Supplementary information

Climate change will lead to pronounced shifts in the diversity of soil microbial communities

Joshua Ladau [1, 2,†], Yu Shi [1,†], Xin Jing [3], Jin-Sheng He [3, 4], Litong Chen [4], Xiangui Lin [1], Noah Fierer [5,6], Jack A Gilbert [7, 8, 9] Katherine S Pollard [2, 10,*], Haiyan Chu [1,*]

[1] State Key Laboratory of Soil and Sustainable Agriculture, Institute of Soil Science, Chinese Academy of Sciences, 71 East Beijing Road, Nanjing 210008, China

[2] Gladstone Institutes, San Francisco, CA 94158, USA

[3] Department of Ecology, College of Urban and Environmental Sciences and Key Laboratory for Earth Surface Processes of the Ministry of Education, Peking University, 5 Yiheyuan Road, Beijing 100871, China

[4] Key Laboratory of Adaptation and Evolution of Plateau Biota, Northwest Institute of Plateau Biology, Chinese Academy of Sciences, 23 Xinning Road, Xining 810008, China

[5] Department of Ecology and Evolutionary Biology, University of Colorado, Boulder, CO 80309, USA

[6] Cooperative Institute for Research in Environmental Sciences, University of Colorado, Boulder, CO 80309, USA

[7] Biosciences Division, The Microbiome Center, Argonne National Laboratory, Argonne, Illinois, USA

[8] Department of Surgery, University of Chicago, Chicago, Illinois, USA

[9] Marine Biological Laboratory, 7 MBL Street, Woods Hole, MA 02543, USA

[10] Division of Biostatistics and Institute for Human Genetics, University of California, San Francisco, CA, USA *Corresponding authors:

H. Chu, Tel.: 86-25-86881356; E-mail: hychu@issas.ac.cn

K.S. Pollard, Tel.: 415-734-2000; E-mail: kpollard@gladstone.ucsf.edu

† These two authors contributed equally to this work

Supplementary Figures

Figure S1. Relative abundance of the dominant bacterial phyla across samples from Tibetan Plateauan Plateau. Relative abundances are based on the proportional frequencies of 16S rDNA sequences that could be classified at the phylum level.
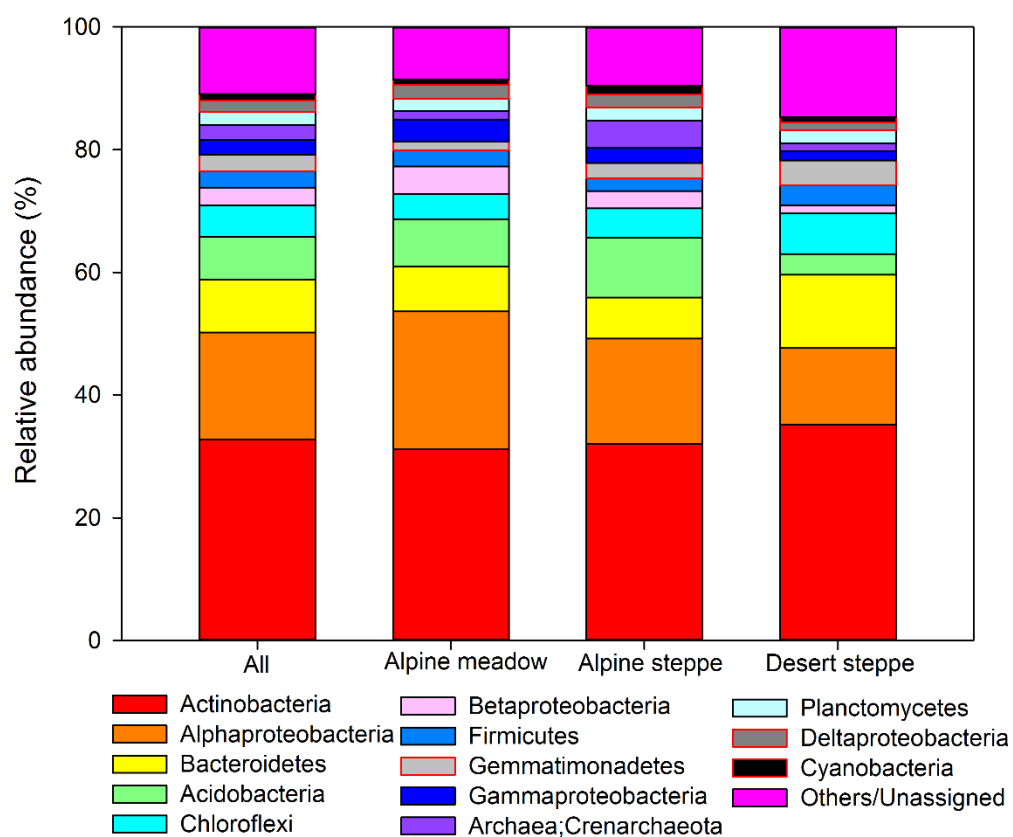
Figure S2. Importance of climate variables for predicting the distributions of bacterial families across Tibetan Plateau as a function of year. When they were chosen in model selection, historic climate variables tended to be as important at predicting contemporary soil microbial distributions as contemporary climate variables.
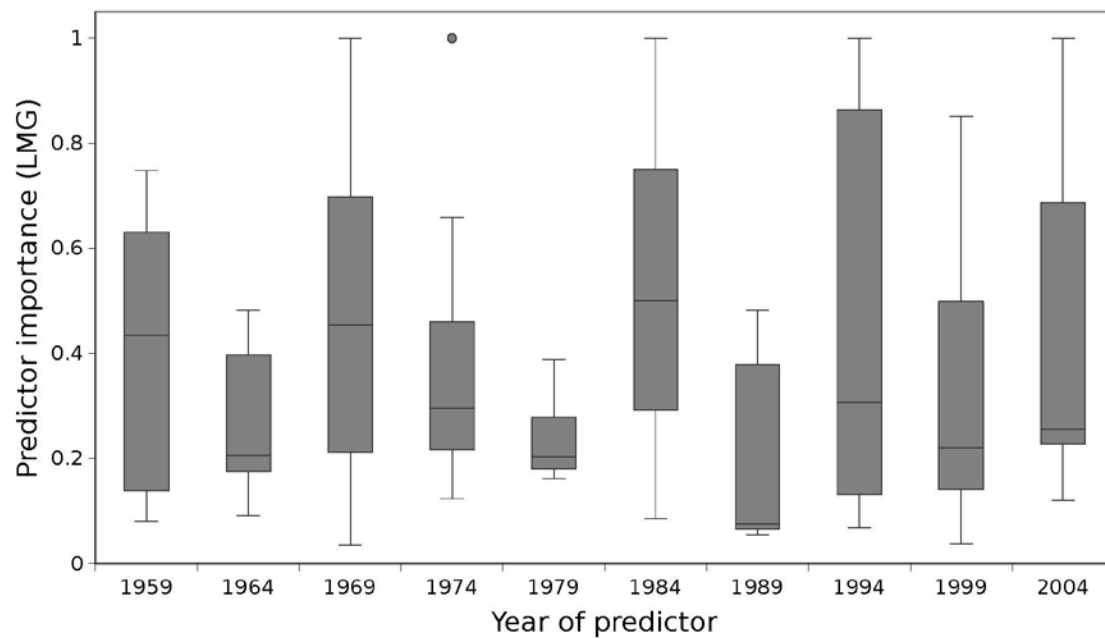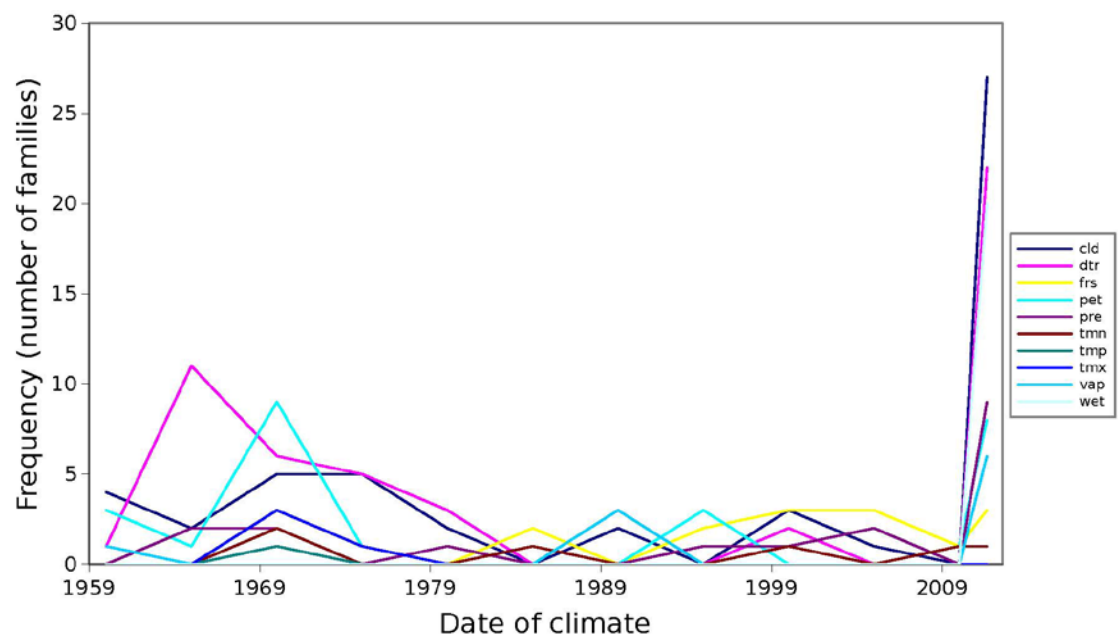
Figure S3. Same as Figure S2, but for OTUs rather than families across Tibetan Plateau.
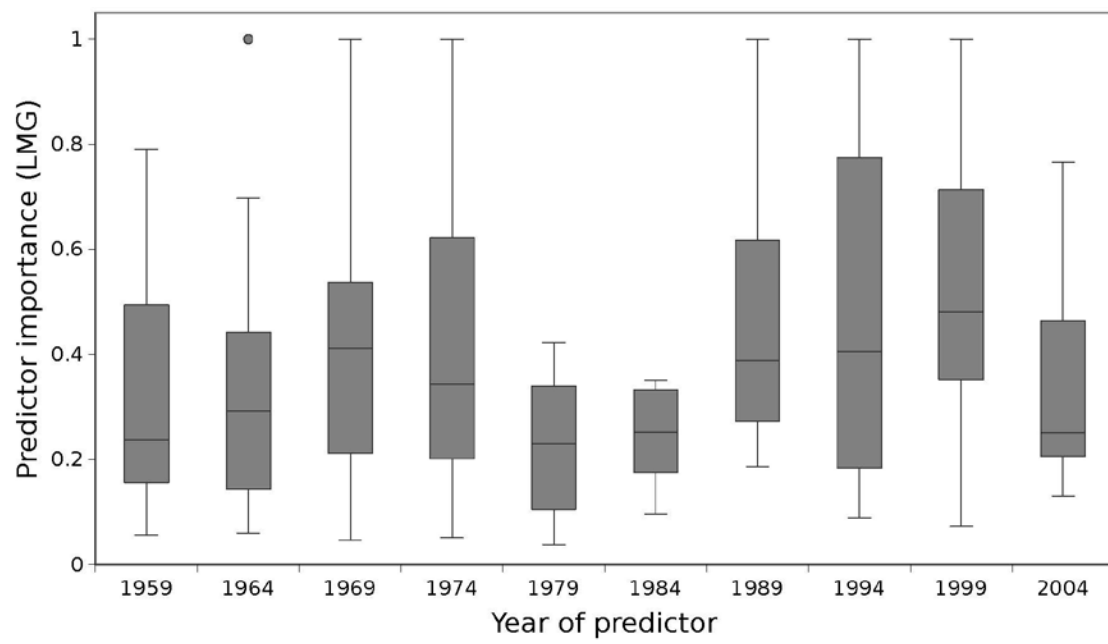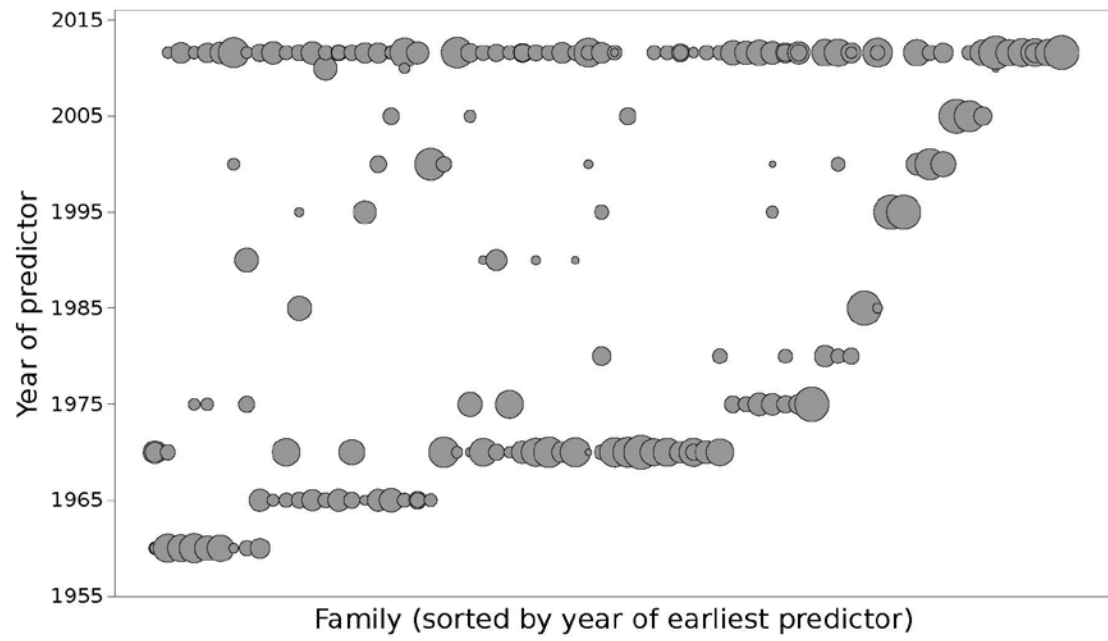
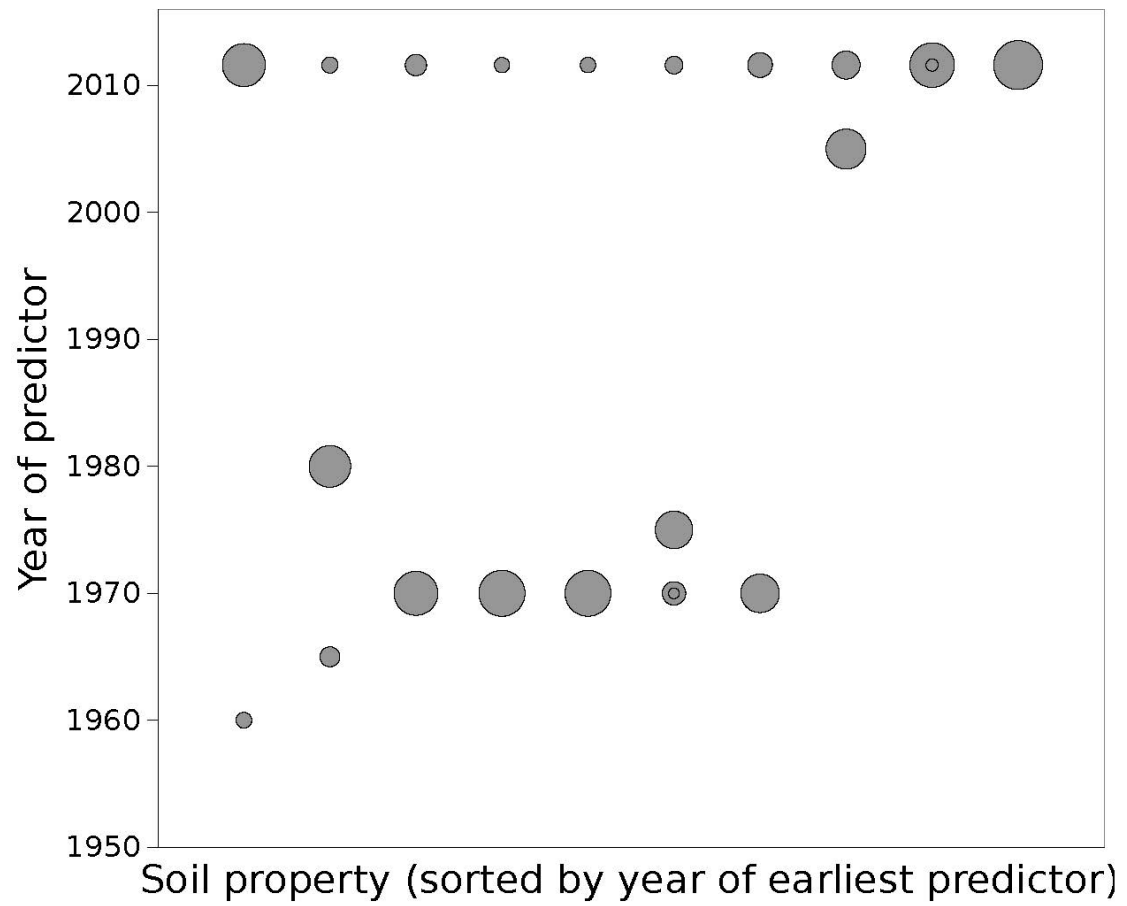**Figure S4.** Same as Figure 1A, but for families across Tibetan Plateau.
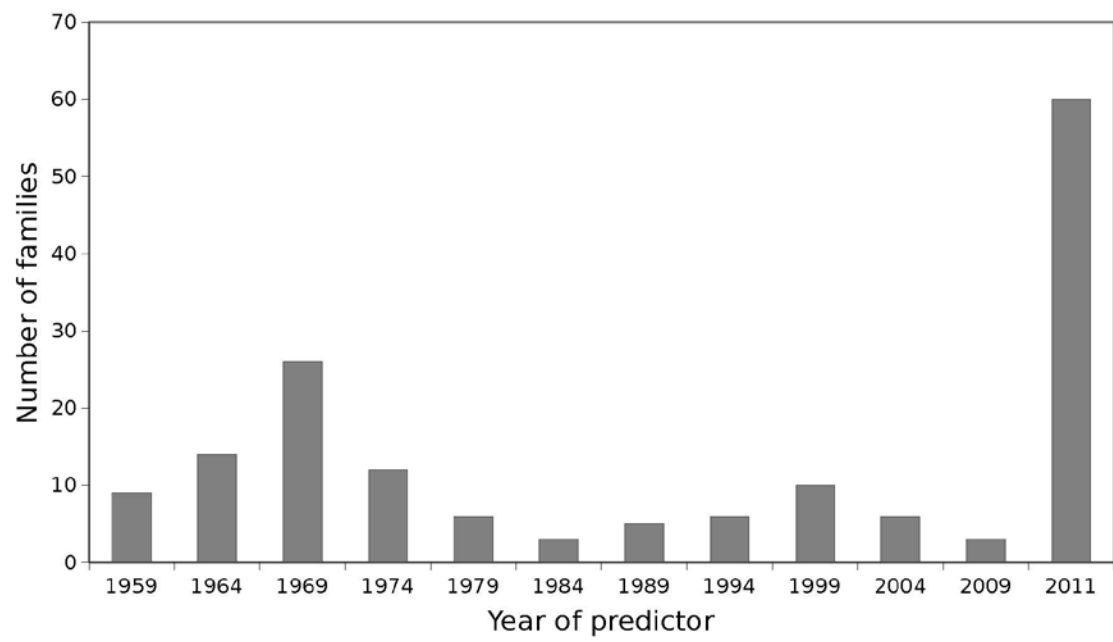
Figure S5. Same as Figure 1B, but for families across Tibetan Plateau.

