

Reporting Summary

Nature Portfolio wishes to improve the reproducibility of the work that we publish. This form provides structure for consistency and transparency in reporting. For further information on Nature Portfolio policies, see our [Editorial Policies](#) and the [Editorial Policy Checklist](#).

Statistics

For all statistical analyses, confirm that the following items are present in the figure legend, table legend, main text, or Methods section.

n/a Confirmed

- | | | |
|-------------------------------------|-------------------------------------|--|
| ☐ | ☒ | The exact sample size (n) for each experimental group/condition, given as a discrete number and unit of measurement |
| ☐ | ☒ | A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly |
| ☐ | ☒ | The statistical test(s) used AND whether they are one- or two-sided
<i>Only common tests should be described solely by name; describe more complex techniques in the Methods section.</i> |
| ☒ | ☐ | A description of all covariates tested |
| ☒ | ☐ | A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons |
| ☐ | ☒ | A full description of the statistical parameters including central tendency (e.g. means) or other basic estimates (e.g. regression coefficient) AND variation (e.g. standard deviation) or associated estimates of uncertainty (e.g. confidence intervals) |
| ☐ | ☒ | For null hypothesis testing, the test statistic (e.g. F , t , r) with confidence intervals, effect sizes, degrees of freedom and P value noted
<i>Give P values as exact values whenever suitable.</i> |
| ☒ | ☐ | For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings |
| ☒ | ☐ | For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes |
| ☒ | ☐ | Estimates of effect sizes (e.g. Cohen's d , Pearson's r), indicating how they were calculated |

Our web collection on [statistics for biologists](#) contains articles on many of the points above.

Software and code

Policy information about [availability of computer code](#)

Data collection Megahit v1.2.8, fastp v0.20.0, SortMeRNA v2.1, prefetch v2.1.5, FastQC v0.11.8, FastUniq v1.1, Bowtie2 v2.4.1

Data analysis HMMER v3.1b2, qiime2 v.2022.2, Parallel-META v.3.5.1, CheckM v.1.0.11, metaWRAP v.1.2.1, dRep v.1.4.3, GTDB-Tk v.1.0.2, Spec1 v.1.0, MAFFT v 7.505, trimAl v1.4, IQ-TREE v 1.611, RAXML v 8.212, iTOL v .4, bwa v.0.7.17, samtools v.1.9, CoverM v.0.4.0, R v.4.2.2, DIAMOND v.0.9.27.128, Prodigal v.2.6.2, KofamScan v.1.1.0, seqtk v1.3, BLASTn v.2.9.0, PyMOL v.2.1.0, Salmon v.1.10.2, cd-hit v.4.8.1.

For manuscripts utilizing custom algorithms or software that are central to the research but not yet described in published literature, software must be made available to editors and reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Portfolio [guidelines for submitting code & software](#) for further information.

Data

Policy information about [availability of data](#)

All manuscripts must include a [data availability statement](#). This statement should provide the following information, where applicable:

- Accession codes, unique identifiers, or web links for publicly available datasets
- A description of any restrictions on data availability
- For clinical datasets or third party data, please ensure that the statement adheres to our [policy](#)

The assembled Contig and MAG sequences data generated in this study have been deposited in the NCBI database under the accession codes PRJNA635214 [<https://www.ncbi.nlm.nih.gov/bioproject/635214>] and PRJNA1051299 [<https://www.ncbi.nlm.nih.gov/bioproject/1051299>]. The raw sequencing data used in this study are available in the NCBI database under accession codes PRJNA524407 [<https://www.ncbi.nlm.nih.gov/bioproject/PRJNA524407>], PRJNA573088 [<https://www.ncbi.nlm.nih.gov/bioproject/PRJNA573088>].

