

## The rice *GRH2* and *GRH4* activate various defense responses to the green rice leafhopper and confer strong insect resistance

Takayuki Asano<sup>1</sup>, Yasumori Tamura<sup>1</sup>, Hiroe Yasui<sup>1</sup>, Kouji Satoh<sup>1</sup>, Makoto Hattori<sup>1</sup>,  
Hideshi Yasui<sup>2</sup>, Shoshi Kikuchi<sup>1,\*</sup>

<sup>1</sup>National Institute of Agrobiological Sciences, Tsukuba, Ibaraki 305-8602, Japan; <sup>2</sup>Plant Breeding Laboratory, Faculty of Agriculture, Graduate School, Kyushu University, Fukuoka 812-8581, Japan

\* E-mail: skikuchi@niasaffrc.go.jp Tel & Fax: +81-29-838-7007

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**Abstract** Rice *GRH2* confers enhanced resistance to green rice leafhoppers (GRH), *Nephrotettix cincticeps* Uhler. A pyramided line carrying *GRH2* and *GRH4* (TGRH29) showed strong resistance to GRH insects compared with a *GRH2* near-isogenic line (TGRH11), although *GRH4* alone did not confer any resistance to GRH. To explore the effects of *GRH2* and *GRH4* on GRH resistance, we investigated the transcriptional response of rice plants to GRH infestation using DNA microarray analysis. The expression of a large number of genes encoding pathogenesis-related proteins, lipoxygenases, terpene synthase (TPS) and WRKY transcription factor, was upregulated in response to GRH infestation in TGRH11 and TGRH29 compared with control plants. Quantitative RT-PCR revealed that expression of *JAmyb* and *TPS* was more strongly and more rapidly upregulated in TGRH29 compared with TGRH11 after GRH infestation. These results suggest that TGRH29 plants can more rapidly and strongly activate the defense response compared with plants carrying *GRH2* alone. Furthermore, sesquiterpenes were emitted from TGRH29 plants in response to attack by GRH. The strong induction of sesquiterpene production in the TGRH29 line was correlated with the transcript levels of *TPS* genes. Our results suggest that *GRH2* and *GRH4* activate various defense responses and confer strong GRH insect resistance.

**Key words:** Defense signaling, green rice leafhopper, insect resistance, rice, sesquiterpene, upregulated genes.

The green rice leafhopper (GRH), *Nephrotettix cincticeps* Uhler, is a major insect pest of cultivated rice in temperate Asia. GRH is closely related to the green leafhopper (GLH) *Nephrotettix virescens* Distant, which transmits rice tungro disease. Rice tungro disease causes major constraints in rice production in southeast Asia (Hull 1996). GRH penetrates plant tissues using stylets and ingests sap from both the phloem and xylem of susceptible rice cultivars (Kawabe 1985), causing considerable losses in rice yield. In addition, GRH also causes severe damage to rice plants indirectly by transmitting several viral and phytoplasma diseases, such as rice dwarf disease and transitory yellowing disease (Nakasugi and Nomura 1968; Shinkai 1962).

Plants have evolved immunity mechanisms to protect themselves against pests, such as bacteria, fungi, viruses and insects (Bernoux et al. 2011; Chisholm et al. 2006; Lukasik and Takken 2009). Resistance (*R*) genes play a central role in plant disease resistance. Plant disease resistance can be triggered by recognition of specific

pathogen effectors by *R* proteins. The recognition often generates a hypersensitive response (HR), which restricts cell death to the pathogen infection site and prevents further expansion of the pathogens. A number of *R* genes have been cloned from many plant species (Bernoux et al. 2011; Chisholm et al. 2006; Dangl and Jones 2001; Goggin 2007; Lukasik and Takken 2009). However, three *R* genes against sucking insects have been cloned to date. These genes encode nucleotide binding and leucine-rich repeat (NB-LRR) proteins. *Mi-1* confers resistance to both root-knot nematodes (*Meloidogyne incognita*) and potato aphids (*Macrosiphum euphorbiae*) (Vos et al. 1998), and *Bph14* and *Bph26* confer resistance to brown planthoppers (BPH; *Nilaparvata lugens*) in rice (Du et al. 2009; Tamura et al. 2014).

Plants activate different defense responses in response to pest species. Insects can be classified into 2 groups: chewing insects and sucking insects. For chewing insects, jasmonic acid (JA) is a ubiquitous signal that activates defense responses (Howe and Jander 2008;

Abbreviations: BPH, Brown planthopper; GRH, Green rice leafhopper; JA, Jasmonic acid; PR, Pathogenesis-related; SA, Salicylic acid; T65, Taichung 65; TPS, Terpene synthase.

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Thompson and Goggin 2006). In fact, the disruption of rice *lipoxygenase* (*OsHI-LOX*) and *CORONATINE INSENSITIVE1* (*OsCOI1*) increases the susceptibility of rice plants to striped stem borer (SSB, *Chilo suppressalis*) and rice leaf folder (LF, *Cnaphalocrocis medinalis*) (Ye et al. 2012; Zhou et al. 2009). In contrast, little is known about the molecular mechanisms underlying sucking insect resistance. Salicylic acid (SA) levels in wild-type plants are increased in response to BPH infestation, whereas no significant difference in JA levels is found between BPH-infested and non-infested rice plants (Tong et al. 2012; Ye et al. 2012). SA synthesis-related genes are expressed more strongly and rapidly in *Bph14*-containing plants than wild-type plants. Therefore, *Bph14* is thought to activate an SA signaling pathway (Du et al. 2009). Suppressed expression of *OsHI-LOX* confers enhanced resistance to BPH, whereas the BPH susceptibility of *OsCOI1* RNAi plants and the GRH susceptibility of the constitutively active JA signaling mutant *rim1* are similar to that of wild-type plants (Ye et al. 2012; Yoshii et al. 2009, 2010; Zhou et al. 2009). These results suggest that rice resistance to BPH and GRH does not depend on JA-mediated defense signaling.

In studies examining plant defense mechanisms against aphids, several components that function downstream of the *R* gene *Mi-1* have been identified. Silencing the mitogen-activated protein kinases (MAPKs) *LeMPK2* and *LeMPK1* or silencing *LeMPK3* and the MAPK kinase *LeMKK2* resulted in the attenuation of *Mi-1* mediated aphid resistance (Li et al. 2006). The co-chaperone SGT1 and the heat shock protein Hsp90-1 are required for *Mi-1* mediated resistance against root-knot nematodes (RKN; *Meloidogyne* spp.) and potato aphids (*Macrosiphum euphorbiae*) (Bhattarai et al. 2007). Virus-induced gene silencing of the transcription factors *SlWRKY72a* and *SlWRKY72b* in tomato resulted in a reduction of *Mi-1*-mediated resistance as well as basal defense against RKN and potato aphids (Bhattarai et al. 2010). The tomato receptor-like kinase *SlSERK1* is required for *Mi-1*-mediated resistance to potato aphids (Mantelin et al. 2011). Thus, pathogen defense-related genes are involved in *Mi-1*-mediated aphid resistance.

Some *indica* varieties exhibit resistance against GRH or GLH (Fujita et al. 2006; Ghani and Khush 1988). Genetic analyses using molecular markers have identified 6 loci and a quantitative trait locus (QTL) with a minor effect on GRH resistance (Fujita et al. 2010). However, none of these GRH resistance genes has been cloned to date. *GRH2* and *GRH4* are found on chromosomes 11 and 3 of Lepe dumai and DV85, respectively (Fukuta et al. 1998; Kadowaki et al. 2003). Two near-isogenic lines (NILs) and a pyramided line (PYL) were developed by introducing *GRH2* and *GRH4* (Fujita et al. 2006, 2010). TGRH11 has a substituted

segment including *GRH2* on chromosome 11 from DV85. The size of the substituted segment is less than 9.3 Mbp. There are no other substituted segments in the Taichung 65 (T65) genetic background. TGRH16 has a substituted segment including *GRH4* (0.6 to 10.3 Mbp) on chromosome 3 from DV85. TGRH16 also carries substituted segments on chromosome 2 (with a size of less than 5.1 Mbp) and on chromosome 9 (with a size of less than 7.9 Mbp). TGRH29 has substituted segments including *GRH2* and *GRH4*. TGRH11 exhibits enhanced resistance to GRH insects: the nymph mortality on *GRH2*-NIL is about 75% at 3 days after infestation (Fujita et al. 2010). *GRH2/GRH4-PYL* showed higher nymph mortality than *GRH2*-NIL (Fujita et al. 2006). Regarding the defense response against insects, the signal transduction pathways that are activated by *R* genes after pest recognition are largely unknown. To explore the molecular mechanisms that underlie *GRH2/GRH4*-mediated insect resistance, we investigated the transcriptional response of rice plants during infestation. We found that the expression of *proteinase inhibitors*, *lipoxygenases* and *terpene synthase* (TPS) genes were upregulated in response to GRH infestation in resistant lines. Furthermore, the transcript levels of TPS genes were correlated with the strong induction of sesquiterpenes in the TGRH29 line. Thus, *GRH2* and *GRH4* activated various defense responses and conferred strong GRH resistance.

## Materials and methods

### Evaluation of GRH resistance

Rice (*Oryza sativa*) plants and insects were grown at 25°C under a 16-h light/8-h dark photoperiod. The GRH resistance test was performed as described previously (Fujita et al. 2010). Briefly, seedlings at the second-leaf stage were infested with 7 to 10 first- or second-instar nymphs in test tubes. GRH resistance was evaluated by calculating the survival rates of GRH. For the honeydew assay, a plastic dish was placed at low position on the plant stem, and filter paper was placed in the dish. An inverted plastic cup was placed onto the filter paper. Five adult GRH insects were introduced into each plastic cup. After 24 h, the filter papers were treated with 0.1% ninhydrin in acetone solution and dried at 55°C for 30 min.

### Oligo DNA microarray analysis

For gene expression analysis, rice plants were grown in a growth chamber at 25°C under a 16-h light/8-h dark photoperiod. Seedlings at the second-leaf stage were infested with 10 to 15 first- or second-instar nymphs in test tubes. Shoot samples were collected at 0 h or 30 h after GRH infestation. For RNA extraction, three independent plant materials were pooled to produce a single sample. Rice total RNA was extracted using an RNeasy Plant Mini Kit (Qiagen, Hilden, Germany), and 16 RNA samples were prepared for

the microarray experiment with two biological replicates. The RNA integrity was evaluated on an Agilent 2100 bioanalyzer using RNA nanochips. The RNA quantity was determined on a Nanodrop ND-1000 spectrophotometer (Nanodrop Technologies). For microarray analysis, the probe and arrays were designed using eArray version 4.5 (supplied by Agilent Technologies), and 43494 probes were selected for this custom array. Four sets of the 43494 probes ( $4 \times 44\text{K}$  microarray formats) were blotted on a glass slide ( $25 \times 75\text{ mm}$ ). Cyanine 3 (Cy3)- or cyanine 5 (Cy5)-labeled complementary RNA (cRNA) samples were synthesized from 850 ng of total RNA using a Quick Amp Labeling Kit (Agilent Technologies) according to the manufacturer's instructions. GRH-infested and uninfested samples were labeled with Cy3 and Cy5, respectively. The hybridization solution was prepared with 825 ng each of Cy3- and Cy5-labeled cRNA preparations using an In Situ Hybridization Kit Plus (Agilent Technologies). Hybridization and washing of the microarray slides were performed according to the manufacturer's protocols. After washing, slide image files were produced using a DNA microarray scanner (G2505B; Agilent Technologies). The signal intensities of Cy3 and Cy5 were extracted from the image files and normalized in each array by Feature Extraction version 9.5 (Agilent Technologies). The signal intensities of all samples were transformed into log<sub>2</sub>-based numbers and normalized according to the quantile method by EXPANDER version 5.0 (Shamir et al. 2005). Gene expression analyses were conducted based on the normalized signal intensities using Excel. The median value of the normalized signal intensities of Cy3 and Cy5 of all the probes are calculated, the resulted value was 6.53. The microarray data were deposited in the Gene Expression Omnibus Database (accession no. GSE46409).

#### Gene expression analysis

RNA isolation and quantitative reverse transcription PCR (qRT-PCR) assays were performed as described previously (Asano et al. 2012). Rice total RNA was extracted from shoots using an RNeasy Plant Mini Kit (Qiagen, Hilden, Germany). The isolated RNA was treated with TURBO DNase (Applied Biosystems/Ambion, Austin, TX, USA). cDNA synthesis was performed using an iScript cDNA Synthesis Kit (Bio-Rad, Hercules, CA, USA). qRT-PCR analysis was performed using the iCycler iQ System (Bio-Rad, Hercules, CA, USA) with iQ SYBR Green Supermix (Bio-Rad, Hercules, CA, USA) in a total volume of 25  $\mu\text{l}$ . The reactions were performed in biological triplicates using RNA samples extracted from 3 independent samples of plant material. The expression values were normalized to the *ubiquitin-conjugating enzyme (UBC)* gene (Jain et al. 2006). The primers that were used for qRT-PCR are listed in Supplementary Table S1.

#### Analysis of volatiles in rice

Seven-day-old seedlings were planted in graduated cylinders and infested with adult GRH. After 24 h of infestation, the volatiles released from the plants were captured using a solid-

phase microextraction (SPME) fiber coated with 100  $\mu\text{m}$  polydimethylsiloxane (PDMS) (Red, Supelco, Bellefonte, PA, USA). Volatile capturing was conducted for 30 min, and the volatiles were immediately analyzed by GC-MS (Agilent 7890A GC system interfaced with a JEOL JMS-T100GC time-of-flight mass spectrometer) equipped with an INNOWax column ( $30\text{ m} \times 0.25\text{ mm i.d.} \times 0.25\text{ }\mu\text{m}$  film thickness; Agilent Technologies). Helium was used as the carrier gas at a flow rate of 1 ml/min. The injection temperature was set to 200°C (splitless mode). The GC oven temperature was set at 50°C for 2 min. The temperature was then ramped to 240°C at 5°C/min (1-min hold). The mass spectrometer was set to electron ionization (EI) mode at 70 eV and 200°C. Mass spectra were recorded with a scanning range of 30 to 400 mass-to-charge ratio ( $m/z$ ), and the mass spectral data were deposited in the NIST mass spectral library.

## Results

#### *GRH2 confers enhanced resistance to GRH*

An *indica* cultivar, DV85, carrying *GRH2* and *GRH4* shows resistance to GRH (Fujita et al. 2010). *GRH2-NIL* (TGRH11), *GRH4-NIL* (TGRH16) and *GRH2/GRH4-PYL* (TGRH29) were developed by introducing *GRH2* and *GRH4* from DV85 (Fujita et al. 2006, 2010). To investigate the effects of *GRH2* and *GRH4* on GRH resistance, we examined the survival rate of GRH on TGRH11, TGRH16 and TGRH29 from 1–4 days after GRH infestation. Two days after infestation, most of the GRH on T65 and TGRH16 survived, whereas most of the GRH on TGRH29 died. The survival rate of GRH on TGRH11 gradually decreased, and 2/3 of the GRH died at 4 days after infestation (Figure 1A). Seven days after infestation, T65 and TGRH16 developed damage symptoms, such as leaf wilting and yellowing. In contrast, TGRH11 and TGRH29 showed significantly less damage compared with T65 and TGRH16 (Figure 1B). Thus, TGRH11 and TGRH29 confer apparent resistance to GRH. Although TGRH16 showed no GRH resistance, TGRH29 had greater resistance to GRH than TGRH11 due to the synergistic effect of *GRH4*.

We subsequently evaluated the feeding activity of GRH insects on the plants by visualizing honeydew deposited on filter paper with ninhydrin reagent. The intensity of stained honeydew was correlated with the levels of GRH resistance of the plants. Intense staining was observed on T65 and TGRH16 lines after 24 h of infestation. The staining was significantly less intense on TGRH29 and TGRH11 lines compared with T65 and TGRH16 lines (Figure 1C, D). This result suggests that *GRH2* confers resistance to GRH by reducing GRH feeding.

#### *Identification of GRH-responsive genes in rice*

To investigate the response of the rice plants to GRH infestation, we performed DNA microarray analysis

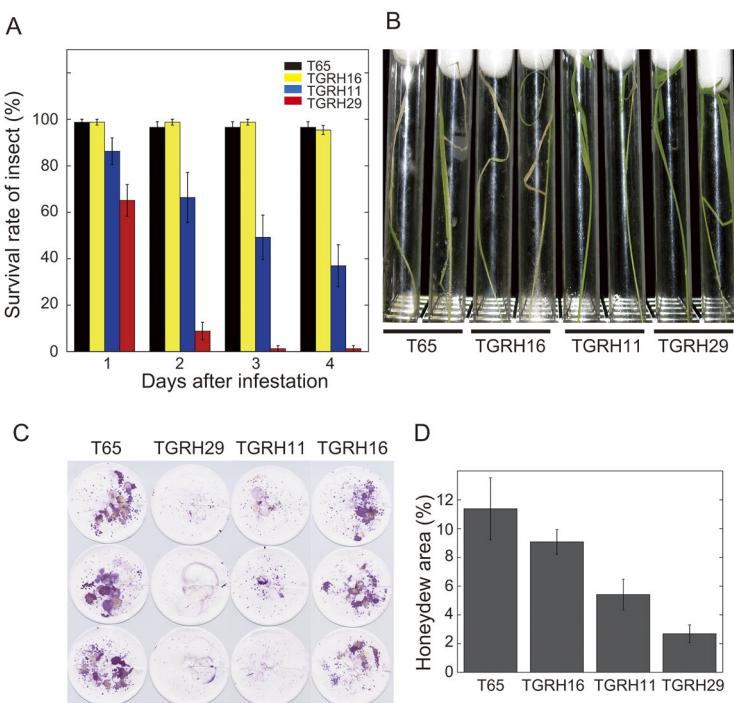


Figure 1. Effects of *GRH2* and *GRH4* on GRH resistance. (A) Survival rate of GRH. GRH insects were placed on 7-day-old rice seedlings. Error bars indicate the standard error of the mean (SEM) ( $n=9$  or 10). Asterisks indicate a significant difference at  $p<0.05$ . (B) Phenotypes of rice plants at 7 days after GRH infestation. (C) Honeydew assay. The size of the honeydew and the intensity of the honeydew color indicate the GRH feeding activity. The honeydew area was evaluated after 24 h of GRH infestation. (D) Honeydew area. The area of honeydew color was estimated by ImageJ. Error bars indicate SEM ( $n=7$ ). Asterisks indicate a significant difference at  $p<0.05$ .

