

# Distinct depth profile of bacterial and archaeal communities between four Alaskan soil cores

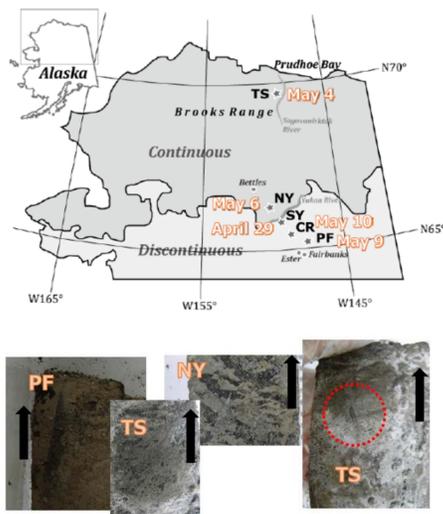
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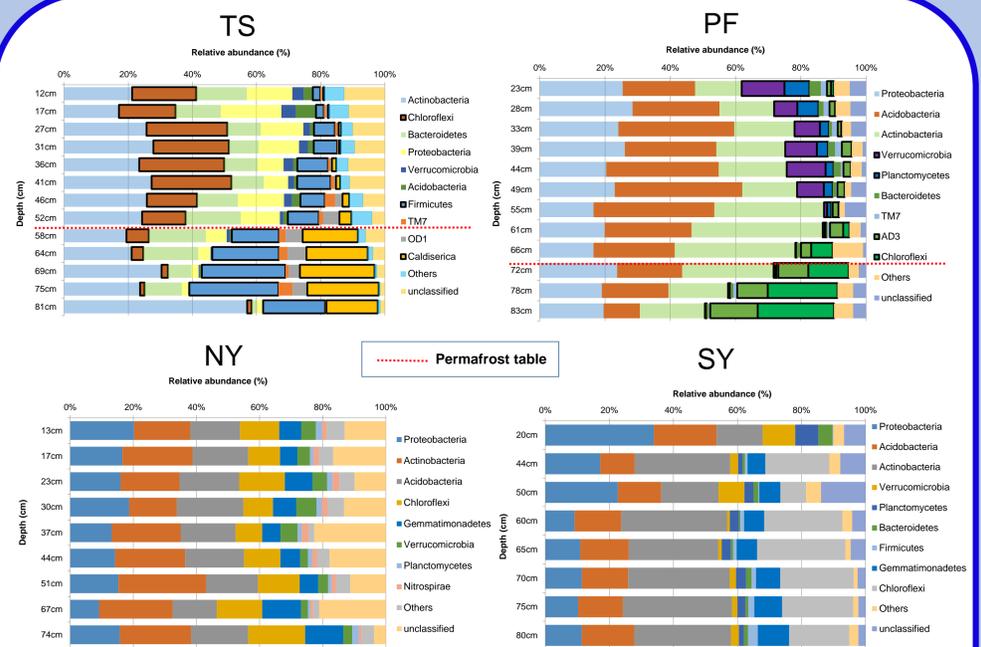
## Abstract

Microbial response to permafrost thaw driven by climate warming varies by sites. Although a great deal of environmental heterogeneity is found across permafrost regions, vertical variation of microbial communities in permafrost affected soils is not well understood. Here, we sampled soil cores at four different sites including both continuous and discontinuous permafrost regions in Alaska. Abundance and community structure of soil bacteria and archaea were compared between cores at different depths using MiSeq sequencing and quantitative PCR targeting 16S rRNA gene. Abundance of bacteria and archaea overall changed in a similar way but did not show any directional pattern across depth. Both bacteria and archaeal communities were primarily structured by site difference, followed by depth and soil chemical properties. Interestingly, there were dramatic shifts in bacterial phyla dominance around permafrost table in two permafrost affected soils. Relative abundance of Chloroflexi was reduced to a great extent, while Caldiserica and Firmicutes markedly increased below 58 cm depth in a tussock tundra site. In a Sphagnum-dominated bog site, Verrucomicrobia and Planctomycetes almost disappeared, while Chloroflexi and candidate phylum AD3 dominated below 72 cm depth. These site-specific vertical variations of microbial community structure will be an important resource to predict how soil microbes respond to permafrost thaw.

