

Table S1 The primers for qRT-PCR and the annotation of chosen genes for q-PCR

<a href="#">GeneID</a>	Primer name	Primer sequence (5'-3')	Sequence length/bp	<a href="#">Gene length</a>	<a href="#">Tc284_2 RPKM</a>	<a href="#">Tc361_1 RPKM</a>	<a href="#">Annotation</a>
<a href="#">CL622.Contig3</a> <a href="#">Tc15_2</a>	RT622	F-CCGAGCTGTA	20	<a href="#">2695</a>	<a href="#">37.80</a>	<a href="#">14.14</a>	<a href="#">mannosyl-oligosaccharide glucosidase activity(GO)</a>
		CGAGGAACTG					
<a href="#">CL3900.Contig1</a> <a href="#">Tc15_2</a>	RT3900	R-CGCCGGTGAT	20	<a href="#">1608</a>	<a href="#">0.79</a>	<a href="#">0.31</a>	<a href="#">Adenosinetriphosphatase (nt)</a>
		AGGGTCATAC					
<a href="#">Unigene18070</a> <a href="#">Tc15_2</a>	RT18070	F-CTTTTGGGAA	20	<a href="#">2660</a>	<a href="#">58.72</a>	<a href="#">26.77</a>	<a href="#">helicase activity;DNA binding;ATP binding(GO)</a>
		CGGCACGAAG					
<a href="#">Unigene1676</a> <a href="#">Tc15_2</a>	RT1676	R-TGCATGGGTA	20	274	0.01	29.28	<a href="#">E3 ubiquitin-protein ligase(ko)</a>
		ACTTGACGCT					
<a href="#">Unigene17170</a> <a href="#">Tc15_2</a>	RT17170	F-TACTGGGGCG	19	385	0.01	40.38	<a href="#">glucose repressible protein 2(KEGG)</a>
		ACTCAGTGTA					
<a href="#">Unigene18727</a> <a href="#">Tc15_2</a>	RT18727	R-CTTCGAGCCG	20	574	12.47	0.01	<a href="#">Cytochrome P450 52A6(nr)</a>
		GTTAGGTGAG					
<a href="#">Unigene1676</a> <a href="#">Tc15_2</a>	RT1676	F-GATAAAGACG	20	274	0.01	29.28	<a href="#">E3 ubiquitin-protein ligase(ko)</a>
		GTGCACCTCC					
<a href="#">Unigene17170</a> <a href="#">Tc15_2</a>	RT17170	R-CGTCGTCATC	19	385	0.01	40.38	<a href="#">glucose repressible protein 2(KEGG)</a>
		CTCTCCTCA					
<a href="#">Unigene18727</a> <a href="#">Tc15_2</a>	RT18727	F-CGGCAAGGAC	20	574	12.47	0.01	<a href="#">Cytochrome P450 52A6(nr)</a>
		TCCATCTCC					
<a href="#">Unigene18727</a> <a href="#">Tc15_2</a>	RT18727	R-CCCTCGTGCT	19	574	12.47	0.01	<a href="#">Cytochrome P450 52A6(nr)</a>
		TCTTCTCGT					
<a href="#">Unigene18727</a> <a href="#">Tc15_2</a>	RT18727	F-TTCTCCTTGAT	20	574	12.47	0.01	<a href="#">Cytochrome P450 52A6(nr)</a>
		CTCCGCCTC					
<a href="#">Unigene18727</a> <a href="#">Tc15_2</a>	RT18727	R-CTGGACAGG	19	574	12.47	0.01	<a href="#">Cytochrome P450 52A6(nr)</a>
		GAGATCAGGC					

