

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 (<i>n</i>) 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. <i>F</i> , <i>t</i> , <i>r</i>) with confidence intervals, effect sizes, degrees of freedom and <i>P</i> 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 <i>d</i> , Pearson's <i>r</i>), 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	DNA was extracted from the three sediment core samples (B1, B2 and C1) using PowerSoil DNA Isolation Kits (MO BIO Laboratories) according to the manufacturer’s instructions. Metagenomic sequencing was performed on DNBSEQ-T1 and BGISEQ500 sequencers (MGI Tech, China).
Data analysis	For metagenome sequencing and analysis, raw reads derived from metagenome libraries were quality-controlled by clipping off primers and adapters and filtering out artefacts and low-quality reads using Read_QC module within the metaWRAP pipeline v1.3.2. Filtered reads were individually assembled and co-assembled using MEGAHIT v1.1.3 (k list: 21, 29, 39, 59, 79, 99, 119). Each assembly was binned using the binning module within the metaWRAP pipeline v1.3.2 (–metabat2 –maxbin2 –concoct for individual assembly and co-assembly from inactive samples; –metabat2 for co-assembly from active samples). For each assembly, the three bin sets (one for co-assembly from active samples) were consolidated into a final bin set with the bin_refinement module of metaWRAP pipeline v1.3.2 (–c 50 –x 10). Finally, 865 MAGs were obtained from the 18 assemblies. They were then combined and dereplicated using dRep v 3.0.0 (–comp 50 –con 10 –sa 0.95) at 95% average nucleotide identity clustering. The completeness and contamination of each MAG were assessed using the lineage-specific workflow of CheckM v1.0.18. After dereplication, a total of 487 dereplicated MAGs were obtained. Contigs in each MAG were renamed using anvi-script-reformat-fasta in anvi’o v6. Each MAG was taxonomically assigned according to the Genome Taxonomy Database (GTDB) (Release R06-RS202) using GTDB-tk v1.5.0. CoverM v0.6.1 “genome” (https://github.com/wwood/CoverM) was used to obtain coverage of genomes.

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](#)

Raw metagenomic sequencing data were deposited in NCBI (<https://www.ncbi.nlm.nih.gov/>; PRJNA739036). Large supplementary tables include geochemical data and metagenome statistics were deposited in Figshare (<https://figshare.com/account/articles/25688694>; 10.6084/m9.figshare.25688694).

Human research participants

Policy information about [studies involving human research participants and Sex and Gender in Research](#).

Reporting on sex and gender

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	In this study, we demonstrate substantial enrichments of mercury (Hg) and methylmercury (MMHg), along with the presence of microbes capable of metabolizing Hg in sediments of the Haima cold seep, South China Sea. We propose that cold seeps function as a previously unrecognized sink for Hg and source for MMHg in the deep ocean.
Research sample	Sediment and bivalve samples were collected from the Haima cold seep in the northern part of the South China Sea.
Sampling strategy	Sediment and bivalve samples were collected by the manned submersible ShenHai YongShi using a manipulator and push core sampler.
Data collection	Total Hg was measured on a Direct Mercury Analyzer (DMA 80, Milestone Inc., Italy). MMHg were analyzed by the combination of gas chromatography and cold vapor atomic fluorescence spectrometry. Hg isotopes were analyzed on a Nu-Plasma II MC-ICP-MS. The pore water DIC concentrations and carbon isotopes were analyzed with a continuous-flow isotope ratio mass spectrometer (MAT253, Gasbench). The sediment TOC and TN concentrations were measured on an elemental analyzer, connected to a stable isotope mass spectrometer (EA/IRMS, Elementar Vario Isotope Cube™/Isoprime 100™). Sulfate concentrations in pore water were measured by ion chromatography (ICS-1100, Thermo Inc., US). Metagenomic sequencing was performed on DNBSEQ-T1 and BGISEQ500 sequencers (MGI Tech, China).
Timing and spatial scale	It is not applicable for this study.
Data exclusions	No data were excluded from the analyses.
Reproducibility	The methods of data collection and analysis are presented in the methods section in detail and to enhance reproducibility. All attempts to repeat the experiment were successful.
Randomization	Samples were collected from three different environments, including the reference area, the active seep area, and the inactive seep area. Thus, we divided different groups according to the origin of the samples.

Blinding

Sediment push cores and bivalves were collected randomly in three different environments. Also, in the sediment column, sediment samples were collected randomly by depth.

Did the study involve field work? ☒ Yes ☐ No

Field work, collection and transport

Field conditions	The sampling field is 1400-1600 meters underwater in the deep ocean, with an ambient temperature of about 2-4°C.
Location	Haima cold seep is located at a water depth of approximately 1360–1400 m at the northern slope of the SCS.
Access & import/export	All samples collection has been fully compliant with local laws and all required permits has been secured for this study.
Disturbance	No disturbance occurred during the process of this study.

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

Methods

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