

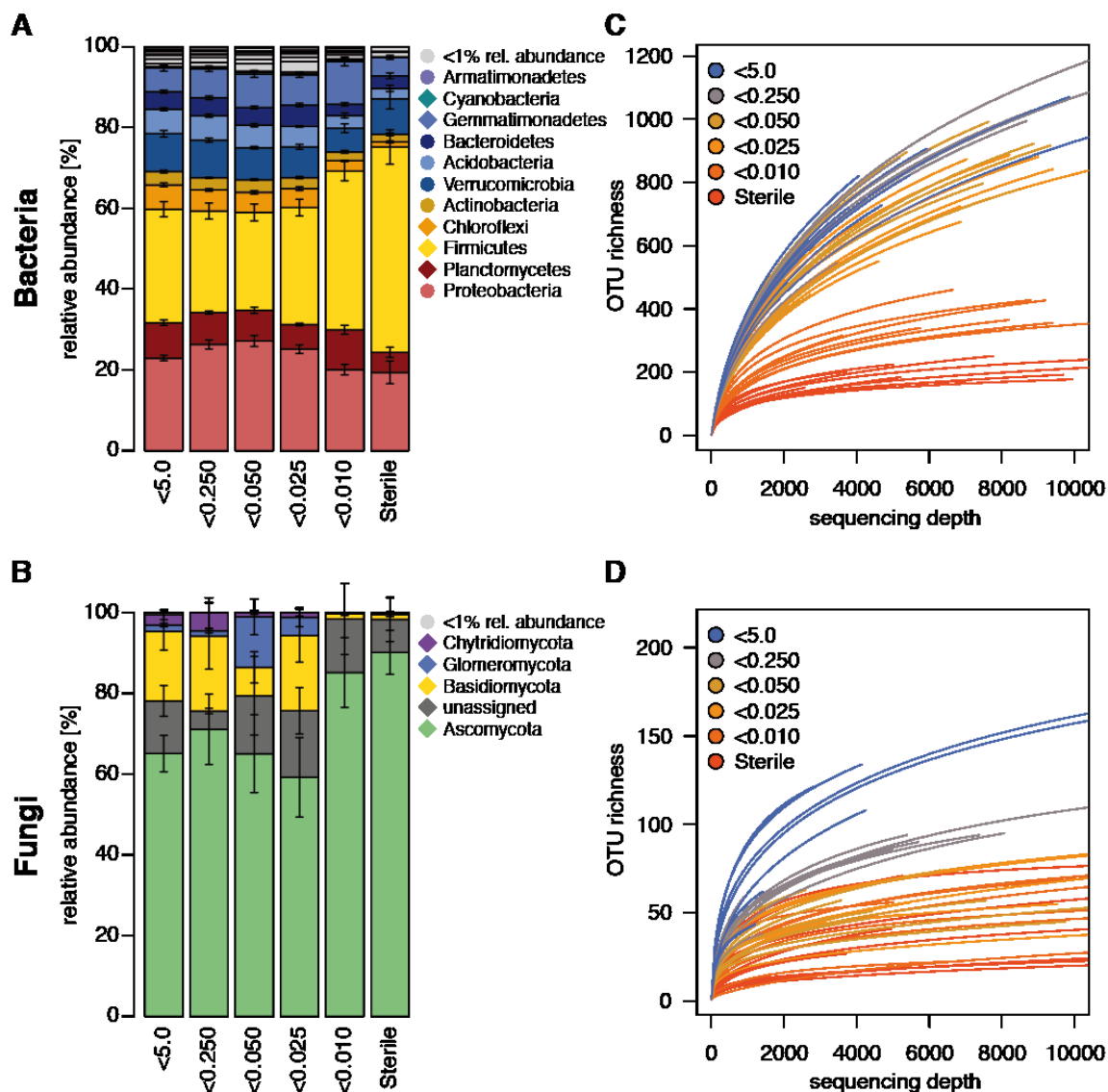
Supplementary Materials

Fungal-bacterial diversity and microbiome complexity predict ecosystem functioning

