Supplementary materials

Microbial quantification and metabarcoding

The DNA and RNA were co-extracted from 500 mg of -80°C frozen soils following the Griffiths et al., (2000) protocol with some modifications according to Nicolaisen et al., 2008 and Monard et al., 2013. Lysing Matrix E tubes (MP Biomedicals, California, USA) were used for the cell lysis and agitated at 30 m.s⁻¹ for 3 min in a bead beating. Glycogen (0.1 mg) was added to precipitate nucleic acids for 2 h at 4 °C that were subsequently pelleted by centrifugation at 18 000 g for 30 min at 4 °C. Nucleic acids were resuspended in 50 µl of DNase-RNase-free water. The DNA and RNA qualities were assessed on a 1% agarose gel and on a nanodrop spectrophotometer (ND-1000, Nyxor Biotech, Palaiseau, France). DNA quantity was assessed by the Qubit fluorimetric (Invitrogen, Carlsbad, California, USA) following the instruction of the broad range quantification. Half of the extract was stored at-20°C before further DNA-based analyses on (pristine soil and 0 days samples); the other half was subjected to a DNAse treatment according to the manufacturer's instructions (Promega, Madison, WI, USA) for further RNA-based analyses on (pristine soil and - 0, 3, 7, 21 and 49 days samples). The absence of DNA was checked by none amplification using PCR on the 16S rRNA gene. RNA quantity was assessed by the Qubit fluorimetric and 200 ng of RNA were used to run the reverse transcription (RT) according to the manufacturer's instructions (RevertAid RT kit, Thermo Scientific, USA). Half of the cDNA products was stored at -20 °C to prepare 16S and ITS1 rRNA amplicons for Illumina sequencing and the other half was used for the quantification of the total bacteria and fungi by quantitative PCR (qPCR) as described further.

The total bacterial (16S rRNA gene) and fungal (ITS2 region) abundances were quantified by qPCR, runned in duplicate, on the BioRad CFX Connect Real-Time detection System. The qPCR reactions were conducted in a final volume of 15 μ l using 1 ng of soil DNA or 2 μ l cDNA 10 times diluted (i.e. 0.8 ng RNA) in 1x iQ SYBR Green Supermix (Bio-Rad Laboratories, USA) with 0.67 mg/ml BSA (New England BioLabs, USA). The following primer sets were used for the bacteria (0.25 μ M each) and fungi (0.3 μ M, 0.23 μ M and 0.075 μ M): 341F and 534R (5'-ATTACCGCGGCTGCTGGCA-3') (Muyzer et al., 1993), gITS7 (5'-

GTGARTCATCGARTCTTTG -3') (Ihrmark et al., 2012), ITS4 (5'-TCCTCCGCTTATTGATATGC-3') (White et al., 1990) and ITS4a (5'-TCCTCGCCTTATTGATATGC-3') (Ihrmark et al., 2012), respectively. The qPCR program for bacteria consisted in 5 min at 95°C, followed by 34 cycles of 15 s at 95°C, 30 s at 60°C, 30 s at 72°C, 5 s at 80°C and a final melting curves step with an increase of 0.5° C/ 5 s from 65°C to 95°C. For fungi, the qPCR program consisted in 5 min at 95°C, followed by 35 cycles of 15 s at 95°C, 30 s at 56°C, 40 s at 72°C, 5 s at 78°C and the final melting curves step. Standard curves for each assay were generated by serial dilutions to obtain numbers of copies ranging from 10⁸ to 10² of linearized plasmids with cloned fragments of the genes of interest (R² = 0.98 and 0.99 for bacteria and fungi, respectively).The quantities of ITS and 16S rRNA gene fragments were expressed in gene copy numbers per g of dry soil and used to replace the normalized number of sequences obtained from the metabarcoding analysis in each samples.

