The role of mycorrhizal type and plant dominance in regulating nitrogen cycling in Oroarctic soils

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1 Supplementary tables and figures

1.1 Methods

Table S1: Plant species removal for the Rare and Dominant (Dom) treatment plots.

Plot	Treat	Emp_nig	Vac_uli	Fes_viv	Cx_big	Bis_viv	Dry_oct	Cas_hyp	Sx_pol	Tha_alp	Gräs_1	Sx_herb	Sil_acu	Dia_lap	Loi_pro	Jun_tri	Ped_lap	Arc_alp	Cx_nig	Pot_cra
B2	Rare		1	1	1	1	1		1								1			
E2	Rare			1	1	1	1	1	1	1	1		1							1
F3	Rare		1	1	1	1		1	1			1	1	1	1	1				
G1	Rare	1	1	1	1	1			1				1					1	1	

Plot	Treat	Ped_lap	Hie_alp	Ant_alp	Cas_hyp	Sx_herb	Dry_opp	Bar_alp	Vac_uli	Sil_acu	Sau_alp	Jun_tri	Ast_alp	Sx_pol	Eup_wet	Sx_ret	Equ_arv	Sx_lan	Vac_vit	Phy_cer	Cx_glac	Vac_myr	Cx_nig	Arc_alp	Cx_vag
A4	Dom					1		1	1					1	1						1		1	1	
C3	Dom	1	1	1				1		1			1						1	1		1			
D4	Dom				1	1	1	1				1		1		1	1	1							
H2	Dom	1	1		1	1				1	1		1	1											1

Table S2: Primer sequences used for qPCR.

Target	Region	Primer Direction	Primer Name	Primer Sequence	Primer concentration (µM)	Reference
Bacteria						
	16S rRNA V4 and V5	Forward	515	5'-GTGYCAGCMGCCGCGGTAA-3'	0.2	(Parada et al., 2016)
		Reverse	926	5'-CCGYCAATTYMTTTRAGTTT-3'		(Quince et al., 2011)
Fungi						
	ITS2	Forward	fITS7	5'-GTGARTCATCGAATCTTTG-3'	0.3	(Ihrmark et al., 2012)
		Reverse	ITS4a	5'-TCCTCGCCTTATTGATATGC-3'		
		Reverse	ITS4	5'-TCCTCCGCTTATTGATATGC-3'		(White et al., 1990)
N-cycling genes						
Ammonia oxidizing bacteria (AOB)	amoA	Forward	amoA-1	5'-GGGGTTTCTACTGGTGGT-3'	0.5	(Rotthauwe et al., 1997)
		Reverse	amoA-2	5'-CCCCTCKGSAAAGCCTTCTTC-3'		
Ammonia oxidizing archaea (AOA)	amoA	Forward	CrenamoA23	5'-ATGGTCTGGCTWAGACG-3'	0.5	(Tourna et al., 2008)
		Reverse	CrenamoA616	5'-GCCATCCATCTGTATGTCCA-3'		
Comammox clade A	amoA	Forward	comaA-244F	5'-TAYAAYTGGGTSAAYTA-3'	1.0	(Pjevac et al., 2017)
		Reverse	comaA-659R	5'-ARATCATSGTGCTRTG-3'		

Comammox clade B	amoA	Forward	comaB-244F	5'-TAYTTCTGGACRTTYTA-3'	1.0	
		Reverse	comaB-659R	5'-ARATCCARACDGTGTG-3'		
Nitrobacter-type nitrite oxidizer	nxrB	Forward	nxrB1-F	5'-ACGTGGAGACCAAGCCGGG-3'	0.5	(Vanparys et al., 2007)
		Reverse	nxrB1-R	5'-CCGTGCTGTTGAYCTCGTTGA-3'		
Nitrospira-type nitrite oxidizer	nxrB	Forward	nxrB169f	5'-TACATGTGGTGGAACA-3'	0.5	(Pester et al., 2014)
		Reverse	nxrB638r	5'-CGGTTCTGGTCRATCA-3'		

Table S3. qPCR cycling conditions for the different N-cycling genes.

Genes	Initial Denaturation	Denaturation	Annealing	Elongation	Signal Reading	Cycles	PCR efficiency
16S rRNA	5 min at 95°C	15 s at 95°C	30 s at 50°C	45 s at 72°C	5 s at 80°C	35	E = 80.2, R^2 = 0.998
ITS	5 min at 95°C	15 s at 95°C	30 s at 56°C	40 s at 72°C	5 s at 78°C	35	E = 78.3, R^2 = 0.999
AOA/AOB	5 min at 95°C	15 s at 95°C	30 s at 55°C	40 s at 72°C	5 s at 77°C	40	E = 84.2, R^2 = 0.997/ E = 77.1, R^2 = 0.995
comaA/comaB	5 min at 95°C	15 s at 95°C	30 s at 52°C	30 s at 72°C	5 s at 80°C	40	E = 68.6, R^2 = 0.998/ E = 85.0, R^2 = 0.997
nxrB NIS	5 min at 95°C	15 s at 95°C	30 s at 56°C	45 s at 72°C	5 s at 78°C	35	E = 78.3, R^2 = 0.999
nxrB NIB	5 min at 95°C	15 s at 95°C	30 s at 72°C - 1°C/cycle	30 s at 72°C		8	E = 70.2, R^2 = 0.998
nxrB NIB		15 s at 95°C	30 s at 67°C	30 s at 72°C	5 s at 78°C	27	

1.2 Soil characteristics

Table S4. Summary of Generalized Linear Mixed Models (GLMMs) for Soil Characteristics: field Soil Moisture (VWC), lab Soil Moisture (GWC (%)), Soil Organic Matter (SOM (%)), and total nitrogen (TN), which follow a Beta distribution; field Soil Temperature (T_{soil} (°C)), which follows a Gamma distribution with a log link function; and pH and the Carbon-to-Nitrogen Ratio (C/N) are modeled using a Gaussian distribution. AM/NM = plants with arbuscular mycorrhizal association or no mycorrhizal association; EcM/ErM = plants with ectomycorrhizal and ericoid mycorrhizal associations; Dominant = rare plant species removed; and Rare = dominant species removed. Bolded p-values are based on alpha < 0.05*, < 0.1#.

