Supplemental Material.

Table S1. Oligonucleotides used for qPCR analysis of the tomato development genes

Gene	Name	Sequence (5´-3´)
SUCS	SUCS-F	ATGAACCGAGTGAGGAATGG
SUCS	SUCS-R	GCTGGACCACCGTGATTAGT
ACCS	ACCS2-F	AAGCGCGATGAGGTTAGGTA
ACCS	ACCS2-R	AAAGTGGACGCAAATCCATC
GAI	GAI-F	ACCTCCGGTGAACAATCAAG
GAI	GAI-R	GAACGCATTTGAACCCAGAT

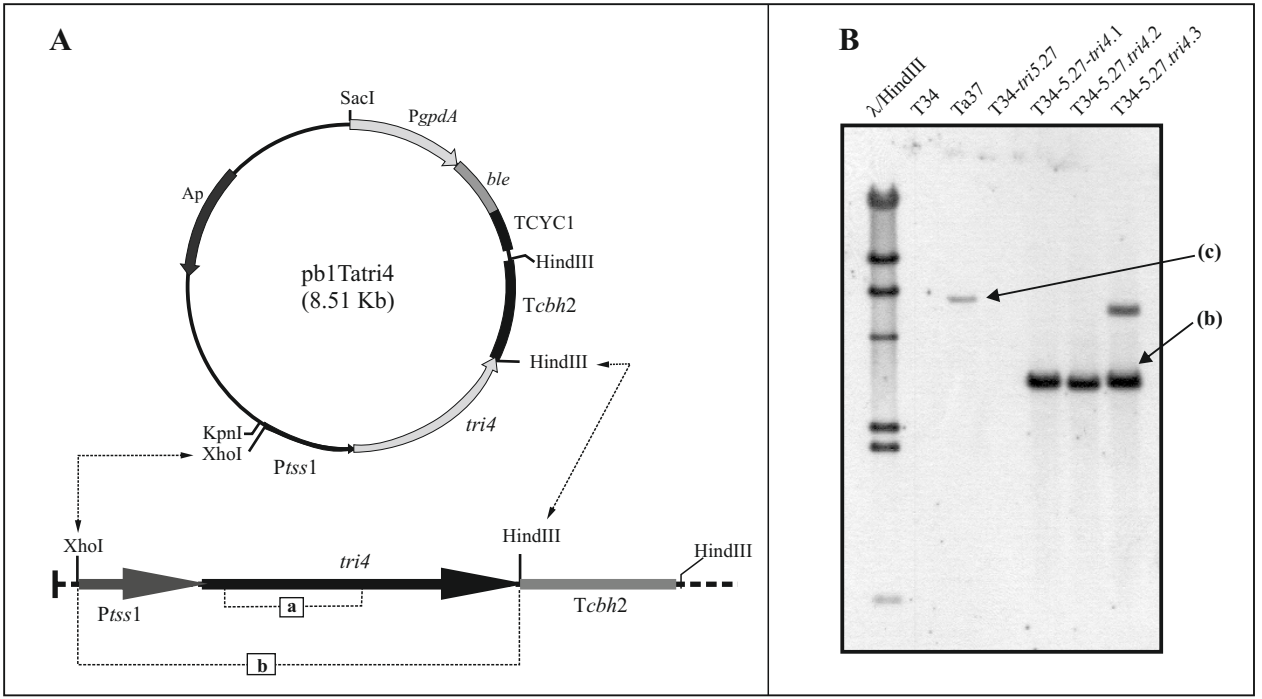


Figure S1. **A.** Representation of plasmid pb1Tatri4. *PgpdA,* promoter of the *gpdA* gene from *Aspergillus nidulans; ble,* phleomycin resistance gene from *Streptoalloteichus hindustanus; TCYC1,* transcriptional terminator of the cytochrome C oxidase I encoding gene from *Saccharomyces cerevisiae*; *tri4, Trichoderma arundianceum* IBT 40837 *tri4* gene; *Ptss1,* promoter of *tss1* gene from *Trichoderma harzianum* and *Tcbh2,* transcriptional terminator of the cellobiohydrolase 2 encoding gene from *Trichoderma reesei.* **B.** Southern of controls and *tri4* overexpressing transformants. DNAs were XhoI-HindIII digested. Note that *Trichoderma harzianum* CECT 2413 (T34) and T34-5.27 strains do not give any hybridization signal since the source of the *tri4* gene was the *Trichoderma arundinaceum* IBT 40837 (Ta37) strain, a producer of the trichothecene HA. **a)** 837 bp fragment used as a probe in this study; **b)** 2997 bp XhoI-HindIII fragment expected in the transformants as result of the hybridization with probe "a". **c)** 5911 bp signal corresponding to the endogenous XhoI-HindIII fragment of the Ta37 strain.

