Supplementary Table 1. PCR primers targetting the 16S rRNA gene hypervariable regions and their percent coverage to the RDP database (version 10.27).

Hypervariable region	**Primer**	**Sequence**	**Bacteria**		**Archaea**		**Reference**
			0 mismatch	**2 mismatches**	**0 mismatch**	**2 mismatches**	
V3	341F	CCTACGGGAGGCAGCAG	94.44%	99.68%	0.00%	64.61%	Bartram et al., 2011
	518R	ATTACCGCGGCTGCTGG	88.52%	99.75%	0.30%	82.09%	(soil)
V5	784DEG	GGMTTAGATACCC	97.31%	99.87%	95.22%	99.75%	Lazarevic et al., 2009
	880RDEG	CRTACTHCHCAGGYG	95.81%	99.90%	83.00%	99.72%	(mouth)
V6	L-V6	CAACGCGARGAACCTTACC	66.46%	97.74%	0.00%	5.06%	Hummelen et al., 2010
	R-V6	ACAACACGAGCTGACGAC	4.67%	99.51%	0.00%	25.76%	(vagina)
	976F	CAACGCGAAGAACCTTACC	66.10%	89.10%	0.00%	0.00%	Sogin et al., 2006 (sea)
	1046R	CGACAGCCATGCANCACCT	42.80%	99.80%	0.00%	71.20%	
	970F	CGCGAAGAACCTTACC	67.30%	99.60%	0.00%	5.50%	Degnan & Ochman, 2011
	1050R	ACGACAGCCATGCANC	43.20%	99.88%	0.00%	92.20%	(feces)
	917F	GAATTGACGGGGRCCCGC	86.10%	99.60%	0.00%	0.04%	Keijser et al., 2008
	1061R	CACGRCACGAGCTGACGAC	92.10%	99.90%	1.40%	65.30%	(mouth)
	E1052-1072	TGCATGGYTGTCGTCAGCTCG	93.07%	n.a.	0.02%	n.a.	Wang & Qian, 2009 (*in silico*)
	U1052-1071	TGCATGGYYGYCGYCAGYTC	95.90%	n.a.	88.92%	n.a.	
	E949-964	ATGTGGTTTAATTCGA	71.36%	n.a.	0.00%	n.a.	
	E917F	GAATTGACGGGRCCC	86.29%	n.a.	0.00%	n.a.	Wang & Qian., 2009;
							Liu et al., 2007 (various)
	E939R	CTTGTGCGGGCCCCCGTCAATTC	54.28%	n.a.	0.00%	n.a.	Wang & Qian, 2009;
							Huws et al., 2007 (*in silico*)

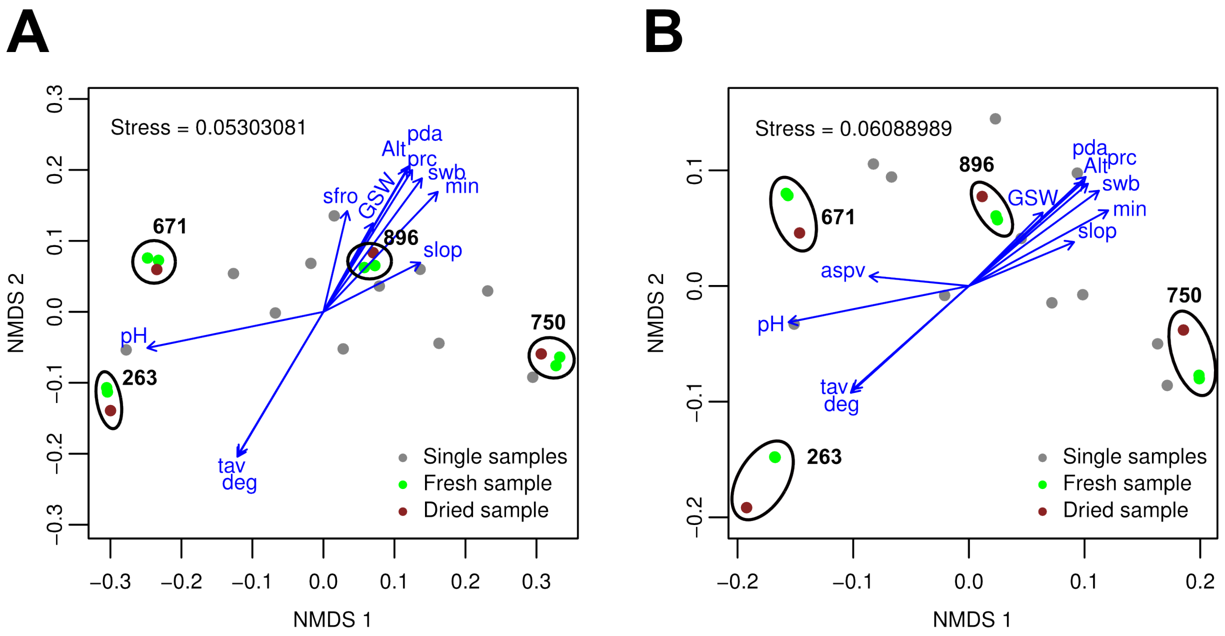
Supplementary Table 2. Complete list of environmental parameters

Environmental parameters	Abbreviation
Soil physico-chemical composition: Edaphic factors	
Soil temperature at depth -5cm (ºC)	ST
pH	pH
Electrical conductivity (µS/cm)	EC
Stable isotopic carbon ratio (per mL vs VPDB)	δ13C / C13
Stable isotopic nitrogen ratio (per mL vs. N_2 in Air)	δ15N / N15
Bulk carbon content (wt %)	C
Bulk hydrogen content (wt %)	H
Bulk nitrogen content (wt %)	N
C:N ratio	CN
Total phosphorus (mg/g)	P
Soluble phosphorus content (mgP/kg DW)	avP
Hydrogen index (mg HC/g TOC)	HI
Oxygen index (mg CO_2/g TOC)	OI
Total organic carbon content (wt %)	TOC
Mineral carbon content (wt %)	MiC
Bulk soil gravimetric water content (40ºC, %)	BSW
Sieved soil gravimetric water content (105ºC, %)	GSW
Temperature of maximal pyrolytic yield (T-max, ºC)	Tmx
Soil physico-chemical composition: Major elements	
SiO_2 (wt %)	Si
TiO_2 (wt %)	Ti
Al_2O_3 (wt %)	Al
Fe_2O_3 (wt %)	Fe
MnO (wt %)	Mn
MgO (wt %)	Mg
CaO (wt %)	Ca
Na_2 (wt %)	Na
K2O	K
P_2O_5 (wt %)	P2O
Cr_2O_3 (wt %)	Cr
NiO (wt %)	Ni
Soil physico-chemical composition: Mineralogy	
Phyllosilicate (%)	PSi
Quartz (%)	Qua
Feldspath-K (%)	Feld
Plagioclase-Na (%)	Pla
Calcite (%)	Cal
Dolomite (%)	Dol
Goethite (%)	Geo
Ankerite (%)	Ank
Indoses (%)	Ind
Organic matter content via loss of ignition (wt %)	OM
Topographic parameters	
Longitude, x (Swiss coordinates system)	Lon
Latitude, y (Swiss coordinates system)	Lat
Elevation (m)	Alt
Terrain slope (º)	slope / slop
Direction that a slope faces (º/%)	asp25 / asp
Sine transformed asp25 (º/%)	aspval / aspv
Topographic position	topos / top
Climatic parameters	
Air temperature (ºC)	N.A.
Annual degree days (day*deg)	ddeg0 / deg
Monthly moisture index ((1/10mm)/month)	mmind68 / min
Daily average of global potential shortwave radiation per month (kJ/day)	summradyy / srd
Monthly average temperature (ºC*100)	taveyy / tav
Annual average site water balance accounting for soil properties (1/10mm / year)	swb
Topographic wetness index	twi25 / twi
Annual average number of frost days during the growing season (day*100)	sfroyy / sfro
Number of precipitation days per growing season (day)	pday / pda
Monthly mean precipitation sum (mm)	precyy / prc

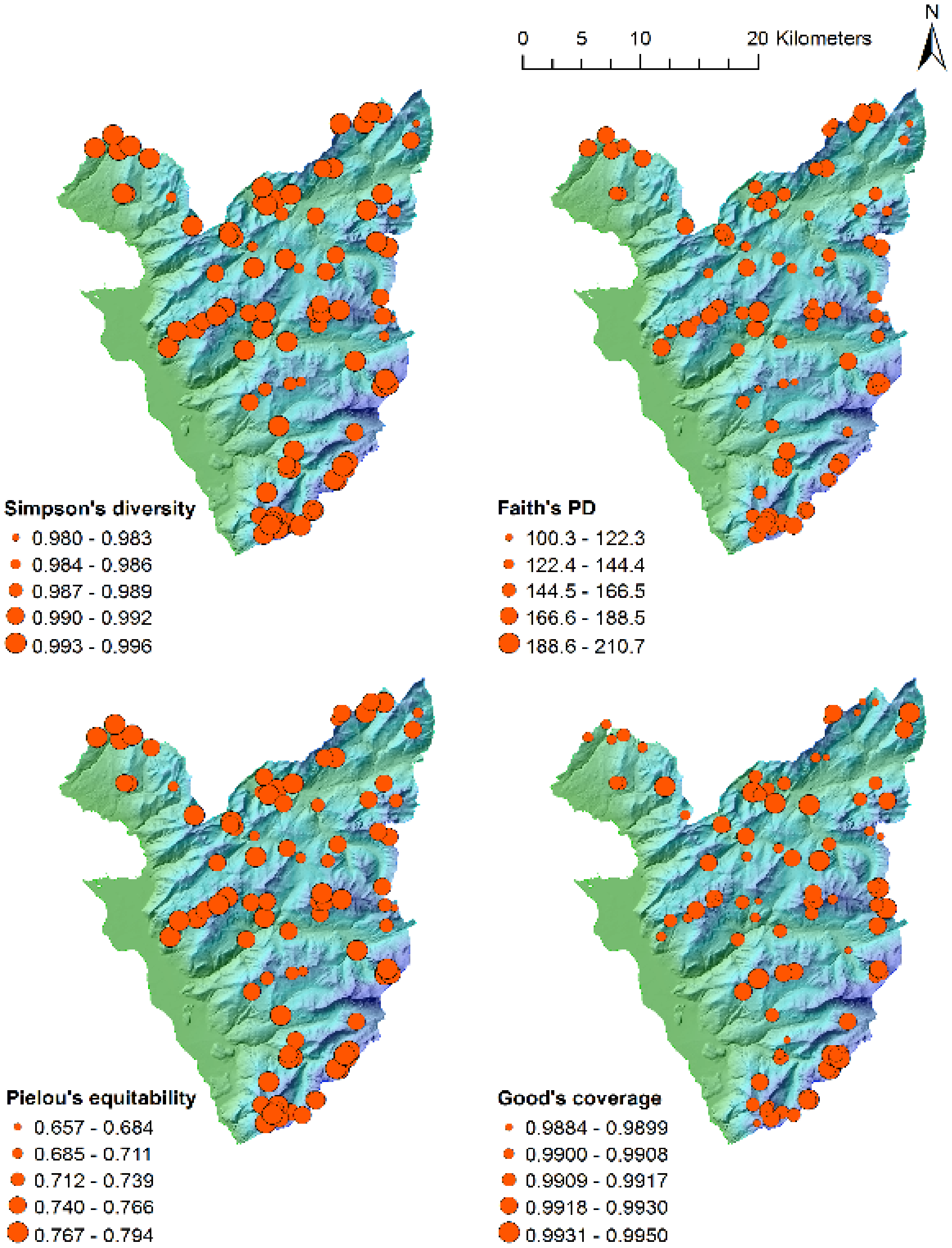
Supplementary Table 3. Spearman correlations between Bacteroidetes groups and soil soluble phosphorus content.

