

# Temperature Dependent Microbial Community Dynamics Modulates Methane Cycle in Permafrost-affected Soils



Nu Ri Myeong<sup>1,2</sup> and Mincheol Kim<sup>1\*</sup>  
<sup>1</sup>Korea Polar Research Institute (KOPRI), <sup>2</sup>Chung-Ang University

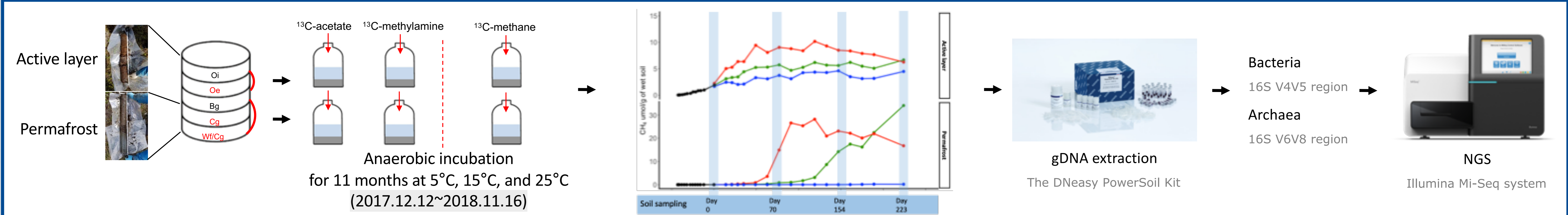


## Introduction

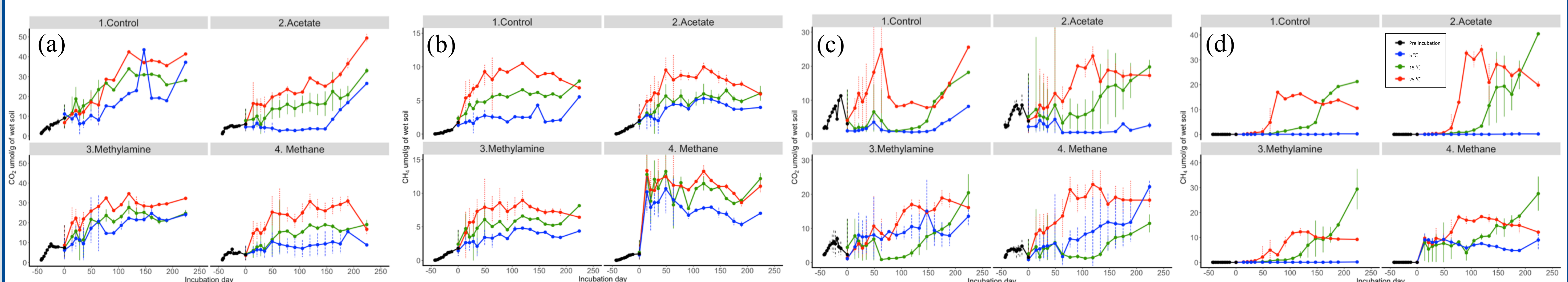
Arctic permafrost soils store large amounts of SOC (soil organic carbon). Thawing permafrost promotes microbial degradation of SOC leading to the biogenic production of green house gas as carbon dioxide and methane. However, the dynamics of microbial community in methane production and oxidation during thawing remains poorly understood. This study aim to understand the temperature-dependent modulation of microbial production and oxidation of methane under anaerobic condition. We anaerobic incubated Alaska Council soil cores with <sup>13</sup>C-labelled acetate, methylamine and methane have the potential for methanogenesis and anaerobic oxidation of methane.

