MICROBIAL DIVERSITY AND SULFUR CYCLING IN AN EARLY EARTH ANALOGUE: FROM ANCIENT NOVELTY TO MODERN COMMONALITY

By

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Abstract: Life emerged and diversified in the absence of molecular oxygen. The prevailing anoxia and unique sulfur chemistry in the Paleo-, Meso- and Neoarchean, and early Proterozoic eons may have supported microbial communities that differ from those currently thriving on the earth's surface. Zodletone spring in southwestern Oklahoma represents a unique habitat where spatial sampling could substitute for geological eons: from the anoxic, surficial light-exposed sediments simulating a preoxygenated earth, to overlaid water column where air exposure simulates oxygen intrusion during the NeoProterozoic. We document a remarkably diverse microbial community in the anoxic spring sediments, with 340/516 (65.89%) of genomes recovered in a metagenomic survey belonging to 200 bacterial and archaeal families that were either previously undescribed or that exhibit an extremely rare distribution on the current earth. Such diversity is underpinned by the widespread occurrence of sulfite-, thiosulfate, tetrathionate-, and sulfur-reduction, and paucity of sulfate-reduction machineries in these taxa; hence greatly expanding lineages mediating reductive sulfur cycling processes in the tree of life. Analysis of the overlaying oxygenated water community demonstrated the development of a significantly less diverse community dominated by well-characterized lineages and a prevalence of oxidative sulfur cycling processes. Such transition from ancient novelty to modern commonality underscores the profound impact of the great oxygenation event on the earth's surficial anoxic community. It also suggests that novel and rare lineages encountered in current anaerobic habitats could represent taxa once thriving in an anoxic earth, but have failed to adapt to earth's progressive oxygenation. Life on earth evolved in an anoxic setting, however, the identity and fate of microorganisms that thrived in a pre-oxygenated earth is poorly understood. Collectively, such patterns strongly suggest that microbial diversity and sulfur cycling processes in a pre-oxygenated earth were drastically different from the currently observed patterns, and that the Great Oxygenation Event has precipitated the near extinction of a wide range of oxygen-sensitive lineages and significantly altered the microbial reductive sulfur-cycling community on earth.

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CHAPTER I

INTRODUCTION

Sulfur is one of the most abundant elements on earth, exhibiting a wide range of oxidation states (-2 to +6). Microorganisms have evolved a plethora of genes and pathways for exploiting sulfur-redox reactions for energy generation. Reductive processes employ sulfur oxyanions or elemental sulfur as terminal electron acceptors in anaerobic respiratory schemes linked to heterotrophic or autotrophic growth. Oxidative processes, on the other hand, employ sulfides or elemental sulfur as electron donors, powering chemolithotrophic and photosynthetic growth.

Thermodynamic considerations limit reductive sulfur processes to habitats where oxygen is limited. This is reflected in the global distribution of sulfate (SO_4^{2-}), sulfite (SO_3^{2-}), thiosulfate ($S_2O_3^{2-}$), tetrathionate ($S_4O_6^{2-}$), and elemental sulfur (S0) reducing microorganisms (henceforth collectively referred to as SRM) in permanently and seasonally anoxic and hypoxic habitats in marine [48, 103, 109], freshwater [39], terrestrial [90], and subsurface [28] ecosystems. Sulfate is highly abundant on the current earth, and hence sulfate-reduction dominates reductive processes in the global sulfur cycle; although reduction and disproportionation of the intermediate sulfur species, e.g. sulfur [45, 98], sulfite [45], thiosulfate and tetrathionate [65, 115] could be significant in localized settings.

The history of earth's sulfur cycle is a prime example of a geological-biological feedback loop, where the evolution of biological processes is driven by, and dramatically impacts, the earth's biogeochemistry. The earth's surface was completely anoxic during the first two billion years of its history, and the availability and speciation of various sulfur species greatly differed from their current values. Sulfate levels were significantly lower when compared to current values in oceanic water (28 mM), with estimates of $< 200\mu M - 1mM$ from the Archean up to the Paleoproterozoic (2.3 Gya) [13, 14, 33, 87]. On the other hand, intermediate sulfur species appear to have played an important role in shaping the ancient sulfur cycle [32]. Modeling suggests that mM levels of SO_3^{2-} were attained in the Archean anoxic shallow surficial aquifers as a result of dissolution of the volcanic SO_2 prevailing in aquatic habitats [87]. Isotopic studies have demonstrated the importance of elemental sulfur, sulfite, and thiosulfate reduction in the Archean [32, 81].

The evolution of life (3.8 to 4.0 Gy) in the early Archean era and the subsequent evolution of major bacterial and archaeal clades in the Archean and early Proterozoic eons [67] occurred within this background of anoxia and characteristic sulfur-chemistry. As such, it has been speculated that organisms using intermediate forms of sulfur were likely more common than sulfate-reducing organisms [32]. However, while isotopic fractionation, modeling, and microscopic studies could provide clues on prevailing sulfur speciation patterns and prevalent biological processes, the identity of microorganisms mediating such processes

Figure 1.1: Zodletone Spring Source Sediments and Overlaid Water

is unknown. This is mostly due to constrains on preservation of nucleic acids and other biological macromolecules, with the oldest successful DNA sequenced sample being only 1.2 M years old [102].

Investigation of the microbial community in modern ecosystems with conditions resembling those prevailing in the ancient earth could provide important clues to the nature and identity of microorganisms that thrived under conditions prevailing prior to earth's oxygenation. In Zodletone spring, a surficial anoxic spring in southwestern Oklahoma, anoxic, surficial, light-exposed conditions are maintained in the sediments by constant emergence of sulfide-saturated water at the spring source from anoxic underground water formations in the Anadarko basin, along with gaseous hydrocarbons, which occur in seeps in the general vicinity. These surficial anoxic conditions also support a sulfur chemistry characterized by high levels of sulfide, sulfite, sulfur (soluble polysulfide), thiosulfate, and a low level of sulfate, as previously reported [12, 21, 97]. Microbial diversity using 16S rRNA amplicon surveys have reported higher level of phylogenetic diversity in the anoxic spring sediments, the affiliation of a fraction of the spring community with previously recognized sulfur-metabolizing lineages, as well as the high proportion of phylogenetically novel taxa in the spring anoxic sediments [21, 113, 112]. As such, the prevailing conditions at the spring source are reminiscent of ancient metabolic capacities prevailing on the earth's surface in the late Archean/early Proterozoic eons, as previously noted [12].

Further, the sediments at the source of the spring are overlaid by an air-exposed water column, and prior microsensor measurements and detailed geochemical analysis [12, 97] demonstrated that oxygen intrusion leads to a vertical oxygen gradient (from oxic in the top

1 µm, to hypoxic in the middle, to anoxic in deeper layers overlaying the sediments) (Figure 1.1). As such, contrasting communities between the anoxic sediments and the oxygen-exposed water column could provide a glimpse on how oxygen evolution has altered such communities. Here, we combined metagenomic, metatranscriptomic, and amplicon-based approaches to fully characterize the microbial community in Zodletone spring. Our results provide a glimpse of the community mediating the ancient sulfur cycle, significantly expand the overall microbial diversity by the description of a wide range of novel lineages, and greatly increase the number of lineages documented to mediate reductive sulfur processes in the microbial tree of life.

CHAPTER II

MATERIALS AND METHODS

2.1 Site description and geochemistry

Zodletone spring is located in the Anadarko Basin of western Oklahoma (N34.99562° W98.68895°). The spring arises from underground, where water is pumped out slowly along with sediments. Sediments settled at the source of the spring, a boxed square $1m^2$ (Figure 1.1), are overlaid with water that collects and settles in a concrete pool erected in the early 1900s. The settled water is 50-cm deep above the sediments and is exposed to atmospheric air. Water and sediments originating from the spring source are highly reduced due to the high dissolved sulfide levels (8-10 mM) in the spring sediments.

Microsensor measurements show a completely anoxic (oxygen levels < 0.1 μM) and highly reduced source sediments. Oxygen levels slowly increase in the overlaid water column from 2–4 μM in the 2 mm above the source to complete oxygen exposure at the top of the water column [12]. The spring geochemistry has regularly been monitored during the last two decades [12, 21, 92] and is remarkably stable. The spring is characterized by low levels of sulfate (50-94 μM), with higher levels of sulfite (0.21 mM), elemental sulfur (0.1 mM), and thiosulfate (0.52) [92, 97].

2.2 Sampling

Samples were collected from the source sediments and standing overlaid water in sterile containers and kept on ice until brought back to the lab (2h drive), where they were immediately processed. For metatranscriptomics, samples were collected at three different time points: morning (9:15 am), afternoon (2:30 pm), and evening (5:30 pm) in June 2019; stored on dry ice until transferred to the lab where they were stored at -80^{o}C until processed for RNA extraction within a week.

2.3 Nucleic acid extraction

DNA was directly extracted from 0.5 grams of source sediments. For water samples, water was filtered on 0.2 µm sterile filters. DNA was directly extracted from filters (20 filters, 10 L of water samples). Extraction was conducted using the DNeasy PowerSoil kit (Qiagen, Valencia, CA, USA). RNA was extracted from 0.5 g sediment samples using RNeasy PowerSoil Total RNA Kit (Qiagen, Valencia, CA, USA) according to the manufacturer's instructions.

2.4 16S rRNA gene amplification, sequencing, and analysis

Triplicate DNA extractions were performed for both sediment and water samples from the Zodletone spring. To characterize the microbial diversity based on 16S rRNA gene sequences, we used the Quick-16S™ NGS Library Prep Kit (Zymo Research, Irvine CA), following the manufacturer's protocol. For amplification of the V4 hypervariable region we used a mix of modified versions of primers 515F-806R [15], tailored to provide better coverage for several under-represented microbial lineages. They included 515FY (5'GTGYCAGCMGCCGCGGTAA) [75], 515F-Cren (5' GTGKCAGCMGCCGCGGTAA, for Crenarchaeota) [82], 515F-Nano (5'GTGGCAGYCGCCRCGGKAA, for Nanoarchaeota) [82], 515F-TM7 (5' GTGCCAGCMGCCGCGGTCA for TM7/Saccharibacteria) [18] as forward mix and 805RB (5' GGACTACNVGGGTWTCTAAT) [108] and 805R-Nano (5'GGAMTACHGGGGTCTCTAAT, for Nanoarchaeota) [82] as reverse mix. Purified barcoded amplicon libraries were sequenced on an Illumina MiSeq instrument (Illumina Inc., San Diego, CA) using a v2 500 cycle kit, according to manufacturer's protocol. Demultiplexed forward and reverse reads were imported as paired fastq files into QIIME2 v. 2020.8 [10] for analysis. The DADA2 plugin was used to trim, denoise, pair, purge chimeras and select amplicon sequence variants (ASVs), using the command "qiime dada2 denoise-paired". Between 44k and 194k non-chimeric sequences were obtained for the individual samples. The ASVs were taxonomically classified in QIIME2 using a trained classifier built based on Silva-138-99 rRNA sequence database. The ASVs were assigned to 1643 taxonomic categories corresponding to taxonomic level 7 (species and above) and to 932 genera (level 6). Alpha rarefaction curves indicated saturation of observed sequence features (ASVs) at a sequencing depth of 70-80k sequences.

2.5 Metagenome sequencing, assembly, and binning

Metagenomic sequencing was conducted using the services of a commercial provider (Novogene, Beijing, China) using two lanes of the Illumina HiSeq 2500 system for each of the water and sediment samples. Transcriptomic sequencing using Illumina HiSeq 2500 2×150bp paired-end technology was conducted using the services of a commercial provider (Novogene Corporation, Beijing, China). Metagenomic reads were assessed for quality using FastQC followed by quality filtering and trimming using Trimmomatic v0.38 [9]. High quality reads were assembled into contigs using MegaHit (v.1.1.3) with minimum Kmer of 27, maximum kmer of 127, Kmer step of 10, and minimum contig length of 1000 bp. Bowtie2 was used to calculate sequencing coverage of each contig by mapping the raw reads back to the contigs. Assembled contigs were searched for ribosomal protein S3 (rpS3) sequences using a custom hidden Markov model (HMM) built from Uniprot reference sequences assigned to the Kegg Orthologies K02982, and K02984 (corresponding to the bacterial, and archaeal RPS3, respectively) using hmmbuild (HMMER 3.1b2). rpS3 Sequences were clustered at 99% ID using CD-HIT as previously suggested for a putative species cutoff for rpS3 data [50]. Taxonomic affiliations of rpS3 groups were identified using Diamond Blast against the GTDB r95 database [76]. Contigs from the sediment and water assemblies were binned into draft genomes using both Metabat [55] and MaxBin2 [111]. DasTool was used to select the highest quality bins from each metagenome assembly [94]. CheckM was used for estimation of genome completeness, strain heterogeneity, and contamination [77]. Genomic bins

showing contamination levels higher than 10%, were further refined based on the taxonomic affiliations of the binned contigs, as well as the GC content, tetranucleotide frequency, and coverage levels using RefineM [78]. Low quality bins (>10% contamination) were cleaned by removal of the identified outlier contigs, and the percentage completeness and contamination were again re-checked using CheckM.

2.6 Genomes classification

Taxonomic classifications followed the Genome Taxonomy Database (GTDB) release r95 [76], and were carried out using the classify workflow in GTDB-Tk (v1.1.0) [16]. Phylogenomic analysis utilized the concatenated alignment of a set of 120 single-copy bacterial genes, and 122 single-copy archaeal genes [76] generated by the GTDB-Tk. Maximum-likelihood phylogenomic tree was constructed in FastTree using the default parameters [83].

2.7 Annotation and metabolic analysis

Protein-coding genes were predicted using Prodigal [42]. GhostKOALA [54] was used for the functional annotation of every predicted open reading frame in every genomic bin and to assign protein-coding genes to KEGG orthologies (KOs).

2.8 Analysis of sulfur cycling genes

To identify taxa mediating key sulfur-transformation processes in the spring sediments, we mapped the distribution of key sulfur-cycling genes in all genomes and deduced capacities in individual genomes by documenting the occurrence of entire pathways (as explained below in details). This was subsequently confirmed by phylogenetic analysis and examining contiguous genes organization in processes requiring multi-subunit and/or multi-gene. Further, expression data was used from three time points to identify the fraction of the community that is metabolically actively involved in the process. Analysis of S cycling capabilities was conducted on individual genomic bins by building and scanning hidden markov model (HMM) profiles as explained below. To build the sulfur-genes HMM profiles, Uniprot reference sequences for all genes with an assigned KO number were downloaded, aligned using Clustal-omega [95], and the alignment was used to build an HMM profile using hmmbuild (HMMER 3.1b2) [69]. For genes not assigned a KO number (e.g. otr, tsdA, tetH), a representative protein was compared against the KEGG Genes database using Blastp and significant hits (those with e-values < e-80) were downloaded and used to build HMM profiles as explained above. The custom-built HMM profiles were then used to scan the analyzed genomes for significant hits using hmmscan (HMMER 3.1b2) [69] with the option -T 100 to limit the results to only those profiles with an alignment score of at least 100. Further confirmation was achieved through phylogenetic assessment and tree building procedures, in which potential candidates identified by hmmscan were aligned to the reference sequences used to build the custom HMM profiles using Clustal-omega [95], followed by maximum likelihood phylogenetic tree construction using FastTree [83]. Only candidates clustering with reference sequences were deemed true hits and were assigned to the corresponding KO.

2.8.1 Sulfate-reduction

Sulfate reduction capacity was assessed by the presence of genes encoding the enzymes 3'-phosphoadenosine 5'-phosphosulfate synthase [Sat; EC:2.7.7.4 2.7.1.25] for sulfate activation to adenylyl sulfate (APS), the enzyme complex adenylylsulfate reductase [AprAB; EC:1.8.99.2] for APS reduction to sulfite, the quinone-interacting membrane-bound oxidoreductase complex [QmoABC] for electron transfer, the enzyme dissimilatory sulfite reductase [DsrAB; EC:1.8.99.5] and its co-substrate DsrC for dissimilatory sulfite reduction to sulfide, and the sulfite reduction-associated membrane complex DsrMKJOP for linking cytoplasmic sulfite reduction to energy conservation.

2.8.2 Sulfite-Reduction

Sulfite could be utilized by most sulfate-reducing microorganisms [86]. Dedicated sulfite-reduction capacity was assessed by the presence of the dissimilatory sulfite reductase system explained above [17, 35] with the lack of sulfate-activation (Sat) and reduction (Apr) genes. In addition, sulfite-reduction was assessed via the sole or co-occurrence of the anaerobic sulfite reductase (AsrABC) system [106], along with the membrane-bound associated complex (HdrABC) for transfer of electrons to the AsrC subunit [105]. The Asr enzyme has been shown to function in the cytoplasm in *Salmonella typhimurium* to reduce the sulfite released from respiratory reduction of tetrathionate and thiosulfate [86]. However, a scenario where the Asr enzyme is involved in sulfite respiration is possible via electron transfer from a membrane-bound associated complex to AsrC (the physiological partner of AsrAB). A plausible candidate for this membrane complex is the heterodisulfide reductase-related enzymes (HdrABC), analogous to what was suggested for DsrC (the physiological partner of DsrAB) in organisms lacking the sulfite reduction-associated membrane complex DsrMKJOP [106].

2.8.3 Polysulfide reduction

In addition to sulfate and sulfite, Zodletone spring is euxinic with extremely high levels of zero valent sulfur, available as soluble polysulfide. Respiratory polysulfide reduction was assessed via the identification of the membrane-bound molybdoenzyme complex PsrABC, which reduces polysulfides with electrons obtained from either a hydrogenase or a formate dehydrogenase through a quinone electron carrier [20]. In addition to the membrane-bound Psr system, representatives of the cytolpasmic sulfurhydrogenase I (HydABCD system), and/or II (ShyABCD system) were identified. However, although these enzymes have been shown to be dissimilatory in the archaeon Pyrococcus furiosus [8, 64], their involvement in an ETS-associated respiration is currently unclear.

2.8.4 Thiosulfate reduction/ disproportionation

Thiosulfate occurs in natural environments as a result of the reaction of sulfite with bisulfide (HS-) [115]. Thiosulfate is relatively stable at neutral pH and is present in high levels in Zodletone spring, Thiosulfate contains two sulfur atoms: a sulfone-sulfur (oxidation state +5), and a sulfane-sulfur (oxidation state -1). As such, thiosulfate can be disproportionated where the sulfone-sulfur is reduced (serves as an electron acceptor), and the

sulfane-sulfur is oxidized (serves as an electron donor), with the products being hydrogen sulfide, and sulfite, respectively. We searched for genes encoding the three known pathways for thiosulfate-disproportionation. First, in pure cultures of several sulfate reducers in the *Desulfobacterota* and *Firmicutes*, e.g. *Desulfovibrio, Desulfotomaculum*, thiosulfate disproportionation is known to occur via a cytochrome c-dependent thiosulfate reductase [EC: 1.8.2.5] [4, 5, 23, 43, 44, 46, 47, 61]. Second, in pure culture members of the family Enterobacteriaceae (*Gammaproteobacteria*), thiosulfate disproportionation is known to occur via the quinone-dependent membrane-bound molybdopterin-containing thiosulfate reductase PhsABC [36]. Finally, thiosulfate disproportionation to sulfite and hydrogen sulfide can also occur via a rhodanase-like enzyme [EC: 2.8.1.1 or EC: 2.8.1.3], as shown for several bacterial lineages [2, 22, 52, 79, 88], although this could be part of a thiosulfate assimilatory pathway as recently shown in E. coli [57]. Following the disproportionation of thiosulfate to sulfite and hydrogen sulfide, microorganisms differ in the fate of the produced sulfite. Some microorganisms reduce the released sulfite to sulfide via a Dsr or Asr dissimilatory sulfite reductase [36]), leading to complete reduction of one thiosulfate molecule to two sulfides (thiosulfate-reduction). Others oxidize the released sulfite to sulfate via the reversal of the sulfate reduction pathway [24, 61], or via the sulfite dehydrogenases SorAB or SoeABC [26], leading to the final conversion of one thiosulfate molecule to one sulfide and one sulfate molecules. The distribution of all thiosulfate disproportionation capacities was assessed by the occurrence of one of the three pathways described above, and the fate of sulfite in genomes mediating the initial disproportionation steps was assessed as described above.

2.8.5 Tetrathionate reduction

Tetrathionate has two sulfur atoms in oxidation state of 0 while the other two are in oxidation state of +5. In nature, tetrathionate is formed via the biotic or abiotic oxidation of thiosulfate under anoxic conditions [115]. Some microorganisms are capable of tetrathionate respiration via membrane-bound tetrathionate reductases that will reduce tetrathionate to thiosulfate serving as the terminal oxidase in a short electron transport system. Enzymes mediating such process include octaheme tetrathionate reductase (otr) [71], as well as the guanylyl molybdenum cofactor-containing tetrathionate reductase (ttrABC) [37]. The produced thiosulfate could be metabolized through disproportionation as described above.

2.8.6 Oxidative sulfur processes

The versatile sulfur oxidation (SOX enzyme complex) system was assessed in all genomes. The SOX system mediates the oxidation of a wide range of reduced sulfur compounds (sulfide, sulfite, thiosulfate, and elemental sulfur) directly to sulfate. Sulfide oxidation to sulfur was also assessed by the presence of the sulfide dehydrogenase FccAB [EC: 1.8.2.3] and/or the sulfide:quinone oxidoreductase Sqr [EC: 1.8.5.4], both known to oxidize sulfide to sulfur or polysulfide. Sulfur/polysulfide oxidation to sulfite was assessed via the reversal of the Dsr system (encompassing the full Dsr system dsrAB+dsrC+dsrMKJOP, in addition to the genes dsrEFH, tusA, and rhdA). Sulfite oxidation to sulfate was assessed via the reversal of AprAB+QmoABC system, the sulfite dehydrogenase (quinone) SoeABC [EC: 1.8.5.6], or the sulfite dehydrogenase (c-type cytochrome) SorAB [EC: 1.8.2.1]. Thiosulfate oxidation

to tetrathionate was assessed via the thiosulfate dehydrogenase tsdA [EC: 1.8.2.2], or the thiosulfate dehydrogenase (quinone) doxAD [EC: 1.8.5.2]. Tetrathionate generated could be cleaved using tetrathionate hydrolase (tetH) [53] that is known to cleave tetrathionate to thiosulfate, sulfur, and sulfate, or converted to sulfite using the rDSR system.

2.9 Expanding lineages mediating reductive sulfur cycling processes

Expanding lineages mediating reductive sulfur cycling processes in the tree of life. Annotree 42 [68] was queried at the family level for the presence of sulfate reduction genes (Figure 3.8) (combined search for the genes AprA, AprB, Sat, QmoA, QmoB, QmoC, DsrA, DsrB, and DsrC), sulfite reduction genes (Figure 3.9) using both the DSR system (combined search for the genes DsrA, DsrB, and DsrC, excluding all duplicate hits from (Figure 3.8) and excluding all hits from phyla known to use the system in the oxidative direction (Proteobacteria, Nitrospira, and Chlorobiaceae), and the ASR system (combined search for the genes AsrA, AsrB, AsrC, HdrA, HdrB, and HdrC), polysulfide reduction genes (Figure 3.10) (combined search for the genes PsrA, PsrB, and PsrC), thiosulfate reduction (Figure 3.11) (combined search for the genes PhsA, PhsB, and PhsC, combined with either DsrA, DsrB, and DsrC , or AsrA, AsrB, and AsrC) and thiosulfate disproportionation (combined search for the genes PhsA, PhsB, and PhsC, combined with either AprA, AprB, and Sat, or SoeA, SoeB, and SoeC, or SorA), and tetrathionate reduction (Figure 3.12) (combined search for the genes TtrA, TtrB, and TtrC).

For each of these searches, all hits were downloaded and sorted and parsed to keep one representative from each family with a hit. The Gtdb accession IDs for all such representatives were used to extract their 120 single-copy-protein concatenated alignment available from the Gtdb downloads repository [16]. These were then combined with the concatenated alignments for family-level representatives in Zodletone with genomic evidence of the corresponding sulfur reductive. The maximum likelihood trees were constructed in FastTree 40 [83]. The branches represent family-level taxonomy and are color coded by phylum. Zodletone lineages staring with ZN depict novel lineages as follows: ZNC, novel class; ZNO, novel order; and ZNF, novel family. The track around the tree represents the distribution of each family level representative as follows: only encountered in Annotree, black; only encountered in Zodletone spring sediment, blue; and encountered in both, red. By comparing the number of lineages with the blue track (only encountered in Zodletone) to the combined number of lineages with the black and red tracks, the level of expansion of lineages mediating reductive sulfur cycling processes in the tree of life can be deduced as follows: with regards to sulfate reduction (Figure 3.8), and as stated in the results section of the main text, lineages encountered in Zodletone spring sediment encoded minimal sulfate reduction capacities. Only 7 new lineages were added to an existing list of 90 lineages in the bacteria tree of life (increase by 7.7%).

On the other hand, with regards to sulfite reduction (Figure 3.9), representatives of 71 new families were added to a list of 76 families already known to encode this function (increase by 93.4%). For polysulfide reduction (Figure 3.10), thiosulfate reduction/disproportionation (Figure 3.11), and tetrathionate reduction (Figure 3.12), increases of 11.8% (12 new lineages added to 102 already known), 30.4% (7 new lineages added to 23 already known), and 34.7% (43 new lineages added to 124 already known), respectively, were encountered.

2.10 Phylogenetic affiliation and contig organization of selected sulfur reduction proteins

Alignments were created in Mafft [56] and maximum likelihood trees were constructed in RaxML [60]. Bootstrap support values are shown as bubbles for nodes with >50% support. Branches and branch labels are color coded by phylum for Zodletone sequences. Branch labels depict classification to family level followed by the NCBI genome accession number. Reference sequences are shown in black with the Uniprot accession numbers. Contig organizations of the DSR and ASR loci in selected Zodletone genomes are shown to the right of the trees in A and B. Genes are color coded as shown in the top right corner. Unrelated genes are shown by grey arrows. Gene maps were created in R using the package genoplotR [31]. Phylum/class classification is depicted to the right of the trees in Figures 3.15, 3.16, 3.17.

2.11 Phylogenetic analysis and operon organization of S cycling genes

The phylogenetic affiliation of the S cycling proteins AsrB, Otr, PhsC, PsrC, and DsrAB was examined by aligning Zodletone genome predicted protein sequences to Uniprot reference sequences using Mafft [56]. The DsrA and DsrB alignments were concatenated in MEGA X [62]. All alignments were used to construct maximum likelihood phylogenetic trees in RAxML [60]. The R package genoPlotR [31] was used to produce gene maps for the DSR and ASR loci in Zodletone genomes using the Prodigal predicted gene starts, ends, and strand direction.

2.12 Transcription of sulfur cycling genes

A total of 21.4 M, 27.9 M, and 22.5 M 150-bp paired-end reads were obtained from the morning, afternoon, and evening RNA-seq libraries. Reads were pseudo-aligned to all Prodigal-predicted genes from all genomes using Kallisto with default settings [11]. The calculated transcripts per million (TPM) were used to obtain total transcription levels for genes identified from genomic analysis as involved in S cycling in the spring.

2.13 Additional metabolic analysis

For all other non-sulfur related functional predictions, combined GhostKOALA outputs of all genomes belonging to a certain order (for orders with 5 genomes or less; n=206), or family (for orders with more than 5 genomes; n=85) were checked for the presence of groups of KOs constituting metabolic pathways (additional file 1). The list of these 291 lineages is shown in Table S3. The presence of at least 80% of KOs assigned to a certain pathway in at least one genome belonging to a certain order/family was used as an indication of the presence of that pathway in that order/family. Such criteria were used for the prediction of autotrophic capabilities, as well as catabolic heterotrophic degradation capabilities of sugars, amino acids, long-chain fatty acids, short chain fatty acids, anaerobic benzoate degradation, anaerobic short chain alkane degradation, aerobic respiration, nitrate reduction, nitrification, and chlorophyll biosynthesis. Glycolytic, and fermentation capabilities were predicted by

feeding the GhostKOALA output to KeggDecoder [30]. Proteases, peptidases, and protease inhibitors were identified using Blastp against the Merops database [89], while CAZymes (glycoside hydrolases [GHs], polysaccharide lyases [PLs], and carbohydrate esterases [CEs]) were identified by searching all ORFs from all genomes against the dbCAN hidden Markov models V9 [41] (downloaded from the dbCAN web server in September 2020) using hmmscan. FeGenie [27] was used to predict the presence of iron reduction and iron oxidation genes in individual bins.

CHAPTER III

RESULTS

3.1 Novel phylogenetic diversity in Zodletone sediments

3.1.1 Overall Sequencing Overview and Diversity Patterns

Metagenomic sequencing of the spring sediments yielded 281 Gbp, 79.54% of which assembled into 12 Gbp contigs, with 6.8 Gbp contigs longer than 1Kbp. 1,848 genomes were binned, but only 683 passed quality control criteria, and 516 remained after dereplication (Table 3.1). These metagenome-assembled genomes (MAGs) represented 64 phyla or candidate phyla (53 bacterial and 11 archaeal), 127 classes, 198 orders, and 300 families (Figure 3.1). Diversity assessment utilizing small subunit ribosomal protein S3 from assembled contigs (n=2079), as well as a complementary 16S rRNA Illumina sequencing effort (n=309,074 amplicons), identified a higher number of taxa (82 phyla and 1679 species in the ribosomal protein S3 dataset, and 69 phyla and 1050 species in 16S rRNA dataset) (Figure 3.2). Nevertheless, the overall community composition profiles generated from all three approaches were broadly similar (Figure 3.2), suggesting that the MAG list largely reflects the sediment microbial community.

Assessment of the novelty and degree of uniqueness of sediment MAGs identified a remarkably high number of previously undescribed lineages (1 phylum, 14 classes, 43 orders, and 97 families) as well as Lineages exhibiting Rare Global Distribution (LRD) pattern (11 phyla, 24 classes, 45 orders, and 113 families) in the spring (Figure 3.1, 3.3, 3.4). We define LRD lineages as those represented by 5 genomes or less in the Genome Taxonomy Database release 95 (GTDB r95). At the family level, 132 (25.58%), and 208 (40.03%) genomes clustered into 97 novel and 113 LRD families respectively, bringing the proportion of genomes belonging to novel or LRD families in Zodletone sediments to 65.89%. The high level of novelty in the sediment MAGs is reflected in an average RED value of 0.76, a value that is slightly lower than the median RED value for designation of a novel family (0.77) [76].

3.1.2 Detailed phylogenetic analysis of Zodletone sediment MAGs

The *Chloroflexota* (n=69), *Planctomycetota* (n=47), *Bacteroidota* (n= 43), *Desulfobacterota* (n= 43), *Spirochaetota* (n= 28 genomes), *Patescibacteria* (n=20 genomes), and the archaeal phylum *Nanoarchaeota* (n=21) were the most abundant phyla in Zodletone spring sediments, albeit representing only 52.52% of the total number of recovered genomes (Figure 3.1, 3.4, 3.5). An extreme paucity of genomes belonging to the *Proteobacteria* (6 genomes) and *Firmicutes* (12 genomes), widely distributed and abundant taxa in current biomes [73], and the absence of oxygen-generating *Cyanobacteria* (0 genomes) were observed (Figure 3.1, 3.5).

Within the *Chloroflexota*, 38/69 genomes belonged to 3 novel orders, 5 novel families, and multiple LRD orders (Thermoflexales, 4572-78, and UBA2777) and families (E44-bin32, Fen-1058, J111, RBG-13-53-26, RBG-16-64-43, UBA11579, UBA11858, UBA2029, UBA2162, UBA3940, UBA4811, UBA4823, UBA5620, UBA5760, and UBA6092) (Figure 3A inside 3.1).

Within the *Planctomycetota*, 17/47 genomes belonged to 2 novel orders, 8 novel families, and multiple LRD orders (FEN-1346, SZUA-567, and UBA8890) and families (Fen-1342, SM23-30, UBA1845, UTPLA1, and UBA8108) (Figure 3c inside 3.1).

Within the *Bacteroidota*, 27/43 genomes belonged to 1 novel family, and multiple LRD families (FEN-979, GCA-2748055, NBLH01, UBA10428, UBA12170, UBA5072, UBA6680, and SZUA-365) (Figure 3b inside 3.1).

Within the *Spirochaetota*, 19/28 genomes belonged to one novel class, 2 novel orders, and 9 novel families, as well as multiple LRD families (ARS1246, *Marispirochaetaceae*, and RPPD01) (Figure 3d inside 3.1).

Within the *Desulfobacterota*, 35/43 genomes belonging to 3 novel classes, 10 novel orders, and 7 novel families were identified, as well as multiple LRD families (B25-G16, BuS5, HGW-15, MLS-D, NaphS2, UBA2210, and UBA3084). Only 6/43 genomes belonged to the well-described families *Desulfovibrionaceae, Geopsychrobacteraceae, Smithellaceae*, and *Syntrophaceae*. (Figure 3e inside 3.1)

Finally, an extremely diverse community of *Patescibacteria* (13 different orders, 3 of which belonging to LRD orders, and 14 different families, including 6 novel and 2 LRD families), and *Nanoarchaeota* (2 orders including the LRD order CG07-land), and 15 different families, including 5 novel and 10 LRD families) were identified in the spring sediments (Figure 3F (Figure 3e inside 3.1)). A similar pattern of high proportion of novel and LRD families was identified throughout all other lineages (Figure 3.1). Therefore, in addition to expanding the number of novel lineages (classes, orders, and families), and greatly enriching available genomes in rare, poorly represented taxa, our results highlight the uniqueness and distinction of the microbial community thriving in Zodletone spring sediments, compared to present earth environments studied so far.

3.2 Hypoxic Waters

3.2.1 Overall Sequencing Overview and Diversity Patterns

Metagenomic sequencing of the oxygen-exposed overlaying water column community yielded 323 Gbp, 80.07% of which assembled into 3.6 Gbp contigs, with 3.1 Gbp contigs >1K. 883 genomes were binned, with only 114 remaining after dereplication. Of these, 62 belonged to families shared with the sediment community, while 52 were water specific. Genomes recovered from the water column belonged to a significantly lower number of phyla (n= 27), classes (n=37), orders (n=52), and families (n=79) when compared to the euxinic sediments (Table 3.1). The community exhibited a much lower level of novelty and rarity at the phylum, class, order, and family levels when compared to the sediment community (Figure 3.3).

3.2.2 Detailed Phylogenetic Analysis of Zodletone Water MAGs

Water-specific genomes (n=52) mostly belonged to well-characterized microbial lineages, e.g. class *Alphaproteobacteria* (5 genomes belonging to *Rhodobacteraceae* and *Rhodospirillaceae*, and 3 belonging to the uncultured lineages NBLK01 and Rs-D84), *Gammaproteobacteria* (9 genomes belonging to the lineages *Thiomicrospiraceae, Halothiobacillaceae, Acidithiobacillaceae, Burkholderiaceae, Chromatiaceae*, and *Methylothermaceae*, and 1 belonging to the uncultured lineage UBA9339), phylum *Camplylobacterota* (8 genomes, belonging to the families *Sulfurimonadaceae, Sulfurovaceae, and Sulfurospirillaceae*), *Firmicutes/Firmicutes_A* (4 genomes, and 6 genomes belonging to the *Bacilli*, and *Clostridia* classes, respectively), and well described families in the phyla *Bacteroidota* (*Flavobacteriaceae, Prolixibacteraceae, Paludibacteraceae, Marinilabiliaceae, Tannerellaceae, Marinifilaceae, Balneolaceae*), *Desulfobacterota* (Families *Geopsychrobacteraceae, Desulfuromonadaceae,), and Spriochaetota (Sphaerochaetaceae, Treponemataceae, Spirochaetaceae_B*) (Figure 3.1, Table 3.1).

Collectively, this demonstrates a pattern where the intrusion of oxygen is associated with a negative impact on novel and LRD lineages that are prevalent in the sediment, and the propagation of communities associated with well-characterized lineages within the bacterial tree of life.

3.3 Reductive sulfur processes dominate Zodletone spring sediment communities

A total of 149 genomes (28.9% of all genomes), belonging to 32 phyla, 51 classes, 69 orders, and 97 families were involved in at least one reductive sulfur processes (Figure 3.6, 3.7, Table 3.2). By comparison, only 21 sediment genomes (4.06% of all genomes) encoded at least one sulfur oxidation pathway (Figure 3.6, 3.7, Table 3.2). The reductive sulfur-community in the spring exhibited two unique traits: First, a majority of genomes encoding such capacities belonged to novel (47 genomes) or LRD (66 genomes) lineages (Figure 3.6, 3.7), and second: sulfite-, polysulfide-, thiosulfate-, and tetrathionate reduction capacities appears to be more prevalent than sulfate-reduction capacities in the sediment genomes.

3.3.1 Sulfate Reduction

Sulfate-reduction capacity was encoded in only 18 sediment genomes (Figure 3.6, 3.7), but exhibited a unique community composition, when compared to well-studied marine and terrestrial habitats [39, 48, 104, 109]. Sulfate-reduction capacities were observed in mostly previously undescribed or LRD lineages within the *Zixibacteria, Acidobacteriota* (members of family *UBA6911*, equivalent to *Acidobacteria* group 18), *Myxococcota, Bacteroidota, Planctomycetota*, candidate phylum *OLB16* (1 genome), as well as rare and novel lineages within the *Desulfobacterota* (Figure 3.6, 3.7, 3.8, Table 3.2). Organization of the sulfate reduction genes differed between different phyla, with *Myxococcota, Zixibacteria, OLB16*, and *Acidobacteriota* genomes encoding all genes for sulfate activation and reduction, dissimilatory sulfite reduction, as well as energy conservation on one locus, while *Desulfobacterota* genomes encoded genes for sulfate activation and reduction as well as energy conservation on one locus with genes for dissimilatory sulfite reduction on another, as previously observed in cultured

Desulfobacterota [72, 23, 114].

3.3.2 Sulfite Reduction

Sulfite (but not sulfate) reduction via the DsrAB+DsrC+DsrKMJOP system was identified in only 8 genomes belonging to 7 families within the phyla *Planctomycetes, Chloroflexota, Spirochaetota*, and *Desulfobacterota* (Figure 3.6, 3.7, 3.9, 3.13, Table 3.2). Gene organization of the dsr locus in the above 9 genomes differed between different phyla, with *Chloroflexota*, and *Spirochaetota* genomes encoding all genes for dissimilatory sulfite reduction (dsrABC plus dsrKMJOP) on one locus, while *Planctomycetota* and *Desulfobacterota* genomes showed a split dsr locus with dsrABC on one locus and dsrMKJOP on another (Figure 3.13).

On the other hand, sulfite-reduction capacity within Zodletone spring sediment solely via the Asr/Hdr system was rampant, being encountered in 104 genomes belonging to 28 phyla, 43 (8 novel and 9 LRD) classes, 56 (18 novel, and 12 LRD) orders, and 72 (31 novel and 25 LRD) families (Figure 3.6, 3.7, 3.14, Table 3.2), with a gene organization of the asr locus adjacent to the hdr locus in the majority of genomes (Figure 3.14). Asr-encoding genomes in the sediment included members of previously undescribed and LRD lineages within the *Chloroflexota, Desulfobacterota. Planctomycetota, and Bacteroidota*. The capacity was also rampant in the yet-uncultured bacterial phyla, many of which have fairly limited global distribution (e.g. the candidate phyla CSSED10-310, FCPU426, RBG-13-66-14, SM23-31, SZUA-182, UBP14, I, and I). Interestingly, all genomes belonging to the novel phylum Krumholzibacteriota, recently described from the spring sediment [99], encoded complete anaerobic sulfite reductase systems. Zodletone dissimilatory sulfite reductase (Figure S6a) and the anaerobic sulfite reductase (Figure 3.14) sequences clustered with reference sequences from the same phylum, generally showing no evidence of LGT.

3.3.3 Sulfur (polysulfide) reduction

Sulfur (polysulfide) reduction capacities were observed in twenty Zodletone sediment genomes that encoded psrABC genes (Figure 3.6, 3.7, 3.10, 3.15,**Table S2**). These genomes belonged mostly to previously undescribed and LRD families within the phyla *Bacteroidota, Desulfobacterota, Myxococota, Acidobacterota, Chloroflexota, and Campylobacterota* (Figure 3.7). In addition, representatives of the cytoplasmic sulfurhydrogenase I (HydABCD system), and/or II (ShyABCD system) were identified in 119 Zodletone sediment genomes (Figure 3.6). However, as explained above, direct involvement of these enzymes in an ETS-associated respiration is not yet clear.

3.3.4 Thiosulfate Disproportionation and Reduction

The quinone-dependent membrane-bound molybdopterin-containing thiosulfate reductase PhsABC was encoded in 11 genomes belonging to 6 phyla, with *Bacteroidota* representing the major phsABC-encoding phylum (4 genomes) (Table S2, Figure 3.11). Within these genomes, only two (a *Chloroflexota* family UBA6092 genome, and a *Desulfatiglandales* family HGW15 genome) also encoded a dissimilatory sulfite reductase (the Asr system) akin to the *Gammaproteobacteria* thiosulfate disproportionating pure culture members [84], where

the final products of thiosulfate disproportionation are expected to be only hydrogen sulfide (Figure 3.6, 3.7, 3.11, Table 3.2). On the other hand, 5 of the 11 phsABC-encoding Zodletone genomes also encoded the sulfite dehydrogenase SoeABC system, akin to *Desulfobacterota* and *Firmicutes* pure culture members, where the final products of thiosulfate disproportionation are expected to be both hydrogen sulfide and sulfate [23, 43] (Figure 3.6, 3.7, 3.11, Table 3.2).

In addition to the phsABC system, 14 Zodletone genomes belonging to 6 phyla (*Desulfobacterota, Acidobacteriota, Chloroflexota, Bacteroidota, Spirochaetota*, and *Myxococcota*) encoded a rhodanase-like enzyme [EC: 2.8.1.1 or EC: 2.8.1.3] for thiosulfate disproportionation, as well as enzymes for both sulfite oxidation (by means of reversal of sulfate reduction via Sat+AprAB, or the sulfite dehydrogenase SoeABC), and sulfite reduction (via the dissimilatory sulfite reductases Dsr or Asr), where the final products of thiosulfate disproportionation are expected to be both hydrogen sulfide and sulfate (Figure 3.6, 3.7, 3.11, Table 3.2).

3.3.5 Tetrathionate Reduction

Tetrathionate reduction capacities were identified in 105 sediment genomes. Seventy-three Zodletone sediment genomes encoded the octaheme tetrathionate reductase (OTR) enzyme. These genomes belonged to 14 phyla with major contribution from *Bacteroidota* (30 genomes), *Chloroflexota* (10 genomes), and *Desulfobacterota* (10 genomes) (Table 3.2, Figure 3.6, 3.7, 3.17). In addition to Otr, 68 Zodletone genomes encoded the Ttr enzyme system. These genomes belonged to 14 phyla with major contribution from *Chloroflexota* (22 genomes), and *Desulfobacterota* (20 genomes) (Table 3.2, Figure 3.6, 3.7, 3.12). As shown previously in *Salmonella typhimurium* [84], in presence of means for thiosulfate disproportionation/reduction and sulfite reduction, the thiosulfate produced as a result of tetrathionate reduction could be further reduced to sulfide. Out of the 105 sediment genomes encoding the Otr, and/or Ttr enzymes, only 12 genomes also encoded thiosulfate and sulfite reduction enzymes. These genomes belonged to the phyla *Acidobacteriota, Chloroflexota, Desulfobacterota, Myxococcota*, and *Spirochaetota* (Table 3.2).

3.4 Substrates supporting sulfidogenic capacities at Zodletone Spring

Within lineages mediating reductive sulfur processes in Zodletone sediments (n=98), a wide range of substrates supporting sulfidogenesis were identified (Table 3.3, Figure 3.7). These included hexoses (26-87% of sulfidogenic lineages), pentoses (30-41% of sulfidogenic lineages), amino acids and peptides (39% of lineages), short chain fatty acids, e.g. lactate, propionate, butyrate, and acetate (22-73% of lineages), long chain fatty acids (29% of lineages), aromatic hydrocarbons (3% of lineages), and short chain alkanes (6% of lineages). Autotrophic capacities with hydrogen as the electron donor were identified in 28% of sulfidogenic lineages.

3.5 Transcriptomic analysis

Transcriptional expression of genes involved in S-species reduction/disproportionation was analyzed, and the identity of the active sulfur-reducing community in the spring sediment was

examined (Figure 3.6). All S-species reduction/ disproportionation genes discussed above were identified in the metatranscriptomic dataset, and transcripts belonging to 51 different phyla were identified. Analysis of the spring sediment revealed the transcription of both the Dsr and Asr systems for sulfite reduction with contributions from *Chloroflexota, Planctomycetota, Desulfobacterota, Bacteroidota, Fermentibacterota, Acidobacteriota, CSSED10-310, Actinobacteriota, Spirochaetota, WOR-3*, and *Fibrobacterota* (Asr), and *Desulfobacterota*, *Acidobacteriota, Zixibacteria*, and *Myxococcota* (Dsr). Sulfate reduction genes (Sat, AprAB, and QmoABC) were also transcribed with major contribution from *Desulfobacterota, Myxococcota, Zixibacteria*, and *Acidobacteriota*.

Total transcription levels of the Asr system were 4-times higher than the Dsr system, consistent with the higher number of Zodletone sediment genomes encoding the Asr system compared to the Dsr system. Transcription of the thiosulfate disproportionating rhodanese-like enzyme [EC: 2.8.1.1 or EC: 2.8.1.3] was detected in the phyla *Desulfobacterota, Actinobacteriota, Firmicutes_A, Chloroflexota, Fibrobacterota, Planctomycetota, Spirochaetota, Bacteroidota, Halobacteriota*, and *Acidobacteriota*, while the transcription of the thiosulfate reductase phsABC was detected in the phyla *Actinobacteriota* and *Bacteroidota*. Transcription of the tetrathionate reduction genes ttrABC was detected in the phyla *Desulfobacterota, Actinobacteriota, Bacteroidota, Chloroflexota, Acidobacteriota*, and *Spirochaetota*, while the octaheme tetrathionate reductase otr transcription was detected in *Desulfobacterota, Bacteroidota, Myxococcota, UBP7A*, and *Chloroflexota*.

Finally, the transcription of psrABC for polysulfide reduction was detected majorly in the phyla *Bacteroidota, Desulfobacterota*, and *Campylobacterota*, while transcription of the cytoplasmic sulfurhydrogenases I and II (hyd/shy systems) was identified in the phyla *Actinobacteriota, Chloroflexota, Planctomycetota, Myxococcota, Acidobacteriota, Bacteroidota*, and *Desulfobacterota*.

3.6 Oxidative sulfur processes dominate Zodletone water community

In contrast to sediment communities, reductive sulfur-processes were identified in only 25 (21.92%) water genomes, as opposed to 149 (29%) sediment genomes (Figure 3.6, 3.7, Table 3.2). Dissimilatory sulfate reduction to sulfide capacity was completely absent in water genomes. The capacity for dissimilatory sulfite reduction via the Dsr system was absent, and the Asr system was only encoded in 7 water genomes. Thiosulfate reduction/disproportionation capacity to sulfide and sulfate (PhsABC + SoeABC, and/or Rhodanase + Dsr/Asr + SoeABC/SorAB) was encoded in only four genomes, all of which also encoded the capacity for tetrathionate reduction (via Otr and/or ttrABC). Finally, respiratory polysulfide reduction (via PsrABC) was encoded in 19 genomes. In all cases, the reductive sulfur community in water was a subset of the sediment community.

In contrast, oxidative sulfur processes dominated the water community, with pathways encoding sulfide, sulfur, thiosulfate, tetrathionate, and/or sulfite oxidation to sulfate present in 59/114 genomes (51.8% of all water genomes) belonging to 13 phyla, 16 classes, 25 orders, and 43 families. The oxidative sulfur community in the water belonged to mostly well-characterized lineages (Figure 3.6, 3.7, Table 3.2). Only 8 and 10 genomes involved in oxidative sulfur processes belonged to novel, and LDR families, respectively.

A complete SOX system, putatively mediating oxidation of a wide range of reduced sulfur-species to sulfate was encoded in genomes belonging to well-characterized families within the *Proteobacteria* (11 genomes total belonging to families *Acidithiobacillaceae, Burkholderiaceae, Halothiobacillaceae, Rhodobacteraceae,* and *Thiomicrospiraceae*) and *Campylobacterota* (3 genomes in the family *Sulfurimonadaceae*) (Figure 3.6, 3.7, Table 3.2).

3.6.1 Sulfide oxidation to sulfur and sulfite

Thirty nine water genomes encoded the sulfide dehydrogenase fccAB [EC: 1.8.2.3] and/or the sulfide:quinone oxidoreductase Sqr [EC: 1.8.5.4] both known to oxidize sulfide to sulfur/ polysulfide (Figure 3.6, 3.7, Table 3.2). These genomes belonged to the phyla *Bacteroidota* (14 genomes in the well characterized families *Chlorobiaceae, Prolixibacteraceae*, and *Paludibacteracaeae*, as well as the uncultured families NBLH01, UBA1556, DTU049, and F082 in the order *Bacteriodales*), *Proteobacteria* (13 genomes in the families *Acidithiobacillaceae, Burkholderiaceae, Chromatiaceae, Halothiobacillaceae, Methylothermaceae, Rhodobacteraceae, Thiomicrospiraceae*), *Campylobacterota* (8 genomes in the families *Sulfurimonadaceae, Sulfurospirillaceae, Sulfurovaceae*), in addition to three genomes in the families *Anaerolineaceae, Geopsychrobacteraceae*, and *UBA2242* within the phyla *Chloroflexota, Desulfobacterota, and Marinisomatota*, respectively, and one genome belonging to a novel *Thermodesulfovibrionales* family (*Nitrospirota*). Only two of the above thirty-nine genomes (one *Proteobacteria* genome and one *Nitrospirota* genome) encoded the capacity to further oxidize the sulfur/polysulfide to sulfite via the reversal of the Dsr system (encompassing the full Dsr system dsrAB+dsrC+dsrMKJOP, in addition to the genes dsrEFH, tusA, and rhdA).

