SUPPLEMENTARY INFORMATION

Phylogenetic and environmental diversity of DsrAB-type dissimilatory (bi)sulfite reductases

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SUPPLEMENTARY MATERIALS AND METHODS

Recovery of *dsrAB* sequences from public databases using tblastx analysis

A bit score threshold for retrieving *dsrAB* sequences from public databases was defined by blasting entries of a *dsrAB* in-house 'seed' database (n=998) against each other with archaeal type *dsrAB* sequences serving as the outgroup for bacterial type *dsrAB* sequences and vice versa. The highest bit score of the outgroup entries + 10% (to make the search more conservative) was then used as a bit score threshold for each *dsrAB* seed entry. Subsequently, each *dsrAB* seed entry with its own threshold was blasted against NCBI's non-redundant and environmental databases (Benson *et al.*, 2014), the IMG/M database (Markowitz *et al.*, 2012) and the Camera database (Sun *et al.*, 2011). Metagenomic databases were filtered to exclude short single reads (<400 bp) in order to enhance search speed. Since we aimed at recovering continuous nucleic acid sequences of *dsrAB* with the intergenic region in addition to partial *dsrA* and *dsrB* sequences, we did not use the FunGene database (Fish *et al.*, 2013) that only collects individual *dsrA* and *dsrB* sequences from GenBank based on a Hidden Markov Model.

Ecological classification of *dsrAB* sequences

To analyze general habitat patterns, *dsrAB* sequences were assigned to broad environmental categories based on the qualitative description submitted with the sequence and/or the information in the publication. Categories based on the environmental origin of the sample (marine, estuarine, freshwater, soil, and industrial) were complemented by categories denoting special microbial lifestyles (thermophilic, alkali-/halophilic, and symbiotic). Sequences were not assigned to multiple categories, in case of sequences fitting in two or more categories, lifestyle categories were given precedence (i.e. a sequence from a marine thermophile would be classified as thermophilic and not as marine).

Tree calculations

Maximum likelihood (RAxML (Stamatakis, 2006), Dayhoff amino acid substitution model) and maximum parsimony (PHYLIP PROTPARS) trees were calculated in ARB. Neighbor joining trees (PHYLIP NEIGHBOR) were calculated in the PHYLIP software package (Felsenstein, 1989) based on the JTT matrix model (Jones *et al.*, 1992). The three trees were combined into a consensus tree by using the extended majority rule in PHYLIP CONSENSE. Branch lengths of the consensus tree were inferred by using the JTT matrix model (PHYLIP PROML). Bootstrap analysis was performed with all three methods with 100 or 1,000 re-samplings, depending on the size of the tree. In order to save computation time, sequences were clustered at 97% amino acid identity using the average neighbor algorithm in mother (Schloss *et al.*, 2009) and only a representative sequence of each cluster was used for calculation of the larger trees. The other sequences were subsequently added to the consensus tree using the ARB Parsimony interactive tool using the same alignment filter as for tree calculation. Trees were visualized using iTOL (Letunic & Bork, 2007).

For comparison of tree topologies, DsrAB and 16S rRNA trees were based on corresponding data sets, that is, the same number of organisms, to avoid sampling artifacts. Consensus trees were constructed using the strict consensus rule setting to allow for more polytomies and thus conservative, but more robust phylogenies (Ludwig *et al.*, 2004). DsrAB trees were calculated as mentioned previously. 16S rRNA trees were calculated using maximum likelihood (RAxML), maximum parsimony (PYHLIP DNAPARS), and neighbor joining (PHYLIP NEIGHBOR) methods and branch lengths in the 16S rRNA consensus tree were adjusted using PHYLIP DNAML.

Uncultured family-level DsrAB lineages

By adapting previously established criteria (Pester *et al.*, 2012), environmental DsrAB sequences were assigned into uncultured family-level lineages. First, sequences sharing ≥64% amino acid identity were clustered into groups using the furthest neighbor algorithm in mothur (Schloss *et al.*, 2009). This very conservative threshold was based on minimum intra-family amino acid sequence identities of known families of sulfate-reducing microorganisms (SRM), which range from 64% to 89%. Second, a ≥64% DsrAB sequence identity cluster was only designated as an "uncultured DsrAB lineage" if it consisted of at least three sequences and formed a monophyletic group in the extended majority rule-based consensus tree with a bootstrap support of >70% in at least two treeing methods. CodeML (PAML 4.8) (Yang, 2007) was used to determine non-synonymous/synonymous substitution rate ratios for the uncultured DsrAB lineages.

Comparisons between *dsrAB* and 16S rRNA gene identities

Gene identity plots of *dsrAB* and 16S rRNA genes of organisms for which both genes are known were performed in R (R Development Core Team, 2008) using nucleic acid distance matrices calculated in ARB without an alignment filter. A nucleotide identity species-level threshold for bacterial type *dsrAB* was inferred from a *dsrAB*/16S rRNA gene identity plot of organisms with non-laterally acquired bacterial type *dsrAB*. A 99% nucleotide similarity was used as a threshold for approximate species level assignment on 16S rRNA level (Stackebrandt & Ebers, 2006).

SUPPLEMENTARY RESULTS AND DISCUSSION

The four families and root of the DsrAB tree

Since *dsrA* and *dsrB* originated from an ancient gene duplication event that likely preceded the divergence of the bacterial and archaeal domains of life (Dahl *et al.*, 1993; Wagner *et al.*, 1998), it is possible to determine the root of the DsrAB tree by paralogous rooting (Iwabe *et al.*, 1989). An alignment of DsrA to DsrB based on 163 conserved homologous amino acid positions supports a nearly bilaterally symmetrical tree in which DsrA and DsrB sequences form mirrored branches converging at the root (Supplementary Figure S4). The family of oxidative DsrAB sequences from sulfide-oxidizing bacteria (SOB) branches off after the split between bacterial type and archaeal type sequences and thus likely represents a secondary, functional diversification. Hence, the branching pattern suggests that ancestral DsrAB functioned in the reductive direction, a finding that is corroborated by geochemical data that suggests that sulfite reduction occurred very early in Earth's history and possibly predated the evolution of sulfate reduction (Skyring & Donnelly, 1982). It is not possible to conclusively determine the root of the DsrAB tree with respect to the fourth type of DsrAB family, constituted by the exceptional second DsrAB copy of *Moorella thermoacetica,* because its position differs in the DsrA and DsrB branches of the tree (Supplementary Figure S4). The basal placement of the *M. thermoacetica* DsrAB copy 2 subunits in the DsrA/DsrB paralog tree might be a treeing artifact caused by long-branch attraction (Bergsten, 2005) between the two subunits. We thus performed long-branch extraction (Siddall & Whiting, 1999) by repeating the tree calculation and by either omitting the DsrA or the DsrB subunit of *M. thermoacetica* DsrAB copy 2 in any one calculation. Erroneous phylogenetic placement of *M. thermoacetica* DsrAB copy 2 is unlikely because the phylogenetic position of the respective subunit in both test trees was identical to the position in the tree calculated with both subunits (data not shown). We thus conclude that the root of the DsrAB tree is either between *M. thermoacetica* DsrAB copy 2 and all other DsrAB sequences or between

the *M. thermoacetica* DsrAB copy 2/reductive archaeal type DsrAB branch and the oxidative/reductive bacterial type DsrAB branch.

DsrAB consensus phylogeny and members of main lineages

***Reductive bacterial type DsrAB*.** The *Deltaproteobacteria* supercluster contains the majority of known bacterial type DsrAB sequences, including *dsrAB* from all deltaproteobacterial SRM, *Deltaproteobacteria*-related *dsrAB* from (mostly) thermophilic sulfate and/or sulfite-reducing members of the phyla *Firmicutes* (i.e., members of *Desulfotomaculum* subclusters Ib, Ic, Id, and Ie, *Ammonifex degensii*, *Candidatus* Desulforudis audaxviator, *Desulfovirgula thermocuniculi*, *Sporotomaculum hydroxybenzoicum*, and *Moorella thermoacetica dsrAB* copy 1) and *Thermodesulfobacteria* (*Thermodesulfobacterium* and *Thermodesulfatator*), uncultured DsrAB lineages 1 and 11 and other environmental sequences (Figure 1, Supplementary Figure S1). We have renamed the *Thermodesulfovibrio* supercluster into *Nitrospirae* supercluster because it now comprises *dsrAB* from two taxa within the phylum *Nitrospirae*, namely the genus *Thermodesulfovibrio* and *Candidatus* Magnetobacterium casensis (Lin *et al.*, 2014). The *Nitrospirae* supercluster additionally contains uncultured DsrAB lineage 10 and 13, and other environmental sequences. The environmental supercluster 1 does so far not contain *dsrAB* from any cultured organism and includes uncultured DsrAB lineages 8, 9, and 12, and other environmental *dsrAB* sequences. Most sequences from cultured organisms in the *Firmicutes* group belong to the phylum *Firmicutes* (i.e., the SRM genera *Desulfotomaculum*, *Desulfosporosinus,* and *Desulfurispora*, the non-SRM genera *Desulfitobacterium*, *Carboxydothermus*, *Desulfitibacter*, and *Thermanaeromonas* that are able to reduce other sulfur compounds, the syntroph *Pelotomaculum propionicum*, and members of the family *Sporomusaceae* (Yutin & Galperin, 2013), the acetogen *Acetonema longum* and the thiosulfate-utilizing *Thermosinus carboxydivorans*) yet these do not form a monophyletic DsrAB cluster. Instead, they are phylogenetically intermingled with members of the taxonomically uncertain genus *Thermodesulfobium* (Mori *et al.*, 2003), *dsrAB*-carrying members of the phyla *Actinobacteria*, *Aigarchaeota* and *Caldiserica*, uncultured DsrAB lineages 2 to 7, and other environmental *dsrAB* sequences (Figure 1, Supplementary Figure S1). Continuous genomic analysis of cultured microorganisms or single microbial cells has led to the discovery of *dsrAB* in members of phyla previously not known to possess these genes. Hence, DsrAB-coding genes were detected on amplified genomes of individual cells belonging to the bacterial phylum *Caldiserica* (JGI_0000059-M03, accession AQSQ01000030) and the archaeal candidate phylum *Aigarchaeota* (pSL4 archaeon JGI_0000106-J15, accession ASPF01000004) (Rinke *et al.*, 2013) (Figure 1). The phylum *Caldiserica* (formerly known as candidate phylum OP5) so far contains only one characterized species, *Caldisericum exile*, which uses thiosulfate, sulfite, and elemental

sulfur, but not sulfate, as electron acceptors, yet its genome (NC_017096) does not contain *dsrAB* (Mori *et al.*, 2009). The genome of the intestinal actinobacterium *Gordonibacter pamelaeae* (NC_021021) (Würdemann *et al.*, 2009) also contains *dsrAB* that consistently cluster with the *Firmicutes* sister genera *Desulfosporosinus* and *Desulfitobacterium*. Importantly, *G. pamelaeae* lacks further genes of the canonical dissimilatory sulfate reduction pathway in its genome and is thus likely not an SRM.

***Oxidative bacterial type DsrAB*.** The majority of oxidative DsrAB sequences belong to the *Gammaproteobacteria* cluster that contains cultivated members of families *Chromatiaceae* (nine genera), *Ectothiorhodospiraceae* (genera *Alkalilimnicola*, *Halorhodospira*, and *Thioalkalivibrio)* and *Thiotrichaceae* (genus *Thiothrix*) (Figure 1, Supplementary Figure S2). Interestingly, DsrAB of *Thioalkalivibrio nitratireducens* does not fall into this *Gammaproteobacteria* cluster, in contrast to sequences of the other members of the genus, *T. sulfidiphilus*, *T. thiocyanodenitrificans*, and *T. paradoxus* [the genome sequence of *T. paradoxus,* NZ_AGFB01000003 was wrongly published as *T. thioycyanoxidans* (D.Y. Sorokin, personal communication) and has since been removed]. The second largest oxidative DsrAB cluster, the *Alphaproteobacteria* cluster, is subdivided into two main branches, one harbors members of the genera *Magnetospirillum* and *Azospirillum* (family *Rhodospirillaceae,* order *Rhodospirillales*), and the other contains *Rhodomicrobium vannielii* (family *Hyphomicrobiaceae,* order *Rhizobiales*) and environmental sequences. The *Betaproteobacteria* cluster contains *dsrAB* from members of the genus *Thiobacillus,* from *Sulfuricella denitrificans* (both family *Hydrogenophilaceae,* order *Hydrogenophilales*), and from *Sideroxydans lithotrophicus* (family *Gallionellaceae*, order *Gallionellales*). The *Chlorobi* cluster contains *dsrAB* from members of the family *Chlorobiaceae*. *Magnetococcus marinus* (family *Magnetococcaceae*, order *Magnetococcales*) has been provisionally included in the *Alphaproteobacteria* (Bazylinski *et al.*, 2013), but its DsrAB is very dissimilar from other alphaproteobacterial DsrAB and instead clusters with DsrAB of *Chlorobi* and the deltaproteobacterial SAR324 clade.

***Reductive archaeal type DsrAB*.** This type of DsrAB is present in three genera of hyperthermophilic *Crenarchaeota* (*Pyrobaculum*, *Vulcanisaeta* and *Caldivirga*). Each of these three genera represents a distinct monophyletic group in the archaeal DsrAB tree with *Caldivirga maquilingensis*, an organism capable of reducing sulfate, thiosulfate and sulfur (Itoh *et al.*, 1999), occupying the deepest branch (Figure 1, Supplementary Figure S3). *C. maquilingensis* is the only organism in which the neighboring genes *dsrA* and *dsrB* are arranged in different directions. *Vulcanisaeta distributa* (Itoh *et al.*, 2002) and *V. moutnovskia* (Prokofeva *et al.*, 2005) utilize elemental sulfur and thiosulfate for growth. However, both species might also be capable

of sulfate reduction (Itoh *et al.*, 2002) since genes for the complete canonical sulfate reduction pathway are present in their genomes (Mavromatis *et al.*, 2010; Gumerov *et al.*, 2011). All *Pyrobaculum* species seem to be capable of using thiosulfate as an electron acceptor (Völkl *et al.*, 1993; Molitor *et al.*, 1998; Huber *et al.*, 2000; Sako *et al.*, 2001; Amo *et al.*, 2002) and some were also shown to use elemental sulfur (*P. arsenaticum* (Huber *et al.*, 2000), *P. islandicum* (Molitor *et al.*, 1998), *P. neutrophilum* (Fischer *et al.*, 1983), *P. oguniense* (Sako *et al.*, 2001)) as a terminal electron acceptor whereas other species are inhibited by elemental sulfur (*P. aerophilum* (Völkl *et al.*, 1993), *P. calidifontis* (Amo *et al.*, 2002)). *P. islandicum* was also shown to utilize other sulfur compounds like sulfite, L-cysteine and oxidized glutathione (Molitor *et al.*, 1998). Interestingly, some but not all *Pyrobaculum* genomes harbor multiple *dsrAB* copies with a phylogeny that indicates a complex evolutionary history of *dsrAB* in members of this genus involving gene duplications, gene losses, and/or intra-genus LGT. Some *Pyrobaculum* species thus possess two (*P. aerophilum*, *P. calidifontis*) or three (*P. arsenaticum*, *P. oguniense*) *dsrAB* copies, all of which have intact reading frames and conserved siroheme binding sites. These multiple copies do not cluster together according to species affiliation (Supplementary Figure S3). No reports exist on function of specific copies of *dsrAB* in *Pyrobaculum* genomes and there is no obvious pattern regarding copy number and/or type and metabolic potential of *Pyrobaculum* species. Gene duplications can be a source of new protein functions because one (or both) of the now functionally redundant paralogs experience a period of relaxed selection and accelerated evolution (Ohno, 1970) in enzymes leading, for example, to different substrate affinities or specificities (Baani & Liesack, 2008). Presence of multiple *dsrAB* in some *Pyrobaculum* species is very unusual as *dsrAB* are mostly present as single-copy genes. The only other organisms known to possess more than one copy of *dsrAB* is *Moorella thermoacetica* with its two significantly different copies of *dsrAB*, and the SOB *Chlorobaculum tepidum*, which possesses two nearly identical *dsrAB* copies, but one has an authentic frameshift in *dsrB* and is likely not functional (Eisen *et al.*, 2002).

Moorella thermoacetica *DsrAB copy 2*. The unusual second *dsrAB* copy of *M. thermoacetica* is the only representative of this type of DsrAB. The two strains of *M. thermoacetica* for which genome sequences are available, strain ATCC 39073 (Pierce *et al.*, 2008) and strain Y72 (Tsukahara *et al.*, 2014), are the only bacteria known to possess two significantly different copies of *dsrAB*. The first copy (NC_007644, 1634923..1637803; BARR01000003, 15717..18335) is a bacterial DsrAB related to *Firmicutes* sequences within the *Deltaproteobacteria* supercluster, whereas the second copy (NC_007644, 1664993..1667213; BARR01000005, 9074..11294) is not closely related to other DsrAB sequences (Pierce *et al.*, 2008). *M. thermoacetica* can reduce

thiosulfate and dimethylsulfoxide (Drake & Daniel, 2004) but nothing specific is known about the individual functions of its DsrAB copies.

Putative lateral gene transfers of *dsrAB*

Consensus trees of corresponding DsrAB and 16S rRNA sequences were compared for topological incongruences as signs of LGT (Figures 2 and 3). Additionally, we plotted identity values of 16S rRNA and *dsrAB* genes of pairs of pure cultures and genomes against each other (Supplementary Figure S6). 16S rRNA gene and *dsrAB* identities are highly correlated, which indicates that these genes generally evolve in parallel at constant mutation rates. Considerable deviations from linear regression in such a plot thus indicate changes in the standard evolutionary mechanism. In comparisons of the major DsrAB families (Supplementary Figure S6), deviations towards the top left of the plot (*dsrAB* identity > 16S rRNA identity) is indicative of laterally acquired *dsrAB* (LA-*dsrAB*), while deviation towards the bottom right of the plot (*dsrAB* identity < 16S rRNA identity) might have multiple causes such as LGT, diversification of *dsrAB* through accelerated mutation or a combination of these processes with gene duplication/loss events.

