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Continental scale structuring of forest and soil diversity via functional traits

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Supplemental Document - Extended Data Tables, Extended Data Figures, and Box 1

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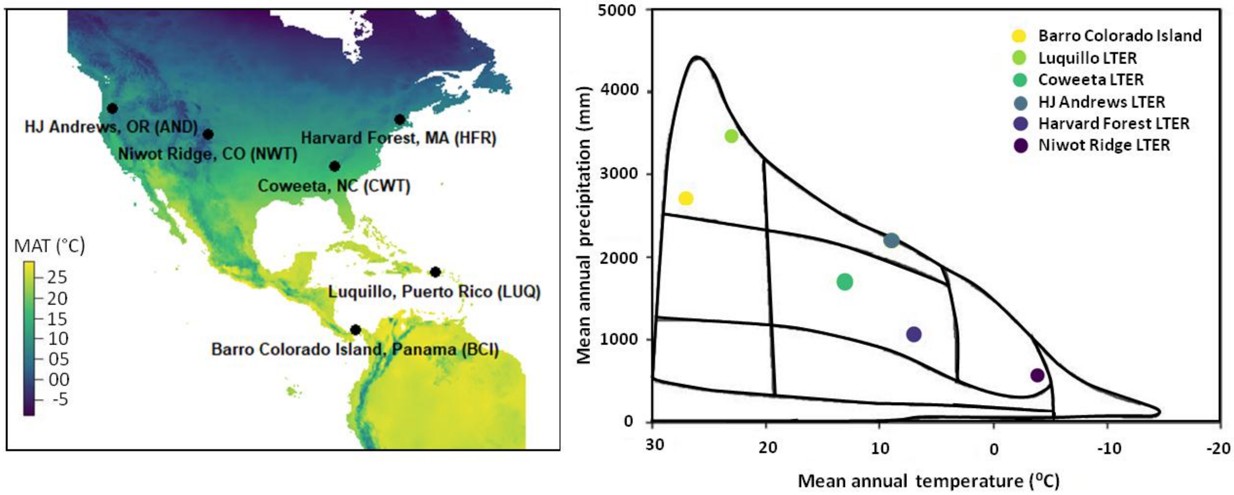
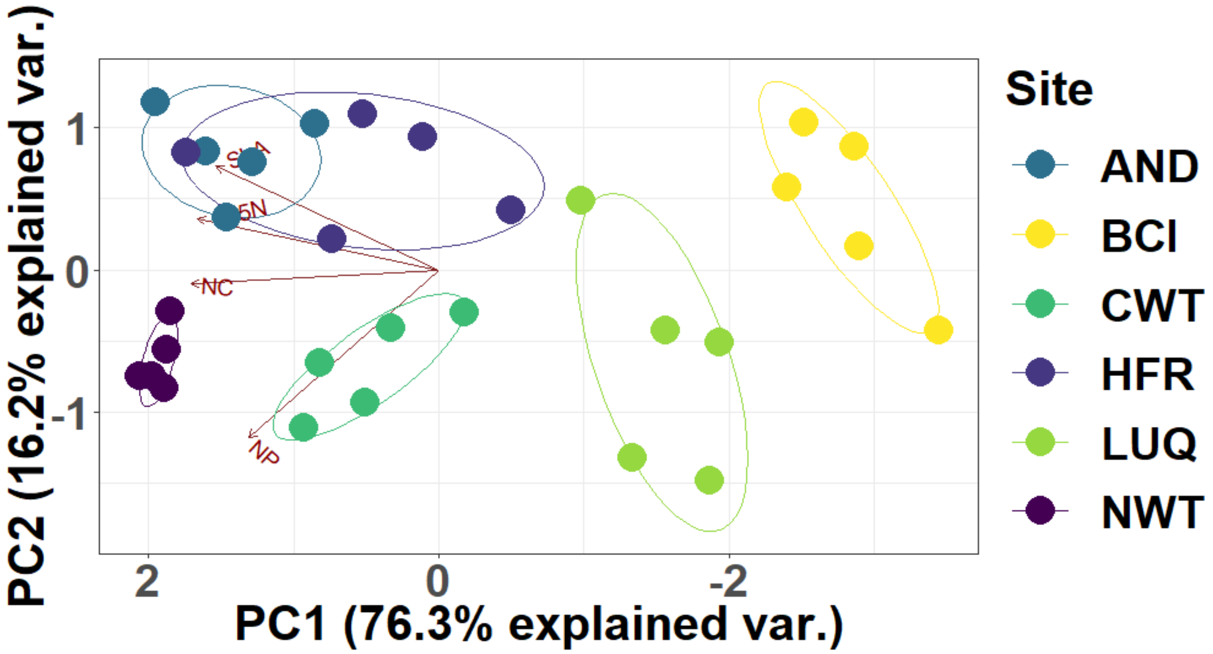
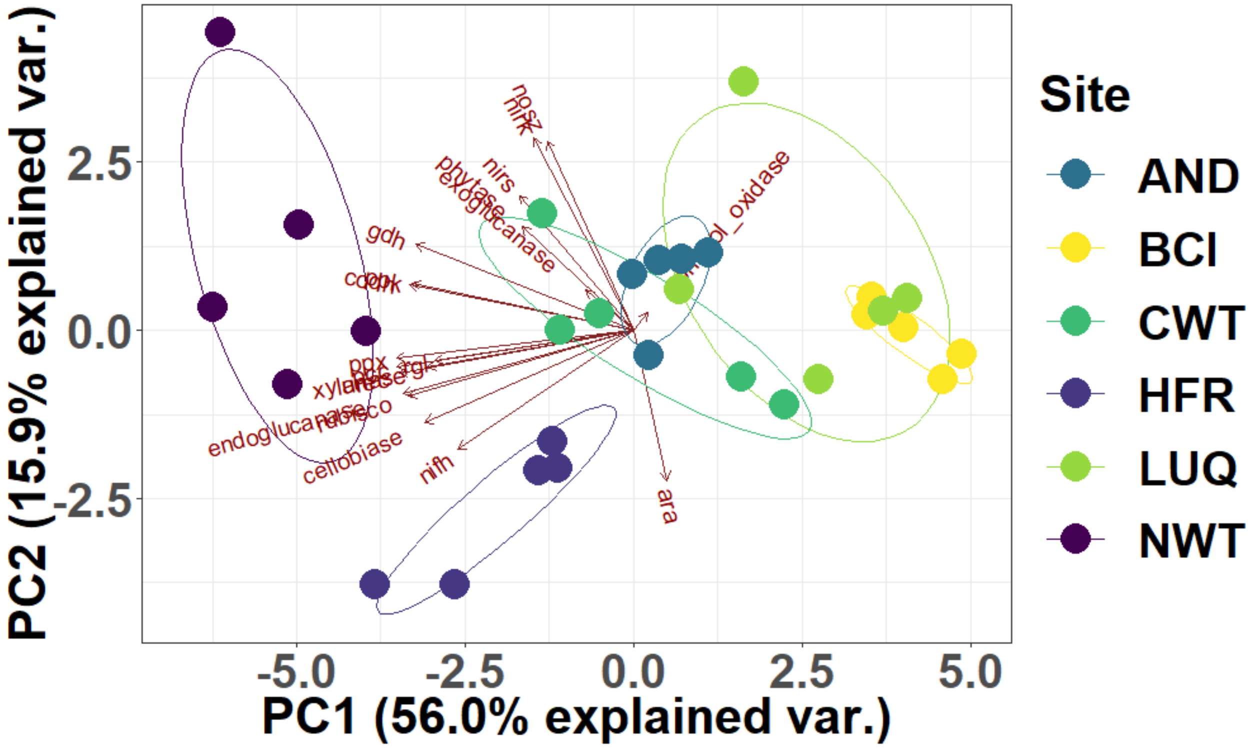
Extended Data Figure 1 | Six sites spanning a broad temperature and latitudinal gradient. (a) Mean annual temperature (MAT) in degrees Celsius overlaid using the MAT climate layer from BioClim. (b) Based on Whittaker's classic graph, the six sites are superimposed on the plot of MAT and mean annual precipitation.