<a href="#">CL3499.Contig</a> <a href="#">2_Tc15_2</a>	RT3499	F-GTGCTCGTGG TTGGGTGG	18	<a href="#">673</a>	9.38	0.01	<a href="#">Flocculation protein</a>
		R-ACTGCATGTC ATACCACTGG	20				
<a href="#">CL2376.Contig</a> <a href="#">1_Tc15_2</a>	RT2376	F-CAAACAGGAA CCGTGCAAGA	20	<a href="#">354</a>	24.97	0.01	<a href="#">ATP-binding cassette transporter 2(GO)</a>
		R-GTCCTTGACC AACGAGCAC	19				
<a href="#">Unigene14763</a> <a href="#">_Tc15_2</a>	RT14763	F-AGTGGTGAAT CGCAAGGTGT	20	<a href="#">550</a>	808.28	394.79	::
		R-TTACCAAGTGC CCCCAAAGTC	20				
<a href="#">Unigene22186</a> <a href="#">_Tc15_2</a>	RT22186	F-TTGCAATCCG TCATGGCAAC	20	<a href="#">992</a>	<a href="#">199.46</a>	<a href="#">41.96</a>	<a href="#">metal ion binding; superoxide dismutase activity(GO)</a>
		R-TTCGCGCCAT GAATGACAAC	20				
<a href="#">CL6956.Contig</a> <a href="#">1_Tc15_2</a>	RT6956	F-TGTTGCTTGG AGAGTACGGC	20	<a href="#">1292</a>	<a href="#">196.15</a>	<a href="#">1501.69</a>	::
		R-CAAGTCTTGG TGTTCCGCC	20				
<a href="#">CL4323.Contig</a> <a href="#">1_Tc15_2</a>	RT4323	F-CTACGGCTTC TCTGGTTGGA	20	<a href="#">365</a>	0.01	20.61	::
		R-GCCACCATTA GCCATGTTGT	20				
<a href="#">Unigene11683</a> <a href="#">_Tc15_2</a>	RT11683	F-GACGAGTCTG TGGTGTCTCT	20	<a href="#">289</a>	24.76	0.01	::
		R-CGTGATGCTC AGTCGCTTAT	20				
<a href="#">Unigene11935</a> <a href="#">_Tc15_2</a>		F-CGCTCAGAAA ACCAAACCTC	20	<a href="#">427</a>	20.70	0.01	::

Table S2 40 specific expressed genes in Tc361\_1 at 144 hpi

Gene ID	Deduced character and function	Gene ID	Deduced character and function
CL6859.	Hypothetical protein	CL5715.Contig	Hypothetical protein CERSUDRAFT_115801
Contig2_Tc15_2	PGTG_07569	2_Tc15_2	( <i>Ceriporiopsis subvermispora</i> )
Unigene12464	Transcription initiation factor TFIIIB(KO);Hypothetical protein RO3G_11938 ( <i>Rhizopus</i>	Unigene15745	histone-lysine N-methyltransferase (KO);Hypothetical protein
_Tc15_2	<i>delemar</i> )	_Tc15_2	DOTSEDRAFT_40277 ( <i>Clostridium perfringens</i> )
Unigene22345	Hypothetical protein	Unigene25145	Hypothetical protein
_Tc15_2	PGTG_10413	_Tc15_2	PGTG_18554
Unigene7211	Hypothetical protein	Unigene2529	Hypothetical protein
_Tc15_2	PGTG_19708	_Tc15_2	PGTG_00998
CL5307.Contig2	Hypothetical protein	Unigene11430	Hypothetical protein
_Tc15_2	PGTG_19579	_Tc15_2	PGTG_03295
CL560.Contig1	Hypothetical protein	Unigene7449	Hypothetical protein
_Tc15_2	PGTG_13958	_Tc15_2	PGTG_05143
CL7155.Contig1	Glucoamylas(KO);Hypothetical protein PGTG_08062	Unigene9988_	Putative uncharacterized protein
_Tc15_2		Tc15_2	YHR217C( <i>S cerevisiae</i> )
Unigene26456	Hypothetical protein	Unigene25109	Hypothetical protein
_Tc15_2	PGTG_13885	_Tc15_2	PGTG_15083

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CL4985.Contig1 _Tc15_2	Asparagine synthase (glutamine-hydrolysing) <i>(Exophiala dermatitidis)</i> (KO)	CL3109.Contig 3_Tc15_2	Hypothetical protein PGTG_18680
Unigene24409 _Tc15_2	Predicted protein ( <i>Pyrenophora tritici-repentis</i> ]	CL1464.Contig 1_Tc15_2	D-amino-acid oxidase( <i>Rhodospodium toruloides</i> )(KO)
Unigene17702 _Tc15_2	Large subunit ribosomal protein L41e( <i>Saccharomyces cerevisiae</i> )	Unigene26432_ Tc15_2	Hypothetical protein PGTG_15563
Unigene11040 _Tc15_2	substrate-specific transmembrane transporter activity(GO);Hypothetical protein MELLADRAFT_71916 <i>(Melampsora larici-populina)</i>	Unigene17170 _Tc15_2	Glucose repressible protein gene( <i>Xanthophyllomyces dendrorhous</i> )(Nt) ; Histone-lysine N-methyltransferase SETD1(ko); Small GTPase mediated signal transduction(GO)
Unigene24199_Tc1 5_2	Hypothetical protein PGTG_07304	Unigene25090 _Tc15_2	Hypothetical protein PGTG_03348
CL5606.Contig1 _Tc15_2	Hypothetical protein PGTG_07990,	CL1408.Contig 1_Tc15_2	Hypothetical protein PGTG_04420,
Unigene7326_Tc15 _2	Hypothetical protein PGTG_05143,	Unigene7450 _Tc15_2	Hypothetical protein PGTG_05143
Unigene11422 _Tc15_2	Nucleolar complex protein 2(S. <i>cerevisiae</i> )	Unigene23304 _Tc15_2	alpha-amylase(KO);Unnamed protein product( <i>Aspergillus oryzae</i> )
Unigene28255 _Tc15_2	Hypothetical protein PGTG_03418	Unigene10946 _Tc15_2	Hypothetical protein PGTG_19367
CL4323.Contig1 _Tc15_2	Hypothetical protein PGTG_05160	CL4476.Contig 1_Tc15_2	Chitinase(KO); Hypothetical protein TRIVIDRAFT_225056 <i>( Trichoderma virens)</i>

