

Supporting Information for

Soil microbial communities shift from plant- to microorganism-derived resources under resource limitation

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Table S1. Bayesian linear regression model testing the microbial trophic position relative to 2. mean_TP and pooled_propagated_SE represent the mean trophic position and the propagated error of microbial communities for each Detritus × Microbes treatment combination. Pr(TP > 2)(%) indicates that posterior probability that the mean trophic position for a given treatment combination exceeded 2, calculated from the Bayesian model after accounting for total error propagation.

Microbes	Detritus	mean_TP	pooled_propagated_SE	Pr(TP > 2)(%)
Mixed	Arable soil	2.58	0.25	100.00
Bacteria	Arable soil	2.41	0.33	99.80
Fungi	Arable soil	2.59	0.32	100.00
Mixed	Beech leaves	2.44	0.29	99.95
Bacteria	Beech leaves	2.38	0.24	99.73
Fungi	Beech leaves	2.23	0.28	96.50
Mixed	Forest soil	2.50	0.29	99.98
Bacteria	Forest soil	2.51	0.28	100.00
Fungi	Forest soil	2.44	0.27	99.93
Mixed	Legume leaves	2.31	0.29	97.50
Bacteria	Legume leaves	2.23	0.23	91.30
Fungi	Legume leaves	2.44	0.28	99.68
Mixed	Lime leaves	2.36	0.28	99.85
Bacteria	Lime leaves	2.12	0.21	88.65
Fungi	Lime leaves	2.01	0.37	52.75
Mixed	Wheat straw	2.49	0.29	99.95
Bacteria	Wheat straw	2.20	0.32	92.55
Fungi	Wheat straw	2.19	0.31	95.48

Table S2 Reclassification table of basal resource groups (bacteria, fungi and plants) generated using the leave-one-out cross-validation method based on linear discriminant analysis (LDA). Correct reclassifications are shown in bold, and the accuracy of samples correctly reclassified for each basal resource group is shown in the right column.

		Initial groups			accuracy (%)
		Bacteria	Fungi	Plants	
Reclassification	Bacteria	12	0	0	100
	Fungi	0	22	0	95.7
	Plant	0	1	52	100

