

Reporting Summary

Nature Research 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 Research policies, see [Authors & Referees](#) and the [Editorial Policy Checklist](#).

Statistical parameters

When statistical analyses are reported, confirm that the following items are present in the relevant location (e.g. 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
- ☐ ☒ An indication of 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
Only common tests should be described solely by name; describe more complex techniques in the Methods section.
- ☐ ☒ 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 statistics 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
Give P values as exact values whenever suitable.
- ☒ ☐ 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
- ☒ ☐ Clearly defined error bars
State explicitly what error bars represent (e.g. SD, SE, CI)

Our web collection on [statistics for biologists](#) may be useful.

Software and code

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

Data collection

CopyRighter v0.46. SingleM v0.2.1. Vegan v2.4. R v3.3.2-v3.4.0. CLC Genomics Cell Assembler 4.4. BamM v1.3.8-v1.7.3. BWA v0.7.12. Samtools v0.1.19-v1.3. MetaBAT 3127e20aa4e7. CheckM v1.0.4. pplacer v1.1 alpha 16. CompareM v0.0.17. Widdowquinn/scripts git_version 56613. GTDB v2.1.8. FastTree v2.1.9. genomereetk v0.0.31. ARB v6.0.6. tax2tree 1.0. Prokka v1.11. HMMER v3.1b2. DIAMOND v0.8.27.89. MAFFT v7.221. MSGFPlus. ProteoWizard.

Data analysis

R v3.3.2

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/reviewers upon request. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Research [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 list of figures that have associated raw data
- A description of any restrictions on data availability

Data described in this manuscript are submitted under NCBI BioProject accession number PRJNA386568.

Field-specific reporting

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

☒ Life sciences ☐ Behavioural & social sciences

For a reference copy of the document with all sections, see nature.com/authors/policies/ReportingSummary-flat.pdf

Life sciences

Study design

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

Sample size	The number of samples from each core, and the number of cores analysed were not subject to a sample-size calculation before sampling. Since the specific differences in metabolism across the thaw gradient were not known before sampling, it was not possible to use statistical power calculations to guide estimation of the number of samples needed to be taken. The sample sizes are sufficient, since conclusions are reported with accompanying p-values.
Data exclusions	While some samples initially chosen did not yield sufficient DNA for sequencing, no data was excluded after raw sequencing reads became available for it.
Replication	Given the observation and discovery basis of the work presented, the reported findings were not reproduced.
Randomization	Experimental groups were not allocated, instead the sample's categories were derived from their natural environmental state.
Blinding	Given the observation and discovery basis of the work presented, blinding was not considered relevant.

Materials & experimental systems

Policy information about [availability of materials](#)

n/a	Involved in the study
<input checked="" type="checkbox"/>	<input type="checkbox"/> Unique materials
<input checked="" type="checkbox"/>	<input type="checkbox"/> Antibodies
<input checked="" type="checkbox"/>	<input type="checkbox"/> Eukaryotic cell lines
<input checked="" type="checkbox"/>	<input type="checkbox"/> Research animals
<input checked="" type="checkbox"/>	<input type="checkbox"/> Human research participants

Method-specific reporting

n/a	Involved in the study
<input checked="" type="checkbox"/>	<input type="checkbox"/> ChIP-seq
<input checked="" type="checkbox"/>	<input type="checkbox"/> Flow cytometry
<input checked="" type="checkbox"/>	<input type="checkbox"/> Magnetic resonance imaging