DsrAB and 16S rRNA branching patterns are generally similar but show previously recognized and newly identified topological inconsistencies. Acquisition of *dsrAB* of a group of *Firmicutes* from deltaproteobacterial ancestors of the *Desulfatiglans anilini* (formerly *Desulfobacterium anilini* (Suzuki et al., 2014)) lineage (Figure 2) (Klein *et al.*, 2001; Zverlov *et al.*, 2005) is confirmed by the *dsrAB*-16S rRNA gene identity plot. When compared with all organisms carrying "standard" vertically inherited bacterial *dsrAB*, non-LA-*dsrAB Firmicutes* cluster along the linear regression, while LA-*dsrAB* Firmicutes show slightly higher *dsrAB* gene identity (Supplementary Figure S6 B). Additionally, *dsrAB* of the latter organisms possess characteristic insertions that are typical for deltaproteobacterial *dsrAB* and provide further independent evidence of a deltaproteobacterial origin (Klein et al., 2001). It has been proposed that members of the phylum *Thermodesulfobacteria* (genera *Thermodesulfobacterium* and *Thermodesulfatator*) also have LA-*dsrAB* (Klein et al., 2001). *Thermodesulfobacteria* form a monophyletic branch within the *Deltaproteobacteria* cluster in the DsrAB tree (Figure 2) and possess the characteristic deltaproteobacterial *dsrAB* insertions, but, in contrast to *Firmicutes* with LA-*dsrAB*, show no deviations in the *dsrAB*-16S rRNA gene identity plot when compared to non-LA bacterial *dsrAB* (Supplementary Figure S6 C). Notably, it has recently been suggested that the phylogenetic inconsistency between 16S rRNA and DsrAB is due to incorrect placement of the phylum *Thermodesulfobacteria* in the 16S rRNA tree (Lang *et al.*, 2013). Phylogenetic analysis of a set of 24 concatenated phylogenetic marker genes identified the *Thermodesulfobacteria* as a

sister-group of the deltaproteobacterial order *Desulfovibrionales* (Lang et al., 2013). However, *Thermodesulfobacteria* were clearly unrelated to *Deltaproteobacteria* in another whole genome tree based on 38 concatenated marker genes (Rinke *et al.*, 2013). Because of these conflicting findings, it currently remains unresolved if *Thermodesulfobacteria* received *dsrAB* via LGT.

All evidence points to a bacterial origin of *dsrAB* in members of the archaeal genus *Archaeoglobus*. *Archaeoglobus* DsrAB branches unambiguously in the reductive bacterial type DsrAB family (Klein et al., 2001) (Figure 2). Furthermore, *Archaeoglobus* species (*Euryarcheota*) are more similar to bacteria on *dsrAB* level than to *Crenarchaeota* and thus deviate considerably from the linear regression of *dsrAB*-16S rRNA sequence identities, whereas *Crenarchaeota* do not (Supplementary Figure S6 C). This is consistent with paralogous rooting analysis and confirms an archaeal origin of *dsrAB* in *Crenarchaeota* members.

Analogous to *Archaeoglobus*, DsrAB in the *Aigarchaeota* member clearly belongs to the reductive bacterial type DsrAB family (Figures 1 and 2). Substantial differences in GC content between host genomes and acquired genes can be used to infer LGT events (Lawrence & Ochman, 1997) and a difference of more than 10% was previously used as an additional indication of LA-*dsrAB* (Klein et al., 2001). The GC content of the *dsrAB* sequence (44%) of the aigarchaeon is more than 10% different from the whole genome (38%), whereas the most closely related *dsrAB* sequences have GC contents between 51 and 55%, suggesting that *dsrAB* was relatively recently acquired from a donor with a higher genomic GC content and is currently undergoing evolutionary adaptation into the new genome (Lawrence & Ochman, 1997). The *Aigarchaeota* member also shows a deviation pattern in the *dsrAB*-16S rRNA gene identity plot that is similar to *Archaeoglobus*, with its *dsrAB* being much more similar to bacterial sequences than its 16S rRNA sequence (Supplementary Figure S6 C).

DsrAB of the actinobacterium *G. pamelaeae* forms a stable monophyletic group with DsrAB of the *Firmicutes* genera *Desulfosporosinus* and *Desulfitobacterium* (Figures 1 and 2), which suggests that *G. pamelaeae dsrAB* were laterally acquired from a *Firmicutes* member. However, there is no evidence that this potential LGT event occurred recently, since the GC content of *dsrAB* (65.3%, the highest value of any known organisms with a bacterial type DsrAB) is similar to the GC content of the whole genome (64%) of *G. pamelaeae*, but considerably higher than the GC content of *dsrAB* and genome sequences of *Desulfosporosinus* and *Desulfitobacterium* species (41-49%). Furthermore, *dsrAB* of *G. pamelaeae* lack a characteristic insertion at position 1053 that is shared by all *Desulfosporosinus* and *Desulfitobacterium* species. The *dsrAB*-16S rRNA gene identity plot does not suggest LGT (Supplementary Figure S6 C). So far *G. pamelaeae* is the only

member of the phylum *Actinobacteria* with *dsrAB* and there are no closely related environmental *dsrAB* sequences with a similar, high GC content that might hint at the presence of further actinobacterial *dsrAB* sequences in the database.

The branching patterns of the only known *dsrAB*-carrying member of the phylum *Caldiserica* do not suggest LGT of its *dsrAB* as it branches deeply in both the DsrAB tree and the 16S rRNA tree (Figure 2). However, the GC content is >10% different between *dsrAB* (44.1%) and genome (35%) and more similar to phylogenetically related *dsrAB* sequences, hinting to lateral acquisition. Furthermore, in the *dsrAB*-16S rRNA gene identity plot it shows considerable deviation from other bacterial *dsrAB* sequences (Supplementary Figure S6 C).

Primers targeting *dsrA* and *dsrB*

The very first *dsrAB*-targeted primers were designed on the basis of nucleotide sequence homologies of only two sequences, namely *dsrAB* from *Archaeoglobus fulgidus* and *Desulfovibrio vulgaris* (Karkhoff-Schweizer *et al.*, 1995). Shortly after, first versions of the now widely used DSR1F and DSR4R primers were published (Wagner *et al.*, 1998). They target highly conserved sequence regions of *dsrAB* and amplify a ~1.9kb fragment that covers approximately 85% of *dsrA*, 70% of *dsrB* and the intergenic spacer region between the two genes (Supplementary Figure S7). These degenerated primers were repeatedly updated by introducing additional primer variants (Loy *et al.*, 2004; Zverlov *et al.*, 2005; Pester *et al.*, 2010) and were modified (Kondo *et al.*, 2004; Suzuki *et al.*, 2005; Schmalenberger *et al.*, 2007; Loy *et al.*, 2009; Lenk *et al.*, 2011; Lever *et al.*, 2013) to adjust their coverage or improve PCR efficiency (Supplementary Tables S1 and S3). Also, several primers were developed that bind within the region amplified by DSR1F/DSR4R primer variants and were applied to amplify shorter fragments of either *dsrA* or *dsrB* for denaturing gradient gel electrophoresis (Geets *et al.*, 2005; Steger *et al.*, 2011), terminal restriction fragment length polymorphism analysis (Santillano *et al.*, 2010), quantitative real-time PCR (Kondo *et al.*, 2004; Ben-Dov *et al.*, 2007; Chin *et al.*, 2008; Gittel *et al.*, 2009; Pereyra *et al.*, 2010) or (nested) PCR (Dhillon *et al.*, 2003; Giloteaux *et al.*, 2010; Akob *et al.*, 2012; Lever *et al.*, 2013). Analogous to primers targeting the reductive bacterial type *dsrAB*, primers were also developed for oxidative bacterial type *dsrAB* of SOB (Loy *et al.*, 2009; Mori *et al.*, 2010; Lenk *et al.*, 2011; Luo *et al.*, 2011; Lever *et al.*, 2013) (Supplementary Tables S2 and S4). Primers for amplification of reductive, archaeal type *dsrAB* sequences or the second *dsrAB* copy of *M. thermoacetica* are not yet available.

References

Akob DM, Lee SH, Sheth M, Küsel K, Watson DB, Palumbo AV *et al*. (2012). Gene Expression Correlates with Process Rates Quantified for Sulfate- and Fe(III)-Reducing Bacteria in U(VI)-Contaminated Sediments. *Front Microbiol* **3:** 280.

Amo T, Paje ML, Inagaki A, Ezaki S, Atomi H, Imanaka T. (2002). Pyrobaculum calidifontis sp. nov., a novel hyperthermophilic archaeon that grows in atmospheric air. *Archaea* **1:** 113-121.

Baani M, Liesack W. (2008). Two isozymes of particulate methane monooxygenase with different methane oxidation kinetics are found in Methylocystis sp. strain SC2. *Proc Natl Acad Sci U S A* **105:** 10203-10208.

Bazylinski DA, Williams TJ, Lefevre CT, Berg RJ, Zhang CLL, Bowser SS *et al*. (2013). Magnetococcus marinus gen. nov., sp nov., a marine, magnetotactic bacterium that represents a novel lineage (Magnetococcaceae fam. nov., Magnetococcales ord. nov.) at the base of the Alphaproteobacteria. *Int J Syst Evol Microbiol* **63:** 801-808.

Ben-Dov E, Brenner A, Kushmaro A. (2007). Quantification of sulfate-reducing bacteria in industrial wastewater, by real-time polymerase chain reaction (PCR) using dsrA and apsA genes. *Microb Ecol* **54:** 439-451.

Benson DA, Clark K, Karsch-Mizrachi I, Lipman DJ, Ostell J, Sayers EW. (2014). GenBank. *Nucleic Acids Res* **42:** D32-37.

Bergsten J. (2005). A review of long-branch attraction. *Cladistics* **21:** 163-193.

Chin KJ, Sharma ML, Russell LA, O'Neill KR, Lovley DR. (2008). Quantifying expression of a dissimilatory (bi) sulfite reductase gene in petroleum-contaminated marine Harbor Sediments. *Microb Ecol* **55:** 489-499.

Dahl C, Kredich NM, Deutzmann R, Trüper HG. (1993). Dissimilatory sulphite reductase from Archaeoglobus fulgidus: physico-chemical properties of the enzyme and cloning, sequencing and analysis of the reductase genes. *J Gen Microbiol* **139:** 1817-1828.

Dhillon A, Teske A, Dillon J, Stahl DA, Sogin ML. (2003). Molecular characterization of sulfate-reducing bacteria in the Guaymas Basin. *Appl Environ Microbiol* **69:** 2765-2772.

Drake HL, Daniel SL. (2004). Physiology of the thermophilic acetogen Moorella thermoacetica (vol 155, pg 422, 2004). *Res Microbiol* **155:** 868-883.

Eisen JA, Nelson KE, Paulsen IT, Heidelberg JF, Wu M, Dodson RJ *et al*. (2002). The complete genome sequence of Chlorobium tepidum TLS, a photosynthetic, anaerobic, green-sulfur bacterium. *Proc Natl Acad Sci U S A* **99:** 9509-9514.

Felsenstein J. (1989). PHYLIP-phylogeny inference package. *Cladistics* **5:** 163-166.

Fischer F, Zillig W, Stetter KO, Schreiber G. (1983). Chemolithoautotrophic metabolism of anaerobic extremely thermophilic archaebacteria. *Nature* **301:** 511-513.

Fish JA, Chai B, Wang Q, Sun Y, Brown CT, Tiedje JM *et al*. (2013). FunGene: the functional gene pipeline and repository. *Front Microbiol* **4:** 291.

Geets J, Borremans B, Vangronsveld J, Diels L, van der Lelie D. (2005). Molecular monitoring of SRB community structure and dynamics in batch experiments to examine the applicability of in situ precipitation of heavy metals for groundwater remediation. *J Soils Sediments* **5:** 149-163.

Giloteaux L, Goni-Urriza M, Duran R. (2010). Nested PCR and new primers for analysis of sulfate-reducing bacteria in low-cell-biomass environments. *Appl Environ Microbiol* **76:** 2856-2865.

Gittel A, Sørensen KB, Skovhus TL, Ingvorsen K, Schramm A. (2009). Prokaryotic Community Structure and Sulfate Reducer Activity in Water from High-Temperature Oil Reservoirs with and without Nitrate Treatment. *Appl Environ Microbiol* **75:** 7086-7096.

Gumerov VM, Mardanov AV, Beletsky AV, Prokofeva MI, Bonch-Osmolovskaya EA, Ravin NV *et al*. (2011). Complete genome sequence of "Vulcanisaeta moutnovskia" strain 768-28, a novel member of the hyperthermophilic crenarchaeal genus Vulcanisaeta. *J Bacteriol* **193:** 2355-2356.

Huber R, Sacher M, Vollmann A, Huber H, Rose D. (2000). Respiration of arsenate and selenate by hyperthermophilic archaea. *Syst Appl Microbiol* **23:** 305-314.

Itoh T, Suzuki K, Sanchez PC, Nakase T. (1999). Caldivirga maquilingensis gen. nov., sp. nov., a new genus of rod-shaped crenarchaeote isolated from a hot spring in the Philippines. *Int J Syst Bacteriol* **49 Pt 3:** 1157-1163.

Itoh T, Suzuki K, Nakase T. (2002). Vulcanisaeta distributa gen. nov., sp. nov., and Vulcanisaeta souniana sp. nov., novel hyperthermophilic, rod-shaped crenarchaeotes isolated from hot springs in Japan. *Int J Syst Evol Microbiol* **52:** 1097-1104.

Iwabe N, Kuma K, Hasegawa M, Osawa S, Miyata T. (1989). Evolutionary relationship of archaebacteria, eubacteria, and eukaryotes inferred from phylogenetic trees of duplicated genes. *Proc Natl Acad Sci U S A* **86:** 9355-9359.

Jones DT, Taylor WR, Thornton JM. (1992). The rapid generation of mutation data matrices from protein sequences. *Comput Appl Biosci* **8:** 275-282.

Karkhoff-Schweizer RR, Huber DP, Voordouw G. (1995). Conservation of the genes for dissimilatory sulfite reductase from Desulfovibrio vulgaris and Archaeoglobus fulgidus allows their detection by PCR. *Appl Environ Microbiol* **61:** 290-296.

Klein M, Friedrich M, Roger AJ, Hugenholtz P, Fishbain S, Abicht H *et al*. (2001). Multiple lateral transfers of dissimilatory sulfite reductase genes between major lineages of sulfate-reducing prokaryotes. *J Bacteriol* **183:** 6028-6035.

Kondo R, Nedwell DB, Purdy KJ, Silva SD. (2004). Detection and enumeration of sulphate-reducing bacteria in estuarine sediments by competitive PCR. *Geomicrobiol J* **21:** 145-157.

Lang JM, Darling AE, Eisen JA. (2013). Phylogeny of bacterial and archaeal genomes using conserved genes: supertrees and supermatrices. *PloS one* **8:** e62510.

Lawrence JG, Ochman H. (1997). Amelioration of bacterial genomes: rates of change and exchange. *J Mol Evol* **44:** 383-397.

Lenk S, Arnds J, Zerjatke K, Musat N, Amann R, Mussmann M. (2011). Novel groups of Gammaproteobacteria catalyse sulfur oxidation and carbon fixation in a coastal, intertidal sediment. *Environ Microbiol* **13:** 758-774.

Letunic I, Bork P. (2007). Interactive Tree Of Life (iTOL): an online tool for phylogenetic tree display and annotation. *Bioinformatics* **23:** 127-128.

Lever MA, Rouxel O, Alt JC, Shimizu N, Ono S, Coggon RM *et al*. (2013). Evidence for microbial carbon and sulfur cycling in deeply buried ridge flank basalt. *Science* **339:** 1305-1308.

Lin W, Deng A, Wang Z, Li Y, Wen T, Wu LF *et al*. (2014). Genomic insights into the uncultured genus 'Candidatus Magnetobacterium' in the phylum Nitrospirae. *ISME J*.

Loy A, Küsel K, Lehner A, Drake HL, Wagner M. (2004). Microarray and functional gene analyses of sulfate-reducing prokaryotes in low-sulfate, acidic fens reveal cooccurrence of recognized genera and novel lineages. *Appl Environ Microbiol* **70:** 6998-7009.

Loy A, Duller S, Baranyi C, Mussmann M, Ott J, Sharon I *et al*. (2009). Reverse dissimilatory sulfite reductase as phylogenetic marker for a subgroup of sulfur-oxidizing prokaryotes. *Environ Microbiol* **11:** 289-299.

Ludwig W, Strunk O, Westram R, Richter L, Meier H, Yadhukumar *et al*. (2004). ARB: a software environment for sequence data. *Nucleic Acids Res* **32:** 1363-1371.

Luo JF, Lin WT, Guo Y. (2011). Functional genes based analysis of sulfur-oxidizing bacteria community in sulfide removing bioreactor. *Appl Microbiol Biotechnol* **90:** 769-778.

Markowitz VM, Chen IM, Chu K, Szeto E, Palaniappan K, Grechkin Y *et al*. (2012). IMG/M: the integrated metagenome data management and comparative analysis system. *Nucleic Acids Res* **40:** D123-129.

Mavromatis K, Sikorski J, Pabst E, Teshima H, Lapidus A, Lucas S *et al*. (2010). Complete genome sequence of Vulcanisaeta distributa type strain (IC-017). *Stand Genomic Sci* **3:** 117-125.

Molitor M, Dahl C, Molitor I, Schäfer U, Speich N, Huber R *et al*. (1998). A dissimilatory sirohaem-sulfite-reductase-type protein from the hyperthermophilic archaeon Pyrobaculum islandicum. *Microbiology* **144 (Pt 2):** 529-541.

Mori K, Kim H, Kakegawa T, Hanada S. (2003). A novel lineage of sulfate-reducing microorganisms: Thermodesulfobiaceae fam. nov., Thermodesulfobium narugense, gen. nov., sp. nov., a new thermophilic isolate from a hot spring. *Extremophiles* **7:** 283-290.

Mori K, Yamaguchi K, Sakiyama Y, Urabe T, Suzuki K. (2009). Caldisericum exile gen. nov., sp. nov., an anaerobic, thermophilic, filamentous bacterium of a novel bacterial phylum, Caldiserica phyl. nov., originally called the candidate phylum OP5, and description of Caldisericaceae fam. nov., Caldisericales ord. nov. and Caldisericia classis nov. *Int J Syst Evol Microbiol* **59:** 2894-2898.

Mori Y, Purdy KJ, Oakley BB, Kondo R. (2010). Comprehensive Detection of Phototrophic Sulfur Bacteria Using PCR Primers That Target Reverse Dissimilatory Sulfite Reductase Gene. *Microbes Environ* **25:** 190-196.

Ohno S. (1970). *Evolution by gene duplication*. London: George Alien & Unwin Ltd. Berlin, Heidelberg and New York: Springer-Verlag.

Pereyra LP, Hiibel SR, Riquelme MVP, Reardon KF, Pruden A. (2010). Detection and Quantification of Functional Genes of Cellulose-Degrading, Fermentative, and Sulfate-Reducing Bacteria and Methanogenic Archaea. *Appl Environ Microbiol* **76:** 2192-2202.

Pester M, Bittner N, Deevong P, Wagner M, Loy A. (2010). A 'rare biosphere' microorganism contributes to sulfate reduction in a peatland. *ISME J* **4:** 1591-1602.

Pester M, Knorr KH, Friedrich MW, Wagner M, Loy A. (2012). Sulfate-reducing microorganisms in wetlands - fameless actors in carbon cycling and climate change. *Front Microbiol* **3:** 72.

Pierce E, Xie G, Barabote RD, Saunders E, Han CS, Detter JC *et al*. (2008). The complete genome sequence of Moorella thermoacetica (f. Clostridium thermoaceticum). *Environ Microbiol* **10:** 2550-2573.

Prokofeva MI, Kublanov IV, Nercessian O, Tourova TP, Kolganova TV, Lebedinsky AV *et al*. (2005). Cultivated anaerobic acidophilic/acidotolerant thermophiles from terrestrial and deep-sea hydrothermal habitats. *Extremophiles* **9:** 437-448.

R Development Core Team. (2008). R: A language and environment for statistical computing.: R Foundation for Statistical Computing, Vienna, Austria. ISBN 3-900051-07-0, URL http://www.R-project.org.