**Figure S6.** Same as Figure 1C, but for families across Tibetan Plateau.

Figure S7. Same as Figure 1C, but for soil properties across Tibetan Plateau.

Figure S8. Distributions of projected shifts in richness within samples as compared tocurrent and future intersample differences in richness across Tibetan Plateau. Projected intrasample changes in richness are of similar magnitude to existing and projected future intersample differences in richness.
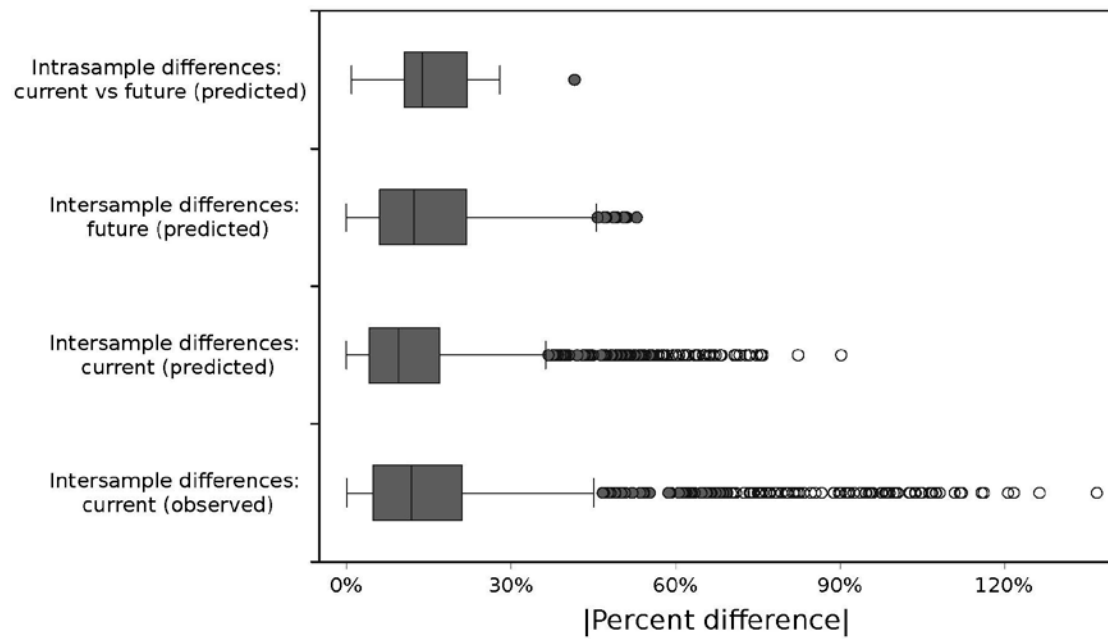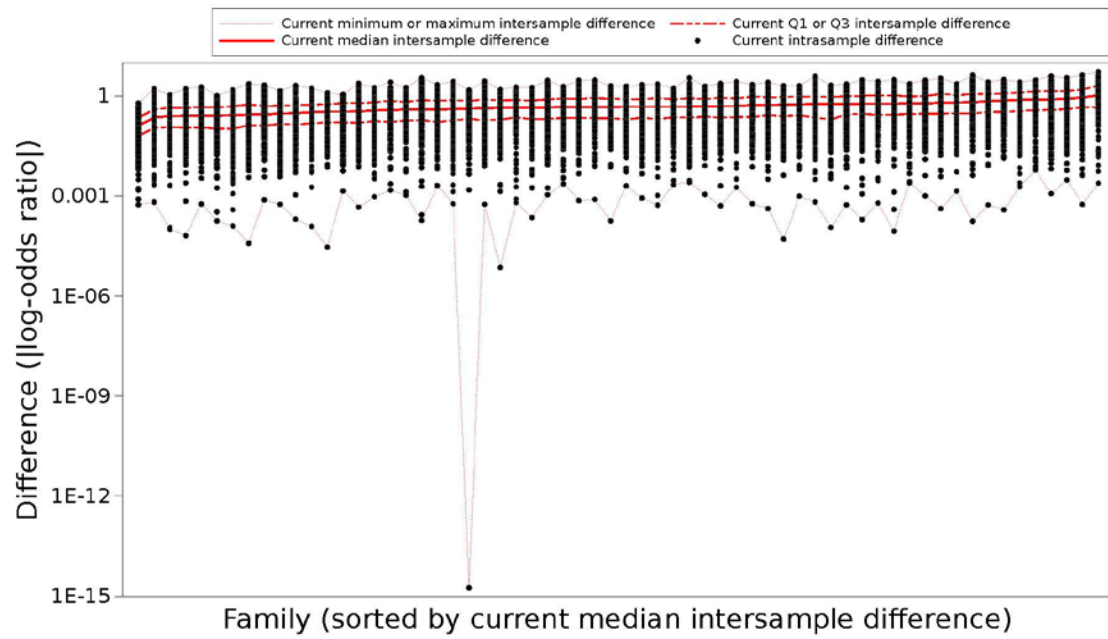
Figure S9. Same as Figure S8, but for Shannon Diversity across Tibetan Plateau.
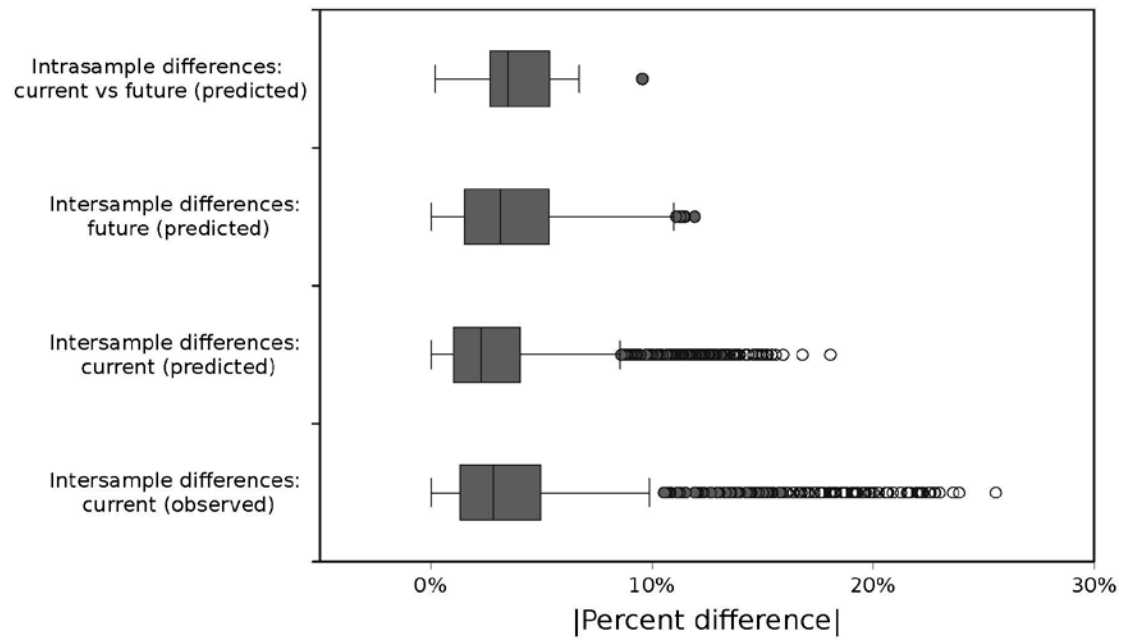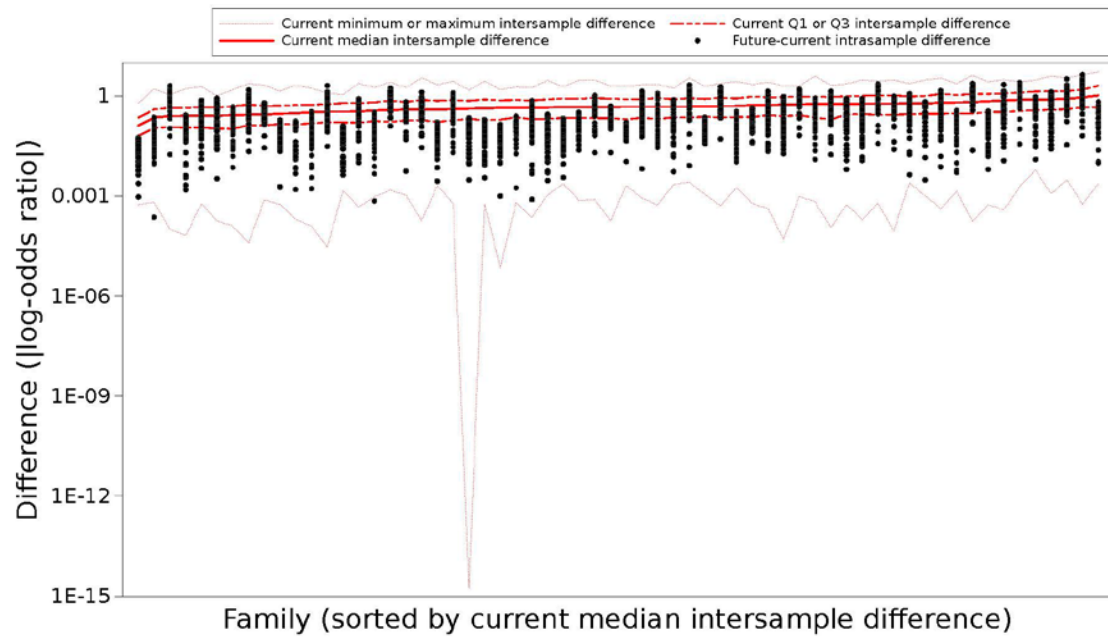
Figure S10. Same as Figure 2B, but for Shannon Diversity across Tibetan Plateau.
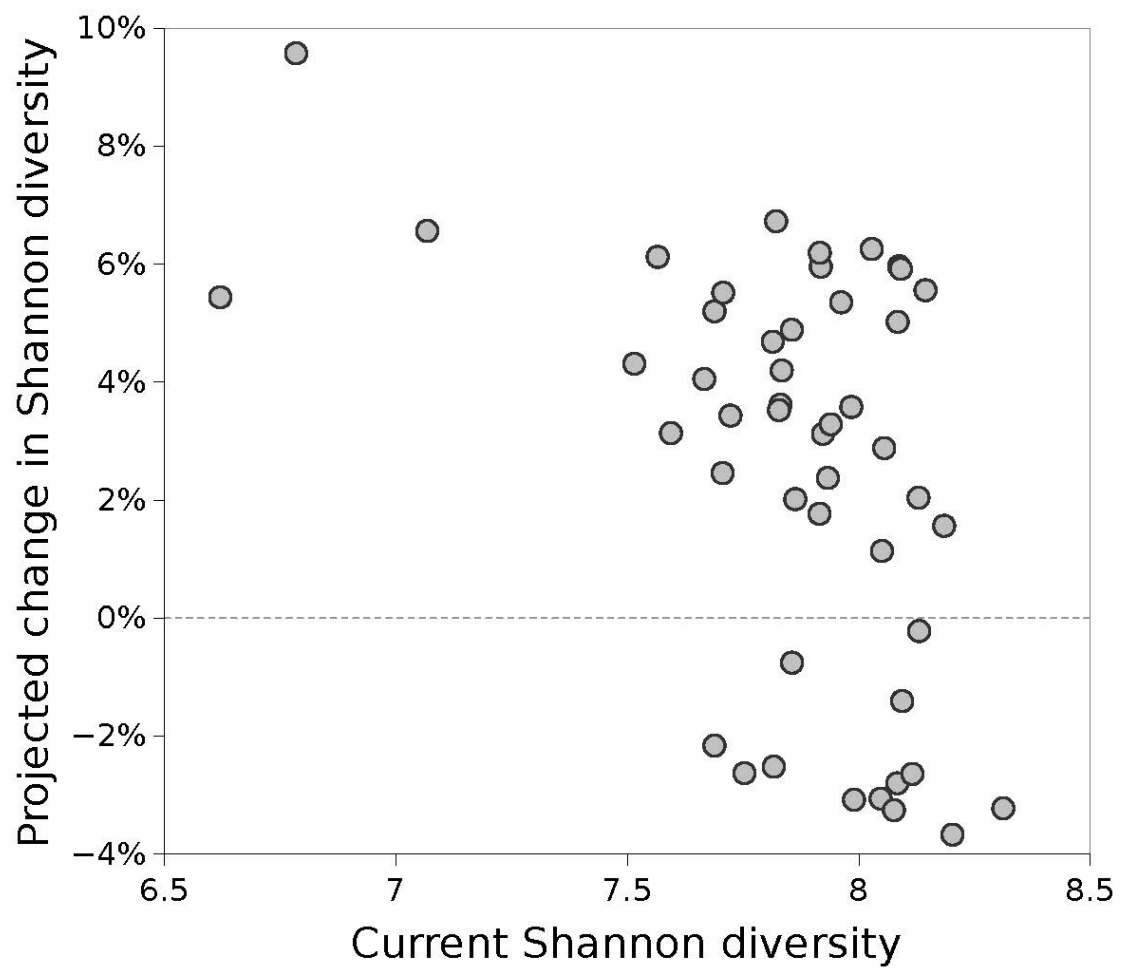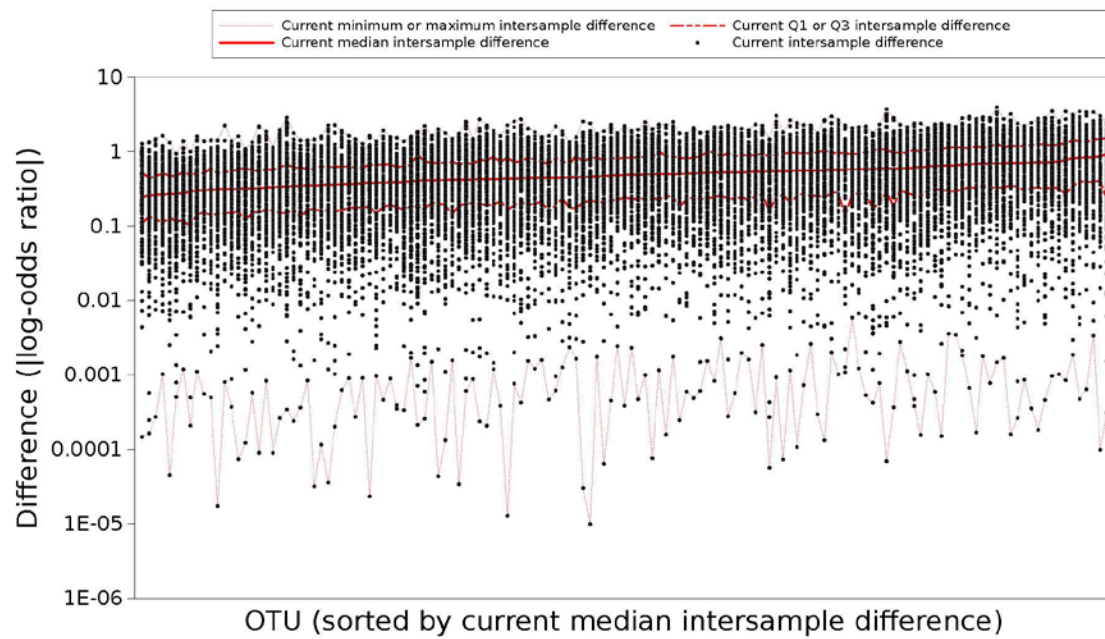
Figure S11. Analogous to Figure 2C, but showing the distribution of current intersample differences in relative abundances of families across Tibetan Plateau.