## Methods

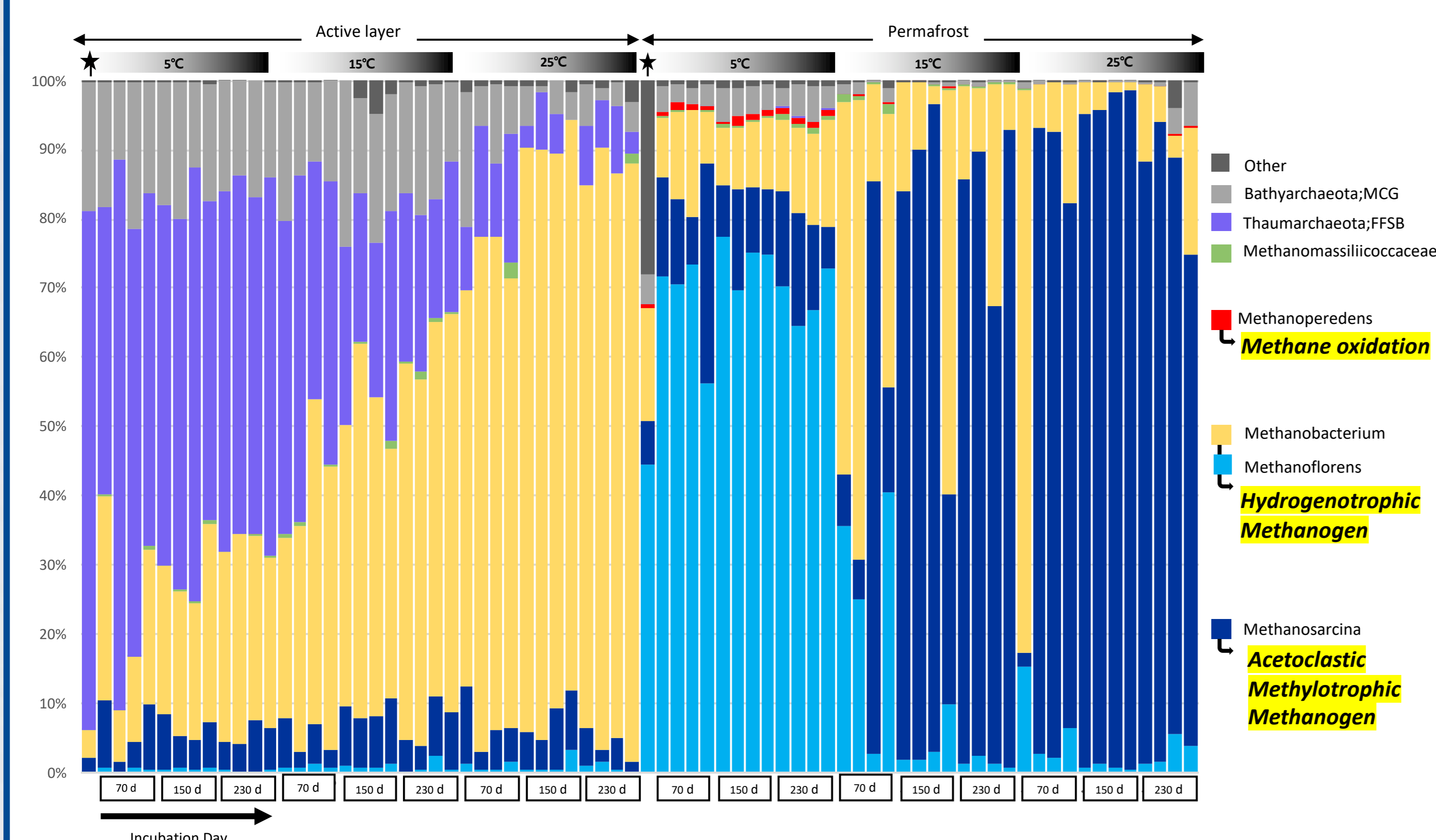
Alaska tundra soil were anaerobically incubated at 5°C, 15°C and 25°C for 11 months with <sup>13</sup>C labeled substrate. Then, extracted genomic DNA from incubated soil and sequencing bacterial and archaeal 16S rRNA gene using Miseq platform. Also, gas concentration of CO<sub>2</sub> and CH<sub>4</sub> in headspace was measured to confirm microbial respiration and methanogenesis.