	VWC			Tsoil			GWC			SOM			pH			C/N			TN		
Predictors	*Estimates*	*z*	*p*	*Estimates*	*z*	*p*	*Estimates*	*z*	*p*	*Estimates*	*z*	*p*	*Estimates*	*z*	*p*	*Estimates*	*z*	*p*	*Estimates*	*z*	*p*
Intercept	0.35 (0.30 – 0.41)	-13.27	**<0.001**	2.37 (2.34 – 2.40)	142.43	**<0.001**	0.56 (0.52 – 0.59)	29.81	**<0.001**	0.59 (0.48 – 0.73)	-5.02	**<0.001**	4.93 (4.82 – 5.05)	84.60	**<0.001**	1.07 (1.06 – 1.07)	30.15	**<0.001**	0.01 (0.01 – 0.01)	-28.03	**<0.001**
AM/NM	1.03 (0.87 – 1.23)	0.38	0.704	1.01 (1.00 – 1.02)	1.48	0.139	-0.04 (-0.09 – 0.01)	-1.49	0.136	0.71 (0.54 – 0.95)	-2.35	**0.019***	-0.07 (-0.22 – 0.09)	-0.86	0.391	1.00 (0.99 – 1.00)	-0.37	0.708	0.83 (0.52 – 1.31)	-0.81	0.421
EcM/ErM	1.21 (1.02 – 1.43)	2.19	**0.028***	0.99 (0.98 – 1.00)	-1.88	**0.060**#	-0.01 (-0.06 – 0.04)	-0.32	0.747	0.86 (0.66 – 1.14)	-1.05	0.294	0.06 (-0.09 – 0.21)	0.79	0.427	1.00 (1.00 – 1.01)	1.53	0.127	1.27 (0.84 – 1.93)	1.12	0.261
Dominant	1.17 (0.94 – 1.46)	1.39	0.166	0.98 (0.97 – 1.00)	-2.44	**0.015***	0.02 (-0.04 – 0.08)	0.61	0.539	1.03 (0.73 – 1.44)	0.15	0.881	0.06 (-0.14 – 0.26)	0.57	0.571	0.99 (0.99 – 1.00)	-1.61	0.108	0.94 (0.54 – 1.62)	-0.23	0.821
Rare	1.20 (0.97 – 1.49)	1.64	0.102	0.99 (0.98 – 1.01)	-0.82	0.412	-0.02 (-0.08 – 0.04)	-0.62	0.538	0.78 (0.55 – 1.10)	-1.41	0.160	0.11 (-0.09 – 0.30)	1.04	0.300	1.00 (0.99 – 1.01)	0.41	0.681	1.03 (0.61 – 1.75)	0.11	0.915
Random Effects																					
σ^2	0.00			0.00			0.00			0.00			0.02			0.01			0.00		
τ_{00}	0.02 $_{Block}$			0.00 $_{Block}$			0.00 $_{Block}$			0.01 $_{Block}$			0.00 $_{Block}$			0.00 $_{Block}$			0.01 $_{Block}$		
ICC	1.00			0.52			0.13			1.00			0.12						1.00		
N	8 $_{Block}$			8 $_{Block}$			8 $_{Block}$			8 $_{Block}$			8 $_{Block}$			8 $_{Block}$			8 $_{Block}$		
Observations	32			32			32			32			32			32			32		
Marginal R^2 / Conditional R^2	0.265 / 1.000			0.230 / 0.629			0.105 / 0.219			0.658 / 1.000			0.116 / 0.226			0.001 / NA			0.819 / 1.000		

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1.3 Gross rates

Table S5: Gross nitrogen (N) transformation rates (mean and 85% confidence interval) estimated using either the ^{15}N tracing model (Ntrace) or the isotope pool dilution (IPD) approach (μmol g^{-1} C d^{-1}). M_{Norg} = Mineralization of organic N; I_{NH4} = Immobilization of NH_4^+; O_{NH4} = NH_4^+ oxidation; I_{NO3} = Immobilization of NO_3^-; Min. = Gross mineralization; Nitr. = Gross nitrification; Control = no plant manipulation; AM/NM = plants with arbuscular mycorrhizal association or no mycorrhizal association; EcM/ErM = plants with ectomycorrhizal and ericoid mycorrhizal associations; Dominant = rare plant species removed, promoting dominant plant species; and Rare = dominant species removed, promoting rare plant species.

	Ntrace				IPD	
	M_{Norg}	I_{NH4}	O_{NH4}	I_{NO3}	Min.	Nitr.
Control	5.0 ± 0.3	5.8 ± 0.4	0.131 ± 0.011	0.149 ± 0.011	7.4 ± 3.6	0.248 ± 0.136
AM/NM	6.5 ± 0.5	9.2 ± 0.6	0.071 ± 0.004	0.077 ± 0.004	8.5 ± 6.3	0.140 ± 0.051
EcM/ErM	8.7 ± 0.4	9.3 ± 0.4	0.165 ± 0.008	0.180 ± 0.008	10.9 ± 4.3	0.224 ± 0.060
Dominant	8.9 ± 0.6	10.0 ± 0.6	0.066 ± 0.007	0.076 ± 0.004	6.5 ± 4.9	0.086 ± 0.034
Rare	7.3 ± 0.6	8.5 ± 0.5	0.090 ± 0.007	0.106 ± 0.007	8.1 ± 2.2	0.162 ± 0.048

1.4 qPCR

Table S6: Total genomic DNA (ng/μL) and gene copy numbers (g^{-1} dry weight soil) in the organic soil horizon at the study site (Tarfala, Sweden). Mean values ± standard errors are reported, with the number of replicates indicated in parentheses. Differences compared with the control, as determined by generalized linear mixed model (GLMM) outputs (Table S7), are denoted by bolded text for p-values less than 0.1 (# = $p < 0.1$).

Treatment	gDNA	16S	ITS
Control	106 ± 15 (8)	2.75e+09 ± 4.64e+08 (8)	1.68e+08 ± 3.65e+07 (8)
AM/NM	96 ± 6 (8)	2.36e+09 ± 2.39e+08 (8)	**1.05e+08 ± 2.00e+07 (8)** #
EcM/ErM	114 ± 6 (8)	2.46e+09 ± 1.38e+08 (8)	1.30e+08 ± 1.87e+07 (8)
Dominant	94 ± 8 (4)	2.31e+09 ± 2.41e+08 (4)	1.61e+08 ± 3.81e+07 (4)
Rare	**78 ± 16 (4)** #	2.07e+09 ± 3.42e+08 (4)	1.14e+08 ± 1.80e+07 (4)

Table S7: Summary of regression models using log-transformed data, except gDNA, which needed no transformation to be normally distributed. The models utilized a Gaussian distribution with a log link function for gDNA, and an identity link function for 16S and ITS. The fixed effect was treatment group, and the random effect was Block. Treatments: removal of plants with arbuscular

mycorrhiza & no mycorrhiza associations = EcM/ErM; removal of plants with ecto and ericoid mycorrhiza associations = AM/NM; removal of dominant plant species = Rare; removal of rare plant species = Dominant. Bolded p-values are based on alpha < 0.1 [#].

	gDNA			**16S**			**ITS**		
Predictors	*Estimates*	*Statistic*	*p*	*Estimates*	*Statistic*	*p*	*Estimates*	*Statistic*	*p*
Intercept	4.67 (4.50 – 4.83)	55.26	**<0.001**	9.39 (9.29 – 9.49)	184.33	**<0.001**	8.14 (7.99 – 8.29)	105.76	**<0.001**
AM/NM	-0.10 (-0.35 – 0.14)	-0.82	0.413	-0.03 (-0.17 – 0.11)	-0.46	0.642	**-0.18 (-0.40 – 0.03)**	**-1.67**	**0.094[#]**
EcM/ErM	0.06 (-0.16 – 0.29)	0.56	0.578	-0.00 (-0.14 – 0.14)	-0.05	0.958	-0.05 (-0.27 – 0.16)	-0.50	0.617
Dominant	-0.13 (-0.44 – 0.19)	-0.80	0.425	-0.03 (-0.21 – 0.14)	-0.38	0.707	0.03 (-0.24 – 0.29)	0.20	0.844
Rare	**-0.32 (-0.68 – 0.05)**	**-1.71**	**0.086[#]**	-0.09 (-0.27 – 0.08)	-1.06	0.288	-0.10 (-0.36 – 0.16)	-0.75	0.455
Random Effects									
σ^2	646.50			0.02			0.05		
τ_{00}	0.00 $_{Block}$			0.00 $_{Block}$			0.00 $_{Block}$		
N	8 $_{Block}$			8 $_{Block}$			8 $_{Block}$		
Observations	32			32			32		
Marginal R^2 / Conditional R^2	0.000 / NA			0.042 / NA			0.110 / NA		

Table S8: Ratios of gene copy numbers (g^{-1} dry weight soil) in the organic soil horizon at the study site (Tarfala, Sweden). Mean values with standard errors (SE) are reported, with the number of replicates indicated in brackets. Treatments: removal of plants

with arbuscular mycorrhiza & no mycorrhiza associations = EcM/ErM; removal of plants with ecto and ericoid mycorrhiza associations = AM/NM; removal of dominant plant species = Rare; removal of rare plant species = Dominant. Differences compared with the control, as determined by generalized linear mixed model (GLMM) outputs (Table S9), are denoted by bolded text for p-values less than 0.05 (* = p < 0.05).

