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* (*1106*) 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. $\log_2 R/S \ge 0.6$ or $\log_2 SS/S \le -0.6$) 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 (tap-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 μ L solution containing a 1- μ L 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 °C, followed by 21 to 40 cycles of PCR (94 °C for 45 sec, 60 °C for 45 sec, and 72 °C for 1 minute), and a final 10 minutes at 72 °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.

	Log2	2 fold cha	inge					
ن NRRox(SS)/LG(S)_1 d	NHlox(R)/LG(S)_l d	Xa21(R)/TP309(S)_2 d =	BTH/SA(hormone)/Mock	JA(hormone)/Mock	REARLAN		President Transfer	Feature
					LOC_Os11g11960 St LOC_Os11g12340 St LOC_Os12g25170 St LOC_Os08g07330 St	tress Biotic: Disease resistance tress Biotic: Disease resistance tress Biotic: Disease resistance tress Biotic: Disease resistance	disease resistance protein RPM1 disease resistance protein RPM1 NB-ARC domain containing disease resistance protein RGH1A	NRR, NH1 NRR, NH1 NRR, NH1, Xa21 NH1, Xa21
					LOC_0s02g43360 R LOC_0s10g28200 R LOC_0s12g08810 R LOC_0s07g48020 M LOC_0s07g48050 M LOC_0s07g28480 M LOC_0s09g29200 M	edox: Respiratory burst edox: Respiratory burst edox: Respiratory burst lise: Respiratory burst lise: Respiratory burst lise: Respiratory burst lise: Respiratory burst	cytochrome b5-like Herne NAD dependent epimense VTC2 peroxidise procursor peroxidise procursor gibantinne S-transferase gibantinne S-transferase	NH1, Xa21 NRR, Xa21 NH1, Xa21 NH1, Xa21 NH1, Xa21 NRR, Xa21 NRR, Xa21 NRR, NH1, Xa21
					LOC 0s04g37619 H LOC 0s02g477610 H LOC 0s04g49194 H LOC 0s10g49194 H LOC 0s10g39140 H LOC 0s08g26820 H LOC 0s08g26820 H LOC 0s12g37360 H LOC 0s12g37350 H LOC 0s03g32314 H LOC 0s03g43714 H LOC 0s03g414 H	ormone Metabolism: ABA ormone Metabolism: Ethylene ormone Metabolism: Ethylene ormone Metabolism: Ethylene ormone Metabolism: Ethylene ormone Metabolism: Ethylene ormone Metabolism: JA ormone Metabolism: JA ormone Metabolism: JA ormone Metabolism: SA	zeazathia epoxidase Josci-epoxycaronenial diaxygenase 1 naringenia, -oxoghtana t-dooxygenase maringenia, -oxoghtana t-dooxygenase flavonol synthuse/flavanene 3-hydroxylase unkrown fanction domain containing protein lipoxygenase 21, cholorophast precursor lipoxygenase protein allene oxide cyclose 4 SAM dependent carboxyl methyltransferase methyltransferase	NRR, Xa21 NRR, Xa21 NRR, NH1 NH1, Xa21 NRR, NH1 NRR, NH1 NRR, NH1 NRR, NH1 NRR, NH1 NH1, Xa21 NH1, Xa21 NH1, Xa21 NH1, Xa21
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					LOC_0s09g20350 RI LOC_0s05g46020 RI LOC_0s09g25060 RI LOC_0s09g25070 RI LOC_0s11g02530 RI LOC_0s11g02530 RI LOC_0s12g02450 RI LOC_0s12g02450 RI	NA Regulation of transcription NA Regulation of transcription	edly/enc-responsive transcription factor WRKY76 WRKY76 WRKY40 WRKY40 WRKY50 WRKY64 WRKY64	NRR, Xa21 NRR, NH1 NRR, NH1, Xa21 NRR, NH1, Xa21 NH1, Xa21 NRR, NH1, Xa21 NH1, Xa21 NH1, Xa21
					LOC_0s03g18850 St LOC_0s12g36800 St LOC_0s12g36800 St LOC_0s12g36800 St LOC_0s12g36880 St LOC_0s12g36880 St LOC_0s12g37960 St LOC_0s12g4380 St LOC_0s01g71350 M LOC_0s01g71350 M LOC_0s07g35560 M	tress Biotic: PR protein tress Biotic: PR protein lise: PR protein lise: PR protein	pathgenesis-related Bet v I pathgenesis-related Bet v I pathgenesis-related Bet v I pathgenesis-related Bet v I WIP3 WIP4 thurnatin ghocosi Jydroiases fam3y 17 ghocosi Jydroiases fam3y 17 ghocasi Jydroiases fam3y 17	NH1, Xa21 NH1, Xa21 NH1, Xa21 NRR, NH1, Xa21 NH1, Xa21 NH1, Xa21 NH1, Xa21 NH1, Xa21 NH1, Xa21 NH1, Xa21 NH2, Xa21 NRR, Xa21
					LOC 0.03g22420 Sc LOC 0.035g05940 Sc LOC 0.035g19910 Sc LOC 0.030g1710 Sc LOC 0.032g21640 Sc LOC 0.03g26140 Sc LOC 0.03g26140 Sc LOC 0.03g4500 Sc	econdary Metabolism econdary Metabolism	AAA-ppe ATPase family protein stress-related protein transferase family protein 1-decxys-D-sykulose 5-phosphate reductoisomerase hydroxymethybutenyl 4-diphosphate synthase terpene synthase terpene synthase dehydrogenase AMP-binding domain containing protein leucoambecyandin reductuse isolitowore reductuse homolog IRL	NH1, Xa21 NRR, Xa21 NRR, Xa21 NRR, Xa21 NH1, Xa21 NH1, Xa21 NH1, Xa21 NRR, Xa21 NH2, Xa21 NH1, Xa21 NH1, Xa21 NH1, Xa21 NH1, Xa21
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					LOC_Os01g01160 St LOC_Os03g31300 St	tress Abiotic tress Abiotic	heat shock protein DnaJ chaperone protein clpB 1	NH1, Xa21 NRR, Xa21

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 (log₂ 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 $\log_2 Xa21/TO309$ 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 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 *NH1*ox 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 H_2O_2 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 (BRI1)-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 Xa21and 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 lipozygenase 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, *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 singling 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 phyotohormones; *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

		log_2	log_2	log_2	Log_2	Log_2	log_2	Feature
Locus_id	Putative Function	NRRox(SS)/	NH1ox(R)/	Xa21(R)/	BTH(hormone)/	JA(hormone)/	LPS(elicitor)/	
		LG(S)_1d	LG(S)_1d	TP309(S)_2d	Mock	Mock_leaf	Mock	
LOC_Os01g01080	decarboxylase, putative, expressed	-0.62166	0.113813	1.032885				Figure 4
LOC_Os01g01160	heat shock protein DnaJ, putative,	0.50816	1.146319	0.782804				Figure 4
	expressed							
LOC_Os01g01180	expressed protein	0.484002	1.028018	1.185149				Figure 4
LOC_Os01g01710	1-deoxy-D-xylulose 5-phosphate	-0.73341	-0.22451	1.15928			0.60495	Figure 4
	reductoisomerase, chloroplast							
	precursor, putative, expressed							
LOC_Os01g01840	helix-loop-helix DNA-binding	-1.57286	2.032539	0.616171	6.470884	-0.58151		Figure 4
	domain containing protein,							
	expressed							
LOC_Os01g04280	calmodulin binding protein,	-0.83571	0.998188	-0.22336	1.556207	0.374425	1.71215	Figure 4
	putative, expressed							
LOC_Os01g10590	osFTL8 FT-Like8 homologous to	-0.75864	1.32332	0.1833				Figure 4
	Flowering Locus T gene; contains							
	Pfam profile PF01161:							
	Phosphatidylethanolamine-binding							
	protein, expressed							
LOC_Os01g13590	isoflavone reductase homolog IRL,	0.829176	1.694336	1.035175				Figure 4
	putative, expressed							

Tabl	e S	1.	List and	l microarray o	data of	genes	associated	with	n enhanced	bacterial	blight r	esistance
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LOC_Os01g14250	expressed protein	1.172973	2.053824	0.75785				Figure 4
LOC_Os01g14810	5-nucleotidase domain-containing	-1.00083	-0.18424	0.875149	0.010906	-1.047	0.3255	Figure 4
	protein, putative, expressed							
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	-0.97823	-0.43121	1.46745	-0.01421	-0.1275	0.23955	Figure 4
	CDA, MAPK, GSK3, and CLKC							
	kinases, expressed							
LOC_Os01g24750	Ser/Thr protein phosphatase family	-0.68218	-0.36161	0.885727	0.312546	0.31625	1.08105	Figure 4
	protein, putative, expressed							
LOC_Os01g28450	SCP-like extracellular protein,	0.372053	1.61947	0.914662	2.037198	4.517	0.8253	Figure 4
	expressed							
LOC_Os01g35330	circumsporozoite protein precursor,	-0.34795	1.918976	1.511377				Figure 4
	putative, expressed							
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,	-0.60312	-0.42046	1.263314	0.301193	-1.75224	0.1247	Figure 4
	putative, expressed							
LOC_Os01g37910	vacuolar-processing enzyme	-1.34885	-0.50324	1.990398	0.193102	-1.02125	-1.1582	Figure 4
	precursor, putative, expressed							
LOC_Os01g38650	expressed protein	0.646583	2.223721	1.45609	6.433319	-0.15985	-0.2508	Figure 4
LOC_Os01g42260	transcriptional corepressor	-0.76208	-0.0509	1.035176	0.045065	0.055	-0.2768	Figure 4
	LEUNIG, putative, expressed							
LOC_Os01g48930	splicing factor-related, putative,	-0.62469	-0.62635	1.411129	0.284588	-0.83453	0.3147	Figure 4
	expressed							
LOC_Os01g53350	anthocyanidin	-0.93493	0.350547	1.431636	0.634006	0.6167	-0.33065	Figure 4
	5,3-O-glucosyltransferase, putative,							
	expressed							
LOC_Os01g55870	chorismate mutase, chloroplast	-0.39654	0.776814	1.198372	0.083726	0.4675	0.94185	Figure 4
	precursor, putative, expressed							
LOC_Os01g58100	polyphenol oxidase, putative,	-0.00841	1.669244	1.401254	1.460684	0.215975		Figure 4
	expressed							
LOC_Os01g58580	ICE-like protease p20 domain	-0.82197	-0.41204	1.178699	0.003101	0.563063	-0.39125	Figure 4
	containing protein, putative,							
	expressed							
LOC_Os01g62460	ZOS1-16 - C2H2 zinc finger	-0.77967	-0.11553	0.9173	0.325713	-1.50676	0.5238	Figure 4
	protein, expressed							
LOC_Os01g64110	glycosyl hydrolase, putative,	-0.85731	0.193286	0.612443	2.460338	0.701125	-0.01565	Figure 4
	expressed							
LOC_Os01g64660	fructose-1,6-bisphosphatase,	-0.82458	-1.66019	0.973493	-0.30016	-2.32073	-0.9129	Figure 4
	putative, expressed							
LOC_Os01g64840	aspartic proteinase nepenthesin-1	0.637163	1.506497	0.868187	-0.03436	0.02125		Figure 4
	precursor, putative, expressed							
LOC_Os01g65900	chitin-inducible	-0.82484	-0.0625	0.808025	0.157345	0.528	1.02565	Figure 4
	gibberellin-responsive protein,							
	putative, expressed							
LOC_Os01g69050	lysine ketoglutarate reductase	-0.68127	0.29725	0.876405	-0.07882	-0.12683		Figure 4
	trans-splicing related 1, putative,							
	expressed							
LOC_Os01g70390	expressed protein	1.405615	1.87148	1.243578	0.023805	0.457775	-0.04995	Figure 4
LOC_Os01g71350	glycosyl hydrolases family 17,	0.500127	0.652049	1.205307	0.593943	1.642625	0.5571	Figure 4
	putative, expressed	0	0					
LOC_Os01g71770	KNA recognition motif containing	-0.69017	0.030101	1.081014	-0.00193	0.372	-0.1018	Figure 4
	protein, putative, expressed							
LOC_Os01g72370	helix-loop-helix DNA-binding	-1.75644	-0.69859	0.646425	0.02924	-1.66145	-0.0425	Figure 4
	domain containing protein,							
	expressed	0	0.000					
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	-0.77905	-0.94952	0.976393	##############	-2.84	0.2955	Figure 4
LOC_Os02g02120	protein, expressed OsWAK11 - OsWAK receptor-like	-1.13558	0.98523	0.673381	0.413338	-0.05999		Figure 4
	protein kinase, expressed							
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,	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,	-0.2034	1.102211	0.62184	0.529439	2.143238	0.33275	Figure 4
LOC_Os02g39160	hydroxymethylbutenyl 4-diphosphate synthase, putative,	-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,	-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,	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,	-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_00123F730 transmetry proving publicks, responsed -0.003 -0.2034 1.240239 -0.19682 -0.17428 -0.20653 Figure 4 LOC_00123F10 NADII 4doptoqueme 1 alpin -0.77657 -0.0214 1.240239 -0.19682 0.355513 -0.00853 Figure 4 LOC_00123F01 OUTbdde cysteme consentemint -0.64714 0.00113 0.97399 -0.2142 0.738975 0.2018 Figure 4 LOC_00123F00 opersond pressor -0.64714 0.00113 0.97399 -0.2142 0.738975 0.2108 Figure 4 LOC_00123F010 opersond pressor -0.64714 0.00113 0.97399 -0.2142 0.738975 0.2108 Figure 4 LOC_00123F010 opersond pressor -0.84711 8.4871 1.85178 1.570655 0.5728 0.310725 Figure 4 LOC_00123F010 DEFs. horisonian defrema-filter 0.48771 1.85178 1.570655 0.5728 0.310725 Figure 4 LOC_00123F020 ponglanc_nanazac_proprinte_nanazac_opersond 0.48775 0.79116 0.99765									
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expensionLOC_00472700ADDL daylogenes Lapida0.77870.20212.120290.10920.205310.0855Fugue 4JOC_00472700OTI-bia cystemotechanila0.818210.49111.277870.11810.141350.81825Fugue 4JOC_00472700OTI-bia cystemotechanila0.471630.00110.979990.20120.7389750.2288Fugue 4JOC_00472700Orgenesi Potorie0.477630.43841.256630.07064-0.45220.0014Fugue 4JOC_00472700Orgenesi Potorie0.474730.581450.518755-0.16867.1682Fugue 4JOC_00472870DERS- Inferion and Driematili0.489711.841731.550650.572480.510725J.16819.1697JOC_00472870DERS- Inferion and Driematili0.439711.811781.550650.257241.6119.1077Fugue 4JOC_00472870Dista strastyre presend0.422710.251010.1077Fugue 4JOC_00472870Orgenesi Patrici Patr		transporter protein, putative,							
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protect protect <t< td=""><td></td><td>subcomplex subunit 9, mitochondrial</td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></t<>		subcomplex subunit 9, mitochondrial							
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protein, putative, expressed	LOC Os02g57410	OTU-like cysteine protease family	-0.81021	-0.42941	1.277887	-0.1184	0.14135	0.81835	Figure 4
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LOC_000301720 paradre, expressed 0.01001 1.0000001 0.01007 Figure 4 1.00000001 1.0018 0.01071 2.1458001 0.05793 Figure 4 1.00000300200 postation simps, copressed 0.01071 2.148002 0.046635 -1.04593 4.05594 1.02594 1.02594 1.02594 1.02594 1.02594 1.025945 1.025945 1.025945	LOC_0s03g02590	nerovisomal biogenesis factor 11	-0 77663	-0 5884	1 276663	0.070674	-1 68225	-0.0034	Figure 4
LOC. 0.043/017 picerality-spinsplane -1.04445 -0.38365 0.879015 -0.1586 -2.554 0.2205 Figure 4 LOC_003/03100 DEFS - Defensional Defensio-like -0.84973 1.581758 1.570025 0.057248 0.516725 Figure 4 DEFA - Entity-expressed -0.82271 -0.22244 1.55009 -0.0723 -1.681 -0.1007 Figure 4 LOC_003/050500 ioregence plonphate transportery -0.87221 0.300406 0.999645 2.454804 0.87935 Figure 4 LOC_003/050500 preterix intras AFRI B, chrosphate -0.87720 0.17711 2.40802 0.652433 -1.65241 0.0579 Figure 4 LOC_003/050700 instinal-3-photentic symbase. -0.9775 0.17711 2.40802 0.85429 -0.5555 Figure 4 LOC_004/03/0308 instinal-3-photent symbase. -0.9775 0.26771 2.40802 0.85425 -0.0666 Figure 4 LOC_004/03/03189 Bood Complex Symbase -0.9775 0.26975 0.962366 0.234875 0.456352 -0.06666 Fig	LOC_0305g02570	putative expressed	-0.77005	-0.5004	1.270005	0.070074	-1.00225	-0.0054	I iguie 4
LOC_0003g0720 professional and Synthesis -1.04433 -1.04431 -1.04433 -1.04431 -1.04433 -1.04431 -1.04433 -1.04513 -1.04431 -0.04773 0.046645 -1.045141 0.04573 -0.026043 -1.052443 -1.04211 1.0178 Figure 4 LOC_0003g08170 proteinse, expressed 0.04475 0.616271 2.06002 0.366453 -1.05508 -0.25515 Figure 4 LOC_0003g10890 debidescent formanics, expressed 0.04775 0.616271 2.06002 0.366455 -1.04508 -6.5241 0.0579 Figure 4 LOC_0003g10890 debidescent formanics, expressed 0.04775 0.104034 1.25788 0.046655 -1	100 0-02-02720	alugeraldebude 2 about to	1.04445	0.29265	0.970045	0.16596	2.554	0 42905	Eiman 4
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DDE-Diright number, expressed -0.82271 -0.27244 1.563009 -0.20723 -1.681 -0.1067 Figure 4 LOC_O03030562 inorganic phosphate transporter, putative, expressed -0.87222 0.360406 0.939645 2.454804 0.87935 - Figure 4 LOC_O03030562 pressors, putative, expressed -0.87271 0.073316 0.006601 -0.61211 1.0178 Figure 4 LOC_O03030502 insons, putative, expressed 0.046422 0.749322 1.095651 1.052493 -1.65241 0.0579 Figure 4 LOC_O03020220 insons, putative, expressed 0.04775 0.616271 2.408002 0.586429 1.58625 -0.2555 Figure 4 LOC_O03020280 BTBNS - Brie-a-Brae, Trantrack, non-phontory bypocry13 NP13 and orif-coil domains, expressed - 1.08665 0.234857 0.066631 -1.04508 Figure 4 LOC_O03021399 C65 proteasome non-ATPase -0.63307 -0.42429 1.59866 -0.31787 0.234857 0.06641 Figure 4 LOC_O0321399 C65 proteasome non-ATPase -0.63307 -0.4	LOC_0s03g03810	DEF8 - Defensin and Defensin-like	-0.84973	1.581/58	1.576025	0.057248	0.516/25		Figure 4
LOC_008/g6590 Cinate transporter protein, putative, expressed -0.2724 1.6810 -0.067 Figure 4 LOC_003/g6520 inorganic phosphate transporter, precursor, putative, expressed -0.87922 0.360406 0.939645 2.454804 0.87935 Figure 4 LOC_003/g60520 precursor, putative, expressed -0.22010 0.975376 0.773161 0.006001 -0.61211 1.0178 Figure 4 LOC_003/g60520 mesiot-3-phosphate synthese, mesiot-3-phosphate synthese, divelopmetary synthese, putative, expressed -0.04775 0.616271 2.408002 0.586429 1.589625 -0.25555 Figure 4 LOC_003/g60520 mesiot-3-phosphate synthese, mon-phototropic hypocotyl 3 NPH3 and colled coil domains, expressed -0.07976 0.263975 0.962386 0.234857 0.865825 -0.0666 Figure 4 LOC_003/g12500 catomer shorting amma-1, ecquieracy shorting amma-1, dicate coil domains, expressed -0.67976 0.263975 0.962386 0.234857 0.865825 -0.0666 Figure 4 LOC_003/g12500 pathotropic hypocotyl 3 NPH3 and colled coil domains, expressed -0.65497 -0.02937 0.486557 -0.0666 Figure 4 LOC_003/g12500 pathotropic-shines, expresse		DEFL family, expressed							
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Induct, expressed Product, expressed Product	LOC_Os03g05620	inorganic phosphate transporter,	-0.87922	0.360406	0.939645	2.454804	0.87935		Figure 4
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LOC_00398999 dehydrogenase, putative, expressed 0.084622 0.749322 1.052493 -1.65241 0.0579 Figure 4 LOC_00390920 mointi		precursor, putative, expressed							
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Inditive expressed Partial expressed Partia expressed Partial expressed	LOC_Os03g09250	inositol-3-phosphate synthase,	-0.04775	0.616271	2.408002	0.586429	1.589625	-0.25555	Figure 4
DCC_0s03g10880 BTBN 5 - Brie-a-Brac, Tramtrack, Broad Complex BTB domain with non-phototropic hypocotyl 3 NPH3 and collect-coil domains, expressed - 1.08046 1.26788 0.046635 -1.04508 Figure 4 LOC_0s03g12590 coatomer subunit garma-1, putative, expressed -0.67976 0.263975 0.962386 0.234857 0.865825 -0.0666 Figure 4 LOC_0s03g12590 coatomer subunit garma-1, regulatory subunit 4, putative, regressed -0.63037 -0.42429 1.059866 -0.13787 0.229375 0.03735 Figure 4 LOC_0s03g1380 expressed protein 1.14035 1.764665 0.98704 - Figure 4 LOC_0s03g1880 patogenesis-related Bet v I family 0.65611 1.045877 1.11257 -4.026657 -4.08613 - Figure 4 LOC_0s03g18960 ATP-dependent RNA helicase, putative, expressed - - -0.73562 2.861238 -0.0509 2.8292 Figure 4 LOC_0s03g24240 AAA-type ATPase family protein, expressed - - - - - - - Figure 4 LOC_0s03g24240 Expressed		putative, expressed							
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putative, expressed valuative,	LOC_Os03g19960	ATP-dependent RNA helicase,	-0.65439	-0.29234	1.163933	-0.22722	-0.01838	0.0664	Figure 4
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LOC_Os03g30190 retrotransposon protein, putative, 1.353919 2.24824 1.355825 Figure 4 unclassified, expressed	LOC_Os03g29190	PDI, putative, expressed	-0.18225	1.172415	0.969791	1.741026	0.366763	0.26155	Figure 4
unclassified, expressed LOC_0s03g31300 chaperone protein clpB 1, putative, -0.69475 0.16005 1.388952 -0.22987 -0.96638 -0.0237 Figure 4 expressed expressed -0.00401 1.094336 0.027076 1.53175 -0.26065 Figure 4 LOC_0s03g36750 cbbY, putative, expressed -0.8416 -0.74637 0.754195 0.09488 -0.94066 0.272 Figure 4	LOC_Os03g30190	retrotransposon protein, putative,	1.353919	2.24824	1.355825				Figure 4
LOC_Os03g31300 chaperone protein clpB 1, putative, -0.69475 0.16005 1.388952 -0.22987 -0.96638 -0.0237 Figure 4 expressed -0.003g32314 allene oxide cyclase 4, chloroplast -0.70565 -0.00401 1.094336 0.027076 1.53175 -0.26065 Figure 4 precursor, putative, expressed -0.74637 0.754195 0.09488 -0.94066 0.272 Figure 4		unclassified, expressed							
expressed LOC_Os03g32314 allene oxide cyclase 4, chloroplast -0.70565 -0.00401 1.094336 0.027076 1.53175 -0.26065 Figure 4 precursor, putative, expressed -0.70565 -0.74637 0.754195 0.09488 -0.94066 0.272 Figure 4	LOC_Os03g31300	chaperone protein clpB 1, putative,	-0.69475	0.16005	1.388952	-0.22987	-0.96638	-0.0237	Figure 4
LOC_0s03g32314 allene oxide cyclase 4, chloroplast -0.70565 -0.00401 1.094336 0.027076 1.53175 -0.26065 Figure 4 precursor, putative, expressed -0.74637 0.754195 0.09488 -0.94066 0.272 Figure 4		expressed							
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LOC_0s03g36750 cbbY, putative, expressed -0.8416 -0.74637 0.754195 0.09488 -0.94066 0.272 Figure 4		precursor, putative, expressed							
	LOC_Os03g36750	cbbY, putative, expressed	-0.8416	-0.74637	0.754195	0.09488	-0.94066	0.272	Figure 4