The bacterial and fungal 16S rRNA and ITS1 libraries were constructed using a twostep PCR approach "16S metagenomics sequencing library preparation" protocol given by Illumina. The following primer sets were used for the bacteria and fungi: 341F (5'-CCTACGGGNGGCWGCAG-3') and 785R (5'-GACTACHVGGGTATCTAATCC-3') (Klindworth et al 2012) and ITS1f (5'-CTTGGTCATTTAGAGGAAGTAA-3') (Gardes and Bruns, 1993) and ITS2 (5'-GCTGCGTTCTTCATCGATGC-3') (White et al., 1990). Each primer set contained the following overhang adapters: forward overhang (5'-ACACTGACGACATGGTTCTACA-3') and reverse overhang (5'-TACGGTAGCAGACTTGGTCT-3'). The first PCR was carried out in two replicates in a total volume of 25 μ L containing each bacterial or fungal primer (0.2 μ M), 12.5 μ l 2X *TransTaq* HiFi PCR SuperMix (1X), 0.5 μl T4 gp32 (100 ng/μl), 2 μl DNA or cDNA and ultrapure water to reach the final volume. The amplification conditions were as follows: for bacteria, 3 min at 94 °C, 30 cycles of 30 s at 94 °C, 30 s at 55 °C and 30 s at 72 °C and a final 10 min extension step at 72 °C; for fungi, 4 min at 94 °C, followed by 35 cycles of 30 s at 94 °C, 30 s at 52 °C and 30 S at 72 °C and a final 10 min extension step at 72 °C. The amplicon quality was assessed on a 1 % agarose gel and the replicate amplicons were pooled and sent to the Génome Québec Innovation Center for normalization, barcoding, multiplexing and Illumina paired-end $(2 \times 300 \text{ bp})$ MiSeq sequencing.



Figure S1 Rarefaction curves of total and active bacteria (from DNA and cDNA) at the different times during the soil incubation and before and after normalization. C=bare soil, CS: bare soil with litter addition, A: soil previously planted with *A. thaliana*, AS: soil previously planted with *A. thaliana* and with plant litter addition, T: soil previously planted with T. *aestivum*, TS: soil previously planted with T. *aestivum* and with plant litter addition. The different sampling times were t = i, 0, 3, 7, 21 and 49 days, i: original soil before soil plant-growing.



Figure S2. Rarefaction curves of total and active fungi (from DNA and cDNA) at the different times during the soil incubation and before and after normalization. C=bare soil, CS: bare soil with litter addition, A: soil previously planted with *A. thaliana*, AS: soil previously planted with *A. thaliana* and with plant litter addition, T: soil previously planted with T. *aestivum*, TS: soil previously planted with T. *aestivum* and with plant litter addition. The different sampling times were t = i, 0, 3, 7, 21 and 49 days, i: original soil before soil plant-growing.



Figure S3. Ternary plots describing the distribution of the bacterial and fungal DNA-based or RNAbased OTUs between the soil treatments at the end of the plant-soil experiment (grey circles) showing the DNA-based or RNA-based enriched or activated OTUs by *A. thaliana* (dark green circles) or by *T. aestivum* (blue circles), depleted or inhibited OTUs by *A. thaliana* (light green) or by *T. aestivum* (light blue), the enriched or activated OTUs by both plants (orange) and the depleted or inhibited by both plants (yellow). This analysis was performed on the abundances (copy number of genes) for the total bacteria and fungi. Each circle depicts one individual OTU and its position is determined by the contribution of the indicated modality to the abundance. The size of the circle reflects the relative abundance of the OTU.

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Figure S4: Relative abundance dynamics of the 12 main active soil bacteria enriched by *A. thaliana* **along the 49 day of incubation in the different soil treatments wihtout and with litter addition.** The error bars indicate the standard error (n=4) and the scale differ according to the OTU and ranging from 0.06 to 1 ‰.



Figure S5: Relative abundance dynamics of the 9 main active soil bacteria enriched by *T. aestivum* **along the 49 day of incubation in the different soil treatments wihtout and with litter addition.** The error bars indicate the standard error (n=4) and the scale differ according to the OTU and ranging from 0.2 to 2 ‰.



Figure S6: Relative abundance dynamics of the 17 main active soil fungi enriched by *A. thaliana* **along the 49 day of incubation in the different soil treatments wihtout and with litter addition.** The error bars indicate the standard error (n=4) and the scale differ according to the OTU and ranging from 0.15 to 150 ‰.



Figure S7: Relative abundance dynamics of the 4 main active soil fungi enriched by *T. aestivum* **along the 49 day of incubation in the different soil treatments wihtout litter and with litter addition.** The error bars indicate the standard error (n=4) and the scale differ according to the OTU and ranging from 0.2 to 10 ‰.