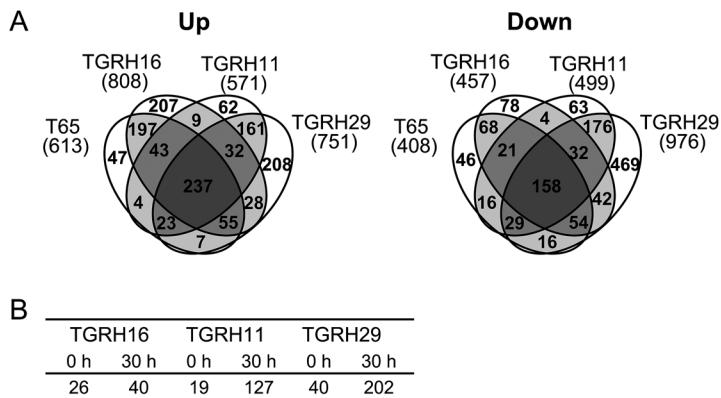


Figure 2. Summary of microarray analysis. (A) The number of GRH-responsive genes. Genes that were 2-fold upregulated or downregulated by GRH infestation (30 h post-infestation) were selected from the microarray data. (B) The number of upregulated genes. Gene expression levels of respective NIL lines were compared with that of T65 at 0 h or 30 h after GRH infestation. Genes that were 2-fold elevated in respective NIL lines were shown.

using a 60-mer oligonucleotide microarray (platform no. GPL7252, available at NCBI GEO). We extracted RNAs from the shoots of the respective rice lines at 0 h or 30 h post-infestation. Transcriptional changes in the respective rice lines were detected by comparison between GRH-infested and non-infested plants. We excluded spots with low signal intensity (<median) and extracted genes that were 2-fold upregulated or downregulated from the microarray data. During GRH infestation at the seedling stage, the expression levels

of 751 and 976 genes were increased and decreased, respectively in the TGRH29 line. The number of GRH-responsive genes is shown in Figure 2. Significantly, the expression levels of fourteen genes such as *transferase family protein* (Os12g27254), *terpene synthase* (Os08g07100 and Os08g07080), *lipoxygenase*, *OsRCI-1* (Os12g37260), *ABC transporter* (Os08g43120), *SAM-dependent carboxyl methyltransferase* (Os06g13390 and Os02g48770), *Bowman-Birk type bran trypsin inhibitor* (Os01g03320), *crocetin dialdehyde* (Os08g28240),

*lipase/acylhydrolase* (Os07g39740), *hypothetical protein* (Os01g40950), *phosphorylase domain containing protein* (Os05g13970), *late embryogenesis abundant protein, group 3* (Os05g46480) and *cinnamoyl CoA reductase* (Os01g18120) were greatly increased (>100-fold) in the TGRH29 line (Supplementary Table S3).

In contrast, only *probenazole-induced protein (PBZ1)* was significantly upregulated (>100-fold) in the T65 line (data not shown). Among the 322 upregulated genes in both TGRH29 and T65, 25 genes overlap with genes induced by JA treatment (GEO accession no. GPL6864) and 54 genes overlap with genes induced by benzothiadiazole (BTH) treatment (Shimono et al. 2007). In contrast, among the 429 remaining upregulated genes in TGRH29, 30 and 21 genes showed altered the expression level in response to treatment with JA and BTH, respectively. Furthermore, the expression levels of JA synthesis- or signaling-related genes such as *allene oxide synthase (AOS)*, *12-oxophytodienoate reductase (OPR7)*, *4-coumarate: CoA ligase (PCL)*, *acyl-coenzyme A oxidase (ACX)* and *COII* were comparable between GRH-infested TGRH29 and GRH-infested T65 plants (data not shown). The expression of *NPR1 homolog 1 (NH1*, a key regulator of SA-mediated systemic acquired resistance) (Yuan et al. 2007) and the pathogenesis-related (PR) gene *PR1b* (Os01g28450) was induced in response to GRH infestation in T65 but not in TGRH29.

#### ***Identification of up-regulated genes in GRH-resistant lines***

To identify the upregulated genes in TGRH11, TGRH16 and TGRH29, we compared the gene expression levels between NILs/PYL and control plants (T65). The expression levels of a few genes were higher in TGRH11, TGRH16 and TGRH29 compared with T65 before GRH infestation (Figure 2B). In contrast, the expression levels of 127 and 202 genes were higher in TGRH11 and TGRH29, respectively, compared with their levels in T65 at 30 h post-infestation. These results suggest that *GRH2* induces the defense response by recognizing GRH invasion. To explore the defense mechanism of TGRH29, we attempted to identify the upregulated genes in this line. However, the significantly upregulated genes, such as *SAM-dependent carboxyl methyltransferase* (>90-fold) and *TPS* (>150-fold) were excluded by the abovementioned filtering (data not shown). To prevent the exclusion of important genes during the filtering process, we first selected the spots with signal intensities > median only in infested TGRH29, and we subsequently selected the genes with a 2-fold/4-fold increase or decrease in spot intensity when comparing NILs/PYL and T65. The intensities of 1504 genes were increased by 2-fold or more in infested TGRH29 compared with their levels in infested T65. Moreover, the expression levels of 497 genes were ≥4-fold

increased in TGRH29. In contrast, the expression levels of 909 and 158 genes were 2-fold and 4-fold decreased, respectively, in TGRH29. These include genes encoding PR proteins, proteinase inhibitors, transcription factors and metabolism-related genes (Supplementary Table S2). Among the 497 highly expressed genes in TGRH29, the expression of 232 genes was increased in response to GRH infestation in TGRH29 but not in T65, and expression levels of 115 genes ≥2-fold increased in TGRH29 compared with TGRH11. Among the 158 downregulated genes in TGRH29, the expression of 43 genes was decreased in response to GRH infestation in TGRH29.

Among the defense-related genes with a 4-fold or greater intensity ratio at 30 h after GRH infestation, the expression levels of *PR6* genes were especially upregulated in response to GRH infestation in TGRH29. Furthermore, 8 *Bowman-Birk type bran trypsin inhibitors*, 2 *wound-induced proteinase inhibitors* and 9 putative *proteinase inhibitors* were significantly upregulated in TGRH29 compared with T65 (Figure 3, Supplementary Tables S2, S3). Thus, several types of proteinase inhibitor genes were highly expressed in the TGRH29 line.

Several metabolism-related genes were also upregulated in the GRH-resistant line and, most of these genes belonged to the cytochrome P450 family. The expression levels of *lipoxygenase* genes (Os12g37260, Os12g37350 and Os03g49350) were found to be significantly upregulated in response to GRH infestation in the TGRH29 line, whereas the expression of one gene (Os08g39840) was significantly downregulated in response to GRH infestation (Figure 3, Supplementary Table S2, S3). In addition, 4 *TPS* genes were highly upregulated in response to GRH infestation in TGRH29 (Figure 4, Supplementary Table S2, S3). Other highly expressed genes encoded SAM-dependent carboxyl methyltransferase, polyphenol oxidase, O-methyltransferase, aminotransferase, phenylalanine ammonia-lyase, lipase and 2OG-Fe(II) oxygenase superfamily proteins (Figure 4, Supplementary Table S3). The transcriptional repressor protein genes *OsJAZ5*, *OsJAZ8*, *OsJAZ9* and *OsJAZ11* were significantly upregulated in the TGRH29 line during GRH infestation. Eight *WRKY* transcription factor genes were upregulated in TGRH29, whereas the expression levels of 2 *WRKY* genes were decreased in TGRH29 compared with T65. Five *MYB* transcription factor genes were upregulated in TGRH29, whereas one *MYB* gene was downregulated (Figure 4).

To assess the validity of the microarray data and to examine gene expression over time, we investigated the expression of 3 *TPS* genes, *transferase family protein (Os12g27254)*, *OsRCI-1*, *OsJAZ8*, *JAmyb*, *PR6 (subtilisin-chymotrypsin inhibitor, Os12g36210)* and *OsCCR24* at 0, 6 and 30 h after GRH infestation by qRT-PCR. The

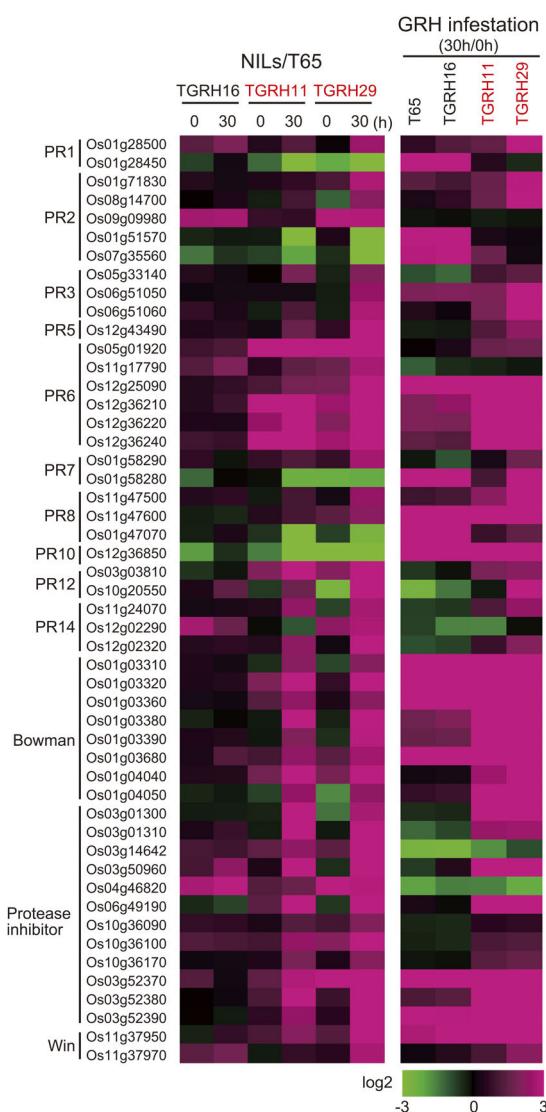


Figure 3. The expression of defense-related genes. The left column indicates the differences in gene expression levels between T65 and NIL lines. The right column shows the transcriptional response to GRH infestation in the respective rice lines. Bowman: *Bowman-Birk type bran trypsin inhibitor*; Win: *Similar to Barwin*.

results indicated that all 9 genes were reproducibly upregulated by GRH infestation in TGRH11 and TGRH29 (Figure 5). The expression of 2 *TPS* genes (*Os04g27670* and *Os08g07080*), *transferase family protein*, *OsRCI-1*, *PR6* and *OsCCR24* was upregulated by GRH infestation in TGRH29, reaching peak expression at 30 h. The expression levels of *OsJAZ8*, *JAmyb* and *TPS2* (*Os02g02930*) in TGRH29 were greater than their levels in T65, and these genes reached maximum expression levels 6 h after GRH infestation. Furthermore, the expression levels of *PR6*, *JAmyb*, *OsCCR24* and *TPS* genes (*Os04g27670* and *Os08g07080*) were higher in TGRH29 than in TGRH11 (Figure 5).

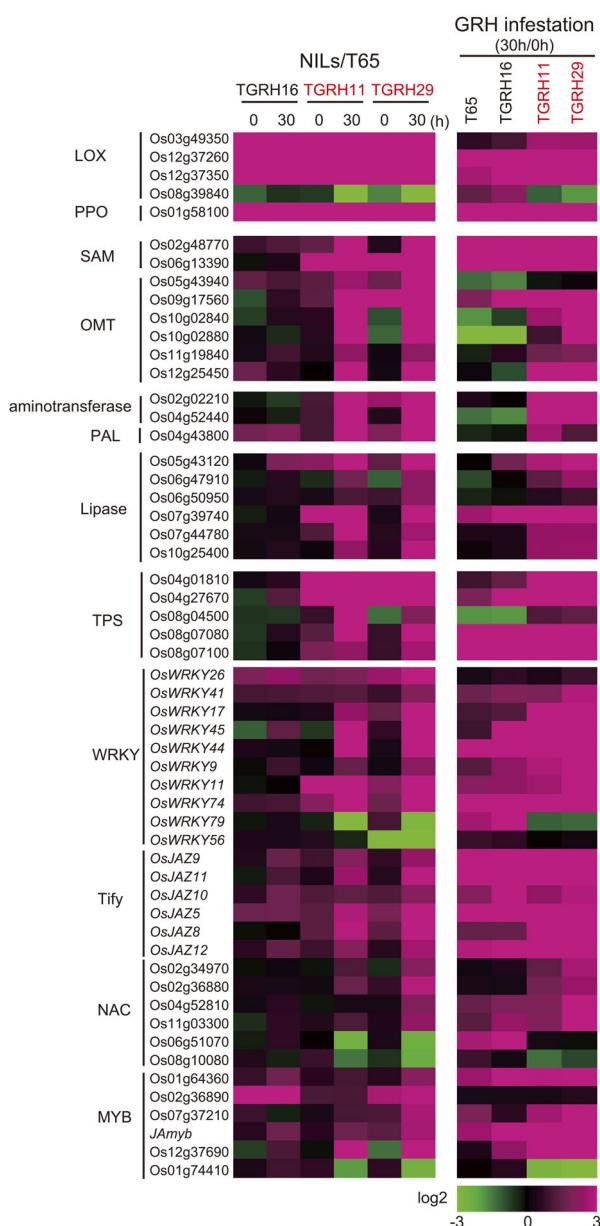


Figure 4. Changes in gene expression during GRH infestation. The left column indicates the differences in gene expression levels between T65 and NIL lines. The right column shows the expression changes induced by GRH infestation in the respective rice lines. LOX: *lipoxygenase*; PPO: *polyphenol oxidase*; SAM: *SAM-dependent carboxyl methyltransferase*; OMT: *O-methyltransferase*; PAL: *phenylalanine ammonia-lyase*.

#### **GRH infestation induced the emission of plant terpenes**

Rice *TPS* genes were among the most highly upregulated genes in response to GRH infestation in TGRH29 (Supplementary Table S2). *TPS* genes constitute a large multigene family consisting of 40 genes in *Arabidopsis thaliana* (Aubourg et al. 2002) and were involved in production of monoterpenes, diterpenes and sesquiterpenes (Lee and Chappell 2008). Rice *TPS* genes showed a high level of sequence similarity with sorghum and maize sesquiterpene synthase genes.

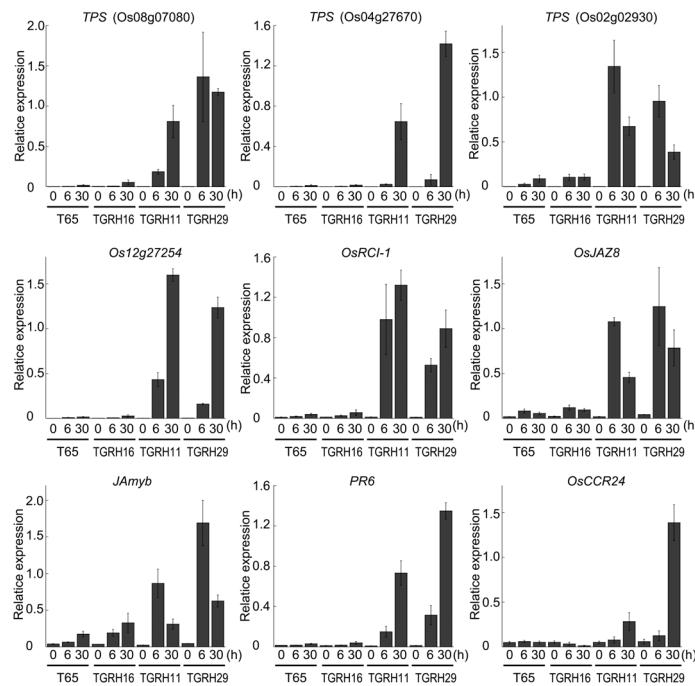


Figure 5. Transcriptional response to GRH infestation. Total RNA was extracted from the shoots and subjected to quantitative RT-PCR analysis. The expression level of each gene relative to the expression level of *UBC* at each time point is indicated. Error bars indicate the SEM of 3 independent experiments.

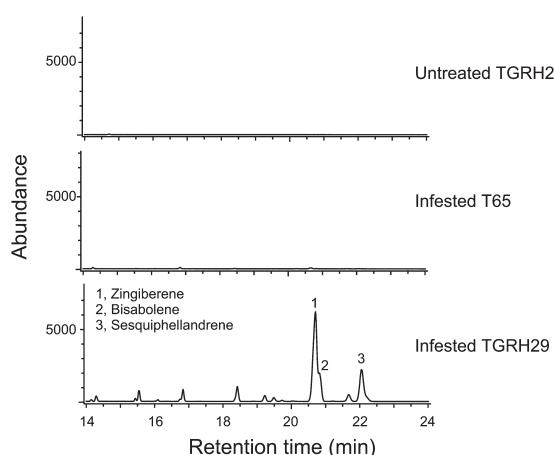


Figure 6. Total ion chromatograph of volatiles emitted in response to GRH infestation. Volatiles were collected after no treatment (control) or after 24 h of GRH infestation and analyzed by GC-MS. The peaks were identified as zingiberene (peak 1),  $\beta$ -bisabolene (peak 2) and  $\beta$ -sesquiphellandrene (peak 3).

Herbivore-induced plant volatiles are thought to be involved in direct/indirect defenses against insects. To determine whether the production of volatiles is induced by GRH infestation, we identified the volatiles emitted from TGRH29 plants using gas chromatography-mass spectrometry (GC-MS). Peaks were detected in samples from GRH-infested TGRH29 plants, whereas no significant peaks were found in GRH-infested T65 plants or TGRH29 plants that were not infested with GRH. GC-MS revealed strong induction of sesquiterpenes such as

zingiberene,  $\beta$ -sesquiphellandrene and  $\beta$ -bisabolene in GRH-infested TGRH29 plants (Figure 6).

