

Supplementary Material

Supplement S1 Details on soil sampling and determination of soil nutrients

The distance between sampling points was 3 m. We took largely undisturbed 40 cm long and 5 cm wide mineral soil samples using a split tube auger (Eijkelkamp, Giesbeek, The Netherlands) and cut the aboveground portion of the vegetation. Then, we prepared a composite sample, which represents the soil of the whole plot by mixing all 14 organic layer and mineral soil samples from the same plot. We air-dried one aliquot of the composite soil sample, stored the another (field moist) at a temperature of +4°C, froze a third at -20°C, and shock froze the forth in liquid nitrogen immediately after the sampling and stored it at -80°C until analyses. A subsample of the field moist mineral soil was used to determine the gravimetric water content. For each plot, we calculated the total volume of the split tubes, the stone volume, and the bulk density using the weight of oven dried mineral soil (105°C). For soil pH, soil texture and CN analyses, we air dried and sieved (<2 mm) soil samples. We measured the soil pH in the supernatant of 1:2.5 mixture of soil and 0.01M CaCl₂ and analyzed soil texture with the pipette method¹. We analyzed total carbon (TC) and nitrogen (N) contents of the soil subsamples by dry combustion in a CN analyzer (Vario Max; Elementar Analysensysteme GmbH, Hanau, Germany). We then determined inorganic carbon (IC) after combustion of organic carbon (OC) in a muffle furnace (450°C for 16 h). The OC equals the difference between TC and IC. We calculated the C/N ratio by dividing organic carbon by total nitrogen concentrations. We further calculated soil OC and TN stocks (kg m²) as a function of OC or TN concentration, the weight of the air-dried fine-earth and its volume. At each site, we classified the soil type according to the World Reference Base of Soil Resources (IUSS Working Group WRB, 2006).

We calculated a Principal Component Analysis with nitrogen stock, total soil N, OC stock, soil IC, soil OC, soil C/N ratio and N_stock and used the first axis as measure of soil nutrients (Table S1-1).

Table S1-1: Detail results of a Principle Component Analysis (PCA) on soil nutrients. The first axis of the combined analyses of all regions was used in the Generalized Dissimilarity Models shown in the main manuscript.

	Schwäbische Alb			Hainich-Dün			Schorfheide-Chorin			All		
	Axis 1	Axis 2	Axis3	Axis 1	Axis 2	Axis3	Axis 1	Axis 2	Axis3	Axis 1	Axis 2	Axis3
% inertia	59.1%	25.1%	13.9%	60.4%	26.9%	10.6%	71.1%	23.9%	2.9%	67.4%	24.9%	5.2%
Loadings												
N_stock	-0.46	-0.08	0.53	-0.47	0.12	-0.52	-0.47	-0.08	0.45	-0.47	0.15	-0.44
OC_stock	-0.45	-0.13	0.51	-0.47	0.12	-0.51	-0.46	-0.20	0.08	-0.48	0.18	-0.08
Soil.InorganicC	0.31	-0.62	0.25	0.19	0.71	-0.07	-0.24	0.70	0.50	-0.26	-0.64	-0.56
SoilCN	0.37	-0.56	0.10	0.32	0.60	-0.09	-0.31	0.59	-0.66	-0.20	-0.69	0.54
SoilN.tot	-0.44	-0.33	-0.37	-0.47	0.23	0.45	-0.46	-0.20	-0.04	-0.48	0.15	0.18
SoilOrganicC	-0.39	-0.40	-0.50	-0.45	0.24	0.52	-0.45	-0.28	-0.32	-0.47	0.17	0.41

Supplement S2 Details on biodiversity assessment and analyses

Bacteria

Briefly, total RNA was isolated from soils and reverse transcribed into cDNA. Amplicons of the V3 region of the 16S rRNA gene were sequenced on an Illumina HiSeq platform using universal bacterial primers as described by Bartram et al². DNA concentrations were quantified with the Qubit® RNA Assay Kit (Life Technologies, Carlsbad, CA U.S.). Quality was checked with a 2100 Bioanalyser (Agilent Technologies, Santa Clara, CA, U.S.). 50 samples were pooled in equal amounts and sequenced in paired-end mode on individual lanes of a HiSeq2500 and Illumina GAII (Illumina®, San Diego, CA, U.S.), yielding reads of 100 bp and 150 bp, respectively. Per lane an equivalent amount of genomic DNA was added to ensure sufficient cluster diversity. Reads were assigned to individual samples using the 6-bp index. Forward and reverse reads from V3 Illumina Amplicon sequencing longer than 100 bp were trimmed and dimers filtered out based on detection methods implemented in FastQC (<http://www.bioinformatics.babraham.ac.uk/projects/fastqc/>). FASTQ-files were synchronized for those rare cases where only one of both reads has been filtered out. Reads were joined using fastq-join³ allowing 20 percent mismatch and a minimum overlap of 6. Converted FASTA files were checked for chimeras by Uchime integrated in Usearch 5.2.32⁴ applying the GOLD database from ChimeraSlayer (<http://drive5.com/otupipe/gold.tz>) as reference. Ca. 1 million reads of approximately 200 bp were obtained per soil sample. Taxonomic-dependent analysis was performed using RDP Multiclassifier 1.1, which is essentially based on RDP classifier^{5,6}. The total number of 1323 bacterial genera was detected in 105 plots (Extended Data Table 1). The abundance data are given as relative abundance: proportion of reads that can be assigned to a specific bacterial genus among all reads obtained from a given plot. Presence/Absence is given as presence (reads could be assigned to a bacterial genus) versus absence (no reads could be assigned to a bacterial genus).

Arbuscular mycorrhizal fungi

For arbuscular mycorrhizal fungi operational taxonomic units (AMF OTUs) we extracted soil microbial genomic DNA from 1 g of each composite sample using a MoBioPowerSoil DNA Isolation Kit (MoBio Laboratories Inc. Carlsbad, CA, USA), according to the manufacturer's instructions. We generated AMF OTU amplicon libraries using fusion primers designed with the pyrosequencing primer B, a barcode and the AM fungal specific primer AM1a or AM1b⁷ as reverse primers, and the pyrosequencing primer A as well as the NS31 primer as forward primers. We used a set of 10bp MID-barcodes provided by Roche (Roche Applied Science). Amplicon libraries were produced from a pool of two dilution levels and three PCR replications. We performed the first PCR reactions in a total volume of 25 µl reaction mix containing 0.5 µl of DNA template (5-20 ng/µl), 12.5 µl GoTaq Green Mastermix 2x (Promega, USA), 1 µl of each primer (25 µM) on a Eppendorf Mastercycler DNA Engine Thermal Cycler PCR (Eppendorf, USA) with the following PCR conditions: 98°C for 30 s, 5 cycles of 94°C for 30 s, 60°C (-1°C/cycle, 4 cycles) for 30 s, 72°C for 1 min, and 25 cycles of 94°C for 30 s, 55°C for 30 s, 72°C for 1 min, and for extension 72°C for 5 min. For the semi-nested PCR, we performed two separate amplifications using 1 µl of the diluted amplified product of PCR I (1:10), 25 µl GoTaq Green Mastermix 2x (Promega), and 1 µl of each primer (25 µM), the 50 µl-reactions were run under following conditions: 98°C for 30 s, followed by 30 cycles of 94°C for 30 s, 63°C for 30 s, 72°C for 1 min., and 72°C for 5 min. Each sample in both PCR amplification steps was amplified in triplicate accompanied by a negative control. The semi-nested PCR amplified products were checked by a 1.5% agarose gel and amplified products were pooled per sample. pooled amplicons (30 µl, each) were purified with the QIAquick Gel Extraction Kit (Qiagen GmbH, Hilden, Germany) following the manufacturer's protocol. The purified products were quantified by fluorescence spectrophotometer (Cary Eclipse, Agilent Technologies, Waldbronn, Germany) using Quant-iTTM PicoGreen® dsDNA Assay Kit (Life Technologies GmbH, Darmstadt, Germany). We subjected an equimolar mix of the 50 amplicon libraries to unidirectional pyrosequencing from the NS31 end of the amplicons, 50 samples per lane on plate separated by four lane gasket, using a 454 titanium amplicon sequencing kit and a Genome Sequencer FLX 454 System (454 Life Sciences/Roche Applied Biosystems, Mannheim, Germany) at the Department of Soil Ecology, Helmholtz Centre for Environmental Research (UFZ, Halle/Germany).

For the bioinformatic analysis, we performed multiple levels of sequence processing and quality filtering. We extracted the 454 fungal 18S rDNA sequences based on 100% barcode similarity. Simultaneously, we removed sequence reads with an average quality score of < 20, ambiguous bases, and homo-polymers of >8 bases and read length of < 300 bp after barcodes and primers removal using MOTHUR⁸. The sequences were normalized to the smallest read number and potential chimeric sequences were checked and removed by using UCHIME⁴ algorithm as implemented in MOTHUR. Quality-filtered sequences were clustered into operational taxonomical units (OTUs) based on a CD-HIT algorithm CD-HIT-EST⁹ with a sequence similarity threshold of 97%. Representative sequences for each OTU were taxonomically assignment to NCBI based fungal reference data set using the default parameters in MOTHUR and all non-glomeromycotan OTUs were removed from the data set (~ 11% of sequences). To avoid over clustering, representative sequences of the glomeromycotan OTU's were aligned using MUSCLE as implemented in Seaview version 4¹⁰. The alignment was used to construct a *phylogenetic tree* using the Quick NJ tree and the OTUs were further re-clustered using the GroupCluster algorithm at a similarity threshold of 97% in TOPALI v2.5¹¹. The taxonomic assignment of representative sequences of these glomeromycotan OTUs were refined using the MaarjaM AMF reference database¹² at a similarity threshold of 90% using the GAST algorithm¹³.

Protist analysis

One gram of the homogenized bulk soil from the upper 10 cm of the A horizon was taken and stored at 4°C while still at field moisture content.

Whole genomic DNA was extracted from one gram of each soil sample using the PowerSoil[®] DNA isolation kit (Mo Bio Laboratories, Inc., Carlsbad, CA), according to the manufacturer's instructions. DNA quality and quantity was assessed and concentrations were adjusted to 100 ng/μl using ddH₂O. The highly variable V4 region of the 18S rRNA gene was directly amplified from the samples using eukaryotic specific primers (590F and 1300R). To separate the sequences, the Titanium primer design and the recommended multiplex identifier (MID) adaptor complex design (Roche, Germany) method was used. The pre-454 sequencing PCR reaction contained: 2μl (100 ng/μl) DNA, 2 μl 10x DNA polymerase buffer with 20 mM MgSO₄, 2μl (1 μM) 590F primer [(5'-3':CGGTAATTCCAGCTCCAATAGC) + Key + MID + Adaptor A] and 2μl (1 μM) 1300R primer (5'-3':CACCAACTAAGAACGGCCATGC), 2μl (2 mM) dNTP each and 0.4 μl (2.5 U/μl) Pfu (*Pyrococcus furiosus*) DNA polymerase

(Fermentas, Germany) and made up to a total volume of 25 µl with ddH₂O. Cycling conditions were: initial denaturation at 95°C for 3 min; 30 cycles at 95°C for 30 s, 55°C for 30 s, 72°C for 2 min; and a final extension at 72°C for 10 min. Each sample was amplified in triplicate and pooled to a final concentration of 20 ng/µl to eliminate possible PCR biases. NGS using the GS-FLX Titanium sequencer (Roche, Germany) was performed by GATC Biotech AG, Germany. Sequencing was done in one direction from the forward primer (adaptor A) or 5'-end. Pyrotags were filtered for (1.) 100% forward primer match; (2.) minimum sequence length of 200bp's; (3.) a maximum sequence length of 710 bp's; and (4.) ambiguities (N's).

Traces in FastA file format were scanned for chimeric sequences against the revised (October 2014) protist ribosomal reference (PR²) database¹⁴ using the UCHIME algorithm⁴. All sequences were trimmed to a length of 530 and dereplication to cluster 100% identical amplicons. Singletons were removed. Sequences were aligned to the PR² database using the nucleotide basic local alignment search tool (BLASTn) algorithm with default parameters. One hit sequence was retained with an E-value $\leq e^{-100}$. Only OTUs with 100% coverage to a reference sequence were considered suitable for analysis. OTUs with high similarity annotations to (1.) taxa for which the V4 region of the 18S rRNA gene is not a suitable barcoding gene¹⁵ and (2.) non-protistan taxa were removed. Taxa removed included Metazoa and Fungi within the supergroup Opisthokonta and Streptophyta within the supergroup Archaeplastida¹⁶. OTUs were converted to presence-absence data where sequences aligning with $\geq 99.7\%$ sequence similarity to PR² database reference sequence were annotated to the species taxonomic level OTUs¹⁷.

Table S2-1 | Overview on clades and trophic groups. Data was assessed on a total of 105 grassland plots across three regions in Germany.

Clade	Trophic group	Number of Individuals	Number of species/OTUs
Aboveground			
Araneae	Secondary consumers	666	76
Coleoptera	Invertebrate decomposers	326	36
	Herbivores	5241	175
	Pollinators	29	5
	Secondary consumers	632	64
Dermoptera	Omnivores*	25	1
Dictyoptera	Omnivores*	5	1
Diptera	Pollinators	12944	408
Hemiptera	Herbivores	35680	185
	Omnivores*	31	11
	Secondary consumers	159	12
Hymenoptera	Herbivores	99	4
	Pollinators	7871	168
Lepidoptera	Pollinators	5848	96
Lichens	„Primary producers“*	#	63
Myriapoda	Invertebrate decomposers	138	4
	Secondary consumers	344	4
Neuroptera	Secondary consumers	33	6
Opiliones	Secondary consumers	5	1
Orthoptera	Herbivores	488	15
	Secondary consumers	5	1
Plants	Primary producers	#	301
Foliar fungal pathogens	Plant pathogens	696	79
Vertebrates	Tertiary consumers (Birds)	1430	65
	Tertiary consumers (Bats)	6491	11
	Vertebrate herbivores (Birds)*	312	15
Belowground			
AMF**	Mycorrhizae	#	308
Bacteria***	Microbial decomposers	#	1323
Protists**	Bacterivores	#	286
Insect larvae****	Herbivores	1305	11
	Predators	2070	16

* these groups were excluded due to low sample size

** in these groups data on OTUs was used

*** based on genera, only active stages (RNA) considered

**** genus level data

due to density measures / molecular data no data on the number of individuals is available

Table S2-2 | Sample coverage of trophic groups based on species abundances. Sample coverage was calculated for each of the 105 studied plots based on the approach proposed by Chao and colleagues^{18,19}. Coverage is defined as the proportion of the total number of individuals in an assemblage that belong to species represented in the sample and is therefore a measure of sampling completeness. Means (SC) and 95% confidence intervals (LC: lower, UC: upper) based on 200 bootstraps are shown. LUI values represent globally standardized values of land-use intensity including mowing frequency and grazing and fertilization intensity averaged across years (2006-2010). Only plots with more than five individuals and two species could be analyzed, others are indicated by NA. Additionally the classification into low and high intensity plots (LUI-Cat) is given. Plant pathogens are missing because for this group no abundance data were available.

