



Supplement of

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

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S1 Supplementary tables and figures

15 S1.1 Methods

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

Treatment	Plot	Total Species Removed	AM/NM Species Removed	EcM/ErM Species Removed	Mixed Myco Species Removed
Rare	B2	7	3	2	2
	E2	10	6	2	2
	F3	11	4	6	1
	G1	9	4	3	2
Dominant	A4	8	4	3	1
	C3	9	6	3	0
	D4	9	3	5	1
	H2	9	6	3	0

20 Table S2. Summary table of 2015 (before treatment) and 2019 (¹⁵N experimental year) absolute abundance ± standard deviation for AM/NM and EcM/ErM plants for each treatment.

	2015		2019	
Treatment	AM/NM	EcM/ErM	AM/NM	EcM/ErM

Control	30 ± 15	27 ± 17	48 ± 17	30 ± 19
AM/NM	41 ± 15	27 ± 12	54 ± 19	0 ± 0
EcM/ErM	44 ± 14	27 ± 17	0 ± 0	15 ± 14
Dominant	25 ± 18	38 ± 35	31 ± 18	43 ± 34
Rare	31 ± 21	38 ± 17	7 ± 5	0.3 ± 0.5

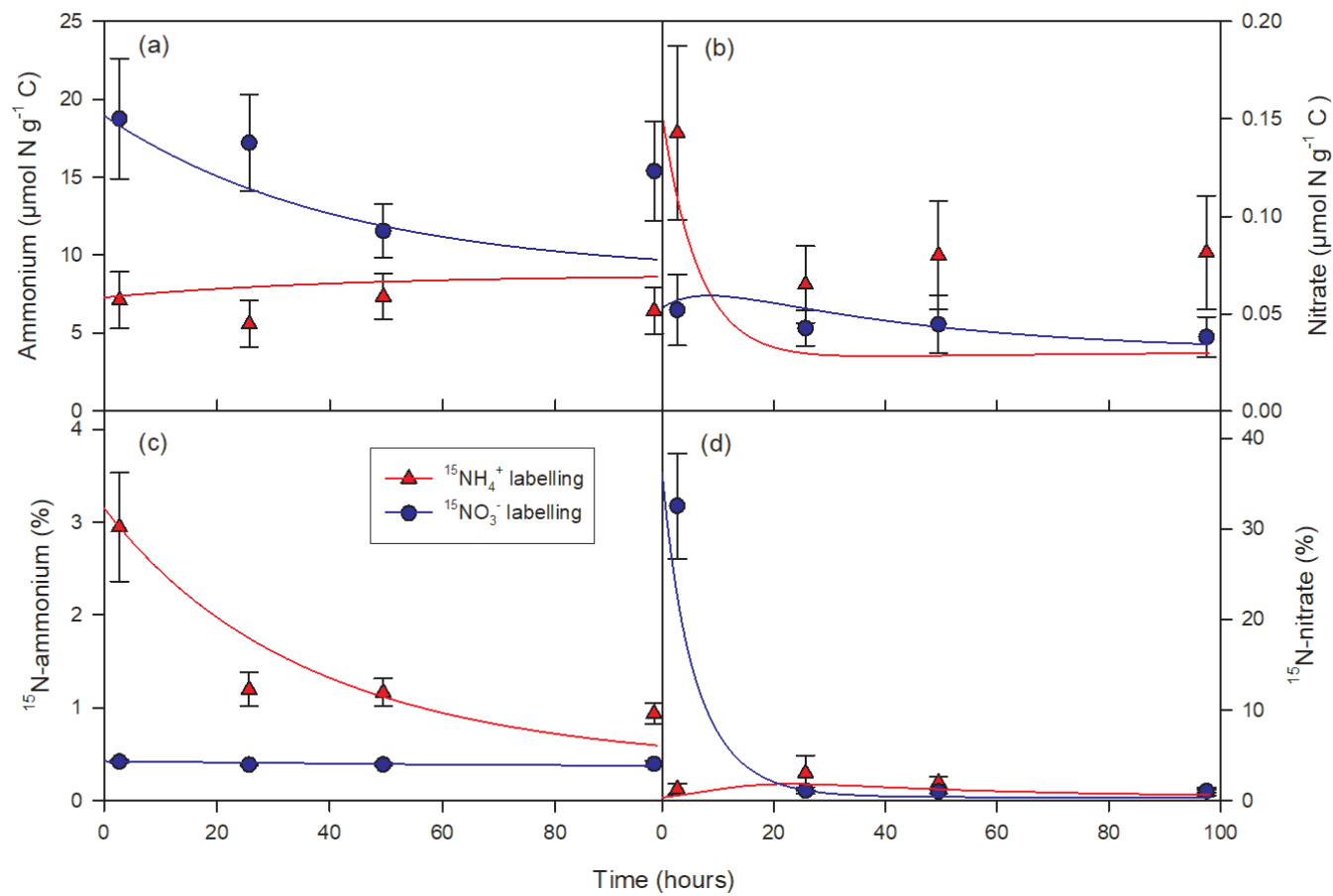


Figure S1: Model fit of Ntrace simulations to observed (a) ammonium, (b) nitrate, (c) ^{15}N -ammonium, and (d) ^{15}N -nitrate enrichments (% of total) for control plots.