3.6.2 Sulfite oxidation to sulfate

A total of twenty-six water genomes encoded the capacity for sulfite oxidation to sulfate via the reversal of AprAB+QmoABC system (1 *Bacteroidales* genome), the sulfite dehydrogenase (quinone) SoeABC [EC: 1.8.5.6] (22 genomes belonging to the order *Bacteroidales*, and the families *Acidithiobacillaceae, Burkholderiaceae, Chromatiaceae, Dethiosulfatibacteraceae, Halothiobacillaceae, Methylothermaceae, Rhodobacteraceae, Thiomicrospiraceae* within *Proteobacteria*, the families *Sulfurimonadaceae*, *Sulfurospirillaceae, Sulfurovaceae* within *Campylobacterota*, the *Syntrophales* family *UBA3084*, and a novel *Thermodesulfovibrionales* family (*Nitrospirota*)), or the sulfite dehydrogenase (cytochrome) SorAB [EC: 1.8.2.1] (3 genomes total within the families *Chromatiaceae*, *Halothiobacillaceae* (*Proteobacteria*), and UBA12059 (*Spirochaetota*)) (Figure 3.6, 3.7, Table 3.2).

3.6.3 Thiosulfate Oxidation

Eight water genomes encoded thiosulfate to tetrathionate oxidation capacities via either the thiosulfate dehydrogenase tsdA [EC: 1.8.2.2] (7 genomes belonging to the families *Sulfurimonadaceae* within *Campylobacterota*, and *Rhodobacteraceae, Burkholderiaceae, Halothiobacillaceae, Thiomicrospiraceae* within *Proteobacteria*), or the thiosulfate dehydrogenase (quinone) doxAD [EC: 1.8.5.2] (1 *Flavobacteriaceae* genome) (Figure 3.6, 3.7, Table 3.2). Two of these 8 genomes (1 *Rhodobacteraceae*, and 1 *Halothiobacillaceae* genomes) also encoded tetrathionate hydrolase (tetH) [53] that is known to cleave tetrathionate to thiosulfate,

sulfur, and sulfate (Figure 3.6, 3.7, Table 3.2). Simultaneous identification of the SOX system and both forms of sulfide dehydrogenase (fccAB and Sqr) imply that these two genomes encode the capacity for complete thiosulfate oxidation to sulfate.

3.6.4 Tetrathionate oxidation

In addition to the above two genomes, ten other water genomes encoded tetrathionate hydrolase, but with no other means of thiosulfate and sulfide oxidation capacities (Figure 3.6, 3.7, Table 3.2). Surprisingly, tetH (without other means of thiosulfate or sulfide oxidation) was also encoded in 100 sediment genomes, belonging to 26 phyla, 37 classes, 49 orders, and 66 families (including 23 novel families). Only nine of these genomes (belonging to 9 families including 4 novel ones) showed tetH transcriptional levels above 1 (Figure 3.6, 3.7, Table 3.2). However, the exact function of tetrathionate hydrolase in these organisms is not entirely clear, as the subsequent steps of oxidation could not be identified.

3.7 Additional metabolic capacities in Zodletone spring sediments

In addition to reductive sulfur processes, strict fermentative capacities were highly prevalent in sediment genomes (Table 3.3) being identified in 100 of the 291 lineages studied. On the other hand, a dearth of aerobic (only 38 lineages), nitrate (only 65 lineages encoded dissimilatory nitrite reduction to ammonium, with 2 of which also encoding the suite of genes for denitrification), Fe3+ respiration (8 lineages), or chemolithotrophic nitrifying (only 1 lineage encoded the combination of ammonia monooxygenase and hydroxylamine dehydrogenase), and photosynthetic capacities were identified (Figure 3.1.a, Table 3.3). Strict fermentative lineages mediate the degradation a wide range of substrates, e.g. sugars (89 of the 100 fermentative lineages), amino acids (85 of the 100 fermentative lineages), short chain fatty acids (37 of the 100 fermentative lineages), complex carbohydrates (36 of the 100 fermentative lineages), long chain fatty acid oxidation (2 lineages), and short chain alkanes (1 lineage) (Table 3.3), producing a wide range of fermentative end products including lactate, formate, acetate, ethanol, succinate, and hydrogen. Primary productivity in the spring sediments appears to be mostly mediated via hydrogen utilization coupled to either sulfur-cycle intermediates reduction (27 lineages, Table 3.3), or to CO2 fixation by hydrogenotrophic methanogens and acetogens using the Wood-Ljungdahl pathway (8 lineages, Table 3.3).

Table 3.1: List of all genomes analyzed in this study
List of all genomes analyzed in this study with their NCBI Assembly accession numbers, taxonomic classification, sequencing statistics, and general genomic features

Table S1. List of all genomes analyzed in this study with their NCBI Assembly accession numbers, taxonomic classification, sequecning statistics, and general genomic features.

Genome	NCBI assembly accession number	% completeness	% contamination	Gtdb classification							RED value	Family Abundance in Gtdb	Median genome coverage	Number of Contigs	Assembly n50	Assembly Size (bp)	Expected Genome Size (bp)	GC %	Number of Genes	Coding %	Avg Gene Length (bp)	Number of ribosomal RNA genes			Number of tRNA genes	Quality Tier
				Domain	Phylum	Class	Order	Family	Genus	Species												5s rRNA	16s rRNA	23s rRNA		
Zod_maxbin.0146	JAFGAJ000000000	71.72	8.12	Bacteria	Acidobacteriota	Aminicenantia	Aminicenantales	Aminicenantaceae			0.786	Abundant	52.34	605	8132	3097255	4318537	42.5	2968	89.44	933	1	0	0	35	MQD
Zod_Metabat.553	JAFGNQ000000000	84.39	6.48	Bacteria	Acidobacteriota	Aminicenantia	Aminicenantales	Aminicenantaceae			0.786	Abundant	10.38	498	10616	4326490	5126780	48.6	3861	89.94	1008	1	0	0	28	MQD
Zod_Metabat.480	JAFGMO000000000	90.37	2.56	Bacteria	Acidobacteriota	Aminicenantia	Aminicenantales	Novel:ZNF011			0.705	Novel	17.18	104	76730	4989209	5520869	45.8	4093	90.36	1101	1	0	0	51	MQD
Zod_maxbin.0003	JAFGAB000000000	83.3	1.33	Bacteria	Acidobacteriota	Aminicenantia	Aminicenantales	RBG-16-66-30	RBG-16-66-30		0.941	Rare	635.54	619	6653	2657141	3189845	66.8	2653	93.28	934	0	1	0	29	MQD
Zod_maxbin.0345_1	JAFGAV000000000	89.4	4.33	Bacteria	Acidobacteriota	Aminicenantia	Aminicenantales	UBA4085			0.762	Rare	19.06	123	33522	2374780	2656353	62.2	2130	91.98	1026	1	1	0	37	MQD
Zod_Metabat.1003	JAFGBC000000000	71.03	2.78	Bacteria	Acidobacteriota	Aminicenantia	Aminicenantales	UBA4085			0.758	Rare	332.73	370	6033	2053444	2890953	66.7	1976	94.15	978	0	0	0	22	MQD
Zod_Metabat.1233	JAFGEN000000000	85.3	1.71	Bacteria	Acidobacteriota	Aminicenantia	Aminicenantales	UBA4085			0.852	Rare	95.54	373	9998	2931239	3436388	61.6	2666	94.07	1034	0	0	0	29	MQD
Zod_Metabat.860	JAFGRZ000000000	62.77	2.14	Bacteria	Acidobacteriota	Aminicenantia	Aminicenantales	UBA8522	UBA8522		0.855	Rare	23.19	345	6728	2127094	3388711	58.9	2028	92.17	967	0	0	0	17	MQD
Zod_Metabat.571	JAFGNX000000000	76.54	3.42	Bacteria	Acidobacteriota	Aminicenantia	UBA2199	UBA2199	UBA876		0.917	Abundant	17.51	216	12209	2049147	2677224	55.6	1978	92.99	963	0	0	0	32	MQD
Zod_Metabat.875	JAFGSF000000000	86.07	0	Bacteria	Acidobacteriota	Aminicenantia	UBA2199	UBA2199			0.879	Abundant	60.34	66	54825	2208932	2566437	51.4	2080	93.44	992	1	0	0	39	MQD
Zod_Metabat.920	JAFGST000000000	79.46	0.85	Bacteria	Acidobacteriota	Aminicenantia	UBA2199	UBA2199	UBA2199		0.925	Abundant	13.11	271	12032	2570893	3235456	63.7	2484	92.22	955	0	0	0	38	MQD
Zod_Metabat.1058	JAFGBY000000000	85.7	2.56	Bacteria	Acidobacteriota	B3-B38	Novel:ZNO05	Novel:ZNF012			0.466	Novel	11.20	178	19392	2332997	2722284	41.4	2114	92.23	1018	2	0	0	28	MQD
Zod_Metabat.850	JAFGRT000000000	91.88	5.13	Bacteria	Acidobacteriota	UBA6911	Novel:ZNO06	Novel:ZNF013			0.492	Novel	14.36	237	33417	4746816	5166321	60.7	3868	88.62	1088	0	0	0	42	MQD
Zod_maxbin.0255	JAFGAO000000000	73.17	2.64	Bacteria	Acidobacteriota	UBA6911	UBA6911	UBA6911	UBA6911		0.923	Rare	28.22	298	23699	3624899	4954078	57.6	3220	87.66	987	1	0	0	33	MQD
Zod_Metabat.240	JAFGIY000000000	95.67	5.98	Bacteria	Acidobacteriota	UBA6911	UBA6911	UBA6911			0.844	Rare	61.55	258	48489	6513361	6808154	52.3	5615	87.11	1011	1	0	0	60	MQD
Zod_Metabat.919	JAFGSS000000000	95.25	5.13	Bacteria	Acidobacteriota	UBA6911	UBA6911	UBA6911			0.838	Rare	27.58	233	21052	3248839	3410855	66.5	3001	92.00	996	1	1	0	35	MQD
Zod_Metabat.95	JAFGTD000000000	93.11	3.42	Bacteria	Acidobacteriota	UBA6911	UBA6911	UBA6911	UBA6911		0.944	Rare	13.46	343	21988	5449249	5852485	51.8	4791	86.74	987	1	0	0	47	MQD
Zod_Metabat.903	JAFGSN000000000	94.11	5.98	Bacteria	Acidobacteriota	Vicinamibacteria_A	Fen-336	Fen-336			0.788	Rare	43.65	247	27424	3977865	4226825	62.6	3430	90.65	1051	1	0	0	44	MQD
Zod_Metabat.708	JAFGPU000000000	76.15	2.14	Bacteria	Actinobacteriota	Acidimicrobiia	Acidimicrobiales	Novel:ZNF014			0.625	Novel	19.04	555	6339	3200401	4202759	73.4	3410	92.67	870	1	0	0	17	MQD
Zod_Metabat.1092	JAFGCH000000000	89.74	3.09	Bacteria	Actinobacteriota	Acidimicrobiia	UBA5794	UBA11373			0.774	Rare	18.71	161	25459	2441669	2720826	70.9	2488	92.74	910	1	0	0	45	MQD
Zod_Metabat.1034	JAFGBM000000000	92.49	0	Bacteria	Actinobacteriota	Actinomycetia	Actinomycetales	Demequinaceae			0.850	Abundant	42.67	15	212669	1885200	2038274	66.1	1802	93.60	979	1	0	0	43	MQD
Zod_Metabat.615	JAFGOK000000000	74.89	3.2	Bacteria	Actinobacteriota	Actinomycetia	Mycobacteriales	Micromonosporaceae	Dactylosporangium		0.883	Abundant	27.24	790	7077	4938482	6594314	67.4	4731	89.54	935	0	0	0	41	MQD
Zod_maxbin.0135_3	JAFGAG000000000	78.33	1.25	Bacteria	Actinobacteriota	Coriobacteriia	OPB41	UBA2279	UBA7930		0.921	Abundant	55.83	84	25368	1680009	2144784	66.4	1684	93.83	936	1	0	0	30	MQD
Zod_Metabat.552	JAFGNP000000000	87.56	4.5	Bacteria	Actinobacteriota	Coriobacteriia	OPB41	UBA2279	UBA6100		0.919	Abundant	11.86	142	19047	1645470	1879249	64	1703	93.14	900	1	0	0	43	MQD
Zod_Metabat.866	JAFGSD000000000	78.9	1.42	Bacteria	Actinobacteriota	Coriobacteriia	OPB41	UBA2279	UBA2279		0.907	Abundant	9.05	288	8351	1952477	2474622	61.8	2168	92.82	836	1	0	0	36	MQD
ZodW_maxbin.211	JAFGUS000000000	91.39	0.83	Bacteria	Actinobacteriota	Coriobacteriia	OPB41	UBA2279	UBA2272		0.930	Abundant	11.72	234	18710	2142970	2344863	67.6	2257	93.10	884	0	0	0	54	MQD
ZodW_maxbin.228	JAFGUU000000000	78.68	7.68	Bacteria	Actinobacteriota	Coriobacteriia	OPB41	UBA2279	UBA7930		0.913	Abundant	9.76	268	19011	2036127	2587858	65.7	2179	92.26	862	0	0	0	46	MQD
ZodW_Metabat.125	JAFGVD000000000	97.5	2.92	Bacteria	Actinobacteriota	Coriobacteriia	OPB41	UBA2279	UBA2279		0.908	Abundant	12.52	49	75379	2133228	2187926	61.9	2138	93.14	929	1	0	0	45	MQD
Zod_Metabat.1040	JAFGBQ000000000	80.6	9.09	Bacteria	Actinobacteriota	RBG-13-55-18	Fen-727	Novel:ZNF015			0.711	Novel	10.99	260	11114	2233910	2771600	50.1	2161	88.26	912	0	0	0	30	MQD
Zod_Metabat.502	JAFGMY000000000	84.62	2.14	Bacteria	Actinobacteriota	RBG-13-55-18	Fen-727	Novel:ZNF015			0.713	Novel	16.00	178	18827	2471909	2921188	52.2	2269	87.89	958	1	0	0	42	MQD
Zod_Metabat.1188	JAFGDU000000000	97.01	0.85	Bacteria	Actinobacteriota	RBG-13-55-18	RBG-13-55-18	RBG-13-55-18	SURF-21		0.916	Rare	14.00	187	29165	3910073	4030588	60.1	3543	87.72	968	1	1	0	75	MQD
Zod_Metabat.188	JAFGIH000000000	72.9	0	Bacteria	Actinobacteriota	Thermoleophilia	RBG-16-64-13	RBG-16-64-13			0.905	Rare	9.90	873	5176	4274456	5863451	64.4	4657	92.38	848	0	0	0	41	MQD
Zod_Metabat.495	JAFGMT000000000	91.75	10.2	Bacteria	Actinobacteriota	Thermoleophilia	RBG-16-64-13	RBG-16-64-13			0.901	Rare	17.94	203	31530	3350424	3651688	64.7	3260	92.13	947	1	0	0	62	MQD
Zod_Metabat.264	JAFGJG000000000	95.09	2.3	Bacteria	Actinobacteriota	Thermoleophilia	Solirubrobacterales	Thermoleophilaceae			0.809	Rare	15.97	193	28566	3462899	3641707	72.5	3655	95.22	902	1	0	0	48	MQD
Zod_maxbin.0406_1	JAFGAW000000000	81.61	1.58	Bacteria	Actinobacteriota	Thermoleophilia	UBA2241	UBA2241	UBA2241		0.877	Abundant	18.65	295	15649	2494662	3056809	71.6	2455	89.35	908	1	0	0	29	MQD
Zod_Metabat.1146	JAFGDA000000000	85.45	3.94	Bacteria	Actinobacteriota	UBA1414	UBA1414	UBA1414			0.837	Abundant	12.15	220	9349	1651713	1932958	40.8	1630	89.47	907	0	0	0	33	MQD
Zod_Metabat.463	JAFGMJ000000000	77.27	3.64	Bacteria	Actinobacteriota	UBA1414	UBA1414	UBA1414			0.830	Abundant	10.17	280	6611	1611886	2086044	37.4	1561	91.49	945	0	0	0	31	MQD
Zod_Metabat.1000	JAFGAZ000000000	79.91	1.4	Archaea	Aenigmatarchaeota	Aenigmatarchaeia	Aenigmatarchaeales	Aenigmatarchaeaceae			0.634	Rare	23.06	21	45990	694169	868689	41.4	843	93.83	773	0	0	1	44	MQD
Zod_Metabat.1300	JAFGFG000000000	92.06	0	Archaea	Aenigmatarchaeota	Aenigmatarchaeia	QMZP01	Novel:ZNF01			0.512	Novel	24.85	9	150048	929379	1009536	46.9	1056	93.51	823	0	1	0	44	MQD
Zod_Metabat.932	JAFGSV000000000	83.02	0	Archaea	Aenigmatarchaeota	Aenigmatarchaeia	QMZP01	QMZP01			0.707	Rare	13.84	35	51596	1238070	1491291	54.1	1285	90.63	873	1	0	0	36	MQD
Zod_Metabat.1100	JAFGCI000000000	89.25	0	Archaea	Aenigmatarchaeota	Aenigmatarchaeia	QMZP01	QMZT01			0.632	Rare	40.82	11	209214	1176130	1317793	42.5	1190	92.80	917	1	1	1	39	MQD
Zod_Metabat.1163	JAFGDH000000000	86.38	0.93	Archaea	Aenigmatarchaeota	Aenigmatarchaeia	QMZP01	QMZT01			0.620	Rare	15.03	43	33415	1137756	1317152	48.1	1208	92.57	872	1	1	2	36	MQD
Zod_maxbin.0093	JAFGAE000000000	84.74	7.87	Archaea	Altarchaeota	Altarchaeia	IMC4	QMZM01			0.778	Rare	75.03	161	28662	1585831	1871408	52	1644	92.02	888	2	0	0	32	MQD
Zod_Metabat.1191	JAFGDV000000000	87.08	2.48	Archaea	Altarchaeota	Altarchaeia	IMC4	QMZM01			0.775	Rare	67.66	46	45205	1550521	1780571	46.8	1696	94.47	864	1	1	0	22	MQD
Zod_Metabat.755	JAFGQM000000000	83.21	0.93	Archaea	Altarchaeota	Novel:ZNC01	Novel:ZNO01	Novel:ZNF02			0.255	Novel	9.34	144	11135	1407565	1691582	50.7	1693	93.82	780	1	0	0	33	MQD
Zod_Metabat.349	JAFGKS000000000	78.15	7.15	Bacteria	Armatimonadota	UBA10988	Novel:ZNO07	Novel:ZNF016			0.452	Novel	11.43	662	7242	4221306	5401543	61.7	4423	89.80	857	0	1	0	51	MQD
Zod_Metabat.460	JAFGMH000000000	86.45	7.94	Archaea	Asgardarchaeota	Heimdallarchaeia	Novel:ZNO02	Novel:ZNF03			0.363	Novel	46.81	88	80509	3792542	4386977	31.5	3486	87.59	953	0	0	0	46	MQD
Zod_Metabat.1044	JAFGBS000000000	94.39	4.21	Archaea	Asgardarchaeota	Lokiarchaeia	CR-4	AMARA-1	AMARA-1		0.900	Rare	29.42	36	303549	3760042	3983517	35.3	3377	88.82	989	0	1	1	46	MQD
Zod_Metabat.1389	JAFGGO000000000	85.98	2.34	Archaea	Asgardarchaeota	Lokiarchaeia	CR-4	SOKP01			0.831	Abundant	18.06	190	33582	3999874	4652098	35.1	3788	85.88	907	0	0	2	33	MQD
Zod_Metabat.578	JAFGOA000000000	90.65	5.14	Archaea	Asgardarchaeota	Lokiarchaeia	CR-4	SOKP01			0.779	Abundant	33.75	238	26265	3880929	4281223	26.2	3603	85.17	917	0	1	0	65	MQD
Zod_Metabat.1055	JAFGBX000000000	81.13	3.74	Archaea	Asgardarchaeota	Lokiarchaeia	Novel:ZNO03	Novel:ZNF04			0.456	Novel	10.57	476	13666	5105683	6293212	60.7	4731	89.67	968	0	0	0	58	MQD
Zod_maxbin.0292	JAFGAR000000000	86.92	4.42	Archaea	Asgardarchaeota	Thorarchaeia	Thorarchaeales	Thorarchaeaceae	MP8T-1		0.909	Abundant	26.35	215	114129	3466336	3987961	42.3	3331	90.25	939	0	0	1	47	MQD
Zod_Metabat.1054	JAFGBW000000000	85.69	2.36	Bacteria	Aureabacteria	Novel:ZNC17	Novel:ZNO08	Novel:ZNF017			0.419	Novel	19.42	300	14417	3137840	3661851	43.6	2851	89.03	980	1	1	0	43	MQD
Zod_Metabat.284	JAFGJP000000000	71.51	1.75	Bacteria	Aureabacteria	Novel:ZNC17	Novel:ZNO08	Novel:ZNF017			0.438	Novel	13.21	327	6879	1969107	2753611	44.7	2018	89.27	871	0	1	0	25	MQD
Zod_Metabat.1009	JAFGBE000000000	82.43	2.7	Bacteria	Aureabacteria	UBA6266	UBA6266	UBA6266	UBA6266		0.939	Rare	9.39	199	10757	1612344	1956016	44.9	1638	94.33	929	1	1	0	38	MQD
Zod_Maxbin.0334	JAFGAU000000000	71.12	5.17	Bacteria	B130-G9	B130-G9	B130-G9	B130-G9	B130-G9		0.862	Rare	20.77	114	60171	2639640	3711530	57.5	2184	89.63	1083	0	0	0	42	MQD
Zod_Metabat.233	JAFGIT000000000	85.01	0.35	Bacteria	B130-G9	B130-G9	B130-G9	B130-G9			0.842	Rare	8.75	423	8976	3190843	3753491	54.5	2796	90.17	1029	0	0	0	41	MQD
Zod_Metabat.1203	JAFGDZ000000000	97.62	3.02	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	BBW3	UBA5206		0.979	Abundant	43.02	82	68692	4077890	4177310	43.7	3360	89.52	1087	0	0	0	53	MQD
ZodW_Metabat.241	JAFGWH000000000	95.95	2.79	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	BBW3	UBA5206		0.979	Abundant	45.59	112	57657	3974724	4142495	43.7	3292	89.44	1080	0	0	0	53	MQD
ZodW_Metabat.234	JAFGWG000000000	96.24	2.69	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	DTU049	BM518		0.949	Abundant	15.83	254	23862	3854161	4004739	37.7	3282	90.79	1066	1	0	0	39	MQD
ZodW_Metabat.54	JAFGXS000000000	93.26	2.96	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	F082	SZUA-53		0.886	Abundant	31.99	93	80686	3037131	3256628	38.6	2617	91.60	1063	0	0	0	49	MQD
ZodW_Metabat.88	JAFGYB000000000	93.17	1.88	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	F082	SZUA-53		0.887	Abundant	29.92	74	97882	3100855	3328169	44.2	2681	91.62	1060	0	0	0	37	MQD
Zod_Metabat.1032	JAFGBL000000000	86.02	2.35	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	FEN-979			0.741	Rare	13.48	314	24690	4466147	5191987	41	3678	91.39	1110	1	0	0	36	MQD
Zod_Metabat.1433	JAFGHD000000000	97.85	1.61	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	FEN-979			0.784	Rare	18.81	197	32910	3674376	3755111	50.9	2976	91.41	1129	1	0	0	38	MQD
Zod_Metabat.457	JAFGME000000000	94.21	8.39	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	FEN-979			0.751	Rare	13.45	317	21583	4356747	4624506	45.6	3494	92.24	1150	1	0	0	29	MQD
Zod_Metabat.574	JAFGNY000000000	70.66	0	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	FEN-979	QYOJ01		0.922	Rare	10.67	405	8263	2820851	3992147	47.4	2577	94.55	1035	0	0	0	21	MQD
Zod_Metabat.612	JAFGOH000000000	73.62	0.48	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	GCA-2748055			0.863	Rare	282.08	69	68339	2388154	3243893	46.4	1930	93.15	1153	1	0	0	24	MQD
Zod_Metabat.664	JAFGOZ000000000	84.05	0	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	GCA-2748055			0.775	Rare	29.15	727	25675	9271116	11030477	35.8	7862	88.65	1045	2	0	0	72	MQD
ZodW_Metabat.292	JAFGWU000000000	90	1.67	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	GCA-2748055			0.861	Rare	14.55	102	66306	3481259	3868066	47.8	2692	92.84	1201	1	0	0	31	MQD
ZodW_Metabat.319	JAFGXD000000000	86.56	1.08	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	GWF2-38-335	GWF2-38-335		0.858	Rare	12.10	192	27576	3582342	4138565	34.2	2850	92.67	1165	1	0	0	30	MQD
ZodW_Metabat.94	JAFGYE000000000	97.85	2.96	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	Marinifilaceae	Labilibaculum		0.992	Abundant	19.67	120	77489	4711564	4815088	36.2	3865	87.68	1069	1	0	0	63	MQD
Zod_Metabat.1042	JAFGBR000000000	91.3	1.09	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	Marinilabiliaceae	Breznakibacter		0.882	Abundant	37.96	82	84401	3911004	4283685	33.8	3005	91.27	1188	0	0	0	44	MQD
ZodW_Metabat.248	JAFGWJ000000000	96.2	3.04	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	Marinilabiliaceae	Breznakibacter	Breznakibacter xylanolytica	N/A	Abundant	13.97	125	43618	3607881	3750396	47.1	3001	86.68	1042	1	0	0	48	MQD
ZodW_Metabat.182	JAFGVU000000000	97.62	6.3	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	ML635J-15	Bact-19		0.945	Abundant	21.80	264	28471	4441848	4550141	34.2	3524	90.13	1136	2	0	0	38	MQD
Zod_Metabat.545	JAFGNL000000000	94.52	2.15	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	NBLH01	NBLH01		0.874	Rare	17.49	278	21168	3697324	3911684	27.9	3203	89.33	1031	0	0	0	23	MQD
ZodW_Metabat.217	JAFGWC000000000	98.71	3.36	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	NBLH01	NBLH01		0.874	Rare	85.07	159	48883	3947023	3998605	27.8	3374	89.37	1046	0	0	0	35	MQD
Zod_Metabat.325	JAFGKI000000000	92.15	4.3	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	Paludibacteraceae	UBA4363		0.880	Abundant	12.45	211	15665	2273582	2467262	35.3	2124	89.34	956	0	1	0	53	MQD
ZodW_Metabat.166	JAFGVL000000000	89.52	1.08	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	Paludibacteraceae	Paludibacter_A		0.862	Abundant	26.78	130	27265	2013096	2248767	35.1	1911	90.68	955	0	0	0	32	MQD
ZodW_Metabat.183	JAFGVV000000000	96.76	0	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	Paludibacteraceae	Paludibacter		0.932	Abundant	62.71	73	88035	3743171	3868511	40.7	2832	88.68	1172	0	0	0	41	MQD
Zod_maxbin.0112	JAFGAF000000000	82.97	2.33	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	Prolixibacteraceae	SKHV01		0.924	Abundant	69.14	584	8598	3218648	3879291	40.5	3033	92.77	985	0	0	0	33	MQD
Zod_Metabat.1198	JAFGDX000000000	77.86	4.41	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	Prolixibacteraceae			0.912	Abundant	24.60	583	6256	3230539	4149164	41.5	3243	90.39	901	0	0	0	21	MQD
Zod_Metabat.1255	JAFGEV000000000	78.15	2.97	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	Prolixibacteraceae	SKHV01		0.905	Abundant	28.00	448	15704	4585703	5867822	40.5	3887	90.50	1068	0	0	0	43	MQD
Zod_Metabat.1376	JAFGGF000000000	91.74	1.52	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	Prolixibacteraceae			0.874	Abundant	14.86	464	11684	4106078	4475777	37.3	3709	91.50	1013	0	0	0	25	MQD
Zod_Metabat.1419	JAFGGY000000000	92.11	2.15	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	Prolixibacteraceae	SKHV01		0.920	Abundant	12.96	216	21404	3308896	3592331	40.6	2855	89.56	1038	0	0	0	44	MQD
ZodW_Metabat.155	JAFGVJ000000000	86.15	2.15	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	Prolixibacteraceae	SKHV01		0.913	Abundant	20.66	403	11200	3371188	3913161	44.5	2958	91.71	1045	0	0	0	39	MQD
ZodW_Metabat.19	JAFGVY000000000	83.76	3.96	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	Prolixibacteraceae			0.874	Abundant	12.52	478	10272	3812368	4551538	37.3	3497	91.59	999	0	1	0	30	MQD
ZodW_Metabat.353	JAFGXJ000000000	87.72	3.49	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	Prolixibacteraceae	SKHV01		0.918	Abundant	22.50	132	44491	3167636	3611076	40.4	2723	89.00	1035	0	0	0	41	MQD
ZodW_Metabat.59	JAFGXU000000000	78.55	7.48	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	Prolixibacteraceae	Draconibacterium		0.926	Abundant	20.99	283	20997	3238956	4123432	36.9	2917	89.39	993	0	0	0	25	MQD
Zod_Metabat.777	JAFGQQ000000000	71.69	0.95	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	PUMT01			0.769	Abundant	32.06	527	6552	3099507	4323486	31.3	2853	90.87	987	1	0	0	24	MQD
ZodW_Metabat.376	JAFGXM000000000	72.42	0.9	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	Tannerellaceae	Parabacteroides_A		0.965	Abundant	13.49	420	7577	2715616	3749815	40.9	2459	92.01	1016	0	0	0	36	MQD
Zod_Metabat.1236	JAFGEO000000000	96.55	8.62	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	UBA10428	UBA10428		0.889	Rare	14.87	168	53329	4824774	4997177	45.1	3958	89.98	1097	0	0	0	35	MQD
Zod_Metabat.217	JAFGIP000000000	97.31	2.87	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	UBA10428	UBA10428		0.868	Rare	33.07	122	76271	4062668	4174975	36.2	3359	89.86	1087	0	0	0	42	MQD
Zod_Metabat.642	JAFGOS000000000	95.61	3.89	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	UBA10428	UBA10428		0.888	Rare	28.39	205	50756	4713847	4930287	36.6	3962	90.12	1072	0	0	0	41	MQD
Zod_Metabat.768	JAFGQO000000000	90.86	6.72	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	UBA10428	UBA10428		0.868	Rare	14.31	225	31427	3799530	4181741	37.7	3219	89.39	1055	0	0	0	34	MQD
Zod_Metabat.800	JAFGQZ000000000	93.65	2.7	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	UBA10428	UBA10428		0.895	Rare	15.96	107	55376	3943945	4211367	41.2	3139	91.14	1145	0	0	0	39	MQD
Zod_Metabat.943	JAFGSZ000000000	94.89	4.84	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	UBA10428			0.815	Rare	28.04	155	68197	4534558	4778752	36.2	3815	89.34	1062	1	0	0	37	MQD
ZodW_Metabat.117	JAFGVA000000000	98.44	2.7	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	UBA10428	UBA10428		0.887	Rare	43.30	239	47140	5220499	5303229	36.6	4329	90.46	1091	0	0	0	40	MQD
Zod_maxbin.0163	JAFGAK000000000	72.42	1.25	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	UBA12170	UBA12170		0.929	Rare	46.06	368	13087	2446505	3378217	36.4	2294	91.92	980	0	0	0	20	MQD
Zod_Metabat.155	JAFGHU000000000	87.46	2.78	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	UBA12170	UBA12170		0.925	Rare	13.25	241	18927	2845310	3253270	36.6	2539	90.64	1016	0	0	0	23	MQD
ZodW_Metabat.232	JAFGWF000000000	87.99	2.15	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	UBA1556	UBA6267		0.981	Abundant	36.32	333	13220	3166573	3598787	37.6	2852	90.49	1005	0	0	0	37	MQD
ZodW_maxbin.137	JAFGUD000000000	95.16	7.1	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	UBA3824			0.789	Rare	24.09	555	23910	4750332	4991942	30.9	4175	88.65	1009	0	0	0	39	MQD
ZodW_Metabat.383	JAFGXO000000000	77.42	0	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	UBA3824			0.783	Rare	15.41	241	25307	3342802	4317750	29.8	2904	89.79	1034	0	0	0	35	MQD
Zod_Metabat.1005	JAFGBD000000000	89.52	1.59	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	UBA5072			0.829	Rare	315.85	88	67592	4046580	4520308	40.5	3244	90.46	1128	1	0	0	45	MQD
Zod_Metabat.1409	JAFGGU000000000	85.11	2.86	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	UBA5072	UBA5072		0.942	Rare	43.32	112	66964	3965572	4659349	44.8	3285	93.13	1124	0	0	0	34	MQD
Zod_Metabat.37	JAFGKY000000000	90.59	4.84	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	UBA5072	UBA5072		0.874	Rare	163.31	173	59852	4802515	5301374	41.7	3844	89.62	1120	1	0	0	45	MQD
Zod_Metabat.64	JAFGOR000000000	87.62	6.43	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	UBA5072	UBA5072		0.920	Rare	34.50	294	15991	3431162	3915958	44.2	2939	91.55	1069	1	0	0	20	MQD
Zod_Metabat.669	JAFGPB000000000	85.87	4.21	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	UBA5072	UBA5072		0.887	Rare	14.43	113	28884	2240971	2609725	44.2	1924	91.18	1062	0	0	0	24	MQD
Zod_Metabat.688	JAFGPL000000000	93.81	3.6	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	UBA5072			0.835	Rare	64.13	332	25222	5315248	5665972	39.9	4301	89.29	1104	1	0	0	47	MQD
Zod_Metabat.810	JAFGRC000000000	97.22	1.83	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	UBA5072	UBA5072		0.884	Rare	67.77	173	24337	2832218	2913205	42.7	2543	90.58	1009	1	0	0	30	MQD
Zod_Metabat.988	JAFGTR000000000	96.43	2.14	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	UBA5072	UBA5072		0.866	Rare	569.83	208	36429	4540757	4708863	41.6	3552	89.34	1142	1	0	0	33	MQD
ZodW_Metabat.13	JAFGVG000000000	75.59	2.71	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	UBA5072	UBA5072		0.927	Rare	15.71	456	7492	2961001	3917186	45.2	2750	92.48	996	0	0	0	18	MQD
ZodW_Metabat.2	JAFGWB000000000	80.79	3.02	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	UBA5072	UBA5072		0.867	Rare	8.54	581	8238	4065314	5031952	42	3442	89.76	1060	0	0	0	27	MQD
Zod_Metabat.638	JAFGOQ000000000	92.22	2.14	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	UBA6680	UBA6680		0.867	Rare	12.47	233	18783	2901786	3146591	34.1	2481	88.05	1030	0	0	0	54	MQD
ZodW_Metabat.352	JAFGXI000000000	99.46	1.61	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	UBA6680			0.753	Rare	45.90	45	149316	2971627	2987761	35.1	2476	93.70	1125	0	0	0	39	MQD
Zod_Metabat.397	JAFGLJ000000000	72.04	2.54	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	VadinHA17	UBA9300		0.932	Abundant	111.28	76	72926	2764806	3837876	41.3	2245	92.02	1133	0	0	0	25	MQD
Zod_Metabat.65	JAFGOV000000000	75.9	4.46	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	VadinHA17	LD21		0.937	Abundant	101.73	282	9570	2346570	3091660	45.1	2060	94.27	1074	0	0	0	15	MQD
ZodW_maxbin.163	JAFGUI000000000	74.33	6.35	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	VadinHA17	LD21		0.936	Abundant	19.33	750	5417	2993422	4027206	40.7	3033	90.13	890	1	0	0	18	MQD
ZodW_Metabat.368	JAFGXK000000000	93.33	5.71	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	VadinHA17	LD21		0.988	Abundant	10.29	343	11926	3147996	3372973	46	2824	92.34	1029	0	0	0	29	MQD
ZodW_Metabat.7	JAFGXX000000000	92.86	3.1	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	VadinHA17	LD21		0.937	Abundant	31.18	257	18946	3211628	3458570	44.7	2767	93.31	1083	0	0	0	28	MQD
ZodW_maxbin.172	JAFGUK000000000	80.29	4.08	Bacteria	Bacteroidota	Bacteroidia	Flavobacteriales	Flavobacteriaceae	Mesoflavibacter		0.983	Abundant	16.99	557	4632	2063726	2570340	31.5	2394	91.86	792	0	0	0	23	MQD
Zod_Metabat.1248	JAFGER000000000	93.13	0.29	Bacteria	Bacteroidota	Chlorobia	Chlorobiales	Chlorobiaceae	Chlorobaculum		0.951	Abundant	14.52	106	31066	2248297	2414149	58	2068	86.48	940	0	0	0	41	MQD
Zod_Metabat.509	JAFGMZ000000000	85.15	0.85	Bacteria	Bacteroidota	Chlorobia	Chlorobiales	Chlorobiaceae	Chlorobium		0.925	Abundant	22.86	188	13461	1930616	2267312	51.4	1940	89.34	889	0	0	0	37	MQD
Zod_Metabat.461	JAFGMI000000000	98.32	1.4	Bacteria	Bacteroidota	Ignavibacteria	Ignavibacteriales	Melioribacteraceae	PGYT01		0.886	Abundant	24.26	59	107155	3850316	3916107	38.3	3238	92.87	1104	1	0	0	41	MQD
Zod_Metabat.179	JAFGID000000000	78.51	1.68	Bacteria	Bacteroidota	Ignavibacteria	Ignavibacteriales	Novel:ZNF018			0.734	Novel	60.61	344	8500	2378876	3030029	31.5	2328	91.04	930	0	0	0	29	MQD
Zod_Metabat.701	JAFGPR000000000	82.03	1.4	Bacteria	Bacteroidota	Ignavibacteria	Ignavibacteriales	Novel:ZNF018			0.732	Novel	142.24	317	11090	2627073	3202576	30.8	2491	91.97	970	0	0	1	25	MQD
Zod_Metabat.193	JAFGII000000000	91.53	3.28	Bacteria	Bacteroidota	Ignavibacteria	SJA-28	B-1AR			0.802	Abundant	124.18	124	41035	2781959	3039396	35.3	2412	89.14	1028	0	0	0	39	MQD
ZodW_Metabat.264	JAFGWN000000000	92.19	1.38	Bacteria	Bacteroidota	Rhodothermia	Balneolales	Balneolaceae	SMO-BIN1		0.888	Abundant	11.03	246	14887	2624021	2846318	45	2515	90.74	947	0	0	0	34	MQD
Zod_Metabat.348	JAFGKR000000000	89.07	2.46	Bacteria	Bacteroidota	SZUA-365	SZUA-365	SZUA-365			0.813	Rare	14.88	375	13600	3767052	4229316	57.8	3193	91.87	1084	0	0	0	36	MQD
Zod_Metabat.377	JAFGLB000000000	95.77	3.37	Bacteria	Bacteroidota	UBA10030	UBA10030	UBA10030	Fen-1298		0.928	Abundant	218.25	224	18515	3155489	3294862	41.4	2860	89.43	987	0	0	0	38	MQD
Zod_Metabat.617	JAFGOL000000000	76.57	1.68	Bacteria	Bdellovibrionota	FAC87	Novel:ZNO09	Novel:ZNF019			0.460	Novel	8.60	298	6443	1739474	2271744	44.1	1921	94.37	855	0	1	0	27	MQD
Zod_Metabat.1330	JAFGFS000000000	88.14	5.08	Bacteria	Bipolaricaulota	Bipolaricaulia	UBA7950	UBA9294	RXOA01	RXOA01 sp003979035	N/A	Rare	9.91	248	13688	2356994	2674148	60.3	2375	88.45	878	1	2	1	40	MQD
ZodW_Metabat.265	JAFGWO000000000	78.21	1.71	Bacteria	BMS3Abin14	BMS3Abin14	BMS3Abin14	Novel:ZNF020			0.672	Novel	9.16	292	6801	1711051	2187765	58.1	1779	88.09	847	0	0	0	26	MQD
Zod_Metabat.864	JAFGSC000000000	72.97	2	Bacteria	Caldatribacteriota	JS1	SB-45	UBA6794			0.804	Rare	51.84	354	5869	1968070	2697095	35.4	2026	85.27	828	0	0	0	37	MQD
Zod_Metabat.370	JAFGKZ000000000	74.66	1.1	Bacteria	Calditrichota	Calditrichia	Calditrichales	Calditrichaceae			0.788	Rare	12.26	291	17140	3691956	4945025	38.7	3099	90.59	1079	0	0	0	21	MQD
Zod_Metabat.858	JAFGRX000000000	86.02	2.2	Bacteria	Calditrichota	Calditrichia	Calditrichales	Calditrichaceae	Zgenome-0002	Zgenome-0002 sp003854985	N/A	Rare	702.58	144	50910	3986471	4634354	39.7	3366	90.27	1069	0	0	0	40	MQD
ZodW_Metabat.275	JAFGWR000000000	92.24	2.2	Bacteria	Calditrichota	Calditrichia	Calditrichales	Calditrichaceae	Zgenome-0002	Zgenome-0002 sp003854985	N/A	Rare	29.61	72	110911	4219898	4574911	39.8	3445	90.45	1108	0	0	0	41	MQD
Zod_Metabat.906	JAFGSO000000000	88.4	1.1	Bacteria	Calditrichota	Calditrichia	RBG-13-44-9	RBG-13-44-9	RQOF01	RQOF01 sp003854955	N/A	Rare	26.87	555	6342	3273137	3702644	42.9	2952	87.40	969	0	0	0	21	MQD
ZodW_maxbin.095	JAFGUB000000000	95	2.24	Bacteria	Campylobacterota	Campylobacteria	Campylobacterales	Sulfurimonadaceae			0.866	Abundant	44.70	62	83590	2854195	3004416	52	2934	94.78	922	0	0	0	44	MQD
ZodW_maxbin.169	JAFGUJ000000000	93.39	1.63	Bacteria	Campylobacterota	Campylobacteria	Campylobacterales	Sulfurimonadaceae	Sulfuricurvum		0.964	Abundant	16.92	216	14161	1817971	1946644	53.8	2006	94.86	860	0	0	0	40	MQD
ZodW_Metabat.126	JAFGVE000000000	98.51	5.04	Bacteria	Campylobacterota	Campylobacteria	Campylobacterales	Sulfurimonadaceae	Sulfurimonas		0.931	Abundant	56.01	44	79408	2255390	2289504	35.6	2289	95.27	939	0	0	0	32	MQD
ZodW_Metabat.179	JAFGVR000000000	70.75	1.15	Bacteria	Campylobacterota	Campylobacteria	Campylobacterales	Sulfurimonadaceae			0.893	Abundant	8.29	270	6331	1511867	2136914	33.4	1656	95.28	870	0	0	0	13	MQD
Zod_Metabat.1333	JAFGFU000000000	98.85	0.38	Bacteria	Campylobacterota	Campylobacteria	Campylobacterales	Sulfurospirillaceae	Sulfurospirillum		0.977	Abundant	24.14	37	93560	2230579	2256529	38.1	2290	94.71	923	0	0	0	34	MQD
ZodW_Metabat.102	JAFGUX000000000	73	0.38	Bacteria	Campylobacterota	Campylobacteria	Campylobacterales	Sulfurospirillaceae	Sulfurospirillum		0.976	Abundant	233.04	258	5777	1466918	2009477	37.3	1692	94.45	819	0	0	0	25	MQD
Zod_maxbin.0142	JAFGAI000000000	84.49	2.77	Bacteria	Campylobacterota	Campylobacteria	Campylobacterales	Sulfurovaceae			0.907	Abundant	53.52	197	17406	1630151	1929401	45.9	1781	90.72	830	0	0	0	37	MQD
ZodW_Metabat.130	JAFGVH000000000	79.82	9.29	Bacteria	Campylobacterota	Campylobacteria	Campylobacterales	Sulfurovaceae	FS08-3		0.954	Abundant	7.87	474	5579	2405797	3014028	39.3	2772	92.52	803	0	0	0	17	MQD
ZodW_Metabat.188	JAFGVX000000000	95.29	0.41	Bacteria	Campylobacterota	Campylobacteria	Campylobacterales	Sulfurovaceae			0.907	Abundant	44.64	108	23001	1494242	1568099	37.2	1622	93.78	864	0	0	0	26	MQD
ZodW_Metabat.273	JAFGWQ000000000	78.84	2.46	Bacteria	Campylobacterota	Campylobacteria	Campylobacterales	Sulfurovaceae	BN30871		0.988	Abundant	9.28	186	7677	1182750	1500190	37.4	1301	92.93	845	0	0	0	22	MQD
Zod_Metabat.862	JAFGSA000000000	92.7	1.12	Bacteria	CG03	SLGR01	SLGR01	Novel:ZNF021			0.687	Novel	15.25	77	56451	2525914	2724826	49.9	2036	95.53	1185	0	0	0	43	MQD
Zod_Metabat.120	JAFGDY000000000	97.27	4.55	Bacteria	Chloroflexota	Anaerolineae	4572-78	J111			0.840	Rare	110.52	320	30251	6061832	6231965	53.6	5009	90.63	1097	1	0	0	47	MQD
Zod_Metabat.569	JAFGNV000000000	94.55	3.64	Bacteria	Chloroflexota	Anaerolineae	4572-78	J111			0.841	Rare	26.44	222	35313	5335393	5642933	53.2	4399	89.75	1089	1	0	0	34	MQD
Zod_maxbin.0001	JAFGAA000000000	82.73	4.55	Bacteria	Chloroflexota	Anaerolineae	Anaerolineales	Anaerolineaceae			0.869	Abundant	778.46	422	17161	2777173	3356912	50.6	2828	90.30	887	0	0	1	80	MQD
Zod_Metabat.1174	JAFGDL000000000	71.02	7.23	Bacteria	Chloroflexota	Anaerolineae	Anaerolineales	Anaerolineaceae			0.834	Abundant	27.81	275	15129	3045478	4288198	53.3	2670	89.43	1020	0	0	0	26	MQD
Zod_Metabat.414	JAFGLU000000000	78.79	4.73	Bacteria	Chloroflexota	Anaerolineae	Anaerolineales	Anaerolineaceae			0.900	Abundant	18.43	147	41309	3968489	5036793	57.9	3428	90.02	1042	0	0	0	62	MQD
ZodW_Metabat.341	JAFGXF000000000	79.09	3.64	Bacteria	Chloroflexota	Anaerolineae	Anaerolineales	Anaerolineaceae			0.790	Abundant	10.64	144	27288	2288619	2893689	49.3	2224	91.44	941	1	0	0	35	MQD
Zod_Metabat.534	JAFGNH000000000	94.55	5	Bacteria	Chloroflexota	Anaerolineae	Anaerolineales	E44-bin32			0.809	Rare	46.11	204	37204	4808938	5086132	51.3	4232	86.80	986	1	1	0	46	MQD
Zod_Metabat.720	JAFGQC000000000	91.36	8.64	Bacteria	Chloroflexota	Anaerolineae	Anaerolineales	E44-bin32			0.813	Rare	38.35	65	79728	3045362	3333365	55.9	2866	90.37	960	1	1	0	47	MQD
Zod_Metabat.109	JAFGCG000000000	90.45	5.64	Bacteria	Chloroflexota	Anaerolineae	Anaerolineales	EnvOPS12	UBA12294		0.940	Abundant	60.57	195	40693	4938462	5459881	54.9	4607	90.23	967	1	0	0	42	MQD
Zod_Metabat.341	JAFGKO000000000	89.55	6.36	Bacteria	Chloroflexota	Anaerolineae	Anaerolineales	EnvOPS12			0.881	Abundant	13.93	402	21489	5507780	6150508	53	5367	90.36	927	1	0	0	49	MQD
Zod_Metabat.498	JAFGMV000000000	96.55	2.73	Bacteria	Chloroflexota	Anaerolineae	Anaerolineales	EnvOPS12	UBA5796		0.871	Abundant	26.68	130	48311	3879211	4017826	52	3523	88.78	978	0	0	0	36	MQD
Zod_Metabat.883	JAFGSI000000000	96.67	1.82	Bacteria	Chloroflexota	Anaerolineae	Anaerolineales	EnvOPS12	UBA877		0.914	Abundant	24.81	88	72409	4089344	4230210	62.4	3692	90.14	998	0	1	0	44	MQD
Zod_Metabat.1134	JAFGCU000000000	97.27	5	Bacteria	Chloroflexota	Anaerolineae	Anaerolineales	RBG-16-64-43	FEN-1073		0.918	Rare	36.63	129	41249	3646931	3749287	61.4	3189	86.15	985	1	0	0	44	MQD
Zod_Metabat.328	JAFGKK000000000	95.45	6.36	Bacteria	Chloroflexota	Anaerolineae	Anaerolineales	RBG-16-64-43	FEN-1073		0.911	Rare	19.77	137	46784	3838895	4021891	62.9	3320	85.00	983	1	0	0	44	MQD
Zod_Metabat.1173	JAFGDK000000000	86.55	4.09	Bacteria	Chloroflexota	Anaerolineae	Anaerolineales	UBA11579	UBA11579		0.928	Rare	94.53	128	41108	3129672	3616028	52.9	2884	90.42	981	1	0	0	33	MQD
Zod_Metabat.604	JAFGOD000000000	72.73	5.45	Bacteria	Chloroflexota	Anaerolineae	Anaerolineales	UBA11579			0.799	Rare	14.43	27	134760	1686174	2318402	45.5	1505	91.97	1031	1	0	0	34	MQD
Zod_Metabat.802	JAFGRA000000000	89.09	0.18	Bacteria	Chloroflexota	Anaerolineae	Anaerolineales	UBA11579			0.801	Rare	11.51	425	15723	4907455	5508424	54.4	4653	89.53	944	1	0	0	36	MQD
Zod_Metabat.154	JAFGHT000000000	73.48	7.91	Bacteria	Chloroflexota	Anaerolineae	Anaerolineales	UBA11858	UBA11858		0.859	Rare	9.35	649	7190	4081391	5554424	56.9	4110	91.12	905	0	0	0	36	MQD
Zod_Metabat.279	JAFGJM000000000	87.27	5.64	Bacteria	Chloroflexota	Anaerolineae	Anaerolineales	UBA4823			0.863	Rare	26.34	61	123016	3913075	4483872	46.6	3474	89.32	1006	0	0	0	39	MQD
Zod_Metabat.636	JAFGOP000000000	86.55	8.18	Bacteria	Chloroflexota	Anaerolineae	Anaerolineales	UBA4823			0.869	Rare	24.49	238	30256	4627765	5346927	59.3	4003	91.97	1063	1	0	0	41	MQD
Zod_Metabat.740	JAFGQI000000000	84.85	6.55	Bacteria	Chloroflexota	Anaerolineae	Anaerolineales	UBA4823			0.867	Rare	15.02	177	43663	4102834	4835397	56.7	3625	93.45	1058	0	0	0	41	MQD
Zod_Metabat.1053	JAFGBV000000000	77.27	0	Bacteria	Chloroflexota	Anaerolineae	Anaerolineales	UBA6092	UBA6092		0.905	Rare	27.65	307	27244	4545903	5883141	55.9	4170	93.47	1019	0	0	0	39	MQD
Zod_Metabat.1210	JAFGED000000000	90.91	5.99	Bacteria	Chloroflexota	Anaerolineae	B4-G1	B4-G1			0.854	Abundant	328.47	481	12512	4810397	5291384	61.8	4234	90.44	1028	0	0	0	38	MQD
Zod_Metabat.1382	JAFGGK000000000	88.03	9.09	Bacteria	Chloroflexota	Anaerolineae	B4-G1	B4-G1			0.854	Abundant	29.52	715	10964	6115851	6947462	60.5	5705	91.87	985	1	0	0	44	MQD
Zod_Metabat.1220	JAFGEI000000000	89.55	2.73	Bacteria	Chloroflexota	Anaerolineae	B4-G1	Novel:ZNF024			0.726	Novel	33.07	236	29354	3868919	4320401	64.7	3215	92.51	1113	1	0	0	47	MQD
Zod_Metabat.614	JAFGOJ000000000	78.45	1.82	Bacteria	Chloroflexota	Anaerolineae	B4-G1	Novel:ZNF024			0.721	Novel	18.89	534	8557	3795705	4838375	64.7	3127	91.89	1115	1	1	0	34	MQD
Zod_Metabat.1205	JAFGEA000000000	94.68	10.99	Bacteria	Chloroflexota	Anaerolineae	B4-G1	SLSP01	SLSP01		0.873	Abundant	62.30	497	25507	7951779	8398584	57.3	6149	91.00	1177	0	0	0	50	MQD
Zod_Metabat.1288	JAFGFB000000000	82.73	0.91	Bacteria	Chloroflexota	Anaerolineae	B4-G1	SLSP01			0.811	Abundant	16.04	330	18906	4347111	5254576	56.5	3647	89.97	1072	0	0	0	25	MQD
Zod_Metabat.1307	JAFGFI000000000	86.36	3.82	Bacteria	Chloroflexota	Anaerolineae	B4-G1	SLSP01	SLSP01		0.870	Abundant	13.47	517	21482	7546492	8738411	51.2	6034	90.40	1131	0	0	0	43	MQD
Zod_Metabat.308	JAFGKB000000000	73.03	1.82	Bacteria	Chloroflexota	Anaerolineae	B4-G1	SLSP01			0.818	Abundant	32.20	336	9771	2753255	3770033	49.1	2346	91.88	1078	0	0	0	21	MQD
Zod_Metabat.538	JAFGNI000000000	87.27	0	Bacteria	Chloroflexota	Anaerolineae	B4-G1	SLSP01			0.893	Abundant	24.24	783	7991	5168239	5922126	62.6	4672	90.88	1005	0	0	0	34	MQD
Zod_Metabat.557	JAFGNR000000000	81.36	4.09	Bacteria	Chloroflexota	Anaerolineae	B4-G1	SLSP01			0.817	Abundant	302.19	460	11942	4295939	5280161	59.3	3816	91.96	1035	0	0	0	34	MQD
Zod_Metabat.892	JAFGSL000000000	85.91	0	Bacteria	Chloroflexota	Anaerolineae	B4-G1	SLSP01	SLSP01		0.870	Abundant	180.80	734	12260	6816906	7934939	56.9	5968	91.88	1050	0	0	0	28	MQD
Zod_Metabat.168	JAFGIA000000000	86.82	4.83	Bacteria	Chloroflexota	Anaerolineae	Novel:ZNO10	Novel:ZNF022			0.531	Novel	38.41	469	25739	6367539	7334185	63.8	5386	92.46	1093	0	0	0	45	MQD
Zod_Metabat.611	JAFGOG000000000	74.34	2	Bacteria	Chloroflexota	Anaerolineae	Novel:ZNO10	Novel:ZNF022			0.596	Novel	37.17	645	13468	5979229	8043084	63	5455	91.93	1008	1	0	0	48	MQD
Zod_Metabat.1280	JAFGEY000000000	91.36	5.76	Bacteria	Chloroflexota	Anaerolineae	Novel:ZNO11	Novel:ZNF023			0.560	Novel	16.92	565	13327	5597726	6127108	59	5051	91.61	1015	1	0	0	33	MQD
Zod_Metabat.182	JAFGIE000000000	86.36	3.64	Bacteria	Chloroflexota	Anaerolineae	Novel:ZNO11	Novel:ZNF023			0.558	Novel	16.38	279	26865	4417294	5114977	67	3671	92.02	1107	1	0	0	37	MQD
Zod_Metabat.263	JAFGJF000000000	93.1	6.9	Bacteria	Chloroflexota	Anaerolineae	Novel:ZNO11	Novel:ZNF023			0.559	Novel	11.54	701	11069	6221095	6682164	56.6	5871	91.62	971	1	0	0	43	MQD
Zod_Metabat.50	JAFGMX000000000	78.64	8.82	Bacteria	Chloroflexota	Anaerolineae	Promineofilales	UBA4811			0.807	Rare	9.15	765	8742	5813529	7392585	50.7	5528	89.69	943	0	0	0	31	MQD
Zod_Metabat.1216	JAFGEG000000000	73.58	9.85	Bacteria	Chloroflexota	Anaerolineae	SBR1031	A4b			0.740	Abundant	8.92	1035	4838	4873934	6623993	64.4	4921	89.55	887	0	0	0	39	MQD
Zod_Metabat.823	JAFGRI000000000	75.29	7.73	Bacteria	Chloroflexota	Anaerolineae	SBR1031	A4b			0.740	Abundant	14.23	683	7099	4144254	5504388	62.4	4012	89.92	929	0	0	0	40	MQD
Zod_Metabat.474	JAFGMM000000000	92.53	1.92	Bacteria	Chloroflexota	Anaerolineae	SBR1031	Novel:ZNF025			0.689	Novel	14.22	425	17985	5102097	5513992	63	4299	89.87	1067	0	0	0	43	MQD
Zod_Metabat.151	JAFGHR000000000	84.55	2.73	Bacteria	Chloroflexota	Anaerolineae	SBR1031	UBA2029	MO-CFX2		0.883	Rare	16.22	132	49214	4038597	4776578	58	3336	89.52	1084	0	0	0	40	MQD
Zod_Metabat.248	JAFGJA000000000	70.98	3.64	Bacteria	Chloroflexota	Anaerolineae	SBR1031	UBA2029	MO-CFX2		0.876	Rare	12.71	695	7192	4473346	6302263	55.4	4172	90.03	965	1	0	0	37	MQD
Zod_Metabat.568	JAFGNU000000000	83.18	4.55	Bacteria	Chloroflexota	Anaerolineae	SBR1031	UBA2029	MO-CFX2		0.886	Rare	40.18	104	59413	3749337	4507498	60.4	3111	90.48	1091	0	0	0	37	MQD
Zod_Metabat.964	JAFGTJ000000000	80	0.91	Bacteria	Chloroflexota	Anaerolineae	SBR1031	UBA2029	MO-CFX2		0.881	Rare	19.72	564	8476	4067076	5083845	59.8	3615	90.39	1017	0	0	0	30	MQD
Zod_Metabat.387	JAFGLD000000000	96.36	0.91	Bacteria	Chloroflexota	Anaerolineae	SBR1031	UBA3940			0.798	Rare	32.83	372	19323	5350260	5552366	54.1	4693	84.62	965	0	0	0	53	MQD
Zod_Metabat.487	JAFGMS000000000	85.3	1.82	Bacteria	Chloroflexota	Anaerolineae	SBR1031	UBA3940			0.793	Rare	121.96	547	11788	5042005	5910909	54.7	4364	83.67	967	0	0	0	30	MQD
Zod_Metabat.549	JAFGNO000000000	74.55	1.82	Bacteria	Chloroflexota	Anaerolineae	SBR1031	UBA3940			0.822	Rare	14.74	249	12238	2276034	3053030	55	2191	91.50	951	0	0	0	40	MQD
Zod_Metabat.663	JAFGOY000000000	96.97	0.91	Bacteria	Chloroflexota	Anaerolineae	SBR1031	UBA3940			0.827	Rare	21.57	82	119540	4611464	4755557	57.2	3980	89.60	1038	0	0	0	50	MQD
Zod_Metabat.132	JAFGFO000000000	89.8	6.36	Bacteria	Chloroflexota	Anaerolineae	Thermoflexales	Fen-1058			0.742	Rare	48.49	486	17689	6210360	6915768	61.2	4930	92.55	1166	0	0	0	36	MQD
Zod_Metabat.4	JAFGLK000000000	85.29	3.67	Bacteria	Chloroflexota	Anaerolineae	UBA1429	UBA1429			0.798	Abundant	14.53	625	7389	3953698	4635594	63.9	3790	90.17	941	0	0	0	28	MQD
Zod_Metabat.323	JAFGKG000000000	83.49	5.05	Bacteria	Chloroflexota	Chloroflexia	Novel:ZNO12	Novel:ZNF026			0.557	Novel	13.75	226	24388	3543452	4244163	63.7	2964	90.72	1085	0	0	0	39	MQD
Zod_Metabat.406	JAFGLQ000000000	93.23	0.33	Bacteria	Chloroflexota	Dehalococcoidia	Dehalococcoidales	Dehalococcoidaceae			0.903	Abundant	11.96	120	17160	1608427	1725225	51.3	1746	91.17	840	0	0	0	43	MQD
Zod_Metabat.1454	JAFGHK000000000	92.74	1.76	Bacteria	Chloroflexota	Dehalococcoidia	Dehalococcoidales	RBG-16-60-22	RBG-13-51-18		0.959	Abundant	55.20	104	26117	1812417	1954299	51.2	1875	91.11	881	1	0	0	42	MQD
Zod_Metabat.597	JAFGOC000000000	81.95	0	Bacteria	Chloroflexota	Dehalococcoidia	Dehalococcoidales	RBG-16-60-22	RBG-13-51-18		0.947	Abundant	84.09	146	15296	1730832	2112059	51.5	1838	90.71	854	0	0	0	41	MQD
Zod_Metabat.674	JAFGPF000000000	76.24	2.48	Bacteria	Chloroflexota	Dehalococcoidia	Dehalococcoidales	RBG-16-60-22	RBG-16-60-22		0.878	Abundant	14.71	82	26841	1483466	1945784	55.4	1538	91.11	879	2	0	0	22	MQD
Zod_maxbin.0226_1	JAFGAN000000000	85.31	7.92	Bacteria	Chloroflexota	Dehalococcoidia	Dehalococcoidales	UBA2162	MGML01		0.910	Rare	34.61	106	88047	3156231	3699720	48.1	2957	88.74	947	0	0	0	43	MQD
Zod_Metabat.1136	JAFGCW000000000	92.9	2.48	Bacteria	Chloroflexota	Dehalococcoidia	Dehalococcoidales	UBA2162	MGML01		0.958	Rare	21.49	96	68079	3509226	3777423	46.1	3462	87.94	891	1	0	0	51	MQD
Zod_Metabat.163	JAFGHZ000000000	82.53	0.99	Bacteria	Chloroflexota	Dehalococcoidia	Dehalococcoidales	UBA3254			0.884	Abundant	12.34	146	10014	1183623	1434173	49.2	1264	89.78	841	1	0	0	34	MQD