Aboveground															Belowground																				
			Primary producers			Herbivores			Pollinators			Invert. decomposers			Secondary consumers			Tertiary consumers			Mycorrhizae			Herbivores			Microbial decomposers			Secondary consumers			Bacterivores		
Plot	LUI	LUI-Cat	SC	LC	UC	SC	LC	UC	SC	LC	UC	SC	LC	UC	SC	SC	LC	SC	SC	LC	SC	LC	UC	SC	LC	UC	SC	LC	UC	SC	LC	UC			
AEG07	0.52	low	0.88	0.82	0.94	0.90	0.87	0.93	0.94	0.93	0.96	NA	NA	NA	0.37	0.07	0.67	0.55	0.33	0.77	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.89	1.00	NA	NA	NA	0.55	0.35	0.76
AEG08	1.31	low	0.97	0.94	1.00	0.96	0.95	0.98	0.85	0.80	0.89	NA	NA	NA	0.90	0.58	1.00	0.63	0.38	0.88	0.33	0.00	0.79	1.00	0.98	1.00	1.00	0.89	1.00	0.92	0.84	0.99	0.77	0.68	0.86
AEG09	0.58	low	0.96	0.91	1.00	0.92	0.89	0.95	0.90	0.88	0.93	1.00	1.00	1.00	0.82	0.66	0.98	0.83	0.74	0.92	0.87	0.76	0.97	0.90	0.57	1.00	1.00	0.90	1.00	NA	NA	NA	1.00	0.97	1.00
AEG22	1.34	low	0.95	0.92	0.99	0.95	0.93	0.98	0.93	0.92	0.95	NA	NA	NA	0.86	0.63	1.00	0.76	0.48	1.00	0.97	0.95	0.99	1.00	0.91	1.00	1.00	0.89	1.00	1.00	1.00	1.00	0.86	0.81	0.92
AEG25	0.88	low	0.95	0.91	0.98	0.98	0.97	0.99	0.91	0.89	0.94	NA	NA	NA	0.86	0.73	0.98	0.77	0.61	0.94	NA	NA	NA	0.88	0.63	1.00	1.00	0.89	1.00	NA	NA	NA	0.72	0.46	0.98
AEG26	1.42	low	0.94	0.91	0.98	0.96	0.94	0.98	0.93	0.91	0.95	NA	NA	NA	0.57	0.25	0.89	0.66	0.41	0.91	1.00	1.00	1.00	0.91	0.74	1.00	1.00	0.89	1.00	NA	NA	NA	0.90	0.80	0.99
AEG27	1.15	low	0.95	0.91	0.99	0.98	0.97	0.99	0.94	0.93	0.96	NA	NA	NA	1.00	0.88	1.00	0.74	0.49	1.00	1.00	0.99	1.00	NA	NA	NA	1.00	0.91	1.00	NA	NA	NA	0.99	0.99	1.00
AEG28	0.66	low	0.96	0.92	1.00	0.94	0.92	0.97	0.95	0.92	0.98	NA	NA	NA	0.80	0.61	0.98	0.86	0.77	0.96	0.97	0.93	1.00	0.92	0.78	1.00	1.00	0.90	1.00	1.00	1.00	1.00	0.72	0.61	0.83
AEG30	1.51	low	0.95	0.91	0.99	0.96	0.94	0.98	0.92	0.89	0.95	NA	NA	NA	0.78	0.57	0.99	0.71	0.45	0.96	0.90	0.85	0.95	0.97	0.97	0.98	1.00	0.88	1.00	NA	NA	NA	0.85	0.80	0.90
AEG31	1.14	low	0.93	0.89	0.97	0.95	0.93	0.98	0.83	0.77	0.89	1.00	1.00	1.00	0.86	0.70	1.00	0.92	0.83	1.00	0.86	0.79	0.93	0.90	0.80	1.00	1.00	0.88	1.00	1.00	1.00	1.00	0.90	0.87	0.94
AEG32	0.57	low	0.99	0.96	1.00	0.92	0.89	0.95	0.97	0.96	0.98	NA	NA	NA	0.74	0.58	0.90	0.93	0.88	0.98	0.98	0.97	0.99	1.00	0.91	1.00	1.00	0.90	1.00	NA	NA	NA	NA	NA	NA
AEG33	1.23	low	0.97	0.94	1.00	0.98	0.97	0.99	0.92	0.90	0.95	NA	NA	NA	0.76	0.45	1.00	0.95	0.81	1.00	0.93	0.89	0.98	1.00	1.00	1.00	1.00	0.90	1.00	1.00	1.00	1.00	0.75	0.63	0.87
AEG34	0.88	low	0.98	0.95	1.00	0.96	0.94	0.97	0.89	0.84	0.93	NA	NA	NA	0.02	0.00	0.34	1.00	1.00	1.00	0.94	0.91	0.98	1.00	1.00	1.00	1.00	0.89	1.00	1.00	1.00	1.00	0.85	0.80	0.90
AEG47	0.82	low	0.95	0.90	1.00	0.97	0.95	0.98	0.89	0.86	0.92	NA	NA	NA	0.84	0.73	0.95	0.72	0.55	0.89	1.00	1.00	1.00	NA	NA	NA	1.00	0.89	1.00	NA	NA	NA	NA	NA	NA

AEG48	0.66	low	0.95	0.88	1.00	0.96	0.94	0.99	0.95	0.93	0.96	NA	NA	NA	0.93	0.84	1.00	0.71	0.49	0.93	1.00	1.00	1.00	0.90	0.70	1.00	1.00	0.90	1.00	1.00	NA	NA	NA	0.83	0.70	0.95
AEG49	0.93	low	0.98	0.95	1.00	0.96	0.94	0.97	0.97	0.96	0.99	NA	NA	NA	0.47	0.14	0.81	0.82	0.60	1.00	0.94	0.92	0.97	0.84	0.73	0.95	1.00	0.89	1.00	1.00	1.00	1.00	1.00	0.82	0.71	0.94
HEG08	1.47	low	0.97	0.93	1.00	0.99	0.99	1.00	0.92	0.89	0.95	NA	NA	NA	0.88	0.80	0.96	0.98	0.96	0.99	0.91	0.87	0.95	1.00	1.00	1.00	1.00	0.89	1.00	1.00	0.93	0.77	1.00	0.79	0.74	0.85
HEG09	0.72	low	0.94	0.87	1.00	0.95	0.93	0.96	0.94	0.93	0.96	NA	NA	NA	0.69	0.51	0.87	0.71	0.57	0.84	0.91	0.87	0.95	1.00	0.96	1.00	1.00	0.89	1.00	1.00	0.85	0.67	1.00	0.74	0.69	0.80
HEG10	1.5	low	0.98	0.95	1.00	0.95	0.93	0.98	0.90	0.86	0.93	NA	NA	NA	0.83	0.71	0.96	0.79	0.68	0.89	0.91	0.88	0.95	1.00	1.00	1.00	1.00	0.90	1.00	1.00	NA	NA	NA	0.83	0.78	0.88
HEG11	1.48	low	0.98	0.93	1.00	0.91	0.86	0.96	0.94	0.92	0.96	NA	NA	NA	0.91	0.80	1.00	0.93	0.88	0.98	0.88	0.83	0.92	1.00	0.99	1.00	1.00	0.89	1.00	1.00	NA	NA	NA	0.79	0.73	0.84
HEG16	0.97	low	0.93	0.87	0.99	0.98	0.97	0.98	0.91	0.89	0.94	1.00	1.00	1.00	0.71	0.56	0.85	0.86	0.74	0.99	0.90	0.87	0.94	0.63	0.35	0.92	1.00	0.89	1.00	1.00	0.85	0.76	0.94	0.85	0.80	0.89
HEG17	0.63	low	0.95	0.90	1.00	0.97	0.95	0.98	0.98	0.98	0.99	NA	NA	NA	0.44	0.05	0.83	0.90	0.80	1.00	0.93	0.91	0.96	0.82	0.68	0.97	1.00	0.89	1.00	1.00	NA	NA	NA	0.84	0.79	0.89
HEG18	0.69	low	0.93	0.86	1.00	0.79	0.72	0.87	0.81	0.76	0.86	NA	NA	NA	0.66	0.44	0.89	0.70	0.59	0.82	0.96	0.94	0.98	1.00	1.00	1.00	1.00	0.89	1.00	1.00	NA	NA	NA	0.73	0.62	0.84
HEG19	0.63	low	0.93	0.88	0.99	0.97	0.95	0.98	0.92	0.89	0.95	NA	NA	NA	0.83	0.71	0.96	0.92	0.84	1.00	0.90	0.85	0.94	0.94	0.90	0.98	1.00	0.88	1.00	1.00	0.95	0.92	0.97	0.69	0.58	0.80
HEG20	0.61	low	0.95	0.90	1.00	0.90	0.87	0.94	0.91	0.89	0.94	NA	NA	NA	0.37	0.05	0.68	0.97	0.95	0.98	0.95	0.93	0.98	0.85	0.66	1.00	1.00	0.89	1.00	1.00	0.87	0.79	0.95	0.42	0.22	0.63
HEG21	0.66	low	0.96	0.91	1.00	0.97	0.96	0.98	0.97	0.96	0.99	NA	NA	NA	0.87	0.78	0.96	0.69	0.48	0.90	0.95	0.93	0.98	1.00	0.90	1.00	1.00	0.89	1.00	1.00	NA	NA	NA	0.76	0.69	0.83
HEG23	1.38	low	0.98	0.91	1.00	0.93	0.90	0.96	0.92	0.89	0.95	NA	NA	NA	0.73	0.52	0.94	0.77	0.57	0.98	0.89	0.85	0.93	1.00	0.98	1.00	1.00	0.89	1.00	1.00	1.00	1.00	1.00	0.86	0.82	0.90
HEG24	1.51	low	0.96	0.92	1.00	0.91	0.87	0.95	0.88	0.84	0.92	NA	NA	NA	0.86	0.69	1.00	0.81	0.70	0.91	0.93	0.91	0.96	1.00	1.00	1.00	1.00	0.88	1.00	1.00	1.00	1.00	1.00	0.88	0.84	0.91
HEG39	1.22	low	0.97	0.93	1.00	0.96	0.94	0.98	0.84	0.78	0.89	NA	NA	NA	0.61	0.31	0.91	0.98	0.93	1.00	0.97	0.95	0.99	0.90	0.81	0.99	1.00	0.89	1.00	1.00	1.00	0.90	1.00	0.72	0.62	0.82
HEG41	0.61	low	0.94	0.87	1.00	0.95	0.94	0.97	0.84	0.78	0.91	NA	NA	NA	0.68	0.47	0.89	0.95	0.87	1.00	0.76	0.61	0.91	1.00	1.00	1.00	1.00	0.89	1.00	1.00	NA	NA	NA	0.27	0.01	0.53
HEG42	0.63	low	0.86	0.76	0.96	0.94	0.92	0.96	0.92	0.89	0.95	0.63	0.34	0.92	0.89	0.81	0.97	0.90	0.80	1.00	0.94	0.92	0.97	0.90	0.85	0.95	1.00	0.88	1.00	1.00	1.00	1.00	1.00	0.60	0.38	0.82
HEG43	0.88	low	0.96	0.91	1.00	0.99	0.98	0.99	0.97	0.95	0.98	1.00	1.00	1.00	0.74	0.59	0.90	0.83	0.72	0.93	0.92	0.88	0.95	0.78	0.52	1.00	1.00	0.90	1.00	1.00	NA	NA	NA	0.87	0.83	0.92
HEG44	0.72	low	0.89	0.82	0.96	0.97	0.96	0.98	0.95	0.93	0.96	NA	NA	NA	0.62	0.41	0.84	0.81	0.62	1.00	0.94	0.92	0.96	1.00	1.00	1.00	1.00	0.88	1.00	1.00	1.00	1.00	1.00	0.69	0.56	0.81
HEG45	0.58	low	0.98	0.94	1.00	0.96	0.94	0.98	0.94	0.93	0.96	NA	NA	NA	0.96	0.84	1.00	0.86	0.75	0.96	0.92	0.89	0.96	0.76	0.44	1.00	1.00	0.89	1.00	1.00	1.00	0.98	1.00	0.69	0.57	0.80
HEG46	0.7	low	0.97	0.92	1.00	0.96	0.95	0.98	0.96	0.94	0.98	NA	NA	NA	0.58	0.36	0.79	0.98	0.96	1.00	0.91	0.87	0.95	1.00	1.00	1.00	1.00	0.88	1.00	1.00	NA	NA	NA	0.76	0.69	0.84
SEG04	1.01	low	1.00	0.98	1.00	0.92	0.88	0.96	0.76	0.65	0.87	0.49	0.00	1.00	0.40	0.06	0.73	0.83	0.72	0.94	0.94	0.89	0.98	0.73	0.46	1.00	1.00	0.87	1.00	1.00	0.96	0.89	1.00	0.46	0.21	0.71
SEG06	1.45	low	0.99	0.97	1.00	0.94	0.91	0.97	0.91	0.87	0.95	NA	NA	NA	0.90	0.83	0.96	0.98	0.96	1.00	0.93	0.89	0.97	0.88	0.65	1.00	1.00	0.87	1.00	1.00	0.93	0.72	1.00	0.85	0.79	0.91
SEG08	1.05	low	0.97	0.94	1.00	0.96	0.93	0.98	0.82	0.77	0.87	0.73	0.44	1.00	0.77	0.58	0.95	0.94	0.90	0.98	0.97	0.95	0.99	1.00	1.00	1.00	1.00	0.87	1.00	1.00	0.94	0.82	1.00	0.63	0.49	0.77
SEG09	1.45	low	0.95	0.92	0.99	0.95	0.93	0.98	0.83	0.77	0.90	NA	NA	NA	0.44	0.16	0.72	0.99	0.98	1.00	0.94	0.91	0.97	NA	NA	NA	1.00	0.88	1.00	1.00	NA	NA	NA	0.88	0.83	0.93

SEG15	1.11	low	0.99	0.96	1.00	0.93	0.90	0.97	0.73	0.56	0.89	NA	NA	NA	0.69	0.45	0.92	0.97	0.94	1.00	0.99	0.99	1.00	NA	NA	NA	1.00	0.86	1.00	0.97	0.91	1.00	0.72	0.58	0.86	
SEG16	1.01	low	0.98	0.96	1.00	0.94	0.92	0.97	0.85	0.75	0.96	1.00	0.94	1.00	0.51	0.24	0.78	0.90	0.81	1.00	0.99	0.98	1.00	0.93	0.66	1.00	1.00	0.87	1.00	1.00	0.96	1.00	0.38	0.11	0.66	
SEG17	1.29	low	0.97	0.94	1.00	0.95	0.93	0.98	0.93	0.90	0.97	1.00	0.96	1.00	1.00	0.95	1.00	1.00	0.99	1.00	0.94	0.90	0.97	1.00	0.97	1.00	1.00	0.86	1.00	1.00	0.90	1.00	0.59	0.43	0.74	
SEG19	0.96	low	0.99	0.97	1.00	0.96	0.93	0.98	0.64	0.48	0.80	NA	NA	NA	0.44	0.09	0.79	0.90	0.83	0.98	0.97	0.96	0.98	1.00	1.00	1.00	1.00	0.87	1.00	NA	NA	NA	0.71	0.58	0.85	
SEG20	1.27	low	0.98	0.95	1.00	0.97	0.95	0.99	0.82	0.73	0.90	NA	NA	NA	0.05	0.00	0.49	0.98	0.94	1.00	0.97	0.96	0.99	NA	NA	NA	1.00	0.88	1.00	NA	NA	NA	0.57	0.41	0.73	
SEG24	1.2	low	0.98	0.94	1.00	0.99	0.98	1.00	0.93	0.89	0.96	NA	NA	NA	0.54	0.30	0.79	1.00	0.98	1.00	0.99	0.98	0.99	1.00	1.00	1.00	1.00	0.89	1.00	0.89	0.82	0.97	0.44	0.18	0.70	
SEG25	1.43	low	0.97	0.93	1.00	0.97	0.96	0.98	0.90	0.87	0.93	0.91	0.86	0.96	1.00	0.95	1.00	1.00	0.99	1.00	0.97	0.96	0.99	0.66	0.31	1.00	1.00	0.88	1.00	0.90	0.80	0.99	0.91	0.85	0.97	
SEG28	1.2	low	0.96	0.93	0.99	0.97	0.96	0.99	0.79	0.74	0.84	0.76	0.54	0.99	0.63	0.42	0.84	0.87	0.77	0.96	0.99	0.98	0.99	NA	NA	NA	1.00	0.89	1.00	NA	NA	NA	0.56	0.38	0.74	
SEG29	0.9	low	0.98	0.96	1.00	0.93	0.90	0.96	0.82	0.74	0.90	NA	NA	NA	0.48	0.22	0.73	0.87	0.80	0.95	0.98	0.97	0.99	NA	NA	NA	1.00	0.86	1.00	0.79	0.61	0.96	NA	NA	NA	
SEG30	1.28	low	0.96	0.93	1.00	0.92	0.87	0.97	0.77	0.61	0.92	NA	NA	NA	0.73	0.43	1.00	0.99	0.97	1.00	0.94	0.92	0.96	NA	NA	NA	1.00	0.89	1.00	NA	NA	NA	0.89	0.85	0.93	
SEG31	1.28	low	0.95	0.91	0.99	0.96	0.94	0.98	0.93	0.91	0.96	NA	NA	NA	0.95	0.86	1.00	0.99	0.98	1.00	0.98	0.97	0.99	0.89	0.68	1.00	1.00	0.90	1.00	1.00	1.00	1.00	0.84	0.80	0.89	
SEG32	1.28	low	0.99	0.96	1.00	0.96	0.93	0.98	0.86	0.78	0.95	NA	NA	NA	0.70	0.48	0.92	0.95	0.92	0.99	0.95	0.94	0.97	1.00	1.00	1.00	1.00	0.88	1.00	NA	NA	NA	0.83	0.76	0.90	
SEG39	1.27	low	0.95	0.91	0.99	0.88	0.83	0.93	0.89	0.85	0.93	NA	NA	NA	0.49	0.00	0.97	0.99	0.98	1.00	0.94	0.93	0.96	1.00	1.00	1.00	1.00	0.89	1.00	1.00	1.00	1.00	0.81	0.75	0.87	
AEG02	3.14	high	0.97	0.94	0.99	0.99	0.98	1.00	0.95	0.93	0.96	NA	NA	NA	0.28	0.00	0.69	1.00	0.98	1.00	0.82	0.71	0.92	0.95	0.93	0.97	1.00	0.90	1.00	1.00	1.00	1.00	0.74	0.64	0.83	
AEG03	2.1	high	0.99	0.97	1.00	0.98	0.97	0.99	0.94	0.92	0.96	NA	NA	NA	0.90	0.72	1.00	0.84	0.64	1.00	0.50	0.18	0.81	1.00	0.98	1.00	1.00	0.90	1.00	1.00	0.91	1.00	0.87	0.82	0.92	
AEG05	1.76	high	0.97	0.94	1.00	0.99	0.99	0.99	0.93	0.91	0.95	NA	NA	NA	0.57	0.40	0.74	0.81	0.66	0.95	0.84	0.62	1.00	1.00	0.97	1.00	1.00	0.90	1.00	0.90	0.84	0.96	0.76	0.63	0.89	
AEG12	2.13	high	0.97	0.95	1.00	0.97	0.96	0.98	0.88	0.85	0.91	NA	NA	NA	0.64	0.39	0.89	NA	NA	NA	0.57	0.25	0.89	1.00	0.95	1.00	1.00	0.89	1.00	1.00	1.00	1.00	0.82	0.75	0.89	
AEG13	2.13	high	0.99	0.97	1.00	0.99	0.98	0.99	0.78	0.70	0.86	1.00	1.00	1.00	0.49	0.02	0.96	0.84	0.72	0.95	0.76	0.50	1.00	1.00	0.92	1.00	1.00	0.89	1.00	1.00	1.00	1.00	0.84	0.79	0.90	
AEG15	2.65	high	0.99	0.97	1.00	0.96	0.95	0.98	0.92	0.89	0.95	NA	NA	NA	0.28	0.00	0.70	1.00	0.98	1.00	0.95	0.93	0.98	0.49	0.00	1.00	1.00	0.89	1.00	0.95	0.92	0.98	0.83	0.78	0.89	
AEG17	2.26	high	0.92	0.88	0.97	0.96	0.94	0.98	0.94	0.93	0.96	NA	NA	NA	0.85	0.71	1.00	0.89	0.74	1.00	0.98	0.96	1.00	NA	NA	NA	1.00	0.90	1.00	0.95	0.92	0.97	0.88	0.84	0.92	
AEG18	2.46	high	0.98	0.95	1.00	0.76	0.60	0.92	0.94	0.92	0.96	1.00	1.00	1.00	0.63	0.12	1.00	1.00	1.00	1.00	0.95	0.91	0.98	NA	NA	NA	1.00	0.90	1.00	1.00	1.00	1.00	0.90	0.87	0.93	
AEG20	1.77	high	0.98	0.96	1.00	0.96	0.94	0.97	0.92	0.89	0.94	NA	NA	NA	0.93	0.84	1.00	0.80	0.68	0.92	0.97	0.95	1.00	0.49	0.00	0.99	1.00	0.89	1.00	NA	NA	NA	0.77	0.66	0.88	
AEG24	2.22	high	0.98	0.97	1.00	0.99	0.98	0.99	0.98	0.97	0.98	NA	NA	NA	0.78	0.56	0.99	0.65	0.42	0.89	0.96	0.93	0.98	1.00	0.99	1.00	1.00	0.89	1.00	1.00	1.00	1.00	0.95	0.94	0.97	
AEG37	1.89	high	0.98	0.96	1.00	0.96	0.94	0.98	0.70	0.56	0.84	NA	NA	NA	0.69	0.46	0.91	1.00	1.00	1.00	0.94	0.91	0.97	1.00	1.00	1.00	1.00	0.90	1.00	1.00	1.00	0.98	1.00	0.74	0.65	0.84
AEG39	1.89	high	1.00	0.98	1.00	0.98	0.97	0.99	0.84	0.75	0.93	NA	NA	NA	0.56	0.24	0.89	0.68	0.45	0.91	0.94	0.89	0.98	0.90	0.73	1.00	1.00	0.90	1.00	1.00	1.00	1.00	0.90	0.84	0.95	