Figure S8 Powered partial least squares discriminant analysis (PPLS-DA) describing the bacterial and fungal community structure at the OTU level overtime for each soils without litter. On the correlation circle, the OTUs in red corresponded to the most abundant OTUs that contributed significantly to the differences according ANOVA. In the bare soil (B) the composition of the active bacterial community at day 0 was significantly different from that at days 3, 7, 21 and 49 and the composition was also different between day 3 and days 7, 21 and 49. The OTUs that were different between day 0 and day 3 were more abundant in day 0 and affiliated to Planctomycetes (OTUs 1202, 769 and 804), Acidobacteria (OTUs 671 and 686), Gemmatimonadetes (OTUs 1611 and 963), Detlaproteobacteria (OTU 424), Chloroflexi (OTU 1242) and Gammaproteobacteria (OTUs 730). The OTUs that were different between day 0 and day 7 were more abundant in day 0 and affiliated to Acidobacteria (OTUs 671 and 686), Actinobacteria (OTUs 204, 856 and 864), Alphaproteobacteria (OTUs 154 and 227), Detlaproteobacteria (OTU 424), Planctomycetes (OTU 859) and Gammaproteobacteria (OTUs 730). The OTUs that were different between day 0 and days 21 and 49 were more abundant in day 0 and affiliated to Acidobacteria (OTUs 31 and 70), Actinobacteria (OTUs 10 and 35), Firmicutes (OTUs 1, 38 and 7), Deltaproteobacteria (OTU 61), Alphaproteobacteria (OTUs 64 and 33) and Chloroflexi (OTU 112). The OTUs that were different between day 3 and day 7 were more abundant in day 3 and affiliated to Planctomycetes (OTUs 1073, 1389, 2106 and 982) and Actinobacteria (OTUs 364 and 864). The OTUs that were different between day 3 and day 21 were more abundant in day 3 and affiliated to Planctomycetes (OTUs 2106, 272 and 982), Actinobacteria (OTUs 364 and 471), Alphaproteobacteria (OTU 334). The OTUs that were different between day 3 and day 49 were more abundant in day 3 and affiliated to Actinobacteria (OTUs 325, 340, 364, 471, 62 and 864) and Alphaproteobacteria (OTUs 242 and 334). In the bare soil (B) the composition of the active fungal community at day 0 was significantly different from that at days 3, 7 and 21 and the composition was also different between day 3 and day 7. At the beginning and at the end of the incubation the active fungal composition was not different. The OTUs that were different were all

more abundant at day 0 or day 3 and all affiliated to *Ascomycota* (*Sordiariomycetes*: OTUs 1, 15, 29, 3, 30 and 40; Dothideomycetes: OTUs 2, 6, 7 and 9) or unknown fungi (OTUs 62, 39, 36 and 88). In the soil that grew *A. thaliana* (A) the composition of the active fungal community at day 0 was different from that at day 3. The composition was also different between day 3 and days 7 and 49. The OTUs that were different were all more abundant at day 3 and affiliated to *Ascomycota* (*Sordiariomycetes*: OTUs 1, 15, 23, 29, 30 and 40; *Dothideomycetes*: OTUs 24, 51, 7 and 9). In the soil that grew *T. aestivum* (T) the composition of the active fungal community at day 3 was different from all the others days and were more abundant at day 3 and affiliated to *Ascomycota* (*Sordiariomycetes*: OTUs 1, 15, 23, 29, 30, and 3; *Dothideomycetes*: OTUs 24, 2, 6, 7 and 9).



Figure S9: Powered partial least squares discriminant analysis (PPLS-DA) describing the bacterial and fungal community structure at the OTU level overtime for each soils with litter addition. On the correlation circle, the OTUs in red corresponded to the most abundant OTUs that contributed significantly to the differences according ANOVA. In the bare soil (B-litter) the composition of the active bacterial community at day 21 was significantly different from that at days 3 and 7. Most of the OTUs that were different were more abundant at day 21 and affiliated to Alphaproteobacteria (OTUs, 48, 336 and 432) and Deltaproteobacteria (OTUs 24, 27, 43, 163, 165 266 and 548). The others were more abundant at day 3 and affiliated to Actinobacteria (OTUs 62 and 104). The composition of the active fungal was only different between day 7 and day 21. The OTUs that were different between were also more abundant at day 21 and affiliated to Ascomycota (Sordariomycetes: OTUs 57 and 85; Saccharomycetes: OTU 290) and Zygomycota (OTUs 28, 13 and 92). In the soil that grew A. thaliana (A-litter) the composition of the active bacterial community at day 3 was significantly different from that at days 7 and 49. The composition was also different between day 7 and day 49. The OTUs that were different were more abundant at day 3 and mainly affiliated to Alphaproteobacteria (Rhizobiales: OTUs 2, 3, 4, 5, 16, 17, 140). The others were more abundant at day 49 and affiliated to Deltaproteobacteria (Myxococcales: OTUs 548, 24 and 103). The composition of the active fungal at day 0 was different from that at days 3, 7, 21 and 49. The composition was also different between day 3 and days 7, 21 and 49 and between day 7 and day 49. The OTUs that were different were more abundant at days 0 or 3 and mainly affiliated to Ascomycota (Sordariomycetes: OTUs 29, 15, 40, 1, 113 and 30). The others were more abundant at day 49 and affiliated to Zygomycota (OTU 541) and Ascomycota (Sordariomycetes: OTU 8). In the soil that grew T. aestivum (T-litter) the composition of the active fungal community was only different between day 0 and day 49. The OTUs that were different were more abundant at day 0 and affiliated Ascomycota (Sordariomycetes: OTUs 23, 29, 15, 40, 1 and 30; Dothideomycetes: OTUs 51, 9 and 7).