Taxonomic group	**rho**	**pval**
Bacteroidetes Richness	**0.3147742**	0.0101
Bacteroidetes abundance	**0.4127544**	0.0006
Class Cytophagia richness	-0.1248956	*0.3177*
Class Cytophagia abundance	-0.1871282	*0.1324*
Class Flavobacteriia richness	-0.1545922	*0.2152*
Class Flavobacteriia abundance	0.02717908	*0.8285*
Class Saprospirae richness	-0.1268913	*0.3100*
Class Saprospirae abundance	-0.1313642	*0.2923*
Class Sphingobacteriia richness	-0.06126204	*0.6251*
Class Sphingobacteriia abundance	-0.03473578	*0.7819*
Cytophagia; family undefined	**0.4825635**	< 0.0001
Cytophagia; family Amoebophilaceae	-0.1930786	*0.1204*
Cytophagia; family Cyclobacteriaceae	-0.1043033	*0.4046*
Cytophagia; family Cytophagaceae	**0.4431108**	0.0002
Cytophagia; family Flammeovirgaceae	**0.3167463**	0.0096
Flavobacteriia; family undefined	0.09165792	*0.4642*
Flavobacteriia; family Weeksellaceae	**0.4547138**	0.0001
Flavobacteriia; family Cryomorphaceae	-0.09854788	*0.4311*
Flavobacteriia; family Flavobacteriaceae	**0.4905593**	0.0000
Saprospirae; family undefined	0.02360067	*0.8508*
Saprospirae; family Chitinophagaceae	**0.3442438**	0.0049
Saprospirae; family Saprospiraceae	-0.06064085	*0.6278*
Sphingobacteriia; family undefined	0.2176436	*0.0792*
Sphingobacteriia; family Sphingobacteriaceae	**0.2901492**	0.0181
OTUs in Bacteroidetes-avP module		
c_Sphingobacteriia; o_Sphingobacteriales; f_; g_; s_	**0.4198781**	0.0004
c_Sphingobacteriia; o_Sphingobacteriales; f_; g_; s_	**0.4296077**	0.0003
c_Sphingobacteriia; o_Sphingobacteriales; f_; g_; s_	**0.6308022**	< 0.0001
c_Sphingobacteriia; o_Sphingobacteriales; f_; g_; s_	**0.4253544**	0.0004
c_Flavobacteriia; o_Flavobacteriales; f_Flavobacteriaceae; g_; s_	**0.3622746**	0.0028
c_Flavobacteriia; o_Flavobacteriales; f_Flavobacteriaceae; g_Flavobacterium; s_	**0.4188436**	0.0005
c_Flavobacteriia; o_Flavobacteriales; f_Flavobacteriaceae; g_Flavobacterium; s_	**0.4653918**	< 0.0001

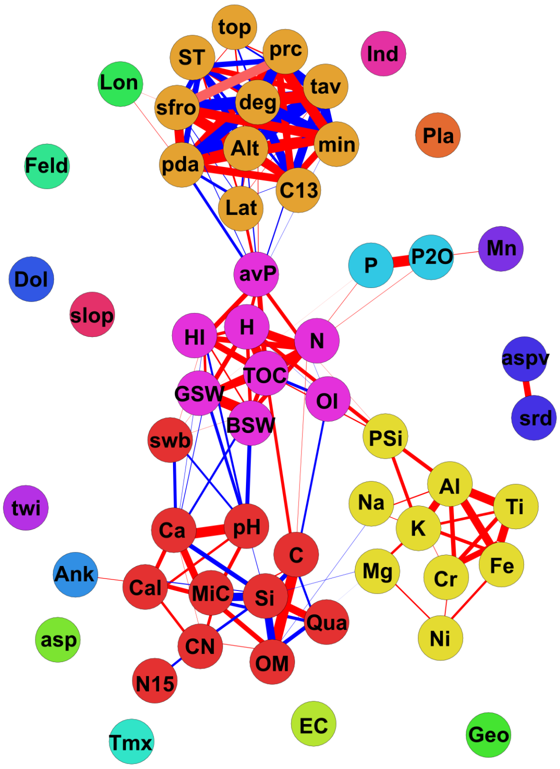
The significant coefficients are indicated in bold letters, while the non-significant p-values are italicised.
Only the results from the four most abundant Bacteroidetes classes are shown.
One Bacteroidetes family was omitted from the analysis because only a single rare OTU was present in the dataset.



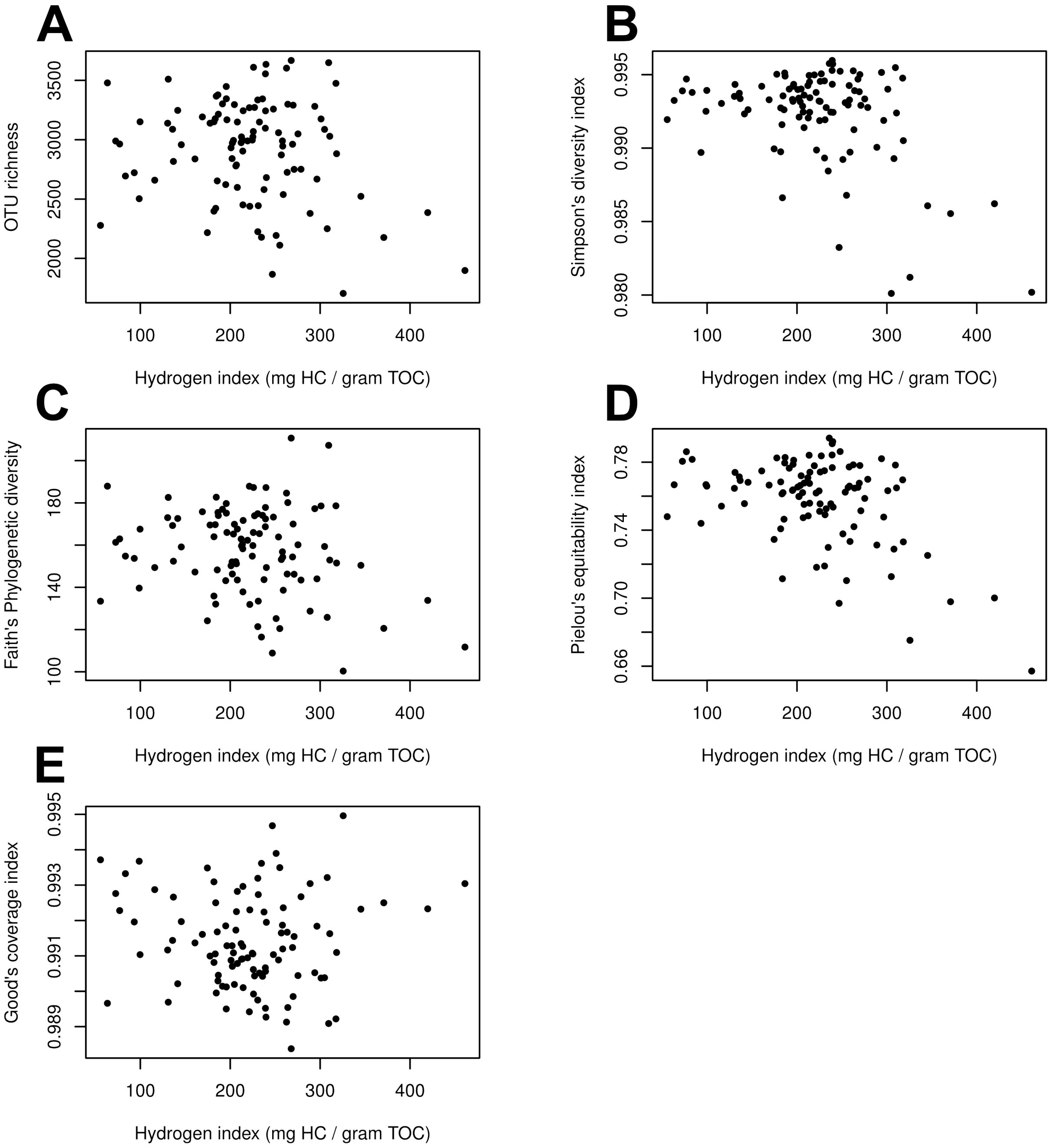
Supplementary Figure 1. Principal coordinate analysis ordination of the (A) unweighted and (B) weighted UniFrac distance matrices of the soil samples where the DNA was extracted from fresh samples (green) or from the dried samples (brown). The duplicate fresh (green) samples for each site are replicate sequencing runs from the same PCR product, used as a reference point in assessing the level of variation that is present within sequenced samples. The communities from freshly extracted soil samples which were not included in the treatment study are colored in gray. The environmental parameters that were available for this small-scale study are the following pH, GSW, deg, slop, min, srd, tav, top, asp, aspv, swb, twi, sfro, Alt, and prc. Those parameters that were significant drivers of the bacterial communities ($p > 0.05$) are shown in the ordination space.



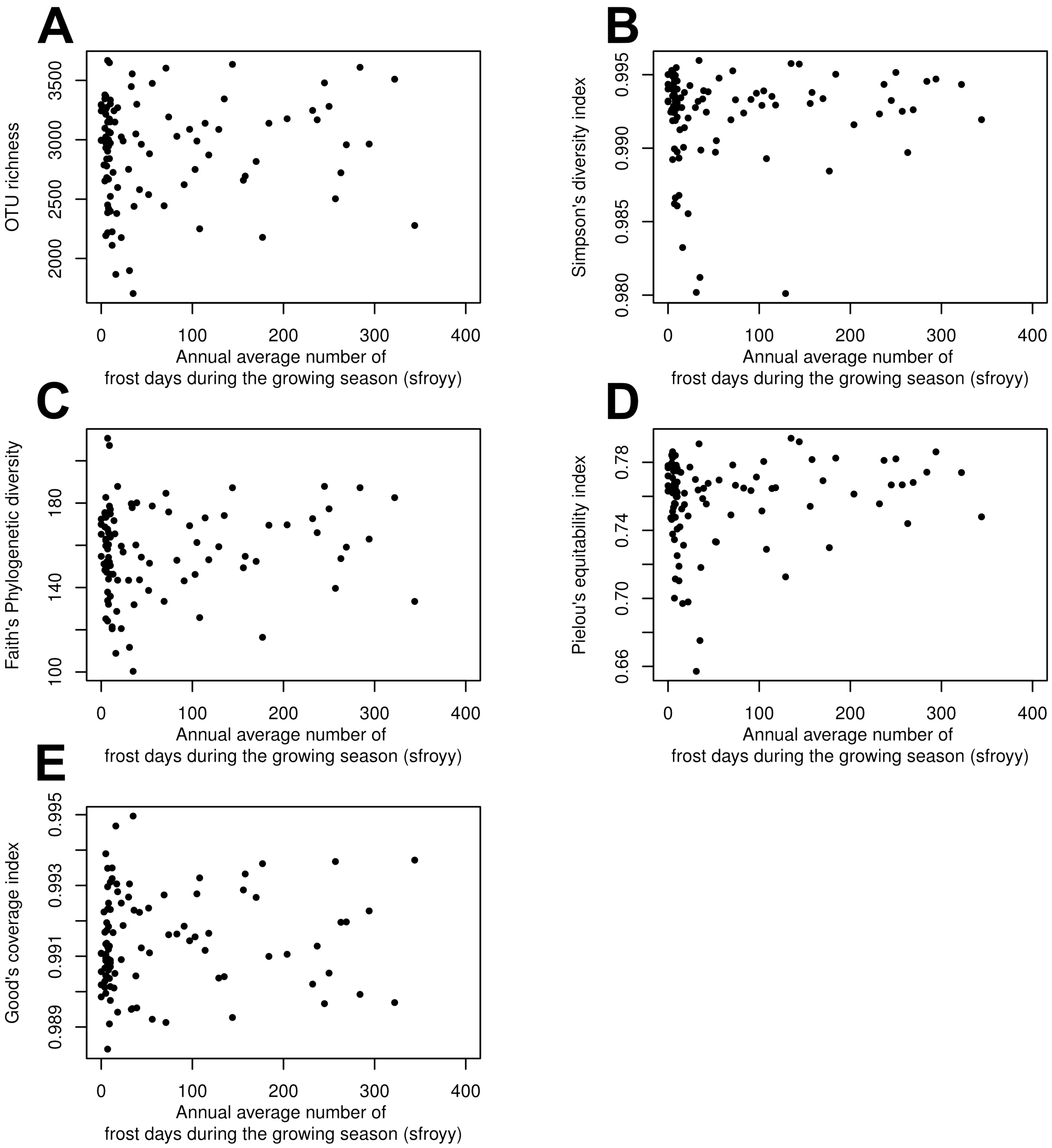
Supplementary Figure 2. Distribution of the bacterial community diversity measures across the alpine landscape.The Simpson's diversity, Faith's phylogenetic diversity, Pielou's equitability, and Good's coverage indices were 0.992 (s.d. 0.003), 157.3 (s.d. 20.8), 0.758 (s.d. 0.025), and 0.991 (s.d. 0.001), respectively. Base maps reproduced by permission of swisstopo (BA16075).