Rinke C, Schwientek P, Sczyrba A, Ivanova NN, Anderson IJ, Cheng JF *et al*. (2013). Insights into the phylogeny and coding potential of microbial dark matter. *Nature* **499:** 431-437.

Sako Y, Nunoura T, Uchida A. (2001). Pyrobaculum oguniense sp. nov., a novel facultatively aerobic and hyperthermophilic archaeon growing at up to 97 degrees C. *Int J Syst Evol Microbiol* **51:** 303-309.

Santillano D, Boetius A, Ramette A. (2010). Improved dsrA-Based Terminal Restriction Fragment Length Polymorphism Analysis of Sulfate-Reducing Bacteria. *Appl Environ Microbiol* **76:** 5308-5311.

Schloss PD, Westcott SL, Ryabin T, Hall JR, Hartmann M, Hollister EB *et al*. (2009). Introducing mothur: open-source, platform-independent, community-supported software for describing and comparing microbial communities. *Appl Environ Microbiol* **75:** 7537-7541.

Schmalenberger A, Drake HL, Kusel K. (2007). High unique diversity of sulfate-reducing prokaryotes characterized in a depth gradient in an acidic fen. *Environ Microbiol* **9:** 1317-1328.

Siddall ME, Whiting MF. (1999). Long-branch abstractions. *Cladistics* **15:** 9-24.

Skyring GW, Donnelly TH. (1982). Precambrian Sulfur Isotopes and a Possible Role for Sulfite in the Evolution of Biological Sulfate Reduction. *Precambrian Res* **17:** 41-61.

Stackebrandt E, Ebers J. (2006). Taxonomic parameters revisited: tarnished gold standards. *Microbiol Today* **33:** 152.

Stamatakis A. (2006). RAxML-VI-HPC: maximum likelihood-based phylogenetic analyses with thousands of taxa and mixed models. *Bioinformatics* **22:** 2688-2690.

Steger D, Wentrup C, Braunegger C, Deevong P, Hofer M, Richter A *et al*. (2011). Microorganisms with Novel Dissimilatory (Bi)Sulfite Reductase Genes Are Widespread and Part of the Core Microbiota in Low-Sulfate Peatlands. *Appl Environ Microbiol* **77:** 1231-1242.

Sun S, Chen J, Li W, Altintas I, Lin A, Peltier S *et al*. (2011). Community cyberinfrastructure for Advanced Microbial Ecology Research and Analysis: the CAMERA resource. *Nucleic Acids Res* **39:** D546-551.

Suzuki D, Cui X, Li Z, Zhang C, Katayama A. (2014). Reclassification of Desulfobacterium anilini as Desulfatiglans anilini comb. nov. to Desulfatiglans gen. nov., and description of a 4-chlorophenol-degrading sulfate-reducing bacterium-Desulfatiglans parachlorophenolica sp. nov. *Int J Syst Evol Microbiol*: ijs-0.

Suzuki Y, Kelly SD, Kemner KM, Banfield JF. (2005). Direct microbial reduction and subsequent preservation of uranium in natural near-surface sediment. *Appl Environ Microbiol* **71:** 1790-1797.

Tsukahara K, Kita A, Nakashimada Y, Hoshino T, Murakami K. (2014). Genome-guided analysis of transformation efficiency and carbon dioxide assimilation by Moorella thermoacetica Y72. *Gene* **535:** 150-155.

Völkl P, Huber R, Drobner E, Rachel R, Burggraf S, Trincone A *et al*. (1993). Pyrobaculum aerophilum sp. nov., a novel nitrate-reducing hyperthermophilic archaeum. *Appl Environ Microbiol* **59:** 2918-2926.

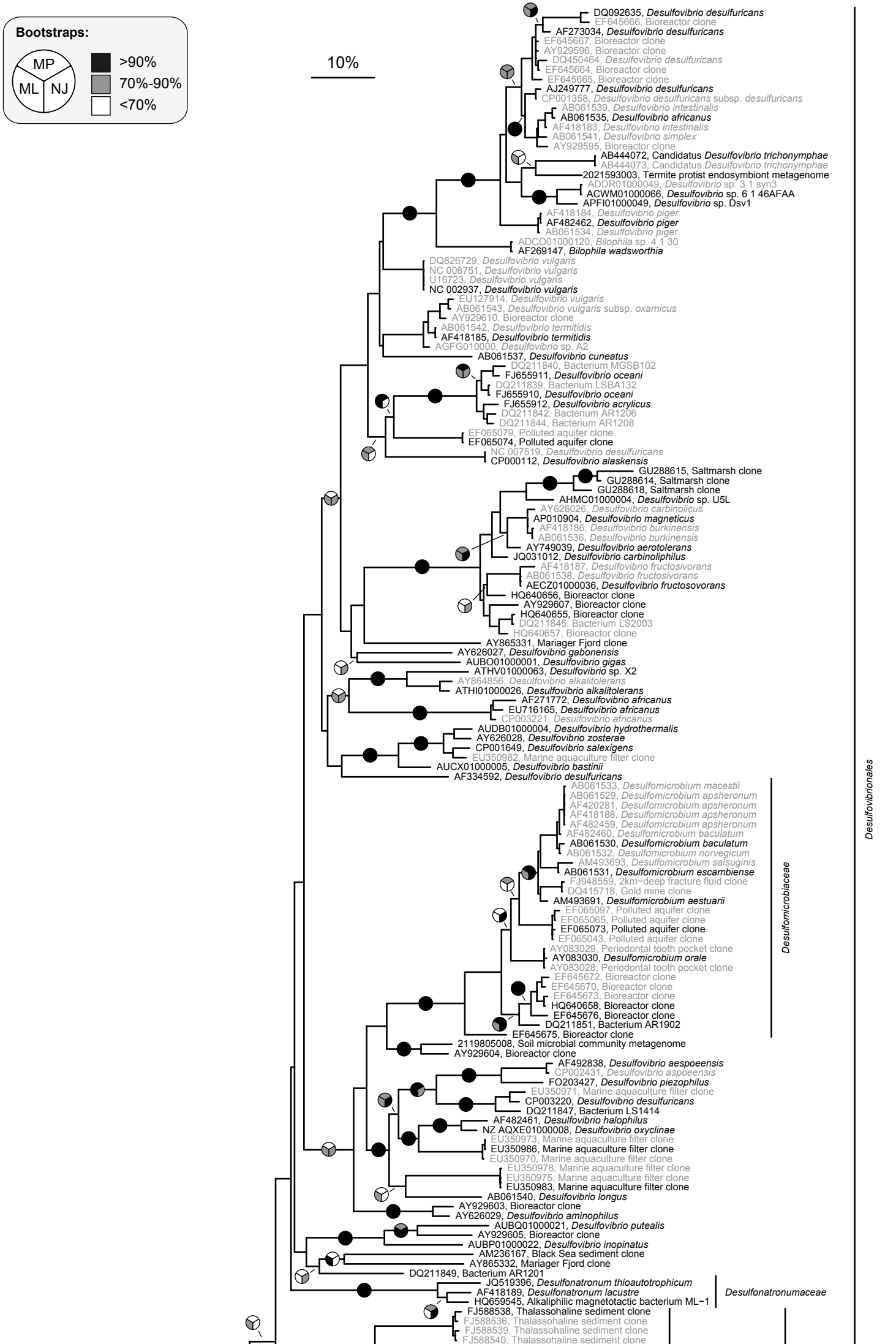
Wagner M, Roger AJ, Flax JL, Brusseau GA, Stahl DA. (1998). Phylogeny of dissimilatory sulfite reductases supports an early origin of sulfate respiration. *J Bacteriol* **180:** 2975-2982.

Würdemann D, Tindall BJ, Pukall R, Lunsdorf H, Strompl C, Namuth T *et al*. (2009). Gordonibacter pamelaeae gen. nov., sp. nov., a new member of the Coriobacteriaceae isolated from a patient with Crohn's disease, and reclassification of Eggerthella hongkongensis Lau et al. 2006 as Paraeggerthella hongkongensis gen. nov., comb. nov. *Int J Syst Evol Microbiol* **59:** 1405-1415.

Yang Z. (2007). PAML 4: phylogenetic analysis by maximum likelihood. *Mol Biol Evol* **24:** 1586-1591.

Yutin N, Galperin MY. (2013). A genomic update on clostridial phylogeny: Gram-negative spore formers and other misplaced clostridia. *Environ Microbiol* **15:** 2631-2641.