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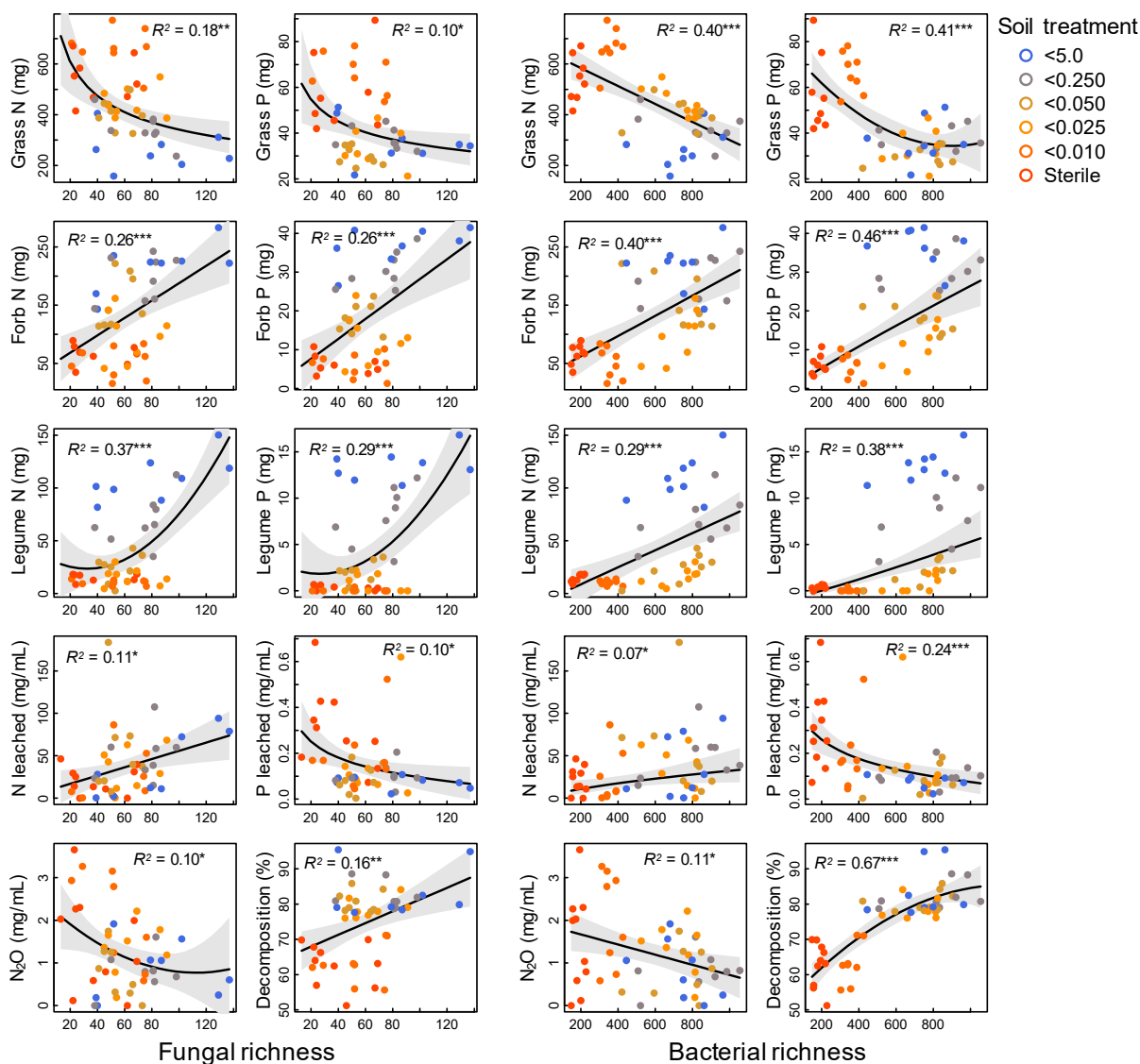
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34 **Fig. S1. Taxonomy and richness of soil bacteria and fungi.** The taxonomic composition of
 35 bacteria (per class) (A, C) and fungi (per phylum) (B, D) in microcosms with progressive
 36 filtering of soil biota. (A, B). Phyla with mean (\pm s.e.m.) relative abundances $>1\%$ are shown
 37 and Phyla varying significantly between treatments are indicated with a diamond symbol in the
 38 colour legend (ANOVA-like likelihood ratio test, $P < 0.05$ (FDR)). (C, D) Rarefaction curves
 39 depicting OTU richness as a function of sequencing depth were constructed by sub-sampling in
 40 increasing steps of 100 sequences per sample (the graphs were cropped at 10,000 sequences
 41 per sample for clarity). Individual samples are colored by treatment groups.

