

Microbial community dynamics of permafrost in response to thermokarst formation

Patrick Neuberger¹, Alireza Saidi-Mehrabad¹, Duane Froese², Brian Lanoil¹

¹Department of Biological Sciences, University of Alberta

²Department of Earth and Atmospheric Sciences, University of Alberta



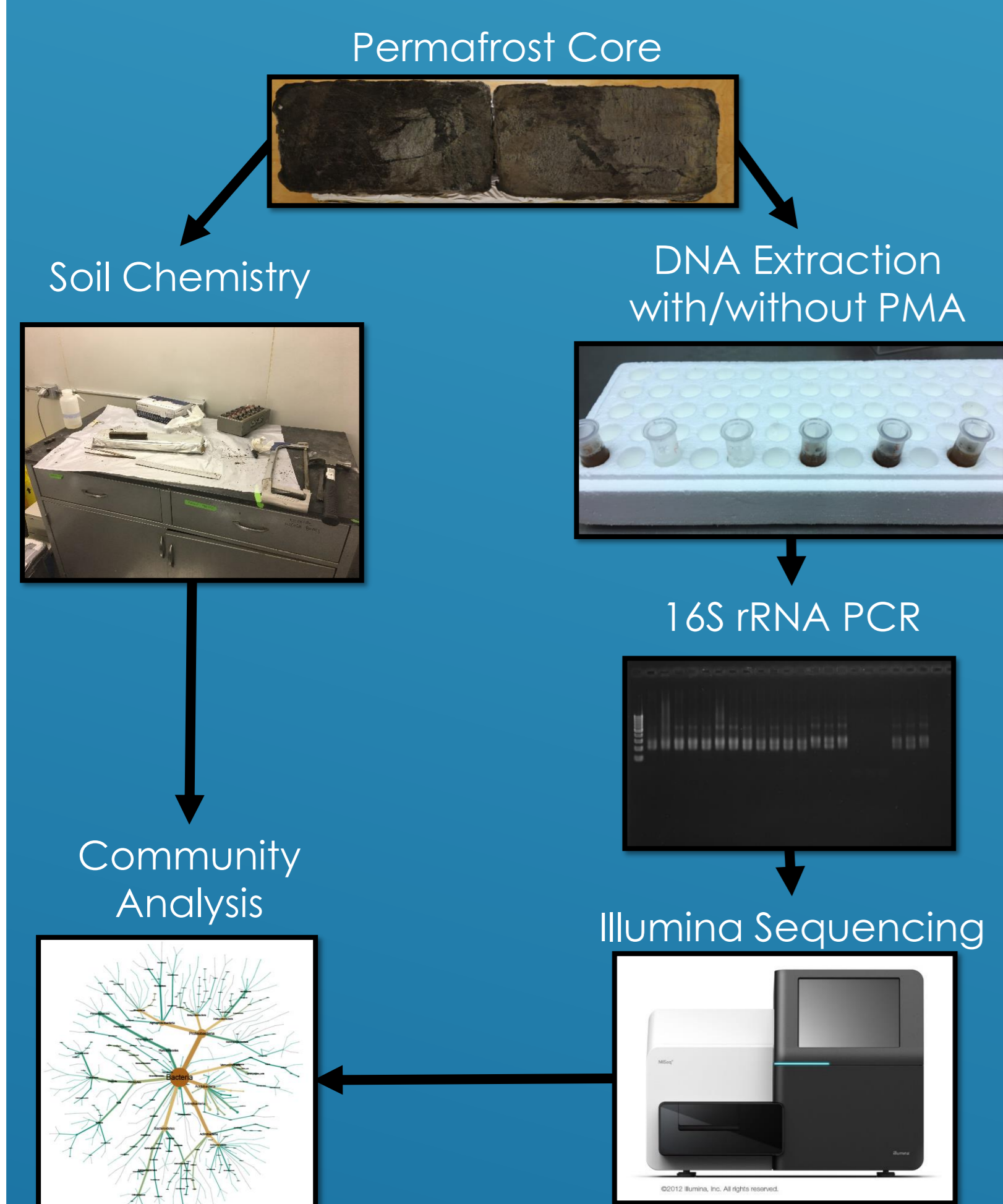
Introduction

Permafrost thaw as a result of climate change can lead to dramatic ecosystem changes, including the formation of thermokarst ponds. Microbial degradation of organic carbon increases with thermokarst development, resulting in increased flux of the greenhouse gases CO₂ and CH₄. Few studies have examined how the microbial community, which controls greenhouse gas flux, changes with thaw under field conditions. Lab-based studies have also not differentiated between nucleic acids derived from living and dead cells, an issue as permafrost can preserve ancient DNA for tens of thousands of years. We aim to characterize both viable and total microbial assemblages across a permafrost thaw gradient.