LOC_Os03g37830	potassium transporter, putative,	-0.16712	0.866306	1.691325	-0.10637	-0.18579	1.8453	Figure 4
LOC_Os03g39560	expressed retrotransposon protein, putative,	0.520306	1.442007	0.633289				Figure 4
	unclassified, expressed							
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,	-0.32707	1.087504	0.795232	0.714943	-0.56433		Figure 4
_ 0	putative, expressed							e
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	-0.70099	-0.05171	1.140078	0.889493	1.46225	2.9079	Figure 4
_ 0	protein, expressed							
LOC_Os03g56280	lactate/malate dehydrogenase,	-0.75105	-0.74289	0.892172	0.094108	-2.65425	-0.0445	Figure 4
	putative, expressed							
LOC_Os03g56460	glucose-6-phosphate isomerase,	-0.83767	-0.81911	1.164797	-0.12843	-0.353	-0.3123	Figure 4
	putative, expressed							
LOC_Os03g57110	expressed protein	-0.66752	-0.26454	1.375674	0.224606	0.0595	-0.7048	Figure 4
LOC_Os03g58470	retrotransposon protein, putative,	0.167802	0.647122	1.262179	0.761888	-0.32875	0.0545	Figure 4
	Ty3-gypsy subclass, expressed							
LOC_Os03g58790	ATPase, putative, expressed	-0.66516	0.747763	1.072476	2.850385	0.992725	0.8413	Figure 4
LOC_Os03g60090	methylenetetrahydrofolate	0.083086	1.138991	1.041158	0.009448	0.51125	0.1575	Figure 4
	reductase, putative, expressed							
LOC_Os03g61130	phosphoesterase family protein,	-0.89047	0.175411	1.228094	-0.36764	0.472125	0.315	Figure 4
	putative, expressed							
LOC_Os03g61960	2Fe-2S iron-sulfur cluster binding	0.228726	1.121364	0.723668	-0.00275	1.679625		Figure 4
	domain containing protein,							
	expressed							
LOC_Os03g62200	ammonium transporter protein,	-0.11178	1.827604	0.747954	0.648322	-0.31638	2.36805	Figure 4
	putative, expressed							
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,	0.178221	1.202952	0.735868				Figure 4
	unclassified							
LOC_Os04g04540	retrotransposon, putative,	0.244272	1.098164	1.062164				Figure 4
	centromere-specific, expressed							
LOC_Os04g12520	transposon protein, putative,	0.620964	0.895447	0.906761				Figure 4
	unclassified, expressed							
LOC_Os04g15690	DSBA-like thioredoxin domain	-1.13414	1.034968	1.427958	1.050473	0.002913	-0.7268	Figure 4
	containing protein, expressed							
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,	-0.87423	-0.83194	1.138305	-0.04861	-3.19063	-0.40825	Figure 4
	putative, expressed							
LOC_Os04g16730	hypothetical protein	-0.15817	0.652854	1.025593				Figure 4
LOC_Os04g24220	OsWAK32 - OsWAK receptor-like	-0.3636	1.049977	0.652823	0.571276	-0.05271	-0.78515	Figure 4
	protein kinase, expressed							
LOC_Os04g27340	terpene synthase, putative,	-0.20764	1.48521	0.967139				Figure 4
	expressed							
LOC_Os04g29790	OsWAK40 - OsWAK receptor-like	-0.99643	0.529033	0.634053				Figure 4
	protein OsWAK-RLP, expressed							
LOC_Os04g31700	methylisocitrate lyase 2, putative,	-0.74025	-0.03289	1.161776	0.014329	0.072388		Figure 4
	expressed	0.720.15	0.007707	1 502201	0.1(5250	0.52225	0.0400	
LUC_Us04g32020	∠-oxogiutarate dehydrogenase E1	-0.72045	0.237/26	1.593301	0.165379	0.53325	0.0699	Figure 4
	productor putative							
LOC 0-04-22050	calraticulin precursor protein	1.00252	0 262940	1 177202	0 422002	1 2005		Figure 4
LOC_0804g52930	nutative expressed	-1.00233	0.203049	1.1//302	0.452092	1.2905		Figure 4
	paanto, orprosou							

_	LOC_Os04g33190	AMP-binding enzyme, putative,	-0.17149	0.638145	1.464633	0.416425	0.651875		Figure 4
	LOC Os04g37619	expressed zeaxanthin epoxidase, chloroplast	-0.63111	-0.10812	1.079638	-0.3939	0.43325		Figure 4
	_ 0	precursor, putative, expressed							Ū
	LOC_Os04g42470	regulatory subunit, putative,	-0.92728	-0.92712	1.813929	-0.21151	-0.50775	-0.19955	Figure 4
	1.00 0-04-42070	expressed	0.000022	0 659219	1 20(19)	0.046657	1 751	1.0725	Eiman 4
	LOC_0s04g43070	ammonium transporter protein,	0.080032	0.658318	1.296181	0.046657	-1./51	1.0725	Figure 4
	1.00.0.04.40104	putative, expressed	0.02056	0.((2057	0.20024	0.041200	0.00005	0.20455	F ' 4
	LOC_0s04g49194	naringenin,2-oxogiutarate	-0.83956	0.663057	0.39834	0.941388	0.88985	0.20455	Figure 4
	100.0.04.40010	3-dioxygenase, putative, expressed	0.21	1 544026	0.010011	2.0175(1	0 (25025	0.27915	F ' 4
	LOC_Os04g49210	naringenin,2-oxoglutarate	-0.31	1.544026	0.818011	3.91/561	0.635925	-0.27815	Figure 4
	100 0 04 51400	3-dioxygenase, putative, expressed	0.017(7	0.72226	1 20017	0.1420	1 200	0.075	F ¹ 4
	LOC_Os04g51400	zinc finger, C3HC4 type domain	-0.91/6/	-0./3336	1.30017	0.1439	-1.389	0.975	Figure 4
	100 0-04-52810	containing protein, expressed	0.00052	0.052720	1 594629	1 544900	0 707012	0.5922	Eiman 4
	LOC_0s04g53810	reucoantnocyanidin reductase,	-0.88053	0.053729	1.584638	1.544892	0.797013	0.5832	Figure 4
	100 0-04-55710	putative, expressed	1 00095	0.281600	0.745261	2 24500	2.09654	0 52525	Eiman 4
	LOC_0s04g55710	transposon protein, putative,	-1.09985	0.281009	0.745501	2.24399	-2.08034	0.55555	Figure 4
	1.00 0-04-55850	unclassified, expressed	0.074205	0.004555	0.676601	0 12204	1.0004	0.05255	Eiman 4
	LOC_0s04g55850	nuclease PA3, putative, expressed	0.074395	0.884555	0.6/6601	-0.12294	0.24295	0.05255	Figure 4
	LOC_Os04g57200	heavy metal transport/detoxification	-0.93951	0.368/01	1.021466	1.620669	0.24285		Figure 4
	100.004.55300	protein, putative, expressed	0.5(054	0.0000	1 2210(1	0.015064	0.15120	0.0(705	E: 4
	LOC_Os04g57300	phosphatidylinositol 3- and 4-kinase	-0.76254	-0.66953	1.321861	0.015864	-0.1/138	-0.06/25	Figure 4
		family protein, putative, expressed	1 57 4107	1 (01204	0.045251	0.02242	0.150020	0.00405	E: 4
	LOC_Os04g57750	plastocyanin-like domain containing	1.5/419/	1.691384	0.945251	-0.03242	0.150838	0.38485	Figure 4
		protein, putative, expressed	0.40(100	1.0(70.40	1.044060				E: 4
	LOC_0s04g58270	expressed protein	0.496199	1.06/049	1.044962	0.222004	0.1204	0.0049	Figure 4
	LOC_0s04g58330	expressed protein	0.009048	0.624041	1.255325	0.233994	0.1294	0.8048	Figure 4
	LOC_Os05g01030	phospholipid-transporting A I Pase,	0.77225	1.276122	1.5119/3	0.4/5/61	2.28595	1.81/1	Figure 4
	100.0.05.01140	putative, expressed	0.1(2507	1.245062	1 7746	0.220424	0.01246	0.7(025	F ¹
	LOC_0s05g01140	methyltransferase, putative,	0.162597	1.245963	1.//46	0.230434	-0.01346	0.76925	Figure 4
	100.0.05.04(20	expressed	0.((520	0.21107	1.2((205	0.00070/	0.27(75	0 10165	F ¹ 1
	LOC_0s05g04630	contransposon protein, putative,	-0.66538	-0.31187	1.266295	0.008/86	0.3/6/5	-0.19165	Figure 4
	1.00.0.05.05020	SINE subclass, expressed	0.01052	0.0550	1 769554	0.01072(0.02(02	1.0450	F ¹
	LOC_0s05g05020	expressed protein	-0.81052	0.8558	1.708004	0.010/36	-0.02603	1.8458	Figure 4
		expressed protein	-0.8/545	0.6/4/62	1.722902	0.333969	-0.55819	-0.6012	Figure 4
	LOC_0s05g05940	stress-related protein, putative,	-0.94015	-0.05886	1.063594	0.151245	0.28675		Figure 4
		expressed	0.004080	0.000925	0 (541)	0 12 492	0.142075		F ¹
	LOC_0s05g06260	Spc9// Spc98 family protein,	0.294082	0.999835	0.65416	-0.13482	0.142975		Figure 4
	1.00 0-05-0(250	putative, expressed	0 70299	0.217046	1.042054	0.15102	0.209625	0.227	Eiman 4
	LOC_0s03g06330	imporun subunit aipna, putative,	-0./9288	0.31/940	1.042954	-0.15195	0.208625	0.227	Figure 4
	LOC 0-05-10010	transforaça family protain putatiya	0 10914	1 207265	0 852067	0.087206	0 7205	0 47465	Eiguro 4
	LOC_0s03g19910	transferase family protein, putative,	-0.19814	1.207265	0.852967	0.08/200	-0.7303	0.4/403	Figure 4
	1.00 0-05-20500	expressed	1.02080	1 441208	0.560114	5 574205	0.50021		Eiguro 4
	LOC_0:05g30300	glyacsyl bydrologog family 17	-1.02089	0.7460	1 959902	0.22171	-0.30921	0 20065	Figure 4
	LOC_0s03g31140	putative expressed	-0.78844	-0.7409	1.636692	0.32171	1.233023	0.39903	Figure 4
	LOC 0s05g33570	putative, expressed	0.061504	0 836358	0.981813	-0.05522	0 56975	1 3279	Figure 4
	LOC_0303g55570	chloroplast precursor, putative	0.001504	0.050550	0.901015	-0.03322	0.50775	1.5277	I iguie 4
		expressed							
	LOC 0s05033610	expressed protein	-0 67743	-0 55813	1 020504	-0 28531	0 1895	0 4506	Figure 4
	LOC Os05g33710	WD domain G-beta reneat domain	-0.89961	-0 43418	0.880772	-0 13261	0.0275	-0 2724	Figure 4
	_00_0000555710	containing protein expressed	0.07701	0.10110	0.000772	0.15201	0.0210	0.2/21	Bare 1
	LOC Os05g34270	inactive receptor kinase At1927190	-1.01778	0.820989	0.305172	0.811334	0 288	1 0468	Figure 4
		precursor, putative. expressed							
	LOC Os05g40270	expressed protein	-0.58008	0.814495	0.644073	-0.15324	-1.21163	-0.2552	Figure 4
									<u> </u>