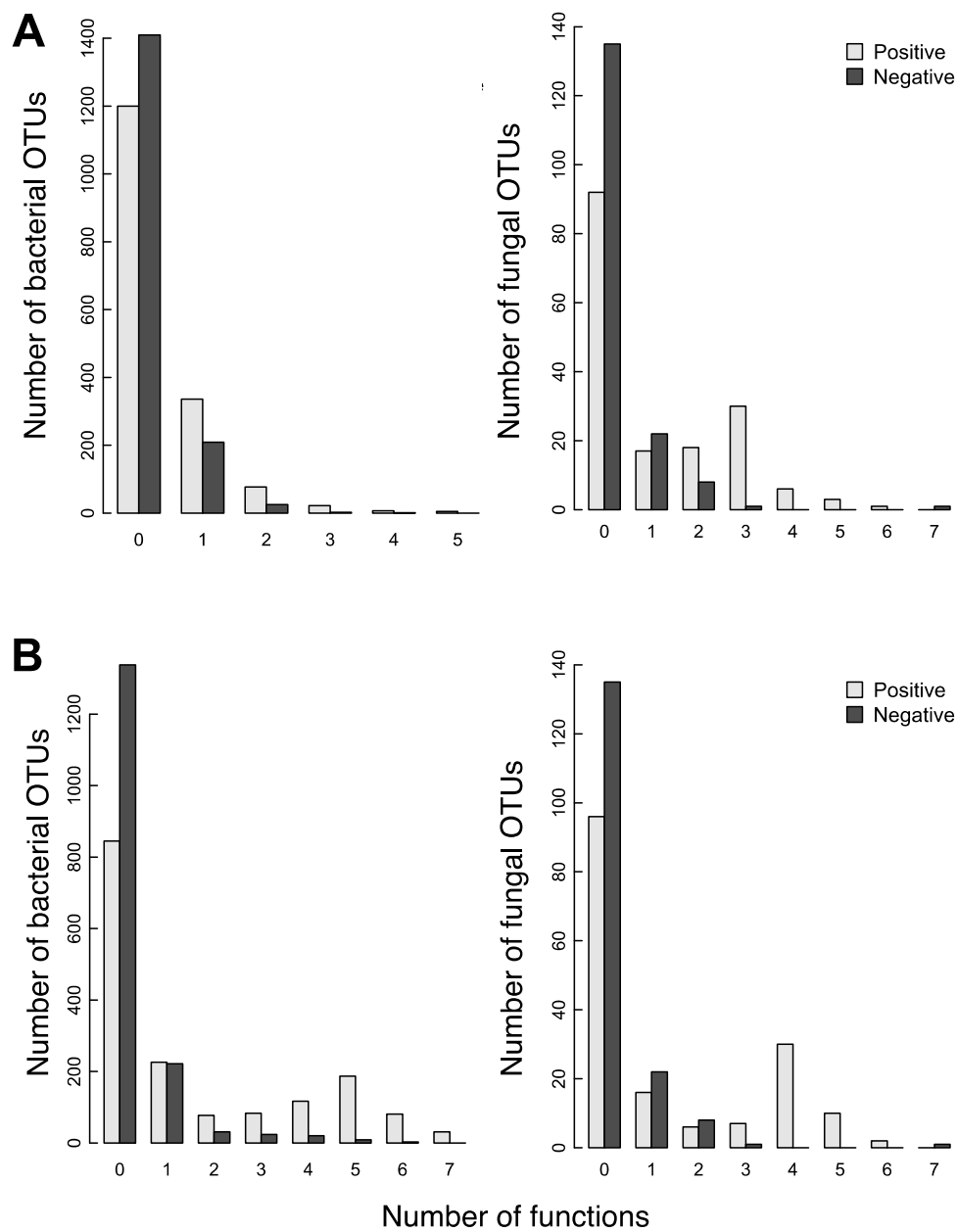
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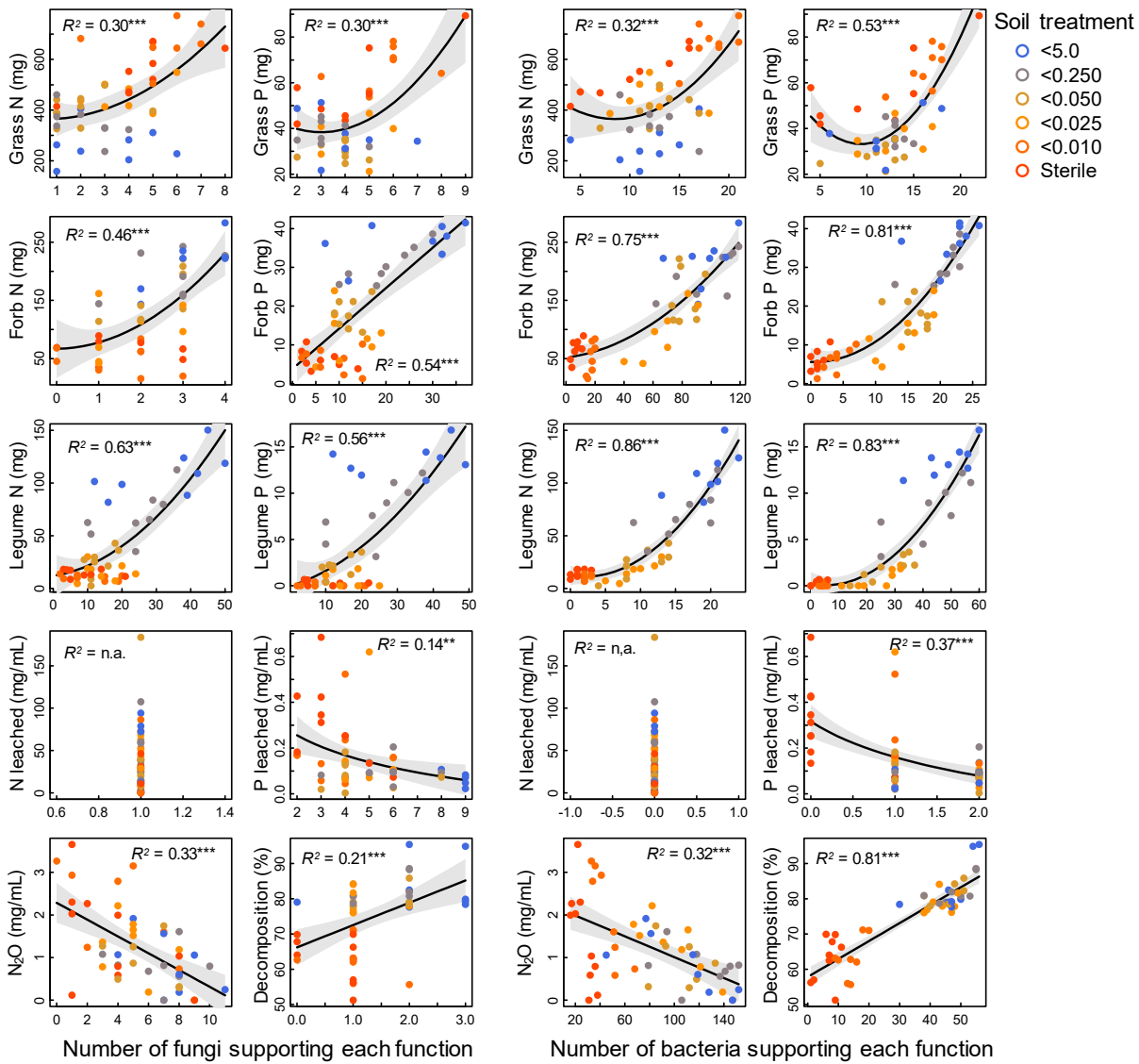
Fig. S2. Relationships between microbial richness and ecosystem functions. Relationships between fungal and bacterial OTU richness and ecosystem functions are shown. Points are colored by the filtering treatment. Solid lines are regression fits with the shaded region indicating the 95% confidence band. Relationships were fit using the best fitting regression (based on adjusted R^2 shown within each panel) using linear, second order polynomial and power function (log-log). Significance for the fit is indicated by * $P < 0.05$, ** $P < 0.01$ and *** $P < 0.001$.