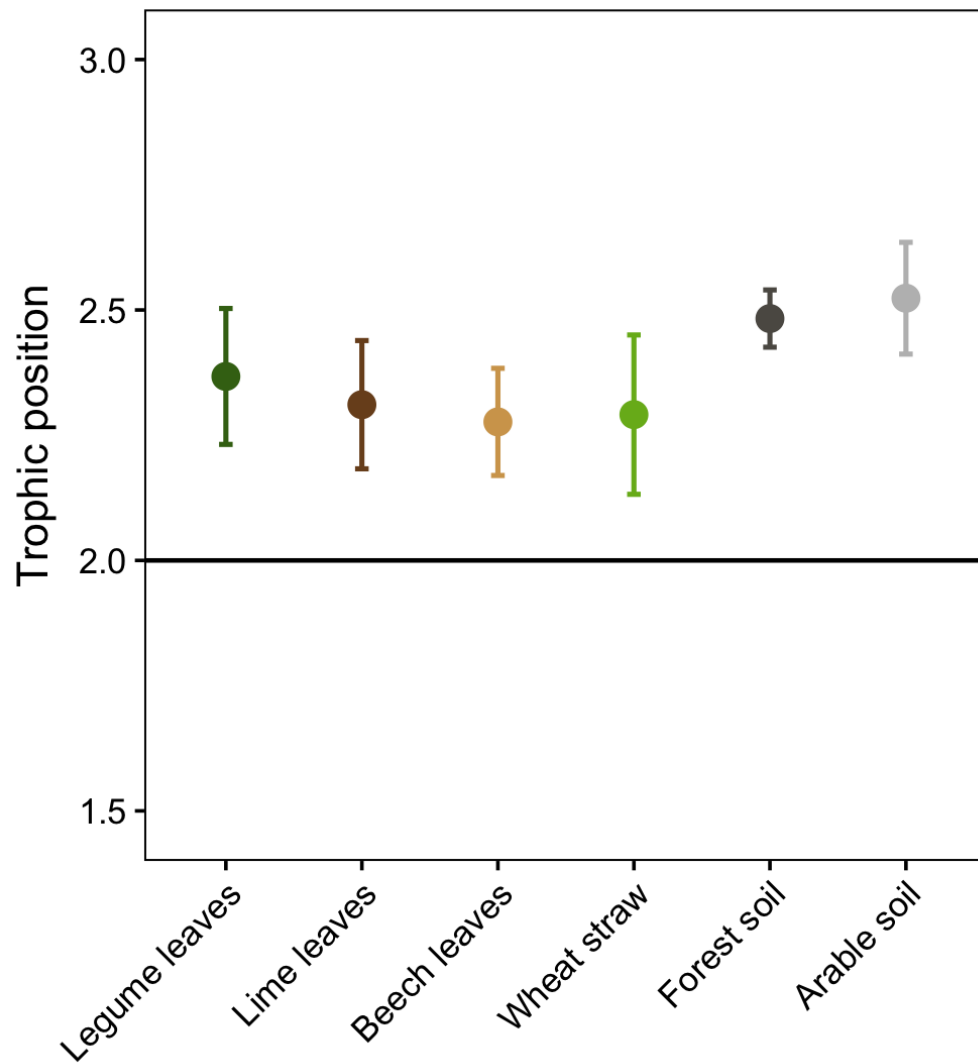


Figure S1 Trophic position of microorganisms calculated using the difference in $\delta^{15}\text{N}$ values between glutamic acid and phenylalanine in microcosms with detrital materials of different quality (decreasing from left to right). Note that we used the C_3 plant β values ($-8.40 \pm 1.60\text{‰}$) taken from literature to calculate the trophic position of microorganisms.

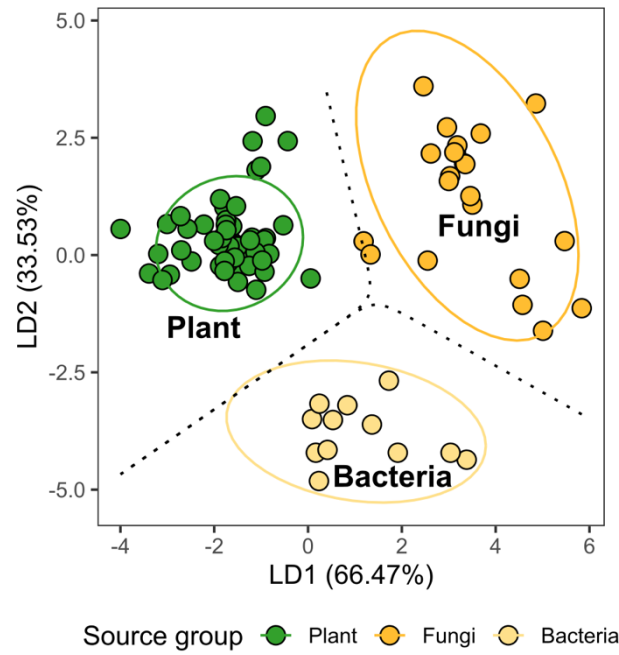


Figure S2. Aggregated basal resource profiles in linear discriminant space. Points represent $\delta^{13}\text{C}$ profiles for essential amino acids (leucine, isoleucine, threonine, phenylalanine and valine). Data are shown with 95% confidence ellipses for plants, bacteria and fungi groups.

