

Tree diversity and mycorrhizal type independently shape multitrophic biodiversity, with stronger effects belowground than aboveground

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Supplementary Methods

Details for trophic groupings

Canopy fauna

Invertebrates were classified into trophic groups based on their ecological roles as predators, fungivores, herbivores, pollinators, and omnivores (details listed Supplementary Data 1^{1–14}). The following taxonomic groups were identified and classified:

Predators: Predatory arthropods included 17 families from the orders Araneae, two families of Opiliones, and three families of Coleoptera (Coccinellidae, Cantharidae, Carabidae). Additional predatory taxa included two families of Diptera (Hybotidae, Dolichopodidae), the genus *Formica* from the family Formicidae, one family from Hemiptera (Reduviidae), and families from Raphidioptera, Odonata, and Mesostigmata. Three families of Prostigmata (Anystidae, Bdellidae, Trombidiidae) were also categorised as predators. We also grouped twelve families of Hymenoptera as predators, including Vespidae, Crabronidae, while the other ten families were categorised as parasitoids.

Fungivores: Fungivore families comprised five families of Coleoptera, four families of Psocoptera, three families of Collembola, and two families of Thysanoptera.

Herbivores: Herbivores included eight families of Coleoptera, eight families of Hemiptera, two families of Diptera (Bibionidae and Drosophilidae), and families (e.g., Rhaphidophoridae and Tettigoniidae) from Orthoptera. Additional herbivores included larvae from Lepidoptera, Hymenoptera, Neuroptera, the genus *Lasius* from the family Formicidae, and two families of Gastropoda.

Omnivores: Omnivores included three families of Coleoptera (Anthicidae, Elateridae, Staphylinidae), and additional representatives from Dermaptera, Diptera, and mites from Oribatida and Prostigmata.

Foliar fungi

Total foliar fungi: From non-sterilised samples representing the entire phyllosphere fungal community¹⁵.

Endophytic (Endo.) fungi: From surface-sterilised samples representing the endophytic community *sensu stricto*.

Epiphytic (Epi.) fungi: A derived subset was generated by subtracting taxa present in the endophytic subset from the non-sterilised phyllosphere data.

Soil surface fauna

Invertebrates at the soil surface were categorised into trophic groups based on their ecological roles as predators, detritivores, herbivores, and omnivores^{1–3,10,12,13,16,17}. The following classifications were established:

Predators: This group comprised 14 families from Araneae and Opiliones, four families of Coleoptera, and three families from Chilopoda. Additional predatory taxa included two

134 families from Diplura, Mesostigmata mites, Pseudoscorpiones, and the family Neanuridae
135 from Collembola.

136 **Detritivores:** Dominated by six families of Diplopoda, detritivores also included two
137 families of Coleoptera (Anobiidae and Cholevidae), the family Campodeidae from Diplura,
138 Enchytraeidae and Lumbricidae (Oligochaeta), and Isopoda.

139 **Herbivores:** The herbivores consisted of seven families of Coleoptera, seven families of
140 Hemiptera, two families of Diptera (Bibionidae and Drosophilidae), larvae from Lepidoptera
141 and Neuroptera, two families from Orthoptera, Tetranychidae mites, and various families
142 from Gastropoda.

143 **Omnivores:** Omnivores included larvae of Coleoptera, two families of Coleoptera (Silphidae
144 and Staphylinidae), larvae of Diptera, three genera of Formicidae, and Dermaptera
145 (Forficulidae).

146 Soil fauna

147 Soil invertebrates were categorised by body size into nematodes, mesofauna, and
148 macrofauna. Different extraction and identification methods were applied based on body size,
149 and taxonomic and trophic groups were classified as follows to ensure comparability:

150 **Nematodes:** Nematodes were analysed as a whole group (Ne:Total) and further classified by
151 feeding preference into herbivores (Ne:Herbivores), fungivores (Ne:Fungivores), and
152 bacterivores (Ne:Bacterivores)^{18–20}. Due to overall low densities and therefore issues with
153 zero inflation, predator and omnivore nematodes were grouped into one group in diversity
154 analyses^{21,22}.

155 **Mesofauna:** Mesofauna was analysed as a whole group, with some taxa further classified by
156 function^{10,17,23,24,24–29}. Fungivores (Me:Fungivores) included seven families of Collembola,
157 three families of Oribatida mites, Protura, Psocoptera, and Thysanoptera. Predators
158 (Me:Predators) included Mesostigmata, two families of Oribatida (Ooppiidae and
159 Hypochthonidae), the family Neanuridae from Collembola, Anajapygidae from Diplura, and
160 Pseudoscorpiones. The remaining mesofauna were considered omnivores (Me:Omnivores).

161 **Macrofauna:** Macrofauna were grouped into herbivores (Ma:Herbivores), fungivores
162 (Ma:Fungivores), predators (Ma:Predators), and omnivores (Ma:Omnivores), and earthworms
163^{1,10,17,30–33}.

164 Soil microbial communities

165 **Total soil microbes:** Total soil microbial abundance was represented by total microbial
166 biomass, and alpha diversity was calculated as the average of both bacterial and fungal alpha
167 diversity (details provided below).

168 **Soil fungi:** Fungal abundance was represented by fungal biomass, and alpha diversity indices
169 were obtained from sequencing data.

170 **Soil bacteria:** Bacterial abundance was represented by bacterial biomass, and alpha diversity
171 indices were obtained from sequencing data.

Construction of Structural Equation Models

For the final SEM framework in Fig. S7, we only included mediators that were significantly affected by the treatments (see Table S9, Fig. S6) and were not strongly correlated with each other (Table S10; details written in lines 823-843). The final set of mediators included ENL, leaf C:N, root Ca, root C, and soil NO_3^- . Soil C was excluded, because its response pattern indicated non-additive treatment effects (e.g., lower values in AM + EcM mixtures than in AM plots; Fig. S1), which could not be adequately represented by the linear coding used in the SEM.

Based on the hypothesized relationships (Fig. S1; Fig. S7), we first fitted a full piecewise structural equation model (SEM) including all plausible pathways among treatment variables, mediators, and multitrophic responses. All component models were fitted as linear mixed-effects models with composition included as a random effect, except for root Ca, for which the random-effect variance was negligible. EcM% represents the proportion of EcM tree species, and $\log(\text{Richness})$ represents log-transformed tree species richness. The multitrophic diversity and abundance are shortened as multi-indices, or multi-abundance, or multi-diversity.

aboveground multi-index $\sim$ Leaf C:N + ENL
surface multi-index $\sim$ ENL + Leaf C:N + root Ca + root C + Soil NO_3^-
belowground multi-index $\sim$ ENL + Leaf C:N + root Ca + root C + Soil NO_3^-
ENL $\sim$ $\log(\text{Richness})$ + EcM%
Leaf C:N $\sim$ $\log(\text{Richness})$ + EcM%
root Ca $\sim$ $\log(\text{Richness})$ + EcM%
root C $\sim$ $\log(\text{Richness})$ + EcM% + $\log(\text{Richness}) \times \text{EcM\%}$
 NO_3^- $\sim$ $\log(\text{Richness})$ + EcM%

The initial SEM was simplified by sequentially removing unsupported paths while monitoring model performance, marginal R^2 , and tests of directed separation. Removal of unsupported predictors had little effect on marginal R^2 or overall model fit. Additional direct pathways were included only when tests of directed separation indicated missing relationships ($p < 0.1$). The final SEMs therefore represent reduced versions of the hypothesized full model.

The final models for multitrophic abundance were:

aboveground multi-abundance $\sim$ Leaf C:N + ENL
surface multi-abundance $\sim$ ENL + Leaf C:N + root Ca
belowground multi-diversity $\sim$ ENL + Leaf C:N + root Ca + $\log(\text{Richness})$

The final models for multitrophic diversity were:

aboveground multi-diversity $\sim$ Leaf C:N + ENL + $\log(\text{Richness})$
surface multi-diversity $\sim$ ENL + Leaf C:N + root Ca
belowground multi-diversity $\sim$ ENL + Leaf C:N + root Ca

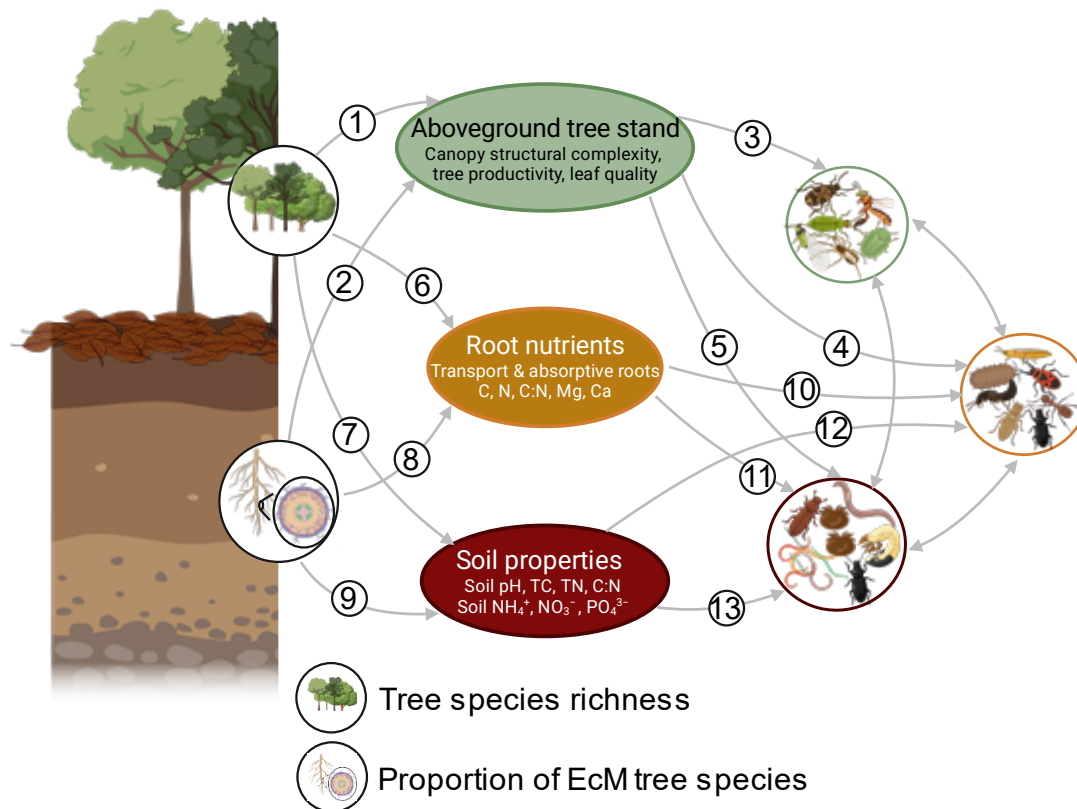


Figure S1: Conceptual figure of the hypothesized structural equation model (SEM) framework for tree and mycorrhizal type effects as well as environmental mediators on multitrophic abundance and diversity across above- and belowground food webs. The invertebrates across the aboveground (green bubbles), soil surface (orange bubbles), and belowground (brown bubbles) strata are displayed on the right side of the framework. Arrows indicate proposed causal relationships. We tested how tree species richness and mycorrhizal types (the proportion of EcM tree species; EcM%) influence multitrophic metrics via a range of mediators representing the aboveground tree stand, root nutrients, and soil properties. Mycorrhizal type was coded as the proportion of EcM tree species (1 = EcM, 0.5 = AM+EcM, 0 = AM). As this is a conceptual figure, the final analysis included only mediators that were significantly affected by the treatment factors (see Table S9, Fig. S6) and were not strongly correlated with each other (Table S10). The theoretical basis for each pathway (indicated with number in the cycles) is described below. Created in BioRender³⁴.

Pathways 1-2: tree diversity and mycorrhizal types → aboveground tree stand characteristics

We hypothesized that tree diversity influences above- and belowground communities indirectly through changes in canopy structure complexity^{35,36}, productivity^{37,38}, and leaf quality³⁹. In addition, we assumed that these variables mediate the effects of mycorrhizal type^{40–43}. Specifically, we assumed that tree canopy structural complexity (measured as the effective number of layers, ENL), aboveground tree productivity (total wood volume), and leaf quality (leaf nitrogen content and C:N ratio) act as key mediators linking tree diversity to biotic communities.

Pathway 3: aboveground tree stand characteristics → aboveground biodiversity

For aboveground communities, we expected canopy structural complexity to increase habitat heterogeneity and resource availability, thereby promoting the abundance and diversity of foliar fungi¹⁵ and invertebrates^{44,45}. Higher tree productivity was expected to increase the overall availability of plant-derived resources⁴⁶, while leaf quality was assumed to influence herbivore and foliar fungal communities through changes in leaf nutrient content and palatability^{47,48}. These effects were expected to propagate to higher trophic levels such as predators⁶.

Pathway 4-5: aboveground tree stand characteristics → soil surface and belowground biodiversity

For soil-surface and belowground communities, we hypothesized that canopy structural complexity enhances microclimatic stability (e.g., temperature buffering and soil moisture)^{49,50}, which benefits invertebrates and microbial communities. In addition, higher aboveground productivity was expected to increase carbon inputs to the soil through root growth, root exudates, and litter production, thereby supporting microbial communities, detritivores, and higher trophic levels⁵¹⁻⁵⁵. Finally, leaf quality was expected to indicate litter quality and decomposition processes, affecting resource availability for microbial communities⁴² and microhabitats for litter and soil fauna^{56,57}.

Pathway 6-9: tree diversity and mycorrhizal types → soil properties and root nutrients

For soil-surface and belowground communities, we hypothesized that the effects of tree diversity are mediated by soil properties^{39,58} and root nutrient contents⁵⁹⁻⁶¹. These variables are also expected to mediate the effects of mycorrhizal type^{42,62-65}. Specifically, we assume that soil properties (soil pH, soil total C and N contents, and C:N ratio), soil nutrient availability (NO_3^- , NH_4^+ , and PO_4^{3-}), and nutrient contents in both transport and absorptive roots (e.g., C, N, Ca, Mg, and root C:N ratio) act as key mediators linking tree diversity and mycorrhizal types to soil-surface and belowground communities.

Pathway 10-11: root nutrients → belowground and soil-surface biodiversity

Root nutrient contents can determine the palatability of roots for root-feeding organisms⁶⁶. Following root turnover, nutrients contained in root litter further regulate the abundance of detritivores, such as earthworms^{67,68}, and influence soil microbial community structure. These effects can propagate through the entire soil food web^{69,70}. In addition, roots, particularly those of ectomycorrhizal (EcM) trees, often forage for nutrients in the top-soil and litter layer, which may also influence soil-surface communities⁷¹.

Pathway 12-13: soil properties → belowground and soil surface biodiversity

Soil properties directly determine the structure of soil microbial communities and nematode assemblages^{42,72-74}. For example, higher nutrient availability was expected to promote soil bacteria and bacterivorous nematodes, whereas higher soil organic matter and carbon contents are likely to favor soil fungi and fungivorous nematodes^{72,75,76}. Soil carbon content and the soil C:N ratio have also been shown to be key predictors of microbial biomass⁷⁷ and oribatid mite diversity⁷⁸.

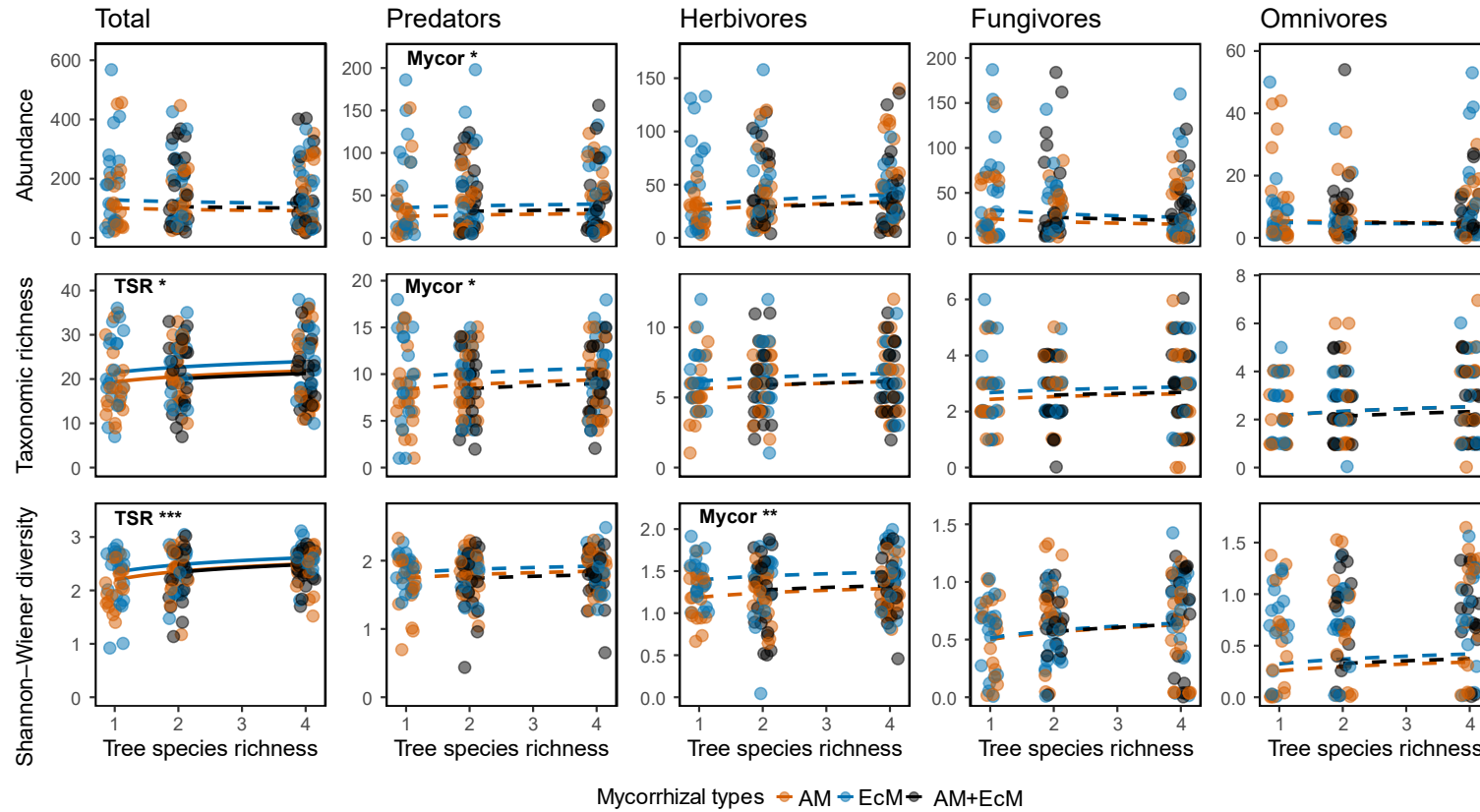
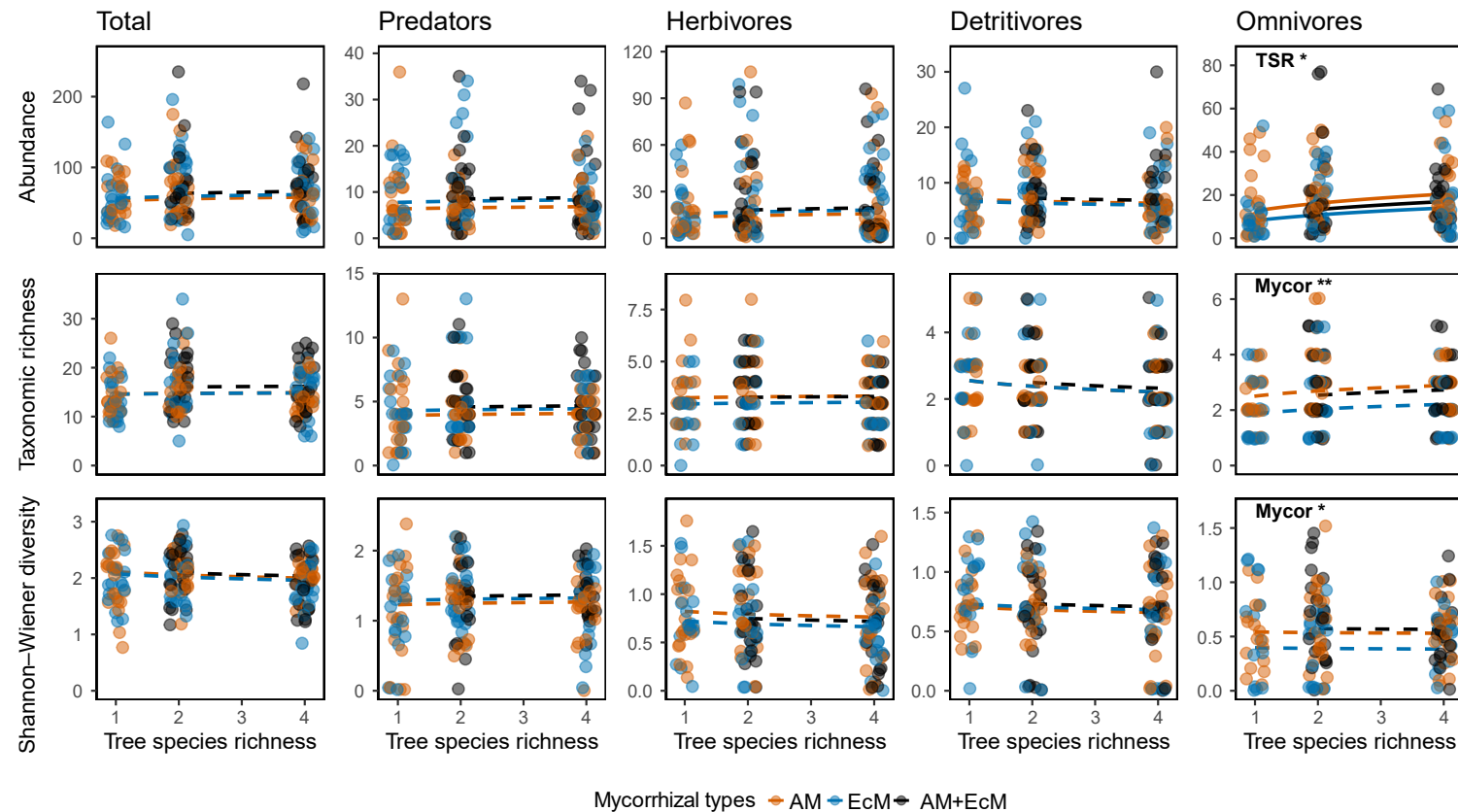