AEG40	2	high	0.96	0.93	0.99	0.97	0.96	0.98	0.91	0.88	0.93	NA	NA	NA	0.67	0.48	0.86	0.95	0.78	1.00	0.94	0.90	0.97	0.90	0.57	1.00	1.00	0.89	1.00	1.00	1.00	1.00	1.00	0.96	0.94	0.98
AEG42	2.24	high	0.98	0.96	1.00	1.00	0.99	1.00	0.88	0.85	0.91	NA	NA	NA	0.87	0.78	0.97	0.79	0.62	0.96	1.00	0.99	1.00	0.83	0.54	1.00	1.00	0.88	1.00	1.00	0.91	1.00	0.53	0.33	0.74	
AEG43	1.99	high	0.97	0.93	1.00	0.98	0.97	0.99	0.92	0.90	0.95	NA	NA	NA	0.68	0.46	0.89	0.92	0.86	0.97	0.96	0.93	0.99	0.90	0.71	1.00	1.00	0.89	1.00	1.00	0.97	1.00	0.92	0.89	0.95	
AEG46	1.59	high	0.95	0.91	0.98	1.00	0.99	1.00	0.85	0.80	0.91	NA	NA	NA	0.64	0.46	0.82	0.91	0.81	1.00	0.96	0.94	0.98	NA	NA	NA	1.00	0.89	1.00	0.97	0.88	1.00	0.88	0.84	0.93	
HEG02	2.62	high	0.97	0.93	1.00	0.90	0.86	0.94	0.88	0.84	0.92	NA	NA	NA	0.79	0.62	0.96	0.93	0.89	0.97	0.90	0.85	0.94	0.78	0.53	1.00	1.00	0.90	1.00	0.93	0.76	1.00	0.87	0.83	0.90	
HEG06	2.05	high	0.98	0.95	1.00	0.95	0.93	0.98	0.94	0.92	0.95	0.89	0.68	1.00	0.91	0.78	1.00	0.91	0.85	0.98	0.95	0.93	0.98	1.00	1.00	1.00	1.00	0.89	1.00	1.00	1.00	1.00	1.00	0.86	0.81	0.90
HEG07	1.52	high	0.96	0.92	1.00	0.97	0.96	0.99	0.94	0.91	0.97	NA	NA	NA	0.73	0.53	0.92	0.92	0.84	0.99	0.93	0.89	0.97	0.76	0.57	0.95	1.00	0.90	1.00	NA	NA	NA	0.89	0.86	0.92	
HEG14	2.27	high	0.96	0.92	1.00	0.97	0.94	0.99	0.76	0.62	0.89	NA	NA	NA	0.88	0.79	0.97	0.79	0.64	0.93	0.94	0.92	0.97	NA	NA	NA	1.00	0.88	1.00	1.00	1.00	1.00	NA	NA	NA	
HEG15	1.84	high	0.97	0.93	1.00	0.93	0.89	0.96	0.97	0.95	0.98	0.88	0.65	1.00	0.86	0.72	1.00	0.87	0.78	0.96	0.92	0.88	0.95	0.86	0.69	1.00	1.00	0.88	1.00	1.00	0.97	1.00	0.90	0.87	0.93	
HEG27	1.69	high	0.97	0.92	1.00	0.94	0.92	0.97	0.87	0.81	0.93	NA	NA	NA	0.86	0.73	0.99	0.71	0.55	0.86	0.93	0.90	0.96	0.95	0.85	1.00	1.00	0.88	1.00	0.96	0.92	1.00	0.85	0.81	0.89	
HEG28	1.94	high	0.94	0.90	0.98	0.89	0.85	0.93	0.87	0.83	0.91	0.88	0.63	1.00	0.84	0.74	0.95	0.80	0.67	0.93	0.97	0.95	0.98	1.00	0.98	1.00	1.00	0.89	1.00	1.00	1.00	1.00	1.00	0.80	0.73	0.87
HEG29	1.86	high	0.97	0.92	1.00	0.94	0.92	0.97	0.93	0.91	0.95	NA	NA	NA	0.92	0.82	1.00	0.89	0.81	0.98	0.93	0.91	0.96	1.00	1.00	1.00	1.00	0.89	1.00	1.00	1.00	0.98	1.00	0.81	0.76	0.86
HEG30	2.29	high	0.95	0.89	1.00	0.98	0.96	1.00	0.86	0.79	0.93	NA	NA	NA	0.78	0.63	0.92	0.74	0.56	0.93	0.95	0.93	0.97	0.97	0.92	1.00	1.00	0.89	1.00	1.00	1.00	1.00	1.00	0.95	0.93	0.97
HEG31	1.91	high	0.96	0.90	1.00	0.92	0.89	0.95	0.97	0.96	0.98	0.85	0.73	0.97	0.54	0.31	0.78	0.35	0.01	0.69	0.96	0.94	0.98	0.95	0.79	1.00	1.00	0.87	1.00	0.92	0.83	1.00	0.68	0.59	0.78	
HEG33	1.92	high	0.98	0.93	1.00	0.97	0.95	0.99	0.87	0.83	0.92	0.63	0.34	0.93	0.42	0.05	0.79	0.77	0.60	0.94	0.96	0.94	0.98	0.69	0.39	0.99	1.00	0.90	1.00	0.87	0.71	1.00	0.81	0.75	0.88	
HEG34	2.05	high	0.96	0.91	1.00	0.95	0.92	0.97	0.97	0.95	0.99	0.93	0.80	1.07	0.75	0.54	0.96	0.94	0.78	1.00	0.92	0.90	0.95	0.80	0.64	0.97	1.00	0.88	1.00	1.00	0.97	1.00	0.91	0.88	0.94	
HEG36	2.01	high	0.94	0.89	1.00	0.99	0.97	1.00	0.91	0.88	0.95	NA	NA	NA	0.82	0.63	1.00	0.68	0.48	0.88	0.89	0.85	0.93	1.00	1.00	1.00	1.00	0.88	1.00	0.94	0.92	0.97	0.68	0.57	0.80	
HEG37	2.05	high	0.98	0.94	1.00	0.96	0.94	0.99	0.92	0.88	0.95	NA	NA	NA	0.49	0.00	0.98	0.87	0.75	0.99	0.93	0.89	0.96	1.00	0.89	1.00	1.00	0.89	1.00	0.81	0.62	1.00	0.68	0.58	0.77	
HEG38	1.64	high	0.92	0.85	0.98	0.87	0.82	0.92	0.81	0.75	0.88	1.00	1.00	1.00	0.70	0.46	0.95	0.76	0.45	1.00	0.92	0.88	0.95	NA	NA	NA	1.00	0.88	1.00	1.00	1.00	1.00	0.36	0.00	0.75	
HEG40	1.57	high	0.97	0.95	1.00	0.92	0.89	0.96	0.91	0.88	0.94	NA	NA	NA	0.77	0.59	0.95	0.94	0.91	0.97	0.93	0.91	0.96	0.90	0.82	0.99	1.00	0.88	1.00	1.00	0.95	1.00	0.90	0.86	0.93	
HEG49	1.63	high	0.97	0.94	1.00	0.94	0.91	0.97	0.85	0.81	0.90	1.00	1.00	1.00	0.79	0.64	0.93	0.90	0.73	1.00	0.92	0.88	0.96	1.00	0.98	1.00	1.00	0.88	1.00	0.97	0.92	1.00	0.86	0.83	0.90	
HEG50	1.93	high	0.96	0.92	1.00	0.90	0.85	0.95	0.86	0.80	0.92	NA	NA	NA	0.93	0.85	1.00	0.81	0.62	1.00	0.97	0.95	0.99	1.00	0.94	1.00	1.00	0.89	1.00	NA	NA	NA	0.88	0.85	0.92	
SEG01	2.39	high	0.97	0.94	1.00	0.97	0.96	0.99	0.76	0.66	0.85	NA	NA	NA	0.75	0.58	0.91	0.98	0.96	1.00	0.98	0.97	0.99	NA	NA	NA	1.00	0.88	1.00	NA	NA	NA	0.57	0.36	0.78	
SEG02	2.2	high	0.96	0.93	1.00	0.97	0.96	0.99	0.82	0.75	0.89	1.00	0.92	1.00	0.76	0.62	0.91	0.89	0.80	0.99	0.98	0.97	0.99	NA	NA	NA	1.00	0.88	1.00	0.49	0.00	0.99	0.80	0.74	0.85	
SEG03	2.21	high	0.96	0.94	0.99	0.96	0.94	0.97	0.86	0.82	0.90	1.00	0.94	1.00	0.74	0.63	0.86	0.98	0.96	1.00	0.97	0.95	0.99	NA	NA	NA	1.00	0.88	1.00	0.85	0.76	0.94	0.63	0.45	0.80	

SEG10	2.21	high	0.98	0.95	1.00	0.96	0.94	0.98	0.94	0.92	0.97	1.00	0.99	1.00	0.54	0.27	0.81	0.99	0.99	1.00	1.00	0.99	1.00	NA	NA	NA	1.00	0.87	1.00	0.96	0.94	0.97	0.44	0.07	0.82
SEG11	2.21	high	0.97	0.94	1.00	0.96	0.94	0.99	0.82	0.76	0.89	1.00	0.91	1.00	1.00	1.00	1.00	0.99	0.98	1.00	0.98	0.97	0.99	NA	NA	NA	1.00	0.86	1.00	0.97	0.94	1.00	0.56	0.32	0.81
SEG22	1.57	high	0.99	0.96	1.00	0.95	0.92	0.97	0.86	0.81	0.92	NA	NA	NA	0.18	0.00	0.71	0.99	0.96	1.00	0.98	0.97	0.99	0.58	0.21	0.96	1.00	0.87	1.00	0.90	0.80	0.99	0.73	0.61	0.86
SEG23	1.59	high	1.00	0.98	1.00	0.99	0.98	1.00	0.83	0.72	0.94	0.79	0.60	0.98	0.73	0.51	0.94	0.97	0.94	1.00	0.99	0.98	1.00	1.00	1.00	1.00	1.00	0.87	1.00	0.85	0.75	0.95	0.81	0.74	0.89
SEG26	1.53	high	0.98	0.95	1.00	0.98	0.97	1.00	0.90	0.87	0.93	NA	NA	NA	0.63	0.40	0.87	0.90	0.83	0.97	0.98	0.97	0.99	NA	NA	NA	1.00	0.87	1.00	NA	NA	NA	0.81	0.72	0.90
SEG33	1.8	high	0.98	0.96	1.00	0.96	0.93	0.98	0.91	0.88	0.94	NA	NA	NA	0.83	0.44	1.00	1.00	1.00	1.00	0.93	0.90	0.96	0.90	0.70	1.00	1.00	0.90	1.00	1.00	0.99	1.00	0.90	0.87	0.93
SEG35	1.95	high	0.98	0.96	1.00	0.97	0.94	0.99	0.84	0.79	0.90	1.00	1.00	1.00	0.67	0.42	0.93	0.95	0.91	1.00	0.96	0.94	0.97	0.63	0.09	1.00	1.00	0.89	1.00	1.00	0.96	1.00	0.89	0.85	0.94
SEG36	1.63	high	0.98	0.95	1.00	0.95	0.92	0.97	0.97	0.95	0.98	NA	NA	NA	0.63	0.33	0.92	0.99	0.98	1.00	0.96	0.94	0.97	1.00	0.94	1.00	1.00	0.91	1.00	0.97	0.88	1.00	0.83	0.79	0.87
SEG37	1.76	high	0.97	0.94	1.00	0.95	0.94	0.97	0.90	0.87	0.92	1.00	1.00	1.00	0.75	0.61	0.89	0.98	0.95	1.00	0.98	0.97	0.99	0.94	0.78	1.00	1.00	0.89	1.00	1.00	0.96	1.00	0.62	0.50	0.74
SEG38	2.53	high	0.99	0.96	1.00	0.99	0.98	1.00	0.84	0.79	0.88	NA	NA	NA	0.84	0.69	0.99	0.99	0.98	1.00	0.95	0.94	0.97	1.00	1.00	1.00	1.00	0.91	1.00	NA	NA	NA	0.72	0.63	0.81
SEG40	2.08	high	0.99	0.96	1.00	0.98	0.97	0.99	0.86	0.82	0.91	0.73	0.52	0.94	0.53	0.26	0.80	0.98	0.97	1.00	0.95	0.94	0.97	0.91	0.86	0.97	1.00	0.90	1.00	0.94	0.80	1.00	0.90	0.88	0.93
SEG41	2.14	high	0.98	0.95	1.00	0.97	0.96	0.99	0.87	0.81	0.94	1.00	1.00	1.00	0.56	0.26	0.86	0.98	0.97	1.00	0.95	0.94	0.97	0.81	0.59	1.00	1.00	0.90	1.00	0.81	0.63	0.99	0.87	0.83	0.92
SEG42	2.86	high	0.98	0.96	1.00	0.89	0.86	0.93	0.86	0.80	0.92	NA	NA	NA	0.11	0.00	0.64	0.99	0.98	1.00	0.92	0.88	0.96	1.00	1.00	1.00	1.00	0.90	1.00	1.00	0.96	1.00	0.78	0.70	0.85
SEG43	2.29	high	0.95	0.92	0.98	0.96	0.94	0.97	0.88	0.83	0.92	NA	NA	NA	0.75	0.56	0.93	0.99	0.99	1.00	0.95	0.94	0.97	1.00	1.00	1.00	1.00	0.90	1.00	0.78	0.53	1.00	0.89	0.86	0.91
SEG48	1.62	high	0.97	0.93	1.00	0.96	0.95	0.98	0.85	0.79	0.91	NA	NA	NA	0.65	0.40	0.90	0.98	0.97	1.00	0.96	0.94	0.97	0.95	0.95	0.96	1.00	0.90	1.00	0.84	0.66	1.00	0.74	0.68	0.81
SEG49	1.82	high	0.95	0.93	0.98	0.97	0.96	0.98	0.87	0.82	0.92	NA	NA	NA	0.90	0.73	1.00	0.99	0.98	1.00	0.90	0.86	0.93	0.90	0.78	1.00	1.00	0.90	1.00	0.98	0.94	1.00	0.74	0.68	0.81

Supplement S3 Details on diversity partitioning

In order to analyze the importance of β - relative to α -diversity in contributing to total γ -diversity we multiplicatively partitioned γ -diversity into independent α - and β -components, based on Whittaker's (1960) formula:

$$\gamma = \alpha_1 \text{ (within plot)} \times \beta_1 \text{ (among plots)} \times \beta_2 \text{ (among regions)}$$

We used true diversities and q-metrics as suggested by Jost²⁰ and Jost et al.²¹ using multipart function in vegan package²². The values for three different q-levels are shown in Table S3-1.

Table S3-1 | Gamma diversity partitioning across trophic groups. Gamma diversity was multiplicatively partitioned into independent α - and β -components following Whittaker²³ and Jost²⁰. Alpha-1: within plot, Alpha-2: within LUI intensity class (low vs. high), Alpha 3: within region; Beta-1: among plots within LUI intensity class, Beta-2: among LUI intensity classes within region, Beta-3: among regions.

