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SUPPLEMENTARY INFORMATION

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Multiple elements of soil biodiversity drive ecosystem functions across biomes

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Supplementary Information for

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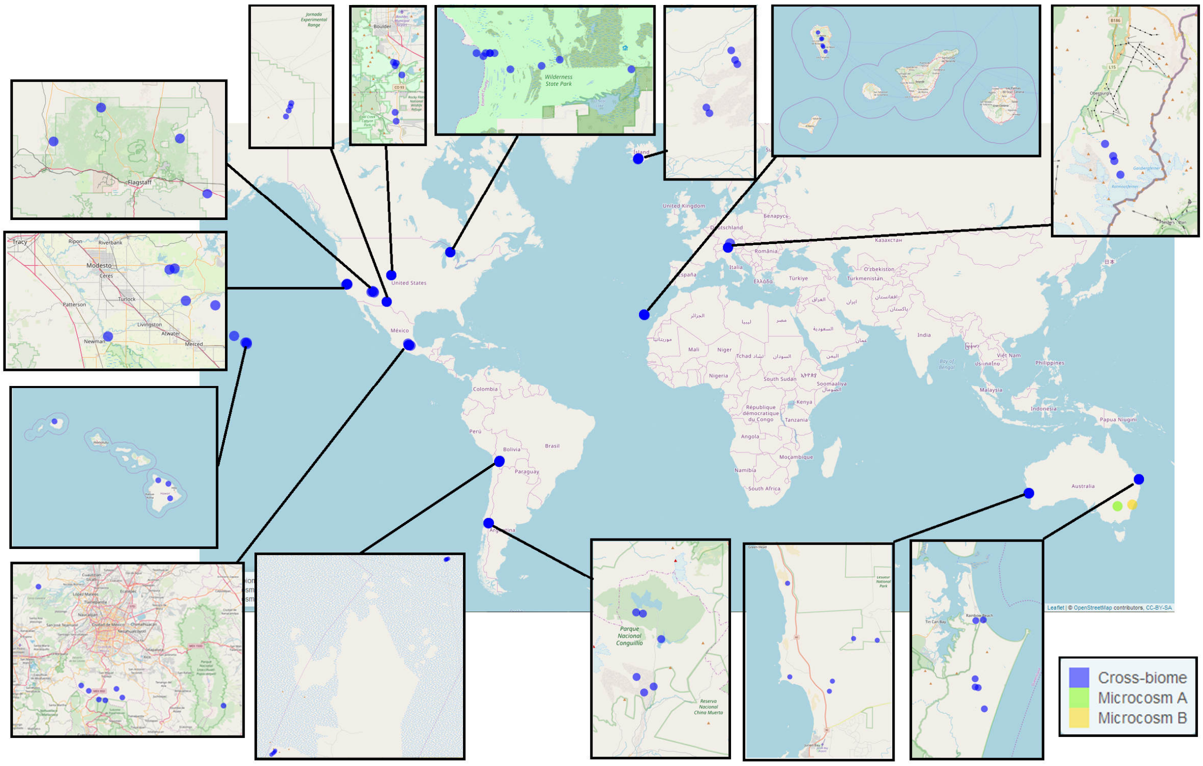
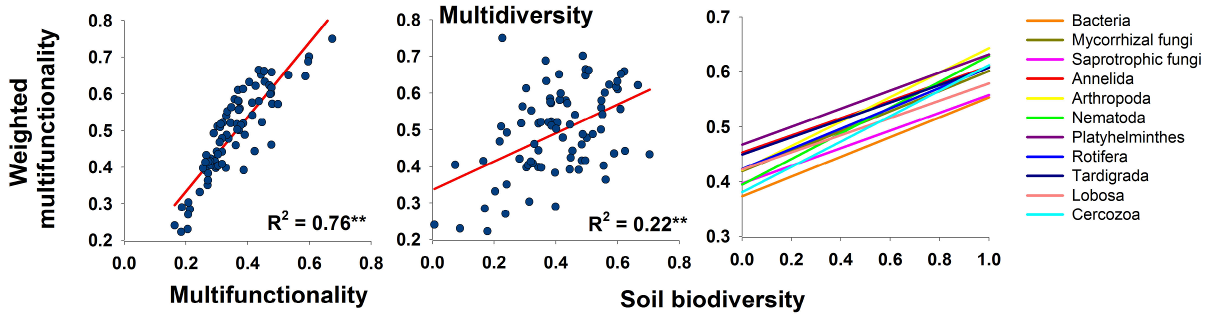
This .PDF file includes:

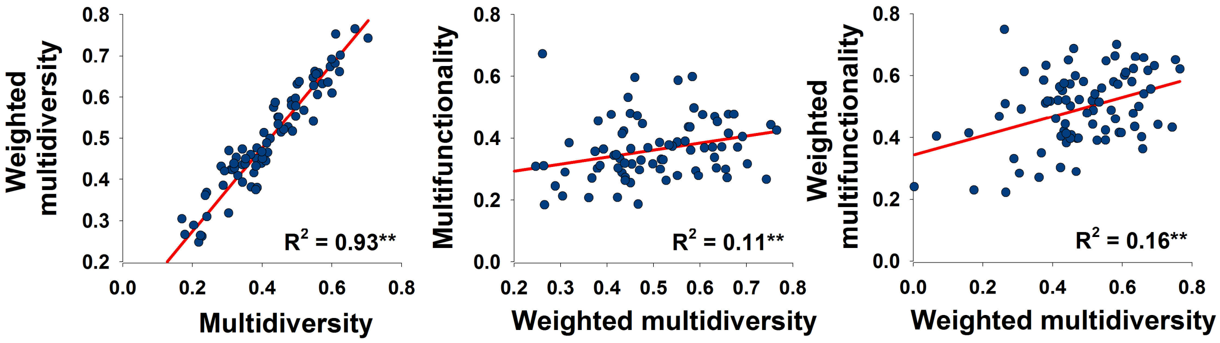
Supplementary Figs. 1–21
Supplementary Tables 1–7, 9 and 10
Legend for Supplementary Table 8



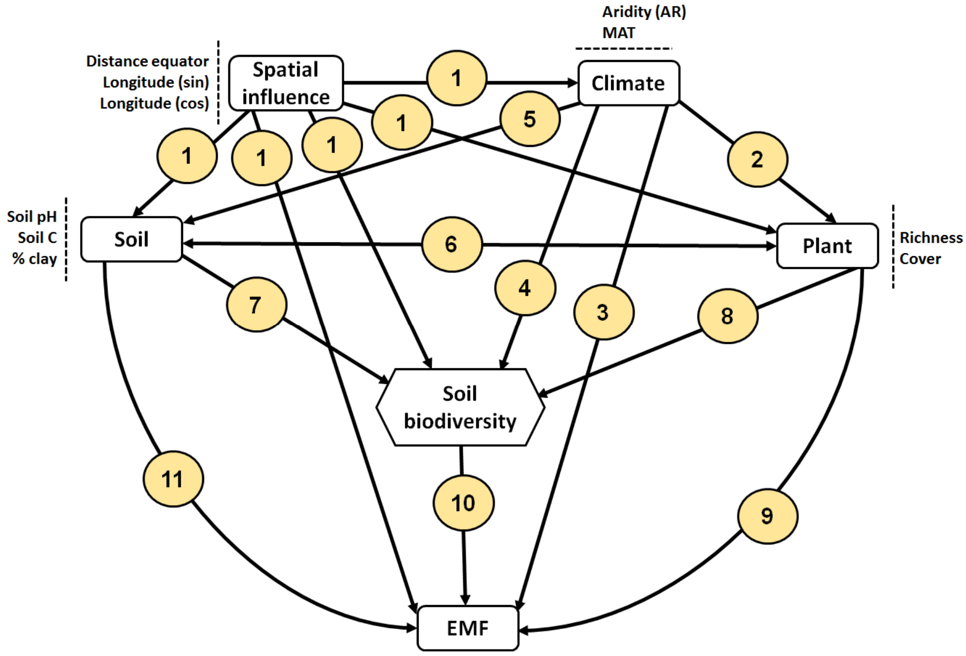
Supplementary Figure 1. Locations for the sites included in this study (n = 83 study sites). This map was generated using the R packages in refs.[52-53].



Supplementary Figure 2. Linear relationships between averaging ecosystem multifunctionality and soil biodiversity (multidiversity and the diversity of single groups of soil organisms; number of phylotypes) with a weighted version of the multifunctionality (n = 81 study sites). For this weighted multifunctionality index, ecosystem functions are averaged into five ecosystem services: plant productivity, ARG control, pathogen control, nutrient cycling and OM decomposition, before multifunctionality is calculated, so that functions from each ecosystem service contributed equally to multifunctionality. P-values (Ordinary least squares linear regressions) as follow: **P < 0.01.



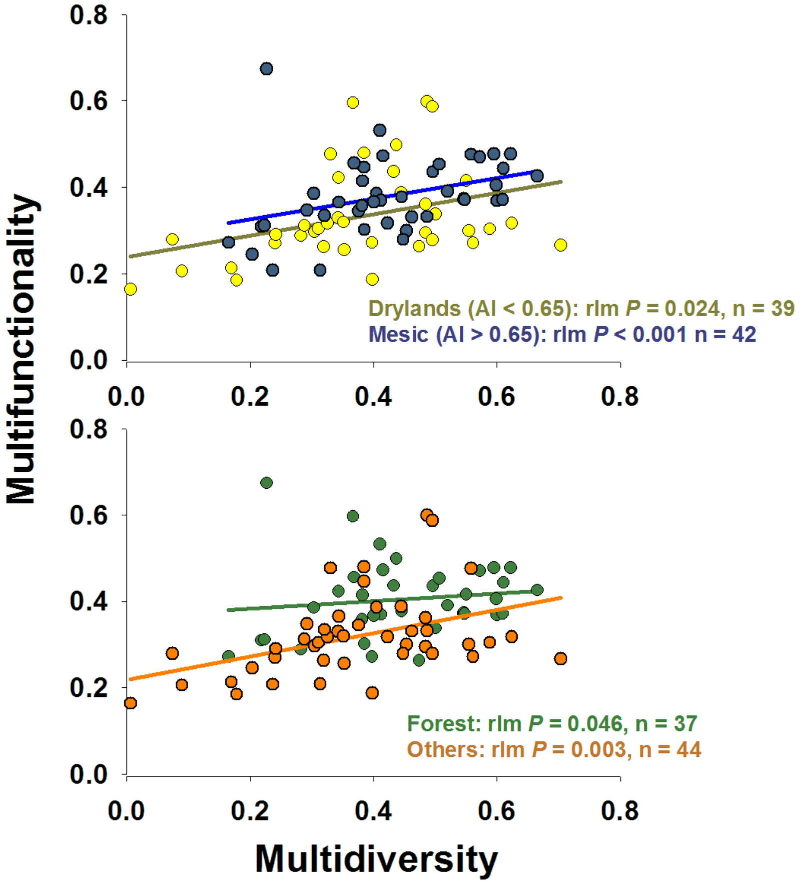
Supplementary Figure 3. Linear relationships between averaging and weighted soil biodiversity (multidiversity) and multifunctionality (n = 81 study sites). For this weighted multifunctionality index, ecosystem functions are averaged into five ecosystem services: plant productivity, ARG control, pathogen control, nutrient cycling and OM decomposition, before multifunctionality is calculated, so that functions from each ecosystem service contributed equally to multifunctionality. For the weighted multidiversity index, soil biodiversity are averaged into four groups of organisms: bacteria, fungi (Mycorrhizal and saprotrophic fungi), protists (Cercozoa, Ciliophora, Lobosa) and invertebrates (Arthropoda, Annelida, Nematoda, Platyhelminthes, Rotifera, Tardigrada), so that richness from each soil group contributed equally to multidiversity. P-values (Ordinary least squares linear regressions) as follow: **P < 0.01.



