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Title: Comparison of transcriptome profiles by *Fusarium oxysporum* inoculation between *Fusarium* yellows resistant and susceptible lines in *Brassica rapa* L.

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Abstract

Key message

Resistant and susceptible lines in *Brassica rapa* have different immune responses against *Fusarium oxysporum* inoculation.

Abstract

Fusarium yellows caused by *Fusarium oxysporum* f. sp. *conglutinans* (*Foc*) is an important disease of Brassicaceae, however the mechanism of how host-plants respond to *Foc* is still unknown. By comparing with and without *Foc* inoculation in both resistant and susceptible lines of Chinese cabbage (*Brassica rapa* var. *pekinensis*), we identified differentially expressed genes (DEGs) between the bulked inoculated (6, 12, 24 and 72 hours after inoculation (HAI)) and non-inoculated samples. Most of the DEGs were up-regulated by *Foc* inoculation. Quantitative real-time RT-PCR showed that most up-regulated genes increased their expression levels from 24 HAI. An independent transcriptome analysis at 24 and 72 HAI was performed in resistant and susceptible lines. GO analysis using up-regulated genes at 24 HAI indicated *Foc* inoculation activates systemic acquired resistance (SAR) in resistant lines and tryptophan biosynthetic process and responses to chitin and ethylene in susceptible lines. By contrast, GO analysis using up-regulated genes at 72 HAI showed the overrepresentation of some categories for the defense response in susceptible lines but not in the resistant lines. We also compared DEGs between *B. rapa* and *Arabidopsis thaliana* after *F. oxysporum* inoculation at the same time point and identified genes related to defense response that were up-regulated in the resistant lines of Chinese cabbage and *A. thaliana*. Particular genes that changed expression levels overlapped between the two species, suggesting that they are candidates for genes involved in the resistance mechanisms against *F. oxysporum*.

Keywords

Fusarium yellows; Chinese cabbage; Transcriptome; Systemic acquired resistance; *Brassica rapa*; *Fusarium oxysporum* f. sp. *conglutinans*

Introduction

Brassica rapa L. is an annual and out-crossing plant species in the Brassicaceae family and has

several subspecies with morphological diversity (Fujimoto and Nishio 2007; Cheng et al. 2016). *B. rapa* includes vegetable crops consumed worldwide such as Chinese cabbage (var. *pekinensis*), pak choi (var. *chinensis*), and komatsuna (var. *perviridis*), and root vegetables including turnip (var. *rapa*). Chinese cabbage forms a head with large pale-green colored leaves and wide white midribs and is an important vegetable, especially in Asian countries. The whole genome sequence of Chinese cabbage (Chiifu-401-42) is available and 199 accessions of *B. rapa* representing various morphotypes have been re-sequenced (Wang et al. 2011; Cheng et al. 2016), which provide informative sources for research.

Biotic stress caused by fungi, bacteria, viruses, or insects results in severe yield losses of crops and vegetables. *Fusarium oxysporum* causes serious disease against a wide range of commercially important plants such as tomato, cotton, melon, banana, cabbage, and Chinese cabbage (Ulloa et al. 2006; Charoenporn et al. 2010; Oumouloud et al. 2013; Ploetz 2006; Beckman 1987; Enya et al. 2008). *Fusarium* yellows (also known as *Fusarium* wilt) is caused by a soil-borne *Fusarium oxysporum* f. sp. *conglutinans* or *F. oxysporum* f. sp. *rapae* in *Brassica* vegetables and is an economically important disease for Chinese cabbage (Daly and Tomkins 1995; Enya et al. 2008). Leaf yellowing, wilting, defoliation, stunted growth, and death of seedlings are caused by infection of this pathogen, which invades the host roots and colonizes in their xylem tissues, especially in warm soil (Walker 1930; Daly and Tomkins 1995). This pathogen can survive for many years in the soil and can spread from field-to-field by heavy rain or flood. It is difficult to prevent the development of this pathogen by seed treatment, crop rotation, improved sanitation, or fungicides. Once this pathogen is found in a crop field, the most successful control method is by cultivation of disease resistant lines (Kawamura et al. 2015).

There are two types of plant immune systems, pathogen-associated molecular pattern (PAMP)-triggered immunity (PTI) and effector-triggered immunity (ETI) (Jones and Dangl 2006). PTI is activated when plant pattern recognition receptors (PRRs) localized in the plant cell membrane recognize pathogen molecules. Transcriptional change caused by pathogen infection is a PTI that induces expression of defense genes; PTI activates not only the mitogen associated protein kinase (MAPK) cascade but also WRKY transcription factors (Bigeard et al. 2015; Li et al. 2016). In *Arabidopsis thaliana*, recognition of the bacterial elicitor flg22 by the receptor kinase FLAGELLIN SENSITIVE2 (FLS2) activates the signaling cascade, MEKK1-MKK4/MKK5-MPK3/MPK6-WRKY22/WRKY29 (Asai et al. 2002). The

MKK4/MKK5-MPK3/MPK6 signaling cascade plays an important role in *Botrytis cinerea*-infected *A. thaliana* to regulate biosynthesis of the major phytoalexin, camalexin (Ren et al. 2008). By contrast, the MAPK cascade is not associated with defense response against infection by *Fusarium* in either *A. thaliana* or the economically important crops such as cotton and tomato (Berrocal-Lobo and Molina 2004). ETI is activated when plant resistance (R) proteins localized within a plant cell recognize specific pathogen effectors (avirulence (Avr) proteins). This recognition of Avr by R is termed ‘gene-for-gene resistance’ (Dangl and Jones 2001). Most R genes encode proteins with leucine-rich repeats (LRR), a central nucleotide binding site (NBS) domain, and a domain in the N-terminus with homology to cytosolic domains of the *Drosophila* Toll animal interleukin-1 receptor (TIR) (termed TIR–NBS–LRR) or a potential coiled-coil (CC) domain (termed CC–NBS–LRR) (Meyers et al. 2003; Joshi and Nayak 2011; Marone et al. 2013). R genes against *Fusarium* yellows have been identified in *A. thaliana* (Diener and Ausubel 2005), *B. rapa* (Shimizu et al. 2014), and *Brassica oleracea* (Lv et al. 2014; Shimizu et al. 2015). A candidate R gene in *B. rapa* and *B. oleracea* is orthologous and encodes a TIR-NBS-LRR protein, while a resistance gene in *A. thaliana* encodes a receptor-like kinase.

Numerous genes are involved in the pathogen infection. Transcriptome analysis by RNA-sequencing (RNA-seq) gives accurate global gene expression profiling, detection of allele specific expression, and alternative splicing variants (Mortazavi et al. 2008; Wang et al. 2009; Saeki et al. 2016). Transcriptome analysis was applied to monitor pathogen response genes in plant containing *Fusarium* fungi. This approach provided insights into the network, pathways, or genes involved in the plant immune response against the pathogen (Zhu et al. 2013; Xing et al. 2016). The aim of our study was to gain insights into the immune responses of host plants against *F. oxysporum* f. sp. *conglutinans* (*Foc*) inoculation in Chinese cabbage. A few differences in the initial *Foc* infection and colonization of roots were observed between susceptible and resistant cabbage cultivars up to 1 to 3 days post-inoculation (dpi). However, hyphae entered the xylem vessels in the susceptible cultivar from 4 to 6 dpi, whereas such colonization was rarely observed in the resistant cultivar (Li et al. 2015). We performed transcriptome analysis by RNA-seq at 24 and 72 hours after *Foc* inoculation in resistant and susceptible lines of Chinese cabbage to examine the broad disease responses. Genes differentially expressed between non-inoculated and inoculated plants and the transcriptional changes between resistant and susceptible lines were

identified.

Materials and methods

Plant materials and inoculation test of *Fusarium oxysporum* f. sp. *conglutinans*

Two Chinese cabbage inbred lines (RJKB-T23 and RJKB-T24) were used as plant material. RJKB-T23 and RJKB-T24 are Fusarium yellows resistant and susceptible lines, respectively. Resistant line, RJKB-T23, has two Fusarium yellows resistance genes, Bra012688 (*FocBr1a*) and Bra012689 (*FocBr1b*) (Shimizu et al. 2014). A field strain Cong; 1-1 (isolated from cabbage) of *F. oxysporum* f. sp. *conglutinans* categorized by race 1, provided by Dr. Kadota (National Agricultural Research Center for Tohoku Region, Japan), was used to prepare the inocula used in this study. Liquid inocula were prepared according to the method described by Pu et al. (2012). Plants were grown in plastic dishes containing Murashige and Skoog (MS) agar medium supplemented with 1.0 % sucrose (pH 5.7) in growth chambers under a 16-h/8-h light/dark cycle at 25 °C for two weeks. Roots of two weeks old plants were dipped into liquid inocula or distilled water for the mock inoculation, and then returned to MS medium. At 6, 12, 24, and 72 hours after inoculation (HAI), whole plants (three independent biological replicates, each containing a pool of six plants) were harvested and frozen with liquid nitrogen.

RNA-sequencing (RNA-seq)

Total RNAs from whole plants with mock inoculation and *F. oxysporum* f. sp. *conglutinans* inoculation were isolated by SV Total RNA Isolation System (Promega Co., WI, USA). We prepared twelve sequence libraries for RNA-seq; (1) Rb-mock, mock-inoculated bulked samples (6, 12, 24, and 72 HAI) from the resistant line (RJKB-T23) (read length; 75 bp, single-end sequencing (SE)); (2) Rb-inf, inoculated bulked samples (6, 12, 24, and 72 HAI) from the resistant line (100 bp, paired-end sequencing (PE)); (3) Sb-mock, mock-inoculated bulked samples (6, 12, 24, and 72 HAI) from the susceptible line (RJKB-T24) (75 bp, SE); (4) Sb-inf, inoculated bulked samples (6, 12, 24, and 72 HAI) from the susceptible line (100 bp, PE); (5) R-24h-mock, mock-inoculated samples of the resistant line at 24 HAI (100 bp, PE); (6) R-24h-inf, inoculated samples of the resistant line at 24 HAI (100 bp, PE); (7) S-24h-mock, mock-inoculated samples of the susceptible line at 24 HAI (100 bp, PE); (8) S-24h-inf,

inoculated samples of the susceptible line at 24 HAI (100 bp, PE); (9) R-72h-mock, mock-inoculated samples of the resistant line at 72 HAI (75 bp, SE); (10) R-72h-inf, inoculated samples of the resistant line at 72 HAI (75 bp, SE); (11) S-72h-mock, mock-inoculated samples of the susceptible line at 72 HAI (75 bp, SE); (12) S-72h-inf, inoculated samples of the susceptible line at 72 HAI (75 bp, SE). For making libraries for RNA-seq, the first strand cDNA was synthesized by random hexamer primers using the short fragmented mRNA, which was purified by beads containing oligo (dT) from total RNA and then fragmented by fragmentation buffer. The second-strand cDNA was synthesized using buffer, dNTPs, RNase H, and DNA polymerase I. Illumina sequencing adaptors were ligated to the short fragments and sequenced on an Illumina HiSeq™ 2000 (100 bp, PE) or Nextseq500 (75 bp, SE). The RNA sequencing data have been deposited with DDBJ under DRA005538 and DRA005976.

Detection of differentially expressed genes (DEGs)

Tophat2 (Kim et al. 2013) was used to align RNA-seq reads against the *B. rapa* reference genome downloaded from the Ensemble Genome database (ftp://ftp.ensemblgenomes.org/pub/release-28/plants/fasta/brassica_rapa/dna/Brassica_rapa.IVFCAASv1.28.dna.genome.fa). Gene expression levels were scored by fragments per kilo-base per million (FPKM) using cufflinks, and cuffdiff was used for identification of differentially expressed genes (DEGs) with and without *F. oxysporum* f. sp. *conglutinans* inoculation (Trapnell et al. 2012). Analysis for enrichment of gene functional ontology terms was completed using the gene ontology (GO) tool, agriGO (Du et al. 2010) following the methods described by Shimizu et al. (2014). Statistical tests for enrichment of functional terms used the hypergeometric test and false discovery rate (FDR) correction for multiple testing to a level of 5% FDR.

Gene expression analysis

cDNA was synthesized from 500 ng total RNA using PrimeScript RT reagent Kit (Takara Bio., Shiga JAPAN). Prior to quantitative real-time RT-PCR (qPCR), the specificity of the primer set for each gene was first tested by electrophoresis of PCR amplified products using QuickTaq®HS DyeMix (TOYOBO Co., Ltd., Osaka JAPAN) on 2.0 % agarose gel in which single products were observed.

Absence of genomic DNA contamination was confirmed by the PCR of no RT control. PCR conditions were 94 °C for 2 min followed by 30 cycles of 94 °C for 30 s, 55 °C for 30 s, and 68 °C for 30 s.

qPCR was performed using a LightCycler 96 (Roche Molecular Systems, Inc., CA, USA). cDNA was amplified using FastStart Essential DNA Green Master (Roche). PCR conditions were 95 °C for 10 min followed by 40 cycles of 95 °C for 10 s, 60 °C for 10 s, and 72 °C for 10 s, and Melting program (65 °C to 97 °C at 0.1 °C/s). After amplification cycles, each reaction was subjected to melt temperature analysis to confirm single amplified products. The relative expression level of each gene relative to *ACTIN* (*Bractin*) was automatically calculated using automatic CQ calling according to the manufacturer's instructions (Roche) (Fujimoto et al. 2006). Data presented are the average and standard error of three biological and experimental replicates and statistically analyzed using the Student's *t*-test, $p < 0.05$. The primers used in this study are listed in Table S1.

Results

RNA-sequencing analysis on samples inoculated by *F. oxysporum* f. sp. *conglutinans*

In our previous study, the whole genome transcriptome of 14-day-old leaves of the Fusarium yellows resistant line, RJKB-T23, and the susceptible line, RJKB-T24, were compared without inoculation of *F. oxysporum* f. sp. *conglutinans* (*Foc*) and two candidate genes for Fusarium yellows resistance, *FocBr1a* (Bra012688) and *FocBr1b* (Bra012689), were identified as a deletion in the genome of the susceptible lines (Shimizu et al. 2014). In the present study, total RNA was isolated from whole plants at 6, 12, 24, and 72 hours after inoculation (HAI) of RJKB-T23 and RJKB-T24. The expression levels of Bra012688 and Bra012689 in RJKB-T23 after inoculation of *Foc* were examined by quantitative real-time RT-PCR (qPCR) and were not drastically altered at any time point except for the expression level of Bra012689 at 72 HAI (Fig. 1a).

Whole genome transcriptome analysis was carried out using RNA-seq on the bulked total RNAs from whole plants collected at 6, 12, 24, and 72 HAI of *Foc* or at the same time points of mock treated RJKB-T23 and RJKB-T24. The RNA-seq libraries from RJKB-T23 and RJKB-T24 with *Foc* inoculation were named Rb-inf and Sb-inf, respectively, and the RNA-seq libraries from RJKB-T23 and RJKB-T24 with mock treatments were named Rb-mock and Sb-mock, respectively. 28.8 M, 28.2 M, 25.8

M, and 26.8 M clean reads were obtained from Rb-mock, Sb-mock, Rb-inf, and Sb-inf, respectively (Table S2). 26.1 M reads (90.6 %) in Rb-mock, 25.6 M reads (90.6 %) in Sb-mock, 18.5 M sequenced reads (71.7 %) in Rb-inf, and 19.4 M reads (72.4 %) in Sb-inf were mapped to the reference genome (Table S2).

Differentially expressed genes with and without *Foc* inoculation

The differentially expressed genes (DEGs) between inoculated and non-inoculated (mock treatment) samples were identified by Tophat/cuffdiff using two criteria, two-fold difference ($\log_2$ ratio ≥ 1.0) and 95% confidence. In the resistant lines of Fusarium yellows after inoculation 200 DEGs were identified between Rb-mock and Rb-inf, including 124 up-regulated and 76 down-regulated genes (Table S3, S4). 174 DEGs, including 137 up-regulated and 37 down-regulated genes, between Sb-mock and Sb-inf in the susceptible lines of Fusarium yellows were detected after inoculation (Table S3, S4). Sixty-six up-regulated genes and 14 down-regulated genes were detected after inoculation in both the resistant and susceptible lines (Table S3). 304 genes showed differential expression levels between Rb-inf and Sb-inf. 154 of the 304 genes (50.7 %) showed differential expression levels between Rb-mock and Sb-mock (data not shown). There were no difference in expression levels of Bra012688 and Bra012689 between Rb-mock and Rb-inf and both were not expressed in Sb-mock and Sb-inf (Fig. 1b).

Detection of gene expression levels after inoculation of *Foc*

Among the DEGs detected by RNA-seq, six genes showing up-regulation after inoculation in the resistant and/or susceptible lines (*GSTF3*, *GSTU13*, *JR1*, *PR3*, *PR4*, and *TPS04*) were selected to examine the expression levels at 6, 12, 24, and 72 HAI. The expression levels increased at 72 HAI (Fig. 2). These expression patterns were categorized into three groups, Group-1; increased expression levels at 72 HAI in the resistant line (*JR1* and *TPS04*), Group-2; increased expression levels at 72 HAI in the susceptible line (*GSTU13*, *PR3*, and *PR4*), and Group-3; increased expression levels at 72 HAI in the both lines (*GSTF3*) (Fig. 2). The results obtained from qPCR analysis corresponded with the RNA-seq data (Fig. 2).

Gene expression levels at 24 and 72 hours after inoculation with *Foc*

The six genes above, which are involved in pathogen resistance or immune response, indicated that gene expression started to increase after 24 HAI in the resistant and/or susceptible lines, thus the RNA-seq analysis was repeated using whole plants at 24 HAI. We also performed RNA-seq analysis using whole plants at 72 HAI before the appearance of disease symptoms in susceptible lines.

RNA-seq of four libraries produced clean reads of 11.6 M, 11.7 M, 11.7 M, and 11.6 M from R-24h-mock, S-24h-mock, R-24h-inf, and S-24h-inf, respectively, and about 80% of these reads were mapped to the reference genome (Table S2). 29.5 M, 28.8 M, 28.8 M, and 26.1 M clean reads were obtained from R-72h-mock, S-72h-mock, R-72h-inf, and S-72h-inf, respectively (Table S2), and about 90 % of these reads were mapped to the reference genome (Table S2).

The DEGs were identified by Tophat/cuffdiff with two criteria, two-fold difference ($\log_2$ ratio ≥ 1.0) and 95% confidence at 24 HAI. 260 DEGs including 245 up-regulated and 15 down-regulated genes were identified between R-24h-mock and R-24h-inf in the resistant line (Table S3, S5). There were 253 DEGs including 207 up-regulated and 46 down-regulated genes identified between S-24h-mock and S-24h-inf in the susceptible line (Table S3, S5). There were 123 up-regulated genes and five down-regulated genes in both the resistant and susceptible lines (Fig. 3a). The expression levels of 344 genes were significantly different between R-24h-inf and S-24h-inf, and 238 of 344 genes (69.2 %) were significantly different between R-24h-mock and S-24h-mock (data not shown).

At 72 HAI, 83 up-regulated and 5 down-regulated genes were identified between R-72h-mock and R-72h-inf in the resistant line (Table S3, S6). There were 87 up-regulated and 22 down-regulated genes obtained between S-72h-mock and S-72h-inf in the susceptible line (Table S3, S6). There were 13 up-regulated genes and one down-regulated gene in both the resistant and susceptible lines (Fig. 3b). The expression levels of 257 genes were significantly different between R-72h-inf and S-72h-inf, and 170 of 257 genes (66.1 %) were significantly different between R-72h-mock and S-72h-mock (data not shown).

There were 13 up-regulated genes and one down-regulated gene common to 24 and 72 HAI in the resistant lines (Fig. 3c, Table 1). There were eight up-regulated genes and three down-regulated genes common to 24 and 72 HAI in the susceptible lines (Fig. 3c, Table 1).

Gene ontology analysis of differentially expressed genes after inoculation of *Foc*

The up- and down-regulated genes at 24 or 72 HAI in the resistant and/or susceptible lines were categorized into GO cellular component (CC), GO molecular function (MF), and GO biological process (BP). At 24 HAI, 83 and 121 categories were overrepresented in up-regulated genes in the resistant and susceptible lines, respectively ($p < 0.001$, $FDR < 0.05$). Seventy-four categories were overrepresented in the up-regulated genes in both resistant and susceptible lines (Table S7). None of the categories was overrepresented in down-regulated genes in the resistant line and two categories were overrepresented in the down-regulated genes in the susceptible line ($p < 0.001$, $FDR < 0.05$) (Table S7). The up-regulated genes from both the resistant and susceptible lines categorized into 'Response to biotic stimulus', 'Secondary metabolic process', 'Response to chemical stimulus', 'Response to stress', 'Defense response', 'Response to jasmonic acid stimulus', and 'Sulfur metabolic process' in BP were overrepresented (Fig. 4, Table S7). The genes categorized into 'Regulation of defense response', 'Response to salicylic acid stimulus', and 'Systemic acquired resistance' in BP tended to be overrepresented in the up-regulated genes of the resistant line (Fig. 4, Table S7). The genes categorized into 'Oxidoreductase activity' in MF and 'Tryptophan biosynthetic process', 'Response to chitin', 'Response to ethylene stimulus', 'Auxin biosynthetic process', 'Cell wall thickening', and 'Callose deposition in cell wall' in BP tended to be overrepresented in up-regulated genes of the susceptible line (Fig. 4, Table S7).

