

Supplementary Information for
Microbial potential to mitigate neurotoxic methylmercury accumulation in
farmlands and rice

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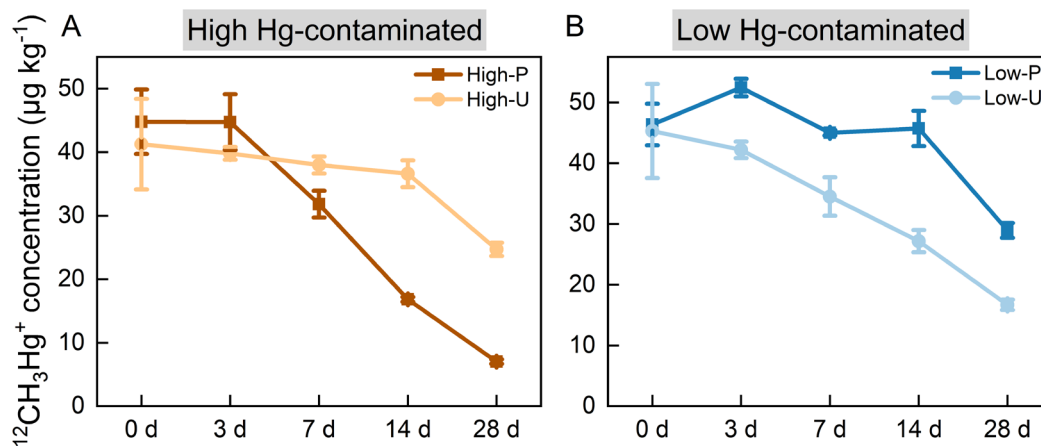
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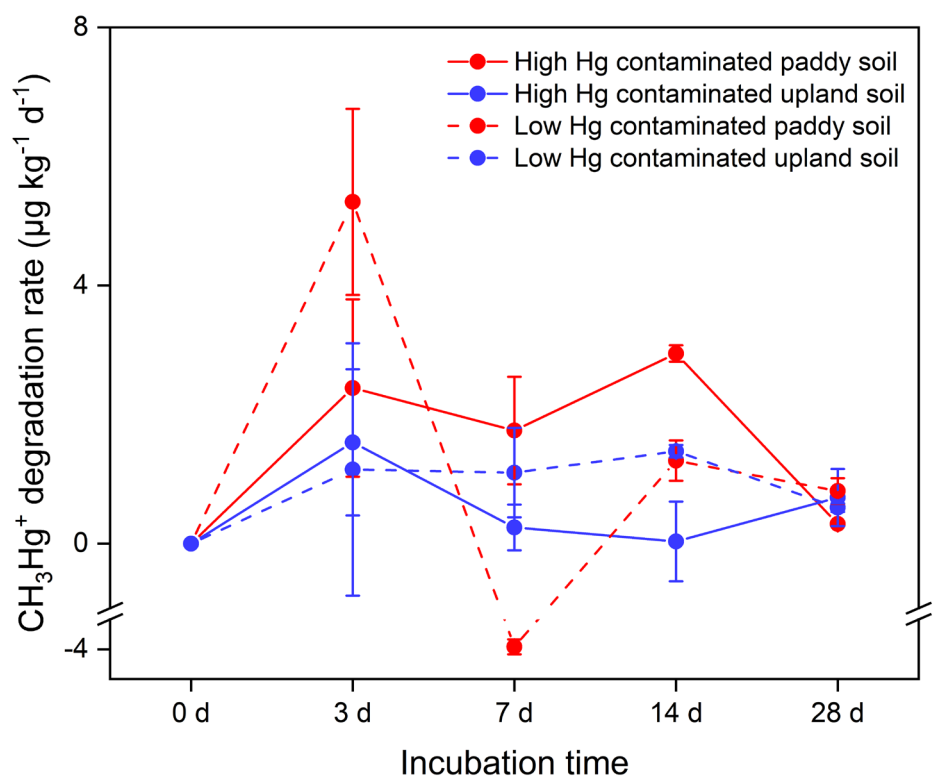
Supplementary Figs. 1 to 10