LOC_Os05g43170	calreticulin precursor protein,	-1.29567	-0.09876	0.986462	0.707302	0.02175	0.48415	Figure 4
100.0.05.4(020	putative, expressed	0.76400	0.0(50	0.015174	2 402010	1 14(2(2		F ' 4
LOC_0s05g46020	WRKY/, expressed	-0.76488	0.8658	0.0151/4	2.482018	1.146363	2 1007	Figure 4
LOC_0s05g48210	expressed protein	-0.75753	0.981228	0.584407	0.772179	1.08/	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,	-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_0s06g09370	PTF1 putative expressed	-0.60589	0.60267	1 120514	0.10838	0.94565	0 7746	Figure 4
LOC_0s06g15360	RAD23 DNA repair protein	-0.71919	-0 27624	0 804288	0.122697	0 259625	0.0224	Figure 4
	putative, expressed							8
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	-2 20891	1 638874	2 282938	3 207274	0 777488	0.08745	Figure 4
200_000627700	Factor RALF family protein	2.20031	1.000071	2.202/30	5.207271	0.777100	0.00712	i iguio i
100.00000000000	precursor, expressed	1 20022	1 501000	1.550020				E: 4
LOC_Os06g29/40	OsFBX19/ - F-box domain	-1.38033	1.581222	1.558929				Figure 4
100 0-0(-20770	burnethetical materia	0.26162	1 294454	0.910///				Eiman 4
LOC_0s06g29770	nypoinetical protein	-0.30103	1.284434	1.284200	0.50(22)(2.046975	0.5551	Figure 4
LOC_0s06g34730	expressed protein	0.14/4//	0.84280	0.992105	0.390320	3.0408/3	-0.5551	Figure 4
LOC_0806g36840	expressed	-0.03889	-0.84289	0.883103	-0.34088	-1.13881	-0.40255	Figure 4
LOC_Os06g40360	OsFBL30 - F-box domain and LRR	-0.94474	0.441776	0.788987	0.490685	-0.49463	-0.2796	Figure 4
LOC Os06g47350	RNA polymerase I specific	-0.90071	-0.16899	1.138781	0.12431	-0.3846	-0.15375	Figure 4
_ 0	transcription initiation factor RRN3							0
	family protein, putative, expressed							
LOC Os06g49040	Myb-like DNA-binding domain	-0.69809	-0.21604	1.70527	-0.63941	-0.31763	-0.2834	Figure 4
_ 0	containing protein, putative,							Ū
	expressed							
LOC Os06g50380	protein phosphatase 2C, putative,	-0.75351	-0.15734	1.32197	-0.13594	-0.09875	0.4257	Figure 4
	expressed							0
LOC_Os07g01550	leucine rich repeat domain	-0.73593	0.08566	1.084281	-0.48409	0.130425	0.13765	Figure 4
	containing protein, putative,							
	expressed							
LOC_Os07g01760	aminotransferase, classes I and II,	-1.08046	-0.94311	1.259548	0.090304	-2.26738	-0.52445	Figure 4
	domain containing protein,							
	expressed							
LOC_Os07g03900	lectin-like receptor kinase, putative,	-0.17543	0.938464	0.828874	-0.01753	-0.0816		Figure 4
	expressed							
LOC_Os07g04180	amino acid transporter, putative,	-1.1317	-0.21078	1.609952	-0.15372	-1.60215	0.2762	Figure 4
	expressed							
LOC_Os07g05820	hydroxyacid oxidase 1, putative,	-1.03291	-0.94306	1.330001	0.206442	-2.524	1.38545	Figure 4
	expressed							
LOC_Os07g06830	gibberellin receptor GID1L2,	-0.62594	0.480929	0.870572	1.181186	2.158875	2.1187	Figure 4
	putative, expressed							
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,	-0.61725	-0.21661	0.886505	0.116204	-0.1642	0.0504	Figure 4
	putative, expressed							
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	-0.76434	0.081198	1.353311	0.035187	0.29975	0.0046	Figure 4
	protein, expressed							
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,	-0.16569	0.663386	0.914085	-0.55364	1.402375	-0.08705	Figure 4
LOC_Os07g35560	glucan endo-1,3-beta-glucosidase	-1.21901	0.426135	1.39239	1.298103	0.991363	-0.2355	Figure 4
LOC_Os07g36470	vacuolar ATP synthase subunit H,	-0.77629	-0.14436	1.333521			0.30085	Figure 4
LOC_Os07g37320	transporter family protein, putative,	-0.76722	-0.46646	0.825372	0.491275	-0.0995		Figure 4
LOC_Os07g39560	RNA recognition motif containing	-0.86229	-0.34553	0.800235	-0.09132	0.819075	0.6439	Figure 4
LOC_Os07g41410	EGG APPARATUS-1, putative,	-2.18787	0.911142	1.147621	2.57855	-1.74084		Figure 4
LOC Os07945570	expressed protein	-0 64508	0 765675	1 906607	0 848385	0.68	0 2768	Figure 4
LOC Os07g46370	WD domain. G-beta repeat domain	-0.61043	0.105536	0.914468	0.036131	0.19775	-0.012	Figure 4
200_0001910010	containing protein, expressed	0.01010	0.1000000	0.011100	0.050151	0.13770	0.012	i igui e i
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,	-0.16103	1.9694	2.452248	2.278653	-0.90539		Figure 4
LOC_Os07g48100	CAMK_KIN1/SNF1/Nim1_like.31 - CAMK includes calcium/calmodulin depedent	-0.56661	0.766023	1.076177	-0.45404	-0.11138	0.12765	Figure 4
LOC_Os08g02230	protein kinases, expressed FAD-binding and arabino-lactone oxidase domains containing protein, putativa expressed	-0.02447	1.174869	0.747826	1.784682	2.55875	0.6397	Figure 4
LOC_Os08g03290	glyceraldehyde-3-phosphate	-0.68219	0.027479	1.727328	-0.15612	1.012	-0.40285	Figure 4
LOC_Os08g04500	terpene synthase, putative,	-0.26414	1.487079	1.611447	0.828786	-0.78225		Figure 4
LOC_Os08g06010	transporter, major facilitator family,	-0.40771	0.62253	1.421575	-0.28354	-0.69498	-0.99025	Figure 4
LOC_Os08g07080	terpene synthase, putative,	-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	-0.75596	-0.17138	0.980372	-0.156	-0.42013	-0.3124	Figure 4
LOC_Os08g13440	cupin domain containing protein,	-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	-0.82197	0.613377	-0.63966	1.823608	-0.42415	0.42165	Figure 4
	domain containing protein,							
	expressed							
LOC_Os08g26840	plant protein of unknown function	-0.93502	0.608336	-0.78005	2.432813	0.313988	-0.28645	Figure 4
	domain containing protein,							
	expressed							
LOC_Os08g27840	phosphoenolpyruvate carboxylase,	-0.8157	0.561896	1.932299	-0.05879	-0.32888	-0.0799	Figure 4
	putative, expressed							
LOC_Os08g31410	sulfate transporter, putative,	-0.51642	0.86571	0.689295	-0.31539	-0.1727	1.3203	Figure 4
	expressed							
LOC_Os08g31470	peptidase, trypsin-like serine and	-0.83115	0.639277	0.770847	-0.07416	-0.3675	-0.03595	Figure 4
	cysteine proteases, putative,							
	expressed							
LOC_Os08g34280	cinnamoyl-CoA reductase, putative,	-0.21915	1.332616	0.84905	-0.49974	-0.5305	2.0953	Figure 4
	expressed							
LOC_Os08g42370	zinc finger DHHC	-0.79692	0.255648	1.192034	1.584436	-0.09238	0.7129	Figure 4
	domain-containing protein, putative,							
	expressed							
LOC_Os08g44210	dihydroneopterin aldolase, putative,	-0.07519	1.221587	0.767862	1.269775	-0.01206		Figure 4
	expressed							
LOC_Os09g02214	Citrate transporter protein, putative,	-0.72081	0.074592	0.955266	0.020841	-1.11475	-0.10675	Figure 4
	expressed							
LOC_Os09g08390	CRAL/TRIO domain containing	-0.30332	1.275875	0.620181	-0.365	1.445625	0.4374	Figure 4
	protein, expressed							
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	-0.68531	-0.1428	1.089021	0.056874	0.047125	0.0824	Figure 4
	factor, putative, expressed							
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,	-1.14163	1.968905	0.777529	1.850103	-0.6581	-0.61455	Figure 4
	expressed							
LOC_Os09g29200	glutathione S-transferase, putative,	-1.05684	0.880411	0.982377	1.165847	-0.06325	-0.1917	Figure 4
	expressed							
LOC_Os09g34280	ankyrin repeat-containing protein,	-0.6773	-0.25578	1.177433	-0.20306	0.236125	-0.03985	Figure 4
	putative, expressed							
LOC_Os09g36200	senescence-inducible chloroplast	-0.03029	1.245938	1.120025	0.406153	3.31125	1.3453	Figure 4
	stay-green protein 1, putative,							
	expressed							
LOC_Os09g36300	OsLonP4 - Putative Lon protease	-0.93291	-0.20606	0.822577	0.417583	0.057125	0.5832	Figure 4
	homologue, expressed							
LOC_Os09g37012	eukaryotic aspartyl protease domain	-0.64697	-0.36589	1.506965	0.041825	-0.08663	0.7824	Figure 4
	containing protein, expressed							
LOC_Os09g39650	protein kinase family protein,	-0.93158	1.144367	0.854584	0.299028	-0.30216	-0.47365	Figure 4
	putative, expressed							
LOC_Os10g05210	OsFBX368 - F-box domain	-0.90651	1.088556	0.461708	-0.09681	0.063588	-0.1622	Figure 4
	containing protein, expressed							
LOC_Os10g10130	OsWAK112d - OsWAK	-1.23226	-0.35722	1.434578	0.464137	-0.18563	-0.15035	Figure 4
	receptor-like protein kinase,							
	expressed							
LOC_Os10g27230	endonuclease/exonuclease/phosphat	-0.82868	-0.27237	0.920414	0.078359	-0.10988	0.0577	Figure 4
	ase family domain containing							
	protein, expressed							

LOC_Os10g28080	glycosyl hydrolase, putative,	-0.11884	0.865343	0.971423	0.288969	1.774362	2.66235	Figure 4
	expressed							
LOC_Os10g28200	NAD dependent	-0.77035	-0.84127	1.2388	0.624559	-0.53288		Figure 4
	epimerase/dehydratase family							
	protein, putative, expressed							
LOC_Os10g34400	expressed protein	-0.97528	-0.1197/1	1.440205	0.214561	-0.91703		Figure 4
LOC_Os10g37/30	pollen ankyrin, putative, expressed	-0.74848	-0.22441	0.988011	0.004502	0.056538	-0.1448	Figure 4
LOC_Os10g39140	flavonol synthase/flavanone	-0.77322	1.514981	-0.05439	3.239305	2.323125	0.1602	Figure 4
100.010.41000	3-hydroxylase, putative, expressed	0.45622	0.72.5202	1 420100	0.500005	1.44006	0.07175	E: 4
LOC_0s10g41980	RALFL26 - Rapid ALkalinization	0.45632	0./35282	1.420188	0.722995	-1.44296	0.0/1/5	Figure 4
	Factor RALF family protein							
100.0.10.42240	precursor, expressed	0.027(0	0 400 40	0 (722(0	0 10100	1 2(570	0.76145	E' 4
LOC_0s10g42240	kinase, pfkB family, putative,	-0.93769	-0.49049	0.6/3269	-0.19108	-1.265/9	-0.76145	Figure 4
100.0.11.00150	expressed	0.00427	0.59257	1.2(2007	0.0021/	0 42175		E' 4
LOC_Os11g02150	saposin-like type B, region 1 family	-0.8043/	-0.58257	1.362907	-0.09216	0.431/5		Figure 4
100 0-11-02520	WDKV40 and a	0.21467	2 100624	0 725402	2.001122	2 0022		Eiman 4
LOC_0s11g02530	WRKY40, expressed	-0.2140/	2.100624	0.733403	2.091132	2.9033		Figure 4
LOC_0s11g02340	wKK i 50, expressed	-0.09727	2.434097	0.938227	0 579296	0.022075		Figure 4
LOC_0511g05250	nucleoside-inphosphatase, putative,	-0.94344	0.721348	0.209449	0.378280	0.033975		Figure 4
LOC 0:11:04030	major facilitator superfamily	0.03804	2 242272	0 600028	0.01716	0 25671	0 2025	Eiguro 4
LOC_0511g04030	antiporter, putative, expressed	-0.03804	2.243273	0.099938	-0.01/10	-0.33071	-0.2025	rigure 4
LOC 0:11:05000	digalactoryldiacyldiacylalyaeral symthese	0 12222	0 885506	0.611005	0.1410	0.552	0 4773	Eiguro 4
LOC_0511g05990	ablaraplact producer putativa	-0.13223	0.885590	0.011005	-0.1419	0.332	0.4775	r igure 4
	emotopiasi precutsor, putative,							
LOC Os11g06200	expressed protein	0 560401	1 515620	0 677455				Figure 4
LOC_0s11g00200	ovidoreductase short chain	0.210138	0.741941	0.815496	0.005564	-2 79648	0 15865	Figure 4
100_0311g07750	dehydrogenase/reductase family	0.210156	0.741741	0.015470	0.005504	-2.79040	0.15605	I igure 4
	domain containing family							
	expressed							
LOC Os11910100	STE MEKK stell MAP3K 3 -	-0.80011	-0 28149	0 934303	0 767809	0 363875		Figure 4
Loc_ostigiotoo	STE_inexex_seri_init of Step	0.00011	0.2011)	0.991505	0.707009	0.505075		i igure i
	sterile 7 sterile 11 and sterile 20							
	from yeast expressed							
LOC Os11g11960	disease resistance protein RPM1.	-1.00802	0.902514	0.398861				Figure 4
5	putative, expressed							0
LOC Os11g12340	disease resistance protein RPM1.	-1.24499	0.871429	-0.1817	1.657166	-0.56688	0.6507	Figure 4
5	putative, expressed							0
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,	-0.6603	-0.16015	0.971524	-0.13517	0.449975	0.6029	Figure 4
_ 0	putative, expressed							Ū.
LOC Os11g28270	zinc finger C-x8-C-x5-C-x3-H type	-0.60218	0.719985	1.200292	0.089814	-0.05121	-1.06215	Figure 4
	family protein, expressed							
LOC_Os11g36430	zinc finger, C3HC4 type domain	-0.87359	-0.43173	0.982362	0.030891	-0.23775	0.0256	Figure 4
	containing protein, expressed							
LOC_Os11g37950	WIP3 - Wound-induced protein	-0.40058	0.890427	1.717969	0.567761	3.542775		Figure 4
	precursor, expressed							
LOC_Os11g37960	WIP4 - Wound-induced protein	0.285787	0.689607	0.867366	0.143319	0.367288	1.5385	Figure 4
	precursor, expressed							
LOC_Os11g39370	BRASSINOSTEROID	-1.04181	1.829413	0.780994	0.943142	0.154625	-0.1077	Figure 4
	INSENSITIVE 1-associated							
	receptor kinase 1 precursor,							
	putative, expressed							
LOC_Os11g46810	retrotransposon protein, putative,	-1.01768	1.377193	-0.47287				Figure 4
	unclassified, expressed							

