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Supplementary Information of

Warmer *Sphagnum* moss, less soil carbon loss: Anaerobic respiration and temperature response along a boreal forest-peatland ecotone

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Introduction

Here we include text and figures in supplement to those in the body of the paper that further explain the trends observed. The first figure is a drone image of the field site, chosen for its perspective of all the field sites. Figures S2 – S7 show the cumulative measured gas flux over the progression of the 140 day incubation. The units are normalized to gram dry weight of sample and expressed in CO_2-C g^{-1} DW, and CH_4-C g^{-1} DW. Figures S8 and S9 display gene counts from a qPCR analysis of each habitat from the pre-incubation material. The amplicon data for the microbial community composition data is included as Supplementary Information, separate from this document.

SI Text

Study Site Description: The Bog site (61.83867°N, 24.170524°E) had some stunted Scots pines (*Pinus sylvestris*) on the raised peat hummocks, but was otherwise an open canopy landscape. Soil cores were collected approximately 5m apart from each other. Being composed almost homogenously of peat, the soil throughout was typical of a Sphagnofibrist with high acidity, low bulk density, continuous saturation and more than 75% *Sphagnum* content in the top 90cm of the soil column (Nachtergaele et al., 2001). The *Sphagnum* moss communities varied in their patchwork patterns of hummocks, lawns and hollows. We sampled from a lawn composed of *Sphagnum papillosum, S. magellanicum and S. balticum* and some sedges, including from genus *Eriophorum.* Further vegetation details and descriptions of Siikaneva peatland can be found in Korrensalo et al., (2016, 2017) and Korpela et al 2020. The top of the water table was visible from the boardwalk, and the peat layer has been found to be approximately 2m thick.

Soil found in the Intermediate habitat (61.83844°N, 24.171650°E) were histosols, with partially decomposed plant fibers throughout (JRC European Commission, 2010). Soil cores were collected approximately 5m apart from each other, and sampling locations aimed to capture the high heterogeneity of the site by including cores with some representation of the variety of vegetation found in this site. Although this site was above the water table, the soil was very moist, and spongey to the touch. Previous field campaigns found the water table to be between 25-35cm below surface. In this margin site, the Scots Pines grew further apart and appeared somewhat stunted in growth, with a strong presence of understory shrub plant community, mostly consisting of blueberry (*Vaccinium myrtillus*). The ground was less sloped and was covered by some *Sphagnum*, and some feather mosses (*Hylocomium splenens*).

The Upland Forest site (61.83837°N, 24.172040°E) is characterized by a canopy of Scots Pines (*Pinus sylvestris*) growing on haplic podzol soil. The cores here were collected approximately 5m apart from each other and subdivided into three horizons characteristic of a podzol with an organic, eluvial, and a bottom sandy horizon that decrease in acidity with depth (JRC European Commission, 2010) The sample site had sparse understory, but some blueberry bush (*Vaccinium myrtillus*) and ferns (*Dryopteris dilatata*), punctuated with protruding granite boulders and ground lichens (Cladonia spp.). Open space between trees with direct access to the top of the shade-adapted feather mosses (*Hylocomium splenens*),was abundant.

The entirety of the sampling site was at a slight west-facing angle from the Upland Forest towards the Bog.

Results. Soil description: Organic soils had similar TOC content, ranging from 36.0 to 46.2 %. Forest-Top had over 30% more N than the horizon with the next most layer (2.7% vs. 1.7%). The mean nitrogen content in the Intermediate site was higher than the other sites (1.3%, 1.2%, and 1.0% in the Intermediate, bog, and Upland Forest, respectively). The amount of nitrogen largely drove the C:N ratio, and varied from site to site. The gradient patterns in pH and bulk density by soil horizon from all habitats support greater levels of decompositions and compression from the top layer to the deeper soil layers

