***Supplementary information for***

**Metagenomic insights into sulfate-reducing bacteria in a revegetated acidic mine wasteland**

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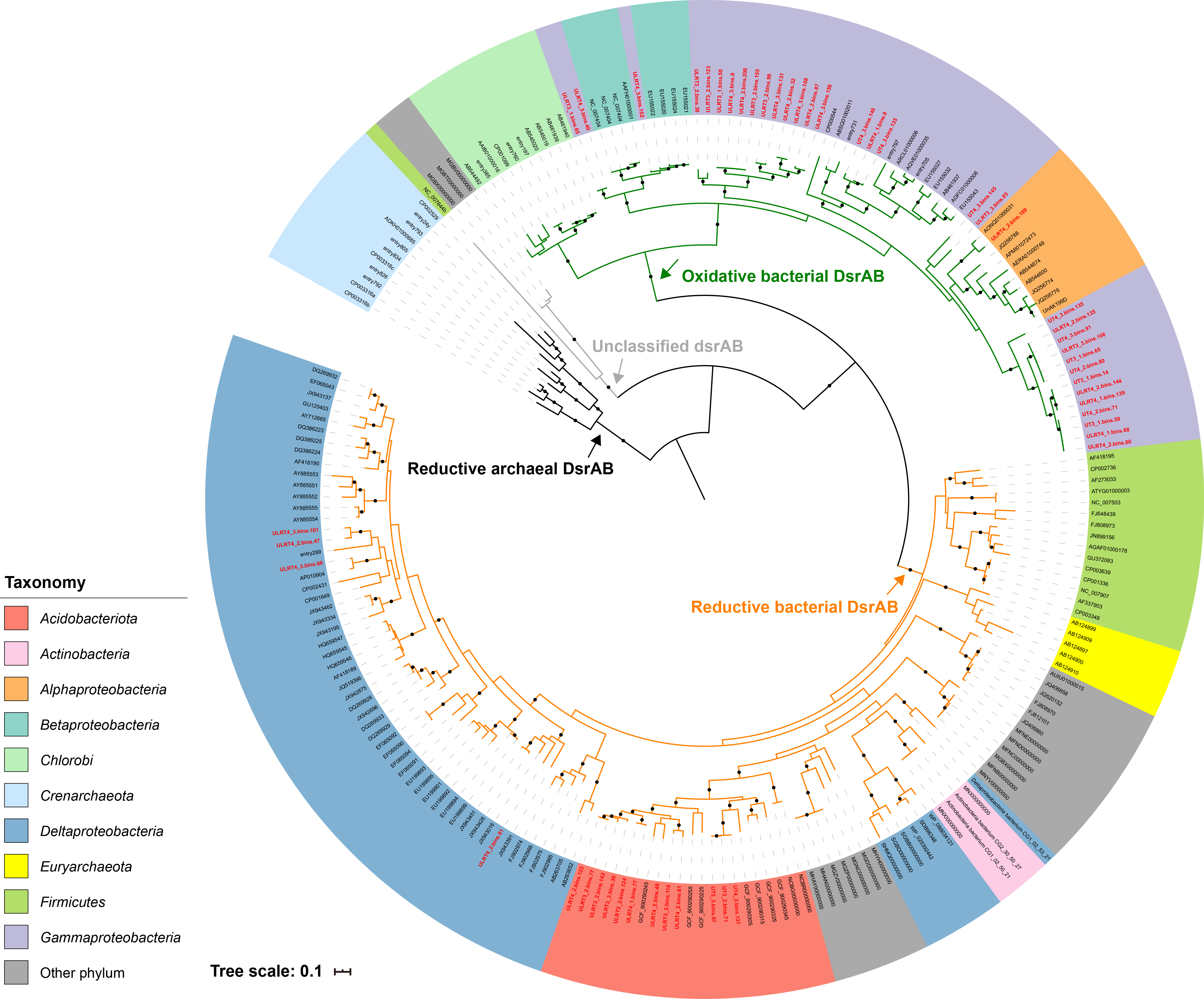
**Supplementary Methods**

