



Additional file 4 Distribution of read pair alignments to the genomes of the soil microorganisms. **(A, B)** Distribution of read pair alignments to the 13 soil microorganisms calculated with the Samtools software [27] and expressed as a percentage (%) of total alignments to the microcosm genome. **(C, D)** Distribution of unique read pairs mapping to genes of the 13 soil microorganisms, counted using HTSeq [29] and expressed as a percentage (%) of total unique read pairs mapping to genes in the microcosm genome. **(E, F)** Percentage (%) of expressed genes (more than one read pair) calculated as compared to the total predicted genes for each soil microorganism. Mean and standard error values of three replicates are reported for each condition: the simplified soil microcosm collected at the beginning of the experiment (SSM₀) and 24 h after incubation either without exogenous fungi (SSM), with the biocontrol agent