nature research

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Last updated by author(s): Apr 13, 2020

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.

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 *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 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 *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

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	Zeiss Stemmi 2000-C stereomicroscope, Zeiss Axioplan 2 Imaging Microscope, Panasonic Lumix GH3 and G85 microfourthirds-lens-mount cameras, Olympus BX51 epifluorescence microscope, Nicolet Magna 860 Fourier transform infrared (FTIR) spectrophotometer, Zeiss 1550VP field emission SEM, Agilent 8800 inductively coupled plasma mass spectrometer, Bio-Rad C1000 Thermal Cycler with CFX96 Real-Time System, Illumina HiSeq2500, Agilent Technologies Bioanalyzer, CAMECA NanoSIMS 50L
Data analysis	Databases: NCBI (ncbi.nlm.nih.gov), JGI IMG (https://img.jgi.doe.gov/cgi-bin/mer/main.cgi), SILVA Ref NR 99 Database Release 119, Genome Taxonomy Database (GTDB) v0.2.2 Data Analysis: QIIME v1.8.0, UCLUST v7.11.0.667, ARB software v6.0.2, SINA v1.2.11, daime v2.1, RTA v1.18.64, bcl2fastq v1.8.4, Trimmomatic v0.36, Spades v3.11.1, mmgenome v0.7.1, bowtie2 v2.3.4.1, CheckM v1.0.6, GTDB v0.2.2, MrBayes v3.2.6, RAxML v8.1.7, sortmerna v2.0, kallisto v0.44.0, sleuth v0.30.0, BBMap v37.93, PRED-TMBB (http://bioinformatics.biol.uoa.gr/PRED-TMBB/), Look@NanoSIMS v2019-05-14 Data Visualization: iTOL (https://itol.embl.de/), Adobe Photoshop CC 2019, Adobe Illustrator CC 2019, Adobe Lightroom CC 2019

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. 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

All sequencing data has been deposited at National Center for Biotechnology Information (NCBI) under BioProject PRJNA562312. The cloned 16S rRNA gene sequences of “Ca. Manganitrophus noduliformans” (Species A) and Ramlibacter lithotrophicus (Species B) from the co-culture have been deposited at GenBank

under accession numbers MN381734 and MN381735, respectively. The iTAG sequences from 3 different enrichments has been deposited at SRA under accession numbers SRR10031198-SRR10031200. Genome sequences of the co-culture, from which the genome of Ca. M. noduliformans was reconstructed, have been deposited under BioSample SAMN12638105 with raw sequences deposited at SRA under accession number SRR10032644; the reconstructed genome of Ca. M. noduliformans has been deposited at DDBJ/ENA/GenBank under accession number VTOW00000000. Genome sequences of R. lithotrophicus strain RBP-1 have been deposited under BioSample SAMN12638106 with raw sequences deposited at SRA under accession number SRR10031379; the reconstructed genome of R. lithotrophicus strain RBP-1 has been deposited at DDBJ/ENA/GenBank under accession number VTOX00000000. Additionally, reconstructed genomes have been deposited in Joint Genome Institute (JGI) Genomes Online Database Study ID Gs0134339, with Integrated Microbial Genome ID 2784132095 for Ca. M. noduliformans and ID 2778260901 for R. lithotrophicus strain RBP-1. Transcriptome sequence data for the 7 biological replicates have been deposited at SRA under accession numbers SRR10060009, SRR10060010, SRR10060011, SRR10060012, SRR10060013, SRR10060017, SRR10060018. Unique biological materials are available upon reasonable request.

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 statistical methods were used to predetermine sample size. "Sample" as intended here seems to more relevant for the concept of deciding sample size in terms of numbers of animals or human subjects to include in a study. Here, as a microbiologist, we are almost always dealing with populations of tens of millions or more, its really quite a different issue. Aside from that, "sample" means very different things in different contexts, and it is not clear at all how statistics would replace sound experimental design in many of them. We have looked at the Nature document that details a past questionnaire, and see several well articulated responses from colleagues that touch on this.
Data exclusions	No data were excluded in the results. No data exclusion criteria were pre established. Again, it seems this tailored for larger studies on animals and human subjects, and not clear how "pre-establishing" would come into play here.
Replication	Technical and biological replication was performed as indicated in individual experiments reported. All attempts at replication were successful.
Randomization	Randomization was not relevant to this study, it was not a randomized controlled trial. As a standard in microbiology, samples were obtained from a larger population of an enrichment culture to inoculate experimental groups.
Blinding	None. This was not a clinical trial or a randomized controlled trial.

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
☒	☐ Animals and other organisms
☒	☐ Human research participants
☒	☐ Clinical data

Methods

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