

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

We conducted a global field survey (83 locations in five continents) and a microcosm experiment. Data collection information is included in the method section of our manuscript.

Data analysis

For Bioinformatic analysis, a combination of Qiime and USEARCH, UPARSE and UCLUST were used. For the Co-occurrence Network, R (<https://cran.r-project.org>) was used for analyses, and Gephi for visualization. The rest of the analysis were made with R 3.4.0.

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 the materials, raw data, and protocols used in the article are available upon request, and all data will be made publicly available in a public repository (Figshare) upon publication.

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	Here, we combined a global field study with microcosm experiments to provide a novel test of the linkages between soil biodiversity and multifunctionality.
Research sample	A total of 415 soil samples were analyzed in this study for soil biodiversity and ecosystem functions.
Sampling strategy	Our sampling was designed to assess soil biodiversity and ecosystem functions at the plot level (50 m × 50 m resolution). Five composite topsoil samples from five 0-10 cm soil cores were collected under the dominant vegetation within each location, meaning that twenty five cores were collected in each plot, and five composite samples were analyzed for functions and soil biodiversity. A total of 415 soil samples were analyzed in this study. We calculated site-level estimates of soil biodiversity and ecosystem functions as explained in the Material and Methods of our paper.
Data collection	We combined a global field survey (87 locations in five continents), across a wide range of ecosystem types, with a microcosm experiment. Our field study included information on ~45,000 soil species, and eleven ecosystem functions associated with multiple ecosystem services including nutrient cycling, organic matter decomposition, primary production and plant pathogen and antibiotic resistance gene control.
Timing and spatial scale	Sample collection of soils took place between 2014 and 2017
Data exclusions	N/A
Reproducibility	Information about the sampled locations and methods used in this paper are included in our material and methods
Randomization	N/A
Blinding	N/A
Did the study involve field work?	☒ Yes ☐ No

Field work, collection and transport

Field conditions	We conducted a global field survey (83 locations in five continents) and a microcosm experiment. These global locations were selected to include a wide range of climates (tropical, temperate, continental, polar and arid) and vegetation types (including grasslands, shrublands, forests, and forblands) in order to represent the wide gradients of soil biodiversity and multifunctionality found across the globe.
Location	We conducted a global field survey (83 locations in five continents). See Extended Data Figure 1.
Access and import/export	Samples were collected by all authors in their respective locations and using local permits.
Disturbance	This study did not cause any environmental disturbance

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 |