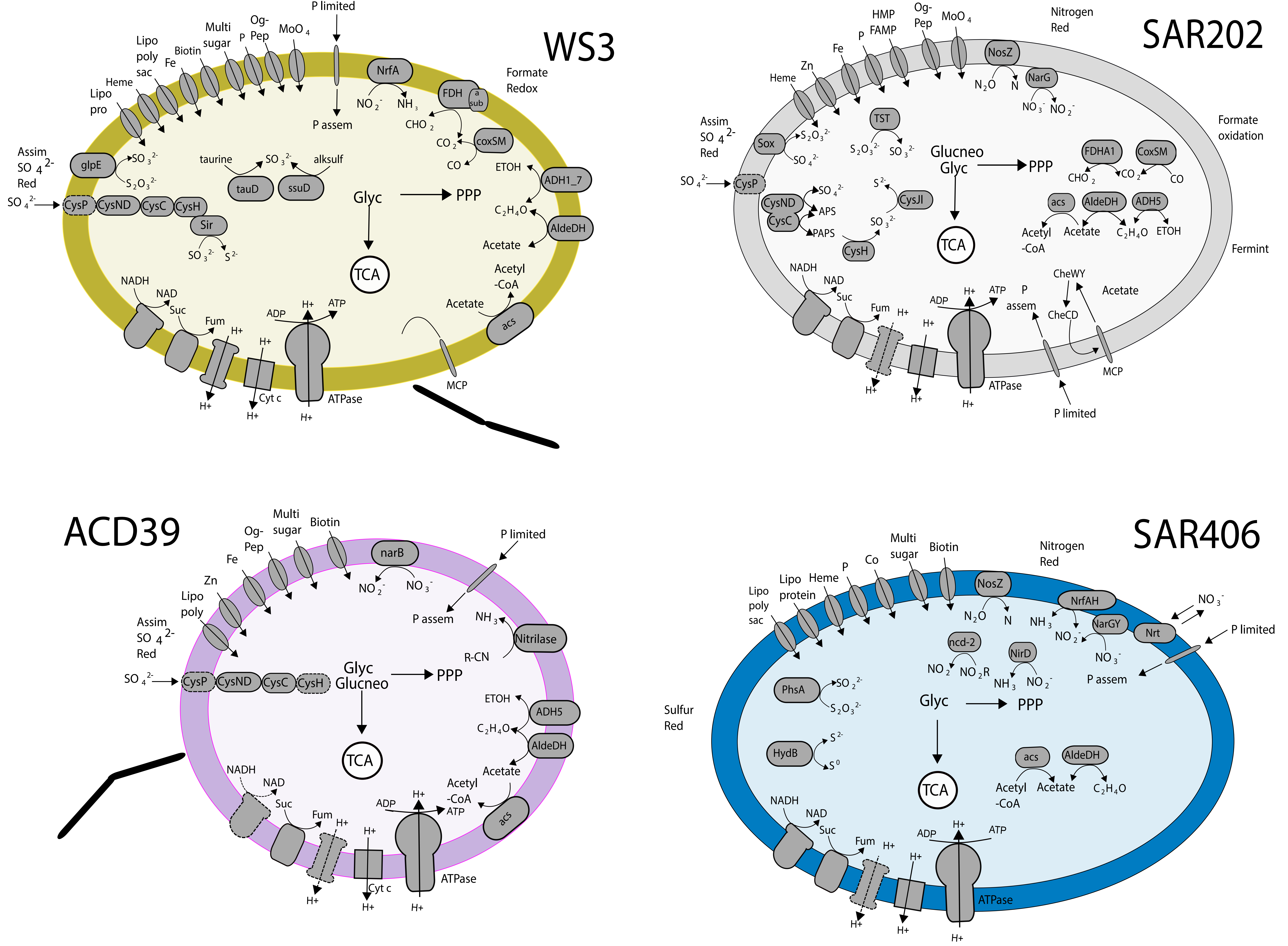
ccoO
ccoP
ccoQ
coxA
coxB
coxC
coxD
cydA
cydB
cyoC
napA
napB
narG
narH
narI
narJ
nirB
nirD
nirK
nirS
norB
norC
nosZ
nrfA
nrfH
RPKM
10000
100
1
sample
D1.RPKM
D2.RPKM
D3.RPKM
E2A.RPKM
E4.RPKM
sample

Figure 5



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MoO 4
Og-Pep
P
Multi sugar
Biotin
Fe
Lipo poly sac
Heme
Lipo pro
NrfA
NO_2^-
NH_3
P assem
FDH
a sub
Formate Redox
CHO_2
CO_2
coxSM
CO
ETOH
ADH1_7
C_2H_4O
AldeDH
Acetate
Acetyl -CoA
acs
Assim SO_4^{2-} Red
glpE
SO_3^{2-}
$S_2O_3^{2-}$
taurine
SO_3^{2-}
alksulf
tauD
ssuD
Glyc
PPP
TCA
SO_4^{2-}
CysP
CysND
CysC
CysH
Sir
SO_3^{2-}
S^{2-}
NADH
NAD
Suc
Fum
H+
ADP
ATP
Cyt c
ATPase
MCP
SAR202
HMP FAMP
Og-Pep
MoO 4
Nitrogen Red
P
Fe
Zn
Heme
NosZ
N_2O
N
NarG
NO_3^-
NO_2^-
Assim SO_4^{2-} Red
Sox
$S_2O_3^{2-}$
SO_4^{2-}
TST
$S_2O_3^{2-}$
SO_3^{2-}
Glucneo Glyc
PPP
Formate oxidation
FDHA1
CoxSM
CHO_2
CO_2
CO
CysP
CysND
CysC
SO_4^{2-}
APS
PAPS
S^{2-}
CysJI
SO_3^{2-}
CysH
TCA
acs
AldeDH
ADH5
Acetyl -CoA
Acetate
C_2H_4O
ETOH
Fermint
NADH
NAD
Suc
Fum
H+
ADP
ATP
P assem
CheWY
Acetate
CheCD
MCP
ATPase
P limited
ACD39
Multi sugar
Biotin
Og-Pep
Fe
Zn
Lipo poly
Assim SO_4^{2-} Red
narB
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NO_3^-
P limited
P assem
NH_3
Nitrilase
R-CN
SO_4^{2-}
CysP
CysND
CysC
CysH
Glyc Glucneo
PPP
ETOH
ADH5
C_2H_4O
AldeDH
Acetate
TCA
Acetyl -CoA
ATP
acs
NADH
NAD
Suc
Fum
H+
ADP
Cyt c
ATPase
SAR406
Multi sugar
Biotin
Co
P
Heme
Lipo protein
Lipo poly sac
Nitrogen Red
NosZ
N_2O
N
NrfAH
NH_3
NO_2^-
NarGY
Nrt
NO_3^-
NO_3^-
P limited
P assem
ncd-2
NO_2
NO_2R
NirD
NH_3
NO_2^-
Sulfur Red
PhsA
SO_3^{2-}
$S_2O_3^{2-}$
HydB
S^{2-}
S^0
Glyc
PPP
TCA
acs
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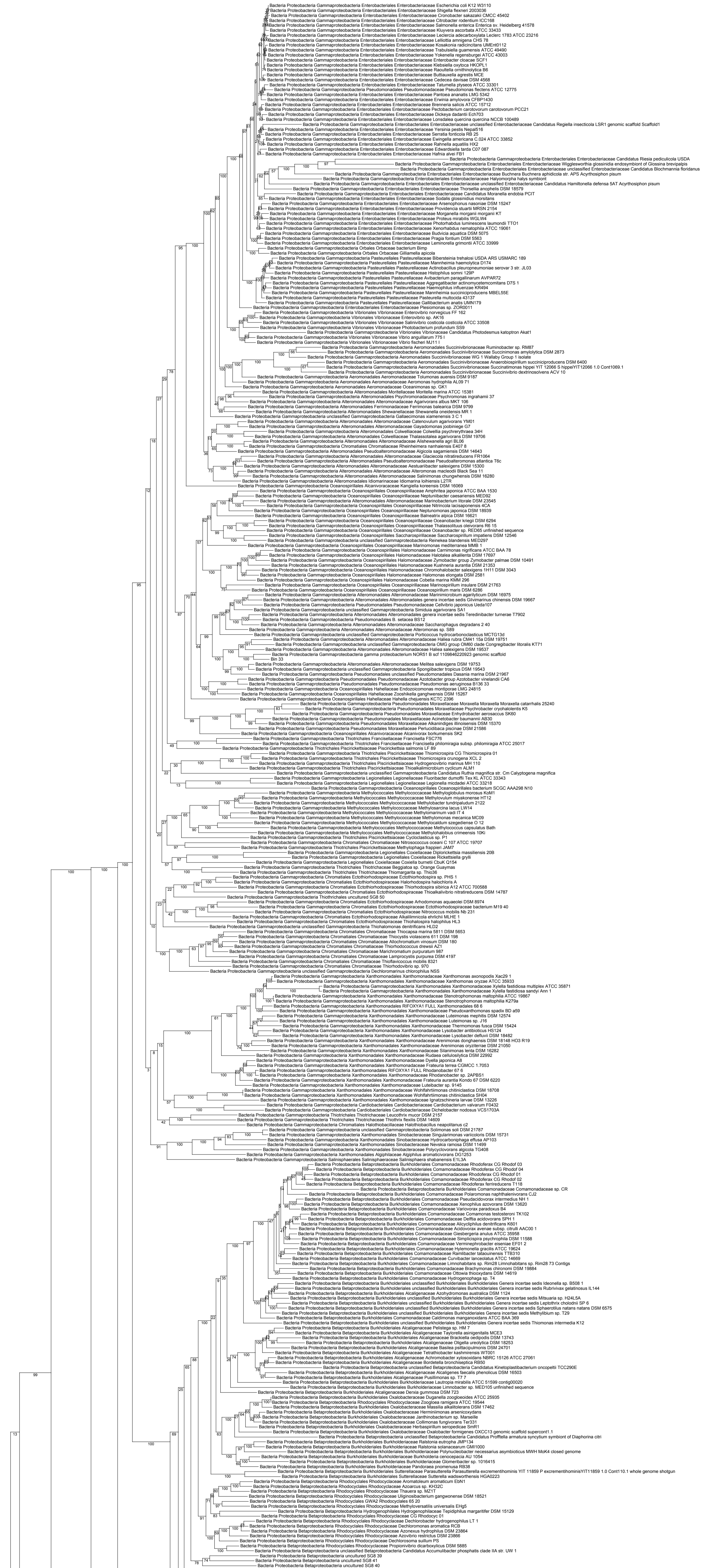
Fum
H+
ADP
ATP
ATPase

