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by

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requirements for the degree of

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Committee in charge:

Professor Jillian F. Banfield, Chair
Professor Mary K. Firestone
Professor Mary E. Power

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Abstract

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Anthropogenic changes in climatic conditions, such as the timing and amount of rainfall, can have profound biotic and abiotic consequences on grassland ecosystems. Grassland's plant and animal phenology are adapted to the ecosystem's wet and cold winters and hot and dry summers and changes to this pattern will have profound consequences in aboveground community structure. Changes in climatic conditions and aboveground communities will also affect the soil biogeochemistry and microbial communities. Soil microbes are an essential component in ecosystem functioning, as they are the key players in nutrient cycling. This thesis investigated the direct and indirect effects of climate change on the structure, composition and abundance of grassland soil microbial communities. The research used the high-throughput technique of 16S rRNA microarrays (Phylochip) to detect changes in the abundances and activities of soil bacterial and archaeal taxa in response to changes in precipitation patterns, aboveground plant communities, and soil environmental conditions. The research took advantage of alongterm climate change experiment that simulated both an increase and an extension of the current winter season in northern California. Five years into the experiment, soil samples and aboveground plant diversity were collected before and after each treatment for two consecutive years. The variability in soil microbial communities after natural wet-dry rainfall events was also investigated. Results showed that, at the community level, soil microbial communities are very robust and resilient to intensified or extended rainfalls during the winter but under extreme and unusual weather events their community structure can be altered. On the other hand, an increased in moss biomass in the plots that received additional water during the spring and fluctuations in soil moisture content (precipitation models and wet-dry patterns) caused changes in soil environmental conditions which in turn affected the activity and abundance of some microbial taxa/guilds. Soil organic carbon and inorganic nitrogen were among the environmental variables that correlated the most with these changes in microbial groups. Considering the great importance soil microbes have in ecosystem functioning, the approach developed here will find application for monitor responses of keystone microbial species/guilds to future changes in climatic conditions. These responses should be taken in consideration for future soil management and conservation practices, and the impacts included in future climate change models.

Table of Contents

Chapter 4: Differences in soil microbial communities underneath bryophytes and grasses.

Chapter 5: Complex short-term responses of soil microbial communities to rainfall events

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Chapter 1

Introduction

Anthropogenic release of greenhouse gases, such as carbon dioxide (CO_2), methane (CH_4), and nitrous oxide (N_2O), have increased 70% from 1970 to 2004 causing an increase in average global temperatures (IPCC 2007a). By consequence, human-induced warming has had repercussions for many physical and biological systems through effects on precipitation and wind patterns, sea level, melting of snow and sea ice, ecosystems adaptation, terrestrial and aquatic biological systems and human health (IPCC 2007b). As a matter of great concern, a lot of research has been done for many years to understand current and predict future effects of climate change in order to mitigate and adapt to the changes. Projection models by the IPCC Special Report on Emission Scenarios (SRES) predict an increase of global green house gases by 25 to 90% (CO_2-equivalents) between 2000 and 2030, which will cause further warming and changes in the physical and biological systems both globally and regionally (IPCC 2007a).

At a regional scale, for example, the state of California, has already experienced climate-related changes such as, increases in temperature, sea level, heavy rainfall, length of growing season and earlier snowmelts, (National Assessment Synthesis Team 2000). Among these, changes in the timing and amount of precipitation patterns are of great concern in California as these might affect grasslands - one of its most important (both economically and biologically) ecosystems. Grasslands occupy over 10% of California's land surface (and 25% of Earth's) and are a vital human resource system as they are highly used for grazing and crop production (Corbin et al. 2007a). Changes in climatic conditions such as fluctuations in the abundance and seasonality of rainfall can have important consequences at the ecosystem level as they can alter plant and animal diversity and aboveground productivity (Knapp et al. 2002, Zavaleta et al. 2003, Harper et al. 2005, Suttle et al. 2007). For instance, simulated extension of the current winter season into the spring in a northern California grassland ecosystem decreased plant and invertebrate species richness and composition (Suttle et al. 2007). These biotic responses could be expected, as plant and animal phenology in a grassland ecosystem are highly dependent on the timing and amount of rainfall (Corbin et al. 2007a, Weltzin et al. 2009). Annual grasses will start to germinate with the onset of the fall rains, followed by slow primary productivity during the winter months and rapid growth and production during the spring when the environmental conditions are favorable (warm temperature, longer days and appropriate soil moisture) (Corbin et al. 2007b).

In addition to changes in aboveground biota, it could also be expected that changes in precipitation patterns will directly and indirectly (via changes in plant communities and environmental conditions) affect the structure, composition and activity of soil microbial and faunal communities (Schnurer et al. 1986, Fierer and Schimel 2002, Waldrop 2006b, a, Weltzin et al. 2009). Soil microbes are an essential component in the process of decomposition and biogeochemical cycling. For this reason, it is of great interest to identify possible changes in microbial community structure and the abundance and activity of keystone microbial groups, as this might have important consequences at the ecosystem level. A key goal of my research was to identify changes in the structure, composition and abundance of soil bacterial and archaeal communities in response to three different precipitation patterns in a northern California grassland ecosystem. The research employed molecular techniques such as 16S rRNA clone libraries and microarrays (Phylochip) to characterize the presence and relative abundance of bacterial and archaeal taxa. In addition, aboveground plant assemblages and soil environmental parameters (e.g., soil moisture, pH, soil temperature, soil inorganic nitrogen, extractable organic carbon, microbial biomass and cation concentrations) were quantified so that microbial responses could be correlated with changes in environmental conditions.

The use of the 16S rRNA microarray was an important tool in the investigation. The Phylochip version G2 has the capability to identify around 8700 different OTUs and quantify the relative abundance of bacterial and archaeal taxa between samples. It rapidly provides much more comprehensive information than would be obtained via other molecular community fingerprinting techniques (*eg*. DGGE, PLFA, TRLFP). My research established that the Phylochip efficiently detected almost of the taxa in the grassland soil samples (only 4% of the taxa were not detected by the array compared to clone libraries). The microarray was used to detect differences in grassland soils microbial communities that: 1) were exposed to a simulated intensified or extended current winter season relative to ambient rainfall 2) were in areas with high moss vs. grass plant biomass and, 3) responded to natural wetting and drying events.

In the first experiment (Chapters 2 and 3), the direct and indirect responses of grassland soil microbial communities to different rainfall amendments (simulating alternative climate change scenarios) were investigated. Since 2001, thirty-six plots in a northern California grassland have been subjected to one of three precipitation-addition regimes designed to mimic predictions of alternative climate change models: 1) an intensified winter season, 2) and extension of the current winter season into the spring and, 3) ambient conditions (National Assessment Synthesis Team 2000, Suttle et al. 2007). Our results showed that grassland soil microbial communities are very robust and resilient to changes in precipitation patterns and aboveground plant and invertebrate communities but they will respond to extreme and unusual weather events. On the other hand, even though the community structure is very resilient to changes in the seasonality of rainfall events, some microbial taxa respond to changes in environmental conditions caused by climate change. These changes might be of great importance at the ecosystem level, as soil microbes are an essential component in biogeochemical cycles and soil structure.

One advantage of using a natural system for climate change experiments is that complex and unpredicted responses can be observed. For instance, an extension of the winter rains into the spring facilitated the growth and proliferation of mosses in these plots. We took advantage of this unexpected result and investigated the effect of mosses (Phylum Bryophyta) on the underlying soil microbial communities. Mosses are non-vascular plants that lack roots and a conductive system, thus obtain most of their nutrients from atmospheric deposition via the plant surface (Tyler 1990, Turetsky 2003). They are extremely important to ecosystem function as they influence the production of organic matter, nutrient cycling, soil stabilization, trapping sediments and water, and providing food and habitat for algae, fungi, invertebrates and amphibians (Turetsky 2003). These physiological and life history traits of mosses can alter the underlying soil geochemistry and microbiology. Here, we show how the high abundance of mosses affected the underlying abundance and activity of some microbial groups by affecting soil environmental conditions such as soil moisture, temperature and nutrient availability (Chapter 4). These results underline the importance of mosses on ecosystem function, as they can directly or indirectly affect microbial guilds involved in nutrient cycling.

In addition of investigating the response of soil microbial communities to simulated climate change models, the responses of these communities to natural wet-dry events was analyzed. Rainfall patterns, especially those involving wet-dry cycles, will release labile carbon and nitrogen substrates (from plant litter, cell lysis and soil aggregates; (Halverson et al. 2000, Denef et al. 2001) into the soil, triggering microbial and faunal activity and changes in biomass (Schnurer et al. 1986, Kieft et al. 1987). Once soil organic compounds become available they will be quickly respired and assimilated by heterotrophic organisms, releasing CO_2 into the atmosphere and available carbon and inorganic nitrogen into the soil system. Here, we show how the composition and abundance of soil microbial communities changed after natural wet-dry events, mainly through changes in soil organic carbon and inorganic nitrogen concentrations (Chapter 5).

This thesis examined the hypothesis that changes in precipitation patterns that alter the composition and productivity of aboveground plant communities also alter underground soil bacterial and archaeal communities. The diversity of soil microbial communities is vast, and this had previously largely precluded analysis of this question. A problem is that there is still only limited (or no) physiological information available for most taxa detected in the Phylochip experiments. Thus, an important product of the correlative-based approach is the generation of hypotheses, only a small subset of which could be tested in the current study. However, new knowledge includes the identification of resilience and response patterns that allow us to begin to incorporate information about soil microbial communities into climate change models. Thus, we can anticipate, and use the approaches developed here to monitor for, consequences at the ecosystem level (eg., nutrient limitation, alterations in biogeochemical cycles). Thus, we may prepare for the inevitable impacts of changes in weather and climate in our grassland ecosystems.

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Chapter 2

Despite strong seasonal responses, soil microbial consortia are more resilient to long-term changes in rainfall than overlying grassland

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Abstract

Climate change impacts on soil microbial communities could alter the structure of terrestrial ecosystems and Earth's biogeochemical cycles. We used 16S rRNA gene microarrays to evaluate changes in the composition of grassland soil microbial communities under rainfall amendments simulating alternative climate change scenarios, and to compare these to responses of overlying plants and invertebrates. Following five years of rainfall manipulation, soil bacteria and archaea in plots where natural rain was supplemented differed little from ambient controls, despite profound treatment-related changes in the overlying grassland. During the sixth and seventh year, seasonal differences in bacterial and archaeal assemblages emerged among treatments, but only when watering exacerbated or alleviated periods of particularly aberrant conditions in the ambient climate. In contrast to effects on plants and invertebrates, effects on bacteria and archaea did not compound across seasons or years, indicating that soil microbial communities may be more robust than associated above-ground macro-organisms to certain alterations in climate.

Introduction

Scientists have now amassed a large body of evidence documenting biological responses to recent climate change (Parmesan 2006, Rosenzweig et al. 2008). This work has focused primarily on macrobiota, while climate change impacts on microbial communities remain little understood. Given the fundamental role of microbial communities in biogeochemical cycling, responses to changing climate could have repercussions for ecosystem structure and feedbacks to the climate system (Wardle et al. 2004b). With relatively short generation times and rapid growth under favorable conditions, microbial communities could be among the fastest components of an ecosystem to respond to changing environmental conditions (Wolters et al. 2000, Prosser et al. 2007). On the other hand, the high functional and genetic diversity, potentially rapid evolutionary rates, and vast dispersal capabilities of microbes may mitigate responses to environmental change (Giller et al. 1997, Finlay and Clarke 1999, Girvan et al. 2005, Prosser et al. 2007). To date, the enormous diversity of soil microbial communities (Rossello-Mora 2001, Torsvik et al. 2002, Gans et al. 2005) has precluded their comprehensive characterization and limited our understanding of climatic effects to broad functional or taxonomic groupings across a community (Fierer et al. 2003b, Zak 2003, Waldrop 2006a, Rinnan et al. 2007) or specific subsets within a community (Horz et al. 2004, Horz et al. 2005). Here, we use 16S rRNA gene microarrays to profile the composition of soil bacterial-archaeal communities in detail and to compare the form and timescale of their ecological response to rainfall manipulation with that of overlying plant and invertebrate communities.

Since 2001, thirty-six plots in a northern California grassland have been subjected to one of three precipitation-addition regimes designed to mimic predictions of alternative climate change models (National Assessment Synthesis Team 2000, Suttle 2007). Previous work has shown that effects of rainfall amendment on plant and invertebrate communities depend heavily on the timing of the increase (Suttle 2007). Increased rainfall during the current winter rainy season has had little discernible effect on aboveground communities. Added spring and summer rainfall that serves to extend the rainy season, on the other hand, has produced dramatic changes in the composition and diversity of grassland plants and invertebrates, in part because seasonal effects have generated strong ecological feedbacks that compound across years (Suttle 2007). Following the fifth year of rainfall manipulation, we initiated work to determine how these different precipitation regimes and associated aboveground changes impact underlying soil bacterial and archaeal communities. Plant and microbial communities are potentially powerful mutual drivers in the response of terrestrial ecosystems to global change (Wardle et al. 2004a), though associations between them are not well understood. With a combined aboveground-belowground, field-based approach, we examined the magnitude of response in each to a shared change in environmental conditions.

Materials and Methods

Experimental background and sample collection

The field experiment was conducted at the Angelo Coast Range Reserve in Mendocino County, California (39° 44' 17.7" N, 123° 37' 48.4" W). Beginning January 2001, rainfall amendments were imposed over replicate 70-m^2 grassland plots in accordance with projections from two leading climate change models (Fig. 1a,b) (National Assessment Synthesis Team 2000). Treatments included increased winter rainfall (January through March), increased spring rainfall (April through June), and a watering control (ambient rainfall). Each water-addition plot receives 14 to 16 mm of rainfall over ambient every three days for 87 days.

After five years of precipitation amendment, we designated twelve neighboring plots for combined analysis of aboveground and belowground communities. Across the following two years (Years 6 and 7 of rainfall amendment), we sampled plant and microbial composition of these plots early in the rainy season (December 10), late in the rainy season (April 1), at peak plant production and diversity (May 31), and during summer drought (July 1). At each time-point, we collected four separate soil subsamples per plot. Subsamples consisted of two 2-cm-diameter 15-cm deep soil cores collected inside pre-designated 400-cm^2 quadrats arrayed within each plot (Fig. 1c). Immediately prior to soil collection, we harvested all aboveground plant tissues within these quadrats for measurement of biomass and species composition. Soil subsamples were combined to obtain measurements of the plot's soil moisture content, pH and available nitrate and ammonium.

Soil DNA extraction and PCR amplification of 16S rRNA genes

We extracted DNA from soils within 24 hours of collection from the field. After soil subsamples were manually homogenized to break down soil aggregates, DNA was extracted from 0.25 grams (approximate dry weight) of each subsample using the Power Soil DNA kit

(MoBio, Carlsbad, Ca) according to the manufacturer's instructions. Extracted DNA was quantified by gel electrophoresis and equal concentrations from each subsample were pooled by plot for further analysis.

A temperature-gradient PCR was performed for each DNA extraction to amplify the bacterial and archaeal 16S rRNA genes. PCR reactions had a final volume of 25µl containing a final concentration of 1X Takara ExTaq PCR buffer with MgCl2, 300 pM of primers 1492R (5'-GGTTACCTTGTTACGACTT-3') and 27F () for bacteria and 1492R with 23F (5'-TGCAGAYCTGGTYGATYCTGCC-3') for archaea, 1 ug/ul BSA, 200 µM dNTPs, 2.5 U ExTaq DNA polymerase (Takara Mirus Bio Inc., Madison, WI) and milliQ H2O to complete volume. PCR cycle was performed with an initial denaturation at 95 °C for 3 min, followed by 25 cycles of 95 °C for 30 sec, annealing gradient from 48 °C – 60 °C for 25 sec, extension of 72 °C for 2 min and a final extension of 72 °C for 10 min. Amplicons were purified using the QIAquick PCR purification kit (Qiagen, Maryland, USA) and quantified with gel electrophoresis.

16S rRNA DNA microarrays

From the corresponding 16S rRNA amplified pools, 500 ng of bacterial and 100 ng of archaeal DNA was fragmented, biotin labeled and hybridized to a 16S rRNA Affymetrix microarray (16S rRNA PhyloChip, Affymetrix) as described in detail elsewhere (Brodie et al. 2006). Briefly, oligonucleotides were synthesized by a photolithographic method by Affymetrix, Inc (Santa Clara, CA) directly onto a 1.28 by 1.28 cm glass surface at a density of 10,000 probes per μm^2. Each unique probe sequence on the array had a copy number of roughly 3 million. The entire array contains 506,944 features that target unique regions in combinations of sequence of the universal gene region 16S rRNA. Probes are grouped into different sets that distinguish among 8,741 distinct taxa, representing 121 bacterial and archaeal orders, 455 families, and 842 subfamilies (Brodie et al. 2006, DeSantis et al. 2007). Errors due to natural sequence diversity (undocumented organisms with 16S rRNA gene sequences that are similar but not identical to those sequences used on the array) were minimized by employing a minimum of 11 different short oligonucleotide probes (and an average of 24) for each taxonomic grouping. PhyloChip washing, staining and scanning were performed as described elsewhere (Masuda and Church 2002). Scanned arrays were recorded as a pixel image and intensities were determined using standard Affymetrix software (GeneChip Microarray Analysis Suite, version 5.1). PhyloChip data were measured at taxon/OTU level (similar to 99% sequence homology) but was summarized to sub-family level (approximately 94% sequence homology). This approach was demonstrated by DeSantis et. al. (DeSantis et al. 2007) to be a conservative way of following community composition while minimizing the influence of cross hybridization occurring between probe-sets targeting closely related sequences. In this data reduction approach we chose the taxon with the highest hybridization signal across all plots as representative for the subfamily.

Clone libraries

We constructed clone libraries to evaluate the level of coverage the microarrays provide for the soil community at the study site. Separate clone libraries were made for each treatment at two time-points, December 2005 and May 2006. Aliquots from the same PCR product used for the microarrays were pooled per treatment, ligated and transformed using the TOPO TA pCR4 cloning kit (Invitrogen, Carlsbad, CA) according to the manufacturer's instructions. Transformed cells were sequenced under the Laboratory Science Program at the Department of Energy, Joint Genome Institute (Walnut Creek, CA). Chimeric sequences were identified using BELLEROPHON, version 3 (Huber et al. 2004, DeSantis et al. 2006a) and removed. Sequences were aligned against the Greengenes 'Core Set" using the NAST algorithm (DeSantis et al. 2006b). Chao1 (Chao 1984) and ACE richness (Chao and Lee 1992) estimators and Shannon's diversity index at 94% sequence similarity were calculated using the software package DOTUR (Schloss and Handelsman 2005).

Accession numbers

Nonchimeric sequences obtained in this study are available in the GenBank database under the accession numbers EF515877 to EF516982.

Environmental correlates

Production and diversity of aboveground communities

At each sampling date, soil and plant samples were collected from within four separate 400cm^2 quadrats spaced widely across each experimental plot. Immediately prior to soil collection, all vegetation within these subplots was clipped at the soil surface and collected along with any residual plant litter. Plants were sorted by species (monocots that could not be identified to species at the time of collection were grouped into either "winter-annual grasses" or "bulbs" (i.e. Liliaceae)), dried at 60 ˚C for 72 hours, and weighed. In addition to species- and group-specific biomass data for each time point, we estimated cumulative production of the plant assemblage across the growing season by summing biomass values for each plant species at its peak production (again, winter annual grasses were grouped together, as were bulbs). Invertebrate sampling followed established protocols for this experiment (Suttle 2007). Briefly, foliar and flying invertebrates were collected in twenty sweeps with a 12-inch diameter net along two perpendicular transects through the center of each plot. Ground-dwelling invertebrates were sampled over 48 hours in pitfall traps containing a solution of water and unscented dish soap. Collected invertebrates were summed by family across all three time points, and subsequent analyses were based on family-level abundance data.

Soil Moisture

Gravimetric soil moisture content was calculated from 10 g composite samples of soil from all four subsamples collected per plot.

Soil pH

A 1:2 w/v solution of fresh soil to 0.01M $CaCl_2$ (10 g soil in 20 ml of 0.01M $CaCl_2$) was shaken for 2 hour at ~100 rpm and allowed to settle overnight. The clear supernatant was then transferred to a clean tube for pH measurement.

Soil Nitrate and Ammonium Concentrations

On the same day of soil collection, we extracted mineral nitrogen for measurement of nitrate and ammonium pools. Within hours of collection, subsamples were individually homogenized by hand (breaking clumps and shaking), and then approximately 20g of soil from each plot (5g per subsample) were added to a 60 ml solution of 2M KCL. The slurry was shaken vigorously for 1 minute, transported to the laboratory, and within 14 hours of collection placed on an orbital shaker for 1 hour at 200 rpm. After shaking, extracts were filtered on pre-leached Whatman 40 Quantitative Grade filter paper (Whatman Group, Middlesex, UK) and frozen until analysis for ammonium and nitrate concentrations (UC Davis ANR Analytical Lab). Concentrations were corrected for gravimetric water content and gravel (>2mm particle size) content in calculating g N per cm^3 of soil.

Data analysis

Community Composition

Analyses of treatment effects on community composition (i.e. taxonomic membership and relative abundance of detected subfamilies across plots) are based on hybridization intensity data only for all taxa that could be detected and identified with high confidence (positive fraction > 0.90). Non-metric multidimensional scaling (NMS) (Kruskal 1978, Clarke 1993) and multi-response permutation procedures (MRPP) (Mielke 1984, 2001) were run in PC-ORD version 4. NMS provides a multivariate approach to structuring high-dimensional data along simpler axes. The approach is particularly suitable for data that are non-normal or on arbitrary scales (McCune 2002). On the resulting ordination, distances among points express relative dissimilarity in species composition among plots. Effects of rainfall amendment on overall community composition were then analyzed with MRPP, a non-parametric procedure for testing the hypothesis of no difference among treatment groups. Following construction of a dissimilarity matrix (Sorensen's Distance) from hybridization intensity data, the analysis compares distances within each group to distances among groups. We identified the specific taxa exhibiting the greatest treatment-based separation in relative abundance by screening hybridization intensity data with univariate tests for each taxon (ANOVA; $P < 0.05$) in the ChipST2C software platform (Peterson 2006). We then conducted post hoc Tukey tests to identify the direction of treatment separation for all taxa showing treatment-based differences at an unadjusted significance level of 0.05.

We verified the depth of coverage provided by microarrays by constructing and sequencing 16S rRNA gene clone libraries for samples collected from each treatment in December 2005 and May 2006 (from 110 to 284 high quality clones used for analysis, Table S1). Only 4% of organisms detected by cloning were not detected by the microarray (at the aforementioned 0.90 detection threshold) (Table S2), supporting the comprehensiveness of microarray coverage for these communities.

Results and Discussion

We tested soils in December 2005 (following the onset of the rainy season but prior to the sixth year of water addition) to evaluate the cumulative impact on the microbial community of the previous five years of rainfall amendment and aboveground change. We found that the overall structure of soil bacterial-archaeal communities was statistically indistinguishable among treatments (Fig. 2a), even as overlying communities of plants and invertebrates had diverged markedly (Suttle 2007); (Fig. 2b). Across the next two years, microbial composition remained statistically indistinguishable among treatments through all but two time-points (Fig. 2a). Treatment-related differences did emerge in April 2006 and July 2006, but these differences did not persist even to the following sampling date (May 2006 and December 2006, respectively). In fact, compositional differences across sampling dates were more pronounced than differences among treatments at any single sample-point (Fig. 3). Under the region's Mediterranean-type climate, winter rainy seasons that can deliver upwards of 200 cm of rainfall in just a few months are followed by prolonged periods of drought in which no rain may fall for six months or more. Sampling across this temporal gradient, we found strong seasonal dynamics in the composition of soil bacterial-archaeal communities, particularly in 2005-2006, when sampling dates were distinguished by sharp contrasts in climatic conditions (Fig. S2).

Treatment-related differences detected in April and July of 2006 were absent in April and July of 2007 (Fig. 2a) suggesting that the 2006 differences were not driven solely by experimental watering, but more likely arose from an interaction between watering and ambient climatic conditions. Both the April and July 2006 sample dates followed periods of aberrant climate at the field site. First, March 2006 was among the wettest Marches on record in northern coastal California (California Climate Tracker. http://www.wrcc.dri.edu/monitor/cal-mon/index.html) (i.e. rank seven in a 113-year record). Against this backdrop of unusually high ambient precipitation (Fig. S2), supplemental watering led to suppressed abundances of many bacterial groups relative to control plots (Fig. 4). The strongest effect was in winter-addition plots, where increased moisture stress would result directly from water addition throughout the rainy season, but we also saw decreased abundances of many groups in spring-addition plots. These differences were attributable, perhaps, to the thick moss covering that had accumulated in spring-addition plots (Table S3), as mosses reduce moisture loss from the soil relative to bare ground or vascular plant cover (Zimov 1995). Following the end of that rainy season, drought conditions began abruptly when an unusually hot period over the first several weeks of May (Fig. S2) dried surface soils and killed annual plant species that had only recently germinated. Over the eight years of the study, this loss of spring-germinating plants was observed only in 2006. The hot spell and rapid soil surface drying appear to have accelerated natural seasonal dynamics in the microbial community, while the addition of water buffered these changes and drove spring-addition plots apart from the other treatments in both overall composition (Fig. 2a) and individual bacterial abundances (Fig. 4).

Variation in the relative abundance of specific taxa among treatments (Fig. 4 and Fig. S1) can be difficult to attribute to specific environmental drivers, given the complexity of the soil system and gaps in our understanding of the physiology and ecology of most soil microorganisms. Where information exists for specific organisms, however, similar responses by less well characterized groups may provide clues to their roles and activities in the soil environment. In July 2006, for example, many Bacteroidetes, Betaproteobacteria and

Gammaproteobacteria were favored in spring-addition plots (Fig. 3). These groups generally adopt a more r-selected life history strategy, typified by rapid responses to high resource availabilities (Smit et al. 2001, Fierer et al. 2007). Such conditions are characteristic of spring-addition plots, where soils remain moist, early-senescing plant species are actively decomposing, and plant species with later phenologies remain active. In contrast, numerous Actinobacteria were suppressed in spring-addition plots at this sampling date. Most Actinobacteria are strict aerobes, generally adopting a slow-growing, K-selected strategy suited to low resource availability (Fierer et al. 2007) and found in lower abundances in wetter soils (Goodfellow and Williams 1983, Alekhina 2001).

Conclusions

Global climate change could have important consequences for patterns of species composition and biodiversity across landscapes, and there is great concern over how these will impact ecosystem productivity and function (Loreau 2001, Tilman et al. 2001, Chapin et al. 2005). Microbial composition and function are sensitive to variability and extremes in soil conditions (Stark and Firestone 1996, Gulledge and Schimel 1998, Fierer et al. 2003a), and researchers working within global change experiments have found that environmental perturbations can impact both individual bacterial groups (Horz et al. 2004, Horz et al. 2005) and aggregate community-level properties such as biomass and respiration (Zak 2000). We detected changes in microbial abundance and composition in response to climatic amendment, but sampling repeatedly across seasons and years found that these responses were short-lived and left little legacy.

Microbial communities in Mediterranean-type grassland soils encounter pronounced fluctuations in soil moisture content across the year. The climatic history of these ecosystems would select for microbial populations that are resilient to highly variable environmental conditions (Waldrop 2006a, b). This may explain why responses to imposed shifts in baseline precipitation regimes were minimal compared to compositional changes observed across the year (Fig. 3). When treatment effects did emerge following periods of more extreme conditions, they were short-lived against background dynamics. Predicted increased frequency of extreme weather events (National Assessment Synthesis Team 2000) and changes in baseline conditions to levels outside the range of historical climatic regimes may be necessary to initiate longer-term or compounding changes in the bacterial and archaeal composition of these soils.

Results from this experiment indicate a degree of robustness to climate alteration, in the form of elevated rainfall, by soil microorganisms not seen in overlying macroorganisms. Through seven years of precipitation amendment, we found much less change in the composition of soil bacterial and archaeal communities than in overlying plants and animals. Most plant and invertebrate taxa in this grassland complete their life cycles within a single year, yet experimental manipulation of the timing of the rainy season generated strong interannual feedbacks that led to dramatic differences in the composition and diversity of aboveground communities five-plus years into the experiment (Fig. 2b) (Suttle 2007). In contrast, soil bacterial and archaeal communities remained statistically indistinguishable among treatments after five years and through most of the two-year sampling period that followed (Fig. 2a). Research has shown that many characteristics of a plant assemblage—composition (Hunt 1988, Bardgett 1999, Smalla 2001, Wieland 2001, Nunan 2003, Ayres 2006), diversity (Gruter 2006), and production (Zak 2003)—can affect the microbial composition of underlying soils. Any snapshot measurement in our experiment might have affirmed this idea for our grassland system as well, but analyzing across seasons we find a soil community characterized by marked seasonal dynamics and longer-term decoupling from aboveground change.

There is speculation that the broad taxonomic distribution of functional traits within microbial communities may confer functional robustness to losses of taxa and changes in composition (Giller et al. 1997, Wolters 2000, Griffiths et al. 2001, Wertz et al. 2007). Intriguingly, this study shows that microbial community composition itself can be robust both to changing climate and to associated changes in plant production and species composition.

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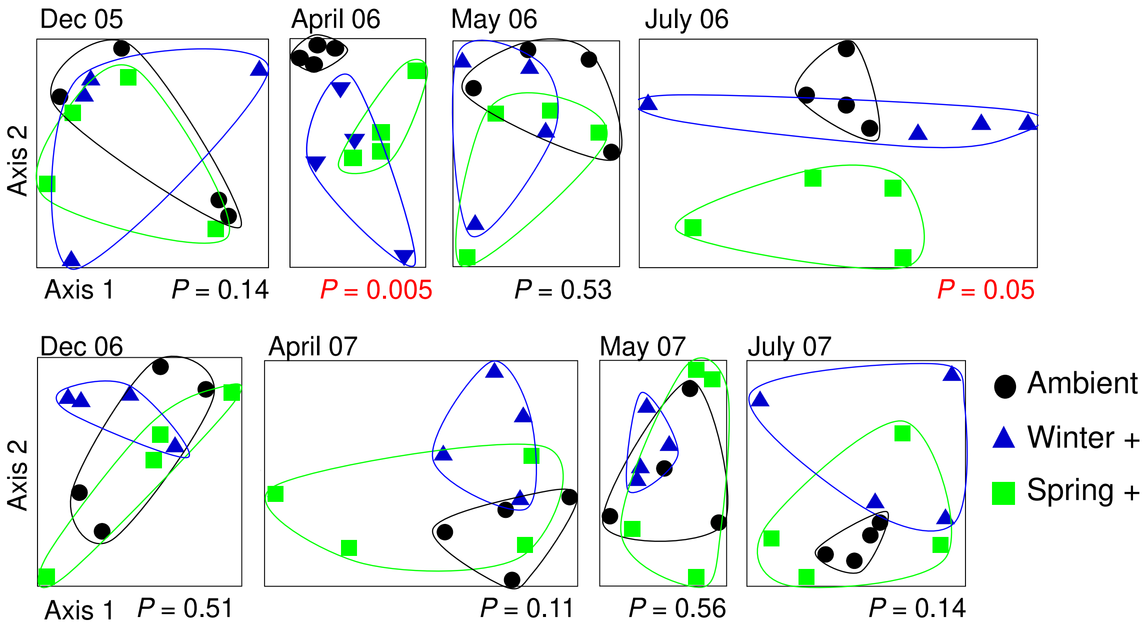
Tables and Figures

Figure 1. The field experiment. Artificial rainfall is delivered from sprinklers (a) that distribute water evenly over replicate 70 m^2 plots (b). Soils and plants were collected for analysis from four quadrants per plot (**c**) at each of four time-points over the year, beginning early in the rainy season (Dec. 10) and continuing into the summer drought (July 1).

a. Belowground



b. Aboveground

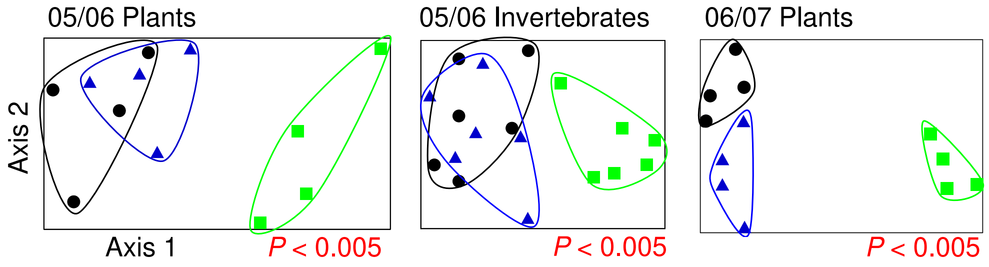


Figure 2. Effects of five-plus years of rainfall amendment on (a) belowground and (b) aboveground communities. Ordinations illustrate results from non-metric multidimensional scaling of (a) taxon-by-taxon abundance data across all subfamilies of bacteria and archaea detected by microarrays at each time-point and (b) species-specific production data and family-specific abundance data across all plants and invertebrates, respectively (Table S4). Distances among points express relative dissimilarities in overall community composition among plots. P values denote significance levels from statistical testing for differences in community composition among treatments using multi-response permutation procedures.

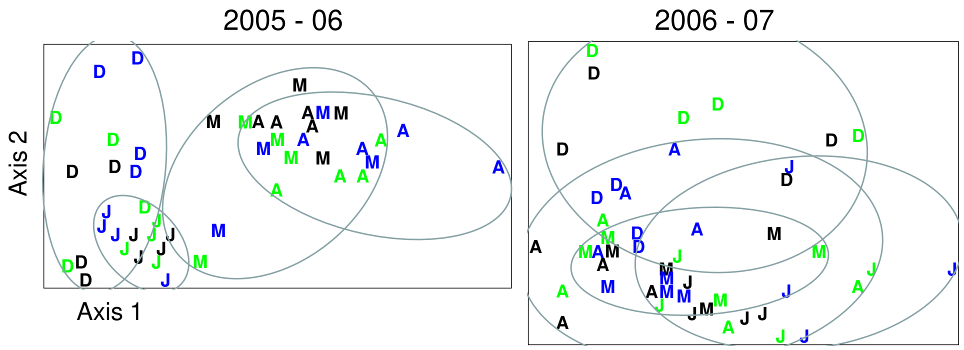


Figure 3. Variation in soil bacterial-archaeal community composition with respect to watering treatment (color) and sampling date (letter). Distances among points express relative dissimilarities in overall community composition among plots and time-points. Blue = Winter-addition plots; Green = Spring-addition plots; and Black = Control plots. D = December 10; A = April 1, M = May 31, J = July 1.

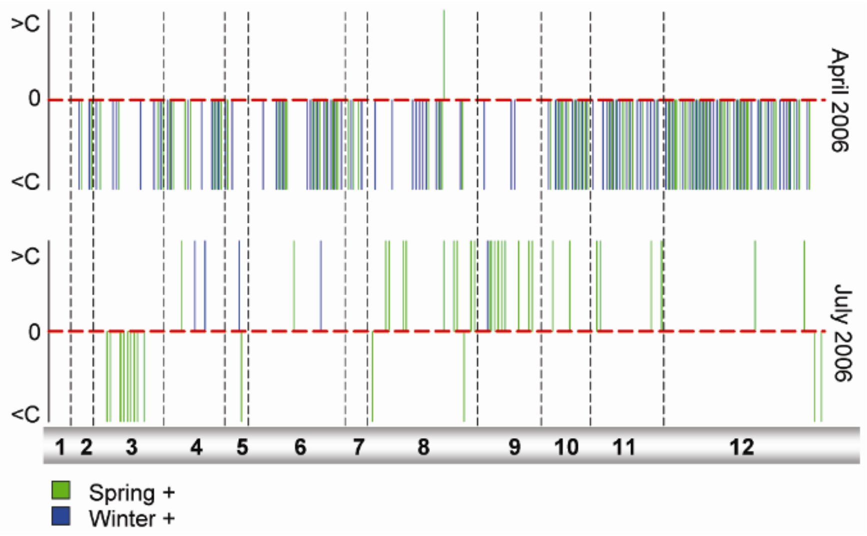


Figure 4. Treatment-based differences in relative abundance of individual subfamilies, as indicated from univariate screening of all subfamily-level data (ANOVA: unadjusted $P \leq 0.05$). Each colored vertical bar represents a subfamily for which abundance in a water-addition treatment (green = spring addition; blue = winter addition) differed statistically from the control. Bars extending upward from the dotted red line to ">C" denote greater abundance in a water-addition treatment than in the control; bars extending downward to "<C" denote lower abundance than in the control. Subfamilies are grouped at broader taxonomic levels as follows: (1) Archaea; the Bacterial phyla (2) Acidobacteria, (3) Actinobacteria, (4) Bacteroidetes, (5) Cyanobacteria, (6) Firmicutes, and (7) Verrucomicrobia, and the Proteobacteria classes (8) Alphaproteobacteria, (9) Betaproteobacteria, (10) Deltaproteobacteria, (11) Gammaproteobacteria, (12) and other phyla.

Supplementary Tables and Figures

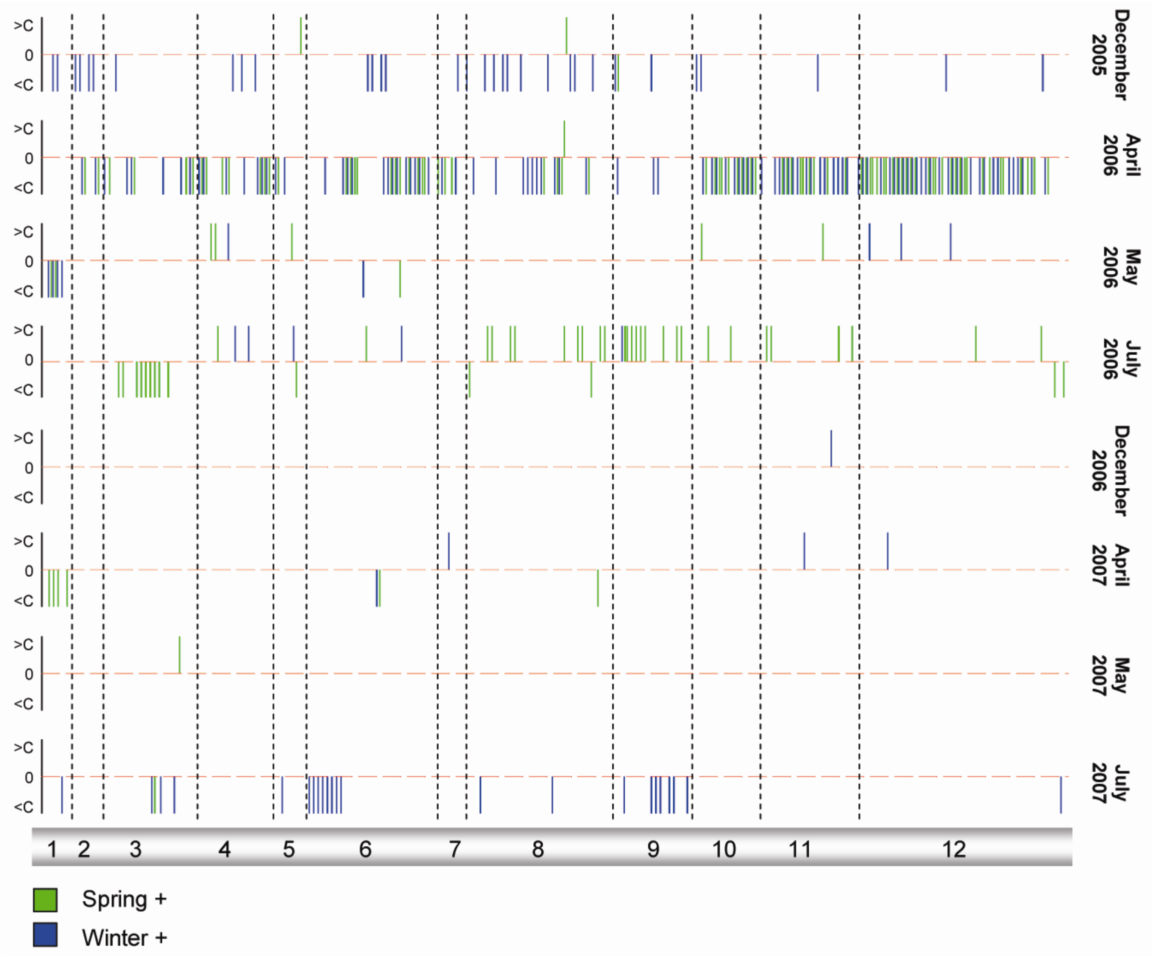


Figure S1: Treatment-based differences in relative abundance of individual subfamilies revealed from univariate screening of all subfamily-level data (ANOVA: unadjusted P ≤ 0.05). Data reflect subfamilies for which abundances in water-addition plots differ from those in control plots. Taxonomic groupings are as follows: (1) Archaea; the Bacterial phyla (2) Acidobacteria, (3) Actinobacteria, (4) Bacteroidetes, (5) Cyanobacteria, (6) Firmicutes, and (7) Verrucomicrobia, and the Proteobacteria classes (8) Alphaproteobacteria, (9) Betaproteobacteria, (10) Deltaproteobacteria, (11) Gammaproteobacteria, and (12) other phyla.

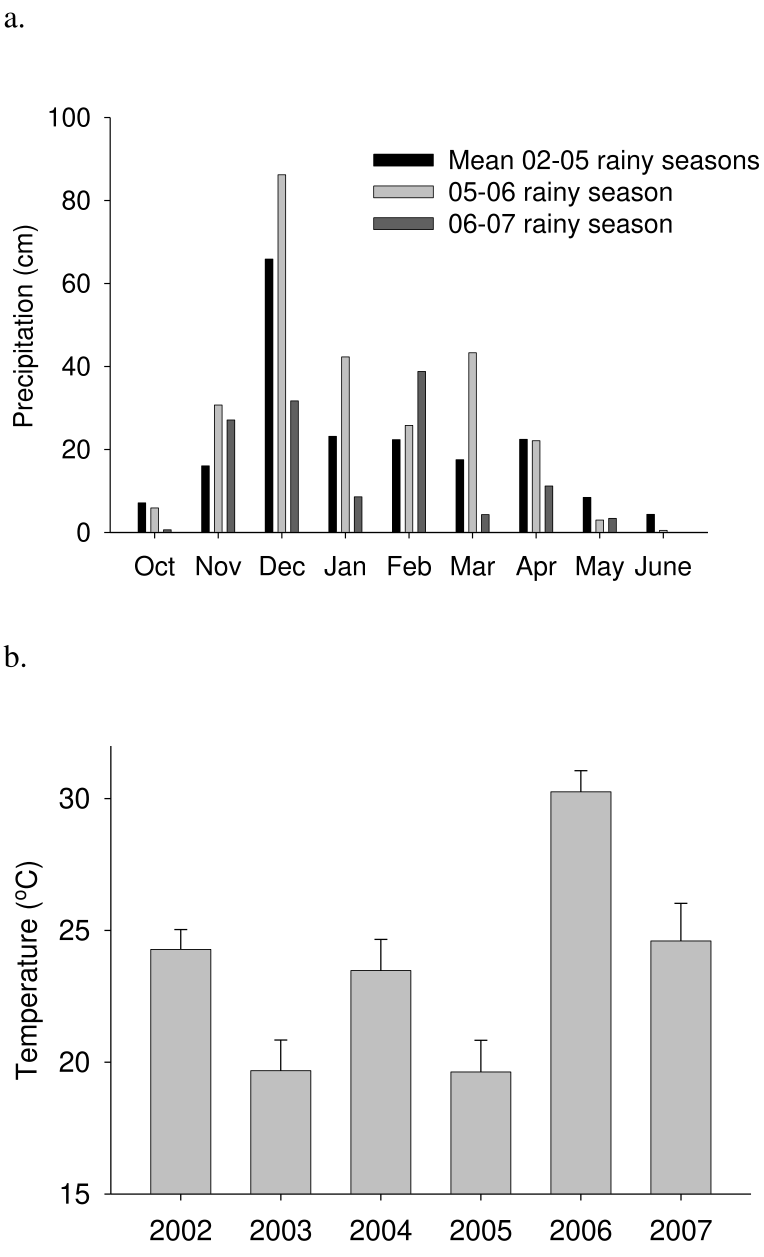


Figure S2: Climatic conditions at the study site. (a) Monthly precipitation data in each of the two years microbial communities were sampled and as an average over the previous three years. (b) Average daily maximum air temperature at the study site over the first three weeks of May from 2002 to 2007.

	NUMBER OF CLONES			ESTIMATED DIVERSITY		PREDICTED RICHNESS [A]		ARRAY RICHNESS
Sample	**Clones Sequenced**	**High Quality[b]**	**Subfamilies detected**	**Shannon's Diversity[c]**	**Shannon's Evenness[c]**	**Chao1[c]**	**ACE[c]**	**Array Richness[c]**
Dec C	373	270	151	4.74	0.85	248-439	272-466	393
Dec S	368	110	78	4.19	0.89	174-534	188-506	402
Dec W	369	182	114	4.56	0.88	172-310	193-367	388
May C	362	204	126	4.62	0.87	222-440	254-489	365
May S	365	213	135	4.68	0.87	316-761	213-409	388
May W	378	284	137	4.54	0.80	238-464	278-507	369

Table S1: Clone library results: Estimated diversity and richness and comparison between array and clone library sub-family richness.

[a] 95% confidence intervals for both Chao1 and ACE richness estimators.

[b] Number of clones after alignment and chimera check

[c] Subfamily-level (6%) sequence divergence

TAXA STRING		NUMBER OF CLONES OBSERVED					
	PF*	**Dec-C**	**Dec-S**	**Dec-W**	**May-C**	**May -S**	**May -W**
Bacteria; Acidobacteria; Acidobacteria-2; Ellin5121/DA052; Unclassified; sf_1	**NP**			1			
Bacteria; Bacteroidetes; Sphingobacteria; Sphingobacteriales; Saprospiraceae; sf_5	**NP**	1	1		1	1	
Bacteria; Bacteroidetes; Sphingobacteria; Sphingobacteriales; Unclassified; sf_5	**0.8**	1					
Bacteria; Chloroflexi; Unclassified; Unclassified; Unclassified; sf_3	**0.75**	1	1	1	1	1	1
Bacteria; Firmicutes; Mollicutes; Unclassified; Unclassified; sf_2	**0.67**						1
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales; Ellin6067/SC-I-66; sf_1	**0.71**			1	1	1	1
Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales; Anaeromyxobacter; sf_1	**0.78**	1			1	1	1
Bacteria; Proteobacteria; Deltaproteobacteria; Unclassified; Unclassified; sf_6	**0.76**		1	1	1	1	1
Bacteria; Termite group 1; Unclassified; Unclassified; Unclassified; sf_1	**0.73**			1			1
Bacteria; TM7; TM7-1; Unclassified; Unclassified; sf_1#	**0.89**	1			3		2
Bacteria; Unclassified; Unclassified; Unclassified; Unclassified; sf_102	**0.59**	1					
Bacteria; Verrucomicrobia; Verrucomicrobiae; Verrucomicrobiales; Opitutaceae; sf_1	**NP**		1	1			1

Table S2: Taxa detected in clone library that did not meet the array detection threshold (PostFrac (PF) > 0.90) for a given treatment and time point (of 1263 total clones yielding high quality sequences).

Detected by the array, but in a different time point or treatment

* Highest positive fraction obtained for that subfamily from the arrays data of December 2005 and May 2007. NP- Not Present in array data from December 2005 and May 2007 time points.

		SOIL MOISTURE (%)	**pH**	**NH4 (ug N /g soil)**	**NO$_3$ (ug N / g soil)**	**VASCULAR PLANT BIOMASS (g/m^2)**	**MOSS BIOMASS (g/m^2)**
Dec. 10 2005	**C**	21.58 ± 0.51	4.81 ± 0.04	23.82 ± 2.36	1.37 ± 0.21	61.75 ± 10.75	ND
	S	20.31 ± 0.47	5.06 ± 0.17	23.21 ± 1.76	1.39 ± 0.35	56.75 ± 18.00	4.50 ± 4.50
	W	**23.73 ± 0.72**	4.96 ± 0.13	23.92 ± 1.22	1.30 ± 0.17	3.86 ± 0.88	23.50 ± 14.25
April 1 2006	**C**	25.58 ± 2.40	4.93 ± 0.03	28.64 ± 1.82	5.87 ± 0.59	96.50 ± 14.50	6.00 ± 5.00
	S	21.29 ± 1.94	5.14 ± 0.13	25.45 ± 1.40	5.24 ± 0.19	159.50 ± 9.50	**43.75 ± 13.50**
	W	24.45 ± 1.96	4.97 ± 0.15	30.76 ± 4.51	6.13 ± 1.51	169.25 ± 16.50	36.26 ± 10.75
May 31 2006	**C**	13.66 ± 0.52	5.06 ± 0.03	34.89 ± 2.97	12.83 ± 2.55	231 ± 22.75	21.75 ± 12.00
	S	**20.19 ± 1.29**	**5.47 ± 0.11**	35.58 ± 3.18	7.54 ± 0.47	306.75 ± 66.75	62.25 ± 14.75
	W	14.98 ± 1.13	5.27 ± 0.07	37.55 ± 3.23	15.56 ± 2.62	268.25 ± 23.75	**78.5 ± 19.75**
July 1 2006	**C**	6.68 ± 0.60	4.98 ± 0.02	61.81 ± 6.54	**82.48 ± 29.91**	268.25 ± 23.75	7.00 ±4.00
	S	**18.67 ± 0.99**	5.18 ± 0.11	39.41 ± 5.75	**13.92 ± 5.91**	323.75 ± 32.5	**82.5 ±17.25**
	W	6.44 ± 0.26	5.20 ± 0.08	51.39 ± 6.13	**93.30 ± 16.73**	275.5 ± 26.25	**51.25 ±11.75**
Dec. 10 2006	**C**	18.13 ± 0.32	4.85 ± 0.04	2.39 ± 0.12	0.69 ± 0.04	ND	3.72 ± 0.95
	S	18.83 ± 0.55	**5.23 ± 0.07**	2.53 ± 0.33	0.59 ± 0.04	ND	3.26 ± 1.69
	W	19.71 ± 0.75	4.99 ± 0.14	2.99 ± 0.60	0.69 ± 0.08	ND	**11.67 ± 2.04**
April 1 2007	**C**	16.43 ± 0.55	4.93 ± 0.02	2.56 ± 0.30	0.59 ± 0.40	101.73 ± 10.11	71.98 ± 36.99
	S	18.17 ± 0.76	5.18 ± 0.12	2.47 ± 0.30	0.40 ± 0.01	106.20 ± 13.46	186.40 ± 59.42
	W	**20.30 ± 0.44**	5.05 ± 0.14	2.26 ± 0.20	0.37 ± 0.05	107.01 ± 10.05	151.55 ± 30.11
May 31 2007	**C**	6.53 ± 0.46	4.93 ± 0.03	3.47 ± 0.43	0.56 ± 0.45	282.66 ± 18.73	25.28 ±14.49
	S	**19.36 ± 0.37**	5.15 ± 0.11	3.39 ± 0.51	0.45 ± 0.04	**377.05 ± 22.35**	**381.55 ± 91.75**
	W	6.01 ± 0.51	5.08 ± 0.14	3.51 ± 0.37	0.55 ± 0.04	247.08 ± 22.18	72.97 ± 26.15
July 1 2007	**C**	4.34 ± 0.23	4.95 ± 0.06	3.50 ± 0.56	0.61 ± 0.16	255.28 ± 27.91	10.59 ± 4.97
	S	**18.34 ± 0.19**	5.22 ± 0.15	3.20 ± 0.74	0.88 ± 0.27	367.00 ± 25.12	**404.31 ± 44.46**
	W	4.38 ± 0.25	5.11 ± 0.11	3.77 ± 1.16	0.49 ± 0.07	276.66 ± 48.99	62.34 ± 16.48

Table S3: Conditions in experimental plots at time of soil collection. Data represent mean values (± standard error) by treatment for gravimetric soil moisture content, soil pH, and aboveground vascular plant biomass and moss biomass. Soil moisture levels are sensitive to prevailing weather conditions immediately preceding soil collection and not necessarily reflective of longer-term differences among treatments. Watering treatment means significantly different from control conditions (ANOVA; P<0.10) are in **bold**.

ND = none detected.

SAMPLE DATE	SOLUTION DIMENSIONALITY	FINAL STRESS	FINAL INSTABILITY
December 10, 2005	2	5.108	0.00001
April 1, 2006	2	3.073	0.00001
May 31, 2006	2	3.543	0.00001
July 1, 2006	2	5.39	0.00001
December 10, 2006	2	0.488	0.000001
April 1, 2007	2	1.435	0.00001
May 31, 2007	2	2.7145	0.00001
July 1, 2007	2	1.104	0.00001

Table S4: Statistics for non-metric multidimensional scaling.

Chapter 3

Responses of soil microbial communities to seasonal changes in precipitation and its associated changes in environmental conditions

Abstract

In a northern California grassland, changes in the seasonality of rainfall that simulate predicted climate change affected the structure and composition of plant and animal communities but had no significant effect on the structure of soil microbial communities. An effect on the overall structure of soil microbial communities was observed only in the first out of two year of sampling. Compared to the second year, weather conditions in the first year were more extreme with high precipitation and intense drought. However, natural seasonal variation and simulated precipitation regimes (increased or extension of the current winter season) affects soil physical and geochemical characteristics, which in turn influences the abundance of specific microbial groups. Among the environmental variables that changed with time in one or more of the water treatment conditions are soil moisture, pH, inorganic nitrogen, available carbon, sodium, calcium and vascular and non-vascular plant biomass. Soil organic carbon and nitrogen availability were the environmental variables that correlated with the abundance of many microbial taxa. Changes in these environmental conditions correlated with different microbial responses in each treatment. An intensification of the winter rains caused a decreased in the abundance of members of the Actinobacteria and Alphaproteobacteria which correlated with the increase in soil moisture content whereas, members of the Gammaproteobacteria, Planctomycetes and Firmicutes showed a positive correlation with the increase in NO_3^- availability in this treatment. Increased carbon availability under ambient conditions had a positive correlation with members of the Bacteroidetes, Actinobacteria, Firmicutes and Alpha, Beta and Gammaproteobacteria whereas, only members of the Firmicutes and Alpha and Gammaproteobacteria responded to carbon availability when the winter rains were extended into the spring. Although correlations do not prove cause and effect, they provide information about the magnitude and possible nature of soil ecosystem cycles and responses of certain taxa to altered precipitation patterns. Changes such as these may have important consequences at the ecosystem level especially where the taxa affected are involved in key ecosystem processes.

Introduction

California Mediterranean grassland ecosystems are adapted to a wide range of climatic conditions. During the winter months the system is exposed to cold and rainy events while in the summer the climate is dry and hot. Changes in the normal climatic cycle such as, anthropogenic changes in the seasonality and amount of rainfall, will affect the structure and composition of grassland's plant and animal communities (Burke et al. 1997, Hughes 2000, Knapp and Smith 2001, Zavaleta et al. 2003, Suttle 2007). Based on intimate relationships involving nutrient cycling between aboveground and belowground communities, it is expected that direct and indirect changes in climatic conditions will also affect the structure, biomass and composition of the underground microbial and faunal communities (Weltzin et al. 2009) but contradictory results have been observed (Kieft et al. 1987, Steenwerth et al. 2005, Waldrop 2006a, b, Cruz-Martinez et al. 2009). Some studies have found changes in microbial biomass and community composition after wetting events (Steenwerth et al. 2005), while others have seen a more robust and resilient community (Waldrop 2006b, a, Cruz-Martinez et al. 2009). Discrepancies in the results might reflect the inherent variability and differences in the type of ecosystem studied (grassland, temperate forest, agricultural soils etc.), the molecular tools used (PLFA, DGGE, microarrays), and the influence of unmeasured environmental parameters (soil type, texture, pressure etc.).

In the grassland ecosystem studied here (northern California), the overall structure of soil microbial communities was shown to be robust to intensified and extended rainfall event as well as to different aboveground plant assemblages, yet the structure was changed by unusual and extreme weather events. During the year 2006, the system experienced the 7th wettest year on record (records from 113 years) and unusual hot and dry events during the summer (Cruz-Martinez et al. 2009). This caused temporary shifts in microbial community structure that did not persist into the following months. This resilience might be due to the high functional and genetic diversity of microbes, which allow them to quickly adapt to environmental changes (Andrén and Balandreau 1999, Behan-Pelletier and Newton 1999, Wall and Virginia 1999, Goddard and Bradford 2003, Reed and Martiny 2007)

Even if the overall structure of the community is robust to environmental changes, individual taxa or guilds may respond to localized and slight variations in environmental conditions such as soil moisture, temperature, pH and nutrient content (Horz et al. 2004, Horz et al. 2005, Fierer et al. 2007)Among these, soil pH and carbon and nitrogen concentrations have been reported as important drivers of the composition and abundance of soil bacteria and are known to influence the bacterial to fungal ratios across soil depth, land use type, soil type and age and ecosystem type (Allison et al. 2007, Fierer et al. 2007, Fierer et al. 2009a, Fierer et al. 2009b, Lauber et al. 2009). It has been previously proposed that low carbon availability will tend to increase the proportional abundance of actinomycetes and gram-positive bacteria relative to gram negative and to decrease the relative abundance of fungi to bacteria and microbial biomass (Blume et al. 2002, Fierer et al. 2003, Allison et al. 2007). In addition, soil inorganic nitrogen is usually a limiting nutrient in grassland ecosystems (Huenneke et al. 1990, Grogan and Chapin 2000) and its abundance and accessibility will affect decomposition rates (Craine et al. 2007) and microbial biomass and activity (Jackson et al. 1988, Schimel et al. 1989), which in turn could alter microbial community composition. Soil pH has also been suggested as a predictor in bacterial community structure at least across larger spatial scales (biomes, continents) (Fierer et al. 2009b, Lauber et al. 2009).

Here we investigate how individual bacterial and archaeal taxa respond to changes in soil environmental conditions caused by changes in the seasonality of rainfall events. This study differs from similar investigations carried out previously in the use of 16S rRNA gene Phylochip microarrays to profile community structure, as it is much more comprehensive and highly resolved. These changes might have important consequences at the ecosystem level if keystone microbial guilds are affected (eg. Nitrogen fixation, methanogenesis) (Schimel 1998, Balser and Firestone 2005, Strickland et al. 2009).

Materials and Methods

Details for the experimental design, soil sampling procedure and protocols for soil moisture, pH, available NH4 and NO3, DNA extraction, 16s rRNA amplification and 16S rRNA microarray experiments and analysis are described in chapter two.

Environmental correlates

Extraction of organic Carbon and exchangeable cations

Water extractable carbon was extracted from 10g of soil by adding 30 ml of deionized water (1:3 w/V), shaken at 900 g for 30 min (Ohno et al. 2007) and filtered through a 0.45 µm syringe filter. Extractable organic carbon was measured using a TIC/TOC analyzer.

Exchangeable cations were extracted and measured at the UC Davis ANR Analytical Lab (Method number 360, (Thomas 1982)).

Statistical Analysis

We identified the taxa that significantly changed across all sampling points (from December 2005 to July 2007) by using univariate analysis of variance (ANOVA, $p \leq 0.01$) in the ChipST2C software platform (Peterson 2006)). The output data were used for clustering analysis (NMS) and Pearson's linear correlations with the measured environmental variables to identify changes in community structure and the variables driving these differences.

Non-metric multidimensional scaling was used to visualize changes in the microbial communities with time. The following clustering analyses were made using each sampling point (December, April, May and July) over the two experimental years (Dec 2005- July 2007): 1) all datafor all treatments (control, winter and spring), 2) significant taxa ($p \leq 0.01$) in control plots 3) significant taxa ($p \leq 0.01$) in spring plots and, 4) significant taxa ($p \leq 0.01$) in winter plots. A second matrix with environmental correlates was overlaid on the first matrix ("species" data) to identify the possible factors driving the observed clustering. Multiple Response Permutation Procedure (MRPP) was used to test the significance of the separation among the groups. Both analyses were done in PC-ORD version 4.

Results and Discussion

Microbial responses to rainfall events over two years

Natural climatic variation from one year to the next was a stronger driver of microbial community structure than additional or extended artificial rainfall within each year (Fig.1). Independent of the treatment, all samples taken in the first year of sampling (Dec 2005- July 2006) were different from samples taken in the following year (Dec 2006- July 2007) (Fig.1). Based on NMS clustering analysis, inorganic nitrogen and moss biomass were the main environmental variables driving these differences. Across both years, ammonium concentrations were the highest in December 2005 (for all treatments) while nitrate was higher in July 2006 (winter and control treatments) (Table 1). As a result of the unusually wet winter/spring season of 2006, the moss biomass rapidly increased in the following year (2007). The effect of increased moss biomass on the composition of the underlying soil microbial communities is further discussed in Chapter 4.

Over the first year of sampling, we detect separation of communities with time but not among treatments (Fig 1). Samples taken in April and May cluster together and separate from the cluster with samples taken in July and December. This pattern was not observed in the second year. The high concentration of inorganic NH_4^+ in December 2005 and NO_3^- in July 2006 are main drivers for this separation (Fig.1 and Table 1). In fact, most of the taxa that showed significant differences across time were correlated with NH_4^+ and NO_3^- concentrations (68 and 76 %, respectively, Table 2). The correlations suggest that many taxa from distinct phylogenetic groups respond to inorganic nitrogen concentrations or respond to environmental factors controlling soil inorganic nitrogen concentrations. This observation suggests that nitrogen is an important nutrient controlling microbial abundances in this system and thus, factors that can directly or indirectly affect its bioavailability such as changes in precipitation patterns, will have important consequences in ecosystem functioning.

For most bacteria, ammonia is the preferred nitrogen source since it is easily assimilated (Kaye and Hart 1997, Cabello et al. 2004). Many archaea, on the other hand, are able to reduce NO_3^- by assimilatory or respiratory pathways and assimilate ammonium via the GS-GOGAT and GDH pathways (Cabello et al. 2004). Interestingly, the abundances of most Archaea in our study were positively correlated to the concentration of NO_3^- but not the NH_4^+concentration (Table 3).The strong response to NO_3^-may reflect their inorganic nitrogen preference in this system. Furthermore, most of the archaeal taxa that responded to $NO_3^-$are known to be strict or facultative anaerobes (eg. Thermoplasmatales sp., Halobacterium sp, Methanogens, Table 3), suggesting that they may be using NO_3^- as their terminal electron acceptor.

Temporal soil geochemical and microbial responses to altered precipitation patterns

Changes in seasonal climatic conditions may influence soil microbial communities both directly and indirectly, by affecting their soil physical and chemical environment. Neither intensification of rainfall during the winter season nor extension of the rainy season into the spring affected the overall structure of soil microbial communities (Cruz-Martinez et al. 2009), but alter soil conditions in response to the treatments (Table 1) did influence specific microbial taxa (Table 4). Extractable organic carbon, inorganic NH_4^+ and aboveground moss and vascular plant biomass are environmental variables that changed significantly with time in all treatments (winter, spring and control) (Table 1). Statistical analyses show that: 1) soil NH_4^+ was significantly higher in December 2005, 2) soil extractable carbon was higher in the control plots in July 2007, in winter plots in May 2007 and in spring plots in April 2006, 3) aboveground moss biomass in the control and winter plots was higher in December 2006 and in the spring plots in May and July 2007 and that 4) the largest vascular plant biomass was in May and July 2007. Other environmental parameters varied only with time in one or two of the treatments. For example, soil pH changed only in control plots, with the lowest pH in December 2005 and 2006, whereas sodium and calcium concentrations were the lowest in the spring plots in April 2006 and 2007. Soil moisture and inorganic NO_3^- changed only in the control and winter plots. The highest soil moisture in these two treatments was recorded in December 2005 and April 2006 and the highest inorganic NO_3^- concentration was observed in July 2006. These changes in soil environmental conditions were strong enough to have an effect on the abundance of some microbial groups.

Based on NMS clustering analysis and Pearson's linear correlations, the environmental variables correlating strongly with the abundance of specific microbial taxa across time in the control plots were; soil moisture, inorganic nitrogen, extractable organic carbon and potassium concentrations (Fig 2a); in spring plots: plant biomass, extractable organic carbon and ammonia, potassium and calcium concentrations (Fig 2b), and in the winter plots were; soil moisture, inorganic nitrogen, moss biomass and potassium concentrations (Fig 2c). This data suggest that the timing and amount of rainfall has a range effects on soil environmental conditions causing different microbial groups to respond to the the variety of environmental alterations resulting from changing patterns and amounts of precipitations.

In the control plots, the higher NH_4^+ concentration in December 2005 and July 2006 influenced 58% of the taxa whereas only 35% and 22% were affected by NH_4^+ in the spring and winter treatment, respectively (based on Pearson linear correlation, Table 4). From all the taxa that correlated with NH_4^+ concentration in one or more of the treatments, 23% of them were only present in the control plots (unique taxa). Among those are members of the Euryarchaeota, Acidobacteria, Actinobacteria, Bacteroidetes, Firmicutes, Proteobacteria (Alpha, Beta, Delta and Gammaproteobacteria) (Table 5). Most showed a positive correlation with NH_4^+ suggesting a response to nitrogen availability.