## Discussion

*R* genes play a central role in the plant defense system. Only 3 insect *R* genes have been cloned to date, whereas a number of *R* genes conferring resistance against pathogens have been cloned from many plant species (Du et al. 2009; Tamura et al. 2014; Vos et al. 1998). Significantly, the *R*-gene-mediated defense mechanism against BPH and GRH is poorly understood. In this study, we investigated the effects of *GRH2* and *GRH4* on GRH resistance. TGRH11 carrying *GRH2* exhibits increased resistance to GRH insects, whereas the susceptibility of TGRH16 carrying *GRH4* is comparable to that of T65. Furthermore, TGRH29 carrying *GRH2* and *GRH4* shows strong insect resistance. The feeding activity of GRH insects on TGRH29 was dramatically reduced (Figure 1). These results suggest that the combination of *GRH2* and *GRH4* confers strong resistance to GRH by reducing GRH feeding.

Elucidation of the insect resistance response of rice plants is important for the production of GRH-resistant rice plants. Gene expression profiles in response to BPH infestation have been analyzed by several groups; however the mechanism of BPH resistance remains unclear (Wang et al. 2008, 2012). In our microarray analyses, the gene expression levels of most JA/SA synthesis- or signaling-related genes in resistant lines

were similar to their levels in T65. These results suggest that JA and SA do not play an important role in GRH resistance. More genes were upregulated in infested TGRH29 compared with T65 than in uninfested TGRH29 compared with T65, suggesting that *GRH2* confers increased resistance to GRH. Our results showed that the expression levels of several types of genes, including *PR* genes, proteinase inhibitors, transcription factors and metabolism-related genes, are increased in response to GRH infestation, and the expression levels are higher in TGRH29 than in T65, suggesting that these genes are involved in GRH resistance.

Sesquiterpenoids are involved in either direct or indirect defenses to insects (Huffaker et al. 2011; Schnee et al. 2006). Rice *TPS* genes (*Os04g01810*, *Os04g27340*, *Os04g27670*, *Os08g07080* and *Os08g07100*) were upregulated in response to GRH infestation in shoots of TGRH29 plants. Maize sesquiterpene synthases, which are closely related to rice TPSs, reportedly function in the production of sesquiterpenes. In fact, highly induced expression of rice *TPS* genes was associated with the strong induction of sesquiterpenes (including zingiberene,  $\beta$ -sesquiphellandrene and  $\beta$ -bisabolene) in the GRH-infested TGRH29 plants. These results suggest that GRH infestation induces the production of sesquiterpenes in the resistant line TGRH29. The accumulation of pathogen-induced sesquiterpenoid phytoalexins has a direct positive relationship with the transcript levels of *Tps6* and *Tps11* (Huffaker et al. 2011), and plants in which these genes are silenced exhibit increased susceptibility to *Ustilago maydis* (van der Linde et al. 2011). Further studies using the loss-of-function lines in which the expression of *TPS* genes is suppressed are needed to elucidate the biological role of rice *TPS* genes in GRH resistance.

Oxylipins encompass a large family of oxidized fatty acids and play pivotal roles as signaling molecules and protective compounds in plant responses to biotic stress. LOX has a central role in the oxylipin biosynthesis pathway (Blee 2002; Farmer et al. 2003; Nalam et al. 2012). The expression level of *OsRCI-1* (*Os12g37260*) was higher in GRH-infested shoots of TGRH29 compared with T65. Furthermore, the expression of *Os3g49350* was upregulated in response to GRH infestation in the shoots of TGRH29. In contrast, the expression of *OsLOX-RLL* (*Os08g39840*) was downregulated in response to GRH infestation in TGRH29. These transcription of these LOX genes was differentially regulated by the *GRH2*/*GRH4*-mediated defense response, although *OsRCI-1* and *OsLOX-RLL* encode 13-LOX, which incorporates oxygen at the C-13 position of the fatty acid to yield a 13-fatty acid hydroperoxide (Ohta et al. 1992, Peng et al. 1994, Schaffrath et al. 2000). The expression of *OsRCI-1* is induced in response to treatment with 2,6-dichloroisonicotinic acid (INA), JA, BTH and

probenazol (Schaffrath et al. 2000). The BTH response of *OsRCI-1* appeared unaffected by the knockdown of either *WRKY45* (*OsWRKY71*) or *NH1*, suggesting that the upregulation of *OsRCI-1* depends on another regulator (Shimono et al. 2007). This result agrees with our data that *NH1* and *PR1b* transcripts are increased in the susceptible line T65, whereas neither gene responded to GRH infestation in TGRH29. Suppression of *OsHI-LOX* (*OsLOX-RLL*) expression confers enhanced resistance to BPH (Zhou et al. 2009). In our microarray analyses, the expression of *OsLOX-RLL* was downregulated in response to GRH infestation in TGRH29. Thus, suppression of *OsLOX-RLL* expression may be associated with plant resistance to GRH. The functional role of LOXs in GRH resistance is unclear, although the modulation of LOX expression is thought to be involved in plant resistance.

TGRH29 exhibited a higher level of GRH resistance compared with TGRH11 (Figure 1). It is noteworthy that TGRH29 has strong insect resistance and defends itself against GRH insects via an inhibition of GRH feeding activity. The results of microarray analyses indicate that a large number of genes were upregulated in response to GRH infestation in TGRH29 compared with TGRH11 (Figure 2B). Furthermore, the expression levels of *TPS* (*Os04g27670*), *PR6* (*Os12g36210*) and *OsCCR24* were higher in TGRH29 than in TGRH11 at 30 h after GRH infestation. Transcripts of *JAmyb* and *TPS* (*Os08g07080*) accumulated to higher levels in TGRH29 than in TGRH11 at 6 h after GRH infestation. These results suggest that TGRH29 plants carrying both *GRH2* and *GRH4* can more rapidly and strongly activate their defense responses compared with plants expressing *GRH2* alone. In TGRH29, *GRH2* is thought to play an important role in GRH resistance and may be involved in the recognition of GRH invasion and the induction of the defense response because expression of *GRH4* alone did not provide any resistance to GRH. However, the presence of *GRH2* alone is not sufficient to protect rice plants against GRH. The GRH resistance of rice plants carrying *GRH2* is broken down by virulent biotypes under experimental conditions in the laboratory. In contrast, a virulent biotype that is effective against rice plants that carry *GRH2* and *GRH4* from Lepe dumai and C203-1 could not be identified by continuously rearing the GRH insects on the resistant rice lines (Hirae et al. 2007). Due to the presence of both *GRH2* and *GRH4*, TGRH29 plants rapidly recognize GRH invasion and subsequently activate various defense-related genes; eventually, these plants not only show strong GRH resistance but also prevent the appearance of a virulent biotype. Thus, *GRH2* and *GRH4* have a synergistic function in plant defense and confer strong GRH resistance.

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**Table S1** PCR primers used in gene expression analysis

Gene	Forward primer	Reverse primer
<i>Terpene synthase</i>		
<i>Os08g07080</i>	5'-GCTTCAACAAAGCGTGAACA-3'	5'-ACGATTTGGTGCAGGTC-3'
<i>Os04g27670</i>	5'-GAGATTGCTCTCGGTTTCG-3'	5'-AGTAGCCCCTTGCGTCATT-3'
<i>Os02g02930</i>	5'-CAGCTACCTCCAGACCTTGC-3'	5'-ATGGCTGTCATCATCCACAC-3'
<i>Transferase family (Os12g27254)</i>		
	5'-AGTCATCGTTGGGAGACCAC-3'	5'-AAAGAGCTCCCTTCCAAA-3'
<i>OsRCI-1</i>	5'-TTGCATGGTTCAGAGACGAG-3'	5'-TCGTGGTAGTCCAGCATGAA-3'
<i>OsJAZ8</i>	5'-CTCGCTCCATAGGTTCTCG-3'	5'-TCCCCACAGATCACTGACA-3'
<i>JAmyb</i>	5'-TTTGCTGCCTCTTCGATCCC-3'	5'-ATATATCTCCTCTGGCCTCTTGAAC-3'
<i>Subtilisin-chymotrypsin inhibitor</i>		
	5'-GGGTCGCCGGTGACCCCTC-3'	5'-ATTAAGATAAAGATGGCCGGG -3'
<i>OsCCR24</i>	5'-CTGTATCTGTTGATCCCGCA-3'	5'-TCATGGCTCCTATTGGGTC-3'
<i>UBC</i>	5'-CCCATCCTGAACCAGACAGT-3'	5'-CCTTTGCACCCCTGGAGTTA-3'

**Table S2** Comparison of gene expression levels between TGRH29 and T65.

Gene class	TGRH29/T65 (30 h after infestation)								GRH infestation (30h/0h)			
	Up		Down		T65		TGRH29					
	FC>2	FC>4	FC>2	FC>4	Up	Down	Up	Down				
PR	PR_01	1	1	1	1	1	0	1	0	1	0	
	PR_02	9	3	5	2	6	0	6	0	6	0	
	PR_03	3	3	1	0	1	0	3	1			
	PR_04	2	0	0	0	0	0	1	0	1	0	
	PR_05	6	1	1	0	4	0	6	0			
	PR_06	6	6	0	0	4	0	5	0			
	PR_07	3	1	4	1	2	0	2	0	2	0	
	PR_08	2	2	1	1	2	0	3	0			
	PR_10	0	0	2	1	2	0	2	0	2	0	
	PR_12	2	2	0	0	0	0	0	0	2	0	
	PR_14	5	3	0	0	0	0	0	0	3	0	
	PR_15_16	4	0	2	0	0	0	0	0	2	1	
PI	Bowman-Birk type bran trypsin inhibitor	8	8	0	0	5	0	8	0			
	Protease inhibitor/seed storage/LTP family protein	17	9	5	0	0	7	6	4			
	Proteinase inhibitor II family protein	3	3	0	0	2	0	3	0			
	Wound-induced protein	3	2	0	0	1	0	3	0			
Peptidase	Papain family cysteine protease	1	1	1	1	1	1	0	1			
	Caspase domain	1	0	1	0	0	0	0	0	0	1	
	Peptidase C26	1	1	0	0	0	0	0	0	1	0	
TF	Tify	9	6	0	0	7	0	9	0			
	WRKY	17	8	6	2	10	0	14	1			
	MYB	8	5	6	1	3	0	6	4			
	MYB-related	4	3	3	1	1	0	3	3			
	NAC	10	4	4	2	3	0	8	0			
	bHLH	9	3	3	0	3	0	4	1			
	bZIP	3	0	4	0	1	0	2	2			
	AP2/ERF	10	3	7	1	3	1	9	3			
	C2H2	5	3	3	0	3	0	4	0			
	P450	48	23	19	3	12	2	36	9			
	Terpene synthase	7	4	1	0	4	1	7	0			
	GDSL-like Lipase/Acylhydrolase	12	6	3	0	0	0	5	1			
	peroxidase	13	3	8	4	3	1	3	7			
	lipoxygenase	4	3	2	1	5	0	5	1			
	The ATP-binding Cassette (ABC) Superfamily	12	3	4	1	4	0	7	1			
	UDP-glucuronosyl and UDP-glucosyl transferase	21	7	13	6	5	2	10	6			
	protein phosphatase 2C	8	2	0	0	2	0	6	0			
	2OG-Fe(II) oxygenogenase superfamily	8	6	4	2	3	0	8	3			
	short chain dehydrogenase	13	6	5	1	3	1	9	2			
	Heavy-metal-associated domain	3	1	8	3	7	0	2	0			
	Glutathion S-transferase	15	6	5	0	6	0	8	0			

The number of genes were shown in this table.

PR: pathogenesis-related protein; PI: proteinase inhibitor; TF: transcription factor.