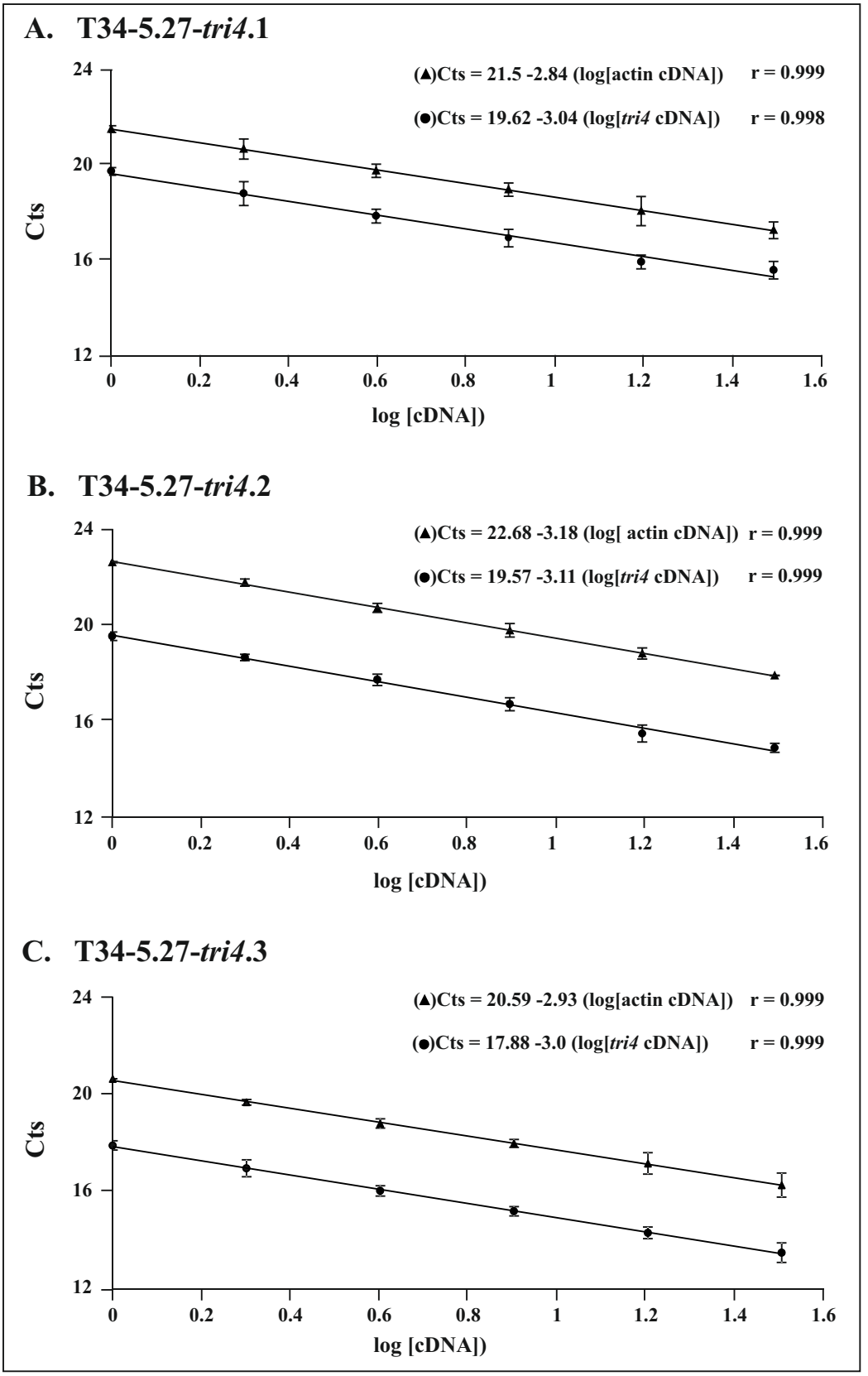


Figure S2. Calibration curves obtained for the genomic DNAs of the three T34-5.27-*tri4* expressing transformants analyzed in the present work to calculate the number of *tri4* gene copies integrated in the genome of each transformant (**A-C**). Oligonucleotides