

Development of Defense Signaling Pathways Against Bacterial Blight Disease in Rice Using Genome-Wide Transcriptome Data

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Abstract

Bacterial blight (BB) disease caused by *Xanthomonas oryzae* pv. *oryzae* (*Xoo*) drives severe yield and quality losses in rice (*Oryza sativa* *Xa1*, *Xa3/Xa26*, *xa5*, *xa13*, *Xa21*, and *Xa27*). Here we employ a transcriptomics approach to elucidate the *Xa21*-, *NH1*- (*NPR1* homolog 1) (*NH1*)-, and *NRR*- (negative regulator of disease resistance) mediated defense response to *Xoo*. Among the candidate genes, we focused on 288 genes showing significant change in at least two of the above comparisons to support the association with an enhanced defense response. Gene Ontology enrichment analysis for this gene list revealed that response to biotic stimulus was 25.0-fold more enriched compared to the control, well qualifying the candidate genes for enhanced resistant response. The biotic stress overview installed in the MapMan toolkit was used to identify diverse components consisting of defense signaling pathways such as genes involved in disease resistance, redox, signaling, regulation of transcription, pathogenesis-related functions, secondary metabolism, and protein degradation. Of these, we validated the expression patterns of genes related to regulation of transcription and pathogenesis-related functions and suggest a functional network model for WRKY transcription factors mediating defense signaling pathways against *Xoo*. We expect that our analysis will contribute to increasing the depth of knowledge on the molecular mechanism for enhanced disease resistance against bacterial blight disease in rice.

Keywords: bacterial blight disease, disease resistance, functional gene network, microarray, rice

1. Introduction

Rice (*Oryza sativa* L.) is an important staple food, feeding more than half of the global population, and is a model for other monocotyledonous species, including most cereal crops. Rice production, however, is severely restricted by biotic stresses, such as pathogenic bacteria, fungi, and viruses. Bacterial blight (BB), a disease which often provokes severe losses of rice grain, is caused by *Xanthomonas oryzae* pv. *oryzae* (*Xoo*) (Nino-Liu, Ronald, & Bogdanove, 2006). Six of the 34 major resistance genes for BB have been cloned and characterized at the molecular level (Lee et al., 2011). Of these, *Xa21* encodes a leucine-rich repeat (LRR) receptor kinase which is positively involved in the defense response (Song et al., 1995). In addition, overexpression of *non-expressor of pathogenesis related gene 1 (NPR1) homolog 1 (NH1)* in rice results in BB resistance and potentiates a benzothiadiazole (BTH)-induced lesion mimic or cell death phenotype (Yuan et al., 2007). Overexpression of a negative regulator of disease resistance (*NRR*) which interacts with *NH1* in rice affects *Xa21*-mediated resistance by enhancing susceptibility to BB (Yuan et al., 2007). Recently, we developed a stress interactome mediated by *Xa21*, *NH1*, and *NRR*, as a hypothetical model to study the molecular mechanism of BB resistance (Seo et al., 2011).

An integrated omics analysis is one of the most powerful methods to unveil a functional network of molecular pathways strongly associated with the candidate genes. Network analysis is dependent on integrated omics analysis. In rice, there are four web tools for this purpose: RiceNet (<http://www.functionalnet.org/ricenet/>), the Rice Interaction Viewer (http://bar.utoronto.ca/interactions/cgi-bin/rice_interactions_viewer.cgi), the Predicted

Rice Interactome Network (PRIN, <http://bis.zju.edu.cn/prin/>), and Planet (<http://aranet.mpimp-golm.mpg.de/ricenet>) (Gu, Zhu, Jiao, Meng, & Chen, 2011; Lee et al., 2011; Mutwil et al., 2011). Of these, RiceNet was successfully used to identify three novel regulators which control resistance mediated by *Xa21*: Regulator of *XA21*-Mediated Immunity 1 (ROX1), ROX2, and ROX3 (Lee et al., 2011).

Oligonucleotide microarray analysis provides a global view of transcriptional regulation mediated by a key gene associated with a significant biological process. More than 4,000 rice oligonucleotide microarray datasets, including gene expression profiles of rice responses to *Xoo* infection, are available in the NCBI gene expression omnibus public microarray database (GEO, <http://www.ncbi.nlm.nih.gov/geo/>) (Barrett et al., 2011; Jung, Jeon, & An, 2011). These data serve as a reference to study the rice defense response against a selected pathogen. Recently, we also generated genome-wide microarray analyses of *Xa21-TP309 vs. TP309*, *NH1ox vs. LiaoGeng (LG)*, and *NRRox vs. LG* after *Xoo* inoculation. These data were used to evaluate the *XA21* interactome. However, we did not provide a detailed analysis of the transcriptome data.

Genome-wide transcriptome data yield a large amount of candidate genes, ranging from several hundreds to thousands, which are differentially expressed under the treatment condition. This feature of the transcriptome data limits further application. Gene ontology (GO) analysis is used to categorize biological meanings of candidate genes from genome-wide transcriptome data using microarray or RNA-seq technology. GO data are provided in three principle categories: biological process, cellular component and molecular function (Jung et al. 2008). MapMan is also useful as a user-driven categorization tool for displaying genomic data sets on diagrams of metabolic pathways and other biological processes (Jung & An, 2012; Peltier, Ytterberg, Sun, & van Wijk, 2004).

Here we analyzed the rice transcriptome to identify genes associated with resistance to *Xoo* infection. Three rice lines with different levels of BB resistance were compared to the susceptible controls through transcriptome analysis: the *Xa21* line carrying functional *Xa21* from wild rice species in *TP309 (Xa21-TP309)* and *NH1overexpressing line (NH1ox)* both had enhanced resistance phenotypes to BB, whereas the *NRR* overexpressing line (*NRRox*) had enhanced susceptibility. We identified 338, and 610 genes which were significantly upregulated in *Xa21* and *NH1ox*, respectively, compared to the susceptible controls. In addition, we identified 186 genes which were significantly downregulated in the *NRRox* line compared to the susceptible control. Among them, we focused on 288 genes showing significant change in at least two of the above comparisons for further scrutiny by GO enrichment analysis, MapMan analysis, and functional gene network.

2. Materials and Methods

2.1 Plant Growth

Seeds from *NRRox*, *NH1ox*, *LG*, *TP309*, and *Xa21-TP309 (I106)* rice plants were germinated by placing them in water for 2 days (d). Seeds were then planted in clay soil and maintained in a greenhouse. After 8 weeks, the plants were moved to a growth chamber with controlled temperature and humidity. The plants were adapted for 2 d and then inoculated on the leaf with *Xoo* isolate *PXO99* by the clipping method. *LG* has the same genetic background as *NRRox* and *NH1ox*, and *TP309* has the same background as *Xa21*. For the microarray experiment, *NRRox* was compared to *LG* (WT), *NH1ox* was compared to *LG* (WT), and *Xa21* was compared to *TP309* (WT). Eight-week-old leaf tissues were collected 1 d after inoculation with *Xoo* for the *NH1ox* and *NRRox* lines, and 2 d after inoculation with *Xoo* for the *Xa21* line. We prepared at least two replicates for each sample and each replicate contained at least five pooled leaves.

2.2 RNA Extraction and Microarray Experiment

At least 500 µg total RNA was isolated using TRIZOL reagent (Invitrogen), followed by DNaseI-treatment for 15 minutes, purification with an RNeasy Midi Kit (Qiagen), and enrichment for poly-A RNA using the Oligotex mRNA Kit (Qiagen). All steps were performed according to the manufacturer's instructions. All hybridizations were conducted at the ArrayCore Microarray Facility at the University of California, Davis (<http://array.ucdavis.edu/home/>) as previously described (Jung et al., 2008).

2.3 Microarray Data Processing and Analysis

Spot intensities were quantified using Axon GenePix Pro 4.0 image analysis software. GenePix Pro 4.0 result data files (.gpr files) were generated using high PMT and low PMT settings. For high PMT, the data were normalized using the Lowess normalization method in the LMGene Package in R (Lu et al., 2008). The LMGene method developed by Rocke (2004) was also used to identify differentially expressed genes. "S" was used to indicate a susceptible response, "ES" an enhanced-susceptible response, and "R" a resistant response. False discovery rates (FDRs) and fold changes of *NRRox* (ES) compared to *LG* (S), *NH1ox* (R) compared to *LG* (S),

and *Xa21* (R) compared to *TP309* (S) were generated. Data with p -values <0.05 by a t -test and >1.5 -fold change (i.e. $\log_2 R/S \geq 0.6$ or $\log_2 SS/S \leq -0.6$) in at least two comparisons are presented in Table S1. These microarray data were deposited in the NCBI GEO with Accession No. GSE22112. Other data were collected from the NCBI gene expression omnibus (GEO, <http://www.ncbi.nlm.nih.gov/geo/>). The marray R package in Bioconductor was used to normalize Agilent 22K array data (GSE5906 and GSE32635), followed by calculation of the average of the \log_2 fold changes for each comparison (Wang, Nygaard, Smith-Sorensen, Hovig, & Myklebost, 2002). To process Agilent 44K array data (GSE7567), median signal intensities of Cy3 were converted to \log_2 median intensities, then normalized using the quantile normalization method (Bolstad et al., 2003).

2.4 Gene Ontology (GO) Enrichment Analysis

The GO terms and assignments for rice genes were downloaded from the Gramene database (<http://www.gramene.org/>) (Youens-Clark et al., 2011). A hypergeometric distribution was then used to calculate the p value for GO enrichment analysis installed in the Rice Oligonucleotide Array Database (ROAD, http://www.ricearray.org/analysis/go_enrichment.shtml) (Cao, Jung, Choi, Hwang, & Ronald, 2012). We uploaded locus IDs of 288 genes in a toolbox for the GO enrichment analysis in the biological process category and identified 333 GO terms assigned to 160 genes. Significant GO terms in the biological process category were identified based on a more than 2-fold enrichment value with less than 0.05 hypergeometric p -values. Eleven GO terms in the biological process category were identified (Figure 1, Tables S2 and S3).

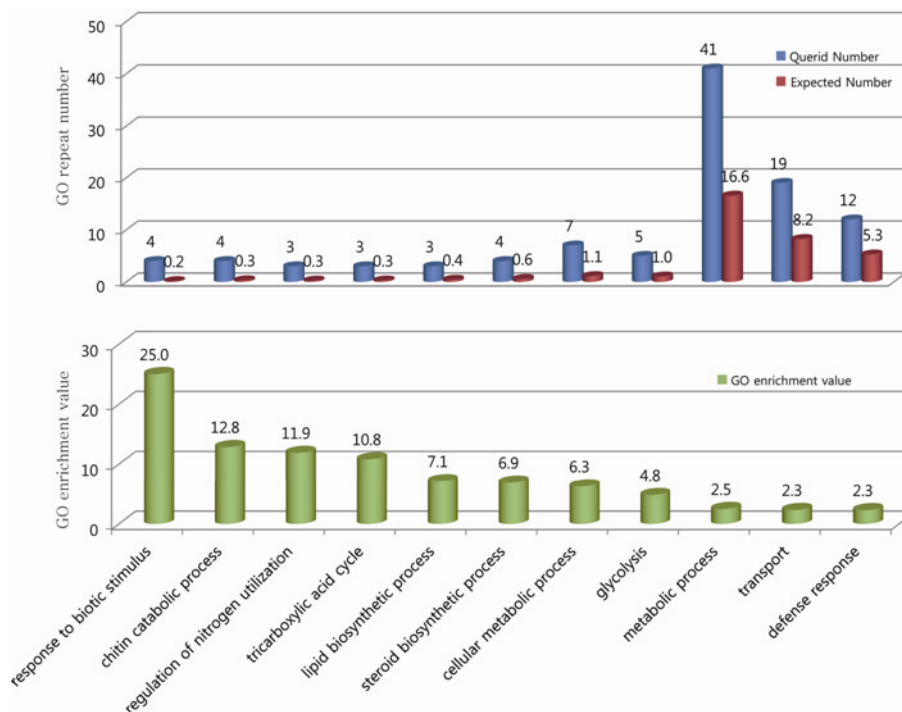


Figure 1. Gene Ontology enrichment analysis of 288 genes associated with enhanced bacterial blight defense. The Gene Ontology (GO) enrichment analysis tool installed in the rice oligonucleotide array database (ROAD, <http://www.ricearray.org/>) was used to identify GO terms enriched in the selected 288 genes. The x-axis indicates the name of the GO term, and the y-axis indicates the GO enrichment value in the lower panel or number of each GO term in the upper panel. The GO enrichment value and number of each GO term are represented as numeric values in this figure. Detailed gene information of enriched GO terms in this analysis is shown in Tables S2 and S3

2.5 MapMan Analysis

A total of 36 MapMan BINs were generated for the Rice MapMan classification; these were extended in a hierarchical manner into subBINs (Urbanczyk-Wochniak et al., 2006; Usadel et al., 2005). We generated a dataset using locus IDs in RGAP version 7 annotation, and a fixed numeric value, 1, indicating 288 genes associated with multiple enhanced defense responses. The data were uploaded to the biotic stress overview which we had recently introduced and installed in the MapMan toolkit (Jung & An, 2012). The image data of the biotic stress overview was used for Figure 2. Detailed information is shown in Table S4.

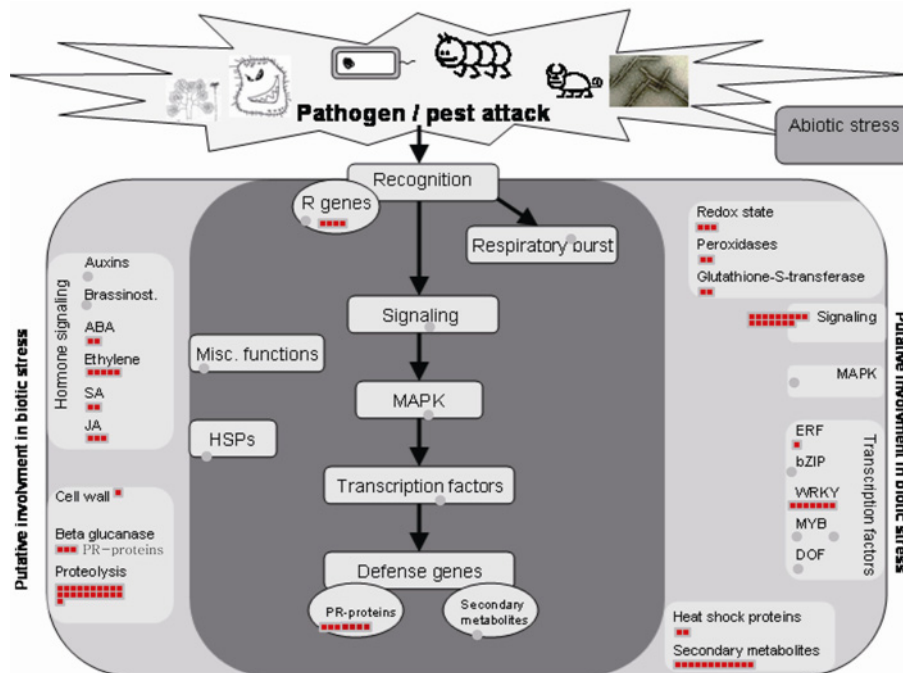


Figure 2. MapMan analysis in biotic stress overview of genes associated with enhanced bacterial blight defense.

The biotic stress overview installed in the MapMan toolkit was integrated with 288 genes associated with enhanced bacterial blight defense. In the overview, 95 elements were identified. Red squares indicate genes associated with enhanced bacterial blight defense in this overview. Detailed information on the MapMan overviews is provided in Table S4

2.6 Generation of Heatmap Using Microarray Data

We used MeV software to generate heatmap expression patterns using the fold data in Table S4 as an input (tab-delimited txt format) (Figure 3).

2.7 RT-PCR Analysis

We isolated 20-50 μg of total RNAs extracted from 8-week-old leaf before inoculation, after 1 d and 2 d *Xoo* (PXO99) inoculation using Trizol reagent, and then treated it with DNaseI for 15 min before purifying it with an RNeasy Midi Kit (Qiagen, USA). Quantities of total RNA and mRNA were determined by measuring A_{260} and A_{280} with a Nanodrop ND-1000. The level of protein contamination in the RNA was estimated based on the A_{260} to A_{280} ratio. Only RNA samples with ratios of 2.0 to 2.2 were used for these experiments. cDNA was synthesized from 2 μg of total RNA using Moloney murine leukemia virus reverse transcriptase (Promega, USA) in a reaction buffer. PCR was performed in a 30 μL solution containing a 1- μL aliquot of the cDNA reaction, 0.2 μM gene-specific primers, 10 mM dNTPs, 1 unit of ExTaq DNA polymerase (Takara, Japan), and reaction buffer. The reaction included an initial 5-minute denaturation at 94 $^{\circ}\text{C}$, followed by 21 to 40 cycles of PCR (94 $^{\circ}\text{C}$ for 45 sec, 60 $^{\circ}\text{C}$ for 45 sec, and 72 $^{\circ}\text{C}$ for 1 minute), and a final 10 minutes at 72 $^{\circ}\text{C}$. The balance of cDNA synthesis was estimated by RT-PCR using rice *Ubiquitin 5* (*OsUbi5/Os01g22490* with forward primer 5'-GCACAAGCACAAGAAGGTGA-3' and reverse primer 5'-GCCTGCTGGTTGTAGACGTA-3'), and rice *Ubiquitin 1* (*OsUbi1/Os03g13170*; forward primer 5'-TGAAGACCCTGACTGGGAAG-3' and reverse primer 5'-CACGGTTCAACAACATCCAG-3'). We then analyzed expression patterns for 18 genes belonging to RNA category and pathogen-related protein group in Figure 3. RT-PCR was conducted as described previously (Jung et al., 2006). Primer sequences are listed in Table S5.

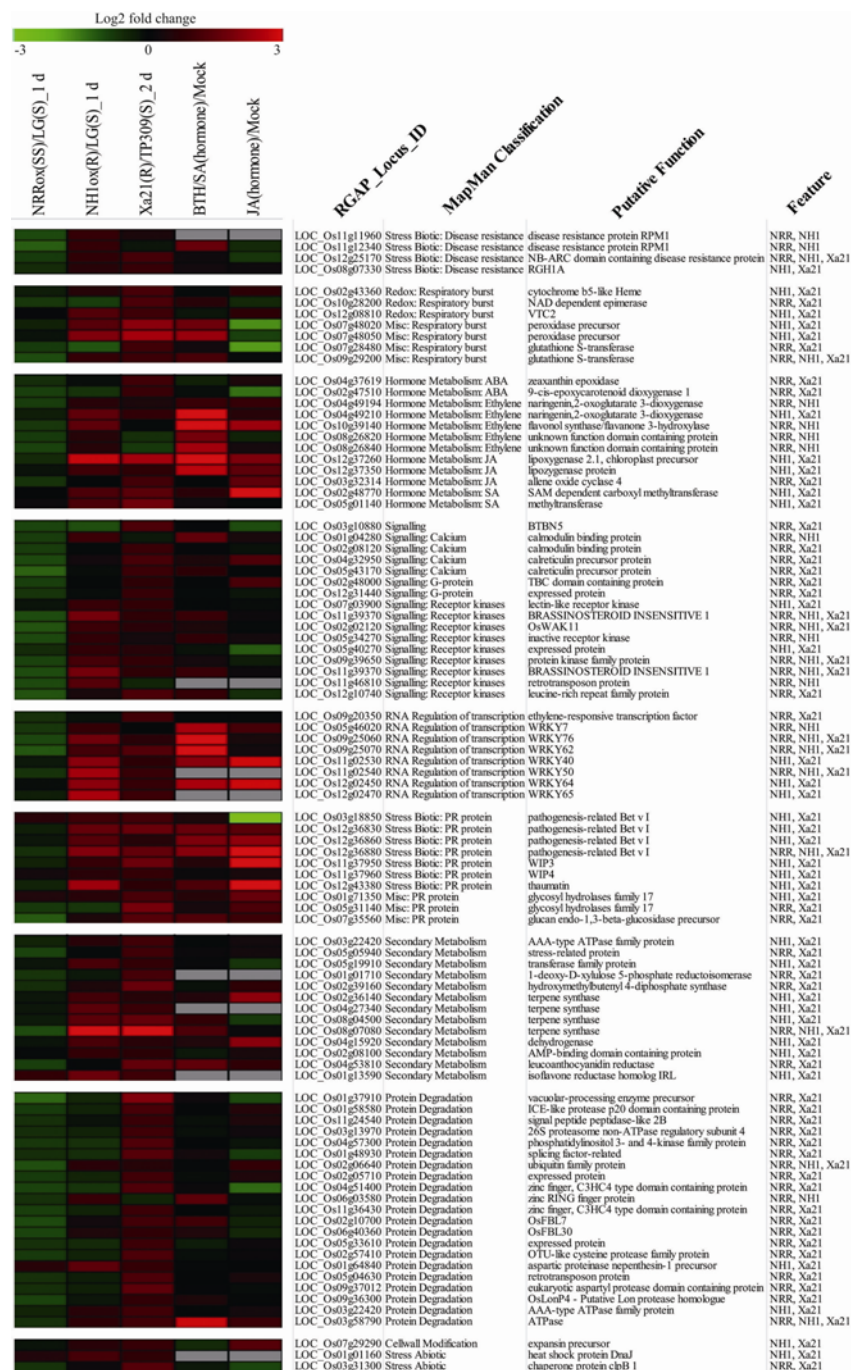


Figure 3. Expression patterns of 95 genes associated with enhanced bacterial blight defense. Two comparisons of enhanced resistance and susceptibility strains and one comparison of enhanced-susceptibility and susceptible strains identified 95 genes in the MapMan biotic stress overview associated with defense response, oxidative burst, protein phosphorylation, transcriptional regulation, hormone signaling, and pathogenesis. In addition, the expression patterns of these genes in response to hormones such as SA/BTH and JA were used to generate a heatmap. Functional groups are assigned according to the order of each defense process after pathogen recognition. Green color indicates downregulation in enhanced resistance or enhanced-susceptible lines after *Xoo* inoculation or treatment with phytohormones, and red indicates upregulation. The detailed experimental conditions are provided in Table 1 and microarray data are provided in Table S4

3. Results and Discussion

3.1 Identification of Rice Genes Differentially Expressed in Response to *Xoo* Infection

To identify rice genes associated with response to *Xoo* infection, we used genome-wide microarray analyses of *Xa21-TP309* vs. *TP309* after 2 d of *Xoo* inoculation, *NH1ox* vs. *LG* after 1 day of *Xoo* inoculation, and *NRRox* vs. *LG* after 1 day of *Xoo* inoculation. In these transcriptome analyses (GSE22112), the *TP309* line (susceptible to *Xoo*) was used as a control for the *TP309* line that carried a functional *Xa21* gene. *LG* was susceptible to *Xoo*, and served as a control for both the *NH1ox* line, which had enhanced resistance, and the *NRRox* line, which had enhanced susceptibility in the *LG* background. Four biological replicates were used to compare *NH1ox* and *NRRox* to *LG*, and two replicates were used to compare *Xa21* to *TP309*. Compared to the controls, upregulated genes in the resistant lines (*Xa21* and *NH1ox*) or downregulated genes in the enhanced susceptibility line (*NRRox*) were candidates for enhanced defense response genes against *Xoo* challenge in rice. A total of 610 genes in *Xa21* and 338 genes in *NH1ox* were upregulated by more than 1.7-fold ($\log_2 0.8$), based on a p-value of <0.05 using a t-test, compared to the susceptible controls (Table S1). In *NRRox*, 186 genes were significantly downregulated compared to the susceptible control (Table S1).

Hormones such as salicylic acid (SA, GSE7567) and jasmonic acid (JA, GSE32635) are also involved in the plant disease response (Table 1) (Desaki et al., 2006). BTH is a functional analog of SA and protects plants from diseases by activating the SA signaling pathway (Shimono et al., 2007). The molecular mechanisms underlying BTH-induced disease resistance, which were elucidated by transcriptome analysis (GSE7567), were used to demonstrate that *OsWRKY45* plays a crucial role in the BTH-inducible defense program in rice (Shimono et al., 2007). To investigate the induction of rice defense responses by JA, transcriptome analyses (GSE32635) were performed. The gene expression patterns in response to hormones were used as reference data to evaluate the gene expression patterns associated with enhanced *Xoo* defense identified in our transcriptome analysis. The overall scheme of our analysis is presented in Figure 4.

As we were more interested in the enhanced defense responses against a broad range of *Xoo* isolates, we identified 288 genes showing significant differential expression patterns in at least two of the following comparisons: upregulation in \log_2 *NH1ox/LG* 1 d after *Xoo* inoculation, upregulation in \log_2 *Xa21/TP309* 2 d after *Xoo* inoculation, and downregulation in \log_2 *NRRox/LG* 1 d after *Xoo* inoculation (Figure 4, Table S1). These genes were used for further analyses.

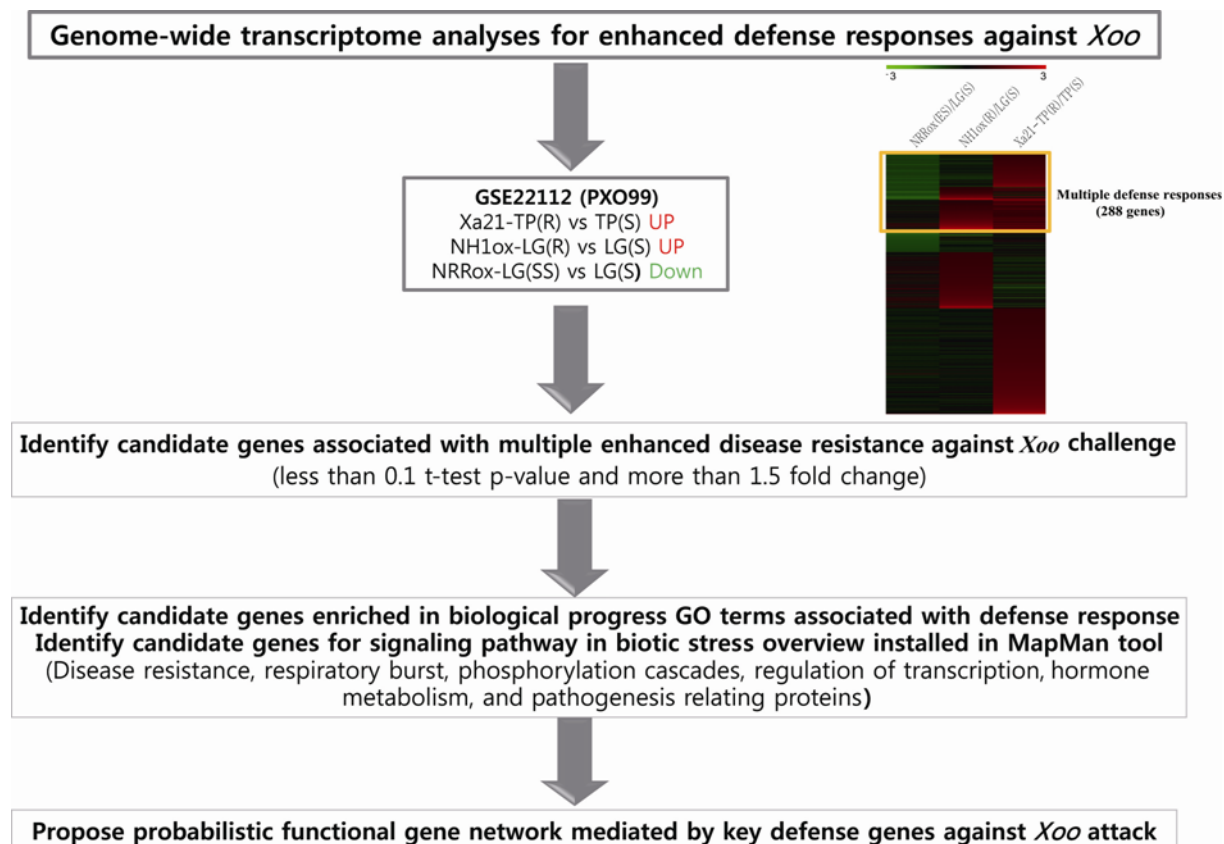


Figure 4. Overall scheme to develop a functional gene network for enhanced bacterial blight defense response in rice

3.2 Identification of Biological Processes Associated With Broad Spectrum Resistance

Recently, we developed a GO enrichment tool to identify the biological meaning of a selected gene list from high-throughput data analysis (Cao et al., 2012). In this tool, p-values are used to support enriched GO terms. The fold enrichment value is the ratio of the queried number of selected GO terms over the expected number (Jung et al., 2008). By applying GO enrichment analysis of the 288 genes found to be involved in the response to a broad range of pathogens, we identified eleven GO terms which were highly overrepresented in the gene list with a smaller than 0.01 p-value and a greater than 2-fold increased enrichment value. Specifically, response to biotic stimulus was 25.0-fold more enriched than the standard; chitin catabolic process, 12.8; regulation of nitrogen utilization, 11.9; tricarboxylic acid cycle, 10.8; lipid biosynthetic process, 7.1; steroid biosynthetic process, 6.9; cellular metabolic process, 6.3; glycolysis, 4.8; metabolic process, 2.5; transport, 2.3; and defense response, 2.3 (Figure 1, Table S2). The gene list belonging to these GO terms is shown in Table S3.

Of these GO terms, response to biotic stimulus showed the highest GO fold enrichment, and the features of genes selected in our analysis were well described by the enrichment of defense response and chitin catabolic process together with response to biotic stimulus GO terms. Close interplay between the plant immune system and plant steroids supported the roles of steroid biosynthetic processes in pathogen responses of rice (Belkhadir et al., 2012). Metabolic process is the most abundant GO term associated with response to a broad range of pathogens. The functions of four of these genes belonging to metabolic process have been identified: LOC_Os02g08100 encoding 4-Coumarate:coenzyme A ligase regulates of a broad range of biological events over the course of rice growth and development (Goodstein et al., 2012); LOC_Os03g09250 encoding myo-inositol 3-phosphate synthase 1, seed phytic acid content (Long et al., 2008); LOC_Os05g31140 encoding β -glucanase, blast resistance (Shimono et al., 2012); and LOC_Os08g03290 encoding cytosolic glyceraldehyde-3-phosphate dehydrogenase GAPDH protein 3, salinity tolerance (Shimono et al., 2007). Of these, β -glucanase was the only gene known so far to be related to pathogen responses. The contribution of glucosinolate transport to *Arabidopsis* defense responses, and depression of auxin transport capacity of infected *Arabidopsis* plants by *A. brassicicola* supported the significance of the transport GO term in the pathogen response of rice (Ellerbrock, Kim, & Jander, 2007; Qi et al., 2012). Among rice genes belonging to the transport

GO term, rice phosphate (Pi) transporter, *OsPht1;1*, is known to function in Pi uptake and translocation in rice under Pi-replete conditions (Sun et al., 2012), but its role in pathogen responses has not yet been analyzed. In summary, GO enrichment analysis effectively suggested the primary candidate genes for an enhanced defense response against *Xoo*.

