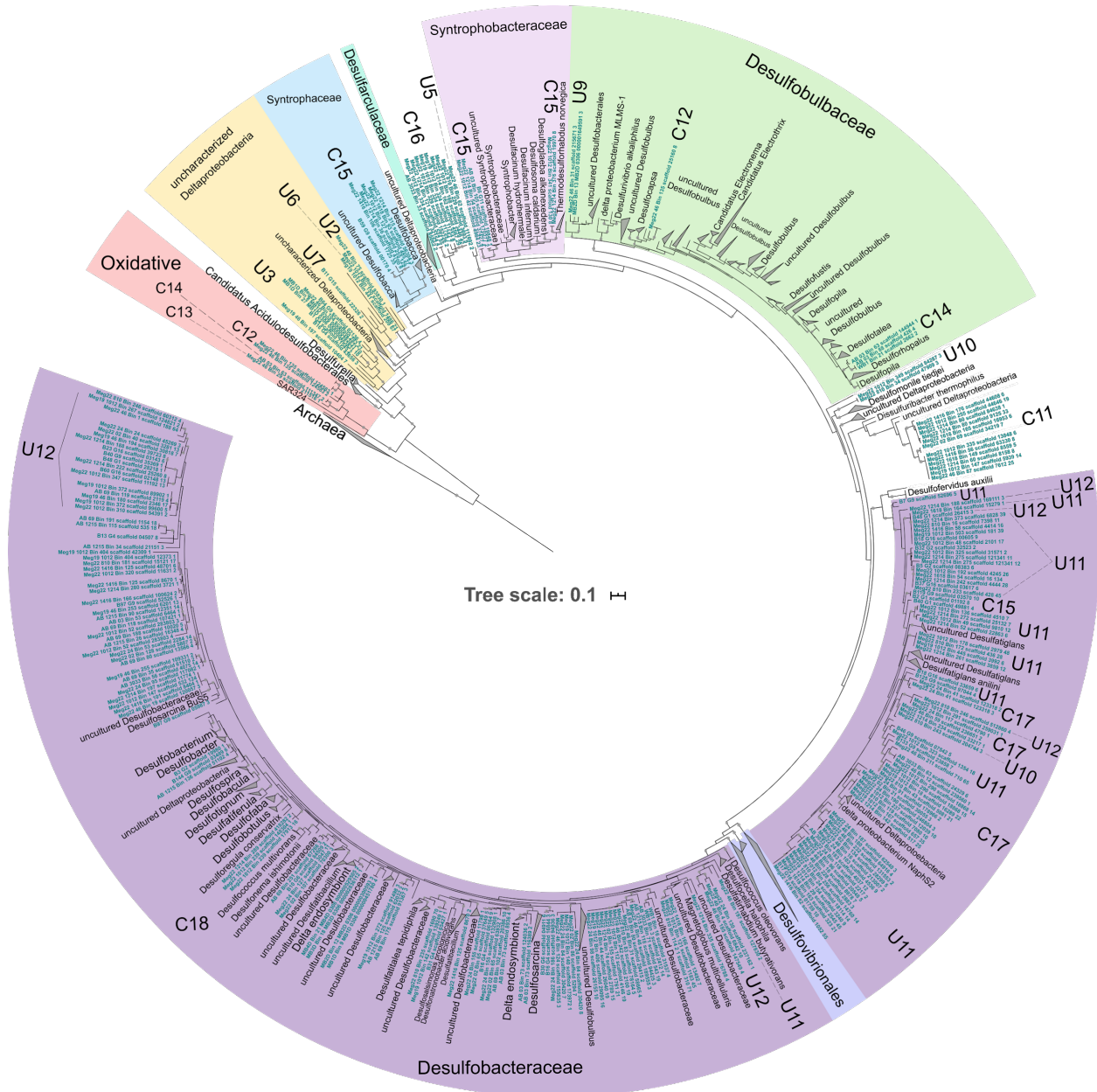


Supplementary Figures

Tree scale: 0.1

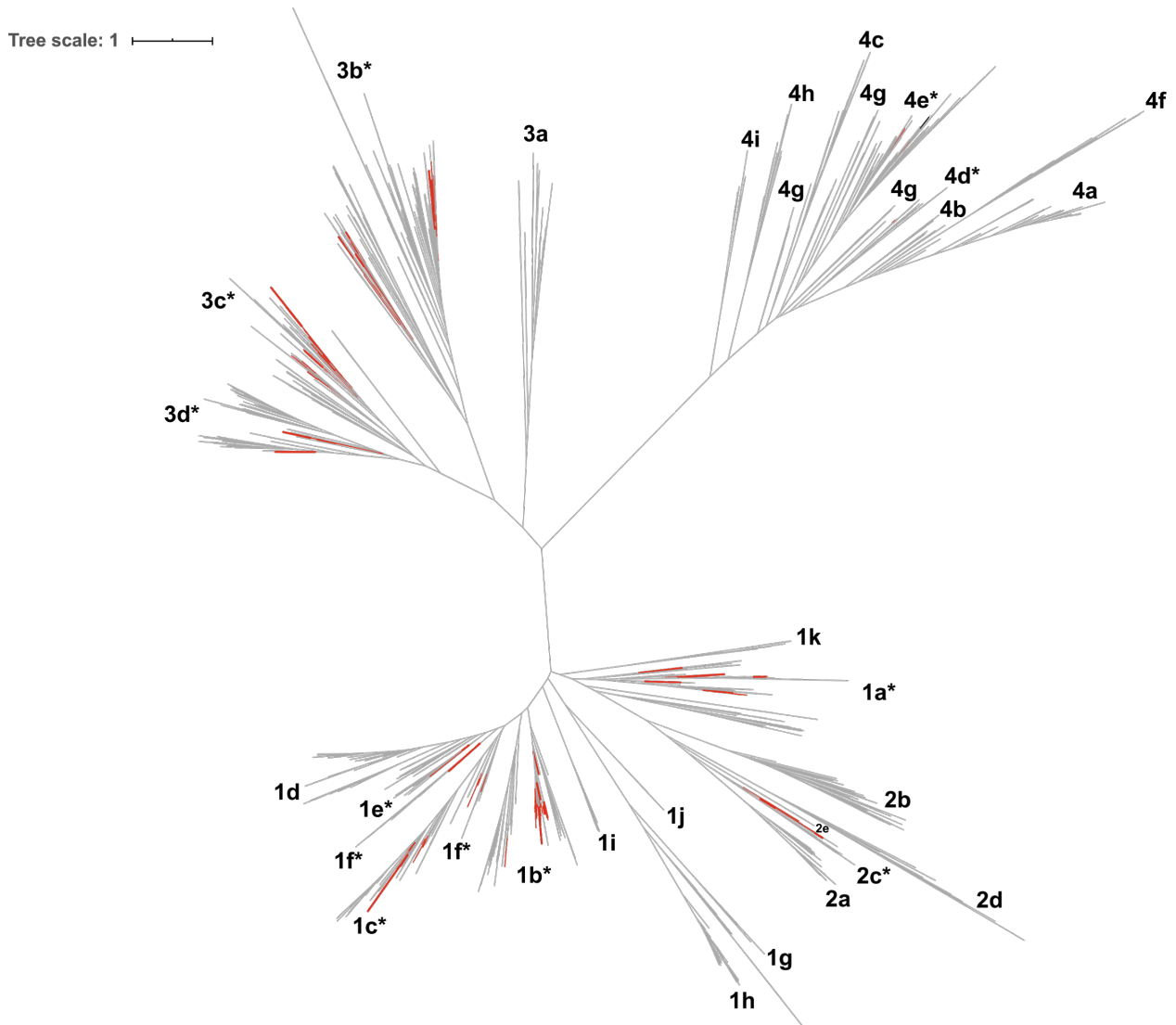


Supplementary Figure 1. 16S rRNA maximum likelihood tree of 55 Deltaproteobacteria MAGs. This tree contains 55 genomes from this analysis and 94 reference genomes obtained from the ARB database. See methods for details on tree construction.



Supplementary Figure 2. Dissimilatory sulfite reductase (DsrB) phylogenetic tree. This tree includes 238 dsrB proteins identified from the 402 MAGs analyzed in this study