Figure S12. Analogous to Figure 2C, but showing the distribution of projected future intersample differences of relative abundances of families across Tibetan Plateau.

Figure S13. Analogous to Figure 2C, but showing the distribution of current intersample differences in relative abundances of OTUs across Tibetan Plateau.

Figure S14. Shifts in the relative abundance of families across Tibetan Plateau as a function of their current relative abundance. Shifts are represented by different colors, with increases and decreases represented by red and blue, respectively. Shifts are significantly inversely associated with current relative abundance, as evidenced by blue symbols being clustered in the upper part of the graph.

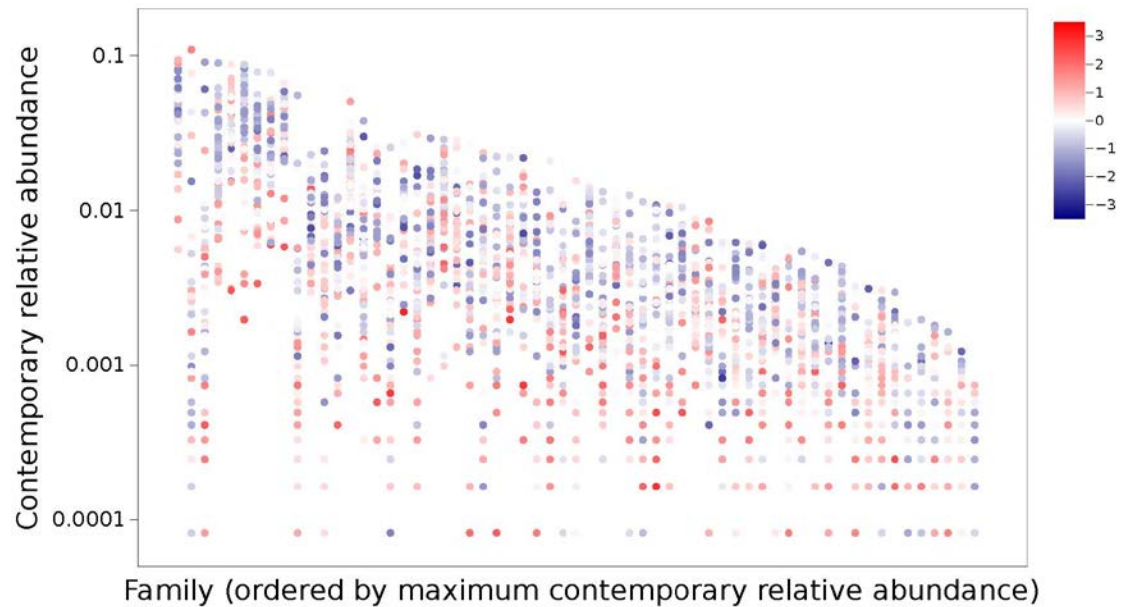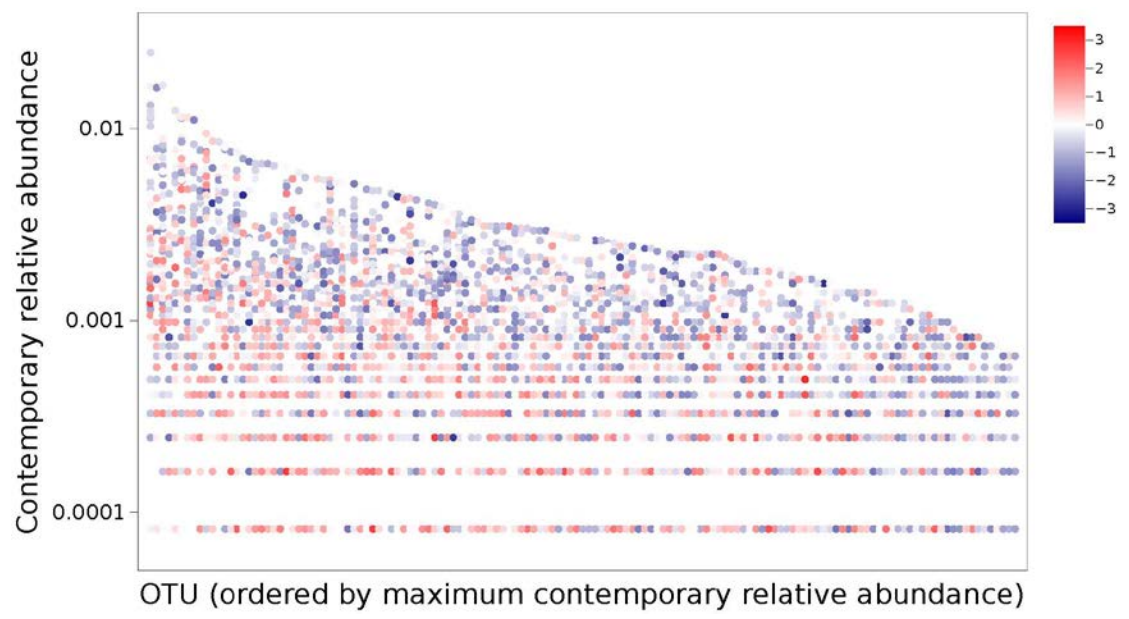**Figure S15.** Same as Figure S14, but for OTUs in Tibetan Plateau.