At 72 HAI, four categories in the resistant lines and 25 categories in the susceptible lines were overrepresented in up-regulated genes ($p < 0.001$, $FDR < 0.05$), and three categories in the resistance lines overlapped with the categories in the susceptible lines (Table S8). None of the categories were overrepresented in the down-regulated genes in resistant or susceptible lines. The up-regulated genes from both the resistant and susceptible lines categorized into 'Catalytic activity' in MF and 'Response to biotic stimulus' and 'Response to stress' in BP were overrepresented (Fig. 4, Table S8). The gene categorized into 'Response to jasmonic acid stimulus', 'Oxylipin metabolic process', 'Response to wounding', 'Fatty acid metabolic process', and 'Response to oxidative stress' in BP tended to be overrepresented in up-regulated genes of the susceptible line (Fig. 4, Table S8).

Validation of differential gene expression by quantitative real-time RT-PCR

Six genes (*BG3*, Bra037877 (Peroxidase superfamily protein), *GULLO2*, *JRG21*, *PDR12*, and *PRB1*) from up-regulated genes at 24 HAI in R-24h-inf/S-24h-inf were selected and the expression levels of these six genes at each time point of 6, 12, 24, or 72 HAI were examined by qPCR (Fig. S1). These genes were categorized into three groups in terms of their expression patterns, Group-1; increased expression levels at 72 HAI in the resistant line (Bra037877), Group-2; increased expression levels at 72 HAI in the susceptible line (*BG3*, *GULLO2*, *PDR12*, and *PRB1*), and Group-3; increased expression levels at 72 HAI in the both lines (*JRG21*) (Fig. S1).

In total, 12 genes (six genes up-regulated in Rb-inf / Sb-inf, six genes up-regulated in R-24h-inf / S-24h-inf) were selected, and two (*GULLO2*, *PDR12*) and one (*BG3*) of 12 genes showed up-regulation in the resistant and susceptible lines, respectively, at 24 HAI and 72 HAI (Table 1). In these 12 genes, the expression levels determined from qPCR analysis and RNA-seq data at 24 and 72 HAI were consistent with the RNA-seq data except for *PRB1* at 24 HAI and Bra037877 at 72 HAI (Fig. S2-S5).

Comparison of *Foc* inoculation responsive genes between species

The transcriptome analysis in *A. thaliana* after infection of *Fusarium oxysporum* has been performed (Zhu et al. 2013). The up- and down-regulated genes at 1 DPI (day-post-inoculation) were compared with our transcriptome data at 24 HAI in *B. rapa*. Twenty-nine up-regulated genes in R-24h-inf and 24 up-regulated genes in S-24h-inf overlapped with the up-regulated genes in *A. thaliana* at 1 DPI (Table 2, Fig. S6). These included genes encoding the peroxidase superfamily protein, chitinase, glutathione S-transferase, ACC OXIDASE 1, CYTOCHROME P450, and transcription factors such as WRKY51 and WRKY53 (Table 2). The expression levels at each time point of 6, 12, 24, or 72 HAI in two genes (Peroxidase superfamily protein (Bra037877/At4g08780) and *PDR12*), which showed up-regulation in R-24h-inf and *A. thaliana* at 1 DPI (Table 2), have been examined by qPCR (Fig. S1). Four genes (*GSTU10*, *HB1*, *WRKY51*, and *WRKY53*) from 29 up-regulated genes in R-24h-inf and *A. thaliana* at 1 DPI were selected and the expression levels of these four genes at each time point of 6, 12, 24, or 72 HAI were examined by qPCR (Table 2, Fig. 5). The qPCR results were consistent with

RNA-seq results at 24 and 72 HAI (Fig. S7, S8).

Discussion

Pathogen attack triggers complex signaling cascades regulated by molecules such as salicylic acid (SA), jasmonic acid (JA), and ethylene (ET), resulting in the expression of defense-related genes such as those encoding pathogenesis-related (PR) proteins (Glazebrook 2001). The SA-signaling pathway is often considered to be effective against the biotroph phase (pathogens that derive nutrients from living host cells), while JA- and ET-signaling pathways tend to be effective against the necrotroph phase (pathogens that derive nutrients from dead cells) (Glazebrook 2005; Beckers and Spoel 2006). *F. oxysporum* is considered a hemi-biotrophic pathogen, because it begins its infection cycle as a biotroph but changes to a necrotroph at the later stage (Lyons et al. 2015).

We previously identified candidates for Fusarium yellows resistance genes, Bra012688 and Bra012689 (Shimizu et al. 2014). In this study, we examined the expression levels of these two genes in the resistant lines at four time points (6, 12, 24, and 72 hours) after *Foc* inoculation by qPCR. Though the expression level of Bra012689 at 72 HAI was slightly higher than those at other time points or with no inoculation, expression levels of these two genes did not change dramatically following *Foc* inoculation. This suggests that expression of resistance genes prior to infection is sufficient for Fusarium yellows resistance. We also examined the expression levels of 16 genes in the resistant and susceptible lines at four time points (6, 12, 24, and 72 hours) after *Foc* inoculation by qPCR. Most genes increased their expression levels at all time points in resistant and/or susceptible lines. Expression of antimicrobial PR genes, *PR3* and *PR4*, was more induced in the susceptible lines than those in the resistant lines at 72 HAI. *PR3* and *PR4* are known as key genes for JA/ET-mediated resistance to necrotroph pathogens (Spoel and Dong 2012), suggesting that the phase change from biotroph to necrotroph occurs in susceptible lines from 24 to 72 HAI. However, the JA/ET-mediated disease resistance response might not be effective in activating resistance in the susceptible line, and up-regulation of *PR3* and *PR4* might be a response to a shift to necrotroph phase. *TPS04*, *JR1*, and Bra037877 (peroxidase) were expressed at higher levels in the resistant lines than in the susceptible lines at 72 HAI, suggesting that they are more involved in defense response than genes showing similar expression patterns between the resistant and susceptible lines, or

with higher expression levels in the susceptible lines than in the resistant lines.

Previous reports of the transcriptome analyses by *F. oxysporum* infection used one line assessing different time points (Zhu et al. 2013; Lyons et al. 2015; Xing et al. 2016). However, we used both resistant and susceptible lines for transcriptome analysis, which enables us to compare the transcriptional change between the resistant and susceptible lines. We identified DEGs between non-inoculated and inoculated plants at 24 and 72 hours after *Foc* inoculation in the resistant and susceptible lines. In both cases, about 80% of DEGs were up-regulated in both resistant and susceptible lines. The constant up-regulation of most DEGs by *F. oxysporum* infection was also observed in *A. thaliana* (Zhu et al. 2013), while no such bias was observed in the same material from a different group (Lyons et al. 2015). In cabbage, a ratio between up- and down-regulated genes by *Foc* infection was dependent on the time point (Xing et al. 2016). These results suggest that the trend of up-regulation by *Foc* inoculation observed in our study is not a fundamental reaction of host plants. About 50% of up-regulated genes overlapped between the resistant and susceptible lines at 24 HAI, while about 15% of up-regulated genes overlapped at 72 HAI. These results suggest that the half of the up-regulated genes were involved in the basic defense response rather than the specific reaction for Fusarium yellows resistance at 24 HAI, but the difference of the reaction between resistant and susceptible lines became clear at 72 HAI.

At 24 HAI, categories in ‘Systemic acquired resistance’, ‘Regulation of defense response’, and ‘Response to salicylic acid stimulus’ were overrepresented in up-regulated genes in the resistant lines. The up-regulated genes in the resistant lines at 24 HAI categorized into ‘Systemic acquired resistance’, *PR2* (Pathogenesis-related 2), *PR4*, *ICS1/SID2* (*ISOCHORISMATE SYNTHASE 1*), and *WRKY70* were involved. *ICS1/SID2* is involved in SA biosynthesis including pathogen-induced biosynthesis, and *WRKY70* is activated by SA (Strawn et al. 2007; Garcion et al. 2008; Li et al. 2004). Overrepresentation in those categories of ‘Systemic acquired resistance’ and ‘Regulation of defense response’ was not observed in the up-regulated genes in the resistant lines at 72 HAI. These results indicate that SA-dependent SAR, which is known as ETI and is effective against a biotroph phase, occurs in the resistant lines of Chinese cabbage at the early time point (24 HAI). A similar hypothesis that SA-dependent SAR is involved in the defense response against *Foc* infection has been discussed in

cabbage (Xing et al. 2016). In contrast, categories of ‘Cell wall thickening’ and ‘Callose deposition in cell wall’ were overrepresented in the susceptible lines at 24 HAI, and categories related to auxin biosynthesis were also overrepresented. Genes involved in tryptophan biosynthesis or IAA (Indole Acetic Acid) and IGs (Indolic Glucosinolates) biosynthesis such as *ASA1* (*ANTHRANILATE SYNTHASE ALPHA SUBUNIT 1*), *TSA1* (*TRYPTOPHAN SYNTHASE ALPHA CHAIN 1*), *TSB2* (*TRYPTOPHAN SYNTHASE BETA-SUBUNIT 2*), and *CYP79B2*, were up-regulated at 24 HAI in the susceptible lines, and some of which were involved in the categories of ‘Cell wall thickening’ and ‘Callose deposition in cell wall’. Genes categorized into the synthesis of tryptophan were induced by *F. oxysporum* infection in *A. thaliana*, but endogenous auxin levels were not affected by the *F. oxysporum* disease development (Kidd et al. 2011). The negative impact of auxin in SA-mediated defense against biotrophic pathogens has been demonstrated (Chen et al. 2007; Wang et al. 2007), suggesting that induction of the genes categorized into ‘Tryptophan biosynthetic process’ results in the failure of SAR induction in the susceptible lines.

At 72 HAI, four categories were overrepresented in the up-regulated genes of the resistant lines, but three of the four categories overlapped with the categories overrepresented in the up-regulated genes of the susceptible lines. By contrast, more categories were overrepresented in the susceptible lines including the categories of ‘Response to jasmonic acid stimulus’, ‘Response to wounding’, and ‘Response to oxidative stress’. Category of ‘Response to ethylene stimulus’ tended to be overrepresented in up-regulated genes of the susceptible line at 24 HAI and category of ‘Response to jasmonic acid stimulus’ was overrepresented in the susceptible line but not in the resistant line at 72 HAI. These results suggest that the susceptible lines activate the JA- and ET-signaling pathways, which are effective against the necrotroph phase, but the resistant lines do not. In the case of cabbage, *F. oxysporum* was observed in an outer layer of a root apex in the susceptible lines at 1 day post infection (dpi) but not in the resistant lines at 1 dpi (Pu et al. 2016), suggesting that the difference of transcriptome reactions in the resistant and susceptible lines becomes clear from 24 and 72 HAI, which might be consistent with the time when *Foc* multiplies in susceptible lines.

We compared our transcriptome profile with previous reports using *A. thaliana* at the same time points after *Foc* inoculation (Zhu et al. 2013). There are few genes that overlapped between the two data sets (*B. rapa* and *A. thaliana*) in the down-regulated genes, suggesting that down-regulated genes

have no relationship with the defense response or are species-specific reactions against *Foc* infection. Some up-regulated genes overlapped between the two data sets and contained genes related to defense responses such as chitinase (*CHI*, *Chitinase family protein*), glutathione S-transferase (*GSTU10*, *GSTU12*), β -glucosidase (*BGLU27*), and peroxidase superfamily proteins. WRKY transcription factors have been implicated in regulating defense responses against pathogen infection (Dong et al. 2003; Pandey and Somssich 2009), and *WRKY51* and *WRKY53* were up-regulated in the resistant lines of Chinese cabbage and *A. thaliana*. *WRKY51* and *WRKY53* are involved in the defense response against *Pseudomonas syringae* in *A. thaliana* (Gao et al. 2011; Murray et al. 2007; Wang et al. 2006). *WRKY70* was also up-regulated in the resistant lines of Chinese cabbage, and *WRKY46*, *WRKY53*, and *WRKY70* play overlapping and synergistic roles in plant basal defense in *A. thaliana* (Hu et al. 2012), suggesting that *WRKY53* and *WRKY70* may act cooperatively as positive regulators for resistance to *Foc* in Chinese cabbage. The shared genes, including fundamental defense response genes, between related species such as Chinese cabbage, cabbage, and *A. thaliana* may contain key genes for resistance to *F. oxysporum*.

In conclusion, our RNA-seq analysis detected that genes tended to be up-regulated in both the resistant and susceptible lines at 24 and 72 HAI with *Foc* infection. About 50% of up-regulated genes at 24 HAI overlapped between resistant and susceptible lines but some resistant or susceptible line-specific GO terms were overrepresented. At 72 HAI, the number of up-regulated genes common to resistant and susceptible lines decreased, suggesting that the difference of gene expression between them becomes clearer. The resistant lines activated the genes involved in disease resistance such as ‘Systemic acquired resistance’, ‘Regulation of defense response’, and ‘Response to salicylic acid stimulus’ at 24 HAI but not 72 HAI, suggesting the defense response against *Foc* may be established by up-regulating the genes involved in resistance reactions at 24 HAI. By contrast, the susceptible lines activated the genes involved in many types of categories such as ‘Response to chitin’, ‘Response to ethylene stimulus’, ‘Auxin biosynthetic process’, ‘Cell wall thickening’, ‘Response to jasmonic acid stimulus’, ‘Response to wounding’, and ‘Response to oxidative stress’ at 24 and/or 72 HAI. However, induction of these genes was not effective against *Foc* infection in the susceptible lines. Our results indicate activation of ETI such as SA-dependent SAR by recognition of Avr by the R protein is important for Fusarium yellows resistance. We detected the SA-dependent SAR-related genes, *PR2*, *PR4*, and some WRKY family genes,

as DEGs in resistant lines. Further research will focus on functional validation of the selected DEGs, which could be useful tools for breeding *Foc* resistance in Chinese cabbage.

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Conflict of interest

The authors declare that they have no conflict of interest.

Author contribution

RF, K. Okazaki, and ESD designed research. NM, M. Shimizu, M. Sato, YE, and ST performed research. M. Shimizu analyzed the RNA-seq data. MK developed materials. NM, MS, JM, K. Osabe, ESD, and RF wrote the paper.

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Figure legends

Figure 1. Expression levels of Bra012688 (*FocBr1a*) and Bra012689 (*FocBr1b*) in the *Fusarium* yellows resistant line, RJKB-T23, and susceptible line, RJKB-T24, after inoculation of *Foc*. (a) Values are means $\pm$ s.e. (three biological and technical replicates) of relative expression levels of

Bra012688 and Bra012689 compared with *Bractin* quantitated by real-time RT-PCR at 6, 12, 24, and 72 hours after inoculation (HAI). NI, non-inoculated samples. (b) The values of fragments per kilo-base per million (FPKM) were calculated by data from RNA-seq analysis. Rb-mock, mock-inoculated bulked samples (6, 12, 24, and 72 HAI) from the resistant line (RJKB-T23); Sb-mock, mock-inoculated bulked samples (6, 12, 24, and 72 HAI) from the susceptible line (RJKB-T24); Rb-inf, inoculated bulked samples (6, 12, 24, and 72 HAI) from the resistant line (RJKB-T23); Sb-inf, inoculated bulked samples (6, 12, 24, and 72 HAI) from the susceptible line (RJKB-T24).

Figure 2. Gene expression levels of up-regulated genes after *Foc* inoculation measured by quantitative real-time RT-PCR. Six genes, *GSTF3* (Group-3), *GSTU13* (Group-2), *JR1* (Group-1), *PR3* (Group-2), *PR4* (Group-2), and *TPS04* (Group-1), whose expression was up-regulated in Rb-inf and/or Sb-inf were examined. Expression levels of these six genes were measured by real-time RT-PCR at 6, 12, 24, and 72 hours after *Foc* inoculation (HAI). Values are means $\pm$ s.e. (three biological and technical replicates) of relative expression levels compared with *Bractin* are shown. The values of fragments per kilo-base per million (FPKM) were calculated by data from RNA-seq analysis. Rb-mock, mock-inoculated bulked samples (6, 12, 24, and 72 HAI) from the resistant line (RJKB-T23); Sb-mock, mock-inoculated bulked samples (6, 12, 24, and 72 HAI) from the susceptible line (RJKB-T24); Rb-inf, inoculated bulked samples (6, 12, 24, and 72 HAI) from the resistant line; Sb-inf, inoculated bulked samples (6, 12, 24, and 72 HAI) from the susceptible line. HAI, hours after inoculation. NI, non-inoculated samples.

Figure 3. Venn diagram of differentially expressed genes in *Foc* inoculated samples compared with mock-inoculated samples. (a) Up- or down-regulated genes in inoculated samples at 24 HAI between resistant and susceptible lines. R-24h-inf UP/DOWN, up- / down-regulated genes in the inoculated whole plants compared with genes in the mock-inoculated whole plants in resistant line (RJKB-T23) at 24 HAI. S-24h-inf UP/DOWN, up- / down-regulated genes in the inoculated whole plants compared with genes in the mock-inoculated whole plants in the susceptible line (RJKB-T24) at 24 HAI. (b) Up- or down-regulated genes in inoculated samples at 72 HAI between resistant and susceptible lines. R-72h-inf

UP/DOWN, up- / down-regulated genes in the inoculated whole plants compared with genes in the mock-inoculated whole plants in resistant line at 72 HAI. S-72h-inf UP/DOWN, up- / down-regulated genes in the inoculated whole plants compared with genes in the mock-inoculated whole plants in the susceptible line at 72 HAI. (c) Up- or down-regulated genes in inoculated samples between 24 and 72 HAI.

Figure 4. Gene ontology classification of up-regulated genes after inoculation. R-24h-inf UP, up-regulated genes at 24 HAI in whole plants of the resistant line (RJKB-T23); S-24h-inf UP, up-regulated genes at 24 HAI in whole plants of the susceptible line (RJKB-T24). R-72h-inf UP, up-regulated genes at 72 HAI in whole plants of the resistant line; S-72h-inf UP, up-regulated genes at 72 HAI in whole plants of the susceptible line.

Figure 5. Gene expression levels after *Foc* inoculation measured by quantitative real-time RT-PCR in the *Fusarium* yellows resistant and susceptible lines. Four genes, *GSTU10*, *HB1*, *WRKY51*, and *WRKY53*, whose expression was up-regulated at 24 HAI in resistant line of *B. rapa* and 1 DPI (day-post-inoculation) in *A. thaliana*, were examined. Expression levels of these four genes were measured by real-time RT-PCR at 6, 12, 24, and 72 hours after *Foc* inoculation (HAI). Values are means $\pm$ s.e. (three biological and technical replicates) of relative expression levels compared with *Bractin* are shown. HAI, hours after inoculation. NI, non-inoculated samples.

Figure S1. Gene expression levels of up-regulated genes after *Foc* inoculation measured by quantitative real-time RT-PCR. Six genes, *BG3* (Group-2), *Bra037877* (Group-1), *GULLO2* (Group-2), *JRG21* (Group-3), *PDR12* (Group-2), and *PRB1* (Group-2), whose expression was up-regulated in R-24h-inf and/or S-24h-inf, were examined. Expression levels of these six genes were measured by real-time RT-PCR at 6, 12, 24, and 72 hours after *Foc* inoculation (HAI). Values are means $\pm$ s.e. (three biological and technical replicates) of relative expression levels compared with *Bractin* were shown. NI, non-inoculated samples.

Figure S2. Validation of six genes at 24 HAI by quantitative real-time RT-PCR. The expression levels quantified by real-time RT-PCR and RNA-seq data at 24 HAI were compared in six genes, whose expression was up-regulated in Rb-inf and/or Sb-inf. Values are means $\pm$ s.e. (three biological and technical replicates) of relative expression levels compared with *Bractin* are shown. The values of fragments per kilo-base per million (FPKM) were calculated by data from RNA-seq analysis. R-24h-mock, mock-inoculated samples of the resistant line (RJKB-T23); S-24h-mock; mock-inoculated samples of the susceptible line (RJKB-T24). R-24h-inf, inoculated samples at 24 HAI of the resistant line; S-24h-inf, inoculated samples at 24 HAI of the susceptible line; HAI, hours after inoculation. NI, non-inoculated samples.

Figure S3. Validation of six genes at 24 HAI by quantitative real-time RT-PCR. The expression levels quantified by real-time RT-PCR and RNA-seq data at 24 HAI were compared in six genes, whose expression was up-regulated in R-24h-inf and/or S-24h-inf. Values are means $\pm$ s.e. (three biological and technical replicates) of relative expression levels compared with *Bractin* are shown. The values of fragments per kilo-base per million (FPKM) were calculated by data from RNA-seq analysis. R-24h-mock, mock-inoculated samples of the resistant line (RJKB-T23); S-24h-mock; mock-inoculated samples of the susceptible line (RJKB-T24). R-24h-inf, inoculated samples at 24 HAI of the resistant line; S-24h-inf, inoculated samples at 24 HAI of the susceptible line; HAI, hours after inoculation. NI, non-inoculated samples.

Figure S4. Validation of six genes at 72 HAI by quantitative real-time RT-PCR. The expression levels quantified by real-time RT-PCR and RNA-seq data at 72 HAI were compared in six genes, whose expression was up-regulated in Rb-inf and/or Sb-inf. Values are means $\pm$ s.e. (three biological and technical replicates) of relative expression levels compared with *Bractin* are shown. The values of fragments per kilo-base per million (FPKM) were calculated by data from RNA-seq analysis. R-72h-mock, mock-inoculated samples of the resistant line (RJKB-T23); S-72h-mock; mock-inoculated samples of the susceptible line (RJKB-T24). R-72h-inf, inoculated samples at 72 HAI of the resistant line; S-72h-inf, inoculated samples at 72 HAI of the susceptible line; HAI, hours after inoculation. NI,

non-inoculated samples.