A similar response was observed to carbon availability where 27% of the taxa that responded to extractable organic carbon were only present in the control plots. Correlation suggests that members of the Bacteroidetes, Actinobacteria, Firmicutes and Alpha, Beta and Gammaproteobacteria had a positive response to carbon availability. Such positive response to available carbon was also observed in this system in response to short term dynamics following rainfall events (Chapter 5). Analogous results have been reported previously by (Fierer et al. 2007). These authors showed a positive correlation between Betaprotoebacteria and Bacteroidetes and carbon utilization rates and suggested that these groups might exhibit a copiothrophic life strategy. Copiotrophs are organisms that will respond quickly to resources by having higher growth rates and low substrate specificity (Sylvia 1999, Fierer et al. 2007). Carbon availability is one of the main drivers of soil microbial community structure across depths, land-use and ecosystems (Fierer et al. 2003, Allison et al. 2007) and could influence several microbial groups differently based on their nutritional requirements and physiological capabilities.

In the spring treatment, soil extractable carbon concentration also had a positive correlation with many microbial taxa (14%, Table 4). However, this effect was less pronounced compared to the ambient conditions. The taxa that mainly responded to carbon availability were members of the Firmicutes and Alpha and Gammaproteobacteria. It is possible that the response to carbon is connected to root exudation from the aboveground vascular plants. The spring plots had larger plant biomass when compared to ambient conditions which will cause higher and more complex inputs of organic compounds. Measurements of extractable organic carbon will represent all types, sizes and complexity of carbon sources in soil. Interestingly, only 1% of the taxa that responded to available carbon also responded to vascular plant biomass (data not shown)., suggesting that soil microorganisms are responding to different types and sources of organic compounds other than those from plant exudates. They could respond to carbon sources originated from microbial cell death and exudates (Van Gestel 1993, Halverson et al. 2000), release of organic matter bound in soil aggregates (Denef et al. 2001), recalcitrant carbon compounds (Bardgett et al. 2007) and inputs from animal (Osler and Sommerkorn 2007) and non-vascular plants (Chapter 4). As previously mentioned, the type, amount and quality of carbon are good predictors on the abundance and composition of bacteria and fungi in soils (Fierer et al. 2003, Fierer et al. 2007).

In the winter plots, high availability of soil NO_3^- in July 2006 and variation in soil moisture were inferred to be the strongest environmental variables (Fig 2c), affecting 71% and 37% of the taxa respectively (Table 4). Soil inorganic NO_3^- had a positive effect mainly on members of the Firmicutes, Planctomycetes and Gammaproteobacteria, while soil moisture had a negative response mainly on members that are known to be sensitive to soil moisture content such as the Actinobacteria (Goodfellow and Williams 1983). By July, the plants have died in the winter and control plots and most of the aboveground plants biomass is in the form of litter. Continuing slow rates of nitrogen mineralization and low uptake of nutrients by the few living plants still remaining, provide a potential mechanism for increasing the soil inorganic nitrate pool. Groups showing a positive correlation of abundance with nitrate concentrations may be directly or indirectly responding to the available nitrate pool.

Conclusions

Grassland soil microbial communities are known to be both genetically and functionally diverse. This high diversity is likely the source for their high resilience and robustness at the community level. The current study detected shifts at the guild or "species" level across seasons and treatments. The groups of bacteria and archaea found to contribute to shifts in soil community structure may be those that confer this robustness to perturbation. Furthermore, correlations with specific environmental parameters suggest factors that motivate these shifts in structure. The environmental factors most likely to drive changes in taxa abundances are soil moisture content and the availability of inorganic nitrogen, sodium, potassium, and organic carbon. Among these, carbon availability and inorganic NH_4^+ and NO_3^- concentrations exhibited the strongest correlations with many taxa, indicating these nutrients are major determinants of microbial abundance patterns across seasons and rainfall patterns (Table 5). The strong correlation with nitrogen availability might indicate that, in this grassland ecosystem, soil microbial communities are nitrogen limited. These findings underline the importance of coupling changes in climatic conditions with the soil abiotic and biotic environment.

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Tables and Figures

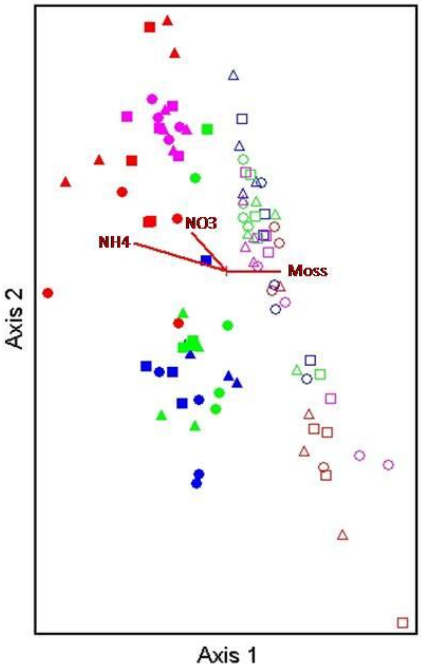

Figure 1: NMS clustering analysis of all the samples taken from December 2005 until July 2007. Environmental variables with a R^2 above 0.10 were overlaid on the clustering analysis. Filled symbols represent samples from year Dec 2005- July 2006 and empty symbols from year Dec 2006 – July 2007. Shape of symbol represents the treatment: triangle = control, square = spring, circle = winter. Color represent the time of sampling; December =red, April = blue, May = green and July = pink. NMS statistical results are shown in Table S3.

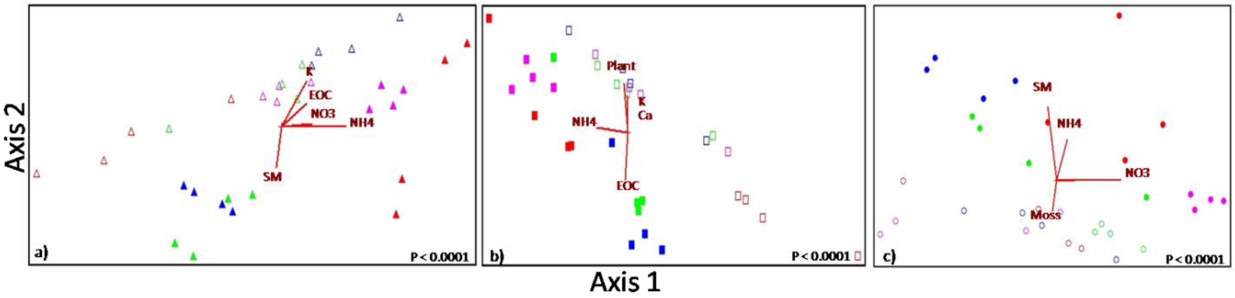

Figure 2: NMS clustering analysis from all time points in the a) control, b) winter and c) spring treatments. Environmental variables with a R^2 above 0.10 were overlaid on the clustering analysis. Filled symbols represent samples from year Dec 2005- July 2006 and empty symbols from year Dec 2006 – July 2007. Color represent the time of sampling; December =red, April = blue, May = green and July = pink. NMS statistical results are shown in Table S4.

		Dec. 10 2005	**April 1 2006**	**May 31 2006**	**July 1 2006**	**Dec. 10 2006**	**April 1 2007**	**May 31 2007**	**July 1 2007**
Soil moisture	**C***	21.58 ± 0.51^{ab}	25.58 ± 2.40 ^{a}	13.66 ± 0.52^{c}	6.68 ± 0.60^{d}	18.13 ± 0.32^{bc}	16.43 ± 0.55^{c}	6.53 ± 0.46^{d}	4.34 ± 0.23^{d}
	S	20.31 ± 0.47	21.29 ± 1.94	20.19 ± 1.29	18.67 ± 0.99	18.83 ± 0.55	18.17 ± 0.76	19.36 ± 0.37	18.34 ± 0.19
	W*	23.73 ± 0.72^{a}	24.45 ± 1.96^{a}	14.98 ± 1.13^{c}	6.44 ± 0.26^{d}	19.71 ± 0.75^{b}	20.30 ± 0.44^{b}	6.01 ± 0.51^{d}	4.38 ± 0.25^{d}
pH	**C***	4.81 ± 0.04^{b}	4.93 ± 0.03^{ab}	5.06 ± 0.03^{a}	4.98 ± 0.02^{ab}	4.85 ± 0.04^{b}	4.93 ± 0.02^{ab}	4.93 ± 0.03^{ab}	4.95 ± 0.06^{ab}
	S	5.06 ± 0.17	5.14 ± 0.13	5.47 ± 0.11	5.18 ± 0.11	5.23 ± 0.07	5.18 ± 0.12	5.15 ± 0.11	5.22 ± 0.15
	W	4.96 ± 0.13	4.97 ± 0.15	5.27 ± 0.07	5.20 ± 0.08	4.99 ± 0.14	5.05 ± 0.14	5.08 ± 0.14	5.11 ± 0.11
NH_4^+	**C ***	23.82 ± 2.36^{a}	2.81 ± 0.18^{b}	3.03 ± 0.25^{b}	4.01 ± 0.44^{b}	2.39 ± 0.12^{b}	2.56 ± 0.30^{b}	3.47 ± 0.43^{b}	3.50 ± 0.56^{b}
	S*	23.21 ± 1.76^{a}	2.49 ± 0.13^{b}	3.12 ± 0.29^{b}	2.63 ± 3.37^{b}	2.53 ± 0.33^{b}	2.47 ± 0.30^{b}	3.39 ± 0.51^{b}	3.20 ± 0.74^{b}
	W*	23.92 ± 1.22^{a}	3.02 ± 0.44^{b}	3.28 ± 0.28^{b}	3.37 ± 0.43^{b}	2.99 ± 0.60^{b}	2.26 ± 0.20^{b}	3.51 ± 0.37^{b}	3.77 ± 1.16^{b}
NO_3^-	**C ***	1.37 ± 0.21^{b}	0.58 ± 0.06^{b}	1.11 ± 0.22^{b}	5.36 ± 1.96^{a}	0.69 ± 0.04^{b}	0.59 ± 0.30^{b}	0.56 ± 0.11^{b}	0.61 ± 0.16^{b}
	S	1.39 ± 0.35	0.51 ± 0.02	0.66 ± 0.04	0.93 ± 0.40	0.59 ± 0.04	0.40 ± 0.01	0.45 ± 0.04	0.88 ± 0.27
	W*	1.30 ± 0.17^{b}	0.60 ± 0.15^{b}	1.36 ± 0.23^{b}	6.13 ± 1.14^{a}	0.69 ± 0.08^{b}	0.37 ± 0.05^{b}	0.55 ± 0.04^{b}	0.49 ± 0.07^{b}
EOC	**C ***	54.19 ± 3.16^{bc}	87.52 20.29^{b}	21.52 2.80^{c}	55.02 7.91^{bc}	17.32 1.25^{c}	25.37 3.73^{c}	100.70 20.20^{b}	187.05 17.45^{a}
	S*	55.79 ±4.41^{b}	93.84 ±18.64^{a}	31.12 ±5.12^{b}	30.82 ±3.17^{b}	28.23 ±3.50^{b}	24.65 ±1.42^{b}	36.80 ± 5.03^{b}	36.72 ± 4.54^{b}
	W*	93.25 ± 26.26	76.00 ± 10.61	26.91 ± 3.39	78.07 ± 9.86	18.73 ± 0.77	39.46 ± 12.13	145.16 ± 38.11	202.81 ± 7.83
K	**C**	170.08 ± 11.68	157.37 ± 9.76	162.26 ± 8.52	198.42 ± 13.95	173.01 ± 11.22	177.90 ± 23.16	183.76 ± 16.59	189.63 ± 22.71
	S	154.44 ±13.96	151.51 ± 8.80	148.57 ±18.68	137.82 ±7.72	136.84 ±5.53	136.84 ±13.64	137.82 ±13.67	151.51 ±14.92
	W	165.19 ± 3.7	152.48 ± 5.76	149.55 ± 6.46	184.74 ± 15.67	158.35 ± 6.87	142.71 ± 7.23	168.12 ± 14.01	154.44 ± 10.88
Na	**C***	14.94 ± 0.66	16.09 ± 0.94	14.37 ± 0.57	14.94 ± 0.66	13.79 ± 0.94	13.79 ± 0.0	13.79 ± 0.0	13.79 ± 0.0
	S*	24.71 ±1.10^{bc}	20.69 ± 2.65^{c}	25.29 ±1.63^{abc}	30.46 ± 1.96^{ab}	27.59 ± 1.63^{abc}	21.84 ± 1.48^{c}	31.61 ± 1.10^{ab}	33.34 ± 2.39^{a}
	W	20.69 ± 0.94	22.42 ± 0.57	20.69 ±0.94	18.97 ±1.72	19.54 ±0.66	21.84 ±0.66	23.56 ± 1.96	22.99 ± 1.33
Ca	**C***	13.03 ± 0.58	14.03 ± 0.82	12.52 ± 0.50	13.03 ±0.58	12.02 ± 0.0	12.02 ± 0.82	12.02 ± 0.0	12.02 ± 0.0
	S*	21.54 ±0.96^{bc}	18.04 ± 2.31^{c}	22.04 ± 1.42^{abc}	26.55 ± 1.71^{ab}	24.05 ± 1.42^{abc}	19.04 ± 1.29^{c}	27.55 ± 0.96^{ab}	29.06 ± 2.09^{a}
	W	18.04 ±0.82	19.54 ± 0.50	18.04 ± 0.82	16.53 ± 1.50	17.03 ± 0.58	19.04 ±0.58	20.54 ±1.71	20.04 ±1.16
Mg	**C**	1009.87 ± 101.69	1051.50 ± 134.59	1016.86 ± 126.84	1016.56 ± 97.56	1046.63 ±104.86	1024.76 ± 77.44	970.68 ± 80.87	1003.49 ±

		Dec. 10 2005	April 1 2006	May 31 2006	July 1 2006	Dec. 10 2006	April 1 2007	May 31 2007	July 1 2007
									115.13
	S	1060.61 ± 35.13	1166.34 ± 49.70	1114.38 ± 41.58	1132.31 ± 23.67	1162.39 ± 35.54	1068.51 ± 26.03	1123.19 ± 34.24	1148.72 ± 42.23
	W	993.16 ± 92.77	1076.71 ± 51.82	1021.42 ± 71.62	1014.43 ±62.57	1058.48 ± 79.58	1031.14 ± 81.31	1004.10 ± 49.79	952.15 ± 67.74
MPB	**C***	ND	5.99 ± 5.04^{b}	21.75 ± 2.00^{ab}	6.98 ± 4.08^{b}	92.95 ± 23.68^{a}	71.98 ± 6.99^{ab}	25.28 ±14.49^{ab}	10.59 ± 4.97^{b}
	S*	4.50 ± 4.50^{c}	43.75 ± 13.50^{c}	62.25 ± 14.75^{c}	82.6 ±17.25^{c}	81.58 ± 42.31^{c}	186.40 ± 59.42^{bc}	381.55 ± 91.75^{ab}	404.31 ± 44.46^{a}
	W*	23.55 ± 14.17^{c}	36.36 ± 10.68^{bc}	78.38 ± 19.87^{bc}	51.25 ±11.70^{bc}	291.65 ± 50.88^{a}	151.55 ±30.11b	72.97 ±26.15^{bc}	62.34 ± 16.48^{bc}
VPB	**C ***	61.75 ± 10.75^{cd}	96.50 ± 14.50^{bc}	231 ± 22.75^{ab}	268.25 ± 23.75^{a}	ND	101.73 ± 10.11^{c}	282.66 ± 18.73^{a}	255.28 ± 27.91^{a}
	S *	56.75 ± 18.00^{c}	159.50 ± 9.50^{bc}	306.75 ±66.75a^{b}	323.75 ± 32.5^{ab}	ND	106.20 ± 13.46^{bc}	377.05 ± 22.35^{a}	367.00 ± 25.12^{a}
	W*	3.86 ± 0.88^{de}	169.25 ± 16.50^{bcd}	268.25 ± 23.75^{abc}	275.5 ± 26.25^{ab}	ND	107.01 ± 10.05c^{de}	247.08 ± 22.18^{a}	276.66 ± 48.99^{a}

Table 1: Mean and ± standard error for the environmental parameters measured at each sampling point and treatment. ANOVA ($P \leq 0.05$) was used to identify differences across time within each treatment. Significant differences across time were labeled with a (*).ND = none detected. EOC = extractable organic carbon, MPB = moss plant biomass, VPB = vascular plant biomass.One outlier was eliminated to calculate the mean and s.e. for EOC. Values with different superscript letter are significantly different.

	SM	pH	NH4	NO3	EOC	K	Na	Ca	Mg	MB	VPB	Total number of taxa
Number of taxa that significantly correlated with environmental variable	352	53	544	608	199	388	53	56	38	304	215	**799**
Percentage	44	7	68	76	25	49	7	7	5	38	27	

Table 2: Number and percentage of taxa that correlated to each environmental variable across time (no treatment separation).

Gene	SM		$NH4^+$		$NO3^-$		K		MB		VPB	
	P	**r**	**P**	**r**	**P**	**r**	**P**	**r**	**P**	**r**	**P**	**r**
Archaea;Crenarchaeota;C1; C1a;Unclassified;sf_1;2583	7.9E-07	-0.48	3.4E-06	-0.45							1.2E-03	0.33
Archaea;Crenarchaeota; C1; C1b;Unclassified;sf_1;2589	1.8E-04	-0.37			1.3E-03	0.32	2.6E-02	0.23			1.2E-04	0.38
Archaea;Crenarchaeota;Thermoprotei; Cenarchaeales;Cenarchaeaceae;sf_1;2593	8.3E-05	-0.39			4.9E-03	0.29	4.0E-02	0.21			4.1E-05	0.41
Archaea;Crenarchaeota;Thermoprotei; Unclassified;Unclassified;sf_7;2582	2.8E-07	-0.50	6.5E-03	-0.28							1.2E-05	0.43
Archaea;Euryarchaeota;Halobacteria; Halobacteriales;Halobacteriaceae;sf_1;2137	2.2E-04	-0.37			1.3E-04	0.38	1.8E-02	0.24			5.0E-04	0.35
Archaea;Euryarchaeota;Methanomicrobia; Methanomicrobiales;Methanomicrobiaceae;sf_3;2274	1.4E-02	-0.25			3.2E-03	0.30						
Archaea;Euryarchaeota;Methanomicrobia; Methanomicrobiales;Methanomicrobiaceae;sf_3;2286					1.0E-03	0.33					5.1E-03	0.28
Archaea;Euryarchaeota;Methanomicrobia; Methanosarcinales;Unclassified;sf_1;2215	7.1E-04	-0.34			5.0E-04	0.35	2.4E-02	0.23			8.1E-04	0.34
Archaea;Euryarchaeota;SAGMEG-1; Unclassified;Unclassified;sf_1;2195	1.5E-02	-0.25			5.4E-04	0.35					1.2E-03	0.33
Archaea;Euryarchaeota;Thermococci; Thermococcales;Thermococcaceae;sf_1;2240			1.3E-02	0.25	1.4E-04	0.38						
Archaea;Euryarchaeota;Thermoplasmata; E2;terrestrial group;sf_2;2204					3.9E-03	0.29			6.3E-03	-0.28		
Archaea;Euryarchaeota;Thermoplasmata;Thermoplasmatales;Cplasma;sf_1;2198	2.3E-04	-0.37			1.1E-03	0.33	4.4E-02	0.21			2.8E-04	0.36
Archaea;Euryarchaeota;Thermoplasmata; Thermoplasmatales;Unclassified;sf_1;2265			5.4E-03	0.28	1.4E-03	0.32						
Archaea;Euryarchaeota;Thermoplasmata; Unclassified;Unclassified;sf_1;2303											2.9E-02	-0.22

Table 3: P-values and Pearson's correlation coefficient (r) of archaea to environmental parameters

		SM	pH	NH4^{+}	NO3^{-}	EOC	K	Na	Ca	Mg	MPB	VPB
Control	Number of taxa that responded to environmental variable	145	61	466	269	234	297	15	10	0	125	80
	% from total	18	8	58	34	29	37	2	2	0	16	10
	% unique taxa	2	7	23	1	27	26	1	1	0	8	5
Spring	Number of taxa that responded to environmental variable	8	22	277	116	114	18	106	71	27	130	114
	% from the total	1	3	35	15	14	2	13	13	3	16	14
	% unique taxa	0	2	4	1	13	2	13	13	3	9	11
Winter	Number of taxa that responded to environmental variable	286	60	174	569	30	181	20	22	6	95	72
	% from total	37	8	22	71	4	23	3	3	1	9	9
	% unique taxa	20	7	3	32	3	12	2	2	1	3	4

Table 4: Actual number and percentage of taxa that correlated to the measured environmental variables on each treatment. Percentage of taxa that were unique to that treatment is also included in the table. Percentages were calculated based on the total number of taxa identified by the microarrays (799 at 0.9 pf threshold). SM = soil moisture, EOC = extractable organic carbon, MPB = moss plant biomass, VPB = vascular plant biomass.

Phyla	**SM**			**NH4**			**NO3**			**EOC**			**K**			**Na**			**MB**			**VPB**		
	C	S	W	C	S	W	C	S	W	C	S	W	C	S	W	C	S	W	C	S	W	C	S	W
Archaea																								
Crenarchaeota						1											4		2			1	4	
Euryarchaeota	1												2				6		4		1	3	3	
Bacteria																								
Acidobacteria			2	7		1			6	4	4		7		1		6			1	1	1		
Actinobacteria		1	28	9	16	1			21	19	8		36	4	7		4	3	28	3	1	4		2
Bacteroidetes			5	14	2				16	22	5	1	11	1	3		7	4	5	6		6	6	2
Chloroflexi	1		4	3		2		1		2	5	1	7		1	1	2			6	1		5	
Cyanobacteria			10	4	1	1				2	3		3		10		1			3	5	2	1	8
Firmicutes	5		13	16		2	1		27	15	11		29	2	7	2	12	3	1	8	1	5	12	
Nitrospira			1	1						2			1									1	1	
Planctomycetes			3	2		1			28	7	2	17	17			2	4			2	1			12
Verrucomicrobia	1		5	9			1	1	16	2	6		4	2			11				1		4	1
Proteobacteria	1	1	68	87	8	8	2	3	92	133	42	2	75	4	60	5	24	7	19	34	10	8	35	7
α-proteobacteria			37	20	5	5	2		22	51	11		21		37	2	4	5	16	20	1	6	5	5
β-proteobacteria			2	14				3	12	30	5	1	4		10	1	1	1	1	6	1	1	1	1
δ-proteobacteria	1	1	8	18		1			23	16	4	1		2	3	1	5			2	2		6	1
ε-proteobacteria				1					1		1		1									1		
γ-proteobacteria	2		17	34	3	2			32	35	17		28	2	10	1	11	1	2	6	4		21	
Total number of taxa	**14**	**2**	**157**	**185**	**29**	**20**	**4**	**5**	**253**	**219**	**103**	**21**	**211**	**15**	**98**	**10**	**102**	**19**	**62**	**73**	**26**	**40**	**88**	**34**

Table 5: Number of taxa that responded to each environmental variable but were only present in one of the three treatments ("unique taxa for that treatment").

SupplementaryTables

Gene	SM	NH4	NO3	K	Na	EOC	MPB	VPB
Archaea;Crenarchaeota;C1; C1a;Unclassified;sf_1;2583	-0.48	-0.45						0.33
Archaea;Crenarchaeota; C1; C1b;Unclassified;sf_1;2589	-0.37		0.32	0.23				0.38
Archaea;Crenarchaeota;Thermoprotei; Cenarchaeales;Cenarchaeaceae;sf_1;2593	-0.39		0.29	0.21				0.41
Archaea;Crenarchaeota;Thermoprotei; Unclassified;Unclassified;sf_7;2582	-0.50	-0.28						0.43
Archaea;Euryarchaeota;Halobacteria; Halobacteriales;Halobacteriaceae;sf_1;2137	-0.37		0.38	0.24				0.35
Archaea;Euryarchaeota;Methanomicrobia; Methanomicrobiales;Methanomicrobiaceae;sf_3;2274	-0.25		0.30					
Archaea;Euryarchaeota;Methanomicrobia; Methanomicrobiales;Methanomicrobiaceae;sf_3;2286			0.33					0.28
Archaea;Euryarchaeota;Methanomicrobia; Methanosarcinales;Unclassified;sf_1;2215	-0.34		0.35	0.23				0.34
Archaea;Euryarchaeota;SAGMEG-1; Unclassified;Unclassified;sf_1;2195	-0.25		0.35					0.33
Archaea;Euryarchaeota;Thermococci; Thermococcales;Thermococcaceae;sf_1;2240		0.25	0.38					
Archaea;Euryarchaeota;Thermoplasmata; E2;terrestrial group;sf_2;2204			0.29				-0.28	
Archaea;Euryarchaeota;Thermoplasmata;Thermoplasmatales;Cplasma;sf_1;2198	-0.37		0.33	0.21				0.36
Archaea;Euryarchaeota;Thermoplasmata; Thermoplasmatales;Unclassified;sf_1;2265		0.28	0.32					
Archaea;Euryarchaeota;Thermoplasmata; Unclassified;Unclassified;sf_1;2303								-0.22
Bacteria;Acidobacteria;Acidobacteria; Acidobacteriales;Acidobacteriaceae;sf_1;6371	0.34	0.36						-0.33
Bacteria;Acidobacteria;Acidobacteria; Acidobacteriales;Acidobacteriaceae;sf_1;877							0.39	
Bacteria;Acidobacteria;Acidobacteria; Acidobacteriales;Acidobacteriaceae;sf_14;401	-0.38		0.20		0.30		0.25	0.37
Bacteria;Acidobacteria;Acidobacteria; Acidobacteriales;Acidobacteriaceae;sf_14;6390		0.25	0.27					
Bacteria;Acidobacteria;Acidobacteria; Acidobacteriales;Acidobacteriaceae;sf_14;6438	-0.25	0.20	0.25	0.20				
Bacteria;Acidobacteria;Acidobacteria; Acidobacteriales;Acidobacteriaceae;sf_16;6414		-0.27	-0.33	-0.21				-0.20
Bacteria;Acidobacteria;Acidobacteria; Acidobacteriales;Acidobacteriaceae;sf_6;6362		-0.30	-0.36				0.24	
Bacteria;Acidobacteria;Acidobacteria; Holophagales;Unclassified;sf_1;734		-0.27	-0.28	-0.20				

Gene	SM	NH4	NO3	K	Na	EOC	MPB	VPB
Bacteria;Acidobacteria;Acidobacteria-10;Unclassified;Unclassified;sf_1;516	0.30		-0.34	-0.22				-0.29
Bacteria;Acidobacteria;Acidobacteria-4;Ellin6075/11-25;Unclassified;sf_1;435	-0.31	-0.43	-0.21				0.45	
Bacteria;Acidobacteria;Acidobacteria-4;Unclassified;Unclassified;sf_1;6455	-0.32							0.30
Bacteria;Acidobacteria;Acidobacteria-4;Unclassified;Unclassified;sf_1;654	-0.51		0.23					0.29
Bacteria;Acidobacteria;Acidobacteria-5;Unclassified;Unclassified;sf_1;523	0.22		-0.26	-0.21				
Bacteria;Acidobacteria;Acidobacteria-6;Unclassified;Unclassified;sf_1;102			0.12		0.21			
Bacteria;Acidobacteria;Acidobacteria-6;Unclassified;Unclassified;sf_1;517		0.37	0.27			0.21		
Bacteria;Acidobacteria;Acidobacteria-6;Unclassified;Unclassified;sf_1;990							0.28	
Bacteria;Acidobacteria;Acidobacteria-7;Unclassified;Unclassified;sf_1;113	-0.49	-0.21					0.31	0.26
Bacteria;Acidobacteria;Acidobacteria-7;Unclassified;Unclassified;sf_1;151		0.55				0.21		-0.24
Bacteria;Acidobacteria;Acidobacteria-9;Unclassified;Unclassified;sf_1;704		-0.28	-0.28					
Bacteria;Acidobacteria;Solibacteres;Unclassified;Unclassified;sf_1;6329	-0.41		0.39	0.31	-0.34			
Bacteria;Acidobacteria;Solibacteres;Unclassified;Unclassified;sf_1;6375		0.42	0.36	0.25	-0.26	0.22	-0.20	
Bacteria;Acidobacteria;Solibacteres;Unclassified;Unclassified;sf_1;6386	-0.27	0.24	0.28	0.27				
Bacteria;Acidobacteria;Solibacteres;Unclassified;Unclassified;sf_1;6444	-0.24	0.26	0.31	0.29				
Bacteria;Acidobacteria;Unclassified;Unclassified;Unclassified;sf_1;572		-0.31	-0.36	-0.26				
Bacteria;Actinobacteria;Actinobacteria;Acidimicrobiales;Acidimicrobiaceae;sf_1;1478		0.45	0.34	0.22				
Bacteria;Actinobacteria;Actinobacteria;Acidimicrobiales;Acidimicrobiaceae;sf_1;1524		0.47	0.39	0.24				
Bacteria;Actinobacteria;Actinobacteria;Acidimicrobiales;Acidimicrobiaceae;sf_1;1532		0.46	0.49	0.29		0.20	-0.28	
Bacteria;Actinobacteria;Actinobacteria;Acidimicrobiales;Microthrixineae;sf_1;2028	0.21	0.55	0.30				-0.25	
Bacteria;Actinobacteria;Actinobacteria;Acidimicrobiales;Microthrixineae;sf_12;1721	-0.26	0.28	0.42	0.36	-0.26		-0.36	
Bacteria;Actinobacteria;Actinobacteria;Acidimicrobiales;Unclassified;sf_1;1100		0.47	0.49	0.26		0.21	-0.23	
Bacteria;Actinobacteria;Actinobacteria;Acidimicrobiales;Unclassified;sf_2;1811		0.37	0.36				-0.43	
Bacteria;Actinobacteria;Actinobacteria;		-0.21	-0.29	-0.23				-0.20

Gene	SM	NH4	NO3	K	Na	EOC	MPB	VPB
Actinomycetales;Acidothermaceae;sf_1;1399								
Bacteria;Actinobacteria;Actinobacteria; Actinomycetales;Actinomycetaceae;sf_1;1672	-0.34	0.24	0.49	0.43			-0.20	
Bacteria;Actinobacteria;Actinobacteria; Actinomycetales;Actinosynnemataceae;sf_1;1126	-0.48		0.48	0.34				
Bacteria;Actinobacteria;Actinobacteria; Actinomycetales;Actinosynnemataceae;sf_1;1951	-0.46		0.30	0.43				0.36
Bacteria;Actinobacteria;Actinobacteria; Actinomycetales;Actinosynnemataceae;sf_1;1984	-0.29	0.29	0.70	0.36			-0.28	
Bacteria;Actinobacteria;Actinobacteria; Actinomycetales;Brevibacteriaceae;sf_1;1745		0.36	0.23	0.30	-0.22		-0.39	
Bacteria;Actinobacteria;Actinobacteria; Actinomycetales;Cellulomonadaceae;sf_1;1592		0.39	0.49	0.36			-0.29	
Bacteria;Actinobacteria;Actinobacteria; Actinomycetales;Cellulomonadaceae;sf_1;2061	-0.21	0.35	0.47	0.31				
Bacteria;Actinobacteria;Actinobacteria; Actinomycetales;Corynebacteriaceae;sf_1;1332	-0.26	0.23	0.47	0.29		0.24		
Bacteria;Actinobacteria;Actinobacteria; Actinomycetales;Dermabacteraceae;sf_1;1736	-0.37		0.47	0.40		0.21		0.25
Bacteria;Actinobacteria;Actinobacteria; Actinomycetales;Dermatophilaceae;sf_1;1852	-0.23	0.38	0.37	0.36			-0.26	
Bacteria;Actinobacteria;Actinobacteria; Actinomycetales;Dietziaceae;sf_1;1143	-0.27	0.31	0.44	0.32		0.24		
Bacteria;Actinobacteria;Actinobacteria; Actinomycetales;Frankiaceae;sf_1;1286			-0.28					
Bacteria;Actinobacteria;Actinobacteria; Actinomycetales;Geodermatophilaceae;sf_1;1245		0.43	0.56	0.36			-0.30	
Bacteria;Actinobacteria;Actinobacteria; Actinomycetales;Geodermatophilaceae;sf_1;1973		0.42	0.53	0.38			-0.31	
Bacteria;Actinobacteria;Actinobacteria; Actinomycetales;Gordoniaceae;sf_1;1209	-0.26	0.34	0.48	0.36		0.21	-0.22	
Bacteria;Actinobacteria;Actinobacteria; Actinomycetales;Intrasporangiaceae;sf_1;1935		0.41	0.42	0.35			-0.40	
Bacteria;Actinobacteria;Actinobacteria; Actinomycetales;Kineosporiaceae;sf_1;2015	-0.31	0.25	0.48	0.39		0.22	-0.21	
Bacteria;Actinobacteria;Actinobacteria; Actinomycetales;Kribbella;sf_1;1839	-0.29	0.27	0.49	0.38			-0.27	
Bacteria;Actinobacteria;Actinobacteria; Actinomycetales;Microbacteriaceae;sf_1;1098	-0.41	-0.25		0.31		0.25		
Bacteria;Actinobacteria;Actinobacteria; Actinomycetales;Microbacteriaceae;sf_1;1507	-0.29	0.28	0.46	0.38		0.21	-0.22	
Bacteria;Actinobacteria;Actinobacteria; Actinomycetales;Microbacteriaceae;sf_1;1513	-0.34	0.29	0.44	0.51	-0.27	0.25	-0.21	
Bacteria;Actinobacteria;Actinobacteria; Actinomycetales;Microbacteriaceae;sf_1;1550	-0.30	0.35	0.46	0.58	-0.36	0.27	-0.33	
Bacteria;Actinobacteria;Actinobacteria; Actinomycetales;Microbacteriaceae;sf_1;1705	-0.35	0.28	0.46	0.45		0.26	-0.23	

Gene	SM	NH4	NO3	K	Na	EOC	MPB	VPB
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Microbacteriaceae;sf_1;1946	-0.42		0.24	0.40				0.25
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Microbacteriaceae;sf_1;1974		0.49	0.52	0.42			-0.36	
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Microbacteriaceae;sf_1;2044	-0.27	0.25	0.39	0.36		0.20		
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Micrococcaceae;sf_1;1099	-0.20	0.34	0.41	0.29		0.28		
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Micrococcaceae;sf_1;1452		0.37	0.50	0.30			-0.24	
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Micromonosporaceae;sf_1;1316	-0.38		0.51	0.43		0.21	-0.22	
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Micromonosporaceae;sf_1;1395	-0.29		0.43	0.38				
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Micromonosporaceae;sf_1;1462	-0.28	0.23	0.61	0.34			-0.24	
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Micromonosporaceae;sf_1;1572		0.33	0.48	0.34			-0.22	
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Micromonosporaceae;sf_1;1821		0.36	0.53	0.35			-0.31	
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Micromonosporaceae;sf_1;1847		0.49	0.49	0.23			-0.39	
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Micromonosporaceae;sf_1;1876	-0.20	0.39	0.49	0.30		0.22	-0.21	
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Micromonosporaceae;sf_1;1997		0.40	0.56	0.29			-0.32	
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Mycobacteriaceae;sf_1;1093	-0.27	0.26	0.61	0.35			-0.27	
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Nocardiaceae;sf_1;1142		0.43	0.43	0.39			-0.28	
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Nocardiaceae;sf_1;1788	-0.29		0.23	0.27		0.22		
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Nocardiaceae;sf_1;1861	-0.21	0.27	0.39	0.30		0.22		
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Nocardiaceae;sf_1;1999		0.43	0.49	0.31			-0.25	
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Nocardioidaceae;sf_1;1854	-0.23			0.24			-0.31	0.26
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Nocardiopsaceae;sf_1;1385	0.22				-0.22		-0.33	
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Promicromonosporaceae;sf_1;1671		0.30		0.26	-0.24		-0.42	
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Propionibacteriaceae;sf_1;1315	-0.32	0.34	0.41	0.42		0.21		
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Propionibacteriaceae;sf_1;2023	-0.34	0.28	0.53	0.37		0.22	-0.20	
Bacteria;Actinobacteria;Actinobacteria;	-0.29		0.75	0.32			-0.20	

Gene	SM	NH4	NO3	K	Na	EOC	MPB	VPB
Actinomycetales;Pseudonocardiaceae;sf_1;1326								
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Pseudonocardiaceae;sf_1;1388		0.39	0.51	0.22			-0.20	
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Pseudonocardiaceae;sf_1;1932		0.33	0.57	0.30			-0.26	
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Pseudonocardiaceae;sf_3;1362	-0.21	0.36	0.49	0.29				
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Sporichthyaceae;sf_1;1223	-0.28	0.31	0.61	0.36			-0.27	
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Sporichthyaceae;sf_1;1701		0.45	0.60	0.29			-0.32	
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Streptomycetaceae;sf_1;1128	-0.32		0.59	0.36			-0.23	
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Streptomycetaceae;sf_1;1697		0.30	0.32			0.26		
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Streptomycetaceae;sf_1;1841	-0.33	0.21	0.54	0.39			-0.21	
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Streptomycetaceae;sf_3;1743	-0.25	0.39	0.43	0.37			-0.24	
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Streptosporangiaceae;sf_1;1224		0.41	0.40	0.36			-0.38	
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Thermomonosporaceae;sf_1;1406	-0.27	0.39	0.57	0.39			-0.31	
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Thermomonosporaceae;sf_1;2043	-0.45		0.22	0.31		0.21		0.26
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Unclassified;sf_3;1114		0.32	0.57	0.31			-0.29	
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Unclassified;sf_3;1252		0.41	0.41	0.34			-0.22	
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Unclassified;sf_3;1369		0.40	0.48	0.33			-0.27	
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Unclassified;sf_3;1410	-0.34	0.22	0.36	0.41		0.23		
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Unclassified;sf_3;1514	-0.27		0.40	0.31				0.23
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Unclassified;sf_3;1806	-0.23	0.39	0.51	0.30		0.20	-0.20	
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Unclassified;sf_4;1337		-0.39	-0.32	-0.22			0.21	
Bacteria;Actinobacteria;Actinobacteria;Bifidobacteriales;Bifidobacteriaceae;sf_1;1444		-0.27						-0.22
Bacteria;Actinobacteria;Actinobacteria;Coriobacteriales;Coriobacteriaceae;sf_1;1800		-0.25	-0.27	-0.20				
Bacteria;Actinobacteria;Actinobacteria;Rubrobacterales;Rubrobacteraceae;sf_1;1107	-0.29		0.37	0.30		0.22		
Bacteria;Actinobacteria;Actinobacteria;Rubrobacterales;Rubrobacteraceae;sf_1;1480		0.46	0.49	0.37	-0.23	0.28	-0.37	

Gene	SM	NH4	NO3	K	Na	EOC	MPB	VPB
Bacteria;Actinobacteria;Actinobacteria;Rubrobacterales;Rubrobacteraceae;sf_1;1536	-0.27	0.34	0.48	0.37		0.23	-0.27	
Bacteria;Actinobacteria;Actinobacteria;Rubrobacterales;Rubrobacteraceae;sf_1;1762		0.42	0.45			0.21	-0.22	
Bacteria;Actinobacteria;Actinobacteria;ubrobacterales;Rubrobacteraceae;sf_1;1919		0.45	0.43				-0.37	
Bacteria;Actinobacteria;Actinobacteria;Rubrobacterales;Rubrobacteraceae;sf_1;1980	-0.26	0.29	0.53	0.35				
Bacteria;Actinobacteria;Actinobacteria;Unclassified;Unclassified;sf_1;1118	-0.36		0.32	0.38		0.27		
Bacteria;Actinobacteria;Actinobacteria;Unclassified;Unclassified;sf_1;1283	-0.30	0.34	0.48	0.38		0.22		
Bacteria;Actinobacteria;Actinobacteria;Unclassified;Unclassified;sf_1;1407	-0.27	0.30	0.51	0.34				
Bacteria;Actinobacteria;Actinobacteria;Unclassified;Unclassified;sf_1;1490	-0.35	0.22	0.41	0.35		0.27		
Bacteria;Actinobacteria;Actinobacteria;Unclassified;Unclassified;sf_1;1588	-0.27	0.39	0.48	0.36		0.20	-0.22	
Bacteria;Actinobacteria;Actinobacteria;Unclassified;Unclassified;sf_1;1848	-0.33			0.20				
Bacteria;Actinobacteria;Actinobacteria;Unclassified;Unclassified;sf_2;1233	0.24	0.31					-0.36	
Bacteria;Actinobacteria;BD2-10 group;Unclassified;Unclassified;sf_1;1732		-0.37	-0.27	-0.20				
Bacteria;Actinobacteria;BD2-10 group;Unclassified;Unclassified;sf_2;1652							-0.23	
Bacteria;AD3;Unclassified;Unclassified;Unclassified;sf_1;2338			-0.21		-0.25		-0.25	
Bacteria;Aquificae;Aquificae;Aquificales;Hydrogenothermaceae;sf_1;737		0.21	0.34					
Bacteria;Aquificae;Aquificae;Aquificales;Unclassified;sf_1;2364	0.30	0.21					-0.24	
Bacteria;Bacteroidetes;Bacteroidetes;Bacteroidales;Bacteroidaceae;sf_12;5950	0.23	0.49	0.44				-0.28	
Bacteria;Bacteroidetes;Bacteroidetes;Bacteroidales;Bacteroidaceae;sf_6;5792		0.29			0.32			
Bacteria;Bacteroidetes;Bacteroidetes;Bacteroidales;Porphyromonadaceae;sf_1;5454		-0.33	-0.32	-0.26				
Bacteria;Bacteroidetes;Bacteroidetes;Bacteroidales;Prevotellaceae;sf_1;5946	-0.20						0.25	
Bacteria;Bacteroidetes;Bacteroidetes;Bacteroidales;Prevotellaceae;sf_1;6118		0.25	0.37					0.22
Bacteria;Bacteroidetes;Bacteroidetes;Bacteroidales;Prevotellaceae;sf_1;6152	-0.20		0.33					
Bacteria;Bacteroidetes;Bacteroidetes;Bacteroidales;Prevotellaceae;sf_1;6259	-0.33							0.32
Bacteria;Bacteroidetes;Bacteroidetes;		-0.35	-0.28				0.22	

Gene	SM	NH4	NO3	K	Na	EOC	MPB	VPB
Bacteroidales;Rikenellaceae;sf_5;5892								
Bacteria;Bacteroidetes;Bacteroidetes; Bacteroidales;Unclassified;sf_15;5874		-0.33	-0.29	-0.21				
Bacteria;Bacteroidetes;Flavobacteria; Flavobacteriales;Blattabacteriaceae;sf_1;5828		-0.39	-0.31	-0.21			0.20	
Bacteria;Bacteroidetes;Flavobacteria; Flavobacteriales;Cryomorphaceae;sf_1;5400								
Bacteria;Bacteroidetes;Flavobacteria; Flavobacteriales;Flavobacteriaceae;sf_1;5339							0.22	
Bacteria;Bacteroidetes;Flavobacteria; Flavobacteriales;Flavobacteriaceae;sf_1;5341		0.48	0.28			0.23		
Bacteria;Bacteroidetes;Flavobacteria; Flavobacteriales;Flavobacteriaceae;sf_1;5362		-0.25					0.33	
Bacteria;Bacteroidetes;Flavobacteria; Flavobacteriales;Flavobacteriaceae;sf_1;5490	0.25	0.56	0.26				-0.22	
Bacteria;Bacteroidetes;Flavobacteria; Flavobacteriales;Flavobacteriaceae;sf_1;5559								
Bacteria;Bacteroidetes;Flavobacteria; Flavobacteriales;Flavobacteriaceae;sf_1;5588	0.49	0.56					-0.26	-0.41
Bacteria;Bacteroidetes;Flavobacteria; Flavobacteriales;Flavobacteriaceae;sf_1;5636	0.22	0.31						
Bacteria;Bacteroidetes;Flavobacteria; Flavobacteriales;Flavobacteriaceae;sf_1;5847	0.27	0.45						
Bacteria;Bacteroidetes;Flavobacteria; Flavobacteriales;Flavobacteriaceae;sf_1;5918	-0.41						0.22	0.32
Bacteria;Bacteroidetes;Flavobacteria; Flavobacteriales;Flavobacteriaceae;sf_1;5933	0.20	0.41						
Bacteria;Bacteroidetes;Flavobacteria; Flavobacteriales;Flavobacteriaceae;sf_1;6077	0.31	0.50						
Bacteria;Bacteroidetes;Flavobacteria; Flavobacteriales;Flavobacteriaceae;sf_1;6200	0.23	0.52						
Bacteria;Bacteroidetes;Flavobacteria; Flavobacteriales;Flavobacteriaceae;sf_1;6241		0.34	0.20			0.25		
Bacteria;Bacteroidetes;Flavobacteria; Flavobacteriales;Flavobacteriaceae;sf_1;6251		0.43				0.29		
Bacteria;Bacteroidetes;Flavobacteria; Flavobacteriales;Unclassified;sf_3;5248		-0.34	-0.36	-0.26			0.21	
Bacteria;Bacteroidetes;KSA1; Unclassified;Unclassified;sf_1;5951		-0.47	-0.35				0.37	
Bacteria;Bacteroidetes;Sphingobacteria; Sphingobacteriales;Crenotrichaceae;sf_11;5266		0.41	0.41	0.25				
Bacteria;Bacteroidetes;Sphingobacteria; Sphingobacteriales;Crenotrichaceae;sf_11;5283							0.23	
Bacteria;Bacteroidetes;Sphingobacteria; Sphingobacteriales;Crenotrichaceae;sf_11;5288		0.51	0.48					
Bacteria;Bacteroidetes;Sphingobacteria; Sphingobacteriales;Crenotrichaceae;sf_11;5381		0.46	0.34					

Gene	SM	NH4	NO3	K	Na	EOC	MPB	VPB
Bacteria;Bacteroidetes;Sphingobacteria; Sphingobacteriales;Crenotrichaceae;sf_11;5387		0.48	0.37			0.24	-0.20	
Bacteria;Bacteroidetes;Sphingobacteria; Sphingobacteriales;Crenotrichaceae;sf_11;5449		0.45	0.30					
Bacteria;Bacteroidetes;Sphingobacteria; Sphingobacteriales;Crenotrichaceae;sf_11;5491		0.47	0.39					
Bacteria;Bacteroidetes;Sphingobacteria; Sphingobacteriales;Crenotrichaceae;sf_11;5581		0.54	0.40					
Bacteria;Bacteroidetes;Sphingobacteria; Sphingobacteriales;Crenotrichaceae;sf_11;5722		0.35	0.32					
Bacteria;Bacteroidetes;Sphingobacteria; Sphingobacteriales;Crenotrichaceae;sf_11;5872		0.32	0.41	0.21				
Bacteria;Bacteroidetes;Sphingobacteria; Sphingobacteriales;Crenotrichaceae;sf_11;5925		0.49	0.34	0.30		0.23	-0.23	
Bacteria;Bacteroidetes;Sphingobacteria; Sphingobacteriales;Crenotrichaceae;sf_11;5948			0.32	0.21				
Bacteria;Bacteroidetes;Sphingobacteria; Sphingobacteriales;Crenotrichaceae;sf_11;5987		0.52	0.43			0.20		
Bacteria;Bacteroidetes;Sphingobacteria; Sphingobacteriales;Crenotrichaceae;sf_11;6003		0.28	0.39					
Bacteria;Bacteroidetes;Sphingobacteria; Sphingobacteriales;Crenotrichaceae;sf_11;6148	-0.23			0.20		0.24		
Bacteria;Bacteroidetes;Sphingobacteria; Sphingobacteriales;Crenotrichaceae;sf_11;6150	-0.22	0.31	0.42	0.21				
Bacteria;Bacteroidetes;Sphingobacteria; Sphingobacteriales;Crenotrichaceae;sf_11;6167		0.32	0.41	0.21			-0.20	
Bacteria;Bacteroidetes;Sphingobacteria; Sphingobacteriales;Crenotrichaceae;sf_11;6196	-0.24							0.20
Bacteria;Bacteroidetes;Sphingobacteria; Sphingobacteriales;Crenotrichaceae;sf_11;6281	-0.43		0.38	0.30		0.25		0.24
Bacteria;Bacteroidetes;Sphingobacteria; Sphingobacteriales;Crenotrichaceae;sf_11;6325			0.24		0.22			
Bacteria;Bacteroidetes;Sphingobacteria; Sphingobacteriales;Flammeovirgaceae;sf_5;6084		-0.32	-0.23	-0.24	0.28		0.56	
Bacteria;Bacteroidetes;Sphingobacteria; Sphingobacteriales;Flexibacteraceae;sf_10;5253		-0.43	-0.21				0.43	
Bacteria;Bacteroidetes;Sphingobacteria; Sphingobacteriales;Flexibacteraceae;sf_19;5805		0.24	0.20					
Bacteria;Bacteroidetes;Sphingobacteria; Sphingobacteriales;Flexibacteraceae;sf_19;6054		0.28	0.31					
Bacteria;Bacteroidetes;Sphingobacteria; Sphingobacteriales;Flexibacteraceae;sf_19;6217	-0.26					0.24		
Bacteria;Bacteroidetes;Sphingobacteria; Sphingobacteriales;Flexibacteraceae;sf_19;6304		0.25			0.39			
Bacteria;Bacteroidetes;Sphingobacteria; Sphingobacteriales;Flexibacteraceae;sf_20;10311		-0.37	-0.28	-0.27			0.32	
Bacteria;Bacteroidetes;Sphingobacteria;		0.49	0.21					

Gene	**SM**	**NH4**	**NO3**	**K**	**Na**	**EOC**	**MPB**	**VPB**
Sphingobacteriales;Sphingobacteriaceae;sf_1;5614								
Bacteria;Bacteroidetes;Sphingobacteria; Sphingobacteriales;Sphingobacteriaceae;sf_1;5840		0.34	0.29	0.29	-0.22	0.23		
Bacteria;Bacteroidetes;Sphingobacteria; Sphingobacteriales;Sphingobacteriaceae;sf_1;5858		0.40	0.29	0.20		0.27		
Bacteria;Bacteroidetes;Sphingobacteria; Sphingobacteriales;Sphingobacteriaceae;sf_1;6273		0.61	0.21		-0.20		-0.23	-0.24
Bacteria;Bacteroidetes;Sphingobacteria; Sphingobacteriales;Unclassified;sf_3;6168		-0.44	-0.37	-0.24			0.25	
Bacteria;Bacteroidetes;Sphingobacteria; Sphingobacteriales;Unclassified;sf_6;5439		-0.44	-0.37	-0.25			0.24	
Bacteria;Bacteroidetes;Unclassified; Unclassified;Unclassified;sf_4;5785		-0.47	-0.36	-0.22			0.33	
Bacteria;Bacteroidetes;Unclassified; Unclassified;Unclassified;sf_9;5519		0.38	0.29					
Bacteria;BRC1;Unclassified; Unclassified;Unclassified;sf_1;5051		-0.43	-0.36	-0.24			0.26	
Bacteria;BRC1;Unclassified; Unclassified;Unclassified;sf_2;118		-0.32	-0.32	-0.24				
Bacteria;Caldithrix;Unclassified; Caldithrales;Caldithraceae;sf_1;2384	0.25	-0.20	-0.28	-0.28		-0.22		-0.25
Bacteria;Caldithrix;Unclassified; Caldithrales;Caldithraceae;sf_2;91		-0.30					0.48	
Bacteria;Chlamydiae;Chlamydiae; Chlamydiales;Chlamydiaceae;sf_1;4820		-0.44	-0.32				0.34	
Bacteria;Chlamydiae;Chlamydiae; Chlamydiales;Parachlamydiaceae;sf_1;4964		-0.26	-0.28	-0.25			0.25	-0.25
Bacteria;Chlamydiae;Chlamydiae; Chlamydiales;Simkaniaceae;sf_1;4702		-0.39	-0.20				0.28	
Bacteria;Chlorobi;Chlorobia; Chlorobiales;Chlorobiaceae;sf_1;995	0.28						-0.36	
Bacteria;Chlorobi;Unclassified; Unclassified;Unclassified;sf_1;5928		-0.21		-0.21			0.30	
Bacteria;Chlorobi;Unclassified; Unclassified;Unclassified;sf_6;5294		-0.48	-0.30				0.40	
Bacteria;Chlorobi;Unclassified; Unclassified;Unclassified;sf_8;549	0.27						-0.32	
Bacteria;Chlorobi;Unclassified; Unclassified;Unclassified;sf_9;6146	0.05	-0.34	-0.36	-0.26				
Bacteria;Chloroflexi;Anaerolineae; Chloroflexi-1a;Unclassified;sf_1;86	-0.29	0.24	0.24	0.22		0.29		
Bacteria;Chloroflexi;Anaerolineae; Chloroflexi-1b;Unclassified;sf_1;1071								-0.20
Bacteria;Chloroflexi;Anaerolineae; Chloroflexi-1b;Unclassified;sf_2;789	-0.38						0.22	
Bacteria;Chloroflexi;Anaerolineae; Chloroflexi-1b;Unclassified;sf_3;432			0.28					

Gene	SM	NH4	NO3	K	Na	EOC	MPB	VPB
Bacteria;Chloroflexi;Anaerolineae; Chloroflexi-1f;Unclassified;sf_1;765								
Bacteria;Chloroflexi;Anaerolineae; Unclassified;Unclassified;sf_1;266	0.37		-0.29	-0.29		-0.24		-0.27
Bacteria;Chloroflexi;Anaerolineae; Unclassified;Unclassified;sf_7;8542		0.40	0.47		-0.21		-0.38	
Bacteria;Chloroflexi;Anaerolineae; Unclassified;Unclassified;sf_9;188	-0.21		0.35					
Bacteria;Chloroflexi;Chloroflexi-3; Roseiflexales;Unclassified;sf_5;119		0.23	0.29				-0.37	
Bacteria;Chloroflexi;Chloroflexi-4; Unclassified;Unclassified;sf_2;2532	0.35		-0.21	-0.21				-0.33
Bacteria;Chloroflexi;Dehalococcoidetes; Unclassified;Unclassified;sf_1;2438		-0.31	-0.30	-0.22				
Bacteria;Chloroflexi;Thermomicrobia; Unclassified;Unclassified;sf_1;1041		0.18			-0.28		-0.30	
Bacteria;Chloroflexi;Thermomicrobia; Unclassified;Unclassified;sf_2;652	-0.35	-0.33					0.24	
Bacteria;Chloroflexi;Unclassified; Unclassified;Unclassified;sf_1;2534	0.25						-0.27	-0.21
Bacteria;Chloroflexi;Unclassified; Unclassified;Unclassified;sf_12;2523	0.41					-0.22	-0.24	-0.44
Bacteria;Chloroflexi;Unclassified; Unclassified;Unclassified;sf_2;818		-0.33	-0.22	-0.29			0.23	
Bacteria;Chloroflexi;Unclassified; Unclassified;Unclassified;sf_5;1051	0.29		-0.28	-0.35		-0.22		-0.36
Bacteria;Chloroflexi;Unclassified; Unclassified;Unclassified;sf_7;757	0.38				-0.20		-0.29	-0.30
Bacteria;Coprothermobacteria;Unclassified; Unclassified;Unclassified;sf_1;751		-0.29	-0.24	-0.32			0.20	
Bacteria;Cyanobacteria;Cyanobacteria; Chloroplasts;Chloroplasts;sf_11;5123		-0.46	-0.35	-0.20			0.34	
Bacteria;Cyanobacteria;Cyanobacteria; Chloroplasts;Chloroplasts;sf_13;5000			0.21	0.25			-0.25	0.24
Bacteria;Cyanobacteria;Cyanobacteria; Chloroplasts;Chloroplasts;sf_5;5026			0.38	0.25				
Bacteria;Cyanobacteria;Cyanobacteria; Chloroplasts;Chloroplasts;sf_5;5158	-0.30		0.25	0.20		0.21		0.29
Bacteria;Cyanobacteria;Cyanobacteria; Chroococcales;Unclassified;sf_1;5219	-0.35		0.43	0.20				0.28
Bacteria;Cyanobacteria;Cyanobacteria; Geitlerinema;Unclassified;sf_1;4999	-0.24		0.27					
Bacteria;Cyanobacteria;Cyanobacteria; Leptolyngbya;Unclassified;sf_1;5157		0.52	0.45					
Bacteria;Cyanobacteria;Cyanobacteria; Nostocales;Unclassified;sf_1;5057								0.31
Bacteria;Cyanobacteria;Cyanobacteria;		0.59	0.22				-0.22	

Gene	SM	NH4	NO3	K	Na	EOC	MPB	VPB
Oscillatoriales;Unclassified;sf_1;5159								
Bacteria;Cyanobacteria;Cyanobacteria;Phormidium;Unclassified;sf_1;4978	-0.31		0.31					0.28
Bacteria;Cyanobacteria;Cyanobacteria;Plectonema;Unclassified;sf_1;5190	-0.23	-0.30	-0.20					0.24
Bacteria;Cyanobacteria;Cyanobacteria;Prochlorales;Unclassified;sf_1;5001	0.20						-0.29	
Bacteria;Cyanobacteria;Cyanobacteria;Pseudanabaena;Unclassified;sf_1;5008	-0.38	-0.22	0.22					0.24
Bacteria;Cyanobacteria;Cyanobacteria;Scytonema;Unclassified;sf_1;5115	-0.29		0.27	0.21				0.33
Bacteria;Cyanobacteria;Cyanobacteria;Spirulina;Unclassified;sf_1;5034	-0.32		0.42					0.22
Bacteria;Cyanobacteria;Cyanobacteria;Symploca;Unclassified;sf_1;5165		0.36	0.53	0.23			-0.24	
Bacteria;Cyanobacteria;Cyanobacteria;Thermosynechococcus;Unclassified;sf_1;5029	-0.27		0.57	0.20			-0.24	
Bacteria;Cyanobacteria;Unclassified;Unclassified;Unclassified;sf_5;4991	-0.35		0.39	0.23				0.26
Bacteria;Cyanobacteria;Unclassified;Unclassified;Unclassified;sf_5;4995	-0.39		0.51	0.22				0.30
Bacteria;Cyanobacteria;Unclassified;Unclassified;Unclassified;sf_5;5087			0.52				-0.20	
Bacteria;Cyanobacteria;Unclassified;Unclassified;Unclassified;sf_5;5104	-0.21	0.31	0.57	0.27			-0.25	
Bacteria;Cyanobacteria;Unclassified;Unclassified;Unclassified;sf_5;5204			0.35					
Bacteria;Cyanobacteria;Unclassified;Unclassified;Unclassified;sf_6;5186		0.38	0.35					
Bacteria;Cyanobacteria;Unclassified;Unclassified;Unclassified;sf_8;5206								0.32
Bacteria;Cyanobacteria;Unclassified;Unclassified;Unclassified;sf_9;5164			0.28					0.23
Bacteria;Deferribacteres;Deferribacer;Unclassified;Unclassified;sf_1;797	-0.24					0.20	0.25	
Bacteria;Deinococcus-Thermus;Unclassified;Unclassified;Unclassified;sf_1;563		-0.27	-0.21	-0.24				
Bacteria;Deinococcus-Thermus;Unclassified;Unclassified;Unclassified;sf_2;637	-0.25						0.30	0.21
Bacteria;Deinococcus-Thermus;Unclassified;Unclassified;Unclassified;sf_3;920		-0.36					0.22	
Bacteria;Dictyoglomi;Dictyoglomi;Dictyoglomales;Dictyoglomaceae;sf_9;7579		-0.25					0.24	
Bacteria;DSS1;Unclassified;Unclassified;Unclassified;sf_1;4405		-0.41	-0.33					
Bacteria;DSS1;Unclassified;Unclassified;Unclassified;sf_2;38	-0.39						0.22	0.30

Gene	SM	NH4	NO3	K	Na	EOC	MPB	VPB
Bacteria;Fibrobacteres;Fibrobacteres;Fibrobacterales;Fibrobacteraceae;sf_1;6422		0.25			-0.41		-0.38	
Bacteria;Firmicutes;Anaerobranca;Unclassified;Unclassified;sf_1;4304	0.21	-0.20						-0.27
Bacteria;Firmicutes;Bacilli;Bacillales;Alicyclobacillaceae;sf_1;3368		0.34	0.25				-0.25	
Bacteria;Firmicutes;Bacilli;Bacillales;Bacillaceae;sf_1;3262	-0.37			0.21				0.26
Bacteria;Firmicutes;Bacilli;Bacillales;Bacillaceae;sf_1;3388	-0.32			0.26				
Bacteria;Firmicutes;Bacilli;Bacillales;Bacillaceae;sf_1;3454		0.32	0.42	0.22			-0.21	
Bacteria;Firmicutes;Bacilli;Bacillales;Bacillaceae;sf_1;3484	-0.26		0.26	0.24				
Bacteria;Firmicutes;Bacilli;Bacillales;Bacillaceae;sf_1;3626		0.34	0.36					
Bacteria;Firmicutes;Bacilli;Bacillales;Bacillaceae;sf_1;3650		-0.31	-0.26					-0.26
Bacteria;Firmicutes;Bacilli;Bacillales;Bacillaceae;sf_1;3656		0.41	0.43				-0.33	
Bacteria;Firmicutes;Bacilli;Bacillales;Bacillaceae;sf_1;3689	-0.31		0.39	0.31				
Bacteria;Firmicutes;Bacilli;Bacillales;Bacillaceae;sf_1;3733	-0.30		0.21	0.25				0.24
Bacteria;Firmicutes;Bacilli;Bacillales;Bacillaceae;sf_1;3878	-0.29		0.30	0.34				
Bacteria;Firmicutes;Bacilli;Bacillales;Bacillaceae;sf_1;3893	-0.37		0.50	0.31				0.26
Bacteria;Firmicutes;Bacilli;Bacillales;Bacillaceae;sf_1;3898		0.20	0.34	0.20				
Bacteria;Firmicutes;Bacilli;Bacillales;Bacillaceae;sf_1;3926	-0.20		0.33	0.22				
Bacteria;Firmicutes;Bacilli;Bacillales;Caryophanaceae;sf_1;3285	-0.47	-0.46						0.28
Bacteria;Firmicutes;Bacilli;Bacillales;Halobacillaceae;sf_1;3554	-0.41		0.27	0.31				0.27
Bacteria;Firmicutes;Bacilli;Bacillales;Paenibacillaceae;sf_1;3254	-0.30		0.35	0.24				0.24
Bacteria;Firmicutes;Bacilli;Bacillales;Paenibacillaceae;sf_1;3731	-0.21		0.34			0.22		0.29
Bacteria;Firmicutes;Bacilli;Bacillales;Paenibacillaceae;sf_1;3735	-0.29						0.23	0.22
Bacteria;Firmicutes;Bacilli;Bacillales;Paenibacillaceae;sf_1;3793	-0.23						0.29	
Bacteria;Firmicutes;Bacilli;Bacillales;Sporolactobacillaceae;sf_1;3747	-0.44	-0.22						0.32
Bacteria;Firmicutes;Bacilli;	-0.28	-0.22						0.28

Gene	SM	NH4	NO3	K	Na	EOC	MPB	VPB
Bacillales;Staphylococcaceae;sf_1;3638								
Bacteria;Firmicutes;Bacilli; Bacillales;Thermoactinomycetaceae;sf_1;3539							0.32	
Bacteria;Firmicutes;Bacilli; Bacillales;Unclassified;sf_3;3743	-0.23	-0.49	-0.28				0.35	
Bacteria;Firmicutes;Bacilli; Lactobacillales;Aerococcaceae;sf_1;3553	-0.42	-0.26		0.30				0.30
Bacteria;Firmicutes;Bacilli; Lactobacillales;Aerococcaceae;sf_1;3736	-0.30	-0.37	-0.21				0.43	
Bacteria;Firmicutes;Bacilli; Lactobacillales;Aerococcaceae;sf_1;3866	-0.35		0.49	0.34	-0.22	0.20		
Bacteria;Firmicutes;Bacilli; Lactobacillales;Carnobacteriaceae;sf_1;3536	-0.36	-0.55					0.33	0.28
Bacteria;Firmicutes;Bacilli; Lactobacillales;Enterococcaceae;sf_1;3433		-0.44	-0.30					
Bacteria;Firmicutes;Bacilli; Lactobacillales;Lactobacillaceae;sf_1;3599			0.32	0.23				
Bacteria;Firmicutes;Bacilli; Lactobacillales;Lactobacillaceae;sf_1;3600		0.53	0.39	0.20		0.21	-0.24	
Bacteria;Firmicutes;Bacilli; Lactobacillales;Leuconostocaceae;sf_1;3286	-0.34							0.21
Bacteria;Firmicutes;Bacilli; Lactobacillales;Streptococcaceae;sf_1;3436	-0.24		0.54	0.24				
Bacteria;Firmicutes;Bacilli; Lactobacillales;Unclassified;sf_1;3434	-0.31		0.22					0.24
Bacteria;Firmicutes;Catabacter; Unclassified;Unclassified;sf_1;4293	0.00	-0.32	-0.26					
Bacteria;Firmicutes;Catabacter; Unclassified;Unclassified;sf_4;2716	0.04	-0.23	-0.26					
Bacteria;Firmicutes;Clostridia; Clostridiales;Clostridiaceae;sf_1;4227	-0.26	0.37	0.35					
Bacteria;Firmicutes;Clostridia; Clostridiales;Clostridiaceae;sf_12;4359	0.22	-0.22	-0.30	-0.20				
Bacteria;Firmicutes;Clostridia; Clostridiales;Clostridiaceae;sf_21;4471	0.28		-0.21					
Bacteria;Firmicutes;Clostridia; Clostridiales;Eubacteriaceae;sf_1;28								
Bacteria;Firmicutes;Clostridia; Clostridiales;Lachnospiraceae;sf_5;2708	0.36	0.59	0.24				-0.26	-0.36
Bacteria;Firmicutes;Clostridia; Clostridiales;Lachnospiraceae;sf_5;2728		0.44	0.30			0.21		
Bacteria;Firmicutes;Clostridia; Clostridiales;Lachnospiraceae;sf_5;2747		0.45	0.25					
Bacteria;Firmicutes;Clostridia; Clostridiales;Lachnospiraceae;sf_5;3007							0.21	
Bacteria;Firmicutes;Clostridia; Clostridiales;Lachnospiraceae;sf_5;3078		0.48	0.45	0.24			-0.21	