*Sequence alignment of DsrD and DsrT proteins*

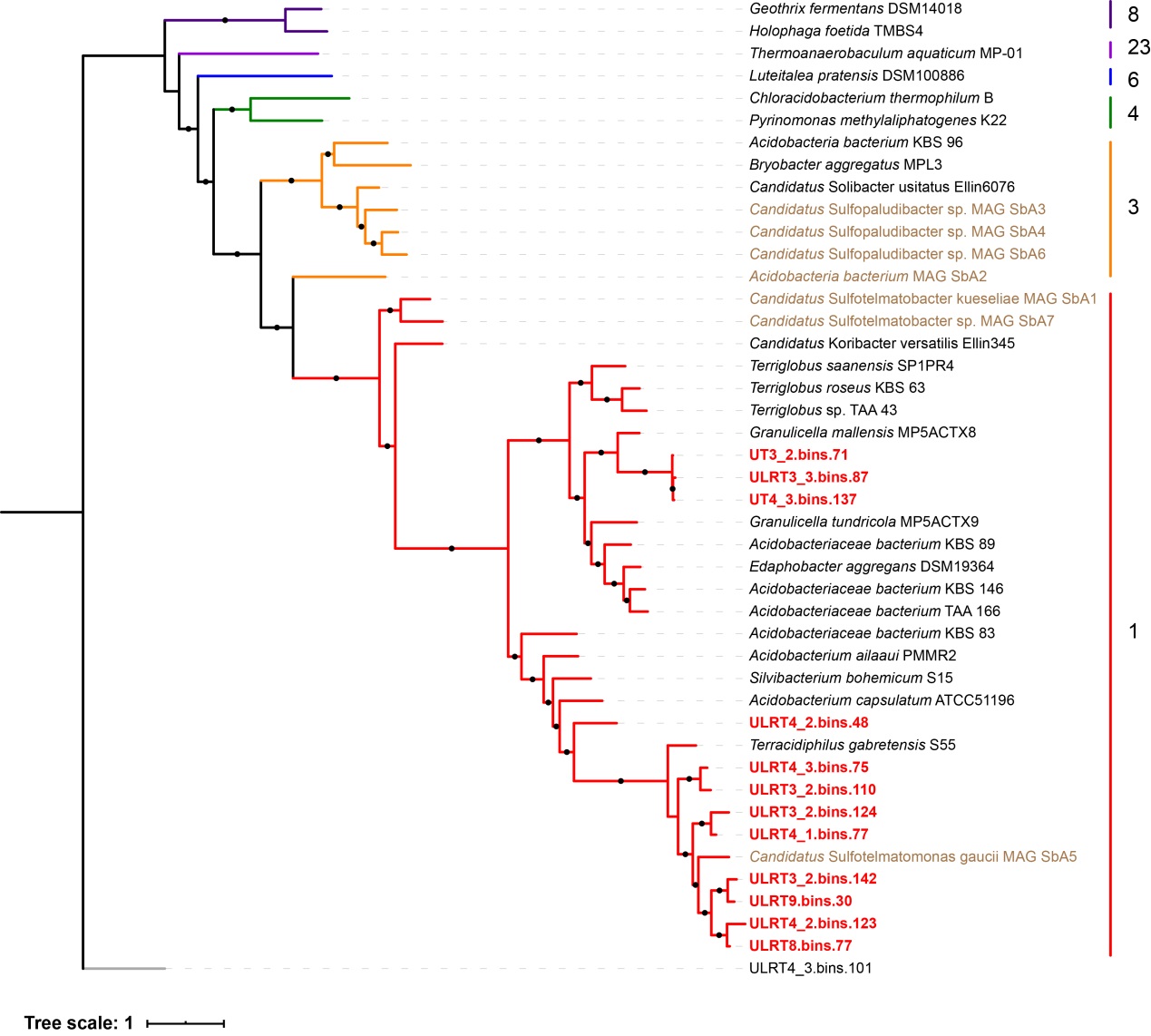
The DsrD and DsrT protein sequences identified in the genomic bins reported in this study were aligned along with the reference sequences respectively, using ClustalW with slow/accurate setting parameters (https://www.genome.jp/tools-bin/clustalw). The alignments were manual corrected and later visualized by ESPript 3.0 [1]. The conserved residues were highlighted.

