

**Table S1. Specific primer pairs used in quantitative Real-time PCR experiments.**

Name	Sequences (5' → 3')	Gene
PR1-fw1	CCTCAAGATTATCTTAACGCTC	Pathogenesis-related 1 ( <i>PR1</i> )
PR1-rev1	TACCATTGCTTCTCATCAACC	
ICS1-fw1	GTTCCCTCTCCAAGAAATGTCC	Isochorismate synthase 1 ( <i>ICS1</i> )
ICS1-rev1	TCCTTCAAGGTCATCAAATC	
LOX f	GCCTCTCTTCTTGATGGA	Lipoxygenase 1 ( <i>Lox1</i> )
LOX r	GTAGTGAGCCACTTCTCCAA	
EIN2 f	GTTGCTAAGTGATGCTGTA	Ethylene-insensitive 2 ( <i>EIN2</i> )
EIN2 r	CGCTCAAGCATGCTGGGCC	
AREB-fw1	GCTCAACAGGAGGGAGTGG	Abscisic acid-responsive element binding transcription factor 2 ( <i>AREB2</i> )
AREB-rev1	CATCAACAGTCTTATGACTCAG	
APX1-fw1	GGTCTTGACATTGCTCTCA	Ascorbate peroxidase 1 ( <i>APX1</i> )
APX1-rev1	CTGGTGGCTCTGGCTTGTC	
SOS1-fw1	GGTGGACTTCTAAGCGCTAC	Salt overly sensitive 1 ( <i>SOS1</i> )
SOS1-rev1	GAAATTAGATGACAGCTCCCC	
Actin-fw	CACCACTGCTGAACGGGAA	Actin
Actin-rev	GGAGCTGCTCCTGGCACTTT	
ABC-fw2	CGAGACGTACCATGGCCAGAT	ABC transporter
ABC-rev2	CTCGTTGAGCGTTGTCGGACT	
Alcohol DH-fw	GCCGAATTTCTTCTTGAACCTACCT	Alcohol dehydrogenase
Alcohol DH-rev	GAATTGTAGCCGCCTCATCC	
CSRP-fw	CCCCTGTACTTACCAGGAGTA	Cellulose signaling related protein
CSRP-rev	GTAAGAGTTGCCGACAATGCC	
DH red-fw2	TTGAGAGAGTCCTGGTAGTCG	Short-chain dehydrogenase reductase
DH red-rev2	AACGCTTGCTTCGACGATATCG	
PG mutase-fw	AGGTTACCGAGCGACCTCACG	Phosphoglycerate mutase
PG mutase-rev	AATGACACCGGCGAGGATCTC	
MAT-fw	CATAAACGACCCGAACCGAC	Malic acid transporter
MAT-rev	TATACGACTAAGCCAATCACCT	
MFS-fw	GTGTCATTCTCATGGCTGGT	Major facilitator superfamily transporter
MFS-rev	TGATGAATCGAGTGAAGAAGGAG	
Monooxygenase-fw	CACTGGAGTCATGACACAGC	Steroid monooxygenase
Monooxygenase-rev	GTCGACAATGTCCTTCTTCCA	
p450-fw	GGGACATTATTCGGGAGAGG	Cytochrome p450 monooxygenase
p450-rev	GATGATGAAAGCCGATGACAG	
Tubulin-fw	GAATATCAACAATACCAGGATGC	$\beta$ -tubulin
Tubulin-rev	AGGATTGGTATTGATCATCAGCA	

**Table S2. *Trichoderma parareesei* T6 physiological processes differentially expressed in response to the presence of tomato plants in the culture medium.**

<b>Up-regulated</b>			
<b>Processes</b>	<b>Probe sets</b>	<b>Probe set number</b>	<b>Orthologous numbering</b>
Metabolism			
Carbohydrate	Endopolygalacturonase	1	Trire2_103049
	Glucan 1,4- $\alpha$ -glucosidase	1	Trire2_105313
Lipid and fatty acid	Phospholipase	1	Trire2_3434
Secondary	Chimeric spermidine synthase/saccharopine dehydrogenase	1	
	Quinate dehydrogenase	1	Trire2_109687
	Non-ribosomal peptide synthase- like enzyme	1	Trire2_71072
Energy	Aldehyde dehydrogenase	1	
Cellular processes and signaling			
Transport	General substrates (Major Facilitator Superfamily transporters)	2	Trire2_54999 Trire2_71059
	ABC transporters	2	Trire2_80028 Trive_36031
Posttranslational events	26S proteasome regulatory complex	1	Trive_111074
Secretion	Mitochondrial import translocase	1	Trive_89707
Cell wall and membranes	Integral membrane protein	2	Trire2_105251 Trive_36530
Signaling	Ankyrin repeat protein	2	Trire2_104219 Trire2_36373
	Cellulose signaling related protein	1	Trire2_50323
Information storage and Processing			
Transcription	Transcription factors	4	Trire2_122448 Trire2_27649 Trive_12973 Trive_501