Figure S5. Validation of six genes at 72 HAI by quantitative real-time RT-PCR. The expression levels quantified by real-time RT-PCR and RNA-seq data at 72 HAI were compared in six genes, whose expression was up-regulated in R-24h-inf and/or S-24h-inf. Values are means $\pm$ s.e. (three biological and technical replicates) of relative expression levels compared with *Bractin* are shown. The values of fragments per kilo-base per million (FPKM) were calculated by data from RNA-seq analysis. R-72h-mock, mock-inoculated samples of the resistant line (RJKB-T23); S-72h-mock; mock-inoculated samples of the susceptible line (RJKB-T24). R-72h-inf, inoculated samples at 72 HAI of the resistant line; S-72h-inf, inoculated samples at 72 HAI of the susceptible line; HAI, hours after inoculation. NI, non-inoculated samples.

Figure S6. Venn diagram of up- or down-regulated genes in inoculated samples of *B. rapa* (24 HAI) compared with *A. thaliana* (1 DPI). R-24h-inf UP/DOWN, up- / down-regulated genes in the inoculated whole plants compared with genes in the mock-inoculated whole plants in resistant line (RJKB-T23) at 24 HAI (hours after inoculation). S-24h-inf UP/DOWN, up- / down-regulated genes in the inoculated whole plants compared with genes in the mock-inoculated whole plants in the susceptible line (RJKB-T24) at 24 HAI. At UP/DOWN, up- / down-regulated genes in inoculated samples at 1 DPI (day-post-inoculation) compared with genes in mock-inoculated samples in *A. thaliana*.

Figure S7. Validation of four genes at 24 HAI by quantitative real-time RT-PCR. The expression levels quantified by real-time RT-PCR and RNA-seq data at 24 HAI were compared in four genes, whose expression was up-regulated at 24 HAI in resistant line of *B. rapa* and 1 DPI (day-post-inoculation) in *A. thaliana*. Values are means $\pm$ s.e. (three biological and technical replicates) of relative expression levels compared with *Bractin* are shown. The values of fragments per kilo-base per million (FPKM) were calculated by data from RNA-seq analysis. R-24h-mock, mock-inoculated samples of the resistant line (RJKB-T23); S-24h-mock; mock-inoculated samples of the susceptible line (RJKB-T24). R-24h-inf, inoculated samples at 24 HAI of the resistant line; S-24h-inf, inoculated samples at 24 HAI of the

susceptible line; HAI, hours after inoculation. NI, non-inoculated samples.

Figure S8. Validation of four genes at 72 HAI by quantitative real-time RT-PCR. The expression levels quantified by real-time RT-PCR and RNA-seq data at 72 HAI were compared in four genes, whose expression was up-regulated at 24 HAI in resistant line of *B. rapa* (RJKB-T23) and 1 DPI (day-post-inoculation) in *A. thaliana*. Values are means $\pm$ s.e. (three biological and technical replicates) of relative expression levels compared with *Bractin* are shown. The values of fragments per kilo-base per million (FPKM) were calculated from the RNA-seq data analysis. R-72h-mock, mock-inoculated samples of the resistant line (RJKB-T23); S-72h-mock; mock-inoculated samples of the susceptible line (RJKB-T24). R-72h-inf, inoculated samples at 72 HAI of the resistant line (RJKB-T23); S-72h-inf, inoculated samples at 72 HAI of the susceptible line (RJKB-T24); HAI, hours after inoculation. NI, non-inoculated samples.

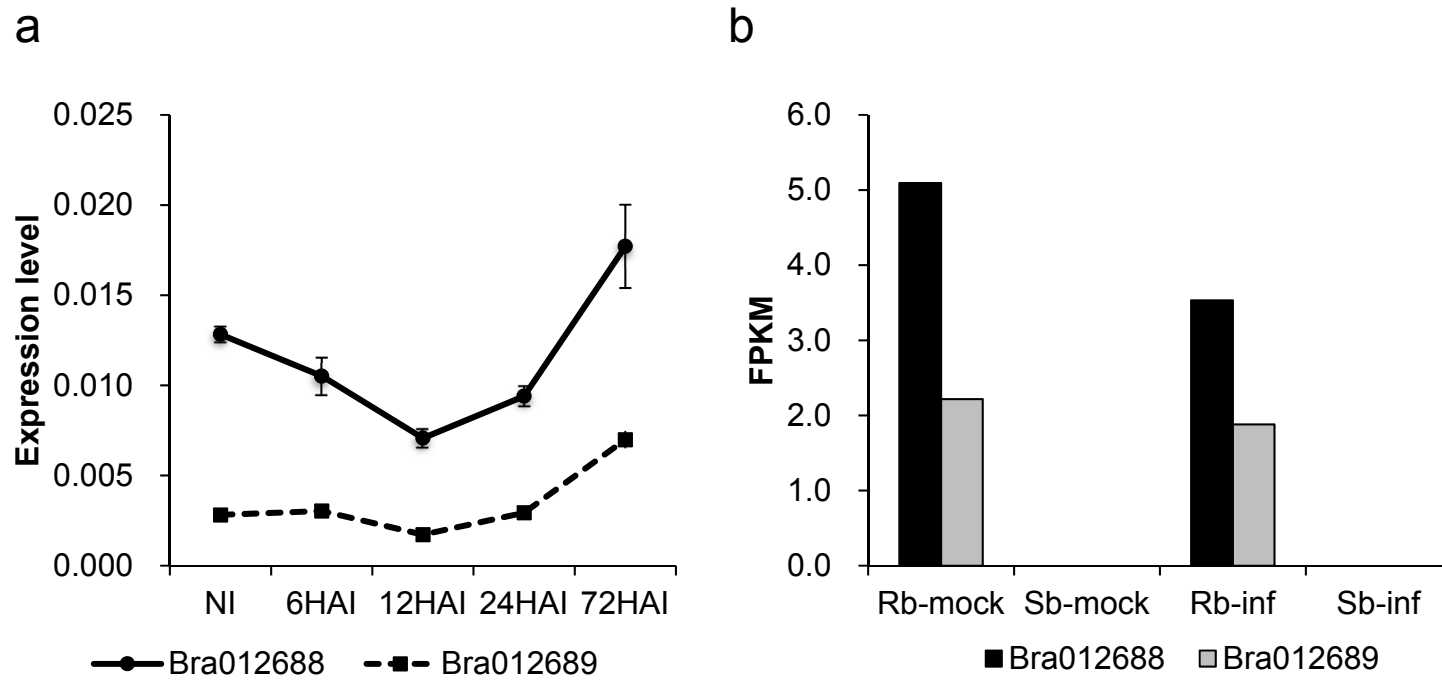


Fig. 1

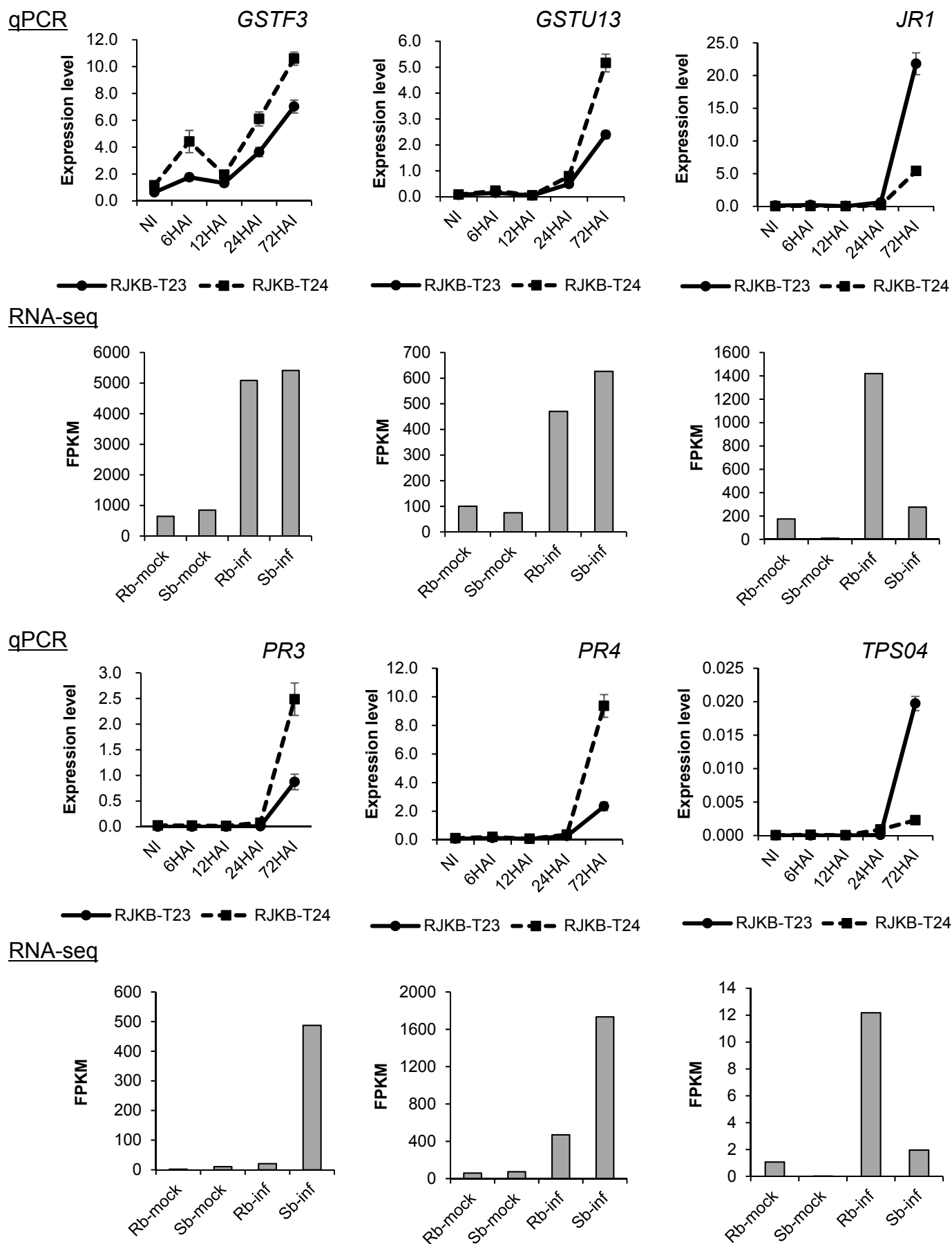
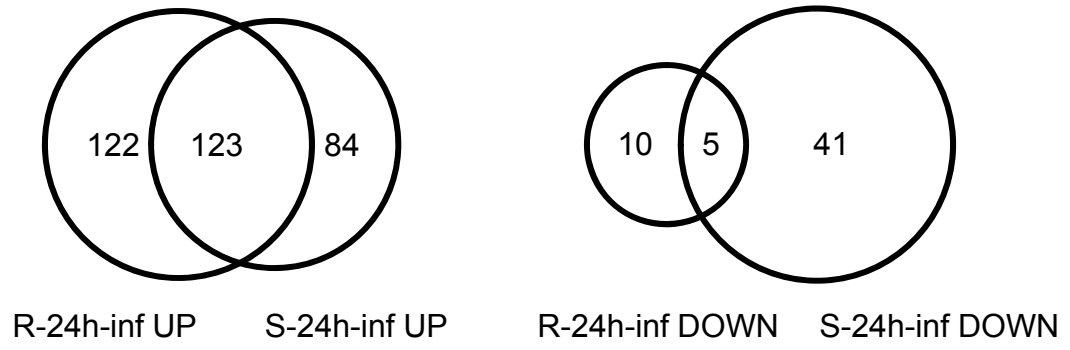
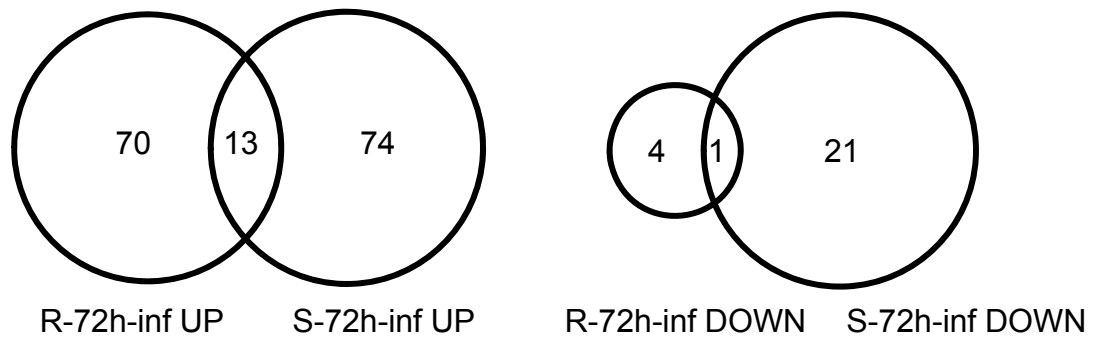


Fig. 2

a



b



c

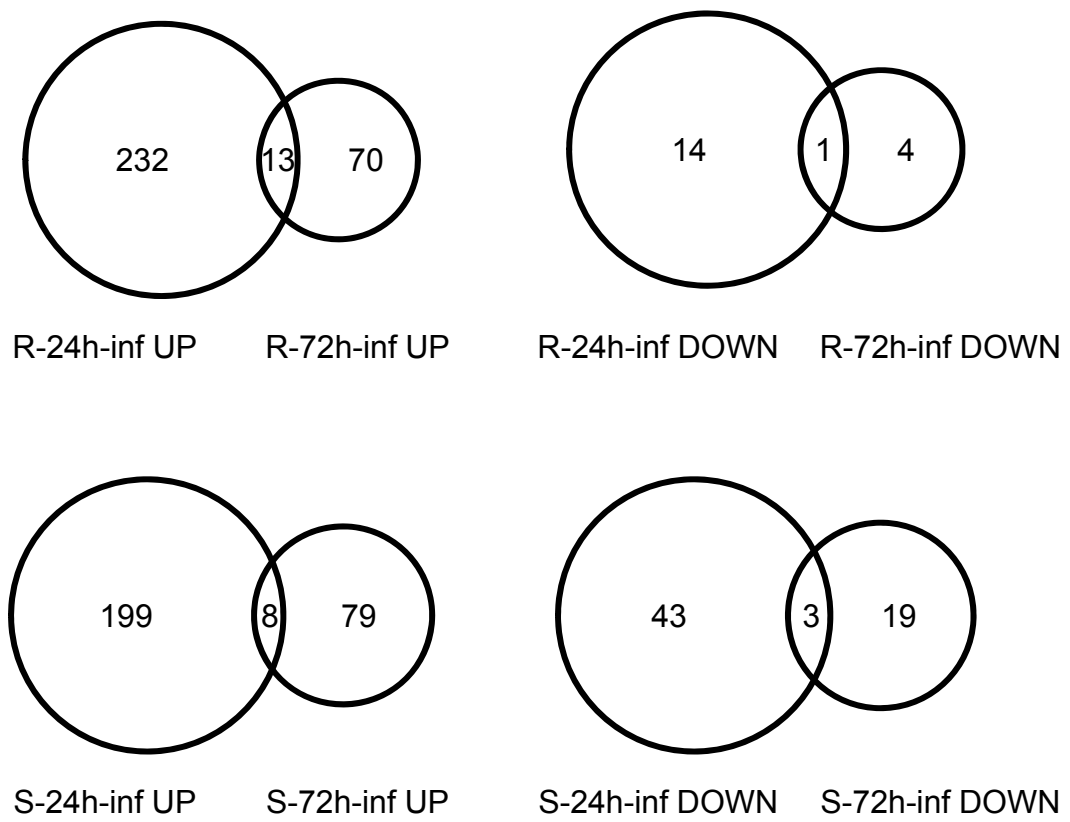


Fig. 3

Molecular Function

Catalytic activity

Hydrolase activity

Oxidoreductase activity

Biological Process

Auxin biosynthetic process

Callose deposition in cell wall

Cell wall thickening

Defense response

Fatty acid metabolic process

Oxylipin metabolic process

Regulation of defense response

Response to biotic stimulus

Response to chemical stimulus

Response to chitin

Response to ethylene stimulus

Response to jasmonic acid stimulus

Response to oxidative stress

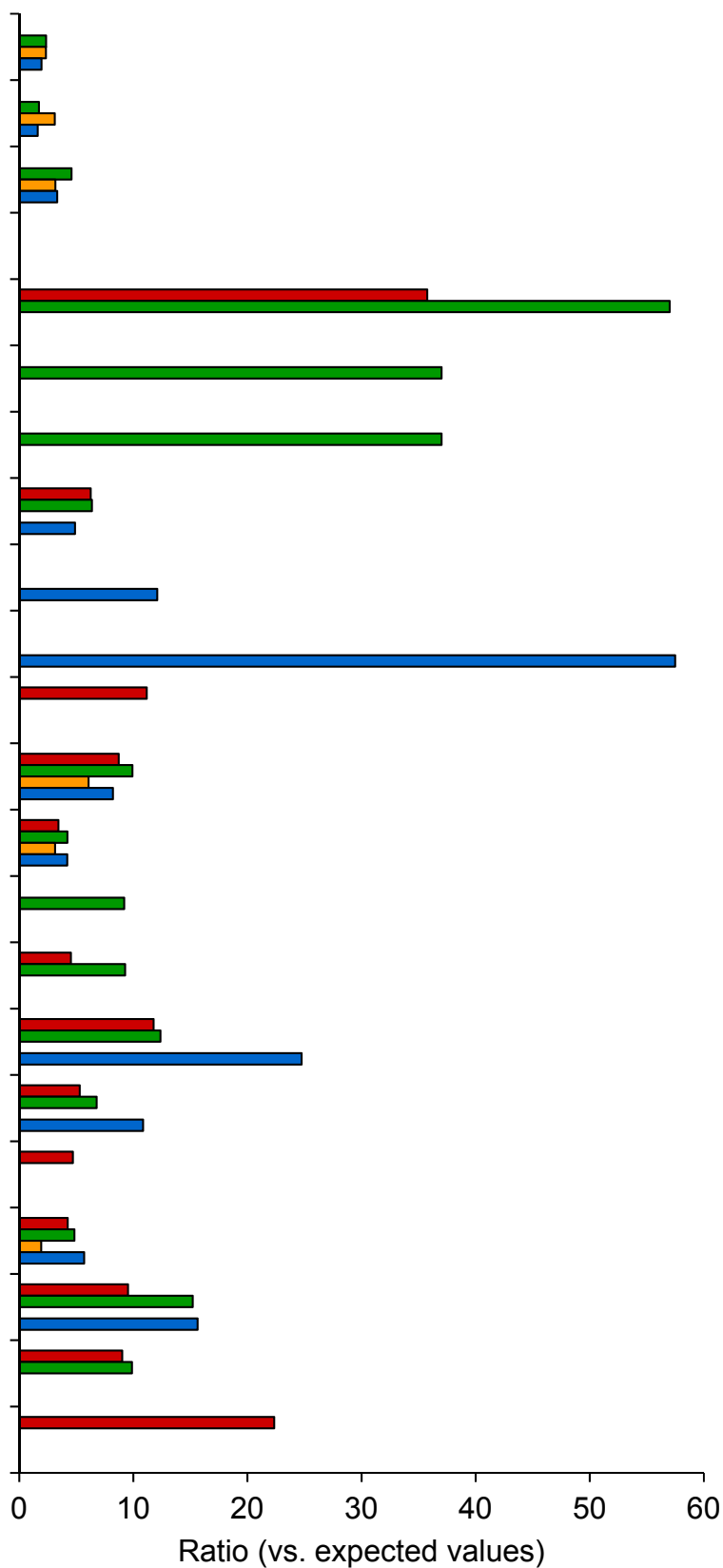
Response to salicylic acid stimulus

Response to stress

Response to wounding

Secondary metabolic process

Systemic acquired resistance



■ R-24h-inf UP ■ S-24h-inf UP ■ R-72h-inf UP ■ S-72h-inf UP

Fig. 4

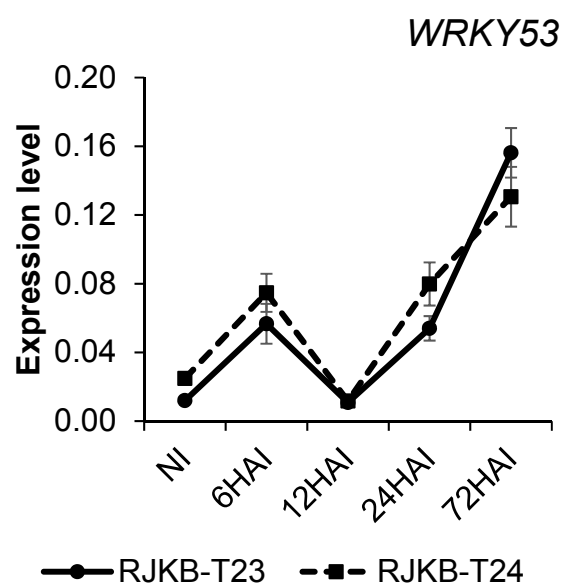
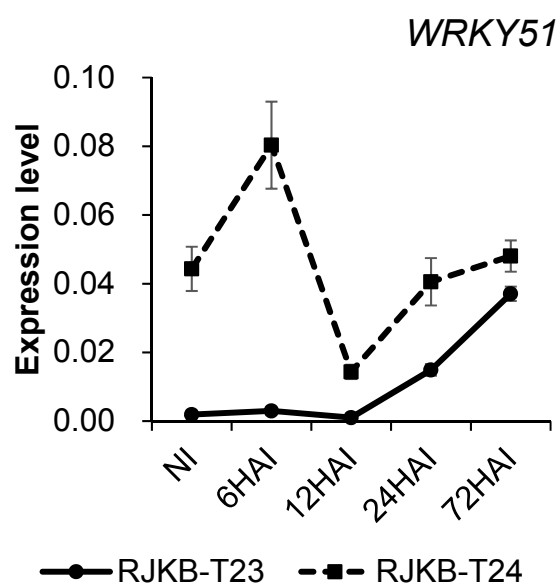
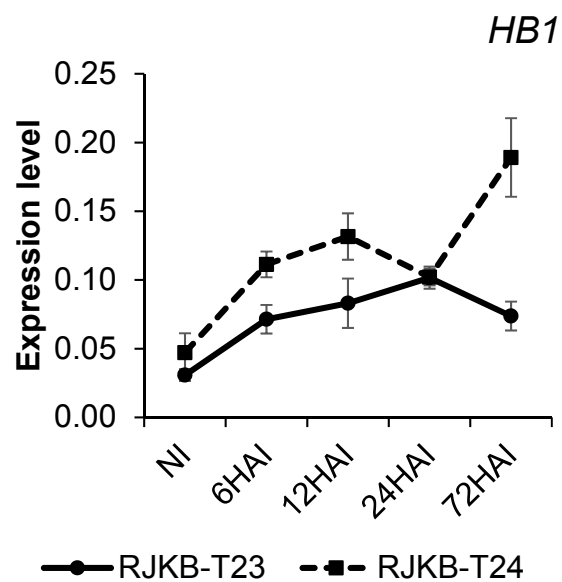
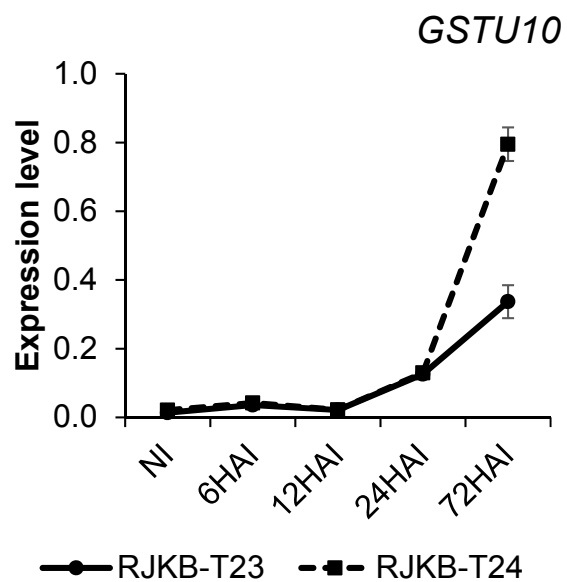


