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From the article: Management effects on temporal and spatial variations in temperate grassland microbiomes

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The condition table (condition_table.csv) corresponds to the description of the sample code, indicating to which treatment (vegetation management practice), block and material it belongs. The sample code (first column) is included in the file names (fastq files). However, information about the sequence (ITS or 16S), the year and the library are in the folder name where these files are included (see the following Zenodo repositories).

The raw sequencing data can be find following the links:

Amplicon sequencing data – 2020:

https://zenodo.org/uploads/17541396?token=eyJhbGciOiJIUzUxMiJ9eyJpZCI6ImlwMGQxNzU0LTRhZWYtNDkzZS1iMDNjLWQzYjE2YzIxMmQ0NSIsImRhGEiOnt9LCJyYW5kb20iOiI1YTAwNWY3MDYxNTA4MDJiOGM5ZTFkZWY4OTZmZml2NiJ9.MxsRCMOPLqwyrBPVfb-CFTIMCWP7ygjmbKQGnV3_Slz8z0NVfBIIQ6CgMBzD-drEBA1e5dYeSyzfyj-td11eow

Amplicon sequencing data – 2021:

Amplicon sequencing data – 2022:

In the condition table, “Perm_exclosure” is the term used to define samples from the passive succession plots, and “Perm_access” for samples from the grazing plots.