*Calculation of the average amino acid identity (AAI)*

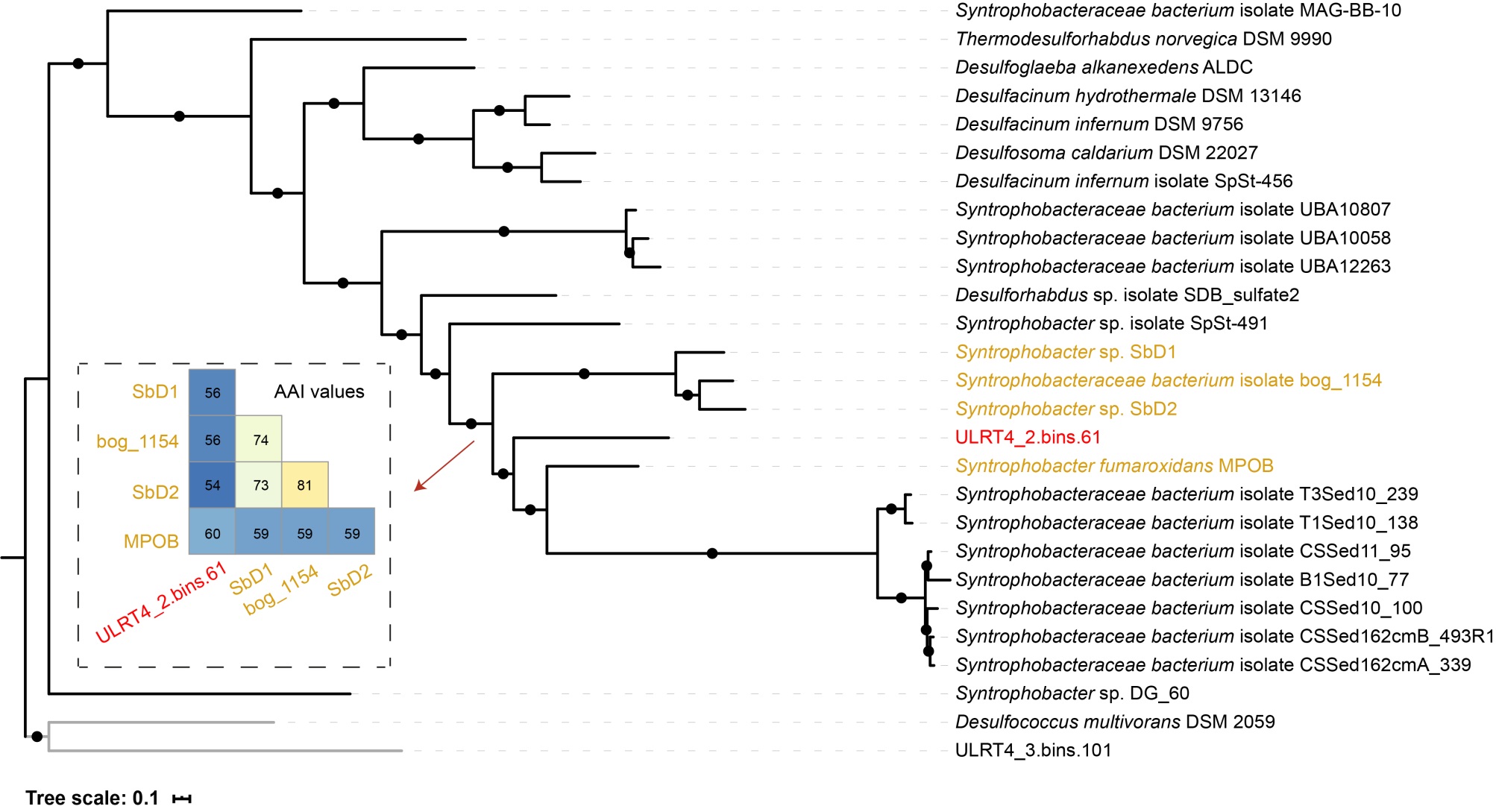
The AAI values between five genomes from *Syntrophobacteraceae* family were calculated by AAI calculator (<http://enve-omics.ce.gatech.edu/aai/index>) with default parameters. The reciprocal best hits (two-way AAI) between two genomic datasets of proteins were used for further comparisons.