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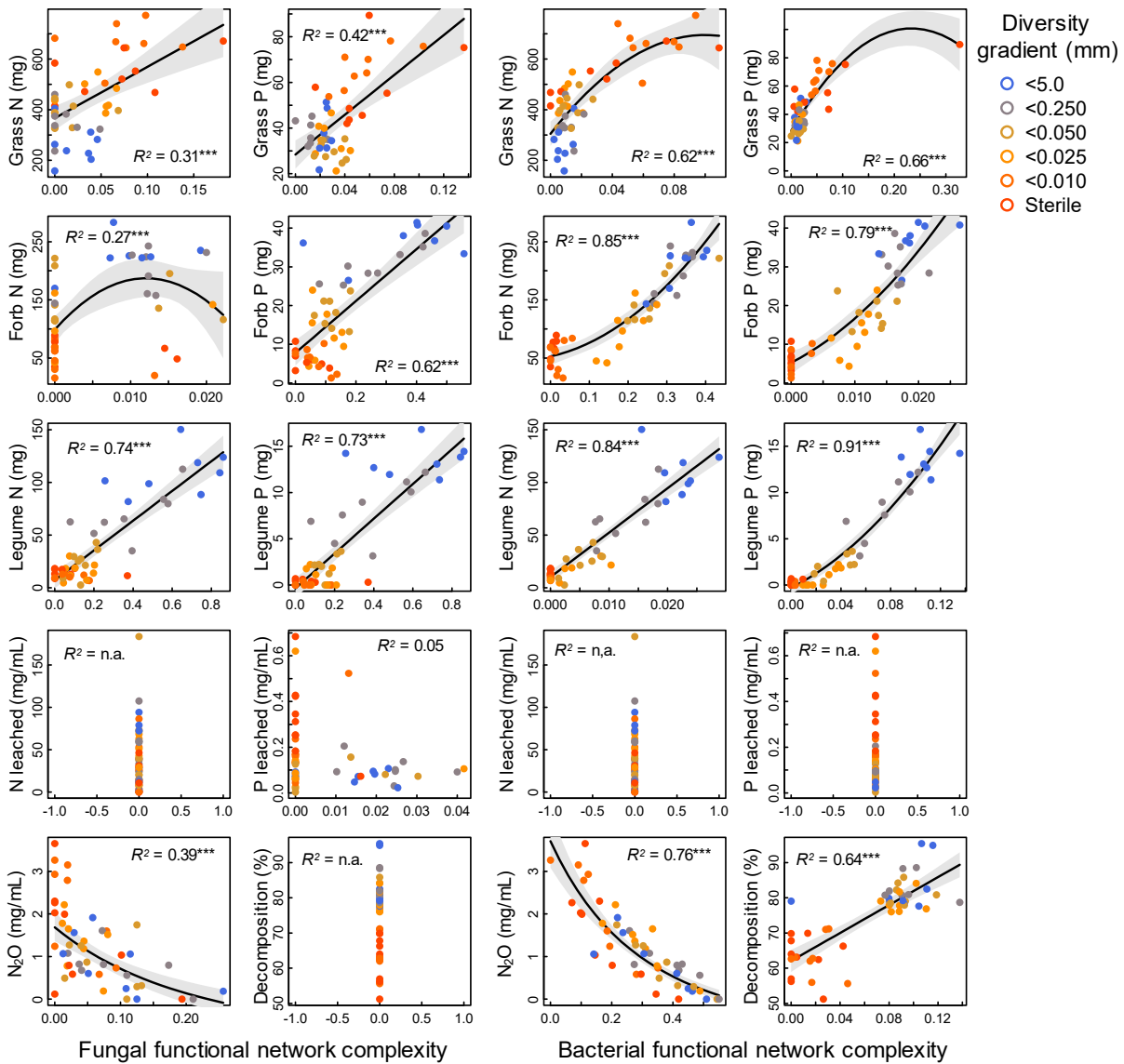
55 **Fig. S3. Number of taxa associated with number of functions.** (A) Using the elastic net
 56 method to simultaneously identify taxa that together best predict ecosystem functions and (B)
 57 using randomization tests considering each taxa independently to identify taxa that
 58 significantly (95% CI) relate to a function.

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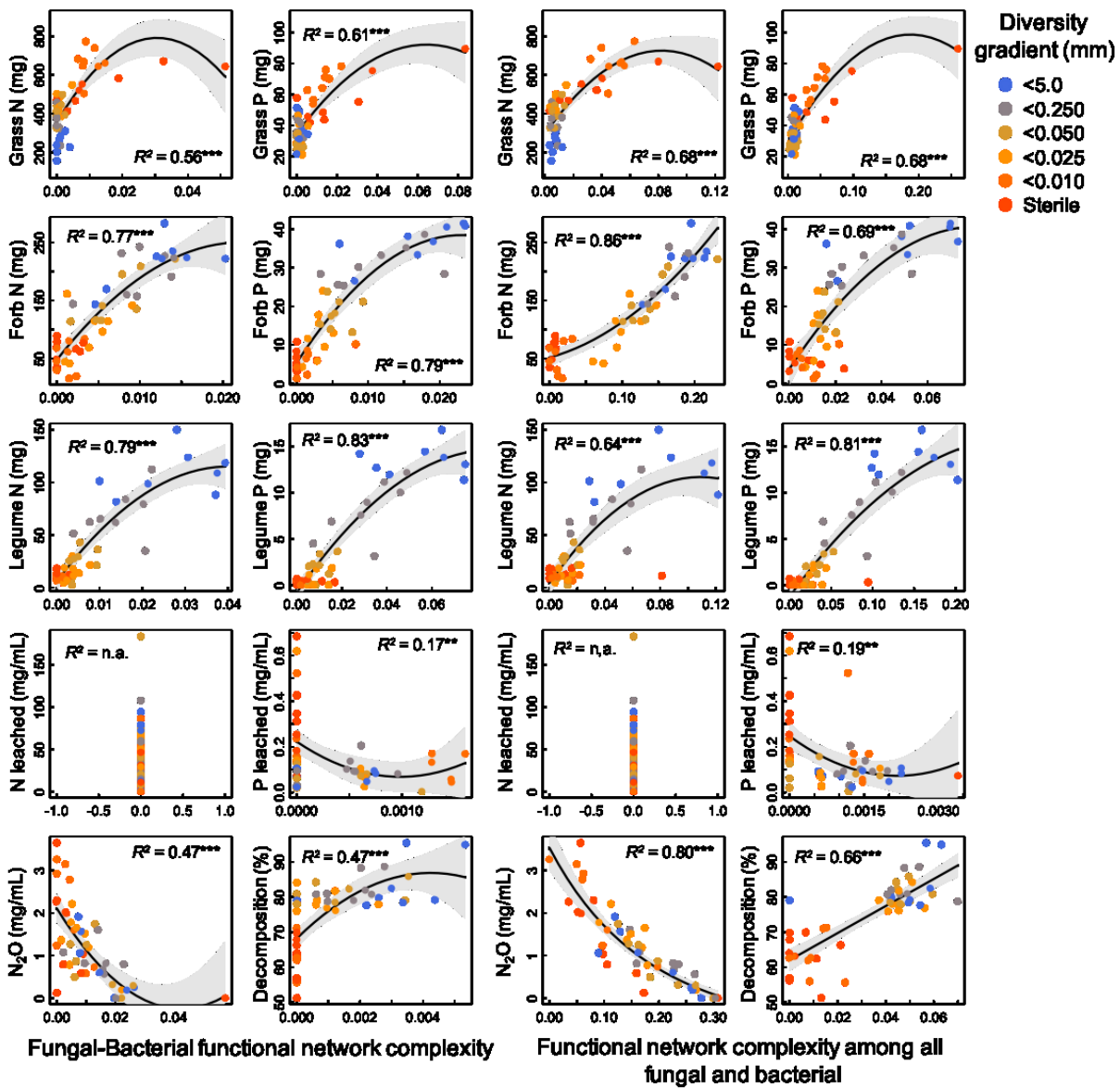


