

Additional file 3. RNA-Seq sequencing and mapping results for each replicate.

Condition ^a	Replicate	Sequenced read pairs ^b	Filtered read pairs (%) ^c	Mapped reads (%) ^d	Unique read pairs (%) ^e	Multi read pairs (%) ^f	Unique read pairs mapping to genes (%) ^g
SSM ₀	1	54,867,635	46,512,002 (85)	45,466,335 (98)	10,442,923 (23)	3,5023,412 (77)	8,981,515 (86)
	2	53,137,108	44,843,649 (84)	43,827,359 (98)	11,547,703 (26)	3,2279,656 (74)	10,025,907 (87)
	3	47,288,179	41,240,720 (87)	40,375,071 (98)	10,878,932 (27)	2,9496,139 (73)	9,482,541 (87)
SSM ₀	1	53,923,704	45,334,672 (84)	44,120,949 (97)	8,078,247 (18)	3,6042,702 (82)	6,228,246 (77)
	2	57,625,098	48,992,138 (85)	47,848,571 (98)	12,114,995 (25)	3,5733,576 (75)	9,893,233 (82)
	3	47,957,873	42,184,246 (88)	41,009,367 (97)	10,371,301 (25)	3,0638,066 (75)	8,358,839 (81)
SSM+T	1	53,770,221	47,001,494 (87)	45,259,937 (96)	10,679,232 (24)	3,4580,705 (76)	8,739,437 (82)
	2	74,788,948	66,797,521 (89)	64,626,032 (97)	14,367,754 (22)	5,0258,278 (78)	11,619,984 (81)
	3	60,209,616	50,657,014 (84)	48,771,238 (96)	11,850,153 (24)	3,6921,085 (76)	9,648,304 (81)
SSM+A	1	45,543,588	40,539,838 (89)	39,071,436 (96)	7,318,891 (19)	3,1752,545 (81)	5,676,838 (78)
	2	47,244,943	39,689,851 (84)	38,478,021 (97)	8,622,139 (22)	2,9855,882 (78)	6,919,365 (80)
	3	54,715,166	46,315,044 (85)	44,902,907 (97)	8,531,929 (19)	3,6370,978 (81)	6,710,241 (79)
SSM+T+A	1	51,885,907	43,582,841 (84)	41,864,067 (96)	8,676,131 (21)	3,3187,936 (79)	6,847,827 (79)
	2	80,245,613	71,084,866 (89)	68,440,718 (96)	14,731,717 (22)	5,3709,001 (78)	11,857,496 (81)
	3	47,733,908	41,138,248 (86)	39,542,785 (96)	8,746,714 (22)	3,0796,071 (78)	7,070,119 (81)

^a Five different conditions were analysed 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 Read pairs of 100 nucleotides were obtained by the RNA-seq protocol followed by Illumina sequencing.

^c Read pairs passing the quality check and the corresponding percentage (%) of the sequenced read pairs.

^d Read pairs mapped to the microcosm genome and the corresponding percentage (%) of filtered read pairs.

^e Read pairs unambiguously mapped to unique locations (unique read pairs) to the microcosm genome and the corresponding percentage (%) of total read pairs mapped to the microcosm genome.

^f Read pairs mapped to more than one location (multi read pairs) to the microcosm genome and the corresponding percentage (%) of total read pairs mapped to the microcosm genome.