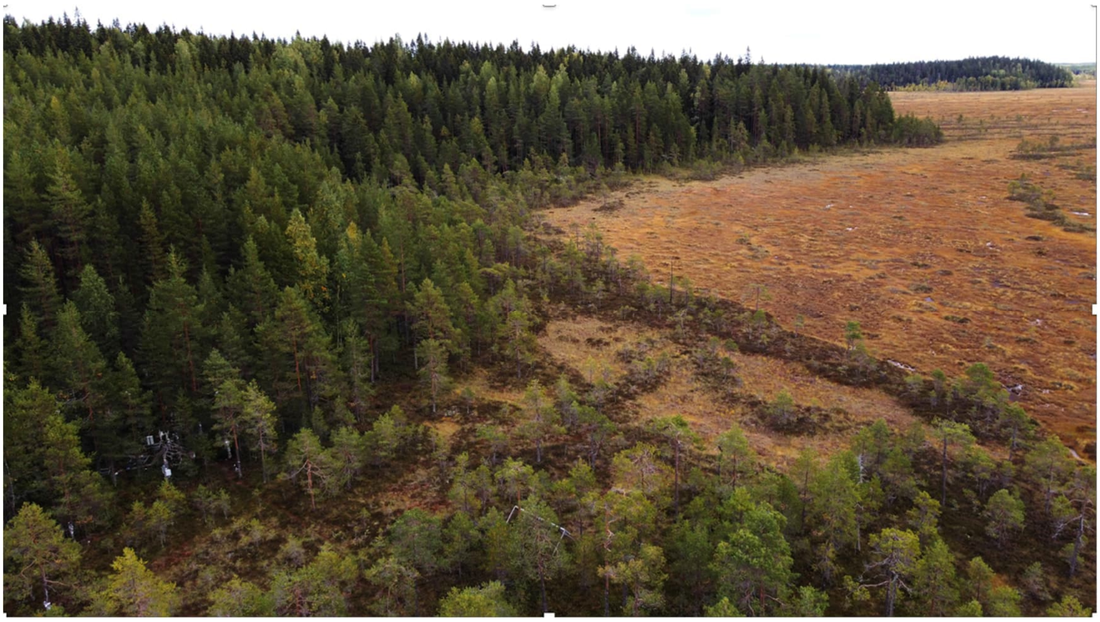

Figure S1: Aerial view of Siikaneva Peatland Complex from drone image. Here, the drone was north of the site, photographing the west-facing transect used in this study. In view are autochambers and boardwalk in the “Intermediate” habitat, bottom left (T. Rettlebach, L. Golde – Autumn 2022).