Zverlov V, Klein M, Lücker S, Friedrich MW, Kellermann J, Stahl DA *et al*. (2005). Lateral gene transfer of dissimilatory (bi)sulfite reductase revisited. *J Bacteriol* **187:** 2203-2208.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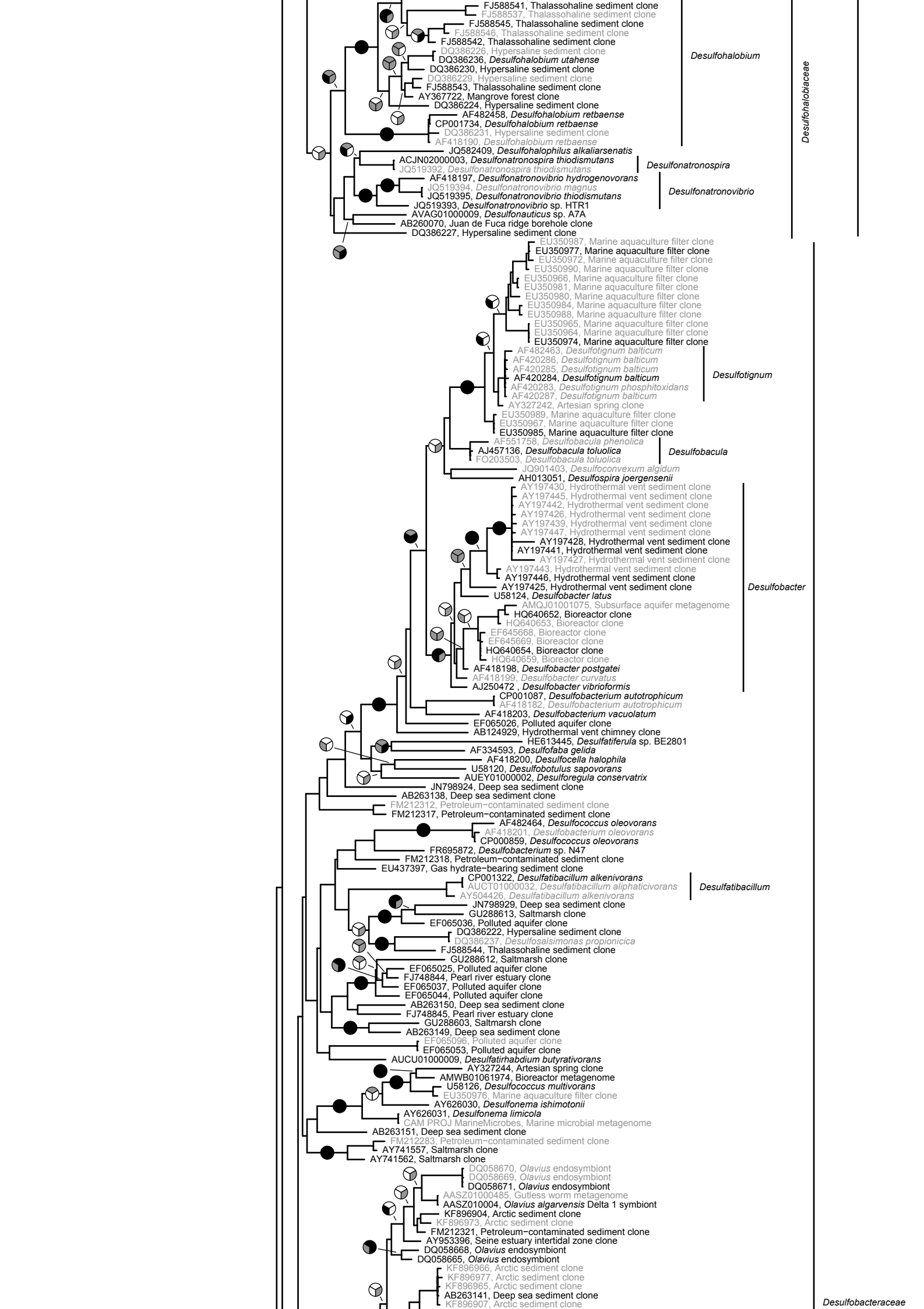
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EU350985, Marine aquaculture filter clone
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JQ901403, Desulfoconvexum algidum
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CP001087, Desulfobacterium autotrophicum
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AF418203, Desulfobacterium vacuolatum
EF065026, Polluted aquifer clone
AB124929, Hydrothermal vent chimney clone
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AF418200, Desulfocella halophila
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AY626031, Desulfonema limicola
CAM PROJ MarineMicrobes, Marine microbial metagenome
AB263151, Deep sea sediment clone
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DQ058671, Olavius endosymbiont
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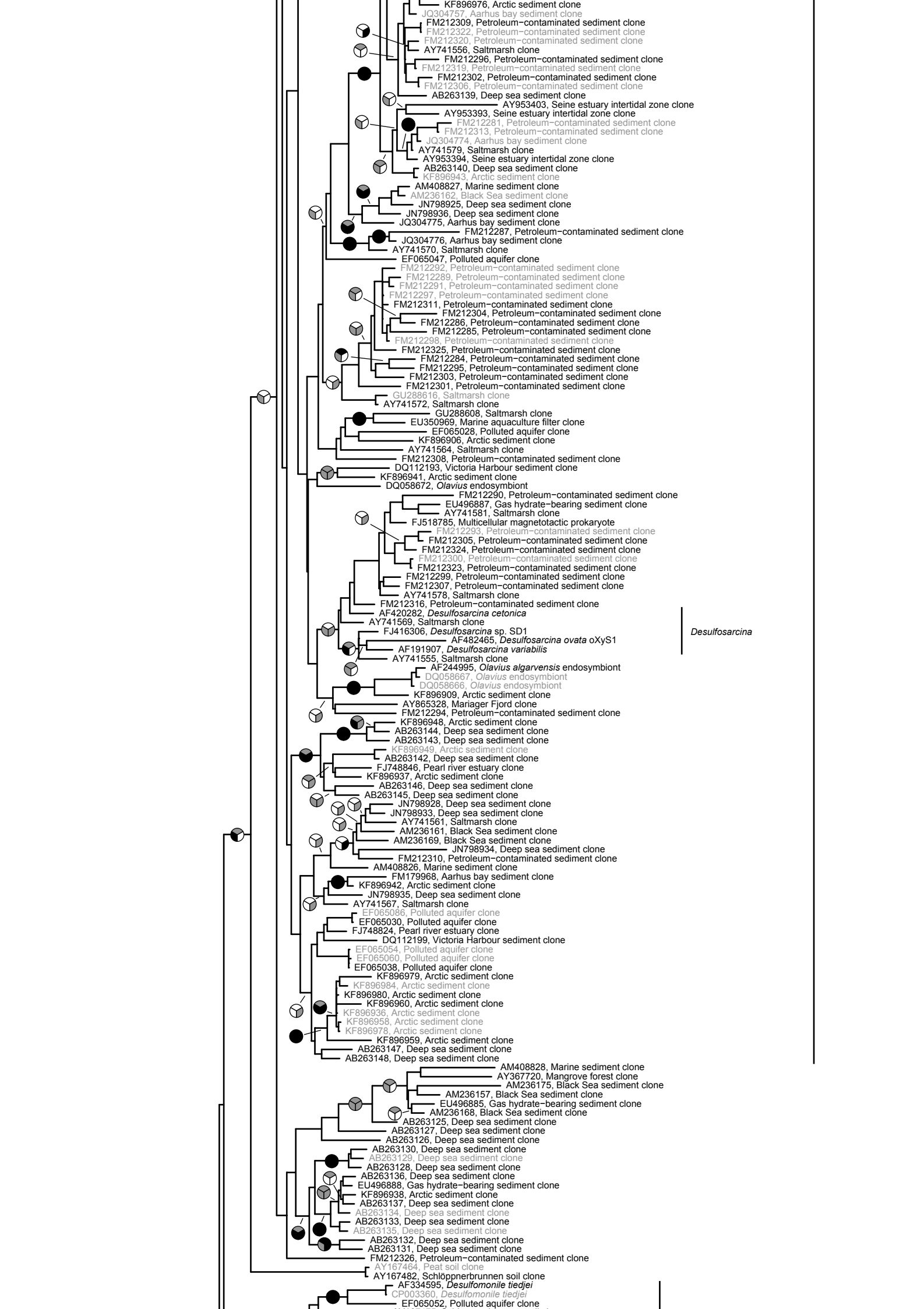
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FM212304, Petroleum−contaminated sediment clone
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FM212295, Petroleum−contaminated sediment clone
FM212303, Petroleum−contaminated sediment clone
FM212301, Petroleum−contaminated sediment clone
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AY741572, Saltmarsh clone
GU288608, Saltmarsh clone
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EF065028, Polluted aquifer clone
KF896906, Arctic sediment clone
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FM212308, Petroleum−contaminated sediment clone
DQ112193, Victoria Harbour sediment clone
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DQ058672, *Olavius* endosymbiont
FM212290, Petroleum−contaminated sediment clone
EU496887, Gas hydrate−bearing sediment clone
AY741581, Saltmarsh clone
FJ518785, Multicellular magnetotactic prokaryote
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FM212305, Petroleum−contaminated sediment clone
FM212324, Petroleum−contaminated sediment clone
FM212300, Petroleum−contaminated sediment clone
FM212323, Petroleum−contaminated sediment clone
FM212299, Petroleum−contaminated sediment clone
FM212307, Petroleum−contaminated sediment clone
AY741578, Saltmarsh clone
FM212316, Petroleum−contaminated sediment clone
AF420282, *Desulfosarcina cetonica*
AY741569, Saltmarsh clone
FJ416306, *Desulfosarcina* sp. SD1
AF482465, *Desulfosarcina ovata* oXyS1
AF191907, *Desulfosarcina variabilis*
AY741555, Saltmarsh clone
Desulfosarcina
AF244995, *Olavius algarvensis* endosymbiont
DQ058667, *Olavius* endosymbiont
DQ058666, *Olavius* endosymbiont
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FM212310, Petroleum−contaminated sediment clone
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FM179968, Aarhus bay sediment clone
KF896942, Arctic sediment clone
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AY741567, Saltmarsh clone
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EF065030, Polluted aquifer clone
FJ748824, Pearl river estuary clone
DQ112199, Victoria Harbour sediment clone
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EF065060, Polluted aquifer clone
EF065038, Polluted aquifer clone
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KF896978, Arctic sediment clone
KF896959, Arctic sediment clone
AB263147, Deep sea sediment clone
AB263148, Deep sea sediment clone
AM408828, Marine sediment clone
AY367720, Mangrove forest clone
AM236175, Black Sea sediment clone
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AY167464, Peat soil clone
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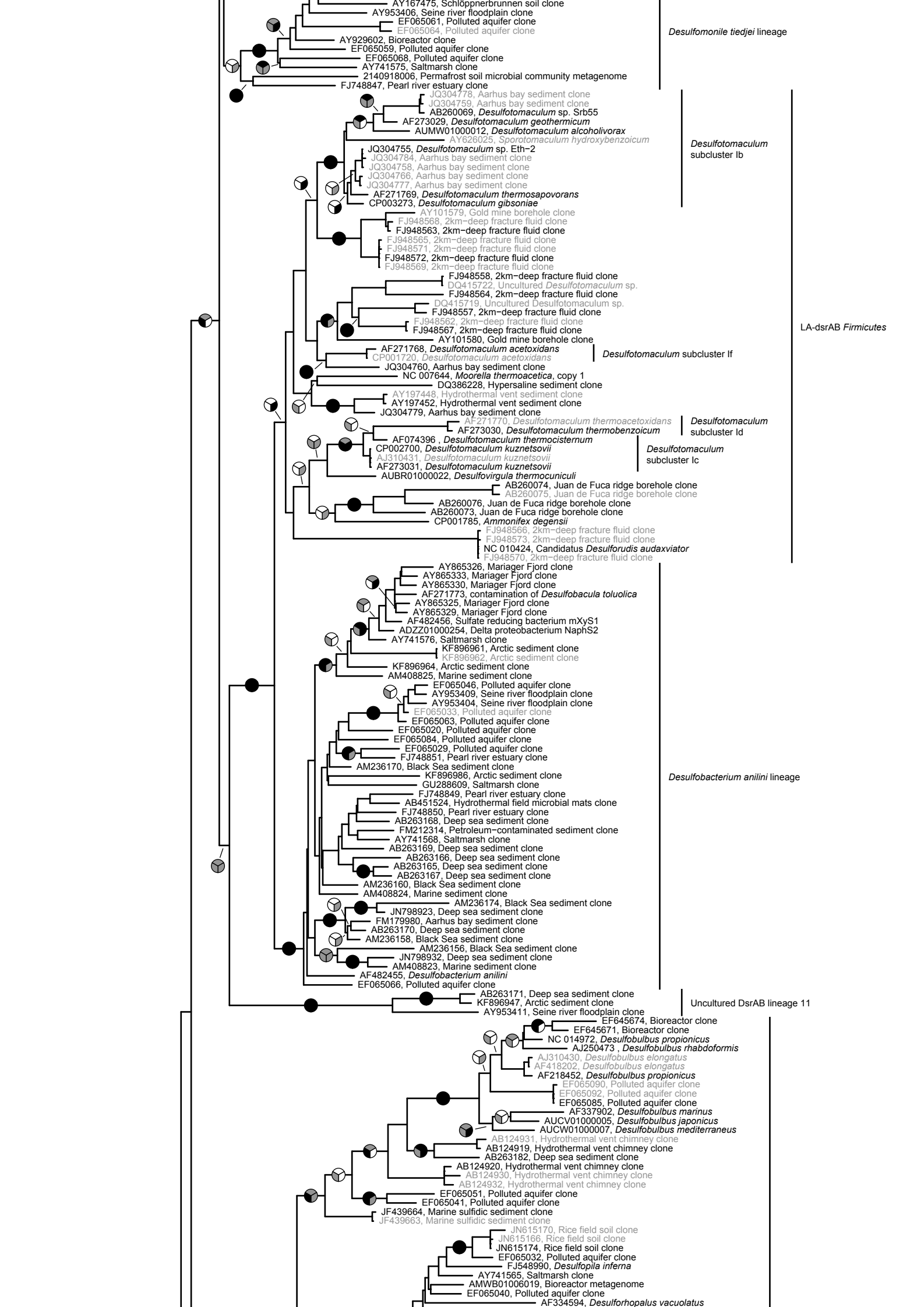
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2140918006, Permafrost soil microbial community metagenome
FJ748847, Pearl river estuary clone
Desulfomonile tiedjei lineage
JQ304778, Aarhus bay sediment clone
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AB260069, Desulfotomaculum sp. Srb55
AF273029, Desulfotomaculum geothermicum
AUMW01000012, Desulfotomaculum alcoholivorax
AY626025, Sporotomaculum hydroxybenzoicum
JQ304755, Desulfotomaculum sp. Eth−2
JQ304784, Aarhus bay sediment clone
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JQ304777, Aarhus bay sediment clone
AF271769, Desulfotomaculum thermosapovorans
CP003273, Desulfotomaculum gibsoniae
Desulfotomaculum subcluster Ib
AY101579, Gold mine borehole clone
FJ948568, 2km−deep fracture fluid clone
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FJ948569, 2km−deep fracture fluid clone
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DQ415722, Uncultured Desulfotomaculum sp.
FJ948564, 2km−deep fracture fluid clone
DQ415719, Uncultured Desulfotomaculum sp.
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FJ948562, 2km−deep fracture fluid clone
FJ948567, 2km−deep fracture fluid clone
AY101580, Gold mine borehole clone
AF271768, Desulfotomaculum acetoxidans
CP001720, Desulfotomaculum acetoxidans
Desulfotomaculum subcluster If
JQ304760, Aarhus bay sediment clone
NC 007644, Moorella thermoacetica, copy 1
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AF271770, Desulfotomaculum thermoacetoxidans
AF273030, Desulfotomaculum thermobenzoicum
Desulfotomaculum subcluster Id
AF074396 , Desulfotomaculum thermocisternum
CP002700, Desulfotomaculum kuznetsovii
AJ310431, Desulfotomaculum kuznetsovii
AF273031, Desulfotomaculum kuznetsovii
Desulfotomaculum subcluster Ic
AUBR01000022, Desulfovirgula thermocuniculi
AB260074, Juan de Fuca ridge borehole clone
AB260075, Juan de Fuca ridge borehole clone
AB260076, Juan de Fuca ridge borehole clone
AB260073, Juan de Fuca ridge borehole clone
CP001785, Ammonifex degensii
FJ948566, 2km−deep fracture fluid clone
FJ948573, 2km−deep fracture fluid clone
NC 010424, Candidatus Desulforudis audaxviator
FJ948570, 2km−deep fracture fluid clone
LA-dsrAB Firmicutes
AY865326, Mariager Fjord clone
AY865333, Mariager Fjord clone
AY865330, Mariager Fjord clone
AF271773, contamination of Desulfobacula toluolica
AY865325, Mariager Fjord clone
AY865329, Mariager Fjord clone
AF482456, Sulfate reducing bacterium mXyS1
ADZZ01000254, Delta proteobacterium NaphS2
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EF065029, Polluted aquifer clone
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AM236156, Black Sea sediment clone
JN798932, Deep sea sediment clone
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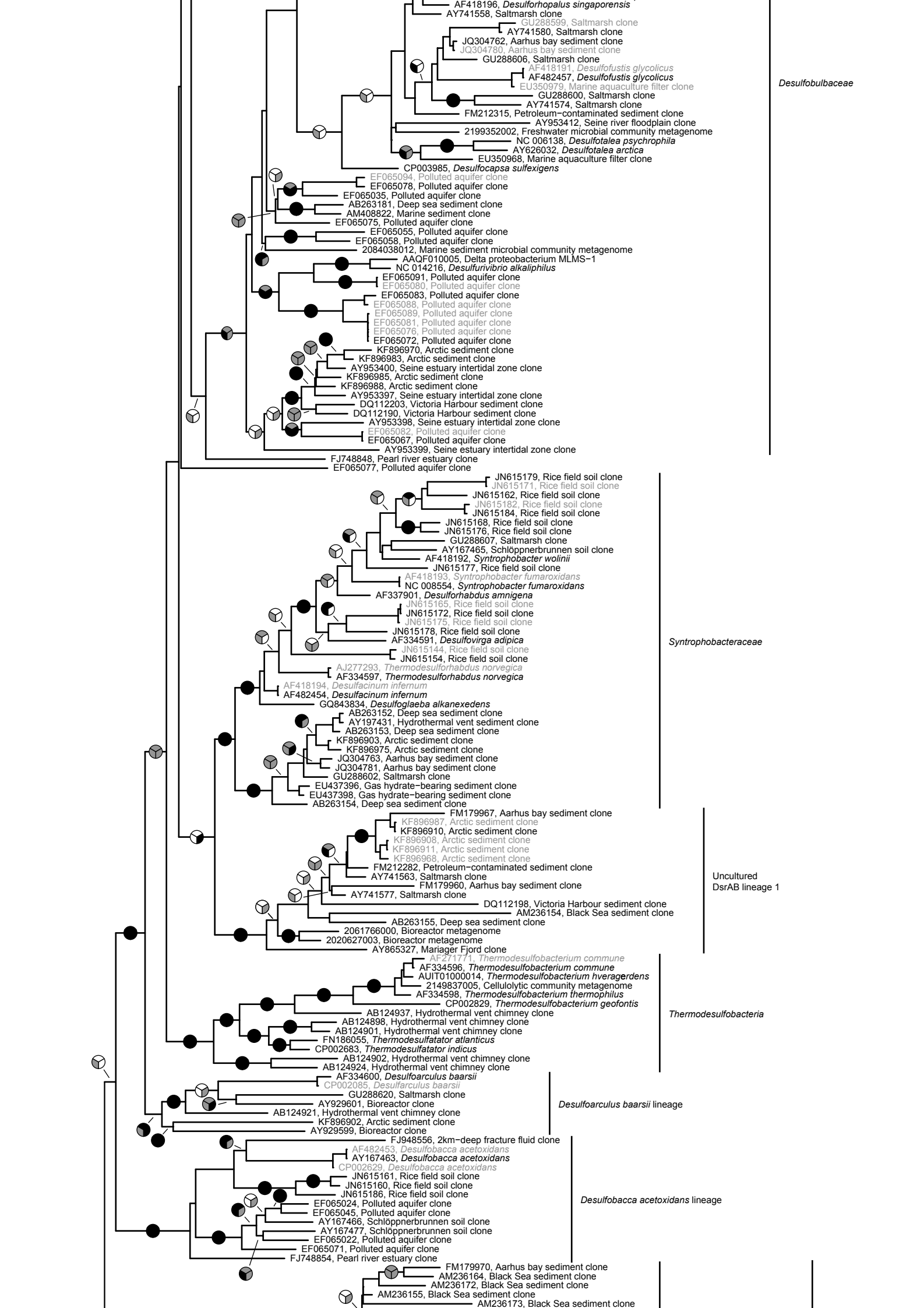
AF482455, Desulfobacterium anilini
EF065066, Polluted aquifer clone
Desulfobacterium anilini lineage
AB263171, Deep sea sediment clone
KF896947, Arctic sediment clone
AY953411, Seine river floodplain clone
Uncultured DsrAB lineage 11
EF645674, Bioreactor clone
EF645671, Bioreactor clone
NC 014972, Desulfobulbus propionicus
AJ250473 , Desulfobulbus rhabdoformis
AJ310430, Desulfobulbus elongatus
AF418202, Desulfobulbus elongatus
AF218452, Desulfobulbus propionicus
EF065090, Polluted aquifer clone
EF065092, Polluted aquifer clone
EF065085, Polluted aquifer clone
AF337902, Desulfobulbus marinus
AUCV01000005, Desulfobulbus japonicus
AUCW01000007, Desulfobulbus mediterraneus
AB124931, Hydrothermal vent chimney clone
AB124919, Hydrothermal vent chimney clone
AB263182, Deep sea sediment clone
AB124920, Hydrothermal vent chimney clone
AB124930, Hydrothermal vent chimney clone
AB124932, Hydrothermal vent chimney clone
EF065051, Polluted aquifer clone
EF065041, Polluted aquifer clone
JF439664, Marine sulfidic sediment clone
JF439663, Marine sulfidic sediment clone
JN615170, Rice field soil clone
JN615166, Rice field soil clone
JN615174, Rice field soil clone
EF065032, Polluted aquifer clone
FJ548990, Desulfopila inferna
AY741565, Saltmarsh clone
AMWB01006019, Bioreactor metagenome
EF065040, Polluted aquifer clone
AF334594, Desulforhopalus vacuolatus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EU350979, Marine aquaculture filter clone
GU288600, Saltmarsh clone
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AY953412, Seine river floodplain clone
2199352002, Freshwater microbial community metagenome
NC 006138, Desulfotalea psychrophila
AY626032, Desulfotalea arctica
EU350968, Marine aquaculture filter clone
CP003985, Desulfocapsa sulfexigens
EF065094, Polluted aquifer clone
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EF065035, Polluted aquifer clone
AB263181, Deep sea sediment clone
AM408822, Marine sediment clone
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EF065055, Polluted aquifer clone
EF065058, Polluted aquifer clone
2084038012, Marine sediment microbial community metagenome
AAQF010005, Delta proteobacterium MLMS−1
NC 014216, Desulfurivibrio alkaliphilus
EF065091, Polluted aquifer clone
EF065080, Polluted aquifer clone
EF065083, Polluted aquifer clone
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EF065081, Polluted aquifer clone
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KF896970, Arctic sediment clone
KF896983, Arctic sediment clone
AY953400, Seine estuary intertidal zone clone
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KF896988, Arctic sediment clone
AY953397, Seine estuary intertidal zone clone
DQ112203, Victoria Harbour sediment clone
DQ112190, Victoria Harbour sediment clone
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EF065082, Polluted aquifer clone
EF065067, Polluted aquifer clone
AY953399, Seine estuary intertidal zone clone
FJ748848, Pearl river estuary clone
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Desulfobulbaceae
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JN615176, Rice field soil clone
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AF418192, Syntrophobacter wolinii
JN615177, Rice field soil clone
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NC 008554, Syntrophobacter fumaroxidans
AF337901, Desulforhabdus amnigena
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AJ277293, Thermodesulforhabdus norvegica
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AF418194, Desulfacinum infernum