Supplementary Tables 1 to 7

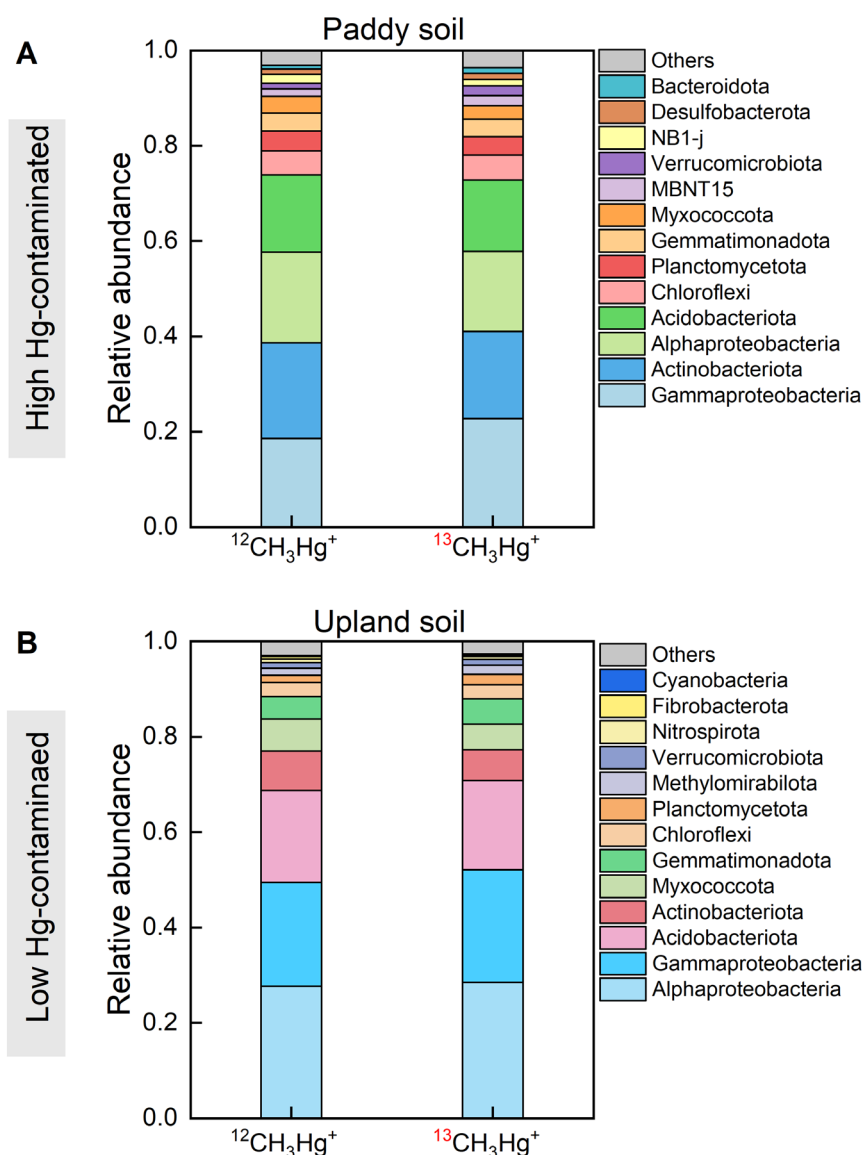
Supplementary References



Supplementary Fig. 1. Dynamics of methylmercury (CH₃Hg⁺) degradation in the ¹²CH₃Hg⁺ treatments. A-B Dynamics of CH₃Hg⁺ degradation in the ¹²CH₃Hg⁺ treatments of the paddy soil and the upland soil from high Hg-contaminated and low Hg-contaminated sites, respectively. Data are shown in average values with standard deviations (three biological replicates, n = 3). Source data are provided as a Source Data file.