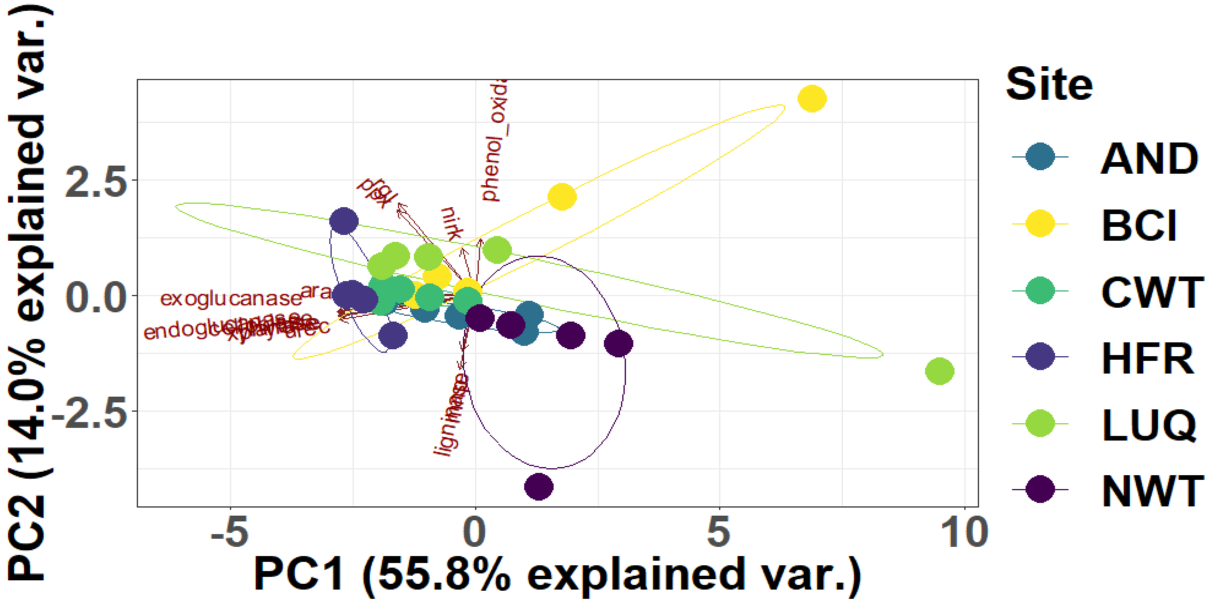
Extended Data Figure 2 | Principal Component Analysis biplot for plant functional traits (Complete list of traits is located in Extended Data Table 1).



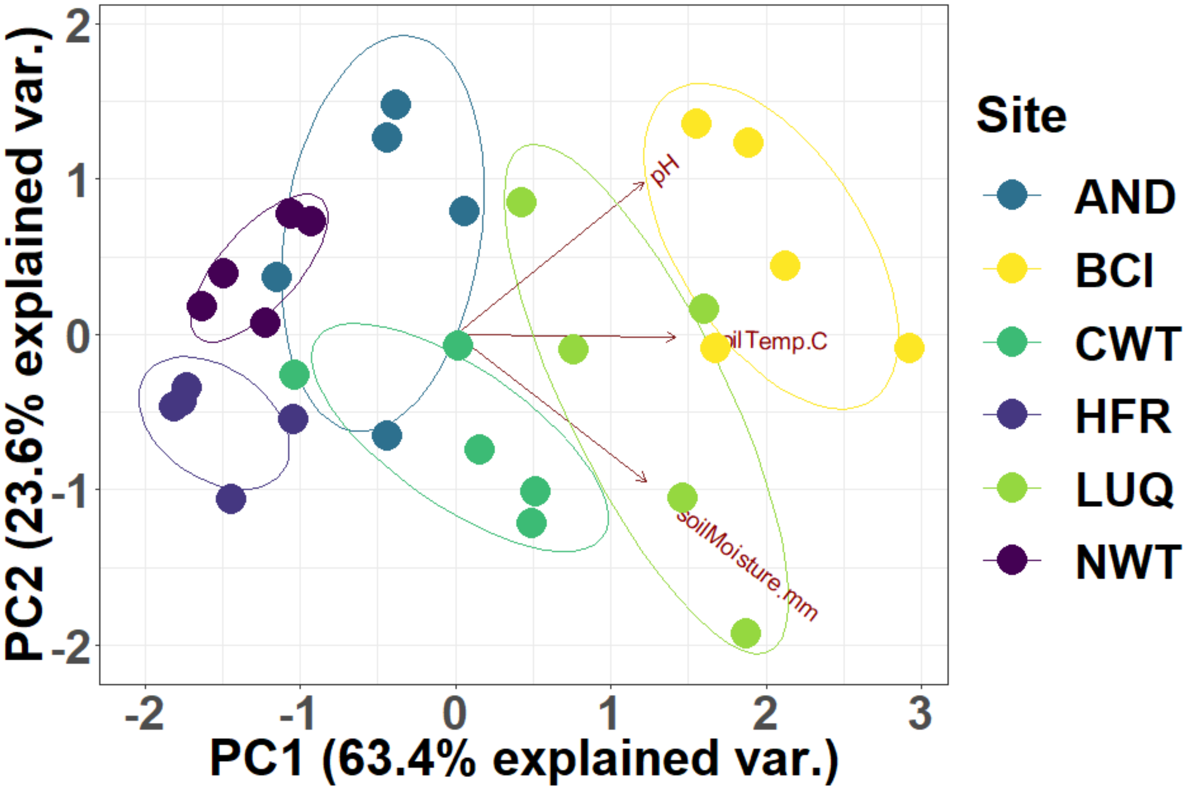
Extended Data Figure 3 | Principal Component Analysis biplot for bacterial functional traits (Complete list of traits is located in Extended Data Table 1).