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GQ843834, Desulfoglaeba alkanexedens
AB263152, Deep sea sediment clone
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AB263153, Deep sea sediment clone
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JQ304763, Aarhus bay sediment clone
JQ304781, Aarhus bay sediment clone
GU288602, Saltmarsh clone
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AB263154, Deep sea sediment clone
Syntrophobacteraceae
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KF896911, Arctic sediment clone
KF896968, Arctic sediment clone
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AY741563, Saltmarsh clone
FM179960, Aarhus bay sediment clone
AY741577, Saltmarsh clone
DQ112198, Victoria Harbour sediment clone
AM236154, Black Sea sediment clone
AB263155, Deep sea sediment clone
2061766000, Bioreactor metagenome
2020627003, Bioreactor metagenome
AY865327, Mariager Fjord clone
Uncultured
DsrAB lineage 1
AF271771, Thermodesulfobacterium commune
AF334596, Thermodesulfobacterium commune
AUIT01000014, Thermodesulfobacterium hveragerdens
2149837005, Cellulolytic community metagenome
AF334598, Thermodesulfobacterium thermophilus
CP002829, Thermodesulfobacterium geofontis
AB124937, Hydrothermal vent chimney clone
AB124898, Hydrothermal vent chimney clone
AB124901, Hydrothermal vent chimney clone
FN186055, Thermodesulfatator atlanticus
CP002683, Thermodesulfatator indicus
AB124902, Hydrothermal vent chimney clone
AB124924, Hydrothermal vent chimney clone
Thermodesulfobacteria
AF334600, Desulfoarculus baarsii
CP002085, Desulfarculus baarsii
GU288620, Saltmarsh clone
AY929601, Bioreactor clone
AB124921, Hydrothermal vent chimney clone
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AY929599, Bioreactor clone
Desulfoarculus baarsii lineage
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AY167463, Desulfobacca acetoxidans
CP002629, Desulfobacca acetoxidans
JN615161, Rice field soil clone
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EF065024, Polluted aquifer clone
EF065045, Polluted aquifer clone
AY167466, Schlöppnerbrunnen soil clone
AY167477, Schlöppnerbrunnen soil clone
EF065022, Polluted aquifer clone
EF065071, Polluted aquifer clone
FJ748854, Pearl river estuary clone
Desulfobacca acetoxidans lineage
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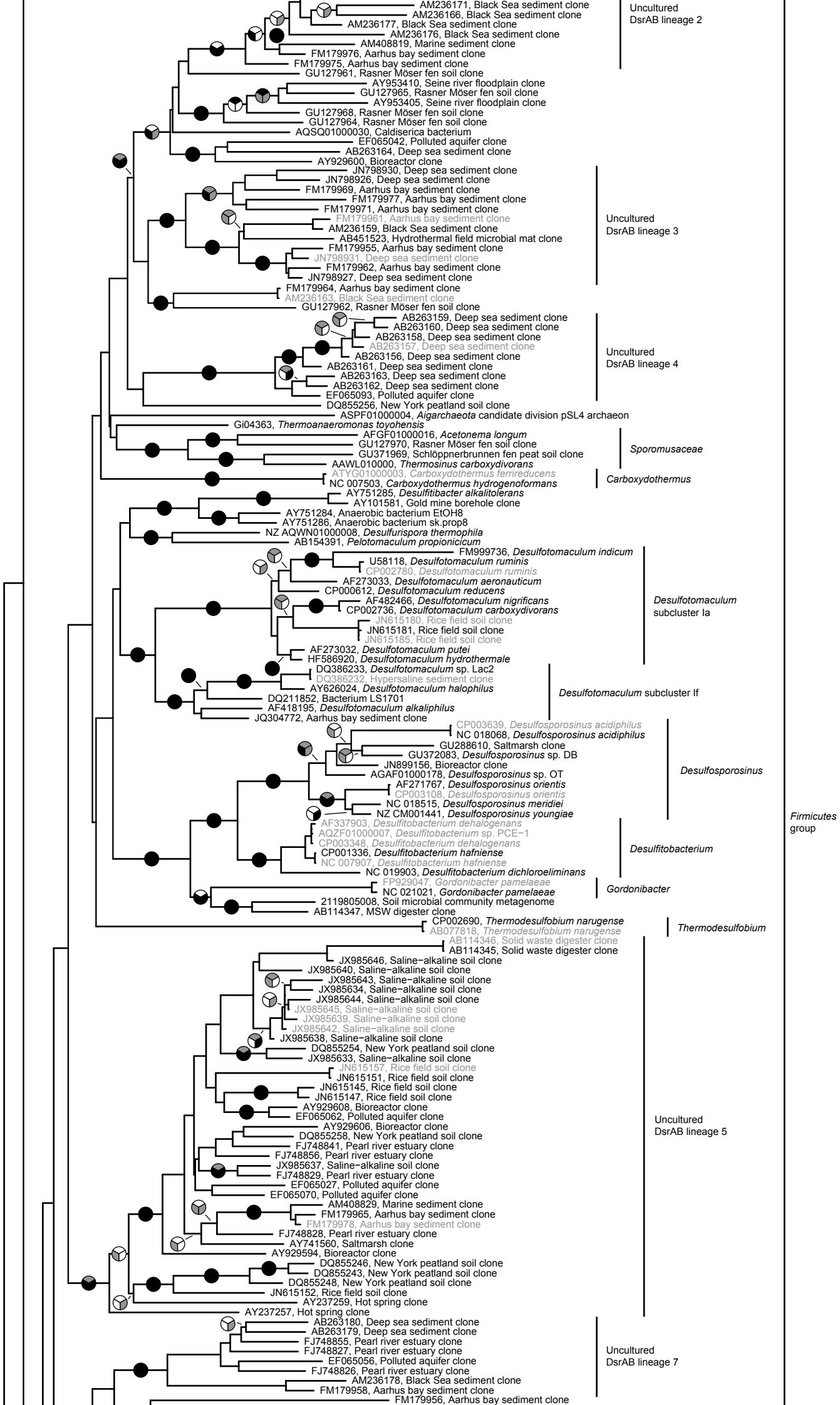
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AY953410, Seine river floodplain clone
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AY953405, Seine river floodplain clone
GU127968, Rasner Möser fen soil clone
GU127964, Rasner Möser fen soil clone
AQSQ01000030, Caldiserica bacterium
EF065042, Polluted aquifer clone
AB263164, Deep sea sediment clone
AY929600, Bioreactor clone
Uncultured DsrAB lineage 2
JN798930, Deep sea sediment clone
JN798926, Deep sea sediment clone
FM179969, Aarhus bay sediment clone
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FM179961, Aarhus bay sediment clone
AM236159, Black Sea sediment clone
AB451523, Hydrothermal field microbial mat clone
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FM179962, Aarhus bay sediment clone
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FM179964, Aarhus bay sediment clone
AM236163, Black Sea sediment clone
GU127962, Rasner Möser fen soil clone
Uncultured DsrAB lineage 3
AB263159, Deep sea sediment clone
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AB263163, Deep sea sediment clone
AB263162, Deep sea sediment clone
EF065093, Polluted aquifer clone
DQ855256, New York peatland soil clone
Uncultured DsrAB lineage 4
ASPF01000004, Aigarchaeota candidate division pSL4 archaeon
Gi04363, Thermoanaeromonas toyohensis
AFGF01000016, Acetonema longum
GU127970, Rasner Möser fen soil clone
GU371969, Schlöppnerbrunnen fen peat soil clone
AAWL010000, Thermosinus carboxydivorans
Sporomusaceae
ATYG01000003, Carboxydothermus ferrireducens
NC 007503, Carboxydothermus hydrogenoformans
Carboxydothermus
AY751285, Desulfitibacter alkalitolerans
AY101581, Gold mine borehole clone
AY751284, Anaerobic bacterium EtOH8
AY751286, Anaerobic bacterium sk.prop8
NZ AQWN01000008, Desulfurispora thermophila
AB154391, Pelotomaculum propionicicum
FM999736, Desulfotomaculum indicum
U58118, Desulfotomaculum ruminis
CP002780, Desulfotomaculum ruminis
AF273033, Desulfotomaculum aeronauticum
CP000612, Desulfotomaculum reducens
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DQ386232, Hypersaline sediment clone
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CP003108, Desulfosporosinus orientis
NC 018515, Desulfosporosinus meridiei
NZ CM001441, Desulfosporosinus youngiae
Desulfosporosinus
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NC 019903, Desulfitobacterium dichloroeliminans
Desulfitobacterium
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Gordonibacter
2119805008, Soil microbial community metagenome
AB114347, MSW digester clone
CP002690, Thermodesulfobium narugense
AB077818, Thermodesulfobium narugense
Thermodesulfobium
Firmicutes group
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JN615152, Rice field soil clone
AY237259, Hot spring clone
AY237257, Hot spring clone
Uncultured DsrAB lineage 5
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EF065056, Polluted aquifer clone
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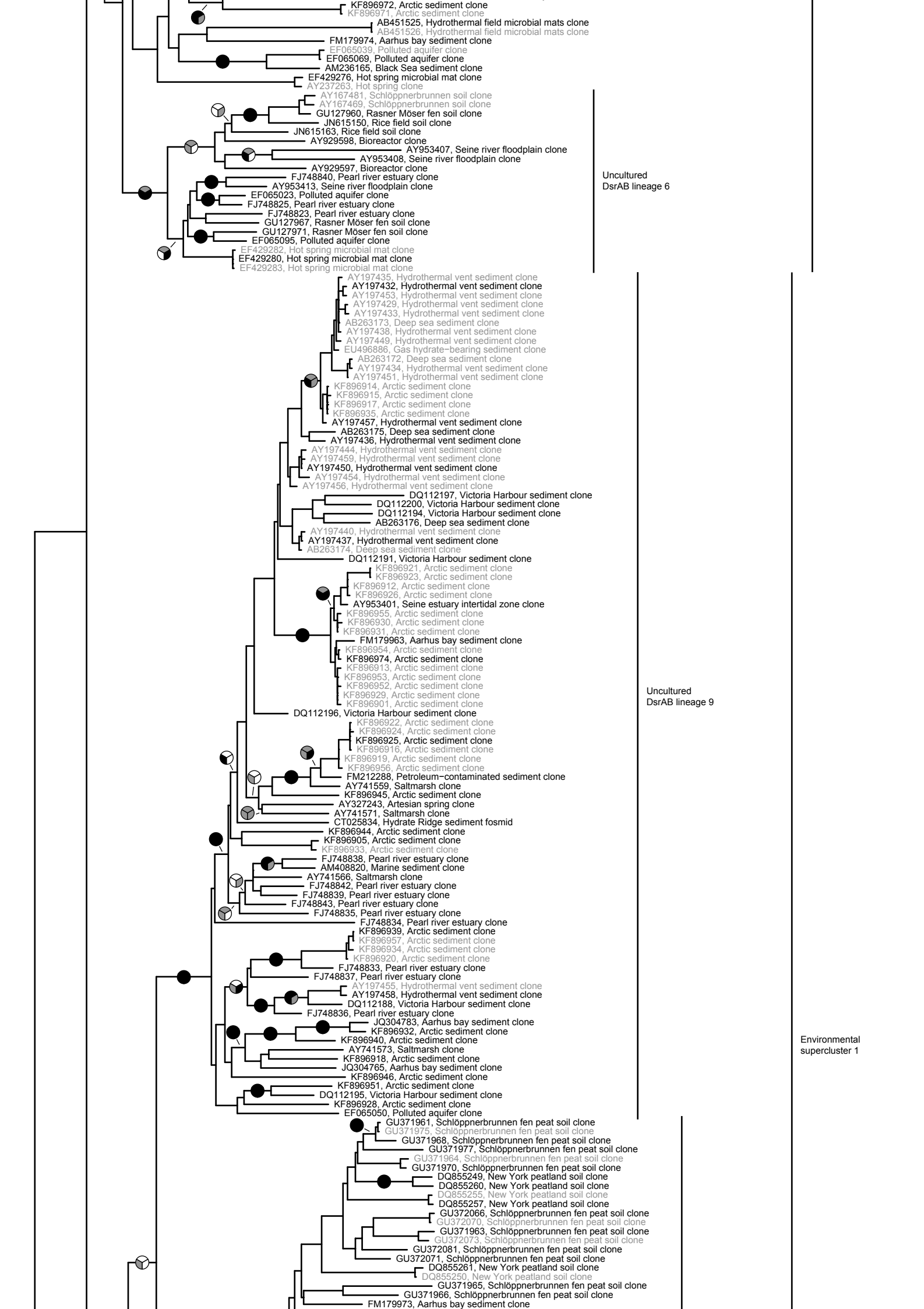
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GU127960, Rasner Möser fen soil clone
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AY929598, Bioreactor clone
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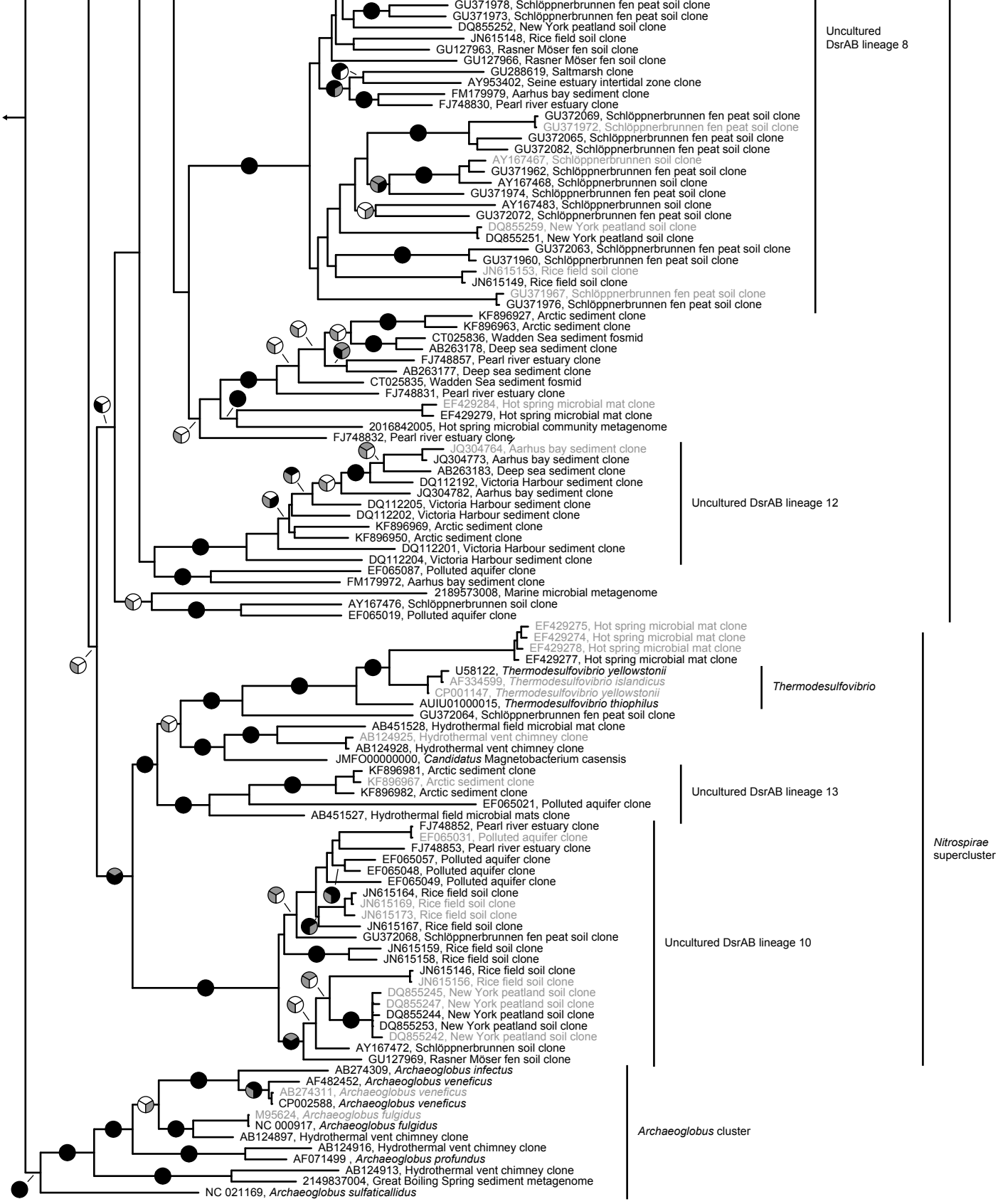
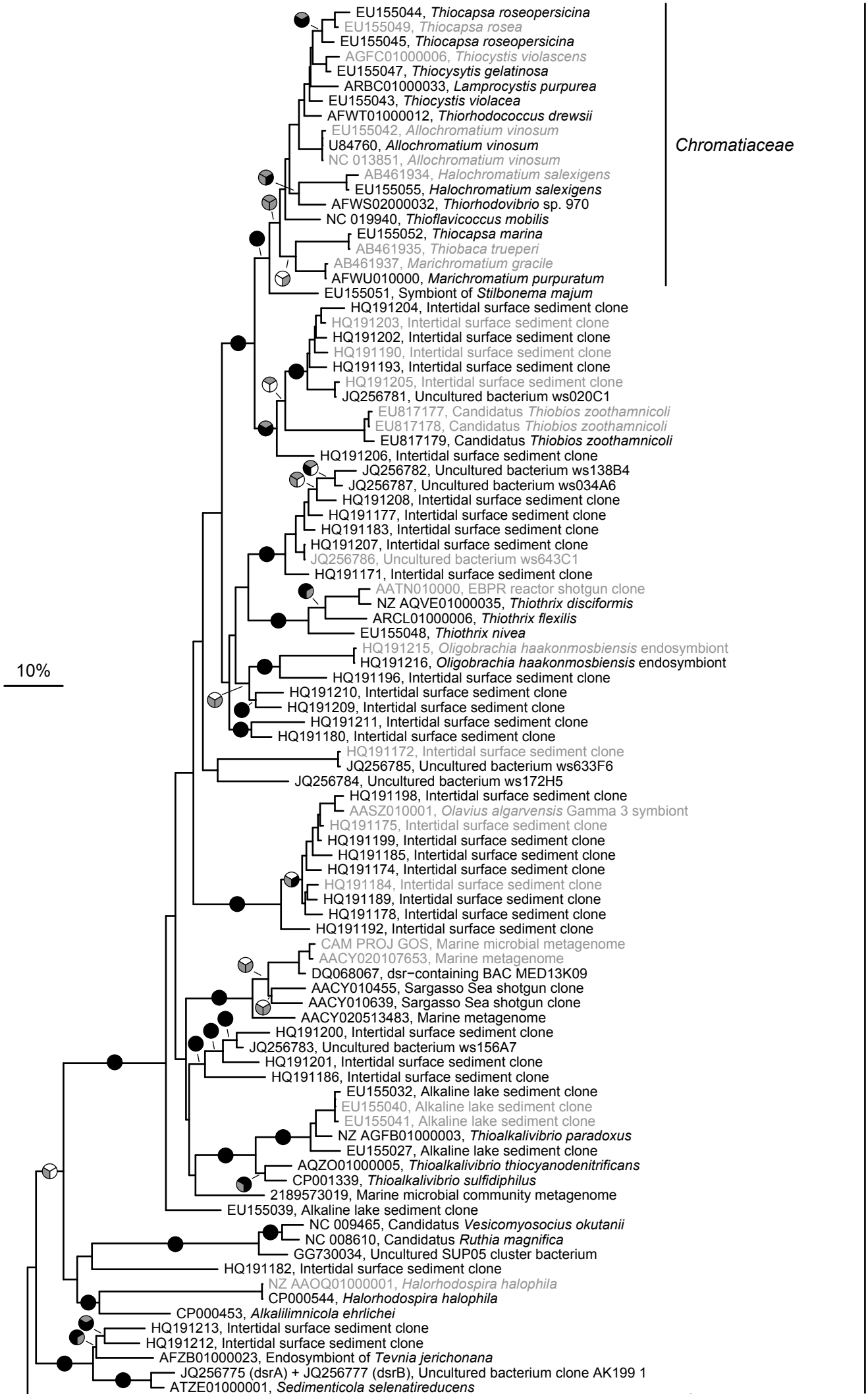
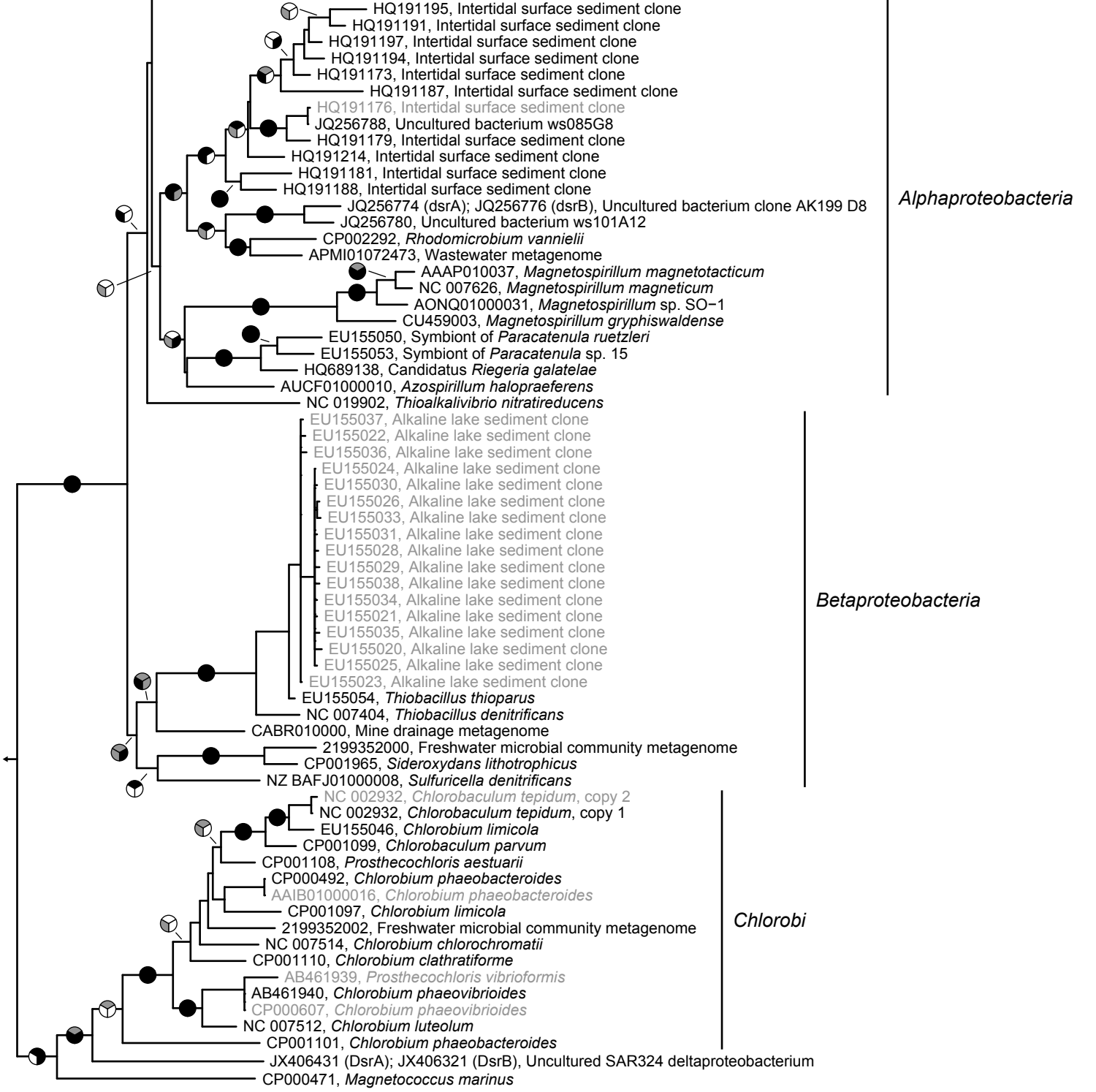
EF429282, Hot spring microbial mat clone
EF429280, Hot spring microbial mat clone
EF429283, Hot spring microbial mat clone
Uncultured
DsrAB lineage 6
AY197435, Hydrothermal vent sediment clone
AY197432, Hydrothermal vent sediment clone
AY197453, Hydrothermal vent sediment clone
AY197429, Hydrothermal vent sediment clone
AY197433, Hydrothermal vent sediment clone
AB263173, Deep sea sediment clone
AY197438, Hydrothermal vent sediment clone
AY197449, Hydrothermal vent sediment clone
EU496886, Gas hydrate−bearing sediment clone
AB263172, Deep sea sediment clone
AY197434, Hydrothermal vent sediment clone
AY197451, Hydrothermal vent sediment clone
KF896914, Arctic sediment clone
KF896915, Arctic sediment clone
KF896917, Arctic sediment clone
KF896935, Arctic sediment clone
AY197457, Hydrothermal vent sediment clone
AB263175, Deep sea sediment clone
AY197436, Hydrothermal vent sediment clone
AY197444, Hydrothermal vent sediment clone
AY197459, Hydrothermal vent sediment clone
AY197450, Hydrothermal vent sediment clone
AY197454, Hydrothermal vent sediment clone
AY197456, Hydrothermal vent sediment clone
DQ112197, Victoria Harbour sediment clone
DQ112200, Victoria Harbour sediment clone
DQ112194, Victoria Harbour sediment clone
AB263176, Deep sea sediment clone
AY197440, Hydrothermal vent sediment clone
AY197437, Hydrothermal vent sediment clone
AB263174, Deep sea sediment clone
DQ112191, Victoria Harbour sediment clone
KF896921, Arctic sediment clone
KF896923, Arctic sediment clone
KF896912, Arctic sediment clone
KF896926, Arctic sediment clone
AY953401, Seine estuary intertidal zone clone
KF896955, Arctic sediment clone
KF896930, Arctic sediment clone
KF896931, Arctic sediment clone
FM179963, Aarhus bay sediment clone
KF896954, Arctic sediment clone
KF896974, Arctic sediment clone
KF896913, Arctic sediment clone
KF896953, Arctic sediment clone
KF896952, Arctic sediment clone
KF896929, Arctic sediment clone
KF896901, Arctic sediment clone
DQ112196, Victoria Harbour sediment clone
KF896922, Arctic sediment clone
KF896924, Arctic sediment clone
KF896925, Arctic sediment clone
KF896916, Arctic sediment clone
KF896919, Arctic sediment clone
KF896956, Arctic sediment clone
FM212288, Petroleum−contaminated sediment clone
AY741559, Saltmarsh clone
KF896945, Arctic sediment clone
AY327243, Artesian spring clone
AY741571, Saltmarsh clone
CT025834, Hydrate Ridge sediment fosmid
KF896944, Arctic sediment clone
KF896905, Arctic sediment clone
KF896933, Arctic sediment clone
FJ748838, Pearl river estuary clone
AM408820, Marine sediment clone
AY741566, Saltmarsh clone
FJ748842, Pearl river estuary clone
FJ748839, Pearl river estuary clone
FJ748843, Pearl river estuary clone
FJ748835, Pearl river estuary clone
FJ748834, Pearl river estuary clone
KF896939, Arctic sediment clone
KF896957, Arctic sediment clone
KF896934, Arctic sediment clone
KF896920, Arctic sediment clone
FJ748833, Pearl river estuary clone
FJ748837, Pearl river estuary clone
AY197455, Hydrothermal vent sediment clone
AY197458, Hydrothermal vent sediment clone
DQ112188, Victoria Harbour sediment clone
FJ748836, Pearl river estuary clone
JQ304783, Aarhus bay sediment clone
KF896932, Arctic sediment clone
KF896940, Arctic sediment clone
AY741573, Saltmarsh clone
KF896918, Arctic sediment clone
JQ304765, Aarhus bay sediment clone
KF896946, Arctic sediment clone
KF896951, Arctic sediment clone
DQ112195, Victoria Harbour sediment clone
KF896928, Arctic sediment clone
EF065050, Polluted aquifer clone
Uncultured
DsrAB lineage 9
GU371961, Schlöppnerbrunnen fen peat soil clone
GU371975, Schlöppnerbrunnen fen peat soil clone
GU371968, Schlöppnerbrunnen fen peat soil clone
GU371977, Schlöppnerbrunnen fen peat soil clone
GU371964, Schlöppnerbrunnen fen peat soil clone
GU371970, Schlöppnerbrunnen fen peat soil clone
DQ855249, New York peatland soil clone
DQ855260, New York peatland soil clone
DQ855255, New York peatland soil clone
DQ855257, New York peatland soil clone
GU372066, Schlöppnerbrunnen fen peat soil clone
GU372070, Schlöppnerbrunnen fen peat soil clone
GU371963, Schlöppnerbrunnen fen peat soil clone
GU372073, Schlöppnerbrunnen fen peat soil clone
GU372081, Schlöppnerbrunnen fen peat soil clone
GU372071, Schlöppnerbrunnen fen peat soil clone
DQ855261, New York peatland soil clone
DQ855250, New York peatland soil clone
GU371965, Schlöppnerbrunnen fen peat soil clone
GU371966, Schlöppnerbrunnen fen peat soil clone
FM179973, Aarhus bay sediment clone
Environmental
supercluster 1