Gene	SM	NH4	NO3	K	Na	EOC	MPB	VPB
Bacteria;Firmicutes;Clostridia; Clostridiales;Lachnospiraceae;sf_5;3107		0.46	0.40	0.25		0.21		
Bacteria;Firmicutes;Clostridia; Clostridiales;Lachnospiraceae;sf_5;4164	-0.23	0.30	0.55	0.25				
Bacteria;Firmicutes;Clostridia; Clostridiales;Lachnospiraceae;sf_5;4316	-0.20						0.20	
Bacteria;Firmicutes;Clostridia; Clostridiales;Peptococc/Acidaminococc;sf_11;185		0.31	0.24					
Bacteria;Firmicutes;Clostridia; Clostridiales;Peptococc/Acidaminococc;sf_11;2473		0.57	0.41				-0.29	
Bacteria;Firmicutes;Clostridia; Clostridiales;Peptococc/Acidaminococc;sf_11;49	-0.25	0.29	0.52	0.25		0.20		
Bacteria;Firmicutes;Clostridia; Clostridiales;Peptococc/Acidaminococc;sf_11;903	-0.24	0.26	0.26	0.31	-0.22	0.30		
Bacteria;Firmicutes;Clostridia; Clostridiales;Peptostreptococcaceae;sf_5;2913			-0.20					
Bacteria;Firmicutes;Clostridia; Clostridiales;Syntrophomonadaceae;sf_5;2456		-0.32	-0.38	-0.28				
Bacteria;Firmicutes;Clostridia; Clostridiales;Unclassified;sf_17;2659			0.26					-0.33
Bacteria;Firmicutes;Clostridia; Unclassified;Unclassified;sf_3;4280	0.24		-0.27	-0.23		-0.22		-0.24
Bacteria;Firmicutes;Clostridia; Unclassified;Unclassified;sf_4;2398		-0.40	-0.39	-0.28		-0.21		
Bacteria;Firmicutes;Clostridia; Unclassified;Unclassified;sf_7;4216	0.29						-0.23	
Bacteria;Firmicutes;Desulfotomaculum; Unclassified;Unclassified;sf_1;894	-0.21	0.36	0.43	0.32		0.22		
Bacteria;Firmicutes;gut clone group; Unclassified;Unclassified;sf_1;4616					-0.38		-0.31	
Bacteria;Firmicutes;Mollicutes; Acholeplasmatales;Acholeplasmataceae;sf_1;4084		0.48	0.48	0.21				
Bacteria;Firmicutes;Mollicutes; Anaeroplasmatales;Erysipelotrichaceae;sf_3;3981		-0.56	-0.41	-0.21			0.37	
Bacteria;Firmicutes;Mollicutes; Entomoplasmatales;Entomoplasmataceae;sf_1;4074	-0.42			0.27		0.23		0.28
Bacteria;Firmicutes;Mollicutes; Mycoplasmatales;Mycoplasmataceae;sf_1;3929		-0.46	-0.33				0.33	
Bacteria;Firmicutes;Mollicutes; Unclassified;Unclassified;sf_6;149							-0.25	0.20
Bacteria;Firmicutes;Symbiobacteria; Symbiobacterales;Unclassified;sf_1;2388		-0.40	-0.38	-0.22			0.26	
Bacteria;Firmicutes;Symbiobacteria; Symbiobacterales;Unclassified;sf_3;3508		-0.38	-0.22	-0.20				
Bacteria;Firmicutes;Unclassified; Unclassified;Unclassified;sf_8;2433	0.27		-0.31	-0.21				
Bacteria;Gemmatimonadetes;Unclassified;		-0.34	-0.22				0.25	

Gene	SM	NH4	NO3	K	Na	EOC	MPB	VPB
Unclassified;Unclassified;sf_5;2047								
Bacteria;Gemmatimonadetes;Unclassified; Unclassified;Unclassified;sf_6;2554							-0.25	
Bacteria;LD1PA group;Unclassified; Unclassified;Unclassified;sf_1;10118		-0.47	-0.33	-0.26			0.32	
Bacteria;Lentisphaerae;Unclassified; Unclassified;Unclassified;sf_5;9704		-0.25	-0.41	-0.22				
Bacteria;marine group A;mgA-1; Unclassified;Unclassified;sf_1;6454		0.24	0.30					
Bacteria;marine group A;mgA-2; Unclassified;Unclassified;sf_1;6344		-0.27	-0.21	-0.22				
Bacteria;Natronoanaerobium;Unclassified; Unclassified;Unclassified;sf_1;2437		-0.37	-0.34	-0.22				
Bacteria;NC10;NC10-1; Unclassified;Unclassified;sf_1;452	0.35		-0.28	-0.24		-0.21		-0.24
Bacteria;NC10;NC10-2; Unclassified;Unclassified;sf_1;10254	0.21						-0.20	
Bacteria;NC10;Unclassified; Unclassified;Unclassified;sf_1;2516	0.27		-0.28	-0.23				-0.20
Bacteria;Nitrospira;Nitrospira; Nitrospirales;Nitrospiraceae;sf_1;860	0.21	0.36			0.30			
Bacteria;Nitrospira;Nitrospira; Nitrospirales;Nitrospiraceae;sf_2;542	0.29		-0.25	-0.21		-0.21		-0.22
Bacteria;Nitrospira;Nitrospira; Nitrospirales;Nitrospiraceae;sf_3;240			0.41	0.21				
Bacteria;OD1;OP11-5; Unclassified;Unclassified;sf_1;515		0.29	0.37					
Bacteria;OP10;CH21 cluster; Unclassified;Unclassified;sf_1;308	-0.29	0.30	0.49	0.23		0.22	-0.21	
Bacteria;OP10;Unclassified; Unclassified;Unclassified;sf_1;8413							-0.24	-0.35
Bacteria;OP10;Unclassified; Unclassified;Unclassified;sf_4;484	0.21				-0.24		-0.37	
Bacteria;OP10;Unclassified; Unclassified;Unclassified;sf_5;9782	0.37					-0.20	-0.25	-0.34
Bacteria;OP11;Unclassified; Unclassified;Unclassified;sf_5;650		0.57	0.34				-0.21	
Bacteria;OP3;Unclassified; Unclassified;Unclassified;sf_3;1015		0.39					-0.28	
Bacteria;OP3;Unclassified; Unclassified;Unclassified;sf_4;628		-0.28	-0.32	-0.21				-0.24
Bacteria;OP8;Unclassified; Unclassified;Unclassified;sf_3;598	-0.20	-0.47	-0.30				0.40	
Bacteria;OP9/JS1;JS1 ;Unclassified;Unclassified;sf_1;2489	0.20	-0.30	-0.35	-0.26		-0.20		-0.22
Bacteria;OP9/JS1;OP9; Unclassified;Unclassified;sf_1;726		-0.43	-0.33	-0.21			0.30	

Gene	SM	NH4	NO3	K	Na	EOC	MPB	VPB
Bacteria;OS-K;Unclassified;Unclassified;Unclassified;sf_1;501							0.21	
Bacteria;Planctomycetes;Planctomycetacia;Planctomycetales;Anammoxales;sf_2;4683		-0.37	-0.25	-0.21				
Bacteria;Planctomycetes;Planctomycetacia;Planctomycetales;Anammoxales;sf_4;4694	0.25	-0.20	-0.24	-0.31		-0.21		-0.28
Bacteria;Planctomycetes;Planctomycetacia;Planctomycetales;Gemmatae;sf_1;4719	-0.55		0.37	0.36		0.29		0.30
Bacteria;Planctomycetes;Planctomycetacia;Planctomycetales;Gemmatae;sf_1;4843	-0.47			0.22				0.29
Bacteria;Planctomycetes;Planctomycetacia;Planctomycetales;Gemmatae;sf_1;4852	-0.63		0.28	0.35		0.28		0.37
Bacteria;Planctomycetes;Planctomycetacia;Planctomycetales;Gemmatae;sf_1;4857	-0.58		0.31	0.37		0.28		0.29
Bacteria;Planctomycetes;Planctomycetacia;Planctomycetales;Gemmatae;sf_1;4866	-0.55		0.33	0.32		0.30		0.30
Bacteria;Planctomycetes;Planctomycetacia;Planctomycetales;Gemmatae;sf_1;4925	-0.60		0.21	0.35		0.29		0.32
Bacteria;Planctomycetes;Planctomycetacia;Planctomycetales;Gemmatae;sf_1;4959	-0.60		0.33	0.34		0.27		0.33
Bacteria;Planctomycetes;Planctomycetacia;Planctomycetales;Isosphaerae;sf_1;4829	-0.59		0.32	0.49	-0.25	0.32		0.24
Bacteria;Planctomycetes;Planctomycetacia;Planctomycetales;Isosphaerae;sf_1;4846	-0.48		0.30	0.39		0.30		0.21
Bacteria;Planctomycetes;Planctomycetacia;Planctomycetales;Pirellulae;sf_3;4687	-0.51		0.31	0.26		0.20		0.34
Bacteria;Planctomycetes;Planctomycetacia;Planctomycetales;Pirellulae;sf_3;4726	-0.57		0.25	0.29		0.25		0.37
Bacteria;Planctomycetes;Planctomycetacia;Planctomycetales;Pirellulae;sf_3;4738	-0.47		0.39	0.31		0.26		0.31
Bacteria;Planctomycetes;Planctomycetacia;Planctomycetales;Pirellulae;sf_3;4744	-0.58	-0.28		0.20			0.21	0.39
Bacteria;Planctomycetes;Planctomycetacia;Planctomycetales;Pirellulae;sf_3;4754	-0.56		0.33	0.23		0.26		0.37
Bacteria;Planctomycetes;Planctomycetacia;Planctomycetales;Pirellulae;sf_3;4782	-0.52		0.38	0.26		0.28		0.33
Bacteria;Planctomycetes;Planctomycetacia;Planctomycetales;Pirellulae;sf_3;4833	-0.45		0.47	0.27		0.25		0.23
Bacteria;Planctomycetes;Planctomycetacia;Planctomycetales;Pirellulae;sf_3;4894	-0.52		0.24	0.23		0.23		0.38
Bacteria;Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;sf_3;4654	-0.41		0.37	0.22		0.20		0.32
Bacteria;Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;sf_3;4682	-0.40	0.25	0.33	0.24		0.20		0.26
Bacteria;Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;sf_3;4759	-0.30	0.33	0.37	0.25		0.20		
Bacteria;Planctomycetes;Planctomycetacia;	-0.58		0.28	0.34		0.30		0.31

Gene	**SM**	**NH4**	**NO3**	**K**	**Na**	**EOC**	**MPB**	**VPB**
Planctomycetales;Planctomycetaceae;sf_3;4821								
Bacteria;Planctomycetes;Planctomycetacia; Planctomycetales;Planctomycetaceae;sf_3;4858	-0.38		0.33	0.35		0.28		
Bacteria;Planctomycetes;Planctomycetacia; Planctomycetales;Planctomycetaceae;sf_3;4873	-0.60		0.38	0.32		0.30		0.28
Bacteria;Planctomycetes;Planctomycetacia; Planctomycetales;Planctomycetaceae;sf_3;4933	-0.50		0.20	0.21		0.26		0.29
Bacteria;Planctomycetes;Planctomycetacia; Planctomycetales;Planctomycetaceae;sf_4;4859	-0.50		0.36	0.29		0.26		0.28
Bacteria;Planctomycetes;Planctomycetacia; Planctomycetales;Planctomycetaceae;sf_5;4940	-0.60		0.30	0.46	-0.28	0.33		0.24
Bacteria;Planctomycetes;Planctomycetacia; Planctomycetales;Unclassified;sf_6;4655	-0.52		0.30	0.38		0.27		0.26
Bacteria;Planctomycetes;Planctomycetacia; Planctomycetales;Unclassified;sf_6;4661	-0.53		0.29	0.35		0.26		0.30
Bacteria;Planctomycetes;Planctomycetacia; Planctomycetales;Unclassified;sf_6;4785	-0.55		0.31	0.36		0.28		0.30
Bacteria;Planctomycetes;Planctomycetacia; Planctomycetales;Unclassified;sf_6;4871	-0.53		0.33	0.34		0.31		0.27
Bacteria;Planctomycetes;Planctomycetacia; Planctomycetales;Unclassified;sf_6;4932	-0.55		0.36	0.37		0.29		0.31
Bacteria;Planctomycetes;Planctomycetacia; Planctomycetales;Unclassified;sf_6;4961	-0.65		0.24	0.38		0.29		0.33
Bacteria;Planctomycetes;Planctomycetacia; WPS-1;Unclassified;sf_1;4897	0.35	0.21					-0.23	
Bacteria;Proteobacteria;Alphaproteobacteria; Acetobacterales;Acetobacteraceae;sf_1;6841	-0.33	0.23	0.54	0.37			-0.23	
Bacteria;Proteobacteria;Alphaproteobacteria; Acetobacterales;Acetobacteraceae;sf_1;7080	-0.31	0.32	0.55	0.37			-0.24	
Bacteria;Proteobacteria;Alphaproteobacteria; Acetobacterales;Acetobacteraceae;sf_1;7408		0.31	0.53	0.31			-0.26	
Bacteria;Proteobacteria;Alphaproteobacteria; Acetobacterales;Acetobacteraceae;sf_1;7414	-0.33		0.52	0.33			-0.20	0.22
Bacteria;Proteobacteria;Alphaproteobacteria; Acetobacterales;Acetobacteraceae;sf_1;7565		0.52	0.47	0.36	-0.26	0.26	-0.35	
Bacteria;Proteobacteria;Alphaproteobacteria; Acetobacterales;Acetobacteraceae;sf_1;7623	-0.30	0.28	0.52	0.35		0.24	-0.22	
Bacteria;Proteobacteria;Alphaproteobacteria; Acetobacterales;Roseococcaceae;sf_1;6708	-0.52		0.44	0.34		0.24		0.28
Bacteria;Proteobacteria;Alphaproteobacteria; Acetobacterales;Roseococcaceae;sf_1;6856		0.36	0.35	0.26		0.25		
Bacteria;Proteobacteria;Alphaproteobacteria; Acetobacterales;Roseococcaceae;sf_1;7106	-0.48	0.25	0.36	0.53	-0.24	0.32	-0.22	0.21
Bacteria;Proteobacteria;Alphaproteobacteria; Acetobacterales;Unclassified;sf_1;6961		0.42	0.39	0.26		0.21	-0.21	
Bacteria;Proteobacteria;Alphaproteobacteria; Acetobacterales;Unclassified;sf_1;7387	-0.26		0.25					

Gene	SM	NH4	NO3	K	Na	EOC	MPB	VPB
Bacteria;Proteobacteria;Alphaproteobacteria;Acetobacterales;Unclassified;sf_1;7475		0.49	0.40	0.20			-0.22	
Bacteria;Proteobacteria;Alphaproteobacteria;Azospirillales;Azospirillaceae;sf_1;7539		-0.23	-0.20		0.23			0.20
Bacteria;Proteobacteria;Alphaproteobacteria;Azospirillales;Magnetospirillaceae;sf_1;6922		0.34	0.31					0.22
Bacteria;Proteobacteria;Alphaproteobacteria;Azospirillales;Unclassified;sf_1;6905		0.32	0.28			0.20		
Bacteria;Proteobacteria;Alphaproteobacteria;Azospirillales;Unclassified;sf_1;7632		0.49	0.40			0.23	-0.20	
Bacteria;Proteobacteria;Alphaproteobacteria;Bradyrhizobiales;Beijerinck/Rhodoplan/Methylocyst;sf_3;6721		0.39	0.39					
Bacteria;Proteobacteria;Alphaproteobacteria;Bradyrhizobiales;Beijerinck/Rhodoplan/Methylocyst;sf_3;6722		0.46	0.49				-0.34	
Bacteria;Proteobacteria;Alphaproteobacteria Bradyrhizobiales;Beijerinck/Rhodoplan/Methylocyst;sf_3;6731		0.44	0.42			0.20		
Bacteria;Proteobacteria;Alphaproteobacteria;Bradyrhizobiales;Beijerinck/Rhodoplan/Methylocyst;sf_3;6780	-0.20	0.36	0.54	0.28		0.21	-0.26	
Bacteria;Proteobacteria;Alphaproteobacteria;Bradyrhizobiales;Beijerinck/Rhodoplan/Methylocyst;sf_3;6826	-0.31	0.22	0.43	0.30				0.21
Bacteria;Proteobacteria;Alphaproteobacteria;Bradyrhizobiales;Beijerinck/Rhodoplan/Methylocyst;sf_3;7117		0.47	0.48	0.21			-0.26	
Bacteria;Proteobacteria;Alphaproteobacteria;Bradyrhizobiales;Beijerinck/Rhodoplan/Methylocyst;sf_3;7228		0.44	0.32				-0.26	
Bacteria;Proteobacteria;Alphaproteobacteria;Bradyrhizobiales;Beijerinck/Rhodoplan/Methylocyst;sf_3;7261	-0.24	0.28	0.44	0.24			-0.29	0.26
Bacteria;Proteobacteria;Alphaproteobacteria;Bradyrhizobiales;Beijerinck/Rhodoplan/Methylocyst;sf_3;7495	-0.32	0.23	0.41	0.27			-0.24	0.22
Bacteria;Proteobacteria;Alphaproteobacteria;Bradyrhizobiales;Beijerinck/Rhodoplan/Methylocyst;sf_3;7620	-0.24	0.35	0.51	0.29			-0.26	
Bacteria;Proteobacteria;Alphaproteobacteria;Bradyrhizobiales;Bradyrhizobiaceae;sf_1;6942	-0.29	0.28	0.40	0.25		0.23		0.20
Bacteria;Proteobacteria;Alphaproteobacteria;Bradyrhizobiales;Bradyrhizobiaceae;sf_1;7077	-0.27	0.35	0.56	0.38			-0.26	
Bacteria;Proteobacteria;Alphaproteobacteria;Bradyrhizobiales;Bradyrhizobiaceae;sf_1;7078	0.31						-0.39	-0.29
Bacteria;Proteobacteria;Alphaproteobacteria;Bradyrhizobiales;Bradyrhizobiaceae;sf_1;7328		0.38	0.54				-0.25	
Bacteria;Proteobacteria;Alphaproteobacteria;Bradyrhizobiales;Hyphomicrobiaceae;sf_1;7530	-0.38		0.28	0.21				0.30
Bacteria;Proteobacteria;Alphaproteobacteria;Bradyrhizobiales;Methylobacteriaceae;sf_1;6744	-0.26	-0.52	-0.23				0.37	
Bacteria;Proteobacteria;Alphaproteobacteria;Bradyrhizobiales;Methylobacteriaceae;sf_1;6782		0.37	0.48	0.31			-0.22	
Bacteria;Proteobacteria;Alphaproteobacteria;Bradyrhizobiales;Methylobacteriaceae;sf_1;7269		0.38	0.28	0.24	-0.28		-0.40	
Bacteria;Proteobacteria;Alphaproteobacteria;	-0.32	0.32	0.54	0.34		0.26	-0.21	

Gene	SM	NH4	NO3	K	Na	EOC	MPB	VPB
Bradyrhizobiales;Methylobacteriaceae;sf_1;7593								
Bacteria;Proteobacteria;Alphaproteobacteria;Bradyrhizobiales;Unclassified;sf_1;7255		0.48	0.47	0.24			-0.33	
Bacteria;Proteobacteria;Alphaproteobacteria;Bradyrhizobiales;Unclassified;sf_1;7306		0.27	0.39	0.29		0.20	-0.25	
Bacteria;Proteobacteria;Alphaproteobacteria;Bradyrhizobiales;Unclassified;sf_1;7557	-0.28	0.36	0.53	0.29		0.26	-0.29	
Bacteria;Proteobacteria;Alphaproteobacteria;Bradyrhizobiales;Xanthobacteraceae;sf_1;6855	-0.29	0.38	0.59	0.32		0.21	-0.30	
Bacteria;Proteobacteria;Alphaproteobacteria;Caulobacterales;Caulobacteraceae;sf_1;6929		0.47	0.32	0.20		0.20		
Bacteria;Proteobacteria;Alphaproteobacteria;Caulobacterales;Caulobacteraceae;sf_1;6930		0.58	0.49	0.26		0.25	-0.31	
Bacteria;Proteobacteria;Alphaproteobacteria;Caulobacterales;Caulobacteraceae;sf_1;6953	-0.34			0.26				0.24
Bacteria;Proteobacteria;Alphaproteobacteria;Caulobacterales;Caulobacteraceae;sf_1;7134		0.43	0.47	0.23			-0.21	
Bacteria;Proteobacteria;Alphaproteobacteria;Caulobacterales;Caulobacteraceae;sf_1;7245		0.63	0.31				-0.23	
Bacteria;Proteobacteria;Alphaproteobacteria;Caulobacterales;Caulobacteraceae;sf_1;7396		0.53	0.33					
Bacteria;Proteobacteria;Alphaproteobacteria;Caulobacterales;Caulobacteraceae;sf_1;7578		0.61	0.43	0.23		0.21	-0.26	
Bacteria;Proteobacteria;Alphaproteobacteria;Consistiales;Caedibacteraceae;sf_3;6807		0.47	0.27					
Bacteria;Proteobacteria;Alphaproteobacteria;Consistiales;Caedibacteraceae;sf_4;7157								
Bacteria;Proteobacteria;Alphaproteobacteria;Consistiales;Caedibacteraceae;sf_5;6947	0.40							
Bacteria;Proteobacteria;Alphaproteobacteria;Consistiales;SAR11;sf_2;7043		-0.36					0.20	-0.20
Bacteria;Proteobacteria;Alphaproteobacteria;Consistiales;Unclassified;sf_4;7105	-0.26	-0.40	-0.25				0.36	
Bacteria;Proteobacteria;Alphaproteobacteria;Consistiales;Unclassified;sf_5;7203	-0.22		0.22	0.24		0.26		
Bacteria;Proteobacteria;Alphaproteobacteria;Devosia;Unclassified;sf_1;7298	-0.23	0.37	0.63	0.31		0.25	-0.24	
Bacteria;Proteobacteria;Alphaproteobacteria;Devosia;Unclassified;sf_1;7626		0.24	0.54	0.31				
Bacteria;Proteobacteria;Alphaproteobacteria;Ellin314/wr0007;Unclassified;sf_1;7103		0.52	0.41					
Bacteria;Proteobacteria;Alphaproteobacteria;Ellin329/Riz1046;Unclassified;sf_1;6945	0.28		-0.28					-0.23
Bacteria;Proteobacteria;Alphaproteobacteria;Fulvimarina;Unclassified;sf_1;7281		0.32	0.41				-0.33	
Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Bartonellaceae;sf_1;7384		-0.36	-0.22					

Gene	SM	NH4	NO3	K	Na	EOC	MPB	VPB
Bacteria;Proteobacteria;Alphaproteobacteria; Rhizobiales;Beijerinck/Rhodoplan/Methylocyst;sf_1;7591	-0.22	-0.42	-0.28					
Bacteria;Proteobacteria;Alphaproteobacteria; Rhizobiales;Bradyrhizobiaceae;sf_1;6824		0.40	0.51	0.24			-0.32	
Bacteria;Proteobacteria;Alphaproteobacteria; Rhizobiales;Bradyrhizobiaceae;sf_1;7629		0.43	0.49	0.24			-0.27	
Bacteria;Proteobacteria;Alphaproteobacteria; Rhizobiales;Brucellaceae;sf_1;6995	0.21							-0.24
Bacteria;Proteobacteria;Alphaproteobacteria; Rhizobiales;Hyphomicrobiaceae;sf_1;6747		0.23	0.48					
Bacteria;Proteobacteria;Alphaproteobacteria; Rhizobiales;Hyphomicrobiaceae;sf_1;6787	-0.29	0.27	0.49	0.27			-0.22	
Bacteria;Proteobacteria;Alphaproteobacteria; Rhizobiales;Hyphomicrobiaceae;sf_1;7144	-0.20	0.24	0.48	0.22				
Bacteria;Proteobacteria;Alphaproteobacteria; Rhizobiales;Phyllobacteriaceae;sf_1;7416	0.33	0.51	0.38				-0.39	-0.28
Bacteria;Proteobacteria;Alphaproteobacteria; Rhizobiales;Rhizobiaceae;sf_1;6813		0.46	0.48	0.29		0.24	-0.26	
Bacteria;Proteobacteria;Alphaproteobacteria; Rhizobiales;Rhizobiaceae;sf_1;6861	-0.31	0.21	0.50	0.31			-0.24	0.30
Bacteria;Proteobacteria;Alphaproteobacteria; Rhizobiales;Rhizobiaceae;sf_1;7070	-0.23	0.21	0.57	0.29		0.26		
Bacteria;Proteobacteria;Alphaproteobacteria; Rhizobiales;Rhizobiaceae;sf_1;7457		0.57	0.40				-0.24	
Bacteria;Proteobacteria;Alphaproteobacteria; Rhizobiales;Rhodobiaceae;sf_1;6891		0.34	0.40	0.23		0.21		
Bacteria;Proteobacteria;Alphaproteobacteria; Rhizobiales;Unclassified;sf_1;6767	-0.29	0.21	0.63	0.21			-0.21	
Bacteria;Proteobacteria;Alphaproteobacteria; Rhizobiales;Unclassified;sf_1;6938		0.43	0.52	0.26			-0.35	
Bacteria;Proteobacteria;Alphaproteobacteria; Rhizobiales;Unclassified;sf_1;6969		0.35	0.51	0.22			-0.30	
Bacteria;Proteobacteria;Alphaproteobacteria; Rhizobiales;Unclassified;sf_1;7012		0.39	0.30			0.32		
Bacteria;Proteobacteria;Alphaproteobacteria; Rhizobiales;Unclassified;sf_1;7173		0.35	0.56	0.22			-0.45	
Bacteria;Proteobacteria;Alphaproteobacteria; Rhizobiales;Unclassified;sf_1;7249		0.47	0.42				-0.32	
Bacteria;Proteobacteria;Alphaproteobacteria; Rhodobacterales;Hyphomonadaceae;sf_1;7584	0.34							-0.35
Bacteria;Proteobacteria;Alphaproteobacteria; Rhodobacterales;Rhodobacteraceae;sf_1;6682		0.31	0.68	0.26			-0.25	
Bacteria;Proteobacteria;Alphaproteobacteria; Rhodobacterales;Rhodobacteraceae;sf_1;6743	-0.27							0.22
Bacteria;Proteobacteria;Alphaproteobacteria; Rhodobacterales;Rhodobacteraceae;sf_1;7021		0.54	0.47				-0.26	
Bacteria;Proteobacteria;Alphaproteobacteria;		0.47	0.55	0.23			-0.29	

Gene	SM	NH4	NO3	K	Na	EOC	MPB	VPB
Rhodobacterales;Rhodobacteraceae;sf_1;7241								
Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae;sf_1;7527		0.48	0.50	0.20			-0.25	
Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae;sf_1;7536		0.45	0.42	0.23				
Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Unclassified;sf_5;7471	0.32			-0.21				-0.28
Bacteria;Proteobacteria;Alphaproteobacteria;Rickettsiales;Anaplasmataceae;sf_3;6648		-0.30	-0.32					-0.21
Bacteria;Proteobacteria;Alphaproteobacteria;Rickettsiales;Rickettsiaceae;sf_1;7556		-0.49	-0.35				0.40	
Bacteria;Proteobacteria;Alphaproteobacteria;Rickettsiales;Unclassified;sf_1;7156	0.43						-0.22	
Bacteria;Proteobacteria;Alphaproteobacteria;Rickettsiales;Unclassified;sf_2;6639	-0.35	-0.20					0.36	0.31
Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;sf_1;6633	-0.30						0.25	
Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;sf_1;6666		0.55	0.42				-0.23	
Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;sf_1;6720		0.58	0.41				-0.23	
Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;sf_1;6800	0.29	0.59	0.25				-0.24	-0.27
Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;sf_1;6808		0.65	0.40			0.27	-0.29	
Bacteria;Proteobacteria;Alphaproteobacteria;phingomonadales;Sphingomonadaceae;sf_1;6839		0.57	0.44			0.20	-0.28	
Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;sf_1;6846	0.22	0.27			0.50			
Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;sf_1;6902		0.68	0.31				-0.28	
Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;sf_1;7011		0.62	0.38				-0.28	
Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;sf_1;7048		0.42	0.43	0.24				
Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;sf_1;7185		0.24						
Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;sf_1;7215	0.28	0.66	0.37				-0.33	
Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;sf_1;7289		0.29	0.24	0.23		0.23		
Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;sf_1;7344		0.75	0.39			0.25	-0.34	
Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;sf_1;7411				0.20				
Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;sf_1;7532	0.22						0.21	-0.21

Gene	SM	NH4	NO3	K	Na	EOC	MPB	VPB
Bacteria;Proteobacteria;Alphaproteobacteria; Sphingomonadales;Sphingomonadaceae;sf_1;7555	0.08	0.52	0.45				-0.23	
Bacteria;Proteobacteria;Alphaproteobacteria; Sphingomonadales;Sphingomonadaceae;sf_1;7570	0.23	0.61	0.25				-0.26	
Bacteria;Proteobacteria;Alphaproteobacteria; Sphingomonadales;Sphingomonadaceae;sf_1;7582								-0.29
Bacteria;Proteobacteria;Alphaproteobacteria; Sphingomonadales;Sphingomonadaceae;sf_15;7035	0.46	0.23					-0.27	-0.24
Bacteria;Proteobacteria;Alphaproteobacteria; Sphingomonadales;Unclassified;sf_1;7052		0.28	0.42	0.24				
Bacteria;Proteobacteria;Alphaproteobacteria; Unclassified;Unclassified;sf_2;7188	0.27	-0.30	-0.31	-0.27				-0.27
Bacteria;Proteobacteria;Alphaproteobacteria; Unclassified;Unclassified;sf_6;6685	-0.27	0.25	0.40	0.31		0.30		
Bacteria;Proteobacteria;Alphaproteobacteria; Unclassified;Unclassified;sf_6;6703		0.46	0.35	0.24		0.25		
Bacteria;Proteobacteria;Alphaproteobacteria; Unclassified;Unclassified;sf_6;6844	-0.38	0.29	0.52	0.42	-0.20	0.24	-0.22	
Bacteria;Proteobacteria;Alphaproteobacteria; Unclassified;Unclassified;sf_6;6970		0.57	0.37			0.21	-0.29	
Bacteria;Proteobacteria;Alphaproteobacteria; Unclassified;Unclassified;sf_6;7166	-0.32		0.26	0.25		0.24		0.21
Bacteria;Proteobacteria;Alphaproteobacteria; Unclassified;Unclassified;sf_6;7368		0.37	0.54	0.27		0.22	-0.25	
Bacteria;Proteobacteria;Alphaproteobacteria; Unclassified;Unclassified;sf_6;7399	-0.26	0.30	0.50	0.22				
Bacteria;Proteobacteria;Alphaproteobacteria; Unclassified;Unclassified;sf_6;7406		0.37	0.33		0.26			
Bacteria;Proteobacteria;Alphaproteobacteria; Unclassified;Unclassified;sf_6;7463		0.61	0.47	0.21		0.21	-0.31	
Bacteria;Proteobacteria;Alphaproteobacteria; Unclassified;Unclassified;sf_6;7534		0.49	0.40					
Bacteria;Proteobacteria;Alphaproteobacteria; Verorhodospirilla;Rhodospirillum;sf_1;7198	-0.28	0.20	0.35	0.23		0.25		0.22
Bacteria;Proteobacteria;Alphaproteobacteria; Verorhodospirilla;Unclassified;sf_1;6740	0.29			-0.21				-0.26
Bacteria;Proteobacteria;Betaproteobacteria; Burkholderiales;Alcaligenaceae;sf_1;7700		0.59	0.31	0.20		0.25		
Bacteria;Proteobacteria;Betaproteobacteria; Burkholderiales;Burkholderiaceae;sf_1;7848		0.28	0.29	0.21				0.21
Bacteria;Proteobacteria;Betaproteobacteria; Burkholderiales;Burkholderiaceae;sf_1;7899				0.22				
Bacteria;Proteobacteria;Betaproteobacteria; Burkholderiales;Burkholderiaceae;sf_1;7914		0.40						
Bacteria;Proteobacteria;Betaproteobacteria; Burkholderiales;Burkholderiaceae;sf_1;7918		0.26	0.32					
Bacteria;Proteobacteria;Betaproteobacteria;		0.37	0.35					

Gene	SM	NH4	NO3	K	Na	EOC	MPB	VPB
Burkholderiales;Burkholderiaceae;sf_1;7934								
Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;sf_1;7754		0.50	0.26					
Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;sf_1;7786		0.49	0.32					
Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;sf_1;7820		0.56	0.33					
Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;sf_1;7854		0.44	0.24			0.24		
Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;sf_1;7863		0.46	0.34			0.21		
Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;sf_1;7872		0.39	0.45			0.22		
Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;sf_1;7884	0.23	0.69	0.38				-0.29	
Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;sf_1;7894		0.53	0.38	0.22		0.21		
Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;sf_1;7905		0.55	0.32					
Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;sf_1;7920							0.24	
Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;sf_1;7937		0.54	0.31			0.20		
Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;sf_1;8028		0.58	0.24			0.21		
Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;sf_1;8047		0.39	0.43	0.30		0.22		
Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;sf_1;8065	0.30	0.20						
Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;sf_1;8070								
Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;sf_1;8075		0.53	0.24					
Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;sf_1;8083		0.48	0.34					
Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;sf_1;8102		0.29	0.30			0.20		
Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;sf_1;8117		0.44						
Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;sf_1;8162		0.39	0.27					
Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Oxalobacteraceae;sf_1;7883		0.44				0.27		
Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Oxalobacteraceae;sf_1;8124	0.45	0.55	0.23				-0.35	-0.32
Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Ralstoniaceae;sf_1;7755	0.24	0.56	0.31				-0.23	

Gene	SM	NH4	NO3	K	Na	EOC	MPB	VPB
Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Unclassified;sf_1;7727		0.61				0.20		
Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Unclassified;sf_1;7832		0.53	0.24					
Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Unclassified;sf_1;7850		0.39	0.22					
Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Unclassified;sf_1;7851		0.55	0.29					
Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Unclassified;sf_1;7879		0.34	0.37				-0.32	
Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Unclassified;sf_1;8038		0.57	0.25			0.21		
Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Unclassified;sf_1;8087		0.21						
Bacteria;Proteobacteria;Betaproteobacteria;Ellin6095/SC-I-39;Unclassified;sf_1;8093		0.49				0.20		
Bacteria;Proteobacteria;Betaproteobacteria;Ellin6095/SC-I-39;Unclassified;sf_1;8148	0.37							-0.34
Bacteria;Proteobacteria;Betaproteobacteria;Hydrogenophilales;Hydrogenophilaceae;sf_1;7953		0.35	0.29					
Bacteria;Proteobacteria;Betaproteobacteria;Hydrogenophilales;Hydrogenophilaceae;sf_2;8756		0.35	0.30	0.21				
Bacteria;Proteobacteria;Betaproteobacteria;Hydrogenophilales;Unclassified;sf_1;8151			-0.38				0.40	
Bacteria;Proteobacteria;Betaproteobacteria;Methylophilales;Methylophilaceae;sf_1;8050		0.33	0.45	0.20				
Bacteria;Proteobacteria;Betaproteobacteria;Methylophilales;Methylophilaceae;sf_1;8159		0.39	0.48	0.21			-0.24	
Bacteria;Proteobacteria;Betaproteobacteria;MND1 clone group;Unclassified;sf_1;7896	0.39	0.65					-0.29	-0.47
Bacteria;Proteobacteria;Betaproteobacteria;MND1 clone group;Unclassified;sf_1;8134		0.42	0.23					
Bacteria;Proteobacteria;Betaproteobacteria;Neisseriales;Neisseriaceae;sf_1;7867		0.47	0.38	0.23		0.20		
Bacteria;Proteobacteria;Betaproteobacteria;Neisseriales;Unclassified;sf_1;8037		0.45						
Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Nitrosomonadaceae;sf_1;8149	0.42	0.40					-0.24	
Bacteria;Proteobacteria;Betaproteobacteria;Procabacteriales;Procabacteriaceae;sf_1;8136							0.25	
Bacteria;Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae;sf_1;7666		0.56	0.28			0.27		
Bacteria;Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae;sf_1;7668								
Bacteria;Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae;sf_1;7692		0.40	0.21	0.28		0.26		
Bacteria;Proteobacteria;Betaproteobacteria;		-0.27	-0.25					

Gene	SM	NH4	NO3	K	Na	EOC	MPB	VPB
Rhodocyclales;Rhodocyclaceae;sf_1;7734								
Bacteria;Proteobacteria;Betaproteobacteria; Rhodocyclales;Rhodocyclaceae;sf_1;7753		0.58	0.22			0.26		
Bacteria;Proteobacteria;Betaproteobacteria; Rhodocyclales;Rhodocyclaceae;sf_1;7875		0.38						
Bacteria;Proteobacteria;Betaproteobacteria; Rhodocyclales;Rhodocyclaceae;sf_1;7956		-0.20	-0.23					-0.28
Bacteria;Proteobacteria;Betaproteobacteria; Rhodocyclales;Rhodocyclaceae;sf_1;7980	0.25	0.50						
Bacteria;Proteobacteria;Betaproteobacteria; Rhodocyclales;Unclassified;sf_3;8109	-0.40					0.24		0.25
Bacteria;Proteobacteria;Betaproteobacteria; Unclassified;Unclassified;sf_3;7679		0.38	0.22					
Bacteria;Proteobacteria;Betaproteobacteria; Unclassified;Unclassified;sf_3;7707		0.69	0.27					-0.21
Bacteria;Proteobacteria;Betaproteobacteria; Unclassified;Unclassified;sf_3;7723					0.21		0.26	
Bacteria;Proteobacteria;Betaproteobacteria; Unclassified;Unclassified;sf_3;8116		0.50	0.47				-0.20	
Bacteria;Proteobacteria;Deltaproteobacteria; AMD clone group;Unclassified;sf_1;3084	0.36		-0.27	-0.25		-0.24		-0.33
Bacteria;Proteobacteria;Deltaproteobacteria; Bdellovibrionales;Bdellovibrionaceae;sf_1;9748		0.55	0.28	0.25		0.25	-0.23	
Bacteria;Proteobacteria;Deltaproteobacteria; Bdellovibrionales;Bdellovibrionaceae;sf_2;10036		0.31	0.31					
Bacteria;Proteobacteria;Deltaproteobacteria; Bdellovibrionales;Unclassified;sf_1;7382		-0.39	-0.27				0.34	
Bacteria;Proteobacteria;Deltaproteobacteria; dechlorinating clone group;Unclassified;sf_1;9959		-0.34	-0.35	-0.26				
Bacteria;Proteobacteria;Deltaproteobacteria; Desulfobacterales;Desulfoarculaceae;sf_2;10227	0.28		-0.30	-0.23		-0.23		-0.23
Bacteria;Proteobacteria;Deltaproteobacteria; Desulfobacterales;Desulfobacteraceae;sf_5;10226						0.21		
Bacteria;Proteobacteria;Deltaproteobacteria; Desulfobacterales;Desulfobacteraceae;sf_5;10276	-0.21	-0.21					0.29	
Bacteria;Proteobacteria;Deltaproteobacteria; Desulfobacterales;Desulfobacteraceae;sf_5;9699		0.36	0.35	0.21		0.22		
Bacteria;Proteobacteria;Deltaproteobacteria; Desulfobacterales;Desulfobacteraceae;sf_5;9810		0.40	0.38	0.22				
Bacteria;Proteobacteria;Deltaproteobacteria; Desulfobacterales;Desulfobacteraceae;sf_5;9885							0.20	
Bacteria;Proteobacteria;Deltaproteobacteria; Desulfobacterales;Desulfobulbaceae;sf_1;10235		0.36	0.23					
Bacteria;Proteobacteria;Deltaproteobacteria; Desulfobacterales;Desulfobulbaceae;sf_1;9931		0.39	0.33					
Bacteria;Proteobacteria;Deltaproteobacteria; Desulfobacterales;Nitrospinaceae;sf_1;580	-0.22	-0.42	-0.26				0.40	

Gene	SM	NH4	NO3	K	Na	EOC	MPB	VPB
Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Nitrospinaceae;sf_2;594	0.30	-0.23	-0.32	-0.25		-0.24		-0.32
Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Unclassified;sf_3;9813	0.44		-0.25	-0.23		-0.27		-0.37
Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Unclassified;sf_4;9951		-0.37	-0.32	-0.23				
Bacteria;Proteobacteria;Deltaproteobacteria;Desulfovibrionales;Desulfohalobiaceae;sf_1;9894	0.30	-0.20	-0.24	-0.23				-0.26
Bacteria;Proteobacteria;Deltaproteobacteria;Desulfovibrionales;Desulfomicrobiaceae;sf_1;10079		-0.32	-0.34	-0.24				
Bacteria;Proteobacteria;Deltaproteobacteria;Desulfovibrionales;Desulfovibrionaceae;sf_1;10105		0.40	0.38					
Bacteria;Proteobacteria;Deltaproteobacteria;Desulfovibrionales;Desulfovibrionaceae;sf_1;10212		0.35	0.27	0.27				
Bacteria;Proteobacteria;Deltaproteobacteria;Desulfovibrionales;Desulfovibrionaceae;sf_1;10292		0.23						
Bacteria;Proteobacteria;Deltaproteobacteria;Desulfovibrionales;Unclassified;sf_1;9828	0.23	-0.21	-0.33	-0.21				-0.20
Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Desulfuromonaceae;sf_1;10020	0.22	-0.31	-0.33	-0.28		-0.25		-0.22
Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;sf_1;10176	-0.24	0.26	0.22	0.33	-0.22	0.22		
Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Unclassified;sf_1;10076		-0.30	-0.38	-0.24				
Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonales;Desulfuromonaceae;sf_1;10129		0.41	0.36					
Bacteria;Proteobacteria;Deltaproteobacteria;EB1021 group;Unclassified;sf_4;9884		-0.40	-0.36	-0.34			0.32	
Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Myxococcaceae;sf_1;10232	-0.25	-0.21					0.33	
Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Myxococcaceae;sf_1;10313		0.36	0.27					
Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Polyangiaceae;sf_3;10104		0.31	0.29	0.23				
Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Polyangiaceae;sf_3;9725		0.22	0.34	0.22				
Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Polyangiaceae;sf_4;9733			0.26		0.21			
Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Unclassified;sf_1;10092		-0.40	-0.28				0.27	
Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;sf_3;9665	0.33		-0.31	-0.26		-0.21		-0.28
Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;sf_1;9845	0.35	-0.20	-0.29	-0.24		-0.26		-0.40
Bacteria;Proteobacteria;Deltaproteobacteria;Unclassified;Unclassified;sf_7;10048		-0.23	-0.22					
Bacteria;Proteobacteria;Deltaproteobacteria;	-0.23	0.26	0.27					

Gene	SM	NH4	NO3	K	Na	EOC	MPB	VPB
Unclassified;Unclassified;sf_9;10174								
Bacteria;Proteobacteria;Deltaproteobacteria;Unclassified;Unclassified;sf_9;10185	0.21	0.37	0.34					-0.24
Bacteria;Proteobacteria;Deltaproteobacteria;Unclassified;Unclassified;sf_9;10206		0.22	0.22			0.20		
Bacteria;Proteobacteria;Deltaproteobacteria;Unclassified;Unclassified;sf_9;9786	-0.36		0.22					0.29
Bacteria;Proteobacteria;Deltaproteobacteria;Unclassified;Unclassified;sf_9;9859		0.31	0.36					
Bacteria;Proteobacteria;Deltaproteobacteria;Unclassified;Unclassified;sf_9;9911	-0.21	0.30	0.29	0.25		0.21		
Bacteria;Proteobacteria;Epsilonproteobacteria;Campylobacterales;Campylobacteraceae;sf_3;10474								-0.28
Bacteria;Proteobacteria;Epsilonproteobacteria;Campylobacterales;Helicobacteraceae;sf_23;10443		-0.26	-0.29	-0.21				-0.20
Bacteria;Proteobacteria;Epsilonproteobacteria;Campylobacterales;Helicobacteraceae;sf_3;10602		-0.29					0.34	
Bacteria;Proteobacteria;Epsilonproteobacteria;Campylobacterales;Helicobacteraceae;sf_5;10610							0.22	-0.27
Bacteria;Proteobacteria;Epsilonproteobacteria;Campylobacterales;Unclassified;sf_1;10384		0.49	0.46				-0.21	
Bacteria;Proteobacteria;Gammaproteobacteria;Acidithiobacillales;Acidithiobacillaceae;sf_1;8304		0.25	0.32			0.22		
Bacteria;Proteobacteria;Gammaproteobacteria;Acidithiobacillales;Acidithiobacillaceae;sf_1;9204		0.35	0.31	0.21				
Bacteria;Proteobacteria;Gammaproteobacteria;acidophile isolate group;Unclassified;sf_1;7909	0.37	0.34						
Bacteria;Proteobacteria;Gammaproteobacteria;Aeromonadales;Aeromonadaceae;sf_1;8621	0.30	0.31						
Bacteria;Proteobacteria;Gammaproteobacteria;Aeromonadales;Succinivibrionaceae;sf_1;8822	-0.38	-0.34					0.39	0.28
Bacteria;Proteobacteria;Gammaproteobacteria;Alteromonadales;Alteromonadaceae;sf_1;8517		0.47	0.32					
Bacteria;Proteobacteria;Gammaproteobacteria;Alteromonadales;Alteromonadaceae;sf_1;8768		0.38	0.25					
Bacteria;Proteobacteria;Gammaproteobacteria;Alteromonadales;Pseudoalteromonadaceae;sf_1;9339	0.20	0.38	0.25					-0.29
Bacteria;Proteobacteria;Gammaproteobacteria;Alteromonadales;Shewanellaceae;sf_1;8201	0.42							
Bacteria;Proteobacteria;Gammaproteobacteria;Alteromonadales;Unclassified;sf_1;8483		0.27	0.22	0.26				
Bacteria;Proteobacteria;Gammaproteobacteria;aquatic clone group;Unclassified;sf_1;9246	0.21	-0.26	-0.36	-0.26				
Bacteria;Proteobacteria;Gammaproteobacteria;Cardiobacteriales;Cardiobacteriaceae;sf_1;9453	0.20	-0.29	-0.46	-0.33			0.35	
Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Chromatiaceae;sf_1;9054	0.33			-0.20				-0.24

Gene	SM	NH4	NO3	K	Na	EOC	MPB	VPB
Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Ectothiorhodospiraceae;sf_1;8818		0.35	0.34			0.22		
Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Ectothiorhodospiraceae;sf_1;9155		0.30	0.27	0.22		0.21		
Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Ectothiorhodospiraceae;sf_11;8306		-0.27	-0.26	-0.24				-0.23
Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Halothiobacillaceae;sf_1;9181	0.22	-0.30	-0.44	-0.31			0.29	
Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Halothiobacillaceae;sf_3;9448		-0.31	-0.41	-0.26			0.35	
Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Unclassified;sf_1;9316		0.48	0.46			0.25		
Bacteria;Proteobacteria;Gammaproteobacteria;Ellin307/WD2124;Unclassified;sf_1;8423		0.49	0.24	0.20	-0.23	0.30		
Bacteria;Proteobacteria;Gammaproteobacteria;Ellin307/WD2124;Unclassified;sf_1;9374	-0.29			0.25				
Bacteria;Proteobacteria;Gammaproteobacteria;Enterobacteriales;Enterobacteriaceae;sf_1;1206							0.28	
Bacteria;Proteobacteria;Gammaproteobacteria;Enterobacteriales;Enterobacteriaceae;sf_1;8236							0.22	
Bacteria;Proteobacteria;Gammaproteobacteria;Enterobacteriales;Enterobacteriaceae;sf_1;8388	-0.30		0.27	0.26		0.23		0.29
Bacteria;Proteobacteria;Gammaproteobacteria;Enterobacteriales;Enterobacteriaceae;sf_1;8564		0.27	0.29					
Bacteria;Proteobacteria;Gammaproteobacteria;Enterobacteriales;Enterobacteriaceae;sf_1;8773	-0.21	0.29	0.47	0.27				
Bacteria;Proteobacteria;Gammaproteobacteria;Enterobacteriales;Enterobacteriaceae;sf_1;8864		0.52	0.41					
Bacteria;Proteobacteria;Gammaproteobacteria;Enterobacteriales;Enterobacteriaceae;sf_1;9276		0.28	0.40	0.22				
Bacteria;Proteobacteria;Gammaproteobacteria;Enterobacteriales;Enterobacteriaceae;sf_1;9337	-0.30		0.34	0.23				0.33
Bacteria;Proteobacteria;Gammaproteobacteria;Enterobacteriales;Enterobacteriaceae;sf_6;103		0.38	0.48				-0.24	
Bacteria;Proteobacteria;Gammaproteobacteria;Enterobacteriales;Unclassified;sf_1;8430	0.29	0.62	0.31				-0.21	
Bacteria;Proteobacteria;Gammaproteobacteria;GAO cluster;Unclassified;sf_1;8980		-0.31	-0.27				0.22	
Bacteria;Proteobacteria;Gammaproteobacteria;Legionellales;Coxiellaceae;sf_3;8378		0.32	0.39					
Bacteria;Proteobacteria;Gammaproteobacteria;Legionellales;Legionellaceae;sf_1;8193	0.43	0.54					-0.22	-0.34
Bacteria;Proteobacteria;Gammaproteobacteria;Legionellales;Legionellaceae;sf_1;8235		0.48	0.47	0.20			-0.23	
Bacteria;Proteobacteria;Gammaproteobacteria;Legionellales;Legionellaceae;sf_1;8372	-0.35					0.24		0.32
Bacteria;Proteobacteria;Gammaproteobacteria;	-0.39						0.29	0.32

Gene	SM	NH4	NO3	K	Na	EOC	MPB	VPB
Legionellales;Legionellaceae;sf_1;9079								
Bacteria;Proteobacteria;Gammaproteobacteria; Legionellales;Legionellaceae;sf_1;9146		0.32	0.26					
Bacteria;Proteobacteria;Gammaproteobacteria; Legionellales;Unclassified;sf_1;9418	0.28	-0.23	-0.32	-0.24				-0.23
Bacteria;Proteobacteria;Gammaproteobacteria; Legionellales;Unclassified;sf_3;8587	0.28	-0.28	-0.36	-0.30				
Bacteria;Proteobacteria;Gammaproteobacteria; Methylococcales;Methylococcaceae;sf_1;8250		0.21	0.24					
Bacteria;Proteobacteria;Gammaproteobacteria; Methylococcales;Methylococcaceae;sf_1;8418		0.50	0.33			0.24		
Bacteria;Proteobacteria;Gammaproteobacteria; Methylococcales;Methylococcaceae;sf_1;9313		0.32	0.39	0.24		0.25		
Bacteria;Proteobacteria;Gammaproteobacteria; Methylococcales;Unclassified;sf_1;9182		0.39	0.34				-0.36	
Bacteria;Proteobacteria;Gammaproteobacteria; Oceanospirillales;Halomonadaceae;sf_1;8331		0.42	0.34					
Bacteria;Proteobacteria;Gammaproteobacteria; Oceanospirillales;Oceanospirillaceae;sf_1;9351		-0.22			0.26		0.45	0.22
Bacteria;Proteobacteria;Gammaproteobacteria; Oceanospirillales;Saccharospirillaceae;sf_1;8889	-0.24	0.22	0.36					0.33
Bacteria;Proteobacteria;Gammaproteobacteria; Oceanospirillales;Unclassified;sf_3;8648			0.23		0.40			0.30
Bacteria;Proteobacteria;Gammaproteobacteria; Oceanospirillales;Unclassified;sf_3;8961	-0.30		0.50	0.29				
Bacteria;Proteobacteria;Gammaproteobacteria; Pasteurellales;Pasteurellaceae;sf_1;9237	-0.35	-0.44					0.39	0.26
Bacteria;Proteobacteria;Gammaproteobacteria; Pseudomonadales;Moraxellaceae;sf_3;9466		-0.38	-0.33	-0.25			0.24	
Bacteria;Proteobacteria;Gammaproteobacteria; Pseudomonadales;Pseudomonadaceae;sf_1;8288		0.53	0.40				-0.20	
Bacteria;Proteobacteria;Gammaproteobacteria; Pseudomonadales;Pseudomonadaceae;sf_1;8635		0.36	0.26			0.27		
Bacteria;Proteobacteria;Gammaproteobacteria; Pseudomonadales;Pseudomonadaceae;sf_1;9553		0.31	0.21					
Bacteria;Proteobacteria;Gammaproteobacteria; Pseudomonadales;Pseudomonadaceae;sf_1;9613		-0.38	-0.28				0.47	
Bacteria;Proteobacteria;Gammaproteobacteria; SAR86;Unclassified;sf_1;8962		-0.31	-0.24		0.20		0.21	
Bacteria;Proteobacteria;Gammaproteobacteria; Shewanella;Unclassified;sf_1;9344		0.21				0.21		0.24
Bacteria;Proteobacteria;Gammaproteobacteria; SUP05;Unclassified;sf_1;8654		-0.35	-0.34	-0.26			0.32	
Bacteria;Proteobacteria;Gammaproteobacteria; Symbionts;Unclassified;sf_1;9107		0.30	0.22	0.21		0.28		
Bacteria;Proteobacteria;Gammaproteobacteria; Thiotrichales;Francisellaceae;sf_1;9554	0.45	0.37						

Gene	SM	NH4	NO3	K	Na	EOC	MPB	VPB
Bacteria;Proteobacteria;Gammaproteobacteria;Thiotrichales;Piscirickettsiaceae;sf_3;9291	0.24							
Bacteria;Proteobacteria;Gammaproteobacteria;Thiotrichales;Thiotrichaceae;sf_3;8221		0.47	0.47	0.23			-0.28	
Bacteria;Proteobacteria;Gammaproteobacteria;Unclassified;Unclassified;sf_3;8291		0.48	0.37					
Bacteria;Proteobacteria;Gammaproteobacteria;Unclassified;Unclassified;sf_3;8391		0.44	0.25			0.23		
Bacteria;Proteobacteria;Gammaproteobacteria;Unclassified;Unclassified;sf_3;8551		0.40	0.34			0.27		
Bacteria;Proteobacteria;Gammaproteobacteria;Unclassified;Unclassified;sf_3;8566	-0.41		0.26	0.23		0.26		0.24
Bacteria;Proteobacteria;Gammaproteobacteria;Unclassified;Unclassified;sf_3;8674		0.22	0.30					0.21
Bacteria;Proteobacteria;Gammaproteobacteria;Unclassified;Unclassified;sf_3;8759		0.35	0.28					
Bacteria;Proteobacteria;Gammaproteobacteria;Unclassified;Unclassified;sf_3;8815			0.31					
Bacteria;Proteobacteria;Gammaproteobacteria;Unclassified;Unclassified;sf_3;8816		0.50	0.41				-0.21	
Bacteria;Proteobacteria;Gammaproteobacteria;Unclassified;Unclassified;sf_3;8832			0.32			0.20		
Bacteria;Proteobacteria;Gammaproteobacteria;Unclassified;Unclassified;sf_3;8867		0.50	0.21					
Bacteria;Proteobacteria;Gammaproteobacteria;Unclassified;Unclassified;sf_3;8883	-0.28			0.24		0.25		0.25
Bacteria;Proteobacteria;Gammaproteobacteria;Unclassified;Unclassified;sf_3;8922	-0.21	-0.27			0.22		0.47	0.22
Bacteria;Proteobacteria;Gammaproteobacteria;Unclassified;Unclassified;sf_3;9021		0.26				0.27		
Bacteria;Proteobacteria;Gammaproteobacteria;Unclassified;Unclassified;sf_3;9040		0.21						
Bacteria;Proteobacteria;Gammaproteobacteria;Unclassified;Unclassified;sf_3;9173		0.30				0.22		
Bacteria;Proteobacteria;Gammaproteobacteria;Unclassified;Unclassified;sf_3;9269		0.21	0.24	0.20		0.20		0.20
Bacteria;Proteobacteria;Gammaproteobacteria;Unclassified;Unclassified;sf_3;9279		0.33	0.34					
Bacteria;Proteobacteria;Gammaproteobacteria;Unclassified;Unclassified;sf_3;9314		0.41	0.40	0.26		0.22		
Bacteria;Proteobacteria;Gammaproteobacteria;Unclassified;Unclassified;sf_3;9403	-0.31						0.32	0.27
Bacteria;Proteobacteria;Gammaproteobacteria;Unclassified;Unclassified;sf_3;9509		0.33	0.39					
Bacteria;Proteobacteria;Gammaproteobacteria;Unclassified;Unclassified;sf_3;9572		0.34	0.39	0.26		0.28		
Bacteria;Proteobacteria;Gammaproteobacteria;			0.21					

Gene	SM	NH4	NO3	K	Na	EOC	MPB	VPB
Unclassified;Unclassified;sf_3;9581								
Bacteria;Proteobacteria;Gammaproteobacteria;Unclassified;Unclassified;sf_3;9590					0.33		0.33	0.25
Bacteria;Proteobacteria;Gammaproteobacteria;Unclassified;Unclassified;sf_3;9605		0.39	0.27	0.21		0.23		
Bacteria;Proteobacteria;Gammaproteobacteria;Unclassified;Unclassified;sf_4;8855	0.36		-0.29	-0.25		-0.22		-0.31
Bacteria;Proteobacteria;Gammaproteobacteria;uranium waste clones;Unclassified;sf_1;8231		-0.23	-0.20	-0.27	0.36		0.49	
Bacteria;Proteobacteria;Gammaproteobacteria;Vibrionales;Vibrionaceae;sf_1;8785	0.67	0.59						-0.47
Bacteria;Proteobacteria;Gammaproteobacteria;Vibrionales;Vibrionaceae;sf_1;8914	0.25	0.37						-0.24
Bacteria;Proteobacteria;Gammaproteobacteria;Xanthomonadales;Xanthomonadaceae;sf_3;8538					0.26		0.35	
Bacteria;Proteobacteria;Gammaproteobacteria;Xanthomonadales;Xanthomonadaceae;sf_3;8612		0.28			0.30			0.25
Bacteria;Proteobacteria;Gammaproteobacteria;Xanthomonadales;Xanthomonadaceae;sf_3;9150		0.25	0.31	0.30		0.21		0.22
Bacteria;Proteobacteria;Gammaproteobacteria;Xanthomonadales;Xanthomonadaceae;sf_3;9623		0.35	0.37					
Bacteria;Proteobacteria;Unclassified;Unclassified;Unclassified;sf_17;7819	0.45	0.49					-0.26	
Bacteria;Proteobacteria;Unclassified;Unclassified;Unclassified;sf_20;6763	-0.33						0.27	
Bacteria;Proteobacteria;Unclassified;Unclassified;Unclassified;sf_20;7365		0.55	0.37					
Bacteria;Proteobacteria;Unclassified;Unclassified;Unclassified;sf_21;8509	0.40							
Bacteria;Proteobacteria;Unclassified;Unclassified;Unclassified;sf_28;10091	-0.28		0.31	0.25				0.23
Bacteria;Proteobacteria;Unclassified;Unclassified;Unclassified;sf_8;8247	0.33		-0.28	-0.26				-0.22
Bacteria;SPAM;Unclassified;Unclassified;Unclassified;sf_1;738	0.27		-0.30	-0.23				-0.31
Bacteria;Spirochaetes;Spirochaetes;Spirochaetales;Leptospiraceae;sf_3;6496		-0.35	-0.33	-0.23				
Bacteria;Spirochaetes;Spirochaetes;Spirochaetales;Serpulinaceae;sf_1;6548		0.40	0.28					
Bacteria;Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;sf_1;6502		-0.25						-0.31
Bacteria;Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;sf_2;6493		-0.40	-0.33				0.30	
Bacteria;Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;sf_3;6558		-0.27	-0.29	-0.22				
Bacteria;SR1;Unclassified;Unclassified;Unclassified;sf_1;2900	-0.38							0.30

Gene	SM	NH4	NO3	K	Na	EOC	MPB	VPB
Bacteria;Synergistes;Unclassified;Unclassified;Unclassified;sf_3;60		-0.28	-0.36	-0.25				
Bacteria;Termite group 1;Unclassified;Unclassified;Unclassified;sf_2;722		-0.41	-0.35	-0.28			0.31	
Bacteria;Thermodesulfobacteria;Thermodesulfobacteria;Thermodesulfobacteriales;Thermodesulfobacteriaceae;sf_1;667		-0.34	-0.21					
Bacteria;Thermotogae;Thermotogae;Thermotogales;Thermotogaceae;sf_4;51		0.30	0.32	0.21				
Bacteria;TM6;Unclassified;Unclassified;Unclassified;sf_1;10203	0.36		-0.37	-0.30				-0.21
Bacteria;TM7;TM7-1;Unclassified;Unclassified;sf_1;3746	0.21	0.33						
Bacteria;TM7;TM7-2;Unclassified;Unclassified;sf_1;5228			0.22				0.21	
Bacteria;TM7;TM7-3;Unclassified;Unclassified;sf_1;3081	0.21	0.24						
Bacteria;TM7;Unclassified;Unclassified;Unclassified;sf_1;3255		0.25						
Bacteria;TM7;Unclassified;Unclassified;Unclassified;sf_1;3464							0.29	
Bacteria;Unclassified;Unclassified;Unclassified;Unclassified;sf_105;1995		0.35	0.63	0.32			-0.33	
Bacteria;Unclassified;Unclassified;Unclassified;Unclassified;sf_106;243	0.25	-0.21	-0.34	-0.27				
Bacteria;Unclassified;Unclassified;Unclassified;Unclassified;sf_119;316	-0.36		0.31					
Bacteria;Unclassified;Unclassified;Unclassified;Unclassified;sf_119;6449	-0.29		0.24					0.23
Bacteria;Unclassified;Unclassified;Unclassified;Unclassified;sf_119;874	-0.33	0.26	0.34	0.22				
Bacteria;Unclassified;Unclassified;Unclassified;Unclassified;sf_119;929	-0.37		0.28					0.22
Bacteria;Unclassified;Unclassified;Unclassified;Unclassified;sf_126;296	-0.35			0.25				
Bacteria;Unclassified;Unclassified;Unclassified;Unclassified;sf_132;9820		0.39	0.28	0.21				
Bacteria;Unclassified;Unclassified;Unclassified;Unclassified;sf_140;6355	0.33		-0.36	-0.24		-0.20		-0.26
Bacteria;Unclassified;Unclassified;Unclassified;Unclassified;sf_148;5062	-0.38		0.24					0.25
Bacteria;Unclassified;Unclassified;Unclassified;Unclassified;sf_156;4291		-0.27	-0.34	-0.24				
Bacteria;Unclassified;Unclassified;Unclassified;Unclassified;sf_160;391	-0.23						0.24	
Bacteria;Unclassified;Unclassified;Unclassified;Unclassified;sf_160;6380		0.32	0.33	0.23				
Bacteria;Unclassified;Unclassified;	-0.34		0.47	0.31	-0.28			

Gene	SM	NH4	NO3	K	Na	EOC	MPB	VPB
Unclassified;Unclassified;sf_160;6387								
Bacteria;Unclassified;Unclassified;Unclassified;Unclassified;sf_160;6388	-0.36		0.34	0.32	-0.53			
Bacteria;Unclassified;Unclassified;Unclassified;Unclassified;sf_160;6396		0.43	0.42	0.25		0.20		
Bacteria;Unclassified;Unclassified;Unclassified;Unclassified;sf_160;6400		0.46	0.34					
Bacteria;Unclassified;Unclassified;Unclassified;Unclassified;sf_160;6435	-0.21	0.37	0.27	0.21		0.21		
Bacteria;Unclassified;Unclassified;Unclassified;Unclassified;sf_160;7444		-0.29					0.26	-0.34
Bacteria;Unclassified;Unclassified;Unclassified;Unclassified;sf_160;883					0.25		0.29	
Bacteria;Unclassified;Unclassified;Unclassified;Unclassified;sf_34;4668	0.29	-0.29	-0.35	-0.29		-0.21		-0.27
Bacteria;Unclassified;Unclassified;Unclassified;Unclassified;sf_67;10326		0.29	0.23			0.25		
Bacteria;Unclassified;Unclassified;Unclassified;Unclassified;sf_72;384		0.49						-0.20
Bacteria;Unclassified;Unclassified;Unclassified;Unclassified;sf_91;260		0.41	0.49	0.24		0.24	-0.25	
Bacteria;Unclassified;Unclassified;Unclassified;Unclassified;sf_92;9999		-0.31					0.22	-0.20
Bacteria;Unclassified;Unclassified;Unclassified;Unclassified;sf_93;925		-0.43	-0.32				0.34	
Bacteria;Unclassified;Unclassified;Unclassified;Unclassified;sf_95;2545		-0.46	-0.37	-0.22			0.26	
Bacteria;Verrucomicrobia;Unclassified;Unclassified;Unclassified;sf_3;486		-0.36	-0.35	-0.23				
Bacteria;Verrucomicrobia;Unclassified;Unclassified;Unclassified;sf_4;288		-0.39	-0.28	-0.23			0.22	
Bacteria;Verrucomicrobia;Unclassified;Unclassified;Unclassified;sf_5;686	0.20		-0.31	-0.24				
Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Unclassified;sf_3;399	-0.30		0.27	0.21				
Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Unclassified;sf_3;417	-0.25	0.24	0.27	0.23				
Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Unclassified;sf_3;430					0.34		0.22	0.21
Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Unclassified;sf_3;44	-0.38		0.25				0.23	0.26
Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Unclassified;sf_3;4840		0.46	0.21					
Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Unclassified;sf_3;4841		0.37	0.23					
Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Unclassified;sf_3;4865		0.35	0.26					

Gene	SM	NH4	NO3	K	Na	EOC	MPB	VPB
Bacteria;Verrucomicrobia;Verrucomicrobiae; Verrucomicrobiales;Unclassified;sf_3;565	-0.38						0.26	
Bacteria;Verrucomicrobia;Verrucomicrobiae; Verrucomicrobiales;Unclassified;sf_3;607	-0.28						0.37	0.25
Bacteria;Verrucomicrobia;Verrucomicrobiae; Verrucomicrobiales;Unclassified;sf_3;610	-0.28		0.22					
Bacteria;Verrucomicrobia;Verrucomicrobiae; Verrucomicrobiales;Unclassified;sf_3;911	-0.32							0.23
Bacteria;Verrucomicrobia;Verrucomicrobiae; Verrucomicrobiales;Unclassified;sf_4;169		-0.29	-0.30	-0.22				
Bacteria;Verrucomicrobia;Verrucomicrobiae; Verrucomicrobiales;Verrucomicrobia subdivision 3;sf_1;712			0.23				0.22	
Bacteria;Verrucomicrobia;Verrucomicrobiae; Verrucomicrobiales;Verrucomicrobia subdivision 5;sf_1;547		-0.32	-0.30	-0.22				
Bacteria;Verrucomicrobia;Verrucomicrobiae; Verrucomicrobiales;Verrucomicrobia subdivision 7;sf_1;760		-0.28	-0.31	-0.21				
Bacteria;Verrucomicrobia;Verrucomicrobiae; Verrucomicrobiales;Verrucomicrobiaceae;sf_1;1024	0.29		-0.26	-0.32		-0.24		-0.31
Bacteria;Verrucomicrobia;Verrucomicrobiae; Verrucomicrobiales;Verrucomicrobiaceae;sf_6;1063	-0.25	0.20	0.42	0.36				
Bacteria;Verrucomicrobia;Verrucomicrobiae; Verrucomicrobiales;Verrucomicrobiaceae;sf_6;282					0.27			
Bacteria;Verrucomicrobia;Verrucomicrobiae; Verrucomicrobiales;Verrucomicrobiaceae;sf_6;303	-0.36						0.26	0.24
Bacteria;Verrucomicrobia;Verrucomicrobiae; Verrucomicrobiales;Verrucomicrobiaceae;sf_6;660	-0.34		0.29					0.24
Bacteria;Verrucomicrobia;Verrucomicrobiae; Verrucomicrobiales;Verrucomicrobiaceae;sf_7;29		0.44	0.29	0.25				
Bacteria;Verrucomicrobia;Verrucomicrobiae ;Verrucomicrobiales;Verrucomicrobiaceae;sf_8;806		-0.20	-0.24	-0.23				
Bacteria;Verrucomicrobia;Verrucomicrobiae; Verrucomicrobiales;Xiphinematobacteraceae;sf_3;352		0.37	0.21					
Bacteria;Verrucomicrobia;Verrucomicrobiae; Verrucomicrobiales;Xiphinematobacteraceae;sf_3;876	-0.24	0.23	0.27					
Bacteria;WS3;Unclassified; Unclassified;Unclassified;sf_1;2537		-0.35	-0.43	-0.29			0.28	
Bacteria;WS3;Unclassified; Unclassified;Unclassified;sf_3;95	-0.29		0.28					
Bacteria;WS5;Unclassified; Unclassified;Unclassified;sf_2;8119	0.24	-0.22						

Table S1: Pearson's linear correlation coefficient (r) for the taxa that showed a significant ($P < 0.05$) correlation with the soil environmental parameters. Colors are meant to easily visualize different taxonomic groups (phyla or class). SM = soil moisture, EOC= extractable organic carbon, MPB= moss plant biomass and VPB= vascular plant biomass.