www.ncbi.nlm.nih.gov/bioproject/PRJNA573088], PRJNA380945 [https://www.ncbi.nlm.nih.gov/bioproject/PRJNA380945], PRJNA504765 [https://www.ncbi.nlm.nih.gov/bioproject/PRJNA504765], PRJEB25358 [https://www.ncbi.nlm.nih.gov/bioproject/PRJEB25358], PRJNA264715 [https://www.ncbi.nlm.nih.gov/bioproject/PRJNA264715], PRJNA309469 [https://www.ncbi.nlm.nih.gov/bioproject/PRJNA309469], PRJNA297058 [https://www.ncbi.nlm.nih.gov/bioproject/PRJNA297058], PRJNA340165 [https://www.ncbi.nlm.nih.gov/bioproject/PRJNA340165], PRJNA341273 [https://www.ncbi.nlm.nih.gov/bioproject/PRJNA341273]. Raw metagenome sequencing and metatranscriptome sequencing data with accession code PRJNA635214 have been published, and raw metagenome sequencing data with accession code PRJNA1051299 have been uploaded and will be released on 2027-10-01 (submission id: SUB14725554). Accession numbers for the previous published metagenomes also can be found in Supplementary Data 2. Public available datasets in this study include the GTDB database release 207 (https://data.gtdb.ecogenomic.org/releases/release207/), the SILVA 138 SSU database (https://www.arb-silva.de/download/archive/), and the Hg MATE database (https://doi.org/10.25573/serc.13105370.v1). Source data are provided with this paper. The custom scripts used in this study are publicly available at GitHub (https://github.com/ZhuoboLi/Mercury_metagenomics) and in Zenodo (https://doi.org/10.5281/zenodo.16269052). (https://zenodo.org/records/16269052). Correspondence and material requests should be directed to Y.Wang (wangyong@sz.tsinghua.edu.cn).

Research involving human participants, their data, or biological material

Policy information about studies with [human participants or human data](#). See also policy information about [sex, gender \(identity/presentation\), and sexual orientation](#) and [race, ethnicity and racism](#).

Reporting on sex and gender

Reporting on race, ethnicity, or other socially relevant groupings

Population characteristics

Recruitment

Ethics oversight

Note that full information on the approval of the study protocol must also be provided in the manuscript.

Field-specific reporting

Please select the one below that is the best fit for your research. If you are not sure, read the appropriate sections before making your selection.

☐ Life sciences ☐ Behavioural & social sciences ☒ Ecological, evolutionary & environmental sciences

For a reference copy of the document with all sections, see nature.com/documents/nr-reporting-summary-flat.pdf

Ecological, evolutionary & environmental sciences study design

All studies must disclose on these points even when the disclosure is negative.

Study description	To understand the ecological impact of mercury on deep-sea ecosystems, we analyzed 32 sediment cores, comprising 101 layers, along with 41 additional global reference sediment metagenomes. Based on these metagenomes data, we analyzed the biotransformation of Hg from marginal slopes to the hadal zone, including 1) the distinct relative abundance of Hg methylation and demethylation genes in the marginal sea compared to the open ocean, 2) the unique adaptations of Hg-methylating microbes in deep-sea sediments, and 3) a large number of novel Hg demethylation taxa in deep-sea sediments. Ultimately, we expand the diversity of Hg-transforming taxa and reveal their unique ecophysiological adaptations in deep-sea sediments.
Research sample	A total of 32 sediment cores were collected from South China Sea, Bashi Channel, northern slope of the Mariana Trench, and Challenger Deep of Mariana Trench at water depths ranging from 1,087 to 10,909 meters. South China Sea and Bashi Channel are close to the mainland, while northern slope of the Mariana Trench and Challenger Deep of Mariana Trench are located in the western Pacific Ocean which is farther away from the mainland (Fig. 1a and Supplementary Data 1). In addition, the 41 metagenomes downloaded from NCBI Sequence Read Archive were from samples collected at depths ranging from 100 m to 9,161 m (Supplementary Data 2).
Sampling strategy	For our sediment samples, we selected those from the South China Sea and Mariana Trench to represent sediments from the South China Sea-Western Pacific. In February 2023, marine sediment metagenomes for the global oceans were collected from NCBI. We selected samples from the marginal seas and open oceans, except for those from specialized environments including cold seeps and hydrothermal fluids.
Data collection	Our 32 sediment cores were collected by Y W and 41 global marine metagenomes were downloaded by ZB L from the NCBI-SRA database.
Timing and spatial scale	Our 32 sediment cores from the South China Sea and Mariana Trench were collected between 2016-2020, and 41 global marine metagenomes were downloaded in February 2023 from the NCBI-SRA database.
Data exclusions	No data were excluded from this manuscript.
Reproducibility	Detection of mercury, total nitrogen, total organic carbon and porewater nutrient concentrations were replicated independently by processing two replicate subsamples. All detections at replications were successful. According to the data and methods provided in

the papers, all results can be reproduced.

Randomization

All sediment cores were used to represent marginal slopes and open ocean sites. Subsamples of sediment cores by 2-cm layers were selected to represent sediment depth profile. We randomly selected sediment layers from oxic and anoxic layers. Samples from each layer were homogenized.