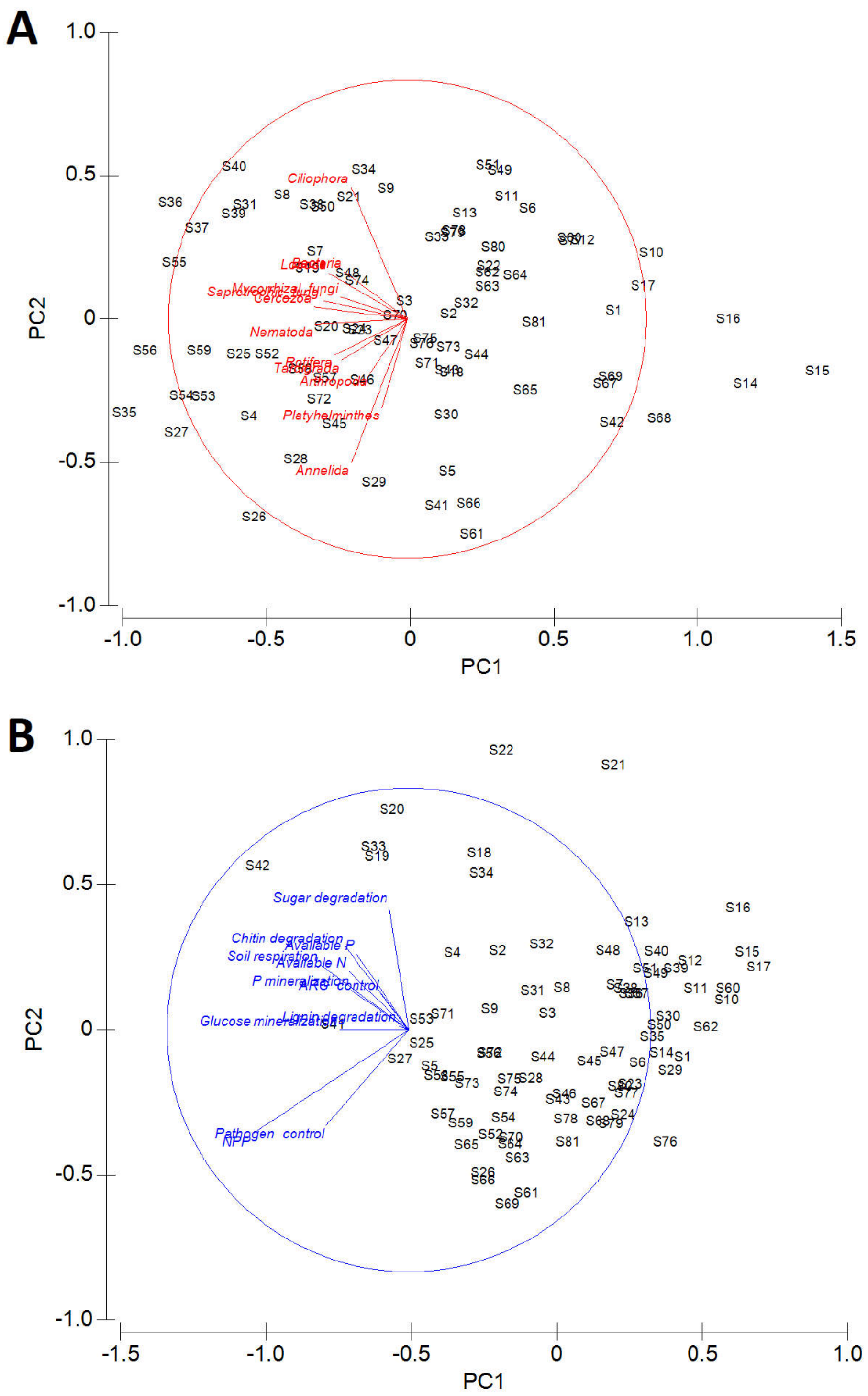
#	Associations	*Rationale*	Ref.
1	**Spatial → Others**	Location is included in our model to account for any potential effect of spatial autocorrelation on our data. Moreover, location on Earth can determine multiple environmental variables. For instance, the farther from the equator the lower the temperature.	25, 38
2	**Climate → Plant attributes**	Climate regulates plant attributes. For example, aridity is expected to be negatively associated with plant cover and richness. Moreover, at the global scale, MAT is expected to be positively associated with plant cover and richness (e.g., tropical regions).	25, 38
3	**Climate → EMF**	Climate is known to control ecosystem multifunctionality. For examples, increases in aridity are known to be negatively associated with ecosystem multifunctionality.	25
4	**Climate → Soil biodiversity**	Climate controls soil biodiversity globally. For example, increases in aridity are known to be negatively related to soil microbial diversity. Moreover, MAT has been reported to be positively associated with the diversity of bacteria.	10
5	**Climate → Soil attributes**	Climate regulates soil properties across the globe. For example, increases in aridity are known to be negatively associated with soil organic matter (soil C). Locations with reduced precipitation often have reduced C fixation and litter decomposition rates reducing the entrance of C into the soil system. MAT is expected to have a positive effect on soil C. Very cold locations (e.g., alpine ecosystems) are expected to have reduced C fixation and decomposition rates. Aridity is also expected to increase soil pH by increasing the amount of caliche in soil and to alter the texture of soil by blowing off the finest fractions (e.g., clay) of soil via promoting soil erosion. Aridity could also influence clay formation via its effect on weathering processes. MAT is expected to affect soil texture and pH via promoting soil weathering.	10,13,38
6	**Soil ↔ plant attributes**	Plant and soil attributes are known to be largely associated with each other via multiple soil/plant processes. For example, plant cover is known to promote soil C via litter production. Moreover, soil fertility is known to promote plant cover. Soil texture and pH can also by factors controlling plant	10,13,38

		cover, but can also be affected by plants via weathering and shifting soil aggregates.	
7	**Soil → Soil biodiversity**	Soil attributes are among the most important drivers of soil biodiversity. For example, soil pH is the major regulator of bacterial diversity. Soil organic matter is also known to be essential for the biodiversity of soil microbes and animals by controlling resource availability. Texture is also critical for soil biodiversity as its control soil aggregates and water availability.	10,20,32
8	**Plant → Soil biodiversity**	Plant attributes are key controllers of soil biodiversity. Plant cover, for example, provide resources and habitats to soil organisms. Moreover, plant richness increases the heterogeneity of resources (e.g., litter heterogeneity) than can increase the number of niches available for soil organisms.	8-10
9	**Plant → EMF**	Plant richness and cover are known to have positive effects on ecosystem multifunctionality. Locations with larger percentages of plant cover can support larger C fixation, plant productivity and resource availability (e.g., litter production). Moreover, plant richness is expected to fuel ecosystem functioning by promoting resource heterogeneity and allowing the co-existence of multiple soil organisms.	25
10	**Soil biodiversity → EMF**	Belowground organisms comprise a large fraction of global terrestrial diversity, and are responsible for essential ecosystem functions and services which are valued at trillions of dollars annually, including plant productivity, nutrient cycling, organic matter (OM) decomposition, pollutant degradation, and pathogen control. We hypothesized that soil biodiversity is positively correlated with the rates of multiple ecosystem functions.	1-6,27
11	**Soil → EMF**	Soil attributes control soil functioning. Locations with higher amounts of organic matter (resources) are expected to support higher organic matter decomposition rates and nutrient cycling. Soil texture is expected to influence ecosystem functioning by regulating water availability and soil aggregates. Finally, pH can largely influence the rates of ecosystem processes as enzymes and metabolic activity is known to be regulated by pH.	9-10, 13

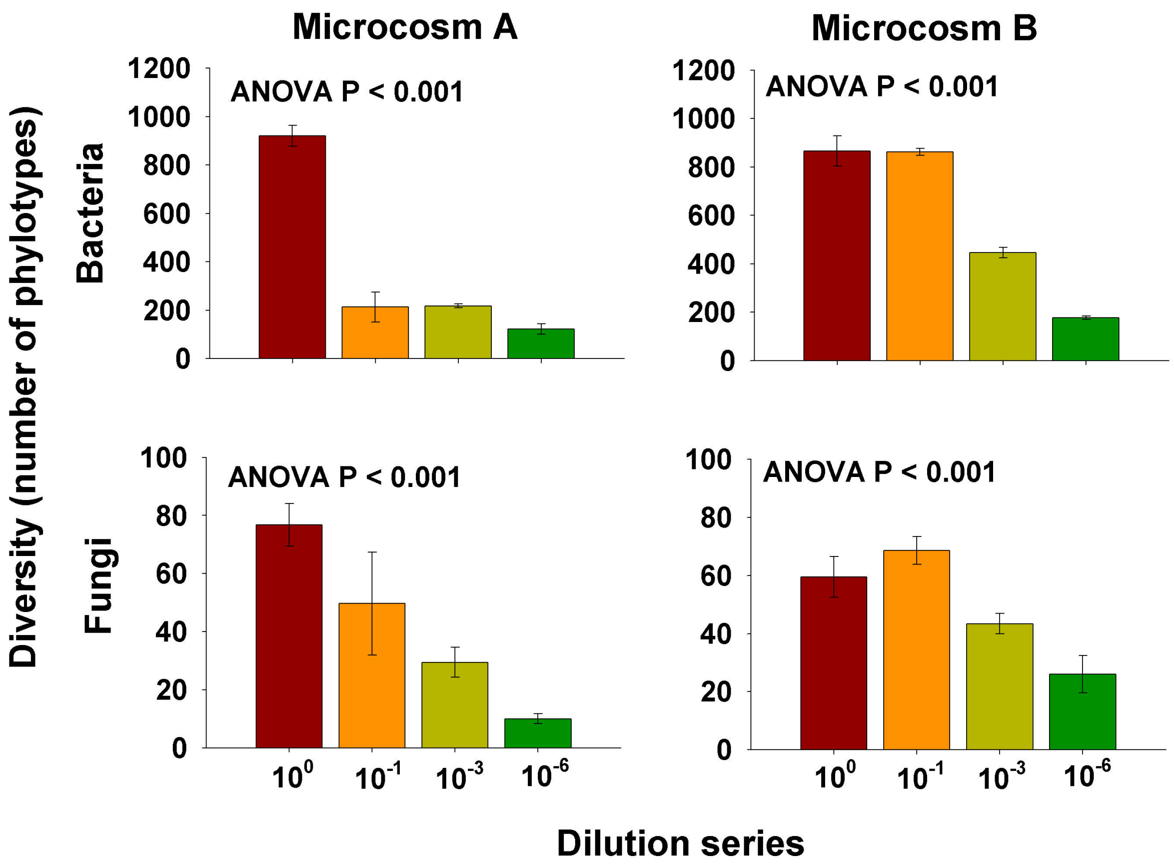
Supplementary Figure 4. *A priori* structural equation modeling (SEM) metamodel aimed to evaluate the link between soil biodiversity and multifunctionality (EMF) after controlling for key ecological predictors such as space, climate, and soil and plant attributes. Hexagons present composite variables. Rectangles represent observable variables. Different categories of predictors were grouped in the same box in the model for graphical simplicity. Aridity = - 1 x Aridity Index. MAT = Mean annual temperature. The fitted model is available in Fig. 2B and **Supplementary Table** 2.