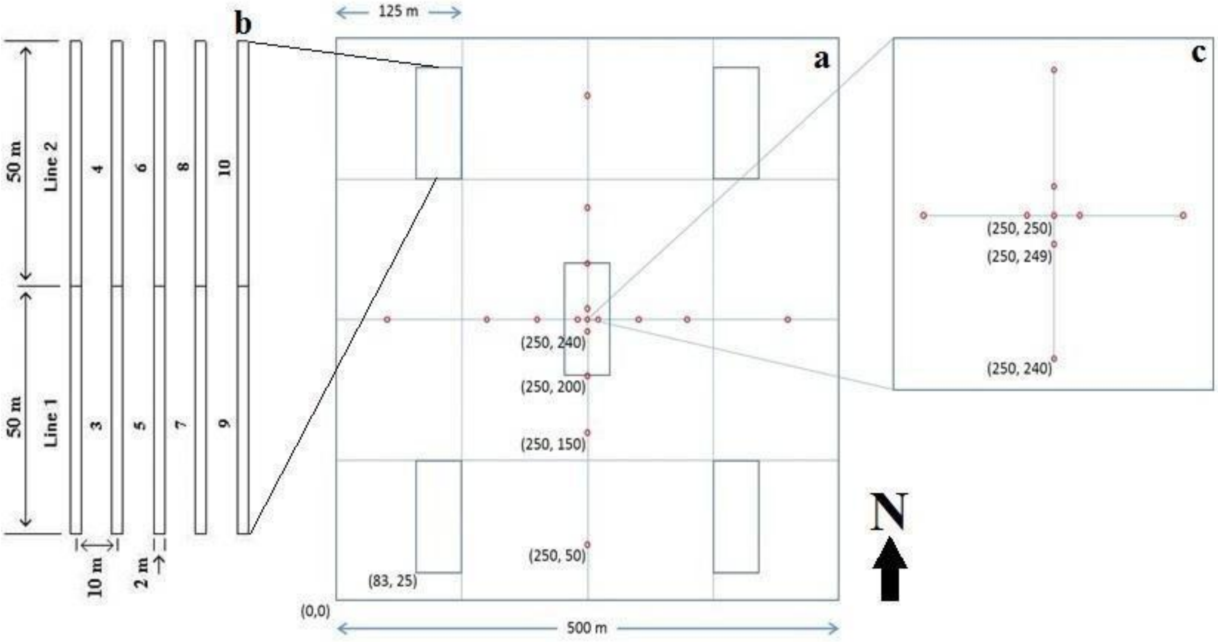
Extended Data Figure 4 | Principal Component Analysis biplot for fungal functional traits (Complete list of traits is located in Extended Data Table 1).



Extended Data Figure 5 | Principal Component Analysis biplot for soil environmental variables (soil moisture, soil temperature, and soil pH).

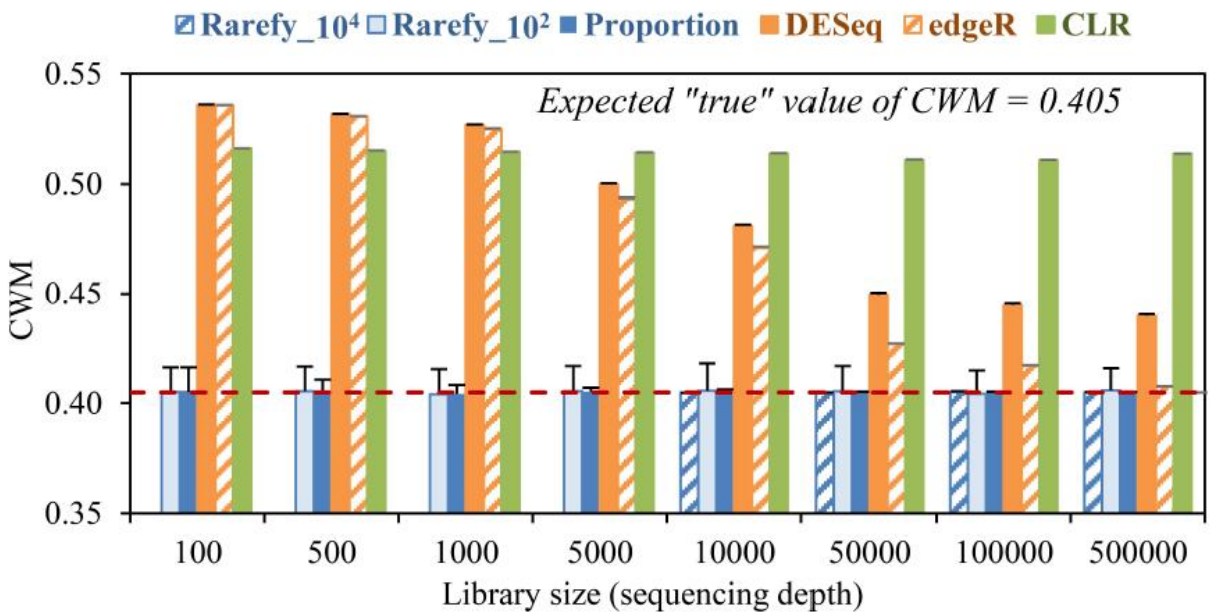


Extended Data Figure 6 | Diagram of sampling design. a) 25ha plot. b) Zoom in of 1 of the 5 Gentry style vegetative plots consisting of 10 transects that are 50m by 2m arranged south to north. c) Zoom in of the center arrangement of the microbial soil plots. Red dots represent the 21 microbial plots that are 1m^2.