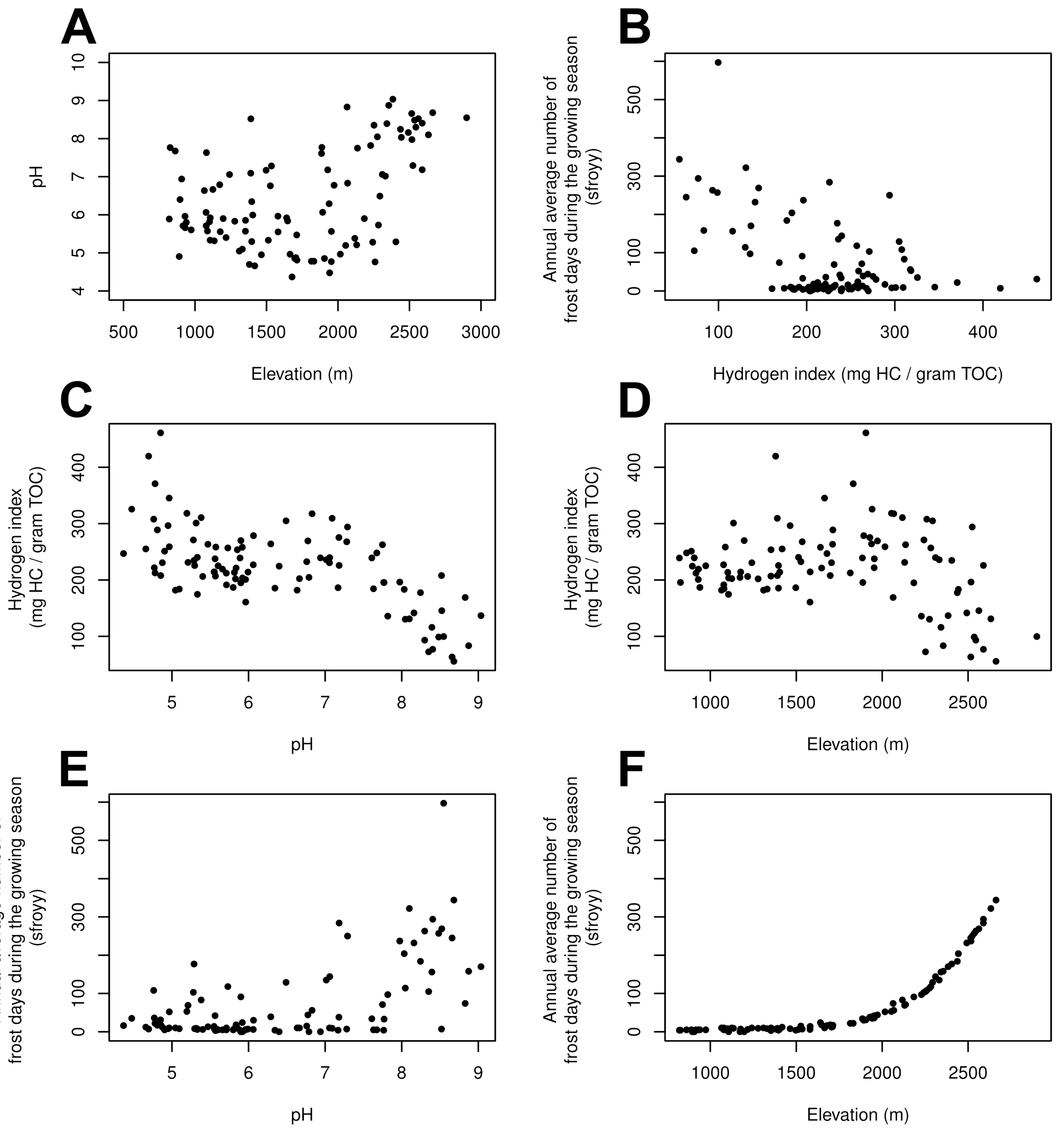
Supplementary Figure 3. The Spearman's rank based correlation networks of the 56 environmental variables measured for the 100 sites. Positive correlations have red edges, while the negative have blue edges. Only those edges with coefficients greater than ± 0.5 are shown, and the edge thickness displays the strength of the correlation. Refer to Supplementary Table 1 for the complete explanation of the environmental parameter abbreviations. Note how several parameters are directly or indirectly dependent, for example Alt (altitude) with deg (degree), etc.



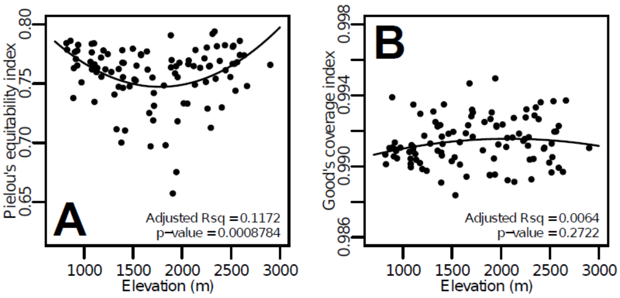
Supplementary Figure 4. Diversity indices of the alpine soil bacteria as a function of the hydrogen index (mg hydrocarbon/g TOC). Note that the hydrogen index indicates the amount of fresh organic matter that is present in the soil. (A) OTU richness, (B) Simpson's diversity, (C) Faith's phylogenetic diversity, (D) Pielou's equitability, and (E) Good's coverage.



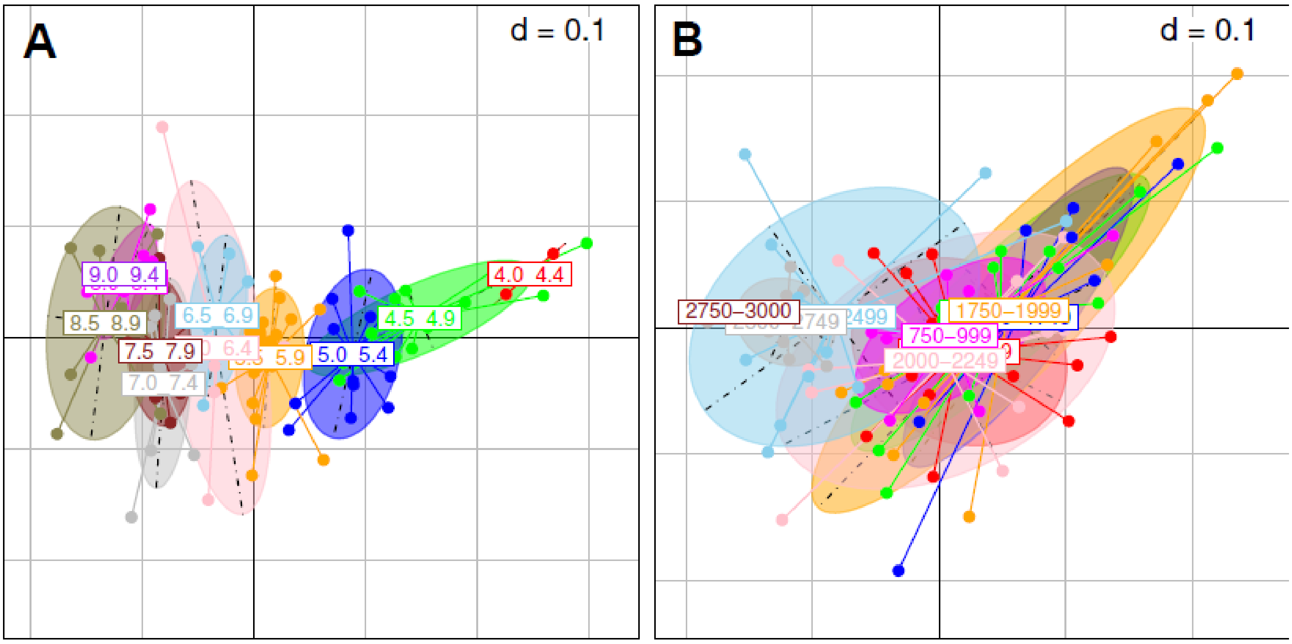
Supplementary Figure 5. Diversity indices of the alpine soil bacteria as a function of the annual average number of frost days during the growing season (sfroyy). (A) OTU richness, (B) Simpson's diversity, (C) Faith's phylogenetic diversity, (D) Pielou's equitability, and (E) Good's coverage.