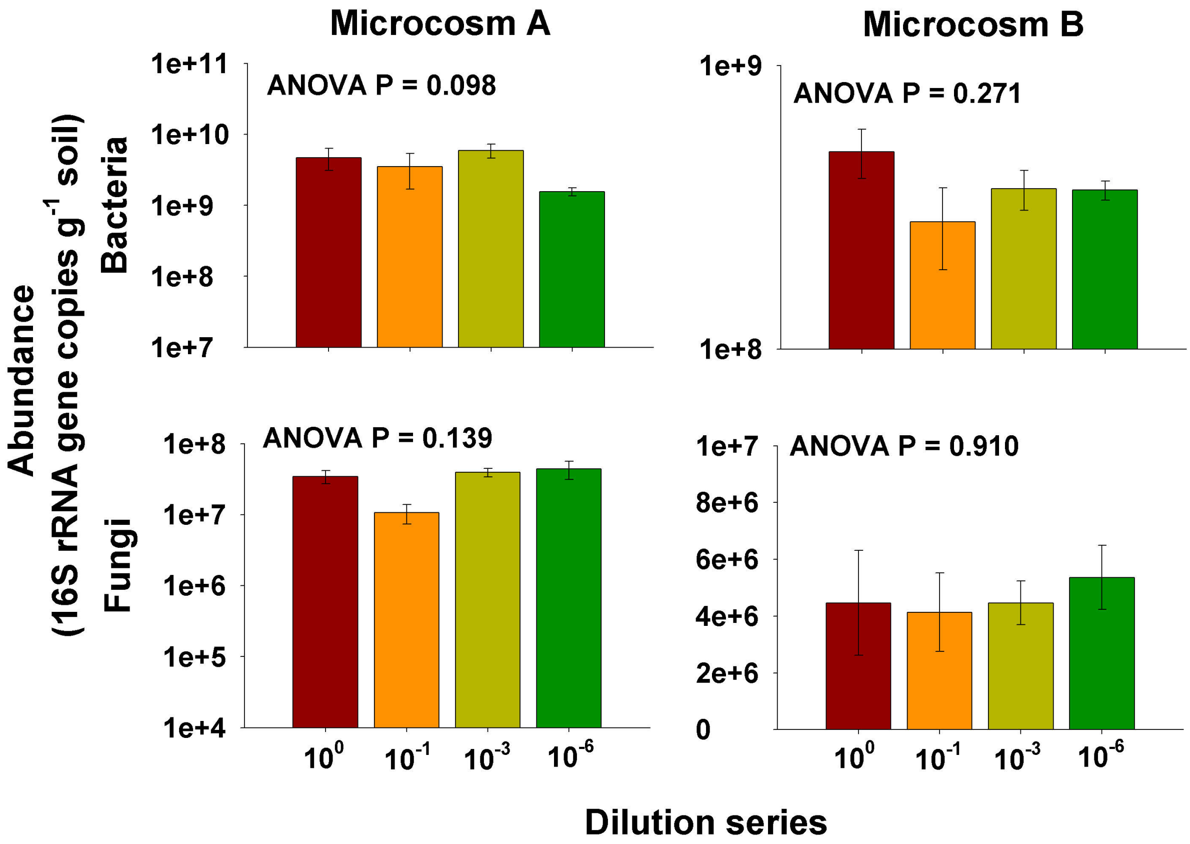
Supplementary Figure 5. Robust linear modeling linking the relationship between soil biodiversity (multidiversity) and average multifunctionality across major biomes and vegetation types included in the global survey database. We used the R Package 'rlm' for these analyses to account for the influence of statistical outliers in our analyses.



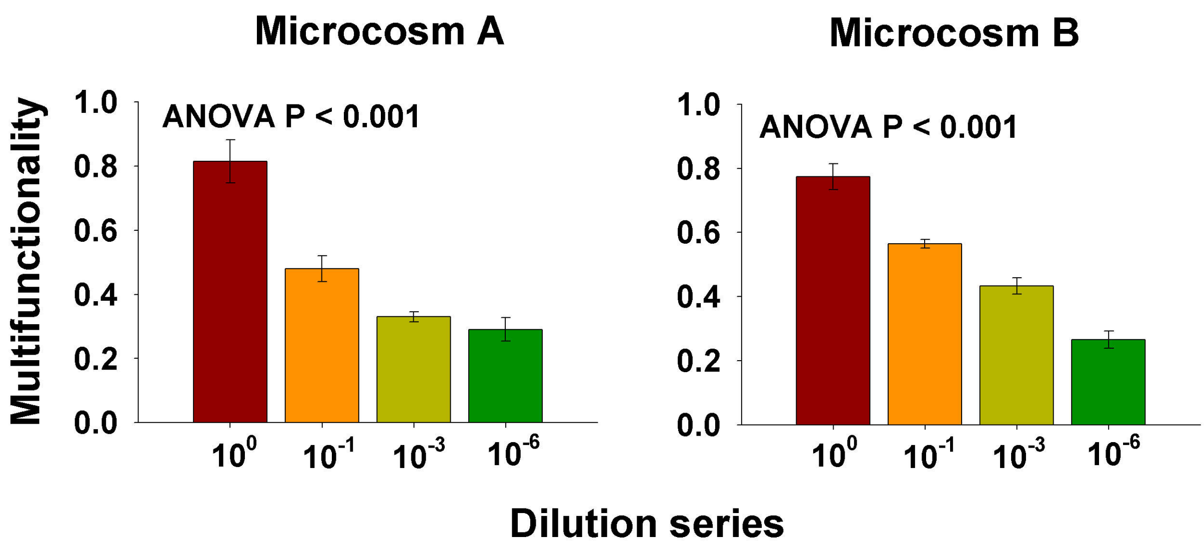
Supplementary Figure 6. PCA showing the distribution of biodiversity and functional data in our global survey (n = 81 study sites). Soil biodiversity PC1 and PC2 explained 44% and 17% of the variation in soil biodiversity, respectively. Soil functional PC1 and PC2 explained 30% and 25% of the variation in functions, respectively.



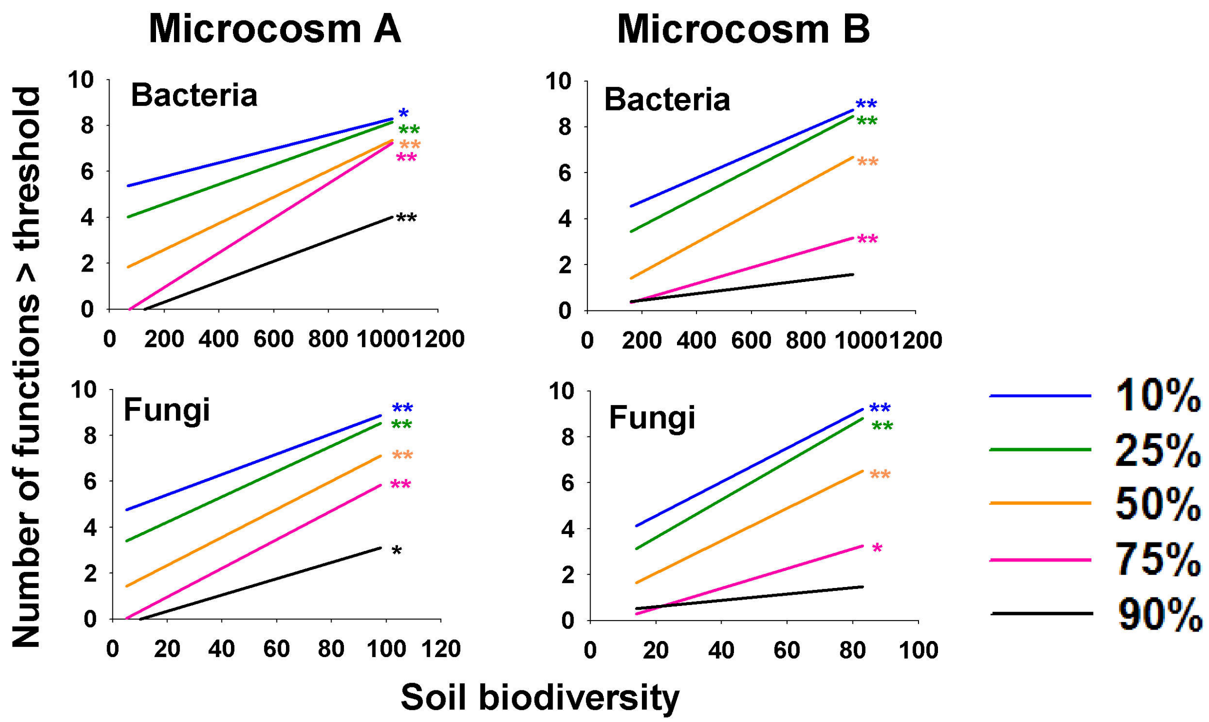
Supplementary Figure 7. Mean (±SE) diversity (number of phylotypes) of bacteria and fungi across an experimentally-created gradient of soil biodiversity using the dilution to extinction approach in two soils from Eastern Australia (n = 5 replicates).



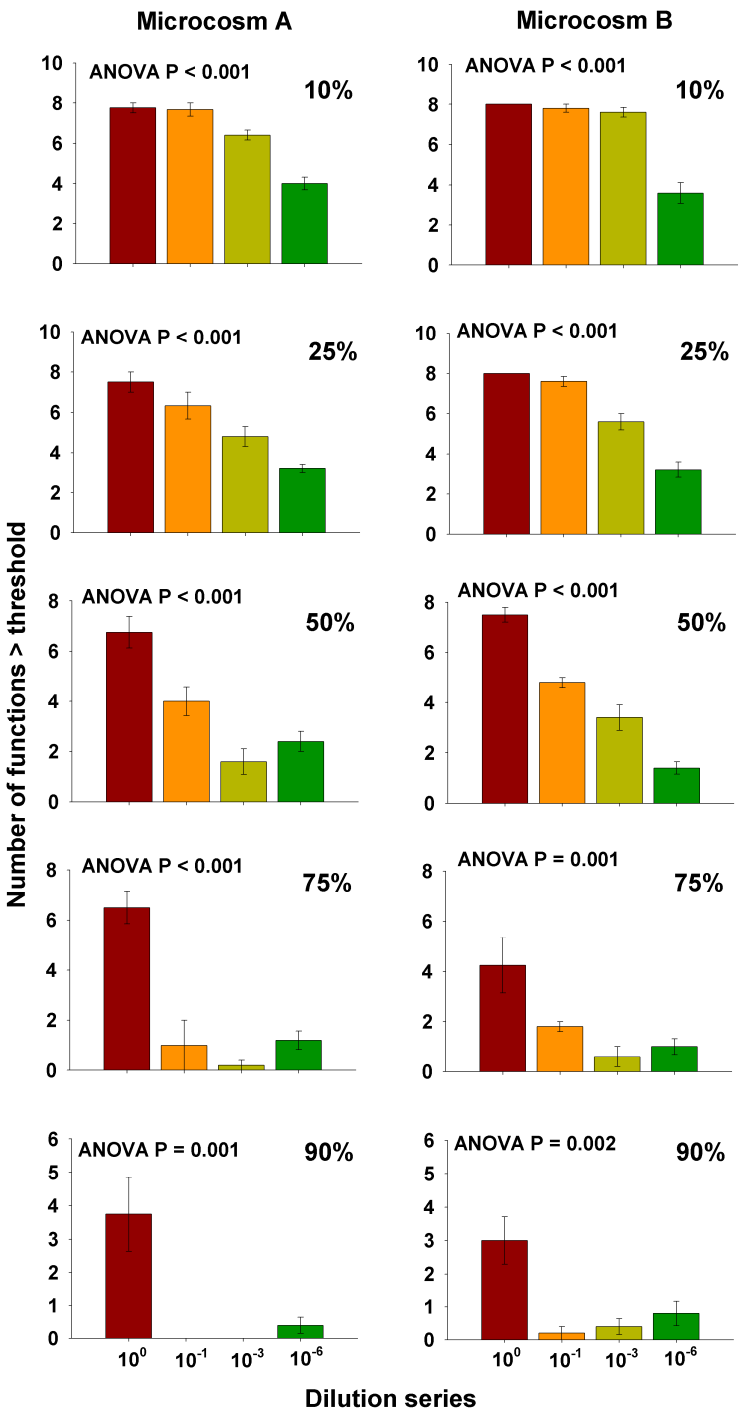
Supplementary Figure 8. Mean (±SE) abundance of bacteria and fungi across an experimentally created gradient of soil biodiversity using the dilution to extinction approach in two soils from Eastern Australia (n = 5 replicates).



