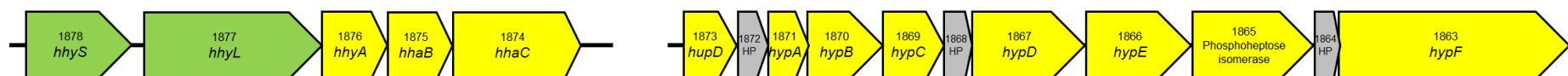


## Supplementary Information

**Table S1 (xlsx).** Transcript read count for RNA-seq experiment comparing gene expression of three exponential phase (carbon-replete) and three stationary phase (carbon-limited) cultures of *Thermomicrobium roseum*.

**Figure S1.** Structure of the putative operons encoding the group 1h [NiFe]-hydrogenase, type I carbon monoxide dehydrogenase, and heterodisulfide reductase / electron transfer flavoprotein complex in *Thermomicrobium roseum*. Genes are differentially coloured depending on whether they encode structural subunits (green), accessory and maturation factors (yellow), or hypothetical proteins (grey).

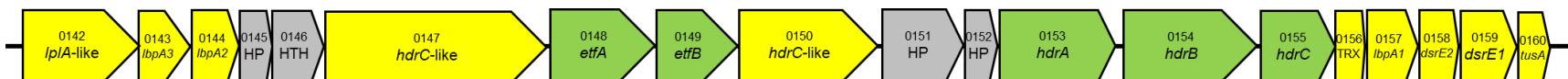
Group 1h [NiFe]-hydrogenase structural and maturation operon



Type I carbon monoxide dehydrogenase structural and maturation operon

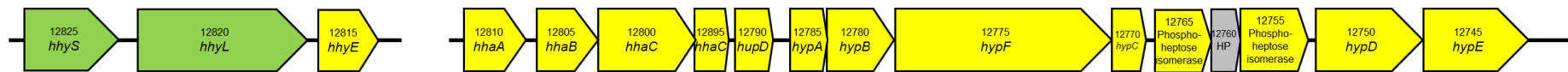


Heterodisulfide reductase and electron transfer flavoprotein complex operon



**Figure S2.** Structure of the putative operons encoding the group 1h [NiFe]-hydrogenase and type I carbon monoxide dehydrogenase in *Thermogemmatispora* sp. T81. Genes are differentially coloured depending on whether they encode structural subunits (green), accessory and maturation factors (yellow), or hypothetical proteins (grey).

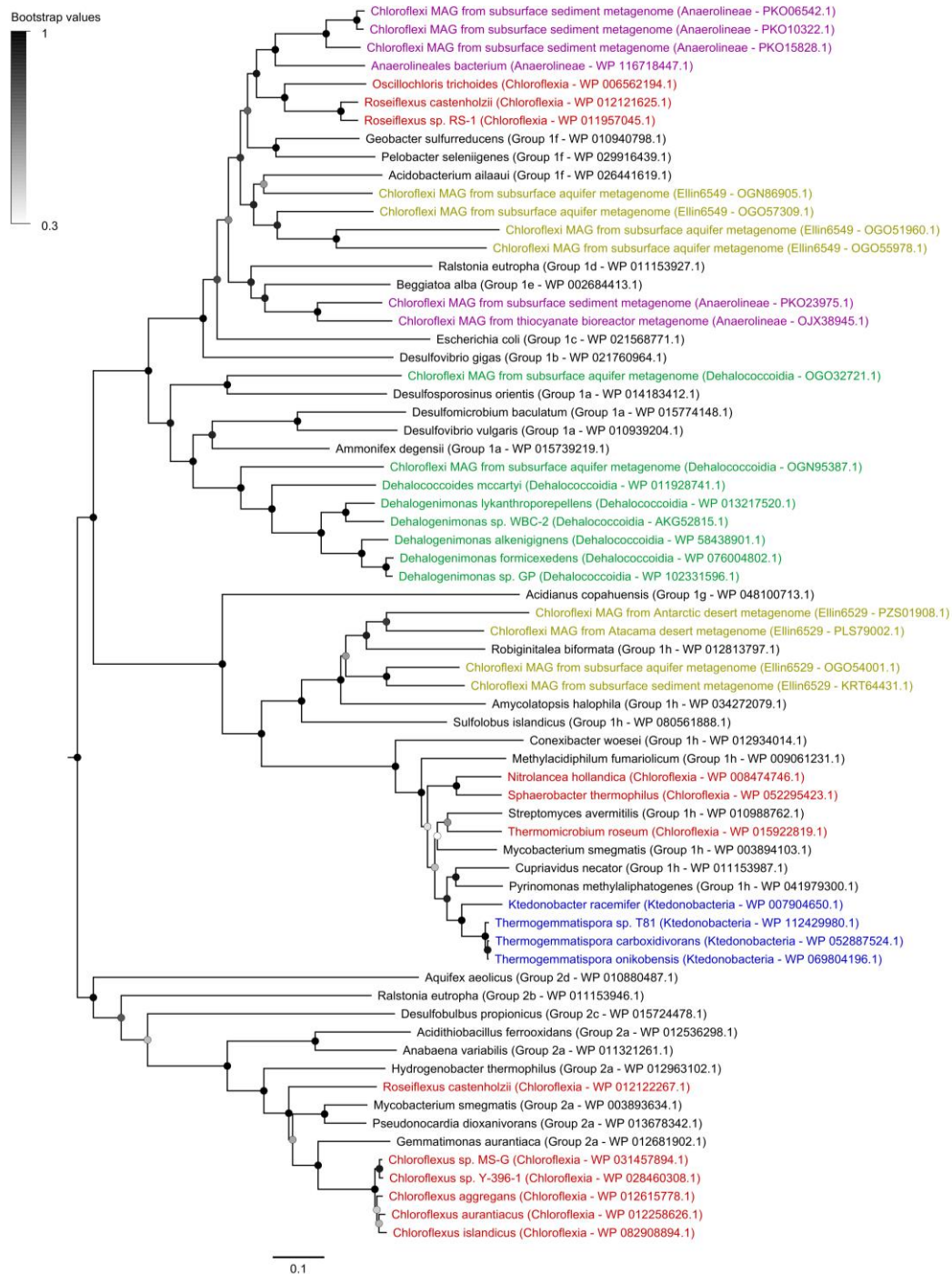
Group 1h [NiFe]-hydrogenase structural and maturation operon



Type I carbon monoxide dehydrogenase structural operon



**Figure S3.** Phylogenetic tree showing the distribution of uptake respiratory hydrogenases in Chloroflexi genomes and metagenome-assembled genomes (MAGs). The genomes encode catalytic subunits of group 1a, group 1e, group 1f, group 1h, and group 2a [NiFe]-hydrogenases. Sequences are coloured by class, where blue = Ktenodobacteria, red = Chloroflexia, green = Dehalococcoidia, purple = Anaerolineae, and yellow = candidate class Ellin6546, with reference sequences in black. The tree was constructed using amino acid sequences of the hydrogenase large subunit using the neighbour-joining method and was bootstrapped with 100 replicates.



**Figure S4.** Phylogenetic tree showing the distribution of type I carbon monoxide dehydrogenases in Chloroflexi genomes and metagenome-assembled genomes (MAGs). Sequences are coloured by class, where blue = Ktenodobacteria, red = Chloroflexia, purple = Anaerolineae, and yellow = candidate class Ellin6546, with reference sequences in black. The tree was constructed using amino acid sequences of the carbon monoxide dehydrogenase large subunit using the neighbour-joining method and was bootstrapped with 100 replicates.