Figure S16. Analogous to Figure 2C, but showing the distribution of projected future intersample differences in relative abundances of families across Tibetan Plateau.
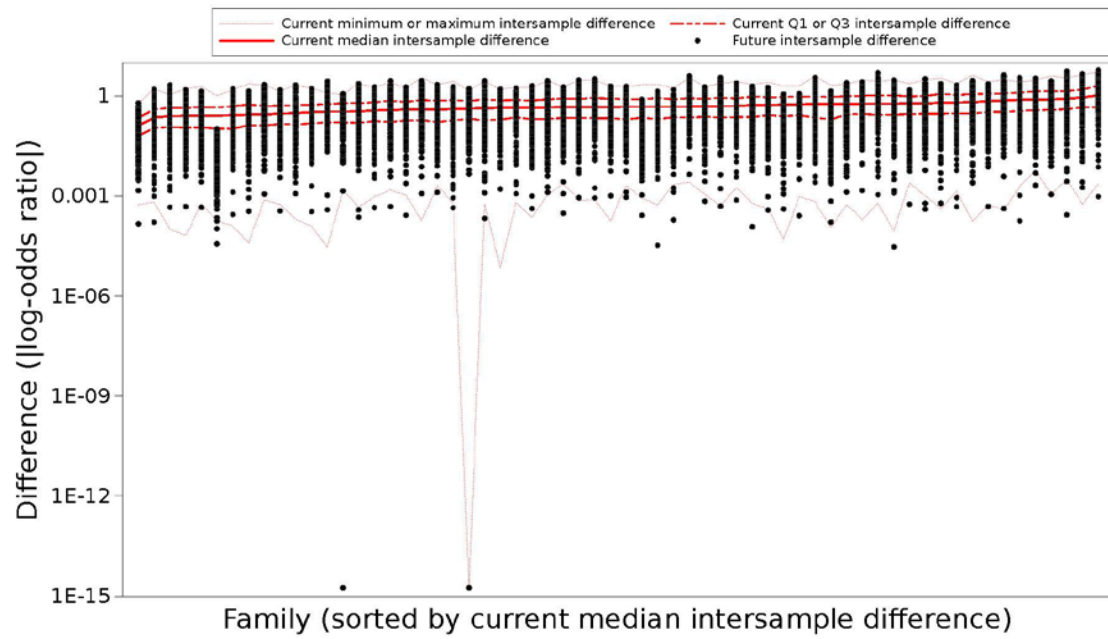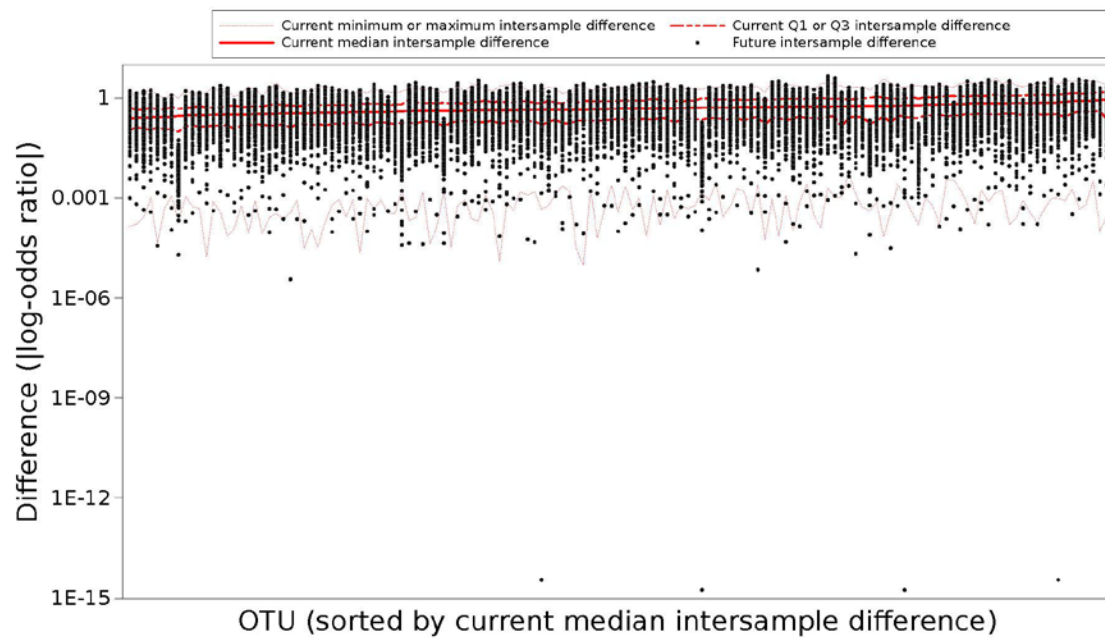
Figure S17. Analogous to Figure 2C, but showing the distribution of projected future intersample differences in relative abundances of OTUs across Tibetan Plateau.

Figure S18. Locations of sampling sites across North America.
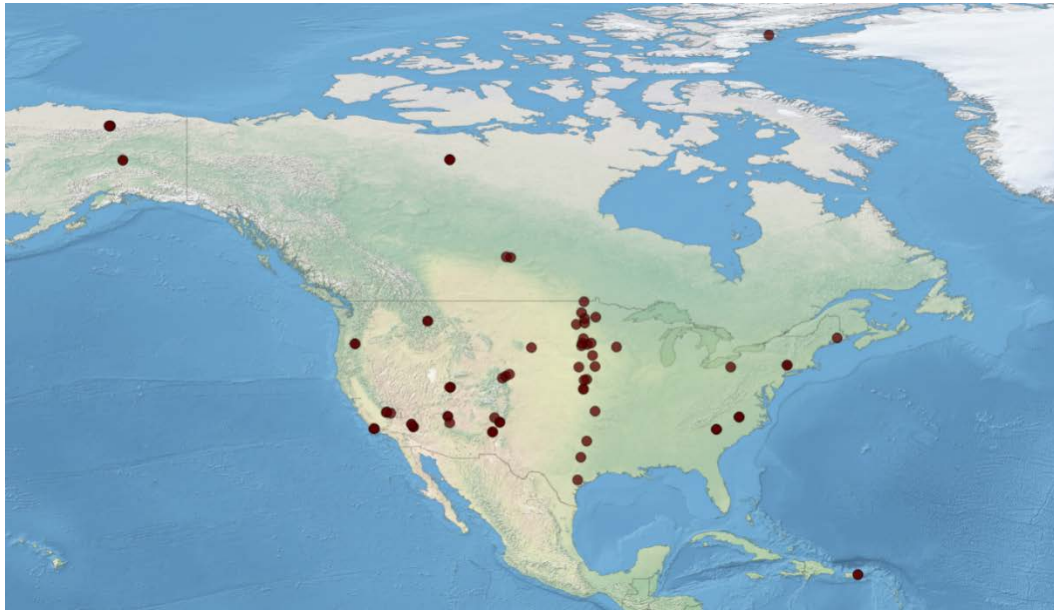
Figure S19. Analogous to Figure 4A, but for families of bacteria across northern North America.

Figure S20. Analogous to Figure 4B, but for families of bacteria across northern North America.

Figure S21. Analogous to Figure S2, but for families across northern North America.

Figure S22. Analogous to Figure S2, but for OTUs across northern North America.

Figure S23. Analogous to Figure 1B, but for families in northern North America.

Figure S24. Analogous to Figure 1B, but for OTUs in northern North America.

Figure S25. Analogous to Figure 2A, but for richness across northern North America.

Figure S26. Analogous to Figure S8, but for richness across northern North America.

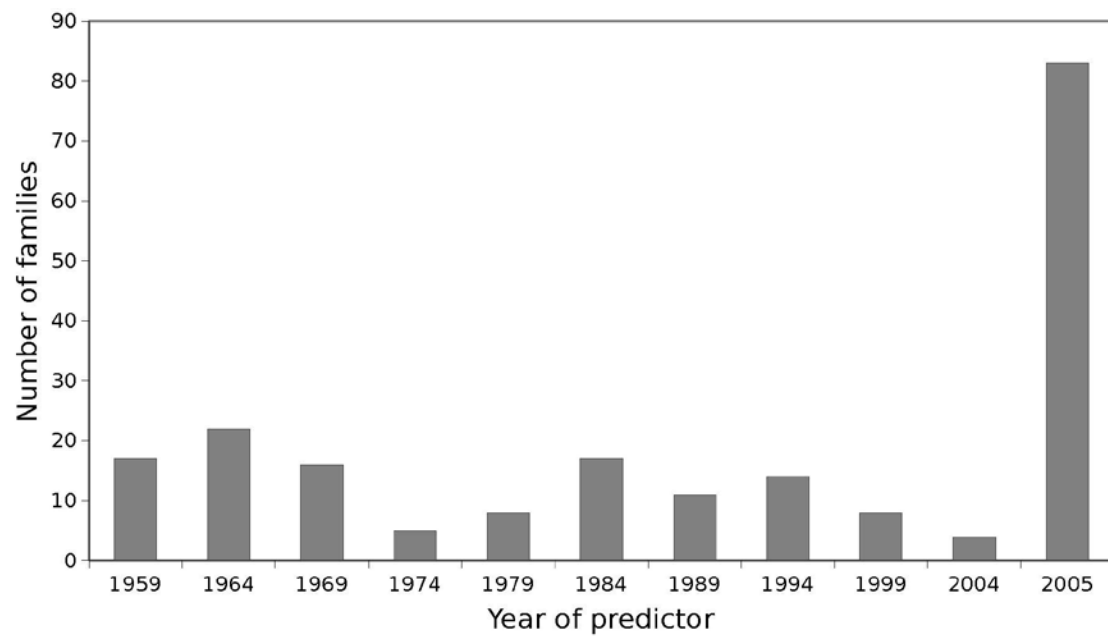**Figure S27.** Analogous to Figure S8, but for Shannon Diversity across northern North America.