Zod_Metabat.409	JAFGLR000000000	88.78	3.96	Bacteria	Chloroflexota	Dehalococcoidia	Dehalococcoidales	UBA3254			0.800	Abundant	23.36	177	18229	2293637	2583506	45	2357	87.74	854	1	0	0	42	MQD
Zod_Metabat.59	JAFGOB000000000	96.37	5.94	Bacteria	Chloroflexota	Dehalococcoidia	Dehalococcoidales	UBA3254	UBA3254		0.897	Abundant	21.85	189	39835	4489829	4658949	49.5	3990	85.18	959	0	0	1	48	MQD
Zod_Metabat.1321	JAFGFP000000000	82.34	3.17	Bacteria	Chloroflexota	Dehalococcoidia	Dehalococcoidales	UBA5760	UBA5760		0.866	Rare	17.03	137	10608	1145560	1391256	59.3	1275	90.75	815	0	0	0	27	MQD
Zod_Metabat.1036	JAFGBN000000000	90.26	4.62	Bacteria	Chloroflexota	Dehalococcoidia	GIF9	AB-539-J10			0.821	Abundant	20.26	125	21803	1931542	2139976	46.8	2043	85.75	811	1	1	0	44	MQD
Zod_Metabat.1332	JAFGFT000000000	87.69	2.97	Bacteria	Chloroflexota	Dehalococcoidia	GIF9	AB-539-J10			0.894	Abundant	61.98	83	55341	2375754	2709264	56.9	2328	88.40	902	1	0	1	45	MQD
Zod_Metabat.609	JAFGOF000000000	73.27	6.93	Bacteria	Chloroflexota	Dehalococcoidia	GIF9	AB-539-J10			0.918	Abundant	15.57	291	5916	1618411	2208832	60	1778	89.08	811	1	0	0	25	MQD
Zod_Metabat.817	JAFGRG000000000	88.89	9.3	Bacteria	Chloroflexota	Dehalococcoidia	GIF9	UBA5620	9FT-COMBO-48-23		0.935	Rare	65.68	169	17114	2008064	2259044	47.9	2107	90.07	858	1	0	0	38	MQD
Zod_Metabat.1459	JAFGHL000000000	94.72	0	Bacteria	Chloroflexota	Dehalococcoidia	GIF9	UBA5629			0.893	Abundant	15.72	131	30416	2618856	2764840	53	2566	91.83	937	1	0	0	47	MQD
Zod_Metabat.405	JAFGLP000000000	75.37	3.96	Bacteria	Chloroflexota	Dehalococcoidia	GIF9	UBA5629	UBA1162		0.925	Abundant	13.12	197	15962	2232682	2962295	48.1	2262	89.50	883	1	0	0	36	MQD
Zod_Metabat.1111	JAFGCL000000000	78.09	4.46	Bacteria	Chloroflexota	Dehalococcoidia	UBA2777	RBG-13-53-26			0.821	Rare	214.56	237	13618	2433981	3116892	58.4	2459	85.86	850	1	0	0	39	MQD
ZodW_Metabat.128	JAFGVF000000000	74.08	0.81	Bacteria	Cloacimonadota	Cloacimonadia	Cloacimonadales	Novel:ZNF027			0.653	Novel	8.06	427	6018	2379343	3211856	39.5	2043	88.80	1034	0	0	0	32	MQD
Zod_Metabat.1219	JAFGEH000000000	73.01	1.1	Bacteria	Cloacimonadota	Cloacimonadia	Cloacimonadales	TCS61			0.821	Rare	74.46	233	7506	1489619	2040294	45.6	1490	94.45	944	0	0	0	25	MQD
Zod_Metabat.458	JAFGMF000000000	73.18	3.85	Bacteria	Cloacimonadota	Cloacimonadia	Cloacimonadales	TCS61			0.798	Rare	149.31	288	6164	1626656	2222815	40.6	1556	93.17	974	0	0	0	26	MQD
Zod_Metabat.824	JAFGRJ000000000	91.69	1.1	Bacteria	Cloacimonadota	Cloacimonadia	Cloacimonadales	TCS61			0.792	Rare	47.81	221	14014	2234959	2437517	43.7	2044	93.98	1028	0	0	0	31	MQD
Zod_Metabat.1183	JAFGDR000000000	94.51	0	Bacteria	Cloacimonadota	Cloacimonadia	JGIOTU-2	JGIOTU-2			0.891	Abundant	14.71	66	50478	2443448	2585386	39	2114	94.23	1089	1	0	1	45	MQD
Zod_Metabat.1246	JAFGEQ000000000	85.42	0.85	Bacteria	CSSED10-310	CSSED10-310	CSSED10-310	CSSED10-310			0.808	Rare	30.42	24	245466	2572111	3011134	48.9	2073	94.16	1168	1	0	0	35	MQD
Zod_Metabat.479	JAFGMN000000000	85.59	5.13	Bacteria	CSSED10-310	CSSED10-310	CSSED10-310	CSSED10-310			0.762	Rare	9.59	360	13125	3457392	4039481	53.2	2993	94.09	1087	1	0	0	30	MQD
Zod_Metabat.252	JAFGJC000000000	68.11	0	Bacteria	CSSED10-310	CSSED10-310	CSSED10-310	Novel:ZNF028			0.647	Novel	8.98	522	9322	3848767	5650810	43.4	3368	93.29	1066	0	0	0	18	MQD
Zod_Metabat.419	JAFGLW000000000	82.85	1.28	Bacteria	CSSED10-310	CSSED10-310	CSSED10-310	Novel:ZNF028			0.664	Novel	25.83	31	180367	3118451	3763972	54	2515	93.96	1165	1	0	0	41	MQD
Zod_Metabat.1153	JAFGDC000000000	86.32	4.75	Bacteria	CSSED10-310	CSSED10-310	Novel:ZNO13	Novel:ZNF029			0.440	Novel	9.54	635	9603	4937956	5720524	58.9	4044	89.05	1087	1	0	0	34	MQD
Zod_Metabat.886	JAFGSJ000000000	95.25	6.27	Bacteria	CSSED10-310	Novel:ZNC05	Novel:ZNO41	Novel:ZNF100			0.396	Novel	365.89	169	44879	5453321	5725271	48.6	4306	89.16	1129	1	0	0	46	MQD
Zod_Metabat.1212	JAFGEE000000000	98.9	4.4	Bacteria	Delongbacteria	UBA4055	UBA4055	UBA4055			0.827	Abundant	30.76	368	33837	5302707	5361686	31.5	4365	88.56	1076	0	0	0	51	MQD
ZodW_maxbin.179	JAFGUL000000000	71.98	0	Bacteria	Delongbacteria	UBA4055	UBA4055	UBA4055	SLFX01		0.882	Abundant	15.73	262	13073	1973847	2742216	40.5	1938	95.14	969	0	0	0	33	MQD
ZodW_Metabat.115	JAFGUZ000000000	98.9	4.4	Bacteria	Delongbacteria	UBA4055	UBA4055	UBA4055			0.831	Abundant	20.87	244	39089	4751544	4804392	31.4	3900	89.28	1088	0	0	0	42	MQD
ZodW_Metabat.17	JAFGVM000000000	97.8	0	Bacteria	Delongbacteria	UBA4055	UBA4055	UBA4055			0.784	Abundant	28.37	99	43884	2745438	2807196	34.6	2350	92.09	1076	0	0	0	31	MQD
Zod_maxbin_2.173	JAFFZZ000000000	72.47	6.81	Bacteria	Dependentiae	Babeliae	Babeliales	Babeliaceae			0.822	Abundant	18.15	159	52406	1147103	1582866	43.2	1137	87.89	887	1	2	1	36	MQD
Zod_Metabat.256	JAFGJD000000000	82.02	0	Bacteria	Dependentiae	Babeliae	Babeliales	GWF2-32-72			0.727	Rare	18.62	10	216852	808977	986317	42.5	786	92.43	951	1	1	0	38	MQD
Zod_Metabat.1348	JAFGFW000000000	97.9	4.52	Bacteria	Desulfobacterota	Desulfobacteria	C00003060	S7086C20			0.830	Rare	55.35	212	25972	3678351	3757253	49.7	3631	85.91	870	1	0	0	44	MQD
Zod_Metabat.558	JAFGNS000000000	71.44	8.29	Bacteria	Desulfobacterota	Desulfobacteria	Desulfatiglandales	B25-G16			0.776	Rare	10.88	484	7126	2976072	4165834	41.4	2861	86.03	895	1	0	0	24	MQD
Zod_Metabat.1085	JAFGCF000000000	80.81	6.77	Bacteria	Desulfobacterota	Desulfobacteria	Desulfatiglandales	HGW-15			0.714	Rare	10.05	616	8406	4276954	5292605	58.2	4259	86.74	871	1	0	0	28	MQD
Zod_Metabat.1158	JAFGDF000000000	90.65	0	Bacteria	Desulfobacterota	Desulfobacteria	Desulfatiglandales	HGW-15			0.709	Rare	22.95	362	23162	4868925	5371125	46	4543	87.50	938	1	0	0	35	MQD
Zod_Metabat.1176	JAFGDM000000000	94.05	1.95	Bacteria	Desulfobacterota	Desulfobacteria	Desulfatiglandales	HGW-15			0.766	Rare	42.27	323	15492	3728176	3964036	51.2	3624	87.97	905	1	0	0	33	MQD
Zod_Metabat.1317	JAFGFM000000000	97.42	4.54	Bacteria	Desulfobacterota	Desulfobacteria	Desulfatiglandales	HGW-15			0.708	Rare	18.62	240	33103	5183859	5321145	42.8	4727	87.67	962	0	0	0	45	MQD
Zod_Metabat.1351	JAFGFY000000000	90.65	0.86	Bacteria	Desulfobacterota	Desulfobacteria	Desulfatiglandales	HGW-15			0.713	Rare	42.52	285	22592	4216487	4651392	48	3900	85.68	926	0	0	0	44	MQD
Zod_Metabat.1361	JAFGGA000000000	92.26	2.26	Bacteria	Desulfobacterota	Desulfobacteria	Desulfatiglandales	HGW-15			0.707	Rare	16.38	224	32622	4696344	5090336	46.3	4368	85.09	915	2	1	0	47	MQD
Zod_Metabat.172	JAFGIC000000000	81.58	4.03	Bacteria	Desulfobacterota	Desulfobacteria	Desulfatiglandales	HGW-15			0.711	Rare	9.73	542	7028	3488432	4276087	46.9	3348	88.44	922	1	0	0	34	MQD
Zod_Metabat.678	JAFGPH000000000	86.72	0	Bacteria	Desulfobacterota	Desulfobacteria	Desulfatiglandales	HGW-15			0.830	Rare	15.42	690	9899	5518067	6363085	57.5	5584	88.53	875	1	0	0	53	MQD
Zod_Metabat.868	JAFGSE000000000	78.2	9.03	Bacteria	Desulfobacterota	Desulfobacteria	Desulfatiglandales	HGW-15			0.707	Rare	56.06	530	6218	3000680	3837187	42.4	3026	88.71	880	1	0	0	26	MQD
Zod_Metabat.483	JAFGMQ000000000	84.95	6.29	Bacteria	Desulfobacterota	Desulfobacteria	Desulfatiglandales	NaphS2			0.826	Rare	60.76	259	13981	2549820	3001554	44.6	2371	88.21	949	0	0	0	32	MQD
Zod_Metabat.1250	JAFGES000000000	96.77	2.47	Bacteria	Desulfobacterota	Desulfobacteria	Desulfobacterales	BuS5			0.801	Rare	40.64	133	47382	3378275	3491035	41.8	3102	88.27	961	1	0	0	46	MQD
Zod_Metabat.542	JAFGNJ000000000	90.97	2.6	Bacteria	Desulfobacterota	Desulfomonilia_A	Novel:ZNO17	Novel:ZNF033			0.845	Novel	38.60	31	159540	2481530	2727855	50.4	2483	89.96	899	0	0	0	38	MQD
Zod_Metabat.184	JAFGIF000000000	77.72	1.31	Bacteria	Desulfobacterota	Desulfomonilia_A	UBA1062	UBA1062			0.789	Rare	75.55	324	8883	2506504	3225044	47	2529	90.43	896	0	0	0	22	MQD
Zod_Metabat.965	JAFGTK000000000	78.3	0	Bacteria	Desulfobacterota	Desulfomonilia_A	UBA1062	UBA1062			0.834	Rare	40.36	360	9205	2698348	3446166	48.9	2700	90.17	901	0	0	0	21	MQD
Zod_Metabat.1050	JAFGBU000000000	98.22	0	Bacteria	Desulfobacterota	Desulfovibrionia	Desulfovibrionales	Desulfovibrionaceae			0.810	Abundant	105.57	49	72293	2483598	2528607	66.7	2353	92.10	972	0	0	0	44	MQD
ZodW_Metabat.6	JAFGXV000000000	85.81	0	Bacteria	Desulfobacterota	Desulfuromonadia	Desulfuromonadales	Desulfuromonadaceae	Pseudodesulfuromonas		0.863	Abundant	17.97	64	73522	2538858	2958697	57.2	2336	91.50	995	1	0	0	47	MQD
Zod_Metabat.1226	JAFGEL000000000	86.94	0.65	Bacteria	Desulfobacterota	Desulfuromonadia	Desulfuromonadales	Geopsychrobacteraceae	BM522		0.919	Abundant	14.11	118	39698	2938963	3380450	52.2	2780	90.95	962	0	0	0	36	MQD
ZodW_Metabat.176	JAFGVQ000000000	84.41	6.29	Bacteria	Desulfobacterota	Desulfuromonadia	Desulfuromonadales	Geopsychrobacteraceae	BM522		0.920	Abundant	17.06	103	54023	3126379	3703802	52.3	2931	91.22	973	0	0	0	37	MQD
Zod_Metabat.652	JAFGOW000000000	81.45	3.25	Bacteria	Desulfobacterota	Desulfuromonadia	Novel:ZNO18	Novel:ZNF034			0.567	Novel	14.02	258	14544	2770735	3401762	60.4	2647	87.72	918	0	0	0	45	MQD
Zod_Metabat.852	JAFGRU000000000	92.63	1.31	Bacteria	Desulfobacterota	Desulfuromonadia	Novel:ZNO18	Novel:ZNF034			0.569	Novel	63.92	136	41021	3576763	3861344	51.1	3213	85.95	957	0	0	0	37	MQD
Zod_Maxbin.0214	JAFGAM000000000	77.74	0.65	Bacteria	Desulfobacterota	Novel:ZNC02	Novel:ZNO14	Novel:ZNF030			0.397	Novel	35.36	146	52974	2677598	3444299	63.3	2363	87.10	987	1	0	0	35	MQD
Zod_Metabat.940	JAFGSY000000000	98.39	0.22	Bacteria	Desulfobacterota	Novel:ZNC02	Novel:ZNO14	Novel:ZNF030			0.397	Novel	97.30	52	95348	2696119	2740237	53.5	2471	89.90	981	0	0	0	46	MQD
ZodW_maxbin.067	JAFGTY000000000	98.39	0.22	Bacteria	Desulfobacterota	Novel:ZNC02	Novel:ZNO14	Novel:ZNF030			0.398	Novel	66.79	94	109869	2745981	2790915	53.6	2543	90.01	972	0	1	0	46	MQD
ZodW_Metabat.137	JAFGVI000000000	88.87	0.65	Bacteria	Desulfobacterota	Novel:ZNC02	Novel:ZNO14	Novel:ZNF030			0.430	Novel	17.35	141	31762	2701266	3039570	52	2439	91.77	1016	0	0	0	41	MQD
ZodW_Metabat.297	JAFGWV000000000	79.42	9.78	Bacteria	Desulfobacterota	Novel:ZNC02	Novel:ZNO14	Novel:ZNF030			0.430	Novel	9.08	419	7295	2759767	3474902	55	2674	89.45	923	0	0	0	47	MQD
Zod_maxbin.0311	JAFGAS000000000	80.65	0.65	Bacteria	Desulfobacterota	Novel:ZNC03	Novel:ZNO16	Novel:ZNF032			0.416	Novel	23.50	86	155667	2944368	3650797	56	2733	86.61	933	1	0	0	46	MQD
Zod_Metabat.1292	JAFGFE000000000	97.42	0	Bacteria	Desulfobacterota	Novel:ZNC03	Novel:ZNO16	Novel:ZNF032			0.414	Novel	76.38	46	138644	3726185	3824867	55.3	3398	87.74	962	1	0	0	47	MQD
Zod_Metabat.24	JAFGIX000000000	98.06	0	Bacteria	Desulfobacterota	Novel:ZNC03	Novel:ZNO16	Novel:ZNF032			0.410	Novel	130.66	92	62768	3762314	3836747	51.3	3350	84.54	949	1	1	0	49	MQD
Zod_Metabat.1117	JAFGCP000000000	75.37	2.26	Bacteria	Desulfobacterota	Novel:ZNC15	Novel:ZNO15	Novel:ZNF031			0.371	Novel	11.43	460	10252	3869006	5133350	52.4	3834	85.82	866	1	0	0	32	MQD
Zod_Metabat.815	JAFGRE000000000	91.94	1.94	Bacteria	Desulfobacterota	Novel:ZNC15	Novel:ZNO15	Novel:ZNF031			0.430	Novel	36.62	246	16106	2804507	3050367	49.7	2696	87.69	912	1	0	0	40	MQD
Zod_Metabat.1020	JAFGBH000000000	92.22	1.94	Bacteria	Desulfobacterota	Syntrophia	Syntrophales	MLS-D			0.713	Rare	439.77	102	40204	2685877	2912467	48.8	2513	88.92	950	1	0	0	43	MQD
Zod_Metabat.1365	JAFGGB000000000	92.9	4.52	Bacteria	Desulfobacterota	Syntrophia	Syntrophales	MLS-D			0.732	Rare	12.17	231	19686	3120465	3358950	52.4	3059	89.35	912	1	0	0	47	MQD
Zod_Metabat.996	JAFGTS000000000	91.61	1.51	Bacteria	Desulfobacterota	Syntrophia	Syntrophales	MLS-D			0.726	Rare	45.15	55	81577	2850888	3111983	55	2556	89.90	1003	1	0	0	50	MQD
ZodW_maxbin.216	JAFGUT000000000	87.71	1.29	Bacteria	Desulfobacterota	Syntrophia	Syntrophales	MLS-D			0.711	Rare	11.90	113	40914	2678671	3054009	48.6	2497	88.79	953	1	2	2	51	MQD
Zod_Metabat.153	JAFGHS000000000	85.16	4.09	Bacteria	Desulfobacterota	Syntrophia	Syntrophales	Novel:ZNF035			0.702	Novel	15.91	192	30747	3807336	4470803	51.6	3539	87.74	944	1	0	0	42	MQD
Zod_Metabat.402	JAFGLN000000000	83.55	2.15	Bacteria	Desulfobacterota	Syntrophia	Syntrophales	Novel:ZNF035			0.645	Novel	171.62	126	44386	3676951	4400899	49.7	3317	87.26	967	1	0	0	43	MQD
Zod_Metabat.717	JAFGPZ000000000	75.43	3.94	Bacteria	Desulfobacterota	Syntrophia	Syntrophales	Novel:ZNF036			0.705	Novel	13.76	331	10536	2827858	3748983	46.2	2827	88.55	886	0	1	0	31	MQD
Zod_Metabat.309	JAFGKC000000000	84.19	1.29	Bacteria	Desulfobacterota	Syntrophia	Syntrophales	Smithellaceae	UBA4810		0.987	Abundant	35.06	222	12285	2105806	2501254	43.9	2220	90.10	855	0	0	0	36	MQD
Zod_Metabat.324	JAFGKH000000000	68.43	1.29	Bacteria	Desulfobacterota	Syntrophia	Syntrophales	Smithellaceae	Smithella		0.992	Abundant	17.31	321	11763	2928647	4279771	43.9	2933	88.26	881	0	0	0	39	MQD
Zod_Metabat.41	JAFGLS000000000	78.06	3.57	Bacteria	Desulfobacterota	Syntrophia	Syntrophales	Smithellaceae	Smithella		0.965	Abundant	23.05	239	22285	3376298	4325260	41.3	3253	86.63	899	0	0	0	43	MQD
Zod_Metabat.27	JAFGJJ000000000	82.24	11.85	Bacteria	Desulfobacterota	Syntrophia	Syntrophales	Syntrophaceae			0.748	Abundant	9.80	564	9032	4093519	4977528	49.5	4187	87.56	856	1	0	0	56	MQD
Zod_Metabat.215	JAFGIO000000000	85.43	10	Bacteria	Desulfobacterota	Syntrophia	Syntrophales	UBA2185			0.720	Abundant	28.22	285	16672	3074372	3598703	56.5	2923	88.25	928	1	0	0	34	MQD
Zod_Metabat.729	JAFGQD000000000	73.89	1.29	Bacteria	Desulfobacterota	Syntrophia	Syntrophales	UBA2210			0.849	Rare	146.44	204	8733	1457726	1972833	48.6	1516	89.69	863	1	0	0	19	MQD
Zod_Metabat.88	JAFGSH000000000	74.42	0	Bacteria	Desulfobacterota	Syntrophia	Syntrophales	UBA2210	UBA6078		0.893	Rare	13.32	290	7530	1928340	2591158	58.2	2029	90.83	863	1	0	0	25	MQD
Zod_maxbin.0017_4	JAFGAD000000000	81.1	2.9	Bacteria	Desulfobacterota	Syntrophia	Syntrophales	UBA3084			0.754	Rare	277.82	448	7723	2186337	2695853	51.8	2243	87.93	857	1	0	0	26	MQD
Zod_Metabat.781	JAFGQS000000000	94.19	3.87	Bacteria	Desulfobacterota	Syntrophia	Syntrophales	UBA3084			0.785	Rare	237.19	196	23381	3058949	3247637	45.1	2920	85.72	898	1	0	0	38	MQD
ZodW_Metabat.303	JAFGWZ000000000	84.79	3.26	Bacteria	Desulfobacterota	Syntrophia	Syntrophales	UBA3084			0.754	Rare	9.18	301	10333	2524195	2976996	51.8	2521	86.81	869	1	0	0	44	MQD
Zod_Metabat.836	JAFGRP000000000	88.46	4.68	Bacteria	Desulfobacterota	Syntrophia	Syntrophales	UBA5619	UBA5619		0.945	Abundant	13.51	265	16271	2869135	3243426	56.9	2789	89.19	918	1	0	0	38	MQD
Zod_Metabat.137	JAFGGD000000000	98.9	0	Bacteria	Eisenbacteria	Novel:ZNC04	Novel:ZNO19	Novel:ZNF037			0.373	Novel	30.73	60	110062	3781923	3823987	66	2923	90.69	1173	1	0	0	43	MQD
Zod_Metabat.707	JAFGPT000000000	73.94	5.09	Bacteria	Eisenbacteria	Novel:ZNC04	Novel:ZNO20	Novel:ZNF038			0.374	Novel	9.21	437	6664	2572855	3479652	63	2488	90.45	935	1	0	0	32	MQD
Zod_Metabat.294	JAFGJU000000000	85.16	1.1	Bacteria	Eisenbacteria	Novel:ZNC04	Novel:ZNO40	Novel:ZNF099			0.431	Novel	56.13	241	11613	2047304	2404068	63.1	1825	90.01	1010	0	0	0	33	MQD
Zod_Metabat.202	JAFGIL000000000	92.13	2.43	Bacteria	Elusimicrobiota	Endomicrobia	Endomicrobiales	Novel:ZNF039			0.635	Novel	17.83	77	52674	2228376	2418730	39.4	1786	94.23	1176	1	1	0	38	MQD
Zod_Metabat.1366	JAFGGC000000000	91.01	1.12	Bacteria	Elusimicrobiota	Endomicrobia	Endomicrobiales	Novel:ZNF101			0.644	Novel	16.24	45	95303	2302584	2530034	51.4	1937	93.89	1116	1	1	0	37	MQD
Zod_Metabat.39	JAFGLF000000000	96.56	5.06	Bacteria	Elusimicrobiota	UBA8919	UBA8919	UBA8919			0.760	Abundant	22.32	87	65380	2372302	2456816	37.7	2121	92.89	1039	1	2	2	40	MQD
Zod_Metabat.219	JAFGIQ000000000	86.84	2.5	Bacteria	FCPU426	Novel:ZNC06	Novel:ZNO21	Novel:ZNF040			0.385	Novel	10.12	327	10736	2832131	3261321	54.1	2434	89.59	1042	0	1	0	36	MQD
Zod_Metabat.684	JAFGPK000000000	92.31	2.2	Bacteria	Fermentibacterota	Fermentibacteria	Fermentibacterales	Fermentibacteraceae	Aegiribacteria		0.908	Abundant	251.46	117	36469	2678320	2901441	58.4	2481	93.56	1010	0	1	0	39	MQD
ZodW_Metabat.82	JAFGYA000000000	85.71	1.2	Bacteria	Fermentibacterota	Fermentibacteria	Fermentibacterales	Fermentibacteraceae	Aegiribacteria		0.907	Abundant	9.40	260	13922	2657834	3100961	58.2	2621	93.28	946	0	1	0	37	MQD
Zod_Metabat.345	JAFGKQ000000000	74.18	0	Bacteria	Fermentibacterota	Fermentibacteria	Fermentibacterales	Novel:ZNF041			0.621	Novel	8.55	337	7680	2307464	3110628	65	2389	93.50	903	0	1	0	33	MQD
Zod_Metabat.355	JAFGKV000000000	91.16	3.3	Bacteria	Fermentibacterota	Novel:ZNC07	Novel:ZNO22	Novel:ZNF042			0.350	Novel	20.47	343	22865	4794814	5259778	62.2	4111	87.87	1025	0	0	0	46	MQD
Zod_Metabat.1030	JAFGBJ000000000	72.03	6.59	Bacteria	Fibrobacterota	Chitinivibrionia	Chitinivibrionales	Chitinispirillaceae			0.847	Rare	10.80	217	11473	1946827	2702800	57.8	1803	91.36	987	0	0	0	22	MQD
Zod_Metabat.118	JAFGDP000000000	81.25	5.49	Bacteria	Fibrobacterota	Chitinivibrionia	Chitinivibrionales	Chitinispirillaceae			0.839	Rare	14.37	156	41783	3953828	4866250	53.7	3333	90.06	1068	1	0	0	43	MQD
Zod_Metabat.1421	JAFGHA000000000	83.52	5.01	Bacteria	Fibrobacterota	Chitinivibrionia	Chitinivibrionales	Chitinispirillaceae			0.728	Rare	12.84	316	27545	5892762	7055510	50.8	4958	87.87	1044	1	0	0	43	MQD
Zod_Metabat.210	JAFGIN000000000	92.24	4.4	Bacteria	Fibrobacterota	Chitinivibrionia	Chitinivibrionales	Chitinispirillaceae			0.730	Rare	29.19	224	61585	6599087	7154257	41	5133	86.95	1118	0	0	0	46	MQD
Zod_Metabat.237	JAFGIW000000000	86.75	2.3	Bacteria	Fibrobacterota	Chitinivibrionia	Chitinivibrionales	Chitinispirillaceae			0.725	Rare	48.72	227	34306	5082896	5859246	52.9	4220	89.16	1074	1	0	0	43	MQD
Zod_Metabat.521	JAFGNB000000000	82.35	3.49	Bacteria	Fibrobacterota	Chitinivibrionia	Chitinivibrionales	Chitinispirillaceae			0.787	Rare	12.27	396	14640	4153719	5043982	53.9	3592	90.47	1046	0	0	0	41	MQD
Zod_Metabat.647	JAFGOU000000000	75.02	0	Bacteria	Fibrobacterota	Chitinivibrionia	Chitinivibrionales	Chitinispirillaceae			0.841	Rare	10.27	594	9231	4624650	6164556	55.5	4182	90.36	999	0	0	0	45	MQD
Zod_Metabat.1207	JAFGEB000000000	95.38	9.89	Bacteria	Fibrobacterota	Chitinivibrionia	Chitinivibrionales	Novel:ZNF043			0.651	Novel	9.94	669	10717	5793365	6073983	46.4	4933	86.80	1019	1	0	0	48	MQD
Zod_Metabat.963	JAFGTI000000000	77.52	3.92	Bacteria	Firmicutes	Bacilli	Acholeplasmatales	Acholeplasmataceae	UBA2284		0.956	Abundant	27.59	136	14322	1372127	1770030	32.2	1348	92.38	940	1	0	0	30	MQD
Zod_Metabat.982	JAFGTQ000000000	92	8.04	Bacteria	Firmicutes	Bacilli	Acholeplasmatales	Acholeplasmataceae	UBA2284		0.992	Abundant	37.47	77	24259	1170208	1271965	33.5	1175	93.87	935	0	0	0	24	MQD
ZodW_maxbin.272	JAFGUV000000000	83.5	0.47	Bacteria	Firmicutes	Bacilli	Erysipelotrichales	Erysipelotrichaceae	GWE2-51-13	GWE2-51-13 sp003520745	N/A	Abundant	8.69	614	3463	1713137	2051661	51.7	2182	93.79	736	0	0	0	21	MQD
ZodW_Metabat.63	JAFGXW000000000	89.33	1.7	Bacteria	Firmicutes	Bacilli	Izemoplasmatales	Izemoplasmataceae	Izemoplasma_A		0.924	Abundant	107.10	148	13609	1487830	1665543	32.5	1528	92.70	903	1	0	1	32	MQD
Zod_Metabat.734	JAFGQH000000000	86.67	0	Bacteria	Firmicutes	Bacilli	Izemoplasmatales	UBA5603	4572-104		0.970	Abundant	15.10	79	32028	1412040	1629214	39.8	1353	93.29	974	0	0	0	25	MQD
Zod_Metabat.782	JAFGQT000000000	85.33	0	Bacteria	Firmicutes	Bacilli	Izemoplasmatales	UBA5603			0.868	Abundant	30.91	132	16300	1400563	1641349	43.5	1373	93.31	952	0	0	0	30	MQD
ZodW_maxbin.140	JAFGUE000000000	96	0	Bacteria	Firmicutes	Bacilli	Izemoplasmatales	UBA5603	4572-104		0.966	Abundant	29.12	277	29625	2007052	2090679	39.3	2036	92.68	914	2	0	0	44	MQD
ZodW_Metabat.270	JAFGWP000000000	83.59	0	Bacteria	Firmicutes	Bacilli	Izemoplasmatales	UBA5603			0.869	Abundant	8.80	162	10273	1334741	1596771	43.4	1322	93.10	940	0	0	0	27	MQD
Zod_maxbin.0317	JAFGAT000000000	74.08	2.82	Bacteria	Firmicutes_A	Clostridia	Lachnospirales	Vallitaleaceae			0.879	Abundant	24.07	698	4571	2356043	3180404	37.9	2576	93.61	856	0	0	0	30	MQD
ZodW_maxbin.062	JAFGTX000000000	92.55	3.19	Bacteria	Firmicutes_A	Clostridia	Peptostreptococcales	Acidaminobacteraceae			0.760	Rare	78.89	438	13965	3215692	3474546	41.8	3145	91.75	938	1	0	1	33	MQD
Zod_maxbin.0011	JAFGAC000000000	92.91	1.06	Bacteria	Firmicutes_A	Clostridia	Peptostreptococcales	DTU036	ML8-F1		0.865	Rare	366.53	221	53382	2381912	2563677	33.6	2406	89.44	886	0	0	0	27	MQD
ZodW_Metabat.172	JAFGVN000000000	96.1	5.67	Bacteria	Firmicutes_A	Clostridia	Peptostreptococcales	Novel:ZNF045			0.741	Novel	18.61	153	42176	4031709	4195327	33.8	3816	90.46	956	2	0	0	23	MQD
Zod_Metabat.2	JAFGIJ000000000	83.12	0	Bacteria	Firmicutes_A	Clostridia	Saccharofermentanales	Novel:ZNF044			0.589	Novel	18.42	229	15085	2227166	2679459	40.5	2201	93.52	946	0	0	0	28	MQD
Zod_Metabat.73	JAFGQE000000000	86.64	0	Bacteria	Firmicutes_A	Clostridia	Saccharofermentanales	Novel:ZNF044			0.645	Novel	11.19	180	19429	2343846	2705270	48.6	2227	92.41	973	0	0	0	35	MQD
ZodW_maxbin.088	JAFGUA000000000	83.22	0	Bacteria	Firmicutes_A	Clostridia	Saccharofermentanales	Novel:ZNF044			0.589	Novel	43.19	540	7419	2361424	2837568	40.7	2539	93.30	868	0	0	0	28	MQD
ZodW_maxbin.207	JAFGUQ000000000	92.83	3.5	Bacteria	Firmicutes_A	Clostridia	Saccharofermentanales	Novel:ZNF044			0.588	Novel	10.85	301	18574	2988528	3219356	37.5	2854	94.17	986	0	0	0	45	MQD
Zod_Metabat.1254	JAFGEU000000000	82.15	7.09	Bacteria	Firmicutes_A	Clostridia	Saccharofermentanales	Saccharofermentanaceae			0.820	Abundant	11.78	133	19789	1826570	2223457	49.1	1724	90.55	959	0	0	0	32	MQD
Zod_Metabat.14	JAFGGR000000000	80.34	2.72	Bacteria	Firmicutes_A	Clostridia	Saccharofermentanales	Saccharofermentanaceae			0.828	Abundant	9.09	239	8686	1717103	2137295	51.9	1704	90.95	917	0	0	0	32	MQD
Zod_Metabat.972	JAFGTM000000000	98.02	1.4	Bacteria	Firmicutes_A	Clostridia	Tissierellales	Dethiosulfatibacteraceae			0.856	Abundant	27.69	259	24196	3142109	3205579	36.9	2953	90.13	959	1	0	0	27	MQD
ZodW_Metabat.12	JAFGVC000000000	95.69	0.7	Bacteria	Firmicutes_A	Clostridia	Tissierellales	Dethiosulfatibacteraceae			0.856	Abundant	53.30	194	21926	2503467	2616226	36.7	2386	92.11	966	0	0	0	17	MQD
Zod_Metabat.1384	JAFGGL000000000	96.47	4.13	Bacteria	Firmicutes_A	Clostridia_A	Christensenellales	CAG-74	Firm-11		0.912	Abundant	17.85	78	45787	2354055	2440194	57.5	2133	90.81	1002	0	0	0	34	MQD
ZodW_maxbin.143	JAFGUF000000000	96.15	3.73	Bacteria	Firmicutes_A	Clostridia_A	Christensenellales	Novel:ZNF046			0.684	Novel	20.56	45	160713	2623415	2728461	41.3	2430	90.10	973	2	0	0	48	MQD
Zod_Metabat.320	JAFGKE000000000	89.97	4.6	Bacteria	Fusobacteriota	Fusobacteriia	Fusobacteriales	Fusobacteriaceae			0.766	Abundant	31.38	153	46180	3252504	3615098	27.3	3103	87.72	919	2	0	2	44	MQD
ZodW_maxbin.210	JAFGUR000000000	79.38	0	Bacteria	Fusobacteriota	Fusobacteriia	Fusobacteriales	Fusobacteriaceae			0.769	Abundant	11.32	304	11240	2246508	2830068	27.7	2268	88.04	872	0	0	0	38	MQD
Zod_Metabat.976	JAFGTO000000000	81.17	0	Bacteria	Gemmatimonadota	Glassbacteria	GWA2-58-10	GWA2-58-10			0.767	Rare	10.30	604	7147	3798706	4679938	60.3	3154	87.38	1052	0	0	0	28	MQD
ZodW_Metabat.199	JAFGWA000000000	93.26	2.25	Bacteria	Goldbacteria	PGYV01	PGYV01	PGYV01	PGYV01		0.983	Rare	13.36	124	31321	2589297	2776428	42.3	2342	90.45	1000	1	1	1	42	HQD
Zod_Metabat.358	JAFGKW000000000	88.24	1.31	Archaea	Halobacteriota	Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	Methanolacinia		0.950	Abundant	45.27	60	41045	1926770	2183556	45.6	1990	91.14	882	1	0	0	39	MQD
Zod_Metabat.564	JAFGNT000000000	84.64	0.65	Archaea	Halobacteriota	Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	LKUD01		0.944	Abundant	158.21	35	95545	1976704	2335425	56.8	2107	90.32	847	0	0	0	40	MQD
ZodW_Metabat.227	JAFGWE000000000	97.39	1.31	Archaea	Halobacteriota	Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	Methanomicrobium		0.913	Abundant	17.87	52	72222	2104177	2160568	40.4	2114	89.98	896	0	0	0	49	MQD
Zod_Metabat.630	JAFGOM000000000	98.04	0.65	Archaea	Halobacteriota	Methanomicrobia	Methanomicrobiales	Methanospirillaceae			0.801	Rare	30.32	121	36056	2936193	2994893	46.5	2798	86.22	905	0	0	0	44	MQD
Zod_Metabat.1106	JAFGCK000000000	96.9	0	Archaea	Halobacteriota	Methanosarcinia	Methanosarcinales	Methanosarcinaceae	Methanolobus		0.934	Abundant	12.21	165	16310	1988439	2052053	47.1	2069	86.59	832	0	0	0	38	MQD
Zod_Metabat.632	JAFGOO000000000	80.55	1.68	Archaea	Halobacteriota	Methanosarcinia	Methanosarcinales	Methanosarcinaceae			0.699	Abundant	90.08	225	8595	1602817	1989841	41.4	1659	83.60	808	0	0	0	26	MQD
Zod_Metabat.786	JAFGQV000000000	80.27	0.98	Archaea	Halobacteriota	Methanosarcinia	Methanosarcinales	Methanosarcinaceae			0.732	Abundant	17.99	191	11990	1803207	2246427	44.4	1869	87.35	843	0	0	0	27	MQD
Zod_Metabat.485	JAFGMR000000000	98.53	0.65	Archaea	Halobacteriota	Methanosarcinia	Methanotrichales	Methanotrichaceae			0.747	Abundant	23.14	94	38897	2317673	2352251	56.1	2271	88.13	899	0	0	0	42	MQD
Zod_Metabat.543	JAFGNK000000000	95.42	1.31	Archaea	Halobacteriota	Methanosarcinia	Methanotrichales	Methanotrichaceae	Methanothrix		0.941	Abundant	99.87	212	13688	2371651	2485486	51.2	2465	85.82	826	0	0	0	43	MQD
Zod_Metabat.1428	JAFGHB000000000	91.18	3.76	Archaea	Halobacteriota	Syntropharchaeia	ANME-1	ANME-1	ANME-1-THS		0.845	Abundant	19.73	87	38372	2227763	2443258	49.2	2262	87.92	866	1	0	0	43	MQD
Zod_Metabat.342	JAFGKP000000000	75.18	4.58	Archaea	Halobacteriota	Syntropharchaeia	ANME-1	ANME-1	ANME-1-THS		0.853	Abundant	68.15	154	12029	1514744	2014823	54.6	1646	88.38	813	1	1	0	36	MQD
Zod_Metabat.968	JAFGTL000000000	89.78	1.2	Bacteria	Hydrogenedentota	Hydrogenedentia	Hydrogenedentiales	UBA2224			0.746	Rare	9.27	806	9054	6040148	6727721	66.3	5133	91.06	1072	0	0	0	25	MQD
Zod_Metabat.1151	JAFGDB000000000	88.32	0	Archaea	Iainarchaeota	Iainarchaeia	Iainarchaeales	GCA-2688035			0.734	Rare	10.48	106	14039	1068444	1209742	46.2	1210	91.63	809	1	0	0	34	MQD
Zod_Metabat.1228	JAFGEM000000000	77.26	0	Archaea	Iainarchaeota	Iainarchaeia	Iainarchaeales	GCA-2688035			0.697	Rare	9.24	128	8609	952776	1233207	41.2	1160	92.14	757	1	0	0	36	MQD
Zod_Metabat.1066	JAFGBZ000000000	90.65	0.93	Archaea	Iainarchaeota	Iainarchaeia	Iainarchaeales	Novel:ZNF05			0.643	Novel	11.12	100	12963	1000661	1103873	29.7	1135	93.28	822	1	0	0	40	MQD
Zod_Metabat.659	JAFGOX000000000	81.31	0	Archaea	Iainarchaeota	Iainarchaeia	Novel:ZNO04	Novel:ZNF06			0.355	Novel	10.52	52	13809	592378	728543	40.1	731	93.58	758	0	2	1	40	MQD
Zod_Metabat.1420	JAFGGZ000000000	84.83	0	Archaea	Iainarchaeota	Iainarchaeia	Novel:ZNO38	Novel:ZNF104			0.338	Novel	11.57	56	22101	839123	989182	55.4	991	93.87	795	1	0	1	27	MQD
Zod_Metabat.1031	JAFGBK000000000	94.51	0.55	Bacteria	Krumholzibacteriota	Krumholzibacteria	Novel:ZNO23	Novel:ZNF047			0.470	Novel	15.93	144	41304	3450757	3651208	71.6	2835	92.86	1130	1	1	1	39	HQD
Zod_Metabat.1015	JAFGBF000000000	95.54	2.2	Bacteria	Krumholzibacteriota	Krumholzibacteria	SSS58A	SSS58A	QTKG01	QTKG01 sp003369455	N/A	Rare	45.68	31	122473	2579306	2699713	49.7	2159	92.40	1104	1	0	0	45	MQD
Zod_Metabat.1142	JAFGCX000000000	97.8	2.2	Bacteria	Krumholzibacteriota	Krumholzibacteria	SSS58A	SSS58A	QTKG01	QTKG01 sp003369535	N/A	Rare	34.11	38	120218	3113963	3184011	50.8	2529	92.55	1140	1	0	0	42	MQD
Zod_Metabat.1283	JAFGEZ000000000	98.9	3.3	Bacteria	Krumholzibacteriota	Krumholzibacteria	SSS58A	SSS58A			0.780	Rare	14.32	51	90145	2967000	3000000	67.6	2456	92.87	1122	1	0	0	44	MQD
Zod_Metabat.682	JAFGPI000000000	92.31	1.1	Bacteria	Krumholzibacteriota	Krumholzibacteria	SSS58A	SSS58A			0.810	Rare	11.17	244	16155	3021010	3272679	55.8	2612	90.27	1044	0	0	0	38	MQD
Zod_Metabat.1132	JAFGCS000000000	79.06	9.89	Bacteria	KSB1	UBA2214	AABM5-25-91	Novel:ZNF048			0.552	Novel	10.31	1072	9255	7883242	9971214	40.4	5943	84.71	1124	0	0	0	33	MQD
Zod_Metabat.1197	JAFGDW000000000	85.65	4.58	Bacteria	KSB1	UBA2214	AABM5-25-91	Novel:ZNF048			0.612	Novel	17.41	381	32018	7894986	9217730	42.4	5971	85.90	1136	0	0	0	42	MQD
Zod_Metabat.436	JAFGMA000000000	96.64	3.4	Bacteria	KSB1	UBA2214	AABM5-25-91	Novel:ZNF048			0.556	Novel	13.85	452	24906	7579817	7843354	46	5452	84.69	1177	1	1	0	47	MQD
Zod_Metabat.605	JAFGOE000000000	87.85	2.2	Bacteria	KSB1	UBA2214	AABM5-25-91	Novel:ZNF048			0.601	Novel	25.74	134	45194	3611166	4110604	44.4	2748	89.11	1171	1	1	0	40	MQD
Zod_Metabat.1209	JAFGEC000000000	77.71	1.28	Bacteria	KSB1	UBA2214	UBA2214	UBA2214			0.702	Rare	48.43	713	13540	7225944	9298602	44	6054	87.68	1047	1	0	0	50	MQD
Zod_Metabat.28	JAFGJN000000000	94.34	2.2	Bacteria	KSB1	UBA2214	UBA2214	UBA2214			0.706	Rare	10.38	366	15219	4046472	4289243	52.4	3400	89.97	1071	0	0	0	40	MQD
Zod_Metabat.930	JAFGSU000000000	77.21	2.2	Bacteria	KSB1	UBA2214	UBA2214	UBA2214			0.781	Rare	9.78	551	8716	4055812	5252962	49.8	3450	86.83	1021	1	0	0	23	MQD
Zod_Metabat.251	JAFGJB000000000	92.12	3.3	Bacteria	KSB1	UBA2214	UBA2214	Zgenome-0027	Zgenome-0027		0.926	Rare	35.59	367	18918	4343692	4715254	50.8	3685	90.31	1065	0	0	0	29	MQD
Zod_Metabat.31	JAFGKD000000000	95.54	1.1	Bacteria	KSB1	UBA2214	UBA2214	Zgenome-0027	Zgenome-0027	Zgenome-0027 sp003854975	N/A	Rare	62.94	136	75161	5997843	6277834	46.8	4544	92.11	1216	0	0	0	44	MQD
Zod_Metabat.326	JAFGKJ000000000	87.85	4.4	Bacteria	KSB1	UBA2214	UBA2214	Zgenome-0027	Zgenome-0027	Zgenome-0027 sp003854995	N/A	Rare	206.43	416	10821	3460858	3939508	52.6	3047	92.05	1046	0	0	0	34	MQD
Zod_Metabat.863	JAFGSB000000000	93.34	2.2	Bacteria	KSB1	UBA2214	UBA2214	Zgenome-0027			0.704	Rare	20.59	179	55450	5391025	5775686	41.8	4214	87.84	1124	0	0	0	45	MQD
Zod_Metabat.481	JAFGMP000000000	94.44	1.1	Bacteria	Latescibacterota	Latescibacteria	Latescibacterales	Latescibacteraceae			0.767	Rare	15.67	521	16153	6093097	6451818	42.7	5061	88.45	1065	1	0	0	43	MQD
Zod_Metabat.1157	JAFGDE000000000	87.61	1.71	Bacteria	Margulisbacteria	WOR-1	O2-12-FULL-45-9	O2-12-FULL-45-9			0.790	Abundant	15.71	31	95689	1668633	1904615	53.6	1609	95.45	990	0	0	1	42	MQD
Zod_Metabat.143	JAFGHC000000000	88.89	0.85	Bacteria	Margulisbacteria	WOR-1	O2-12-FULL-45-9	XYB2-FULL-48-7	2-01-FULL-53-15		0.853	Abundant	37.93	42	47244	1531895	1723360	58	1479	93.19	965	0	1	0	42	MQD
ZodW_Metabat.180	JAFGVT000000000	76.18	0	Bacteria	Marinisomatota	AB16	AB16	Novel:ZNF050			0.696	Novel	12.87	207	7208	1351185	1773674	54.2	1302	92.64	961	1	0	0	24	MQD
Zod_Metabat.977	JAFGTP000000000	90.21	1.1	Bacteria	Marinisomatota	UBA2242	Novel:ZNO24	Novel:ZNF049			0.570	Novel	25.21	69	95686	4215448	4672928	40.8	3338	92.40	1167	0	0	0	44	MQD
ZodW_Metabat.79	JAFGXZ000000000	73.1	2.85	Bacteria	Marinisomatota	UBA2242	UBA2242	UBA2242	B118-G9		0.873	Abundant	9.19	364	7155	2242648	3067918	42.7	2194	93.71	958	1	0	0	27	MQD
ZodW_Metabat.255	JAFGWL000000000	96.63	0	Bacteria	McInerneybacteriota	McInerneyibacteria	Novel:ZNO25	Novel:ZNF088			0.319	Novel	12.01	71	45428	1879816	1945375	51	1876	95.93	961	0	0	0	44	MQD
Zod_Metabat.1406	JAFGGT000000000	76.73	1.27	Archaea	Methanobacteriota	Thermococci	Methanofastidiosales	NM3			0.764	Rare	58.75	120	14674	1236253	1611173	48.9	1426	93.04	807	1	0	0	39	MQD
Zod_Metabat.1079	JAFGCC000000000	93.15	0	Archaea	Micrarchaeota	Micrarchaeia	UBA10214	UBA10214			0.664	Rare	46.13	25	68288	1246214	1337857	52.7	1223	92.25	940	1	1	1	44	HQD
Zod_Metabat.667	JAFGPA000000000	85.75	0	Archaea	Micrarchaeota	Micrarchaeia	UBA10214	UBA10214			0.704	Rare	107.13	39	36011	1047127	1221139	43.2	1175	93.01	829	1	1	1	33	MQD
Zod_Metabat.797	JAFGQX000000000	89.49	0	Archaea	Micrarchaeota	Micrarchaeia	UBA10214	UBA10214			0.683	Rare	10.00	86	12761	845148	944405	39.5	955	94.17	833	0	1	1	31	MQD
Zod_Metabat.807	JAFGRB000000000	85.58	5.56	Bacteria	Myxococcota	B64-G9	B64-G9	B64-G9			0.726	Rare	18.68	481	23865	7741669	9046119	68.2	6252	92.87	1150	1	0	0	42	MQD
Zod_Metabat.1238	JAFGEP000000000	81.29	5.48	Bacteria	Myxococcota	Bradimonadia	Bradymonadales	Novel:ZNF056			0.564	Novel	30.39	167	58267	5703155	7015814	64.2	4157	89.43	1227	1	1	0	44	MQD
Zod_Metabat.575	JAFGNZ000000000	96.75	5.52	Bacteria	Myxococcota	Myxococcia	Myxococcales	Myxococcaceae	Hyalangium		0.964	Abundant	20.46	409	35526	9592223	9914442	69.7	7872	91.06	1110	0	0	0	75	MQD
ZodW_Metabat.263	JAFGWM000000000	86.13	1.77	Bacteria	Myxococcota	Polyangia	HGW-17	HGW-17			0.832	Rare	15.95	85	73658	4109015	4770713	39.4	3327	92.88	1147	0	0	0	45	MQD
Zod_Metabat.1445	JAFGHH000000000	79.57	4.16	Bacteria	Myxococcota	Polyangia	Novel:ZNO26	Novel:ZNF052			0.500	Novel	11.79	611	14516	6417104	8064728	72.8	5359	92.35	1106	0	0	0	39	MQD
Zod_Metabat.76	JAFGQN000000000	94.84	3.87	Bacteria	Myxococcota	Polyangia	Novel:ZNO27	Novel:ZNF053			0.493	Novel	24.82	249	51303	8161753	8605813	50.3	6749	88.18	1066	0	0	0	47	MQD
Zod_Metabat.947	JAFGTB000000000	94.19	3.23	Bacteria	Myxococcota	Polyangia	Novel:ZNO27	Novel:ZNF053			0.491	Novel	27.27	216	41988	6049167	6422303	51.4	5022	91.26	1099	0	0	0	41	MQD
ZodW_Metabat.174	JAFGVO000000000	91.24	3.26	Bacteria	Myxococcota	Polyangia	Novel:ZNO27	Novel:ZNF053			0.490	Novel	9.91	493	11036	4141693	4539339	38.3	3640	91.37	1040	0	0	0	39	MQD
ZodW_Metabat.284	JAFGWT000000000	89.08	3.87	Bacteria	Myxococcota	Polyangia	Novel:ZNO27	Novel:ZNF053			0.489	Novel	10.27	564	14988	6428606	7216666	51.5	5483	89.22	1046	0	0	0	44	MQD
ZodW_Metabat.4	JAFGXQ000000000	96.01	3.23	Bacteria	Myxococcota	Polyangia	Novel:ZNO27	Novel:ZNF053			0.491	Novel	91.32	252	36989	5908543	6154091	51.3	4949	91.36	1091	0	0	0	40	MQD
Zod_Metabat.714	JAFGPX000000000	92.04	2.6	Bacteria	Myxococcota	Polyangia	Palsa-1104	Fen-1088	Fen-1118		0.946	Abundant	69.45	341	26687	5385096	5850821	67.7	4570	90.18	1063	1	0	0	39	MQD
Zod_Metabat.169	JAFGIB000000000	90.7	1.94	Bacteria	Myxococcota	Polyangia	Polyangiales	Novel:ZNF051			0.660	Novel	67.12	462	19535	6222193	6860191	54.4	4931	85.31	1077	1	0	0	42	MQD
Zod_Metabat.1029	JAFGBI000000000	92.69	1.15	Bacteria	Myxococcota	Polyangia	Polyangiales	Polyangiaceae			0.820	Abundant	21.07	464	33939	8251119	8901844	68.4	6759	86.32	1054	1	0	0	43	MQD
Zod_Metabat.23	JAFGIS000000000	90.22	3.71	Bacteria	Myxococcota	Polyangia	Polyangiales	Polyangiaceae			0.824	Abundant	12.45	675	22864	9556717	10592681	66.3	8279	87.78	1013	1	0	0	62	MQD
Zod_Metabat.937	JAFGSX000000000	82.96	3.87	Bacteria	Myxococcota	UBA727	Novel:ZNO28	Novel:ZNF054			0.540	Novel	9.80	613	11879	5603776	6754793	69	4772	93.42	1097	1	0	0	41	MQD
Zod_Metabat.425	JAFGLY000000000	84.71	1.29	Bacteria	Myxococcota	UBA796	UBA796	Novel:ZNF055			0.646	Novel	71.49	216	28837	3989788	4709937	71	3440	93.74	1087	1	1	0	43	MQD
ZodW_Metabat.156	JAFGVK000000000	93.64	1.68	Bacteria	Myxococcota	UBA796	UBA796	Novel:ZNF055			0.685	Novel	34.00	246	34427	5193187	5545907	70.8	4077	87.82	1119	0	0	0	47	MQD
Zod_Metabat.1224	JAFGEK000000000	94.19	0.65	Bacteria	Myxococcota	XYA12-FULL-58-9	XYA12-FULL-58-9	XYA12-FULL-58-9			0.746	Rare	15.90	227	28063	4172418	4429789	40.2	3751	89.53	996	0	1	1	41	MQD
Zod_Metabat.1304	JAFGFH000000000	79.91	0.93	Archaea	Nanoarchaeota	Nanoarchaeia	CG07-land	CG07-land	CG07-land		0.809	Rare	17.29	26	77901	886719	1109647	37.3	1082	94.71	776	1	2	1	43	MQD
Zod_Metabat.390	JAFGLG000000000	90.65	0.93	Archaea	Nanoarchaeota	Nanoarchaeia	Woesearchaeales	B72-G16			0.629	Rare	105.73	17	187687	1483426	1636432	45.4	1493	90.71	901	0	1	1	46	MQD
Zod_Metabat.1084	JAFGCE000000000	78.04	1.87	Archaea	Nanoarchaeota	Nanoarchaeia	Woesearchaeales	CG08-08-20-14			0.668	Rare	10.22	87	14302	927099	1187979	41.9	1065	94.32	821	1	0	0	35	MQD
Zod_Metabat.161	JAFGHY000000000	72.47	0	Archaea	Nanoarchaeota	Nanoarchaeia	Woesearchaeales	GCA-2685855			0.698	Rare	9.52	92	11162	909952	1255626	43.8	1029	87.74	776	1	0	0	26	MQD
Zod_Metabat.297	JAFGJW000000000	86.92	0.93	Archaea	Nanoarchaeota	Nanoarchaeia	Woesearchaeales	GW2011-AR15			0.761	Rare	29.46	20	114087	1531415	1761867	36.8	1554	93.39	920	1	0	1	31	MQD
Zod_Metabat.833	JAFGRO000000000	86.45	1.87	Archaea	Nanoarchaeota	Nanoarchaeia	Woesearchaeales	GW2011-AR15			0.744	Rare	25.26	82	39236	1773445	2051411	33.6	1838	91.61	884	0	0	0	31	MQD
Zod_Metabat.908	JAFGSP000000000	74.3	0	Archaea	Nanoarchaeota	Nanoarchaeia	Woesearchaeales	GW2011-AR15	GW2011-AR15		0.816	Rare	9.28	204	7823	1364004	1835806	40.1	1534	92.57	823	0	0	0	22	MQD
Zod_Metabat.712	JAFGPW000000000	87.38	0	Archaea	Nanoarchaeota	Nanoarchaeia	Woesearchaeales	J091			0.630	Rare	127.01	10	216860	1398368	1600330	61.8	1347	92.13	957	1	0	0	45	MQD
Zod_Metabat.828	JAFGRM000000000	84.58	0	Archaea	Nanoarchaeota	Nanoarchaeia	Woesearchaeales	J091			0.626	Rare	12.48	102	15247	1257203	1486407	42.7	1192	85.41	901	1	0	0	36	MQD
Zod_Metabat.822	JAFGRH000000000	78.07	0	Archaea	Nanoarchaeota	Nanoarchaeia	Woesearchaeales	Novel:ZNF010			0.669	Novel	9.35	82	13323	827365	1059773	47	1033	94.35	756	0	0	0	32	MQD
Zod_Metabat.157	JAFGHW000000000	72.9	0	Archaea	Nanoarchaeota	Nanoarchaeia	Woesearchaeales	Novel:ZNF07			0.636	Novel	42.29	56	19817	873022	1197561	34.1	1014	91.52	788	0	2	2	40	MQD
Zod_Metabat.396	JAFGLI000000000	75.7	1.87	Archaea	Nanoarchaeota	Nanoarchaeia	Woesearchaeales	Novel:ZNF08			0.692	Novel	24.32	23	56580	773797	1022189	33.1	910	91.14	775	1	1	1	36	MQD
Zod_Metabat.513	JAFGNA000000000	80.84	0	Archaea	Nanoarchaeota	Nanoarchaeia	Woesearchaeales	Novel:ZNF09			0.702	Novel	16.53	24	59260	1109711	1372725	57.1	1183	91.24	856	1	0	0	45	MQD
Zod_Metabat.672	JAFGPE000000000	79.69	1.87	Archaea	Nanoarchaeota	Nanoarchaeia	Woesearchaeales	Novel:ZNF106			0.644	Novel	10.67	172	12322	1620839	2033930	41.6	1831	93.30	826	1	0	1	31	MQD
ZodW_maxbin.125	JAFGUC000000000	84.58	0	Archaea	Nanoarchaeota	Nanoarchaeia	Woesearchaeales	Novel:ZNF107			0.632	Novel	29.05	85	411490	1501420	1775148	30.4	1487	93.06	940	1	1	1	39	MQD
Zod_Metabat.644	JAFGOT000000000	72.66	1.25	Archaea	Nanoarchaeota	Nanoarchaeia	Woesearchaeales	SKGA01	SKGA01		0.834	Rare	15.24	40	35651	1016835	1399443	32.2	1047	91.72	891	2	0	0	28	MQD
Zod_Metabat.1039	JAFGBP000000000	76.64	0.93	Archaea	Nanoarchaeota	Nanoarchaeia	Woesearchaeales	SM23-78			0.800	Rare	11.35	85	18899	1266225	1652172	48.7	1309	87.86	850	1	0	0	35	MQD
Zod_Metabat.1155	JAFGDD000000000	77.73	1.87	Archaea	Nanoarchaeota	Nanoarchaeia	Woesearchaeales	SM23-78	SM23-78		0.836	Rare	36.64	28	90600	1338846	1722431	40.5	1422	88.57	834	1	0	0	38	MQD
Zod_Metabat.140	JAFGGS000000000	82.24	0	Archaea	Nanoarchaeota	Nanoarchaeia	Woesearchaeales	SM23-78	SM23-78		0.811	Rare	36.87	22	61056	1300433	1581266	49.7	1293	90.25	908	1	1	0	40	MQD
Zod_Metabat.825	JAFGRK000000000	78.5	0.07	Archaea	Nanoarchaeota	Nanoarchaeia	Woesearchaeales	SM23-78	SM23-78		0.840	Rare	13.39	35	52644	1223909	1559120	44.8	1336	89.22	817	0	0	0	38	MQD
Zod_Metabat.845	JAFGRQ000000000	74.3	1.87	Archaea	Nanoarchaeota	Nanoarchaeia	Woesearchaeales	UBA10107	UBA10107		0.839	Rare	12.46	59	14908	771067	1037775	36.8	955	92.46	747	1	0	0	33	MQD
Zod_Metabat.265	JAFGJH000000000	82.71	0	Archaea	Nanoarchaeota	Nanoarchaeia	Woesearchaeales	UBA11576			0.805	Rare	16.39	60	27002	1207989	1460511	51.1	1208	88.71	887	1	0	0	38	MQD
ZodW_Metabat.371	JAFGXL000000000	98.18	0.91	Bacteria	Nitrospirota	Thermodesulfovibrionia	Thermodesulfovibrionales	Novel:ZNF057			0.715	Novel	12.66	42	92637	1990635	2027536	43.5	1963	93.29	946	1	0	0	42	MQD
Zod_Metabat.949	JAFGTC000000000	94.48	1.12	Bacteria	OLB16	OLB16	SURF-12	SURF-12			0.774	Rare	13.79	316	27003	5958995	6307150	51.4	4792	88.92	1106	1	0	0	41	MQD
Zod_Metabat.1444	JAFGHG000000000	79.06	1.17	Bacteria	Omnitrophota	Koll11	4484-171	4484-171			0.805	Rare	9.51	225	10262	1786960	2260258	39.8	1850	94.64	914	0	0	0	31	MQD
Zod_Metabat.783	JAFGQU000000000	81	2.15	Bacteria	Omnitrophota	Koll11	4484-171	4484-171			0.794	Rare	28.03	24	120448	1812739	2237949	45.8	1783	91.22	927	1	1	0	45	MQD
Zod_Metabat.1076	JAFGCB000000000	88.11	2.15	Bacteria	Omnitrophota	Koll11	4484-171	B32-G15			0.796	Rare	18.39	79	40127	2134372	2422395	41.1	2020	91.59	968	1	1	0	41	MQD
Zod_Metabat.1253	JAFGET000000000	80.51	2.15	Bacteria	Omnitrophota	Koll11	GIF10	UBA6249			0.780	Abundant	9.06	198	8112	1412063	1753898	44.5	1533	94.02	866	0	0	0	28	MQD