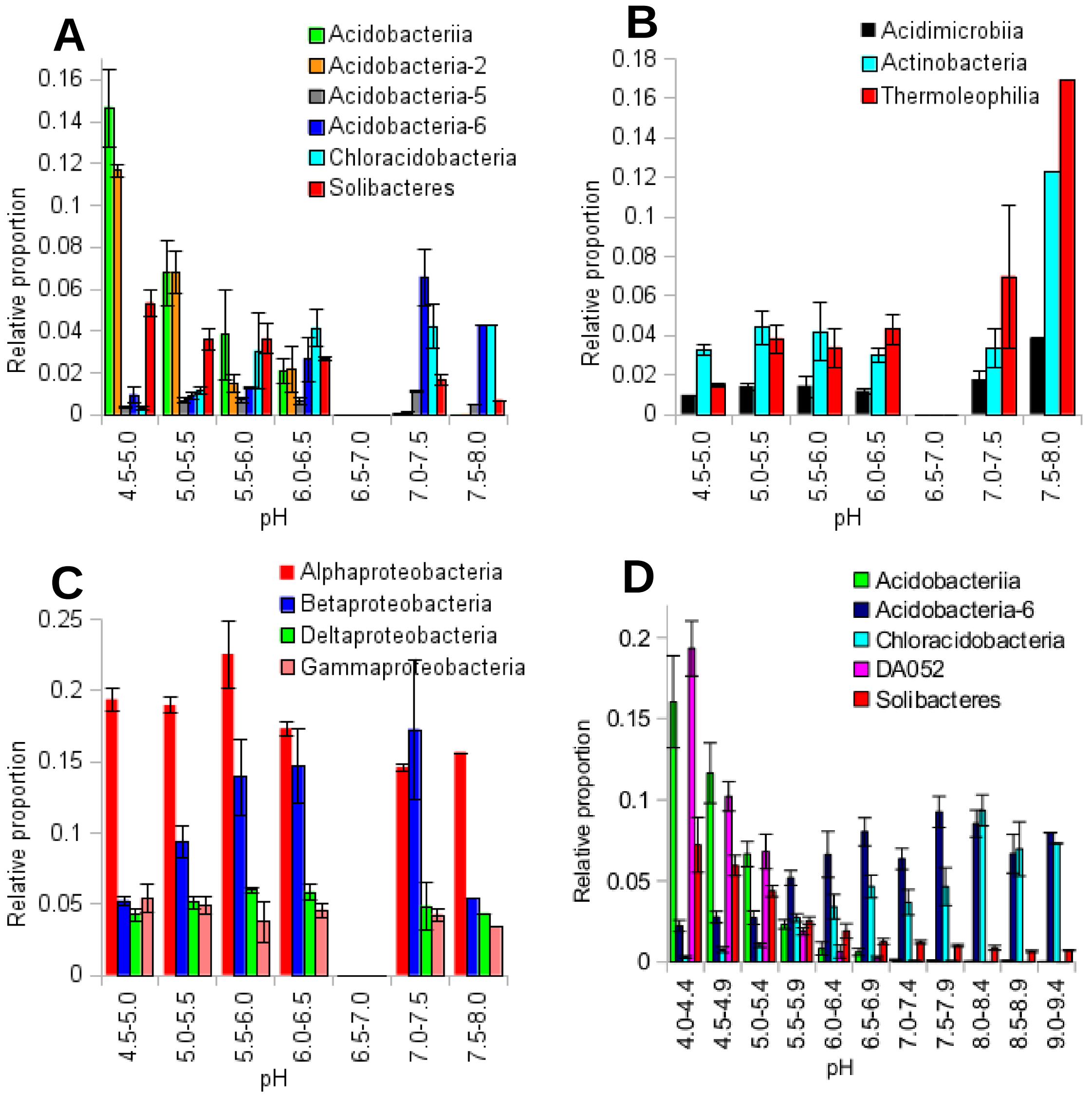
Supplementary Figure 6. Relationship between elevation, pH, hydrogen index, and annual average number of frost days during the growing season. (A) The soil pH across the elevation gradient; (B) the annual average number of frost days as a function of the soil hydrogen index; (C) the soil hydrogen index as a function of soil pH; (D) the soil hydrogen index across the elevation gradient; (E) the annual average number of frost days as a function of pH and (F) across the elevation gradient.

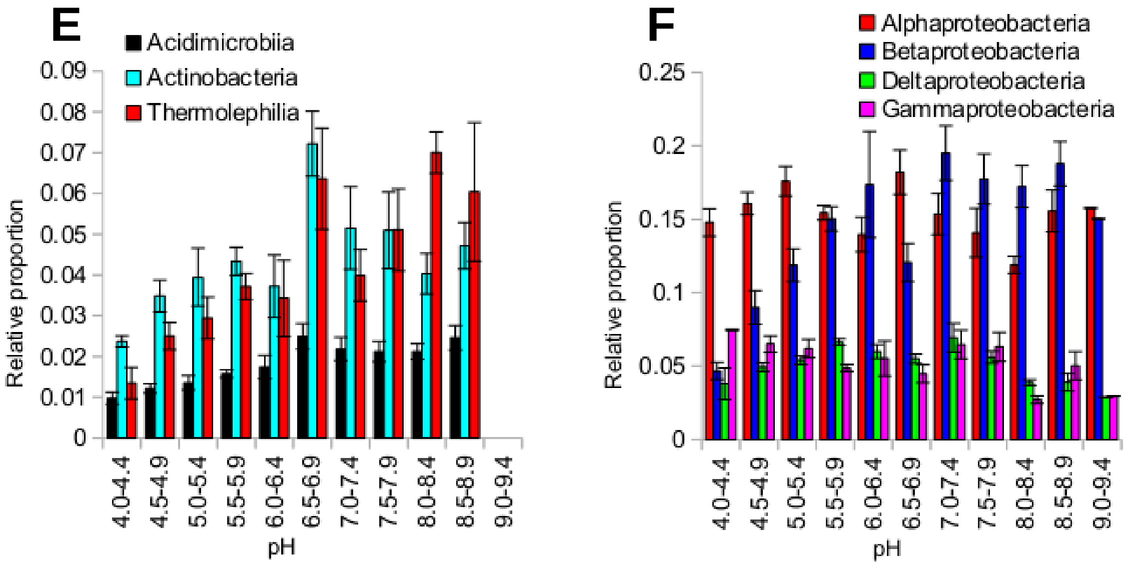


Supplementary Figure 7. Relationship between soil bacterial diversity and elevation. (A) Pielou's equitability index, and (B) Good's coverage index. Points correspond to individual sites. Quadratic trendlines are shown, which were calculated using the lm() function in R. the adjusted R squared values indicate the 'goodness of fit' of the bacterial diversity to respective trendlines. p-values indicate the significance of the overall model.

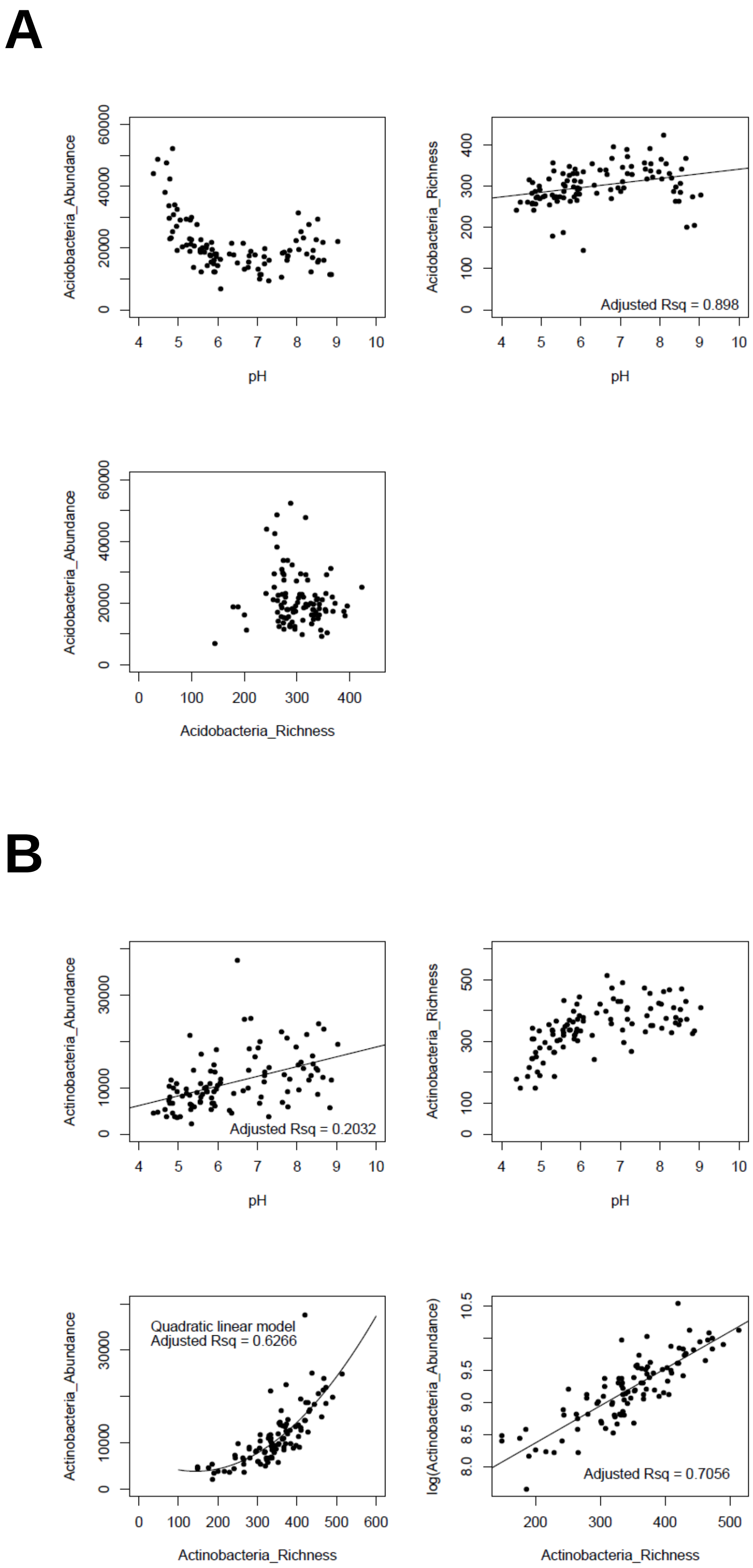


Supplementary Figure 8. Between class analysis of the alpine soil bacterial community structure (NMDS of the weighted UniFrac matrix) as a function of (A) soil pH and (B) elevation. The colors and ellipses show the respective pH or elevation groups.

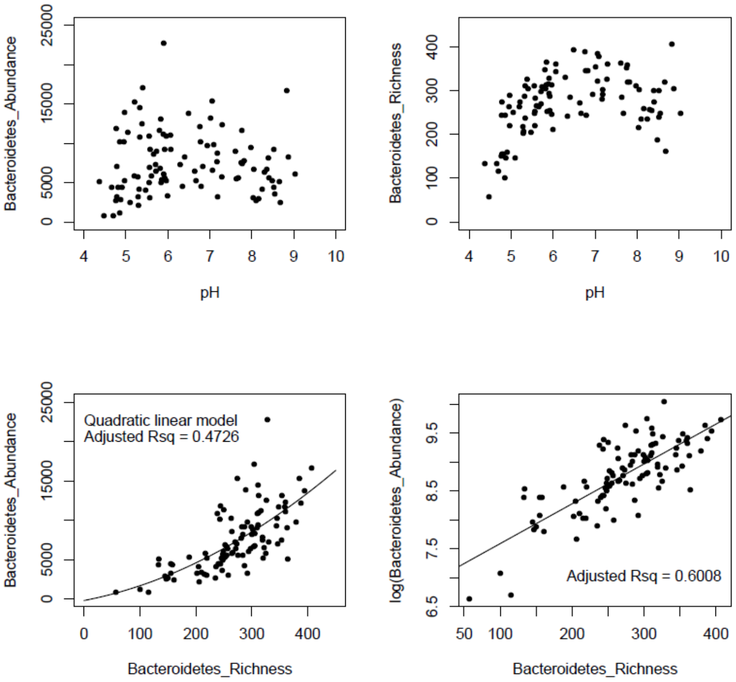

A
Acidobacteriia
Acidobacteria-2
Acidobacteria-5
Acidobacteria-6
Chloracidobacteria
Solibacteres
Relative proportion
0.16
0.14
0.12
0.1
0.08
0.06
0.04
0.02
0
4.5-5.0
5.0-5.5
5.5-6.0
6.0-6.5
6.5-7.0
7.0-7.5
7.5-8.0
pH
B
Acidimicrobiia
Actinobacteria
Thermoleophilia
Relative proportion
0.18
0.16
0.14
0.12
0.1
0.08
0.06
0.04
0.02
0
4.5-5.0
5.0-5.5
5.5-6.0
6.0-6.5
6.5-7.0
7.0-7.5
7.5-8.0
pH
C
Alphaproteobacteria
Betaproteobacteria
Deltaproteobacteria
Gammaproteobacteria
Relative proportion
0.25
0.2
0.15
0.1
0.05
0
4.5-5.0
5.0-5.5
5.5-6.0
6.0-6.5
6.5-7.0
7.0-7.5
7.5-8.0
pH
D
Acidobacteriia
Acidobacteria-6
Chloracidobacteria
DA052
Solibacteres
Relative proportion
0.2
0.15
0.1
0.05
0
4.0-4.4
4.5-4.9
5.0-5.4
5.5-5.9
6.0-6.4
6.5-6.9
7.0-7.4
7.5-7.9
8.0-8.4
8.5-8.9
9.0-9.4
pH



