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Linking Soil Metabolic Potential to Vegetation Type Across Landscape Positions in the East River Watershed, Colorado

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Different vegetation types are associated with a suite of different soil edaphic characteristics, nutrient cycling processes, and microbial assemblages and functions. Identifying associations between vegetation types and potential soil microbial functions may be the key to scaling up point observations from microbial ecological studies to watershed processes at kilometer scales. To provide genome-resolved insights into the association between soil microbial functions and vegetation types, we sampled soils at two depths in four different vegetation types (aspen, conifer, meadow, and sagebrush) in nine blocks distributed across the 275 km² East River watershed in Colorado, USA. These samples collected in 2016 were used for shotgun metagenomic sequencing and to measure soil edaphic characteristics. Over 6 million scaffolds >1kb have been assembled and >100 putative genomes have been preliminary binned. There is evidence that Thaumarchaeota may dominate some soil microbial communities, adding support for this pattern observed in previous genome-resolved studies of soil. In the summer of 2017, 196 samples were collected from four sites to test how soil microbial metabolic potential varies across the growing season. These will be sequenced under a newly awarded Joint Genome Institute Community Science Project award.