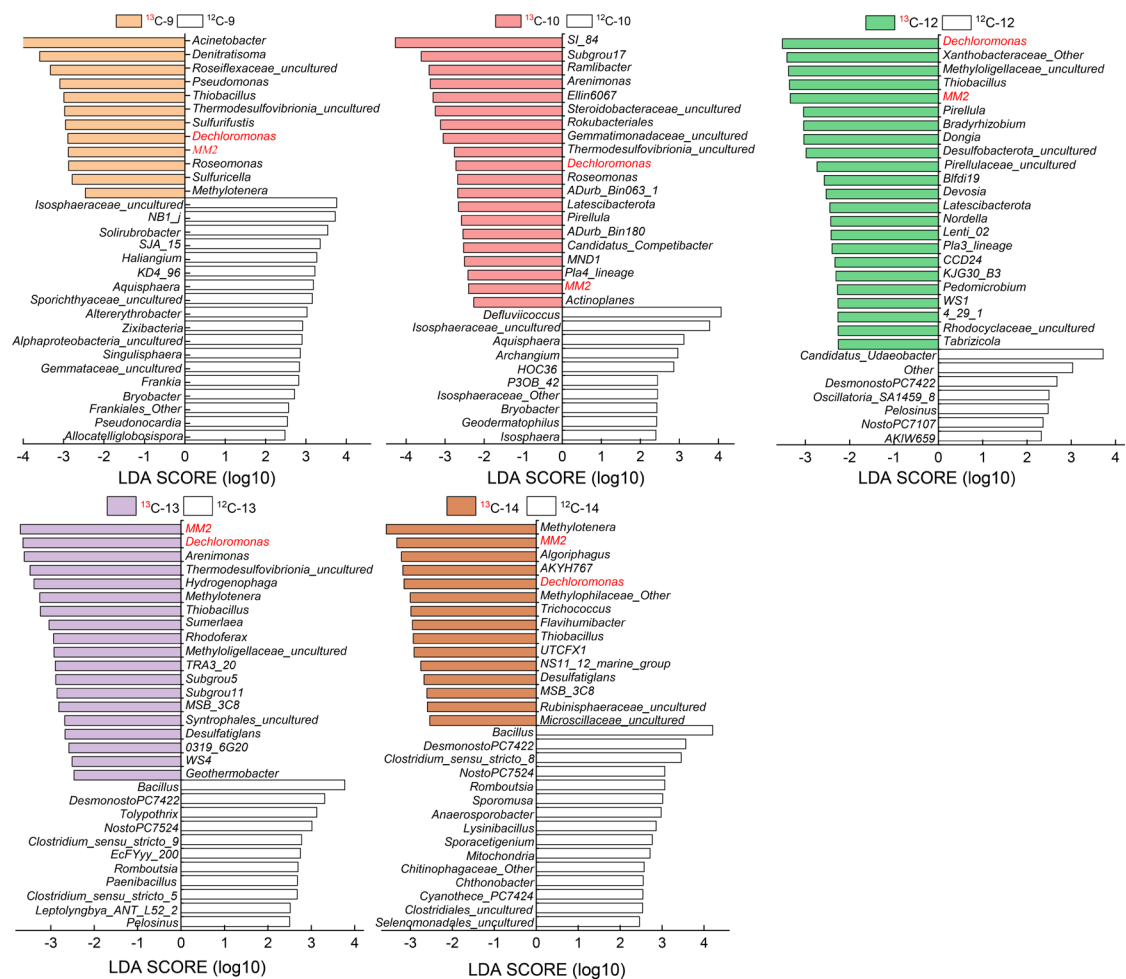


Supplementary Fig. 2. The degradation rates of methylmercury (CH_3Hg^+) in the $^{13}\text{CH}_3\text{Hg}^+$ treatments of the paddy and upland soils from high and low background Hg contamination sites. Data are shown in average values with standard deviations (three biological replicates, $n = 3$). Source data are provided as a Source Data file.

