

Description of Additional Supplementary Files

File Name: Supplementary Data 1

Description: The statistics of sampling locations and overview of the metagenomes and metatranscriptomes generated from the sediments.

File Name: Supplementary Data 2

Description: Metagenomic data downloaded from NCBI database.

File Name: Supplementary Data 3

Description: Mercury concentrations of sediments.

File Name: Supplementary Data 4

Description: Geochemical data (PO_4^{3-} , NH_4^+ , NO_3^- , NO_2^- , SO_4^{2-} , Fe^{3+} , TOC, TN) of sediments.

File Name: Supplementary Data 5

Description: Percentage of novel 16S miTags and microbiome novelty score for samples.

File Name: Supplementary Data 6

Description: Overview of the prokaryotic MAGs identified in this study.

File Name: Supplementary Data 7

Description: Relative abundance (CPM) of mercury transforming genes in the metagenomes.

File Name: Supplementary Data 8

Description: Relative abundance (TPM) of mercury transforming genes in the metatranscriptomes.

File Name: Supplementary Data 9

Description: Taxonomy of putative methylators.

File Name: Supplementary Data 10

Description: Relative abundance of putative methylators in 142 metagenomes.

File Name: Supplementary Data 11

Description: Metabolic gene statistics on the genome of putative methylators.

File Name: Supplementary Data 12

Description: Integrity of the Wood-Ljungdahl pathway and distribution of typical cobalamindependent methyltransferases in MAGs identified in this study.

File Name: Supplementary Data 13

Description: Confidence score statistics for the docking model.

File Name: Supplementary Data 14

Description: The proteinprotein docking interaction site.

File Name: Supplementary Data 15

Description: Taxonomy of putative *merA* carriers.

File Name: Supplementary Data 16

Description: Taxonomy of putative *merB* carriers.

File Name: Supplementary Data 17

Description: Relative abundance of *merA* carriers in 142 metagenomes.

File Name: Supplementary Data 18

Description: Relative abundance of *merB* carriers in 142 metagenomes.