	Trophic group	Alpha-1		Alpha-2		Alpha-3		Beta-1		Beta-2		Beta-3		Gamma
Aboveground	q=0 (species richness)													
	Autotrophs	146.7	(-) ^{***}	275.2	(-) ^{***}	293.6	(-) ^{***}	1.875	(+) ^{***}	1.067	(+) ^{***}	1.025	(+) ^{***}	301
	Plant pathogenes	5.8	(+) ^{***}	37.4	(-) ^{***}	50.3	(-) ^{***}	6.895	(-) ^{***}	1.373	(+) [*]	1.572	(+) ^{***}	79
	Herbivores	67.5	(-) ^{***}	221.1	(-) ^{***}	277.5	(-) ^{***}	3.276	(+) ^{***}	1.253	(+) ^{***}	1.366	(+) ^{***}	379
	Pollinators	95.1	(-) ^{***}	387.5	(-) ^{***}	488.9	(-) ^{***}	4.155	(+) ^{***}	1.26	(+) ^{***}	1.385	(+) ^{***}	677
	Invert. Decomposers	3.3	(-) ^{***}	14.5	(-) ^{***}	21.2	(-) ^{***}	4.502	(+) ^{**}	1.482	(+) [*]	1.888	(+) ^{***}	40
	Second. Consumers	12.0	(-) ^{***}	73.1	(-) ^{***}	101.8	(-) ^{***}	6.131	(+) ^{***}	1.411	(+) ^{***}	1.601	(+) ^{***}	163
Belowground	Tert. Consumers	13.6	(-) ^{***}	45.0	(-) ^{***}	54.9	(-) ^{***}	3.496	(+) ^{***}	1.206	(+) ^{**}	1.385	(+) ^{***}	76
	Mycorrhizae	72.1	(-) ^{***}	219.6	(-) ^{***}	257.9	(-) ^{***}	3.23	(+) ^{***}	1.171	(+) ^{**}	1.195	(+) ^{***}	308
	Herbivores	3.8	(-) ^{***}	9.5	(-) ^{***}	10.4	(-) ^{***}	2.503	(+) ^{***}	1.095	n.s.	1.06	(+) ^{***}	11
	Microbial decomposers	825.5	(-) ^{***}	1136.2	(-) ^{***}	1202.1	(-) ^{***}	1.376	(+) ^{***}	1.058	(+) ^{***}	1.074	(+) ^{***}	1291
	Second. Consumers	4.2	(-) ^{***}	12.0	(-) ^{***}	13.8	(-) ^{***}	2.954	(+) ^{***}	1.152	(+) ^{**}	1.163	(+) ^{***}	16
	Bacterivores	41.8	(-) ^{***}	194.8	(-) ^{***}	237.0	(-) ^{***}	4.762	(+) ^{***}	1.219	(+) ^{***}	1.207	(+) ^{***}	286
Aboveground	q=1 (exponential Shannon diversity)													
	Autotrophs	58.9	(-) ^{***}	64.4	(-) ^{***}	64.6	(-) ^{***}	1.093	(+) ^{***}	1.003	(+) ^{***}	1.002	(+) ^{***}	64.8
	Plant pathogenes	5.5	(+) ^{***}	26.0	(-) ^{***}	30.1	(-) ^{***}	5.062	(-) ^{***}	1.168	n.s.	1.155	(+) ^{***}	34.7
	Herbivores	27.9	(-) ^{***}	35.5	(-) ^{***}	36.0	(-) ^{***}	1.271	(+) ^{***}	1.014	(+) ^{***}	1.011	(+) ^{***}	36.5
	Pollinators	61.5	(-) ^{***}	110.7	(-) ^{***}	114.9	(-) ^{***}	1.833	(+) ^{***}	1.038	(+) ^{***}	1.034	(+) ^{***}	118.7
	Invert. Decomposers	2.9	(-) ^{***}	7.1	(-) ^{***}	7.7	(-) ^{***}	2.515	n.s.	1.106	(+) ^{***}	1.109	(+) ^{***}	8.6
	Second. Consumers	10.6	(-) ^{***}	33.8	(-) ^{***}	37.6	(-) ^{***}	3.218	(+) ^{***}	1.117	(+) ^{***}	1.108	(+) ^{***}	41.7
Belowground	Tert. Consumers	7.9	(-) ^{***}	11.2	(-) ^{**}	11.4	n.s.	1.458	(+) ^{***}	1.022	(+) ^{***}	1.023	n.s.	11.7
	Mycorrhizae	46.0	(-) ^{***}	71.4	(-) ^{***}	73.1	(-) ^{***}	1.638	(+) ^{***}	1.024	(+) ^{***}	1.02	(+) ^{***}	74.6
	Herbivores	3.0	(-) ^{***}	4.3	(-) ^{***}	4.3	(-) ^{***}	1.435	(+) ^{***}	1.013	n.s.	1.008	(+) ^{***}	4.4
	Microbial decomposers	87.7	(-) ^{***}	87.7	(-) ^{***}	87.7	(-) ^{***}	1	(+) ^{***}	1	(+) ^{***}	1	(+) ^{***}	87.7

Aboveground	Second. Consumers	2.3	(-) ^{***}	2.9	(-) ^{***}	3.0	(-) ^{***}	1.288	n.s.	1.013	(+) ^{***}	1.007	(+) ^{***}	3.0
	Bacterivores	20.1	(-) ^{***}	38.1	(-) ^{***}	39.4	n.s.	1.925	(+) ^{***}	1.035	(+) ^{***}	1.025	n.s.	40.4
	q=2 (reciprocal Simpson index)													
	Autotrophs	35.4	(-) ^{***}	36.3	(-) ^{***}	36.3	(-) ^{***}	1.025	(+) ^{***}	1.001	(+) ^{***}	1	(+) ^{***}	36.331
	Plant pathogenes	5.3	(+) ^{***}	19.4	(-) ^{***}	21.1	(-) ^{***}	3.945	(-) ^{***}	1.099	n.s.	1.07	(+) ^{***}	22.615
	Herbivores	12.8	(-) ^{***}	13.2	(-) ^{***}	13.2	(-) ^{***}	1.027	(+) ^{***}	1.001	(+) ^{***}	1	(+) ^{***}	13.178
	Pollinators	41.4	(-) ^{***}	53.6	(-) ^{***}	53.9	(-) ^{***}	1.305	(+) ^{***}	1.007	(+) ^{***}	1.004	(+) ^{***}	54.176
	Invert. Decomposers	2.7	(-) ^{***}	4.9	(-) ^{***}	5.0	(-) ^{***}	1.893	n.s.	1.03	(+) ^{***}	1.014	(+) ^{***}	5.085
	Second. Consumers	9.3	(-) ^{***}	19.0	(-) ^{***}	19.5	(-) ^{***}	2.057	(+) ^{***}	1.03	(+) ^{***}	1.018	(+) ^{***}	19.873
	Tert. Consumers	5.9	(-) ^{***}	6.9	(-) ^{***}	6.9	(-) ^{***}	1.172	(+) [*]	1.004	(+) ^{***}	1.003	(+) ^{***}	6.897
Belowground	Mycorrhizae	30.5	(-) ^{***}	38.2	(-) ^{***}	38.4	(-) ^{***}	1.294	(+) ^{***}	1.006	(+) ^{***}	1.004	(+) ^{***}	38.497
	Herbivores	2.6	(-) ^{***}	3.1	(-) [*]	3.1	(-) ^{**}	1.19	(+) ^{***}	1.004	n.s.	1.001	(+) ^{**}	3.09
	Microbial decomposers	42.8	(-) ^{***}	42.8	(-) ^{***}	42.8	(-) ^{***}	1	(+) ^{***}	1	(+) ^{***}	1	(+) ^{***}	42.77
	Second. Consumers	1.7	n.s.	1.8	(-) ^{***}	1.8	(-) ^{***}	1.011	n.s.	1.001	(+) ^{***}	1	(+) ^{***}	1.757
	Bacterivores	11.1	(-) ^{***}	12.9	(+) ^{***}	13.0	(+) ^{***}	1.176	(+) ^{***}	1.003	(+) ^{***}	1.001	(-) ^{***}	12.988

(-) lower / (+) higher than expected from a random distribution

Significance level: ***p<0.001, **p<0.01, *p<0.05

Table S3-2 | Beta-diversity across trophic groups. Mean beta diversity (Soerensen index) and the mean proportional dissimilarity due to species turnover (SD = standard deviation), based on the approach proposed by Baselga²⁴ and Baselga & Leprieur²⁵ for the seven aboveground and five belowground trophic groups.

	Trophic group	Sørensen dissimilarity β_{sor}		Species turnover β_{sim}		% turnover
		Mean	SD	Mean	SD	
Aboveground	Autotrophs	0.656	±0.153	0.565	±0.162	86.1
	Plant pathogens	0.744	±0.209	0.571	±0.327	76.8
	Herbivores	0.683	±0.113	0.612	±0.136	89.6
	Pollinators	0.763	±0.099	0.664	±0.129	87.0
	Invert. Decomposers	0.794	±0.321	0.384	±0.445	48.4
	Secondary Consumers	0.831	±0.141	0.765	±0.200	92.0
	Tert. Consumers	0.633	±0.196	0.496	±0.242	78.4
Belowground	Mycorrhizae	0.760	±0.143	0.628	±0.186	82.6
	Herbivores	0.489	±0.289	0.332	±0.351	68.0
	Microbial decomposers	0.181	±0.030	0.130	±0.033	71.7
	Secondary Consumers	0.473	±0.204	0.201	±0.245	42.5
	Bacterivores	0.727	±0.119	0.569	±0.169	78.3

Supplement S4 Details on α -diversity

Table S4-1 | Detailed statistics of power law models of α -diversity. The coefficients $\pm$ confidence intervals from power law models fitted to the alpha diversity of each trophic group. Diversity values were produced with different weightings for abundance from $q=0$ (species richness) to $q=2$. Confidence intervals were produced by bootstrapping. Parameters whose confidence intervals do not cross 0 are shown in bold.

		q=0			q=1			q=2		
		a	b	c	a	b	c	a	b	c
Aboveground	Primary producers	0.72$\pm$0.25	-0.64$\pm$0.23	0.41$\pm$0.29	0.79$\pm$0.3	-0.65$\pm$0.28	0.4$\pm$0.33	0.7$\pm$0.32	-0.46$\pm$0.3	0.39 $\pm$ 0.48
	Plant pathogens	0.58$\pm$0.15	-0.16 $\pm$ 0.16	1.07 $\pm$ 2.93	NA	NA	NA	NA	NA	NA
	Herbivores	0.59$\pm$0.29	-0.19 $\pm$ 0.26	0.58 $\pm$ 1.79	0.56$\pm$0.29	-0.1 $\pm$ 0.26	0.58 $\pm$ 3.39	0.49$\pm$0.29	-0.07 $\pm$ 0.26	0.55 $\pm$ 4.81
	Pollinators	0.49$\pm$0.08	0.08 $\pm$ 0.27	2.68 $\pm$ 15.03	0.29$\pm$0.16	0.15 $\pm$ 0.17	1.05 $\pm$ 3.07	0.26$\pm$0.23	0.22$\pm$0.2	0.76 $\pm$ 1.89
	Invert. Decomposers	0.33$\pm$0.23	0.13 $\pm$ 0.21	0.63 $\pm$ 2.48	0.37$\pm$0.23	0.04 $\pm$ 0.21	0.78 $\pm$ 9.78	0.4$\pm$0.29	0.11 $\pm$ 0.26	0.63 $\pm$ 3.68
	Secondary consumers	0.34$\pm$0.15	-0.08 $\pm$ 0.15	0.99 $\pm$ 4.91	0.3$\pm$0.15	-0.06 $\pm$ 0.15	0.98 $\pm$ 6.79	0.31$\pm$0.22	-0.05 $\pm$ 0.2	0.7 $\pm$ 7.67
Belowground	Tertiary consumers	0.63$\pm$0.32	-0.28 $\pm$ 0.31	0.34 $\pm$ 0.67	0.59$\pm$0.31	-0.24 $\pm$ 0.29	0.34 $\pm$ 0.76	0.54$\pm$0.29	-0.2 $\pm$ 0.28	0.38 $\pm$ 1
	Mycorrhizae	0.44$\pm$0.39	0.17 $\pm$ 0.38	0.25 $\pm$ 0.95	0.22 $\pm$ 0.43	0.23 $\pm$ 0.44	0.09 $\pm$ 0.34	0.41$\pm$0.06	-0.16 $\pm$ 0.29	4.05 $\pm$ 9.87
	Herbivores	0.5$\pm$0.08	-0.07 $\pm$ 0.28	2.99 $\pm$ 19.34	NA	NA	NA	NA	NA	NA
	Microbial decomposers	0.3 $\pm$ 0.34	0.21 $\pm$ 0.33	0.34 $\pm$ 0.99	0.44$\pm$0.36	0.14 $\pm$ 0.34	0.36 $\pm$ 1.59	0.51$\pm$0.05	0.25 $\pm$ 0.31	5.76 $\pm$ 9.8
	Secondary consumers	0.06 $\pm$ 0.41	0.51$\pm$0.39	0.32 $\pm$ 0.44	0.15 $\pm$ 0.34	0.31$\pm$0.31	0.5 $\pm$ 1.04	0.23 $\pm$ 0.3	0.29$\pm$0.27	0.54 $\pm$ 1.16
	Bacterivores	0.29$\pm$0.27	0.32$\pm$0.25	0.46 $\pm$ 0.75	0.37$\pm$0.15	0.11 $\pm$ 0.14	0.93 $\pm$ 3.16	0.33$\pm$0.07	0.03 $\pm$ 0.18	2.2 $\pm$ 26.44

Table S4-2 | Detailed statistics of power law models of α -diversity not corrected for soil nutrients. The coefficients $\pm$ confidence intervals from power law models fitted to the alpha diversity of each trophic group. Here species richness and LUI values were not corrected for soil nutrient levels

		q=0			q=1			q=2		
		a	b	c	a	b	c	a	b	c
Aboveground	Primary producers	0.89±0.26	-0.78±0.25	0.25±0.14	0.99±0.32	-0.81±0.31	0.24±0.16	0.87±0.34	-0.6±0.33	0.21±0.2
	Plant pathogens	0.56±0.17	-0.15±0.17	0.92±2.73	0.56±0.15	-0.15±0.16	1±2.9	0.56±0.17	-0.15±0.17	0.92±2.73
	Herbivores	0.58±0.25	-0.19±0.23	0.59±1.68	0.56±0.23	-0.09±0.21	0.66±3.6	0.47±0.22	-0.06±0.2	0.67±5.34
	Pollinators	0.49±0.09	0.08±0.26	2.49±13.68	0.29±0.14	0.15±0.16	1.13±3.11	0.27±0.18	0.21±0.18	0.88±2
	Invert. Decomposers	0.22±0.35	0.18±0.34	0.27±0.91	0.27±0.45	0.07±0.45	0.19±1.95	0.21±0.47	0.25±0.47	0.1±0.36
	Secondary consumers	0.32±0.14	-0.09±0.15	1.05±4.7	0.29±0.14	-0.06±0.15	1.02±6.45	0.3±0.16	-0.04±0.16	0.89±8.38
Belowground	Tertiary consumers	0.69±0.33	-0.34±0.32	0.23±0.38	0.61±0.3	-0.27±0.29	0.27±0.53	0.56±0.28	-0.21±0.27	0.32±0.75
	Mycorrhizae	0.23±0.38	0.26±0.39	0.09±0.27	0.14±0.39	0.26±0.39	0.06±0.22	0.36±0.05	-0.13±0.27	4.25±11.74
	Herbivores	NA	NA	NA	NA	NA	NA	NA	NA	NA
	Microbial decomposers	0.21±0.36	0.28±0.35	0.2±0.44	0.48±0.3	0.09±0.29	0.34±2.07	0.56±0.05	0.16±0.27	6.19±15.3
	Secondary consumers	0.01±0.4	0.55±0.39	0.25±0.31	0.16±0.29	0.3±0.27	0.51±0.99	0.09±0.39	0.4±0.38	0.22±0.36
	Bacterivores	0.23±0.28	0.34±0.27	0.36±0.54	0.35±0.12	0.11±0.13	1.01±3.15	0.33±0.03	0.06±0.32	19.95±271.67

Supplement S5 Details on β -diversity

Table S5-1 | Statistical details of Linear Models (LMs) on the drivers of β -diversity. The numbers give the coefficients from the models and the p-values using permutation-based significance testing. Results are shown for the seven aboveground and five belowground trophic group and for different q-levels (Sørensen q=0, Morisita q=1, Morisita-Horn q=2) and species turnover component β_{sim} .