Figure S2: Effects of tree species richness (TSR), mycorrhizal type (Mycor), and their interaction on the abundance, taxonomic richness and Shannon-Wiener diversity of trophic groups in the aboveground compartment. The significance of fixed effects (TSR, Mycor, and TSR $\times$ Mycor) is indicated within each panel. Significance levels are indicated as *** for $p < 0.001$, ** for $0.001 \leq p < 0.01$, and * for $0.01 \leq p < 0.05$. Effects with $p \geq 0.05$ are not labeled for the visual clarity. Solid lines indicate significant effects of tree species richness, whereas dashed lines indicate non-significant effects. Points represent observed values ($n = 160$), and lines show model-predicted responses from linear mixed-effects models fitted as: $\text{lme}(y_i^t \sim \text{month} + \text{Mycor} \times \log(\text{Richness}), \text{random} = \sim 1 \mid \text{composition/month, data})$. Trophic groups are labeled at the top of each column. Abundance (upper row; number of individuals per 4 m² sampling area), taxonomic richness (middle row; number of taxa, with most organisms identified to the family level) and Shannon–Wiener diversity (lower row) are shown separately.

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282

283 **Figure S3: Effects of tree species richness (TSR), mycorrhizal type (Mycor), and their interaction on the abundance, taxonomic richness**
284 **and Shannon-Wiener diversity of trophic groups in the soil surface compartment.** The significance of fixed effects (TSR, Mycor, and TSR
285 $\times$ Mycor) is indicated within each panel. Significance levels are indicated as *** for $p < 0.001$, ** for $0.001 \leq p < 0.01$, and * for $0.01 \leq p <$
286 0.05 . Effects with $p \geq 0.05$ are not labeled for the visual clarity. Solid lines indicate significant effects of tree species richness, whereas dashed
287 lines indicate non-significant effects. Points represent observed values ($n = 160$), and lines show model-predicted responses from linear mixed-
288 effects models fitted as: $\text{lme}(y_i^t \sim \text{month} + \text{Mycor} \times \log(\text{Richness}), \text{random} = \sim 1 \mid \text{composition/month, data})$. Trophic groups are labeled at the
289 top of each column. Abundance (upper row; number of individuals per $0.5 \times 0.5 \text{ m}^2$ sampling area), taxonomic richness (middle row; number of
290 taxa, with most organisms identified to the family level) and Shannon–Wiener diversity (lower row) are shown separately.

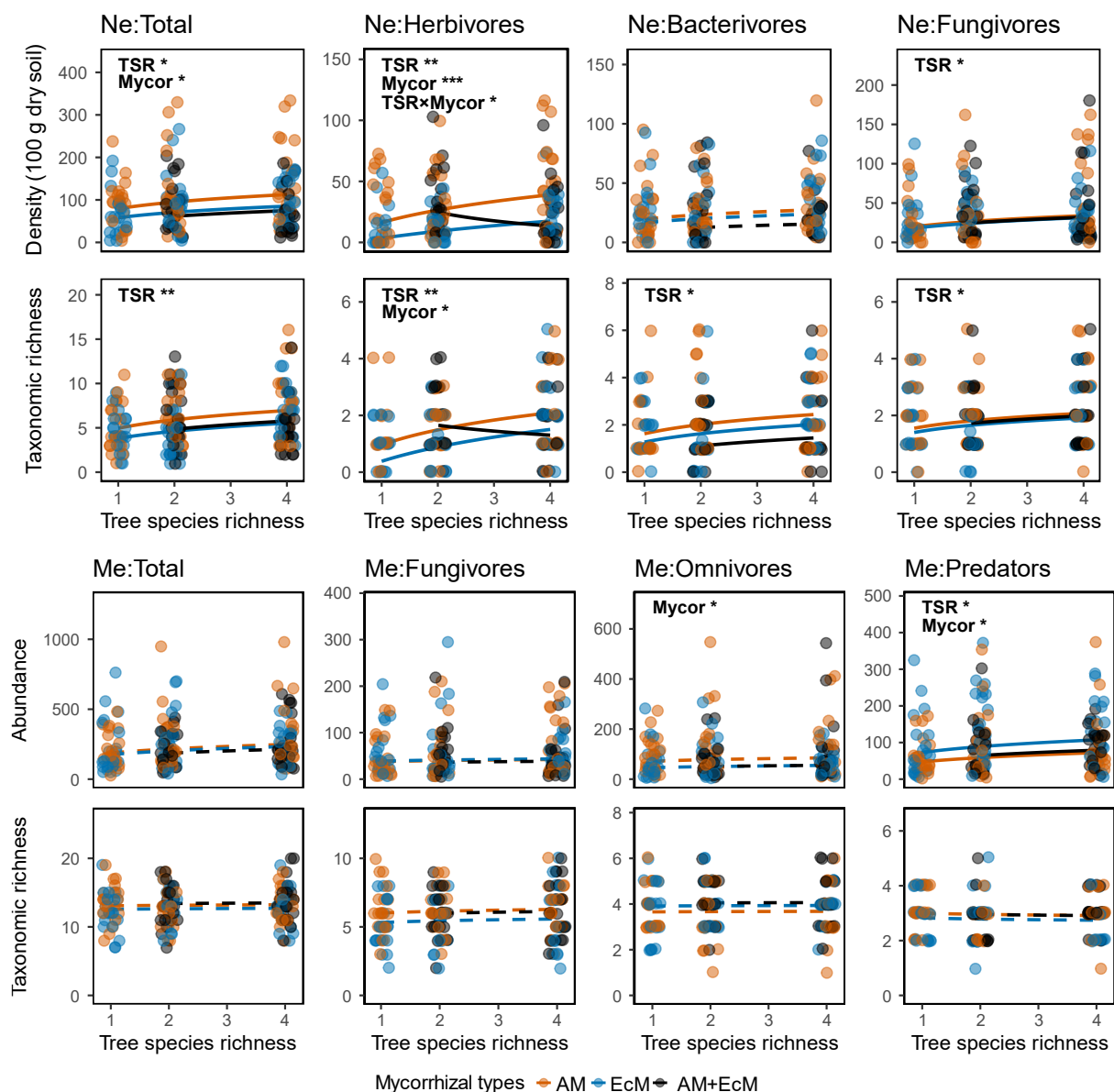


Figure S4: Effects of tree species richness (TSR), mycorrhizal type (Mycor), and their interaction on the abundance and taxonomic richness of trophic groups in the belowground compartment. The significance of fixed effects (TSR, Mycor, and TSR $\times$ Mycor) is indicated within each panel. Significance levels are indicated as *** for $p < 0.001$, ** for $0.001 \leq p < 0.01$, and * for $0.01 \leq p < 0.05$. Effects with $p \geq 0.05$ are not labeled for clarity. Solid lines indicate significant effects of tree species richness, whereas dashed lines indicate non-significant effects. Points represent observed values ($n = 160$), and lines show model-predicted responses from linear mixed-effects models fitted as: $\text{lme}(y_i^t \sim \text{month} + \text{Mycor} \times \log(\text{Richness}), \text{random} = \sim 1 | \text{composition/month, data})$. Trophic groups are labeled at the top of each column. The first two rows represent nematode trophic groups (Ne), with density (number of individuals per 100 g dry soil) in the first row and taxonomic richness (number of taxa, with most identified to the genus level) in the second row. The last two rows represent mesofauna trophic groups (Me), with abundance in the third row (total number of individuals per soil core in each plot, 16 cm diameter and 10 cm depth) and taxonomic richness in the fourth row (number of taxa, with most groups identified to the suborder level).

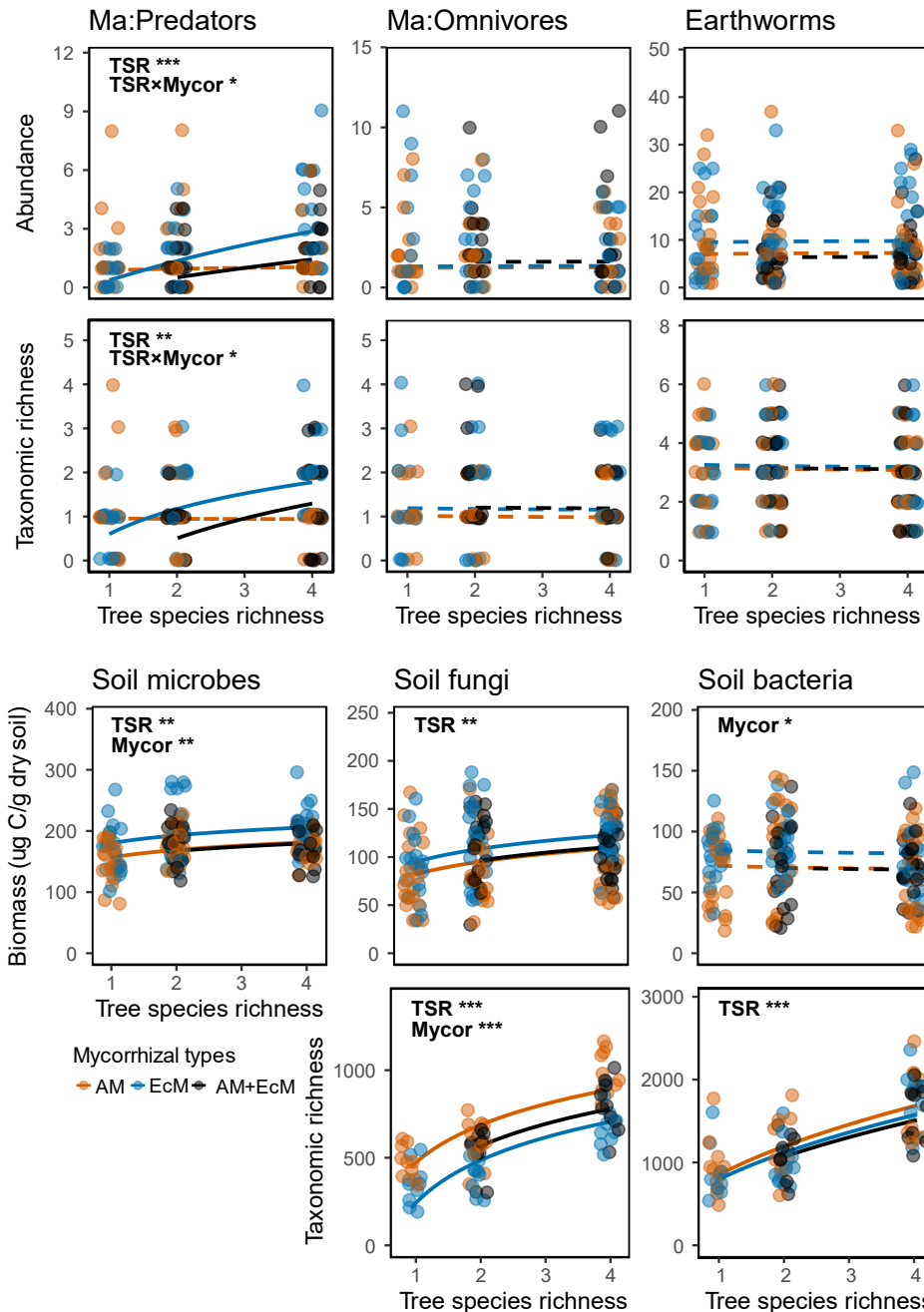


Figure S4 (continued): Effects of tree species richness (TSR), mycorrhizal type (Mycor), and their interaction on the abundance and taxonomic richness of macrofauna (Ma) and soil microbial communities in the belowground compartment. Trophic groups are labeled at the top of each column. Abundance of macrofauna (predators and omnivores) represents the total number of individuals per soil core (16 cm diameter, 10 cm depth), while taxonomic richness represents the number of identified families. For earthworms, abundance corresponds to the total number of individuals sampled from a 0.5 × 0.5 m² area using a mustard extraction solution, and taxonomic richness represents the number of identified species. These metrics are shown in the upper rows. Points represent observed values (n = 160). The lower rows indicate microbial biomass (as a proxy for abundance, n = 160) and estimated taxonomic richness (Chao1; n = 80). Other details, including model specification, significance levels, and line types, are as described in Fig. S3.

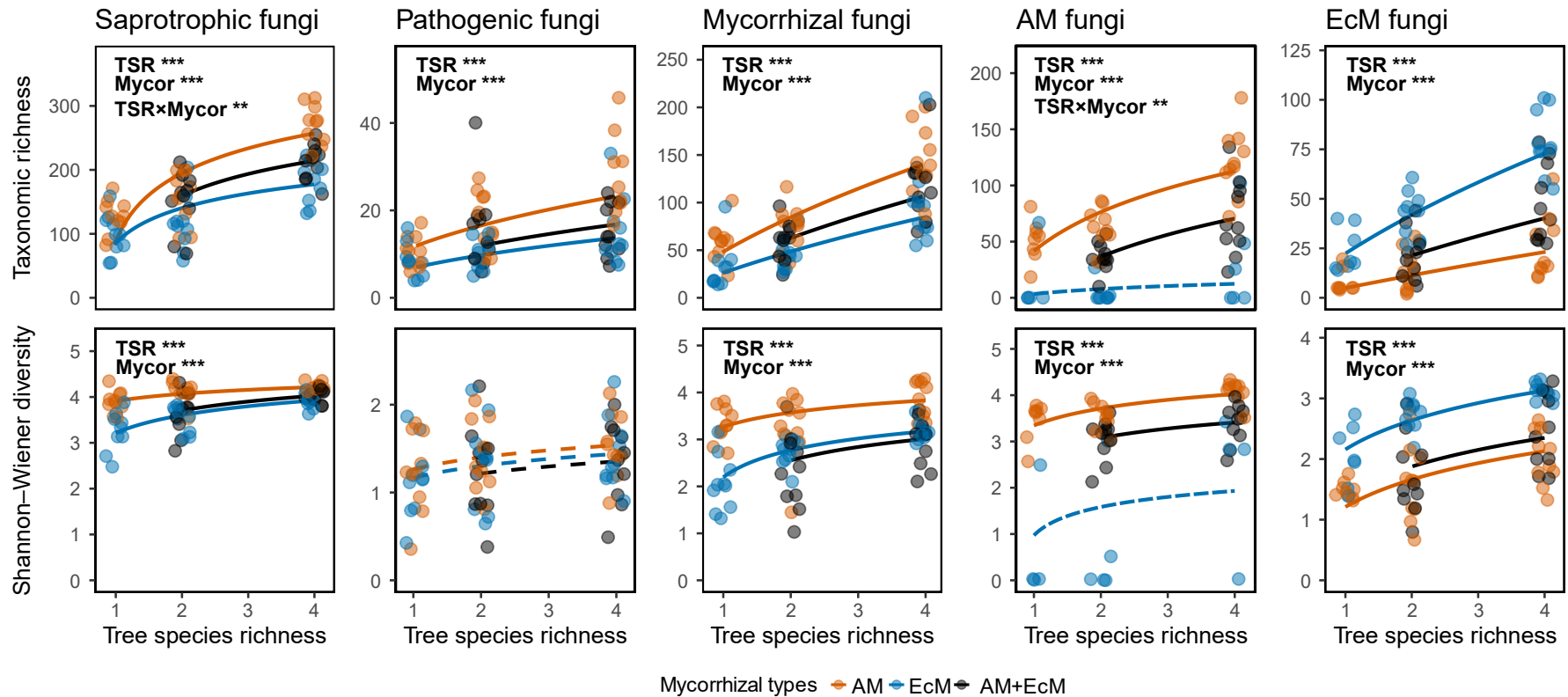


Figure S5: Effects of tree species richness (TSR), mycorrhizal type (Mycor), and their interaction on the taxonomic richness and Shannon-Wiener diversity of fungal functional groups. The significance of fixed effects (TSR, Mycor, and TSR × Mycor) is indicated within each panel. Significance levels are indicated as *** for $p < 0.001$, ** for $0.001 \leq p < 0.01$, and * for $0.01 \leq p < 0.05$. Effects with $p \geq 0.05$ are not labeled for clarity. Solid lines indicate significant effects of tree species richness, whereas dashed lines indicate non-significant effects. Points represent observed values ($n = 80$), and lines show model-predicted responses from linear mixed-effects models fitted as: $\text{lme}(y_i^t \sim \text{Mycor} \times \log(\text{Richness}), \text{random} = \sim 1 \mid \text{composition, data})$. Fungal functional groups are labeled at the top of each column; taxonomic richness (Chao1; upper row) and Shannon-Wiener diversity (lower row) are shown separately.