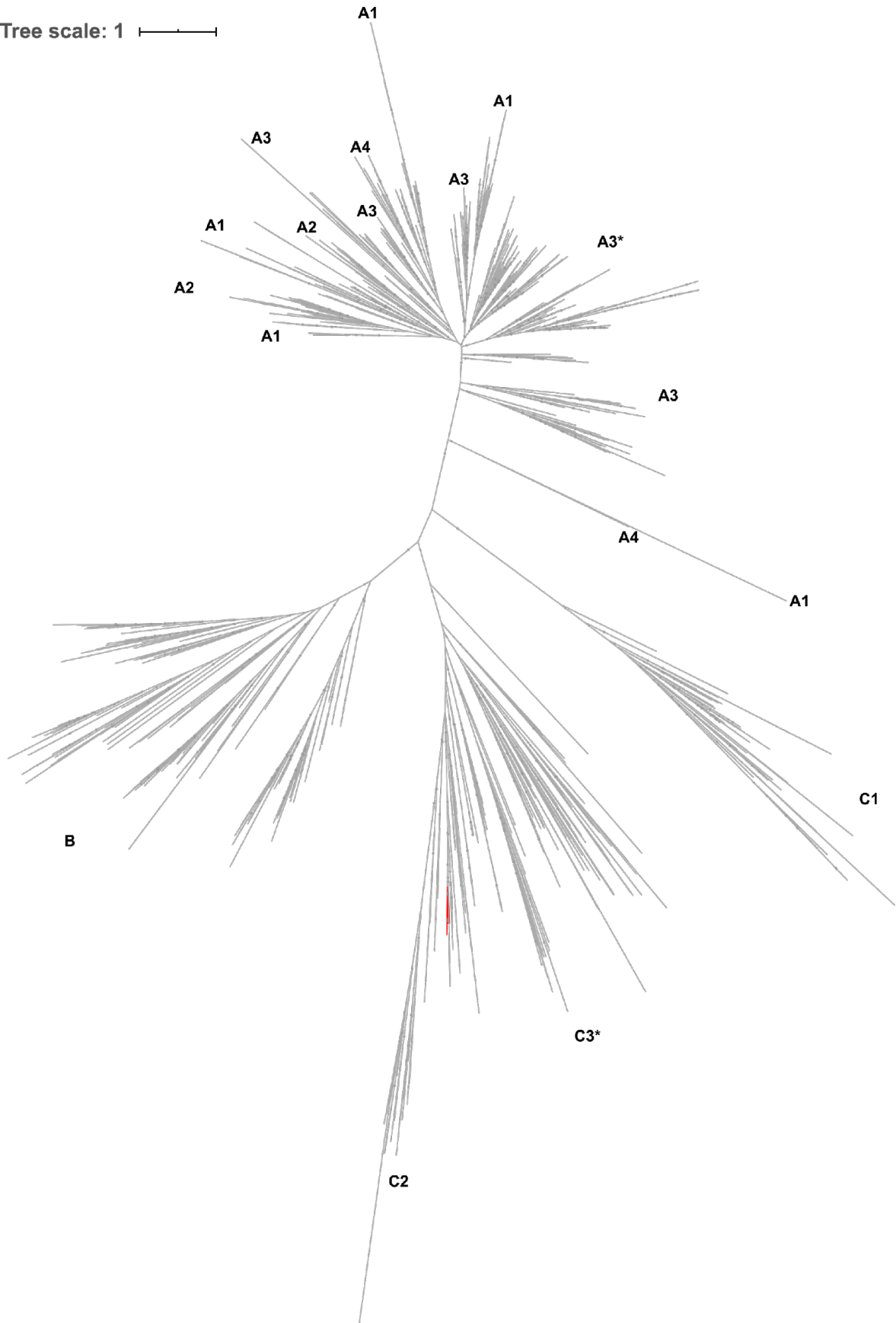
(highlighted in blue and labeled with their group name from Figure 1) and 1306 reference dsrB sequences from public databases. The phylogeny was inferred using IQ-TREE (v.1.6.11, model LG+R7) with the ultrafast bootstrapping option -bb 1000.