corresponding to *tri4* (lower calibration curve of each panel) and to the *actin* genes (upper calibration curve of each panel) were used for qPCR analysis (see Materials and Methods).

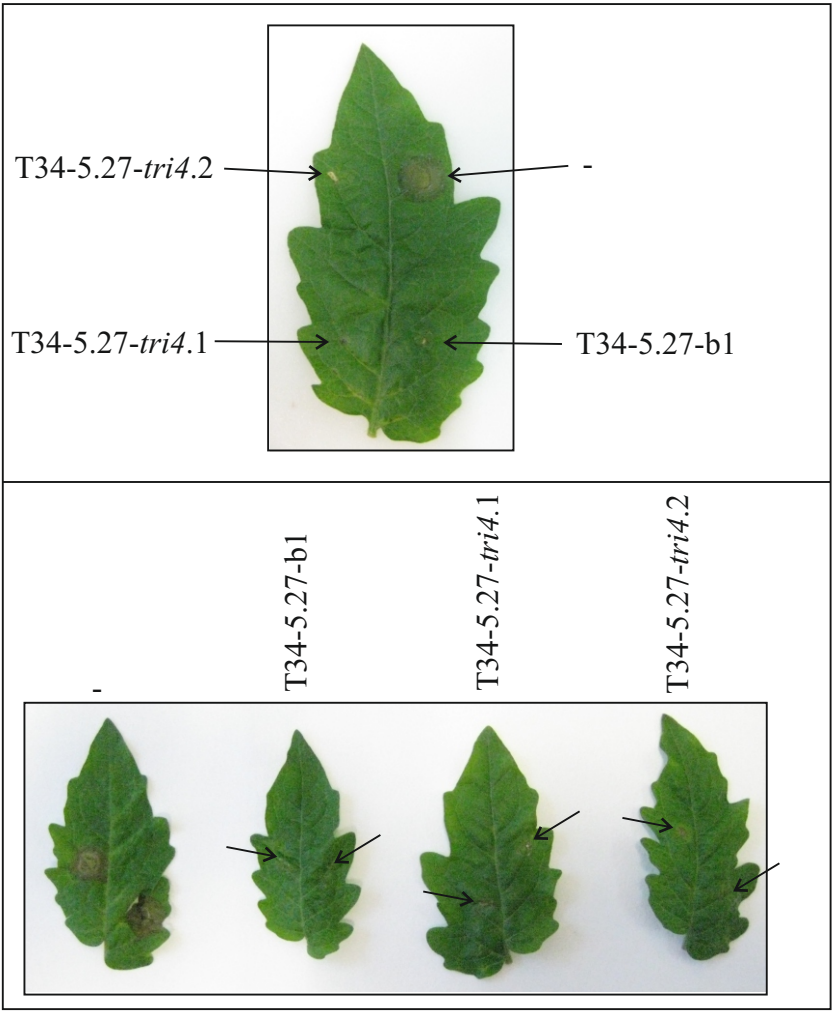
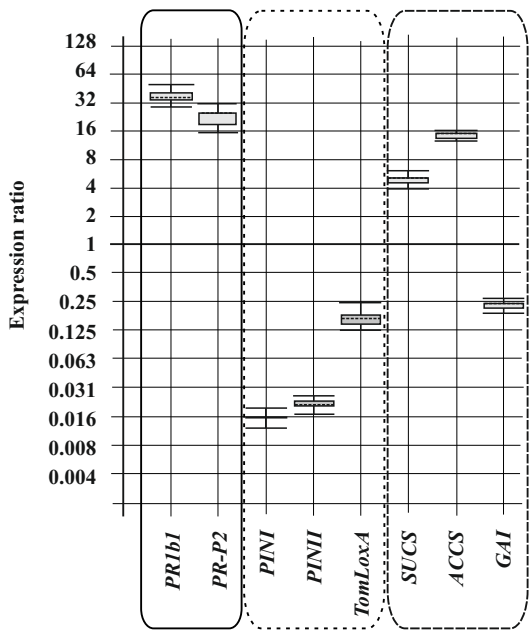
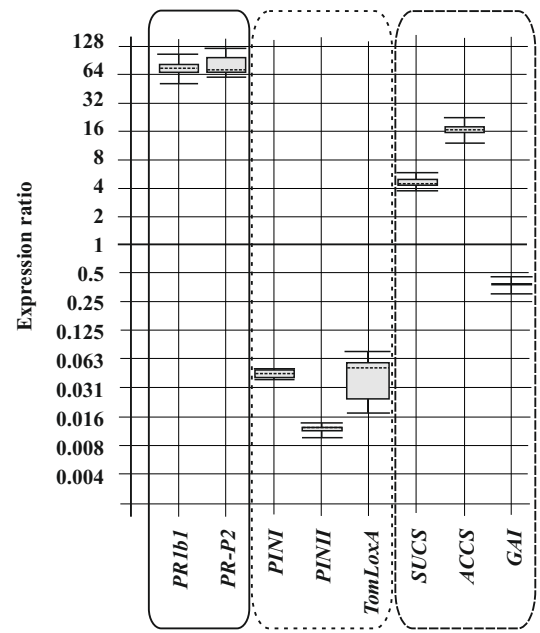