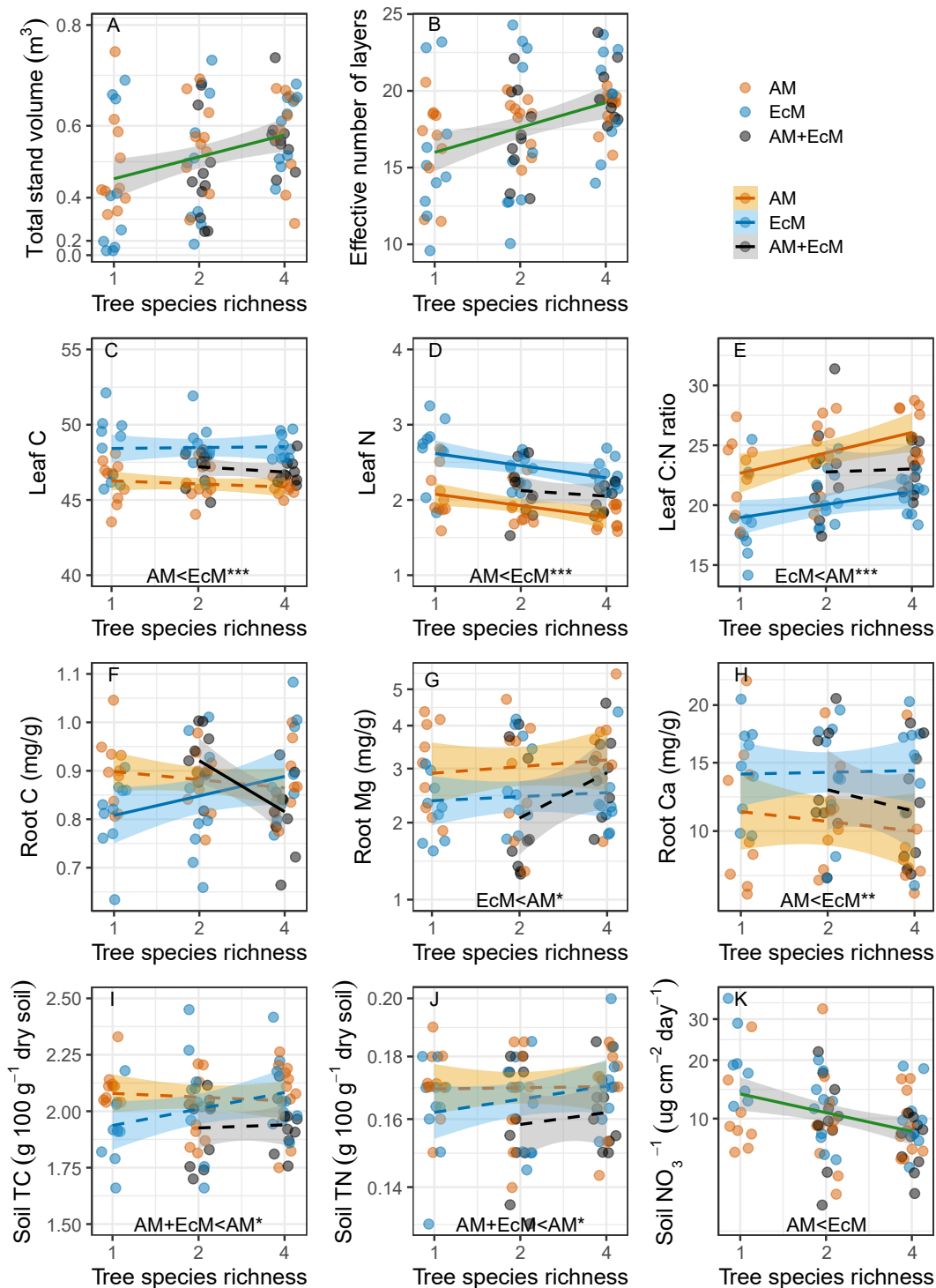


Figure S6. Relationships between parameters for aboveground tree stand (A–C), root nutrient (D–F) and soil properties (G–I) and tree species richness across three mycorrhizal type treatments. Significant relationships with tree species richness are shown with solid lines ($\pm$ SE), while non-significant relationships are shown with dashed lines. Points represent observed values ($n = 80$). Differences among mycorrhizal types are indicated by lines in different colors and labeled at the bottom of each panel; where no difference is present, a single green line is shown. Statistical results from the mixed-effects models are provided in Table S9.

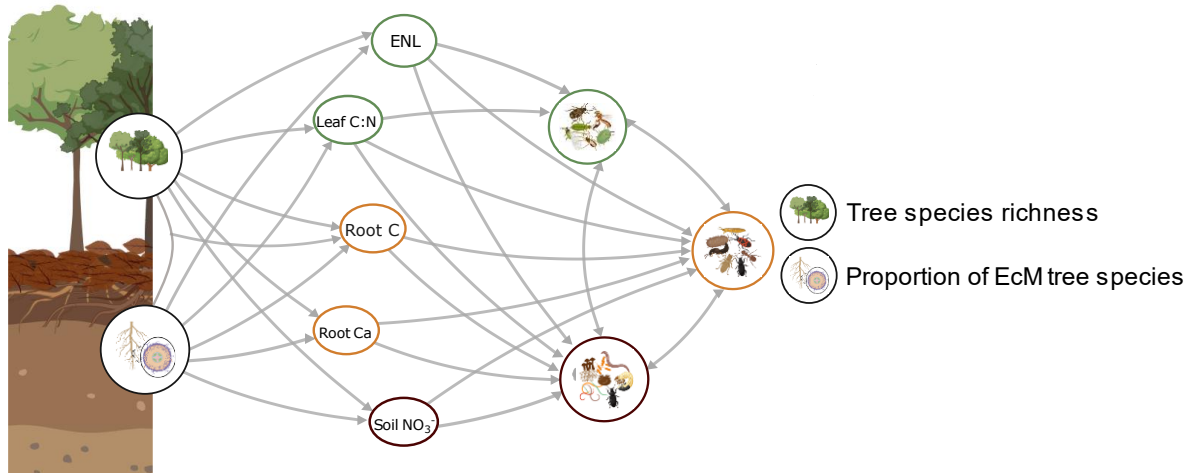


Figure S7: Simplified framework of the hypothesized structural equation model (SEM) for multitrophic abundance and diversity above- and belowground food webs. This is the final framework used for the statistical analysis (see Supplementary Methods: Construction of Structural Equation Models). It was simplified from the hypothesized framework in Fig. S1 by selecting the parameters significantly affected by the treatment factors (Fig. S6) and retaining only those that were not significantly correlated with each other (Tables S9-S10). More specifically, we tested how tree species richness and mycorrhizal types (the proportion of EcM tree species) influence multitrophic metrics via mediators: aboveground tree stand characteristics (ENL and leaf C:N ratio), root C and Ca, and soil NO₃⁻. Mycorrhizal type was coded as the proportion of EcM tree species (1 = EcM, 0.5 = AM+EcM, 0 = AM), but soil C was excluded due to non-additive responses (e.g., the lowest values in AM+EcM plots; Fig. S6). A richness × mycorrhizal interaction was included for root C. The invertebrates across the aboveground (green bubbles), soil surface (orange bubbles), and belowground (brown bubbles) strata are displayed on the right side of the framework. Arrows indicate proposed causal relationships. Direct paths from tree species richness and mycorrhizal types to multitrophic abundance or diversity were retained only if significant/marginal after accounting for mediators ($p < 0.1$). For clarity, covariances between mediators (double arrows) are not shown but were tested and retained only if significant/marginal ($p < 0.1$). Icons from BioRender³⁴.

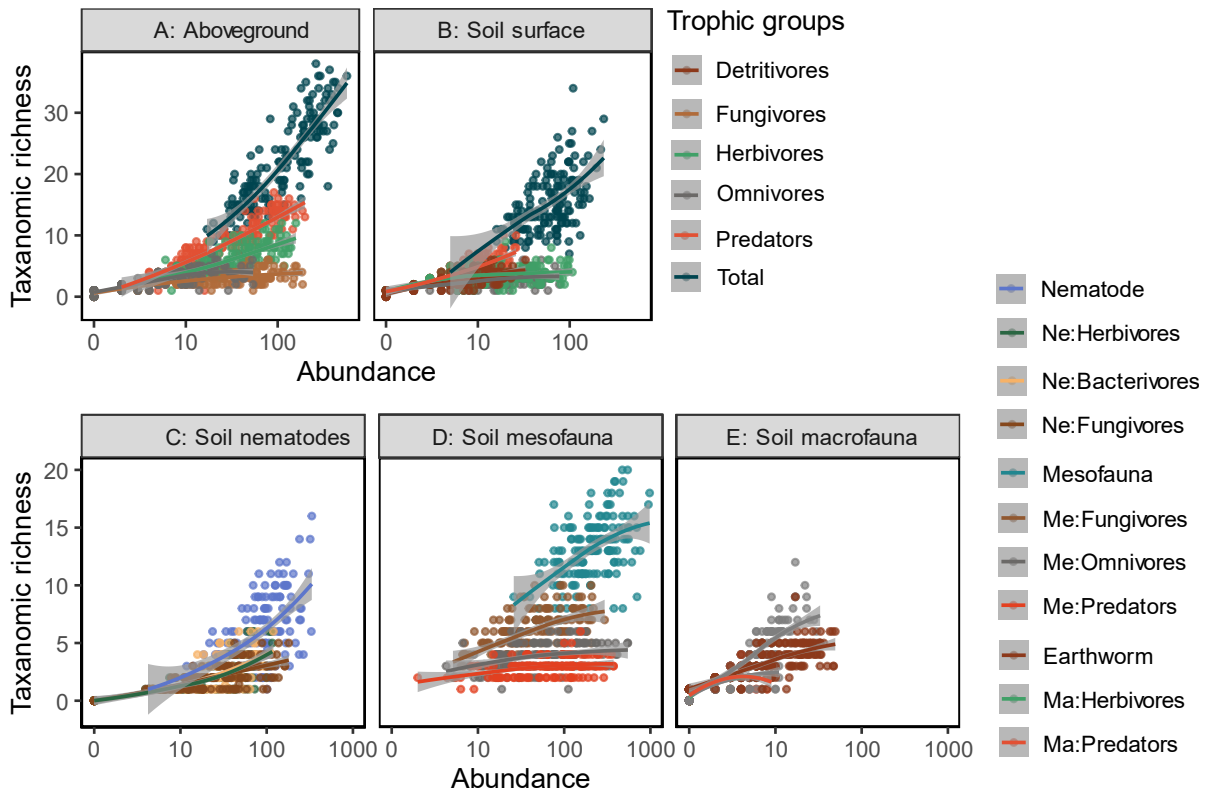


Figure S8. Scatterplots showing the correlation between abundance and taxonomic richness for each trophic group across (A) aboveground, (B) soil surface, and (C–E) belowground compartments. Belowground invertebrates are presented separately as (C) soil nematodes, (D) soil mesofauna, and (E) soil macrofauna. Different functional groups are distinguished by colors. Belowground organisms are abbreviated as Ne (nematodes), Me (mesofauna), and Ma (macrofauna). In general, taxonomic richness increased with abundance. Note: the x-axis (Abundance) is log₁₀-transformed. Points represent observed values, with colors indicating different trophic groups (n = 160 per group).

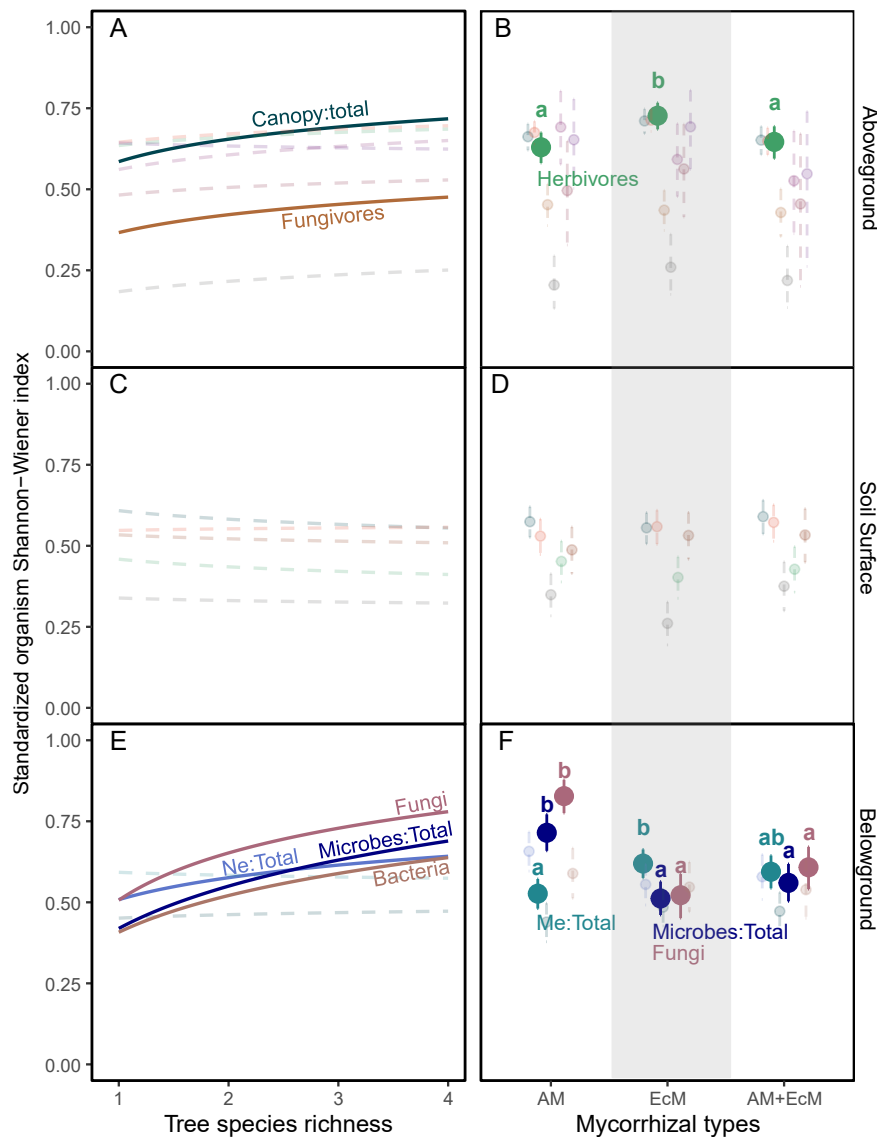


Figure S9: Effects of tree species richness and mycorrhizal types on organism Shannon-Wiener diversity aboveground (A-B), at the soil surface (C-D), and belowground (E-F). All response variables were scaled to [0,1]. Linear mixed-effects models with two-sided tests were fitted separately for each trophic group within each stratum using plot-level observations. Invertebrate models included 160 observations from 80 plots sampled in two seasons. Soil microbial groups were sampled once across 80 plots, and foliar fungal groups were sampled once with fewer plot-level observations (endophytes, $n = 39$; total foliar fungi and epiphytic fungi, $n = 34$ each). Curves (A, C, E) show prediction across the tree species richness gradient; solid lines indicate significant effects ($p < 0.05$), while dashed and transparent lines indicate non-significant effects. Estimated means and 95% confidence intervals for each mycorrhizal type (B, D, F) were obtained using *emmeans* from the fitted models. Solid dots and letters (a, b, ab) denote significant differences among mycorrhizal types after Tukey adjustment ($p < 0.05$); transparent dots indicate non-significant differences. Group names are shown next to lines or points when responses to tree species richness or mycorrhizal type were significant. Belowground organisms are abbreviated as Ne (nematodes), Me (mesofauna), and Ma (macrofauna). Colors correspond to organism groups. See Tables S1-3 for power transformation values and Tables S4-8 for F-values, p-values, degrees of freedom and model R^2 of each model.

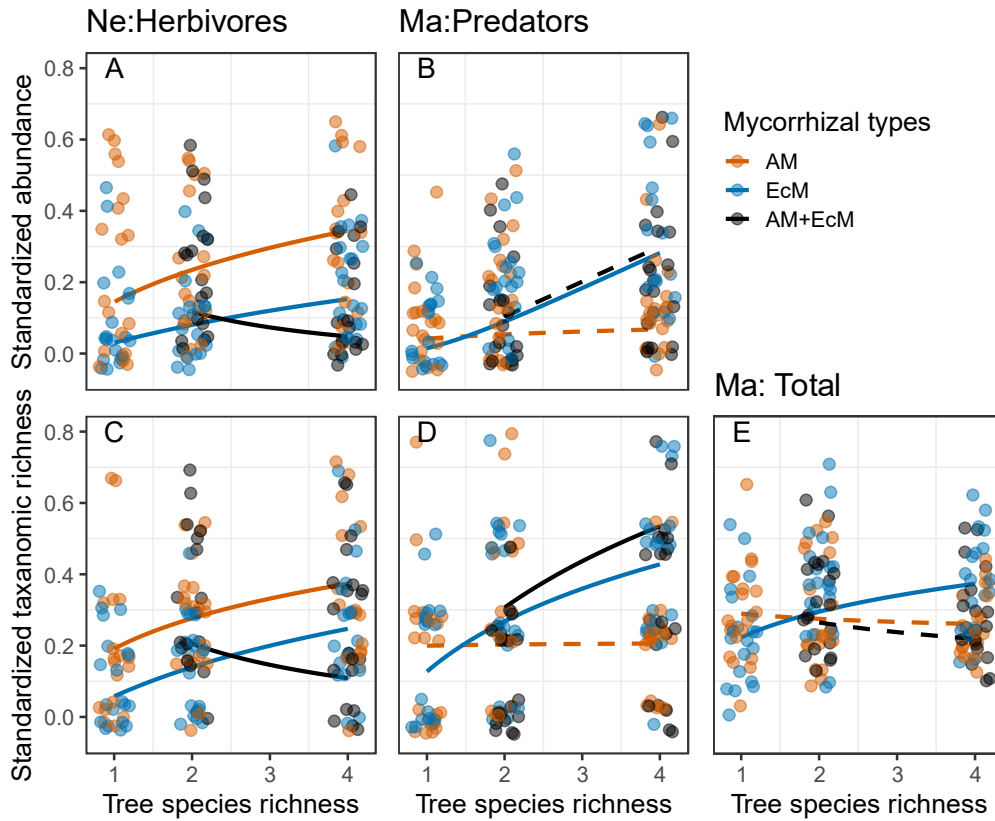


Figure S10. Effects of mycorrhizal type, tree species richness, and their interaction on standardized abundance (A–B) and taxonomic richness (C–E). Only the trophic groups that showed significant interaction effects are presented here (Tables S4–S8). Colors indicate mycorrhizal types. Solid lines represent significant relationships; dashed lines represent non-significant ones. Lines were predicted from the model $lme(y_i \sim \text{Month} + \text{Mycor} \times \log(\text{Richness}), \text{random} = \sim 1 \mid \text{composition/Month}, \text{data})$. For visualization, predictions were averaged across sampling seasons using the *emmeans* package. Panels within each column correspond to the same trophic group: nematode herbivores (Ne:Herbivore), soil macrofauna predators (Ma:Predators), and total soil macrofauna (Ma:Total). Points represent observed values ($n = 160$).