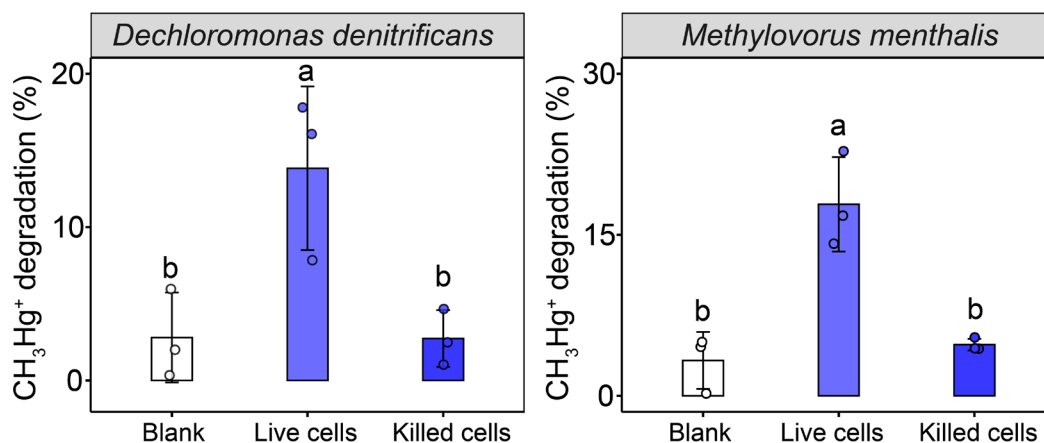


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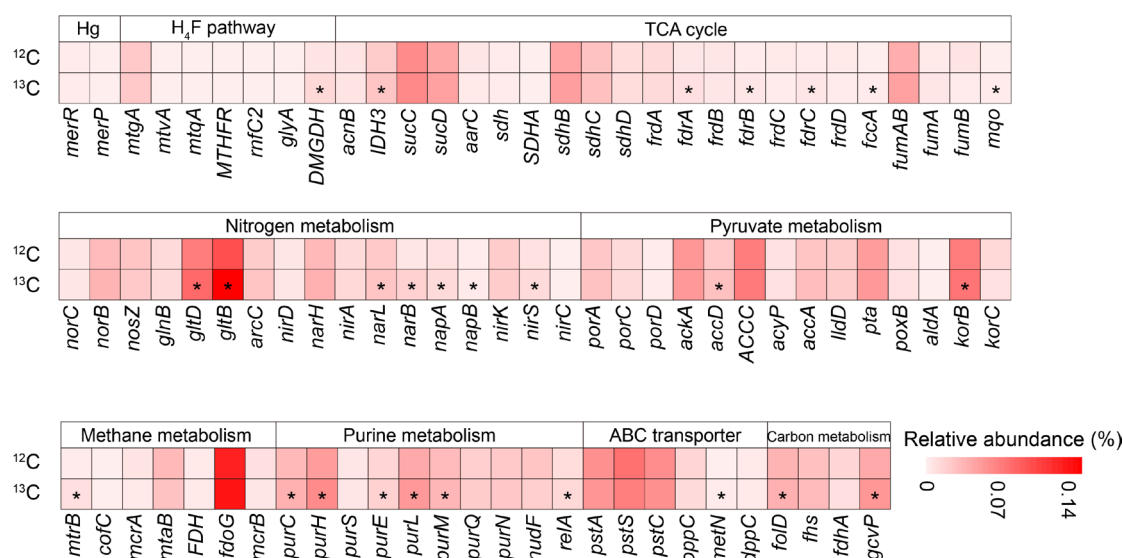
43 **Supplementary Fig. 3. The dominant bacteria phyla in the unlabeled**
 44 **methylmercury ($^{12}\text{CH}_3\text{Hg}^+$) and $^{13}\text{CH}_3\text{Hg}^+$ treatments. A-B indicates the paddy soil**
 45 **and the upland soil from high Hg-contaminated and low Hg-contaminated sites,**
 46 **respectively. Data are shown in average values (three biological replicates, n = 3).**
 47 **Source data are provided as a Source Data file.**



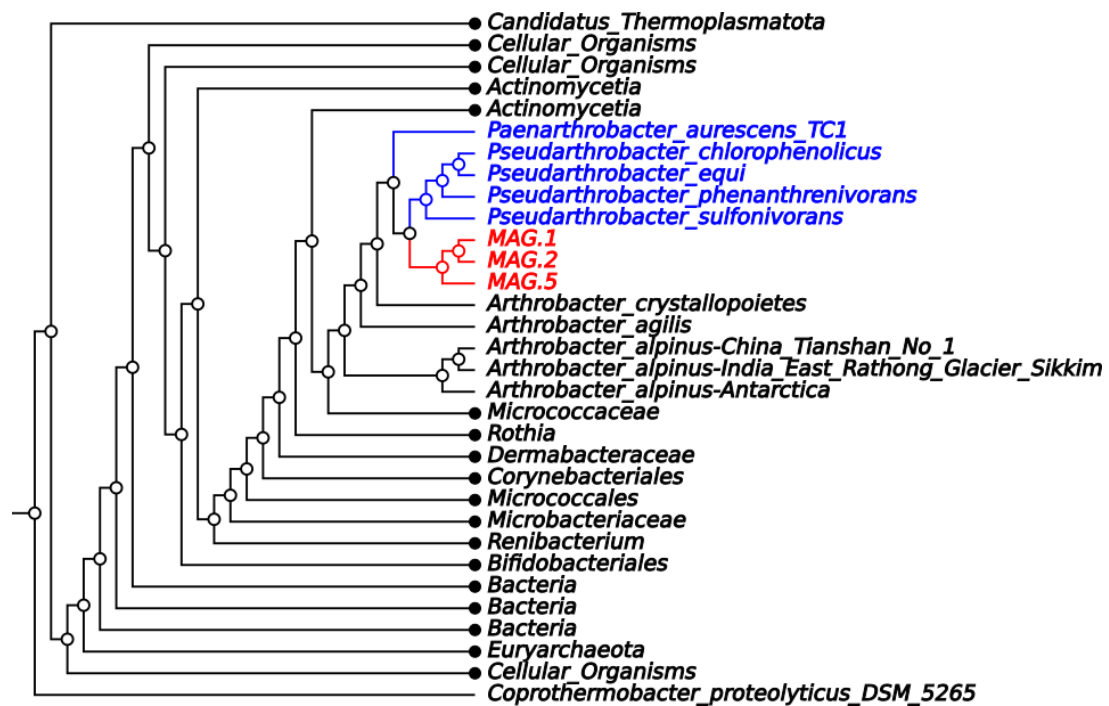
Supplementary Fig. 4. Biomarkers of key genera in the fractions 9, 10, 12, 13 and 14 from the $^{12}\text{CH}_3\text{Hg}^+$ and $^{13}\text{CH}_3\text{Hg}^+$ treatments of the paddy soil from high Hg-contaminated site. Exact p -values and Source data are provided as a Source Data file.



