

From trees to soil: microbial and spatial mediation of tree diversity effects on carbon cycling in subtropical Chinese forests

Der Fakultät für Lebenswissenschaften

der Universität Leipzig

eingereichte

DISSEMINATION APPENDIX

zur Erlangung des akademischen Grades

Doctor rerum naturalium

Dr. rer. nat.

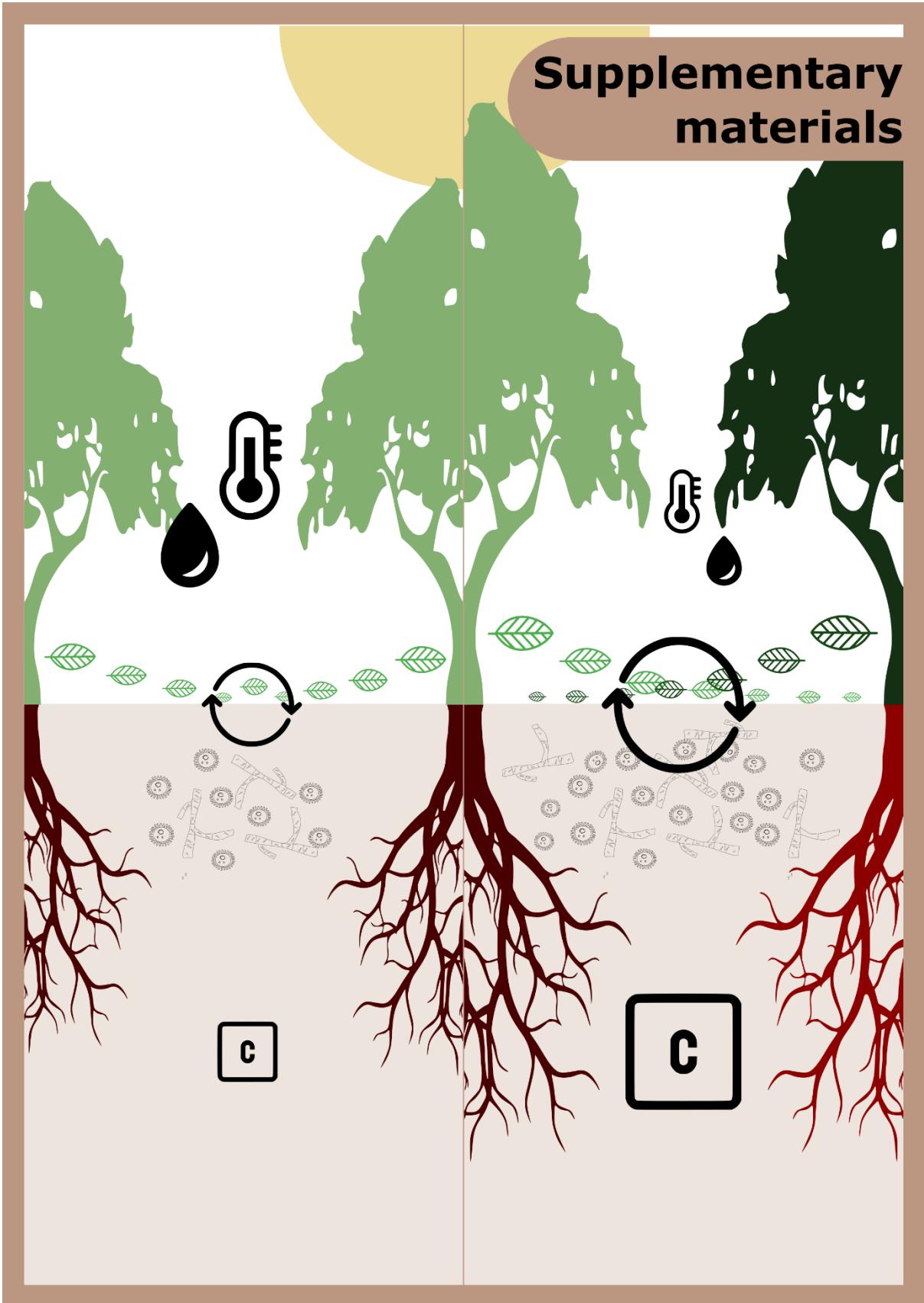
Vorgelegt

von Rémy Beugnon

geboren am 16.03.1993 in Rochefort s/ Mer, France

Leipzig, den 30. September 2021

Supplementary materials



Declaration of independent work

I, Rémy Beugnon, hereby affirm that I take note and accept the doctorate regulations of the Faculty of Biosciences, Pharmacy and Psychology of the University of Leipzig from the 30th of September 2019.

I further affirm that the presented thesis was prepared autonomously without inadmissible help. All aids used in this thesis as well as scientific ideas which are quoted from or based on other sources were cited at the respective point.

All people who helped me to prepared the conception, to select and analyze the materials of this thesis as well as to improve the manuscript are namely cited in the acknowledgments. With exception of the namely mentioned people no other persons were involved in the intellectual work. No Ph.D. consultant service was employed. Third parties did not get money's worth for benefits that were in conjunction with the content of this dissertation.

I declare that this dissertation has been neither presented nationally nor internationally in its entirely or in parts to any institution for the purpose of dissertation or other official or scientific examination and/or publishing.

Previously unsuccessful dissertations had not taken place.

The original document of the verification of the co-authors' parts are deposited in the office of the dean.

Leipzig, the 30th of September 2021



CV



Ph.D candidate in the German Center for Integrative Biodiversity Research (iDiv) Halle – Jena – Leipzig. I am working on tree diversity effects on soil microbial community and soil functioning including litter decomposition and soil carbon storage.

Research interest: BEF, ecosystem ecology, soil ecology, microbial ecology, food web ecology, synthesis

Rémy Beugnon

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Web: <https://remybeugnon.netlify.app/>

Languages

French – native
English – fluent

Field skills

- Subtropical China field campaign
- Litterfall, insect and soil sampling
- Performing decomposition experiment

Lab skills

- Microbial biomass (e.g., PLFA)
- Microbial physiology (e.g., MicroResp®)
- Insect identification

Analysis skills

- Multivariate analysis (e.g. PCA, RDA)
- Frequentist statistic (e.g. linear, non-linear, mixed effects models)
- Spatio-temporal analysis
- Structural Equation Modelling
- Network analysis (basic knowledge)
- Bayesian statistics (basic knowledge)

Programming skills

R – advanced
Bash – basic knowledge
LaTeX – basic knowledge
Python/HTML/SQL/GIS – basic knowledge

Research experiences

07.2018 to now

Ph.D thesis - German Center for Integrative Biodiversity Research (iDiv) Halle – Jena – Leipzig , Leipzig (Germany)

Tree diversity effects on soil microbial communities and soil carbon dynamics

Supervision: Dr. Simone Cesarz, Prof. Dr. Nico Eisenhauer

Main topics: tree interactions effects on litterfall, decomposition, microbial community composition and functions and soil carbon storage

01.2018 to 06.2018

MSc. thesis - Institut des Sciences de l'Evolution de Montpellier ISME, Montpellier (France)

Modelling non-trophic interactions effects on community dynamics.

Supervision: Dr. Sonia Kéfi, Dr. Vasilis Dakos

04.2017 to 07.2017

Internship - Swedish University of Agricultural Sciences (SLU), Umeå (Sweden)

Root trait effects of alpine plant communities on plant-soil feedback effects performed in two greenhouse experiments.

Supervision: Dr. Paul Kardol

Education

09.2017-06.2018

Master's degree in biology, ecology and evolution – Université de Montpellier, France

09.2014-11.2018

Agricultural engineering diploma – Montpellier SupAgro, France

Publications

2019

Beugnon, Rémy; Steinauer, Katja; Barnes, Andrew D.; Ebeling, Anne; Roscher, Christiane; Eisenhauer, Nico (2019): *Plant functional trait identity and diversity effects on soil meso-and macrofauna in an experimental grassland.* In Advances in ecological research 61, p. 163-184. DOI: 10.1016/bs.aecr.2019.06.004

Cesarz, Simone; Schulz, Annika Eva; **Beugnon, Rémy**; Eisenhauer, Nico (2019): *Testing soil nematode extraction efficiency using different variations of the Baermann-funnel method.* In Soil Organisms 91 (2), p. 61. DOI: 10.25674%2Fso91201

2021

Beugnon, Rémy† & Du Jianqing†; Cesarz, Simone; Jurburg, Stephanie D.; Pang, Zhe; Singavarapu, Bala; Wubet, Tesfaye; Xue, Kai; Wangs, Yanfen^S & Eisenhauer, Nico^S (2021): *Tree diversity and soil chemical properties drive the linkages between soil microbial community and ecosystem functioning.* In ISME Communications 1 (1), 1-11. DOI: 10.1038/s43705-021-00040-0

Beugnon, Rémy, Emma Ladouceur, Marie Sünnemann, Simone Cesarz^S & Nico Eisenhauer^S (2021): *Diverse forests are cool: promoting diverse forest to mitigate carbon emission and climate change.* In Journal of Sustainable Agriculture and Environment

Phillips, Helen R. P.; Bach, Elizabeth M.; Bartz, Marie L. C.; Bennett, Joanne M.; **Beugnon, Rémy**; Briones, Maria J. I. et al. (2021): *Global data on earthworm abundance, biomass, diversity and corresponding environmental properties.* In Scientific Data 8 (1), p. 136. DOI: 10.1038/s41597-021-00912-z.

Singavarapu, Bala; **Beugnon, Rémy**; Bruelheide, Helge; Cesarz, Simone; Du, Jianqing; Eisenhauer, Nico; Guo, Liang-Dong; Nawaz, Ali; Wang, Yanfen; Xue, Kai; Wubet, Tesfaye (2021): *Tree mycorrhizal type and tree diversity shape the forest soil microbiome.* In Environmental Microbiology

Thouvenot, Lise; Ferlian, Olga; **Beugnon, Rémy**; Künne, Tom; Lochner, Alfred; Thakur, Madhav P.; Türke, Manfred; Eisenhauer, Nico (2021): *Do invasive earthworms affect the functional traits of native plants?* In Frontiers in plant science 12, p. 424. DOI: 10.3389/fpls.2021.627573

In preparation

Beugnon, Rémy; Bu, Wensheng; Bruelheide, Helge; Davrinche, Andréa; Du, Jianqing; Haider, Sylvia; Kunz, Matthias; von Oheimb, Goddert; Perles-Garcia, Maria D.; Saadani, Mariem; Scholten, Thomas; Seitz, Steffen; Singavarapu, Bala; Trogisch, Stefan; Wang, Yanfen; Wubet, Tesfaye; Xue, Kai; Yang, Bo; Cesarz, Simone^S & Eisenhauer, Nico^S (**under review**): *Abiotic and biotic drivers of scale-dependent tree trait effects on soil microbial biomass and soil carbon concentration.* In Ecological Monographs

Beugnon, Rémy; Eisenhauer, Nico; Bruelheide, Helge; Davrinche, Andréa; Du, Jianqing; Haider, Sylvia; Haehn, Georg; Saadani, Mariem; Singavarapu, Bala; Sünnemann, Marie; Thouvenot, Lise; Wang, Yanfen; Wubet, Tesfaye; Xue, Kai; Cesarz, Simone (**in prep.**): *Tree diversity effects on litter decomposition are mediated by litterfall and microbial processes.*

Schnabel, Florian†; **Beugnon, Rémy**†; Bo, Yang†; Castro Izaguirre, Nadia Cristina; Cesarz, Simone; Eisenhauer, Nico; Garcia, Maria Dolores Perles; Haehn, Georg; Härdtle, Werner; Huang, Yuanyuan; Kunz, Matthias; Liu, Xiaojuan; Niklaus, Pascal A.; von Oheimb, Goddert; Pietsch, Katherine A.; Richter, Ronny; Schmid, Bernhard; Trogisch, Stefan; Wirth, Christian; Ma, Keping^S & Bruelheide Helge^S (**in prep.**): *The role of tree species richness for temperature buffering below forest canopies.*

Reviewer

Nature Communications, Scientific Reports, Pedobiologia, Soil Organisms

Teaching

2021 - Introduction to stats in R for bachelors and master students (12h)

Outreach

2019 to 2021 - Guest editor for Frontiers for Young Minds collection “Soil biodiversity”

2021 - Contribution to the Leipzig’s Long Night of Sciences

Oral presentations and invited talks

2018 - “*Effect of non-trophic interactions on community dynamics*”, Model in Ecology and Evolution conference – Monpellier, France

2019 - “*Effects of tree functional diversity on soil community and function*”, iDiv conference – Leipzig, Germany

2020

“*To a mechanistical understanding of plant diversity effects on soil fauna community*”, Laboratoire d’écologie alpine (LECA) – Grenoble, France

“*Abiotic and biotic mediations of scale dependent tree traits effects on soil carbon concentrations*”, BES annual meeting 2020 – Virtual

2021

“*Tree diversity effects on litter decomposition and microbial processes*”, GfÖ annual meeting – Virtual

Professionalization courses

2021 - Third Party Funding Opportunities

2020

- Scientific writing
- Introduction to ggplot2
- Good scientific practices

2019

- Structural Equation Modeling
- Nematode identification course

Participation to institutional activities

09.2021 - Ph.D representative for iDiv Equal Opportunity comity

2021 - Interviews of senior researcher about “transdisciplinary research” for the GfÖ Twitter account

2018-2021

- Organization of afterwork activities for the Experimental Interaction Ecology (EIE) working group
- Organization of welcome packages for new members of the EIE working group

Article justifications

Nachweis über Anteile der Co-Autoren:

Title: Tree diversity effects on litter decomposition are mediated by litterfall and microbial processes

Journal: Nature Communications (*under review*)

Autoren: Rémy Beugnon, Nico Eisenhauer, Helge Bruelheide, Andréa Davrinche, Jianqing Du, Sylvia Haider, Georg Haehn, Mariem Saadani, Bala Singavarapu, Marie Sünnemann, Lise Thouvenot, Yanfen Wang, Tesfaye Wubet, Kai Xue & Simone Cesarz

Beiträge:

Rémy Beugnon: i. field sampling, ii. lab measurements, iii. project conceptual framework, iv. statistical analyses, v. manuscript writing

Nico Eisenhauer: i. funding; ii. project conceptual framework, iii. framing of the manuscript, iv. writing

Helge Bruelheide: i. project conceptual framework, ii. funding, ii. manuscript revision

Andréa Davrinche: i. field sampling, ii. lab measurements, iii. manuscript revision

Jianqing Du: i. project conceptual framework, ii. manuscript revision

Sylvia Haider: i. funding; ii. trait data; iii. manuscript revision

Georg Haehn: i. field sampling, ii. lab measurements, iii. manuscript revision

Mariem Saadani: i. field sampling, ii. manuscript revision

Bala Singavarapu: i. field sampling, ii. manuscript revision

Marie Sünnemann: i. project conceptual framework, ii. writing

Lise Thouvenot: i. project conceptual framework, ii. writing

Yanfen Wang: i. project conceptual framework, ii. manuscript revision

Tesfaye Wubet: i. project conceptual framework, ii. manuscript revision

Kai Xue: i. project conceptual framework, ii. manuscript revision

Simone Cesarz: i. funding; ii. project conceptual framework, iii. framing of the manuscript, iv. writing

*Nachweis über Anteile der Co-Autoren, Rémy Beugnon
From tree to soil: microbial and spatial mediation of tree diversity effects on carbon cycling
in Subtropical Chinese forests*

Unterschriften:

Rémy Beugnon



Prof. Dr. Nico Eisenhauer

Nico Eisenhauer

Digital unterschrieben von Nico Eisenhauer
Name: Nico Eisenhauer, Ort: Universität Regensburg, aus: Biogeochemie, Hochschulökologie, Email: nico.eisenhauer@idv.de, c:DE Datum: 2021.08.20 19:26:05 +0200

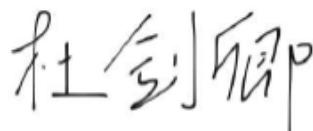
Prof. Dr. Helge Bruelheide



Andréa Davrinche



Dr. Jianqing Du



Dr. Sylvia Haider



Georg Hähn



Mariem Saadani



Bala Singavarapu



Marie Sünnemann



Dr. Lise Thouvenot



Prof. Dr. Yanfen Wang



Dr. Tesfaye Wubet



Dr. Kai Xue



Dr. Simone Cesarz



Nachweis über Anteile der Co-Autoren:

Title: Tree diversity and soil chemical properties drive the linkages between soil microbial community and ecosystem functioning

Journal: ISME Communications

Autoren: Rémy Beugnon & Jianqing Du, Simone Cesarz, Stephanie D. Jurburg, Zhe Pang, Bala Singavarapu, Tesfaye Wubet, Kai Xue, Yanfen Wang & Nico Eisenhauer

Beiträge:

Rémy Beugnon: i. field sampling, ii. lab measurements, iii. project conceptual framework, iv. statistical analyses, v. manuscript writing

Jianqing Du: i. lab measurements, ii. project conceptual framework, iii. contributed to statistical analyses, iv. manuscript writing

Dr. Simone Cesarz: i. contributed to project conceptual framework, ii. contributed to the framing of paper, iii. contributed to writing, iv. funding

Dr. Stephanie D. Jurburg: i. contributed to statistical analyses, ii.

contributed to writing Dr. Zhe Pang: i. lab measurements

Bala Singavarapu: i. field sampling, ii. lab measurements, iii. contributed to statistical analyses, iv. manuscript revisions

Dr. Tesfaye Wubet: i. provided lab support for microbial community profiling ii. bioinformatics, iii. contributed to manuscript revisions, iv. funding

Dr. Kai Xue: i. laboratory support, ii. contributed to project conceptual framework, iii. contributed to writing

Prof. Dr. Yanfen Wang: i. lab support for measurements of soil properties and functional genes, ii. contributed to manuscript revisions, iii. funding

Prof. Dr. Nico Eisenhauer: i. contributed to project conceptual framework, ii. contributed to framing of paper, iii. contributed to writing, iv. funding

Nachweis über Anteile der Co-Autoren, Rémy Beugnon

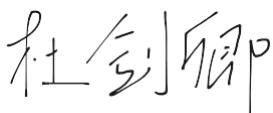
*From tree to soil: microbial and spatial mediation of tree diversity effects on carbon cycling
in Subtropical Chinese forests*

Unterschriften:

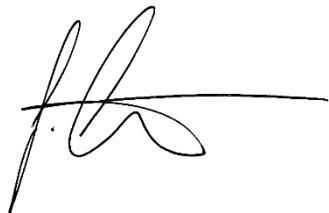
Rémy Beugnon



Jianqing Du



Dr. Simone Cesarz



Dr. Stephanie D.
Jurburg



Dr. Zhe Pang



Bala Singavarapu



Dr. Tesfaye Wubet



Dr. Kai Xue



Prof. Dr. Yanfen
Wang



Prof. Dr. Nico
Eisenhauer



Nachweis über Anteile der Co-Autoren:

Title: Abiotic and biotic drivers of scale-dependent tree trait effects on soil microbial biomass and soil carbon concentration

Journal: Ecological Monographs (*under review*)

Autoren: Rémy Beugnon, Wensheng Bu, Helge Bruelheide, Andréa Davrinche, Jianqing Du, Sylvia Haider, Matthias Kunz, Goddert von Oheimb, Maria D. Perles-Garcia, Mariem Saadani, Thomas Scholten, Steffen Seitz, Bala Singavarapu, Stefan Trogisch, Yanfen Wang, Tesfaye Wubet, Kai Xue, Bo Yang, Simone Cesarz & Nico Eisenhauer.

Beiträge:

Rémy Beugnon: i. field sampling, ii. lab measurements, iii. project conceptual framework, iv. statistical analyses, v. manuscript writing

Dr. Wensheng Bu: i. field sampling, ii. lab measurements

Prof. Dr. Helge Bruelheide: i. securing funding, ii. experimental design, iii. trait and environmental measurements, vi. manuscript revisions.

Andréa Davrinche: i. field sampling (traits), ii. lab measurements (traits), iii. manuscript revisions

Jianqing Du: i. field sampling, ii. lab measurements, iii. manuscript revisions

Dr. Sylvia Haider: i. field sampling (traits), ii. lab measurements (traits), iii. manuscript revisions

Dr. Matthias Kunz: i. field sampling, iii. manuscript revisions

Prof. Dr. Goddert von Oheimb: i. securing funding, ii. manuscript revisions

Maria D. Perles-Garcia: i. field sampling, ii. data calculation, iii. manuscript revisions

Mariem Saadani: i. field sampling (Basal area), ii. manuscript revisions

Prof. Dr. Thomas Scholten: i. field sampling, ii. lab measurements, iii. manuscript revisions

Dr. Steffen Seitz: i. field sampling, ii. lab measurements, iii. manuscript revisions

Bala Singavarapu: i. field sampling, iii. manuscript revisions

Dr. Stefan Trogisch: i. field sampling, ii. manuscript revisions

Nachweis über Anteile der Co-Autoren, Rémy Beugnon

*From tree to soil: microbial and spatial mediation of tree diversity effects on carbon cycling
in Subtropical Chinese forests*

Prof. Dr. Yanfen Wang: i. laboratory support, ii. manuscript revisions

Dr. Tesfaye Wubet: i. field sampling, ii. manuscript revisions

Dr. Kai Xue: i. laboratory support, ii. manuscript revisions

Dr. Bo Yang: i. site establishment, ii. microclimate measurements

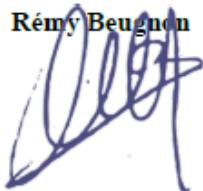
Dr. Simone Cesarz: i. conceived the study, ii. secured relevant funds, iii. project conceptual framework, iv. laboratory support, v. manuscript revisions

Prof. Dr. Nico Eisenhauer: i. conceived the study, ii. secured relevant funds, iii. project conceptual framework, iv. manuscript revisions

Nachweis über Anteile der Co-Autoren, Rémy Beugnon
From tree to soil: microbial and spatial mediation of tree diversity effects on carbon cycling
in Subtropical Chinese forests

Unterschriften:

Rémy Beugnon



Dr. Wensheng Bu



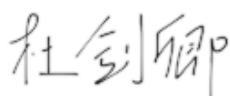
Prof. Dr. Helge Bruelheide



Andréa Davrinche



Jianqing Du



Dr. Sylvia Haider



Dr. Matthias Kunz



Prof. Dr. Goddert von Oheimb



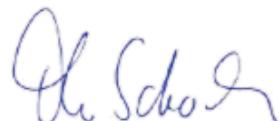
Maria D. Perles-Garcia



Mariem Saadani



Prof. Dr. Thomas Scholten



Dr. Steffen Seitz



Bala Singavarapu



Dr. Stefan Trogisch



Prof. Dr. Yanfen Wang



Dr. Tesfaye Wubet



Dr. Kai Xue



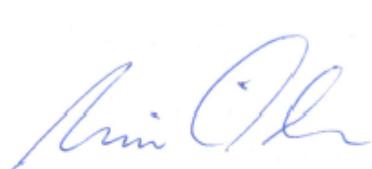
Dr. Bo Yang



Dr. Simone Cesarz



Prof. Dr. Nico Eisenhauer



Nachweis über Anteile der Co-Autoren:

Title: Diverse forests are cool: promoting diverse forests to mitigate carbon emissions and climate change

Journal: Journal of Sustainable Agriculture and Environment

Autoren: Rémy Beugnon, Emma Ladouceur, Marie Sünnemann, Simone Cesarz & Nico Eisenhauer.

Beiträge:

Rémy Beugnon: i. conceptual framework, ii. manuscript writing, iii. manuscript revisions

Dr. Emma Ladouceur: i. conceptual framework, ii. manuscript revisions

Marie Sünnemann: i. conceptual framework, ii. manuscript revisions

Dr. Simone Cesarz: i. conceptual framework, ii. manuscript revisions

Prof. Dr. Nico Eisenhauer: i. conceptual framework, ii. manuscript revisions

Unterschriften:

Rémy Beugnon



Dr. Emma Ladouceur



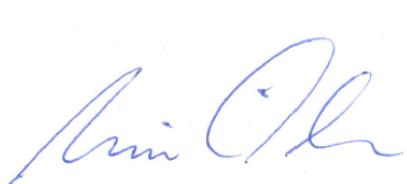
Marie Sünnemann



Dr. Simone Cesarz



Prof. Dr. Nico Eisenhauer



Beugnon, Rémy

From: Journal of Sustainable Agriculture and Environment
<onbehalfof@manuscriptcentral.com>
Sent: Friday, September 17, 2021 3:01 AM
To: Beugnon, Rémy; Ladouceur, Emma Rachel; Sünnemann, Marie-Catherine Elisabeth;
Cesarz, Simone; Eisenhauer, Nico
Subject: [Extern] Journal of Sustainable Agriculture and Environment - Decision on
Manuscript ID JSAE-2021-0005.R1 [email ref: DL-SW-1-a]

16-Sep-2021

Dear Rémy Beugnon:

It is a pleasure to accept your manuscript entitled "Diverse forests are cool: promoting diverse forests to mitigate carbon emissions and climate change" in its current form for publication in Journal of Sustainable Agriculture and Environment. The comments of the reviewer(s) who reviewed your manuscript are included at the bottom of this letter.

Please note although the manuscript is accepted the files will now be checked to ensure that everything is ready for publication, and you may be contacted if final versions of files for publication are required.

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Thank you for your fine contribution. On behalf of the Editors of Journal of Sustainable Agriculture and Environment, we look forward to your continued contributions to the Journal.

TO WHOME IT MAY CONCERN

I, as a Ph.D. supervisor of Rémy Beugnon, confirm that the information about the authors contributions on his Ph.D. manuscript are correct for the cases where either original or electronic signatures of the co-authors are unavailable.



Prof. Dr. Nico Eisenhauer

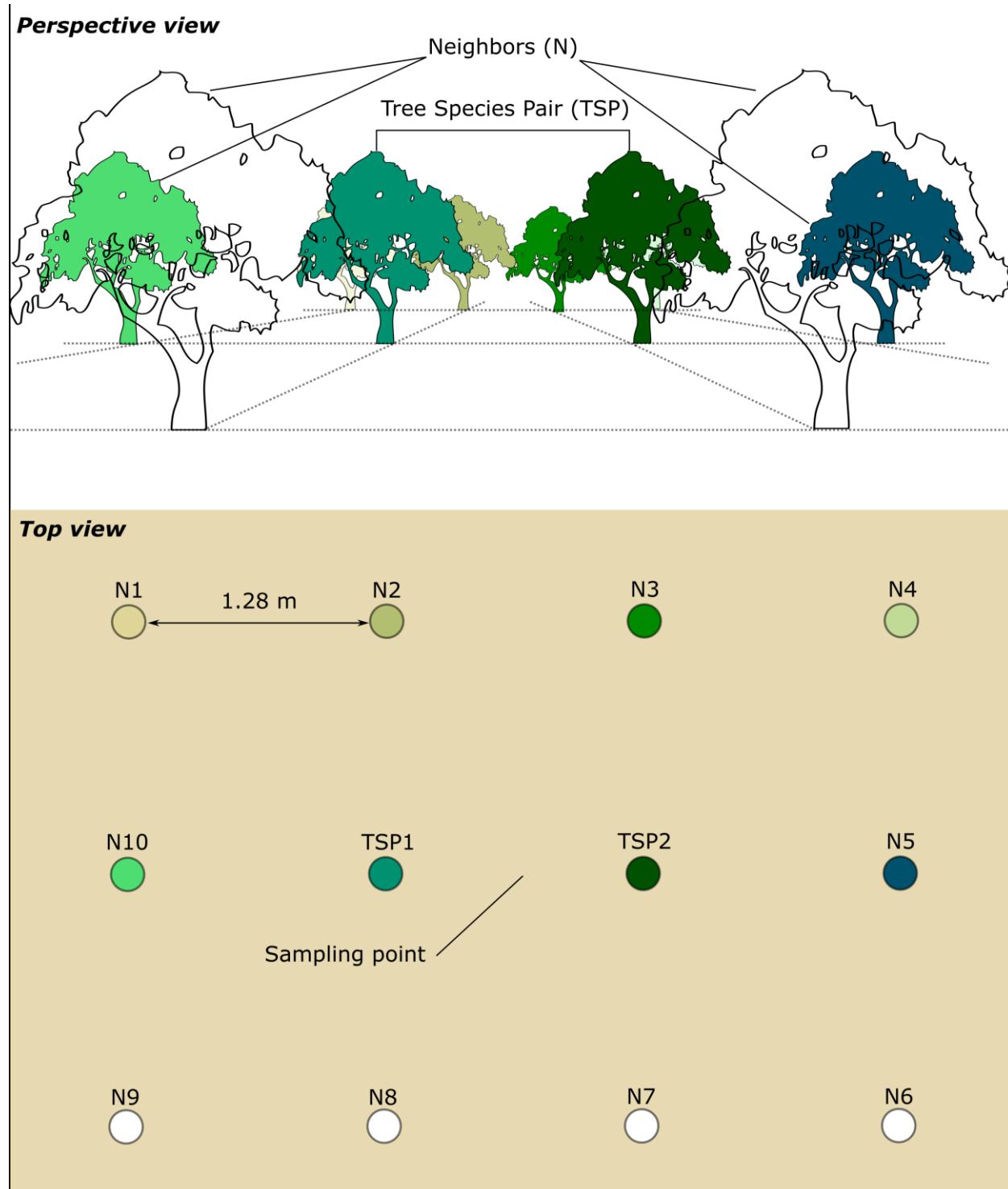
Scientific supplementary materials

*Supplementary material: Chapter I - Tree diversity effects on litter decomposition are mediated
by litterfall and microbial processes*

Supplementary material I – S1 Experimental design

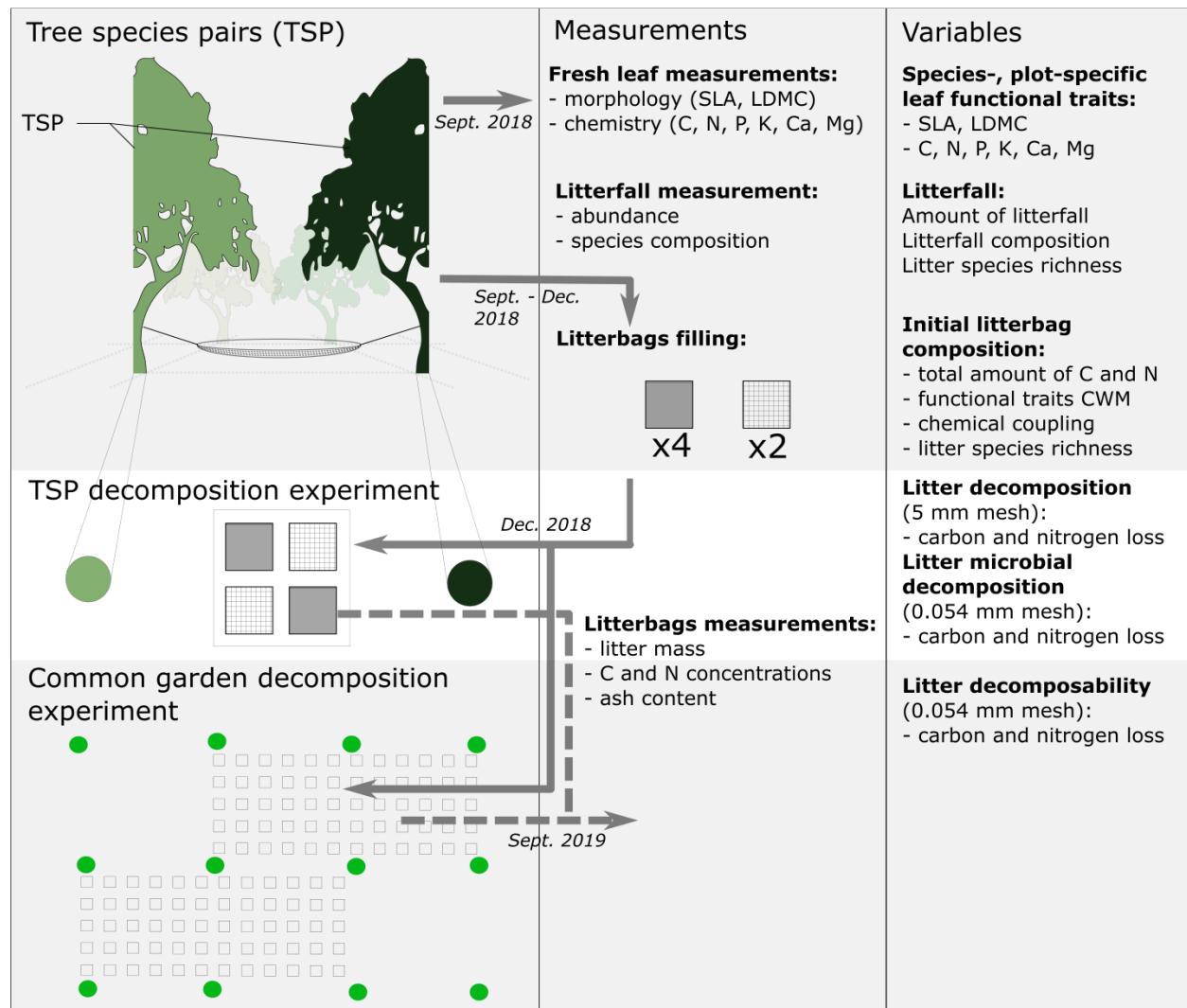
A. Plot design

Plantation design in BEF China plot with example of tree species pair (i.e., TSP) and its neighborhood.



B. Sampling design

Experimental design, realized measurements, and variables used in our study.



C. Tree species selection

List of tree species building the pairs of tree species in the different plots of Site A (BEF China

experiment)	Species	Leaf persistence
<i>Castanea</i>	<i>henryi</i>	deciduous
<i>evergreen</i>	<i>Choerospondias</i>	
<i>axillaris</i>		deciduous
<i>Cyclobalanopsis</i>	<i>glaucia</i>	
<i>evergreen</i>	<i>Koelreuteria bipinnata</i>	
<i>deciduous</i>		
<i>Liquidambar formosana</i>		deciduous
<i>Lithocarpus glaber</i>		evergreen
<i>Nyssa sinensis</i>		deciduous
<i>Quercus fabri</i>		deciduous
<i>Quercus serrata</i>		deciduous
<i>Sapindus mukorossi</i>		deciduous
<i>Sapium sebiferum</i>		deciduous

D. Tree Species Pairs (TSPs) selection

Sampling point description and attributes (paragraphs were added for readability)

Code	Site	Plot	Diversity level	Species 1	Species 2
26-E24	A	E24	1	<i>Liquidambar formosana</i>	<i>Liquidambar formosana</i>
33-E31	A	E31	1	<i>Quercus fabri</i>	<i>Quercus fabri</i>
34-E31	A	E31	1	<i>Quercus fabri</i>	<i>Quercus fabri</i>
27-E33	A	E33	1	<i>Lithocarpus glaber</i>	<i>Lithocarpus glaber</i>
28-E33	A	E33	1	<i>Lithocarpus glaber</i>	<i>Lithocarpus glaber</i>
1-E34	A	E34	1	<i>Castanea henryi</i>	<i>Castanea henryi</i>
2-E34	A	E34	1	<i>Castanea henryi</i>	<i>Castanea henryi</i>
37-F21	A	F21	1	<i>Quercus serrata</i>	<i>Quercus serrata</i>
38-F21	A	F21	1	<i>Quercus serrata</i>	<i>Quercus serrata</i>
10-G17	A	G17	1	<i>Castanopsis sclerophylla</i>	<i>Castanopsis sclerophylla</i>
29-G22	A	G22	1	<i>Lithocarpus glaber</i>	<i>Lithocarpus glaber</i>
22-G24	A	G24	1	<i>Koelreuteria bipinnata</i>	<i>Koelreuteria bipinnata</i>
23-G24	A	G24	1	<i>Koelreuteria bipinnata</i>	<i>Koelreuteria bipinnata</i>
36-G33	A	G33	1	<i>Quercus serrata</i>	<i>Quercus serrata</i>
30-H25	A	H25	1	<i>Nyssa sinensis</i>	<i>Nyssa sinensis</i>
3-I12	A	I12	1	<i>Castanea henryi</i>	<i>Castanea henryi</i>
24-I28	A	I28	1	<i>Liquidambar formosana</i>	<i>Liquidambar formosana</i>
25-I28	A	I28	1	<i>Liquidambar formosana</i>	<i>Liquidambar formosana</i>
14-K9	A	K9	1	<i>Cyclobalanopsis glauca</i>	<i>Cyclobalanopsis glauca</i>
8-L11	A	L11	1	<i>Castanopsis sclerophylla</i>	<i>Castanopsis sclerophylla</i>
9-L11	A	L11	1	<i>Castanopsis sclerophylla</i>	<i>Castanopsis sclerophylla</i>
13-L23	A	L23	1	<i>Choerospondias axillaris</i>	<i>Choerospondias axillaris</i>
43-N11	A	N11	1	<i>Sapindus mukorossi</i>	<i>Sapindus mukorossi</i>
46-N13	A	N13	1	<i>Sapium sebiferum</i>	<i>Sapium sebiferum</i>

Supplementary material: I - Tree diversity effects on litter decomposition are mediated by litterfall and microbial processes

Code	Site	Plot	Diversity level	Species 1	Species 2
47-N13	A	N13	1	<i>Sapium sebiferum</i>	<i>Sapium sebiferum</i>
11-O27	A	O27	1	<i>Choerospondias axillaris</i>	<i>Choerospondias axillaris</i>
21-Q13	A	Q13	1	<i>Koelreuteria bipinnata</i>	<i>Koelreuteria bipinnata</i>
r-21-Q13	A	Q13	1	<i>Koelreuteria bipinnata</i>	<i>Koelreuteria bipinnata</i>
35-Q16	A	Q16	1	<i>Quercus fabri</i>	<i>Quercus fabri</i>
15-R14	A	R14	1	<i>Cyclobalanopsis glauca</i>	<i>Cyclobalanopsis glauca</i>
16-R14	A	R14	1	<i>Cyclobalanopsis glauca</i>	<i>Cyclobalanopsis glauca</i>
44-R17	A	R17	1	<i>Sapindus mukorossi</i>	<i>Sapindus mukorossi</i>
45-W13	A	W13	1	<i>Sapium sebiferum</i>	<i>Sapium sebiferum</i>
32-W14	A	W14	1	<i>Nyssa sinensis</i>	<i>Nyssa sinensis</i>
51-C32	A	C32	2	<i>Castanea henryi</i>	<i>Castanea henryi</i>
52-C32	A	C32	2	<i>Castanea henryi</i>	<i>Nyssa sinensis</i>
96-C32	A	C32	2	<i>Castanea henryi</i>	<i>Nyssa sinensis</i>
95-C32	A	C32	2	<i>Nyssa sinensis</i>	<i>Nyssa sinensis</i>
97-C32	A	C32	2	<i>Nyssa sinensis</i>	<i>Nyssa sinensis</i>
53-F22	A	F22	2	<i>Castanea henryi</i>	<i>Castanea henryi</i>
54-F22	A	F22	2	<i>Castanea henryi</i>	<i>Castanea henryi</i>
55-F22	A	F22	2	<i>Castanea henryi</i>	<i>Nyssa sinensis</i>
98-F22	A	F22	2	<i>Nyssa sinensis</i>	<i>Nyssa sinensis</i>
87-H31	A	H31	2	<i>Liquidambar formosana</i>	<i>Liquidambar formosana</i>
86-H31	A	H31	2	<i>Liquidambar formosana</i>	<i>Sapindus mukorossi</i>
113-H31	A	H31	2	<i>Sapindus mukorossi</i>	<i>Liquidambar formosana</i>
112-H31	A	H31	2	<i>Sapindus mukorossi</i>	<i>Sapindus mukorossi</i>
118-I27	A	I27	2	<i>Sapium sebiferum</i>	<i>Sapium sebiferum</i>
81-J21	A	J21	2	<i>Koelreuteria bipinnata</i>	<i>Koelreuteria bipinnata</i>
82-J21	A	J21	2	<i>Koelreuteria bipinnata</i>	<i>Koelreuteria bipinnata</i>
83-J21	A	J21	2	<i>Koelreuteria bipinnata</i>	<i>Lithocarpus glaber</i>
92-J21	A	J21	2	<i>Lithocarpus glaber</i>	<i>Lithocarpus glaber</i>
72-K3	A	K3	2	<i>Cyclobalanopsis glauca</i>	<i>Cyclobalanopsis glauca</i>
73-K3	A	K3	2	<i>Cyclobalanopsis glauca</i>	<i>Cyclobalanopsis glauca</i>
75-K3	A	K3	2	<i>Cyclobalanopsis glauca</i>	<i>Quercus fabri</i>
64-O6	A	O6	2	<i>Castanopsis sclerophylla</i>	<i>Castanopsis sclerophylla</i>
65-O6	A	O6	2	<i>Castanopsis sclerophylla</i>	<i>Castanopsis sclerophylla</i>
66-O6	A	O6	2	<i>Castanopsis sclerophylla</i>	<i>Quercus serrata</i>
105-O6	A	O6	2	<i>Quercus serrata</i>	<i>Quercus serrata</i>
63-P26	A	P26	2	<i>Castanopsis sclerophylla</i>	<i>Castanopsis sclerophylla</i>
62-P26	A	P26	2	<i>Castanopsis sclerophylla</i>	<i>Quercus serrata</i>
102-P26	A	P26	2	<i>Quercus serrata</i>	<i>Quercus serrata</i>
103-P26	A	P26	2	<i>Quercus serrata</i>	<i>Quercus serrata</i>
104-P26	A	P26	2	<i>Quercus serrata</i>	<i>Quercus serrata</i>
74-Q21	A	Q21	2	<i>Cyclobalanopsis glauca</i>	<i>Cyclobalanopsis glauca</i>
76-Q21	A	Q21	2	<i>Cyclobalanopsis glauca</i>	<i>Quercus fabri</i>
77-Q21	A	Q21	2	<i>Cyclobalanopsis glauca</i>	<i>Quercus fabri</i>
100-Q21	A	Q21	2	<i>Quercus fabri</i>	<i>Quercus fabri</i>
101-Q21	A	Q21	2	<i>Quercus fabri</i>	<i>Quercus fabri</i>
84-Q7	A	Q7	2	<i>Koelreuteria bipinnata</i>	<i>Koelreuteria bipinnata</i>
85-Q7	A	Q7	2	<i>Koelreuteria bipinnata</i>	<i>Lithocarpus glaber</i>

Supplementary material: Chapter I - Tree diversity effects on litter decomposition are mediated by litterfall and microbial processes

Code	Site	Plot	Diversity level	Species 1	Species 2
93-Q7	A	Q7	2	<i>Lithocarpus glaber</i>	<i>Lithocarpus glaber</i>
94-Q7	A	Q7	2	<i>Lithocarpus glaber</i>	<i>Lithocarpus glaber</i>
69-S18	A	S18	2	<i>Choerospondias axillaris</i>	<i>Choerospondias axillaris</i>
70-S18	A	S18	2	<i>Choerospondias axillaris</i>	<i>Sapium sebiferum</i>
71-S18	A	S18	2	<i>Choerospondias axillaris</i>	<i>Sapium sebiferum</i>
119-S18	A	S18	2	<i>Sapium sebiferum</i>	<i>Sapium sebiferum</i>
r-120-S18	A	S18	2	<i>Sapium sebiferum</i>	<i>Sapium sebiferum</i>
88-T17	A	T17	2	<i>Liquidambar formosana</i>	<i>Liquidambar formosana</i>
89-T17	A	T17	2	<i>Liquidambar formosana</i>	<i>Liquidambar formosana</i>
90-T17	A	T17	2	<i>Liquidambar formosana</i>	<i>Sapindus mukorossi</i>
115-T17	A	T17	2	<i>Sapindus mukorossi</i>	<i>Sapindus mukorossi</i>
130-F27	A	F27	4	<i>Castanopsis sclerophylla</i>	<i>Castanopsis sclerophylla</i>
131-F27	A	F27	4	<i>Choerospondias axillaris</i>	<i>Castanopsis sclerophylla</i>
153-F27	A	F27	4	<i>Quercus serrata</i>	<i>Choerospondias axillaris</i>
161-F27	A	F27	4	<i>Sapium sebiferum</i>	<i>Choerospondias axillaris</i>
162-F27	A	F27	4	<i>Sapium sebiferum</i>	<i>Sapium sebiferum</i>
139-F28	A	F28	4	<i>Koelreuteria bipinnata</i>	<i>Koelreuteria bipinnata</i>
132-N20	A	N20	4	<i>Choerospondias axillaris</i>	<i>Choerospondias axillaris</i>
154-N20	A	N20	4	<i>Quercus serrata</i>	<i>Castanopsis sclerophylla</i>
155-N20	A	N20	4	<i>Quercus serrata</i>	<i>Quercus serrata</i>
156-N20	A	N20	4	<i>Quercus serrata</i>	<i>Sapium sebiferum</i>
163-N20	A	N20	4	<i>Sapium sebiferum</i>	<i>Castanopsis sclerophylla</i>
133-N8	A	N8	4	<i>Cyclobalanopsis glauca</i>	<i>Cyclobalanopsis glauca</i>
149-N8	A	N8	4	<i>Quercus fabri</i>	<i>Cyclobalanopsis glauca</i>
125-P19	A	P19	4	<i>Castanea henryi</i>	<i>Castanea henryi</i>
126-P19	A	P19	4	<i>Castanea henryi</i>	<i>Nyssa sinensis</i>
143-P19	A	P19	4	<i>Liquidambar formosana</i>	<i>Sapindus mukorossi</i>
148-P19	A	P19	4	<i>Nyssa sinensis</i>	<i>Sapindus mukorossi</i>
160-P19	A	P19	4	<i>Sapindus mukorossi</i>	<i>Sapindus mukorossi</i>
141-P29	A	P29	4	<i>Liquidambar formosana</i>	<i>Liquidambar formosana</i>
142-P29	A	P29	4	<i>Liquidambar formosana</i>	<i>Nyssa sinensis</i>
147-P29	A	P29	4	<i>Nyssa sinensis</i>	<i>Castanea henryi</i>
159-P29	A	P29	4	<i>Sapindus mukorossi</i>	<i>Castanea henryi</i>
146-W12/X12	A	W12/X12	4	<i>Lithocarpus glaber</i>	<i>Lithocarpus glaber</i>
176-P27	A	P27	8	<i>Cyclobalanopsis glauca</i>	<i>Quercus fabri</i>
181-P27	A	P27	8	<i>Koelreuteria bipinnata</i>	<i>Lithocarpus glaber</i>
166-R16	A	R16	8	<i>Castanea henryi</i>	<i>Liquidambar formosana</i>
171-R16	A	R16	8	<i>Castanopsis sclerophylla</i>	<i>Castanopsis sclerophylla</i>
175-R16	A	R16	8	<i>Choerospondias axillaris</i>	<i>Sapium sebiferum</i>
190-R16	A	R16	8	<i>Nyssa sinensis</i>	<i>Castanea henryi</i>
193-R16	A	R16	8	<i>Quercus serrata</i>	<i>Castanopsis sclerophylla</i>
194-R16	A	R16	8	<i>Quercus serrata</i>	<i>Quercus serrata</i>
198-R16	A	R16	8	<i>Sapindus mukorossi</i>	<i>Sapindus mukorossi</i>
199-R16	A	R16	8	<i>Sapindus mukorossi</i>	<i>Sapindus mukorossi</i>
200-R16	A	R16	8	<i>Sapium sebiferum</i>	<i>Quercus serrata</i>
201-R16	A	R16	8	<i>Sapium sebiferum</i>	<i>Sapium sebiferum</i>
165-S10	A	S10	8	<i>Castanea henryi</i>	<i>Castanea henryi</i>
170-S10	A	S10	8	<i>Castanopsis sclerophylla</i>	<i>Sapium sebiferum</i>