ZodW_Metabat.114	JAFGUY000000000	86.32	1.68	Bacteria	Omnitrophota	Koll11	GIF10	UBA6249	GCA-002774445		0.898	Abundant	15.85	109	12722	1010152	1170241	41.1	1060	94.75	903	0	0	0	33	MQD
Zod_Metabat.234	JAFGIU000000000	92.41	1.08	Bacteria	Omnitrophota	Koll11	Novel:ZNO30	Novel:ZNF059			0.484	Novel	11.58	137	25671	2428575	2628044	55.4	2134	94.83	1079	1	0	0	44	MQD
Zod_Metabat.1390	JAFGGP000000000	86.56	1.08	Bacteria	Omnitrophota	Koll11	Novel:ZNO31	Novel:ZNF060			0.504	Novel	17.33	57	56984	1917213	2214895	50.1	1731	91.02	1008	1	1	0	37	MQD
Zod_Metabat.1113	JAFGCM000000000	81.8	1.61	Bacteria	Omnitrophota	Koll11	Novel:ZNO32	Novel:ZNF061			0.483	Novel	9.39	122	10115	1007404	1231545	45.5	1135	94.60	840	0	0	0	32	MQD
Zod_Metabat.1437	JAFGHF000000000	84.35	3.32	Bacteria	Omnitrophota	Koll11	Novel:ZNO32	Novel:ZNF061			0.483	Novel	11.95	76	40215	1743987	2067560	44.3	1732	95.16	958	1	1	1	40	MQD
Zod_Metabat.364	JAFGKX000000000	82.08	4.3	Bacteria	Omnitrophota	Koll11	Novel:ZNO32	Novel:ZNF062			0.481	Novel	9.23	161	9449	1242218	1513423	41.6	1286	95.65	924	0	0	0	27	MQD
Zod_Metabat.1316	JAFGFL000000000	81.84	1.08	Bacteria	Omnitrophota	Koll11	UBA10015	Kpj58rc	2-02-FULL-52-10		0.878	Abundant	14.67	94	39102	2196924	2684413	47	2009	91.53	1001	1	0	0	44	MQD
Zod_Metabat.276	JAFGJL000000000	93.3	2.69	Bacteria	Omnitrophota	Koll11	UBA1560	2-01-FULL-45-10			0.805	Abundant	12.75	79	28669	1504170	1612186	54.9	1460	94.67	975	1	0	0	43	MQD
Zod_Metabat.83	JAFGRN000000000	76.88	1.08	Bacteria	Omnitrophota	Koll11	UBA1560	2-01-FULL-45-10			0.839	Abundant	12.89	79	21988	1395464	1815120	50.5	1302	95.41	1023	1	0	1	30	MQD
Zod_Metabat.1290	JAFGFD000000000	80.58	4.66	Bacteria	Omnitrophota	Koll11	UBA1560	Novel:ZNF063			0.639	Novel	9.74	162	12634	1604881	1991662	45.3	1671	92.82	892	0	0	0	32	MQD
Zod_Metabat.422	JAFGLX000000000	80.52	2.69	Bacteria	Omnitrophota	Koll11	UBA1560	RBG-13-46-9			0.779	Rare	9.34	189	11600	1732882	2152114	44.5	1633	93.10	988	1	0	0	36	MQD
Zod_Metabat.301	JAFGJY000000000	81.72	1.08	Bacteria	Omnitrophota	Omnitrophia	Novel:ZNO29	Novel:ZNF058			0.436	Novel	25.63	131	17966	1733125	2120809	45.2	1630	91.71	975	0	0	0	32	MQD
Zod_Metabat.1447	JAFGHI000000000	87.28	0	Bacteria	Omnitrophota	Omnitrophia	Omnitrophales	GWA2-52-8			0.726	Rare	13.06	63	66836	2307202	2643449	46.9	1955	93.18	1100	0	0	0	37	MQD
Zod_Metabat.338	JAFGKM000000000	93.73	0	Bacteria	Omnitrophota	UBA8468	UBA8468	B48-G9			0.754	Rare	15.58	94	32890	1950702	2081193	47.3	1836	92.36	981	1	1	0	45	MQD
ZodW_maxbin.059	JAFGTW000000000	72.19	0.99	Bacteria	Patescibacteria	ABY1	BM507	UBA12465	GCA-002841655		0.922	Abundant	76.89	55	28129	800563	1108967	34.7	781	90.33	926	1	1	0	44	MQD
ZodW_maxbin.194	JAFGUO000000000	71.03	3.98	Bacteria	Patescibacteria	ABY1	BM507	UBA12465			0.852	Abundant	13.19	90	12195	739876	1041639	33.8	711	90.24	939	1	1	0	36	MQD
Zod_Metabat.1414	JAFGGX000000000	75.25	0	Bacteria	Patescibacteria	ABY1	Buchananbacterales	UBA6539			0.813	Abundant	13.38	53	20786	897161	1192241	38.5	913	87.83	863	1	1	1	42	MQD
Zod_Metabat.236	JAFGIV000000000	70.46	1.49	Bacteria	Patescibacteria	ABY1	SG8-24	SG8-24			0.807	Abundant	17.51	28	58444	1099857	1560967	57.8	1074	88.92	911	0	2	0	43	MQD
Zod_Metabat.442	JAFGMD000000000	71.29	1.98	Bacteria	Patescibacteria	ABY1	XYB2-FULL-38-15	Novel:ZNF064			0.617	Novel	19.51	42	34808	945878	1326803	35.2	969	88.63	865	1	2	0	46	MQD
Zod_Metabat.1179	JAFGDO000000000	78.29	0.86	Bacteria	Patescibacteria	Dojkabacteria	B142	Novel:ZNF065			0.603	Novel	33.46	32	110462	1463828	1869751	36.9	1334	87.23	957	0	1	2	48	MQD
Zod_Metabat.1309	JAFGFJ000000000	77.43	5.17	Bacteria	Patescibacteria	Dojkabacteria	B142	Novel:ZNF065			0.635	Novel	65.43	10	559650	971167	1254252	37.2	925	88.70	931	1	1	1	47	MQD
Zod_Metabat.46	JAFGMG000000000	71.25	1.12	Bacteria	Patescibacteria	Dojkabacteria	B142	Novel:ZNF065			0.657	Novel	21.60	15	120433	908235	1274716	38.9	880	93.15	961	1	1	1	46	MQD
Zod_Metabat.404	JAFGLO000000000	73.82	0	Bacteria	Patescibacteria	Dojkabacteria	SC72	Novel:ZNF066			0.594	Novel	86.52	15	84631	849368	1150593	38.2	809	90.42	949	0	1	1	44	MQD
Zod_Metabat.1102	JAFGCJ000000000	81.74	1.72	Bacteria	Patescibacteria	Dojkabacteria	SC72	Novel:ZNF067			0.586	Novel	65.12	7	598548	1056757	1292827	40.5	982	90.37	973	1	1	1	49	MQD
Zod_Metabat.200	JAFGIK000000000	80.72	1.72	Bacteria	Patescibacteria	Dojkabacteria	SC72	Novel:ZNF067			0.585	Novel	42.08	109	31320	1586902	1965934	34.8	1438	87.48	965	1	1	1	53	MQD
Zod_Metabat.293	JAFGJT000000000	83.66	0	Bacteria	Patescibacteria	Gracilibacteria	UBA1369	Novel:ZNF068			0.629	Novel	25.84	20	108028	1127696	1347951	38.5	1025	92.43	1017	1	1	1	43	MQD
Zod_Metabat.1128	JAFGCR000000000	81.02	0.93	Bacteria	Patescibacteria	Gracilibacteria	UM-FILTER-43-11	UM-FILTER-43-11			0.798	Rare	69.44	50	32845	1175011	1450273	47.9	1095	89.66	962	0	1	1	47	MQD
Zod_Metabat.1133	JAFGCT000000000	81.94	0.62	Bacteria	Patescibacteria	Gracilibacteria	UM-FILTER-43-11	UM-FILTER-43-11			0.777	Rare	255.04	39	68048	1346587	1643382	35	1261	87.74	937	1	0	1	39	MQD
Zod_Metabat.530	JAFGNE000000000	70.83	0.1	Bacteria	Patescibacteria	Gracilibacteria	UM-FILTER-43-11	UM-FILTER-43-11			0.772	Rare	9.66	99	10391	915282	1292224	50.4	921	93.40	928	0	1	0	37	MQD
Zod_Metabat.950	JAFGTE000000000	75.84	1.12	Bacteria	Patescibacteria	Gracilibacteria	UM-FILTER-43-11	UM-FILTER-43-11			0.770	Rare	15.40	34	35727	1013440	1336287	45.1	975	92.73	964	1	1	0	38	MQD
Zod_Metabat.691	JAFGPN000000000	72.44	0.99	Bacteria	Patescibacteria	Kazan-3B-28	Kazan-3B-28	UBA10110	2-01-FULL-49-10		0.939	Rare	21.04	18	56839	670276	925284	47.5	644	88.72	923	0	1	0	42	MQD
Zod_Metabat.670	JAFGPD000000000	77.43	2.59	Bacteria	Patescibacteria	Microgenomatia	GWA2-44-7	UBA8517			0.739	Abundant	20.88	57	29459	1114049	1438782	37.5	1171	89.90	855	0	0	0	37	MQD
Zod_Metabat.464	JAFGMK000000000	75.71	1.72	Bacteria	Patescibacteria	Microgenomatia	UBA1400	Novel:ZNF069			0.623	Novel	19.29	31	57242	1193203	1576018	43.4	1154	90.34	934	0	0	1	41	MQD
Zod_Metabat.1002	JAFGBB000000000	72.7	0	Bacteria	Patescibacteria	Paceibacteria	UBA6257	UBA9933	UM-FILTER-39-64		0.856	Abundant	24.29	35	22621	608694	837268	31.3	645	89.46	844	0	1	1	46	MQD
Zod_Metabat.1126	JAFGCQ000000000	76.85	0.86	Bacteria	Patescibacteria	Paceibacteria	UBA9983	Zambryskibacteraceae			0.888	Abundant	15.68	33	45949	607940	791074	35.6	664	89.84	823	1	0	0	39	MQD
Zod_Metabat.613	JAFGOI000000000	73.98	1.72	Bacteria	Patescibacteria	WWE3	UBA101185	UBA10185			0.798	Abundant	17.58	13	170802	872428	1179275	38.4	839	92.73	964	1	1	0	34	MQD
Zod_Metabat.715	JAFGPY000000000	78.98	4.55	Bacteria	Planctomycetota	FEN-1346	FEN-1346	Novel:ZNF070			0.625	Novel	20.98	457	12721	4345568	5502112	65.3	3721	87.89	1027	0	0	0	40	MQD
Zod_Metabat.1017	JAFGBG000000000	90.73	1.14	Bacteria	Planctomycetota	Phycisphaerae	Sedimentisphaerales	Anaerohalophaeraceae			0.895	Abundant	81.06	270	22084	4238465	4671514	46	3534	87.62	1051	1	0	0	49	MQD
Zod_Metabat.1071	JAFGCA000000000	90.91	0	Bacteria	Planctomycetota	Phycisphaerae	Sedimentisphaerales	Anaerohalophaeraceae	PLanc-01		0.916	Abundant	11.18	836	12963	7878841	8666638	61.6	6591	87.49	1046	0	2	0	52	MQD
Zod_Metabat.1083	JAFGCD000000000	97.73	0	Bacteria	Planctomycetota	Phycisphaerae	Sedimentisphaerales	Anaerohalophaeraceae			0.887	Abundant	33.72	157	41993	4161664	4258328	54.4	3288	89.53	1133	1	0	0	46	MQD
Zod_Metabat.1177	JAFGDN000000000	97.73	0	Bacteria	Planctomycetota	Phycisphaerae	Sedimentisphaerales	Anaerohalophaeraceae	Fen-1362		0.917	Abundant	22.25	94	47427	2950782	3019321	49.3	2608	89.27	1010	0	0	0	45	MQD
Zod_Metabat.1213	JAFGEF000000000	95.45	1.14	Bacteria	Planctomycetota	Phycisphaerae	Sedimentisphaerales	Anaerohalophaeraceae			0.887	Abundant	115.47	173	41099	4548764	4765599	41.2	3821	88.40	1052	1	0	0	50	MQD
Zod_Metabat.1370	JAFGGE000000000	89.77	2.27	Bacteria	Planctomycetota	Phycisphaerae	Sedimentisphaerales	Anaerohalophaeraceae	FEN-1350		0.854	Abundant	14.62	294	19530	4110405	4578818	54.3	3448	91.00	1085	0	0	0	37	MQD
Zod_Metabat.138	JAFGGH000000000	76.96	0	Bacteria	Planctomycetota	Phycisphaerae	Sedimentisphaerales	Anaerohalophaeraceae			0.820	Abundant	15.90	103	33067	2179384	2831840	44.7	1931	88.65	1001	0	0	0	30	MQD
Zod_Metabat.1380	JAFGGI000000000	97.73	0	Bacteria	Planctomycetota	Phycisphaerae	Sedimentisphaerales	Anaerohalophaeraceae			0.854	Abundant	34.53	64	52163	2454332	2511339	43.7	2101	90.41	1056	0	0	0	51	MQD
Zod_Metabat.1411	JAFGGV000000000	95.45	9.66	Bacteria	Planctomycetota	Phycisphaerae	Sedimentisphaerales	Anaerohalophaeraceae			0.893	Abundant	20.57	188	45541	4693474	4917207	44.6	3944	87.01	1035	2	0	0	54	MQD
Zod_Metabat.289	JAFGJR000000000	96.59	9.09	Bacteria	Planctomycetota	Phycisphaerae	Sedimentisphaerales	Anaerohalophaeraceae	PLanc-01		0.922	Abundant	26.03	340	31377	6611224	6844626	61.3	5394	88.22	1081	0	0	0	52	MQD
Zod_Metabat.331	JAFGKL000000000	82.75	0	Bacteria	Planctomycetota	Phycisphaerae	Sedimentisphaerales	Anaerohalophaeraceae			0.810	Abundant	69.98	179	13606	1833900	2216193	44.5	1709	90.72	974	0	0	0	32	MQD
Zod_Metabat.388	JAFGLE000000000	88.57	8.52	Bacteria	Planctomycetota	Phycisphaerae	Sedimentisphaerales	Anaerohalophaeraceae	RBG-13-46-10		0.871	Abundant	12.63	199	20244	2501228	2824013	47.7	2312	88.57	958	0	0	0	51	MQD
Zod_Metabat.417	JAFGLV000000000	83.32	1.14	Bacteria	Planctomycetota	Phycisphaerae	Sedimentisphaerales	Anaerohalophaeraceae	PLanc-01		0.924	Abundant	18.79	180	49419	5339645	6408599	61.9	4328	88.29	1089	0	0	0	38	MQD
Zod_Metabat.67	JAFGPC000000000	94.32	1.14	Bacteria	Planctomycetota	Phycisphaerae	Sedimentisphaerales	Anaerohalophaeraceae	FEN-1350		0.856	Abundant	35.65	222	37288	5015080	5317091	49.7	4098	90.58	1109	0	0	0	51	MQD
Zod_Metabat.683	JAFGPJ000000000	75.88	3.41	Bacteria	Planctomycetota	Phycisphaerae	Sedimentisphaerales	Anaerohalophaeraceae			0.894	Abundant	20.46	456	10325	3937029	5188494	48.5	3429	89.54	1028	0	0	0	40	MQD
Zod_Metabat.706	JAFGPS000000000	86.56	5.38	Bacteria	Planctomycetota	Phycisphaerae	Sedimentisphaerales	Anaerohalophaeraceae			0.887	Abundant	30.42	217	32676	4356545	5032977	38.8	3698	89.06	1049	0	0	0	43	MQD
Zod_Metabat.769	JAFGQP000000000	81.77	3.41	Bacteria	Planctomycetota	Phycisphaerae	Sedimentisphaerales	Anaerohalophaeraceae	UBA7708		0.987	Abundant	25.82	381	13080	3825677	4678583	51.1	3207	89.76	1071	1	0	0	34	MQD
Zod_Metabat.827	JAFGRL000000000	97.73	9.03	Bacteria	Planctomycetota	Phycisphaerae	Sedimentisphaerales	Anaerohalophaeraceae	B140-G9		0.891	Abundant	13.21	199	20550	2857869	2924249	44.6	2675	87.27	932	2	0	0	59	MQD
Zod_Metabat.96	JAFGTG000000000	81.68	0	Bacteria	Planctomycetota	Phycisphaerae	Sedimentisphaerales	Anaerohalophaeraceae			0.889	Abundant	64.40	634	12526	6317079	7733936	51.4	5354	88.46	1044	1	0	0	56	MQD
Zod_Metabat.999	JAFGTU000000000	76.48	2.27	Bacteria	Planctomycetota	Phycisphaerae	Sedimentisphaerales	Anaerohalophaeraceae			0.884	Abundant	10.71	567	9200	4434503	5798252	54.9	3895	88.79	1011	0	1	0	39	MQD
Zod_Metabat.1166	JAFGDI000000000	72.5	0.1	Bacteria	Planctomycetota	Phycisphaerae	Sedimentisphaerales	Novel:ZNF071			0.693	Novel	9.12	398	7784	2632508	3631046	44.8	2123	86.73	1075	0	1	0	20	MQD
ZodW_maxbin.277	JAFGUW000000000	86.43	0.57	Bacteria	Planctomycetota	Phycisphaerae	Sedimentisphaerales	Novel:ZNF071			0.691	Novel	8.47	716	7456	3692144	4271832	44.9	3047	85.91	1041	0	0	0	36	MQD
Zod_Metabat.1001	JAFGBA000000000	73.02	0	Bacteria	Planctomycetota	Phycisphaerae	Sedimentisphaerales	SM23-30			0.737	Rare	21.94	384	10547	3371326	4616990	51.2	2961	88.92	1013	0	1	0	37	MQD
Zod_Metabat.1349	JAFGFX000000000	83.86	0.57	Bacteria	Planctomycetota	Phycisphaerae	Sedimentisphaerales	SM23-30			0.767	Rare	33.11	406	12239	3901033	4651840	63.3	2949	85.22	1127	0	0	0	35	MQD
Zod_Metabat.1436	JAFGHE000000000	86.86	0	Bacteria	Planctomycetota	Phycisphaerae	Sedimentisphaerales	SM23-30			0.763	Rare	11.36	329	16749	4229061	4868825	47.9	3337	86.92	1102	1	1	0	47	MQD
Zod_Metabat.35	JAFGKT000000000	84.09	0	Bacteria	Planctomycetota	Phycisphaerae	Sedimentisphaerales	SM23-30			0.750	Rare	18.74	80	59654	3073187	3654640	51.1	2439	85.38	1076	0	0	0	40	MQD
Zod_Metabat.916	JAFGSR000000000	89.77	0	Bacteria	Planctomycetota	Phycisphaerae	Sedimentisphaerales	SM23-30			0.781	Rare	16.31	253	25963	4511089	5025163	49.2	3493	86.31	1115	1	1	1	44	MQD
Zod_Metabat.1221	JAFGEJ000000000	89.57	1.14	Bacteria	Planctomycetota	Phycisphaerae	SM23-33	SM23-33	B1-G9		0.859	Abundant	42.07	289	12350	2823786	3152602	59.7	2369	83.71	998	0	0	0	43	MQD
Zod_Metabat.26	JAFGJE000000000	93.99	2.27	Bacteria	Planctomycetota	Phycisphaerae	SM23-33	SM23-33	B1-G9		0.862	Abundant	21.07	263	21786	4161089	4427161	58.5	3432	86.67	1051	1	0	0	43	MQD
Zod_Metabat.846	JAFGRR000000000	83.9	2.27	Bacteria	Planctomycetota	Phycisphaerae	UBA1845	Fen-1342			0.814	Rare	8.68	719	6705	4233034	5045333	63.5	3837	87.44	965	1	1	0	32	MQD
Zod_Metabat.304	JAFGKA000000000	87.81	5.68	Bacteria	Planctomycetota	Phycisphaerae	UBA1845	Novel:ZNF072			0.678	Novel	51.28	606	10805	5282483	6015810	63.8	4496	86.93	1021	1	0	1	37	MQD
Zod_Metabat.429	JAFGLZ000000000	98.86	0.1	Bacteria	Planctomycetota	Phycisphaerae	UBA1845	Novel:ZNF073			0.678	Novel	14.42	274	54993	9250279	9356948	64.4	6920	88.00	1176	0	0	1	-3	MQD
Zod_Metabat.286	JAFGJQ000000000	90.62	5.11	Bacteria	Planctomycetota	Phycisphaerae	UBA1845	UBA1845			0.780	Rare	11.00	530	16059	5803548	6404268	65	4797	87.69	1061	0	1	1	51	MQD
Zod_Metabat.718	JAFGQA000000000	95.45	5.68	Bacteria	Planctomycetota	Phycisphaerae	UBA1845	UTPLA1			0.827	Rare	16.89	506	18313	6384335	6688669	62.6	5199	84.31	1035	2	0	0	59	MQD
Zod_Metabat.1355	JAFGFZ000000000	88.96	2.3	Bacteria	Planctomycetota	Planctomycetes	Pirellulales	Ga0077529			0.795	Abundant	28.90	528	14230	5553417	6242600	54.7	4551	89.37	1091	0	0	0	26	MQD
Zod_Metabat.10	JAFGAY000000000	90.74	1.15	Bacteria	Planctomycetota	Planctomycetes	Pirellulales	UBA11386	UBA11386		0.876	Abundant	19.95	406	11809	3734388	4115482	61.6	2975	85.63	1075	0	0	0	36	MQD
Zod_Metabat.1184	JAFGDS000000000	97.7	0	Bacteria	Planctomycetota	Planctomycetes	Pirellulales	UBA11386			0.837	Abundant	52.22	153	58178	5430075	5557907	66.1	4090	85.76	1139	0	0	0	54	MQD
Zod_Metabat.1299	JAFGFF000000000	95.4	2.87	Bacteria	Planctomycetota	Planctomycetes	Pirellulales	UBA11386			0.848	Abundant	12.69	491	18626	6061764	6354050	61.9	4845	84.55	1058	0	0	0	72	MQD
Zod_Metabat.223	JAFGIR000000000	87.29	0.1	Bacteria	Planctomycetota	Planctomycetes	Pirellulales	UBA11386	UBA11386		0.891	Abundant	10.95	503	12161	4603293	5273563	60.6	3912	85.68	1008	1	0	0	44	MQD
Zod_Metabat.393	JAFGLH000000000	89.08	1.15	Bacteria	Planctomycetota	Planctomycetes	Pirellulales	UBA11386			0.785	Abundant	15.66	269	18863	3623539	4067736	60.8	3040	87.15	1039	0	0	0	56	MQD
Zod_Metabat.711	JAFGPV000000000	96.55	0	Bacteria	Planctomycetota	Planctomycetes	Pirellulales	UBA11386			0.794	Abundant	18.02	212	41036	5375127	5567195	60.4	4108	85.57	1120	0	0	1	60	MQD
Zod_Metabat.813	JAFGRD000000000	93.1	0	Bacteria	Planctomycetota	Planctomycetes	Pirellulales	UBA11386			0.796	Abundant	20.96	172	78477	7102429	7628817	64.6	4806	88.75	1312	0	0	0	43	MQD
Zod_Metabat.975	JAFGTN000000000	78.74	3.45	Bacteria	Planctomycetota	Planctomycetes	Pirellulales	UBA11386			0.839	Abundant	10.39	929	9667	7441541	9450776	54	6512	86.92	993	0	0	0	44	MQD
Zod_Metabat.1381	JAFGGJ000000000	87.81	0.54	Bacteria	Planctomycetota	SZUA-567	Novel:ZNO43	Novel:ZNF075			0.437	Novel	14.75	96	56577	3395508	3866881	61.8	2803	93.49	1133	1	0	0	38	MQD
Zod_Metabat.533	JAFGNG000000000	75.35	1.17	Bacteria	Planctomycetota	SZUA-567	SZUA-567	Novel:ZNF074			0.593	Novel	9.71	297	9153	2327191	3088508	53.3	2130	89.85	982	0	0	0	39	MQD
ZodW_Metabat.298	JAFGWW000000000	74.48	0	Bacteria	Planctomycetota	SZUA-567	SZUA-567	Novel:ZNF074			0.690	Novel	8.43	506	8668	3657461	4910662	54.3	3503	89.60	936	0	0	0	55	MQD
Zod_Metabat.792	JAFGQW000000000	93.75	2.91	Bacteria	Planctomycetota	UBA8108	Novel:ZNO44	Novel:ZNF076			0.460	Novel	25.78	405	18051	4891853	5217977	70.9	3798	88.47	1140	1	0	0	44	MQD
Zod_Metabat.340	JAFGKN000000000	74.73	0	Bacteria	Planctomycetota	UBA8108	UBA8108	UBA8108			0.769	Rare	14.53	871	5562	4424978	5921287	68.6	3582	88.69	1096	0	0	0	24	MQD
Zod_Metabat.384	JAFGLC000000000	86.02	9.14	Bacteria	Planctomycetota	UBA8108	UBA8890	Novel:ZNF077			0.687	Novel	10.07	780	13789	8064695	9375372	69.6	5931	92.66	1260	0	1	0	39	MQD
ZodW_maxbin.058	JAFGTV000000000	96.8	1.06	Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Rhodovulum		0.939	Abundant	84.69	70	126152	2908307	3004449	66.2	2858	91.63	932	0	0	0	36	MQD
ZodW_Metabat.191	JAFGVZ000000000	88.79	1.12	Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Roseibaca		0.980	Abundant	18.35	247	12903	2464395	2775532	61.7	2649	92.90	864	0	0	0	28	MQD
ZodW_Metabat.253	JAFGWK000000000	96.08	0.71	Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Thioclava		0.996	Abundant	27.36	307	13013	2965688	3086686	59.9	3111	90.96	867	0	0	0	43	MQD
ZodW_Metabat.71	JAFGXY000000000	97.8	1.21	Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Cypionkella		0.975	Abundant	12.71	77	56431	3068624	3137652	63.7	3076	90.58	904	0	0	0	39	MQD
ZodW_Metabat.220	JAFGWD000000000	70.11	5.56	Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae	Alpha-05		0.911	Abundant	8.07	333	7549	2173154	3099635	56.6	2248	91.29	883	0	0	0	26	MQD
Zod_Metabat.1412	JAFGGW000000000	74.18	0	Bacteria	Proteobacteria	Alphaproteobacteria	Rs-D84	NBLK01	NBLK01		0.891	Rare	9.15	117	6976	693519	934914	39.4	812	91.01	777	0	0	0	23	MQD
ZodW_Metabat.18	JAFGVS000000000	91.21	0	Bacteria	Proteobacteria	Alphaproteobacteria	Rs-D84	NBLK01	NBLK01		0.894	Rare	10.52	67	17499	852340	934481	39.3	923	89.87	830	1	0	0	31	MQD
ZodW_Metabat.337	JAFGXE000000000	79.02	2.3	Bacteria	Proteobacteria	Alphaproteobacteria	Rs-D84	NBLK01	NBLK01		0.858	Rare	10.55	110	7860	760666	962625	37.8	826	90.99	838	0	0	0	31	MQD
Zod_Metabat.441	JAFGMC000000000	86.01	0	Bacteria	Proteobacteria	Alphaproteobacteria	Rs-D84	Rs-D84	Rs-D84		0.944	Abundant	50.55	14	69326	764220	888525	35.1	765	92.16	921	0	0	0	44	MQD
Zod_Metabat.497	JAFGMU000000000	84.92	0	Bacteria	Proteobacteria	Alphaproteobacteria	Rs-D84	Rs-D84	Rs-D84		0.943	Abundant	29.08	46	21660	779205	917575	36	809	91.93	885	0	1	0	43	MQD
ZodW_Metabat.347	JAFGXG000000000	88.46	1.1	Bacteria	Proteobacteria	Alphaproteobacteria	Rs-D84	Rs-D84	Rs-D84		0.946	Abundant	51.97	12	176852	766725	866748	35.2	775	92.15	912	0	0	0	47	MQD
ZodW_Metabat.30	JAFGWY000000000	90.41	7.25	Bacteria	Proteobacteria	Gammaproteobacteria	Acidithiobacillales	Acidithiobacillaceae	Acidithiobacillus		0.988	Abundant	13.20	177	18328	2241664	2479443	55.3	2330	93.58	900	0	0	0	32	MQD
ZodW_Metabat.308	JAFGXB000000000	91.61	1.5	Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Burkholderiaceae	Thiomonas		0.983	Abundant	9.24	317	12153	2843638	3104069	64.2	2871	91.57	907	0	0	0	36	MQD
ZodW_maxbin.084	JAFGTZ000000000	91.62	2.18	Bacteria	Proteobacteria	Gammaproteobacteria	Chromatiales	Chromatiaceae	Marichromatium		0.915	Abundant	44.49	527	7799	2750919	3002531	65.4	2750	91.59	916	0	0	0	35	MQD
ZodW_maxbin.154	JAFGUH000000000	96.83	3.86	Bacteria	Proteobacteria	Gammaproteobacteria	Halothiobacillales	Halothiobacillaceae	Guyparkeria		0.973	Abundant	22.56	267	23644	2395148	2473560	65.8	2217	88.15	952	0	0	0	19	MQD
ZodW_maxbin.192	JAFGUN000000000	98.28	0	Bacteria	Proteobacteria	Gammaproteobacteria	Halothiobacillales	Halothiobacillaceae	Halothiobacillus	Halothiobacillus sp002281295	N/A	Abundant	12.26	165	22634	2281448	2321376	53.6	2197	91.65	952	0	0	0	34	MQD
Zod_Metabat.401	JAFGLM000000000	96.87	0.35	Bacteria	Proteobacteria	Gammaproteobacteria	HTCC5015	HTCC5015			0.718	Rare	17.98	58	84335	2669552	2755809	47.1	2493	91.40	979	0	0	0	43	MQD
ZodW_Metabat.299	JAFGWX000000000	75.79	1.91	Bacteria	Proteobacteria	Gammaproteobacteria	Methylococcales	Methylothermaceae	Methylohalobius	Methylohalobius crimeensis	N/A	Rare	8.49	380	7755	2617835	3454064	58.2	2852	92.03	845	0	0	0	33	MQD
ZodW_maxbin.150	JAFGUG000000000	96.38	0	Bacteria	Proteobacteria	Gammaproteobacteria	Thiomicrospirales	Thiomicrospiraceae	Thiomicrorhabdus		0.923	Abundant	17.86	108	162652	2933684	3043872	43.5	2693	89.47	975	0	0	0	41	MQD
ZodW_Metabat.390	JAFGXP000000000	98.17	0.61	Bacteria	Proteobacteria	Gammaproteobacteria	Thiomicrospirales	Thiomicrospiraceae	Thiomicrorhabdus		0.937	Abundant	18.21	49	60777	2120385	2159911	47.8	1972	90.44	973	0	0	0	38	MQD
ZodW_Metabat.9	JAFGYC000000000	74.63	0	Bacteria	Proteobacteria	Gammaproteobacteria	Thiomicrospirales	Thiomicrospiraceae	Hydrogenovibrio		0.994	Abundant	43.47	144	16958	1787821	2395580	44.7	1802	91.59	909	0	0	0	28	MQD
Zod_Metabat.15	JAFGHQ000000000	82.27	1.36	Bacteria	Proteobacteria	Gammaproteobacteria	UBA12402	UBA12402			0.833	Abundant	50.79	114	17123	1310027	1592351	37.9	1218	86.67	932	0	1	0	45	MQD
Zod_Metabat.529	JAFGNC000000000	80.77	4.85	Bacteria	Proteobacteria	Gammaproteobacteria	UBA6522	UBA6522	FEN-1219		0.869	Abundant	11.94	619	9026	4553460	5637563	68.5	4348	90.73	950	1	0	0	35	MQD
ZodW_Metabat.305	JAFGXA000000000	89.53	0.58	Bacteria	Proteobacteria	Gammaproteobacteria	UBA9339	UBA9339			0.783	Rare	31.49	59	40683	1334380	1490428	38.1	1280	93.24	972	0	0	0	45	MQD
Zod_Metabat.1115	JAFGCN000000000	83.18	2.8	Archaea	QMZS01	QMZS01	QMZS01	QMZS01			0.694	Rare	15.75	29	60056	1263699	1519234	46.7	1388	91.91	837	1	1	1	31	MQD
Zod_Metabat.53	JAFGND000000000	95.6	0	Bacteria	RBG-13-66-14	Novel:ZNC10	Novel:ZNO32	Novel:ZNF078			0.396	Novel	15.89	109	37911	2991973	3129679	35.9	2725	94.36	1036	0	2	1	45	MQD
Zod_maxbin.0504	JAFGAX000000000	71.43	1.1	Bacteria	SM23-31	SM23-31	QNDG01	Novel:ZNF079			0.598	Novel	13.47	227	22347	2700592	3780753	61.4	2273	90.70	1078	0	0	0	32	MQD
Zod_Metabat.1116	JAFGCO000000000	94.51	4.4	Bacteria	SM23-31	SM23-31	QNDG01	Novel:ZNF079			0.608	Novel	31.85	72	90842	4411322	4667572	43.6	3425	89.45	1152	0	0	0	48	MQD
Zod_Metabat.1186	JAFGDT000000000	96.64	1.1	Bacteria	SM23-31	SM23-31	QNDG01	Novel:ZNF079			0.609	Novel	27.88	140	47009	3536956	3659930	43	3103	89.93	1025	1	0	0	47	MQD
Zod_Metabat.1270	JAFGEX000000000	84.62	3.3	Bacteria	SM23-31	SM23-31	QNDG01	Novel:ZNF079			0.612	Novel	11.07	412	12286	3890793	4597959	56.4	3336	89.30	1042	1	0	0	33	MQD
Zod_Metabat.1387	JAFGGN000000000	95.6	4.4	Bacteria	SM23-31	SM23-31	QNDG01	Novel:ZNF079			0.600	Novel	16.33	141	56034	4994489	5224361	51.5	3898	90.52	1160	1	0	0	45	MQD
Zod_Metabat.86	JAFGRY000000000	94.44	1.1	Bacteria	SM23-31	SM23-31	QNDG01	Novel:ZNF079			0.624	Novel	26.96	52	118982	4399361	4658366	56.2	3563	91.93	1135	0	0	0	38	MQD
Zod_Metabat.958	JAFGTF000000000	96.37	6.4	Bacteria	Spirochaetota	B62-G9	B62-G9	Novel:ZNF081			0.669	Novel	21.23	156	34463	3834888	3979338	53.6	3462	87.36	968	0	0	0	44	MQD
Zod_Metabat.719	JAFGQB000000000	86.05	4.8	Bacteria	Spirochaetota	GWE2-31-10	GWE2-31-10	GWE2-31-10			0.761	Abundant	183.51	310	17962	3717311	4319943	29.8	3428	89.64	972	1	0	0	26	MQD
Zod_Metabat.1289	JAFGFC000000000	97.75	0	Bacteria	Spirochaetota	Novel:ZNC11	Novel:ZNO33	Novel:ZNF080			0.279	Novel	13.21	204	22022	2884471	2950865	40.9	2591	93.71	1043	1	0	0	39	MQD
ZodW_maxbin.202	JAFGUP000000000	94.89	4.16	Bacteria	Spirochaetota	Spirochaetia	Sphaerochaetales	Sphaerochaetaceae			0.873	Abundant	12.29	395	14112	3066969	3232131	50.3	2976	91.30	941	0	0	0	46	MQD
Zod_Metabat.1463	JAFGHN000000000	78.74	2.87	Bacteria	Spirochaetota	Spirochaetia	Spirochaetales	ARS1246			0.791	Rare	21.62	348	9025	2525994	3208019	55.1	2526	93.76	938	0	0	0	22	MQD
Zod_Metabat.752	JAFGQL000000000	73.5	2.3	Bacteria	Spirochaetota	Spirochaetia	Spirochaetales	Marispirochaetaceae			0.741	Rare	38.25	182	26902	2983344	4058971	51.1	2726	93.63	1025	0	0	0	21	MQD
Zod_Metabat.1170	JAFGDJ000000000	84.92	1.72	Bacteria	Spirochaetota	Spirochaetia	Spirochaetales	Novel:ZNF082			0.652	Novel	85.05	260	18934	3256449	3834726	53.2	3116	94.33	986	2	0	0	32	MQD
Zod_Metabat.156	JAFGHV000000000	80.08	8.05	Bacteria	Spirochaetota	Spirochaetia	Spirochaetales	Novel:ZNF083			0.651	Novel	12.08	198	28219	3738850	4668894	47.4	3323	92.32	1039	0	0	0	35	MQD
ZodW_Metabat.38	JAFGXN000000000	97.7	0	Bacteria	Spirochaetota	Spirochaetia	Spirochaetales	Novel:ZNF084			0.656	Novel	12.26	168	27448	3256282	3332940	37.8	2773	93.43	1097	0	0	0	36	MQD
Zod_Metabat.1342	JAFGFV000000000	89.2	0	Bacteria	Spirochaetota	Spirochaetia	Spirochaetales	Novel:ZNF102			0.701	Novel	16.98	640	8232	4253845	4768885	66.5	4370	92.48	900	0	0	0	28	MQD
Zod_Metabat.745	JAFGQJ000000000	80.27	2.83	Bacteria	Spirochaetota	Spirochaetia	Spirochaetales	Novel:ZNF102			0.707	Novel	67.15	426	9965	3288469	4096760	61.6	3236	93.89	954	1	0	0	19	MQD
Zod_Metabat.1464	JAFGHO000000000	96	3.73	Bacteria	Spirochaetota	Spirochaetia	Spirochaetales	Novel:ZNF103			0.715	Novel	67.86	135	59675	5363805	5587297	48.3	4426	89.41	1084	1	0	0	46	MQD
Zod_Metabat.353	JAFGKU000000000	88.4	4.8	Bacteria	Spirochaetota	Spirochaetia	Spirochaetales	Novel:ZNF103			0.763	Novel	12.94	243	29527	5111004	5781679	46.2	4270	91.17	1091	1	0	0	45	MQD
Zod_Metabat.749	JAFGQK000000000	95.6	4.4	Bacteria	Spirochaetota	Spirochaetia	Spirochaetales	Novel:ZNF103			0.714	Novel	24.38	408	23092	6753453	7064281	40.1	5434	88.69	1102	1	0	0	45	MQD
Zod_Metabat.855	JAFGRV000000000	85.39	5.6	Bacteria	Spirochaetota	Spirochaetia	Spirochaetales	Novel:ZNF103			0.726	Novel	13.07	665	13594	6798499	7961704	40	5482	87.61	1087	1	0	0	34	MQD
ZodW_Metabat.242	JAFGWI000000000	92.03	2.4	Bacteria	Spirochaetota	Spirochaetia	Spirochaetales	Novel:ZNF103			0.752	Novel	19.36	335	24094	5088767	5529465	41.2	3978	82.28	1053	0	0	0	40	MQD
Zod_Metabat.1377	JAFGGG000000000	77.6	3.2	Bacteria	Spirochaetota	Spirochaetia	Spirochaetales	RPPD01			0.793	Rare	137.67	46	102953	3230593	4163135	42.9	2949	92.20	1010	0	1	0	36	MQD
Zod_Metabat.281	JAFGJO000000000	97.2	0.8	Bacteria	Spirochaetota	Spirochaetia	Spirochaetales	RPPD01	RPPD01		0.869	Rare	41.00	69	83640	3485276	3585675	45.3	3119	89.70	1002	0	0	0	45	MQD
Zod_Metabat.934	JAFGSW000000000	96	4.53	Bacteria	Spirochaetota	Spirochaetia	Spirochaetales	RPPD01			0.827	Rare	21.86	102	55726	4056940	4225979	59.1	3535	86.41	992	0	0	0	40	MQD
Zod_Metabat.700	JAFGPQ000000000	96.77	6.4	Bacteria	Spirochaetota	Spirochaetia	Spirochaetales	Spirochaetaceae_B	SZUA-368		0.963	Abundant	10.43	368	14534	3932230	4063480	53.9	3943	93.91	937	0	0	0	39	MQD
ZodW_Metabat.41	JAFGXR000000000	90.32	6.4	Bacteria	Spirochaetota	Spirochaetia	Spirochaetales	Spirochaetaceae_B			0.791	Abundant	25.10	134	59100	4727195	5233830	48.2	4225	93.70	1048	2	0	0	46	MQD
ZodW_Metabat.93	JAFGYD000000000	76.93	0	Bacteria	Spirochaetota	Spirochaetia	Spirochaetales	Spirochaetaceae_B	SZUA-382		0.937	Abundant	22.32	284	13965	2847966	3702023	31	2836	95.05	955	1	0	0	36	MQD
Zod_Metabat.209	JAFGIM000000000	79.85	0.35	Bacteria	Spirochaetota	Spirochaetia	Treponematales	Treponemataceae	Spiro-10		0.897	Abundant	11.09	165	18208	2163526	2709488	47.8	2076	95.79	998	0	0	0	34	MQD
ZodW_Metabat.118	JAFGVB000000000	82.11	0	Bacteria	Spirochaetota	Spirochaetia	Treponematales	Treponemataceae	Spiro-10		0.887	Abundant	9.46	342	7434	2252584	2743374	55.2	2227	94.37	955	0	0	0	34	MQD
Zod_Metabat.296	JAFGJV000000000	96.55	0	Bacteria	Spirochaetota	Spirochaetia	Treponematales	UBA12059			0.889	Abundant	23.48	59	67623	2866226	2968644	63.5	2433	92.05	1084	0	0	0	46	MQD
Zod_Metabat.547	JAFGNN000000000	97.7	2.4	Bacteria	Spirochaetota	Spirochaetia	Treponematales	UBA12059			0.765	Abundant	13.53	94	55082	3376908	3456405	67.7	2911	91.68	1064	0	0	0	46	MQD
ZodW_maxbin.191	JAFGUM000000000	88.57	2.3	Bacteria	Spirochaetota	Spirochaetia	Treponematales	UBA12059	SZUA-370		0.937	Abundant	13.75	605	5899	2553449	2882973	58.7	2660	94.10	903	0	0	0	33	MQD
Zod_Metabat.302	JAFGJZ000000000	91.51	1.12	Bacteria	Spirochaetota	UBA4802	Novel:ZNO34	Novel:ZNF086			0.565	Novel	14.55	193	26216	3601690	3935843	36.8	3417	90.28	952	1	0	0	39	MQD
Zod_Metabat.857	JAFGRW000000000	86.52	1.12	Bacteria	Spirochaetota	UBA4802	Novel:ZNO34	Novel:ZNF087			0.555	Novel	28.66	138	54832	3751546	4336045	38.2	3355	87.49	978	3	0	0	38	MQD
ZodW_Metabat.186	JAFGVW000000000	91.01	5.62	Bacteria	Spirochaetota	UBA4802	Novel:ZNO34	Novel:ZNF087			0.551	Novel	13.38	214	31047	3988311	4382278	38	3613	87.75	969	3	0	0	36	MQD
Zod_Metabat.1181	JAFGDQ000000000	92.82	4.49	Bacteria	Spirochaetota	UBA4802	UBA4802	Novel:ZNF085			0.661	Novel	33.83	116	61856	4420346	4762278	37.6	3803	86.49	1005	1	0	0	44	MQD
Zod_Metabat.878	JAFGSG000000000	90.95	2.25	Bacteria	Spirochaetota	UBA4802	UBA4802	Novel:ZNF085			0.661	Novel	268.68	150	40015	3551455	3904843	38.5	3265	87.15	948	2	0	0	47	MQD
Zod_Metabat.1046	JAFGBT000000000	88.7	4.49	Bacteria	Spirochaetota	UBA4802	UBA4802	UBA5550	RBG-16-49-21		0.878	Abundant	168.54	55	143511	4056821	4573643	53.8	3568	88.97	1012	0	0	0	41	MQD
Zod_Metabat.1135	JAFGCV000000000	79.71	6.74	Bacteria	Spirochaetota	UBA4802	UBA4802	UBA5550			0.804	Abundant	38.71	104	64932	3566117	4473864	57.9	3267	89.36	975	0	0	0	37	MQD
Zod_Metabat.271	JAFGJK000000000	77.53	2.43	Bacteria	Spirochaetota	UBA4802	UBA4802	UBA5550			0.736	Abundant	13.55	159	48718	4387639	5659279	59.3	4085	88.18	947	0	0	0	43	MQD
Zod_Metabat.30	JAFGJX000000000	85.33	3.37	Bacteria	Spirochaetota	UBA4802	UBA4802	UBA5550	RBG-16-49-21		0.875	Abundant	14.89	131	46793	3809730	4464702	54	3420	88.93	991	0	0	0	39	MQD
Zod_Metabat.1312	JAFGFK000000000	89.43	6.59	Bacteria	Sumerlaeota	Novel:ZNC16	Novel:ZNO42	Novel:ZNF105			0.571	Novel	12.76	523	11260	4660019	5210801	47.8	3898	91.27	1091	1	0	0	37	MQD
Zod_Metabat.292	JAFGJS000000000	96.56	2.43	Bacteria	Sumerlaeota	Novel:ZNC16	Novel:ZNO42	Novel:ZNF105			0.416	Novel	25.59	161	40426	4546854	4708838	56	3557	87.27	1116	0	1	0	50	MQD
Zod_Metabat.321	JAFGKF000000000	93.26	3.93	Bacteria	Sumerlaeota	Sumerlaeia	UBA8349	Novel:ZNF089			0.578	Novel	14.98	393	14625	4169219	4470533	66.1	3595	90.97	1055	1	0	1	37	MQD
Zod_Metabat.1318	JAFGFN000000000	97.25	0	Bacteria	Sumerlaeota	Sumerlaeia	UBA8349	UBA8349			0.745	Rare	21.99	220	30074	4309893	4431767	63	3419	87.34	1101	1	1	1	45	HQD
Zod_Metabat.437	JAFGMB000000000	74.25	0	Bacteria	Synergistota	Synergistia	Synergistales	Novel:ZNF091			0.705	Novel	9.00	266	10039	2172844	2926389	47.5	2252	89.31	862	0	0	0	34	MQD
Zod_Metabat.896	JAFGSM000000000	88.65	3.7	Bacteria	SZUA-182	Novel:ZNC12	Novel:ZNO35	Novel:ZNF092			0.381	Novel	14.50	272	15665	3163608	3568650	43.8	2691	87.40	1028	0	1	0	33	MQD
Zod_Metabat.1159	JAFGDG000000000	92.25	8	Archaea	Thermoplasmatota	E2	DHVEG-1	DHVEG-1			0.790	Abundant	10.79	161	14939	1618332	1754289	40.6	1708	92.00	872	0	0	0	41	MQD
Zod_Metabat.1324	JAFGFQ000000000	89.2	0.8	Archaea	Thermoplasmatota	E2	DHVEG-1	DHVEG-1	SM1-50		0.917	Abundant	25.86	166	25273	2217355	2485824	42.3	2272	89.59	874	0	1	0	39	MQD
Zod_Metabat.472	JAFGML000000000	74.86	1.6	Archaea	Thermoplasmatota	E2	DHVEG-1	DHVEG-1			0.871	Abundant	42.18	57	38236	1471894	1966196	49.3	1356	92.08	1000	0	0	0	28	MQD
Zod_Metabat.690	JAFGPM000000000	70.36	4.39	Archaea	Thermoplasmatota	E2	DHVEG-1	DHVEG-1	SM1-50		0.929	Abundant	10.25	204	8454	1418629	2016244	45.2	1504	91.01	858	0	0	0	22	MQD
Zod_Metabat.7	JAFGPP000000000	80.4	1.2	Archaea	Thermoplasmatota	E2	DHVEG-1	DHVEG-1			0.730	Abundant	18.90	153	15991	1714040	2131891	34.1	1747	88.92	872	0	0	0	30	MQD
Zod_Metabat.266	JAFGJI000000000	78.81	0	Archaea	Thermoplasmatota	EX4484-6	EX4484-6	EX4484-6			0.749	Rare	10.79	313	9269	2380726	3020843	53.2	2060	92.85	1073	0	0	0	33	MQD
Zod_Metabat.400	JAFGLL000000000	96.8	4	Archaea	Thermoplasmatota	EX4484-6	EX4484-6	EX4484-6			0.747	Rare	19.49	124	32247	2799415	2891958	52.3	2176	92.14	1185	1	0	0	41	MQD
Zod_Metabat.676	JAFGPG000000000	72.85	0	Archaea	Thermoplasmatota	Thermoplasmata	Methanomassiliicoccales	UBA472			0.885	Abundant	38.16	124	16943	1245944	1710287	61.1	1384	92.02	828	0	0	0	30	MQD
Zod_Metabat.1462	JAFGHM000000000	88.69	1.2	Archaea	Thermoplasmatota	Thermoplasmata	UBA10834	UBA10834	COMBO-56-21		0.850	Rare	18.53	125	21408	1829169	2062430	59.2	1788	91.28	934	0	0	0	28	MQD
Zod_Metabat.1386	JAFGGM000000000	86.53	0.93	Archaea	Thermoproteota	Bathyarchaeia	B26-1	BA1	BIN-L-1		0.972	Abundant	63.56	80	21659	1142389	1320223	42.8	1292	86.82	768	1	0	0	28	MQD
Zod_Metabat.411	JAFGLT000000000	90.65	7.01	Archaea	Thermoproteota	Bathyarchaeia	B26-1	UBA233	SG8-32-3		0.951	Abundant	46.39	119	23111	1693721	1868418	45.2	1871	87.22	790	0	0	0	34	MQD
Zod_Metabat.546	JAFGNM000000000	83.64	6.07	Archaea	Thermoproteota	Bathyarchaeia	B26-1	UBA233	SG8-32-3		0.926	Abundant	101.47	133	18971	1928651	2305896	45.9	2119	86.71	789	1	0	0	42	MQD
Zod_Metabat.1465	JAFGHP000000000	86.41	4.85	Archaea	Thermoproteota	Bathyarchaeia	TCS64	TCS64	UBA8941		0.885	Abundant	34.45	111	35522	1792688	2074630	32.9	1947	88.71	817	0	1	1	38	MQD
Zod_Metabat.946	JAFGTA000000000	82.51	2.8	Archaea	Thermoproteota	Bathyarchaeia	TCS64	TCS64	RBG-16-57-9		0.895	Abundant	11.65	230	14843	2691853	3262457	57.5	3037	89.92	797	0	0	0	44	MQD
Zod_maxbin.0139	JAFGAH000000000	76.1	2.35	Bacteria	Thermotogota	Thermotogae	Petrotogales	Kosmotogaceae	Mesotoga		0.991	Abundant	57.29	547	4729	1898949	2495334	45.5	2097	91.90	832	0	0	0	19	MQD
Zod_maxbin.0257_1	JAFGAP000000000	75.71	0.63	Bacteria	Thermotogota	Thermotogae	Petrotogales	Kosmotogaceae	Mesotoga		0.982	Abundant	29.25	260	15558	1980000	2615242	44.7	1987	90.11	898	0	0	0	26	MQD
Zod_Metabat.5	JAFGMW000000000	90.34	1.68	Bacteria	UBA10199	UBA10199	2-02-FULL-44-16	Novel:ZNF093			0.619	Novel	58.57	119	26658	1812637	2006461	63.4	1634	90.99	1009	0	0	0	37	MQD
Zod_Metabat.1399	JAFGGQ000000000	95.6	2.2	Bacteria	UBP14	UBA6098	Novel:ZNO36	Novel:ZNF094			0.493	Novel	12.18	180	22807	2854132	2985494	45.2	2119	92.79	1250	1	0	0	35	MQD
Zod_Metabat.733	JAFGQG000000000	95.6	1.1	Bacteria	UBP14	UBA6098	Novel:ZNO36	Novel:ZNF094			0.494	Novel	15.04	200	28941	3977482	4160546	42.8	2962	88.99	1195	0	1	0	42	MQD
ZodW_Metabat.349	JAFGXH000000000	90.7	1.68	Bacteria	UBP6	Novel:ZNC13	Novel:ZNO37	Novel:ZNF095			0.376	Novel	13.70	380	12558	3590224	3958351	28.9	2924	89.91	1104	0	0	0	36	MQD
Zod_Metabat.1143	JAFGCY000000000	88.46	1.28	Bacteria	UBP7_A	4484-113	4484-113	Novel:ZNF090			0.612	Novel	16.13	113	49629	3705459	4188853	62.2	3032	89.68	1096	1	2	0	44	MQD
Zod_Metabat.1037	JAFGBO000000000	86.66	2.73	Bacteria	Verrucomicrobiota	Kiritimatiellae	Kiritimatiellales	Pontiellaceae	Pontiella		0.882	Abundant	17.30	127	53565	4190486	4835548	54.5	3387	91.88	1137	0	0	0	43	MQD
ZodW_Metabat.175	JAFGVP000000000	92.74	4.08	Bacteria	Verrucomicrobiota	Kiritimatiellae	Kiritimatiellales	Pontiellaceae	Pontiella		0.884	Abundant	13.14	183	34977	4279068	4614048	54.4	3551	91.82	1107	0	0	0	46	MQD
ZodW_Metabat.279	JAFGWS000000000	71.9	4.32	Bacteria	Verrucomicrobiota	Kiritimatiellae	Kiritimatiellales	Pontiellaceae	Pontiella		0.875	Abundant	30.54	187	19610	2644535	3678074	53.2	2311	89.15	1020	1	0	0	42	MQD
ZodW_Metabat.316	JAFGXC000000000	80.31	9.46	Bacteria	Verrucomicrobiota	Kiritimatiellae	Kiritimatiellales	Pontiellaceae	Pontiella		0.877	Abundant	21.72	330	13251	3401861	4235912	52.6	3035	89.08	999	0	0	0	38	MQD
Zod_Metabat.16	JAFGHX000000000	93.58	7.24	Bacteria	Verrucomicrobiota	Kiritimatiellae	Novel:ZNO45	Novel:ZNF097			0.507	Novel	26.65	487	40074	11135617	11899569	65.8	7699	88.75	1284	1	0	0	40	MQD
Zod_Metabat.531	JAFGNF000000000	71.91	5.78	Bacteria	Verrucomicrobiota	Kiritimatiellae	SLAD01	Novel:ZNF096			0.651	Novel	15.78	341	12965	3324085	4622563	65.5	2757	89.65	1081	0	0	0	34	MQD
Zod_Metabat.245	JAFGIZ000000000	80.41	1.35	Bacteria	Verrucomicrobiota	Kiritimatiellae	UBA8416	YA12-FULL-48-11			0.689	Rare	9.14	321	9525	2379530	2959246	67.1	2164	93.90	1033	0	0	0	35	MQD
Zod_Metabat.961	JAFGTH000000000	76.79	1.62	Bacteria	Verrucomicrobiota	Kiritimatiellae	UBA8416	YA12-FULL-48-11			0.736	Rare	8.48	279	9190	2131810	2776156	48.3	2060	92.12	953	1	0	0	29	MQD
Zod_Metabat.847	JAFGRS000000000	79.97	1.38	Bacteria	Verrucomicrobiota	Lentisphaeria	UBA1407	Lenti-02			0.748	Rare	10.89	973	6556	5800582	7253448	68.4	4109	87.19	1231	0	0	0	29	MQD
Zod_Metabat.1329	JAFGFR000000000	79.17	0.07	Bacteria	Verrucomicrobiota	Lentisphaeria	Victivallales	GWF2-50-93			0.738	Rare	10.18	342	9436	2697119	3406744	54	2467	88.93	972	1	0	0	38	MQD
ZodW_Metabat.56	JAFGXT000000000	89.5	2.03	Bacteria	Verrucomicrobiota	Lentisphaeria	Victivallales	SZUA-371			0.839	Rare	10.56	401	14531	4499774	5027680	45.9	3911	91.08	1048	1	0	0	50	MQD
Zod_maxbin.0260_1	JAFGAQ000000000	78.72	0.68	Bacteria	Verrucomicrobiota	Verrucomicrobiae	Opitutales	UBA4506			0.766	Rare	27.58	443	9830	2832865	3598660	54.9	2571	91.39	1007	0	0	0	31	MQD
Zod_Metabat.1145	JAFGCZ000000000	73.65	0.23	Bacteria	Verrucomicrobiota	Verrucomicrobiae	Opitutales	Verruco-01			0.792	Abundant	48.66	15	341759	2108223	2862489	49.7	1858	92.23	1047	0	0	0	43	MQD
Zod_Metabat.372	JAFGLA000000000	95.27	0.81	Bacteria	Verrucomicrobiota	Verrucomicrobiae	Opitutales	Verruco-01	Verruco-01		0.949	Abundant	13.82	105	33480	2488908	2612478	57	2094	88.21	1049	1	0	0	42	MQD
Zod_Metabat.779	JAFGQR000000000	96.62	4.73	Bacteria	Verrucomicrobiota	Verrucomicrobiae	Pedosphaerales	Palsa-1400			0.798	Rare	31.63	200	41496	5285562	5470464	66.6	3652	89.97	1302	0	0	0	38	MQD
Zod_Metabat.1285	JAFGFA000000000	91.22	0	Bacteria	Verrucomicrobiota_A	Chlamydiia	Parachlamydiales	SM23-39			0.769	Abundant	17.76	32	77067	1209137	1325517	38.3	1114	91.75	996	0	0	0	34	MQD
Zod_Metabat.799	JAFGQY000000000	86.49	2.7	Bacteria	Verrucomicrobiota_A	Chlamydiia	Parachlamydiales	SM23-39	O2-12-FULL-27-8		0.869	Abundant	16.15	147	15175	1578817	1825433	29.6	1528	91.59	946	0	1	0	29	MQD
Zod_Metabat.1268	JAFGEW000000000	95.14	5.52	Bacteria	Verrucomicrobiota_A	Novel:ZNC14	Novel:ZNO39	Novel:ZNF098			0.275	Novel	20.20	134	55760	4055620	4262792	65.3	3412	88.88	1057	1	0	0	45	MQD
Zod_Metabat.185	JAFGIG000000000	90.11	0	Bacteria	WOR-3	SDB-A	SDB-A	SDB-A			0.742	Rare	192.06	142	23798	1978835	2196022	42.8	1909	95.84	994	1	0	0	36	MQD
Zod_Metabat.631	JAFGON000000000	90.29	0	Bacteria	WOR-3	SDB-A	SDB-A	SDB-A			0.732	Rare	12.79	106	32167	2148543	2379602	42.3	2024	94.72	1006	1	0	0	46	MQD
Zod_Metabat.912	JAFGSQ000000000	94.14	3.3	Bacteria	WOR-3	SDB-A	SDB-A	SDB-A			0.736	Rare	17.05	76	45564	2234418	2373505	43.4	2064	95.04	1029	1	0	0	39	MQD
Zod_Metabat.145	JAFGHJ000000000	94.04	0	Bacteria	WOR-3	UBA3072	UBA3072	UBA3072			0.837	Rare	48.89	48	103954	2344829	2493438	38	2119	90.06	997	1	0	1	47	MQD
Zod_Metabat.699	JAFGPO000000000	92	2.25	Bacteria	WOR-3	WOR-3	SM23-42	SM23-42			0.781	Rare	11.67	162	22014	2494665	2711592	49.7	2326	92.14	988	1	0	0	39	MQD
Zod_Metabat.887	JAFGSK000000000	95.51	0	Bacteria	WOR-3	WOR-3	UBA2258	B3-TA06			0.877	Rare	70.33	90	51832	3330455	3487022	49.2	3137	88.97	945	1	1	0	43	MQD
Zod_Metabat.732	JAFGQF000000000	82.6	1.65	Bacteria	WOR-3	WOR-3	UBA2258	UBA2258			0.810	Rare	17.64	297	6927	1846171	2235074	68.3	1831	92.80	936	1	0	0	38	MQD
Zod_Metabat.816	JAFGRF000000000	76.86	0	Bacteria	WOR-3	WOR-3	UBA2258	UBA2258	UBA2258		0.950	Rare	10.42	397	7704	2637114	3431062	62.8	2634	87.76	879	1	2	1	42	MQD
Zod_Metabat.57	JAFGNW000000000	93.11	1.1	Bacteria	Zixibacteria	MSB-5A5	GN15	FEB-12			0.843	Rare	14.55	285	16214	3294075	3537832	50.3	2916	90.45	1022	0	0	0	33	MQD
Zod_maxbin.0182_1	JAFGAL000000000	71.36	1.1	Bacteria	Zixibacteria	MSB-5A5	GN15	PGXB01			0.782	Rare	34.34	33	164573	2745777	3847782	52.9	2239	91.35	1120	1	0	0	39	MQD
Zod_Metabat.998	JAFGTT000000000	96.64	2.2	Bacteria	Zixibacteria	MSB-5A5	GN15	PGXB01			0.817	Rare	100.50	38	146970	3383155	3500781	48.6	2883	90.55	1063	1	0	0	45	MQD