## Results

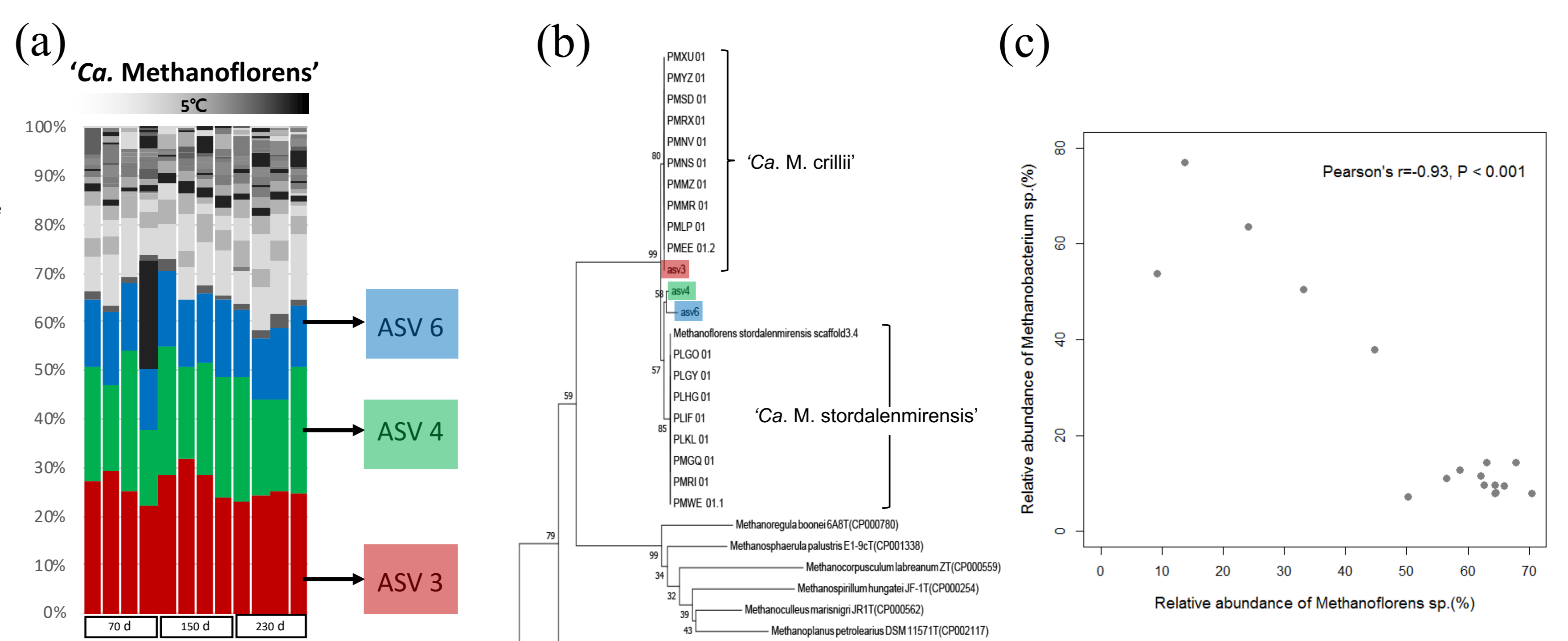


**Fig 1. Head space gas concentration** (a) CO<sub>2</sub> concentration at active layer (b) CH<sub>4</sub> concentration at active layer (c) CO<sub>2</sub> concentration at permafrost (d) CH<sub>4</sub> concentration at permafrost. CO<sub>2</sub> and CH<sub>4</sub> concentration increased with time at all temperatures. CO<sub>2</sub> concentration patterns are similar at both active and permafrost layer.