Translation (protein synthesis)	Translational initiation factor 2 $\beta$	1	
Unknown function		10	*
<b>Down-regulated</b>			
<b>Processes</b>	<b>Probe sets</b>	<b>Probe set number</b>	<b>Orthologous numbering</b>
Metabolism			
Carbohydrate	$\beta$ -galactosidase	2	
	Phosphoglycerate mutase	16	Trire2_121350 Trive_73471
	Glycoside hydrolase (chitinase)	1	Trire2_102837
	Alginate-lyase	1	Trire2_103033
	Polygalacturonase	1	Trire2_122780
	$\beta$ -mannosidase	1	Trire2_5836
	Short-chain dehydrogenase/reductase	3	Trire2_60518 Trire2_69181 Trire2_80019
	Glucose dehydrogenase	1	Trire2_66795
	6-phosphofructo-2-kinase	1	Trire2_78732
	2-hydroxy-3-oxopropionate reductase	1	Trire2_66544
Lipid and fatty acid	Phosphatidylserine decarboxylase	3	Trire2_29642 Trire2_66935
	Fusicocadiene synthase	1	Trire2_107667
	Esterase/lipase	1	Trire2_107835
	Acyl-CoA synthase	1	Trire2_54667
	Secretory phospholipase	1	Trire2_67579
Amino acid	S-adenosylmethionine dependent methyltransferase	2	Trire2_111082 Trire2_5633
	Aromatic amino acid aminotransferase	1	Trire2_105978
	Homoserine dehydrogenase	1	Trire2_122868
	Aspartate kinase	1	Trire2_81896
Protein	Proteasome component (endopeptidase)	1	Trive_85569
	Serine-type endopeptidase inhibitor	1	Trire2_110790
Nucleotide and nucleic acid metabolism	Pyrimidine biosynthesis enzyme	2	Trire2_121620
	Oxidoreductase 2-	1	Trire2_123468

	nitropropane dioxygenase		
	Phosphoribosyl transferase	1	Trire2_55837
	Endoribonuclease L-PSP	1	Trire2_75424
	Deoxyuridine 5'-triphosphate nucleotidohydrolase	1	Trire2_75529
Vitamin	Thiamin biosynthesis protein	1	Trire2_59068
	Vitamin b12 biosynthesis protein	1	Trire2_74681
	C-14 sterol reductase	1	Trire2_81049
Secondary	Non-ribosomal peptide synthase- like enzyme	1	Trire2_23171
	Prenyltransferase	1	Trire2_70040
	Isoflavone reductase	3	Trire2_109239 Trire2_111832 Trire2_81525
	Longiborneol synthase	1	Trire2_67738
Energy	NADH:flavin oxidoreductase	1	Trire2_103015
	FMN-dependent dehydrogenase	1	Trire2_103136
	Flavin oxidoreductase	1	Trire2_122416
	Alcohol dehydrogenase	1	Trire2_30759
	Dynamin GTPase	2	Trire2_61605 Trire2_68192
	ATPase	1	Trire2_74187
	FAD-dependent pyridine nucleotide-disulphide oxidoreductase	1	Trire2_77288
	Aldo-keto reductase	1	Trire2_82204
Inorganic	Ferric reductase	3	Trire2_111750 Trire2_22845 Trire2_23353
Nitrogen compounds	Urease accessory protein UreD	1	Trire2_53187
Cellular processes and signaling			
Transport	General substrates (Major Facilitator Superfamily transporters)	16	Trire2_105752 Trire2_106556