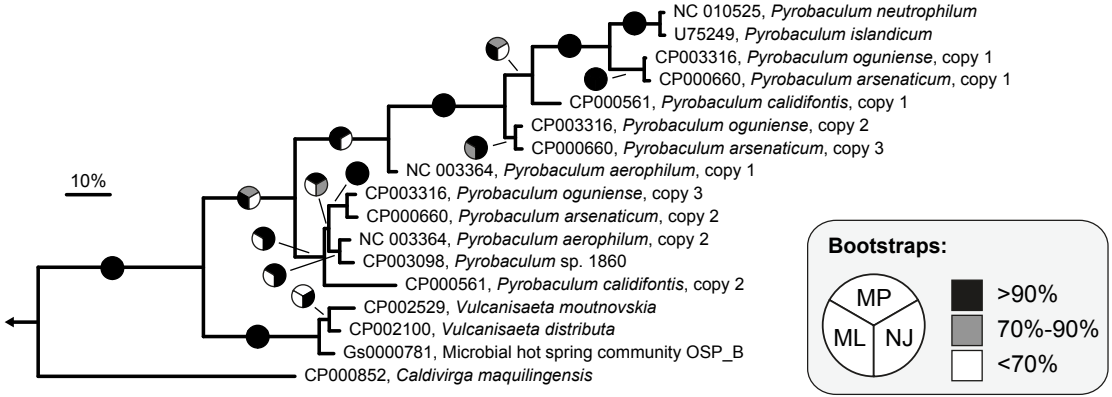


Supplementary Figure S1. Consensus phylogeny of reductive bacterial type DsrAB sequences. This figure shows an un-collapsed version of the consensus tree shown in Figure 1 depicting only reductive bacterial type DsrAB. Sequences in grey were subsequently added to the consensus tree without changing its topology. Scale bar indicates 10% sequence divergence.

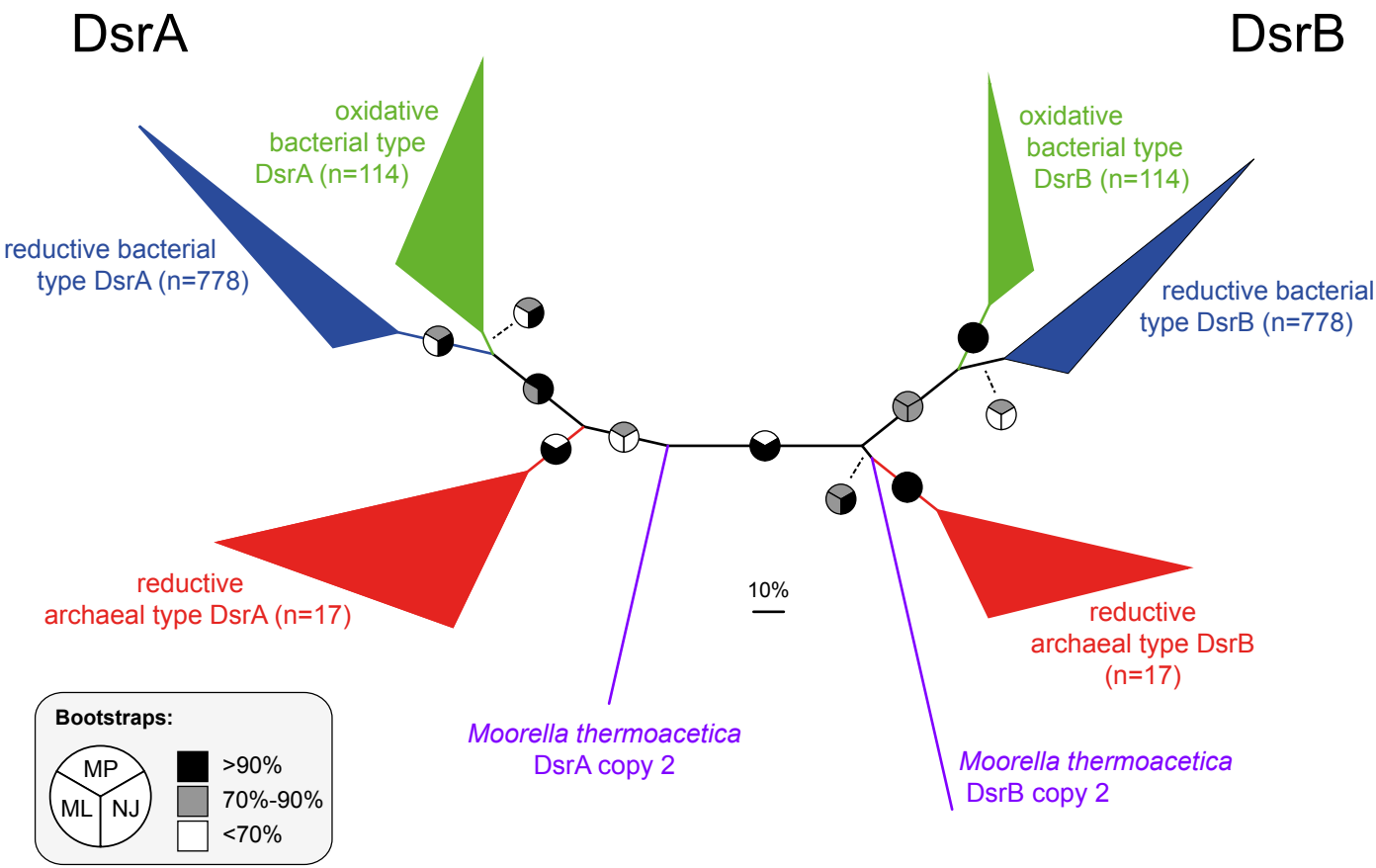

EU155044, Thiocapsa roseopersicina
EU155049, Thiocapsa rosea
EU155045, Thiocapsa roseopersicina
AGFC01000006, Thiocystis violascens
EU155047, Thiocysytis gelatinosa
ARBC01000033, Lamprocystis purpurea
EU155043, Thiocystis violacea
AFWT01000012, Thiorhodococcus drewsii
EU155042, Allochromatium vinosum
U84760, Allochromatium vinosum
NC 013851, Allochromatium vinosum
AB461934, Halochromatium salexigens
EU155055, Halochromatium salexigens
AFWS02000032, Thiorhodovibrio sp. 970
NC 019940, Thioflavicoccus mobilis
EU155052, Thiocapsa marina
AB461935, Thiobaca trueperi
AB461937, Marichromatium gracile
AFWU010000, Marichromatium purpuratum
EU155051, Symbiont of Stilbonema majum
Chromatiaceae
HQ191204, Intertidal surface sediment clone
HQ191203, Intertidal surface sediment clone
HQ191202, Intertidal surface sediment clone
HQ191190, Intertidal surface sediment clone
HQ191193, Intertidal surface sediment clone
HQ191205, Intertidal surface sediment clone
JQ256781, Uncultured bacterium ws020C1
EU817177, Candidatus Thiobios zoothamnicoli
EU817178, Candidatus Thiobios zoothamnicoli
EU817179, Candidatus Thiobios zoothamnicoli
HQ191206, Intertidal surface sediment clone
JQ256782, Uncultured bacterium ws138B4
JQ256787, Uncultured bacterium ws034A6
HQ191208, Intertidal surface sediment clone
HQ191177, Intertidal surface sediment clone
HQ191183, Intertidal surface sediment clone
HQ191207, Intertidal surface sediment clone
JQ256786, Uncultured bacterium ws643C1
HQ191171, Intertidal surface sediment clone
AATN010000, EBPR reactor shotgun clone
NZ AQVE01000035, Thiothrix disciformis
ARCL01000006, Thiothrix flexilis
EU155048, Thiothrix nivea
HQ191215, Oligobrachia haakonmosbiensis endosymbiont
HQ191216, Oligobrachia haakonmosbiensis endosymbiont
HQ191196, Intertidal surface sediment clone
HQ191210, Intertidal surface sediment clone
HQ191209, Intertidal surface sediment clone
HQ191211, Intertidal surface sediment clone
HQ191180, Intertidal surface sediment clone
HQ191172, Intertidal surface sediment clone
JQ256785, Uncultured bacterium ws633F6
JQ256784, Uncultured bacterium ws172H5
HQ191198, Intertidal surface sediment clone
AASZ010001, Olavius algarvensis Gamma 3 symbiont
HQ191175, Intertidal surface sediment clone
HQ191199, Intertidal surface sediment clone
HQ191185, Intertidal surface sediment clone
HQ191174, Intertidal surface sediment clone
HQ191184, Intertidal surface sediment clone
HQ191189, Intertidal surface sediment clone
HQ191178, Intertidal surface sediment clone
HQ191192, Intertidal surface sediment clone
CAM PROJ GOS, Marine microbial metagenome
AACY020107653, Marine metagenome
DQ068067, dsr−containing BAC MED13K09
AACY010455, Sargasso Sea shotgun clone
AACY010639, Sargasso Sea shotgun clone
AACY020513483, Marine metagenome
HQ191200, Intertidal surface sediment clone
JQ256783, Uncultured bacterium ws156A7
HQ191201, Intertidal surface sediment clone
HQ191186, Intertidal surface sediment clone
EU155032, Alkaline lake sediment clone
EU155040, Alkaline lake sediment clone
EU155041, Alkaline lake sediment clone
NZ AGFB01000003, Thioalkalivibrio paradoxus
EU155027, Alkaline lake sediment clone
AQZO01000005, Thioalkalivibrio thiocyanodenitrificans
CP001339, Thioalkalivibrio sulfidiphilus
2189573019, Marine microbial community metagenome
EU155039, Alkaline lake sediment clone
NC 009465, Candidatus Vesicomyosocius okutanii
NC 008610, Candidatus Ruthia magnifica
GG730034, Uncultured SUP05 cluster bacterium
HQ191182, Intertidal surface sediment clone
NZ AAOQ01000001, Halorhodospira halophila
CP000544, Halorhodospira halophila
CP000453, Alkalilimnicola ehrlichei
HQ191213, Intertidal surface sediment clone
HQ191212, Intertidal surface sediment clone
AFZB01000023, Endosymbiont of Tevnia jerichonana
JQ256775 (dsrA) + JQ256777 (dsrB), Uncultured bacterium clone AK199 1
ATZE01000001, Sedimenticola selenatireducens
10%
Gammaproteobacteria



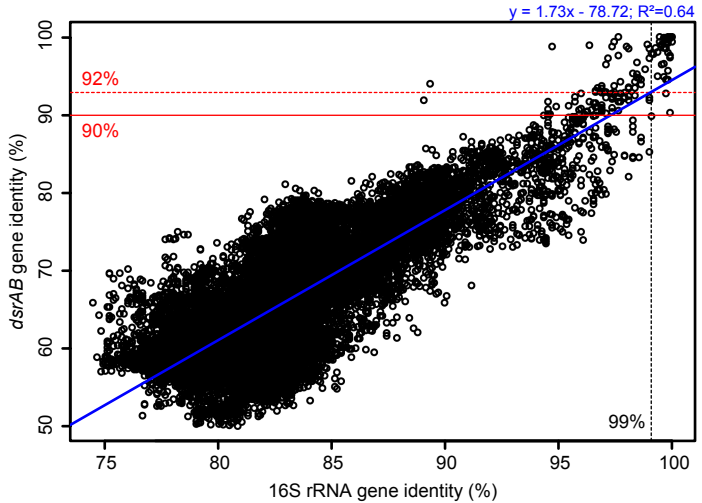
Supplementary Figure S2. Consensus phylogeny of oxidative bacterial type DsrAB sequences. Trees for reconstruction of the consensus tree (extended majority rule) were calculated using an amino acid alignment of 115 representative oxidative DsrAB sequences (clustered at 97% amino acid identity) and a filter covering 552 amino acid positions (omitting insertions/deletions). The tree was rooted with reductive bacterial type DsrAB sequences as outgroup. Sequences in grey (n=45) were subsequently added to the consensus tree without changing its topology. Scale bar indicates 10% sequence divergence. Bootstrap support (1000 re-samplings) is shown by split circles (top: maximum parsimony, bottom left: maximum likelihood, bottom right: neighbor joining) at the respective branches; with black, grey, and white indicating ≥90%, 70%-90%, and <70% support, respectively.



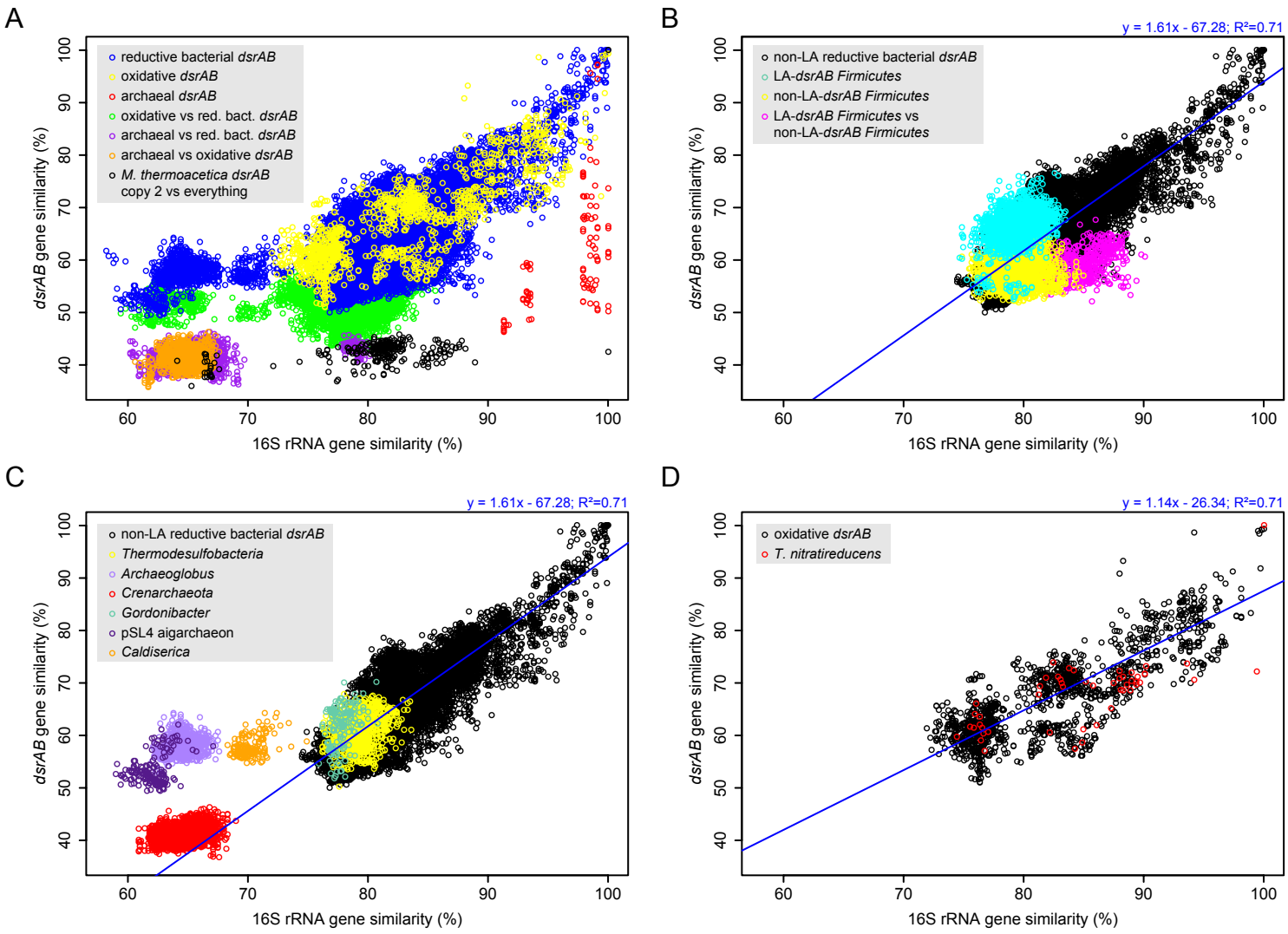
Supplementary Figure S3. Consensus phylogeny of reductive archaeal type DsrAB sequences. Trees for reconstruction of the consensus tree (extended majority rule) were calculated using an amino acid alignment of 17 archaeal type DsrAB sequences and a filter covering 629 amino acid positions (omitting insertions/deletions). The tree was rooted with bacterial DsrAB sequences as outgroup. Scale bar indicates 10% sequence divergence. Bootstrap support (1000 re-samplings) is shown by split circles (top: maximum parsimony, bottom left: maximum likelihood, bottom right: neighbor joining) at the respective branches; with black, grey, and white indicating ≥90%, 70%-90%, and <70% support, respectively.