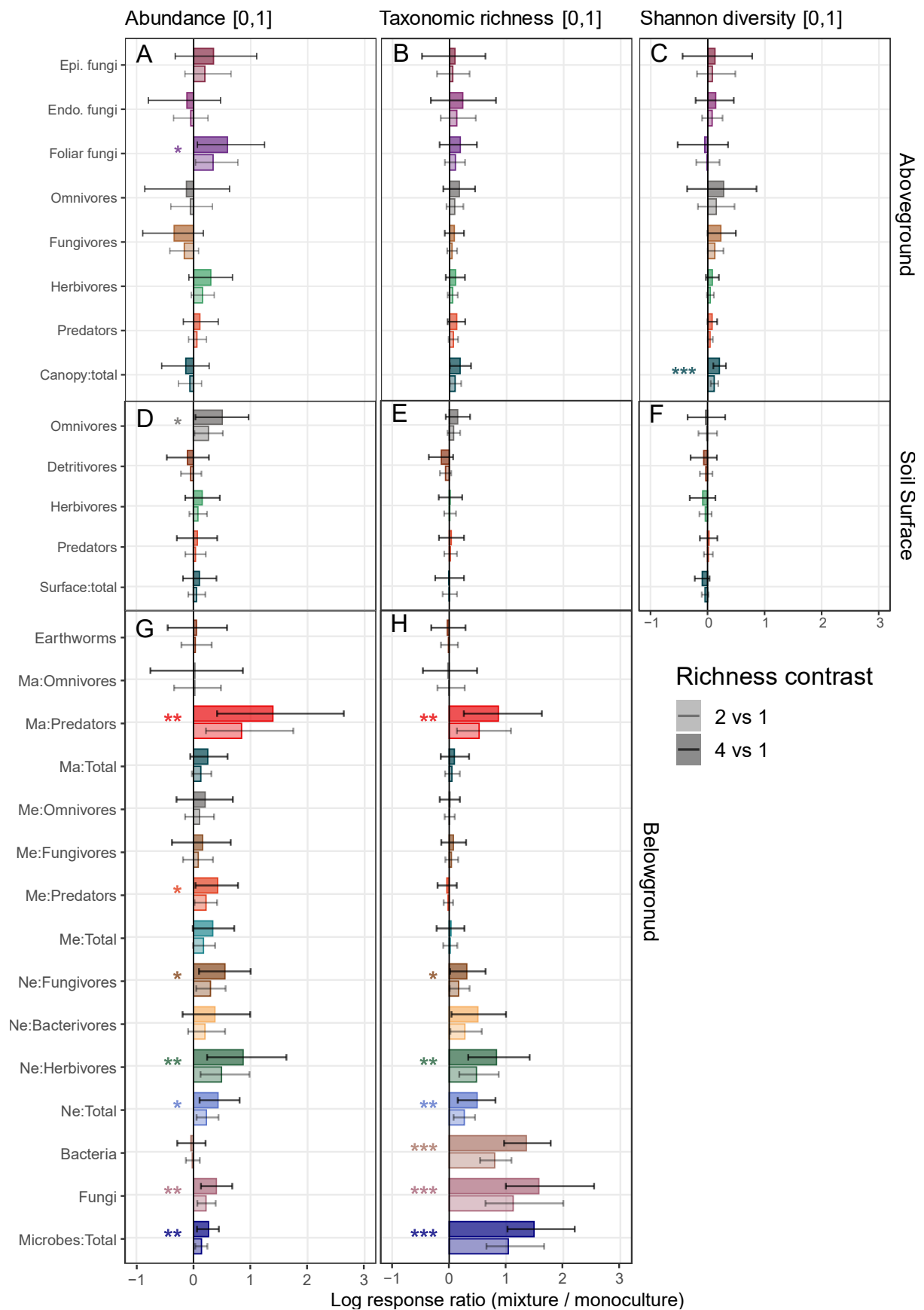
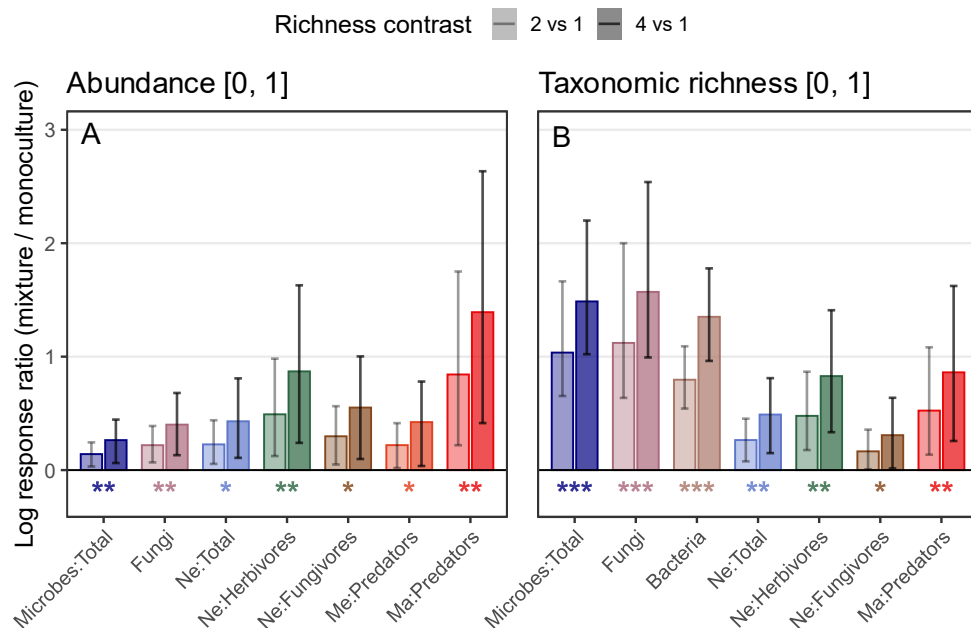


Figure S11. Standardized tree diversity effect sizes on the abundance (A, D, G), taxonomic richness (B, E, H), and Shannon–Wiener diversity (C, F) across trophic

groups and food-web compartments (Aboveground, Soil surface, and Belowground).

Effect sizes were calculated from predicted values for monocultures and tree mixtures (2- and 4-species; indicated with different transparency) obtained from linear mixed-effects models ($lme: y_i^t \sim \text{Month} + \text{Mycor} + \log(\text{Richness})$) fitted to min-max transformed data. The linear mixed-effects models with two-sided tests were fitted separately for each diversity index of each trophic group within each stratum using plot-level observations. Invertebrate models included 160 observations from 80 plots sampled in two seasons. Soil microbial abundance was sampled twice across 80 plots ($n = 160$), but soil microbial taxonomic richness and Shannon-Wiener diversity were only assessed once across 80 plots ($n = 80$). Foliar fungal groups were sampled once with fewer plot-level observations (endophytes, $n = 39$; total foliar fungi and epiphytic fungi, $n = 34$ each). Effect sizes were expressed as the log-response ratio, $\log(\text{mixture}/\text{monoculture})$. Asterisks (*) indicate cases where the effect sizes for both 2- and 4-species mixtures are significantly greater than zero (95% confidence intervals do not overlap zero). These significance levels correspond to those shown in Figs. 1-2 and Fig. S9. For trophic groups not significantly affected by tree diversity, the 95% confidence intervals overlap zero. For belowground trophic groups, abbreviations are as follows: Ne = nematodes, Me = mesofauna, and Ma = macrofauna. The magnitude of biodiversity change for each trophic group was calculated as $\exp(\log\text{-response ratio}) - 1$, representing the percentage change relative to monocultures in two- and four-species mixtures.



Continued Fig. S11. We zoomed in on the belowground trophic groups (G & H) that responded significantly to tree diversity. This allows comparison of effect sizes across trophic groups and helps address Hypothesis (1b). Based on the overlap of the 95% confidence intervals, the effect sizes do not differ significantly among trophic groups.

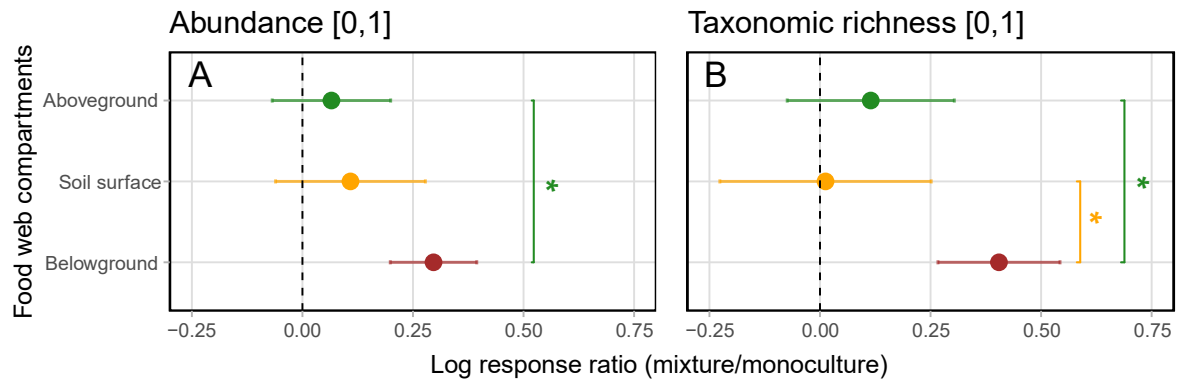


Figure S12. Averaged effect sizes of trophic groups across three food-web

compartments. This figure was derived from Fig. S11 by extracting the mean effect sizes of trophic groups within each compartment for both abundance (A) and taxonomic richness (B). Eight groups were from aboveground compartment, five groups were from soil surface, and 15 groups were from belowground compartment. Differences in effect sizes were tested using the model (mean(log-response ratio) ~ Stratum × Richness contrast) (n = 56). Richness contrast (2- and 4- species) had no significant effect on the averaged effect sizes, whereas effect sizes differed among food-web compartments, indicated by “*” (p < 0.05). Notably, these results may be biased, because more trophic groups were included in the belowground compartment than for aboveground and at the soil surface compartments, and we did not account for variation among effect sizes across trophic groups. Therefore, this figure should be used only as a summary reference, while the main results rely on Fig. S11 and Figs. 1&2.

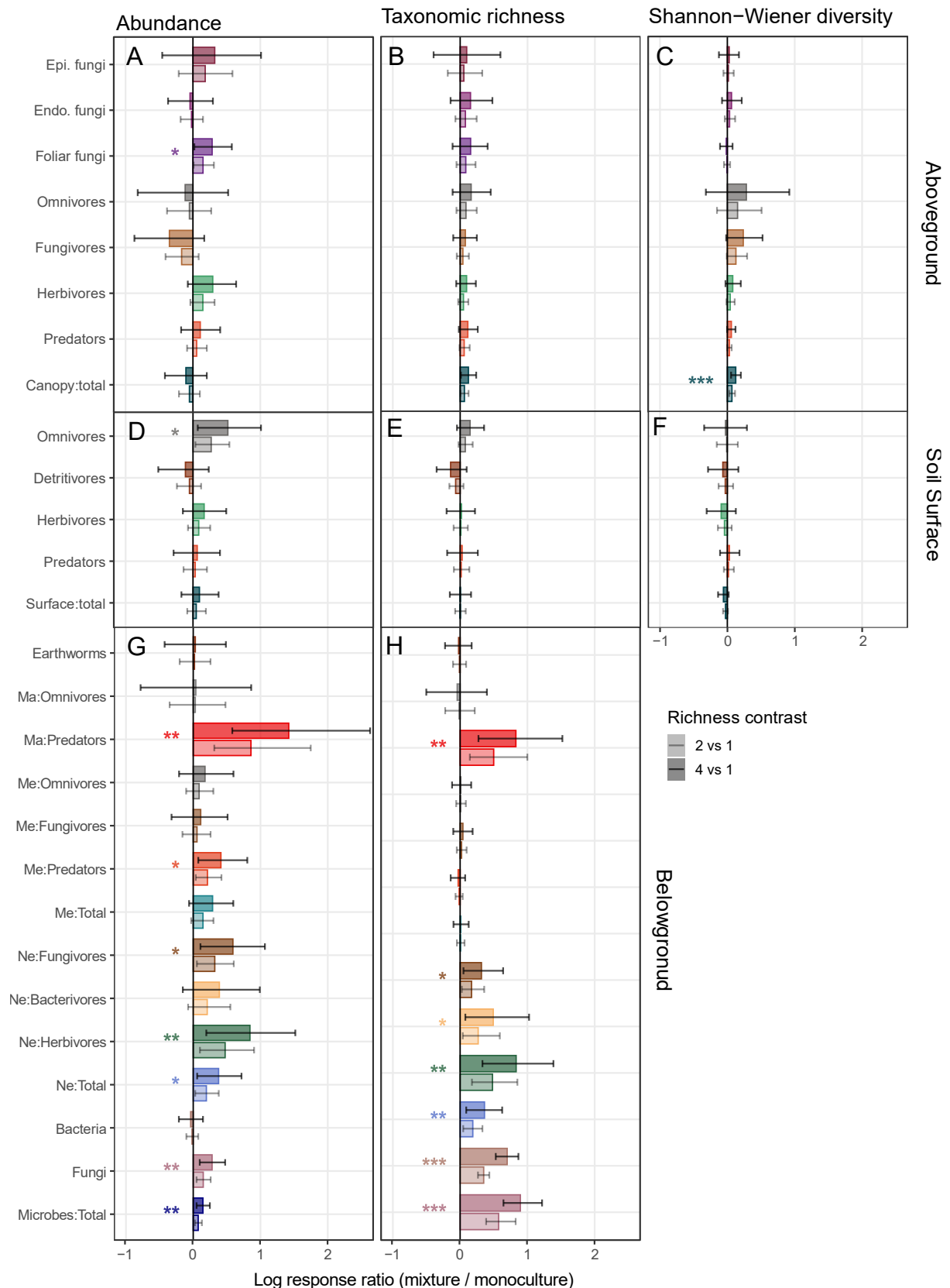


Figure S13. Standardized tree diversity effect sizes on the abundance (A, D, G), taxonomic richness (B, E, H), and Shannon–Wiener diversity (C, F) across trophic groups and food-web compartments. This figure follows the same structure and pattern as Fig. S11, but is based on predictions from models fitted to the original data.

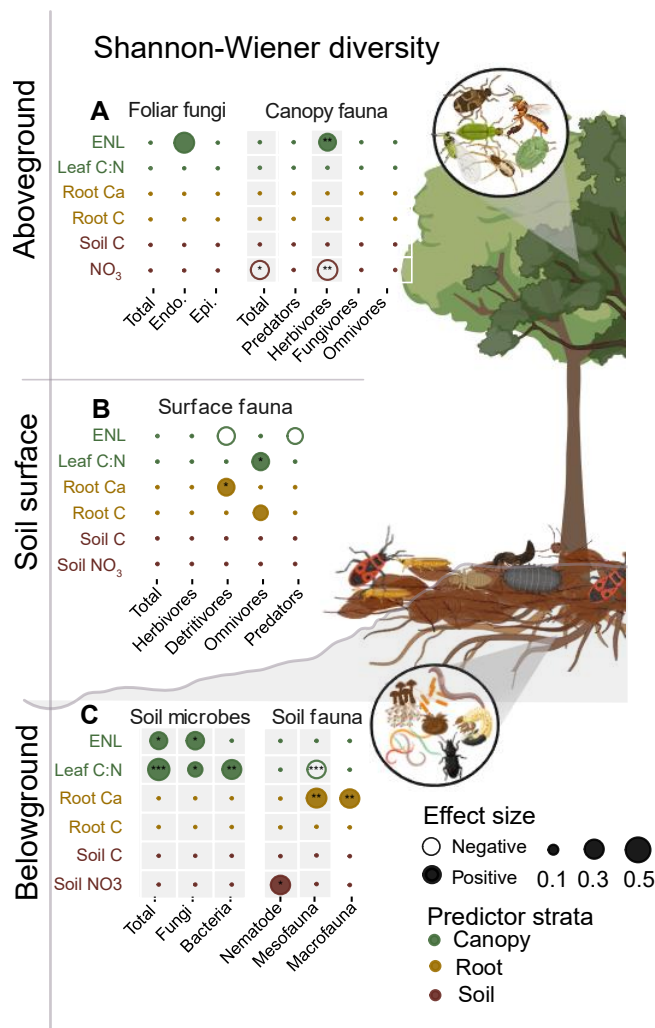


Figure S14. Results of multiple linear regressions showing the effects of six mediators on standardized organism Shannon-Wiener diversity index aboveground (A), at the soil surface (B), and belowground (C). Within each panel, individual trophic groups are shown as columns along the x-axis, grouped into broader categories (e.g., foliar fungi, canopy fauna, soil microbes, soil fauna) labeled at the top. Linear mixed-effects models with two-sided tests were fitted separately for each trophic group within each stratum, using all six proposed explanatory variables. Sample sizes were $n = 80$ for soil microbes and fauna groups, $n = 39$ for endophytes, and $n = 34$ for total foliar fungi and epiphytic fungi. Only variables retained in the best-fit models after backwards selection with the lowest AICc are shown. Standardized coefficients of retained explanatory variables are represented by circles, with filled circles indicating positive effects and open circles indicating negative effects; circle size is proportional to the absolute standardized coefficient. Non-selected variables are shown as small dots. Statistical significance is indicated by asterisks: * $0.01 \leq p < 0.05$, ** $0.001 \leq p < 0.01$, *** $p < 0.001$. Colors indicate the source of each explanatory variable: green for canopy conditions (leaf C:N ratio, ENL), light brown for root nutrients, and earthy brown for soil properties. Marginal R^2 (R^2_m ; fixed effects only) and conditional R^2 (R^2_c ; fixed and random effects) are listed in Tables S15-S17. Panels are shaded when the biodiversity response was significantly affected by tree species richness and/or mycorrhizal type (see Fig. S9). Icons from BioRender³⁴.