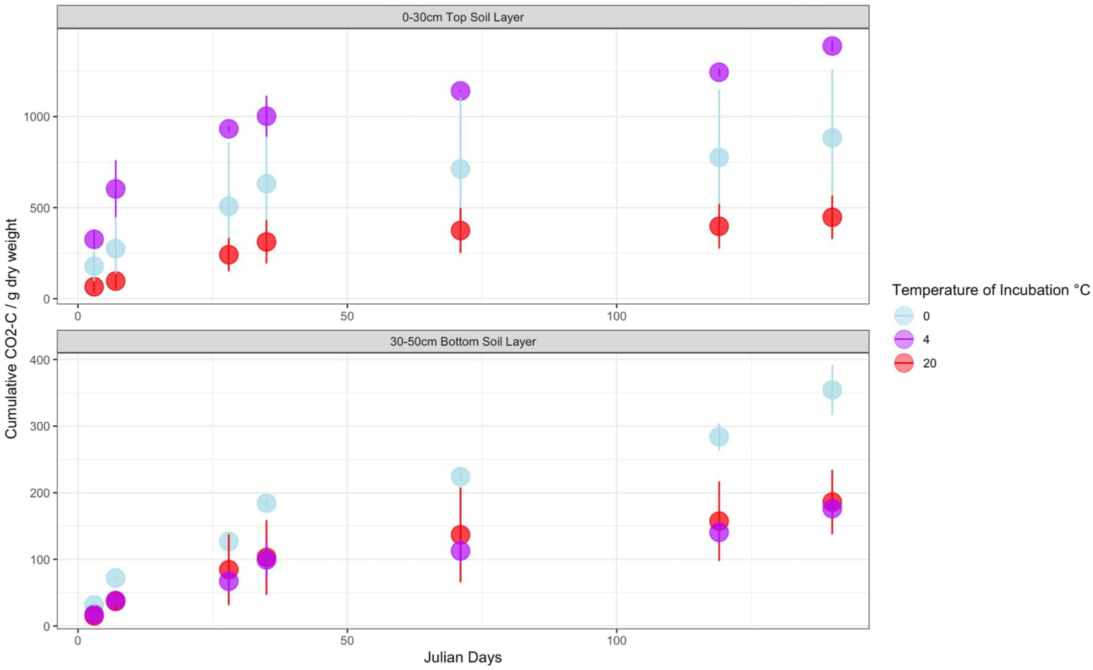

Figure S2: Cumulative CO_2 production over the 140-day incubation from samples taken from bog habitat samples. Each plot represents an average for a depth by temperature group (n=2) as denoted by text header and color of data points, error bars show ± standard deviation.

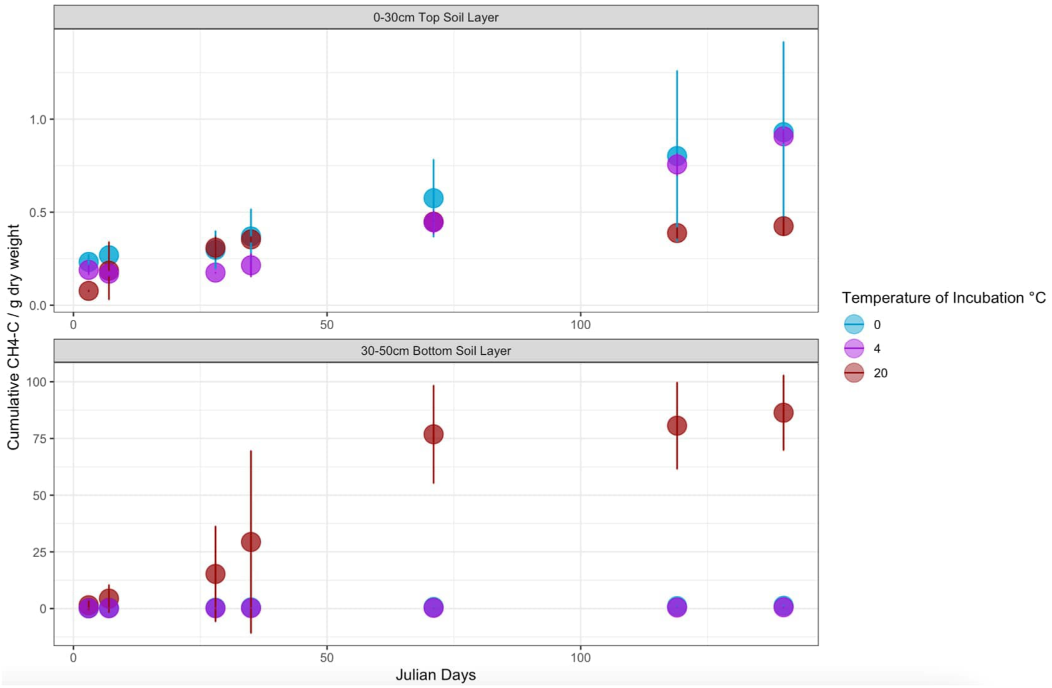

Figure S3: Cumulative CH_4 production over the 140-day incubation from samples taken from bog habitat samples. Each plot represents an average for a depth by temperature group (n=2) as denoted by text header and color of data points, error bars show ± standard deviation