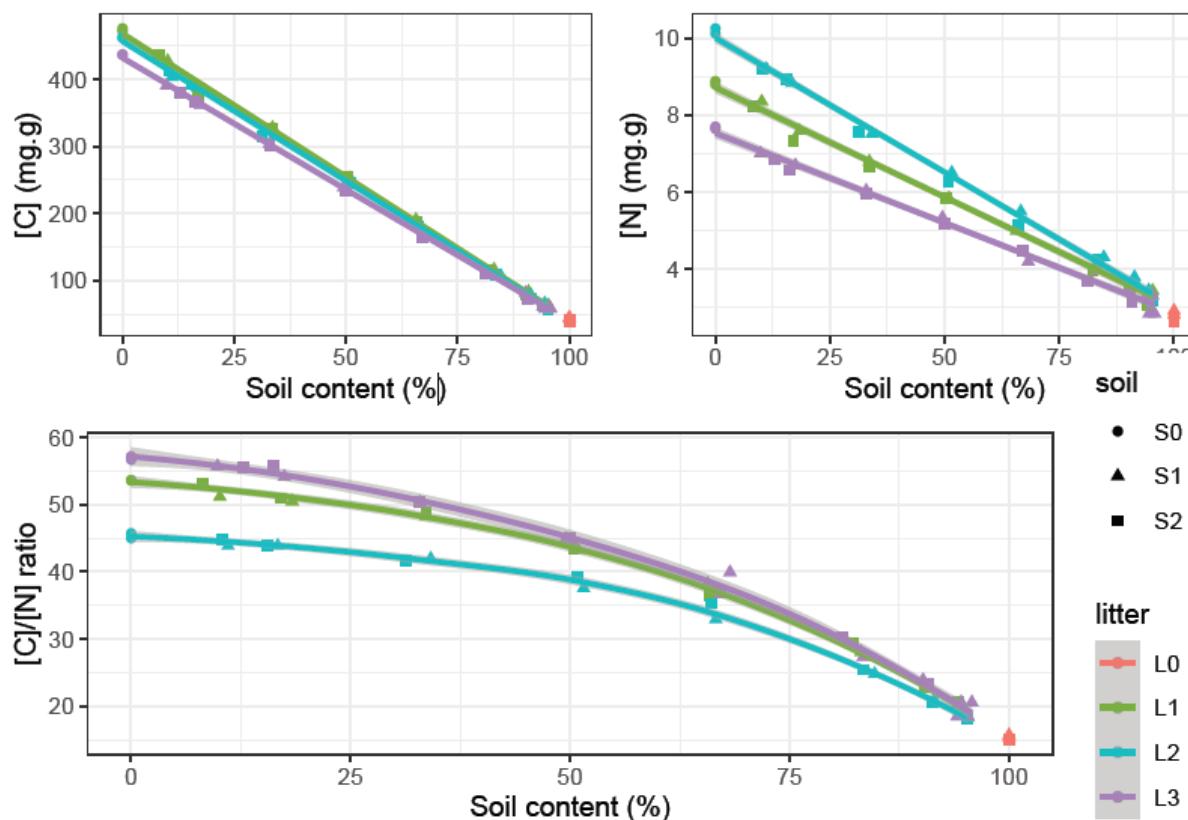
Code	Site	Plot	Diversity level	Species 1	Species 2
173-S10	A	S10	8	<i>Choerospondias axillaris</i>	<i>Castanopsis sclerophylla</i>
174-S10	A	S10	8	<i>Choerospondias axillaris</i>	<i>Choerospondias axillaris</i>
186-S10	A	S10	8	<i>Liquidambar formosana</i>	<i>Liquidambar formosana</i>
185-S10	A	S10	8	<i>Liquidambar formosana</i>	<i>Nyssa sinensis</i>
188-S10	A	S10	8	<i>Nyssa sinensis</i>	<i>Nyssa sinensis</i>
189-S10	A	S10	8	<i>Nyssa sinensis</i>	<i>Sapindus mukorossi</i>
197-S10	A	S10	8	<i>Sapindus mukorossi</i>	<i>Castanea henryi</i>
178-S14	A	S14	8	<i>Cyclobalanopsis glauca</i>	<i>Cyclobalanopsis glauca</i>
183-S15	A	S15	8	<i>Koelreuteria bipinnata</i>	<i>Koelreuteria bipinnata</i>
r-216-S15	A	S15	8	<i>Koelreuteria bipinnata</i>	<i>Lithocarpus glaber</i>
184-S15	A	S15	8	<i>Koelreuteria bipinnata</i>	<i>Quercus fabri</i>
191-T15	A	T15	8	<i>Quercus fabri</i>	<i>Quercus fabri</i>
220-L21	A	L21	16	<i>Liquidambar formosana</i>	<i>Choerospondias axillaris</i>
203-L22	A	L22	16	<i>Castanea henryi</i>	<i>Nyssa sinensis</i>
204-L22	A	L22	16	<i>Castanea henryi</i>	<i>Sapindus mukorossi</i>
217-L22	A	L22	16	<i>Liquidambar formosana</i>	<i>Castanea henryi</i>
219-L22	A	L22	16	<i>Liquidambar formosana</i>	<i>Liquidambar formosana</i>
218-L22	A	L22	16	<i>Liquidambar formosana</i>	<i>Nyssa sinensis</i>
221-L22	A	L22	16	<i>Lithocarpus glaber</i>	<i>Lithocarpus glaber</i>
222-L22	A	L22	16	<i>Quercus fabri</i>	<i>Quercus fabri</i>
230-L22	A	L22	16	<i>Sapium sebiferum</i>	<i>Castanopsis sclerophylla</i>
226-M21	A	M21	16	<i>Quercus serrata</i>	<i>Sapium sebiferum</i>
r-213-U10	A	U10	16	<i>Cyclobalanopsis glauca</i>	<i>Quercus fabri</i>
225-U10	A	U10	16	<i>Quercus serrata</i>	<i>Quercus serrata</i>
229-U10	A	U10	16	<i>Sapindus mukorossi</i>	<i>Sapindus mukorossi</i>
231-U10	A	U10	16	<i>Sapium sebiferum</i>	<i>Sapium sebiferum</i>
232-N9	A	N9	24	<i>Castanea henryi</i>	<i>Castanea henryi</i>
236-N9	A	N9	24	<i>Cyclobalanopsis glauca</i>	<i>Cyclobalanopsis glauca</i>
238-N9	A	N9	24	<i>Koelreuteria bipinnata</i>	<i>Koelreuteria bipinnata</i>
241-N9	A	N9	24	<i>Sapindus mukorossi</i>	<i>Nyssa sinensis</i>
234-R18	A	R18	24	<i>Castanopsis sclerophylla</i>	<i>Quercus serrata</i>
235-R18	A	R18	24	<i>Choerospondias axillaris</i>	<i>Quercus serrata</i>
239-R18	A	R18	24	<i>Nyssa sinensis</i>	<i>Nyssa sinensis</i>

Supplementary material I – S2 Soil contamination correction

Effect of soil contamination on litter carbon (C) and nitrogen (N) measurements

Estimation of soil contamination effect on C and N measurements

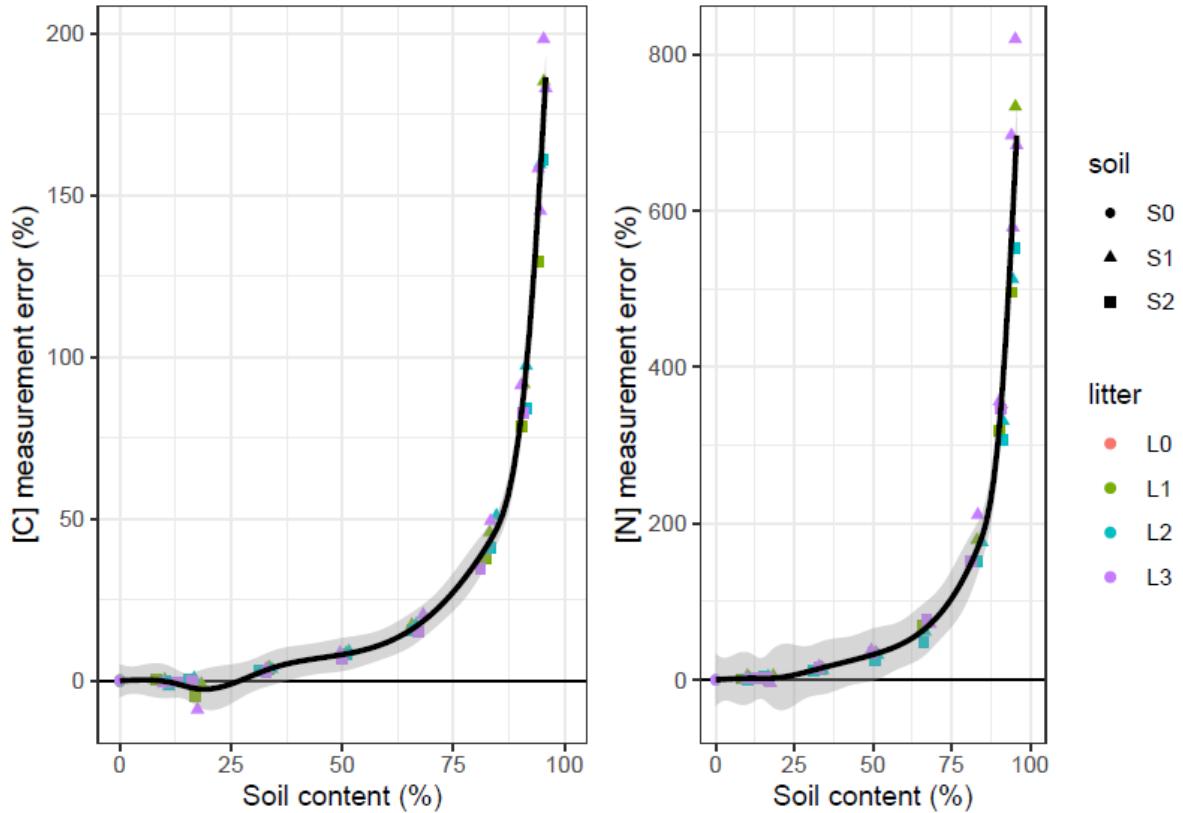
To test the effect of soil contamination on carbon and nitrogen measurements, we prepared calibration samples where soil contamination was manipulated from 0% to 100% of the total sample mass. The litter was collected in litter traps to avoid soil contamination from three monocultures (*Sapium sebiferum*, *Castanea Henryi*, *Liquidambar formosana*), soil was collected from two distant plots (K19 and T17) with contrasting chemical composition (see Scholten *et al.* 2017). For each pair of soil and litter types, 1 g of soil:litter mix was prepared for the following ratio: 1:0, 5:1, 2:1, 1:1, 1:2, 1:5, 1:10, 0:1. The sample carbon and nitrogen content were measured with an elemental analyzer (Vario EL Cube, Elementar, Langenselbold, Germany)



Measurement error due to soil contamination

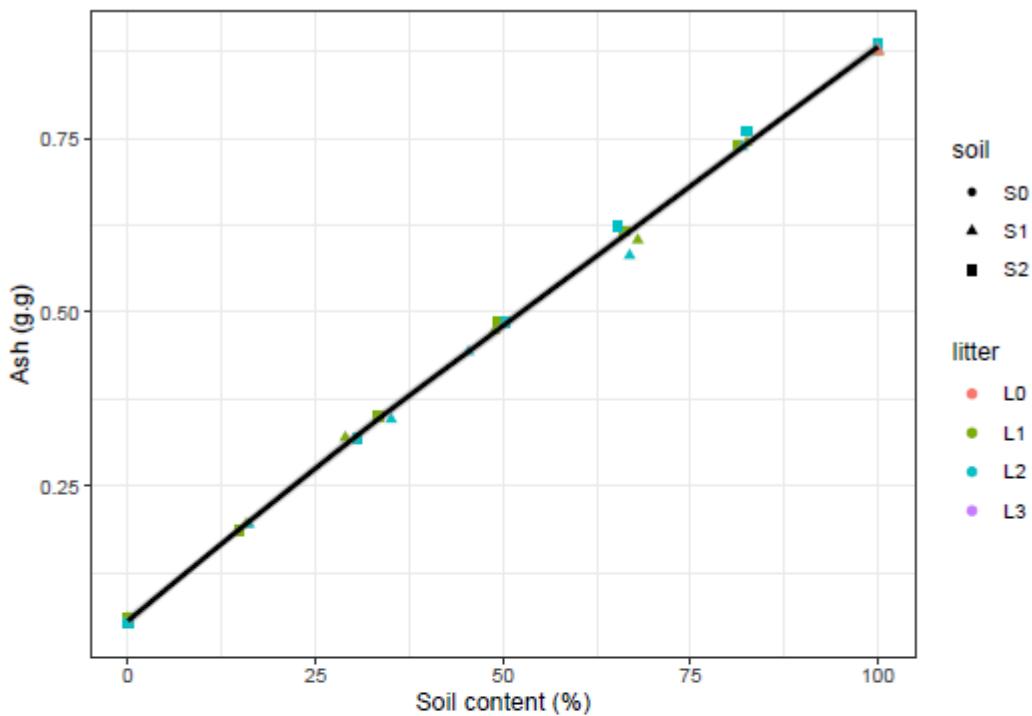
Measurement error calculation:

$$\text{Measurement.error} = 100 \times \frac{(\text{measured} - \text{introduced})}{\text{introduced}}$$



Using ash measurements to estimate and correct soil contamination

To estimate soil contamination from our samples, we used measured ash content from our calibration samples and tested the linear relationship between soil contamination (%) and ash content (g.g). The ash content of the samples was measured using the loss on ignition method where the samples are incinerated in a muffle oven at 550 ° C (Nabertherm GmbH, Lilienthal, Germany)



```
##  
## Call:  
## lm(formula = ash.content ~ soil.conta, data = df.ash)  
##  
## Residuals:  
##      Min       1Q   Median       3Q      Max  
## -0.032487 -0.008449  0.000179  0.007138  0.022679  
##  
## Coefficients:  
##             Estimate Std. Error t value Pr(>|t|)  
## (Intercept) 6.347e-02 3.756e-03   16.9  3.2e-16 ***  
## soil.conta 8.231e-03 6.233e-05   132.1 < 2e-16 ***  
## ---  
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1  
##  
## Residual standard error: 0.01208 on 28 degrees of freedom  
##   (17 observations deleted due to missingness)  
## Multiple R-squared:  0.9984, Adjusted R-squared:  0.9983  
## F-statistic: 1.744e+04 on 1 and 28 DF,  p-value: < 2.2e-16
```

According to our measurements, soil contamination linearly increases ash content. In addition, litter ash content (estimate +/- SE = 0.063 +/- 0.004 g/g, i.e., model intercept) is neglectable in comparison to soil ash content (.886 +/- 0.004 g/g).

Therefore, we can estimate soil carbon and nitrogen addition into the sample using:

$$\begin{aligned}\Leftrightarrow \text{soil.content} &= \frac{\text{Ash}_{\text{sample}}}{\text{Ash}_{\text{soil}}} \\ \Leftrightarrow \text{soil.content} &= \frac{\text{Ash}_{\text{sample}}}{1 - \text{SOM}}, \text{ when } \text{Ash}_{\text{soil}} = 1 - \text{SOM} \\ \Rightarrow [C]_{\text{litter}} &= [C]_{\text{sample}} - [C]_{\text{soil}} \times \text{soil.content} \\ \Leftrightarrow [C]_{\text{litter}} &= [C]_{\text{sample}} - [C]_{\text{soil}} \times \frac{\text{Ash}_{\text{sample}}}{1 - \text{SOM}}\end{aligned}$$

Equivalent for N content with:

$$[N]_{\text{litter}} = [N]_{\text{sample}} - [N]_{\text{soil}} \times \frac{\text{Ash}_{\text{sample}}}{1 - \text{SOM}}$$

Supplementary material I – S3 R Outputs

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Fig. 2.F Decomposability N loss (%)

Figure 3

Fig. 3.A Tree diversity effect on the amount of litterfall and litter species richness
Fig. 3.B: Part of microbial decomposition in litter decomposition
Fig. 3.C: Structural equation model

Figure 4

Fig. 4.A: Decomposability drivers
Fig. 4.B: Litterfall drivers

Fig. 2.A Decomposition C loss (%)

Model output

```
##  
## Call:  
## lm(formula = "C.loss_Mai ~ log(neigh.sp.rich)", data = df)  
##  
## Residuals:  
##     Min      1Q  Median      3Q     Max  
## -50.755 -10.573 - 1.088 10.112 38.701  
##  
## Coefficients:  
##                               Estimate Std. Error t value Pr(>|t|)  
## (Intercept)          59.175      2.236  26.461 <2e-16 ***  
## log(neigh.sp.rich)    1.532      1.927   0.795   0.428  
## ---  
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1  
##  
## Residual standard error: 15.32 on 151 degrees of freedom  
## Multiple R-squared:  0.00417,   Adjusted R-squared:  -0.002425  
## F-statistic: 0.6322 on 1 and 151 DF,  p-value: 0.4278
```

Model quality

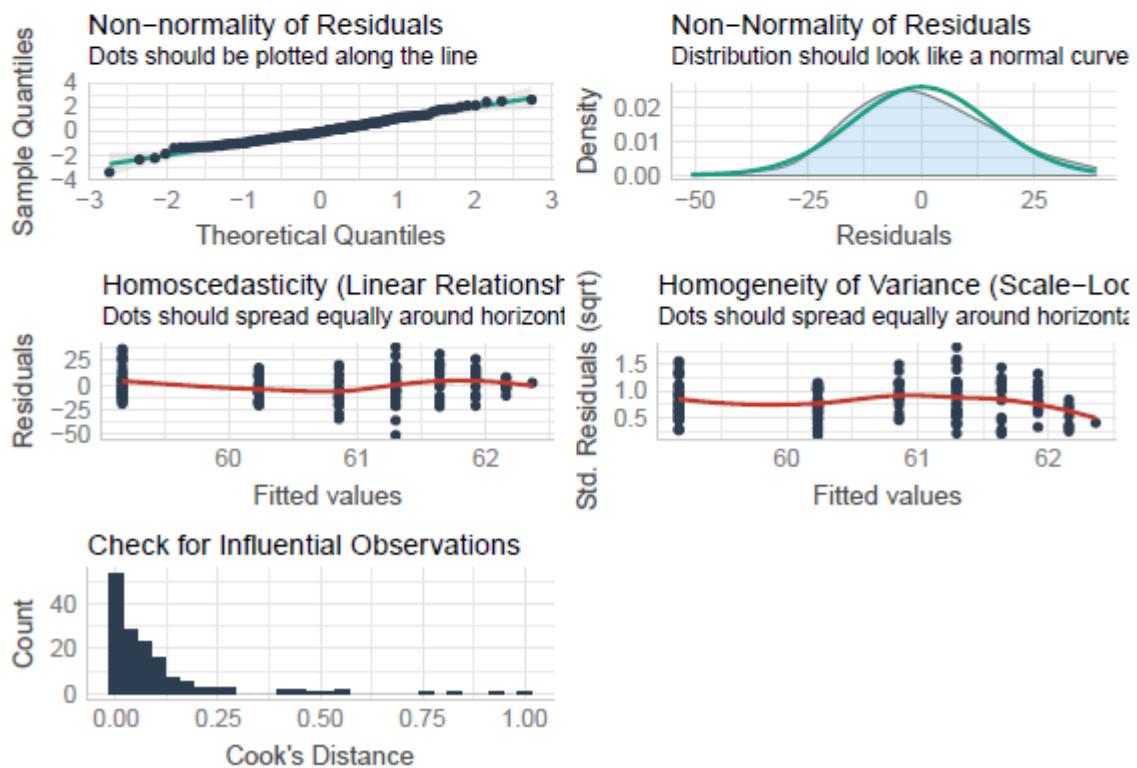


Fig. 2.B Decomposition N loss (%)

Model output

```
##  
## Call:  
## lm(formula = "N.loss_Ma1 ~ log(neigh.sp.rich)", data = df)  
##  
## Residuals:  
##    Min      1Q  Median      3Q     Max  
## -41.429 -12.969   1.371  11.548  34.494  
##  
## Coefficients:  
##                               Estimate Std. Error t value Pr(>|t|)  
## (Intercept)             65.506     2.418  27.094 <2e-16 ***  
## log(neigh.sp.rich)      4.989     2.083   2.395   0.0179 *  
## ---  
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1  
##  
## Residual standard error: 16.56 on 151 degrees of freedom  
## Multiple R-squared:  0.03659,   Adjusted R-squared:  0.03021  
## F-statistic: 5.735 on 1 and 151 DF,  p-value: 0.01785
```

Model quality

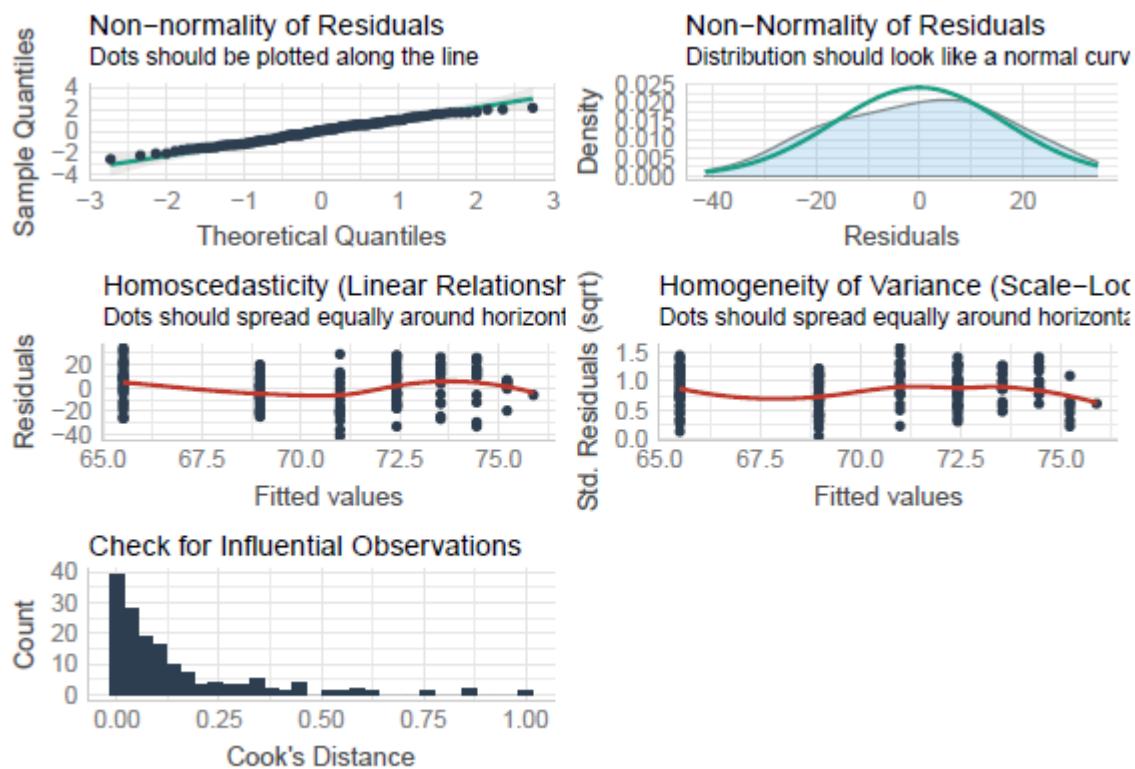


Fig. 2.C Microbial decomposition C loss (%)

Model output

```
##
## Call:
## lm(formula = "C.loss_M11 ~ log(neigh.sp.rich)", data = df)
##
## Residuals:
##    Min      1Q  Median      3Q     Max 
## -25.889 -7.769 -0.531  6.920 36.553 
## 
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)    
## (Intercept) 49.521     1.720   28.783 <2e-16 ***
## log(neigh.sp.rich) -1.826     1.482  -1.231    0.22    
## ---      
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 11.79 on 151 degrees of freedom
## Multiple R-squared:  0.009943, Adjusted R-squared:  0.003386 
## F-statistic: 1.516 on 1 and 151 DF, p-value: 0.2201
```

Model quality

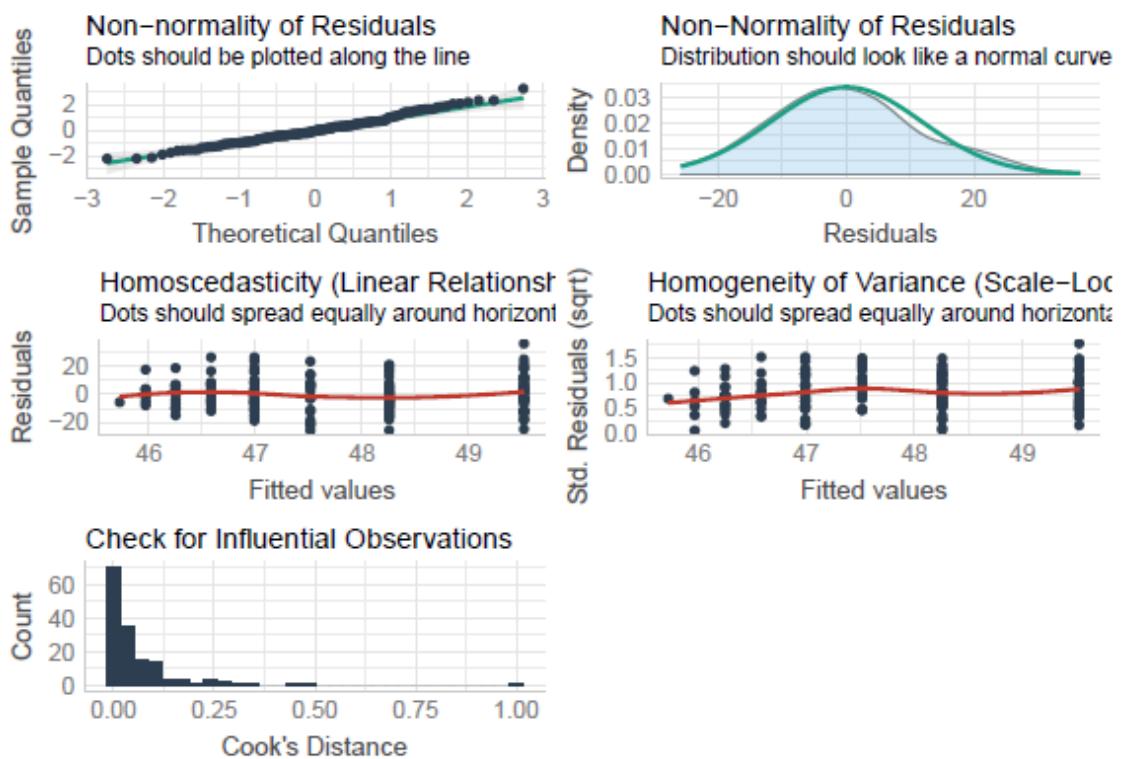


Fig. 2.D Microbial decomposition N loss (%)

Model output

```
##
## Call:
## lm(formula = "N.loss_M11 ~ log(neigh.sp.rich)", data = df)
##
## Residuals:
##    Min      1Q  Median      3Q     Max 
## -36.379 -10.818 - 1.621   7.900  43.181 
## 
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)    
## (Intercept) 56.819     2.308  24.616 <2e-16 ***
## log(neigh.sp.rich) 2.885     1.989   1.451   0.149  
## ---      
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1 
## 
## Residual standard error: 15.81 on 151 degrees of freedom
## Multiple R-squared:  0.01374, Adjusted R-squared:  0.007213 
## F-statistic: 2.104 on 1 and 151 DF, p-value: 0.149
```

Model quality

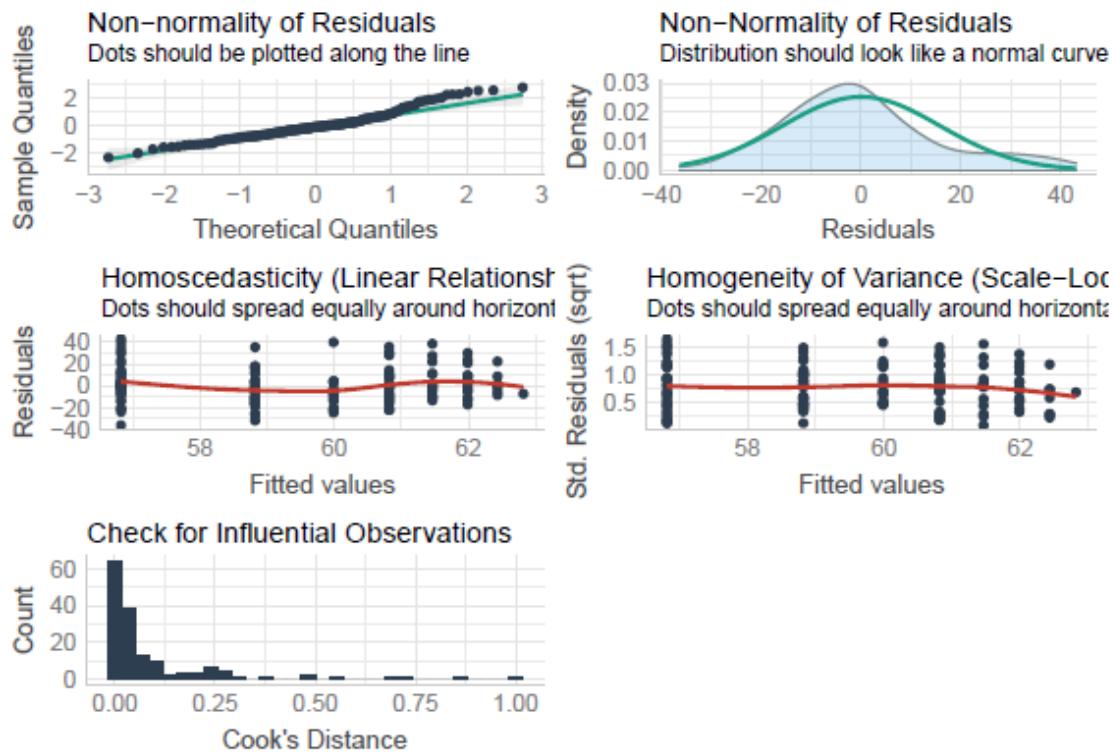


Fig. 2.E Decomposability C loss (%)

Model output

```
##
## Call:
## lm(formula = "C.loss_CG ~ log(lit.rich)", data = df)
##
## Residuals:
##    Min      1Q  Median      3Q     Max 
## -21.659  -5.099  -0.132   5.716  20.047 
## 
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)    
## (Intercept) 43.7478    0.9935  44.032 <2e-16 ***
## log(lit.rich) -1.2590    0.8716  -1.445    0.151    
## ---      
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 8.124 on 151 degrees of freedom
## Multiple R-squared:  0.01363,   Adjusted R-squared:  0.007099 
## F-statistic: 2.087 on 1 and 151 DF,  p-value: 0.1507
```

Model quality

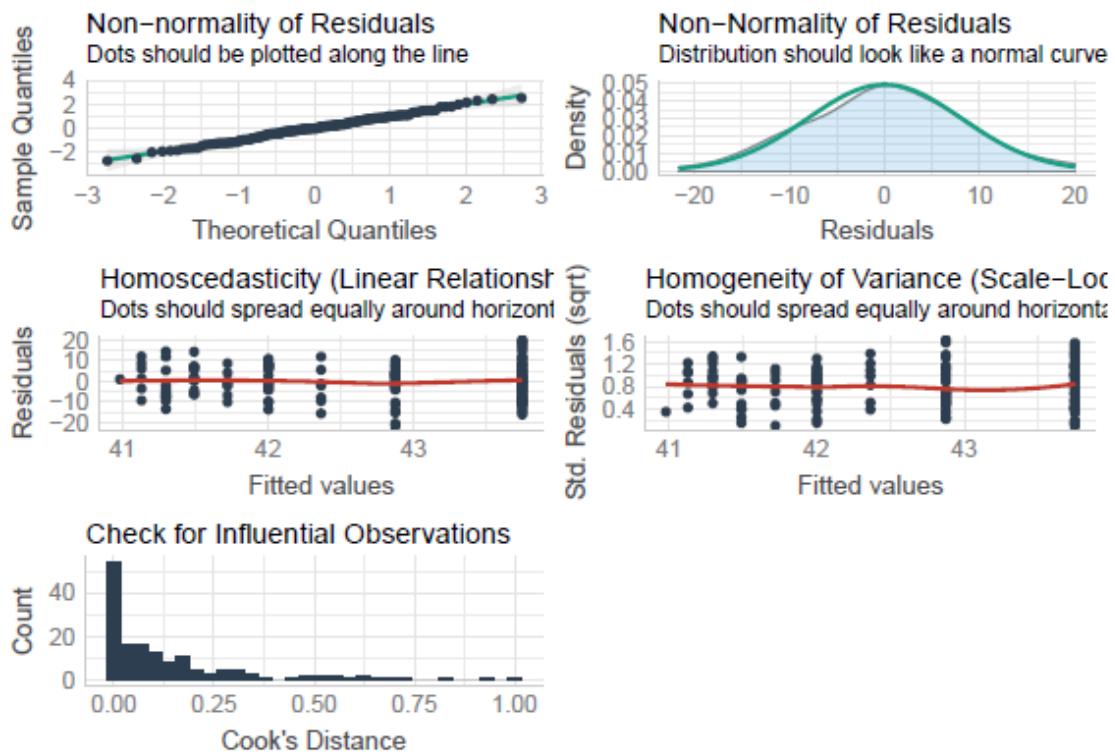
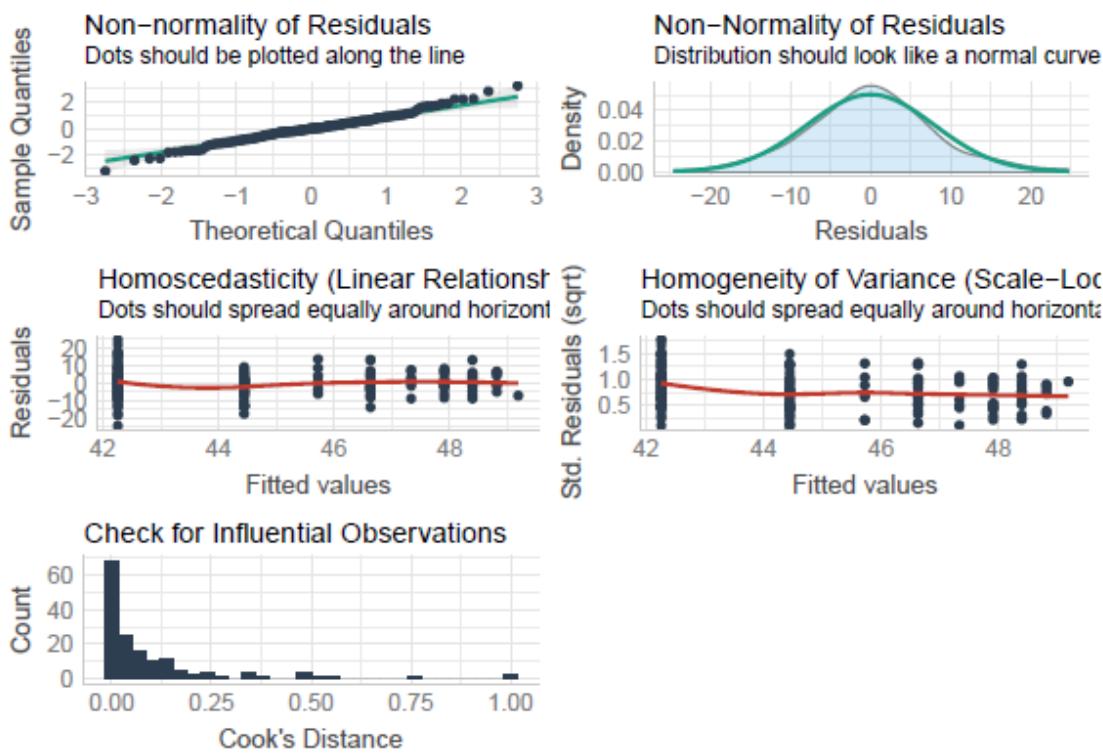


Fig. 2.F Decomposability N loss (%)

Model output

```
##
## Call:
## lm(formula = "N.loss_CG ~ log(lit.rich)", data = df)
##
## Residuals:
##    Min      1Q  Median      3Q     Max 
## -24.5090 -4.9002  0.0964  4.6015 24.6910 
## 
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)    
## (Intercept) 42.2580    0.9720  43.476 < 2e-16 ***
## log(lit.rich) 3.1526    0.8527   3.697 0.000304 *** 
## ---        
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 7.947 on 151 degrees of freedom
## Multiple R-squared:  0.08302, Adjusted R-squared:  0.07694 
## F-statistic: 13.67 on 1 and 151 DF,  p-value: 0.0003043
```

Model quality



Litter species richness

Model

```
##
## Call:
## lm(formula = "lit.rich ~ log(neigh.sp.rich)", data = df)
##
## Residuals:
##     Min      1Q  Median      3Q     Max 
## -3.4450 -1.2606 -0.2954  0.6351  4.6699 
## 
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)    
## (Intercept) 0.3649    0.1996   1.828   0.0695 .  
## log(neigh.sp.rich) 2.8353    0.1720  16.488  <2e-16 ***
## --- 
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 1.367 on 151 degrees of freedom
## Multiple R-squared:  0.6429, Adjusted R-squared:  0.6405 
## F-statistic: 271.9 on 1 and 151 DF,  p-value: < 2.2e-16
```

Model quality .

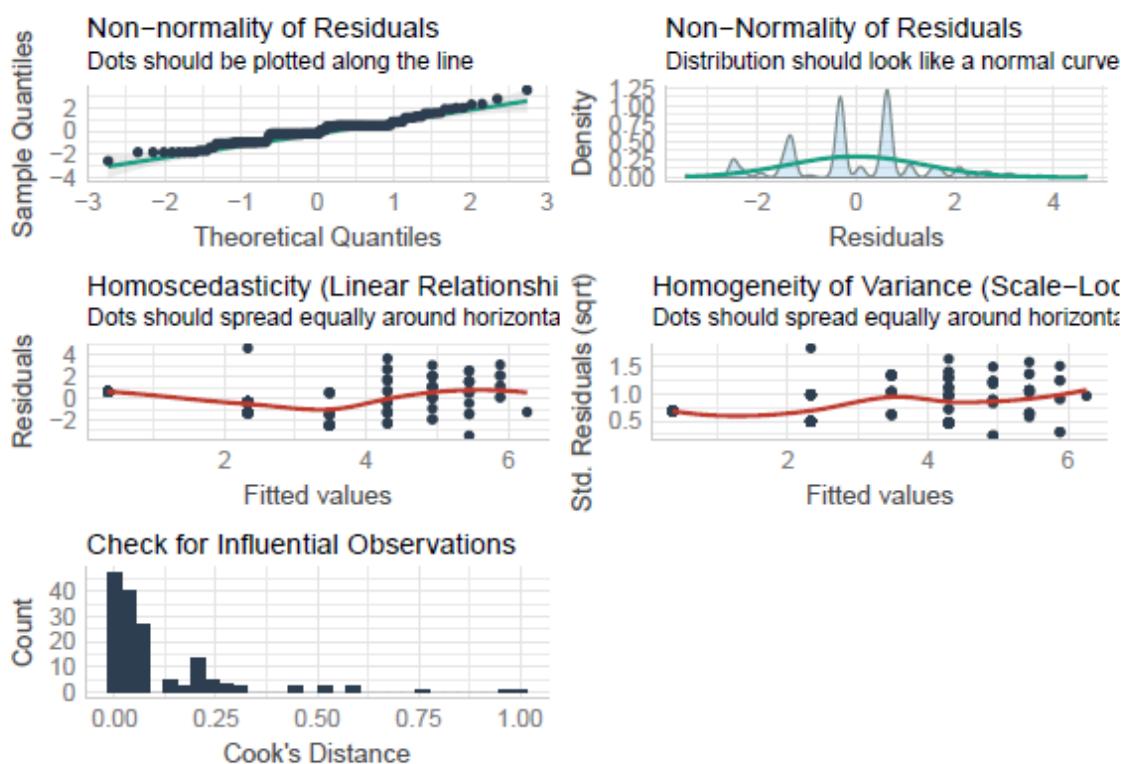


Fig. 3.B: Part of microbial decomposition in litter decomposition

Part of microbial decomposition in total C loss

$$\text{microbial contribution to } C_{\text{loss}} = \frac{C_{\text{loss}}_{\text{microbial}}}{C_{\text{loss}}_{\text{total}}}$$

```
##      Min. 1st Qu. Median   Mean 3rd Qu.   Max.  
##    30.32    64.30   80.55   84.42   97.41  476.48
```

Part of microbial decomposition in total N loss

$$\text{microbial contribution to } N_{\text{loss}} = \frac{N_{\text{loss}}_{\text{microbial}}}{N_{\text{loss}}_{\text{total}}}$$

```
##      Min. 1st Qu. Median   Mean 3rd Qu.   Max.  
##    27.31    74.62   86.59   87.16  100.62  190.34
```

Fig. 3.C: Structural equation model

SEM structure

Labels: "Ma" = total decomposition, "Mi" = microbial decomposition, "CG" = Common Garden (i.e., decomposability), "fall" = amount of litterfall, "lit.rich" = litter species richness, "neigh.sp.rch" = neighborhood tree species richness

```
form.sem =
'
C.loss_Ma1 ~ C.loss_Mi1 + fall + log.lit.rich + log.neigh.sp.rich
N.loss_Ma1 ~ N.loss_Mi1 + fall + log.lit.rich + log.neigh.sp.rich
C.loss_Ma1 ~~ N.loss_Ma1

C.loss_Mi1 ~ C.loss(CG) + fall + log.lit.rich + log.neigh.sp.rich
N.loss_Mi1 ~ N.loss(CG) + fall + log.lit.rich + log.neigh.sp.rich
C.loss_Mi1 ~~ N.loss_Mi1

C.loss(CG) ~ log.lit.rich
N.loss(CG) ~ log.lit.rich
C.loss(CG) ~~ N.loss(CG)

fall ~ log.neigh.sp.rich
log.lit.rich ~ log.neigh.sp.rich
fall ~~ log.lit.rich
'
```

Hypotheses .

Causal relations

Response variable	Explanatory variable	Hypothesis
C.loss_Ma1	C.loss_Mi1	We expect total litter decomposition to be carried out by the microbial community
C.loss_Ma1	fall	We expect litter decomposition rate to increase with the amount of litterfall due to the addatation of the decomposer community to the higher amount of nutrients
C.loss_Ma1	log.lit.rich	We expect litter decomposition rate to increase with litter species richness due to the increase of litter complementarity
N.loss_Ma1	N.loss_Mi1	We expect total litter decomposition to be carried out by the microbial community
N.loss_Ma1	fall	We expect litter decomposition rate to increase with the amount of litterfall due to the addatation of the decomposer community to the higher amount of nutrients
N.loss_Ma1	log.lit.rich	We expect litter decomposition rate to increase with litter species richness due to the increase of litter complementarity
C.loss_Mi1	C.loss(CG)	We expect microbial decomposition to increase with litter decomposability
C.loss_Mi1	fall	We expect litter decomposition rate to increase with the amount of litterfall due to the addatation of the decomposer community to the higher amount of nutrients

(continued)

Response variable	Explanatory variable	Hypothesis
C.loss_Mi1	log.lit.rich	We expect litter decomposition rate to increase with litter species richness due to the increase of litter complementarity
N.loss_Mi1	N.loss(CG	We expect microbial decomposition to increase with litter decomposability
N.loss_Mi1	fall	We expect litter decomposition rate to increase with the amount of litterfall due to the addatation of the decomposer community to the higher amount of nutrients
N.loss_Mi1	log.lit.rich	We expect litter decomposition rate to increase with litter species richness due to the increase of litter complementarity
C.loss(CG	log.lit.rich	We expect litter decomposition rate to increase with litter species richness due to the increase of litter complementarity
N.loss(CG	log.lit.rich	We expect litter decomposition rate to increase with litter species richness due to the increase of litter complementarity
fall	log.neigh.sp.i	We expect tree litterfall to increase with tree species richness
log.lit.rich	log.neigh.sp.ri	We expect litter species richness to increase with tree species richness

Correlations

Covariate 1	Covariate 2	Hypothesis
C.loss_Ma1	N.loss_Ma1	We expect carbon and nitrogen decomposition to be positively correlated
C.loss_Mi1	N.loss_Mi1	We expect carbon and nitrogen decomposition to be positively correlated
C.loss(CG	N.loss(CG	We expect carbon and nitrogen decomposition to be positively correlated
fall	log.lit.rich	We expect the amount of litterfall and litter species richness to be positively correlated as both positively affected by tree species richness

Model outputs

Summary

Labels: "Ma" = total decomposition, "Mi" = microbial decomposition, "CG" = Common Garden (i.e., decomposability), "fall" = amount of litterfall, "lit.rich" = litter species richness, "ngh.sp.rch" = neighborhood tree species richness

```
## lavaan 0.6-7 ended normally after 42 iterations
##
##   Estimator                               ML
## Optimization method                       NLMINB
## Number of free parameters                 32
##
##   Number of observations                  153
##
## Model Test User Model:
##
##   Test statistic                          10.994
##   Degrees of freedom                     12
##   P-value (Chi-square)                   0.529
##
## Parameter Estimates:
##
##   Standard errors                        Standard
##   Information                            Expected
##   Information saturated (h1) model       Structured
##
## Regressions:
##   Estimate   Std.Err  z-value  P(>|z|)  Std.lv  Std.all
##   C.loss_Ma1 ~
##     C.loss_Mi1    0.264   0.052   5.069   0.000   0.264   0.261
##     fall         0.319   0.092   3.468   0.001   0.319   0.314
##     log.lit.rich 0.185   0.158   1.168   0.243   0.185   0.181
##     log.ngh.sp.rch -0.214   0.144  -1.486   0.137  -0.214  -0.210
##   N.loss_Ma1 ~
##     N.loss_Mi1    0.507   0.048  10.511   0.000   0.507   0.492
##     fall         0.235   0.081   2.904   0.004   0.235   0.232
##     log.lit.rich 0.090   0.139   0.649   0.516   0.090   0.089
##     log.ngh.sp.rch -0.053   0.126  -0.423   0.672  -0.053  -0.053
##   C.loss_Mi1 ~
##     C.loss(CG)    0.433   0.055   7.881   0.000   0.433   0.430
##     fall         0.046   0.091   0.502   0.616   0.046   0.045
##     log.lit.rich 0.196   0.156   1.255   0.210   0.196   0.195
##     log.ngh.sp.rch -0.217   0.142  -1.532   0.125  -0.217  -0.216
##   N.loss_Mi1 ~
##     N.loss(CG)    0.350   0.056   6.271   0.000   0.350   0.356
##     fall         0.110   0.089   1.229   0.219   0.110   0.111
##     log.lit.rich 0.235   0.154   1.530   0.126   0.235   0.239
##     log.ngh.sp.rch -0.198   0.139  -1.429   0.153  -0.198  -0.202
##   C.loss(CG) ~
##     log.lit.rich -0.117   0.080  -1.454   0.146  -0.117  -0.117
##   N.loss(CG) ~
##     log.lit.rich  0.288   0.077   3.722   0.000   0.288   0.288
```

```
## fall ~
## log.ngh.sp.rch    0.459    0.072    6.395    0.000    0.459    0.459
## log.lit.rich ~
## log.ngh.sp.rch    0.856    0.042   20.445    0.000    0.856    0.856
##
## Covariances:
##             Estimate Std.Err z-value P(>|z|) Std.lv Std.all
## .C.loss_Ma1 ~~
##   .N.loss_Ma1     0.579    0.075    7.716    0.000    0.579    0.798
## .C.loss_Mi1 ~~
##   .N.loss_Mi1     0.550    0.078    7.062    0.000    0.550    0.695
## .C.loss_CG ~~
##   .N.loss_CG      0.379    0.082    4.604    0.000    0.379    0.401
## .fall ~~
##   .log.lit.rich   0.197    0.040    4.901    0.000    0.197    0.432
##
## Variances:
##             Estimate Std.Err z-value P(>|z|) Std.lv Std.all
## .C.loss_Ma1      0.827    0.095    8.746    0.000    0.827    0.803
## .N.loss_Ma1      0.636    0.073    8.746    0.000    0.636    0.624
## .C.loss_Mi1      0.807    0.092    8.746    0.000    0.807    0.803
## .N.loss_Mi1      0.776    0.089    8.746    0.000    0.776    0.807
## .C.loss_CG       0.980    0.112    8.746    0.000    0.980    0.986
## .N.loss_CG       0.911    0.104    8.746    0.000    0.911    0.917
## .fall            0.784    0.090    8.746    0.000    0.784    0.789
## .log.lit.rich   0.266    0.030    8.746    0.000    0.266    0.268
```

R squared

```
## C.loss_Ma1  N.loss_Ma1  C.loss_Mi1  N.loss_Mi1  C.loss_CG  N.loss_CG
##      0.197      0.376      0.197      0.193      0.014      0.083
##      fall log.lit.rich
##      0.211      0.732
```

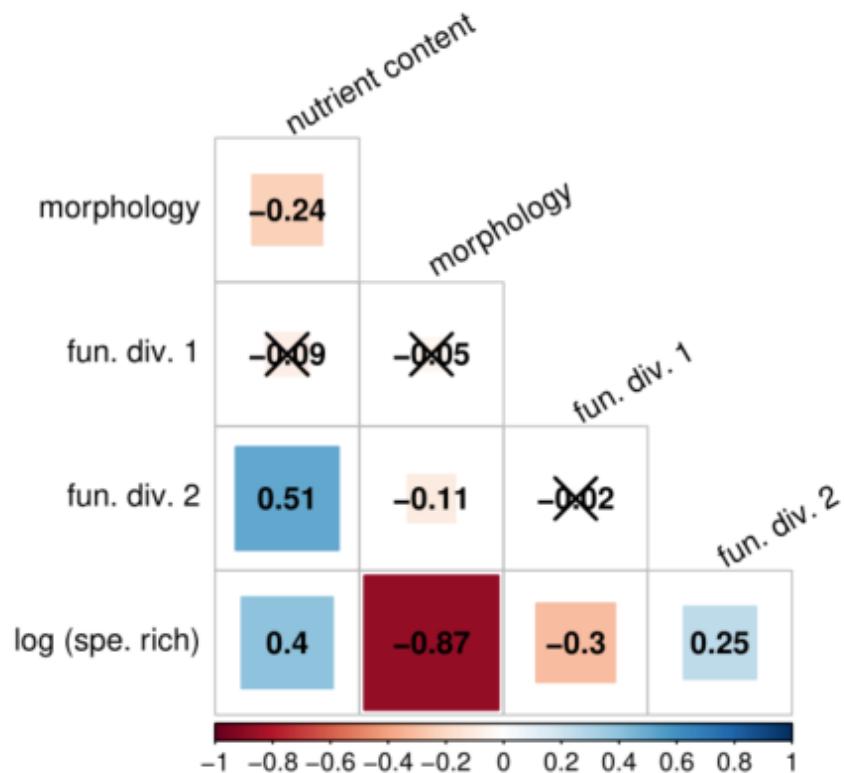
Model quality

```
##   DF   CFI   RMSEA   SRMR
## 12.000 1.000 0.000 0.031
```

Figure 4

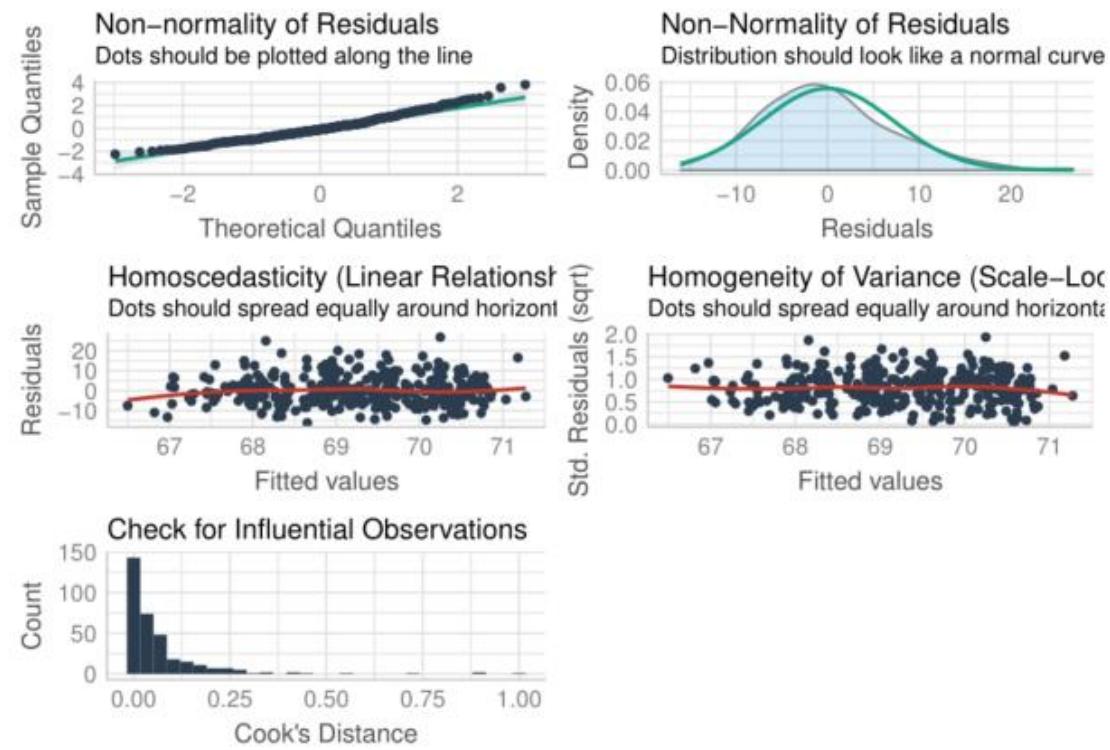
Fig. 4.A: Decomposability drivers

Correlation between explanatory variables



Decomposability C loss

```
##
## Call:
## lm(formula = C.loss ~ compo.pca.1, data = df)
##
## Residuals:
##   Min     1Q Median     3Q    Max
## -16.0580 -5.0609 -0.6945  3.9496 26.8027
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 69.2268    0.3891 177.915 < 2e-16 ***
## compo.pca.1  1.0215    0.3897   2.621  0.00915 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 7.164 on 337 degrees of freedom
## Multiple R-squared:  0.01998, Adjusted R-squared:  0.01707
## F-statistic: 6.872 on 1 and 337 DF, p-value: 0.009155
```