3.3 Identification of MapMan Terms in Biotic Stress Overview With Response to *Xoo* Infection

The biotic stress overview installed in the MapMan tool is useful to identify major elements in signaling pathways for defense response. We uploaded 288 genes to the MapMan tool and identified 95 genes in the biotic stress overview (Figure 2). The primary step is recognition of pathogen attack by R genes related to the defense response, such as pattern recognition receptors (PRRs) located at the plasma membrane (Boller & Felix, 2009; Dardick & Ronald, 2006; Desclos-Theveniau et al., 2012; Lee et al., 2009; Tena, Boudsocq, & Sheen, 2011). Next is an oxidative burst including redox reactions and miscellaneous functions for an early hypersensitive response, hormone metabolism to modulate the defense response, signal transduction by phosphorylation, transcriptional regulation by transcription factors, and defense response by pathogenesis-related (PR) protein genes, genes relating to secondary metabolism and protein degradation (Delteil, Zhang, Lessard, & Morel, 2010). Figure 3 shows the differential expression patterns of these genes in two enhanced resistance lines and an enhanced susceptibility line after *Xoo* inoculation, and after treatment with BTH and JA, compared to controls. Four genes were related to the defense response, 7 to the oxidative burst, 12 to hormone metabolism, 18 to phosphorylation cascades, 8 to transcriptional regulation, 10 to PR genes, 12 to secondary metabolism, 21 to protein degradation, and 3 to other functions (Figure 3; Table S4).

3.4 Defense Response

Among the defense response genes, we identified four genes belonging to the nucleotide-binding site (NBS)-LRR family. Two of these genes (*Os11g11960* and *Os11g12340*) encode resistance to *Pseudomonas syringae* pv. *maculicola* 1 (RPM1) homologous proteins, one (*Os12g25170*) encodes an NBS-LRR protein, and one (*Os08g07330*) encodes resistance gene homolog 1a. Defense response is the most obvious functional group related to enhance BB resistance.

The NBS-LRR genes are particularly important for enhanced defense responses to BB (Bryan et al., 2000; Jeung et al., 2007; Lin et al., 2008; Okuyama et al., 2011; Yoshimura et al., 1998). *Os12g25170* was upregulated in the *NH1ox* and *Xa21* lines and downregulated in the *NRrox* line. *Os11g11960* and *Os11g12340* encoding the RPM1 homolog were upregulated in the *NH1ox* line and downregulated in the *NRrox* line (Figure 3). *Arabidopsis* RPM1 (At3g07040) is a disease resistance protein that specifically recognizes the AvrRpm1 type III effector, a virulence protein from *Pseudomonas syringae*, and protects the plant from the pathogen (Grant et al., 2000). This gene interacts with RPM1-interacting protein 4 (RIN4) and triggers plant resistance when RIN4 is phosphorylated by AvrRpm1 (Mackey, Holt, Wiig, & Dangl, 2002). We expect that rice RPM1 homologs have similar roles to *Arabidopsis* RPM1 in the disease resistance response. Four genes described in this section belonged to different classes of the NBS-LRR protein family, suggesting that there might be diverse routes mediated by NBS-LRR for enhanced defense against BB.

3.5 Respiratory Burst

Among the respiratory burst genes, we identified seven genes associated with redox response and miscellaneous functions. Among them, *Os02g43360* encoding cytochrome b5-like heme protein, *Os10g28200* encoding NAD dependent epimerase, and *Os12g08810* encoding vacuolar transporter chaperone 2 (VTC2) were relating to redox reactions. *Os07g37730* and *Os09g29200* encoding glutathione S-transferase (GST), and *Os07g48020* and *Os0748050* encoding peroxidase were related to genes with miscellaneous functions. All these genes showed upregulation in the *Xa21* lines. In addition, *Os07g48020*, *Os0748050*, *Os09g29200*, and *Os12g08810* were upregulated in the *NH1ox* line, and by SA treatment, except for *Os12g08810*; in contrast, *Os07g37730*, *Os09g29200*, and *Os10g28200* were downregulated in the *NRrox* line (Figure 3). Respiratory burst is an immediate response to a pathogen attack leading to the production of diverse reactive oxygen species (ROS) (Peltier et al., 2004). ROS generation mainly depends on NADPH oxidase and peroxidase activities. GSTs are a major group of enzymes that detoxify ROS produced after an infection (Hayes & Pulford, 1995). A series of redox reactions are required to develop a cooperative network for antioxidant activity (Blokhina, Virolainen, & Fagerstedt, 2003). In plants, hydrogen peroxide (H₂O₂) is generated during the exposure to pathogen attack, and due to its relative stability the level of H₂O₂ is regulated by an array of catalases and peroxidases localized in almost all compartments of the plant cell (Blokhina et al., 2003). Therefore, the seven genes associated with respiratory burst might be components of a cooperative network for antioxidant activity mediated by Xa21 or NH1.

3.6 Signaling

We identified 18 genes involved in signaling (Figure 3). Of them, eight encoded receptor-like protein kinases with an extracellular region and a transmembrane domain, and the others were kinases lacking these structures, a WD40-like protein, and a Tre-2/Bub2/Cdc16 (TBC)-domain-containing protein. The former group included three LRR-receptor-like protein kinases (*Os05g40270*, *Os05g40270*, and *Os12g10740*), one lectin-like receptor kinase (*Os07g03900*), one brassinosteroid insensitive 1 (BR1)-associated receptor kinase (BAK, *Os11g39370*), one wall-associated receptor kinase (*OsWAK11*, *Os02g02120*), and two less well defined receptor-like protein kinases (*Os09g39650* and *Os11g46810*). A functional association between lectin-like receptor kinases and the pathogen defense response was uncovered by identifying *Arabidopsis* LecRK-I.9. The knockout mutant had a gain-of-susceptibility phenotype and the activation mutant had enhanced resistance to *Phytophthora brassicae* (Bouwmeester et al., 2011), suggesting possible involvement of rice lectin-like receptor kinase in the defense response against bacterial pathogen challenge. BAK gene, *Os11g39370*, was upregulated in the *NH1ox* and *Xa21* lines and by BTH (SA) treatment, and was downregulated in the *NRRox* line. These results indicated that BAK was involved in SA-dependent signaling. Recent studies revealed that *Arabidopsis* BAK1 is an important regulator of pathogen-associated molecular pattern (PAMP) signaling (Bari & Jones, 2009; Boller & Felix, 2009; Schulze et al., 2010; Schwessinger et al., 2011). In addition, *Arabidopsis* receptor kinase flagellin sensitive 2 (FLS2)/BAK1 receptor complex triggers the accumulation of SA (Mersmann, Bourdais, Rietz, & Robatzek, 2010; Mishina & Zeier, 2007). This finding supported the significance of finding the above BAK gene in *Xa21*- and *NH1*-mediated defense responses via SA signaling. Expression of the *wall-associated receptor kinase* gene (*OsWAK11*, *Os02g02120*) depended on *NH1*, *XA21* and *NRR*. In summary, we expect that the BB defense mechanism may be modulated by diverse types of LRR-receptor-like kinases, including *Xa21* (Song et al., 1995).

Among the non-receptor kinases, there were one mitogen-activated protein kinase kinase kinase (MAP3K) (*Os11g10100*) and two calcium/calmodulin-dependent protein kinases (CAMKs) (*Os01g10890* and *Os01g18800*). MAP3Ks are components of the MAPK signaling cascade. *Xa21* stimulated expression of *Os11g10100* (encoding a MAP3K) and *NRR* repressed its expression, suggesting that *Os11g10100* may be involved in *Xa21*-mediated defense responses. Calcium/calmodulin-dependent signaling was also implicated in the BB defense response by transcriptome analysis (Figure 3). *Os01g18800* was upregulated in the *NH1ox* line and *Os01g10890* was upregulated in the *Xa21* line, while JA treatment repressed the expression of both genes. Regarding calcium signaling, four genes encoding calmodulin binding protein or calreticulin precursor protein might function upstream of these CAMKs. In addition, we identified two genes relating to G-proteins: one (*Os12g31440*) encoded a WD40-like protein and the other (*Os02g48000*) a TBC-domain-containing protein.

3.7 Hormone Metabolism

Based on our transcriptome analysis, there were 12 genes associated with hormone metabolism (Figure 3). Of these, two were related to ABA, five to ethylene signaling, three to JA signaling, and two to SA signaling. Plants infected with diverse pathogens change their levels of disease-responsive phytohormones such as JA and SA (Bari & Jones, 2009). This report supported the significance of JA and SA signaling in disease resistance. Among the genes related to JA signaling, *Os03g32314* encoding allene oxide cyclase 4 was upregulated in the *Xa21* line and by JA treatment, and was downregulated in the *NRRox* line. *Os12g37260* encoding lipoxygenase and *Os12g37350* encoding lipoxygenase also showed upregulation in response to JA treatment in *NH1ox* and *Xa21* lines. JA stimulated the expression of these genes, suggesting that they might be involved in a JA-dependent BB defense response. Allene oxide cyclase, along with allene oxide synthase, is a key enzyme in JA synthesis. Transgenic rice overexpressing a pathogen-inducible *OsAOS2* gene encoding allene oxide synthase showed JA-dependent induction of PR genes and enhanced Magnaporthe *grisea* (*M. grisea*) resistance (Mei, Qi, Sheng, & Yang, 2006), supporting the possible involvement of allene oxide cyclase 4 in the BB defense response. Regarding ethylene signaling, we identified two genes (*Os04g49194* and *Os04g49210*) encoding naringenin,2-oxoglutarate 3-dioxygenase, one (*Os10g39140*) encoding flavonol synthase/flavanone 3-hydroxylase, and two genes of unknown function (*Os08g26820* and *Os08g26840*). All these genes were commonly upregulated in the *NH1ox* line and by BTH treatment. In addition, *Os04g49194*, *Os04g49210*, and *Os10g39140* were upregulated by JA treatment. Naringenin,2-oxoglutarate 3-dioxygenase with 1-aminocyclopropane-1-carboxylate (ACC) oxidase and flavanone 3-hydroxylase generates products such as ethylene and flavanone, a precursor of JA and SA. This result explains why *Os04g49194*, *Os04g49210*, and *Os10g39140* might be involved in multiple hormone signaling pathways. Regarding SA signaling, we identified two genes (*Os02g48770* and *Os05g01140*) encoding S-adenosyl-L-methionin (SAM)/salicylic acid (SA)-dependent carboxyl methyltransferase which catalyzes the formation of methyl SA from SA. Both showed

upregulation in *NH1ox* and *Xa21* lines. This result suggested that SA signaling regulates a broad range of BB resistance response via these genes. In addition, *Os02g48770* was upregulated by BTH and JA treatments. Crosstalk among different hormones for BB defense response could be enabled by *Os02g48770*. We found two genes related to ABA metabolism. The involvement of ABA signaling in the regulation of Arabidopsis resistance to *R. solanacearum* was demonstrated by the enhanced susceptibility of *abi1-1* and *abi2-1*, two ABA-insensitive mutants (Hernandez-Blanco et al. 2007). This finding supports the role of ABA signaling in BB disease resistance of rice. Direct evidence will require functional analysis using genetic approaches.

3.8 Transcriptional Regulation

Eight genes related to transcriptional regulation were identified (Figure 3). These included seven WRKY transcription factors (TFs) (*Os05g46020*, *Os09g25060*, *Os09g25070*, *Os11g02530*, *Os11g02540*, *Os12g02450*, and *Os12g02470*), and an apetalata2 and ethylene responsive transcription factor (AP2/ERF, *Os09g20350*) (Figure 3). Among the TFs, the WRKY gene family is typically responsible for enhanced pathogen defense (Pandey & Somssich, 2009a) and is the most abundant TF related to enhanced BB resistance (Figure 3). *Os09g25060* (*OsWRKY76*), *Os09g25070* (*OsWRKY62*), *Os11g02530* (*OsWRKY40*), *Os11g02540* (*OsWRKY50*), *Os12g02450* (*OsWRKY64*) and *Os12g02470* (*OsWRKY65*) were upregulated in the *NH1ox* and *Xa21* lines. Of these, *OsWRKY50*, *OsWRKY62*, and *OsWRKY76* were also downregulated in the *NRROx* line, and *OsWRKY40* and *OsWRKY64* were upregulated by SA and JA treatments. *Os05g46020* (*OsWRKY7*) was upregulated in the *Xa21* line and by SA and JA treatments, and was downregulated in the *NRROx* line. Therefore, most WRKYs identified in this study were differentially expressed by multiple factors, suggesting they might be involved in a broad range of BB defense responses. Identification of multiple *WRKY* genes suggested diversity in the detailed mechanism triggering BB defense responses.

In the AP2/ERF family, one gene (*Os09g20350*) was related to a broad range of BB resistance. This gene was upregulated in the *Xa21* line and downregulated in the *NRROx* line. Tobacco (*Nicotiana tabacum*) osmotin promoter binding protein 1 (OPBP1) which belongs to the AP2/ERF family is involved in enhanced resistance to *Pseudomonas syringae* pv *tabaci* and *Phytophthora parasitica* var *nicotianae* (Guo, Chen, Wu, Ling, & Xu, 2004). Overexpressing *Arabidopsis* cytokinin response factor 5 (CRF5) which belongs to the AP2/ERF family increases pathogen resistance and concomitantly activates the expression of a large number of GCC-box pathogenesis-related genes (Liang et al., 2010). These studies suggested that the function of a rice *AP2/ERF* gene might be associated with multiple BB defense responses as demonstrated by transcriptome analysis.

3.9 Pathogenesis Related Protein, Secondary Metabolism and Protein Degradation

To date, 17 groups of pathogenesis-related (PR) genes have been identified (Sels, Mathys, De Coninck, Cammue, & De Bolle, 2008). Two hundred fifty-six putative PR genes were identified from GreenPhyl (<http://greenphyl.cirad.fr/v2/cgi-bin/index.cgi>), a phylogenomic database for plant comparative genomics (Rouard et al., 2011). Of these PR protein genes, 10 were related to multiple BB resistance responses in our analysis. Four genes encoding pathogenesis-related Bet v I family protein (PR10) (*Os03g18850*, *Os12g36830*, *Os12g36860*, and *Os12g36880*) were found to be significantly upregulated in *Xa21* and *NH1ox* lines. In addition, *Os12g36830*, *Os12g36860*, and *Os12g36880* were also upregulated by SA and JA treatments. In the PR2 family, we identified three genes: two (*Os01g71350* and *Os05g31140*) encoding glycosyl hydrolase family 17 proteins and one (*Os07g35560*) encoding a glucan endo-1,3-beta-glucosidase. All of these genes were upregulated in the *Xa21* line and by JA treatment (Figure 3). In addition, *Os01g71350* was upregulated in the *NH1ox* line, and *Os05g31140* and *Os07g35560* were downregulated in the *NRROx* line (Figure 3). Two PR3 family genes were identified. *Os11g37950* and *Os11g37960* encoded wound-induced proteins (WIP). Expression of *Os11g37950* and *Os11g37960* was upregulated in *Xa21* and *NH1ox* lines (Figure 3). In addition, *Os11g37950* was upregulated by JA treatment (Figure 3). *Os12g43380* encodes thaumatin belonging to the PR-5 family and was upregulated in *Xa21* and *NH1ox* lines, as well as by SA and JA treatments (Figure 3). PR proteins are a group of heterogeneous proteins encoded by genes that are rapidly induced in response to a pathogen. Elevated expression of PR genes is associated with systemic acquired resistance (SAR), emphasizing the requirement of PR gene expression for enhanced defense response to BB attack (Seo, Lee, Xiang, & Park, 2008).

We identified 13 and 21 genes involved in secondary metabolism and protein degradation, respectively. These functional groups are also known to contain active molecules for defense response against pathogen attack because higher concentrations of secondary metabolites might result in a more resistant plant (Bednarek, 2012). Exact roles of genes in these functional groups remain to be characterized.

Validation of expression patterns for candidate genes in the mainstream signaling pathway associated with multiple defense responses against bacterial blight disease.

To validate expression patterns of candidate genes in the mainstream signaling pathway associated with multiple defense responses against bacterial blight disease from our study, we carried out real-time PCR analysis for 8 genes belonging to RNA category and 10 to pathogenesis (PR) related protein group in Figure 3. As a result, we confirmed that 7 WRKY genes except *AP2/ERF* gene in RNA category were upregulated in *NH1ox* and *Xa21* lines compared to their background varieties, LG and TP309, in response to *Xoo* (Figure 5, Figure S1). In case of PR genes, all genes except glycosyl hydrolase (*GH17*, *Os05g31140*) were upregulated in *Xa21* line compared with TP309, and expression patterns of PRs (*Os03g18850*, *Os12g36830*, *Os12g36860*, and *Os12g36880*), WIP3 (*Os11g37950*) and glucanase (*Os07g35560*) genes were upregulated in *NH1ox* line compared with LG. Based on this data, 4 PR, WIP3 and glucanase genes are expected to function downstream of multiple defense signaling pathways mediated by *Xa21* or *NH1*, while *WIP4* (*Os11g37960*), *Thaumatin* (*Os12g43380*), and *GH17* (*Os01g71350*) genes show *Xa21* dependent response (Figure 5, Figure S1). This result indicates that candidate genes from our transcriptome data are mostly relevant for further functional analysis to elucidate defense signaling pathways associated with *Xa21* or *NH1*.

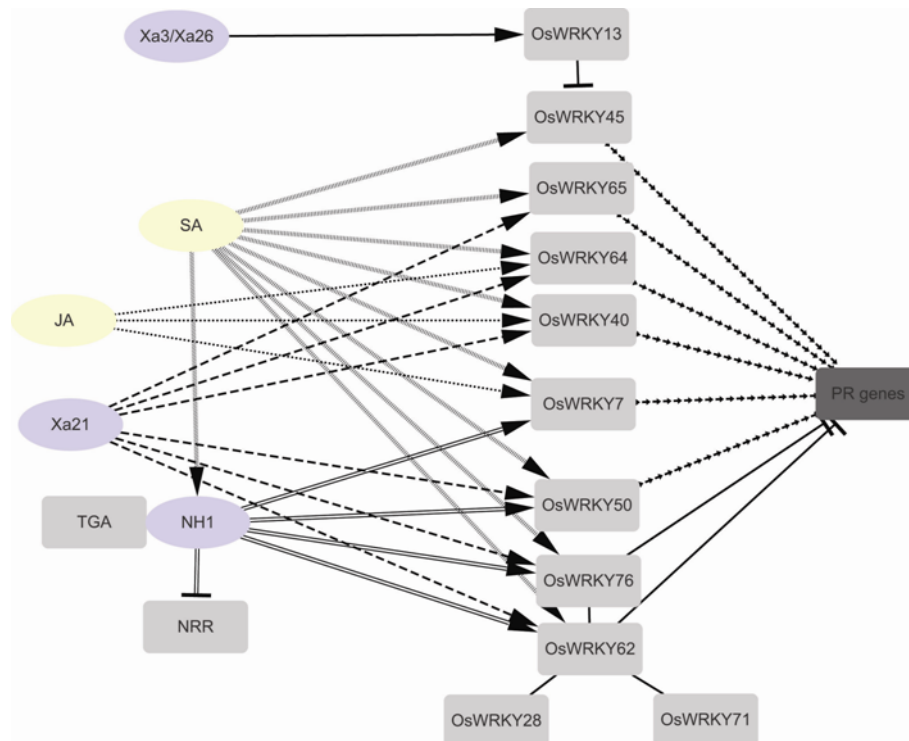


Figure 5. Model of WRKY transcription factors mediating bacterial blight defense responses in rice. Differential expression patterns in Figure 3 were used to develop a model of bacterial blight defense responses. SA and JA in yellow circles are phytohormones; *Xa21*, *Xa3/Xa26*, and *NH1* in weak purple circles are defense genes with known function; genes in weak gray boxes are downstream transcriptional regulators of *Xa21*, *Xa3/Xa26*, and *NH1* genes; and PR genes are indicated as dark gray box

4. Conclusion

Transcriptome analyses using multiple resistance lines or an enhanced-susceptible line against BB revealed diverse views of enhanced BB resistance response. Genes associated with disease resistance, and hormones such as SA and JA, are good candidates to study the molecular mechanism of an enhanced BB defense response (Table S1). Out of our candidate genes in Table S1, functions of 43 genes were identified and 8 of them are related to defense responses (Table S6), suggesting that our transcriptome analysis retains useful information to elucidate molecular mechanism underlining enhanced defense responses against pathogen attack or pathogen responses. Especially, *NH1* is functionally related to multiple WRKYs including three WRKY genes previously characterized: two (*OsWRKY62* and *OsWRKY76*) belonging to the WRKY II-a subfamily, one (*OsWRKY7*) to WRKY II-c, and two (*OsWRKY64* and *OsWRKY65*) to WRKY III. These data suggested that *NH1* mediated diverse defense mechanisms in rice through different types of WRKY subfamilies. Thus, *NH1* may be a hub

modulator of broad-spectrum BB resistance, like *Arabidopsis* NPR1 (Wang, Amornsiripanitch, & Dong, 2006). The functional association with WRKY and NH1 is supported by the recent study that *Arabidopsis* NPR1 was functionally associated with six WRKYs (*WRKY18*, *WRKY38*, *WRKY53*, *WRKY54*, *WRKY58*, and *WRKY70*) (ref plos genetics). In addition, *Arabidopsis* *WRKY6*, an *OsWRKY1* ortholog, was found to be active during NPR1-dependent defense priming by β -amino-butyric acid (Van der Ent et al., 2009). This finding further enhances the functional association between WRKY TFs and NH1. Functions of uncharacterized WRKY genes for enhanced BB defense response remain to be determined. In addition to the above-mentioned WRKYs, *OsWRKY13* mediates the defense response downstream of *Xa1* and *Xa3/Xa26* (Kou & Wang, 2011) and *OsWRKY45-1* negatively regulates rice resistance to *Xoo* in an SA-induced and NH1-independent manner (Tao et al., 2009), indicating that transcriptional regulation, mainly modulated by the WRKY family, plays a central role in BB defense signaling (Liu, Bai, Wang, & Chu, 2007; Pandey & Somssich, 2009b; Peng, Bartley, Canlas, & Ronald, 2010; Peng et al., 2008; Qiu et al., 2007; Ryu et al., 2006; Tao et al., 2009). Since *OsWRKY13* binds to *OsWRKY45-1* promoters and negatively regulates its expression (Tao et al., 2009), we expect that an understanding of the mutual regulation among WRKY genes would provide important clues to explain enhanced defense responses mediated by these TFs.

Mainstream processes for disease resistance signaling pathways were well represented. Assignment of candidates from our transcriptome analyses into each step of the pathway could provide a useful molecular framework to study the defense mechanism through signaling pathways. Ninety-four genes were mapped to nine processes in the mainstream pathway for enhanced BB resistance response. Further functional elucidation of these candidate genes will clarify the detailed molecular mechanism. The integration and refinement of multiple omics data related to BB resistance provides useful information to design or develop crops with enhanced BB defense capabilities. To expand the Xa21- and NH1-mediated defense signaling pathway based on the stress interactome that was recently established, we might need to apply a functional gene networking tool for rice genes with 94 mainstream candidates for enhanced BB resistance response. The information of differentially expressed new linkages associated with Xa21 and NH1 provided the clues for key players associated with enhanced defense response against bacterial blight disease. Systematic functional analysis of the main candidate genes identified in this study might accelerate the discovery of the molecular mechanism for enhanced *Xoo* resistance response.

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Supplementary data/Materials

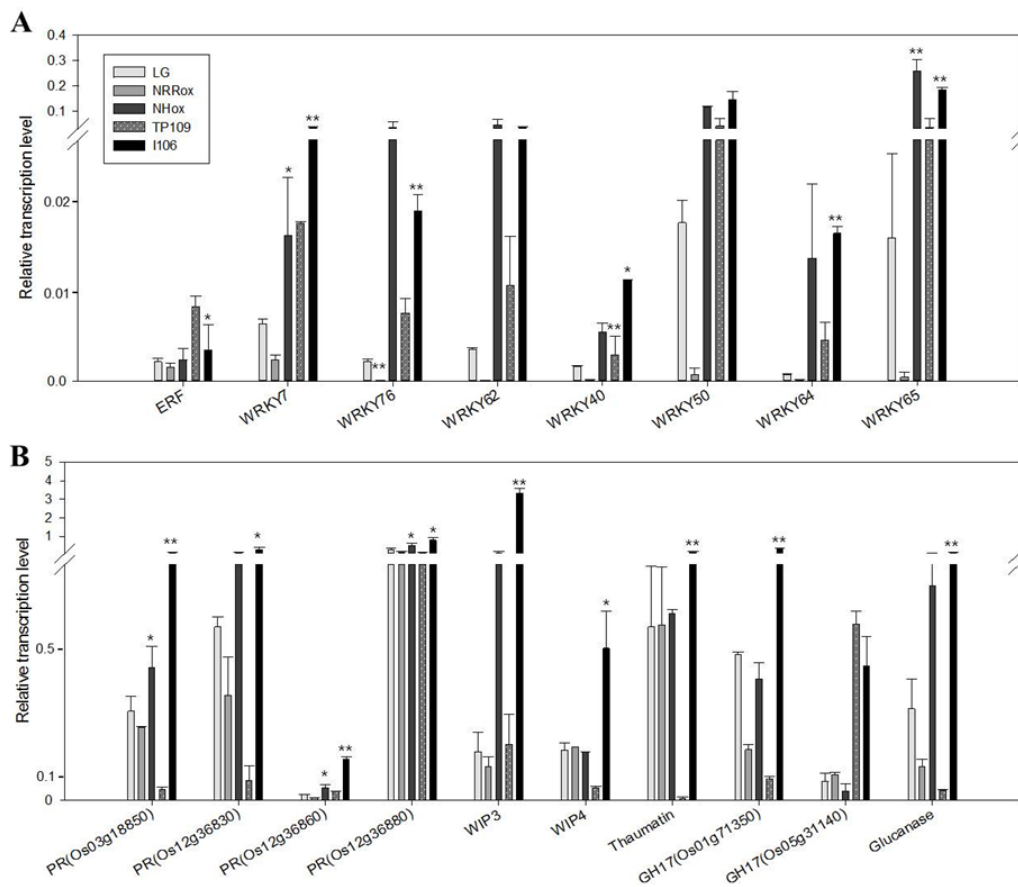


Figure S1. Real-time PCR analysis of genes belonging to RNA and pathogen related protein categories

Table S1. List and microarray data of genes associated with enhanced bacterial blight resistance

Locus_id	Putative Function	log ₂	log ₂	log ₂	Log ₂	Log ₂	log ₂	Feature
		NRRox(SS)/ LG(S)_1d	NH1ox(R)/ LG(S)_1d	Xa21(R)/ TP309(S)_2d	BTH(hormone)/ Mock	JA(hormone)/ Mock_leaf	LPS(elicitor)/ Mock	
LOC_Os01g01080	decarboxylase, putative, expressed	-0.62166	0.113813	1.032885				Figure 4
LOC_Os01g01160	heat shock protein DnaJ, putative, expressed	0.50816	1.146319	0.782804				Figure 4
LOC_Os01g01180	expressed protein	0.484002	1.028018	1.185149				Figure 4
LOC_Os01g01710	1-deoxy-D-xylulose 5-phosphate reductoisomerase, chloroplast precursor, putative, expressed	-0.73341	-0.22451	1.15928			0.60495	Figure 4
LOC_Os01g01840	helix-loop-helix DNA-binding domain containing protein, expressed	-1.57286	2.032539	0.616171	6.470884	-0.58151		Figure 4
LOC_Os01g04280	calmodulin binding protein, putative, expressed	-0.83571	0.998188	-0.22336	1.556207	0.374425	1.71215	Figure 4
LOC_Os01g10590	osFTL8 FT-Like8 homologous to Flowering Locus T gene; contains Pfam profile PF01161: Phosphatidylethanolamine-binding protein, expressed	-0.75864	1.32332	0.1833				Figure 4
LOC_Os01g13590	isoflavone reductase homolog IRL, putative, expressed	0.829176	1.694336	1.035175				Figure 4