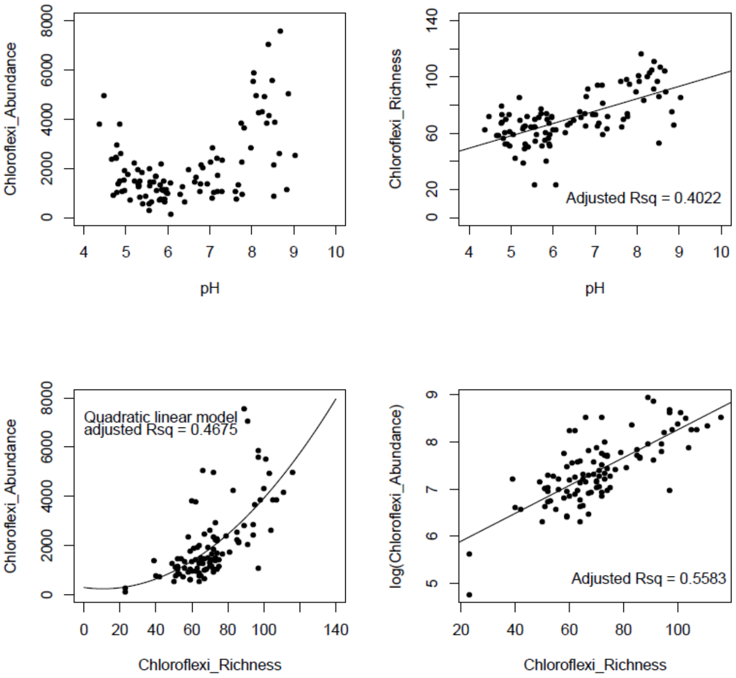
Supplementary Figure 9. pH trend across the major classes within the Acidobacteria, Actinobacteria, and Proteobacteria for the 2011 samples (A-C) and 2012 samples (D-F).


A
Acidobacteria_Abundance
0
20000
40000
60000
4
5
6
7
8
9
10
pH
Acidobacteria_Richness
0
100
200
300
400
Adjusted Rsq = 0.898
pH
Acidobacteria_Abundance
0
100
200
300
400
Acidobacteria_Richness
B
Actinobacteria_Abundance
0
10000
30000
Adjusted Rsq = 0.2032
pH
Actinobacteria_Richness
100
300
500
pH
Actinobacteria_Abundance
Quadratic linear model
Adjusted Rsq = 0.6266
0
100
200
300
400
500
600
Actinobacteria_Richness
log(Actinobacteria_Abundance)
8.0
8.5
9.0
9.5
10.5
Adjusted Rsq = 0.7056
200
300
400
500
Actinobacteria_Richness

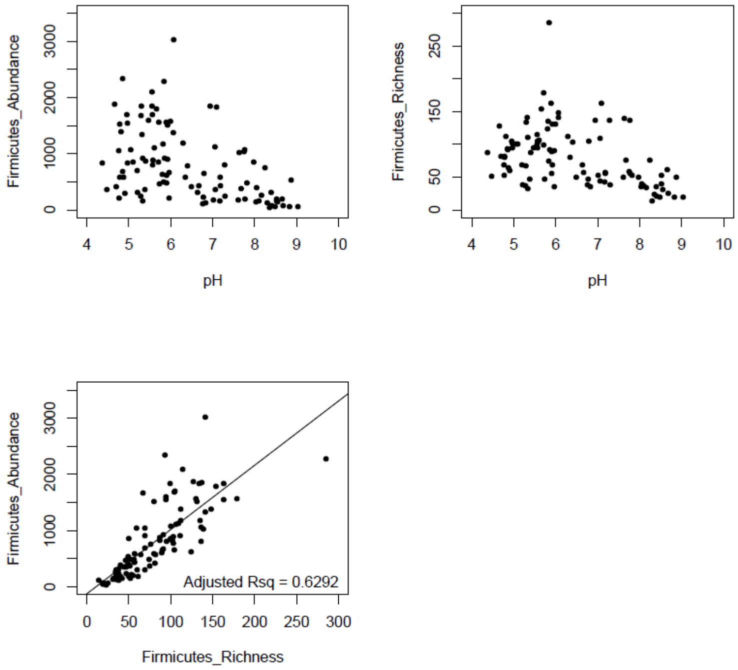
C


Bacteroidetes_Abundance
0
5000
15000
25000
4
5
6
7
8
9
10
pH
Bacteroidetes_Richness
0
100
200
300
400
pH
Quadratic linear model
Adjusted Rsq = 0.4726
Bacteroidetes_Richness
100
200
300
400
log(Bacteroidetes_Abundance)
6.5
7.5
8.5
9.5
Adjusted Rsq = 0.6008
50

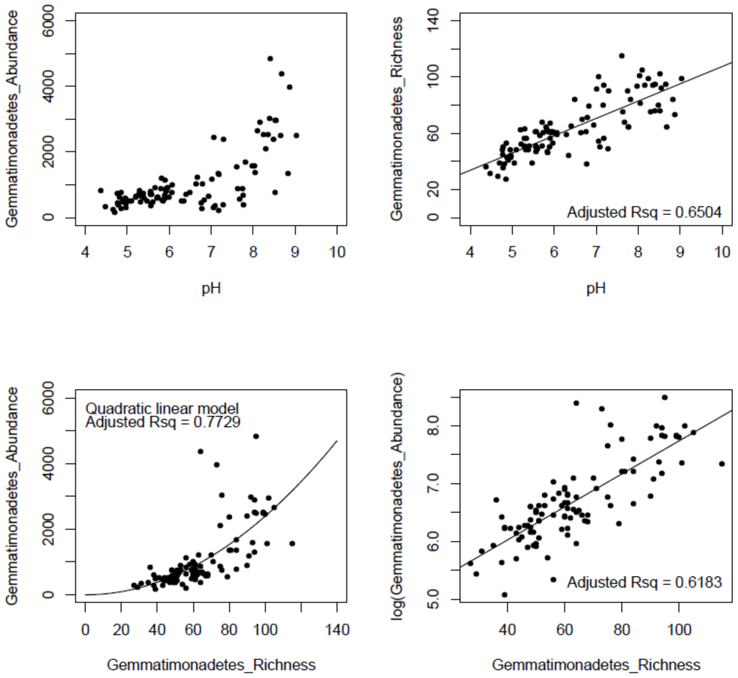
D


Chloroflexi_Abundance
0
2000
4000
6000
8000
4
5
6
7
8
9
10
pH
Chloroflexi_Richness
0
20
60
100
140
Adjusted Rsq = 0.4022
pH
Quadratic linear model
adjusted Rsq = 0.4675
Chloroflexi_Richness
0
20
40
60
80
100
140
log(Chloroflexi_Abundance)
5
6
7
8
9
Adjusted Rsq = 0.5583

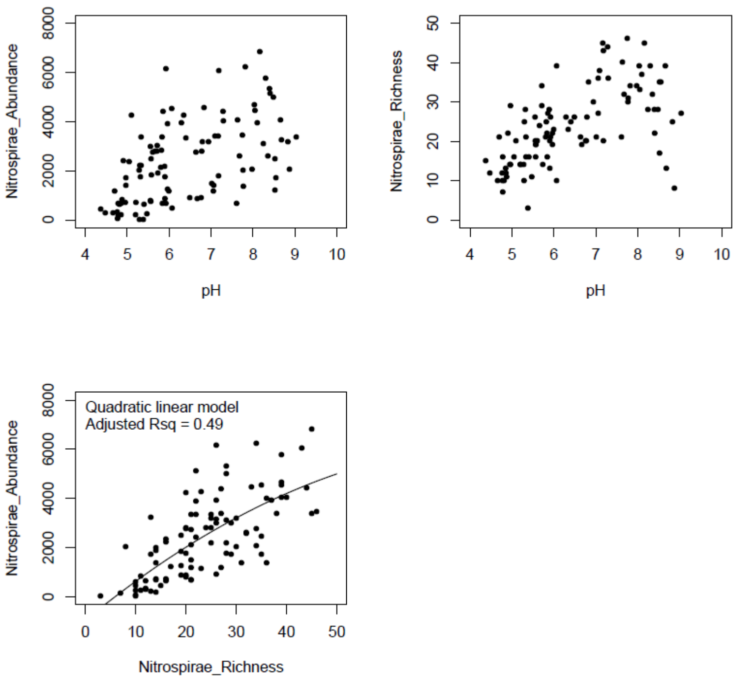
E


Firmicutes_Abundance
0
1000
2000
3000
4
5
6
7
8
9
10
pH
Firmicutes_Richness
0
50
150
250
4
5
6
7
8
9
10
pH
Firmicutes_Abundance
0
1000
2000
3000
Adjusted Rsq = 0.6292
0
50
100
150
200
250
300
Firmicutes_Richness

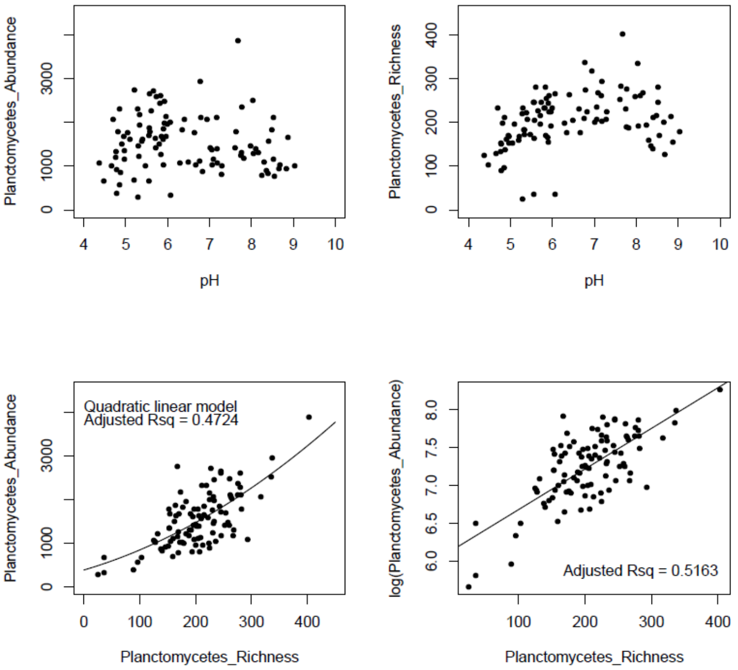
F


Gemmatimonadetes_Abundance
0
2000
4000
6000
4
5
6
7
8
9
10
pH
Gemmatimonadetes_Richness
0
20
60
100
140
Adjusted Rsq = 0.6504
4
5
6
7
8
9
10
pH
Gemmatimonadetes_Abundance
0
2000
4000
6000
Quadratic linear model
Adjusted Rsq = 0.7729
0
20
40
60
80
100
140
Gemmatimonadetes_Richness
log(Gemmatimonadetes_Abundance)
5.0
6.0
7.0
8.0
Adjusted Rsq = 0.6183
40
60
80
100
Gemmatimonadetes_Richness