Table S3. Genes upregulated or downregulated 4 fold or greater in TGRH29

Gene ID	Gene name	NILs/T65						GRH infestation (30h/0h)			
		TGRH16		TGRH11		TGRH29		T65	TGRH16	TGRH11	TGRH29
		0 h	30 h	0 h	30 h	0 h	30 h				
LOC_Os01g01870	helix-loop-helix DNA-binding domain containing protein	0.31	1.11	0.34	1.65	0.52	2.44	0.57	1.38	1.90	2.50
LOC_Os01g03280	expressed protein	-0.52	0.14	0.18	-0.01	7.69	8.28	-0.38	0.04	-0.88	0.07
LOC_Os01g03310	Bowman-Birk type bran trypsin inhibitor precursor	0.43	0.21	-0.46	2.18	-0.80	2.13	3.80	3.50	6.68	6.37
LOC_Os01g03320	Bowman-Birk type bran trypsin inhibitor precursor	0.37	0.49	1.97	3.03	0.74	3.12	5.57	5.62	7.01	7.67
LOC_Os01g03360	Bowman-Birk type bran trypsin inhibitor precursor	0.26	0.15	1.32	2.33	0.37	2.19	4.58	4.42	5.61	6.17
LOC_Os01g03380	Bowman-Birk type bran trypsin inhibitor precursor	-0.30	-0.05	-0.19	4.02	-0.30	3.43	1.72	2.04	6.32	5.35
LOC_Os01g03390	Bowman-Birk type bran trypsin inhibitor precursor	0.39	0.49	-0.16	2.04	-0.49	2.96	1.59	1.67	3.81	4.68
LOC_Os01g03680	Bowman-Birk type bran trypsin inhibitor precursor	0.32	1.25	1.01	2.33	1.37	2.61	5.34	6.16	6.71	6.31
LOC_Os01g03730	nucleus PA3	0.50	0.07	0.08	1.49	0.54	2.53	-0.46	-0.87	0.97	1.50
LOC_Os01g04040	Bowman-Birk type wound-induced proteinase inhibitor WIP1	0.44	0.49	1.77	4.16	1.85	5.04	0.16	0.22	2.56	3.06
LOC_Os01g04050	Bowman-Birk type wound-induced proteinase inhibitor WIP1 precursor	-0.33	-0.18	-0.74	2.38	-1.68	2.27	0.73	0.85	3.78	4.43
LOC_Os01g04620	expressed protein	-0.31	0.35	1.56	2.33	2.64	4.28	0.52	1.18	1.32	2.11
LOC_Os01g06740	protein synthesis inhibitor I	0.84	0.27	0.63	0.90	0.83	2.06	0.43	-0.15	0.70	1.67
LOC_Os01g09080	WRKY transcription factor, OsWRKY26	1.98	2.38	1.76	1.89	2.47	3.05	0.27	0.68	0.40	0.86
LOC_Os01g09130	hypothetical protein	0.79	3.19	0.34	2.67	2.82	5.53	0.28	2.70	2.54	2.92
LOC_Os01g09640	MCB2 protein	2.74	3.23	3.14	4.25	2.29	4.38	-0.10	0.42	1.06	1.99
LOC_Os01g10260	expressed protein	0.81	0.95	-0.27	1.01	0.57	2.10	0.29	0.46	1.60	1.81
LOC_Os01g12750	cytochrome P450 71A4	0.44	0.50	0.51	2.43	0.50	2.27	-0.44	-0.39	1.52	1.33
LOC_Os01g13950	OsGrx_A1 - glutaredoxin subgroup III	1.83	2.34	0.20	1.36	1.73	2.96	1.46	1.96	2.67	2.61
LOC_Os01g16750	disulfide oxidoreductase/ monooxygenase/ oxidoreductase	1.28	1.83	1.41	3.88	0.59	3.63	-0.54	0.04	2.02	2.52
LOC_Os01g18120	cinnamoyl CoA reductase	-0.66	1.17	0.15	4.10	-2.82	4.49	-0.47	1.54	3.67	6.70
LOC_Os01g18930	peroxidase 1 precursor	1.35	1.63	0.91	1.84	1.73	2.18	-1.20	-1.00	-0.33	-0.85
LOC_Os01g19290	nodulin-like protein	-0.23	1.05	-0.04	6.03	0.48	7.76	-1.52	-0.19	4.72	5.66
LOC_Os01g21590	expressed protein	0.04	0.58	0.26	0.07	0.44	2.97	-1.58	-0.91	-1.72	1.14
LOC_Os01g21940	WD-40 repeat protein	1.75	1.58	0.82	1.16	1.61	2.06	-0.26	-0.45	0.10	0.19
LOC_Os01g22352	peroxidase 2 precursor	0.49	0.30	-0.24	1.09	0.25	2.65	-1.06	-1.21	0.34	1.39
LOC_Os01g24710	salt stress-induced protein	-0.09	-0.04	0.25	2.85	-0.65	3.57	-0.26	-0.22	2.29	3.52
LOC_Os01g27490	leucoanthocyanidin dioxygenase	0.19	-0.59	0.46	2.21	1.02	3.70	-1.70	-2.71	-0.11	0.84
LOC_Os01g28500	pathogenesis-related protein PRMS precursor	1.35	1.95	0.49	1.26	0.06	2.50	0.70	1.26	1.49	3.01
LOC_Os01g32560	expressed protein	1.22	0.96	1.39	2.41	1.78	2.30	-0.49	-0.97	0.40	-0.14
LOC_Os01g36294	cytochrome P450 71C4	0.61	0.93	0.60	2.53	-1.25	2.22	1.52	1.79	3.44	4.77
LOC_Os01g36350	cytochrome P450 71C4	1.49	1.65	1.88	2.68	1.83	2.51	0.47	0.60	1.29	1.13
LOC_Os01g37750	glutathione S-transferase GSTU6	0.75	0.32	0.42	1.19	1.12	2.19	1.84	1.40	2.66	2.86
LOC_Os01g38650	expressed protein	0.66	0.64	2.45	3.94	2.01	4.50	2.47	2.40	3.93	4.80
LOC_Os01g39580	anthocyanin regulatory Lc protein	1.40	2.04	1.06	1.89	1.53	2.12	-1.08	-0.56	-0.40	-0.61
LOC_Os01g40950	hypothetical protein	0.31	0.94	0.85	1.51	0.27	2.76	4.67	5.35	5.53	6.94
LOC_Os01g41240	sigma factor sigB regulation protein rsbQ	0.09	0.64	0.08	1.28	2.77	2.40	0.20	0.77	1.42	-0.20
LOC_Os01g42370	PDRS5-like ABC transporter	0.30	-0.03	1.52	3.77	1.46	4.20	0.92	0.59	3.28	3.66
LOC_Os01g45914	expressed protein	-0.28	0.46	1.18	2.44	6.34	2.86	0.33	1.09	1.61	-3.12
LOC_Os01g48870	60S ribosomal protein L37a	2.85	2.48	2.12	2.32	2.52	2.83	0.03	-0.32	0.25	0.28
LOC_Os01g50910	late embryogenesis abundant protein, group 3	1.60	-0.05	0.53	1.22	0.05	2.73	2.60	0.84	3.20	5.00
LOC_Os01g50934	fiber protein Fb11	2.37	2.31	0.60	1.07	2.27	2.39	-0.77	-0.80	-0.27	-0.62
LOC_Os01g50940	DNA binding protein	0.31	1.25	0.30	1.48	0.56	3.23	1.70	2.60	2.92	4.27
LOC_Os01g51360	triacylglycerol lipase	1.96	2.04	0.70	0.69	2.66	2.19	-0.35	-0.26	-0.37	-0.82
LOC_Os01g54510	MAC/Perforin domain containing protein	2.19	2.82	0.99	1.35	2.17	2.75	-0.22	0.41	0.15	0.35
LOC_Os01g55010	EBNA1	1.13	2.38	0.50	1.24	1.29	2.07	-0.63	0.47	-0.12	-0.05
LOC_Os01g55510	dynein light chain LC6, flagellar outer arm	0.42	1.48	0.35	0.96	0.58	2.40	-0.27	0.77	0.35	1.41
LOC_Os01g55720	expressed protein	2.37	2.03	0.92	1.21	2.27	2.73	-0.23	-0.56	0.06	0.20
LOC_Os01g56810	cytokinin dehydrogenase 5 precursor	-0.39	-0.21	-0.05	2.07	-0.06	2.66	-1.29	-1.07	0.89	1.45
LOC_Os01g58100	polyphenol oxidase, chloroplast precursor	0.41	0.81	2.17	4.69	1.39	4.40	3.03	3.35	5.51	5.84
LOC_Os01g58290	cucumisin precursor	0.68	-0.13	0.76	1.18	0.77	2.64	-0.15	-0.97	0.28	1.70
LOC_Os01g60600	WRKY DNA binding domain containing protein, OsWRKY41	1.04	1.11	1.22	1.31	0.83	2.05	1.65	2.04	1.94	2.90
LOC_Os01g61044	amino acid-polyamine transporter	0.99	0.95	0.79	1.41	1.62	2.81	1.05	0.96	1.65	2.19
LOC_Os01g611070	heavy metal-associated domain containing protein	-0.31	0.37	-0.14	1.99	-0.44	2.18	-1.10	-0.32	1.19	1.62
LOC_Os01g63480	AER	0.13	-0.03	0.00	1.90	0.40	3.58	-0.82	-0.96	1.11	2.37
LOC_Os01g63980	TRANSPARENT TESTA 1 protein	-0.24	0.01	0.44	2.35	0.47	2.60	2.69	3.09	4.63	4.64
LOC_Os01g64360	MYB transcription factor	0.83	1.73	0.59	1.04	0.55	2.10	2.51	3.36	2.98	3.97
LOC_Os01g65920	F-box/LRR-repeat protein 2	1.95	2.25	0.57	0.56	1.94	2.16	-0.05	0.24	-0.06	0.14
LOC_Os01g66990	hypothetical protein	-0.28	0.85	0.00	0.50	1.77	2.46	1.48	2.75	2.11	2.39
LOC_Os01g68660	cysteine proteinase inhibitor B	-0.53	0.42	0.50	3.52	0.72	3.50	-0.46	0.61	2.53	2.20
LOC_Os01g70150	hypothetical protein	0.48	1.15	1.37	3.94	2.05	5.45	0.55	1.31	3.25	3.88
LOC_Os01g71090	xylanase inhibitor	0.11	-0.25	0.55	1.72	0.28	2.34	-1.22	-1.55	-0.05	0.83
LOC_Os01g71460	F-box domain containing protein	2.91	2.28	2.69	2.83	2.38	2.31	0.36	-0.30	0.45	0.25
LOC_Os01g71624	expressed protein	-0.96	0.17	-0.19	2.01	-0.56	4.01	1.54	2.76	3.82	5.90
LOC_Os01g71830	glucan endo-1,3-beta-glucosidase GV	0.51	0.22	0.42	0.68	1.10	2.78	1.34	1.03	1.61	2.96
LOC_Os01g71870	ligA	1.25	2.38	1.12	1.34	1.11	2.45	0.27	1.50	0.50	1.57
LOC_Os01g72140	glutathione S-transferase	-0.35	-0.25	1.50	2.37	1.07	2.07	2.20	2.23	3.01	3.02
LOC_Os01g72270	cytochrome P450 86A2	0.96	1.07	2.46	4.05	3.32	4.92	0.82	1.02	2.44	2.32
LOC_Os02g01700	RNA recognition motif containing protein	2.33	2.32	1.98	2.23	2.33	2.59	-0.08	-0.07	0.20	0.19
LOC_Os02g02210	aminotransferase y4uB	-0.16	-0.65	1.10	4.65	2.48	7.34	0.42	0.00	3.92	4.87
LOC_Os02g02230	cytochrome P450 51	-0.08	-0.73	0.29	0.99	0.62	2.44	-0.98	-1.57	-0.15	1.01
LOC_Os02g02780	ATP binding protein	0.40	0.32	0.15	1.42	0.60	2.44	0.34	0.31	1.69	2.24
LOC_Os02g04640	transfector-like protein	0.11	0.32	0.42	2.65	-0.32	3.71	0.85	1.06	3.12	4.83
LOC_Os02g05400	phosphatidate cytidyltransferase	1.87	2.63	-0.32	-0.72	1.93	2.33	-0.35	0.45	-0.76	0.08
LOC_Os02g06090	phytosulfokine receptor precursor	0.13	0.48	-0.27	2.76	0.64	4.89	0.00	0.77	3.20	4.08
LOC_Os02g06300	GTP-binding protein LepA containing protein	2.19	2.26	2.68	2.66	2.44	2.11	-0.73	-0.63	-0.71	-1.02
LOC_Os02g08270	defense-related protein	0.26	1.05	-0.11	3.03	0.35	3.12	1.85	2.63	4.99	4.47
LOC_Os02g10590	FK506 binding protein	2.66	2.84	3.16	3.42	3.07	2.49	-0.14	0.00	0.09	-0.76
LOC_Os02g11640	flavonol-3-O-glycoside-7-O-glucosyltransferase 1	0.14	0.38	0.14	1.90	-0.28	2.02	-0.11	0.11	1.67	2.16
LOC_Os02g11870	expressed protein	-0.96	0.35	0.67	1.80	-0.08	2.48	3.49	4.81	4.57	5.77
LOC_Os02g12680	cytochrome P450 74A3	-1.76	1.11	3.38	5.30	4.15	7.21	1.55	4.36	3.42	4.45
LOC_Os02g21350	expressed protein	1.42	3.00	1.58	3.32	1.43	3.14	-1.43	0.04	0.20	0.16
LOC_Os02g21810	cytochrome P450 51	-0.18	0.16	-0.06	1.73	0.71	2.15	-2.88	-2.44	-0.91	-1.26
LOC_Os02g26794	expressed protein	1.11	0.60	0.57	3.88	-0.13	3.30	1.85	1.27	5.15	4.99
LOC_Os02g30100	cytochrome P450 81E1	0.24	0.20	0.72							

LOC_Os02g36880	NAC domain protein NACS	0.33	0.26	0.16	1.63	0.75	2.94	0.30	0.22	1.80	2.45
LOC_Os02g36890	MYB transcription factor	3.07	3.06	1.13	1.11	2.71	2.93	0.29	0.24	0.25	0.47
LOC_Os02g40840	oxidoreductase	0.28	0.24	0.23	0.94	0.87	2.48	0.90	0.86	1.65	2.43
LOC_Os02g44700	RING-H2 finger protein ATL3D	2.07	2.06	1.75	1.62	2.41	2.24	-0.51	-0.66	-0.79	-0.83
LOC_Os02g44870	dehydriin COR410	2.08	1.79	-1.37	-1.21	1.67	2.09	0.55	0.27	0.72	0.93
LOC_Os02g48770	SAM dependent carboxyl methyltransferase	0.87	1.21	1.50	4.07	0.45	4.62	3.17	3.43	5.73	7.12
LOC_Os02g50350	dihydropyrimidine dehydrogenase precursor	0.88	1.09	1.21	2.12	1.09	2.80	-0.27	-0.05	0.65	1.35
LOC_Os02g50700	expressed protein	-0.16	0.09	0.18	1.50	-0.34	2.24	0.84	1.10	2.15	3.40
LOC_Os02g51100	arsenical pump-driving ATPase	2.03	2.13	1.66	1.85	2.10	2.13	-0.29	-0.17	-0.07	-0.23
LOC_Os02g51404	expressed protein	2.11	2.77	1.69	2.13	2.30	2.69	-0.93	-0.30	-0.52	-0.56
LOC_Os02g51930	cytokinin-O-glycosyltransferase 2	0.60	1.37	0.73	3.51	-0.35	4.28	1.08	1.84	3.88	5.63
LOC_Os02g52670	ethylene-responsive element binding protein 2	-0.16	1.17	0.93	2.40	0.57	3.13	-0.19	1.29	1.42	2.45
LOC_Os02g53100	Superfamily of rice TFs having WRKY and zinc finger domains, OsWRKY17	0.20	0.16	0.35	2.38	1.56	4.01	1.04	1.24	3.01	3.37
LOC_Os03g01300	cortical cell-delineating protein precursor	-0.21	-0.24	-0.31	3.49	-1.39	2.68	-0.47	-0.37	3.52	3.61
LOC_Os03g01310	cortical cell-delineating protein precursor	0.35	0.82	-0.21	3.47	-0.16	3.74	-1.25	-0.81	2.44	2.55
LOC_Os03g01940	expressed protein	3.63	3.09	4.43	2.88	4.03	2.57	1.47	0.90	-0.09	-0.03
LOC_Os03g03034	flavonol synthase/flavanone 3-hydroxylase	0.67	0.74	0.40	1.33	0.74	2.43	1.33	1.42	2.29	2.89
LOC_Os03g03810	flower-specific gamma-thionin precursor	-0.56	-0.15	2.04	4.40	2.14	4.83	-0.61	-0.11	1.89	2.19
LOC_Os03g05880	monooxygenase	-1.14	-1.26	1.66	3.08	0.93	2.88	0.75	0.61	2.20	2.66
LOC_Os03g06520	sulfate transporter 3.1	1.89	2.02	-0.54	0.42	1.93	3.11	0.53	0.63	1.50	1.66
LOC_Os03g08310	OsJAZ9	0.43	1.61	0.92	2.07	0.70	2.36	3.18	4.30	4.31	4.75
LOC_Os03g08320	OsJAZ11	-0.19	1.12	0.40	2.49	0.49	2.97	3.21	4.51	5.37	5.53
LOC_Os03g08330	OsJAZ10	0.67	1.72	1.20	1.45	1.20	2.10	2.08	3.12	2.35	2.89
LOC_Os03g08520	expressed protein	0.34	2.39	-0.05	2.07	0.83	3.36	3.07	5.02	5.15	5.40
LOC_Os03g08900	transparent testa 12 protein	0.00	1.55	0.27	3.00	0.34	2.76	2.90	4.45	5.59	5.04
LOC_Os03g09810	polyamine oxidase precursor	3.00	2.12	2.20	3.37	3.26	5.17	-0.86	-1.60	0.49	1.24
LOC_Os03g12510	non-symbiotic hemoglobin 2	0.74	0.36	0.23	-0.25	0.60	2.77	2.16	1.74	1.65	4.23
LOC_Os03g13050	ACII9	0.16	1.15	-0.13	2.89	-0.40	3.68	1.12	2.11	4.24	5.18
LOC_Os03g14000	acyl CoA binding protein	2.36	2.86	2.42	2.70	2.68	2.99	0.53	1.01	0.79	0.80
LOC_Os03g14100	mybHv5	1.45	2.26	0.76	1.47	1.40	2.03	-1.13	-0.26	-0.41	-0.45
LOC_Os03g14590	calcium ion binding protein	1.10	1.25	1.11	2.37	0.88	2.33	0.06	0.20	1.33	1.49
LOC_Os03g14642	36.4 kDa proline-rich protein	1.07	0.93	1.45	2.28	1.41	3.07	-2.61	-2.68	-1.76	-0.89
LOC_Os03g14840	csPK3	2.47	2.12	2.19	1.85	1.99	2.13	0.07	-0.28	-0.26	0.24
LOC_Os03g16170	protein phosphatase 2C	0.63	0.96	0.83	2.77	0.86	3.20	1.98	2.25	3.94	4.25
LOC_Os03g16940	glyoxalase family protein superfamily	0.00	0.20	0.41	1.60	0.75	2.27	3.24	3.35	4.38	4.59
LOC_Os03g18030	leucoanthocyanidin dioxygenase	-0.57	0.63	0.76	3.06	0.45	3.51	1.34	2.54	3.66	4.36
LOC_Os03g19410	secreted protein	2.21	2.25	2.37	2.77	2.29	2.55	-0.50	-0.45	-0.07	-0.21
LOC_Os03g22680	RING finger and CHY zinc finger domain-containing protein 1	1.33	1.45	1.43	1.69	1.50	2.31	0.50	0.56	0.74	1.27
LOC_Os03g25470	copper transporter 1	3.45	3.18	1.16	0.47	3.67	2.98	-0.24	-0.36	-0.80	-0.78
LOC_Os03g25480	cytochrome P450 72A1	1.65	2.12	-0.10	-0.25	1.63	2.03	-0.20	0.41	-0.31	0.32
LOC_Os03g28090	pectinesterase-2 precursor	-1.11	-0.55	-1.31	2.36	-0.29	4.33	-0.94	-0.41	2.73	3.40
LOC_Os03g32420	expressed protein	0.13	0.36	0.37	1.71	0.20	2.34	1.09	1.35	2.43	3.16
LOC_Os03g38540	glutamate formiminotransferase	0.67	0.94	0.43	1.88	0.47	2.03	-0.14	0.12	1.34	1.41
LOC_Os03g43100	expressed protein	-0.73	0.91	0.57	5.02	-1.11	4.96	-0.18	1.44	4.40	5.75
LOC_Os03g45170	high-affinity cationic amino acid transporter 1	1.39	1.71	0.91	0.91	1.68	2.00	-0.10	0.22	-0.10	0.22
LOC_Os03g45210	cupin, RmLC-type	0.04	0.52	-0.11	2.31	-0.33	5.16	-0.64	-0.12	1.86	4.60
LOC_Os03g49350	lipoxygenase 3	0.06	0.45	0.27	2.18	0.20	2.12	0.67	1.04	2.60	2.55
LOC_Os03g50960	cortical cell-delineating protein precursor	1.04	2.25	0.37	5.57	-0.48	5.09	-0.67	0.48	4.44	4.66
LOC_Os03g52370	expressed protein	1.27	0.16	1.46	2.86	3.65	5.23	4.17	3.14	5.68	5.67
LOC_Os03g52380	expressed protein	-0.01	0.13	1.13	3.46	0.86	4.32	1.15	1.34	3.56	4.54
LOC_Os03g52390	type II proteinase inhibitor family protein	-0.01	-0.19	0.67	2.40	0.59	3.10	3.15	2.96	4.93	5.56
LOC_Os03g53350	cytokinin-O-glycosyltransferase 1	1.04	2.73	-0.12	2.91	1.38	4.29	-1.08	0.41	1.78	1.64
LOC_Os03g57040	AP-1 complex subunit sigma-2	3.45	3.99	3.14	3.94	3.16	4.10	-0.91	-0.38	-0.12	0.03
LOC_Os03g57640	gibberellin receptor GID1L2	0.18	0.58	1.17	2.10	1.27	2.85	1.46	1.83	2.39	2.97
LOC_Os03g58300	indole-3-glycerol phosphate lyase, chloroplast precursor	0.61	0.73	1.25	3.56	0.98	2.69	2.00	2.10	4.33	3.60
LOC_Os03g58500	hypothetical protein	0.21	0.47	-0.21	4.03	0.22	5.05	0.53	0.88	4.98	5.14
LOC_Os03g58530	DNA binding protein	1.91	2.12	1.38	1.61	2.30	2.39	-0.15	0.05	0.05	-0.06
LOC_Os03g59030	UDP-rhamnose rhamnosyltransferase	0.81	0.34	0.34	1.91	0.40	2.07	0.19	-0.22	1.90	1.90
LOC_Os03g60580	actin-depolymerizing factor 4	2.40	2.62	0.94	3.18	2.84	6.52	0.98	1.19	3.26	4.63
LOC_Os03g61150	dnaj domain containing protein	0.17	-0.29	0.11	1.80	0.33	2.20	0.11	-0.33	1.85	2.01
LOC_Os03g63200	powdery mildew resistance protein PM3b	3.05	4.18	1.96	1.89	3.28	3.14	-1.16	-0.17	-1.41	-1.45
LOC_Os03g63330	aspartokinase	1.72	1.77	1.70	3.47	1.67	2.52	-0.83	-0.75	0.98	0.05
LOC_Os03g63870	expressed protein	1.01	0.04	8.52	7.60	6.51	5.95	1.10	0.38	0.18	0.53
LOC_Os04g01690	arginine decarboxylase	0.43	-0.63	-0.68	1.33	0.17	2.82	-0.71	-1.80	1.36	2.02
LOC_Os04g01710	cysteine proteinase At4g11310 precursor	0.45	0.14	0.29	2.65	-0.25	2.17	-1.28	-1.57	1.11	1.14
LOC_Os04g01810	aristolochene synthase	0.18	0.61	5.90	7.97	6.82	9.88	0.92	1.51	3.15	4.00
LOC_Os04g06630	transposon protein, CACTA, En/Spm sub-class	1.15	1.85	1.54	2.66	1.57	2.38	-0.51	0.19	0.59	0.28
LOC_Os04g08560	protein phosphatase 2C containing protein	-0.38	0.68	-0.34	1.89	0.24	2.71	2.79	3.79	5.36	5.30
LOC_Os04g10350	1-aminoacylcopropane-1-carboxylate oxidase	0.32	0.46	0.94	3.56	0.93	3.83	0.49	0.62	3.14	3.26
LOC_Os04g14690	monooxygenase/ oxidoreductase	0.85	0.32	0.23	2.87	0.47	4.12	0.43	-0.11	3.13	4.04
LOC_Os04g15840	alpha-expansin 1 precursor	0.90	0.54	0.70	1.59	0.35	2.84	-2.31	-2.53	-1.24	0.41
LOC_Os04g15920	mannitol dehydrogenase	2.25	3.63	1.49	4.10	2.97	5.00	-0.27	1.15	2.45	1.79
LOC_Os04g24469	jasmonate-induced protein	-0.71	-1.20	-0.67	2.29	1.37	4.03	0.97	0.34	4.00	3.54
LOC_Os04g25950	circumsporozoite protein precursor	0.56	0.98	0.36	1.34	1.19	2.69	0.12	0.58	1.14	1.65
LOC_Os04g27760	retrotransposon protein, unclassified	-0.44	0.42	1.61	5.65	2.05	7.54	-0.60	0.18	3.47	4.67
LOC_Os04g27760	terpene synthase 7	-0.69	1.27	4.43	6.83	5.84	9.31	1.89	3.90	4.26	4.99
LOC_Os04g29890	transposon protein, CACTA, En/Spm sub-class	1.85	2.95	1.50	2.42	2.05	2.81	-0.36	0.76	0.59	0.42
LOC_Os04g31160	acetolactate synthase III, chloroplast precursor	0.60	0.65	1.26	2.48	1.44	2.78	-0.11	-0.01	1.21	1.31
LOC_Os04g32010	acetolactate synthase III, chloroplast precursor	-0.10	0.00	1.33	2.62	0.86	2.64	-0.21	-0.08	1.15	1.63
LOC_Os04g32480	OsJAZ5	1.70	1.73	1.37	2.82	1.87	4.00	3.90	3.79	5.28	5.78
LOC_Os04g32420	sex determination protein tasselseed-2	0.04	-0.23	0.56	1.13	1.01	2.47	1.95	1.65	2.56	3.34
LOC_Os04g35240	serine/threonine-protein kinase SAPK7	3.69	3.00	1.54	2.18	3.41	3.74	0.23	-0.44	0.90	0.57
LOC_Os04g36610	family 9 endoglucanase At1g71380 precursor	0.90	2.10	0.67	2.04	1.14	2.37	-1.73	-0.61	-0.46	-0.56
LOC_Os04g37780	expressed protein	1.25	1.07	1.12	3.32	1.57	3.37	1.14	0.89	3.37	2.86
LOC_Os04g39470	pentatricopeptide repeat protein PPR98E-12	1.07	2.30	0.41	1.74	1.73	2.67	-1.52	-0.41	-0.33	-0.73
LOC_Os04g39980	gibberellin 20 oxidase 2	1.11	1.77	0.78	1.79	1.05	2.44	-0.17	0.53	0.90	1.24
LOC_Os04g42050	hypothetical protein	1.05	2.62	1.60	5.63	1.54	5.14	-1.24	0.13	2.67	2.14
LOC_Os04g43200	caleosin 2	0.00	0.07	0.62	3.44	0.24	3.76	2.28	2.31	5.12	5.68
LOC_Os04g43390	beta-mannosidase 4	-0.67	-0.41								