_	LOC_Os11g48020	fatty acid hydroxylase, putative,	0.3678	0.820391	0.98204			-0.6619	Figure 4
	LOC Os12g02320	LTPL12 - Protease inhibitor/seed	0 31304	1 101199	0 745428	-0 15737	-1.55938		Figure 4
	100_0012602020	storage/LTP family protein	0.01001		0.710120	0.10707	1.00700		i igure i
		precursor, expressed							
	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	acvl-CoA synthetase protein.	-0.86414	-0.25683	0.901445	-0.16841	-0.802	-0.4423	Figure 4
		nutative expressed							8
	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	0 44961	1 752022	1 401411	0.029894	0.21245	-1.1377	Figure 4
		containing protein putative							8
		expressed							
	LOC Os12g09739	pollen signalling protein with	0.54678	0.953602	1.11887	-0.12803	0.132138	0.2602	Figure 4
	5	adenvlvl cvclase activity, putative.							0
		expressed							
	LOC Os12g10740	leucine-rich repeat family protein	-1.13728	0.384152	1 260968	0 895482	-0.61535	0.50175	Figure 4
		nutative expressed							8
	LOC Os12g12560	NADP-dependent oxidoreductase	0 373785	1 001344	0 753859	-0.23166	0 801388	0 30095	Figure 4
	100_0312612500	nutative expressed	0.575705	1.001511	0.755057	0.25100	0.001500	0.50075	i iguie i
	LOC Os12g14440	Jacalin-like lectin domain	-0 66272	2 85033	2 345581	8 118299	1 882363	-0.2118	Figure 4
	200_0312g11110	containing protein putative	0.00272	2.05055	2.5 15501	0.1102//	1.002505	0.2110	rigure i
		expressed							
	LOC Os12g21700	zing finger C-x8-C-x5-C-x3-H type	-0.88214	-0.24038	0.686118	-0.09197	-0.03688	-0.1647	Figure 4
	100_0312g21700	family protein expressed	-0.00214	-0.2-050	0.000110	-0.09197	-0.05000	-0.1047	I igure 4
	LOC Os12g23180	3-beta hydroxysteroid	-0.9701	-0.62121	1 117001	0 160354	-2 508	0.92695	Figure 4
	100_0312g25100	dehydrogenase/isomerase family	-0.9701	-0.02121	1.11///	0.100554	-2.500	0.72075	I igure 4
		protein putative expressed							
	LOC 0s12s25170	NB ABC domain containing disease	0.81503	0 700302	1 147507	0 200279	0 75253	0 15205	Figure 4
	LOC_0312g25170	resistance protein putative	-0.81505	0.799392	1.14/39/	0.200379	-0.75255	0.15205	Figure 4
		avpressed							
	$LOC_{0} = 12\pi 31440$	expressed protein	0 73000	0.0734	0.026051	0.05146	0 1805		Figure 4
	LOC_0s12g31440	expressed protein	-0.73009	2 107820	1.850015	-0.03140	-0.1895		Figure 4
	$LOC_0s12g33470$	expressed protein	0.008304	1.624627	1.639013	1 647240	1 492	1 72945	Figure 4
	LOC_0812g50850	patiogenesis-related Bet v I failing	-0.33330	1.024027	1.0/0813	1.04/349	1.462	1./3645	Figure 4
	LOC 0-12-26860	protein, putative, expressed	0 2086	1 407116	0 6022	1 049627	2 19025		Figure 4
	LOC_0812g50800	pathogenesis-related protein 10,	-0.2080	1.40/110	0.0022	1.946027	2.18025		Figure 4
	100 0-12-26880	putative, expressed	0 (2052	1.006605	1 565020	2.077125	4 229	1.00465	Eiman 4
	LOC_0812g36880	pathogenesis-related Bet v I family	-0.03933	1.990095	1.303929	2.07/135	4.228	1.00465	Figure 4
	100 0-12-272(0	brown, putative, expressed	0.56542	2 914567	2 426765	2 154102	1.04555	0.96425	Eiman 4
	LOC_0812g3/200	npoxygenase 2.1, entoroptast	-0.36342	2.814307	2.420/03	3.134193	1.94555	0.80433	Figure 4
	100 0-12-27250	bin and a sector in a station	0.16202	1.020084	0.770061	2 (91751	1 50(125		Eirona 4
	LOC_0s12g3/350	lipozygenase protein, putative,	-0.16203	1.039084	0.770961	2.081/51	1.506125		Figure 4
	100 0.12 42850	expressed	1 10014	0.00083	1 2002 42	0.10(100	0 (21125	1 1 1 7	E'
	LOC_0s12g42850	amino acid permease, putative,	-1.19914	-0.09983	1.289242	0.196122	0.631125	1.11/	Figure 4
	100 0 10 1000	expressed	0.41707	0.057076	0.700020	1.050/5	2 27 1225		E: 4
	LOC_Os12g43380	thaumatin, putative, expressed	-0.41/86	2.35/3/6	0.709838	1.25965	3.3/4325	1 5200	Figure 4
	LOC_Os08g14570	NADPH reductase, putative,	0.51/6//	1.025565	0.598779	-0.13045	0./508/5	1.7309	
		expressed	0.10005	0.000000	0.500200	0.050450	1.52(20)	0.51105	
	LUC_Us09g29404	giycogen operon protein glgX,	-0.18005	0.880238	0.588289	0.258458	-1.52638	-0.51135	
	100.0.12.05722	putative, expressed	0.2000.17	0.017207	0.50.12.10				
	LOC_Os12g05700	transposon protein, putative,	0.369847	0.817296	0.584349				
		Mutator sub-class, expressed	0.12.02.5	1 2 5 9 2 2	0.5744.1	0.10.10.00	0.054575		
	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_Ox02g1380 early modulin 93 ENOD93 protein, putative, expressed -0.04477 0.822812 0.566767 1.065371 1.572625 0.00655 LOC_Ox01g42620 pentatricoperptide containing protein, putative, expressed 0.87389 0.811243 0.556116 0.019363 -0.05698 -0.87465 LOC_Ox04g06520 expressed protein -0.25421 1.425418 0.540897 1.964411 -0.12266 0.39305 LOC_Ox04g06520 expressed protein -0.25721 1.425418 0.540897 1.964411 -0.12266 0.39305 LOC_Ox02g09490 dehydrogenase, putative, expressed 0.421757 1.108099 0.526731 1.305995 3.3281 1.5933 LOC_Ox02g0454130 cytockrome K9072A1, putative, expressed 0.21826 0.941717 0.521432 0.831575 0.588 LOC_Ox02g454520 oHBXSR - F-box domain 0.219663 1.210373 0.50076 2.145026 2.604875 1.31645 LOC_Ox02g45450 oHBXXR - T-box domain -0.024249 1.550733 0.5076 2.145026 2.604875 1.31645 LOC_
Indexty contraining protein, putative, expressed outsitue, expressed outsitue, expressed LOC_004296520 expressed protein -0.25421 1.425418 0.540897 1.964411 -0.12266 0.39305 LOC_004296520 expressed protein -0.35822 1.801622 0.52121 -
LOC_0x01g4262 pentatricopeptide containing 0.087389 0.811243 0.556116 0.019363 -0.05698 -0.87465 LOC_0x04g04480 expressed protein 0.25421 1.425418 0.54087 1.964411 -0.1266 0.39305 LOC_0x04g04480 retrotransposon protein, putative, expressed 0.536282 0.801622 0.53321 1.340375 0.6383 LOC_0x04g04480 pleiotropic darg resistance protein, 0.12757 1.108099 0.526731 1.305995 3.3281 1.5953 LOC_0x04g42430 pleiotropic darg resistance protein, 0.212767 1.08099 0.526731 0.531875 0.588 LOC_0x02g45430 OFFRX58 F-box domain 0.219663 1.210373 0.520475 0.32171 1.8705 3.1032 protein, putative, expressed 3.1032 LOC_0x12g36860 pathogenesis-related Bet v I family 0.328171 0.520475 0.302171 1.8705 3.1032 protein protein 0.421963 0.520473 0.500728 0.802171 1.8705 3.1032
LOC_0.04/2015 expressed protein -0.25421 1.425418 0.540897 1.964411 -0.1266 0.39305 LOC_0.04/201480 retrotransposon protein, putative, 0.536282 0.801622 0.533211 - - - - - - - - - - - 0.6383 LOC_0.04/2049 dehydrogenase, putative, expressed 0.444607 1.108099 0.526731 1.305995 3.3281 1.5953 LOC_0.04/29410 epicotropic drug resistance protein, -0.12767 1.010999 0.526731 0.531575 0.5588 LOC_0.04/294201 OsfRX58 -F-box domain 0.219663 1.210373 0.520475 0.30171 1.8705 3.1032 protein, putative, expressed - - - - - 2.2737 LOC_0.04/29100 hypothetical protein -0.02872 1.049686 0.495879 - 2.2737 LOC_0.04/292100 hypothetical protein -0.02872 1.049686 0.495879 - 2.2737 LOC_0.04/292100 js
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LOC_0602g0490 dehydrogenase, putative, expressed 0.444607 1.312049 0.532822 -0.28538 1.340375 0.6383 LOC_0801g4238 pletotropic drug resistance protein, expressed -0.21757 1.108099 0.526731 1.305995 3.3281 1.5953 LOC_0807g4130 cytochrome P450 72A1, putative, expressed 0.021826 0.941717 0.521432 0.831575 0.588 LOC_0802g45320 OxFBX58 - F-box domain 0.219663 1.210373 0.520475 0.351903 -0.01745 0.8323 LOC_0802g45320 OxFBX58 - F-box domain 0.219663 1.210373 0.50075 0.351903 -0.01745 0.8323 LOC_0812g36805 CHIT14 - Chitinase family protein protein, putative, expressed - - - 2.2737 LOC_0804g2710 hypothetical protein -0.02872 1.049868 0.49587 - 2.2037 LOC_0804g2710 hypothetical protein -0.02872 1.049868 0.495857 2.2037 LOC_0804g2571 hypothetical protein 0.526735 1.016674 0.46075 1.867619
LOC_0s01g42380 pleiotropic drug resistance protein, putative, expressed -1.108099 0.526731 1.305995 3.3281 1.5953 LOC_0s07g4130 cytochrome P450 72A1, putative, expressed 0.021826 0.941717 0.521432 0.831575 0.588 LOC_0s02g45320 OsFBXS8 F-box domain 0.219663 1.210373 0.520475 0.351903 -0.01745 0.8323 LOC_0s12g36850 pathogenesis-related Bet v I family containing protein, expressed - <td< td=""></td<>
plative, expressedLOC_007g410exprossed0.0218260.9417170.5214320.8315750.5384LOC_007g4503Q608708 L-box domain0.210631.210370.5204750.531903-0.017450.8323LOC_0012g4585Mathy protein, expressedLOC_0012g4586Mathy protein, expressed<
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LOC_0s02g45320 OsFBXS F-box domain containing protein, expressed 1.210373 0.520475 0.351903 -0.01745 0.8323 LOC_0s12g36850 pathogenesis-related Bet v I family protein, putative, expressed -0.38411 1.894099 0.516728 0.802171 1.8705 3.1032 LOC_0s10g39680 CHITI 4 - Chitinase family protein -0.24249 1.550733 0.50076 2.145026 2.604875 1.31645 LOC_0s03g4050 CHITI 4 - Chitinase family protein -0.02872 1.049868 0.495879 - 2.2737 LOC_0s03g4050 SwWAK 7 - OsWAK receptor-like 0.02996 0.49585 - 2.2737 LOC_0s01g72100 Bytothetical protein -0.02872 1.049868 0.495859 - 2.2737 LOC_0s03g4050 Glutathione S-transferase, putative, expressed -0.3265 1.019674 0.464075 1.867619 1.865525 0.2161 LOC_0s00g326774 hypothetical protein 0.55184 2.269339 0.460869 1.0399 1.0399 LOC_0s07g34909 AMP-binding domain containing protein, expressed 0.452941 0.7082
Integration Containing protein, expressed Containing protein, expressed LOC_0s10g3680 CHIT14 - Chitinase family protein -0.34411 1.894099 0.516728 0.802171 1.8705 3.1032 LOC_0s10g3680 CHIT14 - Chitinase family protein -0.24249 1.550733 0.50076 2.145026 2.604875 1.31645 precursor, expressed -
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LOC_0s10g39680 CHITAL Chrintage family protein procursor, expressed -0.24249 1.550733 0.50076 2.145026 2.604875 1.31645 LOC_0s04g27100 hypothetical protein -0.02872 1.049868 0.495879 2.2737 LOC_0s03g44050 OSWAK27 - OSWAK receptor-like 0.209963 0.973302 0.49585 2.2737 LOC_0s01g72120 glutathione S-transferase, putative, protein kinase, expressed -0.3265 1.019674 0.464075 1.867619 1.865525 0.2161 LOC_0s08g32674 hypothetical protein 0.55184 2.269339 0.460869 448075 1.867619 1.865525 0.2161 LOC_0s08g32674 hypothetical protein 0.55184 2.269339 0.460869 449393 1.0399 LOC_0s08g30570 AMP-binding domain containing 0.267325 1.33569 0.452941 0.708217 0.493938 1.0399 LOC_0s08g30570 AMP-binding domain containing 0.267325 1.33569 0.452941 0.708217 0.493938 1.0399 LOC_0s08g30510 rectrotransposon protein, putative, 0.124453 <t< td=""></t<>
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LOC_Os06g32674 hypothetical protein 0.55184 2.269339 0.460869 0.493938 1.0399 LOC_Os06g32674 hypothetical protein 0.55184 2.269339 0.460869 0.493938 1.0399 LOC_Os03g03790 AMP-binding domain containing 0.267325 1.33569 0.452941 0.708217 0.493938 1.0399 protein, expressed
LOC_Os06g32674 hypothetical protein 0.55184 2.269339 0.460869 LOC_Os03g03790 AMP-binding domain containing 0.267325 1.33569 0.452941 0.708217 0.493938 1.0399 protein, expressed protein, expressed 1.00C_Os07g34990 retrotransposon protein, putative, 1.400493 1.117683 0.442836 1.20C_Os10g42130 no apical meristem protein, putative, 0.124453 1.258757 0.427524 0.899073 -1.39631 0.14055 LOC_Os10g42130 no apical meristem protein, putative, 0.124453 1.258757 0.427524 0.899073 -1.39631 0.14055 LOC_Os08g30510 expressed - - - - - - - - - - - 0.3078 - 0.396711 0.302798 -0.67865 0.07365 -
LOC_Os03g03790 AMP-binding domain containing 0.267325 1.33569 0.452941 0.708217 0.493938 1.0399 protein, expressed
protein, expressed 1.400493 1.117683 0.442836 LOC_Os07g34990 retrotransposon protein, putative, unclassified, expressed 1.400493 1.117683 0.442836 LOC_Os10g42130 no apical meristem protein, putative, unclassified, 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, unclassified, expressed -0.03211 0.888445 0.402044 0.078832 0.5771 0.3708 LOC_Os01g38359 peptidyl-prolyl cis-trans isomerase, unclassified, expressed -0.03020 0.851084 0.396711 0.002798 -0.67865 0.07365 LOC_Os00g47200 LTPL85 - Protease inhibitor/seed 0.216743 0.875242 0.39229 -0.0621 0.386563 0.5289 storage/LTP family protein precursor, expressed - <td< td=""></td<>
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_Os10g42130 no apical meristem protein, putative, expressed 0.03211 0.888445 0.402044 0.078832 0.5771 0.3708 LOC_Os01g38359 peptidyl-prolyl cis-trans isomerase, FKBP-type, putative, expressed -0.03902 0.851084 0.396711 0.002798 -0.67865 0.07365 LOC_Os06g47200 LTPL85 - Protease inhibitor/seed 0.216743 0.875242 0.39229 -0.0621 0.386563 0.5289 storage/LTP family protein precursor, expressed
LOC_Os10g42130 no apical meristem protein, putative, 0.124453 1.258757 0.427524 0.899073 -1.39631 0.14055 LOC_Os10g42130 no apical meristem protein, putative, 0.124453 1.258757 0.427524 0.899073 -1.39631 0.14055 LOC_Os08g30510 expressed -0.03211 0.888445 0.402044 0.078832 0.5771 0.3708 LOC_Os01g38359 peptidyl-prolyl cis-trans isomerase, -0.30902 0.851084 0.396711 0.002798 -0.67865 0.07365 FKBP-type, putative, expressed - - - - - - LOC_Os06g47200 LTPL85 - Protease inhibitor/seed 0.216743 0.875242 0.39229 -0.0621 0.386563 0.5289 storage/LTP family protein - - - - - - precursor, expressed - - - - -0.06817 -0.17916 0.8203
LOC_Os10g42130 no apical meristem protein, putative, putative, optical meristem protein, optical meristem protein, putative, optical meristem protein, putative, optical meristem protein, putative, optical meristem protein, protein precursor, 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, optical meristem protein, putative, expressed -0.39902 0.851084 0.396711 0.002798 -0.67865 0.07365 LOC_Os06g47200 LTPL85 - Protease inhibitor/seed 0.216743 0.875242 0.39229 -0.0621 0.386563 0.5289 storage/LTP family protein
LOC_Os08g30510 expressed -0.03211 0.888445 0.402044 0.078832 0.5771 0.3708 LOC_Os01g38359 peptidyl-prolyl cis-trans isomerase, -0.30902 0.851084 0.396711 0.002798 -0.67865 0.07365 FKBP-type, putative, expressed - - - - - - LOC_Os06g47200 LTPL85 - Protease inhibitor/seed 0.216743 0.875242 0.39229 -0.0621 0.386563 0.5289 storage/LTP family protein - - - - - - LOC_Os08g04230 cysteine-rich repeat secretory 1.049796 2.14292 0.384696 -0.06817 -0.17916 0.8203
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 -0.03902 0.851084 0.396711 0.002798 -0.67865 0.07365 LOC_Os06g47200 LTPL85 - Protease inhibitor/seed 0.216743 0.875242 0.39229 -0.0621 0.386563 0.5289 storage/LTP family protein precursor, expressed - - - - - 0.384696 -0.06817 -0.17916 0.8203
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 0.216743 0.875242 0.39229 -0.0621 0.386563 0.5289 storage/LTP family protein precursor, expressed
FKBP-type, putative, expressed LOC_Os06g47200 LTPL85 - Protease inhibitor/seed 0.216743 0.875242 0.39229 -0.0621 0.386563 0.5289 storage/LTP family protein precursor, expressed LOC_Os08g04230 cysteine-rich repeat secretory 1.049796 2.14292 0.384696 -0.06817 -0.17916 0.8203
LOC_Os06g47200 LTPL85 - Protease inhibitor/seed 0.216743 0.875242 0.39229 -0.0621 0.386563 0.5289 storage/LTP family protein precursor, expressed LOC_Os08g04230 cysteine-rich repeat secretory 1.049796 2.14292 0.384696 -0.06817 -0.17916 0.8203
storage/LTP family protein precursor, expressed LOC_0s08g04230 cysteine-rich repeat secretory 1.049796 2.14292 0.384696 -0.06817 -0.17916 0.8203
precursor, expressed LOC_0s08g04230 cysteine-rich repeat secretory 1.049796 2.14292 0.384696 -0.06817 -0.17916 0.8203
LOC_Os08g04230 cysteine-rich repeat secretory 1.049796 2.14292 0.384696 -0.06817 -0.17916 0.8203
protein 55 precursor, putative,
expressed
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, -0.11465 0.903981 0.356786
unclassified, expressed
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_0s11g07850 Protein-tyrosine phosphatase -0.4085 0.812833 0.3279 0.617676 0.73575
domain containing protein,
expressed
LOC_Os08g25310 phosphatidylinositol transfer, 0.275665 0.82753 0.323732 -0.01711 0.219163 0.1328
putative, expressed
LOC_Os12g12090 expressed protein -0.17847 1.458025 0.319071 0.070244 -0.15821 0.56635
LOC_Os12g12090 expressed protein -0.17847 1.458025 0.319071 0.070244 -0.15821 0.56635 LOC_Os12g42980 cysteine synthase, putative, -0.28446 0.967386 0.311369 0.041093 -0.01888 -0.2465
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_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 0.245309 0.903906 0.298568 0.096099 0.745125 0.283