Fig. 5

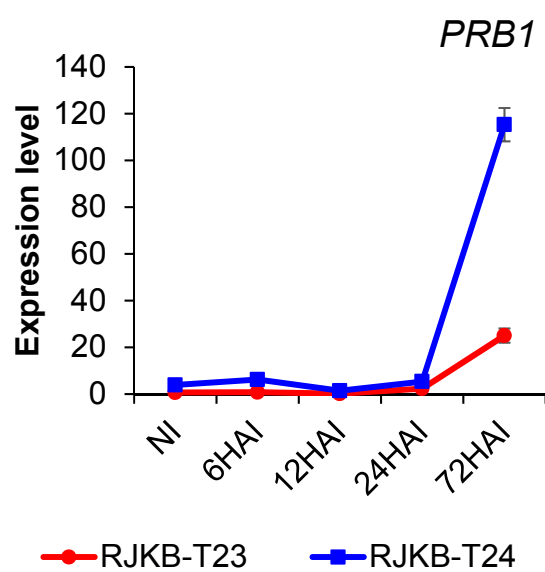
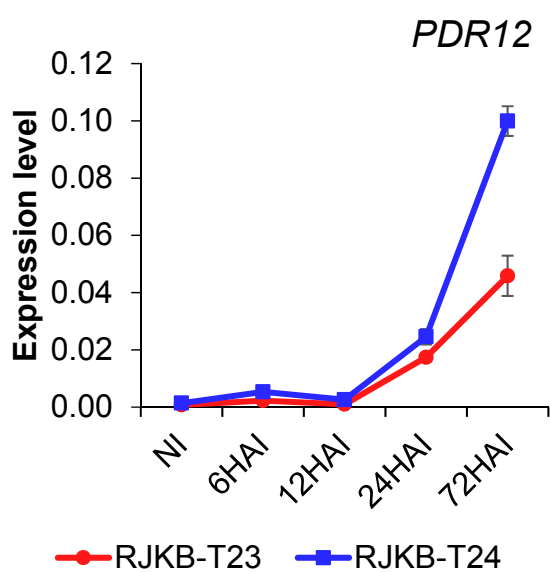
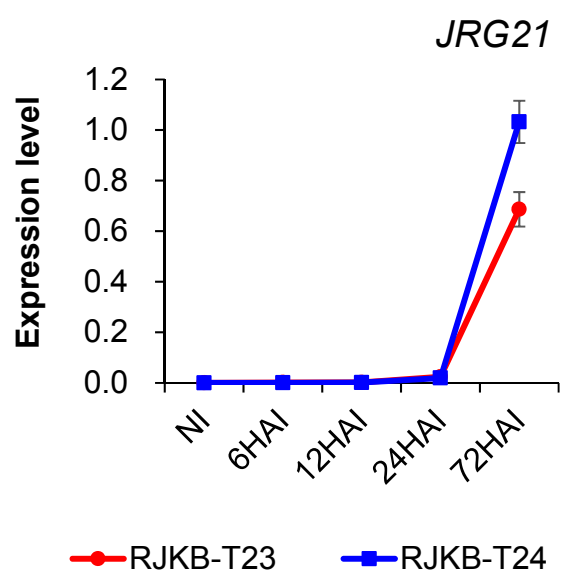
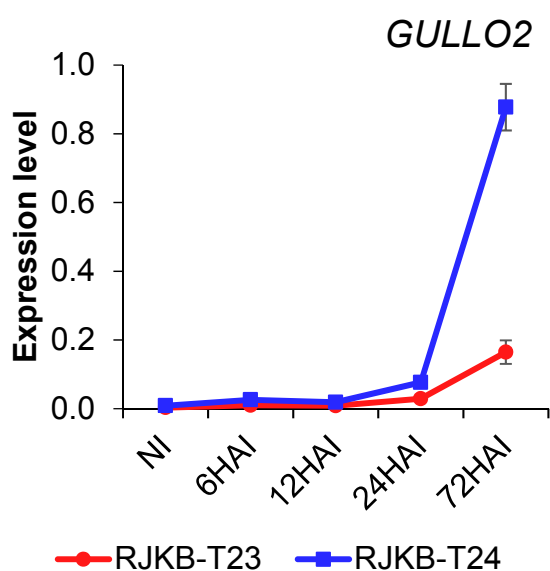
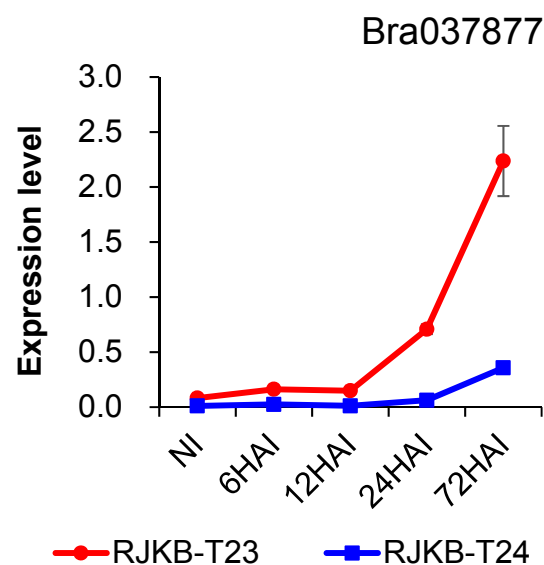
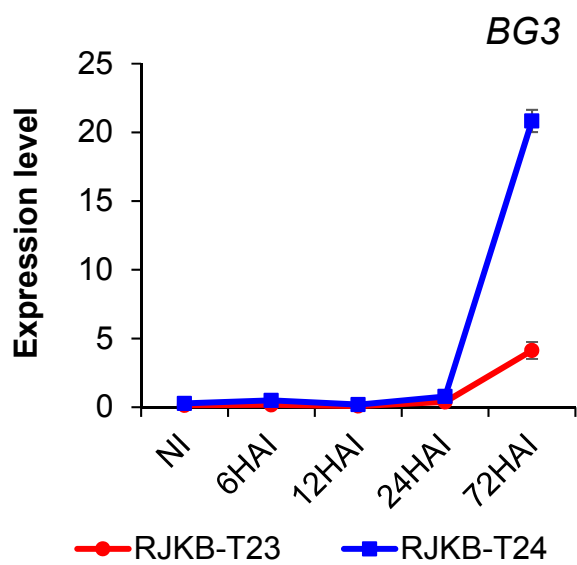
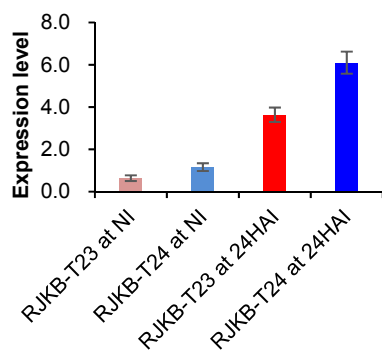


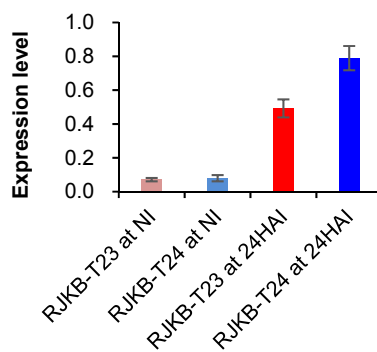
Fig. S1

qPCR

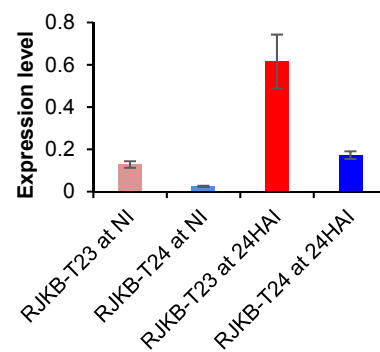
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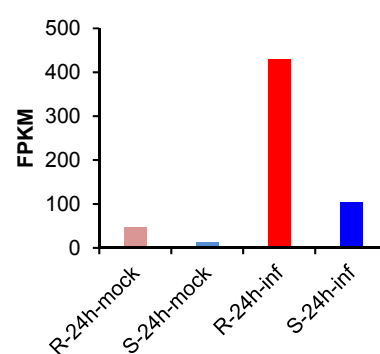
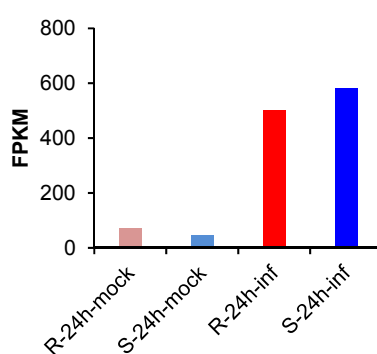
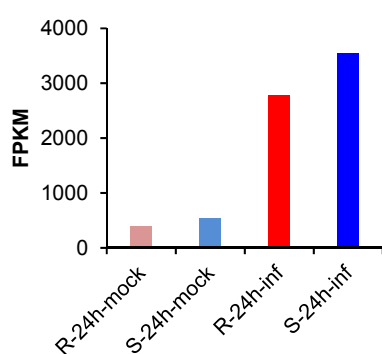
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JR1

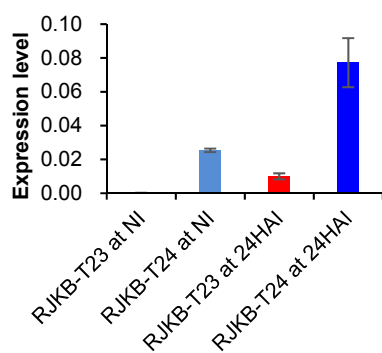


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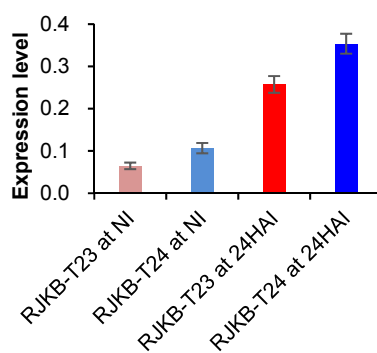


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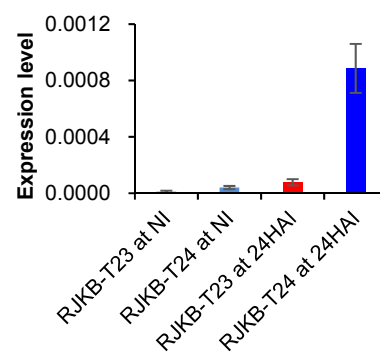
PR3



PR4



TPS04



RNA-seq

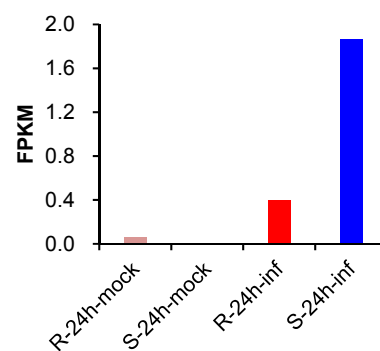
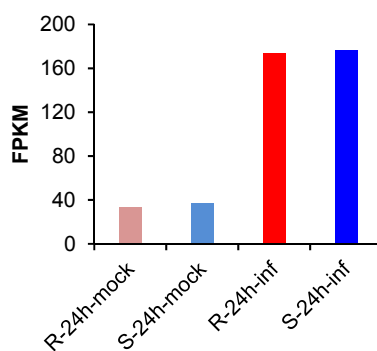
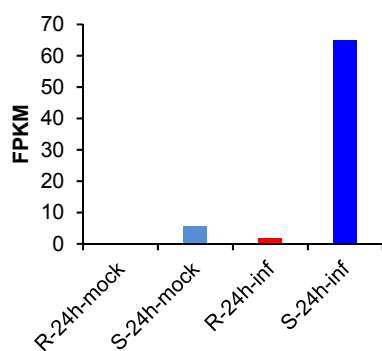


Fig. S2

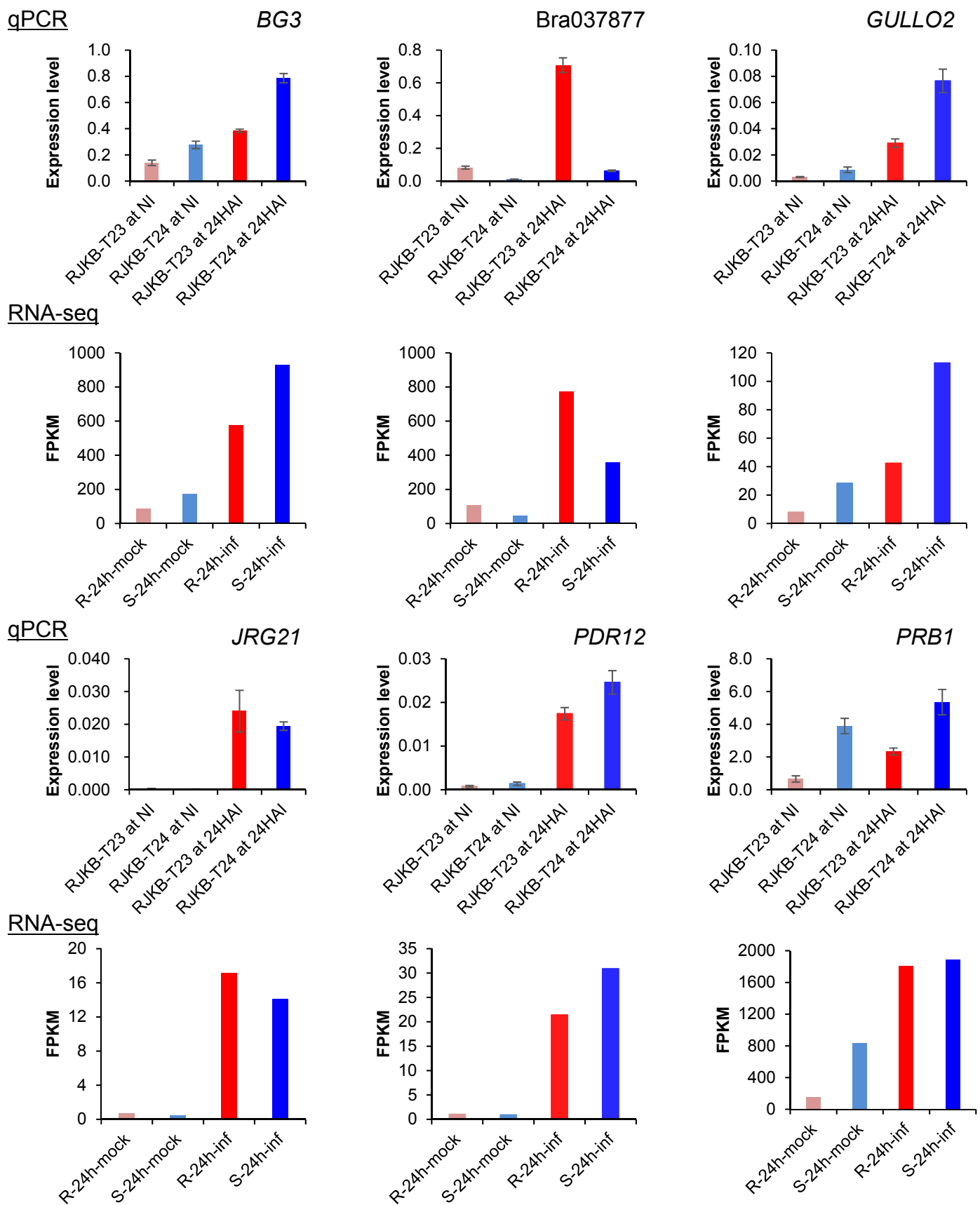
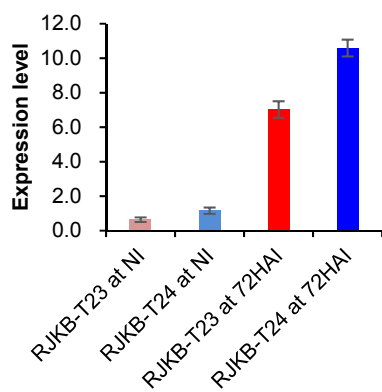


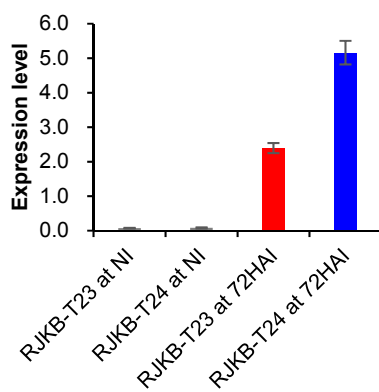
Fig. S3

qPCR

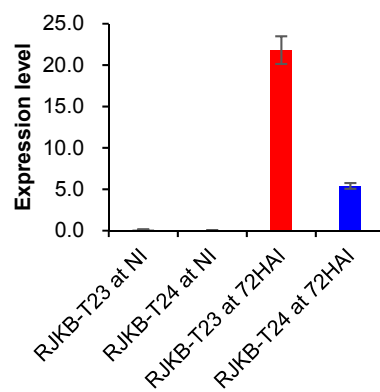
GSTF3



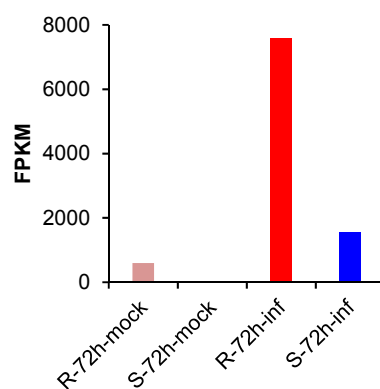
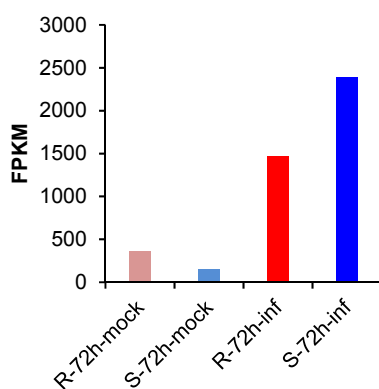
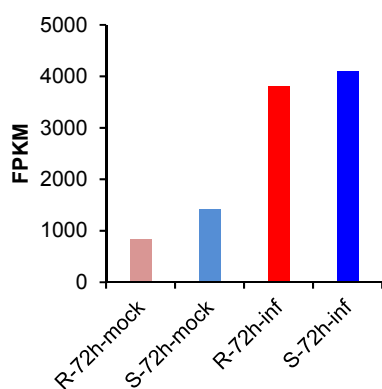
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JR1

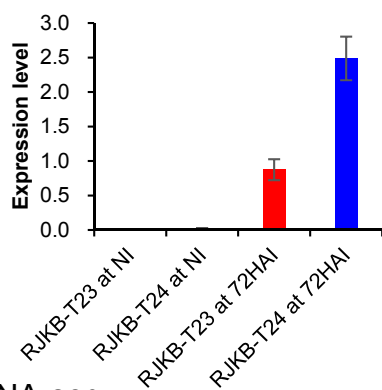


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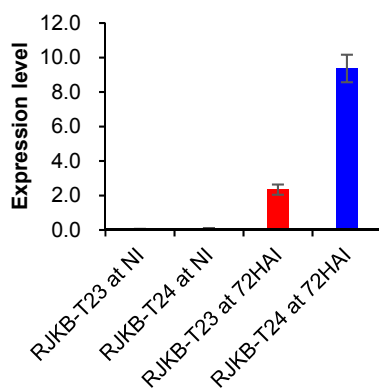


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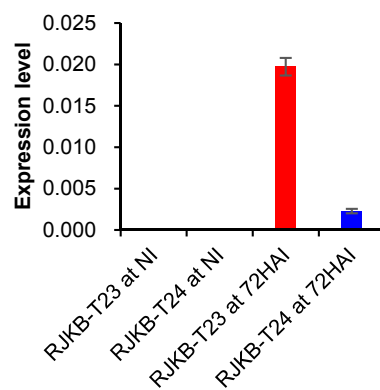
PR3