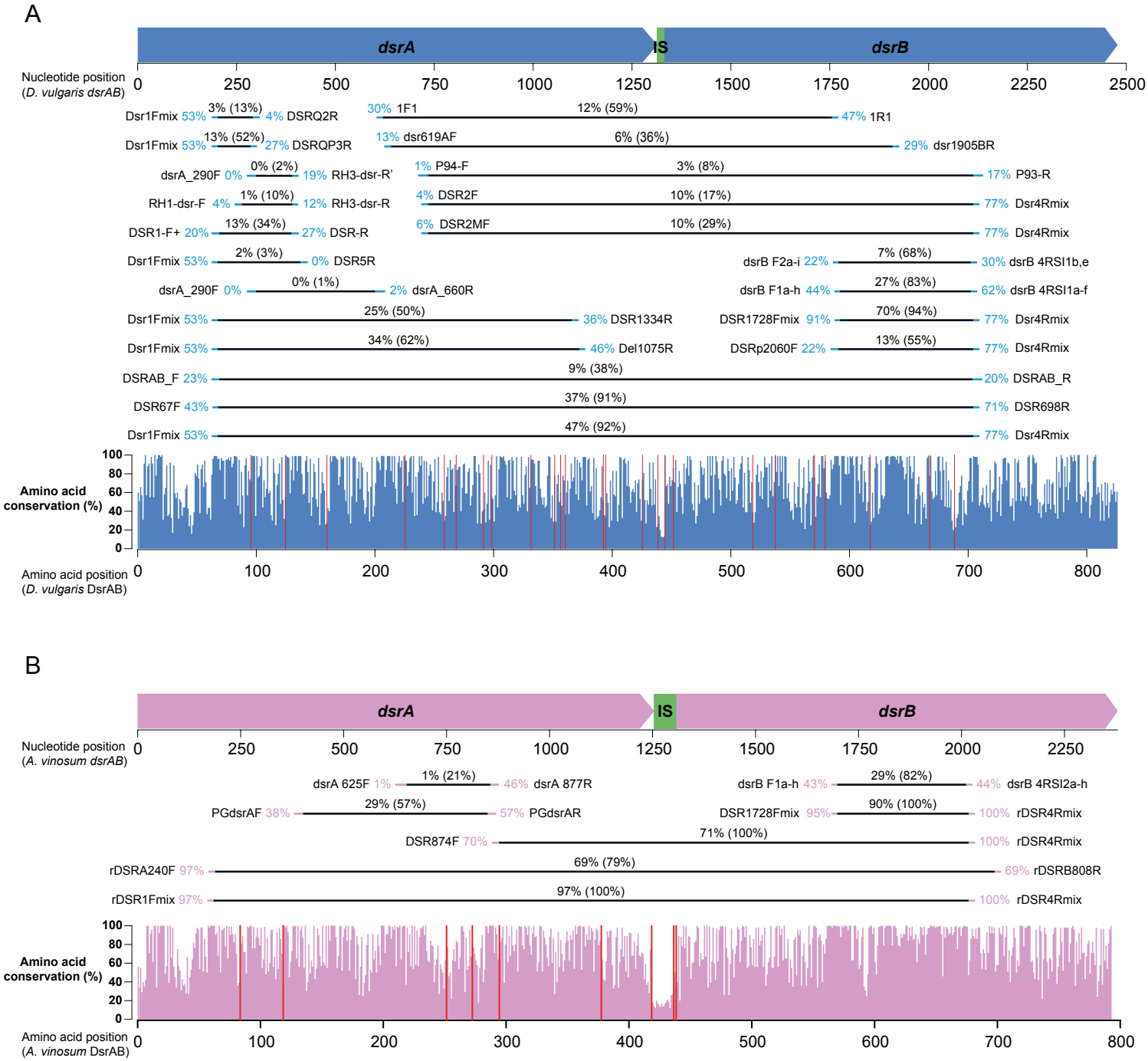
Supplementary Figure S4. Revealing the root in the DsrAB tree by paralogous rooting. Trees for reconstruction of the consensus tree (extended majority rule) were calculated using an alignment of 910 DsrA to corresponding DsrB sequences and a filter covering 163 amino acid positions that are conserved and homologous between DsrA and DsrB subunits. Scale bar indicates 10% sequence divergence. Bootstrap support (100 re-samplings) is shown by split circles (top: maximum parsimony, bottom left: maximum likelihood, bottom right: neighbor joining) at the respective branches; with black, grey, and white indicating ≥90%, 70%-90%, and <70% support, respectively. Clusters of the four, most basal DsrAB branches are collapsed and shown in different colors.



Supplementary Figure S5. Species-level threshold for *dsrAB* nucleotide identity inferred from a gene identity plot of non-laterally acquired bacterial *dsrAB*-carrying organisms using 99% nucleotide identity on 16S rRNA level as threshold for species level.



Supplementary Figure S6. Gene identity plot of *dsrAB* against 16S rRNA. Sequence identities of *dsrAB* and 16S rRNA for pairs of organisms for which both genes are known (mostly pure cultures and genomes) were plotted against each other. A) Pairwise comparisons between 259 corresponding *dsrAB*-16S rRNA pairs. Comparisons within and among the three main DsrAB enzyme families as well as comparisons with *M. thermoacetica dsrAB* copy 2 are highlighted in different colors. B) Comparisons of *Firmicutes* with laterally acquired and vertically inherited *dsrAB* with all organisms that have vertically inherited *dsrAB*. Linear regression of comparisons between organisms with non-laterally acquired reductive bacterial type *dsrAB* is shown for reference. C) Comparisons between organisms with laterally acquired *dsrAB* and organisms with vertically inherited *dsrAB*. Linear regression of comparisons between organisms with non-laterally acquired reductive bacterial type *dsrAB* is shown for reference. D) Comparisons of *T. nitratireducens* with reverse *dsrAB*-carrying organisms. Linear regression of comparisons between organisms with oxidative type dsrAB is shown for reference.



Supplementary Figure S7. Binding sites and *in silico* coverages of reductive (A) and oxidative (B) bacterial type *dsrAB*-targeted primers. Perfect-match coverage values are displayed for individual primers (blue or pink) and primer pairs (black), coverage values using one weighted mismatch are additionally indicated in parentheses for primer pairs. Displayed coverage values for primers binding at the target sites or outside the amplification region of (r)DSR1F/(r)DSR4R are based on full length datasets of reductive (n=115) and oxidative (n=62) bacterial type dsrAB sequences, whereas coverage values for primers binding within the region amplified by (r)DSR1F/(r)DSR4R are based on a core dataset of reductive (n=1110) and oxidative (n=159) bacterial type dsrAB sequences that completely cover this region. Bar charts show positional amino acid sequence variability (calculated in ARB using the ARB_PHYLO 'filter by base frequency' method and indicated in blue or pink bars) and regions with deletions/insertions (red bars) in DsrAB. Sequence numbering and primer binding positions correspond to *dsrAB*/DsrAB of *Desulfovibrio vulgaris* (NC_002937, 449880..452365) or *Allochromatium vinosum* (NC_013851, 1439735 ..1442113).

Supplementary Table S1

Primers targeting reductive bacterial type *dsrAB*[a]					full length *dsrAB*[b] (%)		core dataset *dsrAB*[c] (%)		Phylogenetic clusters[d] (%)					
Name	**Sequence (5'-3')**	**Target gene**	**Position[e]**	**Deg.[f]**	**0 MM**	**1 wMM**	**0 MM**	**1 wMM**	**DpS**	**Fg**	**ES1**	**NsS**	**AgC**	**Reference**
DSR1F	ACSCACTGGAAGCACG	*dsrA*	187-202	2	25	49	*n.a.*	*n.a.*	35	0	0	0	60	Wagner *et al*., 1998
DSR1Fmix (+a-b)		*dsrA*	187-202	5	38	90	*n.a.*	*n.a.*	52	7	0	0	60	Loy *et al*., 2004
DSR1Fa	ACCCAYTGGAAACACG	*dsrA*	187-202	2	11	87	*n.a.*	*n.a.*	17	0	0	0	0	Loy *et al*., 2004
DSR1Fb	GGCCACTGGAAGCACG	*dsrA*	187-202	1	2	26	*n.a.*	*n.a.*	0	7	0	0	0	Loy *et al*., 2004
DSR1Fmix (+a-d)		*dsrA*	187-202	7	49	90	*n.a.*	*n.a.*	68	7	0	0	60	Zverlov *et al*., 2005
DSR1Fc	ACCCATTGGAAACATG	*dsrA*	187-202	1	3	11	*n.a.*	*n.a.*	4	0	0	0	0	Zverlov *et al*., 2005
DSR1Fd	ACTCACTGGAAGCACG	*dsrA*	187-202	1	8	43	*n.a.*	*n.a.*	12	0	0	0	0	Zverlov *et al*., 2005
DSR1Fmix (+a-h)		*dsrA*	187-202	11	53	98	*n.a.*	*n.a.*	68	14	60	0	60	Pester *et al*., 2010
DSR1Fe	GTTCACTGGAAACACG	*dsrA*	187-202	1	2	37	*n.a.*	*n.a.*	0	7	0	0	0	Pester *et al*., 2010
DSR1Ff	AGCCACTGGAAACACG	*dsrA*	187-202	1	1	72	*n.a.*	*n.a.*	0	0	20	0	0	Pester *et al*., 2010
DSR1Fg	GGCCACTGGAAACATG	*dsrA*	187-202	1	1	24	*n.a.*	*n.a.*	0	0	20	0	0	Pester *et al*., 2010
DSR1Fh	GGCTATTGGAAGCACG	*dsrA*	187-202	1	1	2	*n.a.*	*n.a.*	0	0	20	0	0	Pester *et al*., 2010
DSR1-F+	ACSCACTGGAAGCACGGCGG	*dsrA*	187-206	2	20	41	*n.a.*	*n.a.*	31	0	0	0	0	Kondo *et al*., 2004
DSRAB_F	ACSCACTGGAAGCACGGYGG	*dsrA*	187-206	4	23	42	*n.a.*	*n.a.*	35	0	0	0	20	Schmalenberger *et al*., 2007
DSR67F	SCACTGGAARCACGG	*dsrA*	189-203	4	43	100	*n.a.*	*n.a.*	53	21	20	0	60	Suzuki *et al*., 2005
RH1-dsr-F	GCCGTTACTGTGACCAGCC	*dsrA*	245-263	1	9	21	4	13	6	0	0	0	0	Ben-Dov *et al*., 2007
dsrA_290F	CGGCGTTGCGCATTTYCAYACVVT	*dsrA*	276-299	36	0	1	0	3	0	0	0	0	0	Pereyra *et al*., 2010
DSRQP3R	CGCATGGTRTGRAARTG	*dsrA*	286-302	8	17	52	27	60	40	9	3	0	0	Akob *et al*., 2012
DSRQ2R	GTTGAYACGCATGGTRTG	*dsrA*	292-309	4	5	13	4	17	6	0	1	0	0	Chin *et al*., 2007
DSR-R	GTGGMRCCGTGCAKRTTGG	*dsrA*	389-407	16	33	67	27	71	36	18	10	5	0	Kondo *et al*., 2004
RH3-dsr-R	gGTGGAGCCGTGCATGTT	*dsrA*	391-408	1	15	40	12	49	15	15	1	3	0	Ben-Dov *et al*., 2007
RH3-dsr-R'	GTGGMGCCGTGCATGTT	*dsrA*	392-408	2	22	49	19	56	24	3	22	3	0	Pereyra *et al*., 2010
DSR5R	TGCCGAGGAGAACGATGTC	*dsrA*	412-430	1	2	3	0	2	1	0	0	0	0	Wagner et al., 1998
dsrA_660R	GCCGGACGATGCAGHTCRTCCTGRWA	*dsrA*	601-626	24	2	9	2	13	4	0	0	0	0	Pereyra et al., 2010
1F1	CAGGAYGARCTKCACCG	*dsrA*	604-620	8	36	61	30	66	34	39	14	0	0	Dhillon *et al*., 2003
dsr619AF	GYCCGGCVTTCCCSTACAA	*dsrA*	623-641	12	15	38	13	44	18	8	0	8	0	Giloteaux *et al*., 2010
P94-F	ATCGGWACCTGGAAGGAYGACATCAA	*dsrA*	709-734	4	3	8	1	6	1	0	0	0	17	Karkhoff-Schweizer *et al*., 1995
DSR2F	CTGGAAGGAYGACATCAA	*dsrA*	717-734	2	10	17	4	15	6	0	0	0	17	Wagner *et al*., 1998
DSR2MF	CTGGAARGAYGACATCAA	*dsrA*	717-734	4	11	30	6	34	10	0	0	0	17	Akob *et al*., 2012
DSR1334R	TYTTCCATCCACCARTCC	*dsrA*	1098-1115	4	37	50	36	50	56	0	1	0	0	Santillano *et al*., 2010
Del1075R	GYTCVCGGTTCTTDC	*dsrA*	1118-1132	18	45	63	46	61	66	15	2	49	0	Gittel *et al*., 2009
DSRp2060F	CAACATCGTYCAYACCCAGGG	*dsrB*	1752-1772	4	14	56	22	65	23	39	8	0	0	Geets *et al*., 2005
1R1	CCCTGGGTRTGRAYRAT	*dsrB*	1756-1772	16	29	74	47	87	55	54	19	0	50	Dhillon *et al*., 2003
dsrB F2a-i		*dsrB*	1758-1772	9	16	81	22	93	20	40	13	0	25	Lever *et al*., 2013
dsrB F2a	CGTCCACACCCAGGG	*dsrB*	1758-1772	1	10	50	17	69	14	39	9	0	8	Lever *et al*., 2013
dsrB F2b	TGTGCATACCCAGGG	*dsrB*	1758-1772	1	0	7	2	9	2	1	1	0	0	Lever *et al*., 2013
dsrB F2c	CATTCATACCCAGGG	*dsrB*	1758-1772	1	0	25	1	27	1	0	0	0	0	Lever *et al*., 2013
dsrB F2d	TGTTCACACCCAGGG	*dsrB*	1758-1772	1	1	43	1	61	2	0	0	0	0	Lever *et al*., 2013
dsrB F2e	CGTGCACACGCAGGG	*dsrB*	1758-1772	1	3	3	1	5	1	1	3	0	0	Lever *et al*., 2013
dsrB F2f	CGTTCATACACAGGG	*dsrB*	1758-1772	1	1	16	0	12	0	0	0	0	0	Lever *et al*., 2013
dsrB F2g	TGTCCACACTCAGGG	*dsrB*	1758-1772	1	1	11	0	11	0	0	0	0	17	Lever *et al*., 2013
dsrB F2h	CGTGCATACGCAGGG	*dsrB*	1758-1772	1	0	3	0	2	0	0	1	0	0	Lever *et al*., 2013
dsrB F2i	CATCCATACTCAGGG	*dsrB*	1758-1772	1	0	14	0	11	0	0	0	0	0	Lever *et al*., 2013
DSR1728Fmix		*dsrB*	1762-1776	77	90	100	91	100	88	98	95	100	100	Steger *et al*., 2011
DSR1728FmixA	CAYACCCAGGGNTGG	*dsrB*	1762-1776	8	43	77	65	89	71	66	42	56	50	Steger *et al*., 2011
DSR1728FmixB	CAYACBCAAGGNTGG	*dsrB*	1762-1776	24	17	90	7	89	2	9	26	0	0	Steger *et al*., 2011
DSR1728FmixC	CATACDCAGGGHTGG	*dsrB*	1762-1776	9	15	43	6	37	3	2	12	33	0	Steger *et al*., 2011
DSR1728FmixD	CACACDCAGGGNTGG	*dsrB*	1762-1776	12	12	58	10	62	6	21	16	10	50	Steger *et al*., 2011
DSR1728FmixE	CATACHCAGGGNTAY	*dsrB*	1762-1776	24	3	80	4	92	6	0	0	0	0	Steger *et al*., 2011
dsrB F1a-h		*dsrB*	1762-1776	8	35	86	44	89	45	54	31	49	42	Lever *et al*., 2013
dsrB F1a	CACACCCAGGGCTGG	*dsrB*	1762-1776	1	22	59	30	74	30	46	17	21	42	Lever *et al*., 2013
dsrB F1b	CATACTCAGGGCTGG	*dsrB*	1762-1776	1	3	27	1	21	1	1	2	0	0	Lever *et al*., 2013
dsrB F1c	CATACCCAGGGCTGG	*dsrB*	1762-1776	1	8	53	11	65	14	4	6	21	0	Lever *et al*., 2013
dsrB F1d	CACACTCAAGGTTGG	*dsrB*	1762-1776	1	1	26	0	11	0	1	2	0	0	Lever *et al*., 2013
dsrB F1e	CACACACAGGGATGG	*dsrB*	1762-1776	1	0	6	0	10	0	0	0	8	0	Lever *et al*., 2013
dsrB F1f	CACACGCAGGGATGG	*dsrB*	1762-1776	1	0	4	1	5	0	0	3	0	0	Lever *et al*., 2013
dsrB F1g	CACACGCAGGGGTGG	*dsrB*	1762-1776	1	1	3	1	4	0	2	1	0	0	Lever *et al*., 2013
dsrB F1h	CATACGCAAGGTTGG	*dsrB*	1762-1776	1	0	3	0	3	0	1	0	0	0	Lever *et al*., 2013
dsr1905BR	RTGHACSGCGCCGCACAT	*dsrB*	1909-1926	12	25	52	29	69	33	31	13	36	0	Giloteaux *et al*., 2010
dsrB 4RSI1a-f		*dsrB*	2107-2123	1	62	97	*n.a.*	*n.a.*	73	39	60	50	20	Lever *et al*., 2013
dsrB 4RSI1a	CAGTTACCGCAGTACAT	*dsrB*	2107-2123	1	17	58	*n.a.*	*n.a.*	19	11	0	50	20	Lever *et al*., 2013
dsrB 4RSI1b	CAGTTACCGCAGAACAT	*dsrB*	2107-2123	1	12	61	*n.a.*	*n.a.*	19	0	0	0	0	Lever *et al*., 2013
dsrB 4RSI1c	CAGTTGCCGCAGTACAT	*dsrB*	2107-2123	1	15	63	*n.a.*	*n.a.*	12	25	20	0	0	Lever *et al*., 2013
dsrB 4RSI1d	CAGTTTCCGCAGTACAT	*dsrB*	2107-2123	1	1	37	*n.a.*	*n.a.*	0	4	0	0	0	Lever *et al*., 2013
dsrB 4RSI1e	CAGTTGCCGCAGAACAT	*dsrB*	2107-2123	1	17	60	*n.a.*	*n.a.*	24	0	40	0	0	Lever *et al*., 2013
dsrB 4RSI1f	CAGTTTCCACAGAACAT	*dsrB*	2107-2123	1	0	14	*n.a.*	*n.a.*	0	0	0	0	0	Lever *et al*., 2013
DSRAB_R	GTAGCAGTTWCCGCAGWACATG	*dsrB*	2111-2136	4	20	82	*n.a.*	*n.a.*	25	11	0	0	20	Schmalenberger *et al*., 2007
DSR4R	GTGTAGCAGTTACCGCA	*dsrB*	2113-2129	1	28	80	*n.a.*	*n.a.*	31	29	0	0	20	Wagner *et al*., 1998
DSR4Rmix (+a-c)		*dsrB*	2113-2129	5	57	94	*n.a.*	*n.a.*	67	46	20	0	40	Loy *et al*., 2004
DSR4Ra	GTGTAACAGTTTCCACA	*dsrB*	2113-2129	1	1	6	*n.a.*	*n.a.*	0	0	0	0	20	Loy *et al*., 2004
DSR4Rb	GTGTAACAGTTACCGCA	*dsrB*	2113-2129	1	2	37	*n.a.*	*n.a.*	3	0	0	0	0	Loy *et al*., 2004
DSR4Rc	GTGTAGCAGTTKCCGCA	*dsrB*	2113-2129	2	27	83	*n.a.*	*n.a.*	33	18	20	0	0	Loy *et al*., 2004
DSR4Rmix (+a-e)		*dsrB*	2113-2129	7	70	94	*n.a.*	*n.a.*	80	54	20	0	100	Zverlov *et al*., 2005
DSR4Rd	GTGTAGCAGTTACCACA	*dsrB*	2113-2129	1	9	51	*n.a.*	*n.a.*	11	7	0	0	0	Zverlov *et al*., 2005
DSR4Re	GTGTAACAGTTACCACA	*dsrB*	2113-2129	1	4	17	*n.a.*	*n.a.*	3	0	0	0	60	Zverlov *et al*., 2005
DSR4Rmix (+a-g)		*dsrB*	2113-2129	10	77	94	*n.a.*	*n.a.*	83	68	60	0	100	Pester *et al*., 2010
DSR4Rf	GTATAGCARTTGCCGCA	*dsrB*	2113-2129	2	5	42	*n.a.*	*n.a.*	3	14	0	0	0	Pester *et al*., 2010
DSR4Rg	GTGAAGCAGTTGCCGCA	*dsrB*	2113-2129	1	2	34	*n.a.*	*n.a.*	0	0	40	0	0	Pester *et al*., 2010
DSR698R	GTGTARCAGTTRCCRCA	*dsrB*	2113-2129	8	71	91	*n.a.*	*n.a.*	83	50	40	0	80	Suzuki *et al*., 2005
P93-R	GGGCACATSGTGTAGCAGTTACCGCA	*dsrB*	2113-2138	2	17	61	*n.a.*	*n.a.*	20	11	0	0	20	Karkhoff-Schweizer *et al*., 1995