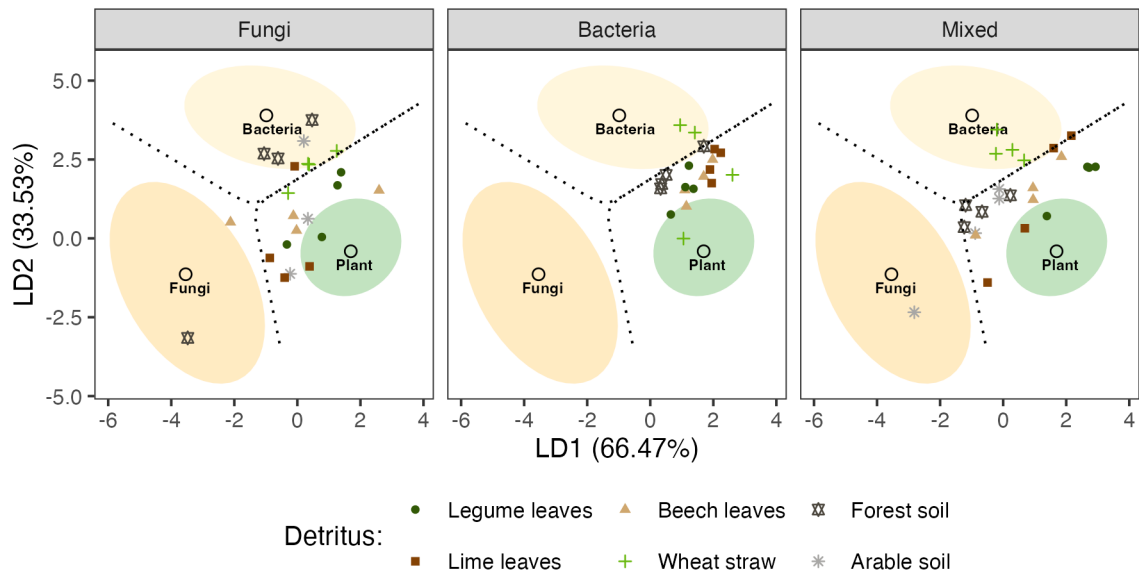


Figure S3 Linear discriminant analysis (LDA) of $\delta^{13}\text{C}$ values in essential amino acids of bacteria, fungi and mixed in the treatment with legume leaves (dark green; circle), lime leaves (dark brown; square), beech leaves (light brown; triangle), wheat straw (light green; cross), forest soil (black; diamond), arable soil (grey; star). Each point represents a single measurement. Training data for plants, bacteria, and fungi were used as endmembers to predict the biosynthetic origin of essential amino acids in microorganisms. Ellipses represent 95% CIs of each resource group, and dashed lines represent the decision boundaries.