PR4



TPS04



RNA-seq

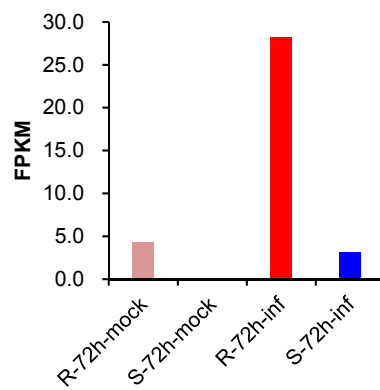
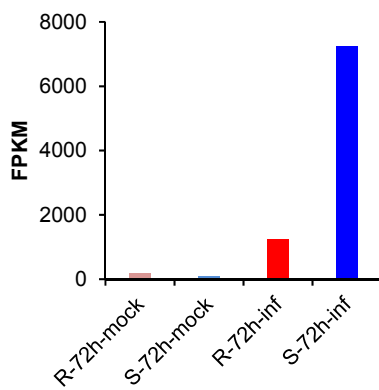
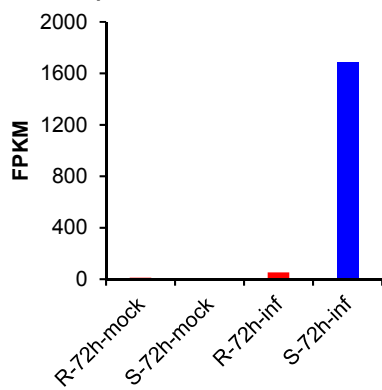


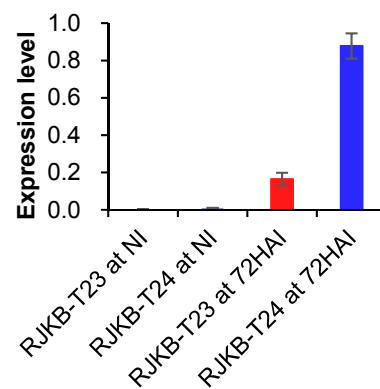
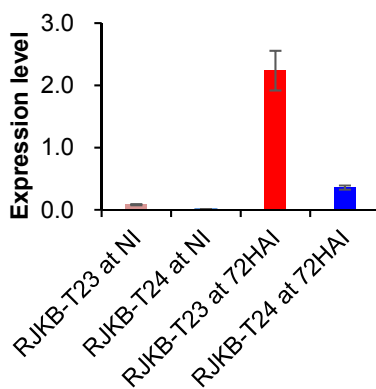
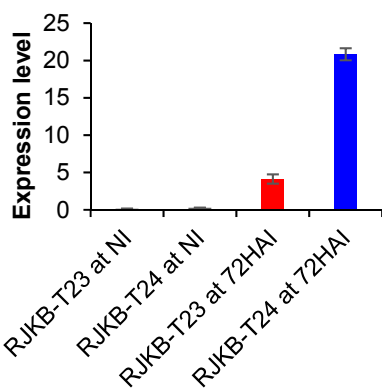
Fig. S4

qPCR

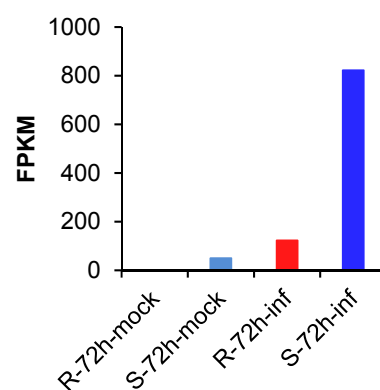
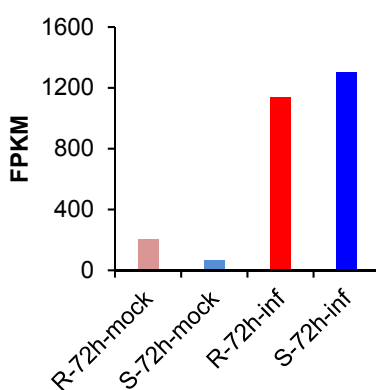
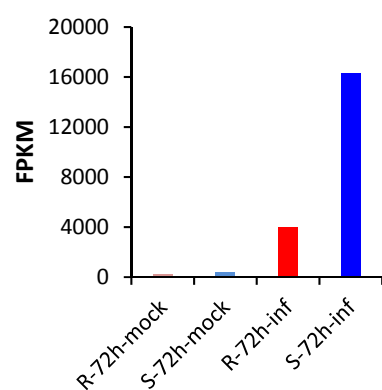
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Bra037877

GULLO2



RNA-seq

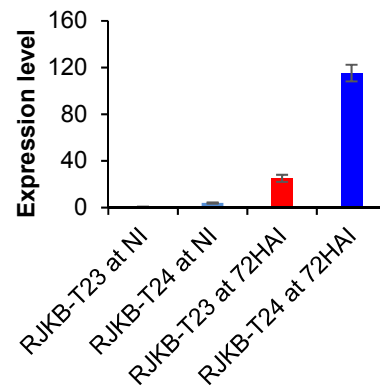
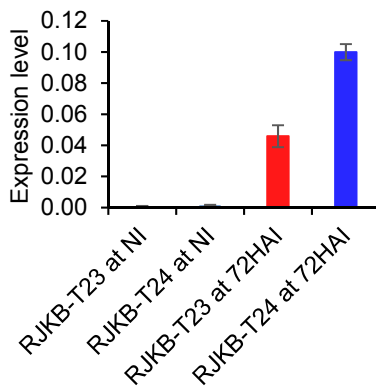
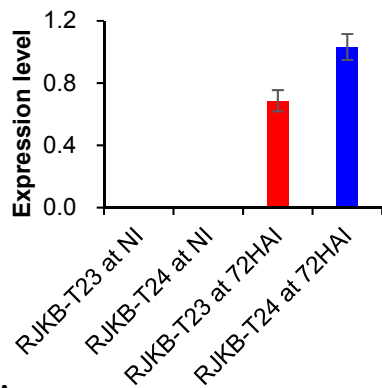


qPCR

JRG21

PDR12

PRB1



RNA-seq

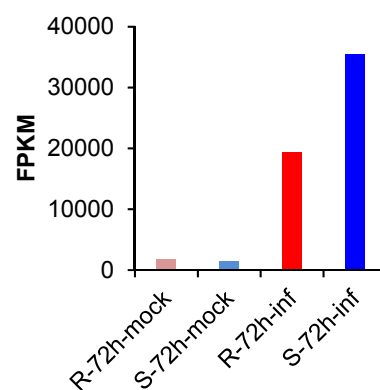
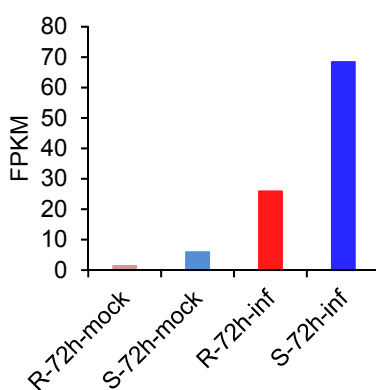
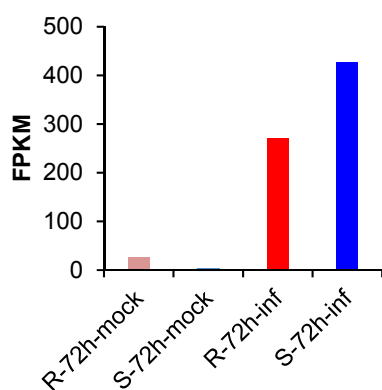


Fig. S5

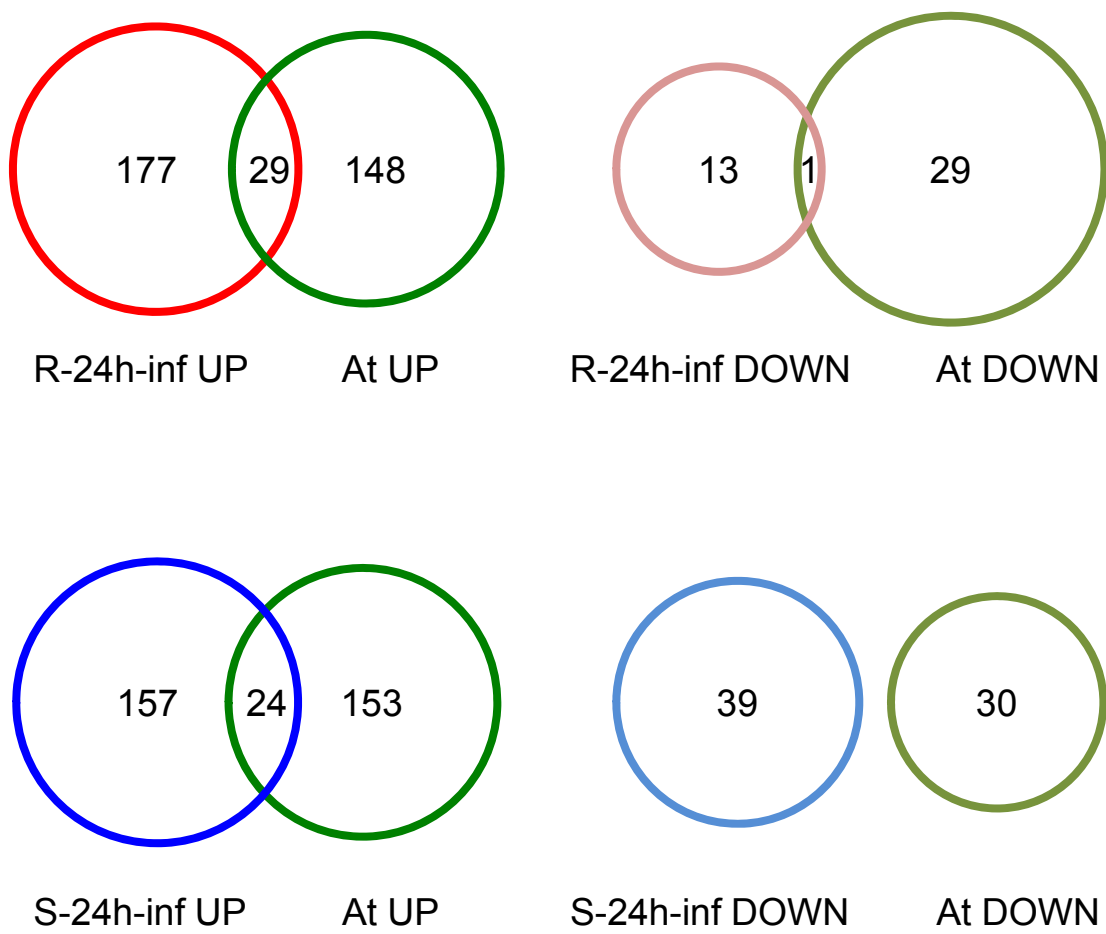
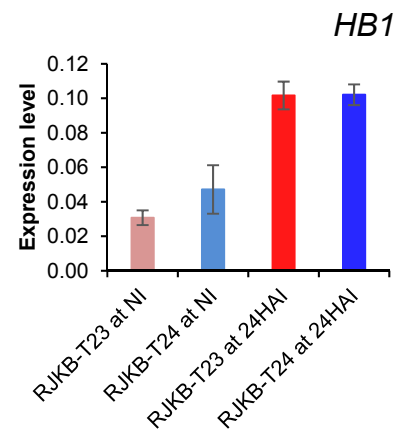
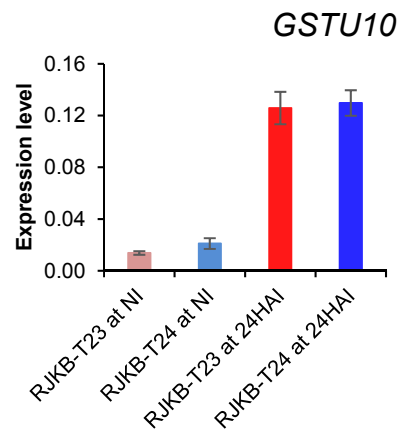
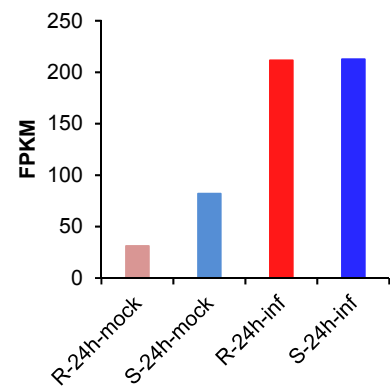
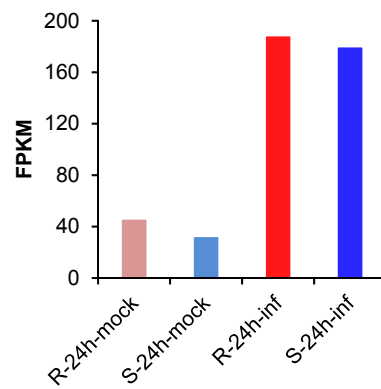


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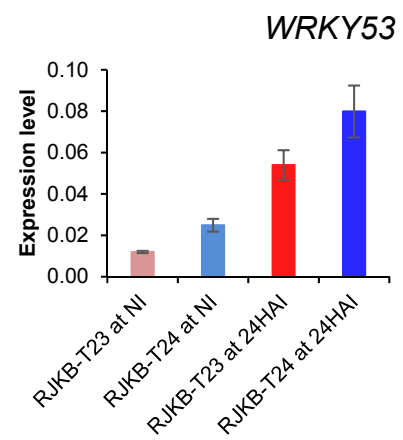
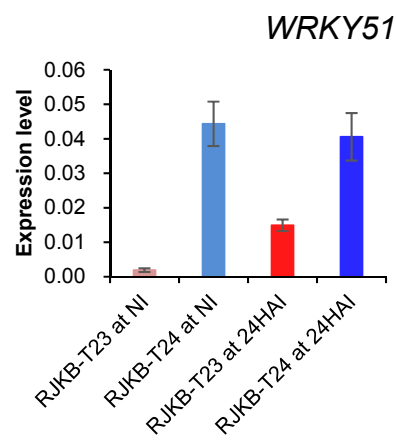
qPCR



RNA-seq



qPCR



RNA-seq

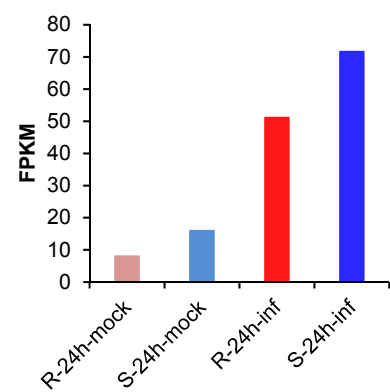
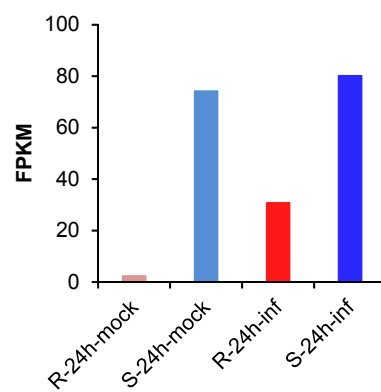
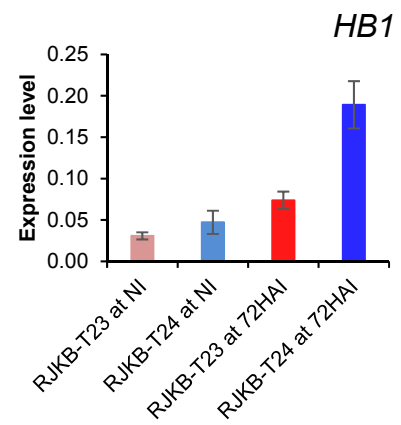
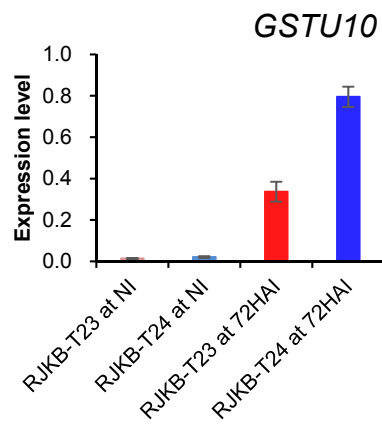
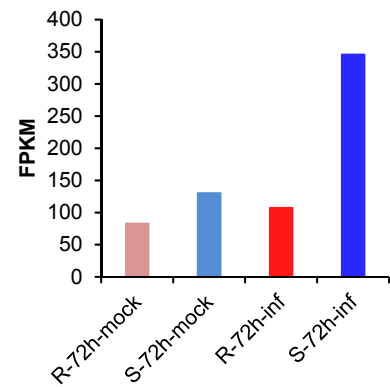
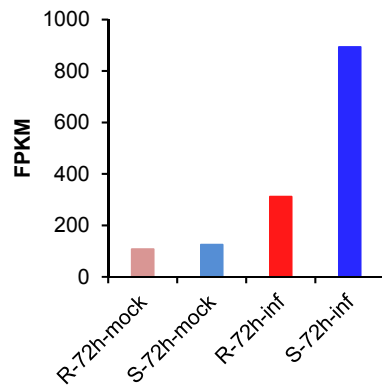


Fig. S7

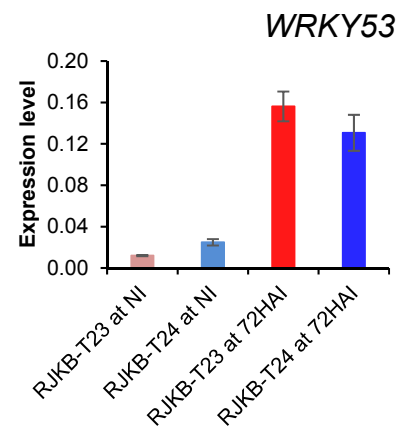
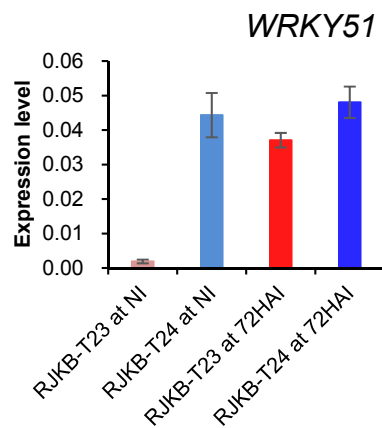
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RNA-seq



qPCR



RNA-seq

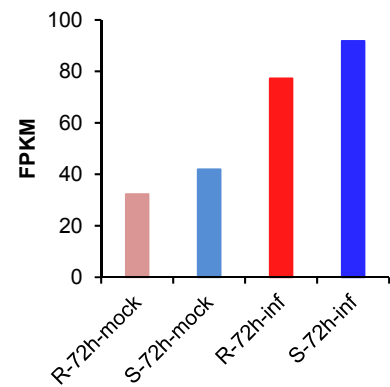
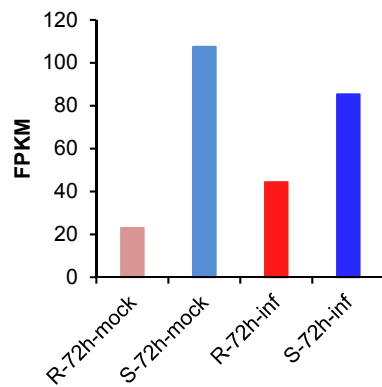


Fig. S8

Table 1 Differentially expressed genes at both 24 and 72 HAI in resistant or susceptible lines

Gene	<i>B. rapa</i>		Highly homologous genes in <i>A. thaliana</i>	
	Fold change (log2) at 24 HAI	Fold change (log2) at 72 HAI	Gene	Annotations
Resistant line				
Up-regulated gene				
Bra000382	4.58	3.72	AT2G45220	PME17 (pectin methylesterase 17)
Bra004511	2.42	4.47	AT2G46750	GULLO2 (L -GULONO-1,4-LACTONE (L -GULL) OXIDASE 2)
Bra004734	No expression in R-24h-mock	No expression in R-72h-mock	AT2G42980	Eukaryotic aspartyl protease family protein
Bra009869	2.79	4.20	AT5G25930	Protein kinase family protein with leucine-rich repeat domain
Bra011746	No expression in R-24h-mock	No expression in R-72h-mock	AT4G36880	CP1 (cysteine proteinase1)
Bra013138	No expression in R-24h-mock	3.96	AT2G13810	ALD1 (AGD2-like defense response protein 1)
Bra016727	No expression in R-24h-mock	No expression in R-72h-mock	AT1G13510	Protein of unknown function
Bra019747	2.85	3.61	AT1G12200	Flavin-binding monooxygenase family protein
Bra020140	4.86	4.48	AT5G20960	AO1 (aldehyde oxidase 1)
Bra023122	2.41	3.90	AT1G30700	FAD-binding Berberine family protein
Bra025730	No expression in R-24h-mock	4.47	AT1G19320	Pathogenesis-related thaumatin superfamily protein
Bra026124	4.38	4.26	AT1G15520	PDR12 (pleiotropic drug resistance 12)
Bra026986	2.87	4.26	AT1G12200	Flavin-binding monooxygenase family protein
Down-regulated gene				
Bra001626	-1.94	-4.58	AT3G16240	DELTA-TIP (delta tonoplast integral protein)
Susceptible line				
Up-regulated gene				
Bra003273	2.43	5.54	AT3G57240	BG3 (beta-1,3-glucanase 3)
Bra009763	2.39	3.94	AT5G24420	PGL5 (6-phosphogluconolactonase 5)
Bra013714	2.60	4.53	AT4G23600	JR2 (jasmonic acid responsive 2)
Bra015719	2.40	4.89	AT1G76790	IGMT5 (INDOLE GLUCOSINOLATE O-METHYLTRANSFERASE 5)
Bra025191	No expression in S-24h-mock	No expression in S-72h-mock	AT3G26190	CYP71B21(cytochrome P450, family 71, subfamily B, polypeptide 21)
Bra025756	2.34	5.54	AT1G19670	COR11 (CORONATINE-INDUCED PROTEIN 1)
Bra026163	No expression in S-24h-mock	5.80	AT1G15125	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
Bra032515	No expression in S-24h-mock	No expression in S-72h-mock	AT1G04350	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
Down-regulated gene				
Bra001012	No expression in S-24h-inf	No expression in S-72h-inf	AT5G15140	Galactose mutarotase-like superfamily protein
Bra019742	-2.37	-5.03	AT1G12090	ELP (extensin-like protein)
Bra022636	No expression in S-24h-inf	No expression in S-72h-inf	AT5G53190	SWEET3 (Nodulin MtN3 family protein)

Table 2 Overlapped genes between up-regulated genes of Chinese cabbage at 24 HAI and up-regulated genes of Arabidopsis at 1 DPI.