Decomposability N loss

```
##
## Call:
## lm(formula = N.loss ~ div.pca.1 + compo.pca.1 + log(lit.rich),
##      data = df)
##
## Residuals:
##    Min      1Q  Median      3Q     Max 
## -25.5671 -4.8384 -0.5727  5.3752 29.4864 
## 
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)    
## (Intercept) 69.7242   0.7842  88.909 < 2e-16 ***
## div.pca.1    0.4594   0.1909   2.406 0.016667 *  
## compo.pca.1   2.0861   0.5152   4.049 6.38e-05 ***
## log(lit.rich) 2.5523   0.7333   3.481 0.000566 *** 
## ---        
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 8.67 on 335 degrees of freedom
## Multiple R-squared:  0.1249, Adjusted R-squared:  0.1171 
## F-statistic: 15.94 on 3 and 335 DF,  p-value: 1.041e-09
```

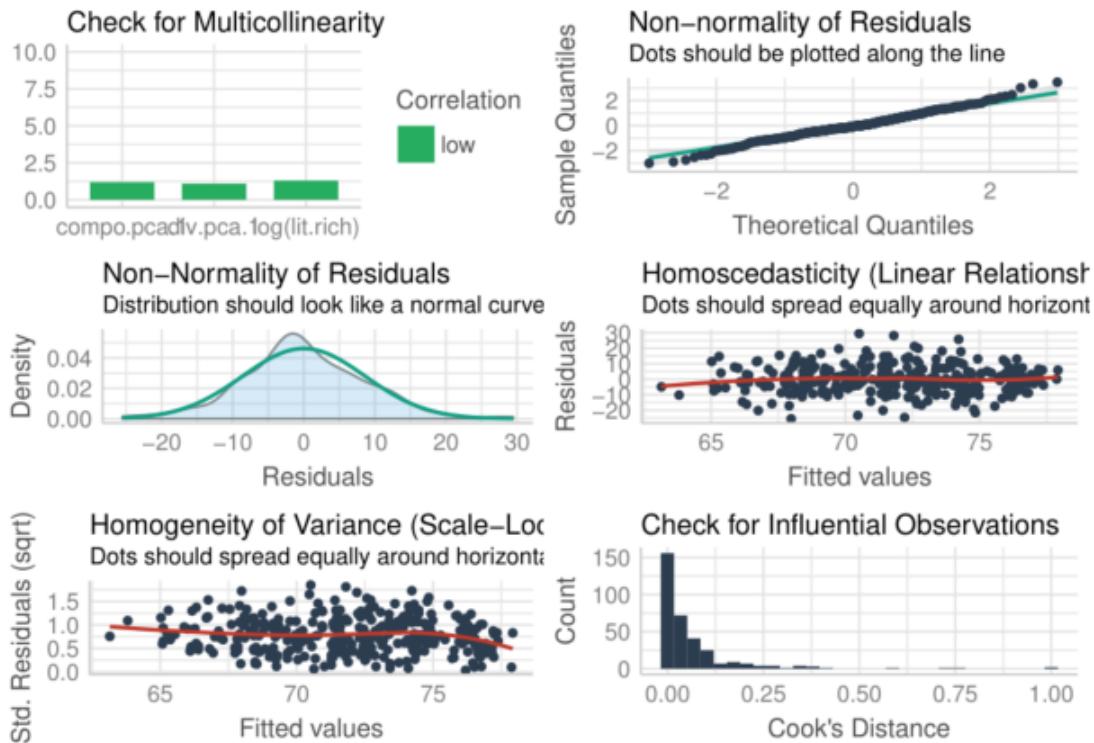
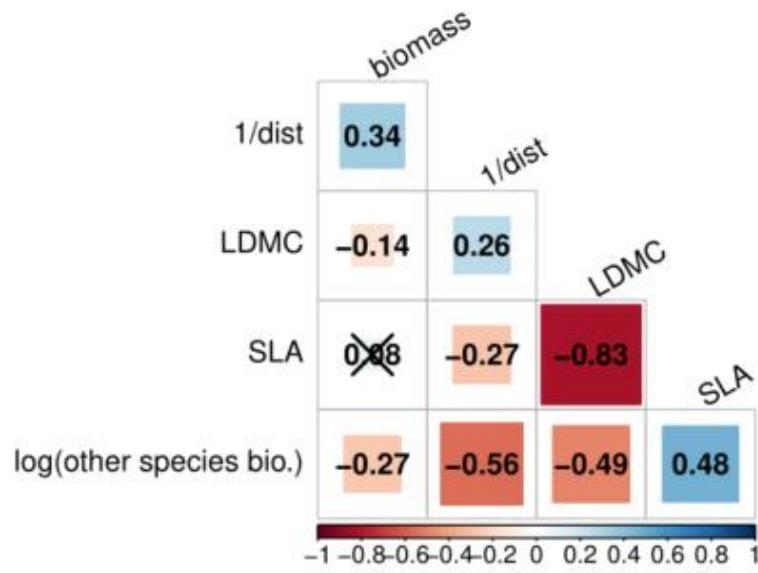


Fig. 4.B: Litterfall drivers

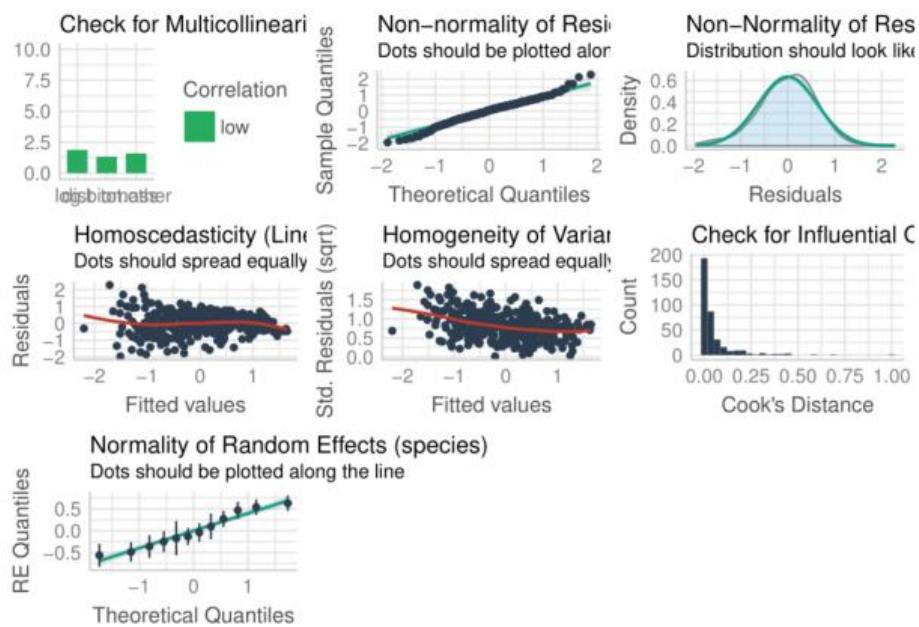
Correlation between explanatory variables



```

## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: log.litter.biomass.area ~ log.biomass + dist + tot.other + (1 |
##     species)
## Data: df.stat
##
## REML criterion at convergence: 767.2
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -3.0497 -0.5819  0.0695  0.6145  3.5516
##
## Random effects:
## Groups   Name        Variance Std.Dev.
## species  (Intercept) 0.1785   0.4225
## Residual           0.4107   0.6408
## Number of obs: 372, groups: species, 12
##
## Fixed effects:
##             Estimate Std. Error      df t value Pr(>|t|)
## (Intercept) -0.10092   0.12795 10.89923 -0.789  0.44707
## log.biomass   0.43985   0.04755 354.96121  9.251 < 2e-16 ***
## dist         0.14263   0.04644 367.58871  3.072  0.00229 **
## tot.other    -0.10310   0.04953 363.68207 -2.082  0.03809 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##          (Intr) lg.bms dist
## log.biomass  0.066
## dist        -0.014 -0.390
## tot.other    0.050  0.047  0.542

```



Supplementary material I – S4 Soil fauna sampling

Fauna collection protocol

In September 2019, we performed several fauna collection during our sampling campaign.

Soil mesofauna collection

Soil mesofauna was collected by heat extraction from two soil cores (5 cm diameter and 10 cm deep) sampled near the Common Garden experiment

Soil macrofauna collection

Soil macrofauna was collected by heat extraction from two soil cores (10 x 10 x 10 cm) sampled near the Common Garden experiment.

Ground macrofauna collection

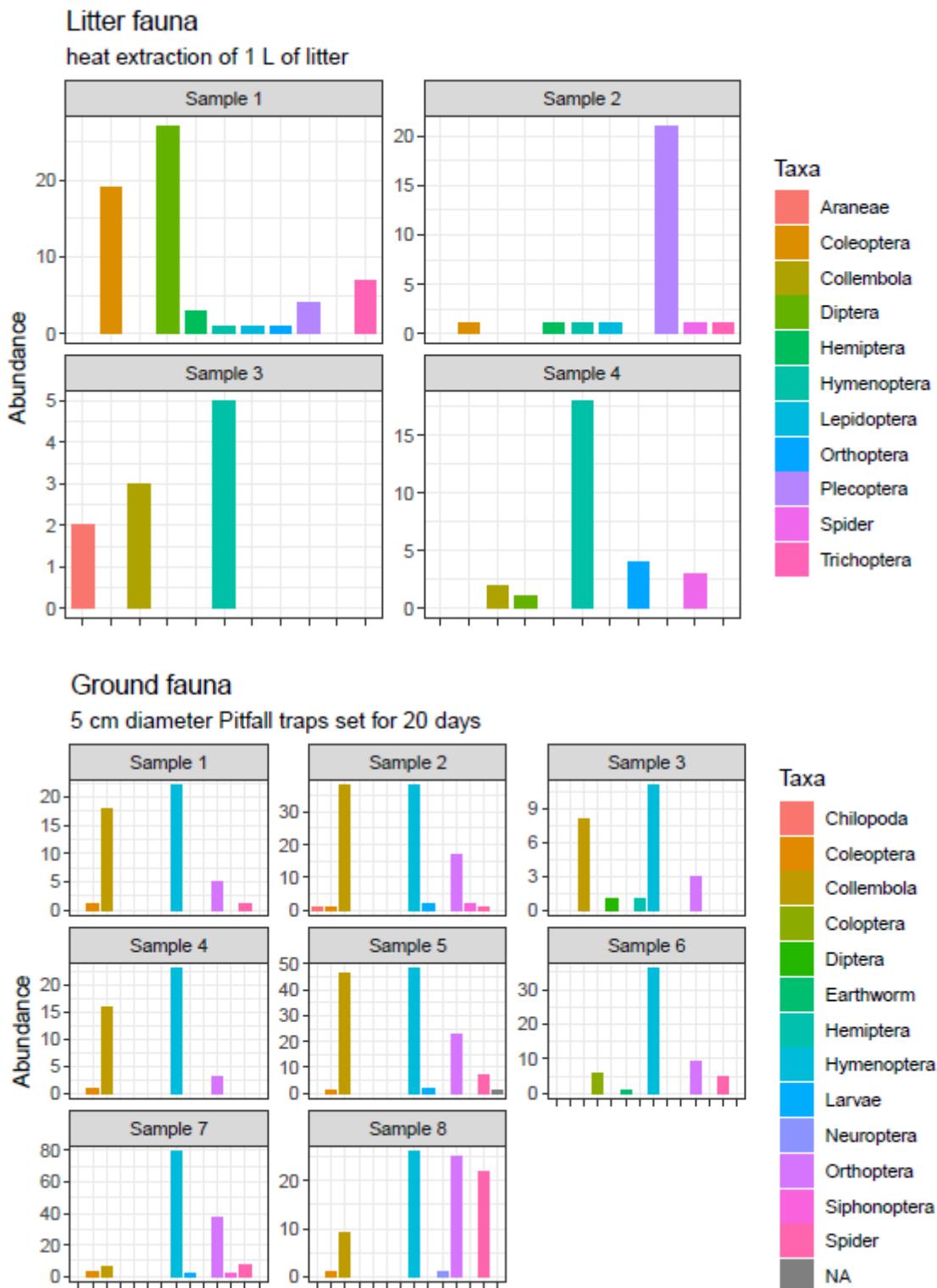
Macrofauna was collected by hand on 50 x 50 cm square during the 10 minutes after litter removal near the Common Garden experiment.

Litter fauna

Litter fauna was collected by heat extraction from 2 L of litter collected near the Common Garden experiment.

Pitfall trap collected

Four pitfall traps of 5 cm diameter filled with Glycerol were set for 20 days in 4 locations across BEF China.



Supplementary material: Chapter II - Tree diversity and soil chemical properties drive the linkages between soil microbial community and ecosystem functioning

Supplementary material II – S1 Material and methods

Study site, study design, and sampling

Our study site was located in south-east China in the Jiangxi province (29.08–29.11° N, 117.90–117.93° E). The region is characterized by a subtropical climate with warm, rainy summers and cold, dry winters (mean temperature of 16.7°C and mean rainfall of 1821 mm) (Yang et al. 2013). Soils in the region are Cambisols and Cambisol derivatives, with Regosol on ridges and crests (Geißler et al. 2012). The natural vegetation consists of species-rich broad-leaved forests dominated by *Quercus glauca*, *Castanopsis eyrei*, *Daphniphyllum oldhamii*, and *Lithocarpus glaber* (Bruelheide et al. 2011; Bruelheide et al. 2014). Sampling took place in BEF China, a tree diversity experiment, including tree species mixture plots (1, 2, 4, 8, and 16 tree species per plot), was planted in 2009 after clear-cutting the original forest (Fig. 1) (Bruelheide et al. 2014). To account for the role of tree diversity and soil quality, we collected 150 soil samples across different levels of tree diversity randomly distributed in the landscape (Fig. 1, Suppl. S2). We sampled from mid-August to late-September 2018, before the litterfall season. To avoid spatio-temporal autocorrelation, the daily sample location was chosen randomly, and to control for the distance to the trees, each sample was extracted on the transect between two trees. For each pair of trees, we extracted four soil cores (5 cm diameter; 10 cm depth), 5 cm and 20 cm away from the centerpoint between the tree pair (Fig. 1). A composite sample was built from these four cores by homogenizing with a 2 mm sieve.

Soil quality analyses

Soil moisture was measured from 25 g of soil by drying at 40°C for two days. A subsample was used to measure soil pH in a 1:2.5 soil-water solution. Soil total organic carbon (TOC) was measured by a TOC Analyzer (Liqui TOC II; Elementar Analysensysteme GmbH, Hanau, Germany). Soil total nitrogen (TN) was measured on an auto-analyzer (SEAL Analytical GmbH, Norderstedt, Germany) using the Kjeldahl method (Bradstreet 1954). Soil total phosphorus (TP) concentration was measured after wet digestion with H₂SO₄ and HClO₄ by a UV-VIS spectrophotometer (UV2700, SHIMADZU, Japan). Carbon to nitrogen and carbon to phosphorus ratios were calculated as TOC:TN and TOC:TP, respectively.

Soil microbial biomass

Microbial biomass was measured using phospholipid fatty acid (PLFA) analysis. PLFAs were extracted from 5 g of frozen soil following Frostegård et al. (1991) (Frostegård et al. 1991). Biomarkers were assigned to microbial functional groups according to Ruess et al. (2010) (Ruess and Chamberlain 2010). These markers targeted bacteria (gram-positive bacteria: i15:0, a15:0, i16:0, i17:0; gram-negative bacteria: cy17:0, cy19:0; general bacterial markers: 16:1ω5; 16:1ω7), arbuscular mycorrhizal fungi (20:1ω9), and saprophytic and ectomycorrhizal association fungi (18:1ω9 and 18:2ω6,9, see Suppl. S3). Total microbial biomass was calculated as the sum of biomasses of all microbial groups. The ratio of bacteria to fungi (B:F) was calculated as the ratio of the sum of all bacterial biomasses to the sum of all fungal biomasses.

Active microbial biomass was measured using the substrate-induced respiration method (Scheu 1992). About 6 g of soil was used to determine soil active microbial biomass, and 8 mg of glucose per gram of dry soil was added to saturated the soil micro-organism catabolism enzymes. O₂ respiration was measured based on electrolyte O₂ micro-compensation using an automated respirometer. Active

microbial biomass was calculated from the maximum initial respiratory response after induction (MIRR).

Soil microbial taxonomic profile

Microbial DNA was extracted from freeze-dried soil samples using a PowerSoil DNA Isolation Kit (MO BIO Laboratories Inc., Carlsbad, CA, United States). DNA concentrations were checked with a NanoDrop spectrophotometer (Thermo Fisher Scientific, Dreieich, Germany), and the extracts were adjusted to 10–15 ng/ul. The bacterial and fungal amplicon libraries were prepared following Schöps et al. (2018) (Schöps et al. 2018) and Nawaz et al. (2019) (Nawaz et al. 2019). Briefly, bacterial and fungal amplicon libraries were built separately using 16S rRNA gene and ITS2 rDNA regions, respectively. The bacterial 16S rRNA gene was amplified with universal primers 515f and 806r (Caporaso et al. 2011) with Illumina adapter sequence overhangs. The fungal ITS2 rDNA region was amplified by performing a semi-nested PCR using the initial primer combination of ITS1F (Gardes and Bruns 1993) and ITS4 (White et al. 1990) followed by the primer pair fITS7 (Ihrmark et al. 2012) and ITS4 containing the Illumina adapter sequences. The amplicon libraries were indexed, purified, quantified, and pooled equimolarly to a final concentration of 4nM which was then mixed in 1:3 ratio to make the final sequencing library. Paired-end sequencing of 2x300 bp was performed on an Illumina MiSeq platform (Illumina Inc., San Diego, CA, United States) using the MiSeq Reagent kit v3 at the Department of Environmental Microbiology, UFZ.

Bioinformatic analysis was performed using the Quantitative Insights into Microbial Ecology – QIIME 2 2020.2 (Bolyen et al. 2019). The forward and reverse reads were demultiplexed, primer sequences were trimmed, denoised, and grouped into Amplicon Sequence Variants (ASVs) using cut-adapt for chimeria removal (q2-cutadapt) (Martin 2011) and DADA2 for non-target taxa removal (via q2-dada2) (Callahan et al. 2016). ASV tables were imported into R with the 'phyloseq' package (McMurdie and Holmes 2013). The fungal and bacterial ASVs were rarefied to 16,542 and 28,897 reads per sample respectively. OTU richness, Shannon diversity, and Pielou evenness were calculated using the 'microbiome' package (Lahti et al. 2017). We inspected the correlations between these indices and focused our analyses on Shannon diversity index (Suppl. S4).

Soil microbial functional profile

DNA was extracted with the FastDNA Spin Kit for Soil (MP Biomedicals, USA) following the manufacturer's instructions. DNA concentrations were checked with a NanoDrop spectrophotometer (Thermo Fisher Scientific, Dreieich, Germany), and DNA concentrations were quantified with the QuantiFluor dsDNA kit (Promega, USA) and a microplate reader (SpectraMax M5, Molecular Devices). DNA was diluted to 50 ng μ l⁻¹ with sterile water and stored at –20 °C.

Microbial functional genes coding for enzymes involved in carbon anabolism and catabolism processes, which are central to soil carbon cycling (complete list in Suppl. S5) (Liang et al. 2017), were quantified using a high-throughput quantitative-PCR-based chip (HT-qPCR; SmartChip Real-time PCR system, WaferGen Biosystems, Fremont, USA). This chip contained 72 primer pairs: 36 designed pairs, 35 published pairs, and the bacterial 16S rRNA gene, which allows to quantify 72 DNA genes in parallel (Zheng et al. 2018). PCR reaction conditions were as follows: initial denaturation of 10 min at 95°C, and 40 cycles of denaturation at 95°C for 30 s, annealing 30 s at 58°C and extension at 72°C for another 30 s. The melting curve was automatically generated by the WaferGen software. Three replicates for each sample were analyzed. Results with multiple melting peaks or with amplification efficiencies less than 80% and over 120% were excluded. Only results with a threshold cycle (C_T) less than 31 (the detection limit for this method) were used for further analysis. The relative copy number of each functional gene was calculated as shown in eq. 1 (Looft et al. 2012). Then, the relative abundance of a

given functional gene was defined as the proportion of the relative copy number of a functional gene to the relative copy number of the 16S rRNA gene.

$$\text{Gene relative copy number (GR): } \text{GR} = (31 - C_T) \times (10/3) / \text{GR}_{16S} \quad (1)$$

To compare abundance patterns across functional genes, we scaled each functional gene abundance between 0 and 1 across all samples using the z-transformation, and we summed the scaled abundance of functional genes related to carbon catabolism (i.e. "Cata", Suppl. S5). To quantify the evenness of the functional gene abundances, the functional gene Pielou evenness was calculated using the R 'diversity' from the 'vegan' package ("FG evenness", respectively).

Soil microbial physiological potential

Microbial physiological potential indices were calculated from substrate-induced respiration assays using the Microresp.® method (Campbell et al. 2003). Fourteen substrates from three chemical classes (i.e. saccharides, amino-acid, and carboxylic acids) were selected to create a gradient of molecular weights (ranging from 89 to 221 g.mol⁻¹), and a gradient of carbon oxidation states (ranging from -2 to 3 e⁻, Suppl. S5). Ten g of soil was evenly distributed on the half of 96 deep-well plate and incubated at 25°C for five days. For each substrate, 30 mg of substrate per gram of soil water was added to three wells. CO₂ production of the wells was fixed in agar – cresol red gel during the six following hours. Total CO₂ production of the wells was measured by colorimetry using a photo-spectrometer. Two indices were calculated from these CO₂ measurements: substrate-use efficiency and substrate-use range. Substrate-use efficiency was calculated as the Pielou evenness (from R 'diversity' function package 'vegan') of the CO₂ production of all substrates. Substrate-use range was defined as the difference in CO₂ production between oxalic acid and alanine, the two substrates on the upper and lower extremes of carbon oxidation. We performed sensitivity analyses to explore the effects of substrate selection on these indices, which showed that substrate selection did not alter our results and conclusions (Suppl. S6).

Soil microbial respiration

Soil microbial respiration was measured on 6 g of fresh soil following Scheu *et al.* (1992) (Scheu 1992) without adding any substrate or water, thereby reflecting the actual respiration at the site. During 24 hours, O₂ consumption was continuously measured using an automated respirometer based on electrolytic O₂ micro-compensation (Scheu 1992). Soil microbial respiration was calculated as the mean of O₂ consumption between the 14 to 24 hours after starting the measurement. Active microbial biomass (with substrate addition) and microbial respiration (without substrate addition) were measured on the same sample and machine. To test the robustness of our results, all following analyses were run with and without active microbial biomass.

Statistical analyses

All data handling and statistical analyses were performed using the R statistical software version 4.0.3, and all R scripts used for this study can be found in our GitHub repository (https://github.com/remybeugnon/Beugnon-Du_et_al_2021_Microbial_community_and_functions). All metrics inferred from soil measurements are summarized in the Suppl. S4. In order to avoid any model-fit deviation due to scale differences between variables, all explanatory variables were centered and divided by two standard deviations for our analyses using the R 'rescale' function from the 'arm' package. For each analysis, we compared the

drivers' effect sizes defined as the standardized estimate of a given variable in the model where the response variable was centered and divided by two standard deviations.

Tree diversity effects on soil microbial community facets and functions

We used linear multivariate models and normal distribution assumptions to test the effects of tree species richness on soil microbial biomass (total and active microbial biomass), taxonomic profile (B:F ratio and Shannon diversity of bacteria and fungi), functional profile (catabolic functional gene abundance and evenness), physiological potential (substrate-use efficiency and range), and microbial respiration. All previous linear multivariate models were tested in R using the 'lm' function and statistical hypotheses of the following linear models were tested in Suppl. S7 using the 'model_check' function from the 'performance' package in R.

Effects of soil microbial facets on microbial functions

We tested the correlation between the microbial facets – soil microbial biomass, taxonomic and functional profiles – using Pearson correlation tests. We used linear multivariate models and normal distribution assumptions to test the effects of microbial biomass (total and active microbial biomass), taxonomic profile (B:F ratio and Shannon diversity of bacteria and fungi) and functional profile (catabolic functional gene abundance, and evenness) on soil microbial physiological potential (substrate-use efficiency and range), and soil microbial respiration. Explanatory variables (microbial biomasses, taxonomic and functional profile indices) were selected using forward and backward step selection based on AIC (i.e., R 'step' function from 'stats' package). A variance partitioning analysis was performed on the final set of variables to disentangle the effects of microbial biomass and taxonomic profile using the R 'varpart' function from the 'vegan' package. All previous linear multivariate models were tested in R using the 'lm' function and statistical hypotheses of the following linear models were tested in Suppl. S8 using the 'model_check' function from the 'performance' package in R

Cascading effects of the different soil microbial community facets on microbial physiological potential and microbial respiration

We tested the relationships between soil microbial biomass, taxonomic and functional profiles, physiological potential, and respiration using a Structural Equation Modeling (SEM) framework. Microbial biomass, taxonomic and functional profiles were linked to each other by correlations, and their effects on physiological potential indices and soil microbial respiration were modeled with causal relations (directed paths). Our SEM was fitted using the R 'sem' function from the 'lavaan' package (Rosseel 2012). The model fit to our data, and model quality were estimated using three complementary indices: (i) the root mean square error of approximation (RMSEA), (ii) the comparative fit index (CFI), and (iii) the standardized root mean squared residuals (SRMR). Model fits were considered acceptable when RMSEA < 0.10, CFI > 0.9 and SRMR < 0.08. All statistical hypotheses and complete outputs can be found in Suppl. S9.

Effects of tree species richness and soil quality on relationships between the soil microbial community and their functions

To test the effects of tree species richness and soil quality on the relationship between the soil microbial community facets and microbial respiration, we added the causal effects of soil quality indices and tree species richness onto the variables of our previous SEM model. To assess which group of response variables was the most affected by soil quality and tree species richness, the effects of soil quality and tree species richness were summarized by a group of response variables (soil microbial biomass, taxonomic profile, functional profile, physiological potential, and microbial respiration). For each group of response variables, we summed all the absolute standardized effects of soil quality or tree species

richness on each of the response variables. Additionally, to assess the importance of soil quality indices and tree species richness for microbial community facets and microbial functions, we summed the absolute standardized effects of each soil quality index and tree species richness. All statistical hypotheses and complete outputs can be found in Suppl. S10.

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Supplementary material II -S2: tree selection

List of tree species building the pairs of tree species in the different plots of Site A (BEF China

experiment)	Species	Leaf persistence
<i>Castanea henryi</i>		
deciduous	<i>Castanopsis</i>	
<i>sclerophylla</i>	evergreen	
<i>Choerospondias</i>	<i>axillaris</i>	
deciduous	<i>Cyclobalanopsis</i>	
<i>glauca</i>	evergreen	<i>Koelreuteria</i>
<i>bipinnata</i>	deciduous	
<i>Liquidambar formosana</i>		deciduous
<i>Lithocarpus glaber</i>		evergreen
<i>Nyssa sinensis</i>		deciduous
<i>Quercus fabri</i>		deciduous
<i>Quercus serrata</i>		deciduous
<i>Sapindus mukorossi</i>		deciduous
<i>Sapium sebiferum</i>		deciduous

Sampling point description and attributes (paragraphs were added for readability)

Code	Site	Plot	Diversity level	Species 1	Species 2
26-E24	A	E24	1	<i>Liquidambar formosana</i>	<i>Liquidambar formosana</i>
33-E31	A	E31	1	<i>Quercus fabri</i>	<i>Quercus fabri</i>
34-E31	A	E31	1	<i>Quercus fabri</i>	<i>Quercus fabri</i>
27-E33	A	E33	1	<i>Lithocarpus glaber</i>	<i>Lithocarpus glaber</i>
28-E33	A	E33	1	<i>Lithocarpus glaber</i>	<i>Lithocarpus glaber</i>
1-E34	A	E34	1	<i>Castanea henryi</i>	<i>Castanea henryi</i>
2-E34	A	E34	1	<i>Castanea henryi</i>	<i>Castanea henryi</i>
37-F21	A	F21	1	<i>Quercus serrata</i>	<i>Quercus serrata</i>
38-F21	A	F21	1	<i>Quercus serrata</i>	<i>Quercus serrata</i>
10-G17	A	G17	1	<i>Castanopsis sclerophylla</i>	<i>Castanopsis sclerophylla</i>
29-G22	A	G22	1	<i>Lithocarpus glaber</i>	<i>Lithocarpus glaber</i>
22-G24	A	G24	1	<i>Koelreuteria bipinnata</i>	<i>Koelreuteria bipinnata</i>
23-G24	A	G24	1	<i>Koelreuteria bipinnata</i>	<i>Koelreuteria bipinnata</i>
36-G33	A	G33	1	<i>Quercus serrata</i>	<i>Quercus serrata</i>
30-H25	A	H25	1	<i>Nyssa sinensis</i>	<i>Nyssa sinensis</i>
3-I12	A	I12	1	<i>Castanea henryi</i>	<i>Castanea henryi</i>
24-I28	A	I28	1	<i>Liquidambar formosana</i>	<i>Liquidambar formosana</i>
25-I28	A	I28	1	<i>Liquidambar formosana</i>	<i>Liquidambar formosana</i>
14-K9	A	K9	1	<i>Cyclobalanopsis glauca</i>	<i>Cyclobalanopsis glauca</i>
8-L11	A	L11	1	<i>Castanopsis sclerophylla</i>	<i>Castanopsis sclerophylla</i>
9-L11	A	L11	1	<i>Castanopsis sclerophylla</i>	<i>Castanopsis sclerophylla</i>
13-L23	A	L23	1	<i>Choerospondias axillaris</i>	<i>Choerospondias axillaris</i>
43-N11	A	N11	1	<i>Sapindus mukorossi</i>	<i>Sapindus mukorossi</i>
46-N13	A	N13	1	<i>Sapium sebiferum</i>	<i>Sapium sebiferum</i>

Supplementary material: Chapter II - Tree diversity and soil chemical properties drive the linkages between soil microbial community and ecosystem functioning

Code	Site	Plot	Diversity level	Species 1	Species 2
47-N13	A	N13	1	<i>Sapium sebiferum</i>	<i>Sapium sebiferum</i>
11-O27	A	O27	1	<i>Choerospondias axillaris</i>	<i>Choerospondias axillaris</i>
21-Q13	A	Q13	1	<i>Koelreuteria bipinnata</i>	<i>Koelreuteria bipinnata</i>
r-21-Q13	A	Q13	1	<i>Koelreuteria bipinnata</i>	<i>Koelreuteria bipinnata</i>
35-Q16	A	Q16	1	<i>Quercus fabri</i>	<i>Quercus fabri</i>
15-R14	A	R14	1	<i>Cyclobalanopsis glauca</i>	<i>Cyclobalanopsis glauca</i>
16-R14	A	R14	1	<i>Cyclobalanopsis glauca</i>	<i>Cyclobalanopsis glauca</i>
44-R17	A	R17	1	<i>Sapindus mukorossi</i>	<i>Sapindus mukorossi</i>
45-W13	A	W13	1	<i>Sapium sebiferum</i>	<i>Sapium sebiferum</i>
32-W14	A	W14	1	<i>Nyssa sinensis</i>	<i>Nyssa sinensis</i>
51-C32	A	C32	2	<i>Castanea henryi</i>	<i>Castanea henryi</i>
52-C32	A	C32	2	<i>Castanea henryi</i>	<i>Nyssa sinensis</i>
96-C32	A	C32	2	<i>Castanea henryi</i>	<i>Nyssa sinensis</i>
95-C32	A	C32	2	<i>Nyssa sinensis</i>	<i>Nyssa sinensis</i>
97-C32	A	C32	2	<i>Nyssa sinensis</i>	<i>Nyssa sinensis</i>
53-F22	A	F22	2	<i>Castanea henryi</i>	<i>Castanea henryi</i>
54-F22	A	F22	2	<i>Castanea henryi</i>	<i>Castanea henryi</i>
55-F22	A	F22	2	<i>Castanea henryi</i>	<i>Nyssa sinensis</i>
98-F22	A	F22	2	<i>Nyssa sinensis</i>	<i>Nyssa sinensis</i>
87-H31	A	H31	2	<i>Liquidambar formosana</i>	<i>Liquidambar formosana</i>
86-H31	A	H31	2	<i>Liquidambar formosana</i>	<i>Sapindus mukorossi</i>
113-H31	A	H31	2	<i>Sapindus mukorossi</i>	<i>Liquidambar formosana</i>
112-H31	A	H31	2	<i>Sapindus mukorossi</i>	<i>Sapindus mukorossi</i>
118-I27	A	I27	2	<i>Sapium sebiferum</i>	<i>Sapium sebiferum</i>
81-J21	A	J21	2	<i>Koelreuteria bipinnata</i>	<i>Koelreuteria bipinnata</i>
82-J21	A	J21	2	<i>Koelreuteria bipinnata</i>	<i>Koelreuteria bipinnata</i>
83-J21	A	J21	2	<i>Koelreuteria bipinnata</i>	<i>Lithocarpus glaber</i>
92-J21	A	J21	2	<i>Lithocarpus glaber</i>	<i>Lithocarpus glaber</i>
72-K3	A	K3	2	<i>Cyclobalanopsis glauca</i>	<i>Cyclobalanopsis glauca</i>
73-K3	A	K3	2	<i>Cyclobalanopsis glauca</i>	<i>Cyclobalanopsis glauca</i>
75-K3	A	K3	2	<i>Cyclobalanopsis glauca</i>	<i>Quercus fabri</i>
64-O6	A	O6	2	<i>Castanopsis sclerophylla</i>	<i>Castanopsis sclerophylla</i>
65-O6	A	O6	2	<i>Castanopsis sclerophylla</i>	<i>Castanopsis sclerophylla</i>
66-O6	A	O6	2	<i>Castanopsis sclerophylla</i>	<i>Quercus serrata</i>
105-O6	A	O6	2	<i>Quercus serrata</i>	<i>Quercus serrata</i>
63-P26	A	P26	2	<i>Castanopsis sclerophylla</i>	<i>Castanopsis sclerophylla</i>
62-P26	A	P26	2	<i>Castanopsis sclerophylla</i>	<i>Quercus serrata</i>
102-P26	A	P26	2	<i>Quercus serrata</i>	<i>Quercus serrata</i>
103-P26	A	P26	2	<i>Quercus serrata</i>	<i>Quercus serrata</i>
104-P26	A	P26	2	<i>Quercus serrata</i>	<i>Quercus serrata</i>
74-Q21	A	Q21	2	<i>Cyclobalanopsis glauca</i>	<i>Cyclobalanopsis glauca</i>
76-Q21	A	Q21	2	<i>Cyclobalanopsis glauca</i>	<i>Quercus fabri</i>
77-Q21	A	Q21	2	<i>Cyclobalanopsis glauca</i>	<i>Quercus fabri</i>
100-Q21	A	Q21	2	<i>Quercus fabri</i>	<i>Quercus fabri</i>
101-Q21	A	Q21	2	<i>Quercus fabri</i>	<i>Quercus fabri</i>
84-Q7	A	Q7	2	<i>Koelreuteria bipinnata</i>	<i>Koelreuteria bipinnata</i>
85-Q7	A	Q7	2	<i>Koelreuteria bipinnata</i>	<i>Lithocarpus glaber</i>

Supplementary material: Chapter II - Tree diversity and soil chemical properties drive the linkages between soil microbial community and ecosystem functioning

Code	Site	Plot	Diversity level	Species 1	Species 2
93-Q7	A	Q7	2	<i>Lithocarpus glaber</i>	<i>Lithocarpus glaber</i>
94-Q7	A	Q7	2	<i>Lithocarpus glaber</i>	<i>Lithocarpus glaber</i>
69-S18	A	S18	2	<i>Choerospondias axillaris</i>	<i>Choerospondias axillaris</i>
70-S18	A	S18	2	<i>Choerospondias axillaris</i>	<i>Sapium sebiferum</i>
71-S18	A	S18	2	<i>Choerospondias axillaris</i>	<i>Sapium sebiferum</i>
119-S18	A	S18	2	<i>Sapium sebiferum</i>	<i>Sapium sebiferum</i>
r-120-S18	A	S18	2	<i>Sapium sebiferum</i>	<i>Sapium sebiferum</i>
88-T17	A	T17	2	<i>Liquidambar formosana</i>	<i>Liquidambar formosana</i>
89-T17	A	T17	2	<i>Liquidambar formosana</i>	<i>Liquidambar formosana</i>
90-T17	A	T17	2	<i>Liquidambar formosana</i>	<i>Sapindus mukorossi</i>
115-T17	A	T17	2	<i>Sapindus mukorossi</i>	<i>Sapindus mukorossi</i>
130-F27	A	F27	4	<i>Castanopsis sclerophylla</i>	<i>Castanopsis sclerophylla</i>
131-F27	A	F27	4	<i>Choerospondias axillaris</i>	<i>Castanopsis sclerophylla</i>
153-F27	A	F27	4	<i>Quercus serrata</i>	<i>Choerospondias axillaris</i>
161-F27	A	F27	4	<i>Sapium sebiferum</i>	<i>Choerospondias axillaris</i>
162-F27	A	F27	4	<i>Sapium sebiferum</i>	<i>Sapium sebiferum</i>
139-F28	A	F28	4	<i>Koelreuteria bipinnata</i>	<i>Koelreuteria bipinnata</i>
132-N20	A	N20	4	<i>Choerospondias axillaris</i>	<i>Choerospondias axillaris</i>
154-N20	A	N20	4	<i>Quercus serrata</i>	<i>Castanopsis sclerophylla</i>
155-N20	A	N20	4	<i>Quercus serrata</i>	<i>Quercus serrata</i>
156-N20	A	N20	4	<i>Quercus serrata</i>	<i>Sapium sebiferum</i>
163-N20	A	N20	4	<i>Sapium sebiferum</i>	<i>Castanopsis sclerophylla</i>
133-N8	A	N8	4	<i>Cyclobalanopsis glauca</i>	<i>Cyclobalanopsis glauca</i>
149-N8	A	N8	4	<i>Quercus fabri</i>	<i>Cyclobalanopsis glauca</i>
125-P19	A	P19	4	<i>Castanea henryi</i>	<i>Castanea henryi</i>
126-P19	A	P19	4	<i>Castanea henryi</i>	<i>Nyssa sinensis</i>
143-P19	A	P19	4	<i>Liquidambar formosana</i>	<i>Sapindus mukorossi</i>
148-P19	A	P19	4	<i>Nyssa sinensis</i>	<i>Sapindus mukorossi</i>
160-P19	A	P19	4	<i>Sapindus mukorossi</i>	<i>Sapindus mukorossi</i>
141-P29	A	P29	4	<i>Liquidambar formosana</i>	<i>Liquidambar formosana</i>
142-P29	A	P29	4	<i>Liquidambar formosana</i>	<i>Nyssa sinensis</i>
147-P29	A	P29	4	<i>Nyssa sinensis</i>	<i>Castanea henryi</i>
159-P29	A	P29	4	<i>Sapindus mukorossi</i>	<i>Castanea henryi</i>
146-W12/X12	A	W12/X12	4	<i>Lithocarpus glaber</i>	<i>Lithocarpus glaber</i>
176-P27	A	P27	8	<i>Cyclobalanopsis glauca</i>	<i>Quercus fabri</i>
181-P27	A	P27	8	<i>Koelreuteria bipinnata</i>	<i>Lithocarpus glaber</i>
166-R16	A	R16	8	<i>Castanea henryi</i>	<i>Liquidambar formosana</i>
171-R16	A	R16	8	<i>Castanopsis sclerophylla</i>	<i>Castanopsis sclerophylla</i>
175-R16	A	R16	8	<i>Choerospondias axillaris</i>	<i>Sapium sebiferum</i>
190-R16	A	R16	8	<i>Nyssa sinensis</i>	<i>Castanea henryi</i>
193-R16	A	R16	8	<i>Quercus serrata</i>	<i>Castanopsis sclerophylla</i>
194-R16	A	R16	8	<i>Quercus serrata</i>	<i>Quercus serrata</i>
198-R16	A	R16	8	<i>Sapindus mukorossi</i>	<i>Sapindus mukorossi</i>
199-R16	A	R16	8	<i>Sapindus mukorossi</i>	<i>Sapindus mukorossi</i>
200-R16	A	R16	8	<i>Sapium sebiferum</i>	<i>Quercus serrata</i>
201-R16	A	R16	8	<i>Sapium sebiferum</i>	<i>Sapium sebiferum</i>
165-S10	A	S10	8	<i>Castanea henryi</i>	<i>Castanea henryi</i>
170-S10	A	S10	8	<i>Castanopsis sclerophylla</i>	<i>Sapium sebiferum</i>

Supplementary material: Chapter II - Tree diversity and soil chemical properties drive the linkages between soil microbial community and ecosystem functioning

Code	Site	Plot	Diversity level	Species 1	Species 2
173-S10	A	S10	8	<i>Choerospondias axillaris</i>	<i>Castanopsis sclerophylla</i>
174-S10	A	S10	8	<i>Choerospondias axillaris</i>	<i>Choerospondias axillaris</i>
186-S10	A	S10	8	<i>Liquidambar formosana</i>	<i>Liquidambar formosana</i>
185-S10	A	S10	8	<i>Liquidambar formosana</i>	<i>Nyssa sinensis</i>
188-S10	A	S10	8	<i>Nyssa sinensis</i>	<i>Nyssa sinensis</i>
189-S10	A	S10	8	<i>Nyssa sinensis</i>	<i>Sapindus mukorossi</i>
197-S10	A	S10	8	<i>Sapindus mukorossi</i>	<i>Castanea henryi</i>
178-S14	A	S14	8	<i>Cyclobalanopsis glauca</i>	<i>Cyclobalanopsis glauca</i>
183-S15	A	S15	8	<i>Koelreuteria bipinnata</i>	<i>Koelreuteria bipinnata</i>
r-216-S15	A	S15	8	<i>Koelreuteria bipinnata</i>	<i>Lithocarpus glaber</i>
184-S15	A	S15	8	<i>Koelreuteria bipinnata</i>	<i>Quercus fabri</i>
191-T15	A	T15	8	<i>Quercus fabri</i>	<i>Quercus fabri</i>
220-L21	A	L21	16	<i>Liquidambar formosana</i>	<i>Choerospondias axillaris</i>
203-L22	A	L22	16	<i>Castanea henryi</i>	<i>Nyssa sinensis</i>
204-L22	A	L22	16	<i>Castanea henryi</i>	<i>Sapindus mukorossi</i>
217-L22	A	L22	16	<i>Liquidambar formosana</i>	<i>Castanea henryi</i>
219-L22	A	L22	16	<i>Liquidambar formosana</i>	<i>Liquidambar formosana</i>
218-L22	A	L22	16	<i>Liquidambar formosana</i>	<i>Nyssa sinensis</i>
221-L22	A	L22	16	<i>Lithocarpus glaber</i>	<i>Lithocarpus glaber</i>
222-L22	A	L22	16	<i>Quercus fabri</i>	<i>Quercus fabri</i>
230-L22	A	L22	16	<i>Sapium sebiferum</i>	<i>Castanopsis sclerophylla</i>
226-M21	A	M21	16	<i>Quercus serrata</i>	<i>Sapium sebiferum</i>
r-213-U10	A	U10	16	<i>Cyclobalanopsis glauca</i>	<i>Quercus fabri</i>
225-U10	A	U10	16	<i>Quercus serrata</i>	<i>Quercus serrata</i>
229-U10	A	U10	16	<i>Sapindus mukorossi</i>	<i>Sapindus mukorossi</i>
231-U10	A	U10	16	<i>Sapium sebiferum</i>	<i>Sapium sebiferum</i>
232-N9	A	N9	24	<i>Castanea henryi</i>	<i>Castanea henryi</i>
236-N9	A	N9	24	<i>Cyclobalanopsis glauca</i>	<i>Cyclobalanopsis glauca</i>
238-N9	A	N9	24	<i>Koelreuteria bipinnata</i>	<i>Koelreuteria bipinnata</i>
241-N9	A	N9	24	<i>Sapindus mukorossi</i>	<i>Nyssa sinensis</i>
234-R18	A	R18	24	<i>Castanopsis sclerophylla</i>	<i>Quercus serrata</i>
235-R18	A	R18	24	<i>Choerospondias axillaris</i>	<i>Quercus serrata</i>
239-R18	A	R18	24	<i>Nyssa sinensis</i>	<i>Nyssa sinensis</i>

Supplementary material II – S3: PLFA biomarkers

PLFA biomarkers used to identify soil microbes' functional groups

Fatty acid	Lipid fraction	Predominant origin	Literature
i15:0	PLFA	Gram-positive bacteria	Zelles (1997, 1999)
a15:0	PLFA	Gram-positive bacteria	Zelles (1997, 1999)
i16:0	PLFA	Gram-positive bacteria	Zelles (1997, 1999)
i17:0	PLFA	Gram-positive bacteria	Zelles (1997, 1999)
16:1n7	PLFA	Bacteria widespread	Guckert et al. (1991), Zelles (1999)
16:1n-5	PLFA	General bacteria	Nichols et al. (1986), Zelles (1997)
cy17:0	PLFA	Gram-negative bacteria	Zelles (1997, 1999)
18:1n9	PLFA	Fungi (saprophytic, EM)	Bååth (2003), Vestal and White (1989), Zelles (1999), Harwood and Russell (1984), Ruess et al. (2007)
cy19:0	PLFA	Gram-negative bacteria	Zelles (1997, 1999)
18:2n6c	PLFA	Fungi (saprophytic, EM)	Frostegård and Bååth (1996), Zelles (1999)
20:1	PLFA	AM fungi (Gigaspora)	Sakamoto et al. (2004)

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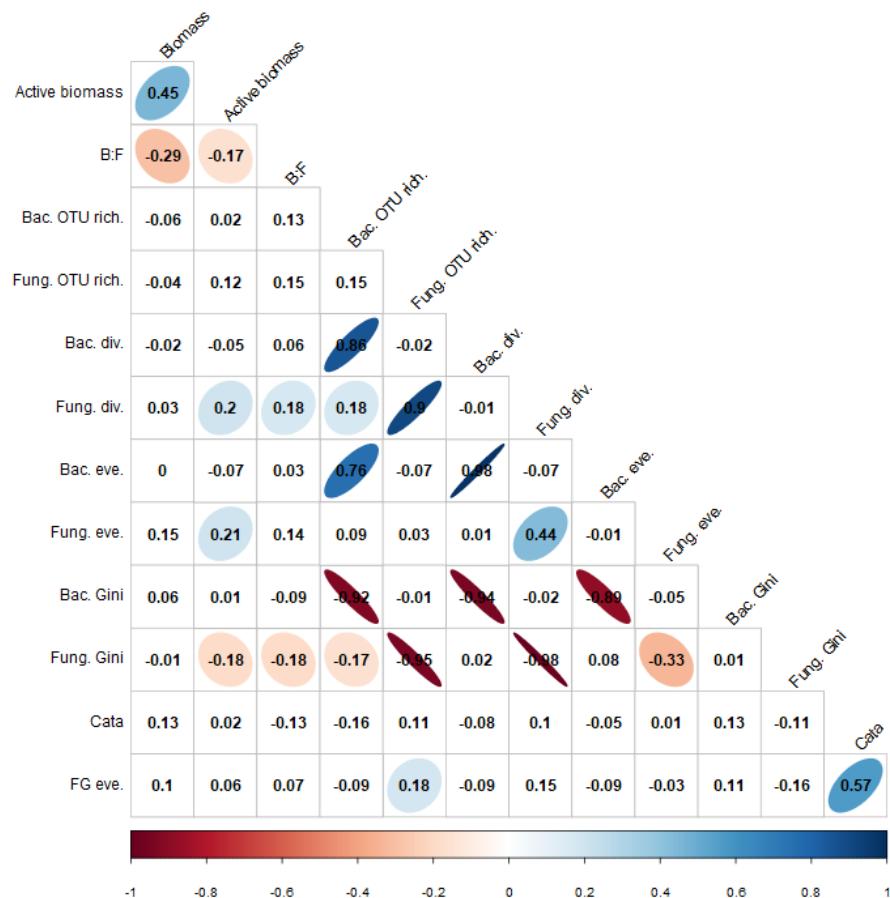
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Supplementary material II – S4: measurements summary

A. Correlations between the microbial variable



B. The structured list of variables used in the analyses.

Variable group	Variable name (acronyms)	Definition and measurement method	Hypotheses and analyses referring to it
Soil chemical properties	Soil carbon content (TOC)	Measured on top soil (0-10 cm) using TOC analyzer	Hypothesis 4, Fig. 5, Suppl. S10
	Soil carbon to nitrogen ratio (C:N)	Calculated on top soil (0-10 cm) measurements	Hypothesis 4, Fig. 5, Suppl. S10
	Soil carbon to nitrogen ratio (C:P)	Calculated on top soil (0-10 cm) measurements	Hypothesis 4, Fig. 5, Suppl. S10
	Soil pH (pH)	Measured on top soil (0-10 cm) using 1:2.5 soil - water solution	Hypothesis 4, Fig. 5, Suppl. S10
	Soil water content (RH)	Measured on 25 g of top soil (0-10 cm) air-dried at 40 °C	Hypothesis 4, Fig. 5, Suppl. S10
Tree Species Richness	Tree species richness	Number of tree species per plot	Hypothesis 1&4, Fig. 1&5, Suppl. S7&10
Soil microbial community facets	Microbial biomass	Total microbial biomass (Biomass)	Hypotheses 1-4, Fig. 1-5, Suppl. S3, S7-10
		Active microbial biomass (Active biomass)	Hypotheses 1-4, Fig. 1-5, Suppl. S3, S7-S10
	Taxonomic profile	Bacteria to fungi ratio (B:F)	Hypotheses 1-4, Fig. 1-5, Suppl. S3, S6-S10
		Bacteria Shannon diversity (Bac. div.)	Hypotheses 1-4, Fig. 1-5, Suppl. S3, S6-S10
	Functional profile	Fungi Shannon diversity (Fung. div.)	Hypotheses 1-4, Fig. 1-5, Suppl. S3, S6-10
		FG evenness	Hypotheses 1-4, Fig. 1-4, Suppl. S5 & S7-9

	Catabolism functional genes (Cata)	Sum of the abundance of functional genes involved in carbon catabolism. The variables can be calculated on the absolute or relative abundance of the functional genes and will be specified.	Hypotheses 1-4, Fig. 1-4, Suppl. S5 & S7-9
Soil physiological potential	Substrate induced-respiration (SIR)	Substrate-induced respiration (i.e. CO ₂ production during six hours after substrate addition) of fourteen substrates (i.e. 5 saccharides, 4 amino-acids, and 5 carboxylic-acids) measured with the Microresp® method.	Hypotheses 1-4, Fig. 1-5, Suppl. S5 & S7-9
	Substrate-induced respiration efficiency (SIR efficiency)	Pielou evenness of the substrate-induced respiration (i.e. CO ₂ production during six hours after substrate addition) of fourteen substrates (i.e. complete list in Suppl. S3)	Hypotheses 1-4, Fig. 1-5, Suppl. S5 & S7-9
	Substrate-induced respiration response range (SIR range)	The absolute difference of CO ₂ production between alamine induced respiration and oxalic-acid induced respiration measured with the Microresp® method.	Hypotheses 1-4, Fig. 1-5, Suppl. S5 & S7-9
Ecosystem function	Microbial respiration (M. resp.)	Soil basal respiration measured (SIR, Scheu 1992)	Hypotheses 1-4, Fig. 1-5, Suppl. S7-9

Supplementary material II – S5: Functional genes

List of functional genes and their functional attributes

Function in the carbon cycle	Functional gene name	Specific functional gene function
Carbon catabolism	abfA	Hemicellulose
	apu	Starch
	cex	Cellulose
	chiA	Chitin
	ipu	Starch
	lig	Lignin
	manB	Hemicellulose
	mnp	Lignin
	mxaF	Methane production
	naglu	Cellulose
	pox	Lignin
	pqq-mdh	Methane production
	sga	Starch
	xylA	Hemicellulose

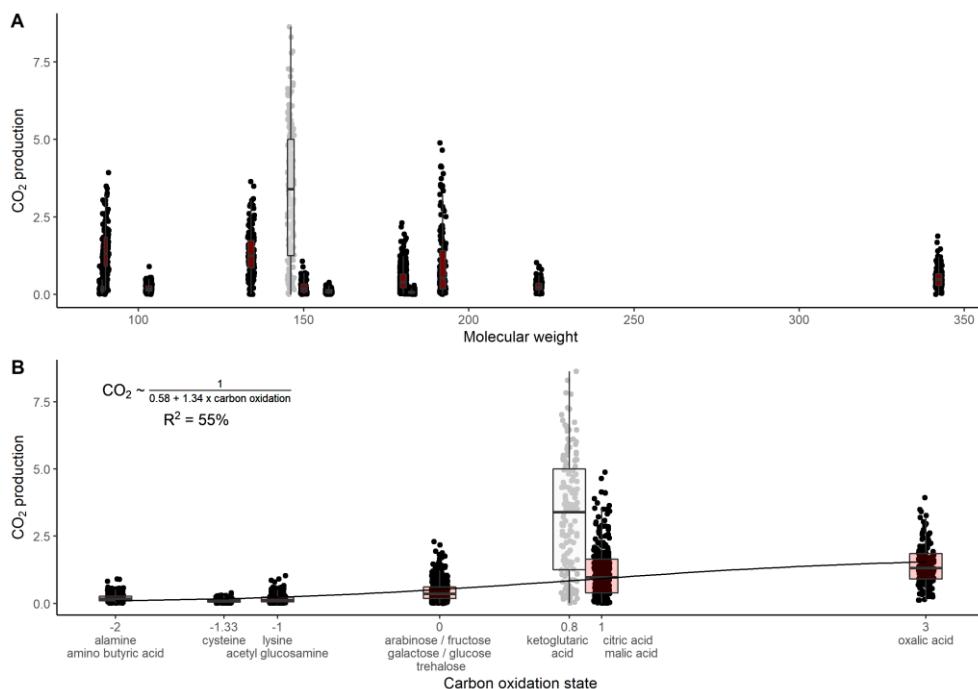
Supplementary material II – S6: MicroResp. ® measurements

- I. List of substrates used in substrate-induced respiration measurements (i.e. Microresp® method) and chemical attributes.