LOC_Os01g14250	expressed protein	1.172973	2.053824	0.75785				Figure 4
LOC_Os01g14810	5-nucleotidase domain-containing protein, putative, expressed	-1.00083	-0.18424	0.875149	0.010906	-1.047	0.3255	Figure 4
LOC_Os01g15470	protein kinase, putative, expressed	-1.05266	-0.219	1.141446	-0.17659	0.11725	0.81305	Figure 4
LOC_Os01g19150	CGMC_GSK.3 - CGMC includes CDA, MAPK, GSK3, and CLKC kinases, expressed	-0.97823	-0.43121	1.46745	-0.01421	-0.1275	0.23955	Figure 4
LOC_Os01g24750	Ser/Thr protein phosphatase family protein, putative, expressed	-0.68218	-0.36161	0.885727	0.312546	0.31625	1.08105	Figure 4
LOC_Os01g28450	SCP-like extracellular protein, expressed	0.372053	1.61947	0.914662	2.037198	4.517	0.8253	Figure 4
LOC_Os01g35330	circumsporozoite protein precursor, putative, expressed	-0.34795	1.918976	1.511377				Figure 4
LOC_Os01g36950	N-rich protein, putative, expressed	-0.98642	0.310588	1.518618	-0.17178	0.281125	1.0989	Figure 4
LOC_Os01g37050	ribonuclease III domain protein, putative, expressed	-0.60312	-0.42046	1.263314	0.301193	-1.75224	0.1247	Figure 4
LOC_Os01g37910	vacuolar-processing enzyme precursor, putative, expressed	-1.34885	-0.50324	1.990398	0.193102	-1.02125	-1.1582	Figure 4
LOC_Os01g38650	expressed protein	0.646583	2.223721	1.45609	6.433319	-0.15985	-0.2508	Figure 4
LOC_Os01g42260	transcriptional corepressor LEUNIG, putative, expressed	-0.76208	-0.0509	1.035176	0.045065	0.055	-0.2768	Figure 4
LOC_Os01g48930	splicing factor-related, putative, expressed	-0.62469	-0.62635	1.411129	0.284588	-0.83453	0.3147	Figure 4
LOC_Os01g53350	anthocyanidin 5,3-O-glucosyltransferase, putative, expressed	-0.93493	0.350547	1.431636	0.634006	0.6167	-0.33065	Figure 4
LOC_Os01g55870	chorismate mutase, chloroplast precursor, putative, expressed	-0.39654	0.776814	1.198372	0.083726	0.4675	0.94185	Figure 4
LOC_Os01g58100	polyphenol oxidase, putative, expressed	-0.00841	1.669244	1.401254	1.460684	0.215975		Figure 4
LOC_Os01g58580	ICE-like protease p20 domain containing protein, putative, expressed	-0.82197	-0.41204	1.178699	0.003101	0.563063	-0.39125	Figure 4
LOC_Os01g62460	ZOS1-16 - C2H2 zinc finger protein, expressed	-0.77967	-0.11553	0.9173	0.325713	-1.50676	0.5238	Figure 4
LOC_Os01g64110	glycosyl hydrolase, putative, expressed	-0.85731	0.193286	0.612443	2.460338	0.701125	-0.01565	Figure 4
LOC_Os01g64660	fructose-1,6-bisphosphatase, putative, expressed	-0.82458	-1.66019	0.973493	-0.30016	-2.32073	-0.9129	Figure 4
LOC_Os01g64840	aspartic proteinase nepenthesisin-1 precursor, putative, expressed	0.637163	1.506497	0.868187	-0.03436	0.02125		Figure 4
LOC_Os01g65900	chitin-inducible gibberellin-responsive protein, putative, expressed	-0.82484	-0.0625	0.808025	0.157345	0.528	1.02565	Figure 4
LOC_Os01g69050	lysine ketoglutarate reductase trans-splicing related 1, putative, expressed	-0.68127	0.29725	0.876405	-0.07882	-0.12683		Figure 4
LOC_Os01g70390	expressed protein	1.405615	1.87148	1.243578	0.023805	0.457775	-0.04995	Figure 4
LOC_Os01g71350	glycosyl hydrolases family 17, putative, expressed	0.500127	0.652049	1.205307	0.593943	1.642625	0.5571	Figure 4
LOC_Os01g71770	RNA recognition motif containing protein, putative, expressed	-0.69017	0.030101	1.081014	-0.00193	0.372	-0.1018	Figure 4
LOC_Os01g72370	helix-loop-helix DNA-binding domain containing protein, expressed	-1.75644	-0.69859	0.646425	0.02924	-1.66145	-0.0425	Figure 4
LOC_Os01g73500	expressed protein	-0.59881	0.980304	1.198605	0.769216	0.429038	-0.57925	Figure 4

LOC_Os02g01150	erythronate-4-phosphate dehydrogenase domain containing protein, expressed	-0.77905	-0.94952	0.976393	#####	-2.84	0.2955	Figure 4
LOC_Os02g02120	OsWAK11 - OsWAK receptor-like protein kinase, expressed	-1.13558	0.98523	0.673381	0.413338	-0.05999		Figure 4
LOC_Os02g05710	expressed protein	-0.82247	-0.46327	1.091058	-0.1026	0.46945	0.43365	Figure 4
LOC_Os02g06640	ubiquitin family protein, putative, expressed	-1.06372	0.693782	0.609578	-0.02649	0.853875	0.19055	Figure 4
LOC_Os02g08080	expressed protein	0.539012	1.241269	0.799832	-0.16171	0.058413	-0.21445	Figure 4
LOC_Os02g08100	AMP-binding domain containing protein, expressed	-0.03591	0.857866	0.696769	-0.22574	0.36825	2.4647	Figure 4
LOC_Os02g08120	calmodulin binding protein, putative, expressed	-0.83634	-0.04884	0.974548	0.068132	-0.15166	-0.0205	Figure 4
LOC_Os02g10700	OsFBL7 - F-box domain and LRR containing protein, expressed	-1.00121	0.261725	1.108338	1.086723	-0.41813	-0.04035	Figure 4
LOC_Os02g12480	expressed protein	-0.80299	0.228533	1.090202	-0.08447	-0.34988	1.22825	Figure 4
LOC_Os02g13840	citrate synthase, putative, expressed	-0.74749	-0.32077	1.245042	0.123813	1.427	-0.1888	Figure 4
LOC_Os02g32110	exostosin family domain containing protein, expressed	-0.60211	-0.08222	1.252702				Figure 4
LOC_Os02g33330	expressed protein	-0.08634	1.878022	0.820267	-0.15051	2.2025	1.2295	Figure 4
LOC_Os02g33820	abscisic stress-ripening, putative, expressed	0.372016	0.879995	0.797212	-0.0076	0.110625	0.65515	Figure 4
LOC_Os02g35039	NAD dependent epimerase/dehydratase family protein, putative, expressed	-0.92128	0.047614	1.146637	-0.03667	0.17125	-0.0425	Figure 4
LOC_Os02g36140	terpene synthase, putative, expressed	-0.2034	1.102211	0.62184	0.529439	2.143238	0.33275	Figure 4
LOC_Os02g39160	hydroxymethylbutenyl 4-diphosphate synthase, putative, expressed	-0.61911	0.433745	1.652625	-0.14289	0.769	1.73225	Figure 4
LOC_Os02g39790	CPuORF9 - conserved peptide uORF-containing transcript, expressed	-0.9079	0.637574	1.993135	0.206664	0.619875	0.0627	Figure 4
LOC_Os02g43360	cytochrome b5-like Heme/Steroid binding domain containing protein, expressed	-0.29904	0.62055	1.187221	-0.06016	0.71975	1.3644	Figure 4
LOC_Os02g43860	amino acid permease, putative, expressed	-1.04365	-0.31184	1.412509	0.021672	0.488375	0.11125	Figure 4
LOC_Os02g44240	expressed protein	0.80848	1.184147	1.044616	-0.02829	0.066163		Figure 4
LOC_Os02g44260	zinc-binding protein, putative, expressed	0.961141	1.759344	1.100723				Figure 4
LOC_Os02g47510	9-cis-epoxycarotenoid dioxygenase 1, chloroplast precursor, putative, expressed	-0.8896	-0.71182	0.943963	-0.11318	-1.44409		Figure 4
LOC_Os02g48000	TBC domain containing protein, expressed	-0.88525	-0.01541	0.754247	-0.01039	1.198638	0.18435	Figure 4
LOC_Os02g48770	SAM dependent carboxyl methyltransferase, putative, expressed	-0.00182	1.239066	1.461013	0.692851	3.978388	0.36415	Figure 4
LOC_Os02g48964	WD-40 repeat family protein, putative, expressed	-0.79626	-0.09659	0.652761	0.112406	0.171838	0.91785	Figure 4
LOC_Os02g50360	nicalin, putative, expressed	-0.8684	0.183329	0.718323	0.040078	-0.03463	-0.0378	Figure 4
LOC_Os02g53700	DENN domain containing protein, expressed	-0.72789	-0.17854	1.068998	-0.31943	-0.13513	0.22165	Figure 4

LOC_Os02g54730	transmembrane amino acid transporter protein, putative, expressed	-0.805	-0.42083	0.812236	-0.20652	-1.47428	-0.3275	Figure 4
LOC_Os02g57180	NADH dehydrogenase 1 alpha subcomplex subunit 9, mitochondrial precursor, putative, expressed	-0.77687	-0.02834	1.260289	-0.10682	0.365613	-0.06855	Figure 4
LOC_Os02g57410	OTU-like cysteine protease family protein, putative, expressed	-0.81021	-0.42941	1.277887	-0.1184	0.14135	0.81835	Figure 4
LOC_Os02g57600	expressed protein	-0.64718	-0.00113	0.97399	-0.2612	0.738975	0.2938	Figure 4
LOC_Os03g02590	peroxisomal biogenesis factor 11, putative, expressed	-0.77663	-0.5884	1.276663	0.070674	-1.68225	-0.0034	Figure 4
LOC_Os03g03720	glyceraldehyde-3-phosphate dehydrogenase, putative, expressed	-1.04445	-0.38365	0.879045	-0.16586	-2.554	0.42805	Figure 4
LOC_Os03g03810	DEF8 - Defensin and Defensin-like DEFL family, expressed	-0.84973	1.581758	1.576025	0.057248	0.516725		Figure 4
LOC_Os03g05390	Citrate transporter protein, putative, expressed	-0.82271	-0.27244	1.563009	-0.20723	-1.681	-0.1067	Figure 4
LOC_Os03g05620	inorganic phosphate transporter, putative, expressed	-0.87922	0.360406	0.939645	2.454804	0.87935		Figure 4
LOC_Os03g08170	protein kinase APK1B, chloroplast precursor, putative, expressed	-0.22801	0.975376	0.773161	0.006001	-0.61211	1.0178	Figure 4
LOC_Os03g08999	dehydrogenase, putative, expressed	0.084622	0.749322	1.095651	1.052493	-1.65241	0.0579	Figure 4
LOC_Os03g09250	inositol-3-phosphate synthase, putative, expressed	-0.04775	0.616271	2.408002	0.586429	1.589625	-0.25555	Figure 4
LOC_Os03g10880	BTBN5 - Bric-a-Brac, Tramtrack, Broad Complex BTB domain with non-phototropic hypocotyl 3 NPH3 and coiled-coil domains, expressed	-0.97051	-1.08046	1.26788	0.046635	-1.04508		Figure 4
LOC_Os03g12590	coatamer subunit gamma-1, putative, expressed	-0.67976	0.263975	0.962386	0.234857	0.865825	-0.0666	Figure 4
LOC_Os03g13970	26S proteasome non-ATPase regulatory subunit 4, putative, expressed	-0.63307	-0.42429	1.059866	-0.13787	0.229375	0.03735	Figure 4
LOC_Os03g17380	expressed protein	1.14035	1.764665	0.98704				Figure 4
LOC_Os03g18850	pathogenesis-related Bet v I family protein, putative, expressed	0.65661	1.045877	1.113257	0.426657	-4.08613		Figure 4
LOC_Os03g19960	ATP-dependent RNA helicase, putative, expressed	-0.65439	-0.29234	1.163933	-0.22722	-0.01838	0.0664	Figure 4
LOC_Os03g20330	VQ domain containing protein, putative, expressed	-0.70253	1.104517	-0.73562	2.861238	-0.75059	2.8292	Figure 4
LOC_Os03g22420	AAA-type ATPase family protein, putative, expressed	-0.44322	0.667829	1.0875	-0.02093	0.284375		Figure 4
LOC_Os03g24040	seven in absentia protein family domain containing protein, expressed	0.637973	0.868475	0.855166			0.7346	Figure 4
LOC_Os03g25070	CAMK_CAMK_like.18 - CAMK includes calcium/calmodulin dependent protein kinases, expressed	-0.6588	-0.46013	1.014203	-0.13715	0.501063	0.1929	Figure 4
LOC_Os03g29190	PDI, putative, expressed	-0.18225	1.172415	0.969791	1.741026	0.366763	0.26155	Figure 4
LOC_Os03g30190	retrotransposon protein, putative, unclassified, expressed	1.353919	2.24824	1.355825				Figure 4
LOC_Os03g31300	chaperone protein clpB 1, putative, expressed	-0.69475	0.16005	1.388952	-0.22987	-0.96638	-0.0237	Figure 4
LOC_Os03g32314	allene oxide cyclase 4, chloroplast precursor, putative, expressed	-0.70565	-0.00401	1.094336	0.027076	1.53175	-0.26065	Figure 4
LOC_Os03g36750	cbbY, putative, expressed	-0.8416	-0.74637	0.754195	0.09488	-0.94066	0.272	Figure 4

LOC_Os03g37830	potassium transporter, putative, expressed	-0.16712	0.866306	1.691325	-0.10637	-0.18579	1.8453	Figure 4
LOC_Os03g39560	retrotransposon protein, putative, unclassified, expressed	0.520306	1.442007	0.633289				Figure 4
LOC_Os03g48660	DUF1336 domain containing protein, expressed	0.052302	0.695765	0.866108	0.023825	0.810625		Figure 4
LOC_Os03g51910	basic helix-loop-helix protein, putative, expressed	-0.32707	1.087504	0.795232	0.714943	-0.56433		Figure 4
LOC_Os03g53520	expressed protein	-0.69831	-0.9415	1.260336	-0.36916	0.496413	-0.4574	Figure 4
LOC_Os03g55540	ZOS3-18 - C2H2 zinc finger protein, expressed	-0.70099	-0.05171	1.140078	0.889493	1.46225	2.9079	Figure 4
LOC_Os03g56280	lactate/malate dehydrogenase, putative, expressed	-0.75105	-0.74289	0.892172	0.094108	-2.65425	-0.0445	Figure 4
LOC_Os03g56460	glucose-6-phosphate isomerase, putative, expressed	-0.83767	-0.81911	1.164797	-0.12843	-0.353	-0.3123	Figure 4
LOC_Os03g57110	expressed protein	-0.66752	-0.26454	1.375674	0.224606	0.0595	-0.7048	Figure 4
LOC_Os03g58470	retrotransposon protein, putative, Ty3-gypsy subclass, expressed	0.167802	0.647122	1.262179	0.761888	-0.32875	0.0545	Figure 4
LOC_Os03g58790	ATPase, putative, expressed	-0.66516	0.747763	1.072476	2.850385	0.992725	0.8413	Figure 4
LOC_Os03g60090	methylenetetrahydrofolate reductase, putative, expressed	0.083086	1.138991	1.041158	0.009448	0.51125	0.1575	Figure 4
LOC_Os03g61130	phosphoesterase family protein, putative, expressed	-0.89047	0.175411	1.228094	-0.36764	0.472125	0.315	Figure 4
LOC_Os03g61960	2Fe-2S iron-sulfur cluster binding domain containing protein, expressed	0.228726	1.121364	0.723668	-0.00275	1.679625		Figure 4
LOC_Os03g62200	ammonium transporter protein, putative, expressed	-0.11178	1.827604	0.747954	0.648322	-0.31638	2.36805	Figure 4
LOC_Os04g04040	expressed protein	-0.04059	1.008227	0.830286				Figure 4
LOC_Os04g04050	expressed protein	2.09564	3.009584	2.162603				Figure 4
LOC_Os04g04440	retrotransposon protein, putative, unclassified	0.178221	1.202952	0.735868				Figure 4
LOC_Os04g04540	retrotransposon, putative, centromere-specific, expressed	0.244272	1.098164	1.062164				Figure 4
LOC_Os04g12520	transposon protein, putative, unclassified, expressed	0.620964	0.895447	0.906761				Figure 4
LOC_Os04g15690	DSBA-like thioredoxin domain containing protein, expressed	-1.13414	1.034968	1.427958	1.050473	0.002913	-0.7268	Figure 4
LOC_Os04g15920	dehydrogenase, putative, expressed	-0.17264	1.196878	0.662445	0.504846	2.102925	0.2482	Figure 4
LOC_Os04g16680	fructose-1,6-bisphosphatase, putative, expressed	-0.87423	-0.83194	1.138305	-0.04861	-3.19063	-0.40825	Figure 4
LOC_Os04g16730	hypothetical protein	-0.15817	0.652854	1.025593				Figure 4
LOC_Os04g24220	OsWAK32 - OsWAK receptor-like protein kinase, expressed	-0.3636	1.049977	0.652823	0.571276	-0.05271	-0.78515	Figure 4
LOC_Os04g27340	terpene synthase, putative, expressed	-0.20764	1.48521	0.967139				Figure 4
LOC_Os04g29790	OsWAK40 - OsWAK receptor-like protein OsWAK-RLP, expressed	-0.99643	0.529033	0.634053				Figure 4
LOC_Os04g31700	methylisocitrate lyase 2, putative, expressed	-0.74025	-0.03289	1.161776	0.014329	0.072388		Figure 4
LOC_Os04g32020	2-oxoglutarate dehydrogenase E1 component, mitochondrial precursor, putative, expressed	-0.72045	0.237726	1.593301	0.165379	0.53325	0.0699	Figure 4
LOC_Os04g32950	calreticulin precursor protein, putative, expressed	-1.00253	0.263849	1.177382	0.432092	1.2905		Figure 4

LOC_Os04g33190	AMP-binding enzyme, putative, expressed	-0.17149	0.638145	1.464633	0.416425	0.651875		Figure 4
LOC_Os04g37619	zeaxanthin epoxidase, chloroplast precursor, putative, expressed	-0.63111	-0.10812	1.079638	-0.3939	0.43325		Figure 4
LOC_Os04g42470	regulatory subunit, putative, expressed	-0.92728	-0.92712	1.813929	-0.21151	-0.50775	-0.19955	Figure 4
LOC_Os04g43070	ammonium transporter protein, putative, expressed	0.080032	0.658318	1.296181	0.046657	-1.751	1.0725	Figure 4
LOC_Os04g49194	naringenin,2-oxoglutarate 3-dioxygenase, putative, expressed	-0.83956	0.663057	0.39834	0.941388	0.88985	0.20455	Figure 4
LOC_Os04g49210	naringenin,2-oxoglutarate 3-dioxygenase, putative, expressed	-0.31	1.544026	0.818011	3.917561	0.635925	-0.27815	Figure 4
LOC_Os04g51400	zinc finger, C3HC4 type domain containing protein, expressed	-0.91767	-0.73336	1.30017	0.1439	-1.389	0.975	Figure 4
LOC_Os04g53810	leucoanthocyanidin reductase, putative, expressed	-0.88053	0.053729	1.584638	1.544892	0.797013	0.5832	Figure 4
LOC_Os04g55710	transposon protein, putative, unclassified, expressed	-1.09985	0.281609	0.745361	2.24599	-2.08654	0.53535	Figure 4
LOC_Os04g55850	nuclease PA3, putative, expressed	0.074395	0.884555	0.676601	-0.12294	1.0904	0.05255	Figure 4
LOC_Os04g57200	heavy metal transport/detoxification protein, putative, expressed	-0.93951	0.368701	1.021466	1.620669	0.24285		Figure 4
LOC_Os04g57300	phosphatidylinositol 3- and 4-kinase family protein, putative, expressed	-0.76254	-0.66953	1.321861	0.015864	-0.17138	-0.06725	Figure 4
LOC_Os04g57750	plastocyanin-like domain containing protein, putative, expressed	1.574197	1.691384	0.945251	-0.03242	0.150838	0.38485	Figure 4
LOC_Os04g58270	expressed protein	0.496199	1.067049	1.044962				Figure 4
LOC_Os04g58330	expressed protein	0.009048	0.624041	1.255325	0.233994	0.1294	0.8048	Figure 4
LOC_Os05g01030	phospholipid-transporting ATPase, putative, expressed	0.77225	1.276122	1.511973	0.475761	2.28595	1.8171	Figure 4
LOC_Os05g01140	methyltransferase, putative, expressed	0.162597	1.245963	1.7746	0.230434	-0.01346	0.76925	Figure 4
LOC_Os05g04630	retrotransposon protein, putative, SINE subclass, expressed	-0.66538	-0.31187	1.266295	0.008786	0.37675	-0.19165	Figure 4
LOC_Os05g05020	expressed protein	-0.81052	0.8558	1.768554	0.010736	-0.02603	1.8458	Figure 4
LOC_Os05g05030	expressed protein	-0.87545	0.674762	1.722902	0.333969	-0.55819	-0.6012	Figure 4
LOC_Os05g05940	stress-related protein, putative, expressed	-0.94015	-0.05886	1.063594	0.151245	0.28675		Figure 4
LOC_Os05g06260	Spc97 / Spc98 family protein, putative, expressed	0.294082	0.999835	0.65416	-0.13482	0.142975		Figure 4
LOC_Os05g06350	importin subunit alpha, putative, expressed	-0.79288	0.317946	1.042954	-0.15193	0.208625	0.227	Figure 4
LOC_Os05g19910	transferase family protein, putative, expressed	-0.19814	1.207265	0.852967	0.087206	-0.7305	0.47465	Figure 4
LOC_Os05g30500	expressed protein	-1.02089	1.441208	0.560114	5.574205	-0.50921		Figure 4
LOC_Os05g31140	glycosyl hydrolases family 17, putative, expressed	-0.78844	-0.7469	1.858892	0.32171	1.235625	0.39965	Figure 4
LOC_Os05g33570	pyruvate, phosphate dikinase, chloroplast precursor, putative, expressed	0.061504	0.836358	0.981813	-0.05522	0.56975	1.3279	Figure 4
LOC_Os05g33610	expressed protein	-0.67743	-0.55813	1.020504	-0.28531	0.1895	0.4506	Figure 4
LOC_Os05g33710	WD domain, G-beta repeat domain containing protein, expressed	-0.89961	-0.43418	0.880772	-0.13261	0.0275	-0.2724	Figure 4
LOC_Os05g34270	inactive receptor kinase At1g27190 precursor, putative, expressed	-1.01778	0.820989	0.305172	0.811334	0.288	1.0468	Figure 4
LOC_Os05g40270	expressed protein	-0.58008	0.814495	0.644073	-0.15324	-1.21163	-0.2552	Figure 4

LOC_Os05g43170	calreticulin precursor protein, putative, expressed	-1.29567	-0.09876	0.986462	0.707302	0.02175	0.48415	Figure 4
LOC_Os05g46020	WRKY7, expressed	-0.76488	0.8658	0.015174	2.482018	1.146363		Figure 4
LOC_Os05g48210	expressed protein	-0.75753	0.981228	0.584407	0.772179	1.087	2.1097	Figure 4
LOC_Os05g50100	expressed protein	0.176906	1.068084	0.785398	1.227359	2.032625	3.3336	Figure 4
LOC_Os06g03580	zinc RING finger protein, putative, expressed	-0.6775	0.916111	-0.4471	1.465421	-0.12158	1.83885	Figure 4
LOC_Os06g03600	transcriptional corepressor SEUSS, putative, expressed	-0.63108	-0.49653	1.196438	-0.11099	-0.19363	0.1537	Figure 4
LOC_Os06g06580	expressed protein	-0.60958	-0.12319	1.102104	0.098034	0.028713		Figure 4
LOC_Os06g09370	PTF1, putative, expressed	-0.60589	0.60267	1.120514	0.10838	0.94565	0.7746	Figure 4
LOC_Os06g15360	RAD23 DNA repair protein, putative, expressed	-0.71919	-0.27624	0.804288	0.122697	0.259625	0.0224	Figure 4
LOC_Os06g15430	expressed protein	0.386732	2.661183	2.884091	0.043752	0.063938		Figure 4
LOC_Os06g15730	expressed protein	0.0023	0.906599	1.025873	0.213153	-2.14595		Figure 4
LOC_Os06g15990	aldehyde dehydrogenase, putative, expressed	-0.91169	-0.41502	0.807655	0.258009	0.485	-0.12365	Figure 4
LOC_Os06g24980	hypothetical protein	0.186696	0.858061	0.762143				Figure 4
LOC_Os06g28600	expressed protein	1.825798	1.993264	1.544256				Figure 4
LOC_Os06g29730	RALFL28 - Rapid ALkalinization Factor RALF family protein precursor, expressed	-2.20891	1.638874	2.282938	3.207274	0.777488	0.08745	Figure 4
LOC_Os06g29740	OsFBX197 - F-box domain containing protein, expressed	-1.38033	1.581222	1.558929				Figure 4
LOC_Os06g29770	hypothetical protein	-0.36163	1.284454	0.819666				Figure 4
LOC_Os06g34730	expressed protein	0.147477	1.463842	1.284309	0.596326	3.046875	-0.5551	Figure 4
LOC_Os06g36840	cysteine synthase, putative, expressed	-0.63889	-0.84289	0.883105	-0.34688	-1.13881	-0.40255	Figure 4
LOC_Os06g40360	OsFBL30 - F-box domain and LRR containing protein, expressed	-0.94474	0.441776	0.788987	0.490685	-0.49463	-0.2796	Figure 4
LOC_Os06g47350	RNA polymerase I specific transcription initiation factor RRN3 family protein, putative, expressed	-0.90071	-0.16899	1.138781	0.12431	-0.3846	-0.15375	Figure 4
LOC_Os06g49040	Myb-like DNA-binding domain containing protein, putative, expressed	-0.69809	-0.21604	1.70527	-0.63941	-0.31763	-0.2834	Figure 4
LOC_Os06g50380	protein phosphatase 2C, putative, expressed	-0.75351	-0.15734	1.32197	-0.13594	-0.09875	0.4257	Figure 4
LOC_Os07g01550	leucine rich repeat domain containing protein, putative, expressed	-0.73593	0.08566	1.084281	-0.48409	0.130425	0.13765	Figure 4
LOC_Os07g01760	aminotransferase, classes I and II, domain containing protein, expressed	-1.08046	-0.94311	1.259548	0.090304	-2.26738	-0.52445	Figure 4
LOC_Os07g03900	lectin-like receptor kinase, putative, expressed	-0.17543	0.938464	0.828874	-0.01753	-0.0816		Figure 4
LOC_Os07g04180	amino acid transporter, putative, expressed	-1.1317	-0.21078	1.609952	-0.15372	-1.60215	0.2762	Figure 4
LOC_Os07g05820	hydroxyacid oxidase 1, putative, expressed	-1.03291	-0.94306	1.330001	0.206442	-2.524	1.38545	Figure 4
LOC_Os07g06830	gibberellin receptor GID1L2, putative, expressed	-0.62594	0.480929	0.870572	1.181186	2.158875	2.1187	Figure 4
LOC_Os07g09010	nodulin, putative, expressed	-0.52245	0.977042	0.654159	0.980485	0.963663	0.08165	Figure 4
LOC_Os07g09320	FHA domain containing protein, putative, expressed	-0.61725	-0.21661	0.886505	0.116204	-0.1642	0.0504	Figure 4
LOC_Os07g16600	expressed protein	2.277472	3.201661	2.064889	0.38583	-0.27873	-0.13045	Figure 4

LOC_Os07g23120	expressed protein	-0.3016	0.742393	2.011276	1.943656	-3.23474	-0.5672	Figure 4
LOC_Os07g26490	ankyrin repeat domain containing protein, expressed	-0.76434	0.081198	1.353311	0.035187	0.29975	0.0046	Figure 4
LOC_Os07g28480	glutathione S-transferase, putative, expressed	-0.81227	-1.14276	1.079337	0.270151	-1.9196	-0.66315	Figure 4
LOC_Os07g29290	expansin precursor, putative, expressed	-0.16569	0.663386	0.914085	-0.55364	1.402375	-0.08705	Figure 4
LOC_Os07g35560	glucan endo-1,3-beta-glucosidase precursor, putative, expressed	-1.21901	0.426135	1.39239	1.298103	0.991363	-0.2355	Figure 4
LOC_Os07g36470	vacuolar ATP synthase subunit H, putative, expressed	-0.77629	-0.14436	1.333521			0.30085	Figure 4
LOC_Os07g37320	transporter family protein, putative, expressed	-0.76722	-0.46646	0.825372	0.491275	-0.0995		Figure 4
LOC_Os07g39560	RNA recognition motif containing protein, putative, expressed	-0.86229	-0.34553	0.800235	-0.09132	0.819075	0.6439	Figure 4
LOC_Os07g41410	Egg apparatus-1, putative, expressed	-2.18787	0.911142	1.147621	2.57855	-1.74084		Figure 4
LOC_Os07g45570	expressed protein	-0.64508	0.765675	1.906607	0.848385	0.68	0.2768	Figure 4
LOC_Os07g46370	WD domain, G-beta repeat domain containing protein, expressed	-0.61043	0.105536	0.914468	0.036131	0.19775	-0.012	Figure 4
LOC_Os07g46460	ferredoxin-dependent glutamate synthase, chloroplast precursor, putative, expressed	-1.00177	-0.09447	1.698099	-0.24174	-1.52268	-0.1921	Figure 4
LOC_Os07g46520	rhythmically expressed gene 2 protein, putative, expressed	0.461344	0.699831	1.231311	-0.32307	-0.72829		Figure 4
LOC_Os07g46920	sex determination protein tasselseed-2, putative, expressed	0.362614	1.437106	1.370873	-0.04603	0.1293		Figure 4
LOC_Os07g47150	expressed protein	-0.25394	0.892945	1.697645	-0.38384	0.252225	0.1655	Figure 4
LOC_Os07g48020	peroxidase precursor, putative, expressed	-0.39394	1.415791	2.109258	1.746237	-1.78905	-1.23325	Figure 4
LOC_Os07g48050	peroxidase precursor, putative, expressed	-0.16103	1.9694	2.452248	2.278653	-0.90539		Figure 4
LOC_Os07g48100	CAMK_KIN1/SNF1/Nim1_like.31 - CAMK includes calcium/calmodulin dependent protein kinases, expressed	-0.56661	0.766023	1.076177	-0.45404	-0.11138	0.12765	Figure 4
LOC_Os08g02230	FAD-binding and arabino-lactone oxidase domains containing protein, putative, expressed	-0.02447	1.174869	0.747826	1.784682	2.55875	0.6397	Figure 4
LOC_Os08g03290	glyceraldehyde-3-phosphate dehydrogenase, putative, expressed	-0.68219	0.027479	1.727328	-0.15612	1.012	-0.40285	Figure 4
LOC_Os08g04500	terpene synthase, putative, expressed	-0.26414	1.487079	1.611447	0.828786	-0.78225		Figure 4
LOC_Os08g06010	transporter, major facilitator family, putative, expressed	-0.40771	0.62253	1.421575	-0.28354	-0.69498	-0.99025	Figure 4
LOC_Os08g07080	terpene synthase, putative, expressed	-1.02679	3.70212	3.052742	1.262063	0.144363		Figure 4
LOC_Os08g07330	RGH1A, putative, expressed	-0.5925	0.636951	0.912574	0.255114	0.179588		Figure 4
LOC_Os08g12750	serine/threonine-protein kinase HT1, putative, expressed	-0.75596	-0.17138	0.980372	-0.156	-0.42013	-0.3124	Figure 4
LOC_Os08g13440	cupin domain containing protein, expressed	-0.80972	-0.40119	1.789424	0.602279	-1.80766	-0.91025	Figure 4
LOC_Os08g14440	uridylyltransferase-related, putative, expressed	-0.83642	-0.39685	0.751591	-0.20914	-1.28334	-0.3443	Figure 4
LOC_Os08g26230	expressed protein	-1.18214	1.42847	-0.72554	1.081431	-1.33206		Figure 4