Figure S1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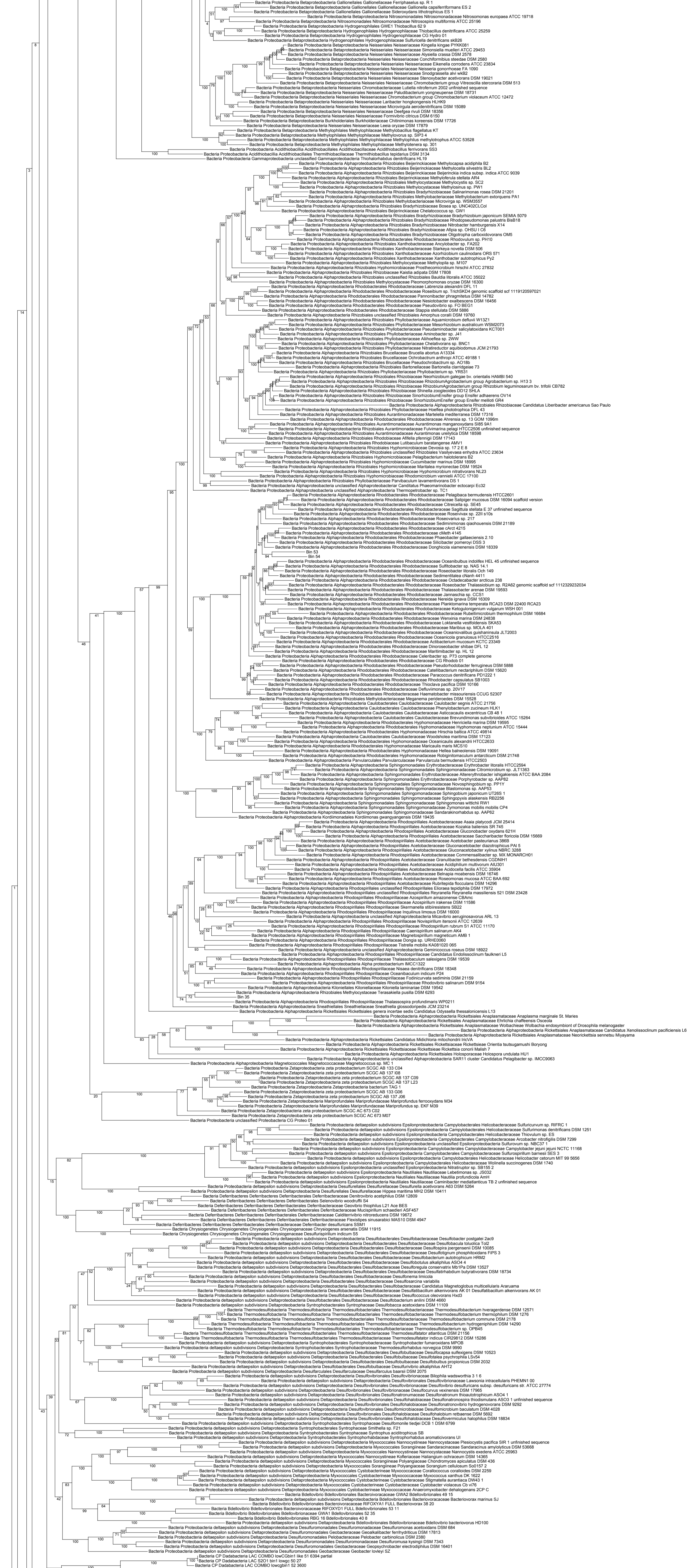
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Bacteria Proteobacteria Alphaproteobacteria Rhizobiales Rhizobiaceae SinorhizobiumEnsifer group Ensifer meliloti GR4
Bacteria Proteobacteria Alphaproteobacteria Rhizobiales Rhizobiaceae Candidatus Liberibacter americanus Sao Paulo
Bacteria Proteobacteria Alphaproteobacteria Rhizobiales Phyllobacteriaceae Hoeflea phototrophica DFL 43
Bacteria Proteobacteria Alphaproteobacteria Rhizobiales Aurantimonadaceae Martelella mediterranea DSM 17316
Bacteria Proteobacteria Alphaproteobacteria Rhodobacterales Rhodobacteraceae Ahrensia sp. 13 GOM 1096m
Bacteria Proteobacteria Alphaproteobacteria Rhizobiales Aurantimonadaceae Aurantimonas manganoxydans SI85 9A1
Bacteria Proteobacteria Alphaproteobacteria Rhizobiales Aurantimonadaceae Fulvimarina pelagi HTCC2506 unfinished sequence
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Bacteria Proteobacteria Alphaproteobacteria Rhizobiales unclassified Rhizobiales Vasilyevaea enhydra ATCC 23634
Bacteria Proteobacteria Alphaproteobacteria Rhizobiales Hyphomicrobiaceae Pelagibacterium halotolerans B2
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Bacteria Proteobacteria Alphaproteobacteria unclassified Alphaproteobacteriar Canditatus Phaeomarinobacter ectocarpi Ec32
Bacteria Proteobacteria Alphaproteobacteria unclassified Alphaproteobacteria Thermopetrobacter sp. TC1
Bacteria Proteobacteria Alphaproteobacteria Rhodobacterales Rhodobacteraceae Pelagibaca bermudensis HTCC2601
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Bacteria Proteobacteria Alphaproteobacteria Rhodobacterales Rhodobacteraceae Citreicella sp. SE45
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Bacteria Proteobacteria Alphaproteobacteria Rhodobacterales Rhodobacteraceae Donghicola xiamenensis DSM 18339
Bin 53
Bin 54
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Bacteria Proteobacteria Alphaproteobacteria Rhodobacterales Rhodobacteraceae Sulfitobacter sp. NAS 14.1
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Bacteria Proteobacteria Alphaproteobacteria Rhodobacterales Rhodobacteraceae Octadecabacter arcticus 238
Bacteria Proteobacteria Alphaproteobacteria Rhodobacterales Rhodobacteraceae Roseobacter Thalassiobium sp. R2A62 genomic scaffold scf 1112329232034
Bacteria Proteobacteria Alphaproteobacteria Rhodobacterales Rhodobacteraceae Thalassobacter arenae DSM 19593
Bacteria Proteobacteria Alphaproteobacteria Rhodobacterales Rhodobacteraceae Jannaschia sp. CCS1
Bacteria Proteobacteria Alphaproteobacteria Rhodobacterales Rhodobacteraceae Nereida ignava DSM 16309
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Bacteria Proteobacteria Alphaproteobacteria Rhodobacterales Rhodobacteraceae Ketogulonigenium vulgarum WSH 001
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Bacteria Proteobacteria Alphaproteobacteria Sphingomonadales Erythrobacteraceae Erythrobacter litoralis HTCC2594
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Bacteria Proteobacteria Alphaproteobacteria Sphingomonadales Erythrobacteraceae Porphyrobacter sp. AAP82
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Bacteria Proteobacteria Alphaproteobacteria Sphingomonadales Sphingomonadaceae Blastomonas sp. AAP53
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Bacteria Proteobacteria Alphaproteobacteria Sphingomonadales Sphingomonadaceae Sphingopyxis alaskensis RB2256
Bacteria Proteobacteria Alphaproteobacteria Sphingomonadales Sphingomonadaceae Sphingomonas wittichii RW1
Bacteria Proteobacteria Alphaproteobacteria Sphingomonadales Sphingomonadaceae Zymomonas mobilis mobilis CP4
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Bacteria Proteobacteria Alphaproteobacteria Rhodospirillales Acetobacteraceae Roseomonas mucosa ATCC BAA 692
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 Rhodospirillales Rhodospirillaceae Azospirillum irakense DSM 11586
Bacteria Proteobacteria Alphaproteobacteria Rhodospirillales Rhodospirillaceae Skermanella stibiiresistens SB22
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Bin 35
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Bacteria Proteobacteria Alphaproteobacteria Rickettsiales Anaplasmataceae Anaplasma marginale St. Maries
Bacteria Proteobacteria Alphaproteobacteria Rickettsiales Anaplasmataceae Ehrlichia chaffeensis Osceola
Bacteria Proteobacteria Alphaproteobacteria Rickettsiales Anaplasmataceae Wolbachieae Wolbachia endosymbiont of Drosophila melanogaster
Bacteria Proteobacteria Alphaproteobacteria Rickettsiales Anaplasmataceae Candidatus Xenolissoclinum pacificiensis L6
Bacteria Proteobacteria Alphaproteobacteria Rickettsiales Anaplasmataceae Neorickettsia sennetsu Miyayama
Bacteria Proteobacteria Alphaproteobacteria Rickettsiales Candidatus Midichloria mitochondrii IricVA
Bacteria Proteobacteria Alphaproteobacteria Rickettsiales Rickettsiaceae Rickettsieae Orientia tsutsugamushi Boryong
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Bacteria Proteobacteria Alphaproteobacteria Rickettsiales Holosporaceae Holospora undulata HU1
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Bacteria Proteobacteria Zetaproteobacteria Mariprofundales Mariprofundaceae Mariprofundus ferrooxydans M34
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Bacteria Proteobacteria Zetaproteobacteria zeta proteobacterium SCGC AC 673 M07
Bacteria Proteobacteria unclassified Proteobacteria CG Proteo 01
Bacteria Proteobacteria deltaepsilon subdivisions Epsilonproteobacteria Campylobacterales Helicobacteraceae Sulfuricurvum sp. RIFRC 1
Bacteria Proteobacteria deltaepsilon subdivisions Epsilonproteobacteria Campylobacterales Helicobacteraceae Sulfurimonas denitrificans DSM 1251
Bacteria Proteobacteria deltaepsilon subdivisions Epsilonproteobacteria Campylobacterales Helicobacteraceae Thiovulum sp. ES
Bacteria Proteobacteria deltaepsilon subdivisions Epsilonproteobacteria Campylobacterales Campylobacteraceae Arcobacter nitrofigilis DSM 7299
Bacteria Proteobacteria deltaepsilon subdivisions Epsilonproteobacteria unclassified Epsilonproteobacteria Sulfurovum sp. NBC37 1
Bacteria Proteobacteria deltaepsilon subdivisions Epsilonproteobacteria Campylobacterales Campylobacteraceae Campylobacter jejuni jejuni NCTC 11168
Bacteria Proteobacteria deltaepsilon subdivisions Epsilonproteobacteria Campylobacterales Campylobacteraceae Sulfurospirillum barnesii SES 3
Bacteria Proteobacteria deltaepsilon subdivisions Epsilonproteobacteria Campylobacterales Helicobacteraceae Helicobacter cetorum MIT 99 5656
Bacteria Proteobacteria deltaepsilon subdivisions Epsilonproteobacteria Campylobacterales Helicobacteraceae Wolinella succinogenes DSM 1740
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Bacteria Proteobacteria deltaepsilon subdivisions Epsilonproteobacteria Nautiliales Nautiliaceae Lebetimonas sp. JS032
Bacteria Proteobacteria deltaepsilon subdivisions Epsilonproteobacteria Nautiliales Nautiliaceae Nautilia profundicola AmH
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Bacteria Proteobacteria deltaepsilon subdivisions Deltaproteobacteria Desulfurellales Desulfurellaceae Desulfurella acetivorans A63 DSM 5264
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Bacteria Deferribacteres Deferribacteres Deferribacterales Deferribacteraceae Denitrovibrio acetiphilus DSM 12809
Bacteria Deferribacteres Deferribacteres Deferribacterales Selenovibrio woodruffii S4
Bacteria Deferribacteres Deferribacteres Deferribacterales Deferribacteraceae Geovibrio thiophilus L21 Ace BES
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Bacteria Chrysiogenetes Chrysiogenetes Chrysiogenales Chrysiogenaceae Chrysiogenes arsenatis DSM 11915
Bacteria Chrysiogenetes Chrysiogenetes Chrysiogenales Chrysiogenaceae Desulfurispirillum indicum S5
Bacteria Proteobacteria deltaepsilon subdivisions Deltaproteobacteria Desulfobacterales Desulfobacteraceae Desulfobacter postgatei 2ac9
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Bacteria Proteobacteria deltaepsilon subdivisions Deltaproteobacteria Myxococcales Nannocystineae Nannocystaceae Plesiocystis pacifica SIR 1 unfinished sequence
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Bacteria Bdellovibrio Bdellovibrionales Bacteroivoracaceae GWA2 Bdellovibrionales 49 15
Bacteria Proteobacteria deltaepsilon subdivisions Deltaproteobacteria Bdellovibrionales Bacteriovoracaceae Bacteriovorax marinus SJ
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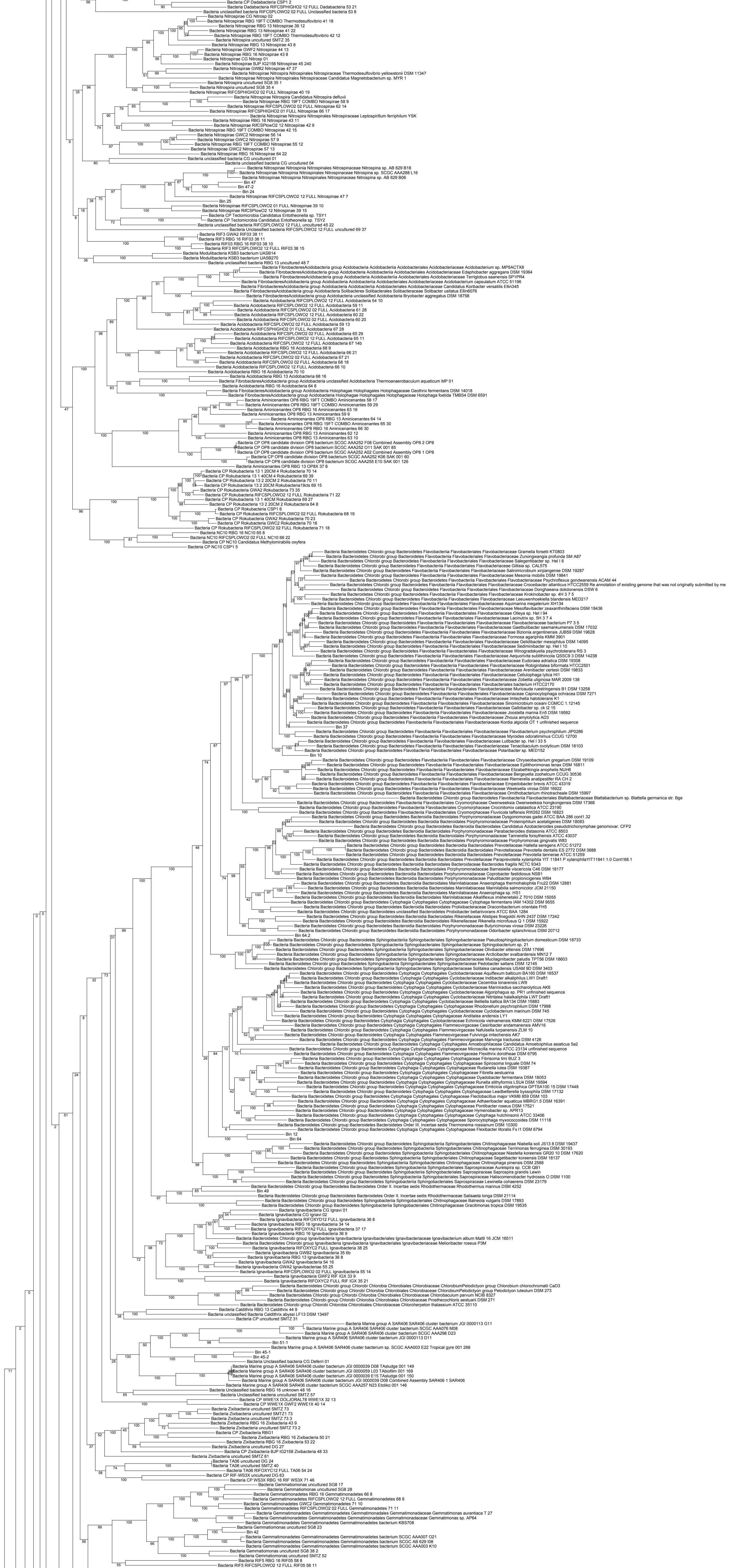
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Bacteria unclassified bacteria RIFCSPLOWO2 02 FULL Unclassified bacteria 53 8
Bacteria Nitrospirae CG Nitrosp 02
Bacteria Nitrospirae RBG 19FT COMBO Thermodesulfovibrio 41 18
Bacteria Nitrospirae RBG 13 Nitrospirae 39 12
Bacteria Nitrospirae RBG 13 Nitrospirae 41 22
Bacteria Nitrospirae RBG 19FT COMBO Thermodesulfovibrio 42 12
Bacteria Nitrospira uncultured SMTZ 35
Bacteria Nitrospirae RBG 13 Nitrospirae 43 8
Bacteria Nitrospirae GWF2 Nitrospirae 44 13
Bacteria Nitrospirae RBG 16 Nitrospirae 43 8
Bacteria Nitrospirae CG Nitrosp 01
Bacteria Nitrospirae BJP IG2158 Nitrospirae 45 240
Bacteria Nitrospirae GWB2 Nitrospirae 47 37
Bacteria Nitrospirae Nitrospira Nitrospirales Nitrospiraceae Thermodesulfovibrio yellowstonii DSM 11347
Bacteria Nitrospirae Nitrospira Nitrospirales Nitrospiraceae Candidatus Magnetobacterium sp. MYR 1
Bacteria Nitrospira uncultured SG8 35 1
Bacteria Nitrospira uncultured SG8 38 4
Bacteria Nitrospirae RIFCSPHIGHO2 02 FULL Nitrospirae 40 19
Bacteria Nitrospirae Nitrospira Candidatus Nitrospira defluvii
Bacteria Nitrospirae RBG 19FT COMBO Nitrospirae 58 9
Bacteria Nitrospirae RIFCSPLOWO2 02 FULL Nitrospirae 62 14
Bacteria Nitrospirae RIFCSPHIGHO2 01 FULL Nitrospirae 66 17
Bacteria Nitrospirae Nitrospira Nitrospirales Nitrospiraceae Leptospirillum ferriphilum YSK
Bacteria Nitrospirae RBG 16 Nitrospirae 43 11
Bacteria Nitrospirae RifCSPlowO2 12 Nitrospirae 42 9
Bacteria Nitrospirae RBG 19FT COMBO Nitrospirae 42 15
Bacteria Nitrospirae GWC2 Nitrospirae 56 14
Bacteria Nitrospirae GWC2 Nitrospirae 57 9
Bacteria Nitrospirae RBG 19FT COMBO Nitrospirae 55 12
Bacteria Nitrospirae GWC2 Nitrospirae 57 13
Bacteria Nitrospirae RBG 16 Nitrospirae 64 22
Bacteria unclassified bacteria CG uncultured 01
Bacteria unclassified bacteria CG uncultured 04
Bacteria Nitrospinae Nitrospinia Nitrospinales Nitrospinaceae Nitrospina sp. AB 629 B18
Bacteria Nitrospinae Nitrospinia Nitrospinales Nitrospinaceae Nitrospina sp. SCGC AAA288 L16
Bacteria Nitrospinae Nitrospinia Nitrospinales Nitrospinaceae Nitrospina sp. AB 629 B06
Bin 47
Bin 47-2
Bin 24
Bacteria Nitrospinae RIFCSPLOWO2 12 FULL Nitrospinae 47 7
Bin 25
Bacteria Nitrospinae RIFCSPLOWO2 01 FULL Nitrospinae 39 10
Bacteria Nitrospinae RifCSPlowO2 12 Nitrospinae 39 15
Bacteria CP Tectomicrobia Candidatus Entotheonella sp. TSY1
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 02 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 Rokubacteria19cts 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 Sanguibacteroides justesenii DSM 17696
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 Contig168.1
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 Marinirадius 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 Cytophagaceae 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
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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
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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
Bacteria Gemmatimonadetes RIFCSPLOWO2 02 FULL Gemmatimonadetes 71 11
Bacteria Gemmatimonadetes Gemmatimonadetes Gemmatimonadales Gemmatimonadaceae Gemmatimonas aurantiaca T 27
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Bacteria Gemmatimonas uncultured SG8 23
Bin 42
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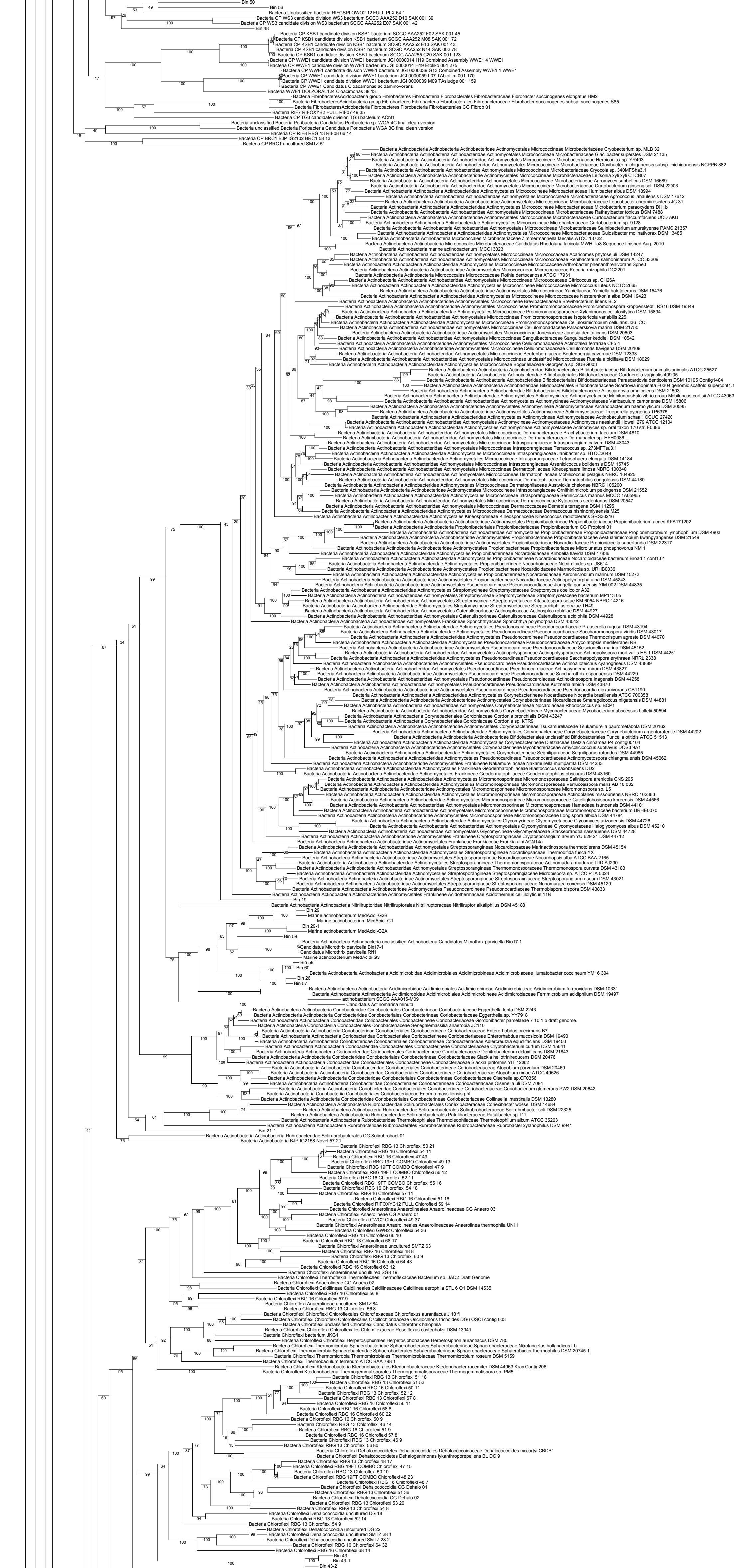
Bacteria Gemmatimonadetes Gemmatimonadetes Gemmatimonadetes bacterium SCGC AAA003 K10
Bacteria Gemmatimonas uncultured SG8 38 2
Bacteria Gemmatimonas uncultured SMTZ 52
Bacteria RIF5 RBG 16 RIF05 58 8
Bacteria RIF5 RIFCSPLOWO2 12 FULL RIF05 58 11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Bin 56
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Bacteria CP WS3 candidate division WS3 bacterium SCGC AAA252 E07 SAK 001 42
Bin 48
Bacteria CP KSB1 candidate division KSB1 bacterium SCGC AAA252 F02 SAK 001 45
Bacteria CP KSB1 candidate division KSB1 bacterium SCGC AAA252 M08 SAK 001 72
Bacteria CP KSB1 candidate division KSB1 bacterium SCGC AAA252 E13 SAK 001 43
Bacteria CP KSB1 candidate division KSB1 bacterium SCGC AAA252 N14 SAK 002 78
Bacteria CP KSB1 candidate division KSB1 bacterium SCGC AAA255 C20 SAK 001 123
Bacteria CP WWE1 candidate division WWE1 bacterium JGI 0000014 H19 Combined Assembly WWE1 4 WWE1
Bacteria CP WWE1 candidate division WWE1 bacterium JGI 0000014 H19 Etoliko 001 275
Bacteria CP WWE1 candidate division WWE1 bacterium JGI 0000039 G13 Combined Assembly WWE1 1 WWE1
Bacteria CP WWE1 candidate division WWE1 bacterium JGI 0000059 L07 TAbiofilm 001 170
Bacteria CP WWE1 candidate division WWE1 bacterium JGI 0000039 M09 TAsludge 001 159
Bacteria CP WWE1 Candidatus Cloacamonas acidaminovorans
Bacteria WWE1 DOLZORAL124 Cloacimonas 38 13
Bacteria FibrobacteresAcidobacteria group Fibrobacteres Fibrobacteria Fibrobacterales Fibrobacteraceae Fibrobacter succinogenes elongatus HM2
Bacteria FibrobacteresAcidobacteria group Fibrobacteres Fibrobacteria Fibrobacterales Fibrobacteraceae Fibrobacter succinogenes subsp. succinogenes S85
Bacteria FibrobacteresAcidobacteria Fibrobacteres Fibrobacteria Fibrobacterales CG Fibrob 01
Bacteria RIF7 RIFOXYB2 FULL RIF07 49 35
Bacteria CP TG3 candidate division TG3 bacterium ACht1
Bacteria unclassified Bacteria Poribacteria Candidatus Poribacteria sp. WGA 4C final clean version
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Bacteria CP RIF8 RBG 13 RIF08 66 14
Bacteria CP BRC1 BJP IG2102 BRC1 58 13
Bacteria CP BRC1 uncultured SMTZ 51
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Bacteria Actinobacteria Actinobacteria Actinobacteridae Actinomycetales Micrococcineae Micrococcaceae Micrococcus luteus NCTC 2665
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Bacteria Actinobacteria Actinobacteria Actinobacteridae Actinomycetales Micrococcineae Promicromonosporaceae Xylanimonas cellulosilytica DSM 15894
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Bin 19
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Bin 29
Marine actinobacterium MedAcidi-G2B
Marine actinobacterium MedAcidi-G1
Bin 29-1
Marine actinobacterium MedAcidi-G2A
Bin 59
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Bin 58
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Bin 26
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Bacteria Actinobacteria Actinobacteria Coriobacteridae Coriobacteriales Coriobacterineae Coriobacteriaceae Collinsella intestinalis DSM 13280
Bacteria Actinobacteria Actinobacteria Rubrobacteridae Solirubrobacterales Conexibacteraceae Conexibacter woesei DSM 14684
Bacteria Actinobacteria Actinobacteria Rubrobacteridae Solirubrobacterales Solirubrobacteraceae Solirubrobacter soli DSM 22325
Bacteria Actinobacteria Actinobacteria Rubrobacteridae Solirubrobacterales Patulibacteraceae Patulibacter sp. I11
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Bacteria Actinobacteria Actinobacteria Rubrobacteridae Rubrobacterales Rubrobacteraceae Rubrobacter xylanophilus DSM 9941
Bin 21-1
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Bacteria Chloroflexi RBG 16 Chloroflexi 54 11
Bacteria Chloroflexi RBG 16 Chloroflexi 47 49
Bacteria Chloroflexi RBG 19FT COMBO Chloroflexi 49 13
Bacteria Chloroflexi RBG 19FT COMBO Chloroflexi 47 9
Bacteria Chloroflexi RBG 19FT COMBO Chloroflexi 56 12
Bacteria Chloroflexi RBG 16 Chloroflexi 52 11
Bacteria Chloroflexi RBG 19FT COMBO Chloroflexi 55 16
Bacteria Chloroflexi RBG 16 Chloroflexi 54 18
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Bacteria Chloroflexi RBG 16 Chloroflexi 51 16
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Bacteria Chloroflexi RBG 13 Chloroflexi 68 17
Bacteria Chloroflexi Anaerolineae uncultured SMTZ 63
Bacteria Chloroflexi RBG 16 Chloroflexi 48 8
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Bacteria Chloroflexi RBG 16 Chloroflexi 64 43
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Bacteria Chloroflexi RBG 16 Chloroflexi 57 9
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Bacteria Chloroflexi bacterium JKG1
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Bacteria Chloroflexi Dehalococcoidetes Dehalogenimonas lykanthroporepellens BL DC 9
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Bacteria Chloroflexi RBG 19FT COMBO Chloroflexi 47 15
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Bacteria Chloroflexi RBG 19FT COMBO Chloroflexi 48 23
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Bacteria Chloroflexi RBG 13 Chloroflexi 52 14
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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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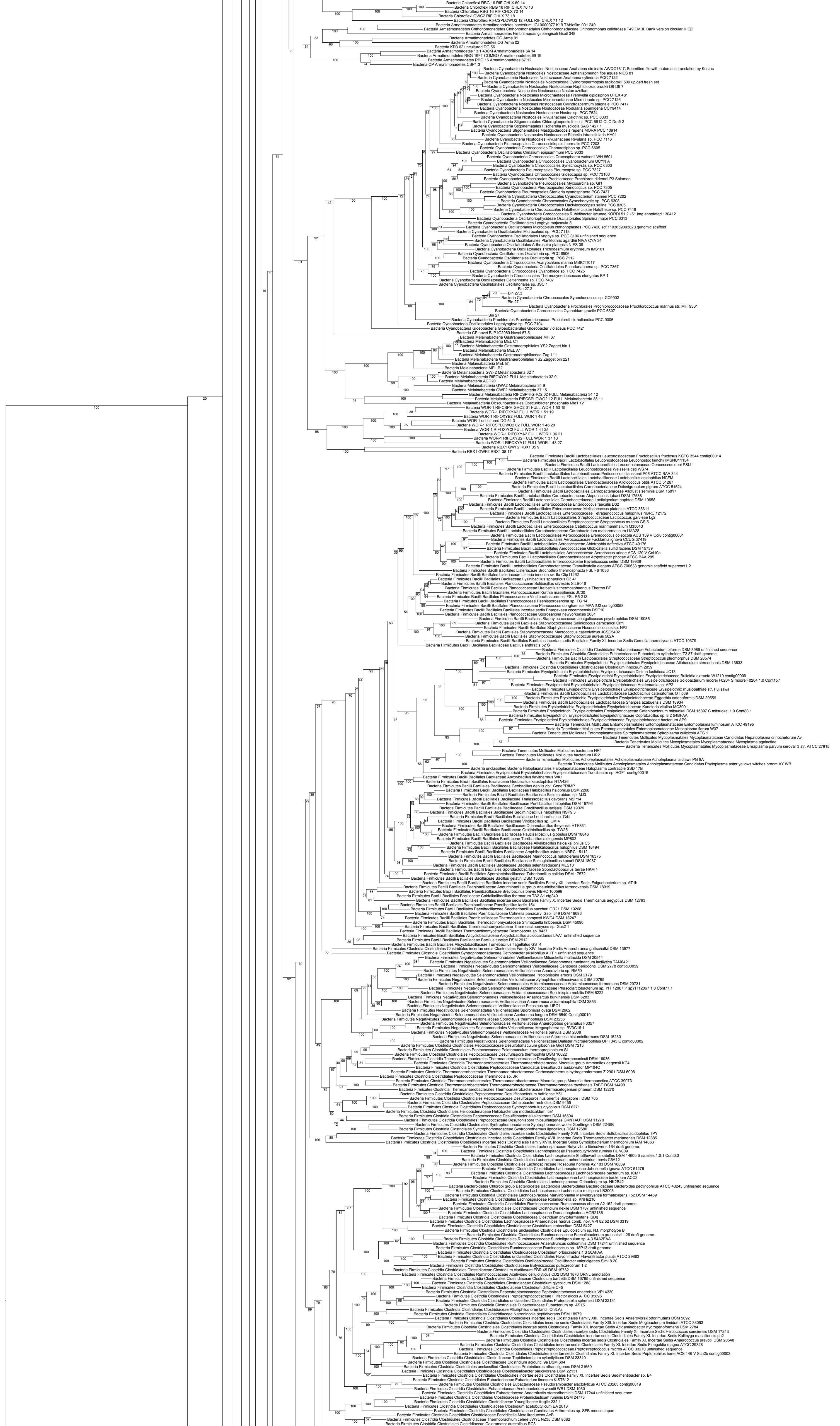
Bacteria Chloroflexi RBG 16 Chloroflexi 68 14
Bin 43
Bin 43-1
Bin 43-2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Bacteria Chloroflexi RIFCSPLOWO2 12 FULL RIF CHLX 71 12
Bacteria Armatimonadetes Armatimonadetes bacterium JGI 0000077 K19 TAbiofilm 001 240
Bacteria Armatimonadetes Chthonomonadetes 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
Bacteria Armatimonadetes RBG 19FT COMBO Armatimonadetes 69 19
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
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Bacteria Cyanobacteria Nostocales Nostocaceae Raphidiopsis brookii D9 D9 7
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Bacteria Cyanobacteria Stigonematales Mastigocladopsis repens MORA PCC 10914
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Bacteria Cyanobacteria Nostocales Rivulariaceae Rivularia sp. PCC 7116
Bacteria Cyanobacteria Pleurocapsales Chroococcidiopsis thermalis PCC 7203
Bacteria Cyanobacteria Chroococcales Chamaesiphon sp. PCC 6605
Bacteria Cyanobacteria Oscillatoriales Crinalium epipsammum PCC 9333
Bacteria Cyanobacteria Chroococcales Crocosphaera watsonii WH 8501
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Bacteria Cyanobacteria Chroococcales Synechocystis sp. PCC 6803
Bacteria Cyanobacteria Pleurocapsales Pleurocapsa sp. PCC 7327
Bacteria Cyanobacteria Chroococcales Gloeocapsa sp. PCC 73106
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Bacteria Cyanobacteria Chroococcales Dactylococcopsis salina PCC 8305
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Bacteria Cyanobacteria Oscillatoriales Lyngbya sp. PCC 8106 unfinished sequence
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Bacteria Cyanobacteria Oscillatoriales Trichodesmium erythraeum IMS101
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Bacteria Cyanobacteria Chroococcales Acaryochloris marina MBIC11017
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Bacteria Cyanobacteria Chroococcales Cyanothece sp. PCC 7425
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Bacteria Cyanobacteria Oscillatoriales Geitlerinema sp. PCC 7407
Bacteria Cyanobacteria Oscillatoriales Oscillatoriales sp. JSC 1
Bin 27.2
Bin 27.3
Bacteria Cyanobacteria Chroococcales Synechococcus sp. CC9902
Bin 27.1
Bacteria Cyanobacteria Prochlorales Prochlorococcaceae Prochlorococcus marinus str. MIT 9301
Bacteria Cyanobacteria Chroococcales Cyanobium gracile PCC 6307
Bin 27
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Bacteria Melainabacteria MEL B2
Bacteria Melainabacteria GWF2 Melainabacteria 32 7
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Bacteria Melainabacteria ACD20
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Bacteria Melainabacteria RIFCSPLOWO2 12 FULL Melainabacteria 35 11
Bacteria Melainabacteria Obscuribacteriales Obscuribacter phosphatis Mle1 12
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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 Negativicutes Selenomonadales Veillonellaceae Anaeromusa acidaminophila DSM 3853
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Bacteria Firmicutes Negativicutes Selenomonadales Veillonellaceae Sporomusa ovata DSM 2662
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Bacteria Firmicutes Negativicutes Selenomonadales Veillonellaceae Anaeroglobus geminatus F0357
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Bacteria Firmicutes Clostridia Clostridiales Peptococcaceae Desulfotomaculum gibsoniae Groll DSM 7213
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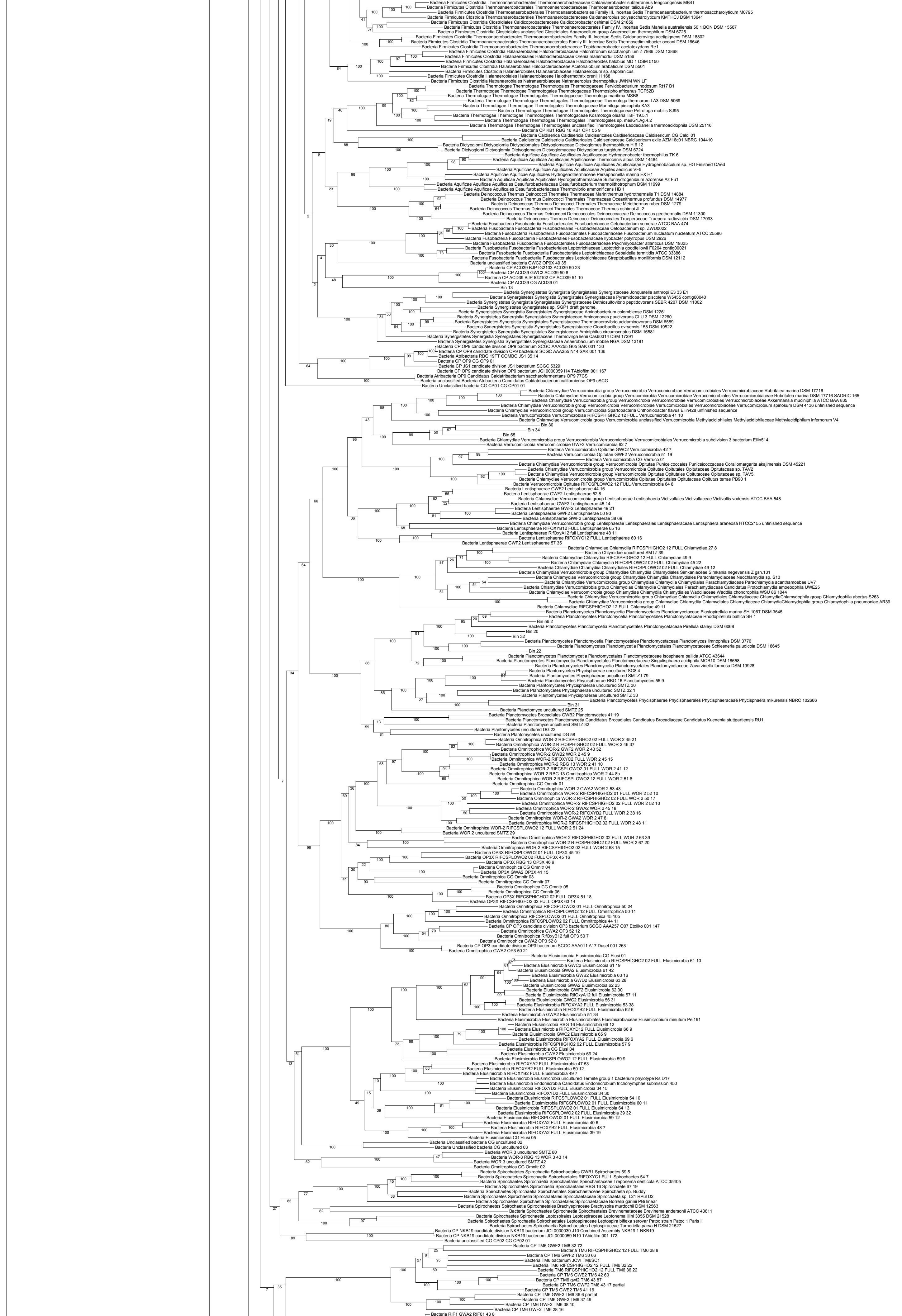
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Bacteria Firmicutes Clostridia Thermoanaerobacterales Thermoanaerobacterales Family III. Incertae Sedis Thermoanaerobacterium thermosaccharolyticum M0795
Bacteria Firmicutes Clostridia Thermoanaerobacterales Thermoanaerobacteraceae Caldanaerobius polysaccharolyticum KMTHCJ DSM 13641
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Bacteria Firmicutes Clostridia Halanaerobiales Halanaerobiaceae Halothermothrix orenii H 168
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Bacteria Aquificae Aquificae Aquificales Aquificaceae Hydrogenobacter thermophilus TK 6
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Bacteria Aquificae Aquificae Aquificales Desulfurobacteriaceae Desulfurobacterium thermolithotrophum DSM 11699
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Bacteria Deinococcus Thermus Deinococci Thermales Thermaceae Marinithermus hydrothermalis T1 DSM 14884
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Bacteria Fusobacteria Fusobacteriia Fusobacteriales Fusobacteriaceae Cetobacterium somerae ATCC BAA 474
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Bacteria unclassified bacteria GWC2 OP9X 49 35
Bacteria CP ACD39 BJP IG2103 ACD39 50 23
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Bin 13
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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
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Bacteria Unclassified bacteria CG CP01 CG CP01 01
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Bin 34
Bin 65
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Bacteria Omnitrophica WOR-2 RBG 13 WOR 2 41 10
Bacteria Omnitrophica WOR-2 RIFCSPLOWO2 01 FULL WOR 2 41 12
Bacteria Omnitrophica WOR-2 RBG 13 Omnitrophica WOR-2 44 8b
Bacteria Omnitrophica WOR-2 RIFCSPLOWO2 12 FULL WOR 2 51 8
Bacteria Omnitrophica CG Omnitr 01
Bacteria Omnitrophica WOR-2 GWA2 WOR 2 53 43
Bacteria Omnitrophica WOR-2 RIFCSPHIGHO2 01 FULL WOR 2 52 10
Bacteria Omnitrophica WOR-2 RIFCSPHIGHO2 02 FULL WOR 2 50 17
Bacteria Omnitrophica WOR-2 RIFCSPHIGHO2 02 FULL WOR 2 52 10
Bacteria Omnitrophica WOR-2 GWA2 WOR 2 45 18
Bacteria Omnitrophica WOR-2 RIFOXYB2 FULL WOR 2 38 16
Bacteria Omnitrophica WOR-2 GWA2 WOR 2 47 8
Bacteria Omnitrophica WOR-2 RIFCSPHIGHO2 02 FULL WOR 2 48 11
Bacteria Omnitrophica WOR-2 RIFCSPLOWO2 12 FULL WOR 2 51 24
Bacteria WOR 2 uncultured SMTZ 29
Bacteria Omnitrophica WOR-2 RIFCSPHIGHO2 02 FULL WOR 2 63 39
Bacteria Omnitrophica WOR-2 RIFCSPHIGHO2 02 FULL WOR 2 67 20
Bacteria Omnitrophica WOR-2 RIFCSPHIGHO2 02 FULL WOR 2 68 15
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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
Bacteria OP3X RIFCSPHIGHO2 02 FULL OP3X 51 18
Bacteria OP3X RIFCSPHIGHO2 02 FULL OP3X 63 14
Bacteria Omnitrophica RIFCSPLOWO2 01 FULL Omnitrophica 50 24
Bacteria Omnitrophica RIFCSPLOWO2 12 FULL Omnitrophica 50 11
Bacteria Omnitrophica RIFCSPLOWO2 01 FULL Omnitrophica 45 10b
Bacteria Omnitrophica RIFCSPLOWO2 02 FULL Omnitrophica 44 11
Bacteria CP OP3 candidate division OP3 bacterium SCGC AAA257 O07 Etoliko 001 147
Bacteria Omnitrophica GWA2 OP3 52 12
Bacteria Omnitrophica RifOxyB12 full OP3 50 7
Bacteria Omnitrophica GWA2 OP3 52 8
Bacteria CP OP3 candidate division OP3 bacterium SCGC AAA011 A17 Dusel 001 263
Bacteria Omnitrophica GWA2 OP3 50 21
Bacteria Elusimicrobia Elusimicrobia CG Elusi 01
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
Bacteria Elusimicrobia Elusimicrobia Elusimicrobiales Elusimicrobiaceae Elusimicrobium minutum Pei191
Bacteria Elusimicrobia RBG 16 Elusimicrobia 66 12
Bacteria Elusimicrobia RIFOXYD12 FULL Elusimicrobia 66 9
Bacteria Elusimicrobia GWC2 Elusimicrobia 65 9
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Bacteria Elusimicrobia RIFCSPHIGHO2 02 FULL Elusimicrobia 57 9
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Bacteria Elusimicrobia GWA2 Elusimicrobia 69 24
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Bacteria Elusimicrobia RIFOXYB2 FULL Elusimicrobia 50 12
Bacteria Elusimicrobia RIFOXYB2 FULL Elusimicrobia 49 7
Bacteria Elusimicrobia Elusimicrobia uncultured Termite group 1 bacterium phylotype Rs D17
Bacteria Elusimicrobia Endomicrobia Candidatus Endomicrobium trichonymphae submission 450
Bacteria Elusimicrobia RIFOXYD2 FULL Elusimicrobia 34 15
Bacteria Elusimicrobia RIFOXYD2 FULL Elusimicrobia 34 30
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Bacteria Elusimicrobia RIFCSPLOWO2 01 FULL Elusimicrobia 60 11
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Bacteria Elusimicrobia RIFOXYB2 FULL Elusimicrobia 48 7
Bacteria Elusimicrobia RIFOXYA2 FULL Elusimicrobia 39 19
Bacteria Elusimicrobia CG Elusi 05
Bacteria Unclassified bacteria CG uncultured 02
Bacteria Unclassified bacteria CG uncultured 03
Bacteria WOR 3 uncultured SMTZ 60
Bacteria WOR-3 RBG 13 WOR 3 43 14
Bacteria WOR 3 uncultured SMTZ 42
Bacteria Omnitrophica CG Omnitr 02
Bacteria Spirochaetes Spirochaetia Spirochaetales GWB1 Spirochaetes 59 5
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Bacteria Spirochaetes Spirochaetia Spirochaetales Spirochaetaceae Treponema denticola ATCC 35405
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Bacteria Spirochaetes Spirochaetia Spirochaetales Spirochaetaceae Spirochaeta sp. Buddy