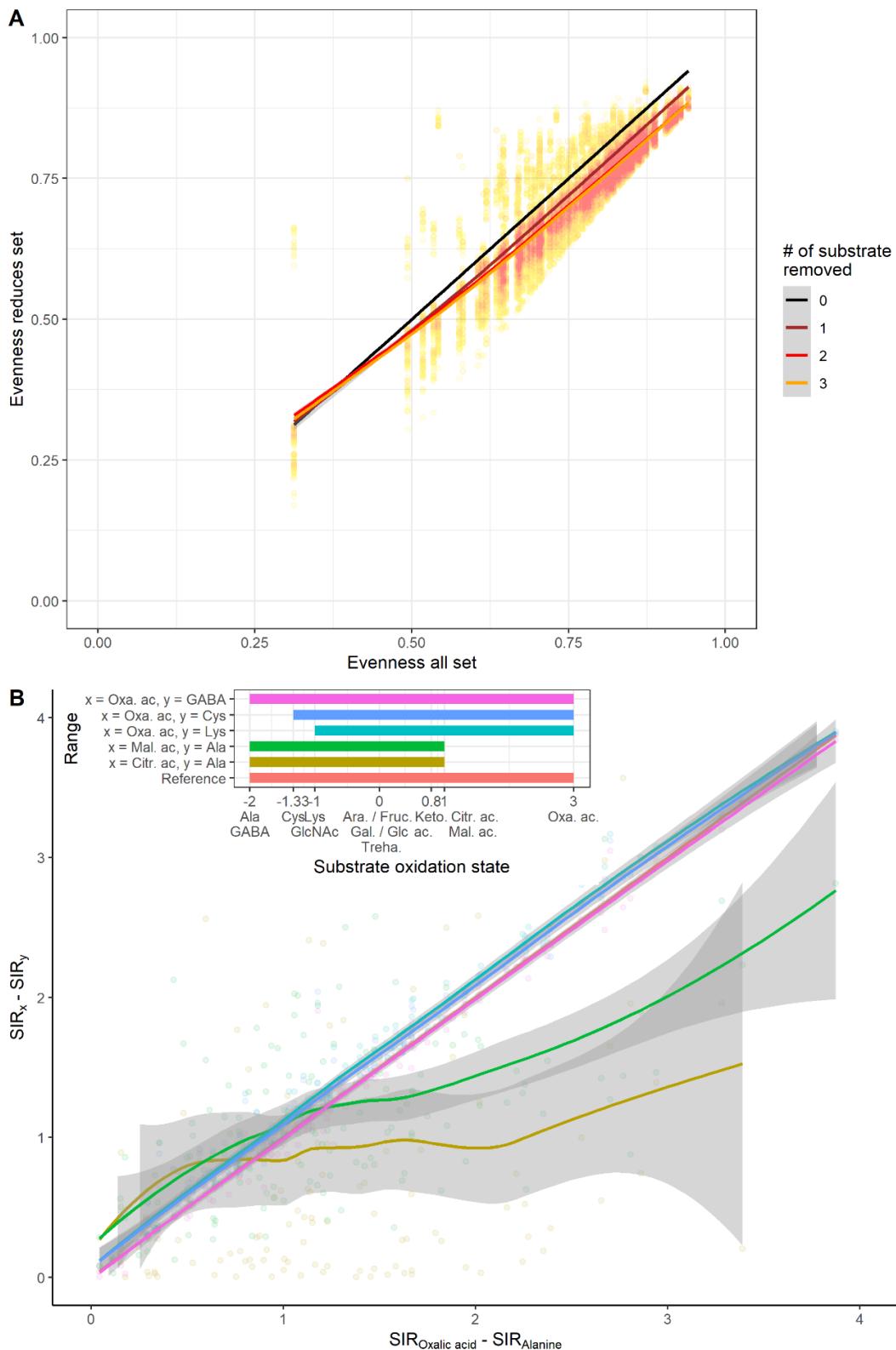
Full name	Chemical group	Formula	Molecular Weight	Mean carbon oxidation state
L-Alanine	Amino acid	C ₃ H ₇ NO ₂	89.094	-2
γ-Aminobutyric acid	Amino acid	C ₄ H ₉ NO ₂	103.121	-2
L-Cysteine-HCl	Amino acid	C ₃ H ₈ ClNO ₂ S	157.612	-1.33
L-Arginine	Amino acid	C ₆ H ₁₄ N ₄ O ₂	174.204	-1
L-Lysine-HCl	Amino acid	C ₆ H ₁₅ ClN ₂ O ₂	182.648	-1
Oxalic acid	Carboxylic acid	(COOH) ₂	90.034	3
L-Malic acid	Carboxylic acid	C ₄ H ₆ O ₅	134.087	1
α-Ketoglutaric acid	Carboxylic acid	C ₅ H ₆ O ₅	146.11	0.8
Citric acid	Carboxylic acid	C ₆ H ₈ O ₇	192.123	1
L-(+)-Arabinose	Sugar	C ₅ H ₁₀ O ₅	150.13	0
D-(-)-Fructose	Sugar	C ₆ H ₁₂ O ₆	180.156	0
D-(+)-Galactose	Sugar	C ₆ H ₁₂ O ₆	180.156	0
D-(+)-Glucose	Sugar	C ₆ H ₁₂ O ₆	180.156	0
N-Acetyl glucosamine	Sugar	C ₈ H ₁₅ NO ₆	221.209	-1

II. CO₂ production during the six hours following the substrate addition in the

Microresp.® measurements. CO₂ production against substrate molecular weight (A.) or against mean carbon oxidation state (B.).



III. Effect of (A.) substrate removal and (B.) change of induction range definition on indices values



Supplementary material II – S7: R output Fig. 2

A. Model shape selection

Tree species richness effect on soil microbial facets and functions. For each soil microbial facets and functions, we tested the shape of the relationship using the ‘lm’ function and the following relations: linear (i.e. $y \sim x$), quadratic (i.e. $y \sim x^2$), polynomial (i.e. $y \sim x + x^2 + x^3$) and logarithmic (i.e. $y \sim \log(x)$). The models were ordered by AIC and considered different when the difference of AIC was higher than 4. When several models had a comparable fit (difference of AIC below 4) the simplest model was chosen (i.e. linear < logarithmic < quadratic < polynomial).

Microbial biomass

Total microbial biomass

Name	Model	AIC	BIC	R2	R2_adjusted	RMSE	Sigma
polynomial	$y \sim \text{poly}(x, \text{degree} = 3)$	2886	2901	0.098	0.079	4013.930	4069.297
linear	$y \sim x$	2889	2898	0.056	0.050	4105.131	4133.153
quadratic	$y \sim x^2$	2889	2898	0.056	0.050	4105.131	4133.153
log	$y \sim \log(x)$	2893	2902	0.027	0.021	4167.715	4196.163

Active microbial biomass

Name	Model	AIC	BIC	R2	R2_adjusted	RMSE	Sigma
polynomial	$y \sim \text{poly}(x, \text{degree} = 3)$	1768	1783	0.049	0.029	91.784	93.050
linear	$y \sim x$	1770	1779	0.010	0.003	93.621	94.260
quadratic	$y \sim x^2$	1770	1779	0.010	0.003	93.621	94.260
log	$y \sim \log(x)$	1771	1780	0.001	-0.006	94.060	94.702

Microbial taxonomic profile

Bacteria to fungi ratio

Name	Model	AIC	BIC	R2	R2_adjusted	RMSE	Sigma
log	$y \sim \log(x)$	207	216	0.016	0.010	0.477	0.480
linear	$y \sim x$	207	216	0.015	0.008	0.477	0.480
quadratic	$y \sim x^2$	207	216	0.015	0.008	0.477	0.480
polynomial	$y \sim \text{poly}(x, \text{degree} = 3)$	211	226	0.017	-0.004	0.476	0.483

Bacterial Shannon diversity

Name	Model	AIC	BIC	R2	R2_adjusted	RMSE	Sigma
log	y ~ log(x)	388	397	0.060	0.053	0.881	0.887
polynomial	y ~ poly(x, degree = 3)	391	406	0.069	0.050	0.876	0.888
linear	y ~ x	391	400	0.044	0.037	0.888	0.894
quadratic	y ~ x^2	391	400	0.044	0.037	0.888	0.894

Fungal Shannon diversity

Name	Model	AIC	BIC	R2	R2_adjusted	RMSE	Sigma
log	y ~ log(x)	-98	-89	0.000	-0.006	0.170	0.171
linear	y ~ x	-98	-89	0.000	-0.007	0.170	0.171
quadratic	y ~ x^2	-98	-89	0.000	-0.007	0.170	0.171
polynomial	y ~ poly(x, degree = 3)	-97	-82	0.014	-0.006	0.169	0.171

Microbial functional profile

Catabolism functional genes

Name	Model	AIC	BIC	R2	R2_adjusted	RMSE	Sigma
log	y ~ log(x)	566	575	0.010	0.003	1.604	1.615
linear	y ~ x	566	575	0.007	0.000	1.607	1.618
quadratic	y ~ x^2	566	575	0.007	0.000	1.607	1.618
polynomial	y ~ poly(x, degree = 3)	569	584	0.014	-0.007	1.601	1.624

Functional genes evenness

Name	Model	AIC	BIC	R2	R2_adjusted	RMSE	Sigma
log	y ~ log(x)	-455	-446	0.003	-0.003	0.051	0.051
linear	y ~ x	-455	-446	0.003	-0.004	0.051	0.051
quadratic	y ~ x^2	-455	-446	0.003	-0.004	0.051	0.051
polynomial	y ~ poly(x, degree = 3)	-452	-437	0.011	-0.010	0.051	0.051

Microbial physiological potential

Substrate-induced respiration efficiency

Name	Model	AIC	BIC	R2	R2_adjusted	RMSE	Sigma
linear	y ~ x	41	50	0.071	0.064	0.272	0.274
quadratic	y ~ x^2	41	50	0.071	0.064	0.272	0.274
log	y ~ log(x)	42	51	0.063	0.057	0.274	0.275
polynomial	y ~ poly(x, degree = 3)	45	60	0.072	0.053	0.272	0.276

Substrate-induced respiration response range

Name	Model	AIC	BIC	R2	R2_adjusted	RMSE	Sigma
log	y ~ log(x)	340	349	0.005	-0.002	0.749	0.754
linear	y ~ x	341	350	0.003	-0.003	0.750	0.755
quadratic	y ~ x^2	341	350	0.003	-0.003	0.750	0.755
polynomial	y ~ poly(x, degree = 3)	345	360	0.004	-0.017	0.749	0.760

Microbial respiration

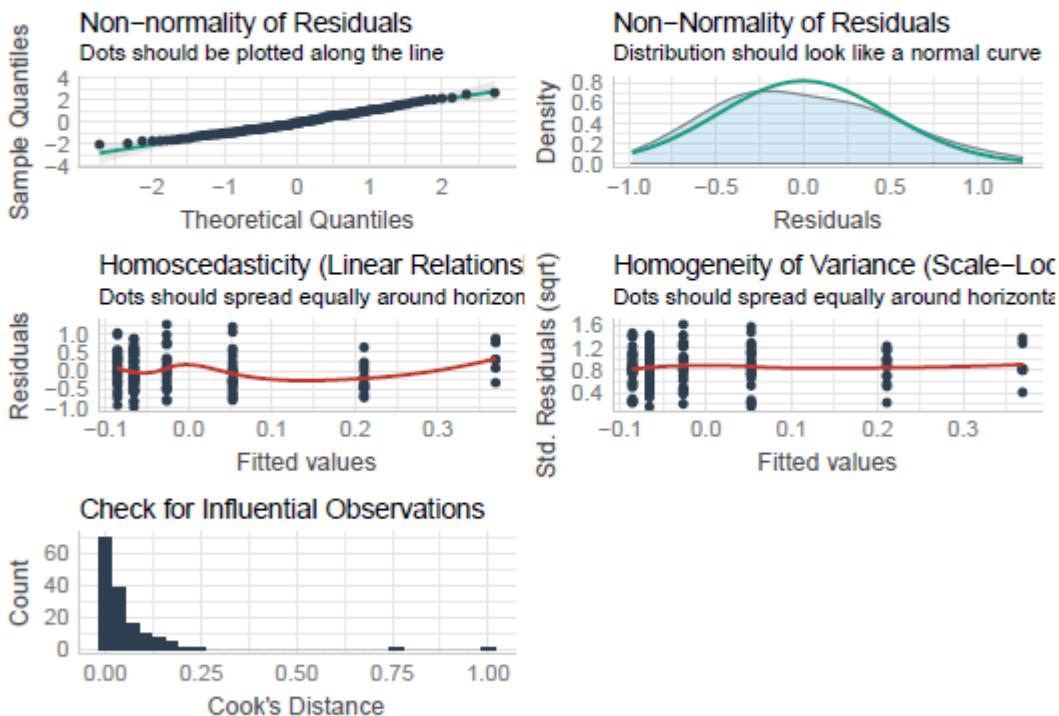
Name	Model	AIC	BIC	R2	R2_adjusted	RMSE	Sigma
linear	y ~ x	149	157	0.023	0.017	0.392	0.394
quadratic	y ~ x^2	149	157	0.023	0.017	0.392	0.394
log	y ~ log(x)	150	159	0.015	0.009	0.393	0.396
polynomial	y ~ poly(x, degree = 3)	151	166	0.035	0.015	0.389	0.395

B. Model quality check

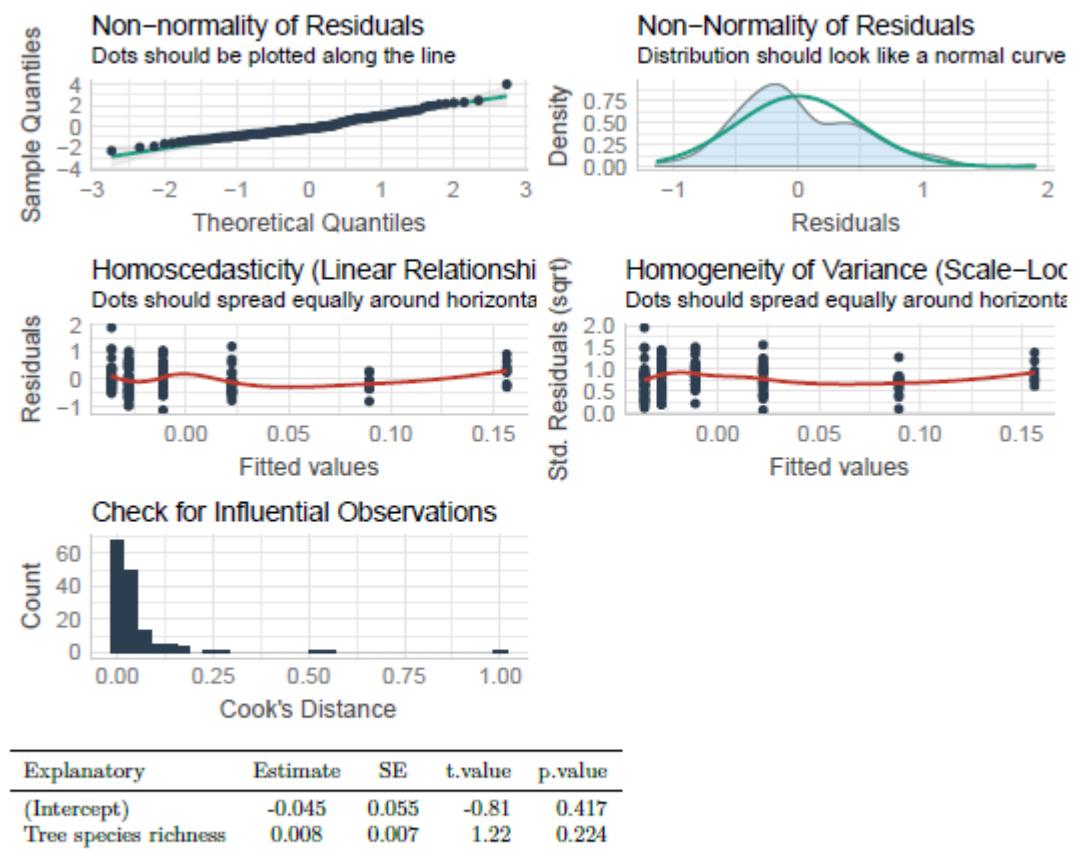
Tree species richness effect on soil microbial facets and functions. The relation was tested using the "lm" function in R. Model statistical assumptions were tested using the "check_model" function from the R package "performance".

Microbial biomass

Total microbial biomass

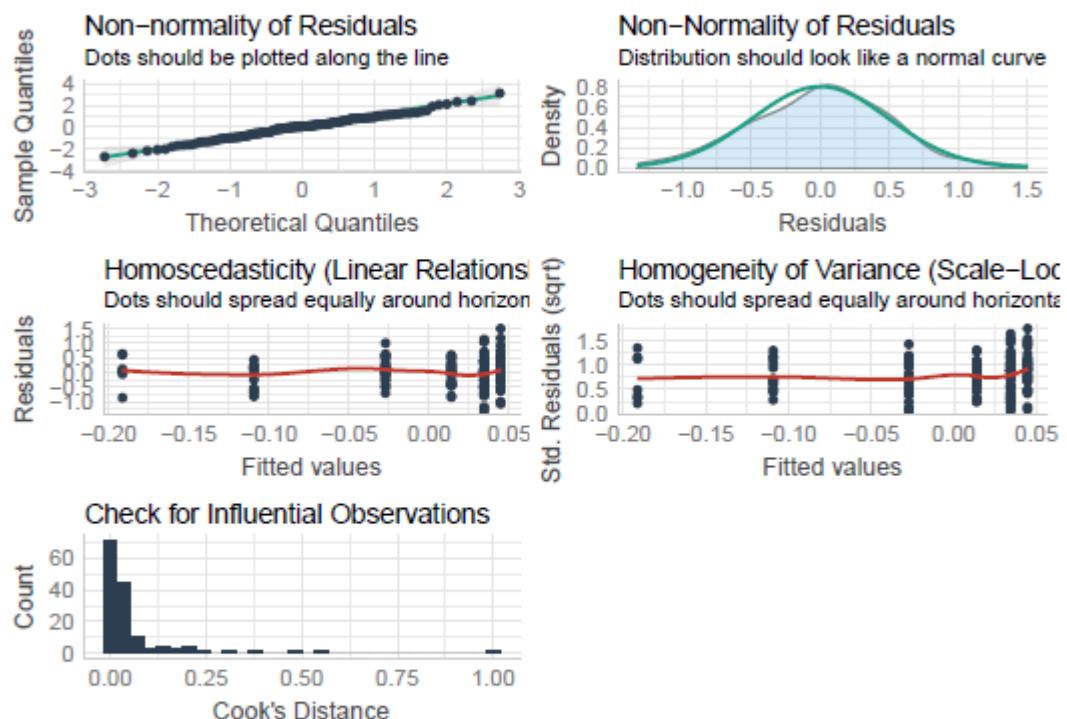


Active microbial biomass

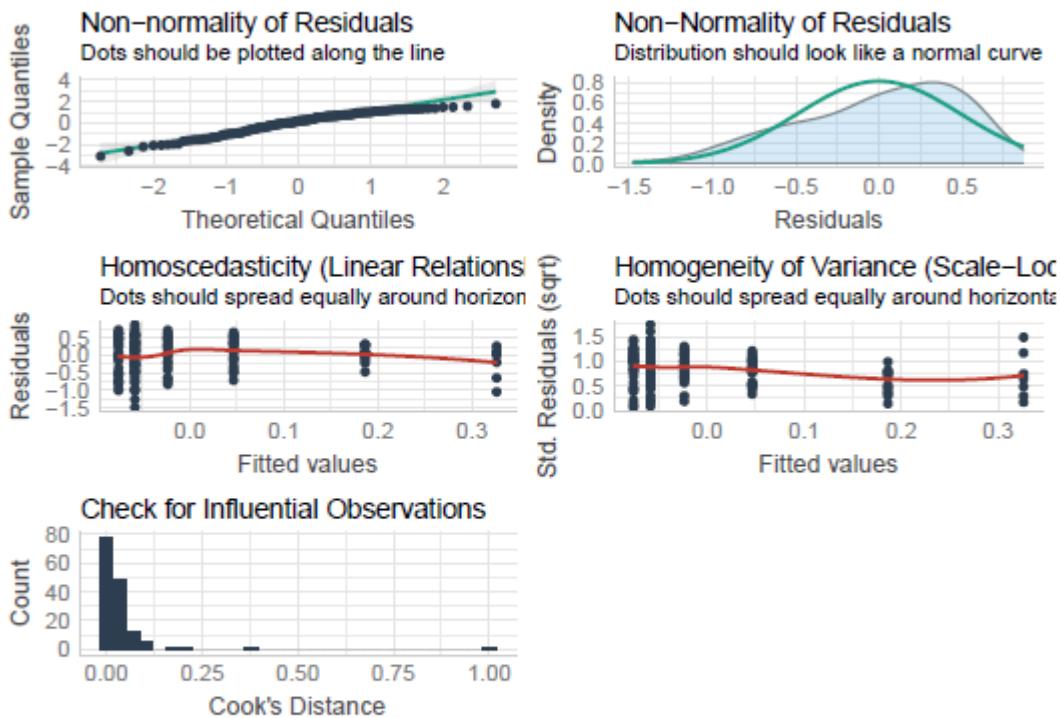


Microbial taxonomic profile

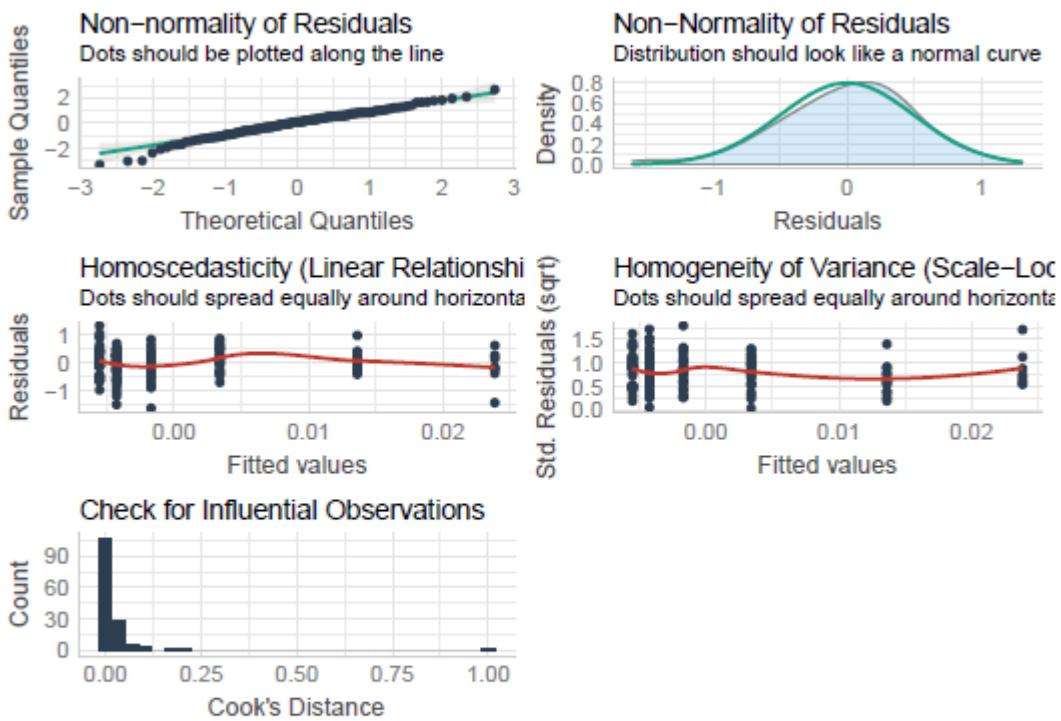
Bacteria to fungi ratio



Bacterial Shannon diversity

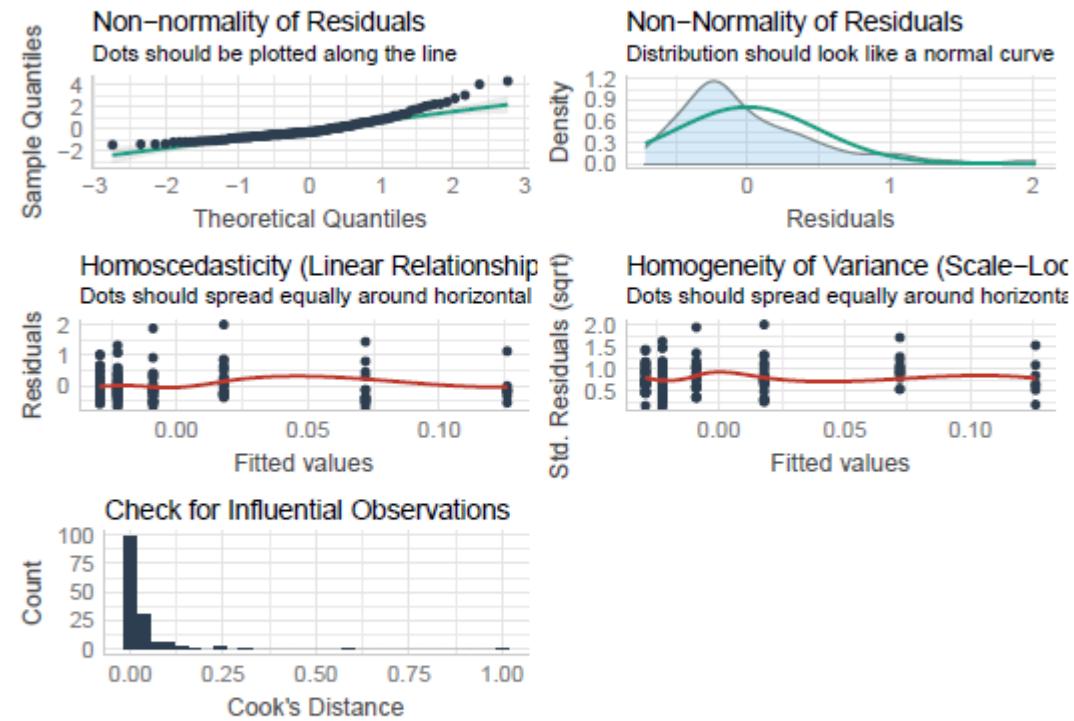


Fungal Shannon diversity



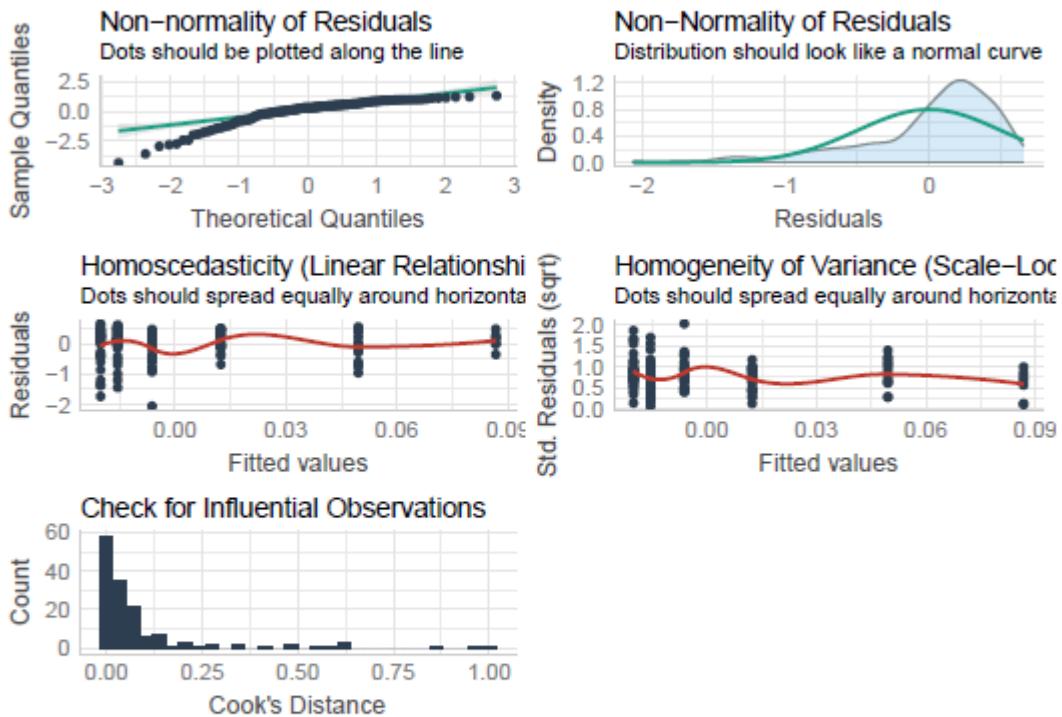
Microbial functional profile

Catabolism functional genes



Explanatory	Estimate	SE	t.value	p.value
(Intercept)	-0.036	0.055	-0.65	0.515
Tree species richness	0.007	0.007	0.98	0.329

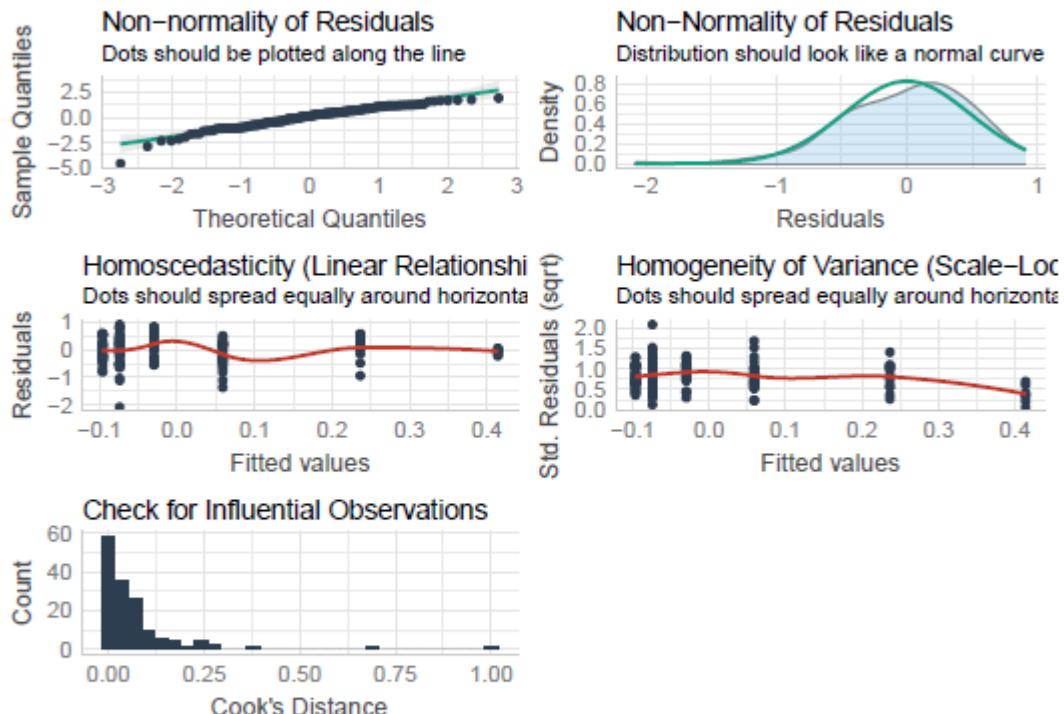
Functional genes evenness



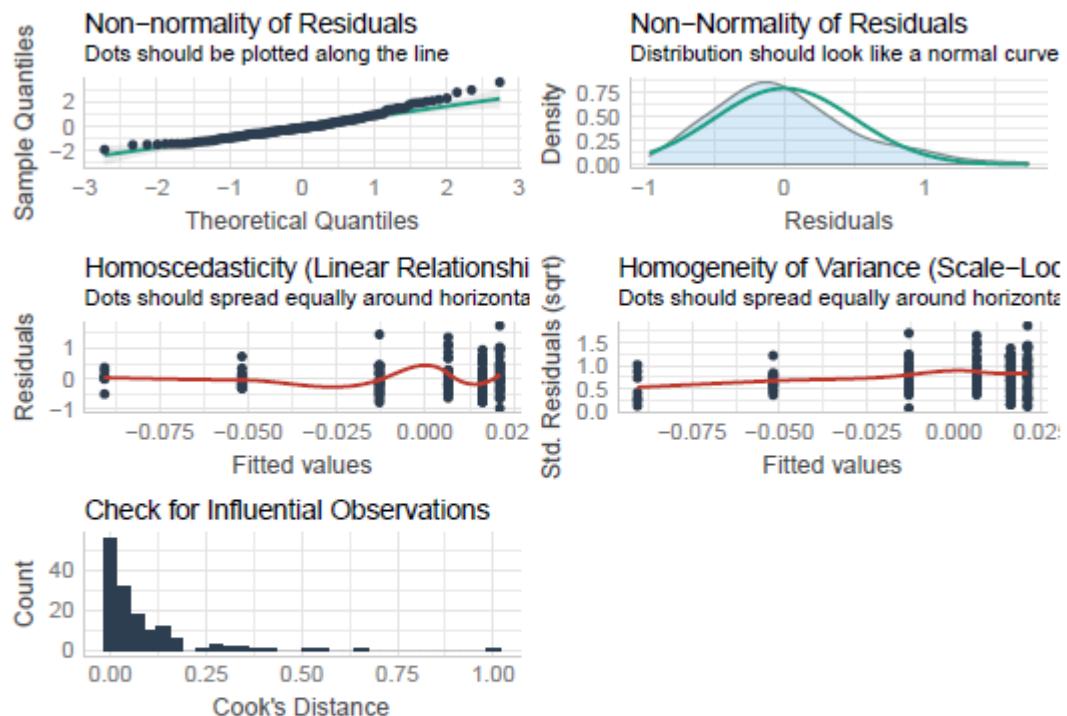
Explanatory	Estimate	SE	t.value	p.value
(Intercept)	-0.025	0.055	-0.45	0.654
Tree species richness	0.005	0.007	0.67	0.501

Microbial physiological potential

Substrate-induced respiration efficiency

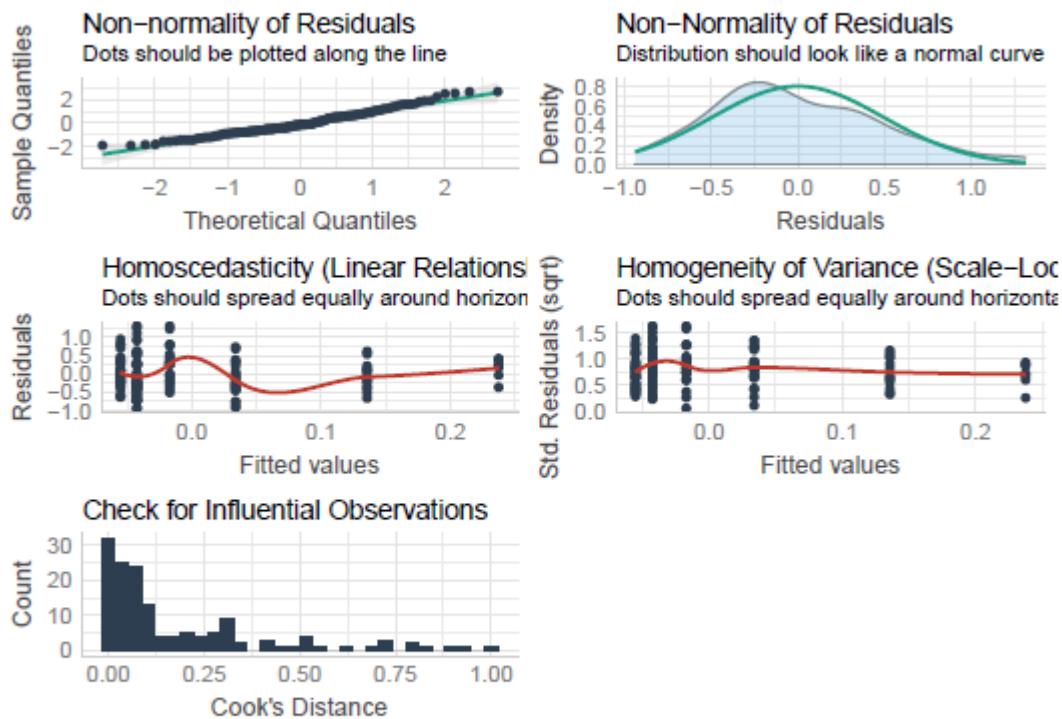


Substrate-induced respiration response range



Explanatory	Estimate	SE	t.value	p.value
(Intercept)	0.026	0.055	0.47	0.639
Tree species richness	-0.005	0.007	-0.7	0.482

Microbial respiration



Explanatory	Estimate	SE	t.value	p.value
(Intercept)	-0.068	0.055	-1.24	0.216
Tree species richness	0.013	0.007	1.86	0.064

Supplementary material II – S8: R output Fig. 3

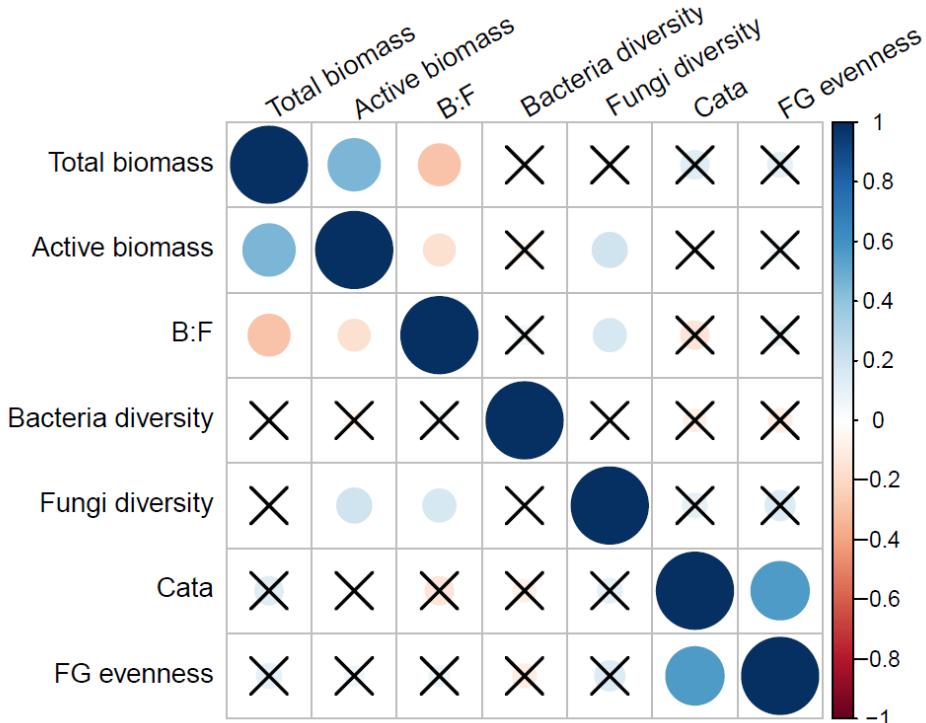
Correlation matrix between microbial facets

Pearson correlation coefficients

	Total biomass	Active biomass	B:F	Bacteria diversity	Fungi diversity	Cata	FG evenness
Total biomass	1.000	0.455	-0.290	-0.016	0.029	0.132	0.102
Active biomass	0.455	1.000	-0.167	-0.055	0.201	0.019	0.062
B:F	-0.290	-0.167	1.000	0.059	0.179	-0.133	0.070
Bacteria diversity	-0.016	-0.055	0.059	1.000	-0.014	-0.083	-0.093
Fungi diversity	0.029	0.201	0.179	-0.014	1.000	0.100	0.150
Cata	0.132	0.019	-0.133	-0.083	0.100	1.000	0.569
FG evenness	0.102	0.062	0.070	-0.093	0.150	0.569	1.000

Pearson correlation | p-value

	Total biomass	Active biomass	B:F	Bacteria diversity	Fungi diversity	Cata	FG evenness
Total biomass	0.00e+00	6.46e-09	3.48e-04	8.49e-01	7.27e-01	1.09e-01	2.18e-01
Active biomass	6.46e-09	0.00e+00	4.24e-02	5.07e-01	1.45e-02	8.22e-01	4.56e-01
B:F	3.48e-04	4.24e-02	0.00e+00	4.79e-01	2.92e-02	1.07e-01	3.96e-01
Bacteria diversity	8.49e-01	5.07e-01	4.79e-01	0.00e+00	8.71e-01	3.19e-01	2.61e-01
Fungi diversity	7.27e-01	1.45e-02	2.92e-02	8.71e-01	0.00e+00	2.27e-01	6.97e-02
Cata	1.09e-01	8.22e-01	1.07e-01	3.19e-01	2.27e-01	0.00e+00	4.42e-14
FG evenness	2.18e-01	4.56e-01	3.96e-01	2.61e-01	6.97e-02	4.42e-14	0.00e+00

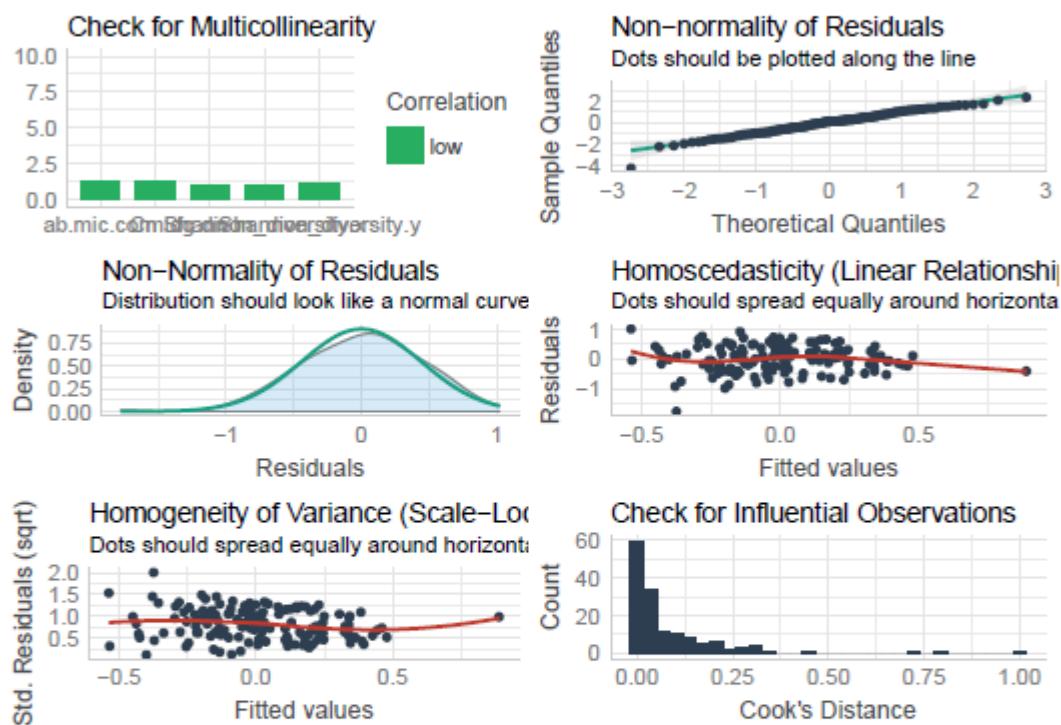


Effect of soil microbial facets on microbial function

Microbial physiological potential

Substrate-induces respiration efficiency

Model statistical assumptions



Model fit

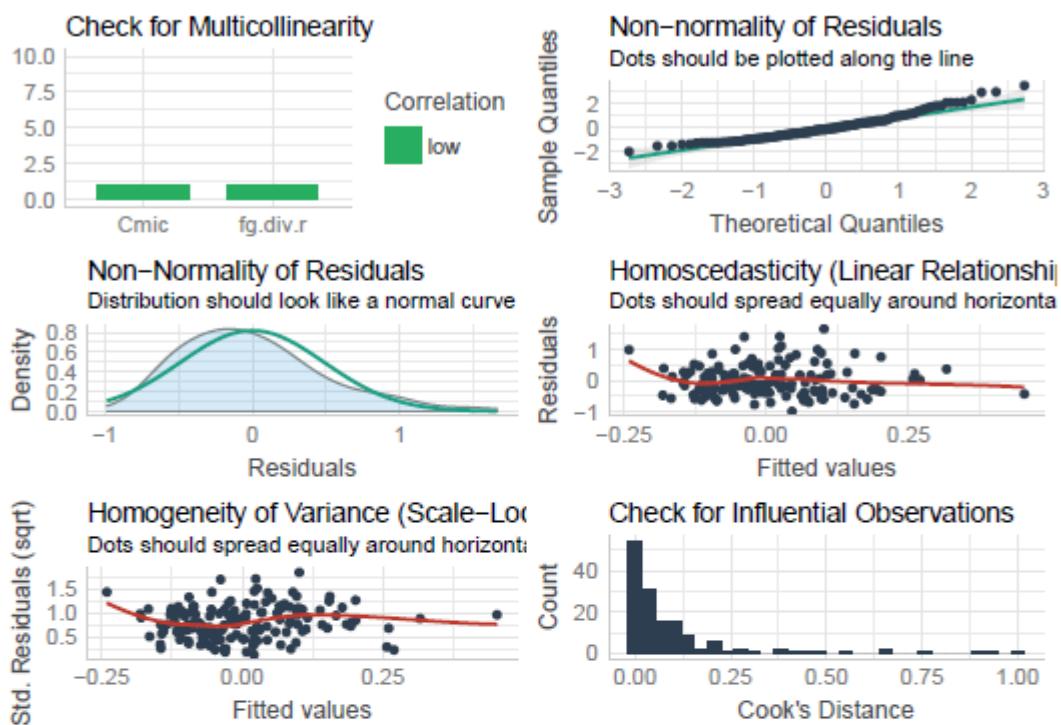
Explanatory	Estimate	SE	t.value	p.value
(Intercept)	0	0.037	0	1
Total biomass	0.238	0.084	2.84	0.005
Active biomass	0.264	0.085	3.09	0.002
Bacteria diversity	0.108	0.074	1.46	0.147
Fungi diversity	-0.152	0.077	-1.98	0.05
PG evenness	-0.166	0.076	-2.2	0.029

Variance partitioning

Explanatory	Df	R squared	Ajusted R squared
Microbial biomass	2	0.150	0.138
Taxonomic profile	2	0.025	0.012
Functional profile	1	0.025	0.018
Microbial biomass + Taxonomic profile	4	0.195	0.172
Microbial biomass + Functional profile	3	0.189	0.172
Taxonomic profile + Functional profile	3	0.043	0.023
All	5	0.221	0.194

Substrate-induced respiration response range

Model statistical assumptions



Model fit

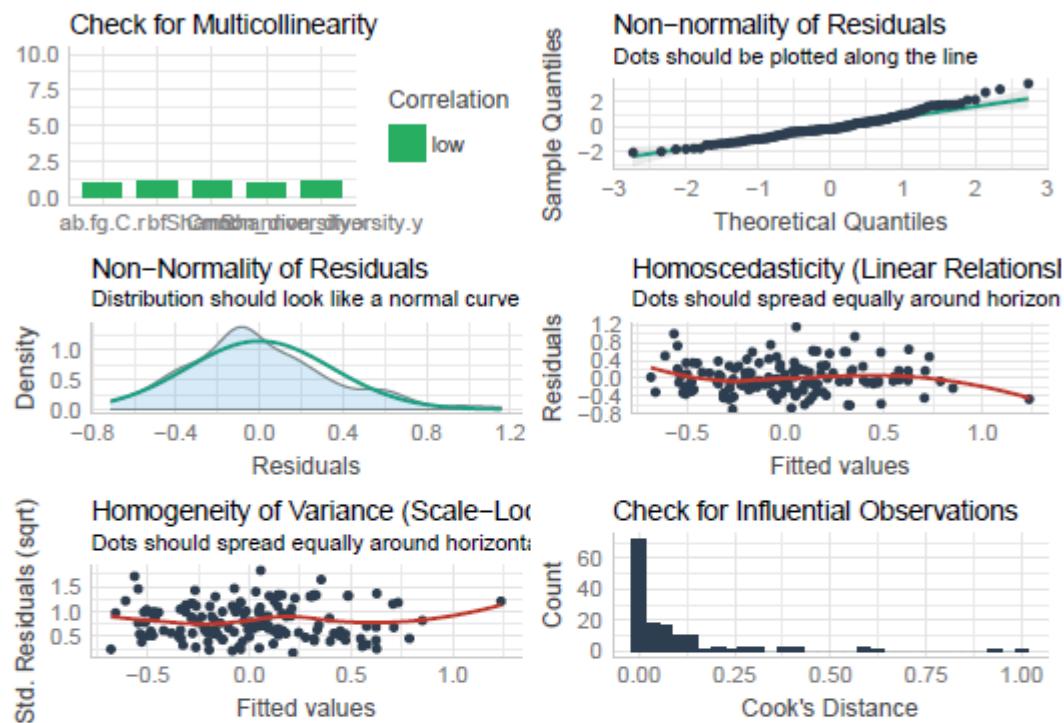
Explanatory	Estimate	SE	t.value	p.value
(Intercept)	0	0.04	0	1
Active biomass	0.175	0.081	2.16	0.033
PG evenness	-0.143	0.081	-1.77	0.079

Variance partitioning

Explanatory	Df	R squared	Ajusted R squared
Microbial biomass	1	0.028	0.021
Functional profile	1	0.018	0.011
All	2	0.048	0.035

Microbial respiration

Model statistical assumptions



Model fit

Explanatory	Estimate	SE	t.value	p.value
(Intercept)	0	0.029	0	1
Active biomass	0.675	0.061	11.07	0
B:F	-0.146	0.061	-2.37	0.019
Bacteria diversity	0.092	0.059	1.57	0.12
Fungi diversity	-0.175	0.062	-2.85	0.005
Cata	-0.132	0.059	-2.21	0.029

Variance partitioning .