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Fig. S4. Relationships between each ecosystem function and the number of taxa present found to support each function. Relationships between the number of fungal and bacterial OTUs present that were found to support each function and the ecosystem function itself are shown. Points are colored by the filtering treatment. Solid lines are regression fits with the shaded region indicating the 95% confidence band. Relationships were fit using the best fitting regression (based on adjusted R^2 shown within each panel) using linear, second order polynomial and power function (log-log). Significance for the fit is indicated by $*P < 0.05$, $**P < 0.01$ and $***P < 0.001$. Note that there was only one fungal OTU detected who's abundance could predict a reduction in N leaching, which was an OTU present in every microcosm. Resultantly there are no relationships between N leaching and the taxa that best predict its reduction as indicated by $R^2 = \text{n.a.}$



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 75 **Fig. S5. Relationships between each ecosystem function and the fungal-fungal and**
 76 **bacterial-bacterial network complexity among taxa that support each function.** Points are
 77 colored by the filtering treatment. Solid lines are regression fits with the shaded region
 78 indicating the 95% confidence band. Relationships were fit using the best fitting regression
 79 (based on adjusted R^2 shown within each panel) using linear, second order polynomial and
 80 power function (log-log). Significance for the fit is indicated by * $P < 0.05$, ** $P < 0.01$ and
 81 *** $P < 0.001$.
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Fig. S6. Relationships between each ecosystem function and the network complexity among fungi-bacteria only and among all fungi and bacteria taxa that support each function. Points are colored by the filtering treatment. Solid lines are regression fits with the shaded region indicating the 95% confidence band. Relationships were fit using the best fitting regression (based on adjusted R^2 shown within each panel) using linear, second order polynomial and power function (log-log). Significance for the fit is indicated by * $P < 0.05$, ** $P < 0.01$ and *** $P < 0.001$.

93 **Table S1. Microbial community characteristics for each soil treatments.** The mean of each
 94 sieving treatment is provided. The F -ratio and degrees of freedom are provided for the
 95 variation across all treatments. ξ is the F -ratio and degrees of freedom for the variation among
 96 treatments after first accounting for the ‘Sterile’ treatment. Significance is indicated by * $P <$
 97 0.05, ** $P < 0.01$, *** $P < 0.001$.

	$F_{5, 37}$	$\xi F_{4, 37}$	< 5.0	< 0.250	< 0.050	< 0.025	< 0.010	Sterile
Bacteria								
Richness	***44.8	***20.2	740.25	817.63	738.63	728.13	357.25	183.73
Positive	***52.3	***28.9	248.63	261.88	226.25	202.38	91.13	49.87
Negative	***22.8	2.6	108.38	116.38	116.63	126.75	104.25	58.69
Uniqueness	***23.7	***20.8	0.097	0.088	0.075	0.065	0.043	0.046
Links	***28.0	***15.2	7347.88	9027.00	7463.38	7174.50	2419.50	880.03
Complexity	***46.9	***18.5	9.67	10.67	9.84	9.74	6.73	4.82
+ Complexity	***40.3	***31.7	0.94	0.95	0.81	0.65	0.33	0.33
- Complexity	**12.8	***14.5	0.25	0.23	0.26	0.31	0.67	0.46
Fungi								
Richness	**3.9	2.4	83.13	73.50	55.00	63.50	53.75	39.70
Positive	***5.9	**5.3	44.25	34.38	23.75	25.50	22.50	18.44
Negative	1.8	1.6	15.63	12.38	9.88	13.88	13.75	10.23
Uniqueness	**4.8	***6.0	0.261	0.213	0.177	0.115	0.152	0.192
Links	**5.1	**4.0	203.00	160.88	101.88	119.00	94.75	65.31
Complexity	***6.8	**4.2	2.34	2.14	1.82	1.84	1.65	1.39
+ Complexity	***18.3	***19.3	1.76	1.18	0.54	0.44	0.42	0.36
- Complexity	***8.5	**4.2	0.10	0.07	0.08	0.12	0.18	0.22
Fungi-Bact.								
Richness†	***21.9	***9.61	0.65	0.66	0.55	0.58	0.37	0.23
Positive†	***35.3	***23.0	0.67	0.60	0.45	0.42	0.22	0.20
Negative†	***8.2	1.2	0.69	0.65	0.63	0.73	0.67	0.46
Uniqueness	***8.1	***10.0	0.178	0.135	0.108	0.082	0.099	0.111
Links	***13.5	***8.0	656.69	652.00	457.19	509.50	222.06	117.50
Complexity	*3.5	*2.8	0.78	0.72	0.58	0.65	0.53	0.50
+ Complexity	***17.8	***21.2	0.23	0.15	0.08	0.06	0.06	0.08
- Complexity	***7.6	*3.4	0.03	0.03	0.03	0.04	0.08	0.10
Network characteristic among all taxa								
Links	***28.4	***15.4	8207.56	9839.88	8022.44	7803.00	2736.31	1062.84
Complexity	***48.3	***19.7	9.73	10.68	9.86	9.75	6.63	4.77
+ Complexity	***44.4	***39.9	1.28	1.13	0.87	0.69	0.40	0.43
- Complexity	***11.7	***12.5	0.27	0.24	0.27	0.33	0.69	0.52