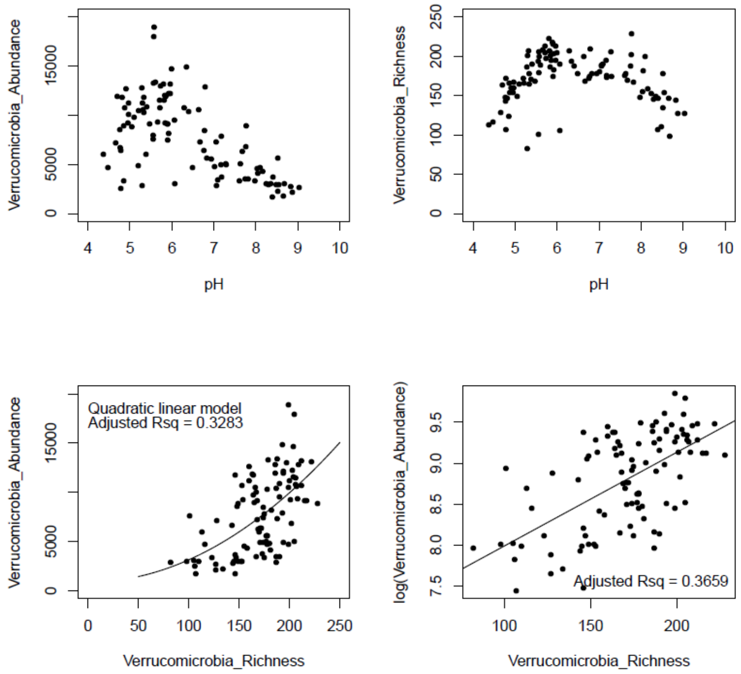
G


Nitrospirae_Abundance
pH
Nitrospirae_Richness
pH
Quadratic linear model
Adjusted Rsq = 0.49
Nitrospirae_Abundance
Nitrospirae_Richness
0
2000
4000
6000
8000
0
10
20
30
40
50
4
5
6
7
8
9
10

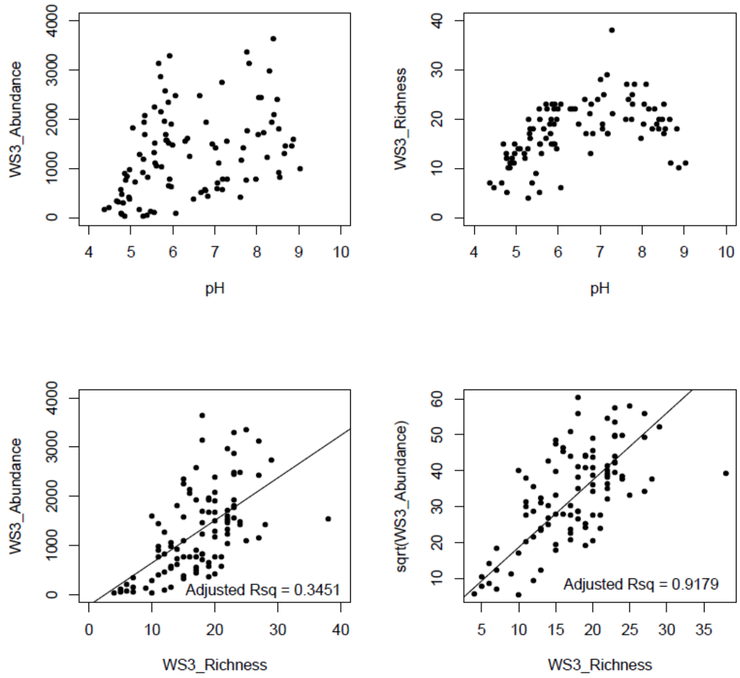
H


Planctomycetes_Abundance
pH
Planctomycetes_Richness
pH
Quadratic linear model
Adjusted Rsq = 0.4724
Planctomycetes_Abundance
Planctomycetes_Richness
log(Planctomycetes_Abundance)
Adjusted Rsq = 0.5163
Planctomycetes_Richness
0
1000
3000
100
200
300
400
6.0
6.5
7.0
7.5
8.0
4
5
6
7
8
9
10

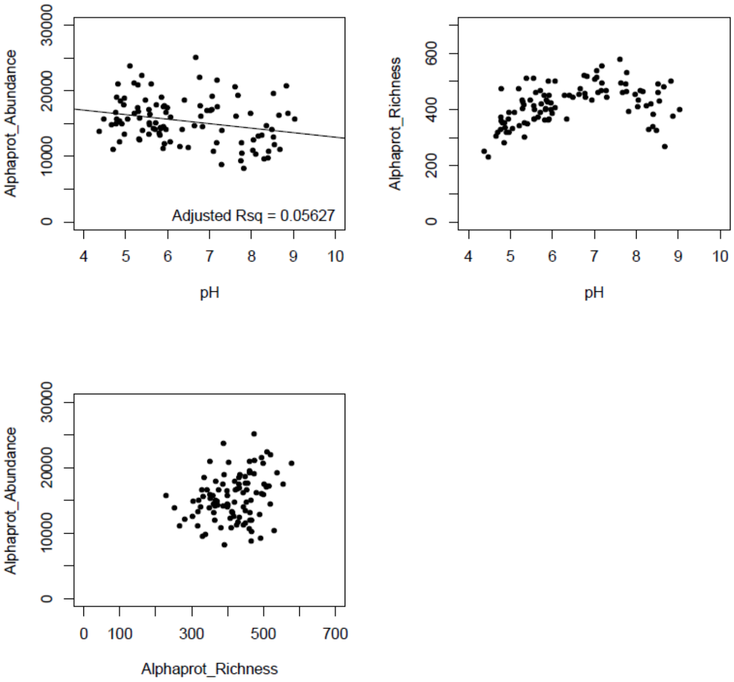
I


Verrucomicrobia_Abundance
0
5000
15000
4
5
6
7
8
9
10
pH
Verrucomicrobia_Richness
0
50
100
150
200
250
pH
Quadratic linear model
Adjusted Rsq = 0.3283
Verrucomicrobia_Abundance
0
50
100
150
200
250
Verrucomicrobia_Richness
log(Verrucomicrobia_Abundance)
7.5
8.0
8.5
9.0
9.5
Adjusted Rsq = 0.3659
Verrucomicrobia_Richness

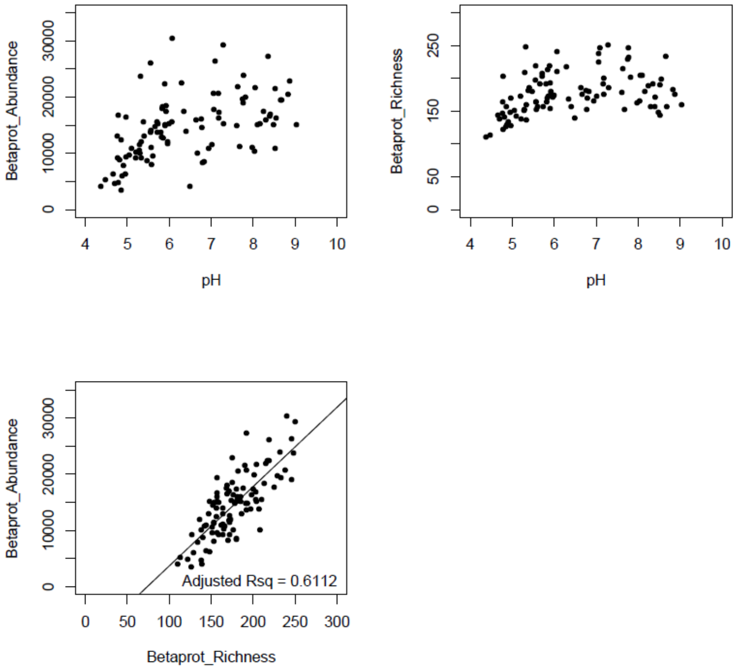
J


WS3_Abundance
0
1000
2000
3000
4000
4
5
6
7
8
9
10
pH
WS3_Richness
0
10
20
30
40
pH
WS3_Abundance
Adjusted Rsq = 0.3451
0
10
20
30
40
WS3_Richness
sqrt(WS3_Abundance)
10
20
30
40
50
60
Adjusted Rsq = 0.9179
5
10
15
20
25
30
35
WS3_Richness

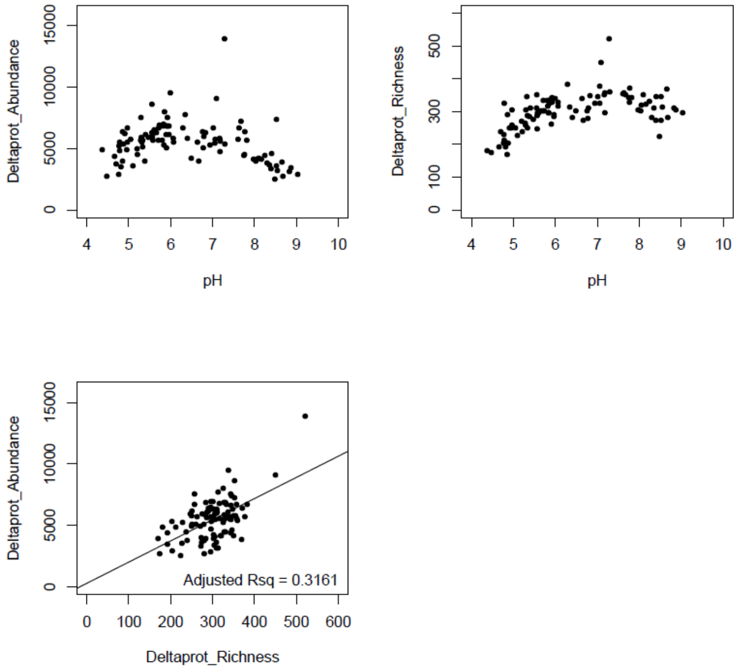
K


Alphaprot_Abundance
0
10000
20000
30000
Adjusted Rsq = 0.05627
4
5
6
7
8
9
10
pH
Alphaprot_Richness
0
200
400
600
4
5
6
7
8
9
10
pH
Alphaprot_Abundance
0
10000
20000
30000
0
100
300
500
700
Alphaprot_Richness

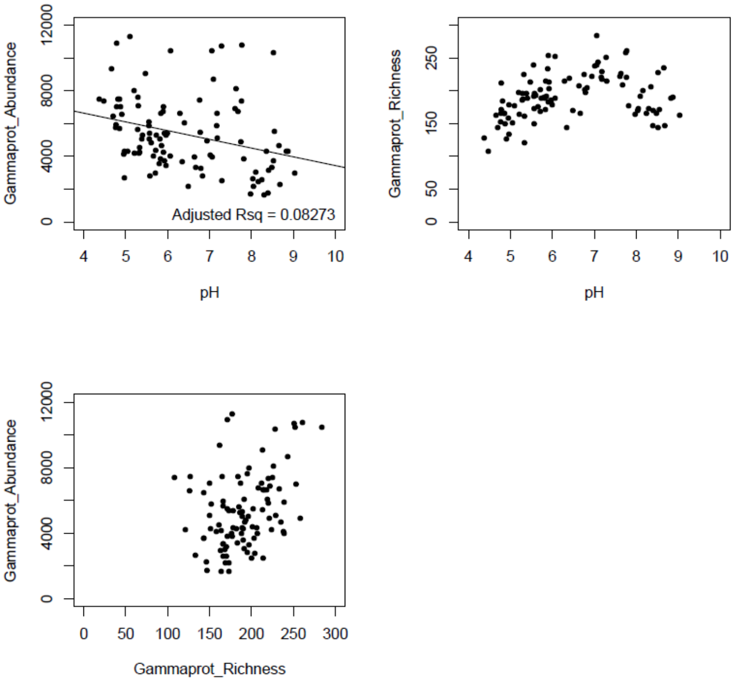
L


Betaprot_Abundance
0
10000
20000
30000
4
5
6
7
8
9
10
pH
Betaprot_Richness
0
50
150
250
4
5
6
7
8
9
10
pH
Betaprot_Abundance
0
10000
20000
30000
Adjusted Rsq = 0.6112
0
50
100
150
200
250
300
Betaprot_Richness