LOC_Os08g26820	plant protein of unknown function domain containing protein, expressed	-0.82197	0.613377	-0.63966	1.823608	-0.42415	0.42165	Figure 4
LOC_Os08g26840	plant protein of unknown function domain containing protein, expressed	-0.93502	0.608336	-0.78005	2.432813	0.313988	-0.28645	Figure 4
LOC_Os08g27840	phosphoenolpyruvate carboxylase, putative, expressed	-0.8157	0.561896	1.932299	-0.05879	-0.32888	-0.0799	Figure 4
LOC_Os08g31410	sulfate transporter, putative, expressed	-0.51642	0.86571	0.689295	-0.31539	-0.1727	1.3203	Figure 4
LOC_Os08g31470	peptidase, trypsin-like serine and cysteine proteases, putative, expressed	-0.83115	0.639277	0.770847	-0.07416	-0.3675	-0.03595	Figure 4
LOC_Os08g34280	cinnamoyl-CoA reductase, putative, expressed	-0.21915	1.332616	0.84905	-0.49974	-0.5305	2.0953	Figure 4
LOC_Os08g42370	zinc finger DHHC domain-containing protein, putative, expressed	-0.79692	0.255648	1.192034	1.584436	-0.09238	0.7129	Figure 4
LOC_Os08g44210	dihydroneopterin aldolase, putative, expressed	-0.07519	1.221587	0.767862	1.269775	-0.01206		Figure 4
LOC_Os09g02214	Citrate transporter protein, putative, expressed	-0.72081	0.074592	0.955266	0.020841	-1.11475	-0.10675	Figure 4
LOC_Os09g08390	CRAL/TRIO domain containing protein, expressed	-0.30332	1.275875	0.620181	-0.365	1.445625	0.4374	Figure 4
LOC_Os09g13440	expressed protein	-1.74367	1.864749	-0.16591	0.176548	-0.24498		Figure 4
LOC_Os09g13460	expressed protein	-1.01061	1.669729	-0.24399				Figure 4
LOC_Os09g14440	hypothetical protein	-0.8808	1.352768	-0.21286				Figure 4
LOC_Os09g20350	ethylene-responsive transcription factor, putative, expressed	-0.68531	-0.1428	1.089021	0.056874	0.047125	0.0824	Figure 4
LOC_Os09g25060	WRKY76, expressed	-0.98184	1.784391	0.679818	4.088948	0.356925	-0.35855	Figure 4
LOC_Os09g25070	WRKY62, expressed	-1.17178	1.135785	1.356364	5.448968	0.26715	1.1186	Figure 4
LOC_Os09g27560	expressed protein	-0.54122	1.61296	0.632241				Figure 4
LOC_Os09g27580	potassium transporter, putative, expressed	-1.14163	1.968905	0.777529	1.850103	-0.6581	-0.61455	Figure 4
LOC_Os09g29200	glutathione S-transferase, putative, expressed	-1.05684	0.880411	0.982377	1.165847	-0.06325	-0.1917	Figure 4
LOC_Os09g34280	ankyrin repeat-containing protein, putative, expressed	-0.6773	-0.25578	1.177433	-0.20306	0.236125	-0.03985	Figure 4
LOC_Os09g36200	senescence-inducible chloroplast stay-green protein 1, putative, expressed	-0.03029	1.245938	1.120025	0.406153	3.31125	1.3453	Figure 4
LOC_Os09g36300	OsLonP4 - Putative Lon protease homologue, expressed	-0.93291	-0.20606	0.822577	0.417583	0.057125	0.5832	Figure 4
LOC_Os09g37012	eukaryotic aspartyl protease domain containing protein, expressed	-0.64697	-0.36589	1.506965	0.041825	-0.08663	0.7824	Figure 4
LOC_Os09g39650	protein kinase family protein, putative, expressed	-0.93158	1.144367	0.854584	0.299028	-0.30216	-0.47365	Figure 4
LOC_Os10g05210	OsFBX368 - F-box domain containing protein, expressed	-0.90651	1.088556	0.461708	-0.09681	0.063588	-0.1622	Figure 4
LOC_Os10g10130	OsWAK112d - OsWAK receptor-like protein kinase, expressed	-1.23226	-0.35722	1.434578	0.464137	-0.18563	-0.15035	Figure 4
LOC_Os10g27230	endonuclease/exonuclease/phosphatase family domain containing protein, expressed	-0.82868	-0.27237	0.920414	0.078359	-0.10988	0.0577	Figure 4

LOC_Os10g28080	glycosyl hydrolase, putative, expressed	-0.11884	0.865343	0.971423	0.288969	1.774362	2.66235	Figure 4
LOC_Os10g28200	NAD dependent epimerase/dehydratase family protein, putative, expressed	-0.77035	-0.84127	1.2388	0.624559	-0.53288		Figure 4
LOC_Os10g34400	expressed protein	-0.97528	-0.11971	1.440205	0.214561	-0.91703		Figure 4
LOC_Os10g37730	pollen ankyrin, putative, expressed	-0.74848	-0.22441	0.988011	0.004502	0.056538	-0.1448	Figure 4
LOC_Os10g39140	flavonol synthase/flavanone 3-hydroxylase, putative, expressed	-0.77322	1.514981	-0.05439	3.239305	2.323125	0.1602	Figure 4
LOC_Os10g41980	RALFL26 - Rapid ALkalinization Factor RALF family protein precursor, expressed	0.45632	0.735282	1.420188	0.722995	-1.44296	0.07175	Figure 4
LOC_Os10g42240	kinase, pfkB family, putative, expressed	-0.93769	-0.49049	0.673269	-0.19108	-1.26579	-0.76145	Figure 4
LOC_Os11g02150	saposin-like type B, region 1 family protein, putative, expressed	-0.80437	-0.58257	1.362907	-0.09216	0.43175		Figure 4
LOC_Os11g02530	WRKY40, expressed	-0.21467	2.100624	0.735403	2.091132	2.9033		Figure 4
LOC_Os11g02540	WRKY50, expressed	-0.69727	2.434097	0.938227				Figure 4
LOC_Os11g03230	nucleoside-triphosphatase, putative, expressed	-0.94344	0.721348	0.209449	0.578286	0.033975		Figure 4
LOC_Os11g04030	major facilitator superfamily antiporter, putative, expressed	-0.03804	2.243273	0.699938	-0.01716	-0.35671	-0.2025	Figure 4
LOC_Os11g05990	digalactosyldiacylglycerol synthase, chloroplast precursor, putative, expressed	-0.13223	0.885596	0.611005	-0.1419	0.552	0.4773	Figure 4
LOC_Os11g06200	expressed protein	0.569491	1.515629	0.677455				Figure 4
LOC_Os11g07930	oxidoreductase, short chain dehydrogenase/reductase family domain containing family, expressed	0.210138	0.741941	0.815496	0.005564	-2.79648	0.15865	Figure 4
LOC_Os11g10100	STE_MEKK_ste11_MAP3K.3 - STE kinases include homologs to sterile 7, sterile 11 and sterile 20 from yeast, expressed	-0.80011	-0.28149	0.934303	0.767809	0.363875		Figure 4
LOC_Os11g11960	disease resistance protein RPM1, putative, expressed	-1.00802	0.902514	0.398861				Figure 4
LOC_Os11g12340	disease resistance protein RPM1, putative, expressed	-1.24499	0.871429	-0.1817	1.657166	-0.56688	0.6507	Figure 4
LOC_Os11g21990	expressed protein	-0.64228	0.244341	1.398549	0.029983	-0.43575	-0.06895	Figure 4
LOC_Os11g24540	signal peptide peptidase-like 2B, putative, expressed	-0.6603	-0.16015	0.971524	-0.13517	0.449975	0.6029	Figure 4
LOC_Os11g28270	zinc finger C-x8-C-x5-C-x3-H type family protein, expressed	-0.60218	0.719985	1.200292	0.089814	-0.05121	-1.06215	Figure 4
LOC_Os11g36430	zinc finger, C3HC4 type domain containing protein, expressed	-0.87359	-0.43173	0.982362	0.030891	-0.23775	0.0256	Figure 4
LOC_Os11g37950	WIP3 - Wound-induced protein precursor, expressed	-0.40058	0.890427	1.717969	0.567761	3.542775		Figure 4
LOC_Os11g37960	WIP4 - Wound-induced protein precursor, expressed	0.285787	0.689607	0.867366	0.143319	0.367288	1.5385	Figure 4
LOC_Os11g39370	BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1 precursor, putative, expressed	-1.04181	1.829413	0.780994	0.943142	0.154625	-0.1077	Figure 4
LOC_Os11g46810	retrotransposon protein, putative, unclassified, expressed	-1.01768	1.377193	-0.47287				Figure 4

LOC_Os11g48020	fatty acid hydroxylase, putative, expressed	0.3678	0.820391	0.98204			-0.6619	Figure 4
LOC_Os12g02320	LTP12 - Protease inhibitor/seed storage/LTP family protein precursor, expressed	0.31304	1.101199	0.745428	-0.15737	-1.55938		Figure 4
LOC_Os12g02450	WRKY64, expressed	-0.09472	2.125418	0.896351	2.50443	2.8683		Figure 4
LOC_Os12g02470	WRKY65, expressed	-0.32874	2.499243	0.980709				Figure 4
LOC_Os12g05110	pyruvate kinase, putative, expressed	-0.60497	0.254239	1.176003	0.031856	0.95775	0.0352	Figure 4
LOC_Os12g07110	acyl-CoA synthetase protein, putative, expressed	-0.86414	-0.25683	0.901445	-0.16841	-0.802	-0.4423	Figure 4
LOC_Os12g08810	VTC2, putative, expressed	0.06484	1.363664	1.037753	-0.18673	0.72975	-0.2396	Figure 4
LOC_Os12g09700	Jacalin-like lectin domain containing protein, putative, expressed	0.44961	1.752022	1.401411	0.029894	0.21245	-1.1377	Figure 4
LOC_Os12g09739	pollen signalling protein with adenylyl cyclase activity, putative, expressed	0.54678	0.953602	1.11887	-0.12803	0.132138	0.2602	Figure 4
LOC_Os12g10740	leucine-rich repeat family protein, putative, expressed	-1.13728	0.384152	1.260968	0.895482	-0.61535	0.50175	Figure 4
LOC_Os12g12560	NADP-dependent oxidoreductase, putative, expressed	0.373785	1.001344	0.753859	-0.23166	0.801388	0.30095	Figure 4
LOC_Os12g14440	Jacalin-like lectin domain containing protein, putative, expressed	-0.66272	2.85033	2.345581	8.118299	1.882363	-0.2118	Figure 4
LOC_Os12g21700	zinc finger C-x8-C-x5-C-x3-H type family protein, expressed	-0.88214	-0.24038	0.686118	-0.09197	-0.03688	-0.1647	Figure 4
LOC_Os12g23180	3-beta hydroxysteroid dehydrogenase/isomerase family protein, putative, expressed	-0.9701	-0.62121	1.117991	0.160354	-2.508	0.92695	Figure 4
LOC_Os12g25170	NB-ARC domain containing disease resistance protein, putative, expressed	-0.81503	0.799392	1.147597	0.200379	-0.75253	0.15205	Figure 4
LOC_Os12g31440	expressed protein	-0.73009	-0.0734	0.926051	-0.05146	-0.1895		Figure 4
LOC_Os12g35470	expressed protein	0.068304	2.197839	1.859015				Figure 4
LOC_Os12g36830	pathogenesis-related Bet v I family protein, putative, expressed	-0.33356	1.624627	1.670813	1.647349	1.482	1.73845	Figure 4
LOC_Os12g36860	pathogenesis-related protein 10, putative, expressed	-0.2086	1.407116	0.6022	1.948627	2.18025		Figure 4
LOC_Os12g36880	pathogenesis-related Bet v I family protein, putative, expressed	-0.63953	1.996695	1.565929	2.077135	4.228	1.00465	Figure 4
LOC_Os12g37260	lipoxygenase 2.1, chloroplast precursor, putative, expressed	-0.56542	2.814567	2.426765	3.154193	1.94555	0.86435	Figure 4
LOC_Os12g37350	lipoxygenase protein, putative, expressed	-0.16203	1.039084	0.770961	2.681751	1.506125		Figure 4
LOC_Os12g42850	amino acid permease, putative, expressed	-1.19914	-0.09983	1.289242	0.196122	0.631125	1.117	Figure 4
LOC_Os12g43380	thaumatin, putative, expressed	-0.41786	2.357376	0.709838	1.25965	3.374325		Figure 4
LOC_Os08g14570	NADPH reductase, putative, expressed	0.517677	1.025565	0.598779	-0.13045	0.750875	1.7309	
LOC_Os09g29404	glycogen operon protein glgX, putative, expressed	-0.18005	0.880238	0.588289	0.258458	-1.52638	-0.51135	
LOC_Os12g05700	transposon protein, putative, Mutator sub-class, expressed	0.369847	0.817296	0.584349				
LOC_Os10g04520	expressed protein	0.134036	1.35022	0.576641	0.104868	0.954575		
LOC_Os01g63389	hypothetical protein	0.803083	1.430825	0.576128				
LOC_Os01g14640	expressed protein	0.370379	1.015062	0.574099	0.068946	-0.03423	-0.16475	

LOC_Os02g13380	early nodulin 93 ENOD93 protein, putative, expressed	-0.09457	0.822812	0.566767	1.065371	1.572625	0.00655
LOC_Os01g42620	pentatricopeptide containing protein, putative, expressed	0.087389	0.811243	0.556116	0.019363	-0.05698	-0.87465
LOC_Os04g06520	expressed protein	-0.25421	1.425418	0.540897	1.964411	-0.12266	0.39305
LOC_Os04g04480	retrotransposon protein, putative, unclassified, expressed	0.536282	0.801622	0.533211			
LOC_Os02g09490	dehydrogenase, putative, expressed	0.444607	1.312049	0.532822	-0.28538	1.340375	0.6383
LOC_Os01g42380	pleiotropic drug resistance protein, putative, expressed	-0.12757	1.108099	0.526731	1.305995	3.3281	1.5953
LOC_Os07g44130	cytochrome P450 72A1, putative, expressed	0.021826	0.941717	0.521432	0.831575	0.588	
LOC_Os02g45320	OsFBX58 - F-box domain containing protein, expressed	0.219663	1.210373	0.520475	0.351903	-0.01745	0.8323
LOC_Os12g36850	pathogenesis-related Bet v I family protein, putative, expressed	-0.38411	1.894099	0.516728	0.802171	1.8705	3.1032
LOC_Os10g39680	CHIT14 - Chitinase family protein precursor, expressed	-0.24249	1.550733	0.50076	2.145026	2.604875	1.31645
LOC_Os04g27100	hypothetical protein	-0.02872	1.049868	0.495879			2.2737
LOC_Os03g44050	OsWAK27 - OsWAK receptor-like protein kinase, expressed	0.209963	0.973302	0.49585			
LOC_Os01g72120	glutathione S-transferase, putative, expressed	-0.3265	1.019674	0.464075	1.867619	1.865525	0.2161
LOC_Os06g32674	hypothetical protein	0.55184	2.269339	0.460869			
LOC_Os03g03790	AMP-binding domain containing protein, expressed	0.267325	1.33569	0.452941	0.708217	0.493938	1.0399
LOC_Os07g34990	retrotransposon protein, putative, unclassified, expressed	1.400493	1.117683	0.442836			
LOC_Os10g42130	no apical meristem protein, putative, expressed	0.124453	1.258757	0.427524	0.899073	-1.39631	0.14055
LOC_Os08g30510	expressed protein	-0.03211	0.888445	0.402044	0.078832	0.5771	0.3708
LOC_Os01g38359	peptidyl-prolyl cis-trans isomerase, FKBP-type, putative, expressed	-0.30902	0.851084	0.396711	0.002798	-0.67865	0.07365
LOC_Os06g47200	LTPL85 - Protease inhibitor/seed storage/LTP family protein precursor, expressed	0.216743	0.875242	0.39229	-0.0621	0.386563	0.5289
LOC_Os08g04230	cysteine-rich repeat secretory protein 55 precursor, putative, expressed	1.049796	2.14292	0.384696	-0.06817	-0.17916	0.8203
LOC_Os11g29870	WRKY72, expressed	0.269616	1.12951	0.380616	1.15141	2.8793	3.64035
LOC_Os09g27520	expressed protein	0.940414	0.968126	0.373085			
LOC_Os01g37390	retrotransposon protein, putative, unclassified, expressed	-0.11465	0.903981	0.356786			
LOC_Os01g32460	expressed protein	-0.20262	0.913044	0.338687	4.661748	-0.27636	
LOC_Os01g09190	expressed protein	-0.57563	0.926198	0.327973	0.389842	-0.18744	0.33465
LOC_Os11g07850	Protein-tyrosine phosphatase domain containing protein, expressed	-0.4085	0.812833	0.3279	0.617676	0.73575	
LOC_Os08g25310	phosphatidylinositol transfer, putative, expressed	0.275665	0.82753	0.323732	-0.01711	0.219163	0.1328
LOC_Os12g12090	expressed protein	-0.17847	1.458025	0.319071	0.070244	-0.15821	0.56635
LOC_Os12g42980	cysteine synthase, putative, expressed	-0.28446	0.967386	0.311369	0.041093	-0.01888	-0.2465
LOC_Os06g47230	coiled-coil domain-containing protein 72, putative, expressed	0.245309	0.903906	0.298568	0.096099	0.745125	0.283

LOC_Os09g38020	Core histone H2A/H2B/H3/H4 domain containing protein, putative, expressed	0.789403	0.92825	0.294242	0.388692	-0.117	
LOC_Os03g38790	expressed protein	0.745584	1.503607	0.292124	0.190029	0.5032	0.17365
LOC_Os07g29960	cytochrome P450, putative, expressed	0.038416	0.979755	0.289449	-0.12992	0.567375	
LOC_Os01g66020	protein kinase family protein, putative, expressed	0.569928	1.435638	0.284799	0.479999	-2.35851	
LOC_Os09g36860	acyl carrier protein, putative, expressed	0.212074	1.144683	0.272877	-0.19698	0.827763	-0.14125
LOC_Os11g08100	eukaryotic aspartyl protease domain containing protein, expressed	0.250838	0.805867	0.271172	0.6558	1.96725	0.4285
LOC_Os03g29810	OsClp6 - Putative Clp protease homologue, expressed	0.380819	0.819027	0.267026	-0.04466	-0.77219	-0.77945
LOC_Os02g47650	universal stress protein domain containing protein, putative, expressed	-0.4703	1.218947	0.263932	1.122829	2.389425	2.2264
LOC_Os08g26350	expressed protein	0.208753	0.932967	0.261943	0.122034	0.277838	
LOC_Os08g13270	expressed protein	0.032641	0.803642	0.255814			0.10205
LOC_Os01g66260	expressed protein	0.489091	1.205067	0.254066			
LOC_Os07g48310	inactive receptor kinase At2g26730 precursor, putative, expressed	-0.00677	0.8385	0.250737	1.015334	0.12645	-0.1533
LOC_Os07g34720	harpin-induced protein 1 domain containing protein, expressed	0.942009	0.927974	0.227188	-0.22752	-0.10996	
LOC_Os03g21470	hypothetical protein	0.539293	1.272535	0.222811	-0.06473	0.035738	
LOC_Os03g16910	SLT1 protein, putative, expressed	0.261247	0.80941	0.212241	0.027945	-0.01338	0.0756
LOC_Os01g10450	protein kinase domain containing protein, expressed	0.062891	1.161433	0.210487	-0.64203	-1.43829	0.37985
LOC_Os01g70380	serine palmitoyltransferase 2, putative, expressed	0.058332	0.850594	0.205318	0.116246	-0.1325	
LOC_Os04g10000	sex determination protein tasselseed-2, putative, expressed	-0.25757	0.81185	0.199029	0.389432	1.531363	
LOC_Os10g42710	RCD1, putative, expressed	0.04682	0.856264	0.197557	0.051698	0.14	0.5074
LOC_Os04g35520	OsAPx7 - Stromal Ascorbate Peroxidase encoding gene 5,8, expressed	-0.56916	0.965237	0.194587	0.181532	0.113625	0.38605
LOC_Os07g48060	peroxidase precursor, putative, expressed	-0.32617	1.278839	0.193109	0.355389	-0.04315	0.20455
LOC_Os06g37070	expressed protein	-0.03137	1.005162	0.191886	0.270714	0.108875	
LOC_Os10g41838	F-box protein interaction domain containing protein, expressed	0.932503	0.894083	0.188818	0.005115	-0.29828	0.03475
LOC_Os06g40240	retrotransposon protein, putative, unclassified, expressed	1.919841	1.371946	0.180104			
LOC_Os01g48620	expressed protein	-0.47494	0.991977	0.178454	0.738433	-0.70741	
LOC_Os10g37160	transposon protein, putative, unclassified, expressed	0.065569	2.424127	0.175901	-0.04364	0.665913	1.3797
LOC_Os05g38520	60S ribosomal protein L36-2, putative, expressed	0.392614	0.830741	0.165846	0.235314	-0.26075	0.15055
LOC_Os10g41190	transporter family protein, putative, expressed	-0.13673	1.622247	0.15234	-0.14834	-1.98736	-0.33545
LOC_Os03g10100	transporter family protein, putative, expressed	-0.00542	1.53672	0.149307	0.174185	-0.20126	-1.46955
LOC_Os10g39710	strictosidine synthase, putative, expressed	-0.33354	1.567622	0.145574	0.645725	-0.30749	0.1142
LOC_Os12g01530	ferritin-1, chloroplast precursor, putative, expressed	0.578497	1.208198	0.127761	0.348227	1.8265	0.34695

LOC_Os11g34920	stripe rust resistance protein Yr10, putative, expressed	-0.05823	0.80677	0.124434	0.136032	-0.07119	0.13935
LOC_Os05g33580	expressed protein	0.144575	0.84638	0.11739	0.2226	-0.33205	-0.40475
LOC_Os03g59080	AMP-binding enzyme, putative, expressed	0.424125	0.85549	0.094652	-0.08367	0.423875	-0.00865
LOC_Os06g13390	SAM dependent carboxyl methyltransferase, putative, expressed	1.107522	1.887983	0.090444	0.089597	5.212725	
LOC_Os03g47280	VQ domain containing protein, putative, expressed	-0.29434	2.331807	0.090302	0.692421	2.440263	2.38675
LOC_Os12g13800	O-methyltransferase, putative, expressed	-0.17371	2.004835	0.090211	-0.05522	1.682625	
LOC_Os03g46070	thaumatin, putative, expressed	-0.28265	1.209647	0.077706	1.451168	5.047762	
LOC_Os03g62420	expressed protein	0.32336	0.856091	0.07758	-0.05128	0.48475	
LOC_Os08g07090	expressed protein	-0.05133	0.990826	0.070316			
LOC_Os06g40030	S-locus-like receptor protein kinase, putative, expressed	-0.05951	0.859538	0.070013	0.979238	-0.40216	1.3066
LOC_Os07g01960	hypothetical protein	1.318828	0.940819	0.060704			
LOC_Os01g58280	OsSub8 - Putative Subtilisin homologue, expressed	0.50634	0.912495	0.040221	2.000822	0.386	1.8865
LOC_Os03g04060	CHIT16 - Chitinase family protein precursor, expressed	-0.29093	1.012936	0.033708	1.032299	-0.30876	0.26405
LOC_Os09g28000	OsSigP6 - Putative Type I Signal Peptidase homologue; employs a putative Ser/Lys catalytic dyad, expressed	-0.20288	0.848405	0.008806	0.708869	0.697875	
LOC_Os08g07470	hypothetical protein	1.099379	1.70653	0.002787			
LOC_Os04g57730	uracil-DNA glycosylase, putative, expressed	0.404662	0.856585	-0.0176	0.031908	-0.30463	
LOC_Os02g18080	NB-ARC domain containing protein, expressed	-0.36652	0.975804	-0.01866	0.026415	-0.21979	
LOC_Os04g33440	DNA-binding protein S1FA, putative, expressed	0.366075	0.971709	-0.02068			
LOC_Os11g44390	retrotransposon protein, putative, Ty1-copia subclass, expressed	0.198537	1.514221	-0.02176			
LOC_Os05g50940	expressed protein	-0.10384	0.944208	-0.0237	0.1101	0.025013	
LOC_Os06g38970	expressed protein	-0.35112	1.253789	-0.03963	0.028584	1.539	-1.0568
LOC_Os11g07780	hypothetical protein	0.051251	0.854665	-0.03969			
LOC_Os04g09900	ent-kaurene synthase, chloroplast precursor, putative, expressed	-0.00479	1.821975	-0.04137	0.237114	2.1666	0.8574
LOC_Os11g25510	protein kinase domain containing protein, expressed	0.220726	0.90918	-0.04551	0.009272	-0.16424	1.62915
LOC_Os07g03200	phytosulfokines precursor, putative, expressed	0.149679	1.30029	-0.05178	0.948779	-0.31156	0.58545
LOC_Os04g02050	bifunctional 3-phosphoadenosine 5-phosphosulfate synthetase, putative, expressed	0.38245	0.925056	-0.0563	-0.23299	0.563375	0.3866
LOC_Os11g11970	expressed protein	-0.35672	1.146147	-0.05637			
LOC_Os03g16890	N-acetylglucosaminyltransferase, putative, expressed	1.57564	0.981103	-0.0605	-0.0341	0.204188	
LOC_Os11g30690	expressed protein	0.001253	1.369467	-0.06305			
LOC_Os07g45350	zinc finger, RING-type, putative, expressed	0.686882	1.160784	-0.08554	-0.31341	-0.52675	-0.30665
LOC_Os12g36250	retrotransposon protein, putative, Ty1-copia subclass, expressed	0.236499	0.962	-0.08726			

LOC_Os01g22370	peroxidase precursor, putative, expressed	0.014049	1.094006	-0.09211	0.693886	-0.2535	1.41475
LOC_Os02g04230	CGMC_MAPKCMGC_2.7 - CGMC includes CDA, MAPK, GSK3, and CLKC kinases, expressed	0.029934	1.0635	-0.09271	0.584453	0.650938	
LOC_Os08g03350	amino acid transporter, putative, expressed	0.049052	0.894679	-0.09731	1.399948	0.88625	1.5317
LOC_Os03g20380	CAMK_KIN1/SNF1/Nim1_like.2 - CAMK includes calcium/calmodulin dependent protein kinases, expressed	0.180244	1.575217	-0.09739	0.346332	0.007988	0.38025
LOC_Os12g10560	clathrin adaptor complex small chain domain containing protein, expressed	0.330111	1.064096	-0.1133	0.09276	0.684913	0.82545
LOC_Os02g13430	receptor-like protein kinase 5 precursor, putative, expressed	-0.34523	0.81309	-0.11722	-0.02805	0.0824	
LOC_Os02g37180	expressed protein	-0.23332	0.803831	-0.13071	1.190802	-0.57273	0.31015
LOC_Os12g16720	cytochrome P450 71A1, putative, expressed	0.018278	1.467189	-0.13188	2.2582	0.828163	1.01775
LOC_Os01g09800	BTBA1 - Bric-a-Brac, Tramtrack, Broad Complex BTB domain with Ankyrin repeat region, expressed	0.602012	3.403062	-0.14062	1.013809	0.65975	
LOC_Os12g42884	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase, putative, expressed	0.544896	1.379718	-0.14124	-0.24333	0.5925	-0.08745
LOC_Os01g18800	CAMK_KIN1/SNF1/Nim1_like.9 - CAMK includes calcium/calmodulin dependent protein kinases, expressed	0.610288	1.656666	-0.14637	0.056477	-0.61825	0.33735
LOC_Os10g34940	expressed protein	1.071994	1.38556	-0.15089	0.086128	-0.06356	-0.5057
LOC_Os08g33740	CSLA11 - cellulose synthase-like family A, expressed	-0.21737	1.511318	-0.15232	2.44081	0.11905	
LOC_Os06g38110	expressed protein	0.518951	0.944784	-0.15453	0.250105	0.783225	
LOC_Os03g21450	bromodomain domain containing protein, expressed	0.939522	1.198147	-0.17603			
LOC_Os03g27960	sodium/calcium exchanger protein, putative, expressed	0.169251	0.956355	-0.17963	0.170158	0.67655	0.2142
LOC_Os09g29930	transcription factor BIM2, putative, expressed	0.494588	0.90453	-0.18447	0.022334	0.5413	-0.0012
LOC_Os04g50790	RNA recognition motif, putative, expressed	0.517584	1.008444	-0.20382	0.461579	1.128363	
LOC_Os10g35770	E2F-related protein, putative, expressed	-0.14211	1.143848	-0.20575	-0.68924	1.518038	1.11
LOC_Os11g09900	expressed protein	0.788367	1.062645	-0.22458	-0.13193	0.002525	
LOC_Os01g64780	COV1, putative, expressed	0.1875	0.836655	-0.22588	0.054963	0.1975	
LOC_Os02g30070	expressed protein	0.209474	0.890075	-0.22634			
LOC_Os10g40740	helix-loop-helix DNA-binding domain containing protein, expressed	0.992924	1.12691	-0.22791	-0.36307	-1.77799	
LOC_Os08g10460	retrotransposon protein, putative, unclassified, expressed	0.829885	1.241416	-0.22964			
LOC_Os06g12120	BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1 precursor, putative, expressed	-0.17064	0.982091	-0.24368	0.586526	-0.53803	0.5637