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Unigene23386 _Tc15_2	Hypothetical protein AURDEDRAFT_149120 ( <i>Auricularia delicata</i> )	Unigene11154 _Tc15_2	Hypothetical protein PGTG_15082(Nr);Nucleic acid binding(GO)
Unigene1676 _Tc15_2	E3 ubiquitin-protein ligase TRIP12	Unigene10945 _Tc15_2	Hypothetical protein PGTG_12382
Unigene4619 _Tc15_2	large subunit ribosomal protein L41e ( <i>Ashbya gossypii</i> )	CL420.Contig2 _Tc15_2	Hypothetical protein PGTG_19367
CL6460.Contig1 _Tc15_2	Asparagine synthase (glutamine-hydrolyzing) ( <i>Rhizopus delemar</i> )	Unigene14298 _Tc15_2	Hypothetical protein PGTG_10756

Table S3 26 specific expressed genes in Tc284\_2 at 144 hpi

Gene ID	Deduced character and function	Gene ID	Deduced character and function
Unigene31407 _Tc15_2	Nitrate reductase (NADPH)( <i>Ustilago maydis</i> )(KO)	Unigene7678 _Tc15_2	Hypothetical protein PGTG_17070
Unigene3535 _Tc15_2	H <sup>+</sup> -transporting ATPase ( <i>P. graminis</i> f. sp. <i>tritici</i> )(KO)	Unigene24030 _Tc15_2	Hypothetical protein PGTG_19367
Unigene31515 _Tc15_2	Cytochrome-b5 reductase( <i>Fomitiporia mediterranea</i> )(KO)	CL5794.Contig1 _Tc15_2	Hypothetical protein AOL_s00110g124 ( <i>Arthrotrrys oligospora</i> )
Unigene15719 _Tc15_2	GTPase activity(GO); Hypothetical protein PGTG_14941	Unigene10373 _Tc15_2	Hypothetical protein PGTG_02401
Unigene2587 2_Tc15_2	—	Unigene18727 _Tc15_2	Cytochrome P450 ( <i>Candida tropicalis</i> )
CL2376.Contig1 _Tc15_2	Putative ABC transport system ( <i>Batrachochytrium dendrobatidis</i> )(KO)	CL1500.Contig2 _Tc15_2	L:anosterol synthase ( <i>Schizosaccharomyces pombe</i> )
Unigene11683	Hypothetical protein	Unigene20992	putative replicase readthrough

_Tc15_2	PGTG_17415	_Tc15_2	protein( <i>Eutypa lata</i> )
Unigene5804	Hypothetical protein	CL3499.Contig2	GTPase activator activity(GO); Hypothetical protein
_Tc15_2	PGTG_01823	_Tc15_2	PGTG_05787
Unigene19721	Terpenoid cyclase	CL5691.Contig1	cell wall integrity and stress response component
_Tc15_2	( <i>P. graminis</i> f. sp. tritici)	_Tc15_2	( <i>S. cerevisiae</i> )
Unigene3471	Hypothetical protein	Unigene337	Hypothetical protein CMQ_2906
_Tc15_2	PGTG_01823	_Tc15_2	( <i>Grossmannia clavigera</i> )
Unigene3938	Hypothetical protein	Unigene11388	uncharacterized protein CPUR_01692
_Tc15_2	PGTG_07937	_Tc15_2	( <i>Claviceps purpurea</i> )
Unigene11935	Hypothetical protein	Unigene20989	Chitinase-like protein
_Tc15_2	PGTG_03017	_Tc15_2	( <i>S. pombe</i> )(KO)
Unigene3933	Hypothetical protein	CL4245.Contig1	Lon-like ATP-dependent protease
_Tc15_2	PGTG_15242	_Tc15_2	( <i>P. graminis</i> f. sp. <i>Tritici</i> ) (KO)