Blinding

Blinding was not applicable to this study. ALL methods and results that we used for analysis sediment samples are objective.

Did the study involve field work?

☒ Yes ☐ No

Field work, collection and transport

Field conditions

The marine sediment samples used in this study were collected from the seafloor of the South China Sea and the Pacific Ocean.

Location

For samples SCS1: 14.31996N, 115.20912E, water depth of 4299m.
 For samples SCS2: 13.424N, 114.83525E, water depth of 2053m.
 For samples SCS3: 14.15771N 115.51419E, water depth of 3797.8m.
 For samples SCS4: 17.98689N, 111.00278E, water depth of 1500m.
 For samples SCS5: 16.7291N, 110.4731E, water depth of 1390m.
 For samples SCS6: 16.11548N, 111.28475E, water depth of 1144m.
 For samples SCS7: 18.5123N, 112.8204E, water depth of 1372m.
 For samples SCS8: 18.4425N, 111.9046E, water depth of 1526m.
 For samples SCS9: 17.4279N, 113.7993E, water depth of 1217m.
 For samples BS1: 21.8729N, 120.0353E, water depth of 1646m.
 For samples BS2: 22.8167N, 123.3148E, water depth of 5991m.
 For samples BS3: 22.185N, 123.0272E, water depth of 4210m.
 For samples BS4: 22.1152N, 119.2855E, water depth of 1087m.
 For samples MT1: 12.616771N, 141.142565E, water depth of 3250m.
 For samples MT2: 12.48232N, 140.74122E, water depth of 3373m.
 For samples MT3: 11.61171N, 140.32451E, water depth of 3279m.
 For samples MT4: 11.43967N, 139.40662E, water depth of 2681m.
 For samples MT5: 11.65369N, 138.6214E, water depth of 3510m.
 For samples MT6: 11.81906N, 138.71595E, water depth of 3249m.
 For samples MC02: 11.764N, 141.976E, water depth of 5400m.
 For samples D1T1: 11.801N, 142.117E, water depth of 5533m.
 For samples D1T2: 11.801N, 142.117E, water depth of 5533m.
 For samples T1B5: 10.924N, 141.799E, water depth of 7061m.
 For samples T1B3: 11.553N, 141.873E, water depth of 7082m.
 For samples T1B8: 11.602N, 142.228E, water depth of 7143m.
 For samples T1L6: 11.091N, 142.073E, water depth of 7850m.
 For samples T1B10: 11.195N, 141.812E, water depth of 8638m.
 For samples T1B11: 11.228N, 141.689E, water depth of 9150m.
 For samples T1L10: 11.328N, 142.202E, water depth of 10900m.
 For samples T3L11: 11.325N, 142.191E, water depth of 10908m.
 For samples T3L8: 11.327N, 142.194E, water depth of 10909m.
 For samples T3L14: 11.325N, 142.189E, water depth of 10909m.

Access & import/export

Not relevant to this study.

Disturbance

None

Reporting for specific materials, systems and methods

We require information from authors about some types of materials, experimental systems and methods used in many studies. Here, indicate whether each material, system or method listed is relevant to your study. If you are not sure if a list item applies to your research, read the appropriate section before selecting a response.

Materials & experimental systems

n/a	Involved in the study
☒	☐ Antibodies
☒	☐ Eukaryotic cell lines
☒	☐ Palaeontology and archaeology
☒	☐ Animals and other organisms
☒	☐ Clinical data
☒	☐ Dual use research of concern
☒	☐ Plants

Methods

n/a	Involved in the study
☒	☐ ChIP-seq
☒	☐ Flow cytometry
☒	☐ MRI-based neuroimaging

Plants

Seed stocks

Report on the source of all seed stocks or other plant material used. If applicable, state the seed stock centre and catalogue number. If plant specimens were collected from the field, describe the collection location, date and sampling procedures.

Novel plant genotypes

Describe the methods by which all novel plant genotypes were produced. This includes those generated by transgenic approaches, gene editing, chemical/radiation-based mutagenesis and hybridization. For transgenic lines, describe the transformation method, the number of independent lines analyzed and the generation upon which experiments were performed. For gene-edited lines, describe the editor used, the endogenous sequence targeted for editing, the targeting guide RNA sequence (if applicable) and how the editor was applied.

Authentication

Describe any authentication procedures for each seed stock used or novel genotype generated. Describe any experiments used to assess the effect of a mutation and, where applicable, how potential secondary effects (e.g. second site T-DNA insertions, mosaicism, off-target gene editing) were examined.