Figure S28. Analogous to Figure 2C, but showing the distribution of current intersample differences in relative abundances of families across northern North America.
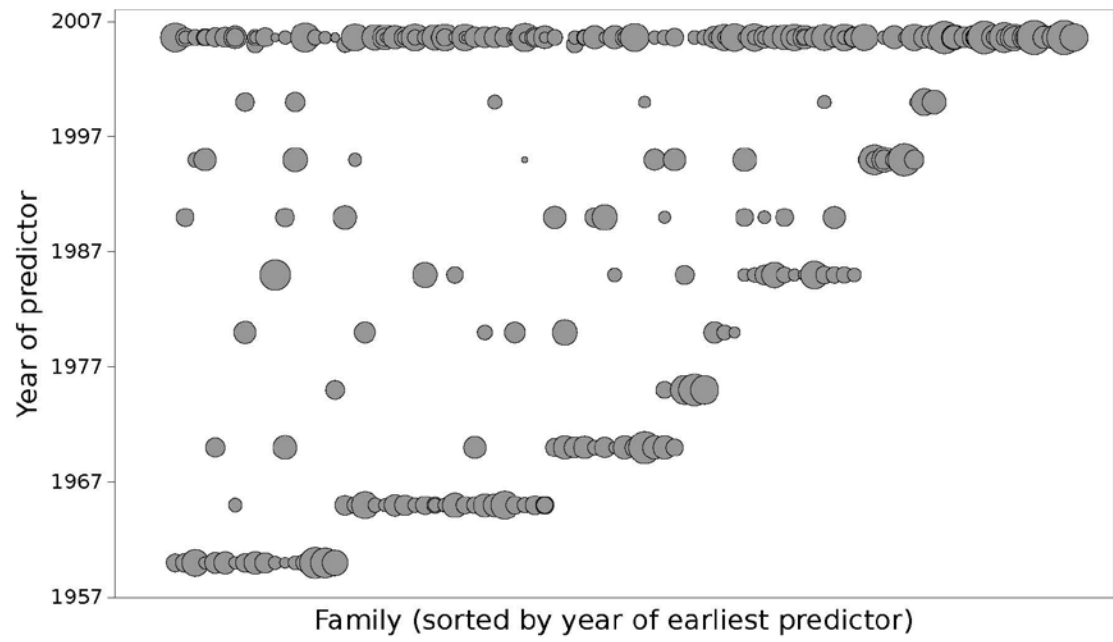
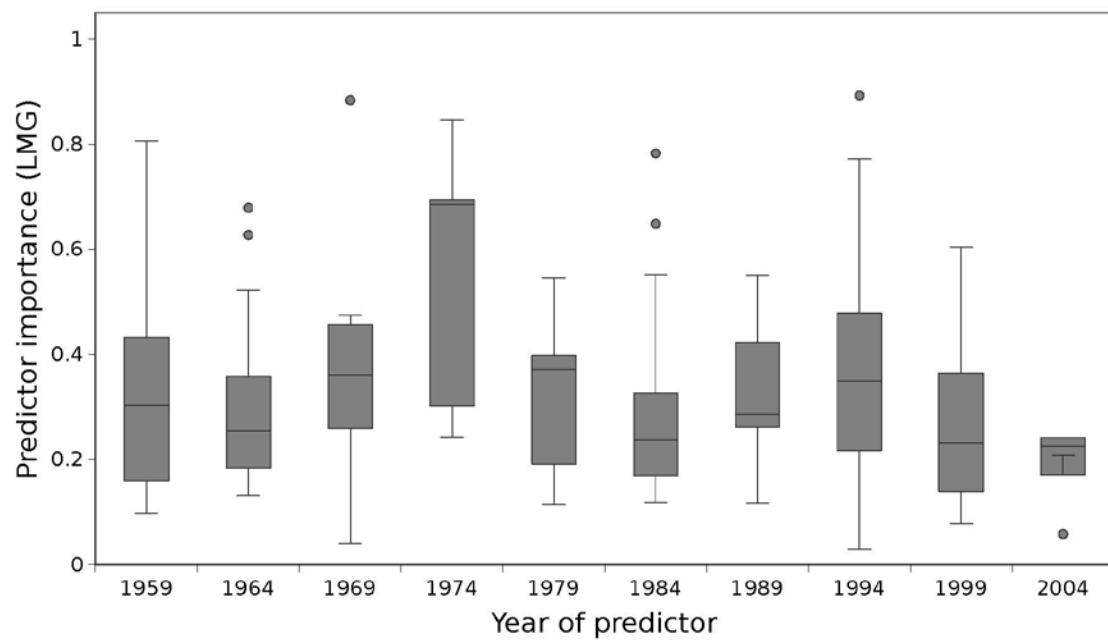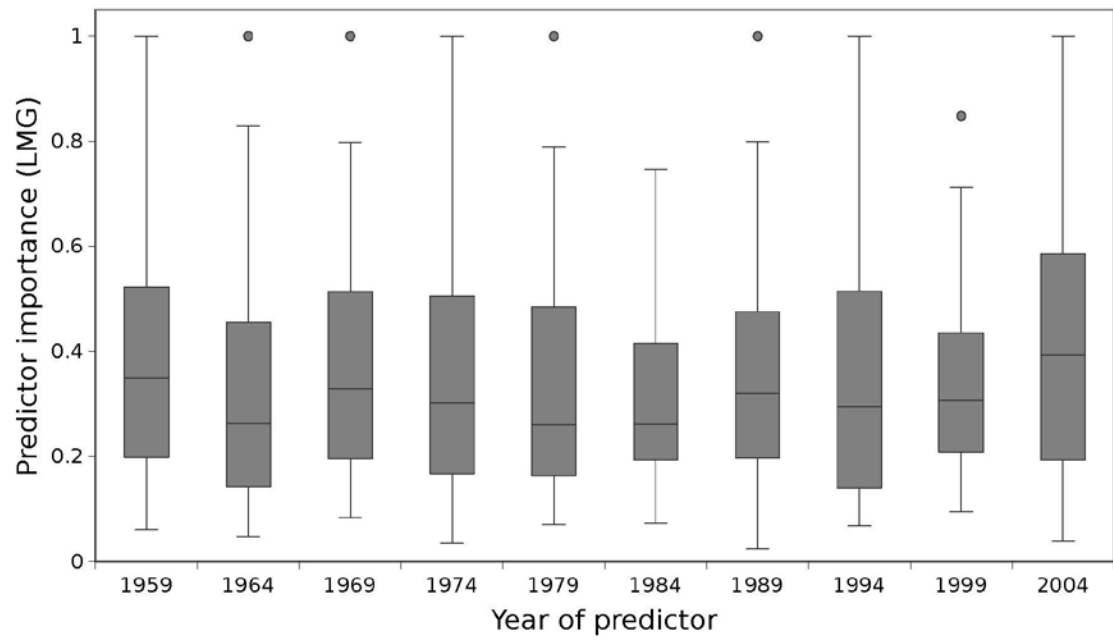**Figure S29.** Analogous to Figure 2C, but for families across northern North America.
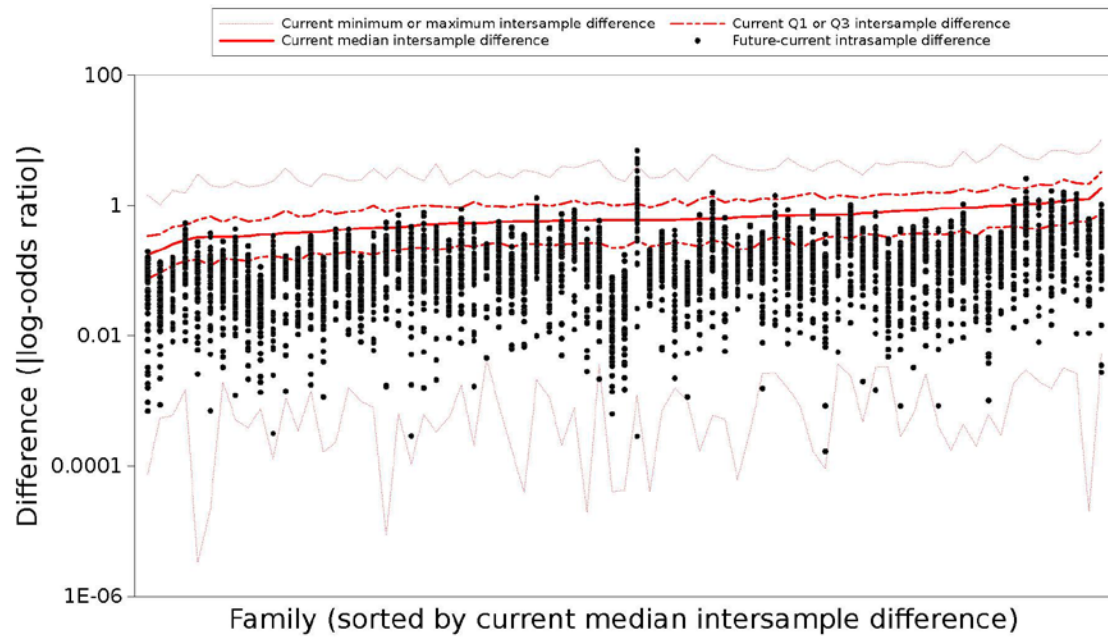
Figure S30. Analogous to Figure 2C, but showing the distribution of current intersample differences in relative abundances of OTUs across northern North America.
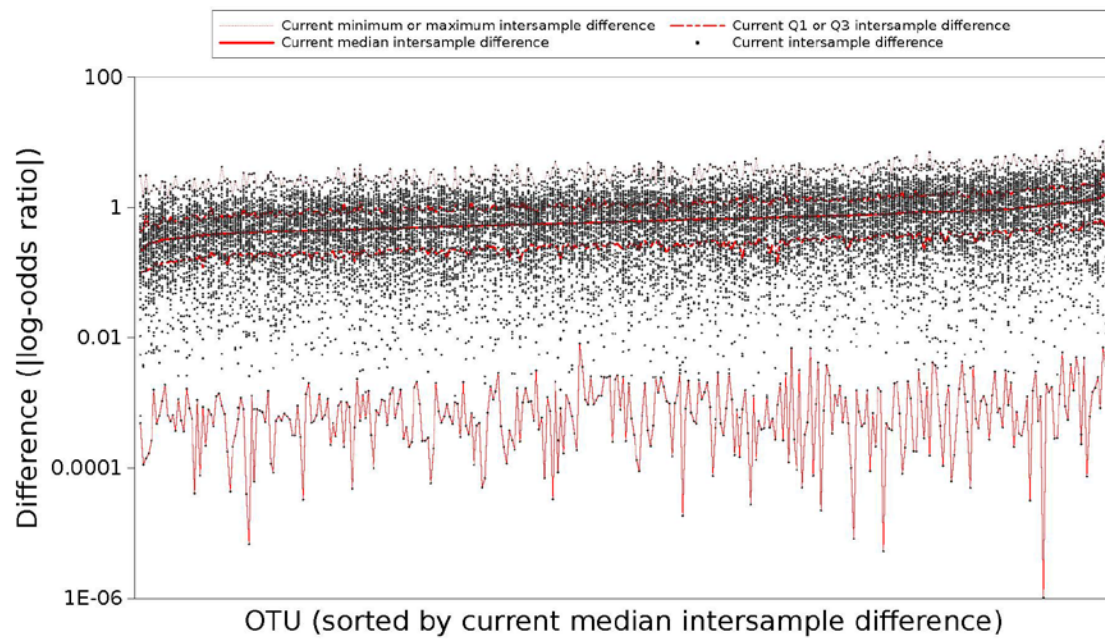
Figure S31. Analogous to Figure 2B, but for richness across northern North America.

Figure S32. Analogous to Figure 2B, but for Shannon Diversity across northern
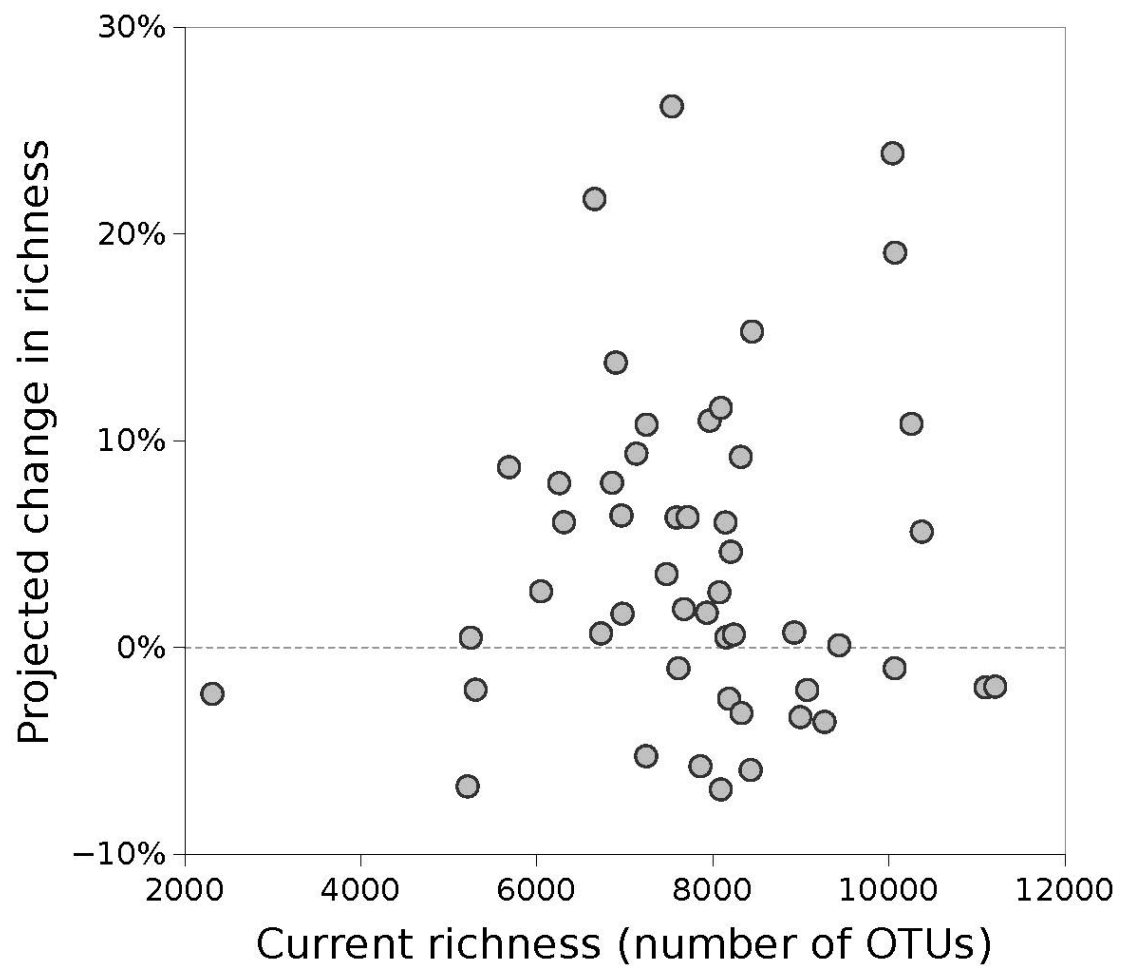
North America.