Hypothesis

If permafrost thaws with exposure to atmospheric temperatures, then the total assemblage will shift to resemble the active layer while the viable microbial community of permafrost will not change.

Methods



Conclusion

- Edaphic parameters do not shift rapidly with thaw.
- Microbial community structure shifts to resemble the active layer, regardless of soil edaphic parameters. Phylogenetic structure changes drastically with permafrost thaw.
- Viable communities are more similar to their total assemblage than to other groups.

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Results

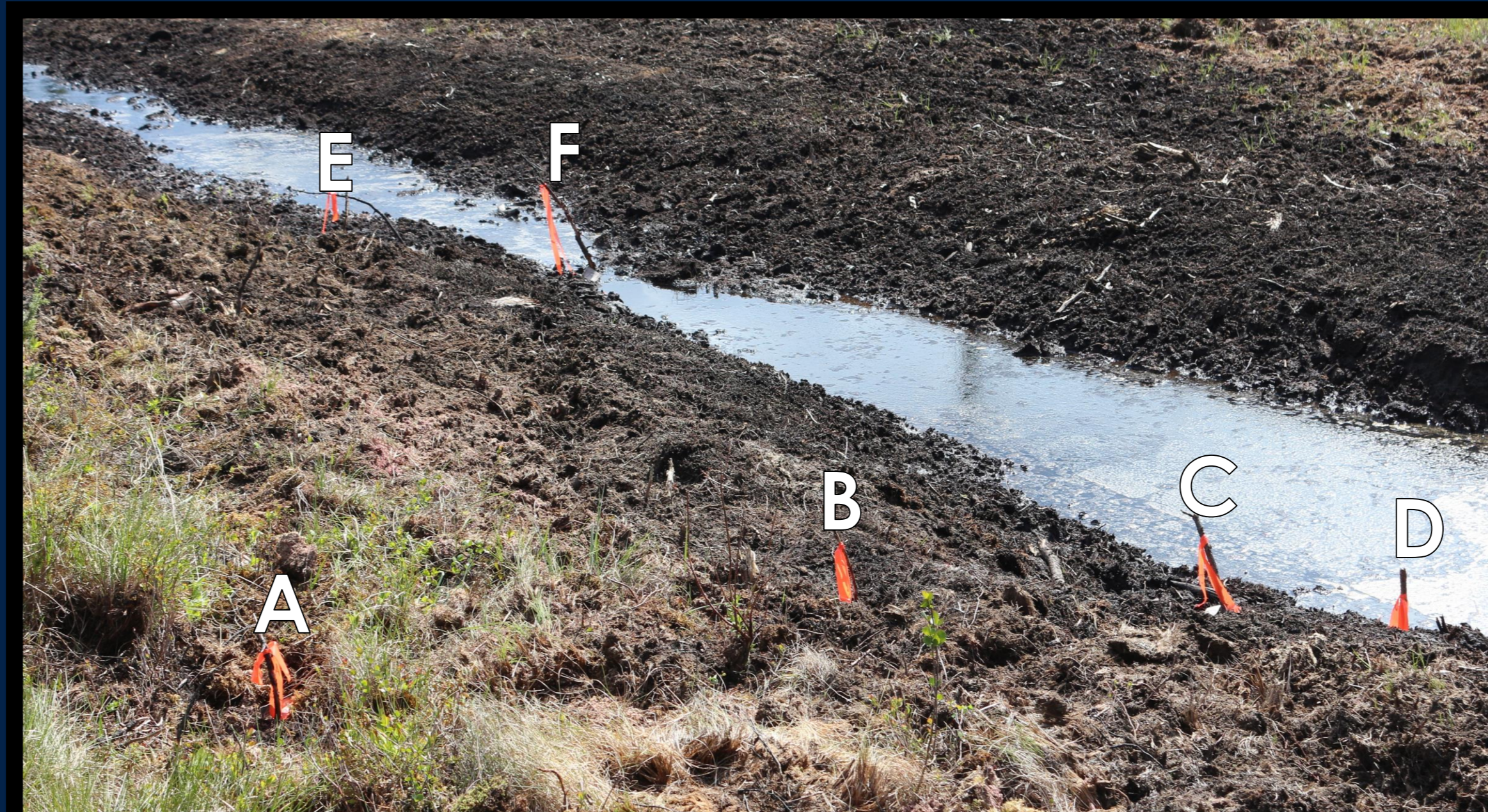


Figure 1. Active layer, permafrost, and thawed permafrost collected at Dominion Creek, Yukon, Canada. The disturbance gradient extends across: **Undisturbed active layer, Disturbed permafrost, and Thermokarst sediments.** Permafrost was cored at three locations adjacent to this gradient: Core 1 (**undisturbed**), Core 2 (**disturbed**) and Core 3 (**thermokarst**).