Treatment	ITS:16S	AOA:AOB	ComaA:ComaB	NIS:NIB
Control	0.060±0.008 (8)	29.6±5.9 (8)	9.3±1.2 (8)	114.9±13.2 (8)
AM/NM	**0.043±0.006 (8)***	34.5±10.2 (8)	8.5±0.9 (8)	130.7±22.1 (8)
EcM/ErM	0.053±0.006 (8)	36.0±11.0 (8)	9.3±1.4 (8)	138.7±28.1 (8)
Dominant	0.067±0.011 (4)	17.1±7.6 (4)	10.6±1.2 (4)	92.9±29.8 (4)
Rare	0.057±0.006 (4)	32.0±14.2 (4)	10.1±1.2 (4)	84.8±13.6 (4)

Table S9: Summary of regression models for gene copy ratios. The models utilized a Gamma distribution with a log link function. The fixed effect was treatment group, and the random effect was Block. Treatments: removal of plants with arbuscular mycorrhiza & no mycorrhiza associations = EcM/ErM; removal of plants with ecto and ericoid mycorrhiza associations = AM/NM; removal of dominant plant species = Rare; removal of rare plant species = Dominant. Bolded p-values are based on alpha = 0.05.

	ITS:16S			AOA:AOB			ComaA:ComaB			NIS:NIB		
Predictors	*Estimates*	*Statistic*	*p*	*Estimates*	*Statistic*	*p*	*Estimates*	*Statistic*	*p*	*Estimates*	*Statistic*	*p*
Intercept	0.06 (0.05 – 0.08)	-24.83	**<0.001**	29.03 (17.24 – 48.87)	12.67	**<0.001**	9.13 (7.38 – 11.31)	20.33	**<0.001**	114.04 (84.40 – 154.10)	30.84	**<0.001**
AM/NM	0.71 (0.52 – 0.97)	-2.13	**0.033***	1.03 (0.56 – 1.90)	0.10	0.918	0.92 (0.71 – 1.20)	-0.59	0.553	1.08 (0.79 – 1.49)	0.48	0.630
EcM/ErM	0.87 (0.64 – 1.19)	-0.87	0.387	1.09 (0.60 – 1.99)	0.29	0.775	1.00 (0.76 – 1.30)	-0.01	0.992	1.13 (0.82 – 1.56)	0.77	0.440
Dominant	1.12 (0.76 – 1.64)	0.56	0.573	0.56 (0.26 – 1.20)	-1.50	0.133	1.26 (0.88 – 1.81)	1.26	0.209	0.81 (0.54 – 1.21)	-1.04	0.299

Rare	0.94 (0.64 – 1.38)	-0.33	0.745	0.92 (0.42 – 1.99)	-0.22	0.826	1.02 (0.72 – 1.44)	0.11	0.915	0.71 (0.47 – 1.08)	-1.61	0.108
Random Effects												
σ^2	0.10			0.31			0.07			0.10		
τ_{00}	0.00 $_{Block}$			0.18 $_{Block}$			0.02 $_{Block}$			0.08 $_{Block}$		
ICC				0.37			0.22			0.46		
N	8 $_{Block}$			8 $_{Block}$			8 $_{Block}$			8 $_{Block}$		
Observations	32			32			32			32		
Marginal R^2 / Conditional R^2	0.195 / NA			0.083 / 0.425			0.086 / 0.287			0.125 / 0.525		

Table S10: Gene copy numbers (g^{-1} dry weight soil) in the organic soil horizon at the study site (Tarfala, Sweden). Mean values with standard errors (SE) are reported. Treatments: ectomycorrhizal and ericoid mycorrhizal associations = EcM/ErM; arbuscular mycorrhizal association or no mycorrhiza association = AM/NM; removal of dominant plant species = Rare; removal of rare plant species = Dominant. Differences compared with the control, as determined by generalized linear mixed model (GLMM) outputs (Table S11), are denoted by bolded text for p-values ** = p < 0.01, # = p < 0.1.

Treatment	n	AOA	AOB	ComaA	ComaB	NIB	NIS
Control	8	3.94e+06 ± 7.39e+05	1.50e+05 ± 2.70e+04	7.05e+06 ± 1.61e+06	8.31e+05 ± 1.72e+05	3.47e+05 ± 7.01e+04	3.98e+07 ± 8.13e+06
AM/NM	8	3.71e+06 ± 5.41e+05	1.43e+05 ± 2.33e+04	5.05e+06 ± 7.48e+05	6.63e+05 ± 1.44e+05	3.11e+05 ± 3.77e+04	3.65e+07 ± 4.20e+06
EcM/ErM	8	4.46e+06 ± 1.45e+06	1.23e+05 ± 5.46e+03	6.13e+06 ± 2.94e+05	7.48e+05 ± 9.98e+04	3.32e+05 ± 2.25e+04	4.49e+07 ± 8.41e+06
Dominant	4	**1.89e+06 ± 7.73e+05****	2.46e+05 ± 1.38e+05	4.61e+06 ± 9.15e+05	4.51e+05 ± 9.63e+04	2.50e+05 ± 3.76e+04	**2.20e+07 ± 6.73e+06**$^{\#}$

Rare	4	3.32e+06 ± 1.39e+06	1.10e+05 ± 1.80e+04	4.75e+06 ± 8.12e+05	4.83e+05 ± 9.71e+04	3.09e+05 ± 2.27e+04	2.69e+07 ± 5.90e+06

Table S11: Summary of regression models using log-transformed data. The models utilized a Gaussian distribution with an identity link function. The fixed effect was treatment group, and the random effect was Block. Treatments: ectomycorrhizal and ericoid mycorrhizal associations = EcM/ErM; arbuscular mycorrhizal association or no mycorrhiza association = AM/NM; removal of dominant plant species = Rare; removal of rare plant species = Dominant. Bolded p-values ** = p < 0.01, # = p < 0.1.