			Trire2_26160 Trire2_28409 Trire2_43347 Trire2_53903 Trire2_54972 Trire2_55630 Trire2_57749 Trire2_69026 Trire2_69164 Trire2_69834 Trire2_80058
	Aquaporin transporter	1	Trire2_105870
	Copper transporter	2	Trire2_52315 Trire2_71029
	Hemolysin III channel protein	2	Trire2_68212 Trire2_82246
Detoxification	Cytochrome-c oxidase chain VI precursor	1	
	Cytochrome p450 monooxygenase	6	Trire2_109811 Trire2_4999 Trire2_58772 Trire2_70984 Trire2_77512 Trire2_78223
	ADP-ribose pyrophosphatase	1	Trire2_104200
	Chloroperoxidase	1	Trire2_123079
	Glutathione-dependent formaldehyde-activating enzyme	1	Trire2_123987
	Glutathione S-transferase	1	Trire2_22453
	Monooxygenase FAD-binding protein	2	Trire2_53430

			Trire2_76905
	β-lactamase	1	Trire2_58717
	Flavin-dependent halogenase O-methyltransferase bifunctional protein	1	Trire2_69652
	Catalase/peroxidase	1	Trire2_70803
	Steroid monooxygenase	1	Trire2_76230
	Agmatine deiminase	1	Trire2_80980
	RTA1 domain protein	1	Trire2_41325
	Acid-phosphatase	2	Trire2_76155 Trive_87714
Posttranslational events	Protein disulfide isomerase	1	
	Glutamate carboxypeptidase	1	
	Thiorredoxin-like protein	1	Trire2_120922
	Similar to tripeptidyl-peptidase	1	Trire2_123865
	Aspartic protease	1	Trire2_53961
	26S proteasome non-ATPase regulatory subunit 9	1	Trire2_56215
	related to histone-lysine N-methyltransferase	1	Trire2_56354
	Radical S-adenosyl methionine domain containing protein	1	Trire2_64288
Adhesion	Fasciclin	1	Trire2_121417
Cell communication	Hydrophobin	1	Trire2_73173
Cell wall and membranes	Integral membrane protein	1	Trire2_69500
	Cell wall protein	1	Trire2_105763
Signaling	WD-repeat containing protein probably involved in G-protein mediated signaling	1	Trire2_30465
	Ankyrin repeat protein	1	Trire2_35186
	G-protein coupled receptor	1	Trire2_38672
	Casein kinase II/ser/thr protein kinase	1	Trire2_5127
	Casein kinase I, subunit delta	1	Trire2_55049
	Regulator of G protein signaling	1	Trire2_63981
Regulation	Phosphotyrosyl phosphatase activator (serine/threonine protein	1	Trire2_79850