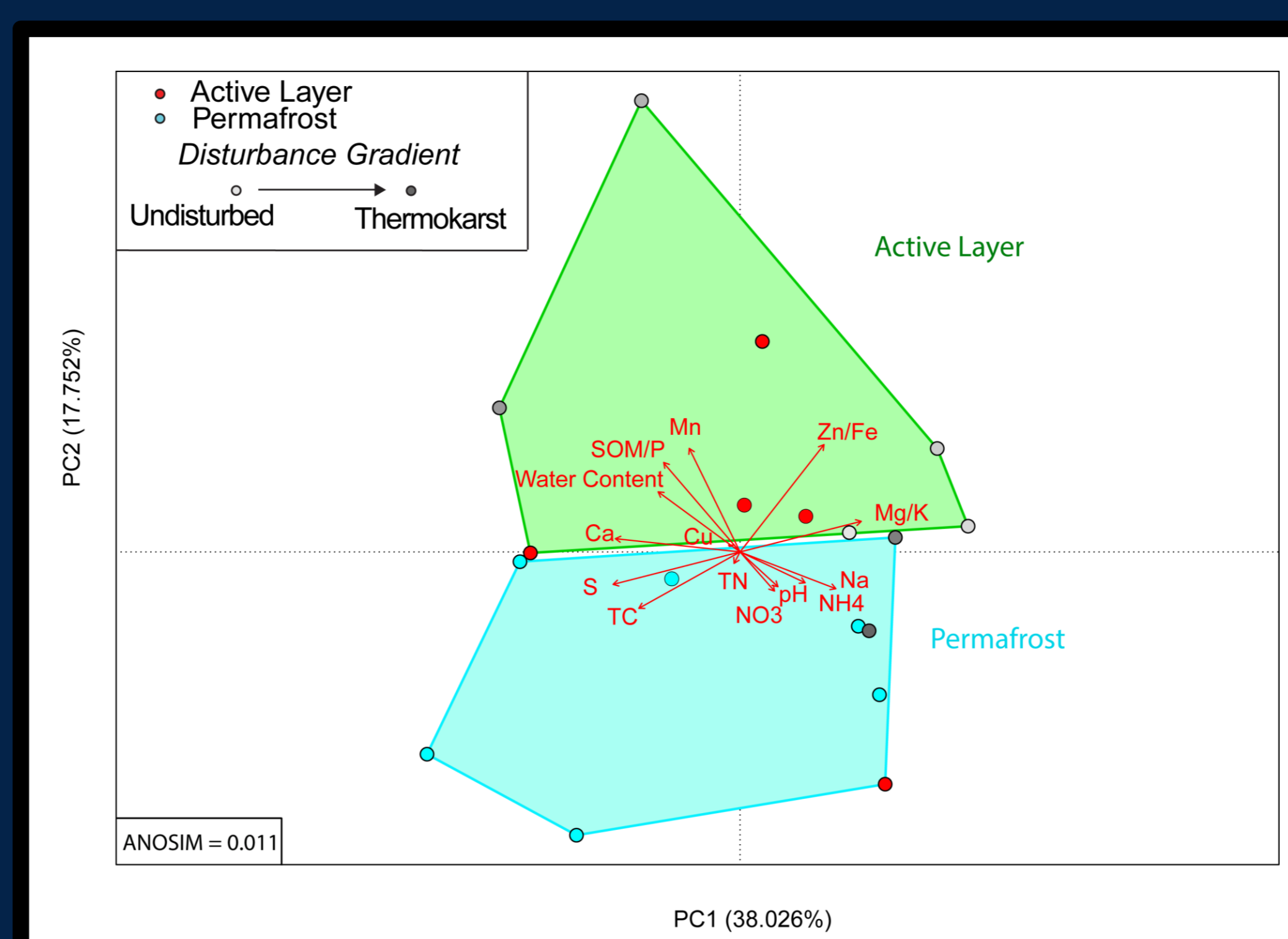


Figure 2. Soil chemistry is distinguishable between Active Layer and Permafrost sourced samples.

Principal component analysis of permafrost, active layer, and the disturbance gradient based on soil physicochemical parameters. Values were normalized to the variable's standard deviation. Vectors depict eigenvectors driving sample location in ordination space. Coloured hulls represent two different clusters: Active Layer (**green**) and Permafrost (**cyan**). Across the disturbance gradient darker circles represent greater disturbance.