	AOA			**AOB**			**ComaA**			**ComaB**			**NIB**			**NIS**		
Predictors	*Estimates*	*Statistic*	*p*	*Estimates*	*Statistic*	*p*	*Estimates*	*Statistic*	*p*	*Estimates*	*Statistic*	*p*	*Estimates*	*Statistic*	*p*	*Estimates*	*Statistic*	*p*
Intercept	6.52 (6.33 – 6.72)	66.46	**<0.001**	5.12 (4.99 – 5.26)	73.32	**<0.001**	6.78 (6.65 – 6.91)	105.45	**<0.001**	5.84 (5.68 – 5.99)	72.79	**<0.001**	5.49 (5.38 – 5.59)	107.32	**<0.001**	7.52 (7.38 – 7.67)	100.70	**<0.001**
AM/NM	0.01 (-0.20 – 0.22)	0.11	0.913	-0.000 (-0.020 – 0.019)	-0.03	0.978	-0.12 (-0.30 – 0.05)	-1.37	0.171	-0.09 (-0.31 – 0.13)	-0.79	0.427	-0.02 (-0.16 – 0.13)	-0.22	0.829	0.02 (-0.17 – 0.20)	0.17	0.864
EcM/ErM	0.02 (-0.19 – 0.23)	0.16	0.877	-0.004 (-0.023 – 0.014)	-0.36	0.721	0.00 (-0.17 – 0.17)	0.05	0.964	0.01 (-0.21 – 0.23)	0.07	0.940	0.03 (-0.11 – 0.17)	0.38	0.703	0.08 (-0.11 – 0.27)	0.84	0.403

	0.22)			0.16)			0.18)			0.23)			0.17)			0.27)			
Dominant	**-0.36 (-0.63 – -0.10)**	**-2.70**	**0.07 ** **	0.10 (-0.13 – 0.34)	0.86	0.390	-0.14 (-0.36 – 0.07)	-1.31	0.190	-0.22 (-0.49 – 0.05)	-1.57	0.116	-0.10 (-0.28 – 0.07)	-1.18	0.239	**-0.22 (-0.46 – 0.01)**	**-1.88**	**0.059 #**	
Rare	-0.13 (-0.39 – 0.14)	-0.95	0.344	-0.10 (-0.33 – 0.14)	-0.82	0.414	-0.12 (-0.34 – 0.09)	-1.13	0.259	-0.18 (-0.45 – 0.10)	-1.27	0.203	0.00 (-0.17 – 0.17)	0.01	0.993	-0.13 (-0.37 – 0.10)	-1.13	0.257	
Random Effects																			
σ^2	0.04			0.04			0.03			0.05			0.02			0.04			
τ_{00}	0.03 $_{Block}$			0.00 $_{Block}$			0.00 $_{Block}$			0.00 $_{Block}$			0.00 $_{Block}$			0.01 $_{Block}$			
ICC	0.42			0.01			0.03									0.19			
N	8 $_{Block}$			8 $_{Block}$			8 $_{Block}$			8 $_{Block}$			8 $_{Block}$			8 $_{Block}$			
Observations	32			32			32			32			32			32			
Marginal	0.174 / 0.519			0.069 / 0.080			0.119 / 0.143			0.124 / NA			0.069 / NA			0.184 / 0.342			

R^2 / Conditional R^2

1.5 Environment

Table S12: Correlation analyses of gene abundances and environmental variables. Results of Spearman rank-order correlation analyses are shown, focusing on relationships among variables. Spearman correlation coefficients (r) quantify these relationships and are categorized as weak (0 < |r| < 0.4), moderate (0.4 < |r| < 0.7), and strong (|r| > 0.7). Original p-values, Holm's corrected p-values (adj p-value), and corresponding confidence intervals are also reported.

Variable1	Variable2	r	p-value	adj p-value	adj CI lower	adj CI upper
Simpsons	VWC	**0.63**	**0.00**	**0.02**	**0.08**	**0.89**
	Tsoil	-0.37	0.04	1.00	-0.78	0.27
	GWC	-0.28	0.12	1.00	-0.74	0.35
	SOM	-0.31	0.08	1.00	-0.75	0.32
	pH	0.11	0.54	1.00	-0.47	0.63
	C/N	-0.46	0.01	1.00	-0.82	0.16
	TN	0.14	0.45	1.00	-0.45	0.65
	BD	0.29	0.10	1.00	-0.34	0.74
	MSL	0.03	0.87	1.00	-0.49	0.53
	gDNA	-0.05	0.78	1.00	-0.56	0.49
	16S	-0.18	0.33	1.00	-0.67	0.43
	ITS	-0.18	0.33	1.00	-0.67	0.43
	AOA	0.07	0.71	1.00	-0.48	0.58
	AOB	-0.25	0.16	1.00	-0.72	0.38
	ComaA	-0.03	0.89	1.00	-0.52	0.48
	ComaB	-0.10	0.59	1.00	-0.61	0.48
	NIB	0.02	0.93	1.00	-0.47	0.49
	NIS	0.04	0.81	1.00	-0.49	0.55
VWC	Tsoil	-0.45	0.01	1.00	-0.82	0.17
	GWC	-0.13	0.47	1.00	-0.64	0.46

Variable1	Variable2	r	p-value	adj p-value	adj CI lower	adj CI upper
	SOM	-0.25	0.17	1.00	-0.72	0.38
	pH	-0.25	0.16	1.00	-0.72	0.38
	C/N	-0.37	0.03	1.00	-0.78	0.26
	TN	0.17	0.36	1.00	-0.44	0.67
	BD	**0.60**	**0.00**	**0.04**	**0.03**	**0.88**
	MSL	0.28	0.13	1.00	-0.36	0.74
	gDNA	-0.01	0.96	1.00	-0.48	0.46
	16S	-0.22	0.23	1.00	-0.70	0.40
	ITS	-0.17	0.34	1.00	-0.67	0.43
	AOA	0.16	0.37	1.00	-0.44	0.66
	AOB	-0.21	0.25	1.00	-0.70	0.41
	ComaA	-0.24	0.18	1.00	-0.72	0.38
	ComaB	-0.41	0.02	1.00	-0.80	0.22
	NIB	-0.10	0.60	1.00	-0.61	0.48
	NIS	0.09	0.61	1.00	-0.48	0.61
Tsoil	GWC	-0.20	0.26	1.00	-0.69	0.41
	SOM	-0.08	0.67	1.00	-0.59	0.48
	pH	-0.26	0.15	1.00	-0.73	0.37
	C/N	-0.03	0.87	1.00	-0.53	0.48
	TN	-0.04	0.82	1.00	-0.55	0.49
	BD	-0.58	0.00	0.08	-0.87	0.01
	MSL	-0.53	0.00	0.30	-0.85	0.08
	gDNA	-0.06	0.75	1.00	-0.57	0.48
	16S	0.05	0.80	1.00	-0.49	0.56
	ITS	-0.17	0.36	1.00	-0.67	0.44
	AOA	0.17	0.34	1.00	-0.43	0.67
	AOB	-0.01	0.95	1.00	-0.48	0.46
	ComaA	0.05	0.78	1.00	-0.49	0.56
	ComaB	-0.07	0.72	1.00	-0.58	0.48

Variable1	Variable2	r	p-value	adj p-value	adj CI lower	adj CI upper
	NIB	0.09	0.64	1.00	-0.48	0.60
	NIS	0.16	0.40	1.00	-0.44	0.66
GWC	SOM	**0.85**	**0.00**	**0.00**	**0.53**	**0.96**
	pH	0.00	0.99	1.00	-0.35	0.35
	C/N	-0.16	0.40	1.00	-0.66	0.44
	TN	0.48	0.01	0.78	-0.14	0.83
	BD	0.09	0.64	1.00	-0.48	0.60
	MSL	0.18	0.33	1.00	-0.43	0.68
	gDNA	0.27	0.13	1.00	-0.36	0.73
	16S	0.15	0.42	1.00	-0.45	0.65
	ITS	0.11	0.55	1.00	-0.47	0.62
	AOA	0.05	0.79	1.00	-0.49	0.56
	AOB	0.09	0.64	1.00	-0.48	0.60
	ComaA	0.09	0.63	1.00	-0.48	0.60
	ComaB	0.24	0.18	1.00	-0.38	0.72
	NIB	0.22	0.23	1.00	-0.40	0.70
	NIS	0.09	0.63	1.00	-0.48	0.61
SOM	pH	-0.13	0.49	1.00	-0.64	0.46
	C/N	-0.14	0.46	1.00	-0.64	0.45
	TN	0.51	0.00	0.39	-0.10	0.84
	BD	-0.02	0.93	1.00	-0.49	0.47
	MSL	0.20	0.28	1.00	-0.42	0.69
	gDNA	0.17	0.36	1.00	-0.44	0.67
	16S	0.07	0.70	1.00	-0.48	0.58
	ITS	0.11	0.56	1.00	-0.47	0.62
	AOA	-0.02	0.89	1.00	-0.52	0.48
	AOB	-0.01	0.97	1.00	-0.45	0.44
	ComaA	0.04	0.82	1.00	-0.49	0.55
	ComaB	0.17	0.34	1.00	-0.43	0.67