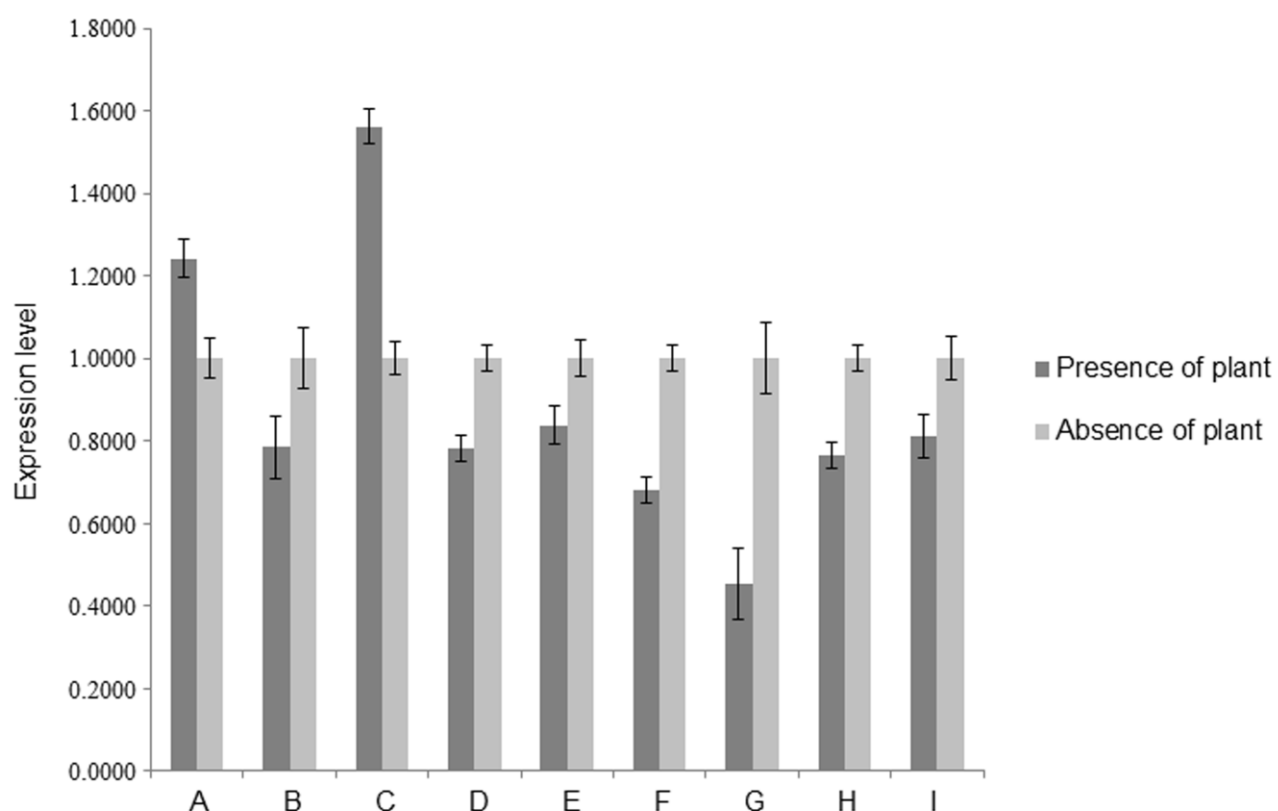
	phosphatase activator)		
Information storage and Processing			
Replication	DNA replication complex	1	Trive_44614
Transcription	DNA-dependent RNA polymerase II	1	
	DNA-directed RNA polymerase III	1	Trive_66115
	Transcription factors	11	Trire2_102673 Trire2_106625 Trire2_111742 Trire2_112131 Trire2_58011 Trire2_68455 Trire2_69695 Trire2_76220 Trire2_77878 Trire2_79726
	tRNAHis guanylyltransferase	1	Trire2_64065
Translation (protein synthesis)	GTP-dependent nucleic acid-binding protein	1	Trive_82125
Repair	Smr domain protein	1	Trire2_56603
	DNA repair protein	1	Trire2_70084
Unknown function		68	**

These physiological processes grouped the 250 differentially expressed probe sets (FC $\geq$ 2 and FDR 0.10), up- and down-regulated, identified in *T. parareesei* T6 in the presence of the plants after Gene Spring GX program analysis.

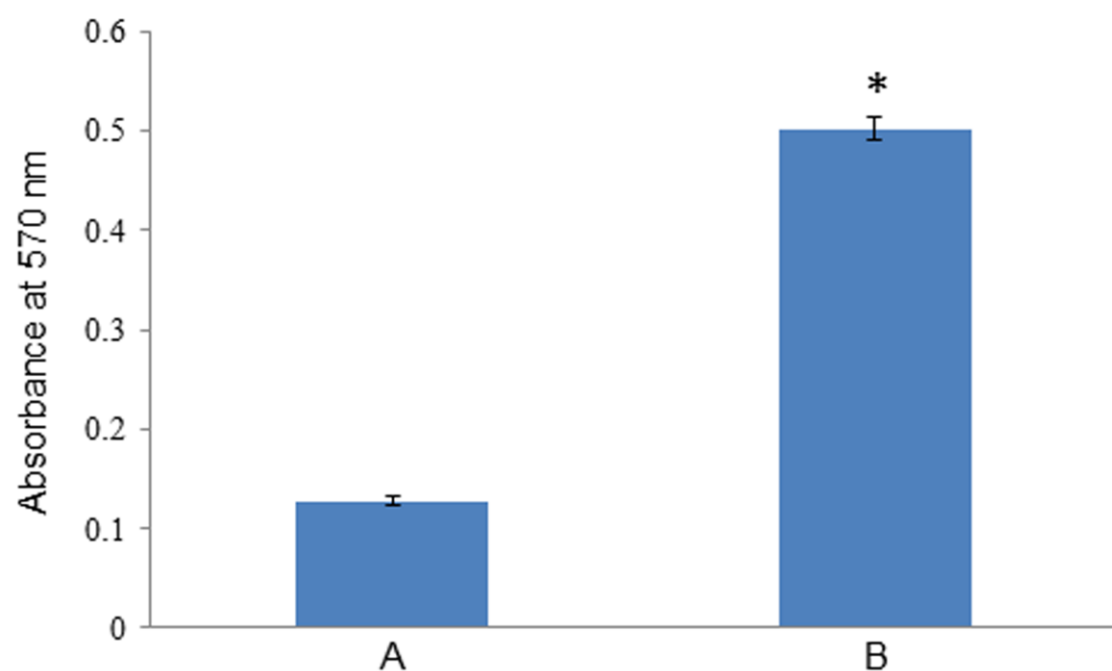
\* Trire2\_107869, Trire2\_120362, Trire2\_122724, Trire2\_122825, Trire2\_1927, Trive\_59121.