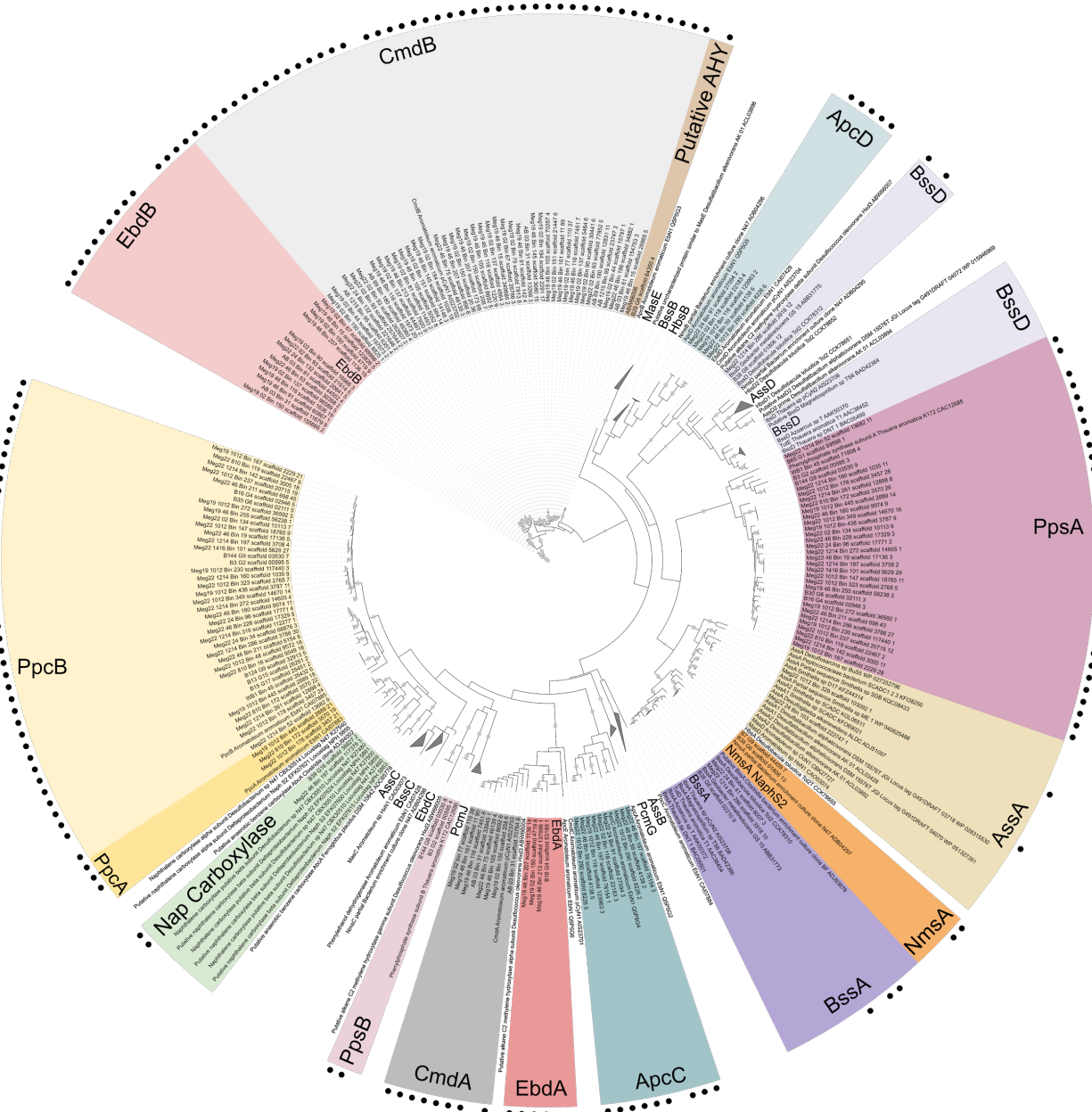
Supplementary Figure 3. Phylogeny of nearly 300 new NiFe hydrogenases recovered in this study. NiFe hydrogenases are compared to characterized groups. Phylogenies were generated using IQ-TREE (v.1.6.11) with the ultrafast bootstrapping option -bb 1000. Hydrogenase sequences identified in this study are highlighted in red and indicated

with an asterisk (*) in the hydrogenase group name. Grey circles signify bootstrap support ≥ 70 .