	R-24h-inf up	S-24h-inf up	Description
AT1G15520	+	+	PDR12 (PLEIOTROPIC DRUG RESISTANCE 12)
AT1G19020	+	-	Unknown protein
AT1G21120	+	+	O-methyltransferase family protein
AT1G23730	+	-	BCA3 (BETA CARBONIC ANHYDRASE 3)
AT1G26390	-	+	FAD-binding Berberine family protein
AT1G26420	+	-	FAD-binding Berberine family protein
AT1G60750	-	+	NAD(P)-linked oxidoreductase superfamily protein
AT1G68450	+	-	VQ motif-containing protein
AT1G69920	+	+	GSTU12 (GLUTATHIONE S-TRANSFERASE TAU 12)
AT1G74590	+	+	GSTU10 (GLUTATHIONE S-TRANSFERASE TAU 10)
AT1G77120	+	+	ADH1 (ALCOHOL DEHYDROGENASE 1)
AT2G02010	+	-	GAD4 (GLUTAMATE DECARBOXYLASE 4)
AT2G16060	+	-	HB1 (HEMOGLOBIN 1)
AT2G18690	+	-	Unknown protein
AT2G19590	+	-	ACO1 (ACC OXIDASE 1)
AT2G23270	+	+	Unknown protein
AT2G38860	+	+	YLS5 (Class I glutamine amidotransferase-like superfamily)
AT2G43570	+	+	CHI (CHITINASE)
AT2G43620	+	+	Chitinase family protein
AT3G02840	+	-	ARM repeat superfamily protein
AT3G15518	+	-	Unknown protein
AT3G29970	-	+	B12D protein
AT3G48450	+	+	RPM1-interacting protein 4 (RIN4) family protein
AT3G54150	+	+	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
AT3G54640	-	+	TSA1 (TRYPTOPHAN SYNTHASE ALPHA CHAIN)
AT3G60120	+	+	BGLU27 (BETA GLUCOSIDASE 27)
AT4G08780	+	+	Peroxidase superfamily protein
AT4G14630	+	+	GLP9 (GERMIN-LIKE PROTEIN 9)
AT4G23810	+	-	WRKY53 (WRKY family transcription factor)
AT4G24110	-	+	Unknown protein
AT4G37290	+	+	Unknown protein
AT4G37370	-	+	CYP81D8 (CYTOCHROME P450, FAMILY 81, SUBFAMILY D, POLYPEPTIDE 8)
AT4G37710	-	+	VQ motif-containing protein
AT4G39950	+	+	CYP79B2 (CYTOCHROME P450, FAMILY 79, SUBFAMILY B, POLYPEPTIDE 2)
AT5G57220	+	+	CYP81F2 (CYTOCHROME P450, FAMILY 81, SUBFAMILY F, POLYPEPTIDE 2)
AT5G64810	+	-	WRKY51 (WRKY DNA-BINDING PROTEIN 51)

+, overlapped with up-regulated genes of Arabidopsis at 1 DPI

-, did not overlap with up-regulated genes of Arabidopsis at 1 DPI

Table S1 Sequences of primers used for qPCR

Name	Primer sequences (5'-3')	
<i>BG3</i>	GCAGAACATCGATAGAGCGGT	TGAATGTCCCACTCGAAGGC
<i>Bra012688</i>	CGATAGGTATTCGAATTTGAGTCT	TCCACACTGTTGTTTGTACTGAGTT
<i>Bra012689</i>	AGATGTCGTTGAGAAGTCTGATACC	TTGTTGTTCTGTTATCATGGGATTA
<i>Bra037877</i>	TTCCTGGTCCAGCTTCTACC	TGAATCGGCATTGGTTTTTA
<i>Bractin</i>	CGGTCCAGCTTCGTCATACTCAGCC	AAATGTGATGTGGATATCAGGAAGG
<i>GSTF3</i>	CCTTTGAAGATGGAGACCTCA	CGAASTGGTGAGCTTCTACTT
<i>GSTU10</i>	CCTCTTCTTGTCATGATGG	CCGAACCTGGGCCCTTTCAT
<i>GSTU13</i>	GTTCTCAACTCAAAGAGCGA	CGTTCGTAAGGGTGAGAAGG
<i>GULLO2</i>	TACCCAACAACCGAAGATGA	CGTCGGTACAAACGAGCTTA
<i>HB1</i>	TTTGAGATTGCACCAACAGC	AAAACAGACATGGCATGAGG
<i>JR1</i>	AAAGCCTGTCCTTGGAATTG	TTCATTCCATACGGGTCAGA
<i>JRG21</i>	ATACACAAACGACATAACTC	TAAGTTTTTGGCGAATTAGC
<i>PDR12</i>	AGCTTGGATTCCAAGATACC	ATTGTCTGGAAGATCGATTCC
<i>PRB1</i>	CGAAAGCTCAAGACAGTCCA	GGCCAAGTTCTCTCCGTAAG
<i>PR3</i>	ATCATTAACGGTGGATTAGAGTGTG	ACGTTACTACCTTCATTAAACGGCC
<i>PR4</i>	ACACAAGGACTAATGCAGCTGTAAC	AACAATGAGATGACCTTTTCGATAG
<i>TPS04</i>	CCYAAACCGTGCAAAGAKAT	AGCCTTCTTAATGTCTTGAA
<i>WRKY51</i>	ACGAGATCAAAGATKGATGT	CTCTTCTTCACCRTGCAACC
<i>WRKY53</i>	CCAAGTTCCCCAGGAGTTAC	AGTGTGTGTYCCTCTGTACG

Table S2 Number of mapped reads

Sample	Total reads	Mapped reads
Rb-mock	28,765,769	26,060,973 (90.6%)
Sb-mock	28,247,856	25,599,320 (90.6%)
Rb-inf*	25,761,116	18,461,656 (71.7%)
Sb-inf*	26,782,986	19,401,760 (72.4 %)
R-24h-mock*	11,591,656	9,423,984 (81.3 %)
S-24h-mock*	11,689,377	9,539,846 (81.6 %)
R-24h-inf*	11,664,261	9,218,782 (79.0 %)
S-24h-inf*	11,616,963	9,157,484 (78.8 %)
R-72h-mock	29,514,321	26,416,528 (89.5%)
S-72h-mock	28,829,880	26,108,887 (90.6%)
R-72h-inf	28,797,472	25,428,059 (88.3%)
S-72h-inf	26,122,374	22,859,275 (87.5%)

*Paired-end

Table S3 Number of differentially expressed genes between inoculated and non-inoculated samples

	Total DEGs	Up-regulated		Down-regulated	
Rb-inf vs. Rb-mock	200	124	62.0%	76	38.0%
Sb-inf vs. Sb-mock	174	137	78.7%	37	21.3%
(Rb-inf vs. Rb-mock) vs. (Sb-inf vs. S-mock)	80	66	82.5%	14	17.5%
R-24h-inf vs. R-24h-mock	260	245	94.2%	15	5.8%
S-24h-inf vs. S-24h-mock	253	207	81.8%	46	18.2%
(R-24h-inf vs. R-24h-mock) vs. (S-24h-inf vs. S-24h-mock)	128	123	96.1%	5	3.9%
R-72h-inf vs. R-72h-mock	88	83	94.3%	5	5.7%
S-72h-inf vs. S-72h-mock	109	87	79.8%	22	20.2%
(R-72h-inf vs. R-72h-mock) vs. (S-72h-inf vs. S-72h-mock)	14	13	92.9%	1	7.1%

Rb-mock, mock-inoculated bulked samples (6, 12, 24, and 72 HAI) from the resistant line (RJKB-T23)

Sb-mock, mock-inoculated bulked samples (6, 12, 24, and 72 HAI) from the resistant line (RJKB-T24)

Rb-inf, inoculated bulked samples (6, 12, 24, and 72 HAI) from the resistant line (RJKB-T23)

Sb-inf, inoculated bulked samples (6, 12, 24, and 72 HAI) from the susceptible line (RJKB-T24)

R-24h-mock, mock-inoculated samples of the resistant line (RJKB-T23)

S-24h-mock; mock-inoculated samples of the susceptible line (RJKB-T24)

R-24h-inf, inoculated samples at 24 HAI of the resistant line (RJKB-T23)

S-24h-inf, inoculated samples at 24 HAI of the susceptible line (RJKB-T24)

R-72h-mock, mock-inoculated samples of the resistant line (RJKB-T23)

S-72h-mock; mock-inoculated samples of the susceptible line (RJKB-T24)

R-72h-inf, inoculated samples at 72 HAI of the resistant line (RJKB-T23)

S-72h-inf, inoculated samples at 72 HAI of the susceptible line (RJKB-T24)

Table S4 Differentially expressed genes between inoculated and non-inoculated bulked samples (6, 12, 24, and 72 HAI)

RJKB-T23				RJKB-T24			
Rb-inf > Rb-mock (up-regulated)		Rb-inf < Rb-mock (down-regulated)		SRb-inf > Sb-mock (up-regulated)		Sb-inf < Sb-mock (down-regulated)	
Gene	Fold change (log2)	Gene	Fold change (log2)	Gene	Fold change (log2)	Gene	Fold change (log2)
Bra000129	2.85	Bra000227	-2.91	Bra000059	No expression in Sb-mock	Bra000227	-3.25
Bra000204	3.79	Bra000329	No expression in Rb-inf	Bra000292	3.01	Bra000299	No expression in Sb-inf
Bra000292	3.33	Bra000376	-2.42	Bra000382	2.98	Bra000947	-2.53
Bra000310	2.50	Bra000935	No expression in Rb-inf	Bra000441	4.11	Bra005423	-2.48
Bra000311	3.24	Bra000947	-2.52	Bra000578	5.34	Bra006913	-2.99
Bra000382	3.69	Bra002741	-3.04	Bra000806	3.05	Bra007230	-2.72
Bra000875	3.23	Bra002944	-2.41	Bra000876	3.51	Bra007451	No expression in Sb-inf
Bra000876	4.56	Bra003381	No expression in Rb-inf	Bra001121	3.54	Bra007946	No expression in Sb-inf
Bra001086	No expression in Rb-mock	Bra006076	No expression in Rb-inf	Bra001123	4.55	Bra008144	-2.43
Bra001090	2.29	Bra006248	-2.40	Bra001453	5.50	Bra008278	No expression in Sb-inf
Bra001121	2.49	Bra006685	-3.49	Bra001921	3.34	Bra008904	No expression in Sb-inf
Bra001122	5.00	Bra007230	-3.06	Bra002165	2.75	Bra009527	No expression in Sb-inf
Bra001123	2.99	Bra007750	-2.95	Bra002747	3.11	Bra009646	No expression in Sb-inf
Bra001921	3.33	Bra008144	-2.90	Bra003696	6.14	Bra009739	-2.77
Bra002422	2.35	Bra008368	No expression in Rb-inf	Bra003699	2.94	Bra015374	No expression in Sb-inf
Bra002747	3.17	Bra008704	No expression in Rb-inf	Bra003923	No expression in Sb-mock	Bra016180	No expression in Sb-inf
Bra003019	No expression in Rb-mock	Bra008896	No expression in Rb-inf	Bra003977	No expression in Sb-mock	Bra019267	No expression in Sb-inf
Bra003696	5.94	Bra009386	No expression in Rb-inf	Bra004057	5.83	Bra020907	No expression in Sb-inf
Bra003699	3.55	Bra009527	No expression in Rb-inf	Bra004058	4.21	Bra021959	No expression in Sb-inf
Bra004057	3.81	Bra009646	No expression in Rb-inf	Bra004511	3.63	Bra022843	No expression in Sb-inf
Bra004058	2.82	Bra013045	No expression in Rb-inf	Bra004528	3.49	Bra024426	No expression in Sb-inf
Bra004511	3.46	Bra013054	No expression in Rb-inf	Bra004749	3.56	Bra026338	No expression in Sb-inf
Bra004749	3.70	Bra013342	-2.34	Bra004768	2.74	Bra027254	-3.06
Bra004771	4.28	Bra014130	No expression in Rb-inf	Bra004771	3.18	Bra027657	No expression in Sb-inf
Bra005345	3.07	Bra015142	No expression in Rb-inf	Bra004838	No expression in Sb-mock	Bra029961	No expression in Sb-inf
Bra005919	2.95	Bra015439	No expression in Rb-inf	Bra005231	3.38	Bra030263	No expression in Sb-inf
Bra006178	4.15	Bra017306	No expression in Rb-inf	Bra006178	4.80	Bra031232	No expression in Sb-inf
Bra006702	3.92	Bra017920	-2.90	Bra006197	2.22	Bra031911	No expression in Sb-inf
Bra007051	2.89	Bra018121	No expression in Rb-inf	Bra006702	4.27	Bra031948	No expression in Sb-inf
Bra007315	3.87	Bra018307	No expression in Rb-inf	Bra006830	No expression in Sb-mock	Bra032388	No expression in Sb-inf
Bra008033	2.44	Bra019125	No expression in Rb-inf	Bra007051	3.01	Bra035536	No expression in Sb-inf
Bra008187	3.76	Bra019267	No expression in Rb-inf	Bra007225	3.03	Bra036128	-2.85
Bra008846	3.16	Bra021234	No expression in Rb-inf	Bra007315	3.14	Bra036812	No expression in Sb-inf
Bra009149	2.85	Bra021706	No expression in Rb-inf	Bra007507	3.20	Bra037006	No expression in Sb-inf
Bra009221	3.36	Bra022327	No expression in Rb-inf	Bra008010	No expression in Sb-mock	Bra037775	No expression in Sb-inf
Bra009234	2.83	Bra023418	-2.56	Bra008025	6.52	Bra038930	No expression in Sb-inf
Bra009464	2.37	Bra023842	No expression in Rb-inf	Bra008026	No expression in Sb-mock	Bra039943	-2.88
Bra009763	3.28	Bra023901	No expression in Rb-inf	Bra008033	2.75		
Bra009869	3.05	Bra023909	No expression in Rb-inf	Bra008037	5.23		
Bra010320	3.49	Bra024287	-2.68	Bra008187	3.99		
Bra010627	3.26	Bra024426	No expression in Rb-inf	Bra008846	4.02		
Bra010644	3.42	Bra024598	No expression in Rb-inf	Bra009149	2.36		
Bra010740	2.74	Bra025533	No expression in Rb-inf	Bra009221	2.79		
Bra010822	No expression in Rb-mock	Bra027192	-2.68	Bra009234	2.54		
Bra011019	4.35	Bra027223	No expression in Rb-inf	Bra009763	2.91		
Bra011500	2.85	Bra027254	-2.98	Bra009869	2.84		

Bra011686	3.98	Bra027339	No expression in Rb-inf	Bra009967	2.38
Bra011722	4.17	Bra027354	No expression in Rb-inf	Bra010153	2.92
Bra011761	No expression in Rb-mock	Bra027448	No expression in Rb-inf	Bra010627	3.15
Bra011821	3.88	Bra028394	No expression in Rb-inf	Bra010644	3.64
Bra012269	2.64	Bra028557	-4.29	Bra011506	2.73
Bra012274	3.24	Bra028674	No expression in Rb-inf	Bra011821	2.42
Bra012384	3.47	Bra030263	No expression in Rb-inf	Bra012384	4.21
Bra012702	3.04	Bra031097	-2.61	Bra013426	3.04
Bra013426	3.54	Bra031800	No expression in Rb-inf	Bra013714	2.98
Bra013660	2.53	Bra031948	No expression in Rb-inf	Bra013744	2.46
Bra013714	4.04	Bra032388	No expression in Rb-inf	Bra014205	No expression in Sb-mock
Bra013732	2.95	Bra032620	-2.47	Bra014510	4.22
Bra014510	3.78	Bra032899	No expression in Rb-inf	Bra015481	2.75
Bra016002	3.10	Bra032978	No expression in Rb-inf	Bra015531	2.91
Bra016070	2.85	Bra033875	-2.90	Bra015719	2.76
Bra016073	5.16	Bra034032	No expression in Rb-inf	Bra015981	2.57
Bra016432	2.97	Bra034717	-2.65	Bra016002	5.23
Bra016495	2.41	Bra034985	No expression in Rb-inf	Bra016056	2.56
Bra016511	5.48	Bra035456	No expression in Rb-inf	Bra016432	2.74
Bra016604	3.32	Bra036193	-2.48	Bra016589	2.49
Bra017117	2.89	Bra036244	-2.41	Bra016604	4.55
Bra017637	3.26	Bra036924	No expression in Rb-inf	Bra016708	2.91
Bra017700	3.00	Bra038071	No expression in Rb-inf	Bra017117	2.35
Bra017871	3.13	Bra038930	No expression in Rb-inf	Bra017154	No expression in Sb-mock
Bra018907	2.23	Bra039043	No expression in Rb-inf	Bra017272	4.41
Bra018970	2.90	Bra039161	No expression in Rb-inf	Bra017350	3.55
Bra018998	2.50	Bra039362	No expression in Rb-inf	Bra017637	3.62
Bra019250	3.18	Bra039943	-3.37	Bra018463	2.73
Bra019366	2.82	Bra040525	-2.69	Bra019366	2.58
Bra019747	3.19	Bra041173	No expression in Rb-inf	Bra019544	No expression in Sb-mock
Bra020071	No expression in Rb-mock			Bra019747	3.19
Bra020140	3.48			Bra020037	3.02
Bra020470	2.57			Bra020140	2.86
Bra020813	2.69			Bra020470	6.48
Bra021220	2.64			Bra021164	2.74
Bra023122	2.85			Bra022161	4.71
Bra024614	3.52			Bra023122	2.46
Bra025668	3.08			Bra024410	4.20
Bra025713	3.93			Bra024577	2.53
Bra025728	4.50			Bra024659	3.07
Bra025756	3.15			Bra024717	2.38
Bra025874	2.92			Bra024719	3.84
Bra025875	2.26			Bra025191	No expression in Sb-mock
Bra026124	3.88			Bra025192	2.48
Bra026157	3.06			Bra025403	2.68
Bra026167	4.47			Bra025450	2.63
Bra026303	2.50			Bra025637	No expression in Sb-mock
Bra026365	2.78			Bra025668	3.14
Bra026986	3.67			Bra025713	4.33
Bra027323	2.72			Bra025756	3.31

Bra027357	2.47		Bra025874	2.47
Bra027397	2.19		Bra026124	3.55
Bra027987	3.49		Bra026157	2.91
Bra028399	3.59		Bra026166	No expression in Sb-mock
Bra029278	2.42		Bra026167	5.53
Bra029393	4.89		Bra026986	3.96
Bra029784	2.85		Bra027020	3.37
Bra029933	2.72		Bra027238	2.33
Bra030917	3.94		Bra027257	3.57
Bra031065	3.27		Bra027323	2.72
Bra032348	2.50		Bra027357	2.86
Bra032515	No expression in Rb-mock		Bra028523	2.59
Bra032845	2.59		Bra028980	3.09
Bra033549	3.71		Bra029056	3.75
Bra034754	3.93		Bra029393	3.25
Bra035320	2.44		Bra029933	3.22
Bra035384	2.99		Bra030917	2.82
Bra036490	3.09		Bra031065	4.23
Bra036772	3.29		Bra031074	3.18
Bra036882	2.50		Bra032362	No expression in Sb-mock
Bra036981	No expression in Rb-mock		Bra032433	3.48
Bra036986	No expression in Rb-mock		Bra032515	No expression in Sb-mock
Bra036988	No expression in Rb-mock		Bra033138	4.65
Bra037954	4.04		Bra033436	2.50
Bra039268	3.20		Bra033549	6.26
Bra039755	2.93		Bra035384	3.19
Bra040633	2.61		Bra035628	2.74
Bra040817	2.52		Bra036172	2.84
			Bra036259	2.46
			Bra036490	2.98
			Bra036882	2.61
			Bra036984	No expression in Sb-mock
			Bra036988	No expression in Sb-mock
			Bra037877	3.50
			Bra037954	5.15
			Bra038569	No expression in Sb-mock
			Bra038799	2.41
			Bra039067	No expression in Sb-mock
			Bra039755	4.43
			Bra040817	3.22
			Bra041155	10.17

Table S5 Differentially expressed genes between inoculated and non-inoculated samples at 24 HAI