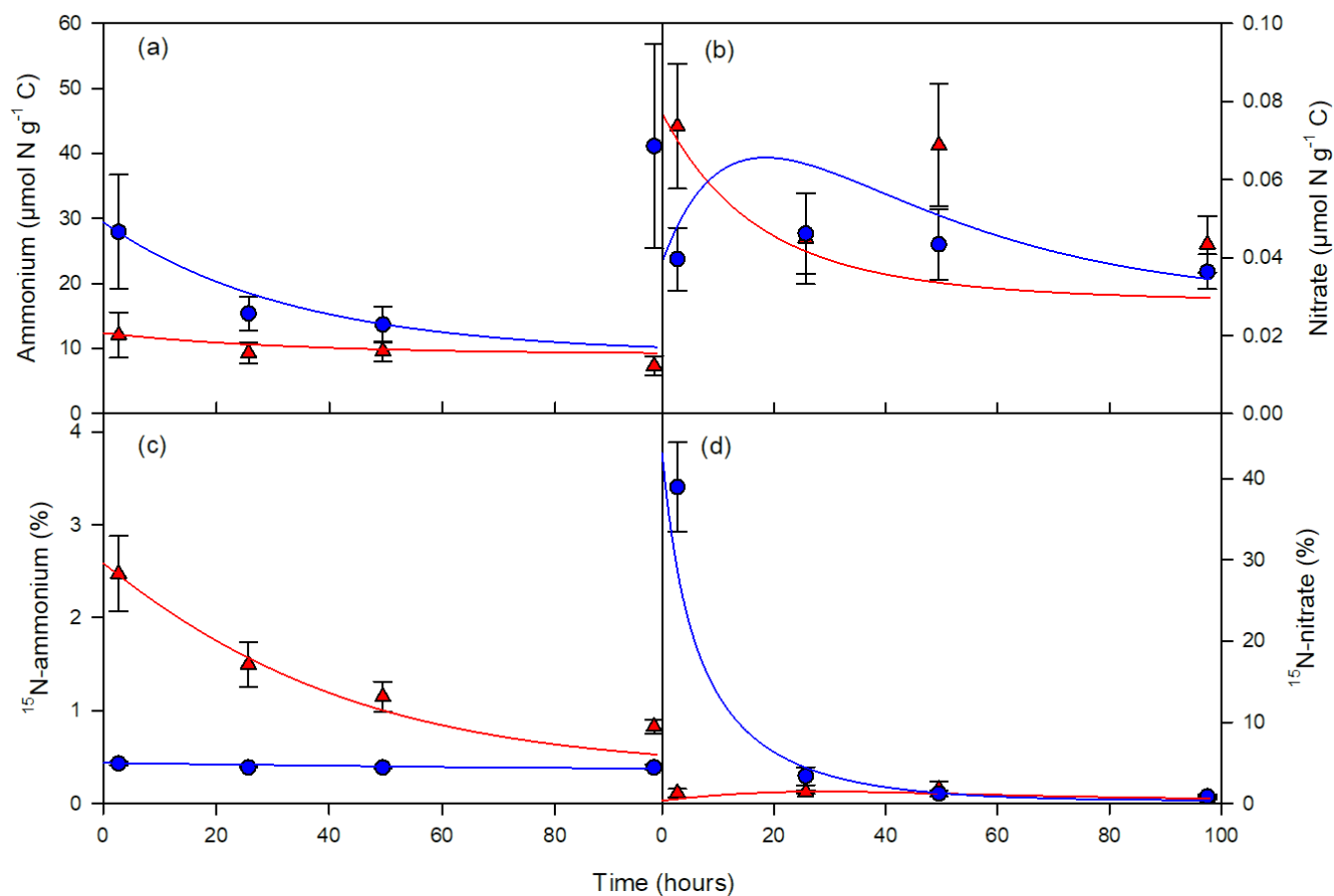


Figure S2: Model fit of Ntrace simulations to observed (a) ammonium, (b) nitrate, (c) ^{15}N -ammonium, and (d) ^{15}N -nitrate