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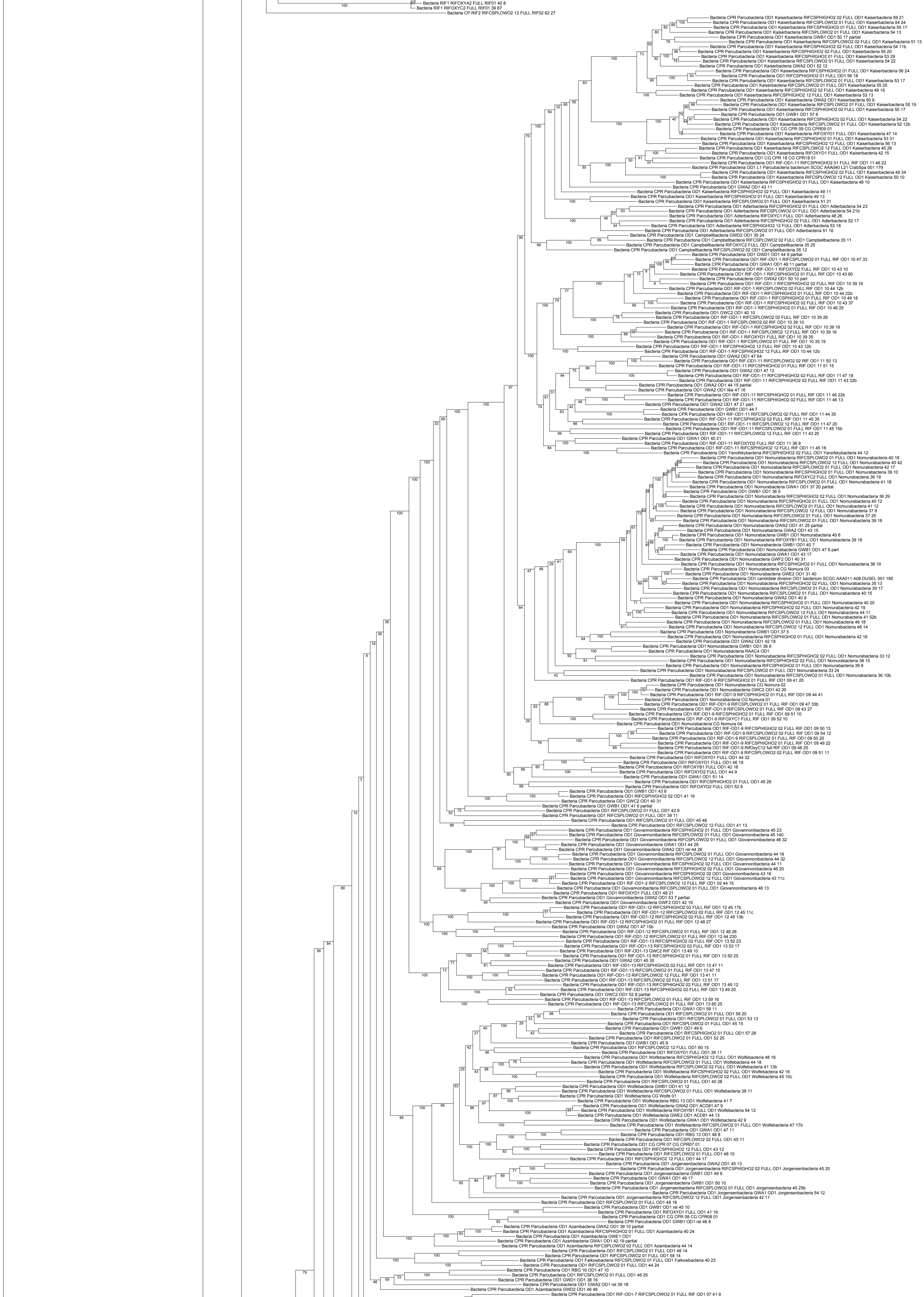
Bacteria Spirochaetes Spirochaetia Spirochaetales Leptospiraceae Turneriella parva H DSM 21527
Bacteria CP NKB19 candidate division NKB19 bacterium JGI 0000039 J10 Combined Assembly NKB19 1 NKB19
Bacteria CP NKB19 candidate division NKB19 bacterium JGI 0000059 N10 TAbiofilm 001 172
Bacteria unclassified CG CP02 CG CP02 01
Bacteria CP TM6 GWF2 TM6 32 72
Bacteria TM6 RIFCSPHIGHO2 12 FULL TM6 38 8
Bacteria CP TM6 GWF2 TM6 30 66
Bacteria TM6 bacterium JCVI TM6SC1
Bacteria TM6 RIFCSPHIGHO2 12 FULL TM6 32 22
Bacteria TM6 RIFCSPHIGHO2 12 FULL TM6 36 22
Bacteria CP TM6 GWE2 TM6 42 60
Bacteria CP TM6 gwf2 TM6 43 87
Bacteria CP TM6 GWF2 TM6 43 17 partial
Bacteria CP TM6 GWE2 TM6 41 16
Bacteria CP TM6 GWF2 TM6 36 6 partial
Bacteria CP TM6 GWF2 TM6 37 49
Bacteria CP TM6 GWF2 TM6 38 10
Bacteria CP TM6 GWF2 TM6 28 16
Bacteria RIF1 GWA2 RIF01 43 8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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
Bacteria CPR Parcubacteria OD1 Kaiserbacteria RIFCSPHIGHO2 02 FULL OD1 Kaiserbacteria 55 20
Bacteria CPR Parcubacteria OD1 Kaiserbacteria RIFCSPHIGHO2 01 FULL OD1 Kaiserbacteria 53 29
Bacteria CPR Parcubacteria OD1 Kaiserbacteria RIFCSPLOWO2 01 FULL OD1 Kaiserbacteria 54 22
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Bacteria CPR Parcubacteria OD1 Kaiserbacteria RIFCSPHIGHO2 02 FULL OD1 Kaiserbacteria 49 11
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 Adlerbacteria RIFOXYC1 FULL OD1 Adlerbacteria 48 26
Bacteria CPR Parcubacteria OD1 Adlerbacteria RIFCSPHIGHO2 02 FULL OD1 Adlerbacteria 52 17
Bacteria CPR Parcubacteria OD1 Adlerbacteria RIFCSPHIGHO2 12 FULL OD1 Adlerbacteria 53 18
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Bacteria CPR Parcubacteria OD1 Campbellbacteria GWD2 OD1 35 24
Bacteria CPR Parcubacteria OD1 Campbellbacteria RIFCSPLOWO2 02 FULL OD1 Campbellbacteria 35 11
Bacteria CPR Parcubacteria OD1 Campbellbacteria RIFOXYC2 FULL OD1 Campbellbacteria 35 25
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
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Bacteria CPR Parcubacteria OD1 RIF-OD1-1 RIFCSPHIGHO2 01 FULL RIF OD1 10 49 18
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Bacteria CPR Parcubacteria OD1 RIF-OD1-1 RIFCSPHIGHO2 02 FULL RIF OD1 10 39 19
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Bacteria CPR Parcubacteria OD1 GWA2 OD1 47 64
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Bacteria CPR Parcubacteria OD1 RIF-OD1-11 RIFCSPHIGHO2 01 FULL RIF OD1 11 51 15
Bacteria CPR Parcubacteria OD1 GWA2 OD1 47 12
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Bacteria CPR Parcubacteria OD1 GWA2 OD1 47 21 part
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Bacteria CPR Parcubacteria OD1 GWB1 OD1 36 5
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Bacteria CPR Parcubacteria OD1 Nomurabacteria GWB1 OD1 40 7
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Bacteria CPR Parcubacteria OD1 RIFOXYD1 FULL OD1 44 32
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Bacteria CPR Parcubacteria OD1 GWA1 OD1 51 14
Bacteria CPR Parcubacteria OD1 RIFCSPHIGHO2 01 FULL OD1 45 26
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Bacteria CPR Parcubacteria OD1 GWB1 OD1 43 8
Bacteria CPR Parcubacteria OD1 RIFCSPHIGHO2 02 OD1 41 19
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Bacteria CPR Parcubacteria OD1 RIFCSPLOWO2 01 FULL OD1 39 11
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Bacteria CPR Parcubacteria OD1 RIFCSPLOWO2 12 FULL OD1 41 13
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Bacteria CPR Parcubacteria OD1 Giovannonibacteria RIFCSPLOWO2 01 FULL OD1 Giovannonibacteria 45 140
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Bacteria CPR Parcubacteria OD1 Giovannonibacteria GWA1 OD1 44 29
Bacteria CPR Parcubacteria OD1 Giovannonibacteria GWA2 OD1 rel 44 26
Bacteria CPR Parcubacteria OD1 Giovannonibacteria RIFCSPLOWO2 01 FULL OD1 Giovannonibacteria 44 16
Bacteria CPR Parcubacteria OD1 Giovannonibacteria RIFCSPLOWO2 12 FULL OD1 Giovannonibacteria 44 32
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Bacteria CPR Parcubacteria OD1 Giovannonibacteria RIFCSPHIGHO2 02 FULL OD1 Giovannonibacteria 46 20
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Bacteria CPR Parcubacteria OD1 RIFOXYD1 FULL OD1 48 21
Bacteria CPR Parcubacteria OD1 Giovannonibacteria GWA2 OD1 53 7 partial
Bacteria CPR Parcubacteria OD1 Giovannonibacteria GWF2 OD1 42 19
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Bacteria CPR Parcubacteria OD1 Wolfebacteria RIFCSPLOWO2 01 FULL OD1 Wolfebacteria 47 17b
Bacteria CPR Parcubacteria OD1 GWA1 OD1 47 11
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Bacteria CPR Parcubacteria OD1 GWA2 OD1 rel 39 18
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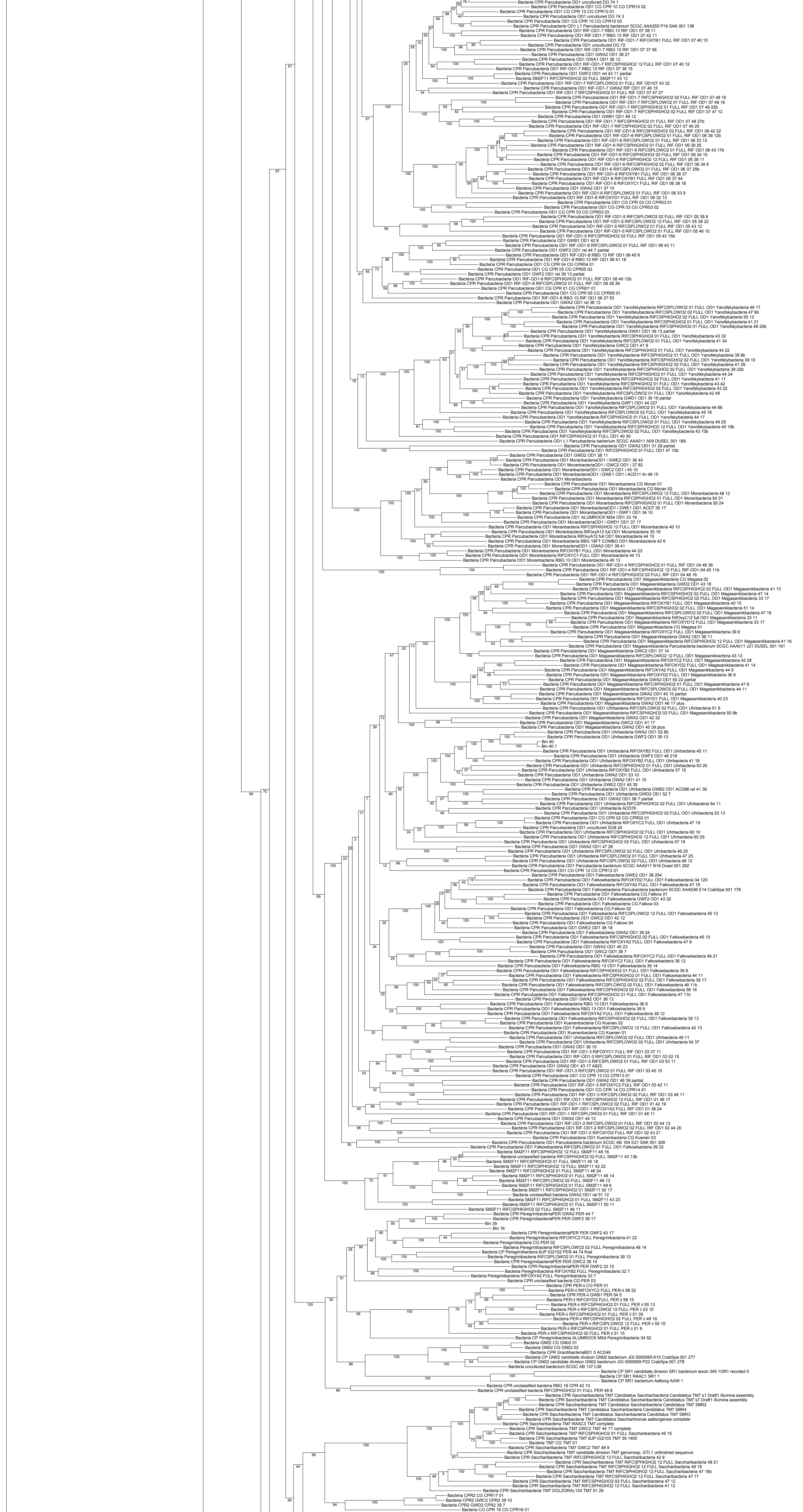
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Bacteria SM2F11 RIFCSPHIGHO2 02 FULL SM2F11 43 13
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Bacteria CPR Parcubacteria OD1 GWF2 OD1 rel 39 13 partial
Bacteria CPR Parcubacteria OD1 RIF-OD1-8 RIFCSPHIGHO2 01 FULL RIF OD1 08 40 12b
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Bacteria CPR Parcubacteria OD1 RIF-OD1-8 RBG 13 RIF OD1 08 37 53
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Bacteria CPR Parcubacteria OD1 Yanofskybacteria RIFCSPHIGHO2 01 FULL OD1 Yanofskybacteria 38 22b
Bacteria CPR Parcubacteria OD1 Yanofskybacteria RIFCSPHIGHO2 01 FULL OD1 Yanofskybacteria 44 24
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Bacteria CPR Parcubacteria OD1 GWC2 OD1 38 7
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Bacteria CPR Parcubacteria OD1 Falkowbacteria RBG 13 OD1 Falkowbacteria 39 14
Bacteria CPR Parcubacteria OD1 Falkowbacteria RIFCSPHIGHO2 01 FULL OD1 Falkowbacteria 39 8
Bacteria CPR Parcubacteria OD1 Falkowbacteria RIFCSPHIGHO2 01 FULL OD1 Falkowbacteria 44 11
Bacteria CPR Parcubacteria OD1 Falkowbacteria RIFCSPHIGHO2 02 FULL OD1 Falkowbacteria 39 17
Bacteria CPR Parcubacteria OD1 Falkowbacteria RIFCSPLOWO2 02 FULL OD1 Falkowbacteria 46 11b
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Bacteria CPR Parcubacteria OD1 GWA2 OD1 38 13
Bacteria CPR Parcubacteria OD1 Falkowbacteria RBG 13 OD1 Falkowbacteria 36 9
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Bacteria CPR Parcubacteria OD1 Falkowbacteria RifOXYA2 FULL OD1 Falkowbacteria 38 12
Bacteria CPR Parcubacteria OD1 Falkowbacteria RIFCSPHIGHO2 02 FULL OD1 Falkowbacteria 39 13
Bacteria CPR Parcubacteria OD1 Kuenenbacteria CG Kuenen 02
Bacteria CPR Parcubacteria OD1 Falkowbacteria RIFCSPLOWO2 12 FULL OD1 Falkowbacteria 42 13
Bacteria CPR Parcubacteria OD1 Kuenenbacteria CG Kuenen 01
Bacteria CPR Parcubacteria OD1 Uhrbacteria RIFCSPHIGHO2 02 FULL OD1 Uhrbacteria 49 11
Bacteria CPR Parcubacteria OD1 Uhrbacteria RIFCSPHIGHO2 02 FULL OD1 Uhrbacteria 54 37
Bacteria CPR Parcubacteria OD1 GWA2 OD1 36 10
Bacteria CPR Parcubacteria OD1 RIF-OD1-3 RIFOXYC1 FULL RIF OD1 03 37 11
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Bacteria CPR Parcubacteria OD1 GWA2 OD1 44 12
Bacteria CPR Parcubacteria OD1 RIF-OD1-2 RIFCSPLOWO2 01 FULL RIF OD1 02 44 13
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Bacteria CPR Parcubacteria OD1 Parcubacteria bacterium SCGC AB 164 E21 SAK 001 209
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Bacteria SM2F11 RIFCSPHIGHO2 12 FULL SM2F11 42 22
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Bacteria unclassified bacteria GWA2 OD1 rel 51 12
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Bacteria CPR PeregrinibacteriaPER GWA2 PER 44 7
Bacteria CPR PeregrinibacteriaPER PER GWF2 39 17
Bin 39
Bin 16
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Bacteria Peregrinibacteria RIFOXYC2 FULL Peregrinibacteria 41 22
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Bacteria Peregrinibacteria RIFCSPLOWO2 02 FULL Peregrinibacteria 48 14
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Bacteria CPR PER-ii CG PER 01
Bacteria PER-ii RIFOXYC2 FULL PER ii 58 32
Bacteria CPR PER-ii GWB1 PER 54 5
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Bacteria PER-ii RIFCSPHIGHO2 01 FULL PER ii 55 13
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Bacteria PER-ii RIFCSPHIGHO2 01 FULL PER ii 51 35
Bacteria PER-ii RIFCSPHIGHO2 01 FULL PER ii 49 16
Bacteria PER-ii RIFCSPLOWO2 12 FULL PER ii 55 15
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Bacteria CP Peregrinibacteria ALUMROCK MS4 Peregrinibacteria 34 52
Bacteria GN02 CG GN02 01
Bacteria GN02 CG GN02 02
Bacteria CPR GracilibacteriaBD1 5 ACD49
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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 fOR1 recoded II
Bacteria CP SR1 RAAC1 SR1 1
Bacteria CP SR1 bacterium Aalborg AAW 1
Bacteria CPR unclassified bacteria RBG 16 CPR 42 10
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Bacteria CPR Saccharibacteria TM7 Candidatus Saccharibacteria Candidatus TM7 SBR4
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Bacteria CPR Saccharibacteria TM7 RAAC3 TM7 complete
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Bacteria CPR Saccharibacteria TM7 BJP IG2103 TM7 39 1400
Bacteria TM7 CG TM7 01
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Bacteria CPR Saccharibacteria TM7 candidate division TM7 genomosp. GTL1 unfinished sequence
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Bacteria CPR Saccharibacteria TM7 RIFCSPHIGHO2 02 FULL Saccharibacteria 47 12
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Bacteria CPR Saccharibacteria TM7 DOLZORAL124 TM7 51 29
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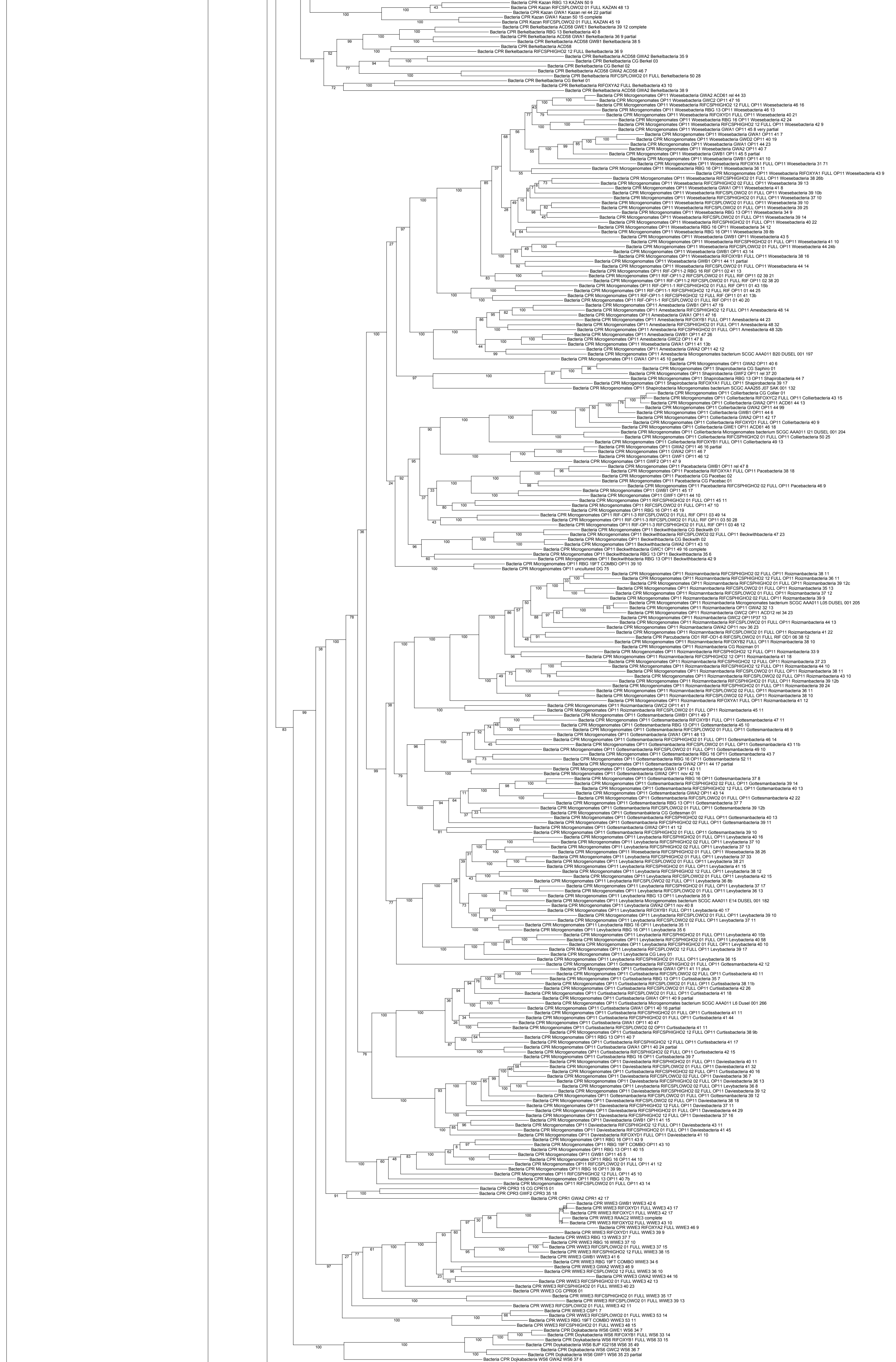
Bacteria CPR2 GWC2 CPR2 39 10
Bacteria CPR2 GWD2 CPR2 39 7
Bacteria CG CPR 16 CG CPR16 01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Bacteria CPR Kazan RIFCSPLOWO2 01 FULL KAZAN 45 19
Bacteria CPR Berkelbacteria ACD58 GWE1 Berkelbacteria 39 12 complete
Bacteria CPR Berkelbacteria RBG 13 Berkelbacteria 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
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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
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Bacteria CPR Microgenomates OP11 Woesebacteria RBG 13 OP11 Woesebacteria 46 13
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Bacteria CPR Microgenomates OP11 Woesebacteria RBG 16 OP11 Woesebacteria 42 24
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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
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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 RBG 13 OP11 Woesebacteria 34 9
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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
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Bacteria CPR Microgenomates OP11 Woesebacteria RIFOXYB1 FULL OP11 Woesebacteria 38 16
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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 GWA2 OP11 42 17
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Bacteria CPR Microgenomates OP11 Collierbacteria RIFCSPHIGHO2 01 FULL OP11 Collierbacteria 50 25
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Bacteria CPR Microgenomates OP11 GWA2 OP11 46 16 partial
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Bacteria CPR Microgenomates OP11 Levybacteria GWA2 OP11 nov 40 8
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
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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
Bacteria CPR Microgenomates OP11 Levybacteria CG Levy 01
Bacteria CPR Microgenomates OP11 Levybacteria RIFCSPHIGHO2 01 FULL OP11 Levybacteria 36 15
Bacteria CPR Microgenomates OP11 Gottesmanbacteria RIFCSPHIGHO2 01 FULL OP11 Gottesmanbacteria 42 12
Bacteria CPR Microgenomates OP11 Curtissbacteria GWA1 OP11 41 11 plus
Bacteria CPR Microgenomates OP11 Curtissbacteria RIFCSPLOWO2 02 FULL OP11 Curtissbacteria 40 11
Bacteria CPR Microgenomates OP11 Curtissbacteria RBG 13 OP11 Curtissbacteria 35 7
Bacteria CPR Microgenomates OP11 Curtissbacteria RIFCSPLOWO2 01 FULL OP11 Curtissbacteria 38 11b
Bacteria CPR Microgenomates OP11 Curtissbacteria RIFCSPLOWO2 01 FULL OP11 Curtissbacteria 42 26
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Bacteria CPR Microgenomates OP11 Curtissbacteria GWA1 OP11 40 9 partial
Bacteria CPR Microgenomates OP11 Curtissbacteria Microgenomates bacterium SCGC AAA011 L6 Dusel 001 266
Bacteria CPR Microgenomates OP11 Curtissbacteria GWA1 OP11 40 16 partial
Bacteria CPR Microgenomates OP11 Curtissbacteria RIFCSPHIGHO2 01 FULL OP11 Curtissbacteria 41 11
Bacteria CPR Microgenomates OP11 Curtissbacteria RIFCSPHIGHO2 01 FULL OP11 Curtissbacteria 41 44
Bacteria CPR Microgenomates OP11 Curtissbacteria GWA1 OP11 40 47
Bacteria CPR Microgenomates OP11 Curtissbacteria RIFCSPLOWO2 02 OP11 Curtissbacteria 41 11
Bacteria CPR Microgenomates OP11 Curtissbacteria RIFCSPHIGHO2 12 FULL OP11 Curtissbacteria 38 9b
Bacteria CPR Microgenomates OP11 RBG 13 OP11 40 7
Bacteria CPR Microgenomates OP11 Curtissbacteria RIFCSPHIGHO2 12 FULL OP11 Curtissbacteria 41 17
Bacteria CPR Microgenomates OP11 Curtissbacteria GWA1 OP11 40 24 partial
Bacteria CPR Microgenomates OP11 Curtissbacteria RIFCSPHIGHO2 02 FULL OP11 Curtissbacteria 42 15
Bacteria CPR Microgenomates OP11 Curtissbacteria RBG 16 OP11 Curtissbacteria 39 7
Bacteria CPR Microgenomates OP11 Daviesbacteria RIFCSPHIGHO2 01 FULL OP11 Daviesbacteria 40 11
Bacteria CPR Microgenomates OP11 Daviesbacteria RIFCSPLOWO2 01 FULL OP11 Daviesbacteria 41 32
Bacteria CPR Microgenomates OP11 Curtissbacteria RIFCSPHIGHO2 02 FULL OP11 Curtissbacteria 40 16
Bacteria CPR Microgenomates OP11 Daviesbacteria RIFCSPLOWO2 02 FULL OP11 Daviesbacteria 36 7
Bacteria CPR Microgenomates OP11 Daviesbacteria RIFCSPHIGHO2 02 FULL OP11 Daviesbacteria 36 13
Bacteria CPR Microgenomates OP11 Levybacteria RIFCSPLOWO2 02 FULL OP11 Levybacteria 36 8
Bacteria CPR Microgenomates OP11 Daviesbacteria RIFCSPHIGHO2 02 FULL OP11 Daviesbacteria 39 12
Bacteria CPR Microgenomates OP11 Gottesmanbacteria RIFCSPLOWO2 01 FULL OP11 Gottesmanbacteria 39 12
Bacteria CPR Microgenomates OP11 Daviesbacteria RIFCSPLOWO2 02 FULL OP11 Daviesbacteria 38 18
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
Bacteria CPR Microgenomates OP11 RIFCSPLOWO2 01 FULL OP11 41 12
Bacteria CPR Microgenomates OP11 RBG 16 OP11 39 9b
Bacteria CPR Microgenomates OP11 RIFCSPHIGHO2 12 FULL OP11 45 10
Bacteria CPR Microgenomates OP11 RBG 13 OP11 40 7b
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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
Bacteria CPR WWE3 RIFCSPLOWO2 01 FULL WWE3 39 13
Bacteria CPR WWE3 RIFCSPLOWO2 01 FULL WWE3 42 11
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 Doykabacteria WS6 RIFOXYB1 FULL WS6 33 14
Bacteria CPR Doykabacteria WS6 RIFOXYB1 FULL WS6 33 15
Bacteria CPR Doykabacteria WS6 BJP IG2158 WS6 35 49
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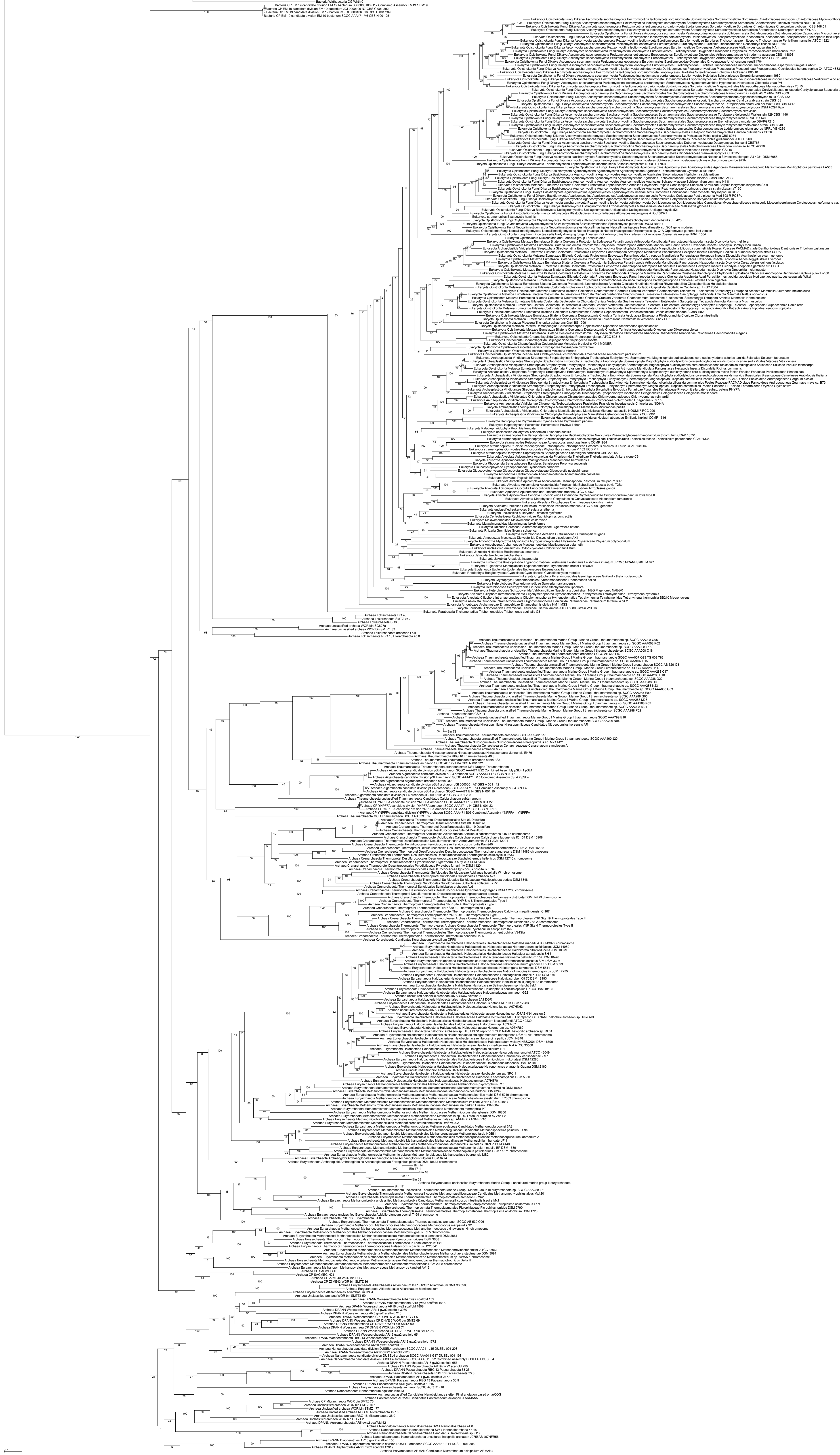
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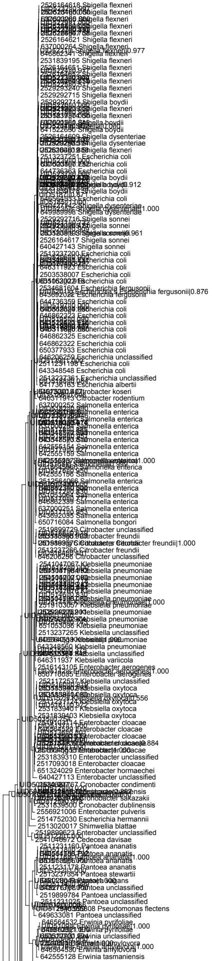
Figure S2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2529293240 Shigella flexneri
2529292715 Shigella flexneri
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641522656 Shigella boydii
2526164609 Shigella dysenteriae
2513237251 Escherichia coli
644736363 Escherichia coli
646564533 Escherichia coli
649989906 Shigella dysenteriae
2529292716 Shigella sonnei
2526164617 Shigella sonnei
640427143 Shigella sonnei
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646311923 Escherichia coli
2503538007 Escherichia coli
2534681604 Escherichia fergusonii
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644736359 Escherichia coli
646862323 Escherichia coli
646862325 Escherichia coli
646862322 Escherichia coli
650377933 Escherichia coli
646206259 Escherichia unclassified
2511231198 Escherichia coli
643348548 Escherichia coli
2513237361 Escherichia unclassified
641736163 Escherichia albertii
646311913 Citrobacter rodentium
637000252 Salmonella enterica
642555154 Salmonella enterica
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637000251 Salmonella enterica
643692095 Salmonella enterica
650716084 Salmonella bongori
2519899729 Citrobacter unclassified
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2541047067 Klebsiella pneumoniae
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2513237265 Klebsiella unclassified
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646311937 Klebsiella variicola
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2521172537 Klebsiella unclassified
2531839401 Klebsiella oxytoca
2531839403 Klebsiella oxytoca
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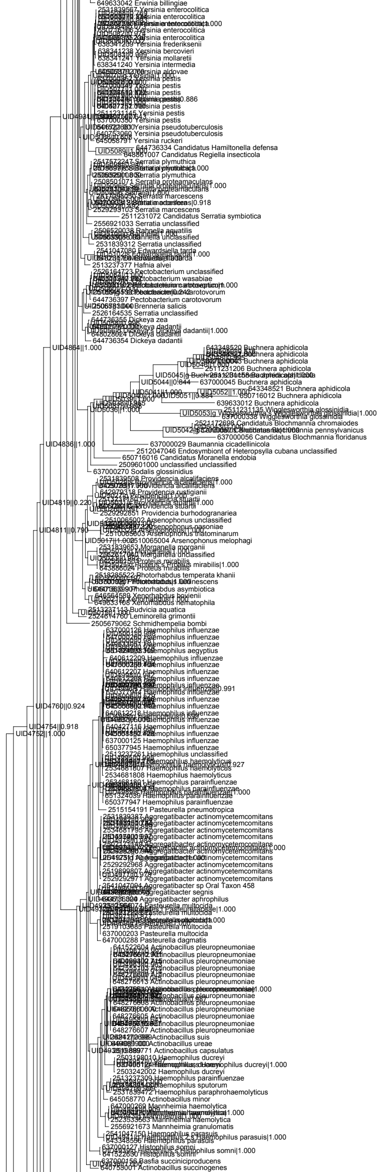
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638341238 Yersinia bercovieri
638341241 Yersinia mollaretii
638341240 Yersinia intermedia
Yersinia aldovae
Yersinia pestis
Yersinia pestis
Yersinia pestis
Yersinia pestis|0.886
Yersinia pestis
2511231145 Yersinia pestis
637000350 Yersinia pestis
Yersinia pseudotuberculosis
640753060 Yersinia pseudotuberculosis
645058791 Yersinia ruckeri
644736334 Candidatus Hamiltonella defensa
648861007 Candidatus Regiella insecticola
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Serratia plymuthica|1.000
Serratia plymuthica
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Serratia proteamaculans|1.000
Serratia marcescens
Serratia marcescens|0.918
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2511231072 Candidatus Serratia symbiotica
2556921033 Serratia unclassified
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Rahnella unclassified
2531839312 Serratia unclassified
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Edwardsiella tarda|1.000
2513237377 Hafnia alvei
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Pectobacterium wasabiae
Pectobacterium atrosepticum|1.000
Pectobacterium carotovorum
644736397 Pectobacterium carotovorum
Brenneria salicis
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644736355 Dickeya zea
Dickeya dadantii
Dickeya dadantii|1.000
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644736354 Dickeya dadantii
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Buchnera aphidicola
Buchnera aphidicola
Buchnera aphidicola
2511231206 Buchnera aphidicola
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UID5044||0.844
637000045 Buchnera aphidicola
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UID5051||0.884
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UID5036||1.000
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2521172698 Candidatus Blochmannia chromaiodes
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Candidatus Blochmannia pennsylvanicus
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637000029 Baumannia cicadellinicola
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Providencia alcalifaciens|1.000
Providencia alcalifaciens
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Providencia stuartii
Providencia stuartii|1.000
Providencia stuartii
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Arsenophonus nasoniae
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UID5017||1.000
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Morganella unclassified
Proteus mirabilis
Proteus mirabilis|1.000
643886024 Proteus mirabilis
2518285522 Photorhabdus temperata khanii
Photorhabdus luminescens
Photorhabdus asymbiotica
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649633108 Xenorhabdus nematophila
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2524614760 Leminorella grimontii
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Haemophilus influenzae
Haemophilus influenzae
Haemophilus aegyptius
640612209 Haemophilus influenzae
Haemophilus influenzae
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Haemophilus influenzae
Haemophilus influenzae
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Haemophilus influenzae
Haemophilus influenzae
Haemophilus influenzae
640612218 Haemophilus influenzae
Haemophilus influenzae
640427116 Haemophilus influenzae
Haemophilus influenzae
637000125 Haemophilus influenzae
650377945 Haemophilus influenzae
UID4760||0.924
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Haemophilus parainfluenzae
Haemophilus parainfluenzae|1.000
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Aggregatibacter actinomycetemcomitans
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Actinobacillus pleuropneumoniae
Actinobacillus pleuropneumoniae
Actinobacillus pleuropneumoniae
Actinobacillus pleuropneumoniae
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Actinobacillus pleuropneumoniae
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Haemophilus sputorum
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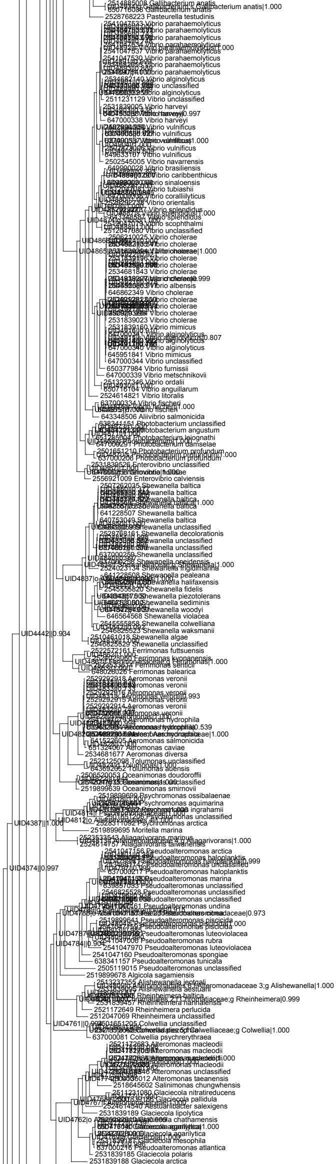
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Vibrio parahaemolyticus
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Vibrio vulnificus
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Vibrio orientalis
Vibrio splendidus
Vibrio splendidus
Vibrio scophthalmi
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2513237346 Vibrio ordalii
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Vibrio fischeri
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Pseudoalteromonas marina
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Glaciecola pallidula
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Glaciecola agarilytica
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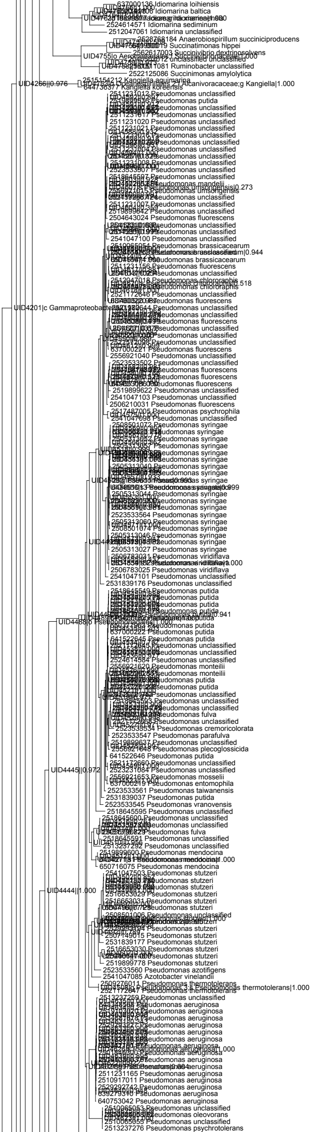
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Succinatimonas hippei
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Alcanivoracaceae;g Kangiella|1.000
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Pseudomonas chlororaphis|0.518
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Pseudomonas fluorescens
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Pseudomonas unclassified
Pseudomonas fluorescens
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2541047103 Pseudomonas unclassified
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2508501072 Pseudomonas syringae
Pseudomonas syringae|0.999
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2505313060 Pseudomonas syringae
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2505313046 Pseudomonas syringae
2505313027 Pseudomonas syringae
2506783031 Pseudomonas viridiflava
Pseudomonas viridiflava|1.000
2506783025 Pseudomonas viridiflava
2541047101 Pseudomonas unclassified
2531839176 Pseudomonas unclassified
2518645549 Pseudomonas putida
Pseudomonas putida|0.941
UID4488|o Pseudomonadales|1.000
637000222 Pseudomonas putida
641522645 Pseudomonas putida
2524614584 Pseudomonas unclassified
2556921620 Pseudomonas monteilii
Pseudomonas monteilii
Pseudomonas putida
Pseudomonas fulva
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Pseudomonas plecoglossicida
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UID4445||0.972
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Pseudomonas mendocina|1.000
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UID4444||1.000
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2519899778 Pseudomonas stutzeri
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Pseudomonas thermotolerans|1.000
2521172647 Pseudomonas thermotolerans
2513237259 Pseudomonas unclassified
Pseudomonas aeruginosa
Pseudomonas aeruginosa|1.000
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2510917011 Pseudomonas aeruginosa
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Pseudomonas oleovorans
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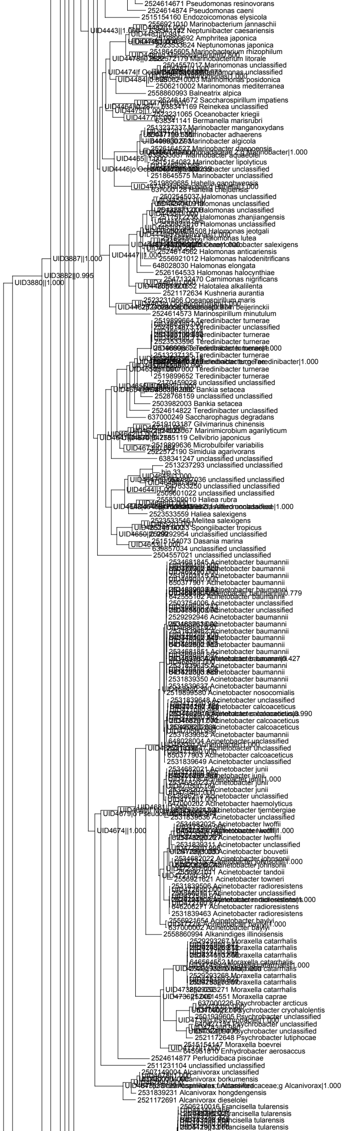
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2523533624 Neptunomonas japonica
2518645605 Marinobacterium rhizophilum
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Marinomonas unclassified
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Marinobacter algicola
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Marinobacter aquaeolei
Marinobacter|1.000
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Halomonas unclassified
Halomonas unclassified
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Halomonas unclassified
Halomonas jeotgali
Halomonas lutea
Chromohalobacter salexigens
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UID4447||1.000
2556921012 Halomonas halodenitrificans
648028030 Halomonas elongata
2526164533 Halomonas halocynthiae
2547132470 Carnimonas nigrificans
Halotalea alkalilenta
2521172634 Kushneria aurantia
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Oceanospirillum beijerinckii
2524614573 Marinospirillum minutulum
2519899664 Teredinibacter turnerae
2524614873 Teredinibacter unclassified
Teredinibacter turnerae
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Teredinibacter turnerae|1.000
2513237135 Teredinibacter turnerae
Teredinibacter|1.000
Teredinibacter turnerae
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
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unclassified unclassified
unclassified unclassified
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Spongiibacter tropicus
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UID3880||1.000
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Acinetobacter baumannii
Acinetobacter baumannii
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Acinetobacter baumannii|0.779
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2531839552 Acinetobacter baumannii
648028004 Acinetobacter unclassified
Acinetobacter unclassified
650377903 Acinetobacter calcoaceticus
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2534682021 Acinetobacter junii
Acinetobacter junii
Acinetobacter junii|1.000
Acinetobacter junii
Acinetobacter junii
Acinetobacter unclassified
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Acinetobacter tjernbergiae
2531839536 Acinetobacter unclassified
UID4679|o Pseudo
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2531839311 Acinetobacter unclassified