LOC_Os11g48030	skp1 family, tetramerisation domain containing protein, expressed	1.03037	0.866145	-0.25868			-0.25205
LOC_Os05g21180	phosphatidic acid phosphatase-related, putative, expressed	-0.04158	1.193427	-0.27326	0.639835	0.909925	1.50625
LOC_Os05g10930	OsGrx_C15 - glutaredoxin subgroup III, expressed	-0.27119	0.861877	-0.27403	0.033054	-0.76391	
LOC_Os09g31180	ribosomal protein L6, putative, expressed	0.653113	1.003725	-0.27667	0.281798	-0.25125	
LOC_Os08g05480	OsFBX261 - F-box domain containing protein, expressed	-0.4005	0.834846	-0.28147	0.778569	-1.19444	2.6675
LOC_Os12g11410	retrotransposon protein, putative, LINE subclass, expressed	0.181072	0.981873	-0.29539			
LOC_Os11g12320	disease resistance protein RPM1, putative, expressed	0.814494	0.845938	-0.29987			
LOC_Os06g47790	hypothetical protein	-0.26	1.097089	-0.3111			
LOC_Os11g41640	helix-loop-helix DNA-binding domain containing protein, expressed	0.422971	0.820754	-0.31563			
LOC_Os09g39540	40S ribosomal protein S25, putative, expressed	0.393994	0.907492	-0.35488	0.126288	-0.126	-0.0918
LOC_Os05g46430	60S ribosomal protein L28-1, putative, expressed	0.86141	0.993909	-0.36429	0.194403	-0.09875	-0.31085
LOC_Os08g42760	methyltransferase domain containing protein, expressed	0.459036	0.870726	-0.36606	-0.0855	-0.34428	-0.63445
LOC_Os11g23080	retrotransposon protein, putative, unclassified, expressed	0.262367	1.010006	-0.36828			0.3105
LOC_Os04g54200	diacylglycerol kinase, putative, expressed	-0.31537	0.819092	-0.38319	0.223355	2.334363	0.34755
LOC_Os05g11780	mitochondrial carrier protein, putative, expressed	0.317856	0.978359	-0.38368	-0.00799	0.551	0.203
LOC_Os01g53770	expressed protein	0.793173	1.367017	-0.38774	0.007046	0.03975	0.54465
LOC_Os02g06200	phytosulfokine receptor precursor, putative, expressed	-0.23775	0.963097	-0.4035			
LOC_Os12g02630	cytochrome P450 72A1, putative, expressed	0.636741	0.891183	-0.41761	-0.02864	0.576725	0.5624
LOC_Os07g48430	nucleoside-triphosphatase, putative, expressed	0.011404	0.825611	-0.41889	0.258704	0.985125	0.5101
LOC_Os01g01660	isoflavone reductase, putative, expressed	0.357105	0.907572	-0.42496			0.43165
LOC_Os08g31630	uncharacterized glycosyl hydrolase Rv2006/MT2062, putative, expressed	0.349091	0.948004	-0.43089	-0.36445	-1.3734	
LOC_Os11g27470	expressed protein	0.336224	0.810269	-0.43192			
LOC_Os03g09840	C2 domain containing protein, putative, expressed	-0.15963	1.209152	-0.43786	-0.03411	-0.45338	
LOC_Os08g24770	protein kinase, putative, expressed	-0.1905	0.808784	-0.43984	0.119215	0.324788	
LOC_Os03g18590	malonyl CoA-acyl carrier protein transacylase, mitochondrial precursor, putative, expressed	0.351416	0.964893	-0.44108	-0.13675	-1.08286	-0.25845
LOC_Os08g44450	L1P family of ribosomal proteins domain containing protein, expressed	0.568743	0.939071	-0.44478	0.045145	-0.25238	-0.0618
LOC_Os05g45410	HSF-type DNA-binding domain containing protein, expressed	0.021431	1.022224	-0.4558	1.27458	1.556725	2.2887

LOC_Os08g42910	peptidase, M24 family protein, putative, expressed	-0.13001	1.194551	-0.45691	0.116872	0.559125	
LOC_Os01g45250	DUF1645 domain containing protein, putative, expressed	-0.16	1.177335	-0.45929	1.190503	1.65775	
LOC_Os01g47420	pterin-4-alpha-carbinolamine dehydratase, putative, expressed	0.80168	0.853765	-0.4842	0.140474	-0.22623	0.29945
LOC_Os04g16780	hypothetical protein	0.458576	1.413518	-0.49487			0.5908
LOC_Os01g03100	protein binding protein, putative, expressed	0.141046	0.809181	-0.50467			-0.34325
LOC_Os09g04310	expressed protein	0.489907	0.869788	-0.51495	0.666936	1.211788	1.8719
LOC_Os08g33920	60S ribosomal protein L34, putative, expressed	0.697323	1.088552	-0.51768	0.174417	-0.116	-0.1015
LOC_Os03g63400	transcription factor BTF3, putative, expressed	0.785985	1.038759	-0.52127	-0.02628	0.8548	-0.4193
LOC_Os08g41300	60S ribosomal protein L32, putative, expressed	0.467819	0.815883	-0.53093	0.192694	-0.03763	
LOC_Os10g20910	40S ribosomal protein S23, putative	0.699975	0.887183	-0.53508			
LOC_Os05g46830	proline-rich protein, putative, expressed	-0.23184	1.341589	-0.5424	0.067859	1.564138	2.46675
LOC_Os11g40320	expressed protein	0.349056	0.825271	-0.54896			
LOC_Os08g05530	LSM domain containing protein, expressed	0.537188	0.962806	-0.55309	0.104619	-0.215	-0.33355
LOC_Os02g32520	ERD1 protein, chloroplast precursor, putative, expressed	-0.08501	0.881185	-0.56084	1.547589	2.486875	1.9809
LOC_Os10g35920	OsFBX389 - F-box domain containing protein, expressed	-0.13792	1.031605	-0.5682	0.583063	0.239625	0.1726
LOC_Os01g62430	C2 domain containing protein, putative, expressed	-0.29593	0.992829	-0.5741	2.030325	2.347925	
LOC_Os11g07280	coatamer subunit beta-1, putative, expressed	0.340602	0.966965	-0.57603	0.121668	0.801625	
LOC_Os02g48030	expressed protein	-0.13645	0.986382	-0.58061			
LOC_Os06g06760	protein kinase, putative, expressed	-0.12825	0.976154	-0.59279	0.77159	-0.515	-0.1646
LOC_Os09g15420	NAD dependent epimerase/dehydratase family protein, putative, expressed	0.092497	1.158289	-0.59332	0.257708	2.370713	1.83845
LOC_Os04g49757	purine permease, putative, expressed	0.617191	1.166246	-0.61023	0.676582	-1.16581	0.388
LOC_Os04g27020	cytochrome P450, putative, expressed	0.047259	2.27759	-0.61485	0.629121	0.4977	
LOC_Os10g41410	nucleoside diphosphate kinase, putative, expressed	0.207868	1.210656	-0.62351	1.389964	0.14325	-0.22565
LOC_Os08g17784	purple acid phosphatase, putative, expressed	0.416011	1.011075	-0.62441	-0.19014	-0.09669	-0.09855
LOC_Os04g22720	expressed protein	0.145743	0.967069	-0.63247	-0.03504	0.134525	0.107
LOC_Os09g24690	60S ribosomal protein L34, putative, expressed	0.821378	0.923766	-0.63807	0.092311	-0.078	-0.199
LOC_Os07g33910	transporter family protein, putative, expressed	0.975399	0.899675	-0.64215	-0.70319	0.907875	0.17375
LOC_Os02g03400	microtubule associated protein, putative, expressed	0.725835	1.033361	-0.64373	0.036009	-0.02354	0.50255
LOC_Os05g48220	60S ribosomal protein L35a-3, putative, expressed	0.568089	1.104001	-0.66322	0.040336	0.192013	-0.8111
LOC_Os08g24780	hypothetical protein	0.939827	1.561257	-0.67731			
LOC_Os11g31960	hypothetical protein	0.172582	0.836706	-0.68384			
LOC_Os11g29014	retrotransposon protein, putative, unclassified, expressed	0.773511	0.906192	-0.69406			

LOC_Os02g03710	UP-9A, putative, expressed	0.795204	0.907471	-0.71385	1.427998	0.011088	1.2943
LOC_Os07g45340	expressed protein	1.579777	1.535197	-0.71771			
LOC_Os11g28910	transposon protein, putative, CACTA, En/Spm sub-class, expressed	0.756482	0.839797	-0.74493	0.08992	0.258575	
LOC_Os10g40080	expressed protein	0.623923	0.830665	-0.75885			
LOC_Os09g11460	AP2 domain containing protein, expressed	0.539806	1.274692	-0.79289	-0.05673	0.73315	0.0576
LOC_Os04g39320	expressed protein	0.737449	1.126122	-0.8303	1.795706	1.807063	1.44965
LOC_Os05g11710	ribosomal protein L5, putative, expressed	0.658685	1.216823	-0.84018	0.190448	0.372	
LOC_Os11g44870	expressed protein	-0.08178	0.900852	-0.8517	-0.07349	-0.4875	1.313
LOC_Os05g48320	60S ribosomal protein L37a, putative, expressed	1.018265	0.827976	-0.89178	0.113323	-0.109	-0.5055
LOC_Os08g20010	expressed protein	0.616284	1.134932	-0.91882			
LOC_Os05g08360	rRNA 2-O-methyltransferase fibrillarin 2, putative, expressed	0.814896	1.114097	-0.9797	0.376706	-0.17776	
LOC_Os11g23180	hypothetical protein	0.834672	1.190009	-1.00164			
LOC_Os08g17760	expressed protein	0.627955	0.921569	-1.03155			
LOC_Os11g46950	wall-associated receptor kinase-like 18 precursor, putative, expressed	-0.11669	0.865413	-1.04704	-0.12548	0.056238	
LOC_Os02g05370	retrotransposon protein, putative, Ty3-gypsy subclass, expressed	0.402893	0.85194	-1.07973			
LOC_Os02g11870	expressed protein	-0.06684	1.097439	-1.08248	0.844755	2.32635	4.13655
LOC_Os10g35450	serine/threonine-protein kinase, putative, expressed	0.56968	0.965738	-1.17005	-0.49038	-0.34683	-0.6278
LOC_Os02g27480	membrane attack complex component/perforin/complement C9, putative, expressed	0.054664	0.847496	-1.20102	0.06561	0.325275	1.9167
LOC_Os08g24190	OsFBX286 - F-box domain containing protein, expressed	1.075303	0.984956	-1.31262	-0.07762	0.975625	
LOC_Os04g40630	BTBZ4 - Bric-a-Brac, Tramtrack, Broad Complex BTB domain with TAZ zinc finger and Calmodulin-binding domains, expressed	1.218921	1.31717	-1.3625	-0.46337	1.187875	2.96815
LOC_Os11g36510	retrotransposon protein, putative, unclassified, expressed	1.221531	1.316739	-1.39647	0.389854	0.567038	
LOC_Os05g50380	glucose-1-phosphate adenylyltransferase large subunit, chloroplast precursor, putative, expressed	0.581913	1.038034	-1.45629	-0.15622	2.4029	-0.5485
LOC_Os08g23960	OsFBL46 - F-box domain and LRR containing protein, expressed	0.74187	1.097278	-1.49533	-0.032	-0.05131	
LOC_Os03g56160	lectin-like receptor kinase 7, putative, expressed	-0.45436	1.613115	-1.55169	0.8599	0.85475	
LOC_Os08g19200	expressed protein	0.864661	1.090907	-1.6212			
LOC_Os08g35160	heat shock protein DnaJ, putative, expressed	0.333641	1.991116	-1.84475	0.934194	-0.64553	0.05065
LOC_Os01g65610	expressed protein	0.470391	0.120046	3.104297			
LOC_Os07g32710	retrotransposon protein, putative, unclassified, expressed	2.366842	0.460799	3.02609	0.03042	0.130313	0.63045
LOC_Os02g41680	phenylalanine ammonia-lyase, putative, expressed	-0.08075	0.469767	2.752294	0.605036	-0.784	3.60465
LOC_Os03g52390	PIII1 - Proteinase inhibitor II family protein precursor, expressed	0.230628	0.591478	2.455296	1.283272	2.066	2.4384

LOC_Os04g02490	expressed protein	0.25447	0.202314	2.380529	-0.06247	0.628363	
LOC_Os01g10890	CAMK_KIN1/SNF1/Nim1_like.8 - CAMK includes calcium/calmodulin dependent protein kinases, expressed	0.159278	0.008341	2.325187	-1.12806	-2.08753	
LOC_Os01g17396	expressed protein	-0.07005	-0.15031	2.183089	-0.0582	0.07315	0.1159
LOC_Os07g18990	LTPL40 - Protease inhibitor/seed storage/LTP family protein precursor, expressed	-0.22407	-0.33285	2.164805	-0.38161	-1.30263	0.7675
LOC_Os06g05230	retrotransposon protein, putative, unclassified, expressed	0.091616	0.316795	2.159462			
LOC_Os04g31120	OsFBK14 - F-box domain and kelch repeat containing protein, expressed	-0.4348	-0.57179	2.109069	0.755325	-0.24233	
LOC_Os03g60580	actin-depolymerizing factor, putative, expressed	0.309457	-0.25407	2.013691	0.239195	0.573875	
LOC_Os08g33710	ribonuclease T2 family domain containing protein, expressed	0.141643	0.123274	1.99959	-0.825	-0.47701	0.15635
LOC_Os06g51060	CHIT8 - Chitinase family protein precursor, expressed	0.022889	-0.1662	1.999407	1.16594	1.0355	1.2868
LOC_Os03g57880	glucan endo-1,3-beta-glucosidase precursor, putative, expressed	0.285945	0.034413	1.975122	-0.39709	1.774225	
LOC_Os08g06110	MYB family transcription factor, putative, expressed	-0.37638	-0.1035	1.942447	-0.24468	-0.95353	-0.17155
LOC_Os04g46880	transporter, major facilitator family, putative, expressed	-0.1387	0.364692	1.908629	-0.16371	-0.86968	2.07555
LOC_Os08g39140	heat shock protein, putative, expressed	-0.57939	0.006477	1.851955	-0.05243	0.817625	-0.5244
LOC_Os03g13540	Ser/Thr protein phosphatase family protein, putative, expressed	-0.23539	0.261718	1.837805	-1.66641	1.912375	1.06805
LOC_Os12g38660	expressed protein	0.700296	0.327909	1.823683	-0.48384	-0.67675	-0.3479
LOC_Os01g55540	aminotransferase, classes I and II, domain containing protein, expressed	-0.41636	0.276277	1.802218	0.043507	0.942375	-0.288
LOC_Os01g09570	6-phosphofructokinase, putative, expressed	-0.53747	0.003369	1.774486	-0.11409	0.32325	
LOC_Os05g04610	ABC transporter, ATP-binding protein, putative, expressed	-0.31227	-0.33239	1.738652	-0.6838	-2.72748	1.24895
LOC_Os03g48190	expressed protein	0.239911	-0.0995	1.72994	0.246745	-0.68351	0.11565
LOC_Os03g12290	glutamine synthetase, catalytic domain containing protein, expressed	-0.06426	0.288342	1.722727	0.189553	-0.528	
LOC_Os03g39760	cytochrome P450, putative, expressed	-0.13983	-0.0365	1.712995	0.030716	-3.26888	0.86205
LOC_Os03g37840	potassium transporter, putative, expressed	-0.5234	0.5539	1.712992	0.41608	-1.66333	0.38685
LOC_Os01g31100	retrotransposon, putative, centromere-specific	0.340402	-0.14551	1.698301			
LOC_Os03g49630	expressed protein	-0.29505	-0.01083	1.69613	0.277418	-2.46779	0.29455
LOC_Os03g52370	PIII4 - Proteinase inhibitor II family protein precursor, expressed	-0.03898	0.065326	1.676255	0.361409	0.537638	1.3359
LOC_Os02g57060	OsCttP2 - Putative C-terminal processing peptidase homologue, expressed	-0.15097	-0.14081	1.669211	-0.08294	-1.23544	-0.1757
LOC_Os05g50840	mitochondrial carrier protein, putative, expressed	-0.14442	-0.07275	1.664499	0.203986	-0.00413	

LOC_Os03g05290	aquaporin protein, putative, expressed	0.117806	-0.4643	1.649945	-0.79695	0.18525	
LOC_Os06g01760	ligA, putative, expressed	-0.43976	-0.45435	1.649658	-0.15805	-0.775	
LOC_Os04g58710	AMP-binding domain containing protein, expressed	0.580699	-0.07495	1.646555	1.463947	-0.10675	0.8732
LOC_Os03g55240	cytochrome P450, putative, expressed	-0.07001	-0.33214	1.64239	0.099796	-0.31638	0.52395
LOC_Os01g52230	phosphoethanolamine/phosphocholine phosphatase, putative, expressed	0.307707	0.16564	1.630064	-2.15971	0.68415	1.4454
LOC_Os11g36180	receptor kinase, putative, expressed	-0.40071	-0.02072	1.623519			
LOC_Os08g14950	receptor-like protein kinase 2 precursor, putative, expressed	-0.00724	-0.1331	1.604925			
LOC_Os07g42250	strictosidine synthase, putative, expressed	-0.29293	-0.22317	1.60161	-0.21389	-1.88511	-0.0833
LOC_Os01g04920	glycosyl transferase, group 1 domain containing protein, expressed	-0.42365	0.496614	1.591279	-1.73096	-1.63008	-1.49295
LOC_Os06g21890	basic proline-rich protein precursor, putative, expressed	-0.28882	0.199713	1.578644	0.077735	-0.15604	0.6951
LOC_Os06g03860	uncharacterized membrane protein, putative, expressed	0.219387	-0.24087	1.576973	-0.28168	0.111275	
LOC_Os07g43940	X8 domain containing protein, expressed	-0.08947	-0.07741	1.575404	-0.17198	-0.39713	-0.0486
LOC_Os11g08670	NAD kinase, putative, expressed	-0.47924	-0.41816	1.569675	0.224285	-0.62188	0.04455
LOC_Os03g19290	mitochondrial import inner membrane translocase subunit Tim17, putative, expressed	0.020656	-0.29482	1.565506	0.149452	-0.19608	-0.6073
LOC_Os01g56360	wax synthase, putative, expressed	0.019516	-0.27605	1.559191	-0.1878	-1.33109	
LOC_Os03g52170	4-hydroxy-3-methylbut-2-enyl diphosphate reductase, putative, expressed	-0.25606	0.208098	1.558048	-0.52021	-0.033	
LOC_Os08g34210	aldehyde dehydrogenase, putative, expressed	-0.12576	-0.42752	1.545683	-0.27298	-1.59188	-0.22315
LOC_Os02g54140	hsp20/alpha crystallin family protein, putative, expressed	-0.04761	-0.26412	1.542395	-1.03339	-1.23978	0.0633
LOC_Os01g62840	mannose-1-phosphate guanylttransferase, putative, expressed	-0.27282	-0.04399	1.540741	0.508205	-0.15783	0.15685
LOC_Os01g07370	KIP1, putative, expressed	-0.38016	0.565146	1.54032	0.762761	0.480625	-0.6225
LOC_Os02g58100	expressed protein	0.249995	-0.03633	1.535223	-0.2254	-1.115	
LOC_Os09g38070	expressed protein	-0.47433	-0.72867	1.524207	-0.51424	-0.63388	0.4403
LOC_Os01g08560	DnaK family protein, putative, expressed	-0.4394	0.222786	1.513481	-0.25983	0.203038	-0.13045
LOC_Os04g45360	retrotransposon protein, putative, unclassified, expressed	-0.46935	-0.86578	1.510922			
LOC_Os04g54230	wound induced protein, putative, expressed	-0.3721	-0.30099	1.501586	0.008147	0.4178	0.88065
LOC_Os01g15900	expressed protein	-0.22287	-0.22212	1.496699	0.831606	-0.54308	0.243
LOC_Os01g45460	serine esterase, putative, expressed	-0.01954	-0.09801	1.486874	-0.11684	-0.08374	0.40295
LOC_Os11g43860	sodium/calcium exchanger protein, putative, expressed	-0.29585	0.520314	1.480552	0.459985	0.08165	0.3121
LOC_Os09g06499	sulfate transporter 4.1, chloroplast precursor, putative, expressed	-0.49266	-0.06766	1.47355	-0.11393	-0.26435	0.07215
LOC_Os06g05630	GDSL-like lipase/acylhydrolase, putative, expressed	0.563935	-0.22254	1.464149	-0.71512	-1.1426	0.06435

LOC_Os01g71340	glycosyl hydrolases family 17, putative, expressed	-0.29051	0.305427	1.457615	0.61339	4.36325	1.1184
LOC_Os07g37560	myosin-Vb, putative, expressed	0.021894	0.168476	1.451504	-0.10787	-0.20688	
LOC_Os12g32760	transporter family protein, putative, expressed	-0.17724	-0.20521	1.43865	0.052844	-0.21798	
LOC_Os12g43340	actin-depolymerizing factor, putative, expressed	0.235272	0.287315	1.434862	-0.44723	-0.8392	
LOC_Os03g43870	expressed protein	-0.00237	-0.75916	1.430551			
LOC_Os08g14940	receptor kinase, putative, expressed	-0.10012	0.398548	1.426802	-0.03314	-0.34788	
LOC_Os02g31030	glycerophosphoryl diester phosphodiesterase family protein, putative, expressed	0.415283	0.412523	1.426115	-1.85783	-0.29829	2.62115
LOC_Os02g29510	DUF803 domain containing, putative, expressed	0.166694	0.183054	1.423737	-0.19935	-1.16695	-0.55855
LOC_Os03g43720	transporter family protein, putative, expressed	0.119785	-0.02671	1.423368	-0.14075	0.336963	0.21255
LOC_Os04g46960	glutathione peroxidase domain containing protein, expressed	-0.03305	0.131359	1.412068	0.387975	0.459375	0.40885
LOC_Os03g21890	potassium transporter, putative, expressed	-0.19303	-0.09029	1.410098	-0.19149	-0.4482	
LOC_Os01g14900	glycerol-3-phosphate acyltransferase, putative, expressed	0.11633	0.130731	1.40459	-0.00518	0.242525	
LOC_Os03g08430	SAC domain containing protein, putative, expressed	-0.22198	-0.14205	1.403178	-0.07642	0.337313	1.55945
LOC_Os05g41930	N-rich protein, putative, expressed	-0.5814	-0.4815	1.393921	-0.01852	-0.17213	-0.0705
LOC_Os12g31850	ureide permease, putative, expressed	0.237948	-0.68813	1.387038	-0.11175	0.505075	0.60795
LOC_Os04g23890	AGC_PVPK_like_kin82y.10 - ACG kinases include homologs to PKA, PKG and PKC, expressed	-0.43627	-0.563	1.38335	-0.01447	-1.83238	0.1493
LOC_Os03g20730	chaperone protein dnaJ, putative, expressed	-0.2423	-0.16449	1.383296	1.308946	-0.45438	0.0888
LOC_Os04g54300	wound induced protein, putative, expressed	0.057619	-0.2692	1.382769	0.397519	0.66075	
LOC_Os03g17800	phosphatidylinositol transfer protein alpha isoform, putative, expressed	-0.08126	0.197204	1.371122	-1.16267	0.371613	0.0953
LOC_Os01g67320	expressed protein	0.227811	0.015442	1.366539	0.105538	-1.24725	0.194
LOC_Os02g42940	MSP domain containing protein, expressed	-0.18089	-0.0881	1.363976	-0.11135	-0.4437	0.59285
LOC_Os03g43100	expressed protein	0.962316	0.447866	1.359162	4.370815	0.016788	-0.31555
LOC_Os09g09930	heavy metal transport/detoxification protein, putative, expressed	-0.02987	-0.12745	1.355495	-0.24259	-1.8946	0.0623
LOC_Os03g03510	CAMK_KIN1/SNF1/Nim1_like.15 - CAMK includes calcium/calmodulin dependent protein kinases, expressed	0.315179	-0.21288	1.353872	0.02246	0.057588	
LOC_Os01g62810	regulator of chromosome condensation, putative, expressed	0.480613	0.16726	1.349774	0.002758	0.553313	-0.44225
LOC_Os08g29720	mitochondrial carrier protein, putative, expressed	-0.28508	0.59744	1.346159	0.214802	-0.14433	-0.2947
LOC_Os04g35840	T-complex protein 11, putative, expressed	-0.38842	0.111143	1.345561	-0.0359	0.2115	-0.48625
LOC_Os08g02860	transposon protein, putative, unclassified, expressed	-0.01801	0.034977	1.343484	0.074998	-0.27975	1.1677

LOC_Os10g41780	chlorophyllide a oxygenase, chloroplast precursor, putative, expressed	0.055264	-0.22434	1.340079	-0.83212	-1.60838	
LOC_Os06g13560	SAM dependent carboxyl methyltransferase, putative, expressed	0.112941	0.511587	1.339616	0.803892	4.82265	0.0075
LOC_Os07g35510	glucan endo-1,3-beta-glucosidase precursor, putative, expressed	-0.56113	-0.29182	1.334085	0.546757	1.568875	-0.00225
LOC_Os01g28770	hypothetical protein	-0.15015	-0.19693	1.332129			
LOC_Os05g30250	Os5bglu19 - beta-glucosidase homologue, similar to G. max isohydroxyurate hydrolase, expressed	0.071367	0.087921	1.32999	-0.14677	-1.63395	0.9521
LOC_Os07g22690	expressed protein	0.12094	-0.21474	1.322673			
LOC_Os01g09320	NADP-dependent malic enzyme, chloroplast precursor, putative, expressed	0.09046	0.424401	1.32228	-0.23099	-0.14514	
LOC_Os04g48860	hypothetical protein	-0.03147	0.162068	1.322139	-0.70628	-1.67025	-0.4471
LOC_Os02g03860	mitochondrial ATP synthase precursor, putative, expressed	-0.43355	-0.13614	1.322057	-0.04703	0.27	-0.061
LOC_Os04g23440	helix-loop-helix DNA-binding domain containing protein, expressed	-0.56276	0.30396	1.320267			
LOC_Os08g33750	myb-like DNA-binding domain containing protein, expressed	-0.37054	-0.06583	1.317998	-0.27326	-0.98398	-0.0077
LOC_Os03g06240	YT521-B-like family domain containing protein, expressed	-0.58694	0.243364	1.316985	-0.08421	-0.40175	-0.0477
LOC_Os01g22010	S-adenosylmethionine synthetase, putative, expressed	-0.06022	0.411495	1.314552	0.395094	0.426625	0.26425
LOC_Os09g30414	aspartic proteinase nepenthesin-2 precursor, putative, expressed	0.032302	-0.45264	1.311794	0.119275	-0.0715	1.7456
LOC_Os04g58110	pyruvate kinase, putative, expressed	-0.511	0.09382	1.304513	-0.22783	0.33375	0.1368
LOC_Os02g04710	cycloartenol synthase, putative, expressed	0.18135	0.378945	1.293952	-0.17863	-0.26063	
LOC_Os01g11240	DUF538 domain containing protein, putative, expressed	0.289558	-0.12975	1.293233	-0.23991	-0.08825	0.3005
LOC_Os10g22430	gibberellin response modulator protein, putative, expressed	-0.19887	-0.29667	1.289106	0.02698	-0.15163	0.1432
LOC_Os09g06464	CCT/B-box zinc finger protein, putative, expressed	0.289411	0.009049	1.283868	-0.36088	-0.9599	
LOC_Os10g35560	expressed protein	-0.39459	0.074125	1.277643	0.099433	0.20225	0.2122
LOC_Os08g30790	hypersensitive-induced response protein, putative, expressed	-0.50303	-0.47608	1.275392	-0.01632	-0.42965	0.19765
LOC_Os03g09020	dehydrogenase, putative, expressed	-0.25692	-0.27869	1.271753	0.523695	0.081625	1.74675
LOC_Os03g49050	possible lysine decarboxylase domain containing protein, expressed	0.242084	0.029849	1.271703	-0.21973	0.045113	
LOC_Os01g14410	early light-induced protein, chloroplast precursor, putative, expressed	-0.23578	0.001652	1.270832	-0.38573	-1.97991	0.2953
LOC_Os09g36620	hypothetical protein	-0.24041	-0.32582	1.269612			
LOC_Os06g39900	agenet domain containing protein, putative, expressed	-0.12052	-0.38212	1.269401	-0.39862	-0.48971	0.13125
LOC_Os05g51370	hypothetical protein	-0.06281	0.105053	1.264357			
LOC_Os12g22510	retrotransposon protein, putative, Ty3-gypsy subclass	-0.09809	-0.08304	1.264134			

LOC_Os02g01060	harpin-induced protein 1 domain containing protein, expressed	-0.44587	0.06355	1.260665	-0.40334	-0.78301	-0.31735
LOC_Os11g41150	nitrilase-associated protein, putative, expressed	0.234155	-0.18725	1.259466	-0.75189	2.310488	-0.47235
LOC_Os03g59320	expressed protein	-0.09846	0.057192	1.259103	-0.16604	0.78825	1.61625
LOC_Os12g37650	DUF538 domain containing protein, putative, expressed	-0.10336	-0.43799	1.258531	0.006814	-1.63746	-0.49895
LOC_Os07g48160	alpha-galactosidase precursor, putative, expressed	-0.08042	-0.1902	1.256744	-0.33812	1.25815	
LOC_Os01g63380	transposon protein, putative, unclassified, expressed	0.325032	0.238514	1.25066			
LOC_Os02g57790	ZOS2-19 - C2H2 zinc finger protein, expressed	-0.0853	-0.14267	1.250554			
LOC_Os12g03060	expressed protein	-0.36405	-0.4763	1.243288	0.075722	0.58375	0.09805
LOC_Os01g56780	plus-3 domain containing protein, expressed	-0.37727	0.35635	1.239628	-0.2439	-0.59638	-0.36155
LOC_Os10g31640	glycine-rich cell wall structural protein 2 precursor, putative, expressed	0.341043	-0.26132	1.237072	-0.13426	0.0063	
LOC_Os12g04020	hydroxymethylglutaryl-CoA lyase, putative, expressed	-0.4664	-0.17888	1.233948	-0.18859	0.67025	1.6773
LOC_Os02g16040	ubiquitin-conjugating enzyme, putative, expressed	0.042054	0.244525	1.232284	0.024861	1.393125	
LOC_Os01g12810	retrotransposon protein, putative, unclassified, expressed	0.154694	0.294055	1.2313	0.276908	-1.74551	0.04975
LOC_Os03g42810	endonuclease/exonuclease/phosphatase family domain containing protein, expressed	0.500267	0.310071	1.230129	0.070647	1.68855	
LOC_Os01g68330	antigen peptide transporter-like 1, chloroplast precursor, putative, expressed	-0.03351	-0.62467	1.228882	-0.34221	0.13445	0.4354
LOC_Os06g45350	protein kinase domain containing protein, expressed	0.047958	0.314365	1.226662	-0.433	1.447375	-0.2465
LOC_Os07g39900	interferon-related developmental regulator, putative, expressed	-0.39919	-0.17935	1.226136	-0.55571	0.353375	-0.4126
LOC_Os06g40120	SPX domain containing protein, putative, expressed	-0.35321	0.316101	1.221792	-0.26056	-0.83714	0.1464
LOC_Os01g18080	retrotransposon protein, putative, unclassified, expressed	-0.29719	-0.53398	1.221785	0.534189	1.18875	0.4055
LOC_Os05g50500	secretory protein, putative, expressed	-0.17277	-0.22007	1.220852	-0.13186	-0.64946	
LOC_Os07g48630	ethylene-insensitive 3, putative, expressed	-0.50258	-0.21481	1.220723	1.046094	0.911375	1.56175
LOC_Os01g58640	nucleotide pyrophosphatase/phosphodiesterase, putative, expressed	-0.31399	0.033456	1.219181	-1.25104	-1.26933	-0.69095
LOC_Os06g18990	embryogenesis transmembrane protein, putative, expressed	-0.27091	-0.07965	1.217188	-0.24976	-0.34878	0.22385
LOC_Os01g47630	expressed protein	-0.29105	0.140064	1.216656	-0.26661	-0.63484	
LOC_Os03g31230	MYB family transcription factor, putative, expressed	-0.55293	-0.30742	1.215568	-0.13181	-0.0502	0.54205
LOC_Os08g39150	expressed protein	-0.41377	0.320661	1.213102	-0.32646	0.110375	0.2091
LOC_Os03g61090	expressed protein	0.048187	-0.49068	1.210753	0.078606	-2.35795	
LOC_Os02g44870	dehydrin, putative, expressed	0.181634	-0.19167	1.206707	0.035625	-0.15905	-0.01905
LOC_Os12g09480	retrotransposon protein, putative, Ty3-gypsy subclass, expressed	-0.37801	-0.08338	1.206474			