% completeness and % contamination: calculated in CheckM

GTDB classification to the species level: obtained by running the classify_workflow in GTDB-Tk (v1.1.0) {Chaumeil, 2019 #48}.

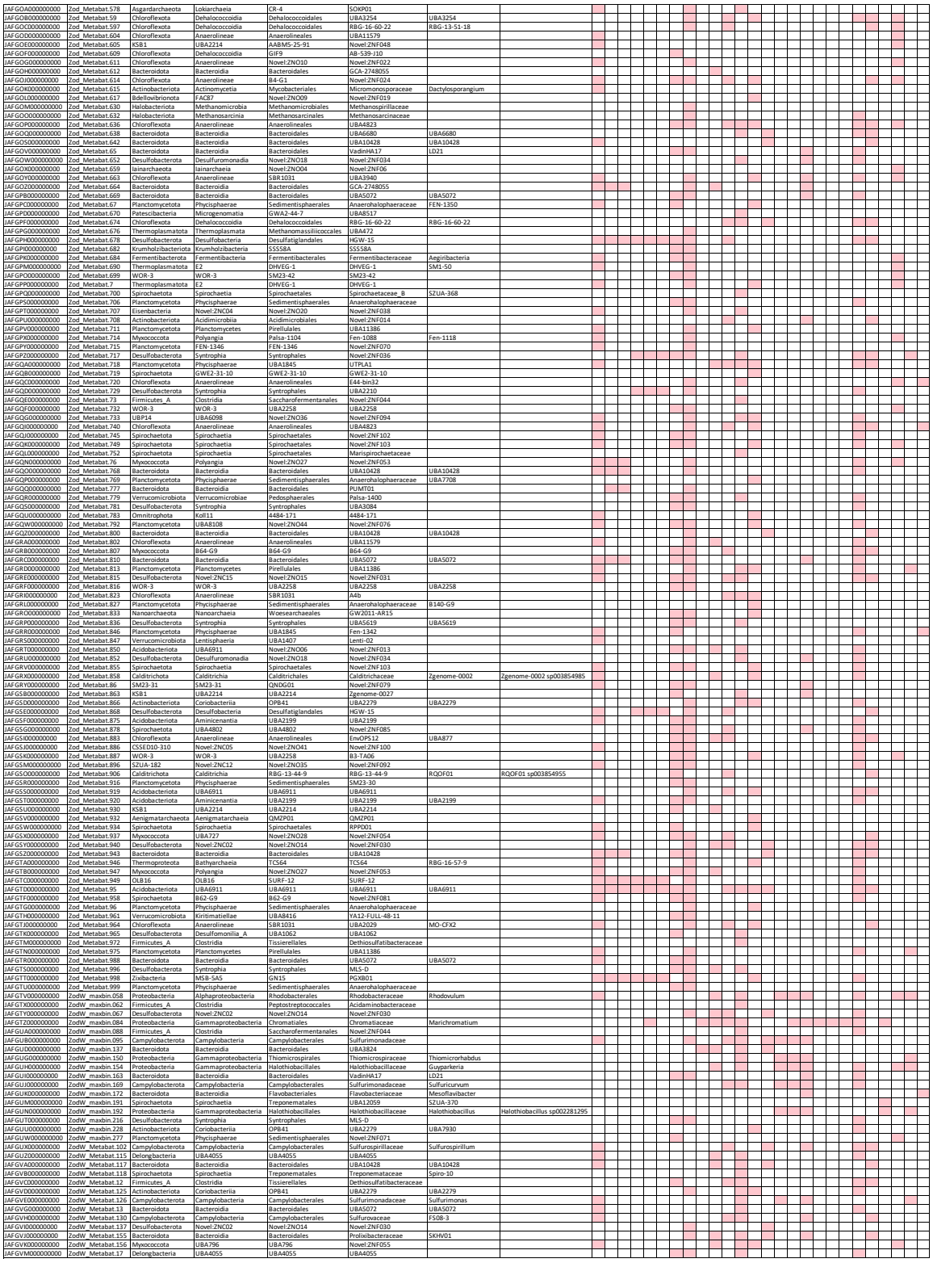
RED value: Relative evolutionary divergence value calculated for each genome in GTDB-TK. No RED value was obtained when a genome is classified down to the species level.
Family abundance in GTDB: Families were classified according to how abundant they were in Gtdb based on the available number of genomes. Abundant, more than 5 genomes are available in Gtdb for the family; Rare, 5 genomes or less are available in Gtdb for the family; Novel, no genomes were available in Gtdb (these correspond to novel families binned from Zodletone spring).
Median genome coverage: Median contig coverage for each MAG calculated based on the number of reads (125bp) mapped to each contig and the length of each contig as follows: contig coverage= (Number of reads mapped to the contig x 125)/ contig length.
Number of contigs: Number of contigs binned for each genome.
Assembly N50: Calculated using the module Proch-NGS-1.3.0 available at (https://r.metagen.org/release/Proch-NGS).
Assembly size (bp): refers to the size of binned contigs for each genome.
Expected genome size (bp): genome size extrapolated based on the % completeness of the genome.
GC%: Percentage G+C for each genome calculated using an in-house perl script.
Number of genes: Total number of protein coding genes as predicted by Prodigal [Hyatt, 2010 #50].
Coding %: Percentage of genome that is gene-coding. Calculated as cumulative size of all predicted genes/ genome size x 100.
Average gene length: Average size of all genes (bp).
Number of rRNA genes: Predicted number of rRNA genes as determined using barrnap 0.8 (https://github.com/tseemann/barrnap).
Number of tRNA genes: Predicted number of tRNA genes as determined using tRNAscan-SE [Chan, 2019 #128].
Quality bin: Genomes were classified as medium-quality draft (MQD), or high-quality draft (HQD) based on the criteria set forth by [Bowers, 2017 #129].

Table 3.2: S-cycling genes predicted in Zodletone genomes
Genes are shown in the table header and actual gene names are shown in the corresponding cells.

Table S2: S-cycling genes predicted in Zodletone genomes. Genes are shown in the table header and actual gene names are shown in the corresponding cells.