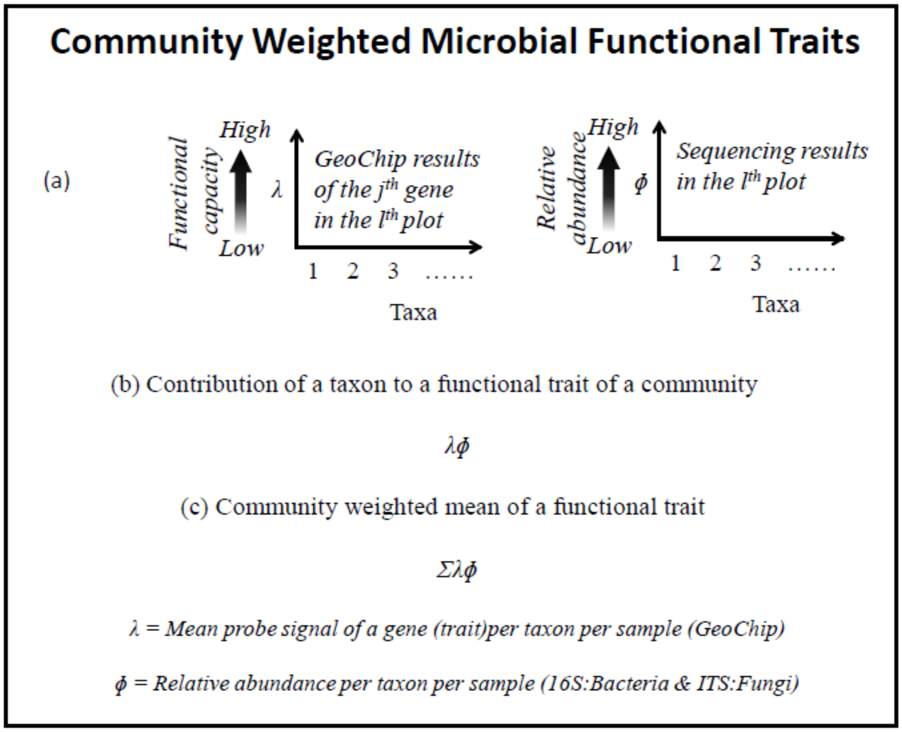


Extended Data Figure 7 | Community weighted mean (CWM) calculated from simulated sequencing results with different library sizes after normalized by different methods. Rarefy_ 104, rarefying to 10,000 reads per sample;

Rarefy_ 102, rarefying to 100 reads per sample; Proportion, directly use the relative abundance without any normalization; DESeq and edgeR are methods described previously[1]; CLR, centered log-ratio recommended previously[2].. Red dash line, the expected "true" value of CWM. Error bars indicate standard deviation from 100-time simulation.



Box 1. Community weighted microbial functional traits.


Community Weighted Microbial Functional Traits

(b) Contribution of a taxon to a functional trait of a community

$$\lambda\phi$$

(c) Community weighted mean of a functional trait

$$\Sigma\lambda\phi$$

λ = Mean probe signal of a gene (trait)per taxon per sample (GeoChip)

ϕ = Relative abundance per taxon per sample (16S:Bacteria & ITS:Fungi)

Extended Data Table 1 | Microbial functional traits (represented by functional genes) broken down by C, N, or P category and further noted with their associated subcategories. Whether the trait is present in bacteria, fungi or both is noted along with the total number of probes used per trait, and the total number of taxa detected per trait.

Category	Subcategory 1	Subcategory 2	Traits	Present	Number of GeoChip probes	Total taxa per trait
Nitrogen	Nitrogen Fixation		*Dinitrogenase reductase (nifH)*	Bacteria	1331	131
Nitrogen	Ammonification		*Glutamate dehydrogenase (gdh)*	Bacteria	396	113
Nitrogen	Ammonification		*Urease alpha subunit (ureC)*	Both	562	212
Nitrogen	Denitrification		*Dissimilatory nitrite reductase, Cytochrome* cd_1 *(nirS)*	Bacteria	459	18
Nitrogen	Denitrification		*Nitrite reductase, copper-containing (nirK)*	Both	336	32
Nitrogen	Denitrification		*Nitrous oxide reductase (nosZ)*	Bacteria	651	94
Phosphorus	Phosphorus synthesis		*Polyphosphate kinase (ppk)*	Bacteria	483	134
Phosphorus	Phosphorus degradation		*Exopolyphosphatase (ppx)*	Both	1450	378
Phosphorus	Phytic acid hydrolysis		*Phytase (phytase)*	Both	235	70
Carbon	Carbon fixation		*Ribulose bisphosphate carboxylase, large chain (rbcL)*	Bacteria	470	124
Carbon	Carbon fixation		*Carbon-monoxide dehydrogenase (CODH)*	Bacteria	319	70
Carbon	Carbon fixation		*Propionyl-CoA carboxylase (pcc)*	Bacteria	505	142
Carbon	Carbon degradation	Lignin	*Ligninase (ligninase)*	Fungi	22	8
Carbon	Carbon degradation	Lignin	*Manganese peroxidase (MnP)*	Fungi	63	19

Carbon	Carbon degradation	Lignin	*Laccase (phenol oxidase)*	Both	560	88
Carbon	Carbon degradation	Cellulose	*Endoglucanase (endoglucanase)*	Both	446	111
Carbon	Carbon degradation	Cellulose	*Exoglucanase (exoglucanase)*	Both	219	52
Carbon	Carbon degradation	Cellulose	*Beta-glucosidase (cellobiase)*	Both	721	162
Carbon	Carbon degradation	Hemicellulose	*xylanase (xylanase)*	Both	803	143
Carbon	Carbon degradation	Hemicellulose	*Arabinofuranosidase (ara)*	Both	715	148
Carbon	Carbon degradation	Pectin	*Rhamnogalacturonan lyase (RGL)*	Both	289	62

Extended Data Table 2 | Linear regression of soil chemistry (TC= total carbon, TN= total nitrogen, TNC= total N:C ratio) as a function of soil properties (MAST= natural log of mean annual soil temperature, MASM= square root of mean annual soil moisture). Bold, $p < 0.05$.