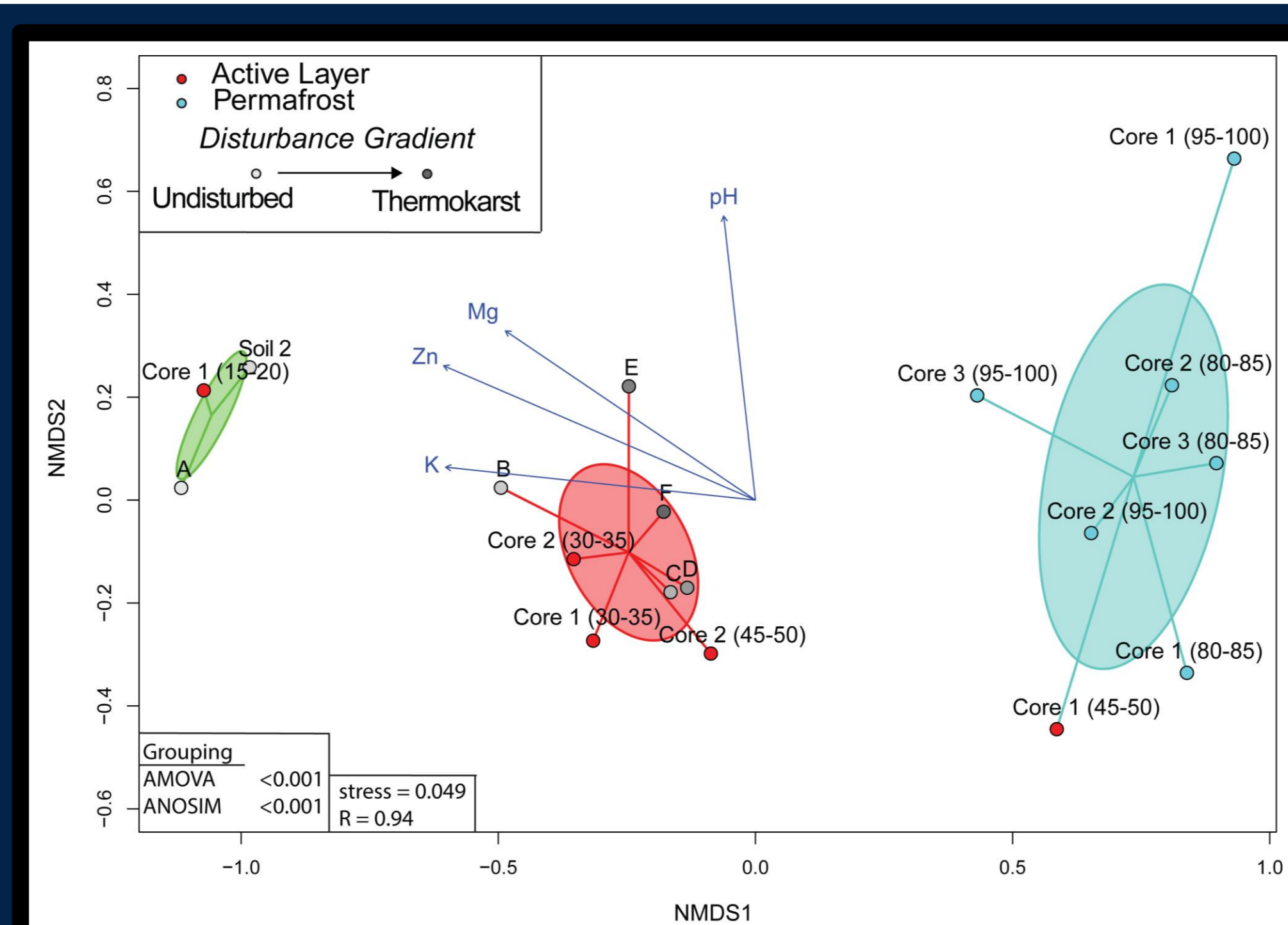


Figure 3a. Microbial community structure of permafrost shifts to resemble lower active layer samples. Non-metric Multidimensional Scaling (NMDS) plot of total microbial assemblage. Ellipses denote clusters determined by weighted average algorithms. Vectors denote chemical parameters correlating with community shifts ($r^2 > 0.3$, $p \leq 0.05$).