Genome accession number	Genome	Phylum	Class	Order	Family	Genus	Species	*sat*	*aprAB*	*qmoABC*	*dsrAB*	*dsrC*	*dsrMKJOP*	*asrABC*	*hdrABCD*	*phsABC*	*otr*	*ttrABC*	*glpE/sseA/rdl*	*hydCNqhAC*	*psrABC*	*Sox system*	*fccAB*	*sqr*	*rDSR*	*dsrMKJOP*	*dsrEFH*	*tusA*	*soeAB*	*soxA*	*tetH*	*tsdA*	*dimDA*
JAFFZZ000000000	Zod_maxbin_2_173	Dependentiae	Babeliae	Babeliales	Babeliaceae																												
JAFGAA000000000	Zod_maxbin.0001	Chloroflexota	Anaerolineae	Anaerolineales	Anaerolineaceae																												
JAFGAB000000000	Zod_maxbin.0003	Acidobacteriota	Aminicenantia	Aminicenantales	RBG-16-66-30	RBG-16-66-30																											
JAFGAC000000000	Zod_maxbin.0011	Firmicutes_A	Clostridia	Peptostreptococcales	DTU036	MLB-F1																											
JAFGAD000000000	Zod_maxbin.0017_A	Desulfobacterota	Syntrophia	Syntrophales	UBA3084																												
JAFGAE000000000	Zod_maxbin.0093	Altarchaeota	Altarchaeia	IMC4	QMZM01																												
JAFGAF000000000	Zod_maxbin.0112	Bacteroidota	Bacteroidia	Bacteroidales	Prolixibacteraceae	SKHV01																											
JAFGAI000000000	Zod_maxbin.0142	Campylobacterota	Campylobacteria	Campylobacterales	Sulfurovaceae																												
JAFGAJ000000000	Zod_maxbin.0146	Acidobacteriota	Aminicenantia	Aminicenantales	Aminicenantaceae																												
JAFGAK000000000	Zod_maxbin.0163	Bacteroidota	Bacteroidia	Bacteroidales	UBA12170	UBA12170																											
JAFGAL000000000	Zod_maxbin.0182_1	Zixibacteria	MSB-5A5	GN15	PGXB01																												
JAFGAM000000000	Zod_Maxbin.0214	Desulfobacterota	Novel:ZNC02	Novel:ZNO14	Novel:ZNF030																												
JAFGAO000000000	Zod_maxbin.0255	Acidobacteriota	UBA6911	UBA6911	UBA6911	UBA6911																											
JAFGAQ000000000	Zod_maxbin.0260_1	Verrucomicrobiota	Opitutales	UBA4506	UBA4506																												
JAFGAR000000000	Zod_maxbin.0292	Asgardarchaeota	Thorarchaeia	Thorarchaeales	MP8T-1																												
JAFGAS000000000	Zod_maxbin.0311	Desulfobacterota	Novel:ZNC03	Novel:ZNO16	Novel:ZNF032																												
JAFGAT000000000	Zod_maxbin.0317	Firmicutes_A	Clostridia	Lachnospirales	Vallitaleaceae																												
JAFGAV000000000	Zod_maxbin.0345_1	Acidobacteriota	Aminicenantia	Aminicenantales	UBA4085																												
JAFGAW000000000	Zod_maxbin.0406_1	Actinobacteriota	Thermoleophilia	UBA2241	UBA2241	UBA2241																											
JAFGAX000000000	Zod_maxbin.0504	SM23-31	SM23-31	QNDG01	Novel:ZNF079																												
JAFGAY000000000	Zod_Metabat.10	Planctomycetota	Planctomycetes	Pirellulales	UBA11386	UBA11386																											
JAFGBA000000000	Zod_Metabat.1001	Planctomycetota	Phycisphaerae	Sedimentisphaerales	SM23-30																												
JAFGBC000000000	Zod_Metabat.1003	Acidobacteriota	Aminicenantia	Aminicenantales	UBA4085																												
JAFGBD000000000	Zod_Metabat.1005	Bacteroidota	Bacteroidia	Bacteroidales	UBA5072																												
JAFGBF000000000	Zod_Metabat.1015	Krumholzibacteriota	Krumholzibacteria	SSS58A	SSS58A	QTKG01	QTKG01 sp003369455																										
JAFGBG000000000	Zod_Metabat.1017	Planctomycetota	Phycisphaerae	Sedimentisphaerales	Anaerohalosphaeraceae																												
JAFGBH000000000	Zod_Metabat.1020	Desulfobacterota	Syntrophia	Syntrophales	MLS-D																												
JAFGBI000000000	Zod_Metabat.1029	Myxococcota	Polyangia	Polyangiales	Polyangiaceae																												
JAFGBJ000000000	Zod_Metabat.1030	Fibrobacterota	Chitinivibrionia	Chitinivibrionales	Chitinispirillaceae																												
JAFGBK000000000	Zod_Metabat.1031	Krumholzibacteriota	Krumholzibacteria	Novel:ZNO23	Novel:ZNF047																												
JAFGBL000000000	Zod_Metabat.1032	Bacteroidota	Bacteroidia	Bacteroidales	FEN-979																												
JAFGBM000000000	Zod_Metabat.1034	Actinobacteriota	Actinomycetia	Actinomycetales	Demequinaceae																												
JAFGBN000000000	Zod_Metabat.1036	Chloroflexota	Dehalococcoidia	GIF9	AB-539-J10																												
JAFGBO000000000	Zod_Metabat.1037	Verrucomicrobiota	Kiritimatiellae	Kiritimatiellales	Pontiellaceae	Pontiella																											
JAFGBQ000000000	Zod_Metabat.1040	Actinobacteriota	RBG-13-55-18	Fen-727	Novel:ZNF015																												
JAFGBR000000000	Zod_Metabat.1042	Bacteroidota	Bacteroidia	Bacteroidales	Marinilabiliaceae	Breznakibacter																											
JAFGBS000000000	Zod_Metabat.1044	Asgardarchaeota	Lokiarchaeia	CR-4	AMARA-1	AMARA-1																											
JAFGBT000000000	Zod_Metabat.1046	Spirochaetota	UBA4802	UBA4802	UBA5550	RBG-16-49-21																											
JAFGBU000000000	Zod_Metabat.1050	Desulfobacterota	Desulfovibrionia	Desulfovibrionales	Desulfovibrionaceae																												
JAFGBV000000000	Zod_Metabat.1053	Chloroflexota	Anaerolineae	Anaerolineales	UBA6092	UBA6092																											
JAFGBW000000000	Zod_Metabat.1054	Aureabacteria	Novel:ZNC17	Novel:ZNO08	Novel:ZNF017																												
JAFGBX000000000	Zod_Metabat.1055	Asgardarchaeota	Lokiarchaeia	Novel:ZNO03	Novel:ZNF04																												
JAFGBY000000000	Zod_Metabat.1058	Acidobacteriota	B3-B38	Novel:ZNO05	Novel:ZNF012																												
JAFGCA000000000	Zod_Metabat.1071	Planctomycetota	Phycisphaerae	Sedimentisphaerales	Anaerohalosphaeraceae	Planc-01																											
JAFGCD000000000	Zod_Metabat.1083	Planctomycetota	Phycisphaerae	Sedimentisphaerales	Anaerohalosphaeraceae																												
JAFGCF000000000	Zod_Metabat.1085	Desulfobacterota	Desulfobacteria	Desulfatiglandales	HGW-15																												
JAFGCG000000000	Zod_Metabat.109	Chloroflexota	Anaerolineae	Anaerolineales	EmOPS-12	UBA12294																											
JAFGCH000000000	Zod_Metabat.1092	Actinobacteriota	Acidimicrobiia	UBA5794	UBA11373																												
JAFGCI000000000	Zod_Metabat.1100	Aenigmatarchaeota	Aenigmatarchaeia	QMZP01	QMZT01																												
JAFGCK000000000	Zod_Metabat.1106	Halobacteriota	Methanosarcinia	Methanosarcinales	Methanosarcinaceae	Methanolobus																											
JAFGCL000000000	Zod_Metabat.1111	Chloroflexota	Dehalococcoidia	UBA2777	RBG-13-53-26																												
JAFGCO000000000	Zod_Metabat.1116	SM23-31	SM23-31	QNDG01	Novel:ZNF079																												
JAFGCP000000000	Zod_Metabat.1117	Desulfobacterota	Novel:ZNC15	Novel:ZNO15	Novel:ZNF031																												
JAFGCS000000000	Zod_Metabat.1132	KSB1	UBA2214	AABM5-25-91	Novel:ZNF048																												
JAFGCU000000000	Zod_Metabat.1134	Chloroflexota	Anaerolineae	Anaerolineales	RBG-16-64-43	FEN-1073																											
JAFGCV000000000	Zod_Metabat.1135	Spirochaetota	UBA4802	UBA4802	UBA5550																												
JAFGCW000000000	Zod_Metabat.1136	Chloroflexota	Dehalococcoidia	Dehalococcoidales	UBA2162	MGML01																											
JAFGCX000000000	Zod_Metabat.1142	Krumholzibacteriota	Krumholzibacteria	SSS58A	SSS58A	QTKG01	QTKG01 sp003369535																										
JAFGCY000000000	Zod_Metabat.1143	UBP7_A	4484-113	4484-113	Novel:ZNF090																												
JAFGDA000000000	Zod_Metabat.1146	Actinobacteriota	UBA1414	UBA1414	UBA1414																												
JAFGDB000000000	Zod_Metabat.1151	Iainarchaeota	Iainarchaeia	GCA-2688035	GCA-2688035																												
JAFGDC000000000	Zod_Metabat.1153	CSSED10-310	CSSED10-310	Novel:ZNO13	Novel:ZNF029																												
JAFGDE000000000	Zod_Metabat.1157	Margulisbacteria	WOR-1	O2-12-FULL-45-9	O2-12-FULL-45-9																												
JAFGDF000000000	Zod_Metabat.1158	Desulfobacterota	Desulfobacteria	Desulfatiglandales	HGW-15																												
JAFGDG000000000	Zod_Metabat.1159	Thermoplasmatota	E2	DHVEG-1	DHVEG-1																												
JAFGDI000000000	Zod_Metabat.1170	Spirochaetota	Spirochaetia	Spirochaetales	Novel:ZNF082																												
JAFGDK000000000	Zod_Metabat.1173	Chloroflexota	Anaerolineae	Anaerolineales	UBA11579	UBA11579																											
JAFGDL000000000	Zod_Metabat.1174	Chloroflexota	Anaerolineae	Anaerolineales	Anaerolineaceae																												
JAFGDM000000000	Zod_Metabat.1176	Desulfobacterota	Desulfobacteria	Desulfatiglandales	HGW-15																												
JAFGDN000000000	Zod_Metabat.1177	Planctomycetota	Phycisphaerae	Sedimentisphaerales	Anaerohalosphaeraceae	Fen-1362																											
JAFGDO000000000	Zod_Metabat.1179	Patescibacteria	Dojkabacteria	B142	Novel:ZNF065																												
JAFGDP000000000	Zod_Metabat.118	Fibrobacterota	Chitinivibrionia	Chitinivibrionales	Chitinispirillaceae																												
JAFGDQ000000000	Zod_Metabat.1181	Spirochaetota	UBA4802	UBA4802	Novel:ZNF085																												
JAFGDR000000000	Zod_Metabat.1183	Cloacimonadota	Cloacimonadia	JGIOTU-2	JGIOTU-2																												
JAFGDS000000000	Zod_Metabat.1184	Planctomycetota	Planctomycetes	Pirellulales	UBA11386																												
JAFGDT000000000	Zod_Metabat.1186	SM23-31	SM23-31	QNDG01	Novel:ZNF079																												
JAFGDU000000000	Zod_Metabat.1188	Actinobacteriota	RBG-13-55-18	RBG-13-55-18	RBG-13-55-18	SURF-21																											
JAFGDV000000000	Zod_Metabat.1191	Altarchaeota	Altarchaeia	IMC4	QMZM01																												
JAFGDW000000000	Zod_Metabat.1197	KSB1	UBA2214	AABM5-25-91	Novel:ZNF048																												
JAFGDX000000000	Zod_Metabat.1198	Bacteroidota	Bacteroidia	Bacteroidales	Prolixibacteraceae																												
JAFGDY000000000	Zod_Metabat.120	Chloroflexota	Anaerolineae	4572-78	JJ11																												
JAFGDZ000000000	Zod_Metabat.1203	Bacteroidota	Bacteroidia	Bacteroidales	BBW3	UBA5206																											
JAFGEA000000000	Zod_Metabat.1205	Chloroflexota	Anaerolineae	B4-G1	SLSP01	SLSP01																											
JAFGEB000000000	Zod_Metabat.1207	Fibrobacterota	Chitinivibrionia	Chitinivibrionales	Novel:ZNF043																												
JAFGEC000000000	Zod_Metabat.1209	KSB1	UBA2214	UBA2214	UBA2214																												
JAFGED000000000	Zod_Metabat.1210	Chloroflexota	Anaerolineae	B4-G1	B4-G1																												
JAFGEE000000000	Zod_Metabat.1212	Delongbacteria	UBA4055	UBA4055	UBA4055																												
JAFGEF000000000	Zod_Metabat.1213	Planctomycetota	Phycisphaerae	Sedimentisphaerales	Anaerohalosphaeraceae																												
JAFGEG000000000	Zod_Metabat.1216	Chloroflexota	Anaerolineae	SBR1031	A4b																												
JAFGEI000000000	Zod_Metabat.1220	Chloroflexota	Anaerolineae	B4-G1	Novel:ZNF024																												
JAFGEK000000000	Zod_Metabat.1224	Myxococcota	XYA12-FULL-58-9	XYA12-FULL-58-9	XYA12-FULL-58-9																												
JAFGEL000000000	Zod_Metabat.1226	Desulfobacterota	Desulfuromonadia	Desulfuromonadales	Geopsychrobacteraceae	BM522																											
JAFGEN000000000	Zod_Metabat.1233	Acidobacteriota	Aminicenantia	Aminicenantales	UBA4085																												
JAFGEO000000000	Zod_Metabat.1236	Bacteroidota	Bacteroidia	Bacteroidales	UBA10428	UBA10428																											
JAFGEP000000000	Zod_Metabat.1238	Myxococcota	Bradimonadia	Bradymonadales	Novel:ZNF056																												
JAFGEQ000000000	Zod_Metabat.1246	CSSED10-310	CSSED10-310	CSSED10-310	CSSED10-310																												
JAFGER000000000	Zod_Metabat.1248	Bacteroidota	Chlorobia	Chlorobiales	Chlorobiaceae	Chlorobaculum																											
JAFGES000000000	Zod_Metabat.1250	Desulfobacterota	Desulfobacteria	Desulfobacterales	BuS5																												
JAFGEU000000000	Zod_Metabat.1254	Firmicutes_A	Clostridia	Saccharofermentanales	Saccharofermentanaceae																												
JAFGEV000000000	Zod_Metabat.1255	Bacteroidota	Bacteroidia	Bacteroidales	Prolixibacteraceae	SKHV01																											
JAFGEX000000000	Zod_Metabat.1270	SM23-31	SM23-31	QNDG01	Novel:ZNF079																												
JAFGEZ000000000	Zod_Metabat.1283	Krumholzibacteriota	Krumholzibacteria	SSS58A	SSS58A																												
JAFGFB000000000	Zod_Metabat.1288	Chloroflexota	Anaerolineae	B4-G1	SLSP01																												
JAFGFC000000000	Zod_Metabat.1289	Spirochaetota	Novel:ZNC11	Novel:ZNO33	Novel:ZNF080																												
JAFGFE000000000	Zod_Metabat.1292	Desulfobacterota	Novel:ZNC03	Novel:ZNO16	Novel:ZNF032																												
JAFGFG000000000	Zod_Metabat.1300	Aenigmatarchaeota	Aenigmatarchaeia	QMZP01	Novel:ZNF01																												
JAFGFI000000000	Zod_Metabat.1307	Chloroflexota	Anaerolineae	B4-G1	SLSP01	SLSP01																											
JAFGFK000000000	Zod_Metabat.1312	Sumerlaeota	Novel:ZNC16	Novel:ZNO42	Novel:ZNF105																												
JAFGFM000000000	Zod_Metabat.1317	Desulfobacterota	Desulfobacteria	Desulfatiglandales	HGW-15																												
JAFGFO000000000	Zod_Metabat.132	Chloroflexota	Anaerolineae	Thermoflexales	Fen-1058																												
JAFGFP000000000	Zod_Metabat.1321	Chloroflexota	Dehalococcoidia	Dehalococcoidales	UBA5760	UBA5760																											
JAFGFQ000000000	Zod_Metabat.1324	Thermoplasmatota	E2	DHVEG-1	DHVEG-1	SM1-50																											
JAFGFS000000000	Zod_Metabat.1330	Bipolaricaulota	Bipolaricaulia	UBA7950	UBA9294	RXOA01	RXOA01 sp003979035																										
JAFGFT000000000	Zod_Metabat.1332	Chloroflexota	Dehalococcoidia	GIF9	AB-539-J10																												
JAFGFU000000000	Zod_Metabat.1333	Campylobacterota	Campylobacteria	Campylobacterales	Sulfurospirillaceae	Sulfurospirillum																											
JAFGFV000000000	Zod_Metabat.1342	Spirochaetota	Spirochaetia	Spirochaetales	Novel:ZNF102																												
JAFGFW000000000	Zod_Metabat.1348	Desulfobacterota	Desulfobacteria	C00003060	S70866Z20																												
JAFGFX000000000	Zod_Metabat.1349	Planctomycetota	Phycisphaerae	Sedimentisphaerales	SM23-30																												
JAFGFY000000000	Zod_Metabat.1351	Desulfobacterota	Desulfobacteria	Desulfatiglandales	HGW-15																												
JAFGFZ000000000	Zod_Metabat.1355	Planctomycetota	Planctomycetes	Pirellulales	Ga0077529																												
JAFGGA000000000	Zod_Metabat.1361	Desulfobacterota	Desulfobacteria	Desulfatiglandales	HGW-15																												
JAFGGB000000000	Zod_Metabat.1365	Desulfobacterota	Syntrophia	Syntrophales	MLS-D																												
JAFGGD000000000	Zod_Metabat.137	Eisenbacteria	Novel:ZNC04	Novel:ZNO19	Novel:ZNF037																												
JAFGGE000000000	Zod_Metabat.1370	Planctomycetota	Phycisphaerae	Sedimentisphaerales	Anaerohalosphaeraceae	FEN-1350																											
JAFGGF000000000	Zod_Metabat.1376	Bacteroidota	Bacteroidia	Bacteroidales	Prolixibacteraceae																												
JAFGGG000000000	Zod_Metabat.1377	Spirochaetota	Spirochaetia	Spirochaetales	RPP01																												
JAFGGH000000000	Zod_Metabat.138	Planctomycetota	Phycisphaerae	Sedimentisphaerales	Anaerohalosphaeraceae																												
JAFGGJ000000000	Zod_Metabat.1381	Planctomycetota	SZUA-567	Novel:ZNO43	Novel:ZNF075																												
JAFGGK000000000	Zod_Metabat.1382	Chloroflexota	Anaerolineae	B4-G1	B4-G1																												
JAFGGM000000000	Zod_Metabat.1386	Thermoproteota	Bathyarchaeia	B26-1	BA1	BIN-L-1																											
JAFGGO000000000	Zod_Metabat.1389	Asgardarchaeota	Lokiarchaeia	CR-4	SOKP01																												
JAFGGQ000000000	Zod_Metabat.1399	UBP14	UBA6098	Novel:ZNO36	Novel:ZNF094																												
JAFGGT000000000	Zod_Metabat.1406	Methanobacteriota	Thermococci	Methanofastidiosales	NM3																												
JAFGGU000000000	Zod_Metabat.1409	Bacteroidota	Bacteroidia	Bacteroidales	UBA5072	UBA5072																											
JAFGGV000000000	Zod_Metabat.1411	Planctomycetota	Phycisphaerae	Sedimentisphaerales	Anaerohalosphaeraceae																												

JAFGGY000000000	Zod_Metabat.1419	Bacteroidota	Bacteroidia	Bacteroidales	Prolixibacteraceae	SKHV01	
JAFGHA000000000	Zod_Metabat.1421	Fibrobacterota	Chitinivibrionia	Chitinivibrionales	Chitinispirillaceae		
JAFGHB000000000	Zod_Metabat.1428	Halobacteriota	Syntropharchaeia	ANME-1	ANME-1	ANME-1-THS	
JAFGHD000000000	Zod_Metabat.1433	Bacteroidota	Bacteroidia	Bacteroidales	FEN-979		
JAFGHE000000000	Zod_Metabat.1436	Planctomycetota	Phycisphaerae	Sedimentisphaerales	SM23-30		
JAFGHG000000000	Zod_Metabat.1444	Omnitrophota	Koll11	4484-171	4484-171		
JAFGHH000000000	Zod_Metabat.1445	Myxococcota	Polyangia	Novel:ZNO26	Novel:ZNF052		
JAFGHJ000000000	Zod_Metabat.145	WOR-3	UBA3072	UBA3072	UBA3072		
JAFGHK000000000	Zod_Metabat.1454	Chloroflexota	Dehalococcoidia	Dehalococcoidales	RBG-16-60-22	RBG-13-51-18	
JAFGHL000000000	Zod_Metabat.1459	Chloroflexota	Dehalococcoidia	GIF9	UBA5629		
JAFGHM000000000	Zod_Metabat.1462	Thermoplasmatota	Thermoplasmata	UBA10834	UBA10834	COMBO-56-21	
JAFGHN000000000	Zod_Metabat.1463	Spirochaetota	Spirochaetia	Spirochaetales	ARS1246		
JAFGHO000000000	Zod_Metabat.1464	Spirochaetota	Spirochaetia	Spirochaetales	Novel:ZNF103		
JAFGHP000000000	Zod_Metabat.1465	Thermoproteota	Bathyarchaeia	TCS64	TCS64	UBA8941	
JAFGHQ000000000	Zod_Metabat.15	Proteobacteria	Gammaproteobacteria	UBA12402	UBA12402		
JAFGHR000000000	Zod_Metabat.151	Chloroflexota	Anaerolineae	SBR1031	UBA2029	MO-CFX2	
JAFGHS000000000	Zod_Metabat.153	Desulfobacterota	Syntrophia	Syntrophales	Novel:ZNF035		
JAFGHT000000000	Zod_Metabat.154	Chloroflexota	Anaerolineae	Anaerolineales	UBA11858	UBA11858	
JAFGHU000000000	Zod_Metabat.155	Bacteroidota	Bacteroidia	Bacteroidales	UBA12170	UBA12170	
JAFGHV000000000	Zod_Metabat.156	Spirochaetota	Spirochaetia	Spirochaetales	Novel:ZNF083		
JAFGHX000000000	Zod_Metabat.16	Verrucomicrobiota	Kiritimatiellae	Novel:ZNO45	Novel:ZNF097		
JAFGIA000000000	Zod_Metabat.168	Chloroflexota	Anaerolineae	Novel:ZNO10	Novel:ZNF022		
JAFGIB000000000	Zod_Metabat.169	Myxococcota	Polyangia	Polyangiales	Novel:ZNF051		
JAFGIC000000000	Zod_Metabat.172	Desulfobacterota	Desulfobacteria	Desulfatiglandales	HGW-15		
JAFGID000000000	Zod_Metabat.179	Bacteroidota	Ignavibacteria	Ignavibacteriales	Novel:ZNF018		
JAFGIE000000000	Zod_Metabat.182	Chloroflexota	Anaerolineae	Novel:ZNO11	Novel:ZNF023		
JAFGIG000000000	Zod_Metabat.185	WOR-3	SDB-A	SDB-A	SDB-A		
JAFGIH000000000	Zod_Metabat.188	Actinobacteriota	Thermoleophilia	RBG-16-64-13	RBG-16-64-13		
JAFGII000000000	Zod_Metabat.193	Bacteroidota	Ignavibacteria	SJA-28	B-1AR		
JAFGIJ000000000	Zod_Metabat.2	Firmicutes_A	Clostridia	Saccharofermentanales	Novel:ZNF044		
JAFGIN000000000	Zod_Metabat.210	Fibrobacterota	Chitinivibrionia	Chitinivibrionales	Chitinispirillaceae		
JAFGIO000000000	Zod_Metabat.215	Desulfobacterota	Syntrophia	Syntrophales	UBA2185		
JAFGIP000000000	Zod_Metabat.217	Bacteroidota	Bacteroidia	Bacteroidales	UBA10428	UBA10428	
JAFGIQ000000000	Zod_Metabat.219	FCPU426	Novel:ZNC06	Novel:ZNO21	Novel:ZNF040		
JAFGIR000000000	Zod_Metabat.223	Planctomycetota	Planctomycetes	Pirellulales	UBA11386	UBA11386	
JAFGIS000000000	Zod_Metabat.23	Myxococcota	Polyangia	Polyangiales	Polyangiaceae		
JAFGIT000000000	Zod_Metabat.233	B130-G9	B130-G9	B130-G9	B130-G9		
JAFGIW000000000	Zod_Metabat.237	Fibrobacterota	Chitinivibrionia	Chitinivibrionales	Chitinispirillaceae		
JAFGIX000000000	Zod_Metabat.24	Desulfobacterota	Novel:ZNC03	Novel:ZNO16	Novel:ZNF032		
JAFGIY000000000	Zod_Metabat.240	Acidobacteriota	UBA6911	UBA6911	UBA6911		
JAFGJA000000000	Zod_Metabat.248	Chloroflexota	Anaerolineae	SBR1031	UBA2029	MO-CFX2	
JAFGJB000000000	Zod_Metabat.251	KSB1	UBA2214	UBA2214	Zgenome-0027	Zgenome-0027	
JAFGJF000000000	Zod_Metabat.263	Chloroflexota	Anaerolineae	Novel:ZNO11	Novel:ZNF023		
JAFGJG000000000	Zod_Metabat.264	Actinobacteriota	Thermoleophilia	Solirubrobacterales	Thermoleophilaceae		
JAFGJH000000000	Zod_Metabat.265	Nanoarchaeota	Nanoarchaeia	Woesearchaeales	UBA11576		
JAFGJJ000000000	Zod_Metabat.27	Desulfobacterota	Syntrophia	Syntrophales	Syntrophaceae		
JAFGJK000000000	Zod_Metabat.271	Spirochaetota	UBA4802	UBA4802	UBA5550		
JAFGJL000000000	Zod_Metabat.276	Omnitrophota	Koll11	UBA1560	2-01-FULL-45-10		
JAFGJM000000000	Zod_Metabat.279	Chloroflexota	Anaerolineae	Anaerolineales	UBA4823		
JAFGJN000000000	Zod_Metabat.28	KSB1	UBA2214	UBA2214	UBA2214		
JAFGJO000000000	Zod_Metabat.281	Spirochaetota	Spirochaetia	Spirochaetales	RPPD01	RPPD01	
JAFGJP000000000	Zod_Metabat.284	Aureabacteria	Novel:ZNC17	Novel:ZNO08	Novel:ZNF017		
JAFGJQ000000000	Zod_Metabat.286	Planctomycetota	Phycisphaerae	UBA1845	UBA1845		
JAFGJR000000000	Zod_Metabat.289	Planctomycetota	Phycisphaerae	Sedimentisphaerales	Anaerohalophaeraceae	PLanc-01	
JAFGJS000000000	Zod_Metabat.292	Sumerlaeota	Novel:ZNC16	Novel:ZNO42	Novel:ZNF105		
JAFGJU000000000	Zod_Metabat.294	Eisenbacteria	Novel:ZNC04	Novel:ZNO40	Novel:ZNF099		
JAFGJV000000000	Zod_Metabat.296	Spirochaetota	Spirochaetia	Treponematales	UBA12059		
JAFGJW000000000	Zod_Metabat.297	Nanoarchaeota	Nanoarchaeia	Woesearchaeales	GW2011-AR15		
JAFGJX000000000	Zod_Metabat.30	Spirochaetota	UBA4802	UBA4802	UBA5550	RBG-16-49-21	
JAFGJZ000000000	Zod_Metabat.302	Spirochaetota	UBA4802	Novel:ZNO34	Novel:ZNF086		
JAFGKA000000000	Zod_Metabat.304	Planctomycetota	Phycisphaerae	UBA1845	Novel:ZNF072		
JAFGKB000000000	Zod_Metabat.308	Chloroflexota	Anaerolineae	B4-G1	SLSP01		
JAFGKC000000000	Zod_Metabat.309	Desulfobacterota	Syntrophia	Syntrophales	Smithellaceae	UBA4810	
JAFGKD000000000	Zod_Metabat.31	KSB1	UBA2214	UBA2214	Zgenome-0027	Zgenome-0027	Zgenome-0027 sp003854975
JAFGKE000000000	Zod_Metabat.320	Fusobacteriota	Fusobacteriia	Fusobacteriales	Fusobacteriaceae		
JAFGKF000000000	Zod_Metabat.321	Sumerlaeota	Sumerlaeia	UBA8349	Novel:ZNF089		
JAFGKG000000000	Zod_Metabat.323	Chloroflexota	Chloroflexia	Novel:ZNO12	Novel:ZNF026		
JAFGKJ000000000	Zod_Metabat.326	KSB1	UBA2214	UBA2214	Zgenome-0027	Zgenome-0027	Zgenome-0027 sp003854995
JAFGKK000000000	Zod_Metabat.328	Chloroflexota	Anaerolineae	Anaerolineales	RBG-16-64-43	FEN-1073	
JAFGKL000000000	Zod_Metabat.331	Planctomycetota	Phycisphaerae	Sedimentisphaerales	Anaerohalophaeraceae		
JAFGKM000000000	Zod_Metabat.338	Omnitrophota	UBA8468	UBA8468	B48-G9		
JAFGKO000000000	Zod_Metabat.341	Chloroflexota	Anaerolineae	Anaerolineales	EnvOPS12		
JAFGKP000000000	Zod_Metabat.342	Halobacteriota	Syntropharchaeia	ANME-1	ANME-1	ANME-1-THS	
JAFGKQ000000000	Zod_Metabat.345	Fermentibacterota	Fermentibacteria	Fermentibacterales	Novel:ZNF041		
JAFGKR000000000	Zod_Metabat.348	Bacteroidota	SZUA-365	SZUA-365	SZUA-365		
JAFGKS000000000	Zod_Metabat.349	Armatimonadota	UBA10988	Novel:ZNO07	Novel:ZNF016		
JAFGKU000000000	Zod_Metabat.353	Spirochaetota	Spirochaetia	Spirochaetales	Novel:ZNF103		
JAFGKV000000000	Zod_Metabat.355	Fermentibacterota	Novel:ZNC07	Novel:ZNO22	Novel:ZNF042		
JAFGKW000000000	Zod_Metabat.358	Halobacteriota	Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	Methanolacinia	
JAFGKY000000000	Zod_Metabat.37	Bacteroidota	Bacteroidia	Bacteroidales	UBA5072	UBA5072	
JAFGKZ000000000	Zod_Metabat.370	Calditrichota	Calditrichia	Calditrichales	Calditrichaceae		
JAFGLA000000000	Zod_Metabat.372	Verrucomicrobiota	Verrucomicrobiae	Opitutales	Verruco-01	Verruco-01	
JAFGLB000000000	Zod_Metabat.377	Bacteroidota	UBA10030	UBA10030	UBA10030	Fen-1298	
JAFGLC000000000	Zod_Metabat.384	Planctomycetota	UBA8108	UBA8890	Novel:ZNF077		
JAFGLD000000000	Zod_Metabat.387	Chloroflexota	Anaerolineae	SBR1031	UBA3940		
JAFGLE000000000	Zod_Metabat.388	Planctomycetota	Phycisphaerae	Sedimentisphaerales	Anaerohalophaeraceae	RBG-13-46-10	
JAFGLJ000000000	Zod_Metabat.397	Bacteroidota	Bacteroidia	Bacteroidales	VadinHA17	UBA9300	
JAFGLK000000000	Zod_Metabat.4	Chloroflexota	Anaerolineae	UBA1429	UBA1429		
JAFGLL000000000	Zod_Metabat.400	Thermoplasmatota	EX4484-6	EX4484-6	EX4484-6		
JAFGLM000000000	Zod_Metabat.401	Proteobacteria	Gammaproteobacteria	HTCC5015	HTCC5015		
JAFGLN000000000	Zod_Metabat.402	Desulfobacterota	Syntrophia	Syntrophales	Novel:ZNF035		
JAFGLP000000000	Zod_Metabat.405	Chloroflexota	Dehalococcoidia	GIF9	UBA5629	UBA1162	
JAFGLQ000000000	Zod_Metabat.406	Chloroflexota	Dehalococcoidia	Dehalococcoidales	Dehalococcoidaceae		
JAFGLR000000000	Zod_Metabat.409	Chloroflexota	Dehalococcoidia	Dehalococcoidales	UBA3254		
JAFGLS000000000	Zod_Metabat.41	Desulfobacterota	Syntrophia	Syntrophales	Smithellaceae	Smithella	
JAFGLT000000000	Zod_Metabat.411	Thermoproteota	Bathyarchaeia	B26-1	UBA233	SG8-32-3	
JAFGLU000000000	Zod_Metabat.414	Chloroflexota	Anaerolineae	Anaerolineales	Anaerolineaceae		
JAFGLV000000000	Zod_Metabat.417	Planctomycetota	Phycisphaerae	Sedimentisphaerales	Anaerohalophaeraceae	PLanc-01	
JAFGLW000000000	Zod_Metabat.419	CSSED10-310	CSSED10-310	CSSED10-310	Novel:ZNF028		
JAFGLY000000000	Zod_Metabat.425	Myxococcota	UBA796	UBA796	Novel:ZNF055		
JAFGLZ000000000	Zod_Metabat.429	Planctomycetota	Phycisphaerae	UBA1845	Novel:ZNF073		
JAFGMA000000000	Zod_Metabat.436	KSB1	UBA2214	AABM5-25-91	Novel:ZNF048		
JAFGMB000000000	Zod_Metabat.437	Synergistota	Synergistia	Synergistales	Novel:ZNF091		
JAFGMD000000000	Zod_Metabat.442	Patescibacteria	ABY1	XYB2-FULL-38-15	Novel:ZNF064		
JAFGME000000000	Zod_Metabat.457	Bacteroidota	Bacteroidia	Bacteroidales	FEN-979		
JAFGMH000000000	Zod_Metabat.460	Asgardarchaeota	Heimdallarchaeia	Novel:ZNO02	Novel:ZNF03		
JAFGMI000000000	Zod_Metabat.461	Bacteroidota	Ignavibacteria	Ignavibacteriales	Melioribacteraceae	PGYT01	
JAFGMJ000000000	Zod_Metabat.463	Actinobacteriota	UBA1414	UBA1414	UBA1414		
JAFGML000000000	Zod_Metabat.472	Thermoplasmatota	E2	DHVEG-1	DHVEG-1		
JAFGMM000000000	Zod_Metabat.474	Chloroflexota	Anaerolineae	SBR1031	Novel:ZNF025		
JAFGMN000000000	Zod_Metabat.479	CSSED10-310	CSSED10-310	CSSED10-310	CSSED10-310		
JAFGMO000000000	Zod_Metabat.480	Acidobacteriota	Aminicenantia	Aminicenantales	Novel:ZNF011		
JAFGMP000000000	Zod_Metabat.481	Latescibacterota	Latescibacteria	Latescibacterales	Latescibacteraceae		
JAFGMQ000000000	Zod_Metabat.483	Desulfobacterota	Desulfobacteria	Desulfatiglandales	NaphS2		
JAFGMR000000000	Zod_Metabat.485	Halobacteriota	Methanosarcinia	Methanotrichales	Methanotrichaceae		
JAFGMS000000000	Zod_Metabat.487	Chloroflexota	Anaerolineae	SBR1031	UBA3940		
JAFGMT000000000	Zod_Metabat.495	Actinobacteriota	Thermoleophilia	RBG-16-64-13	RBG-16-64-13		
JAFGMV000000000	Zod_Metabat.498	Chloroflexota	Anaerolineae	Anaerolineales	EnvOPS12	UBA5796	
JAFGMX000000000	Zod_Metabat.50	Chloroflexota	Anaerolineae	Promineofilales	UBA4811		
JAFGMY000000000	Zod_Metabat.502	Actinobacteriota	RBG-13-55-18	Fen-727	Novel:ZNF015		
JAFGMZ000000000	Zod_Metabat.509	Bacteroidota	Chlorobia	Chlorobiales	Chlorobiaceae	Chlorobium	
JAFGNC000000000	Zod_Metabat.529	Proteobacteria	Gammaproteobacteria	UBA6522	UBA6522	FEN-1219	
JAFGND000000000	Zod_Metabat.53	RBG-13-66-14	Novel:ZNC10	Novel:ZNO32	Novel:ZNF078		
JAFGNF000000000	Zod_Metabat.531	Verrucomicrobiota	Kiritimatiellae	SLAD01	Novel:ZNF096		
JAFGNG000000000	Zod_Metabat.533	Planctomycetota	SZUA-567	SZUA-567	Novel:ZNF074		
JAFGNH000000000	Zod_Metabat.534	Chloroflexota	Anaerolineae	Anaerolineales	E44-bin32		
JAFGNI000000000	Zod_Metabat.538	Chloroflexota	Anaerolineae	B4-G1	SLSP01		
JAFGNJ000000000	Zod_Metabat.542	Desulfobacterota	Desulfomonilia_A	Novel:ZNO17	Novel:ZNF033		
JAFGNK000000000	Zod_Metabat.543	Halobacteriota	Methanosarcinia	Methanotrichales	Methanotrichaceae	Methanothrix	
JAFGNL000000000	Zod_Metabat.545	Bacteroidota	Bacteroidia	Bacteroidales	NBLH01	NBLH01	
JAFGNM000000000	Zod_Metabat.546	Thermoproteota	Bathyarchaeia	B26-1	UBA233	SG8-32-3	
JAFGNO000000000	Zod_Metabat.549	Chloroflexota	Anaerolineae	SBR1031	UBA3940		
JAFGNP000000000	Zod_Metabat.552	Actinobacteriota	Coriobacteriia	OPB41	UBA2279	UBA6100	
JAFGNQ000000000	Zod_Metabat.553	Acidobacteriota	Aminicenantia	Aminicenantales	Aminicenantaceae		
JAFGNS000000000	Zod_Metabat.558	Desulfobacterota	Desulfobacteria	Desulfatiglandales	B25-G16		
JAFGNT000000000	Zod_Metabat.564	Halobacteriota	Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	LKUD01	
JAFGNU000000000	Zod_Metabat.568	Chloroflexota	Anaerolineae	SBR1031	UBA2029	MO-CFX2	
JAFGNV000000000	Zod_Metabat.569	Chloroflexota	Anaerolineae	4572-78	J111		
JAFGNW000000000	Zod_Metabat.57	Zixibacteria	MSB-5A5	GN15	FEB-12		
JAFGNY000000000	Zod_Metabat.574	Bacteroidota	Bacteroidia	Bacteroidales	FEN-979	QYOJ01	
JAFGNZ000000000	Zod_Metabat.575	Myxococcota	Myxococcia	Myxococcales	Myxococcaceae	Hyalangium	

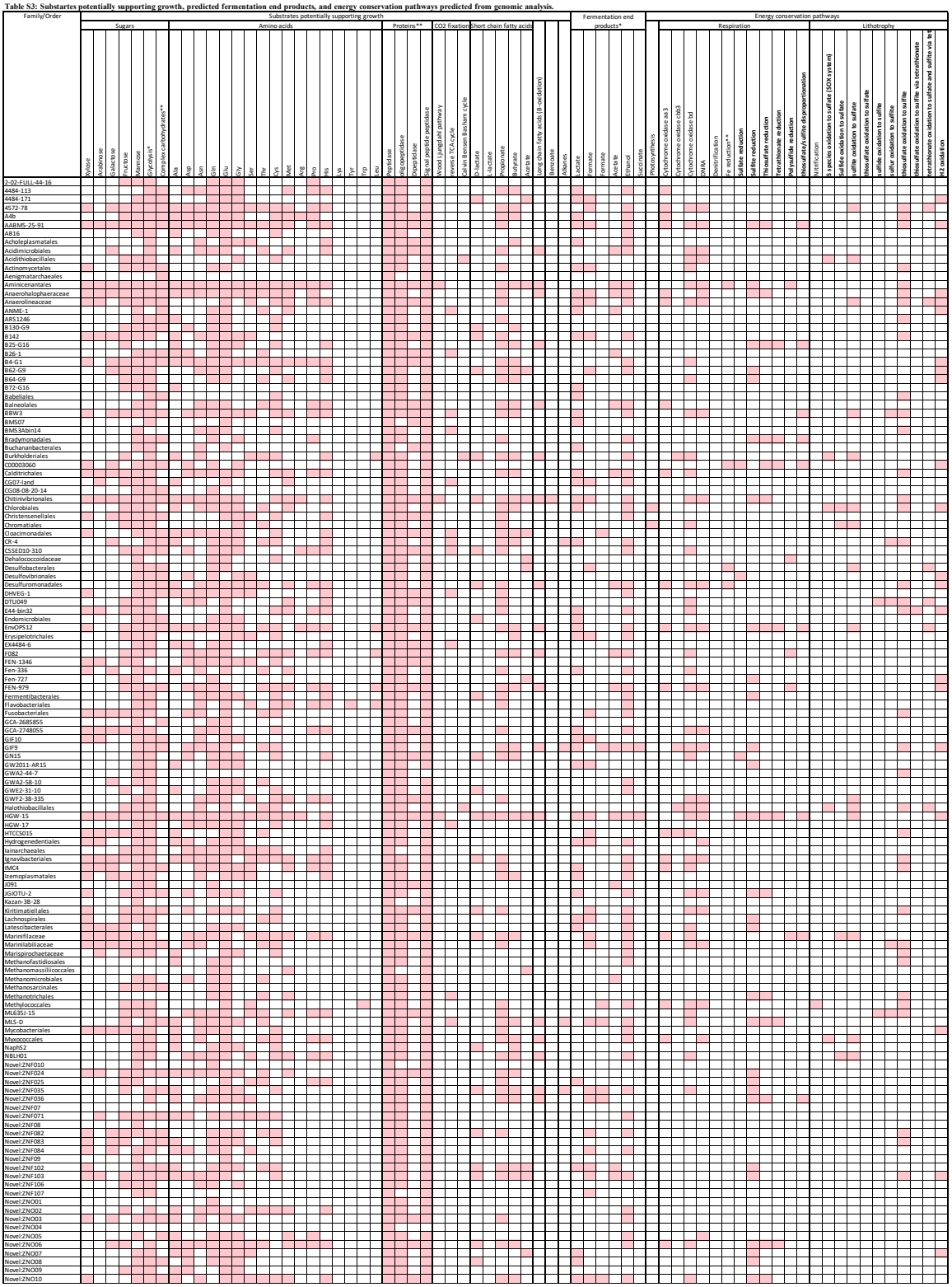


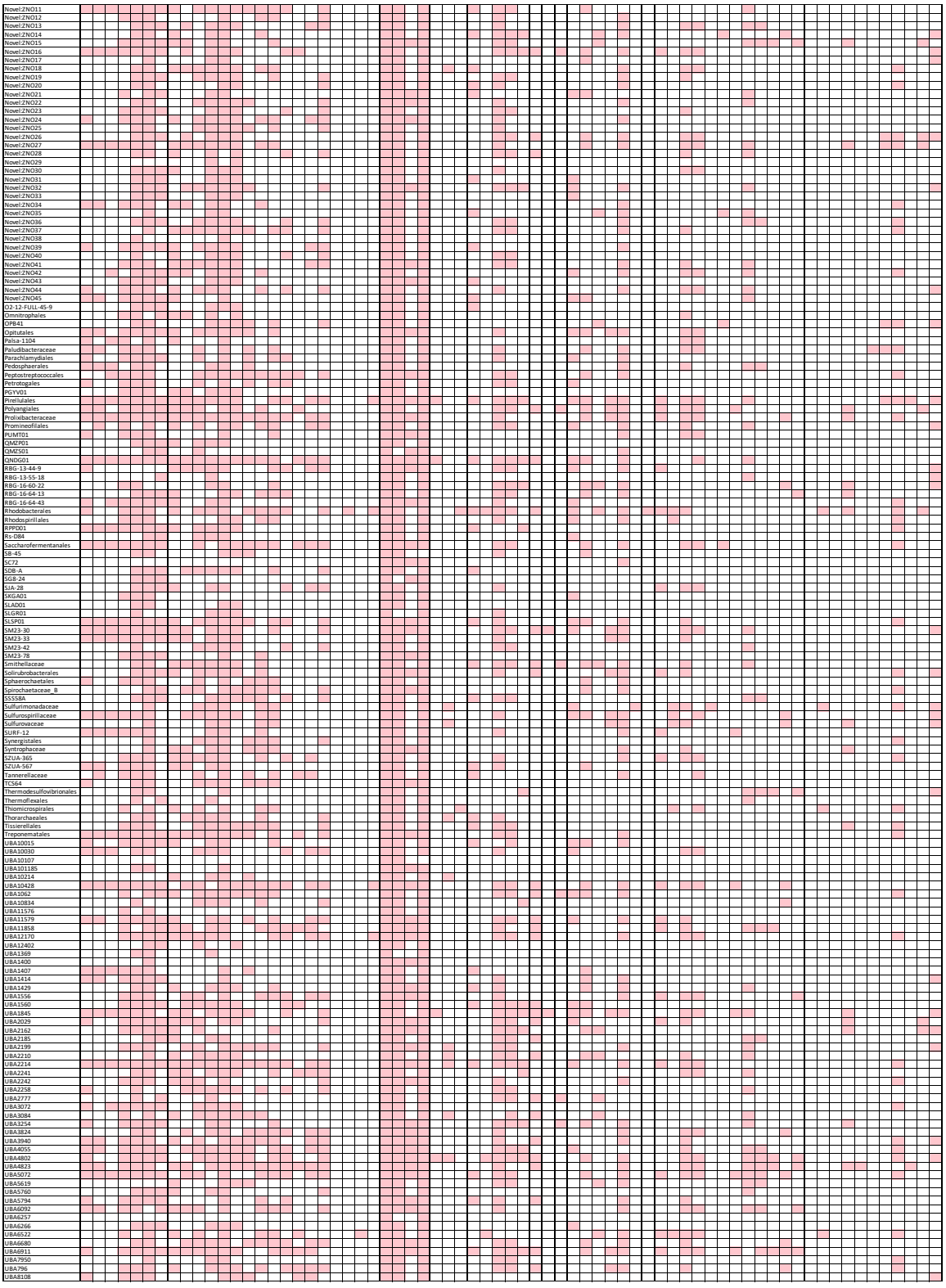
JAFGOA000000000	Zod_Metabat.578	Asgardarchaeota	Lokiarchaeia	CR-4	SOKP01			
JAFGOB000000000	Zod_Metabat.59	Chloroflexota	Dehalococcoidia	Dehalococcoidales	UBA3254	UBA3254		
JAFGOC000000000	Zod_Metabat.597	Chloroflexota	Dehalococcoidia	Dehalococcoidales	RBG-16-60-22	RBG-13-51-18		
JAFGOD000000000	Zod_Metabat.604	Chloroflexota	Anaerolineae	Anaerolineales	UBA11579			
JAFGOE000000000	Zod_Metabat.605	KSB1	UBA2214	AABM5-25-91	Novel:ZNF048			
JAFGOF000000000	Zod_Metabat.609	Chloroflexota	Dehalococcoidia	GIF9	AB-539-J10			
JAFGOG000000000	Zod_Metabat.611	Chloroflexota	Anaerolineae	Novel:ZNO10	Novel:ZNF022			
JAFGOH000000000	Zod_Metabat.612	Bacteroidota	Bacteroidia	Bacteroidales	GCA-2748055			
JAFGOJ000000000	Zod_Metabat.614	Chloroflexota	Anaerolineae	B4-G1	Novel:ZNF024			
JAFGOK000000000	Zod_Metabat.615	Actinobacteriota	Actinomycetia	Mycobacteriales	Micromonosporaceae	Dactylosporangium		
JAFGOL000000000	Zod_Metabat.617	Bdellovibrionota	FAC87	Novel:ZNO09	Novel:ZNF019			
JAFGOM000000000	Zod_Metabat.630	Halobacteriota	Methanomicrobia	Methanomicrobiales	Methanospirillaceae			
JAFGOO000000000	Zod_Metabat.632	Halobacteriota	Methanosarcinia	Methanosarcinales	Methanosarcinaceae			
JAFGOP000000000	Zod_Metabat.636	Chloroflexota	Anaerolineae	Anaerolineales	UBA4823			
JAFGOQ000000000	Zod_Metabat.638	Bacteroidota	Bacteroidia	Bacteroidales	UBA6680	UBA6680		
JAFGOS000000000	Zod_Metabat.642	Bacteroidota	Bacteroidia	Bacteroidales	UBA10428	UBA10428		
JAFGOV000000000	Zod_Metabat.65	Bacteroidota	Bacteroidia	Bacteroidales	VadinHA17	LD21		
JAFGOW000000000	Zod_Metabat.652	Desulfobacterota	Desulfuromonadia	Novel:ZNO18	Novel:ZNF034			
JAFGOX000000000	Zod_Metabat.659	Iainarchaeota	Iainarchaeia	Novel:ZNO04	Novel:ZNF06			
JAFGOY000000000	Zod_Metabat.663	Chloroflexota	Anaerolineae	SBR1031	UBA3940			
JAFGOZ000000000	Zod_Metabat.664	Bacteroidota	Bacteroidia	Bacteroidales	GCA-2748055			
JAFGPB000000000	Zod_Metabat.669	Bacteroidota	Bacteroidia	Bacteroidales	UBA5072	UBA5072		
JAFGPC000000000	Zod_Metabat.67	Planctomycetota	Phycisphaerae	Sedimentisphaerales	Anaerohalosphaeraceae	FEN-1350		
JAFGPD000000000	Zod_Metabat.670	Patescibacteria	Microgenomatia	GWA2-44-7	UBA8517			
JAFGPF000000000	Zod_Metabat.674	Chloroflexota	Dehalococcoidia	Dehalococcoidales	RBG-16-60-22	RBG-16-60-22		
JAFGPG000000000	Zod_Metabat.676	Thermoplasmatota	Thermoplasmata	Methanomassiliicoccales	UBA472			
JAFGPH000000000	Zod_Metabat.678	Desulfobacterota	Desulfobacteria	Desulfatiglandales	HGW-15			
JAFGPI000000000	Zod_Metabat.682	Krumholzibacteriota	Krumholzibacteria	SSS58A	SSS58A			
JAFGPK000000000	Zod_Metabat.684	Fermentibacterota	Fermentibacteria	Fermentibacterales	Fermentibacteraceae	Aegiribacteria		
JAFGPM000000000	Zod_Metabat.690	Thermoplasmatota	E2	DHVEG-1	DHVEG-1	SM1-50		
JAFGPO000000000	Zod_Metabat.699	WOR-3	WOR-3	SM23-42	SM23-42			
JAFGPP000000000	Zod_Metabat.7	Thermoplasmatota	E2	DHVEG-1	DHVEG-1			
JAFGPQ000000000	Zod_Metabat.700	Spirochaetota	Spirochaetia	Spirochaetales	Spirochaetaceae_B	SZUA-368		
JAFGPS000000000	Zod_Metabat.706	Planctomycetota	Phycisphaerae	Sedimentisphaerales	Anaerohalosphaeraceae			
JAFGPT000000000	Zod_Metabat.707	Eisenbacteria	Novel:ZNC04	Novel:ZNO20	Novel:ZNF038			
JAFGPU000000000	Zod_Metabat.708	Actinobacteriota	Acidimicrobiia	Acidimicrobiales	Novel:ZNF014			
JAFGPV000000000	Zod_Metabat.711	Planctomycetota	Planctomycetes	Pirellulales	UBA11386			
JAFGPX000000000	Zod_Metabat.714	Myxococcota	Polyangia	Palsa-1104	Fen-1088	Fen-1118		
JAFGPY000000000	Zod_Metabat.715	Planctomycetota	FEN-1346	FEN-1346	Novel:ZNF070			
JAFGPZ000000000	Zod_Metabat.717	Desulfobacterota	Syntrophia	Syntrophales	Novel:ZNF036			
JAFGQA000000000	Zod_Metabat.718	Planctomycetota	Phycisphaerae	UBA1845	UTPLA1			
JAFGQB000000000	Zod_Metabat.719	Spirochaetota	GWE2-31-10	GWE2-31-10	GWE2-31-10			
JAFGQC000000000	Zod_Metabat.720	Chloroflexota	Anaerolineae	Anaerolineales	E44-bin32			
JAFGQD000000000	Zod_Metabat.729	Desulfobacterota	Syntrophia	Syntrophales	UBA2210			
JAFGQE000000000	Zod_Metabat.73	Firmicutes_A	Clostridia	Saccharofermentanales	Novel:ZNF044			
JAFGQF000000000	Zod_Metabat.732	WOR-3	WOR-3	UBA2258	UBA2258			
JAFGQG000000000	Zod_Metabat.733	UBP14	UBA6098	Novel:ZNO36	Novel:ZNF094			
JAFGQI000000000	Zod_Metabat.740	Chloroflexota	Anaerolineae	Anaerolineales	UBA4823			
JAFGQJ000000000	Zod_Metabat.745	Spirochaetota	Spirochaetia	Spirochaetales	Novel:ZNF102			
JAFGQK000000000	Zod_Metabat.749	Spirochaetota	Spirochaetia	Spirochaetales	Novel:ZNF103			
JAFGQL000000000	Zod_Metabat.752	Spirochaetota	Spirochaetia	Spirochaetales	Marispirochaetaceae			
JAFGQN000000000	Zod_Metabat.76	Myxococcota	Polyangia	Novel:ZNO27	Novel:ZNF053			
JAFGQO000000000	Zod_Metabat.768	Bacteroidota	Bacteroidia	Bacteroidales	UBA10428	UBA10428		
JAFGQP000000000	Zod_Metabat.769	Planctomycetota	Phycisphaerae	Sedimentisphaerales	Anaerohalosphaeraceae	UBA7708		
JAFGQQ000000000	Zod_Metabat.777	Bacteroidota	Bacteroidia	Bacteroidales	PUMT01			
JAFGQR000000000	Zod_Metabat.779	Verrucomicrobiota	Verrucomicrobiae	Pedosphaerales	Palsa-1400			
JAFGQS000000000	Zod_Metabat.781	Desulfobacterota	Syntrophia	Syntrophales	UBA3084			
JAFGQU000000000	Zod_Metabat.783	Omnitrophota	Koll11	4484-171	4484-171			
JAFGQW000000000	Zod_Metabat.792	Planctomycetota	UBA8108	Novel:ZNO44	Novel:ZNF076			
JAFGQZ000000000	Zod_Metabat.800	Bacteroidota	Bacteroidia	Bacteroidales	UBA10428	UBA10428		
JAFGRA000000000	Zod_Metabat.802	Chloroflexota	Anaerolineae	Anaerolineales	UBA11579			
JAFGRB000000000	Zod_Metabat.807	Myxococcota	B64-G9	B64-G9	B64-G9			
JAFGRC000000000	Zod_Metabat.810	Bacteroidota	Bacteroidia	Bacteroidales	UBA5072	UBA5072		
JAFGRD000000000	Zod_Metabat.813	Planctomycetota	Planctomycetes	Pirellulales	UBA11386			
JAFGRE000000000	Zod_Metabat.815	Desulfobacterota	Novel:ZNC15	Novel:ZNO15	Novel:ZNF031			
JAFGRF000000000	Zod_Metabat.816	WOR-3	WOR-3	UBA2258	UBA2258	UBA2258		
JAFGRI000000000	Zod_Metabat.823	Chloroflexota	Anaerolineae	SBR1031	A4b			
JAFGRL000000000	Zod_Metabat.827	Planctomycetota	Phycisphaerae	Sedimentisphaerales	Anaerohalosphaeraceae	B140-G9		
JAFGRO000000000	Zod_Metabat.833	Nanoarchaeota	Woesearchaeales	GW2011-AR15	Novel:ZNF044			
JAFGRP000000000	Zod_Metabat.836	Desulfobacterota	Syntrophia	Syntrophales	UBAS619	UBAS619		
JAFGRR000000000	Zod_Metabat.846	Planctomycetota	Phycisphaerae	UBA1845	Fen-1342			
JAFGRS000000000	Zod_Metabat.847	Verrucomicrobiota	Lentisphaeria	UBA1407	Lenti-02			
JAFGRT000000000	Zod_Metabat.850	Acidobacteriota	UBA6911	Novel:ZNO06	Novel:ZNF013			
JAFGRU000000000	Zod_Metabat.852	Desulfobacterota	Desulfuromonadia	Novel:ZNO18	Novel:ZNF034			
JAFGRV000000000	Zod_Metabat.855	Spirochaetota	Spirochaetia	Spirochaetales	Novel:ZNF103			
JAFGRX000000000	Zod_Metabat.858	Calditrichota	Calditrichia	Calditrichales	Calditrichaceae	Zgenome-0002	Zgenome-0002 sp003854985	
JAFGRY000000000	Zod_Metabat.86	SM23-31	SM23-31	QNDG01	Novel:ZNF079			
JAFGSB000000000	Zod_Metabat.863	KSB1	UBA2214	UBA2214	Zgenome-0027			
JAFGSD000000000	Zod_Metabat.866	Actinobacteriota	Coriobacteriia	OPB41	UBA2279	UBA2279		
JAFGSE000000000	Zod_Metabat.868	Desulfobacterota	Desulfobacteria	Desulfatiglandales	HGW-15			
JAFGSF000000000	Zod_Metabat.875	Acidobacteriota	Aminicenantia	UBA2199	UBA2199			
JAFGSG000000000	Zod_Metabat.878	Spirochaetota	UBA4802	UBA4802	Novel:ZNF085			
JAFGSI000000000	Zod_Metabat.883	Chloroflexota	Anaerolineae	Anaerolineales	EmOPS12	UBA877		
JAFGSJ000000000	Zod_Metabat.886	CSSED10-310	Novel:ZNC05	Novel:ZNO41	Novel:ZNF100			
JAFGSK000000000	Zod_Metabat.887	WOR-3	WOR-3	UBA2258	B3-TA06			
JAFGSM000000000	Zod_Metabat.896	SZUA-182	Novel:ZNC12	Novel:ZNO35	Novel:ZNF092			
JAFGSO000000000	Zod_Metabat.906	Calditrichota	Calditrichia	RBG-13-44-9	RBG-13-44-9	RQOF01	RQOF01 sp003854955	
JAFGSR000000000	Zod_Metabat.916	Planctomycetota	Phycisphaerae	Sedimentisphaerales	SM23-30			
JAFGSS000000000	Zod_Metabat.919	Acidobacteriota	UBA6911	UBA6911	UBA6911			
JAFGST000000000	Zod_Metabat.920	Acidobacteriota	Aminicenantia	UBA2199	UBA2199	UBA2199		
JAFGSU000000000	Zod_Metabat.930	KSB1	UBA2214	UBA2214	UBA2214			
JAFGSV000000000	Zod_Metabat.932	Aenigmatarchaeota	Aenigmatarchaeia	QMZP01	QMZP01			
JAFGSW000000000	Zod_Metabat.934	Spirochaetota	Spirochaetia	Spirochaetales	RPP001			
JAFGSX000000000	Zod_Metabat.937	Myxococcota	UBA727	Novel:ZNO28	Novel:ZNF054			
JAFGSY000000000	Zod_Metabat.940	Desulfobacterota	Novel:ZNC02	Novel:ZNO14	Novel:ZNF030			
JAFGSZ000000000	Zod_Metabat.943	Bacteroidota	Bacteroidia	Bacteroidales	UBA10428			
JAFGTA000000000	Zod_Metabat.946	Thermoprotota	Bathyarchaeia	TCS64	RBG-16-57-9			
JAFGTB000000000	Zod_Metabat.947	Myxococcota	Polyangia	Novel:ZNO27	Novel:ZNF053			
JAFGTC000000000	Zod_Metabat.949	OLB16	OLB16	SURF-12	SURF-12			
JAFGTD000000000	Zod_Metabat.95	Acidobacteriota	UBA6911	UBA6911	UBA6911	UBA6911		
JAFGTF000000000	Zod_Metabat.958	Spirochaetota	B62-G9	B62-G9	Novel:ZNF081			
JAFGTG000000000	Zod_Metabat.96	Planctomycetota	Phycisphaerae	Sedimentisphaerales	Anaerohalosphaeraceae			
JAFGTH000000000	Zod_Metabat.961	Verrucomicrobiota	Kiritimatiellae	UBA8416	YA12-FULL-48-11			
JAFGTJ000000000	Zod_Metabat.964	Chloroflexota	Anaerolineae	SBR1031	UBA2029	MO-CFX2		
JAFGTK000000000	Zod_Metabat.965	Desulfobacterota	Desulfomonilia_A	UBA1062	UBA1062			
JAFGTM000000000	Zod_Metabat.972	Firmicutes_A	Clostridia	Tissierellales	Dethiosulfatibacteraceae			
JAFGTN000000000	Zod_Metabat.975	Planctomycetota	Planctomycetes	Pirellulales	UBA11386			
JAFGTR000000000	Zod_Metabat.988	Bacteroidota	Bacteroidia	Bacteroidales	UBA5072	UBA5072		
JAFGTS000000000	Zod_Metabat.996	Desulfobacterota	Syntrophia	Syntrophales	MLS-D			
JAFGTT000000000	Zod_Metabat.998	Zixibacteria	MSB-5A5	GN15	PGXB01			
JAFGTU000000000	Zod_Metabat.999	Planctomycetota	Phycisphaerae	Sedimentisphaerales	Anaerohalosphaeraceae			
JAFGTV000000000	ZodW_maxbin.058	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Rhodovulum		
JAFGTX000000000	ZodW_maxbin.062	Firmicutes_A	Clostridia	Peptostreptococcales	Acidaminobacteraceae			
JAFGTY000000000	ZodW_maxbin.067	Desulfobacterota	Novel:ZNC02	Novel:ZNO14	Novel:ZNF030			
JAFGTZ000000000	ZodW_maxbin.084	Proteobacteria	Gammaproteobacteria	Chromatiales	Chromatiaceae	Marichromatium		
JAFGUA000000000	ZodW_maxbin.088	Firmicutes_A	Clostridia	Saccharofermentanales	Novel:ZNF044			
JAFGUB000000000	ZodW_maxbin.095	Campylobacterota	Campylobacteria	Campylobacterales	Sulfurimonadaceae			
JAFGUD000000000	ZodW_maxbin.137	Bacteroidota	Bacteroidia	Bacteroidales	UBA3824			
JAFGUG000000000	ZodW_maxbin.150	Proteobacteria	Gammaproteobacteria	Thiomicrospirales	Thiomicrospiraceae	Thiomicrorhabdus		
JAFGUH000000000	ZodW_maxbin.154	Proteobacteria	Gammaproteobacteria	Halothiobacillales	Halothiobacillaceae	Guyparkeria		
JAFGUI000000000	ZodW_maxbin.163	Bacteroidota	Bacteroidia	Bacteroidales	VadinHA17	LD21		
JAFGUJ000000000	ZodW_maxbin.169	Campylobacterota	Campylobacteria	Campylobacterales	Sulfurimonadaceae	Sulfuricurvum		
JAFGUK000000000	ZodW_maxbin.172	Bacteroidota	Bacteroidia	Flavobacteriales	Flavobacteriaceae	Mesoflavibacter		
JAFGUM000000000	ZodW_maxbin.191	Spirochaetota	Spirochaetia	Treponematales	UBA12059	SZUA-370		
JAFGUN000000000	ZodW_maxbin.192	Proteobacteria	Gammaproteobacteria	Halothiobacillales	Halothiobacillaceae	Halothiobacillus	Halothiobacillus sp002281295	
JAFGUT000000000	ZodW_maxbin.216	Desulfobacterota	Syntrophia	Syntrophales	MLS-D			
JAFGUU000000000	ZodW_maxbin.228	Actinobacteriota	Coriobacteriia	OPB41	UBA2279	UBA7930		
JAFGUW000000000	ZodW_maxbin.277	Planctomycetota	Phycisphaerae	Sedimentisphaerales	Novel:ZNF071			
JAFGUX000000000	ZodW_Metabat.102	Campylobacterota	Campylobacteria	Campylobacterales	Sulfurospirillaceae	Sulfurospirillum		
JAFGUZ000000000	ZodW_Metabat.115	Delongbacteria	UBA4055	UBA4055	UBA4055			
JAFGVA000000000	ZodW_Metabat.117	Bacteroidota	Bacteroidia	Bacteroidales	UBA10428	UBA10428		
JAFGVB000000000	ZodW_Metabat.118	Spirochaetota	Spirochaetia	Treponematales	Treponemataceae	Spiro-10		
JAFGVC000000000	ZodW_Metabat.12	Firmicutes_A	Clostridia	Tissierellales	Dethiosulfatibacteraceae			
JAFGVD000000000	ZodW_Metabat.125	Actinobacteriota	Coriobacteriia	OPB41	UBA2279	UBA2279		
JAFGVE000000000	ZodW_Metabat.126	Campylobacterota	Campylobacteria	Campylobacterales	Sulfurimonadaceae	Sulfurimonas		
JAFGVG000000000	ZodW_Metabat.13	Bacteroidota	Bacteroidia	Bacteroidales	UBA5072	UBA5072		
JAFGVH000000000	ZodW_Metabat.130	Campylobacterota	Campylobacteria	Campylobacterales	Sulfurovaceae	FS08-3		
JAFGVI000000000	ZodW_Metabat.137	Desulfobacterota	Novel:ZNC02	Novel:ZNO14	Novel:ZNF030			
JAFGVJ000000000	ZodW_Metabat.155	Bacteroidota	Bacteroidia	Bacteroidales	Prolixibacteraceae	SKHV01		
JAFGVK000000000	ZodW_Metabat.156	Myxococcota	UBA796	UBA796	Novel:ZNF055			
JAFGVM000000000	ZodW_Metabat.17	Delongbacteria	UBA4055	UBA4055	UBA4055			