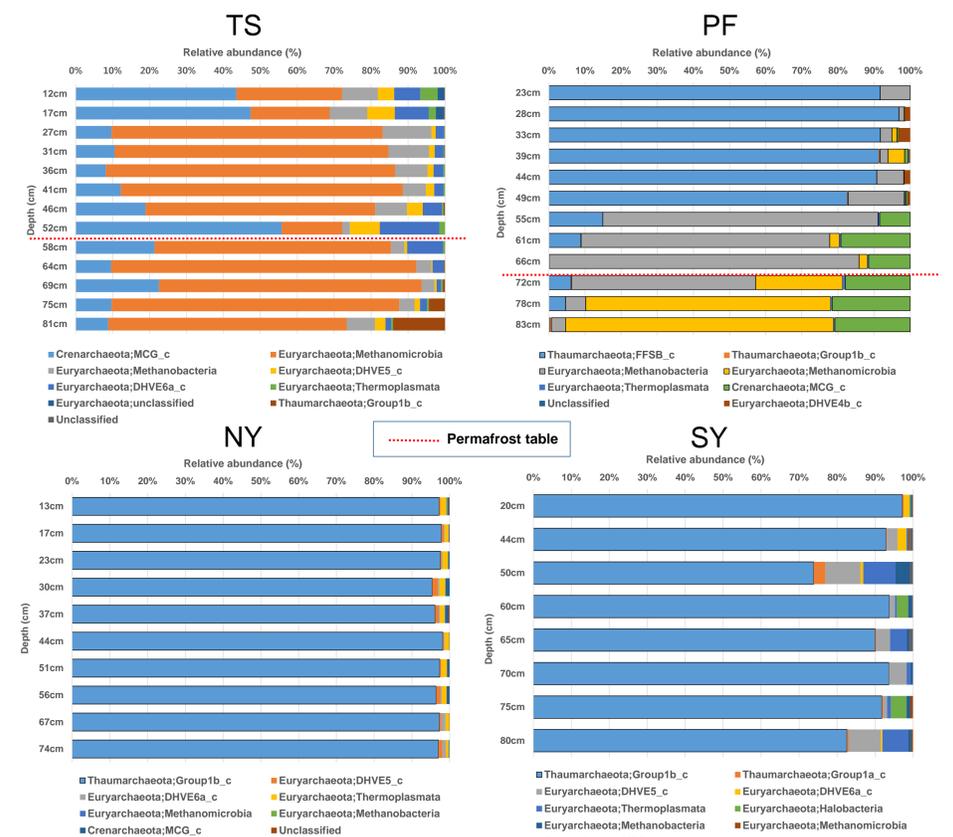
## Sampling sites



	Location °N, °W (masl)	Vegetation
TS	69.7, 148.7 (107)	Tundra near Sag River, with dominant surface vegetation as tussock grass, Dwarf Birch, American native willow, and sedge
NY	66.1, 151.2 (229)	Black spruce forest on north of Yukon River, shrubs and Dwarf Birch, and lichen layer in surface.
SY	65.8, 149.6 (361)	Black spruce forest on south of Yukon River, shrubs and feather moss surface.
CR	65.4, 148.9 (258)	Forest fire in 2010, burned black spruce trees with reed canarygrass vegetation
PF	65.1, 147.5 (210)	Bogs predominated by Sphagnum spp. and feather moss residing under shrubs and cotton grass

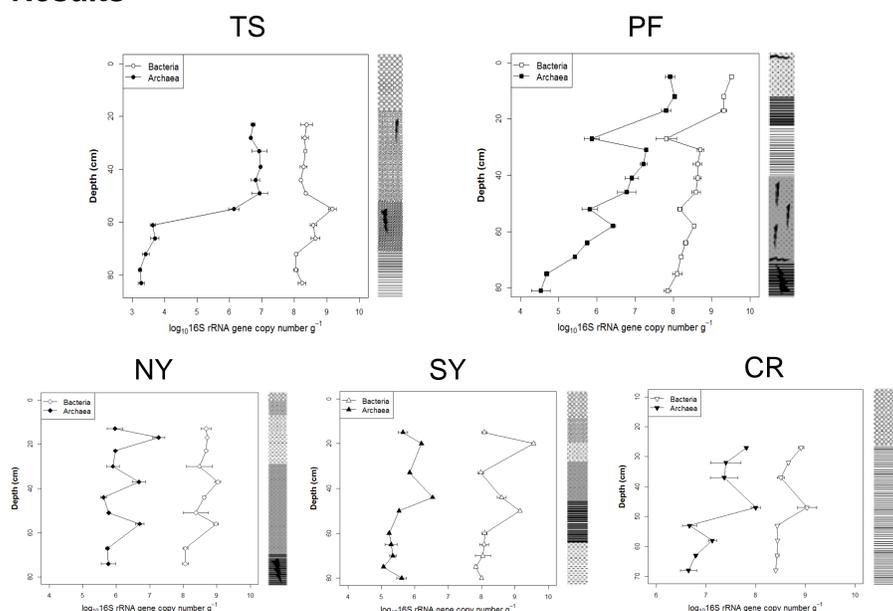


## ✓ Bacterial phyla distribution across depth

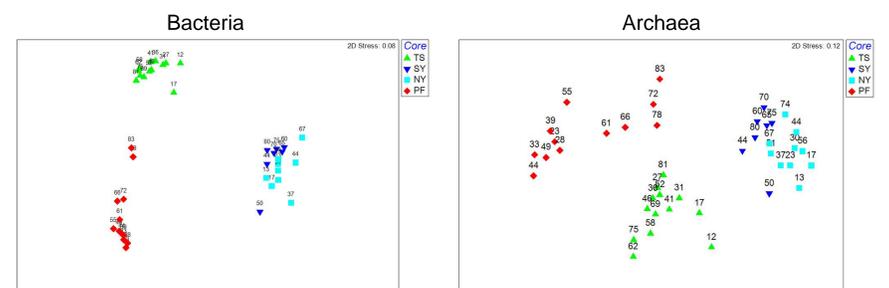


## ✓ Archaeal class distribution across depth

## Results



## ✓ Changes of bacterial and archaeal rRNA copy numbers across depth



## ✓ Clustering pattern of bacterial and archaeal community compositions

## Conclusions

- ✓ Abundance of bacteria and archaea overall changed in a similar way but did not show any directional pattern across depth.
- ✓ There were dramatic shifts in bacterial phyla dominance around permafrost table in permafrost affected soils.
- ✓ Both bacterial and archaeal communities were structured more by site difference rather than depth.