RJKB-T23				RJKB-T24			
R-24h-inf > R-24h-mock (up-regulated)		R-24h-inf < R-24h-mock (down-regulated)		S-24h-inf > S-24h-mock (up-regulated)		S-24h-inf < S-24h-mock (down-regulated)	
Gene	Fold change (log2)	Gene	Fold change (log2)	Gene	Fold change (log2)	Gene	Fold change (log2)
Bra000064	1.95	Bra001626	-1.94	Bra000202	No expression in S-24h-mock	Bra000087	No expression in S-24h-inf
Bra000129	2.29	Bra002189	-2.37	Bra000310	3.19	Bra000777	No expression in S-24h-inf
Bra000310	4.35	Bra003112	No expression in R-24h-inf	Bra000311	2.24	Bra001012	No expression in S-24h-inf
Bra000311	3.75	Bra004655	No expression in R-24h-inf	Bra000315	3.81	Bra001320	-3.51
Bra000315	2.84	Bra007462	No expression in R-24h-inf	Bra000382	2.67	Bra001626	-2.02
Bra000382	4.58	Bra018065	-2.06	Bra000441	4.94	Bra001631	-4.39
Bra000548	No expression in R-24h-mock	Bra019742	-1.89	Bra000513	No expression in S-24h-mock	Bra002189	-2.07
Bra000795	No expression in R-24h-mock	Bra022447	-2.95	Bra000703	No expression in S-24h-mock	Bra002309	No expression in S-24h-inf
Bra000875	4.33	Bra022636	No expression in R-24h-inf	Bra000875	3.29	Bra002475	No expression in S-24h-inf
Bra000963	2.54	Bra023457	No expression in R-24h-inf	Bra000876	3.62	Bra003112	No expression in S-24h-inf
Bra001067	No expression in R-24h-mock	Bra024943	-2.67	Bra001090	2.79	Bra003506	No expression in S-24h-inf
Bra001090	3.42	Bra026262	-2.16	Bra001122	2.33	Bra004502	No expression in S-24h-inf
Bra001122	4.87	Bra031685	No expression in R-24h-inf	Bra001123	2.24	Bra005053	-2.19
Bra001123	2.39	Bra035844	No expression in R-24h-inf	Bra001457	2.65	Bra010165	-4.65
Bra001457	2.39	Bra036638	No expression in R-24h-inf	Bra001874	3.25	Bra012092	No expression in S-24h-inf
Bra001488	2.26			Bra001921	4.12	Bra012534	No expression in S-24h-inf
Bra001874	3.03			Bra001988	3.79	Bra013307	No expression in S-24h-inf
Bra001914	2.27			Bra002165	2.80	Bra013419	No expression in S-24h-inf
Bra001921	5.19			Bra002539	No expression in S-24h-mock	Bra013943	No expression in S-24h-inf
Bra001958	2.77			Bra002954	1.99	Bra014398	No expression in S-24h-inf
Bra002165	3.59			Bra003126	2.83	Bra014399	No expression in S-24h-inf
Bra002539	No expression in R-24h-mock			Bra003148	No expression in S-24h-mock	Bra015028	No expression in S-24h-inf
Bra002747	3.02			Bra003273	2.43	Bra017446	No expression in S-24h-inf
Bra002773	No expression in R-24h-mock			Bra003526	2.27	Bra017796	No expression in S-24h-inf
Bra002914	3.40			Bra003588	No expression in S-24h-mock	Bra019741	-2.16
Bra003273	2.70			Bra004193	2.49	Bra019742	-2.37
Bra003923	No expression in R-24h-mock			Bra004261	2.05	Bra019922	No expression in S-24h-inf
Bra004129	No expression in R-24h-mock			Bra004511	1.99	Bra021177	-3.27
Bra004193	3.60			Bra004771	2.71	Bra021179	-3.00
Bra004511	2.42			Bra005104	2.84	Bra022160	-2.44
Bra004518	No expression in R-24h-mock			Bra005197	No expression in S-24h-mock	Bra022636	No expression in S-24h-inf
Bra004537	1.83			Bra006137	No expression in S-24h-mock	Bra022714	No expression in S-24h-inf
Bra004734	No expression in R-24h-mock			Bra006197	2.12	Bra024101	No expression in S-24h-inf
Bra004749	2.00			Bra006830	No expression in S-24h-mock	Bra024194	No expression in S-24h-inf
Bra004771	4.17			Bra007051	2.46	Bra025040	No expression in S-24h-inf
Bra004840	No expression in R-24h-mock			Bra007085	2.22	Bra026249	No expression in S-24h-inf
Bra004980	No expression in R-24h-mock			Bra007204	No expression in S-24h-mock	Bra027198	-2.88
Bra005345	2.03			Bra007225	2.10	Bra029766	No expression in S-24h-inf
Bra006816	No expression in R-24h-mock			Bra007315	2.68	Bra030190	No expression in S-24h-inf
Bra007051	3.31			Bra007507	4.13	Bra030606	No expression in S-24h-inf
Bra007204	No expression in R-24h-mock			Bra008033	2.39	Bra030607	No expression in S-24h-inf
Bra007828	No expression in R-24h-mock			Bra008132	2.78	Bra030915	-4.23
Bra008033	2.29			Bra008157	2.65	Bra032218	No expression in S-24h-inf
Bra008132	2.87			Bra008165	2.22	Bra035431	No expression in S-24h-inf
Bra008157	2.13			Bra008187	4.44	Bra039079	No expression in S-24h-inf
Bra008165	2.80			Bra008435	3.77	Bra039929	No expression in S-24h-inf

Bra008187	4.60
Bra008333	2.23
Bra009149	5.06
Bra009234	2.02
Bra009370	2.21
Bra009771	3.03
Bra009869	2.79
Bra009925	2.58
Bra010283	3.39
Bra010320	4.76
Bra010419	2.28
Bra010528	2.25
Bra010627	2.54
Bra010644	5.55
Bra010645	No expression in R-24h-mock
Bra010794	No expression in R-24h-mock
Bra010980	2.78
Bra011033	2.28
Bra011201	1.91
Bra011506	2.67
Bra011510	No expression in R-24h-mock
Bra011611	2.72
Bra011746	No expression in R-24h-mock
Bra011752	No expression in R-24h-mock
Bra011821	4.33
Bra011822	No expression in R-24h-mock
Bra012268	2.39
Bra012270	4.41
Bra012274	2.64
Bra012384	4.29
Bra013120	3.40
Bra013123	3.59
Bra013138	No expression in R-24h-mock
Bra013144	3.45
Bra013596	No expression in R-24h-mock
Bra013674	2.61
Bra013678	1.98
Bra013714	2.98
Bra013732	2.70
Bra013790	No expression in R-24h-mock
Bra014510	3.03
Bra014511	No expression in R-24h-mock
Bra014635	2.69
Bra014692	2.16
Bra015047	2.33
Bra015615	No expression in R-24h-mock
Bra015693	3.10
Bra015719	2.85
Bra015935	3.41
Bra016070	No expression in R-24h-mock

Bra009130	2.16
Bra009149	3.78
Bra009234	2.36
Bra009300	No expression in S-24h-mock
Bra009763	2.39
Bra009869	2.47
Bra009967	2.16
Bra010153	2.14
Bra010283	3.35
Bra010419	2.64
Bra010528	2.10
Bra010594	No expression in S-24h-mock
Bra010608	No expression in S-24h-mock
Bra010644	4.67
Bra010980	2.39
Bra011201	2.34
Bra011506	3.53
Bra011611	2.11
Bra011752	No expression in S-24h-mock
Bra011821	3.51
Bra012269	2.13
Bra012274	2.16
Bra012702	No expression in S-24h-mock
Bra013120	3.08
Bra013144	3.50
Bra013161	2.08
Bra013209	2.67
Bra013579	1.99
Bra013714	2.60
Bra013763	No expression in S-24h-mock
Bra013856	2.52
Bra014510	2.49
Bra014511	4.11
Bra015478	No expression in S-24h-mock
Bra015693	3.67
Bra015719	2.40
Bra015740	2.50
Bra015935	3.31
Bra016007	2.00
Bra016025	No expression in S-24h-mock
Bra016252	2.59
Bra016432	3.34
Bra016433	2.08
Bra016510	No expression in S-24h-mock
Bra016520	2.97
Bra016589	2.71
Bra016607	2.26
Bra017031	No expression in S-24h-mock
Bra017120	3.60
Bra017184	1.92

Bra016250	2.63
Bra016252	2.54
Bra016432	4.54
Bra016433	2.78
Bra016515	No expression in R-24h-mock
Bra016589	2.68
Bra016607	2.08
Bra016727	No expression in R-24h-mock
Bra016844	2.26
Bra017117	2.29
Bra017120	3.52
Bra017210	1.85
Bra017429	No expression in R-24h-mock
Bra017637	5.29
Bra017702	No expression in R-24h-mock
Bra017725	3.15
Bra017871	4.55
Bra018058	No expression in R-24h-mock
Bra018468	2.06
Bra018493	No expression in R-24h-mock
Bra018543	2.41
Bra018969	2.48
Bra018970	2.68
Bra019014	No expression in R-24h-mock
Bra019075	1.98
Bra019339	No expression in R-24h-mock
Bra019366	3.21
Bra019747	2.85
Bra020140	4.86
Bra020295	No expression in R-24h-mock
Bra020472	2.07
Bra020836	2.09
Bra021101	2.00
Bra021673	2.80
Bra021802	2.24
Bra022161	3.20
Bra022378	2.21
Bra022607	No expression in R-24h-mock
Bra022724	2.02
Bra022803	2.12
Bra022815	2.46
Bra022816	1.99
Bra022870	1.96
Bra023009	3.12
Bra023110	2.06
Bra023122	2.41
Bra023297	2.50
Bra023336	2.36
Bra023373	No expression in R-24h-mock
Bra023676	4.00

Bra017210	2.21
Bra017299	No expression in S-24h-mock
Bra017455	No expression in S-24h-mock
Bra017637	4.17
Bra017702	No expression in S-24h-mock
Bra017819	1.85
Bra018058	No expression in S-24h-mock
Bra018468	2.71
Bra018543	2.46
Bra018941	2.02
Bra018969	3.27
Bra018998	2.25
Bra019075	2.11
Bra019339	No expression in S-24h-mock
Bra019366	2.72
Bra019747	3.32
Bra020037	2.67
Bra020071	No expression in S-24h-mock
Bra020140	2.94
Bra020836	1.95
Bra021048	No expression in S-24h-mock
Bra021101	2.46
Bra021164	3.11
Bra021673	2.59
Bra021775	No expression in S-24h-mock
Bra022128	No expression in S-24h-mock
Bra022161	3.14
Bra022378	2.14
Bra022803	2.53
Bra022815	2.59
Bra023009	2.79
Bra023122	2.86
Bra023336	2.53
Bra023676	2.33
Bra023748	No expression in S-24h-mock
Bra024269	2.81
Bra024634	2.69
Bra024659	3.62
Bra024719	5.22
Bra025191	No expression in S-24h-mock
Bra025192	2.09
Bra025407	No expression in S-24h-mock
Bra025481	2.32
Bra025494	2.03
Bra025668	3.99
Bra025713	3.70
Bra025723	No expression in S-24h-mock
Bra025756	2.34
Bra025874	2.58
Bra026124	5.11

Bra023940	No expression in R-24h-mock
Bra024328	No expression in R-24h-mock
Bra024459	2.42
Bra024634	2.65
Bra024659	2.83
Bra024717	2.24
Bra025481	2.73
Bra025668	4.00
Bra025704	No expression in R-24h-mock
Bra025707	No expression in R-24h-mock
Bra025713	3.09
Bra025723	No expression in R-24h-mock
Bra025728	3.41
Bra025730	No expression in R-24h-mock
Bra025756	3.02
Bra025874	2.57
Bra025875	2.28
Bra026124	4.38
Bra026156	2.57
Bra026157	2.50
Bra026515	2.12
Bra026796	3.51
Bra026919	2.20
Bra026986	2.87
Bra027236	No expression in R-24h-mock
Bra027257	3.30
Bra027357	2.63
Bra027700	1.90
Bra027740	2.99
Bra027848	No expression in R-24h-mock
Bra027940	2.36
Bra027987	No expression in R-24h-mock
Bra028091	4.02
Bra028463	No expression in R-24h-mock
Bra028825	2.14
Bra028896	No expression in R-24h-mock
Bra029278	2.14
Bra029414	3.06
Bra029505	1.93
Bra029740	1.93
Bra029933	2.52
Bra030029	No expression in R-24h-mock
Bra030385	2.03
Bra030917	2.87
Bra031042	2.65
Bra031392	2.46
Bra031627	2.15
Bra031715	No expression in R-24h-mock
Bra031795	No expression in R-24h-mock
Bra031896	3.03

Bra026163	No expression in S-24h-mock
Bra026515	2.30
Bra026864	2.72
Bra026986	3.96
Bra027047	2.57
Bra027049	2.15
Bra027098	No expression in S-24h-mock
Bra027257	4.29
Bra027357	2.89
Bra028091	2.76
Bra028103	No expression in S-24h-mock
Bra028463	No expression in S-24h-mock
Bra028523	2.26
Bra028571	No expression in S-24h-mock
Bra028896	No expression in S-24h-mock
Bra029145	No expression in S-24h-mock
Bra029278	2.28
Bra029302	No expression in S-24h-mock
Bra029393	4.64
Bra029505	2.05
Bra029933	3.31
Bra029946	1.89
Bra030385	2.06
Bra030917	2.07
Bra031074	1.89
Bra031392	2.37
Bra031486	2.51
Bra031795	No expression in S-24h-mock
Bra031896	3.14
Bra032177	No expression in S-24h-mock
Bra032515	No expression in S-24h-mock
Bra033138	2.33
Bra033549	3.21
Bra033568	2.44
Bra034848	2.32
Bra034941	3.08
Bra035384	2.42
Bra035574	2.23
Bra036172	2.80
Bra036259	2.74
Bra036316	2.74
Bra036490	2.98
Bra036575	2.10
Bra036846	3.26
Bra036882	3.40
Bra037555	1.93
Bra037647	2.44
Bra037877	2.93
Bra038302	No expression in S-24h-mock
Bra038647	No expression in S-24h-mock

Bra031934		1.91	Bra038663		2.22
Bra032177	No expression in R-24h-mock		Bra038734		2.48
Bra032472	No expression in R-24h-mock		Bra038799		3.09
Bra032515	No expression in R-24h-mock		Bra039727	No expression in S-24h-mock	
Bra032555		2.32	Bra039818		3.26
Bra033170	No expression in R-24h-mock		Bra039976		2.35
Bra033549		2.33	Bra040159		2.80
Bra033774		2.57	Bra040274	No expression in S-24h-mock	
Bra033934	No expression in R-24h-mock		Bra040633		3.09
Bra034404		2.56	Bra040999		2.56
Bra034611		3.07	Bra041119	No expression in S-24h-mock	
Bra034754		1.98			
Bra034808		2.47			
Bra034848		2.48			
Bra034941		3.28			
Bra035320		2.07			
Bra035384		2.28			
Bra036172		3.17			
Bra036259		3.35			
Bra036316		2.63			
Bra036490		3.55			
Bra036846		4.20			
Bra036882		3.52			
Bra037113		2.73			
Bra037141	No expression in R-24h-mock				
Bra037252	No expression in R-24h-mock				
Bra037520		2.10			
Bra037555		2.28			
Bra037647		3.14			
Bra037796	No expression in R-24h-mock				
Bra037877		2.82			
Bra037954		3.34			
Bra038302	No expression in R-24h-mock				
Bra038546		3.01			
Bra038611		3.02			
Bra038647	No expression in R-24h-mock				
Bra038734		2.16			
Bra038799		3.62			
Bra039006		2.64			
Bra039130		2.45			
Bra039193	No expression in R-24h-mock				
Bra039316	No expression in R-24h-mock				
Bra039353	No expression in R-24h-mock				
Bra039727	No expression in R-24h-mock				
Bra039818		3.45			
Bra040107		4.17			
Bra040633		4.86			
Bra040999		2.58			
Bra041119	No expression in R-24h-mock				

Table S6 Differentially expressed genes between inoculated and non-inoculated samples at 72 HAI

RJKB-T23				RJKB-T24			
R-72h-inf > R-72h-mock (up-regulated)		R-72h-inf < R-72h-mock (down-regulated)		S-24h-inf > S-24h-mock (up-regulated)		S-24h-inf < S-24h-mock (down-regulated)	
Gene	Fold change (log2)	Gene	Fold change (log2)	Gene	Fold change (log2)	Gene	Fold change (log2)
Bra000382	3.72	Bra001626	-4.58	Bra000059	No expression in S-72h-mock	Bra001012	No expression in S-72h-inf
Bra000441	4.99	Bra002329	No expression in R-72h-inf	Bra000129	6.97	Bra001476	No expression in S-72h-inf
Bra000469	No expression in R-72h-mock	Bra007905	No expression in R-72h-inf	Bra000137	No expression in S-72h-mock	Bra001482	-4.01
Bra002211	No expression in R-72h-mock	Bra019376	No expression in R-72h-inf	Bra000578	5.32	Bra003874	-4.38
Bra002474	No expression in R-72h-mock	Bra019741	-4.44	Bra003273	5.54	Bra006736	No expression in S-72h-inf
Bra002543	No expression in R-72h-mock			Bra003296	No expression in S-72h-mock	Bra008209	No expression in S-72h-inf
Bra003019	No expression in R-72h-mock			Bra003511	5.29	Bra011017	No expression in S-72h-inf
Bra003816	No expression in R-72h-mock			Bra003696	6.69	Bra011470	No expression in S-72h-inf
Bra003837	No expression in R-72h-mock			Bra003707	4.26	Bra014177	No expression in S-72h-inf
Bra004415	No expression in R-72h-mock			Bra003977	No expression in S-72h-mock	Bra016791	-4.50
Bra004470	No expression in R-72h-mock			Bra003982	No expression in S-72h-mock	Bra016855	-3.70
Bra004511	4.47			Bra004057	7.22	Bra019376	No expression in S-72h-inf
Bra004734	No expression in R-72h-mock			Bra004175	No expression in S-72h-mock	Bra019742	-5.03
Bra005870	No expression in R-72h-mock			Bra004837	5.29	Bra020330	No expression in S-72h-inf
Bra006178	4.20			Bra004842	No expression in S-72h-mock	Bra022636	No expression in S-72h-inf
Bra006655	No expression in R-72h-mock			Bra005919	4.83	Bra028859	No expression in S-72h-inf
Bra006951	No expression in R-72h-mock			Bra005937	5.50	Bra029355	No expression in S-72h-inf
Bra006978	No expression in R-72h-mock			Bra005940	5.34	Bra033350	-4.14
Bra007332	No expression in R-72h-mock			Bra006178	4.88	Bra034095	No expression in S-72h-inf
Bra007887	4.14			Bra007239	No expression in S-72h-mock	Bra035929	-5.32
Bra008490	No expression in R-72h-mock			Bra008026	No expression in S-72h-mock	Bra035955	No expression in S-72h-inf
Bra009221	3.57			Bra008037	5.47	Bra038442	No expression in S-72h-inf
Bra009225	No expression in R-72h-mock			Bra008456	No expression in S-72h-mock		
Bra009869	4.20			Bra008846	5.22		
Bra010056	No expression in R-72h-mock			Bra008858	5.64		
Bra011625	No expression in R-72h-mock			Bra009148	No expression in S-72h-mock		
Bra011722	4.20			Bra009261	6.28		
Bra011746	No expression in R-72h-mock			Bra009463	No expression in S-72h-mock		
Bra012184	No expression in R-72h-mock			Bra009763	3.94		
Bra012482	4.34			Bra010332	5.64		
Bra013138	3.96			Bra010627	3.70		
Bra013234	No expression in R-72h-mock			Bra010898	3.77		
Bra014439	No expression in R-72h-mock			Bra011722	5.41		
Bra015238	No expression in R-72h-mock			Bra012482	5.18		
Bra016213	No expression in R-72h-mock			Bra012597	No expression in S-72h-mock		
Bra016727	No expression in R-72h-mock			Bra013138	4.22		
Bra016867	No expression in R-72h-mock			Bra013714	4.53		
Bra017342	No expression in R-72h-mock			Bra014716	7.20		
Bra018991	No expression in R-72h-mock			Bra015481	3.98		
Bra019314	No expression in R-72h-mock			Bra015719	4.89		
Bra019612	No expression in R-72h-mock			Bra015854	4.25		
Bra019711	No expression in R-72h-mock			Bra016382	4.66		
Bra019747	3.61			Bra016417	No expression in S-72h-mock		
Bra020140	4.48			Bra016604	4.88		
Bra020315	No expression in R-72h-mock			Bra017350	5.28		
Bra020322	5.14			Bra018803	No expression in S-72h-mock		