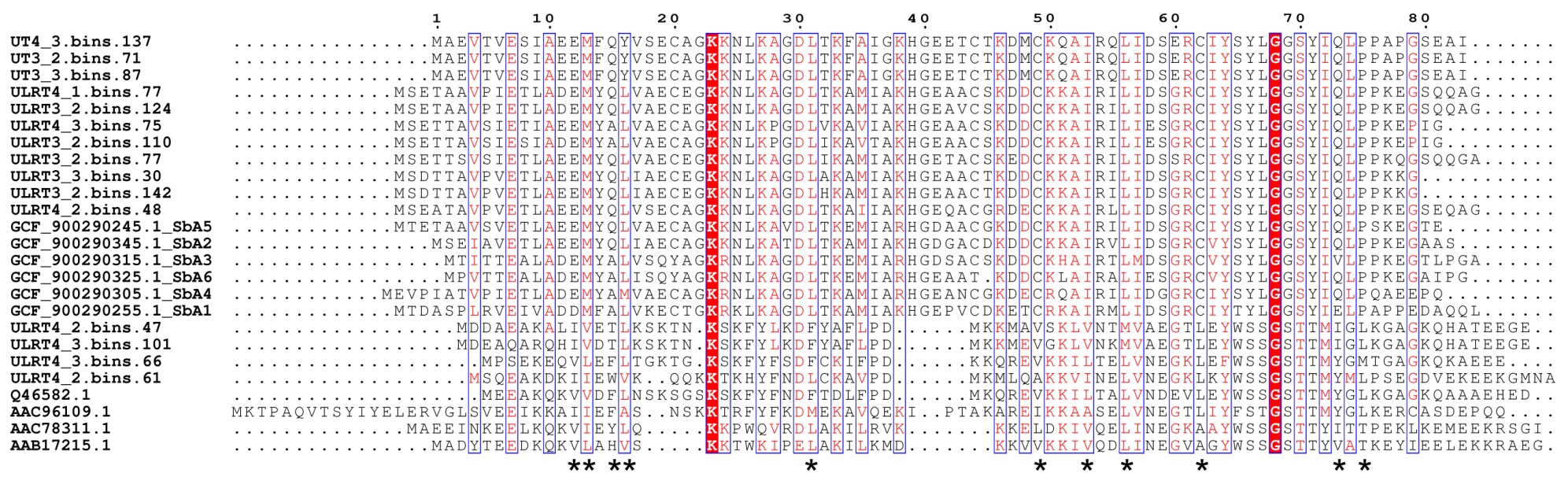
**Figure S1.** Phylogenic analysis of dissimilatory sulfite reductases DsrAB. Concatenated DsrAB protein sequences identified in this study are marked in bold red. Assignment of oxidative/reductive, bacterial/archaeal type DsrAB was according to previous studies [2, 3]. Bootstrap values were based on 100 replicates, and only bootstrap values higher than 70% are shown with black circles.