enrichments (% of total) for arbuscular mycorrhizal and non-mycorrhizal (AM/NM) plots.

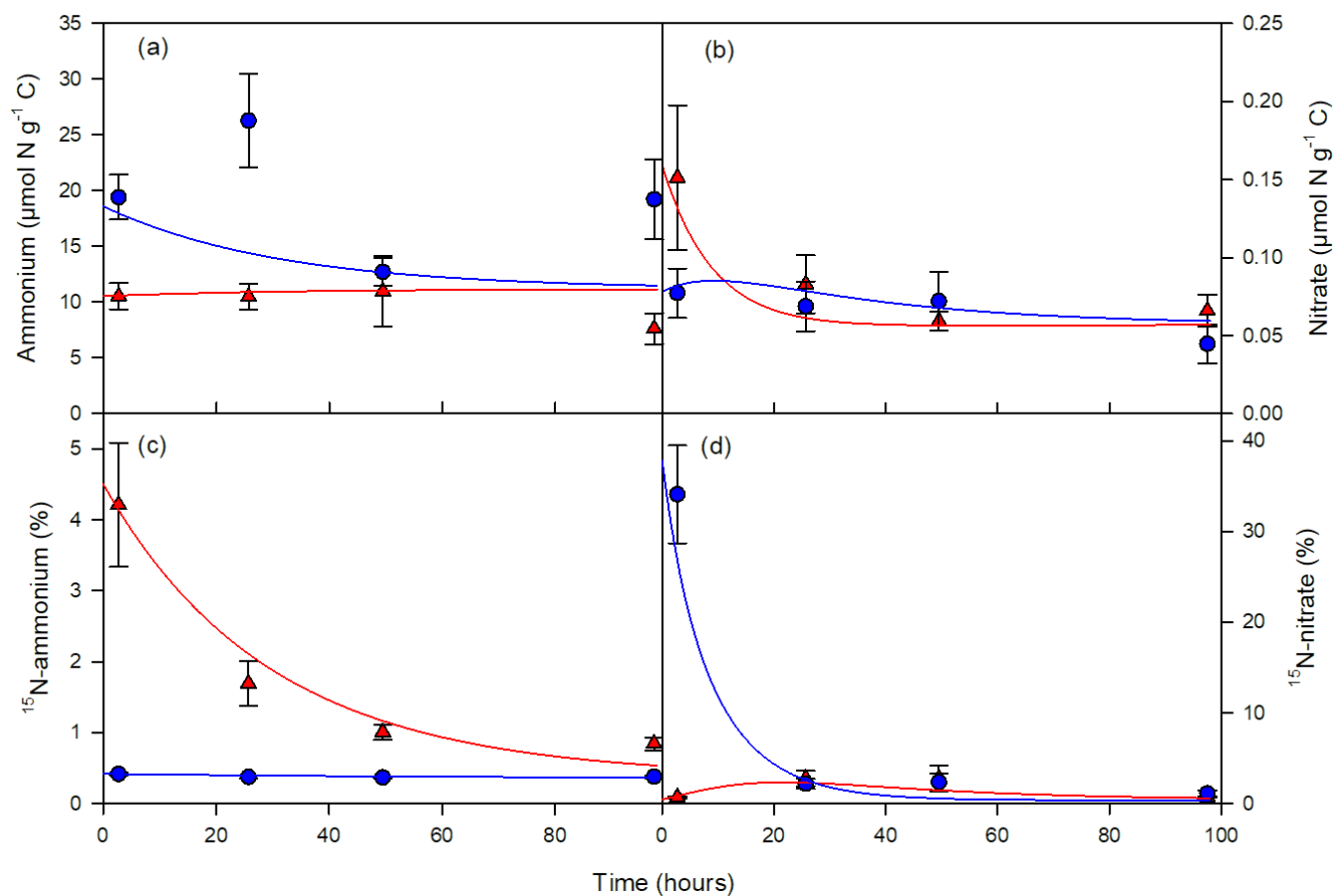
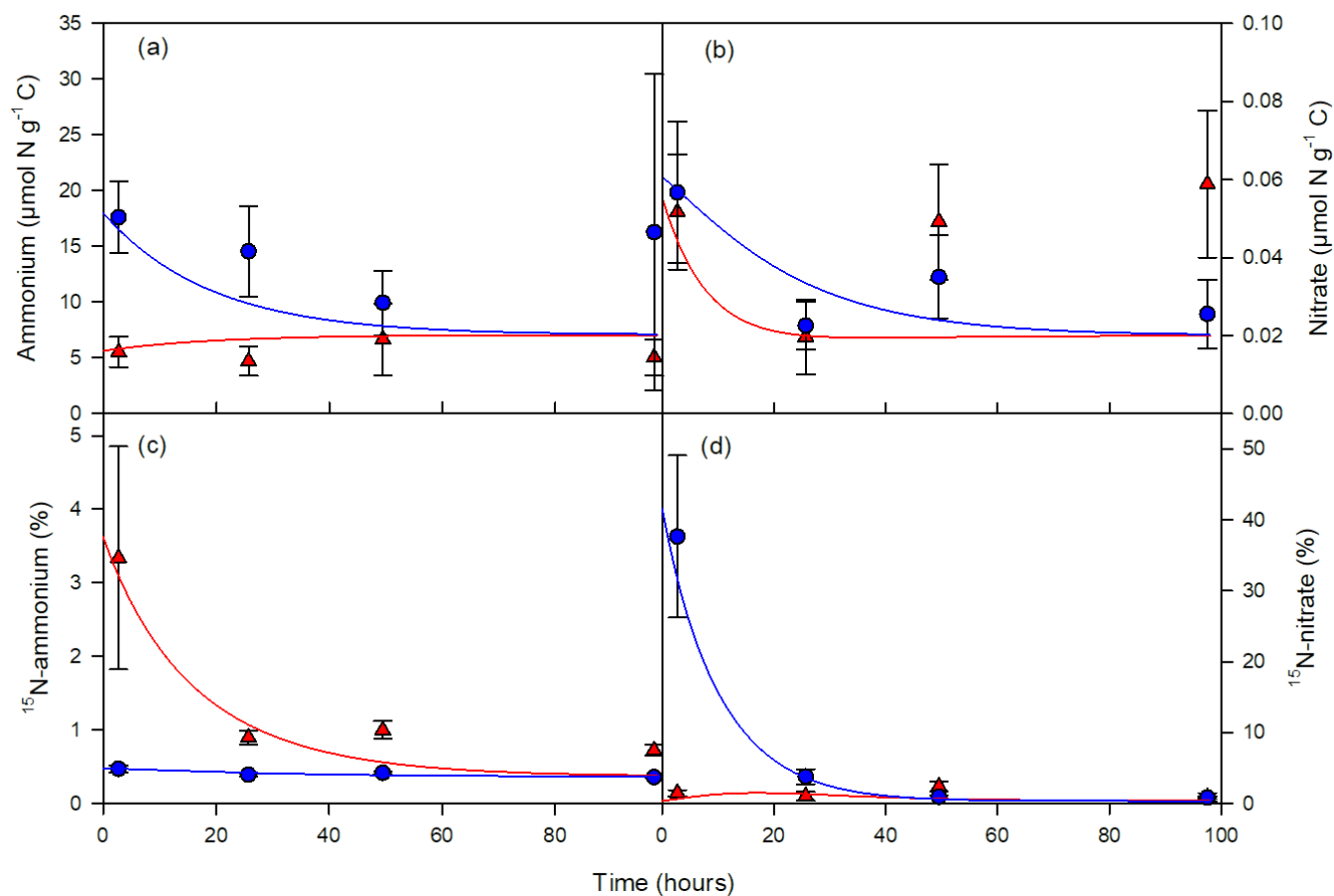