Explanatory	Df	R squared	Ajusted R squared
Microbial biomass	1	0.431	0.427
Taxonomic profile	3	0.078	0.059
Functional profile	1	0.016	0.009
Microbial biomass + Taxonomic profile	4	0.501	0.487
Microbial biomass + Functional profile	2	0.450	0.442
Taxonomic profile + Functional profile	4	0.101	0.076
All	5	0.518	0.501

VIF analysis

Active microbial biomass	B:F	Bacteria diversity
1.09	1.11	1.01
Fungi diversity	Cata	
1.11	1.04	

Supplementary material II – S9: SEM hypotheses

Expected causal relationships

Response variable	Explanatory variable	Hypothesis [Reference from the main text]
Basal respiration	Total microbial biomass	Increasing soil microbial biomass should increase basal respiration [19]
Basal respiration	Active microbial biomass	Increasing active soil microbial biomass should increase basal respiration [19]
Basal respiration	B:F	Increasing B:F is expected to increase microbial community activity and thereafter, respiration [7-10]
Basal respiration	Bacteria diversity	Bacteria diversity should increase microbial respiration by increasing resource use [7-10]
Basal respiration	Fungi diversity	Fungi diversity should increase microbial respiration by increasing resource use [7-10]
Basal respiration	Cata	Increasing catabolism functional genes abundance (i.e. Cata) should increase microbial respiration by increasing the genetic material supporting the catabolism processes [30, 36]
Basal respiration	FG evenness	Increasing catabolism functional gene evenness should increase microbial respiration by increasing the physiological pathways supported by the genetic material [30, 36]
Basal respiration	SIR efficiency	Increasing microbial SIR efficiency should increase microbial respiration due to a higher number of physiological pathways supported [40 - 41]
Basal respiration	SIR range	Increasing microbial SIR range should increase microbial respiration due to a stronger response of the microbial community to complex substrates with longer pathways [40 - 41]
Basal respiration	TOC	Soil chemical properties affect soil functions by changing resource limitations and physiological processes [12, 13, 25, 26, 46]
Basal respiration	C:N	Soil chemical properties affect soil functions by changing resource limitations and physiological processes [12, 13, 25, 26, 46]
Basal respiration	C:P	Soil chemical properties affect soil functions by changing resource limitations and physiological processes [12, 13, 25, 26, 46]

Basal respiration	pH	Soil chemical properties affect soil functions by changing resource limitations and physiological processes [12, 13, 25, 26, 46]
Basal respiration	RH	Soil chemical properties affect soil functions by changing resource limitations and physiological processes [12, 13, 25, 26, 46]
Basal respiration	Tree species richness	Increasing tree species richness should increase microbial respiration by providing a higher amount and diversity of substrates [11, 21-22, 24]
SIR efficiency	Biomass	Increasing microbial biomass should increase SIR efficiency by reducing microbial lag time before the exponential growth [19, 45]
SIR efficiency	Active microbial biomass	Increasing microbial biomass should increase SIR efficiency by reducing microbial lag time before the exponential growth [19, 45]
SIR efficiency	B:F	Changes in microbial community composition are expected to affect microbial processes [42 - 44]
SIR efficiency	Bacteria diversity	Changes in microbial community composition are expected to affect microbial processes [42 - 44]
SIR efficiency	Fungi diversity	Changes in microbial community composition are expected to affect microbial processes [42 - 44]
SIR efficiency	Cata	Increasing catabolism functional genes should increase SIR efficiency by reducing microbial lag time before the exponential growth [37, 39]
SIR efficiency	FG evenness	Increasing catabolism functional gene evenness should increase SIR efficiency by optimizing all physiological pathways [37, 39]
SIR efficiency	TOC	Soil chemical properties affect soil functions by changing resource limitations and physiological processes [12, 13, 25, 26, 27]
SIR efficiency	C:N	Soil chemical properties affect soil functions by changing resource limitations and physiological processes [12, 13, 25, 26]
SIR efficiency	C:P	Soil chemical properties affect soil functions by changing resource limitations and physiological processes [12, 13, 25, 26]
SIR efficiency	pH	Soil chemical properties affect soil functions by changing resource limitations and physiological processes [12, 13, 25, 26]

SIR efficiency	RH	Soil chemical properties affect soil functions by changing resource limitations and physiological processes [12, 13, 25, 26]
SIR efficiency	Tree species richness	Increasing tree species richness should increase microbial physiological potential by providing a higher amount and diversity of substrates [11, 21-22, 24]
SIR range	Biomass	Increasing microbial biomass should increase SIR range by reducing microbial lag time before the exponential growth and favor long physiological pathways [19, 45]
SIR range	Active microbial biomass	Increasing microbial biomass should increase SIR efficiency by reducing microbial lag time before the exponential growth [19, 45]
SIR range	B:F	Changes in microbial community composition are expected to affect microbial processes [42 - 44]
SIR range	Bacteria diversity	Changes in microbial community composition are expected to affect microbial processes [42 - 44]
SIR range	Fungi diversity	Changes in microbial community composition are expected to affect microbial processes [42 - 44]
SIR range	Cata	Increasing catabolism functional genes should increase SIR range by reducing microbial lag before the exponential growth and favor long physiological pathways [37, 39]
SIR range	FG evenness	Increasing catabolism functional gene evenness should increase SIR range by optimizing all physiological pathways [37, 39]
SIR range	TOC	Soil chemical properties affect soil microbial functions (such as microbial growth) by changing resource limitations and physiological processes [13]
SIR range	C:N	Soil chemical properties affect soil microbial functions (such as microbial growth) by changing resource limitations and physiological processes [13]
SIR range	C:P	Soil chemical properties affect soil microbial functions (such as microbial growth) by changing resource limitations and physiological processes [13]
SIR range	pH	Soil chemical properties affect soil microbial functions (such as microbial growth) by changing resource limitations and physiological processes [13]
SIR range	RH	Soil chemical properties affect soil microbial functions (such as microbial

		growth) by changing resource limitations and physiological processes [13]
SIR range	Tree species richness	Increasing tree species richness should increase microbial physiological potential by providing a higher amount and diversity of substrates [11, 21-22, 24]
Biomass	TOC	Soil chemical properties affect soil microbial functions (such as microbial growth) by affecting resource limitations and physiological processes [13]
Biomass	C:N	Soil chemical properties affect soil microbial functions (such as microbial growth) by affecting resource limitations and physiological processes [13]
Biomass	C:P	Soil chemical properties affect soil microbial functions (such as microbial growth) by affecting resource limitations and physiological processes [13]
Biomass	pH	Soil chemical properties affect soil microbial functions (such as microbial growth) by affecting resource limitations and physiological processes [13]
Biomass	RH	Soil chemical properties affect soil microbial functions (such as microbial growth) by affecting resource limitations and physiological processes [13]
Biomass	Tree species richness	Increase of tree species richness should increase substrate abundance and therefore the system's carrying capacity [16, 21-22, 24]
Active microbial biomass	TOC	Soil chemical properties affect soil microbial functions (such as microbial growth) by changing resource limitations and physiological processes [13]
Active microbial biomass	C:N	Soil chemical properties affect soil microbial functions (such as microbial growth) by changing resource limitations and physiological processes [13]
Active microbial biomass	C:P	Soil chemical properties affect soil microbial functions (such as microbial growth) by changing resource limitations and physiological processes [13]
Active microbial biomass	pH	Soil chemical properties affect soil microbial functions (such as microbial growth) by changing resource limitations and physiological processes [13]
Active microbial biomass	RH	Soil chemical properties affect soil microbial functions (such as microbial growth) by changing resource limitations and physiological processes [13]

Active microbial biomass	Tree species richness	Increase of tree species richness increases substrate abundance and therefore the system's carrying capacity [21-22]
B:F	TOC	Soil chemical properties shape microbial community structure [13, 16]
B:F	C:N	Soil chemical properties shape microbial community structure [13, 16]
B:F	C:P	Soil chemical properties shape microbial community structure [13, 16]
B:F	pH	Soil chemical properties shape microbial community structure [13, 16]
B:F	RH	Soil chemical properties shape microbial community structure [13, 16]
B:F	Tree species richness	Tree species richness should increase bacteria to fungi ratio [21]
Bacteria diversity	TOC	Soil chemical properties shape microbial community structure [13, 16]
Bacteria diversity	C:N	Soil chemical properties shape microbial community structure [13, 16]
Bacteria diversity	C:P	Soil chemical properties shape microbial community structure [13, 16]
Bacteria diversity	pH	Soil chemical properties shape microbial community structure [13, 16]
Bacteria diversity	RH	Soil chemical properties shape microbial community structure [13, 16]
Bacteria diversity	Tree species richness	Increase of tree species richness increases substrate diversity and therefore functional niche complementarity [21-22]
Fungi diversity	TOC	Soil chemical properties shape microbial community structure [13, 16]
Fungi diversity	C:N	Soil chemical properties shape microbial community structure [13, 16]
Fungi diversity	C:P	Soil chemical properties shape microbial community structure [13, 16]
Fungi diversity	pH	Soil chemical properties shape microbial community structure [13, 16]
Fungi diversity	RH	Soil chemical properties shape microbial community structure [13, 16]
Fungi diversity	Tree species richness	Increase of tree species richness increases substrate diversity and therefore functional niche complementarity [21-22]
Cata	TOC	Soil chemical properties shape microbial community structure [12, 13, 25, 26, 30-32]
Cata	C:N	Soil chemical properties shape microbial community structure [12, 13, 25, 26, 30-32]
Cata	C:P	Soil chemical properties shape microbial community structure [12, 13, 25, 26, 30-32]
Cata	pH	Soil chemical properties shape microbial community structure [12, 13, 25, 26, 30-32]
Cata	RH	Soil chemical properties shape microbial community structure [12, 13, 25, 26, 30-32]

Cata	Tree species richness	Increase of tree species richness increases substrate diversity and therefore functional niche complementarity [21-22]
FG evenness	TOC	Soil chemical properties affect soil microbial community composition by changing resource limitations and therefore species selection [12, 13, 25, 26, 30-32]
FG evenness	C:N	Soil chemical properties affect soil microbial community composition by changing resource limitations and therefore species selection [12, 13, 25, 26, 30-32]
FG evenness	C:P	Soil chemical properties affect soil microbial community composition by changing resource limitations and therefore species selection [12, 13, 25, 26, 30-32]
FG evenness	pH	Soil chemical properties affect soil microbial community composition by changing resource limitations and therefore species selection [12, 13, 25, 26, 30-32]
FG evenness	RH	Soil chemical properties affect soil microbial community composition by changing resource limitations and therefore species selection [12, 13, 25, 26, 30-32]
FG evenness	Tree species richness	Increasing tree species richness increases substrate diversity and therefore functional niche complementarity [21-22]

Correlations (relationships where directionality of effects is not clear from the literature)

First variable	Second variable	Hypothesis [Reference from the main text]
Biomass	Active microbial biomass	We expect the biomass of active microbes to increase with increasing total microbial biomass
Biomass	B:F	We expect the B:F ratio to positively correlate with the microbial biomass
Biomass	Bacteria diversity	We expect a positive biomass ~ diversity relationship
Biomass	Fungi diversity	We expect a positive biomass ~ diversity relationship
Biomass	Cata	The number of genes copies is expected to increase with the number of cells
Biomass	FG evenness	We expect a positive biomass ~ diversity relationship
Active microbial biomass	B:F	We expect the B:F ratio to positively correlate with the microbial biomass
Active microbial biomass	Bacteria diversity	We expect a positive biomass ~ diversity relationship
Active microbial biomass	Fungi diversity	We expect a positive biomass ~ diversity relationship
Active microbial biomass	Cata	The number of genes copies is expected to increase with the number of cells
Active microbial biomass	FG evenness	We expect a positive biomass ~ diversity relationship
B:F	Bacteria diversity	We expect a positive biomass ~ diversity relationship, which also implies a positive B:F ~ bacteria diversity relationship
B:F	Fungi diversity	We expect a positive biomass ~ diversity relationship, which also implies a positive B:F ~ bacteria diversity relationship
B:F	Cata	We expect a positive relationship, as most of the measured genes are bacterial
B:F	FG evenness	We expect a positive relationship, as most of the measured genes are bacterial
Bacteria diversity	Fungi diversity	We expect bacteria and fungi diversity to be positively correlated to each another as driven by similar processes
Bacteria diversity	Cata	We expect a positive biomass ~ diversity relationship [33]
Bacteria diversity	FG evenness	We expect taxonomic and functional diversity to be strongly positively correlated to each another as driven by similar processes [33]
Fungi diversity	Cata	We expect a positive biomass ~ diversity relationship [33]

Fungi diversity	FG evenness	We expect taxonomic and functional diversity to be strongly correlated to each another as driven by similar processes [33]
Cata	FG evenness	We expect a positive biomass ~ diversity relationship
SIR efficiency	SIR range	We expect SIR range and efficiency to be positively correlated
TOC	C:N	We expect soil chemical properties to be correlated [see Scholten et al. 2017]
TOC	C:P	We expect soil chemical properties to be correlated [see Scholten et al. 2017]
TOC	pH	We expect soil chemical properties to be correlated [see Scholten et al. 2017]
TOC	RH	We expect soil chemical properties to be correlated [see Scholten et al. 2017]
TOC	Tree species richness	We expect soil chemical properties and tree species richness may be correlated; while significant tree diversity effects on soil properties can be expected, initial plot selection could also have caused non-causal relationships
C:N	C:P	We expect soil chemical properties to be correlated [see Scholten et al. 2017]
C:N	pH	We expect soil chemical properties to be correlated [see Scholten et al. 2017]
C:N	RH	We expect soil chemical properties to be correlated [see Scholten et al. 2017]
C:N	Tree species richness	We expect soil chemical properties and tree species richness may be correlated; while significant tree diversity effects on soil properties can be expected, initial plot selection could also have caused non-causal relationships
C:P	pH	We expect soil chemical properties to be correlated [see Scholten et al. 2017]
C:P	RH	We expect soil chemical properties to be correlated [see Scholten et al. 2017]
C:P	Tree species richness	We expect soil chemical properties and tree species richness may be correlated; while significant tree diversity effects on soil properties can be expected, initial plot selection could also have caused non-causal relationships
pH	RH	We expect soil chemical properties to be correlated [see Scholten et al. 2017]
pH	Tree species richness	We expect soil chemical properties and tree species richness may be correlated; while significant tree diversity effects on soil properties can be expected, initial plot selection could also have caused non-causal relationships
RH	Tree species richness	We expect soil chemical properties and tree species richness may be correlated; while significant tree diversity effects on soil properties can be expected, initial plot selection could also have caused non-causal relationships

Supplementary material II – S10: R outputs Fig. 4

Contents

1	Introduction
2	Model structure
3	Model fit
3.1	Fit quality
3.2	Explained variance
3.3	Model output
4	Model inflation by measurement methods
4.1	Fit quality
4.2	Explained variance
4.3	Model output

1 Introduction

The following document will display the R summary after fitting the structural equation model displayed in figure Fig. 4. The model was fitted using the “lavaan” package. (See all hypotheses rational and references in S9)

2 Model structure

```
form =  
'  
# Causal relations  
  
Basal respiration ~ Biomass + Active biomass +  
    B:F + Bacteria diversity + Fungi diversity +  
    Cata + FG evenness +  
    SIR efficiency + SIR range  
  
SIR efficiency ~ Biomass + Active biomass +  
    B:F + Bacteria diversity + Fungi diversity +  
    Cata + FG evenness  
  
SIR range ~ Biomass + Active biomass +  
    B:F + Bacteria diversity + Fungi diversity +  
    Cata + FG evenness  
  
# Correlations  
  
Biomass -- Active biomass  
Biomass -- B:F  
Biomass -- Bacteria diversity  
Biomass -- Fungi diversity  
Biomass -- Cata  
Biomass -- FG evenness  
  
Active biomass -- B:F  
Active biomass -- Bacteria diversity  
Active biomass -- Fungi diversity  
Active biomass -- Cata  
Active biomass -- FG evenness  
  
B:F -- Bacteria diversity  
B:F -- Fungi diversity  
B:F -- Cata  
B:F -- FG evenness  
  
Bacteria diversity -- Fungi diversity  
Bacteria diversity -- Cata  
Bacteria diversity -- FG evenness  
  
Fungi diversity -- Cata  
Fungi diversity -- FG evenness  
  
Cata -- FG evenness  
  
SIR range -- SIR efficiency'
```

3 Model fit

3.1 Fit quality

Fit index	Value
cfi	1
rmsea	0
srmr	0

3.2 Explained variance

Variable	R.squared
Basal respiration	0.573
SIR eff.	0.232
SIR range	0.084

3.3 Model output

Response	Relation	Explanatory	Estimate	SE	p value
Basal respiration	~	Total biomass	-0.034	0.065	0.595
Basal respiration	~	Active biomass	0.590	0.060	< 0.001 ***
Basal respiration	~	B:F	-0.109	0.060	0.067
Basal respiration	~	Bacteria diversity	0.046	0.055	0.409
Basal respiration	~	Fungi diversity	-0.128	0.058	0.027 *
Basal respiration	~	Cata	-0.113	0.067	0.094
Basal respiration	~	FG evenness	0.020	0.068	0.771
Basal respiration	~	SIR eff.	0.176	0.062	0.005 **
Basal respiration	~	SIR range	0.213	0.057	< 0.001 ***
SIR eff.	~	Total biomass	0.209	0.083	0.012 *
SIR eff.	~	Active biomass	0.258	0.082	0.002 **
SIR eff.	~	B:F	-0.096	0.079	0.222
SIR eff.	~	Bacteria diversity	0.115	0.072	0.11
SIR eff.	~	Fungi diversity	-0.134	0.076	0.077
SIR eff.	~	Cata	0.037	0.090	0.685
SIR eff.	~	FG evenness	-0.179	0.089	0.045 *
SIR range	~	Total biomass	0.096	0.092	0.295
SIR range	~	Active biomass	0.148	0.091	0.103
SIR range	~	B:F	-0.047	0.086	0.586
SIR range	~	Bacteria diversity	0.111	0.079	0.16
SIR range	~	Fungi diversity	-0.099	0.083	0.233
SIR range	~	Cata	-0.039	0.099	0.694
SIR range	~	FG evenness	-0.101	0.098	0.302
Total biomass	~~	Active biomass	0.455	0.065	< 0.001 ***
Total biomass	~~	B:F	-0.290	0.075	< 0.001 ***
Total biomass	~~	Bacteria diversity	-0.016	0.082	0.847
Total biomass	~~	Fungi diversity	0.029	0.082	0.725
Total biomass	~~	Cata	0.132	0.081	0.101
Total biomass	~~	FG evenness	0.102	0.081	0.211
Active biomass	~~	B:F	-0.167	0.080	0.037 *
Active biomass	~~	Bacteria diversity	-0.055	0.082	0.503
Active biomass	~~	Fungi diversity	0.201	0.079	0.011 *
Active biomass	~~	Cata	0.019	0.082	0.82
Active biomass	~~	FG evenness	0.062	0.082	0.451
B:F	~~	Bacteria diversity	0.059	0.082	0.474
B:F	~~	Fungi diversity	0.179	0.080	0.024 *
B:F	~~	Cata	-0.133	0.081	0.1
B:F	~~	FG evenness	0.070	0.082	0.39
Bacteria diversity	~~	Fungi diversity	-0.014	0.082	0.869
Bacteria diversity	~~	Cata	-0.083	0.082	0.312
Bacteria diversity	~~	FG evenness	-0.093	0.081	0.254
Fungi diversity	~~	Cata	0.100	0.081	0.22
Fungi diversity	~~	FG evenness	0.150	0.080	0.063
Cata	~~	FG evenness	0.569	0.056	< 0.001 ***
SIR eff.	~~	SIR range	-0.185	0.079	0.02 *
Basal respiration	~~	Basal respiration	0.427	0.053	< 0.001 ***

(continued)

Response	Relation	Explanatory	Estimate	SE	p value
SIR eff.	~~	SIR eff.	0.768	0.061	< 0.001***
SIR range	~~	SIR range	0.916	0.044	< 0.001***

4 Model inflation by measurement methods

Active microbial biomass and microbial respiration were measured using the same machine and subsample. Therefore, we are testing the stability of our observation and results when removing microbial biomass.

4.1 Fit quality

Fit index	Value
cfi	1
rmsea	0
srmr	0

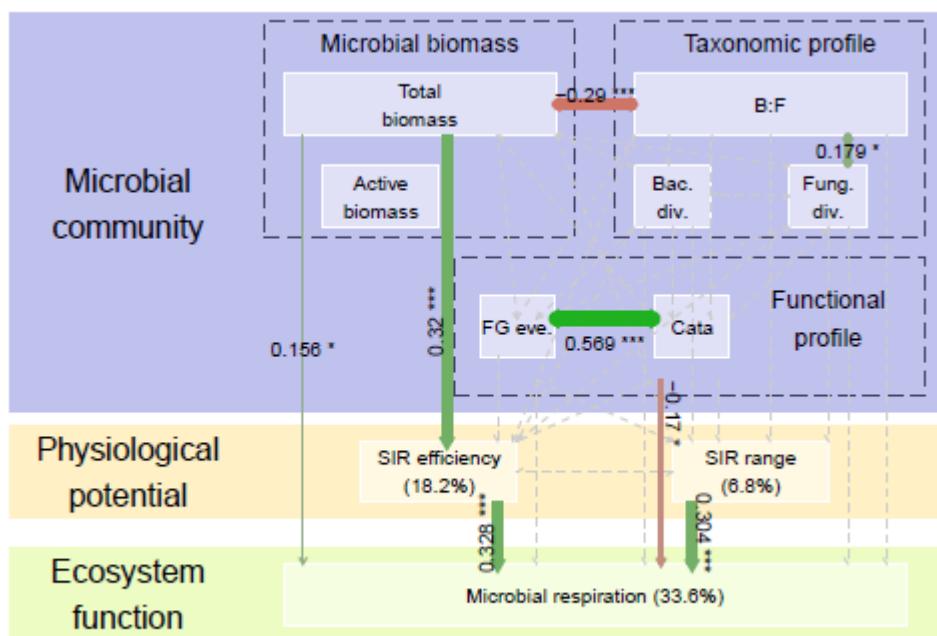
4.2 Explained variance

Variable	R.squared
Basal respiration	0.336
SIR eff.	0.182
SIR range	0.068

4.3 Model output

Response	Relation	Explanatory	Estimate	SE	p value
Basal respiration	~	Total biomass	0.156	0.076	0.039 *
Basal respiration	~	B:F	-0.141	0.074	0.056
Basal respiration	~	Bacteria diversity	-0.006	0.068	0.935
Basal respiration	~	Fungi diversity	0.013	0.070	0.855
Basal respiration	~	Cata	-0.170	0.083	0.041 *
Basal respiration	~	FG evenness	0.082	0.085	0.333
Basal respiration	~	SIR eff.	0.328	0.072	< 0.001***
Basal respiration	~	SIR range	0.304	0.068	< 0.001***
SIR eff.	~	Total biomass	0.320	0.075	< 0.001***
SIR eff.	~	B:F	-0.121	0.081	0.135
SIR eff.	~	Bacteria diversity	0.104	0.075	0.162
SIR eff.	~	Fungi diversity	-0.081	0.076	0.292
SIR eff.	~	Cata	0.010	0.093	0.911
SIR eff.	~	FG evenness	-0.167	0.092	0.07
SIR range	~	Total biomass	0.159	0.083	0.055
SIR range	~	B:F	-0.061	0.087	0.482
SIR range	~	Bacteria diversity	0.104	0.080	0.189
SIR range	~	Fungi diversity	-0.068	0.082	0.404
SIR range	~	Cata	-0.054	0.099	0.586
SIR range	~	FG evenness	-0.094	0.099	0.341
Total biomass	~~	B:F	-0.290	0.075	< 0.001***
Total biomass	~~	Bacteria diversity	-0.016	0.082	0.847
Total biomass	~~	Fungi diversity	0.029	0.082	0.725
Total biomass	~~	Cata	0.132	0.081	0.101
Total biomass	~~	FG evenness	0.102	0.081	0.211
B:F	~~	Bacteria diversity	0.059	0.082	0.474
B:F	~~	Fungi diversity	0.179	0.080	0.024 *
B:F	~~	Cata	-0.133	0.081	0.1
B:F	~~	FG evenness	0.070	0.082	0.39
Bacteria diversity	~~	Fungi diversity	-0.014	0.082	0.869
Bacteria diversity	~~	Cata	-0.083	0.082	0.312
Bacteria diversity	~~	FG evenness	-0.093	0.081	0.254
Fungi diversity	~~	Cata	0.100	0.081	0.22
Fungi diversity	~~	FG evenness	0.150	0.080	0.063
Cata	~~	FG evenness	0.569	0.056	< 0.001***
SIR eff.	~~	SIR range	-0.145	0.080	0.071
Basal respiration	~~	Basal respiration	0.664	0.063	< 0.001***
SIR eff.	~~	SIR eff.	0.818	0.057	< 0.001***
SIR range	~~	SIR range	0.932	0.040	< 0.001***

```
## Warning: package 'readxl' was built under R version 4.0.3
```



Supplementary material II – S11: R outputs Fig. 5

Contents

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5.2	Complete R summary

1 Introduction

The following document will display the R summary after fitting the structural equation model displayed in figure Fig. 5. The model was fitted using the “lavaan” package.(See all hypotheses rational and references in S9)

2 Model structure

```
form =  
,  
# Causal relations  
## Ecosystem function  
Basal respiration ~ Biomass + Active biomass +  
    B:F + Bacteria diversity + Fungi diversity +  
    Cata + FG evenness +  
    SIR efficiency + SIR range +  
    TOC + C:N + C:P + pH + RH + Tree.species.richness  
  
## Physiological potential  
SIR efficiency ~ Biomass + Active biomass +  
    B:F + Bacteria diversity + Fungi diversity +  
    Cata + FG evenness +  
    TOC + C:N + C:P + pH + RH + Tree.species.richness  
  
SIR range ~ Biomass + Active biomass +  
    B:F + Bacteria diversity + Fungi diversity +  
    Cata + FG evenness +  
    TOC + C:N + C:P + pH + RH + Tree.species.richness  
  
## Genetic potential  
Cata ~ TOC + C:N + C:P + pH + RH + Tree.species.richness  
  
FG evenness ~ TOC + C:N + C:P + pH + RH + Tree.species.richness  
  
## Community structure  
B:F ~ TOC + C:N + C:P + pH + RH + Tree.species.richness  
  
Bacteria diversity ~ TOC + C:N + C:P + pH + RH + Tree.species.richness  
  
Fungi diversity ~ TOC + C:N + C:P + pH + RH + Tree.species.richness  
  
## Microbial biomass  
Biomass ~ TOC + C:N + C:P + pH + RH + Tree.species.richness  
  
Active biomass ~ TOC + C:N + C:P + pH + RH + Tree.species.richness  
  
# Correlations  
## Microbial community  
  
Biomass -- Active biomass  
Biomass -- B:F  
Biomass -- Bacteria diversity  
Biomass -- Fungi diversity  
Biomass -- Cata  
Biomass -- FG evenness  
  
Active biomass -- B:F  
Active biomass -- Bacteria diversity  
Active biomass -- Fungi diversity
```

```
Active biomass -- Cata
Active biomass -- FG evenness

B:F -- Bacteria diversity
B:F -- Fungi diversity
B:F -- Cata
B:F -- FG evenness

Bacteria diversity -- Fungi diversity
Bacteria diversity -- Cata
Bacteria diversity -- FG evenness

Fungi diversity -- Cata
Fungi diversity -- FG evenness

Cata -- FG evenness

# Physiological potential
SIR range -- SIR efficiency

# Soil chemical properties & tree species richness
Tree.species.richness -- TOC
Tree.species.richness -- C:P
Tree.species.richness -- C:N
Tree.species.richness -- pH
Tree.species.richness -- RH

TOC -- C:P
TOC -- C:N
TOC -- pH
TOC -- RH

C:P -- C:N
C:P -- pH
C:P -- RH

C:N -- pH
C:N -- RH

pH -- RH'
```

3 Model fit

3.1 Fit quality

Fit index	Value
cfi	1
rmsea	0
srmr	0

4 Model output

4.1 Explained variance

Variable	R.squared
Basal respiration	0.68
SIR eff.	0.335
SIR range	0.172
Cata	0.037
FG evenness	0.045
Fungi diversity	0.055
Bacteria diversity	0.079
B:F	0.053
Active biomass	0.166
Total biomass	0.465

4.2 Summarized effects

4.2.1 Effect of soil and tree species richness

Total effects of soil chemical properties and tree species richness on microbial community facets and functions.

Variable	Total.effect
TOC	1.384
C:N	0.000
C:P	0.269
RH	0.546
pH	0.585
TreeD.	0.489

4.2.2 Link between the groups

Response	Relation	Explanatory	Total.effect
Microbial biomass	~	Soil chemical properties	1.474
Taxonomic profile	~	Soil chemical properties	0.199
Functional profile	~	Soil chemical properties	0.000
Physiological potential	~	Soil chemical properties	0.799
Microbial respiration	~	Soil chemical properties	0.312
Microbial biomass	~	Tree species richness	0.173
Taxonomic profile	~	Tree species richness	0.164
Functional profile	~	Tree species richness	0.000
Physiological potential	~	Tree species richness	0.152
Microbial respiration	~	Tree species richness	0.000
Taxonomic profile	~~	Microbial biomass	0.568
Functional profile	~~	Microbial biomass	0.000
Physiological potential	~~	Microbial biomass	0.543
Microbial respiration	~~	Microbial biomass	0.567
Functional profile	~~	Taxonomic profile	0.000
Physiological potential	~~	Taxonomic profile	0.182
Microbial respiration	~~	Taxonomic profile	0.138
Physiological potential	~~	Functional profile	0.186
Microbial respiration	~~	Functional profile	0.000
Microbial respiration	~~	Physiological potential	0.175
Soil chemical properties	~~	Soil chemical properties	1.440
Microbial biomass	~~	Microbial biomass	0.334
Taxonomic profile	~~	Taxonomic profile	0.188
Functional profile	~~	Functional profile	0.554
Physiological potential	~~	Physiological potential	0.000

4.3 Complete R summary

Response	Relation	Explanatory	Estimate	SE	p value
Basal respiration	~	Total biomass	0.085	0.072	0.236
Basal respiration	~	Active biomass	0.567	0.057	< 0.001***
Basal respiration	~	B:F	-0.138	0.053	0.009 **
Basal respiration	~	Bacteria diversity	0.025	0.051	0.619
Basal respiration	~	Fungi diversity	-0.094	0.051	0.067
Basal respiration	~	Cata	-0.094	0.059	0.11
Basal respiration	~	FG evenness	0.011	0.060	0.859
Basal respiration	~	SIR eff.	0.090	0.058	0.12
Basal respiration	~	SIR range	0.175	0.052	< 0.001***
Basal respiration	~	TOC	-0.113	0.077	0.14
Basal respiration	~	C:P	0.096	0.064	0.134
Basal respiration	~	C:N	-0.046	0.049	0.348
Basal respiration	~	pH	-0.078	0.057	0.169
Basal respiration	~	RH	0.312	0.054	< 0.001***
Basal respiration	~	TreeD.	0.019	0.052	0.718
SIR eff.	~	Total biomass	0.093	0.101	0.356
SIR eff.	~	Active biomass	0.258	0.079	0.001 **
SIR eff.	~	B:F	-0.078	0.075	0.295
SIR eff.	~	Bacteria diversity	0.024	0.072	0.737
SIR eff.	~	Fungi diversity	-0.094	0.072	0.193
SIR eff.	~	Cata	0.044	0.084	0.603
SIR eff.	~	FG evenness	-0.186	0.085	0.028 *
SIR eff.	~	TOC	0.038	0.108	0.725
SIR eff.	~	C:P	0.113	0.089	0.204
SIR eff.	~	C:N	0.076	0.070	0.282
SIR eff.	~	pH	-0.205	0.078	0.009 **
SIR eff.	~	RH	0.042	0.075	0.578
SIR eff.	~	TreeD.	0.152	0.073	0.038 *
SIR range	~	Total biomass	0.285	0.111	0.01 *
SIR range	~	Active biomass	0.129	0.089	0.147
SIR range	~	B:F	-0.057	0.083	0.494
SIR range	~	Bacteria diversity	0.182	0.079	0.021 *
SIR range	~	Fungi diversity	-0.086	0.081	0.287
SIR range	~	Cata	-0.023	0.094	0.808
SIR range	~	FG evenness	-0.079	0.095	0.406
SIR range	~	TOC	-0.325	0.118	0.006 **
SIR range	~	C:P	0.269	0.098	0.006 **
SIR range	~	C:N	-0.051	0.078	0.518
SIR range	~	pH	0.168	0.088	0.056
SIR range	~	RH	0.151	0.083	0.069
SIR range	~	TreeD.	-0.104	0.082	0.207
Cata	~	TOC	0.089	0.103	0.391
Cata	~	C:P	-0.130	0.105	0.217
Cata	~	C:N	0.092	0.082	0.259
Cata	~	pH	-0.017	0.092	0.855
Cata	~	RH	-0.106	0.084	0.205

(continued)

Response	Relation	Explanatory	Estimate	SE	p value
Cata	~	TreeD.	0.073	0.084	0.388
FG evenness	~	TOC	0.058	0.103	0.57
FG evenness	~	C:P	-0.166	0.105	0.113
FG evenness	~	C:N	0.138	0.081	0.088
FG evenness	~	pH	-0.053	0.091	0.565
FG evenness	~	RH	-0.070	0.084	0.403
FG evenness	~	TreeD.	0.039	0.084	0.639
Fungi diversity	~	TOC	0.171	0.102	0.092
Fungi diversity	~	C:P	-0.110	0.104	0.292
Fungi diversity	~	C:N	-0.006	0.081	0.944
Fungi diversity	~	pH	0.199	0.090	0.026 *
Fungi diversity	~	RH	-0.017	0.083	0.839
Fungi diversity	~	TreeD.	0.043	0.084	0.607
Bacteria diversity	~	TOC	0.089	0.101	0.379
Bacteria diversity	~	C:P	-0.026	0.103	0.799
Bacteria diversity	~	C:N	0.100	0.080	0.212
Bacteria diversity	~	pH	-0.112	0.089	0.209
Bacteria diversity	~	RH	0.068	0.082	0.41
Bacteria diversity	~	TreeD.	0.164	0.082	0.045 *
B:F	~	TOC	-0.058	0.102	0.574
B:F	~	C:P	-0.042	0.105	0.69
B:F	~	C:N	-0.097	0.081	0.232
B:F	~	pH	0.068	0.091	0.451
B:F	~	RH	0.132	0.083	0.112
B:F	~	TreeD.	-0.108	0.083	0.194
Active biomass	~	TOC	0.407	0.092	< 0.001***
Active biomass	~	C:P	-0.033	0.098	0.74
Active biomass	~	C:N	0.037	0.076	0.631
Active biomass	~	pH	0.181	0.085	0.032 *
Active biomass	~	RH	0.067	0.078	0.391
Active biomass	~	TreeD.	0.086	0.078	0.275
Total biomass	~	TOC	0.652	0.069	< 0.001***
Total biomass	~	C:P	-0.072	0.079	0.36
Total biomass	~	C:N	0.106	0.061	0.082
Total biomass	~	pH	0.018	0.068	0.797
Total biomass	~	RH	-0.234	0.063	< 0.001***
Total biomass	~	TreeD.	0.173	0.063	0.006 **
Active biomass	~~	Total biomass	0.334	0.073	< 0.001***
B:F	~~	Total biomass	-0.244	0.077	0.002 **
Bacteria diversity	~~	Total biomass	-0.163	0.080	0.041 *
Fungi diversity	~~	Total biomass	-0.046	0.082	0.577
Cata	~~	Total biomass	0.095	0.081	0.242
FG evenness	~~	Total biomass	0.099	0.081	0.226
B:F	~~	Active biomass	-0.153	0.080	0.057
Bacteria diversity	~~	Active biomass	-0.119	0.081	0.143
Fungi diversity	~~	Active biomass	0.161	0.080	0.045 *
Cata	~~	Active biomass	0.002	0.082	0.977
FG evenness	~~	Active biomass	0.069	0.082	0.401

(continued)

Response	Relation	Explanatory	Estimate	SE	p value
Bacteria diversity	~~	B:F	0.104	0.081	0.202
Fungi diversity	~~	B:F	0.188	0.079	0.018 *
Cata	~~	B:F	-0.109	0.081	0.178
FG evenness	~~	B:F	0.097	0.081	0.235
Fungi diversity	~~	Bacteria diversity	-0.003	0.082	0.975
Cata	~~	Bacteria diversity	-0.107	0.081	0.189
FG evenness	~~	Bacteria diversity	-0.119	0.081	0.143
Cata	~~	Fungi diversity	0.084	0.082	0.305
FG evenness	~~	Fungi diversity	0.143	0.081	0.076
Cata	~~	FG evenness	0.554	0.057	< 0.001***
SIR eff.	~~	SIR range	-0.161	0.080	0.044 *
C:P	~~	TreeD.	-0.001	0.082	0.993
C:N	~~	TreeD.	0.008	0.082	0.922
pH	~~	TreeD.	-0.246	0.077	0.001 **
RH	~~	TreeD.	0.081	0.082	0.324
TOC	~~	TreeD.	0.132	0.081	0.102
TOC	~~	C:P	0.603	0.052	< 0.001***
TOC	~~	C:N	0.012	0.082	0.883
TOC	~~	pH	-0.263	0.077	< 0.001***
TOC	~~	RH	0.108	0.081	0.182
C:P	~~	C:N	-0.038	0.082	0.642
C:P	~~	pH	-0.328	0.073	< 0.001***
C:P	~~	RH	0.016	0.082	0.848
C:N	~~	pH	0.142	0.081	0.078
C:N	~~	RH	-0.123	0.081	0.129
pH	~~	RH	-0.246	0.077	0.001 **
Basal respiration	~~	Basal respiration	0.320	0.043	< 0.001***
SIR eff.	~~	SIR eff.	0.665	0.063	< 0.001***
SIR range	~~	SIR range	0.828	0.056	< 0.001***
Cata	~~	Cata	0.963	0.031	< 0.001***
FG evenness	~~	FG evenness	0.955	0.033	< 0.001***
Fungi diversity	~~	Fungi diversity	0.945	0.037	< 0.001***
Bacteria diversity	~~	Bacteria diversity	0.921	0.042	< 0.001***
B:F	~~	B:F	0.947	0.036	< 0.001***
Active biomass	~~	Active biomass	0.834	0.056	< 0.001***
Total biomass	~~	Total biomass	0.535	0.060	< 0.001***

5 Model simplification

In order to simplify our model, soil parameter have been added into a latent variable. The model fit was tested and the estimates were compared to the full model. The difference between the model output been neglectable, we favored the full model in our manuscript to leave the reader the opportunity to explore the different mechanisms. Below the simplified model and its outputs

```
form =
#
# Latent variable
```

```
fert == TOC + C:N + C:P + pH + RH

# Causal relations
## Ecosystem function
Basal respiration ~ Biomass + Active biomass +
    B:F + Bacteria diversity + Fungi diversity +
    Cata + FG evenness +
    SIR efficiency + SIR range +
    fert + Tree.species.richness

## Physiological potential
SIR efficiency ~ Biomass + Active biomass +
    B:F + Bacteria diversity + Fungi diversity +
    Cata + FG evenness +
    fert + Tree.species.richness

SIR range ~ Biomass + Active biomass +
    B:F + Bacteria diversity + Fungi diversity +
    Cata + FG evenness +
    fert + Tree.species.richness

## Genetic potential
Cata ~ fert + Tree.species.richness

FG evenness ~ fert + Tree.species.richness

## Community structure
B:F ~ fert + Tree.species.richness

Bacteria diversity ~ fert + Tree.species.richness

Fungi diversity ~ fert + Tree.species.richness

## Microbial biomass
Biomass ~ fert + Tree.species.richness

Active biomass ~ fert + Tree.species.richness

# Correlations
## Microbial community

Biomass -- Active biomass
Biomass -- B:F
Biomass -- Bacteria diversity
Biomass -- Fungi diversity
Biomass -- Cata
Biomass -- FG evenness

Active biomass -- B:F
Active biomass -- Bacteria diversity
Active biomass -- Fungi diversity
Active biomass -- Cata
Active biomass -- FG evenness
```

```

B:F -- Bacteria diversity
B:F -- Fungi diversity
B:F -- Cata
B:F -- FG evenness

Bacteria diversity -- Fungi diversity
Bacteria diversity -- Cata
Bacteria diversity -- FG evenness

Fungi diversity -- Cata
Fungi diversity -- FG evenness

Cata -- FG evenness

# Physiological potential
SIR range -- SIR efficiency

# Soil chemical properties & tree species richness
Tree.species.richness -- fert
,

```

5.1 Fit quality

	Fit index	Value
cfi	0.82251	
rmsea	0.11403	
srmr	0.07261	

5.2 Complete R summary

Response	Relation	Explanatory	Estimate	SE	p value
Basal respiration	~	Total biomass	-0.078	0.075	0.3
Basal respiration	~	Active biomass	0.587	0.060	< 0.001***
Basal respiration	~	B:F	-0.110	0.060	0.065
Basal respiration	~	Bacteria diversity	0.024	0.057	0.674
Basal respiration	~	Fungi diversity	-0.132	0.058	0.022 *
Basal respiration	~	Cata	-0.115	0.067	0.086
Basal respiration	~	FG evenness	0.020	0.068	0.765
Basal respiration	~	SIR eff.	0.156	0.063	0.014 *
Basal respiration	~	SIR range	0.224	0.057	< 0.001***
Basal respiration	~	fert	0.057	0.067	0.394
Basal respiration	~	TreeD.	0.068	0.058	0.245
SIR eff.	~	Total biomass	0.076	0.098	0.437
SIR eff.	~	Active biomass	0.239	0.080	0.003 **
SIR eff.	~	B:F	-0.096	0.077	0.214
SIR eff.	~	Bacteria diversity	0.052	0.073	0.479

(continued)

Response	Relation	Explanatory	Estimate	SE	p value
SIR eff.	~	Fungi diversity	-0.141	0.073	0.055
SIR eff.	~	Cata	0.027	0.087	0.757
SIR eff.	~	FG evenness	-0.171	0.087	0.05
SIR eff.	~	fert	0.162	0.088	0.065
SIR eff.	~	TreeD.	0.189	0.073	0.01 *
SIR range	~	Total biomass	0.212	0.107	0.049 *
SIR range	~	Active biomass	0.165	0.090	0.065
SIR range	~	B:F	-0.044	0.086	0.604
SIR range	~	Bacteria diversity	0.161	0.080	0.045 *
SIR range	~	Fungi diversity	-0.093	0.082	0.254
SIR range	~	Cata	-0.031	0.097	0.746
SIR range	~	FG evenness	-0.110	0.097	0.254
SIR range	~	fert	-0.153	0.097	0.112
SIR range	~	TreeD.	-0.134	0.082	0.1
Cata	~	fert	0.008	0.080	0.921
Cata	~	TreeD.	0.080	0.082	0.332
FG evenness	~	fert	-0.030	0.080	0.709
FG evenness	~	TreeD.	0.060	0.083	0.471
Fungi diversity	~	fert	0.062	0.080	0.443
Fungi diversity	~	TreeD.	0.007	0.083	0.929
Bacteria diversity	~	fert	0.102	0.078	0.193
Bacteria diversity	~	TreeD.	0.196	0.079	0.013 *
B:F	~	fert	-0.083	0.080	0.297
B:F	~	TreeD.	-0.112	0.081	0.168
Active biomass	~	fert	0.346	0.074	< 0.001***
Active biomass	~	TreeD.	0.056	0.077	0.469
Total biomass	~	fert	0.569	0.064	< 0.001***
Total biomass	~	TreeD.	0.164	0.065	0.012 *
Active biomass	~~	Total biomass	0.321	0.075	< 0.001***
B:F	~~	Total biomass	-0.274	0.075	< 0.001***
Bacteria diversity	~~	Total biomass	-0.159	0.080	0.047 *
Fungi diversity	~~	Total biomass	-0.012	0.081	0.885
Cata	~~	Total biomass	0.138	0.080	0.083
FG evenness	~~	Total biomass	0.134	0.080	0.094
B:F	~~	Active biomass	-0.137	0.080	0.089
Bacteria diversity	~~	Active biomass	-0.122	0.081	0.132
Fungi diversity	~~	Active biomass	0.191	0.079	0.016 *
Cata	~~	Active biomass	0.008	0.082	0.918
FG evenness	~~	Active biomass	0.071	0.081	0.382
Bacteria diversity	~~	B:F	0.096	0.081	0.236
Fungi diversity	~~	B:F	0.189	0.079	0.017 *
Cata	~~	B:F	-0.124	0.081	0.125
FG evenness	~~	B:F	0.076	0.082	0.354
Fungi diversity	~~	Bacteria diversity	-0.024	0.082	0.774
Cata	~~	Bacteria diversity	-0.103	0.081	0.203
FG evenness	~~	Bacteria diversity	-0.105	0.081	0.198
Cata	~~	Fungi diversity	0.099	0.081	0.225

(continued)

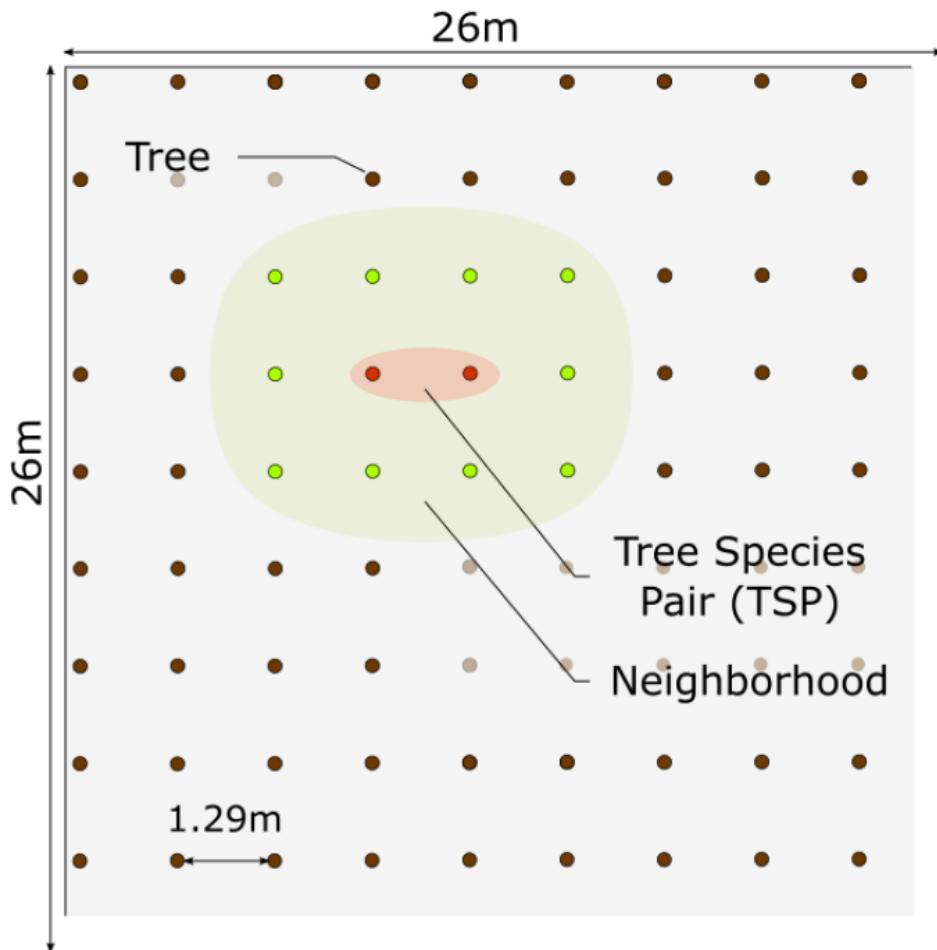
Response	Relation	Explanatory	Estimate	SE	p value
FG evenness	~~	Fungi diversity	0.151	0.080	0.06
Cata	~~	FG evenness	0.568	0.056	< 0.001***
SIR eff.	~~	SIR range	-0.148	0.080	0.065
fert	~~	TreeD.	0.129	0.079	0.103
TOC	~~	TOC	-0.054	0.122	0.656
C:P	~~	C:P	0.655	0.074	< 0.001***
C:N	~~	C:N	1.000	0.002	< 0.001***
pH	~~	pH	0.939	0.038	< 0.001***
RH	~~	RH	0.987	0.018	< 0.001***
Basal respiration	~~	Basal respiration	0.422	0.053	< 0.001***
SIR eff.	~~	SIR eff.	0.722	0.062	< 0.001***
SIR range	~~	SIR range	0.887	0.049	< 0.001***
Cata	~~	Cata	0.993	0.013	< 0.001***
FG evenness	~~	FG evenness	0.996	0.010	< 0.001***
Fungi diversity	~~	Fungi diversity	0.996	0.010	< 0.001***
Bacteria diversity	~~	Bacteria diversity	0.946	0.036	< 0.001***
B:F	~~	B:F	0.978	0.024	< 0.001***
Active biomass	~~	Active biomass	0.872	0.052	< 0.001***
Total biomass	~~	Total biomass	0.625	0.073	< 0.001***
fert	==	TOC	1.027	0.059	< 0.001***
fert	==	C:P	0.587	0.063	< 0.001***
fert	==	C:N	0.009	0.080	0.905
fert	==	pH	-0.246	0.077	0.001 **
fert	==	RH	0.112	0.079	0.156

*Supplementary material: Chapter III - Abiotic and biotic drivers of scale-dependent tree trait
effects on soil microbial biomass and soil carbon concentration*

Supplementary material III – S1: design

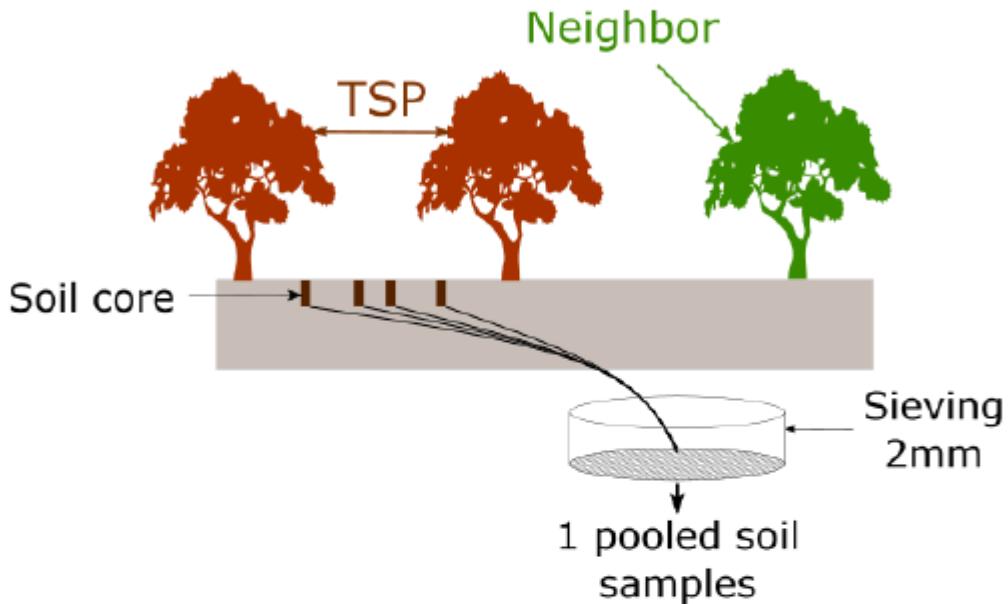
A. Plot design

Plantation design in BEF China plot with example of tree species pair (i.e. TSP in red) and its neighborhood (in green).