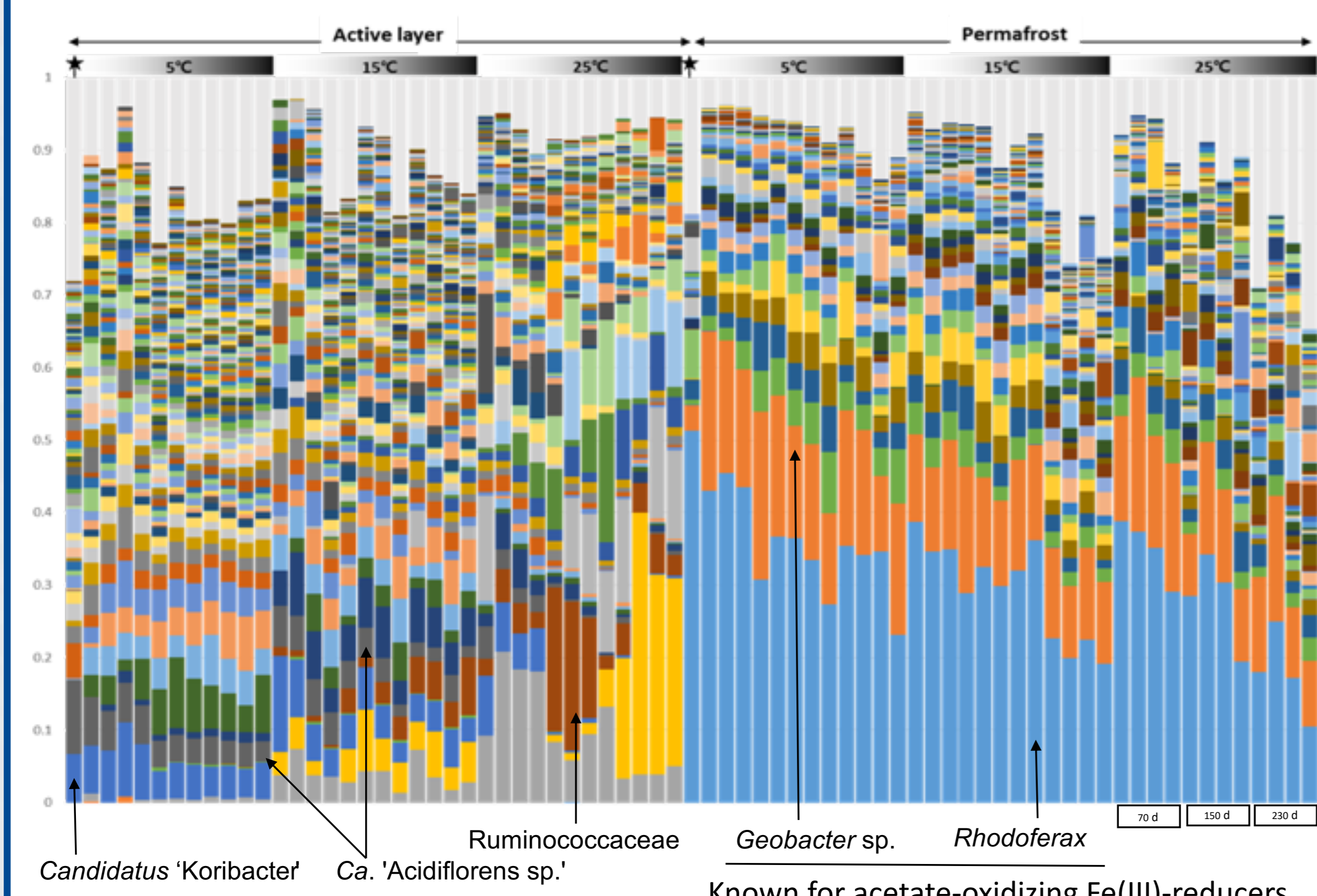
**Fig 2. Relative abundance of archaeal community (genus level)**

The relative abundance of the *Methanobacterium* increased with temperature at active layer. In contrast to active layer, in permafrost, the relative abundance of the *Methanoflorens* dominant at 5°C and *Methanosarcina* dominant at over 15°C. Also *Methanoperedens* known as methane oxidation archaea were identified in permafrost samples incubated at 5°C.