Variable1	Variable2	r	p-value	adj p-value	adj CI lower	adj CI upper
	NIB	0.10	0.57	1.00	-0.47	0.62
	NIS	-0.04	0.83	1.00	-0.54	0.49
pH	C/N	0.24	0.18	1.00	-0.38	0.71
	TN	-0.11	0.54	1.00	-0.63	0.47
	BD	-0.21	0.24	1.00	-0.70	0.41
	MSL	-0.22	0.23	1.00	-0.70	0.40
	gDNA	-0.04	0.84	1.00	-0.54	0.49
	16S	0.02	0.91	1.00	-0.48	0.51
	ITS	0.20	0.26	1.00	-0.41	0.69
	AOA	-0.16	0.39	1.00	-0.66	0.44
	AOB	0.01	0.98	1.00	-0.43	0.44
	ComaA	0.18	0.33	1.00	-0.43	0.68
	ComaB	0.20	0.28	1.00	-0.42	0.69
	NIB	-0.08	0.68	1.00	-0.59	0.48
	NIS	-0.24	0.18	1.00	-0.72	0.38
C/N	TN	-0.50	0.00	0.54	-0.84	0.12
	BD	-0.22	0.23	1.00	-0.70	0.40
	MSL	0.02	0.92	1.00	-0.48	0.50
	gDNA	-0.15	0.42	1.00	-0.65	0.45
	16S	0.01	0.96	1.00	-0.45	0.47
	ITS	0.25	0.18	1.00	-0.38	0.72
	AOA	-0.39	0.03	1.00	-0.79	0.24
	AOB	0.12	0.51	1.00	-0.46	0.63
	ComaA	-0.13	0.48	1.00	-0.64	0.46
	ComaB	-0.11	0.53	1.00	-0.63	0.47
	NIB	-0.20	0.28	1.00	-0.69	0.42
	NIS	-0.39	0.03	1.00	-0.79	0.24
TN	BD	0.02	0.92	1.00	-0.48	0.51
	MSL	0.07	0.71	1.00	-0.48	0.58

Variable1	Variable2	r	p-value	adj p-value	adj CI lower	adj CI upper
	gDNA	0.15	0.40	1.00	-0.44	0.66
	16S	-0.03	0.86	1.00	-0.54	0.49
	ITS	-0.17	0.34	1.00	-0.67	0.43
	AOA	0.03	0.86	1.00	-0.49	0.53
	AOB	-0.01	0.96	1.00	-0.46	0.45
	ComaA	-0.08	0.67	1.00	-0.59	0.48
	ComaB	0.08	0.67	1.00	-0.48	0.59
	NIB	0.20	0.26	1.00	-0.41	0.69
	NIS	0.22	0.24	1.00	-0.40	0.70
BD	MSL	**0.60**	**0.00**	**0.04**	**0.03**	**0.88**
	gDNA	0.09	0.62	1.00	-0.48	0.61
	16S	0.07	0.71	1.00	-0.48	0.58
	ITS	0.11	0.55	1.00	-0.47	0.62
	AOA	-0.00	0.99	1.00	-0.40	0.39
	AOB	0.07	0.72	1.00	-0.48	0.58
	ComaA	-0.02	0.93	1.00	-0.50	0.47
	ComaB	-0.08	0.65	1.00	-0.60	0.48
	NIB	0.01	0.98	1.00	-0.41	0.42
	NIS	0.03	0.87	1.00	-0.48	0.53
MSL	gDNA	-0.23	0.21	1.00	-0.71	0.39
	16S	-0.26	0.15	1.00	-0.73	0.37
	ITS	-0.09	0.62	1.00	-0.61	0.48
	AOA	-0.33	0.07	1.00	-0.76	0.31
	AOB	-0.11	0.55	1.00	-0.63	0.47
	ComaA	-0.35	0.05	1.00	-0.77	0.28
	ComaB	-0.19	0.31	1.00	-0.68	0.43
	NIB	-0.18	0.31	1.00	-0.68	0.43
	NIS	-0.27	0.14	1.00	-0.73	0.36
gDNA	16S	**0.79**	**0.00**	**0.00**	**0.37**	**0.94**

Variable1	Variable2	r	p-value	adj p-value	adj CI lower	adj CI upper
	ITS	0.49	0.00	0.57	-0.12	0.84
	AOA	0.34	0.06	1.00	-0.30	0.77
	AOB	**0.64**	**0.00**	**0.01**	**0.10**	**0.89**
	ComaA	**0.64**	**0.00**	**0.01**	**0.09**	**0.89**
	ComaB	0.52	0.00	0.37	-0.10	0.84
	NIB	**0.82**	**0.00**	**0.00**	**0.44**	**0.95**
	NIS	**0.60**	**0.00**	**0.04**	**0.03**	**0.88**
16S	ITS	**0.73**	**0.00**	**0.00**	**0.25**	**0.92**
	AOA	0.14	0.45	1.00	-0.45	0.65
	AOB	**0.73**	**0.00**	**0.00**	**0.25**	**0.92**
	ComaA	**0.77**	**0.00**	**0.00**	**0.33**	**0.93**
	ComaB	**0.67**	**0.00**	**0.00**	**0.14**	**0.90**
	NIB	**0.75**	**0.00**	**0.00**	**0.28**	**0.93**
	NIS	0.34	0.06	1.00	-0.29	0.77
ITS	AOA	-0.16	0.37	1.00	-0.66	0.44
	AOB	**0.69**	**0.00**	**0.00**	**0.17**	**0.91**
	ComaA	0.55	0.00	0.16	-0.05	0.86
	ComaB	0.39	0.03	1.00	-0.24	0.79
	NIB	0.38	0.03	1.00	-0.26	0.79
	NIS	-0.06	0.72	1.00	-0.57	0.48
AOA	AOB	-0.08	0.65	1.00	-0.60	0.48
	ComaA	0.09	0.64	1.00	-0.48	0.60
	ComaB	0.11	0.56	1.00	-0.47	0.62
	NIB	0.28	0.12	1.00	-0.36	0.74
	NIS	**0.81**	**0.00**	**0.00**	**0.42**	**0.95**
AOB	ComaA	**0.63**	**0.00**	**0.02**	**0.07**	**0.89**
	ComaB	0.39	0.03	1.00	-0.24	0.79
	NIB	0.57	0.00	0.10	-0.02	0.86
	NIS	0.20	0.26	1.00	-0.41	0.69

Variable1	Variable2	r	p-value	adj p-value	adj CI lower	adj CI upper
ComaA	ComaB	**0.72**	**0.00**	**0.00**	**0.23**	**0.92**
	NIB	**0.63**	**0.00**	**0.02**	**0.07**	**0.89**
	NIS	0.25	0.17	1.00	-0.38	0.72
ComaB	NIB	**0.60**	**0.00**	**0.04**	**0.03**	**0.88**
	NIS	0.32	0.07	1.00	-0.31	0.76
NIB	NIS	0.51	0.00	0.41	-0.10	0.84