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Acinetobacter johnsonii
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2531839506 Acinetobacter radioresistens
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Acinetobacter radioresistens|1.000
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2558860994 Alkanindiges illinoisensis
2529293267 Moraxella catarrhalis
Moraxella catarrhalis
Moraxella catarrhalis
Moraxella catarrhalis
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Moraxella catarrhalis
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637000226 Psychrobacter arcticus
Psychrobacter cryohalolentis
2501939605 Psychrobacter unclassified
Psychrobacter unclassified
Psychrobacter unclassified
2521172648 Psychrobacter lutiphocae
2515154147 Moraxella boevrei
643561810 Enhydrobacter aerosaccus
2524614877 Perlucidibaca piscinae
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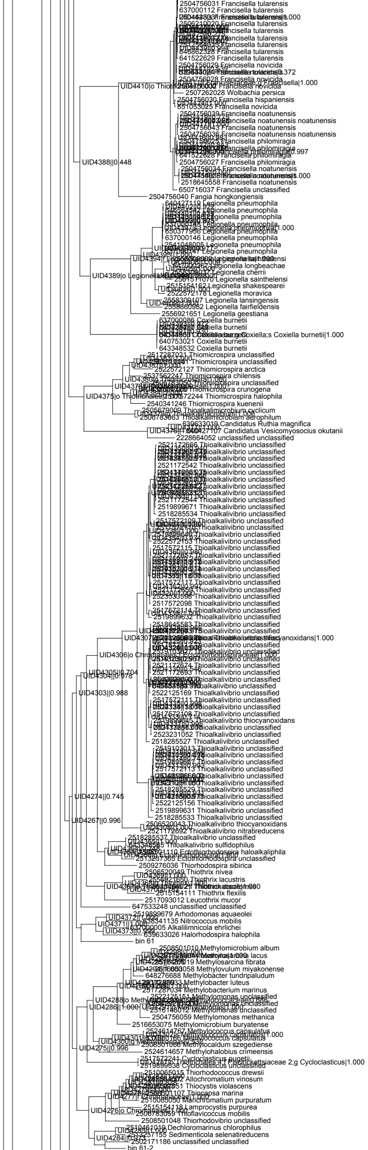
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2504756029 Francisella novicida
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2507262028 Wolbachia persica
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651053025 Francisella novicida
UID4410|o Thiotrichales
2504756039 Francisella noatunensis
Francisella noatunensis noatunensis
2504756043 Francisella noatunensis
2504756036 Francisella noatunensis noatunensis
Francisella philomiragia
Francisella philomiragia
641522628 Francisella philomiragia
2504756027 Francisella philomiragia
2504756034 Francisella noatunensis
2518645558 Francisella noatunensis
650716037 Francisella unclassified
UID4388||0.448
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640427119 Legionella pneumophila
Legionella pneumophila
Legionella pneumophila
Legionella pneumophila
650377956 Legionella pneumophila
637000146 Legionella pneumophila
2541948005 Legionella pneumophila
Legionella pneumophila
Legionella longbeachae
Legionella cherrii
2561511070 Legionella sainthelensi
2515154162 Legionella shakespearei
2522572178 Legionella moravica
2558309107 Legionella lansingensis
2558860982 Legionella fairfieldensis
2556921651 Legionella geestiana
UID4389|o Legionellales
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
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Thiomicrospira unclassified
Thiomicrospira crunogena
UID4375|o Thiotrichales
Thiomicrospira halophila
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Thioalkalivibrio thiocyanoxidans|1.000
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2518285537 Thioalkalivibrio unclassified
Thioalkalivibrio sulfidophilus
Ectothiorhodospira haloalkaliphila
2513237365 Ectothiorhodospira unclassified
2509276036 Thiorhodospira sibirica
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2515154111 Thiothrix flexilis
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UID4372||1.000
638341135 Nitrococcus mobilis
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UID4373||0.999
639633026 Halorhodospira halophila
bin 61
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Methylomonas lacus
Methylosarcina fibrata
Methylovulum miyakonense
648276688 Methylobacter tundripaludum
Methylobacter luteus
2517287034 Methylobacterium marinus
2522125151 Methylomonas unclassified
Methylomonas unclassified
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UID4286||1.000
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2516653075 Methylomicrobium buryatense
2524614767 Methylococcus capsulatus
Methylococcus capsulatus
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UID4300|o Methylococcales
UID4275||0.996
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Piscirickettsiaceae 2;g Cycloclasticus|1.000
Cycloclasticus unclassified
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Allochromatium vinosum
Thiocystis violascens
Thiocapsa marina
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UID4276|o Chromatiales
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2508501048 Thiorhodovibrio unclassified
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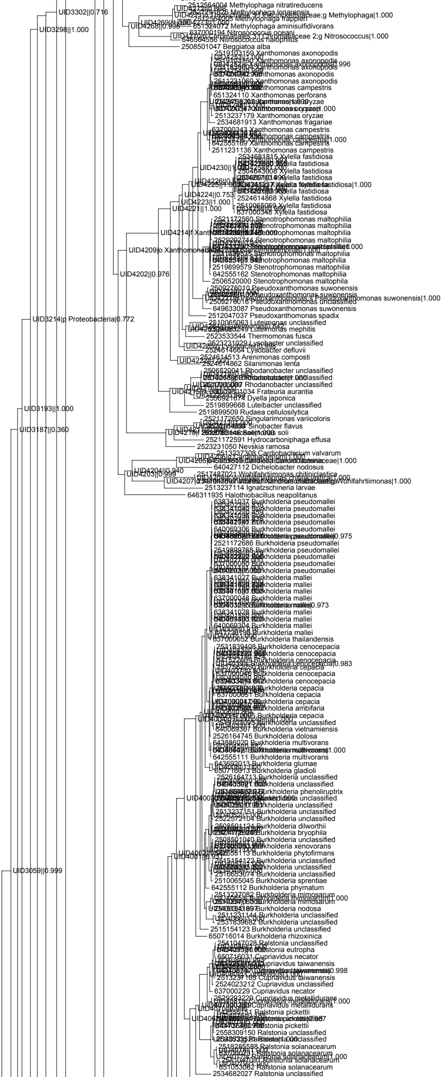
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651324072 Methylophaga aminisulfidivorans
637000194 Nitrosococcus oceani
Chromatiales 3;f Chromatiaceae 2;g Nitrosococcus|1.000
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Xanthomonas axonopodis
2511231060 Xanthomonas axonopodis
Xanthomonas campestris
651324110 Xanthomonas perforans
Xanthomonas oryzae
Xanthomonas oryzae|1.000
2513237179 Xanthomonas oryzae
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Xanthomonas campestris
Xanthomonas campestris|1.000
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Xylella fastidiosa
2504643008 Xylella fastidiosa
Xylella fastidiosa
Xylella fastidiosa|1.000
Xylella fastidiosa
2524614868 Xylella fastidiosa
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Stenotrophomonas maltophilia
2529292744 Stenotrophomonas maltophilia
Stenotrophomonas maltophilia|1.000
Stenotrophomonas maltophilia
Stenotrophomonas maltophilia
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Pseudoxanthomonas suwonensis|1.000
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649633087 Pseudoxanthomonas suwonensis
2512047037 Pseudoxanthomonas spadix
2510065063 Luteimonas unclassified
Luteimonas mephitis
2523533544 Thermomonas fusca
2523231029 Lysobacter unclassified
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Rhodanobacter unclassified
Rhodanobacter|1.000
Rhodanobacter unclassified
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Burkholderia pseudomallei
Burkholderia pseudomallei
Burkholderia pseudomallei
640069306 Burkholderia pseudomallei
Burkholderia pseudomallei|0.975
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Burkholderia pseudomallei
637000050 Burkholderia pseudomallei
Burkholderia pseudomallei
638341027 Burkholderia mallei
Burkholderia mallei
Burkholderia mallei
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Burkholderia mallei|0.973
638341028 Burkholderia mallei
Burkholderia mallei
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637000052 Burkholderia thailandensis
2531839408 Burkholderia cenocepacia
Burkholderia cenocepacia
Burkholderia cenocepacia
Burkholderia cenocepacia|0.983
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637000046 Burkholderia cenocepacia
Burkholderia cenocepacia
Burkholderia cepacia
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
2515154122 Burkholderia unclassified
Burkholderia unclassified
2516653074 Burkholderia unclassified
2510065045 Burkholderia sprentiae
642555112 Burkholderia phymatum
UID3059||0.999
UID4001||0.931
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Burkholderia mimosarum|1.000
Burkholderia mimosarum
Burkholderia nodosa
2511231144 Burkholderia unclassified
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2515154123 Burkholderia unclassified
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Ralstonia eutropha
650716031 Cupriavidus necator
Cupriavidus taiwanensis
Cupriavidus taiwanensis|0.998
2513237165 Cupriavidus taiwanensis
2524023212 Cupriavidus unclassified
637000229 Cupriavidus necator
2529293220 Cupriavidus metallidurans
Cupriavidus metallidurans|1.000
Ralstonia pickettii
Ralstonia pickettii|0.987
Ralstonia pickettii
2558309150 Ralstonia unclassified
Ralstonia|1.000
2518285588 Ralstonia solanacearum
Ralstonia solanacearum
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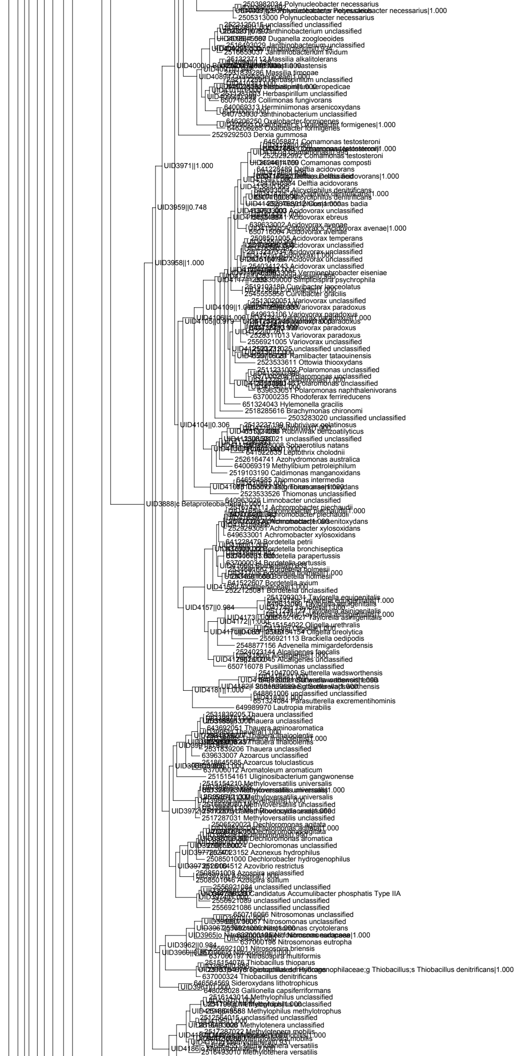
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Janthinobacterium unclassified
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2516493029 Janthinobacterium unclassified
2516653037 Janthinobacterium lividum
2513237112 Massilia alkalitolerans
UID4000|o Burkholderiales
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646206250 Oxalobacter formigenes
Oxalobacter formigenes|1.000
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641228489 Delftia acidovorans
Delftia acidovorans|1.000
Delftia acidovorans
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Alicycliphilus denitrificans|1.000
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Comamonas badia
Acidovorax unclassified
Acidovorax ebreus
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Acidovorax avenae|1.000
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2508501005 Acidovorax temperans
Acidovorax unclassified
Acidovorax unclassified
Acidovorax unclassified
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Verminephrobacter eiseniae
Simplicispira psychrophila
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Variovorax paradoxus
UID4109||1.000
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UID4105||0.979
649633106 Variovorax paradoxus
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Variovorax paradoxus
2528311013 Variovorax paradoxus
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unclassified unclassified
Ramlibacter tataouinensis
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unclassified unclassified
Sphaerotilus natans
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640069319 Methylibium petroleiphilum
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Thiomonas arsenitoxydans
2523533526 Thiomonas unclassified
UID3888|c Betaproteobacteria|1.000
640963026 Limnobacter unclassified
Achromobacter piechaudii
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
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UID4173||1.000
2515154022 Oligella urethralis
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Oligella ureolytica
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2548877156 Advenella mimigardefordensis
2524023144 Alcaligenes faecalis
Alcaligenes|1.000
Alcaligenes unclassified
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648861006 unclassified unclassified
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649989970 Lautropia mirabilis
2531839205 Thauera unclassified
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Thauera linaloolentis|1.000
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2531839206 Thauera unclassified
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637000012 Aromatoleum aromaticum
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Methyloversatilis universalis|1.000
Methyloversatilis universalis
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Dechloromonas agitata|1.000
Dechloromonas agitata
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Azonexus hydrophilus
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Azovibrio restrictus
2508501008 Azospira unclassified
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Candidatus Accumulibacter phosphatis Type IIA
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637000324 Thiobacillus denitrificans
646564569 Sideroxydans lithotrophicus
648028028 Gallionella capsiferriformans
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Methylophilus unclassified
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2516493026 Methylotenera unclassified
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Methylotenera versatilis
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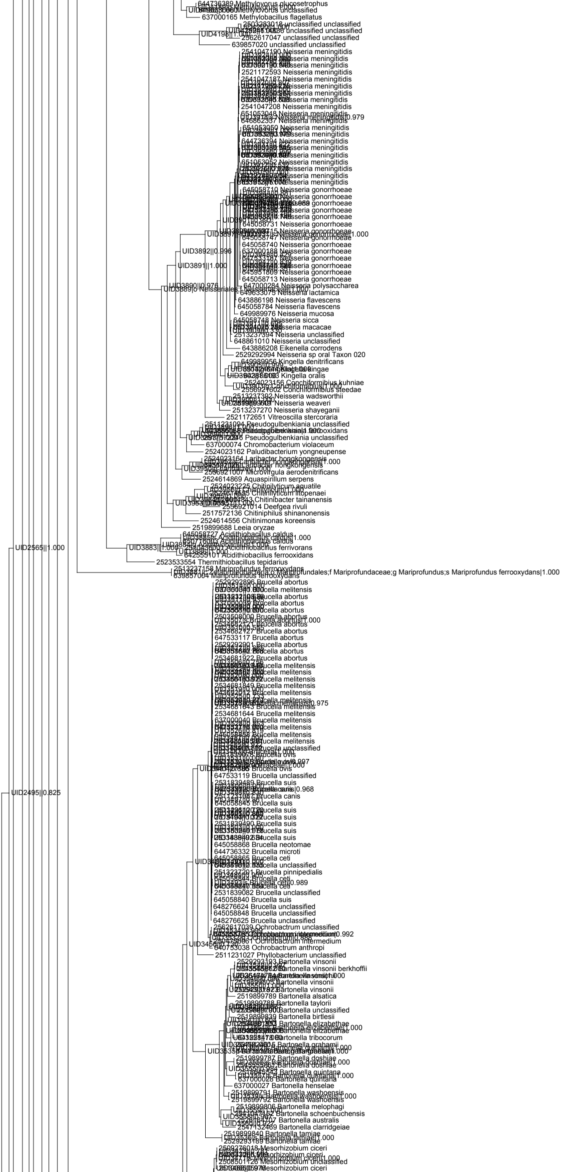
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644736394 Neisseria meningitidis
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645058710 Neisseria gonorrhoeae
645058731 Neisseria gonorrhoeae
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637000188 Neisseria gonorrhoeae
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649989956 Kingella denitrificans
2524023156 Conchiformibius kuhniae
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2513237270 Neisseria shayeganii
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2517572136 Chitiniphilus shinanonensis
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2519899839 Bartonella birtlesii
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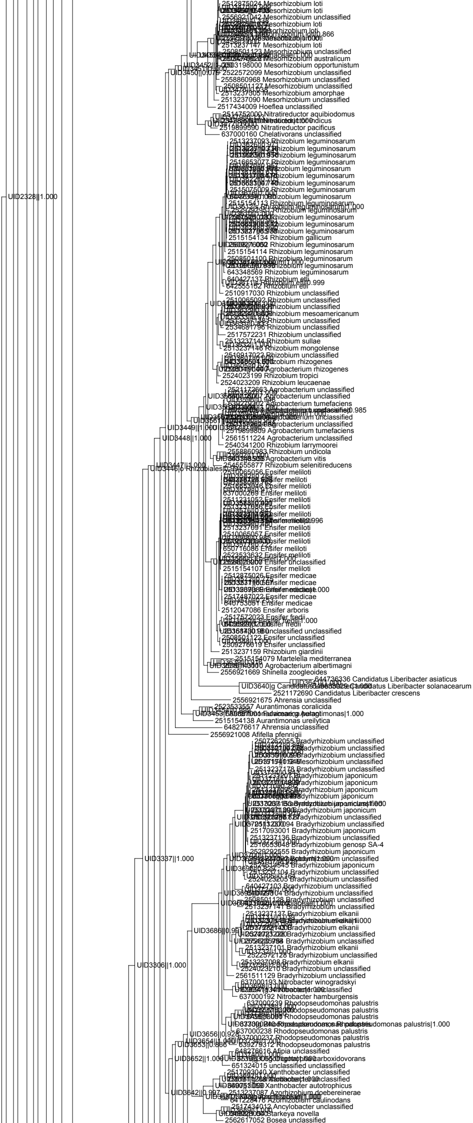
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Mesorhizobium australicum
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2516899590 Nitratireductor pacificus
637000160 Chelativorans unclassified
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2513237144 Rhizobium sullae
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2510917022 Rhizobium unclassified
Rhizobium rhizogenes
Agrobacterium rhizogenes
2524023199 Rhizobium tropici
2524023209 Rhizobium leucaenae
2521172663 Agrobacterium unclassified
Agrobacterium unclassified
Agrobacterium tumefaciens
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Agrobacterium vitis
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Ensifer unclassified
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2512875026 Ensifer medicae
2517487022 Ensifer medicae
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2513237159 Rhizobium giardinii
2515154079 Martelella mediterranea
Agrobacterium albertimagni
2556921669 Shinella zoogleoides
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Candidatus Liberibacter solanacearum
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2515154138 Aurantimonas ureilytica
648276617 Ahrensia unclassified
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Bradyrhizobium unclassified
Mesorhizobium unclassified
2513237178 Bradyrhizobium unclassified
Bradyrhizobium japonicum
2517093001 Bradyrhizobium japonicum
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2513237104 Bradyrhizobium unclassified
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Bradyrhizobium elkanii
Bradyrhizobium unclassified
2513237101 Bradyrhizobium elkanii
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2561511129 Bradyrhizobium unclassified
637000193 Nitrobacter winogradskyi
Nitrobacter unclassified
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Rhodopseudomonas palustris
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639279312 Rhodopseudomonas palustris
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carboxidovorans
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Xanthobacter unclassified
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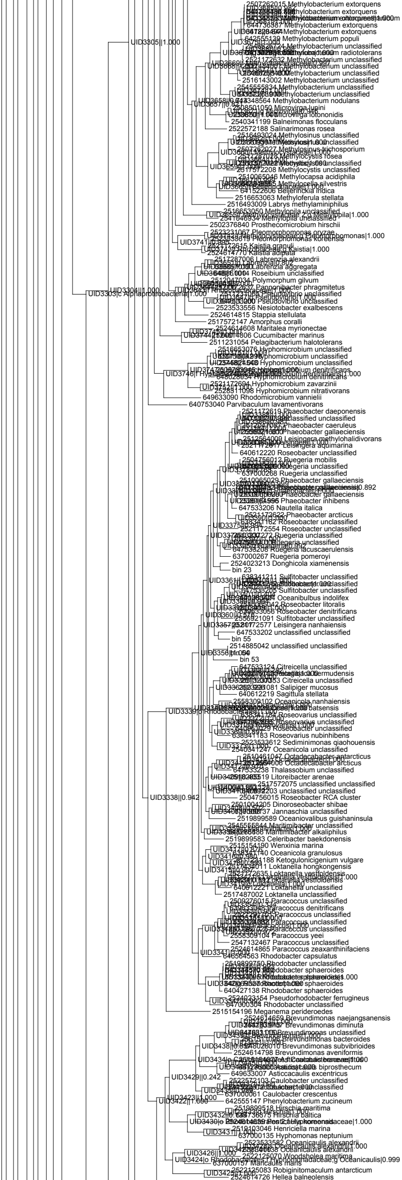
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Methylobacterium nodulans
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Microvirga lotononidis
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2522572188 Salinarimonas rosea
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Methylocystis rosea
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Pleomorphomonas koreensis
2521172615 Kaistia granuli
2524614770 Kaistia adipata
2517287006 Labrenzia alexandrii
Labrenzia aggregata
Roseibium unclassified
2512047034 Polymorphum gilvum
Pannonibacter phragmitetus
Pseudovibrio unclassified
Pseudovibrio unclassified
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2517572147 Amorphus coralli
2524614608 Maritalea myrionectae
Cucumibacter marinus
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2516653076 Hyphomicrobium unclassified
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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Ruegeria unclassified
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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
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Leisingera nanhaiensis
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bin 55
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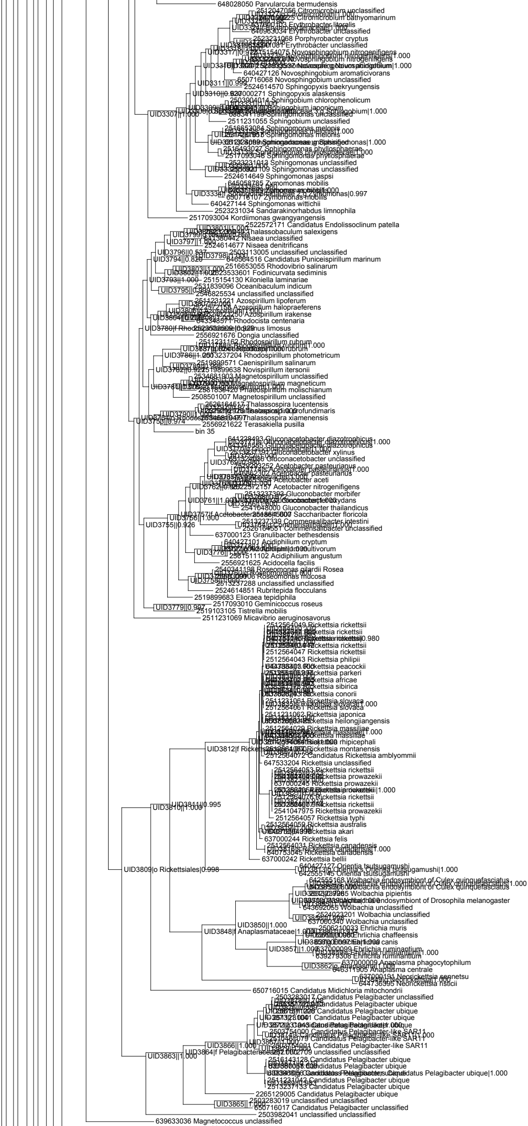
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Erythrobacter unclassified
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Gluconacetobacter diazotrophicus
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Gluconacetobacter unclassified
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Acetobacter pasteurianus
Acetobacter aceti
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Roseomonas mucosa
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Rickettsia parkeri
Rickettsia africae
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Rickettsia conorii
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Rickettsia massiliae
Rickettsia rhipicephali
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Rickettsia montanensis
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647533204 Rickettsia unclassified
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Rickettsia prowazekii
637000245 Rickettsia prowazekii
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Rickettsia rickettsii
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2541047975 Rickettsia prowazekii
2512564057 Rickettsia typhi
2512564059 Rickettsia australis
Rickettsia akari
637000244 Rickettsia felis
2512564031 Rickettsia canadensis
640753045 Rickettsia canadensis
637000242 Rickettsia bellii
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Orientia tsutsugamushi|1.000
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Wolbachia endosymbiont of Culex quinquefasciatus|1.000
Wolbachia pipientis
endosymbiont of Drosophila melanogaster
643692055 Wolbachia unclassified
2524023201 Wolbachia unclassified
637000340 Wolbachia unclassified
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2506210033 Ehrlichia muris
Ehrlichia chaffeensis
UID3848|f Anaplasmataceae|1.000
Ehrlichia canis
UID3857||1.000
637000099 Ehrlichia ruminantium
Ehrlichia ruminantium|1.000
639279308 Ehrlichia ruminantium
637000009 Anaplasma phagocytophilum
UID3862|g Anaplasma|1.000
646311905 Anaplasma centrale
637000191 Neorickettsia sennetsu
Neorickettsia|1.000
644736395 Neorickettsia risticii
650716015 Candidatus Midichloria mitochondrii
2503283017 Candidatus Pelagibacter unclassified
Candidatus Pelagibacter ubique
Candidatus Pelagibacter ubique
Candidatus Pelagibacter ubique
Candidatus Pelagibacter ubique|1.000
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2524023209 unclassified unclassified
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Candidatus Pelagibacter ubique|1.000
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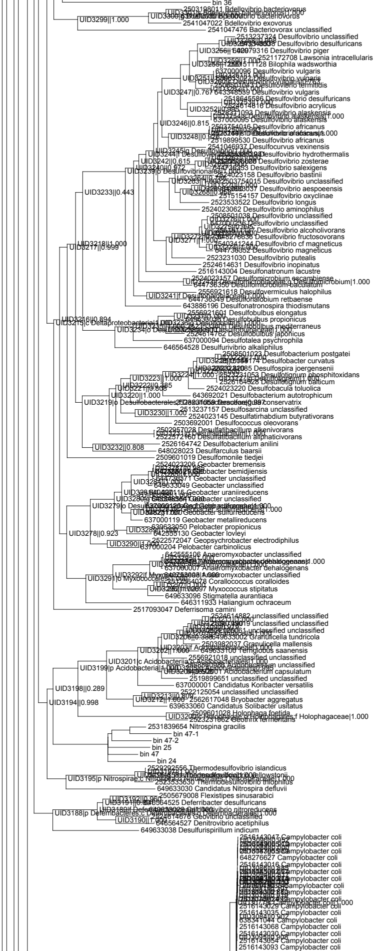
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Desulfovibrio salexigens
UID3239|o Desulfovibrionales
UID3233||0.443
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Desulfovibrio unclassified
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2524614631 Desulfovibrio inopinatus
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UID3241|f Desulfohalobiaceae|1.000
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UID3234|o Desulfobulbaceae|1.000
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2524023220 Desulfobacula toluolica
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conservatrix
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UID3230||1.000
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Desulfatibacillum|1.000
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UID3232||0.808
2526164742 Desulfobacterium anilini
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2524023206 Geobacter bremensis
Geobacter bemidjiensis
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UID3284||1.000
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Geobacter uraniireducens
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bin 24
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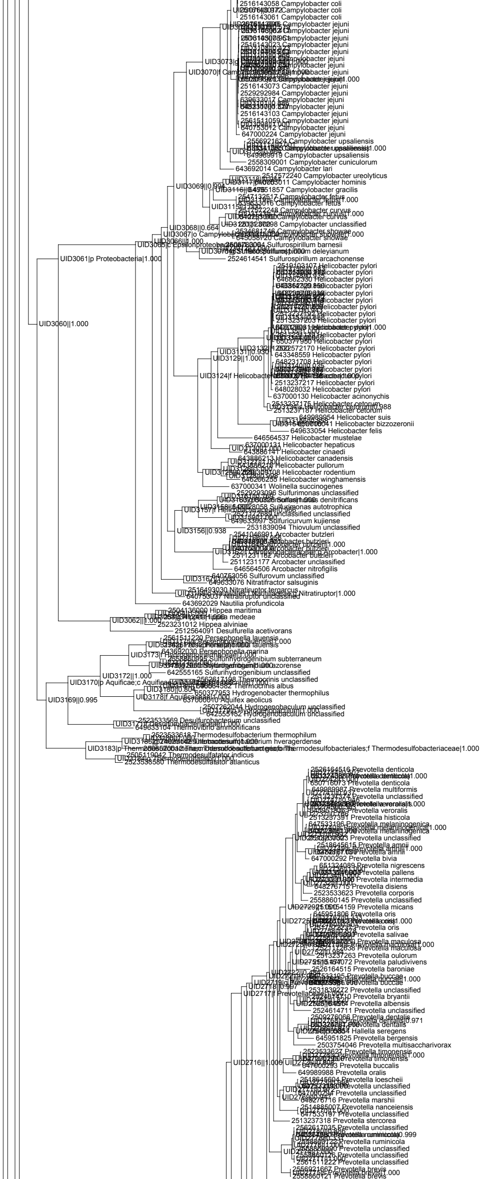
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640753012 Campylobacter jejuni
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2558309001 Campylobacter cuniculorum
643692014 Campylobacter lari
2517572240 Campylobacter ureolyticus
UID3073|g
UID3070|f Campylobacteraceae
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2547132517 Campylobacter fetus
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UID3115||1.000
2517572248 Campylobacter curvus
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Sulfurospirillum barnesii
Sulfurospirillum deleyianum
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2513237175 Helicobacter cetorum
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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
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Sulfurimonas autotrophica
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2511231182 Arcobacter butzleri
2511231177 Arcobacter unclassified
646564506 Arcobacter nitrofigilis
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2516493030 Nitratiruptor tergarcus
640753037 Nitratiruptor unclassified
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Hippea medeae
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2523533580 Thermodesulfatator atlanticus
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650716073 Prevotella denticola
649989987 Prevotella multiformis
2513237374 Prevotella unclassified
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2513237391 Prevotella histicola
647533196 Prevotella melaninogenica
Prevotella melaninogenica
Prevotella unclassified
2518645615 Prevotella amnii
Prevotella amnii
647000292 Prevotella bivia
651324089 Prevotella nigrescens
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Prevotella intermedia
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2523533623 Prevotella corporis
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Prevotella oris
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Prevotella buccae
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Prevotella bryantii
Prevotella albensis
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Hallella seregens
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647533197 Prevotella unclassified
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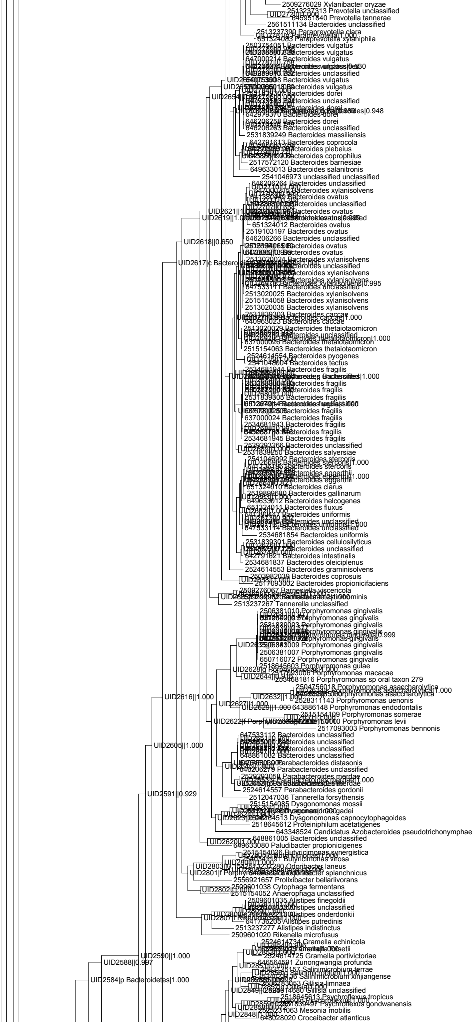
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2513020024 Bacteroides xylanisolvens
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Bacteroides xylanisolvens
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2531839303 Bacteroides caccae
Bacteroides caccae|1.000
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637000026 Bacteroides thetaiotaomicron
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Bacteroides eggerthii
Bacteroides eggerthii|1.000
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651324010 Bacteroides clarus
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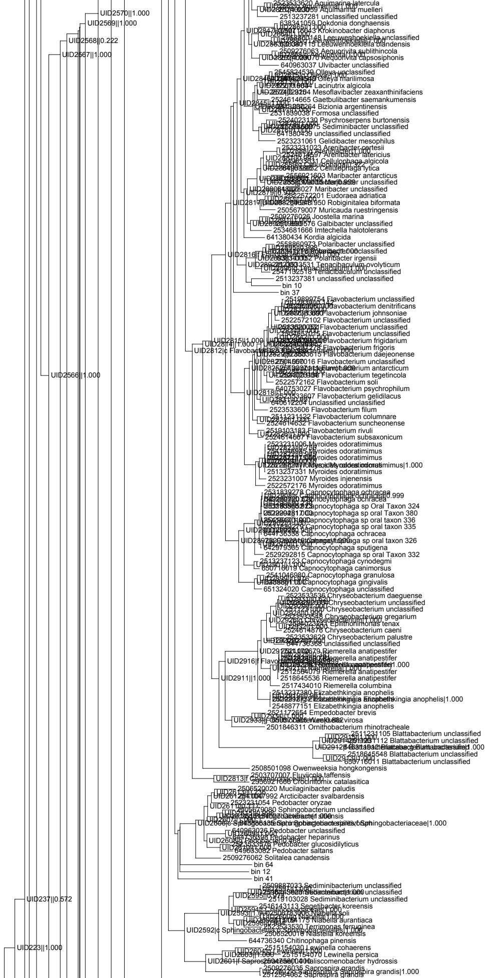
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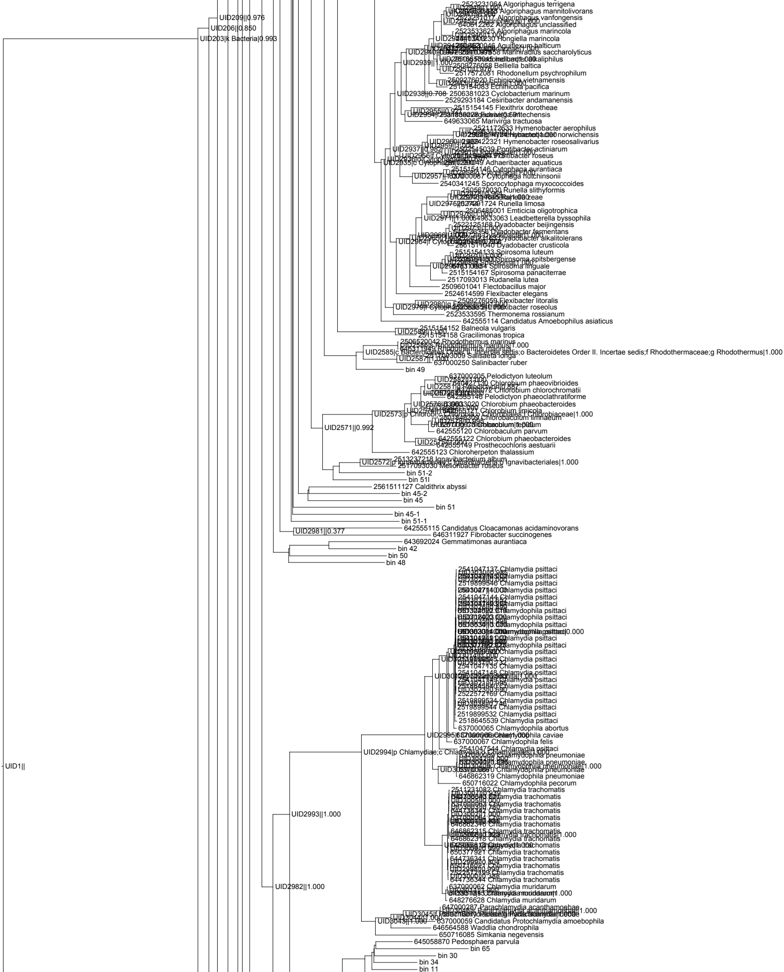
2508501098 Owenweeksia hongkongensis
2503707007 Fluviicola taffensis
UID2813|f Cryomorphaceae|1.000
2556921666 Crocinitomix catalasitica
2506520020 Mucilaginibacter paludis
Arcticibacter svalbardensis
2523231054 Pedobacter oryzae
2505679080 Sphingobacterium unclassified
UID2606|c Sphingobacteriia|o Sphingobacteriales|f 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
Niastella soli
Niabella aurantiaca
2523533530 Terrimonas ferruginea
2506520016 Niastella koreensis
644736340 Chitinophaga pinensis
UID2592|c Sphingobacteriia
UID2593||1.000
2515154030 Lewinella cohaerens
2515154070 Lewinella persica
UID2603||1.000
UID2601|f Saprospiraceae
Haliscomenobacter hydrossis
2509276035 Saprospira grandis
Saprospira grandis|1.000
2512564062 Saprospira grandis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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
UID2940
UID2939||1.000
UID2938||0.708
2506381023 Cyclobacterium marinum
2529293184 Cesiribacter andamanensis
2515154145 Flexithrix dorotheae
UID2955||0.927
UID2954
649633065 Marivirga tractuosa
2521172633 Hymenobacter aerophilus
Hymenobacter norwichensis
Hymenobacter roseosalivarius
2522545039 Pontibacter actiniarum
Pontibacter roseus
UID2937||0.982
UID2960||0.962
UID2959||1.000
UID2956|f Cytophagaceae
UID2935|c Cytophagia
Adhaeribacter aquaticus
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UID2957||1.000
Cytophaga hutchinsonii
2540341245 Sporocytophaga myxococcoides
2505679030 Runella slithyformis
Runella zeae
UID2975
Runella limosa
2506485001 Emticicia oligotrophica
UID2971||1.000
649633063 Leadbetterella byssophila
2522125168 Dyadobacter beijingensis
Dyadobacter fermentans
Dyadobacter alkalitolerans
2561511040 Dyadobacter crusticola
UID2964|f Cytophagaceae
2515154133 Spirosoma luteum
Spirosoma spitsbergense
Spirosoma linguale
2515154167 Spirosoma panaciterrae
2517093013 Rudanella lutea
2509601041 Flectobacillus major
2524614599 Flexibacter elegans
2509276059 Flexibacter litoralis
UID2980
UID2979|f Cytophagaceae
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
UID2581
Chlorobium chlorochromatii
642555146 Pelodictyon phaeoclathratiforme
Chlorobium phaeobacteroides
Chlorobium limicola
UID2573|p Chlorobi;c Chlorobia;o Chlorobiales;f Chlorobiaceae|1.000
Chlorobaculum limnaeum
Chlorobaculum tepidum
642555120 Chlorobaculum parvum
UID2571||0.992
642555122 Chlorobium phaeobacteroides
642555149 Prosthecochloris aestuarii
642555123 Chloroherpeton thalassium
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
2519899546 Chlamydia psittaci
2541047144 Chlamydia psittaci
Chlamydophila psittaci
Chlamydophila psittaci|0.000
2541047135 Chlamydia psittaci
2541047148 Chlamydia psittaci
2522572169 Chlamydia psittaci
2519899534 Chlamydia psittaci
2519899544 Chlamydia psittaci
2519899532 Chlamydia psittaci
2518645539 Chlamydia psittaci
637000065 Chlamydophila abortus
UID2995
Chlamydophila caviae
637000067 Chlamydophila felis
UID2994|p Chlamydiae;c Chlamydiia
2541047544 Chlamydia psittaci
Chlamydophila pneumoniae
Chlamydophila pneumoniae|1.000
646862319 Chlamydophila pneumoniae
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UID2993||1.000
2511231082 Chlamydia trachomatis
Chlamydia trachomatis
646862315 Chlamydia trachomatis
Chlamydia trachomatis|1.000
646862318 Chlamydia trachomatis
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UID2982||1.000
637000062 Chlamydia muridarum
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647000287 Parachlamydia acanthamoebae
UID3045
UID3043||1.000
637000059 Candidatus Protochlamydia amoebophila
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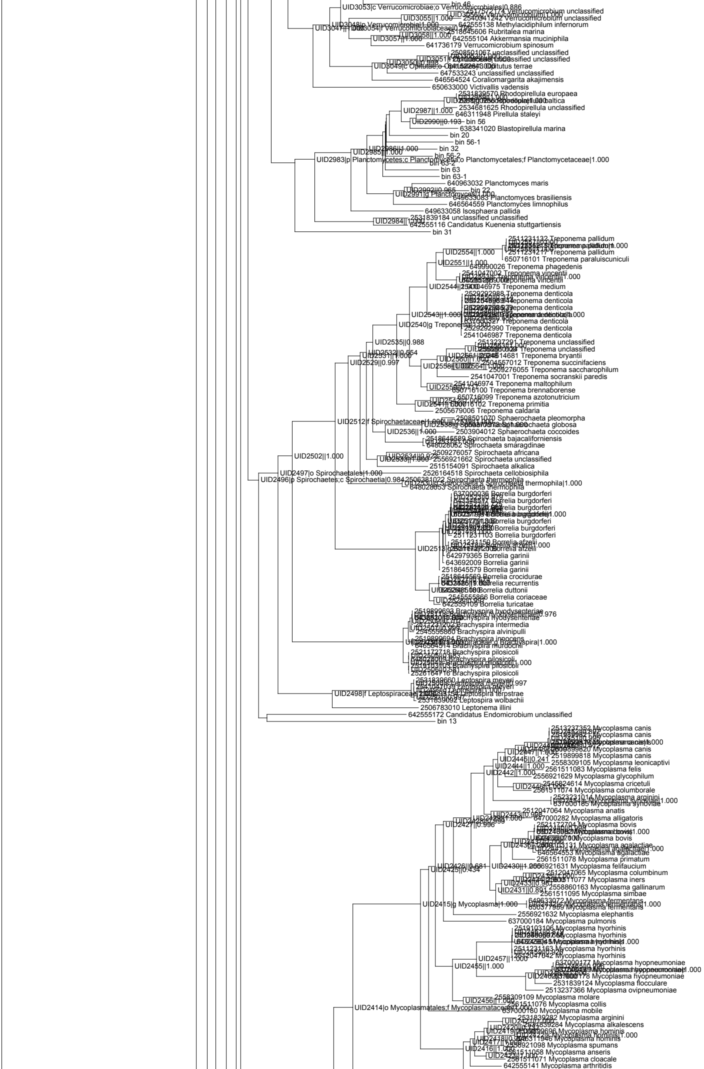
645058870 Pedosphaera parvula
bin 65
bin 30
bin 34
bin 11