	SM		pH		NH4^{+}		NO3^{-}		K		Na		Ca		Mg		EOC		MB		VPB	
	P	r	P	r	P	r	P	r	P	r	P	r	P	r	P	r	P	r	P	r	P	r
SM					0.01	0.27	0.00	-0.31	0.0001	-0.38	0.01	0.28	0.01	0.28	0.02	0.24	0.03	-0.22			<1E-4	-0.45
pH									0.01	-0.28	<1E-4	0.61	<1E-4	0.61	<1E-4	0.69			0.06	0.20	0.003	0.30
NH4+	0.01	0.27																	0.01	-0.26	0.002	-0.32
NO3-	0.002	-0.31							0.0003	0.36												
K	0.0001	-0.38	0.01	-0.28			0.00	0.36			<1E-4	-0.48	<1E-4	-0.48			0.01	0.27	<1E-4	-0.39		
Na	0.01	0.28	<1E-4	0.61					<1E-4	-0.48					<1E-4	0.45			<1E-4	0.50	0.001	0.32
Ca	0.01	0.28	<1E-4	0.61					<1E-4	-0.48	<1E-4	1.00			<1E-4	0.45			<1E-4	0.50	0.001	0.32
Mg	0.02	0.24	<1E-4	0.69					0.09	-0.17	<1E-4	0.45	<1E-4	0.45								
EOC	0.03	-0.22							0.01	0.27	0.08	-0.18							0.03	-0.23		
MB			0.06	0.20	0.01	-0.26			<1E-4	-0.39	<1E-4	0.50	<1E-4	0.50			0.03	-0.23			0.02	0.23
VPB	<1E-4	-0.45	0.003	0.30	0.002	-0.32					<1E-4	0.32	0.001	0.32					0.02	0.23		

Table S2: P-values and Pearson’s linear correlation coefficient (r) among the measured environmental variables.

NMS Statistical data

Table S3: Microbial communities' responses over two years.

Pearson and Kendall Correlations with Ordination Axes   N= 96

```
Axis:               1                    2
r      r-sq   tau    r      r-sq   tau

SM          .215   .046   .118  -.151   .023  -.120
pH          .012   .000   .006   .021   .000  -.005
NH4 (ug/   -.285   .081  -.229  -.544   .296  -.331
NO3(ug/g   -.350   .123  -.154  -.360   .129  -.329
K (ug/g)   -.251   .063  -.136  -.173   .030  -.144
Na (ug/g   -.001   .000   .021   .117   .014   .058
Ca (ug/g   -.001   .000   .015   .117   .014   .053
Mg (ug/g    .007   .000   .014  -.010   .000  -.009
EOC        -.193   .037  -.087  -.079   .006  -.127
Moss bio    .049   .002   .073   .393   .154   .339
Plant Bi   -.179   .032  -.105   .044   .002   .015
```

Coefficients of determination for the correlations between ordination distances and distances in the original n-dimensional space:

```
            R Squared
Axis   Increment   Cumulative
 1       .875         .875
 2       .115         .990
```

Increment and cumulative R-squared were adjusted for any lack of orthogonality of axes.

```
Axis pair     r     Orthogonality,% = 100(1-r^2)
  1 vs 2     0.570     67.5
```

Number of entities = 96
Number of entity pairs used in correlation = 4560
Distance measure for ORIGINAL distance: Sorensen (Bray-Curtis)
MRPP (time) =P<0.0001, A=0.305.
MRPP (tmt) = P > 0.05, A = 0.0003.

Table S4a: Microbial communities' responses over two years in the control treatment.

Pearson and Kendall Correlations with Ordination Axes   N= 32

```
Axis:              1                   2
r      r-sq   tau    r      r-sq   tau
SM         -.156   .024  -.045  -.387   .150  -.235
pH         -.145   .021  -.115  -.169   .028  -.115
NH4 (ug/    .548   .300   .410  -.035   .001   .059
NO3(ug/g    .377   .142   .228   .102   .010  -.083
K (ug/g)    .343   .118   .250   .409   .167   .241
Na (ug/g    .019   .000   .044  -.279   .078  -.201
Ca (ug/g    .019   .000   .044  -.279   .078  -.201
Mg (ug/g   -.003   .000   .034  -.093   .009  -.002
EOC         .342   .117   .192   .294   .087   .155
Moss bio   -.277   .077  -.290   .195   .038   .082
Plant Bi   .091   .008  -.034   .037   .001  -.038
```

Coefficients of determination for the correlations between ordination
distances and distances in the original n-dimensional space:

```
            R Squared
Axis   Increment   Cumulative
 1       .919        .919
 2       .073        .992
```

Increment and cumulative R-squared were adjusted for any lack
of orthogonality of axes.

```
Axis pair     r     Orthogonality,% = 100(1-r^2)
  1 vs 2     0.553     69.5
```

Number of entities = 32
Number of entity pairs used in correlation = 496
Distance measure for ORIGINAL distance: Sorensen (Bray-Curtis)
MRPP <0.0001 A=0,45

Table S4b: Microbial communities' responses over two years in the winter treatment.

Pearson and Kendall Correlations with Ordination Axes   N= 32

```
Axis:          1                    2
        r      r-sq   tau      r      r-sq   tau

SM   -.230   .053  -.109   .584   .341   .408
pH    .259   .067   .197  -.163   .027  -.136
NH4   .252   .063   .293   .433   .188   .087
NO3   .613   .376   .406  -.041   .002   .174
K     .328   .107   .188  -.051   .003   .043
Na   -.137   .019  -.066  -.156   .024  -.155
Ca   -.137   .019  -.066  -.156   .024  -.155
Mg    .097   .009   .030   .060   .004   .067
EOC   .027   .001   .065  -.215   .046  -.117
MB   -.160   .026  -.022  -.380   .145  -.313
VPB   .089   .008   .061  -.243   .059  -.170
```

Coefficients of determination for the correlations between ordination distances and distances in the original n-dimensional space:

```
           R Squared
Axis   Increment   Cumulative
 1       .840        .840
 2       .150        .990
```

Increment and cumulative R-squared were adjusted for any lack of orthogonality of axes.

```
Axis pair      r     Orthogonality,% = 100(1-r^2)
  1 vs 2    -0.228     94.8
```

Number of entities = 32
Number of entity pairs used in correlation = 496
Distance measure for ORIGINAL distance: Sorensen (Bray-Curtis)
MRPP <0.0001 A=0,36

Table S4c: Microbial communities' responses over two years in the spring treatment.

Pearson and Kendall Correlations with Ordination Axes   N= 32

```
Axis:          1                    2
        r      r-sq   tau    r      r-sq   tau
SM    -.150   .022  -.065  -.114   .013  -.105
pH     .061   .004   .051  -.101   .010  -.087
NH4   -.409   .167  -.278   .136   .018   .065
NO3   -.276   .076  -.093   .158   .025  -.121
K     -.133   .018  -.044  -.079   .006  -.060
Na    -.054   .003  -.079   .359   .129   .244
Ca    -.054   .003  -.079   .359   .129   .244
Mg     .059   .004   .044  -.067   .005  -.056
EOC   -.110   .012  -.129  -.403   .162  -.157
MB     .209   .044   .123   .295   .087   .168
VPB   -.145   .021  -.095   .408   .167   .220
```

Coefficients of determination for the correlations between ordination
distances and distances in the original n-dimensional space:

```
            R Squared
Axis   Increment   Cumulative
 1       .903        .903
 2       .093        .996
```

Increment and cumulative R-squared were adjusted for any lack
of orthogonality of axes.

```
Axis pair     r     Orthogonality,% = 100(1-r^2)
  1 vs 2    -0.677     54.2
```

Number of entities = 32
Number of entity pairs used in correlation = 496
Distance measure for ORIGINAL distance: Sorensen (Bray-Curtis)
MRPP <0.0001 A= .35

CHAPTER 4

Differences in soil microbial communities underneath bryophytes and grasses

Abstract

Bryophytes are globally distributed non vascular plants that are essential for ecosystem functioning. We investigated the effects of moss (Bryophyta, a subgroup of the Bryophytes) biomass on the underlying soil geochemistry and the structure and composition of soil microbial communities. Eight, 10 cm deep soil cores, were taken from areas dominated by mosses or grasses on a meadow at the Angelo Reserve in Northern California subjected to a rainfall amendment study. Geochemical analyses showed increased soil moisture, pH and Na concentration and decreased soil temperature, dissolved organic carbon, Mn, K and Al concentrations underneath areas dominated by mosses relative to grasses. Many of these variables were also affected by soil depth. DNA was hybridized to 16S rRNA gene DNA Phylochips to compare the compositions of microbial communities under the two plant assemblages and cDNA was hybridized to compare activity levels. Aboveground moss biomass did not strongly influence overall microbial community structure but significant responses were observed for a subset of microorganisms (t-test $p < 0.05$) and at the activity level. Interestingly, different correlations with environmental variables were observed for taxa that changed in abundance with plant assemblage than for those that responded at the activity level. Higher soil moisture and lower temperatures underneath mosses had a negative influence on the abundance of mostly aerobic organisms (e.g., Actinobacteria, Alpha and Betaproteobacteria), probably due to anaerobic micro-niches. On the other hand, higher carbon availability, warmer temperatures and lower soil moisture underneath grasses correlated with increased abundances of Acidobacteria, Firmicutes, Planctomycetes, Verrucomicrobia and Gammaproteobacteria. Actinobacteria, Alpha and Betaproteobacteria showed increased activity under grasses, with levels correlating with increased Mn concentrations and aboveground plant biomass. At a depth of 8-10 cm, we detected no significant impact of the overlying plant assemblage, yet soil depth had a strong effect on microbial community structure. The 8-10 cm region was dominated by Acidobacteria, Chloroflexi, Firmicutes, Planctomycetes, Deltaproteobacteria and Verrucomicrobia and had lower abundances of Actinobacteria, Bacteroidetes, Cyanobacteria, TM7 group, and Alpha, Beta and Gamma proteobacteria. Correlations suggest that lower dissolved organic carbon and higher Al concentrations in deeper soil caused this stratification. In conclusion, we infer that through their effects on soil parameters such as moisture, temperature, cation concentration, pH and carbon availability, mosses and grasses have different impacts on the structure, composition and activity of soil microbial communities.

Introduction

Bryophytes are nonvascular land plants comprising of three taxonomic groups: the Marchantiophyta (liverworts), Anthocerotophyta (hornworts), and Bryophyta (mosses) (Glime 2007). They are the second largest land plant group (after the flowering plant group, Magnoliophyta) consisting of 15,000 (Gradstein 2001) to 25,000 species (Crum 2001) and can be found in most aquatic and terrestrial ecosystems. They are physiologically different from the tracheophytes in: 1) lack of lignin in their cells walls, 2) do not have a well developed conductive system, 3) have no real roots, just filamentous rhizoids for anchorage and, 4) the gametophyte is the dominant generation while in vascular plants it is the sporophyte. Due to the absence of a protecting cuticle and conductive system, high cation exchange capacity, and large surface to weight ratio, bryophytes can obtain water, nutrients, and minerals from atmospheric deposition onto their cell surfaces (Tyler 1990). They evolved to be tolerant to water stress (by poikilohydry) and wide temperature changes, traits that together with the absence of a rooting system, allow them to colonize habitats that vascular plants cannot (e.g., rocks and wood) (Turetsky 2003). These physiological and life history characteristics allow them to survive in a wide variety of climates, but very few species are truly cosmopolitan. For example, species found in tropical rain forest adapted to constant shade and moisture and recover slower after long dry periods than species exposed to the sun on bare rocks (Gignac 2001).

Bryophytes are important contributors to the ecosystem function, influencing the production of organic matter, nutrient cycling, soil stabilization, trapping sediments and water, and providing food and habitat for algae, fungi, invertebrates and amphibians (Turetsky 2003). They are the primary form of carbon storage in many northern ecosystems (temperate, boreal and artic) (O'Neill 2000). For instance, boreal and subartic peatlands store approximately 455 Pg of carbon; two to three times the amount of carbon stored in tropical rainforest (Post et al 1982 (Gorham 1991, O'Neill 2000). This large amount of carbon is frozen in permafrost soils but as climate change and increases in temperature occurs, this carbon could be rapidly decomposed, releasing large amounts of CO_2 and CH_4 into the atmosphere, a negative feedback into the current global warming (O'Neill 2000). The role of mosses at the ecosystem level is so important that efforts for their conservation are included in conservation management plans worldwide (Hallingback 2000). Due to their ability to obtain nutrients and water from the atmosphere they have been used as biological sensors of atmospheric pollutants and heavy metals (Tyler 1990) and as indicators of past (macrofossils) and future (mathematical modeling) changes in climate (Gignac 2001)

Bryophytes coexist with many vascular plants but their singular impact on underlying soil microbial communities in a natural setting has been little studied. They are known to have antimicrobial capabilities (Basile 1999) and form associations with cyanobacteria (Rai 2000, DeLuca 2002) and other bacterial (Opelt and Berg 2004, Raghoebarsing et al. 2005) and fungal species (Tsuneda 2001, Thormann 2002). Most of these associations are with the aboveground leafy structures. Little is known about the effects of mosses on the underlying soil microbial community structure, activity and composition. One can predict that due to the capability of bryophytes to stabilize soils, produce organic matter, store nutrients, reduce soil temperatures and/or retain soil moisture, they will alter soil geochemistry and microbial activity. For instance, wetter conditions can create anaerobic hotspots, affecting decomposition by aerobic heterotrophs (Tsuneda 2001) and possibly leading to the production of greenhouse gases such as nitrous oxide and methane by anaerobic microorganisms. Here we investigate the effect of aboveground moss and grass biomass on the underground geochemistry and soil microbial community composition and activity.

Materials and Methods

Sampling description

Soil samples were collected on May 4, 2008 from a single experimental plot that had received a spring rainfall amendment in the climate change experimental field site previously described (Chapter 1 and (Cruz-Martinez et al. 2009). Spring plot number 9 was selected as it had the highest moss biomass of all of the plots, based on visual inspection. Eight 10 cm deep by 4.45 cm wide soil cores were collected from areas with high moss biomass and eight from areas soil overlain predominantly by annual grasses and forbs. Aboveground moss, grass and forb biomass was collected and stored prior to taking the cores. At the Angelo Reserve laboratory, each core was subdivided into 2 cm sections and homogenized by hand to break down soil clumps. From the homogenized sample, approximately 2 grams of soil was saved for further DNA and RNA extractions and 3 grams of soil were stored for measurements of microbial biomass. Samples for biological analysis were transported in dry ice to the laboratory, where they were stored at -80°C until DNA or RNA extraction. On the same day of sampling, 3 grams of soils was added to 15 ml 2M KCl in a specimen cup for extraction of inorganic nitrogen on the following day. The rest of the soil was transported to the UC Berkeley laboratory and stored at 4°C for further analyses. On the following day, 2 grams of soil was used for measurements of gravimetric soil moisture and 3 grams of soil from depths 0-2 and 8-10 was added to 25 ml of 0.05M K_2SO_4 in specimen cups for extraction of dissolved organic. The rest of the soil was air-dried and sieved (<2mm fraction) for measurements of exchangeable cations and pH.

Environmental correlates

Biomass of aboveground communities

Immediately after to soil collection, all aboveground vegetation was removed and stored in paper bags. Back in the laboratory, plants were divided into two groups: vascular plants (grasses) and bryophytes. Among the vascular plants were Lotus sp., Galium sp., Aira caryophyllea and other grasses. The dominant bryophyte species was Homalothecium pinnatifidum followed by less abundant species such as Timiella crassinervis, Didymodon vinealis and several species of Bryum. To measure plants biomass, samples were dried at 60°C for 72 hours, and weighed.

Soil Moisture

Gravimetric soil moisture was calculated by oven-dry 2 grams of soil at 105 °C for 24 hours or until a constant weight was achieved.

Soil pH and exchangeable cations

A modification of the $BaCl_2$ extraction method described by Hendershot, W. H. and Lalande, H (Hendershot 1993) was used to measure soil exchangeable cations and pH. Briefly, 3 grams of air-dried (< 2 mm) soil was added to 30 ml 0.1 M $BaCl_2$ (1:10 w/v) in a 50 ml Falcon tube and shaken on a platform shaker (40 rpm) for 2 hours. Each sample was centrifuged at 700 g for 15 minutes at 4°C and the supernatant divided into two 15 ml falcon tubes, one for measurement of exchangeable cations and the other for pH determination.

Exchangeable cations Al, Ca, Fe, K, P, Mg, Mn, Na and Si were analyzed by Inductively Coupled with Optical Emission System (ICP-OES) by using a Perkin Elmer 5300 DV optimal emission ICP with auto sampler. Blanks and internal controls were included in the analysis. Soil pH was measured with a Fisher Acumet AR 20 pH meter.

Extractable inorganic nitrogen

Soil inorganic nitrogen (NH_4^+ and NO_3^-) was measured from each depth by using a modification of the protocol of (Maynard 1993). Three grams of moist soil was added to 15 ml 2.0 M KCl (1:5 w/v) in a specimen cup, either on the date of sampling or on the following day. Within 24 hours, samples were shaken for 1 hour at 150 rpm and filtered using a Whatman No. 1 filter (pre-washed with 2M KCl). Extracts were frozen (-20°C) and shipped to the UC Davis Agricultural and Natural Resources Analytical Laboratory (Davis, Ca) for analysis of NH_4^+ and NO_3^- concentrations using an automated flow injection analyzer method (Hofer 2003, Knepel 2003).

Extractable organic Carbon (non-fumigated samples)

Within 24 hours of sample collection, 3 grams of wet soil from depths 0-2 and 8-10 was added to 25 ml 0.05M K_2SO_4 (1:8 w/v), shaken at 150 rpm for 2 hours and filtered using a Whatman No. 1 filter (Soil Sampling and methods of analysis, Canadian Society of Soil Science). Organic Carbon extracts were measured using a TIC/TOC analyzer.

Microbial biomass Carbon

Chloroform fumigation was performed on three grams of frozen samples (-80 °C) incubated in the dark for seven days (Brooks et al. 1989, Voroney and Winter 1993). Organic carbon was extracted and quantified from the fumigated samples, as described in the previous section. Microbial biomass C was calculated as follows: microbial biomass C = EC/kEC, where EC = (organic C extracted from fumigated soils) - (organic C extracted from non-fumigated soils) and kEC = 0.45 (Beck 1997).

Soil DNA and RNA extractions and cDNA amplification

DNA was extracted from 0.25 grams (approximate dry weight) of homogenized soil from subsamples at depths 0-2 and 8-10 using the Power Soil DNA kit (MO BIO, Carlsbad, CA, USA) according to the manufacturer’s instructions. Four random samples at depth 0-2 from the areas with high moss and four from the areas with low moss were selected for simultaneously extraction of DNA and RNA following a modified procedure described by DeAngelis et al. (Griffiths RI 2000, DeAngelis et al. 2008). Briefly, 0.5 g of frozen soil was added to a Lysing matrix E tube (containing 1.4 mm ceramic spheres, 0.1 mm silica spheres and one 4 mm glass bead; Qbiogene Inc., Irvine, CA, US), 0.5 ml of modified CTAB extraction buffer (equal volumes of 10% hexadecyltrimethylammonium bromide in 1 M NaCl and 0.5 M potassium phosphate buffer, pH 8.0), 50 µl of ammonium aluminum sulfate (AmAlS) and 0.5 ml of phenol:chloroform:isoamylalcohol (25:24:1) and then shaken in a FastPrep Instrument (Qbiogene Inc., Irvine, CA, USA) at 5.5 m/s for 30 s. Following bead-beating, soils were extracted with an equal volume of chloroform:isoamylalcohol (24:1), DNA was precipitated with PEG6000/NaCl solution, washed in cold 70% ethanol washing and resuspended in 50 µl of DNAse/RNAse –free TE buffer. To increase DNA and RNA yield, two or three soil extractions were made per sample and the extraction procedure was repeated for each. For DNA and RNA purification, the Qiagen Allprep DNA/RNA kit and the Qiagen DNAse-free RNAse set were used following the published protocol (Qiagen Sciences, Valencia, CA, USA).

To prepare cDNA from the RNA extracts, two different master mix were prepared: master mix one (MM1) consisted of 1 µl of 300 ng/µl Random primers (Invitrogen, Carlsbad, CA) and 4 µl of dNTP mix (2.5 mM each) per reaction and, master mix two (MM2) obtained 4 µl of 5X First-strand buffer, 2 µl 0.1 M DTT and 1 µl RNAse OUT (Invitrogen Carlsbad, CA) per reaction. Seven µl of RNA was added to 5 µl of MM1, heated at 65 °C for 5 minutes then quickly chilled on ice. Later, 7 µl of MM2 was added to the reaction and incubated at 25 °C for 2 minutes. At the end of this incubation, 0.5 µl of SuperaseII reverse transcriptase (Invitrogen Carlsbad, CA) was added to each sample and incubated at 25 °C for 10 min, followed by another incubation at 42 °C for 50 min and finally the enzyme was denatured by incubating the sample at 70 °C for 15 minutes.

PCR amplification of 16S rRNA genes

For the amplification of the bacterial 16S rRNA gene, a temperature-gradient PCR was performed for each DNA and cDNA extraction using the primers 1492R (5’-GGTTACCTTGTTACGACTT-3’) and 27F (5’-GTTTGATCCTGGCTCAG-3’). For the archaeal 16S rRNA gene amplification, two rounds of PCR were performed. On the first round, one reaction per sample was done using the primers 1492R and the 4Fa (5’-TCCGGTTGATCCTGCCRG-3’) and on the second round, a gradient PCR was done using primers 1406R (5’-ACGGGCGGTGWGTRCAA-3’) and 23F (5’-TGCAGAYCTGGTYGATYCTGCC-3’). PCR reactions had a final volume of 25 µl containing a final concentration of 1X Takara ExTaq PCR buffer with $MgCl_2$, 300 pM of primers, 1 µg/ul BSA, 200 µM dNTPs, 2.5 U ExTaq DNA polymerase (Takara Mirus Bio Inc., Madison, WI) and milliQ H_2O to complete volume. PCR cycle for the bacterial 16S rRNA amplification was performed with a initial denaturation at 95 °C for 3 min, followed by 25 cycles of 95 °C for 30 sec, annealing gradient from 48 °C – 60 °C for 25 sec, extension of 72 °C for 2 min and a final extension of 72 °C for 10 min. The first round of archaeal PCR had a initial denaturation at 95 °C for 3 min, followed by 25 cycles of 95 °C for 30 sec, annealing temperature of 50 °C for 25 sec, extension of 72 °C for 2 min and a final extension of 72 °C for 10 min and the second round had the same cycle but with an annealing gradient of 53 °C – 65 °C for 25 sec. Amplicons were purified using the QIAquick PCR purification kit (Qiagen, Maryland, USA) and quantified with gel electrophoresis.

16S rRNA gene DNA microarrays

From the corresponding 16S rRNA amplified pools, 500 ng of bacterial and 100 ng of archaeal DNA were fragmented, biotin labeled and hybridized to a 16S rRNA Affymetrix microarray (16S rRNA PhyloChip, Affymetrix) as described in detail elsewhere (Brodie et al. 2006). PhyloChip washing, staining and scanning were performed as described elsewhere (Masuda and Church 2002). Scanned arrays were recorded as a pixel image and intensities were determined using standard Affymetrix software (GeneChip Microarray Analysis Suite, version 5.1). PhyloChip data was measured at taxon/OTU level (similar to 99% sequence homology) but was summarized to sub-family level (approximately 94% sequence homology) by selecting the OTUs from which 90% of its probes are positive and their hybridization signal is the highest across all experiments. This approach was demonstrated by DeSantis et al. (DeSantis et al. 2007) to be a conservative way of following community composition while minimizing the influence of cross hybridization occurring between probe-sets targeting closely related sequences. In this data reduction approach we chose the taxon with the highest hybridization signal that met our across all experiments to be the representative for each subfamily.

Data analysis

Environmental Parameters with depth and between plant groups

To identify the effect of depth or plant group on the measured environmental parameters Analysis of Variance (ANOVA) and Student's t-test with a p-value cut off of 0.05 was performed, respectively. The effect of plant was ignored when testing the effect of depth and vice versa. A follow up Tukey test was used to identify the directionality of the difference.

Community Composition

Analyses of the effects of aboveground plant type and soil depth on community composition (i.e. taxonomic membership and relative abundance of detected subfamilies across plots) are based only on hybridization intensity data for all taxa that could be detected and identified with high confidence (positive fraction > 0.90). Non-metric multidimensional scaling (NMS) (Kruskal 1978, Clarke 1993) and multi-response permutation procedures (MRPP) (Mielke 1984, 2001) were used to visualize and test dissimilarities in species composition between plant types (moss and grass) on the 1) active (by using cDNA) microbial communities and 2) whole microbial communities (by using DNA) on the top 2cm of the soil profile and between depths (0-2 and 8-10 cm), ignoring plant type. Environmental variables were superimposed on the ordination analysis to identify the variables that could be responsible for driving the observed clustering.

We identified the specific taxa exhibiting the greatest separation in relative abundance between plant types or depths by screening hybridization intensity data with univariate tests for each taxon (Student's t-test; $P < 0.05$) in the ChipST2C software platform (Peterson 2006). We then conducted post hoc Tukey tests to identify the direction of the separation for all taxa showing differences between plant types or depths. Pearson's linear correlation was used to establish relationships between environmental variables and each of the significant taxa.

For the response of environmental variables to microbial biomass, a forward stepwise regression procedure was used to select the best model. We used the following soil and site characteristics in the statistical analysis: aboveground plant type, depth, dissolved organic carbon, pH, soil moisture, ammonium and nitrate concentrations, cation exchange capacity and aluminum, manganese, cation, magnesium, potassium, sodium, iron, phosphorus concentrations.

Cation concentrations were log transform to achieve a normal distribution. The threshold for inclusion in the final model was set at $P < 0.05$. All statistical analyses were performed using JMP (SAS Institute Inc. 2004).

Results and Discussion

Effects of soil depth and aboveground grass and bryophyte abundance in soil geochemistry

Differences between mosses and grasses

On the annual grassland at the Angelo Reserve, a high abundance of moss biomass significantly increased the gravimetric soil moisture, at least in the top 10 cm of the soil profile (Table 1). An increase in soil moisture could affect soil dynamics by limiting the diffusion of oxygen needed for aerobic heterotrophic decomposition and by stimulating the growth of anaerobic microorganisms capable of producing greenhouse gases (eg., CH_4, N_2O) (Turetsky 2003). Dissolved organic carbon was significantly higher underneath grasses (Table 1), possibly due to root exudation of organic compounds (eg., organic acids) and higher decomposition rates by heterotrophic microorganism. Increase in organic compound concentration was probably the main cause for a slight, but significant decrease in pH on the top 6 cm of the soil profile underneath grasses (Table 1). It has been previously proposed that bryophytes can decrease soil pH and inhibit microbial population and/or activity due to their high cation exchange capacity (release of protons from cation exchange sites) (Spearing 1972). However, in this case the higher abundance of dissolved organic compounds (most probably due to root exudates; Table 1) and root respiration associated with the rhizosphere of grasses might be one of the stronger plantfactors influencing soil acidity (creation of H^+/HCO_3^-) (Marschner and Romheld 1996, De Kroon and Visser 2003). An increase in soil acidity under grasses might have increased the dissolution of many elements from minerals (Table 2, De Kroon and Visser 2003). Changes in pH and cation concentrations (particularly Al) may be deleterious to many plant species and certain microorganism types, affecting their enzymatic activity and hence their abundance and activity.

Differences among depths

Microbial biomass was significantly higher in the top 2 cm of the soil profile where the nutritional and aerobic conditions are optimal for microbial growth (Table 1). Litter deposition from the aboveground plant assemblages can be quickly decomposed by invertebrates and microbes, providing a labile pool of carbon and nitrogen that is quickly cycled through the system. In the top 4 cm of the soil profile ammonia concentrations were higher under both moss and grasses. In contrast, NO3-was evenly distributed across all depths probably due to its high solubility in water (no significant depth differences for soil moisture). The effects of soil depth and associated environmental condition on microorganisms will be discussed below.

Differences in microbial community structure underneath grasses and bryophytes (DNA level)

Because aboveground moss vs. grass assemblage influences soil moisture, dissolved organic carbon, pH and cation concentrations, the plant assemblage may also affect the structure, composition and activity of soil microbial communities. Based on hybridization of DNA to the Phylochip, aboveground moss abundance had no significant effect on the overall structure of the underlying soil microbial communities (Fig 1a). However, a subset of the community (taxa that showed a significant difference between plant groups) did respond to the aboveground plant assemblage (t-test $p<0.05$; Fig 1b). Actinobacteria, Alpha and Betaproteobacteria had the highest number of taxa responding to differences in aboveground plant assemblage (30%, 24% and 17% respectively, Fig. 3). In general, members of the Actinobacteria, Alpha and Betaproteobacteria were in higher relative abundance underneath grasses whereas members of the Acidobacteria, Firmicutes, Planctomycetes, Verrucomicrobia and Gammaproteobacteria were significantly more abundant underneath mosses (Table 3). Soil moisture, pH, soil temperature, manganese concentration and dissolved organic carbon are among the environmental variables whose correlation patterns suggest they may have driven these differences (Fig 1b, Table 4). Higher soil moisture and lower temperature underneath mosses relative to grasses decreased the relative abundances of members of the Actinobacteria and Alphaproteobacteria (Table 4). An increase in soil moisture could have limited oxygen diffusion into the soil, thus limiting the growth of strict aerobes such as many Actinobacteria (Goodfellow and Williams 1983).

A slightly lower pH (~4.2) and higher concentrations of aluminum and manganese in pore fluids underneath grasses correlated with the high abundance of members of the families Burkholderiaceae, Comamonadaceae (Class Betaprotoebacteria) and Bradyrhizobia (Class Alphaproteobacteria) (Table 4). These groups have members able to reduce nitrate, have metal resistance capabilities and/or are tolerant to acidic environments (Khan et al. 2002, Akob et al. 2007). Tolerance mechanisms may vary among bacteria. In the case of aluminum, bacteria can eliminate the toxic ion by extrusion, chemical transformation, intra or extracellular chelation and membrane or cell wall binding (Garcidueñas Piña 1996).

Differences in microbial activity underneath bryophytes and grasses (RNA level)

When the active microbial community was analyzed (by cDNA microarrays), strong differences in the community structure underneath the two plant types were observed (Fig 2). Contrary to the DNA NMS clustering analysis (Fig.1), soil moisture and temperature did not strongly influence the activity of these communities (Fig. 2) but aluminum, magnesium, manganese and soil pH did. In addition to these variables, aboveground plant biomass, nitrate, iron, silica, sodium and phosphorus concentrations show correlations indicating that they may have influenced the active community. Among these variables, the high manganese concentration underneath grasses and the amount of aboveground plant biomass had strong positive effects on the relative abundance of members of the Actinobacteria, which was the group with the highest number of taxa that significantly responded to differences in aboveground plant type (20% of the significant taxa; Fig 3, Table 6). Alpha and Gammaproteobacteria where the second largest groups (10% each) that responded to the aboveground plant assemblage, but few of the significant taxa showed a correlation with the measured environmental variables (Table 5 and 6), suggesting that other variables are driving their responses.

Together, these results suggest that, as a group, Actinobacteria are negatively affected by the high aboveground moss biomass, probably due to their sensitivity to soil moisture, temperature, pH (which can affect cation concentrations), organic matter content and composition (McCarthy et al. 1990, Xu et al. 2006, Jenkins et al. 2009).

Response to Manganese

An interesting finding was evidence suggesting a response of many bacterial taxa to manganese concentrations in the top 2 cm of the soil profile. Most of the taxa that showed a significant difference among both plant groups (moss and grasses) also showed a correlation with Mn concentrations. At the DNA level, 34 out of 120 significant taxa (~28%) showed a response to Mn whereas at the cDNA level, 33 out of 157 (21%) showed a response. Interestingly, the response of bacterial groups to manganese differed in the DNA vs. RNA analysis. For example, at the DNA level, members of the Actinobacteria and Alphaprotoebacteria were the dominant groups responding to manganese concentrations while at the RNA level it was mostly Actinobacteria with some Cyanobacteria and Gammaproteobacteria (Tables 4 and 6).

A number of taxonomically unrelated bacterial groups have been found to be involved in the reduction and oxidation of manganese. For example, it has been previously shown how members of the Actinobacteria (eg. Arthrobacter sp. and Streptomyces sp) and Gammaproteobacteria (eg. Aeromonas sp. and some Pseudomonas sp.) are involved in manganese oxidation while other members of the Gammaproteobacteria (Shewanella sp. some Pseudomonas sp. and Acinetobacter sp.) are involved in manganese reduction (Nealson 1978). In our study, several families within the Actinobacteria such as, Streptomycetaceae, Micromonosporaceae, Mycobacteriaceae, Microbacteriaceae, Cellulomonadaceae, and others showed a positive response to manganese concentration. As some members of these families have been previously shown to be involved in the oxidation of Mn^{2+}, it is a possibility that these groups are involved in a similar manner. Members of the Cyanobacteria and Gammaproteobacteria showed a negative correlation (activity levels) to manganese concentrations, suggesting that manganese and/or pH had a deleterious or toxic effect on these groups. An indirect effect of pH on these bacterial taxa is a possibility, but very few taxa (only 9 of the 33 taxa) that correlated with Mn also correlated with soil pH suggesting that manganese concentrations is the main driver. In addition, contrary to what is expected, pH does not seem to strongly affect the dissolution of Mn minerals. (Table 2, $p = 0.057$).

Differences in microbial community structure at 0-2 and 8-10 cm of the soil profile

Under both plant types, moss and grass, the structure and biomass of microbial communities showed a significant difference with depth (0-2 cm vs 8-10 cm) (Fig 4), but no significant impact of moss vs. grass plant assemblage could be detected in the 8-10 cm depth interval. At this depth, very few roots were present, as grass roots were mainly on the top 6 to 8 cm of the soil profile and mosses lack a root system. The lack of high root biomass at this depth will limit the transport of water and nutrients to/from the soil surface and above depth layers. Most measured environmental parameters showed no significant differences between plant groups in deeper soil layers (8-10 cm), and this may explain why there was no difference in the structure of microbial communities. The effect of soil depth on the structure, composition and biomass of microbial communities has been previously shown in different ecosystems and at different depths (Fierer et al. 2003, Steenwerth et al. 2005, Allison et al. 2007). Nutrient (especially carbon) availability is the factor known to directly or indirectly shape these differences (Fierer et al. 2003, Allison et al. 2007).

Our study showed a decrease in microbial biomass and changes in microbial community structure and composition across the top 10 cm of the soil (Fig 4a and b). In the top 10 cm, significant increases with depth in aluminum concentration and decreases in soil temperature, dissolved organic carbon, ammonia, soil pH and cation concentration were observed (Table 1). Among these variables, dissolved organic carbon and manganese and aluminum concentrations are the variables most likely to have driven differences in microbial biomass and community structure, based on observed correlations (Fig 4 and table 7 and 8). The groups that were more abundant on the top 2 cm of the soil profile were the Actinobacteria, Bacteroidetes, Cyanobacteria, Alpha, Beta and Gamma proteobacteria whereas the Firmicutes, Planctomycetes, Deltaproteobacteria and Verrucomicrobia were more abundant on the 8-10 cm of the soil profile.

Carbon inputs, via litter deposition or root exudation, can stimulate taxa that are able to rapidly utilize these labile carbon substrates (copiotrophs) and stimulate their growth and hence biomass (Fierer et al. 2007). It has been previously proposed that higher rates of carbon addition to soil will increase the fungal to bacteria ratio in the microbial community and lower the proportions of Actinomycetes and Gram-positive bacteria relative to Gram negative bacteria (Griffiths et al. 1998). As the availability and quality of carbon decrease with soil depth (Ajwa et al. 1998, Trumbore 2000) a similar pattern in relation to soil depth has been observed (Fierer et al. 2003, Allison et al. 2007), where fungal and gram negative bacteria are more abundant in the soil surface whereas the relative abundances of Actinobacteria and gram positive bacteria increases with depth.

In the current study, we observed somewhat different patterns in the relative abundances of several taxonomic groups with soil depth and available carbon to those reported previously. For instance, high carbon availability near the surface soil had a positive correlation with the relative abundances of the Gram-positive Actinobacteria and TM7 and the Gram-negative Bacteroidetes, Cyanobacteria and the Alpha, Beta and Gammaproteobacteria , whereas an opposite correlation was observed for the Gram-positive Firmicutes, Chloroflexi and Gram-negative Planctomycetes, Verrucomicrobia and Acidobacteria (Table 7 and 8). Discrepancies between the abundance patterns of Actinobacteria and other Gram-positive bacteria with depth reported here and those reported in previous studies may be due to differences in the depths studied or related to the accuracy of identifying specific taxa within bacterial groups given differences in the molecular methods used in the current (microarrays) vs. previous (eg. PLFA) studies (Fierer et al. 2003, Marschner 2007).

In addition to carbon availability, the concentrations of soil ammonium, phosphorus, aluminum, magnesium and manganese correlated with the differences in microbial community structure with depth (Table 8) and pH, soil temperature and ammonium and cation concentrations correlated with the amount of microbial biomass carbon (Table 9). Variations in the bioavailability of soil phosphorous, magnesium, aluminum and manganese concentrations can directly or indirectly affect the structure of microbial communities (Garcidueñas Piña 1996, Allison et al. 2007, Marschner 2007). These nutrients are essential macro or micronutrients for cell growth but in high quantities can be toxic. Bioavailability of phosphorous, magnesium and manganese decreases with soil acidity while aluminum has the inverse response. Members of almost all taxonomic groups exhibited abundance patterns that correlated positively or negatively with phosphorous, magnesium and aluminum (Table 8). There was a strong positive correlation of members of the Actinobacteria, Bacteroidetes and Proteobacteria to manganese concentrations and a negative response to members of the Acidobacteria, Firmicutes, Chloroflexi and Verrucomicrobia. As discussed in the previous section, is a possibility that many members of these groups have the ability oxidize manganese in this heterogenous system or are unable to survive under high manganese concentrations.

Based on the variation among replicates at each depth that is apparent in the clustering analysis (by NMS), there may be more variability in the microbial community composition in the top 2 cm of the soil profile compared to the bottom two (8-10) cm (Fig. 3b). Such variation could reflect more dynamic and changing environmental conditions in the top soil due to the continuous input of nutrients, water and mesofauna activity, factors that may be less variable deeper in the soil.

Conclusions

In an annual grassland, aboveground bryophyte abundance has an effect on the underlying soil biotic and abiotic conditions. Physiological differences between bryophytes and tracheophytes are probably the causative agent of these environmental changes. Altered environmental conditions influenced the relative activity levels of many bacterial groups. Although a pronounced effect on the total microbial community composition was not evident, some groups responded negatively to aboveground moss compared to grass-dominated biomass, probably due to increased soil moisture and reduced soil temperature. These conditions and low availability of dissolved organic carbon stimulated the growth of members of the Cyanobacteria, Chloroflexi, Acidobacteria, Bacteroidetes, Firmicutes and Delta and Gammaproteobacteria. Interestingly, aboveground plant assemblage had no detectable effect on the composition or activity of soil microbial communities in deeper soil layers (8-10 cm). On the other hand, soil depth (independently of the aboveground plant assemblage) had a strong influence on the structure and biomass of soil microbial communities. Carbon availability and cation concentrations were the variables whose abundance patterns suggest they could have driven most of the differences between the two depths studied.

In light of climate change, changes in the seasonality and amount of rainfall might affect the abundance of moss biomass and the associated soil microbial community structure. For example, extending the winter rainfalls into the spring is expected to increase the abundance of moss biomass affecting plant community structure and composition and the activity and abundance of the associated microbes. This could have important consequences at the ecosystem level as changes in the abundance of keystone members in the community (e.g., nitrogen fixers, nitrifiers) can affect nutrient cycling and ecosystem processes.

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Tables and Figures

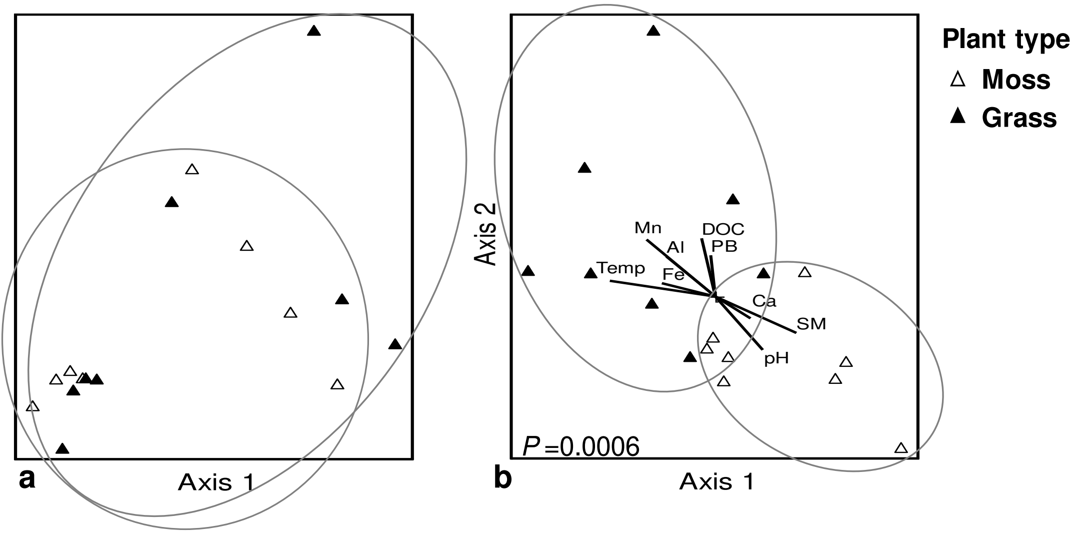

Figure 1: Non-metric multidimensional scaling (NMDS) showing the a) whole and b) "dynamic" microbial communities (DNA level) on the top 2 cm of the soil profile underneath grasses (fill triangle) and mosses (empty triangle). The environmental variables that correlated (above 15%) with the ordination (dynamic taxa) are overlaid in figure b. NMS statistics for figure b are shown in Table 4.

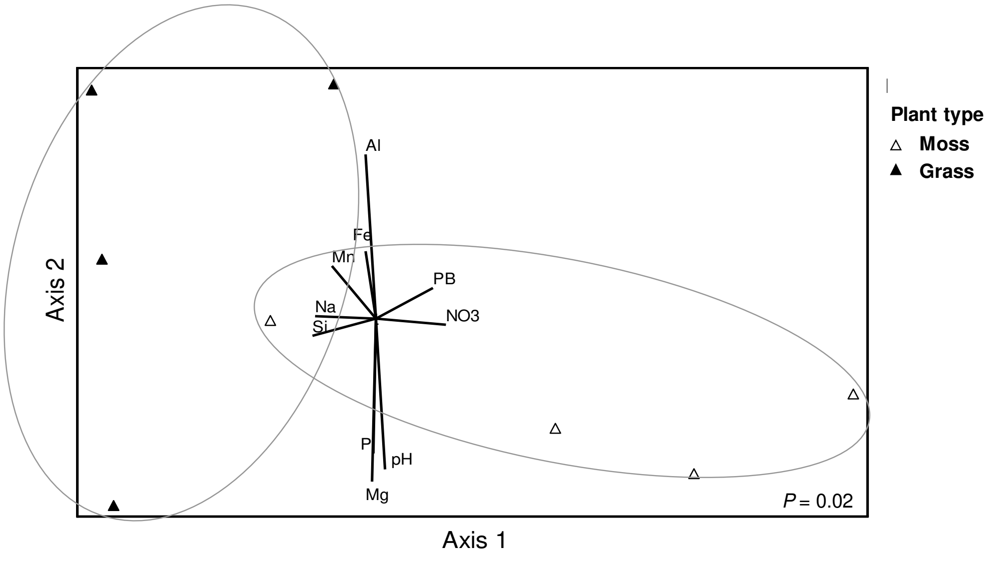

Figure 2: Non-metric multidimensional scaling (NMDS) of the active (cDNA) community on the top 2 cm underneath grass (solid triangles) and mosses (empty triangles). Probability of a smaller or equal delta, P = 0.024 (from MRPP using Sorensen distance) and within-group homogeneity, A= 0.14. Environmental variables that had more than 15% correlation (R^2 =0.15)

with the data are showed. Pearson's and Kendall correlations with ordination axes are shown in Table 4.

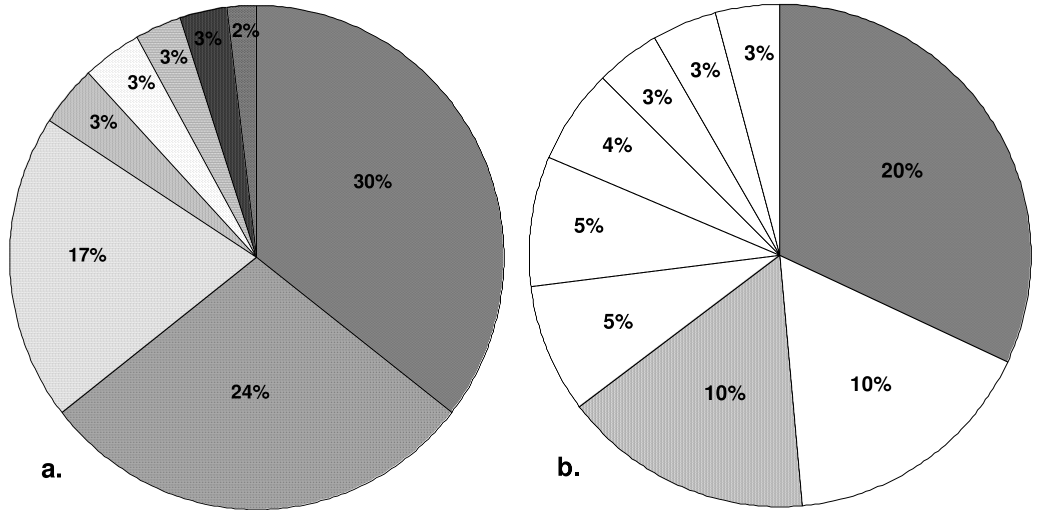

Figure 3: Proportion of the a) total (DNA) and b) active (cDNA) microbial community that showed a significant difference (t-test, p ≤ 0.05) between aboveground plant type (mosses and grasses). Only the Classes with the highest percentages are shown.

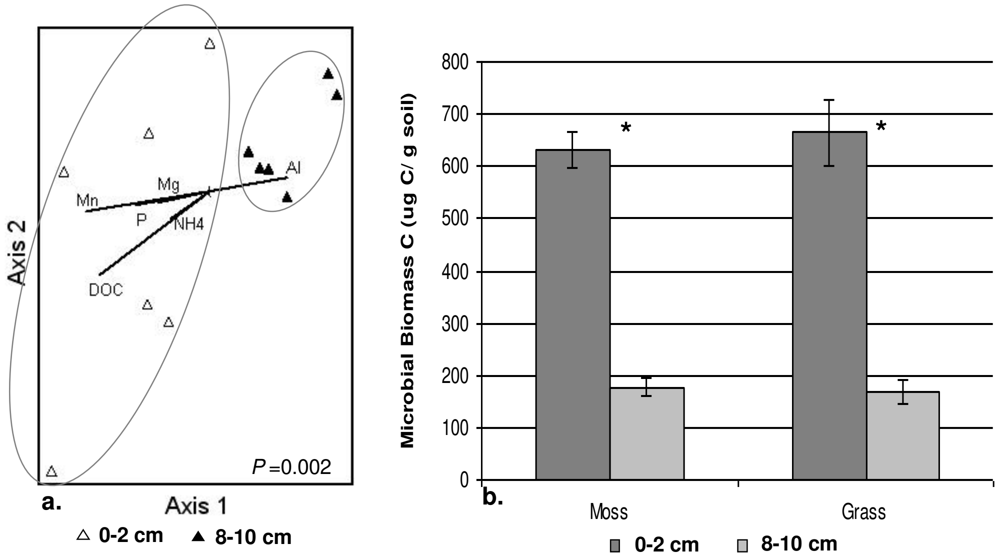

Figure 4: Effects of depth a) on the structure and b) biomass of soil microbial communities on the top 10 cm of the soil profile. Environmental variables that correlated above 20% (R^2>0.20) with the ordination axes are overlaid in figure a. Correlation coefficients are shown in Table 4. P values for NMDS and bar graph were obtained from MRPP and t-test, respectively. *P<0.0001.

Environmental variable	**Moss vs Grass**	**0-2 cm**	**2-4 cm**	**4-6 cm**	**6-8 cm**	**8-10 cm**
#DOC (ug C/ g soil)	Moss	55.00 (3.94)	82.5 (7.29)	72.5 (6.47)	88.2 (6.07)	38.02 (3.85)
	Grass	72.88 (5.46)	85.9 (8.02)	104.3 (15.50)	79.8 (7.39)	52.96 (9.32)
	*Moss + Grass	64.75 (4.14)	34.61 (2.16)	36.33 (3.74)	41.64 (29.78)	45.48 (20.96)
***Microbial Biomass C** (ug C/ g soil)	Moss	630.18 (34.57)	NA	NA	NA	177.69 (15.78)
	Grass	664.28 (62.28)	NA	NA	NA	166.96 (22.63
	*Moss + Grass	633.90 (34.37)	NA	NA	NA	172.33 (18.90)
***NH_4** (ug/ g soil)	Moss	1.06 (0.125)	0.83 (0.058)	0.83 (0.118)	0.74 (0.07)	0.84 (0.056)
	Grass	1.17 (0.216)	0.93 (0.052)	0.77 (0.108)	0.79 (0.047)	0.69 (0.074)
	*Moss + Grass	1.12 (0.12)	0.88 (0.04)	0.80 (0.08)	0.76 (0.62)	0.77 (0.62)
NO_3 (ug/ g soil)	Moss	0.85 (0.33)	0.67 (0.26)	0.66 (0.25)	0.96 (0.30)	1.19 (0.25)
	Grass	0.81 (0.17)	0.98 (0.24)	0.60 (0.32)	1.15 (0.20)	0.82 (0.27)
	Moss + Grass	0.83 (0.18)	0.83 (0.18)	0.63 (0.20)	1.05 (0.18)	1.01 (0.19)
***#pH**	Moss	4.57 (0.05)	4.46 (0.05)	4.29 (0.03)	4.19 (0.02)	4.16 (0.03)
	Grass	4.33 (0.05)	4.22 (0.04)	4.20 (0.03)	4.15 (0.02)	4.12 (0.01)
	*Moss + Grass	4.45 (0.05)	4.34 (0.04)	4.25 (0.02)	4.17 (0.01)	4.14 (0.02)
***#Soil Temperature** (°C)	Moss	22.25 (1.31)	NA	NA	NA	17.72 (0.36)
	Grass	22.01 (0.90)	NA	NA	NA	20.58 (0.83)
#Soil Moisture (%)	Moss	18.17 (0.50)	16.97 (0.81)	16.56 (0.43)	17.14 (0.86)	17.17 (0.59)
	Grass	15.50 (1.33)	14.89 (0.71)	14.54 (0.70)	13.95 (0.68)	14.09 (0.77)
	Moss + Grass	16.83 (0.77)	15.91 (0.58)	15.54 (0.47)	15.54 (2.67)	15.61 (2.45)

***#Al** (ug/g soil)	Moss	5.77 (1.92)	16.19 (4.86)	35.73 (7.88)	57.92 (9.22)	64.63 (0.34)
	Grass	17.84 (5.45)	42.96 (12.0)	50.21 (10.74)	61.60 (8.04)	71.44 (6.70)
	*Moss + Grass	11.81 (3.20)	29.58 (7.14)	42.97 (6.70)	59.76 (5.93)	68.04 (5.62)
***Ca** (ug/g soil)	Moss	1453.51 (51.52)	1383.65 (61.31)	1235.01 (89.61)	1364.45 (106.83)	1203.18 (80.66)
	Grass	1336.75 (29.54)	1327.80 (73.84)	1116.88 (54.60)	1332.89 (99.02)	1300.98 (47.14)
	*Moss + Grass	1395.13 (43.81)	1355.73 (46.92)	1175.95 (52.93)	1348.67 (70.48)	1252.08 (46.86)
***Fe** (ug/g soil)	Moss	0.24 (0.04)	0.29 (0.08)	0.46 (0.09)	0.57 (0.06)	0.58 (0.09)
	Grass	0.31 (0.05)	0.49 (0.10)	0.37 (0.07)	0.53 (0.12)	0.44 (0.09)
	*Moss + Grass	0.27 (0.03)	0.39 (0.07)	0.42 (0.05)	0.55 (0.06)	0.51 (0.25)
***#K** (ug/g soil)	Moss	103.21 (9.94)	80.20 (11.85)	75.30 (10.93)	68.99 (7.65)	68.72 (10.03)
	Grass	108.41 (8.89)	90.39 (11.61)	90.84 (9.50)	81.88 (10.08)	87.39 (7.25)
	*Moss + Grass	105.81 (6.48)	85.30 (8.12)	83.07 (7.28)	75.44 (6.33)	78.05 (6.44)
***P** (ug/g soil)	Moss	6.42 (0.20)	5.86 (0.27)	5.56 (0.22)	5.03 (0.21)	4.56 (0.21)
	Grass	5.98 (0.29)	5.30 (0.33)	4.96 (0.34)	4.56 (0.21)	4.61 (0.14)
	*Moss + Grass	6.20 (0.18)	5.58 (0.28)	5.26 (0.21)	4.80 (0.16)	4.58 (0.12)
***#Mg** (ug/g soil)	Moss	413.42 (17.14)	370.18 (18.99)	345.23 (16.62)	296.58 (13.23)	265.79 (12.61)
	Grass	366.92 (26.41)	319.27 (26.07)	289.28 (22.81)	267.67 (14.56)	267.75 (8.00)
	*Moss + Grass	390.17 (16.35)	344.73 (16.91)	317.25 (15.43)	282.12 (10.21)	266.77 (28.87)
***#Mn** (ug/g soil)	Moss	2.48 (0.38)	1.28 (0.21)	0.68 (0.12)	0.82 (0.16)	0.72 (0.17)
	Grass	7.57 (1.11)	4.12 (0.75)	2.35 (0.54)	0.87 (0.28)	0.81 (0.15)
	*Moss + Grass	5.02 (0.87)	2.70 (0.52)	1.52 (0.34)	0.85 (0.16)	0.77 (0.11)
#Na (ug/g soil)	Moss	18.77 (1.72)	21.38 (2.17)	25.14 (3.41)	25.39 (3.31)	23.23 (2.52)

	Grass	15.51 (1.89)	12.19 (1.71)	11.29 (1.35)	10.37 (1.52)	10.86 (1.44)
	Moss + Grass	17.14 (1.3)	16.78 (1.78)	18.22 (2.52)	17.88 (2.62)	17.04 (2.12)
Si (ug/g soil)	Moss	4.22 (0.28)	4.09 (0.22)	4.72 (0.32)	5.06 (0.15)	4.98 (0.29)
	Grass	4.22 (0.45)	3.89 (0.55)	3.29 (0.41)	4.17 (0.50)	4.02 (0.39)
	Moss + Grass	4.22 (3.66)	3.97 (3.41)	4.01 (3.45)	4.62 (0.28)	4.50 (0.28)

Table 1: Environmental variables measured on the top 10 cm of the soil profile underneath grasses and mosses. Each soil core was subdivided in 2 cm intervals. Values are the average from eight replica and the standard error of the mean is in parenthesis * Variables that showed significant ($p \leq 0.05$) differences among depths (ignoring plant group). $^{\#}$ Variables that showed significant ($p \leq 0.05$) differences between plant groups (ignoring depth). Cations were log transformed forunivariate (t-test or ANOVA) analysis. For DOC, one sample from depth 6-8 was considered an outlier and removed from the statistical analysis. NA = Not available.

Environmental variable	**p-value**	**Pearson's r**	**R^2**
Log Al (uM)	<0.0001	-0.94	0.89
Log Mn (uM)*	0.0570	0.21	0.05
Log Ca (uM)	<0.0001	0.74	0.53
Log K (uM)	0.0006	0.38	0.14
Log Mg (uM)	<0.0001	0.84	0.71
Log Na (uM)	0.0024	0.33	0.11
Log Fe (uM)	0.0009	-0.34	0.13
Log P (uM)	<0.0001	0.76	0.64
Log CEC (cmol (+)/kg)	<0.0001	0.75	0.57
SM (%)	0.0014	0.36	0.13
NH4 (ug N/ g soil)	0.01	0.28	0.08
MBC (ug C/ g soil)	<0.0001	0.69	0.49

Table 2: Environmental variables that showed a significant ($p<0.05$) relationship with pH. Table shows p-values from linear regression, Pearson's product-moment correlation coefficient and coefficient of determination.* Log Mn was included as its p-value is close to 0.05.