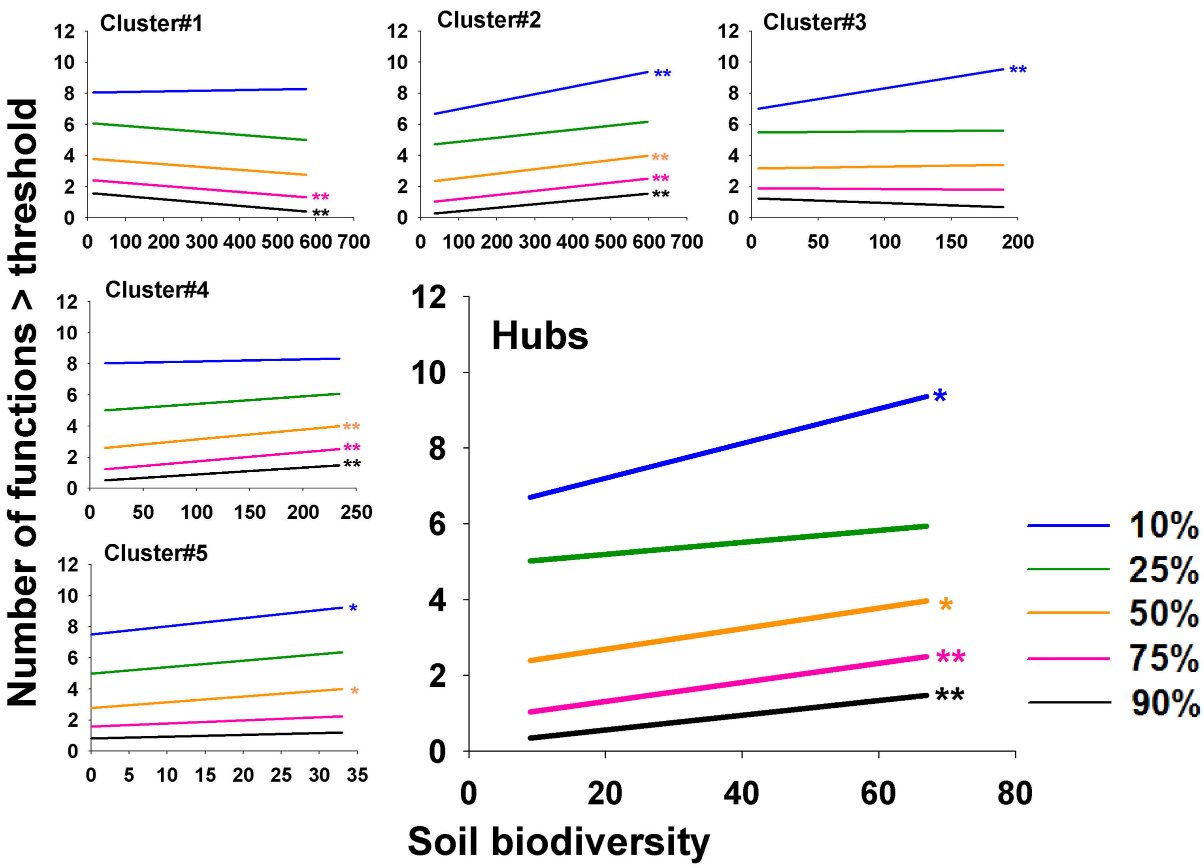
Supplementary Figure 9. Mean (±SE) multifunctionality across an experimentally-created gradient of soil biodiversity using the dilution to extinction approach in two soils from Eastern Australia (n = 5 replicates).



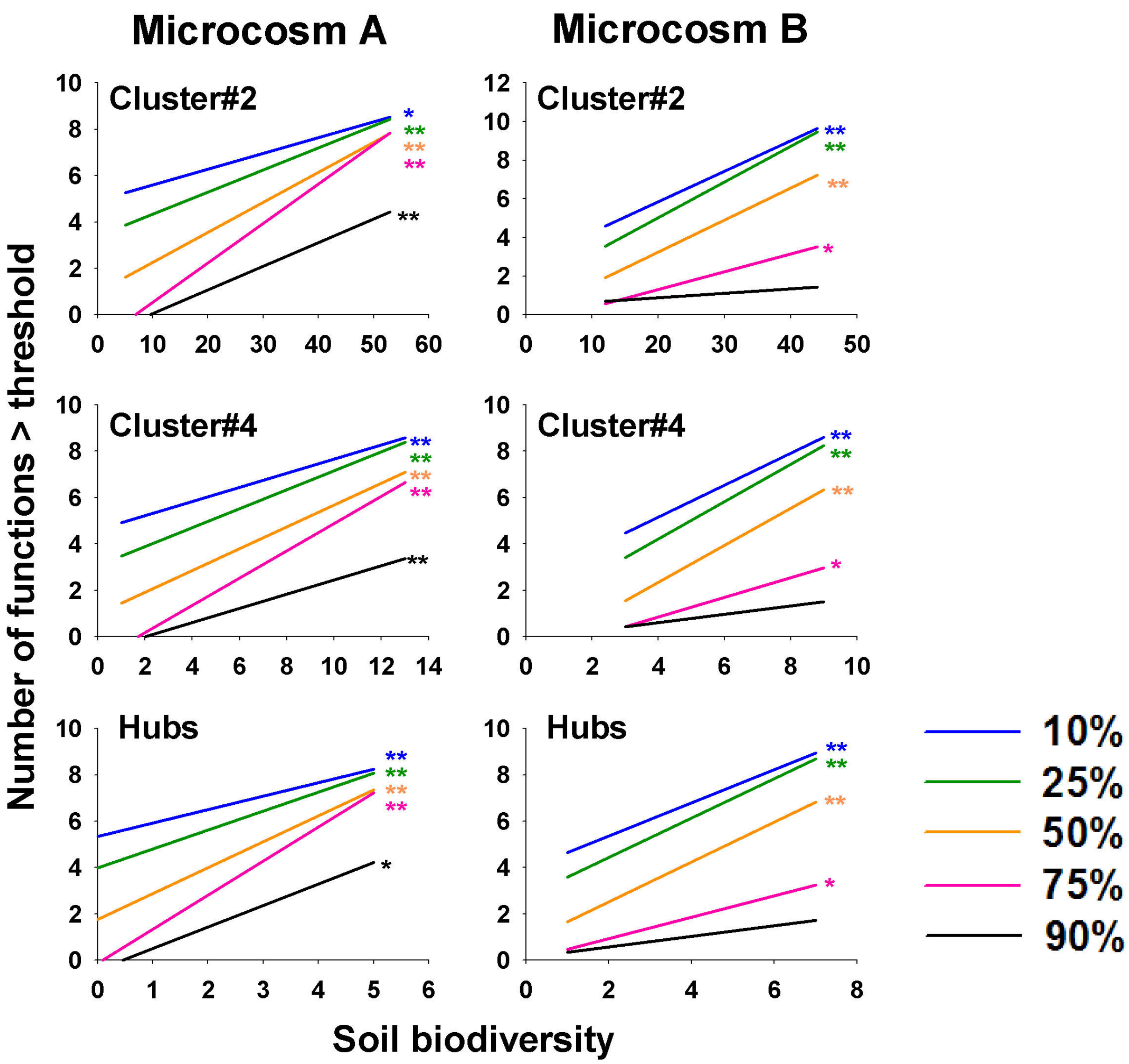
Supplementary Figure 10. Relationships between the diversity (number of phylotypes) of bacteria or fungi and the number of functions beyond threshold in a microcosm study including two soils from Eastern Australia (n = 5 replicates x four dilution levels). P-values (Ordinary least squares linear regressions) as follow: *P < 0.05; **P < 0.01.



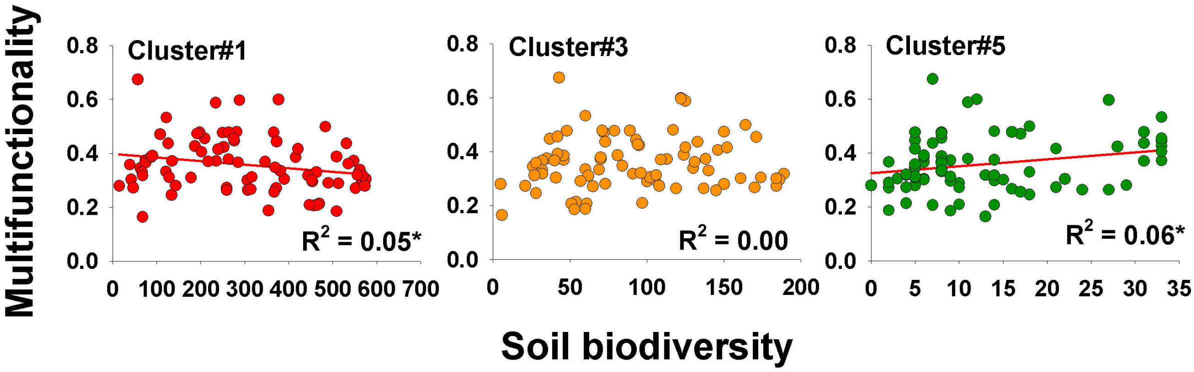
Supplementary Figure 11. Number of functions (±SE) beyond threshold across an experimentally-created gradient of soil biodiversity using the dilution to extinction approach in two soils from Eastern Australia (n = 5 replicates).



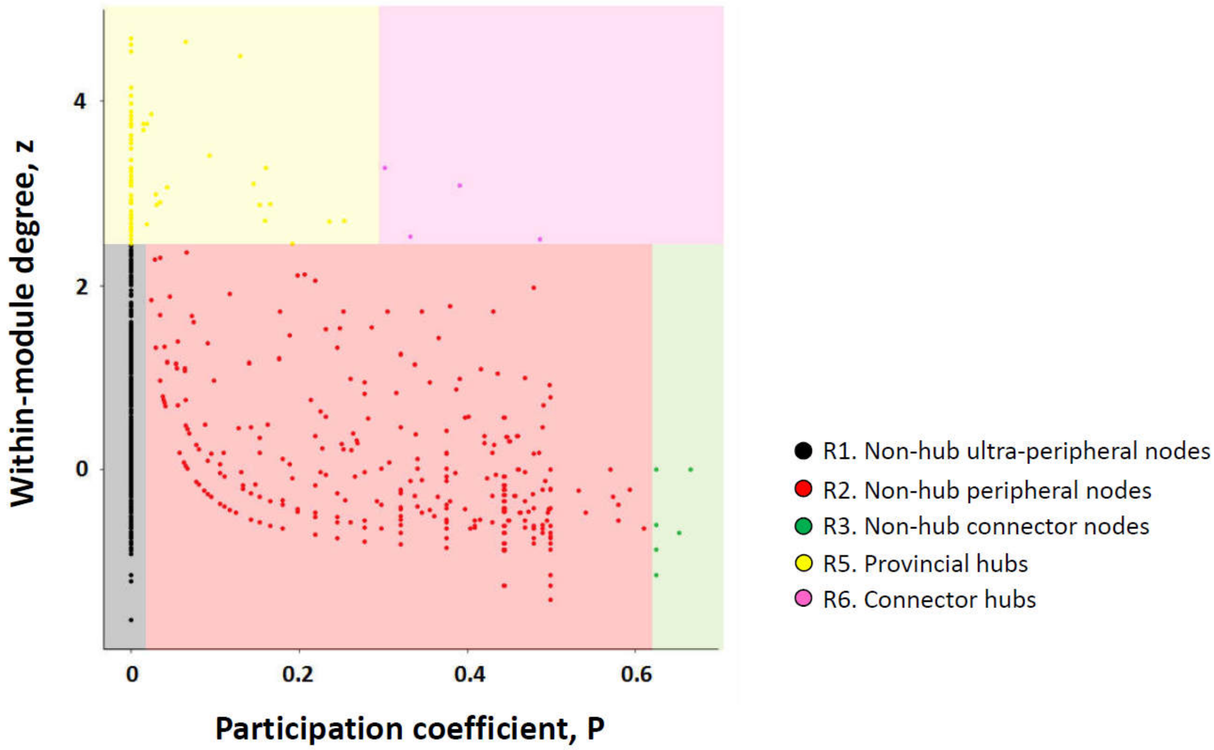
Supplementary Figure 12. Relationships between the diversity (number of phylotypes) of ecological clusters for highly connected taxa and the number of functions beyond threshold in a global field survey (n = 81 study sites). P-values (Ordinary least squares linear regressions) as follow: *P < 0.05; **P < 0.01.