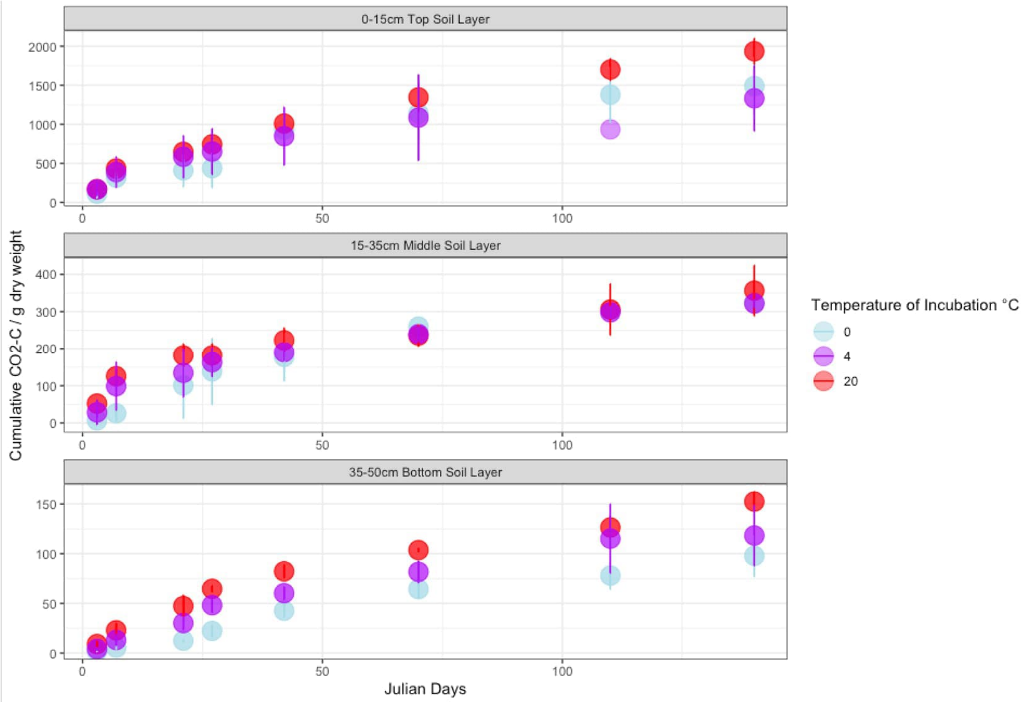

Figure S4**.** Shown is the 140 day progression of CO_2 production from samples taken from the intermediate habitat samples. Each plot represents an average for a depth by temperature group (n=2) as denoted by text header and color of data points, error bars show ± standard deviation.