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

LOC_Os11g34920	stripe rust resistance protein Yr10,	-0.05823	0.80677	0.124434	0.136032	-0.07119	0.13935	
	putative, expressed							
LOC_Os05g33580	expressed protein	0.144575	0.84638	0.11739	0.2226	-0.33205	-0.40475	
LOC_Os03g59080	AMP-binding enzyme, putative,	0.424125	0.85549	0.094652	-0.08367	0.423875	-0.00865	
	expressed							
LOC_Os06g13390	SAM dependent carboxyl	1.107522	1.887983	0.090444	0.089597	5.212725		
	methyltransferase, putative,							
	expressed							
LOC_Os03g47280	VQ domain containing protein,	-0.29434	2.331807	0.090302	0.692421	2.440263	2.38675	
	putative, expressed							
LOC_Os12g13800	O-methyltransferase, putative,	-0.17371	2.004835	0.090211	-0.05522	1.682625		
	expressed							
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,	-0.05951	0.859538	0.070013	0.979238	-0.40216	1.3066	
	putative, expressed							
LOC_Os07g01960	hypothetical protein	1.318828	0.940819	0.060704				
LOC_Os01g58280	OsSub8 - Putative Subtilisin	0.50634	0.912495	0.040221	2.000822	0.386	1.8865	
	homologue, expressed							
LOC_Os03g04060	CHIT16 - Chitinase family protein	-0.29093	1.012936	0.033708	1.032299	-0.30876	0.26405	
	precursor, expressed							
LOC_Os09g28000	OsSigP6 - Putative Type I Signal	-0.20288	0.848405	0.008806	0.708869	0.697875		
	Peptidase homologue; employs a							
	putative Ser/Lys catalytic dyad,							
	expressed							
LOC_Os08g07470	hypothetical protein	1.099379	1.70653	0.002787				
LOC_Os04g57730	uracil-DNA glycosylase, putative,	0.404662	0.856585	-0.0176	0.031908	-0.30463		
	expressed							
LOC_Os02g18080	NB-ARC domain containing	-0.36652	0.975804	-0.01866	0.026415	-0.21979		
	protein, expressed							
LOC_Os04g33440	DNA-binding protein SIFA,	0.366075	0.971709	-0.02068				
	putative, expressed							
LOC_Os11g44390	retrotransposon protein, putative,	0.198537	1.514221	-0.02176				
	Tyl-copia subclass, expressed							
LOC_Os05g50940	expressed protein	-0.10384	0.944208	-0.0237	0.1101	0.025013	4.0.5.0	
LOC_Os06g38970	expressed protein	-0.35112	1.253789	-0.03963	0.028584	1.539	-1.0568	
LOC_Osl1g07780	hypothetical protein	0.051251	0.854665	-0.03969				
LOC_Os04g09900	ent-kaurene synthase, chloroplast	-0.00479	1.821975	-0.04137	0.237114	2.1666	0.8574	
	precursor, putative, expressed	0.000506	0.00010	0.04551	0.000050	0.16404	1 (2015	
LOC_0s11g25510	protein kinase domain containing	0.220726	0.90918	-0.04551	0.009272	-0.16424	1.62915	
100.007.0000	protein, expressed	0.140(70	1 20020	0.05150	0.040550	0.01156	0.50545	
LOC_Os0/g03200	phytosulfokines precursor, putative,	0.149679	1.30029	-0.051/8	0.948779	-0.31156	0.58545	
100 0-04-02050	expressed	0 29245	0.025056	0.0562	0.22200	0 562275	0.2966	
LOC_0804g02030	5 mb comb could to comb atom	0.38243	0.925056	-0.0363	-0.23299	0.303375	0.3800	
	5-phosphosultate synthetase,							
100 0 11 11070	putative, expressed	0.25(72)	1 14(147	0.05(27				
LOC_0511g119/0	N aastulaluoosominutenen form	-0.556/2	1.14014/	-0.03037	0.0241	0 204199		
LUC_USU3g16890	n-accivigiucosaminyitransferase,	1.3/364	0.981103	-0.0605	-0.0341	0.204188		
LOC 0-11-20(00	putative, expressed	0.001252	1 260467	0.06205				
LOC_0507-45250	zing finger BING time autotion	0.001255	1.30940/	-0.00303	0 21241	0.52675	0 20465	
LUC_US0/g45550	zine iniger, Knyo-type, putative,	0.000882	1.100/84	-0.08334	-0.51541	-0.32073	-0.50005	
LOC 0s12~26250	retratransposon protein sutativ-	0 236400	0.062	0.09726				
LOC_0312g50250	Tul-copia subclass appressed	0.230499	0.902	-0.08/20				
	1 J 1-copia subciass, expressed							

LOC_Os01g22370	peroxidase precursor, putative,	0.014049	1.094006	-0.09211	0.693886	-0.2535	1.41475
1.00 0-02-04220	CCMC MARKENCE 27	0.020024	1.0625	0.00271	0 594452	0.650028	
LOC_0502g04230	CGMC_mArKCMOC_2./-	0.029934	1.0035	-0.092/1	0.384433	0.050958	
	GSK3 and CLKC kinases						
	expressed						
LOC Os08g03350	amino acid transporter, putative,	0.049052	0.894679	-0.09731	1.399948	0.88625	1.5317
_ 0	expressed						
LOC_Os03g20380	CAMK_KIN1/SNF1/Nim1_like.2 -	0.180244	1.575217	-0.09739	0.346332	0.007988	0.38025
	CAMK includes						
	calcium/calmodulin depedent						
	protein kinases, expressed						
LOC_Os12g10560	clathrin adaptor complex small	0.330111	1.064096	-0.1133	0.09276	0.684913	0.82545
	chain domain containing protein,						
	expressed						
LOC_Os02g13430	receptor-like protein kinase 5	-0.34523	0.81309	-0.11722	-0.02805	0.0824	
	precursor, putative, expressed						
LOC_Os02g37180	expressed protein	-0.23332	0.803831	-0.13071	1.190802	-0.57273	0.31015
LOC_Os12g16720	cytochrome P450 71A1, putative,	0.018278	1.467189	-0.13188	2.2582	0.828163	1.01775
100.0.01.00000	expressed	0.00010	2 4020(2	0.140/2	1 012000	0.65075	
LOC_0501g09800	BIBAI - Bric-a-Brac, Iramirack, Broad Complex BTB domain with	0.602012	3.403062	-0.14062	1.013809	0.03975	
	Ankyrin repeat region expressed						
LOC Os12942884	5-methyltetrahydronteroyltriglutama	0 544896	1 379718	-0 14124	-0 24333	0 5925	-0.08745
100_0312g12001	tehomocysteine methyltransferase	0.5 11090	1.577710	0.11121	0.21555	0.0720	0.00715
	putative, expressed						
LOC Os01g18800	CAMK KIN1/SNF1/Nim1 like.9 -	0.610288	1.656666	-0.14637	0.056477	-0.61825	0.33735
_ 0	CAMK includes						
	calcium/calmodulin depedent						
	protein kinases, expressed						
LOC_Os10g34940	expressed protein	1.071994	1.38556	-0.15089	0.086128	-0.06356	-0.5057
LOC_Os08g33740	CSLA11 - cellulose synthase-like	-0.21737	1.511318	-0.15232	2.44081	0.11905	
	family A, expressed						
LOC_Os06g38110	expressed protein	0.518951	0.944784	-0.15453	0.250105	0.783225	
LOC_Os03g21450	bromodomain domain containing	0.939522	1.198147	-0.17603			
	protein, expressed						
LOC_Os03g27960	sodium/calcium exchanger protein,	0.169251	0.956355	-0.17963	0.170158	0.67655	0.2142
	putative, expressed	0.404500	0.00452	0.10.445	0.000004	0.5412	0.0010
LOC_Os09g29930	transcription factor BIM2, putative,	0.494588	0.90453	-0.1844/	0.022334	0.5413	-0.0012
LOC 0c04g50790	PNA recognition motif, putative	0.517584	1.008444	0 20382	0.461570	1 128262	
LOC_0304g50790	expressed	0.517584	1.008444	-0.20382	0.401379	1.128505	
LOC Os10g35770	E2E-related protein putative	-0 14211	1 143848	-0 20575	-0 68924	1 518038	1.11
200_0010800770	expressed	0.11211	1.1.10010	0.20070	0.00721	1.010000	
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	0.992924	1.12691	-0.22791	-0.36307	-1.77799	
	domain containing protein,						
	expressed						
LOC_Os08g10460	retrotransposon protein, putative,	0.829885	1.241416	-0.22964			
	unclassified, expressed						
LOC_Os06g12120	BRASSINOSTEROID	-0.17064	0.982091	-0.24368	0.586526	-0.53803	0.5637
	INSENSITIVE 1-associated						
	receptor kinase 1 precursor,						
	putative, expressed						

LOC_Os11g48030	skp1 family, tetramerisation domain	1.03037	0.866145	-0.25868			-0.25205
	containing protein, expressed						
LOC_Os05g21180	phosphatidic acid	-0.04158	1.193427	-0.27326	0.639835	0.909925	1.50625
	phosphatase-related, putative,						
	expressed						
LOC_Os05g10930	OsGrx_C15 - glutaredoxin	-0.27119	0.861877	-0.27403	0.033054	-0.76391	
	subgroup III, expressed						
LOC_Os09g31180	ribosomal protein L6, putative,	0.653113	1.003725	-0.27667	0.281798	-0.25125	
	expressed						
LOC_Os08g05480	OsFBX261 - F-box domain	-0.4005	0.834846	-0.28147	0.778569	-1.19444	2.6675
	containing protein, expressed						
LOC_Os12g11410	retrotransposon protein, putative,	0.181072	0.981873	-0.29539			
	LINE subclass, expressed						
LOC_Os11g12320	disease resistance protein RPM1,	0.814494	0.845938	-0.29987			
	putative, expressed						
LOC_Os06g47790	hypothetical protein	-0.26	1.097089	-0.3111			
LOC_Os11g41640	helix-loop-helix DNA-binding	0.422971	0.820754	-0.31563			
	domain containing protein,						
	expressed						
LOC_Os09g39540	40S ribosomal protein S25, putative,	0.393994	0.907492	-0.35488	0.126288	-0.126	-0.0918
	expressed						
LOC_Os05g46430	60S ribosomal protein L28-1,	0.86141	0.993909	-0.36429	0.194403	-0.09875	-0.31085
	putative, expressed						
LOC_Os08g42760	methyltransferase domain	0.459036	0.870726	-0.36606	-0.0855	-0.34428	-0.63445
	containing protein, expressed						
LOC_Os11g23080	retrotransposon protein, putative,	0.262367	1.010006	-0.36828			0.3105
	unclassified, expressed						
LOC_Os04g54200	diacylglycerol kinase, putative,	-0.31537	0.819092	-0.38319	0.223355	2.334363	0.34755
	expressed						
LOC_Os05g11780	mitochondrial carrier protein,	0.317856	0.978359	-0.38368	-0.00799	0.551	0.203
	putative, expressed						
LOC_Os01g53770	expressed protein	0.793173	1.367017	-0.38774	0.007046	0.03975	0.54465
LOC_Os02g06200	phytosulfokine receptor precursor,	-0.23775	0.963097	-0.4035			
	putative, expressed						
LOC_Os12g02630	cytochrome P450 72A1, putative,	0.636741	0.891183	-0.41761	-0.02864	0.576725	0.5624
	expressed						
LOC_Os07g48430	nucleoside-triphosphatase, putative,	0.011404	0.825611	-0.41889	0.258704	0.985125	0.5101
	expressed						
LOC_Os01g01660	isoflavone reductase, putative,	0.357105	0.907572	-0.42496			0.43165
	expressed						
LOC Os08g31630	uncharacterized glycosyl hydrolase	0.349091	0.948004	-0.43089	-0.36445	-1.3734	
	Rv2006/MT2062, putative,						
	expressed						
LOC Os11g27470	expressed protein	0.336224	0.810269	-0.43192			
LOC Os03g09840	C2 domain containing protein,	-0.15963	1.209152	-0.43786	-0.03411	-0.45338	
_ •	putative, expressed						
LOC Os08g24770	protein kinase, putative, expressed	-0.1905	0.808784	-0.43984	0.119215	0.324788	
LOC Os03g18590	malonyl CoA-acyl carrier protein	0.351416	0.964893	-0.44108	-0.13675	-1.08286	-0.25845
_ 0	transacylase, mitochondrial						
	precursor, putative, expressed						
LOC Os08g44450	L1P family of ribosomal proteins	0.568743	0.939071	-0.44478	0.045145	-0.25238	-0.0618
	domain containing protein						
	expressed						
LOC Os05g45410	HSF-type DNA-binding domain	0.021431	1.022224	-0.4558	1.27458	1,556725	2.2887
	containing protein expressed						
	0 r						

LOC_Os08g42910	peptidase, M24 family protein,	-0.13001	1.194551	-0.45691	0.116872	0.559125		
1.00.0.01.45250	putative, expressed	0.16	1 177225	0.45020	1 100502	1 (5775		
LOC_Os01g45250	DUF 1645 domain containing protein, putative, expressed	-0.16	1.1//335	-0.45929	1.190503	1.65775		
LOC_Os01g47420	pterin-4-alpha-carbinolamine	0.80168	0.853765	-0.4842	0.140474	-0.22623	0.29945	
	dehydratase, putative, expressed							
LOC_Os04g16780	hypothetical protein	0.458576	1.413518	-0.49487			0.5908	
LOC_Os01g03100	protein binding protein, putative,	0.141046	0.809181	-0.50467			-0.34325	
	expressed							
LOC_Os09g04310	expressed protein	0.489907	0.869788	-0.51495	0.666936	1.211788	1.8719	
LOC_Os08g33920	60S ribosomal protein L34,	0.697323	1.088552	-0.51768	0.174417	-0.116	-0.1015	
	putative, expressed							
LOC_Os03g63400	transcription factor BTF3, putative,	0.785985	1.038759	-0.52127	-0.02628	0.8548	-0.4193	
	expressed							
LOC_Os08g41300	60S ribosomal protein L32,	0.467819	0.815883	-0.53093	0.192694	-0.03763		
	putative, expressed							
LOC_Os10g20910	40S ribosomal protein S23, putative	0.699975	0.887183	-0.53508				
LOC_Os05g46830	proline-rich protein, putative,	-0.23184	1.341589	-0.5424	0.067859	1.564138	2.46675	
	expressed							
LOC_Os11g40320	expressed protein	0.349056	0.825271	-0.54896				
LOC_Os08g05530	LSM domain containing protein,	0.537188	0.962806	-0.55309	0.104619	-0.215	-0.33355	
	expressed							
LOC_Os02g32520	ERD1 protein, chloroplast	-0.08501	0.881185	-0.56084	1.547589	2.486875	1.9809	
	precursor, putative, expressed							
LOC_Os10g35920	OsFBX389 - F-box domain	-0.13792	1.031605	-0.5682	0.583063	0.239625	0.1726	
	containing protein, expressed	0.00500	0.000000	0.57.41	2 020225	2.2.17025		
LOC_0s01g62430	C2 domain containing protein,	-0.29593	0.992829	-0.5/41	2.030325	2.34/925		
LOC 0-11-07280	putative, expressed	0.240602	0.066065	0 57602	0 121669	0.801625		
LOC_0511g07280	expressed	0.540002	0.900905	-0.57005	0.121008	0.801025		
I OC Os02948030	expressed protein	-0 13645	0.986382	-0 58061				
LOC_0s02g48050	protein kinase, putative, expressed	-0.12825	0.976154	-0.59279	0 77159	-0.515	-0 1646	
LOC_0s09g15420	NAD dependent	0.092497	1.158289	-0.59332	0.257708	2 370713	1 83845	
	epimerase/dehydratase family							
	protein, putative, expressed							
LOC_Os04g49757	purine permease, putative,	0.617191	1.166246	-0.61023	0.676582	-1.16581	0.388	
	expressed							
LOC_Os04g27020	cytochrome P450, putative,	0.047259	2.27759	-0.61485	0.629121	0.4977		
	expressed							
LOC_Os10g41410	nucleoside diphosphate kinase,	0.207868	1.210656	-0.62351	1.389964	0.14325	-0.22565	
	putative, expressed							
LOC_Os08g17784	purple acid phosphatase, putative,	0.416011	1.011075	-0.62441	-0.19014	-0.09669	-0.09855	
	expressed							
LOC_Os04g22720	expressed protein	0.145743	0.967069	-0.63247	-0.03504	0.134525	0.107	
LOC_Os09g24690	60S ribosomal protein L34,	0.821378	0.923766	-0.63807	0.092311	-0.078	-0.199	
	putative, expressed							
LOC_Os07g33910	transporter family protein, putative,	0.975399	0.899675	-0.64215	-0.70319	0.907875	0.17375	
	expressed							
LOC_Os02g03400	microtubule associated protein,	0.725835	1.033361	-0.64373	0.036009	-0.02354	0.50255	
100.000	putative, expressed	0.500000	1 10 1001	0.0000	0.040224	0.100010	0.0111	
LOC_Os05g48220	bus ribosomal protein L35a-3,	0.568089	1.104001	-0.66322	0.040336	0.192013	-0.8111	
LOC 0-09-24780	putative, expressed	0.020927	1 561257	0 67721				
$LOC_Os11s21060$	hypothetical protein	0.222827	0.826704	-0.62294				
LOC_0s11g51900	retrotransposon protein putative	0.172362	0.050700	-0.00304				
200_0011620014	unclassified, expressed	0.775511	0.700172	0.07400				

