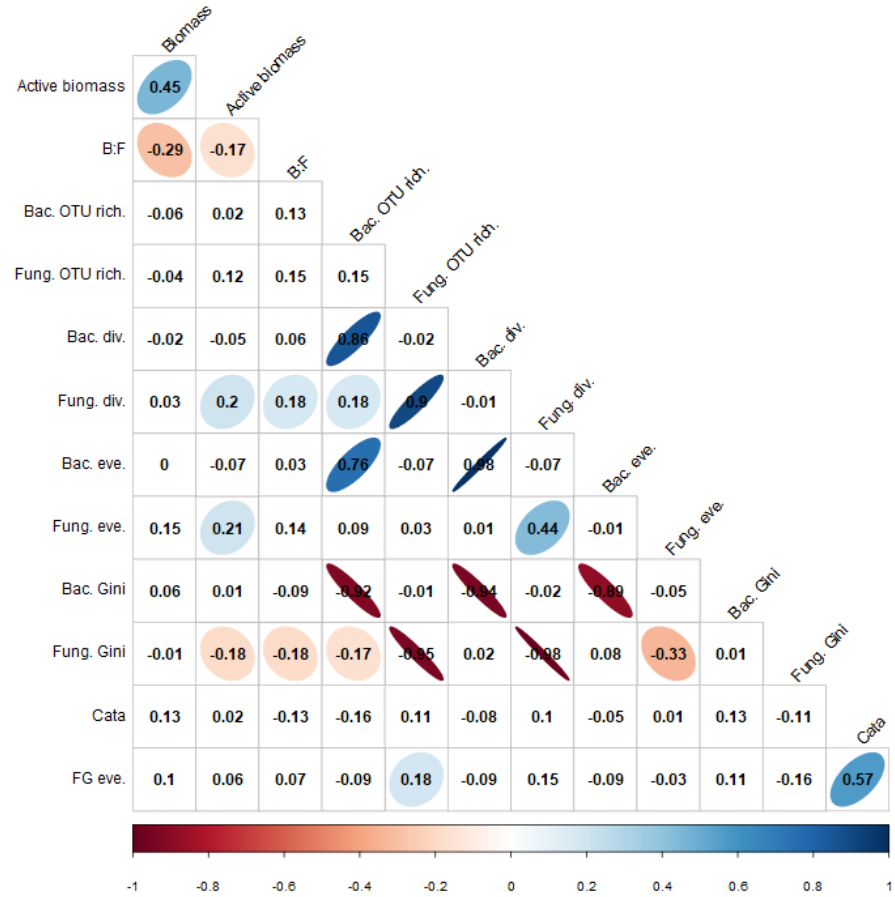


Supplementary material II-S4

A. Correlations between the microbial variable



B. The structured list of variables used in the analyses.

Variable group	Variable name (acronyms)		Definition and measurement method	Hypotheses and analyses referring to it
Soil chemical properties	Soil carbon content (TOC)		Measured on top soil (0-10 cm) using TOC analyzer	Hypothesis 4, Fig. 5, Suppl. S10
	Soil carbon to nitrogen ratio (C:N)		Calculated on top soil (0-10 cm) measurements	Hypothesis 4, Fig. 5, Suppl. S10
	Soil carbon to nitrogen ratio (C:P)		Calculated on top soil (0-10 cm) measurements	Hypothesis 4, Fig. 5, Suppl. S10
	Soil pH (pH)		Measured on top soil (0-10 cm) using 1:2.5 soil - water solution	Hypothesis 4, Fig. 5, Suppl. S10
	Soil water content (RH)		Measured on 25 g of top soil (0-10 cm) air-dried at 40 °C	Hypothesis 4, Fig. 5, Suppl. S10
Tree Species Richness	Tree species richness		Number of tree species per plot	Hypothesis 1&4, Fig. 1&5, Suppl. S7&10
Soil microbial community facets	Microbial biomass	Total microbial biomass (Biomass)	Total microbial biomass calculated from PLFA markers measurements	Hypotheses 1-4, Fig. 1-5, Suppl. S3, S7-10
		Active microbial biomass (Active biomass)	The active fraction of the total microbial biomass calculated from substrate-induced respiration (SIR, Scheu 1992)	Hypotheses 1-4, Fig. 1-5, Suppl. S3, S7-S10
	Taxonomic profile	Bacteria to fungi ratio (B:F)	Bacteria to fungi ratio was calculated using microbial functional groups biomass measured by PLFA analyses	Hypotheses 1-4, Fig. 1-5, Suppl. S3, S6-S10

		Bacteria Shannon diversity (Bac. div.)	Bacterial community Shannon diversity calculated from 16S sequencing data	Hypotheses 1-4, Fig. 1-5, Suppl. S3, S6-S10
		Fungi Shannon diversity (Fung. div.)	Fungi community Shannon diversity calculated from ITS sequencing data	Hypotheses 1-4, Fig. 1-5, Suppl. S3, S6-10
	Functional profile	FG evenness	The absolute or relative abundance of functional genes measured by qPCR. See Suppl. S5 for a complete list of measured functional genes	Hypotheses 1-4, Fig. 1-4, Suppl. S5 & S7-9
		Catabolism functional genes (Cata)	Sum of the abundance of functional genes involved in carbon catabolism. The variables can be calculated on the absolute or relative abundance of the functional genes and will be specified.	Hypotheses 1-4, Fig. 1-4, Suppl. S5 & S7-9
Soil physiological potential	Substrate induced-respiration (SIR)		Substrate-induced respiration (i.e. CO ₂ production during six hours after substrate addition) of fourteen substrates (i.e. 5 saccharides, 4 amino-acids, and 5 carboxylic-acids) measured with the Microresp [®] method.	Hypotheses 1-4, Fig. 1-5, Suppl. S5 & S7-9
	Substrate-induced respiration efficiency (SIR efficiency)		Pielou evenness of the substrate-induced respiration (i.e. CO ₂ production during six hours after substrate addition) of fourteen substrates (i.e. complete list in Suppl. S3)	Hypotheses 1-4, Fig. 1-5, Suppl. S5 & S7-9
	Substrate-induced respiration response range (SIR range)		The absolute difference of CO ₂ production between alanine induced respiration and oxalic-acid induced respiration measured with the Microresp [®] method.	Hypotheses 1-4, Fig. 1-5, Suppl. S5 & S7-9
Ecosystem function	Microbial respiration (M. resp.)		Soil basal respiration measured (SIR, Scheu 1992)	Hypotheses 1-4, Fig. 1-5, Suppl. S7-9