Taxa that significantly responded to aboveground plant type on the top 2 cm (DNA)	Higher relative abundance under Moss (M) or Grass (G)
Bacteria;Acidobacteria;Acidobacteria;Holophagales;Unclassified;sf_1;734	**M**
Bacteria;Acidobacteria;Acidobacteria-4;Ellin6075/11-25;Unclassified;sf_1;435	**M**
Bacteria;Acidobacteria;Acidobacteria-9;Unclassified;Unclassified;sf_1;704	**M**
Bacteria;Acidobacteria;Unclassified;Unclassified;Unclassified;sf_1;572	**M**
Bacteria;Actinobacteria;Actinobacteria;Acidimicrobiales;Unclassified;sf_1;1318	**G**
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Actinosynnemataceae;sf_1;1951	**G**
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Actinosynnemataceae;sf_1;1984	**G**
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Cellulomonadaceae;sf_1;1592	**G**
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Cellulomonadaceae;sf_1;2061	**G**
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Corynebacteriaceae;sf_1;1374	**G**
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Dermabacteraceae;sf_1;1736	**G**
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Geodermatophilaceae;sf_1;1245	**G**
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Geodermatophilaceae;sf_1;1973	**G**
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Kribbella;sf_1;1839	**G**
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Microbacteriaceae;sf_1;1098	**G**
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Microbacteriaceae;sf_1;1507	**G**
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Microbacteriaceae;sf_1;1513	**G**
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Microbacteriaceae;sf_1;1550	**G**
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Microbacteriaceae;sf_1;1640	**G**
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Microbacteriaceae;sf_1;1705	**G**
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Micrococcaceae;sf_1;1099	**G**
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Micrococcaceae;sf_1;1452	**G**
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Micromonosporaceae;sf_1;1395	**G**
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Micromonosporaceae;sf_1;1572	**G**
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Mycobacteriaceae;sf_1;1093	**G**
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Nocardiaceae;sf_1;1142	**G**
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Nocardiaceae;sf_1;1809	**G**
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Nocardiaceae;sf_1;1861	**G**
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Nocardiaceae;sf_1;1999	**G**
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Propionibacteriaceae;sf_1;1315	**G**
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Sporichthyaceae;sf_1;1223	**G**
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Sporichthyaceae;sf_1;1701	**G**
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Streptomycetaceae;sf_3;1743	**G**
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Streptosporangiaceae;sf_1;1535	**G**
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Thermomonosporaceae;sf_1;1406	**G**
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Unclassified;sf_3;1114	**G**
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Unclassified;sf_3;1369	**G**
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Unclassified;sf_3;1410	**G**
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Unclassified;sf_3;1564	**G**
Bacteria;Actinobacteria;Actinobacteria;Unclassified;Unclassified;sf_1;1283	**G**
Bacteria;Bacteroidetes;Sphingobacteria;Sphingobacteriales;Flexibacteraceae;sf_20;10311	**M**
Bacteria;Caldithrix;Unclassified;Caldithrales;Caldithraceae;sf_1;2384	**M**
Bacteria;Chloroflexi;Anaerolineae;Unclassified;Unclassified;sf_1;266	**M**
Bacteria;Chloroflexi;Unclassified;Unclassified;Unclassified;sf_12;2523	**M**
Bacteria;Chloroflexi;Unclassified;Unclassified;Unclassified;sf_5;1051	**M**
Bacteria;Cyanobacteria;Unclassified;Unclassified;Unclassified;sf_6;5186	**M**

Taxa that significantly responded to aboveground plant type on the top 2 cm (DNA)	**Higher relative abundance under Moss (M) or Grass (G)**
Bacteria;Firmicutes;Bacilli;Bacillales;Bacillaceae;sf_1;3893	**M**
Bacteria;Firmicutes;Bacilli;Bacillales;Staphylococcaceae;sf_1;3684	**M**
Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiaceae;sf_12;4359	**M**
Bacteria;Firmicutes;Clostridia;Unclassified;Unclassified;sf_4;2398	**M**
Bacteria;Firmicutes;Clostridia;Unclassified;Unclassified;sf_7;4216	**M**
Bacteria;Firmicutes;Desulfotomaculum;Unclassified;Unclassified;sf_1;894	**G**
Bacteria;Firmicutes;Symbiobacteria;Symbiobacterales;Unclassified;sf_1;2388	**M**
Bacteria;LD1PA group;Unclassified;Unclassified;Unclassified;sf_1;10118	**M**
Bacteria;Planctomycetes;Planctomycetacia;Planctomycetales;Anammoxales;sf_4;4694	**M**
Bacteria;Planctomycetes;Planctomycetacia;Planctomycetales;Pirellulae;sf_3;4687	**M**
Bacteria;Planctomycetes;Planctomycetacia;WPS-1;Unclassified;sf_1;4930	**M**
Bacteria;Proteobacteria;Alphaproteobacteria;Acetobacterales;Acetobacteraceae;sf_1;6841	**G**
Bacteria;Proteobacteria;Alphaproteobacteria;Acetobacterales;Acetobacteraceae;sf_1;7080	**G**
Bacteria;Proteobacteria;Alphaproteobacteria;Acetobacterales;Acetobacteraceae;sf_1;7414	**G**
Bacteria;Proteobacteria;Alphaproteobacteria;Acetobacterales;Acetobacteraceae;sf_1;7452	**G**
Bacteria;Proteobacteria;Alphaproteobacteria;Acetobacterales;Acetobacteraceae;sf_1;7565	**G**
Bacteria;Proteobacteria;Alphaproteobacteria;Acetobacterales;Acetobacteraceae;sf_1;7623	**G**
Bacteria;Proteobacteria;Alphaproteobacteria;Acetobacterales;Roseococcaceae;sf_1;6708	**G**
Bacteria;Proteobacteria;Alphaproteobacteria;Bradyrhizobiales;Beijerinck/ Rhodoplan/Methylocyst;sf_3;7000	**G**
Bacteria;Proteobacteria;Alphaproteobacteria;Bradyrhizobiales;Bradyrhizobiaceae;sf_1;7077	**G**
Bacteria;Proteobacteria;Alphaproteobacteria;Bradyrhizobiales;Bradyrhizobiaceae;sf_1;7631	**G**
Bacteria;Proteobacteria;Alphaproteobacteria;Bradyrhizobiales;Hyphomicrobiaceae;sf_1;7389	**M**
Bacteria;Proteobacteria;Alphaproteobacteria;Bradyrhizobiales;Methylobacteriaceae;sf_1;6782	**G**
Bacteria;Proteobacteria;Alphaproteobacteria;Caulobacterales;Caulobacteraceae;sf_1;6929	**G**
Bacteria;Proteobacteria;Alphaproteobacteria;Caulobacterales;Caulobacteraceae;sf_1;6930	**G**
Bacteria;Proteobacteria;Alphaproteobacteria;Caulobacterales;Caulobacteraceae;sf_1;7134	**G**
Bacteria;Proteobacteria;Alphaproteobacteria;Caulobacterales;Caulobacteraceae;sf_1;7245	**G**
Bacteria;Proteobacteria;Alphaproteobacteria;Caulobacterales;Caulobacteraceae;sf_1;7562	**G**
Bacteria;Proteobacteria;Alphaproteobacteria;Devosia;Unclassified;sf_1;7626	**G**
Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Bradyrhizobiaceae;sf_1;6824	**G**
Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Brucellaceae;sf_1;6995	**M**
Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Unclassified;sf_5;7471	**M**
Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;sf_1;7289	**G**
Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;sf_1;7344	**G**
Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;sf_1;7411	**G**
Bacteria;Proteobacteria;Alphaproteobacteria;Unclassified;Unclassified;sf_6;6844	**G**
Bacteria;Proteobacteria;Alphaproteobacteria;Unclassified;Unclassified;sf_6;7166	**G**
Bacteria;Proteobacteria;Alphaproteobacteria;Unclassified;Unclassified;sf_6;7368	**G**
Bacteria;Proteobacteria;Alphaproteobacteria;Unclassified;Unclassified;sf_6;7463	**M**
Bacteria;Proteobacteria;Alphaproteobacteria;Verorhodospirilla;Unclassified;sf_1;6740	**M**
Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae;sf_1;7899	**G**
Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae;sf_1;7914	**G**
Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae;sf_1;7934	**G**
Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;sf_1;7754	**G**
Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;sf_1;7775	**G**

Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;sf_1;7820	**G**
Taxa that significantly responded to aboveground plant type on the top 2 cm (DNA)	**Higher relative abundance under Moss (M) or Grass (G)**
Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;sf_1;7920	**G**
Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;sf_1;7937	**G**
Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;sf_1;8028	**G**
Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;sf_1;8075	**G**
Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;sf_1;8083	**G**
Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;sf_1;8117	**G**
Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Unclassified;sf_1;7832	**G**
Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Unclassified;sf_1;7944	**G**
Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Unclassified;sf_1;8038	**G**
Bacteria;Proteobacteria;Betaproteobacteria;Ellin6095/SC-I-39;Unclassified;sf_1;8093	**M**
Bacteria;Proteobacteria;Betaproteobacteria;Neisseriales;Neisseriaceae;sf_1;7867	**G**
Bacteria;Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae;sf_1;7666	**G**
Bacteria;Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae;sf_1;7875	**G**
Bacteria;Proteobacteria;Betaproteobacteria;Unclassified;Unclassified;sf_3;7723	**M**
Bacteria;Proteobacteria;Epsilonproteobacteria;Campylobacterales;Unclassified;sf_1;10530	**M**
Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Chromatiaceae;sf_1;9571	**M**
Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Ectothiorhodospiraceae;sf_11;8306	**M**
Bacteria;Proteobacteria;Gammaproteobacteria;Ellin307/WD2124;Unclassified;sf_1;9374	**G**
Bacteria;Proteobacteria;Gammaproteobacteria;Legionellales;Unclassified;sf_1;9418	**M**
Bacteria;Proteobacteria;Unclassified;Unclassified;Unclassified;sf_28;10091	**G**
Bacteria;Termite group 1;Unclassified;Unclassified;Unclassified;sf_2;722	**M**
Bacteria;Unclassified;Unclassified;Unclassified;Unclassified;sf_34;4668	**M**
Bacteria;Verrucomicrobia;Unclassified;Unclassified;Unclassified;sf_3;486	**M**
Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Unclassified;sf_3;4840	**M**
Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales; Verrucomicrobia subdivision 5;sf_1;547	**M**
Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales; Verrucomicrobia subdivision 7;sf_1;760	**M**
Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales; Verrucomicrobiaceae;sf_1;1024	**M**
Bacteria;WS5;Unclassified;Unclassified;Unclassified;sf_2;8119	**M**

Table 3: Taxa that significantly responded (t-test; $p \leq 0.05$) to aboveground plant type (moss vs grass) on the top 2cm of the soil profile. Post hoc Tukey HSD test revealed the directionality of the difference; higher relative abundance under moss (M) or grass (G).

Taxa string	DOC		Al		Ca		Fe		Mn		pH		SM		VPB		Soil Temp	
	P	r	P	r	P	r	P	r	P	r	P	r	P	r	P	r	P	r
Bacteria;Acidobacteria;Acidobacteria;Holophagales;Unclassified;sf_1;734					0.040	0.52												
Bacteria;Acidobacteria;Acidobacteria-4;Ellin6075/11-25;Unclassified;sf_1;435							0.024	-0.56									0.022	-0.57
Bacteria;Acidobacteria;Acidobacteria-9;Unclassified;Unclassified;sf_1;704	0.006	-0.66	0.017	-0.59					0.050	-0.50	0.023	0.57						
Bacteria;Acidobacteria;Unclassified;Unclassified;Unclassified;sf_1;572	0.029	-0.55																
Bacteria;Actinobacteria;Actinobacteria;Acidimicrobiales;Unclassified;sf_1;1318							0.029	0.54			0.048	-0.50						
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Actinosynnemataceae;sf_1;1951													0.052	-0.49			0.042	0.51
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Actinosynnemataceae;sf_1;1984									0.014	0.60			0.004	-0.68			0.040	0.52
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Cellulomonadaceae;sf_1;1592													0.011	-0.61			0.014	0.60
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Cellulomonadaceae;sf_1;2061																	0.015	0.59
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Corynebacteriaceae;sf_1;1374																	0.044	0.51
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Dermabacteraceae;sf_1;1736													0.002	-0.72				
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Geodermatophilaceae;sf_1;1245									0.002	0.72			0.001	-0.75			0.037	0.53
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Geodermatophilaceae;sf_1;1973									0.007	0.65			0.001	-0.77			0.009	0.63
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Microbacteriaceae;sf_1;1098																	0.039	0.52
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Microbacteriaceae;sf_1;1507					0.020	-0.57							0.004	-0.67				
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Microbacteriaceae;sf_1;1513					0.004	-0.68					0.054	-0.49					0.003	0.69
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Microbacteriaceae;sf_1;1550																	0.016	0.59

Taxa string	DOC		Al		Ca		Fe		Mn		pH		SM		VPB		Soil Temp	
	P	r	P	r	P	r	P	r	P	r	P	r	P	r	P	r	P	r
Bacteria;Actinobacteria;Actinobacteria; Actinomycetales;Microbacteriaceae; sf_1;1640																	0.004	0.67
Bacteria;Actinobacteria;Actinobacteria; Actinomycetales;Microbacteriaceae; sf_1;1705																	0.009	0.63
Bacteria;Actinobacteria;Actinobacteria; Actinomycetales;Micrococcaceae; sf_1;1452					0.016	-0.59							0.039	-0.52				
Bacteria;Actinobacteria;Actinobacteria; Actinomycetales;Micromonosporaceae; sf_1;1395	0.015	0.59	0.026	0.55					0.001	0.76	0.011	-0.61	0.023	-0.56				
Bacteria;Actinobacteria;Actinobacteria; Actinomycetales;Micromonosporaceae; sf_1;1572													0.036	-0.53			0.021	0.57
Bacteria;Actinobacteria;Actinobacteria; Actinomycetales;Mycobacteriaceae; sf_1;1093									0.000	0.80			0.002	-0.72				
Bacteria;Actinobacteria;Actinobacteria; Actinomycetales;Nocardiaceae;sf_1;1142																	0.055	0.49
Bacteria;Actinobacteria;Actinobacteria; Actinomycetales;Nocardiaceae;sf_1;1809					0.052	-0.49												
Bacteria;Actinobacteria;Actinobacteria; Actinomycetales;Nocardiaceae;sf_1;1999									0.050	0.50			0.002	-0.72				
Bacteria;Actinobacteria;Actinobacteria; Actinomycetales;Sporichthyaceae ;sf_1;1223									0.003	0.70	0.040	-0.52	0.013	-0.61				
Bacteria;Actinobacteria;Actinobacteria; Actinomycetales;Sporichthyaceae; sf_1;1701													0.020	-0.58			0.004	0.67
Bacteria;Actinobacteria;Actinobacteria; Actinomycetales;Streptomycetaceae; sf_3;1743																	0.035	0.53
Bacteria;Actinobacteria;Actinobacteria; Actinomycetales;Streptosporangiaceae; sf_1;1535													0.022	-0.57			0.014	0.60
Bacteria;Actinobacteria;Actinobacteria; Actinomycetales;Thermomonosporaceae; sf_1;1406													0.030	-0.54			0.013	0.60
Bacteria;Actinobacteria;Actinobacteria; Actinomycetales;Unclassified;sf_3;1114	0.053	0.49	0.016	0.59					0.001	0.75	0.044	-0.51	0.013	-0.60				
Bacteria;Actinobacteria;Actinobacteria; Actinomycetales;Unclassified;sf_3;1369													0.047	-0.50			0.012	0.61
Bacteria;Actinobacteria;Actinobacteria; Actinomycetales;Unclassified;sf_3;1410													0.020	-0.57			0.007	0.65

Taxa string	DOC		Al		Ca		Fe		Mn		pH		SM		VPB		Soil Temp	
	P	**r**	**P**	**r**	**P**	**r**	**P**	**r**	**P**	**r**	**P**	**r**	**P**	**r**	**P**	**r**	**P**	**r**
Bacteria;Actinobacteria;Actinobacteria; Actinomycetales;Unclassified;sf_3;1564									0.000	0.77			0.002	-0.72			0.022	0.57
Bacteria;Actinobacteria;Actinobacteria; Unclassified;Unclassified;sf_1;1283																	0.019	0.58
Bacteria;Bacteroidetes;Sphingobacteria; Sphingobacteriales;Flexibacteraceae;sf_20;103					0.055	0.49							0.023	0.56				
Bacteria;Chloroflexi;Unclassified; Unclassified;Unclassified;sf_12;2523															0.031	-0.54	0.007	-0.65
Bacteria;Chloroflexi;Unclassified; Unclassified;Unclassified;sf_5;1051									0.003	-0.69								
Bacteria;Cyanobacteria;Unclassified; Unclassified;Unclassified;sf_6;5186																	0.038	-0.52
Bacteria;Firmicutes;Bacilli; Bacillales;Bacillaceae;sf_1;3893	0.030	-0.54	0.007	-0.64					0.010	-0.62	0.000	0.78						
Bacteria;Firmicutes;Bacilli; Bacillales;Staphylococcaceae;sf_1;3684			0.041	-0.51									0.001	0.73			0.025	-0.56
Bacteria;Firmicutes;Clostridia; Clostridiales;Clostridiaceae;sf_12;4359											0.027	0.55			0.017	-0.59		
Bacteria;Firmicutes;Clostridia; Unclassified;Unclassified;sf_7;4216							0.014	-0.60					0.046	0.51			0.017	-0.59
Bacteria;Firmicutes;Desulfotomaculum; Unclassified;Unclassified;sf_1;894	0.358	0.25	0.004	0.68	0.031	-0.54			0.011	0.62	0.015	-0.60	0.002	-0.71			0.039	0.52
Bacteria;Firmicutes;Symbiobacteria; Symbiobacterales;Unclassified;sf_1;2388	0.005	-0.66																
Bacteria;Proteobacteria;Alphaproteobacteria; Acetobacterales;Acetobacteraceae; sf_1;6841									0.007	0.65			0.014	-0.60				
Bacteria;Proteobacteria;Alphaproteobacteria; Acetobacterales;Acetobacteraceae; sf_1;7080			0.009	0.63					0.001	0.76			0.003	-0.68				
Bacteria;Proteobacteria;Alphaproteobacteria; Acetobacterales;Acetobacteraceae; sf_1;7414									0.001	0.74			0.019	-0.58			0.038	0.52
Bacteria;Proteobacteria;Alphaproteobacteria; Acetobacterales;Acetobacteraceae; sf_1;7452			0.030	0.54									0.027	-0.55			0.054	0.49
Bacteria;Proteobacteria;Alphaproteobacteria; Acetobacterales;Acetobacteraceae; sf_1;7565									0.003	0.69	0.048	-0.50						
Bacteria;Proteobacteria;Alphaproteobacteria; Acetobacterales;Acetobacteraceae; sf_1;7623			0.003	0.69					0.005	0.67	0.054	-0.49	0.002	-0.72			0.032	0.54
Bacteria;Proteobacteria;Alphaproteobacteria; Acetobacterales;Roseococcaceae; sf_1;6708													0.033	-0.54			0.010	0.62

Taxa string	DOC		Al		Ca		Fe		Mn		pH		SM		VPB		Soil Temp	
	P	r	P	r	P	r	P	r	P	r	P	r	P	r	P	r	P	r
Bacteria;Proteobacteria;Alphaproteobacteria;Bradyrhizobiales;Beijerinck/Rhodoplan/Methylocyst;sf_3;7000			0.050	0.50	0.007	-0.64					0.037	-0.52	0.032	-0.54				
Bacteria;Proteobacteria;Alphaproteobacteria;Bradyrhizobiales;Bradyrhizobiaceae;sf_1;7077			0.050	0.50	0.180	-0.35			0.000	0.86	0.026	-0.56	0.005	-0.66				
Bacteria;Proteobacteria;Alphaproteobacteria Bradyrhizobiales;Bradyrhizobiaceae;sf_1;7631									0.036	0.53			0.008	-0.64				
Bacteria;Proteobacteria;Alphaproteobacteria;Bradyrhizobiales;Hyphomicrobiaceae;sf_1;7389	0.013	-0.60															0.004	-0.68
Bacteria;Proteobacteria;Alphaproteobacteria;Caulobacterales;Caulobacteraceae;sf_1;6929	0.053	0.49	0.018	0.58	0.022	-0.57			0.029	0.55	0.003	-0.69	0.017	-0.59			0.007	0.64
Bacteria;Proteobacteria;Alphaproteobacteria;Caulobacterales;Caulobacteraceae;sf_1;6930			0.001	0.74					0.032	0.54	0.010	-0.62	0.014	-0.60				
Bacteria;Proteobacteria;Alphaproteobacteria;Caulobacterales;Caulobacteraceae;sf_1;7134																		
Bacteria;Proteobacteria;Alphaproteobacteria;Caulobacterales;Caulobacteraceae;sf_1;7245	0.027	0.55	0.022	0.57					0.003	0.69	0.007	-0.64	0.013	-0.61			0.010	0.62
Bacteria;Proteobacteria;Alphaproteobacteria;Caulobacterales;Caulobacteraceae;sf_1;7562									0.022	0.57								
Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Bradyrhizobiaceae;sf_1;6824			0.028	0.55					0.024	0.56			0.021	-0.57				
Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Unclassified;sf_5;7471			0.022	-0.57			0.044	-0.51			0.038	0.52						
Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;sf_1;7289	0.052	0.49													0.041	0.52		
Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;sf_1;7344					0.023	-0.56			0.029	0.55			0.001	-0.76			0.024	0.56
Bacteria;Proteobacteria;Alphaproteobacteria;Unclassified;Unclassified;sf_6;6844									0.003	0.69	0.054	-0.49	0.006	-0.65			0.007	0.64
Bacteria;Proteobacteria;Alphaproteobacteria;Unclassified;Unclassified;sf_6;7166																	0.015	0.60
Bacteria;Proteobacteria;Alphaproteobacteria;Unclassified;Unclassified;sf_6;7368	0.032	0.54							0.004	0.68			0.047	-0.50				
Bacteria;Proteobacteria;Alphaproteobacteria;Verorhodospirilla;Unclassified;sf_1;6740			0.056	-0.49			0.011	-0.62										

Taxa string	**DOC**		**Al**		**Ca**		**Fe**		**Mn**		**pH**		**SM**		**VPB**		**Soil Temp**	
	P	**r**	**P**	**r**	**P**	**r**	**P**	**r**	**P**	**r**	**P**	**r**	**P**	**r**	**P**	**r**	**P**	**r**
Bacteria;Proteobacteria;Betaproteobacteria; Burkholderiales;Burkholderiaceae; sf_1;7899			0.020	0.57							0.004	-0.68						
Bacteria;Proteobacteria;Betaproteobacteria; Burkholderiales;Burkholderiaceae; sf_1;7914					0.039	-0.52					0.016	-0.59			0.040	0.52		
Bacteria;Proteobacteria;Betaproteobacteria; Burkholderiales;Burkholderiaceae; sf_1;7934			0.005	0.66					0.015	0.59	0.004	-0.68	0.045	-0.51				
Bacteria;Proteobacteria;Betaproteobacteria; Burkholderiales;Comamonadaceae; sf_1;7754											0.031	-0.54						
Bacteria;Proteobacteria;Betaproteobacteria; Burkholderiales;Comamonadaceae; sf_1;7775			0.033	0.53	0.050	-0.50					0.023	-0.56						
Bacteria;Proteobacteria;Betaproteobacteria; Burkholderiales;Comamonadaceae;sf_1;7820	0.027	0.55							0.014	0.60	0.043	-0.51						
Bacteria;Proteobacteria;Betaproteobacteria; Burkholderiales;Comamonadaceae;sf_1;7920	0.034	0.53													0.010	0.62		
Bacteria;Proteobacteria;Betaproteobacteria; Burkholderiales;Comamonadaceae;sf_1;7937					0.025	-0.56					0.047	-0.50					0.001	0.76
Bacteria;Proteobacteria;Betaproteobacteria; Burkholderiales;Comamonadaceae;sf_1;8028									0.042	0.51								
Bacteria;Proteobacteria;Betaproteobacteria; Burkholderiales;Comamonadaceae;sf_1;8075			0.005	0.67							0.006	-0.66						
Bacteria;Proteobacteria;Betaproteobacteria; Burkholderiales;Comamonadaceae;sf_1;8083	0.045	0.51	0.009	0.63	0.052	-0.49					0.005	-0.67						
Bacteria;Proteobacteria;Betaproteobacteria; Burkholderiales;Comamonadaceae;sf_1;8117			0.017	0.59							0.007	-0.64						
Bacteria;Proteobacteria;Betaproteobacteria; Burkholderiales;Unclassified;sf_1;7832											0.004	-0.68			0.045	0.51		
Bacteria;Proteobacteria;Betaproteobacteria; Burkholderiales;Unclassified;sf_1;7944					0.019	-0.58					0.016	-0.59						
Bacteria;Proteobacteria;Betaproteobacteria; Burkholderiales;Unclassified;sf_1;8038											0.033	-0.53					0.039	0.52
Bacteria;Proteobacteria;Betaproteobacteria; Ellin6095/SC-I-39;Unclassified;sf_1;8093	0.019	-0.58	0.043	-0.51							0.041	0.52						
Bacteria;Proteobacteria;Betaproteobacteria; Neisseriales;Neisseriaceae;sf_1;7867			0.015	0.59					0.034	0.53	0.011	-0.62						
Bacteria;Proteobacteria;Betaproteobacteria; Rhodocyclales;Rhodocyclaceae;sf_1;7666															0.024	0.56		
Bacteria;Proteobacteria;Betaproteobacteria; Rhodocyclales;Rhodocyclaceae;sf_1;7875											0.043	-0.51						
Bacteria;Proteobacteria;Betaproteobacteria; Unclassified;Unclassified;sf_3;7723															0.053	-0.49		

Taxa string	DOC		Al		Ca		Fe		Mn		pH		SM		VPB		Soil Temp	
	P	r	P	r	P	r	P	r	P	r	P	r	P	r	P	r	P	r
Bacteria;Proteobacteria;Gammaproteobacteria Chromatiales;Chromatiaceae;sf_1;9571	0.031	-0.54																
Bacteria;Proteobacteria;Gammaproteobacteria Chromatiales;Ectothiorhodospiraceae;sf_11;83					0.052	0.49												
Bacteria;Proteobacteria;Gammaproteobacteria Ellin307/WD2124;Unclassified;sf_1;9374	0.030	0.54							0.019	0.58								
Bacteria;Proteobacteria;Gammaproteobacteria Legionellales;Unclassified;sf_1;9418									0.273	-0.29								
Bacteria;Proteobacteria;Unclassified; Unclassified;Unclassified;sf_28;10091									0.016	0.59								
Bacteria;Termite group 1;Unclassified; Unclassified;Unclassified;sf_2;722																	0.018	-0.58
Bacteria;Verrucomicrobia;Verrucomicrobiae; Verrucomicrobiales;Verrucomicrobia subdi 7;sf_1;760	0.040	-0.52																
Bacteria;Verrucomicrobia;Verrucomicrobiae; Verrucomicrobiales;Verrucomicrobiaceae;sf_1 4							0.008	-0.64										

Table 4: Environmental variables that showed a significant (P ≤ 0.55) linear correlation (Pearson's r) with taxa that showed a significant difference (t-test p≤ 0.50) between moss and grass on the top 2 cm of the soil profile (DNA level). Abbreviations are as follows: DOC; dissolved organic carbon, Al; aluminum, Ca; calcium, Fe; iron, Mn; manganese, SM; soil moisture, VPB; vascular plant biomass

Active taxa that significantly responded to aboveground plant type ($p \leq 0.05$)	**Higher relative abundance under Moss (M) or Grass (G)**
Archaea;Crenarchaeota;C1;C1a;Unclassified;sf_1;2583	**G**
Archaea;Crenarchaeota;Thermoprotei;Unclassified;Unclassified;sf_7;2582	**G**
Bacteria;Acidobacteria;Acidobacteria;Acidobacteriales;Acidobacteriaceae;sf_14;6368	**M**
Bacteria;Acidobacteria;Acidobacteria;Acidobacteriales;Acidobacteriaceae;sf_16;6414	**M**
Bacteria;Actinobacteria;Actinobacteria;Acidimicrobiales;Acidimicrobiaceae;sf_1;1478	**G**
Bacteria;Actinobacteria;Actinobacteria;Acidimicrobiales;Acidimicrobiaceae;sf_1;1524	**G**
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Acidothermaceae;sf_1;1399	**M**
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Actinomycetaceae;sf_1;1684	**M**
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Cellulomonadaceae;sf_1;1592	**G**
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Corynebacteriaceae;sf_1;1374	**G**
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Geodermatophilaceae;sf_1;1973	**G**
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Intrasporangiaceae;sf_1;1481	**G**
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Kineosporiaceae;sf_1;1424	**G**
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Kineosporiaceae;sf_1;2015	**G**
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Kribbella;sf_1;1839	**G**
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Microbacteriaceae;sf_1;1098	**G**
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Microbacteriaceae;sf_1;1513	**G**
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Microbacteriaceae;sf_1;1548	**G**
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Microbacteriaceae;sf_1;1705	**G**
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Micromonosporaceae;sf_1;1395	**G**
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Micromonosporaceae;sf_1;1572	**G**
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Micromonosporaceae;sf_1;1847	**G**
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Mycobacteriaceae;sf_1;1175	**G**
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Nocardiaceae;sf_1;1142	**G**
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Sporichthyaceae;sf_1;1223	**G**
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Streptomycetaceae;sf_1;1697	**G**
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Streptomycetaceae;sf_3;1743	**G**
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Unclassified;sf_3;1114	**G**
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Unclassified;sf_3;1369	**G**
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Unclassified;sf_3;1410	**G**
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Unclassified;sf_4;1337	**M**
Bacteria;Actinobacteria;Actinobacteria;Coriobacteriales;Coriobacteriaceae;sf_1;1800	**M**
Bacteria;Actinobacteria;Actinobacteria;Rubrobacterales;Rubrobacteraceae;sf_1;1480	**G**
Bacteria;Actinobacteria;Actinobacteria;Unclassified;Unclassified;sf_1;1283	**G**
Bacteria;Actinobacteria;Actinobacteria;Unclassified;Unclassified;sf_1;1588	**G**
Bacteria;AD3;Unclassified;Unclassified;Unclassified;sf_1;2338	**M**
Bacteria;Bacteroidetes;Bacteroidetes;Bacteroidales;Porphyromonadaceae;sf_1;5454	**M**
Bacteria;Bacteroidetes;Bacteroidetes;Bacteroidales;Unclassified;sf_15;5874	**M**
Bacteria;Bacteroidetes;Flavobacteria;Flavobacteriales;Blattabacteriaceae;sf_1;5828	**M**
Bacteria;Bacteroidetes;Flavobacteria;Flavobacteriales;Cryomorphaceae;sf_1;5400	**G**
Bacteria;Bacteroidetes;KSA1;Unclassified;Unclassified;sf_1;5951	**M**
Bacteria;Bacteroidetes;Sphingobacteria;Sphingobacteriales;Flexibacteraceae;sf_20;10311	**M**
Bacteria;Bacteroidetes;Sphingobacteria;Sphingobacteriales;Unclassified;sf_3;6298	**M**
Bacteria;Bacteroidetes;Sphingobacteria;Sphingobacteriales;Unclassified;sf_6;5439	**M**
Bacteria;Bacteroidetes;Unclassified;Unclassified;Unclassified;sf_4;5785	**M**

Active taxa that significantly responded to aboveground plant type ($p \leq 0.05$)	**Higher relative abundance under Moss (M) or Grass (G)**
Bacteria;Caldithrix;Unclassified;Caldithrales;Caldithraceae;sf_1;2384	**M**
Bacteria;Chlamydiae;Chlamydiae;Chlamydiales;Chlamydiaceae;sf_1;4820	**M**
Bacteria;Chlorobi;Unclassified;Unclassified;Unclassified;sf_6;5294	**M**
Bacteria;Chlorobi;Unclassified;Unclassified;Unclassified;sf_9;6146	**M**
Bacteria;Chloroflexi;Anaerolineae;Chloroflexi-1a;Unclassified;sf_1;258	**M**
Bacteria;Chloroflexi;Anaerolineae;Chloroflexi-1b;Unclassified;sf_2;789	**G**
Bacteria;Chloroflexi;Anaerolineae;Chloroflexi-1b;Unclassified;sf_3;2399	**G**
Bacteria;Chloroflexi;Chloroflexi-4;Unclassified;Unclassified;sf_2;2532	**M**
Bacteria;Chloroflexi;Dehalococcoidetes;Unclassified;Unclassified;sf_1;2497	**M**
Bacteria;Chloroflexi;Thermomicrobia;Unclassified;Unclassified;sf_2;652	**G**
Bacteria;Chloroflexi;Unclassified;Unclassified;Unclassified;sf_1;2534	**M**
Bacteria;Cyanobacteria;Cyanobacteria;Chloroplasts;Chloroplasts;sf_11;5123	**M**
Bacteria;Cyanobacteria;Cyanobacteria;Plectonema;Unclassified;sf_1;5190	**M**
Bacteria;Cyanobacteria;Cyanobacteria;Prochlorales;Unclassified;sf_1;5001	**M**
Bacteria;Cyanobacteria;Cyanobacteria;Thermosynechococcus;Unclassified;sf_1;5012	**M**
Bacteria;Deinococcus-Thermus;Unclassified;Unclassified;Unclassified;sf_3;920	**M**
Bacteria;Firmicutes;Bacilli;Bacillales;Alicyclobacillaceae;sf_1;3368	**G**
Bacteria;Firmicutes;Bacilli;Bacillales;Bacillaceae;sf_1;3898	**G**
Bacteria;Firmicutes;Bacilli;Bacillales;Paenibacillaceae;sf_1;3641	**M**
Bacteria;Firmicutes;Bacilli;Bacillales;Sporolactobacillaceae;sf_1;3365	**G**
Bacteria;Firmicutes;Catabacter;Unclassified;Unclassified;sf_1;4293	**M**
Bacteria;Firmicutes;Catabacter;Unclassified;Unclassified;sf_4;2716	**M**
Bacteria;Firmicutes;Clostridia;Clostridiales;Peptostreptococcaceae;sf_5;2913	**M**
Bacteria;Firmicutes;Clostridia;Clostridiales;Syntrophomonadaceae;sf_5;2456	**M**
Bacteria;Firmicutes;Mollicutes;Anaeroplasmatales;Erysipelotrichaceae;sf_3;3981	**M**
Bacteria;Firmicutes;Mollicutes;Mycoplasmatales;Mycoplasmataceae;sf_1;3929	**M**
Bacteria;marine group A;mgA-2;Unclassified;Unclassified;sf_1;6344	**M**
Bacteria;Natronoanaerobium;Unclassified;Unclassified;Unclassified;sf_1;2437	**M**
Bacteria;OP10;Unclassified;Unclassified;Unclassified;sf_5;9782	**M**
Bacteria;OP3;Unclassified;Unclassified;Unclassified;sf_2;349	**G**
Bacteria;OP3;Unclassified;Unclassified;Unclassified;sf_3;1015	**G**
Bacteria;OP8;Unclassified;Unclassified;Unclassified;sf_3;598	**M**
Bacteria;OP9/JS1;OP9;Unclassified;Unclassified;sf_1;969	**M**
Bacteria;Planctomycetes;Planctomycetacia;Planctomycetales;Anammoxales;sf_4;4695	**G**
Bacteria;Planctomycetes;Planctomycetacia;Planctomycetales;Gemmatae;sf_1;4857	**G**
Bacteria;Planctomycetes;Planctomycetacia;Planctomycetales;Isosphaerae;sf_1;4749	**G**
Bacteria;Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;sf_3;4948	**G**
Bacteria;Proteobacteria;Alphaproteobacteria;Acetobacterales;Acetobacteraceae;sf_1;6841	**G**
Bacteria;Proteobacteria;Alphaproteobacteria;Acetobacterales;Acetobacteraceae;sf_1;7080	**G**
Bacteria;Proteobacteria;Alphaproteobacteria;Acetobacterales;Acetobacteraceae;sf_1;7414	**G**
Bacteria;Proteobacteria;Alphaproteobacteria;Acetobacterales;Acetobacteraceae;sf_1;7565	**G**
Bacteria;Proteobacteria;Alphaproteobacteria;Bradyrhizobiales;Bradyrhizobiaceae;sf_1;6942	**G**
Bacteria;Proteobacteria;Alphaproteobacteria;Bradyrhizobiales;Methylobacteriaceae;sf_1;7593	**G**
Bacteria;Proteobacteria;Alphaproteobacteria;Bradyrhizobiales;Xanthobacteraceae;sf_1;6971	**M**
Bacteria;Proteobacteria;Alphaproteobacteria;Caulobacterales;Caulobacteraceae;sf_1;7578	**G**

Active taxa that significantly responded to aboveground plant type ($p \leq 0.05$)	**Higher relative abundance under Moss (M) or Grass (G)**
Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Beijerinck/Rhodoplan/Methylocyst;sf_1;7591	**M**
Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Unclassified;sf_1;6938	**G**
Bacteria;Proteobacteria;Alphaproteobacteria;Rickettsiales;Rickettsiaceae;sf_1;7556	**M**
Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;sf_1;7344	**G**
Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;sf_15;7035	**M**
Bacteria;Proteobacteria;Alphaproteobacteria;Unclassified;Unclassified;sf_2;7188	**M**
Bacteria;Proteobacteria;Alphaproteobacteria;Unclassified;Unclassified;sf_6;6844	**G**
Bacteria;Proteobacteria;Alphaproteobacteria;Unclassified;Unclassified;sf_6;7166	**G**
Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae;sf_1;7899	**G**
Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;sf_1;7754	**G**
Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;sf_1;7786	**G**
Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Oxalobacteraceae;sf_1;8032	**M**
Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Ralstoniaceae;sf_1;7778	**M**
Bacteria;Proteobacteria;Betaproteobacteria;Hydrogenophilales;Hydrogenophilaceae;sf_1;7975	**G**
Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Nitrosomonadaceae;sf_1;7789	**M**
Bacteria;Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae;sf_1;7875	**G**
Bacteria;Proteobacteria;Deltaproteobacteria;dechlorinating clone group;Unclassified;sf_1;9959	**M**
Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Unclassified;sf_4;9951	**M**
Bacteria;Proteobacteria;Deltaproteobacteria;Desulfovibrionales;Desulfohalobiaceae;sf_1;9894	**M**
Bacteria;Proteobacteria;Deltaproteobacteria;Desulfovibrionales;Desulfomicrobiaceae;sf_1;10079	**M**
Bacteria;Proteobacteria;Deltaproteobacteria;EB1021 group;Unclassified;sf_4;9741	**M**
Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Myxococcaceae;sf_1;10358	**M**
Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Unclassified;sf_1;10092	**M**
Bacteria;Proteobacteria;Deltaproteobacteria;Unclassified;Unclassified;sf_9;9786	**G**
Bacteria;Proteobacteria;Epsilonproteobacteria;Campylobacterales;Campylobacteraceae;sf_3;10538	**M**
Bacteria;Proteobacteria;Epsilonproteobacteria;Campylobacterales;Helicobacteraceae;sf_3;10442	**M**
Bacteria;Proteobacteria;Epsilonproteobacteria;Campylobacterales;Unclassified;sf_1;10530	**M**
Bacteria;Proteobacteria;Gammaproteobacteria;Aeromonadales;Aeromonadaceae;sf_1;9294	**M**
Bacteria;Proteobacteria;Gammaproteobacteria;Alteromonadales;Alteromonadaceae;sf_1;8578	**M**
Bacteria;Proteobacteria;Gammaproteobacteria;aquatic clone group;Unclassified;sf_1;9246	**M**
Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Ectothiorhodospiraceae;sf_1;9598	**M**
Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Unclassified;sf_1;9316	**G**
Bacteria;Proteobacteria;Gammaproteobacteria;Legionellales;Coxiellaceae;sf_3;8457	**M**
Bacteria;Proteobacteria;Gammaproteobacteria;Legionellales;Unclassified;sf_3;8587	**M**
Bacteria;Proteobacteria;Gammaproteobacteria;Oceanospirillales;Alcanivoraceae;sf_1;8335	**M**
Bacteria;Proteobacteria;Gammaproteobacteria;Oceanospirillales;Unclassified;sf_3;9010	**M**
Bacteria;Proteobacteria;Gammaproteobacteria;Pseudomonadales;Moraxellaceae;sf_3;9466	**M**
Bacteria;Proteobacteria;Gammaproteobacteria;Pseudomonadales;Pseudomonadaceae;sf_1;9005	**M**
Bacteria;Proteobacteria;Gammaproteobacteria;SAR86;Unclassified;sf_1;8962	**M**
Bacteria;Proteobacteria;Gammaproteobacteria;Symbionts;Unclassified;sf_1;8403	**G**
Bacteria;Proteobacteria;Gammaproteobacteria;Thiotrichales;Thiotrichaceae;sf_3;8559	**M**
Bacteria;Proteobacteria;Gammaproteobacteria;uranium waste clones;Unclassified;sf_1;8747	**M**
Bacteria;Proteobacteria;Gammaproteobacteria;Xanthomonadales;Xanthomonadaceae;sf_3;9150	**G**
Bacteria;Proteobacteria;Unclassified;Unclassified;Unclassified;sf_28;10091	**G**

Active taxa that significantly responded to aboveground plant type ($p \leq 0.05$)	**Higher relative abundance under Moss (M) or Grass (G)**
Bacteria;Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;sf_1;6479	**M**
Bacteria;Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;sf_2;6493	**M**
Bacteria;Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;sf_3;6558	**M**
Bacteria;SR1;Unclassified;Unclassified;Unclassified;sf_1;2900	**G**
Bacteria;TM7;TM7-3;Unclassified;Unclassified;sf_1;8155	**M**
Bacteria;TM7;Unclassified;Unclassified;Unclassified;sf_1;3255	**G**
Bacteria;Unclassified;Unclassified;Unclassified;Unclassified;sf_119;874	**G**
Bacteria;Unclassified;Unclassified;Unclassified;Unclassified;sf_126;296	**G**
Bacteria;Unclassified;Unclassified;Unclassified;Unclassified;sf_156;4291	**M**
Bacteria;Unclassified;Unclassified;Unclassified;Unclassified;sf_160;6380	**G**
Bacteria;Unclassified;Unclassified;Unclassified;Unclassified;sf_72;450	**G**
Bacteria;Unclassified;Unclassified;Unclassified;Unclassified;sf_92;9999	**M**
Bacteria;Unclassified;Unclassified;Unclassified;Unclassified;sf_93;925	**M**
Bacteria;Unclassified;Unclassified;Unclassified;Unclassified;sf_95;2545	**M**
Bacteria;Verrucomicrobia;Unclassified;Unclassified;Unclassified;sf_3;486	**M**
Bacteria;Verrucomicrobia;Unclassified;Unclassified;Unclassified;sf_5;686	**G**
Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Unclassified;sf_3;430	**G**
Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Unclassified;sf_3;565	**G**
Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobia subdivision 5;sf_1;547	**M**
Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobiaceae;sf_6;660	**G**
Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobiaceae;sf_7;29	**G**
Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Xiphinematobacteraceae;sf_3;888	**M**
Bacteria;WS5;Unclassified;Unclassified;Unclassified;sf_2;8119	**M**

Table 5: Taxa, from the active community (cDNA), that significantly (t-test; $p < 0.05$)) responded to the aboveground plant type (moss or grass). Post hoc Tukey HSD test revealed the directionality of the difference; higher relative abundance under moss (M) or grass (G).

Active taxa that significantly responded to aboveground plant type	**Ca**		**Mn**		**pH**		**SM**		**VPB**	
	P	**r**	**P**	**r**	**P**	**r**	**P**	**r**	**P**	**r**
Bacteria;Acidobacteria;Acidobacteria;Acidobacteriales;Acidobacteriaceae;sf_16;6414									0.027	-0.77
Bacteria;Actinobacteria;Actinobacteria;Acidimicrobiales;Acidimicrobiaceae;sf_1;1478										
Bacteria;Actinobacteria;Actinobacteria;Acidimicrobiales;Acidimicrobiaceae;sf_1;1524			0.008	0.84					0.032	0.75
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Cellulomonadaceae;sf_1;1592	0.052	-0.70	0.038	0.73						
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Corynebacteriaceae;sf_1;1374	0.011	-0.83	0.000	0.95	0.049	-0.71			0.005	0.87
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Geodermatophilaceae;sf_1;1973			0.052	0.70						
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Intrasporangiaceae;sf_1;1481	0.032	-0.75	0.031	0.75			0.018	-0.79		
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Kineosporiaceae;sf_1;1424			0.031	0.75						
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Kineosporiaceae;sf_1;2015			0.017	0.80						
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Kribbella;sf_1;1839							0.055	-0.70		
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Microbacteriaceae;sf_1;1098	0.011	-0.83	0.013	0.82					0.027	0.76
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Microbacteriaceae;sf_1;1513	0.018	-0.80								
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Microbacteriaceae;sf_1;1548	0.055	-0.70	0.026	0.77					0.036	0.74
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Microbacteriaceae;sf_1;1705										
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Micromonosporaceae;sf_1;1395			0.032	0.75			0.020	-0.79		
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Micromonosporaceae;sf_1;1847			0.012	0.82	0.038	-0.73			0.010	0.83
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Mycobacteriaceae;sf_1;1175			0.003	0.89	0.021	-0.79			0.038	0.74
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Nocardiaceae;sf_1;1142			0.002	0.90					0.008	0.85
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Streptomycetaceae;sf_1;1697			0.007	0.85					0.017	0.80
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Streptomycetaceae;sf_3;1743			0.005	0.87					0.033	0.75
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Unclassified;sf_3;1369			0.009	0.84					0.024	0.78
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Unclassified;sf_3;1410			0.040	0.73						
Bacteria;Actinobacteria;Actinobacteria;Unclassified;Unclassified;sf_1;1283			0.006	0.86					0.040	0.73
Bacteria;Actinobacteria;Actinobacteria;Unclassified;Unclassified;sf_1;1588			0.009	0.84					0.035	0.74
Bacteria;AD3;Unclassified;Unclassified;Unclassified;sf_1;2338					0.034	0.74			0.015	-0.81
Bacteria;Chlorobi;Unclassified;Unclassified;Unclassified;sf_9;6146			0.027	-0.76					0.011	-0.83
Bacteria;Cyanobacteria;Cyanobacteria;Plectonema;Unclassified;sf_1;5190	0.052	0.70	0.003	-0.89	0.012	0.82			0.000	-0.96
Bacteria;Cyanobacteria;Cyanobacteria;Prochlorales;Unclassified;sf_1;5001	0.019	0.79	0.043	-0.72					0.004	-0.87
Bacteria;Cyanobacteria;Cyanobacteria;Thermosynechococcus;Unclassified;sf_1;5012	0.019	0.79			0.046	0.71			0.024	-0.78
Bacteria;Firmicutes;Clostridia;Clostridiales;Syntrophomonadaceae;sf_5;2456									0.035	-0.74
Bacteria;OP3;Unclassified;Unclassified;Unclassified;sf_2;349					0.031	-0.75				
Bacteria;OP8;Unclassified;Unclassified;Unclassified;sf_3;598					0.028	0.76				
Bacteria;Planctomycetes;Planctomycetacia;Planctomycetales;Anammoxales;sf_4;4695			0.016	0.80	0.008	-0.84			0.003	0.89

Active taxa that significantly responded to aboveground plant type	Ca		Mn		pH		SM		VPB	
	P	r	P	r	P	r	P	r	P	r
Bacteria;Proteobacteria;Alphaproteobacteria;Bradyrhizobiales;Bradyrhizobiaceae;sf_1;6942					0.032	-0.75				
Bacteria;Proteobacteria;Alphaproteobacteria;Bradyrhizobiales;Xanthobacteraceae;sf_1;6971	0.010	0.83	0.007	-0.85					0.044	-0.72
Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Oxalobacteraceae;sf_1;8032			0.044	-0.72					0.033	-0.75
Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Ralstoniaceae;sf_1;7778					0.019	0.79				
Bacteria;Proteobacteria;Deltaproteobacteria;Unclassified;Unclassified;sf_9;9786	0.026	-0.77	0.024	0.77					0.047	0.71
Bacteria;Proteobacteria;Gammaproteobacteria;Aeromonadales;Aeromonadaceae;sf_1;9294	0.011	0.83	0.018	-0.80	0.016	0.80			0.004	-0.88
Bacteria;Proteobacteria;Gammaproteobacteria;Alteromonadales;Alteromonadaceae;sf_1;8578	0.022	0.78	0.035	-0.74	0.010	0.83			0.010	-0.83
Bacteria;Proteobacteria;Gammaproteobacteria;Legionellales;Unclassified;sf_3;8587			0.040	-0.73					0.042	-0.72
Bacteria;Proteobacteria;Gammaproteobacteria;Pseudomonadales;Pseudomonadaceae;sf_1;9005	0.005	0.87	0.016	-0.80	0.050	0.71			0.007	-0.85
Bacteria;Proteobacteria;Gammaproteobacteria;Symbionts;Unclassified;sf_1;8403					0.007	-0.85				
Bacteria;Proteobacteria;Gammaproteobacteria;uranium waste clones;Unclassified;sf_1;8747	0.044	0.72								
Bacteria;SR1;Unclassified;Unclassified;Unclassified;sf_1;2900			0.004	0.88					0.011	0.83
Bacteria;Unclassified;Unclassified;Unclassified;Unclassified;sf_72;450			0.024	0.77	0.050	-0.71			0.016	0.81
Bacteria;Unclassified;Unclassified;Unclassified;Unclassified;sf_92;9999			0.053	-0.70			0.032	0.75		
Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Unclassified;sf_3;565					0.012	-0.82				

Table 6: Environmental variables that showed a significant ($P \leq 0.50$) correlation (Pearson's r) with taxa from the active (cDNA) community that showed a significant difference (t-test $p \leq 0.50$) between moss and grass. Abbreviations are as follows: Ca; calcium, Mn; manganese, SM; soil moisture, VPB; vascular plant biomass.

Taxa that significantly responded to depth (0-2 cm vs 8-10 cm)	Higher relative Abundance on top (T) or bottom (B) 2 cm of soil profile
Bacteria;Acidobacteria;Acidobacteria;Acidobacteriales;Acidobacteriaceae;sf_1;6371	**B**
Bacteria;Acidobacteria;Acidobacteria;Acidobacteriales;Acidobacteriaceae;sf_1;877	**B**
Bacteria;Acidobacteria;Acidobacteria;Acidobacteriales;Acidobacteriaceae;sf_14;401	**B**
Bacteria;Acidobacteria;Acidobacteria;Acidobacteriales;Acidobacteriaceae;sf_6;6362	**B**
Bacteria;Acidobacteria;Acidobacteria-10;Unclassified;Unclassified;sf_1;516	**B**
Bacteria;Acidobacteria;Acidobacteria-4;Ellin6075/11-25;Unclassified;sf_1;435	**T**
Bacteria;Acidobacteria;Acidobacteria-6;Unclassified;Unclassified;sf_1;1014	**T**
Bacteria;Acidobacteria;Acidobacteria-7;Unclassified;Unclassified;sf_1;588	**B**
Bacteria;Acidobacteria;Acidobacteria-9;Unclassified;Unclassified;sf_1;704	**B**
Bacteria;Acidobacteria;Unclassified;Unclassified;Unclassified;sf_1;572	**B**
Bacteria;Actinobacteria;Actinobacteria;Acidimicrobiales;Microthrixineae;sf_1;1408	**B**
Bacteria;Actinobacteria;Actinobacteria;Acidimicrobiales;Unclassified;sf_2;1811	**B**
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Acidothermaceae;sf_1;1399	**B**
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Actinomycetaceae;sf_1;1672	**T**
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Actinosynnemataceae;sf_1;1951	**T**
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Brevibacteriaceae;sf_1;1745	**T**
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Cellulomonadaceae;sf_1;1592	**T**
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Cellulomonadaceae;sf_1;2061	**T**
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Corynebacteriaceae;sf_1;1374	**T**
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Dermabacteraceae;sf_1;1736	**T**
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Dermatophilaceae;sf_1;1852	**T**
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Frankiaceae;sf_1;1286	**B**
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Geodermatophilaceae;sf_1;1245	**T**
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Geodermatophilaceae;sf_1;1973	**T**
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Kineosporiaceae;sf_1;2015	**T**
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Kribbella;sf_1;1839	**T**
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Microbacteriaceae;sf_1;1507	**T**
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Microbacteriaceae;sf_1;1513	**T**
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Microbacteriaceae;sf_1;1550	**T**
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Microbacteriaceae;sf_1;1640	**T**
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Microbacteriaceae;sf_1;1705	**T**
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Micrococcaceae;sf_1;1099	**T**
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Micrococcaceae;sf_1;1452	**T**
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Micromonosporaceae;sf_1;1316	**T**
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Micromonosporaceae;sf_1;1395	**T**
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Micromonosporaceae;sf_1;1462	**T**
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Micromonosporaceae;sf_1;1876	**T**
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Nocardiaceae;sf_1;1142	**T**
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Nocardiaceae;sf_1;1809	**T**
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Nocardioidaceae;sf_1;1854	**T**
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Propionibacteriaceae;sf_1;1315	**T**
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Sporichthyaceae;sf_1;1223	**T**
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Streptomycetaceae;sf_1;1128	**B**

Taxa that significantly responded to depth (0-2 cm vs 8-10 cm)	**Higher relative Abundance on top (T) or bottom (B) 2 cm of soil profile**
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Streptomycetaceae;sf_3;1743	**T**
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Streptosporangiaceae;sf_1;1535	**T**
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Unclassified;sf_3;1564	**T**
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Unclassified;sf_3;1806	**T**
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Unclassified;sf_4;1337	**B**
Bacteria;Actinobacteria;Actinobacteria;Coriobacteriales;Coriobacteriaceae;sf_1;1459	**B**
Bacteria;Actinobacteria;Actinobacteria;Rubrobacterales;Rubrobacteraceae;sf_1;1980	**T**
Bacteria;Actinobacteria;Actinobacteria;Unclassified;Unclassified;sf_1;1118	**B**
Bacteria;Actinobacteria;Actinobacteria;Unclassified;Unclassified;sf_1;1490	**B**
Bacteria;Actinobacteria;Actinobacteria;Unclassified;Unclassified;sf_1;1498	**B**
Bacteria;Actinobacteria;Actinobacteria;Unclassified;Unclassified;sf_1;1588	**T**
Bacteria;Actinobacteria;Actinobacteria;Unclassified;Unclassified;sf_2;1233	**B**
Bacteria;Actinobacteria;BD2-10 group;Unclassified;Unclassified;sf_1;1675	**B**
Bacteria;AD3;Unclassified;Unclassified;Unclassified;sf_1;2338	**B**
Bacteria;Bacteroidetes;Bacteroidetes;Bacteroidales;Bacteroidaceae;sf_6;5792	**T**
Bacteria;Bacteroidetes;Bacteroidetes;Bacteroidales;Porphyromonadaceae;sf_1;5454	**T**
Bacteria;Bacteroidetes;Bacteroidetes;Bacteroidales;Prevotellaceae;sf_1;6118	**T**
Bacteria;Bacteroidetes;Bacteroidetes;Bacteroidales;Prevotellaceae;sf_1;6152	**T**
Bacteria;Bacteroidetes;Bacteroidetes;Bacteroidales;Rikenellaceae;sf_5;5892	**T**
Bacteria;Bacteroidetes;Flavobacteria;Flavobacteriales;Cryomorphaceae;sf_1;5400	**T**
Bacteria;Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae;sf_1;5341	**T**
Bacteria;Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae;sf_1;5559	**T**
Bacteria;Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae;sf_1;5636	**T**
Bacteria;Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae;sf_1;5906	**B**
Bacteria;Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae;sf_1;5918	**B**
Bacteria;Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae;sf_1;6200	**T**
Bacteria;Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae;sf_1;6241	**T**
Bacteria;Bacteroidetes;Sphingobacteria;Sphingobacteriales;Crenotrichaceae;sf_11;5266	**T**
Bacteria;Bacteroidetes;Sphingobacteria;Sphingobacteriales;Crenotrichaceae;sf_11;5283	**T**
Bacteria;Bacteroidetes;Sphingobacteria;Sphingobacteriales;Crenotrichaceae;sf_11;5288	**T**
Bacteria;Bacteroidetes;Sphingobacteria;Sphingobacteriales;Crenotrichaceae;sf_11;5354	**T**
Bacteria;Bacteroidetes;Sphingobacteria;Sphingobacteriales;Crenotrichaceae;sf_11;5387	**T**
Bacteria;Bacteroidetes;Sphingobacteria;Sphingobacteriales;Crenotrichaceae;sf_11;5491	**T**
Bacteria;Bacteroidetes;Sphingobacteria;Sphingobacteriales;Crenotrichaceae;sf_11;5581	**T**
Bacteria;Bacteroidetes;Sphingobacteria;Sphingobacteriales;Crenotrichaceae;sf_11;5872	**T**
Bacteria;Bacteroidetes;Sphingobacteria;Sphingobacteriales;Crenotrichaceae;sf_11;5925	**T**
Bacteria;Bacteroidetes;Sphingobacteria;Sphingobacteriales;Crenotrichaceae;sf_11;5948	**T**
Bacteria;Bacteroidetes;Sphingobacteria;Sphingobacteriales;Crenotrichaceae;sf_11;5970	**T**
Bacteria;Bacteroidetes;Sphingobacteria;Sphingobacteriales;Crenotrichaceae;sf_11;5987	**T**
Bacteria;Bacteroidetes;Sphingobacteria;Sphingobacteriales;Crenotrichaceae;sf_11;6003	**T**
Bacteria;Bacteroidetes;Sphingobacteria;Sphingobacteriales;Crenotrichaceae;sf_11;6148	**T**
Bacteria;Bacteroidetes;Sphingobacteria;Sphingobacteriales;Crenotrichaceae;sf_11;6196	**T**
Bacteria;Bacteroidetes;Sphingobacteria;Sphingobacteriales;Crenotrichaceae;sf_11;6245	**T**
Bacteria;Bacteroidetes;Sphingobacteria;Sphingobacteriales;Crenotrichaceae;sf_11;6281	**T**
Bacteria;Bacteroidetes;Sphingobacteria;Sphingobacteriales;Crenotrichaceae;sf_11;6325	**T**

Taxa that significantly responded to depth (0-2 cm vs 8-10 cm)	**Higher relative Abundance on top (T) or bottom (B) 2 cm of soil profile**
Bacteria;Bacteroidetes;Sphingobacteria;Sphingobacteriales;Flammeovirgaceae;sf_5;6084	**T**
Bacteria;Bacteroidetes;Sphingobacteria;Sphingobacteriales;Flexibacteraceae;sf_19;6048	**T**
Bacteria;Bacteroidetes;Sphingobacteria;Sphingobacteriales;Flexibacteraceae;sf_19;6054	**T**
Bacteria;Bacteroidetes;Sphingobacteria;Sphingobacteriales;Flexibacteraceae;sf_19;6304	**T**
Bacteria;Bacteroidetes;Sphingobacteria;Sphingobacteriales;Sphingobacteriaceae;sf_1;5840	**T**
Bacteria;Bacteroidetes;Sphingobacteria;Sphingobacteriales;Unclassified;sf_4;6030	**T**
Bacteria;Bacteroidetes;Unclassified;Unclassified;Unclassified;sf_4;5814	**T**
Bacteria;BRC1;Unclassified;Unclassified;Unclassified;sf_1;5051	**B**
Bacteria;Chlorobi;Unclassified;Unclassified;Unclassified;sf_6;5294	**T**
Bacteria;Chloroflexi;Anaerolineae;Chloroflexi-1a;Unclassified;sf_1;258	**B**
Bacteria;Chloroflexi;Anaerolineae;Chloroflexi-1f;Unclassified;sf_1;765	**B**
Bacteria;Chloroflexi;Anaerolineae;Unclassified;Unclassified;sf_1;266	**B**
Bacteria;Chloroflexi;Anaerolineae;Unclassified;Unclassified;sf_7;663	**B**
Bacteria;Chloroflexi;Chloroflexi-4;Unclassified;Unclassified;sf_2;2532	**B**
Bacteria;Chloroflexi;Unclassified;Unclassified;Unclassified;sf_12;2523	**B**
Bacteria;Chloroflexi;Unclassified;Unclassified;Unclassified;sf_5;1051	**B**
Bacteria;Cyanobacteria;Cyanobacteria;Chloroplasts;Chloroplasts;sf_13;5000	**T**
Bacteria;Cyanobacteria;Cyanobacteria;Chloroplasts;Chloroplasts;sf_5;5026	**T**
Bacteria;Cyanobacteria;Cyanobacteria;Chroococcales;Unclassified;sf_1;5219	**T**
Bacteria;Cyanobacteria;Cyanobacteria;Nostocales;Unclassified;sf_1;5057	**T**
Bacteria;Cyanobacteria;Cyanobacteria;Oscillatoriales;Unclassified;sf_1;5159	**B**
Bacteria;Cyanobacteria;Cyanobacteria;Phormidium;Unclassified;sf_1;4978	**T**
Bacteria;Cyanobacteria;Cyanobacteria;Scytonema;Unclassified;sf_1;5115	**T**
Bacteria;Cyanobacteria;Unclassified;Unclassified;Unclassified;sf_9;5164	**T**
Bacteria;Deferribacteres;Deferribacer;Unclassified;Unclassified;sf_1;797	**B**
Bacteria;Deinococcus-Thermus;Unclassified;Unclassified;Unclassified;sf_2;637	**T**
Bacteria;Dictyoglomi;Dictyoglomi;Dictyoglomales;Dictyoglomaceae;sf_9;7579	**T**
Bacteria;Firmicutes;Anaerobranca;Unclassified;Unclassified;sf_1;4304	**B**
Bacteria;Firmicutes;Bacilli;Bacillales;Alicyclobacillaceae;sf_1;3368	**B**
Bacteria;Firmicutes;Bacilli;Bacillales;Bacillaceae;sf_1;3370	**B**
Bacteria;Firmicutes;Bacilli;Bacillales;Bacillaceae;sf_1;3626	**B**
Bacteria;Firmicutes;Bacilli;Bacillales;Caryophanaceae;sf_1;3285	**B**
Bacteria;Firmicutes;Bacilli;Bacillales;Halobacillaceae;sf_1;3756	**B**
Bacteria;Firmicutes;Bacilli;Bacillales;Paenibacillaceae;sf_1;3247	**B**
Bacteria;Firmicutes;Bacilli;Bacillales;Paenibacillaceae;sf_1;3766	**B**
Bacteria;Firmicutes;Bacilli;Bacillales;Sporolactobacillaceae;sf_1;3365	**B**
Bacteria;Firmicutes;Bacilli;Bacillales;Staphylococcaceae;sf_1;3684	**B**
Bacteria;Firmicutes;Bacilli;Bacillales;Thermoactinomycetaceae;sf_1;3301	**B**
Bacteria;Firmicutes;Bacilli;Bacillales;Unclassified;sf_3;3743	**B**
Bacteria;Firmicutes;Bacilli;Lactobacillales;Carnobacteriaceae;sf_1;3536	**B**
Bacteria;Firmicutes;Bacilli;Lactobacillales;Enterococcaceae;sf_1;3433	**B**
Bacteria;Firmicutes;Bacilli;Lactobacillales;Unclassified;sf_1;3434	**B**
Bacteria;Firmicutes;Catabacter;Unclassified;Unclassified;sf_4;2716	**B**
Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiaceae;sf_12;4359	**B**

Taxa that significantly responded to depth (0-2 cm vs 8-10 cm)	Higher relative Abundance on top (T) or bottom (B) 2 cm of soil profile
Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiaceae;sf_21;4471	**B**
Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;sf_5;4316	**B**
Bacteria;Firmicutes;Clostridia;Clostridiales;Peptococc/Acidaminococc;sf_11;177	**T**
Bacteria;Firmicutes;Clostridia;Clostridiales;Peptococc/Acidaminococc;sf_11;185	**B**
Bacteria;Firmicutes;Clostridia;Clostridiales;Peptococc/Acidaminococc;sf_11;49	**B**
Bacteria;Firmicutes;Clostridia;Clostridiales;Peptococc/Acidaminococc;sf_11;903	**B**
Bacteria;Firmicutes;Clostridia;Clostridiales;Peptostreptococcaceae;sf_5;2913	**B**
Bacteria;Firmicutes;Clostridia;Clostridiales;Syntrophomonadaceae;sf_5;2456	**B**
Bacteria;Firmicutes;Clostridia;Clostridiales;Unclassified;sf_17;2659	**T**
Bacteria;Firmicutes;Clostridia;Unclassified;Unclassified;sf_3;2373	**B**
Bacteria;Firmicutes;Clostridia;Unclassified;Unclassified;sf_4;2398	**B**
Bacteria;Firmicutes;Desulfotomaculum;Unclassified;Unclassified;sf_1;894	**T**
Bacteria;Firmicutes;gut clone group;Unclassified;Unclassified;sf_1;4616	**B**
Bacteria;Firmicutes;Symbiobacteria;Symbiobacterales;Unclassified;sf_1;2388	**B**
Bacteria;Firmicutes;Symbiobacteria;Symbiobacterales;Unclassified;sf_3;3508	**B**
Bacteria;Firmicutes;Unclassified;Unclassified;Unclassified;sf_8;546	**T**
Bacteria;Lentisphaerae;Unclassified;Unclassified;Unclassified;sf_5;10330	**B**
Bacteria;marine group A;mgA-1;Unclassified;Unclassified;sf_1;6454	**B**
Bacteria;marine group A;mgA-2;Unclassified;Unclassified;sf_1;6344	**T**
Bacteria;NC10;NC10-1;Unclassified;Unclassified;sf_1;452	**B**
Bacteria;NC10;NC10-2;Unclassified;Unclassified;sf_1;10254	**B**
Bacteria;NC10;Unclassified;Unclassified;Unclassified;sf_1;2516	**B**
Bacteria;Nitrospira;Nitrospira;Nitrospirales;Nitrospiraceae;sf_1;860	**B**
Bacteria;Nitrospira;Nitrospira;Nitrospirales;Nitrospiraceae;sf_2;697	**B**
Bacteria;OP10;Unclassified;Unclassified;Unclassified;sf_1;8413	**B**
Bacteria;OP3;Unclassified;Unclassified;Unclassified;sf_3;1015	**B**
Bacteria;OP3;Unclassified;Unclassified;Unclassified;sf_4;628	**B**
Bacteria;OP9/JS1;JS1;Unclassified;Unclassified;sf_1;2489	**B**
Bacteria;OS-K;Unclassified;Unclassified;Unclassified;sf_1;501	**B**
Bacteria;Planctomycetes;Planctomycetacia;Planctomycetales;Anammoxales;sf_2;4683	**B**
Bacteria;Planctomycetes;Planctomycetacia;Planctomycetales;Gemmatae;sf_1;4866	**B**
Bacteria;Planctomycetes;Planctomycetacia;Planctomycetales;Isosphaerae;sf_1;4856	**T**
Bacteria;Planctomycetes;Planctomycetacia;Planctomycetales;Pirellulae;sf_3;4687	**B**
Bacteria;Planctomycetes;Planctomycetacia;Planctomycetales;Pirellulae;sf_3;4712	**T**
Bacteria;Planctomycetes;Planctomycetacia;Planctomycetales;Pirellulae;sf_3;4726	**B**
Bacteria;Planctomycetes;Planctomycetacia;Planctomycetales;Pirellulae;sf_3;4744	**T**
Bacteria;Planctomycetes;Planctomycetacia;Planctomycetales;Pirellulae;sf_3;4754	**B**
Bacteria;Planctomycetes;Planctomycetacia;Planctomycetales;Pirellulae;sf_3;4894	**B**
Bacteria;Planctomycetes;Planctomycetacia;Planctomycetales;Unclassified;sf_6;4655	**B**
Bacteria;Planctomycetes;Planctomycetacia;Planctomycetales;Unclassified;sf_6;4661	**B**
Bacteria;Planctomycetes;Planctomycetacia;Planctomycetales;Unclassified;sf_6;4714	**B**
Bacteria;Planctomycetes;Planctomycetacia;Planctomycetales;Unclassified;sf_6;4932	**B**
Bacteria;Planctomycetes;Planctomycetacia;Planctomycetales;Unclassified;sf_6;4961	**B**
Bacteria;Planctomycetes;Planctomycetacia;WPS-1;Unclassified;sf_1;4930	**B**
Bacteria;Proteobacteria;Alphaproteobacteria;Acetobacterales;Acetobacteraceae;sf_1;6841	**T**