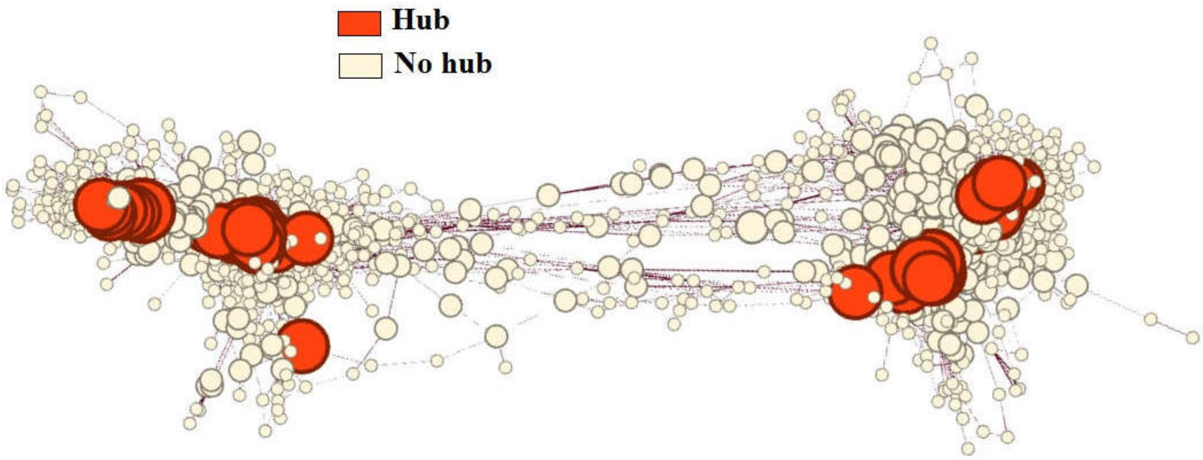
Supplementary Figure 13. Relationships between the diversity (number of phylotypes) of selected ecological clusters and highly connected taxa and the number of functions beyond threshold in a microcosm experiment (n = 5 replicates x four dilution levels). P-values (Ordinary least squares linear regressions) as follow: *P < 0.05; **P < 0.01.



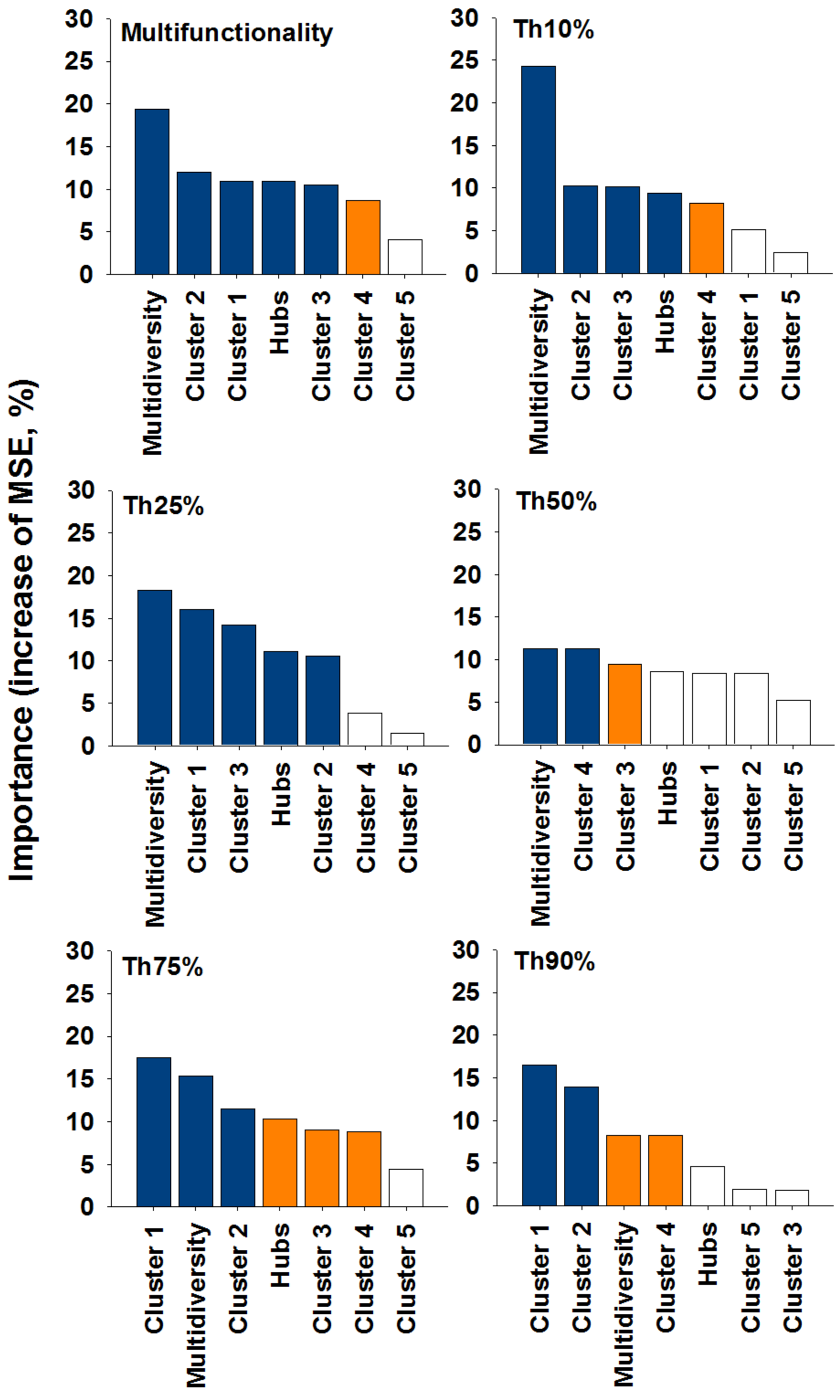
Supplementary Figure 14. Relationships between the diversity (number of phylotypes) within ecological clusters #1, 3 and 5 in a correlation network and averaging multifunctionality in the global suervey (n = 81 study sites). P-values (Ordinary least squares linear regressions) as follow: *P < 0.05.



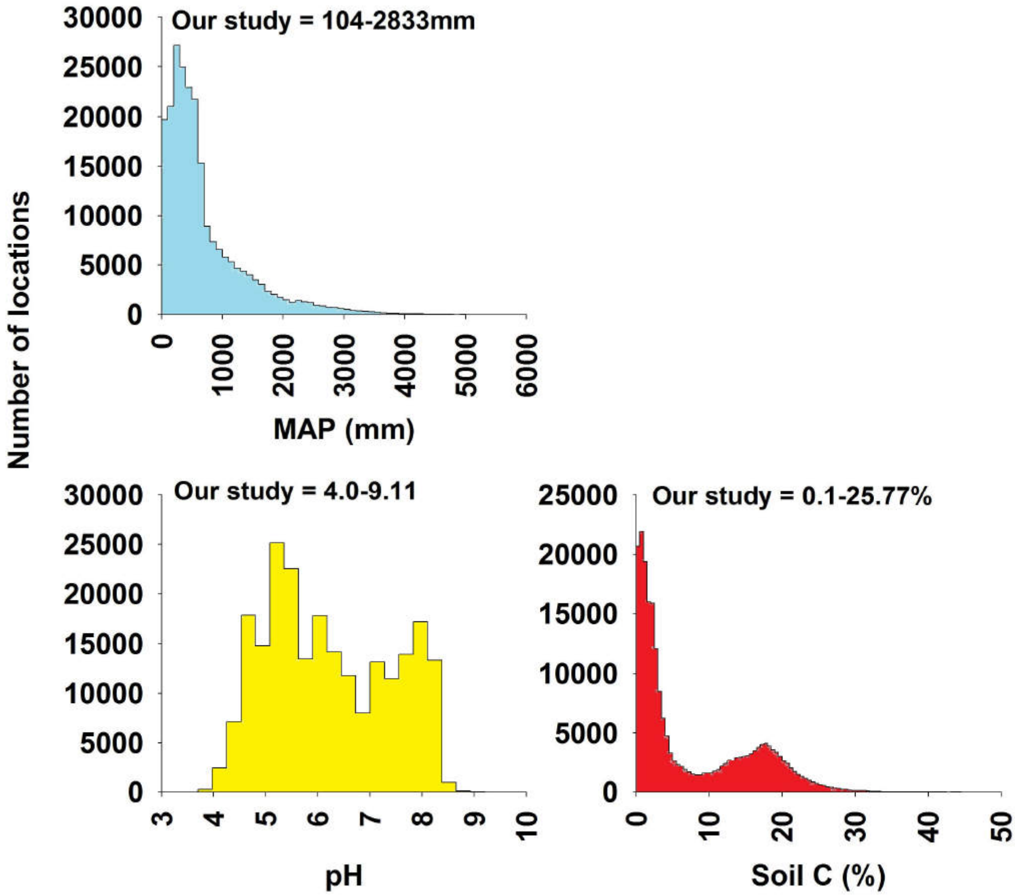
Supplementary Figure 15. Roles and regions in the z–P parameter space. Module = ecological cluster. This figure is based on Fig. 2 from ref.[21]. Each dot represents a soil phylotypes.



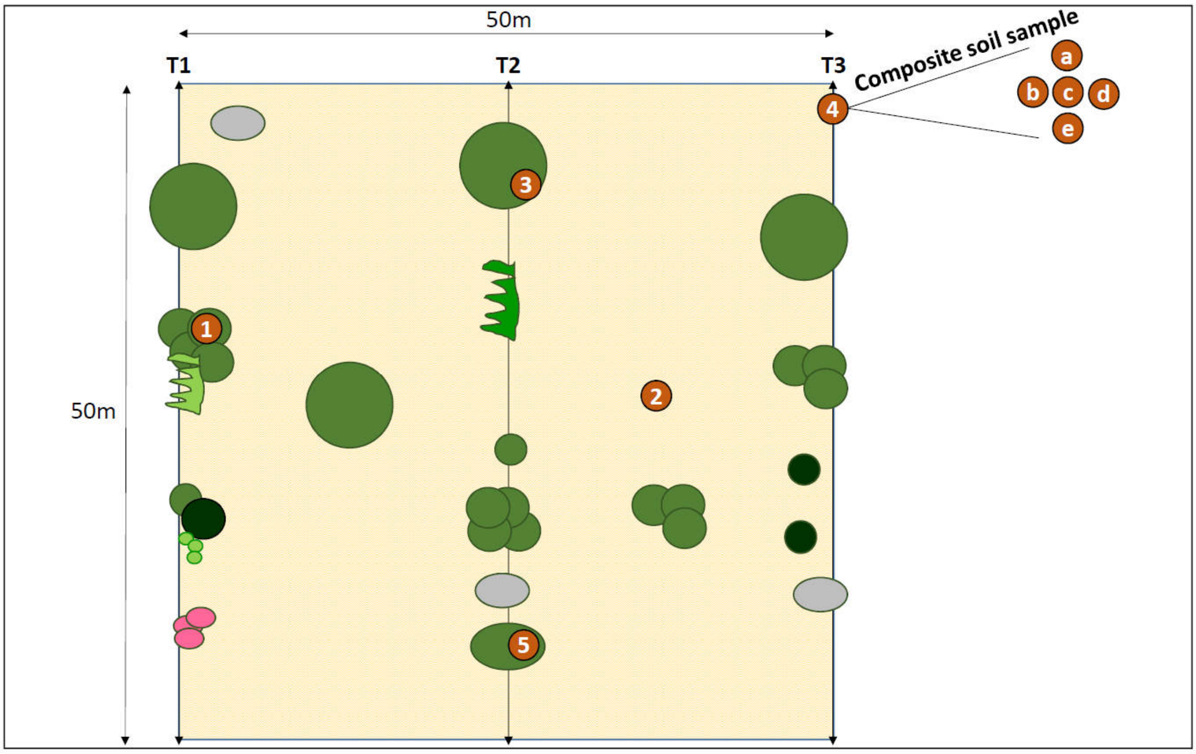
Supplementary Figure 16. Ecological network diagram highlighting the presence of highly connected soil taxa within the food web.