Soil Property (x)	Soil Chemistry (y)	r^2	*p*-value	intercept	slope	degrees of freedom	residual standard error
MAST	**TC**	**0.292**	**0.0020**	**2.948**	**-0.045**	**28**	**0.572**
MAST	TN	0.001	0.8667	2.437	-0.131	28	0.679
MAST	**TNC**	**0.740**	**0.0000**	**1.177**	**26.641**	**28**	**0.347**
MAST	**pH**	**0.171**	**0.0232**	**0.370**	**0.414**	**28**	**0.619**
MASM	**TC**	**0.363**	**0.0004**	**20.930**	**-0.611**	**28**	**6.602**
MASM	TN	0.080	0.1290	0.413	-0.296	28	0.167
MASM	**TNC**	**0.305**	**0.0016**	**0.086**	**4.367**	**28**	**0.145**
MASM	pH	**0.139**	**0.0427**	**-0.179**	**0.095**	**28**	**0.161**

Extended Data Table 3 | Linear regression of plant, bacteria, and fungi community weighted traits as a function of the natural log of mean annual soil temperature (MAST) and/or the square root of mean annual soil moisture (MASM). Bold, $p < 0.05$.

Organism	Environment (x)	Trait (y)	r^2 or adjusted R^2	p-value	intercept	slope	degrees of freedom	residual standard error	AICc
Plant	**MAST**	**NP**	**0.463**	**0.0000**	**1.24**	**7.77**	**28**	**5.68**	**194.23**
Plant	**MASM**	**NP**	**0.350**	**0.0006**	**12.24**	**26.43**	**28**	**6.25**	**199.97**
Plant	**MAST +MASM**	**NP**	**0.496**	**0.0000**	**1.95**		**27**	**5.41**	**192.85**
Plant	**Latitude**	**NP**	**0.636**	**0.0000**	**-4.51**	**7.33**	**28**	**3.77**	**169.60**
Plant	**MAST**	**SLA**	**0.187**	**0.0171**	**8.52**	**15.54**	**28**	**5.63**	**193.69**
Plant	**MASM**	**SLA**	**0.609**	**0.0000**	**-4.52**		**27**	**3.84**	**172.28**
Plant	**MAST +MASM**	**SLA**	**0.693**	**0.0000**	**0.13**	**1.37**	**28**	**0.62**	**61.10**
Plant	**MAST**	**NC**	**0.310**	**0.0014**	**2.36**	**3.58**	**28**	**0.93**	**85.43**
Plant	**MASM**	**NC**	**0.686**	**0.0000**	**0.17**		**27**	**0.61**	**62.36**
Plant	**MAST +MASM**	**NC**	**0.713**	**0.0000**	**-8.88**	**2.75**	**28**	**1.19**	**100.26**
Plant	**MAST**	**$\delta^{15}N$**	**0.210**	**0.0109**	**-3.99**	**5.84**	**28**	**1.97**	**130.60**
Plant	**MASM**	**$\delta^{15}N$**	**0.713**	**0.0000**	**-8.88**		**27**	**1.21**	**102.93**
Plant	**MAST +MASM**	**$\delta^{15}N$**	**0.825**	**0.0000**	**-5.66**	**2.38**	**28**	**0.74**	**72.19**
Plant	**MAST**	**PC1**	**0.330**	**0.0009**	**-1.67**	**5.89**	**28**	**1.46**	**112.52**

Plant	**MASM**	**PC1**	**0.821**	**0.0000**	**-5.60**		**27**	**0.74**	**73.44**
Plant	**MAST +MASM**	**PC1**	**0.463**	**0.0000**	**1.24**	**7.77**	**28**	**5.68**	**194.23**
Bacteria	**MAST**	***nifH***	**0.279**	**0.0027**	**0.47**	**-0.12**	**28**	**0.13**	**-34.18**
Bacteria	MASM	*nifH*	**0.151**	**0.0340**	**0.29**	**-0.33**	**28**	**0.14**	**-29.29**
Bacteria	**MAST +MASM**	***nifH***	**0.240**	**0.0094**	**0.47**		**27**	**0.13**	**-32.09**
Bacteria	**MAST**	***gdh***	**0.613**	**0.0000**	**0.31**	**-0.07**	**28**	**0.04**	**-103.42**
Bacteria	**MASM**	***gdh***	**0.156**	**0.0311**	**0.17**	**-0.15**	**28**	**0.06**	**-79.99**
Bacteria	**MAST +MASM**	***gdh***	**0.587**	**0.0000**	**0.31**		**27**	**0.04**	**-100.89**
Bacteria	**MAST**	***ureC***	**0.787**	**0.0000**	**1.77**	**-0.49**	**28**	**0.17**	**-14.73**
Bacteria	**MASM**	***ureC***	**0.326**	**0.0010**	**0.95**	**-1.25**	**28**	**0.31**	**19.87**
Bacteria	**MAST +MASM**	***ureC***	**0.782**	**0.0000**	**1.76**		**27**	**0.17**	**-13.50**
Bacteria	**MAST**	***nirS***	**0.185**	**0.0178**	**0.03**	**-0.01**	**28**	**0.01**	**-187.64**
Bacteria	MASM	*nirS*	0.120	0.0603	0.02	-0.02	28	0.01	-185.36
Bacteria	**MAST +MASM**	***nirS***	**0.143**	**0.0473**	**0.03**		**27**	**0.01**	**-185.62**
Bacteria	MAST	*nirK*	0.068	0.1625	0.08	-0.01	28	0.02	-132.19
Bacteria	MASM	*nirK*	0.003	0.7705	0.06	-0.01	28	0.03	-130.15