LOC_Os02g36490	expressed protein	0.328013	0.050174	1.20632	0.610348	0.39645	
LOC_Os12g29520	auxin response factor, putative, expressed	-0.53621	-0.42738	1.205519	0.132073	-0.07775	
LOC_Os12g44230	expressed protein	-0.51668	0.325442	1.20443	0.348358	-0.17848	-0.0803
LOC_Os04g31390	vacuolar protein sorting-associated protein 11, putative, expressed	0.384655	0.106093	1.203065	0.02966	0.034625	0.30625
LOC_Os09g02270	cyclase family protein, putative, expressed	0.986741	-0.50003	1.199572	0.160669	0.315013	1.70195
LOC_Os07g02340	expressed protein	0.120101	0.211513	1.195652	-0.249	0.470875	0.3318
LOC_Os01g13390	expressed protein	0.806562	0.578907	1.19308	-0.56324	-2.34364	
LOC_Os02g48720	mitochondrial carrier protein, putative, expressed	-0.2503	0.307055	1.192688	0.116405	1.550125	-0.01725
LOC_Os06g28630	expressed protein	-0.26872	-0.51383	1.187432	-0.22798	-0.13634	-0.1547
LOC_Os03g62240	expressed protein	-0.19563	-0.04657	1.183856	-0.23968	-1.12611	0.0731
LOC_Os05g39700	hypothetical protein	-0.30074	-0.03064	1.18192			
LOC_Os03g63580	phosphoesterase family protein, putative, expressed	-0.17846	-0.04959	1.180262	-0.41344	#####	
LOC_Os06g49120	Complex I intermediate-associated protein 30 domain containing protein, putative, expressed	-0.30772	-0.84889	1.179567	0.221483	-2.39248	
LOC_Os04g13140	vignain precursor, putative, expressed	-0.03917	0.047869	1.178027	-0.00341	0.049675	
LOC_Os03g27310	histone H3, putative, expressed	-0.39507	0.04916	1.176369	-0.04195	0.134625	0.0209
LOC_Os11g06010	helix-loop-helix DNA-binding protein, putative, expressed	-0.26898	-0.12246	1.173904	-0.04048	0.396475	-0.8507
LOC_Os01g60830	expressed protein	0.897806	0.570377	1.170648	-0.66755	-1.74385	
LOC_Os07g44060	haloacid dehalogenase-like hydrolase family protein, putative, expressed	0.433766	0.456103	1.170408	-0.31247	0.295663	
LOC_Os03g19240	AMP-binding enzyme, putative, expressed	-0.23764	-0.00225	1.168932	-0.16444	-0.875	
LOC_Os01g53930	hexokinase, putative, expressed	0.044709	-0.2552	1.164149	-0.45172	-0.32461	
LOC_Os05g02020	protein kinase APK1A, chloroplast precursor, putative, expressed	-0.42971	-0.58317	1.163681	-0.11543	-0.09913	0.83875
LOC_Os09g38920	thiol protease SEN102 precursor, putative, expressed	0.48973	0.344826	1.162962	-0.06649	0.7911	-0.5456
LOC_Os04g40090	zinc finger, ZZ type family protein, expressed	-0.498	0.257141	1.156063	0.125155	-0.3272	-0.23275
LOC_Os03g62670	expressed protein	0.110074	0.137405	1.150797	-0.40509	-5.19375	
LOC_Os08g41960	OsMADS37 - MADS-box family gene with MIKC* type-box, expressed	-0.29905	0.05266	1.150011	-0.22538	-0.4035	
LOC_Os01g48680	two pore calcium channel protein 1, putative, expressed	-0.55134	-0.00607	1.149163	0.003772	-1.02104	0.851
LOC_Os01g68270	hypothetical protein	-0.07815	-0.48779	1.147298			
LOC_Os03g49720	PAP fibrillin family domain containing protein, expressed	-0.12428	-0.25451	1.147003	-0.51011	-0.39348	1.4857
LOC_Os09g25150	cinnamoyl-CoA reductase, putative, expressed	-0.07477	0.046599	1.139748	-0.49846	-2.8484	0.3165
LOC_Os03g63020	protein kinase domain containing protein, expressed	-0.58531	-0.68288	1.13762	-0.36063	0.234188	-0.0644
LOC_Os12g08060	universal stress protein family protein, expressed	-0.03519	0.076099	1.137483			
LOC_Os02g46660	SNARE associated Golgi protein, putative, expressed	-0.1782	-0.27549	1.136795	-0.64708	-1.11264	-0.08805

LOC_Os12g18650	Regulator of chromosome condensation domain containing protein, expressed	0.007808	-0.8847	1.135683	-0.1154	0.293088	0.5959
LOC_Os06g12320	transmembrane amino acid transporter protein, putative, expressed	0.206656	-0.20898	1.130373	-0.60465	1.984425	0.2901
LOC_Os04g08550	oxidoreductase, aldo/keto reductase family protein, putative, expressed	-0.46204	0.244233	1.129256	1.254635	1.577375	0.81755
LOC_Os05g07090	acyl-coenzyme A dehydrogenase, mitochondrial precursor, putative, expressed	-0.24294	-0.21336	1.127209	0.030344	0.794038	0.4984
LOC_Os02g51290	HVA22, putative, expressed	-0.41325	0.112281	1.125723	-0.43038	1.0189	-0.45765
LOC_Os03g51030	phytochrome A, putative, expressed	-0.58801	-0.10434	1.123147	-0.06637	-0.16475	-0.9871
LOC_Os08g06480	lissencephaly type-1-like homology motif, putative, expressed	-0.28372	0.203639	1.120602	0.007266	0.279075	0.5318
LOC_Os05g48760	protein of unknown function DUF1421 domain containing protein, expressed	0.066379	0.585729	1.119257	0.349112	-0.22131	
LOC_Os07g36800	UPF0041 domain containing protein, putative, expressed	0.41107	-0.32729	1.117751	0.052251	0.02875	0.6103
LOC_Os08g04430	expressed protein	0.26873	0.214622	1.106868	-0.1952	-0.017	1.2635
LOC_Os09g20930	expressed protein	-0.36991	-0.02629	1.105611	-0.15174	0.056138	0.0031
LOC_Os02g05330	DEAD-box ATP-dependent RNA helicase, putative, expressed	-0.41632	-0.1386	1.104676	0.150606	0.683875	-0.0982
LOC_Os12g32980	potyvirus VPg interacting protein, putative, expressed	-0.19729	0.051664	1.102846	0.165383	0.2045	
LOC_Os08g10500	expressed protein	0.320289	-0.12027	1.102291	0.274456	0.3405	0.69805
LOC_Os09g32820	uridine/cytidine kinase-like 1, putative, expressed	-0.51524	-0.37	1.101382	-0.03576	-0.36338	-0.4805
LOC_Os06g24190	expressed protein	-0.20236	-0.41818	1.099426	0.105074	-0.22195	0.3046
LOC_Os11g04210	hydroxymethylglutaryl-CoA lyase, putative, expressed	-0.15358	0.433137	1.098403	-0.16084	0.445225	
LOC_Os02g28980	peptidyl-prolyl isomerase, putative, expressed	-0.27476	-0.11376	1.094579	-0.19176	-0.02863	-0.3079
LOC_Os05g41460	cysteine proteinase inhibitor precursor protein, putative, expressed	-0.40899	0.31428	1.093339	0.113253	-0.125	0.30685
LOC_Os12g12934	peptide transporter PTR3-A, putative, expressed	-0.06925	-0.38932	1.093157	-0.43295	-1.00473	
LOC_Os05g48660	MRH1, putative, expressed	-0.20034	-0.33807	1.092702	-0.19292	0.9925	
LOC_Os03g19250	AMP-binding enzyme, putative, expressed	-0.16074	-0.22461	1.091017	-0.06423	1.109375	-0.0536
LOC_Os03g30950	acyl-desaturase, chloroplast precursor, putative, expressed	-0.11192	0.136272	1.090354	-0.17436	-0.1047	0.17145
LOC_Os09g38080	retrotransposon protein, putative, unclassified, expressed	0.261327	-0.29016	1.088508	-0.29391	0.859913	0.32025
LOC_Os11g02100	peroxidase precursor, putative, expressed	-0.54112	-0.36393	1.086922	0.062408	-0.31075	-0.3057
LOC_Os04g42420	nodulin, putative, expressed	-0.15788	0.01602	1.085176	0.51516	-0.03775	-0.45615
LOC_Os11g14180	expressed protein	-0.55127	0.548044	1.082046	-0.11956	-0.4745	0.25215
LOC_Os03g51000	3,4-dihydroxy-2-butanone kinase, putative, expressed	-0.52282	-0.17063	1.081765	-0.33823	-0.25858	0.1209
LOC_Os03g14570	expressed protein	0.088861	0.344485	1.081324	0.204319	-1.45838	
LOC_Os01g22510	cyclase/dehydrase family protein, expressed	-0.32732	-0.24986	1.078861	-0.09353	0.4653	
LOC_Os05g02420	expressed protein	0.119834	-0.22646	1.075074	0.164037	-1.1541	0.42975

LOC_Os05g07030	arginyl-tRNA synthetase, putative, expressed	-0.24674	-0.30547	1.074287	0.109058	-0.0095	-0.2099
LOC_Os10g05130	expressed protein	-0.25923	-0.59408	1.071806	-0.16853	0.127625	
LOC_Os05g01570	auxin-induced protein 5NG4, putative, expressed	-0.54067	-0.60173	1.07162	-0.50998	0.7339	
LOC_Os04g35590	thioesterase family protein, putative, expressed	-0.43749	-0.15268	1.070574	0.086598	0.069625	-0.0041
LOC_Os03g14160	hypothetical protein	0.100735	-0.02458	1.070315			
LOC_Os01g43030	tetratricopeptide repeat domain containing protein, expressed	-0.42843	-0.29044	1.070132	0.074843	-0.08275	
LOC_Os06g05100	transketolase, putative, expressed	-0.54191	-0.47143	1.06697	-0.15485	-0.2606	-0.6091
LOC_Os05g40420	2,3-bisphosphoglycerate-independent phosphoglycerate mutase, putative, expressed	-0.27958	0.015546	1.06462	-0.06929	0.1365	-0.2629
LOC_Os09g28740	gibberellin receptor GID1L2, putative, expressed	-0.10773	-0.58761	1.063714	-0.54699	-0.808	-0.55515
LOC_Os11g40540	transporter family protein, putative, expressed	0.018132	-0.26863	1.062409	-0.19457	-0.25071	0.25945
LOC_Os01g72480	zinc finger, C3HC4 type domain containing protein, expressed	-0.50383	-0.35123	1.062257	-0.30968	0.219638	0.4181
LOC_Os08g42040	LTPL80 - Protease inhibitor/seed storage/LTP family protein precursor, expressed	0.054544	-0.47588	1.062106	-0.25953	0.0192	-0.22515
LOC_Os10g36650	actin, putative, expressed	-0.1588	-0.02492	1.060544	-0.44769	-0.00863	-0.45965
LOC_Os01g69030	sucrose-phosphate synthase, putative, expressed	0.079348	0.128285	1.056808	-0.42691	-0.80596	
LOC_Os09g28910	carbonic anhydrase, chloroplast precursor, putative, expressed	-0.24202	-0.07622	1.054319	0.404322	1.04325	0.25025
LOC_Os04g49350	PPR repeat domain containing protein, putative, expressed	-0.21721	0.40794	1.053956			0.01315
LOC_Os03g60850	peptide transporter PTR2, putative, expressed	-0.40765	-0.09754	1.053886	0.058761	-0.27748	0.2621
LOC_Os03g22800	OsFBT5 - F-box and tubby domain containing protein, expressed	-0.14899	-0.03947	1.051548	0.026613	0.862863	-0.1252
LOC_Os03g58580	nodulin, putative, expressed	-0.22586	-0.21003	1.051069	0.229347	-0.25113	0.63175
LOC_Os12g38150	osmotin, putative, expressed	-0.0697	-0.22	1.049965	-0.83868	2.205188	
LOC_Os01g06660	thiamine pyrophosphate enzyme, C-terminal TPP binding domain containing protein, expressed	-0.13967	0.52488	1.049452	0.762345	1.1188	0.64255
LOC_Os11g05810	expressed protein	-0.42933	-0.36326	1.047226	0.585963	0.40125	0.26725
LOC_Os02g47800	monodehydroascorbate reductase, putative, expressed	-0.34908	-0.71376	1.046721	-0.12916	-1.038	0.62625
LOC_Os12g39660	calcium-transporting ATPase, plasma membrane-type, putative, expressed	-0.31604	-0.02244	1.045158	0.123435	0.315125	0.04975
LOC_Os09g25710	keratin, type I cytoskeletal 9, putative, expressed	0.191817	0.130082	1.043402	-0.2112	-1.20523	
LOC_Os03g50480	phosphoglucomutase, putative, expressed	-0.33013	-0.10303	1.042341	-0.45637	-0.59638	-0.2779
LOC_Os06g48750	DEAD-box ATP-dependent RNA helicase, putative, expressed	-0.56423	-0.4224	1.036989	0.12172	-0.146	-0.16555
LOC_Os02g52860	phosphate carrier protein, mitochondrial precursor, putative, expressed	-0.44223	0.389755	1.035635	0.108075	0.736	0.1836
LOC_Os01g72100	OsCML10 - Calmodulin-related calcium sensor protein, expressed	0.006688	0.369373	1.032705	-0.19663	-0.24963	-0.41665

LOC_Os01g48420	peroxiredoxin, putative, expressed	-0.22509	-0.02932	1.031877	-0.12011	-0.08275	-0.22195
LOC_Os02g53320	universal stress protein domain containing protein, putative, expressed	-0.05634	0.073099	1.031667	-0.42087	-0.00179	0.61115
LOC_Os05g09440	NADP-dependent malic enzyme, chloroplast precursor, putative, expressed	-0.53193	0.189053	1.031565	-0.65779	-0.1106	2.34375
LOC_Os04g12530	amino acid transporter family protein, putative, expressed	-0.15149	-0.14904	1.030677			
LOC_Os09g14670	phosphoenolpyruvate carboxylase, putative, expressed	-0.54232	-0.06101	1.02944	-0.72492	-0.0785	
LOC_Os05g39250	phosphatidylethanolamine-binding protein, putative, expressed	-0.06532	0.241144	1.02797	0.345626	0.752175	
LOC_Os10g22050	expressed protein	0.577465	-0.78696	1.027306	-0.2366	1.03845	
LOC_Os03g09110	mitochondrial carrier protein, putative, expressed	-0.49234	-0.17141	1.025791	0.163494	-0.12014	
LOC_Os03g43010	expressed protein	-0.58527	-0.9586	1.024259	0.083629	-0.29059	-1.0102
LOC_Os03g08900	MATE efflux family protein, putative, expressed	-0.12457	0.032906	1.024011	1.276876	1.4326	
LOC_Os12g39320	DUF221 domain containing protein, expressed	-0.55327	0.142651	1.023979	0.125373	0.3887	0.0673
LOC_Os03g53910	tetratricopeptide repeat domain containing protein, expressed	0.040796	0.091853	1.022612	-0.35569	-0.976	-0.77135
LOC_Os07g49150	26S protease regulatory subunit 4, putative, expressed	-0.43265	0.117105	1.021848	0.13891	0.30025	0.00385
LOC_Os03g57790	ubiquitin-conjugating enzyme, putative, expressed	-0.40841	-0.1756	1.021733	-0.11332	-0.55425	
LOC_Os03g64080	retrotransposon protein, putative, Ty1-copia subclass, expressed	-0.53751	0.076514	1.020101	-0.04934	-0.09113	
LOC_Os04g39300	heavy metal transport/detoxification protein, putative, expressed	0.180227	0.580248	1.019349			
LOC_Os03g53190	Core histone H2A/H2B/H3/H4 domain containing protein, putative, expressed	-0.3335	-0.2775	1.017954	0.082156	0.80555	
LOC_Os09g27210	lecithine cholesterol acyltransferase, putative, expressed	-0.39944	-0.38428	1.017228	6.00E-04	-1.00868	-0.0873
LOC_Os03g29240	PDI, putative, expressed	0.293096	0.250577	1.014347	0.236438	1.354875	
LOC_Os03g16670	haloacid dehalogenase-like hydrolase family protein, putative, expressed	-0.27331	0.451622	1.012712	-1.27	0.8325	0.2639
LOC_Os07g47110	OsFBT11 - F-box and tubby domain containing protein, expressed	-0.15422	-0.33492	1.012662	-0.15939	0.504	0.3903
LOC_Os10g11310	expressed protein	-0.21577	-0.12126	1.012405	-0.90308	-0.32756	0.2846
LOC_Os06g51150	catalase isozyme B, putative, expressed	0.104165	-0.0047	1.01136	-0.18283	1.9255	0.1393
LOC_Os04g40910	OsFBX146 - F-box domain containing protein, expressed	-0.30441	-0.247	1.011335	0.034055	0.296163	-0.2837
LOC_Os05g06690	HECT-domain domain containing protein, expressed	-0.26418	0.26078	1.010832	-0.09234	0.067375	0.04175
LOC_Os03g09220	stage II sporulation protein E, putative, expressed	0.254703	-0.12094	1.010014	-0.08671	-0.79063	0.33465
LOC_Os08g12120	retrotransposon protein, putative, unclassified, expressed	0.084349	-0.39533	1.006446			
LOC_Os05g44360	oligosaccharyl transferase, putative, expressed	-0.15719	-0.67189	1.004314	0.111088	0.131625	-0.1905

LOC_Os03g39000	inositol-1-monophosphatase, putative, expressed	-0.14858	0.06116	1.00401	-0.46813	0.453425	-0.20775
LOC_Os03g22690	nucleoporin interacting component, putative, expressed	-0.50319	0.130692	1.003887	0.084782	-0.01069	-0.39085
LOC_Os08g34700	GDU1, putative, expressed	-0.10001	-0.01659	1.001906	-0.84406	-1.76784	
LOC_Os06g25439	NAD dependent epimerase/dehydratase family protein, putative, expressed	-0.38199	-0.02434	1.000954	-0.12921	-1.28958	0.41145
LOC_Os01g73170	peroxidase precursor, putative, expressed	-0.14406	0.132066	0.999368	0.621027	1.945875	
LOC_Os01g03730	nuclease PA3, putative, expressed	-0.32053	0.450476	0.996529	-0.10037	1.344213	0.37935
LOC_Os07g43950	RNA recognition motif containing protein, putative, expressed	-0.11806	-0.0796	0.993747	-0.36902	0.380138	0.0013
LOC_Os08g10080	no apical meristem protein, putative, expressed	0.181963	0.389629	0.990803	-0.60271	2.041238	0.96545
LOC_Os05g38530	DnaK family protein, putative, expressed	0.618571	-0.04209	0.98978	-0.20952	-0.64549	
LOC_Os01g07170	HORMA domain containing protein, putative, expressed	0.490974	-0.04741	0.989615	-0.14852	0.008825	
LOC_Os10g42730	expressed protein	-0.33884	0.151668	0.989363			-0.4344
LOC_Os04g42430	EF hand family protein, putative, expressed	-0.29251	0.06572	0.988155	0.26279	0.042	0.0947
LOC_Os06g07780	vesicle-associated membrane protein, putative, expressed	-0.21536	-0.24507	0.98809	0.095614	-0.3425	-0.07455
LOC_Os09g23660	ZIM motif family protein, expressed	0.027808	-0.02236	0.987433	0.847961	0.267988	0.69895
LOC_Os12g38850	DUF1336 domain containing protein, expressed	0.044845	0.126746	0.984692	0.106978	-1.15936	-0.4629
LOC_Os03g18690	26S protease regulatory subunit 4, putative, expressed	-0.58587	0.060749	0.983933	-0.01071	-0.14275	-0.3428
LOC_Os06g49990	UPF0183 protein, putative, expressed	-0.55074	-0.62192	0.971985	0.022064	0.70105	0.40735
LOC_Os11g11100	bZIP transcription factor domain containing protein, expressed	-0.20968	0.366779	0.970571	-0.24061	-0.008	0.0924
LOC_Os04g41460	transporter family protein, putative, expressed	-0.13945	0.079014	0.968329	0.316185	0.820313	0.10985
LOC_Os03g53750	nuclear prelamin A recognition factor, putative, expressed	0.219473	0.050967	0.967272	0.326895	0.629775	-0.00635
LOC_Os04g10680	zinc finger, C3HC4 type domain containing protein, expressed	-0.59401	0.153401	0.965815	0.039396	0.066125	0.34315
LOC_Os06g01390	acyl-coenzyme A oxidase 1.2, peroxisomal, putative, expressed	-0.38116	-0.25495	0.960934	0.027744	1.319625	0.1414
LOC_Os10g38710	glutathione S-transferase, putative, expressed	-0.47756	-0.71346	0.958159	-0.179	-4.60589	
LOC_Os05g33880	cysteine proteinase inhibitor precursor protein, putative, expressed	0.038099	-0.32454	0.957805	-0.06224	0.178875	0.0182
LOC_Os03g32580	BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1 precursor, putative, expressed	-0.57558	0.447174	0.956571	1.061583	0.790338	0.8929
LOC_Os01g14630	polyprenyl synthetase, putative, expressed	-0.00893	-0.26621	0.954226			
LOC_Os04g34230	RING-H2 finger protein, putative, expressed	0.636271	-0.25669	0.953731	-0.50699	-0.03531	
LOC_Os10g26620	dof zinc finger domain containing protein, putative, expressed	0.075263	-0.40047	0.953127	-0.62638	0.328488	0.3899

LOC_Os03g10500	adenylyl-sulfate kinase, putative, expressed	-0.04053	0.195067	0.953105			
LOC_Os08g28670	pathogenesis-related Bet v I family protein, putative, expressed	0.508105	-0.49746	0.953034	-0.94187	-1.13256	-0.2104
LOC_Os07g08710	AT hook-containing DNA-binding protein, putative, expressed	-0.12135	0.145286	0.95296	-0.13783	-0.882	-0.08055
LOC_Os02g02980	MATE domain containing protein, expressed	-0.27363	-0.32832	0.952817	-0.01301	0.500888	
LOC_Os06g10520	pantothenate kinase, putative, expressed	-0.39789	-0.02842	0.952438	1.122785	2.181963	0.7178
LOC_Os01g33784	lipase family protein, putative, expressed	-0.26582	0.129191	0.951342	-0.1599	0.195988	0.56145
LOC_Os07g47510	stress-related protein, putative, expressed	-0.19998	-0.31335	0.950471	-0.30777	-0.67575	-0.72635
LOC_Os08g32870	aldehyde dehydrogenase, putative, expressed	-0.34967	-0.44655	0.949209	-0.13667	0.45675	-0.0291
LOC_Os05g51480	cleavage and polyadenylation specificity factor, putative, expressed	-0.50767	0.538376	0.94136	0.041876	-0.00175	-0.2642
LOC_Os10g28360	1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase protein, putative, expressed	-0.23444	-0.42388	0.940983	-0.83293	-0.42488	0.48755
LOC_Os03g31170	inosine-uridine preferring nucleoside hydrolase family protein, putative, expressed	-0.41041	-0.6169	0.936446	-0.10343	-0.06238	0.06215
LOC_Os03g37470	MATE efflux family protein, putative, expressed	-0.42537	0.047182	0.935713	-0.47235	-0.70395	-0.31705
LOC_Os03g40100	ACT domain containing protein, expressed	-0.04836	0.597238	0.93264	0.697239	-0.64331	-0.0025
LOC_Os03g15000	Zinc finger, C3HC4 type domain containing protein, expressed	-0.16019	-0.10785	0.931465	0.067046	0.3025	0.3585
LOC_Os06g11310	plastocyanin-like domain containing protein, putative, expressed	0.181089	0.125639	0.930544	-1.48508	-1.31138	0.2308
LOC_Os02g11640	UDP-glucuronosyl and UDP-glucosyl transferase, putative, expressed	0.105678	0.017209	0.926131	-0.42564	-0.42626	
LOC_Os06g05130	myristoyl-acyl carrier protein thioesterase, chloroplast precursor, putative, expressed	-0.23713	0.463926	0.925612	0.039041	0.2511	2.42285
LOC_Os08g09690	nuclear transcription factor Y subunit, putative, expressed	-0.05626	0.099756	0.924744	-0.61638	-0.56145	-0.2188
LOC_Os04g56160	plasma membrane ATPase, putative, expressed	-0.45533	-0.03629	0.924593	0.047113	0.173875	0.2996
LOC_Os01g66720	NADP-dependent oxidoreductase, putative, expressed	-0.12324	-0.28079	0.924044	-0.09884	-0.34989	-0.24285
LOC_Os04g57870	expressed protein	0.039956	0.258814	0.923658	-0.01474	#####	-0.2498
LOC_Os01g53880	OsIAA6 - Auxin-responsive Aux/IAA gene family member, expressed	0.264048	-0.51953	0.921864	0.335769	0.42325	0.1149
LOC_Os04g39190	cell division protease ftsH homolog 4, putative, expressed	-0.48118	-0.49971	0.919882	-0.05561	0.026188	
LOC_Os07g36190	hydrolase, NUDIX family, domain containing protein, expressed	0.347625	0.250483	0.917119	-0.24771	-1.88038	-0.3294
LOC_Os06g22060	pyrophosphate--fructose 6-phosphate 1-phosphotransferase subunit alpha, putative, expressed	-0.05982	-0.23702	0.916024	-0.07601	-1.28843	-0.66225

LOC_Os08g27010	APE1, putative, expressed	-0.55259	-0.5823	0.91329	-0.17276	-2.31463	0.17095
LOC_Os05g38550	ubiquitin-conjugating enzyme, putative, expressed	-0.45461	-0.20611	0.912858	0.011173	-0.21763	
LOC_Os06g02420	ATOZ1, putative, expressed	0.168433	-0.42336	0.910915	-0.40661	-1.8432	-0.81195
LOC_Os09g38130	auxin efflux carrier component, putative, expressed	0.402758	0.51029	0.909661	0.318828	1.52	0.1604
LOC_Os04g56620	molybdopterin biosynthesis protein CNX1, putative, expressed	-0.35423	0.02123	0.909087			
LOC_Os03g27010	expressed protein	-0.05657	0.280987	0.908628	-0.0967	1.071625	-0.22905
LOC_Os08g09200	aconitate hydratase protein, putative, expressed	-0.45228	0.279104	0.908333	-0.06238	2.100625	0.15155
LOC_Os11g37730	glutathione S-transferase, N-terminal domain containing protein, expressed	-0.35628	-0.344	0.906745	0.272657	1.43675	0.9467
LOC_Os06g39690	SOUL heme-binding protein, putative, expressed	-0.32928	-0.27064	0.90282	-0.17921	-0.73008	-0.63805
LOC_Os08g16930	expressed protein	-0.39588	-0.51175	0.902631	0.044066	0.327	0.78295
LOC_Os06g23530	pre-mRNA-splicing factor ATP-dependent RNA helicase, putative, expressed	-0.52396	-0.32974	0.901173	-0.12048	-0.1842	0.00525
LOC_Os03g20900	Myb transcription factor, putative, expressed	-0.18326	-0.03901	0.896889	-0.4615	-0.0525	-0.1282
LOC_Os07g43700	lactate/malate dehydrogenase, putative, expressed	0.085509	-0.20581	0.892387	-1.01888	-2.05089	1.00E-04
LOC_Os10g35250	vacuolar protein-sorting protein bro1, putative, expressed	0.21204	-0.11224	0.890238	0.101033	0.34025	0.2251
LOC_Os02g03840	expressed protein	0.157645	0.057189	0.887944	-0.08485	0.228375	0.0866
LOC_Os03g62660	transposon protein, putative, unclassified, expressed	-0.43332	0.038827	0.886737	-0.00603	0.17365	-0.0078
LOC_Os07g10150	coatamer subunit gamma-2, putative, expressed	-0.49127	0.254893	0.886018	0.034845	0.72725	0.28335
LOC_Os09g26670	expressed protein	-0.09807	-0.39363	0.885966	-2.61947	-1.84009	0.169
LOC_Os02g18450	GTP-binding protein typA/bipA, putative, expressed	-0.35267	0.078962	0.885346	-0.24902	-2.55079	-0.5319
LOC_Os05g01090	pex14, putative, expressed	-0.45647	-0.14013	0.883355	0.233186	0.1025	0.3559
LOC_Os01g31360	expressed protein	-0.13371	0.310415	0.881878	-0.53127	0.85225	-0.32245
LOC_Os01g17390	OsFBX5 - F-box domain containing protein, expressed	0.036931	0.065427	0.881167	-0.00263	-0.93379	-0.0278
LOC_Os04g45070	remorin, putative, expressed	-0.31149	-0.48699	0.878158	-0.14335	-1.08863	-0.37375
LOC_Os07g10460	5-nucleotidase surE, putative, expressed	-0.35841	-0.02737	0.877157	-0.10429	0.611063	0.12145
LOC_Os02g20310	expressed protein	-0.24624	-0.48923	0.876941	0.033403	-0.42238	0.0791
LOC_Os10g07440	expressed protein	0.125591	-0.09947	0.875301	-0.27255	0.091375	0.42775
LOC_Os04g43800	phenylalanine ammonia-lyase, putative, expressed	-0.22079	0.173247	0.874567	3.276763	-1.99279	2.9547
LOC_Os03g19580	expressed protein	-0.16672	0.299404	0.873189	0.487985	1.694875	1.13015
LOC_Os04g40040	copper methylamine oxidase precursor, putative, expressed	0.08753	-0.39684	0.867393	0.475336	0.277	-1.19655
LOC_Os01g71240	calcium-transporting ATPase, plasma membrane-type, putative, expressed	-0.32338	-0.18442	0.867241	0.07072	-0.0215	0.70065
LOC_Os05g01760	lysine ketoglutarate reductase trans-splicing related 1, putative, expressed	0.11533	-0.32697	0.866619	-0.43484	0.829	0.37055
LOC_Os07g44610	pyrrolidone-carboxylate peptidase, putative, expressed	-0.09326	-0.26084	0.864527	0.066857	0.86925	-0.31845