Taxa that significantly responded to depth (0-2 cm vs 8-10 cm)	Higher relative Abundance on top (T) or bottom (B) 2 cm of soil profile
Bacteria;Proteobacteria;Alphaproteobacteria;Acetobacterales;Acetobacteraceae;sf_1;7080	**T**
Bacteria;Proteobacteria;Alphaproteobacteria;Acetobacterales;Acetobacteraceae; sf_1;7452	**T**
Bacteria;Proteobacteria;Alphaproteobacteria;Acetobacterales;Acetobacteraceae; sf_1;7565	**T**
Bacteria;Proteobacteria;Alphaproteobacteria;Acetobacterales;Acetobacteraceae; sf_1;7623	**T**
Bacteria;Proteobacteria;Alphaproteobacteria;Azospirillales;Unclassified; sf_1;6905	**B**
Bacteria;Proteobacteria;Alphaproteobacteria;Bradyrhizobiales; Beijerinck/Rhodoplan/Methylocyst; sf_3;7228	**B**
Bacteria;Proteobacteria;Alphaproteobacteria;Bradyrhizobiales; Beijerinck/Rhodoplan/Methylocyst;sf_3;7495	**B**
Bacteria;Proteobacteria;Alphaproteobacteria;Bradyrhizobiales;Bradyrhizobiaceae; sf_1;7077	**T**
Bacteria;Proteobacteria;Alphaproteobacteria;Bradyrhizobiales;Methylobacteriaceae; sf_1;6782	**T**
Bacteria;Proteobacteria;Alphaproteobacteria;Bradyrhizobiales;Methylobacteriaceae; sf_1;7593	**T**
Bacteria;Proteobacteria;Alphaproteobacteria;Bradyrhizobiales;Unclassified;sf_1;7306	**T**
Bacteria;Proteobacteria;Alphaproteobacteria;Bradyrhizobiales;Unclassified;sf_1;7557	**T**
Bacteria;Proteobacteria;Alphaproteobacteria;Bradyrhizobiales;Xanthobacteraceae; sf_1;7483	**B**
Bacteria;Proteobacteria;Alphaproteobacteria;Caulobacterales;Caulobacteraceae; sf_1;6929	**T**
Bacteria;Proteobacteria;Alphaproteobacteria;Caulobacterales;Caulobacteraceae; sf_1;7245	**T**
Bacteria;Proteobacteria;Alphaproteobacteria;Caulobacterales;Caulobacteraceae; sf_1;7562	**T**
Bacteria;Proteobacteria;Alphaproteobacteria;Caulobacterales;Caulobacteraceae; sf_1;7578	**T**
Bacteria;Proteobacteria;Alphaproteobacteria;Consistiales;Caedibacteraceae; sf_3;7010	**T**
Bacteria;Proteobacteria;Alphaproteobacteria;Consistiales;Caedibacteraceae; sf_4;7157	**T**
Bacteria;Proteobacteria;Alphaproteobacteria;Consistiales;Caedibacteraceae; sf_5;6947	**T**
Bacteria;Proteobacteria;Alphaproteobacteria;Consistiales;SAR11;sf_2;7043	**T**
Bacteria;Proteobacteria;Alphaproteobacteria;Consistiales;Unclassified;sf_4;7105	**T**
Bacteria;Proteobacteria;Alphaproteobacteria;Consistiales;Unclassified;sf_5;7203	**T**
Bacteria;Proteobacteria;Alphaproteobacteria;Fulvimarina;Unclassified;sf_1;7281	**T**
Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Hyphomicrobiaceae; sf_1;6747	**T**
Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Hyphomicrobiaceae; sf_1;7144	**B**
Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Phyllobacteriaceae; sf_1;7216	**T**
Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Rhodobiaceae;sf_1;6891	**T**
Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Unclassified;sf_1;6938	**B**
Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Hyphomonadaceae; sf_1;7584	**T**
Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae; sf_1;6728	**T**
Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae; sf_1;7618	**T**
Bacteria;Proteobacteria;Alphaproteobacteria;Rickettsiales;Anaplasmataceae;sf_3;6648	**T**
Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae; sf_1;6812	**T**

Taxa that significantly responded to depth (0-2 cm vs 8-10 cm)	**Higher relative Abundance on top (T) or bottom (B) 2 cm of soil profile**
Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;sf_1;7011	**T**
Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;sf_1;7132	**T**
Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;sf_1;7215	**T**
Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;sf_1;7289	**T**
Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;sf_1;7532	**T**
Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;sf_1;7555	**T**
Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;sf_15;7035	**T**
Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Unclassified;sf_1;6653	**T**
Bacteria;Proteobacteria;Alphaproteobacteria;Unclassified;Unclassified;sf_6;6685	**T**
Bacteria;Proteobacteria;Alphaproteobacteria;Unclassified;Unclassified;sf_6;6844	**T**
Bacteria;Proteobacteria;Alphaproteobacteria;Unclassified;Unclassified;sf_6;7166	**T**
Bacteria;Proteobacteria;Alphaproteobacteria;Unclassified;Unclassified;sf_6;7516	**B**
Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae;sf_1;7914	**T**
Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae;sf_1;7918	**T**
Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae;sf_1;7934	**T**
Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;sf_1;7775	**T**
Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;sf_1;7786	**T**
Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;sf_1;7820	**T**
Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;sf_1;7884	**T**
Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;sf_1;7905	**T**
Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;sf_1;7920	**T**
Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;sf_1;7937	**T**
Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;sf_1;8028	**T**
Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;sf_1;8047	**T**
Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;sf_1;8070	**T**
Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;sf_1;8083	**T**
Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;sf_1;8117	**T**
Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Unclassified;sf_1;7832	**T**
Bacteria;Proteobacteria;Betaproteobacteria;Ellin6095/SC-I-39;Unclassified;sf_1;8093	**B**
Bacteria;Proteobacteria;Betaproteobacteria;Hydrogenophilales;Unclassified;sf_1;8151	**B**
Bacteria;Proteobacteria;Betaproteobacteria;MND1 clone group;Unclassified;sf_1;7896	**T**
Bacteria;Proteobacteria;Betaproteobacteria;Neisseriales;Neisseriaceae;sf_1;7867	**T**
Bacteria;Proteobacteria;Betaproteobacteria;Neisseriales;Neisseriaceae;sf_1;8143	**T**

Taxa that significantly responded to depth (0-2 cm vs 8-10 cm)	**Higher relative Abundance on top (T) or bottom (B) 2 cm of soil profile**
Bacteria;Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae;sf_1;7666	**T**
Bacteria;Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae;sf_1;7692	**B**
Bacteria;Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae;sf_1;7980	**B**
Bacteria;Proteobacteria;Deltaproteobacteria;Bdellovibrionales;Bdellovibrionaceae;sf_1;10010	**B**
Bacteria;Proteobacteria;Deltaproteobacteria;Bdellovibrionales;Bdellovibrionaceae;sf_2;10036	**T**
Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;sf_5;9810	**T**
Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Nitrospinaceae;sf_2;594	**B**
Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Unclassified;sf_3;468	**B**
Bacteria;Proteobacteria;Deltaproteobacteria;Desulfovibrionales;Unclassified;sf_1;9828	**B**
Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;sf_1;10176	**T**
Bacteria;Proteobacteria;Deltaproteobacteria;EB1021 group;Unclassified;sf_4;9884	**B**
Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Polyangiaceae;sf_4;9733	**T**
Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Unclassified;sf_1;10230	**B**
Bacteria;Proteobacteria;Deltaproteobacteria;Unclassified;Unclassified;sf_7;10048	**B**
Bacteria;Proteobacteria;Deltaproteobacteria;Unclassified;Unclassified;sf_9;10174	**T**
Bacteria;Proteobacteria;Deltaproteobacteria;Unclassified;Unclassified;sf_9;10185	**T**
Bacteria;Proteobacteria;Gammaproteobacteria;Aeromonadales;Succinivibrionaceae;sf_1;8822	**T**
Bacteria;Proteobacteria;Gammaproteobacteria;Alteromonadales;Alteromonadaceae;sf_1;8768	**T**
Bacteria;Proteobacteria;Gammaproteobacteria;Alteromonadales;Shewanellaceae;sf_1;8662	**B**
Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Chromatiaceae;sf_1;9571	**B**
Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Halothiobacillaceae;sf_1;9181	**B**
Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Halothiobacillaceae;sf_3;9448	**B**
Bacteria;Proteobacteria;Gammaproteobacteria;Enterobacteriales;Enterobacteriaceae;sf_1;1206	**T**
Bacteria;Proteobacteria;Gammaproteobacteria;Enterobacteriales;Enterobacteriaceae;sf_1;8236	**T**
Bacteria;Proteobacteria;Gammaproteobacteria;Enterobacteriales;Enterobacteriaceae;sf_1;9266	**T**
Bacteria;Proteobacteria;Gammaproteobacteria;Enterobacteriales;Enterobacteriaceae;sf_6;103	**T**
Bacteria;Proteobacteria;Gammaproteobacteria;Enterobacteriales;Unclassified;sf_1;8430	**T**
Bacteria;Proteobacteria;Gammaproteobacteria;Legionellales;Coxiellaceae;sf_3;8378	**B**
Bacteria;Proteobacteria;Gammaproteobacteria;Oceanospirillales;Oceanospirillaceae;sf_1;9351	**B**
Bacteria;Proteobacteria;Gammaproteobacteria;Oceanospirillales;Unclassified;sf_3;8648	**T**
Bacteria;Proteobacteria;Gammaproteobacteria;Pasteurellales;Pasteurellaceae;sf_1;9237	**T**
Bacteria;Proteobacteria;Gammaproteobacteria;SAR86;Unclassified;sf_1;8962	**T**
Bacteria;Proteobacteria;Gammaproteobacteria;Thiotrichales;Francisellaceae;sf_1;9554	**B**
Bacteria;Proteobacteria;Gammaproteobacteria;Thiotrichales;Piscirickettsiaceae;sf_3;9291	**T**
Bacteria;Proteobacteria;Gammaproteobacteria;Unclassified;Unclassified;sf_3;8391	**B**

Taxa that significantly responded to depth (0-2 cm vs 8-10 cm)	**Higher relative Abundance on top (T) or bottom (B) 2 cm of soil profile**
Bacteria;Proteobacteria;Gammaproteobacteria;Unclassified;Unclassified;sf_3;8551	**T**
Bacteria;Proteobacteria;Gammaproteobacteria;Unclassified;Unclassified;sf_3;8922	**T**
Bacteria;Proteobacteria;Gammaproteobacteria;Unclassified;Unclassified;sf_3;9040	**B**
Bacteria;Proteobacteria;Gammaproteobacteria;Unclassified;Unclassified;sf_3;9340	**T**
Bacteria;Proteobacteria;Gammaproteobacteria;Unclassified;Unclassified;sf_3;9605	**B**
Bacteria;Proteobacteria;Gammaproteobacteria;Xanthomonadales;Xanthomonadaceae; sf_3;8612	**T**
Bacteria;Proteobacteria;Gammaproteobacteria;Xanthomonadales;Xanthomonadaceae; sf_3;9623	**T**
Bacteria;Proteobacteria;Unclassified;Unclassified;Unclassified;sf_20;8479	**B**
Bacteria;Proteobacteria;Unclassified;Unclassified;Unclassified;sf_28;10091	**T**
Bacteria;Spirochaetes;Spirochaetes;Spirochaetales;Serpulinaceae;sf_1;6548	**T**
Bacteria;Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;sf_1;6502	**B**
Bacteria;Termite group 1;Unclassified;Unclassified;Unclassified;sf_2;722	**B**
Bacteria;Thermotogae;Thermotogae;Thermotogales;Thermotogaceae;sf_4;51	**T**
Bacteria;TM6;Unclassified;Unclassified;Unclassified;sf_1;9803	**B**
Bacteria;TM7;TM7-2;Unclassified;Unclassified;sf_1;5228	**T**
Bacteria;TM7;TM7-3;Unclassified;Unclassified;sf_1;3081	**T**
Bacteria;TM7;Unclassified;Unclassified;Unclassified;sf_1;3255	**T**
Bacteria;TM7;Unclassified;Unclassified;Unclassified;sf_1;3338	**T**
Bacteria;TM7;Unclassified;Unclassified;Unclassified;sf_1;3464	**T**
Bacteria;TM7;Unclassified;Unclassified;Unclassified;sf_1;3847	**T**
Bacteria;TM7;Unclassified;Unclassified;Unclassified;sf_1;3888	**T**
Bacteria;Unclassified;Unclassified;Unclassified;Unclassified;sf_106;243	**B**
Bacteria;Unclassified;Unclassified;Unclassified;Unclassified;sf_119;316	**T**
Bacteria;Unclassified;Unclassified;Unclassified;Unclassified;sf_119;916	**T**
Bacteria;Unclassified;Unclassified;Unclassified;Unclassified;sf_126;296	**T**
Bacteria;Unclassified;Unclassified;Unclassified;Unclassified;sf_140;6355	**B**
Bacteria;Unclassified;Unclassified;Unclassified;Unclassified;sf_148;5062	**T**
Bacteria;Unclassified;Unclassified;Unclassified;Unclassified;sf_160;6388	**T**
Bacteria;Unclassified;Unclassified;Unclassified;Unclassified;sf_160;6435	**B**
Bacteria;Unclassified;Unclassified;Unclassified;Unclassified;sf_34;4668	**B**
Bacteria;Unclassified;Unclassified;Unclassified;Unclassified;sf_67;10326	**T**
Bacteria;Unclassified;Unclassified;Unclassified;Unclassified;sf_92;9999	**T**
Bacteria;Unclassified;Unclassified;Unclassified;Unclassified;sf_93;925	**B**
Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Unclassified; sf_3;399	**B**
Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Unclassified; sf_3;430	**T**
Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Unclassified; sf_3;4840	**B**
Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Unclassified; sf_3;4865	**B**
Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Unclassified; sf_3;565	**B**
Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Unclassified; sf_3;610	**B**
Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Unclassified; sf_3;911	**B**
Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales; Verrucomicrobiasubdivision 3;sf_1;712	**B**

Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales; Verrucomicrobiaceae; sf_6;660	**B**
Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales; Xiphinematobacteraceae; sf_3;352	**B**
Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales; Xiphinematobacteraceae; sf_3;876	**B**
Bacteria;WS3;Unclassified;Unclassified;Unclassified;sf_1;2537	**B**

Table 7: Taxa that significantly responded (t-test; $p \leq 0.05$) to depth, independently of aboveground plant type. Post hoc Tukey HSD test revealed the directionality of the difference; relative abundance higher on the top (T; 0-2 cm) or bottom (B; 8-10cm) 2 cm of the soil profile.

Taxa string	DOC		Al		P		Mg		Mn		NH4	
	P	r	P	r	P	r	P	r	P	r	P	r
Bacteria;Acidobacteria;Acidobacteria;Acidobacteriales;Acidobacteriaceae;sf_1;6371			0.002	0.80	0.002	-0.79	0.015	-0.68	0.022	-0.65		
Bacteria;Acidobacteria;Acidobacteria;Acidobacteriales;Acidobacteriaceae;sf_1;877			0.030	0.62	0.022	-0.65						
Bacteria;Acidobacteria;Acidobacteria;Acidobacteriales;Acidobacteriaceae;sf_14;401									0.021	-0.66		
Bacteria;Acidobacteria;Acidobacteria;Acidobacteriales;Acidobacteriaceae;sf_6;6362	0.020	-0.66	0.013	0.69	0.031	-0.62			0.047	-0.58		
Bacteria;Acidobacteria;Acidobacteria-10;Unclassified;Unclassified;sf_1;516												
Bacteria;Acidobacteria;Acidobacteria-4;Ellin6075/11-25;Unclassified;sf_1;435			0.000	-0.86	0.000	0.86	0.002	0.79				
Bacteria;Acidobacteria;Acidobacteria-6;Unclassified;Unclassified;sf_1;1014			0.041	-0.60	0.042	0.59	0.022	0.65				
Bacteria;Acidobacteria;Acidobacteria-7;Unclassified;Unclassified;sf_1;588	0.022	-0.65										
Bacteria;Acidobacteria;Acidobacteria-9;Unclassified;Unclassified;sf_1;704	0.015	-0.68							0.011	-0.70		
Bacteria;Acidobacteria;Unclassified;Unclassified;Unclassified;sf_1;572	0.006	-0.73										
Bacteria;Actinobacteria;Actinobacteria;Acidimicrobiales;Microthrixineae;sf_1;1408			0.002	0.79	0.001	-0.81	0.008	-0.72	0.032	-0.62		
Bacteria;Actinobacteria;Actinobacteria;Acidimicrobiales;Unclassified;sf_2;1811									0.020	-0.66		
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Actinomycetaceae;sf_1;1672			0.030	-0.63	0.030	0.62			0.006	0.73		
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Actinosynnemataceae;sf_1;1951	0.005	0.75							0.000	0.85		
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Brevibacteriaceae;sf_1;1745	0.002	0.81							0.010	0.71	0.028	0.63
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Cellulomonadaceae;sf_1;1592	0.002	0.79							0.001	0.83		
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Cellulomonadaceae;sf_1;2061	0.001	0.84										
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Corynebacteriaceae;sf_1;1374	0.003	0.78							0.012	0.70	0.021	0.65
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Dermabacteraceae;sf_1;1736									0.000	0.86		
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Dermatophilaceae;sf_1;1852									0.018	0.66		
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Geodermatophilaceae;sf_1;1245	0.027	0.63							0.000	0.90		
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Geodermatophilaceae;sf_1;1973	0.011	0.70							0.000	0.93		
Bacteria;Actinobacteria;Actinobacteria;									0.023	0.65		

Taxa string	DOC		Al		P		Mg		Mn		NH4	
	P	r	P	r	P	r	P	r	P	r	P	r
Actinomycetales;Kineosporiaceae;sf_1;2015												
Bacteria;Actinobacteria;Actinobacteria; Actinomycetales;Kribbella;sf_1;1839									0.006	0.74		
Bacteria;Actinobacteria;Actinobacteria; Actinomycetales;Microbacteriaceae;sf_1;1507	0.004	0.76							0.002	0.79		
Bacteria;Actinobacteria;Actinobacteria; Actinomycetales;Microbacteriaceae;sf_1;1513	0.001	0.84							0.005	0.75		
Bacteria;Actinobacteria;Actinobacteria; Actinomycetales;Microbacteriaceae;sf_1;1550	0.001	0.83							0.000	0.96		
Bacteria;Actinobacteria;Actinobacteria; Actinomycetales;Microbacteriaceae;sf_1;1640	<0.001	0.91							0.004	0.76		
Bacteria;Actinobacteria;Actinobacteria; Actinomycetales;Microbacteriaceae;sf_1;1705	0.003	0.78							<0.001	0.94		
Bacteria;Actinobacteria;Actinobacteria; Actinomycetales;Micrococcaceae;sf_1;1099	0.033	0.62							0.021	0.66		
Bacteria;Actinobacteria;Actinobacteria; Actinomycetales;Micrococcaceae;sf_1;1452	0.004	0.76										
Bacteria;Actinobacteria;Actinobacteria; Actinomycetales;Micromonosporaceae;sf_1;1316	0.017	0.67							0.012	0.69		
Bacteria;Actinobacteria;Actinobacteria; Actinomycetales;Micromonosporaceae;sf_1;1395	0.003	0.78							0.001	0.84		
Bacteria;Actinobacteria;Actinobacteria; Actinomycetales;Micromonosporaceae;sf_1;1462									0.002	0.80		
Bacteria;Actinobacteria;Actinobacteria; Actinomycetales;Micromonosporaceae;sf_1;1876	0.004	0.77										
Bacteria;Actinobacteria;Actinobacteria; Actinomycetales;Nocardiaceae;sf_1;1142	0.002	0.80							0.004	0.76		
Bacteria;Actinobacteria;Actinobacteria; Actinomycetales;Nocardiaceae;sf_1;1809	0.001	0.81							0.009	0.71		
Bacteria;Actinobacteria;Actinobacteria; Actinomycetales;Nocardioidaceae;sf_1;1854	0.009	0.72							0.002	0.78		
Bacteria;Actinobacteria;Actinobacteria; Actinomycetales;Propionibacteriaceae;sf_1;1315	0.017	0.67							0.014	0.69		
Bacteria;Actinobacteria;Actinobacteria; Actinomycetales;Sporichthyaceae;sf_1;1223	0.039	0.60							0.001	0.81		
Bacteria;Actinobacteria;Actinobacteria; Actinomycetales;Streptomycetaceae;sf_1;1128			0.001	0.85	0.004	-0.77	0.010	-0.71				
Bacteria;Actinobacteria;Actinobacteria; Actinomycetales;Streptomycetaceae;sf_3;1743												
Bacteria;Actinobacteria;Actinobacteria; Actinomycetales;Streptosporangiaceae;sf_1;1535	0.015	0.68							0.003	0.78		
Bacteria;Actinobacteria;Actinobacteria; Actinomycetales;Unclassified;sf_3;1564	0.012	0.70							<0.001	0.95		
Bacteria;Actinobacteria;Actinobacteria; Actinomycetales;Unclassified;sf_3;1806	0.007	0.73										

Taxa string	DOC		Al		P		Mg		Mn		NH4	
	P	r	P	r	P	r	P	r	P	r	P	r
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Unclassified;sf_4;1337	0.044	-0.59										
Bacteria;Actinobacteria;Actinobacteria;Coriobacteriales;Coriobacteriaceae;sf_1;1459	0.031	-0.62										
Bacteria;Actinobacteria;Actinobacteria;Rubrobacterales;Rubrobacteraceae;sf_1;1980			0.006	-0.74	0.018	0.67	0.025	0.64				
Bacteria;Actinobacteria;Actinobacteria;Unclassified;Unclassified;sf_1;1118			0.018	0.67	0.016	-0.68						
Bacteria;Actinobacteria;Actinobacteria;Unclassified;Unclassified;sf_1;1490			0.020	0.66	0.008	-0.72	0.025	-0.64				
Bacteria;Actinobacteria;Actinobacteria;Unclassified;Unclassified;sf_1;1498	0.036	-0.61	0.023	0.65	0.015	-0.68	0.045	-0.59				
Bacteria;Actinobacteria;Actinobacteria;Unclassified;Unclassified;sf_1;1588	0.011	0.70							0.013	0.69		
Bacteria;Actinobacteria;Actinobacteria;Unclassified;Unclassified;sf_2;1233	0.017	-0.67										
Bacteria;Actinobacteria;BD2-10 group;Unclassified;Unclassified;sf_1;1675									0.027	-0.63		
Bacteria;AD3;Unclassified;Unclassified;Unclassified;sf_1;2338	0.031	-0.62	0.007	0.73	0.011	-0.70	0.026	-0.64				
Bacteria;Bacteroidetes;Bacteroidetes;Bacteroidales;Bacteroidaceae;sf_6;5792	0.018	0.66	0.014	-0.68	0.040	0.60			0.029	0.63		
Bacteria;Bacteroidetes;Bacteroidetes;Bacteroidales;Porphyromonadaceae;sf_1;5454			0.001	-0.85	<0.001	0.86	0.006	0.74			0.038	0.60
Bacteria;Bacteroidetes;Bacteroidetes;Bacteroidales;Prevotellaceae;sf_1;6118			0.050	-0.58								
Bacteria;Bacteroidetes;Bacteroidetes;Bacteroidales;Prevotellaceae;sf_1;6152	0.033	0.62	0.053	-0.57								
Bacteria;Bacteroidetes;Bacteroidetes;Bacteroidales;Rikenellaceae;sf_5;5892			0.050	-0.58	0.028	0.63					0.022	0.65
Bacteria;Bacteroidetes;Flavobacteria;Flavobacteriales;Cryomorphaceae;sf_1;5400	0.016	0.68										
Bacteria;Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae;sf_1;5341	0.023	0.65										
Bacteria;Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae;sf_1;5559	0.018	0.67										
Bacteria;Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae;sf_1;5636	0.007	0.73										
Bacteria;Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae;sf_1;5906			0.006	0.74	0.006	-0.74	0.031	-0.62				
Bacteria;Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae;sf_1;5918					0.051	-0.57			0.014	-0.68	0.028	-0.63
Bacteria;Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae;sf_1;6200	0.007	0.73	0.052	-0.57								
Bacteria;Bacteroidetes;Flavobacteria;	0.010	0.71										

Taxa string	DOC		Al		P		Mg		Mn		NH4	
	P	r	P	r	P	r	P	r	P	r	P	r
Flavobacteriales;Flavobacteriaceae;sf_1;6241												
Bacteria;Bacteroidetes;Sphingobacteria; Sphingobacteriales;Crenotrichaceae;sf_11;5266	0.013	0.69	0.015	-0.68	0.009	0.72	0.032	0.62	0.026	0.64		
Bacteria;Bacteroidetes;Sphingobacteria; Sphingobacteriales;Crenotrichaceae;sf_11;5283	0.030	0.62	0.003	-0.77	0.006	0.74	0.020	0.66				
Bacteria;Bacteroidetes;Sphingobacteria; Sphingobacteriales;Crenotrichaceae;sf_11;5288	0.011	0.70	0.006	-0.74	0.008	0.72	0.022	0.65				
Bacteria;Bacteroidetes;Sphingobacteria; Sphingobacteriales;Crenotrichaceae;sf_11;5354	0.014	0.68	0.005	-0.75	0.007	0.73	0.028	0.63	0.030	0.63		
Bacteria;Bacteroidetes;Sphingobacteria; Sphingobacteriales;Crenotrichaceae;sf_11;5387	0.003	0.78	0.044	-0.59								
Bacteria;Bacteroidetes;Sphingobacteria; Sphingobacteriales;Crenotrichaceae;sf_11;5491	0.006	0.74	0.044	-0.59					0.014	0.69		
Bacteria;Bacteroidetes;Sphingobacteria; Sphingobacteriales;Crenotrichaceae;sf_11;5581	0.007	0.73	0.040	-0.60					0.051	0.57		
Bacteria;Bacteroidetes;Sphingobacteria; Sphingobacteriales;Crenotrichaceae;sf_11;5872	0.052	0.57	0.011	-0.70	0.004	0.76	0.015	0.68	0.037	0.60		
Bacteria;Bacteroidetes;Sphingobacteria; Sphingobacteriales;Crenotrichaceae;sf_11;5925	0.035	0.61	0.013	-0.69	0.025	0.64			0.037	0.61		
Bacteria;Bacteroidetes;Sphingobacteria; Sphingobacteriales;Crenotrichaceae;sf_11;5948			0.001	-0.81	0.001	0.83	0.002	0.79				
Bacteria;Bacteroidetes;Sphingobacteria; Sphingobacteriales;Crenotrichaceae;sf_11;5970			0.005	-0.75	0.003	0.78	0.023	0.65				
Bacteria;Bacteroidetes;Sphingobacteria; Sphingobacteriales;Crenotrichaceae;sf_11;5987			0.037	-0.61								
Bacteria;Bacteroidetes;Sphingobacteria; Sphingobacteriales;Crenotrichaceae;sf_11;6003	0.029	0.63	0.014	-0.69	0.022	0.65						
Bacteria;Bacteroidetes;Sphingobacteria; Sphingobacteriales;Crenotrichaceae;sf_11;6148	0.027	0.63	0.015	-0.68	0.016	0.68	0.047	0.58				
Bacteria;Bacteroidetes;Sphingobacteria; Sphingobacteriales;Crenotrichaceae;sf_11;6196			0.010	-0.71	0.006	0.74	0.029	0.63				
Bacteria;Bacteroidetes;Sphingobacteria; Sphingobacteriales;Crenotrichaceae;sf_11;6245			0.005	-0.75	0.009	0.72	0.032	0.62				
Bacteria;Bacteroidetes;Sphingobacteria; Sphingobacteriales;Crenotrichaceae;sf_11;6281	0.035	0.61	0.054	-0.57					0.004	0.76		
Bacteria;Bacteroidetes;Sphingobacteria; Sphingobacteriales;Crenotrichaceae;sf_11;6325	0.008	0.72	0.006	-0.74	0.011	0.70	0.038	0.60	0.024	0.64		
Bacteria;Bacteroidetes;Sphingobacteria; Sphingobacteriales;Flammeovirgaceae;sf_5;6084			0.000	-0.86	0.000	0.86	0.001	0.81				
Bacteria;Bacteroidetes;Sphingobacteria; Sphingobacteriales;Flexibacteraceae;sf_19;6048	0.039	0.60										
Bacteria;Bacteroidetes;Sphingobacteria; Sphingobacteriales;Flexibacteraceae;sf_19;6304			0.006	-0.74	0.008	0.72	0.007	0.73				
Bacteria;Bacteroidetes;Sphingobacteria; Sphingobacteriales;Sphingobacteriaceae;sf_1;5840	0.022	0.65							0.000	0.85		

Taxa string	DOC		Al		P		Mg		Mn		NH4	
	P	r	P	r	P	r	P	r	P	r	P	r
Bacteria;Bacteroidetes;Sphingobacteria;Sphingobacteriales;Unclassified;sf_4;6030			0.008	-0.73	0.015	0.68	0.037	0.61	0.405	0.27		
Bacteria;Bacteroidetes;Unclassified;Unclassified;Unclassified;sf_4;5814	0.029	0.63										
Bacteria;BRC1;Unclassified;Unclassified;Unclassified;sf_1;5051	0.008	-0.72										
Bacteria;Chlorobi;Unclassified;Unclassified;Unclassified;sf_6;5294			0.033	-0.62	0.050	0.58						
Bacteria;Chloroflexi;Anaerolineae;Chloroflexi-1a;Unclassified;sf_1;258	0.032	-0.62										
Bacteria;Chloroflexi;Anaerolineae;Chloroflexi-1f;Unclassified;sf_1;765	0.047	-0.58	0.005	0.74	0.013	-0.69	0.045	-0.59	0.020	-0.66		
Bacteria;Chloroflexi;Anaerolineae;Unclassified;Unclassified;sf_1;266	0.009	-0.71										
Bacteria;Chloroflexi;Anaerolineae;Unclassified;Unclassified;sf_7;663			0.022	0.65	0.037	-0.61			0.030	-0.62		
Bacteria;Chloroflexi;Chloroflexi-4;Unclassified;Unclassified;sf_2;2532	0.006	-0.74							0.008	-0.72		
Bacteria;Chloroflexi;Unclassified;Unclassified;Unclassified;sf_12;2523	0.009	-0.71	0.046	0.58					0.007	-0.73		
Bacteria;Chloroflexi;Unclassified;Unclassified;Unclassified;sf_5;1051	0.020	-0.66	0.016	0.67	0.028	-0.63			0.005	-0.75		
Bacteria;Cyanobacteria;Cyanobacteria;Chloroplasts;Chloroplasts;sf_13;5000			0.037	-0.61	0.022	0.65	0.026	0.64				
Bacteria;Cyanobacteria;Cyanobacteria;Chloroplasts;Chloroplasts;sf_5;5026					0.038	0.60						
Bacteria;Cyanobacteria;Cyanobacteria;Chroococcales;Unclassified;sf_1;5219					0.036	0.61	0.033	0.62			0.011	0.70
Bacteria;Cyanobacteria;Cyanobacteria;Nostocales;Unclassified;sf_1;5057			0.013	-0.69	0.009	0.72	0.017	0.67			0.055	0.57
Bacteria;Cyanobacteria;Cyanobacteria;Phormidium;Unclassified;sf_1;4978			0.054	-0.57								
Bacteria;Cyanobacteria;Cyanobacteria;Scytonema;Unclassified;sf_1;5115			0.016	-0.68	0.014	0.69	0.021	0.65				
Bacteria;Cyanobacteria;Unclassified;Unclassified;Unclassified;sf_9;5164			0.006	-0.74	0.002	0.79	0.006	0.74				
Bacteria;Deinococcus-Thermus;Unclassified;Unclassified;Unclassified;sf_2;637			0.037	-0.60	0.045	0.59						
Bacteria;Dictyoglomi;Dictyoglomi;Dictyoglomales;Dictyoglomaceae;sf_9;7579	0.001	0.83	0.008	-0.72	0.037	0.61			0.046	0.58		
Bacteria;Firmicutes;Anaerobranca;Unclassified;Unclassified;sf_1;4304	0.038	-0.60										
Bacteria;Firmicutes;Bacilli;Bacillales;Alicyclobacillaceae;sf_1;3368												
Bacteria;Firmicutes;Bacilli;Bacillales;Bacillaceae;sf_1;3370			0.005	0.75	0.007	-0.73	0.018	-0.67				

Taxa string	DOC		Al		P		Mg		Mn		NH4	
	P	r	P	r	P	r	P	r	P	r	P	r
Bacteria;Firmicutes;Bacilli; Bacillales;Bacillaceae;sf_1;3626			0.003	0.77	0.002	-0.79	0.005	-0.75				
Bacteria;Firmicutes;Bacilli; Bacillales;Caryophanaceae;sf_1;3285	0.010	-0.71	0.048	0.58	0.049	-0.58						
Bacteria;Firmicutes;Bacilli; Bacillales;Halobacillaceae;sf_1;3756	0.025	-0.64	0.016	0.68	0.015	-0.68	0.036	-0.61	0.025	-0.64		
Bacteria;Firmicutes;Bacilli; Bacillales;Paenibacillaceae;sf_1;3247	0.050	-0.58							0.016	-0.68		
Bacteria;Firmicutes;Bacilli; Bacillales;Paenibacillaceae;sf_1;3766			0.003	0.78	0.028	-0.63			0.035	-0.61		
Bacteria;Firmicutes;Bacilli; Bacillales;Sporolactobacillaceae;sf_1;3365			0.008	0.72	0.009	-0.71	0.020	-0.66				
Bacteria;Firmicutes;Bacilli; Bacillales;Staphylococcaceae;sf_1;3684	0.025	-0.64							0.005	-0.75		
Bacteria;Firmicutes;Bacilli; Bacillales;Thermoactinomycetaceae;sf_1;3301	0.011	-0.70							0.028	-0.63		
Bacteria;Firmicutes;Bacilli; Bacillales;Unclassified;sf_3;3743	0.026	-0.64										
Bacteria;Firmicutes;Bacilli; Lactobacillales;Carnobacteriaceae;sf_1;3536	0.008	-0.72										
Bacteria;Firmicutes;Bacilli; Lactobacillales;Enterococcaceae;sf_1;3433	0.023	-0.65										
Bacteria;Firmicutes;Bacilli; Lactobacillales;Unclassified;sf_1;3434			0.005	0.75	0.012	-0.70	0.045	-0.59	0.005	-0.75		
Bacteria;Firmicutes;Clostridia; Clostridiales;Clostridiaceae;sf_12;4359	0.010	-0.71							0.040	-0.60		
Bacteria;Firmicutes;Clostridia; Clostridiales;Clostridiaceae;sf_21;4471	0.013	-0.69										
Bacteria;Firmicutes;Clostridia; Clostridiales;Lachnospiraceae;sf_5;4316												
Bacteria;Firmicutes;Clostridia; Clostridiales;Peptococc/Acidaminococc;sf_11;177	0.003	0.78										
Bacteria;Firmicutes;Clostridia; Clostridiales;Peptococc/Acidaminococc;sf_11;185	0.029	-0.63	0.001	0.84	0.001	-0.83	0.004	-0.76	0.013	-0.69		
Bacteria;Firmicutes;Clostridia; Clostridiales;Peptococc/Acidaminococc;sf_11;49			0.001	0.82	0.001	-0.82	0.007	-0.73				
Bacteria;Firmicutes;Clostridia; Clostridiales;Peptococc/Acidaminococc;sf_11;903			0.004	0.76	0.008	-0.72	0.007	-0.73				
Bacteria;Firmicutes;Clostridia; Clostridiales;Peptostreptococcaceae;sf_5;2913	0.014	-0.68										
Bacteria;Firmicutes;Clostridia; Clostridiales;Syntrophomonadaceae;sf_5;2456	0.040	-0.60										
Bacteria;Firmicutes;Clostridia; Clostridiales;Unclassified;sf_17;2659			0.030	-0.62								
Bacteria;Firmicutes;Clostridia;												

Taxa string	DOC		Al		P		Mg		Mn		NH4	
	P	r	P	r	P	r	P	r	P	r	P	r
Unclassified;Unclassified;sf_3;2373												
Bacteria;Firmicutes;Clostridia; Unclassified;Unclassified;sf_4;2398	0.025	-0.64							0.047	-0.58		
Bacteria;Firmicutes;Desulfotomaculum; Unclassified;Unclassified;sf_1;894	0.015	0.68							0.001	0.83		
Bacteria;Firmicutes;gut clone group; Unclassified;Unclassified;sf_1;4616			0.007	0.73	0.006	-0.74	0.028	-0.63				
Bacteria;Firmicutes;Symbiobacteria; Symbiobacterales;Unclassified;sf_1;2388	0.009	-0.71										
Bacteria;Firmicutes;Unclassified; Unclassified;Unclassified;sf_8;546	0.003	0.78							0.028	0.63	0.016	0.68
Bacteria;Lentisphaerae;Unclassified; Unclassified;Unclassified;sf_5;10330	0.046	-0.58							0.002	-0.80		
Bacteria;marine group A;mgA-1;Unclassified; Unclassified;sf_1;6454	0.013	-0.69							0.016	-0.67		
Bacteria;marine group A;mgA-2;Unclassified; Unclassified;sf_1;6344			0.022	-0.65	0.055	0.57						
Bacteria;NC10;NC10-1; Unclassified;Unclassified;sf_1;452	0.018	-0.67										
Bacteria;NC10;NC10-2; Unclassified;Unclassified;sf_1;10254	0.009	-0.72										
Bacteria;NC10;Unclassified; Unclassified;Unclassified;sf_1;2516	0.010	-0.71							0.030	-0.62		
Bacteria;Nitrospira;Nitrospira; Nitrospirales;Nitrospiraceae;sf_1;860	0.011	-0.70										
Bacteria;OP3;Unclassified; Unclassified;Unclassified;sf_3;1015	0.004	-0.77			0.051	-0.57			0.017	-0.67	0.037	-0.61
Bacteria;OP3;Unclassified; Unclassified;Unclassified;sf_4;628	0.027	-0.63							0.044	-0.59		
Bacteria;OP9/JS1;JS1; Unclassified;Unclassified;sf_1;2489	0.052	-0.57										
Bacteria;OS-K;Unclassified; Unclassified;Unclassified;sf_1;501			0.001	0.81	<0.001	-0.85	0.002	-0.79				
Bacteria;Planctomycetes;Planctomycetacia; Planctomycetales;Anammoxales;sf_2;4683	0.004	-0.76							0.045	-0.59		
Bacteria;Planctomycetes;Planctomycetacia; Planctomycetales;Gemmatae;sf_1;4866			0.003	0.78	0.001	-0.82	0.005	-0.75				
Bacteria;Planctomycetes;Planctomycetacia; Planctomycetales;Isosphaerae;sf_1;4856	0.020	0.66							0.003	0.78		
Bacteria;Planctomycetes;Planctomycetacia; Planctomycetales;Pirellulae;sf_3;4687	0.010	-0.71	0.015	0.68	0.010	-0.71	0.038	-0.60	0.029	-0.63	0.039	-0.60
Bacteria;Planctomycetes;Planctomycetacia; Planctomycetales;Pirellulae;sf_3;4726	0.016	-0.68	0.037	0.61	0.029	-0.63						
Bacteria;Planctomycetes;Planctomycetacia; Planctomycetales;Pirellulae;sf_3;4744	0.030	0.62									0.027	0.63

Taxa string	DOC		Al		P		Mg		Mn		NH4	
	P	r	P	r	P	r	P	r	P	r	P	r
Bacteria;Planctomycetes;Planctomycetacia; Planctomycetales;Pirellulae;sf_3;4754	0.026	-0.64										
Bacteria;Planctomycetes;Planctomycetacia; Planctomycetales;Pirellulae;sf_3;4894			0.052	0.57	0.053	-0.57						
Bacteria;Planctomycetes;Planctomycetacia; Planctomycetales;Unclassified;sf_6;4655			0.006	0.74	0.005	-0.76	0.025	-0.64				
Bacteria;Planctomycetes;Planctomycetacia; Planctomycetales;Unclassified;sf_6;4661			<0.001	0.87	<0.001	-0.86	0.002	-0.78				
Bacteria;Planctomycetes;Planctomycetacia; Planctomycetales;Unclassified;sf_6;4714			0.016	0.67	0.007	-0.73	0.036	-0.61				
Bacteria;Planctomycetes;Planctomycetacia; Planctomycetales;Unclassified;sf_6;4932			0.004	0.76	0.004	-0.76	0.014	-0.68				
Bacteria;Planctomycetes;Planctomycetacia; Planctomycetales;Unclassified;sf_6;4961			0.004	0.76	0.006	-0.74	0.013	-0.69				
Bacteria;Proteobacteria;Alphaproteobacteria; Acetobacterales;Acetobacteraceae;sf_1;6841	0.052	0.57							0.002	0.80		
Bacteria;Proteobacteria;Alphaproteobacteria; Acetobacterales;Acetobacteraceae;sf_1;7080	0.027	0.63							<0.001	0.88		
Bacteria;Proteobacteria;Alphaproteobacteria; Acetobacterales;Acetobacteraceae;sf_1;7452	0.046	0.58							0.001	0.81		
Bacteria;Proteobacteria;Alphaproteobacteria; Acetobacterales;Acetobacteraceae;sf_1;7565	0.019	0.66							0.006	0.74		
Bacteria;Proteobacteria;Alphaproteobacteria; Acetobacterales;Acetobacteraceae;sf_1;7623	0.019	0.66							0.000	0.88		
Bacteria;Proteobacteria;Alphaproteobacteria; Azospirillales;Unclassified;sf_1;6905			0.009	0.72	0.015	-0.68						
Bacteria;Proteobacteria;Alphaproteobacteria; Bradyrhizobiales;Beijerinck/Rhodoplan/Methylocyst;sf_3;7228	0.045	-0.59	<0.001	0.90	0.001	-0.84	0.008	-0.72	0.033	-0.62		
Bacteria;Proteobacteria;Alphaproteobacteria; Bradyrhizobiales;Beijerinck/Rhodoplan/Methylocyst;sf_3;7495			0.001	0.84	0.002	-0.80	0.014	-0.68				
Bacteria;Proteobacteria;Alphaproteobacteria; Bradyrhizobiales;Bradyrhizobiaceae;sf_1;7077	0.040	0.60							<0.001	0.91		
Bacteria;Proteobacteria;Alphaproteobacteria; Bradyrhizobiales;Methylobacteriaceae;sf_1;6782	0.001	0.83										
Bacteria;Proteobacteria;Alphaproteobacteria; Bradyrhizobiales;Methylobacteriaceae;sf_1;7593	0.011	0.70							0.010	0.71		
Bacteria;Proteobacteria;Alphaproteobacteria; Bradyrhizobiales;Unclassified;sf_1;7306	0.002	0.79	0.053	-0.57								
Bacteria;Proteobacteria;Alphaproteobacteria; Bradyrhizobiales;Unclassified;sf_1;7557	0.052	0.57	0.048	-0.58					0.003	0.78		
Bacteria;Proteobacteria;Alphaproteobacteria; Bradyrhizobiales;Xanthobacteraceae;sf_1;7483			0.015	0.68	0.010	-0.71	0.043	-0.59				
Bacteria;Proteobacteria;Alphaproteobacteria; Caulobacterales;Caulobacteraceae;sf_1;6929	0.005	0.75							0.011	0.70		
Bacteria;Proteobacteria;Alphaproteobacteria;	0.001	0.83							0.001	0.82		

Taxa string	DOC		Al		P		Mg		Mn		NH4	
	P	r	P	r	P	r	P	r	P	r	P	r
Caulobacterales;Caulobacteraceae;sf_1;7245												
Bacteria;Proteobacteria;Alphaproteobacteria;Caulobacterales;Caulobacteraceae;sf_1;7562	0.005	0.75							0.006	0.74		
Bacteria;Proteobacteria;Alphaproteobacteria;Caulobacterales;Caulobacteraceae;sf_1;7578	0.032	0.62										
Bacteria;Proteobacteria;Alphaproteobacteria;Consistiales;Caedibacteraceae;sf_3;7010	0.014	0.69	0.026	-0.64	0.030	0.62	0.051	0.57				
Bacteria;Proteobacteria;Alphaproteobacteria;Consistiales;Caedibacteraceae;sf_4;7157	0.050	0.58	0.012	-0.70	0.012	0.70	0.020	0.66			0.043	0.59
Bacteria;Proteobacteria;Alphaproteobacteria;Consistiales;Caedibacteraceae;sf_5;6947			0.029	-0.63	0.035	0.61	0.054	0.57			0.051	0.57
Bacteria;Proteobacteria;Alphaproteobacteria;Consistiales;SAR11;sf_2;7043	0.027	0.63	0.039	-0.60								
Bacteria;Proteobacteria;Alphaproteobacteria;Consistiales;Unclassified;sf_4;7105			0.006	-0.74	0.002	0.80	0.003	0.78			0.005	0.75
Bacteria;Proteobacteria;Alphaproteobacteria;Consistiales;Unclassified;sf_5;7203	0.004	0.76							0.047	0.58		
Bacteria;Proteobacteria;Alphaproteobacteria;Fulvimarina;Unclassified;sf_1;7281	0.055	0.57										
Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Hyphomicrobiaceae;sf_1;6747	0.018	0.67	0.033	-0.61	0.046	0.58	0.050	0.58				
Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Hyphomicrobiaceae;sf_1;7144					0.027	-0.63						
Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Phyllobacteriaceae;sf_1;7216	0.015	0.68							0.048	0.58		
Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Rhodobiaceae;sf_1;6891	0.005	0.75										
Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Hyphomonadaceae;sf_1;7584			0.007	-0.73	0.021	0.66	0.024	0.64				
Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae;sf_1;6728	0.016	0.68										
Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae;sf_1;7618	0.001	0.81	0.023	-0.65	0.051	0.57						
Bacteria;Proteobacteria;Alphaproteobacteria;Rickettsiales;Anaplasmataceae;sf_3;6648			0.001	-0.83	0.001	0.83	0.005	0.75				
Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;sf_1;6812	0.004	0.76							0.052	0.57		
Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;sf_1;7011	0.004	0.76										
Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;sf_1;7132			0.026	-0.64								
Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;sf_1;7215	0.002	0.80										
Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;sf_1;7289	0.002	0.81							0.044	0.59		

Taxa string	DOC		Al		P		Mg		Mn		NH4	
	P	r	P	r	P	r	P	r	P	r	P	r
Bacteria;Proteobacteria;Alphaproteobacteria; Sphingomonadales;Sphingomonadaceae;sf_1;7532	0.014	0.68	0.033	-0.62	0.034	0.61	0.051	0.57				
Bacteria;Proteobacteria;Alphaproteobacteria; Sphingomonadales;Sphingomonadaceae;sf_1;7555	0.002	0.79										
Bacteria;Proteobacteria;Alphaproteobacteria; Sphingomonadales;Sphingomonadaceae;sf_15;7035	0.035	0.61							0.005	0.74		
Bacteria;Proteobacteria;Alphaproteobacteria; Unclassified;Unclassified;sf_6;6685	0.009	0.71							0.006	0.74		
Bacteria;Proteobacteria;Alphaproteobacteria; Unclassified;Unclassified;sf_6;6844	0.011	0.70							<0.001	0.89		
Bacteria;Proteobacteria;Alphaproteobacteria; Unclassified;Unclassified;sf_6;7166	<0.001	0.88	0.046	-0.58					0.013	0.69		
Bacteria;Proteobacteria;Alphaproteobacteria; Unclassified;Unclassified;sf_6;7516	0.029	-0.63	0.002	0.80	0.007	-0.73	0.041	-0.60				
Bacteria;Proteobacteria;Betaproteobacteria; Burkholderiales;Burkholderiaceae;sf_1;7914	<0.001	0.85							0.019	0.66		
Bacteria;Proteobacteria;Betaproteobacteria; Burkholderiales;Burkholderiaceae;sf_1;7934	0.016	0.67							0.007	0.73		
Bacteria;Proteobacteria;Betaproteobacteria; Burkholderiales;Comamonadaceae;sf_1;7775	0.021	0.65							0.023	0.65		
Bacteria;Proteobacteria;Betaproteobacteria; Burkholderiales;Comamonadaceae;sf_1;7786	0.010	0.71							0.051	0.57		
Bacteria;Proteobacteria;Betaproteobacteria; Burkholderiales;Comamonadaceae;sf_1;7820	0.005	0.75							0.006	0.74		
Bacteria;Proteobacteria;Betaproteobacteria; Burkholderiales;Comamonadaceae;sf_1;7884	0.004	0.76										
Bacteria;Proteobacteria;Betaproteobacteria; Burkholderiales;Comamonadaceae;sf_1;7905	0.016	0.68							0.016	0.67		
Bacteria;Proteobacteria;Betaproteobacteria; Burkholderiales;Comamonadaceae;sf_1;7920	0.023	0.65										
Bacteria;Proteobacteria;Betaproteobacteria; Burkholderiales;Comamonadaceae;sf_1;7937	0.005	0.75	0.023	-0.65	0.030	0.62	0.050	0.58	0.017	0.67		
Bacteria;Proteobacteria;Betaproteobacteria; Burkholderiales;Comamonadaceae;sf_1;8028	0.009	0.72	0.033	-0.61	0.041	0.60			0.007	0.73		
Bacteria;Proteobacteria;Betaproteobacteria; Burkholderiales;Comamonadaceae;sf_1;8047	0.006	0.74							0.008	0.72		
Bacteria;Proteobacteria;Betaproteobacteria; Burkholderiales;Comamonadaceae;sf_1;8070	0.028	0.63										
Bacteria;Proteobacteria;Betaproteobacteria; Burkholderiales;Comamonadaceae;sf_1;8083	0.001	0.83							0.009	0.72		
Bacteria;Proteobacteria;Betaproteobacteria; Burkholderiales;Comamonadaceae;sf_1;8117	0.001	0.83							0.005	0.75		
Bacteria;Proteobacteria;Betaproteobacteria; Burkholderiales;Unclassified;sf_1;7832	0.005	0.75							0.049	0.58		
Bacteria;Proteobacteria;Betaproteobacteria;	0.012	-0.70	0.002	0.79	0.006	-0.74	0.018	-0.67	0.008	-0.72		

Taxa string	DOC		Al		P		Mg		Mn		NH4	
	P	**r**	**P**	**r**	**P**	**r**	**P**	**r**	**P**	**r**	**P**	**r**
Ellin6095/SC-I-39;Unclassified;sf_1;8093												
Bacteria;Proteobacteria;Betaproteobacteria; Hydrogenophilales;Unclassified;sf_1;8151	0.031	-0.62										
Bacteria;Proteobacteria;Betaproteobacteria; Neisseriales;Neisseriaceae;sf_1;7867	0.029	0.63							0.016	0.68		
Bacteria;Proteobacteria;Betaproteobacteria; Neisseriales;Neisseriaceae;sf_1;8143												
Bacteria;Proteobacteria;Betaproteobacteria; Rhodocyclales;Rhodocyclaceae;sf_1;7666	0.001	0.83							0.049	0.58		
Bacteria;Proteobacteria;Betaproteobacteria; Rhodocyclales;Rhodocyclaceae;sf_1;7980	0.011	-0.70							0.009	-0.71		
Bacteria;Proteobacteria;Deltaproteobacteria; Bdellovibrionales;Bdellovibrionaceae;sf_2;10036			0.039	-0.60	0.033	0.62						
Bacteria;Proteobacteria;Deltaproteobacteria; Desulfobacterales;Desulfobacteraceae;sf_5;9810	0.017	0.67	0.051	-0.57								
Bacteria;Proteobacteria;Deltaproteobacteria; Desulfobacterales;Unclassified;sf_3;468	0.035	-0.61										
Bacteria;Proteobacteria;Deltaproteobacteria; Desulfovibrionales;Unclassified;sf_1;9828	0.043	-0.59										
Bacteria;Proteobacteria;Deltaproteobacteria; EB1021 group;Unclassified;sf_4;9884	0.006	-0.74	0.033	0.62	0.025	-0.64	0.032	-0.62				
Bacteria;Proteobacteria;Deltaproteobacteria; Myxococcales;Polyangiaceae;sf_4;9733			0.020	-0.66	0.052	0.57						
Bacteria;Proteobacteria;Deltaproteobacteria; Myxococcales;Unclassified;sf_1;10230	0.028	-0.63	0.002	0.80	0.001	-0.82	0.009	-0.72	0.028	-0.63		
Bacteria;Proteobacteria;Deltaproteobacteria; Unclassified;Unclassified;sf_7;10048	0.003	-0.78	0.018	0.67	0.044	-0.59						
Bacteria;Proteobacteria;Deltaproteobacteria; Unclassified;Unclassified;sf_9;10174	0.021	0.65										
Bacteria;Proteobacteria;Deltaproteobacteria; Unclassified;Unclassified;sf_9;10185	0.015	0.68										
Bacteria;Proteobacteria;Gammaproteobacteria; Aeromonadales;Succinivibrionaceae;sf_1;8822	0.021	0.65										
Bacteria;Proteobacteria;Gammaproteobacteria; Alteromonadales;Alteromonadaceae;sf_1;8768	0.008	0.72										
Bacteria;Proteobacteria;Gammaproteobacteria; Chromatiales;Chromatiaceae;sf_1;9571	0.013	-0.69										
Bacteria;Proteobacteria;Gammaproteobacteria; Chromatiales;Halothiobacillaceae;sf_1;9181	0.011	-0.70										
Bacteria;Proteobacteria;Gammaproteobacteria; Chromatiales;Halothiobacillaceae;sf_3;9448	0.028	-0.63										
Bacteria;Proteobacteria;Gammaproteobacteria; Enterobacteriales;Enterobacteriaceae;sf_1;8236	0.027	0.63										
Bacteria;Proteobacteria;Gammaproteobacteria; Enterobacteriales;Enterobacteriaceae;sf_1;9266	0.022	0.65	0.046	-0.58								

Taxa string	DOC		Al		P		Mg		Mn		NH4	
	P	r	P	r	P	r	P	r	P	r	P	r
Bacteria;Proteobacteria;Gammaproteobacteria; Enterobacteriales;Enterobacteriaceae;sf_6;103	0.039	0.60							0.016	0.68		
Bacteria;Proteobacteria;Gammaproteobacteria; Enterobacteriales;Unclassified;sf_1;8430			0.003	-0.78	0.002	0.80	0.002	0.79				
Bacteria;Proteobacteria;Gammaproteobacteria; Legionellales;Coxiellaceae;sf_3;8378			0.012	0.70	0.050	-0.58			0.016	-0.67		
Bacteria;Proteobacteria;Gammaproteobacteria; Oceanospirillales;Oceanospirillaceae;sf_1;9351	0.026	-0.64										
Bacteria;Proteobacteria;Gammaproteobacteria; Pasteurellales;Pasteurellaceae;sf_1;9237			0.033	-0.61	0.029	0.63						
Bacteria;Proteobacteria;Gammaproteobacteria; SAR86;Unclassified;sf_1;8962	0.011	0.70	0.028	-0.63	0.041	0.59			0.006	0.74		
Bacteria;Proteobacteria;Gammaproteobacteria; Thiotrichales;Francisellaceae;sf_1;9554			0.028	0.63	0.014	-0.68	0.041	-0.59				
Bacteria;Proteobacteria;Gammaproteobacteria; Thiotrichales;Piscirickettsiaceae;sf_3;9291	0.020	0.66			0.027	0.63	0.051	0.57	0.017	0.67		
Bacteria;Proteobacteria;Gammaproteobacteria ;Unclassified;Unclassified;sf_3;8391			0.003	0.78	0.026	-0.64						
Bacteria;Proteobacteria;Gammaproteobacteria; Unclassified;Unclassified;sf_3;8551	0.016	0.68										
Bacteria;Proteobacteria;Gammaproteobacteria; Unclassified;Unclassified;sf_3;8922			0.042	-0.59								
Bacteria;Proteobacteria;Gammaproteobacteria; Unclassified;Unclassified;sf_3;9605			0.005	0.75	0.022	-0.65						
Bacteria;Proteobacteria;Gammaproteobacteria; Xanthomonadales;Xanthomonadaceae;sf_3;8612									0.010	0.71		
Bacteria;Proteobacteria;Unclassified; Unclassified;Unclassified;sf_28;10091	0.047	0.58							0.010	0.71		
Bacteria;Spirochaetes;Spirochaetes; Spirochaetales;Serpulinaceae;sf_1;6548												
Bacteria;Spirochaetes;Spirochaetes; Spirochaetales;Spirochaetaceae;sf_1;6502									0.017	-0.67		
Bacteria;Termite group 1;Unclassified; Unclassified;Unclassified;sf_2;722	0.001	-0.81							0.010	-0.71		
Bacteria;Thermotogae;Thermotogae; Thermotogales;Thermotogaceae;sf_4;51	0.016	0.68							0.010	0.71		
Bacteria;TM6;Unclassified; Unclassified;Unclassified;sf_1;9803	0.004	-0.76										
Bacteria;TM7;Unclassified; Unclassified;Unclassified;sf_1;3255									0.019	0.66		
Bacteria;TM7;Unclassified; Unclassified;Unclassified;sf_1;3464	0.029	0.63										
Bacteria;Unclassified;Unclassified; Unclassified;Unclassified;sf_106;243	0.002	-0.81							0.015	-0.68		
Bacteria;Unclassified;Unclassified;			0.016	-0.67								

Taxa string	**DOC**		**Al**		**P**		**Mg**		**Mn**		**NH4**	
	P	**r**	**P**	**r**	**P**	**r**	**P**	**r**	**P**	**r**	**P**	**r**
Unclassified;Unclassified;sf_119;316												
Bacteria;Unclassified;Unclassified; Unclassified;Unclassified;sf_119;916			0.004	-0.76	0.006	0.74	0.005	0.75				
Bacteria;Unclassified;Unclassified; Unclassified;Unclassified;sf_126;296	0.015	0.68										
Bacteria;Unclassified;Unclassified; Unclassified;Unclassified;sf_140;6355	0.010	-0.71	0.040	0.60	0.047	-0.58						
Bacteria;Unclassified;Unclassified; Unclassified;Unclassified;sf_148;5062			0.031	-0.62	0.031	0.62						
Bacteria;Unclassified;Unclassified; Unclassified;Unclassified;sf_160;6388	<0.001	0.89							0.006	0.74		
Bacteria;Unclassified;Unclassified; Unclassified;Unclassified;sf_160;6435												
Bacteria;Unclassified;Unclassified; Unclassified;Unclassified;sf_34;4668	0.021	-0.65										
Bacteria;Unclassified;Unclassified; Unclassified;Unclassified;sf_67;10326												
Bacteria;Unclassified;Unclassified; Unclassified;Unclassified;sf_92;9999	0.048	0.58										
Bacteria;Unclassified;Unclassified; Unclassified;Unclassified;sf_93;925	0.021	-0.66										
Bacteria;Verrucomicrobia;Verrucomicrobiae; Verrucomicrobiales;Unclassified;sf_3;399			0.001	0.81	0.001	-0.81	0.008	-0.72	0.041	-0.60		
Bacteria;Verrucomicrobia;Verrucomicrobiae; Verrucomicrobiales;Unclassified;sf_3;430	0.049	0.58										
Bacteria;Verrucomicrobia;Verrucomicrobiae; Verrucomicrobiales;Unclassified;sf_3;4840			0.010	0.71	0.009	-0.72	0.025	-0.64	0.021	-0.65		
Bacteria;Verrucomicrobia;Verrucomicrobiae; Verrucomicrobiales;Unclassified;sf_3;4865			0.009	0.72	0.020	-0.66	0.031	-0.62	0.052	-0.57		
Bacteria;Verrucomicrobia;Verrucomicrobiae; Verrucomicrobiales;Unclassified;sf_3;565			0.052	0.57					0.029	-0.63		
Bacteria;Verrucomicrobia;Verrucomicrobiae; Verrucomicrobiales;Unclassified;sf_3;610			0.010	0.71	0.009	-0.72	0.038	-0.60				
Bacteria;Verrucomicrobia;Verrucomicrobiae; Verrucomicrobiales;Unclassified;sf_3;911	0.034	-0.61	0.001	0.81	0.002	-0.79	0.012	-0.69	0.008	-0.72		
Bacteria;Verrucomicrobia;Verrucomicrobiae; Verrucomicrobiales;Verrucomicrobiaceae;sf_6;660			0.022	0.65	0.034	-0.61						
Bacteria;Verrucomicrobia;Verrucomicrobiae; Verrucomicrobiales;Xiphinematobacteraceae;sf_3;352	0.040	-0.60	0.023	0.65	0.038	-0.60						
Bacteria;Verrucomicrobia;Verrucomicrobiae; Verrucomicrobiales;Xiphinematobacteraceae;sf_3;876					0.028	-0.63	0.015	-0.68				
Bacteria;WS3;Unclassified; Unclassified;Unclassified;sf_1;2537	0.005	-0.75							0.046	-0.58		

Table 8: Environmental variables that showed a significant (P≤ 0.55) correlation (Pearson's r) with taxa that showed a significant difference (t-test p≤ 0.50) between depths (0-2 and 8-10 cm).

	P	**r**
pH	<0.0001	0.69
Soil Temp	0.0003	0.60
DOC	0.007	0.47
NH4+	0.008	0.46
Mn	<0.0001	0.85
P	<0.0001	0.83
Mg	<0.0001	0.83
Al	<0.0001	-0.81
Ca	<0.0001	0.71
K	0.0001	0.62
Fe	0.001	-0.55

Table 9: P-values and Pearson's linear correlation coefficient (r) for variables that correlated with microbial biomass carbon. Cation concentrations were log transformed for the correlation. Units for dissolved organic carbon (DOC), microbial biomass carbon and NH4+ concentrations were in ug/ g soil, cations were in µM and soil temperature in ºC.

Supplemantary Tables

	Aboveground grass biomass (g dry weight)	Aboveground moss biomass (g dry weight)
Moss plots	1.22 (0.08)	2.66 (0.06)
Grass plots	3.06 (0.08)	0

Table S1: Moss and grassbiomass average and SEM above cores taken from areas with high visual abundance of moss and grass.

Significant taxa between moss and grass (DNA level)						
Environmental variables		**Axis 1**			**Axis 2**	
	r	**R^2**	**tau**	**r**	**R^2**	**tau**
PB (Plant Biomass)	.386	.149	.500	.293	.086	-.071
NH4	.010	.000	-.071	.381	.145	.214
NO3	.427	.183	.000	-.130	.017	-.143
MBC	.354	.125	.286	-.043	.002	.000
DOC	-.060	.004	.143	.317	.101	.000
Al	-.160	.026	-.143	.675	.456	.286
Ca	.356	.127	.071	-.226	.051	-.071
Fe	-.160	.026	-.214	.434	.188	.214
K	-.013	.000	.000	-.374	.140	-.286
P	-.079	.006	.071	-.611	.373	-.357
Mg	-.101	.010	.214	-.673	.453	-.643
Mn	-.338	.114	-.071	.381	.145	.214
Na	-.399	.159	-.429	.072	.005	.143
Si	-.409	.167	-.286	-.215	.046	-.286
pH	.153	.023	.214	-.647	.418	-.357
SM (soilmoisture)	.322	.104	.000	.200	.040	.000
Temp (Soil temperature)	-.298	.089	-.143	-.191	.036	-.286
Significant taxa between moss and grass (cDNA level)		**Axis 1**			**Axis 2**	
	r	**R^2**	**tau**	**r**	**R^2**	**tau**
PB	.386	.149	.500	.293	.086	-.071
NH4	.010	.000	-.071	.381	.145	.214
NO3	.427	.183	.000	-.130	.017	-.143
MBC	.354	.125	.286	-.043	.002	.000
DOC	-.060	.004	.143	.317	.101	.000
Al	-.160	.026	-.143	.675	**.456**	.286
Ca	.356	.127	.071	-.226	.051	-.071
Fe	-.160	.026	-.214	.434	.188	.214
K	-.013	.000	.000	-.374	.140	-.286
P	-.079	.006	.071	-.611	.373	-.357
Mg	-.101	.010	.214	-.673	**.453**	-.643
Mn	-.338	.114	-.071	.381	.145	.214
Na	-.399	.159	-.429	.072	.005	.143

Si	-.409	.167	-.286	-.215	.046	-.286
pH	.153	.023	.214	-.647	**.418**	-.357
SM (soil moisture)	.322	.104	.000	.200	.040	.000
Temp (soil temperature)	-.298	.089	-.143	-.191	.036	-.286
Significant taxa between top and bottom 2cm of soil profile (DNA level)		**Axis 1**			**Axis 2**	
	r	**R^2**	**tau**	**r**	**R^2**	**tau**
NH4	.231	.054	.182	-.435	.19	-.485
NO3	.406	.165	.303	-.342	.117	-.242
DOC	.425	.181	.182	-.747	.558	-.364
Al	-.024	.001	.091	.512	.262	.333
Ca	-.116	.013	-.061	-.018	0	0
Fe	.1	.01	.152	.248	.062	.03
K	-.413	.17	-.394	-.123	.015	-.091
P	.02	0	-.091	-.5	.25	-.333
Mg	.038	.001	-.03	-.425	.181	-.333
Mn	.006	0	.091	-.641	.411	-.515
Na	.226	.051	.061	-.058	.003	-.121
Si	.04	.002	.03	.348	.121	.212
pH	-.09	.008	-.062	-.304	.092	-.277
SM (soil moisture)	.115	.013	-.152	.088	.008	.152
Temp (soil temperature)	.091	.008	.03	-.393	.155	-.152

Table S2: Pearson (Pearson's r) and Kendall (Kendall's tau) correlation values for environmental variables overlaid on the NMDS ordination.

