

**Supplementary Table S1.** Number of NGS-RNASeq reads before and after quality check on the raw sequencing data from *Trichoderma hamatum* FBL 587.

**Supplementary Table S2.** Trimmed Mean of M-values (TMM) obtained by normalization applied to the raw fragment from *Trichoderma hamatum* FBL 587.

**Supplementary Table S3.** Reads Per Kilobase Million (RPKM) obtained by normalization applied to the raw fragment from *Trichoderma hamatum* FBL 587.

**Supplementary Table S4.** The concentrations of DDT metabolites and isomers detected in soil and plant organs (mg/kg) of two *Cucurbita pepo* accessions inoculated with *Trichoderma hamatum* FBL 587.

ND – not detected,  $\Sigma$ DDT = sum of DDT metabolites and isomers.

**Supplementary Table S5.** Carbohydrate active enzymes (CAZymes) in *Trichoderma hamatum* FBL 587 identified with the dbCAN2, which integrates three different tools: (1) HMMER, (2) DIAMOND, (3) Hotpep (see text).

**Supplementary Table S6.** The secondary metabolite gene clusters identification in *Trichoderma hamatum* FBL 587 performed with antiSMASH v. 6.0.0 (see text).

**Supplementary Table S7.** The secondary metabolite gene clusters identification in *Trichoderma asperellum* CBS 433.97 performed with antiSMASH v. 6.0.0 (see text).

**Supplementary Table S8.** The secondary metabolite gene clusters identification in *Trichoderma atroviride* IMI 206040 performed with antiSMASH v. 6.0.0 (see text).

**Supplementary Table S9.** The secondary metabolite gene clusters identification in *Trichoderma gamsii* T6085 performed with antiSMASH v. 6.0.0 (see text).

**Supplementary Table S10.** The secondary metabolite gene clusters identification in *Trichoderma hamatum* GD12 performed with antiSMASH v. 6.0.0 (see text).

**Supplementary Table S11.** The secondary metabolite gene clusters identification in *Trichoderma lixii* MUT3171 performed with antiSMASH v. 6.0.0 (see text).

**Supplementary Figure S1.** Low expression filtering step on transcriptome sequencing data from *Trichoderma hamatum* FBL 587; the algorithm calculated a Global Jaccard index of similarity (on the Y-axis) between the samples in function of different minimum normalized read counts (on the X-axis). The graphic shows the threshold at  $s = 13.294$  in which the replicates have the highest similarity.