Table S4 The expression of candidate effectors in Tc284\_2 and Tc361\_1

Gene ID	RPKM in Tc284_2	RPKM of Tc361_1	Gene ID	RPKM in Tc284_2	RPKM in Tc361_1
CL146.Contig1_Tc15_2	24.6	3.3	Unigene8006_Tc15_2	145.9	554.9
CL1243.Contig1_Tc15_2	408.3	170.2	Unigene8096_Tc15_2	34.9	105.1
CL1492.Contig1_Tc15_2	1578.8	315.2	Unigene8115_Tc15_2	621.9	156.8
CL2307.Contig2_Tc15_2	22.8	58.7	Unigene8591_Tc15_2	601.1	1257.7
CL2876.Contig2_Tc15_2	46.9	8.8	Unigene8845_Tc15_2	23.0	3.6
CL3157.Contig2_Tc15_2	178.5	16.2	Unigene9122_Tc15_2	89.0	180.6
CL4021.Contig2_Tc15_2	3351.4	740.0	Unigene9803_Tc15_2	345.2	114.6
CL4323.Contig1_Tc15_2	0.0	20.6	Unigene10149_Tc15_2	22.9	8.3
CL4576.Contig2_Tc15_2	31.1	65.7	Unigene10936_Tc15_2	147.8	33.3

CL4624.Contig2_Tc15_2	340.8	36.2	Unigene11651_Tc15_2	48.0	175.8
CL5603.Contig1_Tc15_2	73.5	16.4	Unigene11683_Tc15_2	24.8	0.0
CL5885.Contig1_Tc15_2	132.0	48.9	Unigene11893_Tc15_2	99.7	17.8
CL6152.Contig2_Tc15_2	11.3	35.7	Unigene11935_Tc15_2	20.7	0.0
CL6413.Contig2_Tc15_2	5.5	21.8	Unigene12071_Tc15_2	30.1	5.4
CL6671.Contig1_Tc15_2	2.0	24.5	Unigene12860_Tc15_2	45.6	15.7
CL6956.Contig1_Tc15_2	196.2	1501.7	Unigene12905_Tc15_2	27.4	307.9
Unigene683_Tc15_2	41.5	8.6	Unigene13232_Tc15_2	51.8	17.9
Unigene2822_Tc15_2	36.3	6.8	Unigene13539_Tc15_2	42.2	15.4
Unigene3256_Tc15_2	34.5	3.2	Unigene14191_Tc15_2	164.6	43.0
Unigene3561_Tc15_2	127.5	59.3	Unigene14763_Tc15_2	808.3	394.8
Unigene3795_Tc15_2	212.2	41.0	Unigene15092_Tc15_2	10.5	426.8
Unigene4093_Tc15_2	50.4	242.7	Unigene15143_Tc15_2	199.4	50.4
Unigene4156_Tc15_2	110.8	776.2	Unigene15605_Tc15_2	123.8	31.8
Unigene4204_Tc15_2	991.4	237.5	Unigene16185_Tc15_2	37.0	7.0
Unigene4298_Tc15_2	318.7	4804.0	Unigene16387_Tc15_2	5331.4	14187.2
Unigene4450_Tc15_2	758.8	155.2	Unigene16734_Tc15_2	3.4	28.0
Unigene4469_Tc15_2	5.3	59.7	Unigene17088_Tc15_2	41.6	11.6
Unigene4609_Tc15_2	8.5	85.4	Unigene17187_Tc15_2	626.7	1639.0
Unigene4690_Tc15_2	153.1	18.0	Unigene17565_Tc15_2	92.0	234.8
Unigene4702_Tc15_2	82.0	23.0	Unigene17566_Tc15_2	608.5	20.9
Unigene4712_Tc15_2	141.6	68.7	Unigene17799_Tc15_2	25.6	168.2
Unigene5013_Tc15_2	111.6	353.3	Unigene18229_Tc15_2	62.9	143.9
Unigene6906_Tc15_2	16.3	1.9	Unigene18358_Tc15_2	168.2	39.7
Unigene7571_Tc15_2	24.9	3.1			

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