

Additional file 6. Pearson's correlation coefficients among replicates and conditions for RNA-Seq analysis.

Condition ^a	Correlations among replicates ^b		Correlations among conditions ^b				
	2 nd replicate	3 rd replicate	SSM ₀	SSM	SSM+T	SSM+A	SSM+T+A
SSM ₀	0.968	0.989	1				
SSM	0.996	0.963	0.854	1			
SSM+T	0.997	0.995	0.855	0.982	1		
SSM+A	0.989	0.994	0.875	0.992	0.983	1	
SSM+T+A	0.990	0.986	0.877	0.975	0.969	0.987	1

^a Five different conditions were analyzed in triplicate (named from 1 to 3) by RNA-Seq: 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 *Trichoderma atroviride* (SSM+T), with the plant pathogen *Armillaria mellea* (SSM +A) or with both (SSM+T+A).

^b Pearson's correlations between the first replicate and the second or the third replicates were calculated for each condition based on the expression levels of all genes of the simplified soil microcosm ($P = 0.00001$).

^b Pairwise Pearson's correlations among the five different conditions of the simplified soil microcosm were calculated based on the mean expression levels of all genes ($P = 0.00001$).