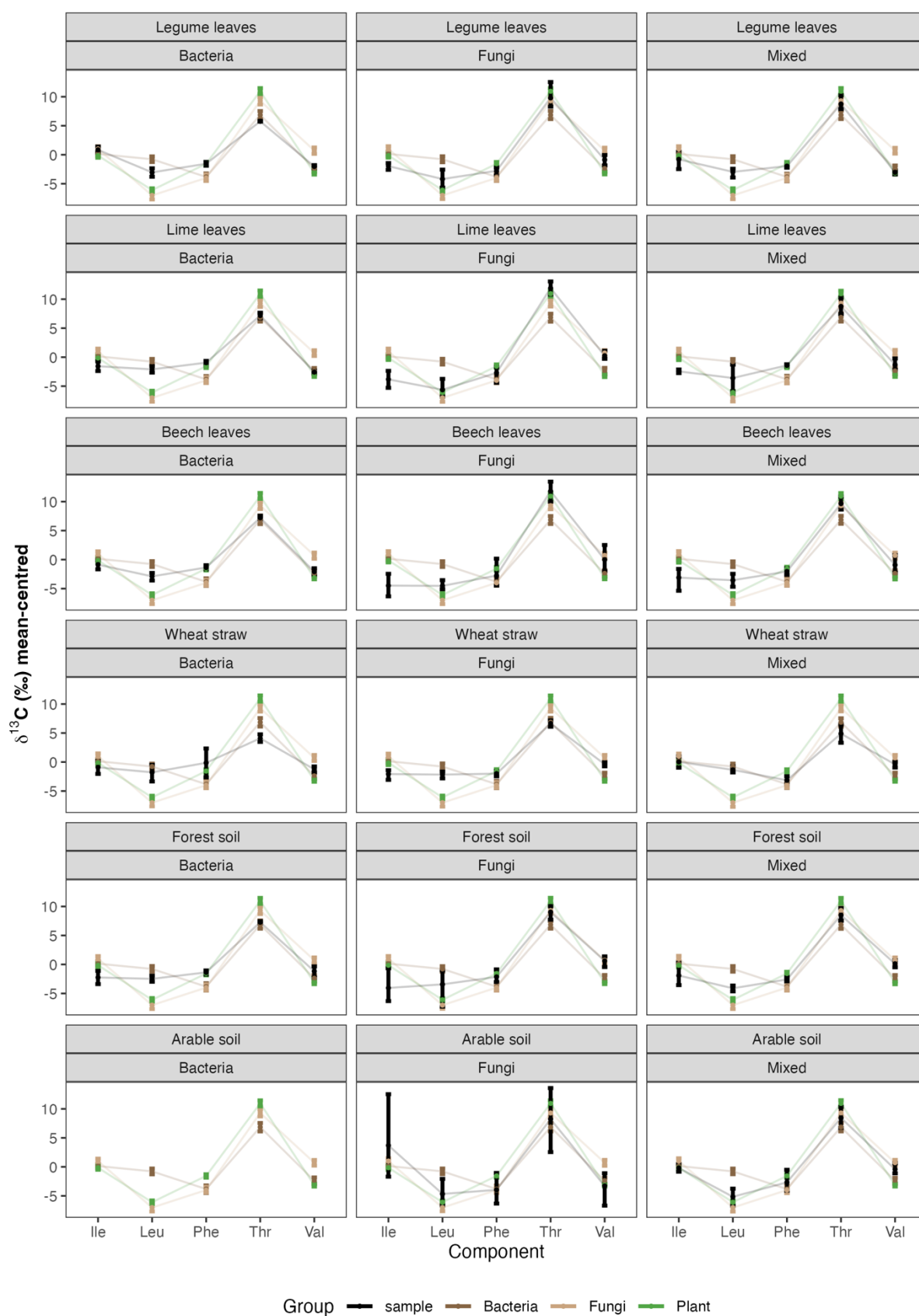


Figure S4 Mean-centred $\delta^{13}\text{C}$ values (arithmetic means $\pm$ 95% CIs) of all five available essential amino acids (Isoleucine, leucine, phenylalanine, Threonine and valine) in

samples (i.e., bacteria, fungi or mixed) and sources data (i.e., bacteria, fungi and plant) in the treatments with different detritus types (legume leaves, lime leaves, beech leaves, wheat straw, forest soil, arable soil).