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,	0.756482	0.839797	-0.74493	0.08992	0.258575		
	CACTA, En/Spm sub-class,							
100 0-10-40090	expressed	0 (22022	0.920665	0.75995				
LOC_0s10g40080	A D2 domain containing most in	0.623923	0.830665	-0./5885	0.05672	0 72215	0.0576	
LOC_0s09g11460	AP2 domain containing protein,	0.539806	1.2/4692	-0.79289	-0.05673	0.73315	0.0576	
1.00 0-04-20220	expressed	0 727440	1 126122	0.8202	1 705706	1 807062	1 44065	
LOC_0s05g11710	ribosomal protein I.5, putative	0.737449	1.120122	-0.8303	0.100448	0 272	1.44905	
LOC_0505g11/10	expressed	0.038085	1.210625	-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,	1.018265	0.827976	-0.89178	0.113323	-0.109	-0.5055	
	putative, expressed							
LOC_Os08g20010	expressed protein	0.616284	1.134932	-0.91882				
LOC_Os05g08360	rRNA 2-O-methyltransferase	0.814896	1.114097	-0.9797	0.376706	-0.17776		
	fibrillarin 2, putative, expressed							
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	-0.11669	0.865413	-1.04704	-0.12548	0.056238		
100.000.000	18 precursor, putative, expressed	0.402002	0.05104	1 05052				
LOC_Os02g05370	T 2	0.402893	0.85194	-1.0/9/3				
100 0-02-11970	1 y3-gypsy subclass, expressed	0.06694	1.007420	1.09249	0.944755	2 22625	4 12655	
LOC_0s02g11870	expressed protein	-0.00084	0.065728	-1.08248	0.844/55	2.32033	4.15055	
LOC_0810g33430	serine/infeonine-protein kinase,	0.30908	0.965/38	-1.17005	-0.49038	-0.34083	-0.0278	
LOC Os02g27480	membrane attack complex	0.054664	0 847496	-1 20102	0.06561	0 325275	1 9167	
LOC_0302g27480	component/perforin/complement	0.054004	0.047470	-1.20102	0.00501	0.525215	1.7107	
	C9 putative expressed							
LOC Os08g24190	OsFBX286 - F-box domain	1 075303	0 984956	-1 31262	-0.07762	0 975625		
	containing protein, expressed							
LOC Os04g40630	BTBZ4 - Bric-a-Brac, Tramtrack,	1.218921	1.31717	-1.3625	-0.46337	1.187875	2.96815	
_ 0	Broad Complex BTB domain with							
	TAZ zinc finger and							
	Calmodulin-binding domains,							
	expressed							
LOC_Os11g36510	retrotransposon protein, putative,	1.221531	1.316739	-1.39647	0.389854	0.567038		
	unclassified, expressed							
LOC_Os05g50380	glucose-1-phosphate	0.581913	1.038034	-1.45629	-0.15622	2.4029	-0.5485	
	adenylyltransferase large subunit,							
	chloroplast precursor, putative,							
	expressed							
LOC_Os08g23960	OsFBL46 - F-box domain and LRR	0.74187	1.097278	-1.49533	-0.032	-0.05131		
	containing protein, expressed							
LOC_Os03g56160	lectin-like receptor kinase 7,	-0.45436	1.613115	-1.55169	0.8599	0.85475		
	putative, expressed							
LOC_Os08g19200	expressed protein	0.864661	1.090907	-1.6212				
LOC_Os08g35160	neat 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,	2.366842	0.460799	3.02609	0.03042	0.130313	0.63045	
-	unclassified, expressed							
LOC_Os02g41680	phenylalanine ammonia-lyase,	-0.08075	0.469767	2.752294	0.605036	-0.784	3.60465	
	putative, expressed							
LOC_Os03g52390	PIII1 - Proteinase inhibitor II family	0.230628	0.591478	2.455296	1.283272	2.066	2.4384	
	protein precursor, expressed							

LOC_Os04g02490	expressed protein	0.25447	0.202314	2.380529	-0.06247	0.628363		
LOC_Os01g10890	CAMK_KIN1/SNF1/Nim1_like.8 -	0.159278	0.008341	2.325187	-1.12806	-2.08753		
	CAMK includes							
	calcium/calmodulin depedent							
	protein kinases, expressed							
LOC_Os01g17396	expressed protein	-0.07005	-0.15031	2.183089	-0.0582	0.07315	0.1159	
LOC_Os07g18990	LTPL40 - Protease inhibitor/seed	-0.22407	-0.33285	2.164805	-0.38161	-1.30263	0.7675	
	storage/LTP family protein							
	precursor, expressed							
LOC Os06g05230	retrotransposon protein, putative,	0.091616	0.316795	2.159462				
_ 0	unclassified, expressed							
LOC Os04g31120	OsFBK14 - F-box domain and kelch	-0.4348	-0.57179	2.109069	0.755325	-0.24233		
_ 0	repeat containing protein, expressed							
LOC Os03g60580	actin-depolymerizing factor,	0.309457	-0.25407	2.013691	0.239195	0.573875		
_ 0	putative, expressed							
LOC Os08g33710	ribonuclease T2 family domain	0.141643	0.123274	1.99959	-0.825	-0.47701	0.15635	
_ 0	containing protein, expressed							
LOC Os06g51060	CHIT8 - Chitinase family protein	0.022889	-0.1662	1.999407	1.16594	1.0355	1.2868	
	precursor, expressed							
LOC Os03g57880	glucan endo-1.3-beta-glucosidase	0.285945	0.034413	1.975122	-0.39709	1.774225		
	precursor putative expressed							
LOC Os08ø06110	MYB family transcription factor	-0 37638	-0 1035	1 942447	-0 24468	-0.95353	-0 17155	
200_0300500110	nutative expressed	0.57050	0.1055	1.912117	0.21100	0.95555	0.17155	
LOC 0s04g46880	transporter major facilitator family	-0.1387	0 364692	1 908629	-0 16371	-0 86968	2 07555	
100_0304g40880	nutative expressed	-0.1567	0.504072	1.900029	-0.10571	-0.00700	2.07355	
LOC 0s08g20140	heat shock protein putative	0 57030	0.006477	1 851055	0.05243	0.817625	0.5244	
LOC_0508g39140	avpressed	-0.37939	0.000477	1.651955	-0.03243	0.817025	-0.5244	
LOC 0s03g13540	Sar/Thr protein phosphatase family	0 22520	0 261718	1 837805	1 66641	1 012275	1.06805	
LOC_0s03g13340	protein puteting approaced	-0.23339	0.201/18	1.057805	-1.00041	1.912373	1.00805	
LOC 0:12:28660	protein, putative, expressed	0 700206	0.227000	1 072602	0 49394	0 67675	0.2470	
LOC_0s12g38660		0.700296	0.32/909	1.823083	-0.48384	-0.0/0/5	-0.3479	
LOC_0801g55540	aminotransferase, classes I and II,	-0.41030	0.276277	1.802218	0.043307	0.942373	-0.288	
	domain containing protein,							
1.00 0-01-00570	expressed	0.52747	0.002260	1 774496	0.11400	0 22225		
LOC_Os01g09570	6-pnospnotructokinase, putative,	-0.53/4/	0.003369	1.//4486	-0.11409	0.32325		
	expressed	0.01007	0.22220	1 730/73	0.6020	0 707 10	1.04005	
LUC_Us05g04610	ABC transporter, ATP-binding	-0.31227	-0.33239	1.738652	-0.6838	-2.72748	1.24895	
	protein, putative, expressed	0.000000	0.000	1 2000 /	0.04/5/5	0.000	0.11575	
LOC_Os03g48190	expressed protein	0.239911	-0.0995	1.72994	0.246745	-0.68351	0.11565	
LOC_Os03g12290	glutamine synthetase, catalytic	-0.06426	0.288342	1.722727	0.189553	-0.528		
	domain containing protein,							
	expressed	0.44	0.67-7-				0.048	
LOC_Os03g39760	cytochrome P450, putative,	-0.13983	-0.0365	1.712995	0.030716	-3.26888	0.86205	
	expressed							
LOC_Os03g37840	potassium transporter, putative,	-0.5234	0.5539	1.712992	0.41608	-1.66333	0.38685	
	expressed							
LOC_Os01g31100	retrotransposon, putative,	0.340402	-0.14551	1.698301				
	centromere-specific							
LOC_Os03g49630	expressed protein	-0.29505	-0.01083	1.69613	0.277418	-2.46779	0.29455	
LOC_Os03g52370	PIII4 - Proteinase inhibitor II family	-0.03898	0.065326	1.676255	0.361409	0.537638	1.3359	
	protein precursor, expressed							
LOC_Os02g57060	OsCttP2 - Putative C-terminal	-0.15097	-0.14081	1.669211	-0.08294	-1.23544	-0.1757	
	processing peptidase homologue,							
	expressed							
LOC_Os05g50840	mitochondrial carrier protein,	-0.14442	-0.07275	1.664499	0.203986	-0.00413		
	putative, expressed							

LOC_Os03g05290	aquaporin protein, putative,	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	0.580699	-0.07495	1.646555	1.463947	-0.10675	0.8732
_ 0	protein, expressed						
LOC_Os03g55240	cytochrome P450, putative,	-0.07001	-0.33214	1.64239	0.099796	-0.31638	0.52395
	expressed						
LOC_Os01g52230	phosphoethanolamine/phosphocholi	0.307707	0.16564	1.630064	-2.15971	0.68415	1.4454
	ne phosphatase, putative, expressed						
LOC_Os11g36180	receptor kinase, putative, expressed	-0.40071	-0.02072	1.623519			
LOC_Os08g14950	receptor-like protein kinase 2	-0.00724	-0.1331	1.604925			
	precursor, putative, expressed						
LOC_Os07g42250	strictosidine synthase, putative,	-0.29293	-0.22317	1.60161	-0.21389	-1.88511	-0.0833
	expressed						
LOC_Os01g04920	glycosyl transferase, group 1	-0.42365	0.496614	1.591279	-1.73096	-1.63008	-1.49295
	domain containing protein,						
	expressed						
LOC_Os06g21890	basic proline-rich protein precursor,	-0.28882	0.199713	1.578644	0.077735	-0.15604	0.6951
	putative, expressed						
LOC_Os06g03860	uncharacterized membrane protein,	0.219387	-0.24087	1.576973	-0.28168	0.111275	
	putative, expressed						
LOC_Os07g43940	X8 domain containing protein,	-0.08947	-0.07741	1.575404	-0.17198	-0.39713	-0.0486
	expressed						
LOC_Os11g08670	NAD kinase, putative, expressed	-0.47924	-0.41816	1.569675	0.224285	-0.62188	0.04455
LOC_Os03g19290	mitochondrial import inner	0.020656	-0.29482	1.565506	0.149452	-0.19608	-0.6073
	membrane translocase subunit						
	Tim17, putative, expressed						
LOC_Os01g56360	wax synthase, putative, expressed	0.019516	-0.27605	1.559191	-0.1878	-1.33109	
LOC_Os03g52170	4-hydroxy-3-methylbut-2-enyl	-0.25606	0.208098	1.558048	-0.52021	-0.033	
	diphosphate reductase, putative,						
	expressed						
LOC_Os08g34210	aldehyde dehydrogenase, putative,	-0.12576	-0.42752	1.545683	-0.27298	-1.59188	-0.22315
	expressed						
LOC_Os02g54140	hsp20/alpha crystallin family	-0.04761	-0.26412	1.542395	-1.03339	-1.23978	0.0633
	protein, putative, expressed						
LOC_Os01g62840	mannose-1-phosphate	-0.27282	-0.04399	1.540741	0.508205	-0.15783	0.15685
	guanyltransferase, putative,						
	expressed						
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,	-0.4394	0.222786	1.513481	-0.25983	0.203038	-0.13045
	expressed						
LOC_Os04g45360	retrotransposon protein, putative,	-0.46935	-0.86578	1.510922			
	unclassified, expressed	0.2721	0.20000	1 501506	0.0001.47	0.4170	0.00075
LOC_Os04g54230	wound induced protein, putative,	-0.3/21	-0.30099	1.501586	0.00814/	0.41/8	0.88065
100.001.15000	expressed	0 22297	0 22212	1.40((00)	0.021(0/	0.54200	0.242
LOC_0s01g15900	expressed protein	-0.22287	-0.22212	1.490099	0.11694	-0.34308	0.243
LOC_0s01g45460	sodium/calcium exchanger protein	-0.01934	-0.09801	1.4000/4	-0.11084	-0.085/4	0.40295
LOC_0811g43860	socium/calcium exchanger protein,	-0.29383	0.320314	1.400332	0.439983	0.08103	0.3121
	sulfate transporter 4.1 chloroplast	-0 40266	-0.06766	1 47355	-0 11303	-0 26425	0.07215
LOC_0509g00499	nrecursor putative expressed	-0.49200	-0.00/00	1.+/333	-0.11393	-0.20433	0.07213
LOC 0s06a05630	GDSL-like linase/acvlhvdrolase	0 563935	-0 22254	1 464149	-0 71512	-1 1426	0.06435
LCC_0300g05050	nutative expressed	0.000700	0.22234	1.101147	0.71012	1.1720	0.00730
	r						

LOC_Os01g71340	glycosyl hydrolases family 17,	-0.29051	0.305427	1.457615	0.61339	4.36325	1.1184
100 0-07-27560	putative, expressed	0.021804	0 169476	1 451504	0 10797	0.20699	
LOC_0s07g37360	myosin-vo, putative, expressed	0.021894	0.108470	1.431304	-0.10/8/	-0.20088	
LOC_0812g32760	transporter family protein, putative,	-0.17/24	-0.20321	1.43803	0.052844	-0.21/98	
100 0-12-42240	expressed	0 225272	0 297215	1 424962	0 44722	0.8202	
LOC_0812g43340	actili-depolymenzing factor,	0.233272	0.28/313	1.454802	-0.44723	-0.8392	
LOC 0:02:042870	overseed protoin	0.00227	0.75016	1 420551			
LOC_0:08g43870	expressed protein	-0.00237	-0.75910	1.430331	0.02214	0 24799	
LOC_0:03g14940	alvastanhamharil diastar	-0.10012	0.396346	1.420802	1 05702	-0.34788	2 62115
LOC_0802g51050	phoephodiosteraça family protain	0.415285	0.412323	1.420115	-1.03/03	-0.29829	2.02115
	putative expressed						
LOC 0s02g29510	DUE803 domain containing	0 166694	0 183054	1 423737	-0 10035	-1 16695	-0.55855
100_0302g2)510	putative expressed	0.1000)4	0.105054	1.423737	-0.17755	-1.10055	-0.55855
LOC Os03943720	transporter family protein putative	0 119785	-0.02671	1 42368	-0 14075	0 336963	0.21255
200_0305615720	expressed	0.119705	0.02071	1.12500	0.11075	0.550705	0.21255
LOC Os04946960	glutathione peroxidase domain	-0.03305	0 131359	1 412068	0 387975	0 459375	0 40885
100_000 ig 10,000	containing protein expressed	0.00000	0.101009	1.112000	0.007770	0.109070	0.10000
LOC Os03g21890	potassium transporter putative	-0 19303	-0.09029	1 410098	-0 19149	-0 4482	
	expressed						
LOC Os01g14900	glycerol-3-phosphate	0.11633	0.130731	1.40459	-0.00518	0.242525	
	acyltransferase, putative, expressed						
LOC_Os03g08430	SAC domain containing protein,	-0.22198	-0.14205	1.403178	-0.07642	0.337313	1.55945
	putative, expressed						
LOC_Os05g41930	N-rich protein, putative, expressed	-0.5814	-0.4815	1.393921	-0.01852	-0.17213	-0.0705
LOC_Os12g31850	ureide permease, putative,	0.237948	-0.68813	1.387038	-0.11175	0.505075	0.60795
	expressed						
LOC_Os04g23890	AGC_PVPK_like_kin82y.10 - ACG	-0.43627	-0.563	1.38335	-0.01447	-1.83238	0.1493
	kinases include homologs to PKA,						
	PKG and PKC, expressed						
LOC_Os03g20730	chaperone protein dnaJ, putative,	-0.2423	-0.16449	1.383296	1.308946	-0.45438	0.0888
	expressed						
LOC_Os04g54300	wound induced protein, putative,	0.057619	-0.2692	1.382769	0.397519	0.66075	
	expressed						
LOC_Os03g17800	phosphatidylinositol transfer protein	-0.08126	0.197204	1.371122	-1.16267	0.371613	0.0953
	alpha isoform, putative, expressed						
LOC_Os01g67320	expressed protein	0.227811	0.015442	1.366539	0.105538	-1.24725	0.194
LOC_Os02g42940	MSP domain containing protein,	-0.18089	-0.0881	1.363976	-0.11135	-0.4437	0.59285
	expressed						
LOC_Os03g43100	expressed protein	0.962316	0.447866	1.359162	4.370815	0.016788	-0.31555
LOC_Os09g09930	heavy metal transport/detoxification	-0.02987	-0.12745	1.355495	-0.24259	-1.8946	0.0623
100.0.02.02510	protein, putative, expressed	0.215170	0.21200	1 252972	0.02246	0.057500	
LOC_0s03g03310	CAMK_KIN1/SNF1/NIM1_like.15	0.3131/9	-0.21288	1.5558/2	0.02246	0.03/388	
	- CAMK includes						
	protein kingses, expressed						
LOC Os01g62810	regulator of chromosome	0.480613	0 16726	1 3/1977/	0.002758	0 553313	-0.44225
LOC_0301g02010	condensation putative expressed	0.400015	0.10720	1.547774	0.002758	0.555515	-0.44223
LOC Os08029720	mitochondrial carrier protein	-0 28508	0.59744	1.346159	0.214802	-0 14433	-0 2947
0000527720	putative, expressed						
LOC Os04g35840	T-complex protein 11, putative.	-0.38842	0.111143	1.345561	-0.0359	0.2115	-0.48625
	expressed		-				
LOC_Os08g02860	transposon protein, putative,	-0.01801	0.034977	1.343484	0.074998	-0.27975	1.1677
	unclassified, expressed						

