

## Supplementary Material

### 1 SUPPLEMENTARY DATA

#### 1.1 gpkg files

The gpkg files built in this study can be found at [github.com/garciafertson/mmfl1\\_gpkgs](https://github.com/garciafertson/mmfl1_gpkgs)

#### 1.2 network files

The [Supplementary\\_network\\_files.zip](#) file contains a folder with cytoscape CYS network files constructed as explained in **Materials and Methods section**. Ovals represent Genus and squares represent KOs. An edge represents if a KO-genus pair is present, and edge width is proportional to the log<sub>2</sub> of total counts. Methane metabolism is shown in light gray and methanogenesis in gray; sulfur oxidation in ocre, sulfate reduction in yellow and sulfur uptake/assimilation in lime; nitrate reduction/denitrification in sky blue and nitrogen metabolism in blue; alkanes/hydrocarbon degradation in dark brown, aromatics degradation in brown and chlorinated compound degradation in purple; oxygenic photosynthesis in green and aerobic respiration in pink. File names ending with *min10.cys* display only edges with a total count above 10. File names ending with *complete.cys* display edges with at least one count.

### 2 SUPPLEMENTARY TABLES AND FIGURES

#### 2.1 Tables

Tables are included as separate XLSX files.

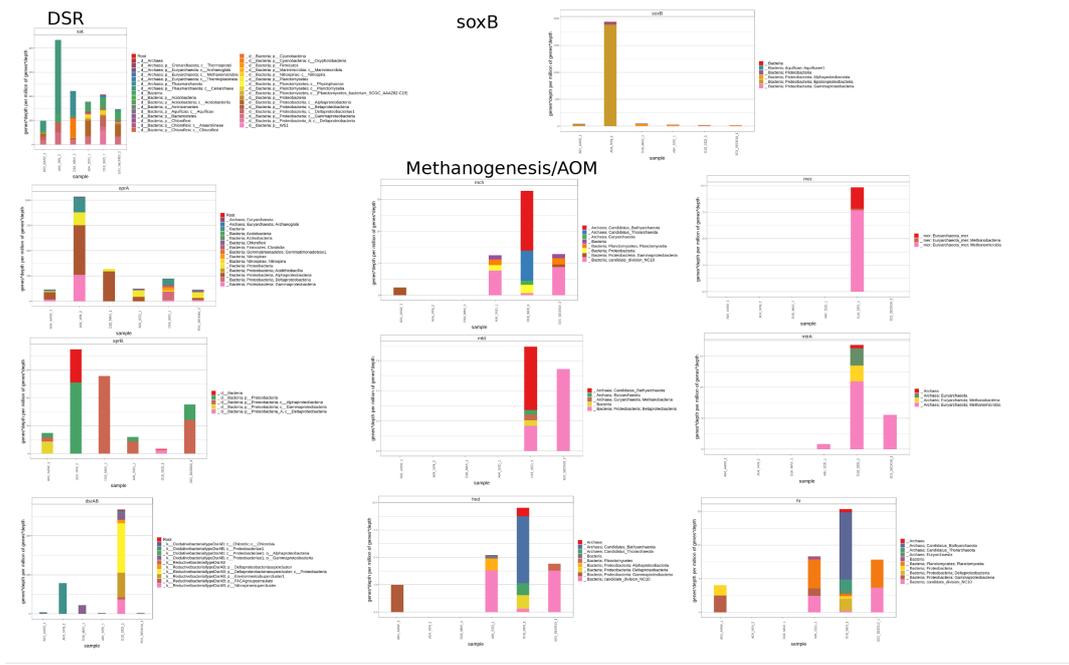
**Supplementary\_Table\_1** CTD\_DATA. **water\_column sheet**) CTD data statistics by water column level **region sheet**) CTD data statistics by region.

**Supplementary\_Table\_2** Sample stats. **WMS sheet**) Sequencing and assembly statistics for Whole Metagenomic Shotgun data. **Amplicon sheet**) Sequencing statistics and alpha diversity for Amplicon, OTU analysis. **ASVs Amplicon sheet**) Alpha diversity for Amplicon, ASV analysis.

**Supplementary\_Table\_3** KO numbers. **Searched KO list sheet**) Selected gene list (as KO numbers) displayed in networks. **Key genes and genus found sheet**) Key KO numbers and genera found in networks by water column level.

#### 2.2 Figures

Figures are also included as separate PNG files.



**Figure S1.** The bar plots show the relative abundance and most likely taxonomic assignment using graftM packages for genes related to **(DSR)** Dissimilatory Sulfite reduction: *sat*, *aprA*, *dsrAB*, **(soxB)** Sulfate oxidation: *soxB* and **(Methanogenesis/AOM)** *mcrA*, *mer*, *fmd*, *ftr*, *mch*, *mtd*, *mtrA*