B. Tree Species pair sampling design

Soil sampling design between the tree species pairs, where four soil cores were taken and pooled together.



C. Tree species selection

List of tree species building the tree species pairs (TSPs) in the different plots of Site A (BEF China experiment)

Species	Leaf persistence
<i>Castanea henryi</i>	deciduous
<i>Castanopsis sclerophylla</i>	evergreen
<i>Choerospondias axillaris</i>	deciduous
<i>Cyclobalanopsis glauca</i>	evergreen
<i>Koelreuteria bipinnata</i>	deciduous
<i>Liquidambar formosana</i>	deciduous
<i>Lithocarpus glaber</i>	evergreen
<i>Nyssa sinensis</i>	deciduous
<i>Quercus fabri</i>	deciduous
<i>Quercus serrata</i>	deciduous
<i>Sapindus mukorossi</i>	deciduous
<i>Sapium sebiferum</i>	deciduous

D. Tree Species Pairs (TSPs) selection

Tree species pairs description and attributes (paragraphs were added for readability)

TSP code	Site	Plot	Diversity level	Species 1	Species 2
26-E24	A	E24	1	<i>Liquidambar formosana</i>	<i>Liquidambar formosana</i>
33-E31	A	E31	1	<i>Quercus fabri</i>	<i>Quercus fabri</i>
34-E31	A	E31	1	<i>Quercus fabri</i>	<i>Quercus fabri</i>
27-E33	A	E33	1	<i>Lithocarpus glaber</i>	<i>Lithocarpus glaber</i>
28-E33	A	E33	1	<i>Lithocarpus glaber</i>	<i>Lithocarpus glaber</i>
1-E34	A	E34	1	<i>Castanea henryi</i>	<i>Castanea henryi</i>
2-E34	A	E34	1	<i>Castanea henryi</i>	<i>Castanea henryi</i>
37-F21	A	F21	1	<i>Quercus serrata</i>	<i>Quercus serrata</i>
38-F21	A	F21	1	<i>Quercus serrata</i>	<i>Quercus serrata</i>
10-G17	A	G17	1	<i>Castanopsis sclerophylla</i>	<i>Castanopsis sclerophylla</i>
29-G22	A	G22	1	<i>Lithocarpus glaber</i>	<i>Lithocarpus glaber</i>
22-G24	A	G24	1	<i>Koelreuteria bipinnata</i>	<i>Koelreuteria bipinnata</i>
23-G24	A	G24	1	<i>Koelreuteria bipinnata</i>	<i>Koelreuteria bipinnata</i>
36-G33	A	G33	1	<i>Quercus serrata</i>	<i>Quercus serrata</i>
30-H25	A	H25	1	<i>Nyssa sinensis</i>	<i>Nyssa sinensis</i>
3-I12	A	I12	1	<i>Castanea henryi</i>	<i>Castanea henryi</i>
24-I28	A	I28	1	<i>Liquidambar formosana</i>	<i>Liquidambar formosana</i>
25-I28	A	I28	1	<i>Liquidambar formosana</i>	<i>Liquidambar formosana</i>
14-K9	A	K9	1	<i>Cyclobalanopsis glauca</i>	<i>Cyclobalanopsis glauca</i>
8-L11	A	L11	1	<i>Castanopsis sclerophylla</i>	<i>Castanopsis sclerophylla</i>
9-L11	A	L11	1	<i>Castanopsis sclerophylla</i>	<i>Castanopsis sclerophylla</i>
13-L23	A	L23	1	<i>Choerospondias axillaris</i>	<i>Choerospondias axillaris</i>
42-N11	A	N11	1	<i>Sapindus mukorossi</i>	<i>Sapindus mukorossi</i>
43-N11	A	N11	1	<i>Sapindus mukorossi</i>	<i>Sapindus mukorossi</i>
46-N13	A	N13	1	<i>Sapium sebiferum</i>	<i>Sapium sebiferum</i>
47-N13	A	N13	1	<i>Sapium sebiferum</i>	<i>Sapium sebiferum</i>
11-O27	A	O27	1	<i>Choerospondias axillaris</i>	<i>Choerospondias axillaris</i>
12-O27	A	O27	1	<i>Choerospondias axillaris</i>	<i>Choerospondias axillaris</i>
21-Q13	A	Q13	1	<i>Koelreuteria bipinnata</i>	<i>Koelreuteria bipinnata</i>
r-21-Q13	A	Q13	1	<i>Koelreuteria bipinnata</i>	<i>Koelreuteria bipinnata</i>
35-Q16	A	Q16	1	<i>Quercus fabri</i>	<i>Quercus fabri</i>
15-R14	A	R14	1	<i>Cyclobalanopsis glauca</i>	<i>Cyclobalanopsis glauca</i>
16-R14	A	R14	1	<i>Cyclobalanopsis glauca</i>	<i>Cyclobalanopsis glauca</i>
44-R17	A	R17	1	<i>Sapindus mukorossi</i>	<i>Sapindus mukorossi</i>
45-W13	A	W13	1	<i>Sapium sebiferum</i>	<i>Sapium sebiferum</i>
31-W14	A	W14	1	<i>Nyssa sinensis</i>	<i>Nyssa sinensis</i>
32-W14	A	W14	1	<i>Nyssa sinensis</i>	<i>Nyssa sinensis</i>
51-C32	A	C32	2	<i>Castanea henryi</i>	<i>Castanea henryi</i>
52-C32	A	C32	2	<i>Castanea henryi</i>	<i>Nyssa sinensis</i>
96-C32	A	C32	2	<i>Castanea henryi</i>	<i>Nyssa sinensis</i>
95-C32	A	C32	2	<i>Nyssa sinensis</i>	<i>Nyssa sinensis</i>
97-C32	A	C32	2	<i>Nyssa sinensis</i>	<i>Nyssa sinensis</i>
53-F22	A	F22	2	<i>Castanea henryi</i>	<i>Castanea henryi</i>
54-F22	A	F22	2	<i>Castanea henryi</i>	<i>Castanea henryi</i>
55-F22	A	F22	2	<i>Castanea henryi</i>	<i>Nyssa sinensis</i>

(continued)

TSP code	Site	Plot	Diversity level	Species 1	Species 2
98-F22	A	F22	2	<i>Nyssa sinensis</i>	<i>Nyssa sinensis</i>
87-H31	A	H31	2	<i>Liquidambar formosana</i>	<i>Liquidambar formosana</i>
86-H31	A	H31	2	<i>Liquidambar formosana</i>	<i>Sapindus mukorossi</i>
113-H31	A	H31	2	<i>Sapindus mukorossi</i>	<i>Liquidambar formosana</i>
112-H31	A	H31	2	<i>Sapindus mukorossi</i>	<i>Sapindus mukorossi</i>
114-H31	A	H31	2	<i>Sapindus mukorossi</i>	<i>Sapindus mukorossi</i>
67-I27	A	I27	2	<i>Choerospondias axillaris</i>	<i>Choerospondias axillaris</i>
68-I27	A	I27	2	<i>Choerospondias axillaris</i>	<i>Choerospondias axillaris</i>
116-I27	A	I27	2	<i>Sapium sebiferum</i>	<i>Choerospondias axillaris</i>
117-I27	A	I27	2	<i>Sapium sebiferum</i>	<i>Choerospondias axillaris</i>
118-I27	A	I27	2	<i>Sapium sebiferum</i>	<i>Sapium sebiferum</i>
81-J21	A	J21	2	<i>Koelreuteria bipinnata</i>	<i>Koelreuteria bipinnata</i>
82-J21	A	J21	2	<i>Koelreuteria bipinnata</i>	<i>Koelreuteria bipinnata</i>
83-J21	A	J21	2	<i>Koelreuteria bipinnata</i>	<i>Lithocarpus glaber</i>
91-J21	A	J21	2	<i>Lithocarpus glaber</i>	<i>Koelreuteria bipinnata</i>
r-91-J21	A	J21	2	<i>Lithocarpus glaber</i>	<i>Koelreuteria bipinnata</i>
92-J21	A	J21	2	<i>Lithocarpus glaber</i>	<i>Lithocarpus glaber</i>
72-K3	A	K3	2	<i>Cyclobalanopsis glauca</i>	<i>Cyclobalanopsis glauca</i>
73-K3	A	K3	2	<i>Cyclobalanopsis glauca</i>	<i>Cyclobalanopsis glauca</i>
75-K3	A	K3	2	<i>Cyclobalanopsis glauca</i>	<i>Quercus fabri</i>
99-K3	A	K3	2	<i>Quercus fabri</i>	<i>Quercus fabri</i>
64-O6	A	O6	2	<i>Castanopsis sclerophylla</i>	<i>Castanopsis sclerophylla</i>
65-O6	A	O6	2	<i>Castanopsis sclerophylla</i>	<i>Castanopsis sclerophylla</i>
66-O6	A	O6	2	<i>Castanopsis sclerophylla</i>	<i>Quercus serrata</i>
105-O6	A	O6	2	<i>Quercus serrata</i>	<i>Quercus serrata</i>
63-P26	A	P26	2	<i>Castanopsis sclerophylla</i>	<i>Castanopsis sclerophylla</i>
62-P26	A	P26	2	<i>Castanopsis sclerophylla</i>	<i>Quercus serrata</i>
w-104-P26	A	P26	2	<i>Quercus serrata</i>	<i>Castanopsis sclerophylla</i>
102-P26	A	P26	2	<i>Quercus serrata</i>	<i>Quercus serrata</i>
103-P26	A	P26	2	<i>Quercus serrata</i>	<i>Quercus serrata</i>
104-P26	A	P26	2	<i>Quercus serrata</i>	<i>Quercus serrata</i>
74-Q21	A	Q21	2	<i>Cyclobalanopsis glauca</i>	<i>Cyclobalanopsis glauca</i>
76-Q21	A	Q21	2	<i>Cyclobalanopsis glauca</i>	<i>Quercus fabri</i>
77-Q21	A	Q21	2	<i>Cyclobalanopsis glauca</i>	<i>Quercus fabri</i>
100-Q21	A	Q21	2	<i>Quercus fabri</i>	<i>Quercus fabri</i>
101-Q21	A	Q21	2	<i>Quercus fabri</i>	<i>Quercus fabri</i>
84-Q7	A	Q7	2	<i>Koelreuteria bipinnata</i>	<i>Koelreuteria bipinnata</i>
85-Q7	A	Q7	2	<i>Koelreuteria bipinnata</i>	<i>Lithocarpus glaber</i>
93-Q7	A	Q7	2	<i>Lithocarpus glaber</i>	<i>Lithocarpus glaber</i>
94-Q7	A	Q7	2	<i>Lithocarpus glaber</i>	<i>Lithocarpus glaber</i>
69-S18	A	S18	2	<i>Choerospondias axillaris</i>	<i>Choerospondias axillaris</i>
70-S18	A	S18	2	<i>Choerospondias axillaris</i>	<i>Sapium sebiferum</i>
71-S18	A	S18	2	<i>Choerospondias axillaris</i>	<i>Sapium sebiferum</i>
119-S18	A	S18	2	<i>Sapium sebiferum</i>	<i>Sapium sebiferum</i>
r-120-S18	A	S18	2	<i>Sapium sebiferum</i>	<i>Sapium sebiferum</i>
88-T17	A	T17	2	<i>Liquidambar formosana</i>	<i>Liquidambar formosana</i>
89-T17	A	T17	2	<i>Liquidambar formosana</i>	<i>Liquidambar formosana</i>

(continued)

TSP code	Site	Plot	Diversity level	Species 1	Species 2
90-T17	A	T17	2	<i>Liquidambar formosana</i>	<i>Sapindus mukorossi</i>
115-T17	A	T17	2	<i>Sapindus mukorossi</i>	<i>Sapindus mukorossi</i>
130-F27	A	F27	4	<i>Castanopsis sclerophylla</i>	<i>Castanopsis sclerophylla</i>
131-F27	A	F27	4	<i>Choerospondias axillaris</i>	<i>Castanopsis sclerophylla</i>
153-F27	A	F27	4	<i>Quercus serrata</i>	<i>Choerospondias axillaris</i>
161-F27	A	F27	4	<i>Sapium sebiferum</i>	<i>Choerospondias axillaris</i>
162-F27	A	F27	4	<i>Sapium sebiferum</i>	<i>Sapium sebiferum</i>
139-F28	A	F28	4	<i>Koelreuteria bipinnata</i>	<i>Koelreuteria bipinnata</i>
132-N20	A	N20	4	<i>Choerospondias axillaris</i>	<i>Choerospondias axillaris</i>
154-N20	A	N20	4	<i>Quercus serrata</i>	<i>Castanopsis sclerophylla</i>
155-N20	A	N20	4	<i>Quercus serrata</i>	<i>Quercus serrata</i>
156-N20	A	N20	4	<i>Quercus serrata</i>	<i>Sapium sebiferum</i>
163-N20	A	N20	4	<i>Sapium sebiferum</i>	<i>Castanopsis sclerophylla</i>
133-N8	A	N8	4	<i>Cyclobalanopsis glauca</i>	<i>Cyclobalanopsis glauca</i>
149-N8	A	N8	4	<i>Quercus fabri</i>	<i>Cyclobalanopsis glauca</i>
125-P19	A	P19	4	<i>Castanea henryi</i>	<i>Castanea henryi</i>
126-P19	A	P19	4	<i>Castanea henryi</i>	<i>Nyssa sinensis</i>
143-P19	A	P19	4	<i>Liquidambar formosana</i>	<i>Sapindus mukorossi</i>
148-P19	A	P19	4	<i>Nyssa sinensis</i>	<i>Sapindus mukorossi</i>
160-P19	A	P19	4	<i>Sapindus mukorossi</i>	<i>Sapindus mukorossi</i>
124-P29	A	P29	4	<i>Castanea henryi</i>	<i>Liquidambar formosana</i>
141-P29	A	P29	4	<i>Liquidambar formosana</i>	<i>Liquidambar formosana</i>
142-P29	A	P29	4	<i>Liquidambar formosana</i>	<i>Nyssa sinensis</i>
147-P29	A	P29	4	<i>Nyssa sinensis</i>	<i>Castanea henryi</i>
159-P29	A	P29	4	<i>Sapindus mukorossi</i>	<i>Castanea henryi</i>
150-U15	A	U15	4	<i>Quercus fabri</i>	<i>Quercus fabri</i>
140-V12/W12	A	V12/W12	4	<i>Koelreuteria bipinnata</i>	<i>Lithocarpus glaber</i>
146-W12/X12	A	W12/X12	4	<i>Lithocarpus glaber</i>	<i>Lithocarpus glaber</i>
176-P27	A	P27	8	<i>Cyclobalanopsis glauca</i>	<i>Quercus fabri</i>
181-P27	A	P27	8	<i>Koelreuteria bipinnata</i>	<i>Lithocarpus glaber</i>
187-P27	A	P27	8	<i>Lithocarpus glaber</i>	<i>Lithocarpus glaber</i>
166-R16	A	R16	8	<i>Castanea henryi</i>	<i>Liquidambar formosana</i>
171-R16	A	R16	8	<i>Castanopsis sclerophylla</i>	<i>Castanopsis sclerophylla</i>
175-R16	A	R16	8	<i>Choerospondias axillaris</i>	<i>Sapium sebiferum</i>
190-R16	A	R16	8	<i>Nyssa sinensis</i>	<i>Castanea henryi</i>
193-R16	A	R16	8	<i>Quercus serrata</i>	<i>Castanopsis sclerophylla</i>
194-R16	A	R16	8	<i>Quercus serrata</i>	<i>Quercus serrata</i>
198-R16	A	R16	8	<i>Sapindus mukorossi</i>	<i>Sapindus mukorossi</i>
199-R16	A	R16	8	<i>Sapindus mukorossi</i>	<i>Sapindus mukorossi</i>
200-R16	A	R16	8	<i>Sapium sebiferum</i>	<i>Quercus serrata</i>
201-R16	A	R16	8	<i>Sapium sebiferum</i>	<i>Sapium sebiferum</i>
165-S10	A	S10	8	<i>Castanea henryi</i>	<i>Castanea henryi</i>
170-S10	A	S10	8	<i>Castanopsis sclerophylla</i>	<i>Sapium sebiferum</i>
173-S10	A	S10	8	<i>Choerospondias axillaris</i>	<i>Castanopsis sclerophylla</i>
174-S10	A	S10	8	<i>Choerospondias axillaris</i>	<i>Choerospondias axillaris</i>
172-S10	A	S10	8	<i>Choerospondias axillaris</i>	<i>Quercus serrata</i>
186-S10	A	S10	8	<i>Liquidambar formosana</i>	<i>Liquidambar formosana</i>
185-S10	A	S10	8	<i>Liquidambar formosana</i>	<i>Nyssa sinensis</i>

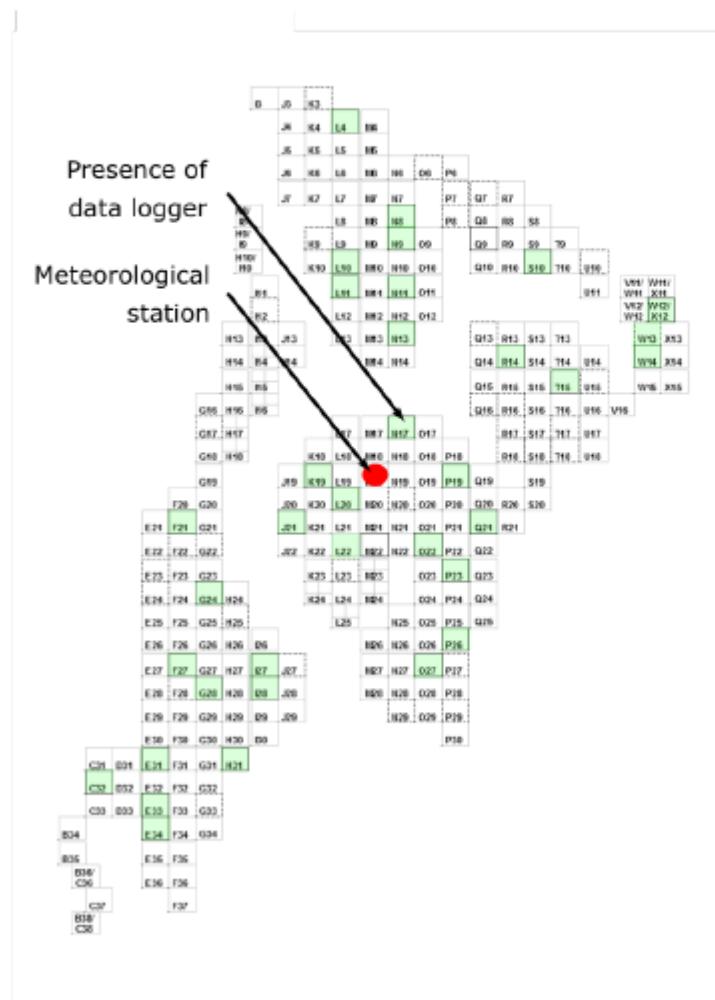
(continued)

TSP code	Site	Plot	Diversity level	Species 1	Species 2
188-S10	A	S10	8	<i>Nyssa sinensis</i>	<i>Nyssa sinensis</i>
189-S10	A	S10	8	<i>Nyssa sinensis</i>	<i>Sapindus mukorossi</i>
197-S10	A	S10	8	<i>Sapindus mukorossi</i>	<i>Castanea henryi</i>
178-S14	A	S14	8	<i>Cyclobalanopsis glauca</i>	<i>Cyclobalanopsis glauca</i>
183-S15	A	S15	8	<i>Koelreuteria bipinnata</i>	<i>Koelreuteria bipinnata</i>
r-216-S15	A	S15	8	<i>Koelreuteria bipinnata</i>	<i>Lithocarpus glaber</i>
184-S15	A	S15	8	<i>Koelreuteria bipinnata</i>	<i>Quercus fabri</i>
191-T15	A	T15	8	<i>Quercus fabri</i>	<i>Quercus fabri</i>
220-L21	A	L21	16	<i>Liquidambar formosana</i>	<i>Choerospondias axillaris</i>
216-L21	A	L21	16	<i>Sapindus mukorossi</i>	<i>Lithocarpus glaber</i>
203-L22	A	L22	16	<i>Castanea henryi</i>	<i>Nyssa sinensis</i>
204-L22	A	L22	16	<i>Castanea henryi</i>	<i>Sapindus mukorossi</i>
209-L22	A	L22	16	<i>Choerospondias axillaris</i>	<i>Castanopsis sclerophylla</i>
210-L22	A	L22	16	<i>Choerospondias axillaris</i>	<i>Choerospondias axillaris</i>
r-213-L22	A	L22	16	<i>Cyclobalanopsis glauca</i>	<i>Quercus fabri</i>
217-L22	A	L22	16	<i>Liquidambar formosana</i>	<i>Castanea henryi</i>
219-L22	A	L22	16	<i>Liquidambar formosana</i>	<i>Liquidambar formosana</i>
218-L22	A	L22	16	<i>Liquidambar formosana</i>	<i>Nyssa sinensis</i>
221-L22	A	L22	16	<i>Lithocarpus glaber</i>	<i>Lithocarpus glaber</i>
222-L22	A	L22	16	<i>Quercus fabri</i>	<i>Quercus fabri</i>
230-L22	A	L22	16	<i>Sapium sebiferum</i>	<i>Castanopsis sclerophylla</i>
r-220-M21	A	M21	16	<i>Liquidambar formosana</i>	<i>Sapindus mukorossi</i>
226-M21	A	M21	16	<i>Quercus serrata</i>	<i>Sapium sebiferum</i>
208-M22	A	M22	16	<i>Castanopsis sclerophylla</i>	<i>Castanopsis sclerophylla</i>
211-M22	A	M22	16	<i>Choerospondias axillaris</i>	<i>Sapium sebiferum</i>
213-U10	A	U10	16	<i>Cyclobalanopsis glauca</i>	<i>Quercus fabri</i>
r-213-U10	A	U10	16	<i>Cyclobalanopsis glauca</i>	<i>Quercus fabri</i>
225-U10	A	U10	16	<i>Quercus serrata</i>	<i>Quercus serrata</i>
229-U10	A	U10	16	<i>Sapindus mukorossi</i>	<i>Sapindus mukorossi</i>
231-U10	A	U10	16	<i>Sapium sebiferum</i>	<i>Sapium sebiferum</i>
232-N9	A	N9	24	<i>Castanea henryi</i>	<i>Castanea henryi</i>
236-N9	A	N9	24	<i>Cyclobalanopsis glauca</i>	<i>Cyclobalanopsis glauca</i>
238-N9	A	N9	24	<i>Koelreuteria bipinnata</i>	<i>Koelreuteria bipinnata</i>
241-N9	A	N9	24	<i>Sapindus mukorossi</i>	<i>Nyssa sinensis</i>
234-R18	A	R18	24	<i>Castanopsis sclerophylla</i>	<i>Quercus serrata</i>
235-R18	A	R18	24	<i>Choerospondias axillaris</i>	<i>Quercus serrata</i>
239-R18	A	R18	24	<i>Nyssa sinensis</i>	<i>Nyssa sinensis</i>

Supplementary material III – S2: temperature modeling

A. Temperature and humidity data logger distribution

Spatial distribution of temperature and humidity data logger and position of the meteorological station in BEF China Site A



B. Variables

Description of the variables used to predict air temperature at the plot level.

Variables	Name	Usage	Units
Logger daily minimum temperature	T.min	Response	Celsius
Logger daily average temperature	T.mean	Response	Celsius
Logger daily maximum temperature	T.max	Response	Celsius
Station daily minimum temperature	T.station.min	Explanatory	Celsius
Station daily minimum temperature	T.station.mean	Explanatory	Celsius
Station daily minimum temperature	T.station.max	Explanatory	Celsius
Daily solar radiation	Radiation	Explanatory	W/qm
Rainfall	Rain	Explanatory	mm
Latitudinal position	X	Explanatory	No unit
Longitudinal position	Y	Explanatory	No unit
Gaussian radial basis vectors	B1 - B12	Explanatory	No unit
Date	date	Explanatory	dd.mm.yyyy hh:mm
Altitude	Alt	Explanatory	m
Eastness	East	Explanatory	Celsius
Northness	North	Explanatory	Celsius
Slope	Slope	Explanatory	Celsius
Plot profile curvature	Curve.Pr	Explanatory	%
Plot plan curvature	Curve.Pl	Explanatory	%
Annual solar radiation	Solar.radiation	Explanatory	W/qm
Tree Species Richness	Sp.Rich	Explanatory	No unit
Forest vertical stratification	ENL	Explanatory	No unit

C. Model structure

Structure of the model used to predict air temperature.

$$\begin{aligned}
 min.T &\sim (X + Y + date)^2 \\
 + poly(T.station.min, 3) + poly(T.station.mean, 3) + poly(T.station.max, 3) \\
 + Solar * Radiation + Rainfall + Rainfall.week \\
 + ENL + Spe.Rich \\
 + Alt + East + North + Slope + Curve.Pr + Curve.Pl \\
 + B1 + B2 + B3 + B4 + B5 + B6 + B7 + B8 + B9 + B10 + B11 + B12
 \end{aligned} \tag{1}$$

$$\begin{aligned}
 mean.T &\sim (X + Y + date)^2 \\
 + poly(T.station.min, 3) + poly(T.station.mean, 3) + poly(T.station.max, 3) \\
 + Solar * Radiation + Rainfall + Rainfall.week \\
 + ENL + Spe.Rich \\
 + Alt + East + North + Slope + Curve.Pr + Curve.Pl \\
 + B1 + B2 + B3 + B4 + B5 + B6 + B7 + B8 + B9 + B10 + B11 + B12
 \end{aligned} \tag{2}$$

$$\begin{aligned}
 & \max.T \sim (X + Y + date)^2 \\
 & + \text{poly}(T.station.min, 3) + \text{poly}(T.station.mean, 3) + \text{poly}(T.station.max, 3) \\
 & \quad + \text{Solar} * \text{Radiation} + \text{Rainfall} + \text{Rainfall.week} \\
 & \quad + \text{ENL} + \text{Spe.Rich} \\
 & \quad + \text{Alt} + \text{East} + \text{North} + \text{Slope} + \text{Curve.Pr} + \text{Curve.Pl} \\
 & \quad + \text{B1} + \text{B2} + \text{B3} + \text{B4} + \text{B5} + \text{B6} + \text{B7} + \text{B8} + \text{B9} + \text{B10} + \text{B11} + \text{B12}
 \end{aligned} \tag{3}$$

D. Model fit

Model fit output of each response variable.

Minimum temperature

```

Call:
lm(formula = min.T ~ X_DD + poly(mean.T.station, degree = 3) +
   poly(min.T.station, degree = 3) + poly(max.T.station, degree = 3) +
   ENL + East + Slope + Curve.Pr + Rain.day + Rain.week + B1 +
   B4 + B5 + B7 + B8 + B9 + B10 + B11 + B12, data = df.comp2.mod)

Residuals:
    Min      1Q  Median      3Q     Max 
-3.07162 -0.75806  0.04286  0.75880  2.45860 

Coefficients:
              Estimate Std. Error t value Pr(>|t|)    
(Intercept) 1.283e+05  3.684e+04  3.481 0.000513 ***
X_DD        -1.088e+03  3.124e+02 -3.481 0.000514 ***
poly(mean.T.station, degree = 3)1 -4.309e+02  3.512e+01 -12.269 < 2e-16 ***
poly(mean.T.station, degree = 3)2  1.578e+02  1.562e+01 10.108 < 2e-16 ***
poly(mean.T.station, degree = 3)3  1.744e+00  5.514e+00  0.316 0.751776  
poly(min.T.station, degree = 3)1  3.895e+02  2.158e+01 18.048 < 2e-16 ***
poly(min.T.station, degree = 3)2 -1.153e+02  9.136e+00 -12.624 < 2e-16 ***
poly(min.T.station, degree = 3)3  2.222e+00  3.991e+00  0.557 0.577733  
poly(max.T.station, degree = 3)1  1.561e+02  1.494e+01 10.452 < 2e-16 ***
poly(max.T.station, degree = 3)2 -7.778e+01  7.647e+00 -10.172 < 2e-16 ***
poly(max.T.station, degree = 3)3  8.440e+00  3.512e+00  2.403 0.016386 *  
ENL          9.234e-03  1.165e-03  7.926 4.36e-15 ***
East         -1.711e-01  8.767e-02 -1.951 0.051208 .  
Slope        -2.317e-02  8.658e-03 -2.677 0.007515 ** 
Curve.Pr     -3.246e-03  9.069e-04 -3.579 0.000356 *** 
Rain.day     -1.006e-01  8.358e-03 -12.033 < 2e-16 *** 
Rain.week    -6.798e-02  3.920e-03 -17.341 < 2e-16 *** 
B1           3.001e+00  1.706e+00  1.759 0.078740 .  
B4           -4.969e+00  1.635e+00 -3.039 0.002416 ** 
B5           7.599e+00  1.578e+00  4.814 1.63e-06 *** 
B7           1.194e+01  3.418e+00  3.492 0.000493 *** 
B8           -1.210e+01  2.034e+00 -5.948 3.38e-09 *** 
B9           1.294e+01  2.045e+00  6.328 3.26e-10 *** 

```

```

B10          -1.030e+01  4.591e+00  -2.245 0.024941 *
B11          1.631e+01  3.432e+00   4.751 2.21e-06 ***
B12          -9.278e+00  2.230e+00  -4.160 3.36e-05 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.9883 on 1511 degrees of freedom
(232 observations deleted due to missingness)
Multiple R-squared:  0.8833,    Adjusted R-squared:  0.8813
F-statistic: 457.3 on 25 and 1511 DF,  p-value: < 2.2e-16

```

Average temperature

```

Call:
lm(formula = mean.T ~ X_DD + date + poly(mean.T.station, degree = 3) +
poly(min.T.station, degree = 3) + poly(max.T.station, degree = 3) +
Solar.radiation + Radiation + ENL + Sp.Rich + Alt + North +
Slope + Curve.Pr + Curve.Pl + Rain.day + Rain.week + B1 +
B2 + B3 + B4 + B5 + B6 + B7 + B8 + B9 + B10 + B11 + B12,
data = df.comp2.mod)

Residuals:
    Min      1Q  Median      3Q     Max 
-3.2275 -0.6104 -0.0125  0.5653  3.2355 

Coefficients:
            Estimate Std. Error t value Pr(>|t|)    
(Intercept) 1.973e+05  5.839e+04   3.379 0.000747 ***
X_DD        -1.677e+03  4.952e+02  -3.386 0.000728 ***
date         2.820e-02  2.958e-03   9.533 < 2e-16 ***
poly(mean.T.station, degree = 3)1 -4.432e+01  3.269e+01  -1.356 0.175356  
poly(mean.T.station, degree = 3)2  6.870e+01  1.534e+01   4.478 8.10e-06 ***
poly(mean.T.station, degree = 3)3 -2.283e+01  4.994e+00  -4.572 5.24e-06 ***
poly(min.T.station, degree = 3)1  8.654e+01  1.984e+01   4.363 1.37e-05 ***
poly(min.T.station, degree = 3)2 -5.637e+01  9.049e+00  -6.229 6.07e-10 ***
poly(min.T.station, degree = 3)3  1.998e+01  3.690e+00   5.415 7.11e-08 ***
poly(max.T.station, degree = 3)1  7.204e+01  1.413e+01   5.098 3.86e-07 ***
poly(max.T.station, degree = 3)2 -4.363e+01  7.576e+00  -5.759 1.02e-08 ***
poly(max.T.station, degree = 3)3  1.352e+01  3.129e+00   4.322 1.65e-05 ***
Solar.radiation -1.681e-05  2.673e-06  -6.288 4.20e-10 ***
Radiation      5.556e-04  2.815e-05   19.736 < 2e-16 ***
ENL           -2.099e-02  1.480e-03  -14.181 < 2e-16 ***
Sp.Rich        -2.372e-02  7.208e-03  -3.291 0.001023 ** 
Alt            3.373e-02  6.170e-03   5.466 5.39e-08 ***
North          -4.303e+00  6.038e-01  -7.127 1.59e-12 ***
Slope          -1.013e-01  2.008e-02  -5.046 5.06e-07 ***
Curve.Pr       9.134e-03  1.350e-03   6.764 1.91e-11 ***
Curve.Pl       6.286e-03  1.421e-03   4.425 1.03e-05 ***
Rain.day       -1.142e-01  7.552e-03  -15.117 < 2e-16 ***
Rain.week      -5.896e-02  3.699e-03  -15.940 < 2e-16 ***
B1             -7.099e+01  4.995e+00  -14.212 < 2e-16 ***
B2             2.340e+01  2.285e+00   10.240 < 2e-16 ***

```

```

B3          -3.943e+01  4.178e+00 -9.438 < 2e-16 ***
B4          4.069e+01  2.434e+00 16.716 < 2e-16 ***
B5          -5.834e+01  3.737e+00 -15.612 < 2e-16 ***
B6          1.583e+01  2.988e+00  5.297 1.36e-07 ***
B7          -9.252e+01  6.319e+00 -14.642 < 2e-16 ***
B8          5.345e+01  3.705e+00 14.427 < 2e-16 ***
B9          -6.078e+01  4.586e+00 -13.253 < 2e-16 ***
B10         2.737e+01  5.692e+00  4.809 1.67e-06 ***
B11         -6.597e+01  6.047e+00 -10.909 < 2e-16 ***
B12         1.885e+01  3.752e+00  5.024 5.67e-07 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.8796 on 1502 degrees of freedom
(232 observations deleted due to missingness)
Multiple R-squared:  0.9143,    Adjusted R-squared:  0.9124
F-statistic: 471.5 on 34 and 1502 DF,  p-value: < 2.2e-16

```

Maximum temperature

```

Call:
lm(formula = max.T ~ Y_DD + date + poly(mean.T.station, degree = 3) +
   poly(min.T.station, degree = 3) + poly(max.T.station, degree = 3) +
   Solar.radiation + Radiation + ENL + Sp.Rich + Alt + North +
   Curve.Pr + Curve.Pl + Rain.day + Rain.week + B1 + B2 + B3 +
   B4 + B5 + B6 + B7 + B8 + B9 + B10 + B11 + B12, data = df.comp2.mod)

Residuals:
    Min      1Q  Median      3Q      Max 
-7.2717 -1.1448 -0.0354  1.1209  6.3630 

Coefficients:
            Estimate Std. Error t value Pr(>|t|)    
(Intercept) -1.031e+05  5.531e+04 -1.864  0.06256 .  
Y_DD        3.488e+03  1.899e+03  1.837  0.06645 .  
date        9.851e-02  6.316e-03 15.598 < 2e-16 ***
poly(mean.T.station, degree = 3)1 -1.154e+02  6.980e+01 -1.654  0.09833 .  
poly(mean.T.station, degree = 3)2  6.833e+00  3.276e+01  0.209  0.83479  
poly(mean.T.station, degree = 3)3 -7.794e+01  1.066e+01 -7.309 4.35e-13 *** 
poly(min.T.station, degree = 3)1  5.100e+01  4.235e+01  1.204  0.22872  
poly(min.T.station, degree = 3)2  6.042e+00  1.932e+01  0.313  0.75452  
poly(min.T.station, degree = 3)3  6.303e+01  7.879e+00  8.000 2.46e-15 *** 
poly(max.T.station, degree = 3)1  2.174e+02  3.017e+01  7.206 9.08e-13 *** 
poly(max.T.station, degree = 3)2 -3.558e+01  1.618e+01 -2.200  0.02797 *  
poly(max.T.station, degree = 3)3  3.403e+01  6.681e+00  5.094 3.96e-07 *** 
Solar.radiation -1.998e-05  3.090e-06 -6.437 1.63e-10 *** 
Radiation     1.505e-03  6.011e-05 25.035 < 2e-16 *** 
ENL          -1.180e-01  2.766e-03 -42.656 < 2e-16 *** 
Sp.Rich       -5.137e-02  1.634e-02 -3.143  0.00170 ** 
Alt           3.165e-02  1.173e-02  2.699  0.00704 ** 
North         -6.390e+00  7.255e-01 -8.808 < 2e-16 *** 
Curve.Pr      4.041e-02  2.958e-03 13.659 < 2e-16 *** 

```

```
Curve.P1           1.757e-02 2.924e-03  6.010 2.32e-09 ***
Rain.day          -1.492e-01 1.613e-02 -9.254 < 2e-16 ***
Rain.week         -7.077e-02 7.898e-03 -8.960 < 2e-16 ***
B1               -2.250e+02 1.078e+01 -20.865 < 2e-16 ***
B2                6.613e+01 3.865e+00 17.113 < 2e-16 ***
B3               -1.278e+02 9.322e+00 -13.705 < 2e-16 ***
B4                1.354e+02 7.032e+00 19.251 < 2e-16 ***
B5               -1.960e+02 7.642e+00 -25.642 < 2e-16 ***
B6                4.253e+01 6.425e+00  6.619 5.02e-11 ***
B7               -3.138e+02 1.275e+01 -24.600 < 2e-16 ***
B8                1.852e+02 7.700e+00 24.047 < 2e-16 ***
B9               -2.249e+02 9.658e+00 -23.284 < 2e-16 ***
B10              6.914e+01 1.631e+01  4.239 2.38e-05 ***
B11              -2.324e+02 1.141e+01 -20.358 < 2e-16 ***
B12              5.648e+01 1.007e+01  5.611 2.39e-08 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 1.878 on 1503 degrees of freedom
(232 observations deleted due to missingness)
Multiple R-squared:  0.8818,    Adjusted R-squared:  0.8792
F-statistic: 339.7 on 33 and 1503 DF,  p-value: < 2.2e-16
```

Supplementary material III – S3: PLFA biomarkers

PLFA biomarkers used to identify soil microbes' functional groups

Fatty acid	Lipid fraction	Predominant origin	Literature
i15:0	PLFA	Gram-positive bacteria	Zelles (1997, 1999)
a15:0	PLFA	Gram-positive bacteria	Zelles (1997, 1999)
i16:0	PLFA	Gram-positive bacteria	Zelles (1997, 1999)
i17:0	PLFA	Gram-positive bacteria	Zelles (1997, 1999)
16:1n7	PLFA	Bacteria widespread	Guckert et al. (1991), Zelles (1999)
16:1n-5	PLFA	General bacteria	Nichols et al. (1986), Zelles (1997)
cy17:0	PLFA	Gram-negative bacteria	Zelles (1997, 1999)
18:1n9	PLFA	Fungi (saprophytic, EM)	Bååth (2003), Vestal and White (1989), Zelles (1999), Harwood and Russell (1984), Ruess et al. (2007)
cy19:0	PLFA	Gram-negative bacteria	Zelles (1997, 1999)
18:2n6c	PLFA	Fungi (saprophytic, EM)	Frostegård and Bååth (1996), Zelles (1999)
20:1	PLFA	AM fungi (Gigaspora)	Sakamoto et al. (2004)

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- Guckert, J. B., Ringelberg, D. B., White, D. C., Hanson, R. S., & Bratina, B. J. (1991). Membrane fatty acids as phenotypic markers in the polyphasic taxonomy of methylotrophs within the Proteobacteria. *Microbiology*, 137(11), 2631-2641.
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- Nichols, P. D., Antworth, C. P., Parsons, J., White, D. C., Henson, J. M., & Wilson, J. T. (1987). Detection of a microbial consortium, including type II methanotrophs, by use of phospholipid fatty acids in an aerobic halogenated hydrocarbon-degrading soil column enriched with natural gas. *Environmental Toxicology and Chemistry: An International Journal*, 6(2), 89-97.

Ruess, L., & Chamberlain, P. M. (2010). The fat that matters: soil food web analysis using fatty acids and their carbon stable isotope signature. *Soil Biology and Biochemistry*, 42(11), 1898-1910.

Sakamoto, K., Iijima, T., & Higuchi, R. (2004). Use of specific phospholipid fatty acids for identifying and quantifying the external hyphae of the arbuscular mycorrhizal fungus *Gigaspora rosea*. *Soil Biology and Biochemistry*, 36(11), 1827-1834.

Vestal, J. R., & White, D. C. (1989). Lipid analysis in microbial ecology. *Bioscience*, 39(8), 535-541.

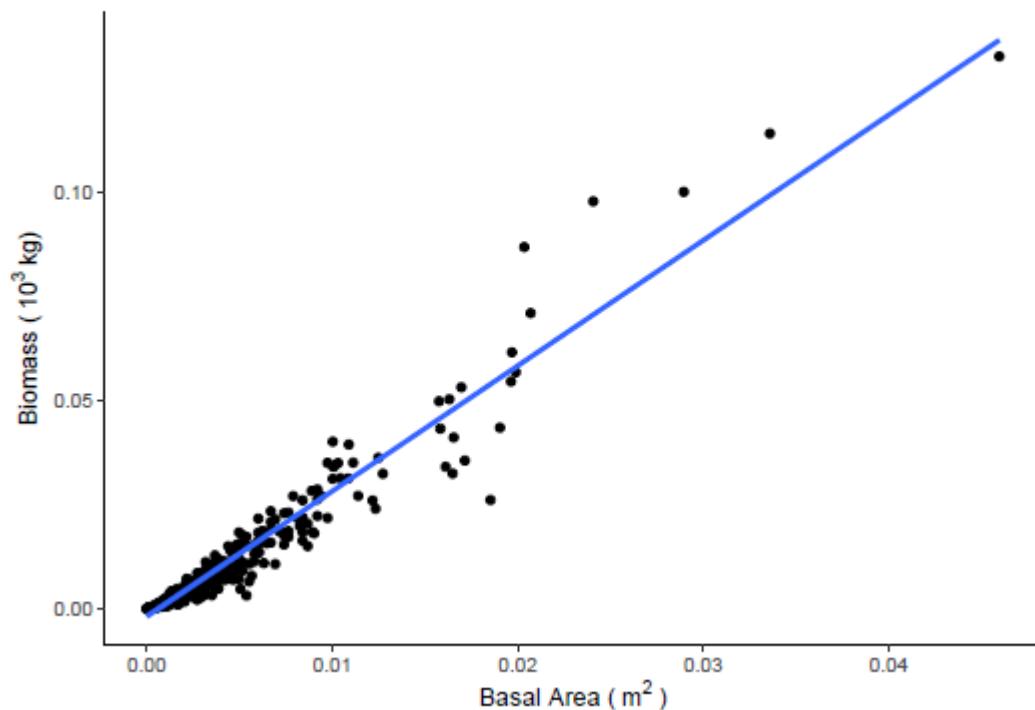
Zelles, L., Palojaervi, A., Kandeler, E., Von Luetzow, M., Winter, K., & Bai, Q. Y. (1997). Changes in soil microbial properties and phospholipid fatty acid fractions after chloroform fumigation. *Soil Biology and Biochemistry*, 29(9-10), 1325-1336.

Zelles, L. (1999). Fatty acid patterns of phospholipids and lipopolysaccharides in the characterisation of microbial communities in soil: a review. *Biology and fertility of soils*, 29(2), 111-129.