bin 46
UID3053|c Verrucomicrobiae;o Verrucomicrobiales|0.886
2540341242 Verrucomicrobium unclassified
UID3055||1.000
UID3048|o Verrucomicrobiales|1.000
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UID3051
UID3050||0.998
UID3049|c Opitutae;o Opitutales
Opitutus terrae
647533243 unclassified unclassified
646564524 Coraliomargarita akajimensis
650633000 Victivallis vadensis
2531839570 Rhodopirellula europaea
UID2987||1.000
2534681625 Rhodopirellula unclassified
646311948 Pirellula staleyi
UID2990||0.193
bin 56
638341020 Blastopirellula marina
bin 20
bin 56-1
UID2986||1.000
UID2985||1.000
bin 32
bin 56-2
UID2983|p Planctomycetes;c Planctomycetia;o Planctomycetales;f Planctomycetaceae|1.000
bin 63-2
bin 63
bin 63-1
640963032 Planctomyces maris
UID2992||0.965
bin 22
UID2991|g Planctomyces|1.000
649633083 Planctomyces brasiliensis
646564559 Planctomyces limnophilus
649633058 Isosphaera pallida
2531839184 unclassified unclassified
UID2984||1.000
642555116 Candidatus Kuenenia stuttgartiensis
bin 31
2511231132 Treponema pallidum
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650716101 Treponema paraluiscuniculi
UID2551||1.000
649990026 Treponema phagedenis
2541047002 Treponema vincentii
Treponema vincentii
UID2544||1.000
2541046975 Treponema medium
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Treponema denticola
Treponema denticola
UID2543||1.000
Treponema denticola
UID2540|g Treponema|1.000
637000327 Treponema denticola
2529292990 Treponema denticola
2541046987 Treponema denticola
2513237291 Treponema unclassified
Treponema unclassified
UID2535||0.988
UID2532||0.554
UID2531||1.000
UID2561
2524614681 Treponema bryantii
UID2529||0.997
UID2560||1.000
2504557012 Treponema succinifaciens
UID2558
2509276055 Treponema saccharophilum
2541047001 Treponema socranskii paredis
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650716100 Treponema brennaborense
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UID2541
650716102 Treponema primitia
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2508501070 Sphaerochaeta pleomorpha
UID2512|f Spirochaetaceae|1.000
Sphaerochaeta globosa
UID2538|g Sphaerochaeta|1.000
UID2536||1.000
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648028052 Spirochaeta smaragdinae
2509276057 Spirochaeta africana
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UID2497|o Spirochaetales|1.000
2526164518 Spirochaeta cellobiosiphila
UID2496|p Spirochaetes;c Spirochaetia|0.984
2506381022 Spirochaeta thermophila
UID2530|g Spirochaeta;s Spirochaeta thermophila|1.000
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637000036 Borrelia burgdorferi
Borrelia burgdorferi
Borrelia burgdorferi|1.000
Borrelia burgdorferi
Borrelia burgdorferi
2511231103 Borrelia burgdorferi
2511231150 Borrelia afzelii
Borrelia afzelii|1.000
UID2518
Borrelia afzelii
642979365 Borrelia garinii
643692009 Borrelia garinii
2518645579 Borrelia garinii
2518645569 Borrelia crocidurae
Borrelia recurrentis
Borrelia duttonii
2545555866 Borrelia coriaceae
UID2528||0.997
642555109 Borrelia turicatae
2519899693 Brachyspira hyodysenteriae
Brachyspira hyodysenteriae|0.976
2511231202 Brachyspira intermedia
2545555860 Brachyspira alvinipulli
2519899694 Brachyspira innocens
Brachyspira|1.000
646564514 Brachyspira murdochii
2521172718 Brachyspira pilosicoli
Brachyspira pilosicoli
Brachyspira pilosicoli|1.000
Brachyspira pilosicoli
2526164116 Brachyspira pilosicoli
2531839660 Leptospira meyeri
Leptospira meyeri|0.997
Leptospira meyeri
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Leptospira|1.000
Leptospira terpstrae
2531839092 Leptospira wolbachii
2506783010 Leptonema illini
642555172 Candidatus Endomicrobium unclassified
bin 13
2513237352 Mycoplasma canis
Mycoplasma canis
Mycoplasma canis|1.000
2519899820 Mycoplasma canis
UID2447||1.000
UID2445||0.241
2519899818 Mycoplasma canis
UID2444||1.000
2558309105 Mycoplasma leonicaptivi
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UID2442||1.000
2556921629 Mycoplasma glycophilum
2545824614 Mycoplasma cricetuli
UID2446
2561511074 Mycoplasma columborale
2523231014 Mycoplasma arginini
637000185 Mycoplasma synoviae
Mycoplasma synoviae|1.000
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UID2443||0.998
UID2428||0.999
647000282 Mycoplasma alligatoris
UID2427||0.996
2521172704 Mycoplasma bovis
Mycoplasma bovis|1.000
Mycoplasma bovis
2561511078 Mycoplasma agalactiae
Mycoplasma agalactiae|1.000
646564553 Mycoplasma agalactiae
2561511078 Mycoplasma primatum
UID2426||0.681
UID2430||1.000
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UID2425||0.434
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2561511077 Mycoplasma iners
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2558860163 Mycoplasma gallinarum
UID2431||0.891
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UID2415|g Mycoplasma|1.000
Mycoplasma fermentans|1.000
650377955 Mycoplasma fermentans
2556921632 Mycoplasma elephantis
637000184 Mycoplasma pulmonis
2519103106 Mycoplasma hyorhinis
Mycoplasma hyorhinis
Mycoplasma hyorhinis|1.000
2511231163 Mycoplasma hyorhinis
UID2457||1.000
2512047042 Mycoplasma hyorhinis
UID2455||1.000
637000177 Mycoplasma hyopneumoniae
Mycoplasma hyopneumoniae|1.000
637000178 Mycoplasma hyopneumoniae
2531839124 Mycoplasma flocculare
2513237366 Mycoplasma ovipneumoniae
2558309109 Mycoplasma molare
UID2456||1.000
2561511076 Mycoplasma collis
UID2414|o Mycoplasmatales;f Mycoplasmataceae|1.000
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2531839282 Mycoplasma arginini
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2531839284 Mycoplasma alkalescens
UID2420
UID2419
Mycoplasma hominis
Mycoplasma hominis|1.000
UID2418
646311946 Mycoplasma hominis
UID2417||1.000
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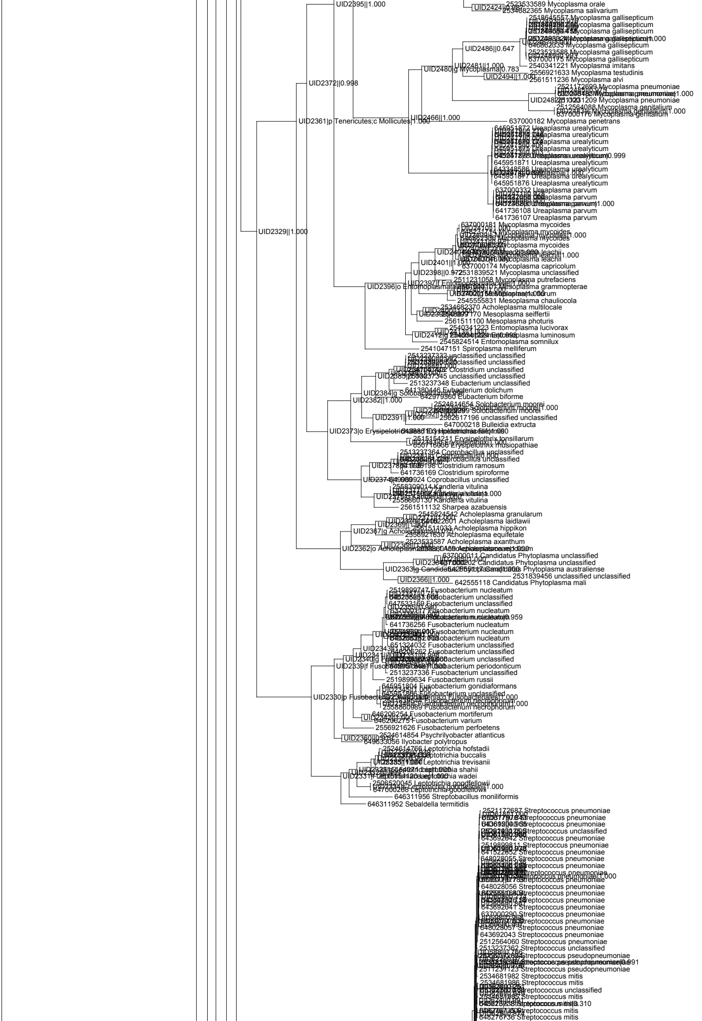
UID2423||1.000
2561511071 Mycoplasma cloacale
642555141 Mycoplasma arthritidis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UID2424
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Mycoplasma gallisepticum
1.000
646862833 Mycoplasma gallisepticum
UID2486||0.647
2523533588 Mycoplasma gallisepticum
637000175 Mycoplasma gallisepticum
UID2481||1.000
2540341221 Mycoplasma imitans
UID2480|g Mycoplasma|0.783
2556921633 Mycoplasma testudinis
UID2494||1.000
2561511236 Mycoplasma alvi
UID2372||0.998
2521172699 Mycoplasma pneumoniae
Mycoplasma pneumoniae|1.000
2511231209 Mycoplasma pneumoniae
2512564088 Mycoplasma genitalium
637000176 Mycoplasma genitalium|1.000
UID2466||1.000
UID2361|p Tenericutes;c Mollicutes|1.000
637000182 Mycoplasma penetrans
645951872 Ureaplasma urealyticum
Ureaplasma urealyticum
Ureaplasma urealyticum
Ureaplasma urealyticum
Ureaplasma urealyticum
Ureaplasma urealyticum|0.999
645951871 Ureaplasma urealyticum
643348586 Ureaplasma urealyticum
645951877 Ureaplasma urealyticum
645951876 Ureaplasma urealyticum
637000332 Ureaplasma parvum
Ureaplasma parvum
Ureaplasma parvum|1.000
641736108 Ureaplasma parvum
641736107 Ureaplasma parvum
UID2329||1.000
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Mycoplasma mycoides|1.000
Mycoplasma mycoides
Mycoplasma mycoides
Mycoplasma leachii
Mycoplasma leachii|1.000
637000174 Mycoplasma capricolum
UID2401||1.000
UID2398||0.972
2531839521 Mycoplasma unclassified
2511231058 Mycoplasma putrefaciens
UID2397|f Entomoplasmataceae|1.000
Mesoplasma grammopterae
Mesoplasma florum
UID2396|o Entomoplasmatales
2545555831 Mesoplasma chauliocola
2534682370 Acholeplasma multilocale
Mesoplasma seiffertii
2561511100 Mesoplasma photuris
2540341223 Entomoplasma lucivorax
Entomoplasma luminosum
UID2412|g Entomoplasma
2545824514 Entomoplasma somnilux
2541047151 Spiroplasma melliferum
2513237332 unclassified unclassified
unclassified unclassified
Clostridium unclassified
2513237345 unclassified unclassified
2513237348 Eubacterium unclassified
641380446 Eubacterium dolichum
UID2384|g Solobacterium
642979360 Eubacterium biforme
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2524614654 Solobacterium moorei
Solobacterium moorei|1.000
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
Coprobacillus unclassified
Clostridium ramosum
641736169 Clostridium spiroforme
UID2374
649989924 Coprobacillus unclassified
2558309014 Kandleria vitulina
Kandleria vitulina|1.000
2558860130 Kandleria vitulina
2561511132 Sharpea azabuensis
2545824542 Acholeplasma granularum
Acholeplasma laidlawii
UID2367|g Acholeplasma
2561511033 Acholeplasma hippikon
2556921630 Acholeplasma equifetale
2523533587 Acholeplasma axanthum
UID2362|o Acholeplasmatales
637000011 Candidatus Phytoplasma unclassified
Candidatus Phytoplasma unclassified
UID2363|g Candidatus Phytoplasma
Phytoplasma australiense
2531839456 unclassified unclassified
UID2366||1.000
642555118 Candidatus Phytoplasma mali
2519899747 Fusobacterium nucleatum
Fusobacterium unclassified
647533169 Fusobacterium unclassified
637000117 Fusobacterium nucleatum
Fusobacterium nucleatum|0.959
641736256 Fusobacterium nucleatum
Fusobacterium nucleatum
Fusobacterium nucleatum
651324032 Fusobacterium unclassified
Fusobacterium unclassified
Fusobacterium unclassified
UID2340|g Fusobacterium
UID2339|f Fusobacteriaceae
Fusobacterium periodonticum
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645951804 Fusobacterium gonidiaformans
Fusobacterium unclassified
UID2330|p Fusobacteria
Fusobacterium necrophorum
Fusobacterium necrophorum|1.000
2558860969 Fusobacterium necrophorum
646206254 Fusobacterium mortiferum
646206273 Fusobacterium varium
2556921626 Fusobacterium perfoetens
UID2360||0.994
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649633056 Ilyobacter polytropus
2524614766 Leptotrichia hofstadii
Leptotrichia buccalis
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UID2331
Leptotrichia wadei
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647000268 Leptotrichia goodfellowii|1.000
646311956 Streptobacillus moniliformis
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Streptococcus pneumoniae
Streptococcus pneumoniae
Streptococcus unclassified
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641522652 Streptococcus pneumoniae
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Streptococcus pneumoniae
Streptococcus pneumoniae
Streptococcus pneumoniae|1.000
Streptococcus pneumoniae
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643692041 Streptococcus pneumoniae
637000290 Streptococcus pneumoniae
Streptococcus pneumoniae
648028057 Streptococcus pneumoniae
643692043 Streptococcus pneumoniae
2512564060 Streptococcus pneumoniae
2513237362 Streptococcus unclassified
Streptococcus pseudopneumoniae
Streptococcus pseudopneumoniae|0.991
2511231123 Streptococcus pseudopneumoniae
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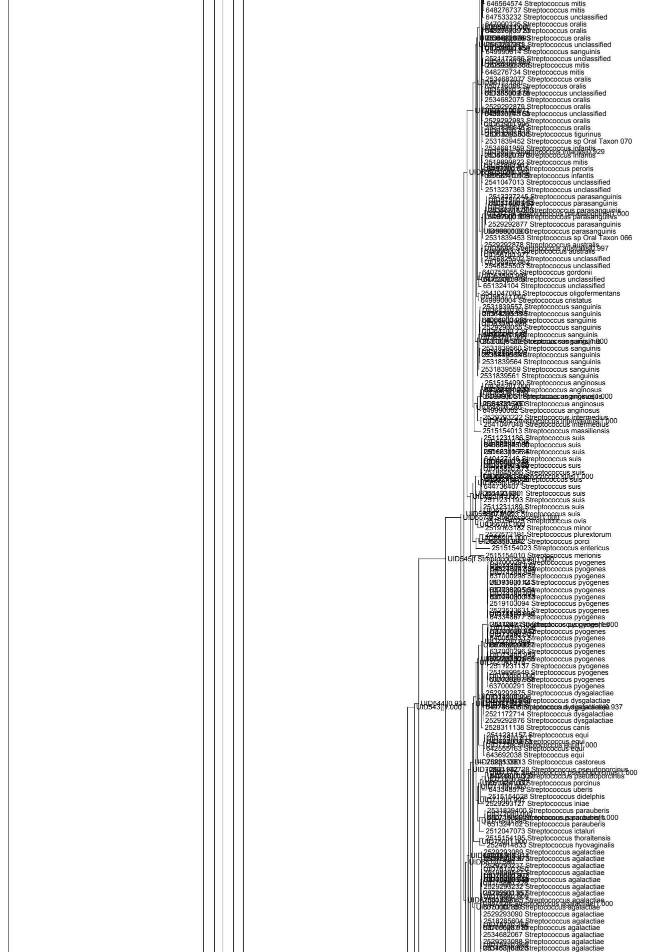
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Streptococcus oralis
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2521172586 Streptococcus unclassified
Streptococcus mitis
648276734 Streptococcus mitis
2534682077 Streptococcus oralis
Streptococcus oralis
Streptococcus unclassified
2534682075 Streptococcus oralis
2529292879 Streptococcus oralis
Streptococcus unclassified
2529292983 Streptococcus oralis
UID629|0.996
Streptococcus oralis
Streptococcus tigurinus
2531839452 Streptococcus sp Oral Taxon 070
2534681959 Streptococcus infantis
Streptococcus infantis|0.929
Streptococcus infantis
2519899822 Streptococcus mitis
Streptococcus peroris
Streptococcus infantis
2541047013 Streptococcus unclassified
2513237363 Streptococcus unclassified
2513237245 Streptococcus parasanguinis
Streptococcus parasanguinis
Streptococcus parasanguinis
Streptococcus parasanguinis|1.000
Streptococcus parasanguinis
2529292877 Streptococcus parasanguinis
Streptococcus parasanguinis
2531839453 Streptococcus sp Oral Taxon 066
2529292878 Streptococcus australis
Streptococcus australis|0.997
Streptococcus australis
UID567|0.977
2546825502 Streptococcus unclassified
UID569|0.982
2546825503 Streptococcus unclassified
640753055 Streptococcus gordonii
UID635|0.998
Streptococcus unclassified
651324104 Streptococcus unclassified
2541047083 Streptococcus oligofermentans
UID563|1.000
649990004 Streptococcus cristatus
2531839557 Streptococcus sanguinis
Streptococcus sanguinis
Streptococcus sanguinis
2529293055 Streptococcus sanguinis
UID641|0.739
Streptococcus sanguinis
Streptococcus sanguinis|1.000
2531839560 Streptococcus sanguinis
Streptococcus sanguinis
2531839564 Streptococcus sanguinis
2531839559 Streptococcus sanguinis
2531839561 Streptococcus sanguinis
2515154090 Streptococcus anginosus
UID652|1.000
Streptococcus anginosus
Streptococcus anginosus|1.000
Streptococcus anginosus
649990002 Streptococcus anginosus
2529293222 Streptococcus intermedius
Streptococcus intermedius|1.000
2541047048 Streptococcus intermedius
2515154013 Streptococcus massiliensis
2511231186 Streptococcus suis
UID665|0.798
Streptococcus suis
Streptococcus suis
640427146 Streptococcus suis
Streptococcus suis
Streptococcus suis
Streptococcus suis|1.000
Streptococcus suis
UID655|0.899
644736407 Streptococcus suis
Streptococcus suis
UID653|1.000
2511231193 Streptococcus suis
2511231189 Streptococcus suis
UID657|0.961
Streptococcus suis
Streptococcus|1.000
2515154025 Streptococcus ovis
UID667|1.000
2519103182 Streptococcus minor
2522572191 Streptococcus plurextorum
UID659|1.000
Streptococcus porci
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Streptococcus pyogenes
Streptococcus pyogenes
637000298 Streptococcus pyogenes
Streptococcus pyogenes
Streptococcus pyogenes
Streptococcus pyogenes
2519103094 Streptococcus pyogenes
2523533631 Streptococcus pyogenes
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Streptococcus pyogenes|1.000
Streptococcus pyogenes
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Streptococcus pyogenes
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UID730|0.000
Streptococcus pyogenes
637000291 Streptococcus pyogenes
2529292875 Streptococcus dysgalactiae
Streptococcus dysgalactiae
Streptococcus dysgalactiae|0.937
2521172714 Streptococcus dysgalactiae
2529292876 Streptococcus dysgalactiae
2528311138 Streptococcus canis
UID544|0.934
UID543||1.000
2511231157 Streptococcus equi
Streptococcus equi
Streptococcus equi|1.000
642555163 Streptococcus equi
643692038 Streptococcus equi
Streptococcus castoreus
Streptococcus pseudoporcinus
Streptococcus pseudoporcinus|1.000
Streptococcus pseudoporcinus
Streptococcus porcinus
643348578 Streptococcus uberis
2515154028 Streptococcus didelphis
UID712|0.997
2529293127 Streptococcus iniae
2531839400 Streptococcus parauberis
UID720|0.000
Streptococcus parauberis|1.000
UID718|0.995
651324102 Streptococcus parauberis
2512047073 Streptococcus ictaluri
2515154195 Streptococcus thoraltensis
UID750|1.000
2524614633 Streptococcus hyovaginalis
2529293089 Streptococcus agalactiae
Streptococcus agalactiae
2529293237 Streptococcus agalactiae
UID761|0.950
Streptococcus agalactiae
Streptococcus agalactiae
2529293232 Streptococcus agalactiae
Streptococcus agalactiae
UID766|0.909
Streptococcus agalactiae
Streptococcus agalactiae|1.000
Streptococcus agalactiae
2529293090 Streptococcus agalactiae
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Streptococcus agalactiae
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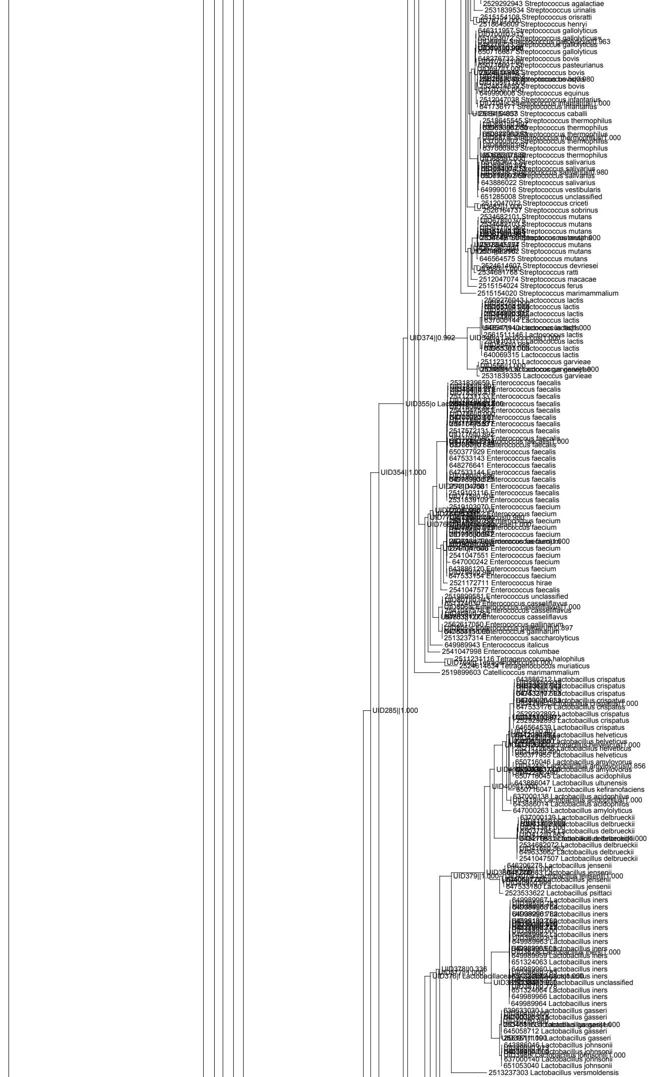
Streptococcus agalactiae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Streptococcus caballi
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Streptococcus thermophilus
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637000303 Streptococcus thermophilus
Streptococcus thermophilus
Streptococcus salivarius
Streptococcus salivarius
Streptococcus salivarius
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649990016 Streptococcus vestibularis
651285008 Streptococcus unclassified
2512047072 Streptococcus criceti
2526164737 Streptococcus sobrinus
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Streptococcus mutans
Streptococcus mutans
Streptococcus mutans
Streptococcus mutans
646564575 Streptococcus mutans
2524614607 Streptococcus devriesei
2534681768 Streptococcus ratti
2512047074 Streptococcus macacae
2515154024 Streptococcus ferus
2515154020 Streptococcus marimammalium
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Lactococcus lactis
Lactococcus lactis
637000144 Lactococcus lactis
UID374||0.992
2561511146 Lactococcus lactis
Lactococcus lactis
Lactococcus lactis
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2531839335 Lactococcus garvieae
2531839659 Enterococcus faecalis
UID355|o Lac
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647533143 Enterococcus faecalis
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UID354||1.000
2519103116 Enterococcus faecalis
2531839109 Enterococcus faecalis
2519103070 Enterococcus faecium
2541047551 Enterococcus faecium
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651324030 Enterococcus casseliflavus
Enterococcus casseliflavus
2562617050 Enterococcus gallinarum
Enterococcus gallinarum
2513237314 Enterococcus saccharolyticus
649989943 Enterococcus italicus
2541047998 Enterococcus columbae
2511231116 Tetragenococcus halophilus
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2519899603 Catellicoccus marimammalium
643886212 Lactobacillus crispatus
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UID285||1.000
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Lactobacillus helveticus
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650716046 Lactobacillus amylovorus
650716045 Lactobacillus acidophilus
643886047 Lactobacillus ultunensis
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2534682072 Lactobacillus delbrueckii
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2541047507 Lactobacillus delbrueckii
646206278 Lactobacillus jensenii
UID379||1.000
647533180 Lactobacillus jensenii
2523533622 Lactobacillus psittaci
649989967 Lactobacillus iners
649989963 Lactobacillus iners
649989959 Lactobacillus iners
651324063 Lactobacillus iners
649989960 Lactobacillus iners
UID378||0.336
Lactobacillus unclassified
651324064 Lactobacillus iners
649989966 Lactobacillus iners
649989964 Lactobacillus iners
639633030 Lactobacillus gasseri
645058712 Lactobacillus gasseri
Lactobacillus gasseri
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637000140 Lactobacillus johnsonii
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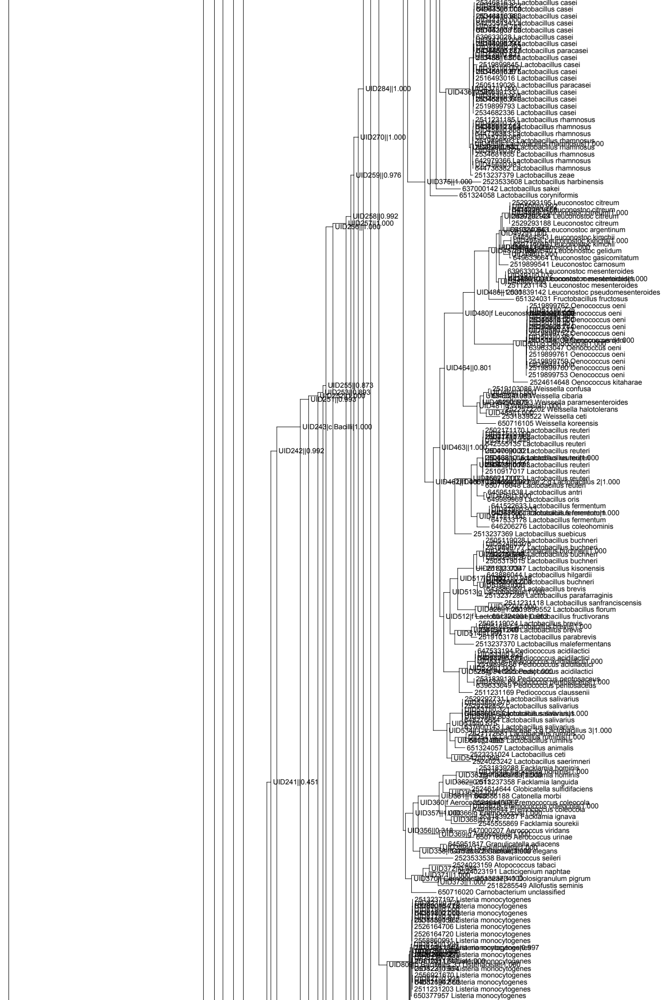
2513237303 Lactobacillus versmoldensis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Lactobacillus casei
Lactobacillus casei
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Lactobacillus paracasei
Lactobacillus casei
2519899845 Lactobacillus casei
Lactobacillus casei
2516493016 Lactobacillus casei
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UID284||1.000
UID436
Lactobacillus casei
Lactobacillus casei
2519899793 Lactobacillus casei
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2511231185 Lactobacillus rhamnosus
Lactobacillus rhamnosus
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Lactobacillus rhamnosus
Lactobacillus rhamnosus
Lactobacillus rhamnosus
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UID375||1.000
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2529293195 Leuconostoc citreum
Leuconostoc citreum
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UID256||1.000
Leuconostoc argentinum
645564543 Leuconostoc kimchii
Leuconostoc gelidum
649633064 Leuconostoc gasicomitatum
2519899541 Leuconostoc carnosum
639633034 Leuconostoc mesenteroides
2511231143 Leuconostoc mesenteroides
UID486
2501839142 Leuconostoc pseudomesenteroides
651324031 Fructobacillus fructosus
2519899762 Oenococcus oeni
UID480|f Leuconost
Oenococcus oeni
Oenococcus oeni
Oenococcus oeni
Oenococcus oeni
639633047 Oenococcus oeni
2519899761 Oenococcus oeni
2519899759 Oenococcus oeni
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UID255||0.873
2519103086 Weissella confusa
Weissella cibaria
Weissella paramesenteroides
Weissella halotolerans
2531839522 Weissella ceti
UID243|c Bacilli|1.000
650716105 Weissella koreensis
2502171170 Lactobacillus reuteri
Lactobacillus reuteri
UID242||0.992
UID463||1.000
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Lactobacillus reuteri
Lactobacillus reuteri
Lactobacillus reuteri
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UID462
Lactobacillus reuteri
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641522633 Lactobacillus fermentum
647533178 Lactobacillus fermentum
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Lactobacillus buchneri
Lactobacillus buchneri
2505313015 Lactobacillus buchneri
Lactobacillus kisonensis
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UID517
Lactobacillus buchneri
Lactobacillus brevis
UID513
2513237286 Lactobacillus parafarraginis
2511231118 Lactobacillus sanfranciscensis
Lactobacillus florum
UID512|f Lactob
Lactobacillus fructivorans
2505119024 Lactobacillus brevis
Lactobacillus brevis
2519103178 Lactobacillus parabrevis
2513237370 Lactobacillus malefermentans
647533194 Pediococcus acidilactici
Pediococcus acidilactici
Pediococcus acidilactici
Pediococcus acidilactici
2531839139 Pediococcus pentosaceus
639633046 Pediococcus pentosaceus
2511231169 Pediococcus claussenii
2529292731 Lactobacillus salivarius
Lactobacillus salivarius
Lactobacillus salivarius
Lactobacillus salivarius
Lactobacillus ruminis
651324057 Lactobacillus animalis
2523231024 Lactobacillus ceti
2524023242 Lactobacillus saerimneri
2531839288 Facklamia hominis
UID241||0.451
UID362
2513237358 Facklamia languida
2524614644 Globicatella sulfidifaciens
Catonella morbi
UID360|f Aeroco
Eremococcus coleocola
Eremococcus coleocola
UID357
Facklamia ignava
2545555869 Facklamia sourekii
UID356||0.318
647000207 Aerococcus viridans
650716005 Aerococcus urinae
645951817 Granulicatella adiacens
Granulicatella elegans
2523533538 Bavariicoccus seileri
2524023159 Atopococcus tabaci
2524023191 Lacticigenium naphtae
UID370
Dolosigranulum pigrum
2518285549 Allofustis seminis
650716020 Carnobacterium unclassified
2513237197 Listeria monocytogenes
Listeria monocytogenes
Listeria monocytogenes
Listeria monocytogenes
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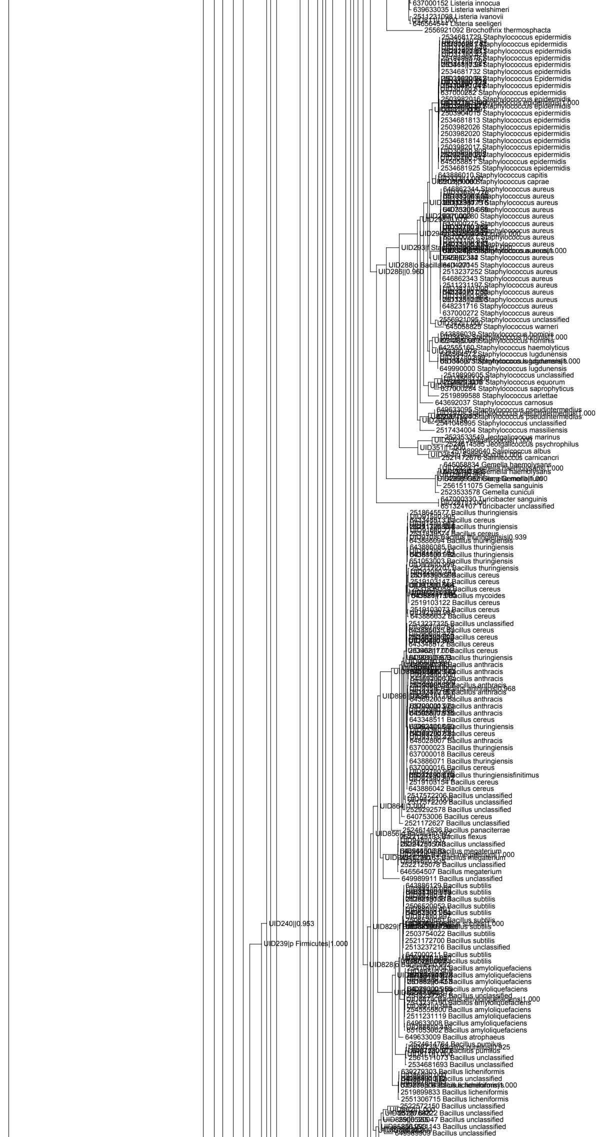
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2534681729 Staphylococcus epidermidis
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2534681813 Staphylococcus epidermidis
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2534681814 Staphylococcus epidermidis
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645058851 Staphylococcus epidermidis
2534681925 Staphylococcus epidermidis
643886010 Staphylococcus capitis
Staphylococcus caprae
646862344 Staphylococcus aureus
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UID293|f Sta
UID288|o Bacillales
UID286||0.960
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2513237252 Staphylococcus aureus
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648231716 Staphylococcus aureus
637000272 Staphylococcus aureus
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645058825 Staphylococcus warneri
643886039 Staphylococcus hominis
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Staphylococcus lugdunensis
649990000 Staphylococcus lugdunensis
2519899605 Staphylococcus unclassified
Staphylococcus equorum
637000284 Staphylococcus saprophyticus
2519899588 Staphylococcus arlettae
643692037 Staphylococcus carnosus
649633095 Staphylococcus pseudintermedius
2541046995 Staphylococcus unclassified
2517434004 Staphylococcus massiliensis
2523533549 Jeotgalicoccus marinus
2524614585 Jeotgalicoccus psychrophilus
UID351||1.000
2519899640 Salinicoccus albus
2521172676 Salinicoccus carnicancri
645058834 Gemella haemolysans
Gemella haemolysans
2561511075 Gemella sanguinis
2523533578 Gemella cuniculi
647000330 Turicibacter sanguinis
651324107 Turicibacter unclassified
2518645577 Bacillus thuringiensis
Bacillus cereus
Bacillus thuringiensis
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Bacillus thuringiensis
Bacillus cereus
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Bacillus cereus
Bacillus mycoides
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Bacillus cereus
643348512 Bacillus cereus
Bacillus thuringiensis
Bacillus anthracis
UID896||
643692005 Bacillus anthracis
643348511 Bacillus cereus
648028007 Bacillus anthracis
637000023 Bacillus thuringiensis
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643886071 Bacillus thuringiensis
637000016 Bacillus cereus
Bacillus thuringiensisfinitimus
2519103154 Bacillus cereus
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2517572206 Bacillus unclassified
Bacillus unclassified
UID864||
2529292578 Bacillus unclassified
640753006 Bacillus cereus
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UID856|
Bacillus flexus
Bacillus unclassified
Bacillus megaterium
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646564507 Bacillus megaterium
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Bacillus subtilis
Bacillus subtilis
2506520052 Bacillus subtilis
UID240||0.953
UID829|
UID239|p Firmicutes|1.000
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647000211 Bacillus subtilis
UID828|o Bacillales
Bacillus subtilis
Bacillus amyloliquefaciens
Bacillus unclassified
2545555800 Bacillus amyloliquefaciens
2511231119 Bacillus amyloliquefaciens
649633008 Bacillus amyloliquefaciens
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649633009 Bacillus atrophaeus
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Bacillus pumilus
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2534681693 Bacillus unclassified
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Bacillus unclassified
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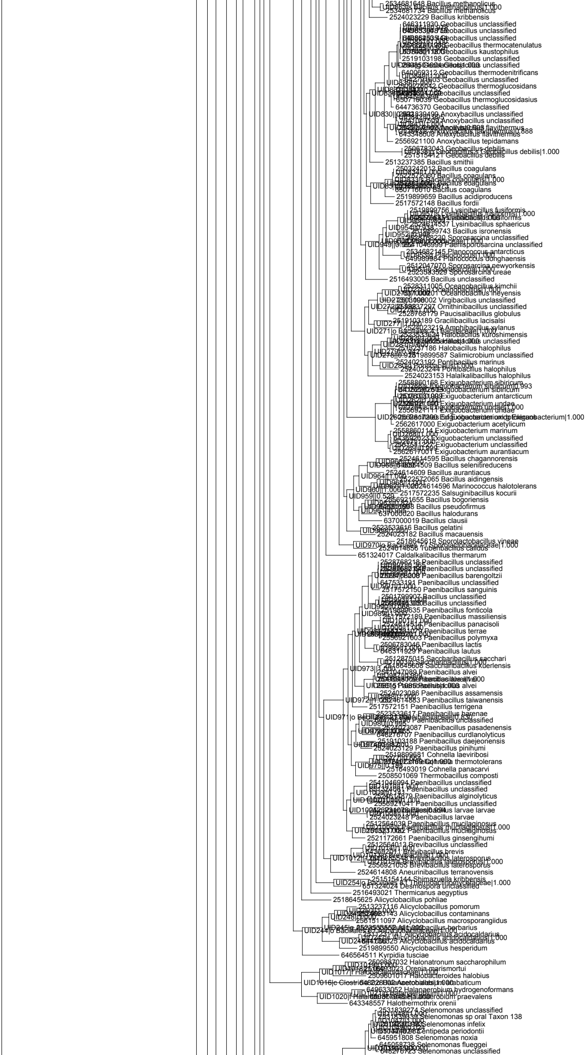
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Bacillus methanolicus|1.000
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2524023229 Bacillus kribbensis
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Geobacillus unclassified
Geobacillus thermocatenulatus
Geobacillus kaustophilus
2519103198 Geobacillus unclassified
Geobacillus unclassified
640069312 Geobacillus thermodenitrificans
Geobacillus unclassified
Geobacillus thermoglucosidans
Geobacillus unclassified
650716039 Geobacillus thermoglucosidasius
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UID830|0.993
Anoxybacillus unclassified
Anoxybacillus unclassified
Anoxybacillus flavithermus
643348508 Anoxybacillus flavithermus
2556921100 Anoxybacillus tepidamans
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Geobacillus debilis|1.000
2515154121 Geobacillus debilis
2513237385 Bacillus smithii
2503242012 Bacillus coagulans
2522572060 Bacillus coagulans
Bacillus coagulans|1.000
Bacillus coagulans
650716010 Bacillus coagulans
2519899659 Bacillus acidiproducens
2517572148 Bacillus fordii
2519899756 Lysinibacillus fusiformis
Lysinibacillus fusiformis|1.000
Lysinibacillus fusiformis
Lysinibacillus sphaericus
Bacillus isronensis
Sporosarcina unclassified
Paenisporosarcina unclassified
2534682145 Planococcus antarcticus
649989984 Planococcus donghaensis
2512047070 Sporosarcina newyorkensis
2523533529 Sporosarcina ureae
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Oceanobacillus iheyensis
Virgibacillus unclassified
Ornithinibacillus unclassified
2528768179 Paucisalibacillus globulus
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2524023219 Amphibacillus xylanus
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Halobacillus kuroshimensis
Halobacillus unclassified
Halobacillus halophilus
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2524023192 Pontibacillus marinus
2524023244 Pontibacillus halophilus