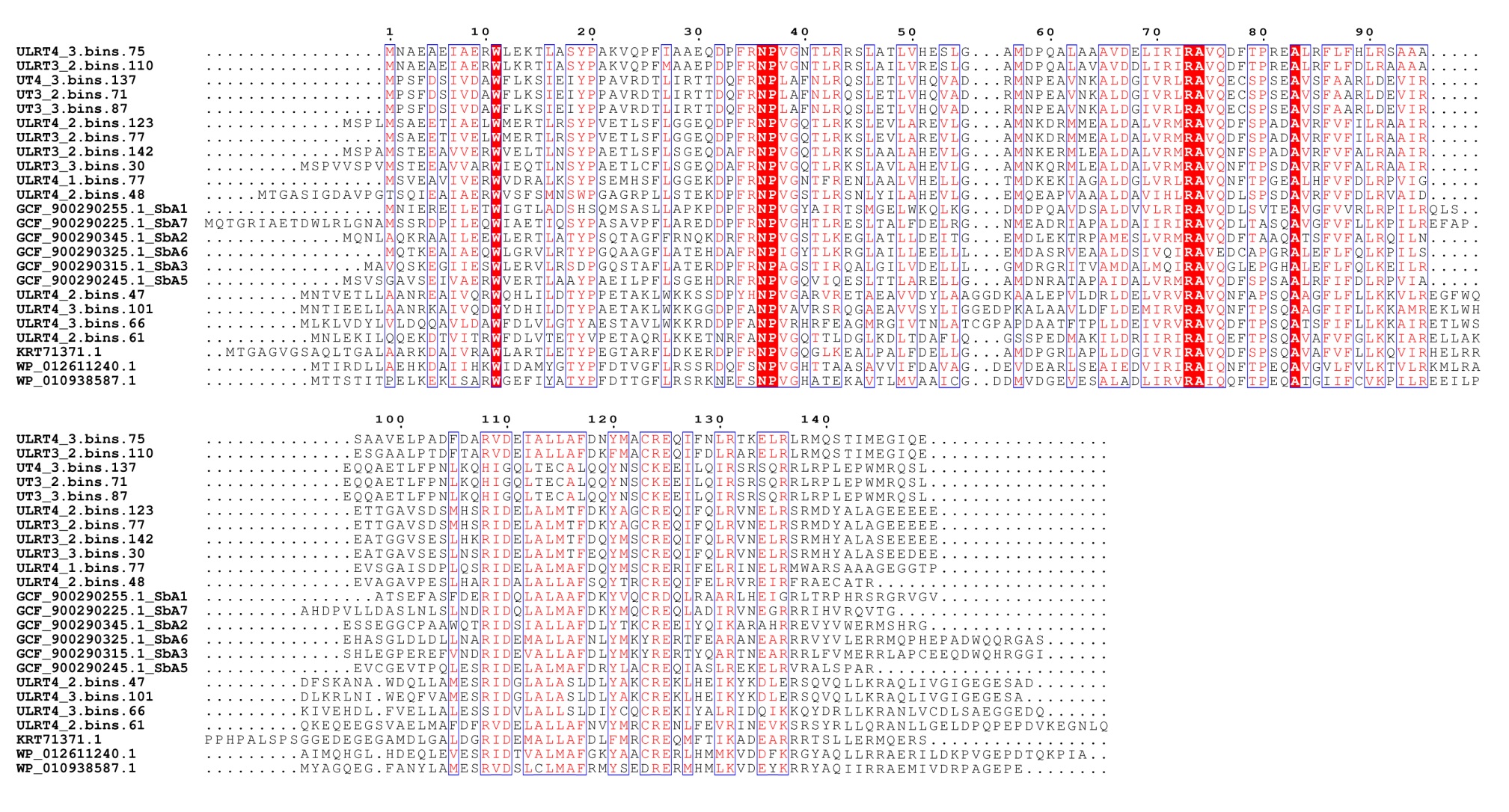
**Figure S2.** Phylogenic analysis of the genomes from *Acidobacteria* phylum. The maximum-likelihood phylogenetic tree was constructed based on a concatenated dataset of 400 universally conserved marker proteins using PhyloPhlAn. Subdivisions are indicated to the right of the tree. The 12 metagenome-assembled genomes (MAGs) harboring sequences of *dsrAB* genes reported in this study are marked in bold red. The 7 MAGs previously reported to have a dissimilatory sulfur metabolism potential are marked in brown. Bootstrap values were based on 100 replicates, and percentages higher than 70% are shown with black circles. The MAG (ULRT4\_3.bins.101) from *Deltaproteobacteria* was used as an outgroup.



