

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](#).

Please do not complete any field with "not applicable" or n/a. Refer to the help text for what text to use if an item is not relevant to your study.

For final submission: please carefully check your responses for accuracy; you will not be able to make changes later.

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

- | | | |
|-------------------------------------|-------------------------------------|--|
| <input type="checkbox"/> | <input checked="" type="checkbox"/> | The exact sample size (n) for each experimental group/condition, given as a discrete number and unit of measurement |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> | A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> | 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> |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> | A description of all covariates tested |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> | A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> | 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) |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> | 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> |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> | For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> | For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> | 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 Leica-X for fluorescence microscopy image acquisition. Shimadzu LabSolutions GC/MS for GC and GCMS analysis.

Data analysis Fiji/imageJ for FISH image analyses. Test-Probe for in silico FISH probe tests. QIIME2 for 16S rRNA and mcrA gene amplicon analysis. SPAdes for sequence filtering and assembly. CheckM for analysis of bin quality. Phylogenetic analyses via IQtree2. Sequence alignment via SSU-align (16S rRNA), MUSCLE (single copy markers), and MAFFT (McrA). Annotation via IMG/M and HydDB.

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](#)

16S rRNA gene and mcrA gene amplicon data, metagenomic reads, and metatranscriptomic reads are deposited at NCBI under BioProject PRJNA913929. Metagenomes and genomes are available on IMG/M (JGI) under IMG Genome IDs 3300005860 (WHS), 3300043541 (LCB058), 3300028675 (LCB003), 8012931703

(Ca. M. washburnensis strain LCB3), 8015587805 (Archaeoglobaceae archaeon LCB3), 8015589684 (Thermofilum sp. LCB3-A), 8015591669 (Thermofilum sp. LCB3-B), 8015593670 (Fervidicoccaceae archaeon LCB3), 8015596852 (Ignisphaera sp. LCB3), 8015595177 (Desulfurococcaceae archaeon LCB3).

Human research participants

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

Reporting on sex and gender

N/A

Population characteristics

N/A

Recruitment

N/A

Ethics oversight

N/A

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

Life sciences study design

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

Sample size

No sample size calculations were performed. Sample sizes were chosen depending on how much biomass was available for experimentation and it was always attempted to maximize the number of biological replicates. Cultivation experiments were performed on at least 2 independent biological samples and are stated in the figure legends. All attempts of replication were successful.

Data exclusions

No data were excluded from the analysis.

Replication

FISH was performed many times for several biological replicates along different points of the growth curve. Time points are indicated in the figures. Sample size for growth, stable isotope, and BONCAT experiments were chosen depending on how much biomass was available at the time, and it was always attempted to maximize the number of biological replicates. Cultivation experiments were performed on at least 2 independent biological samples and are stated in the figure legends. All attempts of replication were successful. For transcriptomics, 6 biological replicates had to be pooled to obtain enough RNA for a single RNA sequencing experiments.

Randomization

Randomization was not relevant for this study because it did not involve participant groups.

Blinding

Blinding was not relevant for this study because the researchers needed to verify culture samples and controls for all experiments.

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