Bacteria



Fungi CA PCA CA PCA 1.0 0.5 T-litter-t49 0.8 T-litter-t49 T-t0 11.00 % 0.4 0.6 58.53 % A-itter-t49 11.49 % B-litter-t49 B-litter-t49 A-litter-t49 T-t0 0.2 -0.5 0.0 A-t0 Ņ B-t0 A-10 10 -0.2 0.0 0.5 1.0 42.04 % 2.0 0.2 0.4 0.6 1.0 -0.5 1.5 -1 2 43.39 % 3 -0.2 0.0 0.8 1 29.77 % 2 3 60.12 % вмс Coinertia axis ĉ Coinertia axis 1 Coinertia axis 1 Coinertia axis 1 Coinertia axis 1

Figure S10: Co-inertia analysis of the relationships between active bacteria and active fungi (RNAbased OTUs), soil carbon and nutrients pools according to soils treatments 7 days after litter addition for bacteria and at the beginning (day 0) or 49 days after litter addition for fungi. The coinertia analysis was performed between a correspondence analysis (CA) of the OTUs composition according to soils and a principal component analysis (PCA) of the carbon and nutrients contents according to soils. The clusters (OTUs) in red, green and blue are the OTUs that contributed significantly to the differences observed between the bare soil and the soil that grew *A. thaliana*, between the soil that grew *A. thaliana* and the one that grew *T. aestivum* and between the bare soil and the soil that grew *T. aestivum* according to ANOVA's, respectively. For bacteria, the OTUs were more abundant in the bare soil and affiliated to *Alphaproteobacteria* (*Caulobacteraceae* OTUs 109,301, 432; *Sphingomonadaceae*: OTU 65), *Bacteroidetes* (*Cytophagaceae* OTU 322, *Microscillaceae* OTU 522), *Gammaproteobacteria* (*Burkholdericeae* OTU 326 and *Cellvibrio* OTU 8) and Actinobacteria (*Catenulispora* OTU 182). The relative abundances ranging from 1.6 to 112 ‰ in the bare soil. For fungi at day 0, the OTUs that were more abundant in the bare soil compared to the soil that grew *A. thaliana* were affiliated to *Ascomycota* (*Sordariomycetes*: OTUS 1, 15, 29 and 30; *Dothideomycetes*: OTUS 2, 6, 7 and 9) while the ones that were more abundant in the soil that grew *A. thaliana* were affiliated to *Basidiomycota* (*Tremellales* OTU 4 and *Zygomycota* (*Mortierella* OTU 5). The OTUs that were more abundant in the soil that grew *T. aestivum* compared to the bare soil were affiliated to *Basidiomycota* (*Solicoccozyma* OTU 16), *Ascomycota* (*Epicoccum* OTU 24; *Acrostalagmus* OTU 40). The OTUs that were more abundant in the soil that grew *A. thaliana* compared to the one that grew. *T aestivum* were affiliated to *Zygomycota* (*Mortierella*, OTUS 11 and 5), *Ascomycota* (*Sordariomycetes* OTUS 19 and 8) and unknown fungi. The relative abundances ranging from 0.3 to 481 ‰ in all the soils. For fungi at day 49, the OTUs that were more abundant in the soil that grew *A. thaliana* compared to the bare soil were affiliated to *Zygomycota* (*Mortierella* OTUS 11, 13, 21, 28 and 5) and *Basidiomycota* (*Solicoccozyma* OTUs 10 and 16; *Tremellales* OTU 4).



Figure S11: Microbial community richness in the original soil and after terminating the plant-soil experiment (*A. thaliana, T. aestivum* and bare soil). The richness (number of OTUs) of the total bacteria and fungi were obtained from DNA extracts and the richness (number of OTUs) of active bacteria and fungi from RNA extracts. The different letters indicate significant differences between treatments according to ANOVA and Tukey's tests (n=4, p<0.05).

Supplementary references

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