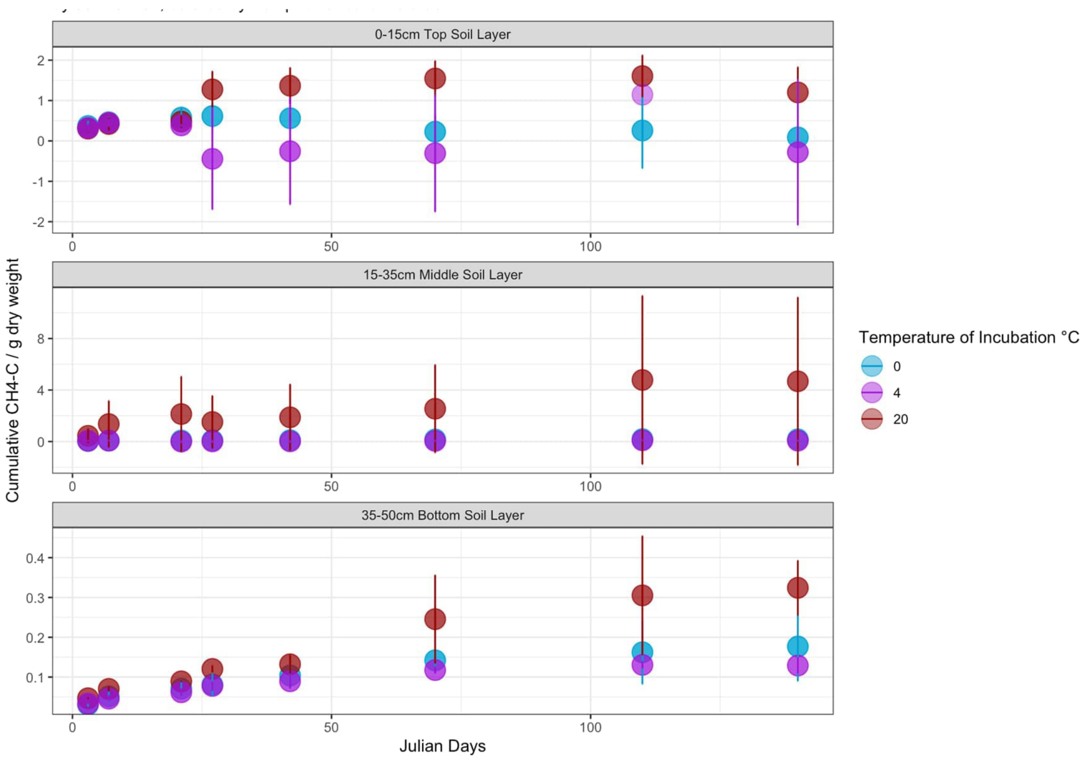

Figure S5. Shown is the 140 day progression of CH_4 production from samples taken from the intermediate habitat samples. Each plot represents an average for a depth by temperature group (n=2) as denoted by text header and color of data points, error bars show ± standard deviation.

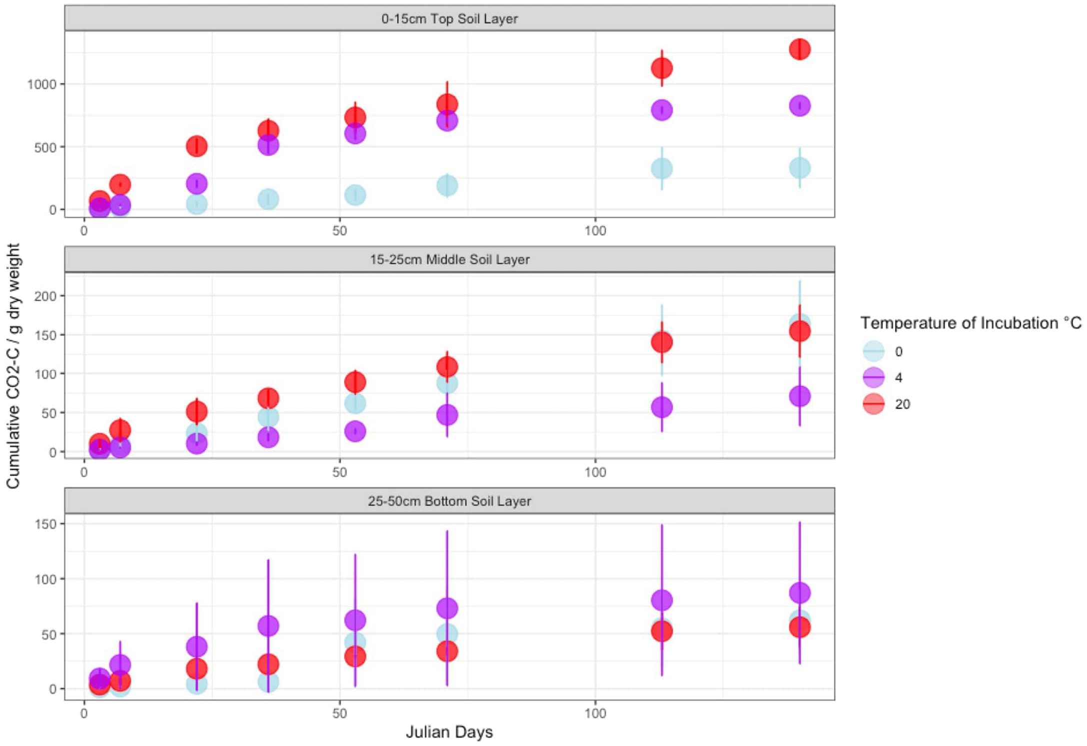

Figure S6. Shown is the 140 day progression of CO_2 production from samples taken from the upland forest habitat samples. Each plot represents an average for a depth by temperature group (n=2) as denoted by text header and color of data points, error bars show ± standard deviation.