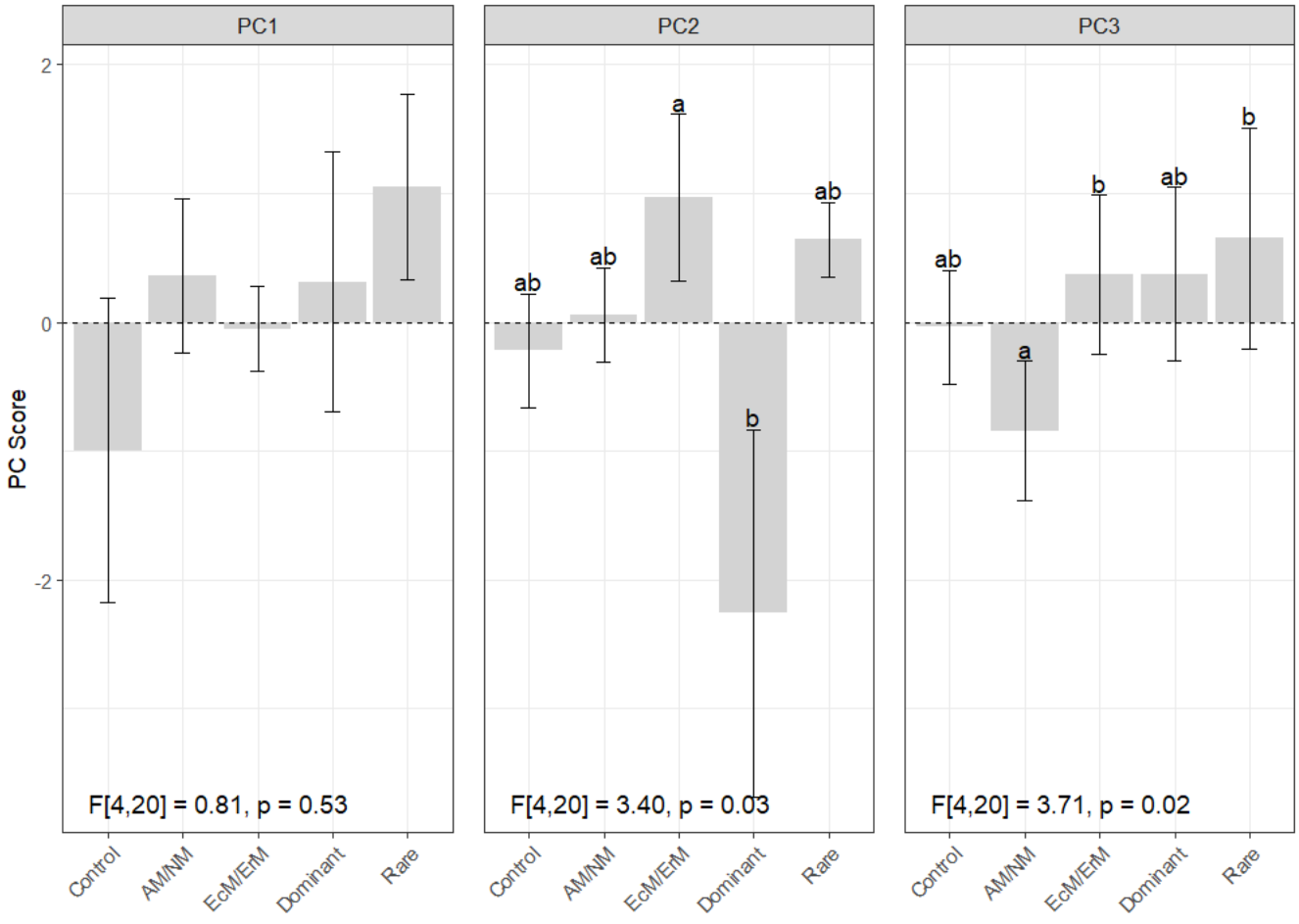


Figure S1: Principal Component Analysis (PCA) scores for soil characteristics, vegetation diversity metrics, and gene abundances across different treatments: removal of plants with ecto- and ericoid mycorrhiza associations (AM/NM), removal of plants with arbuscular mycorrhiza and no mycorrhiza associations (EcM/ErM), removal of rare plant species (Dominant), and removal of dominant plant species (Rare). The study was conducted at the Tarfala Research Station in the Tarfala Valley, northern Sweden. ANOVA was used to generate statistics for each principal component. Letters indicate significant differences from post hoc Tukey's

test; there were no significant differences if letters are absent. The percentage of variance explained by each component is PC1 (25.9%), PC2 (18.5%), and PC3 (13.7%). Error bars represent the standard error of the mean.