[a] Recommended primers are highlighted in gray.

[b] Data indicate primer coverage of all full length reductive bacterial type *dsrAB* sequences (n=115); 0 MM, no mismatches; 1 wMM, one weighted mismatch.

[c] Data indicate primer coverage of all core reductive bacterial type *dsrAB* sequences (n=1110); 0 MM, no mismatches; 1 wMM, one weighted mismatch; n.a., not applicable for primers binding at the target sites or outside the amplification region of DSR1F/DSR4R.

[d] Primer coverage of full length/core dataset *dsrAB* sequences in higher taxonomic clusters. DpS, *Deltaproteobacteria* supercluster (n=75/709); Fg, *Firmicutes* group (n=28/180); ES1, Environmental supercluster 1 (n=5/170); NsS, *Nitrospirae* supercluster (n=2/39); AgC, *Archaeoglobus* cluster (n=5/12). The larger core dataset is used for primers binding within the DSR1F/DSR4R region.

[e] Position is relative to *Desulfovibrio vulgaris* Hildenborough *dsrAB* (NC_002937, 449888..452365).

[f] Degeneracy is given as the number of oligonucleotides that comprise the primer.

Supplementary Table S2

Primers targeting oxidative bacterial type *dsrAB*[a]					full length *dsrAB*[b] (%)		core dataset *dsrAB*[c] (%)		
Name	**Sequence (5'-3')**	**Target gene**	**Position**[d]	**Deg.**[e]	**0 MM**	**1 wMM**	**0 MM**	**1 wMM**	**Reference**
rDSR1Fmix		*dsrA*	169-184	80	97	100	*n.a.*	*n.a.*	Loy *et al.*, 2009
rDSR1Fa	AARGGNTAYTGGAARG	*dsrA*	169-184	32	69	98	*n.a.*	*n.a.*	Loy *et al.*, 2009
rDSR1Fb	TTYGGNTAYTGGAARG	*dsrA*	169-184	32	0	69	*n.a.*	*n.a.*	Loy *et al.*, 2009
rDSR1Fc	ATGGGNTAYTGGAARG	*dsrA*	169-184	16	27	71	*n.a.*	*n.a.*	Loy *et al.*, 2009
rDSRA240F	GGNTAYTGGAARGGNGG	*dsrA*	172-188	64	97	100	*n.a.*	*n.a.*	Lenk *et al*., 2011
PGdsrAF	CAYGGBCAGACCGGBRAYATYATG	*dsrA*	379-402	144	39	56	38	61	Mori *et al*., 2010
dsrA 625F	TTCAAGTTCTCCGGCTGCSCNAAYGACTG	*dsrA*	625-653	16	2	26	1	21	Luo *et al*., 2011
PGdsrAR	RCAGTGCATRCAKCGHACRCA	*dsrA*	850-870	48	60	81	57	89	Mori *et al*., 2010
dsrA 877R	CGTTSANRCAGTGCATGCAGCG	*dsrA*	856-877	16	39	79	46	86	Luo *et al*., 2011
DSR874F	TGYATGCAYTGYYTVAAYG	*dsrA*	859-877	96	71	100	70	100	Loy *et al.*, 2009
DSR1728Fmix		*dsrB*	1684-1698	77	90	100	95	99	Steger *et al*., 2011
DSR1728FmixA	CAYACCCAGGGNTGG	*dsrB*	1684-1698	8	56	74	65	82	Steger *et al*., 2011
DSR1728FmixB	CAYACBCAAGGNTGG	*dsrB*	1684-1698	24	18	97	14	98	Steger *et al*., 2011
DSR1728FmixC	CATACDCAGGGHTGG	*dsrB*	1684-1698	9	6	27	6	28	Steger *et al*., 2011
DSR1728FmixD	CACACDCAGGGNTGG	*dsrB*	1684-1698	12	10	63	9	68	Steger *et al*., 2011
DSR1728FmixE	CATACHCAGGGNTAY	*dsrB*	1684-1698	24	0	74	0	82	Steger *et al*., 2011
dsrB F1a-h		*dsrB*	1684-1698	8	47	90	43	89	Lever *et al*., 2013
dsrB F1a	CACACCCAGGGCTGG	*dsrB*	1684-1698	1	35	63	32	70	Lever *et al*., 2013
dsrB F1b	CATACTCAGGGCTGG	*dsrB*	1684-1698	1	0	18	1	13	Lever *et al*., 2013
dsrB F1c	CATACCCAGGGCTGG	*dsrB*	1684-1698	1	10	53	9	61	Lever *et al*., 2013
dsrB F1d	CACACTCAAGGTTGG	*dsrB*	1684-1698	1	0	21	1	11	Lever *et al*., 2013
dsrB F1e	CACACACAGGGATGG	*dsrB*	1684-1698	1	0	11	0	13	Lever *et al*., 2013
dsrB F1f	CACACGCAGGGATGG	*dsrB*	1684-1698	1	2	8	1	7	Lever *et al*., 2013
dsrB F1g	CACACGCAGGGGTGG	*dsrB*	1684-1698	1	0	6	0	5	Lever *et al*., 2013
dsrB F1h	CATACGCAAGGTTGG	*dsrB*	1684-1698	1	0	8	0	5	Lever *et al*., 2013
dsrB 4RSI2a-h		*dsrB*	2011-2027	1	44	90	*n.a.*	*n.a.*	Lever *et al*., 2013
dsrB 4RSI2a	CAGGCGCCGCAGCAGAT	*dsrB*	2011-2027	1	23	60	*n.a.*	*n.a.*	Lever *et al*., 2013
dsrB 4RSI2b	CAGGCGCCGCAGCACAC	*dsrB*	2011-2027	1	8	15	*n.a.*	*n.a.*	Lever *et al*., 2013
dsrB 4RSI2c	CATGCTCCGCAGCAGAT	*dsrB*	2011-2027	1	2	13	*n.a.*	*n.a.*	Lever *et al*., 2013
dsrB 4RSI2d	CACGCGCCGCAAGCCAC	*dsrB*	2011-2027	1	3	3	*n.a.*	*n.a.*	Lever *et al*., 2013
dsrB 4RSI2e	CATGCACCACAACAAAT	*dsrB*	2011-2027	1	2	13	*n.a.*	*n.a.*	Lever *et al*., 2013
dsrB 4RSI2f	CAGGCACCACAGCAGAT	*dsrB*	2011-2027	1	0	18	*n.a.*	*n.a.*	Lever *et al*., 2013
dsrB 4RSI2g	CAGGCTCCGCAGCAGAT	*dsrB*	2011-2027	1	5	44	*n.a.*	*n.a.*	Lever *et al*., 2013
dsrB 4RSI2h	CAGGCGCCGCAGTACAT	*dsrB*	2011-2027	1	2	42	*n.a.*	*n.a.*	Lever *et al*., 2013
rDSR4Rmix		*dsrB*	2017-2033	96	100	100	*n.a.*	*n.a.*	Loy *et al.*, 2009
rDSR4Ra	CCRAARCAIGCNCCRCA	*dsrB*	2017-2033	32	23	50	*n.a.*	*n.a.*	Loy *et al.*, 2009
rDSR4Rb	GGRWARCAIGCNCCRCA	*dsrB*	2017-2033	64	77	100	*n.a.*	*n.a.*	Loy *et al.*, 2009
rDSRB808R	CCDCCNACCCADATNGC	*dsrB*	2011-2027	144	69	79	*n.a.*	*n.a.*	Lenk *et al*., 2011

[a] Recommended primers are highlighted in gray.

[b] Data indicate primer coverage of all full length oxidative bacterial type *dsrAB* sequences (n=62); 0 MM, no mismatches; 1 wMM, one weighted mismatch.

[c] Data indicate primer coverage of core dataset oxidative bacterial type dsrAB sequences (n=159); 0 MM, no mismatches; 1 wMM, one weighted mismatch; n.a., not applicable for primers binding at the target sites or outside the amplification region of rDSR1F/rDSR4R.

[d] Position is relative to *Allochromatium vinosum dsrAB* (NC_013851, 1439735..1442113).

[e] Degeneracy is given as the number of oligonucleotides that comprise the primer.

Supplementary Table S3

Primer pairs targeting reductive bacterial type *dsrAB* [a]				full length *dsrAB* [b] (%)		core dataset *dsrAB* [c] (%)		Phylogenetic clusters [d] (%)					
Primers	**Target gene**	**Position** [e]	**Length** [f]	**0 MM**	**1 wMM**	**0 MM**	**1 wMM**	**DpS**	**Fg**	**ES1**	**NsS**	**AgC**	**Reference**
DSR1Fmix/DSR1334R	*dsrA*	187-1115	929	25	50	n.a.	n.a.	39	0	0	0	0	Santillano *et al*., 2010
DSR1Fmix/Del1075R	*dsrA*	187-1132	946	34	62	n.a.	n.a.	51	0	20	0	0	Gittel *et al*., 2009
DSR1Fmix/DSR4Rmix	*dsrAB*	187-2129	1943	47	92	n.a.	n.a.	39	7	0	0	40	Pester *et al*., 2010
DSRAB_F/DSRAB_R	*dsrAB*	187-2136	1950	9	38	n.a.	n.a.	13	0	0	0	0	Schmalenberger *et al*., 2007
DSR1Fmix/DSRQP3R	*dsrA*	187-302	116	13	52	n.a.	n.a.	19	0	20	0	0	Akob *et al*., 2012
DSR1Fmix/DSRQ2R	*dsrA*	187-309	123	3	13	n.a.	n.a.	5	0	0	0	0	Chin *et al*., 2007
DSR1-F+/DSR-R	*dsrA*	187-407	221	13	34	n.a.	n.a.	20	0	0	0	0	Kondo *et al*., 2004
DSR1Fmix/DSR5R	*dsrA*	187-430	244	2	3	n.a.	n.a.	3	0	0	0	0	Wagner *et al*., 1998
DSR67F/DSR698R	*dsrAB*	189-2129	1941	37	91	n.a.	n.a.	45	18	20	0	40	Suzuki *et al*., 2005
RH1-dsr-F/RH3-dsr-R	*dsrAB*	245-408	164	3	18	1	10	2	0	0	0	0	Ben-Dov *et al*., 2007
dsr_290F/RH3-dsr-R'	*dsrAB*	276-408	133	0	1	0	2	0	0	0	0	0	Pereyra *et al*., 2010
dsr_290F/dsrA_660R	*dsrAB*	276-626	351	0	0	0	1	0	0	0	0	0	Pereyra *et al*., 2010
1F1/1R1	*dsrAB*	604-1778	1175	13	47	12	59	34	39	14	0	0	Dhillon *et al*., 2003
dsr619AF/dsr1905BR	*dsrAB*	623-1926	1304	10	36	6	36	8	4	0	3	0	Giloteaux *et al*., 2010
P94-F/P93-R	*dsrAB*	709-2138	1430	3	8	n.a.	n.a.	4	0	0	0	20	Karkhoff-Schweizer *et al*., 1995
DSR2MF/DSR4Rmix	*dsrAB*	717-2129	1413	10	29	n.a.	n.a.	15	0	0	0	20	Akob *et al*., 2012
DSR2F/DSR4Rmix	*dsrAB*	717-2129	1413	10	17	n.a.	n.a.	13	0	0	0	20	Wagner *et al*., 1998
DSRp2060F/DSR4Rmix	*dsrB*	1752-2129	378	13	55	n.a.	n.a.	20	0	0	0	0	Geets *et al*., 2005
dsrB F2a-i/4RSI1b,e	*dsrB*	1758-2123	366	7	68	n.a.	n.a.	11	0	0	0	0	Lever *et al*., 2013
dsrB F1a-h/4RSI1a-f	*dsrB*	1762-2123	362	27	83	n.a.	n.a.	36	14	0	0	0	Lever *et al*., 2013
DSR1728mix/DSR4Rmix	*dsrB*	1762-2129	368	70	94	n.a.	n.a.	72	64	60	0	100	Steger *et al*., 2011

[a] Coverage values for primer pairs published using DSR1F or DSR4R are calculated using the most up to date version of the primer mix. Recommended primer pairs are highlighted in gray.

[b] Data indicate primer coverage of all full length reductive bacterial type *dsrAB* sequences (n=115); 0 MM, no mismatches; 1 wMM, one weighted mismatch.

[c] Data indicate primer coverage of all core reductive bacterial type *dsrAB* sequences (n=1110); 0 MM, no mismatches; 1 wMM, one weighted mismatch; n.a., not applicable for primers binding at the target sites or outside the amplification region of DSR1F/DSR4R.

[d] Primer coverage of full length/core dataset *dsrAB* sequences in higher taxonomic clusters. DpS, *Deltaproteobacteria* supercluster (n=75/709); Fg, *Firmicutes* group (n=28/180); ES1, Environmental supercluster 1 (n=5/170); NsS, Nitrospirae supercluster (n=2/39); AgC, *Archaeoglobus* cluster (n=5/12). The larger core dataset is used for primers binding within the DSR1F/DSR4R region.

[e] Position is relative to *Desulfovibrio vulgaris* Hildenborough *dsrAB* (NC_002937, 449888..452365).

[f] Expected length of the PCR amplicon.

Supplementary Table S4

Primer pairs targeting oxidative bacterial type *dsrAB*[a]				full length *dsrAB*[b] (%)		core dataset *dsrAB*[c] (%)		
Name	**Target gene**	**Position**[d]	**Length**[e]	**0 MM**	**1 wMM**	**0 MM**	**1 wMM**	**Reference**
rDSR1Fmix/rDSR4Rmix	*dsrAB*	169-2033	1865	97	100	n.a.	n.a.	Loy *et al* ., 2009
rDSRA240F/rDSRB808R	*dsrAB*	172-2027	1856	69	79	n.a.	n.a.	Lenk *et al* ., 2011
PGdsrAF/PGdsrAR	*dsrA*	379-870	492	32	53	29	57	Mori *et al* ., 2010
dsrA 625F/dsrA 877R	*dsrA*	625-877	253	2	26	1	21	Luo *et al* ., 2011
DSR874F/rDSR4Rmix	*dsrAB*	859-2033	1175	71	100	n.a.	n.a.	Loy *et al* ., 2009
dsrB F1a-h/4RSI2a-h	*dsrB*	1684-2027	344	29	82	n.a.	n.a.	Lever *et al* ., 2013
DSR1728mix/rDSR4Rmix	*dsrB*	1684-2033	350	90	100	n.a.	n.a.	Steger *et al* ., 2011

[a] Recommended primer pairs are highlighted in gray.

[b] Data indicate primer coverage of all full length reverse *dsrAB* sequences (n=62); 0 MM, no mismatches; 1 wMM, one weighted mismatch.

[c] Data indicate primer coverage of core dataset reverse *dsrAB* sequences (n=159); 0 MM, no mismatches; 1 wMM, one weighted mismatch; n.a., not applicable for primers binding at the target sites or outside the amplification region of rDSR1F/rDSR4R.

[d] Position is relative to *Allochromatium vinosum dsrAB* (NC_013851, 1439735..1442113).

[e] Expected length of the PCR amplicon.