98 Note: All richness measures are number of OTUs (‘Richness’, Richness of OTUs with
 99 ‘Positive’ or ‘Negative’ coefficients to ecosystem functions). Links are number of links
 100 between OTUs (among ‘Bacteria’ only, ‘Fungi’ only, ‘Fungi-Bacteria’ only, or among ‘All’
 101 fungi and bacteria). Complexity refers to the number of network links per OTUs (nodes). †
 102 indices are the average of the scaled (between 1 and 0) values of fungi and bacteria.

103 **Table S2. Microbial network complexity characteristics for each soil treatments after de-**
 104 **trending for richness.** The mean of each sieving treatment is provided. The F -ratio and
 105 degrees of freedom are provided. ξ is the F -ratio and degrees of freedom for the variation
 106 among treatments after first accounting for the ‘Sterile’ treatment. Significance is indicated by
 107 * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$.

	$F_{5, 37}$	$\xi F_{4, 37}$	< 5.0	< 0.250	< 0.050	< 0.025	< 0.010	Sterile
Bacteria								
Complexity	***5.8	***6.2	8.24	8.55	8.42	8.41	8.69	8.31
+ Complexity	***5.7	***7.2	0.81	0.75	0.68	0.52	0.52	0.66
- Complexity	**4.8	**5.3	0.32	0.33	0.32	0.37	0.58	0.30
Fungi								
Complexity	1.7	1.2	1.99	1.94	1.90	1.79	1.75	1.70
+ Complexity	***11.8	***14.7	1.36	0.96	0.64	0.39	0.54	0.71
- Complexity	**4.9	*3.0	0.13	0.08	0.08	0.12	0.17	0.20
Fungi-Bact.								
Complexity	2.3	2.0	0.62	0.63	0.62	0.62	0.58	0.64
+ Complexity	***15.5	***18.7	0.19	0.13	0.09	0.05	0.07	0.13
- Complexity	0.5	0.3	0.05	0.05	0.04	0.05	0.06	0.06
All								
Complexity	**3.9	**3.9	8.28	8.53	8.41	8.40	8.62	8.32
+ Complexity	***10.2	***12.6	1.04	0.89	0.80	0.57	0.59	0.83
- Complexity	**3.8	*4.3	0.37	0.35	0.32	0.39	0.60	0.34

108 Note: All richness measures are number of OTUs (‘Richness’, Richness of OTUs with
 109 ‘Positive’ or ‘Negative’ coefficients). All network characteristics are number of links between
 110 OTUs (among ‘Bacteria’ only, ‘Fungi’ only, ‘Fungi-Bacteria’ only, or among ‘All’ fungi and
 111 bacteria). Complexity refers to the number of network links per number of OTUs (nodes). †
 112 indices are the average of the scaled (between 1 and 0) values of fungi and bacteria.

113 **Table S3.** ANOVA results for each ecosystem function and their composite multifunctional
 114 variable in relationship to fungal and bacterial OTU richness. Relationships were fit using
 115 linear regression (Linear) second order polynomial (Poly) and power function (Power). The
 116 sieving treatment was fit after to capture the residual variation among treatments in functioning
 117 that is not explained by fungal and bacterial richness and is highlighted in bold when
 118 significant ($P < 0.05$).

Function	Terms	Df	Bacterial richness			Terms	Df	Fungal richness		
			MS	F	P			MS	F	P
Grass N	Linear	1	428084.70	82.29	<0.001	Power	1	1.19	36.71	<0.001
	Treat.	5	79304.32	15.24	<0.001	Treat.	5	0.68	21.03	<0.001
	Resid.	41	5202.13			Resid.	41	0.03		
Grass P	Poly	2	2711.44	28.13	<0.001	Power	1	0.68	16.41	<0.001
	Treat.	5	651.02	6.75	<0.001	Treat.	5	0.63	15.24	<0.001
	Resid.	40	96.41			Resid.	41	0.04		
Forb N	Linear	1	102485.80	73.10	<0.001	Linear	1	68987.72	54.76	<0.001
	Treat.	5	17918.36	12.78	<0.001	Treat.	5	25784.53	20.47	<0.001
	Resid.	41	1402.02			Resid.	41	1259.76		
Forb P	Power	1	13.34	101.90	<0.001	Linear	1	2045.12	107.06	<0.001
	Treat.	5	1.94	14.83	<0.001	Treat.	5	913.95	47.85	<0.001
	Resid.	41	0.13			Resid.	41	19.10		
Legume N	Linear	1	22193.08	154.00	<0.001	Poly	2	14468.44	86.80	<0.001
	Treat.	5	8903.54	61.78	<0.001	Treat.	5	7402.93	44.41	<0.001
	Resid.	41	144.11			Resid.	40	166.69		
Legume P	Power	1	20.01	232.19	<0.001	Poly	2	211.76	84.97	<0.001
	Treat.	5	5.59	64.91	<0.001	Treat.	5	158.62	63.64	<0.001
	Resid.	41	0.09			Resid.	40	2.49		
N leaching	Power	1	7.21	4.50	0.040	Linear	1	7914.27	7.44	0.009
	Treat.	5	1.22	0.76	0.582	Treat.	5	1295.12	1.22	0.317
	Resid.	43	1.60			Resid.	43	1063.82		
P leaching	Power	1	0.17	16.96	<0.001	Power	1	0.08	7.68	0.008
	Treat.	5	0.01	1.23	0.314	Treat.	5	0.03	3.02	0.020
	Resid.	43	0.01			Resid.	43	0.01		
N ₂ O	Linear	1	5.24	7.31	0.010	Poly	2	2.70	4.02	0.025
	Treat.	5	1.03	1.43	0.232	Treat.	5	1.52	2.26	0.066
	Resid.	43	0.72			Resid.	42	0.67		
Decomposition	Poly	2	1771.26	66.48	<0.001	Linear	1	932.97	33.60	<0.001
	Treat.	5	108.34	4.07	0.004	Treat.	5	615.23	22.15	<0.001
	Resid.	42	26.64			Resid.	43	27.77		
Multifunction.	Linear	1	2.04	288.53	<0.001	Linear	1	1.28	193.5	<0.001
	Treat.	5	0.33	46.09	<0.001	Treat.	5	0.48	72.3	<0.001
	Resid.	41	0.01			Resid.	41	0.01		