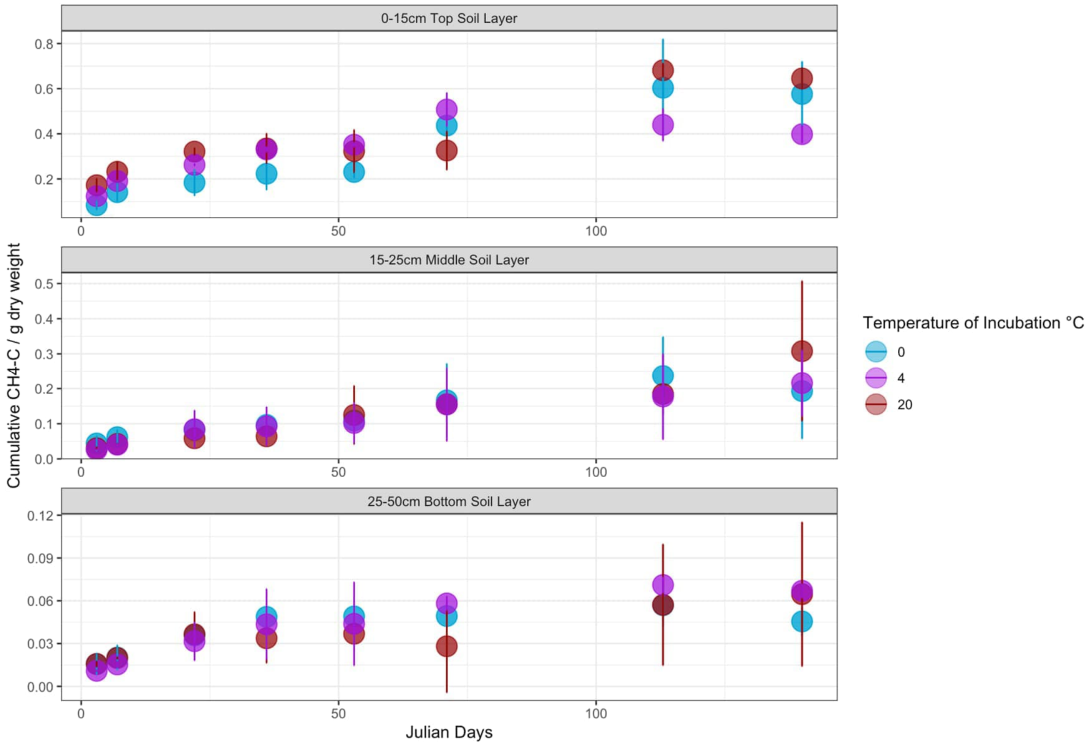

Figure S7. Shown is the 140 day progression of CH_4 production from samples taken from the upland forest habitat samples. Each plot represents an average for a depth by temperature group (n=2) as denoted by text header and color of data points, error bars show ± standard deviation.