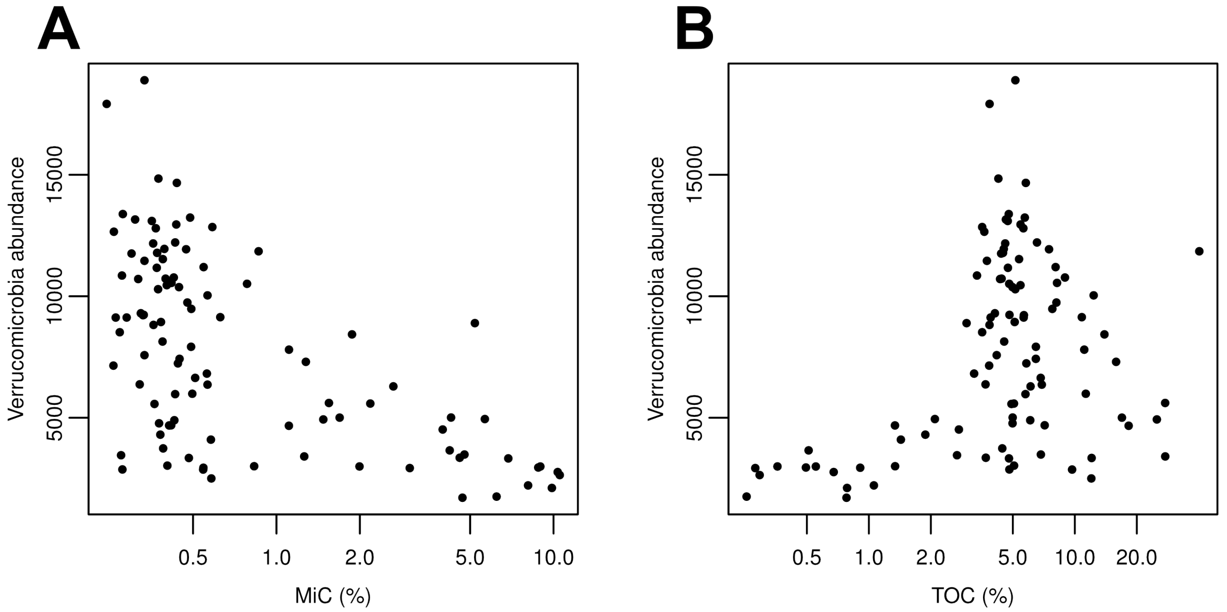
M



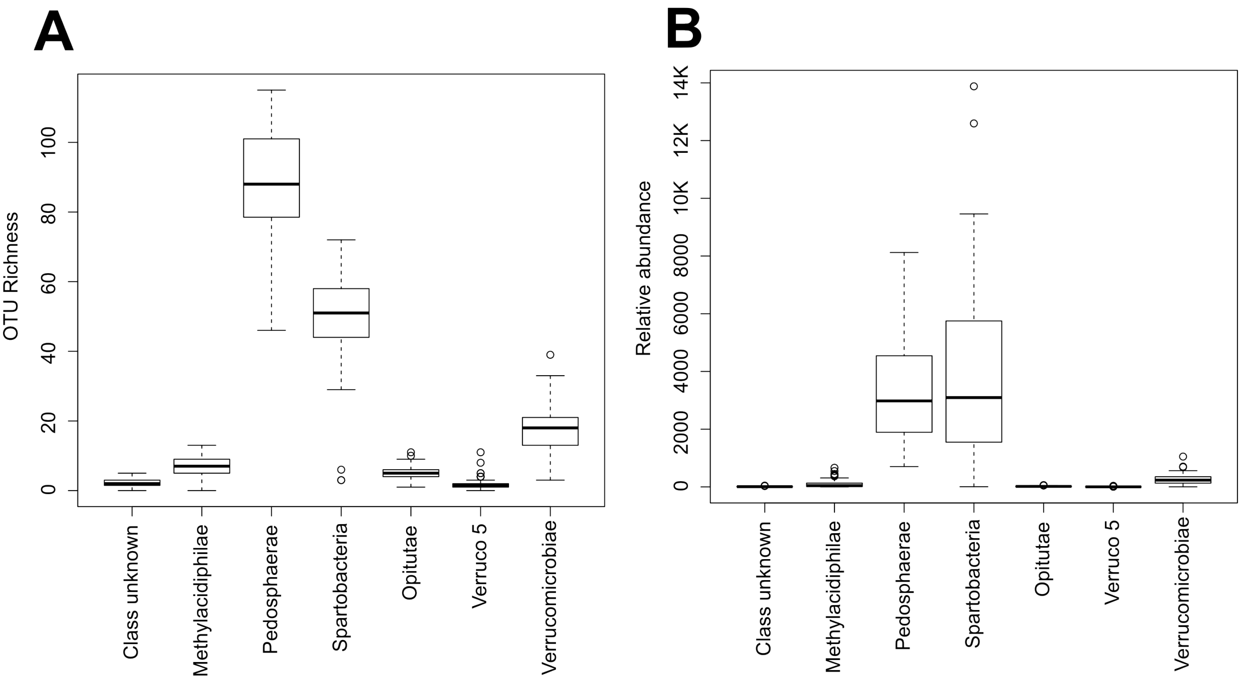
N



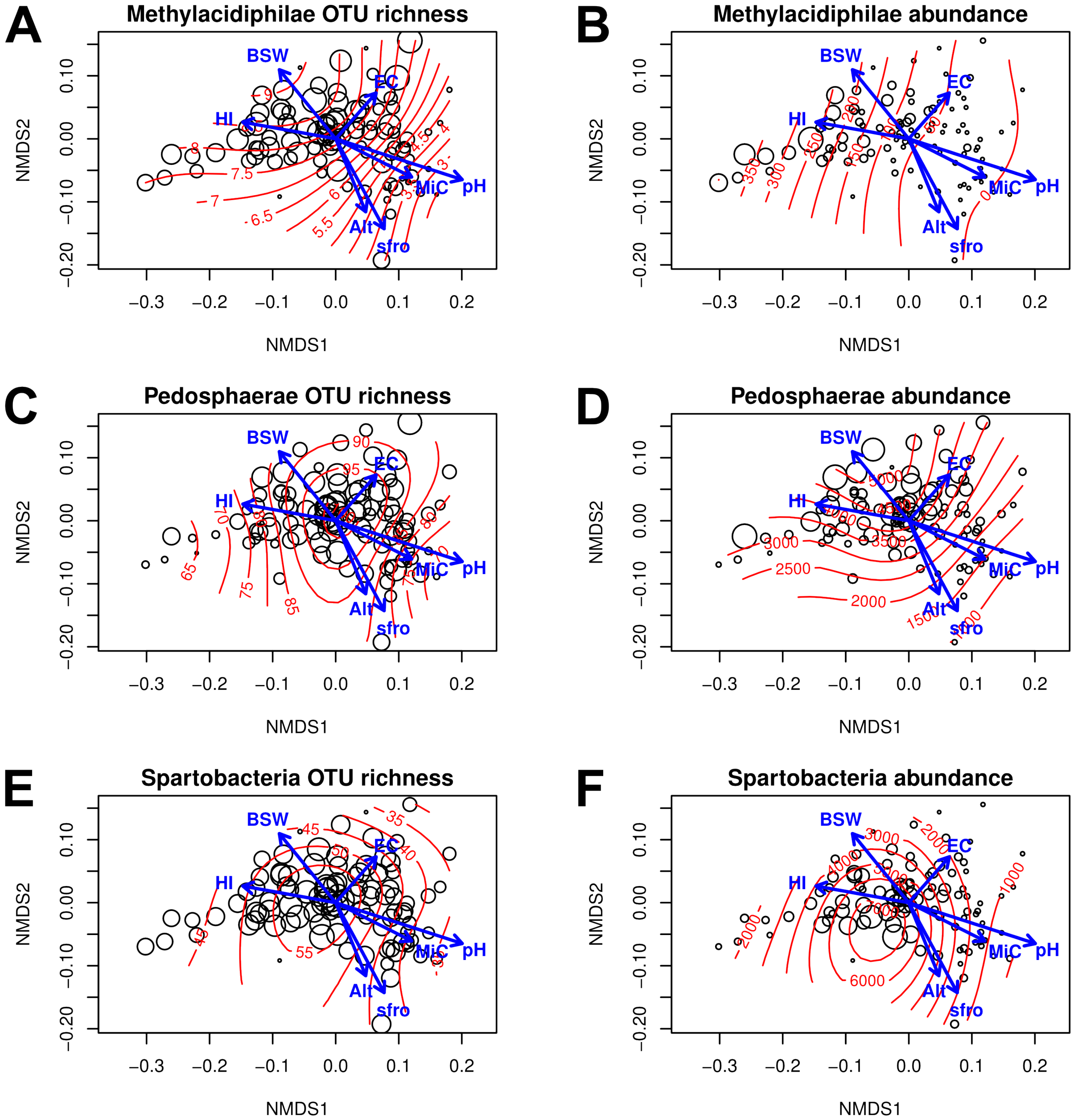
Supplementary figure 10. Relationships between relative abundance, OTU richness, and pH of the most abundant taxonomic groups. (A) Acidobacteria, (B) Actinobacteria, (C) Bacteroidetes, (D) Chloroflexi, (E) Firmicutes, (F) Gemmatimonadetes, (G) Nitrospirae, (H) Planctomycetes, (I) Verrucomicrobia, (J) WS3, (K) Alphaproteobacteria, (L) Betaproteobacteria, (M) Deltaproteobacteria, and (N) Gammaproteobacteria.

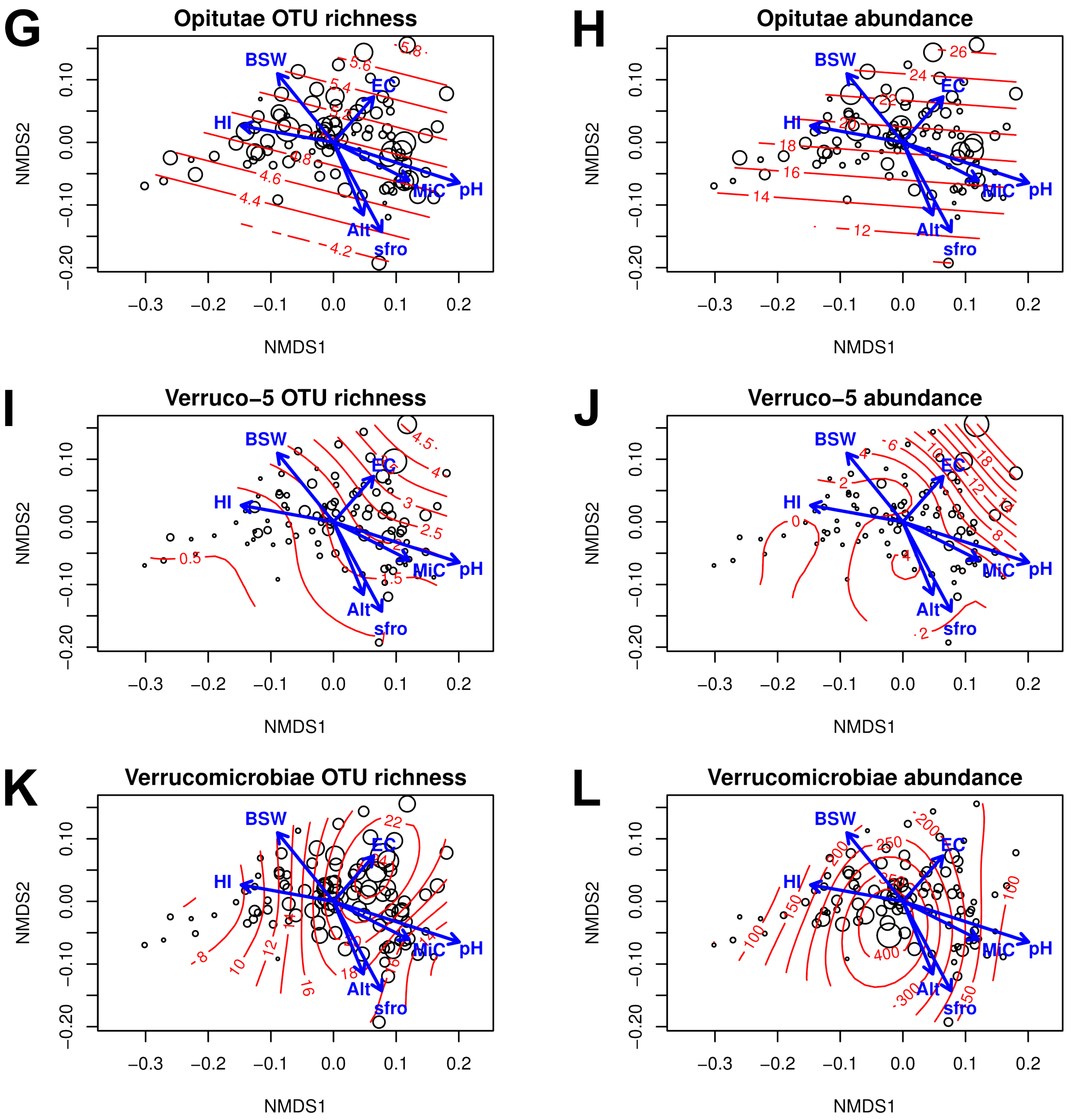


Supplementary Figure 11. Relationship between Verrucomicrobial relative abundance and (A) the soil mineral carbon content and (B) the soil total organic carbon content.