LOC_Os04g52430	expressed protein	0.36	1.49	0.58	3.50	0.22	4.18	-0.50	0.51	2.31	3.23
LOC_Os04g52440	aminotransferase y4uB	0.08	-0.28	1.03	5.32	0.45	6.85	-1.37	-1.70	3.15	5.17
LOC_Os04g52810	no apical meristem protein	0.18	0.61	-0.15	0.32	0.28	2.01	1.57	1.99	2.00	3.22
LOC_Os04g53130	GTE8	2.06	2.49	2.56	2.66	1.94	2.03	-0.16	0.28	-0.04	-0.04
LOC_Os04g53350	expressed protein	1.82	1.83	1.47	1.59	1.55	2.10	-0.13	-0.11	0.00	0.42
LOC_Os04g53810	leucoanthocyanidin reductase	0.85	0.52	1.23	2.70	0.77	2.82	3.60	3.19	5.06	5.49
LOC_Os04g55260	vacuolar membrane protein	3.29	4.21	1.74	2.53	3.61	4.10	-0.45	0.29	0.16	-0.15
LOC_Os04g56110	ATP binding protein	1.51	1.75	0.88	1.51	1.44	2.95	0.92	1.13	1.57	2.38
LOC_Os04g56130	ATP binding protein	1.24	1.50	1.05	1.66	1.34	2.51	0.19	0.44	0.81	1.36
LOC_Os04g57710	conserved hypothetical protein	2.20	2.30	1.57	1.77	2.11	2.07	-0.45	-0.31	-0.21	-0.46
LOC_Os04g57880	dnaJ domain containing protein	0.52	0.36	0.35	2.46	0.59	3.09	2.61	2.40	4.73	5.04
LOC_Os05g01920	subtilisin-chymotrypsin inhibitor Cl-1B	0.94	1.15	3.87	5.39	4.51	6.18	0.03	0.33	1.63	1.74
LOC_Os05g02200	protein kinase	-0.34	-0.61	0.38	1.18	1.14	2.01	1.06	0.79	1.88	1.89
LOC_Os05g03640	flavonol synthase/flavanone 3-hydroxylase	-0.32	0.86	0.16	2.58	0.45	2.48	0.34	1.50	2.81	2.33
LOC_Os05g06160	trehalose-phosphatase	-0.11	0.25	0.32	0.57	1.25	2.11	-0.08	0.29	0.19	0.78
LOC_Os05g06920	guanosine-3,5-bis 3-pyrophosphohydrolase	1.80	1.39	1.39	2.96	1.43	2.88	-0.11	-0.51	1.49	1.29
LOC_Os05g08920	late embryogenesis abundant protein	1.63	2.14	1.45	2.20	1.63	2.37	-0.94	-0.35	-0.11	-0.12
LOC_Os05g09280	ischemia related factor NYW-1	0.62	0.51	0.65	3.26	0.87	3.08	-0.14	-0.18	2.65	2.20
LOC_Os05g10310	acid phosphatase	-0.76	0.20	0.34	2.47	0.77	2.86	0.79	1.82	3.01	2.80
LOC_Os05g10370	acid phosphatase	2.87	3.65	2.11	4.95	2.98	5.99	-0.98	-0.11	2.00	2.10
LOC_Os05g10690	MYBR2	0.84	0.97	0.24	1.39	0.25	2.18	-0.68	-0.54	0.50	1.26
LOC_Os05g12040	cytochrome P450 51	-0.04	2.08	1.86	4.58	2.20	6.32	1.37	3.59	4.18	5.40
LOC_Os05g13620	glycine-rich RNA-binding protein GRP2A	1.79	1.32	1.48	3.60	1.34	3.16	2.66	2.10	4.79	4.37
LOC_Os05g13970	phosphorylase domain containing protein	-1.69	-0.64	1.06	1.30	0.50	2.38	5.12	6.09	5.41	6.84
LOC_Os05g14370	WRKY transcription factor, OsWRKY45	-1.12	1.45	-0.61	4.09	0.69	4.44	0.93	3.21	5.80	4.57
LOC_Os05g15530	4-amino-4-deoxychorismate lyase	-0.20	0.16	-0.03	0.87	-0.61	2.17	0.91	1.27	1.81	3.63
LOC_Os05g17980	retrotransposon protein, unclassified	1.31	2.39	0.99	3.37	1.00	2.81	-1.36	-0.34	1.02	0.35
LOC_Os05g25890	expressed protein	-0.76	-0.41	1.46	3.59	0.48	3.68	1.00	1.28	3.12	3.94
LOC_Os05g31380	GRAS family transcription factor containing protein	1.52	2.20	1.23	1.88	1.62	2.01	-0.57	0.02	-0.04	-0.29
LOC_Os05g31760	annexin-like protein RJ4	0.69	0.86	0.22	1.19	0.71	2.33	0.45	0.60	1.40	1.85
LOC_Os05g33140	basic endochitinase 1 precursor	0.51	0.18	-0.02	1.87	-0.32	2.03	-0.92	-1.23	1.00	1.41
LOC_Os05g33630	hydrolase	0.29	0.67	0.07	1.64	0.02	2.13	0.36	0.73	1.94	2.42
LOC_Os05g35594	expressed protein	0.69	0.38	0.34	1.70	0.96	2.11	-0.97	-1.28	0.42	0.20
LOC_Os05g36260	soluble inorganic pyrophosphatase	0.30	0.79	0.73	2.36	0.49	2.29	-1.20	-0.69	0.46	0.63
LOC_Os05g37190	TRANSPARENT TESTA 1 protein	-1.72	0.19	-0.09	3.13	-1.28	2.87	1.93	3.89	5.23	5.90
LOC_Os05g41080	histone H3	1.56	1.09	1.17	2.25	1.06	2.42	-0.35	-0.76	0.80	1.06
LOC_Os05g42080	hypothetical protein	0.00	0.39	1.30	2.29	0.90	2.19	1.49	1.86	2.48	2.73
LOC_Os05g42210	serine/threonine-protein kinase receptor precursor	0.75	1.13	0.76	2.37	0.69	3.44	0.33	0.71	1.99	3.04
LOC_Os05g43120	esterase precursor	0.14	1.95	2.19	4.92	1.46	5.08	0.00	1.76	2.80	3.50
LOC_Os05g43940	O-methyltransferase ZRP4	1.47	1.09	1.38	2.51	1.66	3.01	-1.30	-1.63	-0.15	0.07
LOC_Os05g45090	anthocyanidin 5,3-O-glucosyltransferase	-0.32	0.78	-0.04	2.44	-0.74	3.14	0.02	1.14	2.56	3.84
LOC_Os05g45100	anthocyanidin 5,3-O-glucosyltransferase	-0.12	0.11	-0.04	3.47	-0.14	4.20	2.02	2.19	5.95	6.32
LOC_Os05g45740	hydrogen-transferring ATP synthase, rotational mechanism	2.16	1.58	1.59	2.14	1.79	2.35	-0.85	-1.40	-0.30	-0.27
LOC_Os05g46220	ADP/ATP translocase 2	2.50	2.58	2.83	2.44	1.82	2.06	0.54	0.54	0.06	0.73
LOC_Os05g46480	late embryogenesis abundant protein, group 3	-0.14	1.03	0.92	3.30	1.29	6.02	2.35	3.21	4.84	6.78
LOC_Os05g48650	tumor-related protein-like	0.46	1.03	0.36	1.97	0.64	2.84	0.05	0.61	1.65	2.20
LOC_Os05g50610	Superfamily of rice TFs having WRKY and zinc finger domains, OsWRKY44	0.40	0.20	-0.03	3.31	0.26	3.07	3.74	3.75	7.35	6.49
LOC_Os06g01440	integral membrane protein	0.21	0.38	0.29	2.43	0.56	2.26	0.38	0.52	2.52	2.05
LOC_Os06g03099	expressed protein	0.57	-0.02	-0.54	1.19	-0.49	2.06	-0.71	-1.28	1.06	1.85
LOC_Os06g03520	expressed protein	0.42	1.02	0.37	0.88	0.15	2.22	2.36	2.91	2.87	4.34
LOC_Os06g03900	esterase precursor	1.08	1.13	0.75	2.46	0.96	3.21	-2.42	-2.23	-0.57	-0.02
LOC_Os06g05940	lipopolysaccharide-modifying protein	1.14	0.97	0.74	1.61	1.02	2.28	-0.67	-0.83	0.19	0.59
LOC_Os06g08790	origin recognition complex subunit 1	1.74	2.30	0.35	2.25	1.28	3.46	-1.47	-0.96	0.38	0.65
LOC_Os06g08960	retrotransposon protein, Ty3-gypsy subclass	1.16	1.71	-0.12	-0.98	2.30	2.52	0.62	1.32	-0.10	0.91
LOC_Os06g11090	gibberellin receptor GID1L2	2.02	2.68	2.34	3.33	2.13	3.13	-0.66	-0.10	0.25	0.25
LOC_Os06g11660	phi-1-like phosphate-induced protein	0.29	0.23	0.31	1.58	0.31	2.41	-0.21	-0.28	1.03	1.69
LOC_Os06g11760	expressed protein	-0.49	0.68	0.53	3.47	0.12	2.73	-1.10	0.08	1.86	1.50
LOC_Os06g13390	SAM dependent carboxyl methyltransferase	-0.11	0.42	4.71	5.60	3.28	5.87	5.51	5.86	6.50	7.81
LOC_Os06g14010	MYB transcription factor TaMYB1	1.52	2.75	1.57	2.49	1.74	2.82	-1.45	-0.35	-0.69	-0.51
LOC_Os06g15202	3-ketoacyl-CoA synthase	0.73	-0.12	0.54	1.64	1.21	2.12	0.12	-0.73	1.26	1.03
LOC_Os06g24180	cytochrome P450 8A4A1	0.12	-0.29	1.90	4.04	-0.15	3.60	-0.15	-0.63	1.91	3.43
LOC_Os06g28050	3Fe-4S ferredoxin	-0.25	1.01	2.46	3.50	0.99	2.61	4.60	5.72	5.45	5.89
LOC_Os06g34730	expressed protein	-0.01	0.53	0.18	2.30	0.20	2.80	-0.54	0.01	1.61	2.05
LOC_Os06g36250	conserved hypothetical protein	2.79	2.68	1.50	1.22	2.86	2.47	-0.22	-0.30	-0.48	-0.60
LOC_Os06g36800	diacylglycerol acyltransferase	1.46	2.13	1.35	2.18	1.75	2.46	-0.60	0.11	0.27	0.14
LOC_Os06g37150	L-ascorbate oxidase precursor	0.24	0.37	-0.15	3.29	-0.80	3.55	0.11	0.21	3.51	4.03
LOC_Os06g38080	von Willebrand factor type A domain containing protein	1.04	0.07	-0.61	1.19	-0.83	3.39	-0.62	-1.54	1.35	3.66
LOC_Os06g40170	phospholipase D alpha 2	0.15	0.11	-0.05	1.41	0.45	2.01	-0.54	-0.57	0.97	1.04
LOC_Os06g43304	cytochrome P450 71D7	0.54	0.60	-0.08	1.72	-0.07	2.43	0.19	0.24	2.03	2.64
LOC_Os06g43320	cytochrome P450 71D10	2.08	2.42	0.33	1.82	1.34	2.91	-0.42	-0.05	1.15	1.22
LOC_Os06g44080	RUB1	2.43	2.06	0.32	0.62	1.96	2.57	-0.31	-0.67	-0.01	0.29
LOC_Os06g44190	expressed protein	-0.55	-0.26	0.41	2.03	-0.49	2.44	1.88	2.15	3.53	4.72
LOC_Os06g46284	alpha-glucosidase precursor	0.10	0.04	0.48	2.12	0.31	2.32	-0.42	-0.47	1.24	1.54
LOC_Os06g46740	early nodulin 20 precursor	0.52	-0.15	0.30	0.66	0.68	2.95	2.14	1.45	2.51	4.37
LOC_Os06g47910	alpha-L-fucosidase 2 precursor	-0.21	0.56	-0.43	1.76	-1.14	2.24	-0.83	-0.03	1.40	2.44
LOC_Os06g49000	expressed protein	1.47	2.60	1.70	2.82	2.03	2.90	0.05	1.04	1.04	0.74
LOC_Os06g49190	nonspecific lipid-transfer protein precursor	-0.41	-0.78	1.42	5.43	-0.59	4.78	0.32	-0.07	4.40	5.66
LOC_Os06g50950	anther-specific proline-rich protein APG precursor	0.24	0.46	0.28	1.13	0.93	2.21	-0.34	-0.11	0.53	0.92
LOC_Os06g51050	basic endochitinase 1 precursor	0.12	0.23	0.24	0.23	-0.24	2.40	1.98	2.07	1.96	4.56
LOC_Os06g51100	basic endochitinase 1 precursor	0.74	0.34	-0.25	1.15	-0.25	2.78	0.49	0.09	1.91	3.38
LOC_Os07g03377	pathogenesis-related protein 1 precursor	0.12	0.31	-1.35	-0.13	1.77	2.24	5.86	6.06	7.10	5.98
LOC_Os07g03810	lectin-like receptor kinase 7	0.57	0.35	0.50	1.76	-0.27	2.13	1.64	1.41	2.89	3.81
LOC_Os07g04990	aldo-keto reductase/ oxidoreductase	0.57	0.66	0.53	3.47	-0.17	3.07	-0.12	-0.03	2.87	3.04
LOC_Os07g05940	viviparous-14	-0.58	-1.80	0.30	2.15	0.03	2.54	3.95	2.79	5.82	6.29
LOC_Os07g06710	TPR Domain containing protein	1.89	2.13	0.76	0.95	1.80	2.05	-0.16	0.07	0.03	0.10
LOC_Os07g07320	glutathione S-transferase GSTU6	0.15	0.64	0.26	1.76	0.09	2.07	0.47	0.95	2.00	2.40
LOC_Os07g07460	hypothetical protein	2.28	2.31	1.79	1.32	2.51	2.29	-0.23	-0.22	-0.80	-0.47
LOC_Os07g08240	ZmEBE-1 protein	-0.26	1.79	1.35	3.33	2.81	6.11	2.21	4.22	4.16	5.30
LOC_Os07g09710	F-box domain containing protein	0.59	0.15	0.46	1.39	0					