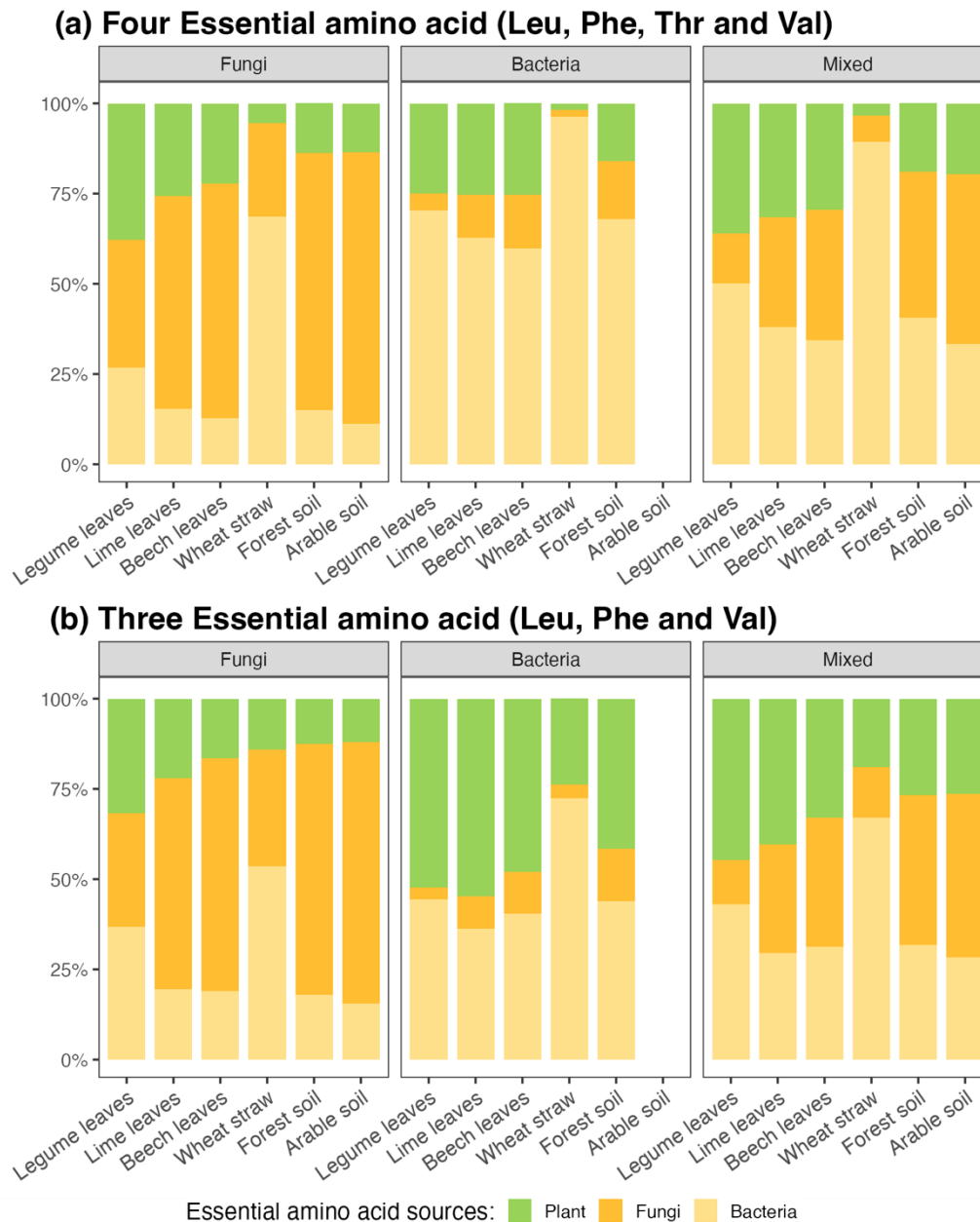


Figure S5 Relative proportion of bacterial- (light yellow), fungal- (orange) and plant-derived essential amino acids (light green) in microcosms with fungi only, bacteria only and both bacteria and fungi in the treatments with detrital materials of different quality (decreasing from left to right) as estimated by Bayesian mixing model based on the mean-centred $\delta^{13}\text{C}$ values of (a) four essential amino acids (leucine, phenylalanine, threonine and valine), and (b) three essential amino acids (leucine, phenylalanine and valine). Each combination of microbial community $\times$ detritus type was replicated four times.