Bacteria	MAST +MASM	*nirK*	0.011	0.3263	0.08		27	0.02	-129.87
Bacteria	MAST	*nosZ*	0.065	0.1727	0.09	-0.01	28	0.03	-129.00
Bacteria	MASM	*nosZ*	0.040	0.2889	0.08	-0.03	28	0.03	-128.20
Bacteria	MAST +MASM	*nosZ*	0.002	0.3730	0.09		27	0.03	-126.49
Bacteria	**MAST**	***ppk***	**0.705**	**0.0000**	**0.82**	**-0.23**	**28**	**0.10**	**-48.14**
Bacteria	**MASM**	***ppk***	**0.262**	**0.0039**	**0.43**	**-0.54**	**28**	**0.16**	**-20.65**
Bacteria	**MAST +MASM**	***ppk***	**0.687**	**0.0000**	**0.81**		**27**	**0.10**	**-45.83**
Bacteria	**MAST**	***ppx***	**0.747**	**0.0000**	**1.61**	**-0.44**	**28**	**0.17**	**-15.27**
Bacteria	**MASM**	***ppx***	**0.294**	**0.0020**	**0.87**	**-1.08**	**28**	**0.29**	**15.55**
Bacteria	**MAST +MASM**	***ppx***	**0.736**	**0.0000**	**1.60**		**27**	**0.17**	**-13.37**
Bacteria	MAST	*phytase*	**0.174**	**0.0217**	**0.11**	**-0.02**	**28**	**0.03**	**-115.69**
Bacteria	MASM	*phytase*	0.016	0.5031	0.07	-0.03	28	0.04	-110.43
Bacteria	MAST +MASM	*phytase*	0.129	0.0588	0.11		27	0.03	-113.56
Bacteria	**MAST**	***rbcL***	**0.589**	**0.0000**	**1.13**	**-0.31**	**28**	**0.18**	**-13.88**
Bacteria	**MASM**	***rbcL***	**0.299**	**0.0018**	**0.63**	**-0.87**	**28**	**0.23**	**2.12**
Bacteria	**MAST +MASM**	***rbcL***	**0.583**	**0.0000**	**1.11**		**27**	**0.18**	**-12.90**

Bacteria	**MAST**	***CODH***	**0.748**	**0.0000**	**0.81**	**-0.23**	**28**	**0.09**	**-55.15**
Bacteria	**MASM**	***CODH***	**0.281**	**0.0026**	**0.42**	**-0.54**	**28**	**0.15**	**-23.67**
Bacteria	**MAST+MASM**	***CODH***	**0.734**	**0.0000**	**0.80**		**27**	**0.09**	**-52.98**
Bacteria	**MAST**	***pcc***	**0.724**	**0.0000**	**1.48**	**-0.40**	**28**	**0.17**	**-17.39**
Bacteria	**MASM**	***pcc***	**0.290**	**0.0021**	**0.82**	**-0.99**	**28**	**0.27**	**10.99**
Bacteria	**MAST+MASM**	***pcc***	**0.712**	**0.0000**	**1.47**		**27**	**0.17**	**-15.51**
Bacteria	MAST	*phenol oxidase*	0.057	0.2023	0.00	0.01	28	0.02	-140.82
Bacteria	MASM	*phenol oxidase*	0.021	0.4430	0.02	0.02	28	0.02	-139.69
Bacteria	MAST+MASM	*phenol oxidase*	-0.012	0.4486	0.00		27	0.02	-138.15
Bacteria	**MAST**	***endoglucanase***	0.674	**0.0000**	1.13	-0.32	**28**	0.15	-24.00
Bacteria	**MASM**	***endoglucanase***	**0.297**	**0.0018**	**0.61**	**-0.82**	**28**	**0.22**	**-0.95**
Bacteria	**MAST+MASM**	***endoglucanase***	0.663	**0.0000**	1.12		**27**	0.15	-22.51
Bacteria	MAST	*exoglucanase*	0.007	0.6511	0.03	0.00	28	0.02	-134.04
Bacteria	MASM	*exoglucanase*	0.011	0.5808	0.02	0.01	28	0.02	-134.15
Bacteria	MAST+MASM	*exoglucanase*	-0.030	0.5712	0.03		27	0.02	-132.38

Bacteria	**MAST**	***cellobiase***	**0.439**	**0.0001**	**0.70**	**-0.18**	**28**	**0.14**	**-29.50**
Bacteria	**MASM**	***cellobiase***	**0.210**	**0.0109**	**0.41**	**-0.48**	**28**	**0.16**	**-19.23**
Bacteria	**MAST +MASM**	***cellobiase***	**0.411**	**0.0003**	**0.69**		**27**	**0.13**	**-27.51**
Bacteria	**MAST**	***xylanase***	**0.590**	**0.0000**	**0.78**	**-0.21**	**28**	**0.12**	**-36.81**
Bacteria	**MASM**	***xylanase***	**0.157**	**0.0305**	**0.40**	**-0.43**	**28**	**0.17**	**-15.16**
Bacteria	**MAST +MASM**	***xylanase***	**0.561**	**0.0000**	**0.78**		**27**	**0.12**	**-34.21**
Bacteria	MAST	*ara*	0.068	0.1631	0.98	0.01	28	0.02	-145.21
Bacteria	MASM	*ara*	0.000	0.9451	1.00	0.00	28	0.02	-143.10
Bacteria	MAST +MASM	*ara*	0.025	0.2691	0.98		27	0.02	-143.33
Bacteria	**MAST**	***RGL***	**0.611**	**0.0000**	**0.37**	**-0.10**	**28**	**0.05**	**-86.64**
Bacteria	**MASM**	***RGL***	**0.149**	**0.0351**	**0.20**	**-0.19**	**28**	**0.08**	**-63.19**
Bacteria	**MAST +MASM**	***RGL***	**0.585**	**0.0000**	**0.37**		**27**	**0.05**	**-84.17**
Bacteria	**MAST**	**PC1**	**0.754**	**0.0000**	**-10.10**	**4.24**	**28**	**1.65**	**119.95**
Bacteria	**MASM**	**PC1**	**0.277**	**0.0028**	**-2.85**	**10.07**	**28**	**2.82**	**152.26**
Bacteria	**MAST +MASM**	**PC1**	**0.739**	**0.0000**	**-10.03**		**27**	**1.67**	**122.20**
Fungi	MAST	*ureC*	0.010	0.6036	0.09	-0.01	28	0.07	-69.65