Figure S3: Model fit of Ntrace simulations to observed (a) ammonium, (b) nitrate, (c) ^{15}N -ammonium, and (d) ^{15}N -nitrate enrichments (% of total) for ectomycorrhizal and ericoid mycorrhizal (EcM/ErM) plots.



35 **Figure S4: Model fit of Ntrace simulations to observed (a) ammonium, (b) nitrate, (c) ^{15}N -ammonium, and (d) ^{15}N -nitrate enrichments (% of total) for Dominant plots.**

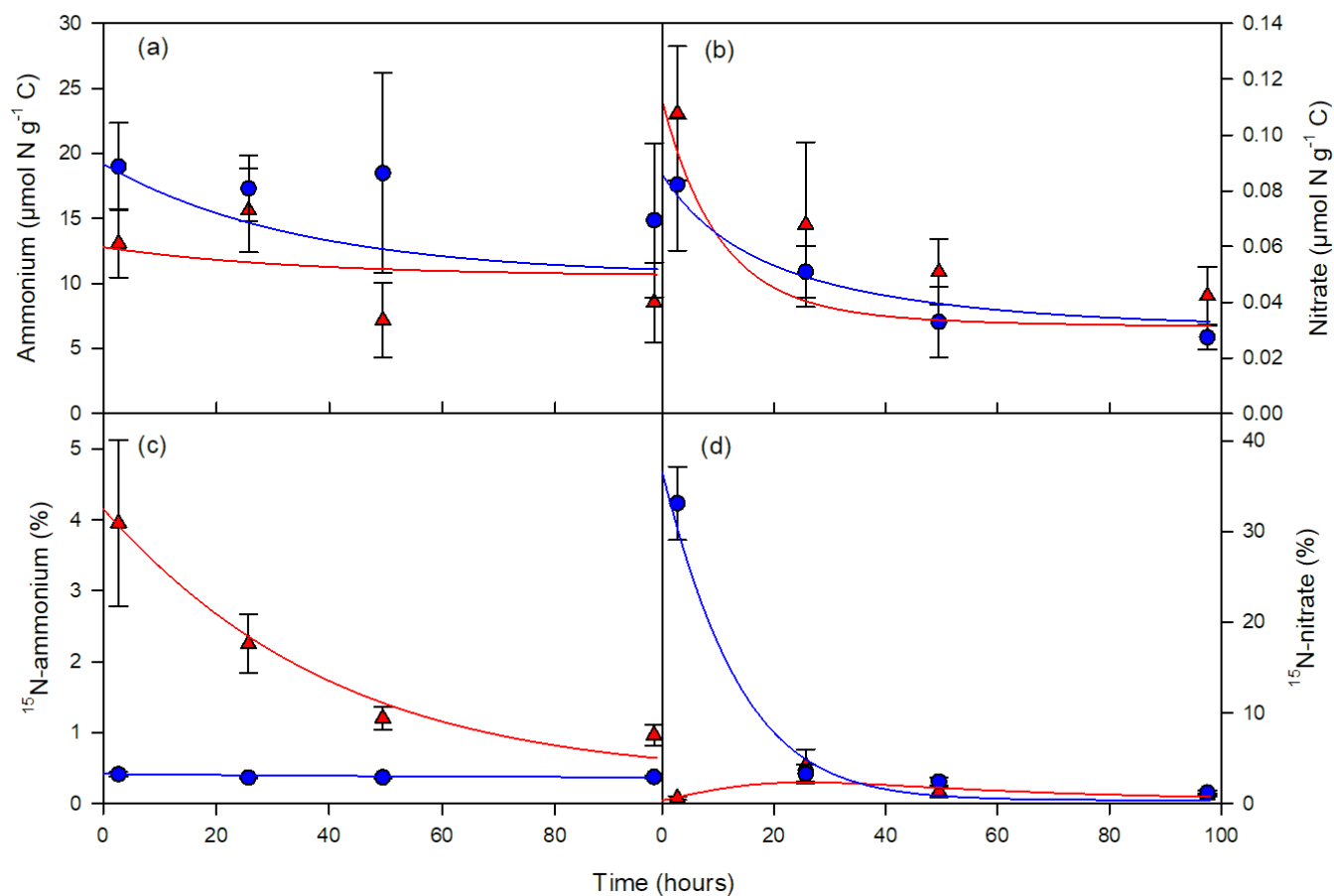


Figure S5: Model fit of Ntrace simulations to observed (a) ammonium, (b) nitrate, (c) ^{15}N -ammonium, and (d) ^{15}N -nitrate enrichments (% of total) for Rare plots.

Table S3: 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	(Tournu 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	nxB	Forward	nxB1-F	5'-ACGTGGAGACCAAGCCGGG-3'	0.5	(Vanparys et al., 2007)
		Reverse	nxB1-R	5'-CCGTGCTGTTGAYCTCGTTGA-3'		
Nitrospira-type nitrite oxidizer	nxB	Forward	nxB169f	5'-TACATGTGGTGGAACA-3'	0.5	(Pester et al., 2014)

		Reverse	nxB638r	5'-CGGTTCTGGTCRATCA-3'		

Table S4. 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
nxB 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
nxB 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
nxB NIB		15 s at 95°C	30 s at 67°C	30 s at 72°C	5 s at 78°C	27	

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S1.2 Soil characteristics

Table S5. 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#.

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	VWC			T _{soil}			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 .43 001	<0. 001	0.56 (0.52 - 0.59)	29. 81 001	<0. 001	0.59 (0.48 - 0.73)	- 5. 02	<0. 001	4.93 (4.82 - 5.05)	84. 60 001	<0. 001	1.07 (1.06 - 1.07)	30. 15 001	<0. 001	0.01 (0.01 - 0.01)	- 28. 03	<0. 001
AM/NM	1.03 (0.87 - 1.23)	0.3 8	0.70 4	1.01 (1.00 - 1.02)	1.4 8	0.13 9	-0.04 (- 0.09 - 0.01)	- 1.4 9	0.13 6	0.71 (0.54 - 0.95)	- 2. 35	0.01 9*	-0.07 (- 0.22 - 0.09)	- 0.8 6	0.39 1	1.00 (0.99 - 1.00)	- 0.3 7	0.70 8	0.83 (0.52 - 1.31)	- 0.8 1	0.42 1

EcM/Er	1.21	2.1	0.02	0.99	-	0.06	-0.01	-	0.74	0.86	-	0.29	0.06	0.7	0.42	1.00	1.5	0.12	1.27	1.1	0.26
M	(1.02	9	8*	(0.98	1.8	0[#]	(-	0.3	7	(0.66	1.	4	(-	9	7	(1.00	3	7	(0.84	2	1
	-			-	8		0.06	2		-	05		0.09			-		-			
	1.43)			1.00)			-			1.14)			-			1.01)			1.93)		
							0.04)						0.21)								
Domina	1.17	1.3	0.16	0.98	-	0.01	0.02	0.6	0.53	1.03	0.	0.88	0.06	0.5	0.57	0.99	-	0.10	0.94	-	0.82
nt	(0.94	9	6	(0.97	2.4	5*	(-	1	9	(0.73	15	1	(-	7	1	(0.99	1.6	8	(0.54	0.2	1
	-			-	4		0.04			-			0.14			-	1	-	3		
	1.46)			1.00)			-			1.44)			-			1.00)			1.62)		
							0.08)						0.26)								
Rare	1.20	1.6	0.10	0.99	-	0.41	-0.02	-	0.53	0.78	-	0.16	0.11	1.0	0.30	1.00	0.4	0.68	1.03	0.1	0.91
	(0.97	4	2	(0.98	0.8	2	(-	0.6	8	(0.55	1.	0	(-	4	0	(0.99	1	1	(0.61	1	5
	-			-	2		0.08	2		-	41		0.09			-		-			
	1.49)			1.01)			-			1.10)			-			1.01)			1.75)		
							0.04)						0.30)								
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		
Margin al R ² / Condi ti onal 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		

S1.3 Gross rates

Table S6: Gross nitrogen (N) transformation rates (mean and 85% confidence interval) estimated using either the ¹⁵N 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 NH₄⁺; O_{NH4} = NH₄⁺ oxidation; I_{NO3} = Immobilization of NO₃⁻; 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.

	<i>Ntrace</i>				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

S1.4 qPCR

65 **Table S7: 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)

70 **Table S8: 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 #.**

<i>Predictors</i>	gDNA			16S			ITS		
	<i>Estimates</i>	<i>Statistic</i>	<i>p</i>	<i>Estimates</i>	<i>Statistic</i>	<i>p</i>	<i>Estimates</i>	<i>Statistic</i>	<i>p</i>
Intercept	4.67	55.26	<0.001	9.39	184.33	<0.001	8.14	105.76	<0.001
	(4.50 –			(9.29 –			(7.99 –		
	4.83)			9.49)			8.29)		

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	0.000 / NA			0.042 / NA			0.110 / NA		
Conditional R ²									

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Table S9: 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)

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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 S10: 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.