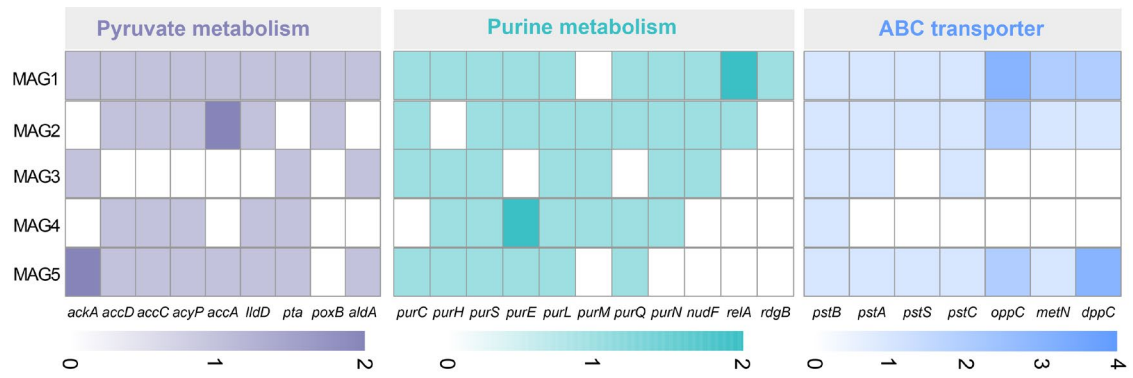
Supplementary Fig. 5. Methylmercury (CH₃Hg⁺) degradation assays with washed cells (5×10^8 cells·mL⁻¹) of *Dechloromonas denitrificans* and *Methylovorus menthalis* in PBS buffer (pH 7.2) during the 24 h incubation. The initial added CH₃Hg⁺ concentration was 1 ng mL⁻¹. Data are shown in average values with standard deviations (three biological replicates, n = 3). Different lowercase letters indicate significant differences between the treatments of blank (control), live cells and killed cells based on one-way ANOVA followed by two-sided Tukey post hoc test. Exact *p*-values and Source data are provided as a Source Data file.



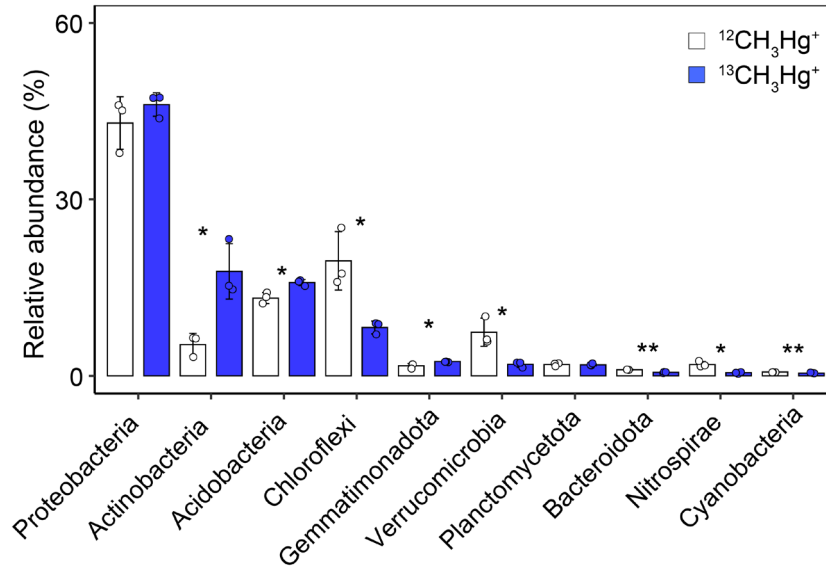
Supplementary Fig. 6. Relative abundance of key genes in the pathway of Hg reduction, H₄F pathway, methane metabolism, nitrogen metabolism, TCA cycle, pyruvate metabolism, purine metabolism, ABC transporter and carbon metabolism as represented by Kyoto Encyclopedia of Genes and Genome (KEGG). The color gradient represents the relative abundances of genes of metagenomic analysis in the heavy DNA fraction from the ¹³CH₃Hg⁺ treatment and the corresponding fraction in the ¹²CH₃Hg⁺ treatment. The definitions of genes are listed in the Source data. Data are shown in average values (three biological replicates, n = 3). * indicates genes that exhibited significant enrichment in the fraction of the highest 16S rRNA gene copies from ¹³CH₃Hg⁺ treatment compared to the fraction in the corresponding ¹²C control at levels of *p* < 0.05 based on two-sided T-Test. Exact *p*-values and Source data are provided as a Source Data file.