A: Multitrophic abundances

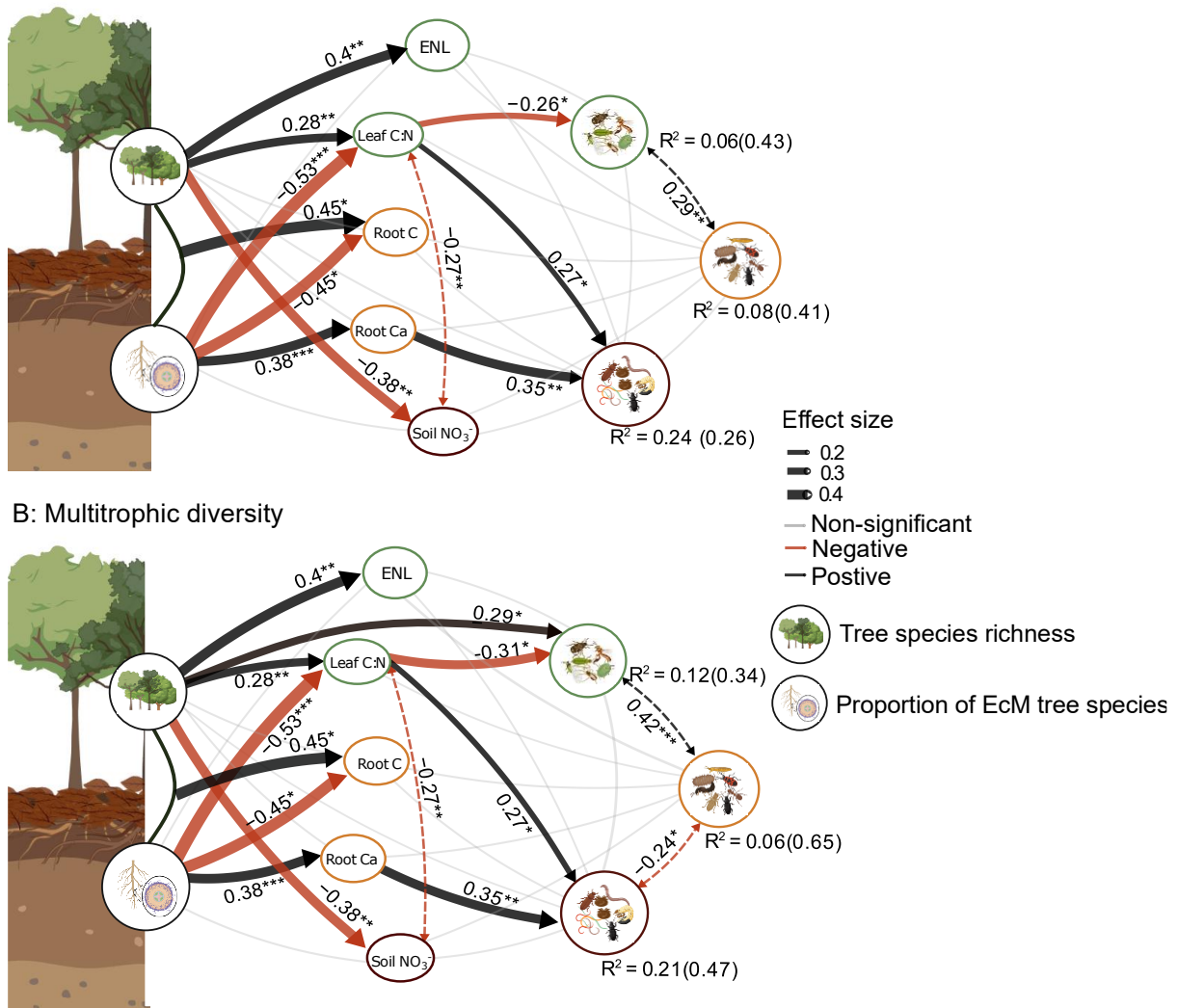


Figure S15. Sensitivity analysis on how tree species richness and mycorrhizal type (proportion of EcM tree species) affect multitrophic abundance (A) and diversity (B) of invertebrates. The invertebrates across the aboveground (green bubbles), soil surface (orange bubbles), and belowground (brown bubbles) strata are displayed on the right side of each model. The multitrophic abundance/diversity were calculated by using z-score transformation. Pathways include direct and indirect effects through tree stand characteristics (ENL and leaf C:N ratio), root C and Ca, and soil NO₃⁻. Panel (A) represents multitrophic abundance (Fisher's C = 34.98, df = 44, p = 0.83); panel (B) shows multitrophic diversity (Fisher's C = 32.48, df = 44, p = 0.90). Significant and marginal paths (p < 0.1) are shown as solid black (positive) or red (negative) lines; non-significant paths are shown in grey. Significant covariances are indicated with dashed lines with double arrows. Standardized path coefficients are shown along each line, with significance denoted as *** (p < 0.001), ** (0.001 ≤ p < 0.01), and * (0.01 ≤ p < 0.05). Interactive effects of tree species richness and mycorrhizal type on root C are shown by a connecting line between two icons. Conditional R² values for each final endogenous variable are noted next to their icons (marginal R² values in bracket ()). For clarity, conditional R² values for mediating variables are not shown here but are reported in Table S12. Icons from BioRender³⁴.

Table S1: Summary of response variables for aboveground specimens on the original scale. Specimens identified aboveground were categorized into five functional groups, with summaries provided for diversity indices, abundance (a), taxon richness (b), and Shannon-Wiener diversity (c). This table can be used to compute transformed values y' for each observation y_i in each plot and sampling season, using the formula: $y' = \frac{y_i - y_{min}}{y_{max} - y_{min}}$.

	(a) Abundance					(b) Taxonomic richness					(c) Shannon-Wiener diversity				
<i>Func.group</i>	<i>Min.</i>	<i>Med.</i>	<i>Mean</i>	<i>Max.</i>	<i>t.value</i>	<i>Min.</i>	<i>Med.</i>	<i>Mean</i>	<i>Max.</i>	<i>t.value</i>	<i>Min.</i>	<i>Med.</i>	<i>Mean</i>	<i>Max.</i>	<i>t.value</i>
Total	17	114	151	568	0.37	7	21	22	38	0.92	0.96	2.44	2.35	3.15	1.93
Predators	2	34	46	198	0.40	1	9	9	18	1.22	0.45	1.83	1.78	2.40	1.66
Herbivores	3	32	44	158	0.35	1	6	6	12	0.87	0.00	1.33	1.29	2.00	1.92
Fungivores	0	22	38	187	0.29	0	3	3	6	0.76	0.00	0.65	0.58	1.46	0.96
Omnivores	0	5	9	54	0.30	0	2	2	7	0.76	0.00	0.64	0.58	1.63	0.46
Foliar.fungi	42810	82592	89577	140679	0.89	50	257	256	395	1.15	2.83	3.76	3.68	4.22	0.74
Endo.fungi	34512	94750	96120	189292	0.86	55	132	138	273	1.20	1.50	2.56	2.62	3.37	1.60
Epi.fungi	41	1239	1474	4062	0.85	6	69	77	159	0.53	2.49	3.41	3.34	4.22	0.85

Notes: Diversity indices for foliar fungi were derived from DNA sequence data. Abundance was measured as the total number of sequence reads, and taxonomic richness was estimated using the Chao index. Outliers were identified and removed using the interquartile range (IQR) method. This resulted in the exclusion of one sample for predator abundance (= 278; n =1), five samples for herbivore abundance (≥ 229 ; n =5), one sample for fungivore abundance (= 222; n =1), and four samples for omnivore abundance (≥ 60 ; n =5). For foliar fungi, outliers in abundance included one sample for total foliar fungi (= 13,113; n =1) and one for epiphytes (= 6,715; n=1). Outliers in Shannon-Wiener diversity included one sample for total foliar fungi (value = 1.71; n =1), one for endophytes (= 0.349; n =1), and one for epiphytes (= 1.55; n =1). No outliers were identified in the remaining datasets.

497 **Table S2: Summary of response variables for soil surface specimens on the original**
498 **scale.** Specimens from the soil surface were categorized into five functional groups.
499 Summaries are provided for abundance (a), taxonomic richness (b), and Shannon-Wiener
500 diversity (c). This table can be used to compute transformed values y' for each observation y_i
501 in each plot and sampling season, using the formula: $y' = \frac{y_i - y_{min}}{y_{max} - y_{min}}$.

	(a) Abundance					(b) Taxonomic richness					(c) Shannon-Wiener diversity				
<i>Func.group</i>	<i>Min.</i>	<i>Median</i>	<i>Mean</i>	<i>Max.</i>	<i>t.value</i>	<i>Min.</i>	<i>Median</i>	<i>Mean</i>	<i>Max.</i>	<i>t.value</i>	<i>Min.</i>	<i>Median</i>	<i>Mean</i>	<i>Max.</i>	<i>t.value</i>
Total	5	64	70	235	0.40	5	14	15	34	0.78	0.81	2.03	1.99	2.95	1.60
Predators	0	7	8	30	0.49	0	4	4	10	0.81	0.00	1.16	1.10	2.16	1.55
Omnivores	0	13	18	77	0.28	0	2	3	6	0.54	0.00	0.50	0.48	1.53	0.93
Herbivores	0	12	25	107	0.30	0	3	3	9	0.65	0.00	0.68	0.72	1.72	1.12
Detritivores	0	7	9	33	0.57	0	3	3	6	0.96	0.00	0.84	0.81	1.56	1.33

502 Notes: Outliers were identified and removed using the interquartile range (IQR) method.
503 This resulted in the exclusion of four sample for total abundance (values ≥ 271 ; $n = 4$), three
504 samples for predator abundance (≥ 32 ; $n = 3$), six sample for detritivores abundance (≥ 43 ; n
505 $=6$). One sample of total taxonomic richness ($=36$; $n =1$) and one for predators ($=12$; $n =1$)
506 were removed. No outliers were identified in the remaining datasets.

507

Table S3: Summary of response variables for belowground specimens on the original scale. Specimens from the belowground compartment were first categorized into nematodes (Ne), mesofauna (Me), and macrofauna (Ma) based on body size. Within each broad group, specimens were further classified into functional groups based on feeding preference. Summaries of diversity indices, abundance (a), taxonomic richness (b), and Shannon-Wiener diversity (c) are provided below. This table can be used to compute transformed values y' for each observation y_i in each plot and sampling season, using the formula: $y' = \frac{y_i - y_{min}}{y_{max} - y_{min}}$.

Func.group	(a) Abundance					(b) Taxonomic richness					(c) Shannon-Wiener diversity				
(a) Abundance	Min.	Median	Mean	Max.	t.value	Min.	Median	Mean	Max.	t.value	Min.	Median	Mean	Max.	t.value
Ne:Total	4	83	95	334	0.43	1	5	6	16	0.59	0.00	1.55	1.46	2.52	1.21
Ne:Herbivores	0	17	25	116	0.52	0	1	2	6	0.61					0.75
Ne:Bacterivores	0	20	27	120	0.47	0	2	2	6	0.60					0.99
Ne:Fungivores	0	23	36	180	0.50	0	2	2	5	0.76					1.02
Me:Total	26	204	256	980	0.35	7	13	13	20	1.01	0.50	1.74	1.71	2.61	1.24
Me:Fungivores	5	37	58	295	0.31	2	6	6	10	0.89					2.04
Me:Omnivores	4	64	94	547	0.26	1	4	4	6	0.92					0.59
Me:Predators	2	73	97	374	0.31	1	3	3	6	0.78					1.33
Ma:Total					0.38					0.66					0.99
Ma:Predators	0	1	2	9	0.54	0	1	1	4	0.89	0.00	0.00	0.22	1.39	0.70
Ma:Omnivores	0	1	2	11	0.53	0	1	1	4	0.94	0.00	0.00	0.24	1.33	0.90
Earthworms	1	9	13	49	0.55	1	3	3	9	0.87	0.00	0.91	0.85	2.00	1.37
Total.microbes	81	178	179	296	0.89					1.15					0.74
Soil.fungi	30	101	103	188	0.86	191	582	604	1165	1.20	3.34	4.53	4.46	5.15	1.60
Soil.bacteria	18	78	76	149	0.85	488	1236	1271	2462	0.53	5.68	6.26	6.27	6.76	0.85

Note: Shannon-Wiener diversity for each functional group of nematode and mesofauna was excluded due to excessive zeros. Soil fungal and bacterial biomass served as proxies for abundance. For soil microbes, taxonomic richness (Chao) and Shannon-Wiener diversity were derived from DNA sequence data. Total macrofauna (*Ma:Total*) combines macrofauna extracted by heat and mustard methods, using the average of min-max transformed values. Microbial richness and diversity represent the average of min-max transformed values for soil fungi and bacteria; thus, no separate summaries are shown. Outliers were removed, but only found in abundance data, including: total nematodes (≥ 414 , $n=3$), nematode herbivores (≥ 142 , $n=2$), bacterivores (≥ 146 , $n=5$), fungivores ($=280$, $n=1$); total mesofauna (≥ 1069 , $n=4$), mesofauna fungivores (≥ 228 , $n=3$), omnivores (≥ 628 , $n=4$), predators ($=583$, $n=1$); macrofauna predators (≥ 10 , $n=3$), omnivores (≥ 21 , $n=4$), earthworms ($=25$, $n=1$); and total soil microbial (≥ 362 , $n=1$) and fungal biomass (≥ 262 , $n=1$).

Table S4: Summary of mixed-effects model testing the effects of sampling season (Month), tree species richness (TSR; 1, 2, 4 species) and mycorrhizal type (Mycor; AM, EcM, AM+EcM), and their interactions on the diversity indices of aboveground invertebrates. Three diversity indices included (a) abundance, (b) taxonomic richness, and (c) Shannon-Wiener diversity index.

<i>Predictors</i>	<i>Total</i>	<i>Predators</i>	<i>Herbivores</i>	<i>Fungivores</i>	<i>Omnivores</i>
(A) Abundance					
Month	$F_{1,59} = 312.4^{***}$	$F_{1,59} = 472.7^{***}$	$F_{1,55} = 155.3^{***}$	$F_{1,58} = 89.2^{***}$	$F_{1,58} = 94.9^{***}$
Mycor	$F_{2,54} = 1.5$	$F_{2,54} = 3.8^*$	$F_{2,54} = 0.9$	$F_{2,54} = 1.4$	$F_{2,53} = 0.0$
Log(TSR)	$F_{1,54} = 0.5$	$F_{1,54} = 0.3$	$F_{1,54} = 2.6$	$F_{1,54} = 1.4$	$F_{1,53} = 0.1$
Mycor×Log(TSR)	$F_{2,54} = 0.4$	$F_{2,54} = 1.1$	$F_{2,54} = 2.5$	$F_{2,54} = 0.1$	$F_{2,53} = 0.3$
R2m(R2c)	0.60(0.80)	0.73(0.85)	0.52(0.68)	0.38(0.52)	0.29(0.54)
(B) Taxonomic richness					
Month	$F_{1,59} = 279.7^{***}$	$F_{1,59} = 213.3^{***}$	$F_{1,59} = 119.3^{***}$	$F_{1,59} = 82.8^{***}$	$F_{1,59} = 101.2^{***}$
Mycor	$F_{2,54} = 2.4$	$F_{2,54} = 4.0^*$	$F_{2,54} = 1.3$	$F_{2,54} = 0.6$	$F_{2,54} = 0.1$
Log(TSR)	$F_{1,54} = 3.8$	$F_{1,54} = 2.4$	$F_{1,54} = 1.6$	$F_{1,54} = 0.7$	$F_{1,54} = 1.4$
Mycor×Log(TSR)	$F_{2,54} = 0.2$	$F_{2,54} = 0.2$	$F_{2,54} = 0.7$	$F_{2,54} = 0.5$	$F_{2,54} = 0.0$
R2m(R2c)	0.63(0.82)	0.59(0.76)	0.46(0.67)	0.35(0.35)	0.36(0.49)
(C) Shannon-Wiener diversity					
Month	$F_{1,59} = 58.9^{***}$	$F_{1,58} = 62.5^{***}$	$F_{1,59} = 32.4^{***}$	$F_{1,59} = 24.9^{***}$	$F_{1,59} = 87.8^{***}$
Mycor	$F_{2,54} = 1.6$	$F_{2,54} = 2.3$	$F_{2,54} = 5.4^{**}$	$F_{2,54} = 0.1$	$F_{2,54} = 0.4$
Log(TSR)	$F_{1,54} = 14.6^{***}$	$F_{1,54} = 3.2$	$F_{1,54} = 1.8$	$F_{1,54} = 4.6^*$	$F_{1,54} = 0.8$
Mycor×Log(TSR)	$F_{2,54} = 0.2$	$F_{2,54} = 0.1$	$F_{2,54} = 0.1$	$F_{2,54} = 0.8$	$F_{2,54} = 0.1$
R2m(R2c)	0.38(0.70)	0.32(0.39)	0.24(0.47)	0.20(0.30)	0.37(0.48)

Note: Statistical significance is indicated by asterisks: * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$. Marginal significance ($0.05 < p \leq 0.1$) is in italic. For each parameter of each trophic group (y_i), min–max transformed data were further power-transformed using the t-values reported in Table S1. Models were then fitted as linear mixed-effects models: $lme(y_i^t \sim \text{Month} + \text{Mycor} \times \log(\text{Richness}), \text{random} = \sim 1 | \text{composition}/\text{Month})$, using Type I sums of squares. Outlier removal was conducted separately for each biodiversity index and functional group, resulting in different final numbers of observations among models. Therefore, the numerator and denominator degrees of freedom ($F_{\text{numDF}, \text{denDF}}$) are reported specifically for each response variable and parameter.

Table S5: Summary of mixed-effects model testing the effects of tree species richness (TSR; 1, 2, 4 species) and mycorrhizal type (Mycor; AM, EcM, AM+EcM), and their interaction on the diversity indices of foliage fungi. Three diversity indices included (a) abundance, (b) taxonomic richness, and (c) Shannon-Wiener diversity index, which derived from DNA sequence data.