		x- Intercept	Geographic distance		Isolation				LUI				sd LUI				pH				Soil nutrients			
					diff	mean			diff	mean			diff	mean			diff	mean			diff	mean		
Aboveground	q=0	P	Coef	p	Coef	p	Coef	p	Coef	p	Coef	p	Coef	p	Coef	p	Coef	p	Coef	p	Coef	p	Coef	p
	Primary producers	<0.001	0.147	<0.001	-0.018	<0.001	0.070	<0.001	0.205	<0.001	-0.362	<0.001	0.061	<0.001	-0.111	<0.001	0.007	0.451	-0.133	<0.001	0.156	<0.001	0.023	<0.001
	Plant pathogens	<0.001	0.251	<0.001	-0.104	<0.001	0.121	<0.001	0.104	<0.001	-0.144	<0.001	-0.022	0.010	-0.079	<0.001	-0.019	<0.001	-0.756	<0.001	-0.116	<0.001	0.254	<0.001
	Herbivores	<0.001	0.154	<0.001	0.012	0.001	0.029	<0.001	0.100	<0.001	-0.202	<0.001	<0.001	1.000	-0.032	<0.001	-0.002	1.000	0.105	<0.001	0.063	<0.001	-0.055	<0.001
	Pollinators	<0.001	0.076	<0.001	0.008	0.172	-0.117	<0.001	0.042	<0.001	-0.013	0.102	0.019	<0.001	0.020	0.006	0.025	<0.001	0.104	<0.001	0.060	<0.001	0.017	<0.001
	Invert. Decomposers	<0.001	0.152	<0.001	-0.017	1.000	-0.056	<0.001	0.020	1.000	-0.085	<0.001	0.061	<0.001	-0.160	<0.001	-0.006	0.441	-0.141	0.038	0.079	0.054	-0.054	<0.001
	Secondary consumers	<0.001	0.121	<0.001	0.001	0.922	0.024	<0.001	0.022	<0.001	0.026	0.005	-0.005	0.303	0.005	1.000	0.005	1.000	-0.035	0.033	0.130	<0.001	0.005	1.000
Tertiary consumers	<0.001	0.197	<0.001	0.084	<0.001	0.461	<0.001	0.085	<0.001	0.062	0.001	-0.052	<0.001	-0.106	<0.001	0.020	<0.001	-0.130	<0.001	-0.181	<0.001	0.120	<0.001	
Belowground	Mycorrhizae	<0.001	0.170	<0.001	-0.064	<0.001	0.072	<0.001	0.090	<0.001	-0.170	<0.001	-0.001	1.000	-0.003	0.430	0.020	1.000	-0.144	<0.001	0.021	<0.001	0.128	<0.001
	Herbivores	<0.001	0.044	<0.001	0.103	<0.001	-0.246	<0.001	0.044	0.007	0.160	<0.001	-0.139	<0.001	0.224	<0.001	0.088	<0.001	0.309	<0.001	0.115	<0.001	0.178	<0.001
	Microbial decomposers	<0.001	0.030	<0.001	-0.017	<0.001	0.016	<0.001	0.019	<0.001	-0.025	<0.001	<0.001	1.000	-0.015	<0.001	-0.001	0.062	-0.061	<0.001	0.026	<0.001	0.017	<0.001
	Secondary consumers	<0.001	0.038	<0.001	-0.057	<0.001	-0.013	0.296	0.050	<0.001	0.067	<0.001	-0.037	<0.001	-0.064	<0.001	0.012	0.069	-0.030	1.000	0.078	<0.001	0.016	0.563
	Bacterivores	<0.001	0.054	<0.001	-0.054	<0.001	0.037	<0.001	0.089	<0.001	-0.185	<0.001	-0.034	<0.001	0.028	<0.001	0.022	<0.001	0.137	<0.001	0.107	<0.001	0.086	<0.001
Aboveground	β _{sim}																							
	Primary producers	<0.001	0.140	<0.001	-0.053	<0.001	0.065	<0.001	0.120	<0.001	-0.282	<0.001	0.048	<0.001	-0.051	<0.001	0.006	1.000	-0.144	<0.001	0.139	<0.001	0.071	<0.001
	Plant pathogens	<0.001	0.285	<0.001	-0.038	0.034	0.160	<0.001	0.193	<0.001	-0.258	<0.001	-0.026	0.035	0.101	<0.001	-0.059	<0.001	-0.415	<0.001	-0.166	<0.001	0.272	<0.001
	Herbivores	<0.001	0.172	<0.001	-0.002	0.236	0.035	<0.001	0.099	<0.001	-0.229	<0.001	0.004	0.340	-0.028	0.244	0.005	1.000	0.121	<0.001	0.069	<0.001	-0.050	<0.001
	Pollinators	<0.001	0.080	<0.001	0.026	<0.001	-0.091	<0.001	0.061	<0.001	-0.005	0.482	0.036	<0.001	0.100	<0.001	0.019	<0.001	0.213	<0.001	0.081	<0.001	0.038	<0.001
	Invert. Decomposers	<0.001	0.188	<0.001	-0.145	<0.001	-0.361	<0.001	-0.121	<0.001	0.258	<0.001	0.077	0.026	-0.045	0.029	0.067	<0.001	0.315	<0.001	0.057	1.000	0.101	<0.001
	Secondary consumers	<0.001	0.163	<0.001	0.017	1.000	0.049	<0.001	0.045	<0.001	0.017	0.096	0.006	1.000	0.043	<0.001	0.004	1.000	0.003	1.000	0.191	<0.001	-0.010	0.765
Tertiary consumers	<0.001	0.138	<0.001	0.069	<0.001	0.279	<0.001	0.082	<0.001	-0.120	<0.001	0.028	0.046	-0.244	<0.001	0.024	0.002	-0.065	0.010	-0.079	<0.001	0.005	1.000	
Belowground	Mycorrhizae	<0.001	0.135	<0.001	0.010	0.044	0.093	<0.001	0.097	<0.001	-0.117	<0.001	-0.036	<0.001	0.138	<0.001	0.055	<0.001	0.142	<0.001	0.051	<0.001	0.152	<0.001
	Herbivores	<0.001	0.086	<0.001	0.043	<0.001	-0.159	<0.001	0.051	<0.001	0.163	<0.001	-0.147	<0.001	0.295	<0.001	0.147	<0.001	0.474	<0.001	0.116	<0.001	0.114	<0.001
	Microbial decomposers	<0.001	0.007	<0.001	0.003	0.340	-0.006	<0.001	0.008	<0.001	0.019	<0.001	0.002	0.218	0.012	<0.001	0.013	<0.001	0.065	<0.001	0.049	<0.001	-0.010	<0.001
	Secondary consumers	<0.001	0.018	<0.001	-0.011	0.219	-0.053	<0.001	-0.034	<0.001	0.425	<0.001	-0.032	0.001	-0.240	<0.001	0.063	<0.001	0.583	<0.001	0.163	<0.001	-0.147	<0.001
	Bacterivores	<0.001	0.064	<0.001	0.011	1.000	0.069	<0.001	0.039	<0.001	-0.217	<0.001	-0.008	0.592	-0.047	<0.001	0.028	0.074	-0.106	<0.001	0.043	<0.001	0.230	<0.001

Aboveground	q=1																							
	Primary producers	<0.001	0.141	<0.001	-0.030	<0.001	0.087	<0.001	0.224	<0.001	-0.442	<0.001	0.027	<0.001	-0.066	<0.001	-0.001	1.000	-0.240	<0.001	0.124	<0.001	0.049	<0.001
	Herbivores	<0.001	0.165	<0.001	0.012	0.081	0.018	0.804	0.163	<0.001	-0.322	<0.001	-0.020	0.045	-0.035	0.005	0.050	<0.001	0.162	<0.001	0.034	<0.001	-0.112	<0.001
	Pollinators	<0.001	0.075	<0.001	0.047	<0.001	-0.203	<0.001	0.043	<0.001	-0.042	<0.001	0.008	0.383	0.006	0.392	0.024	<0.001	0.167	<0.001	0.056	<0.001	0.010	0.045
	Invert. Decomposers	<0.001	0.163	<0.001	0.004	0.249	0.053	0.089	0.012	1.000	-0.224	<0.001	0.080	<0.001	-0.223	<0.001	-0.045	<0.001	-0.411	<0.001	0.052	<0.001	-0.110	<0.001
	Secondary consumers	<0.001	0.150	<0.001	-0.014	0.038	0.026	0.036	0.045	<0.001	0.022	0.023	-0.013	0.941	0.056	<0.001	0.007	0.291	0.048	<0.001	0.158	<0.001	-0.042	<0.001
	Tertiary consumers	<0.001	0.342	<0.001	0.043	<0.001	0.301	<0.001	0.052	<0.001	0.048	<0.001	0.003	0.843	-0.029	0.021	0.016	0.164	0.142	<0.001	-0.074	<0.001	-0.018	0.024
Belowground	Mycorrhizae	<0.001	0.196	<0.001	-0.053	<0.001	0.133	<0.001	0.139	<0.001	-0.177	<0.001	-0.008	0.099	0.035	<0.001	0.033	0.020	-0.107	<0.001	0.011	1.000	0.187	<0.001
	Herbivores	<0.001	0.052	<0.001	0.068	<0.001	-0.227	<0.001	0.054	<0.001	0.225	<0.001	-0.169	<0.001	0.264	<0.001	0.086	<0.001	0.530	<0.001	0.152	<0.001	0.044	<0.001
	Microbial decomposers	<0.001	0.119	<0.001	-0.027	<0.001	-0.018	<0.001	0.027	<0.001	0.013	<0.001	0.041	<0.001	0.052	<0.001	0.026	<0.001	-0.082	<0.001	0.146	<0.001	-0.092	<0.001
	Secondary consumers	<0.001	0.035	<0.001	-0.101	<0.001	-0.130	<0.001	0.151	<0.001	-0.161	<0.001	-0.127	<0.001	0.161	<0.001	0.008	1.000	0.354	<0.001	0.058	<0.001	0.039	0.667
	Bacterivores	<0.001	0.044	<0.001	-0.053	<0.001	0.120	<0.001	0.120	<0.001	-0.200	<0.001	-0.044	<0.001	0.019	1.000	0.030	<0.001	0.265	<0.001	0.228	<0.001	0.059	<0.001
Aboveground	q=2																							
	Primary producers	<0.001	0.104	<0.001	-0.006	1.000	0.090	<0.001	0.208	<0.001	-0.388	<0.001	0.017	<0.001	-0.027	<0.001	0.003	1.000	-0.141	<0.001	0.107	<0.001	0.019	0.032
	Herbivores	<0.001	0.124	<0.001	0.030	<0.001	0.013	1.000	0.166	<0.001	-0.340	<0.001	-0.023	0.034	-0.007	0.155	0.073	<0.001	0.338	<0.001	-0.007	1.000	-0.109	<0.001
	Pollinators	<0.001	0.046	<0.001	0.047	<0.001	-0.194	<0.001	0.030	<0.001	-0.056	<0.001	0.006	1.000	-0.009	1.000	0.016	0.026	0.190	<0.001	0.046	<0.001	0.006	1.000
	Invert. Decomposers	<0.001	0.143	<0.001	0.009	0.159	0.060	0.032	0.008	1.000	-0.176	<0.001	0.073	<0.001	-0.196	<0.001	-0.047	<0.001	-0.389	<0.001	0.031	<0.001	-0.091	<0.001
	Secondary consumers	<0.001	0.146	<0.001	-0.028	<0.001	0.027	1.000	0.062	<0.001	0.001	1.000	-0.014	0.980	0.087	<0.001	0.010	1.000	0.127	<0.001	0.152	<0.001	-0.064	<0.001
	Tertiary consumers	<0.001	0.358	<0.001	0.038	<0.001	0.179	<0.001	0.023	0.001	0.024	0.015	0.016	1.000	0.030	0.238	0.016	0.028	0.286	<0.001	-0.002	1.000	-0.077	<0.001
Belowground	Mycorrhizae	<0.001	0.171	<0.001	-0.038	<0.001	0.133	<0.001	0.130	<0.001	-0.159	<0.001	-0.005	0.153	0.053	<0.001	0.027	<0.001	-0.130	<0.001	0.046	<0.001	0.177	<0.001
	Herbivores	<0.001	0.044	<0.001	0.050	<0.001	-0.228	<0.001	0.054	<0.001	0.213	<0.001	-0.148	<0.001	0.214	<0.001	0.081	<0.001	0.593	<0.001	0.155	<0.001	-0.062	<0.001
	Microbial decomposers	<0.001	0.251	<0.001	-0.034	<0.001	-0.109	<0.001	0.014	0.028	0.087	<0.001	0.136	<0.001	0.163	<0.001	0.052	<0.001	-0.166	<0.001	0.254	<0.001	-0.308	<0.001
	Secondary consumers	<0.001	0.033	<0.001	-0.077	<0.001	-0.094	<0.001	0.174	<0.001	-0.214	<0.001	-0.143	<0.001	0.208	<0.001	0.020	0.001	0.426	<0.001	0.038	0.059	0.080	<0.001
	Bacterivores	<0.001	0.022	0.293	-0.059	<0.001	0.184	<0.001	0.114	<0.001	-0.128	<0.001	-0.053	<0.001	0.045	<0.001	0.020	<0.001	0.327	<0.001	0.286	<0.001	<0.001	1.000

Table S5-2 | Statistical details on the Generalized Dissimilarity Models (GDMs). The numbers give the coefficients of each variable in each model (i.e. the maximum height of the spline for that variable; Coef), the percentage of unique variance explained by each driver in all models and the total variance explained by each model (VarExp) and the p-values (p). Results are shown for the seven aboveground and five belowground trophic group and for different q-levels (Sørensen q=0, Morisita q=1, Morisita-Horn q=2) and species turnover component β_{sim} . Bold numbers indicate the most important variable (highest coefficient) for each trophic group. All values are also shown for models with and without soil nutrients included.

With soil nutrients in GDM		Geographic distance			Isolation			LUI			sd LUI			pH			Soil nutrients			Total
	q=0	Coef	VarExp	p	Coef	VarExp	p	Coef	VarExp	p	Coef	VarExp	p	Coef	VarExp	p	Coef	VarExp	p	VarExp
Aboveground	Primary producers	0.47	23.6	<0.01	0.05	0.3	0.46	0.61	30.1	<0.01	0.17	2.5	0.14	0.04	0.2	0.39	0.45	16.8	<0.01	35.4
	Plant pathogens	1.26	77.9	<0.01	<0.01	<0.1	0.96	0.36	5.8	0.12	0.15	1.3	0.37	0.38	3.9	0.10	0.04	0.1	0.79	26.6
	Herbivores	0.48	53.2	<0.01	0.05	0.3	0.40	0.38	25.5	<0.01	<0.01	<0.1	1.00	<0.01	<0.1	0.78	0.14	2.8	0.07	18.4
	Pollinators	0.28	24.5	<0.01	0.26	7.3	0.02	0.13	2.7	0.23	0.09	0.9	0.39	0.13	3.2	0.09	0.32	14.7	0.02	24.3
	Invert. Decomposers	1.10	70.1	<0.01	0.06	0.3	0.67	0.18	1.8	0.41	0.06	0.1	0.73	0.06	0.3	0.60	0.29	4.5	0.29	17.4
	Secondary consumers	0.80	37.4	<0.01	0.06	0.3	0.52	0.10	0.5	0.47	0.04	<0.1	0.74	0.08	0.1	0.55	0.81	20.8	<0.01	17.4
	Tertiary consumers	0.54	62.0	<0.01	0.30	17.2	0.02	0.50	10.0	0.08	0.07	0.8	0.58	0.05	0.4	0.56	<0.01	<0.1	0.97	17.4
Belowground	Mycorrhizae	0.66	54.1	<0.01	<0.01	0.0	0.98	0.34	11.1	0.03	0.05	0.2	0.62	0.14	0.9	0.34	0.41	12.3	<0.01	9.3
	Herbivores	0.11	2.4	<0.01	0.43	13.2	0.02	0.24	3.2	0.26	<0.01	<0.1	0.96	0.33	11.5	0.05	0.43	20.7	0.02	33.2
	Microbial decomposers	0.04	37.2	<0.01	<0.01	<0.1	0.99	0.03	9.8	0.02	0.01	1.6	0.24	0.01	0.9	0.33	0.04	25.5	<0.01	27.0
	Secondary consumers	0.06	8.1	0.07	<0.01	<0.1	0.90	0.11	16.5	0.15	0.02	1.0	0.63	0.04	2.5	0.45	0.21	44.4	0.07	18.9
	Bacterivores	0.12	4.9	<0.01	<0.01	<0.1	0.99	0.33	21.8	<0.01	<0.01	<0.1	0.99	0.17	5.5	0.04	0.55	43.6	<0.01	27.2
Aboveground	β_{sim}																			
	Primary producers	0.40	33.3	<0.01	<0.01	<0.1	0.75	0.28	15.0	<0.01	0.09	1.7	0.22	0.05	0.4	0.38	0.35	21.3	<0.01	27.0
	Plant pathogens	0.89	83.7	<0.01	0.08	0.9	0.44	0.53	12.3	0.06	0.03	0.1	0.80	<0.01	<0.1	0.98	<0.01	<0.1	0.94	53.3
	Herbivores	0.42	54.9	<0.01	0.02	0.1	0.67	0.30	20.3	<0.01	0.01	<0.1	0.65	0.03	0.2	0.54	0.14	3.7	0.06	53.2
	Pollinators	0.19	16.8	<0.01	0.18	4.9	0.06	0.12	3.0	0.14	0.20	5.1	0.07	0.12	4.2	0.02	0.34	21.2	<0.01	17.3
	Invert. Decomposers	0.29	20.6	0.02	0.27	11.8	0.24	<0.01	<0.1	0.93	0.15	2.6	0.54	0.24	5.4	0.44	0.27	12.8	0.22	2.4
	Secondary consumers	0.76	35.6	<0.01	0.12	0.7	0.40	0.23	1.1	0.31	0.14	0.4	0.53	0.05	0.2	0.62	0.86	19.8	<0.01	2.4
	Tertiary consumers	0.25	44.2	<0.01	0.09	4.1	0.41	0.25	21.6	0.06	0.13	6.8	0.23	0.03	0.5	0.56	<0.01	<0.1	0.95	2.1
	Mycorrhizae	0.33	40.0	<0.01	0.04	0.4	0.55	0.24	8.4	0.01	0.04	0.2	0.61	0.18	2.7	0.10	0.37	19.0	<0.01	3.8
	Herbivores	0.14	7.3	<0.01	0.10	1.8	0.40	0.19	4.0	0.19	<0.01	<0.1	0.99	0.35	19.0	0.01	0.33	22.0	0.04	20.0
	Microbial decomposers	0.01	2.4	<0.01	<0.01	0.4	0.53	0.02	2.9	0.14	<0.01	0.5	0.48	0.02	4.1	0.07	0.05	52.1	<0.01	20.0
	Secondary consumers	0.01	0.5	<0.01	<0.01	<0.1	1.00	0.19	18.8	0.11	0.06	7.3	0.33	0.10	18.8	0.10	0.22	33.5	0.04	10.0
	Bacterivores	0.14	7.0	<0.01	0.02	0.1	0.75	0.21	14.1	<0.01	0.01	<0.1	0.83	0.13	2.0	0.27	0.48	45.4	<0.01	13.1

