

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	No software was used.
Data analysis	Metagenome sequencing data processing: Trimmomatic v0.39, IDBA-UD v1.1.3, Non-pareil (R), OPERA-MS v0.9.0 Metagenome binning and refinement: metaWRAP v1.3.2, dRep v3.5.0, GTDB-Tk release 202. Data Analysis: R 4.3.0, with packages: ape 5.8, lme4 1.1-35.3.

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 metagenomic sequence data for this study have been deposited in the Genome Sequence Archive in National Genomics Data Center, China National Center for Bioinformation / Beijing Institute of Genomics, Chinese Academy of Sciences (<https://ngdc.cncb.ac.cn/gsa>). The Illumina sequencing data are archived under the

GSA accession CRA013105. The Nanopore sequencing data are archived under the GSA accession CRA013130. All data needed to evaluate the conclusions in the paper are present in the paper and/or the Supplementary Information. Source Data are provided with this paper.

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	Not applicable
Reporting on race, ethnicity, or other socially relevant groupings	Not applicable
Population characteristics	Not applicable
Recruitment	Not applicable
Ethics oversight	Not applicable

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](https://www.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	A series of hot spring sediment samples were collected for DNA extraction and metagenome sequencing. Metagenome-assembled genomes were reconstructed to build co-occurrence networks and metabolic complementarity networks. Two networks were co-analyzed to discover that higher temperatures in the hot spring could compact the mutualistic networks of thermophiles. Besides, commensalism was revealed to be the prevalent pattern of microorganisms' syntrophic dependencies. The study provides a novel workflow that combines metabolic modeling and co-occurrence determination based on the rancom matrix theory (RMT) method.
Research sample	The research sediment samples were collected from a hot spring site located in Tengchong, Yunnan Province, China (N24°56' ~ 25° 27', E98°26' ~ 98°27') in June 2020. The temperature gradient along the waterflow ranges from 85.8°C to 63.5°C. Metagenomic sequencing data are available in the Genome Sequence Archive in National Genomics Data Center, China National Center for Bioinformation / Beijing Institute of Genomics, Chinese Academy of Sciences (https://ngdc.cncb.ac.cn/gsa). The Illumina sequencing data are archived under the GSA accession CRA013105. The Nanopore sequencing data are archived under the GSA accession CRA013130. All data needed to evaluate the conclusions in the paper are present in the paper and/or the Supplementary Information.
Sampling strategy	Each sample for one temperature site consists of 5 replicates. In this case, 8 temperature sites (each one with 5 replicates), a total of 40 samples, were included in the analysis.
Data collection	Total DNA were extracted by Xi Peng. The acquired DNA was used for Illumina NovaSeq6000 PE250 metagenomic sequencing (DNA library insertion size: 450bp) and Oxford Nanopore sequencing (the PromethION R9.4 flow cells FLO-PRO002, Oxford Nanopore PromethION sequencer). The Illumina sequencing was conducted on all 40 samples by Magigene Biotechnology Co., Ltd. (Guangzhou, China). Replicate samples of each site were mixed and sequenced using Nanopore sequencing by Benagen Technology Co., Ltd (Wuhan, China).
Timing and spatial scale	N/A
Data exclusions	No data were excluded from the analyses.
Reproducibility	Our workflow can provide reproducibility. In our latest version of manuscript, we once used two sets of MAGs (different completeness and contamination standards) to run our pipeline and the results remain consistent. Besides, a set of MAGs from a composting system experiment was used to validate the pattern we found using our workflow with hot spring microbial community. The results were confirmed to be similar.
Randomization	The temperature groups were divided based on the dissimilarity test of MAG relative abundance distribution.
Blinding	Data analysis was not blinded because all related parameters were known and used in the analyses.
Did the study involve field work?	☐ Yes ☒ No

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	N/A
Novel plant genotypes	N/A
Authentication	N/A