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120 **Table S4. Taxonomy of soil fungi and bacteria linked to functions.** Number of fungal
 121 OTUs per fungal class with positive/negative coefficients for predicting a given ecosystem
 122 function (by column). Note that positive here refers to reducing nutrient leaching and N₂O
 123 emissions.

Fungal class	N	Decom.	N ₂ O	P leach.	N leach.	Leg. N	Gr. N	Forb N	Leg. P	Gr. P	Forb P
Agaricomycetes	55	1/1	5/1	0/3	0/1	13/0	2/0	0/0	12/0	3/0	9/0
Chytridiomycetes	7	0/0	1/0	0/0	0/1	3/0	0/1	1/0	3/0	0/2	3/0
Cystobasidiomycetes	1	0/0	0/0	0/0	0/0	1/0	0/1	0/0	1/0	0/0	1/0
Dothideomycetes	14	0/1	2/2	1/4	1/0	3/0	2/0	1/0	3/0	4/0	3/2
Eurotiomycetes	13	0/0	0/1	1/3	0/0	4/0	2/1	1/0	4/0	0/0	3/0
Glomeromycetes	5	1/0	1/0	1/0	0/0	2/0	0/1	0/0	2/0	0/0	1/0
Lecanoromycetes	3	0/0	0/0	1/1	0/0	1/0	0/0	0/0	1/0	0/0	0/0
Leotiomycetes	4	0/0	0/0	0/0	0/0	1/0	0/0	0/0	1/0	0/0	1/0
Orbiliomycetes	3	0/0	0/0	0/1	0/0	1/0	0/1	0/0	1/0	0/0	1/0
Pezizomycetes	11	0/0	1/0	1/0	0/1	4/0	0/1	0/0	5/0	0/0	2/0
Pucciniomycetes	3	0/0	0/0	0/0	0/0	1/0	0/0	0/0	1/0	0/0	1/0
Saccharomycetes	7	0/0	0/0	0/0	0/2	2/0	1/0	0/0	2/0	1/0	1/0
Sordariomycetes	37	1/1	2/4	4/3	0/0	13/0	1/1	1/0	13/0	1/0	9/2
Tremellomycetes	4	0/0	0/0	0/0	0/0	3/0	0/1	0/0	3/0	0/0	3/0
Bacterial class	N	Decom.	N ₂ O	P leach.	N leach.	Leg. N	Gr. N	Forb N	Leg. P	Gr. P	Forb P
Actinobacteria	128	4/1	15/12	0/0	0/0	3/0	1/0	15/3	10/0	0/2	6/2
Alphaproteobacteria	167	7/4	24/15	1/2	0/1	1/2	4/4	14/4	5/4	4/1	2/2
Anaerolineae	9	0/0	1/0	0/0	0/0	0/0	0/1	0/0	0/0	0/0	0/0
Aquificae	4	1/0	0/0	0/0	0/0	1/0	0/1	1/0	1/0	0/0	0/0
Armatimonadia	1	0/0	0/0	0/1	0/0	0/0	0/0	0/0	0/0	0/0	0/0
Bacilli	131	4/5	15/19	0/1	0/0	1/0	3/0	10/1	4/0	3/0	3/0
Bacteroidia	13	0/0	5/3	0/0	0/0	0/0	0/0	2/0	1/0	0/0	0/0
Betaproteobacteria	63	1/0	6/12	0/0	0/0	3/0	1/2	5/1	5/0	1/1	1/0
Caldilineae	9	0/0	2/1	0/0	0/0	0/0	0/0	1/0	1/0	0/0	0/0
Chlamydiae	20	0/0	2/0	0/0	0/0	0/1	0/0	0/0	0/1	0/0	0/0
Chlorobia	1	0/0	0/0	0/0	0/0	0/0	0/0	0/0	1/0	0/0	0/0
Chloroflexi	5	0/0	0/1	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0
Clostridia	208	6/0	31/15	1/0	0/3	2/0	3/3	18/6	5/2	4/4	2/1
Deferribacteres	1	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0
Deltaproteobacteria	174	4/2	33/11	0/0	0/1	4/0	3/0	13/1	10/1	2/2	3/0
Epsilonproteobacteria	4	0/0	0/0	0/0	0/1	0/0	0/0	0/0	0/0	0/0	0/0
Erysipelotrichia	14	1/0	0/1	0/0	0/0	0/0	0/0	1/1	0/0	0/0	0/0
Fibrobacteria	4	0/0	0/1	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0
Flavobacteria	4	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0
Gammaproteobacteria	167	7/1	23/18	0/1	0/1	4/0	0/3	15/1	9/0	2/2	3/0
Gemmatimonadetes	41	3/0	8/7	0/0	0/0	2/0	0/0	8/0	3/0	1/1	1/0
Holophagae	1	0/0	1/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0
Ignavibacteria	2	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0
Ktedonobacteria	2	0/0	0/0	0/0	0/0	0/0	0/0	0/0	1/0	0/0	0/0
Mollicutes	11	0/0	2/0	0/0	0/0	0/0	0/0	1/0	0/0	0/0	0/0
Negativicutes	20	1/0	3/0	0/0	0/0	0/0	0/0	0/0	2/0	0/0	0/0