		q=1																		
		Coef	VarExp	p	Coef	VarExp	p	Coef	VarExp	p	Coef	VarExp	p	Coef	VarExp	p	Coef	VarExp	p	VarExp
Aboveground	Primary producers	0.59	25.7	<0.01	0.07	0.4	0.49	0.85	36.9	<0.01	0.12	1.0	0.26	0.07	0.2	0.56	0.47	13.7	<0.01	20.7
	Herbivores	0.59	58.6	<0.01	0.02	<0.1	0.73	0.72	29.0	<0.01	<0.01	0.0	0.98	0.09	0.6	0.33	<0.01	<0.1	0.77	15.3
	Pollinators	0.29	14.8	<0.01	0.77	25.3	<0.01	0.17	2.2	0.25	0.06	0.1	0.66	0.18	2.9	0.09	0.42	10.5	0.04	18.1
	Invert. Decomposers	1.92	74.4	<0.01	0.60	10.8	0.11	0.33	2.8	0.30	0.31	2.2	0.42	0.09	0.3	0.64	<0.01	0.0	0.80	4.3
	Secondary consumers	1.01	46.4	<0.01	0.03	0.1	0.70	0.24	1.4	0.22	0.11	0.2	0.55	0.06	0.1	0.64	0.75	13.8	<0.01	9.8
	Tertiary consumers	1.20	90.5	<0.01	0.24	3.6	0.08	0.25	1.8	0.15	0.05	0.1	0.62	<0.01	<0.1	0.80	<0.01	<0.1	1.00	9.7
Belowground	Mycorrhizae	0.90	49.4	<0.01	0.02	<0.1	0.64	0.65	11.2	0.03	0.09	0.4	0.60	0.20	1.1	0.41	0.55	12.4	<0.01	4.3
	Herbivores	0.13	3.3	<0.01	0.35	9.0	0.17	0.47	11.3	0.08	<0.01	<0.1	0.96	0.29	12.9	0.02	0.48	20.0	0.06	15.8
	Microbial decomposers	0.14	37.2	<0.01	<0.01	<0.1	0.92	0.03	0.6	0.17	0.06	1.6	0.07	0.03	0.7	0.13	0.25	24.9	<0.01	16.3
	Secondary consumers	0.03	2.8	0.40	<0.01	<0.1	0.98	0.17	34.7	0.16	<0.01	<0.1	0.94	0.08	11.3	0.30	0.15	29.5	0.25	13.3
	Bacterivores	0.08	2.1	<0.01	0.04	0.3	0.51	0.37	16.9	0.02	<0.01	<0.1	0.98	0.23	7.1	0.04	0.74	49.2	<0.01	14.7
		q=2																		
		Coef	VarExp	p	Coef	VarExp	p	Coef	VarExp	p	Coef	VarExp	p	Coef	VarExp	p	Coef	VarExp	p	VarExp
Aboveground	Primary producers	0.63	19.8	<0.01	0.17	1.5	0.19	1.21	43.1	<0.01	0.10	0.2	0.61	0.12	0.2	0.51	0.57	12.5	<0.01	14.8
	Herbivores	0.81	53.8	<0.01	0.13	0.3	0.47	1.20	33.2	<0.01	0.01	<0.1	0.74	0.12	0.5	0.50	<0.01	<0.1	1.00	29.3
	Pollinators	0.24	6.6	<0.01	1.50	36.2	<0.01	0.23	1.8	0.33	0.02	<0.1	0.69	0.28	3.3	0.09	0.60	9.4	0.02	6.8
	Invert. Decomposers	2.00	74.4	<0.01	0.70	13.0	0.08	0.30	2.1	0.35	0.39	2.6	0.39	0.09	0.2	0.74	<0.01	<0.1	0.98	23.0
	Secondary consumers	1.20	51.4	<0.01	<0.01	<0.1	0.99	0.40	2.6	0.26	0.23	0.8	0.40	0.12	0.6	0.41	0.69	9.3	0.02	22.8
	Tertiary consumers	1.72	88.5	<0.01	0.19	1.1	0.12	0.17	0.6	0.32	0.14	0.3	0.45	<0.01	<0.1	0.80	0.22	0.6	0.32	20.9
Belowground	Mycorrhizae	1.20	38.6	<0.01	0.15	0.7	0.42	0.71	8.1	0.03	0.17	0.6	0.56	0.35	1.7	0.22	0.99	19.4	<0.01	12.6
	Herbivores	0.12	2.2	<0.01	0.40	10.5	0.12	0.64	17.9	0.06	<0.01	<0.1	0.78	0.33	14.9	0.09	0.59	18.2	0.07	11.5
	Microbial decomposers	0.35	31.1	<0.01	<0.01	<0.1	0.97	0.02	0.1	0.42	0.27	4.4	<0.01	0.03	0.2	0.35	0.73	32.9	<0.01	9.5
	Secondary consumers	0.03	1.6	0.25	<0.01	<0.1	0.75	0.26	37.7	0.16	<0.01	<0.1	0.98	0.11	11.7	0.35	0.21	28.2	0.26	6.8
	Bacterivores	0.04	0.4	<0.01	0.12	1.9	0.41	0.39	12.9	0.08	<0.01	<0.1	1.00	0.27	8.0	0.09	1.04	54.3	<0.01	7.3

Without soil nutrients in GDM		Geographic distance			Isolation			LUI			sd LUI			pH			Soil nutrients			Total
	q=0	Coef	VarExp	p	Coef	VarExp	p	Coef	VarExp	p	Coef	VarExp	p	Coef	VarExp	p	Coef	VarExp	p	VarExp
Aboveground	Primary producers	0.55	41.6	<0.01	0.10	0.8	0.36	0.60	32.7	<0.01	0.18	3.6	0.06	0.17	2.6	0.05	NA	NA	NA	29.4
	Plant pathogens	1.27	87.4	<0.01	<0.01	<0.1	0.98	0.36	5.7	0.14	0.15	1.3	0.38	0.38	3.9	0.19	NA	NA	NA	23.0
	Herbivores	0.51	62.6	<0.01	0.08	0.9	0.20	0.37	24.8	<0.01	<0.01	<0.1	0.97	0.03	0.2	0.50	NA	NA	NA	16.1
	Pollinators	0.34	48.3	<0.01	0.37	19.2	<0.01	0.12	3.0	0.22	0.10	1.0	0.41	0.20	10.0	0.02	NA	NA	NA	19.1
	Invert. Decomposers	1.16	88.5	<0.01	0.15	0.6	0.64	0.17	1.4	0.47	0.07	0.2	0.63	0.13	1.4	0.37	NA	NA	NA	17.4
	Secondary consumers	0.94	79.5	<0.01	0.15	1.2	0.35	0.09	0.5	0.46	0.05	0.1	0.77	0.27	3.1	0.15	NA	NA	NA	17.3
	Tertiary consumers	0.54	62.0	<0.01	0.30	17.2	0.04	0.50	10.0	0.08	0.07	0.8	0.58	0.05	0.4	0.63	NA	NA	NA	17.3
Belowground	Mycorrhizae	0.75	82.8	<0.01	<0.01	<0.1	0.99	0.31	10.2	0.05	0.06	0.4	0.61	0.23	1.9	0.25	NA	NA	NA	9.3
	Herbivores	0.18	8.7	<0.01	0.65	43.4	<0.01	0.27	4.7	0.25	<0.01	<0.1	0.99	0.38	25.7	0.02	NA	NA	NA	32.3
	Microbial decomposers	0.05	77.3	<0.01	<0.01	<0.1	0.99	0.02	8.9	0.09	0.01	3.3	0.28	0.01	2.3	0.18	NA	NA	NA	27.0
	Secondary consumers	0.10	42.9	0.15	<0.01	<0.1	0.97	0.10	25.5	0.16	0.03	2.2	0.53	0.09	22.4	0.18	NA	NA	NA	18.9
	Bacterivores	0.24	29.0	0.01	0.07	1.1	0.44	0.29	29.3	0.02	<0.01	<0.1	0.98	0.29	31.3	<0.01	NA	NA	NA	26.1

		β_{sim}																		
Aboveground	Primary producers	0.47	62.7	<0.01	0.02	0.1	0.71	0.26	15.9	<0.01	0.10	2.7	0.19	0.14	5.9	0.05	NA	NA	NA	20.1
	Plant pathogens	0.89	86.9	<0.01	0.08	0.9	0.57	0.53	12.3	0.03	0.03	0.1	0.80	<0.01	<0.1	1.00	NA	NA	NA	40.0
	Herbivores	0.44	66.2	<0.01	0.05	0.5	0.43	0.29	19.7	<0.01	0.02	0.1	0.66	0.06	1.2	0.20	NA	NA	NA	35.8
	Pollinators	0.26	40.2	<0.01	0.29	17.2	<0.01	0.10	3.2	0.13	0.20	5.8	0.11	0.19	14.7	<0.01	NA	NA	NA	8.3
	Invert. Decomposers	0.36	43.1	0.01	0.35	22.0	0.10	0.01	<0.1	0.84	0.15	3.2	0.57	0.29	11.7	0.21	NA	NA	NA	1.3
	Secondary consumers	0.90	75.3	<0.01	0.21	2.2	0.24	0.19	1.1	0.32	0.15	0.7	0.52	0.20	3.4	0.04	NA	NA	NA	1.7
	Tertiary consumers	0.25	44.2	<0.01	0.09	4.1	0.32	0.25	21.6	0.06	0.13	6.8	0.23	0.03	0.5	0.72	NA	NA	NA	1.5
	Mycorrhizae	0.38	64.3	<0.01	0.09	1.0	0.51	0.22	8.2	0.06	0.01	<0.1	0.84	0.24	9.1	<0.01	NA	NA	NA	2.6
	Herbivores	0.19	17.6	0.01	0.25	13.9	0.07	0.23	6.7	0.29	<0.01	<0.1	0.97	0.40	40.8	<0.01	NA	NA	NA	11.3
Belowground	Microbial decomposers	0.02	28.9	<0.01	0.02	11.6	0.05	0.02	6.7	0.15	0.01	1.1	0.46	0.03	30.2	<0.01	NA	NA	NA	10.1
	Secondary consumers	0.04	9.7	0.05	<0.01	<0.1	0.99	0.19	26.6	0.19	0.06	10.3	0.38	0.13	51.6	0.04	NA	NA	NA	4.6
	Bacterivores	0.19	29.3	<0.01	0.21	16.3	0.01	0.16	16.5	0.01	0.04	0.9	0.57	0.19	15.2	0.01	NA	NA	NA	7.1
	q=1																			
Aboveground	Primary producers	0.69	41.6	<0.01	0.09	0.4	0.45	0.84	39.0	<0.01	0.14	1.5	0.24	0.19	1.6	0.15	NA	NA	NA	17.7
	Herbivores	0.59	60.2	<0.01	0.02	<0.1	0.74	0.72	29.0	<0.01	<0.01	<0.1	0.99	0.09	0.6	0.33	NA	NA	NA	13.9
	Pollinators	0.38	27.3	<0.01	0.92	43.8	<0.01	0.16	2.3	0.22	0.05	0.1	0.66	0.27	8.7	0.03	NA	NA	NA	14.3
	Invert. Decomposers	1.92	78.2	<0.01	0.60	10.8	0.12	0.33	2.8	0.34	0.31	2.2	0.43	0.09	0.3	0.58	NA	NA	NA	4.1
	Secondary consumers	1.15	82.5	<0.01	0.08	0.2	0.60	0.22	1.4	0.26	0.14	0.4	0.56	0.26	2.5	0.09	NA	NA	NA	9.8
	Tertiary consumers	1.20	91.0	<0.01	0.24	3.6	0.08	0.25	1.8	0.08	0.05	0.1	0.61	<0.01	<0.1	0.73	NA	NA	NA	9.7
	Mycorrhizae	1.01	78.6	<0.01	<0.01	<0.1	0.82	0.59	11.0	0.02	0.11	0.6	0.50	0.36	2.8	0.11	NA	NA	NA	3.8
	Herbivores	0.21	10.9	0.01	0.55	31.3	<0.01	0.50	15.3	0.07	<0.01	<0.1	0.76	0.36	28.5	0.01	NA	NA	NA	12.5
	Microbial decomposers	0.15	74.4	<0.01	<0.01	<0.1	0.68	0.01	0.3	0.35	0.08	5.3	0.02	0.11	8.2	<0.01	NA	NA	NA	14.1
Belowground	Secondary consumers	0.05	10.2	0.40	0.05	4.5	0.46	0.15	40.9	0.16	<0.01	<0.1	0.96	0.11	38.1	0.11	NA	NA	NA	12.0
	Bacterivores	0.21	20.5	0.01	0.06	0.5	0.50	0.33	25.0	0.03	<0.01	<0.1	0.97	0.38	42.3	0.01	NA	NA	NA	11.8
	q=2																			
	Aboveground	Primary producers	0.74	32.1	<0.01	0.21	1.4	0.26	1.19	45.6	<0.01	0.12	0.5	0.56	0.27	1.9	0.17	NA	NA	NA
Herbivores		0.81	53.8	<0.01	0.13	0.3	0.55	1.20	33.2	<0.01	0.01	<0.1	0.76	0.12	0.5	0.45	NA	NA	NA	29.1
Pollinators		0.35	12.8	<0.01	1.73	59.7	<0.01	0.21	1.8	0.29	<0.01	<0.1	0.77	0.41	9.1	0.05	NA	NA	NA	6.8
Invert. Decomposers		2.00	76.3	<0.01	0.70	13.0	0.07	0.30	2.1	0.38	0.39	2.6	0.32	0.09	0.2	0.76	NA	NA	NA	20.2
Secondary consumers		1.33	82.2	<0.01	0.01	<0.1	0.76	0.34	2.5	0.11	0.26	1.1	0.34	0.26	3.2	0.10	NA	NA	NA	20.0
Tertiary consumers		1.72	92.5	<0.01	0.19	1.2	0.17	0.16	0.5	0.23	0.17	0.3	0.48	0.02	<0.1	0.67	NA	NA	NA	16.8
Mycorrhizae		1.37	77.0	<0.01	0.10	0.4	0.57	0.62	8.4	0.08	0.20	1.0	0.50	0.59	4.2	0.08	NA	NA	NA	10.2
Herbivores		0.21	9.7	<0.01	0.56	28.2	0.02	0.66	22.3	0.06	<0.01	<0.1	0.80	0.40	28.8	0.01	NA	NA	NA	9.1
Microbial decomposers		0.38	63.9	<0.01	<0.01	<0.1	0.86	0.01	<0.1	0.67	0.41	16.5	<0.01	0.19	5.4	0.01	NA	NA	NA	7.6
Belowground	Secondary consumers	0.06	5.9	0.38	0.10	9.1	0.46	0.22	42.0	0.15	<0.01	<0.1	0.98	0.15	36.5	0.13	NA	NA	NA	5.5
	Bacterivores	0.20	16.6	0.02	0.06	1.2	0.64	0.35	20.1	0.08	<0.01	<0.1	0.98	0.44	52.1	0.02	NA	NA	NA	5.7

Supplement S6 Details on correlations among trophic groups

Table S6-1 | The correlation of β -diversity between different trophic groups. R^2 - and p-values from matrix regressions for overall β -diversity ($q=0, 1, 2$) and the species turnover component (β_{sim}) are given for low (52) and high (53) land-use intensity (LUI) plots. AG=Aboveground, BG=Belowground, NA: for plant pathogens no abundance data was available and for invertebrate decomposers calculations for higher q-levels were not possible due to low abundance.