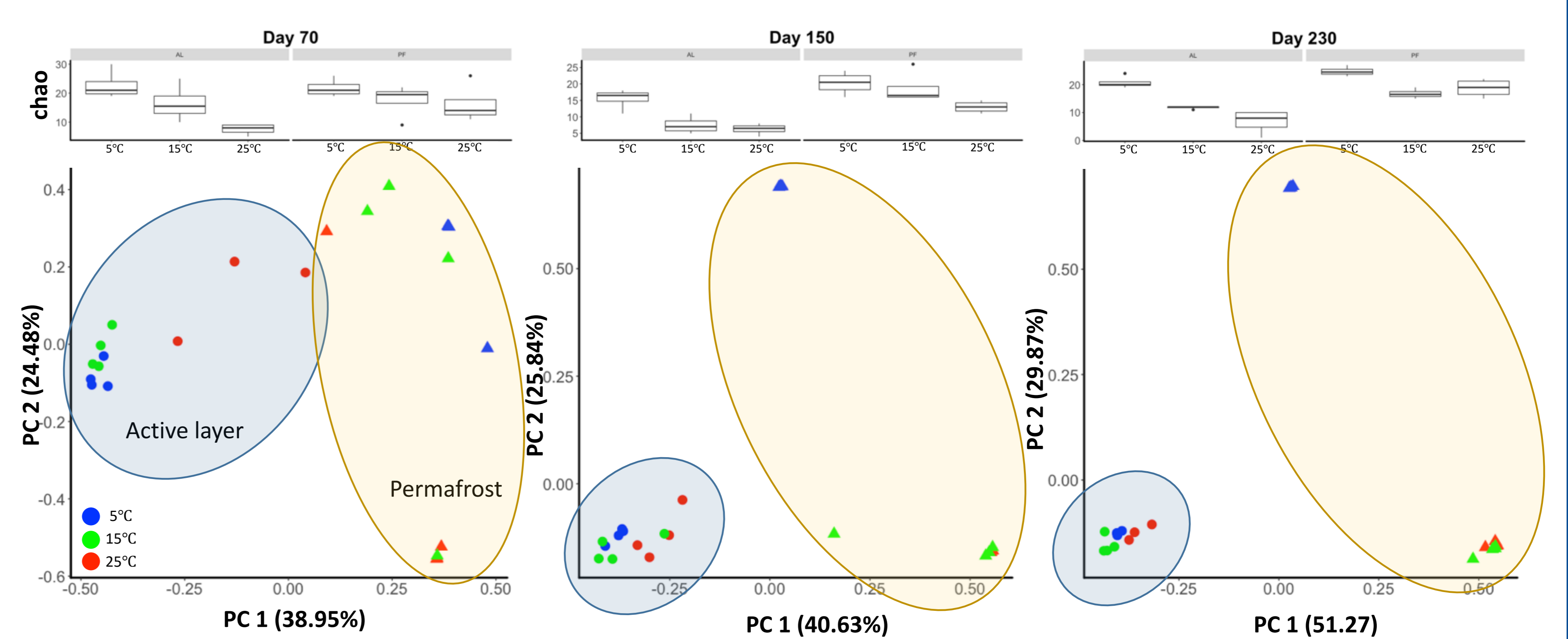
**Fig 3. 'Ca. Methanoflorens' Amplicon Sequence Variant (ASVs)** (a) relative abundance, (b) taxonomic position and (c) correlation with *Methanobacterium*

(a) Belonging to the uncultivated lineage 'Rice Cluster II' *Methanoflorens*, which is mainly found in the permafrost. 'Ca. Methanoflorens' dominated in permafrost sample at 5°C incubated only. Three of 'Ca. Methanoflorens' ASVs identified dominant. (b) 'Ca. M. stordalenmirensis', and 'Ca. M. crillii' genome assembled by metagenome study in thawing permafrost (Mondav 2014 & Woodcroft 2018) (c) Correlation between methanogen 'Ca. Methanoflorens' and *Methanobacterium*.



**Fig 4. Relative abundance of bacterial community (genus level)**

In active layer, there were clear shifts in major bacterial groups depending on temperature and incubation time. However, no discernible differences were observed in permafrost bacterial communities between different temperatures but there were gradual composition changes along incubation time.



**Fig 5. Alpha diversity (chao richness) and PCoA ordination of archaeal communities that varied by incubation temperature and time**

chao richness and Bray-Curtis dissimilarity matrix was calculated based on archaea ASVs profiles of incubated soil samples.

## Summary

Patterns of GHG concentration and microbial community differed by soil layer, temperature, and incubation time. CH<sub>4</sub> production in permafrost, increase abruptly over two month anaerobic incubation. There are distinct patterns in bacterial and archaeal community composition between active layer and permafrost. Considerable reduction in relative abundance of both 'Ca. Methanoflorens' and *Methanoperedens* at higher temperature indirectly confirmed they have adapted to cold niches in the Arctic permafrost. Furthermore methanogen ('Ca. Methanoflorens', *Methanosarcina* and *Methanobacterium*) composition was shifted by rising temperature. These results help to understand the direct effect of different temperature and substrates on metabolic interactions between anaerobic microbes in an Arctic tundra.