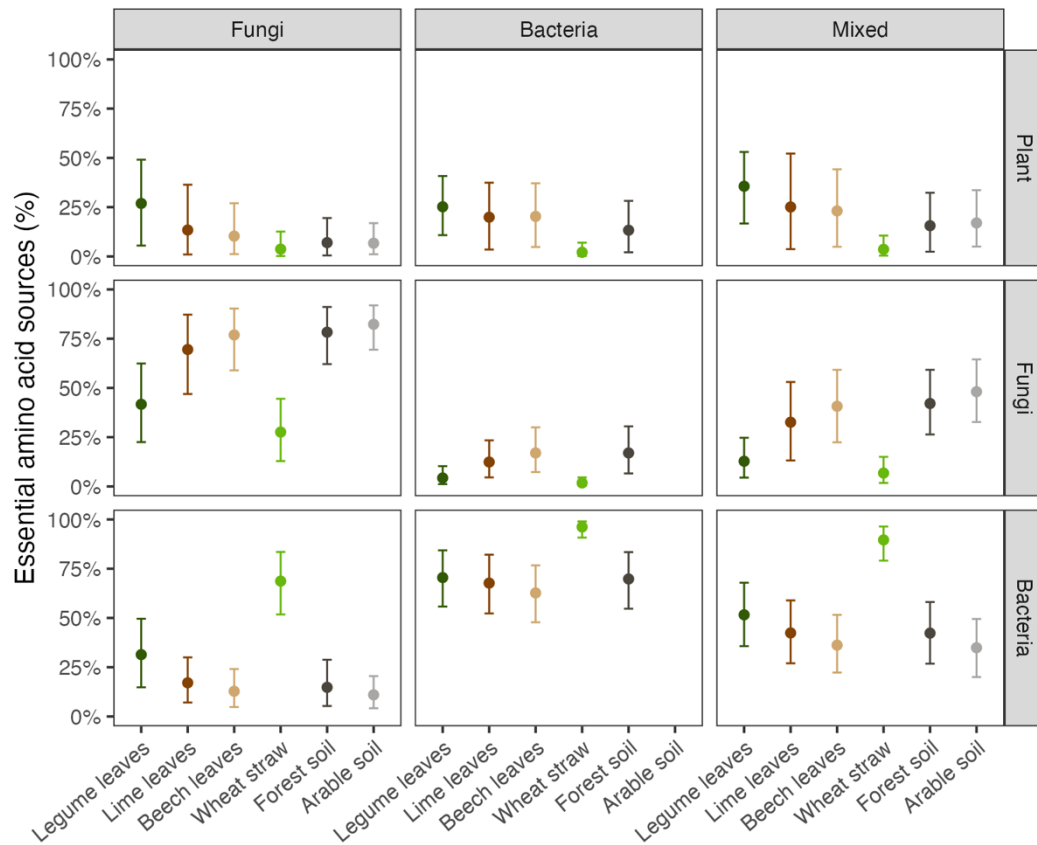


Figure S6. Relative proportion of plant-, fungal- and bacterial-derived essential amino acids in the microcosms with fungi only, bacteria only and both bacteria and fungi in the treatments with different detritus types. The proportion was estimated by Bayesian mixing models based on the mean-centered $\delta^{13}\text{C}$ values of all five available essential amino acids, Isoleucine, leucine, phenylalanine, Threonine and valine. Dots represent the mean relative proportion of plant-, fungal- and bacterial-derived essential amino acids in the respective treatments, the bar represents 95% credible interval.

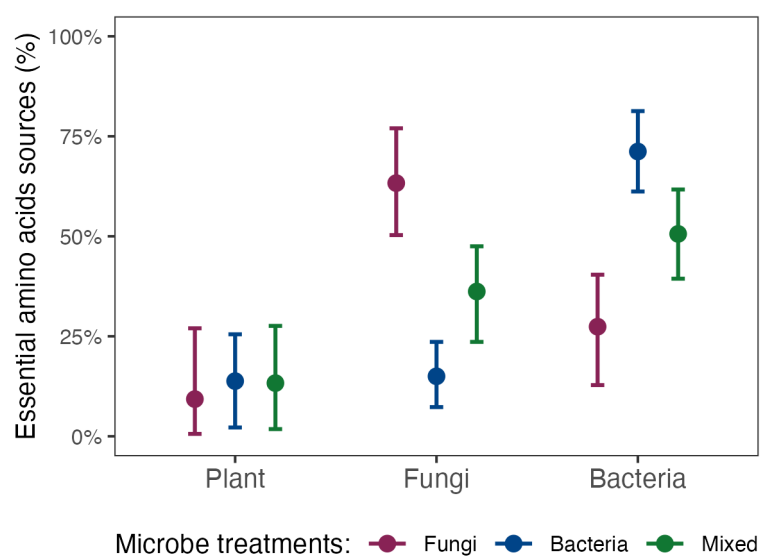


Figure S7. Overall relative proportion of bacterial- fungal- and plant-derived essential amino acids in microcosms with fungi only (purple), bacteria only (blue) and both bacteria and fungi (green).