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Exiguobacterium sibiricum|0.993
Exiguobacterium sibiricum
Exiguobacterium antarcticum
Exiguobacterium undae
Exiguobacterium undae|1.000
Exiguobacterium undae
Exiguobacterium|1.000
2562617000 Exiguobacterium acetylicum
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Exiguobacterium unclassified
Exiguobacterium unclassified
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Bacillus selenitireducens
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2522572065 Bacillus aidingensis
2524614596 Marinococcus halotolerans
2517572235 Salsuginibacillus kocurii
UID959|0.528
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Bacillus pseudofirmus
637000020 Bacillus halodurans
637000019 Bacillus clausii
2523533616 Bacillus gelatini
2524023182 Bacillus macauensis
2518645619 Sporolactobacillus vineae
UID970|o Bacillales 7 f Sporolactobacillaceae|1.000
2524614856 Tuberibacillus calidus
651324017 Caldalkalibacillus thermarum
2528768218 Paenibacillus unclassified
Paenibacillus unclassified
Paenibacillus barengoltzii
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Bacillus unclassified
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Paenibacillus panacisoli
Paenibacillus terrae
2556921003 Paenibacillus polymyxa
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646311929 Paenibacillus lautus
2512875015 Saccharibacillus sacchari
Saccharibacillus|1.000
2518645608 Saccharibacillus kuerlensis
UID973|1.000
2541047089 Paenibacillus alvei
Paenibacillus alvei|1.000
Paenibacillus alvei
2524023086 Paenibacillus assamensis
2524614883 Paenibacillus taiwanensis
2517572151 Paenibacillus terrigena
UID971|o Bacillales
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Paenibacillus unclassified
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Cohnella thermotolerans
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Paenibacillus larvae larvae
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Paenibacillus mucilaginosus|1.000
Paenibacillus mucilaginosus
2521172661 Paenibacillus ginsengihumi
2512564013 Brevibacillus unclassified
Brevibacillus brevis
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Brevibacillus laterosporus|1.000
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651324024 Desmospora unclassified
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Alicyclobacillus herbarius
Alicyclobacillus acidocaldarius
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Alicyclobacillus acidocaldarius
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Orenia marismortui
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UID1016|c Clostridia
Acetohalobium arabaticum
649633052 Halanaerobium hydrogenoformans
UID1020|f Halanaerobiaceae
Halanaerobium praevalens
643348557 Halothermothrix orenii
2531839274 Selenomonas unclassified
2531839039 Selenomonas sp oral Taxon 138
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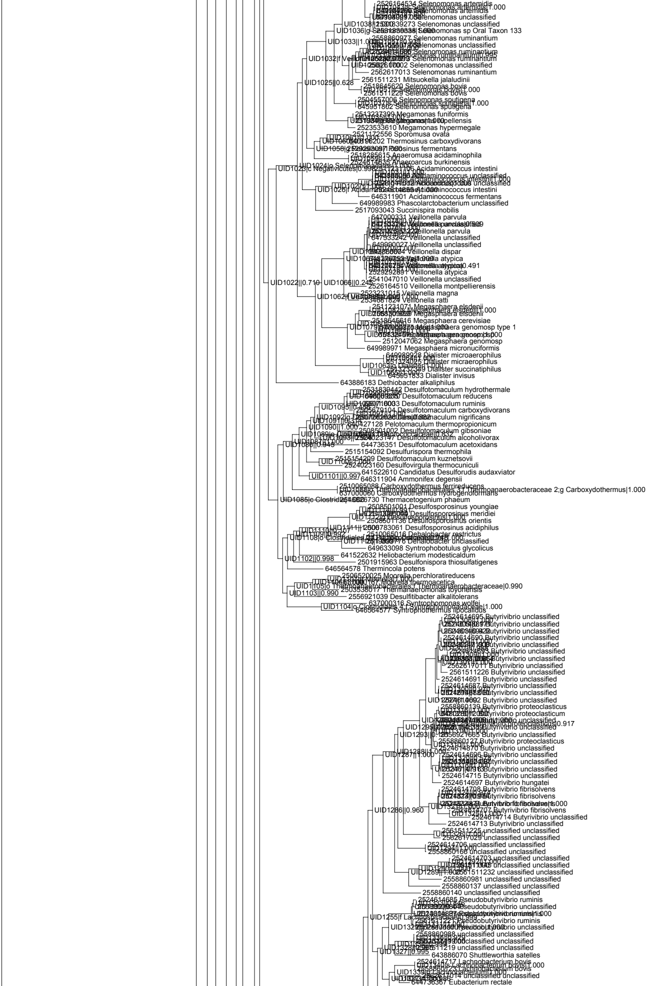
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Selenomonas sp Oral Taxon 133
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Selenomonas unclassified
Selenomonas ruminantium
UID1032|f Veillonellaceae
Selenomonas ruminantium
2562617002 Selenomonas unclassified
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UID1025||0.628
2561511231 Mitsuokella jalaludinii
2518645620 Selenomonas bovis
Selenomonas bovis|1.000
2561511229 Selenomonas bovis
2504557006 Selenomonas sputigena
Selenomonas sputigena|1.000
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2513237399 Megamonas funiformis
Megamonas rupellensis
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2521172556 Sporomusa ovata
Thermosinus carboxydivorans
UID1058
Thermosinus fermentans
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UID1024|o Selenomonadales
UID1023|c Negativicutes|0.998
Acidaminococcus intestini
Acidaminococcus unclassified
Acidaminococcus unclassified
UID1027
UID1026|f Acidaminococcaceae
Acidaminococcus intestini
646311901 Acidaminococcus fermentans
649989983 Phascolarctobacterium unclassified
2517093043 Succinispira mobilis
647000331 Veillonella parvula
Veillonella parvula
Veillonella parvula
647533242 Veillonella unclassified
649990027 Veillonella unclassified
Veillonella dispar
Veillonella atypica
Veillonella atypica|0.491
2529292891 Veillonella atypica
2541047010 Veillonella unclassified
UID1022||0.710
UID1066||0.245
2526164510 Veillonella montpellierensis
2523231015 Veillonella magna
UID1062
2534681624 Veillonella ratti
2511231071 Megasphaera elsdenii
Megasphaera elsdenii|1.000
2518645616 Megasphaera cerevisiae
Megasphaera genomosp type 1
Megasphaera genomosp
2512047062 Megasphaera genomosp
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649989928 Dialister microaerophilus
Dialister micraerophilus
UID1063|g Dialister|1.000
Dialister succinatiphilus
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2531839442 Desulfotomaculum hydrothermale
Desulfotomaculum reducens
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Thermoanaerobacterales 2;f Thermoanaerobacteraceae 2;g Carboxydothermus|1.000
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2508501136 Desulfosporosinus orientis
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2506783061 Desulfosporosinus acidiphilus
UID1110
UID1109
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Dehalobacter unclassified
649633098 Syntrophobotulus glycolicus
UID1102||0.998
641522632 Heliobacterium modesticaldum
2501915963 Desulfonispora thiosulfatigenes
646564578 Thermincola potens
2506520025 Moorella perchloratireducens
Moorella thermoacetica
Thermoanaerobacterales 1;f Thermoanaerobacteraceae|0.990
2503538017 Thermanaeromonas toyohensis
UID1103||0.990
2556921039 Desulfitibacter alkalitolerans
637000316 Syntrophomonas wolfei
UID1104|o Clostridiales 4;f Syntrophomonadaceae|1.000
646564577 Syntrophothermus lipocalidus
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Butyrivibrio unclassified
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Butyrivibrio unclassified
Butyrivibrio unclassified
Butyrivibrio unclassified
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Butyrivibrio unclassified
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Butyrivibrio unclassified
UID1295
UID1293
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UID1289
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Pseudobutyrivibrio unclassified
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Pseudobutyrivibrio ruminis
Pseudobutyrivibrio unclassified
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unclassified unclassified
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UID1327||0.995
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Lachnobacterium bovis
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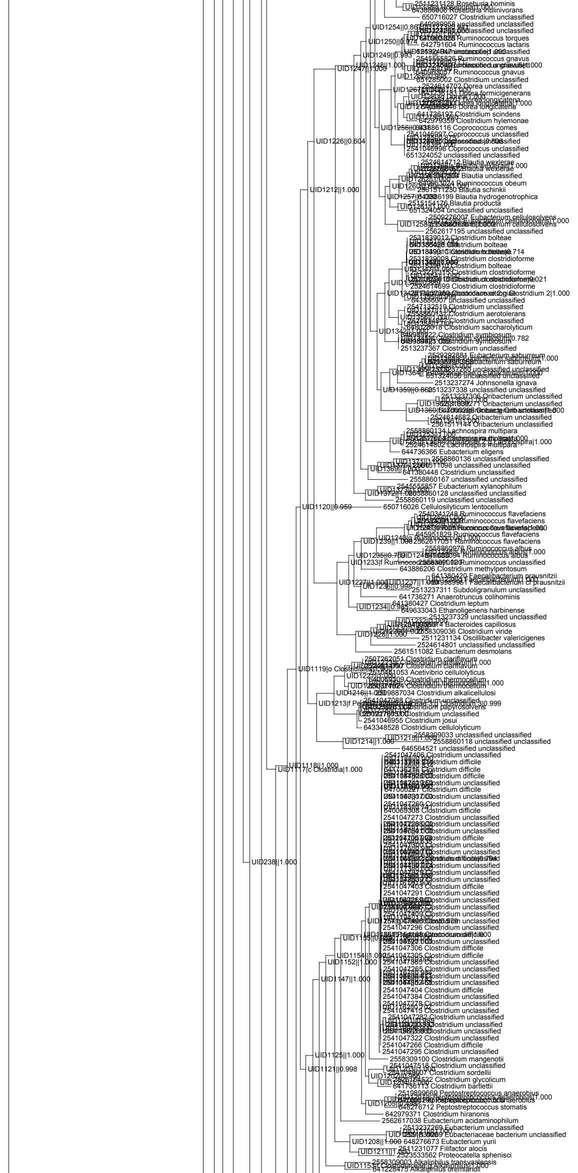
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2545555826 Ruminococcus gnavus
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Ruminococcus gnavus
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Dorea formicigenerans
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Blautia unclassified
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UID1258
Eubacterium cellulosolvens
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Clostridium bolteae
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Clostridium bolteae
Clostridium clostridioforme
2524614699 Clostridium clostridioforme
Clostridium 2|1.000
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2547132519 Clostridium unclassified
Clostridium aerotolerans
Clostridium unclassified
UID1342||1.000
Clostridium saccharolyticum
Clostridium symbiosum
Clostridium symbiosum
2513237367 Clostridium unclassified
Eubacterium saburreum
Eubacterium saburreum
unclassified unclassified
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2524614682 Oribacterium unclassified
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Lachnospira multipara
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unclassified unclassified
641380448 Clostridium unclassified
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Ruminococcus unclassified
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Acetivibrio cellulolyticus
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Clostridium 3|0.999
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Clostridium unclassified
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UID1155
Clostridium unclassified
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Clostridium unclassified
Clostridium unclassified
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Clostridium glycolicum
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Peptostreptococcus anaerobius
648276712 Peptostreptococcus stomatis
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Eubacteriaceae bacterium unclassified
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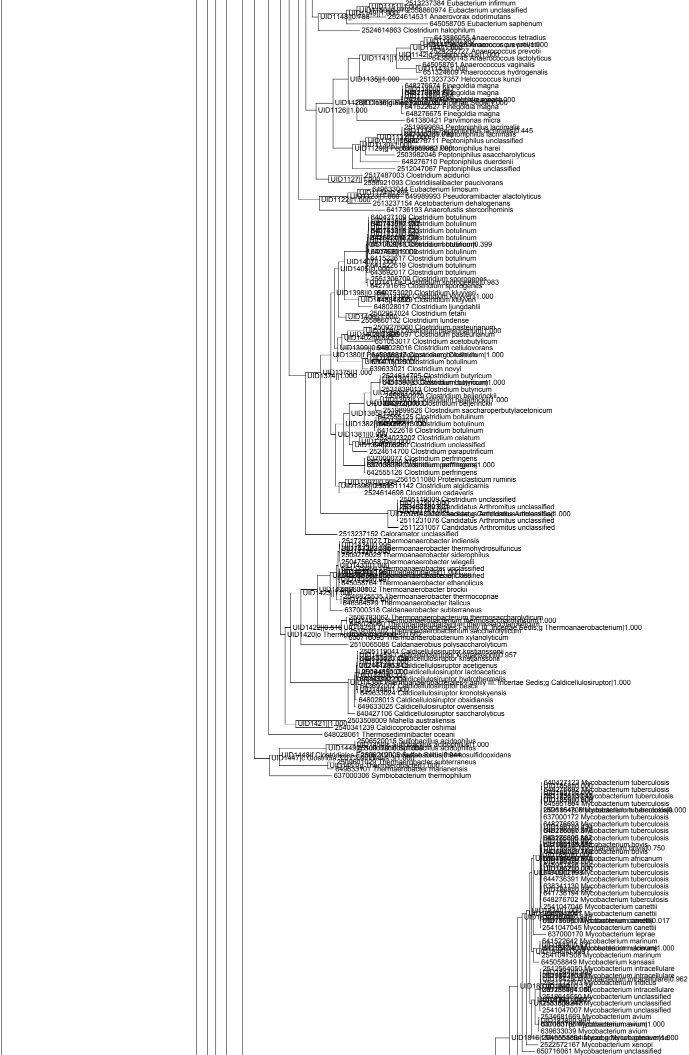
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641380421 Parvimonas micra
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Peptoniphilus lacrimalis
648276711 Peptoniphilus unclassified
Peptoniphilus harei
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Clostridium kluyveri
Clostridium kluyveri|1.000
648028017 Clostridium ljungdahlii
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Thermoanaerobacter brockii
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Thermoanaerobacterium thermosaccharolyticum
Thermoanaerobacterium saccharolyticum
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650716095 Thermoanaerobacterium xylanolyticum
2510065085 Caldanaerobius polysaccharolyticus
2505119041 Caldicellulosiruptor kristjanssonii
Caldicellulosiruptor kristjanssonii
Caldicellulosiruptor acetigenus
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Caldicellulosiruptor hydrothermalis
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Sulfobacillus acidophilus
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649633101 Thermaerobacter marianensis
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Mycobacterium tuberculosis
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Mycobacterium canettii
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Mycobacterium intracellulare
Mycobacterium indicus
Mycobacterium intracellulare
2518645550 Mycobacterium unclassified
Mycobacterium unclassified
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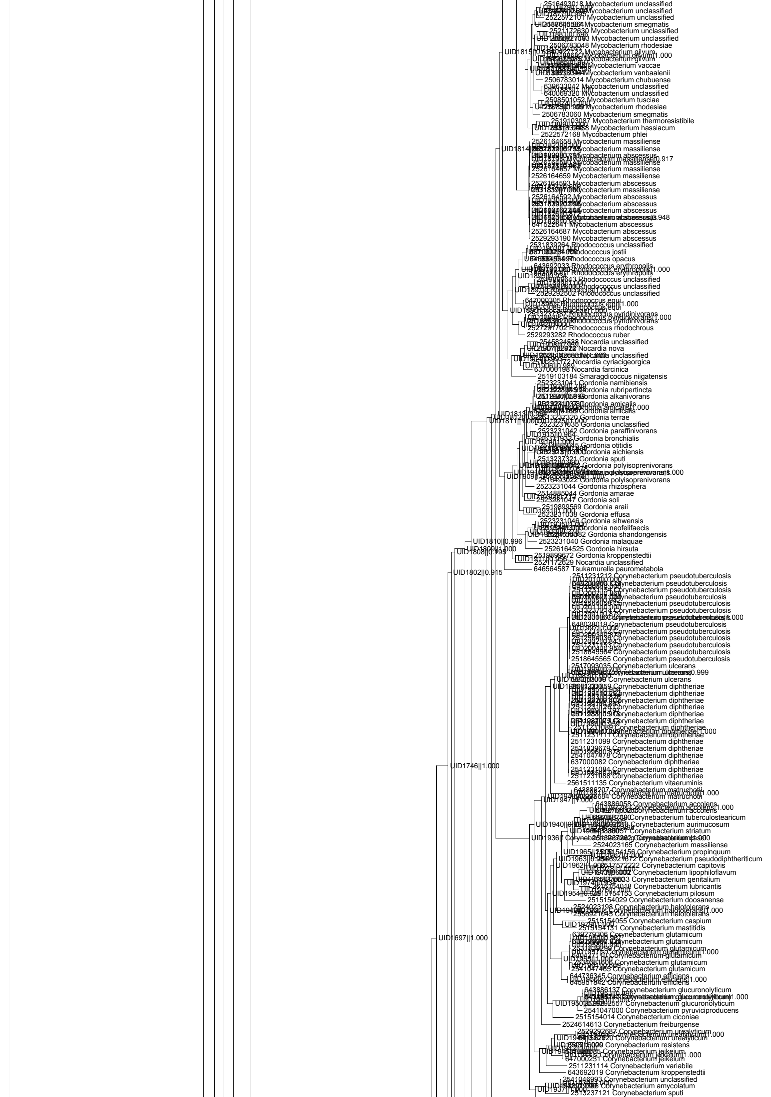
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Mycobacterium massiliense
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Rhodococcus unclassified
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Gordonia aichiensis
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Corynebacterium accolens
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Corynebacterium striatum
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UID1936
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Corynebacterium pseudodiphtheriticum
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Corynebacterium lipophiloflavum
Corynebacterium genitalium
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Corynebacterium efficiens
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Corynebacterium glucuronolyticum
2541047000 Corynebacterium pyruviciproducens
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Corynebacterium urealyticum
Corynebacterium resistens
Corynebacterium jeikeium
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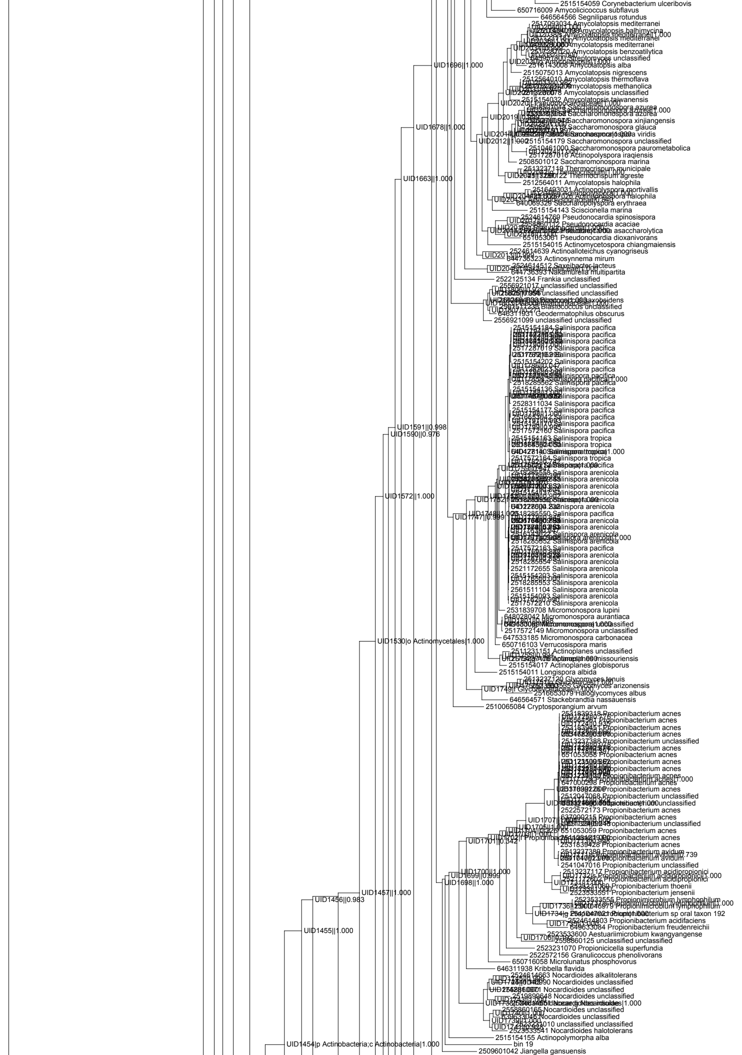
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Streptomyces unclassified
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Pseudonocardia asaccharolytica
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Blastococcus saxobsidens
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2531839708 Micromonospora lupini
648028042 Micromonospora aurantiaca
Micromonospora unclassified
2517572149 Micromonospora unclassified
647533185 Micromonospora carbonacea
UID1530|o Actinomycetales|1.000
650716103 Verrucosispora maris
2511231151 Actinoplanes unclassified
Actinoplanes missouriensis
2515154017 Actinoplanes globisporus
2515154011 Longispora albida
2513237120 Glycomyces tenuis
Glycomyces arizonensis
UID1749|f Glycomycetaceae|1.000
2516653079 Haloglycomyces albus
646564571 Stackebrandtia nassauensis
2510065084 Cryptosporangium arvum
2531839318 Propionibacterium acnes
Propionibacterium acnes
Propionibacterium acnes
Propionibacterium acnes
2513237388 Propionibacterium unclassified
Propionibacterium acnes
651053058 Propionibacterium acnes
Propionibacterium acnes
Propionibacterium acnes
Propionibacterium acnes
Propionibacterium acnes||1.000
647000298 Propionibacterium acnes
Propionibacterium acnes
2512047068 Propionibacterium unclassified
Propionibacterium unclassified
2522572173 Propionibacterium acnes
637000215 Propionibacterium acnes
Propionibacterium unclassified
651053059 Propionibacterium acnes
Propionibacterium acnes
2531839428 Propionibacterium acnes
2513237389 Propionibacterium avidum
Propionibacterium avidum||0.739
Propionibacterium avidum
2541047016 Propionibacterium unclassified
2513237117 Propionibacterium acidipropionici
Propionibacterium acidipropionici||1.000
Propionibacterium acidipropionici
Propionibacterium thoenii
2523533551 Propionibacterium jensenii
UID1707
UID1705||1.000
UID1703||1.000
UID1701||0.342
UID1700||1.000
UID1699||0.999
UID1698||1.000
UID1457||1.000
UID1456||0.983
UID1455||1.000
2523533555 Propionimicrobium lymphophilum
Propionimicrobium lymphophilum||1.000
UID1736
UID1734
Propionibacterium sp oral taxon 192
2524614803 Propionibacterium acidifaciens
649633084 Propionibacterium freudenreichii
2523533600 Aestuariimicrobium kwangyangense
UID1706
2558860125 unclassified unclassified
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650716058 Microlunatus phosphovorus
646311938 Kribbella flavida
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Nocardioides unclassified
Nocardioides unclassified
2519899648 Nocardioides unclassified
Nocardioides|1.000
2558860165 Nocardioides unclassified
639633045 Nocardioides unclassified
2523231010 unclassified unclassified
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bin 19
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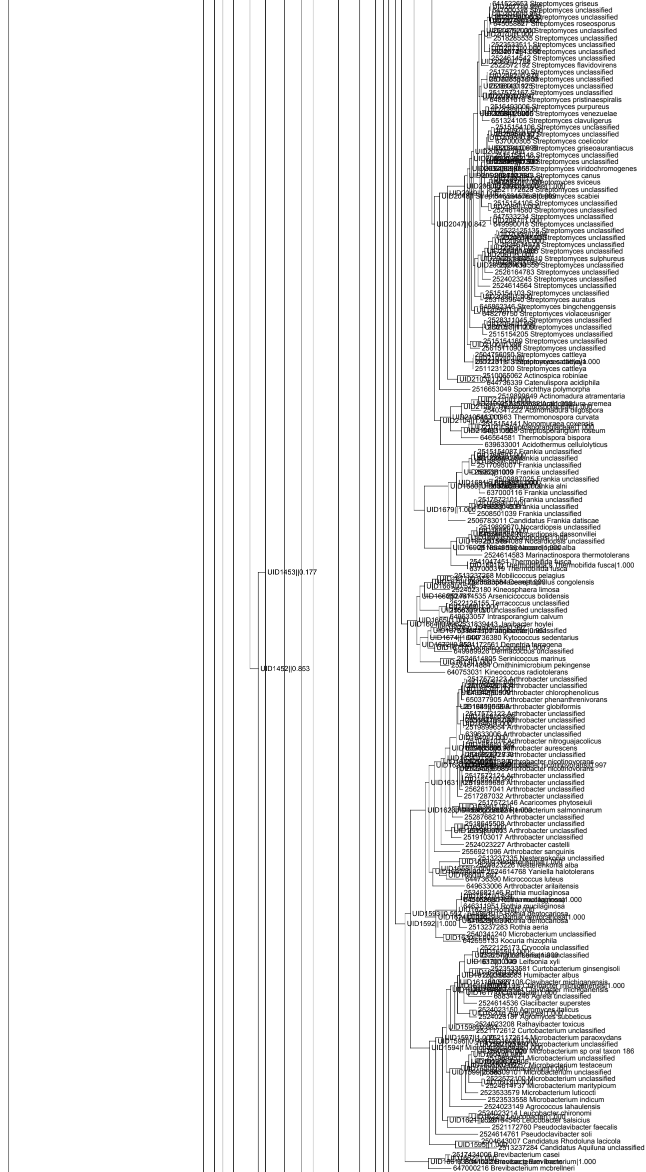
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2515154106 Streptomyces unclassified
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637000305 Streptomyces coelicolor
Streptomyces griseoaurantiacus
Streptomyces unclassified
Streptomyces unclassified
Streptomyces viridochromogenes
Streptomyces canus
Streptomyces sviceus
2521172628 Streptomyces unclassified
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UID2048||Streptomyces scabiei
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649990016 Streptomyces unclassified
2522125135 Streptomyces unclassified
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
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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
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2519899670 Nocardiopsis unclassified
Nocardiopsis dassonvillei
Nocardiopsis unclassified
Nocardiopsis alba
2524614583 Marinactinospora thermotolerans
2541047451 Thermobifida fusca
Thermobifida fusca|1.000
637000319 Thermobifida fusca
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2513237258 Mobilicoccus pelagius
congolensis
2524023180 Kineosphaera limosa
2524614535 Arsenicicoccus bolidensis
2522125155 Terracoccus unclassified
unclassified
649633057 Intrasporangium calvum
UID1665||1.000
2531839443 Janibacter hoylei
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
Arthrobacter nitroguajacolicus
Arthrobacter aurescens
Arthrobacter unclassified
Arthrobacter nicotinovorans
Arthrobacter nicotinovorans
2517572124 Arthrobacter unclassified
UID1631
2519899686 Arthrobacter unclassified
2562617041 Arthrobacter unclassified
2517287032 Arthrobacter unclassified
2517572146 Acaricomes phytoseiuli
Renibacterium salmoninarum
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644736390 Micrococcus luteus
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2534682146 Rothia mucilaginosa
Rothia mucilaginosa|1.000
646311954 Rothia mucilaginosa
Rothia dentocariosa
Rothia dentocariosa|1.000
UID1592||1.000
2513237283 Rothia aeria
2540341240 Microbacterium unclassified
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unclassified
Leifsonia xyli
2523533581 Curtobacterium ginsengisoli
Humibacter albus
Clavibacter michiganensis
Clavibacter michiganensis|1.000
Clavibacter michiganensis
Agreia unclassified
2524614536 Glaciibacter superstes
2524023150 Agromyces italicus
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2524023208 Rathayibacter toxicus
2521172612 Curtobacterium unclassified
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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
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Brevibacterium|1.000
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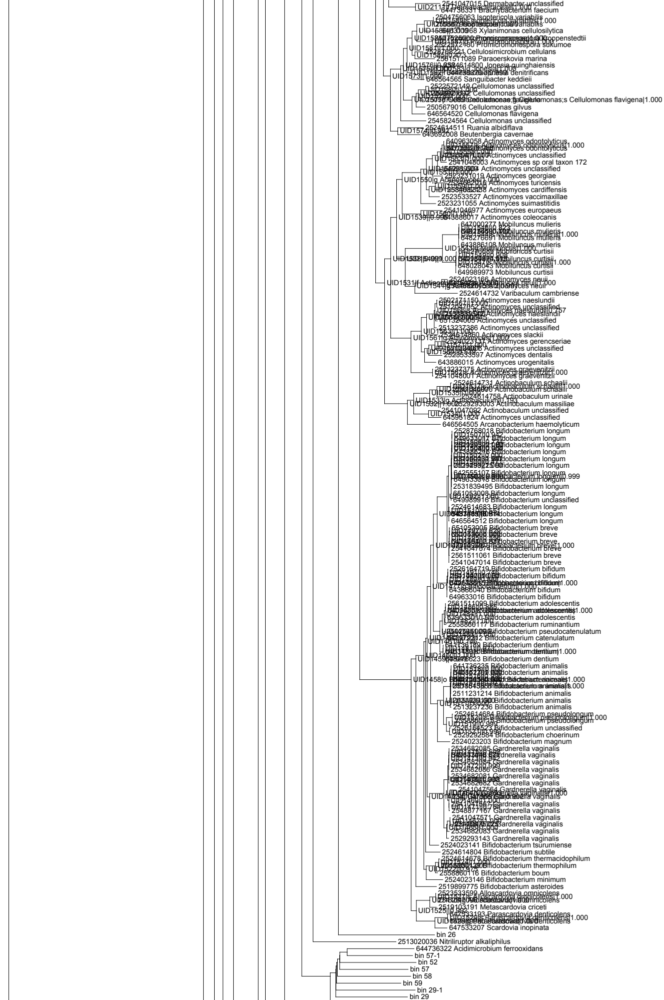
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2528768221 Cellulosimicrobium cellulans
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Jonesia quinghaiensis
denitrificans
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2522572149 Cellulomonas unclassified
Cellulomonas unclassified
Cellulomonas flavigena|1.000
2505679016 Cellulomonas gilvus
646564520 Cellulomonas flavigena
2545824564 Cellulomonas unclassified
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643692008 Beutenbergia cavernae
640963058 Actinomyces odontolyticus
Actinomyces odontolyticus|1.000
Actinomyces unclassified
2541048003 Actinomyces sp oral taxon 172
Actinomyces unclassified
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Actinomyces turicensis
Actinomyces cardiffensis
2523533527 Actinomyces vaccimaxillae
2523231055 Actinomyces suimastitidis
2541046977 Actinomyces europaeus
UID1539|0.998
643886017 Actinomyces coleocanis
647000277 Mobiluncus mulieris
Mobiluncus mulieris|1.000
648276691 Mobiluncus mulieris
643886108 Mobiluncus mulieris
Mobiluncus curtisii
Mobiluncus curtisii|1.000
648028043 Mobiluncus curtisii
649989973 Mobiluncus curtisii
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Actinomyces neuii|1.000
UID1531|f Actinomycetaceae
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Actinomyces unclassified
Actinomyces naeslundii|0.757
651324005 Actinomyces unclassified
2513237386 Actinomyces unclassified
Actinomyces slackii
UID1561|g Actinomyces|1.000
Actinomyces gerencseriae
Actinomyces unclassified
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643886015 Actinomyces urogenitalis
2513237375 Actinomyces graevenitzii
Actinomyces graevenitzii|1.000
2541046001 Actinomyces graevenitzii
2524614731 Actinobaculum schaalii
Actinobaculum schaalii|1.000
2524614758 Actinobaculum urinale
UID1533|g Actinobaculum|0.193
UID1532|1.000
2529293003 Actinobaculum massiliae
2541047092 Actinobaculum unclassified
645951824 Actinomyces unclassified
646564505 Arcanobacterium haemolyticum
2528768018 Bifidobacterium longum
Bifidobacterium longum
Bifidobacterium longum
Bifidobacterium longum
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Bifidobacterium longum
Bifidobacterium longum
642555107 Bifidobacterium longum
Bifidobacterium longum|0.999
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649989916 Bifidobacterium unclassified
2524614683 Bifidobacterium longum
Bifidobacterium longum
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Bifidobacterium breve
Bifidobacterium breve
Bifidobacterium breve|1.000
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Bifidobacterium bifidum|1.000
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2561511099 Bifidobacterium adolescentis
Bifidobacterium adolescentis|1.000
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Bifidobacterium pseudocatenulatum
Bifidobacterium catenulatum
Bifidobacterium dentium
Bifidobacterium dentium|1.000
Bifidobacterium dentium
641736235 Bifidobacterium animalis
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UID1458|o Bifidobacteriales|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
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Gardnerella vaginalis|1.000
Gardnerella vaginalis
Gardnerella vaginalis
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Gardnerella vaginalis
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Bifidobacterium thermophilum
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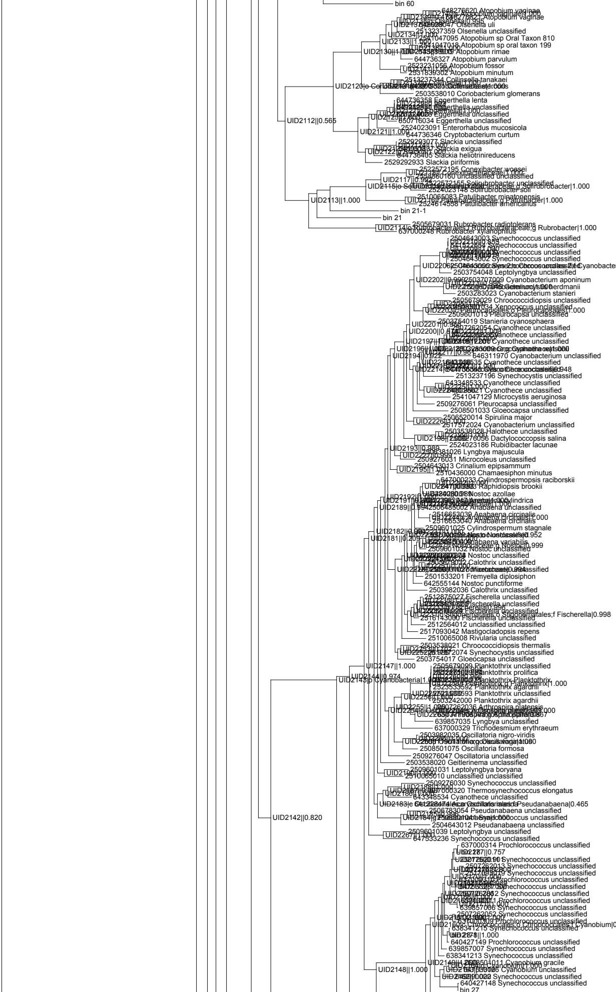
bin 29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2047 Olsenella uli
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UID2120|o Coriobacteriales
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Eggerthella unclassified
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Slackia exigua
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2529292933 Slackia piriformis
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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
Rubrobacter|1.000
637000248 Rubrobacter xylanophilus
2504643003 Synechococcus unclassified
Synechococcus unclassified
Synechococcus unclassified
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UID2206
Cyanobacterium|1.000
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Xenococcus unclassified
Pleurocapsales|1.000
2509601013 Pleurocapsa unclassified
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UID2201||0.986
UID2200||0.874
2507262054 Cyanothece unclassified
Cyanothece unclassified
UID2197||1.000
Cyanothece unclassified
UID2196||1.000
UID2194||0.922
646311970 Cyanobacterium unclassified
Cyanothece unclassified
UID2214
0.948
2513237196 Synechocystis unclassified
643348533 Cyanothece unclassified
Cyanothece unclassified
2541047129 Microcystis aeruginosa
2509276061 Pleurocapsa unclassified
2508501033 Gloeocapsa unclassified
2506520014 Spirulina major
UID2226||1.000
2517572024 Cyanobacterium unclassified
2503538028 Halothece unclassified
Dactylococcopsis salina
2524023186 Rubidibacter lacunae
UID2193||0.989
2506381026 Lyngbya majuscula
UID2227||0.999
2509276031 Microcoleus unclassified
2504643013 Crinalium epipsammum
UID2195||1.000
2510436000 Chamaesiphon minutus
647000233 Cylindrospermopsis raciborskii
Raphidiopsis brookii
Nostoc azollae
UID2192||1.000
UID2191
UID2189||0.994
Anabaena cylindrica
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2509601025 Cylindrospermum stagnale
UID2182||0.999
UID2181||0.209
0.952
Anabaena variabilis
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2509601032 Nostoc unclassified
Nostoc unclassified
2505679032 Calothrix unclassified
UID2228
0.994
2501533201 Fremyella diplosiphon
642555144 Nostoc punctiforme
2503982036 Calothrix unclassified
2512875027 Fischerella unclassified
Fischerella unclassified
Fischerella unclassified
Stigonematales;f Fischerella|0.998
2516143090 Fischerella unclassified
2512564012 unclassified unclassified
2517093042 Mastigocladopsis repens
2510065008 Rivularia unclassified
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UID2252
2517572074 Synechocystis unclassified
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UID2147||1.000
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Planktothrix prolifica
UID2144||0.974
UID2143|p Cyanobacteria|1.000
Planktothrix|1.000
2523533592 Planktothrix agardhii
UID2256||1.000
2523533593 Planktothrix unclassified
2503242000 Planktothrix agardhii
UID2255||1.000
2507262036 Arthrospira platensis
UID2254
1.000
0.867
639857035 Lyngbya unclassified
637000329 Trichodesmium erythraeum
2503982035 Oscillatoria nigro-viridis
Oscillatoria|1.000
2508501075 Oscillatoria formosa
2509276047 Oscillatoria unclassified
2503538020 Geitlerinema unclassified
2509601031 Leptolyngbya boryana
UID2190||1.000
2510065010 unclassified unclassified
2509276030 Synechococcus unclassified
637000320 Thermosynechococcus elongatus
UID2186||1.000
643348534 Cyanothece unclassified
UID2183
Pseudanabaena|0.465
2506783054 Pseudanabaena unclassified
UID2184
Synechococcus unclassified
2504643012 Pseudanabaena unclassified
UID2142||0.820
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UID2267||1.000
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637000314 Prochlorococcus unclassified
UID2287||0.757
Synechococcus unclassified
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639857006 Synechococcus unclassified
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Prochlorococcus unclassified
UID2160
Chroococcales;f Cyanobium|0.557
638341215 Synechococcus unclassified
UID2278||1.000
640427149 Prochlorococcus unclassified
639857007 Synechococcus unclassified
638341213 Synechococcus unclassified
UID2148||1.000
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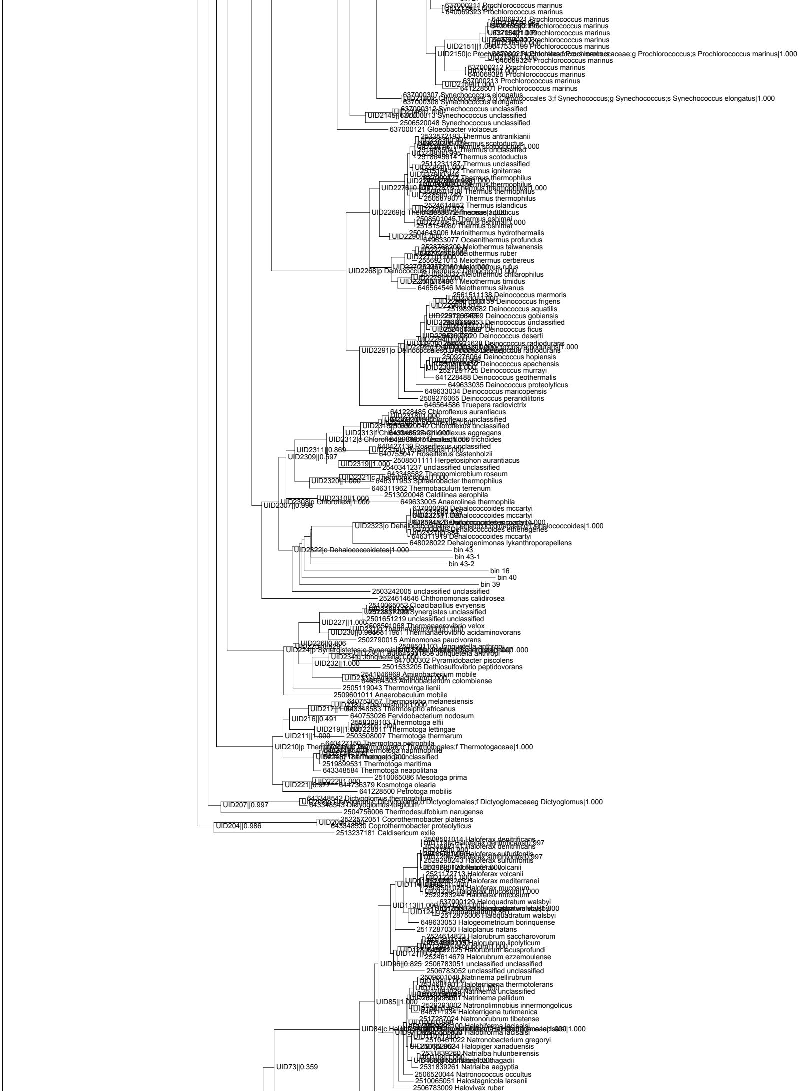
Cyanobium unclassified
Synechococcus unclassified
640427148 Synechococcus unclassified
bin 27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640069323 Prochlorococcus marinus
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UID2151||1.000
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640069324 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||1.000
637000313 Synechococcus unclassified
2506520048 Synechococcus unclassified
637000121 Gloeobacter violaceus
2522572193 Thermus antranikianii
Thermus scotoductus
2514885041 Thermus unclassified
2518645614 Thermus scotoductus
2511231187 Thermus unclassified
Thermus igniterrae
Thermus thermophilus
UID2276||0.
Thermus thermophilus|1.000
2505679077 Thermus thermophilus
2524614852 Thermus islandicus
UID2269|o Thermales;f Thermaceae|1.000
2508501045 Thermus oshimai
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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
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640753047 Roseiflexus castenholzii
UID2309||0.597
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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
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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
2501651219 unclassified unclassified
UID227||1.000
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
646564503 Aminobacterium colombiense
2505119043 Thermovirga lienii
2509601011 Anaerobaculum mobile
640753057 Thermosipho melanesiensis
UID218|g 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 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
UID207||0.997
c Dictyoglomi;o Dictyoglomales;f Dictyoglomaceaeg Dictyoglomus|1.000
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
2529293243 Haloferax sulfurifontis
Haloferax volcanii
2521172713 Haloferax volcanii
Haloferax mediterranei
Haloferax mucosum
Haloferax mucosum|1.000
2529293244 Haloferax mucosum
637000129 Haloquadratum walsbyi
UID113||1.000
Haloquadratum walsbyi|1.000
UID124||
2512875006 Haloquadratum walsbyi
649633053 Halogeometricum borinquense
2517287030 Haloplanus natans
2524614823 Halorubrum saccharovorum
Halorubrum lipolyticum
Halorubrum lacusprofundi
2524614679 Halorubrum ezzemoulense
UID96||0.825
2506783051 unclassified unclassified
2506783052 unclassified unclassified
2509601048 Natrinema pellirubrum
Haloterrigena thermotolerans
Natrinema unclassified
Natrinema pallidum
UID85||1.000
2529293002 Natronolimnobius innermongolicus
646311934 Haloterrigena turkmenica
2517287024 Natronorubrum tibetense
Halobiforma lacisalsi
UID84|c Halobacteria
Halobiforma lacisalsi
2510461022 Natronobacterium gregoryi
Halopiger xanaduensis
2531839260 Natrialba hulunbeirensis
Natrialba magadii
2531839261 Natrialba aegyptia
UID73||0.359
2506520044 Natronococcus occultus
2510065051 Halostagnicola larsenii
2506783009 Halovivax ruber

