Supplementary Figures: Arsenate reduction coupled to anaerobic oxidation of methane by members of the *Methanoperedenaceae*

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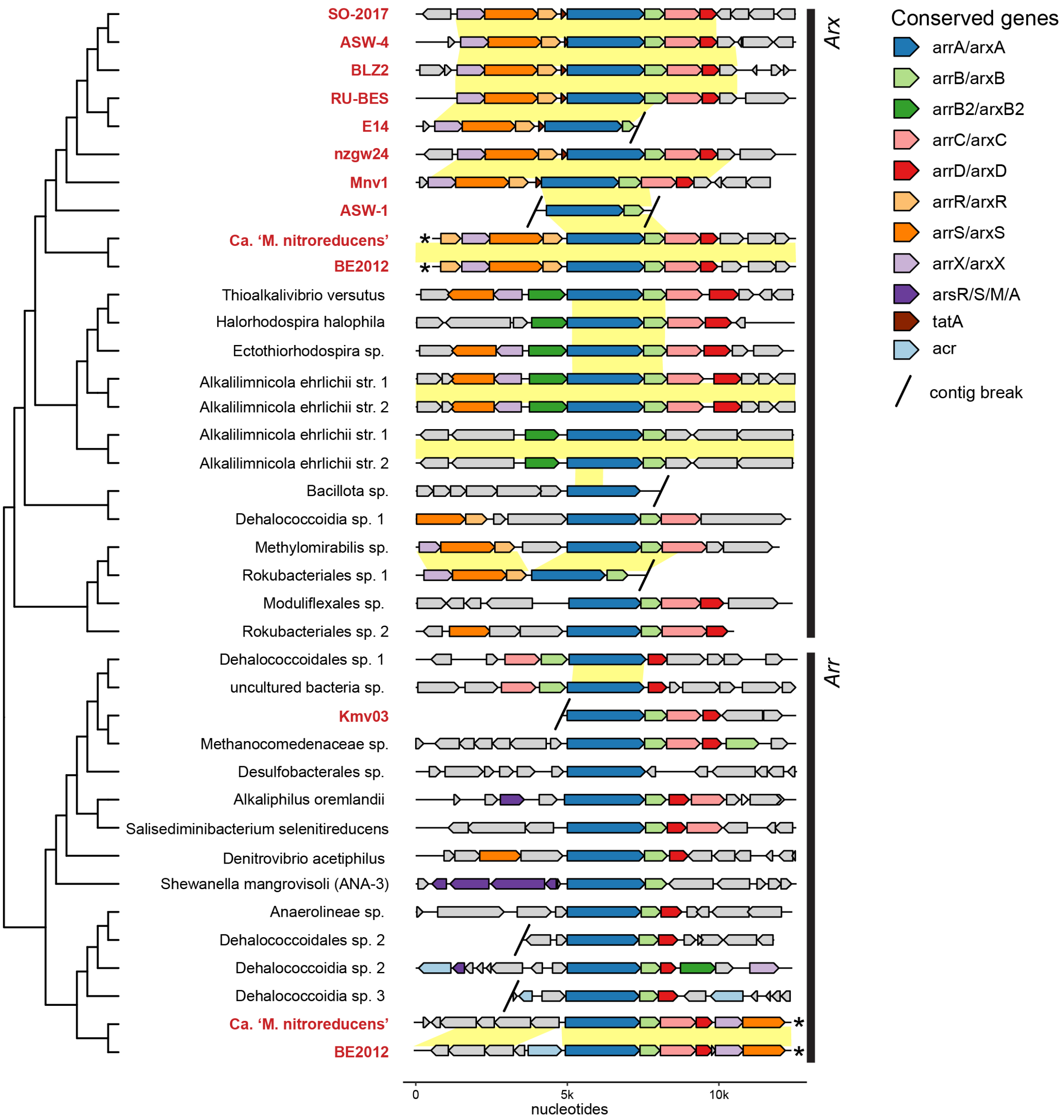
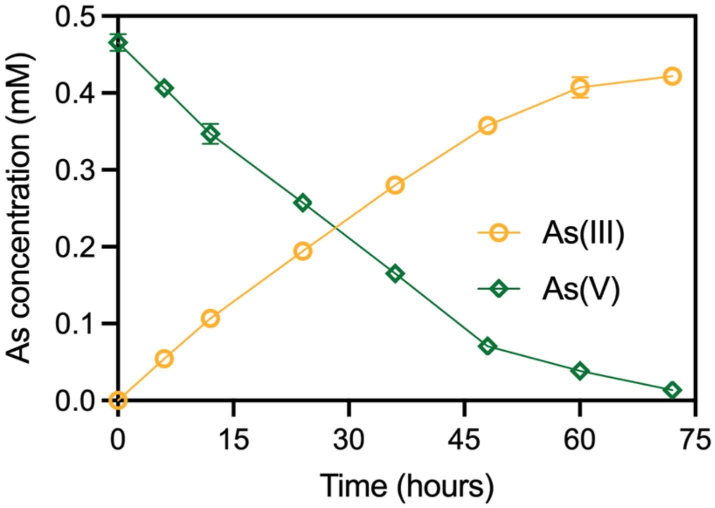
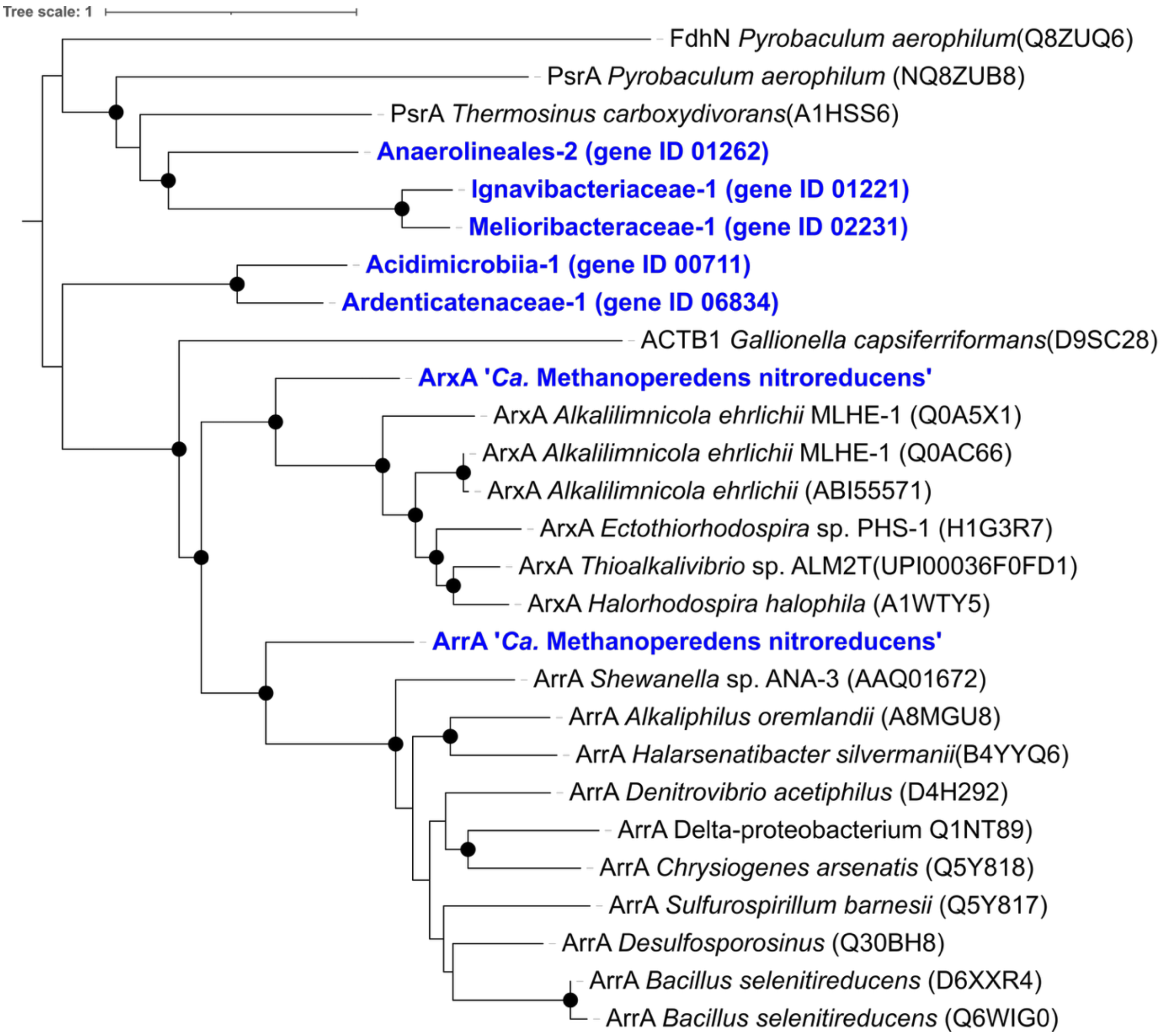