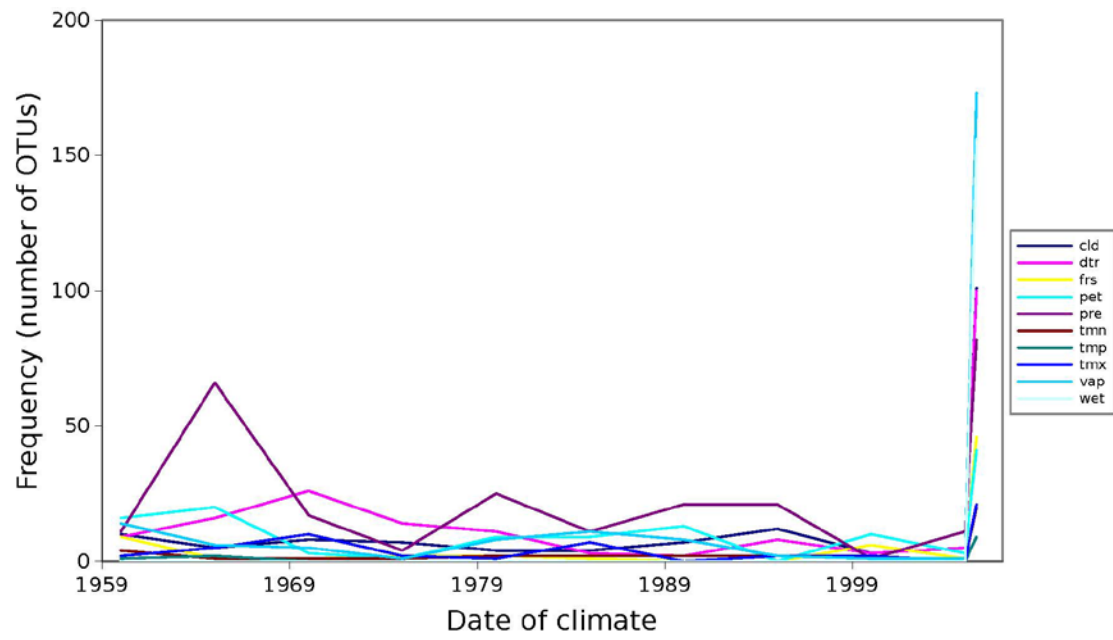**Figure S33.** Analogous to Figure S14, but for families across northern North America.
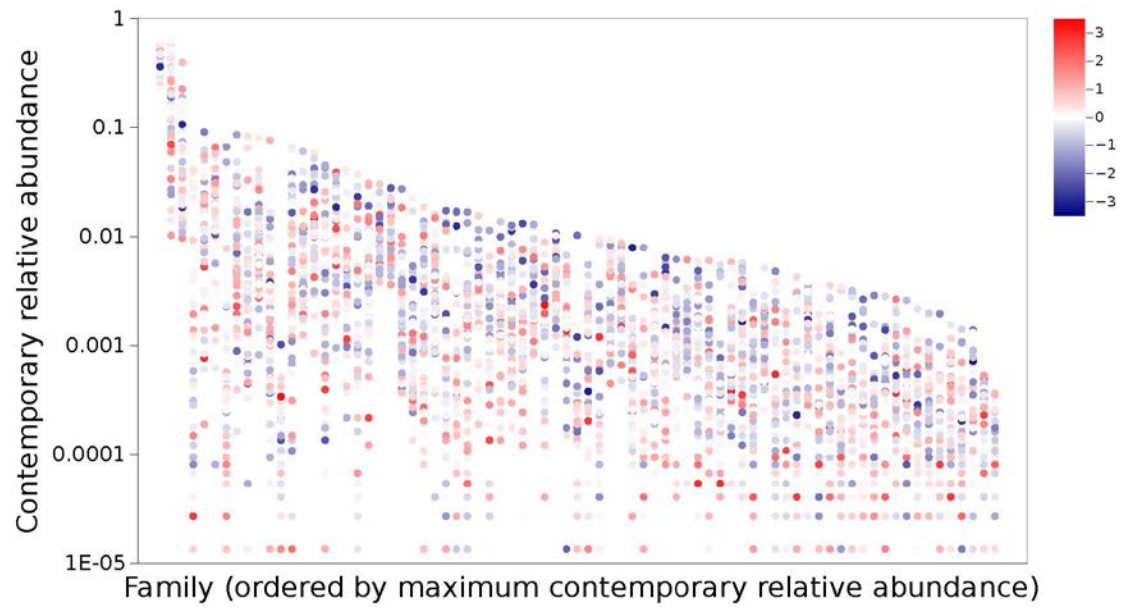
Figure S34. Analogous to Figure S14, but for OTUs across northern North America.
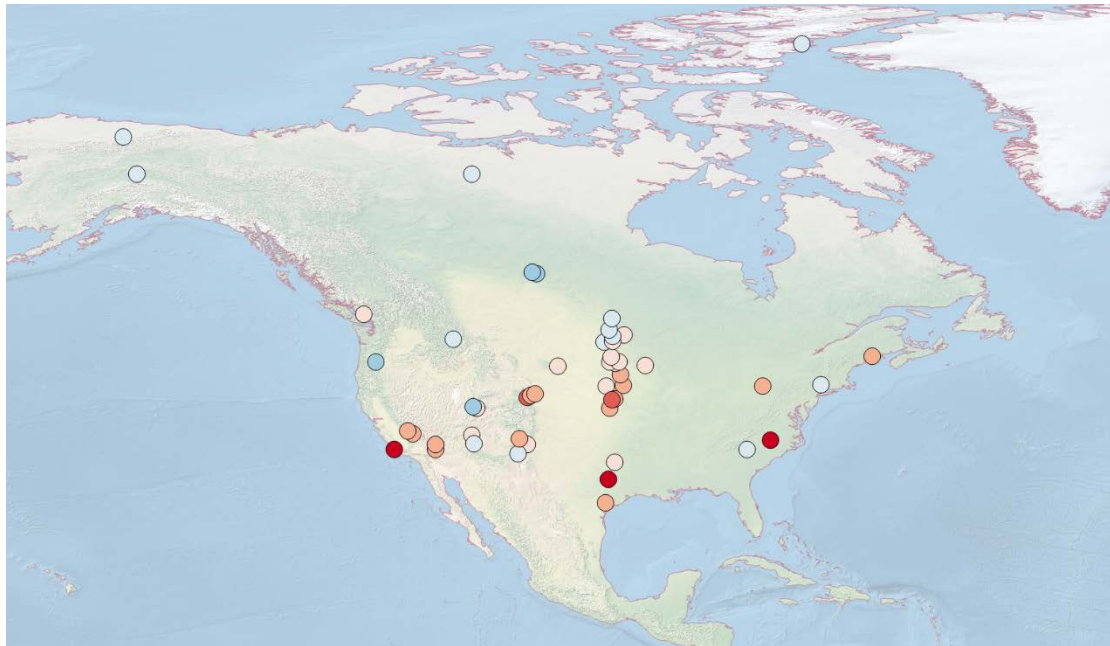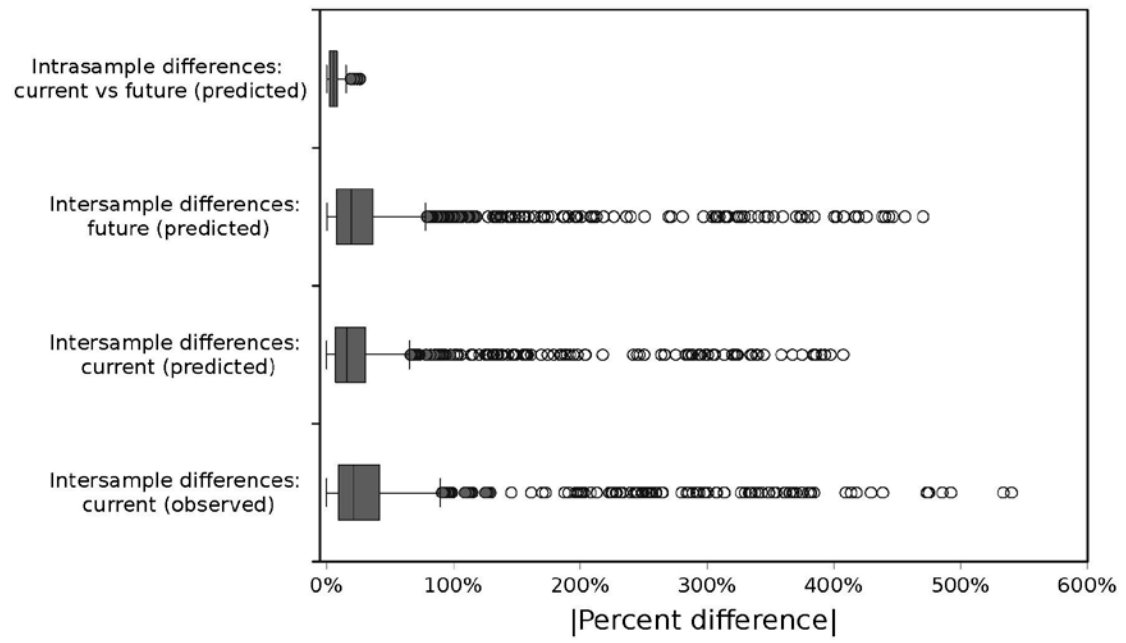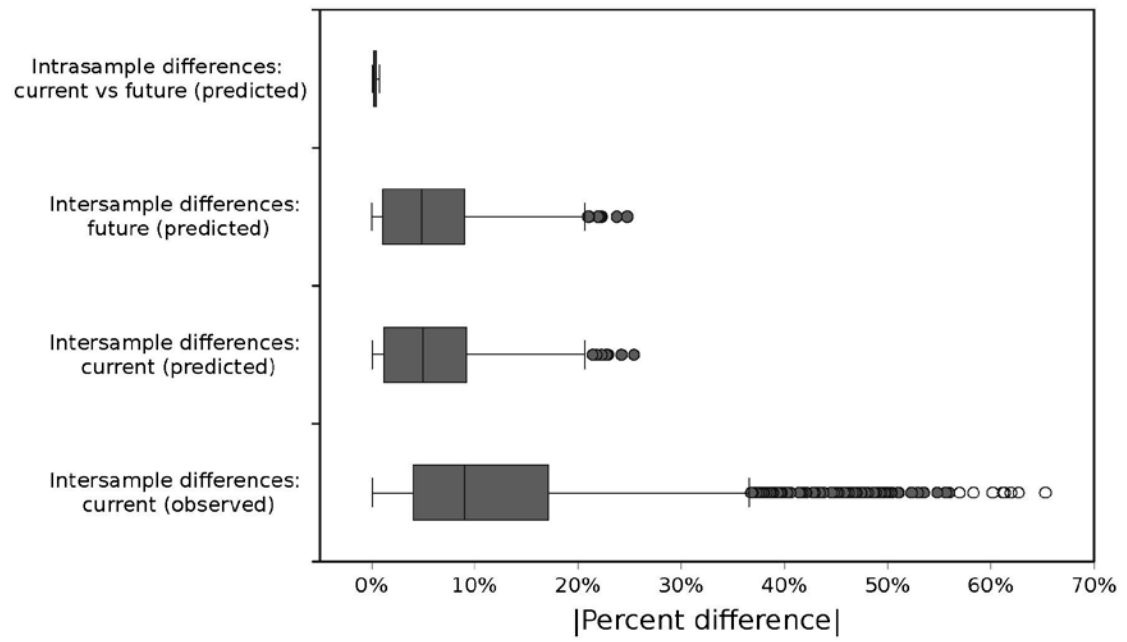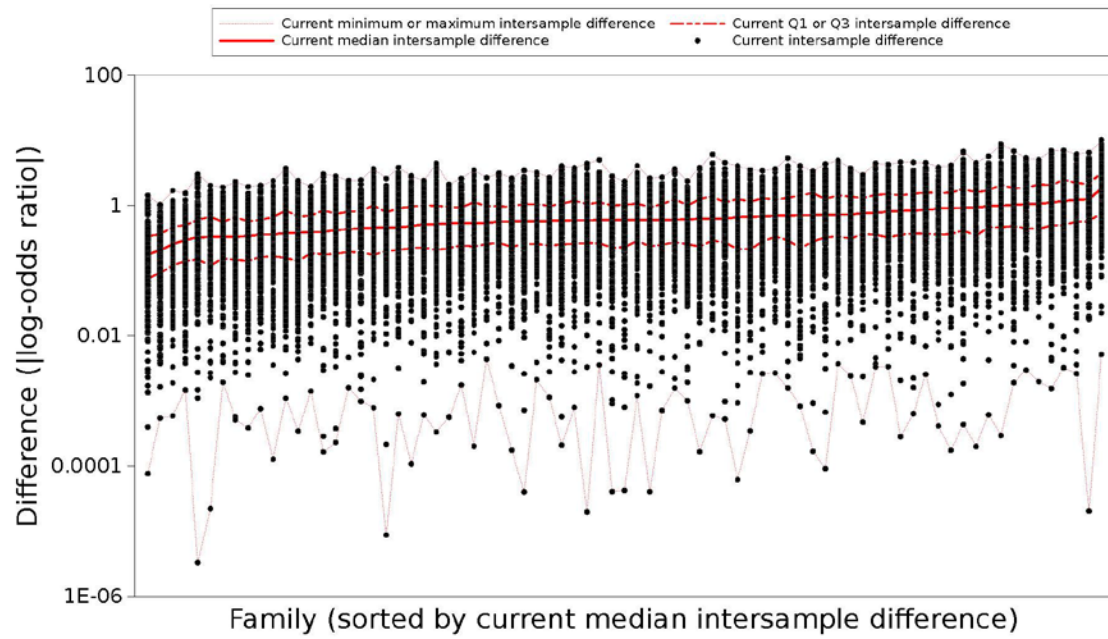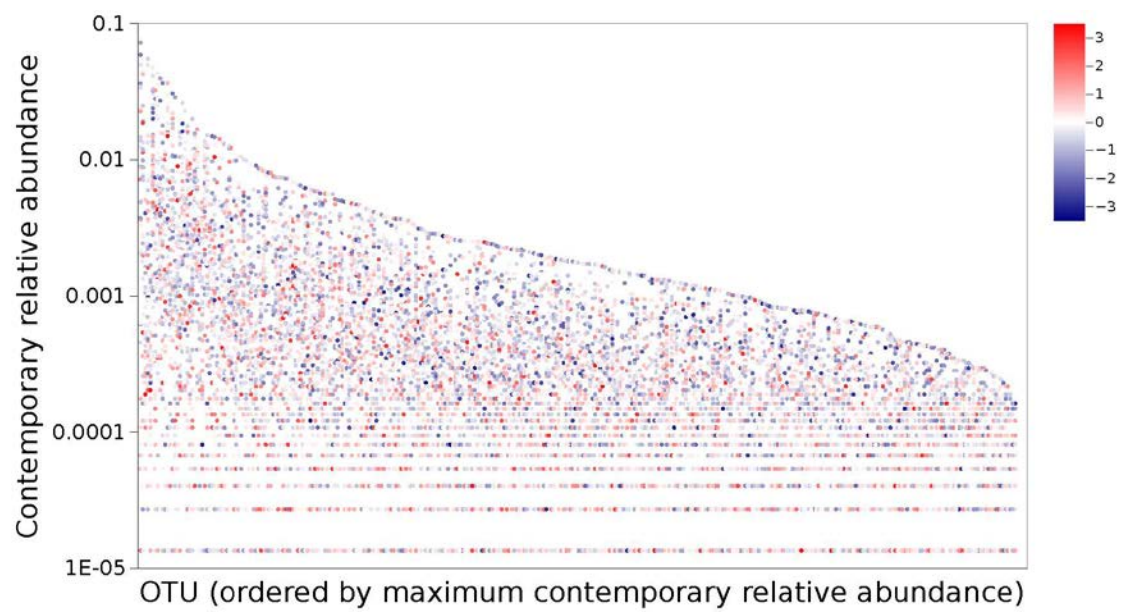
Figure S35. Analogous to Figure 2C, but showing the distribution of predicted future intersample differences in relative abundances of families across northern North America.
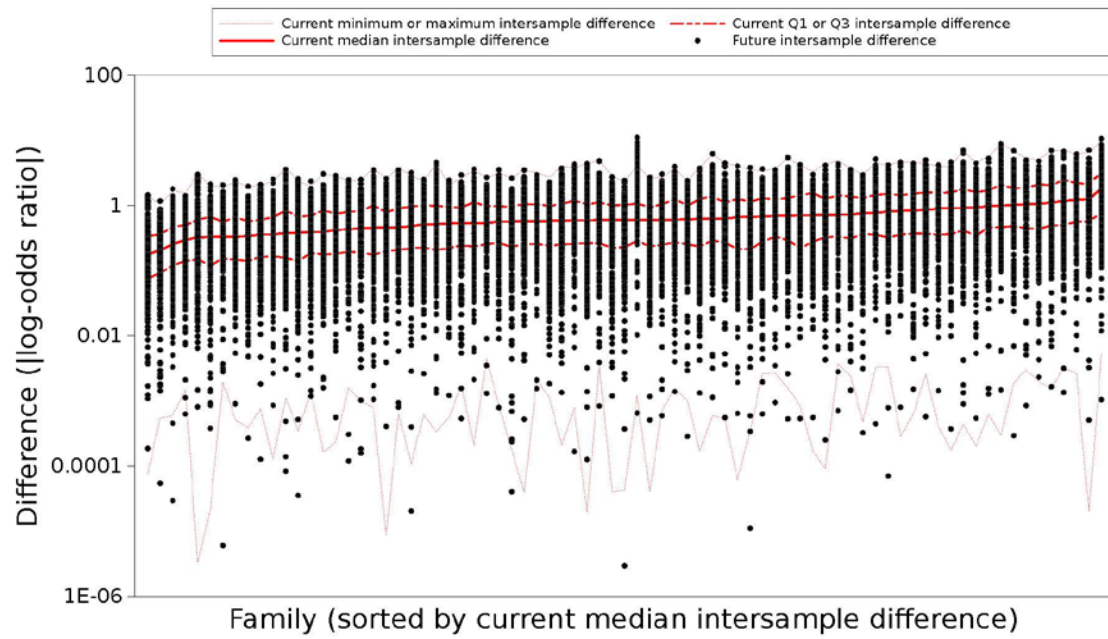
Figure S36. Analogous to Figure 2C, but showing the distribution of predicted