JAFGVN000000000	ZodW_Metabat.172	Firmicutes_A	Clostridia	Peptostreptococcales	Novel:ZNF045			
JAFGVO000000000	ZodW_Metabat.174	Myxococcota	Polyangia	Novel:ZNO27	Novel:ZNF053			
JAFGVP000000000	ZodW_Metabat.175	Verrucomicrobiota	Kiritimatiellae	Kiritimatiellales	Pontiellaceae	Pontiella		
JAFGVQ000000000	ZodW_Metabat.176	Desulfobacterota	Desulfuromonadia	Desulfuromonadales	Geopsychrobacteraceae	BM522		
JAFGVR000000000	ZodW_Metabat.179	Campylobacterota	Campylobacteria	Campylobacterales	Sulfurimonadaceae			
JAFGVU000000000	ZodW_Metabat.182	Bacteroidota	Bacteroidia	Bacteroidales	ML635J-15	Bact-19		
JAFGVV000000000	ZodW_Metabat.183	Bacteroidota	Bacteroidia	Bacteroidales	Paludibacteraceae	Paludibacter		
JAFGVW000000000	ZodW_Metabat.186	Spirochaetota	UBA4802	Novel:ZNO34	Novel:ZNF087			
JAFGVX000000000	ZodW_Metabat.188	Campylobacterota	Campylobacteria	Campylobacterales	Sulfurovaceae			
JAFGVY000000000	ZodW_Metabat.19	Bacteroidota	Bacteroidia	Bacteroidales	Prolixibacteraceae			
JAFGVZ000000000	ZodW_Metabat.191	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Roseibaca		
JAFGWB000000000	ZodW_Metabat.2	Bacteroidota	Bacteroidia	Bacteroidales	UBA5072	UBA5072		
JAFGWC000000000	ZodW_Metabat.217	Bacteroidota	Bacteroidia	Bacteroidales	NBLH01	NBLH01		
JAFGWD000000000	ZodW_Metabat.220	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae	Alpha-05		
JAFGWE000000000	ZodW_Metabat.227	Halobacteriota	Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	Methanomicrobium		
JAFGWF000000000	ZodW_Metabat.232	Bacteroidota	Bacteroidia	Bacteroidales	UBA1556	UBA6267		
JAFGWG000000000	ZodW_Metabat.234	Bacteroidota	Bacteroidia	Bacteroidales	DTU049	BM518		
JAFGWH000000000	ZodW_Metabat.241	Bacteroidota	Bacteroidia	Bacteroidales	BBW3	UBA5206		
JAFGWI000000000	ZodW_Metabat.242	Spirochaetota	Spirochaetia	Spirochaetales	Novel:ZNF103			
JAFGWJ000000000	ZodW_Metabat.248	Bacteroidota	Bacteroidia	Bacteroidales	Marinilabiliaceae	Breznakibacter	Breznakibacter xylanolytica	
JAFGWK000000000	ZodW_Metabat.253	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Thioclava		
JAFGWM000000000	ZodW_Metabat.263	Myxococcota	Polyangia	HGW-17	HGW-17			
JAFGWN000000000	ZodW_Metabat.264	Bacteroidota	Rhodothermia	Balneolales	Balneolaceae	SMO-BIN1		
JAFGWO000000000	ZodW_Metabat.265	BMS3Abin14	BMS3Abin14	BMS3Abin14	Novel:ZNF020			
JAFGWQ000000000	ZodW_Metabat.273	Campylobacterota	Campylobacteria	Campylobacterales	Sulfurovaceae	BN30871		
JAFGWR000000000	ZodW_Metabat.275	Calditrichota	Calditrichia	Calditrichales	Calditrichaceae	Zgenome-0002	Zgenome-0002 sp003854985	
JAFGWT000000000	ZodW_Metabat.284	Myxococcota	Polyangia	Novel:ZNO27	Novel:ZNF053			
JAFGWU000000000	ZodW_Metabat.292	Bacteroidota	Bacteroidia	Bacteroidales	GCA-2748055			
JAFGWV000000000	ZodW_Metabat.297	Desulfobacterota	Novel:ZNC02	Novel:ZNO14	Novel:ZNF030			
JAFGWX000000000	ZodW_Metabat.299	Proteobacteria	Gammaproteobacteria	Methylococcales	Methylothermaceae	Methylohalobius	Methylohalobius crimeensis	
JAFGWY000000000	ZodW_Metabat.30	Proteobacteria	Gammaproteobacteria	Acidithiobacillales	Acidithiobacillaceae	Acidithiobacillus		
JAFGWZ000000000	ZodW_Metabat.303	Desulfobacterota	Syntrophia	Syntrophales	UBA3084			
JAFGXA000000000	ZodW_Metabat.305	Proteobacteria	Gammaproteobacteria	UBA9339	UBA9339			
JAFGXB000000000	ZodW_Metabat.308	Proteobacteria	Gammaproteobacteria	Burkholderiales	Burkholderiaceae	Thiomonas		
JAFGXD000000000	ZodW_Metabat.319	Bacteroidota	Bacteroidia	Bacteroidales	GWF2-38-335	GWF2-38-335		
JAFGXF000000000	ZodW_Metabat.341	Chloroflexota	Anaerolineae	Anaerolineales	Anaerolineaceae			
JAFGXH000000000	ZodW_Metabat.349	UBP6	Novel:ZNC13	Novel:ZNO37	Novel:ZNF095			
JAFGXI000000000	ZodW_Metabat.352	Bacteroidota	Bacteroidia	Bacteroidales	UBA6680			
JAFGXJ000000000	ZodW_Metabat.353	Bacteroidota	Bacteroidia	Bacteroidales	Prolixibacteraceae	SKHV01		
JAFGXK000000000	ZodW_Metabat.368	Bacteroidota	Bacteroidia	Bacteroidales	VadinHA17	LD21		
JAFGXL000000000	ZodW_Metabat.371	Nitrospirota	Thermodesulfovibrionia	Thermodesulfovibrionales	Novel:ZNF057			
JAFGXM000000000	ZodW_Metabat.376	Bacteroidota	Bacteroidia	Bacteroidales	Tannerellaceae	Parabacteroides_A		
JAFGXP000000000	ZodW_Metabat.390	Proteobacteria	Gammaproteobacteria	Thiomicrospirales	Thiomicrospiraceae	Thiomicrorhabdus		
JAFGXQ000000000	ZodW_Metabat.4	Myxococcota	Polyangia	Novel:ZNO27	Novel:ZNF053			
JAFGXR000000000	ZodW_Metabat.41	Spirochaetota	Spirochaetia	Spirochaetales	Spirochaetaceae_B			
JAFGXS000000000	ZodW_Metabat.54	Bacteroidota	Bacteroidia	Bacteroidales	F082	SZUA-53		
JAFGXU000000000	ZodW_Metabat.59	Bacteroidota	Bacteroidia	Bacteroidales	Prolixibacteraceae	Draconibacterium		
JAFGXV000000000	ZodW_Metabat.6	Desulfobacterota	Desulfuromonadia	Desulfuromonadales	Desulfuromonadaceae	Pseudodesulfuromonas		
JAFGXX000000000	ZodW_Metabat.7	Bacteroidota	Bacteroidia	Bacteroidales	VadinHA17	LD21		
JAFGXY000000000	ZodW_Metabat.71	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Cypionkella		
JAFGXZ000000000	ZodW_Metabat.79	Marinisomatota	UBA2242	UBA2242	UBA2242	B118-G9		
JAFGYA000000000	ZodW_Metabat.82	Fermentibacterota	Fermentibacteria	Fermentibacterales	Fermentibacteraceae	Aegiribacteria		
JAFGYB000000000	ZodW_Metabat.88	Bacteroidota	Bacteroidia	Bacteroidales	F082	SZUA-53		
JAFGYC000000000	ZodW_Metabat.9	Proteobacteria	Gammaproteobacteria	Thiomicrospirales	Thiomicrospiraceae	Hydrogenovibrio		
JAFGYD000000000	ZodW_Metabat.93	Spirochaetota	Spirochaetia	Spirochaetales	Spirochaetaceae_B	SZUA-382		
JAFGYE000000000	ZodW_Metabat.94	Bacteroidota	Bacteroidia	Bacteroidales	Marinifilaceae	Labilibaculum		

Analysis of was conducted on individual genomic bins by building and scanning hidden markov model (HMM) profiles for the individual genes in the column headers. To build the sulfur-genes HMM profiles, Uniprot reference sequences for all genes with an assigned KO number were downloaded, aligned using Clustal-omega *(51)* , and the alignment was used to build an HMM profile using hmmbuild (HMMER 3.1b2) *(52)* . For genes not assigned a KO number (e.g. otr, tsdA, tetH), a representative protein was compared against the KEGG Genes database using Blastp and significant hits (those with e-values < e-80) were downloaded and used to build HMM profiles as explained above. The custom-built HMM profiles were then used to scan the analyzed genomes for significant hits using hmmscan (HMMER 3.1b2) *(52)* with the option -T 100 to limit the results to only those profiles with an alignment score of at least 100. Further confirmation was achieved through phylogenetic assessment and tree building procedures, in which potential candidates identified by hmmscan were aligned to the reference sequences used to build the custom HMM profiles using Clustal-omega *(51)* , followed by maximum likelihood phylogenetic tree construction using FastTree *(32)* . Only candidates clustering with reference sequences were deemed true hits and were assigned to the corresponding KO.

Table 3.3: Substrates potentially supporting growth
Substrates potentially supporting growth, predicted fermentation end products, and energy conservation pathways predicted from genomic analysis.




Novel:ZNO11
Novel:ZNO12
Novel:ZNO13
Novel:ZNO14
Novel:ZNO15
Novel:ZNO16
Novel:ZNO17
Novel:ZNO18
Novel:ZNO19
Novel:ZNO20
Novel:ZNO21
Novel:ZNO22
Novel:ZNO23
Novel:ZNO24
Novel:ZNO25
Novel:ZNO26
Novel:ZNO27
Novel:ZNO28
Novel:ZNO29
Novel:ZNO30
Novel:ZNO31
Novel:ZNO32
Novel:ZNO33
Novel:ZNO34
Novel:ZNO35
Novel:ZNO36
Novel:ZNO37
Novel:ZNO38
Novel:ZNO39
Novel:ZNO40
Novel:ZNO41
Novel:ZNO42
Novel:ZNO43
Novel:ZNO44
Novel:ZNO45
O2-12-FULL-45-9
Omnitrophales
OPB41
Opitutales
Palsa-1104
Paludibacteraceae
Parachlamydiales
Pedosphaerales
Peptostreptococcales
Petrotogales
PGYV01
Pirellulales
Polyangiales
Proteobacteraceae
Promineofilales
PUMT01
QMZP01
QMZS01
QNDG01
RBG-13-44-9
RBG-13-55-18
RBG-16-60-22
RBG-16-64-13
RBG-16-64-43
Rhodobacterales
Rhodospirillales
RPPD01
Rs-D84
Saccharofermentanales
SB-45
SC72
SDB-A
SG8-24
SJA-28
SKGA01
SLAD01
SLGR01
SLSP01
SM23-30
SM23-33
SM23-42
SM23-78
Smithellaceae
Solirubrobacterales
Sphaerochaetales
Spirochaetaceae_B
SS55BA
Sulfurimonadaceae
Sulfurospirillaceae
Sulfurovaceae
SURF-12
Synergistales
Syntrophaceae
SZUA-365
SZUA-567
Tannerellaceae
TC5G4
Thermodesulfovibrionales
Thermoflexales
Thiomicrospirales
Thorarchaeales
Tissierellales
Treponematales
UBA10015
UBA10030
UBA10107
UBA101185
UBA10214
UBA10428
UBA1062
UBA10834
UBA11576
UBA11579
UBA11858
UBA12170
UBA12402
UBA1369
UBA1400
UBA1407
UBA1414
UBA1429
UBA1556
UBA1560
UBA1845
UBA2029
UBA2162
UBA2185
UBA2199
UBA2210
UBA2214
UBA2241
UBA2242
UBA2258
UBA2777
UBA3072
UBA3084
UBA3254
UBA3824
UBA3940
UBA4055
UBA4802
UBA4823
UBA5072
UBA5619
UBA5760
UBA5794
UBA6092
UBA6257
UBA6266
UBA6522
UBA6680
UBA6911
UBA7950
UBA796
UBA8108

Filled cells correspond to the detection of a full pathway. For all non-sulfur related functional predictions, combined GhostKoala *(50)* outputs of all genomes belonging to a certain order (for orders with 5 genomes or less; n=206), or family (for orders with more than 5 genomes; n=85) were checked for the presence of groups of KOs constituting metabolic pathways (additional file 1). The list of these 291 lineages is shown in Column A. The presence of at least 80% of KOs assigned to a certain pathway in at least one genome belonging to a certain order/family was used as an indication of the presence of that pathway in that order/family. Analysis of S cycling and H2 metabolism (column header in Boldface) capabilities was conducted on individual genomic bins by building and scanning hidden markov model (HMM) profiles as explained in the main text under Materials and Methods.

*: Glycolytic, and fermentation capabilities were predicted by feeding the GhostKOALA output to KeggDecoder.

**: Proteases, peptidases, and protease inhibitors were identified using Blastp against the Merops database *(87)*, while CAZymes (glycoside hydrolases [GHs], polysaccharide lyases [PLs], and carbohydrate esterases [CEs]) were identified by searching all ORFs from all genomes against the dbCAN hidden Markov models V9 *(88)* (downloaded from the dbCAN web server in September 2020) using hmmscan. FeGenie *(89)* was used to predict the presence of iron reduction and iron oxidation genes in individual bins.

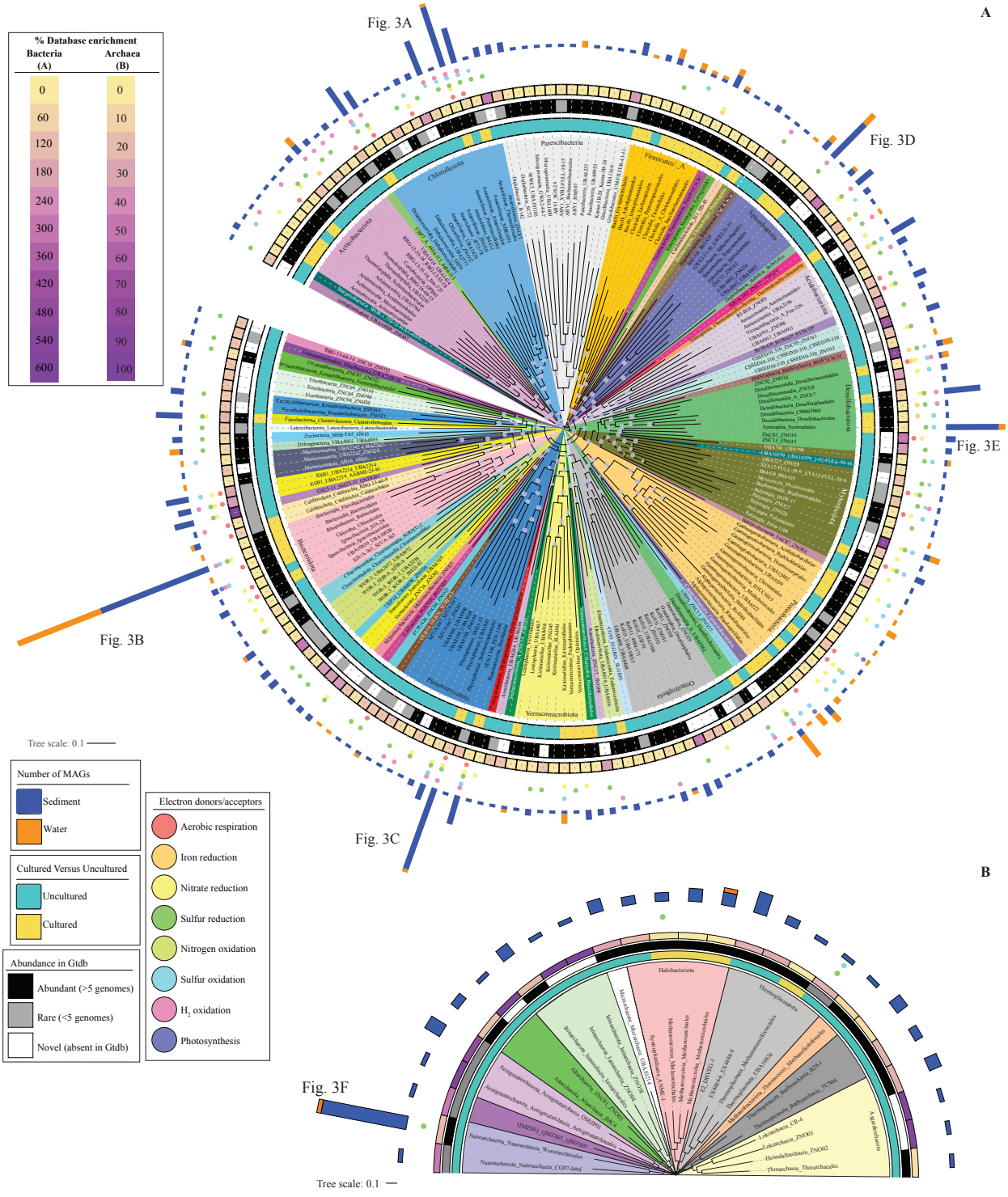


Figure 3.1: Phylogenomics of the bacterial and archaeal genomes

Figure 3.1: Detailed caption of Figure 3.1

Phylogenomics of the 516 bacterial (A), and 114 archaeal (B) genomes analyzed in this study. The maximum likelihood trees were constructed in FastTree [83] based on the concatenated alignments of 120 (bacterial), and 122 (archaeal) housekeeping genes obtained from GTDB-TK (85). The branches represent order-level taxonomy and are color coded by phylum. For phyla with 4 orders or less branches are labeled as Phylum_Class_Order. For phyla with more than 4 orders, the phylum is shown at the base of the colored wedge and the branches are labeled as Class_Order. Lineages staring with ZN depict novel lineages (ZNC = novel class; ZNO = novel order). Bootstrap support values are shown as bubbles for nodes with >70% support. Tracks around the tree represent (from innermost to outermost): cultured status at the order level (cultured versus uncultured), abundance in GTDB based on the number of available genomes (abundant with more than 5 genomes, rare with 5 genomes or less, and novel with no genomes in GTDB), percentage database enrichment (calculated as number of genomes belonging to a certain order binned in the current study as a percentage of the number of genomes belonging to the same order in GTDB), energy conservation capabilities depicted by colored circles (salmon, aerobic respiration; orange, Fe3+ respiration; yellow, nitrate/nitrite reduction; dark green, reductive sulfur processes; lime green, nitrogen oxidation; cyan, oxidative sulfur-processes; pink, respiratory hydrogen oxidation; and purple, photosynthesis), and the number of MAGs belonging to each order binned from the sediment (blue bars) and the water (orange bars). For orders with 20 or more genomes, the family-level delineation is shown in Figure 3. These orders are: *Anaerolineales* (Fig. 3A), *Bacteroidales* (Fig. 3B), *Sedimentisphaerales* (Fig. 3C), *Spirochaetales* (Fig. 3D), *Syntrophales* (Fig. 3E), and *Woesearchaeales* (Fig. 3F).

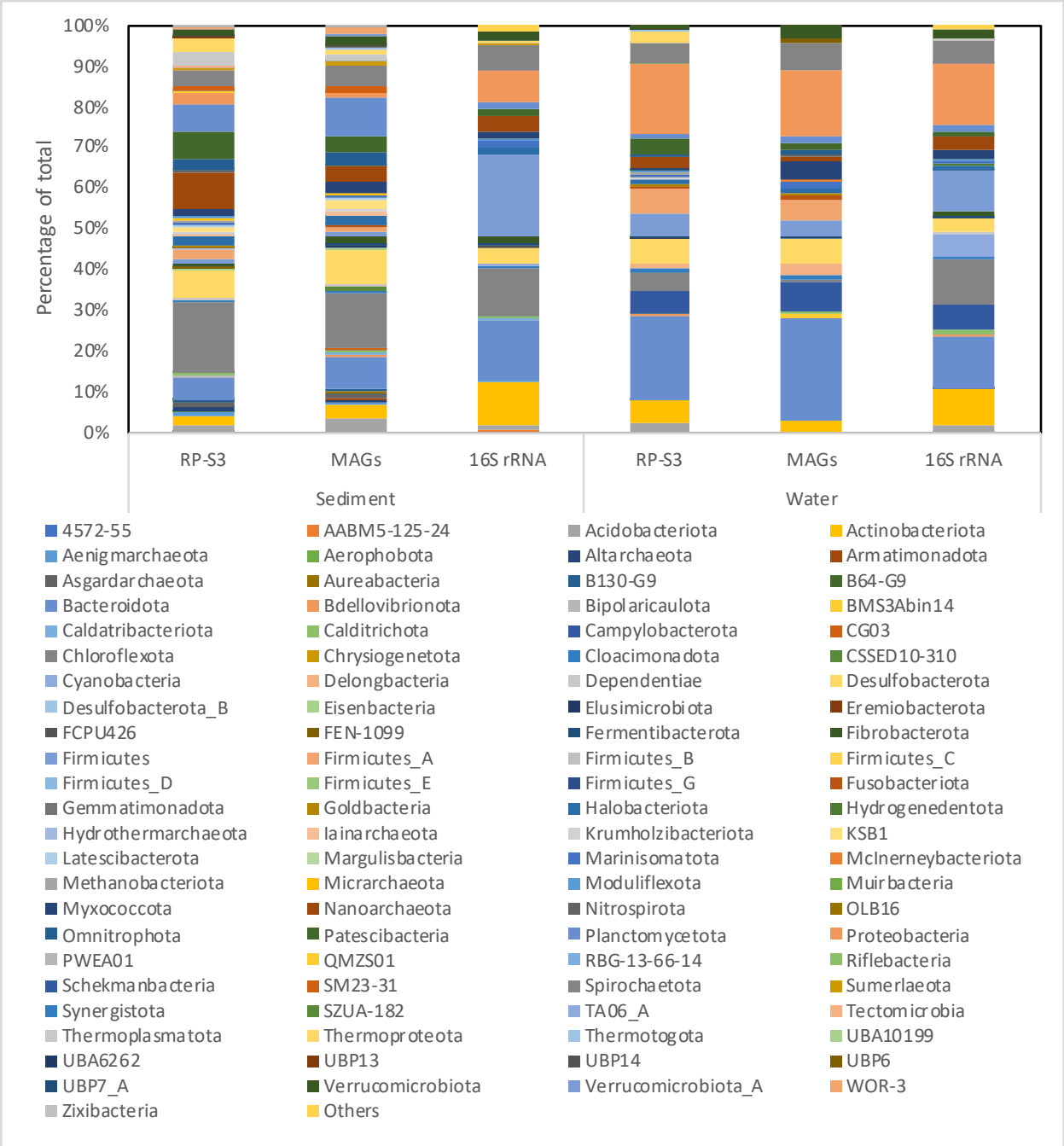


Figure 3.2: Zodletone spring phylum-level community composition

Zodletone spring phylum-level community composition based on ribosomal protein S3 (RP-S3), binned genomes (MAGs), as well as the gene for 16S rRNA for both the sediment and the water samples.

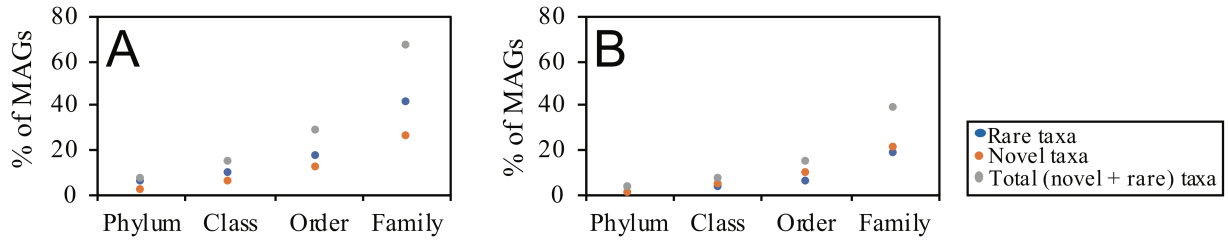


Figure 3.3: Novelty, rarity, and phylum-level makeup in Zodletone

Novelty, rarity, and phylum-level makeup in Zodletone sediment and water communities. Genomes belonging to novel (orange), and LRD (blue) lineages are shown as a percentage of total binned genomes in the sediment (A) and the water (B) communities. The sum of novel and LRD genomes percentages is shown in grey.

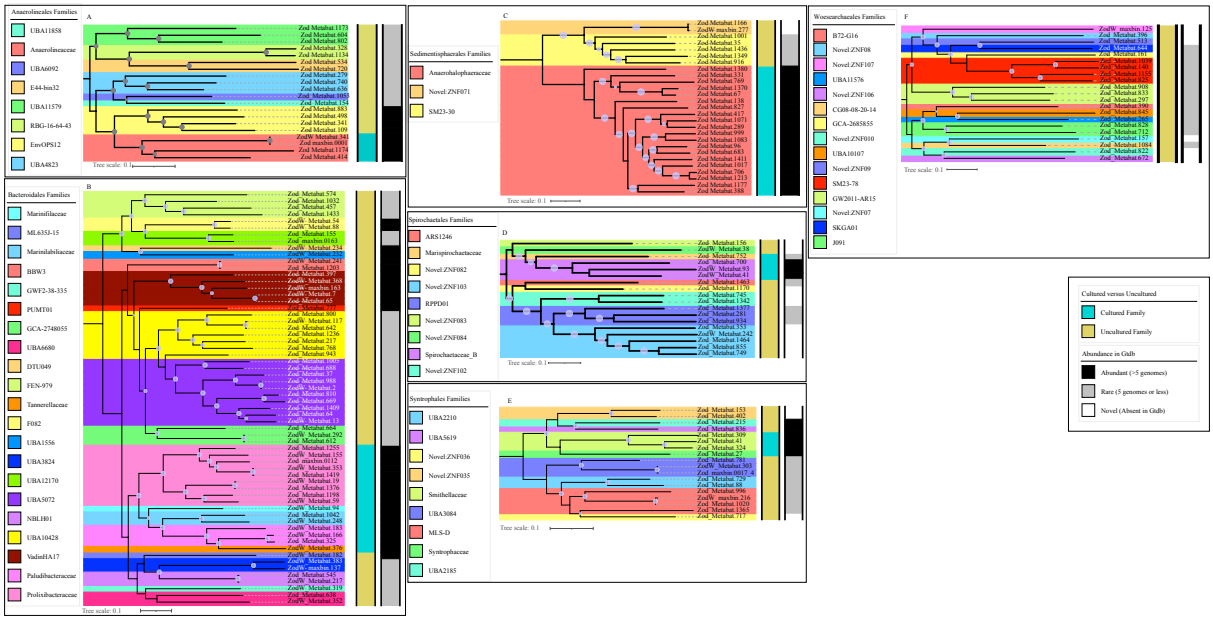


Figure 3.4: Family-level delineation for orders

Family-level delineation for orders with 20 or more genomes. The maximum likelihood trees were constructed in FastTree [83] based on the concatenated alignments of 120-, and 122- single copy genes, respectively, obtained from GTDB-TK (85). Bootstrap support values are shown as bubbles for nodes with >70% support. Families are color-coded. To the right of the trees, tracks are shown for cultured status at the family level (cultured versus uncultured), and abundance in GTDB based on the number of available genomes (abundant with more than 5 genomes, rare with 5 genomes or less, and novel with no genomes in GTDB).

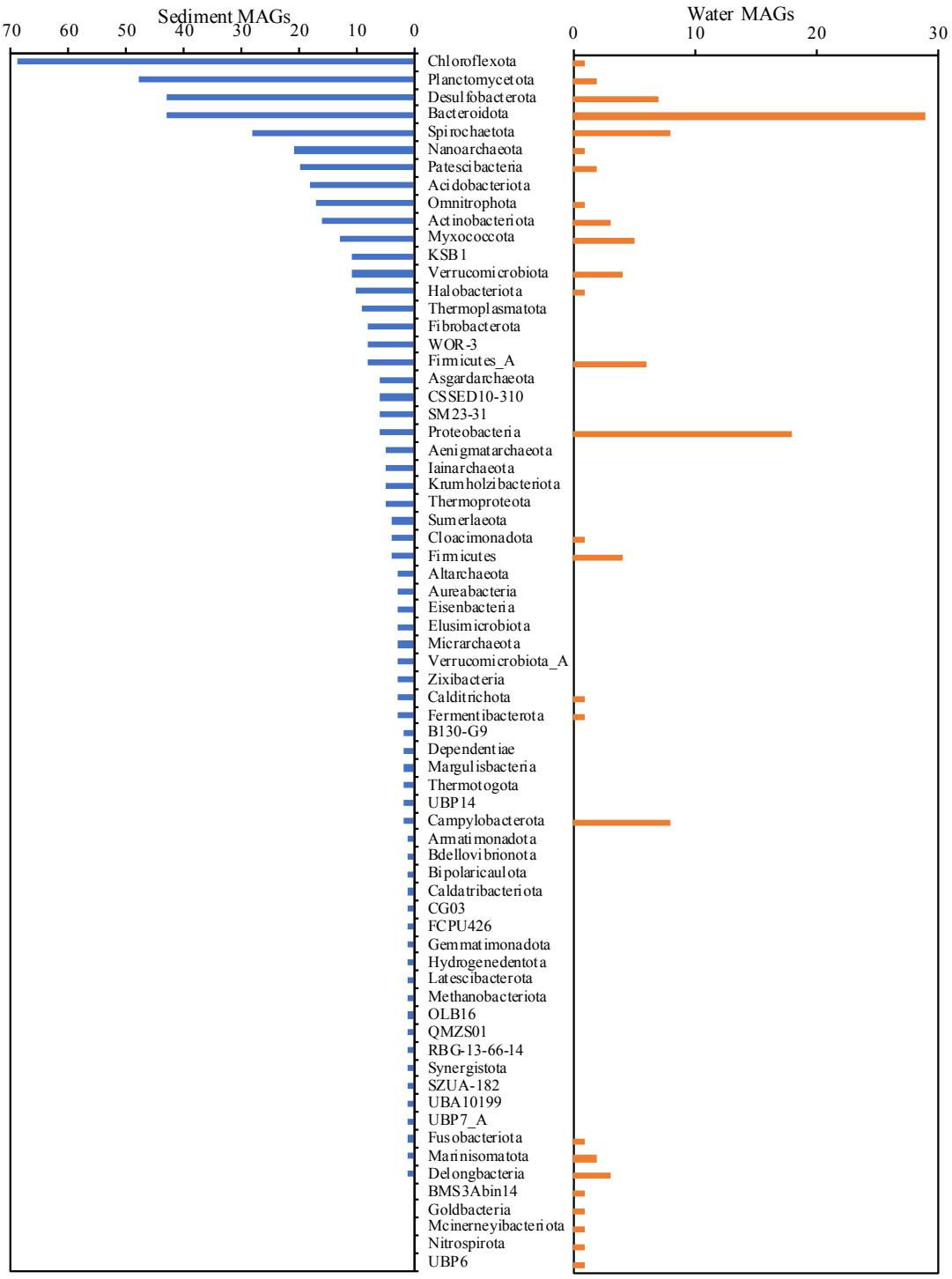


Figure 3.5: Phylum-level affiliation for sediment versus water genomes

Number of genomes belonging to each phylum is shown for the sediment (blue bars on the left) and the water (orange bars on the right).

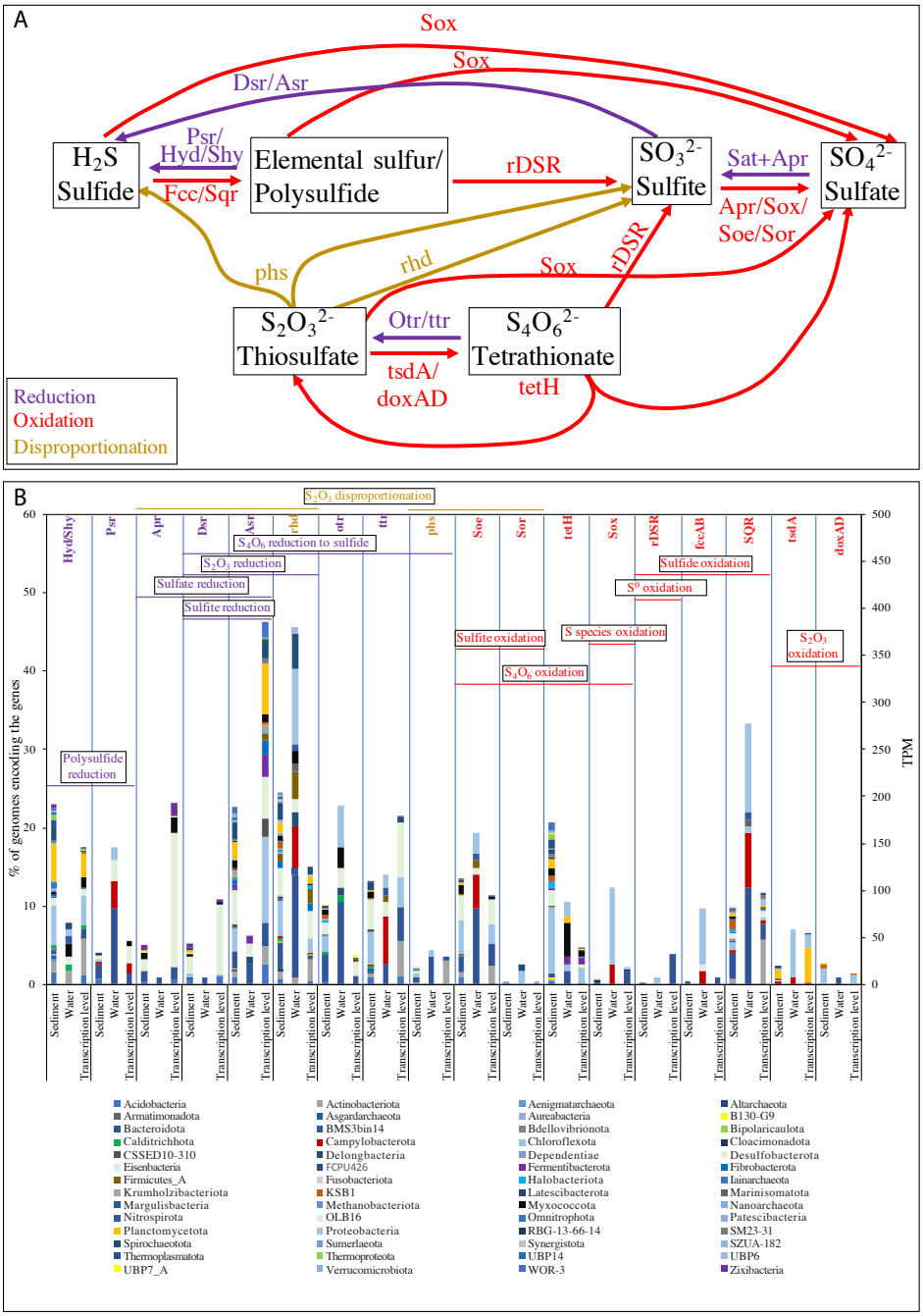


Figure 3.6: Sulfur cycle in Zodletone spring

Figure 3.6: Sulfur cycle in Zodletone spring continued
(A) Diagram of sulfur transformations predicted to take place in the spring. Different sulfur species are shown in black boxes. Reduction reactions are depicted by purple arrows, oxidation reactions are depicted by red arrows, while disproportionation reactions are depicted by golden brown arrows. The gene(s) names are shown on the arrows. (B) Phylum-level distribution of the S-cycling genes shown at the top of the figure in sediment and water genomes, as well as the transcriptomic dataset. Processes involving more than one gene are highlighted by horizontal bars and are color coded by reduction (purple), oxidation (red), or disproportionation (golden brown), with the name of the process shown on top of the horizontal bar. RNA-seq reads were pseudo-aligned to the S-cycling genes predicted in Zodletone genomes to detect exact matches using Kallisto (95). The transcripts per million are shown on the secondary Y-axis for the gene/ group of genes depicted at the top of the figure.

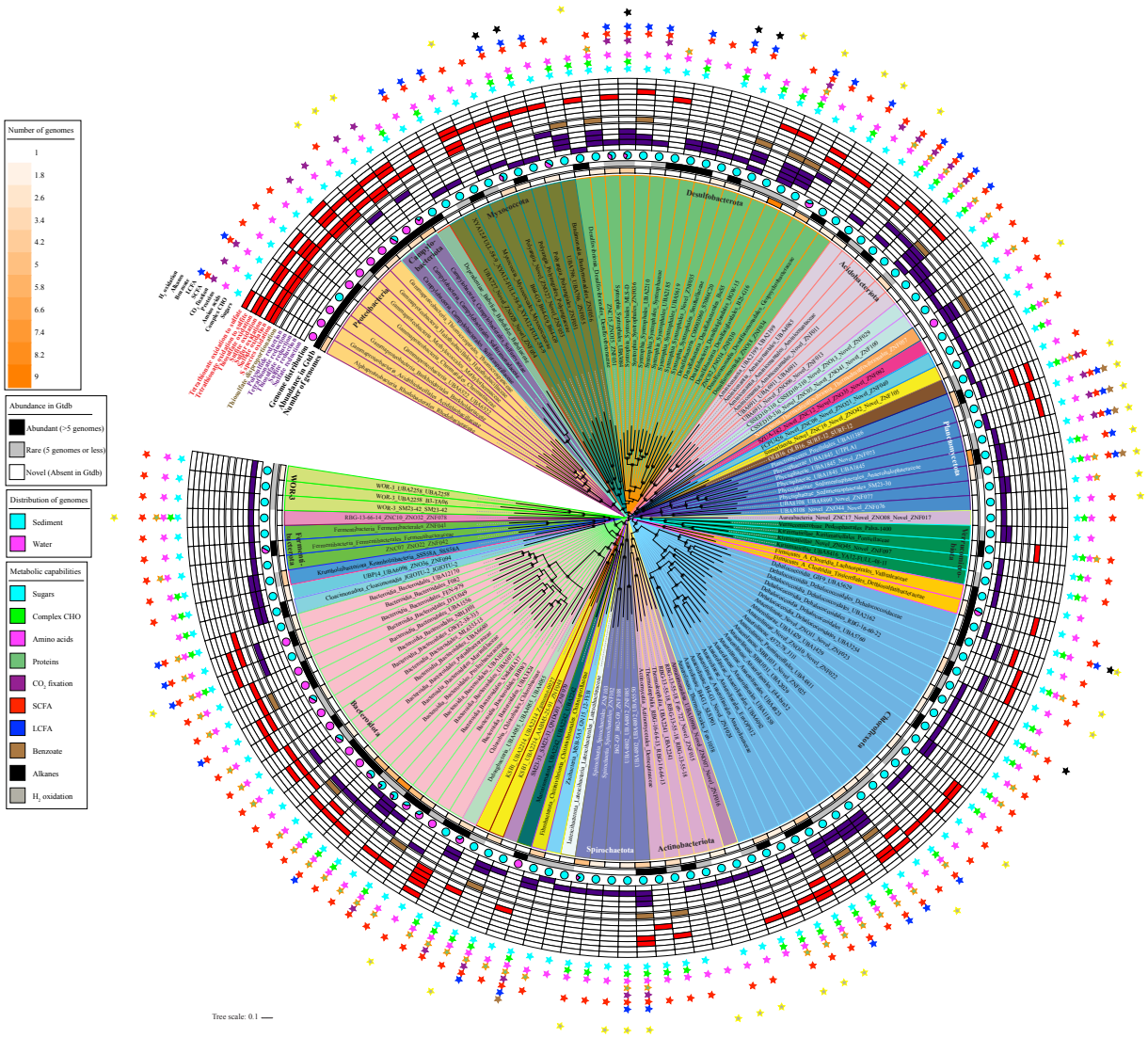


Figure 3.7: Family-level distribution of the genomes involved in S cycling

Figure 3.7: Family-level distribution of the genomes involved in S cycling continued
The maximum likelihood tree was constructed in FastTree 40 based on the concatenated alignments of 120 single-copy genes obtained from Gtdb-TK 41. The branches represent family-level taxonomy and are color coded by phylum. For phyla with 2 families or less involved in S cycling, branches are labeled as Phylum_Class_Order_Family. For phyla where 3 or more families are involved in S cycling, the phylum is shown at the base of the colored wedge and the branches are labeled as Class_Order_Family. Lineages staring with ZN depict novel lineages as follows: ZNC, novel class; ZNO, novel order; and ZNF, novel family. Bootstrap support values are shown as bubbles for nodes with >70% support. Tracks around the tree represent (from innermost to outermost): heatmap for the number of genomes in each family, abundance in Gtdb based on the number of available genomes (abundant with more than 5 genomes, rare with 5 genomes or less, and novel with no genomes in Gtdb), pie charts of the breakdown of the number of genomes in the sediment (cyan) versus water (magenta), sulfur reduction pathways (5 tracks in purple), thiosulfate disproportionation pathways (1 track in golden brown), sulfur oxidation pathways (7 tracks in red), and substrates predicted to support growth depicted by colored stars (cyan, sugars; lime green, complex carbohydrates; magenta, amino acids; orange, proteins; purple, CO2 fixation; red, short-chain fatty acids (SCFA); blue, beta oxidation of long-chain fatty acids; brown, anaerobic benzoate/aromatic hydrocarbon degradation; black, anaerobic alkane degradation; and grey, Hydrogen oxidation).