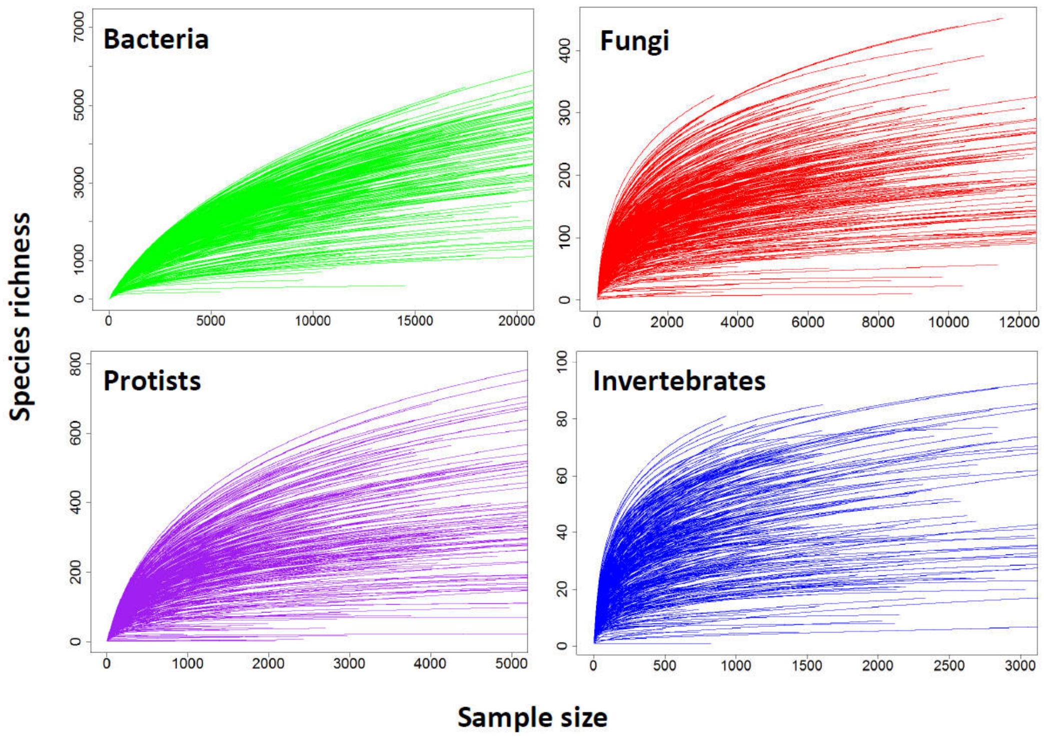
Supplementary Figure 17. Random Forest analysis, as described in ref.[10], aiming to identify the relative importance of different soil biodiversity indexes in predicting ecosystem multifunctionality (n = 81 study sites). Cluster# indicates richness within a given network ecological cluster. Hubs indicate richness of soil taxa classified as hubs. Increase of MSE indicates the increase of the Mean Squared Error when a given variable is randomly permuted.



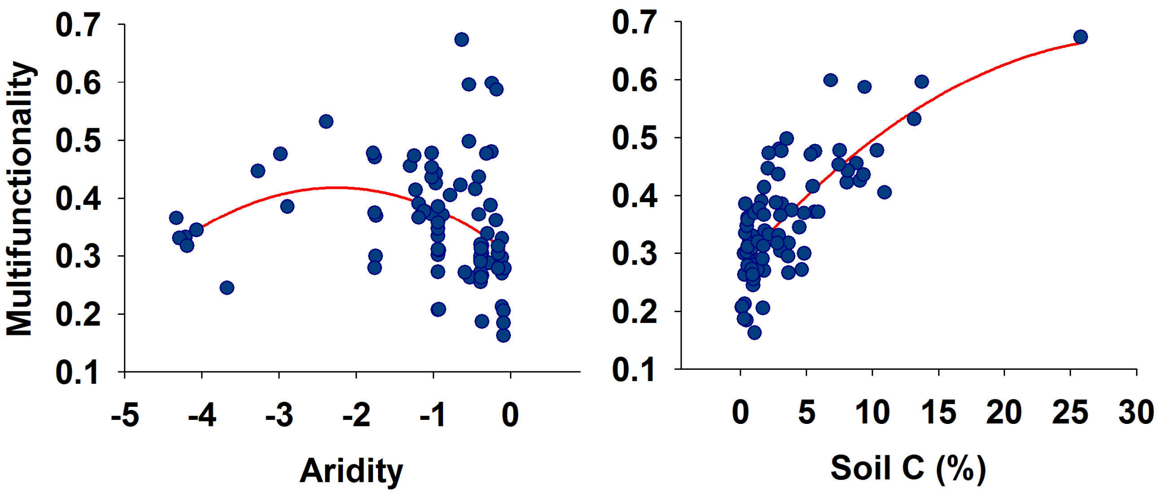
Supplementary Figure 18. Global distribution of mean annual precipitation, and soil pH and carbon. Ranges for these variables covered by our global survey are highlighted within each panel.



Supplementary Figure 19. Soil sampling design within each plot.



Supplementary Figure 20. Rarefaction curves for the richness of four groups of soil organisms. Each line represents a soil sample (n = 81 study sites).



Environmental Predictor	Direction	Response	Model	Adj-R^2	P value	AICc	DeltaAICc
Plant cover	→	EMF	Linear	0.148	<0.001	-149.148	0.00
			Quadratic	0.170	<0.001	-149.006	0.14
Plant richness	→	EMF	Linear	0.000	0.930		
			Quadratic	0.020	0.449		
MAT	→	EMF	Linear	0.048	0.049		
			Quadratic	0.049	0.138		
% of Clay	→	EMF	Linear	0.146	<0.001	-148.871	0.27
			Quadratic	0.171	<0.001	-149.136	0.00
Soil pH	→	EMF	Linear	0.212	<0.001	-156.445	0.00
			Quadratic	0.223	<0.001	-156.438	0.01
Soil C	→	EMF	Linear	0.549	<0.001	-200.545	2.16
			Quadratic	0.572	<0.001	-202.705	0.00
Aridity	→	EMF	Linear	0.013	0.302		
			Quadratic	0.101	0.015		

Supplementary Figure 21. Linear and quadratic fits for the relationships between environmental factors and multifunctionality included (n = 81 study sites).

Supplementary Table 1. Ecosystem type in each location.

Location ID	Ecosystem type
ALPS1	Forbland
ALPS2	Forbland
ALPS3	Grassland
ALPS4	Grassland
ALPS5	Cold Forest
AZ1	Dry Forest
AZ2	Dry Forest
AZ3	Dry Forest
AZ4	Dry Forest
BOS1	Shrubland
BOS2	Shrubland
BOS3	Shrubland
BOS4	Shrubland
BOV1	Shrubland
BOV2	Shrubland
BOV3	Shrubland
BOV4	Shrubland
CAL1	Shrubland
CAL2	Shrubland
CAL3	Grassland
CAL4	Grassland
CAL5	Grassland
CH1	Moss health
CH2	Shrubland
CH3	Temperate Forest
CH4	Temperate Forest
CH5	Temperate Forest
CH6	Temperate Forest
CI1	Temperate Forest
CI2	Temperate Forest
CI3	Temperate Forest
CI4	Temperate Forest
CI5	Temperate Forest
CI6	Temperate Forest
CO1	Grassland
CO2	Grassland
CO3	Grassland
CO4	Grassland
CO5	Grassland

CO6	Grassland
HA1	Tropical Forest
HA3	Tropical Forest
ICE1	Moss health
ICE2	Moss health
ICE3	Moss health
ICE4	Moss health
ICE5	Shrubland
JOR1	Forbland
JOR2	Grassland
JOR3	Forbland
JOR4	Forbland
MEX1	Temperate Forest
MEX2	Temperate Forest
MEX3	Temperate Forest
MEX4	Temperate Forest
MEX5	Temperate Forest
MEX6	Temperate Forest
MEX7	Temperate Forest
MEX8	Temperate Forest
MI1	Grassland
MI10	ColdForest
MI2	Grassland
MI3	Shrubland
MI4	Shrubland
MI5	ColdForest
MI6	ColdForest
MI7	ColdForest
MI8	ColdForest
MI9	ColdForest
QL1	Temperate Forest
QL2	Temperate Forest
QL3	Temperate Forest
QL4	Temperate Forest
QL5	Temperate Forest
QL6	Temperate Forest
WA1	Shrubland
WA2	Shrubland
WA3	Shrubland
WA4	Shrubland
WA5	Shrubland
WA6	Shrubland

Supplementary Table 2. Standardized and unstandardized direct effects of all biotic and abiotic factors on ecosystem multifunctionality from Fig. 2B. This table includes all significant and non-significant path considered by our model, and also includes those variable which were allow to covary. Information on variables included in BOXA-D in Fig. 2B is highlighted in this table in the column “BOX”.

BOX	Parameters			Standardized regression weights	Regression weights	*P*
	Distance equator	→	Multifunctionality	-0.184	-0.002	0.235
	Plant cover	→	Multifunctionality	0.157	0.001	0.115
	Plant richness	→	Multifunctionality	-0.100	-0.001	0.132
	MAT	→	Multifunctionality	0.156	0.003	0.060
	Clay %	→	Multifunctionality	0.123	0.003	0.131
	Soil pH	→	Multifunctionality	-0.128	-0.010	0.250
	Soil C	→	Multifunctionality	0.581	0.014	<0.001
	Longuitude (sine)	→	Multifunctionality	-0.485	-0.066	<0.001
	Longuitude (cosine)	→	Multifunctionality	0.095	0.016	0.482
	Soil biodiversity	→	Multifunctionality	0.295	0.000	0.023
	Aridity	→	Multifunctionality	-0.208	-0.057	0.109
	Aridity	→	Plant cover	0.146	3.899	0.259
	Aridity	→	Plant richness	-0.432	-5.454	0.003
	Aridity	→	Soil C	-0.356	-1.322	0.014
	Aridity	→	Soil pH	0.342	0.393	0.011
	Aridity	→	Clay %	0.305	1.159	0.022
B	Aridity	→	Richness Lobosa	0.062	0.757	0.723
B	Aridity	→	Richness Ciliophora	0.267	12.292	0.018
B	Aridity	→	Richness Platyhelminthes	-0.395	-0.392	0.031
B	Aridity	→	Richness Cercozoa	-0.373	-23.435	0.025
B	Aridity	→	Richness Bacteria	-0.279	-320.389	0.107
B	Aridity	→	Richness Saprotrophic fungi	-0.099	-2.017	0.585
B	Aridity	→	Richness Mycorrhizal fungi	-0.245	-2.551	0.176
B	Aridity	→	Richness Tardigrada	-0.074	-0.180	0.678
B	Aridity	→	Richness Rotifera	-0.168	-1.447	0.261
B	Aridity	→	Richness Nematoda	-0.444	-6.895	0.005
B	Aridity	→	Richness Arthropoda	-0.180	-1.279	0.255
B	Aridity	→	Richness Annelida	-0.151	-0.306	0.414
	Aridity^2	↔	Longuitude (cosine)	-0.124	-0.335	0.27
	Aridity^2	↔	Longuitude (sine)	0.597	2.046	<0.001
	Aridity^2	↔	Distance equator	-0.679	-37.197	<0.001
	Aridity^2	↔	Clay %	0.016	0.266	0.420
	Aridity^2	↔	Soil pH	-0.083	-0.409	<0.001

	$Aridity^2$	↔	Soil C	0.069	1.184	<0.001
	$Aridity^2$	↔	Plant richness	0.022	1.313	0.230
	$Aridity^2$	↔	Plant cover	0.077	8.478	<0.001
	$Aridity^2$	↔	Aridity	0.659	2.43	<0.001
	$Aridity^2$	↔	MAT	0.142	3.013	0.070
C	Clay %	→	Richness Annelida	0.043	0.023	0.752
C	Clay %	→	Richness Arthropoda	-0.066	-0.123	0.566
C	Clay %	→	Richness Nematoda	-0.161	-0.658	0.160
C	Clay %	→	Richness Rotifera	0.044	0.100	0.684
C	Clay %	→	Richness Tardigrada	0.102	0.066	0.428
C	Clay %	→	Richness Mycorrhizal fungi	0.066	0.180	0.619
C	Clay %	→	Richness Saprotrophic fungi	-0.151	-0.816	0.250
C	Clay %	→	Richness Bacteria	-0.311	-94.136	0.014
C	Clay %	→	Richness Cercozoa	0.003	0.052	0.979
C	Clay %	→	Richness Platyhelminthes	0.080	0.021	0.549
C	Clay %	→	Richness Ciliophora	-0.138	-1.669	0.093
C	Clay %	→	Richness Lobosa	0.036	0.116	0.777
	Clay %	↔	Soil pH	-0.346	-1.301	<0.001
	Clay %	↔	Soil C	0.476	6.216	<0.001
	Distance equator	→	Aridity	-0.439	-0.040	<0.001
	Distance equator	→	MAT	-0.556	-0.260	<0.001
	Distance equator	→	Plant cover	0.090	0.221	0.560
	Distance equator	→	Plant richness	0.051	0.059	0.773
	Distance equator	→	Soil C	-0.416	-0.142	0.015
	Distance equator	→	Soil pH	-0.008	-0.001	0.960
	Distance equator	→	Clay %	-0.279	-0.098	0.078
	Distance equator	→	Richness Annelida	-0.037	-0.007	0.836
	Distance equator	→	Richness Arthropoda	0.125	0.081	0.415
	Distance equator	→	Richness Nematoda	-0.253	-0.362	0.096
	Distance equator	→	Richness Rotifera	0.058	0.046	0.688
	Distance equator	→	Richness Tardigrada	0.055	0.012	0.748
	Distance equator	→	Richness Mycorrhizal fungi	-0.506	-0.485	0.004
	Distance equator	→	Richness Saprotrophic fungi	0.156	0.293	0.372
	Distance equator	→	Richness Bacteria	-0.162	-17.138	0.333
	Distance equator	→	Richness Cercozoa	0.056	0.323	0.728
	Distance equator	→	Richness Platyhelminthes	-0.450	-0.041	0.011
	Distance equator	→	Richness Ciliophora	0.643	2.729	<0.001
	Distance equator	→	Richness Lobosa	0.240	0.272	0.153
	Distance equator	↔	Longuitude (sine)	-0.719	-6.339	<0.001
	Distance equator	↔	Longuitude (cosine)	-0.157	-1.097	0.170
	Longuitude (cosine)	→	Aridity	-0.012	-0.023	0.882