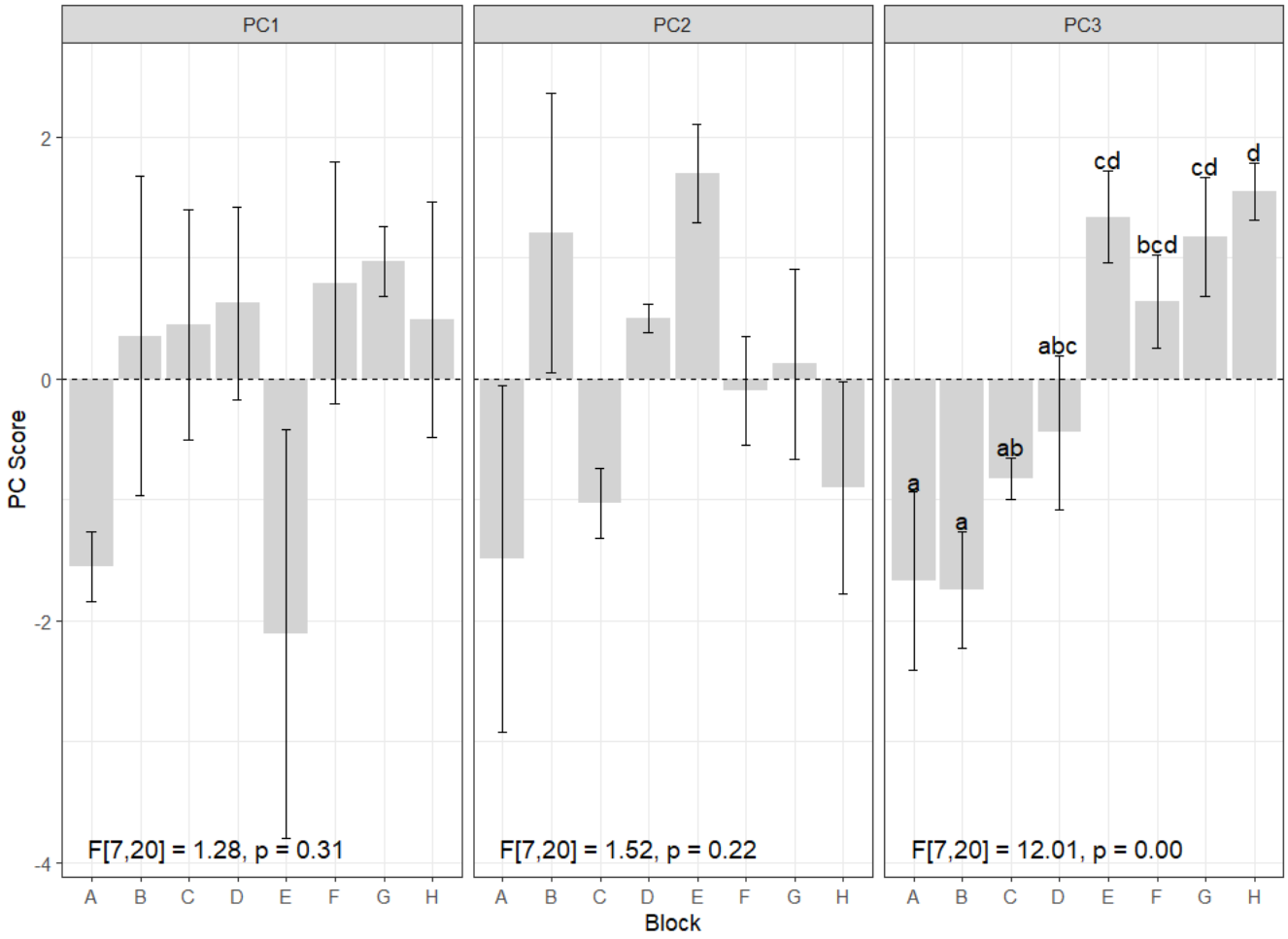


Figure S2: Principal Component Analysis (PCA) scores for soil characteristics, vegetation diversity metrics, and gene abundances across different blocks. The study was conducted at the Tarfala Research Station in the Tarfala Valley, northern Sweden. ANOVA was used to generate statistics for each principal component. Letters indicate significant differences from post hoc Tukey's test; there were no significant differences if letters are absent. The percentage of variance explained by each component is PC1 (25.9%), PC2 (18.5%), and PC3 (13.7%). Error bars represent the standard error of the mean.

Table S13: Principal Component Analysis (PCA) loadings for each variable: Simpson's diversity for vegetation (VD), field soil moisture (SMf), field soil temperature (STf), laboratory soil moisture (SM), soil organic matter (SOM), pH, soil bulk density by block (BD), elevation in meters above sea level (MSL), genomic DNA in ng/microliter (gDNA), and gene abundances in gene copies per gram of dry soil (16S, ITS, AOA, AOB, ComaA, ComaB, NIB, NIS). The study was conducted at Tarfala Research Station in the Tarfala Valley, northern Sweden. The percentage of variance explained by each component is as follows: PC1 (25.9%), PC2 (18.5%), and PC3 (13.7%).

Variable	PC1	PC2	PC3

VD	0.134	0.446	0.126
VWC	0.176	0.318	0.315
Tsoil	-0.036	-0.008	-0.516
GWC	-0.102	-0.204	0.323
SOM	-0.066	-0.279	0.285
pH	-0.078	-0.208	0.085
C/N	-0.013	-0.355	-0.132
BD	-0.141	0.204	0.356
MSL	0.127	-0.056	0.415
16S	-0.443	0.075	0.058
ITS	-0.353	-0.136	0.083
AOA	-0.043	0.317	-0.253
AOB	-0.248	-0.268	-0.084
ComaA	-0.437	0.115	0.038
ComaB	-0.37	0.065	-0.03
NIB	-0.39	0.193	0.08
NIS	-0.17	0.34	-0.138

Table S14: Raw values for environmental and soil characteristics by block. Data collected in 2019 from the Tarfala Research Station, northern Sweden include: Elevation in meters above sea level (Elevation), Simpson's diversity index for vegetation (Simpson), Ecto- and Ericoid mycorrhizal cover (EcM/ErM), field volumetric water content (VWC (%)), field soil temperature (°C) (T_{soil}), gravimetric soil water content (GWC (g/g)), soil organic matter (SOM (%)), pH in H_2O (pH), carbon to nitrogen ratio (C/N), total N (TN), gross nitrification (µmol g^{-1} C d^{-1}) (Nit), and gross mineralization (µmol g^{-1} C d^{-1}) (Min). Data are presented as mean ± standard error, n = 4 except for Nit Block B and D, and Min Block A and C where n = 3. Significance is based on general linear models using the following distributions: Elevation, pH, and C/N (Gaussian); Simpson and EcM/ErM (zero-inflated beta with a logit link); VWC, GWC, and SOM (beta); T_{soil}, TN, and Nitrification (Gamma with a log link); and Mineralization (zero-inflated Gamma with a log link). Significance codes in reference to Block A: "*" p < 0.001, "**" p < 0.01, "*" p < 0.05, "#" p < 0.1.**

Block	Elevation	Simpson	EcM/ErM	VWC	T_{soil}	GWC	SOM	pH	C/N	TN	Nit	Min
A	1098.8±0.3	0.8±0.1	0.4±0.2	21.3±1.7	11.0±0.2	56.4±4.0	35.1±5.8	5.1±0.1	15.6±0.7	1.3±0.1	0.3±0.1	14.2±3.8
B	1101.3±0.2 ***	0.9±0.0	0.2±0.2	29.2±1.3 ***	11.2±0.1	53.4±2.5	33.7±4.7	4.8±0.1 **	15.2±0.9	0.8±0.2	0.1±0.0 **	10.7±5.8
C	1103.6±0.3 ***	0.9±0.0	0.2±0.1	24.5±1.2	10.8±0.1	49.5±2.3 *	32.2±2.7	5.0±0.1	16.2±0.5	0.8±0.1	0.1±0.0 #	6.4±2.7
D	1101.9±0.2 ***	0.9±0.0	0.2±0.1 #	29.0±2.1 ***	10.5±0.3 *	53.6±1.9	29.9±1.3	5.0±0.0	14.6±0.4	0.8±0.1	0.2±0.0	16.8±5.3

E	1103.2±0.2 ***	1.0±0.0 #	0.1±0.1 #	31.4±2.3 ***	10.5±0.2 *	52.4±3.6	30.6±3.7	5.0±0.1	14.4±0.9	1.5±0.7	0.2±0.0	2.4±1.4 #
F	1105.4±0.3 ***	0.9±0.0	0.1±0.1 *	31.3±3.3 ***	10.4±0.2 **	53.9±2.4	29.8±1.5	5.0±0.0	15.6±0.3	0.7±0.1 #	0.1±0.0 #	5.5±2.3
G	1107.8±0.4 ***	0.9±0.0	0.0±0.0 **	29.7±2.0 ***	10.1±0.1 ***	56.8±1.7	37.4±3.2	4.9±0.1 #	14.6±1.6	1.5±0.4	0.2±0.0	7.4±2.5
H	1113.2±0.3 ***	0.9±0.0	0.2±0.1 *	27.5±1.0 **	10.5±0.2 *	60.7±1.9	42.4±3.3 #	4.9±0.1	15.5±1.0	1.2±0.1	0.2±0.1	5.1±2.3