Bra020438	No expression in R-72h-mock		Bra018970	6.12
Bra021367	No expression in R-72h-mock		Bra020370	5.36
Bra021397	No expression in R-72h-mock		Bra021113	4.49
Bra021998	No expression in R-72h-mock		Bra021451	No expression in S-72h-mock
Bra022221	No expression in R-72h-mock		Bra021998	No expression in S-72h-mock
Bra023122	3.90		Bra022535	No expression in S-72h-mock
Bra023487	No expression in R-72h-mock		Bra023278	No expression in S-72h-mock
Bra025665	No expression in R-72h-mock		Bra023749	No expression in S-72h-mock
Bra025730	4.47		Bra024275	No expression in S-72h-mock
Bra026007	No expression in R-72h-mock		Bra024410	4.80
Bra026124	4.26		Bra025191	No expression in S-72h-mock
Bra026167	3.97		Bra025728	7.44
Bra026365	4.19		Bra025756	5.54
Bra026767	No expression in R-72h-mock		Bra026163	5.80
Bra026986	4.26		Bra026167	4.91
Bra027716	No expression in R-72h-mock		Bra028251	No expression in S-72h-mock
Bra027756	No expression in R-72h-mock		Bra029056	4.68
Bra027853	No expression in R-72h-mock		Bra031065	4.90
Bra028698	No expression in R-72h-mock		Bra031432	No expression in S-72h-mock
Bra028980	3.55		Bra031990	No expression in S-72h-mock
Bra029393	3.99		Bra032433	3.86
Bra029472	No expression in R-72h-mock		Bra032515	No expression in S-72h-mock
Bra029755	No expression in R-72h-mock		Bra033632	No expression in S-72h-mock
Bra031065	3.57		Bra035004	No expression in S-72h-mock
Bra031079	No expression in R-72h-mock		Bra036158	No expression in S-72h-mock
Bra036981	No expression in R-72h-mock		Bra036981	No expression in S-72h-mock
Bra036982	No expression in R-72h-mock		Bra036982	No expression in S-72h-mock
Bra036986	No expression in R-72h-mock		Bra036984	No expression in S-72h-mock
Bra036988	No expression in R-72h-mock		Bra036985	No expression in S-72h-mock
Bra037177	4.06		Bra036986	No expression in S-72h-mock
Bra037700	No expression in R-72h-mock		Bra036988	No expression in S-72h-mock
Bra038094	No expression in R-72h-mock		Bra037643	No expression in S-72h-mock
Bra038824	No expression in R-72h-mock		Bra037954	6.97
Bra039673	No expression in R-72h-mock		Bra037958	4.98
Bra039700	No expression in R-72h-mock		Bra038094	No expression in S-72h-mock
Bra040464	No expression in R-72h-mock		Bra038174	No expression in S-72h-mock
Bra040826	No expression in R-72h-mock		Bra038215	No expression in S-72h-mock
			Bra038216	No expression in S-72h-mock
			Bra039067	No expression in S-72h-mock
			Bra039755	5.97
			Bra040826	No expression in S-72h-mock

Table S7 GO term of differentially expressed genes with and without Foc inoculation at 24 HAI in the resistant or susceptible lines

GO accession	Term	p value	FDR
Up-regulated genes in resistant line			
GO:0009607	BP Response to biotic stimulus	6.90E-18	4.10E-15
GO:0051707	BP Response to other organism	9.70E-18	4.10E-15
GO:0019748	BP Secondary metabolic process	4.50E-16	1.10E-13
GO:0051704	BP Multi-organism process	6.50E-16	1.10E-13
GO:0006950	BP Response to stress	6.80E-16	1.10E-13
GO:0009617	BP Response to bacterium	3.30E-15	4.70E-13
GO:0050896	BP Response to stimulus	7.90E-14	9.40E-12
GO:0006952	BP Defense response	1.10E-13	1.10E-11
GO:0042742	BP Defense response to bacterium	1.20E-11	1.10E-09
GO:0006790	BP Sulfur metabolic process	1.70E-11	1.40E-09
GO:0009620	BP Response to fungus	2.90E-11	2.20E-09
GO:0044272	BP Sulfur compound biosynthetic process	3.30E-11	2.30E-09
GO:0009814	BP Defense response, incompatible interaction	9.00E-11	5.80E-09
GO:0009753	BP Response to jasmonic acid stimulus	1.20E-10	7.20E-09
GO:0016144	BP S-glycoside biosynthetic process	1.80E-10	8.90E-09
GO:0019761	BP Glucosinolate biosynthetic process	1.80E-10	8.90E-09
GO:0019758	BP Glycosinolate biosynthetic process	1.80E-10	8.90E-09
GO:0042221	BP Response to chemical stimulus	6.10E-10	2.80E-08
GO:0009404	BP Toxin metabolic process	2.00E-09	8.30E-08
GO:0009407	BP Toxin catabolic process	2.00E-09	8.30E-08
GO:0050832	BP Defense response to fungus	4.40E-09	1.80E-07
GO:0019760	BP Glucosinolate metabolic process	7.40E-09	2.60E-07
GO:0016143	BP S-glycoside metabolic process	7.40E-09	2.60E-07
GO:0019757	BP Glycosinolate metabolic process	7.40E-09	2.60E-07
GO:0045087	BP Innate immune response	1.10E-08	3.60E-07
GO:0019438	BP Aromatic compound biosynthetic process	1.20E-08	3.90E-07
GO:0042435	BP Indole derivative biosynthetic process	1.60E-08	5.10E-07
GO:0002376	BP Immune system process	2.10E-08	6.00E-07
GO:0006955	BP Immune response	2.10E-08	6.00E-07
GO:0006725	BP Cellular aromatic compound metabolic process	3.60E-08	1.00E-06
GO:0016138	BP Glycoside biosynthetic process	4.40E-08	1.20E-06
GO:0042434	BP Indole derivative metabolic process	6.00E-08	1.50E-06
GO:0042430	BP Indole and derivative metabolic process	6.00E-08	1.50E-06
GO:0009611	BP Response to wounding	1.20E-07	3.00E-06
GO:0009851	BP Auxin biosynthetic process	1.30E-07	3.20E-06
GO:0044283	BP Small molecule biosynthetic process	1.60E-07	3.70E-06
GO:0030312	CC External encapsulating structure	2.10E-07	1.10E-05
GO:0005618	CC Cell wall	2.10E-07	1.10E-05
GO:0016137	BP Glycoside metabolic process	3.80E-07	8.50E-06
GO:0042398	BP Cellular amino acid derivative biosynthetic process	8.60E-07	1.90E-05
GO:0009505	CC Plant-type cell wall	9.10E-07	3.00E-05
GO:0042446	BP Hormone biosynthetic process	1.00E-06	2.20E-05
GO:0006575	BP Cellular amino acid derivative metabolic process	1.50E-06	3.20E-05
GO:0009627	BP Systemic acquired resistance	2.10E-06	4.40E-05
GO:0006519	BP Cellular amino acid and derivative metabolic process	3.80E-06	7.60E-05
GO:0009850	BP Auxin metabolic process	4.10E-06	8.00E-05
GO:0016053	BP Organic acid biosynthetic process	8.70E-06	0.00016
GO:0046394	BP Carboxylic acid biosynthetic process	8.70E-06	0.00016
GO:0005576	CC Extracellular region	8.90E-06	0.00022
GO:0010033	BP Response to organic substance	1.10E-05	0.0002
GO:0009605	BP Response to external stimulus	1.50E-05	0.00027
GO:0071554	BP Cell wall organization or biogenesis	1.90E-05	0.00034
GO:0034641	BP Cellular nitrogen compound metabolic process	2.50E-05	0.00042
GO:0044281	BP Small molecule metabolic process	2.50E-05	0.00042
GO:0009719	BP Response to endogenous stimulus	3.70E-05	0.0006
GO:0034637	BP Cellular carbohydrate biosynthetic process	4.20E-05	0.00067
GO:0042445	BP Hormone metabolic process	5.90E-05	0.00091
GO:0043436	BP Oxoacid metabolic process	6.10E-05	0.00091
GO:0006082	BP Organic acid metabolic process	6.10E-05	0.00091
GO:0019752	BP Carboxylic acid metabolic process	6.10E-05	0.00091
GO:0042180	BP Cellular ketone metabolic process	7.30E-05	0.0011
GO:0031347	BP Regulation of defense response	8.20E-05	0.0012
GO:0044271	BP Cellular nitrogen compound biosynthetic process	9.00E-05	0.0013
GO:0009628	BP Response to abiotic stimulus	9.60E-05	0.0013
GO:0006979	BP Response to oxidative stress	1.60E-04	0.0022
GO:0042545	BP Cell wall modification	1.90E-04	0.0026
GO:0008152	BP Metabolic process	2.20E-04	0.0029
GO:0080134	BP Regulation of response to stress	2.40E-04	0.0032
GO:0033554	BP Cellular response to stress	2.60E-04	0.0033
GO:0006520	BP Cellular amino acid metabolic process	2.60E-04	0.0033
GO:0009056	BP Catabolic process	3.30E-04	0.0041
GO:0044106	BP Cellular amine metabolic process	3.70E-04	0.0046

GO:0009699	BP	Phenylpropanoid biosynthetic process	4.80E-04	0.0058
GO:0016051	BP	Carbohydrate biosynthetic process	4.90E-04	0.0058
GO:0071555	BP	Cell wall organization	5.20E-04	0.0061
GO:0048046	BP	Apoplast	6.00E-04	0.012
GO:0044262	BP	Cellular carbohydrate metabolic process	6.00E-04	0.0069
GO:0008652	CC	Cellular amino acid biosynthetic process	6.00E-04	0.0069
GO:0044237	BP	Cellular metabolic process	7.60E-04	0.0086
GO:0051716	BP	Cellular response to stimulus	8.10E-04	0.009
GO:0005829	CC	Cytosol	8.20E-04	0.014
GO:0009309	BP	Amine biosynthetic process	8.50E-04	0.0094
GO:0009698	BP	Phenylpropanoid metabolic process	9.10E-04	0.0099
Up-regulated genes in susceptible line				
GO:0009607	BP	Response to biotic stimulus	3.30E-19	2.30E-16
GO:0051707	BP	Response to other organism	5.00E-19	2.30E-16
GO:0006950	BP	Response to stress	8.60E-18	2.60E-15
GO:0050896	BP	Response to stimulus	6.00E-17	1.40E-14
GO:0051704	BP	Multi-organism process	2.70E-16	4.80E-14
GO:0019748	BP	Secondary metabolic process	3.20E-16	4.80E-14
GO:0042435	BP	Indole derivative biosynthetic process	8.40E-16	1.10E-13
GO:0042434	BP	Indole derivative metabolic process	8.80E-15	8.80E-13
GO:0042430	BP	Indole and derivative metabolic process	8.80E-15	8.80E-13
GO:0006790	BP	Sulfur metabolic process	1.20E-14	1.10E-12
GO:0042221	BP	Response to chemical stimulus	5.10E-13	4.10E-11
GO:0006586	BP	Indolalkylamine metabolic process	7.60E-13	5.20E-11
GO:0006568	BP	Tryptophan metabolic process	7.60E-13	5.20E-11
GO:0009611	BP	Response to wounding	8.20E-13	5.20E-11
GO:0042398	BP	Cellular amino acid derivative biosynthetic process	1.00E-12	6.20E-11
GO:0009617	BP	Response to bacterium	1.20E-12	6.60E-11
GO:0006952	BP	Defense response	1.90E-12	9.90E-11
GO:0019438	BP	Aromatic compound biosynthetic process	2.10E-12	1.00E-10
GO:0006575	BP	Cellular amino acid derivative metabolic process	5.20E-12	2.30E-10
GO:0000162	BP	Tryptophan biosynthetic process	5.70E-12	2.30E-10
GO:0046219	BP	Indolalkylamine biosynthetic process	5.70E-12	2.30E-10
GO:0009851	BP	Auxin biosynthetic process	5.70E-12	2.30E-10
GO:0016491	MF	Oxidoreductase activity	7.60E-12	1.50E-09
GO:0044272	BP	Sulfur compound biosynthetic process	9.20E-12	3.60E-10
GO:0003824	MF	Catalytic activity	1.10E-11	1.50E-09
GO:0006725	BP	Cellular aromatic compound metabolic process	1.40E-11	5.10E-10
GO:0044283	BP	Small molecule biosynthetic process	2.60E-11	9.40E-10
GO:0006576	BP	Cellular biogenic amine metabolic process	6.90E-11	2.40E-09
GO:0006519	BP	Cellular amino acid and derivative metabolic process	1.30E-10	4.30E-09
GO:0042446	BP	Hormone biosynthetic process	1.60E-10	5.00E-09
GO:0042401	BP	Cellular biogenic amine biosynthetic process	2.90E-10	8.90E-09
GO:0009753	BP	Response to jasmonic acid stimulus	4.10E-10	1.20E-08
GO:0042742	BP	Defense response to bacterium	5.50E-10	1.60E-08
GO:0009850	BP	Auxin metabolic process	1.40E-09	3.90E-08
GO:0009605	BP	Response to external stimulus	1.80E-09	4.90E-08
GO:0009620	BP	Response to fungus	2.60E-09	6.80E-08
GO:0016144	BP	S-glycoside biosynthetic process	3.30E-09	8.00E-08
GO:0019761	BP	Glucosinolate biosynthetic process	3.30E-09	8.00E-08
GO:0019758	BP	Glycosinolate biosynthetic process	3.30E-09	8.00E-08
GO:0009072	BP	Aromatic amino acid family metabolic process	3.80E-09	9.00E-08
GO:0016829	MF	Lyase activity	6.70E-09	5.90E-07
GO:0016053	BP	Organic acid biosynthetic process	8.80E-09	2.00E-07
GO:0046394	BP	Carboxylic acid biosynthetic process	8.80E-09	2.00E-07
GO:0044281	BP	Small molecule metabolic process	9.80E-09	2.20E-07
GO:0043648	BP	Dicarboxylic acid metabolic process	1.10E-08	2.30E-07
GO:0046417	BP	Chorismate metabolic process	1.40E-08	2.90E-07
GO:0009073	BP	Aromatic amino acid family biosynthetic process	1.40E-08	2.90E-07
GO:0008652	BP	Cellular amino acid biosynthetic process	3.10E-08	6.20E-07
GO:0010033	BP	Response to organic substance	3.70E-08	7.20E-07
GO:0043436	BP	Oxoacid metabolic process	4.00E-08	7.30E-07
GO:0006082	BP	Organic acid metabolic process	4.00E-08	7.30E-07
GO:0019752	BP	Carboxylic acid metabolic process	4.00E-08	7.30E-07
GO:0009404	BP	Toxin metabolic process	4.20E-08	7.40E-07
GO:0009407	BP	Toxin catabolic process	4.20E-08	7.40E-07
GO:0034641	BP	Cellular nitrogen compound metabolic process	5.10E-08	8.70E-07
GO:0042180	BP	Cellular ketone metabolic process	5.10E-08	8.70E-07
GO:0006520	BP	Cellular amino acid metabolic process	5.80E-08	9.60E-07
GO:0009309	BP	Amine biosynthetic process	5.90E-08	9.60E-07
GO:0004364	MF	Glutathione transferase activity	6.30E-08	4.10E-06
GO:0042445	BP	Hormone metabolic process	7.70E-08	1.20E-06
GO:0019760	BP	Glucosinolate metabolic process	7.70E-08	1.20E-06
GO:0016143	BP	S-glycoside metabolic process	7.70E-08	1.20E-06
GO:0019757	BP	Glycosinolate metabolic process	7.70E-08	1.20E-06

GO:0044106	BP	Cellular amine metabolic process	1.00E-07	1.50E-06
GO:0052482	BP	Cell wall thickening during defense response	1.30E-07	1.80E-06
GO:0052386	BP	Cell wall thickening	1.30E-07	1.80E-06
GO:0044271	BP	Cellular nitrogen compound biosynthetic process	1.30E-07	1.80E-06
GO:0052543	BP	Callose deposition in cell wall	1.30E-07	1.80E-06
GO:0052544	BP	Callose deposition in cell wall during defense response	1.30E-07	1.80E-06
GO:0009814	BP	Defense response, incompatible interaction	1.80E-07	2.40E-06
GO:0016138	BP	Glycoside biosynthetic process	3.60E-07	4.70E-06
GO:0052542	BP	Callose deposition during defense response	3.60E-07	4.70E-06
GO:0052545	BP	Callose localization	3.60E-07	4.70E-06
GO:0046483	BP	Heterocycle metabolic process	5.10E-07	6.40E-06
GO:0009308	BP	Amine metabolic process	5.10E-07	6.40E-06
GO:0033037	BP	Polysaccharide localization	5.50E-07	6.90E-06
GO:0050832	BP	Defense response to fungus	6.30E-07	7.80E-06
GO:0009723	BP	Response to ethylene stimulus	7.40E-07	8.90E-06
GO:0002376	BP	Immune system process	2.10E-06	2.50E-05
GO:0006955	BP	Immune response	2.10E-06	2.50E-05
GO:0030312	CC	External encapsulating structure	2.20E-06	0.0001
GO:0005618	CC	Cell wall	2.20E-06	0.0001
GO:0016137	BP	Glycoside metabolic process	2.30E-06	2.70E-05
GO:0030246	MF	Carbohydrate binding	3.00E-06	0.00016
GO:0018130	BP	Heterocycle biosynthetic process	7.40E-06	8.40E-05
GO:0071554	BP	Cell wall organization or biogenesis	7.40E-06	8.40E-05
GO:0009719	BP	Response to endogenous stimulus	7.70E-06	8.70E-05
GO:0004553	MF	Hydrolase activity, hydrolyzing o-glycosyl compounds	8.00E-06	0.00035
GO:0045087	BP	Innate immune response	8.90E-06	9.80E-05
GO:0010817	BP	Regulation of hormone levels	9.30E-06	0.0001
GO:0006979	BP	Response to oxidative stress	1.00E-05	0.00011
GO:0009058	BP	Biosynthetic process	1.10E-05	0.00012
GO:0010200	BP	Response to chitin	1.30E-05	0.00014
GO:0004497	MF	Monooxygenase activity	1.60E-05	0.00059
GO:0009505	CC	Plant-type cell wall	1.70E-05	0.00053
GO:0016798	MF	Hydrolase activity, acting on glycosyl bonds	2.40E-05	0.00078
GO:0044249	BP	Cellular biosynthetic process	2.70E-05	0.00029
GO:0016741	MF	Transferase activity, transferring one-carbon groups	4.10E-05	0.00096
GO:0008168	MF	Methyltransferase activity	4.10E-05	0.00096
GO:0016684	MF	Oxidoreductase activity, acting on peroxide as acceptor	4.70E-05	0.00096
GO:0016765	MF	Transferase activity, transferring alkyl or aryl (other than methyl) groups	4.70E-05	0.00096
GO:0004601	MF	Peroxidase activity	4.70E-05	0.00096
GO:0050660	MF	Fad binding	5.30E-05	0.001
GO:0009628	BP	Response to abiotic stimulus	5.80E-05	0.0006
GO:0042545	BP	Cell wall modification	9.70E-05	0.00099
GO:0008152	BP	Metabolic process	1.00E-04	0.001
GO:0009056	BP	Catabolic process	1.00E-04	0.001
GO:0019825	MF	Oxygen binding	1.10E-04	0.0019
GO:0016209	MF	Antioxidant activity	1.40E-04	0.0023
GO:0034637	BP	Cellular carbohydrate biosynthetic process	1.40E-04	0.0013
GO:0044237	BP	Cellular metabolic process	1.80E-04	0.0017
GO:0016705	MF	Oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen	2.00E-04	0.0031
GO:0009699	BP	Phenylpropanoid biosynthetic process	2.50E-04	0.0024
GO:0009743	BP	Response to carbohydrate stimulus	2.60E-04	0.0025
GO:0071555	BP	Cell wall organization	2.70E-04	0.0026
GO:0016614	MF	Oxidoreductase activity, acting on ch-oh group of donors	4.50E-04	0.0063
GO:0050662	MF	Coenzyme binding	4.50E-04	0.0063
GO:0009698	BP	Phenylpropanoid metabolic process	4.80E-04	0.0045
GO:0005576	CC	Extracellular region	7.90E-04	0.019
GO:0016740	MF	Transferase activity	8.70E-04	0.011
GO:0032787	BP	Monocarboxylic acid metabolic process	9.60E-04	0.0089
Down-regulated genes in susceptible line				
GO:0022891	MF	Substrate-specific transmembrane transporter activity	6.70E-04	0.0091
GO:0015075	MF	Ion transmembrane transporter activity	8.40E-04	0.0091

CC, Cellular component; MF, Molecular function; BP, Biological process

Table S8 GO term of up-regulated genes at 72h after Foc inoculation in the resistant or susceptible lines

GO accession	Term	p value	FDR
Up-regulated genes in resistant line			
GO:0003824	MF Catalytic activity	2.10E-05	0.001
GO:0016787	MF Hydrolase activity	4.50E-05	0.0011
GO:0009607	BP Response to biotic stimulus	0.00025	0.038
GO:0050896	BP Response to stimulus	0.00077	0.039
Up-regulated genes in susceptible line			
GO:0009753	BP Response to jasmonic acid stimulus	2.50E-11	7.80E-09
GO:0006950	BP Response to stress	1.30E-10	2.00E-08
GO:0050896	BP Response to stimulus	9.10E-09	9.60E-07
GO:0031407	BP Oxylipin metabolic process	2.50E-08	2.00E-06
GO:0051707	BP Response to other organism	5.30E-07	3.30E-05
GO:0009607	BP Response to biotic stimulus	9.80E-07	5.20E-05
GO:0009605	BP Response to external stimulus	2.30E-06	0.0001
GO:0009611	BP Response to wounding	3.40E-06	0.00013
GO:0042221	BP Response to chemical stimulus	3.60E-06	0.00013
GO:0051704	BP Multi-organism process	4.40E-06	0.00014
GO:0006631	BP Fatty acid metabolic process	1.50E-05	0.00043
GO:0009719	BP Response to endogenous stimulus	2.00E-05	0.00053
GO:0006979	BP Response to oxidative stress	2.80E-05	0.00063
GO:0032787	BP Monocarboxylic acid metabolic process	2.80E-05	0.00063
GO:0019752	BP Carboxylic acid metabolic process	6.50E-05	0.0012
GO:0006082	BP Organic acid metabolic process	6.50E-05	0.0012
GO:0043436	BP Oxoacid metabolic process	6.50E-05	0.0012
GO:0042180	BP Cellular ketone metabolic process	7.30E-05	0.0013
GO:0044255	BP Cellular lipid metabolic process	0.00012	0.0019
GO:0010033	BP Response to organic substance	0.00016	0.0026
GO:0051716	BP Cellular response to stimulus	0.00039	0.0056
GO:0006952	BP Defense response	0.00039	0.0056
GO:0006629	BP Lipid metabolic process	0.0005	0.0068
GO:0044281	BP Small molecule metabolic process	0.0008	0.01
GO:0003824	MF Catalytic activity	0.00093	0.032

MF, Molecular function; BP, Biological process