Trophic group 1	Trophic group 2	Soerensen Index β_{sor} (q0)				Species turnover component β_{sim}				exp. Shannon (q1)				inv. Simpson (q2)			
		Low LUI		High LUI		Low LUI		High LUI		Low LUI		High LUI		Low LUI		High LUI	
		R^2	p	R^2	p	R^2	p	R^2	p	R^2	p	R^2	p	R^2	p	R^2	p
AG_Primary producer	AG_Plant pathogens	0.315	0.001	0.019	0.001	0.215	0.001	0.045	0.001	NA	NA	NA	NA	NA	NA	NA	NA
AG_Primary producer	AG_Herbivores	0.413	0.001	0.111	0.001	0.311	0.001	0.098	0.001	0.237	0.001	0.064	0.001	0.079	0.001	0.025	0.001
AG_Primary producer	AG_Pollinators	0.193	0.001	0.052	0.001	0.076	0.001	0.068	0.001	0.090	0.001	0.041	0.001	0.026	0.001	0.015	0.001
AG_Primary producer	AG_Invert. decomposers	0.024	0.001	0.030	0.001	0.003	0.070	0.007	0.014	NA	NA	NA	NA	NA	NA	NA	NA
AG_Primary producer	AG_Secondary consumers	0.162	0.001	0.070	0.001	0.101	0.001	0.062	0.001	0.125	0.001	0.019	0.001	0.068	0.001	0.007	0.003
AG_Primary producer	AG_Tertiary consumers	0.125	0.001	<0.001	0.925	0.140	0.001	0.002	0.233	0.137	0.001	0.076	0.001	0.067	0.001	0.082	0.001
AG_Primary producer	BG_Mycorrhizae	0.372	0.001	0.154	0.001	0.061	0.001	0.047	0.001	0.185	0.001	0.098	0.001	0.060	0.001	0.040	0.001
AG_Primary producer	BG_Herbivores	0.033	0.001	0.038	0.001	0.044	0.001	0.021	0.002	0.009	0.004	0.013	0.002	0.001	0.210	0.009	0.003
AG_Primary producer	BG_Microbial decomposers	0.420	0.001	0.165	0.001	0.015	0.001	0.148	0.001	0.297	0.001	0.158	0.001	0.121	0.001	0.050	0.001
AG_Primary producer	BG_Secondary consumers	0.006	0.004	0.041	0.001	0.021	0.001	0.018	0.001	0.005	0.011	0.015	0.001	<0.001	0.589	0.007	0.006
AG_Primary producer	BG_Bacterivores	0.149	0.001	0.110	0.001	0.034	0.001	0.071	0.001	0.049	0.001	0.158	0.001	0.006	0.010	0.060	0.001
AG_Plant pathogens	AG_Herbivores	0.175	0.001	0.069	0.001	0.107	0.001	0.043	0.001	NA	NA	NA	NA	NA	NA	NA	NA
AG_Plant pathogens	AG_Pollinators	0.022	0.001	0.016	0.001	0.004	0.055	0.007	0.002	NA	NA	NA	NA	NA	NA	NA	NA
AG_Plant pathogens	AG_Invert. decomposers	0.005	0.009	0.028	0.001	0.004	0.023	0.009	0.001	NA	NA	NA	NA	NA	NA	NA	NA
AG_Plant pathogens	AG_Secondary consumers	0.036	0.001	0.009	0.002	0.011	0.001	<0.001	0.822	NA	NA	NA	NA	NA	NA	NA	NA
AG_Plant pathogens	AG_Tertiary consumers	0.160	0.001	0.076	0.001	0.130	0.001	0.014	0.001	NA	NA	NA	NA	NA	NA	NA	NA
AG_Plant pathogens	BG_Mycorrhizae	0.199	0.001	0.094	0.001	0.006	0.007	0.017	0.001	NA	NA	NA	NA	NA	NA	NA	NA
AG_Plant pathogens	BG_Herbivores	0.004	0.033	<0.001	0.544	<0.001	0.521	0.004	0.013	NA	NA	NA	NA	NA	NA	NA	NA

AG_Plant pathogens	BG_Microbial decomposers	0.189	0.001	0.057	0.001	0.011	0.001	<0.001	0.464	NA	NA	NA	NA	NA	NA	NA	NA
AG_Plant pathogens	BG_Secondary consumers	0.004	0.029	0.020	0.001	0.008	0.002	0.041	0.001	NA	NA	NA	NA	NA	NA	NA	NA
AG_Plant pathogens	BG_Bacterivores	0.074	0.001	0.025	0.001	0.004	0.023	0.002	0.093	NA	NA	NA	NA	NA	NA	NA	NA
AG_Herbivores	AG_Pollinators	0.147	0.001	0.058	0.001	0.078	0.001	0.069	0.001	0.107	0.001	0.032	0.001	0.029	0.001	0.018	0.001
AG_Herbivores	AG_Invert. decomposers	0.021	0.001	0.023	0.001	0.015	0.001	0.012	0.001	NA	NA	NA	NA	NA	NA	NA	NA
AG_Herbivores	AG_Secondary consumers	0.117	0.001	0.035	0.001	0.098	0.001	0.030	0.001	0.098	0.001	0.017	0.001	0.028	0.001	<0.001	0.609
AG_Herbivores	AG_Tertiary consumers	0.138	0.001	0.090	0.001	0.126	0.001	0.018	0.001	0.107	0.001	0.135	0.001	0.054	0.001	0.051	0.001
AG_Herbivores	BG_Mycorrhizae	0.238	0.001	0.120	0.001	0.045	0.001	0.053	0.001	0.131	0.001	0.041	0.001	0.048	0.001	0.004	0.052
AG_Herbivores	BG_Herbivores	0.033	0.001	0.005	0.032	0.032	0.001	<0.001	0.958	0.007	0.009	0.006	0.011	<0.001	0.513	0.007	0.004
AG_Herbivores	BG_Microbial decomposers	0.284	0.001	0.063	0.001	0.027	0.001	0.067	0.001	0.176	0.001	0.029	0.001	0.049	0.001	0.005	0.064
AG_Herbivores	BG_Secondary consumers	0.004	0.036	0.033	0.001	<0.001	0.554	0.016	0.001	0.014	0.001	0.044	0.001	0.003	0.048	0.018	0.001
AG_Herbivores	BG_Bacterivores	0.102	0.001	0.047	0.001	0.034	0.001	0.008	0.003	0.039	0.001	0.022	0.001	0.006	0.011	0.013	0.001
AG_Pollinators	AG_Invert. decomposers	0.017	0.001	0.002	0.139	0.011	0.002	0.001	0.423	NA	NA	NA	NA	NA	NA	NA	NA
AG_Pollinators	AG_Secondary consumers	0.188	0.001	0.007	0.011	0.142	0.001	0.025	0.001	0.200	0.001	0.007	0.009	0.112	0.001	0.001	0.178
AG_Pollinators	AG_Tertiary consumers	0.011	0.005	0.009	0.003	0.007	0.009	0.003	0.104	0.003	0.110	0.013	0.001	<0.001	0.907	0.001	0.345
AG_Pollinators	BG_Mycorrhizae	0.048	0.001	0.046	0.001	0.047	0.001	0.019	0.001	0.020	0.001	0.022	0.001	0.014	0.002	0.008	0.005
AG_Pollinators	BG_Herbivores	0.104	0.001	0.003	0.122	0.028	0.001	0.008	0.003	0.067	0.001	0.001	0.255	0.025	0.001	0.001	0.420
AG_Pollinators	BG_Microbial decomposers	0.054	0.001	0.053	0.001	0.054	0.001	0.056	0.001	0.107	0.001	0.016	0.003	0.035	0.001	<0.001	0.679
AG_Pollinators	BG_Secondary consumers	0.003	0.108	0.002	0.184	0.008	0.007	0.004	0.050	0.014	0.002	<0.001	0.956	0.003	0.142	<0.001	0.636
AG_Pollinators	BG_Bacterivores	0.044	0.001	0.065	0.001	0.069	0.001	0.017	0.002	0.021	0.001	0.027	0.001	0.007	0.017	0.001	0.487
AG_Invert. decomposers	AG_Secondary consumers	0.015	0.001	0.023	0.001	0.003	0.101	0.037	0.001	NA	NA	NA	NA	NA	NA	NA	NA
AG_Invert. decomposers	AG_Tertiary consumers	0.001	0.246	0.006	0.008	0.014	0.001	0.017	0.001	NA	NA	NA	NA	NA	NA	NA	NA
AG_Invert. decomposers	BG_Mycorrhizae	0.007	0.003	<0.001	0.683	0.007	0.008	0.004	0.100	NA	NA	NA	NA	NA	NA	NA	NA
AG_Invert. decomposers	BG_Herbivores	0.001	0.358	0.009	0.003	0.001	0.462	0.035	0.001	NA	NA	NA	NA	NA	NA	NA	NA
AG_Invert. decomposers	BG_Microbial decomposers	0.009	0.001	0.004	0.049	0.024	0.001	0.013	0.001	NA	NA	NA	NA	NA	NA	NA	NA
AG_Invert. decomposers	BG_Secondary consumers	0.004	0.024	<0.001	0.427	<0.001	0.574	<0.001	0.490	NA	NA	NA	NA	NA	NA	NA	NA
AG_Invert. decomposers	BG_Bacterivores	0.001	0.294	0.002	0.111	0.002	0.195	0.027	0.001	NA	NA	NA	NA	NA	NA	NA	NA
AG_Secondary consumers	AG_Tertiary consumers	<0.001	0.666	0.002	0.215	0.001	0.249	0.002	0.164	0.025	0.001	0.018	0.001	0.041	0.001	0.014	0.001
AG_Secondary consumers	BG_Mycorrhizae	0.057	0.001	0.041	0.001	0.039	0.001	0.001	0.272	0.047	0.001	0.010	0.001	0.031	0.001	0.001	0.349

AG_Secondary consumers	BG_Herbivores	0.044	0.001	0.011	0.001	0.022	0.001	0.003	0.059	0.045	0.001	0.004	0.049	0.035	0.001	0.001	0.249
AG_Secondary consumers	BG_Microbial decomposers	0.062	0.001	0.043	0.001	0.054	0.001	0.021	0.001	0.177	0.001	0.066	0.001	0.095	0.001	0.031	0.001
AG_Secondary consumers	BG_Secondary consumers	0.017	0.001	0.032	0.001	0.003	0.084	0.002	0.175	0.018	0.001	0.012	0.001	0.009	0.001	0.002	0.072
AG_Secondary consumers	BG_Bacterivores	0.075	0.001	0.011	0.001	0.044	0.001	0.009	0.004	0.039	0.001	0.009	0.004	0.008	0.008	0.005	0.017
AG_Tertiary consumers	BG_Mycorrhizae	0.122	0.001	0.026	0.001	0.007	0.004	0.005	0.041	0.085	0.001	0.086	0.001	0.043	0.001	0.043	0.001
AG_Tertiary consumers	BG_Herbivores	0.002	0.183	<0.001	0.945	0.004	0.020	<0.001	0.686	0.004	0.032	<0.001	0.888	0.002	0.212	<0.001	0.844
AG_Tertiary consumers	BG_Microbial decomposers	0.125	0.001	0.010	0.004	<0.001	0.633	0.016	0.001	0.112	0.001	0.121	0.001	0.111	0.001	0.147	0.001
AG_Tertiary consumers	BG_Secondary consumers	<0.001	0.809	0.001	0.305	0.027	0.001	0.008	0.007	<0.001	0.754	0.002	0.089	<0.001	0.836	0.002	0.097
AG_Tertiary consumers	BG_Bacterivores	0.025	0.001	0.004	0.051	<0.001	0.516	0.013	0.001	0.007	0.006	0.030	0.001	0.001	0.243	0.016	0.001
BG_Mycorrhizae	BG_Herbivores	0.021	0.001	0.007	0.016	0.046	0.001	0.028	0.001	0.006	0.020	0.011	0.002	0.001	0.361	0.009	0.002
BG_Mycorrhizae	BG_Microbial decomposers	0.356	0.001	0.281	0.001	0.076	0.001	0.064	0.001	0.233	0.001	0.153	0.001	0.113	0.001	0.028	0.001
BG_Mycorrhizae	BG_Secondary consumers	0.003	0.043	0.081	0.001	<0.001	0.574	0.005	0.047	0.021	0.001	0.019	0.001	0.016	0.001	0.028	0.001
BG_Mycorrhizae	BG_Bacterivores	0.209	0.001	0.140	0.001	0.011	0.002	0.032	0.001	0.084	0.001	0.083	0.001	0.008	0.002	0.021	0.001
BG_Herbivores	BG_Microbial decomposers	0.023	0.001	0.030	0.001	0.008	0.013	0.019	0.002	0.035	0.001	0.006	0.053	0.035	0.001	<0.001	0.705
BG_Herbivores	BG_Secondary consumers	0.036	0.001	0.002	0.097	<0.001	0.680	0.007	0.007	0.094	0.001	0.056	0.001	0.058	0.001	0.036	0.001
BG_Herbivores	BG_Bacterivores	0.072	0.001	0.074	0.001	0.003	0.112	0.024	0.001	0.033	0.001	0.077	0.001	0.014	0.001	0.057	0.001
BG_Microbial decomposers	BG_Secondary consumers	0.001	0.166	0.077	0.001	0.009	0.003	0.001	0.304	0.021	0.001	0.023	0.001	0.009	0.009	0.002	0.160
BG_Microbial decomposers	BG_Bacterivores	0.103	0.001	0.197	0.001	0.010	0.003	0.072	0.001	0.069	0.001	0.050	0.001	0.011	0.003	0.001	0.494
BG_Secondary consumers	BG_Bacterivores	0.051	0.001	0.034	0.001	0.001	0.232	0.009	0.008	0.017	0.001	0.005	0.022	<0.001	0.730	0.004	0.026

Table S6-2 | Null model approach to test for significant differences in correlations between low and high land-use intensity (LUI) plots.

Differences in observed R²-values (see Table S6-1) between low and high LUI plots were compared to a distribution of simulated R²-values differences (n=1899) where we randomized the LUI differences between plots. Based on this random distribution we calculated z-scores (zsc) and p-values (p). Significant values thus indicate stronger trophic interactions at lower (or higher) LUI than expected by chance. mean.ran: mean of the randomization per pair of groups and per diversity level (q0, β_{sim} , q1, q2), sd.ran: sd of the randomization per pair of groups and per diversity level, diffR.true: true value for the difference R_{2highLUI} - R_{2lowLUI}, AG=Aboveground, BG=Belowground, NA: for plant pathogens no abundance data was available and for invertebrate decomposers calculations for higher q-levels were not possible due to low abundance.

Trophic group 1	Trophic group 2	CatCo mpart	CatTroph	Soerensen Index β_{sor} (q0)					Species turnover component β_{sim}					exp. Shannon (q1)					inv. Simpson (q2)				
				mean .ran	sd.r an	diffR. true	zsc	p	mean .ran	sd.r an	diffR. true	zsc	p	mean .ran	sd.r an	diffR. true	zsc	p	mean .ran	sd.r an	diffR. true	zsc	p
AG_Primary producer	AG_Plant pathogens	AG-AG	PrimProdPr imCons	<0.00 15	0.0 271	0.296 0	10.90 21	<<0.0 011	<0.00 13	0.0 257	0.170 0	6.63 56	<<0.0 011	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
AG_Primary producer	AG_Herbivores	AG-AG	PrimProdPr imCons	<0.00 16	0.0 327	0.302 0	9.255 9	<<0.0 011	<0.00 16	0.0 313	0.213 0	6.77 68	<<0.0 011	<0.00 12	0.0 314	0.173 0	5.497 4	<<0.0 011	<0.00 12	0.0 226	0.054 0	2.395 5	0.016 6
AG_Primary producer	AG_Pollinators	AG-AG	PrimProdPr imCons	<0.00 14	0.0 187	0.141 0	7.559 7	<<0.0 011	<0.00 12	0.0 156	0.008 0	0.49 73	0.619 0	<0.00 13	0.0 146	0.049 0	3.364 7	<0.00 18	<0.00 12	0.0 088	0.011 0	1.265 6	0.205 7
AG_Primary producer	AG_Invert. decomposers	AG-AG	others	<0.00 11	0.0 130	0.006 0	0.468 6	0.639 4	<0.00 11	0.0 013	0.004 0	3.05 61	0.002 2	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
AG_Primary producer	AG_Secondary consumers	AG-AG	others	<0.00 11	0.0 196	0.092 0	4.697 6	<<0.0 011	<0.00 12	0.0 174	0.039 0	2.24 67	0.024 7	<0.00 11	0.0 149	0.106 0	7.124 1	<<0.0 011	<0.00 13	0.0 110	0.061 0	5.533 6	<<0.0 011
AG_Primary producer	AG_Tertiary consumers	AG-AG	others	<0.00 14	0.0 197	0.125 0	6.311 1	<<0.0 011	<0.00 12	0.0 185	0.138 0	7.44 04	<<0.0 011	<0.00 15	0.0 200	0.061 0	3.025 1	0.002 5	<0.00 12	0.0 169	0.015 0	0.896 7	0.369 9
AG_Primary producer	BG_Mycorrhizae	AG-BG	PrimProdPr imCons	<0.00 11	0.0 326	0.218 0	6.697 7	<<0.0 011	<0.00 15	0.0 240	0.014 0	0.56 41	0.572 7	<<0.0 011	0.0 294	0.087 0	2.960 2	0.003 1	<0.00 17	0.0 236	0.020 0	0.817 1	0.413 9
AG_Primary producer	BG_Herbivores	AG-BG	PrimProdPr imCons	<0.00 11	0.0 072	0.005 0	0.703 1	0.482 0	<0.00 15	0.0 108	0.023 0	2.17 95	0.029 3	<<0.0 011	0.0 018	0.004 0	2.217 4	0.026 6	<0.00 11	0.0 016	0.008 0	5.023 9	<<0.0 011
AG_Primary producer	BG_Microbial decomposers	AG-BG	others	<0.00 12	0.0 310	0.255 0	8.245 3	<<0.0 011	<0.00 11	0.0 126	0.133 0	10.5 349	<<0.0 011	<0.00 14	0.0 231	0.139 0	6.005 4	<<0.0 011	<0.00 12	0.0 114	0.071 0	6.215 5	<<0.0 011