Fungi	MASM	*ureC*	0.001	0.8624	0.06	0.01	28	0.07	-69.39
Fungi	MAST +MASM	*ureC*	-0.052	0.7543	0.10		27	0.07	-67.30
Fungi	**MAST**	***nirK***	**0.398**	**0.0002**	**-0.01**	**0.00**	**28**	**0.00**	**-265.13**
Fungi	**MASM**	***nirK***	0.147	0.1467	0.00	0.01	28	0.00	-254.68
Fungi	**MAST +MASM**	***nirK***	**0.355**	**0.0010**	**-0.01**		**27**	**0.00**	**-262.55**
Fungi	**MAST**	***ppx***	**0.136**	**0.0450**	**-0.02**	**0.01**	**28**	**0.02**	**-141.39**
Fungi	**MASM**	***ppx***	0.114	0.0684	-0.01	0.04	28	0.02	-140.63
Fungi	**MAST +MASM**	***ppx***	0.100	0.0922	-0.02		27	0.02	-139.63
Fungi	MAST	*phytase*	0.006	0.6915	0.08	-0.01	28	0.06	-74.82
Fungi	MASM	*phytase*	0.002	0.8131	0.06	0.02	28	0.06	-74.71
Fungi	MAST +MASM	*phytase*	-0.056	0.7994	0.08		27	0.06	-72.47
Fungi	MAST	*ligninase*	0.016	0.5122	0.00	0.00	28	0.01	-195.59
Fungi	MASM	*ligninase*	0.001	0.8796	0.01	0.00	28	0.01	-195.14
Fungi	MAST +MASM	*ligninase*	-0.043	0.6717	0.00		27	0.01	-193.33
Fungi	MAST	*MnP*	0.055	0.2108	0.01	0.00	28	0.01	-208.50
Fungi	MASM	*MnP*	0.008	0.6328	0.00	0.00	28	0.01	-207.04
Fungi	MAST	*MnP*	-0.012	0.4500	0.01		27	0.01	-205.89

	+MASM								
Fungi	MAST	*phenol oxidase*	0.021	0.4401	-0.01	0.02	28	0.09	-54.95
Fungi	MASM	*phenol oxidase*	0.008	0.6367	0.05	-0.05	28	0.09	-54.55
Fungi	MAST +MASM	*phenol oxidase*	-0.006	0.4154	-0.01		27	0.09	-53.58
Fungi	MAST	*endoglucanase*	0.002	0.8313	0.07	0.00	28	0.08	-64.51
Fungi	MASM	*endoglucanase*	0.017	0.4953	0.06	0.06	28	0.08	-64.97
Fungi	MAST +MASM	*endoglucanase*	-0.055	0.7814	0.07		27	0.08	-62.33
Fungi	MAST	*exoglucanase*	0.014	0.5318	0.05	0.01	28	0.07	-66.72
Fungi	MASM	*exoglucanase*	0.015	0.5184	0.07	0.05	28	0.07	-66.75
Fungi	MAST +MASM	*exoglucanase*	-0.054	0.7736	0.06		27	0.07	-64.19
Fungi	MAST	*cellobiase*	0.001	0.8869	0.08	0.00	28	0.07	-71.16
Fungi	MASM	*cellobiase*	0.005	0.6996	0.06	0.03	28	0.07	-71.30
Fungi	MAST +MASM	*cellobiase*	-0.061	0.8505	0.08		27	0.07	-68.82
Fungi	MAST	*xylanase*	0.001	0.8766	0.08	0.00	28	0.07	-71.75
Fungi	MASM	*xylanase*	0.004	0.7413	0.06	0.02	28	0.07	-71.84

Fungi	MAST +MASM	*xylanase*	-0.063	0.8749	0.08		27	0.07	-69.35
Fungi	MAST	*ara*	0.038	0.3032	0.04	0.02	28	0.08	-60.92
Fungi	MASM	*ara*	0.063	0.1819	0.06	0.12	28	0.08	-61.71
Fungi	MAST +MASM	*ara*	-0.002	0.3900	0.05		27	0.08	-59.18
Fungi	**MAST**	***RGL***	**0.326**	**0.0010**	**-0.04**	**0.02**	**28**	**0.02**	**-133.37**
Fungi	**MASM**	***RGL***	**0.161**	**0.0282**	**0.00**	**0.07**	**28**	**0.03**	**-126.80**
Fungi	**MAST +MASM**	***RGL***	**0.287**	**0.0039**	**-0.04**		**27**	**0.02**	**-131.18**
Fungi	MAST	PC1	0.008	0.6285	-0.88	0.37	28	2.73	150.23
Fungi	MASM	PC1	0.024	0.4129	-0.69	2.45	28	2.71	149.76
Fungi	MAST +MASM	PC1	-0.048	0.7189	-0.76		27	2.76	152.43

Extended Table 4 | Mycorrhizal associations of ectomycorrhiza (ECM) and arbuscular mycorrhiza (AM) for plants and fungi for each site. Percent was calculated as the total abundance of all taxa within a given guild divided by all taxa in each site. All mycorrhizal associations were summed and the percent of total mycorrhiza to no observed mycorrhizal association were calculated and recorded as percent symbiont.

Site	**Percent ECM**	**Percent AM**	**Percent Symbiont**
Plants			
H. J. Andrews (AND)	37.8%	28.4%	96.1%
Barro Colorado Island (BCI)	0.0%	20.8%	25.2%
Coweeta LTER (CWT)	16.6%	13.4%	88.8%
Harvard Forest LTER (HFR)	77.5%	12.2%	99.1%
Luquillo LTER (LUQ)	0.0%	29.0%	29.3%
Niwot Ridge LTER (NWT)	99.1%	0.0%	100.0%
Fungi			
H. J. Andrews (AND)	16.3%	0.136%	18.5%
Barro Colorado Island (BCI)	2.5%	0.184%	3.2%
Coweeta LTER (CWT)	18.5%	0.059%	20.0%
Harvard Forest LTER (HFR)	48.4%	0.010%	49.1%
Luquillo LTER (LUQ)	6.8%	0.427%	9.6%
Niwot Ridge LTER (NWT)	22.1%	0.008%	24.7%

Extended Table 5 | Relative importance of explanatory variables in multiple linear regression (Trait=a+SoilTemperature(x)+SoilMoisture(x)) to determine importance of soil temperature compared with soil moisture. *, model is significant at $p < 0.05$. N.S., model is not significant. Bold, represents variable with greater relative importance.