\*\* Trire2\_102908, Trire2\_103048, Trire2\_104549, Trire2\_104838, Trire2\_105156,  
Trire2\_105311, Trire2\_105445, Trire2\_106353, Trire2\_106490, Trire2\_106584,  
Trire2\_106623, Trire2\_107793, Trire2\_107901, Trire2\_108261, Trire2\_108996,  
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Trire2\_121415, Trire2\_121427, Trire2\_122374, Trire2\_122971, Trire2\_123261,  
Trire2\_123429, Trire2\_22426, Trire2\_33359, Trire2\_33827, Trire2\_2433,  
Trire2\_39426, Trire2\_43115, Trire2\_53747, Trire2\_54230, Trire2\_34297, Trire2\_5924,  
Trire2\_59368, Trire2\_60493, Trire2\_63157, Trire2\_63526, Trire2\_64011,  
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Trire2\_71123, Trire2\_71851, Trire2\_76075, Trire2\_77887, Trire2\_82041,  
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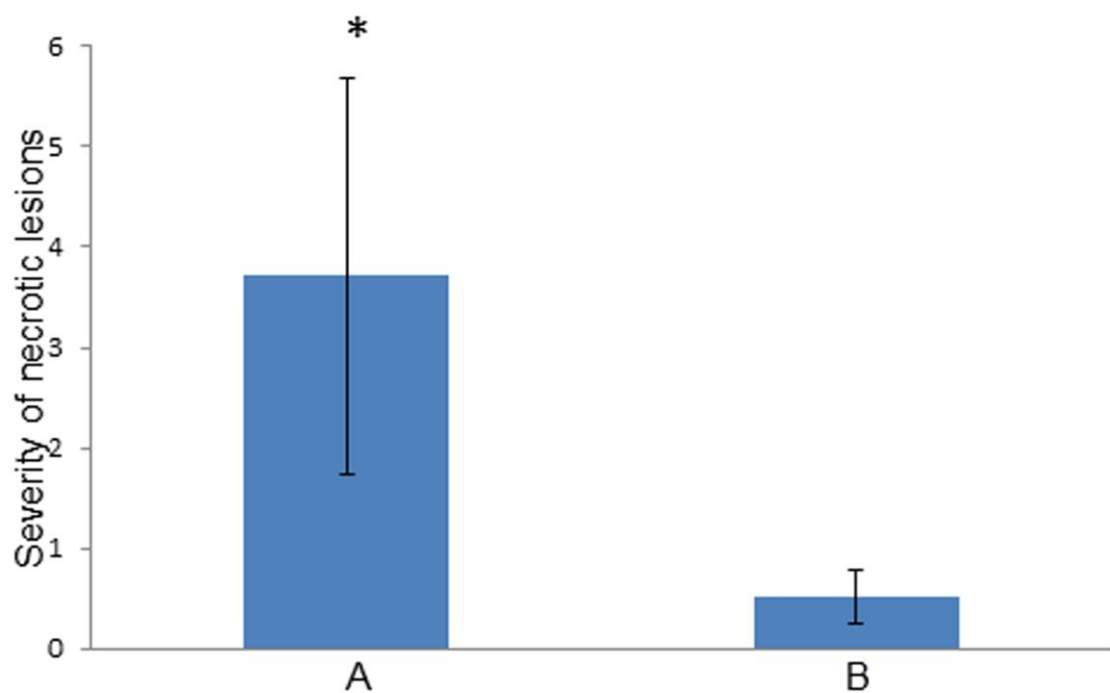