LOC_Os08g07960	mitotic checkpoint protein, putative, expressed	-0.1899	-0.15662	0.862359	0.098055	0.35525	-0.1822
LOC_Os05g34210	expressed protein	-0.4021	-0.23351	0.860503	0.035063	0.645	
LOC_Os08g40620	rabGAP/TBC domain-containing protein, putative, expressed	-0.53594	0.059602	0.859402	0.128107	0.758	0.17955
LOC_Os01g64930	expressed protein	-0.12075	0.040431	0.858285	-0.08236	-0.31309	-0.11055
LOC_Os04g52400	oxidoreductase, short chain dehydrogenase/reductase family protein, putative, expressed	-0.27208	0.036475	0.857444	0.072639	-0.02725	-0.13495
LOC_Os10g35490	hydrolase, alpha/beta fold family domain containing protein, expressed	0.054089	-0.76912	0.855528	-0.92646	-0.08981	-0.4031
LOC_Os02g08440	WRKY71, expressed	-0.47413	0.007454	0.854112	2.052449	0.973375	1.6468
LOC_Os09g32690	zinc finger, C3HC4 type domain containing protein, expressed	-0.5495	-0.27768	0.854035	-0.31063	0.089263	-0.13275
LOC_Os12g02700	harpin-induced protein 1 domain containing protein, expressed	-0.28076	0.004513	0.852895	-0.07453	1.044563	0.29895
LOC_Os04g57210	actin-6, putative, expressed	-0.35831	0.178287	0.850886	0.074543	-0.146	0.90795
LOC_Os02g04260	expressed protein	-0.51645	0.132159	0.848921	-0.2984	-0.17863	-0.5867
LOC_Os03g38020	mgs one binder kinase activator-like 1A, putative, expressed	-0.18298	-0.01507	0.848658	-0.14961	-0.23475	-0.36265
LOC_Os01g43420	expressed protein	-0.21818	0.288031	0.848465	0.077794	-0.016	0.1221
LOC_Os08g04840	MYB family transcription factor, putative, expressed	0.011449	0.106286	0.847558	-0.14165	-0.74614	0.1596
LOC_Os01g64650	VAMP-like protein YKT62, putative, expressed	-0.31844	-0.50098	0.845032	-0.04264	0.3475	0.45925
LOC_Os01g70980	expressed protein	0.049629	0.064648	0.843423	0.062306	0.379625	0.055
LOC_Os03g56860	expressed protein	0.016011	-0.42589	0.842445	0.57521	1.024925	
LOC_Os03g48930	peptidase, T1 family, putative, expressed	-0.3156	-0.01438	0.842149	-0.07643	0.335875	-0.12655
LOC_Os03g59090	retrotransposon protein, putative, unclassified, expressed	-0.17188	-0.20476	0.841384	-0.31224	-2.00045	
LOC_Os03g17590	cat eye syndrome critical region protein 5 precursor, putative, expressed	0.030441	-0.19414	0.84115	-0.13114	-0.73764	-0.0591
LOC_Os04g39290	heavy metal transport/detoxification protein, putative, expressed	-0.00431	0.263241	0.840143			
LOC_Os06g35160	CAMK_KIN1/SNF1/Nim1_like.26 - CAMK includes calcium/calmodulin dependent protein kinases, expressed	-0.32916	-0.09363	0.840086	-0.49926	-1.94425	-0.557
LOC_Os02g47000	expressed protein	-0.43421	-0.18495	0.837074	-0.32926	-0.27038	
LOC_Os03g01880	possible lysine decarboxylase domain containing protein, expressed	0.152933	-0.44603	0.830364	-0.06343	1.963125	-1.24905
LOC_Os08g06140	no apical meristem protein, putative, expressed	-0.43648	-0.21526	0.827665	0.229323	0.58575	0.52855
LOC_Os07g23550	expressed protein	-0.26275	-0.16058	0.826972	-0.09168	-0.248	0.15645
LOC_Os01g70550	heparan-alpha-glucosaminide N-acetyltransferase, putative, expressed	0.021875	-0.22136	0.826637	-0.05771	-1.7656	-0.47855
LOC_Os07g31340	regulator of nonsense transcripts 1, putative, expressed	-0.24961	-0.15508	0.82605	-0.00124	-0.10788	
LOC_Os01g56180	expressed protein	0.145358	-0.29868	0.825376	-0.19569	0.951225	0.64425
LOC_Os02g32730	neutral/alkaline invertase, putative, expressed	-0.57031	-0.0594	0.822657	0.202511	-0.30475	

LOC_Os03g52010	lecithin cholesterol acyltransferase, putative, expressed	0.398442	0.338636	0.819373	3.75E-04	-0.94103	-0.33725
LOC_Os01g04930	MYB family transcription factor, putative, expressed	-0.01295	0.055304	0.819314	-0.22055	0.140738	-0.2583
LOC_Os01g04350	hsp20/alpha crystallin family protein, putative, expressed	-0.24291	0.223939	0.816001	-0.1836	-0.29675	1.58775
LOC_Os03g04770	beta-amylase, putative, expressed	-0.22317	0.02765	0.814081	-0.70403	-2.76675	0.55655
LOC_Os10g42100	pyruvate kinase, putative, expressed	-0.2822	-0.03503	0.813794	-0.18236	0.21125	-0.297
LOC_Os04g35190	OsFBX133 - F-box domain containing protein, expressed	-0.21578	-0.0268	0.812853	-0.13265	-0.23963	-0.48655
LOC_Os06g49030	activator of 90 kDa heat shock protein ATPase homolog, putative, expressed	-0.18459	-0.07275	0.809719	-0.14561	0.85225	-0.0357
LOC_Os03g50540	2Fe-2S iron-sulfur cluster binding domain containing protein, expressed	-0.4094	0.023369	0.809633	-0.18206	0.28075	-0.34695
LOC_Os02g56900	thioredoxin family protein, putative, expressed	-0.07804	0.198618	0.808507	0.47091	1.566088	0.61405
LOC_Os02g38020	inorganic phosphate transporter 2-1, chloroplast precursor, putative, expressed	-0.56644	-1.41308	0.807135	0.136627	-2.89613	-0.35445
LOC_Os08g41250	signal recognition particle receptor subunit beta, putative, expressed	-0.35516	0.39582	0.806449	0.139672	0.804288	0.13225
LOC_Os02g34950	ATP binding protein, putative, expressed	-0.22906	0.012093	0.805621	-0.11701	-0.22088	-0.16445
LOC_Os03g27280	CAMK_CAMK_like.19 - CAMK includes calcium/calmodulin dependent protein kinases, expressed	-0.1623	-0.30819	0.803886	1.188188	0.266875	0.8234
LOC_Os03g50160	plastocyanin-like domain containing protein, putative, expressed	0.169646	0.400857	0.792071	-0.10237	-1.30999	-0.031
LOC_Os01g28500	SCP-like extracellular protein, expressed	-1.27654	0.156779	0.510968	0.319973	3.092325	
LOC_Os01g01280	expressed protein	-0.92657	-0.76745	0.565966	0.107372	-1.52293	
LOC_Os08g44850	C2 domain containing protein, putative, expressed	-1.10551	-0.42785	0.561437	0.208983	-0.12338	1.02175
LOC_Os04g49450	MYB family transcription factor, putative, expressed	-1.20391	-1.44493	0.546397	1.502378	-0.90873	0.78825
LOC_Os11g42970	membrane associated DUF588 domain containing protein, putative, expressed	-0.94065	-0.40201	0.537829	0.430146	-0.32045	0.16165
LOC_Os01g04950	peptide transporter PTR2, putative, expressed	-0.8949	-0.26131	0.508428	0.084373	-0.85049	-0.0532
LOC_Os08g09840	WRKY117, expressed	-1.17757	0.446533	0.486271			
LOC_Os01g26240	retrotransposon protein, putative, Ty1-copia subclass, expressed	-0.9164	0.283896	0.485366			
LOC_Os04g32110	ACT domain containing protein, expressed	-0.9244	-1.19439	0.484351	1.49141	0.968438	
LOC_Os03g25500	cytochrome P450 72A1, putative, expressed	-0.87996	-0.02776	0.474355	-0.03431	0.021075	1.43285
LOC_Os05g48390	ubiquitin conjugating enzyme protein, putative, expressed	-0.8938	0.022004	0.470622	-0.12392	0.313725	
LOC_Os01g51410	glycine dehydrogenase, putative, expressed	-1.17287	-0.1527	0.463928	-0.07181	-2.65488	-0.46645
LOC_Os05g05950	TOC159, putative, expressed	-0.94748	0.37116	0.459822	-0.04824	-0.42888	-0.5627
LOC_Os04g53860	reductase, putative, expressed	-0.81926	0.150901	0.44403	-0.10544	-0.57735	0.2428

LOC_Os07g18240	lectin-like receptor kinase, putative, expressed	-0.91644	-0.16499	0.438785			
LOC_Os04g42480	receptor-like protein kinase At3g46290 precursor, putative, expressed	-0.95343	0.165115	0.434655	0.549117	0.2085	1.0897
LOC_Os10g03570	RGH1A, putative, expressed	-0.85295	-0.12991	0.433056			
LOC_Os09g18594	protein kinase domain containing protein, expressed	-1.22572	0.38545	0.393538	0.771443	-0.51548	-0.0381
LOC_Os10g22560	peptide transporter PTR2, putative, expressed	-0.8836	-0.18276	0.345746	0.105738	-0.06888	-0.29805
LOC_Os04g41960	NADP-dependent oxidoreductase, putative, expressed	-1.19039	-0.15611	0.344807	1.916629	0.384375	1.30305
LOC_Os09g25760	tetraspanin family protein, putative, expressed	-0.80015	-0.21851	0.337457	0.601217	0.148125	
LOC_Os07g12890	metal cation transporter, putative, expressed	-0.99955	0.583405	0.327977	1.680573	-1.00849	
LOC_Os11g07020	fructose-bisphosphate aldolase isozyme, putative, expressed	-1.00126	-0.39168	0.323839	-0.45039	-2.11388	-0.22875
LOC_Os06g40640	fructose-bisphosphate aldolase isozyme, putative, expressed	-1.3972	-1.39504	0.318024	0.156639	-2.673	0.2687
LOC_Os07g47290	xylose isomerase, putative, expressed	-0.8127	0.024919	0.284689	0.051438	-0.41068	-0.17735
LOC_Os10g41550	beta-amylase, putative, expressed	-1.14388	-1.25697	0.282577	0.85704	0.667575	
LOC_Os12g13350	retrotransposon protein, putative, Ty1-copia subclass, expressed	-0.83569	-0.74303	0.280265			
LOC_Os06g19444	CCT/B-box zinc finger protein, putative, expressed	-1.61839	-1.28844	0.274135	0.571109	-0.24734	
LOC_Os03g28940	ZIM domain containing protein, putative, expressed	-0.95214	-0.65904	0.26272	1.480131	2.049875	0.3204
LOC_Os01g05530	expressed protein	-0.91885	-0.19477	0.25055	-0.16191	-0.06725	-0.337
LOC_Os01g66820	inactive receptor kinase At1g27190 precursor, putative, expressed	-0.82449	0.217705	0.248969	0.112999	-0.24355	
LOC_Os04g54840	DNA-directed RNA polymerase subunit, putative, expressed	-0.83773	-0.17416	0.248168	-0.15713	-0.024	-0.7632
LOC_Os01g36350	cytochrome P450, putative, expressed	-0.80902	-0.7103	0.242662	0.088498	-0.03906	1.0506
LOC_Os09g36680	ribonuclease T2 family domain containing protein, expressed	-1.02395	-1.30235	0.225962	-0.66071	-0.5	-0.12115
LOC_Os08g17390	expressed protein	-0.99865	-1.02892	0.223714	0.119238	-4.44279	0.1205
LOC_Os02g43370	transposon protein, putative, unclassified, expressed	-1.00615	-0.05865	0.221107	-0.08313	-0.04174	
LOC_Os01g56200	BTBA2 - Bric-a-Brac, Tramtrack, Broad Complex BTB domain with Ankyrin repeat region, expressed	-0.89483	0.112626	0.214182	0.603712	0.08725	0.59835
LOC_Os11g39190	NB-ARC domain containing protein, putative, expressed	-0.90255	-0.82414	0.198438	0.041085	-1.09833	-0.575
LOC_Os10g38292	hypothetical protein	-0.86794	-0.48054	0.197663			0.18515
LOC_Os01g41780	expressed protein	-0.88313	0.00626	0.190092	0.204918	-0.05775	1.37775
LOC_Os01g15490	phosphoadenosine phosphosulfate, putative, expressed	-0.80472	-0.56236	0.18581	0.204022	-0.47325	0.5413
LOC_Os01g67054	calreticulin precursor protein, putative, expressed	-1.02093	0.152575	0.176661	0.359649	0.6315	0.80815
LOC_Os06g39730	hypothetical protein	-1.10294	-0.74241	0.175028			
LOC_Os01g58020	ribulose bisphosphate carboxylase large chain precursor, putative, expressed	-1.13135	-1.61236	0.16403			

LOC_Os11g05260	phosphoglycerate mutase, putative, expressed	-0.91507	-0.50071	0.138497	-0.2328	-1.23975	0.36745
LOC_Os01g03820	C2 domain containing protein, putative, expressed	-1.04919	0.560898	0.115682	-0.01628	0.023088	
LOC_Os01g22980	OsSCP3 - Putative Serine Carboxypeptidase homologue, expressed	-0.86341	-0.61157	0.022632	-0.27986	-0.58364	-0.0994
LOC_Os01g02570	protein kinase domain containing protein, expressed	-0.88617	0.100562	0.014902	0.663198	-0.07761	
LOC_Os02g49800	eukaryotic aspartyl protease domain containing protein, expressed	-0.93869	0.344194	-0.0015	0.372282	0.141625	0.1934
LOC_Os12g36110	calmodulin binding protein, putative, expressed	-0.96476	0.497316	-0.00529	1.124285	-0.02036	1.90655
LOC_Os08g15460	preprotein translocase subunit secY, putative, expressed	-0.80462	-0.33823	-0.00607	-0.11058	-2.64404	-0.74025
LOC_Os02g49780	expressed protein	-0.89868	0.276333	-0.01359	-0.14391	-0.29863	
LOC_Os03g46440	BTBA4 - Bric-a-Brac, Tramtrack, Broad Complex BTB domain with Ankyrin repeat region, expressed	-1.03721	0.594456	-0.02212	1.756894	-0.02814	
LOC_Os05g34630	hydrolase, alpha/beta fold family domain containing protein, expressed	-0.79664	-0.47977	-0.0314	0.102746	-1.75278	-0.3509
LOC_Os12g38170	osmotin, putative, expressed	-0.83262	-1.05173	-0.04608	0.633234	1.955875	0.53475
LOC_Os12g19030	copine, putative, expressed	-0.9805	0.596323	-0.06467	0.49064	0.668888	0.12815
LOC_Os12g17430	NBS-LRR disease resistance protein, putative, expressed	-0.90915	-0.01035	-0.06937			
LOC_Os06g38450	vignain precursor, putative, expressed	-0.99007	0.140468	-0.1464	0.829805	-1.6048	-0.65525
LOC_Os12g39420	nucleobase-ascorbate transporter, putative, expressed	-0.95533	-0.05573	-0.1547	0.219221	-0.379	0.029
LOC_Os09g19380	receptor-like protein kinase precursor, putative, expressed	-1.39523	-0.19256	-0.17787			
LOC_Os10g42410	zinc-binding protein, putative, expressed	-0.82606	-0.3669	-0.2089	1.112846	0.637375	
LOC_Os02g14250	transposon protein, putative, unclassified, expressed	-1.23327	0.526342	-0.21481			
LOC_Os01g09540	HAD superfamily phosphatase, putative, expressed	-0.90027	-0.94828	-0.21719	0.274522	-2.80386	0.0606
LOC_Os01g18630	aspartic proteinase oryzasin-1 precursor, putative, expressed	-1.14608	0.113063	-0.21789	-0.20188	0.015875	-0.4473
LOC_Os09g19500	senescence-induced receptor-like serine/threonine-protein kinase precursor, putative, expressed	-1.13816	-0.9396	-0.23492	-0.029	-0.18153	-0.1472
LOC_Os09g19390	senescence-induced receptor-like serine/threonine-protein kinase precursor, putative, expressed	-1.37248	0.38207	-0.28151			
LOC_Os01g48300	ATP synthase protein I related, putative, expressed	-0.91854	-0.45885	-0.33156	-0.28296	-0.16436	-0.24695
LOC_Os07g18230	lectin-like receptor kinase, putative, expressed	-0.84463	0.413007	-0.34929			
LOC_Os06g07932	flavonol synthase/flavanone 3-hydroxylase, putative, expressed	-0.80454	-0.38232	-0.37278	0.95579	0.52	
LOC_Os02g20360	tyrosine aminotransferase, putative, expressed	-2.07831	0.31498	-0.37521			

LOC_Os03g22050	CAMK_KIN1/SNF1/Nim1_like.16 - CAMK includes calcium/calmodulin dependent protein kinases, expressed	-0.79706	-0.19025	-0.45877	-0.82048	-0.11495	
LOC_Os02g07690	VQ domain containing protein, putative, expressed	-0.89399	-0.11783	-0.46589	1.091729	1.234625	1.87625
LOC_Os01g46720	expressed protein	-1.02193	0.014271	-0.4954	0.0631	-0.07969	0.22795
LOC_Os02g07360	pentatricopeptide containing protein, putative, expressed	-0.91086	-0.6471	-0.52923	-0.38557	-1.676	0.80255
LOC_Os04g10940	expressed protein	-0.88186	-0.49618	-0.5622			
LOC_Os01g38229	peptidyl-prolyl isomerase, putative, expressed	-1.07743	0.385145	-0.57081	0.663906	0.222413	0.1631
LOC_Os04g47360	OsPOP9 - Putative Prolyl Oligopeptidase homologue, expressed	-0.88908	-0.04737	-0.57198	0.034263	-0.0699	0.26605
LOC_Os02g14440	peroxidase precursor, putative, expressed	-1.10051	-2.13442	-0.66823	0.356743	-3.11048	
LOC_Os01g02780	TAK33, putative, expressed	-1.22064	-0.40119	-0.85837	0.374814	-0.2223	
LOC_Os11g32880	DEAD-box ATP-dependent RNA helicase, putative, expressed	-0.89188	-0.54618	-0.93644	-0.10063	-1.08054	
LOC_Os04g21350	flowering promoting factor-like 1, putative, expressed	-0.84815	-0.59328	-1.26687	0.351238	-2.08903	
LOC_Os01g22900	neutral/alkaline invertase, putative, expressed	-1.57882	-0.90151	-1.26889	0.631526	1.450375	1.02665
LOC_Os03g47610	thiamine biosynthesis protein thiC, putative, expressed	-1.40209	-0.63	-2.42225	0.069719	-1.58694	-0.87805

Table S2. Detailed data used for GO enrichment analysis in Figure 4

GO ID	GO Name	GO Level	Ref Total	Ref Number	Query Total	Query Number	Query Exp	Hyper value	p value	GO enrichment value
GO:0009607	response to biotic stimulus	3	39571	19	333	4	0.2	0	25	
GO:0006032	chitin catabolic process	8	39571	37	333	4	0.3	0.0002	12.8	
GO:0006008	regulation of nitrogen utilization	3, 4	39571	30	333	3	0.3	0.0019	11.9	
GO:0006099	tricarboxylic acid cycle	7, 8	39571	33	333	3	0.3	0.0025	10.8	
GO:0008610	lipid biosynthetic process	4	39571	50	333	3	0.4	0.0078	7.1	
GO:0006694	steroid biosynthetic process	6	39571	69	333	4	0.6	0.0025	6.9	
GO:0044237	cellular metabolic process	3	39571	133	333	7	1.1	0.0001	6.3	
GO:0006096	glycolysis	5	39571	124	333	5	1	0.0034	4.8	
GO:0008152	metabolic process	2	39571	1968	333	41	16.6	0	2.5	
GO:0006610	transport	3, 4	39571	978	333	19	8.2	0.0004	2.3	
GO:0006952	defense response	4	39571	626	333	12	5.3	0.0045	2.3	

Table S3. Gene list associated with 11 enriched GO terms in the biological process category

Locus ID	RGAP Ver 6 Annotation	GO ID	GO Name	GO Type
LOC_Os02g35039	NAD dependent epimerase/dehydratase family protein, putative, expressed	GO:0044237	cellular metabolic process	biological_pr ocess
LOC_Os02g39160	hydroxymethylbutenyl 4-diphosphate synthase, putative, expressed	GO:0044237	cellular metabolic process	biological_pr ocess
LOC_Os02g57180	NADH dehydrogenase 1 alpha subcomplex subunit 9, mitochondrial precursor, putative, expressed	GO:0044237	cellular metabolic process	biological_pr ocess
LOC_Os04g53810	leucoanthocyanidin reductase, putative, expressed	GO:0044237	cellular metabolic process	biological_pr ocess
LOC_Os08g34280	cinnamoyl-CoA reductase, putative, expressed	GO:0044237	cellular metabolic process	biological_pr ocess
LOC_Os10g28200	NAD dependent epimerase/dehydratase family protein, putative, expressed	GO:0044237	cellular metabolic process	biological_pr ocess
LOC_Os12g23180	3-beta hydroxysteroid dehydrogenase/isomerase family protein, putative, expressed	GO:0044237	cellular metabolic process	biological_pr ocess
LOC_Os01g64110	glycosyl hydrolase, putative, expressed	GO:0006032	chitin catabolic process	biological_pr ocess
LOC_Os10g28080	glycosyl hydrolase, putative, expressed	GO:0006032	chitin catabolic process	biological_pr ocess
LOC_Os11g37950	WIP3 - Wound-induced protein precursor, expressed	GO:0006032	chitin catabolic process	biological_pr ocess
LOC_Os11g37960	WIP4 - Wound-induced protein precursor, expressed	GO:0006032	chitin catabolic process	biological_pr ocess
LOC_Os02g36140	terpene synthase, putative, expressed	GO:0006952	defense response	biological_pr ocess
LOC_Os03g03810	DEF8 - Defensin and Defensin-like DEFL family, expressed	GO:0006952	defense response	biological_pr ocess
LOC_Os03g18850	pathogenesis-related Bet v I family protein, putative, expressed	GO:0006952	defense response	biological_pr ocess
LOC_Os08g07330	RGH1A, putative, expressed	GO:0006952	defense response	biological_pr ocess
LOC_Os09g36300	OsLonP4 - Putative Lon protease homologue, expressed	GO:0006952	defense response	biological_pr ocess
LOC_Os11g11960	disease resistance protein RPM1, putative, expressed	GO:0006952	defense response	biological_pr ocess
LOC_Os11g12340	disease resistance protein RPM1, putative, expressed	GO:0006952	defense response	biological_pr ocess
LOC_Os12g09739	pollen signalling protein with adenylyl cyclase activity, putative, expressed	GO:0006952	defense response	biological_pr ocess
LOC_Os12g25170	NB-ARC domain containing disease resistance protein, putative, expressed	GO:0006952	defense response	biological_pr ocess
LOC_Os12g36830	pathogenesis-related Bet v I family protein, putative, expressed	GO:0006952	defense response	biological_pr ocess
LOC_Os12g36860	pathogenesis-related protein 10, putative, expressed	GO:0006952	defense response	biological_pr ocess
LOC_Os12g36880	pathogenesis-related Bet v I family protein, putative, expressed	GO:0006952	defense response	biological_pr ocess

LOC_Os03g56280	lactate/malate dehydrogenase, putative, expressed	GO:0006096	glycolysis	biological_pr ocess
LOC_Os03g56460	glucose-6-phosphate isomerase, putative, expressed	GO:0006096	glycolysis	biological_pr ocess
LOC_Os04g32020	2-oxoglutarate dehydrogenase E1 component, mitochondrial precursor, putative, expressed	GO:0006096	glycolysis	biological_pr ocess
LOC_Os08g03290	glyceraldehyde-3-phosphate dehydrogenase, putative, expressed	GO:0006096	glycolysis	biological_pr ocess
LOC_Os12g05110	pyruvate kinase, putative, expressed	GO:0006096	glycolysis	biological_pr ocess
LOC_Os05g33570	pyruvate, phosphate dikinase, chloroplast precursor, putative, expressed	GO:0008610	lipid biosynthetic process	biological_pr ocess
LOC_Os12g37260	lipoxigenase 2.1, chloroplast precursor, putative, expressed	GO:0008610	lipid biosynthetic process	biological_pr ocess
LOC_Os12g37350	lipozygenase protein, putative	GO:0008610	lipid biosynthetic process	biological_pr ocess
LOC_Os01g01710	1-deoxy-D-xylulose 5-phosphate reductoisomerase, chloroplast precursor, putative, expressed	GO:0008152	metabolic process	biological_pr ocess
LOC_Os01g13590	isoflavone reductase homolog IRL, putative	GO:0008152	metabolic process	biological_pr ocess
LOC_Os01g53350	anthocyanidin 5,3-O-glucosyltransferase, putative, expressed	GO:0008152	metabolic process	biological_pr ocess
LOC_Os01g58100	polyphenol oxidase, putative	GO:0008152	metabolic process	biological_pr ocess
LOC_Os01g71350	glycosyl hydrolases family 17, putative, expressed	GO:0008152	metabolic process	biological_pr ocess
LOC_Os02g01150	erythronate-4-phosphate dehydrogenase domain containing protein, expressed	GO:0008152	metabolic process	biological_pr ocess
LOC_Os02g08100	AMP-binding domain containing protein, expressed	GO:0008152	metabolic process	biological_pr ocess
LOC_Os02g35039	NAD dependent epimerase/dehydratase family protein, putative, expressed	GO:0008152	metabolic process	biological_pr ocess
LOC_Os02g36140	terpene synthase, putative, expressed	GO:0008152	metabolic process	biological_pr ocess
LOC_Os02g48964	WD-40 repeat family protein, putative, expressed	GO:0008152	metabolic process	biological_pr ocess
LOC_Os02g57180	NADH dehydrogenase 1 alpha subcomplex subunit 9, mitochondrial precursor, putative, expressed	GO:0008152	metabolic process	biological_pr ocess
LOC_Os03g03720	glyceraldehyde-3-phosphate dehydrogenase, putative, expressed	GO:0008152	metabolic process	biological_pr ocess
LOC_Os03g08999	dehydrogenase, putative, expressed	GO:0008152	metabolic process	biological_pr ocess
LOC_Os03g09250	inositol-3-phosphate synthase, putative, expressed	GO:0008152	metabolic process	biological_pr ocess
LOC_Os03g36750	cbbY, putative, expressed	GO:0008152	metabolic process	biological_pr ocess
LOC_Os03g56280	lactate/malate dehydrogenase, putative, expressed	GO:0008152	metabolic process	biological_pr ocess

LOC_Os04g15920	dehydrogenase, putative, expressed	GO:0008152	metabolic process	biological_pr ocess
LOC_Os04g27340	terpene synthase, putative, expressed	GO:0008152	metabolic process	biological_pr ocess
LOC_Os04g31700	methylisocitrate lyase 2, putative, expressed	GO:0008152	metabolic process	biological_pr ocess
LOC_Os04g32020	2-oxoglutarate dehydrogenase E1 component, mitochondrial precursor, putative, expressed	GO:0008152	metabolic process	biological_pr ocess
LOC_Os04g33190	AMP-binding enzyme, putative, expressed	GO:0008152	metabolic process	biological_pr ocess
LOC_Os04g37619	zeaxanthin epoxidase, chloroplast precursor, putative, expressed	GO:0008152	metabolic process	biological_pr ocess
LOC_Os04g53810	leucoanthocyanidin reductase, putative, expressed	GO:0008152	metabolic process	biological_pr ocess
LOC_Os05g31140	glycosyl hydrolases family 17, putative, expressed	GO:0008152	metabolic process	biological_pr ocess
LOC_Os06g15990	aldehyde dehydrogenase, putative, expressed	GO:0008152	metabolic process	biological_pr ocess
LOC_Os06g36840	cysteine synthase, putative, expressed	GO:0008152	metabolic process	biological_pr ocess
LOC_Os07g05820	hydroxyacid oxidase 1, putative, expressed	GO:0008152	metabolic process	biological_pr ocess
LOC_Os07g06830	gibberellin receptor GID1L2, putative, expressed	GO:0008152	metabolic process	biological_pr ocess
LOC_Os07g46460	ferredoxin-dependent glutamate synthase, chloroplast precursor, putative, expressed	GO:0008152	metabolic process	biological_pr ocess
LOC_Os07g46520	rhythmically expressed gene 2 protein, putative, expressed	GO:0008152	metabolic process	biological_pr ocess
LOC_Os07g46920	sex determination protein tasselseed-2, putative, expressed	GO:0008152	metabolic process	biological_pr ocess
LOC_Os08g03290	glyceraldehyde-3-phosphate dehydrogenase, putative, expressed	GO:0008152	metabolic process	biological_pr ocess
LOC_Os08g04500	terpene synthase, putative, expressed	GO:0008152	metabolic process	biological_pr ocess
LOC_Os08g07080	terpene synthase, putative, expressed	GO:0008152	metabolic process	biological_pr ocess
LOC_Os08g34280	cinnamoyl-CoA reductase, putative, expressed	GO:0008152	metabolic process	biological_pr ocess
LOC_Os10g28080	glycosyl hydrolase, putative, expressed	GO:0008152	metabolic process	biological_pr ocess
LOC_Os10g28200	NAD dependent epimerase/dehydratase family protein, putative, expressed	GO:0008152	metabolic process	biological_pr ocess
LOC_Os11g07930	oxidoreductase, short chain dehydrogenase/reductase family domain containing family, expressed	GO:0008152	metabolic process	biological_pr ocess
LOC_Os12g07110	acyl-CoA synthetase protein, putative, expressed	GO:0008152	metabolic process	biological_pr ocess
LOC_Os12g12560	NADP-dependent oxidoreductase, putative, expressed	GO:0008152	metabolic process	biological_pr ocess