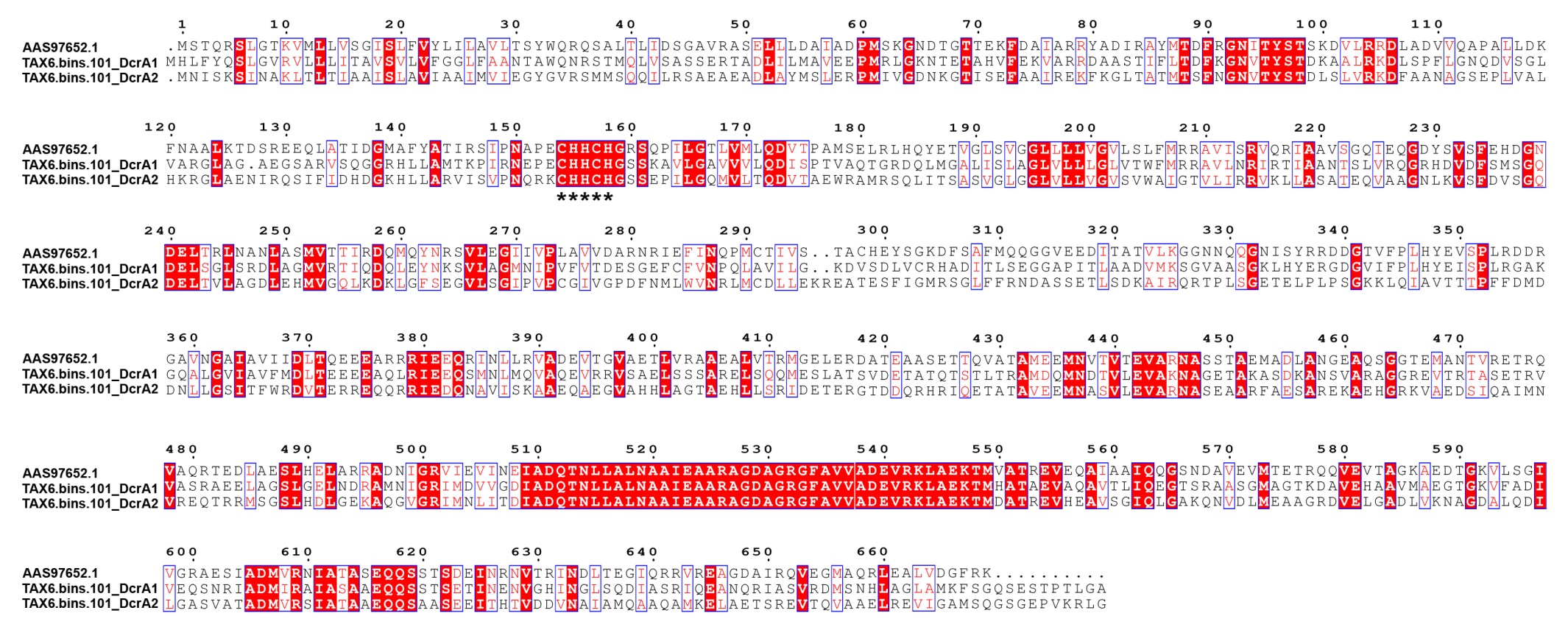
**Figure S3.** Phylogenic analysis of the genomes from *Syntrophobacteraceae* family. The maximum-likelihood phylogenetic tree was constructed using PhyloPhlAn. The *dsrAB*-containing MAG reported in this study is marked in bold red. The four reference genomes of the two closest genera to the MAG are marked in brown. The average amino acid identity (AAI) values between the 5 closest genomes are shown in the inset. Bootstrap values were based on 100 replicates, and percentages higher than 70% are shown with black circles. The genomes (ULRT4\_3.bins.101 and *Desulfococcus multivorans* DSM 2059) from *Deltaproteobacteria* were used as the outgroup.



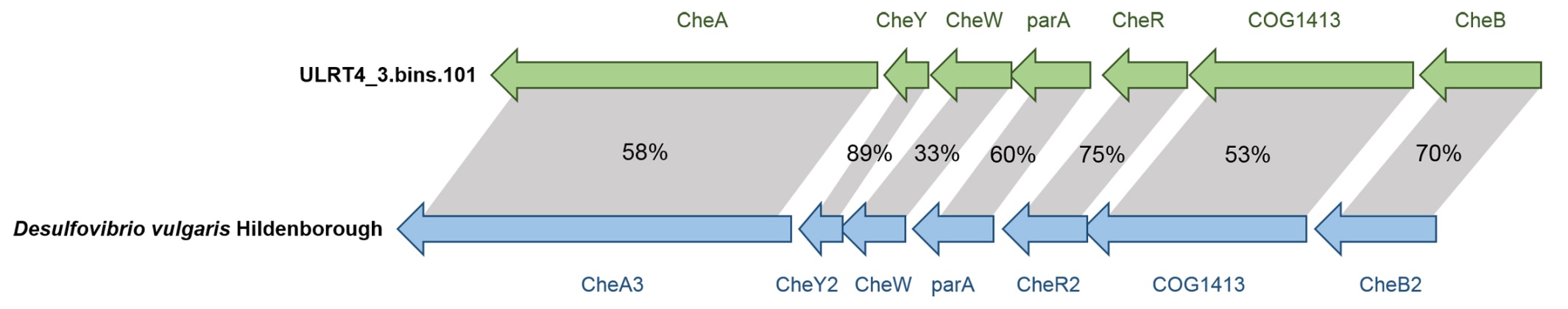
**Figure S4.** Sequence alignment of DsrD proteins identified in this study with reference sequences. Positions of conserved, hydrophobic residues in the DsrD family are marked with asterisks [4]. Highly conserved residues of the same type are highlighted in red background.