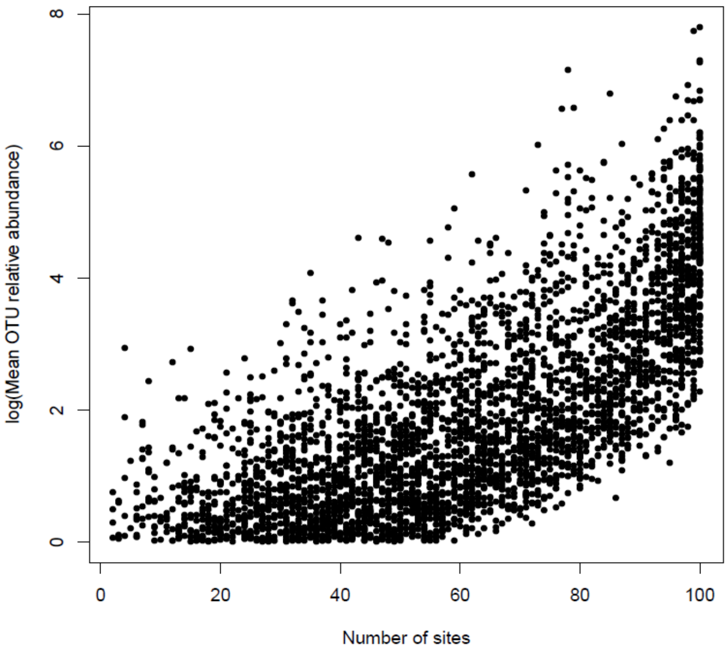


Supplementary Figure 12. Proportion of Verrucomicrobial classes across the alpine landscape. (A) Verrucomicrobial OTU richness and (B) relative abundance in the respective sites.

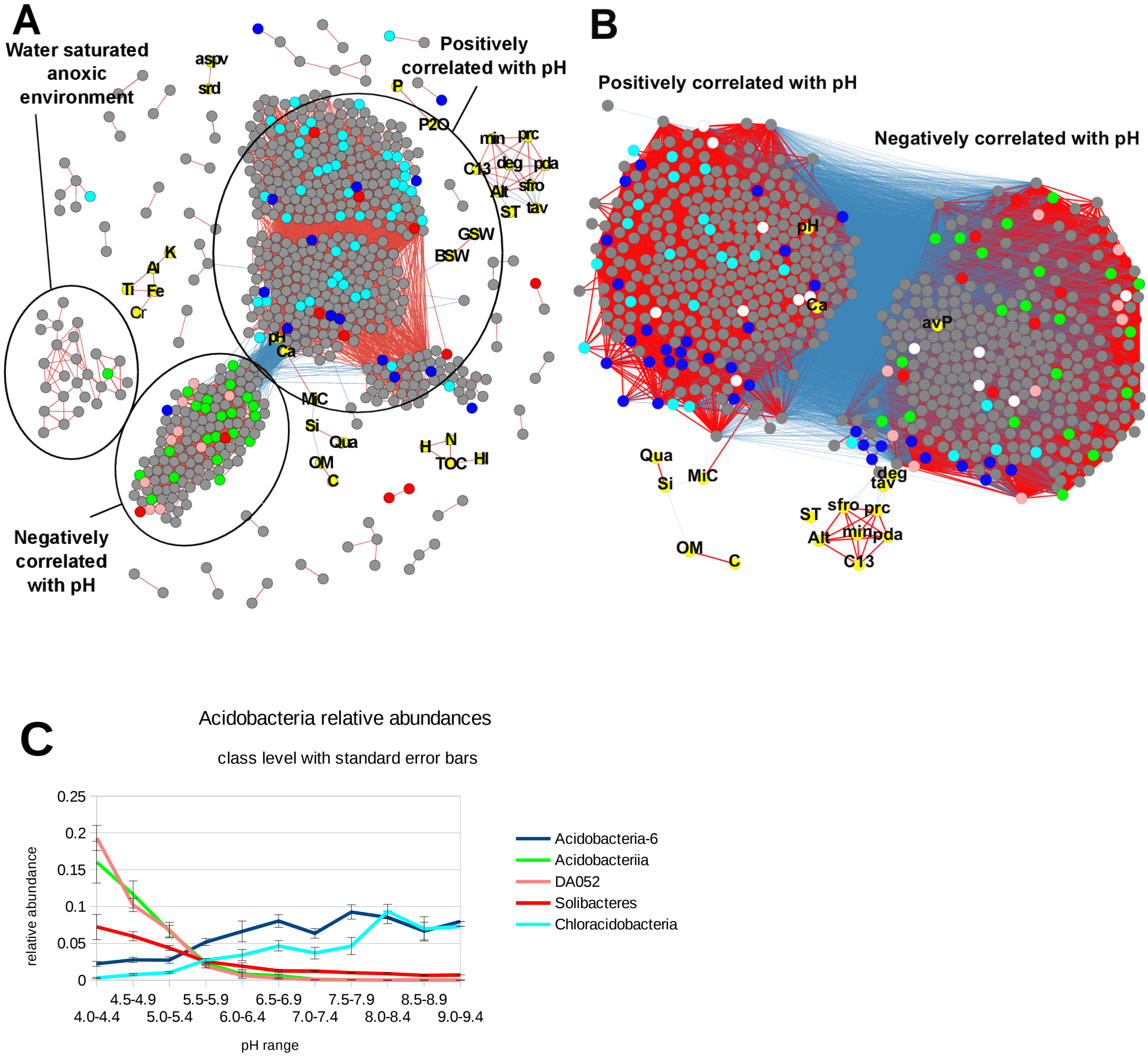

A
Methylacidiphilae OTU richness
B
Methylacidiphilae abundance
C
Pedosphaerae OTU richness
D
Pedosphaerae abundance
E
Spartobacteria OTU richness
F
Spartobacteria abundance
NMDS1
NMDS2
−0.3
−0.2
−0.1
0.0
0.1
0.2
−0.20
−0.10
0.00
0.10
BSW
EC
HI
MiC
pH
Alt
sfro
9
8
7.5
7
6.5
6
5.5
4.5
4
3.5
3
350
300
250
200
150
100
50
0
90
95
85
80
75
70
65
5000
4000
3500
3000
2500
2000
1500
1000
45
50
55
40
35
7000
6000



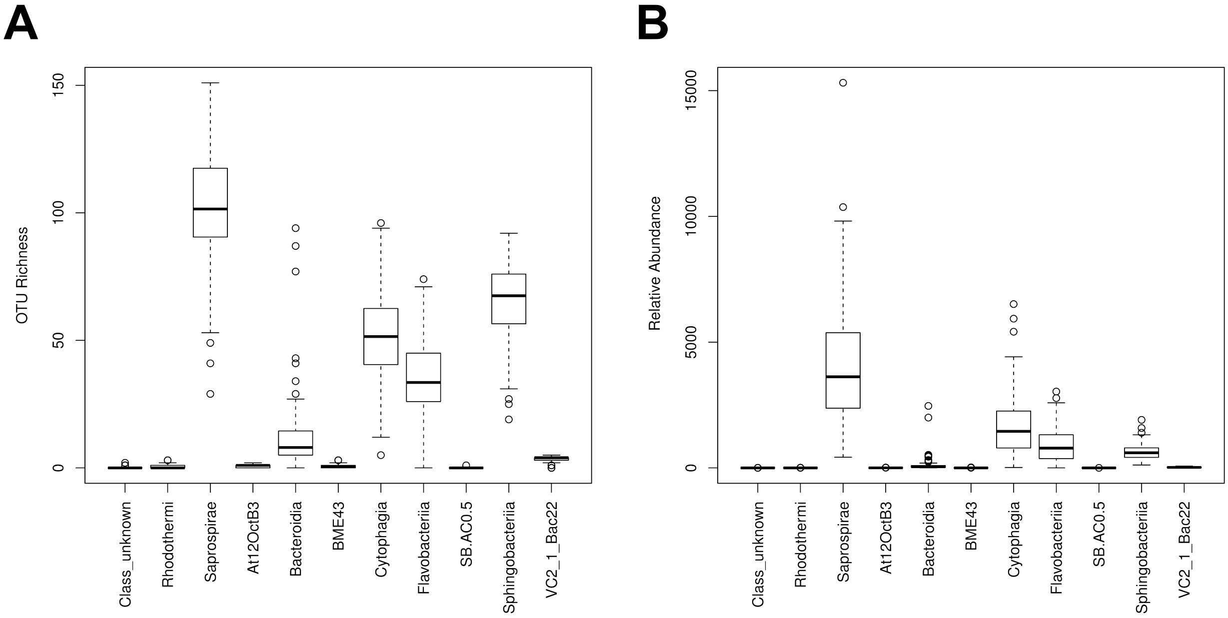
Supplementary Figure 13. Distribution of Verrucomicrobial class richness and abundance across ordination space, respectively of the (A-B) Methylacidophiliae, (C-D) Pedosphaerae, (E-F) Spartobacteria, (G-H) Opitutae, (I-J) Verruco 5, and (K-L) Verrucomicrobiae. The bubble size depicts the relative richness or abundance of a Verrucomicrobial class at each sampling site, while the red contours show the smooth response surface of the respective richness or relative abundance. Only the most relevant environmental variables are shown as envfit vectors.



Supplementary Figure 14. Abundance vs. occupancy plot for the alpine soil bacterial OTUs determined according to a similarity threshold of 97%.



Supplementary Figure 15. Correlation between the relative abundance of Acidobacteria and soil pH at the class and OTU levels. Global co-occurrence networks with nodes color-coded according to the different classes of Acidobacteria: Solibacteres (red), DA052 (pink), Acidobacteriia (green), Acidobacteria-6 (blue), Chloracidobacteria (cyan), and other bacteria (gray). Positive correlations are red edges and negative correlations are blue edges. (A) Yifan Hu Multilevel network of the less commonly found bacterial OTUs; (B) Force Atlas 2 network of the more commonly found bacterial OTUs from just the major cluster excluding the module with the spurious correlations; and (C) the relative abundance of the different acidobacterial classes as a function of pH.



Supplementary Figure 16. Proportion of Bacteroidetes classes across the alpine landscape. (A) The OTU richness and (B) the relative abundance in the respective sites.

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