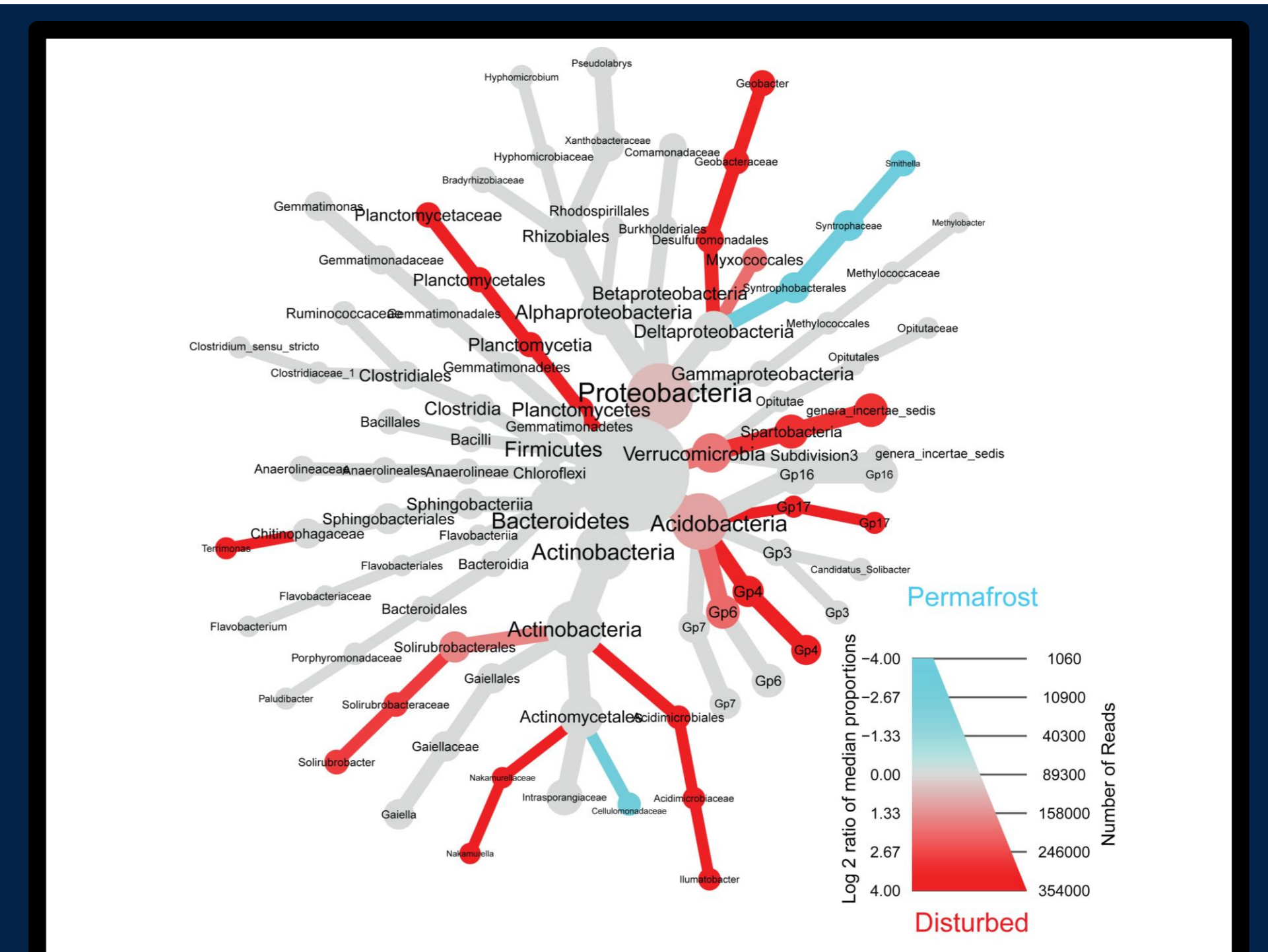


Figure 3b. Permafrost thaw induces higher taxon abundance across taxa. Heat tree depicting the log₂ difference from median for each taxon between permafrost and disturbed clusters with only significant differences shown based on a Wilcoxon rank test ($p \leq 0.05$). Node size indicates the number of sequences per taxon.