<i>Predictors</i>	<i>Phyllosphere</i>	<i>Endophytes</i>	<i>Epiphytes</i>
(A) Abundance			
Mycor	$F_{2,22} = 0.1$	$F_{2,24} = 0.1$	$F_{2,22} = 0.7$
Log(TSR)	$F_{1,22} = 4.6^*$	$F_{1,24} = 0.1$	$F_{1,22} = 0.8$
Mycor×Log(TSR)	$F_{2,22} = 1.2$	$F_{2,24} = 0.9$	$F_{2,22} = 0.1$
R2m(R2c)	0.18(0.18)	0.05(0.05)	0.08(0.29)
(B) Taxonomic richness (Chao1)			
Mycor	$F_{2,22} = 1.1$	$F_{2,24} = 0.8$	$F_{2,22} = 0.3$
Log(TSR)	$F_{1,22} = 1.4$	$F_{1,24} = 0.7$	$F_{1,22} = 0.1$
Mycor×Log(TSR)	$F_{2,22} = 0.4$	$F_{2,24} = 1.2$	$F_{2,22} = 0.2$
R2m(R2c)	0.12(0.12)	0.11(0.11)	0.03(0.03)
(C) Shannon-Wiener diversity			
Mycor	$F_{2,21} = 0.9$	$F_{2,24} = 1.5$	$F_{2,21} = 0.3$
Log(TSR)	$F_{1,21} = 0.0$	$F_{1,24} = 0.8$	$F_{1,21} = 0.1$
Mycor×Log(TSR)	$F_{2,21} = 0.3$	$F_{2,24} = 1.5$	$F_{2,21} = 0.2$
R2m(R2c)	0.07(0.18)	0.16(0.16)	0.04(0.15)

Notes: In total, we sampled 37 plots for foliar fungi. Statistical significance is indicated by asterisks: * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$. Marginal significance ($0.05 \leq p < 0.1$) is in italic. For each parameter of each trophic group (y_i), min–max transformed data were further power-transformed using the t-values reported in Table S1. Models were then fitted as linear mixed-effects models: $lme(y_i^t \sim \text{Mycor} \times \log(\text{Richness}), \text{random} = \sim 1 | \text{composition})$, using Type I sums of squares. The variable “Month” was not included because foliar fungi were assessed only once, in September 2021. Outlier removal was conducted separately for each biodiversity index and functional group, resulting in different final numbers of observations among models. Therefore, the numerator and denominator degrees of freedom ($F_{\text{numDF}, \text{denDF}}$) are reported specifically for each response variable and parameter.

Table S6: Summary of mixed-effects model testing the effects of sampling season (Month), tree species richness (TSR; 1, 2, 4 species) and mycorrhizal type (Mycor; AM, EcM, AM+EcM), and their interaction on diversity indices of surface invertebrates. Three diversity indices included (a) abundance, (b) taxonomic richness, and (c) Shannon-Wiener diversity index.

<i>Predictors</i>	<i>Total</i>	<i>Predators</i>	<i>Omnivores</i>	<i>Herbivores</i>	<i>Detritivores</i>
(A) Abundance					
Month	$F_{1,59} = 9.6^{**}$	$F_{1,59} = 44.7^{***}$	$F_{1,59} = 0.3$	$F_{1,59} = 0.6$	$F_{1,59} = 0.1$
Mycor	$F_{2,54} = 1.0$	$F_{2,54} = 0.8$	$F_{2,54} = 5.6^{**}$	$F_{2,54} = 0.8$	$F_{2,54} = 0.1$
Log(TSR)	$F_{1,54} = 0.0$	$F_{1,54} = 0.6$	$F_{1,54} = 2.6$	$F_{1,54} = 0.2$	$F_{1,54} = 1.5$
Mycor×Log(TSR)	$F_{2,54} = 0.5$	$F_{2,54} = 0.7$	$F_{2,54} = 0.6$	$F_{2,54} = 1.7$	$F_{2,54} = 0.1$
R2m(R2c)	0.09(0.60)	0.24(0.34)	0.09(0.22)	0.04(0.19)	0.01(0.19)
(B) Taxonomic richness					
Month	$F_{1,59} = 14.6^{***}$	$F_{1,59} = 45.1^{***}$	$F_{1,59} = 0.1$	$F_{1,59} = 0.4$	$F_{1,59} = 0.0$
Mycor	$F_{2,54} = 0.9$	$F_{2,54} = 1.0$	$F_{2,54} = 5.1^{**}$	$F_{2,54} = 0.6$	$F_{2,54} = 0.0$
Log(TSR)	$F_{1,54} = 0.0$	$F_{1,54} = 0.1$	$F_{1,54} = 1.8$	$F_{1,54} = 0.0$	$F_{1,54} = 1.7$
Mycor×Log(TSR)	$F_{2,54} = 0.7$	$F_{2,54} = 0.5$	$F_{2,54} = 0.5$	$F_{2,54} = 1.5$	$F_{2,54} = 0.1$
R2m(R2c)	0.12(0.62)	0.26(0.48)	0.08(0.22)	0.03(0.26)	0.01(0.22)
(C) Shannon-Wiener diversity					
Month	$F_{1,59} = 16.8^{***}$	$F_{1,59} = 35.2^{***}$	$F_{1,59} = 0.0$	$F_{1,59} = 0.3$	$F_{1,59} = 0.2$
Mycor	$F_{2,54} = 1.1$	$F_{2,54} = 1.1$	$F_{2,54} = 4.1^{*}$	$F_{2,54} = 0.6$	$F_{2,54} = 0.1$
Log(TSR)	$F_{1,54} = 0.0$	$F_{1,54} = 0.2$	$F_{1,54} = 1.1$	$F_{1,54} = 0.0$	$F_{1,54} = 1.6$
Mycor×Log(TSR)	$F_{2,54} = 0.7$	$F_{2,54} = 0.4$	$F_{2,54} = 0.5$	$F_{2,54} = 1.4$	$F_{2,54} = 0.1$
R2m(R2c)	0.14(0.77)	0.23(0.71)	0.07(0.19)	0.03(0.26)	0.01(0.24)

Note: Statistical significance is indicated by asterisks: * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$. Marginal significance ($0.05 \leq p < 0.1$) is in italic. For each parameter of each trophic group (y_i), min–max transformed data were further power-transformed using the t-values reported in Table S2. Models were then fitted as linear mixed-effects models: $lme(y_i^t \sim \text{Month} + \text{Mycor} \times \log(\text{Richness}), \text{random} = \sim 1 \mid \text{composition/Month})$, using Type I sums of squares. Outlier removal was conducted separately for each biodiversity index and functional group, resulting in different final numbers of observations among models. Therefore, the numerator and denominator degrees of freedom ($F_{\text{numDF}, \text{denDF}}$) are reported specifically for each response variable and parameter.

Table S7: Summary of mixed-effects model testing the effects of sampling season (Month), tree species richness (TSR; 1, 2, 4 species) and mycorrhizal type (Mycor; AM, EcM, AM+EcM), and their interaction on diversity indices of belowground invertebrates. Three diversity indices included (a) abundance, (b) taxonomic richness, and (c) Shannon-Wiener diversity index.

<i>Predictors</i>	<i>Nematode</i>				<i>Mesofauna</i>				<i>Macrofauna</i>			
	<i>Total</i>	<i>Herbi-</i>	<i>Bacteri-</i>	<i>Fungi-</i>	<i>Total</i>	<i>Fungi-</i>	<i>Omni-</i>	<i>Pred-</i>	<i>Total</i>	<i>Pred-</i>	<i>Omni-</i>	<i>Earthworms</i>
(A) Abundance												
Month	$F_{1,56} = 23.3^{***}$	$F_{1,58} = 7.7^{**}$	$F_{1,54} = 1.0$	$F_{1,58} = 52.8^{***}$	$F_{1,56} = 5.1^*$	$F_{1,57} = 62.7^{***}$	$F_{1,57} = 10.0^{**}$	$F_{1,58} = 21.6^{***}$	$F_{1,58} = 22.0^{***}$	$F_{1,58} = 4.8^*$	$F_{1,58} = 2.2$	$F_{1,59} = 41.0^{***}$
Mycor	$F_{2,54} = 3.5^*$	$F_{2,54} = 8.9^{***}$	$F_{2,54} = 1.8$	$F_{2,54} = 0.3$	$F_{2,54} = 0.1$	$F_{2,54} = 0.2$	$F_{2,54} = 3.4^*$	$F_{2,54} = 3.5^*$	$F_{2,54} = 2.0$	$F_{2,54} = 1.0$	$F_{2,54} = 0.3$	$F_{2,54} = 2.8$
Log(TSR)	$F_{1,54} = 6.3^*$	$F_{1,54} = 7.9^{**}$	$F_{1,54} = 1.7$	$F_{1,54} = 5.6^*$	$F_{1,54} = 3.0$	$F_{1,54} = 0.3$	$F_{1,54} = 0.7$	$F_{1,54} = 4.9^*$	$F_{1,54} = 2.1$	$F_{1,54} = 11.6^{**}$	$F_{1,54} = 0.0$	$F_{1,54} = 0.1$
Mycor×Log(TSR)	$F_{2,54} = 1.9$	$F_{2,54} = 3.5^*$	$F_{2,54} = 1.1$	$F_{2,54} = 0.9$	$F_{2,54} = 0.1$	$F_{2,54} = 0.5$	$F_{2,54} = 0.3$	$F_{2,54} = 0.2$	$F_{2,54} = 1.7$	$F_{2,54} = 3.4^*$	$F_{2,54} = 0.3$	$F_{2,54} = 0.8$
R2m(R2c)	0.21(0.21)	0.22(0.26)	0.06(0.18)	0.28(0.28)	0.06(0.30)	0.25(0.41)	0.11(0.21)	0.18(0.20)	0.17(0.31)	0.17(0.50)	0.02(0.18)	0.21(0.37)
(B) Taxonomic richness												
Month	$F_{1,59} = 3.5$	$F_{1,57} = 2.3$	$F_{1,59} = 7.0^*$	$F_{1,59} = 20.9^{***}$	$F_{1,59} = 34.9^{***}$	$F_{1,59} = 50.9^{***}$	$F_{1,59} = 0.0$	$F_{1,59} = 10.8^{**}$	$F_{1,58} = 23.1^{***}$	$F_{1,59} = 9.3^{**}$	$F_{1,59} = 2.9$	$F_{1,58} = 23.8^{***}$
Mycor	$F_{2,54} = 2.6$	$F_{2,54} = 4.2^*$	$F_{2,54} = 2.5$	$F_{2,54} = 0.4$	$F_{2,54} = 0.9$	$F_{2,54} = 2.3$	$F_{2,54} = 1.3$	$F_{2,54} = 0.8$	$F_{2,54} = 0.4$	$F_{2,54} = 1.2$	$F_{2,54} = 0.5$	$F_{2,54} = 0.1$
Log(TSR)	$F_{1,54} = 8.2^{**}$	$F_{1,54} = 11.2^{**}$	$F_{1,54} = 3.8$	$F_{1,54} = 4.2^*$	$F_{1,54} = 0.1$	$F_{1,54} = 0.4$	$F_{1,54} = 0.0$	$F_{1,54} = 0.2$	$F_{1,54} = 0.5$	$F_{1,54} = 10.2^{**}$	$F_{1,54} = 0.0$	$F_{1,54} = 0.1$
Mycor×Log(TSR)	$F_{2,54} = 1.7$	$F_{2,54} = 2.4$	$F_{2,54} = 0.4$	$F_{2,54} = 0.2$	$F_{2,54} = 0.5$	$F_{2,54} = 0.4$	$F_{2,54} = 0.3$	$F_{2,54} = 1.5$	$F_{2,54} = 3.3^*$	$F_{2,54} = 4.1^*$	$F_{2,54} = 1.5$	$F_{2,54} = 0.9$
R2m(R2c)	0.13(0.19)	0.17(0.25)	0.11(0.34)	0.14(0.15)	0.16(0.40)	0.24(0.44)	0.03(0.21)	0.10(0.39)	0.16(0.39)	0.20(0.49)	0.04(0.17)	0.13(0.23)

556 Continued table S7

(C) Shannon-Wiener diversity	<i>Nematodes</i>	<i>Mesofauna</i>	<i>Macrofauna</i>
Month	$F_{1,59} = 1.7$	$F_{1,59} = \mathbf{41.4^{***}}$	$F_{1,59} = \mathbf{11.4^{**}}$
Mycor	$F_{2,54} = 3.0$	$F_{2,54} = \mathbf{4.6^*}$	$F_{2,54} = 0.6$
Log(TSR)	$F_{1,54} = \mathbf{7.2^{**}}$	$F_{1,54} = 0.2$	$F_{1,54} = 0.7$
Mycor×Log(TSR)	$F_{2,54} = 1.4$	$F_{2,54} = 0.3$	$F_{2,54} = \mathbf{3.2^*}$
R2m(R2c)	0.13(0.24)	0.24(0.31)	0.13(0.40)

557 Herbi- denotes herbivores, Bacteri- denotes bacterivores, Fungi- denotes fungivores, Omni-
558 denotes omnivores, and Pred- denotes predators.

559 Note: Statistical significance is indicated by asterisks: * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$.
560 Marginal significance ($0.05 \leq p < 0.1$) is in italic. For each parameter of each trophic group
561 (y_i), min–max transformed data were further power-transformed using the t-values reported in
562 Table S3. Models were then fitted as linear mixed-effects models: $lme(y_i^t \sim \text{Month} + \text{Mycor} \times$
563 $\log(\text{Richness})$, random = $\sim 1 \mid \text{composition/Month}$), using Type I sums of squares. Outlier
564 removal was conducted separately for each biodiversity index and functional group, resulting
565 in different final numbers of observations among models. Therefore, the numerator and
566 denominator degrees of freedom ($F_{\text{numDF}, \text{denDF}}$) are reported specifically for each response
567 variable and parameter.

Table S8: Summary of mixed-effects model testing the effects of sampling season (Month), tree species richness (TSR; 1, 2, 4 species) and mycorrhizal type (Mycor; AM, EcM, AM+EcM), and their interaction on diversity indices of soil microbes

Predictors	Soil microbes	Soi fungi	Soil bacteria
(A) Abundance (biomass)			
Month	$F_{1,58} = 4.8^*$	$F_{1,58} = 0.0$	$F_{1,59} = 5.7^*$
Mycor	$F_{2,54} = 5.5^{**}$	$F_{2,54} = 1.5$	$F_{2,54} = 3.0$
Log(TSR)	$F_{1,54} = 7.5^{**}$	$F_{1,54} = 8.5^{**}$	$F_{1,54} = 0.1$
Mycor×Log(TSR)	$F_{2,54} = 0.9$	$F_{2,54} = 1.1$	$F_{2,54} = 0.1$
R2m(R2c)	0.19(0.38)	0.12(0.42)	0.08(0.30)
(B) Taxonomic richness (Chao1)			
Mycor	$F_{2,54} = 6.3^{**}$	$F_{2,54} = 14.8^{***}$	$F_{2,54} = 1.1$
Log(TSR)	$F_{1,54} = 82.8^{***}$	$F_{1,54} = 79.2^{***}$	$F_{1,54} = 59.8^{***}$
Mycor×Log(TSR)	$F_{2,54} = 0.9$	$F_{2,54} = 2.2$	$F_{2,54} = 0.2$
R2m(R2c)	0.61(0.76)	0.68(0.90)	0.46(0.50)
(C) Shannon-Wiener diversity			
Mycor	$F_{2,54} = 16.4^{***}$	$F_{2,54} = 31.7^{***}$	$F_{2,54} = 0.5$
Log(TSR)	$F_{1,54} = 43.0^{***}$	$F_{1,54} = 30.5^{***}$	$F_{1,54} = 13.9^{***}$
Mycor×Log(TSR)	$F_{2,54} = 2.5$	$F_{2,54} = 1.9$	$F_{2,54} = 0.1$
R2m(R2c)	0.55(0.67)	0.61(0.78)	0.17(0.25)

Note: Statistical significance is indicated by asterisks: * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$. Marginal significance ($0.05 \leq p < 0.1$) is in italic. For microbial, fungal and bacterial abundance (y_i), min–max transformed data were further power-transformed using the t-values reported in Table S3. Models were then fitted as linear mixed-effects models: $lme(y_i^t \sim \text{Month} + \text{Mycor} \times \log(\text{Richness}), \text{random} = \sim 1 \mid \text{composition}/\text{Month})$, using Type I sums of squares. For taxonomic richness and Shannon diversity, min–max transformed data were power-transformed using the t-values in Table S3, and models were fitted as $lme(y_i^t \sim \text{Mycor} \times \log(\text{Richness}), \text{random} = \sim 1 \mid \text{composition})$. “Month” was excluded because soil fungal and microbial diversity were measured only once (September 2021). Outlier removal was conducted separately for each biodiversity index and functional group, resulting in different final numbers of observations among models. Therefore, the numerator and denominator degrees of freedom ($F_{\text{numDF}, \text{denDF}}$) are reported specifically for each response variable and parameter.

Table S9: Summary of mixed-effects model analyses testing the effects of tree species richness (TSR; 1, 2, 4 species) and mycorrhizal types (Mycor; AM, EcM, AM+EcM) on potential mediators. The potential mediators included (a) aboveground tree stand conditions, (b) adsorptive root carbon and nutrients, (c) transportation root carbon and nutrients and (d) soil properties.

(A) Aboveground tree stand characteristics

<i>predictors</i>	<i>Df</i>	<i>denDF</i>	<i>Leaf C</i>	<i>Leaf N</i>	<i>Leaf C:N</i>	<i>Wood volumes</i>	<i>ENL</i>
Mycor	2	54	21.39***	22.92***	14.40***	0.37	0.65
Log(TSR)	1	54	0.26	9.52**	6.61*	7.70**	7.03*
Mycor:Log(TSR)	2	54	0.24	0.19	0.53	0.45	0.36
R ² m(R ² c)			0.42(0.71)	0.46(0.64)	0.37(0.61)	0.14(0.61)	0.14(0.89)

(B) Absorptive root nutrient concentration

<i>Predictors</i>	<i>Df</i>	<i>denDF</i>	<i>C</i>	<i>N</i>	<i>C:N</i>	<i>Mg</i>	<i>Ca</i>
Mycor	2	54	1.25	0.47	0.97	3.99*	6.40**
Log(TSR)	1	54	0.03	0.01	0.13	2.19	0.56
Mycor:Log(TSR)	2	54	6.90**	0.42	1.39	1.82	0.47
R ² m(R ² c)			0.17(0.22)	0.02(0.02)	0.06(0.06)	0.15(0.20)	0.15(0.15)

(C) Transportation root nutrient concentration

<i>Predictors</i>	<i>Df</i>	<i>denDF</i>	<i>C</i>	<i>N</i>	<i>C:N</i>	<i>Mg</i>	<i>Ca</i>
Mycor	2	54	0.26	1.94	2.92	0.35	3.21*
Log(TSR)	1	54	0.01	0.35	0.86	0.00	2.68
Mycor:Log(TSR)	2	54	0.46	1.56	1.35	0.30	0.80
R ² m(R ² c)			0.02(0.02)	0.09(0.09)	0.11(0.11)	0.02(0.02)	0.12(0.12)

(D) Soil properties

<i>Predictors</i>	<i>Df</i>	<i>denDF</i>	<i>pH</i>	<i>TC</i>	<i>TN</i>	<i>C:N</i>	<i>NO₃⁻</i>	<i>PO₄⁻</i>
Mycor	2	54	0.37	3.56*	2.79	0.03	4.00*	0.39
Log(TSR)	1	54	0.01	1.03	1.31	0.03	7.12*	1.78
Mycor:Log(TSR)	2	54	0.06	1.31	0.35	0.67	1.30	0.11
R ² m(R ² c)			0.01(0.62)	0.13(0.35)	0.09(0.09)	0.02(0.26)	0.22(0.53)	0.04(0.28)

Statistical significance is indicated by asterisks: *p < 0.05, **p < 0.01, ***p < 0.001. Marginal significance (0.05 ≤ p < 0.1) is in italic.