Summary of Fit

RSquare	0.932258
RSquareAdj	0.91871
Root Mean Square Error	73.30581
Mean of Response	395.6696
Observations (or Sum Wgts)	31

Analysis of Variance

Source	**DF**	**Sum of Squares**	**Mean Square**	**F Ratio**
Model	5	1848820.0	369764	68.8094
Error	25	134343.5	5374	**Prob> F**
C. Total	30	1983163.5		<.0001

Parameter Estimates

Term	**Estimate**	**Std Error**	**t Ratio**	**Prob>|t|**
Intercept	-1469.436	373.0305	-3.94	0.0006
Treatment[Grass]	-33.65962	15.36061	-2.19	0.0380
Depth[0-2]	63.450841	32.01176	1.98	0.0586
log Mn (uM)	250.16984	55.08937	4.54	0.0001
log K (uM)	229.9752	120.1878	1.91	0.0672
log CEC	1178.2996	356.8874	3.30	0.0029

Table S3: Model statistics for the effect of environmental variables on soil microbial biomass. Forward stepwise regression was done prior to fit model to select the combination of effects that best explain the dependent variable.

Chapter 5

Short-term responses of soil microbial communities to rainfall events

Abstract

In a Mediterranean grassland ecosystem, plant and animal phenology, productivity, biogeochemical cycles and food web dynamics will be mainly controlled by the timing of rainfall events. Variability in dry and wet periods will affect biotic and abiotic conditions which in turn will have consequences on the structure and composition of soil microbial communities; the key players in nutrient cycling and soil health. Here, we look at changes in the structure and composition of soil microbial communities in response to natural rainfall events (wet-dry-wet) at the beginning of the rainy season in a California grassland. We used 16S rRNA microarrays to track changes in the relative microbial abundance after and between the first two rainfall events of the season (total of 4 sampling points in 32 days) and analyze this in response to the associated changes in soil environmental conditions. Data on microbial community composition and relative abundance were obtained for the top 5 cm of the soil profile and soil chemical properties were measured at 5 cm intervals over the top 35 cm of the soil profile. Soil moisture, temperature, extractable organic carbon, ammonium, manganese, and potassium concentrations and microbial carbon and nitrogen were significantly higher in the top 5 cm of the soil compared to deeper soil layers. Following the first rainfall event soil moisture, available carbon, pH and ammonium concentration changed significantly with time in the top five cm. Soil ammonium concentration decreased significantly with time after the first rainfall event and then increased immediately after the second event whereas soil available organic carbon had an inverse response. This pattern indicates a strong coupling between carbon and nitrogen availability in soil. Ordination analyses separate the soil microbial communities into two clusters: time points one and three in one cluster and time points two and four in another cluster. Soil moisture and concentrations of available carbon, ammonium and magnesium are the main environmental parameters correlated with these changes as demonstrated by the ordination and Pearson's linear correlation analysis. Soil pH was not important in separating the clusters, but strongly correlated with many taxa. Two main patterns were observed in the bacterial response to changes in environmental variables after the rainfall events. Members of the phyla Actinobacteria, Bacteroidetes, Planctomycetacia, TM7 groups, Verrucomicrobiae and some of the classes Alpha and Beta and Gamma proteobacteria, responded positively to available carbon but had a negative response to soil moisture, ammonium and pH, whereas members of the phylas Acidobacteria, Chlamydiae, Chloroflexi, Spirochaetes and the class Delta proteobacteria and had an opposite response. Soil microbial communities are known to be robust and resilient to change over longer time periods, yet they clearly respond to changes in soil moisture, chemical and nutritional conditions after and between rainfall events.

Introduction

California's grassland ecosystems are highly dependent in the timing and amount of rainfall events. Variation in precipitation patterns will affect plant and animal phenology, food web structure and nutrient cycling. Rainfall, especially events involving wet-dry cycles, release labile carbon and nitrogen substrates into the soil through heterotrophic decomposition, microbial death, cell lysis (Van Gestel 1993, Halverson et al. 2000) and release of soil organic matter bound in soil aggregates (Denef et al. 2001). An increase in water and nutrient availability after a dry period will trigger microbial and faunal activity, which can result in increased biomass (Schnurer et al. 1986, Kieft et al. 1987). This increase in biomass could be mainly due to the increased availability of soil organic carbon that, once available, will be quickly respired and assimilated by heterotrophic organisms (Fierer et al. 2009a). The magnitude of wetting-drying cycles may determine the size of CO_2 pulses into the atmosphere (due to soil respiration, (Birch 1958, Denef et al. 2001), which could decrease with time, if frequent rewetting events reduce the available organic pool (Fierer and Schimel 2002).

Rainfall events, together with plant life cycle, will also affect nitrogen availability. During the dry summer and early autumn months, soil nitrogen pools will be highest, as plants are not active and nitrogen is bound in viable and non viable microbial biomass and standing litter (Jackson et al. 1988). Once a rainfall event occurs, heterotrophic microorganisms will transform the available organic nitrogen into inorganic NH_4^+ and NO_3^-. This newly available nitrogen pool could be quickly immobilized into new microbial biomass, taken up by the growing plants and/or lost via leaching (in the case of NO_3^-) (Jackson et al. 1989, Schimel et al. 1989). Microbes are better competitors than plants for uptake of inorganic nitrogen (especially NH_4^+), hence the main consumers of inorganic nitrogen once is available (Jones and Woodmansee 1979, Schimel et al. 1989, Kaye and Hart 1997). Microorganisms are integral to nitrogen cycling and understanding how they respond seasonally is key to understanding grassland nitrogen dynamics.

Rainfall should directly or indirectly (through biotic or abiotic conditions) influence the structure, composition and activity of soil microbial communities. Changes (or the lack of them) in structure and activity probably depend on the ecosystem type (oak vs grassland (Waldrop 2006a, b, Fierer et al. 2009b) and time scale measured (Cruz-Martinez et al. 2009). In grassland ecosystems, microbial communities appear to be robust and resilience to long term changes in rainfall-related climatic change across years (Waldrop 2006b, a, Cruz-Martinez et al. 2009). This resilience may be due to adaptation of these communities to the wide range of climatic conditions characteristic of grassland Mediterranean ecosystems (cold and wet winters and hot and dry summers). However, on shorter time frames, significant responses may be observed to changes in environmental conditions such as the ones caused by wet-dry patterns (Schnurer et al. 1986, Fierer and Schimel 2002).

Among the key environmental parameters known to drive microbial community structure are soil moisture and pH (Waldrop 2006a, Allison et al. 2007, Fierer et al. 2007, Lauber et al. 2009) but the quantity and quality of nutrients, such as carbon and nitrogen, could also be important (Fierer et al. 2003, Balser and Firestone 2005). Here, we used newly developed microbial community profiling methods, coupled to measurements of soil parameters over time and as a function of soil depth, to investigate the short term effects of natural wetting-drying episodes on the structure and composition of soil microbial communities in a California grassland. In this study we focus on the response of bacterial and archaeal communities on the top 5 cm of the soil profile. However, changes in microbial composition with depth could be expected (Fierer et al. 2003, Allison et al. 2007), but these changes are considered in Chapter 4. The findings may have broader importance at the ecosystem level. Alterations in the timing and intensity of fall rainfall could modify microbial community composition and dynamics, with major consequences in nutrient and biogeochemical cycles. Understanding of how rainfall events control nitrogen and carbon cycling is the first step for prediction of climate change impacts.

Material and Methods

Sampling description:

Soil sampling was performed at the northern end of South meadow at the Angelo Coast Range Reserve in Mendocino Country, California, US (39°44'N, 123°39'W). Sampling dates were determined in relation to current weather conditions to study the dynamics of short-term soil moisture cycles between precipitation events. We used the weather station at the Angelo Reserve's headquarters to track the local rainfall and air temperature conditions (data at 15 min intervals). The winter rains started on October 9th, 2007. By the time of the first sampling (October 22nd (T1)) the reserve has received 165 mm of precipitation (Figure 1). The following two sampling dates were October 26th (T2) and November 8th (T3). There was only 1.8 mm of precipitation between T1 and T3. On November 11th, the rainfall resumed, and continued through to the final sampling time on November 12th (17.4 mm of precipitation between T3 and T4).The average air temperature during the sampling period was 8.6 °C, with the maximum temperature recorded at 19.0 °C and the minimum temperature at 0 °C at night. To account for diurnal cycles, sampling was initiated at 2 pm PST and finished within 2 hours. At each sampling point, five 20 x 20 cm squares were randomly selected within the experimental plot of 20 x 12 meters at the northern end of the meadow. Dead plant litter was collected for each square. Soil cores (3 cores at T1 and T2, and 2 cores at T3 and T4) were collected within each square to a depth of 30 cm deep (4.45 cm diameter) after the removal of aboveground vegetation. Soil temperature was recorded at 3, 10 and 27cm depth using a soil thermometer. Soil cores were stored at 4 °C until further processing and analysis.

Sample preparation

All soil cores were processed at the Angelo Reserve's laboratory within 8 hours of collection. Each soil core was subdivided into 5 cm sections (depths 0-5, 5-10, 10-15, 15-20, 20-25 and 25-30 cm) and manually homogenized in a plastic bag with its corresponding replica (2 or 3 cores per square). A total of 30 soil samples were obtained at each sampling point. However, square 7 from T2 was excluded from further analysis due to experimental errors at the time of subdividing the soil core. From the homogenized soil, 20 g subsamples were transported in dry ice and later stored at –80 °C for further DNA extraction and at -20 °C for chloroform fumigation. In addition, 10 g of soil was weighted and stored at room temperature in pre-weighted foil containers for gravimetric soil moisture; 20 g was stored over night at +4 °C for extraction of organic carbon and nitrogen and 20 g was stored over night at +4 °C in sampling cups with 1:5 w/V of 2 M KCl for extraction of inorganic nitrogen. The remaining of the soil was air dried at room temperature and dry sieved to <2 mm fraction size. The >2 mm fraction was wet sieved and dried at 80 °C for 72 hours to record the weight of the stone fraction. Dead plant material was dried at 80 °C for 72 hours and weighted.

Environmental correlates

Extraction of inorganic nitrogen

Within 24 hours of sampling, inorganic nitrogen, NH_4^+ and NO_3^-, was extracted by shaking in 2 M KCl at 150 rpm for 1 hour (Maynard 1993). Extracts were filtered through a Whatman No.1 filter (pre-washed with 2 M KCl) and stored at -20 °C for further analysis. One blank was included for each set of extractions. At the end of the sampling period, all extracts were shipped to the UC Davis Agricultural and Natural Resources Analytical Laboratory (Davis, Ca) for analysis of NH_4^+ and NO_3^+ concentrations using an automated flow injection analyzer method (Hofer 2003, Knepel 2003).

Extraction of organic Carbon and Nitrogen

Organic carbon and nitrogen were extracted by adding 20g of soil to 100 ml 0.05 M K_2SO_4 (1:5 w/V), shaken at 150 rpm for 2 hours (Voroney and Winter 1993) and filtered using a Whatman No.1 filter (pre-washed with 0.05M K_2SO_4). Extractable organic carbon was measured using a TIC/TOC analyzer. Samples from the upper soil horizons were diluted (1:2 or 1:5) to fit within the standard set for the TIC/TOC analyzer.

Total nitrogen was measured by digesting the extracts in a 1:1 mixture with 5% alkaline potassium persulfate reagent, and autoclaved for 40 min at 121 °C (Cabrera and Beare 1993). Nitrate in the samples was measured with a QC8000 flow injection analyzer (Lachat Instruments, Milwaukee, WI, USA).

Microbial biomass Carbon and Nitrogen

Microbial biomass carbon and nitrogen were estimated by fumigating 20 g of frozen soil for 7 days in a dessicator with an ethanol-free chloroform atmosphere. Organic carbon and nitrogen was extracted and measured from fumigated soils according to the procedure described above. Microbial biomass carbon was calculated as follows: microbial biomass C = EC/kEC, where EC = (organic C extracted from fumigated soils) - (organic C extracted from non-fumigated soils) and kEC= 0.45 (Beck et al, 1997). Microbial biomass nitrogen was calculated as follows: microbial biomass N = EN/kEN, where EN = (total N extracted from fumigated soils) - (total N extracted from non-fumigated soils) and kEN = 0.54 (Brooks et al 1985).

pH

Within 24 hours of sampling, fresh soil was extracted in 1:5 w/v 0.01 M $CaCl_2$ (2g soil in10 ml of 0.01 M $CaCl_2$) was shaken for 2 hours at ~100 rpm and centrifuged for 5 minutes. The clear supernatant was transferred to a clean tube for pH measurement (Fisher Acumet AR 20, Fisher Scientific).

Gravimetric soil moisture

Gravimetric soil moisture was calculated from the soil dry weight after oven-drying 10 g of fresh soil at 105°C for 24 hours or until a constant weight was achieved. Dry weight was subtracted from fresh weight and the moisture difference divided by the dry weight to obtain the soil moisture percentage.

Organic matter content

The organic matter content of the <2 mm fraction was determined by dry ashing at 350 °C (Ayud and Bioyd, 1994). Dry weights were measured after heating at 105 °C over night both before and after ashing.

Exchangeable cations (modified from (Hendershot 1993)

Exchangeable cations were extracted from 4 g of air-dried soil (<2 mm) added to 20 ml 0.1 M $BaCl_2$ (1:5 w/V) and shaken on a vertical shaker at 45 rpm for 2 hours. One internal extraction control and one blank were included with every set of extractions. The supernatant was separated by centrifugation at 7000 rpm for 5 minutes.

Exchangeable cations Al, Ca, Fe, K, P, Mg, Mn, Na and Si were analyzed by Inductively Coupled with Optical Emission System (ICP-OES) by using a Perkin Elmer 5300 DV optimal emission ICP with auto sampler. Blanks and internal controls were included in the analysis.

Soil DNA extractions and 16S rRNA Bacterial and Archaeal amplification

Within 24 hours of soil collection, DNA was extracted from 0.25 g (approximate dry weight) of homogenized soil using the Power Soil DNA kit (MO BIO, Carlsbad, CA, USA) according to the manufacturer's instructions. Approximately, 6 to 10 ng of DNA was used for further 16S rRNA amplification. For the amplification of the bacterial 16S rRNA gene a temperature-gradient PCR was performed for each sample using the primers 1492R (5'-GGTTACCTTGTTACGACTT-3') and 27F (5'-GTTTGATCCTGGCTCAG-3'). For the archaeal 16S rRNA gene amplification two rounds of PCR were performed. On the first round, one reaction per sample was done using the primers 1492R and the 4Fa (5'-TCCGGTTGATCCTGCCRG-3') and on the second round, a gradient PCR was done using primers 1406R (5'-ACGGGCGGTGWGTRCAA-3') and 23F (5'-TGCAGAYCTGGTYGATYCTGCC-3'). PCR reactions had a final volume of 25µl containing a final concentration of 1X Takara ExTaq PCR buffer with $MgCl_2$, 300 pM of primers, 1 ug/ul BSA, 200 µM dNTPs, 2.5 U ExTaq DNA polymerase (Takara Mirus Bio Inc., Madison, WI) and milliQ H_2O to complete volume. PCR cycle for the bacterial 16S rRNA amplification was performed with a initial denaturation at 95 °C for 3 min, followed by 25 cycles of 95 °C for 30 sec, annealing gradient from 48 °C – 60 °C for 25 sec, extension of 72 °C for 2 min and a final extension of 72 °C for 10 min. The first round of archaeal PCR had a initial denaturation at 95 °C for 3 min, followed by 25 cycles of 95 °C for 30 sec, annealing temperature of 50 °C for 25 sec, extension of 72 °C for 2 min and a final extension of 72 °C for 10 min and the second round had the same cycle but with an annealing gradient of 53 °C – 65 °C for 25 sec. Amplicons were purified using the QIAquick PCR purification kit (Qiagen, Maryland, USA) and quantified with gel electrophoresis.

16S rRNA DNA microarrays

From the corresponding 16S rRNA amplified pools, 500 ng of bacterial and 100 ng of archaeal DNA was fragmented, biotin labeled and hybridized to a 16S rRNA Affymetrix microarray (16S rRNAPhyloChip, Affymetrix) as described in detail elsewhere (Brodie et al. 2006). PhyloChip washing, staining and scanning were performed as described elsewhere (Masuda and Church 2002). Phylochip data was normalized to total array intensity and analyzed at the sub-family level (approximately 94% sequence homology). The representative taxa selected for further analysis were the ones with the best probe sets (gPM), which can give more than one representative per sub-family.

Data analysis

Environmental parameters across time and depth

Analysis of variance (ANOVA) followed by a post-hoc Tukey HSD test was used to find and localize significant changes across time and depth for each environmental parameter measured. We analyzed variation with 1) time at each individual depth, 2) across depths at each individual time and 3) time by depth interactions. All depths were compiled when looking at the effect of time and all times were compiled when looking at the effect of depth. To examine environmental variables in the top 5 cm, all other depths were excluded. Time by depth interactions were also analyzed using the standard least square modeling. All statistical analyses were performed using JMP (SAS Institute Inc. 2004).

Community Composition

Analyses of the effects of the first rainfall of the season and the following events on community composition (i.e., taxonomic membership and relative abundance of detected subfamilies across plots) are based only on hybridization intensity data for taxa that could be detected and identified with high confidence (positive fraction > 0.90). Intensities were normalized to the total array intensity to minimize variations between arrays. Non-metric multidimensional scaling (NMS) (Kruskal 1978, Clarke 1993) and/or Canonical Correspondence Analysis (CCA) (Ter Braak 1986, Ter Braak 1994) and multi-response permutation procedures (MRPP) (Mielke 1984, 2001) were used to visualize and test dissimilarities in species composition across time in the top 5 cm of the soil profile. Environmental variables were superimposed on the CCA ordination analysis to identify the variables that could be responsible for driving the observed clustering. We identified the taxa that showed significant variation in relative abundance across time in the top 5 cm by using one way analysis of variance for each taxon (ANOVA; $P < 0.05$) in the ChipST2C software platform (Peterson 2006). We then conducted post-hoc Tukey tests to identify the direction of the separation for all taxa showing differences across times or depths. Pearson's linear correlation was used to establish relationships between environmental variables and each of the taxa whose variation with time or depth was significant (i.e., "significant taxa"). Those Phyla that have taxa that showed a similar response to environmental parameters were grouped. Statistical analyses were performed using JMP (SAS Institute Inc. 2004). Pearson's linear correlations were done using the program R (http://www.R-project.org).

Results

Change of environmental parameters across depths and time

Soil environmental variables changed with time and depth gradients in response to wetting-drying events. At almost all time points, the top five cm of the soil profile had the highest soil moisture, temperature, microbial biomass carbon and nitrogen, extractable organic carbon and ammonium, manganese and potassium concentrations (Table 1). On the other hand, soil moisture, temperature, extractable organic carbon, inorganic ammonium and nitrate, microbial C:N ratios, pH and manganese concentration significantly varied with time at one or more different depths (Table 1). Soil moisture, extractable organic carbon and ammonium concentrations were the only environmental variables that had a time by depth interaction (Table 1). The highest soil moisture was after the second rainfall event (T4, 0-5 cm), the highest concentration of extractable organic carbon was after the third sampling point (T3, 0-5 cm) and the highest concentration of ammonium was after the first rainfall (T1, 0-5 cm).

In the top 5 cm, where microbial community data were measured, the environmental variables that changed significantly with time were soil moisture and temperature, pH concentrations of extractable organic carbon and ammonium (Table 1). The initial high ammonium concentration was accompanied by one of the lowest available carbon measured. As soil moisture decreased over time, available ammonium also decreased while carbon availability increased, reaching its lowest and highest, respectively, at time point 3 (29 days after first rainfall and 16 days after T1) (Fig 1). Soil pH also changed with time, where the highest pH was measured at the second sampling point. After the second rainfall event, a slight increase in inorganic nitrogen and decrease in available carbon was observed.

Soil bacterial and archaeal communities in the top 5 cm of soil across time.

In the top 5 cm of the soil profile, soil bacterial and archaeal communities changed significantly with time following the first of the four rainfall event. Canonical correspondence analysis (CCA) shows two main clusters; one cluster with communities from T1 and T3 and the second cluster with communities from T2 and T4 (Fig 2). Overlay of environmental variables on ordination space suggest that extractable organic carbon, magnesium, soil moisture and ammonium concentrations are factors driving the separation of the two clusters (Fig 2). Soil pH also changed significantly with time in the top 5 cm (Table 1) and was strongly correlated with many taxa (Table 3). However, soil pH was not inferred to be a driving environmental variable in the CCA analysis (Fig 2).

Univariate analysis of variance (ANOVA, $p \leq 0.05$) identified a total of 253 subfamilies (from a dataset with 608 subfamilies) that changed significantly in abundance over time. Pearson's linear correlation was performed to identify the correlation of each taxa with significant change against all environmental variable. As expected from the CCA analysis, soil moisture, extractable organic carbon, pH and ammonium concentration were the variables that correlated with the abundance of most the taxa (Table 3). Even though magnesium was observed in the CCA analysis, it did not correlated with many taxa (Table 3).

Interestingly, two contrasting response patterns to soil moisture, pH and available carbon and ammonium concentrations were identified for the bacterial phyla with significant change in abundance over time. We propose that the patterns correspond to distinct guilds in the soil microbial community. The first guild includes some members of the phyla Actinobacteria, Bacteroidetes, Planctomycetacia, TM7 groups, Verrucomicrobiae and some of the classes Alpha and Beta and Gamma proteobacteria. This guild responded positively to available carbon but had a negative response to soil moisture, ammonia and pH. The second guild includes members of the phylas Acidobacteria, Chlamydiae, Chloroflexi, Spirochaetes and the class Delta proteobacteria and had an opposite response (Table 3).

Discussion

Here, we show that soil microbial community composition changes in response to changes in soil moisture and availability of carbon and nitrogen during a natural drying and re-wetting event. After the first rainfall event, soil carbon concentrations increased with time but rapidly decreased following the second event. Ammonium concentrations, on the other hand, had the opposite response (Fig. 1). This response could be due to the decomposition of the aboveground litter and the rapid germination of grasses and forbs (Fig 3). Litter decomposition and root and microbial exudations will release organic carbon nitrogen sources into the soil. The active microbial communities and the growing plants quickly assimilate nitrogen and thus compete for this limiting nutrient in this ecosystem (Kaye and Hart 1997, Grogan and Chapin 2000, Harpole 2007). This may explain the rapid decreased in ammonium availability following the first rainfall event. As nitrogen availability decreased, the microbial biomass may get increasingly nitrogen limited. Such conditions may induce microbial decomposition of organic substrates to acquire nitrogen, resulting in release of organic carbon to the soil available pools (Craine et al. 2007). Microbial decomposition of organic matter and plant root exudation may explain the increase in organic carbon after the first rainfall event. The distribution of carbon and nitrogen between the available soil pool and microbial biomass are intimately linked. Thus, interpretation of carbon and nitrogen dynamics is complicated.

Here we observe two main microbial groups or guilds, representing contrasting responses to the aforementioned changes in soil moisture, carbon and nitrogen availability and pH (Table 3). These responses might suggest some similarities in the physiology and nutritional requirements among taxonomic groups of the proposed guilds. For instance, in agreement with our results, previous studies have demonstrated a negative response in the abundance of Acidobacteria and a positive response in the abundance of Betaproteobacteria and Bacteroidetes to carbon availability (Fierer et al. 2007) as well as a negative response of Actinobacteria to soil moisture (Goodfellow and Williams 1983).

These results suggest that diverse bacterial groups might have similar ecological roles and responses to environmental variables. Based on their response to nutrient availability microbes are categorized as copiotrophs or oligotrophs. This concept is similar to the r-K theory of colonization and succession used for macroorganisms. Copiotrophic organisms will have higher growth rates, lower substrate specificity and inefficient conversion of substrate to cell biomass under high substrate availability (similar to r-strategy), whereas oligotrophic organisms are better competitor under low resource availability with high substrate specificity and a more efficient substrate utilization (similar to K-strategy) (Sylvia 1999, Fierer et al. 2007). The availability of nutrients after the first rainfall event probably stimulated the activity of those taxa that are able to quickly respond to the new labile carbon sources (first guild-copiotrophs) but as nutrient quantity and/or quality declines, the relative abundance of oligotrophic organisms might increase (second guild).

On the other hand, not all taxa might be strictly driven by carbon availability but another of environmental parameter. For instance, the Actinobacteria are considered to be oligotrophic organisms as they have slower growth rates and prefer complex organic compounds yet they responded as a copiotrophic organism in this study. This might suggest that other environmental factor, such as soil moisture in this case, might be a stronger driver affecting the abundance of this group. An increase in soil moisture can create anaerobic micro-niches, which can negatively affect the growth of strict aerobic organisms such as the Actinobacteria, but can also create the adequate environment for strict or facultative anaerobes. This could be the case, for example, for some members of the Deltaproteobacteria. These are known to be strict anaerobes (e.g., Desulfobacterales, Desulfovibrio) and are positively correlated to the increase in soil moisture in this study. At least for these two groups, is a possibility that aerobic conditions in soil will be a significant driver in their abundance. To best of our knowledge this is the first time these microbial guilds are observed in relation to short time rainfall events.

Conclusions

Changes in soil moisture, pH and soil nutrient availability (mainly carbon and nitrogen) that result from natural drying and rewetting events affect the structure of soil microbial communities in the top 5 cm of the soil profile. Even though, over long time scales, grassland soil microbial communities are robust and resilience to the wide range of temperatures and moisture conditions that characterize their Mediterranean-type climate, they respond to short term changes in moisture, chemical and nutritional conditions after rainfall events. We detect two main microbial guilds of bacteria, one with a positive response to available carbon and a negative response to soil moisture, ammonia and pH and the other with the opposite response. We proposed that soil microbial communities will respond to changes in soil environmental conditions, due to wetting and drying events, and that their responses to nutrient availability could be predicted if the copiotroph-oligotroph concept applies.

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Tables and Figures

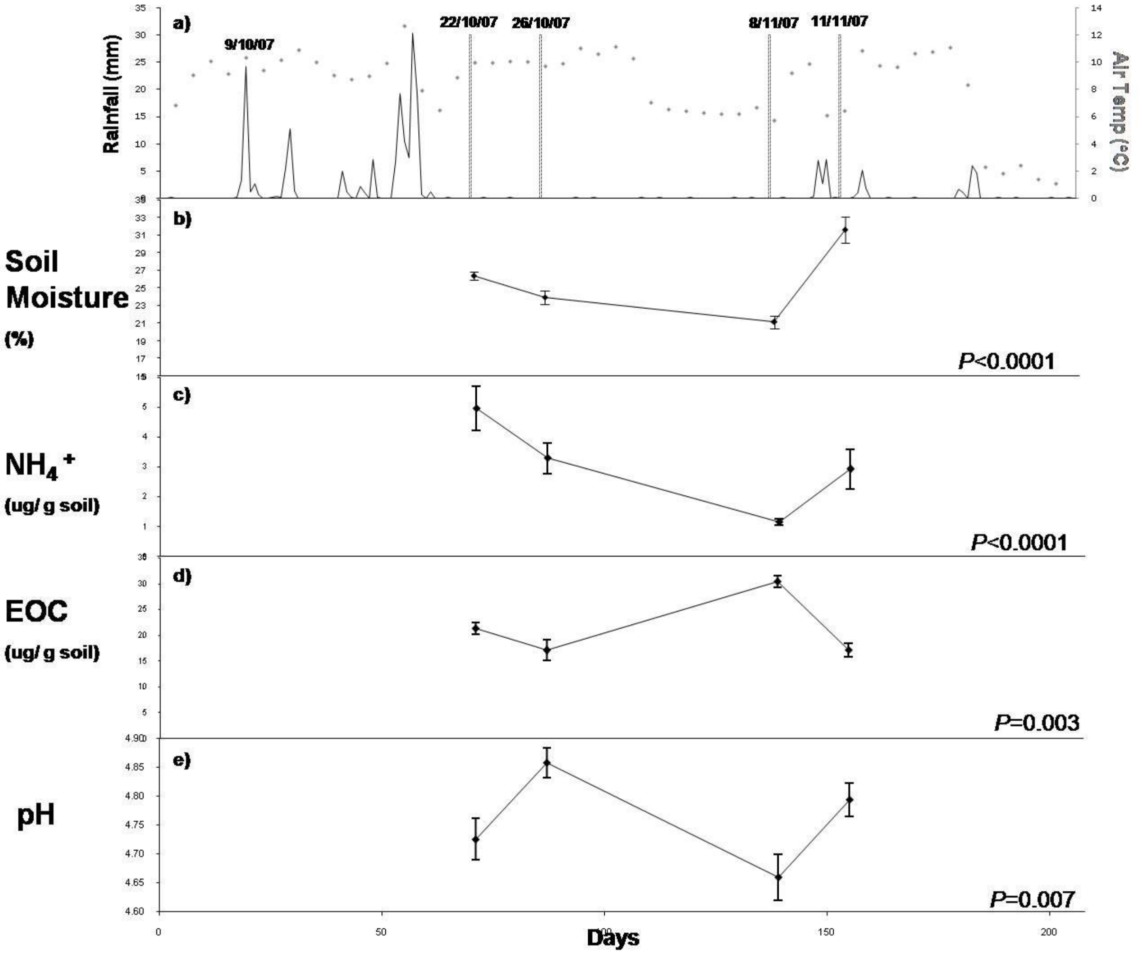

Figure 1: a) Daily rainfall (black lines), air temperature (gray dots) and dates of sampling (dd/mm/yy) and the response of b) soil moisture, c) ammonium (NH_4), d) extractable organic carbon (EOC) and e) pH on the top 5 cm of the soil profile across all four sampling points.

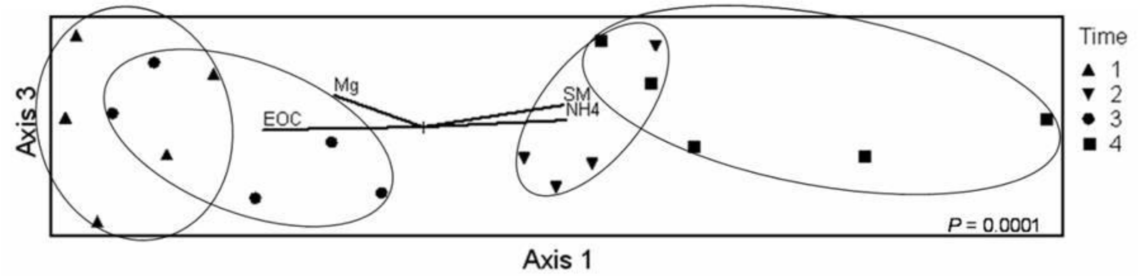

Figure 2: Canonical correspondence analysis (CCA) showing microbial community structure on the top 5 cm of the soil profile at each sampling point. CCA statistics and correlation coefficient with environmental variables are shown in table 3. Axes 1 and 3 were selected to represent the data.

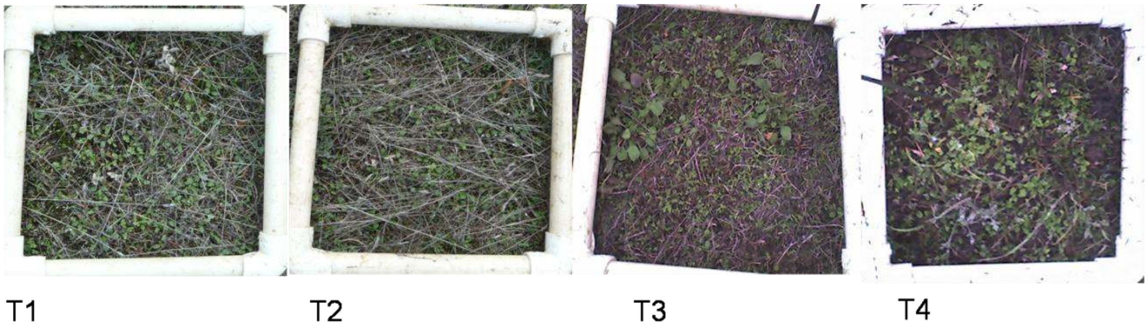

Figure 3: Representative pictures showing changes in aboveground plant biomass at each sampling point.

Soil Moisture (%)	**Depth (cm)**	**Time 1#**	**Time 2**	**Time 3**	**Time 4#**
	0-5*	26.41 (0.44)^{b,A}	23.95 (0.78)^{c}	21.17 (0.72)^{c}	31.62 (1.50)^{a,A}
	5-10*	22.19 (0.71)^{ab,B}	20.65 (0.70)^{b}	20.26 (0.66)^{ab}	23.55 (0.48)^{a,B}
	10-15*	21.96 (0.50)^{ab,B}	20.31 (0.76)^{ab}	19.64 (0.71)^{b}	23.18 (0.48)^{a,B}
	15-20*	22.19 (0.30)^{a,B}	21.37 (1.01)^{a}	19.42 (0.45)^{b}	21.71 (0.40)^{a,BC}
	20-25*	21.09 (0.66)^{ab,B}	21.49 (0.35)^{ab}	19.12 (0.46)^{b}	22.42 (0.42)^{a,BC}
	25-30	20.16 (0.89)^{B}	20.05 (0.76)	18.71 (0.59)	20.77 (0.83)^{BC}
	30-35	17.94^{B}	19.23 (0.79)	18.60 (0.38)	19.07 (0.97)^{C}
pH	**Depth (cm)**	**Time 1**	**Time 2**	**Time 3**	**Time 4**
	0-5*	4.73 (0.04)^{ab}	4.86 (0.03)^{a}	4.66 (0.04)^{b}	4.79 (0.03)^{ab}
	5-10*	4.72 (0.04)^{ab}	4.77 (0.04)^{a}	4.60 (0.03)^{b}	4.67 (0.04)^{ab}
	10-15	4.70 (0.04)	4.76 (0.05)	4.63 (0.04)	4.69 (0.06)
	15-20*	4.75 (0.02)^{ab}	4.81 (0.04)^{a}	4.65 (0.03)^{b}	4.72 (0.05)^{ab}
	20-25	4.70 (0.04)	4.83 (0.02)	4.68 (0.03)	4.74 (0.05)
	25-30	4.79 (0.08)	4.84 (0.03)	4.69 (0.03)	4.76 (0.04)
	30-35*	4.59^{bc}	4.89 (0.02)^{a}	4.68 (0.03)^{c}	4.80 (0.05)^{ab}
NH_4^+ (ug N/ g soil)	**Depth (cm)**	**Time 1#**	**Time 2#**	**Time 3**	**Time 4#**
	0-5*	4.96 (0.73)^{a,A}	3.48 (0.55)^{ab,A}	1.16 (0.11)^{b}	2.93 (0.67)^{ab,A}
	5-10*	2.30 (0.51)^{a,AB}	0.85 (0.31)^{ab,B}	1.07 (0.38)^{ab}	0.69 (0.13)^{b,B}
	10-15	2.52 (1.37)^{AB}	0.38 (0.07)^{B}	1.47 (0.95)	0.58 (0.11)^{B}
	15-20	0.93 (0.25)^{B}	0.30 (0.02)^{B}	0.88 (0.48)	0.38 (0.10)^{B}
	20-25	0.53 (0.15)^{B}	0.22 (0.04)^{B}	0.32 (0.10)	0.24 (0.04)^{B}
	25-30	0.34 (0.06)^{B}	0.12 (0.03)^{B}	0.22 (0.12)	0.50 (0.42)^{B}
	30-35	0.81 (0.51)^{AB}	0.08 (0.03)^{B}	0.53 (0.40)	0.08 (0.04)^{B}

NO$_3^-$ (ug N/ g soil)	**Depth (cm)**	**Time 1**	**Time 2**	**Time 3**	**Time 4**
	0-5	0.25 (0.12)	0.16 (0.10)	0.06 (0.06)	0.14 (0.11)
	5-10*	0.43 (0.10)^{a}	0.07 (0.04)^{b}	0.13 (0.09)^{b}	0.04 (0.03)^{b}
	10-15	0.89 (0.62)	0.07 (0.06)	0.23 (0.07)	0.13 (0.06)
	15-20	0.69 (0.41)	0.05 (0.03)	0.18 (0.08)	0.24 (0.12)
	20-25	0.61 (0.38)	0.09 (0.06)	0.15 (0.08)	0.37 (0.15)
	25-30	1.50 (0.85)	0.15 (0.06)	0.18 (0.18)	0.37 (0.17)
	30-35	0.87 (0.10)	0.14 (0.09)	0.16 (0.08)	0.34 (0.19)
EOC (ug C/ g soil)	**Depth (cm)**	**Time 1#**	**Time 2#**	**Time 3#**	**Time 4#**
	0-5*	21.31 (1.18)^{b,A}	17.80 (1.35)^{b,A}	30.42 (1.15)^{a,A}	17.14 (1.31)^{b,A}
	5-10	14.28 (2.52)^{AB}	8.92 (0.94)^{B}	14.01 (2.13)^{B}	8.95 (1.00)^{B}
	10-15	9.55 (1.18)^{BC}	7.68 (0.61)^{B}	11.26 (2.60)^{BC}	6.69 (0.31)^{BC}
	15-20	10.62 (2.17)^{BC}	7.68 (2.13)^{B}	8.34 (1.00)^{BC}	4.56 (0.59)^{C}
	20-25	6.29 (1.630)^{BC}	8.15 (2.04)^{B}	7.43 (1.28)^{BC}	4.47 (0.48)^{C}
	25-30	5.68 (0.41)^{C}	7.90 (1.69)^{B}	7.17 (1.23)^{BC}	3.51 (0.29)^{C}
	30-35	4.76 ^{BC}	8.21 (2.27)^{B}	6.06 (0.40)^{C}	3.65 (0.38)^{C}
Soil Temperature (°C)	**Depth (cm)**	**Time 1**	**Time 2#**	**Time 3#**	**Time 4#**
	0-5*	18.65 (0.21)^{b}	19.80 (0.39)^{a,A}	15.32 (0.28)^{c,A}	12.26 (0.11)$^{d, AB}$
	5-10	NA	17.30 (0.25)^{B}	12.68 (0.34)^{B}	11.86 (0.05)^{B}
	10-15	NA	17.30 (0.25)^{B}	12.68 (0.34)^{B}	11.86 (0.05)^{B}
	15-20	NA	NA	NA	NA
	20-25	NA	NA	NA	NA
	25-30	NA	NA	NA	NA
	30-35	NA	15.58 (0.15)^{C}	13.08 (0.12)^{B}	12.68 (0.13)^{A}
Microbial C/N ratios	**Depth (cm)**	**Time 1#**	**Time 2**	**Time 3**	**Time 4#**
	0-5	5.42 (0.63)^{B}	6.65 (1.15)	10.11 (1.27)	11.77 (5.51)^{B}

	5-10*	6.50 (1.08)^{ab,AB}	4.15 (1.41)^{b}	9.18 (2.29)^{ab}	20.85 (6.71)^{a,AB}
	10-15	5.86 (0.37)^{B}	5.16 (0.79)	7.71 (2.40)	10.51 (1.94)^{B}
	15-20	6.18 (0.90)^{AB}	4.79 (0.80)	7.78 (1.83)	22.90 (8.92)^{AB}
	20-25	8.42 (1.82) ^{AB}	8.05 (1.86)	5.17 (1.88)	13.42 (4.30)^{B}
	25-30	12.36 (2.52)^{A}	19.27 (8.02)	11.16 (6.38)	26.44 (12.70)^{AB}
	30-35	10.88 ^{AB}	22.71 (14.42)	21.32 (7.67)	103.83 (53.63)^{A}
Microbial Nitrogen (ug N / g soil)	**Depth (cm)**	**Time 1#**	**Time 2#**	**Time 3**	**Time 4#**
	0-5	145.20 (5.88)^{A}	111.95 (15.46)^{A}	76.82 (12.76)	136.95 (66.27)^{A}
	5-10	36.21 (3.06)^{B}	81.40 (46.63)^{AB}	34.35 (8.72)	16.13 (4.59)^{B}
	10-15	21.59 (1.40)^{C}	22.08 (3.09)^{B}	65.88 (41.90)	16.69 (3.05)^{AB}
	15-20	17.15 (2.28)^{CD}	17.11 (1.57)^{B}	16.20 (3.39)	8.13 (2.78)^{B}
	20-25	8.65 (1.53)^{CD}	9.72 (2.43)^{B}	6.20 (6.12)	5.98 (2.17)^{B}
	25-30	4.24 (1.08)^{D}	5.15 (0.92)^{B}	5.40 (1.83)	3.15 (1.50)^{B}
	30-35	2.27 ^{CD}	1.87 (0.47)^{B}	2.63 (1.26)	1.40 (0.95)^{B}
Microbial Carbon (ug C / g soil)	**Depth (cm)**	**Time 1#**	**Time 2#**	**Time 3#**	**Time 4#**
	0-5	774.84 (63.26)^{A}	695.60 (46.90)^{A}	747.02 (134.97)^{A}	702.45 (109.28)^{A}
	5-10	239.81 (49.83)^{B}	190.11 (45.07)^{B}	237.75 (19.77)^{B}	238.19 (40.11)^{B}
	10-15	126.44 (11.95)^{BC}	109.03 (12.90)^{BC}	181.48 (18.69)^{B}	189.38 (69.84)^{B}
	15-20	101.92 (17.10)^{BC}	78.51 (7.97)^{BC}	106.61 (17.09)^{B}	107.73 (11.43)^{B}
	20-25	65.51 (8.57)^{C}	72.99 (21.58)^{BC}	71.58 (14.63)^{B}	76.99 (12.57)^{B}
	25-30	44.44 (8.34)^{C}	85.00 (37.48)^{BC}	60.75 (15.23)^{B}	55.88 (9.70)^{B}
	30-35	24.65 ^{BC}	31.41 (16.25)^{C}	62.29 (21.11)^{B}	33.49 (3.35)^{B}
Al (ug/g soil)	**Depth (cm)**	**Time 1#**	**Time 2#**	**Time 3#**	**Time 4#**
	0-5	15.86	19.84	28.84	21.54

		(3.42)^{D}	(2.52)^{A}	(3.81)^{A}	(2.52)^{a}
	5-10	41.69 (4.63)^{A}	35.94 (4.89)^{A}	39.46 (3.64)^{A}	41.19 (5.06)^{A}
	10-15	38.54 (1.41)^{AB}	38.02 (4.16)^{A}	39.14 (3.07)^{A}	39.00 (7.32)^{A}
	15-20	34.86 (3.52)^{ABC}	34.44 (5.66)^{A}	33.49 (3.31)^{A}	30.04 (5.23)^{A}
	20-25	26.18 (2.18)^{BCD}	31.85 (5.56)^{A}	31.14 (1.96)^{A}	25.09 (4.63)^{A}
	25-30	22.18 (2.47)^{CD}	26.50 (3.59)^{A}	26.44 (0.003)^{A}	18.85 (5.83)^{A}
	30-35	16.19^{BCD}	21.73 (3.11)^{A}	27.77 (2.62)^{A}	18.74 (3.59)^{A}
Ca (ug/g soil)	**Depth (cm)**	**Time 1**	**Time 2**	**Time 3**	**Time 4**
	0-5	1861.70 (111.51)^{d}	1819.79 (92.54)	1720.60 (58.06)	1822.90 (98.46)
	5-10	1742.20 (89.08)^{a}	1646.18 (129.70)	1714.42 (73.50)	1906.21 (129.00
	10-15	1728.78 (179.10)^{ab}	1803.17 (157.96)	1848.76 (77.57)	1957.38 (144.35)
	15-20	1827.01 (75.15)^{abc}	1924.54. (147.34)	1825.51 (75.73)	1830.30 (145.35)
	20-25	1786.28 (60.08)^{bcd}	1878.72 (72.20)	1838.40 (34.34)	1778.11 (75.05)
	25-30	1662.09 (97.79)^{cd}	1817.78 (108.90)	1853.22 (105.05)	1694.70 (108.83)
	30-35	1921.71^{bcd}	1753.27 (205.96)	1831.58 (53.51)	1768.85 (127.03)
Fe (ug/ g soil)	**Depth (cm)**	**Time 1**	**Time 2**	**Time 3**	**Time 4**
	0-5	0.56 (0.39)	1.31 (1.20)	1.08 (0.49)	2.66 (1.05)
	5-10	1.03 (0.44)	1.06 (0.86)	1.03 (0.85)	2.62 (0.87)
	10-15	1.12 (0.65)	0.84 (0.62)	0.90 (0.49)	1.18 (0.57)
	15-20	0.68 (0.24)	0.87 (0.50)	0.85 (0.67)	0.31 (0.15)
	20-25	0.41 (0.27)	0.42 (0.34)	1.26 (0.48)	0.41 (0.32)
	25-30	2.10 (1.99)	0.84 (0.30)	0.25 (0.09)	0.22 (0.11)
	30-35	0.33	1.12 (0.78)	0.75 (0.38)	0.71 (0.38)
K (ug/g soil)	**Depth (cm)**	**Time 1#**	**Time 2#**	**Time 3#**	**Time 4#**
	0-5	152.64 (15.24)^{A}	138.58 (18.57)^{A}	148.61 (14.36)^{A}	121.38 (12.36)^{A}

	5-10	110.08 (10.73)^{AB}	77.72 (16.55)^{B}	81.26 (11.40)^{B}	76.14 (5.32)^{B}
	10-15	95.33 (9.95)^{AB}	84.45 (18.72)^{B}	85.47 (13.03)^{AB}	83.22 (6.98)^{AB}
	15-20	92.62 (7.13)^{AB}	86.28 (10.89)^{B}	80.80 (10.13)^{B}	77.94 (3.70)^{B}
	20-25	75.89 (6.95)^{B}	82.60 (10.40)^{B}	77.67 (7.61)^{B}	70.42 (6.34)^{B}
	25-30	59.47 (4.95)^{B}	71.40 (2.24)^{B}	76.78 (7.15)^{B}	63.97 (8.23)^{B}
	30-35	58.31^{AB}	61.21 (6.28)^{B}	72.41 (7.39)^{B}	63.91 (8.29)^{AB}
Mg (ug/g soil)	**Depth (cm)**	**Time 1#**	**Time 2**	**Time 3#**	**Time 4#**
	0-5	241.65 (9.28)^{A}	238.06 (14.18)^{A}	227.53 (8.30)^{A}	219.69 (9.15)^{A}
	5-10	206.37 (11.11)^{AB}	210.96 (8.68)^{A}	208.33 (6.38)^{A}	199.91 (9.56)^{A}
	10-15	182.54 (7.73)^{B}	201.73 (10.45)^{A}	200.69 (7.95)^{A}	183.05 (11.18)^{A}
	15-20	191.43 (10.61)^{B}	206.80 (16.39)^{A}	194.38 (8.62)^{A}	170.72 (12.77)^{A}
	20-25	194.94 (12.65)^{AB}	209.06 (20.55)^{A}	189.57 (8.65)^{A}	177.98 (14.79)^{A}
	25-30	193.72 (13.16)^{AB}	215.76 (16.91)^{A}	211.24 (10.50)^{A}	190.87 (11.91)^{A}
	30-35	205.29^{AB}	230.09 (23.96)^{A}	227.51 (9.89)^{A}	214.00 (10.17)^{A}
Mn (ug/g soil)	**Depth (cm)**	**Time 1#**	**Time 2**	**Time 3#**	**Time 4#**
	0-5	17.74 (1.61)^{A}	17.62 (1.40)	19.93 (2.39)^{A}	17.62 (2.80)^{A}
	5-10	5.25 (0.60)^{BC}	3.76 (0.31)	4.11 (0.48)^{B}	3.90 (0.50)^{B}
	10-15	4.84 (0.41)^{BC}	4.31 (0.51)	4.41 (0.66)^{B}	3.95 (0.44)^{B}
	15-20*	6.11 (0.60)^{a,B}	6.51 (0.60)^{a}	4.74 (0.33)^{ab,B}	3.72 (0.28)^{b,B}
	20-25*	4.77 (0.22)^{b,BC}	6.83 (0.66)^{a}	4.67 (0.32)^{bc,B}	3.50 (0.31)^{c,B}
	25-30*	3.90 (0.20)^{ab,C}	5.80 (0.64)^{a}	4.27 (0.47)^{ab,B}	2.84 (0.57)^{b,B}
	30-35	3.47^{BC}	4.32 (0.72)	4.77 (1.14)^{B}	2.99 (0.39)^{B}
Si (ug/g soil)	**Depth (cm)**	**Time 1**	**Time 2**	**Time 3**	**Time 4**
	0-5	4.53 (0.91)	6.31 (2.96)	6.15 (1.23)	9.29 (2.68)
	5-10	5.93	5.55	5.87	9.75

		(1.17)	(2.35)	(1.87)	(1.84)
	10-15	6.30 (1.59)	5.78 (1.58)	6.57 (1.21)	6.84 (1.29)
	15-20	6.23 0.76)	6.44 (1.27)	6.99 (1.69)	4.91 (0.63)
	20-25	5.45 (0.70)	6.05 (1.26)	8.52 (0.64)	5.40 (0.86)
	25-30	9.03 (4.49)	7.18 (1.07)	6.14 (0.54)	5.04 (0.47)
	30-35	6.08	8.05 (2.07)	8.03 (1.02)	7.13 (1.03)

Table 1: Environmental variables measured at each depth (5 cm intervals) and sampling point (4 time points). Values are the average from five replicas and the standard error of the mean is in parenthesis. Numbers in italics are samples with only one replica. Manganese, Silica and Iron concentrations were log transformed for univariate analysis (ANOVA). Letters denote differences (Tukey-Kramer HSD test) through time for each individual depth (small letter) and among depths within each time point (capital letter). Environmental variables in italics have a significant ($p \leq 0.05$) time by depth interaction. *Significant differences ($p \leq 0.05$) with time for that specific depth. $^{\#}$ Significant difference ($p \leq 0.05$) among depths at that specific time point. NA = data not available.

	pH	**SM**	**EOC**	**NH4**	**MBC**	**MBN**	**MC:N**	**Al**	**Ca**	**Log Fe**	**K**	**Log Mn**	**Log Si**
pH			<0.0001 (-0.78)	0.029 (0.50)				0.002 (-0.67)		0.034 (0.20)		0.052 (-0.47)	
SM					<0.0001 (0.55)							< 0.0001 (0.46)	
EOC					<0.0001 (0.76)			0.023 (0.52)				< 0.0001 (0.76)	
NH4					<0.0001 (0.58)								
MBN					<0.0001 (0.66)		0.029 (-0.50)						
MBC								0.02 (0.21)			<0.0001 (0.64)	< 0.0001 (0.77)	
Al						0.023 (0.52)			0.015 (-0.55)	0.0006 (0.31)			0.006 (0.24)
Ca										0.01 (0.22)	0.049 (0.47)		0.001 (0.29)
Mg												<0.0001 (0.47)	
K												0.058 (0.46)	
Log Mn													0.007 (0.60)

Table 2: Significant (p-value) correlations (Pearson's linear correlation shown in parenthesis) among the measured environmental variables. Iron, Manganese and Silica concentrations were

log transform to achieve normality. Inorganic nitrogen, cations, extractable organic carbon (EOC) and microbial biomass carbon and nitrogen were measured in ug /g soil.

Phyla/Class	**Guild 1** **(Copiotrophs)** **+C, -pH, -SM, -NH_4^+**	**Guild 2** **(Oligotrophs)** **-C, +pH, +SM, +NH_4^+**
Acidobacteria	2	7
Actinobacteria	36	6
Bacteroidetes	13	6
Chlamydiae	0	3
Chloroflexi	0	3
Firmicutes	10	9
Planctomycetes	16	2
Spirochaetes	1	4
TM7	6	0
Verrucomicrobia	10	4
Alphaproteobacteria	46	13
Betaproteobacteria	24	2
Deltaproteobacteria	8	16
Gammaprotebacteria	19	4

Table 3: Number of taxa present on each assigned guild. Guild 1 consists of taxa that showed a positive correlation to available carbon and a negative correlation to pH, soil moisture (SM), and ammonium (in at least 3 out of the 4 variables). Guild 2 consists of taxa that showed the inverse response. The Phyla Proteobacteria was subdivided into classes.

Supplementary Tables and Figures

	SM		NH4		EOC		pH		Mg	
Gene	**P**	**r**	**P**	**r**	**P**	**r**	**P**	**r**	**P**	**r**
Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales; Methanomicrobiaceae;sf_3;2286			0.04	-0.45	0.04	0.45	0.02	-0.55		
Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales; Methanosarcinaceae;sf_3;2101									0.01	0.57
Archaea;Euryarchaeota;Thermococci;Thermococcales; Thermococcaceae;sf_1;2240									0.01	0.57
Bacteria;Acidobacteria;Acidobacteria;Acidobacteriales; Acidobacteriaceae;sf_1;877					0.01	0.55	0.01	-0.60		
Bacteria;Acidobacteria;Acidobacteria;Acidobacteriales; Acidobacteriaceae;sf_14;6368	0.01	0.54	0.02	0.53	0.01	-0.57	0.01	0.57		
Bacteria;Acidobacteria;Acidobacteria;Acidobacteriales; Acidobacteriaceae;sf_16;6414	0.04	0.46	0.02	0.53	0.04	-0.46	0.04	0.48		
Bacteria;Acidobacteria;Acidobacteria;Acidobacteriales; cidobacteriaceae;sf_6;6362									0.05	-0.46
Bacteria;Acidobacteria;Acidobacteria;Holophagales; Unclassified;sf_1;734	0.01	0.57	0.01	0.54	0.02	-0.53	0.01	0.57		
Bacteria;Acidobacteria;Acidobacteria-4;Ellin6075/11-25; Unclassified;sf_1;435					0.01	-0.57	0.00	0.62		
Bacteria;Acidobacteria;Acidobacteria-4;Unclassified; Unclassified;sf_1;6455			0.04	-0.47						
Bacteria;Acidobacteria;Acidobacteria-4;Unclassified; Unclassified;sf_1;654			0.02	-0.53						
Bacteria;Acidobacteria;Acidobacteria-5;Unclassified; Unclassified;sf_1;523	0.02	0.53	0.01	0.60	0.02	-0.53	0.01	0.57		
Bacteria;Acidobacteria;Acidobacteria-6;Unclassified; Unclassified;sf_1;102			0.02	-0.53	0.03	0.49				
Bacteria;Acidobacteria;Acidobacteria-6;Unclassified; Unclassified;sf_1;517	0.05	-0.44	0.01	-0.54	0.03	0.50				
Bacteria;Acidobacteria;Acidobacteria-6;Unclassified; Unclassified;sf_1;990										
Bacteria;Acidobacteria;Acidobacteria-7;Unclassified; Unclassified;sf_1;588	0.02	0.52	0.01	0.59	0.00	-0.60	0.01	0.57		
Bacteria;Acidobacteria;Acidobacteria-9;Unclassified; Unclassified;sf_1;704			0.04	0.47	0.01	-0.54	0.01	0.59		
Bacteria;Acidobacteria;Solibacteres;Unclassified; Unclassified;sf_1;6386			0.02	-0.50	0.00	0.62	0.01	-0.58		
Bacteria;Acidobacteria;Unclassified;Unclassified; Unclassified;sf_1;572			0.03	0.48	0.02	-0.51	0.02	0.51		
Bacteria;Actinobacteria;Actinobacteria;Acidimicrobiales; Acidimicrobiaceae;sf_1;1478	0.04	-0.46	0.00	-0.61	0.00	0.64	0.00	-0.63		

	SM		NH4		EOC		pH		Mg	
Gene	**P**	**r**	**P**	**r**	**P**	**r**	**P**	**r**	**P**	**r**
Bacteria;Actinobacteria;Actinobacteria;Acidimicrobiales;Acidimicrobiaceae;sf_1;1532			0.01	-0.54	0.01	0.54	0.04	-0.48		
Bacteria;Actinobacteria;Actinobacteria;Acidimicrobiales; Unclassified;sf_1;1217	0.05	0.45	0.02	0.51	0.02	-0.51	0.03	0.50		
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales; Acidothermaceae;sf_1;1399	0.05	0.44	0.03	0.48	0.01	-0.54	0.01	0.55		
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales; Actinomycetaceae;sf_1;1684	0.05	0.44			0.01	-0.54			0.01	-0.57
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales; Actinosynnemataceae;sf_1;1951			0.05	-0.45	0.05	0.45	0.01	-0.56		
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales; Actinosynnemataceae;sf_1;1984			0.04	-0.46	0.03	0.48	0.02	-0.52		
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales; Brevibacteriaceae;sf_1;1745	0.04	-0.47	0.04	-0.47	0.04	0.47	0.04	-0.48		
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales; Cellulomonadaceae;sf_1;1592			0.03	-0.47	0.01	0.54	0.02	-0.52		
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales; Cellulomonadaceae;sf_1;2061			0.05	-0.45						
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales; Corynebacteriaceae;sf_1;1374	0.03	-0.50	0.02	-0.51	0.02	0.52	0.01	-0.57		
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales; Dermatophilaceae;sf_1;1216	0.03	-0.48	0.01	-0.56	0.02	0.53	0.01	-0.58		
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales; Dietziaceae;sf_1;1143			0.02	-0.53	0.02	0.51	0.02	-0.53		
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales; Frankiaceae;sf_1;1286									0.01	-0.58
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales; Geodermatophilaceae;sf_1;1245			0.03	-0.47	0.03	0.49	0.03	-0.49		
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales; Geodermatophilaceae;sf_1;1973			0.03	-0.47	0.02	0.51	0.02	-0.54		
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales; Gordoniaceae;sf_1;1209			0.03	-0.48	0.02	0.51	0.02	-0.53		
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales; Intrasporangiaceae;sf_1;1935					0.03	0.48	0.04	-0.47		
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales; Kineosporiaceae;sf_1;2015			0.02	-0.53	0.02	0.51	0.02	-0.53		
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales; Microbacteriaceae;sf_1;1098							0.04	-0.47		
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales; Microbacteriaceae;sf_1;1451	0.04	-0.46	0.03	-0.48	0.00	0.72	0.00	-0.71		
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales; Microbacteriaceae;sf_1;1513			0.03	-0.49	0.01	0.58	0.01	-0.56		
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales; Microbacteriaceae;sf_1;1548			0.04	-0.46						
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales; Microbacteriaceae;sf_1;1549										

	SM		NH4		EOC		pH		Mg	
Gene	**P**	**r**	**P**	**r**	**P**	**r**	**P**	**r**	**P**	**r**
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales; Microbacteriaceae;sf_1;1550										
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales; Microbacteriaceae;sf_1;1640			0.05	-0.45	0.03	0.48	0.04	-0.48		
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales; Microbacteriaceae;sf_1;1705										
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales; Micrococcaceae;sf_1;1452			0.03	-0.50	0.04	0.47	0.03	-0.50		
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales; Micromonosporaceae;sf_1;1316			0.05	-0.45						
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales; Micromonosporaceae;sf_1;1395	0.01	-0.54	0.04	-0.47	0.02	0.50	0.01	-0.61		
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales; Micromonosporaceae;sf_1;1462			0.03	-0.48	0.04	0.47	0.04	-0.48		
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales; Micromonosporaceae;sf_1;1572			0.02	-0.53	0.05	0.45	0.04	-0.47		
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales; Micromonosporaceae;sf_1;1821			0.05	-0.45	0.04	0.46	0.05	-0.45		
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales; Micromonosporaceae;sf_1;1847					0.02	0.51	0.01	-0.56		
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales; Mycobacteriaceae;sf_1;1175	0.05	-0.44	0.05	-0.44	0.01	0.58	0.01	-0.58		
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales; Nocardiaceae;sf_1;1142	0.03	-0.49			0.04	0.46				
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales; Nocardiaceae;sf_1;1861			0.02	-0.53	0.03	0.48	0.02	-0.52		
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales; Nocardiaceae;sf_1;1999			0.05	-0.45						
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales; Nocardioidaceae;sf_1;1854	0.03	-0.48	0.05	-0.44	0.04	0.46	0.04	-0.48		
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales; Promicromonosporaceae;sf_1;1671	0.04	-0.46			0.04	0.47				
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales; Pseudonocardiaceae;sf_1;1863					0.01	0.60	0.01	-0.61		
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales; Sporichthyaceae;sf_1;1701			0.03	-0.48	0.04	0.45	0.05	-0.46		
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales; Streptomycetaceae;sf_1;1128			0.05	-0.44	0.07	0.42	0.04	-0.48		
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales; Unclassified;sf_3;1114			0.03	-0.48	0.00	0.62	0.00	-0.68		
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales; Unclassified;sf_3;1252			0.03	-0.49	0.01	0.55	0.01	-0.55		
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales; Unclassified;sf_3;1369			0.03	-0.50	0.02	0.51	0.03	-0.49		
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales; Unclassified;sf_3;1410			0.03	-0.48	0.01	0.54	0.01	-0.56		

	SM		NH4		EOC		pH		Mg	
Gene	P	r	P	r	P	r	P	r	P	r
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Unclassified;sf_3;1514			0.03	-0.49	0.02	0.52	0.01	-0.60		
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Unclassified;sf_3;1806			0.04	-0.47	0.05	0.45				
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Unclassified;sf_4;1337	0.04	0.47	0.02	0.51	0.01	-0.55	0.01	0.56		
Bacteria;Actinobacteria;Actinobacteria;Bifidobacteriales;Bifidobacteriaceae;sf_1;1444	0.03	0.49	0.00	0.66	0.00	-0.67	0.00	0.65		
Bacteria;Actinobacteria;Actinobacteria;Coriobacteriales;Coriobacteriaceae;sf_1;1800	0.02	0.51	0.04	0.46	0.00	-0.62	0.01	0.59		
Bacteria;Actinobacteria;Actinobacteria;Rubrobacterales;Rubrobacteraceae;sf_1;1210			0.02	-0.53	0.02	0.50	0.02	-0.55		
Bacteria;Actinobacteria;Actinobacteria;Rubrobacterales;Rubrobacteraceae;sf_1;1480			0.02	-0.53	0.01	0.57	0.01	-0.59		
Bacteria;Actinobacteria;Actinobacteria;Rubrobacterales;Rubrobacteraceae;sf_1;1536			0.03	-0.47	0.03	0.48	0.04	-0.48		
Bacteria;Actinobacteria;Actinobacteria;Rubrobacterales;Rubrobacteraceae;sf_1;1539			0.02	-0.52	0.01	0.54	0.03	-0.51		
Bacteria;Actinobacteria;Actinobacteria;Unclassified;Unclassified;sf_1;1118			0.04	-0.45	0.03	0.49				
Bacteria;Actinobacteria;Actinobacteria;Unclassified;Unclassified;sf_1;1283			0.03	-0.49	0.04	0.46				
Bacteria;Actinobacteria;Actinobacteria;Unclassified;Unclassified;sf_1;1588			0.04	-0.46	0.02	0.52	0.03	-0.50		
Bacteria;Actinobacteria;Actinobacteria;Unclassified;Unclassified;sf_1;1848			0.02	-0.52	0.05	0.44				
Bacteria;Actinobacteria;BD2-10 group;Unclassified;Unclassified;sf_1;1732					0.00	-0.68	0.00	0.69		
Bacteria;Actinobacteria;BD2-10 group;Unclassified;Unclassified;sf_2;1652			0.01	0.56	0.02	-0.52	0.00	0.67		
Bacteria;Bacteroidetes;Bacteroidetes;Bacteroidales;Porphyromonadaceae;sf_1;5454			0.02	0.52	0.01	-0.54	0.02	0.53		
Bacteria;Bacteroidetes;Bacteroidetes;Bacteroidales;Prevotellaceae;sf_1;5946			0.01	-0.54	0.04	0.47	0.05	-0.46		
Bacteria;Bacteroidetes;Bacteroidetes;Bacteroidales;Rikenellaceae;sf_5;5892							0.04	0.48		
Bacteria;Bacteroidetes;Bacteroidetes;Bacteroidales;Unclassified;sf_15;5874	0.02	0.50	0.04	0.45						
Bacteria;Bacteroidetes;Flavobacteria;Flavobacteriales;Blattabacteriaceae;sf_1;5828	0.02	0.51	0.02	0.53	0.00	-0.61	0.02	0.53		
Bacteria;Bacteroidetes;Flavobacteria;Flavobacteriales;Cryomorphaceae;sf_1;5400	0.03	-0.49			0.03	0.48	0.01	-0.58		
Bacteria;Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae;sf_1;5918			0.00	-0.61	0.02	0.52	0.03	-0.51		
Bacteria;Bacteroidetes;KSA1;Unclassified;Unclassified;sf_1;5951	0.03	0.47	0.03	0.48	0.01	-0.59	0.02	0.54		