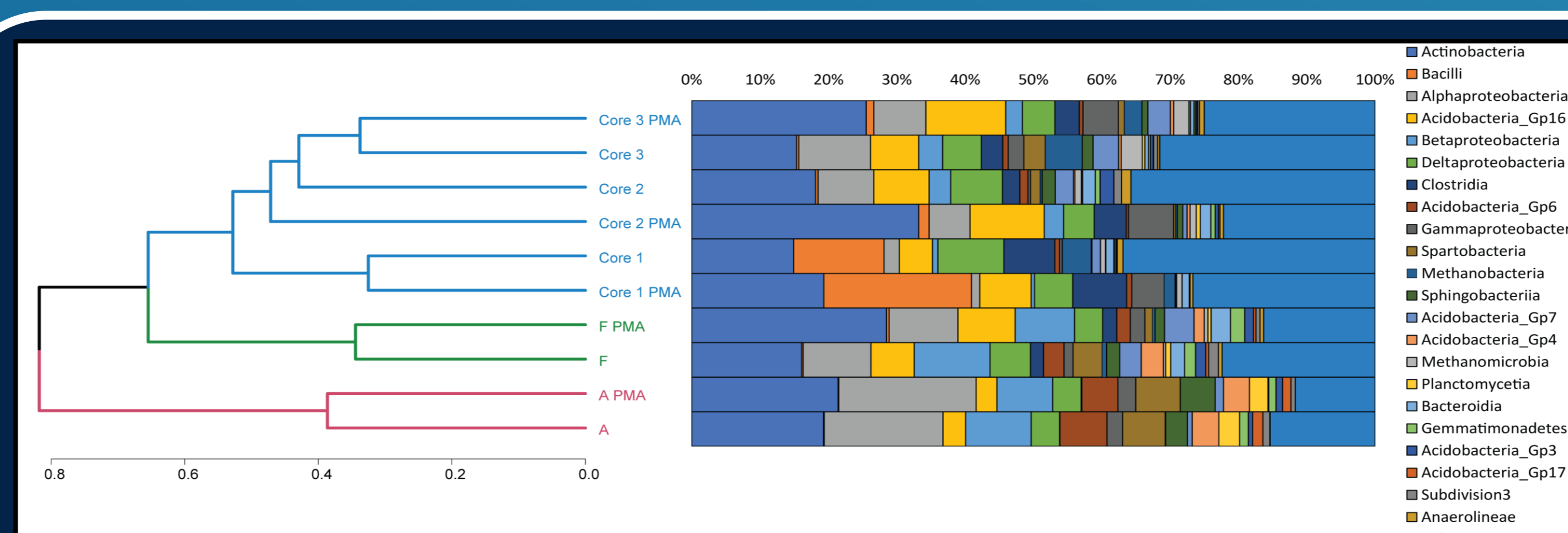


Figure 4. The viable community of permafrost and active layer soils were most similar to their total assemblage. Left: Hierarchical clustering of viable vs. total microbial assemblage. Right: Relative abundance Microbial taxa at the class level. Taxa with $<1\%$ in any sample was combined into "Other".