Supplementary Figure 1: Arrangement of *arr* and *arx* gene clusters found across '*Ca.* Methanoperedenaceae' MAGs (red) compared to other prokaryotes. The dendrogram represents a structure-informed protein tree based on alignment of the A-subunit of the *arr* and *arx*, inferred by maximum likelihood, and support values were calculated via nonparametric bootstrapping with 1000 replicates. Gene functional predictions are noted by colour ("conserved genes"), with other genes including hypothetical genes coloured light grey. Pairwise nucleotide synteny between adjacent leaves is displayed in light yellow, as determined using minimap2 (see methods). Leaves are named as per GTDB taxonomy, with full taxonomies and genbank/refseq accessions provided in supplementary dataset S7. Asterisks (adjacent to MAG BE2012 and *Ca.* 'M. nitroreducens') indicate contiguity of the genome sequence, with the sequence continuing at the genome's corresponding asterisk.



Supplementary Figure 2: Monitoring of As(V) and As(III) during the operation of the arsenate-fed anaerobic methane oxidising batches. Error bars represent the standard deviation of two biological replicates.



Supplementary Figure 3: Phylogenetic placement of complex iron-sulphur molybdoenzyme oxidoreductase A-subunits encoded by MAGs in As-AOM batches (blue text). Black text = reference proteins, with Uniprot/Uniparc ID in brackets. Bootstrap support > 85% (1000 replicates) is indicated by a black circle.