LOC_Os07g26440	CIP7	3.41	4.19	1.72	2.69	3.33	4.39	-1.22	-0.33	-0.13	-0.09
LOC_Os07g26974	expressed protein	2.63	2.84	3.14	3.55	2.53	2.79	-0.04	0.15	0.35	0.19
LOC_Os07g27580	stem 28 kDa glycoprotein precursor	0.39	2.21	1.10	3.73	1.86	4.42	-0.32	1.43	2.25	2.11
LOC_Os07g31260	expressed protein	2.34	3.92	1.14	2.28	2.34	3.59	-1.35	0.33	-0.09	0.01
LOC_Os07g31720	ZAC	0.14	0.23	-0.98	1.78	-1.26	2.28	0.14	0.18	2.76	3.31
LOC_Os07g32290	hypothetical protein	2.53	2.30	-0.34	-0.25	2.76	2.30	-0.51	-0.75	-0.42	-0.95
LOC_Os07g34240	gibberellin receptor GID1L2	0.21	1.31	0.71	2.63	1.56	2.57	1.67	2.73	3.60	2.62
LOC_Os07g35510	glycosyl hydrolases family 17 protein	0.25	0.69	0.00	1.50	-0.77	2.62	0.39	0.82	1.90	3.69
LOC_Os07g37210	MYB transcription factor	0.88	-0.29	0.29	1.07	1.14	2.72	1.89	0.63	2.62	3.39
LOC_Os07g37780	40S ribosomal protein S11	2.30	2.18	-0.35	0.15	1.89	2.64	-0.68	-0.76	-0.17	0.02
LOC_Os07g39740	lipase/acylhydrolase	-0.24	0.17	3.20	5.04	0.33	4.80	2.55	3.07	4.67	7.09
LOC_Os07g40250	sex determination protein tasselseed-2	-0.13	-0.67	0.49	2.20	0.26	2.63	0.40	-0.15	2.14	2.76
LOC_Os07g42240	SKP1-like protein 1B	0.03	-0.28	0.34	1.36	0.39	2.37	-0.07	-0.38	1.02	1.94
LOC_Os07g44140	cytochrome P450 72A1	-0.05	0.13	0.03	0.31	-0.99	2.09	-1.41	-1.18	-1.07	1.78
LOC_Os07g44440	peroxiredoxin	0.20	0.04	0.10	2.44	1.01	3.26	2.30	2.11	5.04	4.64
LOC_Os07g44780	esterase precursor	0.27	0.27	1.20	3.19	0.50	2.57	0.37	0.37	2.39	2.42
LOC_Os07g44920	expressed protein	-0.11	-0.26	1.09	2.15	1.21	2.61	-0.08	-0.22	1.04	1.37
LOC_Os07g46840	sex determination protein tasselseed-2	2.12	2.69	-0.30	-0.28	2.17	2.77	-1.07	-0.43	-1.03	-0.42
LOC_Os07g46910	sex determination protein tasselseed-2	1.01	-0.06	0.80	2.37	1.63	2.95	1.05	-0.07	2.64	2.34
LOC_Os07g46920	sex determination protein tasselseed-2	0.24	0.39	2.25	2.54	1.54	2.58	3.65	3.76	3.97	4.50
LOC_Os07g46930	sex determination protein tasselseed-2	0.12	0.10	0.48	2.26	-0.12	2.68	-0.73	-0.75	1.10	2.07
LOC_Os07g47670	hypoxia induced protein conserved region containing protein	0.12	0.44	0.69	0.62	0.27	2.07	-0.10	0.22	-0.17	1.72
LOC_Os08g01120	sulfate transporter	-0.03	-0.17	0.82	2.30	0.83	2.52	-0.16	-0.29	1.35	1.52
LOC_Os08g01980	expressed protein	-0.19	0.44	-0.33	-0.31	6.10	4.98	0.00	0.64	0.00	-1.23
LOC_Os08g02180	expressed protein	0.01	0.51	0.66	0.84	1.07	2.24	-0.86	-0.34	-0.66	0.31
LOC_Os08g04250	protein kinase	-0.26	-0.09	-0.41	0.88	2.54	4.30	-2.34	-1.96	-1.02	-0.49
LOC_Os08g04500	terpene synthase	-0.55	-0.60	0.80	3.83	-1.33	2.02	-1.82	-1.88	1.19	1.47
LOC_Os08g05670	HEAT repeat family protein	0.18	1.10	0.81	1.51	1.87	3.12	-1.03	-0.21	-0.49	0.13
LOC_Os08g06190	reticuline oxidase precursor	0.52	-0.22	1.81	1.22	1.96	2.54	1.33	0.61	0.69	1.79
LOC_Os08g07080	terpene synthase	-0.60	0.54	1.34	4.80	0.78	5.00	3.77	4.87	7.23	7.76
LOC_Os08g07100	terpene synthase	-0.53	0.09	1.91	2.27	0.81	2.64	6.57	7.16	6.89	8.10
LOC_Os08g07340	mla1	-0.65	-1.73	-0.53	-1.58	6.24	4.92	1.12	0.00	0.00	-0.34
LOC_Os08g08970	germin-like protein subfamily 1 member 11 precursor	0.36	0.81	-0.33	1.72	1.69	2.52	0.09	0.53	2.16	0.88
LOC_Os08g10440	NBS-LRR disease resistance protein	0.74	0.57	0.53	0.40	3.13	3.10	-0.08	-0.19	-0.18	-0.06
LOC_Os08g10500	expressed protein	0.79	1.50	0.31	0.68	0.66	2.20	0.18	0.87	0.56	1.65
LOC_Os08g12830	ethanolamine-phosphate cytidylyltransferase	2.03	2.06	2.53	2.57	2.34	2.47	0.17	0.19	0.22	0.30
LOC_Os08g13130	conserved hypothetical protein	-0.45	-0.03	0.14	1.05	6.33	6.51	0.13	0.49	1.15	0.17
LOC_Os08g13890	exonuclease	0.40	0.06	0.12	0.37	2.56	2.54	-0.47	-0.80	-0.20	-0.50
LOC_Os08g14200	xyloglucan endotransglucosylase/hydrolase protein 23 precursor	-0.10	-0.76	0.10	0.87	5.51	4.53	0.46	0.00	1.35	-0.51
LOC_Os08g14220	expressed protein	-0.81	0.02	-0.28	-0.15	2.57	3.53	-1.04	-0.17	-0.85	-0.14
LOC_Os08g14700	glucan endo-1,3-beta-glucosidase 4 precursor	-0.01	0.37	-0.25	1.02	-1.16	2.17	0.31	0.68	1.62	3.61
LOC_Os08g16450	NBS-LRR disease resistance protein	-0.86	-0.99	0.54	0.09	7.23	5.31	0.06	0.03	-0.38	-1.81
LOC_Os08g16860	F-box domain containing protein	-0.13	-0.32	-0.37	4.98	-0.24	4.75	0.00	0.00	5.51	4.75
LOC_Os08g18974	expressed protein	-0.19	0.02	1.28	4.35	0.75	4.10	1.66	1.96	4.92	4.97
LOC_Os08g20130	flavonol 3-sulfotransferase	0.75	0.54	-0.23	3.40	1.58	5.32	-0.09	-0.24	3.68	3.73
LOC_Os08g21670	conserved hypothetical protein	0.50	0.85	-0.05	2.32	0.94	2.27	-0.67	-0.19	1.89	0.80
LOC_Os08g22210	retrotransposon protein, unclassified	-0.79	-0.62	-0.15	-0.29	6.13	5.67	0.50	0.58	0.67	-0.10
LOC_Os08g22604	expressed protein	0.13	-0.40	-0.17	0.59	0.98	2.19	-0.51	-1.06	0.26	0.75
LOC_Os08g24750	fucosyltransferase 7	-0.78	-1.17	0.23	2.71	-0.03	3.56	1.21	0.59	3.50	4.40
LOC_Os08g25690	expressed protein	-0.37	0.44	0.76	1.61	-0.26	5.78	-0.71	0.21	0.25	5.45
LOC_Os08g26850	expressed protein	2.57	2.09	1.69	0.78	3.25	2.93	0.56	0.12	-0.34	0.25
LOC_Os08g28240	crocetin dialdehyde	-1.02	-0.21	-0.78	4.00	-1.24	7.43	-0.68	0.00	4.06	7.57
LOC_Os08g29160	protein tyrosine/serine/threonine phosphatase	0.12	0.38	-0.11	-0.03	1.43	2.43	-0.52	-0.17	-0.36	0.54
LOC_Os08g29980	retrotransposon protein, unclassified	0.85	1.85	1.05	1.76	2.58	3.15	0.10	1.14	0.76	0.70
LOC_Os08g31980	trehalose 6-phosphate synthase	0.62	0.75	0.42	0.42	1.76	2.38	0.24	0.37	0.24	0.84
LOC_Os08g33740	CSLA11 - cellulose synthase-like family A	1.64	1.10	0.48	3.56	1.35	3.89	0.10	-0.42	3.28	2.66
LOC_Os08g35630	MTD1	0.28	0.40	0.40	1.49	-0.30	2.22	1.23	1.33	2.36	3.73
LOC_Os08g36480	nitrate reductase 1	0.37	0.47	0.41	1.26	0.21	2.07	-1.30	-1.18	-0.44	0.56
LOC_Os08g36680	carbonic anhydrase precursor	-0.49	0.66	0.00	1.49	-0.75	2.42	0.58	1.79	2.10	3.63
LOC_Os08g38500	transposon protein, unclassified	2.66	2.75	-1.65	-2.20	3.29	2.58	-0.02	0.11	-0.49	-0.70
LOC_Os08g38910	caffeooyl-CoA O-methyltransferase 2	0.87	1.01	0.50	1.66	1.27	2.20	0.41	0.53	1.57	1.32
LOC_Os08g39730	cytochrome P450 76C2	-1.37	-1.58	0.29	2.12	0.33	2.79	2.50	2.11	4.29	4.73
LOC_Os08g404680	xylanase inhibitor protein 2 precursor	-0.17	2.19	1.02	3.92	0.91	4.82	2.06	4.26	4.87	5.55
LOC_Os08g41880	nucleotide pyrophosphatase/phosphodiesterase	0.37	-0.63	1.08	4.15	0.68	4.19	0.02	-1.03	3.17	3.54
LOC_Os08g42010	nodulin-like protein	1.67	3.24	2.35	3.79	1.88	3.39	-1.81	-0.35	-0.48	-0.41
LOC_Os08g42750	calcium-dependent protein kinase, isoform AK1	0.37	1.09	-0.06	1.45	0.71	2.00	-0.49	0.35	1.15	0.92
LOC_Os08g43120	ABC transporter	-0.02	-0.65	-0.37	3.82	-0.45	5.96	1.48	0.89	5.84	7.82
LOC_Os08g44020	lyase	1.65	1.98	2.77	3.12	1.98	2.02	-0.41	-0.13	-0.12	-0.44
LOC_Os08g44210	dihydronoepterin aldolase	1.78	1.99	1.37	3.52	1.47	2.96	0.61	0.78	2.77	2.06
LOC_Os08g44670	calreticulin precursor	1.62	2.01	1.70	2.66	1.72	2.48	-1.24	-0.85	-0.30	-0.49
LOC_Os09g01620	RNA binding protein	1.85	2.63	0.65	1.55	1.45	2.92	-1.56	-0.71	-0.62	-0.01
LOC_Os09g02270	cyclase	-0.03	0.15	-0.02	1.15	0.07	2.34	0.28	0.47	1.47	2.56
LOC_Os09g08720	cinnamoyl CoA reductase, OsCCR24	-0.97	-1.96	0.37	3.46	0.25	5.29	-1.27	-1.98	2.04	3.92
LOC_Os09g09920	cytochrome P450 76C1	0.31	0.65	0.02	1.03	0.96	2.52	-0.55	-0.15	0.53	1.07
LOC_Os09g09890	flavonoid 3-monooxygenase	0.36	0.72	0.52	2.55	0.59	4.26	-0.64	-0.29	1.45	3.01
LOC_Os09g09980	glucan endo-1,3-beta-glucosidase 5 precursor	2.62	2.67	0.78	0.71	2.87	2.89	-0.14	-0.08	-0.25	-0.14
LOC_Os09g10340	cytochrome P450 71D7	-0.11	-0.02	2.53	4.26	0.28	2.79	0.34	0.49	2.17	2.74
LOC_Os09g12480	conserved hypothetical protein	-0.42	0.44	0.33	1.08	1.56	3.01	-0.67	0.26	0.10	0.86
LOC_Os09g12660	glucose-1-phosphate adenylyltransferase small subunit, chloroplast precursor	1.99	1.96	1.25	2.50	1.83	2.94	-0.94	-0.92	0.34	0.21
LOC_Os09g13310	retrotransposon protein, Ty3-gypsy subclass	1.01	1.44	1.40	1.91	0.42	2.48	-0.22	0.25	0.32	1.82
LOC_Os09g14950	hypothetical protein	3.52	4.86	2.71	3.77	3.12	4.00	-0.89	0.49	0.24	0.03
LOC_Os09g17110	retrotransposon protein, Ty1-copia subclass	-0.46	0.87	0.22	0.67	2.60	3.98	-1.26	0.02	-0.87	0.11
LOC_Os09g17560	O-methyltransferase ZRP4	-0.92	0.69	1.40	5.20	3.01	6.46	2.01	3.59	5.80	5.21
LOC_Os09g21180	homeodomain leucine zipper protein CPHB-5	-0.24	-0.10	0.29	1.08	0.66	3.79	2.15	2.26	2.98	5.21
LOC_Os09g22410	pyruvate kinase-like	0.18	2.02	0.61	0.13	7.06	8.78	-1.60	0.08	-2.38	-0.14
LOC_Os09g22540	transcription factor/ ubiquitin-protein ligase/ zinc ion binding protein	0.52	0.96	0.62	0.24	2.92	2.72	0.15	0.61	-0.25	-0.01
LOC_Os09g23350	ATTPS6	1.67	1.94	1.59	1.32	1.54	2.01	0.40	0.64	0.13	0.79
LOC_Os09g25470	hypothetical protein	-0.36	0.10	-0.82	-0.10	2.89	4.36	-1.22	-1.12	-0.67	-0.07
LOC_Os09g26210	zinc finger protein 2	0.07	0.12	1.10	1.88	1					