AG_Primary producer	BG_Secondary consumers	AG-BG	others	- <0.00 12	0.0 077	0.035 0	4.572 9	<<0.0 011	- <0.00 11	0.0 100	- 0.003 0	- 0.28 69	0.774 2	- <0.00 12	0.0 097	0.010 0	1.049 8	0.293 8	- <0.00 11	0.0 060	0.007 0	1.173 0	0.240 8
AG_Primary producer	BG_Bacterivores	AG-BG	others	- 0.001 3	0.0 311	- 0.039 0	- 1.212 8	0.225 2	<0.00 12	0.0 187	0.037 0	1.96 73	0.049 1	0.001 5	0.0 267	0.109 0	4.029 5	<0.00 11	<0.00 11	0.0 154	0.054 0	3.500 3	<0.00 15
AG_Plant pathogens	AG_Herbivores	AG-AG	others	- <0.00 18	0.0 246	0.106 0	- 4.275 2	<<0.0 011	<0.00 13	0.0 224	0.064 0	2.86 25	0.004 2	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
AG_Plant pathogens	AG_Pollinators	AG-AG	others	<0.00 14	0.0 122	- 0.006 0	- 0.522 9	0.601 0	<0.00 12	0.0 056	0.003 0	0.51 13	0.609 1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
AG_Plant pathogens	AG_Invert. decomposers	AG-AG	others	- <0.00 14	0.0 111	0.023 0	2.102 0	0.035 6	<<0.0 011	0.0 013	0.005 0	3.76 48	<0.00 12	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
AG_Plant pathogens	AG_Secondary consumers	AG-AG	others	<0.00 12	0.0 103	0.027 0	2.610 4	0.009 0	<<0.0 011	0.0 049	0.011 0	2.25 73	0.024 0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
AG_Plant pathogens	AG_Tertiary consumers	AG-AG	others	0.001 0	0.0 241	- 0.084 0	- 3.529 4	<0.00 14	<0.00 11	0.0 191	- 0.116 0	- 6.08 96	<<0.0 011	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
AG_Plant pathogens	BG_Mycorrhizae	AG-BG	others	- <0.00 11	0.0 267	- 0.105 0	- 3.933 1	<0.00 11	- <0.00 11	0.0 115	0.011 0	0.96 33	0.335 4	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
AG_Plant pathogens	BG_Herbivores	AG-BG	others	<0.00 11	0.0 026	0.004 0	1.600 4	0.109 5	<0.00 12	0.0 032	0.004 0	1.21 53	0.224 3	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
AG_Plant pathogens	BG_Microbial decomposers	AG-BG	others	- <0.00 12	0.0 236	0.132 0	- 5.589 0	<<0.0 011	<<0.0 011	0.0 028	- 0.011 0	- 3.93 66	<0.00 11	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
AG_Plant pathogens	BG_Secondary consumers	AG-BG	others	- <0.00 11	0.0 058	0.016 0	2.763 0	0.005 7	<0.00 11	0.0 027	0.033 0	12.1 087	<<0.0 011	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
AG_Plant pathogens	BG_Bacterivores	AG-BG	others	<0.00 15	0.0 182	0.049 0	2.721 5	0.006 5	<<0.0 011	0.0 054	0.002 0	0.36 02	0.718 7	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
AG_Herbivores	AG_Pollinators	AG-AG	others	<0.00 15	0.0 182	0.089 0	4.922 6	<<0.0 011	<0.00 11	0.0 172	0.009 0	0.52 95	0.596 4	<0.00 12	0.0 164	0.075 0	4.559 6	<<0.0 011	<0.00 14	0.0 109	0.011 0	1.049 4	0.294 0
AG_Herbivores	AG_Invert. decomposers	AG-AG	others	- <0.00 12	0.0 117	0.002 0	0.190 2	0.849 1	<<0.0 011	0.0 048	- 0.003 0	- 0.61 51	0.538 5	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
AG_Herbivores	AG_Secondary consumers	AG-AG	PrimConsS ecCons	<0.00 11	0.0 169	- 0.082 0	- 4.849 6	<<0.0 011	<0.00 17	0.0 166	- 0.068 0	- 4.12 96	<<0.0 011	<0.00 11	0.0 135	- 0.081 0	- 5.997 7	<<0.0 011	<<0.0 011	0.0 057	- 0.028 0	- 4.963 5	<<0.0 011
AG_Herbivores	AG_Tertiary consumers	AG-AG	PrimConsT ertCons	<0.00 14	0.0 251	- 0.048 0	- 1.930 2	0.053 6	- <0.00 17	0.0 201	- 0.108 0	- 5.34 16	<<0.0 011	<0.00 11	0.0 242	0.028 0	1.158 4	0.246 7	<0.00 11	0.0 146	- 0.003 0	- 0.215 1	0.829 7

AG_Herbivores	BG_Mycorrhizae	AG-BG	others	0.001 0	0.0 285	0.118 0	4.103 7	<<0.0 011	<0.00 14	0.0 197	0.008 0	0.38 69	0.698 8	<0.00 19	0.0 258	0.090 0	3.531 3	<0.00 14	<0.00 11	0.0 151	0.044 0	2.930 8	0.003 4
AG_Herbivores	BG_Herbivores	AG-BG	others	<<0.0 011	0.0 059	0.028 0	4.781 9	<<0.0 011	<<0.0 011	0.0 066	0.032 0	4.86 98	<<0.0 011	<0.00 11	0.0 012	0.001 0	0.869 0	0.384 8	<0.00 11	0.0 019	0.007 0	3.723 3	<0.00 12
AG_Herbivores	BG_Microbial decomposers	AG-BG	others	<0.00 19	0.0 292	0.221 0	7.534 0	<<0.0 011	<0.00 13	0.0 113	0.040 0	3.52 63	<0.00 14	<0.00 12	0.0 179	0.147 0	8.234 7	<<0.0 011	<<0.0 011	0.0 059	0.044 0	7.447 0	<<0.0 011
AG_Herbivores	BG_Secondary consumers	AG-BG	others	<0.00 11	0.0 052	0.029 0	5.581 4	<<0.0 011	<0.00 11	0.0 057	0.016 0	2.79 43	0.005 2	<0.00 11	0.0 127	0.030 0	2.355 6	0.018 5	<0.00 11	0.0 087	0.015 0	1.710 5	0.087 2
AG_Herbivores	BG_Bacterivores	AG-BG	others	<0.00 16	0.0 243	0.055 0	2.232 6	0.025 6	<0.00 11	0.0 139	0.026 0	1.85 56	0.063 5	<0.00 11	0.0 153	0.017 0	1.116 3	0.264 3	<0.00 11	0.0 068	0.007 0	1.011 5	0.311 8
AG_Pollinators	AG_Invert. decomposers	AG-AG	others	<<0.0 011	0.0 050	0.015 0	2.999 7	0.002 7	<<0.0 011	0.0 043	0.010 0	2.32 72	0.020 0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
AG_Pollinators	AG_Secondary consumers	AG-AG	PrimConsS ecCons	<0.00 14	0.0 173	0.181 0	10.47 52	<<0.0 011	<0.00 16	0.0 168	0.117 0	7.00 57	<<0.0 011	<0.00 12	0.0 164	0.193 0	11.76 76	<<0.0 011	<<0.0 011	0.0 104	0.111 0	10.65 58	<<0.0 011
AG_Pollinators	AG_Tertiary consumers	AG-AG	PrimConsT ertCons	<0.00 11	0.0 019	0.002 0	1.100 2	0.271 2	<0.00 11	0.0 042	0.004 0	0.98 19	0.326 2	<0.00 11	0.0 026	0.010 0	3.855 4	<0.00 11	<<0.0 011	0.0 013	0.001 0	0.717 6	0.473 0
AG_Pollinators	BG_Mycorrhizae	AG-BG	others	<0.00 12	0.0 158	0.002 0	0.112 4	0.910 5	<0.00 11	0.0 130	0.028 0	2.16 44	0.030 4	<0.00 13	0.0 104	0.002 0	0.218 2	0.827 2	<0.00 11	0.0 065	0.006 0	0.933 7	0.350 5
AG_Pollinators	BG_Herbivores	AG-BG	others	<0.00 12	0.0 152	0.101 0	6.631 5	<<0.0 011	<0.00 12	0.0 107	0.020 0	1.88 96	0.058 8	<0.00 12	0.0 106	0.066 0	6.208 3	<<0.0 011	<0.00 11	0.0 068	0.024 0	3.493 5	<0.00 15
AG_Pollinators	BG_Microbial decomposers	AG-BG	others	<0.00 15	0.0 154	0.001 0	0.032 3	0.974 2	<<0.0 011	0.0 169	0.002 0	0.11 76	0.906 4	<<0.0 011	0.0 114	0.091 0	8.005 7	<<0.0 011	<<0.0 011	0.0 027	0.035 0	13.13 95	<<0.0 011
AG_Pollinators	BG_Secondary consumers	AG-BG	others	<0.00 11	0.0 031	0.001 0	0.352 1	0.724 8	<<0.0 011	0.0 051	0.004 0	0.78 61	0.431 8	<0.00 11	0.0 061	0.014 0	2.303 6	0.021 2	<<0.0 011	0.0 026	0.003 0	1.172 6	0.241 0
AG_Pollinators	BG_Bacterivores	AG-BG	others	<0.00 11	0.0 173	0.021 0	1.218 2	0.223 1	<0.00 13	0.0 135	0.052 0	3.82 32	<0.00 11	<0.00 14	0.0 120	0.006 0	0.466 7	0.640 7	<0.00 12	0.0 050	0.006 0	1.232 4	0.217 8
AG_Invert. decomposers	AG_Secondary consumers	AG-AG	PrimConsS ecCons	<<0.0 011	0.0 112	0.008 0	0.712 5	0.476 2	<0.00 13	0.0 084	0.034 0	3.99 32	<0.00 11	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
AG_Invert. decomposers	AG_Tertiary consumers	AG-AG	PrimConsT ertCons	<0.00 12	0.0 079	0.005 0	0.651 2	0.514 9	<0.00 11	0.0 013	0.003 0	2.24 61	0.024 7	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
AG_Invert. decomposers	BG_Mycorrhizae	AG-BG	others	<<0.0 011	0.0 061	0.007 0	1.150 8	0.249 8	<0.00 12	0.0 060	0.003 0	0.52 71	0.598 1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
AG_Invert. decomposers	BG_Herbivores	AG-BG	others	<0.00 11	0.0 037	0.008 0	2.194 9	0.028 2	<0.00 11	0.0 083	0.034 0	4.09 59	<<0.0 011	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA

AG_Invert. decomposers	BG_Microbial decomposers	AG-BG	others	- <0.00 11	0.0 079	- 0.005 0	- 0.611 5	0.540 9	- <0.00 14	0.0 085	- 0.011 0	- 1.25 68	0.208 8	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
AG_Invert. decomposers	BG_Secondary consumers	AG-BG	others	<<0.0 011	0.0 019	- 0.004 0	- 2.069 8	0.038 5	<0.00 11	0.0 028	<<0.0 011	- 0.02 19	0.982 6	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
AG_Invert. decomposers	BG_Bacterivores	AG-BG	others	<<0.0 011	0.0 049	0.001 0	0.211 2	0.832 7	- <0.00 12	0.0 047	0.025 0	5.32 51	<<0.0 011	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
AG_Secondary consumers	AG_Tertiary consumers	AG-AG	SecConsTer tCons	<<0.0 011	0.0 014	0.002 0	1.470 2	0.141 5	<0.00 11	0.0 023	0.001 0	0.39 80	0.690 6	- <0.00 12	0.0 128	- 0.007 0	- 0.535 0	0.592 7	<<0.0 011	0.0 145	- 0.027 0	- 1.855 0	0.063 6
AG_Secondary consumers	BG_Mycorrhizae	AG-BG	others	<0.00 14	0.0 174	- 0.016 0	- 0.944 6	0.344 9	<0.00 12	0.0 097	- 0.038 0	- 3.92 74	<0.00 11	<0.00 11	0.0 137	- 0.037 0	- 2.717 8	0.006 6	<0.00 11	0.0 099	- 0.030 0	- 3.015 0	0.002 6
AG_Secondary consumers	BG_Herbivores	AG-BG	others	<0.00 13	0.0 119	- 0.033 0	- 2.806 1	0.005 0	- <0.00 12	0.0 082	0.019 0	2.29 67	0.021 6	<<0.0 011	0.0 107	0.041 0	- 3.837 3	<0.00 11	<0.00 12	0.0 085	0.034 0	- 3.979 1	<0.00 11
AG_Secondary consumers	BG_Microbial decomposers	AG-BG	others	<0.00 12	0.0 161	- 0.019 0	- 1.198 8	0.230 6	- <0.00 11	0.0 128	- 0.033 0	- 2.56 15	0.010 4	- <0.00 16	0.0 218	- 0.111 0	- 5.064 4	<<0.0 011	<0.00 11	0.0 165	- 0.064 0	- 3.882 0	<0.00 11
AG_Secondary consumers	BG_Secondary consumers	AG-BG	others	<0.00 12	0.0 084	0.015 0	1.760 4	0.078 3	<<0.0 011	0.0 021	- 0.001 0	- 0.48 13	0.630 3	<0.00 13	0.0 064	- 0.006 0	- 0.984 9	0.324 7	<0.00 11	0.0 040	- 0.007 0	- 1.801 3	0.071 6
AG_Secondary consumers	BG_Bacterivores	AG-BG	others	- <0.00 11	0.0 148	- 0.064 0	- 4.302 3	<<0.0 011	- <0.00 13	0.0 096	- 0.035 0	- 3.60 52	<0.00 13	<0.00 13	0.0 139	- 0.030 0	- 2.182 5	0.029 1	- <0.00 14	0.0 090	- 0.003 0	- 0.283 0	0.777 2
AG_Tertiary consumers	BG_Mycorrhizae	AG-BG	others	<0.00 13	0.0 198	- 0.096 0	- 4.874 2	<<0.0 011	<0.00 13	0.0 084	- 0.002 0	- 0.27 66	0.782 1	<0.00 19	0.0 213	0.001 0	0.003 2	0.997 4	- <0.00 13	0.0 160	<<0.0 011	0.020 3	0.983 8
AG_Tertiary consumers	BG_Herbivores	AG-BG	others	<0.00 11	0.0 032	- 0.002 0	- 0.650 2	0.515 5	<0.00 11	0.0 023	- 0.004 0	- 1.77 97	0.075 1	<<0.0 011	0.0 028	- 0.004 0	- 1.423 3	0.154 6	<<0.0 011	0.0 012	- 0.002 0	- 1.626 9	0.103 8
AG_Tertiary consumers	BG_Microbial decomposers	AG-BG	others	- <0.00 12	0.0 187	- 0.115 0	- 6.142 3	<<0.0 011	- <0.00 11	0.0 065	0.016 0	2.46 24	0.013 8	- <0.00 12	0.0 217	0.009 0	0.425 2	0.670 7	- <0.00 11	0.0 214	0.036 0	1.682 1	0.092 6
AG_Tertiary consumers	BG_Secondary consumers	AG-BG	others	<<0.0 011	0.0 013	0.001 0	0.780 2	0.435 3	- <0.00 13	0.0 091	- 0.019 0	- 2.04 57	0.040 8	<<0.0 011	0.0 012	0.002 0	1.740 3	0.081 8	<0.00 11	0.0 015	0.002 0	1.250 5	0.211 1
AG_Tertiary consumers	BG_Bacterivores	AG-BG	others	<0.00 11	0.0 079	- 0.021 0	- 2.686 4	0.007 2	<0.00 11	0.0 048	0.013 0	2.70 75	0.006 8	- <0.00 11	0.0 089	0.023 0	2.586 2	0.009 7	<<0.0 011	0.0 059	0.015 0	2.554 7	0.010 6
BG_Mycorrhizae	BG_Herbivores	BG-BG	others	<0.00 11	0.0 060	- 0.014 0	- 2.344 4	0.019 1	<0.00 11	0.0 125	- 0.018 0	- 1.45 05	0.146 9	<0.00 11	0.0 040	0.005 0	1.270 8	0.203 8	<<0.0 011	0.0 031	0.008 0	2.561 7	0.010 4
BG_Mycorrhizae	BG_Microbial decomposers	BG-BG	others	- <0.00 12	0.0 274	- 0.075 0	- 2.731 9	0.006 3	<0.00 11	0.0 163	- 0.012 0	- 0.74 60	0.455 6	<0.00 11	0.0 245	- 0.080 0	- 3.276 1	0.001 1	<<0.0 011	0.0 147	- 0.085 0	- 5.785 0	<<0.0 011

BG_Mycorrhizae	BG_Secondary consumers	BG-BG	others	<0.00 12	0.0 098	0.078 0	7.967 1	<<0.0 011	<<0.0 011	0.0 020	0.005 0	2.47 54	0.013 3	- 0.00 12	0.0 105	- 0.002 0	- 0.167 7	0.866 8	- 0.00 14	0.0 109	0.012 0	1.138 0	0.255 1
BG_Mycorrhizae	BG_Bacterivores	BG-BG	others	<<0.0 011	0.0 322	0.069 0	2.143 9	0.032 0	<<0.0 011	0.0 138	0.021 0	1.52 88	0.126 3	- 0.00 12	0.0 235	- 0.001 0	- 0.035 0	0.972 1	- 0.00 13	0.0 107	0.013 0	1.244 5	0.213 3
BG_Herbivores	BG_Microbial decomposers	BG-BG	others	<0.00 11	0.0 097	0.007 0	0.712 1	0.476 4	<0.00 11	0.0 096	0.011 0	1.13 91	0.254 7	<<0.0 011	0.0 102	- 0.029 0	- 2.852 0	0.004 3	<0.00 11	0.0 060	0.035 0	5.798 2	<<0.0 011
BG_Herbivores	BG_Secondary consumers	BG-BG	PrimConsS ecCons	<0.00 13	0.0 102	- 0.034 0	- 3.362 2	<0.00 18	<<0.0 011	0.0 013	0.007 0	5.20 97	<<0.0 011	<<0.0 011	0.0 163	- 0.038 0	- 2.335 0	0.019 5	<0.00 11	0.0 113	- 0.022 0	- 1.959 6	0.050 0
BG_Herbivores	BG_Bacterivores	BG-BG	others	<<0.0 011	0.0 168	0.002 0	0.119 6	0.904 8	<0.00 11	0.0 084	0.021 0	2.50 24	0.012 3	- 0.00 11	0.0 155	0.044 0	2.841 9	0.004 5	<<0.0 011	0.0 128	0.043 0	3.351 8	<0.00 18
BG_Microbial decomposers	BG_Secondary consumers	BG-BG	others	<<0.0 011	0.0 064	0.076 0	11.93 85	<<0.0 011	<0.00 11	0.0 054	0.008 0	- 1.50 44	0.132 5	<0.00 12	0.0 075	0.002 0	0.237 6	0.812 2	<0.00 11	0.0 014	- 0.007 0	- 5.096 4	<<0.0 011
BG_Microbial decomposers	BG_Bacterivores	BG-BG	PrimConsS ecCons	- 0.00 11	0.0 245	0.094 0	3.844 6	<0.00 11	<0.00 13	0.0 098	0.062 0	6.29 03	<<0.0 011	<0.00 13	0.0 170	- 0.019 0	- 1.136 1	0.255 9	- 0.00 11	0.0 047	- 0.010 0	- 2.085 2	0.037 0
BG_Secondary consumers	BG_Bacterivores	BG-BG	others	<0.00 13	0.0 149	- 0.017 0	- 1.160 2	0.246 0	<0.00 11	0.0 048	0.008 0	1.66 46	0.096 0	<0.00 14	0.0 097	- 0.012 0	- 1.281 1	0.200 2	<<0.0 011	0.0 022	0.004 0	1.806 5	0.070 8

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