

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](#).

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 ( <i>n</i> ) 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 type="checkbox"/>            | <input checked="" type="checkbox"/> The statistical test(s) used AND whether they are one- or two-sided<br><i>Only common tests should be described solely by name; describe more complex techniques in the Methods section.</i>                                                               |
| <input type="checkbox"/>            | <input checked="" type="checkbox"/> A description of all covariates tested                                                                                                                                                                                                                     |
| <input type="checkbox"/>            | <input checked="" type="checkbox"/> A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons                                                                                                                                        |
| <input type="checkbox"/>            | <input checked="" 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 type="checkbox"/>            | <input checked="" type="checkbox"/> For null hypothesis testing, the test statistic (e.g. <i>F</i> , <i>t</i> , <i>r</i> ) with confidence intervals, effect sizes, degrees of freedom and <i>P</i> value noted<br><i>Give P values as exact values whenever suitable.</i>                     |
| <input type="checkbox"/>            | <input checked="" type="checkbox"/> For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings                                                                                                                                                           |
| <input type="checkbox"/>            | <input checked="" 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 <i>d</i> , Pearson's <i>r</i> ), 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 | Amino acids Isotope peak detection and integration were performed using Isodat software, which was used to quantify stable isotope signals from chromatographic data. Bacterial and fungal community composition were analyzed using DNA amplicon sequencing targeting the bacterial 16S rRNA gene (V3-V4, region) and the fungal ITS1 region. |
| Data analysis   | All statistical analyses were run in R version 4.4.043. All figures were drawn using “ggplot2”. Bayesian linear regression model was conducted using “brms” package. Bayesian mixing models were run using the “MixSIAR” package44; statistical results of linear models were obtained using the “vegan” and “stats” packages.                 |

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](#)

The data and code were included in Zenodo (link for peer review process:  
[https://zenodo.org/records/20476876?preview=1&token=eyJhbGciOiJIUzUxMiJ9.eyJpZCI6IjYxMjU4NDZlTlI3YmItNGJmMy05ZWYwLTgzMzZkZjlyZmF0SIsImRhdGEiOnt9LCJyYW5kb20iOiJhY2UxMTEzMmUxNDJkYzQzMmRiMjU3ZTA4ZmFiNjc3NCJ9.bCqSgMQuNr3TksrOO-hZxCBEt\\_npmtJmCAjU4FZopQNXuH\\_znjvQJcvzYgPevelCTYI3r1jUliiWo4fiXDhdw](https://zenodo.org/records/20476876?preview=1&token=eyJhbGciOiJIUzUxMiJ9.eyJpZCI6IjYxMjU4NDZlTlI3YmItNGJmMy05ZWYwLTgzMzZkZjlyZmF0SIsImRhdGEiOnt9LCJyYW5kb20iOiJhY2UxMTEzMmUxNDJkYzQzMmRiMjU3ZTA4ZmFiNjc3NCJ9.bCqSgMQuNr3TksrOO-hZxCBEt_npmtJmCAjU4FZopQNXuH_znjvQJcvzYgPevelCTYI3r1jUliiWo4fiXDhdw)).  
 Raw DNA sequencing data was submitted to NCBI with the Sequence Read Archive database under accession number PRJNA1465384.

## Research involving human participants, their data, or biological material

Policy information about studies with [human participants or human data](#). See also policy information about [sex, gender \(identity/presentation\)](#), [and sexual orientation](#) and [race, ethnicity and racism](#).

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| Reporting on sex and gender                                        | N/A |
| Reporting on race, ethnicity, or other socially relevant groupings | 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](https://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        | The study explores the trophic niches of soil microbes under different litter quality                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |
| Research sample          | Not applicable                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| Sampling strategy        | Not applicable                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| Data collection          | compound-specific isotope analysis of amino acids and 16S rDNA sequencing.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |
| Timing and spatial scale | Not applicable                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| Data exclusions          | No data were excluded from the analysis                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |
| Reproducibility          | R code and statistical model specifications are available in Zenodo (link for peer review process:<br><a href="https://zenodo.org/records/20476876?preview=1&amp;token=eyJhbGciOiJIUzUxMiJ9.eyJpZCI6IjYxMjU4NDZlTlI3YmItNGJmMy05ZWYwLTgzMzZkZjlyZmF0SIsImRhdGEiOnt9LCJyYW5kb20iOiJhY2UxMTEzMmUxNDJkYzQzMmRiMjU3ZTA4ZmFiNjc3NCJ9.bCqSgMQuNr3TksrOO-">https://zenodo.org/records/20476876?preview=1&amp;token=eyJhbGciOiJIUzUxMiJ9.eyJpZCI6IjYxMjU4NDZlTlI3YmItNGJmMy05ZWYwLTgzMzZkZjlyZmF0SIsImRhdGEiOnt9LCJyYW5kb20iOiJhY2UxMTEzMmUxNDJkYzQzMmRiMjU3ZTA4ZmFiNjc3NCJ9.bCqSgMQuNr3TksrOO-</a> |

hZxCBEt\_npmtJmCAjU4FZopQNXuH\_znjvQJcvzZYgPevelCTYI3r1jUliiWo4fiXDhdw) allowing to reproduce the data analysis in the supplementary.

Randomization

Not applicable for this microcosm experimental

Blinding

Not applicable

Did the study involve field work?

☐ Yes

☒ No

## 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

### Methods

- n/a Involved in the study
- ☒ ☐ Antibodies
  - ☒ ☐ Eukaryotic cell lines
  - ☒ ☐ Palaeontology and archaeology
  - ☒ ☐ Animals and other organisms
  - ☒ ☐ Clinical data
  - ☒ ☐ Dual use research of concern
  - ☒ ☐ Plants

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

### Plants

Seed stocks

NA

Novel plant genotypes

NA

Authentication

NA