LOC_Os09g36470	minus agglutinin	1.02	-0.56	-0.41	-0.15	2.44	3.96	-1.86	-3.28	-1.53	-0.26
LOC_Os09g36480	ribonuclease 3 precursor	0.67	0.94	0.40	3.10	-0.31	3.08	-0.70	-0.45	1.86	2.35
LOC_Os09g36700	extracellular ribonuclease LE precursor	1.05	0.58	0.68	3.34	1.08	4.91	-1.03	-1.45	1.67	2.75
LOC_Os09g36930	aquaporin PIP2.7	-0.31	-0.48	0.63	4.37	0.27	3.05	-3.44	-3.56	0.33	-0.64
LOC_Os09g37120	ornithine decarboxylase	0.18	0.40	1.77	2.94	2.35	2.95	0.96	1.22	2.08	1.47
LOC_Os09g37958	legumin-like protein	0.53	0.93	0.87	2.44	1.22	3.46	-0.10	0.36	1.52	2.19
LOC_Os09g37976	legumin-like protein	0.28	0.47	0.91	2.77	1.09	3.85	1.24	1.39	3.07	3.90
LOC_Os09g38768	cell division control protein 50	2.74	2.82	1.54	1.33	2.68	2.45	-0.37	-0.29	-0.59	-0.61
LOC_Os10g01660	hypersensitivity-related gene	-0.52	0.96	0.58	5.03	0.44	4.88	-0.77	0.64	3.58	3.36
LOC_Os10g01680	hypersensitivity-related gene	1.37	2.23	1.15	3.50	1.45	3.72	-0.53	0.38	1.88	1.74
LOC_Os10g01930	acyltransferase	0.51	0.66	0.17	3.10	0.72	3.19	-0.85	-0.66	2.17	1.68
LOC_Os10g02840	O-methyltransferase ZRP4	-0.70	0.47	0.57	5.04	-0.95	5.35	-1.82	-0.72	2.53	4.11
LOC_Os10g02880	O-methyltransferase ZRP4	0.19	-0.42	0.54	4.69	-1.22	6.27	-3.31	-3.88	0.93	4.17
LOC_Os10g03920	zinc finger, RING-type	0.14	-0.27	-0.48	-0.37	3.59	4.07	-0.18	-0.50	-0.07	0.28
LOC_Os10g04730	protein kinase	1.16	2.59	0.93	1.19	1.13	2.14	-0.32	0.95	-0.28	0.47
LOC_Os10g05020	transposon protein, unclassified	0.20	0.21	0.98	1.56	1.60	2.04	1.17	1.15	1.76	1.56
LOC_Os10g07229	alcohol dehydrogenase 2	0.67	0.92	0.38	1.58	0.20	2.02	-0.16	0.09	1.06	1.65
LOC_Os10g08319	cytochrome P450 76B1	0.70	0.64	-0.06	2.24	-0.27	3.12	-0.52	-0.49	1.95	2.95
LOC_Os10g11889	expressed protein	-0.06	0.67	1.13	2.46	5.83	2.84	0.34	1.10	1.71	-2.67
LOC_Os10g20550	expressed protein	0.38	1.46	-0.64	1.70	-2.68	3.14	-2.59	-1.44	-0.18	3.23
LOC_Os10g21590	carbohydrate transporter/ sugar porter	0.66	1.06	0.14	1.66	0.11	2.91	2.36	2.70	3.93	5.09
LOC_Os10g223240	retrotransposon protein, unclassified	-0.09	1.93	1.06	1.41	-0.91	4.40	0.12	1.95	0.43	5.04
LOC_Os10g25040	red chlorophyll catabolite reductase	-0.17	0.42	1.00	3.01	1.24	4.08	0.62	1.26	2.69	3.45
LOC_Os10g25290	OsJAZ12	0.62	1.50	0.88	2.08	0.55	2.61	2.87	3.74	4.11	4.79
LOC_Os10g25400	esterase precursor	0.21	0.48	0.10	2.34	0.59	2.97	0.08	0.35	2.38	2.45
LOC_Os10g34760	ripening-related protein 6 precursor	2.83	3.41	2.66	2.16	2.97	2.17	-0.36	0.12	-0.99	-1.28
LOC_Os10g36090	nonspecific lipid-transfer protein precursor	0.73	0.68	0.37	1.29	0.99	2.03	-0.34	-0.40	0.59	0.67
LOC_Os10g36100	nonspecific lipid-transfer protein precursor	1.24	1.11	1.00	2.37	2.11	3.66	-0.29	-0.40	1.11	1.25
LOC_Os10g36170	nonspecific lipid-transfer protein precursor	0.13	0.17	0.41	1.88	0.39	2.12	-0.14	-0.10	1.34	1.55
LOC_Os10g36180	expressed protein	0.97	0.57	0.05	2.36	0.97	4.18	1.50	1.06	3.87	4.64
LOC_Os10g38160	glutathione S-transferase GSTU6	-0.35	-0.72	0.47	1.94	0.36	2.54	-1.04	-1.27	0.61	1.30
LOC_Os10g38340	glutathione S-transferase GSTU6	-0.46	-0.66	0.54	0.50	0.62	2.08	0.58	0.38	0.55	1.98
LOC_Os10g38590	glutathione S-transferase GSTU6	1.56	2.41	1.82	2.85	1.65	3.04	-0.56	0.32	0.54	0.88
LOC_Os10g39936	RING-H2 finger protein ATL1R	1.53	2.80	2.35	3.88	1.30	2.48	-1.93	-0.75	-0.47	-0.84
LOC_Os10g40770	hypothetical protein	3.20	3.12	2.16	1.76	3.35	2.90	-0.38	-0.58	-0.92	-0.95
LOC_Os10g40880	flavonol synthase/flavonone 3-hydroxylase	0.31	-0.07	0.49	2.43	0.21	2.22	-0.69	-1.00	1.38	1.41
LOC_Os10g41550	beta-amylase	4.47	4.02	2.24	2.24	3.19	5.14	2.57	2.19	2.70	4.58
LOC_Os11g02130	peroxidase 52 precursor	0.23	-0.04	0.31	1.48	0.63	2.26	-0.12	-0.38	1.07	1.53
LOC_Os11g02389	nonspecific lipid-transfer protein 1 precursor	0.02	0.16	-0.58	1.30	-1.15	2.24	-0.74	-0.63	1.07	2.29
LOC_Os11g02520	WRKY transcription factor, OsWRKY9	-0.07	0.89	0.12	1.58	0.16	2.22	1.31	2.27	2.82	3.31
LOC_Os11g02540	Superfamily of rice TFs having WRKY and zinc finger domains, OsWRKY11	-0.12	0.04	3.12	3.57	2.10	3.27	2.17	2.31	2.59	3.22
LOC_Os11g02810	conserved hypothetical protein	0.90	2.00	0.73	1.70	1.04	2.26	-1.29	-0.25	-0.42	-0.15
LOC_Os11g03300	NAC domain transcription factor	-0.47	0.67	0.45	1.17	0.41	2.31	1.34	2.44	2.05	3.17
LOC_Os11g03540	AP2/EREBP transcriptional factor WRI1	-0.01	0.79	-0.51	1.15	-0.13	2.22	0.15	0.99	1.85	2.49
LOC_Os11g04300	retrotransposon protein, unclassified	-0.11	-0.20	1.64	3.70	-0.03	2.86	-0.01	0.05	2.20	2.81
LOC_Os11g05830	hypothetical protein	1.75	2.81	-0.58	0.06	2.00	2.82	-1.25	-0.09	-0.44	-0.34
LOC_Os11g09110	receptor-like protein kinase 5 precursor	-0.04	0.14	0.11	0.84	0.46	2.59	1.06	1.31	1.82	3.13
LOC_Os11g10590	expressed protein	0.48	0.96	2.96	5.49	2.84	5.90	2.52	2.98	4.98	5.23
LOC_Os11g10850	dirigent-like protein pDIR14	0.15	0.73	2.12	4.56	2.16	4.91	0.01	0.69	2.62	2.88
LOC_Os11g11210	ATP-dependent peptidase	3.09	2.81	1.91	1.72	3.06	2.51	-0.52	-0.77	-0.69	-1.02
LOC_Os11g16320	expressed protein	2.82	2.87	2.23	2.72	2.55	3.17	-0.93	-0.80	-0.37	-0.23
LOC_Os11g17720	expressed protein	3.25	3.38	1.55	0.63	3.63	2.77	-1.83	-1.61	-2.68	-2.61
LOC_Os11g17790	subtilisin-chymotrypsin inhibitor Cl-1C	1.27	2.02	0.57	1.44	1.67	2.70	-1.11	-0.43	-0.32	-0.15
LOC_Os11g19840	O-methyltransferase ZRP4	0.24	1.00	0.45	2.31	0.11	2.23	-0.31	0.58	1.68	1.92
LOC_Os11g24070	nonspecific lipid-transfer protein 1 precursor	0.22	0.33	0.43	2.32	-0.77	2.65	-0.72	-0.58	1.16	2.36
LOC_Os11g25330	nucleoside-triphosphatase	0.27	0.13	0.67	1.81	0.45	2.63	-1.68	-1.79	-0.51	0.53
LOC_Os11g26760	dehydri Rab16C	-0.13	1.69	-0.90	3.44	-1.24	5.35	-1.23	0.50	3.10	5.11
LOC_Os11g29290	cytochrome P450 86A2	0.41	1.71	0.62	1.32	1.96	3.00	1.10	2.36	1.82	2.07
LOC_Os11g37040	expressed protein	0.99	0.81	4.36	4.06	2.87	2.75	0.83	0.67	0.50	0.67
LOC_Os11g37950	win2 precursor	-0.30	0.74	1.11	2.13	1.26	3.97	2.76	3.77	3.75	5.35
LOC_Os11g37970	win1 precursor	1.41	1.79	-0.20	0.74	0.56	2.71	0.12	0.51	1.09	2.20
LOC_Os11g41550	expressed protein	-0.02	0.16	8.34	10.88	5.86	5.98	-0.39	0.00	2.10	-0.41
LOC_Os11g41650	adenylyl-sulfate kinase 1, chloroplast precursor	-0.51	-0.16	2.02	2.84	1.69	2.43	-0.32	0.06	0.51	0.40
LOC_Os11g41710	cytochrome P450 71D10	0.18	0.07	-0.80	1.62	0.16	2.49	-2.42	-2.52	0.01	-0.09
LOC_Os11g45740	JAMYb	0.57	1.71	0.59	1.69	1.37	2.67	2.54	3.61	3.58	3.70
LOC_Os11g45990	protein binding protein	0.99	0.15	-1.89	0.61	-2.15	3.93	-1.59	-2.40	0.95	4.43
LOC_Os11g47500	xylanase inhibitor protein 1 precursor	0.52	0.67	-0.20	1.02	0.22	2.37	0.92	1.06	2.19	3.05
LOC_Os11g47600	xylanase inhibitor protein 1 precursor	-0.24	-0.37	0.50	1.04	1.39	2.19	4.47	4.31	5.01	5.12
LOC_Os12g01160	trans-2-enoyl-CoA reductase, mitochondrial precursor	2.70	2.77	0.71	0.56	2.84	2.81	0.11	0.19	-0.04	0.04
LOC_Os12g02080	peroxidase 52 precursor	0.11	0.03	0.44	2.27	0.97	2.99	0.01	-0.07	1.88	2.02
LOC_Os12g02290	nonspecific lipid-transfer protein 5 precursor	2.65	1.65	-0.07	-0.99	2.26	2.78	-0.73	-1.59	-1.60	-0.08
LOC_Os12g02320	nonspecific lipid-transfer protein 1 precursor	0.53	0.67	0.50	2.23	0.16	3.16	-0.92	-0.76	0.83	2.06
LOC_Os12g02470	Superfamily of rice TFs having WRKY and zinc finger domains, OsWRKY74	0.95	1.04	2.14	3.72	1.67	3.87	3.84	3.88	5.41	5.84
LOC_Os12g02980	aprasine precursor	0.38	0.18	0.32	3.06	-0.03	2.74	-0.04	-0.25	2.76	2.76
LOC_Os12g03290	AP2/EREBP transcriptional factor WRI1	0.38	0.76	0.24	1.46	0.27	2.10	-0.22	0.17	1.04	1.60
LOC_Os12g04080	agmatine coumaroyltransferase	0.16	0.21	0.36	1.93	0.53	2.31	-1.50	-1.35	0.22	0.43
LOC_Os12g05580	expressed protein	1.78	2.98	1.99	2.81	1.61	2.18	-1.27	-0.23	-0.61	-0.88
LOC_Os12g06120	expressed protein	-0.18	1.71	-0.78	1.06	1.75	4.75	-1.92	-0.15	-0.24	0.91
LOC_Os12g06930	expressed protein	3.08	3.24	1.25	1.21	2.88	2.99	-0.04	0.11	-0.08	0.02
LOC_Os12g08860	hypothetical protein	1.01	0.40	0.30	2.13	1.55	3.70	0.34	-0.28	2.21	2.52
LOC_Os12g09700	jasmonate-induced protein	0.32	-0.29	-2.93	1.10	-2.62	4.55	-2.29	-2.81	1.81	4.95
LOC_Os12g09720	jasmonate-induced protein	-0.03	2.16	2.86	6.35	1.45	5.73	0.92	2.94	4.59	5.12
LOC_Os12g12580	NADP-dependent oxidoreductase P2	0.37	0.33	0.48	1.89	0.71	2.27	-0.18	-0.21	1.23	1.35
LOC_Os12g13890	glycine-rich cell wall structural protein 2 precursor	0.58	2.50	1.49	1.92	0.88	3.43	2.72	4.66	3.24	5.20
LOC_Os12g16080	expressed protein	0.71	1.12	0.11	0.56	0.24	2.07	0.17	0.54	0.59	2.00
LOC_Os12g17950	expressed protein	-0.43	0.28	-0.29	1.92	-0.82	2.80	1.41	2.10	3.77	4.78
LOC_Os12g22970	expressed protein	-0.41	-0.47	0.34	2.19	-0.79	2.68	0.31	0.21	2.11	3.47
LOC_Os12g25090	expressed protein	0.46	0.73	1.13	1.83	1.87	3.66	3.52	3.74	4.23	5.11
LOC_Os12g25450	O-methyltransferase ZRP4	1.64	0.63	0.01	3.41	0.15	3.69	0.10	-0.89	3.59</td	

LOC_Os12g36240	subtilisin-chymotrypsin inhibitor Cl-1B	0.95	0.81	3.51	6.15	2.61	6.30	1.45	1.28	4.05	4.90
LOC_Os12g37260	lipoxygenase, OsRCI-1	0.72	1.00	1.12	3.40	1.46	3.57	6.17	6.35	8.45	7.93
LOC_Os12g37320	lipoxygenase 2.2, chloroplast precursor	-0.04	-0.43	2.55	5.02	1.49	4.03	2.00	1.58	4.45	4.44
LOC_Os12g37350	lipoxygenase 2.2, chloroplast precursor	0.24	0.63	1.92	3.64	1.09	3.14	2.66	3.03	4.38	4.38
LOC_Os12g37690	MYB transcription factor	-0.69	1.10	-0.08	3.02	-1.35	4.35	0.39	2.33	3.64	6.06
LOC_Os12g38180	heat shock cognate 70 kDa protein 2	0.08	0.45	0.15	1.98	0.29	2.18	-0.21	0.16	1.68	1.69
LOC_Os12g38270	metallothionein-like protein 1	0.54	0.62	0.17	2.19	-0.18	3.28	1.31	1.39	3.35	4.54
LOC_Os12g39310	cytochrome P450 81E1	0.47	0.61	0.30	1.76	0.12	2.28	0.92	1.02	2.40	3.07
LOC_Os12g43140	late embryogenesis abundant protein D-34	-0.42	-0.94	-0.20	2.38	-0.78	2.35	-0.88	-1.41	1.84	2.36
LOC_Os12g43490	alpha-amylase/trypsin inhibitor	0.43	0.50	0.20	1.63	0.69	3.21	-0.26	-0.20	1.21	2.23
LOC_Os12g44190	ATPase 3	0.81	1.48	0.36	0.31	1.70	3.35	-0.19	0.58	-0.16	1.54
LOC_Os12g444380	sucrose transport protein SUC4	1.83	2.03	2.35	2.90	1.72	2.32	-0.50	-0.28	0.08	0.09
LOC_Os01g02770	YRK1	0.00	0.09	-0.01	-1.81	0.30	-2.15	1.41	1.46	-0.43	-1.11
LOC_Os01g03549	copper ion binding protein	0.05	-0.43	0.16	-1.95	0.12	-2.66	-0.62	-1.10	-2.77	-3.43
LOC_Os01g04280	calmodulin binding protein	-0.71	-0.27	-0.60	-1.89	-0.88	-2.67	2.79	3.23	1.49	0.97
LOC_Os01g04540	ATP binding protein	-0.18	-0.06	-0.56	-2.91	0.11	-2.37	2.01	2.12	-0.41	-0.51
LOC_Os01g04550	ATP binding protein	-0.41	0.09	-0.18	-3.89	-0.07	-3.24	2.24	2.71	-1.52	-0.95
LOC_Os01g04570	Ser/Thr protein kinase	-0.01	-0.10	0.06	-2.47	0.71	-2.55	1.23	1.13	-1.35	-2.10
LOC_Os01g11160	cationic amino acid transporter 4	-0.58	-0.61	-0.13	-1.84	-0.19	-2.41	1.28	1.25	-0.44	-0.94
LOC_Os01g14410	early light-induced protein, chloroplast precursor	-0.85	-0.31	-0.08	-1.43	0.13	-2.81	1.35	1.88	0.00	-1.58
LOC_Os01g28450	pathogenesis-related (PR) gene PR1b	-0.74	0.20	-1.27	-5.53	-2.14	-7.35	4.80	5.69	0.55	-0.42
LOC_Os01g29330	expressed protein	-0.46	0.78	0.43	-1.81	-0.74	-2.54	0.73	1.94	-1.53	-1.11
LOC_Os01g41430	flavonol-3-O-glycoside-7-O-glucosyltransferase 1	-0.39	0.00	-0.42	-3.42	-1.27	-3.26	3.68	4.04	0.67	1.63
LOC_Os01g47070	acidic endochitinase precursor	-0.27	0.35	-0.54	-3.17	-0.73	-2.67	3.43	4.01	0.85	1.51
LOC_Os01g48620	expressed protein	-0.98	0.04	-0.25	-4.32	-0.71	-5.88	4.35	5.39	0.25	-0.86
LOC_Os01g51570	glucan endo-1,3-beta-glucosidase GII precursor	-0.35	-0.19	-0.21	-4.05	0.38	-3.59	4.05	4.12	0.33	0.14
LOC_Os01g58280	cucumisin precursor	-1.24	-0.04	-0.08	-2.32	-2.30	-2.16	3.41	4.59	1.03	3.16
LOC_Os01g58350	conserved hypothetical protein	-0.64	0.21	-0.07	-4.02	-0.28	-4.28	2.02	2.87	-1.97	-2.00
LOC_Os01g66840	carboxylic ester hydrolase	-0.73	-0.15	-0.13	-1.09	0.67	-2.54	1.25	1.83	0.25	-0.24
LOC_Os01g70220	histone-lysine N-methyltransferase, H3 lysine-9 specific SUVH6	-4.24	-5.45	-5.36	-5.28	-4.98	-4.27	-0.13	-1.23	0.02	0.73
LOC_Os01g73200	peroxidase 12 precursor	-0.77	-0.61	-0.31	-2.89	-0.13	-3.16	0.90	1.02	-1.71	-2.13
LOC_Os01g74410	MYB59	0.35	0.94	0.68	-1.94	0.68	-2.49	-0.02	0.57	-2.68	-3.19
LOC_Os02g11130	cytokinin-O-glucosyltransferase 3	-0.58	-0.59	0.05	-1.12	-0.48	-2.06	1.33	1.30	0.18	-0.25
LOC_Os02g13510	receptor-like protein kinase 5 precursor	-0.99	-1.35	-0.30	-2.37	-0.62	-2.95	2.19	1.78	0.13	-0.16
LOC_Os02g36280	cytochrome P450 76C2	-0.73	0.14	-1.54	-3.30	-1.44	-2.10	3.80	4.66	1.96	2.90
LOC_Os02g37180	expressed protein	0.02	0.16	-0.20	-1.87	-0.38	-2.42	2.40	2.51	0.73	0.34
LOC_Os02g37290	metal ion binding protein	-0.26	0.22	-0.27	-1.75	-0.70	-2.17	1.01	1.51	-0.46	-0.45
LOC_Os02g42160	OsWAK15 - OsWAK receptor-like protein kinase	-0.57	0.25	-0.15	-1.71	-0.05	-2.38	2.09	2.90	0.50	-0.29
LOC_Os02g48194	expressed protein	-1.05	-1.21	-0.94	-2.37	-0.68	-2.02	0.64	0.47	-0.82	-0.73
LOC_Os02g50460	immediate-early fungal elicitor protein CMPG1	-0.46	0.41	-0.33	-2.58	0.36	-2.21	3.52	4.34	1.17	0.80
LOC_Os02g50470	expressed protein	0.10	-0.17	0.20	-3.21	0.37	-3.25	3.14	2.83	-0.35	-0.52
LOC_Os03g16950	serine/threonine kinase-like protein	-1.12	-0.67	-0.43	-2.52	-0.22	-2.16	3.29	3.71	1.24	1.33
LOC_Os03g29930	expressed protein	-0.15	0.10	0.08	-2.20	0.36	-2.35	3.01	3.22	0.70	0.25
LOC_Os03g31750	pyruvate, phosphate dikinase, chloroplast precursor	0.26	0.27	-0.10	-2.85	0.29	-2.89	0.27	0.26	-2.54	-2.90
LOC_Os03g36500	conserved hypothetical protein	-1.03	-1.12	-0.43	-0.67	-1.79	-2.20	0.21	0.11	-0.02	-0.21
LOC_Os03g37840	potassium transporter 16	-0.13	-0.05	0.46	-1.88	0.59	-2.22	1.36	1.45	-1.04	-1.51
LOC_Os03g55010	cytokinin-O-glucosyltransferase 2	0.33	0.44	0.48	-1.98	0.01	-2.24	1.38	1.51	-1.08	-0.84
LOC_Os03g56160	lectin-like receptor kinase 7	-0.51	-0.13	-0.71	-3.15	-0.23	-2.56	2.86	3.24	0.46	0.54
LOC_Os03g59180	expressed protein	-0.19	-0.14	-0.05	-1.96	-0.63	-2.05	-0.21	-0.16	-2.17	-1.62
LOC_Os03g59770	calcium-binding allergen Ole e 8	-1.01	0.02	-0.46	-1.23	-1.79	-2.64	2.59	3.61	1.79	1.67
LOC_Os04g01470	cafféic acid 3-O-methyltransferase	-0.78	-0.30	0.07	-1.16	-0.76	-2.04	1.94	2.40	0.72	0.64
LOC_Os04g03920	expressed protein	-0.61	-0.01	-1.38	-2.58	-0.77	-2.24	2.22	2.82	1.01	0.73
LOC_Os04g07110	expressed protein	-1.50	-0.52	-0.97	-3.69	-0.12	-3.99	3.01	3.99	0.27	-0.92
LOC_Os04g10530	amidase	-0.87	-0.22	-0.08	-2.38	0.44	-2.07	2.76	3.41	0.42	0.20
LOC_Os04g25800	cytokinin-O-glucosyltransferase 2	-0.80	-0.69	-0.67	-3.08	-0.12	-3.36	1.90	1.99	-0.53	-1.38
LOC_Os04g39350	ATFP4	0.34	0.09	0.34	-2.87	0.34	-2.82	3.21	2.84	0.02	0.05
LOC_Os04g43070	ammonium transporter 1, member 2	-0.73	-0.74	-0.33	-2.24	-0.14	-2.35	0.16	0.13	-1.77	-2.06
LOC_Os04g43440	NB-ARC domain containing protein	-0.57	0.46	-0.36	-2.30	-0.98	-2.39	2.41	3.43	0.40	0.91
LOC_Os04g47770	cis-zeatin O-glucosyltransferase	-0.37	-0.52	-0.14	-1.83	-0.11	-2.21	-0.09	-0.26	-1.80	-2.16
LOC_Os04g51030	wall-associated kinase 1	-0.78	-0.75	-0.09	-2.18	-0.21	-2.87	1.78	1.80	-0.36	-0.94
LOC_Os04g52190	vacuolar sorting receptor 7 precursor	-0.19	-0.12	-0.24	-2.42	0.50	-2.22	2.08	2.13	-0.10	-0.63
LOC_Os04g53860	leucoanthocyanidin reductase	-0.55	-0.25	0.23	-1.41	0.07	-2.21	1.95	2.25	0.32	-0.32
LOC_Os04g56600	glycine-rich protein	-0.78	-0.33	-1.96	-3.62	-1.29	-2.02	3.03	3.47	1.36	2.26
LOC_Os04g56910	anthranilate N-benzoyltransferase protein 1	-0.34	0.36	-0.82	-1.10	-0.40	-2.29	4.02	4.67	3.67	1.98
LOC_Os04g59200	peroxidase 12 precursor	-0.57	-0.16	-0.57	-2.28	-1.21	-2.94	0.25	0.63	-1.50	-1.50
LOC_Os05g31170	chloroplast nucleoid DNA binding protein	-0.04	0.33	-0.27	-3.32	-0.44	-4.23	1.04	1.41	-2.06	-2.76
LOC_Os05g31890	expressed protein	-0.95	-0.44	-0.07	-2.45	1.22	-3.21	1.09	1.60	-1.28	-3.32
LOC_Os05g34854	gibberellin 20 oxidase 2	-0.55	-0.88	0.29	-3.18	-0.04	-3.68	0.53	0.22	-2.93	-3.04
LOC_Os05g36360	photoperiod responsive protein	-0.32	-0.77	0.27	-1.40	0.00	-2.00	1.41	0.95	-0.23	-0.60
LOC_Os05g39580	AT-rich element binding factor 3	-0.23	-0.23	-0.06	-4.03	0.32	-4.33	-0.18	-0.18	-4.22	-4.81
LOC_Os05g43820	rac-like GTP-binding protein 2	-0.58	-0.45	-0.40	-3.24	-0.32	-3.02	2.19	2.33	-0.65	-0.49
LOC_Os05g48700	gibberellin 2-beta-dioxygenase	-0.44	-0.52	-0.07	-2.37	0.76	-2.09	-0.28	-0.38	-2.65	-3.15
LOC_Os05g50340	RADIALIS	-0.02	-0.59	0.46	-1.41	-0.45	-2.73	-0.60	-1.16	-2.52	-2.90
LOC_Os06g03810	expressed protein	-0.24	0.35	-0.77	-2.94	-1.10	-3.03	3.67	4.21	1.47	1.65
LOC_Os06g03830	retinol dehydrogenase 14	-1.69	-0.85	-0.47	-2.05	-0.97	-2.05	2.68	3.51	1.11	1.60
LOC_Os06g04070	arginine decarboxylase	0.20	-0.16	0.71	-0.49	-0.08	-2.02	0.69	0.33	-0.49	-1.26
LOC_Os06g10190	monoxygenase	0.45	0.70	0.34	-2.44	0.61	-2.02	2.10	2.33	-0.70	-0.53
LOC_Os06g12620	expressed protein	-0.31	0.04	-0.44	-3.33	-0.08	-2.74	2.06	2.39	-0.82	-0.56
LOC_Os06g20150	peroxidase 1 precursor	0.28	0.38	-0.14	-2.68	1.07	-2.26	0.31	0.39	-2.24	-3.01
LOC_Os06g333100	peroxidase 2 precursor	-0.49	-0.69	-0.78	-1.97	0.21	-2.14	0.21	0.00	-1.02	-2.20
LOC_Os06g33970	VQ motif family protein	0.57	0.85	0.37	-2.73	-0.66	-2.89	4.01	4.20	0.83	1.68
LOC_Os06g35060	heavy metal-associated domain containing protein	-0.16	0.33	0.20	-2.61	-1.00	-3.65	2.05	2.49	-0.82	-0.63
LOC_Os06g37300	ent-kaurene oxidase	0.54	0.06	-0.03	-4.40	-0.42	-5.00	6.09	5.55	1.69	1.42
LOC_Os06g38450	vignain precursor	-0.40	0.14	-0.12	-1.96	-0.15	-4.18	2.24	2.76	0.42	-1.83
LOC_Os06g38764	expressed protein	0.13	0.59	-0.37	-2.50	0.25	-2.42	4.64	5.04	2.44	1.81
LOC_Os06g46149	expressed protein	-0.24	-0.03	0.07	-2.01	1.14	-2.21	3.71	3.88	1.64	0.29
LOC_Os06g51070	NAC domain-containing protein 68	-0.23	0.67	0.02	-2.41	0.34	-2.40	2.69	3.56	0.23	-0.09
LOC_Os07g03050	expressed protein	-0.83	-0.95	-0.81	-2.11	-1.20	-2.14	1.58	1.47	0.23	0.60
LOC_Os07g03690	pathogenesis-related protein PRB1-2 precursor	-0.71	-0.17	-0.67	-2.40						