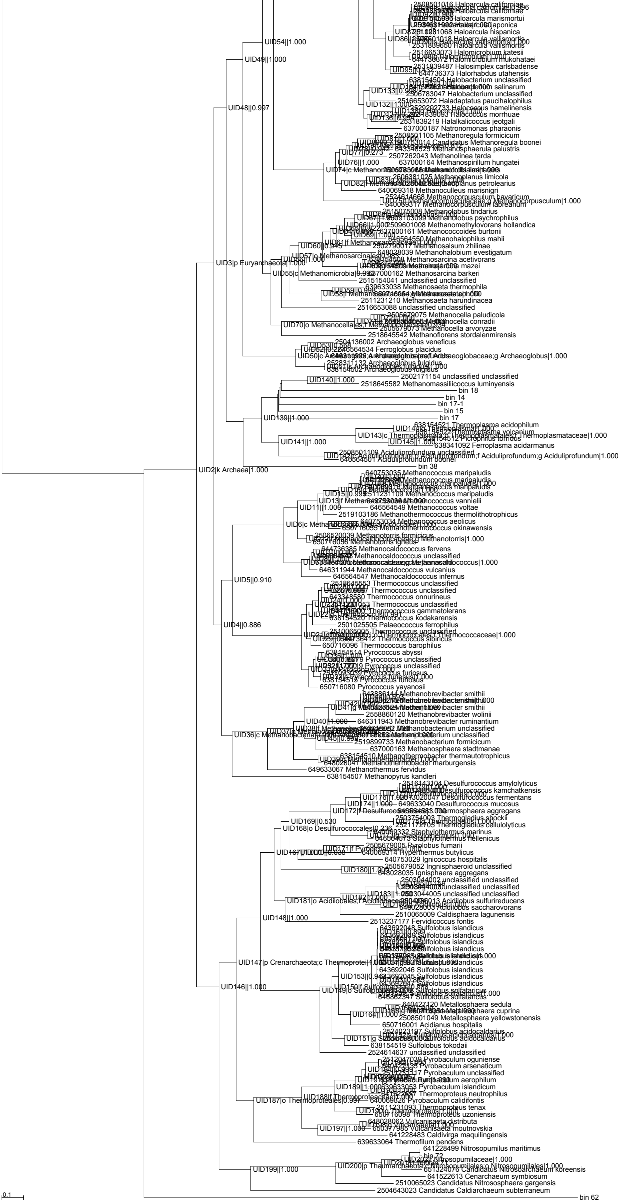

2508501016 Haloarcula californiae
Haloarcula californiae
Haloarcula marismortui
Haloarcula japonica
2511231068 Haloarcula hispanica
Haloarcula vallismortis
2531839650 Haloarcula vallismortis
2516653073 Halomicrobium katesii
644736372 Halomicrobium mukohataei
2531839487 Halosimplex carlsbadense
644736373 Halorhabdus utahensis
638154504 Halobacterium unclassified
Halobacterium salinarum
2506783047 Halobacterium unclassified
2516653072 Haladaptatus paucihalophilus
Halococcus hamelinensis
Halococcus morrhuae
2531839219 Halalkalicoccus jeotgali
637000187 Natronomonas pharaonis
2508501105 Methanoregula formicicum
Candidatus Methanoregula boonei
643348525 Methanosphaerula palustris
2507262043 Methanolinea tarda
637000164 Methanospirillum hungatei
2506381025 Methanoplanus limicola
Methanoplanus petrolearius
640069318 Methanoculleus marisnigri
2524614668 Methanocorpusculum bavaricum
UID75|f Methanocorpusculaceae;g Methanocorpusculum|1.000
640069317 Methanocorpusculum labreanum
2515075008 Methanolobus tindarius
Methanolobus psychrophilus
2509601008 Methanomethylovorans hollandica
637000161 Methanococcoides burtonii
646564550 Methanohalophilus mahii
2502790017 Methanosalsum zhilinae
648028039 Methanohalobium evestigatum
638154508 Methanosarcina acetivorans
Methanosarcina mazei
637000162 Methanosarcina barkeri
2515154041 unclassified unclassified
639633038 Methanosaeta thermophila
2511231210 Methanosaeta harundinacea
2516653088 unclassified unclassified
2505679075 Methanocella paludicola
Methanocella conradii
2505679073 Methanocella arvoryzae
2518645542 Methanoflorens stordalenmirensis
2504136002 Archaeoglobus veneficus
646546534 Ferroglobus placidus
Archaeoglobaceae;g Archaeoglobus|1.000
2528311132 Archaeoglobus fulgidus
638154502 Archaeoglobus fulgidus
2502171154 unclassified unclassified
2518645582 Methanomassiliicoccus luminyensis
bin 18
bin 14
bin 17-1
bin 15
bin 17
638154521 Thermoplasma acidophilum
Thermoplasma volcanium
Thermoplasmatales;f Thermoplasmataceae|1.000
Picrophilus torridus
638341092 Ferroplasma acidarmanus
2508501109 Aciduliprofundum unclassified
Aciduliprofundum;f Aciduliprofundum;g Aciduliprofundum|1.000
646564501 Aciduliprofundum boonei
bin 38
640753035 Methanococcus maripaludis
Methanococcus maripaludis
2511231109 Methanococcus maripaludis
Methanococcus vannielii
646564549 Methanococcus voltae
2519103186 Methanothermococcus thermolithotrophicus
640753034 Methanococcus aeolicus
650716055 Methanothermococcus okinawensis
2506520039 Methanotorris formicicus
Methanotorris|1.000
650716056 Methanotorris igneus
644736385 Methanocaldococcus fervens
Methanocaldococcus unclassified
Methanocaldococcus|1.000
646311944 Methanocaldococcus vulcanius
646564547 Methanocaldococcus infernus
2518645553 Thermococcus unclassified
Thermococcus unclassified
643348580 Thermococcus onnurineus
Thermococcus unclassified
Thermococcus gammatolerans
638154520 Thermococcus kodakarensis
2501025505 Palaeococcus ferrophilus
2510065005 Thermococcus unclassified
Thermococcaceae|1.000
Thermococcus sibiricus
650716096 Thermococcus barophilus
638154514 Pyrococcus abyssi
Pyrococcus unclassified
Pyrococcus unclassified
Pyrococcus furiosus
638154513 Pyrococcus furiosus
650716080 Pyrococcus yayanosii
643886144 Methanobrevibacter smithii
Methanobrevibacter smithii
Methanobrevibacter smithii
2558860120 Methanobrevibacter wolinii
646311943 Methanobrevibacter ruminantium
Methanobacterium unclassified
Methanobacterium unclassified
2519899733 Methanobacterium formicicum
637000163 Methanosphaera stadtmanae
638154510 Methanothermobacter thermautotrophicus
648028041 Methanothermobacter marburgensis
649633067 Methanothermus fervidus
638154507 Methanopyrus kandleri
2516143104 Desulfurococcus amylolyticus
Desulfurococcus kamchatkensis
2513020047 Desulfurococcus fermentans
649633040 Desulfurococcus mucosus
Thermosphaera aggregans
2503754003 Thermogladius shockii
2521172705 Thermogladius cellulolyticus
640069332 Staphylothermus marinus
646564573 Staphylothermus hellenicus
2505679005 Pyrolobus fumarii
640069314 Hyperthermus butylicus
640753029 Ignicoccus hospitalis
2505679052 Ingnisphaeroid unclassified
648028035 Ignisphaera aggregans
2503044002 unclassified unclassified
unclassified unclassified
2503044005 unclassified unclassified
Acidilobus sulfurireducens
648028003 Acidilobus saccharovorans
2510065009 Caldisphaera lagunensis
2513237177 Fervidicoccus fontis
643692048 Sulfolobus islandicus
643692049 Sulfolobus islandicus
Sulfolobus islandicus
Sulfolobus islandicus
Sulfolobus islandicus
Sulfolobus islandicus
Sulfolobus islandicus
643692046 Sulfolobus islandicus
643692045 Sulfolobus islandicus
Sulfolobus islandicus
643692047 Sulfolobus islandicus
Sulfolobus solfataricus
646862347 Sulfolobus solfataricus
640427120 Metallosphaera sedula
Metallosphaera cuprina
2508501049 Metallosphaera yellowstonensis
650716001 Acidianus hospitalis
2524023197 Sulfolobus acidocaldarius
Sulfolobus acidocaldarius
638154519 Sulfolobus tokodaii
2524614637 unclassified unclassified
2512047039 Pyrobaculum oguniense
Pyrobaculum arsenaticum
Pyrobaculum unclassified
Pyrobaculum aerophilum
639633053 Pyrobaculum islandicum
Thermoproteus neutrophilus
640069326 Pyrobaculum calidifontis
2511231093 Thermoproteus tenax
650716098 Thermoproteus uzoniensis
648028062 Vulcanisaeta distributa
650377985 Vulcanisaeta moutnovskia
641228483 Caldivirga maquilingensis
639633064 Thermofilum pendens
641228499 Nitrosopumilus maritimus
bin 72
UID202|f Nitrosopumilaceae|1.000
Nitrosopumilales;o Nitrosopumilales|1.000
651324076 Candidatus Nitrosoarchaeum koreensis
641522613 Cenarchaeum symbiosum
2510065023 Candidatus Nitrososphaera gargensis
2504643023 Candidatus Caldiarchaeum subterraneum
bin 62
UID54||1.000
UID49||1.000
UID48||0.997
UID3|p Euryarchaeota|1.000
UID2|k Archaea|1.000
UID139||1.000
UID141||1.000
UID140||1.000
UID5||0.910
UID4||0.886
UID36|c Methanobacteria
UID148||1.000
UID147|p Crenarchaeota;c Thermoprotei|1.000
UID146||1.000
UID187|o Thermoproteales|0.997
UID199||1.000
UID200|p Thaumarchaeota
0.1

Figure S3

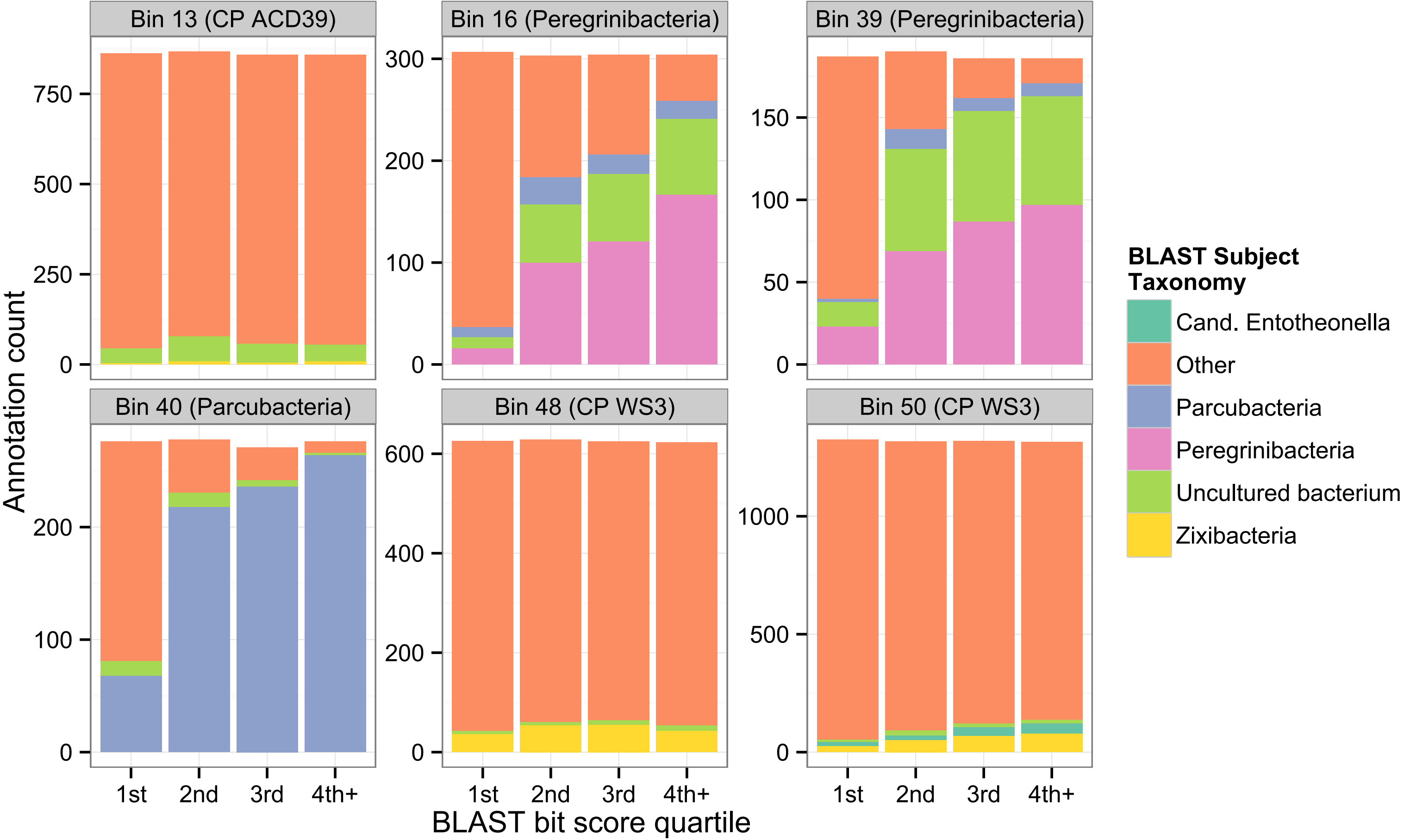

Bin 13 (CP ACD39)
Bin 16 (Peregrinibacteria)
Bin 39 (Peregrinibacteria)
Bin 40 (Parcubacteria)
Bin 48 (CP WS3)
Bin 50 (CP WS3)
Annotation count
0
250
500
750
0
100
200
300
0
50
100
150
0
100
200
0
200
400
600
0
500
1000
1st
2nd
3rd
4th+
BLAST bit score quartile
BLAST Subject Taxonomy
Cand. Entotheonella
Other
Parcubacteria
Peregrinibacteria
Uncultured bacterium
Zixibacteria

Figure S4

"Reductive Bacterial"
"Oxidative Bacterial"
"Reductive Archaeal"

Figure S5

4
3
2
1
Lipoprotein
Lipopolysaccharide
Biotin
Phosphate
Multi-sugar transporter
Heme
Cobalt
Ogliopeptides
MicrocinC
Tungstate
Lipo-oligo
NO_2^-
NO_3^-
NO_2^-
NO_3^-
Glycolysis
Glucose
Hexokinase, Glucokinase
Glucose-6P
Glucose-6P-isomerase
Fructose-6P
6-Phospho-fructokinase
Fructose-1,6-bisphosphatase
Fructose-1,6bP
Aldolase
Glyceralaldehyde-3P
Triose-P-Isomerase
Dihydroxy-acetone-P
Glyceraldehyde-3P-DH
1,3bP-glycerate
Phosphoglycerate kinase
3P-glycerate
Phosphoglycerate mutase
2P-glycerate
Enolase
Phosphoenolpyruvate
PEP carboxylase
Oxalacetate
PEP synthetase
Pyruvate kinase
Pyruvate
Pyruvate DH
2-Hydroxyethyl-ThPP
Pyruvate DH
Acetyl-dihydrolipoamide-E
Lipoate transacetylase
Pyruvate synthetase
Phospho-transacetylase
Acetate kinase
Acetate
Acetyl-P
Acetyl-CoA
Acetyl-CoA synthetase
Acetaldehyde
Acetaldehyde DH
Alcohol DH
Ethanol
Nitric oxide
Nitric oxide reductase
Nitrous oxide
Nitrous oxide reductase
Nitrogen
Nitrogenase
Nitrate reductase (NO-forming)
Nitrate
Nitrite
Nitrite reductease
Ammonia
Carbamoyl-P synthase
Carbamoyl-P
Nitrate metabolism
Respiratory nitrate reductase
Nitroalkane
Hydroxylamine
Hydroxylamine DH
Ammonia monooxygenase
Nitrile
Nitrilase
Glutamate
Glutamate DH
SOX
Thiosulfate
Sulfate
Sulfite DH
Sulfite
Sulfite reductase
Sulfide
Cystein synthase
L-Cystein
Sulfur dioxygenase
Sulfide DH
Sulfur
APS
PAPS
PAP
Sulfate metabolism
TCA
CI
Succinate
Fumarate
CII
CIII
CVI
ADP
H+
ATP
CV
H+
oxidative phosphorylation
Pentose-Phosphate-Pathway
Ribose-5P
Transketolase
Ribose-5P Isomerase
Ribulose-5P
Glyceraldehyde-3P
+
Sedoheptulose-7P
Transaldolase
Fructose-6P + Erythrose-4P
Xylulose-5P
Ribulose-5P 3-epimerase
Transketolase
Xylulose-5P
Transketolase
Glycolysis/ Gluconeogenesis
Glyceraldehyde-3P + Fructose-6P
Phospho ribulokinase
reductive Pentose-Phosphate-Pathway
Glyceraldehyde-3-P DH
CO_2
Ribulose-1,5-bisP
Ribulose-1,5-bisphosphate carboxylase
Glycerate-3P
Phosphoglycerate kinase
1,3-bisP-glycerate
Phosphate Response Regulator
SenX3
PstS
RegX3
PhoD
PhoP
PhoA
PhoB
PhoR
Acetyl-CoA
Pyruvate
Malic enzyme
OAA
Malate-DH
Citrate synthase
L-Malate
Citrate
Fumarase
Aconitase
Fumarate
Succinate-DH
TCA
Isocitrate
Succinate
Succinyl-CoA synthetase
Isocitrate-DH
Succinyl-CoA
2-oxoglutarate synthase
Oxoglutarate

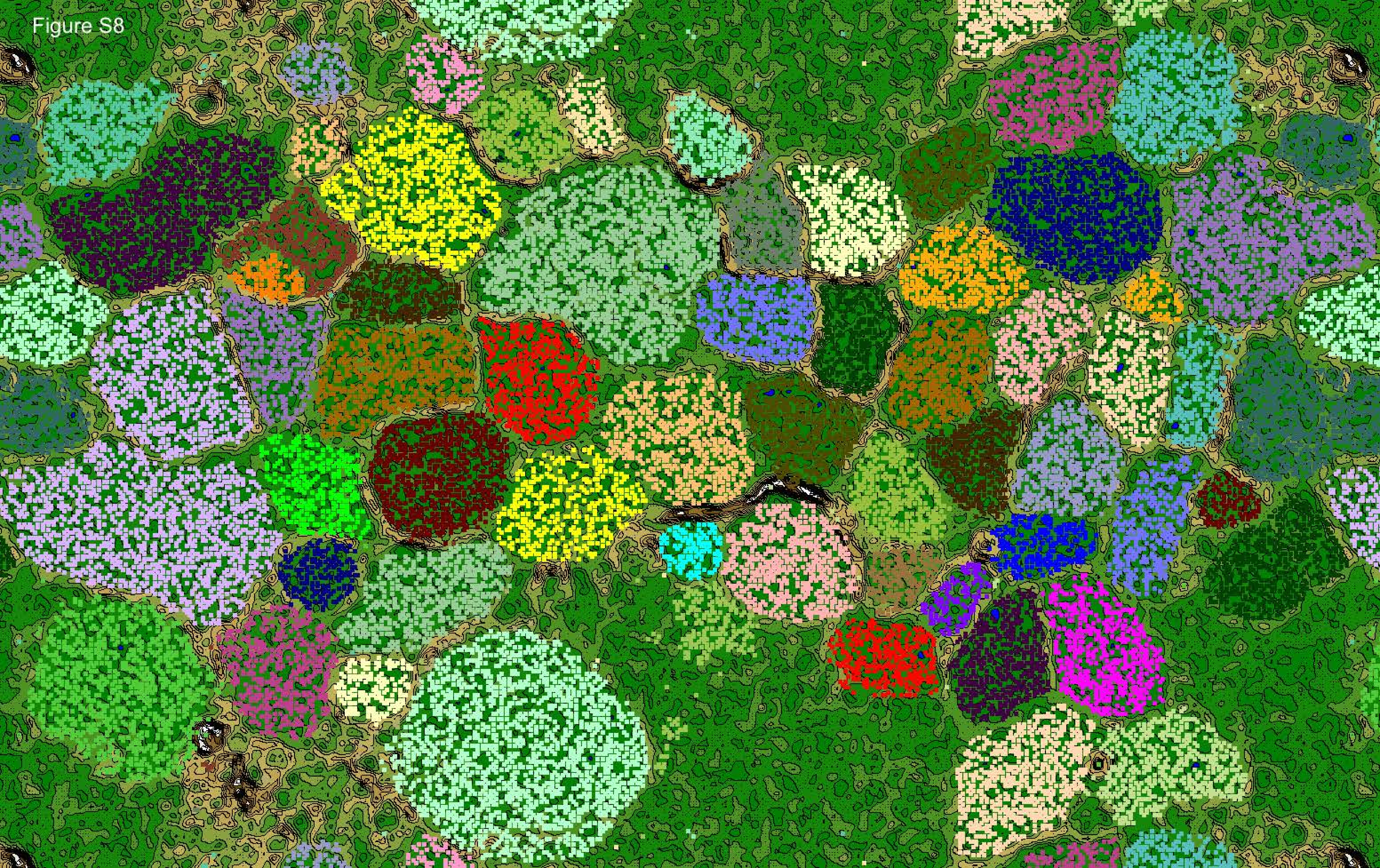
Figure S6

3
2
1
Zinc
Molybdate
Phosphate
Oligopeptides
HMP/FAMP
Heme
Iron
Glycolysis
Pentose-Phosphate-Pathway
Glucose
Hexokinase, Glucokinase
Glucose-6P
Glucose -6P-DH
6-phospho-gluconolactone
Glucono-lactonase
6-phospho-gluconate
6-phospho-gluconate-DH
Ribulose-5P
Glucose-6P-isomerase
Fructose-6P
6-Phospho-fructokinase
Fructose-1,6-bisphosphatase
Fructose-1,6bP
Aldolase
Glyceralaldehyde-3P
Triose-P-Isomerase
Dihydroxy-acetone-P
Glyceraldehyde -3P-DH
1,3bP-glycerate
Phosphoglycerate kinase
3P-glycerate
Phosphoglycerate mutase
2P-glycerate
Enolase
Phosphoenolpyruvate
PEP synthetase
Pyruvate kinase
Pyruvate
Pyruvate DH
2-Hydroxyethyl-ThPP
Pyruvate DH
Acetyl-dihydrolipoamide-E
Lipoate transacetylase
Pyruvate synthetase
Acetate
Acetyl-CoA
Acetyl-CoA sythetase (ADP)
Acetyl-CoA sythetase
Acetaldehyde
Acetaldehyde DH
Ethanol
Alcohol DH
Pyruvate fermentation
Phospho ribulokinase
Ribose-5P Isomerase
Ribulose-5P 3-epimerase
Ribulose-1,5-bisP
CO_2
Ribulose-1,5-bisphosphate carboxylase
Ribose-5P
Xylulose-5P
Transketolase
Glyceraldehyde-3P + Sedoheptulose-7P
Transaldolase
Fructose-6P + Erythrose-4P Xylulose-5P
Transketolase
Glycerate-3P
Phosphoglycerate kinase
1,3-bisP-glycerate
Glyceraldehyde-3-P DH
Glyceraldehyde-3P + Fructose-6P
reductive Pentose-Phosphate-Pathway
Formamide
Formaidase
Formyl-glutathione
Glutathione-DH
Hydroxy methyl-glutathione
Glutathione synthetase
Formaldehyde
Methane metabolism
Formyl glutathione hydrolase
Formate- DH
Formate
CO_2
CO-DH
CO
Nitric oxide
Nitric oxide reductase
Nitrous oxide
Nitrous oxide reductase
Nitrogen
Nitrate reductase (NO-forming)
Nitrogenase
Nitrate
Nitrite
Nitrite reductease
Ammonia
Carbamoyl-P synthase
Carbamoyl-P
Nitrate metabolism
Hydroxylamine
Respiratory nitrate reductase
Hydroxylamine DH
Ammonia monooxygenase
Nitrilase
Glutamate DH
Glutamate
Nitrile
ATP
Secretion System
Sec
TAT
SOX
Thiosulfate
Sulfate
Sulfite DH
Sulfite
Sulfite reductease
Sulfide
Sulfide DH
Sulfur dioxygenase
Sulfur
APS
PAPS
PAP
Sulfate metabolism
CheX
Response Regulator CheY
Response Regulator CheV
Sensor kinase CheW
Response Regulator CheB
CheC
CheD
Aer
MCP
Methyl transferase CheR
Chemotaxis
TCA
Succinate
Fumarate
CI
CII
CIII
CVI
CV
ADP
H+
ATP
H+
oxidative phosphorylation
Pyruvate
Acetyl-CoA
Malate enzyme
Pyruvate carboxylase
OAA
L-Malate
Malate-DH
Citrate synthase
Citrate
Fumarase
Aconitase
Fumarate
TCA
Isocitrate
Succinate-DH
Succinate
Succinyl-CoA synthetase
Isocitrate-DH
Succinyl-CoA
2-oxoglutarate synthase
Oxoglutarate
PstS
RegX3
SenX3
PhoD
PhoP
PhoA
PhoB
PhoR
Phosphate Response Regulator

Figure S7

1
Phosphate Response Regulator
SenX3
PhoR
RegX3
PhoP
PhoB
PstS
PhoD
PhoA
Lipopolysaccaride
Microcin C
Oligopeptide
Zinc
Iron
Glycerol-3P
Multi-sugar
Biotin
Glycolysis
Glucose
Hexokinase, Glucokinase
Glucose-6P
Glucose-6P-isomerase
Fructose-6P
6-Phospho-fructokinase
Fructose-1,6-bisphosphatase
Fructose-1,6bP
Aldolase
Glyceralaldehyde-3P
Triose-P-Isomerase
Dihydroxy-acetone-P
Glyceraldehyde-3P-DH
1,3bP-glycerate
Phosphoglycerate kinase
3P-glycerate
Phosphoglycerate mutase
2P-glycerate
Enolase
Phosphoenolpyruvate
PEP carboxylase
Oxalacetate
PEP synthetase
Pyruvate kinase
Pyruvate
Pyruvate DH
2-Hydroxyethyl-ThPP
Pyruvate DH
Acetyl-dihydrolipoamide-E
Lipoate transacetylase
Pyruvate synthetase
Acetyl-CoA
Acetaldehyde
Ethanol
Acetaldehyde DH
Alcohol DH
Acetyl-P
Phospho-transacetylase
Acetate
Acetate kinase
Acetyl-CoA synthetase
SOX
Thiosulfate
Sulfate
Sulfite DH
Sulfite
Sulfite reductase
Sulfide
Cystein synthase
L-Cystein
Sulfur dioxygenase
Sulfide DH
Sulfur
APS
PAPS
PAP
Sulfate metabolism
Nitric oxide reductase
Nitric oxide
Nitrous oxide
Nitrous oxide reductase
Nitrogen
Nitrate reductase (NO-forming)
Nitrogenase
Nitrate
Nitrite
Nitrite reductease
Ammonia
Carbamoyl-P synthase
Carbamoyl-P
Nitrate metabolism
Respiratory nitrate reductase
Hydroxylamine DH
Hydroxylamine
Ammonia monooxygenase
Nitrilase
Nitrile
Glutamate DH
Glutamate
Pentose-Phosphate-Pathway
Ribose-5P
Transketolase
Ribose-5P Isomerase
Ribulose-5P
Glyceraldehyde-3P
+
Sedoheptulose-7P
Transaldolase
Fructose-6P + Erythrose-4P
Xylulose-5P
Ribulose-5P 3-epimerase
Transketolase
Xylulose-5P
Transketolase
Glycolysis/ Gluconeogenesis
Glyceraldehyde-3P + Fructose-6P
Phospho ribulokinase
Glyceraldehyde-3-P DH
CO_2
Ribulose-1,5-bisP
Ribulose-1,5-bisphosphate carboxylase
Glycerate-3P
Phosphoglycerate kinase
1,3-bisP-glycerate
reductive Pentose-Phosphate-Pathway
Acetyl-CoA
Pyruvate
Malic enzyme
OAA
L-Malate
Malate-DH
Citrate synthase
Citrate
Fumarase
Aconitase
Fumarate
Succinate-DH
TCA
Isocitrate
Succinate
Isocitrate-DH
Succinyl-CoA synthetase
Succinyl-CoA
2-oxoglutarate synthase
Oxoglutarate
Succinate
Fumarate
oxidative phosphorylation
CI
CII
CIII
CVI
CV
ADP
H+
ATP
H+
Flagellar Assembly

Figure S8



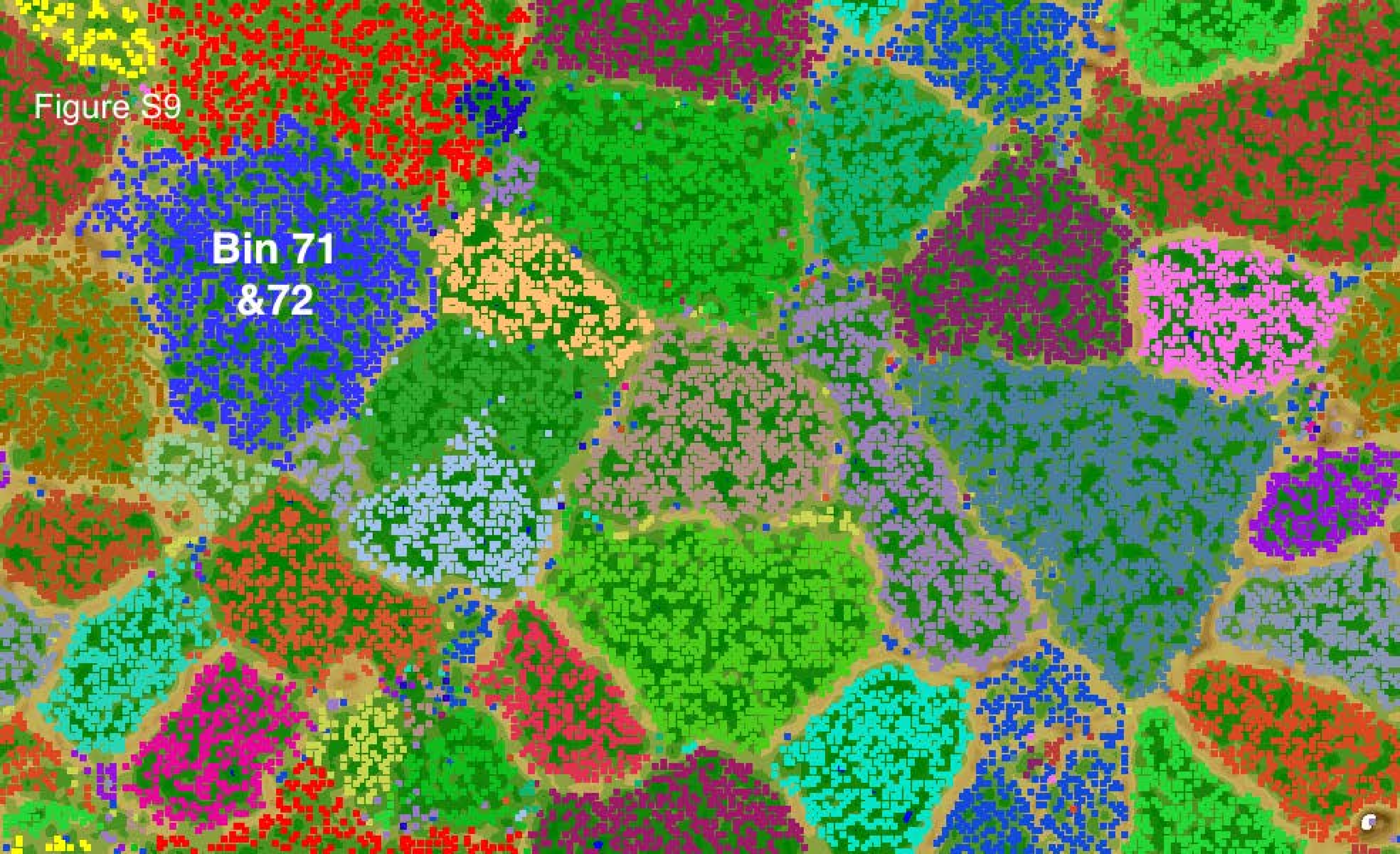
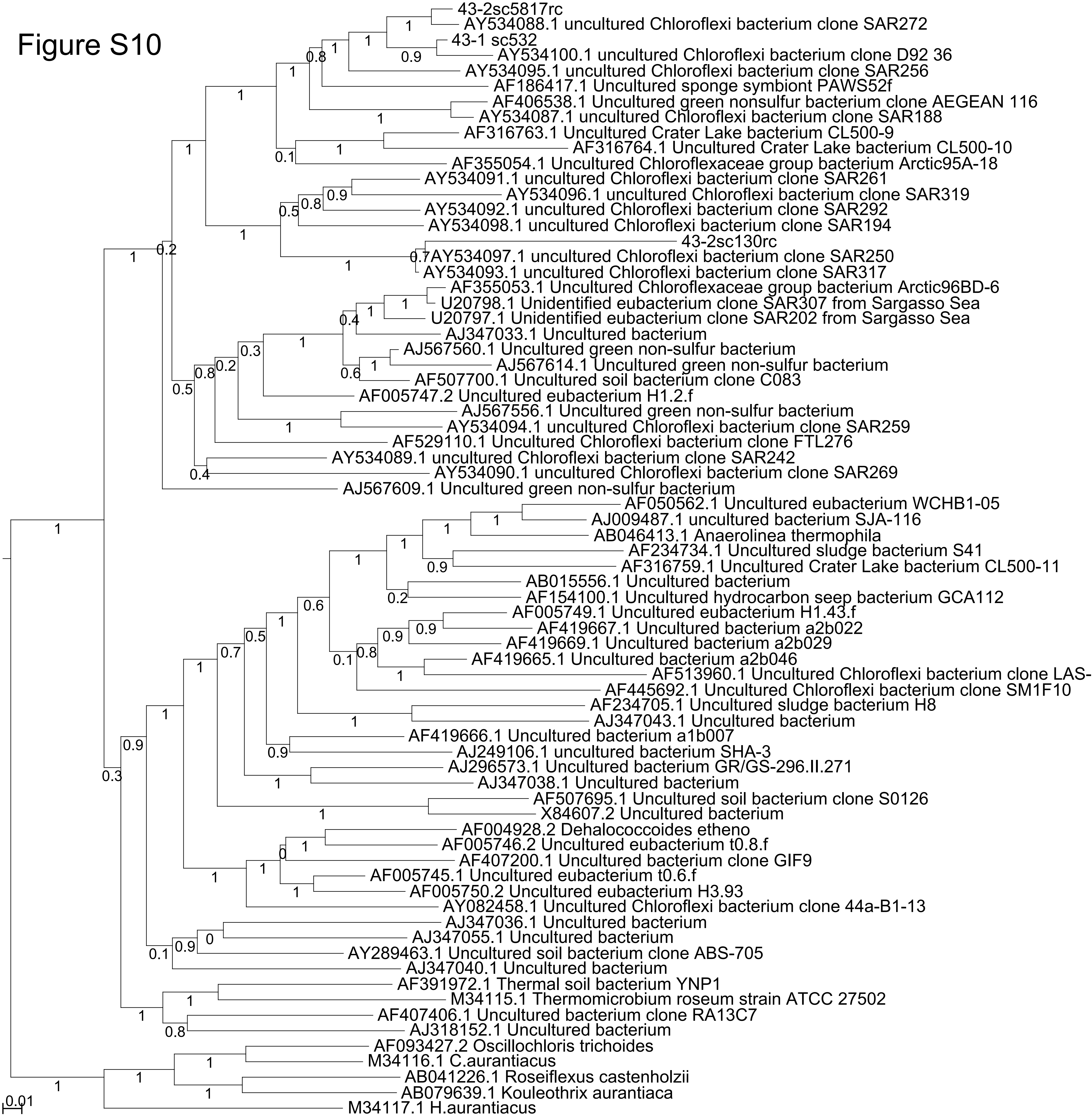


Figure S9

Figure S10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AF186417.1 Uncultured sponge symbiont PAWS52f
AF406538.1 Uncultured green nonsulfur bacterium clone AEGEAN 116
AY534087.1 uncultured Chloroflexi bacterium clone SAR188
AF316763.1 Uncultured Crater Lake bacterium CL500-9
AF316764.1 Uncultured Crater Lake bacterium CL500-10
AF355054.1 Uncultured Chloroflexaceae group bacterium Arctic95A-18
AY534091.1 uncultured Chloroflexi bacterium clone SAR261
AY534096.1 uncultured Chloroflexi bacterium clone SAR319
AY534092.1 uncultured Chloroflexi bacterium clone SAR292
AY534098.1 uncultured Chloroflexi bacterium clone SAR194
43-2sc130rc
AY534097.1 uncultured Chloroflexi bacterium clone SAR250
AY534093.1 uncultured Chloroflexi bacterium clone SAR317
AF355053.1 Uncultured Chloroflexaceae group bacterium Arctic96BD-6
U20798.1 Unidentified eubacterium clone SAR307 from Sargasso Sea
U20797.1 Unidentified eubacterium clone SAR202 from Sargasso Sea
AJ347033.1 Uncultured bacterium
AJ567560.1 Uncultured green non-sulfur bacterium
AJ567614.1 Uncultured green non-sulfur bacterium
AF507700.1 Uncultured soil bacterium clone C083
AF005747.2 Uncultured eubacterium H1.2.f
AJ567556.1 Uncultured green non-sulfur bacterium
AY534094.1 uncultured Chloroflexi bacterium clone SAR259
AF529110.1 Uncultured Chloroflexi bacterium clone FTL276
AY534089.1 uncultured Chloroflexi bacterium clone SAR242
AY534090.1 uncultured Chloroflexi bacterium clone SAR269
AJ567609.1 Uncultured green non-sulfur bacterium
AF050562.1 Uncultured eubacterium WCHB1-05
AJ009487.1 uncultured bacterium SJA-116
AB046413.1 Anaerolinea thermophila
AF234734.1 Uncultured sludge bacterium S41
AF316759.1 Uncultured Crater Lake bacterium CL500-11
AB015556.1 Uncultured bacterium
AF154100.1 Uncultured hydrocarbon seep bacterium GCA112
AF005749.1 Uncultured eubacterium H1.43.f
AF419667.1 Uncultured bacterium a2b022
AF419669.1 Uncultured bacterium a2b029
AF419665.1 Uncultured bacterium a2b046
AF513960.1 Uncultured Chloroflexi bacterium clone LAS-
AF445692.1 Uncultured Chloroflexi bacterium clone SM1F10
AF234705.1 Uncultured sludge bacterium H8
AJ347043.1 Uncultured bacterium
AF419666.1 Uncultured bacterium a1b007
AJ249106.1 uncultured bacterium SHA-3
AJ296573.1 Uncultured bacterium GR/GS-296.II.271
AJ347038.1 Uncultured bacterium
AF507695.1 Uncultured soil bacterium clone S0126
X84607.2 Uncultured bacterium
AF004928.2 Dehalococcoides etheno
AF005746.2 Uncultured eubacterium t0.8.f
AF407200.1 Uncultured bacterium clone GIF9
AF005745.1 Uncultured eubacterium t0.6.f
AF005750.2 Uncultured eubacterium H3.93
AY082458.1 Uncultured Chloroflexi bacterium clone 44a-B1-13
AJ347036.1 Uncultured bacterium
AJ347055.1 Uncultured bacterium
AY289463.1 Uncultured soil bacterium clone ABS-705
AJ347040.1 Uncultured bacterium
AF391972.1 Thermal soil bacterium YNP1
M34115.1 Thermomicrobium roseum strain ATCC 27502
AF407406.1 Uncultured bacterium clone RA13C7
AJ318152.1 Uncultured bacterium
AF093427.2 Oscillochloris trichoides
M34116.1 C.aurantiacus
AB041226.1 Roseiflexus castenholzii
AB079639.1 Kouleothrix aurantiaca
M34117.1 H.aurantiacus
0.01