Supplementary Fig. 7. Phylogenomic tree of MAGs obtained based on metagenomic sequencing of the heavy DNA fraction from the $^{13}\text{CH}_3\text{Hg}^+$ treatment.



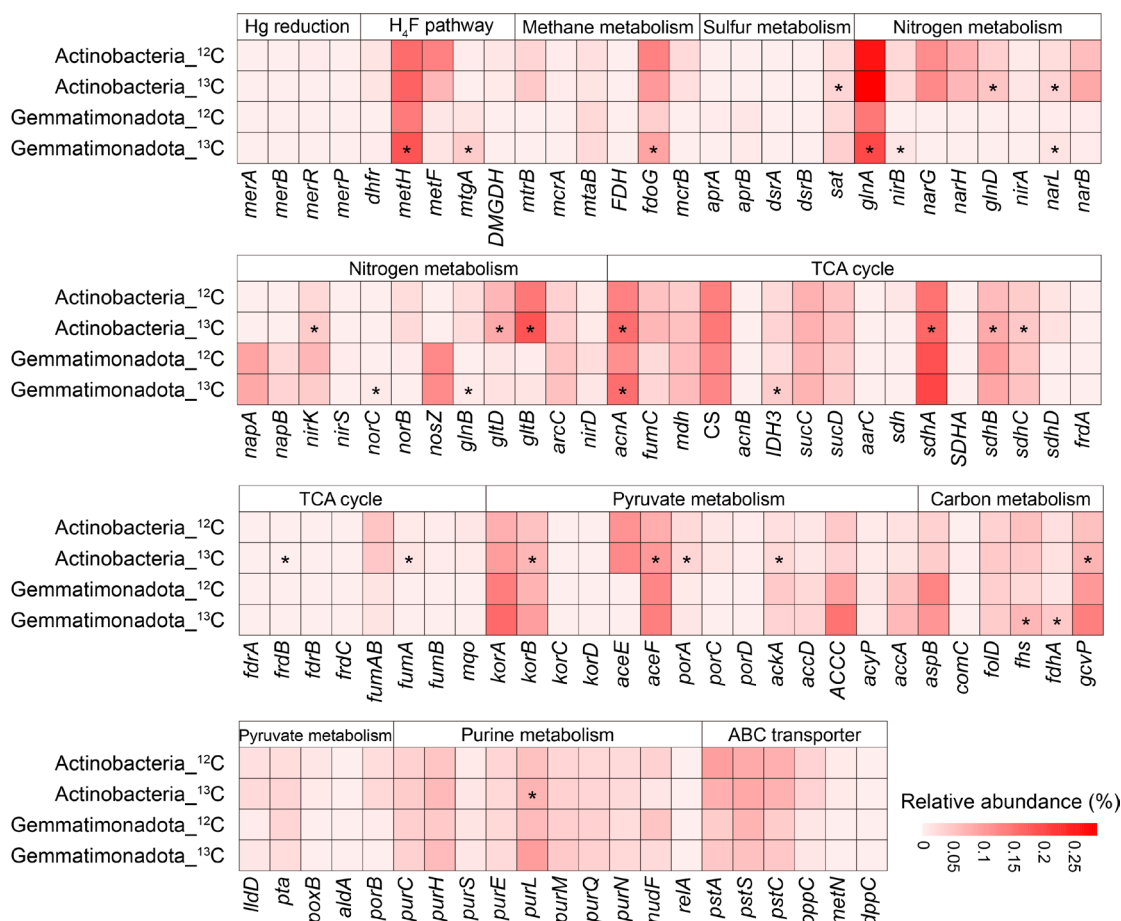
Supplementary Fig. 8. Heatmap represents the numbers of the genes involved in pyruvate metabolism, purine metabolism, and ABC transporter detected in the MAGs. The definitions of genes are listed in the Source data. The colors indicate the number of the gene(s) detected in the MAGs. Source data are provided as a Source Data file.