	SM		NH4		EOC		pH		Mg	
Gene	**P**	**r**	**P**	**r**	**P**	**r**	**P**	**r**	**P**	**r**
Bacteria;Bacteroidetes;Sphingobacteria;Sphingobacteriales; Crenotrichaceae;sf_11;5266	0.01	-0.54	0.04	-0.46						
Bacteria;Bacteroidetes;Sphingobacteria;Sphingobacteriales; Crenotrichaceae;sf_11;5283	0.04	-0.47	0.02	-0.53			0.05	-0.45		
Bacteria;Bacteroidetes;Sphingobacteria;Sphingobacteriales; Crenotrichaceae;sf_11;5288	0.03	-0.49			0.02	0.50	0.04	-0.48		
Bacteria;Bacteroidetes;Sphingobacteria;Sphingobacteriales; Crenotrichaceae;sf_11;5449	0.02	-0.52	0.01	-0.54	0.02	0.53	0.01	-0.58		
Bacteria;Bacteroidetes;Sphingobacteria;Sphingobacteriales; Crenotrichaceae;sf_11;5491	0.02	-0.51	0.05	-0.44			0.04	-0.47		
Bacteria;Bacteroidetes;Sphingobacteria;Sphingobacteriales; Crenotrichaceae;sf_11;5581									0.04	0.48
Bacteria;Bacteroidetes;Sphingobacteria;Sphingobacteriales; Crenotrichaceae;sf_11;5872	0.01	-0.55			0.00	0.67	0.00	-0.63		
Bacteria;Bacteroidetes;Sphingobacteria;Sphingobacteriales; Crenotrichaceae;sf_11;5925					0.01	0.56	0.04	-0.48	0.04	0.48
Bacteria;Bacteroidetes;Sphingobacteria;Sphingobacteriales; Crenotrichaceae;sf_11;5948	0.01	-0.56	0.02	-0.51	0.01	0.55	0.01	-0.57		
Bacteria;Bacteroidetes;Sphingobacteria;Sphingobacteriales; Crenotrichaceae;sf_11;5987			0.04	-0.47						
Bacteria;Bacteroidetes;Sphingobacteria;Sphingobacteriales; Crenotrichaceae;sf_11;6003	0.02	-0.50	0.03	-0.49						
Bacteria;Bacteroidetes;Sphingobacteria;Sphingobacteriales; Crenotrichaceae;sf_11;6148	0.01	-0.58					0.03	-0.49		
Bacteria;Bacteroidetes;Sphingobacteria;Sphingobacteriales; Crenotrichaceae;sf_11;6167					0.02	0.53	0.03	-0.50		
Bacteria;Bacteroidetes;Sphingobacteria;Sphingobacteriales; Crenotrichaceae;sf_11;6196	0.04	-0.47	0.01	-0.57	0.01	0.58	0.00	-0.64		
Bacteria;Bacteroidetes;Sphingobacteria;Sphingobacteriales; Crenotrichaceae;sf_11;6281	0.03	-0.47					0.05	-0.45		
Bacteria;Bacteroidetes;Sphingobacteria;Sphingobacteriales; Flexibacteraceae;sf_10;5253					0.02	-0.51	0.03	0.50		
Bacteria;Bacteroidetes;Sphingobacteria;Sphingobacteriales; Flexibacteraceae;sf_19;5805			0.04	-0.47						
Bacteria;Bacteroidetes;Sphingobacteria;Sphingobacteriales; Flexibacteraceae;sf_20;10311	0.02	0.52	0.05	0.44	0.03	-0.49	0.05	0.45		
Bacteria;Bacteroidetes;Sphingobacteria;Sphingobacteriales; Sphingobacteriaceae;sf_1;5614	0.00	-0.60			0.01	0.55	0.01	-0.59		
Bacteria;Bacteroidetes;Sphingobacteria;Sphingobacteriales; Sphingobacteriaceae;sf_1;5840	0.01	-0.55			0.00	0.64	0.00	-0.70		
Bacteria;Bacteroidetes;Sphingobacteria;Sphingobacteriales; Sphingobacteriaceae;sf_1;6273	0.02	-0.53			0.03	0.48	0.01	-0.55		
Bacteria;Bacteroidetes;Sphingobacteria;Sphingobacteriales; Unclassified;sf_6;5439	0.03	0.49	0.02	0.52	0.01	-0.58	0.01	0.58		
Bacteria;Bacteroidetes;Unclassified;Unclassified;Unclassified;sf_4;5785	0.02	0.51	0.02	0.50	0.01	-0.58	0.01	0.55		

	SM		NH4		EOC		pH		Mg	
Gene	**P**	**r**	**P**	**r**	**P**	**r**	**P**	**r**	**P**	**r**
Bacteria;BRC1;Unclassified;Unclassified;Unclassified;sf_1;5051	0.04	0.47	0.03	0.48	0.02	-0.52	0.01	0.57		
Bacteria;BRC1;Unclassified;Unclassified;Unclassified;sf_2;118	0.02	0.51	0.01	0.56	0.01	-0.57	0.01	0.58		
Bacteria;Caldithrix;Unclassified;Caldithrales;Caldithraceae;sf_1;2384					0.02	-0.52	0.02	0.52		
Bacteria;Chlamydiae;Chlamydiae;Chlamydiales;Chlamydiaceae;sf_1;4820	0.03	0.50	0.02	0.50	0.01	-0.58	0.02	0.54		
Bacteria;Chlamydiae;Chlamydiae;Chlamydiales;Parachlamydiaceae;sf_1;4964			0.01	0.59	0.00	-0.62	0.00	0.67		
Bacteria;Chlamydiae;Chlamydiae;Chlamydiales;Simkaniaceae;sf_1;4702	0.01	0.54	0.01	0.59	0.02	-0.52				
Bacteria;Chlorobi;Unclassified;Unclassified;Unclassified;sf_1;5928										
Bacteria;Chlorobi;Unclassified;Unclassified;Unclassified;sf_6;5294	0.05	0.44			0.02	-0.53				
Bacteria;Chlorobi;Unclassified;Unclassified;Unclassified;sf_8;549	0.01	0.56								
Bacteria;Chlorobi;Unclassified;Unclassified;Unclassified;sf_9;6146			0.02	0.52	0.02	-0.50	0.02	0.54		
Bacteria;Chloroflexi;Anaerolineae;Chloroflexi-1a;Unclassified;sf_1;258	0.01	0.54	0.05	0.44						
Bacteria;Chloroflexi;Anaerolineae;Unclassified;Unclassified;sf_1;266	0.03	0.48			0.04	-0.46				
Bacteria;Chloroflexi;Chloroflexi-4;Unclassified;Unclassified;sf_2;2532					0.03	-0.50	0.01	0.59		
Bacteria;Chloroflexi;Dehalococcoidetes;Unclassified;Unclassified;sf_1;2497	0.02	0.52	0.02	0.50	0.01	-0.59	0.01	0.58		
Bacteria;Chloroflexi;Thermomicrobia;Unclassified;Unclassified;sf_1;1041	0.00	-0.61	0.01	-0.58						
Bacteria;Chloroflexi;Thermomicrobia;Unclassified;Unclassified;sf_2;652					0.04	-0.46				
Bacteria;Chloroflexi;Unclassified;Unclassified;Unclassified;sf_1;2534			0.03	0.48	0.01	-0.57	0.00	0.66		
Bacteria;Chloroflexi;Unclassified;Unclassified;Unclassified;sf_2;818	0.02	0.50	0.01	0.57	0.00	-0.66	0.01	0.58		
Bacteria;Chloroflexi;Unclassified;Unclassified;Unclassified;sf_5;1051					0.03	-0.48			0.02	-0.52
Bacteria;Chloroflexi;Unclassified;Unclassified;Unclassified;sf_7;757	0.05	0.45								
Bacteria;Coprothermobacteria;Unclassified;Unclassified;Unclassified;sf_1;751	0.04	0.46	0.03	0.48	0.00	-0.61	0.01	0.60		
Bacteria;Cyanobacteria;Cyanobacteria;Chloroplasts;Chloroplasts;sf_11;5123	0.03	0.49	0.04	0.47	0.01	-0.59	0.02	0.55		
Bacteria;Cyanobacteria;Cyanobacteria;Chloroplasts;Chloroplasts;sf_5;5147			0.01	0.59	0.03	-0.48	0.00	0.62		
Bacteria;Cyanobacteria;Cyanobacteria;Geitlerinema;Unclassified;sf_1;4999			0.01	-0.58			0.02	-0.54		
Bacteria;Cyanobacteria;Cyanobacteria;Oscillatoriales;Unclassified;sf_1;5159			0.03	-0.48	0.01	0.57	0.01	-0.59		
Bacteria;Cyanobacteria;Cyanobacteria;Pseudanabaena;Unclassified;sf_1;5008	0.04	-0.46	0.01	-0.56	0.04	0.47	0.01	-0.61		
Bacteria;Cyanobacteria;Unclassified;Unclassified;Unclassified;sf_6;5186			0.01	-0.59	0.02	0.52	0.01	-0.58		
Bacteria;Cyanobacteria;Unclassified;Unclassified;Unclassified;sf_8;5206	0.00	-0.62	0.02	-0.53	0.01	0.56	0.00	-0.70		
Bacteria;Deinococcus-Thermus;Unclassified;Unclassified;Unclassified;sf_1;563	0.04	0.47	0.02	0.52	0.00	-0.62	0.00	0.65		
Bacteria;Deinococcus-Thermus;Unclassified;Unclassified;Unclassified;sf_2;637			0.02	-0.53						
Bacteria;Deinococcus-Thermus;Unclassified;Unclassified;Unclassified;sf_3;920	0.02	0.50	0.02	0.52	0.01	-0.55	0.00	0.63		
Bacteria;DSS1;Unclassified;Unclassified;Unclassified;sf_1;4405	0.01	0.58	0.03	0.49	0.02	-0.50	0.02	0.53		

	SM		NH4		EOC		pH		Mg	
Gene	**P**	**r**	**P**	**r**	**P**	**r**	**P**	**r**	**P**	**r**
Bacteria;Firmicutes;Bacilli;Bacillales;Alicyclobacillaceae;sf_1;3368	0.01	-0.56	0.04	-0.47						
Bacteria;Firmicutes;Bacilli;Bacillales;Bacillaceae;sf_1;3370									0.05	0.46
Bacteria;Firmicutes;Bacilli;Bacillales;Bacillaceae;sf_1;3506									0.02	0.52
Bacteria;Firmicutes;Bacilli;Bacillales;Bacillaceae;sf_1;3650	0.05	0.44	0.01	0.59	0.00	-0.64	0.01	0.59		
Bacteria;Firmicutes;Bacilli;Bacillales;Bacillaceae;sf_1;3656					0.04	0.45				
Bacteria;Firmicutes;Bacilli;Bacillales;Bacillaceae;sf_1;3689									0.05	0.45
Bacteria;Firmicutes;Bacilli;Bacillales;Bacillaceae;sf_1;3893					0.05	0.44				
Bacteria;Firmicutes;Bacilli;Bacillales;Bacillaceae;sf_1;3895										
Bacteria;Firmicutes;Bacilli;Bacillales;Bacillaceae;sf_1;3898										
Bacteria;Firmicutes;Bacilli;Bacillales;Bacillaceae;sf_1;3926	0.04	-0.47								
Bacteria;Firmicutes;Bacilli;Bacillales;Paenibacillaceae;sf_1;3247			0.05	-0.44					0.05	0.45
Bacteria;Firmicutes;Bacilli;Bacillales;Paenibacillaceae;sf_1;3567	0.05	-0.44	0.02	-0.53	0.03	0.49	0.05	-0.46		
Bacteria;Firmicutes;Bacilli;Bacillales;Paenibacillaceae;sf_1;3711									0.03	0.49
Bacteria;Firmicutes;Bacilli;Bacillales;Paenibacillaceae;sf_1;3793			0.03	-0.48						
Bacteria;Firmicutes;Bacilli;Bacillales;Sporolactobacillaceae;sf_1;3502									0.05	0.45
Bacteria;Firmicutes;Bacilli;Bacillales;Staphylococcaceae;sf_1;3638									0.02	0.55
Bacteria;Firmicutes;Bacilli;Bacillales;Unclassified;sf_3;3743	0.05	0.44	0.03	0.49	0.02	-0.51	0.03	0.51		
Bacteria;Firmicutes;Bacilli;Lactobacillales;Aerococcaceae;sf_1;3553									0.01	0.57
Bacteria;Firmicutes;Bacilli;Lactobacillales;Aerococcaceae;sf_1;3866									0.00	0.64
Bacteria;Firmicutes;Bacilli;Lactobacillales;Carnobacteriaceae;sf_1;3536			0.03	0.49	0.03	-0.49	0.01	0.61		
Bacteria;Firmicutes;Bacilli;Lactobacillales;Lactobacillaceae;sf_1;3600			0.02	-0.53	0.02	0.50	0.03	-0.51		
Bacteria;Firmicutes;Bacilli;Lactobacillales;Lactobacillaceae;sf_1;3874			0.05	-0.44						
Bacteria;Firmicutes;Bacilli;Lactobacillales;Leuconostocaceae;sf_1;3497	0.05	0.44	0.00	0.60	0.04	-0.47	0.03	0.51		
Bacteria;Firmicutes;Bacilli;Lactobacillales;Unclassified;sf_1;3434	0.03	-0.48	0.01	-0.54	0.04	0.46	0.03	-0.50		
Bacteria;Firmicutes;Catabacter;Unclassified;Unclassified;sf_1;4293	0.04	0.46	0.01	0.55	0.03	-0.48	0.02	0.54		
Bacteria;Firmicutes;Catabacter;Unclassified;Unclassified;sf_4;2716	0.03	0.48	0.04	0.46			0.05	0.46		
Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiaceae;sf_12;4359	0.05	0.45			0.01	-0.58	0.02	0.52		
Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiaceae;sf_21;4471					0.03	-0.48				
Bacteria;Firmicutes;Clostridia;Clostridiales;Eubacteriaceae;sf_1;28	0.03	-0.49	0.02	-0.52						
Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;sf_5;2708			0.02	-0.51	0.01	0.58	0.02	-0.54		
Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;sf_5;2747			0.01	-0.56	0.01	0.54	0.01	-0.55		
Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;sf_5;3007			0.00	-0.61	0.01	0.54	0.00	-0.63		

	SM		**NH4**		**EOC**		**pH**		**Mg**	
Gene	**P**	**r**	**P**	**r**	**P**	**r**	**P**	**r**	**P**	**r**
Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;sf_5;3107			0.02	-0.52	0.01	0.57	0.01	-0.58		
Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;sf_5;4164			0.05	-0.44			0.05	-0.46		
Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;sf_5;4316			0.01	-0.54	0.03	0.48	0.05	-0.45		
Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;sf_5;4474			0.03	-0.48	0.01	0.56	0.01	-0.58		
Bacteria;Firmicutes;Clostridia;Clostridiales;Peptococc/Acidaminococc;sf_11;903	0.02	-0.52	0.01	-0.60	0.00	0.74	0.00	-0.73		
Bacteria;Firmicutes;Clostridia;Clostridiales;Syntrophomonadaceae;sf_5;2456	0.03	0.49	0.02	0.51	0.03	-0.49	0.03	0.51		
Bacteria;Firmicutes;Clostridia;Unclassified;Unclassified;sf_3;4280	0.03	0.49	0.02	0.51	0.01	-0.58	0.01	0.60		
Bacteria;Firmicutes;Clostridia;Unclassified;Unclassified;sf_4;2398					0.02	-0.51	0.00	0.62		
Bacteria;Firmicutes;Desulfotomaculum;Unclassified;Unclassified;sf_1;894			0.04	-0.46						
Bacteria;Firmicutes;Mollicutes;Acholeplasmatales;Acholeplasmataceae;sf_1;4044	0.01	0.57			0.02	-0.51				
Bacteria;Firmicutes;Mollicutes;Mycoplasmatales;Mycoplasmataceae;sf_1;3929	0.01	0.57	0.03	0.48	0.01	-0.57	0.03	0.50		
Bacteria;Fusobacteria;Fusobacteria;Fusobacterales;Fusobacteriaceae;sf_3;558	0.04	0.47	0.01	0.56	0.02	-0.53	0.02	0.54		
Bacteria;LD1PA group;Unclassified;Unclassified;Unclassified;sf_1;10118			0.04	0.46	0.01	-0.56	0.01	0.61		
Bacteria;marine group A;mgA-1;Unclassified;Unclassified;sf_1;6454	0.02	-0.51	0.01	-0.58	0.01	0.57	0.05	-0.46		
Bacteria;marine group A;mgA-2;Unclassified;Unclassified;sf_1;6344			0.01	0.60	0.01	-0.55	0.01	0.59		
Bacteria;Natronoanaerobium;Unclassified;Unclassified;Unclassified;sf_1;2437	0.01	0.54	0.02	0.52	0.01	-0.59	0.01	0.60		
Bacteria;NC10;NC10-1;Unclassified;Unclassified;sf_1;452	0.05	0.44	0.05	0.44			0.03	0.51		
Bacteria;Nitrospira;Nitrospira;Nitrospirales;Nitrospiraceae;sf_1;984	0.02	0.53								
Bacteria;Nitrospira;Nitrospira;Nitrospirales;Nitrospiraceae;sf_2;542	0.04	0.46	0.01	0.58	0.02	-0.53	0.02	0.52		
Bacteria;Nitrospira;Nitrospira;Nitrospirales;Nitrospiraceae;sf_3;240			0.01	-0.57			0.02	-0.54		
Bacteria;OD1;OP11-5;Unclassified;Unclassified;sf_1;515			0.00	-0.63	0.00	0.69	0.00	-0.67		
Bacteria;OP10;Unclassified;Unclassified;Unclassified;sf_1;8413			0.03	0.49						
Bacteria;OP10;Unclassified;Unclassified;Unclassified;sf_4;484			0.04	0.47						
Bacteria;OP10;Unclassified;Unclassified;Unclassified;sf_5;9782			0.04	0.46	0.00	-0.62	0.00	0.69		
Bacteria;OP3;Unclassified;Unclassified;Unclassified;sf_2;349							0.01	0.57		
Bacteria;OP3;Unclassified;Unclassified;Unclassified;sf_4;628	0.04	0.47	0.02	0.51	0.00	-0.65	0.01	0.59		
Bacteria;OP8;Unclassified;Unclassified;Unclassified;sf_3;598			0.05	0.44	0.00	-0.64	0.01	0.56		
Bacteria;OP9/JS1;JS1;Unclassified;Unclassified;sf_1;2489	0.02	0.53	0.02	0.50	0.00	-0.61	0.01	0.60		
Bacteria;OP9/JS1;OP9;Unclassified;Unclassified;sf_1;726	0.02	0.52	0.05	0.44	0.00	-0.65	0.01	0.61		
Bacteria;Planctomycetes;Planctomycetacia;Planctomycetales; Anammoxales;sf_2;4683	0.05	0.44	0.02	0.51	0.00	-0.62	0.00	0.62		
Bacteria;Planctomycetes;Planctomycetacia;Planctomycetales; Anammoxales;sf_4;4694	0.04	0.45	0.04	0.47	0.02	-0.51	0.03	0.49		
Bacteria;Planctomycetes;Planctomycetacia;Planctomycetales;	0.04	-0.45	0.02	-0.53	0.01	0.58	0.01	-0.56		

	SM		NH4		EOC		pH		Mg	
Gene	P	r	P	r	P	r	P	r	P	r
Gemmatae;sf_1;4843										
Bacteria;Planctomycetes;Planctomycetacia;Planctomycetales; Gemmatae;sf_1;4852	0.04	-0.47	0.02	-0.53	0.00	0.61	0.00	-0.62		
Bacteria;Planctomycetes;Planctomycetacia;Planctomycetales; Gemmatae;sf_1;4857	0.04	-0.45	0.02	-0.50	0.01	0.54	0.02	-0.54		
Bacteria;Planctomycetes;Planctomycetacia;Planctomycetales; emmatae;sf_1;4866	0.03	-0.49	0.02	-0.52	0.00	0.61	0.01	-0.59		
Bacteria;Planctomycetes;Planctomycetacia;Planctomycetales; Gemmatae;sf_1;4925	0.03	-0.48	0.02	-0.51	0.02	0.53	0.02	-0.53		
Bacteria;Planctomycetes;Planctomycetacia;Planctomycetales; Isosphaerae;sf_1;4846	0.03	-0.49	0.03	-0.50	0.01	0.57	0.02	-0.52		
Bacteria;Planctomycetes;Planctomycetacia;Planctomycetales; Pirellulae;sf_3;4687			0.01	-0.55	0.02	0.53	0.02	-0.53		
Bacteria;Planctomycetes;Planctomycetacia;Planctomycetales; Pirellulae;sf_3;4726			0.02	-0.51	0.01	0.57	0.01	-0.57		
Bacteria;Planctomycetes;Planctomycetacia;Planctomycetales; Pirellulae;sf_3;4744	0.05	-0.45	0.02	-0.52	0.04	0.47				
Bacteria;Planctomycetes;Planctomycetacia;Planctomycetales; Pirellulae;sf_3;4782					0.00	0.63	0.01	-0.58		
Bacteria;Planctomycetes;Planctomycetacia;Planctomycetales; Pirellulae;sf_3;4894			0.03	-0.50	0.02	0.52	0.02	-0.54		
Bacteria;Planctomycetes;Planctomycetacia;Planctomycetales; Planctomycetaceae;sf_3;4948			0.04	0.47			0.03	0.50		
Bacteria;Planctomycetes;Planctomycetacia;Planctomycetales; Unclassified;sf_6;4655	0.04	-0.47	0.02	-0.51	0.01	0.55	0.02	-0.51		
Bacteria;Planctomycetes;Planctomycetacia;Planctomycetales; Unclassified;sf_6;4661	0.04	-0.47	0.02	-0.53	0.01	0.56	0.01	-0.58		
Bacteria;Planctomycetes;Planctomycetacia;Planctomycetales; Unclassified;sf_6;4785	0.05	-0.44	0.04	-0.47	0.02	0.53	0.02	-0.52		
Bacteria;Planctomycetes;Planctomycetacia;Planctomycetales; Unclassified;sf_6;4871	0.04	-0.47	0.02	-0.51	0.02	0.53	0.03	-0.49		
Bacteria;Planctomycetes;Planctomycetacia;Planctomycetales; Unclassified;sf_6;4932	0.05	-0.44	0.02	-0.51	0.01	0.56	0.01	-0.57		
Bacteria;Planctomycetes;Planctomycetacia;WPS-1; Unclassified;sf_1;4897			0.01	-0.54	0.02	0.52	0.02	-0.54		
Bacteria;Proteobacteria;Alphaproteobacteria;Acetobacterales; Acetobacteraceae;sf_1;6841			0.02	-0.53	0.00	0.61	0.01	-0.60		
Bacteria;Proteobacteria;Alphaproteobacteria;Acetobacterales; Acetobacteraceae;sf_1;7080	0.05	-0.45	0.04	-0.46	0.02	0.52	0.01	-0.60		
Bacteria;Proteobacteria;Alphaproteobacteria;Acetobacterales; Acetobacteraceae;sf_1;7408	0.05	-0.45	0.02	-0.52	0.01	0.56	0.00	-0.62		
Bacteria;Proteobacteria;Alphaproteobacteria;Acetobacterales; Acetobacteraceae;sf_1;7414					0.01	0.55	0.01	-0.57		
Bacteria;Proteobacteria;Alphaproteobacteria;Acetobacterales; Acetobacteraceae;sf_1;7565	0.03	-0.49	0.03	-0.48	0.00	0.66	0.00	-0.64		

	SM		NH4		EOC		pH		Mg	
Gene	P	r	P	r	P	r	P	r	P	r
Bacteria;Proteobacteria;Alphaproteobacteria;Acetobacterales; Acetobacteraceae;sf_1;7623			0.03	-0.47	0.02	0.51	0.01	-0.60		
Bacteria;Proteobacteria;Alphaproteobacteria;Acetobacterales; Roseococcaceae;sf_1;7106	0.03	-0.48			0.05	0.44	0.03	-0.49		
Bacteria;Proteobacteria;Alphaproteobacteria;Acetobacterales; Unclassified;sf_1;7475			0.01	-0.57	0.00	0.65	0.01	-0.59		
Bacteria;Proteobacteria;Alphaproteobacteria;Azospirillales; Magnetospirillaceae;sf_1;6922	0.01	-0.57	0.02	-0.53	0.00	0.62	0.00	-0.64		
Bacteria;Proteobacteria;Alphaproteobacteria;Azospirillales; Unclassified;sf_1;6905	0.04	-0.46	0.01	-0.57	0.00	0.64	0.00	-0.66		
Bacteria;Proteobacteria;Alphaproteobacteria;Azospirillales; Unclassified;sf_1;7632					0.00	0.61	0.00	-0.75		
Bacteria;Proteobacteria;Alphaproteobacteria;Bradyrhizobiales; Beijerinck/Rhodoplan/Methylocyst;sf_3;6721			0.05	-0.45	0.02	0.53	0.02	-0.53		
Bacteria;Proteobacteria;Alphaproteobacteria;Bradyrhizobiales; Beijerinck/Rhodoplan/Methylocyst;sf_3;6722					0.03	0.49	0.02	-0.53		
Bacteria;Proteobacteria;Alphaproteobacteria;Bradyrhizobiales; Beijerinck/Rhodoplan/Methylocyst;sf_3;6780	0.05	-0.45	0.02	-0.50	0.01	0.58	0.00	-0.63		
Bacteria;Proteobacteria;Alphaproteobacteria;Bradyrhizobiales; Beijerinck/Rhodoplan/Methylocyst;sf_3;6826			0.03	-0.48	0.01	0.60	0.00	-0.62		
Bacteria;Proteobacteria;Alphaproteobacteria;Bradyrhizobiales; Beijerinck/Rhodoplan/Methylocyst;sf_3;7228			0.02	-0.52	0.01	0.59	0.01	-0.59		
Bacteria;Proteobacteria;Alphaproteobacteria;Bradyrhizobiales; Beijerinck/Rhodoplan/Methylocyst;sf_3;7261	0.04	-0.46	0.05	-0.45	0.00	0.63	0.00	-0.66		
Bacteria;Proteobacteria;Alphaproteobacteria;Bradyrhizobiales; Beijerinck/Rhodoplan/Methylocyst;sf_3;7495	0.03	-0.50	0.04	-0.46	0.01	0.57	0.01	-0.55		
Bacteria;Proteobacteria;Alphaproteobacteria;Bradyrhizobiales; Beijerinck/Rhodoplan/Methylocyst;sf_3;7620			0.04	-0.46	0.02	0.53	0.01	-0.58		
Bacteria;Proteobacteria;Alphaproteobacteria;Bradyrhizobiales; Bradyrhizobiaceae;sf_1;6942	0.05	-0.44	0.05	-0.44	0.02	0.51	0.02	-0.51		
Bacteria;Proteobacteria;Alphaproteobacteria;Bradyrhizobiales; Hyphomicrobiaceae;sf_1;7641	0.02	-0.51	0.02	-0.50	0.01	0.59	0.01	-0.60		
Bacteria;Proteobacteria;Alphaproteobacteria;Bradyrhizobiales; Methylobacteriaceae;sf_1;6782			0.05	-0.45	0.05	0.45	0.02	-0.53		
Bacteria;Proteobacteria;Alphaproteobacteria;Bradyrhizobiales; Methylobacteriaceae;sf_1;7593			0.02	-0.50	0.02	0.53	0.01	-0.55		
Bacteria;Proteobacteria;Alphaproteobacteria;Bradyrhizobiales; Unclassified;sf_1;7255			0.02	-0.53	0.01	0.60	0.01	-0.56		
Bacteria;Proteobacteria;Alphaproteobacteria;Bradyrhizobiales; Unclassified;sf_1;7557			0.03	-0.48	0.01	0.57	0.01	-0.57		
Bacteria;Proteobacteria;Alphaproteobacteria;Bradyrhizobiales; Xanthobacteraceae;sf_1;6855					0.02	0.50	0.02	-0.53		
Bacteria;Proteobacteria;Alphaproteobacteria;Caulobacterales; Caulobacteraceae;sf_1;6929	0.02	-0.50	0.03	-0.49	0.01	0.57	0.01	-0.57		
Bacteria;Proteobacteria;Alphaproteobacteria;Caulobacterales; Caulobacteraceae;sf_1;6930	0.04	-0.47	0.02	-0.52	0.00	0.63	0.00	-0.66		

	SM		NH4		EOC		pH		Mg	
Gene	**P**	**r**	**P**	**r**	**P**	**r**	**P**	**r**	**P**	**r**
Bacteria;Proteobacteria;Alphaproteobacteria;Caulobacterales;Caulobacteraceae;sf_1;6953	0.05	-0.45	0.01	-0.57	0.02	0.53	0.00	-0.63		
Bacteria;Proteobacteria;Alphaproteobacteria;Caulobacterales;Caulobacteraceae;sf_1;7134			0.03	-0.49	0.02	0.51	0.02	-0.51		
Bacteria;Proteobacteria;Alphaproteobacteria;Caulobacterales;Caulobacteraceae;sf_1;7245	0.05	-0.45	0.03	-0.48	0.01	0.59	0.01	-0.60		
Bacteria;Proteobacteria;Alphaproteobacteria;Caulobacterales;Caulobacteraceae;sf_1;7578			0.05	-0.44	0.03	0.48	0.03	-0.49		
Bacteria;Proteobacteria;Alphaproteobacteria;Consistiales;Caedibacteraceae;sf_3;7010	0.02	-0.53	0.04	-0.46						
Bacteria;Proteobacteria;Alphaproteobacteria;Consistiales;SAR11;sf_2;7043			0.02	0.51	0.00	-0.63	0.01	0.57		
Bacteria;Proteobacteria;Alphaproteobacteria;Consistiales;Unclassified;sf_4;7105			0.02	0.52	0.00	-0.63	0.02	0.52		
Bacteria;Proteobacteria;Alphaproteobacteria;Consistiales;Unclassified;sf_5;6735			0.02	0.51	0.00	-0.61	0.03	0.51		
Bacteria;Proteobacteria;Alphaproteobacteria;Ellin314/wr0007;Unclassified;sf_1;7123			0.01	0.56	0.02	-0.53	0.01	0.59		
Bacteria;Proteobacteria;Alphaproteobacteria;Fulvimarina;Unclassified;sf_1;7281	0.04	-0.47			0.00	0.61	0.01	-0.59		
Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Bartonellaceae;sf_1;7384			0.01	0.58	0.00	-0.62	0.01	0.56		
Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Beijerinck/Rhodoplan/Methylocyst;sf_1;7591	0.03	0.48	0.02	0.51	0.00	-0.67	0.02	0.53		
Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Bradyrhizobiaceae;sf_1;6824	0.05	-0.44	0.05	-0.44	0.03	0.49	0.03	-0.50		
Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Hyphomicrobiaceae;sf_1;6787			0.02	-0.53	0.01	0.55	0.01	-0.57		
Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Hyphomicrobiaceae;sf_1;7144			0.05	-0.44			0.04	-0.48		
Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Phyllobacteriaceae;sf_1;7216			0.02	-0.54	0.00	0.61	0.00	-0.69		
Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Rhizobiaceae;sf_1;6813									0.04	0.47
Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Rhizobiaceae;sf_1;6861					0.01	0.54	0.02	-0.52		
Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Unclassified;sf_1;6938	0.03	-0.49	0.05	-0.44	0.01	0.57	0.02	-0.52		
Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;nclassified;sf_1;6969			0.05	-0.45	0.02	0.51	0.01	-0.57		
Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Unclassified;sf_1;7173			0.03	-0.49	0.01	0.58	0.00	-0.64		
Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Hyphomonadaceae;sf_1;7584			0.00	0.65	0.02	-0.53	0.01	0.56		
Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae;sf_1;6682					0.05	0.45				

	SM		NH4		EOC		pH		Mg	
Gene	**P**	**r**	**P**	**r**	**P**	**r**	**P**	**r**	**P**	**r**
Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales; Rhodobacteraceae;sf_1;6743	0.05	-0.45	0.03	-0.49	0.01	0.56	0.01	-0.57		
Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales; Rhodobacteraceae;sf_1;7527			0.04	-0.47	0.03	0.48	0.05	-0.46		
Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales; Unclassified;sf_5;7471	0.04	0.47	0.01	0.58	0.01	-0.59	0.00	0.69		
Bacteria;Proteobacteria;Alphaproteobacteria;Rickettsiales; Anaplasmataceae;sf_3;6648			0.01	0.57	0.01	-0.55	0.00	0.65		
Bacteria;Proteobacteria;Alphaproteobacteria;Rickettsiales; Rickettsiaceae;sf_1;7556	0.02	0.53	0.05	0.45	0.00	-0.64	0.01	0.55		
Bacteria;Proteobacteria;Alphaproteobacteria;Rickettsiales; Unclassified;sf_1;7156			0.05	0.44						
Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales; Sphingomonadaceae;sf_1;6720	0.05	-0.45	0.05	-0.44	0.05	0.45	0.05	-0.46		
Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales; Sphingomonadaceae;sf_1;7011	0.04	-0.46	0.02	-0.51	0.03	0.48	0.03	-0.49		
Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales; Sphingomonadaceae;sf_1;7048					0.03	0.48	0.05	-0.45		
Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales; Sphingomonadaceae;sf_1;7289	0.01	-0.58	0.03	-0.49	0.01	0.58	0.01	-0.61		
Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales; Sphingomonadaceae;sf_1;7411			0.03	-0.49						
Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales; Unclassified;sf_1;6653			0.04	0.46	0.04	-0.46	0.01	0.58		
Bacteria;Proteobacteria;Alphaproteobacteria;Unclassified; nclassified;sf_2;7188	0.04	0.47	0.02	0.51	0.00	-0.62	0.00	0.64		
Bacteria;Proteobacteria;Alphaproteobacteria;Unclassified; Unclassified;sf_6;6703			0.02	-0.50	0.01	0.55	0.03	-0.49		
Bacteria;Proteobacteria;Alphaproteobacteria;Unclassified; Unclassified;sf_6;6844	0.05	-0.44	0.05	-0.44	0.04	0.46	0.02	-0.52		
Bacteria;Proteobacteria;Alphaproteobacteria;Unclassified; Unclassified;sf_6;6845					0.05	0.44				
Bacteria;Proteobacteria;Alphaproteobacteria;Unclassified; Unclassified;sf_6;6970			0.01	-0.54	0.00	0.69	0.00	-0.68		
Bacteria;Proteobacteria;Alphaproteobacteria;Unclassified; nclassified;sf_6;7166	0.01	-0.54								
Bacteria;Proteobacteria;Alphaproteobacteria;Unclassified; Unclassified;sf_6;7207			0.01	0.58	0.00	-0.73	0.00	0.68		
Bacteria;Proteobacteria;Alphaproteobacteria;Unclassified; Unclassified;sf_6;7463			0.02	-0.51	0.01	0.58	0.02	-0.53		
Bacteria;Proteobacteria;Alphaproteobacteria;Unclassified; Unclassified;sf_6;7516	0.04	-0.47	0.00	-0.60	0.01	0.59	0.01	-0.56		
Bacteria;Proteobacteria;Alphaproteobacteria;Unclassified; Unclassified;sf_6;7534			0.03	-0.49	0.04	0.46	0.03	-0.51		
Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales; Alcaligenaceae;sf_1;7932			0.05	0.45	0.05	-0.45	0.04	0.47		

	SM		NH4		EOC		pH		Mg	
Gene	**P**	**r**	**P**	**r**	**P**	**r**	**P**	**r**	**P**	**r**
Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae;sf_1;7934	0.00	-0.62	0.02	-0.52	0.00	0.63	0.01	-0.59		
Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;sf_1;7754	0.05	-0.44	0.02	-0.53	0.02	0.50	0.03	-0.50		
Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;sf_1;7786	0.05	-0.44	0.02	-0.51	0.02	0.51	0.03	-0.51		
Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;sf_1;7820	0.01	-0.54	0.03	-0.49	0.02	0.53	0.04	-0.48		
Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;sf_1;7854			0.01	-0.57	0.02	0.52	0.01	-0.55		
Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;sf_1;7884	0.02	-0.52	0.05	-0.44	0.04	0.46	0.05	-0.46		
Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;sf_1;7905	0.04	-0.46	0.02	-0.50	0.01	0.55	0.03	-0.50		
Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;sf_1;7920	0.03	-0.49					0.04	-0.48		
Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;sf_1;7937									0.04	0.49
Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;sf_1;8075	0.10	-0.38	0.02	-0.52	0.02	0.52	0.01	-0.59		
Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;sf_1;8083	0.03	-0.50	0.04	-0.47	0.01	0.55	0.01	-0.56		
Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;sf_1;8117	0.03	-0.47	0.05	-0.45			0.02	-0.52		
Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Oxalobacteraceae;sf_1;8032	0.04	0.46	0.02	0.51	0.03	-0.50	0.01	0.57		
Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Unclassified;sf_1;7727	0.05	-0.44	0.04	-0.47	0.00	0.69	0.00	-0.67		
Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Unclassified;sf_1;7850			0.01	-0.54	0.05	0.44	0.04	-0.47		
Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Unclassified;sf_1;8038	0.04	-0.46								
Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Unclassified;sf_1;8055	0.02	-0.51	0.05	-0.45	0.02	0.50	0.03	-0.50		
Bacteria;Proteobacteria;Betaproteobacteria;Ellin6095/SC-I-39;Unclassified;sf_1;8093	0.01	-0.57	0.02	-0.52	0.01	0.59	0.05	-0.46		
Bacteria;Proteobacteria;Betaproteobacteria;Ellin6095/SC-I-39;Unclassified;sf_1;8148							0.03	0.51		
Bacteria;Proteobacteria;Betaproteobacteria;Hydrogenophilales;Hydrogenophilaceae;sf_1;7953	0.02	-0.51	0.01	-0.57	0.01	0.55	0.01	-0.56		
Bacteria;Proteobacteria;Betaproteobacteria;Hydrogenophilales;Hydrogenophilaceae;sf_2;8756			0.00	-0.66	0.00	0.75	0.00	-0.70		
Bacteria;Proteobacteria;Betaproteobacteria;Methylophilales;Methylophilaceae;sf_1;8159			0.04	-0.46			0.03	-0.49		
Bacteria;Proteobacteria;Betaproteobacteria;MND1 clone group;Unclassified;sf_1;7896					0.00	0.74	0.00	-0.71	0.02	0.53

	SM		NH4		EOC		pH		Mg	
Gene	**P**	**r**	**P**	**r**	**P**	**r**	**P**	**r**	**P**	**r**
Bacteria;Proteobacteria;Betaproteobacteria;MND1 clone group;Unclassified;sf_1;8134			0.01	-0.55	0.01	0.55	0.01	-0.57		
Bacteria;Proteobacteria;Betaproteobacteria;Neisseriales;Neisseriaceae;sf_1;7867	0.03	-0.49	0.04	-0.47	0.03	0.49	0.05	-0.45		
Bacteria;Proteobacteria;Betaproteobacteria;Neisseriales;Unclassified;sf_1;8037	0.00	-0.65			0.05	0.45				
Bacteria;Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae;sf_1;7666			0.01	-0.54	0.02	0.50	0.03	-0.51		
Bacteria;Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae;sf_1;7668			0.01	-0.59	0.03	0.49	0.01	-0.55		
Bacteria;Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae;sf_1;7692			0.04	-0.47						
Bacteria;Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae;sf_1;7753			0.00	-0.64	0.00	0.64	0.01	-0.58		
Bacteria;Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae;sf_1;7980			0.01	-0.55	0.00	0.61	0.00	-0.63		
Bacteria;Proteobacteria;Betaproteobacteria;Rhodocyclales;Unclassified;sf_3;8109			0.01	-0.56			0.01	-0.57		
Bacteria;Proteobacteria;Betaproteobacteria;Unclassified;Unclassified;sf_3;7679			0.02	-0.50	0.00	0.60	0.02	-0.51		
Bacteria;Proteobacteria;Betaproteobacteria;Unclassified;Unclassified;sf_3;7723	0.03	-0.48	0.02	-0.51	0.02	0.52				
Bacteria;Proteobacteria;Deltaproteobacteria;AMD clone group;Unclassified;sf_1;9945	0.02	0.51	0.01	0.57	0.01	-0.57	0.01	0.56		
Bacteria;Proteobacteria;Deltaproteobacteria;Bdellovibrionales;Bdellovibrionaceae;sf_1;10010	0.02	0.51	0.04	0.47	0.04	-0.47				
Bacteria;Proteobacteria;Deltaproteobacteria;Bdellovibrionales;Bdellovibrionaceae;sf_2;10036	0.05	-0.45	0.01	-0.58			0.03	-0.50		
Bacteria;Proteobacteria;Deltaproteobacteria;Bdellovibrionales;Unclassified;sf_1;7382			0.03	0.49	0.03	-0.47	0.04	0.48		
Bacteria;Proteobacteria;Deltaproteobacteria;dechlorinating clone group;Unclassified;sf_1;9959	0.03	0.49	0.01	0.56	0.01	-0.55	0.01	0.57		
Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfoarculaceae;sf_2;10227	0.02	0.52	0.03	0.49	0.03	-0.49	0.04	0.48		
Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobulbaceae;sf_1;9739	0.02	0.52	0.01	0.56	0.01	-0.56	0.01	0.56		
Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Nitrospinaceae;sf_2;594	0.01	0.54	0.02	0.52	0.02	-0.52	0.04	0.48		
Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Unclassified;sf_3;468			0.02	0.51	0.04	-0.46	0.04	0.47		
Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Unclassified;sf_4;9951	0.02	0.52	0.02	0.51	0.01	-0.60	0.01	0.58		
Bacteria;Proteobacteria;Deltaproteobacteria;Desulfovibrionales;Desulfohalobiaceae;sf_1;9894	0.02	0.53	0.01	0.60	0.01	-0.55	0.02	0.55		
Bacteria;Proteobacteria;Deltaproteobacteria;Desulfovibrionales;Desulfomicrobiaceae;sf_1;10079	0.04	0.47	0.03	0.49	0.01	-0.55	0.02	0.52		

Gene	SM		NH4		EOC		pH		Mg	
	P	r	P	r	P	r	P	r	P	r
Bacteria;Proteobacteria;Deltaproteobacteria;Desulfovibrionales;Desulfovibrionaceae;sf_1;10212			0.03	-0.49	0.02	0.50	0.02	-0.54		
Bacteria;Proteobacteria;Deltaproteobacteria;Desulfovibrionales;Unclassified;sf_1;9828									0.04	-0.47
Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Desulfuromonaceae;sf_1;10020	0.03	0.49								
Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;sf_1;10171	0.02	0.52	0.03	0.49	0.05	-0.45	0.05	0.45		
Bacteria;Proteobacteria;Deltaproteobacteria;EB1021 group;Unclassified;sf_4;9741	0.02	0.50			0.03	-0.49	0.03	0.49		
Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Myxococcaceae;sf_1;10313	0.03	-0.48	0.04	-0.47	0.05	0.44				
Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Polyangiaceae;sf_3;10104	0.04	-0.47	0.02	-0.53	0.04	0.45	0.03	-0.50		
Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Unclassified;sf_1;10092	0.02	0.50	0.03	0.48	0.04	-0.47				
Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;sf_3;9665			0.03	0.50	0.01	-0.56	0.00	0.62		
Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;sf_1;9731	0.05	0.44	0.03	0.49	0.04	-0.46	0.04	0.48		
Bacteria;Proteobacteria;Deltaproteobacteria;Unclassified;Unclassified;sf_9;10093			0.02	-0.52	0.00	0.68	0.00	-0.64		
Bacteria;Proteobacteria;Deltaproteobacteria;Unclassified;Unclassified;sf_9;10174			0.03	-0.48	0.03	0.49	0.04	-0.48		
Bacteria;Proteobacteria;Deltaproteobacteria;Unclassified;Unclassified;sf_9;9786	0.03	-0.48	0.01	-0.56	0.01	0.60	0.00	-0.63		
Bacteria;Proteobacteria;Deltaproteobacteria;Unclassified;Unclassified;sf_9;9859			0.01	-0.57	0.02	0.52	0.03	-0.49		
Bacteria;Proteobacteria;Epsilonproteobacteria;Campylobacterales;Helicobacteraceae;sf_23;10443	0.03	0.49	0.01	0.58	0.04	-0.46	0.03	0.50		
Bacteria;Proteobacteria;Epsilonproteobacteria;Campylobacterales;Helicobacteraceae;sf_3;10448	0.01	0.57	0.02	0.53	0.02	-0.52	0.03	0.50		
Bacteria;Proteobacteria;Epsilonproteobacteria;Campylobacterales;Unclassified;sf_1;10384			0.03	-0.49						
Bacteria;Proteobacteria;Gammaproteobacteria;Acidithiobacillales;Acidithiobacillaceae;sf_1;8304			0.02	-0.51	0.00	0.61	0.00	-0.66		
Bacteria;Proteobacteria;Gammaproteobacteria;Acidithiobacillales;Acidithiobacillaceae;sf_1;8951			0.01	-0.59	0.03	0.50	0.01	-0.57		
Bacteria;Proteobacteria;Gammaproteobacteria;Alteromonadales;Alteromonadaceae;sf_1;8768			0.01	-0.56	0.05	0.44	0.02	-0.53		
Bacteria;Proteobacteria;Gammaproteobacteria;Alteromonadales;Pseudoalteromonadaceae;sf_1;9339			0.02	-0.51	0.03	0.47	0.03	-0.49		
Bacteria;Proteobacteria;Gammaproteobacteria;aquatic clone group;Unclassified;sf_1;9246	0.02	0.53	0.03	0.48	0.03	-0.48	0.05	0.45		
Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Ectothiorhodospiraceae;sf_1;8818			0.01	-0.54	0.01	0.58	0.00	-0.62		

	SM		NH4		EOC		pH		Mg	
Gene	**P**	**r**	**P**	**r**	**P**	**r**	**P**	**r**	**P**	**r**
Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Ectothiorhodospiraceae;sf_1;9155			0.01	-0.54	0.01	0.55	0.01	-0.56		
Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Halothiobacillaceae;sf_3;9448									0.03	-0.50
Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Unclassified;sf_1;9316	0.03	-0.49	0.03	-0.49	0.00	0.78	0.00	-0.72		
Bacteria;Proteobacteria;Gammaproteobacteria;Ellin307/WD2124;Unclassified;sf_1;9374	0.02	-0.50	0.01	-0.54	0.00	0.65	0.00	-0.74		
Bacteria;Proteobacteria;Gammaproteobacteria;Enterobacteriales;Enterobacteriaceae;sf_1;8564			0.01	-0.60	0.00	0.72	0.01	-0.61		
Bacteria;Proteobacteria;Gammaproteobacteria;Enterobacteriales;Enterobacteriaceae;sf_1;8864			0.01	-0.57	0.01	0.59	0.01	-0.58		
Bacteria;Proteobacteria;Gammaproteobacteria;Enterobacteriales;Enterobacteriaceae;sf_6;103			0.02	-0.53	0.00	0.67	0.00	-0.68		
Bacteria;Proteobacteria;Gammaproteobacteria;GAO cluster;Unclassified;sf_1;8980					0.05	-0.44				
Bacteria;Proteobacteria;Gammaproteobacteria;Legionellales;Coxiellaceae;sf_3;8378			0.00	-0.62	0.01	0.59	0.01	-0.56		
Bacteria;Proteobacteria;Gammaproteobacteria;Legionellales;Legionellaceae;sf_1;8235	0.04	-0.46	0.01	-0.55						
Bacteria;Proteobacteria;Gammaproteobacteria;Legionellales;Unclassified;sf_1;9418	0.02	0.52	0.01	0.55	0.01	-0.55	0.01	0.55		
Bacteria;Proteobacteria;Gammaproteobacteria;Legionellales;Unclassified;sf_3;8587	0.02	0.52	0.05	0.44	0.02	-0.50	0.04	0.48		
Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;sf_1;9313			0.01	-0.56	0.01	0.57	0.01	-0.59		
Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Unclassified;sf_1;9182	0.00	-0.62	0.02	-0.50	0.01	0.60	0.00	-0.64		
Bacteria;Proteobacteria;Gammaproteobacteria;Oceanospirillales;Halomonadaceae;sf_1;8514	0.02	-0.52	0.01	-0.54	0.00	0.61	0.00	-0.65		
Bacteria;Proteobacteria;Gammaproteobacteria;Oceanospirillales;Oceanospirillaceae;sf_1;9351			0.01	-0.54	0.00	0.71	0.00	-0.84		
Bacteria;Proteobacteria;Gammaproteobacteria;Oceanospirillales;Saccharospirillaceae;sf_1;8889	0.02	-0.52	0.04	-0.47			0.03	-0.51		
Bacteria;Proteobacteria;Gammaproteobacteria;Oceanospirillales;Unclassified;sf_3;8648			0.01	-0.56	0.01	0.59	0.01	-0.60		
Bacteria;Proteobacteria;Gammaproteobacteria;Oceanospirillales;Unclassified;sf_3;8961									0.02	0.53
Bacteria;Proteobacteria;Gammaproteobacteria;Pseudomonadales;Moraxellaceae;sf_3;9466	0.02	0.51	0.03	0.48	0.01	-0.59	0.03	0.50		
Bacteria;Proteobacteria;Gammaproteobacteria;Pseudomonadales;Pseudomonadaceae;sf_1;8288			0.00	-0.61	0.00	0.60	0.02	-0.53		
Bacteria;Proteobacteria;Gammaproteobacteria;Pseudomonadales;Pseudomonadaceae;sf_1;8635			0.00	-0.63	0.00	0.63	0.01	-0.59		
Bacteria;Proteobacteria;Gammaproteobacteria;SUP05;Unclassified;sf_1;8654			0.04	0.45						

	SM		NH4		EOC		pH		Mg	
Gene	**P**	**r**	**P**	**r**	**P**	**r**	**P**	**r**	**P**	**r**
Bacteria;Proteobacteria;Gammaproteobacteria;Thiotrichales;Thiotrichaceae;sf_3;8221			0.02	-0.51	0.00	0.61	0.00	-0.66		
Bacteria;Proteobacteria;Gammaproteobacteria;Unclassified;Unclassified;sf_3;8391							0.05	-0.45		
Bacteria;Proteobacteria;Gammaproteobacteria;Unclassified;Unclassified;sf_3;8566			0.00	-0.63	0.00	0.73	0.00	-0.73		
Bacteria;Proteobacteria;Gammaproteobacteria;Unclassified;Unclassified;sf_3;8759					0.00	0.62	0.00	-0.62		
Bacteria;Proteobacteria;Gammaproteobacteria;Unclassified;Unclassified;sf_3;8883	0.01	-0.57			0.02	0.53	0.00	-0.67		
Bacteria;Proteobacteria;Gammaproteobacteria;Unclassified;Unclassified;sf_3;9040	0.05	-0.45	0.04	-0.46	0.01	0.60	0.01	-0.55		
Bacteria;Proteobacteria;Gammaproteobacteria;Unclassified;Unclassified;sf_3;9269	0.03	-0.48	0.01	-0.55	0.00	0.60	0.00	-0.62		
Bacteria;Proteobacteria;Gammaproteobacteria;Unclassified;Unclassified;sf_3;9581	0.01	-0.55	0.02	-0.51	0.00	0.62	0.01	-0.60		
Bacteria;Proteobacteria;Gammaproteobacteria;uranium waste clones;Unclassified;sf_1;8747			0.03	0.48						
Bacteria;Proteobacteria;Gammaproteobacteria;Xanthomonadales;Xanthomonadaceae;sf_3;8612	0.02	-0.53	0.02	-0.51	0.00	0.71	0.00	-0.75		
Bacteria;Proteobacteria;Gammaproteobacteria;Xanthomonadales;Xanthomonadaceae;sf_3;9150	0.03	-0.48	0.00	-0.61	0.00	0.73	0.00	-0.70		
Bacteria;Proteobacteria;Unclassified;Unclassified;Unclassified;sf_20;6763			0.03	-0.50	0.02	0.52	0.01	-0.61		
Bacteria;Proteobacteria;Unclassified;Unclassified;Unclassified;sf_28;10091	0.05	-0.45	0.02	-0.53	0.02	0.53	0.01	-0.61		
Bacteria;Proteobacteria;Unclassified;Unclassified;Unclassified;sf_8;9558			0.04	0.46	0.01	-0.54	0.00	0.63		
Bacteria;SPAM;Unclassified;Unclassified;Unclassified;sf_1;738	0.02	0.50	0.01	0.55	0.01	-0.54	0.01	0.57		
Bacteria;Spirochaetes;Spirochaetes;Spirochaetales;Leptospiraceae;sf_3;6496	0.03	0.50	0.01	0.58	0.01	-0.58	0.01	0.60		
Bacteria;Spirochaetes;Spirochaetes;Spirochaetales;Serpulinaceae;sf_1;6548			0.01	-0.57	0.03	0.50	0.03	-0.51		
Bacteria;Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;sf_1;6502	0.02	0.51			0.02	-0.50	0.04	0.48		
Bacteria;Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;sf_2;6493	0.02	0.52	0.02	0.51	0.00	-0.61	0.01	0.55		
Bacteria;Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;sf_3;6558	0.02	0.53	0.01	0.59	0.00	-0.61	0.01	0.60		
Bacteria;Synergistes;Unclassified;Unclassified;Unclassified;sf_3;717	0.09	-0.39	0.01	-0.55	0.01	0.56	0.01	-0.60		
Bacteria;Thermodesulfobacteria;Thermodesulfobacteria;Thermodesulfobacteriales;Thermodesulfobacteriaceae;sf_1;667	0.04	0.47	0.00	0.64	0.01	-0.60	0.00	0.67		
Bacteria;Thermotogae;Thermotogae;Thermotogales;Thermotogaceae;sf_4;51	0.01	-0.55	0.02	-0.53	0.02	0.53	0.02	-0.54		
Bacteria;TM6;Unclassified;Unclassified;Unclassified;sf_1;9803					0.02	-0.52	0.03	0.50		
Bacteria;TM7;TM7-1;Unclassified;Unclassified;sf_1;3664			0.01	-0.57	0.00	0.74	0.00	-0.71		
Bacteria;TM7;TM7-1;Unclassified;Unclassified;sf_1;3746	0.04	-0.47	0.01	-0.57	0.00	0.63	0.00	-0.62		
Bacteria;TM7;TM7-2;Unclassified;Unclassified;sf_1;5228			0.00	-0.68	0.01	0.58	0.00	-0.64		

	SM		NH4		EOC		pH		Mg	
Gene	**P**	**r**	**P**	**r**	**P**	**r**	**P**	**r**	**P**	**r**
Bacteria;TM7;TM7-3;Unclassified;Unclassified;sf_1;3081			0.03	-0.48	0.01	0.60	0.01	-0.60		
Bacteria;TM7;Unclassified;Unclassified;Unclassified;sf_1;3255	0.05	-0.44	0.01	-0.56	0.01	0.59	0.00	-0.63		
Bacteria;TM7;Unclassified;Unclassified;Unclassified;sf_1;3464			0.01	-0.59	0.01	0.59	0.00	-0.71		
Bacteria;Unclassified;Unclassified;Unclassified;Unclassified;sf_105;1995			0.05	-0.44	0.00	0.61	0.00	-0.68		
Bacteria;Unclassified;Unclassified;Unclassified;Unclassified;sf_106;243	0.05	0.45			0.04	-0.46	0.03	0.49		
Bacteria;Unclassified;Unclassified;Unclassified;Unclassified;sf_119;316	0.02	-0.50	0.04	-0.46						
Bacteria;Unclassified;Unclassified;Unclassified;Unclassified;sf_119;6449			0.02	-0.51						
Bacteria;Unclassified;Unclassified;Unclassified;Unclassified;sf_119;874			0.02	-0.53	0.02	0.52	0.05	-0.45		
Bacteria;Unclassified;Unclassified;Unclassified;Unclassified;sf_126;296	0.05	-0.44	0.04	-0.45	0.00	0.74	0.00	-0.63		
Bacteria;Unclassified;Unclassified;Unclassified;Unclassified;sf_132;9820	0.02	-0.53	0.01	-0.57	0.00	0.67	0.00	-0.66		
Bacteria;Unclassified;Unclassified;Unclassified;Unclassified;sf_140;6355									0.05	-0.46
Bacteria;Unclassified;Unclassified;Unclassified;Unclassified;sf_148;5062			0.01	-0.59			0.03	-0.49		
Bacteria;Unclassified;Unclassified;Unclassified;Unclassified;sf_156;4291	0.01	0.56	0.02	0.53	0.02	-0.50	0.03	0.50		
Bacteria;Unclassified;Unclassified;Unclassified;Unclassified;sf_160;2363			0.01	-0.56			0.05	-0.45		
Bacteria;Unclassified;Unclassified;Unclassified;Unclassified;sf_160;6380	0.04	-0.46	0.03	-0.49	0.01	0.58	0.01	-0.59		
Bacteria;Unclassified;Unclassified;Unclassified;Unclassified;sf_160;6387			0.02	-0.52	0.03	0.48	0.03	-0.50		
Bacteria;Unclassified;Unclassified;Unclassified;Unclassified;sf_160;6435			0.01	-0.55	0.02	0.51	0.03	-0.51		
Bacteria;Unclassified;Unclassified;Unclassified;Unclassified;sf_34;4668	0.02	0.51	0.05	0.45	0.03	-0.50	0.05	0.45		
Bacteria;Unclassified;Unclassified;Unclassified;Unclassified;sf_93;925	0.03	0.49	0.03	0.50	0.01	-0.57	0.01	0.55		
Bacteria;Unclassified;Unclassified;Unclassified;Unclassified;sf_95;2545	0.02	0.51	0.02	0.51	0.01	-0.59	0.01	0.56		
Bacteria;Verrucomicrobia;Unclassified;Unclassified;Unclassified;sf_3;486	0.03	0.48	0.01	0.55	0.01	-0.59	0.01	0.60		
Bacteria;Verrucomicrobia;Unclassified;Unclassified;Unclassified;sf_4;288			0.05	0.45	0.02	-0.54	0.03	0.51		
Bacteria;Verrucomicrobia;Unclassified;Unclassified;Unclassified;sf_5;686					0.02	-0.53	0.01	0.56	0.03	-0.49
Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Unclassified;sf_3;399			0.01	-0.58	0.01	0.56	0.03	-0.51		
Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Unclassified;sf_3;417	0.03	-0.49	0.01	-0.56	0.03	0.49				
Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Unclassified;sf_3;430	0.03	-0.48	0.01	-0.57	0.02	0.50	0.05	-0.46		
Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Unclassified;sf_3;44	0.03	-0.49	0.00	-0.62	0.00	0.68	0.00	-0.73		
Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Unclassified;sf_3;4841			0.03	-0.47	0.02	0.52				
Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Unclassified;sf_3;4865	0.03	-0.49	0.01	-0.54	0.02	0.52	0.04	-0.47		
Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;			0.00	-0.69	0.00	0.78	0.00	-0.76		

	SM		NH4		EOC		pH		Mg	
Gene	**P**	**r**	**P**	**r**	**P**	**r**	**P**	**r**	**P**	**r**
Unclassified;sf_3;565										
Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales; Unclassified;sf_3;607	0.04	-0.46	0.00	-0.62	0.00	0.77	0.00	-0.77		
Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales; Unclassified;sf_3;610			0.01	-0.59	0.00	0.64	0.00	-0.63		
Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales; Verrucomicrobia subdivision 5;sf_1;547	0.02	0.52	0.01	0.56	0.01	-0.56	0.01	0.56		
Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales; Verrucomicrobia subdivision 7;sf_1;760	0.03	0.47	0.01	0.57	0.01	-0.56	0.00	0.63		
Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales; Verrucomicrobiaceae;sf_6;660			0.00	-0.61	0.00	0.79	0.00	-0.73		
Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales; Verrucomicrobiaceae;sf_7;29	0.03	-0.49	0.01	-0.59	0.00	0.60	0.00	-0.65		
Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales; Xiphinematobacteraceae;sf_3;352									0.03	0.49
Bacteria;WS3;Unclassified;Unclassified;Unclassified;sf_1;2537	0.02	0.52			0.03	-0.49				
Bacteria;WS5;Unclassified;Unclassified;Unclassified;sf_2;8119	0.04	0.47			0.01	-0.57			0.04	-0.47

Table S1: Pearson's linear correlations (r) and p-values (P) for taxa that showed a significant difference (ANOVA, p≤ 0.05) among time points and soil moisture, ammonia concentrations (NH4), extractable organic carbon (EOC), magnesium concentrations (Mg) and pH. The main phylogenetic groups are color coded by their Phyla.

Table S2 : CCA statistics

PC-ORD Version 4.34

Coefficients of determination for the correlations between ordination distances and distances in the original n-dimensional space:

	R Squared	
Axis	Increment	Cumulative
1	.759	.759
2	.002	.762
3	.007	.768

Increment and cumulative R-squared were adjusted for any lack of orthogonality of axes.

Axis pair	r	Orthogonality,% = 100(1-r^2)
1 vs 2	0.000	100.0
1 vs 3	0.000	100.0
2 vs 3	0.000	100.0

Number of entities = 19
Number of entity pairs used in correlation = 171
Distance measure for ORIGINAL distance: Relative Euclidean

Pearson and Kendall Correlations with Ordination Axes N= 19

Axis:		1			2			3	
	r	r-sq	tau	r	r-sq	tau	r	r-sq	tau
pH	.348	.121	.344	-.051	.003	-.297	-.019	.000	.059
SM	.494	.244	.439	-.116	.014	-.310	.399	.159	.275
NH4	.505	.255	.228	-.295	.087	-.216	.120	.014	.018
NO3	-.372	.139	-.277	-.212	.045	.006	-.223	.050	-.097
Al	.040	.002	.099	.651	.424	.450	-.104	.011	-.111
Ca	.079	.006	.076	-.437	.191	-.368	.014	.000	.053
Fe	.363	.132	.099	.017	.000	-.135	.328	.108	.076
K	-.051	.003	-.076	-.465	.216	-.333	.173	.030	.135
Mg	-.314	.098	-.263	-.449	.202	-.287	.573	.328	.415
Mn	-.058	.003	-.064	-.030	.001	.006	-.007	.000	.006
Si	.319	.102	.111	-.025	.001	-.170	.300	.090	.088
EOC	-.562	.316	-.439	.313	.098	.240	-.051	.003	.076

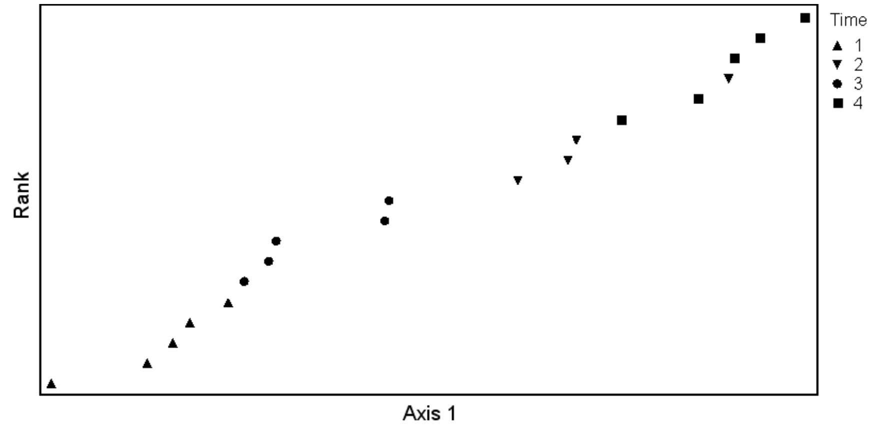

Figure S1: Non metric multidimensional scaling (NMS) showing microbial community structure on the top 5 cm of the soil profile with time in response to rainfall events. NMS statistics and correlations with environmental variables are shown in table S1.

Table S3: NMS statistics

PC-ORD Version 4.34
Coefficients of determination for the correlations between ordination distances and distances in the original n-dimensional space:

	R Squared	
Axis	Increment	Cumulative
1	.983	.983

Number of entities = 19
Number of entity pairs used in correlation = 171
Distance measure for ORIGINAL distance: Sorensen (Bray-Curtis)
Pearson and Kendall Correlations with Ordination Axes N=19

Axis		1	
	r	r-sq	tau
pH	-.343	.118	-.309
SM	-.488	.238	-.392
NH4	-.486	.237	-.251
NO3	.379	.143	.277
Al	-.042	.002	-.099
Ca	-.076	.006	-.123
Fe	-.351	.123	-.123
K	.032	.001	.053
Mg	.288	.083	.240
Mn	.041	.002	-.006
Si	-.311	.097	-.135
EOC	.529	.280	.368