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Bacterial Community in Ancient Permafrost Alluvium at the Mammoth Mountain (Eastern Siberia)

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Running Head: Bacteria in ancient permafrost alluvium

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Abstract

Permanently frozen (approx. 3.5 Ma) alluvial Neogene sediments exposed in the Aldan river valley at the Mammoth Mountain (Eastern Siberia) are unique, ancient, and poorly studied permafrost environments. So far, the structure of the indigenous bacterial community has remained unknown. Use of 16S metagenomic analysis with total DNA isolation using DNA Spin Kit for Soil (MO-Bio) and QIAamp DNA Stool Mini Kit (Qiagen) has revealed the major and minor bacterial lineages in the permafrost alluvium sediments. In sum, 61 Operational Taxonomic Units (OTUs) with 31,239 reads (Qiagen kit) and 15,404 reads (Mo-Bio kit) could be assigned to the known taxa. Only three phyla, *Bacteroidetes*, *Proteobacteria* and *Firmicutes*, comprised more than 5% of the OTUs abundance and accounted for 99% of the total reads. OTUs pertaining to the top families (*Chitinophagaceae*, *Caulobacteraceae*, *Sphingomonadaceae*, *Bradyrhizobiaceae*, *Halomonadaceae*) held more than 90% of reads. The abundance of *Actinobacteria* was less (0.7%), whereas members of other phyla (*Deinococcus-Thermus*, *Cyanobacteria/Chloroplast*, *Fusobacteria*, and *Acidobacteria*) constituted a minor fraction of reads. The bacterial community in the studied ancient alluvium differs from other permafrost sediments, mainly by

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