LOC_Os07g48260	Superfamily of rice TFs having WRKY and zinc finger domains, OsWRKY79	-0.14	0.32	-0.31	-4.05	1.03	-2.85		2.63	3.07	-1.14	-1.26
LOC_Os08g02110	peroxidase 47 precursor	-0.45	-0.63	0.34	-2.55	0.96	-2.03		-0.92	-1.11	-3.90	-3.93
LOC_Os08g03310	RNA binding protein	0.27	0.22	0.73	0.79	-4.64	-4.70		-0.79	-0.84	-0.71	-0.84
LOC_Os08g04090	expressed protein	0.41	0.33	-0.07	-0.10	-1.94	-2.19		0.01	-0.08	-0.02	-0.24
LOC_Os08g04150	RNA polymerase II complex component SRB7	-0.18	-0.24	0.45	0.49	-1.83	-2.05		0.19	0.13	0.22	-0.04
LOC_Os08g04830	expressed protein	0.23	0.42	0.69	0.34	-1.58	-2.57		-0.11	0.08	-0.45	-1.13
LOC_Os08g05960	expressed protein	-0.84	-0.16	-0.30	-2.52	-0.53	-3.78		3.14	3.82	0.92	-0.15
LOC_Os08g06120	RAV-like protein	-1.13	-1.27	-0.44	-0.73	-1.82	-2.39		0.52	0.39	0.23	-0.05
LOC_Os08g07660	expressed protein	-0.03	0.41	-0.30	-1.91	-0.75	-3.20		2.81	3.22	1.16	0.28
LOC_Os08g08920	germin-like protein subfamily 1 member 7 precursor	-0.28	-0.10	-0.26	-1.09	-0.97	-2.89		0.14	0.30	-0.71	-1.79
LOC_Os08g09100	expressed protein	0.23	0.06	-0.09	0.36	-4.25	-4.14		-0.62	-0.77	-0.16	-0.48
LOC_Os08g10080	NAC domain-containing protein 21/22	0.44	-0.29	0.84	-1.40	-0.53	-2.27		0.90	0.18	-1.35	-0.81
LOC_Os08g13440	germin-like protein subfamily 1 member 17 precursor	-0.02	0.19	-0.24	-1.81	-0.72	-3.22		0.81	0.97	-0.77	-1.70
LOC_Os08g13840	Superfamily of rice TFs having WRKY and zinc finger domains, OsWRKY56	0.43	0.30	0.47	-0.37	-4.20	-4.85		0.82	0.68	-0.03	0.16
LOC_Os08g15650	expressed protein	0.27	0.47	-0.67	-1.09	-3.14	-3.37		1.08	1.26	0.66	0.88
LOC_Os08g16010	N-acetyltransferase	-0.22	-0.17	-0.11	-0.21	-3.17	-3.54		-0.76	-0.74	-0.88	-1.15
LOC_Os08g23680	FHA domain containing protein	0.22	0.43	0.30	-0.38	-1.58	-2.39		0.15	0.37	-0.56	-0.65
LOC_Os08g28214	tesmin/TSO1-like CXC domain containing protein	-0.91	-0.60	-0.05	-0.26	-2.06	-2.66		0.42	0.71	0.21	-0.18
LOC_Os08g29370	peptidyl-prolyl cis-trans isomerase, chloroplast precursor	-0.62	-0.58	-0.14	0.10	-1.83	-2.62		-0.99	-0.96	-0.77	-1.81
LOC_Os08g29570	PDR-type ABC transporter 1	0.02	0.42	-0.07	-2.43	-0.42	-2.54		1.27	1.65	-1.13	-0.88
LOC_Os08g31228	50S ribosomal protein L27	-0.06	-0.27	-0.21	-0.15	-4.81	-5.16		0.06	-0.15	0.13	-0.27
LOC_Os08g31814	OsAPRL4 - <i>Oryza sativa</i> adenosine 5'-phosphosulfate reductase-like	-0.30	-0.14	0.16	0.08	-1.97	-2.24		0.17	0.33	0.11	-0.11
LOC_Os08g31830	expressed protein	0.09	0.16	-0.02	0.01	-1.57	-2.24		0.14	0.22	0.17	-0.52
LOC_Os08g31970	expressed protein	-0.24	-0.23	0.21	0.03	-2.41	-2.77		0.43	0.45	0.26	0.08
LOC_Os08g32520	expressed protein	-0.29	-0.13	0.13	1.33	-4.01	-2.37		0.09	0.23	1.31	1.76
LOC_Os08g32750	carbonic anhydrase precursor	-0.46	0.27	-1.14	-2.10	-0.14	-2.60		0.60	1.34	-0.37	-1.84
LOC_Os08g37790	blight-associated protein p12 precursor	-0.06	-0.21	-0.14	-3.91	-0.07	-4.68		3.51	3.34	-0.28	-1.13
LOC_Os08g39840	lipoxygenase, OsLOX-RLL	-1.20	-0.54	-0.64	-3.32	-1.62	-5.04		1.51	2.18	-1.15	-1.89
LOC_Os08g40910	expressed protein	-1.98	-2.50	-0.65	-1.08	-0.51	-4.40		3.68	3.20	3.31	-0.23
LOC_Os08g42700	resistance protein	-0.60	0.08	-0.59	-3.11	-0.05	-3.10		0.50	1.17	-2.08	-2.60
LOC_Os09g00998	expressed protein	-0.27	-0.10	0.25	0.19	-0.68	-2.07		-0.17	-0.02	-0.23	-1.55
LOC_Os09g01000	expressed protein	-0.52	-0.37	0.34	0.32	-0.99	-2.38		-0.14	0.01	-0.14	-1.53
LOC_Os09g08130	indole-3-glycerol phosphate synthase, chloroplast precursor	-0.62	-0.19	0.00	-1.71	-0.82	-2.30		5.84	6.19	3.98	4.10
LOC_Os09g18260	senescence-induced receptor-like serine/threonine-protein kinase precursor	-0.46	-0.04	0.17	-1.14	-0.47	-2.41		0.23	0.63	-1.14	-1.76
LOC_Os09g19720	expressed protein	0.07	0.11	0.02	0.29	-2.68	-2.76		-0.24	-0.19	0.03	-0.33
LOC_Os09g19820	aminopeptidase-like protein	-0.04	0.12	0.37	0.00	-3.45	-3.14		0.01	0.16	-0.37	0.32
LOC_Os09g24860	hypothetical protein	-1.44	-1.56	-0.29	-0.62	-2.18	-2.65		0.28	0.17	-0.05	-0.17
LOC_Os09g26144	glutamate receptor 2.8 precursor	0.08	-0.25	0.04	-3.68	1.19	-2.94		3.34	2.96	-0.43	-0.87
LOC_Os09g277680	expressed protein	-1.99	-3.81	0.35	-0.59	-2.10	-2.97		0.23	-1.63	-0.73	-0.65
LOC_Os09g29520	OsWAK81 - OsWAK receptor-like cytoplasmic kinase (OsWAK-RLCK)	-4.33	-5.52	-0.30	-2.56	-0.13	-2.66		2.88	1.75	0.55	0.26
LOC_Os10g10130	OsWAK112d - OsWAK receptor-like protein kinase	-0.73	-0.33	-0.27	-2.75	-0.65	-2.42		2.66	3.05	0.18	0.89
LOC_Os10g26940	polygalacturonase-1 non-catalytic beta subunit precursor	0.16	0.40	0.35	-4.93	0.84	-4.59		1.41	1.57	-3.78	-3.81
LOC_Os10g34940	expressed protein	0.00	0.56	0.07	-1.79	0.16	-2.15		2.81	3.31	0.89	0.43
LOC_Os10g38940	beta-carotene hydroxylase	-0.17	-0.44	0.32	-0.92	0.28	-2.02		-0.88	-1.18	-2.15	-3.18
LOC_Os10g39260	aspartic proteinase nepenthesin-1 precursor	-0.70	0.36	-0.75	-2.70	-0.43	-3.38		4.07	5.08	2.08	1.08
LOC_Os10g39270	nucleoid DNA-binding-like protein	-0.39	0.52	-1.03	-2.28	-1.36	-3.05		2.78	3.67	1.56	1.10
LOC_Os10g39300	aspartic proteinase nepenthesin-1 precursor	-0.35	0.58	-0.63	-2.28	-0.89	-2.98		4.12	5.01	2.48	2.03
LOC_Os10g39330	aspartic proteinase nepenthesin-1 precursor	-0.33	0.59	-0.90	-2.23	-1.19	-2.93		3.16	4.02	1.83	1.34
LOC_Os10g39350	aspartic proteinase nepenthesin-1 precursor	-0.95	0.24	-1.67	-2.88	-1.75	-3.35		2.90	4.07	1.74	1.34
LOC_Os10g39360	aspartic-type endopeptidase/ pepsin A	-0.49	0.60	-1.22	-2.61	-1.36	-3.03		3.19	4.24	1.77	1.46
LOC_Os10g39380	aspartic proteinase nepenthesin-1 precursor	-0.75	0.31	-1.88	-3.07	-1.57	-3.13		2.69	3.72	1.53	1.13
LOC_Os10g39390	aspartic proteinase nepenthesin-2 precursor	-0.75	0.08	-1.83	-3.36	-1.14	-3.30		2.78	3.60	1.27	0.62
LOC_Os10g41330	ethylene-responsive transcription factor 5	0.39	0.67	0.06	-1.09	-0.09	-2.13		2.02	2.26	0.87	-0.05
LOC_Os10g42040	expressed protein	-1.92	-0.47	-1.20	-3.42	-1.70	-3.97		3.73	5.21	1.53	1.41
LOC_Os11g04860	indole-3-acetate beta-glucosyltransferase	-0.11	-0.29	0.25	-0.91	-0.60	-2.67		-0.53	-0.70	-1.73	-2.66
LOC_Os11g05800	pathogenicity protein PATH531-like protein	-0.64	-0.18	-0.59	-2.90	0.58	-2.07		4.60	4.99	2.18	1.78
LOC_Os11g11780	serine/threonine protein kinase	-0.45	-0.49	-0.38	-2.24	0.44	-2.23		3.12	3.02	1.20	0.36
LOC_Os11g11960	NBS-LRR type disease resistance protein	-0.48	-0.24	0.06	-2.14	-0.23	-2.65		1.86	2.10	-0.34	-0.56
LOC_Os11g13860	transposon protein, unclassified	-0.15	-0.14	0.48	0.46	-1.23	-2.01		0.13	0.12	0.12	-0.66
LOC_Os11g40009	patatin precursor	0.61	0.82	-3.96	-3.95	-3.92	-3.61		0.18	0.40	0.20	0.49
LOC_Os11g40200	expressed protein	-0.09	-0.53	-2.28	-2.22	-2.45	-2.58		0.08	-0.38	0.16	-0.03
LOC_Os11g42970	plant integral membrane protein TIGR01569 containing protein	-0.37	-0.10	0.30	-1.59	-0.05	-2.32		1.75	2.01	-0.13	-0.51
LOC_Os11g45130	pollen signalling protein with adenyl cyclase activity	0.48	0.27	-0.29	-2.86	1.47	-2.30		2.43	2.18	-0.17	-1.37
LOC_Os11g46810	retrotransposon protein, unclassified	-1.18	-0.49	-2.47	-4.51	-1.98	-4.06		3.27	3.97	1.25	1.15
LOC_Os12g03370	harpin-induced protein	-0.45	0.16	-0.10	-2.35	0.81	-2.57		2.47	3.05	0.19	-0.99
LOC_Os12g10880	hypothetical protein	-0.10	0.12	0.03	-4.32	0.31	-4.23		4.34	4.53	-0.07	-0.26
LOC_Os12g12090	expressed protein	-1.24	-0.37	-0.41	-2.59	-1.79	-3.47		2.77	3.65	0.60	1.10
LOC_Os12g24320	cell Division Protein AAA ATPase family	-1.33	-0.24	-0.69	-3.77	-0.21	-2.43		5.30	6.43	2.04	2.71
LOC_Os12g28590	cell Division Protein AAA ATPase family	-1.07	-0.44	-0.74	-2.90	-0.06	-2.65		3.80	4.42	1.64	1.19
LOC_Os12g33120	expressed protein	-0.52	-0.27	0.04	-1.67	-0.22	-2.01		1.46	1.63	-0.24	-0.37
LOC_Os12g34320	S-locus-like receptor protein kinase	0.08	-0.35	0.05	-2.22	-0.02	-2.08		1.86	1.41	-0.41	-0.20
LOC_Os12g36850	major pollen allergen Bet v 1-D/H	-1.93	-0.49	-1.53	-3.71	-3.33	-3.36		5.16	6.59	3.06	5.09

Fold change in gene expression indicates as a normalized log<sub>2</sub> ratio.