Predictors	ITS:16S			AOA:AOB			ComaA:ComaB			NIS:NIB		
	Estimate	Statisti	p	Estimate	Statisti	p	Estimate	Statisti	p	Estimate	Statisti	p
	s	c		s	c		s	c		s	c	
Intercept	0.06 (0.05 – 0.08)	-24.83	<0.00 1	29.03 (17.24 – 48.87)	12.67	<0.00 1	9.13 (7.38 – 11.31)	20.33	<0.00 1	114.04 (84.40 – 154.10)	30.84	<0.00 1
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}		

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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 S11: 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 S12), 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 ±	1.50e+05 ±	7.05e+06 ±	8.31e+05 ±	3.47e+05 ±	3.98e+07 ±
		7.39e+05	2.70e+04	1.61e+06	1.72e+05	7.01e+04	8.13e+06
AM/NM	8	3.71e+06 ±	1.43e+05 ±	5.05e+06 ±	6.63e+05 ±	3.11e+05 ±	3.65e+07 ±
		5.41e+05	2.33e+04	7.48e+05	1.44e+05	3.77e+04	4.20e+06
EcM/ErM	8	4.46e+06 ±	1.23e+05 ±	6.13e+06 ±	7.48e+05 ±	3.32e+05 ±	4.49e+07 ±
		1.45e+06	5.46e+03	2.94e+05	9.98e+04	2.25e+04	8.41e+06
Dominant	4	1.89e+06 ±	2.46e+05 ±	4.61e+06 ±	4.51e+05 ±	2.50e+05 ±	2.20e+07 ±
		7.73e+05**	1.38e+05	9.15e+05	9.63e+04	3.76e+04	6.73e+06[#]
Rare	4	3.32e+06 ±	1.10e+05 ±	4.75e+06 ±	4.83e+05 ±	3.09e+05 ±	2.69e+07 ±
		1.39e+06	1.80e+04	8.12e+05	9.71e+04	2.27e+04	5.90e+06

95 **Table S12: 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		
Predictor s	Estima tes	Statis tic	p	Estima tes	Statis tic	p	Estima tes	Statis tic	p	Estima tes	Statis tic	p	Estima tes	Statis tic	p	Estima tes	Statis tic	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)	105.4 5	<0.001	5.84 (5.68 – 5.99)	72.79	<0.001	5.49 (5.38 – 5.59)	107.3 2	<0.001	7.52 (7.38 – 7.67)	100.7 0	<0.001
AM/NM	0.01 (-0.20 – 0.22)	0.11	0.913	-0.00 (-0.20 – 0.19)	-0.03 8	0.97	-0.12 (-0.30 – 0.05)	-1.37 1	0.17	-0.09 (-0.31 – 0.13)	-0.79 7	0.42	-0.02 (-0.16 – 0.13)	-0.22 9	0.82	0.02 (-0.17 – 0.20)	0.17 4	0.86
EcM/Er M	0.02 (-0.19 – 0.22)	0.16	0.877	-0.04 (-0.23 – 0.16)	-0.36 1	0.72	0.00 (-0.17 – 0.18)	0.05 4	0.96	0.01 (-0.21 – 0.23)	0.07 0	0.94	0.03 (-0.11 – 0.17)	0.38 3	0.70	0.08 (-0.11 – 0.27)	0.84 3	0.40
Dominan t	-0.36 (-0.63 – 0.10)	-2.70	0.007 **	0.10 (-0.13 – 0.34)	0.86 0	0.39	-0.14 (-0.36 – 0.07)	-1.31 0	0.19	-0.22 (-0.49 – 0.05)	-1.57 6	0.11	-0.10 (-0.28 – 0.07)	-1.18 9	0.23	-0.22 (-0.46 – 0.01)	-1.88 9[#]	0.05
Rare	-0.13 (-0.39 – 0.14)	-0.95	0.344	-0.10 (-0.33 – 0.14)	-0.82 4	0.41	-0.12 (-0.34 – 0.09)	-1.13 9	0.25	-0.18 (-0.45 – 0.10)	-1.27 3	0.20	0.00 (-0.17 – 0.17)	0.01 3	0.99	-0.13 (-0.37 – 0.10)	-1.13 7	0.25
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 R^2 / Conditional R^2	0.174 / 0.519	0.069 / 0.080	0.119 / 0.143	0.124 / NA	0.069 / NA	0.184 / 0.342

S1.5 Environment

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Table S13: 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
	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

Variable1	Variable2	r	p-value	adj p-value	adj CI lower	adj CI upper
	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
	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

Variable1	Variable2	r	p-value	adj p-value	adj CI lower	adj CI upper
	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
	pH	-0.13	0.49	1.00	-0.64	0.46
	C/N	-0.14	0.46	1.00	-0.64	0.45
SOM	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
	NIB	0.10	0.57	1.00	-0.47	0.62
	NIS	-0.04	0.83	1.00	-0.54	0.49
	C/N	0.24	0.18	1.00	-0.38	0.71
	TN	-0.11	0.54	1.00	-0.63	0.47
pH						

Variable1	Variable2	r	p-value	adj p-value	adj CI lower	adj CI upper
C/N	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
	TN	-0.50	0.00	0.54	-0.84	0.12
TN	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
	BD	0.02	0.92	1.00	-0.48	0.51
TN	MSL	0.07	0.71	1.00	-0.48	0.58
	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

Variable1	Variable2	r	p-value	adj p-value	adj CI lower	adj CI upper
BD	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
	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
	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

Variable1	Variable2	r	p-value	adj p-value	adj CI lower	adj CI upper
16S	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
	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
ITS	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
	AOA	-0.16	0.37	1.00	-0.66	0.44
	AOB	0.69	0.00	0.00	0.17	0.91
AOA	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
	AOB	-0.08	0.65	1.00	-0.60	0.48
	ComaA	0.09	0.64	1.00	-0.48	0.60
AOB	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
	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
ComaA	NIS	0.20	0.26	1.00	-0.41	0.69
	ComaB	0.72	0.00	0.00	0.23	0.92
	NIB	0.63	0.00	0.02	0.07	0.89
ComaB	NIS	0.25	0.17	1.00	-0.38	0.72
	NIB	0.60	0.00	0.04	0.03	0.88

Variable1	Variable2	r	p-value	adj p-value	adj CI lower	adj CI upper
	NIS	0.32	0.07	1.00	-0.31	0.76
NIB	NIS	0.51	0.00	0.41	-0.10	0.84