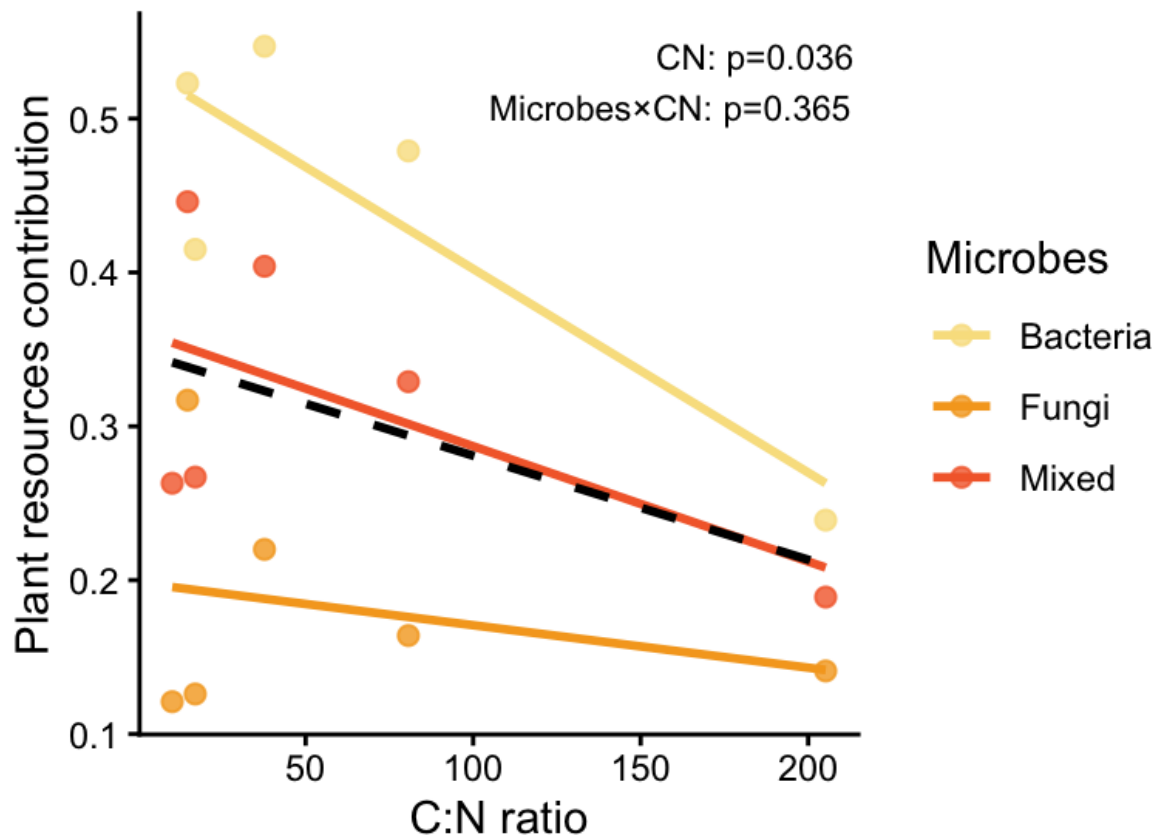


Figure S8. Relationships between litter mass-based C:N ratio and plant resource contribution. Solid lines indicate model fits for each microbial group (bacteria, fungi, mixed), and the dashed line shows the overall trend.