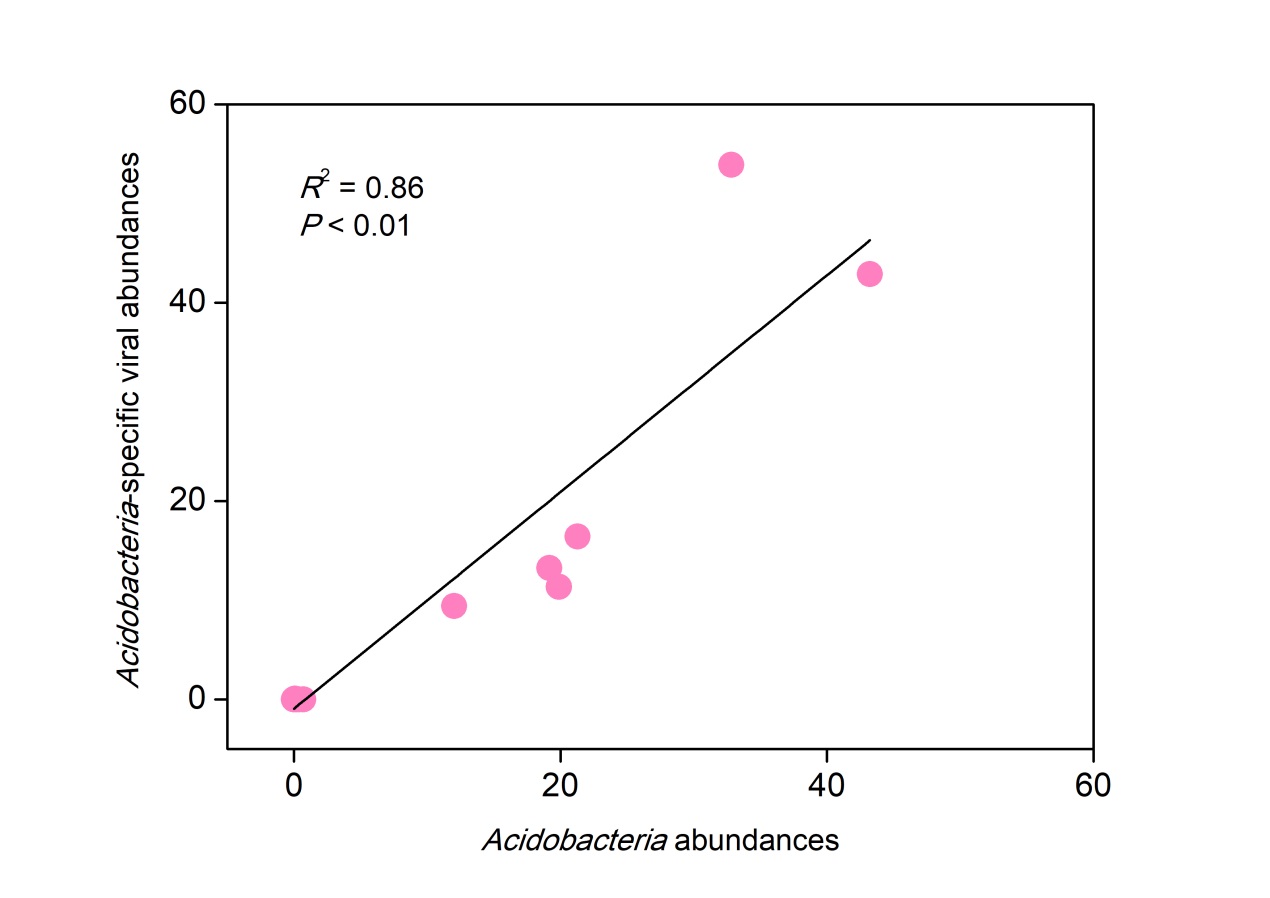
**Figure S5.** Sequence alignment of DsrT proteins identified in this study with reference sequences. Highly conserved residues of the same type are highlighted in red background.



**Figure S6**. Sequence alignment of DcrA proteins identified in this study with reference sequence DcrA identified in *Desulfovibrio vulgaris* str. Hildenborough. Specific sequences, CHHCH, corresponding to a consensus c-type heme-binding site are marked with asterisks [5]. Highly conserved residues of the same type are highlighted in red background.



**Figure S7.** Operons encoding the *cheA* chemotaxis gene in ULRT4\_3.bins.101 and *D. vulgaris* [6]. Arrows represented the coding regions. The percentages in grey shadings indicated sequence similarities.



**Figure S8.** Virus/host abundance ratio for *Acidobacteria* with a dissimilatory sulphur metabolism. *Acidobacteria* abundance and the abundance of their viruses (both calculated as the mean coverage depth from reads mapping, normalized by the number of reads in each metagenomic dataset) are plotted for each sample. Pearson correlation analysis was used to correlate the host and viral abundances.

**Supplementary References**

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