Longuitude (cosine)	→	MAT	-0.101	-0.952	0.286
Longuitude (cosine)	→	Plant cover	-0.415	-20.648	<0.001
Longuitude (cosine)	→	Plant richness	-0.060	-1.417	0.575
Longuitude (cosine)	→	Soil C	0.183	1.262	0.082
Longuitude (cosine)	→	Soil pH	0.395	0.845	<0.001
Longuitude (cosine)	→	Clay %	0.367	2.596	<0.001
Longuitude (cosine)	→	Richness Annelida	0.110	0.413	0.445
Longuitude (cosine)	→	Richness Arthropoda	0.121	1.594	0.325
Longuitude (cosine)	→	Richness Nematoda	0.484	13.992	<0.001
Longuitude (cosine)	→	Richness Rotifera	-0.113	-1.803	0.332
Longuitude (cosine)	→	Richness Tardigrada	-0.067	-0.305	0.627
Longuitude (cosine)	→	Richness Mycorrhizal fungi	0.102	1.983	0.466
Longuitude (cosine)	→	Richness Saprotrophic fungi	0.292	11.116	0.037
Longuitude (cosine)	→	Richness Cercozoa	0.363	42.548	0.005
Longuitude (cosine)	→	Richness Bacteria	0.386	824.979	0.004
Longuitude (cosine)	→	Richness Platyhelminthes	-0.049	-0.090	0.732
Longuitude (cosine)	→	Richness Ciliophora	0.611	52.406	<0.001
Longuitude (cosine)	→	Richness Lobosa	0.301	6.875	0.026
Longuitude (sine)	→	Aridity	0.297	0.438	0.012
Longuitude (sine)	→	MAT	0.016	0.118	0.907
Longuitude (sine)	→	Clay %	-0.330	-1.848	0.021
Longuitude (sine)	→	Soil pH	-0.008	-0.013	0.956
Longuitude (sine)	→	Soil C	-0.022	-0.122	0.885
Longuitude (sine)	→	Plant richness	0.241	4.476	0.127
Longuitude (sine)	→	Plant cover	-0.005	-0.180	0.974
Longuitude (sine)	→	Richness Lobosa	0.101	1.827	0.499
Longuitude (sine)	→	Richness Ciliophora	0.214	14.522	0.027
Longuitude (sine)	→	Richness Platyhelminthes	-0.269	-0.393	0.089
Longuitude (sine)	→	Richness Bacteria	0.045	76.926	0.760
Longuitude (sine)	→	Richness Saprotrophic fungi	0.120	3.603	0.441
Longuitude (sine)	→	Richness Mycorrhizal fungi	-0.005	-0.075	0.975
Longuitude (sine)	→	Richness Tardigrada	-0.363	-1.313	0.017
Longuitude (sine)	→	Richness Rotifera	0.155	1.963	0.228
Longuitude (sine)	→	Richness Nematoda	0.083	1.893	0.540
Longuitude (sine)	→	Richness Arthropoda	0.354	3.697	0.009
Longuitude (sine)	→	Richness Annelida	-0.033	-0.097	0.837
Longuitude (sine)	→	Richness Cercozoa	0.131	12.092	0.360
Longuitude (sine)	↔	Longuitude (cosine)	0.025	0.011	0.82
MAT	→	Plant cover	0.346	1.824	0.002
MAT	→	Plant richness	0.056	0.141	0.664
MAT	→	Soil C	0.067	0.049	0.598
MAT	→	Clay %	-0.122	-0.091	0.301

	MAT	→	Soil pH	-0.298	-0.068	0.012
B	MAT	→	Richness Lobosa	0.111	0.270	0.386
B	MAT	→	Richness Ciliophora	0.198	1.803	0.017
B	MAT	→	Richness Platyhelminthes	0.030	0.006	0.828
B	MAT	→	Richness Cercozoa	-0.050	-0.623	0.683
B	MAT	→	Richness Bacteria	-0.007	-1.613	0.956
B	MAT	→	Richness Saprotrophic fungi	0.063	0.255	0.636
B	MAT	→	Richness Mycorrhizal fungi	-0.259	-0.532	0.053
B	MAT	→	Richness Tardigrada	0.144	0.070	0.271
B	MAT	→	Richness Rotifera	0.114	0.194	0.301
B	MAT	→	Richness Nematoda	-0.232	-0.709	0.046
B	MAT	→	Richness Arthropoda	0.018	0.025	0.878
B	MAT	→	Richness Annelida	-0.132	-0.052	0.337
	MAT	↔	Aridity	0.239	0.878	0.04
A	Plant cover	→	Richness Annelida	0.007	0.001	0.964
A	Plant cover	→	Richness Arthropoda	0.136	0.036	0.315
A	Plant cover	→	Richness Nematoda	0.633	0.368	<0.001
A	Plant cover	→	Richness Rotifera	0.323	0.104	0.012
A	Plant cover	→	Richness Tardigrada	-0.036	-0.003	0.814
A	Plant cover	→	Richness Mycorrhizal fungi	0.465	0.181	0.003
A	Plant cover	→	Richness Saprotrophic fungi	0.533	0.408	<0.001
A	Plant cover	→	Richness Bacteria	0.479	20.591	0.001
A	Plant cover	→	Richness Cercozoa	0.642	1.512	<0.001
A	Plant cover	→	Richness Platyhelminthes	0.035	0.001	0.824
A	Plant cover	→	Richness Ciliophora	0.525	0.906	<0.001
A	Plant cover	→	Richness Lobosa	0.526	0.242	<0.001
	Plant cover	↔	Plant richness	0.394	121.863	<0.001
	Plant cover	↔	Clay %	0.222	18.671	0.05
	Plant cover	↔	Soil pH	-0.423	-10.826	<0.001
	Plant cover	↔	Soil C	0.451	40.103	<0.001
A	Plant richness	→	Richness Lobosa	-0.011	-0.011	0.923
A	Plant richness	→	Richness Ciliophora	0.191	0.696	0.009
A	Plant richness	→	Richness Platyhelminthes	-0.080	-0.006	0.503
A	Plant richness	→	Richness Cercozoa	0.017	0.087	0.871
A	Plant richness	→	Richness Saprotrophic fungi	0.006	0.010	0.957
A	Plant richness	→	Richness Mycorrhizal fungi	0.007	0.006	0.954
A	Plant richness	→	Richness Tardigrada	0.132	0.026	0.250
A	Plant richness	→	Richness Rotifera	0.151	0.103	0.121
A	Plant richness	→	Richness Nematoda	-0.010	-0.012	0.925
A	Plant richness	→	Richness Arthropoda	-0.143	-0.080	0.165
A	Plant richness	→	Richness Annelida	0.063	0.010	0.598
A	Plant richness	→	Richness Bacteria	0.015	1.389	0.892

	Plant richness	↔	Clay %	-0.014	-0.633	0.89
	Plant richness	↔	Soil C	-0.026	-1.232	0.79
	Richness Annelida	↔	Aridity^2	0.036	0.323	0.04
D	Richness Arthropoda	↔	Richness Annelida	0.271	3.156	0.02
D	Richness Arthropoda	↔	Richness Rotifera	0.249	9.958	0.03
D	Richness Arthropoda	↔	Richness Tardigrada	0.089	1.203	0.43
D	Richness Arthropoda	↔	Richness Mycorrhizal fungi	0.295	17.266	0.01
D	Richness Arthropoda	↔	Richness Saprotrophic fungi	0.293	33.592	0.01
D	Richness Arthropoda	↔	Richness Bacteria	0.162	1001.086	0.15
D	Richness Arthropoda	↔	Richness Cercozoa	0.212	68.892	0.06
D	Richness Arthropoda	↔	Richness Platyhelminthes	0.108	0.611	0.34
D	Richness Arthropoda	↔	Richness Ciliophora	0.269	43.299	0.02
D	Richness Arthropoda	↔	Richness Nematoda	0.339	25.673	0
D	Richness Arthropoda	↔	Richness Lobosa	0.342	22.689	0
	Richness Arthropoda	↔	Aridity^2	0.042	1.131	0.02
D	Richness Bacteria	↔	Richness Annelida	0.13	267.106	0.25
D	Richness Bacteria	↔	Richness Platyhelminthes	0.083	83.742	0.46
D	Richness Bacteria	↔	Richness Ciliophora	0.624	17766.161	<0.001
D	Richness Bacteria	↔	Richness Lobosa	0.615	7225.417	<0.001
D	Richness Bacteria	↔	Richness Cercozoa	0.7	40227.581	<0.001
	Richness Bacteria	↔	Aridity^2	0.037	179.289	0.04
D	Richness Cercozoa	↔	Richness Annelida	0.272	29.416	0.02
D	Richness Cercozoa	↔	Richness Ciliophora	0.652	976.836	<0.001
D	Richness Cercozoa	↔	Richness Platyhelminthes	0.124	6.565	0.27
D	Richness Cercozoa	↔	Richness Lobosa	0.804	496.319	<0.001
	Richness Cercozoa	↔	Aridity^2	0.033	8.283	0.06
D	Richness Ciliophora	↔	Richness Annelida	-0.053	-2.827	0.64
D	Richness Ciliophora	↔	Richness Lobosa	0.648	198.35	<0.001
	Richness Ciliophora	↔	Aridity^2	0.023	2.87	0.19
D	Richness Lobosa	↔	Richness Annelida	0.223	4.941	0.05
	Richness Lobosa	↔	Aridity^2	0.025	1.277	0.16
D	Richness Mycorrhizal fungi	↔	Richness Annelida	0.015	0.29	0.89
D	Richness Mycorrhizal fungi	↔	Richness Saprotrophic fungi	0.657	126.62	<0.001
D	Richness Mycorrhizal fungi	↔	Richness Platyhelminthes	0.106	1.008	0.35
D	Richness Mycorrhizal fungi	↔	Richness Ciliophora	0.647	174.97	<0.001
D	Richness Mycorrhizal fungi	↔	Richness Bacteria	0.726	7522.123	<0.001
D	Richness Mycorrhizal fungi	↔	Richness Cercozoa	0.638	347.735	<0.001
D	Richness Mycorrhizal fungi	↔	Richness Lobosa	0.611	68.027	<0.001
	Richness Mycorrhizal fungi	↔	Aridity^2	0.038	1.722	0.03
D	Richness Nematoda	↔	Richness Annelida	0.327	8.275	0.01
D	Richness Nematoda	↔	Richness Tardigrada	0.458	13.443	<0.001
D	Richness Nematoda	↔	Richness Mycorrhizal fungi	0.646	82.244	<0.001
D	Richness Nematoda	↔	Richness Saprotrophic fungi	0.685	170.871	<0.001