Tree scale: 1 

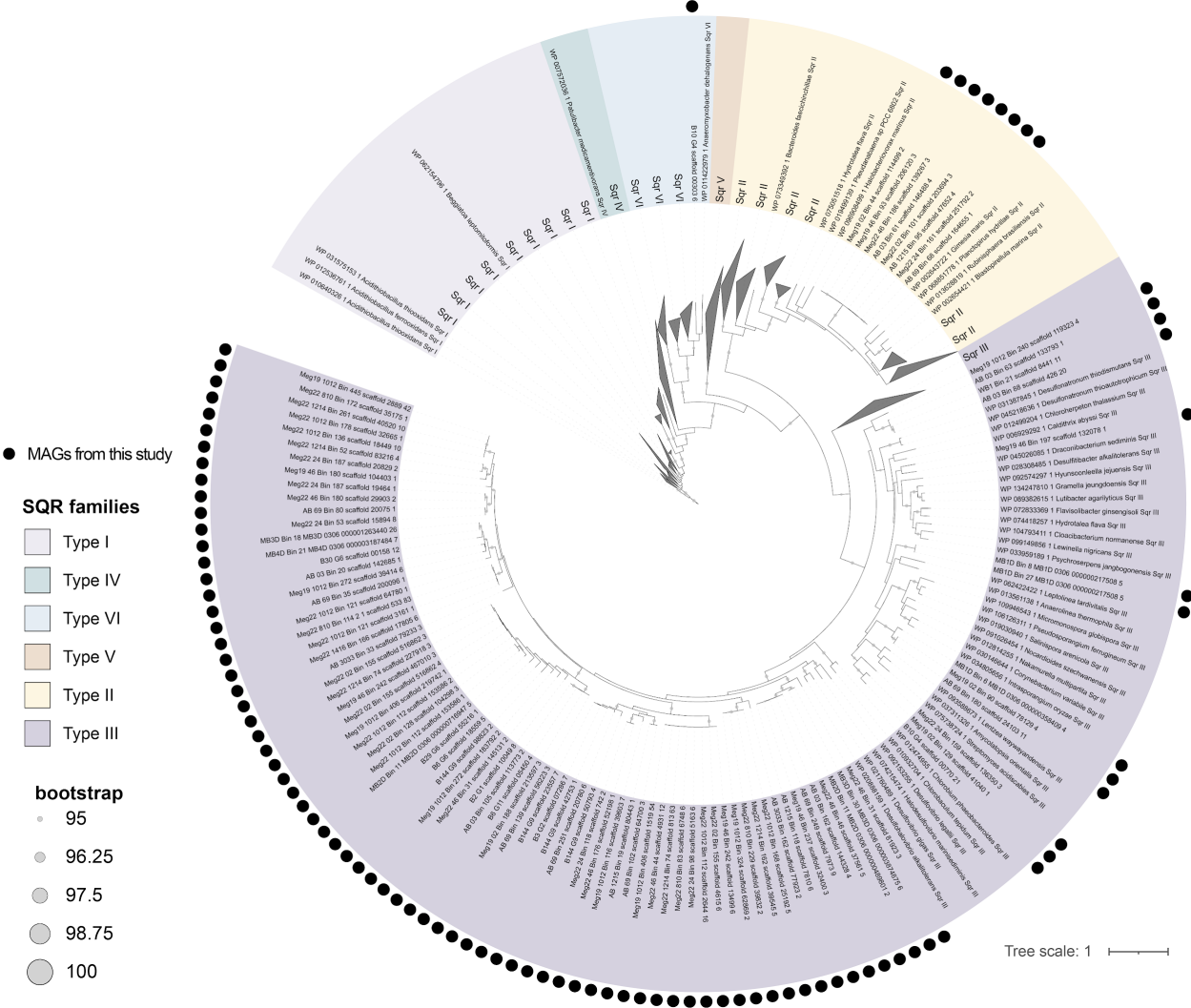


Supplementary Figure 4. Phylogeny of FeFe hydrogenases generated using IQ-TREE (v.1.6.11) with the ultrafast bootstrapping option -bb 1000. Nine FeFe hydrogenase sequences were identified in this study and are highlighted in red and indicated with an asterisk (*) in the hydrogenase group name. Grey circles signify bootstrap support ≥ 70 .