Figure S3. Pathogenicity assay of *B. cinerea* on detached tomato leaves of the Marmande variety. Leaves were inoculated with B05.10 spores in combination with broths from strains T34-5.27-b1, T34-5.27-*tri4*.1 and T34-5.27-*tri4*.2, compared with the control (-) in which uninoculated PDB medium was added.



Gene	Expression ratio	p(H1)
PR1b1	35.431*	0.023
PR-P2	20.341*	0.035
PINI	0.016*	0.000
PINII	0.022*	0.000
TomLoxA	0.169*	0.000
SUCS	4.679*	0.018
ACCS	14.110*	0.043
GAI	0.229*	0.000



Gene	Expression ratio	p(H1)
PR1b1	70.573*	0.000
PR-P2	77.378*	0.024
PINI	0.044*	0.000
PINII	0.012*	0.018
TomLoxA	0.042*	0.046
SUCS	4.595*	0.018
ACCS	16.328*	0.024
GAI	0.385*	0.018

Figure S4. qPCR analysis of the relative level of expression of five tomato defense-related genes (*PR1b1*, *PR-P2, PINI, PINII* and *TomLoxA*) and three development-related genes *(SUCS, ACCS* and *GA1*) in leaves collected from tomato plants whose seeds were coated with conidia of T34-5.27-b1 or T34-5.27-*tri4*.2 strains, in both cases the plants were infected with B05.10 (+B) after four weeks of growth (see Material and Methods) *versus* the level of expression of these genes in plants not inoculated with *Trichoderma* nor infected with B05.10 (-T-B)(**A, B**). Comparison and graphic representations were carried out using the REST© software (*****). Those values indicated with an asterisk (boxed in the graphic representation) correspond to genes significantly diffentially expressed ($p \leq 0.05$) in comparison with the reference condition.

***Pfaffl MW, Horgan GW, Dempfle L.** 2002. Relative expression software tool (REST) for group-wise comparison and statistical analysis of relative expression results in real-time PCR. Nucleic Acids Res **30**: e36.