LOC_Os10g41780	chlorophyllide a oxygenase, chloroplast precursor, putative,	0.055264	-0.22434	1.340079	-0.83212	-1.60838	
LOC_Os06g13560	expressed SAM dependent carboxyl methyltransferase, putative,	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			0.4040-
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	-0.44587	0.06355	1.260665	-0.40334	-0.78301	-0.31735	
	100 0-11-41150	containing protein, expressed	0.224155	0 19725	1 250466	0.75190	2 210499	0 47225	
	LOC_Os11g41150	putative, expressed	0.234155	-0.18/25	1.259466	-0.75189	2.310488	-0.4/235	
	LOC Os03g59320	expressed protein	-0.09846	0.057192	1.259103	-0.16604	0.78825	1.61625	
	LOC_Os12g37650	DUF538 domain containing protein,	-0.10336	-0.43799	1.258531	0.006814	-1.63746	-0.49895	
		putative, expressed							
	LOC_Os07g48160	alpha-galactosidase precursor,	-0.08042	-0.1902	1.256744	-0.33812	1.25815		
		putative, expressed							
	LOC_Os01g63380	transposon protein, putative,	0.325032	0.238514	1.25066				
		unclassified, expressed							
	LOC_Os02g57790	ZOS2-19 - C2H2 zinc finger	-0.0853	-0.14267	1.250554				
		protein, expressed							
	LOC_Os12g03060	expressed protein	-0.36405	-0.4763	1.243288	0.075722	0.58375	0.09805	
	LOC_Os01g56780	plus-3 domain containing protein,	-0.37727	0.35635	1.239628	-0.2439	-0.59638	-0.36155	
		expressed							
	LOC_Os10g31640	glycine-rich cell wall structural	0.341043	-0.26132	1.237072	-0.13426	0.0063		
		protein 2 precursor, putative,							
		expressed	0.4664	0.17000	1 2220 40	0 100 50	0.67025	1 (772)	
	LOC_0s12g04020	hydroxymethylglutaryl-CoA lyase,	-0.4664	-0.1/888	1.233948	-0.18859	0.67025	1.6//3	
	LOC 0s02s16040	ubiquitin conjugating anzume	0.042054	0.244525	1 222284	0.024861	1 202125		
	LOC_0502g10040	nutative expressed	0.042034	0.244323	1.232264	0.024801	1.393123		
	LOC Os01g12810	retrotransposon protein putative	0 154694	0 294055	1 2313	0 276908	-1 74551	0.04975	
	L0C_0301g12010	unclassified. expressed	0.151071	0.291055	1.2515	0.270700	1.71551	0.01775	
	LOC Os03g42810	endonuclease/exonuclease/phosphat	0.500267	0.310071	1.230129	0.070647	1.68855		
	_ 0	ase family domain containing							
		protein, expressed							
	LOC_Os01g68330	antigen peptide transporter-like 1,	-0.03351	-0.62467	1.228882	-0.34221	0.13445	0.4354	
		chloroplast precursor, putative,							
		expressed							
	LOC_Os06g45350	protein kinase domain containing	0.047958	0.314365	1.226662	-0.433	1.447375	-0.2465	
		protein, expressed							
	LOC_Os07g39900	interferon-related developmental	-0.39919	-0.17935	1.226136	-0.55571	0.353375	-0.4126	
		regulator, putative, expressed							
	LOC_Os06g40120	SPX domain containing protein,	-0.35321	0.316101	1.221792	-0.26056	-0.83714	0.1464	
		putative, expressed							
	LOC_Os01g18080	retrotransposon protein, putative,	-0.29/19	-0.53398	1.221/85	0.534189	1.188/5	0.4055	
	LOC 0:05:50500	unclassified, expressed	0 17277	0.22007	1 220852	0 12196	0.64046		
	LOC_0505g50500	expressed	-0.1/2//	-0.22007	1.220832	-0.13180	-0.04940		
	LOC Os07g48630	ethylene-insensitive 3 putative	-0.50258	-0 21481	1 220723	1 046094	0.911375	1 56175	
	200_0007910000	expressed	0.00200	0.21101	1.220723	1.010091	0.911070	1.00170	
	LOC Os01g58640	nucleotide	-0.31399	0.033456	1.219181	-1.25104	-1.26933	-0.69095	
	_ 0	pyrophosphatase/phosphodiesterase,							
		putative, expressed							
	LOC_Os06g18990	embryogenesis transmembrane	-0.27091	-0.07965	1.217188	-0.24976	-0.34878	0.22385	
		protein, putative, expressed							
	LOC_Os01g47630	expressed protein	-0.29105	0.140064	1.216656	-0.26661	-0.63484		
	LOC_Os03g31230	MYB family transcription factor,	-0.55293	-0.30742	1.215568	-0.13181	-0.0502	0.54205	
		putative, expressed							
	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,	-0.37801	-0.08338	1.206474				
		1 v3-gypsy subclass expressed							

LOC_Os02g36490	expressed protein	0.328013	0.050174	1.20632	0.610348	0.39645	
LOC_Os12g29520	auxin response factor, putative,	-0.53621	-0.42738	1.205519	0.132073	-0.07775	
	expressed						
LOC_Os12g44230	expressed protein	-0.51668	0.325442	1.20443	0.348358	-0.17848	-0.0803
LOC_Os04g31390	vacuolar protein sorting-associated	0.384655	0.106093	1.203065	0.02966	0.034625	0.30625
	protein 11, putative, expressed						
LOC_Os09g02270	cyclase family protein, putative,	0.986741	-0.50003	1.199572	0.160669	0.315013	1.70195
	expressed						
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,	-0.2503	0.307055	1.192688	0.116405	1.550125	-0.01725
	putative, expressed						
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,	-0.17846	-0.04959	1.180262	-0.41344	#########	
	putative, expressed						
LOC_Os06g49120	Complex I intermediate-associated	-0.30772	-0.84889	1.179567	0.221483	-2.39248	
	protein 30 domain containing						
	protein, putative, expressed						
LOC_Os04g13140	vignain precursor, putative,	-0.03917	0.047869	1.178027	-0.00341	0.049675	
	expressed						
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	-0.26898	-0.12246	1.173904	-0.04048	0.396475	-0.8507
	protein, putative, expressed						
LOC_Os01g60830	expressed protein	0.897806	0.570377	1.170648	-0.66755	-1.74385	
LOC_Os07g44060	haloacid dehalogenase-like	0.433766	0.456103	1.170408	-0.31247	0.295663	
	hydrolase family protein, putative,						
1.00 0.02 10240	expressed	0.227(4	0.00225	1 1 (00 2 2	0.16444	0.075	
LOC_0s03g19240	AMP-binding enzyme, putative,	-0.23/64	-0.00225	1.168932	-0.16444	-0.875	
LOC 0:01:52020	expressed	0.044700	0.2552	1 164140	0.45172	0 22461	
LOC_0s01g55950	protein kinase APK1A, chloroplast	-0.42971	-0.58317	1.163681	-0.11543	-0.09913	0.83875
LOC_0505g02020	procursor putative expressed	-0.42971	-0.38317	1.105081	-0.11545	-0.09915	0.85875
LOC 0s09g38920	thiol protease SEN102 precursor	0 48973	0 344826	1 162962	-0.06649	0 7911	-0 5456
100_0307g50720	nutative expressed	0.10975	0.511020	1.102902	0.00017	0.7911	0.5150
LOC Os04940090	zinc finger 77 type family protein	-0 498	0 257141	1 156063	0 125155	-0 3272	-0 23275
100_030 ig 10090	expressed	0.190	0.257111	1.150005	0.125155	0.5272	0.23275
LOC Os03g62670	expressed protein	0 110074	0 137405	1 150797	-0 40509	-5 19375	
LOC_0s08g41960	OsMADS37 - MADS-box family	-0 29905	0.05266	1.150011	-0.22538	-0 4035	
	gene with MIKC* type-box.						
	expressed						
LOC Os01g48680	two pore calcium channel protein 1,	-0.55134	-0.00607	1.149163	0.003772	-1.02104	0.851
	putative, expressed						
LOC Os01g68270	hypothetical protein	-0.07815	-0.48779	1.147298			
LOC Os03g49720	PAP fibrillin family domain	-0.12428	-0.25451	1.147003	-0.51011	-0.39348	1.4857
_ 0	containing protein, expressed						
LOC Os09g25150	cinnamoyl-CoA reductase, putative,	-0.07477	0.046599	1.139748	-0.49846	-2.8484	0.3165
	expressed						
LOC_Os03g63020	protein kinase domain containing	-0.58531	-0.68288	1.13762	-0.36063	0.234188	-0.0644
-	protein, expressed						
LOC_Os12g08060	universal stress protein family	-0.03519	0.076099	1.137483			
	protein, expressed						
LOC_Os02g46660	SNARE associated Golgi protein,	-0.1782	-0.27549	1.136795	-0.64708	-1.11264	-0.08805
	putative, expressed						

LOC_Os12g18650	Regulator of chromosome	0.007808	-0.8847	1.135683	-0.1154	0.293088	0.5959	
	condensation domain containing							
	protein, expressed							
LOC_Os06g12320	transmembrane amino acid	0.206656	-0.20898	1.130373	-0.60465	1.984425	0.2901	
	transporter protein, putative,							
	expressed							
LOC_Os04g08550	oxidoreductase, aldo/keto reductase	-0.46204	0.244233	1.129256	1.254635	1.577375	0.81755	
	family protein, putative, expressed							
LOC_Os05g07090	acyl-coenzyme A dehydrogenase,	-0.24294	-0.21336	1.127209	0.030344	0.794038	0.4984	
	mitochondrial precursor, putative,							
	expressed							
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	-0.28372	0.203639	1.120602	0.007266	0.279075	0.5318	
100.005.405(0	motif, putative, expressed	0.044270	0.505500	1 110255	0.040110	0.00101		
LOC_Os05g48/60	protein of unknown function	0.066379	0.585729	1.119257	0.349112	-0.22131		
	DUF1421 domain containing							
100 0-07-26800	LIDE0041 domain containing	0.41107	0 22720	1 117751	0.052251	0.02975	0.6102	
LUC_0s0/g30800	OPF0041 domain containing	0.4110/	-0.32729	1.11//31	0.032231	0.02875	0.0103	
100.0-08-04420	protein, putative, expressed	0.26972	0.214622	1 106969	0 1052	0.017	1 2625	
LOC_0s08g04430	expressed protein	0.20873	0.214022	1.105611	-0.1952	-0.017	0.0021	
LOC_0s03g20330	DEAD box ATP dependent PNA	-0.50991	-0.02029	1.103011	-0.15174	0.050158	0.0031	
LOC_0502g05550	belicase putative expressed	-0.41032	-0.1380	1.104070	0.150000	0.085875	-0.0982	
LOC 0s12g32980	notwirus VPg interacting protein	-0 19729	0.051664	1 102846	0 165383	0 2045		
LOC_0812g32980	putative expressed	-0.19729	0.051004	1.102840	0.105585	0.2045		
LOC Os08g10500	expressed protein	0 320289	-0 12027	1 102291	0 274456	0 3405	0.69805	
LOC_0s09g32820	uridine/cytidine kinase-like 1	-0 51524	-0.37	1 101382	-0.03576	-0.36338	-0.4805	
100_0307652020	nutative expressed	0.51521	0.57	1.101502	0.05570	0.50550	0.1005	
LOC Os06g24190	expressed protein	-0 20236	-0 41818	1 099426	0 105074	-0 22195	0 3046	
LOC Os11g04210	hvdroxvmethvlglutarvl-CoA lvase.	-0.15358	0.433137	1.098403	-0.16084	0.445225		
	putative, expressed							
LOC Os02g28980	peptidyl-prolyl isomerase, putative,	-0.27476	-0.11376	1.094579	-0.19176	-0.02863	-0.3079	
	expressed							
LOC_Os05g41460	cysteine proteinase inhibitor	-0.40899	0.31428	1.093339	0.113253	-0.125	0.30685	
	precursor protein, putative,							
	expressed							
LOC_Os12g12934	peptide transporter PTR3-A,	-0.06925	-0.38932	1.093157	-0.43295	-1.00473		
	putative, expressed							
LOC_Os05g48660	MRH1, putative, expressed	-0.20034	-0.33807	1.092702	-0.19292	0.9925		
LOC_Os03g19250	AMP-binding enzyme, putative,	-0.16074	-0.22461	1.091017	-0.06423	1.109375	-0.0536	
	expressed							
LOC_Os03g30950	acyl-desaturase, chloroplast	-0.11192	0.136272	1.090354	-0.17436	-0.1047	0.17145	
	precursor, putative, expressed							
LOC_Os09g38080	retrotransposon protein, putative,	0.261327	-0.29016	1.088508	-0.29391	0.859913	0.32025	
	unclassified, expressed							
LOC_Os11g02100	peroxidase precursor, putative,	-0.54112	-0.36393	1.086922	0.062408	-0.31075	-0.3057	
	expressed							
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,	-0.52282	-0.17063	1.081765	-0.33823	-0.25858	0.1209	
	putative, expressed							
LOC_Os03g14570	expressed protein	0.088861	0.344485	1.081324	0.204319	-1.45838		
LOC_Os01g22510	cyclase/dehydrase family protein,	-0.32732	-0.24986	1.078861	-0.09353	0.4653		
	expressed	0.4						
LOC_Os05g02420	expressed protein	0.119834	-0.22646	1.075074	0.164037	-1.1541	0.42975	

LOC_Os05g0703	0 arginyl-tRNA synthetase, putative,	-0.24674	-0.30547	1.074287	0.109058	-0.0095	-0.2099	
LOC Os10g0513	expressed	0 25023	0 59408	1.071806	0 16853	0 127625		
LOC_0s05g0157	0 expressed protein	-0.23923	-0.39408	1.07162	-0.10855	0.127025		
LOC_0505g0157	nutative expressed	-0.54007	-0.00175	1.07102	-0.50998	0.7559		
LOC 0e04g3559	0 thioesterase family protein putative	-0 43749	-0 15268	1.070574	0.086598	0.069625	-0.0041	
200_0301g5555	expressed	0.15717	0.15200	1.070574	0.000570	0.009025	0.0011	
LOC 0s03g1416	0 hypothetical protein	0 100735	-0.02458	1.070315				
LOC_0s01g4303	0 tetratricopeptide repeat domain	-0 42843	-0 29044	1.070132	0 074843	-0.08275		
	containing protein, expressed							
LOC Os06g0510	0 transketolase, putative, expressed	-0.54191	-0.47143	1.06697	-0.15485	-0.2606	-0.6091	
LOC Os05g4042	0 2.3-bisphosphoglycerate-independe	-0.27958	0.015546	1.06462	-0.06929	0.1365	-0.2629	
_ 0	nt phosphoglycerate mutase,							
	putative, expressed							
LOC_Os09g2874	0 gibberellin receptor GID1L2,	-0.10773	-0.58761	1.063714	-0.54699	-0.808	-0.55515	
	putative, expressed							
LOC_Os11g4054	0 transporter family protein, putative,	0.018132	-0.26863	1.062409	-0.19457	-0.25071	0.25945	
	expressed							
LOC_Os01g7248	0 zinc finger, C3HC4 type domain	-0.50383	-0.35123	1.062257	-0.30968	0.219638	0.4181	
	containing protein, expressed							
LOC_Os08g4204	0 LTPL80 - Protease inhibitor/seed	0.054544	-0.47588	1.062106	-0.25953	0.0192	-0.22515	
	storage/LTP family protein							
	precursor, expressed							
LOC_Os10g3665	0 actin, putative, expressed	-0.1588	-0.02492	1.060544	-0.44769	-0.00863	-0.45965	
LOC_Os01g6903	0 sucrose-phosphate synthase,	0.079348	0.128285	1.056808	-0.42691	-0.80596		
	putative, expressed							
LOC_Os09g2891	0 carbonic anhydrase, chloroplast	-0.24202	-0.07622	1.054319	0.404322	1.04325	0.25025	
	precursor, putative, expressed							
LOC_Os04g4935	0 PPR repeat domain containing	-0.21721	0.40794	1.053956			0.01315	
	protein, putative, expressed							
LOC_Os03g6085	0 peptide transporter PTR2, putative,	-0.40765	-0.09754	1.053886	0.058761	-0.27748	0.2621	
	expressed							
LOC_Os03g2280	0 OsFBT5 - F-box and tubby domain	-0.14899	-0.03947	1.051548	0.026613	0.862863	-0.1252	
	containing protein, expressed			4.0540.00				
LOC_Os03g5858	0 nodulin, putative, expressed	-0.22586	-0.21003	1.051069	0.229347	-0.25113	0.63175	
LOC_0s12g3815	0 osmotin, putative, expressed	-0.069/	-0.22	1.049965	-0.83868	2.205188	0 (1255	
LOC_Os01g0666	C torminal TDD hinding demain	-0.1396/	0.52488	1.049452	0.762345	1.1188	0.64255	
	c-terminal TPP binding domain							
LOC Os11:0581	avprassed protein	0 42022	0 26226	1.047226	0 585063	0.40125	0.26725	
LOC_0s02g4780	0 monodehydroascorbate reductase	-0.42933	-0.30320	1.047220	-0 12916	-1 038	0.20725	
200_0302g1/00	nutative expressed	0.51500	0.71570	1.010/21	0.12910	1.050	0.02025	
LOC Os12g3966	0 calcium-transporting ATPase.	-0.31604	-0.02244	1.045158	0.123435	0.315125	0.04975	
5	plasma membrane-type, putative,							
	expressed							
LOC Os09g2571	0 keratin, type I cytoskeletal 9,	0.191817	0.130082	1.043402	-0.2112	-1.20523		
	putative, expressed							
LOC_Os03g5048	0 phosphoglucomutase, putative,	-0.33013	-0.10303	1.042341	-0.45637	-0.59638	-0.2779	
	expressed							
LOC_Os06g4875	0 DEAD-box ATP-dependent RNA	-0.56423	-0.4224	1.036989	0.12172	-0.146	-0.16555	
	helicase, putative, expressed							
LOC_Os02g5286	0 phosphate carrier protein,	-0.44223	0.389755	1.035635	0.108075	0.736	0.1836	
	mitochondrial precursor, putative,							
	expressed							
LOC_Os01g7210	0 OsCML10 - Calmodulin-related	0.006688	0.369373	1.032705	-0.19663	-0.24963	-0.41665	
	calcium sensor protein, expressed							