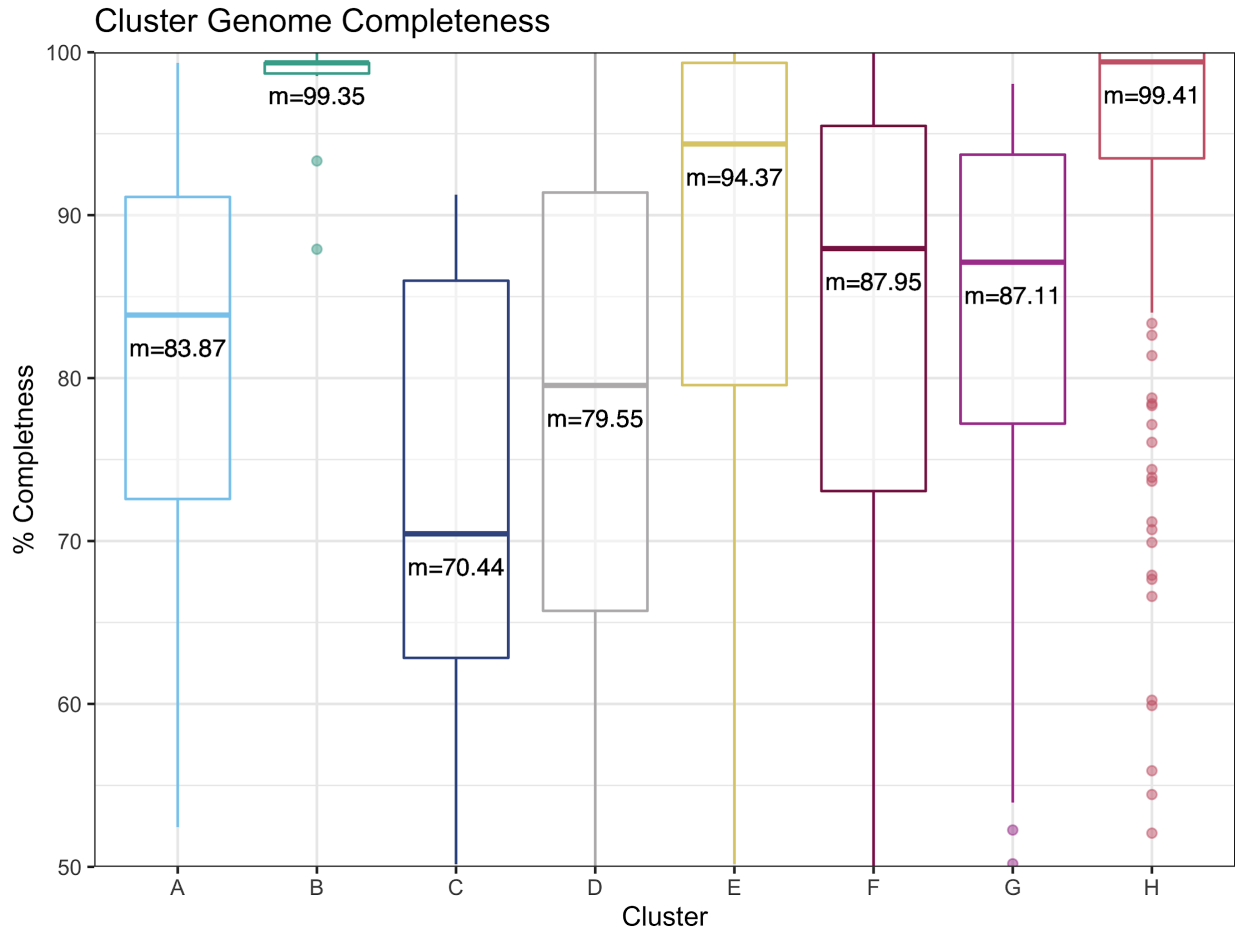
Tree scale: 10

Supplementary Figure 6. Reductive dehalogenase phylogenetic tree. This tree includes 285 reductive dehalogenase genes identified in 106/402 MAGs (highlighted in blue with black dots, and listed in Supplementary Table 14) and 1,040 reference sequences obtained from the reductive dehalogenase database (Molenda et al. 2020, Environ Sci-Proc Imp.). Group names are shown for reductive dehalogenases that branch closely to MAG sequences (see <https://rdasedb.biozone.utoronto.ca/protein>). The phylogeny was inferred using IQ-TREE (v.1.6.11, model LG+F+R10) with the ultrafast bootstrapping option -bb 1000.