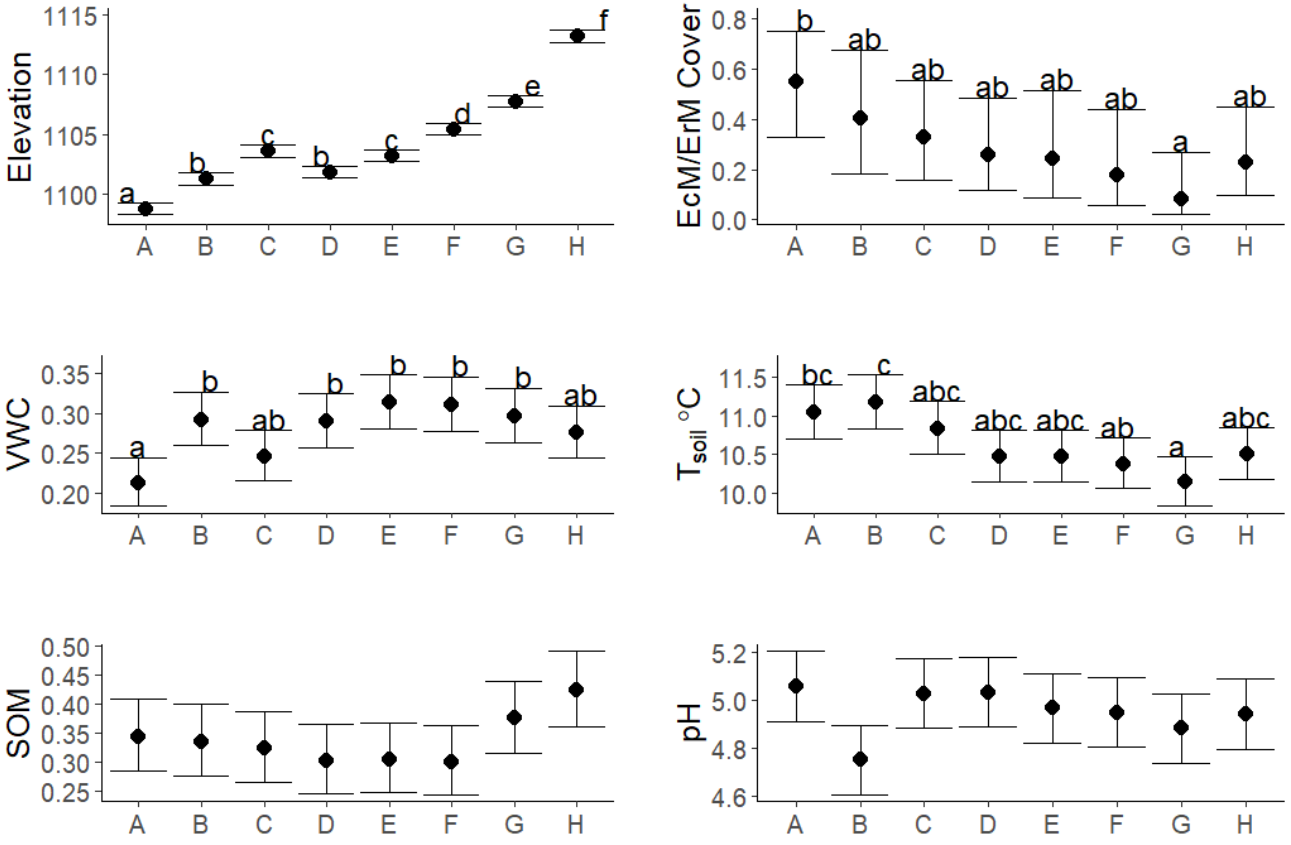
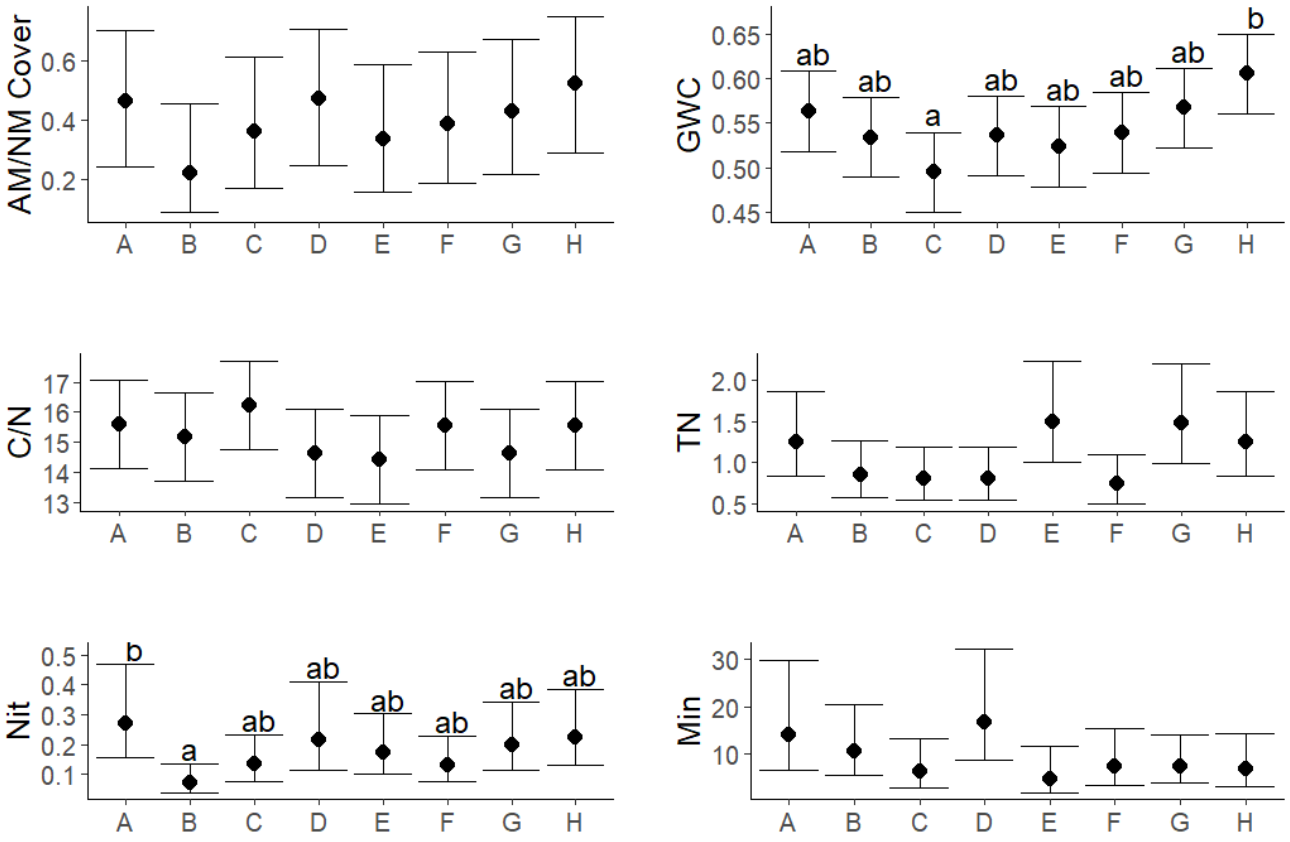


Figure S3a: Environmental gradients by block. Modeled data based on general linear models using the following distributions: Elevation (ma.s.l.) follows a Gaussian distribution; EcM/ErM Species Cover follows a zero-inflated beta distribution with a logit link; volumetric water content (VWC) and Soil Organic Matter (SOM) follow beta distributions; Field Soil Temperature (T_{soil}) follows a Gamma distribution with a log link; and pH follows a Gaussian distribution. Letters in the figures represent significance from pairwise post-hoc comparisons; absent letters indicate no significant differences.



125 **Figure S3b: Environmental gradients by block. Modeled data based on general linear models using the following distributions: AM/NM Species Cover follows a zero-inflated beta distribution with a logit link; gravimetric soil water content (GWC (g/g)) follows a beta distribution; C/N ratio follows a Gaussian distribution; total N (TN) and gross Nitrification (µmol g^{-1} C d^{-1}) (Nit) follows a Gamma distribution with a log link; and gross Mineralization (µmol g^{-1} C d^{-1}) (Min) follows a zero-inflated Gamma distribution with a log link. Letters in the figures represent significance from pairwise post-hoc comparisons; absent letters indicate no significant**
130 **differences.**

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