Supplementary material III – S4: tree biomass estimations

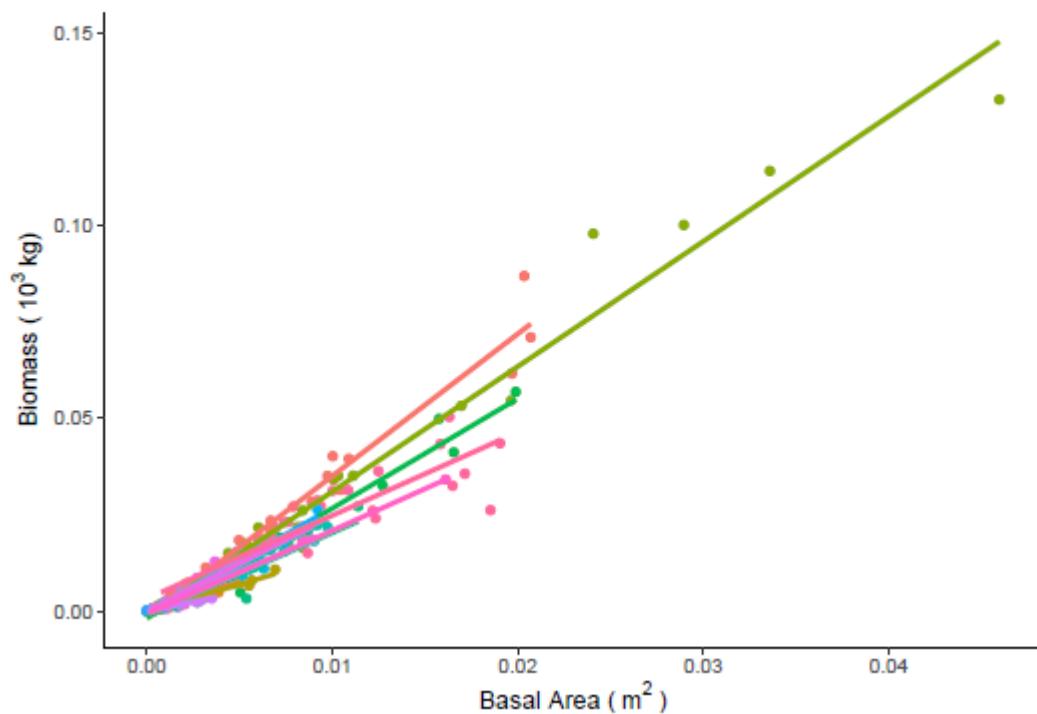
Tree allometric relationships

```
## `geom_smooth()` using formula 'y ~ x'
```



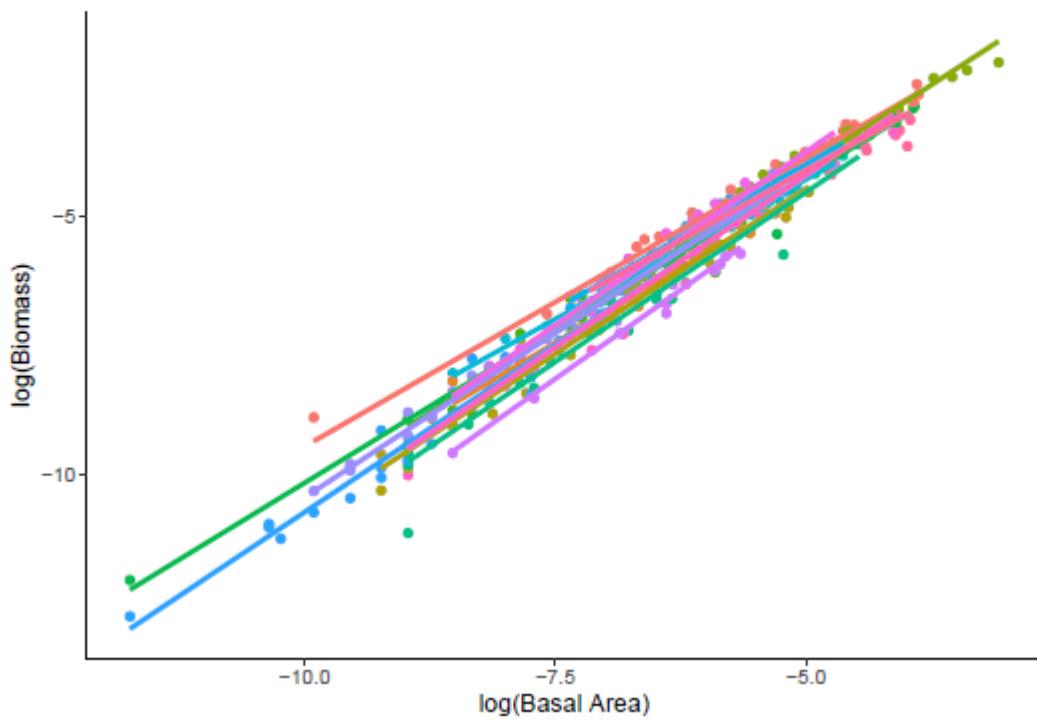
Tree species-specific allometric relationship

```
## `geom_smooth()` using formula 'y ~ x'
```



Tree species-specific allometric relationship log - log transformed

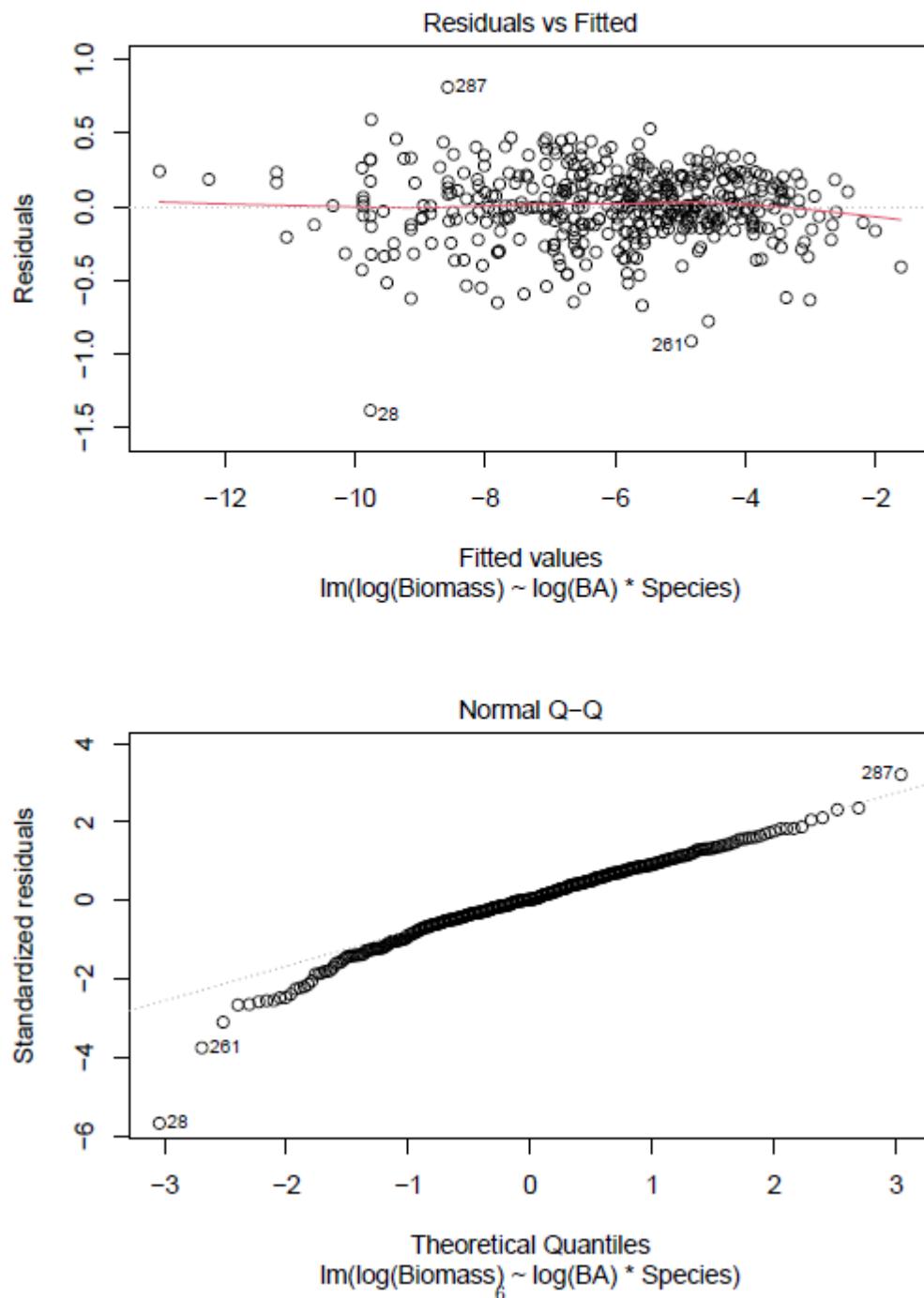
```
## `geom_smooth()` using formula 'y ~ x'
```

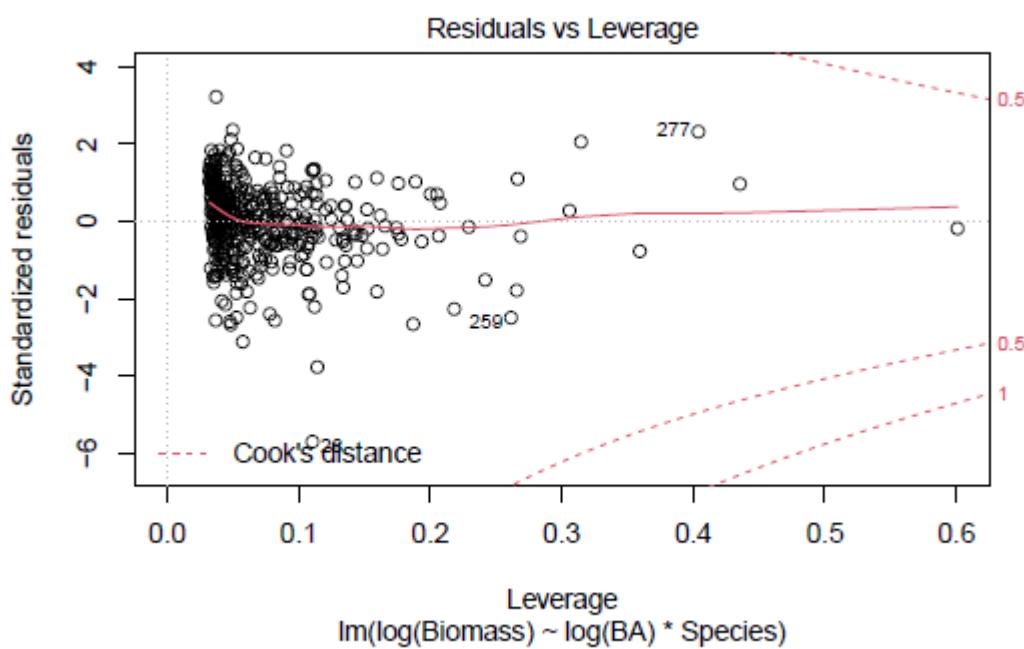
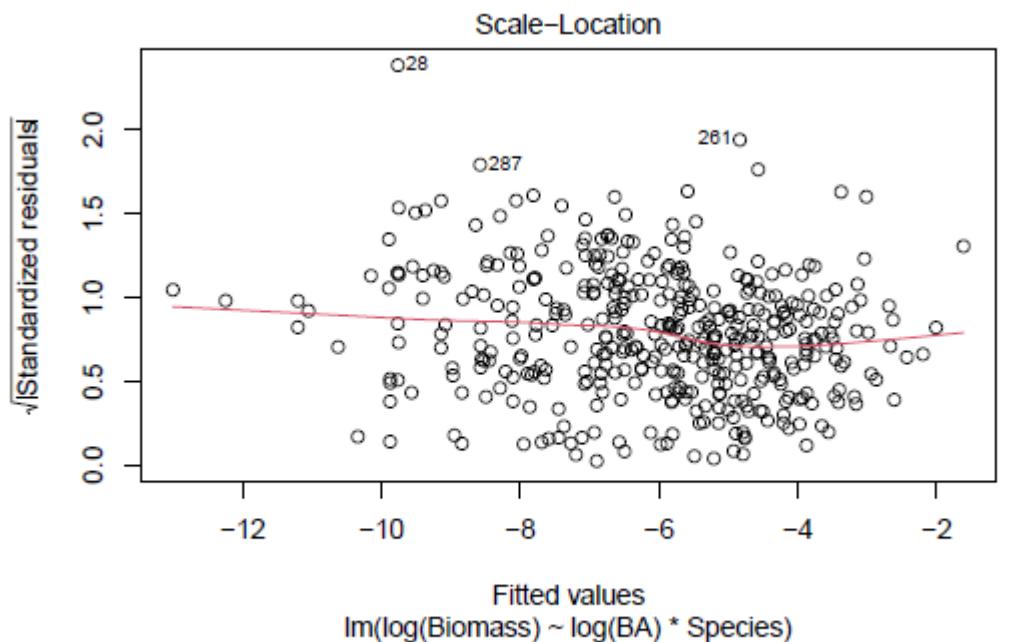


Model summary

	Estimate	Std Error	t-value	p-value
(Intercept)	1.736	0.220	7.904	0.000
log(BA)	1.120	0.037	29.895	0.000
SpeciesCastanopsis eyrei	-0.505	0.534	-0.946	0.345
SpeciesCastanopsis fargesii	-0.694	0.263	-2.641	0.009
SpeciesCastanopsis sclerophylla	0.196	0.345	0.566	0.571
SpeciesChoerospondias axillaris	0.540	0.300	1.802	0.072
SpeciesCyclobalanopsis glauca	0.321	0.424	0.757	0.449
SpeciesCyclobalanopsis myrsinaefolia	-0.018	0.294	-0.061	0.952
SpeciesKoelreuteria bipinnata	0.309	0.353	0.875	0.382
SpeciesLiquidambar formosana	0.556	0.423	1.315	0.189
SpeciesLithocarpus glaber	-0.613	0.394	-1.556	0.120
SpeciesNyssa sinensis	-0.127	0.523	-0.243	0.808
SpeciesQuercus fabri	0.510	0.390	1.307	0.192
SpeciesQuercus serrata	0.571	0.384	1.486	0.138
SpeciesRhus chinensis	0.445	0.652	0.683	0.495
SpeciesSapindus mukorossi	1.237	0.414	2.991	0.003
SpeciesSapium sebiferum	0.743	0.384	1.933	0.054
SpeciesSchima superba	-0.418	0.363	-1.151	0.250
log(BA):SpeciesCastanopsis eyrei	0.038	0.081	0.470	0.639
log(BA):SpeciesCastanopsis sclerophylla	0.160	0.054	2.977	0.003
log(BA):SpeciesChoerospondias axillaris	0.142	0.053	2.664	0.008
log(BA):SpeciesCyclobalanopsis glauca	0.121	0.064	1.894	0.059
log(BA):SpeciesCyclobalanopsis myrsinaefolia	0.069	0.048	1.435	0.152
log(BA):SpeciesKoelreuteria bipinnata	0.196	0.054	3.662	0.000
log(BA):SpeciesLiquidambar formosana	0.148	0.070	2.122	0.034
log(BA):SpeciesLithocarpus glaber	-0.038	0.065	-0.577	0.564
log(BA):SpeciesNyssa sinensis	0.002	0.092	0.019	0.985
log(BA):SpeciesQuercus fabri	0.178	0.053	3.356	0.001
log(BA):SpeciesQuercus serrata	0.156	0.054	2.888	0.004
log(BA):SpeciesRhus chinensis	0.258	0.100	2.568	0.011
log(BA):SpeciesSapindus mukorossi	0.225	0.064	3.504	0.001
log(BA):SpeciesSapium sebiferum	0.216	0.060	3.592	0.000
log(BA):SpeciesSchima superba	-0.035	0.068	-0.510	0.611

Model fit





Supplementary material III – S5: variables

A. List of variables

Variables	Code	Unit	Calculation	Hypothesis
<i>Tree variables</i>				
Plot diversity level	Diversity_level	none	Treatment	①②③
Forest vertical stratification	ENL	none	Calculated from laser scanning measurements (Perles-Garcia et al. 2021 <i>under review</i>)	①②③
Diameter at Breast Height	DBH	m	Measured	○
Basal Area	BA	m^2	$BA = \frac{(DBH)^2}{4\pi}$	○
TSP biomass	TSP _{biomass}	m^2	Calculated from BA (Appendix S4)	①②③
Surrounding trees biomass	tree _{biomass}	m^2	Calculated from BA (Appendix S4)	①②③
Specific Root Length	SRL	$m.g^{-1}$	Measured	○
Root Diameter	RD	m	Measured	○
Fungal association	AM or EM	none	Estimated from literature	○
Root diameter community weighted mean at TSP level	TSP _{CWM RD}	m	$TSP CWM RD = \sum_{i \in TSP species} \frac{RD_i \times BA_i}{TSP_{biomass}}$	①②③
Specific root length community weighted mean at TSP level	TSP _{CWM SRL}	$m.g^{-1}$	$TSP CWM SRL = \sum_{i \in TSP species} \frac{SRL_i \times BA_i}{TSP_{biomass}}$	①②③
Fugal association ratio at TSP level	TSP _{AM/EM}	none	$TSP \frac{AM}{EM} = \sum_{i \in TSP species} \frac{a_i \times BA_i}{TSP_{biomass}}$ $a_i = -1 \text{ or } 1 \text{ if EM or AM association}$	①②③
Root Diameter community weighted mean at neighborhood level	CWM _{RD}	m	$CWM RD = \sum_{i \in species} \frac{RD_i \times BA_i}{tree_{biomass}}$	①②③
Specific Root Length community weighted mean at neighborhood level	CWM _{SRL}	$m.g^{-1}$	$CWM SRL = \sum_{i \in species} \frac{SRL_i \times BA_i}{tree_{biomass}}$	①②③
Fugal association ratio at neighborhood level	AM/EM	none	$TSP \frac{AM}{EM} = \sum_{i \in species} \frac{a_i \times BA_i}{tree_{biomass}}$ $a_i = -1 \text{ or } 1 \text{ if EM or AM association}$	①②③
Root diameter functional richness at TSP level	TSP _{FRic RD}	m	$TPS FRic RD = f(RD)_{TSP}, \text{‘FD’ package}$	①②③
Specific root length functional richness at TSP level	TSP _{FRic SRL}	$m.g^{-1}$	$TPS FRic SRL = f(SRL)_{TSP}, \text{‘FD’ package}$	①②③
Root diameter functional	FDis _{RD}	m	$FDis RD = f(RD, BA), \text{‘FD’ package}$	①②③

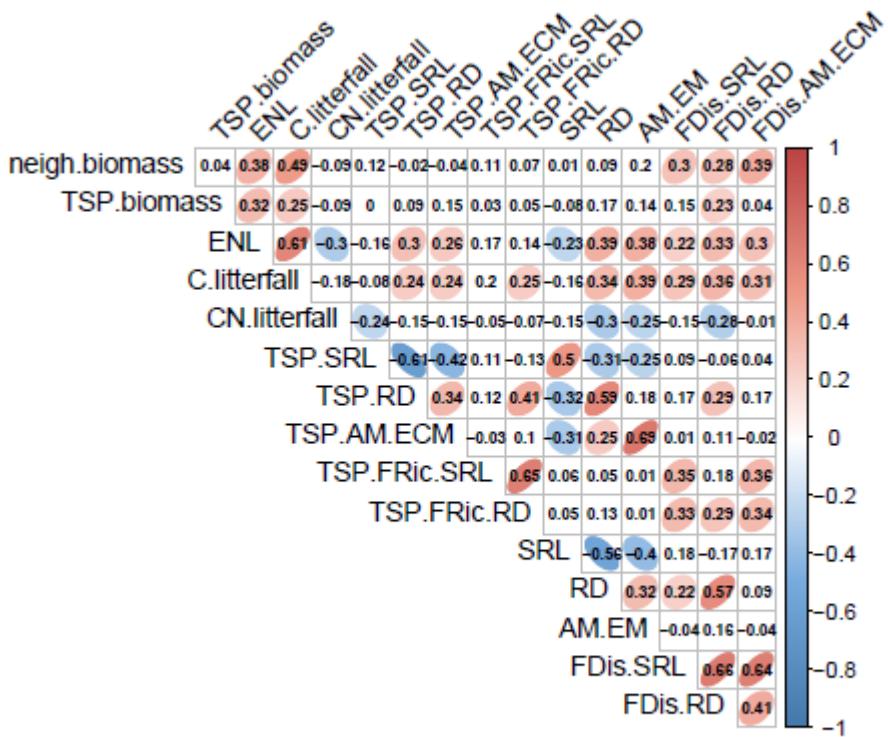
dissimilarity at neighborhood level				
Specific root length functional dissimilarity at neighborhood level	FDis _{SRL}	m.g ⁻¹	$FDis\ SRL = f(SRL, BA)$, 'FD' package	① ② ③
Specific root length functional dissimilarity at neighborhood level	FDis _{AM/EM}	none	$FDis\frac{AM}{EM} = f(\frac{AM}{EM}, BA)$, 'FD' package	① ② ③
Tree community root functional dissimilarity	FDis	none	$FDis = f(\frac{AM}{EM}, RD, SRL, BA)$, 'FD' package	① ② ③
Leaf carbon content	[C] _{leaf}	g.g ⁻¹	Measured	○
Leaf nitrogen content	[N] _{leaf}	g.g ⁻¹	Measured	○
Annual litter productivity	m _{litterfall}	g	Measured	○
Annual litter carbon deposition	C _{litterfall}	g	$C_{litterfall} = m_{litterfall} \times [C]_{leaf}$	① ② ③
Annual litter nitrogen deposition	N _{litterfall}	g	$N_{litterfall} = m_{litterfall} \times [N]_{leaf}$	① ② ③
Soil microbial community				
Soil microbial biomass	mic.bio	mg.g ⁻¹	Measured	② ② ③ ③
MICRO-ENVIRONMENTAL VARIABLES				
<i>Biotic environmental variables</i>				
Litter abundance observed on the ground	Litter.ab	none	Estimated	③
Litter carbon content	[C] _{litter}	g.g ⁻¹	Measured	③
Litter nitrogen content	[N] _{litter}	g.g ⁻¹	Measured	③
Root biomass	root.bioma ss	g.m ⁻³	Measured from soil cores	③
Understory plant abundance	plant.ab	none	Estimated	③
<i>Soil chemistry variables</i>				
Soil carbon stock 2010	Soil _C ²⁰¹⁰	g.g ⁻¹	Measured	① ② ③
Soil carbon stock 2018	Soil _C ²⁰¹⁸	g.g ⁻¹	Measured	① ② ③
Soil nitrogen content in 2018	TN	g.g ⁻¹	Measured	③
Soil phosphorus content in 2018	TP	g.g ⁻¹	Measured	③
Soil C:N ratio	C:N	none	$C:N = \frac{Soil_C^{2018}}{TN}$	③
Soil C:P ratio	C:P	none	$C:P = \frac{Soil_C^{2018}}{TP}$	③
<i>Micro-climatic variables</i>				
Soil water content	RH	g.g ⁻¹	Measured	③
Minimum, average and maximum air temperature of the sampling day and T.min.wee	T.min, T.mean, T.max, T.min.wee	°C	Estimated from climatic models (Supplementary S2)	○

week before sampling	k, T.mean.week, T.max.week			
Temperature conditions	Temperature	none	First PCA axis of climatic variables	(3)
<i>Plot topography</i>				
Slope	Slope	°	Design (Scholten <i>et al.</i> 2017)	(1) (2) (3)
Plan curvature	Curv. PL	°	Design (Scholten <i>et al.</i> 2017)	(1) (2) (3)
Profile curvature	Curv. PR	°	Design (Scholten <i>et al.</i> 2017)	(1) (2) (3)
Altitude	Altitude	m	Design (Scholten <i>et al.</i> 2017)	(1) (2) (3)

B. Hypotheses

Hypothesis	Response variable	Explanatory variable
H1	$Soil_C^{2018}$	$Soil_C^{2010}$, TSP _{biomass} , tree _{biomass} , C _{litterfall} , N _{litterfall} , TSP _{CWM RD} , TSP _{CWM SRL} , TSP _{AM/EM} , TSP _{FRic RD} , TSP _{FRic SRL} , CWM _{RD} , CWM _{SRL} , AM/EM, FDis _{RD} , FDis _{SRL} , FDis _{AM/EM} , FDis
H2.1	$Soil_C^{2018}$	mic.bio
H2.2	<i>mic. bio</i>	$Soil_C^{2010}$, TSP _{biomass} , tree _{biomass} , C _{litterfall} , N _{litterfall} , TSP _{CWM RD} , TSP _{CWM SRL} , TSP _{AM/EM} , TSP _{FRic RD} , TSP _{FRic SRL} , CWM _{RD} , CWM _{SRL} , AM/EM, FDis _{RD} , FDis _{SRL} , FDis _{AM/EM} , FDis
H3.1	<i>mic. bio</i>	<i>env. var</i> ∈ [Temperature, RH, TN, TP, C.N, C.P, root. biomass, plant. ab, litter. ab, [C] _{litter} , [N] _{litter}]
H3.2	<i>env. var</i> ∈ [RH, TN, TP, C.N, C.P, root. biomass, plant. ab, litter. ab, [C] _{litter} , [N] _{litter}]	$Soil_C^{2010}$, TSP _{biomass} , tree _{biomass} , C _{litterfall} , N _{litterfall} , TSP _{CWM RD} , TSP _{CWM SRL} , TSP _{AM/EM} , TSP _{FRic RD} , TSP _{FRic SRL} , CWM _{RD} , CWM _{SRL} , AM/EM, FDis _{RD} , FDis _{SRL} , FDis _{AM/EM} , FDis
	<i>Temperature</i>	TSP _{biomass} , tree _{biomass} , C _{litterfall} , N _{litterfall} ,

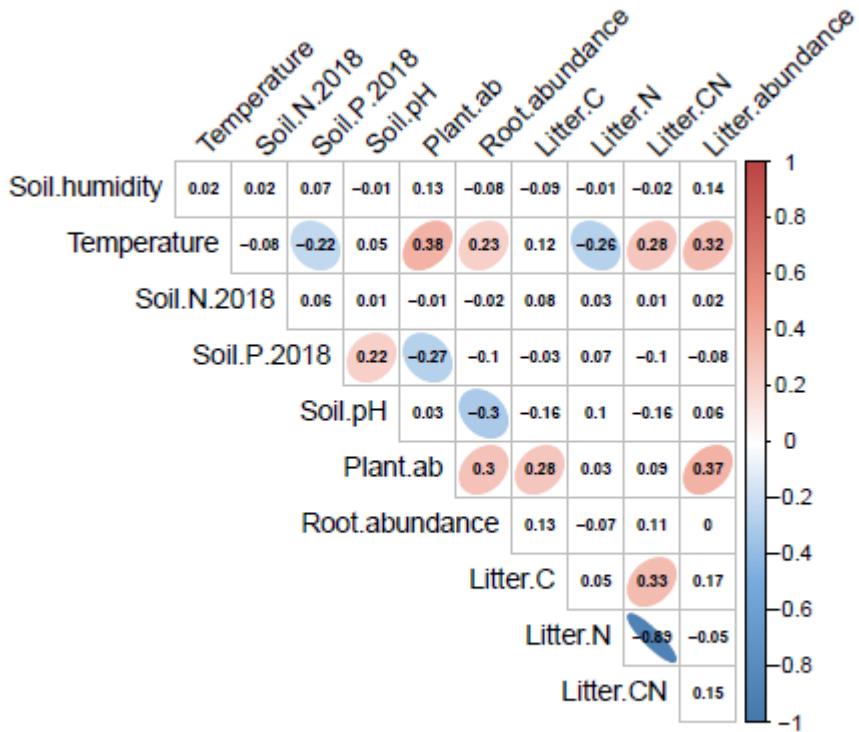
Supplementary material III – S6: correlation between traits



Correlation between root functional traits indices. Ellipses were only displayed when the correlation was significant, and, were sized, colored and oriented by correlation strength and direction.

Supplementary material III – S7: climate variables

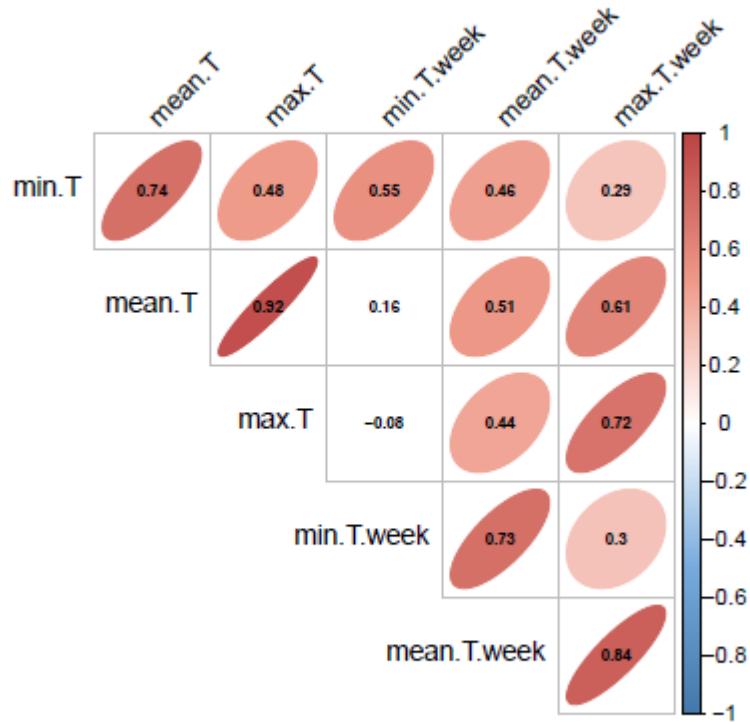
A. Correlation between micro-environmental variables



Correlation between micro-environmental variables. Ellipses were only displayed when the correlation was significant, and were sized, colored and oriented by correlation strength and direction.

B. Microclimate primary component analyses

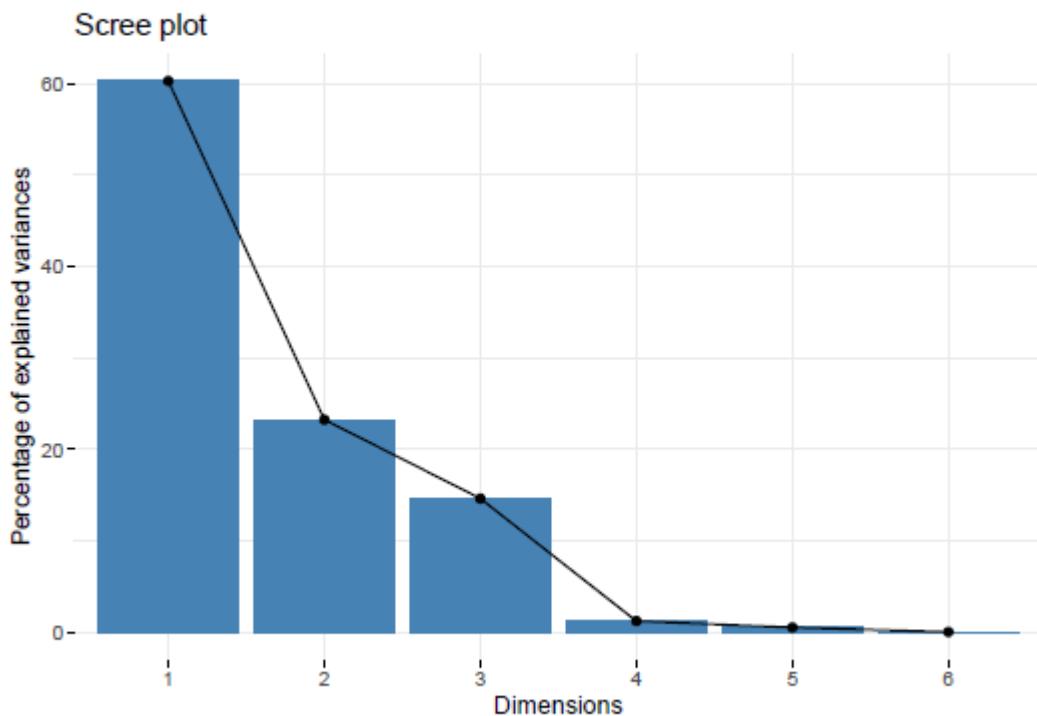
B.1. Correlation between micro-climatic variables



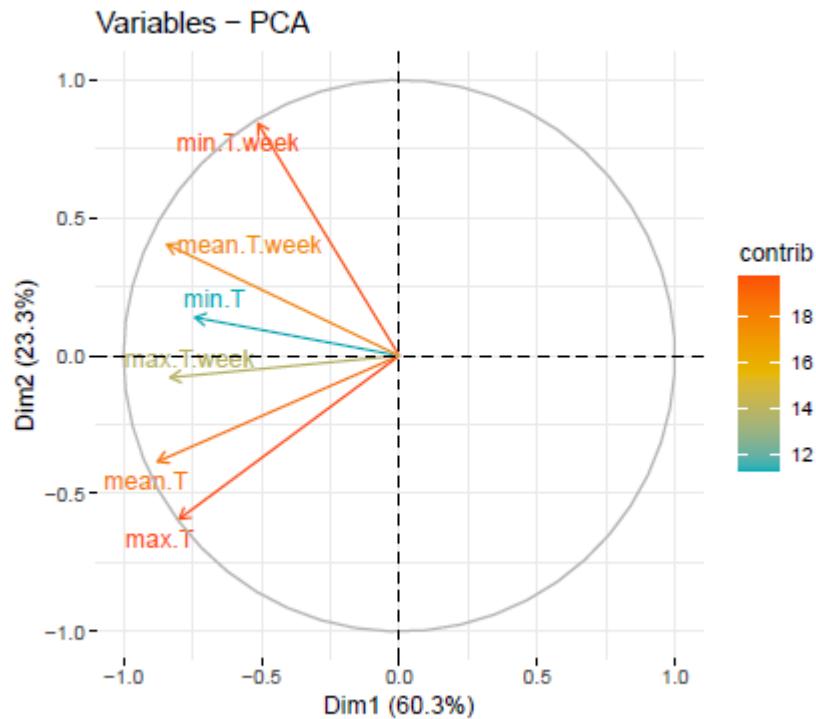
Correlation between micro-climatic variables. Ellipses were only displayed when the correlation was significant, and, were sized, colored and oriented by correlation strength and direction.

B.2. Primary component analysis of micro-climatic variables

B.2.1. PCA Scree plot



B.2.2. Micro-climatic variables projection on the two first axes of the PCA projection



Supplementary material III – S8: model assumptions

The assumptions of the linear models fitted in our analyses were tested using the “check_model” function from the R package performance.

Models Hypothesis H1

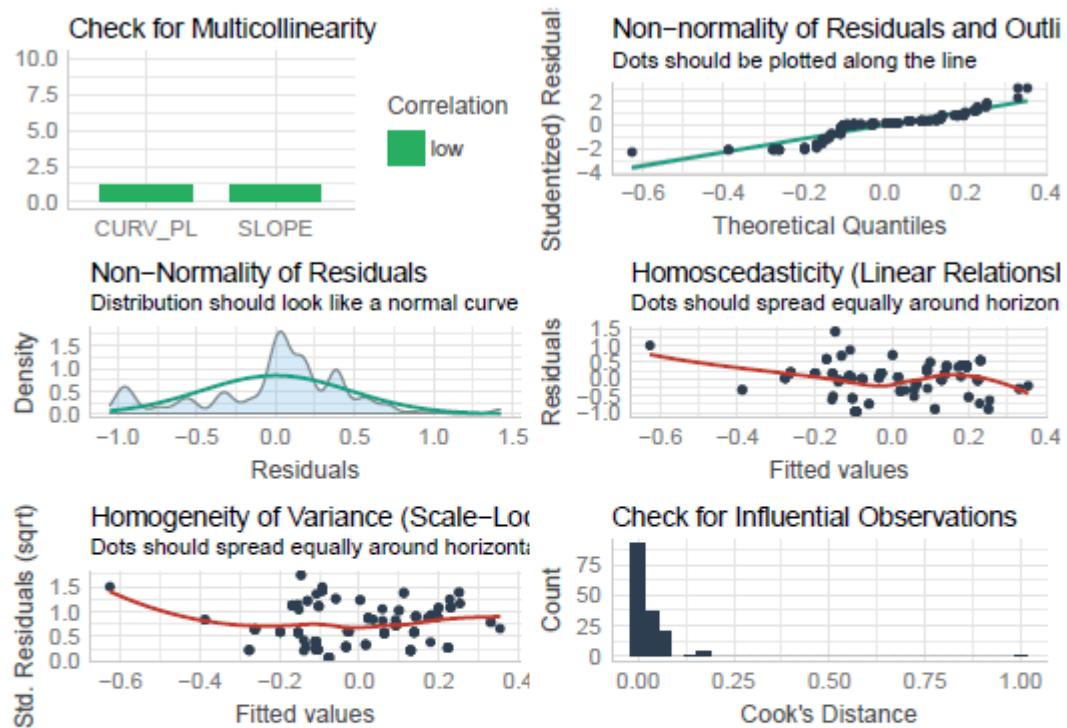
Soil historical carbon concentration model

Summary

	Estimate	Std Error	t-value	p-value
(Intercept)	0.000	0.038	0.000	1.000
CURV_PL	0.357	0.084	4.258	0.000
SLOPE	0.175	0.084	2.090	0.038