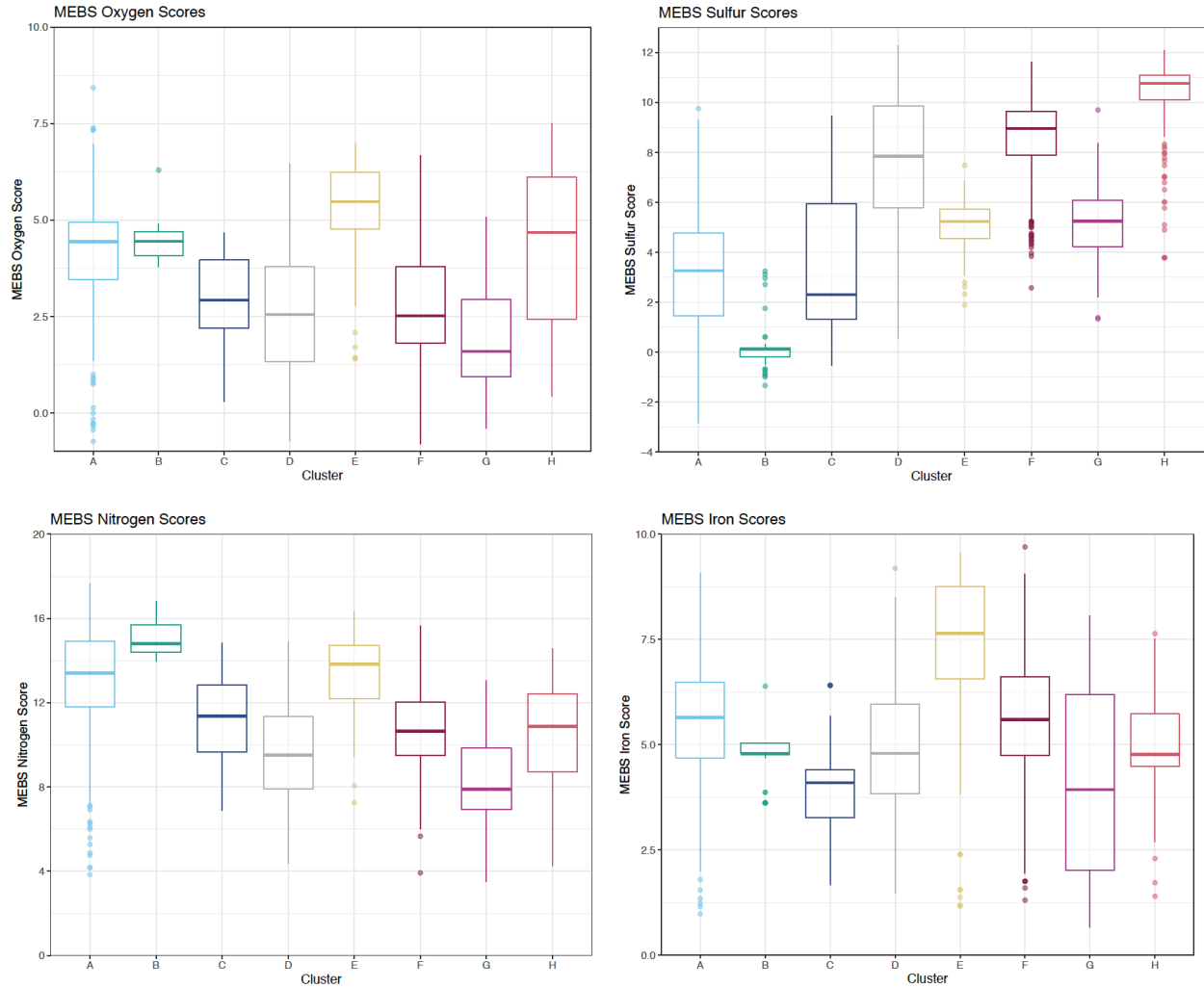


Supplementary Figure 7. Sulfide:quinone oxidoreductase (SQR) phylogenetic tree of 95 SQRs identified in 79/402 MAGs (labeled with black dots) and 333 reference SQRs (custom database, ref 58). SQR families (type I-VI) are shown with unique background

colors. The phylogeny was inferred using IQ-TREE (v.1.6.11, model LG+R8) with the ultrafast bootstrapping option -bb 1000.



Supplementary Figure 8. Genome completeness values for all genomes in each cluster. Genome completeness values were computed using CheckM. The upper boundary of a box plot represents the 75% quantile and the lower boundary is the 25% quantile. The middle line in each box plot represents the median. Upper whiskers are the largest observation less than or equal to the upper hinge + 1.5 * the interquartile range (IQR), while lower whiskers are the smallest observation greater than or equal to the lower hinge - 1.5 * IQR.



Supplementary Figure 9. MEBS scores of major metabolic cycles calculated for each cluster (A-H). The upper boundary of a box plot represents the 75% quantile and the lower boundary is the 25% quantile. The middle line in each box plot represents the median. Upper whiskers are the largest observation less than or equal to the upper hinge +1.5 * the interquartile range (IQR), while lower whiskers are the smallest observation greater than or equal to the lower hinge -1.5 *IQR.