Samples – top 5 genera

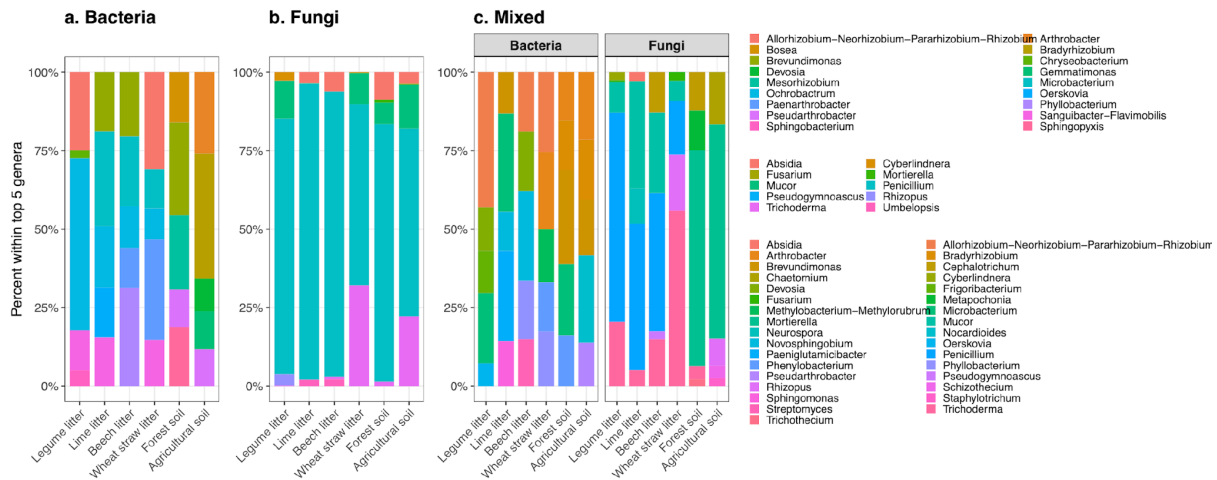


Fig. S9 Dominant microbial genera detected in the experimental microcosms. Relative composition of the top five bacterial and fungal genera detected by DNA amplicon sequencing in the bacteria-only, fungi-only and mixed inoculation treatments across the six detrital substrates. Bars show the percentage contribution of each genus within the top five genera detected in each treatment. Panels show (a) bacteria-only treatments, (b) fungi-only treatments and (c) mixed treatments, separated into bacterial and fungal communities.

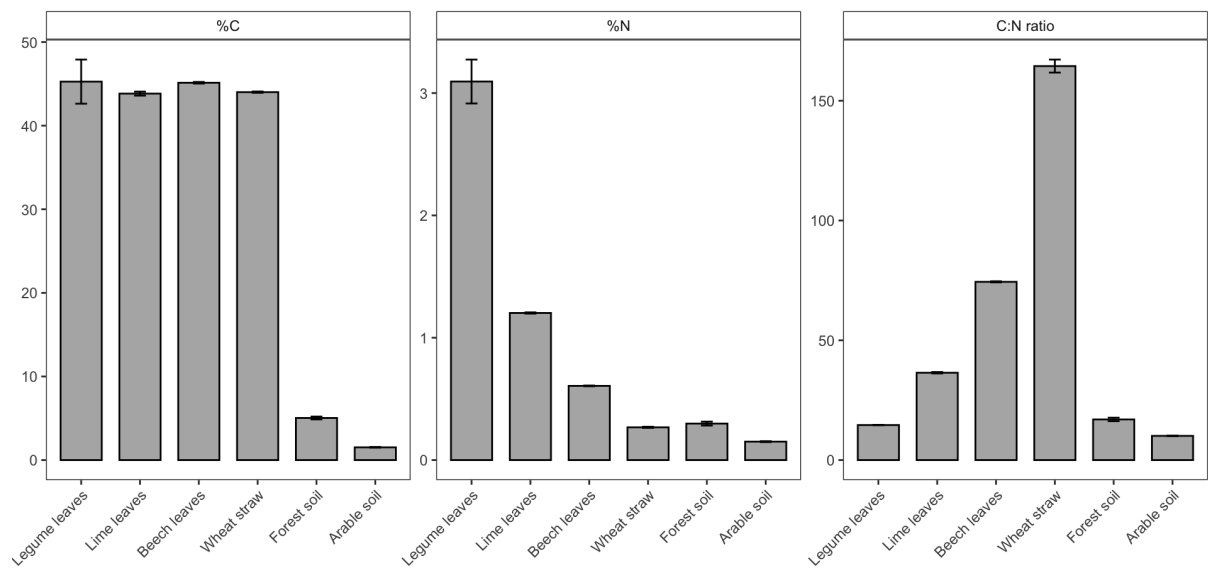


Figure S10. %C, %N and C:N ratio of the six detrital resources used in the experiment (mean $\pm$ SE). C:N ratios were calculated from carbon and nitrogen contents and are expressed on a mass basis.