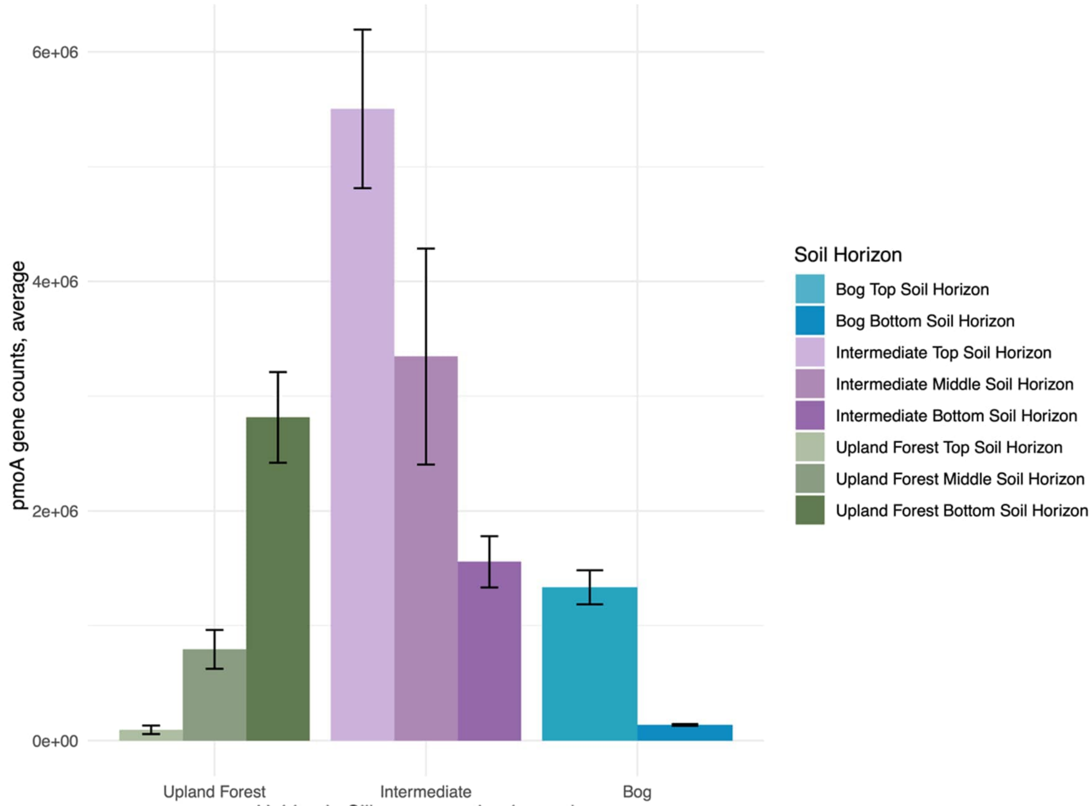

Figure S8. In this figure, the results of a qPCR analysis for gene counts are represented by the height of the bars. The pmoA gene was targeted as it is known to represent the methanotroph community within the soil column. Error bars represent the standard deviation (n=3).

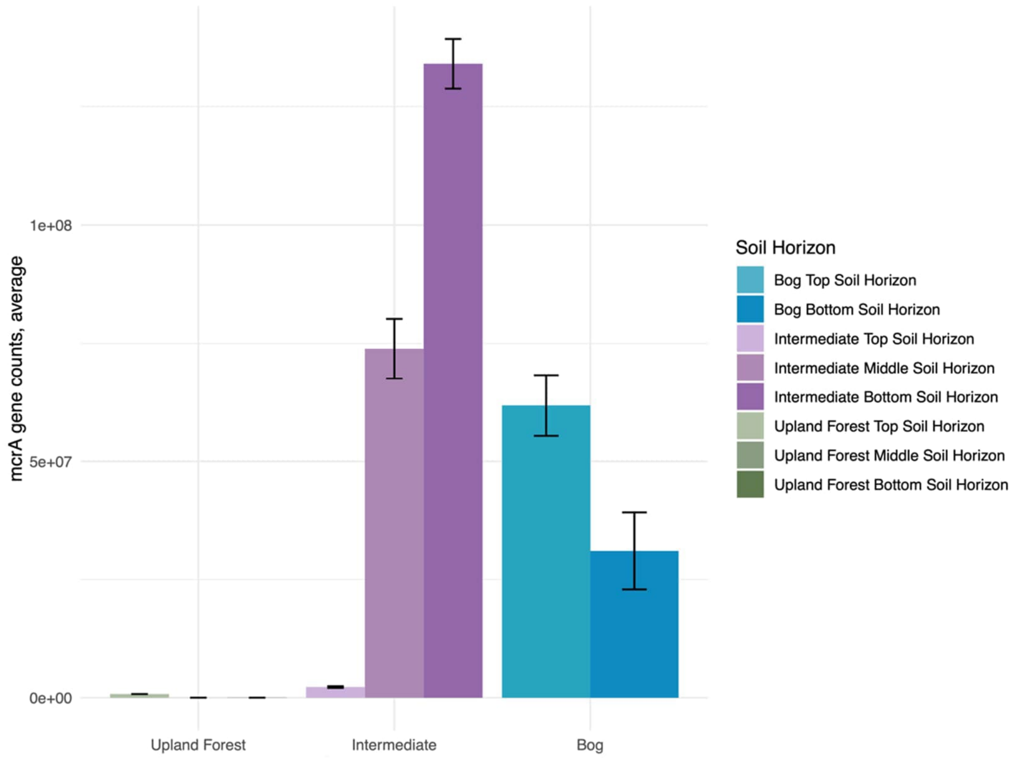

Figure S9**.** In this figure, the results of a qPCR analysis for gene counts are represented by the height of the bars. The mcrA gene was targeted as it is known to represent the methanogen community within the soil column. Error bars represent the standard deviation (n=3).