LOC_Os12g23180	3-beta hydroxysteroid dehydrogenase/isomerase family protein, putative, expressed	GO:0008152	metabolic process	biological_pr ocess
LOC_Os01g13590	isoflavone reductase homolog IRL, putative	GO:0006808	regulation of nitrogen utilization	biological_pr ocess
LOC_Os02g57180	NADH dehydrogenase 1 alpha subcomplex subunit 9,mitochondrial precursor, putative, expressed	GO:0006808	regulation of nitrogen utilization	biological_pr ocess
LOC_Os08g34280	cinnamoyl-CoA reductase, putative, expressed	GO:0006808	regulation of nitrogen utilization	biological_pr ocess
LOC_Os03g18850	pathogenesis-related Bet v I family protein, putative, expressed	GO:0009607	response to biotic stimulus	biological_pr ocess
LOC_Os12g36830	pathogenesis-related Bet v I family protein, putative, expressed	GO:0009607	response to biotic stimulus	biological_pr ocess
LOC_Os12g36860	pathogenesis-related protein 10, putative, expressed	GO:0009607	response to biotic stimulus	biological_pr ocess
LOC_Os12g36880	pathogenesis-related Bet v I family protein, putative, expressed	GO:0009607	response to biotic stimulus	biological_pr ocess
LOC_Os02g35039	NAD dependent epimerase/dehydratase family protein, putative, expressed	GO:0006694	steroid biosynthetic process	biological_pr ocess
LOC_Os02g57180	NADH dehydrogenase 1 alpha subcomplex subunit 9,mitochondrial precursor, putative, expressed	GO:0006694	steroid biosynthetic process	biological_pr ocess
LOC_Os08g34280	cinnamoyl-CoA reductase, putative, expressed	GO:0006694	steroid biosynthetic process	biological_pr ocess
LOC_Os12g23180	3-beta hydroxysteroid dehydrogenase/isomerase family protein, putative, expressed	GO:0006694	steroid biosynthetic process	biological_pr ocess
LOC_Os01g64660	fructose-1,6-bisphosphatase, putative, expressed	GO:0006810	transport	biological_pr ocess
LOC_Os02g43860	amino acid permease, putative, expressed	GO:0006810	transport	biological_pr ocess
LOC_Os02g54730	transmembrane amino acid transporter protein, putative, expressed	GO:0006810	transport	biological_pr ocess
LOC_Os03g05620	inorganic phosphate transporter, putative, expressed	GO:0006810	transport	biological_pr ocess
LOC_Os03g12590	coatomer subunit gamma-1, putative, expressed	GO:0006810	transport	biological_pr ocess
LOC_Os03g37830	potassium transporter, putative, expressed	GO:0006810	transport	biological_pr ocess
LOC_Os03g62200	ammonium transporter protein, putative, expressed	GO:0006810	transport	biological_pr ocess
LOC_Os04g15920	dehydrogenase, putative, expressed	GO:0006810	transport	biological_pr ocess
LOC_Os04g43070	ammonium transporter protein, putative, expressed	GO:0006810	transport	biological_pr ocess
LOC_Os05g06350	importin subunit alpha, putative, expressed	GO:0006810	transport	biological_pr ocess
LOC_Os07g26490	ankyrin repeat domain containing protein, expressed	GO:0006810	transport	biological_pr ocess
LOC_Os07g36470	vacuolar ATP synthase subunit H, putative, expressed	GO:0006810	transport	biological_pr ocess

LOC_Os07g37320	transporter family protein, putative, expressed	GO:0006810	transport	biological_pr ocess
LOC_Os08g31410	sulfate transporter, putative, expressed	GO:0006810	transport	biological_pr ocess
LOC_Os09g08390	CRAL/TRIO domain containing protein, expressed	GO:0006810	transport	biological_pr ocess
LOC_Os09g27580	potassium transporter, putative, expressed	GO:0006810	transport	biological_pr ocess
LOC_Os12g02320	LTPL12 - Protease inhibitor/seed storage/LTP family protein precursor, expressed	GO:0006810	transport	biological_pr ocess
LOC_Os12g07110	acyl-CoA synthetase protein, putative, expressed	GO:0006810	transport	biological_pr ocess
LOC_Os12g42850	amino acid permease, putative, expressed	GO:0006810	transport	biological_pr ocess
LOC_Os02g13840	citrate synthase, putative, expressed	GO:0006099	tricarboxylic cycle	acid biological_pr ocess
LOC_Os03g56280	lactate/malate dehydrogenase, putative, expressed	GO:0006099	tricarboxylic cycle	acid biological_pr ocess
LOC_Os08g27840	phosphoenolpyruvate carboxylase, putative, expressed	GO:0006099	tricarboxylic cycle	acid biological_pr ocess

Table S4. List and microarray data of 95 candidate genes associated with enhanced bacterial blight resistance from microarray experiments

RGAP_Locus_ID	MapMan Classification	Putative Function	Feature	log ₂ NRRox(SS)/ LG(S)_1d	log ₂ NH1ox(R)/ LG(S)_1d	log ₂ Xa21(R)/ TP309(S)_2d	Log ₂ BTH/ SA(hormone) /Mock	Log ₂ JA(hormone) /Mock_leaf
LOC_Os11g11960	Stress Biotic: Disease resistance	disease resistance protein RPM1	NRR, NH1	-1.008	0.903	0.399		
LOC_Os11g12340	Stress Biotic: Disease resistance	disease resistance protein RPM1	NRR, NH1	-1.245	0.871	-0.18	1.657	-0.57
LOC_Os12g25170	Stress Biotic: Disease resistance	NB-ARC domain containing disease resistance protein	NRR, NH1, Xa21	-0.815	0.799	1.148	0.2	-0.75
LOC_Os08g07330	Stress Biotic: Disease resistance	RGH1A	NH1, Xa21	-0.593	0.637	0.913	0.255	0.18
LOC_Os02g43360	Redox: Respiratory burst	cytochrome b5-like Heme	NH1, Xa21	-0.299	0.621	1.187	-0.06	0.72
LOC_Os10g28200	Redox: Respiratory burst	NAD dependent epimerase	NRR, Xa21	-0.77	-0.84	1.239	0.625	-0.53
LOC_Os12g08810	Redox: Respiratory burst	VTC2	NH1, Xa21	0.065	1.364	1.038	-0.19	0.73
LOC_Os07g48020	Misc: Respiratory burst	peroxidase precursor	NH1, Xa21	-0.394	1.416	2.109	1.746	-1.79
LOC_Os07g48050	Misc: Respiratory burst	peroxidase precursor	NH1, Xa21	-0.161	1.969	2.452	2.279	-0.91
LOC_Os07g28480	Misc: Respiratory	glutathione	NRR, Xa21	-0.812	-1.14	1.079	0.27	-1.92

	burst	S-transferase						
LOC_Os09g29200	Misc: Respiratory burst	glutathione S-transferase	NRR, NH1, Xa21	-1.057	0.88	0.982	1.166	-0.06
LOC_Os04g37619	Hormone Metabolism: ABA	zeaxanthin epoxidase	NRR, Xa21	-0.631	-0.11	1.08	-0.39	0.433
LOC_Os02g47510	Hormone Metabolism: ABA	9-cis-epoxycarotenoid dioxygenase 1	NRR, Xa21	-0.89	-0.71	0.944	-0.11	-1.44
LOC_Os04g49194	Hormone Metabolism: Ethylene	naringenin,2-oxoglutarate 3-dioxygenase	NRR, NH1	-0.84	0.663	0.398	0.941	0.89
LOC_Os04g49210	Hormone Metabolism: Ethylene	naringenin,2-oxoglutarate 3-dioxygenase	NH1, Xa21	-0.31	1.544	0.818	3.918	0.636
LOC_Os10g39140	Hormone Metabolism: Ethylene	flavonol synthase/flavanone 3-hydroxylase	NRR, NH1	-0.773	1.515	-0.05	3.239	2.323
LOC_Os08g26820	Hormone Metabolism: Ethylene	unknown function domain containing protein	NRR, NH1	-0.822	0.613	-0.64	1.824	-0.42
LOC_Os08g26840	Hormone Metabolism: Ethylene	unknown function domain containing protein	NRR, NH1	-0.935	0.608	-0.78	2.433	0.314
LOC_Os12g37260	Hormone Metabolism: JA	lipoxygenase 2.1, chloroplast precursor	NH1, Xa21	-0.565	2.815	2.427	3.154	1.946
LOC_Os12g37350	Hormone Metabolism: JA	lipoxygenase protein	NH1, Xa21	-0.162	1.039	0.771	2.682	1.506
LOC_Os03g32314	Hormone Metabolism: JA	allene oxide cyclase 4	NRR, Xa21	-0.706	-0	1.094	0.027	1.532
LOC_Os02g48770	Hormone Metabolism: SA	SAM dependent carboxyl methyltransferase	NH1, Xa21	-0.002	1.239	1.461	0.693	3.978
LOC_Os05g01140	Hormone Metabolism: SA	methyltransferase	NH1, Xa21	0.163	1.246	1.775	0.23	-0.01
LOC_Os03g10880	Signalling	BTBN5	NRR, Xa21	-0.971	-1.08	1.268	0.047	-1.05
LOC_Os01g04280	Signalling: Calcium	calmodulin binding protein	NRR, NH1	-0.836	0.998	-0.22	1.556	0.374
LOC_Os02g08120	Signalling: Calcium	calmodulin binding protein	NRR, Xa21	-0.836	-0.05	0.975	0.068	-0.15
LOC_Os04g32950	Signalling: Calcium	calreticulin precursor protein	NRR, Xa21	-1.003	0.264	1.177	0.432	1.291
LOC_Os05g43170	Signalling: Calcium	calreticulin precursor protein	NRR, Xa21	-1.296	-0.1	0.986	0.707	0.022
LOC_Os02g48000	Signalling:	TBC domain	NRR, Xa21	-0.885	-0.02	0.754	-0.01	1.199

	G-protein	containing protein						
LOC_Os12g31440	Signalling: G-protein	expressed protein	NRR, Xa21	-0.73	-0.07	0.926	-0.05	-0.19
LOC_Os07g03900	Signalling: Receptor kinases	lectin-like receptor kinase	NH1, Xa21	-0.175	0.938	0.829	-0.02	-0.08
LOC_Os11g39370	Signalling: Receptor kinases	BRASSINOSTEROID INSENSITIVE 1	NRR, NH1, Xa21	-1.042	1.829	0.781	0.943	0.155
LOC_Os02g02120	Signalling: Receptor kinases	OsWAK11	NRR, NH1, Xa21	-1.136	0.985	0.673	0.413	-0.06
LOC_Os05g34270	Signalling: Receptor kinases	inactive receptor kinase	NRR, NH1	-1.018	0.821	0.305	0.811	0.288
LOC_Os05g40270	Signalling: Receptor kinases	expressed protein	NH1, Xa21	-0.58	0.814	0.644	-0.15	-1.21
LOC_Os09g39650	Signalling: Receptor kinases	protein kinase family protein	NRR, NH1, Xa21	-0.932	1.144	0.855	0.299	-0.3
LOC_Os11g39370	Signalling: Receptor kinases	BRASSINOSTEROID INSENSITIVE 1	NRR, NH1, Xa21	-1.042	1.829	0.781	0.943	0.155
LOC_Os11g46810	Signalling: Receptor kinases	retrotransposon protein	NRR, NH1	-1.018	1.377	-0.47		
LOC_Os12g10740	Signalling: Receptor kinases	leucine-rich repeat family protein	NRR, Xa21	-1.137	0.384	1.261	0.895	-0.62
LOC_Os09g20350	RNA Regulation of transcription	ethylene-responsive transcription factor	NRR, Xa21	-0.685	-0.14	1.089	0.057	0.047
LOC_Os05g46020	RNA Regulation of transcription	WRKY7	NRR, NH1	-0.765	0.866	0.015	2.482	1.146
LOC_Os09g25060	RNA Regulation of transcription	WRKY76	NRR, NH1, Xa21	-0.982	1.784	0.68	4.089	0.357
LOC_Os09g25070	RNA Regulation of transcription	WRKY62	NRR, NH1, Xa21	-1.172	1.136	1.356	5.449	0.267
LOC_Os11g02530	RNA Regulation of transcription	WRKY40	NH1, Xa21	-0.215	2.101	0.735	2.091	2.903
LOC_Os11g02540	RNA Regulation of transcription	WRKY50	NRR, NH1, Xa21	-0.697	2.434	0.938		
LOC_Os12g02450	RNA Regulation of transcription	WRKY64	NH1, Xa21	-0.095	2.125	0.896	2.504	2.868
LOC_Os12g02470	RNA Regulation of transcription	WRKY65	NH1, Xa21	-0.329	2.499	0.981		
LOC_Os03g18850	Stress Biotic: PR protein	pathogenesis-related Bet v I	NH1, Xa21	0.66	1.05	1.11	0.43	-4.09
LOC_Os12g36830	Stress Biotic: PR protein	pathogenesis-related Bet v I	NH1, Xa21	-0.33	1.62	1.67	1.65	1.48

LOC_Os12g36860	Stress Biotic: PR protein	pathogenesis-related Bet v I	NH1, Xa21	-0.21	1.41	0.6	1.95	2.18
LOC_Os12g36880	Stress Biotic: PR protein	pathogenesis-related Bet v I	NRR, NH1, Xa21	-0.64	2	1.57	2.08	4.23
LOC_Os11g37950	Stress Biotic: PR protein	WIP3	NH1, Xa21	-0.401	0.89	1.718	0.568	3.543
LOC_Os11g37960	Stress Biotic: PR protein	WIP4	NH1, Xa21	0.286	0.69	0.867	0.143	0.367
LOC_Os12g43380	Stress Biotic: PR protein	thaumatin	NH1, Xa21	-0.418	2.357	0.71	1.26	3.374
LOC_Os01g71350	Misc: PR protein	glycosyl hydrolases family 17	NH1, Xa21	0.5	0.652	1.205	0.594	1.643
LOC_Os05g31140	Misc: PR protein	glycosyl hydrolases family 17	NRR, Xa21	-0.788	-0.75	1.859	0.322	1.236
LOC_Os07g35560	Misc: PR protein	glucan endo-1,3-beta-glucosidase precursor	NRR, Xa21	-1.219	0.426	1.392	1.298	0.991
LOC_Os03g22420	Secondary Metabolism	AAA-type ATPase family protein	NH1, Xa21	-0.443	0.668	1.087	-0.02	0.284
LOC_Os05g05940	Secondary Metabolism	stress-related protein	NRR, Xa21	-0.94	-0.06	1.064	0.151	0.287
LOC_Os05g19910	Secondary Metabolism	transferase family protein	NH1, Xa21	-0.198	1.207	0.853	0.087	-0.73
LOC_Os01g01710	Secondary Metabolism	1-deoxy-D-xylulose 5-phosphate reductoisomerase	NRR, Xa21	-0.733	-0.22	1.159		
LOC_Os02g39160	Secondary Metabolism	hydroxymethylbutenyl 4-diphosphate synthase	NRR, Xa21	-0.619	0.434	1.653	-0.14	0.769
LOC_Os02g36140	Secondary Metabolism	terpene synthase	NH1, Xa21	-0.203	1.102	0.622	0.529	2.143
LOC_Os04g27340	Secondary Metabolism	terpene synthase	NH1, Xa21	-0.208	1.485	0.967		
LOC_Os08g04500	Secondary Metabolism	terpene synthase	NH1, Xa21	-0.264	1.487	1.611	0.829	-0.78
LOC_Os08g07080	Secondary Metabolism	terpene synthase	NRR, NH1, Xa21	-1.027	3.702	3.053	1.262	0.144
LOC_Os04g15920	Secondary Metabolism	dehydrogenase	NH1, Xa21	-0.173	1.197	0.662	0.505	2.103
LOC_Os02g08100	Secondary Metabolism	AMP-binding domain containing protein	NH1, Xa21	-0.036	0.858	0.697	-0.23	0.368

LOC_Os04g53810	Secondary Metabolism	leucoanthocyanidin reductase	NRR, Xa21	-0.881	0.054	1.585	1.545	0.797
LOC_Os01g13590	Secondary Metabolism	isoflavone reductase homolog IRL	NH1, Xa21	0.829	1.694	1.035		
LOC_Os01g37910	Protein Degradation	vacuolar-processing enzyme precursor	NRR, Xa21	-1.349	-0.5	1.99	0.193	-1.02
LOC_Os01g58580	Protein Degradation	ICE-like protease p20 domain containing protein	NRR, Xa21	-0.822	-0.41	1.179	0.003	0.563
LOC_Os11g24540	Protein Degradation	signal peptide peptidase-like 2B	NRR, Xa21	-0.66	-0.16	0.972	-0.14	0.45
LOC_Os03g13970	Protein Degradation	26S proteasome non-ATPase regulatory subunit 4	NRR, Xa21	-0.633	-0.42	1.06	-0.14	0.229
LOC_Os04g57300	Protein Degradation	phosphatidylinositol 3- and 4-kinase family protein	NRR, Xa21	-0.763	-0.67	1.322	0.016	-0.17
LOC_Os01g48930	Protein Degradation	splicing factor-related	NRR, Xa21	-0.625	-0.63	1.411	0.285	-0.83
LOC_Os02g06640	Protein Degradation	ubiquitin family protein	NRR, NH1, Xa21	-1.064	0.694	0.61	-0.03	0.854
LOC_Os02g05710	Protein Degradation	expressed protein	NRR, Xa21	-0.822	-0.46	1.091	-0.1	0.469
LOC_Os04g51400	Protein Degradation	zinc finger, C3HC4 type domain containing protein	NRR, Xa21	-0.918	-0.73	1.3	0.144	-1.39
LOC_Os06g03580	Protein Degradation	zinc RING finger protein	NRR, NH1	-0.678	0.916	-0.45	1.465	-0.12
LOC_Os11g36430	Protein Degradation	zinc finger, C3HC4 type domain containing protein	NRR, Xa21	-0.874	-0.43	0.982	0.031	-0.24
LOC_Os02g10700	Protein Degradation	OsFBL7	NRR, Xa21	-1.001	0.262	1.108	1.087	-0.42
LOC_Os06g40360	Protein Degradation	OsFBL30	NRR, Xa21	-0.945	0.442	0.789	0.491	-0.49
LOC_Os05g33610	Protein Degradation	expressed protein	NRR, Xa21	-0.677	-0.56	1.021	-0.29	0.19
LOC_Os02g57410	Protein Degradation	OTU-like cysteine protease family protein	NRR, Xa21	-0.81	-0.43	1.278	-0.12	0.141
LOC_Os01g64840	Protein Degradation	aspartic proteinase nepenthesin-1 precursor	NH1, Xa21	0.637	1.506	0.868	-0.03	0.021

LOC_Os05g04630	Protein Degradation	retrotransposon protein	NRR, Xa21	-0.665	-0.31	1.266	0.009	0.377
LOC_Os09g37012	Protein Degradation	eukaryotic aspartyl protease domain containing protein	NRR, Xa21	-0.647	-0.37	1.507	0.042	-0.09
LOC_Os09g36300	Protein Degradation	OsLonP4 - Putative Lon protease homologue	NRR, Xa21	-0.933	-0.21	0.823	0.418	0.057
LOC_Os03g22420	Protein Degradation	AAA-type ATPase family protein	NH1, Xa21	-0.443	0.668	1.087	-0.02	0.284
LOC_Os03g58790	Protein Degradation	ATPase	NRR, NH1, Xa21	-0.665	0.748	1.072	2.85	0.993
LOC_Os07g29290	Cellwall Modification	expansin precursor	NH1, Xa21	-0.166	0.663	0.914	-0.55	1.402
LOC_Os01g01160	Stress Abiotic	heat shock protein DnaJ	NH1, Xa21	0.508	1.146	0.783		
LOC_Os03g31300	Stress Abiotic	chaperone protein clpB 1	NRR, Xa21	-0.695	0.16	1.389	-0.23	-0.97

Table S5. Primer sequences of genes used for real-time RT-PCR analysis

Locus ID	Forward primer	Reverse primer
<i>Os09g20350</i>	TGCAGCTATAGATCTGTCAG	TGGATGTAGTGCATCTGGG
<i>Os05g46020</i>	AAGAAGTCCGTCAAGAACAG	GCGTAGTACACCGTGCTG
<i>Os09g25060</i>	ACGCTCGACCTACCAAGAA	AACTTGGGGTTCGCTGGTGAG
<i>Os09g25070</i>	TTCCGCTGCGCATTCGCG	TGCTGGCTCGTAGTGCAG
<i>Os11g02530</i>	GCCAACAGCTACAATGGC	TTCCGCAGCCTGCAGATC
<i>Os11g02540</i>	CATGCCGACAGATGATCGC	CAAGGAGCAAATCGTCCATC
<i>Os12g02450</i>	GCCAACAGCTACAATGGC	CGCAGCCTGCAGCTCGCT
<i>Os12g02470</i>	GACGACCACCTCTGGTTCT	CAAATGGGTGATGTTAGCGC
<i>Os03g18850</i>	GTCAGGCAGTTCAACTTCAC	CGGCTCCACCTTGATGTG
<i>Os12g36830</i>	CTGTCACCACCATGAAGCTC	GCCAAGCAAGAGCCGCA
<i>Os12g36860</i>	CAATGCAGCACGCGTGCTA	GAAGTAGCCGTCGACCATC
<i>Os12g36880</i>	CGCCGCAAGTCATGTCCTA	ATAGTAGCCATCCACGATG
<i>Os11g37950</i>	GTCAGAAGTATGGCTGGAC	TGTCCCAGTCCAGGTCAAG
<i>Os11g37960</i>	GAAGTATGGATGGACCGCT	AGCCTTGACCGTCGCTGT
<i>Os12g43380</i>	AGCATCTCGATCCTACCACA	ACCGGTTGGTGATGGTGAA
<i>Os01g71350</i>	CGTACAACCAGAAGCTTATC	TAATTTTGTAGGACGGCGAC
<i>Os05g31140</i>	TCTACAACCAGAACCTCATC	AGAAGCTGATGGGGTAGAC
<i>Os07g35560</i>	TATTGTCTACAAGCCTTCAC	CTTGGTGTGAGGGTCAAAGC
<i>Os01g22490(OsUbi5)</i>	GCACAAGCACAGAAGGTGA	GCCTGCTGGTTGTAGACGTA
<i>Os03g08010(OseEF1)</i>	TCAAGTTTGCTGAGCTGGTG	TTTGCTCATGTCCCGCAC

Table S6. Summary of functionally characterized genes in our candidate genes

Locus_ID	Gene name	Abbreviation of gene name	Category of function	Description of gene function	References (DOI)
LOC_Os01g09800	NONEXPRESSOR OF PATHOGENESIS-RELATED GENES1	OsNPR1	Bacterial blight resistance	Enhanced bacterial blight resistance and herbivore susceptibility.	10.1111/j.1467-7652.2007.00243.x
LOC_Os09g25070	OsWRKY62	OsWRKY62	Bacterial blight resistance	Resistance to <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> .	10.1093/mp/ssn024
LOC_Os02g08440	OsWRKY71	OsWRKY71	Bacterial blight resistance	Resistance to <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> .	10.1016/j.jplph.2006.07.006
LOC_Os09g25060	OsWRKY76	OsWRKY76	Bacterial blight resistance	Resistance to <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> .	10.1007/s12284-010-9039-6
LOC_Os10g41980	RALFL26	Rir1b	Blast resistance	Resistance to <i>Magnaporthe grisea</i> .	10.1023/A:1006423232753
LOC_Os06g03580	zinc RING finger protein	osbbi1	Blast resistance	Resistance to <i>Magnaporthe oryzae</i> . Cell wall defense.	10.1038/cr.2011.4
LOC_Os05g31140	beta-glucanase1	Gns1	Blast resistance	Resistance to <i>Magnaporthe grisea</i> . Lesion mimic.	10.1023/A:1020714426540
LOC_Os03g51030	phytochromeA	phyA	Blast resistance	Resistance to <i>Magnaporthe grisea</i> .	10.1093/mp/ssr005
LOC_Os03g20380	calcineurin B-like protein-interacting protein kinase03	OsCIPK03	Cold tolerance	Cold tolerance.	10.1104/pp.107.101295
LOC_Os03g12290	glutamine synthetase1;2	GS1;2	Cold tolerance	"Leaf nitrogen content. Cold, drought and salinity tolerance. Basta selection resistance."	10.1007/s00299-008-0665-z
LOC_Os03g24040	drought-induced SINA protein 1	OsDIS1	Drought tolerance	Drought tolerance.	10.1104/pp.111.180893
LOC_Os07g45570	BL-enhanced 2	OsBLE2	Culm leaf	Dwarfism. Leaf angle. Brassinosteroid sensitivity.	10.1023/A:1025001304994
LOC_Os02g09490	GOLDHULLAN DINTERNODE2	gh2	Culm leaf	Lignin content. Seed color. Internode color.	10.1104/pp.105.073007
LOC_Os02g08100	4-Coumarate:coenzyme A ligase	Os4CL3	Dwarf	Lignin content. Dwarfism. Culm length. Anther development.	10.1104/pp.111.178301
LOC_Os08g06480	Lisencephaly type-1-like 1	OsLIS-L1	Dwarf	Dwarfism. Elongation of uppermost internode. Pollen development.	10.1007/s00425-011-1532-7
LOC_Os01g22010	S-Adenosyl-l-methionine synthetase2	OsSAMS2	Dwarf	Dwarfism. Fertility. Germination rate. Flowering time.	10.1016/j.jplph.2011.05.020
LOC_Os01g48680	two-pore channel 1	Ostpc1	Dwarf	Sensitivity to Ca ⁺ in growth rate.	10.1093/pcp/pch082
LOC_Os01g55540	Aspartate aminotransferase 2	OsAAT2	Eating quality	Seed amino acid and protein content.	10.1007/s00122-009-0988-3
LOC_Os08g32870	betaine aldehyde dehydrogenase2	Badh2	Eating quality	Fragrance rice. 2-acetyl-1-pyrroline	10.1105/tpc.108.058917

				biosynthesis.	
LOC_Os05g33570	floury endosperm-4	flo4	Eating quality	Seed protein and lipid content.	10.1111/j.1365-313X.2005.02423.x
LOC_Os09g29404	isoamylase3	isa3	Eating quality	Seed starch content.	10.1093/pcp/pcr058
LOC_Os03g09250	rice myo -inositol 3-phosphate synthase 1	RINO1	Eating quality	Seed phytic acid content.	10.1093/pcp/pcp071
LOC_Os02g43370	yellow stripe 1 like 2	OsYSL2	Eating quality	Fe and Mn translocation from root to shoot and endosperm.	10.1111/j.1365-313X.2010.04158.x
LOC_Os09g06464	CONSTANS-LIKE 3	OsCO3	Flowering	Flowering time under short day condition.	10.1007/s00425-008-0742-0
LOC_Os01g15900	rice Dof daily fluctuations 1	Rdd1	Flowering	Grain length and width. 1000-grain weight. Flowering time.	10.1111/j.1365-3040.2009.01954.x
LOC_Os03g13970	26S proteasome non-ATPase regulatory subunit 4	RPN10	Other soil stress tolerance	Canavanine resistance.	10.5511/plantbiotechnology.21.233
LOC_Os01g72370	bHLH	OsIRO2	Other soil stress tolerance	Fe uptake under Fe-deficient conditions. Secretion of mugineic acid family phytosiderophores.	10.1111/j.1365-313X.2007.03149.x
LOC_Os07g12890	metal cation transporter	OsZIP8	Other soil stress tolerance	Zn uptake and translocation.	10.1007/s10059-010-0069-0
LOC_Os05g45410	Heat shock transcription factor A4a	OsHsfA4a	Other soil stress tolerance	Cadmium tolerance.	10.1105/tpc.109.066902
LOC_Os05g48390	LEAF TIP NECROSIS 1	ltn1	Other soil stress tolerance	Phosphate uptake and translocation.	10.1104/pp.110.170209
LOC_Os02g20360	Nicotianamine aminotransferase1	naat1	Other soil stress tolerance	Fe acquisition strategy.	10.1104/pp.107.107912
LOC_Os03g05620	PHOSPHATE TRANSPORTER 1	OsPT1	Other soil stress tolerance	Phosphate starvation tolerance. Phosphate uptake.	10.1104/pp.112.196345
LOC_Os06g09370	Pi starvation induced transcription factor 1	OsPTF1	Other soil stress tolerance	Phosphate starvation tolerance.	10.1104/pp.105.063115
LOC_Os06g40120	SYG/PHO81/XPR1 domain1	OsSPX1	Other soil stress tolerance	Phosphate homeostasis.	10.1111/j.1365-313X.2008.03734.x
LOC_Os03g55240	cytochrome P450	bel	Other stress resistance	Herbicide resistance.	10.1007/s11103-006-0058-z
LOC_Os01g01660	isoflavone reductase-like	OsIRL	Other stress resistance	Resistance to reactive oxygen species.	10.1111/j.1399-3054.2009.01290.x
LOC_Os08g03290	cytosolic GAPDH	OsGAPC3	Salinity tolerance	Salinity tolerance.	10.1007/s11240-

	protein 3					011-9950-6
LOC_Os07g48430	root hairless1	rth1	Root	Root hair formation.		10.1270/jsbbs.5 9.13
LOC_Os01g64660	cytosolic fructose-1,6-bisph osphatase1	oscfbp1	Source activity	Photosynthetic sucrose biosynthesis. Growth retardation.		10.1111/j.1365- 3040.2008.0189 0.x
LOC_Os07g04180	amino acid transporter60	OsAAT60	Source activity	Carbon content.		10.1007/s11738- 012-0995-x
LOC_Os10g41780	Chlorophyllide a oxygenase	cao	Source activity	Chlorophyll content.		10.1270/jsbbs.5 5.361
LOC_Os09g36200	staygreen	sgr	Source activity	Leaf senescence. Chlorophyll degradation.		10.1105/tpc.106. 044891
LOC_Os01g01280	Thylakoid lumen protein 27	OsTLP27	Source activity	Photochemical efficiency. Size and number of grana.		10.1016/j.plants ci.2012.06.006

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