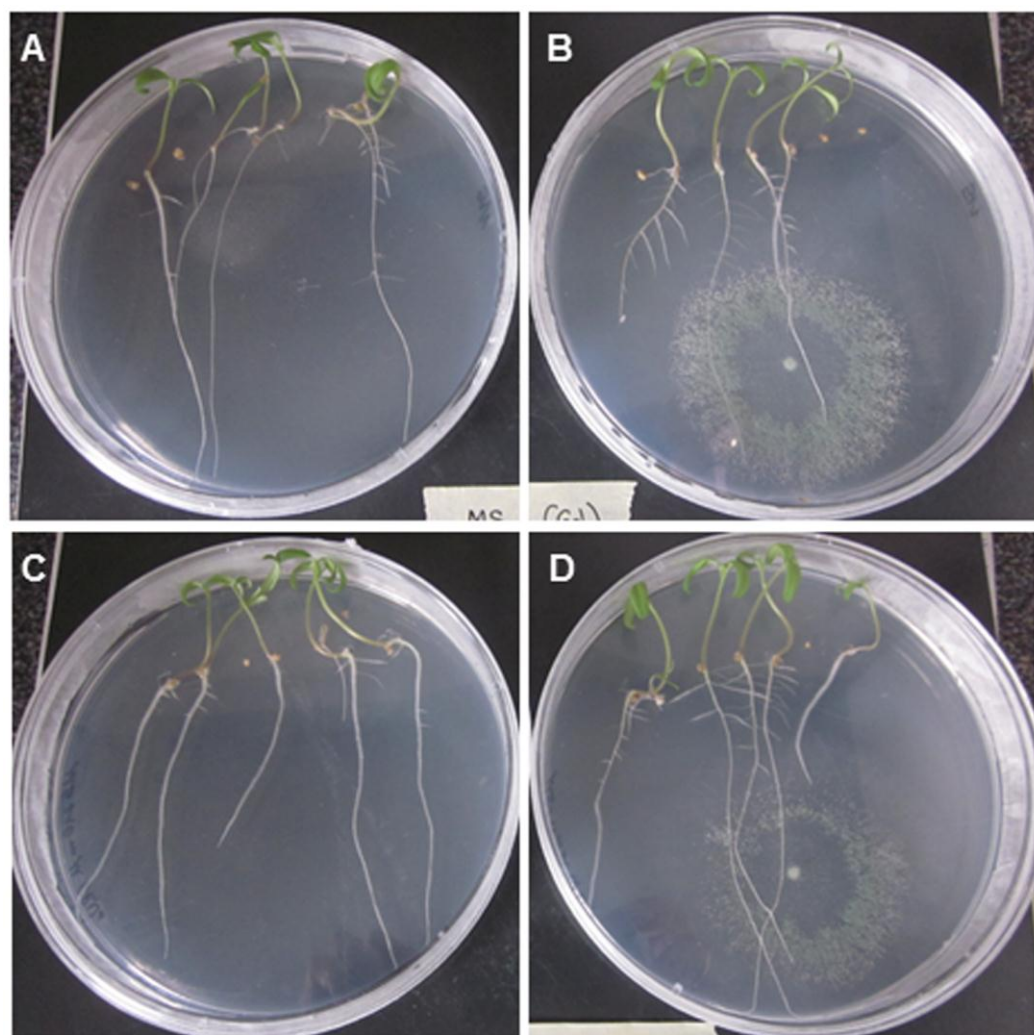
**Figure S1. Validation of microarray experiments.** Real-time PCR of an ABC transporter (Trire2\_80028) (A), an alcohol dehydrogenase (Trire2\_30759) (B), a cellulose signaling-related gene (Trire2\_50323) (C), a dehydrogenase reductase (Trire2\_69181) (D), two MFS transporters (Trire2\_105752 and Trire2\_106556) (E and F), a phosphoglycerate mutase (Trire2\_121350) (G), a steroid monooxygenase (Trire2\_76230) (H) and a cytochrome P450 monooxygenase (Trire2\_4999) (I) genes in *Trichoderma parareesei* T6 after 20 h of incubation in the presence of tomato plants. Values correspond to relative measurements against T6 incubated without plant ( $2^{-\Delta\Delta C_t} = 1$ ). The *Trichoderma*  $\beta$ -tubulin gene was used as an internal reference gene. Bars represent standard deviations of the mean values of three biological replicates.