Nitrospira	8	0/0	3/0	0/0	0/0	0/0	0/0	2/0	0/1	0/0	0/0
Opiritae	32	1/1	5/4	0/0	0/0	1/0	2/2	4/2	1/1	1/0	3/0
Phycisphaerae	13	2/0	1/0	0/0	0/0	1/0	0/0	2/0	3/0	0/0	0/0
Planctomycetacia	226	9/3	27/22	0/0	0/1	1/0	6/2	10/4	4/2	5/1	0/1
Sphingobacteria	74	2/1	10/2	0/0	0/1	1/0	3/0	3/2	3/0	2/0	1/0
Spirochaetes	12	0/0	0/0	0/0	0/0	0/0	1/0	1/0	2/0	1/0	0/0
Synergistia	11	0/0	1/1	0/0	0/0	0/0	0/0	1/0	0/0	0/0	0/0
Thermodesulfobacteria	1	0/0	0/1	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0
Thermomicrobia	12	1/1	0/0	0/0	0/0	0/0	0/0	0/2	0/0	1/0	0/0
Verrucomicrobiae	54	4/0	12/6	0/0	0/0	1/0	1/0	9/0	4/0	0/1	2/1

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126 **Table S5. Similarity among functions in the microbial taxa they are linked to.** Shown are
 127 the ten different ecosystem functions (diagonal) assessed in this study. Values represent
 128 percent (%) overlap among microbial taxa (OTUs) in affecting two different ecosystem
 129 functions for combinations of taxa that have positive coefficients (upper triangle) or negative
 130 coefficients (lower triangle) in predicting each ecosystem function. For instance, litter
 131 decomposition (Decom.) is associated with 7.64 % of the same microbial taxa that are
 132 associated with reducing N₂O emissions.

Positive									
Decom.	7.64	3.33	0.00	14.29	0.00	18.56	15.04	0.00	14.12
4.68	N₂O	0.86	0.00	2.34	3.10	15.30	7.87	2.33	3.11
0.00	2.55	P leach	0.00	0.00	0.00	1.45	0.00	0.00	0.00
0.00	0.00	0.00	N leach	0.00	0.00	0.00	0.00	0.00	0.00
0.00	0.00	0.00	0.00	Leg N	0.00	18.52	51.49	0.00	30.19
0.00	0.00	0.00	0.00	0.00	Gr N	0.00	0.00	54.55	0.00
0.00	10.00	0.00	0.00	6.45	0.00	Forb N	28.44	0.00	25.77
0.00	2.41	0.00	8.70	23.53	0.00	4.76	Leg P	0.00	23.53
0.00	0.00	0.00	8.33	0.00	30.30	0.00	0.00	Gr P	0.00
0.00	2.53	0.00	0.00	22.22	0.00	29.41	10.00	0.00	Forb P

Negative

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137 **Table S6. Effects of soil microbial community characteristics on multifunctionality using**
 138 **randomization tests.** Based on associating OTUs to functions using randomizations test
 139 considering each taxa independently (instead of elastic net considering all taxa
 140 simultaneously). Effects are shown before and after de-trending community characteristics for
 141 richness prior to analysis. Standardized effect (*SES*) and associated standard error (*SE*), R^2 and
 142 *AICc* for each community characteristic as an independent predictor. † average z-transformed
 143 values of bacteria and fungi.

	<i>SES</i>	<i>SE</i>	<i>P</i>	R^2	<i>AICc</i>
Functional richness					
Bacteria (+)	0.842	0.083	< 0.001	0.693	85.1
Fungi (+)	0.757	0.097	< 0.001	0.568	101.4
†Both (+)	0.902	0.068	< 0.001	0.792	66.4
Bacteria (-)	0.460	0.136	0.002	0.199	131.1
Fungi (-)	-0.105	0.150	0.489	0.010	141.2
†Both (-)	0.245	0.151	0.111	0.054	139.1
Functional richness (post de-trending)					
Bacteria (+)	0.565	0.120	< 0.001	0.327	122.8
Fungi (+)	0.599	0.115	< 0.001	0.370	119.6
†Both (+)	0.538	0.124	< 0.001	0.291	125.3
Bacteria (-)	-0.418	0.133	0.003	0.176	132.4
Fungi (-)	-0.620	0.117	< 0.001	0.379	118.9
†Both (-)	-0.443	0.134	0.002	0.193	131.5
Functional complexity					
Bact-Bact (+)	0.921	0.059	< 0.001	0.840	53.9
Fungi-Fungi (+)	0.772	0.093	< 0.001	0.601	97.6
Bact-Fungi (+)	0.833	0.079	< 0.001	0.708	82.7
Among all (+)	0.927	0.057	< 0.001	0.852	50.2
Bact-Bact (-)	-0.778	0.091	< 0.001	0.613	96.2
Fungi-Fungi (-)	-0.657	0.113	< 0.001	0.423	115.3
Bact-Fungi (-)	-0.676	0.108	< 0.001	0.459	112.3
Among all (-)	-0.783	0.091	< 0.001	0.619	95.4
Functional complexity (post de-trending)					
Bact-Bact (+)	0.567	0.118	< 0.001	0.334	122.2
Fungi-Fungi (+)	0.514	0.123	< 0.001	0.274	126.4
Bact-Fungi (+)	0.481	0.128	< 0.001	0.234	129.0
Among all (+)	0.520	0.124	< 0.001	0.276	126.2
Bact-Bact (-)	-0.333	0.137	0.019	0.114	136.0
Fungi-Fungi (-)	-0.453	0.130	0.001	0.208	130.6
Bact-Fungi (-)	-0.263	0.145	0.077	0.067	138.4
Among all (-)	-0.301	0.139	0.036	0.092	137.1