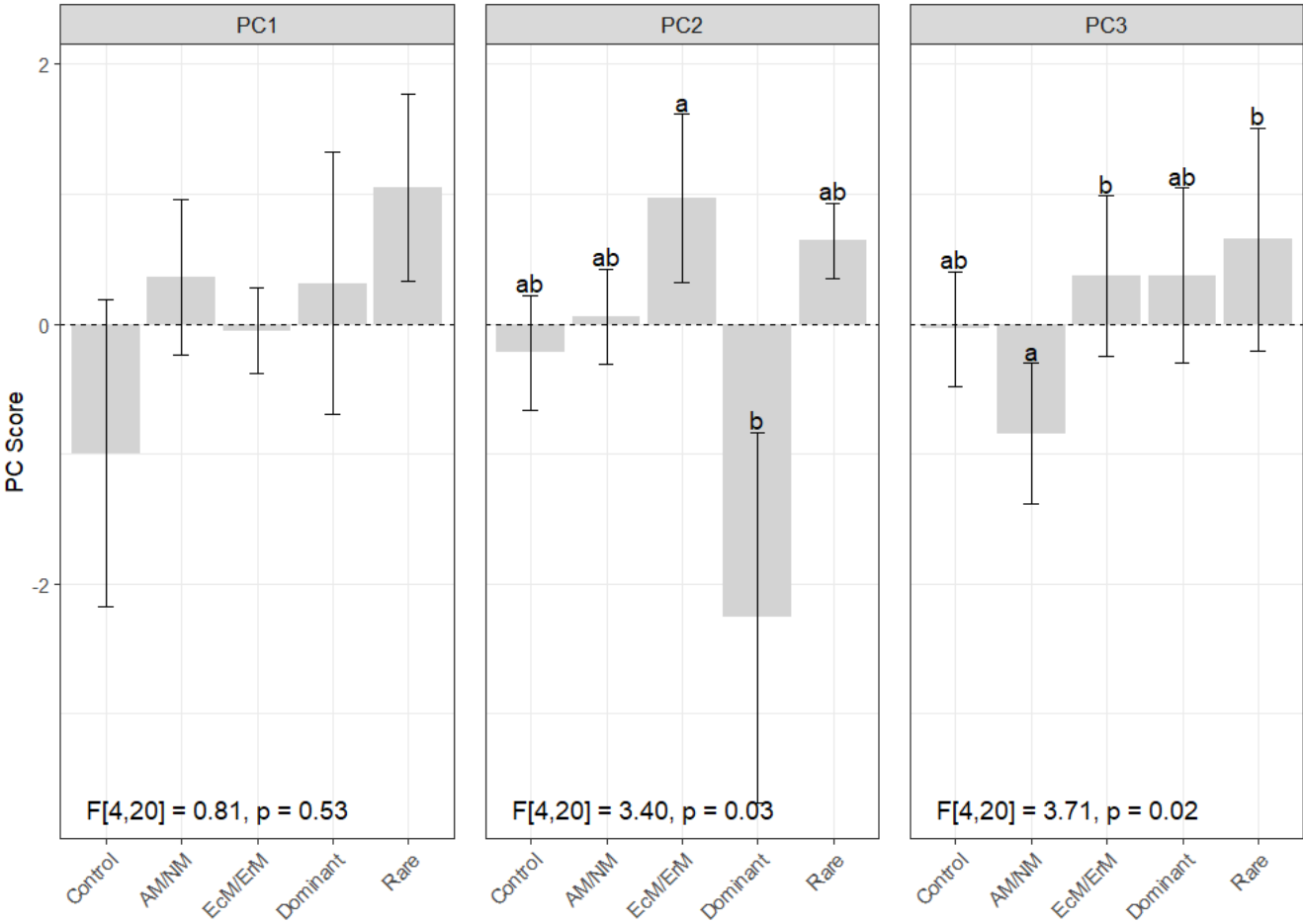


Figure S6: Principal Component Analysis (PCA) scores for soil characteristics, vegetation diversity metrics, and gene abundances across different treatments: removal of plants with ecto- and ericoid mycorrhiza associations (AM/NM), removal of plants with arbuscular mycorrhiza and no mycorrhiza associations (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.

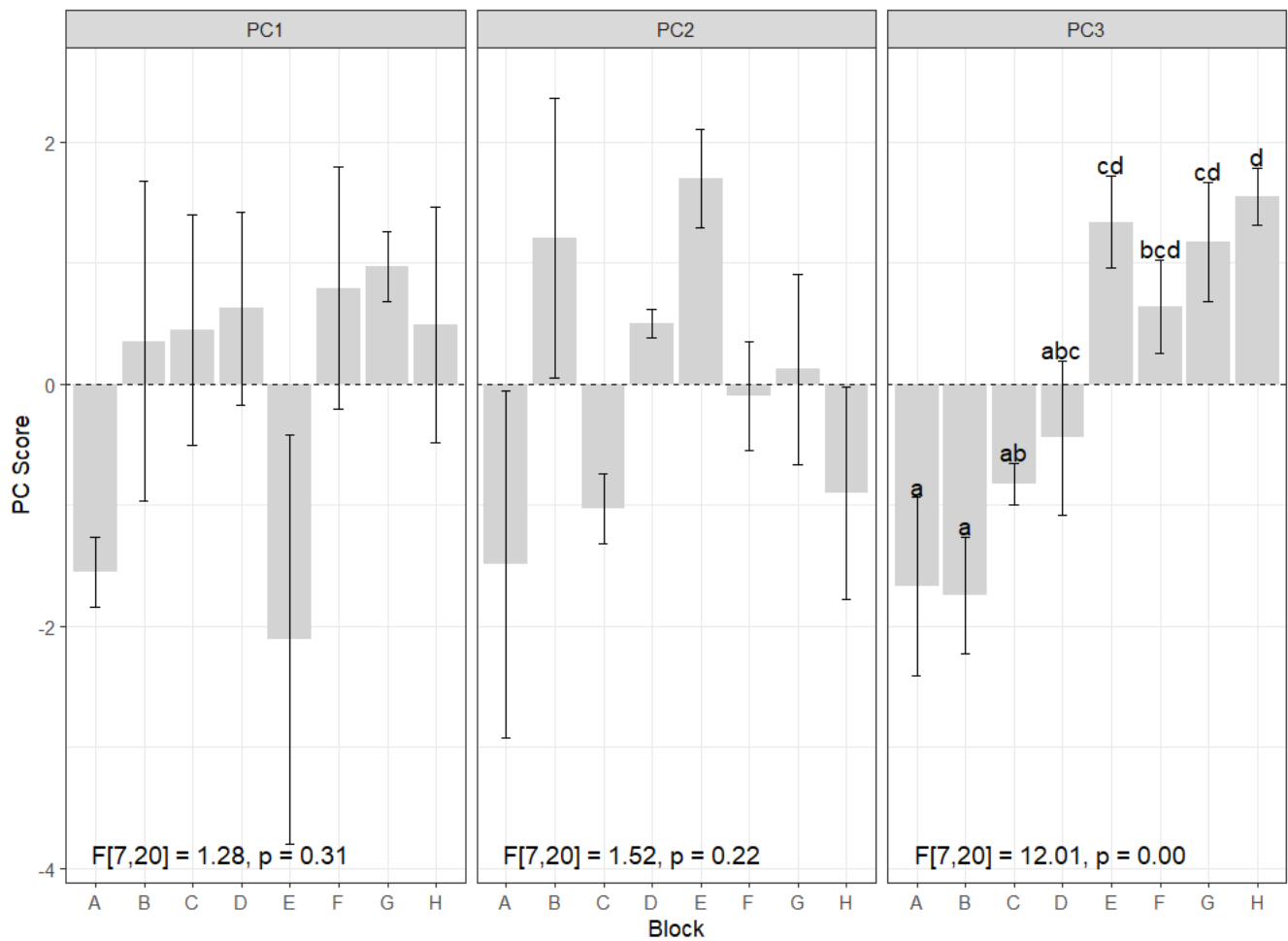


Figure S7: Principal Component Analysis (PCA) scores for soil characteristics, vegetation diversity metrics, and gene abundances across different blocks. ANOVA was used to generate statistics for each principal component. Letters indicate significant differences from post hoc Tukey's test; there were 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.