future intersample differences in relative abundances of OTUs across northern

North America.
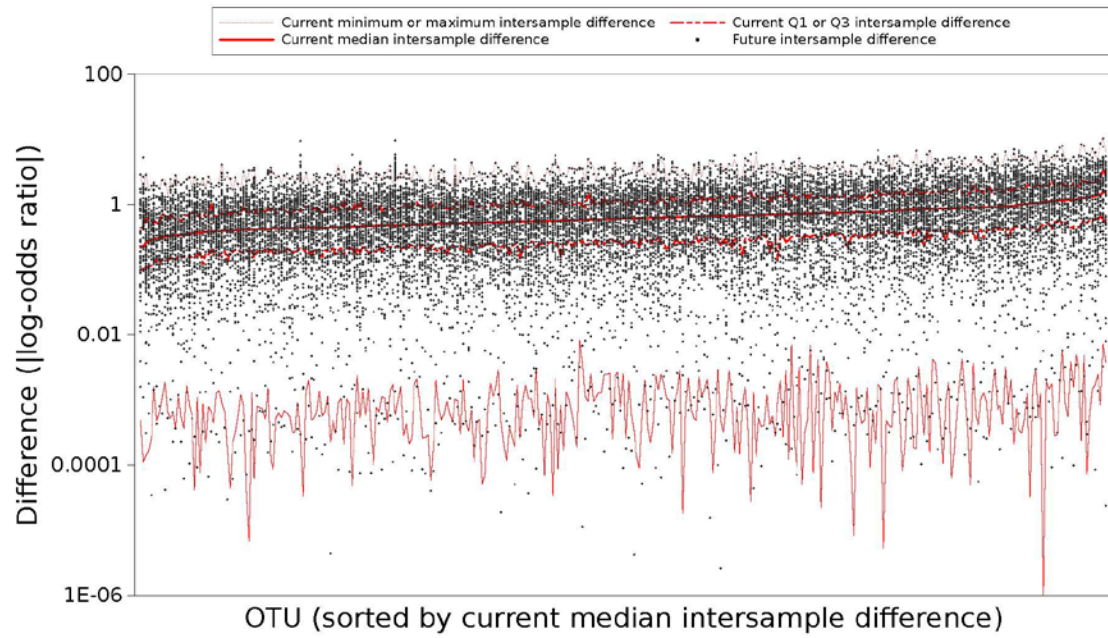
Figure S37. Bacterial community compositional structure in the Tibetan Plateauan Plateau soils as indicated by non-metric multidimensional scaling plots. Sites are color coded according to soil moisture content. A: Based on Bray-Curtis distance. B: Based on Unweighted Unifrac distance. C: Based on Weighted Unifrac distance.
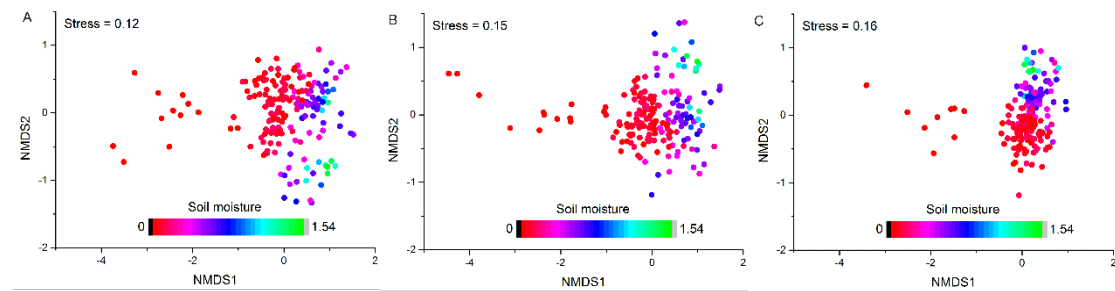
Figure S38. Relationship between relative abundance of dominant bacterial phyla and soil C:N ratio. Linear regressions were used to test Pearson correlation between the relative abundance of each taxon and soil C:N ratio.
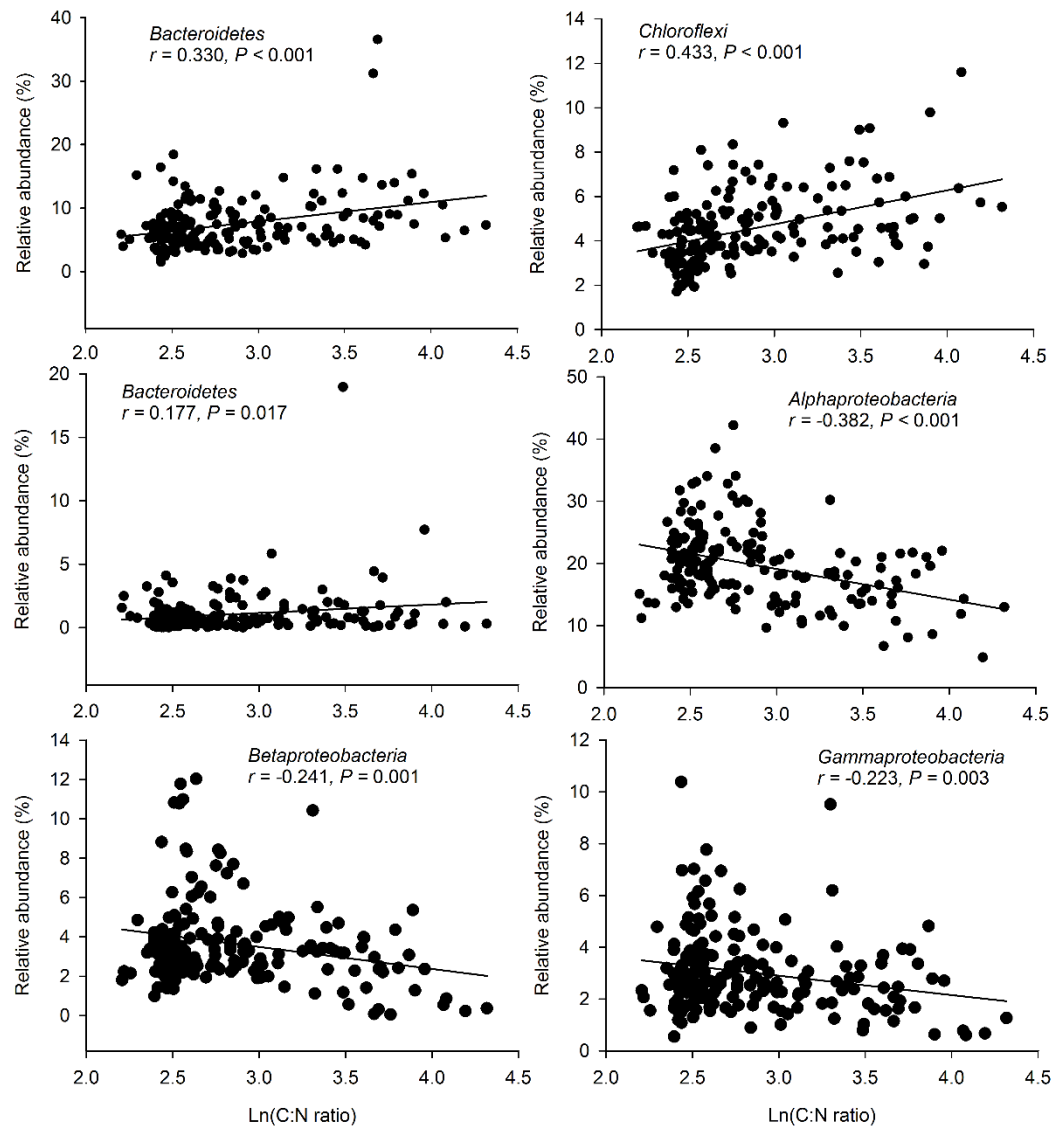
Figure S39. Relationship between relative abundance of dominant bacterial phyla and soil moisture (SM). Linear regressions were used to test Pearson correlation between each taxon's relative abundance and SM.
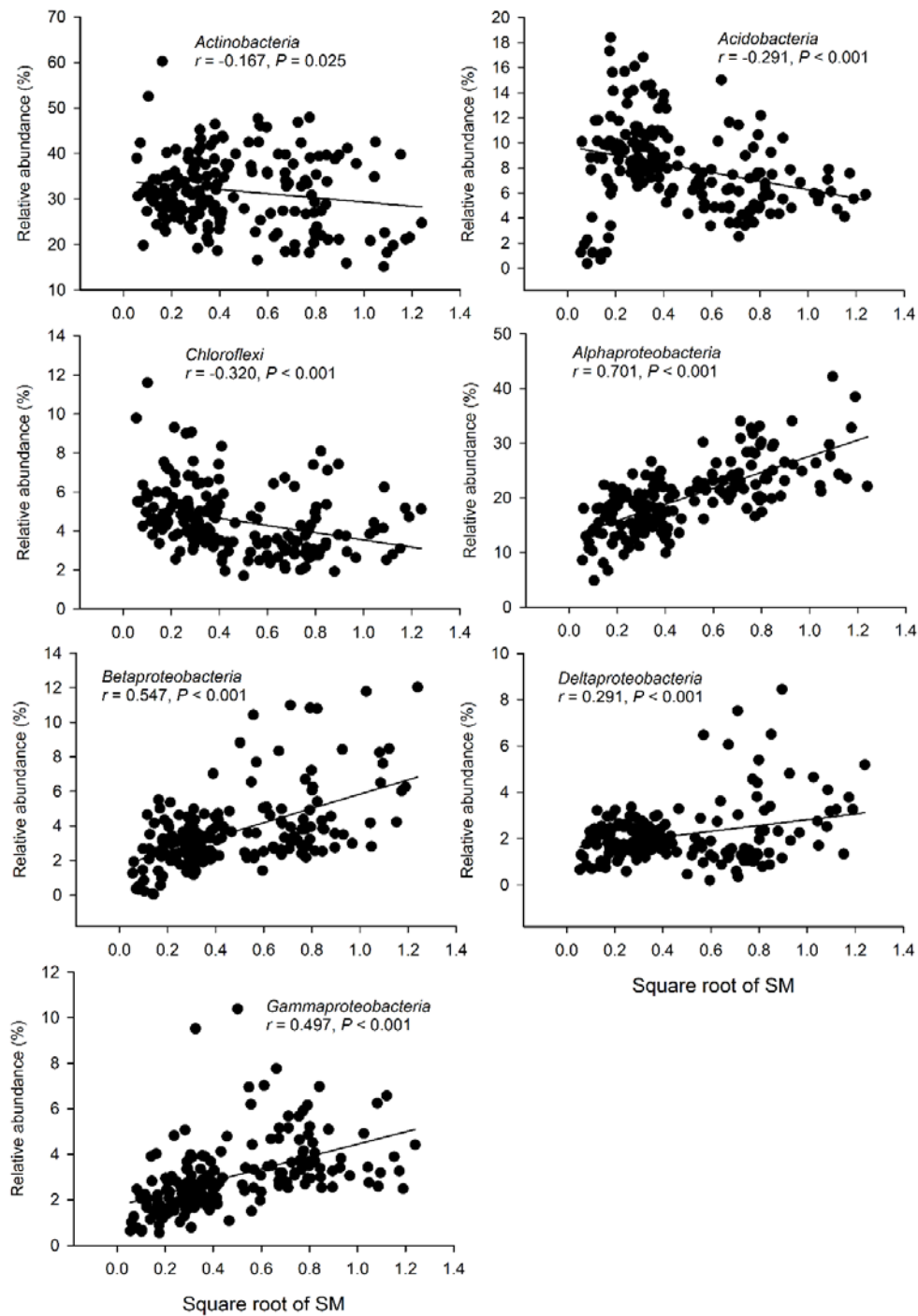
Figure S40. Like bacterial diversity and the relative abundance of many bacterial orders, in Tibetan Plateau key soil properties, including C:N, ratios are most closely associated with climate from approximately 50 years ago. Distributions of vegetation tend to be associated with current climate, however. Plots are the analogous to those in Figure 1. Because C:N ratios and other soil properties are strongly associated with bacterial community structure in Tibetan Plateau, we suggest that the disequilibrium between current bacterial distributions and climate in Tibetan Plateau is mediated by the soil properties: the soil properties respond slowly to changes in climate, and bacterial distributions change most directly in response to the soil properties.
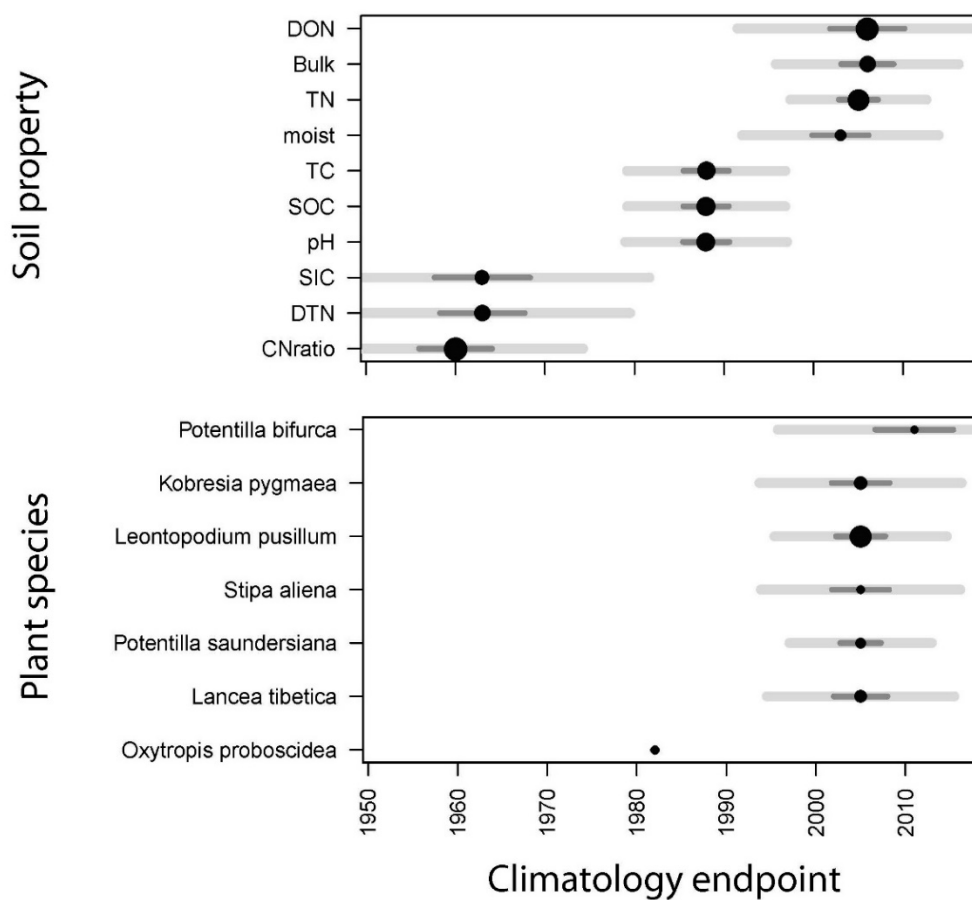
Figure S41. Locations of sampling sites across Tibetan Plateau.
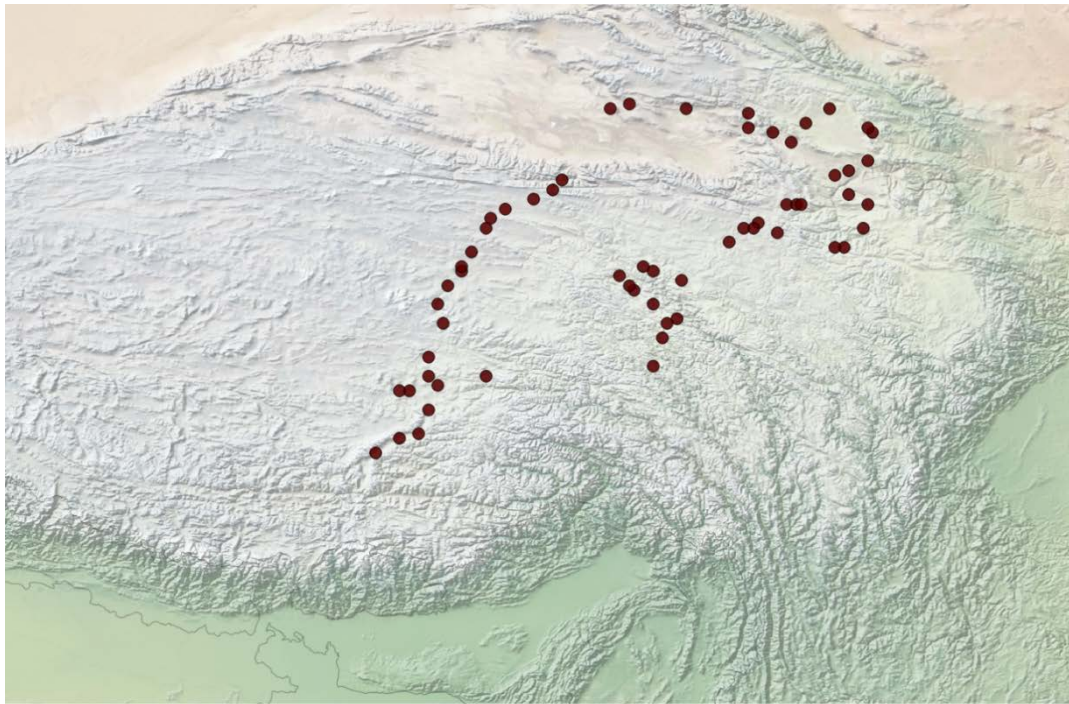
Figure S42. Amount of extrapolation necessary to make geographic projections of diversity. The maps show multivariate environmental similarity surface values (MESS values), which give how far out of the observed range of climate conditions are at each location. Almost all locations within the Tibetan Plateau and northern North America are less than 20% out of range (greater than -20 on the map) both for current and future projections, indicating that to make geographic projections, minimal extrapolation beyond the range of the observed data is necessary.
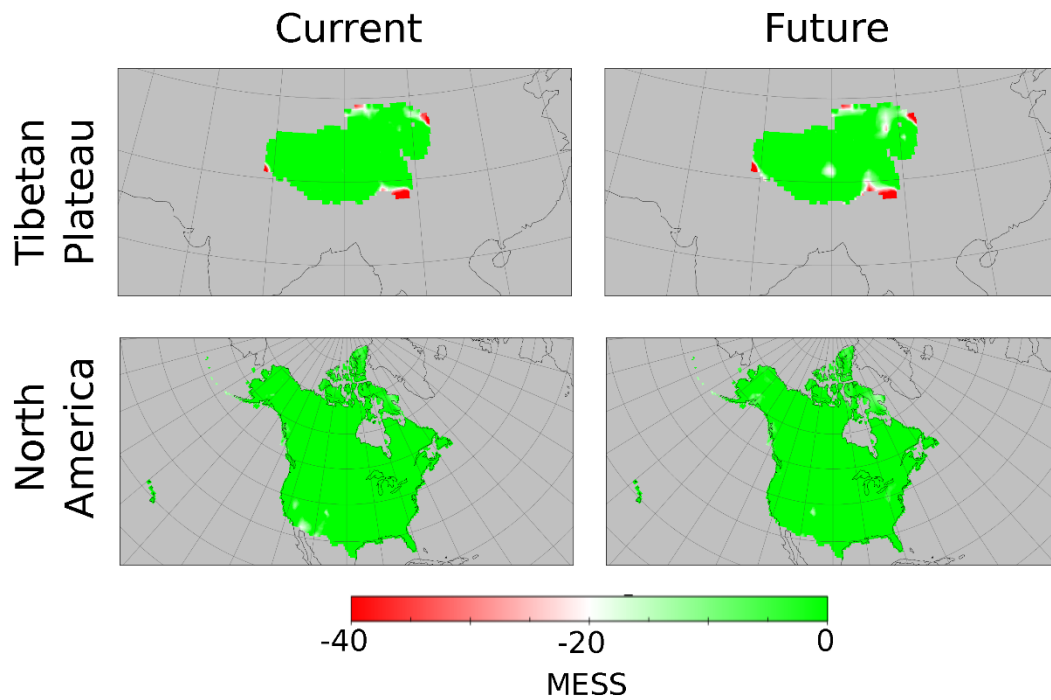
Supplementary Tables