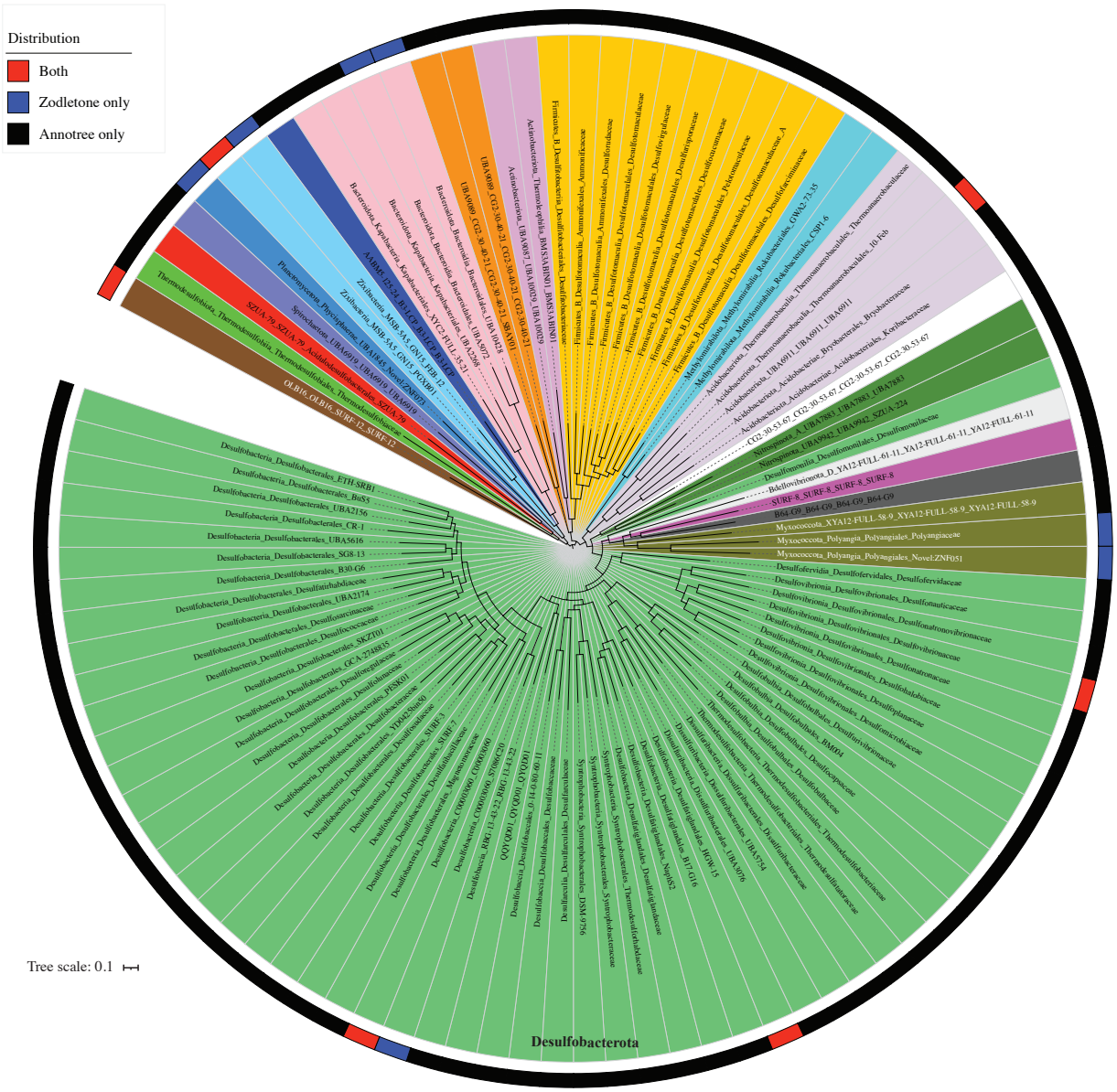


Figure 3.8: Expanding Lineages with sulfate reduction genes

Expanding lineages mediating reductive sulfur cycling processes in the tree of life. Annotree 42 was queried at the family level for the presence of sulfate reduction genes (combined search for the genes AprA, AprB, Sat, QmoA, QmoB, QmoC, DsrA, DsrB, and DsrC).

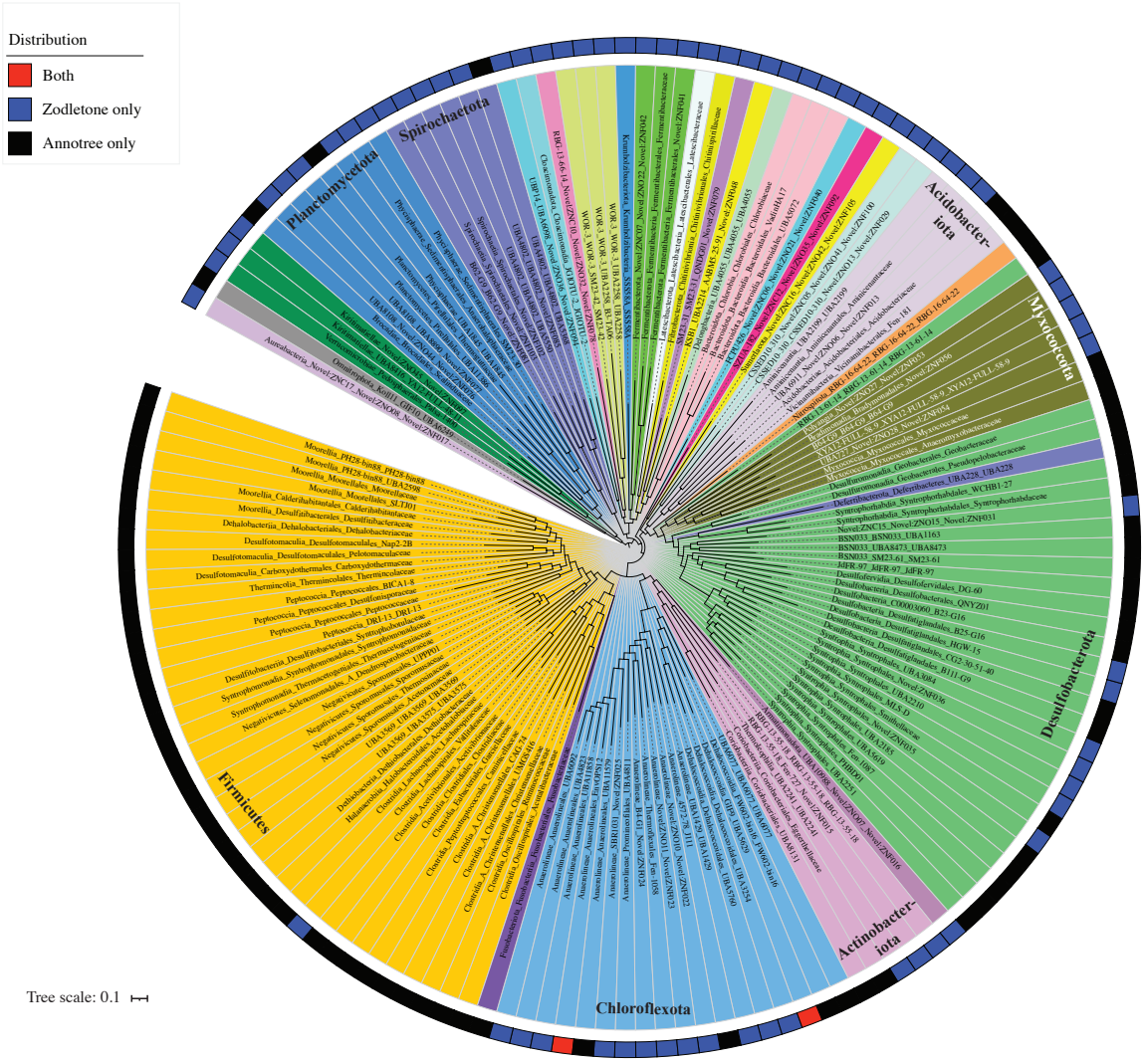


Figure 3.9: Expanding Lineages with sulfite reduction genes

Expanding lineages mediating reductive sulfur cycling processes in the tree of life. Annotree 42 was queried at the family level for the presence of sulfite reduction genes using both the DSR system (combined search for the genes DsrA, DsrB, and DsrC, excluding all duplicate hits from (A) and excluding all hits from phyla known to use the system in the oxidative direction (Proteobacteria, Nitrospira, and Chlorobiaceae), and the ASR system (combined search for the genes AsrA, AsrB, AsrC, HdrA, HdrB, and HdrC).

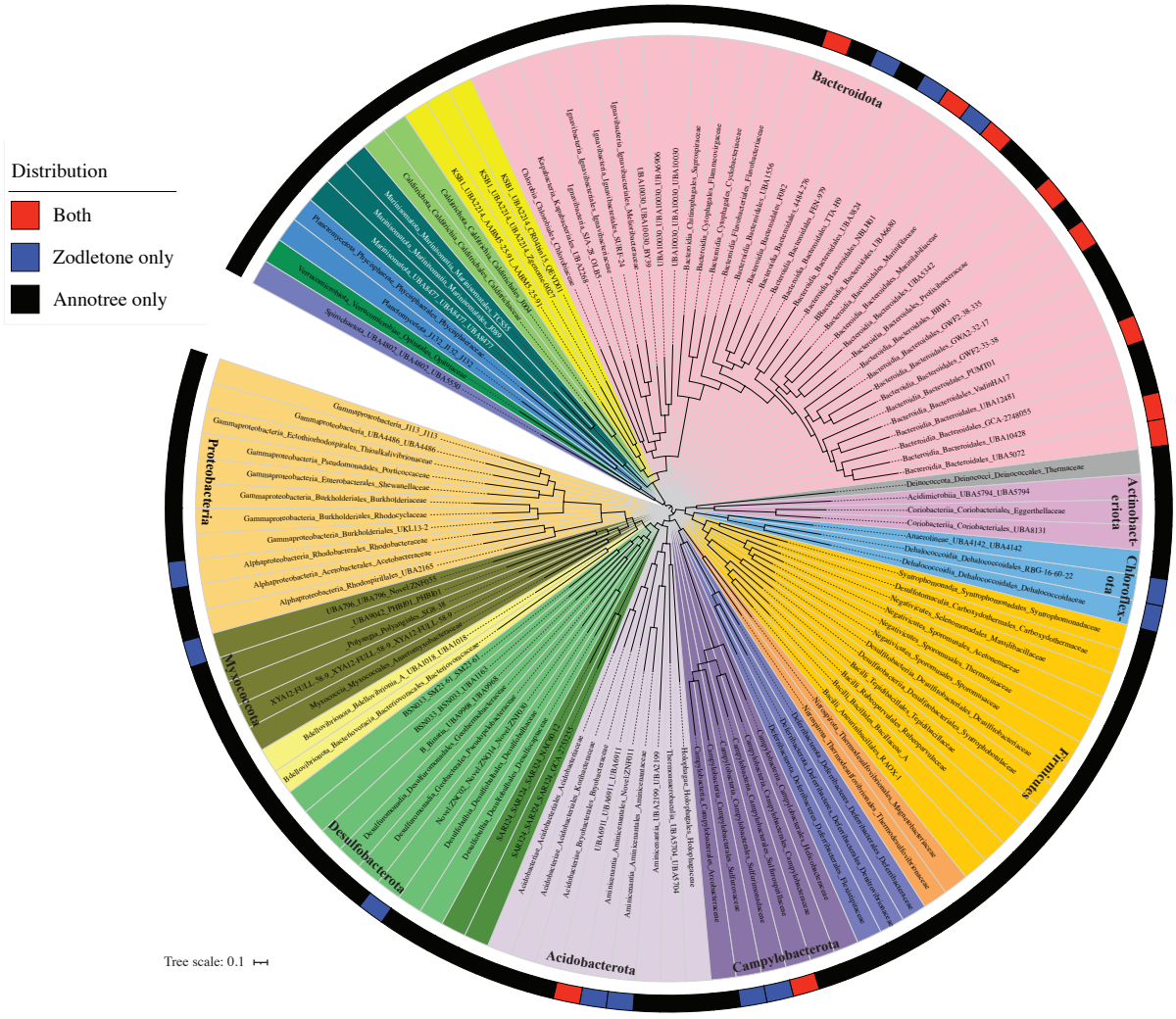


Figure 3.10: Expanding Lineages with polysulfide reduction genes

Expanding lineages mediating reductive sulfur cycling processes in the tree of life. Annotree 42 was queried at the family level for the presence of polysulfide reduction genes (combined search for the genes PsrA, PsrB, and PsrC).

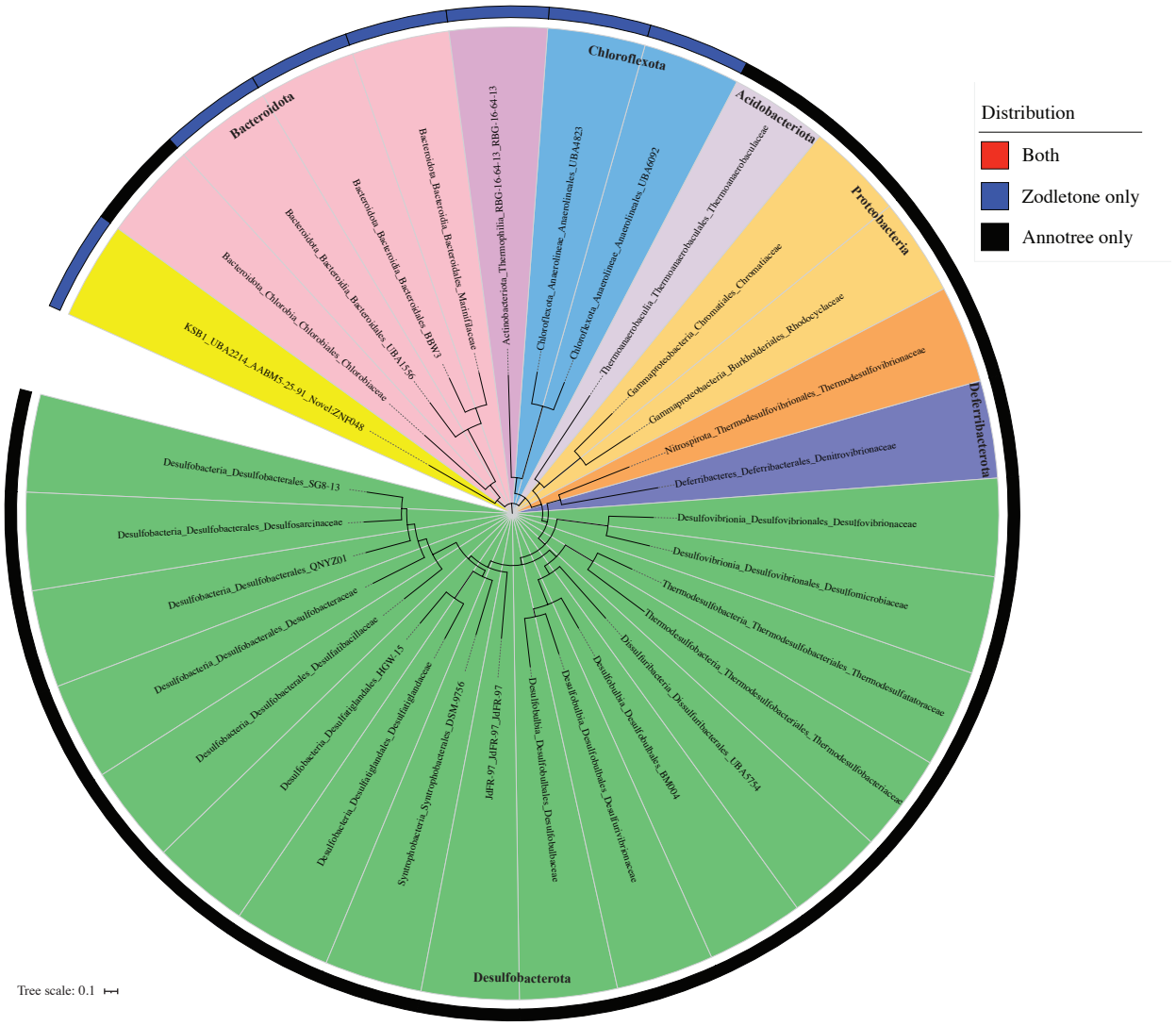


Figure 3.11: Expanding Lineages with thiosulfate reduction genes

Expanding lineages mediating reductive sulfur cycling processes in the tree of life. Annotree 42 was queried at the family level for the presence of thiosulfate reduction (combined search for the genes PhsA, PhsB, and PhsC, combined with either DsrA, DsrB, and DsrC , or AsrA, AsrB, and AsrC) and thiosulfate disproportionation (combined search for the genes PhsA, PhsB, and PhsC, combined with either AprA, AprB, and Sat, or SoeA, SoeB, and SoeC, or SorA).

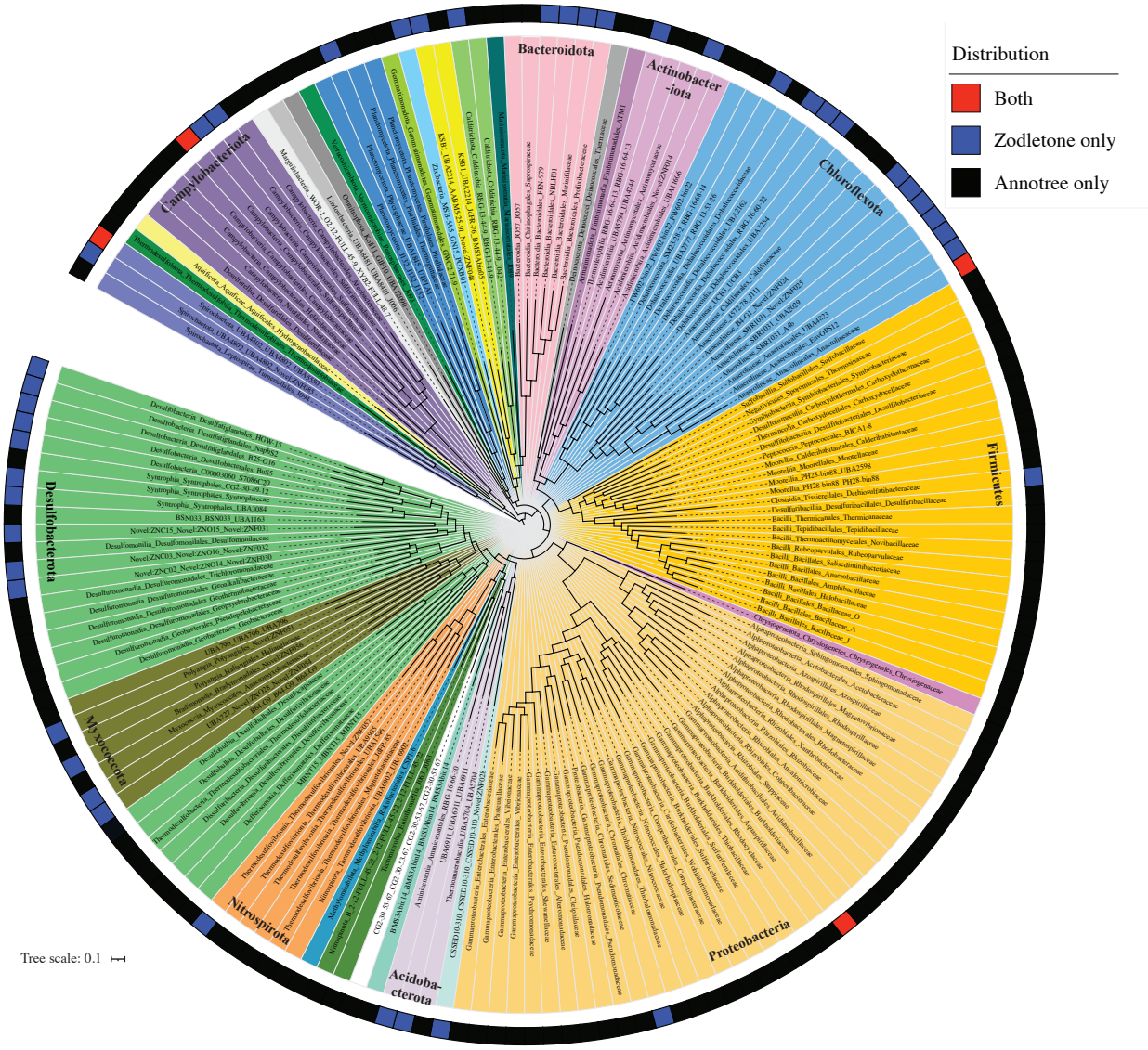


Figure 3.12: Expanding Lineages with tetrathionate reduction genes

Expanding lineages mediating reductive sulfur cycling processes in the tree of life. Annotree 42 was queried at the family level for the presence of tetrathionate reduction (combined search for the genes TtrA, TtrB, and TtrC).

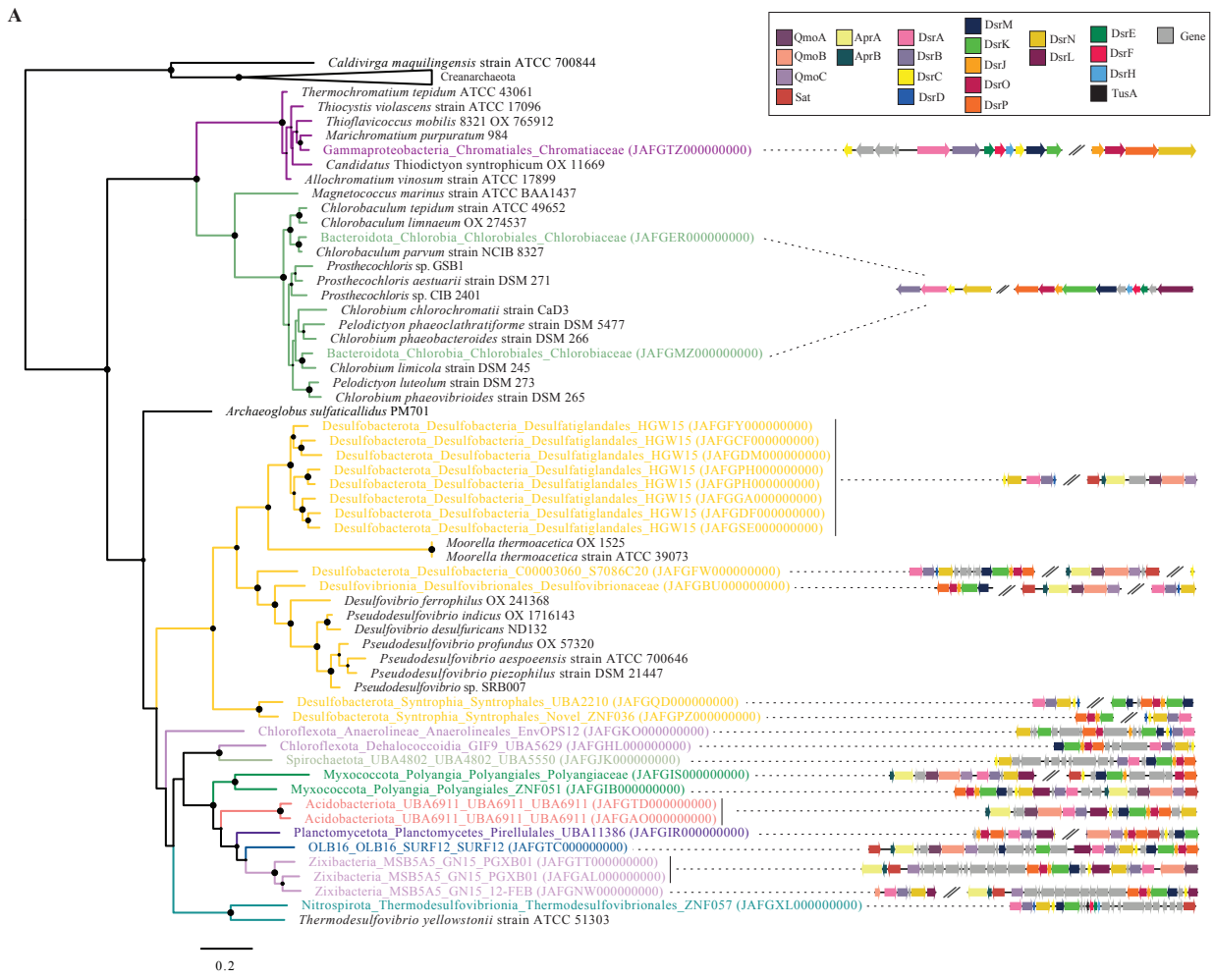


Figure 3.13: Phylogenetic affiliation and contig organization of DsrAB

Phylogenetic affiliation and contig organization of selected sulfur reduction proteins. Phylogeny of the dissimilatory sulfite reductase DsrAB [EC:1.8.99.5] concatenated proteins. , anaerobic sulfite reductase subunit B AsrB.

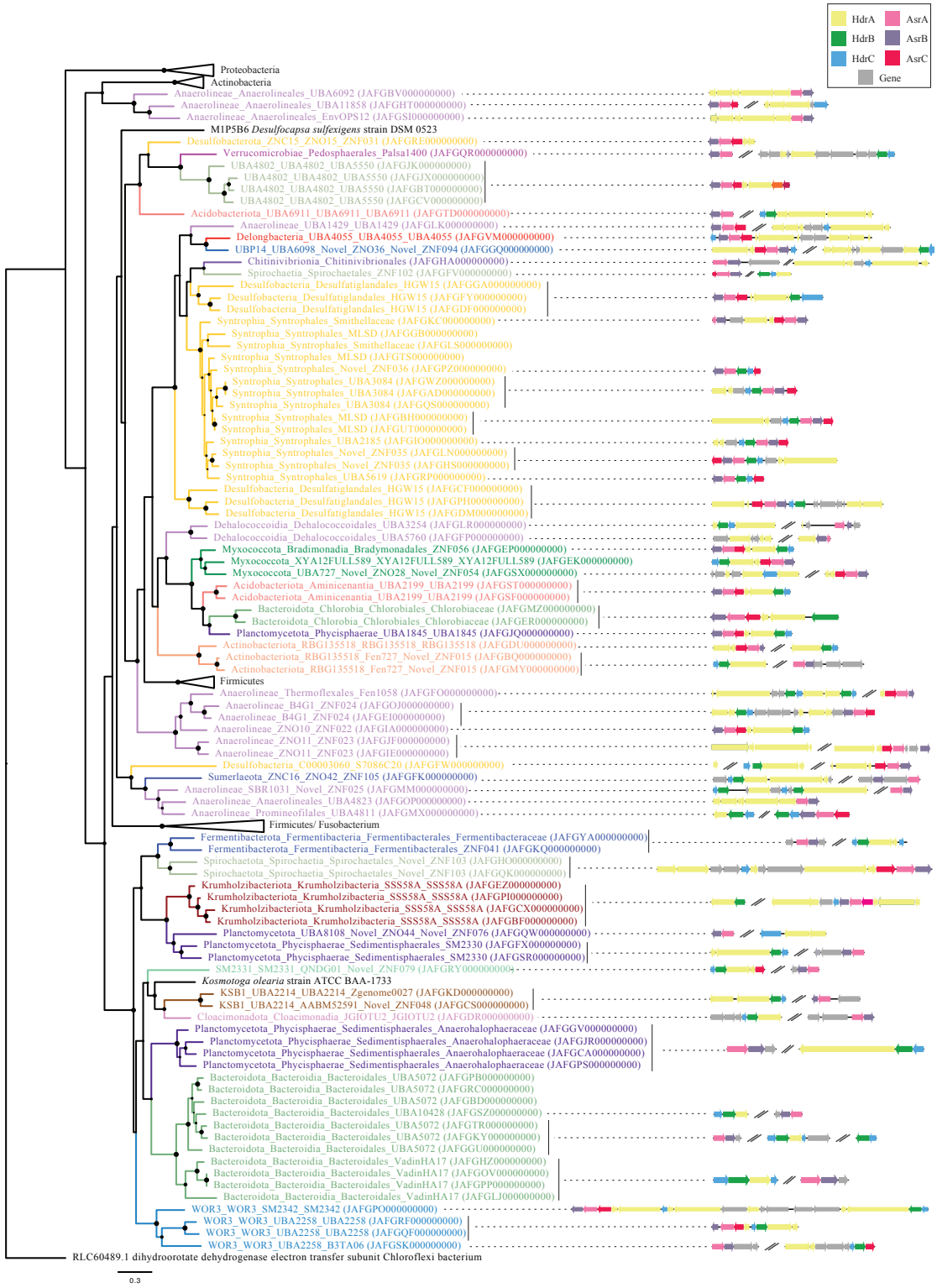


Figure 3.14: Phylogenetic affiliation and contig organization of AsrB

Phylogenetic affiliation and contig organization of selected sulfur reduction proteins. Phylogeny of the anaerobic sulfite reductase subunit B AsrB.

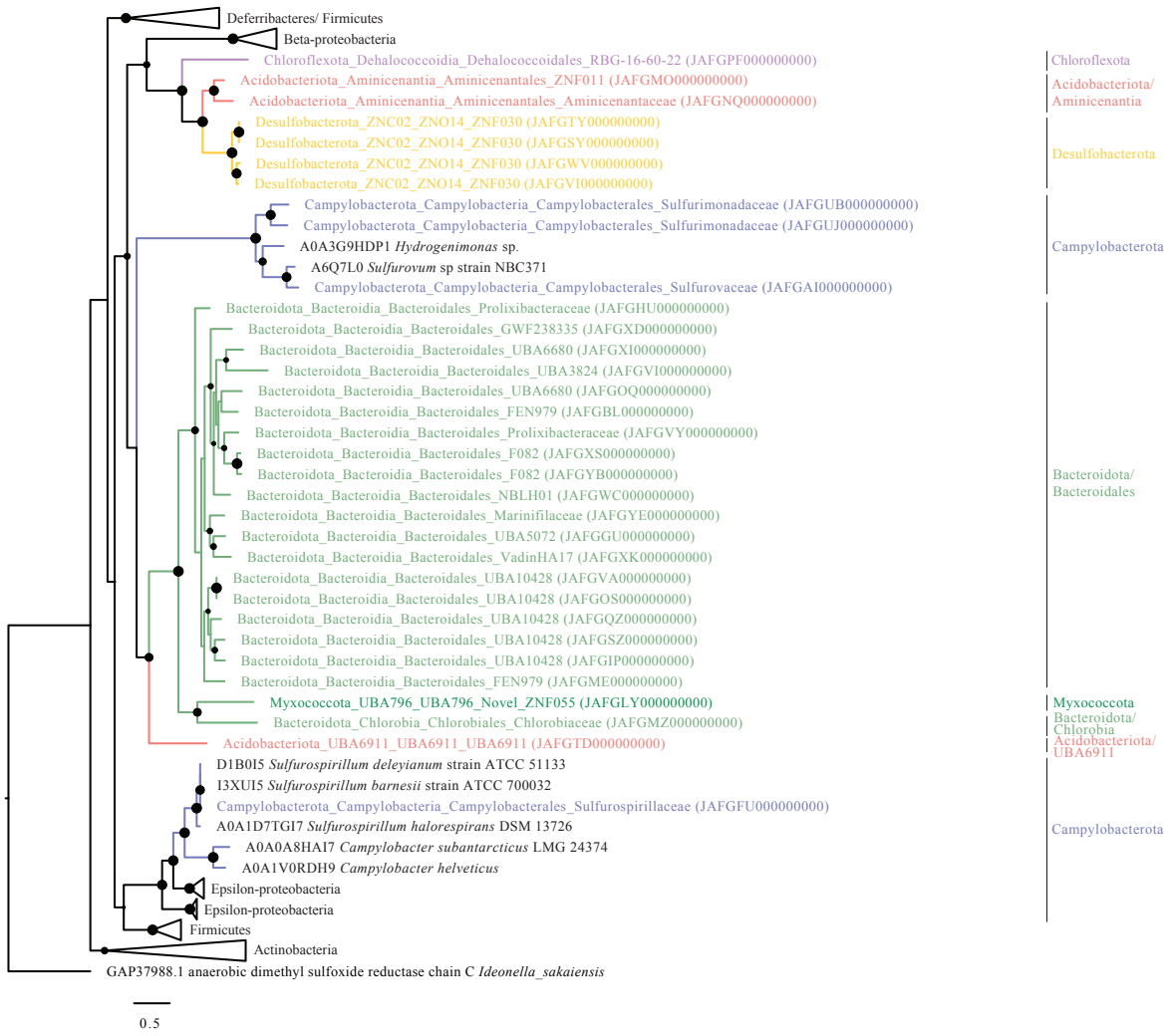


Figure 3.15: Phylogenetic affiliation and contig organization of PsrC

Phylogenetic affiliation and contig organization of selected sulfur reduction proteins. Phylogeny of the epolysulfide reductase subunit gamma PsrC. , and thiosulfate reductase cytochrome b subunit PhsC.

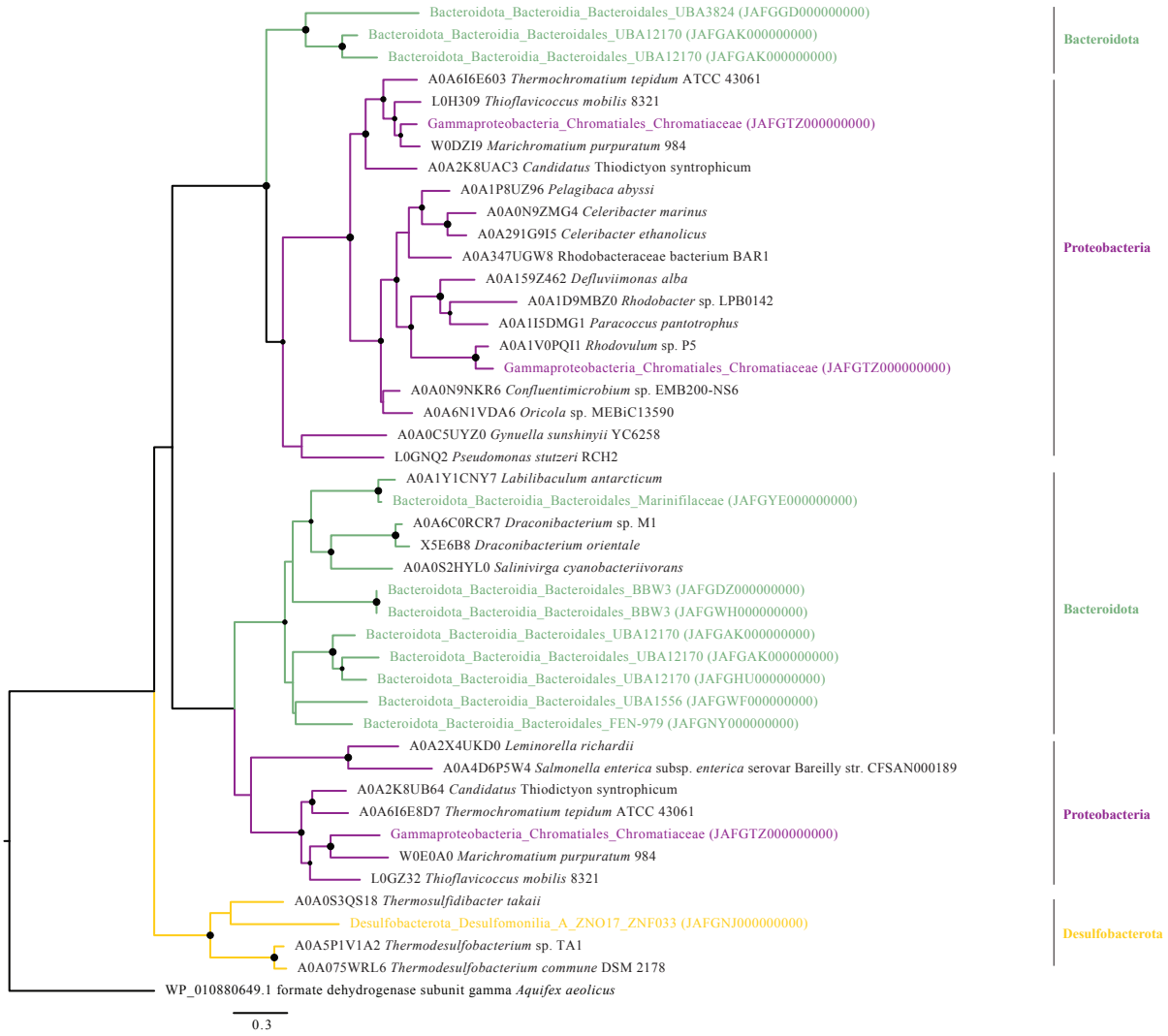


Figure 3.16: Phylogenetic affiliation and contig organization of PhsC

Phylogenetic affiliation and contig organization of selected sulfur reduction proteins. Phylogeny of the thiosulfate reductase cytochrome b subunit PhsC.

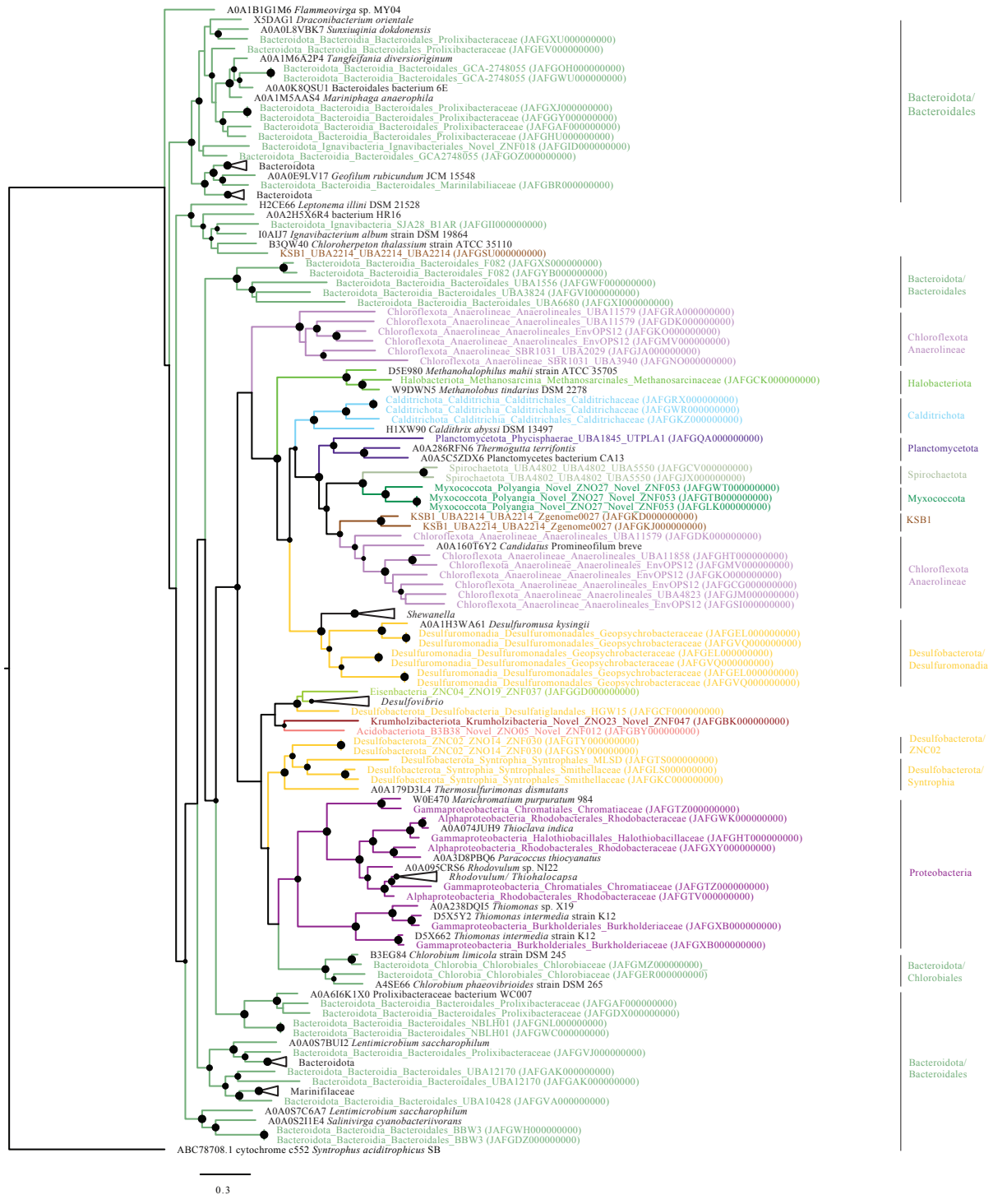


Figure 3.17: Phylogenetic affiliation and contig organization of Otr

Phylogenetic affiliation and contig organization of selected sulfur reduction proteins. Phylogeny of the octaheme tetrathionate reductase Otr.

CHAPTER IV

DISCUSSION

The microbial community in Zodletone spring sediments exhibited a high level of phylogenetic diversity, novelty, and rarity (Figure 3.1, 3.3, 3.4, 3.5). Conversely, representatives of lineages that predominate in most present earth environments, e.g. Proteobacteria, Firmicutes, and Cyanobacteria were absent or extremely sparse within the sediments. The community in the spring sediments was also characterized by a high proportion of SRM, and the prevalence of lineages mediating the reduction of sulfur cycle intermediates (sulfite, thiosulfate, tetrathionate, and elemental sulfur) over sulfate-reducers. Many of the organisms mediating reductive sulfur-cycling processes belonged to novel and LRD lineages (Figure 3.7), hence expanding the range of SRM within the tree of life (Figure 3.8, 3.9, 3.10, 3.11, 3.12).

What drives the assembly, propagation, and maintenance of such a diverse, novel, and distinct community in the spring sediments? The high level of diversity, novelty, and rarity within Zodletone spring sediment SRM community could be attributed to two main factors. First, the availability of a wide range of sulfur cycle intermediates in concentrations much higher than sulfate, in contrast to sulfate-predominance in current ecosystems [109]. Such pattern selects for a more diverse community of SRM in the spring, when compared to predominantly sulfate-driven marine and freshwater ecosystems (Figure 3.7). Second, additional factors usually constraining SRM growth in several habitats such as diel or seasonal intrusion of oxygen, Fe and NO_3 [1, 29, 48, 70], recalcitrance of available substrates [19, 28, 50], temperature [49, 91], pH [100, 96, 104], salinity [101], and pressure extremes [6, 19], or combinations thereof, are absent in the spring. Therefore, while the reductive global sulfur cycle appears to be dominated by a few sulfate-reducing lineages within the Desulfobacterota, and to a lesser extent the Firmicutes, as well as Thermodesulfobacteria and *Archaeoglobus* in high temperature habitat, the SRM community in Zodletone is extremely diverse, encompassing a wide range of previously undescribed and LRD lineages (Figure 4, S4, S5, S6). Sulfate-reducing organisms are the most prevalent component of the reductive sulfur cycle in most marine and aquatic ecosystems. Aspects of the ecology [109], physiology [85], and biochemistry [7, 80, 110] of dissimilatory sulfate reduction have been extensively investigated [86]. While not the most prevalent process, the sulfate-reducing community in Zodletone spring sediment exhibited a unique composition, with members of the Zixibacteria, Acidobacteriota, Myxococcota, Bacteroidota, Planctomycetota, and candidate phylum OLB16 constituting the major players, as well as rare and novel lineages within the Desulfobacterota (Desulfatiglandales, and Order C00003060), with scarce representation of canonical Desulfobacterota sulfate reducers (1 genome). While the identification of the dissimilatory sulfate reducing machinery in some of these lineages (e.g. Zixibacteria, Aci-

dobacteriota, and Planctomycetota) has been shown before [3, 25, 35], these members rarely appear to be the dominant players in a single ecosystem.

Compared to sulfate-reduction, the ecology and diversity of microbial dissimilatory sulfite reduction has not been extensively studied. The biochemistry of the process has been examined in sulfate-reducers, when grown on sulfite [86], as well as in a few other dedicated sulfite reducers such as *Desulfitobacterium* [107], *Salmonella* [40], *Shewanella* [93], and Wolinella [58]. A recent study suggested the importance and ancient nature of sulfite reduction in an extreme thermophilic environment in a limited diversity biofilm [17]. We document a plethora of microorganisms within the phyla Planctomycetes, Chloroflexota, Spirochaetota, and Desulfobacterota encoding the dissimilatory sulfite reductase DSR, as well as 72 additional families (31 novel and 25 LRD) encoding the anaerobic sulfite reductase. These organisms expand the known sulfite reduction capacity within the domain Bacteria (Figure 3.8, 3.9, 3.10, 3.11, 3.12). Further, the novelty or rarity of some of these families is a reflection of the dearth of present-time habitats that could support this mode of metabolism, once predominant on ancient earth.

The bulk of knowledge on thiosulfate reduction and or disproportionation comes from studies in pure cultures, e.g. members of the Desulfobulbaceae (e.g. *Desulfocapsa*) [23, 26] and the genera *Desulfovibrio* and *Desulfomonile* [34, 99, 72] within Desulfobacterota, the gammaproteobacterium *Pantoea agglomerans* [74], members of Thermodesulfobacteria [66] and Firmicutes [43] . Radioisotope tracing of different sulfur atoms showed a significant contribution of thiosulfate disproportionation to the sulfur cycle in marine [46], as well as freshwater sediments [51]. However, the lack of a marker gene for the process hinders ecological culture-independent studies. Similar to sulfite, the high levels, and constant generation of thiosulfate in Zodletone sediments sustains a highly diverse thiosulfate reducing (thiosulfate reductase plus a sulfite reduction complex), or disproportionating (thiosulfate reductase plus both sulfite reduction and sulfite oxidation systems) community with major contribution from novel or rare families in the Acidobacteriota, Chloroflexota, Desulfobacterota, KSB1, Myxococcota, and Spirochaetota. Finally, the extremely high levels of zero valent sulfur, available as soluble polysulfide, result in enriching the community with a plethora of polysulfide-reducing organisms.

As described above, this study infers that the microbial communities thriving in ancient conditions of anoxia and high proportion of sulfur cycle intermediates were extremely diverse. In comparison, communities in the oxygen-exposed water column were markedly less diverse. What drives this drastic shift in diversity and community structure? We argue that oxygen introduction into the system is responsible for such shift, as evident by the shift to oxidative sulfur processes in the water samples. The prevailing conditions in the water column are hence more akin to microbial communities that would thrive in sulfur-rich yet air-exposed habitat on the current earth.

The comparison presented here between both communities could putatively demonstrate how ancient metabolic pathways and lineages mediating them have been curtailed due to oxygen evolution and predominance in the current surficial earth. The evolution of oxygenic photosynthesis has led to the steady and inexorable accumulation of O_2 in Earth's atmosphere (the great oxidation event, GOE), with the rise of atmospheric O_2 to 1-5% of current levels between 2.4 and 2.1 billion years (Gyr) ago, and its accumulation to values comparable to modern values 500-600 Mya [63]. Due to the expected sensitivity and lack of adaptive

mechanisms to cope with atmospheric oxygen in multiple strict anaerobes, as well as the chemical instability of multiple S species in an oxygenated atmosphere, the GOE exerted a profound negative impact on anaerobic surficial life forms (the oxygen catastrophe) leading to the first and arguably most profound extinction event in earth's history [63]. In addition to suppressing anaerobiosis in atmospherically-exposed habitats, the GOE also led to a significant change in the S cycle, from one based on atmospheric inputs to one dependent on oxidative weathering leading to the release of huge amount of sulfate derived from the oxidation of pyrite and the dissolution of sulfate minerals [59], hitherto a minor byproduct of Archean abiotic and biotic reactions [32, 38]. Therefore, it appears that loss of niches associated with geological transformations could be one of the possible explanations for high extinction rates for microorganisms on earth, as well as the constant identification of rare, novel taxa within anaerobic settings. It is notable that phylogenetically novel branches with extremely rare distribution in earth (defined as phyla with 5 genomes or less in GTDB) have been consistently identified in anaerobic habitats.

In summary, by examining microbial diversity in Zodletone spring, we greatly expand the overall diversity within the tree of life via the discovery and characterization of a wide range of novel lineages, and significantly enrich representation of a wide range of LRD lineages. We also describe a unique sulfur-cycling community in the spring that is largely dependent on sulfite, thiosulfate, sulfur, and tetrathionate, rather than sulfate, as an electron acceptor. Given the remarkable similarity to conditions prevailing prior to the GOE, we consider the spring an invaluable portal to investigate the community thriving on the earth's surface during these eons, and posit that GOE precipitated the near extinction of a wide range of phylogenetically distinct oxygen-sensitive lineages and drastically altered the reductive sulfur-cycling community from sulfite, sulfur, and thiosulfate reducers to predominantly sulfate reduction in the current earth.

The full paper can be found here: https://doi.org/10.1128/mbio.00016-22

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