588 **Table S10: Pearson's correlations among mediators significantly influenced by the**
589 **treatment factors (tree species richness and/or mycorrhizal type).**

<i>Variables</i>	<i>Wood volume</i>	<i>ENL</i>	<i>Leaf C</i>	<i>Leaf N</i>	<i>Leaf C:N</i>	<i>Root C</i>	<i>Root Mg</i>	<i>Root Ca</i>	<i>Soil TC</i>	<i>Soil TN</i>
ENL	0.73***									
Leaf C	-0.29**	-0.06								
Leaf N	-0.17	-0.16	0.52***							
Leaf C:N	0.12	0.15	-0.38***	-0.97***						
Root C	0.14	<i>0.2</i>	-0.1	-0.14	0.08					
Root Mg	0.03	0.08	-0.24*	-0.18	0.12	-0.1				
Root Ca	0.07	0.05	0.22*	<i>0.19</i>	-0.14	-0.11	-0.62***			
Soil TC	0.09	0	-0.15	-0.13	0.09	-0.06	0.29**	-0.01		
Soil TN	0.16	0.11	-0.1	-0.03	0	-0.04	0.3**	0.01	0.74***	
Soil NO ₃ ⁻	-0.28*	<i>-0.21</i>	0.28*	0.41***	-0.35**	-0.04	-0.1	<i>0.2</i>	-0.31**	-0.14

590 Note: Statistical significance is indicated by asterisks: *p < 0.05, **p < 0.01, ***p < 0.001.
591 Marginal significance (0.05 ≤ p < 0.1) is in italic.

Table S11 A: The structural equation model for multitrophic abundance of invertebrates, with min-max transformation

<i>Response</i>	<i>Predictor</i>	<i>DF</i>	<i>Std.Estimate</i>	<i>Std.Error</i>	<i>p-value</i>
Canopy organisms	Leaf C:N	18	-0.257*	0.005	0.042
	ENL	18	0.026	0.0052	0.830
Surface organisms	ENL	17	-0.193	0.0055	0.133
	Leaf C:N	17	-0.172	0.0052	0.163
	Root Ca	17	0.129	0.0268	0.236
Soil organisms	ENL	17	0.105	0.0025	0.347
	Leaf C:N	17	0.319**	0.0024	0.008
	Root Ca	17	0.345**	0.0133	0.003
	Log(TSR)	58	0.170	0.0166	0.144
ENL	Log(TSR)	57	0.397**	0.8434	0.005
	EcM%	57	-0.051	0.9918	0.694
Leaf C:N	Log(TSR)	57	0.285**	0.6425	0.007
	EcM%	57	-0.537***	0.7809	<0.001
Root Ca	Log(TSR)	77	-0.084	0.1136	0.424
	EcM%	77	0.380***	0.1419	<0.001
Root C	Log(TSR)	56	-0.272	0.0273	0.116
	EcM%	56	-0.455*	0.0361	0.015
	Log(TSR)	56	0.450*	0.0406	0.047
Soil NO3-	Log(TSR)	57	-0.379**	0.0873	0.003
	EcM%	57	<i>0.208</i>	0.1055	0.079
~~Canopy organisms	~~Surface organisms	80	0.254*	-	0.012
~~Canopy organisms	~~Soil organisms	80	<i>0.153</i>	-	0.089
~~Soil organisms	~~Surface organisms	80	0.069	-	0.273
~~Leaf C:N	~~Soil NO3-	80	-0.272**	-	0.008
~~Root C	~~ENL	80	0.016	-	0.445

Note: Statistical significance (in bold) is indicated by asterisks: * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$. Marginal significance ($0.05 \leq p < 0.1$) is in italic. EcM% represents to the proportion of EcM tree species in each plot. The model fit was good (Fisher's $C = 34.249$, df

595 = 40, p = 0.726). Likelihood-based χ^2 statistics could not be calculated because the model
 596 structures (combined both simple linear regression and mixed effect models).

<i>Response</i>	<i>family</i>	<i>Marginal Rm2</i>	<i>Conditional R2c</i>
Canopy organisms	gaussian	0.06	0.40
Surface organisms	gaussian	0.09	0.58
Soil organisms	gaussian	0.27	0.36
ENL	gaussian	0.15	0.88
Leaf C:N	gaussian	0.37	0.59
Root Ca	gaussian	0.15	NA
Root C	gaussian	0.08	0.16
Soil NO3-	gaussian	0.18	0.54

597

Table S11 B: The structural equation model for multitrophic diversity of invertebrates, with min-max transformation

<i>Response</i>	<i>Predictor</i>	<i>DF</i>	<i>Std.Estimate</i>	<i>Std.Error</i>	<i>p-value</i>
Canopy organisms	Leaf C:N	19	-0.306*	0.0041	0.014
	Log(TSR)	58	0.297*	0.0273	0.016
Surface organisms	ENL	17	-0.252	0.0055	0.057
	Leaf C:N	17	0.003	0.005	0.982
	Root Ca	17	0.117	0.025	0.252
Soil organisms	ENL	17	0.125	0.0029	0.267
	Leaf C:N	17	0.301*	0.0028	0.012
	Root Ca	17	0.333**	0.0155	0.005
ENL	Log(TSR)	57	0.397**	0.8434	0.005
	EcM%	57	-0.051	0.9918	0.694
Leaf C:N	Log(TSR)	57	0.285**	0.6425	0.007
	EcM%	57	-0.537***	0.7809	<0.001
Root Ca	Log(TSR)	77	-0.084	0.1136	0.424
	EcM%	77	0.380***	0.1419	<0.001
Root C	Log(TSR)	56	-0.272	0.0273	0.116
	EcM%	56	-0.455*	0.0361	0.015
	Log(TSR)	56	0.450*	0.0406	0.047
Soil NO3-	Log(TSR)	57	-0.379**	0.0873	0.003
	EcM%	57	0.208	0.1055	0.079
~~Canopy organisms	~~Surface organisms	80	0.411***	-	<0.001
~~Canopy organisms	~~Soil organisms	80	-0.011	-	0.460
~~Soil organisms	~~Surface organisms	80	-0.206*	-	0.034
~~Leaf C:N	~~Soil NO3-	80	-0.272**	-	0.008
~~Root C	~~ENL	80	0.016	-	0.445

Note: Statistical significance (in bold) is indicated by asterisks: * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$. Marginal significance ($0.05 \leq p < 0.1$) is in italic. EcM% represents to the proportion of EcM tree species in each plot. The model fit was good (Fisher's $C = 33.551$, $df = 42$, p -value = 0.821). Likelihood-based χ^2 statistics could not be calculated because the model structures (combined both simple linear regression and mixed effect models).

<i>Response</i>	<i>family</i>	<i>Marginal Rm2</i>	<i>Conditional R2c</i>
Canopy organisms	gaussian	0.13	0.32
Surface organisms	gaussian	0.07	0.69
Soil organisms	gaussian	0.20	0.42
ENL	gaussian	0.15	0.88
Leaf C:N	gaussian	0.37	0.59
Root Ca	gaussian	0.15	NA
Root C	gaussian	0.08	0.16
Soil NO3-	gaussian	0.18	0.54

603

Table S12 A: The structural equation model for multitrophic abundance of invertebrates, with z-score transformation

<i>Response</i>	<i>Predictor</i>	<i>DF</i>	<i>Std.Estimate</i>	<i>Std.Error</i>	<i>p-values</i>
Canopy organisms	Leaf C:N	18	-0.26*	0.02	0.042
	ENL	18	0.03	0.02	0.837
Surface organisms	ENL	17	-0.19	0.03	0.134
	Leaf C:N	17	-0.13	0.03	0.295
	Root Ca	17	0.14	0.15	0.222
Soil organisms	ENL	17	0.12	0.01	0.274
	Leaf C:N	17	0.27*	0.01	0.02
	Root Ca	17	0.35**	0.06	0.003
	Log(TSR)	58	0.15	0.07	0.178
ENL	Log(TSR)	57	0.4**	0.84	0.005
	EcM%	57	-0.05	0.99	0.694
Leaf C:N	Log(TSR)	57	0.28**	0.64	0.007
	EcM%	57	-0.54***	0.78	<0.001
Root Ca	Log(TSR)	77	-0.08	0.11	0.424
	EcM%	77	0.38***	0.14	<0.001
Root C	Log(TSR)	56	-0.27	0.03	0.116
	EcM%	56	-0.45*	0.04	0.015
	Log(TSR)	56	0.45*	0.04	0.047
Soil NO ₃ -	Log(TSR)	57	-0.38**	0.09	0.003
	EcM%	57	<i>0.21</i>	0.11	0.079
~~Canopy organisms	~~Surface organisms	80	0.29**		0.005
~~Canopy organisms	~~Soil organisms	80	<i>0.17</i>		0.066
~~Soil organisms	~~Surface organisms	80	-0.02		0.42
~~Leaf C:N	~~Soil NO ₃ -	80	-0.27**		0.008
~~Root C	~~ENL	80	0.02		0.445

Note: Statistical significance (in bold) is indicated by asterisks: *p < 0.05, **p < 0.01, ***p < 0.001. Marginal significance (0.05 ≤ p < 0.1) is in italic. EcM% represents to the proportion of EcM tree species in each plot. The model fit was good (Fisher's C = 26.232, df

607 = 40, P = 0.954). Likelihood-based χ^2 statistics could not be calculated because the model
 608 structures (combined both simple linear regression and mixed effect models).

<i>Response</i>	<i>family</i>	<i>Marginal Rm2</i>	<i>Conditional R2c</i>
Canopy organisms	gaussian	0.06	0.43
Surface organisms	gaussian	0.08	0.41
Soil organisms	gaussian	0.24	0.26
ENL	gaussian	0.15	0.88
Leaf C:N	gaussian	0.37	0.59
Root Ca	gaussian	0.15	NA
Root C	gaussian	0.08	0.16
Soil NO ₃ -	gaussian	0.18	0.54

609

Table S12 B: The structural equation model for multitrophic diversity of invertebrates, with z-score transformation

<i>Response</i>	<i>Predictor</i>	<i>DF</i>	<i>Std.Estimate</i>	<i>Std.Error</i>	<i>p-values</i>
Canopy organisms	Leaf C:N	19	-0.31*	0.02	0.014
	Log(TSR)	58	0.29*	0.15	0.019
Surface organisms	ENL	18	-0.23	0.03	0.078
	Root Ca	18	0.1	0.12	0.315
Soil organisms	ENL	17	0.18	0.01	0.108
	Leaf C:N	17	0.27*	0.01	0.024
	Root Ca	17	0.35**	0.06	0.003
ENL	Log(TSR)	57	0.4**	0.84	0.005
	EcM%	57	-0.05	0.99	0.694
Leaf C:N	Log(TSR)	57	0.28**	0.64	0.007
	EcM%	57	-0.54***	0.78	<0.001
Root Ca	Log(TSR)	77	-0.08	0.11	0.424
	EcM%	77	0.38***	0.14	<0.001
Root C	Log(TSR)	56	-0.27	0.03	0.116
	EcM%	56	-0.45*	0.04	0.015
	Log(TSR)	56	0.45*	0.04	0.047
Soil NO ₃ -	Log(TSR)	57	-0.38**	0.09	0.003
	EcM%	57	0.21	0.11	0.079
~~Canopy organisms	~~Surface organisms	80	0.41***		<0.001
~~Canopy organisms	~~Soil organisms	80	-0.03		0.409
~~Soil organisms	~~Surface organisms	80	-0.24*		0.015
~~Leaf C:N	~~Soil NO ₃ -	80	-0.27**		0.008
~~Root C	~~ENL	80	0.02		0.445

Note: Statistical significance (in bold) is indicated by asterisks: * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$. Marginal significance ($0.05 < p \leq 0.1$) is in italic. EcM% represents to the proportion of EcM tree species in each plot. The model fit was good (Fisher's $C = 34.818$, $df = 44$, $p\text{-value} = 0.837$). Likelihood-based χ^2 statistics could not be calculated because the model structures (combined both simple linear regression and mixed effect models).

<i>Response</i>	<i>family</i>	<i>Marginal Rm2</i>	<i>Conditional R2c</i>
Canopy organisms	gaussian	0.12	0.34
Surface organisms	gaussian	0.06	0.65
Soil organisms	gaussian	0.21	0.47
ENL	gaussian	0.15	0.88
Leaf C:N	gaussian	0.37	0.59
Root Ca	gaussian	0.15	NA
Root C	gaussian	0.08	0.16
Soil NO ₃ -	gaussian	0.18	0.54

615

Table S13 A: The structural equation model for multitrophic abundance of invertebrates (min-max transformation), replacing ENL with tree wood volume as a mediator

<i>Response</i>	<i>Predictor</i>	<i>DF</i>	<i>Std.Estimate</i>	<i>Std.Error</i>	<i>p-values</i>
Canopy organisms	Wood volume	18	0.05	0.12	0.66
	Leaf C:N	18	-0.26*	0.00	0.038
Surface organisms	Wood volume	17	0.03	0.12	0.776
	Leaf C:N	17	-0.2	0.00	0.108
	Root Ca	17	0.11	0.03	0.3
Soil organisms	Wood volume	17	0.04	0.05	0.745
	Leaf C:N	17	0.31*	0.00	0.01
	Root Ca	17	0.34**	0.01	0.004
	Log(TSR)	58	0.19	0.01	0.101
Wood volume	Log(TSR)	57	0.32*	0.03	0.014
	EcM%	57	-0.1	0.04	0.432
Leaf C:N	Log(TSR)	57	0.28**	0.64	0.007
	EcM%	57	-0.54***	0.78	<0.001
Root Ca	Log(TSR)	77	-0.08	0.11	0.424
	EcM%	77	0.38***	0.14	<0.001
Root C	Log(TSR)	56	-0.27	0.03	0.116
	EcM%	56	-0.45*	0.04	0.015
	Log(TSR)	56	0.45*	0.04	0.047
Soil NO ₃ -	Log(TSR)	57	-0.38**	0.09	0.003
	EcM%	57	<i>0.21</i>	0.11	0.079
~~Canopy organisms	~~Surface organisms	80	0.25*		0.014
~~Canopy organisms	~~Soil organisms	80	<i>0.17</i>		0.073
~~Soil organisms	~~Surface organisms	80	0.05		0.322
~~Leaf C:N	~~Soil NO ₃ -	80	-0.27**		0.008
~~Root C	~~Wood volume	80	0.12		0.139

Note: Statistical significance (in bold) is indicated by asterisks: * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$. Marginal significance ($0.05 \leq p < 0.1$) is in italic. EcM% represents to the proportion

618 of EcM tree species in each plot. The model fit was good (Fisher's $C = 35.715$, $df = 40$, p -
619 value = 0.663). Likelihood-based χ^2 statistics could not be calculated because the model
620 structures (combined both simple linear regression and mixed effect models).

<i>Response</i>	<i>family</i>	<i>Marginal Rm2</i>	<i>Conditional R2c</i>
Canopy organisms	gaussian	0.06	0.42
Surface organisms	gaussian	0.06	0.56
Soil organisms	gaussian	0.24	0.28
Wood volume	gaussian	0.11	0.59
Leaf C:N	gaussian	0.37	0.59
Root Ca	gaussian	0.15	NA
Root C	gaussian	0.08	0.16
Soil NO ₃ -	gaussian	0.18	0.54

621

Table S13 B: The structural equation model for multitrophic diversity of invertebrates (min-max transformation), replacing ENL with Wood volume as a mediator

<i>Response</i>	<i>Predictor</i>	<i>DF</i>	<i>Std.Estimate</i>	<i>Std.Error</i>	<i>p-values</i>
Canopy organisms	Wood volume	18	0.08	0.10	0.475
	Leaf C:N	18	-0.31*	0.00	0.015
	Log(TSR)	58	0.27*	0.03	0.036
Surface organisms	Wood volume	17	-0.06	0.12	0.615
	Leaf C:N	17	-0.02	0.00	0.85
	Root Ca	17	0.11	0.03	0.317
Soil organisms	Wood volume	17	0.08	0.06	0.448
	Leaf C:N	17	0.31*	0.00	0.01
	Root Ca	17	0.34**	0.02	0.004
Wood volume	Log(TSR)	57	0.32*	0.03	0.014
	EcM%	57	-0.1	0.04	0.432
Leaf C:N	Log(TSR)	57	0.28**	0.64	0.007
	EcM%	57	-0.54***	0.78	<0.001
Root Ca	Log(TSR)	77	-0.08	0.11	0.424
	EcM%	77	0.38***	0.14	<0.001
Root C	Log(TSR)	56	-0.27	0.03	0.116
	EcM%	56	-0.45*	0.04	0.015
	Log(TSR)	56	0.45*	0.04	0.047
Soil NO ₃ -	Log(TSR)	57	-0.38**	0.09	0.003
	EcM%	57	<i>0.21</i>	0.11	0.079
~~Canopy organisms	~~Surface organisms	80	0.4***		<0.001
~~Canopy organisms	~~Soil organisms	80	-0.01		0.465
~~Soil organisms	~~Surface organisms	80	-0.23*		0.02
~~Leaf C:N	~~Soil NO ₃ -	80	-0.27**		0.008
~~Root C	~~Wood volume	80	0.12		0.139

Note: Statistical significance (in bold) is indicated by asterisks: *p < 0.05, **p < 0.01, ***p < 0.001. Marginal significance (0.05 ≤ p < 0.1) is in italic. EcM% represents to the proportion

624 of EcM tree species in each plot. The model fit was good (Fisher's $C = 37.285$, $df = 40$, p -
625 value = 0.593). Likelihood-based χ^2 statistics could not be calculated because the model
626 structures (combined both simple linear regression and mixed effect models).