TableS1-3 are ".csv" format. Table S6 is ".xlsx" format. Table S8 and S9 are ".sql" format.

Table S1. Relative average abundances of phyla classified with Greengenes database (http://greengenes.lbl.gov) across all soils.

Table S2. The shifts in relative abundance of the bacterial families (Tibetan Plateau).

Table S3. The shifts in relative abundance of the bacterial families (North American).

Table S6. Description of the geographic, climatic and soil variables by study sites.

Table S8. Climate data used for modeling microbial communities in the Tibetan Plateau. Data are in SQLite format. Data fields are SAMPLE_ID = identifier for sampling location, CLIMATOLOGY_LENGTH_YEARS = number of years over which climate records are averaged, CLIMATOLOGY_VARIABLE = name of climatology variable following CRU conventions, CLIMATOLOGY = end date of climatology, VALUE = value of climatology.

Table S9. Climate data used for modeling microbial communities in northern North America. Data are in SQLite format. Data fields are SAMPLE_ID = identifier for sampling location, CLIMATOLOGY_LENGTH_YEARS = number of years over which climate records are averaged, CLIMATOLOGY_VARIABLE = name of climatology variable following CRU conventions, CLIMATOLOGY = end date of climatology, VALUE = value of climatology.

Table S4 Correlations (R) between bacterial phylotype richness (OTU), phylogenetic diversity (PD) and soil characteristics and plant Shannon index as well as plant species richness. Values in bold indicate significant correlations (P < 0.05). AET: Annual evapotranspiration; PET: potential evapotranspiration; DON: dissolved organic carbon; TN: total nitrogen; SM: soil moisture content; SOC: soil organic carbon content; TC: total carbon content; DOC: dissolved organic carbon.

Environmental variables	OTU		PD	
	Pearson correlation	Sig. (2-tailed)	Pearson correlation	Sig. (2-tailed)
CN ratio	-0.52	<0.001	-0.44	<0.001
Plant Shannon index	0.48	<0.001	0.36	<0.001
Plant species richness	0.43	<0.001	0.30	<0.001
DON	0.22	<0.001	0.06	0.45
Plant evenness index	0.22	<0.001	0.18	0.02
SIC	-0.29	<0.001	-0.14	0.06
Bulk density	-0.20	0.01	-0.14	0.06
DTN	0.17	0.03	0.03	0.64
TN	0.13	0.08	0.03	0.68
NO_3^--N	0.12	0.12	0.03	0.72
SOC	0.04	0.63	-0.03	0.66
NH_4^+-N	0.03	0.65	-0.03	0.65
TC	0.03	0.66	-0.03	0.65
DOC	-0.02	0.84	-0.05	0.50
SM	-0.04	0.58	-0.03	0.67
pH	-0.13	0.08	0.01	0.93

Table S5 Soil variables that significantly correlated with bacterial communities were listed below. The correlations (r) and significance (P) were determined by Mantel tests between the community structure and soil variables. C/N: soil carbon and nitrogen ration; SM: soil moisture content; TN: total nitrogen; SIC: soil organic carbon; SOC: soil organic carbon content; TC: total carbon content; DOC: dissolved organic carbon. DTN: dissolve total organic carbon; DON: dissolved organic carbon.

Soil variables	r	p
CN ratio	0.44	0.001
SM	0.32	0.001
Bulk density	0.32	0.001
SIC	0.31	0.001
TN	0.30	0.001
SOC	0.29	0.001
TC	0.29	0.001
pH	0.27	0.001
DOC	0.16	0.002
NH_4^+-N	0.14	0.002
DTN	0.14	0.005
DON	0.14	0.005
NO_3^--N	0.10	0.037

Table S7 Climate variables used in modeling.

Virable	Measurement	Units
Cloudiness	Monthly mean	Percentage
Daytime temperature range	Monthly mean	Degree Celsius
Frost	Monthly frequency	Days
Potential evapotranspiration	Monthly mean	mm per day
Preciptation	Monthly frequency	Days
Preciptation	Monthly mean	mm
Temperature	Monthly maximum	Degree Celsius
Temperature	Monthly mean	Degree Celsius
Temperature	Monthly minimum	Degree Celsius
Vapour pressure	Monthly mean	hPa