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

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The metadata of the sample are present in the condition_table.csv document, and include 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). The same metadata table should be used for each dataset (meaning each sampling year, and both 16S and ITS analysis). 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://doi.org/10.5281/zenodo.17541396

Amplicon sequencing data – 2021: https://doi.org/10.5281/zenodo.17581178

Amplicon sequencing data – 2022: https://doi.org/10.5281/zenodo.17589353

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.