<i>Response</i>	<i>family</i>	<i>Marginal Rm2</i>	<i>Conditional R2c</i>
Canopy organisms	gaussian	0.13	0.33
Surface organisms	gaussian	0.01	0.63
Soil organisms	gaussian	0.19	0.40
Wood volume	gaussian	0.11	0.59
Leaf C:N	gaussian	0.37	0.59
Root Ca	gaussian	0.15	NA
Root C	gaussian	0.08	0.16
Soil NO ₃ -	gaussian	0.18	0.54

627

Table S14 A: The structural equation model for multitrophic abundance of invertebrates (min-max transformation), including tree wood volume as a mediator

<i>Response</i>	<i>Predictor</i>	<i>DF</i>	<i>Std.Estimate</i>	<i>Std.Error</i>	<i>p-values</i>
Canopy organisms	Wood volume	18	0.05	0.12	0.66
	Leaf C:N	18	-0.26*	0.00	0.038
Surface organisms	Wood volume	16	0.31	0.16	0.069
	ENL	16	-0.42*	0.01	0.023
	Leaf C:N	16	-0.17	0.00	0.154
	Root Ca	16	0.12	0.03	0.258
Soil organisms	Wood volume	16	-0.03	0.07	0.84
	ENL	16	0.1	0.00	0.531
	Leaf C:N	16	0.31*	0.00	0.011
	Root Ca	16	0.34**	0.01	0.005
	Log(TSR)	58	0.17	0.01	0.141
ENL	Log(TSR)	57	0.4**	0.84	0.005
	EcM%	57	-0.05	0.99	0.694
Wood volume	Log(TSR)	57	0.32*	0.03	0.014
	EcM%	57	-0.1	0.04	0.432
Leaf C:N	Log(TSR)	57	0.28**	0.64	0.007
	EcM%	57	-0.54***	0.78	<0.001
Root Ca	Log(TSR)	77	-0.08	0.11	0.424
	EcM%	77	0.38***	0.14	<0.001
Root C	Log(TSR)	56	-0.27	0.03	0.116
	EcM%	56	-0.45*	0.04	0.015
	Log(TSR)	56	0.45*	0.04	0.047
Soil NO ₃ -	Log(TSR)	57	-0.38**	0.09	0.003
	EcM%	57	0.21	0.11	0.079
~~Canopy organisms	~~Surface organisms	80	0.22*		0.027
~~Canopy organisms	~~Soil organisms	80	0.17		0.069
~~Soil organisms	~~Surface organisms	80	0.07		0.272

~~Leaf C:N	~~Soil NO ₃ -	80	-0.27**		0.008
~~Root C	~~Wood volume	80	0.12	NA	0.139
~~ENL	~~Wood volume	80	0.48***	NA	<0.001

628 Note: Statistical significance (in bold) is indicated by asterisks: * $p < 0.05$, ** $p < 0.01$, *** $p <$
629 0.001. Marginal significance ($0.05 \leq p < 0.1$) is in italic. EcM% represents to the proportion
630 of EcM tree species in each plot. The model fit was good (Fisher's $C = 45.006$, $df = 50$, p -
631 value = 0.674). Likelihood-based χ^2 statistics could not be calculated because the model
632 structures (combined both simple linear regression and mixed effect models).

<i>Response</i>	<i>family</i>	<i>Marginal Rm2</i>	<i>Conditional R2c</i>
Canopy organisms	gaussian	0.06	0.42
Surface organisms	gaussian	0.13	0.57
Soil organisms	gaussian	0.24	0.29
ENL	gaussian	0.15	0.88
Wood volume	gaussian	0.11	0.59
Leaf C:N	gaussian	0.37	0.59
Root Ca	gaussian	0.15	NA
Root C	gaussian	0.08	0.16
Soil NO ₃ -	gaussian	0.18	0.54

633

Table S14 B: The structural equation model for multitrophic diversity of invertebrates (min-max transformation), including tree wood volume as a mediator

<i>Response</i>	<i>Predictor</i>	<i>DF</i>	<i>Std.Estimate</i>	<i>Std.Error</i>	<i>p-values</i>
Canopy organisms	Wood volume	18	0.08	0.10	0.475
	Leaf C:N	18	-0.31*	0.00	0.015
	Log(TSR)	58	0.27*	0.03	0.036
Surface organisms	Wood volume	16	0.17	0.15	0.263
	ENL	16	-0.38*	0.01	0.034
	Leaf C:N	16	0	0.00	0.979
	Root Ca	16	0.11	0.02	0.262
Soil organisms	Wood volume	16	-0.01	0.09	0.956
	ENL	16	0.13	0.00	0.415
	Leaf C:N	16	0.3*	0.00	0.014
	Root Ca	16	0.33**	0.02	0.005
ENL	Log(TSR)	57	0.4**	0.84	0.005
	EcM%	57	-0.05	0.99	0.694
Wood volume	Log(TSR)	57	0.32*	0.03	0.014
	EcM%	57	-0.1	0.04	0.432
Leaf C:N	Log(TSR)	57	0.28**	0.64	0.007
	EcM%	57	-0.54***	0.78	<0.001
Root Ca	Log(TSR)	77	-0.08	0.11	0.424
	EcM%	77	0.38***	0.14	<0.001
Root C	Log(TSR)	56	-0.27	0.03	0.116
	EcM%	56	-0.45*	0.04	0.015
	Log(TSR)	56	0.45*	0.04	0.047
Soil NO ₃ -	Log(TSR)	57	-0.38**	0.09	0.003
	EcM%	57	0.21	0.11	0.079
~~Canopy organisms	~~Surface organisms	80	0.4***		<0.001
~~Canopy organisms	~~Soil organisms	80	-0.01		0.464
~~Soil organisms	~~Surface organisms	80	-0.21*		0.032

~~Leaf C:N	~~Soil NO ₃ -	80	-0.27**	0.008
~~Root C	~~Wood volume	80	0.12	0.139
~~Wood volume	~~ENL	80	0.48***	<0.001

634 Note: Statistical significance (in bold) is indicated by asterisks: *p < 0.05, **p < 0.01, ***p <
635 0.001. Marginal significance (0.05 ≤ p < 0.1) is in italic. EcM% represents to the proportion
636 of EcM tree species in each plot. The model fit was good (Fisher's C = 44.71, df = 50, p-
637 value = 0.685). Likelihood-based χ^2 statistics could not be calculated because the model
638 structures (combined both simple linear regression and mixed effect models).

<i>Response</i>	<i>family</i>	<i>Marginal Rm2</i>	<i>Conditional R2c</i>
Canopy organisms	gaussian	0.13	0.33
Surface organisms	gaussian	0.08	0.70
Soil organisms	gaussian	0.19	0.41
ENL	gaussian	0.15	0.88
Wood volume	gaussian	0.11	0.59
Leaf C:N	gaussian	0.37	0.59
Root Ca	gaussian	0.15	NA
Root C	gaussian	0.08	0.16
Soil NO ₃ -	gaussian	0.18	0.54

639

Table S15: Model structure and performance for detecting mediator effects on biodiversity indices of aboveground organisms. Each biodiversity index for each trophic group was power transformed using the corresponding t-value (power-trans(y, t-value)).
A: Abundance

<i>Fauna group</i>	<i>t-value</i>	<i>Final model structures</i>
Total	0.66	power-trans(y, 0.66) ~ Leaf C:N , random = ~ 1 composition; R ² m=0.039 (R ² c=0.53)
Herbivores	0.56	power-trans(y, 0.56) ~ 1 , random = ~ 1 composition;
Fungivores	0.55	power-trans(y, 0.55) ~ 1 , random = ~ 1 composition;
Omnivores	0.37	power-trans(y, 0.37) ~ Soil C + Root C + Leaf C:N + ENL , random = ~ 1 composition; R ² m=0.195 (R ² c=0.311)
Predators	0.51	power-trans(y, 0.51) ~ Leaf C:N , random = ~ 1 composition; R ² m=0.043 (R ² c=0.577)
Foliar fungi	0.77	power-trans(y, 0.77) ~ 1 , random = ~ 1 composition;
Endo. fungi	0.68	power-trans(y, 0.68) ~ Soil C, random = ~ 1 composition; R ² m=0.063 (R ² c=0.063)
Epi.fungi	0.72	power-trans(y, 0.72) ~ Leaf C:N + Root Ca, random = ~ 1 composition; R ² m=0.261 (R ² c=0.528)

640

B: Taxonomic richness

<i>Fauna group</i>	<i>t-value</i>	<i>Final model structures</i>
Total	0.88	power-trans(y, 0.88) ~ Soil C + Leaf C:N + Soil NO ₃ ⁻ , random = ~ 1 composition; R ² m=0.152 (R ² c=0.579)
Herbivores	0.85	power-trans(y, 0.85) ~ Soil C , random = ~ 1 composition; R ² m=0.056 (R ² c=0.501)
Fungivores	0.99	power-trans(y, 0.99) ~ Leaf C:N + Soil NO ₃ ⁻ , random = ~ 1 composition; R ² m=0.065 (R ² c=0.065)
Omnivores	0.76	power-trans(y, 0.76) ~ Soil C , random = ~ 1 composition; R ² m=0.047 (R ² c=0.125)
Predators	0.95	power-trans(y, 0.95) ~ Leaf C:N , random = ~ 1 composition; R ² m=0.073 (R ² c=0.581)
Foliar fungi	1.38	power-trans(y, 1.38) ~ 1 , random = ~ 1 composition;
Endo. fungi	0.80	power-trans(y, 0.8) ~ Root C , random = ~ 1 composition; R ² m=0.063 (R ² c=0.063)
Epi.fungi	0.70	power-trans(y, 0.7) ~ 1 , random = ~ 1 composition;

641

C: Shannon-Wiener diversity index

<i>Fauna group</i>	<i>t-value</i>	<i>Final model structures</i>
Total	2.80	power-trans(y, 2.8) ~ Leaf C:N + Soil NO ₃ ⁻ , random = ~ 1 composition; R ² m=0.099 (R ² c=0.535)
Herbivores	1.70	power-trans(y, 1.7) ~ Root C, random = ~ 1 composition; R ² m=0.026 (R ² c=0.508)
Fungivores	1.45	power-trans(y, 1.45) ~ Leaf C:N + ENL + Soil NO ₃ ⁻ , random = ~ 1 composition; R ² m=0.194 (R ² c=0.334)
Omnivores	1.21	power-trans(y, 1.21) ~ 1, random = ~ 1 composition
Predators	1.76	power-trans(y, 1.76) ~ Soil NO ₃ ⁻ , random = ~ 1 composition; R ² m=0.029 (R ² c=0.276)
Foliar fungi	0.71	power-trans(y, 0.71) ~ Leaf C:N + Root Ca, random = ~ 1 composition; R ² m=0.189 (R ² c=0.189)
Endo. fungi	1.39	power-trans(y, 1.39) ~ Soil C + Root C + ENL, random = ~ 1 composition; R ² m=0.232 (R ² c=0.232)
Epi.fungi	1.63	power-trans(y, 1.63) ~ 1, random = ~ 1 composition

642

Table S16: Model structure and performance for detecting mediator effects on biodiversity indices of soil surface organisms. Each biodiversity index for each trophic group was power transformed using the corresponding t-value (power-trans(y, t-value)).

A: Abundance

<i>Fauna group</i>	<i>t-value</i>	<i>Final model structures</i>
Total	0.41	power-trans(y, 0.41) ~ ENL , random = ~ 1 composition; R ² m=0.032 (R ² c=0.304)
Herbivores	0.43	power-trans(y, 0.43) ~ Leaf C:N , random = ~ 1 composition; R ² m=0.028 (R ² c=0.028)
Detritivores	0.63	power-trans(y, 0.63) ~ ENL + Root Ca, random = ~ 1 composition; R ² m=0.068 (R ² c=0.068)
Omnivores	0.48	power-trans(y, 0.48) ~ ENL, random = ~ 1 composition; R ² m=0.034 (R ² c=0.259)
Predators	0.42	power-trans(y, 0.42) ~ Leaf C:N, random = ~ 1 composition; R ² m=0.052 (R ² c=0.724)

643

B: Taxonomic richness

<i>Fauna group</i>	<i>t-value</i>	<i>Final model structures</i>
Total	0.88	power-trans(y, 0.88) ~ ENL, random = ~ 1 composition; R ² m=0.041 (R ² c=0.716)
Herbivores	0.77	power-trans(y, 0.77) ~ 1 , random = ~ 1 composition
Detritivores	0.86	power-trans(y, 0.86) ~ ENL + Root Ca, random = ~ 1 composition; R ² m=0.102 (R ² c=0.440)
Omnivores	0.79	power-trans(y, 0.79) ~ Leaf C:N, random = ~ 1 composition; R ² m=0.058 (R ² c=0.058)
Predators	0.68	power-trans(y, 0.68) ~ Root C, random = ~ 1 composition; R ² m=0.031 (R ² c=0.679)

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C: Shannon-Wiener diversity index

<i>Fauna group</i>	<i>t-value</i>	<i>Final model structures</i>
Total	1.24	power-trans(y, 1.24) ~ ENL, random = ~ 1 composition; R ² m=0.03 (R ² c=0.307)
Herbivores	1.32	power-trans(y, 1.32) ~ 1 , random = ~ 1 composition
Detritivores	1.24	power-trans(y, 1.24) ~ ENL + Root Ca, random = ~ 1 composition; R ² m=0.11 (R ² c=0.437)
Omnivores	0.67	power-trans(y, 0.67) ~ Root C + Leaf C:N, random = ~ 1 composition; R ² m=0.101 (R ² c=0.101)
Predators	1.51	power-trans(y, 1.51) ~ ENL, random = ~ 1 composition; R ² m=0.044 (R ² c=0.501)

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Table S17: Model structure and performance for detecting mediator effects on biodiversity indices of belowground organisms. Each biodiversity index for each trophic group was power transformed using the corresponding t-value (power-trans(y, t-value)).
A: Abundance

<i>Fauna group</i>	<i>t-value</i>	<i>Final model structures</i>
Nematode (Ne)	0.54	power-trans(y, 0.54) ~ Soil C + Leaf C:N, random = ~ 1 composition; R ² m=0.15 (R ² c=0.635)
Ne:Herbivores	0.47	power-trans(y, 0.47) ~ Leaf C:N, random = ~ 1 composition; R ² m=0.143 (R ² c=0.196)
Ne:Bacterivores	0.55	power-trans(y, 0.55) ~ Leaf C:N + Soil NO ₃ ⁻ , random = ~ 1 composition; R ² m=0.096 (R ² c=0.096)
Ne:Fungivores	0.60	power-trans(y, 0.6) ~ Soil NO ₃ ⁻ , random = ~ 1 composition; R ² m=0.061 (R ² c=0.156)
Mesofauna (Me)	0.44	power-trans(y, 0.44) ~ Soil C + ENL, random = ~ 1 composition; R ² m=0.173 (R ² c=0.52)
Me:Fungivores	0.26	power-trans(y, 0.26) ~ ENL + Root Ca, random = ~ 1 composition; R ² m=0.095 (R ² c=0.095)
Me:Omnivores	0.23	power-trans(y, 0.23) ~ Soil C + Root C + ENL, random = ~ 1 composition; R ² m=0.203 (R ² c=0.358)
Me:Predators	0.31	power-trans(y, 0.31) ~ ENL + Root Ca, random = ~ 1 composition; R ² m=0.098 (R ² c=0.194)
Macrofauna (Ma)	0.43	power-trans(y, 0.43) ~ Soil C + Root Ca, random = ~ 1 composition; R ² m=0.109 (R ² c=0.109)
Ma: Predators	0.58	power-trans(y, 0.58) ~ ENL + Root Ca, random = ~ 1 composition; R ² m=0.111 (R ² c=0.569)
Ma: Omnivores	0.58	power-trans(y, 0.58) ~ ENL + Root Ca, random = ~ 1 composition; R ² m=0.094 (R ² c=0.094)
Earthworm	0.46	power-trans(y, 0.46) ~ Soil C + Root C + Soil NO ₃ ⁻ , random = ~ 1 composition; R ² m=0.144 (R ² c=0.144)
Microbe: total	0.69	power-trans(y, 0.69) ~ Root C + ENL, random = ~ 1 composition; R ² m=0.192 (R ² c=0.287)
Soil fungi	0.71	power-trans(y, 0.71) ~ Root C + ENL + Root Ca, random = ~ 1 composition; R ² m=0.121 (R ² c=0.388)
Soil bacteria	0.84	power-trans(y, 0.84) ~ ENL, random = ~ 1 composition; R ² m=0.058 (R ² c=0.144)

B: Taxonomic richness

<i>Fauna group</i>	<i>t-value</i>	<i>Final model structures</i>
Nematode (Ne)	0.53	power-trans(y, 0.53) ~ Leaf C:N + Soil NO ₃ ⁻ , random = ~ 1 composition; R ² m=0.108 (R ² c=0.409)
Ne:Herbivores	0.78	power-trans(y, 0.78) ~ Leaf C:N , random = ~ 1 composition; R ² m=0.111 (R ² c=0.372)
Ne:Bacterivores	0.63	power-trans(y, 0.63) ~ Leaf C:N + Soil NO ₃ ⁻ , random = ~ 1 composition; R ² m=0.128 (R ² c=0.37)
Ne:Fungivores	0.76	power-trans(y, 0.76) ~ 1 , random = ~ 1 composition;
Mesofauna (Me)	1.00	power-trans(y, 1) ~ Soil C + ENL, random = ~ 1 composition; R ² m=0.088 (R ² c=0.088)
Me:Fungivores	1.05	power-trans(y, 1.05) ~ ENL, random = ~ 1 composition; R ² m=0.044 (R ² c=0.215)
Me:Omnivores	0.91	power-trans(y, 0.91) ~ Root Ca , random = ~ 1 composition; R ² m=0.031 (R ² c=0.031)
Me:Predators	0.96	power-trans(y, 0.96) ~ Soil C, random = ~ 1 composition; R ² m=0.048 (R ² c=0.089)
Macrofauna (Ma)	1.07	power-trans(y, 1.07) ~ Soil C + Root Ca, random = ~ 1 composition; R ² m=0.151 (R ² c=0.381)
Ma: Predators	0.75	power-trans(y, 0.75) ~ Root Ca, random = ~ 1 composition; R ² m=0.034 (R ² c=0.529)
Ma: Omnivores	1.09	power-trans(y, 1.09) ~ ENL, random = ~ 1 composition; R ² m=0.128 (R ² c=0.166)
Earthworm	0.65	power-trans(y, 0.65) ~ Soil C, random = ~ 1 composition; R ² m=0.089 (R ² c=0.167)
Microbe: total	0.20	power-trans(y, 0.2) ~ Leaf C:N + ENL, random = ~ 1 composition; R ² m=0.276 (R ² c=0.758)
Soil fungi	0.56	power-trans(y, 0.56) ~ Leaf C:N + ENL, random = ~ 1 composition; R ² m=0.221 (R ² c=0.875)
Soil bacteria	0.48	power-trans(y, 0.48) ~ Leaf C:N + ENL, random = ~ 1 composition; R ² m=0.184 (R ² c=0.539)

C: Shannon-Wiener diversity index

<i>Fauna group</i>	<i>t-value</i>	<i>Final model structures</i>
Nematode	1.19	power-trans(y, 1.19) ~ Leaf C:N + + Soil NO ₃ ⁻ , random = ~ 1 composition; R ² m=0.11 (R ² c=0.434)
Mesofauna	0.93	power-trans(y, 0.93) ~ Leaf C:N + Root Ca + + Soil NO ₃ ⁻ , random = ~ 1 composition; R ² m=0.284 (R ² c=0.284)
Macrofauna	1.28	power-trans(y, 1.28) ~ Root Ca, random = ~ 1 composition; R ² m=0.087 (R ² c=0.653)
Microbe: total	1.24	power-trans(y, 1.24) ~ Leaf C:N + ENL, random = ~ 1 composition; R ² m=0.267 (R ² c=0.624)
Soil fungi	1.30	power-trans(y, 1.3) ~ Leaf C:N + ENL, random = ~ 1 composition; R ² m=0.134 (R ² c=0.795)
Soil bacteria	0.89	power-trans(y, 0.89) ~ Leaf C:N + ENL, random = ~ 1 composition; R ² m=0.147 (R ² c=0.276)

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