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87 **Supplementary Fig. 9. The dominant bacteria phyla (top 10) in the $^{12}\text{CH}_3\text{Hg}^+$ and**
 88 **$^{13}\text{CH}_3\text{Hg}^+$ treatments based on metagenomics.** Data are shown in average values with
 89 standard deviations (three biological replicates, $n = 3$). * indicates statistically
 90 significant levels of $p < 0.05$, and ** indicates $p < 0.01$ based on two-sided T-Test. Exact
 91 p -values and Source data are provided as a Source Data file.

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Supplementary Fig. 10. Relative abundance of major genes in the key biochemistry pathways involved in *Actinobacteria* and *Gemmatimonadota*. The color gradient represents the relative abundances of genes involved in *Actinobacteria* and *Gemmatimonadota* of metagenomic analysis in the heavy DNA fraction from the $^{13}\text{CH}_3\text{Hg}^+$ treatment and the corresponding fraction in the $^{12}\text{CH}_3\text{Hg}^+$ treatment. The definitions of genes are listed in the Source data. Data are shown in average values (three biological replicates, $n = 3$). * indicates genes that exhibited significant enrichment in the heavy fraction of the $^{13}\text{CH}_3\text{Hg}^+$ treatment compared to the fraction in the corresponding ^{12}C control at levels of $p < 0.05$ based on two-sided T-Test. Exact p -values and Source data are provided as a Source Data file.

104 **Supplementary Table 1.** The initial soil properties from Hg-contaminated and low Hg level sites.

Sites	Hg levels	Types	Longitude (E)	Latitude (N)	Total Hg ($\mu\text{g kg}^{-1}$)	CH_3Hg^+ ($\mu\text{g kg}^{-1}$)	pH	DOC (mg kg^{-1})
Wanshan	High Hg-contaminated	Paddy	109.21369	27.51796	4575.00 ± 166.62	1.55 ± 0.07	6.54 ± 0.18	160.54 ± 4.76
		Upland	109.53333	28.33333	5781.71 ± 85.68	3.48 ± 0.26	6.40 ± 0.20	103.91 ± 13.41
Xianning	Low Hg-contaminated	Paddy	114.2332133	29.90300	55.56 ± 3.24	0.92 ± 0.27	6.02 ± 0.12	80.05 ± 10.24
		Upland	114.24125	29.90561	28.60 ± 3.24	0.45 ± 0.02	5.95 ± 0.08	75.01 ± 6.38

105 Note: The mean values and standard deviations are presented.

106 **Supplementary Table 2.** Genome-based MAGs that represent microbial taxa
 107 determined to be ¹³C-labeled in SIP experiments.

MAGs	Completeness (%)	Contamination (%)	Phylum	Genus
MAG1	84.44	1.97	Actinobacteriota	<i>Arthrobacter_I</i>
MAG2	76.49	1.69	Actinobacteriota	<i>Arthrobacter_I</i>
MAG3	76.05	2.20	Desulfobacterota	<i>CG2-30-66-27</i>
MAG4	72.89	3.30	Gemmatimonadota	<i>UBA4720</i>
MAG5	71.59	2.61	Actinobacteriota	<i>Arthrobacter_I</i>

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Supplementary Table 3. The key parameters and rate coefficients of Hg fluxes among different paddy soils.

Site	Microbial degradation efficiency of CH ₃ Hg ⁺ (%) ^a	Soil CH ₃ Hg ⁺ (μg kg ⁻¹) ^a	BAF ^b	Rice ingestion rate (g d ⁻¹) ^c
Nanjing	64.26	1.1	2.97	217.98
Wuhan	60.79	0.87	2.97	288.29
Yueyang	52.53	0.56	3.26	335.99
Guangzhou	50.25	0.96	2.83	329.14
Panjin	37.3	0.78	2.45	130.29
Wuchang	35.79	0.43	3.86	136.61
Jian	38.28	2.18	2.7	349.79
Jiujiang	8.16	0.46	2.7	349.79
Dalian	38.25	0.36	2.45	130.29
Taoyuan	49.34	1.01	3.26	335.99

^a Data from unpublished data.

^b Rate coefficient. Data from ref ¹.

^c Rate coefficient. Data from ref ².