Figure S11

1
Lipopolysaccharide
Oligopeptide
Phosphate
Biotin
Phosphonate
Na+
Molydabate
Lipoprotein
Iron
Biotin
Heme
Phosphate Response Regulator
SenX3
RegX3
PhoR
PstS
PhoP
PhoD
PhoB
PhoA
Glycolysis
Glucose
Hexokinase, Glucokinase
Glucose-6P
Glucose-6P-isomerase
Fructose-6P
6-Phospho-fructokinase
Fructose-1,6-bisphosphatase
Fructose-1,6bP
Aldolase
Glyceralaldehyde-3P
Triose-P-Isomerase
Dihydroxy-acetone-P
Glyceraldehyde -3P-DH
1,3bP-glycerate
Phosphoglycerate kinase
3P-glycerate
Phosphoglycerate mutase
2P-glycerate
Enolase
Phosphoenolpyruvate
PEP carboxylase
Oxalacetate
PEP synthetase
Pyruvate kinase
Pyruvate
Pyruvate DH
2-Hydroxyethyl-ThPP
Pyruvate DH
Acetyl-dihydrolipoamide-E
Lipoate transacetylase
Pyruvate synthetase
Acetyl-CoA
Acetaldehyde
Acetaldehyde DH
Ethanol
Alcohol DH
Acetyl-P
Phospho-transacetylase
Acetate
Acetate kinase
Acetyl-CoA synthetase
Methane metabolism
Formamide
Formaidase
Formyl-glutathione
Glutathione-DH
Hydroxy methyl-glutathione
Glutathione synthetase
Formaldehyde
Formyl glutathione hydrolase
Formate
Formate- DH
CO2
CO-DH
CO
Nitrate metabolism
Nitric oxide
Nitric oxide reductase
Nitrous oxide
Nitrous oxide reductase
Nitrogen
Nitrate reductase (NO-forming)
Nitrogenase
Nitrate
Nitrite
Nitrite reductase
Ammonia
Carbamoyl-P synthase
Carbamoyl-P
Respiratory nitrate reductase
Nitroalkane
Hydroxylamine DH
Hydroxylamine
Ammonia monooxygenase
Nitrilase
Nitrile
Glutamate DH
Glutamate
TCA
Acetyl-CoA
Pyruvate
Malic enzyme
OAA
Malate-DH
Citrate synthase
L-Malate
Citrate
Fumarase
Aconitase
Fumarate
Succinate-DH
Isocitrate
Succinate
Isocitrate-DH
Succinyl-CoA synthetase
Succinyl-CoA
2-oxoglutarate synthase
Oxoglutarate
TCA
CI
Succinate
Fumarate
CII
CIII
CVI
CV
ADP
H+
ATP
H+
oxidative phosphorylation
Sulfate metabolism
SOX
Thiosulfate
Sulfate
Sulfite DH
Sulfite
Sulfite reductase
Sulfide
Sulfur dioxygenase
Sulfide DH
Sulfur
APS
PAPS
PAP
Pentose-Phosphate-Pathway
Ribose-5P
Transketolase
Ribose-5P Isomerase
Ribulose-5P
Glyceraldehyde-3P + Sedoheptulose-7P
Transaldolase
Fructose-6P + Erythrose-4P
Xylulose-5P
Ribulose-5P 3-epimerase
Transketolase
Xylulose-5P
Transketolase
Glycolysis/ Gluconeogenesis
Glyceraldehyde-3P + Fructose-6P
Phospho ribulokinase
Glyceraldehyde-3-P DH
CO2
Ribulose-1,5-bisP
Ribulose-1,5-bisphosphate carboxylase
Glycerate-3P
Phosphoglycerate kinase
1,3-bisP-glycerate
reductive Pentose-Phosphate-Pathway

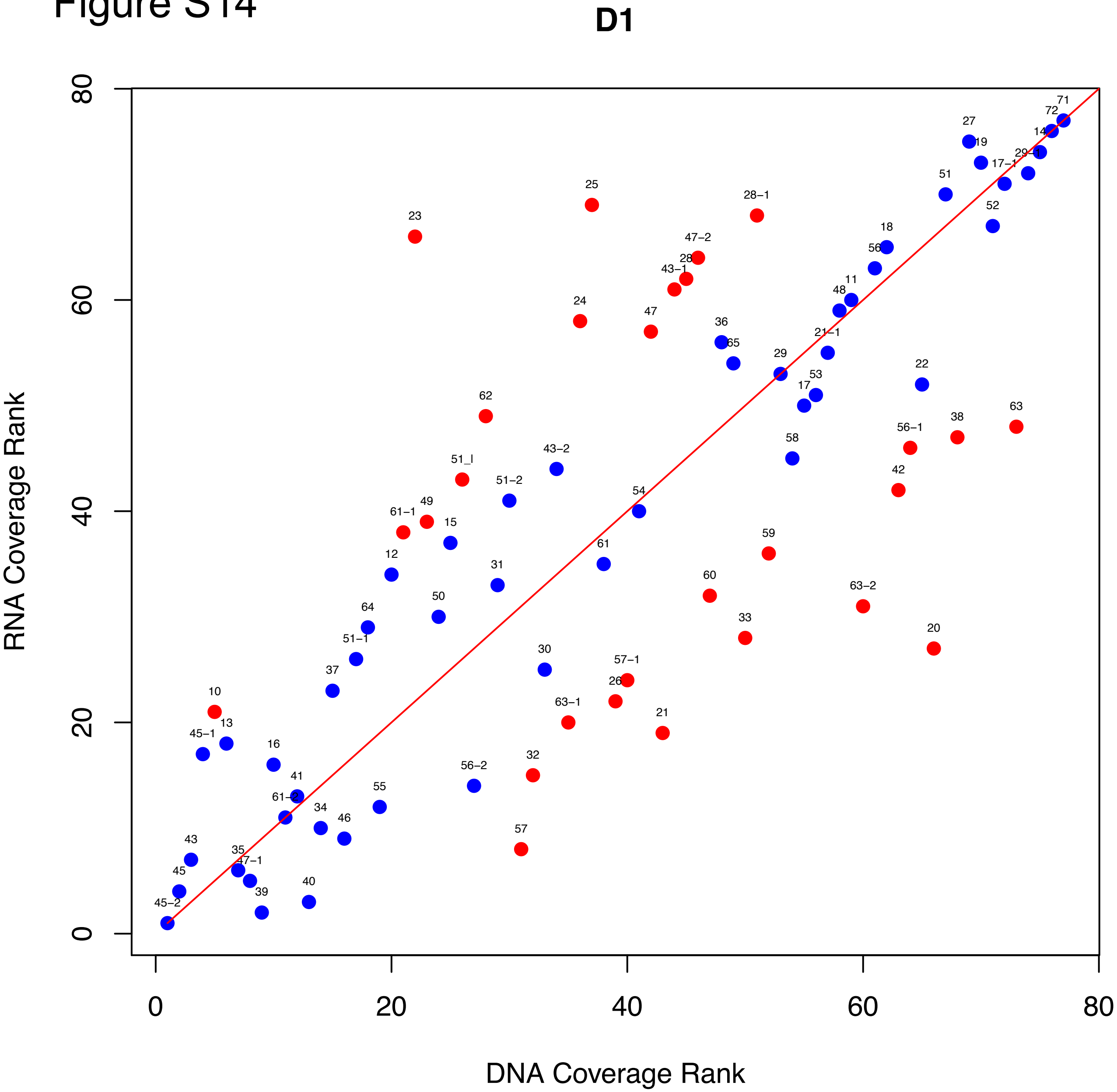
Figure S12

2
1
Glycerol
Phosphate
Iron
Glucoside
Phosphonate
Zn Mn
Fe2+
Lipoprotein
Zinc
hydroxypropionate-hydroxybutyrate cycle
Acetyl-CoA
Acetoacetyl-CoA
Acetoacetyl-CoA beta-ketothiolase
HCO3- ATP
Acetyl-CoA carboxylase
ADP Phosphate H+
S-3-Hydroxy-butyryl-CoA DH
Malonyl-CoA
Malonate-seimaldehyde oxidoreductase
4-Hydroxybutanoyl-CoA
3-Oxopropanoate
Crotonyl-CoA hydratase
3-Hydroxypropionate oxidoreductase
3-Hydroxypropanoate
Crotonyl-CoA
3-Hydroxypropionate DH
4-hydroxybutyryl-CoA-dehydratase
3-Hydroxylpropanoyl-CoA
3-Hydroxypropionyl CoA-dehydratase
Acryloyl-CoA
4-Hydroxybutanoyl-CoA
Acrylyl-CoA reductase
4-hydroxybutyryl-CoA-synthetase
Propanoyl-CoA
Propionyl-CoA carboxylase
HCO3-
S-methylmalonyl-CoA
4-Hydroxybutanoate
Methylmalonyl-CoA epimerase
R-methylmalonyl-CoA
Succinyl semialdehyde reductase
Methylmalonyl-CoA mutase
Succinyl-CoA reductase
Succinyl-CoA
Succinyl semialdehyde
Glycolysis
Glucose
Hexokinase, Glucokinase
Glucose-6P
Glucose-6P-isomerase
Fructose-6P
6-Phospho-fructokinase
Fructose-1,6-bisphosphatase
Fructose-1,6bP
Aldolase
Glyceralaldehyde-3P
Triose-P-Isomerase
Dihydroxy-acetone-P
Glyceraldehyde-3P-DH
1,3bP-glycerate
Phosphoglycerate kinase
3P-glycerate
Phosphoglycerate mutase
2P-glycerate
Enolase
Phosphoenolpyruvate
PEP carboxylase
Oxalacetate
PEP synthetase
Pyruvate kinase
Isocitrate
Pyruvate
Pyruvate DH
2-Hydroxyethyl-ThPP
Pyruvate DH
Pyruvate synthetase
Acetyl-dihydrolipoamide-E
Lipoate transacetylase
Phospho-transacetylase
Acetate kinase
Acetate
Acetyl-P
Acetyl-CoA
Acetaldehyde
Ethanol
Acetyl-CoA synthetase
Acetaldehyde DH
Alcohol DH
Pentose-Phosphate-Pathway
Ribose-5P
Transketolase
Ribose-5P Isomerase
Ribulose-5P
Glyceraldehyde-3P
+
Sedoheptulose-7P
Transaldolase
Fructose-6P + Erythrose-4P
Xylulose-5P
Ribulose-5P 3-epimerase
Transketolase
Xylulose-5P
Transketolase
Glycolysis/ Gluconeogenesis
Glyceraldehyde-3P + Fructose-6P
Phospho ribulokinase
Glyceraldehyde-3-P DH
CO2
Ribulose-1,5-bisP
Ribulose-1,5-bisphosphate carboxylase
Glycerate-3P
Phosphoglycerate kinase
1,3-bisP-glycerate
reductive Pentose-Phosphate-Pathway
SOX
Thiosulfate
Sulfate
Sulfite DH
Sulfite
Sulfite reductease
Sulfide
Cystein synthase
L-Cystein
Sulfur dioxygenase
Sulfide DH
APS
Sulfur
Sulfate metabolism
PAPS
PAP
Phosphoenol-pyruvate
Acetyl-CoA
PEP carboxylase
OAA
Malate-DH
Citrate synthase
L-Malate
Citrate
Fumarase
Aconitase
Fumarate
TCA
Succinate-DH
Succinate
Isocitrate-DH
Succinyl-CoA synthetase
Succinyl-CoA
2-oxoglutarate synthase
Oxoglutarate
TCA
Succinate
Fumarate
CI
CII
CIII
CVI
CV
ADP
H+
ATP
H+
Nitric oxide
Nitrous oxide
Nitrogen
Nitric oxide reductase
Nitrous oxide reductase
Nitrate reductase (NO-forming)
Nitrogenase
Nitrate
Nitrite
Nitrite reductease
Ammonia
Carbamoyl-P
Carbamoyl-P synthase
Nitrilase
Nitrate metabolism
Glutamate
Hydroxylamine
Nitrile
Glutamate DH
Hydroxylamine DH
Ammonia monooxygenase
oxidative phosphorylation

Figure S13

4
3
2
1
Nitrogen Response Regulator
Nitrate
Molybdate
Lipopolysaccharide
Urea
Oligopeptide
Heme
Lipoprotein
Phospholipid
Phosphonate
Microcin C
Zinc
Ribose
Phosphate
Iron
GlnL
NtrY
GlnG
NtrX
Uridylyltransferase P-II
GlnA
NifA
Glutamate metabolism
Nitrogen regulator P-II
Nitric oxide reductase
Nitrous oxide reductase
Nitric oxide
Nitrous oxide
Nitrogen
Nitrate reductase (NO-forming)
Nitrogenase
Nitrate
Nitrite
Nitrite reductase
Ammonia
Carbamoyl-P
Carbamoyl-P synthase
Nitrate metabolism
Nitrilase
Respiratory nitrate reductase
Hydroxylamine DH
Hydroxylamine
Ammonia monooxygenase
Nitrile
Glutamate DH
Glutamate
Glycolysis
Glucose
Hexokinase, Glucokinase
Glucose-6P
Glucose-6P-isomerase
Fructose-6P
6-Phospho-fructokinase
Fructose-1,6-bisphosphatase
Fructose-1,6bP
Aldolase
Glyceral aldehyde-3P
Triose-P-Isomerase
Dihydroxy-acetone-P
Glyceraldehyde -3P-DH
1,3bP-glycerate
Phosphoglycerate kinase
3P-glycerate
Phosphoglycerate mutase
2P-glycerate
Enolase
Phosphoenolpyruvate
PEP carboxylase
Oxalacetate
PEP synthetase
Pyruvate kinase
Pyruvate
Pyruvate DH
2-Hydroxyethyl-ThPP
Pyruvate DH
Acetyl-dihydrolipoamide-E
Lipoate transacetylase
Pyruvate synthetase
Acetyl-CoA synthetase (ADP)
Acetate
Acetyl-CoA
Acetyl-CoA sythetase
Pyruvate fermentation
Pyruvate
Pyruvate-formate-lyase
Pyruvate ferredoxin oxidoreductase
Acetyl-CoA
Phospho-transacetylase
Acetaldehyde DH
Acetyl-P
Acetaldehyde
Acetate kinase
Alcohol DH
Acetate
Ethanol
PhoR
PhoB
PhoA
PhoP
PstS
Phosphate Response Regulator
SOX
Thiosulfate
Sulfate
Sulfite DH
Sulfite
Sulfite reductease
Sulfide
Cystein synthase
L-Cystein
Sulfur dioxygenase
Sulfide DH
Sulfur
APS
PAPS
PAP
Sulfate metabolism
Pyruvate
Acetyl-CoA
Malate enzyme
Pyruvate carboxylase
OAA
Malate-DH
Citrate synthase
L-Malate
Citrate
Fumarase
Aconitase
Fumarate
TCA
Isocitrate
Succinate-DH
Succinate
Isocitrate-DH
Succinyl-CoA synthetase
Succinyl-CoA
2-oxoglutarate synthase
Oxoglutarate
TCA
CI
Succinate
Fumarate
CII
CIII
CVI
CV
ADP
H+
ATP
H+
oxidative phosphorylation
ATP
ATP
Sec
TII
TAT
Secretion System
Response Regulator CheB
Sensor kinase CheA
Response Regulator CheY
Response Regulator CheV
Aer
MCP
Chemotaxis
Flagellar Assembly

Figure S14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18
28
43−1
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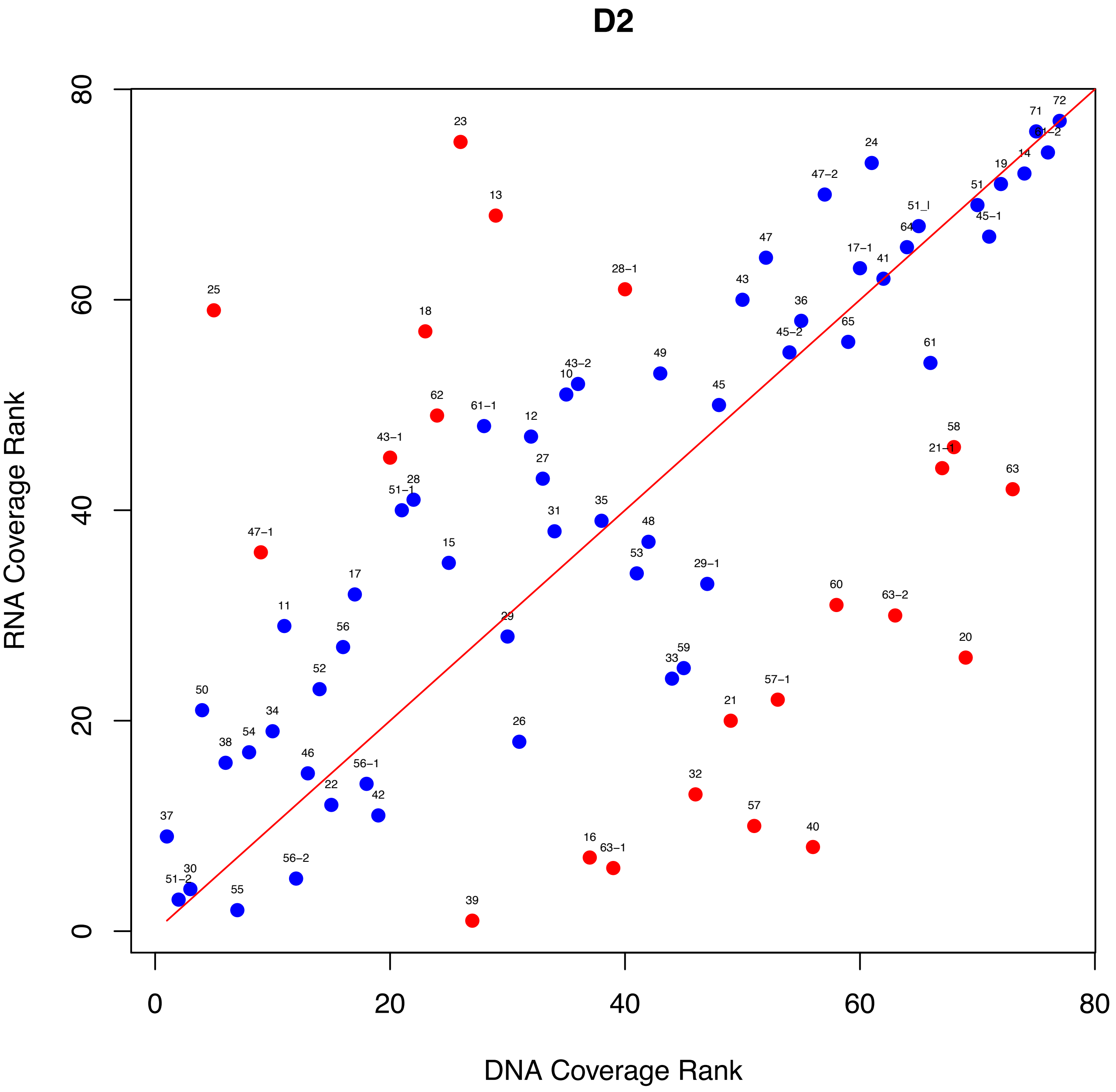
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17−1
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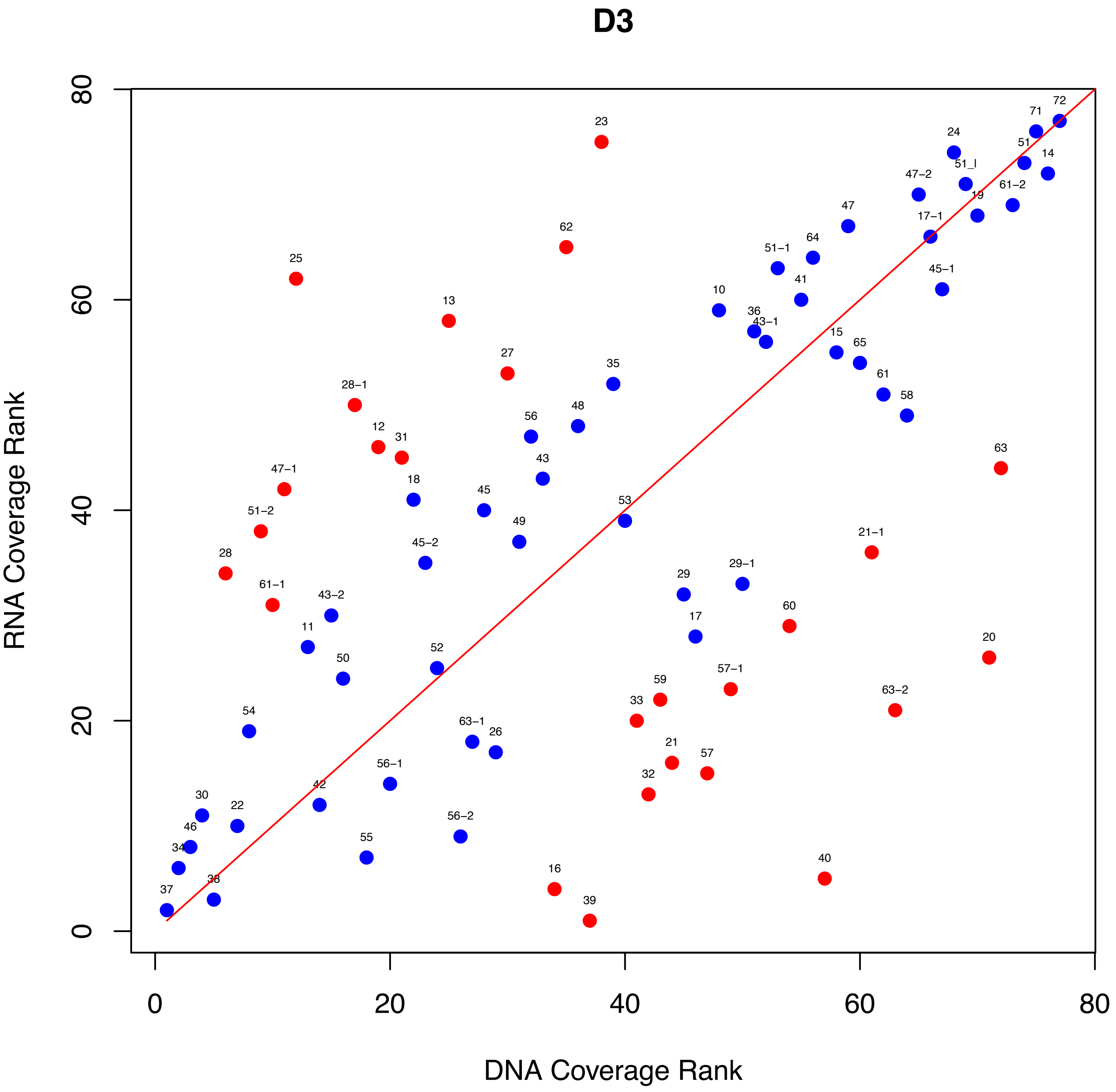
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61–1
29
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43–2
11
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17
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50
59
57–1
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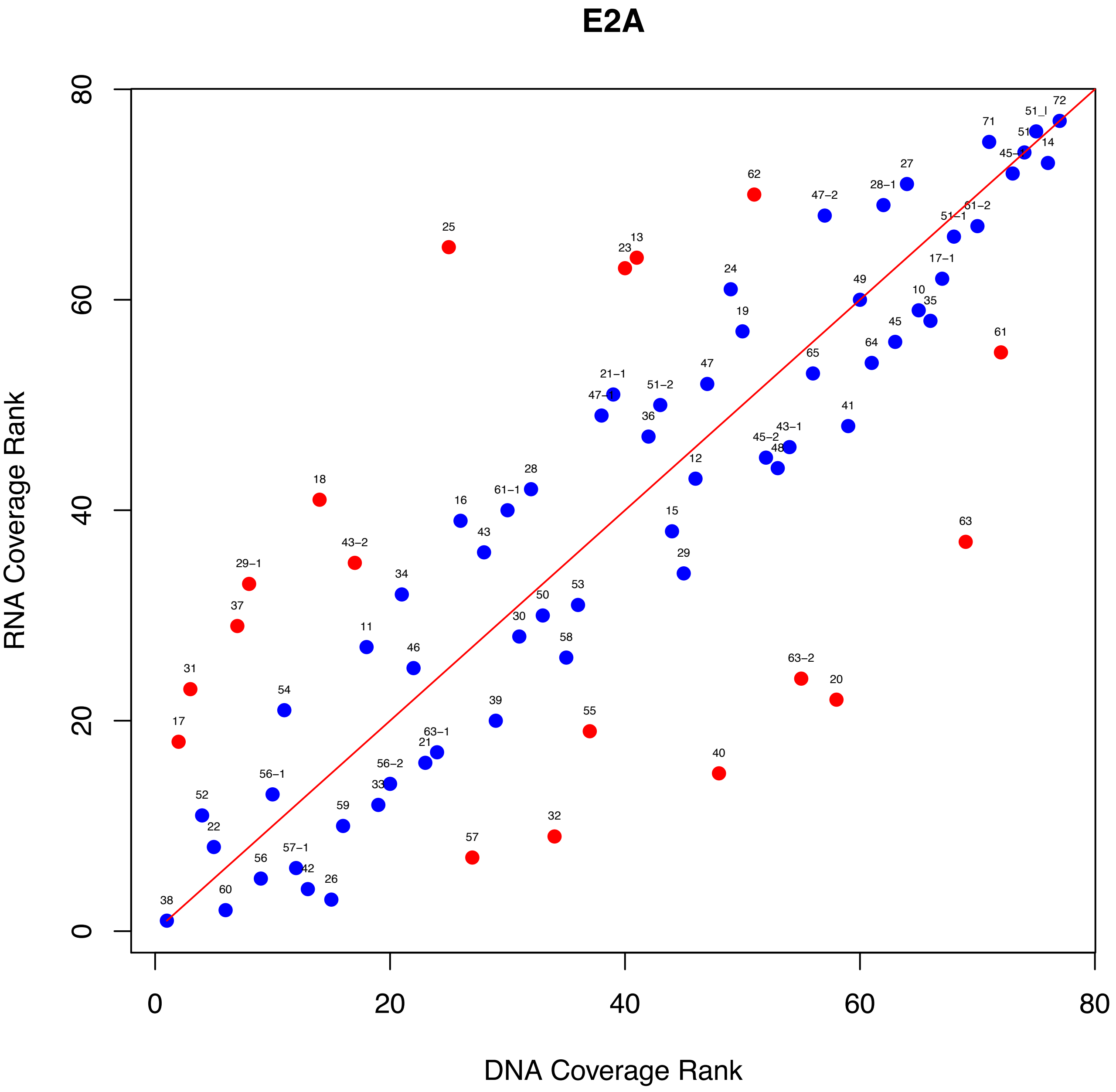
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21–1
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51–2
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43–1
45–2
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28
18
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15
29
43–2
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63–2
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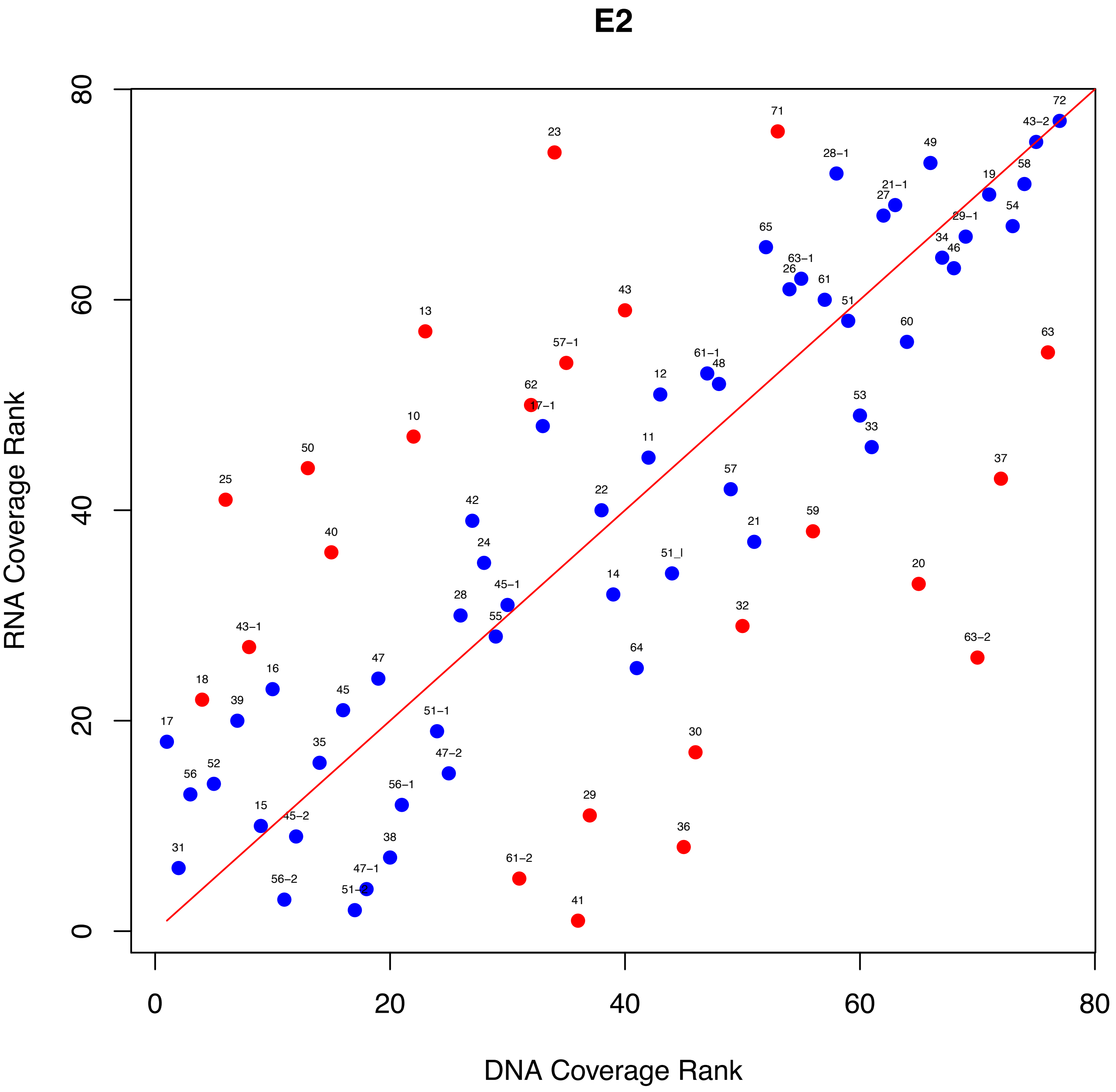
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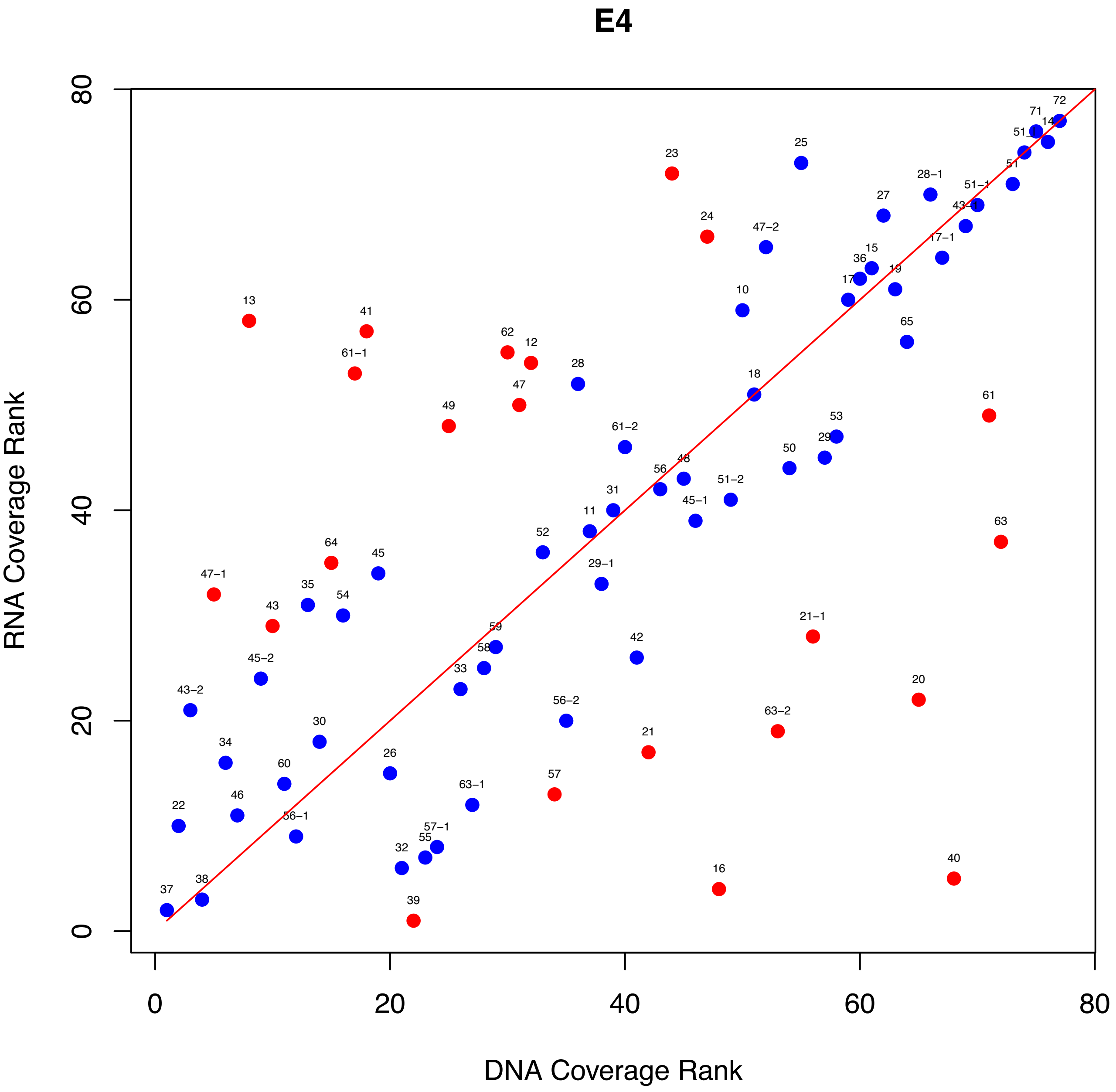
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63–2
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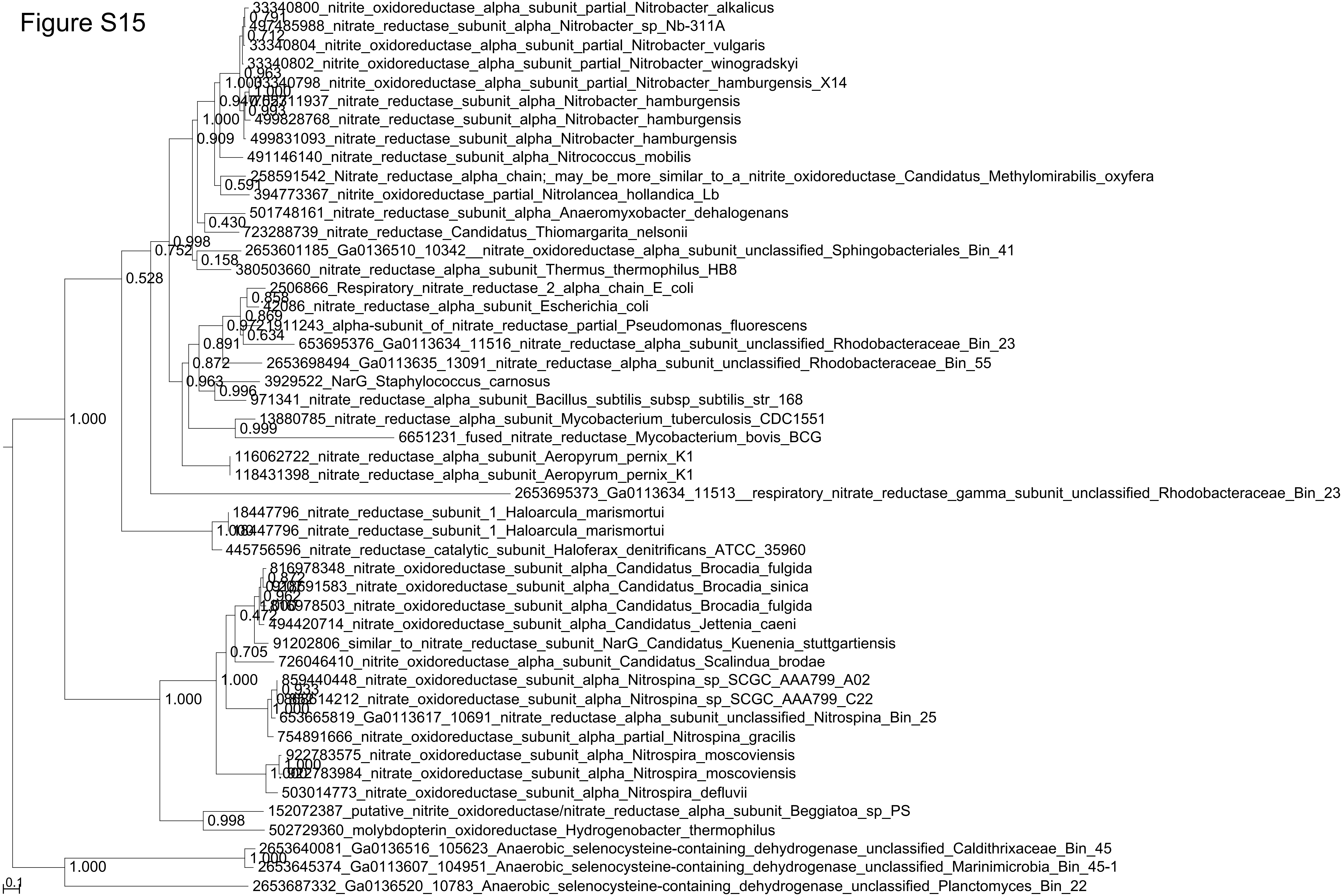
Figure S15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0.918
921691583_nitrate_oxidoreductase_subunit_alpha_Candidatus_Brocadia_sinica
0.962
1.000
816978503_nitrate_oxidoreductase_subunit_alpha_Candidatus_Brocadia_fulgida
0.472
494420714_nitrate_oxidoreductase_subunit_alpha_Candidatus_Jettenia_caeni
91202806_similar_to_nitrate_reductase_subunit_NarG_Candidatus_Kuenenia_stuttgartiensis
0.705
726046410_nitrite_oxidoreductase_alpha_subunit_Candidatus_Scalindua_brodae
1.000
1.000
859440448_nitrate_oxidoreductase_subunit_alpha_Nitrospina_sp_SCGC_AAA799_A02
0.933
0.882
886614212_nitrate_oxidoreductase_subunit_alpha_Nitrospina_sp_SCGC_AAA799_C22
1.000
653665819_Ga0113617_10691_nitrate_reductase_alpha_subunit_unclassified_Nitrospina_Bin_25
754891666_nitrate_oxidoreductase_subunit_alpha_partial_Nitrospina_gracilis
922783575_nitrate_oxidoreductase_subunit_alpha_Nitrospira_moscoviensis
1.000
1.000
922783984_nitrate_oxidoreductase_subunit_alpha_Nitrospira_moscoviensis
503014773_nitrate_oxidoreductase_subunit_alpha_Nitrospira_defluvii
152072387_putative_nitrite_oxidoreductase/nitrate_reductase_alpha_subunit_Beggiatoa_sp_PS
0.998
502729360_molybdopterin_oxidoreductase_Hydrogenobacter_thermophilus
2653640081_Ga0136516_105623_Anaerobic_selenocysteine-containing_dehydrogenase_unclassified_Caldithrixaceae_Bin_45
1.000
1.000
2653645374_Ga0113607_104951_Anaerobic_selenocysteine-containing_dehydrogenase_unclassified_Marinimicrobia_Bin_45-1
2653687332_Ga0136520_10783_Anaerobic_selenocysteine-containing_dehydrogenase_unclassified_Planctomyces_Bin_22
0.1