D	Richness Nematoda	↔	Richness Bacteria	0.608	8155.193	<0.001
D	Richness Nematoda	↔	Richness Cercozoa	0.813	573.334	<0.001
D	Richness Nematoda	↔	Richness Platyhelminthes	0.118	1.459	0.29
D	Richness Nematoda	↔	Richness Ciliophora	0.593	207.364	<0.001
D	Richness Nematoda	↔	Richness Lobosa	0.717	103.285	<0.001
D	Richness Nematoda	↔	Richness Rotifera	0.582	50.591	<0.001
	Richness Nematoda	↔	$Aridity^2$	0.061	3.615	<0.001
D	Richness Platyhelminthes	↔	Richness Ciliophora	0.052	1.364	0.64
D	Richness Platyhelminthes	↔	Richness Annelida	0.181	0.343	0.11
D	Richness Platyhelminthes	↔	Richness Lobosa	0.141	1.523	0.21
	Richness Platyhelminthes	↔	$Aridity^2$	0.01	0.042	0.58
D	Richness Rotifera	↔	Richness Annelida	0.162	2.161	0.15
D	Richness Rotifera	↔	Richness Mycorrhizal fungi	0.389	26.141	0
D	Richness Rotifera	↔	Richness Saprotrophic fungi	0.44	57.902	<0.001
D	Richness Rotifera	↔	Richness Cercozoa	0.478	177.848	<0.001
D	Richness Rotifera	↔	Richness Ciliophora	0.482	89.03	<0.001
D	Richness Rotifera	↔	Richness Lobosa	0.473	35.997	<0.001
D	Richness Rotifera	↔	Richness Tardigrada	0.46	7.132	<0.001
D	Richness Rotifera	↔	Richness Bacteria	0.331	2342.696	0.01
D	Richness Rotifera	↔	Richness Platyhelminthes	0.07	0.456	0.53
	Richness Rotifera	↔	$Aridity^2$	0.023	0.718	0.18
D	Richness Saprotrophic fungi	↔	Richness Annelida	0.377	14.439	<0.001
D	Richness Saprotrophic fungi	↔	Richness Bacteria	0.636	12911.391	<0.001
D	Richness Saprotrophic fungi	↔	Richness Cercozoa	0.737	786.905	<0.001
D	Richness Saprotrophic fungi	↔	Richness Ciliophora	0.534	282.806	<0.001
D	Richness Saprotrophic fungi	↔	Richness Platyhelminthes	0.27	5.037	0.020
D	Richness Saprotrophic fungi	↔	Richness Lobosa	0.718	156.768	<0.001
	Richness Saprotrophic fungi	↔	$Aridity^2$	0.049	4.42	0.010
D	Richness Tardigrada	↔	Richness Annelida	0.102	0.461	0.360
D	Richness Tardigrada	↔	Richness Mycorrhizal fungi	0.336	7.622	<0.001
D	Richness Tardigrada	↔	Richness Saprotrophic fungi	0.521	23.143	<0.001
D	Richness Tardigrada	↔	Richness Bacteria	0.393	939.147	<0.001
D	Richness Tardigrada	↔	Richness Cercozoa	0.594	74.721	<0.001
D	Richness Tardigrada	↔	Richness Platyhelminthes	0.179	0.392	0.120
D	Richness Tardigrada	↔	Richness Ciliophora	0.401	25.009	<0.001
D	Richness Tardigrada	↔	Richness Lobosa	0.449	11.536	<0.001
	Richness Tardigrada	↔	$Aridity^2$	0.024	0.257	0.160
C	Soil C	→	Richness Annelida	0.132	0.072	0.367
C	Soil C	→	Richness Arthropoda	-0.184	-0.352	0.141
C	Soil C	→	Richness Nematoda	0.050	0.209	0.688
C	Soil C	→	Richness Rotifera	-0.025	-0.058	0.832
C	Soil C	→	Richness Tardigrada	0.233	0.154	0.095
C	Soil C	→	Richness Mycorrhizal fungi	-0.189	-0.530	0.187

C	Soil C	→	Richness Saprotrophic fungi	0.118	0.648	0.409
C	Soil C	→	Richness Bacteria	0.194	60.189	0.155
C	Soil C	→	Richness Cercozoa	0.022	0.375	0.866
C	Soil C	→	Richness Platyhelminthes	-0.069	-0.018	0.634
C	Soil C	→	Richness Ciliophora	-0.004	-0.044	0.968
C	Soil C	→	Richness Lobosa	0.104	0.343	0.450
C	Soil pH	→	Richness Annelida	-0.287	-0.504	0.047
C	Soil pH	→	Richness Arthropoda	-0.619	-3.819	<0.001
C	Soil pH	→	Richness Nematoda	-0.096	-1.302	0.432
C	Soil pH	→	Richness Rotifera	-0.296	-2.211	0.011
C	Soil pH	→	Richness Tardigrada	-0.066	-0.141	0.634
C	Soil pH	→	Richness Mycorrhizal fungi	-0.127	-1.150	0.369
C	Soil pH	→	Richness Saprotrophic fungi	0.117	2.074	0.408
C	Soil pH	→	Richness Bacteria	0.258	257.927	0.056
C	Soil pH	→	Richness Cercozoa	0.001	0.044	0.995
C	Soil pH	→	Richness Platyhelminthes	-0.233	-0.201	0.105
C	Soil pH	→	Richness Ciliophora	0.415	16.626	<0.001
C	Soil pH	→	Richness Lobosa	0.126	1.343	0.354
	Soil pH	↔	Soil C	-0.53	-2.103	<0.001

Supplementary Table 3. R^2 values corresponding to the regressions in Fig. 3.

Organism group	Threshold	R^2
Bacteria	10%	0.233
	25%	0.031
	50%	0.053
	75%	0.021
	90%	0.000
Mycorrhizal fungi	10%	0.135
	25%	0.055
	50%	0.053
	75%	0.020
	90%	0.001
Saprotrophic fungi	10%	0.143
	25%	0.012
	50%	0.046
	75%	0.004
	90%	0.000
Annelida	10%	0.042
	25%	0.008
	50%	0.029
	75%	0.077
	90%	0.074
Arthropoda	10%	0.013
	25%	0.015
	50%	0.033
	75%	0.054

	90%	0.127
Nematoda	10%	0.268
	25%	0.060
	50%	0.050
	75%	0.045
	90%	0.040
Platyhelminthes	10%	0.022
	25%	0.031
	50%	0.043
	75%	0.075
	90%	0.042
Tardigrada	10%	0.134
	25%	0.031
	50%	0.047
	75%	0.059
	90%	0.032
Rotifera	10%	0.080
	25%	0.030
	50%	0.058
	75%	0.036
	90%	0.022
Ciliophora	10%	0.087
	25%	0.002
	50%	0.003
	75%	0.047
	90%	0.035

Cercozoa	10%	0.274
	25%	0.047
	50%	0.062
	75%	0.033
	90%	0.025
Lobosa	10%	0.238
	25%	0.033
	50%	0.062
	75%	0.017
	90%	0.000
Multidiversity	10%	0.285
	25%	0.055
	50%	0.090
	75%	0.060
	90%	0.032

Supplementary Table 4. Significant correlations (Spearman) between the diversity of single groups of organisms and the different dimensions (dim) of multifunctionality represented by the multiple axes from a PCA analysis including the eleven functions in the global field survey. *P < 0.05; **P < 0.01. The selected five axes accounted for >80% in the variation of multiple ecosystem functions. Red and blue colors correspond with positive and negative relationships, respectively.

Functions	Dim1	Dim2	Dim3	Dim4	Dim5
Reduced ARG abundance		-.273*	.390**	.245*	
Reduced plant pathogens	.522**	.604**	.284*	-.343**	
NPP	.815**	.559**	-.332**	.236*	
P availability	.260*	-.579**	.249*	-.384**	.335**
N availability	.391**	-.359**	.268*		.487**
Sugar degradation		-.825**			
Chitin degradation	.471**	-.405**	-.350**		-.370**
P mineralization	.602**	-.324**	-.325**		
Lignin degradation				-.405**	
Soil respiration	.590**	-.357**	.417**		
Glucose mineralization	.529**		.513**		
Soil biodiversity					
Annelida	.356**	.293**		-.228*	
Arthropoda	.410**	.262*			-.275*
Nematoda	.361**		.261*		
Platyhelminthes	.325**				
Rotifera	.405**	.255*		.309**	
Tardigrada	.323**				
Mycorrhizal fungi	.286**				
Saprotrophic fungi					
Cercozoa	.339**				
Ciliophora		-.418**			
Lobosa	.236*				.212*
Bacteria			.287**		

Supplementary Table 5. Significant correlations (Spearman) between the diversity of nematode functional groups and average multifunctionality in the global field survey. *P < 0.05; **P < 0.01. Red colors correspond with positive correlations

Functions	Animal Predator	Bacterivore	Herbivore
Reduced ARG abundance			.251*
Reduced plant pathogens	.235*	.233*	.227*
NPP	.229*	.281*	
P availability			.233*
N availability	.305**	.264*	.381**
Sugar degradation			
Chitin degradation			
P mineralization		.257*	
Lignin degradation			
Soil respiration	.233*	.319**	.402**
Glucose mineralization		.325**	.227*
Averaging multifunctionality		.383**	.286**
Functions beyond a 10% threshold	.225*	.379**	.387**
Functions beyond a 25% threshold		.343**	
Functions beyond a 50% threshold		.210*	
Functions beyond a 75% threshold			
Functions beyond a 90% threshold	.239*		

Supplementary Table 6. Significant correlations (Spearman) between the diversity of single groups of organisms and single ecosystem functions in a microcosm experiment. *P < 0.05; **P < 0.01. Red colors correspond with positive correlations

	Soil A		Soil B	
	Bacteria	**Fungi**	**Bacteria**	**Fungi**
P availability			.902**	.732**
N availability	.809**	.885**	.865**	.735**
Sugar degradation	.762**	.896**	.920**	.770**
Chitin degradation	.799**	.867**	.869**	.655**
P mineralization	.708**	.781**	.834**	.787**
Soil respiration				
Lignin degradation	.784**	.603*		
Glucose mineralization			.481*	

Supplementary Table 7. Partial correlations between soil biodiversity and averaging multifunctionality, controlling for microbial abundance and community composition – first axis of an NMDS including the relative abundance of microbial taxa at the phylotype level – in a microcosm experiment. *P < 0.05; **P < 0.01. Red colors correspond with positive correlations

		Multifunctionality
Soil A	Bacteria	0.61*
	Fungal	0.70**
Soil B	Bacteria	0.57*
	Fungal	0.64**

Supplementary Table 8. List of identified dominant soil phylotypes across the globe belonging to different ecological clusters and connectivity classification.

Supplementary Table 8 is available online as a Separate .XLS file under the Supplementary Information for this article.

Table S9. Significant correlations (Spearman) between the diversity of ecological clusters and hub taxa with average multifunctionality in the global field survey. *P < 0.05; **P < 0.01. Red and blue colors correspond with positive and negative relationships, respectively.

	Cluster #1	Cluster #2	Cluster #3	Cluster #4	Cluster #5	Hubs
Reduced ARG abundance	.228*		.344**			
Reduced plant pathogens	-.534**	.526**	-.301**	.587**		.466**
NPP	-.437**	.396**		.633**		.343**
P availability			.219*	-.217*	.222*	
N availability		.334**	.213*		.273*	.233*
Sugar degradation	.307**	-.261*	.264*	-.344**		-.291**
Chitin degradation				.227*		
P mineralization			.279*	.300**	.246*	
Lignin degradation						
Soil respiration		.406**				.220*
Glucose mineralization		.299**		.273*		.295**

Supplementary Table 10. Significant correlations (Spearman) between the richness of soil taxa within ecological clusters and classified as highly connected taxa (hubs) and the different dimensions of multifunctionality calculated using PCA analyses in the global field survey. *P < 0.05; **P < 0.01. Red and blue colors correspond with positive and negative relationships, respectively.

	Dim1	Dim2	Dim3	Dim4	Dim5
Cluster #1	-.404**	-.386**			
Cluster #2	.459**	.250*	.220*		
Cluster #3		-.295**			
Cluster #4	.540**	.509**			
Cluster #5	.241*				.265*
Hubs	.362**	.283*			

References

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