Supplementary Table 4. Reduction in the accumulation of CH₃Hg⁺ in rice and the associated intelligence quotient decrements (ΔIQ) and hazard quotient (HQ) resulting from microbial demethylation of soil CH₃Hg⁺.

Site	Decreases in rice CH ₃ Hg ⁺ (μg kg ⁻¹)	Decreases in ΔIQ (%)	Decreases in HQ (%)
Nanjing	2.10	1.65	7.99
Wuhan	1.57	1.63	7.90
Yueyang	0.96	1.16	5.62
Guangzhou	1.37	1.62	7.84
Panjin	0.71	0.33	1.62
Wuchang	0.59	0.29	1.42
Jian	2.25	2.84	13.75
Jiujiang	0.10	0.13	0.62
Dalian	0.34	0.16	0.77
Taoyuan	1.62	1.97	9.53

119 **Supplementary Table 5.** Sensitivity analysis of key parameters.

Microbial degradation efficiency (%)	Soil CH ₃ Hg ⁺ (µg kg ⁻¹)	BAF	Rice ingestion rate (g d ⁻¹)	ΔRice CH ₃ Hg ⁺ (µg kg ⁻¹)	ΔEDI	ΔHQ	ΔΔIQ
8.16	0.87	2.95	260.42	0.21	0.95	0.0095	0.0020
64.26	0.87	2.95	260.42	1.65	7.49	0.0749	0.0155
37.89	0.36	2.95	260.42	0.40	1.83	0.0183	0.0038
37.89	2.18	2.95	260.42	2.43	11.05	0.1105	0.0228
37.89	0.87	2.45	260.42	0.81	3.67	0.0367	0.0076
37.89	0.87	3.86	260.42	1.27	5.79	0.0579	0.0119
37.89	0.87	2.95	217.98	0.97	3.70	0.0370	0.0076
37.89	0.87	2.95	349.79	0.97	5.93	0.0593	0.0122

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121 **Supplementary Table 6.** Sensitivity coefficient of key parameters.

Parameters	$\Delta\text{Rice CH}_3\text{Hg}^+$ ($\mu\text{g kg}^{-1}$)	ΔHQ	$\Delta\Delta\text{IQ}$
Microbial degradation efficiency (%)	2.57	0.1166	0.024048
Soil CH_3Hg^+ ($\mu\text{g kg}^{-1}$)	1.12	0.0507	0.01046
BAF	0.33	0.0150	0.00309
Rice ingestion rate (g d^{-1})	/	0.0002	0.00003

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Supplementary Table 7. Uncertainty analysis based on interval methods of key parameters.

Microbial degradation efficiency (%)	Soil CH ₃ Hg ⁺ (µg kg ⁻¹)	BAF	Rice ingestion rate (g d ⁻¹)	ΔRice CH ₃ Hg ⁺ (µg kg ⁻¹)	ΔEDI	ΔHQ	ΔΔIQ
8.16	0.36	2.45	217.98	0.07	0.27	0.0027	0.0006
8.16	0.36	2.45	349.79	0.07	0.44	0.0044	0.0009
8.16	2.18	3.86	217.98	0.69	2.61	0.0261	0.0054
8.16	2.18	3.86	349.79	0.69	4.19	0.0419	0.0086
64.26	0.36	2.45	217.98	0.57	2.16	0.0216	0.0044
64.26	0.36	2.45	349.79	0.57	3.46	0.0346	0.0071
64.26	2.18	3.86	217.98	5.41	20.57	0.2057	0.0424
64.26	2.18	3.86	349.79	5.41	33.01	0.3301	0.0681
8.16	0.36	3.86	217.98	0.11	0.43	0.0043	0.0009
8.16	0.36	3.86	349.79	0.11	0.69	0.0069	0.0014
8.16	2.18	2.45	217.98	0.44	1.66	0.0166	0.0034
8.16	2.18	2.45	349.79	0.44	2.66	0.0266	0.0055
64.26	0.36	3.86	217.98	0.89	3.40	0.0340	0.0070
64.26	0.36	3.86	349.79	0.89	5.45	0.0545	0.0112
64.26	2.18	2.45	217.98	3.43	13.06	0.1306	0.0269
64.26	2.18	2.45	349.79	3.43	20.95	0.2095	0.0432

126 **Supplementary References**

- 127 1. Zhong, H. et al., Soil geobacteraceae are the key predictors of neurotoxic
128 methylmercury bioaccumulation in rice. *Nat Food* **5**, 301-311 (2024).
- 129 2. Chen, L. et al., Trans-provincial health impacts of atmospheric mercury
130 emissions in china. *Nat Commun* **10**, 1484 (2019).

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