Model statistical hypotheses

```
## `geom_smooth()` using formula 'y ~ x'  
## `geom_smooth()` using formula 'y ~ x'  
## `geom_smooth()` using formula 'y ~ x'  
  
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```

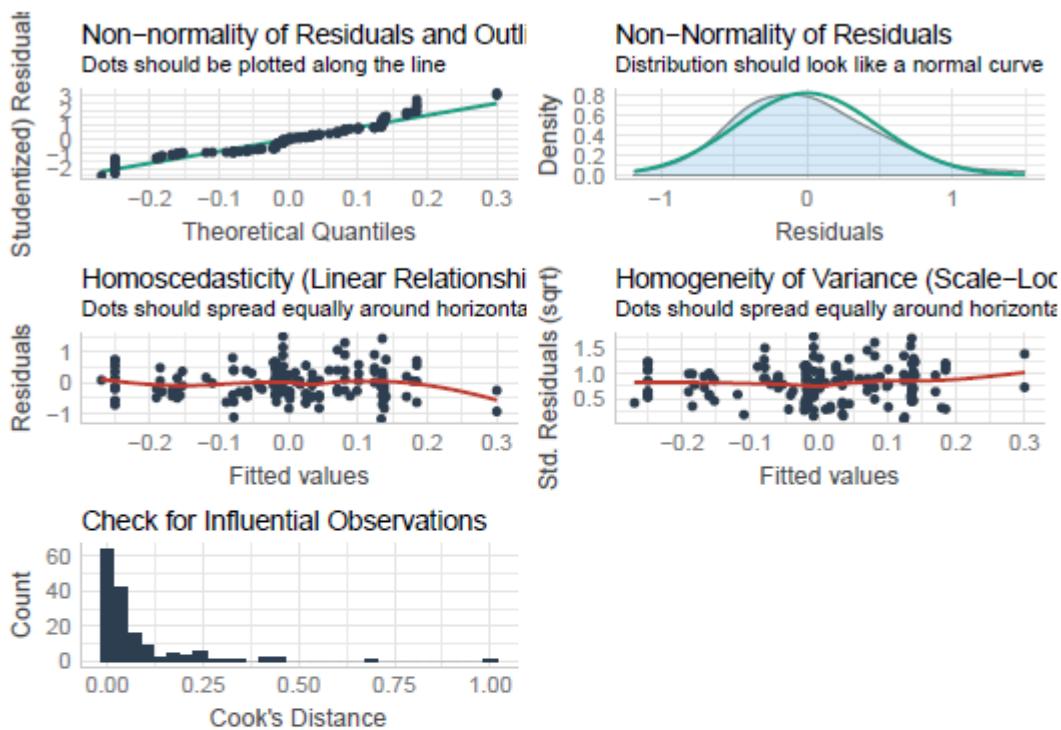


Tree diversity effects on carbon concentration model

Summary

	Estimate	Std Error	t-value	p-value
(Intercept)	0.000	0.039	0.00	1.000
Soil.C.2010	0.236	0.079	2.99	0.003

Model statistical hypotheses

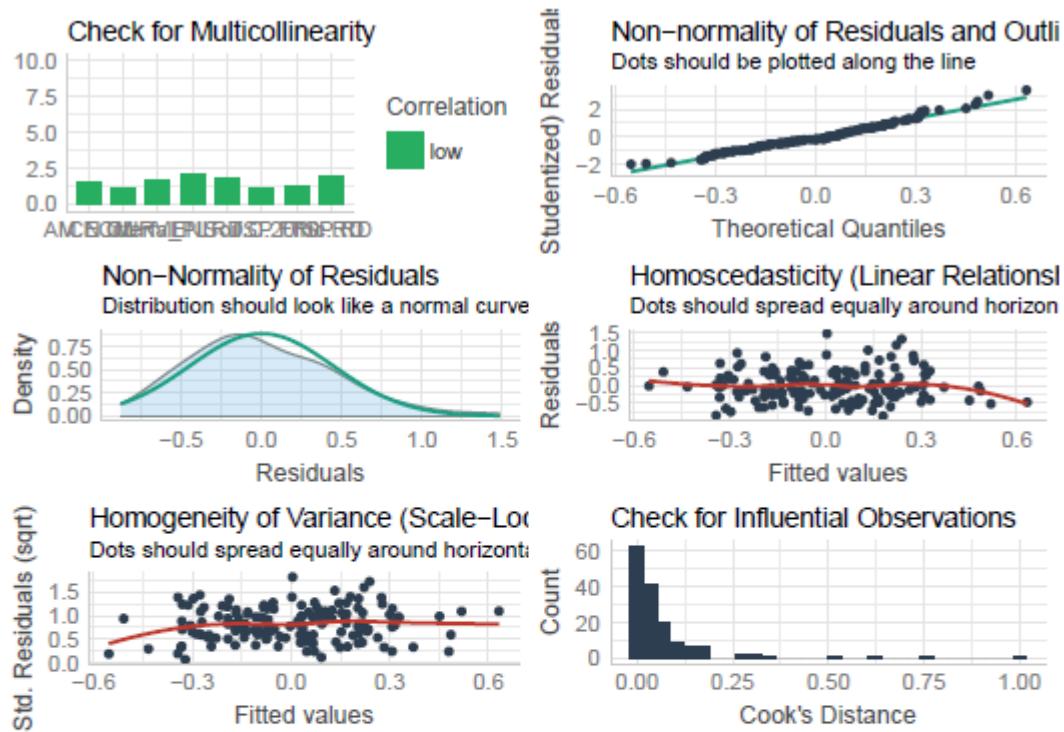


Tree functional traits effects on carbon concentration model

Summary

	Estimate	Std Error	t-value	p-value
(Intercept)	0.000	0.037	0.000	1.000
CURV_PL	0.236	0.095	2.482	0.014
CN.litterfall	-0.218	0.081	-2.701	0.008
ENL	0.344	0.106	3.228	0.002
TSP.RD	0.206	0.103	2.010	0.046
TSP.FRic.RD	-0.135	0.084	-1.613	0.109
RD	-0.286	0.101	-2.829	0.005
AM.ECM	-0.155	0.093	-1.659	0.099
Soil.C.2010	0.294	0.080	3.673	0.000

Model statistical hypotheses



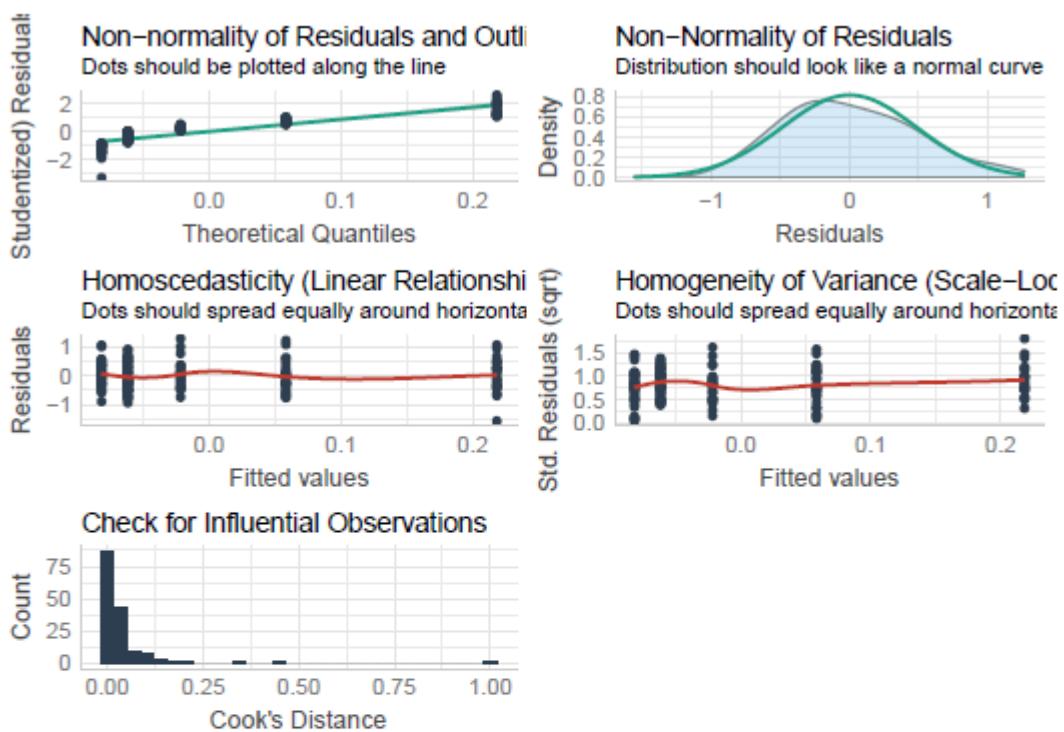
Models Hypothesis H2

Tree diversity effects on microbial biomass

Summary

	Estimate	Std Error	t-value	p-value
(Intercept)	0.000	0.040	0.000	1.000
Sp.rich	0.202	0.079	2.544	0.012

Model statistical hypotheses

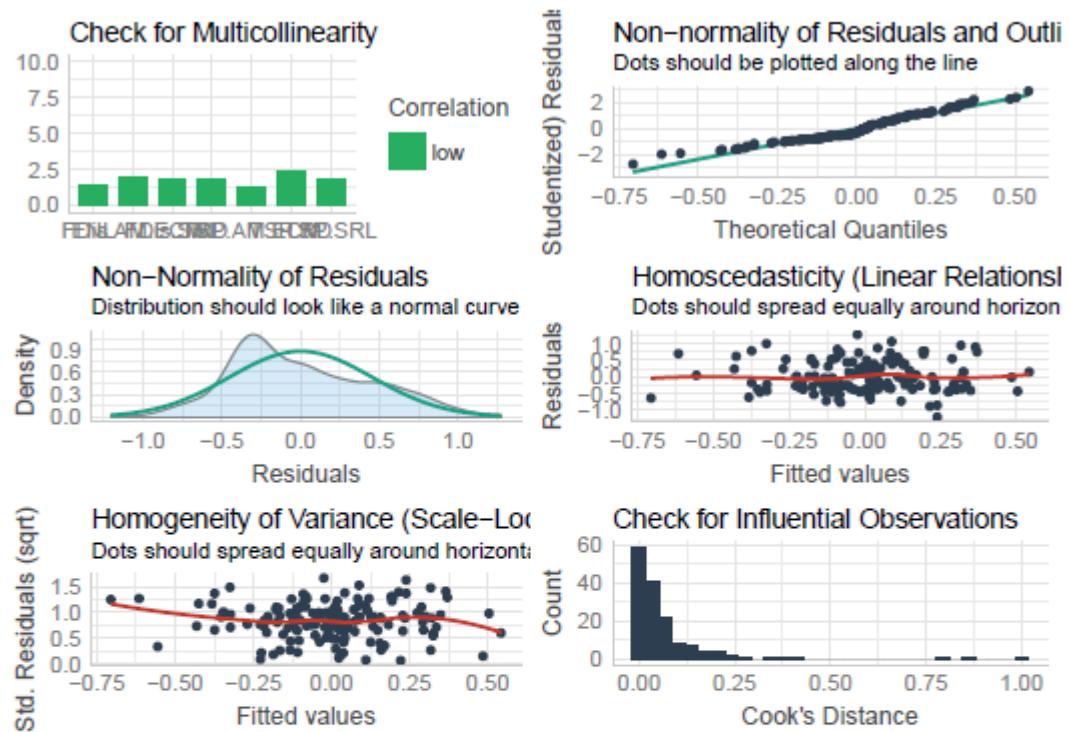


Tree functional traits effects on microbial biomass

Summary

	Estimate	Std Error	t-value	p-value
(Intercept)	0.000	0.037	0.000	1.000
ENL	0.177	0.087	2.037	0.043
TSP.SRL	0.223	0.103	2.176	0.031
TSP.RD	0.308	0.116	2.643	0.009
TSP.AM.ECM	-0.145	0.085	-1.695	0.092
FDis.SRL	-0.216	0.102	-2.124	0.035
FDis.AM.ECM	0.153	0.103	1.488	0.139
RD	-0.349	0.100	-3.494	0.001

Model statistical hypotheses



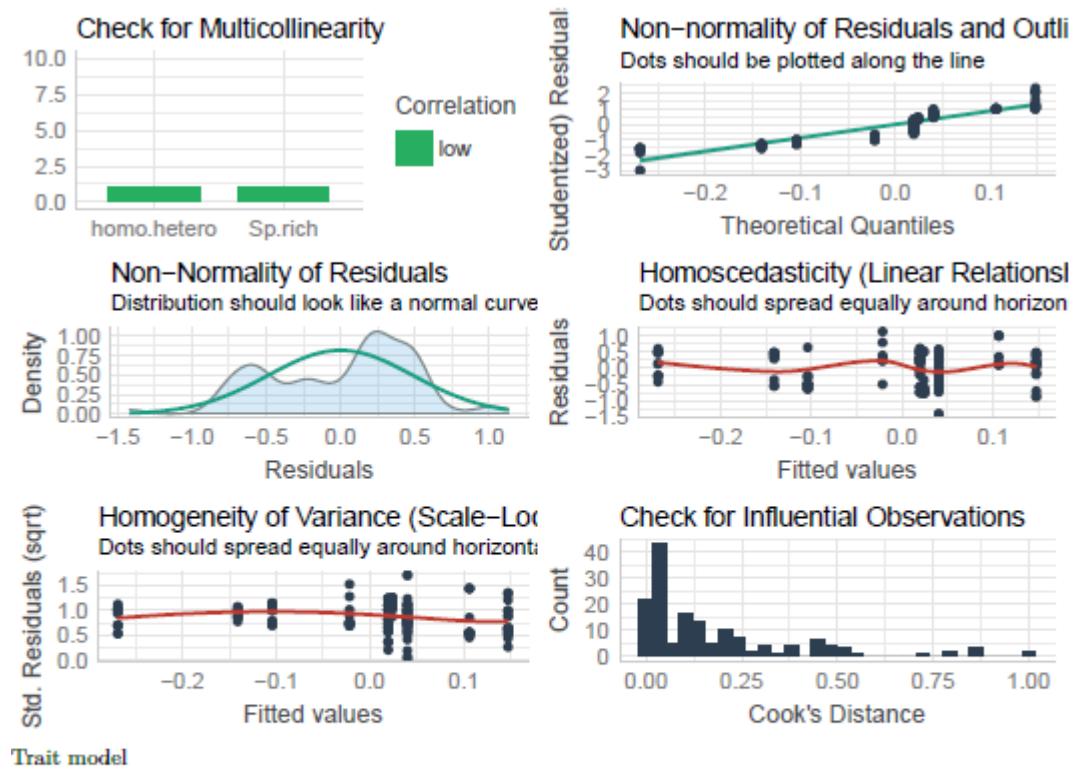
Models Hypothesis H3

Tree diversity and traits effects on environmental conditions

Temperature

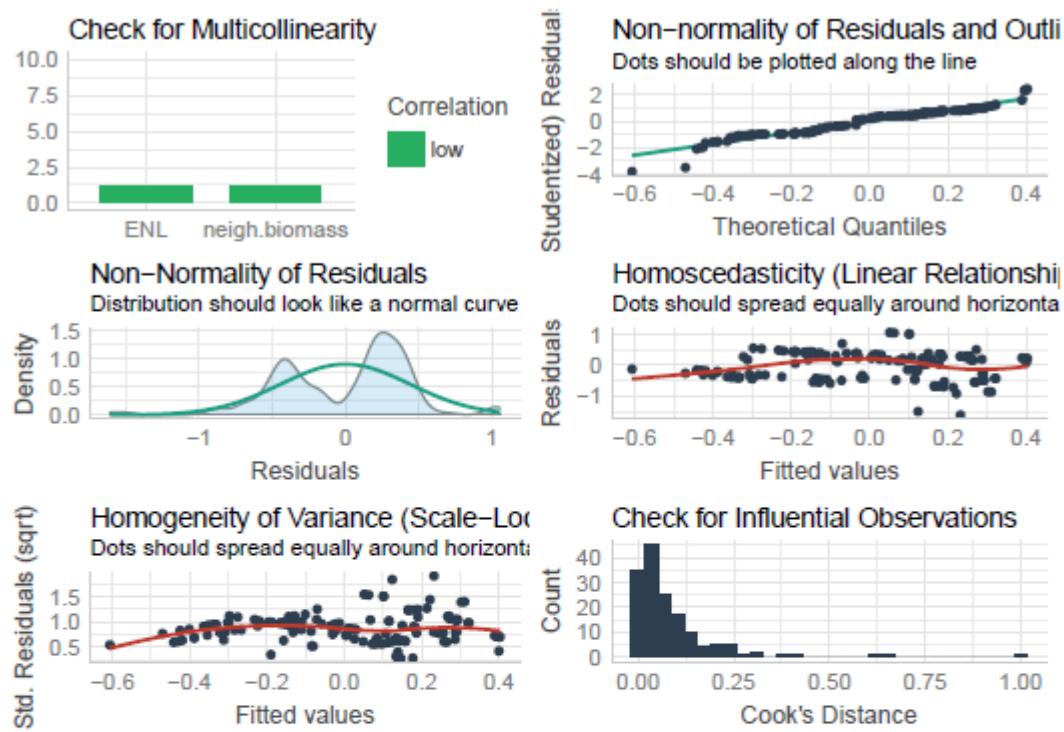
Species richness model

	Estimate	Std Error	t-value	p-value
(Intercept)	0.000	0.040	0.000	1.000
Sp.rich	-0.208	0.082	-2.534	0.012
homo.hetero	0.128	0.086	1.484	0.140



Trait model

	Estimate	Std Error	t-value	p-value
(Intercept)	0.000	0.036	0.000	1.000
neigh.biomass	-0.113	0.078	-1.452	0.149
ENL	-0.406	0.078	-5.207	0.000



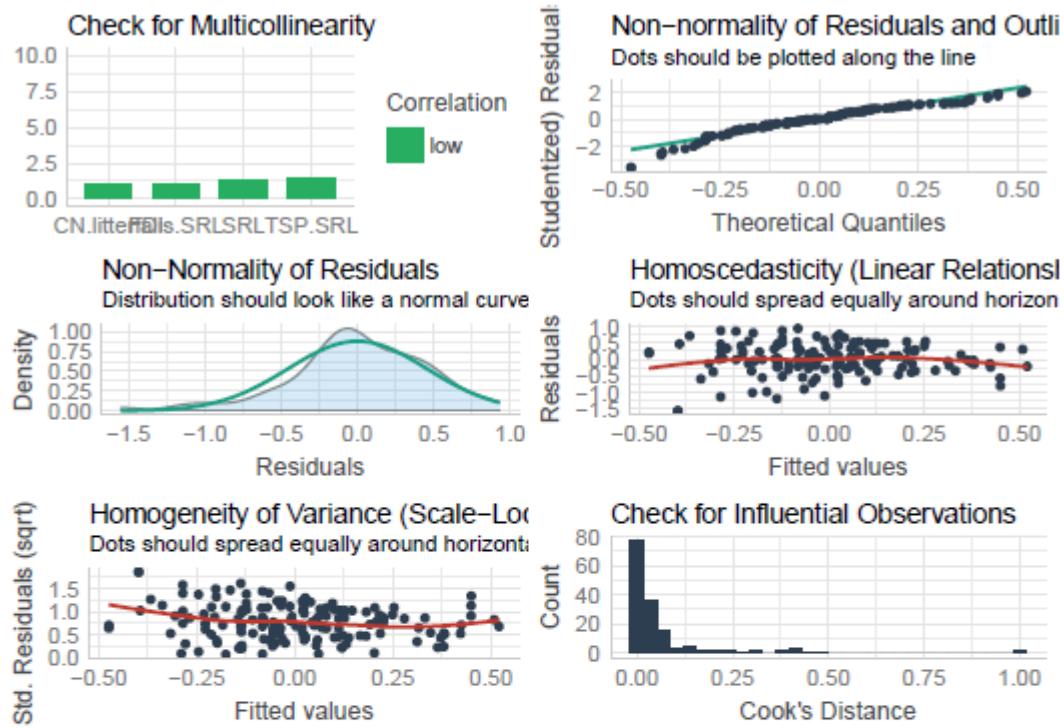
Soil relative humidity

Species richness model

(No variable selected)

Trait model

	Estimate	Std Error	t-value	p-value
(Intercept)	0.000	0.037	0.000	1.000
CN.litterfall	-0.247	0.077	-3.192	0.002
TSP.SRL	-0.290	0.088	-3.301	0.001
FDis.SRL	0.111	0.076	1.454	0.148
SRL	-0.145	0.087	-1.656	0.100



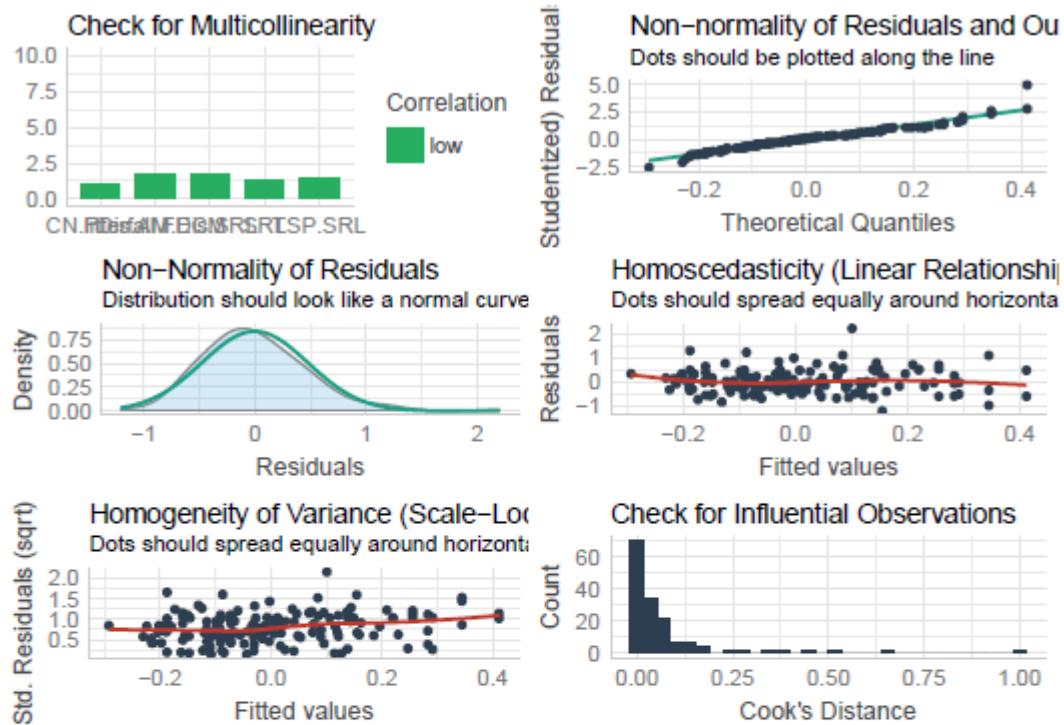
Soil nitrogen

Species richness model

(No variable selected)

Trait model

	Estimate	Std Error	t-value	p-value
(Intercept)	0.000	0.039	0.000	1.000
CN.litterfall	-0.189	0.082	-2.300	0.023
TSP.SRL	-0.135	0.093	-1.460	0.146
FDis.SRL	-0.253	0.104	-2.422	0.017
FDis.AM.ECM	0.149	0.104	1.442	0.151
SRL	0.214	0.092	2.318	0.022



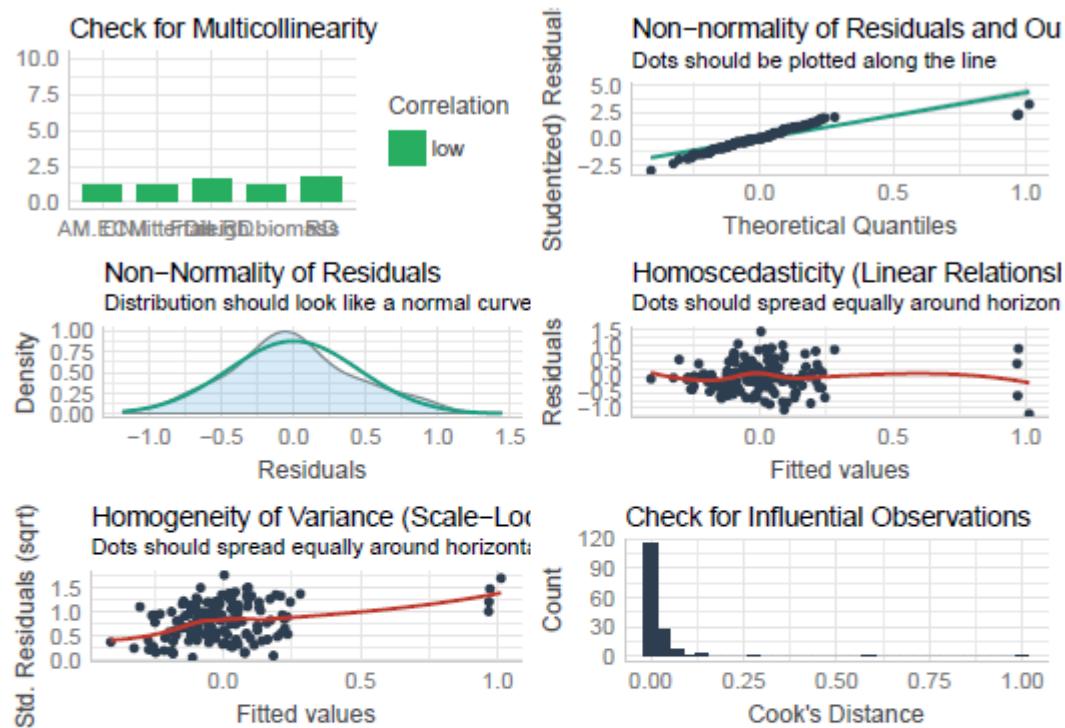
Soil phosphorus

Species richness model

(No variable selected)

Trait model

	Estimate	Std Error	t-value	p-value
(Intercept)	0.000	0.037	0.000	1.000
CN.litterfall	-0.186	0.080	-2.309	0.022
neigh.biomass	0.149	0.080	1.866	0.064
FDis.RD	-0.446	0.096	-4.622	0.000
RD	0.408	0.097	4.214	0.000
AM.ECM	-0.127	0.082	-1.552	0.123

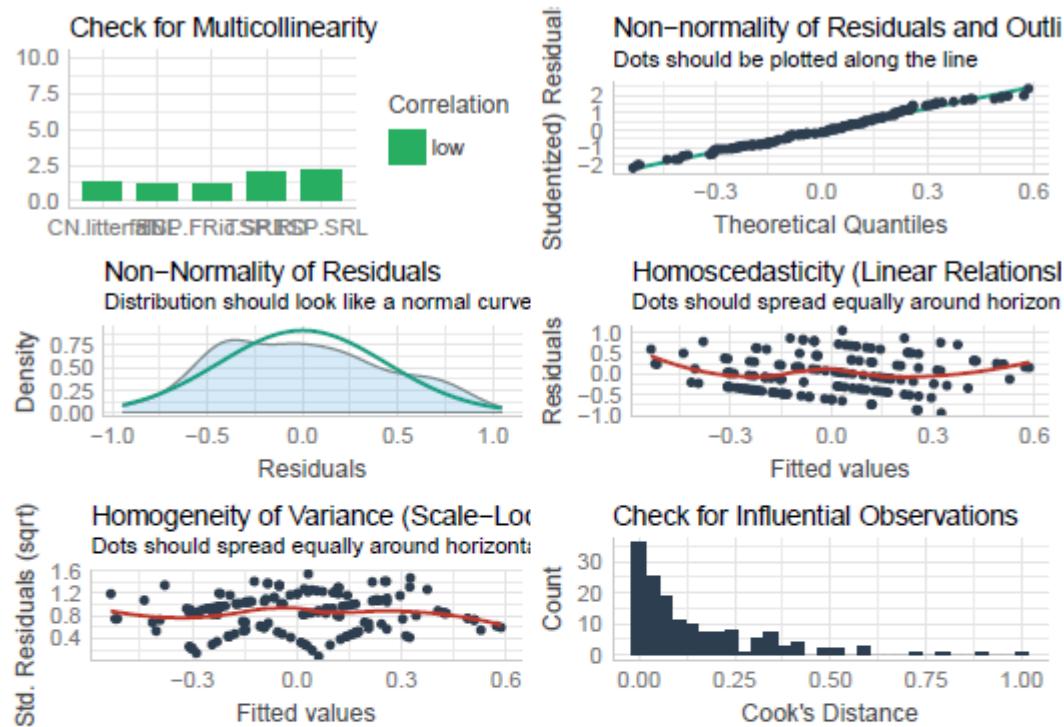


Plant abundance

Species richness model

	Estimate	Std Error	t-value	p-value
(Intercept)	0.000	0.040	0.000	1.000
Sp.rich	-0.129	0.083	-1.559	0.121
homo.hetero	0.135	0.087	1.545	0.124





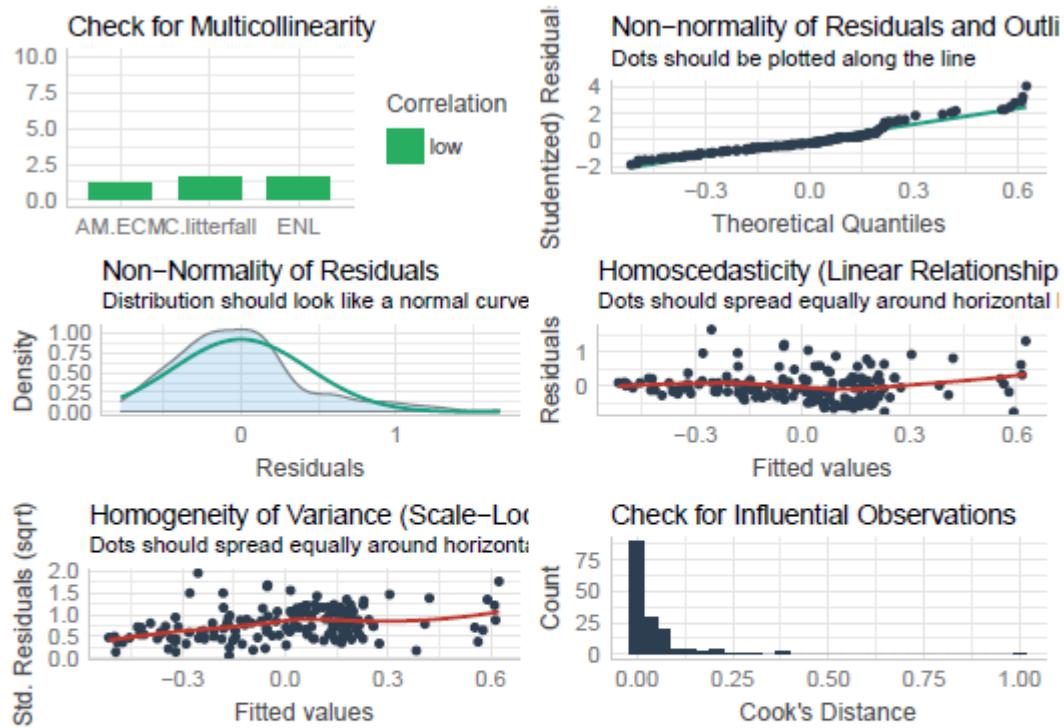
Root biomass

Species richness model

(No variable selected)

Trait model

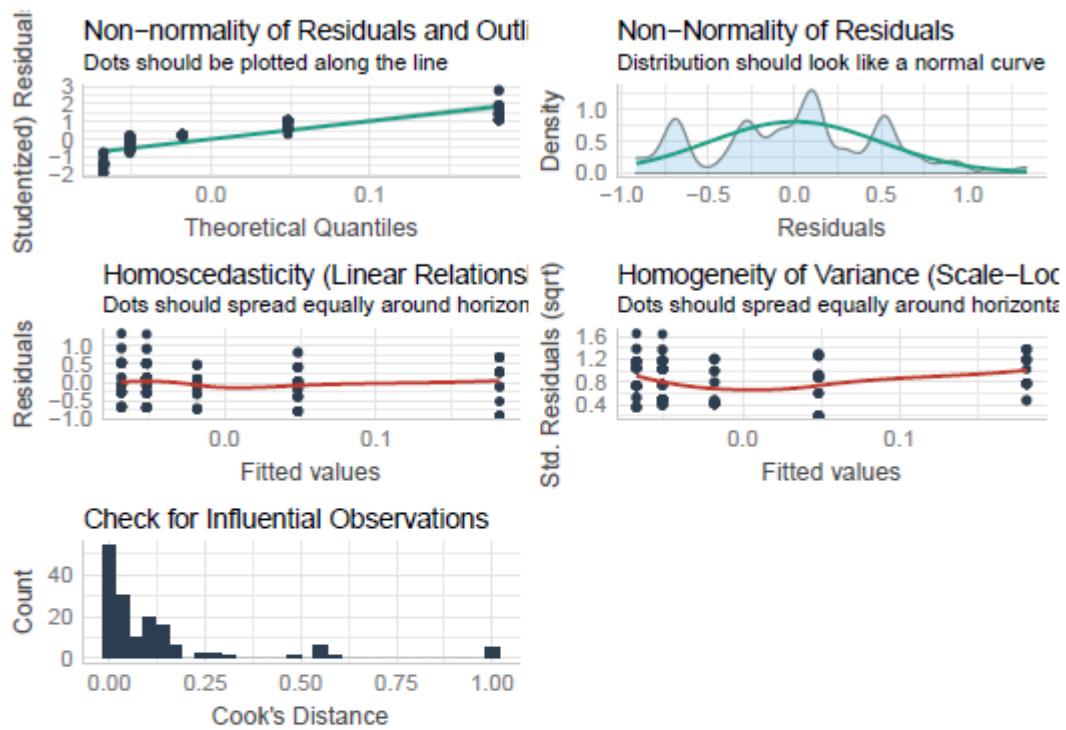
	Estimate	Std Error	t-value	p-value
(Intercept)	0.000	0.035	0.000	1.000
C.litterfall	-0.218	0.091	-2.393	0.018
ENL	-0.389	0.091	-4.275	0.000
AM.ECM	0.237	0.079	3.022	0.003



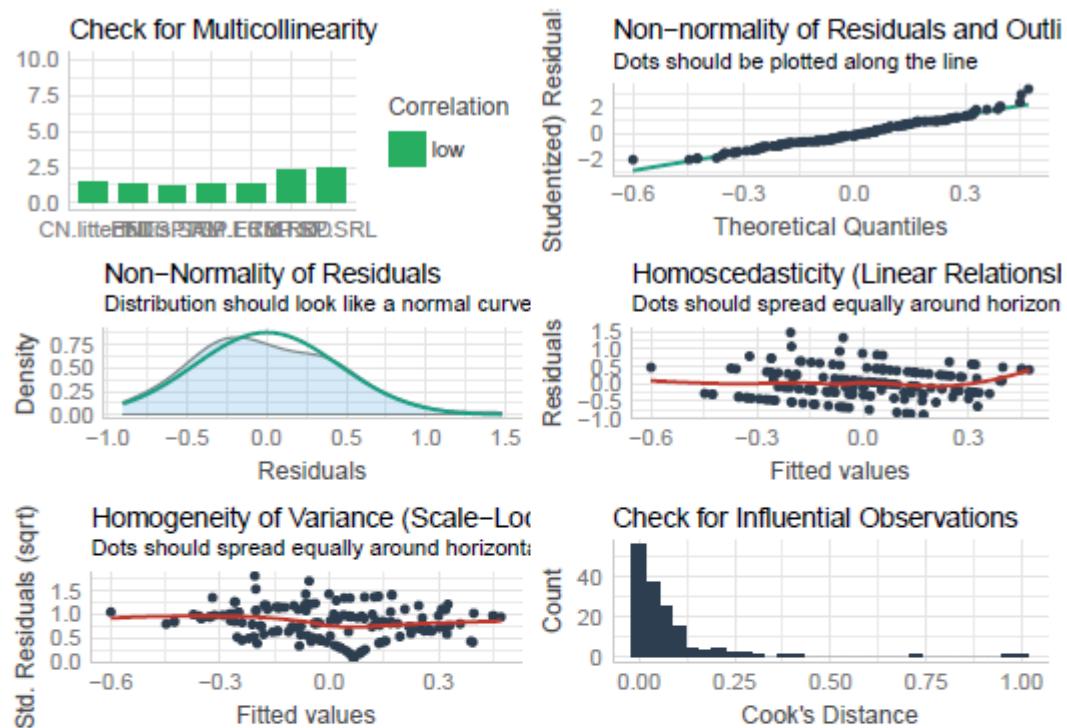
Litter abundance

Species richness model

	Estimate	Std Error	t-value	p-value
(Intercept)	0.000	0.04	0.000	1.000
Sp.rich	0.168	0.08	2.098	0.038



	Estimate	Std Error	t-value	p-value
(Intercept)	0.000	0.037	0.000	1.000
CN.litterfall	-0.153	0.090	-1.698	0.092
ENL	-0.294	0.084	-3.502	0.001
TSP.SRL	-0.365	0.116	-3.135	0.002
TSP.RD	-0.254	0.115	-2.206	0.029
TSP.AM.ECM	-0.205	0.087	-2.358	0.020
TSP.FRic.RD	0.120	0.087	1.391	0.166
FDis.SRL	0.217	0.083	2.620	0.010



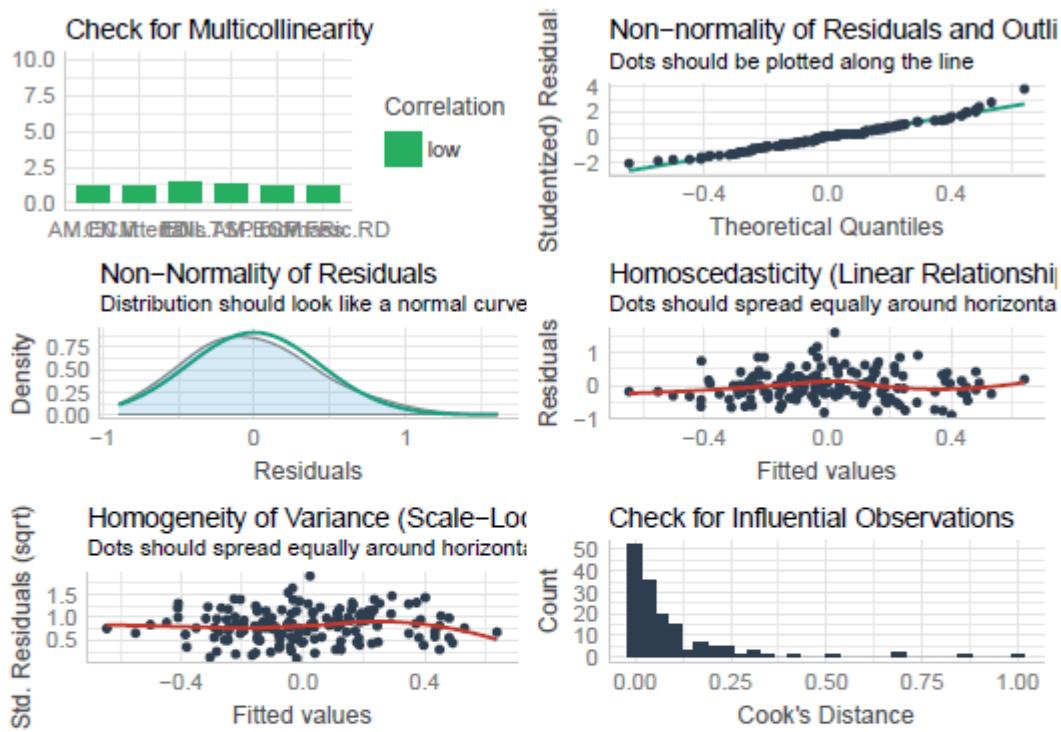
Litter CN

Species richness model

(No variable selected)

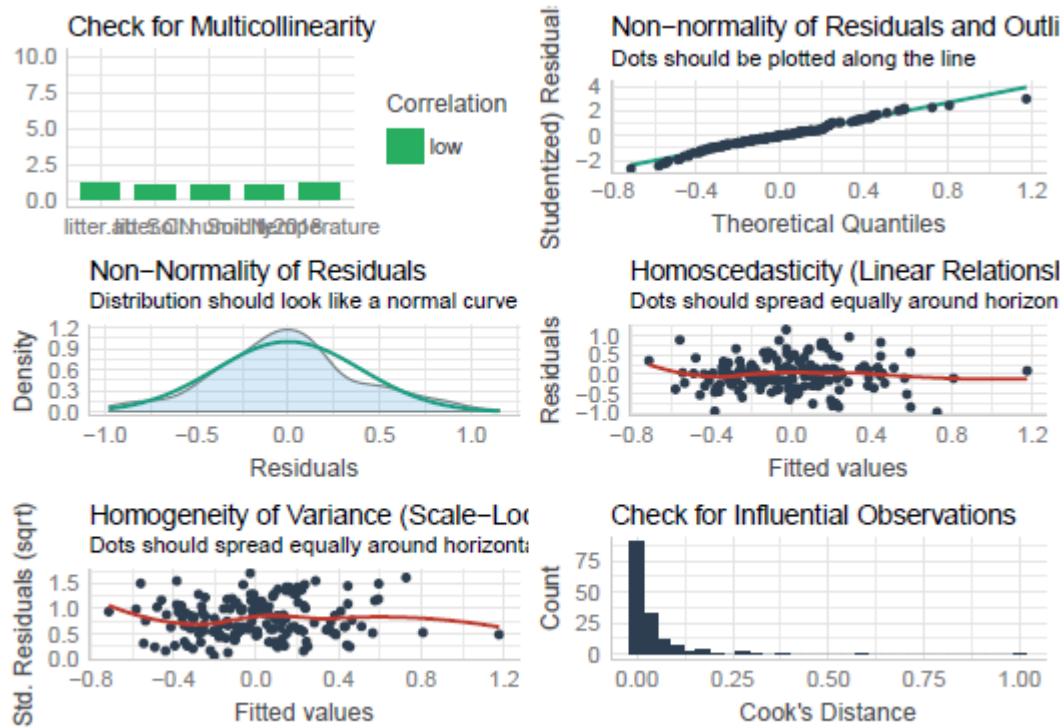
Trait model

	Estimate	Std Error	t-value	p-value
(Intercept)	0.000	0.036	0.000	1.000
CN.litterfall	0.233	0.077	3.046	0.003
TSP.biomass	-0.116	0.076	-1.523	0.130
ENL	-0.306	0.089	-3.440	0.001
TSP.FRic.RD	0.159	0.077	2.065	0.041
FDis.AM.ECM	0.133	0.081	1.641	0.103
A.M.ECM	0.369	0.080	4.612	0.000



Environmental effects on microbial biomass

	Estimate	Std Error	t-value	p-value
(Intercept)	0.000	0.033	0.000	1.000
Soil.humidity	-0.221	0.066	-3.334	0.001
temperature	-0.379	0.072	-5.282	0.000
Soil.N.2018	0.385	0.066	5.846	0.000
litter.CN	0.239	0.068	3.494	0.001
litter.ab	0.117	0.070	1.669	0.097



Supplementary material III – S9: hypothesis 1 – model and complete output

Model

```
model = '
Soil.C.2018 ~ Soil.C.2010 +
    CURV_PR +
    CN.litterfall + ENL +
    TSP.RD + RD

Soil.C.2010 ~ SLOPE + CURV_PL

ENL ~ Sp.rich + SLOPE + CURV_PL + CURV_PR
'
```

Results

Explained variance

Variable	R-squared (%)
Soil.C.2018	18.9
Soil.C.2010	10.8
ENL	34.5

Grouped summary

Relation	Effect size
Neighbors aboveground productivity & traits ~ Topography	0.5162866
Neighbors aboveground productivity & traits ~ Tree species richness	0.2479653
Neighbors aboveground productivity & traits ~~ Neighbors aboveground productivity & traits	0.1626817
Soil C 2010 ~ Topography	0.5325655
Soil C 2010 ~~ Soil C 2010	0.2215195
Soil C 2018 ~ Neighbors aboveground productivity & traits	0.4486591
Soil C 2018 ~ Neighbors root traits	0.2840925
Soil C 2018 ~ Soil C 2010	0.2632744
Soil C 2018 ~~ Soil C 2018	0.2063895

Full summary

Response	Operator	Explanatory	Estimate	SE	p-value
Soil.C.2018	~	Soil.C.2010	0.2632744	0.0767597	0.0006039
Soil.C.2018	~	CURV_PL	0.1635409	0.0873078	0.0610472
Soil.C.2018	~	CN.litterfall	-0.1999060	0.0771914	0.0096047
Soil.C.2018	~	ENL	0.2487531	0.0835579	0.0029107
Soil.C.2018	~	TSP.RD	0.1402681	0.0916951	0.1260854
Soil.C.2018	~	RD	-0.2840925	0.0949800	0.0027800
Soil.C.2010	~	SLOPE	0.1753615	0.0830657	0.0347621
Soil.C.2010	~	CURV_PL	0.3572040	0.0830657	0.0000171
ENL	~	Sp.rich	0.2479653	0.0687963	0.0003129
ENL	~	SLOPE	0.2151081	0.0723778	0.0029585
ENL	~	CURV_PL	-0.1897751	0.0971164	0.0506896
ENL	~	CURV_PR	0.3011785	0.1008265	0.0028164
Soil.C.2018	~~	Soil.C.2018	0.2063895	0.0235203	0.0000000
Soil.C.2010	~~	Soil.C.2010	0.2215195	0.0252445	0.0000000
ENL	~~	ENL	0.1626817	0.0185393	0.0000000
CURV_PL	~~	CURV_PL	0.2483766	0.0000000	NA
CURV_PL	~~	CN.litterfall	0.0176342	0.0000000	NA
CURV_PL	~~	TSP.RD	-0.0364343	0.0000000	NA
CURV_PL	~~	RD	-0.0332459	0.0000000	NA
CURV_PL	~~	SLOPE	-0.0995559	0.0000000	NA
CURV_PL	~~	Sp.rich	0.0228885	0.0000000	NA
CURV_PL	~~	CURV_PR	-0.1797195	0.0000000	NA
CN.litterfall	~~	CN.litterfall	0.2483766	0.0000000	NA
CN.litterfall	~~	TSP.RD	-0.0382589	0.0000000	NA
CN.litterfall	~~	RD	-0.0754086	0.0000000	NA
CN.litterfall	~~	SLOPE	0.0082185	0.0000000	NA
CN.litterfall	~~	Sp.rich	-0.0201507	0.0000000	NA
CN.litterfall	~~	CURV_PR	-0.0147584	0.0000000	NA
TSP.RD	~~	TSP.RD	0.2483766	0.0000000	NA
TSP.RD	~~	RD	0.1472590	0.0000000	NA
TSP.RD	~~	SLOPE	0.0013656	0.0000000	NA
TSP.RD	~~	Sp.rich	0.0031850	0.0000000	NA
TSP.RD	~~	CURV_PR	0.0277585	0.0000000	NA
RD	~~	RD	0.2483766	0.0000000	NA
RD	~~	SLOPE	0.0009270	0.0000000	NA
RD	~~	Sp.rich	0.0146583	0.0000000	NA
RD	~~	CURV_PR	0.0575185	0.0000000	NA
SLOPE	~~	SLOPE	0.2483766	0.0000000	NA
SLOPE	~~	Sp.rich	-0.0167863	0.0000000	NA
SLOPE	~~	CURV_PR	0.1002248	0.0000000	NA
Sp.rich	~~	Sp.rich	0.2483766	0.0000000	NA
Sp.rich	~~	CURV_PR	-0.0686821	0.0000000	NA
CURV_PR	~~	CURV_PR	0.2483766	0.0000000	NA

Supplementary material III – S10: hypothesis 2 – model and complete output

Model

```
model = '
Soil.C.2018 ~ Soil.C.2010 +
    CURV_PR +
    CN.litterfall + ENL +
    TSP.RD + RD + mic.bio

Soil.C.2010 ~ SLOPE + CURV_PL

ENL ~ Sp.rich + SLOPE + CURV_PL + CURV_PR

mic.bio ~ ENL + TSP.SRL + TSP.RD + FDis.SRL + RD + Soil.C.2018
'
```

Results

Explained variance

Variable	R-squared (%)
Soil.C.2018	28.9
Soil.C.2010	10.8
ENL	34.5
mic.bio	47.7

Grouped summary

Relation	Effect size
Mic. biomass ~ Neighbors root traits	0.2847093
Mic. biomass ~ Soil C 2018	0.5058328
Mic. biomass ~ TSP root traits	0.4384361
Mic. biomass ~~ Mic. biomass	0.1346658
Neighbors aboveground productivity & traits ~ Topography	0.5162879
Neighbors aboveground productivity & traits ~ Tree species richness	0.2479654
Neighbors aboveground productivity & traits ~~ Neighbors aboveground productivity & traits	0.1626817
Soil C 2010 ~ Topography	0.5325641
Soil C 2010 ~~ Soil C 2010	0.2215195
Soil C 2018 ~ Neighbors aboveground productivity & traits	0.4067151
Soil C 2018 ~ Soil C 2010	0.2474918
Soil C 2018 ~~ Soil C 2018	0.1807433

Full summary

Response	Operator	Explanatory	Estimate	SE	p-value
Soil.C.2018	~	Soil.C.2010	0.2474918	0.0770108	0.0013102
Soil.C.2018	~	CURV_PL	0.1434109	0.0833647	0.0853808
Soil.C.2018	~	CN.litterfall	-0.1886355	0.0801345	0.0185733
Soil.C.2018	~	ENL	0.2180795	0.0910763	0.0166444
Soil.C.2018	~	TSP.RD	0.1215180	0.0916470	0.1848610
Soil.C.2018	~	RD	-0.2336665	0.1279800	0.0678796
Soil.C.2018	~	mic.bio	0.1170902	0.2045576	0.5670461
Soil.C.2010	~	SLOPE	0.1753612	0.0830657	0.0347624
Soil.C.2010	~	CURV_PL	0.3572028	0.0830657	0.0000171
ENL	~	Sp.rich	0.2479654	0.0687963	0.0003129
ENL	~	SLOPE	0.2151080	0.0723778	0.0029585
ENL	~	CURV_PL	-0.1897739	0.0971164	0.0506911
ENL	~	CURV_PR	0.3011799	0.1008265	0.0028163
mic.bio	~	ENL	0.1037488	0.0636897	0.1033191
mic.bio	~	TSP.SRL	0.2098794	0.0797900	0.0085285
mic.bio	~	TSP.RD	0.2285567	0.0947419	0.0158473
mic.bio	~	FDis.SRL	-0.0949518	0.0629932	0.1317253
mic.bio	~	RD	-0.2847093	0.0819990	0.0005164
mic.bio	~	Soil.C.2018	0.5058328	0.1446843	0.0004721
Soil.C.2018	~~	Soil.C.2018	0.1807433	0.0447773	0.0000543
Soil.C.2010	~~	Soil.C.2010	0.2215195	0.0252445	0.0000000
ENL	~~	ENL	0.1626817	0.0185393	0.0000000
mic.bio	~~	mic.bio	0.1346658	0.0160947	0.0000000
CURV_PL	~~	CURV_PL	0.2483766	0.0000000	NA
CURV_PL	~~	CN.litterfall	0.0176342	0.0000000	NA
CURV_PL	~~	TSP.RD	-0.0364343	0.0000000	NA
CURV_PL	~~	RD	-0.0332459	0.0000000	NA
CURV_PL	~~	SLOPE	-0.0995559	0.0000000	NA
CURV_PL	~~	Sp.rich	0.0228885	0.0000000	NA
CURV_PL	~~	CURV_PR	-0.1797195	0.0000000	NA
CURV_PL	~~	TSP.SRL	0.0113570	0.0000000	NA
CURV_PL	~~	FDis.SRL	-0.0351465	0.0000000	NA
CN.litterfall	~~	CN.litterfall	0.2483766	0.0000000	NA
CN.litterfall	~~	TSP.RD	-0.0382589	0.0000000	NA
CN.litterfall	~~	RD	-0.0754086	0.0000000	NA
CN.litterfall	~~	SLOPE	0.0082185	0.0000000	NA
CN.litterfall	~~	Sp.rich	-0.0201507	0.0000000	NA
CN.litterfall	~~	CURV_PR	-0.0147584	0.0000000	NA
CN.litterfall	~~	TSP.SRL	-0.0594828	0.0000000	NA
CN.litterfall	~~	FDis.SRL	-0.0380842	0.0000000	NA
TSP.RD	~~	TSP.RD	0.2483766	0.0000000	NA
TSP.RD	~~	RD	0.1472590	0.0000000	NA
TSP.RD	~~	SLOPE	0.0013656	0.0000000	NA
TSP.RD	~~	Sp.rich	0.0031850	0.0000000	NA
TSP.RD	~~	CURV_PR	0.0277585	0.0000000	NA
TSP.RD	~~	TSP.SRL	-0.1526118	0.0000000	NA

(continued)

Response	Operator	Explanatory	Estimate	SE	p-value
TSP.RD	~~	FDis.SRL	0.0417814	0.0000000	NA
RD	~~	RD	0.2483766	0.0000000	NA
RD	~~	SLOPE	0.0009270	0.0000000	NA
RD	~~	Sp.rich	0.0146583	0.0000000	NA
RD	~~	CURV_PR	0.0575185	0.0000000	NA
RD	~~	TSP.SRL	-0.0763342	0.0000000	NA
RD	~~	FDis.SRL	0.0557553	0.0000000	NA
SLOPE	~~	SLOPE	0.2483766	0.0000000	NA
SLOPE	~~	Sp.rich	-0.0167863	0.0000000	NA
SLOPE	~~	CURV_PR	0.1002248	0.0000000	NA
SLOPE	~~	TSP.SRL	0.0101562	0.0000000	NA
SLOPE	~~	FDis.SRL	-0.0000568	0.0000000	NA
Sp.rich	~~	Sp.rich	0.2483766	0.0000000	NA
Sp.rich	~~	CURV_PR	-0.0686821	0.0000000	NA
Sp.rich	~~	TSP.SRL	0.0098234	0.0000000	NA
Sp.rich	~~	FDis.SRL	0.0794879	0.0000000	NA
CURV_PR	~~	CURV_PR	0.2483766	0.0000000	NA
CURV_PR	~~	TSP.SRL	-0.0123199	0.0000000	NA
CURV_PR	~~	FDis.SRL	-0.0095466	0.0000000	NA
TSP.SRL	~~	TSP.SRL	0.2483766	0.0000000	NA
TSP.SRL	~~	FDis.SRL	0.0212875	0.0000000	NA
FDis.SRL	~~	FDis.SRL	0.2483766	0.0000000	NA

Supplementary material III – S11: hypothesis 3 – model and complete output

Model

```
model = '
Soil.C.2018 ~ Soil.C.2010 +
    CURV_PR +
    CN.litterfall + ENL +
    TSP.RD + RD

Soil.C.2010 ~ SLOPE + CURV_PL

ENL ~ Sp.rich + SLOPE + CURV_PL + CURV_PR

mic.bio ~ ENL +
    TSP.SRL + TSP.RD + FDis.SRL + RD +
    Soil.C.2018 +
    temperature + Soil.humidity +
    Soil.N.2018 +
    litter.CN

temperature ~ ENL
Soil.humidity ~ CN.litterfall + TSP.SRL
Soil.N.2018 ~ CN.litterfall + FDis.SRL + SRL
litter.CN ~ CN.litterfall + ENL + TSP.FRic.RD + AM.ECM
'
```

Results

Explained variance

Variable	R-squared (%)
Soil.C.2018	18.9
Soil.C.2010	10.8
ENL	34.5
mic.bio	54.2
temperature	20.2
Soil.humidity	15.0
Soil.N.2018	6.3
litter.CN	26.1

Grouped summary

Relation	Effect size
Environment ~ Neighbors aboveground productivity & traits	1.2486435
Environment ~ Neighbors root traits	0.5059349
Environment ~ TSP root traits	0.5529788
Environment ~~ Environment	0.8391214
Mic. biomass ~ Environment	0.6101499
Mic. biomass ~ Neighbors root traits	0.1750829
Mic. biomass ~ Soil C 2018	0.5616956
Mic. biomass ~ TSP root traits	0.3851936
Mic. biomass ~~ Mic. biomass	0.1101626
Neighbors aboveground productivity & traits ~ Topography	0.5162855
Neighbors aboveground productivity & traits ~ Tree species richness	0.2479654
Neighbors aboveground productivity & traits ~~ Neighbors aboveground productivity & traits	0.1626816
Soil C 2010 ~ Topography	0.5325651
Soil C 2010 ~~ Soil C 2010	0.2215193
Soil C 2018 ~ Neighbors aboveground productivity & traits	0.4486605
Soil C 2018 ~ Neighbors root traits	0.2840931
Soil C 2018 ~ Soil C 2010	0.2632743
Soil C 2018 ~~ Soil C 2018	0.2063896

Full summary

Response	Operator	Explanatory	Estimate	SE	p-value
Soil.C.2018	~	Soil.C.2010	0.2632743	0.0767598	0.0006039
Soil.C.2018	~	CURV_PL	0.1635416	0.0873079	0.0610464
Soil.C.2018	~	CN.litterfall	-0.1999060	0.0771914	0.0096047
Soil.C.2018	~	ENL	0.2487545	0.0835580	0.0029106
Soil.C.2018	~	TSP.RD	0.1402688	0.0916951	0.1260836
Soil.C.2018	~	RD	-0.2840931	0.0949800	0.0027799
Soil.C.2010	~	SLOPE	0.1753616	0.0830657	0.0347620
Soil.C.2010	~	CURV_PL	0.3572036	0.0830657	0.0000171
ENL	~	Sp.rich	0.2479654	0.0687963	0.0003129
ENL	~	SLOPE	0.2151084	0.0723778	0.0029585
ENL	~	CURV_PL	-0.1897770	0.0971164	0.0506872
ENL	~	CURV_PR	0.3011770	0.1008265	0.0028165
mic.bio	~	ENL	-0.0058516	0.0638538	0.9269837
mic.bio	~	TSP.SRL	0.1962537	0.0728819	0.0070863
mic.bio	~	TSP.RD	0.1889399	0.0827128	0.0223546
mic.bio	~	FDis.SRL	-0.0425622	0.0571996	0.4568165
mic.bio	~	RD	-0.1750829	0.0691727	0.0113706
mic.bio	~	Soil.C.2018	0.5616956	0.0546386	0.0000000
mic.bio	~	temperature	-0.2864916	0.0600708	0.0000018
mic.bio	~	Soil.humidity	-0.1118651	0.0566677	0.0483756
mic.bio	~	Soil.N.2018	-0.0257387	0.0545010	0.6367402
mic.bio	~	litter.CN	0.2117932	0.0556415	0.0001410
temperature	~	ENL	-0.4492955	0.0719909	0.0000000
Soil.humidity	~	CN.litterfall	-0.2589748	0.0765287	0.0007143
Soil.humidity	~	TSP.SRL	-0.3562751	0.0765287	0.0000032
Soil.N.2018	~	CN.litterfall	-0.1512382	0.0795412	0.0572520
Soil.N.2018	~	FDis.SRL	-0.1530869	0.0799635	0.0555616
Soil.N.2018	~	SRL	0.1590020	0.0798791	0.0465322
litter.CN	~	CN.litterfall	0.2412895	0.0743530	0.0011737
litter.CN	~	ENL	-0.2990837	0.0720974	0.0000335
litter.CN	~	TSP.FRic.RD	0.1967037	0.0719495	0.0062586
litter.CN	~	AM.ECM	0.3469329	0.0742888	0.0000030
Soil.C.2018	~~	Soil.C.2018	0.2063896	0.0235203	0.0000000
Soil.C.2010	~~	Soil.C.2010	0.2215193	0.0252445	0.0000000
ENL	~~	ENL	0.1626816	0.0185393	0.0000000
mic.bio	~~	mic.bio	0.1101626	0.0125542	0.0000000
temperature	~~	temperature	0.1982378	0.0225913	0.0000000
Soil.humidity	~~	Soil.humidity	0.2111682	0.0240649	0.0000000
Soil.N.2018	~~	Soil.N.2018	0.2327641	0.0265259	0.0000000
litter.CN	~~	litter.CN	0.1969512	0.0224447	0.0000000
CURV_PL	~~	CURV_PL	0.2483766	0.0000000	NA
CURV_PL	~~	CN.litterfall	0.0176342	0.0000000	NA
CURV_PL	~~	TSP.RD	-0.0364343	0.0000000	NA
CURV_PL	~~	RD	-0.0332459	0.0000000	NA
CURV_PL	~~	SLOPE	-0.0995559	0.0000000	NA
CURV_PL	~~	Sp.rich	0.0228885	0.0000000	NA

(continued)

Response	Operator	Explanatory	Estimate	SE	p-value
CURV_PL	~~	CURV_PR	-0.1797195	0.0000000	NA
CURV_PL	~~	TSP.SRL	0.0113570	0.0000000	NA
CURV_PL	~~	FDis.SRL	-0.0351465	0.0000000	NA
CURV_PL	~~	SRL	0.0121095	0.0000000	NA
CURV_PL	~~	TSP.FRic.RD	-0.0020780	0.0000000	NA
CURV_PL	~~	AM.ECM	0.0430630	0.0000000	NA
CN.litterfall	~~	CN.litterfall	0.2483766	0.0000000	NA
CN.litterfall	~~	TSP.RD	-0.0382589	0.0000000	NA
CN.litterfall	~~	RD	-0.0754086	0.0000000	NA
CN.litterfall	~~	SLOPE	0.0082185	0.0000000	NA
CN.litterfall	~~	Sp.rich	-0.0201507	0.0000000	NA
CN.litterfall	~~	CURV_PR	-0.0147584	0.0000000	NA
CN.litterfall	~~	TSP.SRL	-0.0594828	0.0000000	NA
CN.litterfall	~~	FDis.SRL	-0.0380842	0.0000000	NA
CN.litterfall	~~	SRL	-0.0363731	0.0000000	NA
CN.litterfall	~~	TSP.FRic.RD	-0.0178646	0.0000000	NA
CN.litterfall	~~	AM.ECM	-0.0608569	0.0000000	NA
TSP.RD	~~	TSP.RD	0.2483766	0.0000000	NA
TSP.RD	~~	RD	0.1472590	0.0000000	NA
TSP.RD	~~	SLOPE	0.0013656	0.0000000	NA
TSP.RD	~~	Sp.rich	0.0031850	0.0000000	NA
TSP.RD	~~	CURV_PR	0.0277585	0.0000000	NA
TSP.RD	~~	TSP.SRL	-0.1526118	0.0000000	NA
TSP.RD	~~	FDis.SRL	0.0417814	0.0000000	NA
TSP.RD	~~	SRL	-0.0784069	0.0000000	NA
TSP.RD	~~	TSP.FRic.RD	0.1007104	0.0000000	NA
TSP.RD	~~	AM.ECM	0.0438371	0.0000000	NA
RD	~~	RD	0.2483766	0.0000000	NA
RD	~~	SLOPE	0.0009270	0.0000000	NA
RD	~~	Sp.rich	0.0146583	0.0000000	NA
RD	~~	CURV_PR	0.0575185	0.0000000	NA
RD	~~	TSP.SRL	-0.0763342	0.0000000	NA
RD	~~	FDis.SRL	0.0557553	0.0000000	NA
RD	~~	SRL	-0.1397787	0.0000000	NA
RD	~~	TSP.FRic.RD	0.0324377	0.0000000	NA
RD	~~	AM.ECM	0.0800884	0.0000000	NA
SLOPE	~~	SLOPE	0.2483766	0.0000000	NA
SLOPE	~~	Sp.rich	-0.0167863	0.0000000	NA
SLOPE	~~	CURV_PR	0.1002248	0.0000000	NA
SLOPE	~~	TSP.SRL	0.0101562	0.0000000	NA
SLOPE	~~	FDis.SRL	-0.0000568	0.0000000	NA
SLOPE	~~	SRL	0.0014794	0.0000000	NA
SLOPE	~~	TSP.FRic.RD	-0.0252828	0.0000000	NA
SLOPE	~~	AM.ECM	-0.0436689	0.0000000	NA
Sp.rich	~~	Sp.rich	0.2483766	0.0000000	NA
Sp.rich	~~	CURV_PR	-0.0686821	0.0000000	NA
Sp.rich	~~	TSP.SRL	0.0098234	0.0000000	NA
Sp.rich	~~	FDis.SRL	0.0794879	0.0000000	NA

(continued)

Response	Operator	Explanatory	Estimate	SE	p-value
Sp.rich	~~	SRL	0.0135911	0.0000000	NA
Sp.rich	~~	TSP.FRic.RD	0.0419447	0.0000000	NA
Sp.rich	~~	AM.ECM	0.0171725	0.0000000	NA
CURV_PR	~~	CURV_PR	0.2483766	0.0000000	NA
CURV_PR	~~	TSP.SRL	-0.0123199	0.0000000	NA
CURV_PR	~~	FDis.SRL	-0.0095466	0.0000000	NA
CURV_PR	~~	SRL	-0.0384493	0.0000000	NA
CURV_PR	~~	TSP.FRic.RD	-0.0060808	0.0000000	NA
CURV_PR	~~	AM.ECM	-0.0153894	0.0000000	NA
TSP.SRL	~~	TSP.SRL	0.2483766	0.0000000	NA
TSP.SRL	~~	FDis.SRL	0.0212875	0.0000000	NA
TSP.SRL	~~	SRL	0.1250474	0.0000000	NA
TSP.SRL	~~	TSP.FRic.RD	-0.0318750	0.0000000	NA
TSP.SRL	~~	AM.ECM	-0.0632655	0.0000000	NA
FDis.SRL	~~	FDis.SRL	0.2483766	0.0000000	NA
FDis.SRL	~~	SRL	0.0442603	0.0000000	NA
FDis.SRL	~~	TSP.FRic.RD	0.0825569	0.0000000	NA
FDis.SRL	~~	AM.ECM	-0.0094878	0.0000000	NA
SRL	~~	SRL	0.2483766	0.0000000	NA
SRL	~~	TSP.FRic.RD	0.0121057	0.0000000	NA
SRL	~~	AM.ECM	-0.0982008	0.0000000	NA
TSP.FRic.RD	~~	TSP.FRic.RD	0.2483766	0.0000000	NA
TSP.FRic.RD	~~	AM.ECM	0.0024365	0.0000000	NA
AM.ECM	~~	AM.ECM	0.2483766	0.0000000	NA