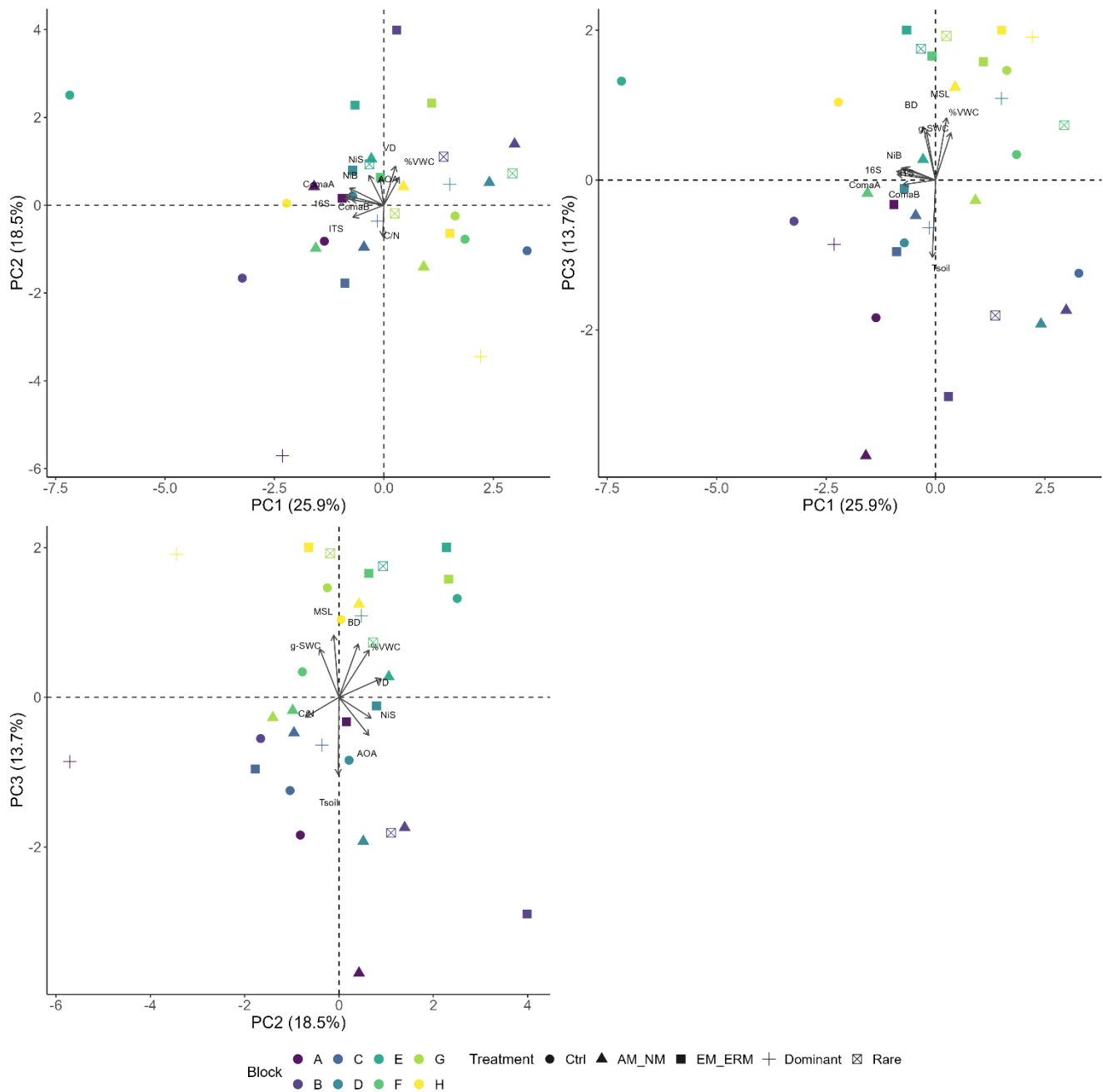


Figure S8: Principal Component Analysis (PCA) biplots for the first three components, showing relationships between soil characteristics, vegetation diversity metrics, and gene abundances across treatments: removal of plants with ecto- and ericoid mycorrhiza associations (AM/NM), removal of plants with arbuscular mycorrhiza and no mycorrhiza associations (EcM/ErM), removal of rare plant species (Dominant), and removal of dominant plant species (Rare). Arrows represent variable loadings. Only variables with loadings greater than 0.3 on the respective components are shown.

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Table S14: 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 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

