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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	All data were collected using publicly available software; flow cytometry data was collected using the BD C6 Accuri software, all fluorescence/ luminescence data was collected using BioTek Gen5 Data Analysis software. Sequencing data were generated using the Illumina MiSeq platform and related software.
Data analysis	All data were analysed using R and related packages as cited in the text. DNA sequence data were initially processed using QIIME before being passed to R. All software used is publicly available.

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

The data used in the analysis are available in the FigShare repository with digital object identifiers 10.6084/m9.figshare.6100181 (phylotype table) and 10.6084/m9.figshare.6100340 (functional data). Sequence data that support the findings of this study have been deposited in NCBI Short Read Archive with accession number SRP145037.

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 ☒ Ecological, evolutionary & environmental sciences

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

Ecological, evolutionary & environmental sciences study design

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

Study description	Bacterial communities collected from the field were assayed in a common laboratory environment.
Research sample	Each bacterial community was a research sample.
Sampling strategy	Sample sizes were selected based on time and cost constraints.
Data collection	Data were collected by coauthor DWR using automated plate readers and flow cytometer.
Timing and spatial scale	Timing of data collection was based on growth curves of the communities (see supplementary information).
Data exclusions	The only data to be excluded from the analysis were from samples that were unable to reach the threshold for read coverage during 16S rRNA gene sequencing as described in the text. All other data were included in the analysis.
Reproducibility	Communities were independently revived and assayed 4 times.
Randomization	Communities were randomised across the microcosms.
Blinding	No formal blinding was possible, but data were collected by automated readers.

Did the study involve field work? ☒ Yes ☐ No

Field work, collection and transport

Field conditions	Study locations and timing are described in the text.
Location	Study locations were in southern England. Specific locations are described in the text.
Access and import/export	Local collection sites. No permits necessary.
Disturbance	Any disturbance would be very ephemeral.

Reporting for specific materials, systems and methods

Materials & experimental systems

n/a	Involved in the study
☐	☒ Unique biological materials
☒	☐ Antibodies
☒	☐ Eukaryotic cell lines
☒	☐ Palaeontology
☒	☐ Animals and other organisms
☒	☐ Human research participants

Methods

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

Unique biological materials

Policy information about availability of materials

Obtaining unique materials	All unique bacterial communities used in this experiment are available from the corresponding author upon request.

Flow Cytometry

Plots

Confirm that:

☐ The axis labels state the marker and fluorochrome used (e.g. CD4-FITC).

☐ The axis scales are clearly visible. Include numbers along axes only for bottom left plot of group (a 'group' is an analysis of identical markers).

☐ All plots are contour plots with outliers or pseudocolor plots.

☒ A numerical value for number of cells or percentage (with statistics) is provided.

Methodology

Sample preparation	Samples were extracted from the microcosms and immediately diluted in water containing 42 nM thiazole orange to stain "live" cells. Cells were then incubated at room temperature in the dark for at least 5 minutes prior to analysis.
Instrument	BD Biosciences C6 Accuri (C6 SN 4408)
Software	Flow cytometry data were collected using the BD Accuri™ C6 Software provided with the C6 Accuri flow cytometer.
Cell population abundance	Cell abundances were total absolute counts. There was no counting of subpopulations except to exclude background noise.
Gating strategy	Gates were created to exclude background fluorescence relative to negative controls (sterile media).

☐ Tick this box to confirm that a figure exemplifying the gating strategy is provided in the Supplementary Information.