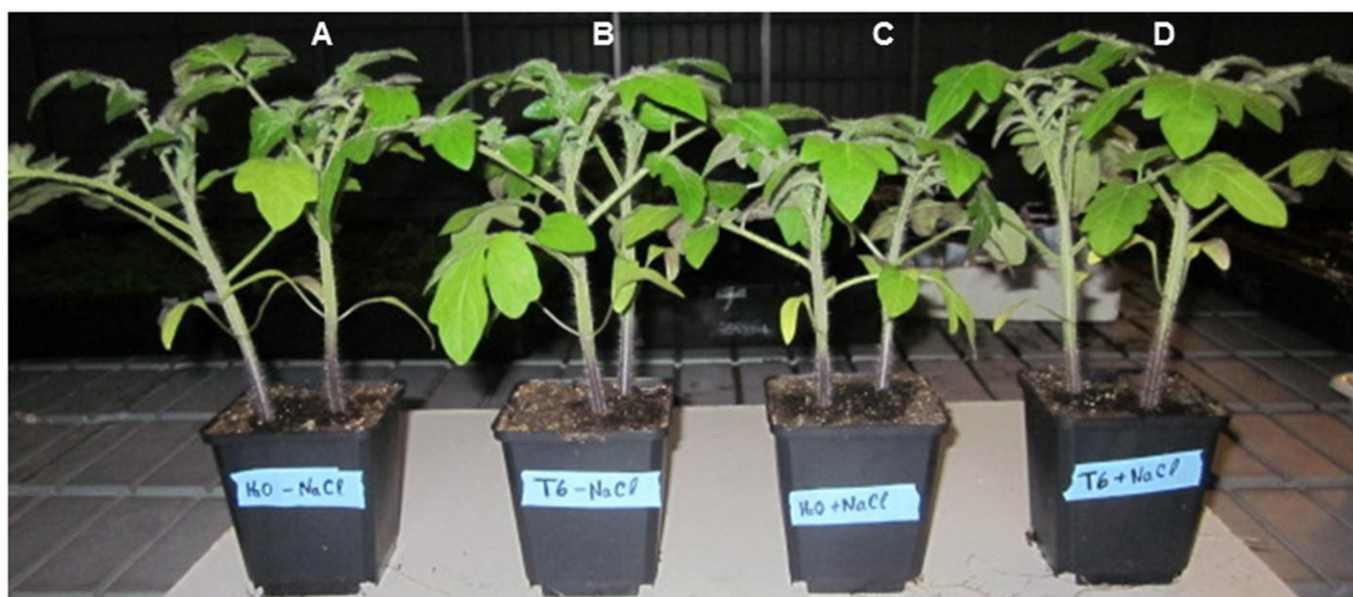
**Figure S2. Effect of tomato exudates on *Trichoderma parareesei* T6 growth.** Absorbance values at 570 nm were measured after the inoculation of 96-well E plates with 2,000 conidia of T6 per well containing MS medium + 1% sucrose (control) (A) or MS medium + 1% sucrose plus tomato exudates (B) and incubation at 28°C for 120 h.



**Figure S3.** Severity of necrotic lesions observed in tomato leaves 3 days after *Trichoderma parareesei* T6 treatment of 4-week old tomato plants and *Botrytis cinerea* B05.10 conidia infection. Untreated (A) and T6-treated plants (B). Necrotic lesion data were recorded 4 days after *B. cinerea* infection. The standard deviation bars were obtained from at least two different experiments, with eight replicates of infection spots. Asterisk represents statistically significant differences (Duncan's test).



**Figure S4. Effect of *Trichoderma parareesei* T6 and salt-stress treatments on tomato plant growth in an *in vitro* assay.** Tomato seedlings grown on MS medium, supplemented with 1% (w/v) sucrose and 0.8% agar, pH 5.7 (A and B) plus 25 mM NaCl (C and D) were inoculated with water (A and C) or *T. parareesei* T6 (B and D). Photographs were taken 4 days after inoculating  $1 \times 10^6$  *Trichoderma* spores.



**Figure S5. Effect of *Trichoderma parareesei* T6 and salt-stress treatments on the growth of tomato plants in an *in vivo* assay.** Image of 4-week-old tomato plants developed from untreated (A and C) or *T. parareesei* T6-treated (B and D) seeds, treated daily with 5 mL of either water (A and B) or 100 mM NaCl (C and D) for 10 days.