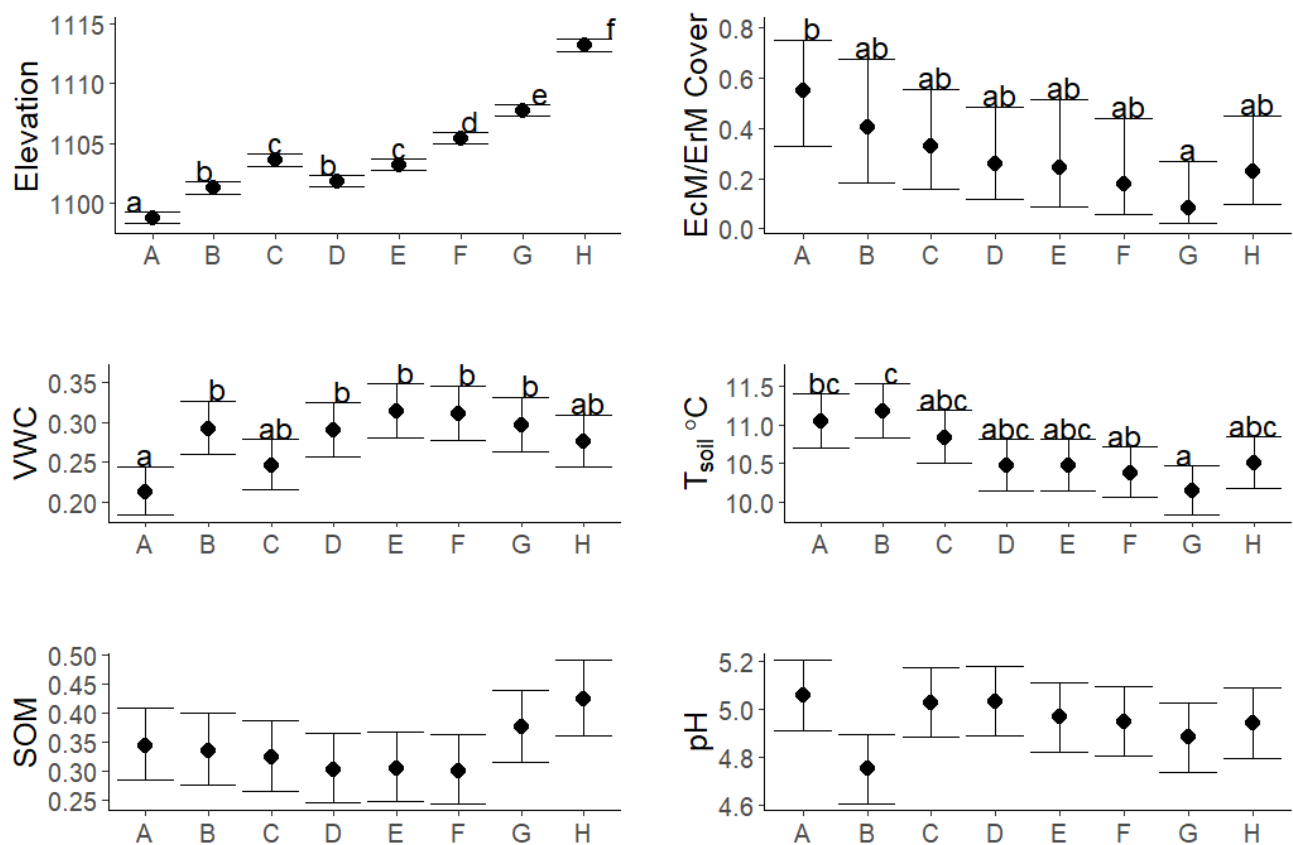
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Table S15: Raw values for environmental and soil characteristics by block. Data collected in 2019 from the Tarfala Research Station, northern Sweden include: Elevation in meters above sea level (Elevation), Simpson's diversity index for vegetation (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 H₂O (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.**

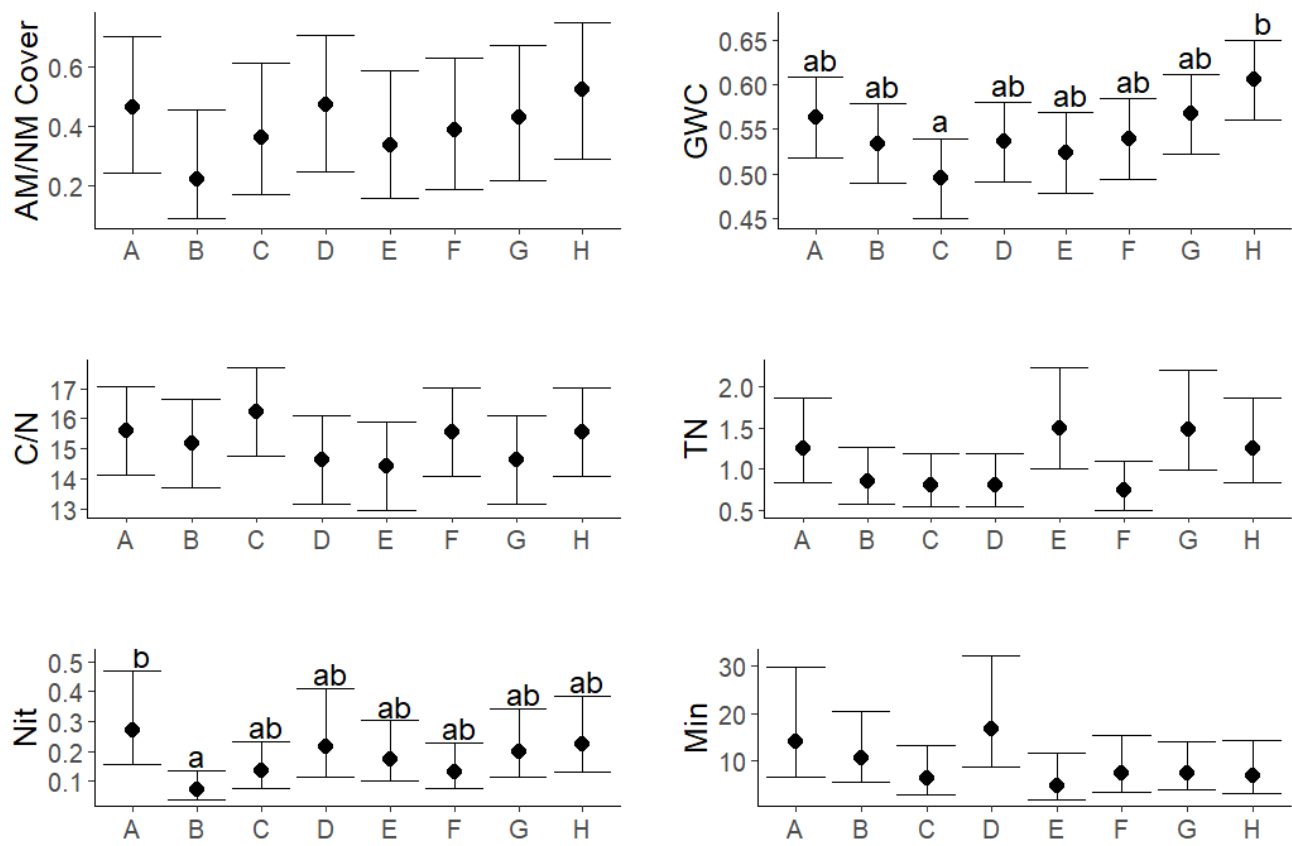
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Block	Elevation	Simpson	EcM/ErM	VWC	T _{soil}	GWC	SOM	pH	C/N	TN	Nit	Min
A	1098.8±0.3	0.8±0.1	0.4±0.2	21.3±1.7	11.0±0.2	56.4±4.0	35.1±5.8	5.1±0.1	15.6±0.7	1.3±0.1	0.3±0.1	14.2±3.8
B	1101.3±0.2 ***	0.9±0.0	0.2±0.2	29.2±1.3 ***	11.2±0.1	53.4±2.5	33.7±4.7	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



150 **Figure S9a: 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.



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Figure S9b: 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 ($\mu\text{mol g}^{-1} \text{C d}^{-1}$) (Nit) follows a Gamma distribution with a log link; and gross Mineralization ($\mu\text{mol g}^{-1} \text{C d}^{-1}$) (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 differences.

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