Organism	Trait	Soil Temperature Relative Importance	Soil Moisture Relative Importance	Significance based on linear regression (Extended Data Table 3)
Plant	NP	**0.853**	0.147	*
Plant	SLA	**0.607**	0.393	*
Plant	NC	**0.771**	0.229	*
Plant	δ^{15}N	**0.853**	0.147	*
Plant	PC1	**0.797**	0.203	*
Bacteria	*nifH*	**0.718**	0.282	*
Bacteria	*gdh*	**0.872**	0.128	*
Bacteria	*ureC*	**0.789**	0.211	*
Bacteria	*nirS*	**0.659**	0.341	N.S.
Bacteria	*nirK*	**0.911**	0.089	N.S.
Bacteria	*nosZ*	**0.679**	0.321	N.S.
Bacteria	*ppk*	**0.813**	0.187	*
Bacteria	*ppx*	**0.801**	0.199	*
Bacteria	*phytase*	**0.918**	0.082	N.S.
Bacteria	*rbcL*	**0.737**	0.263	*

Bacteria	*CODH*	**0.811**	0.189	*
Bacteria	*pcc*	**0.797**	0.203	*
Bacteria	*phenol oxidase*	**0.814**	0.186	N.S.
Bacteria	*endoglucanase*	**0.775**	0.225	*
Bacteria	*exoglucanase*	0.455	**0.545**	N.S.
Bacteria	*cellobiase*	**0.754**	0.246	*
Bacteria	*xylanase*	**0.867**	0.133	*
Bacteria	*ara*	**0.868**	0.132	N.S.
Bacteria	*RGL*	**0.876**	0.124	*
Bacteria	*PC1*	**0.815**	0.185	*
Fungi	*ureC*	**0.709**	0.291	N.S.
Fungi	*nirK*	**0.814**	0.186	*
Fungi	*ppx*	**0.569**	0.431	*
Fungi	*phytase*	**0.612**	0.388	N.S.
Fungi	*ligninase*	**0.752**	0.248	N.S.
Fungi	*MnP*	**0.910**	0.090	N.S.
Fungi	*phenol oxidase*	**0.606**	0.394	N.S.

Fungi	*endoglucanase*	0.082	**0.918**	N.S.
Fungi	*exoglucanase*	0.475	**0.525**	N.S.
Fungi	*cellobiase*	0.304	**0.696**	N.S.
Fungi	*xylanase*	0.344	**0.656**	N.S.
Fungi	*ara*	0.315	**0.685**	N.S.
Fungi	*RGL*	**0.745**	0.255	*
Fungi	*PC1*	**0.823**	0.177	N.S.

Extended Table 6 | Plant genra measured at each site.

Site	**Genus**
H. J. Andrews (AND)	*Acer*
H. J. Andrews (AND)	*Pseudotsuga*
H. J. Andrews (AND)	*Taxus*
H. J. Andrews (AND)	*Thuja*
H. J. Andrews (AND)	*Tsuga*
H. J. Andrews (AND)	*Vaccinium*
Barro Colorado Island (BCI)	*Alseis*
Barro Colorado Island (BCI)	*Anacardium*
Barro Colorado Island (BCI)	*Casearia*
Barro Colorado Island (BCI)	*Chrysophyllum*
Barro Colorado Island (BCI)	*Cojoba*
Barro Colorado Island (BCI)	*Coussarea*
Barro Colorado Island (BCI)	*Guapira*
Barro Colorado Island (BCI)	*Hura*

Barro Colorado Island (BCI)	*Inga*
Barro Colorado Island (BCI)	*Licania*
Barro Colorado Island (BCI)	*Luehea*
Barro Colorado Island (BCI)	*Platypodium*
Barro Colorado Island (BCI)	*Pouteria*
Barro Colorado Island (BCI)	*Protium*
Barro Colorado Island (BCI)	*Tabebuia*
Barro Colorado Island (BCI)	*Tetragastris*
Barro Colorado Island (BCI)	*Trichilia*
Coweeta LTER (CWT)	*Acer*
Coweeta LTER (CWT)	*Carya*
Coweeta LTER (CWT)	*Kalmia*
Coweeta LTER (CWT)	*Liriodendron*
Coweeta LTER (CWT)	*Nyssa*
Coweeta LTER (CWT)	*Oxydendrum*
Coweeta LTER (CWT)	*Quercus*
Coweeta LTER (CWT)	*Rhododendron*
Harvard Forest LTER (HFR)	*Acer*
Harvard Forest LTER (HFR)	*Betula*
Harvard Forest LTER (HFR)	*Fagus*
Harvard Forest LTER (HFR)	*Picea*
Harvard Forest LTER (HFR)	*Pinus*
Harvard Forest LTER (HFR)	*Quercus*

Harvard Forest LTER (HFR)	*Tsuga*
Luquillo LTER (LUQ)	*Alchornea*
Luquillo LTER (LUQ)	*Alchorneopsis*
Luquillo LTER (LUQ)	*Byrsonima*
Luquillo LTER (LUQ)	*Calophyllum*
Luquillo LTER (LUQ)	*Cananga*
Luquillo LTER (LUQ)	*Casearia*
Luquillo LTER (LUQ)	*Cecropia*
Luquillo LTER (LUQ)	*Cordia*
Luquillo LTER (LUQ)	*Croton*
Luquillo LTER (LUQ)	*Dacryodes*
Luquillo LTER (LUQ)	*Dendropanax*
Luquillo LTER (LUQ)	*Drypetes*
Luquillo LTER (LUQ)	*Eugenia*
Luquillo LTER (LUQ)	*Faramea*
Luquillo LTER (LUQ)	*Gerascanthus*
Luquillo LTER (LUQ)	*Guarea*
Luquillo LTER (LUQ)	*Hirtella*
Luquillo LTER (LUQ)	*Inga*

Luquillo LTER (LUQ)	*Ixora*
Luquillo LTER (LUQ)	*Manilkara*
Luquillo LTER (LUQ)	*Marcgravia*
Luquillo LTER (LUQ)	*Matayba*
Luquillo LTER (LUQ)	*Meliosma*
Luquillo LTER (LUQ)	*Micropholis*
Luquillo LTER (LUQ)	*Myrcia*
Luquillo LTER (LUQ)	*Ocotea*
Luquillo LTER (LUQ)	*Prestoea*
Luquillo LTER (LUQ)	*Psychotria*
Luquillo LTER (LUQ)	*Sapium*
Luquillo LTER (LUQ)	*Schefflera*
Luquillo LTER (LUQ)	*Sloanea*
Luquillo LTER (LUQ)	*Syzygium*
Luquillo LTER (LUQ)	*Tetragastris*
Luquillo LTER (LUQ)	*Trichilia*
Niwot Ridge LTER (NWT)	*Abies*
Niwot Ridge LTER (NWT)	*Juniperus*
Niwot Ridge LTER (NWT)	*Picea*

Niwot Ridge LTER (NWT)	*Pinus*

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