Metadata

**Plant-driven changes in soil microbial communities influence seed germination through negative feedbacks**Miller, E.C., Perron, G.G., Collins. C.D.

**Data file**: Miller\_et-al\_FungalCommunities.csv

**Description:** ASV sequences for fungi in soil conditioned for three months by seven different plant species.

**Columns**

SampleID: A unique identifier for each soils sample.

Plant: the conditioning treatment, or species identity of plant that conditioned the soil.

*Bromus* = *Bromus inermis*

*Desmodium*=*Desmodium illinoense*

*Solidago* = *Solidago Canadensis*

*Geum* = *Geum candense*

*Ageratina* = *Ageratina altissima*

*Pycnanthemum* = *Pycnanthemum tenuifolium*

*Poa* = *Poa pratensis*

*Control = Field-collected soils that were in conetainer pots for three months, but did not contain plants.*

*Day0 = Field-collected soils that were not conditioned by plants. Day 0 provided the “baseline” for the three month conditioning period.*

Conetainer: The size of the pot in which the soil-conditioning occurred. NA means that soils were never conditioned (i.e., Day0 soils).

Columns D-SK: Each column is a unique amplicon sequence variant (ASV), similar to operational taxonomic units (OTUs) used in traditional metagenomic pipelines, but based on estimates of true sequence variation rather than grouping by sequence similarity