 LOC_Os01g48420	peroxiredoxin, putative, expressed	-0.22509	-0.02932	1.031877	-0.12011	-0.08275	-0.22195	
LOC_Os02g53320	universal stress protein domain	-0.05634	0.073099	1.031667	-0.42087	-0.00179	0.61115	
	containing protein, putative,							
	expressed							
LOC_Os05g09440	NADP-dependent malic enzyme,	-0.53193	0.189053	1.031565	-0.65779	-0.1106	2.34375	
	chloroplast precursor, putative,							
	expressed							
LOC_Os04g12530	amino acid transporter family	-0.15149	-0.14904	1.030677				
	protein, putative, expressed							
LOC_Os09g14670	phosphoenolpyruvate carboxylase,	-0.54232	-0.06101	1.02944	-0.72492	-0.0785		
	putative, expressed							
LOC_Os05g39250	phosphatidylethanolamine-binding	-0.06532	0.241144	1.02797	0.345626	0.752175		
1.00.0.10.22050	protein, putative, expressed	0.5774/5	0.70(0)	1.027207	0.22((1.029.45		
LOC_0s10g22030	mitachandrial carrier protain	0.377403	-0.78090	1.02/300	-0.2300	0.12014		
LOC_0s03g09110	nutocionaria carrier protein,	-0.49234	-0.1/141	1.025791	0.103494	-0.12014		
LOC Os03ø43010	expressed protein	-0 58527	-0.9586	1 024259	0.083629	-0 29059	-1.0102	
LOC_0s03g08900	MATE efflux family protein	-0 12457	0.032906	1.024011	1 276876	1 4326	1.0102	
	putative expressed							
LOC Os12g39320	DUF221 domain containing protein.	-0.55327	0.142651	1.023979	0.125373	0.3887	0.0673	
5	expressed							
LOC Os03g53910	tetratricopeptide repeat domain	0.040796	0.091853	1.022612	-0.35569	-0.976	-0.77135	
	containing protein, expressed							
LOC_Os07g49150	26S protease regulatory subunit 4,	-0.43265	0.117105	1.021848	0.13891	0.30025	0.00385	
	putative, expressed							
LOC_Os03g57790	ubiquitin-conjugating enzyme,	-0.40841	-0.1756	1.021733	-0.11332	-0.55425		
	putative, expressed							
LOC_Os03g64080	retrotransposon protein, putative,	-0.53751	0.076514	1.020101	-0.04934	-0.09113		
	Ty1-copia subclass, expressed							
LOC_Os04g39300	heavy metal transport/detoxification	0.180227	0.580248	1.019349				
	protein, putative, expressed							
LOC_Os03g53190	Core histone H2A/H2B/H3/H4	-0.3335	-0.2775	1.017954	0.082156	0.80555		
	domain containing protein, putative,							
	expressed				6.007-0.4	1 000 00		
LOC_Os09g27210	lecithine cholesterol acyltransferase,	-0.39944	-0.38428	1.017228	6.00E-04	-1.00868	-0.0873	
100 0-02-20240	PDL putative, expressed	0 202006	0 250577	1.014247	0 226429	1 254975		
LOC_0s03g29240	haloagid dehalogenase like	0.293090	0.250577	1.014347	1.27	0.8225	0 2620	
LOC_0s03g10070	haloaciu uchalogenase-like	-0.2/331	0.431022	1.012/12	-1.27	0.8323	0.2039	
	expressed							
LOC Os07g47110	OsFBT11 - F-box and tubby domain	-0 15422	-0 33492	1 012662	-0.15939	0.504	0 3903	
	containing protein, expressed							
LOC Os10g11310	expressed protein	-0.21577	-0.12126	1.012405	-0.90308	-0.32756	0.2846	
LOC_Os06g51150	catalase isozyme B, putative,	0.104165	-0.0047	1.01136	-0.18283	1.9255	0.1393	
	expressed							
LOC_Os04g40910	OsFBX146 - F-box domain	-0.30441	-0.247	1.011335	0.034055	0.296163	-0.2837	
	containing protein, expressed							
LOC_Os05g06690	HECT-domain domain containing	-0.26418	0.26078	1.010832	-0.09234	0.067375	0.04175	
	protein, expressed							
LOC_Os03g09220	stage II sporulation protein E,	0.254703	-0.12094	1.010014	-0.08671	-0.79063	0.33465	
	putative, expressed							
LOC_Os08g12120	retrotransposon protein, putative,	0.084349	-0.39533	1.006446				
	unclassified, expressed							
LOC_Os05g44360	oligosaccharyl transferase, putative,	-0.15719	-0.67189	1.004314	0.111088	0.131625	-0.1905	
	expressed							

1.0C: 0x1291000 noticity and sequence of the seq	_									
Dot: pubmers. 4.9019 0.19672 1.00287 4.0009 4.9035 Dot: pubmers. 9.0018 0.0018 0.0018 0.0018 0.01292 1.20293 0.1135 Dot: pubmers. 0.0018 0.0019 0.00194 0		LOC_Os03g39000	inositol-1-monophosphatase,	-0.14858	0.06116	1.00401	-0.46813	0.453425	-0.20775	
L0C_008/2269 naclesport 4.0199 0.01897 0.01872 0.01872 0.01872 0.01872 0.01872 0.01872 0.01872 0.01872 0.01872 0.01872 0.01872 0.01872 0.01872 0.01872 0.01874 0.01187 0.01187 0.01187 0.01187 0.01187 0.01187 0.01187 0.01187 0.01187 0.01187 0.01187 0.01187 0.01187 0.01187 0.01187 0.01187 0.01187 0.01187 0.0118 0.01087 0.02107 1.91557 0.0013			putative, expressed							
Deams pathols		LOC_Os03g22690	nucleoporin interacting component,	-0.50319	0.130692	1.003887	0.084782	-0.01069	-0.39085	
LOC_00402100 UD11 UD104 400059 100056 400059 100056 400059 LOC_00402101 Participation Call 100056 400059 100056 400059 100056 400059 100056 400059 100056 400059 100056 400057 100056 400057 100056 400057 100056 400057		100.0.09.24700	CDU1 ct c	0 10001	0.01(50	1.001007	0.04407	1 7 7 9 4		
LDC_006g2349 CAU dependent JULE 00052 JULE 000		LOC_0s08g34700	GDU1, putative, expressed	-0.10001	-0.01659	1.001906	-0.84406	-1./6/84		
cpinnericklysidianse family i protein, pratifix, expressed 0.12406 0.999368 0.621027 1.945975 LOC_0.001j0710 medense PA3, pratinive, expressed 0.33553 0.450476 0.996529 0.10107 1.342133 0.37935 LOC_0.001j07100 medense PA3, pratinive, expressed 0.033 0.990803 0.400271 2.041228 0.99545 LOC_0.001j0750 max family protein, pratinive, pratinive, 0.611571 0.02290 0.99783 0.404271 2.041228 0.99545 LOC_0.001j07100 DRMK family protein, pratinive, 0.611571 0.05721 0.998455 -0.44549 - LOC_0.001j27101 expressed -0.23215 0.05721 0.989455 -0.44549 - LOC_0.001j27101 expressed -0.23215 0.06272 0.989453 0.24799 0.99743 LOC_0.001j27101 expressed -0.21545 -0.22451 0.977433 0.45979 0.94249 LOC_0.001j27140 EPhand family protein, pratineve, repressed -0.2154 0.997413 0.41475 0.47974 LOC_0.001j281600 DIT1356 domina commining <td></td> <td>LOC_Os06g25439</td> <td>NAD dependent</td> <td>-0.38199</td> <td>-0.02434</td> <td>1.000954</td> <td>-0.12921</td> <td>-1.28958</td> <td>0.41145</td> <td></td>		LOC_Os06g25439	NAD dependent	-0.38199	-0.02434	1.000954	-0.12921	-1.28958	0.41145	
protein, putative, expressed -0.1406 0.13206 0.99348 0.62/027 1.045875 LOC, Ob/192710 medmare PA3, putative, expressed 4.32053 0.450476 0.900529 -0.10007 1.342133 0.37935 LOC, Ob/192710 McA recognition multi containing 0.11806 -0.079 0.90077 1.242138 0.97645 LOC, Ob/192710 monitorin putative, expressed - <			epimerase/dehydratase family							
LOC_0001g7317 peckaska processes, patienty, expressed -0.1406 0.1506 0.99368 0.01207 1.945875 LOC_0001g0373 mckase PAA, patienty, expressed -0.23053 0.45076 0.993747 -0.36602 0.380138 0.0013 LOC_0005g1050 no quical meristem protein, patienty, expressed -0.1866 -0.0796 0.993747 -0.36602 0.380138 0.0013 LOC_0005g1053 no quical meristem protein, patienty, expressed 0.181671 -0.04209 0.99978 -0.20752 -0.64549 LOC_0005g10537 DioX family protein, patienty, expressed 0.01371 -0.04209 0.99978 -0.2052 -0.64549 LOC_00045g1057 DioX family protein, patienty, expressed 0.01384 0.15168 0.989763 -0.1452 0.00857 LOC_0045g1057 Picker, patienty, expressed 0.02251 0.06572 0.988195 0.26279 0.042 0.0947 LOC_0045g1058 DLF1336 domaa contaming 0.012516 0.98733 0.01271 0.4144 LOC_0045g1059 DLF1336 domaa contaming 0.012516 0.987433 0.827961 0.42298 0.01953 LOC_0045g1059 <			protein, putative, expressed							
i-currend i-bit 2-bit 2-bi		LOC_Os01g73170	peroxidase precursor, putative,	-0.14406	0.132066	0.999368	0.621027	1.945875		
LOC_00/01/01739 modense PAJ, puntarive, ergressed -0.32835 0.454476 0.998529 -0.1007 1.34213 0.37935 LOC_00/02/04590 RNA recognitions endiremating -0.11806 -0.0796 0.999347 -0.36902 0.380138 0.0013 LOC_00/02/0450730 nata first protein, putative, 0.181961 0.380629 0.999303 -0.6271 2.011238 0.98515 LOC_00/02/07707 Text first protein, putative, 0.618571 -0.04209 0.989787 -0.20522 -0.64549 LOC_00/02/07707 HORMA durania containing 0.390974 -0.01711 0.989163 -0.4344 LOC_00/02/07707 vesice-sanciald membrane -0.21536 -0.24507 0.988195 0.26279 0.0422 0.99971 LOC_00/02/07708 vesice-sanciald membrane containing -0.21536 -0.24507 0.988195 0.26279 0.0422 0.99971 LOC_00/02/07708 vesice-sanciald membrane containing -0.12546 0.987433 0.847961 0.26798 LOC_00/02/0780 ZMP to the matrix protein, putative, ergressid -0.12754 0			expressed							
LOC_004794999 RNA recognition medi containing potein, putative, expressed -0.11806 -0.0796 0.9993147 -0.36902 0.380138 0.0013 LOC_0049109 no agrical meters protein, putative, expressid 0.018571 -0.04209 0.999313 -0.02272 2.041238 0.96545 LOC_0040313331 Deak fumily portein gratative, expressid 0.018571 -0.04209 0.98978 -0.20552 .04.64549 - LOC_004031737 HORMA domain containing portein, putative, expressed -0.04314 0.989153 0.18522 0.008823 - LOC_004042138 EF hand family protein, gratesice -0.22516 -0.02457 0.988155 0.1852 -0.04344 LOC_004042138 DF hand family protein, gratesice -0.2256 -0.987433 0.847961 -0.3428 -0.04755 LOC_004042038 DFIT is domain containing -0.02386 -0.02256 0.987433 0.847961 -0.3428 -0.04755 LOC_004040779 Vesilot-sance containing -0.02366 0.02179 0.02644 -0.14275 -0.3428 LOC_004040789 DEF is domain a co		LOC_Os01g03730	nuclease PA3, putative, expressed	-0.32053	0.450476	0.996529	-0.10037	1.344213	0.37935	
protein protein <t< td=""><td></td><td>LOC_Os07g43950</td><td>RNA recognition motif containing</td><td>-0.11806</td><td>-0.0796</td><td>0.993747</td><td>-0.36902</td><td>0.380138</td><td>0.0013</td><td></td></t<>		LOC_Os07g43950	RNA recognition motif containing	-0.11806	-0.0796	0.993747	-0.36902	0.380138	0.0013	
LOC_OM28410080 requested 0.9181963 0.9389629 0.990033 -0.64271 2.041238 0.96545 LOC_OM2942830 Dark family protein, putative, expressed 0.490974 -0.04741 0.99978 -0.2052 -0.64519 LOC_OM1907170 HORMA domain containing protein, putative, expressed 0.33884 0.151668 0.989363 -0.4344 LOC_OM0942430 EF hand family protein, putative, expressed -0.23251 0.06772 0.988195 0.26279 0.04947 LOC_OM0942430 EF hand family protein, expressed -0.23251 0.06772 0.988195 0.26279 0.14525 0.07435 LOC_OM0942430 EF hand family protein, expressed 0.027608 -0.4226 0.987433 0.847961 0.26798 0.669895 LOC_OM0923660 DIM moinf family protein, expressed 0.127764 0.987933 -0.01071 -0.4225 0.987433 LOC_OM0923660 DIM sensitif main protein, expressed 0.99749 0.987933 -0.01017 -0.4275 -0.428 LOC_OM0923660 DIPO is janomin omain in 0.55876 0.60977 0.97195			protein, putative, expressed							
expressed sepressed LOC_Ood528353 MoR fambry protein, putative, expressed 0.40827 0.40827 0.40828 0.40849 LOC_Ood528470 MORMA domain containing 0.490974 0.00871 0.989815 0.41852 0.08825 LOC_Ood528470 Meressed protein 0.33848 0.151668 0.989815 0.26279 0.042 0.0947 LOC_Ood520470 Meressed protein 0.21356 0.24570 0.988105 0.26279 0.042 0.0947 LOC_Ood520470 Verside-seccessed 0.21356 0.42470 0.998101 0.43245 0.07455 LOC_Ood520480 Muntif family protein, putative, expressed 0.02748 0.998102 0.997433 0.94761 0.43429 LOC_Ood520480 DUH335 domain containing 0.14845 0.00774 0.94735 0.42475 0.43429 LOC_Ood520480 DUH35 domain containing 0.44849 0.90778 0.90183 0.9018 0.40725 LOC_Ood5204900 DUH35 domain containing 0.53877 0.907191 0.40725 0.40725		LOC_Os08g10080	no apical meristem protein, putative,	0.181963	0.389629	0.990803	-0.60271	2.041238	0.96545	
LOC_Od/§28330 Park Emdy protein, putative, expressed 0.04209 0.98978 -0.20952 -0.4549 LOC_Od/§2770 IORMA domain containing protein, putative, expressed 0.09074 0.04711 0.989615 0.14852 0.008225 LOC_Od/§2770 Expressed protein 0.03384 0.151668 0.989615 0.26279 0.042 0.09471 LOC_Od/§2760 EF hand family protein, putative, expressed 0.21536 -0.24501 0.989514 -0.3255 0.00752 0.98619 0.095614 -0.4344 LOC_Od/§2760 EF hand family protein, expressed 0.02708 0.02256 0.987433 0.847961 0.257988 0.66985 LOC_Od/§2760 ZM meerif family protein, expressed 0.02708 0.02256 0.987433 0.847961 0.257988 0.66985 LOC_Od/§2760 ZM protein, putative, expressed 0.02704 0.980533 -0.10105 0.4029 LOC_Od/§2760 UPF015 protein, putative, expressed 0.22044 0.70105 0.4075 LOC_Od/§4999 UPF015 protein, putative, expressed 0.23041 0.96214 0.20661			expressed							
expressed express		LOC_Os05g38530	DnaK family protein, putative,	0.618571	-0.04209	0.98978	-0.20952	-0.64549		
LOC_0.001g07177 HORMA domain comaining protein, putative, expressed 0.49874 0.989615 -0.14852 0.008825 LOC_0.001g0778 expressed protein -0.3344 0.151668 0.89363 -0.4344 LOC_0.001g0778 vesicle-associated membrane -0.21516 0.98615 0.26279 0.042 0.0947 LOC_0.001g0778 vesicle-associated membrane -0.21516 0.98607 0.98609 0.095614 -0.3425 -0.07455 LOC_0.001g07780 vesicle-associated membrane -0.21506 0.98743 0.847961 0.26798 0.69995 LOC_0.001g23680 DMotif family protein, expressed 0.02788 0.02716 0.988492 0.10678 -1.1336 -0.4629 LOC_0.001g1800 Z65 protease regulatory submit 4, 0.38587 0.060749 0.983933 -0.01071 -0.14275 -0.3428 LOC_0.001g1800 Directine, putative, expressed 0.20798 0.20798 0.202064 0.70105 0.40735 expressed -0.2068 0.366779 0.97117 -0.42661 -0.008 0.9224 LOC_0.0			expressed							
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LOC_0810942730 expressed protein -0.33884 0.151668 0.989363 -0.4344 LOC_004942430 EF hand family protein, putative, expressed -0.29251 0.06572 0.988105 0.26279 0.042 0.0947 LOC_004967780 vesicle-associated membrane -0.21536 0.28570 0.98809 0.095614 -0.3425 0.07455 LOC_004962760 ZM monif family protein, expressed 0.027808 -0.02236 0.987433 0.847961 0.267988 0.69895 LOC_004923660 ZM monif family protein, expressed 0.126746 0.984692 0.169778 -1.15936 -0.4259 LOC_004918690 26 protease regulatory submit 4 -0.85857 0.060749 0.98933 -0.01071 -0.14275 -0.3428 LOC_0040949900 UPF0183 protein, putative, expressed -			protein, putative, expressed							
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cupressed cupressed LOC_0.006g07780 veside-associated membrane protein, putative, expressed 0.21536 -0.24507 0.98809 0.095614 -0.3425 -0.07455 LOC_0.00923460 ZM motif family protein, spressed 0.027808 -0.02746 0.984692 0.106978 -1.15936 -0.4629 LOC_0.012g38850 DUF1335 domain containing 0.044845 0.126746 0.984692 0.106978 -1.15936 -0.4629 LOC_0.003g18690 285 protease regulatory submit 4, putative, expressed -0.55074 -0.61292 0.971985 0.02064 0.70105 0.40735 LOC_0.005g18699 UPF0183 protein, putative, expressed -0.55074 -0.61292 0.971985 0.02064 0.70105 0.40735 LOC_0.046g41640 transporter family protein, guartive, expressed -0.5074 0.61929 0.971951 -0.24061 -0.008 0.0924 LOC_0.041g11100 K2IP transporter family protein, matrive, expressed -0.07914 0.968329 0.316185 0.820313 0.10985 LOC_0.041g10800 rine finger, C31424 type domain expressed -0.59401		LOC Os04g42430	EF hand family protein, putative,	-0.29251	0.06572	0.988155	0.26279	0.042	0.0947	
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LOC_0512g1303 DOT 150 description domining 0.010740 0.120400 0.010710 0.112750 0.00071 LOC_0503g18690 265 protease regulatory subunit 4, 0.55587 0.060749 0.983933 -0.01071 -0.14275 -0.3428 LOC_0506g4990 UPF0183 protein, putative, expressed -0.55074 -0.62192 0.971985 0.022064 0.70105 0.40735 LOC_0511g11100 DLPF0183 protein, putative, -0.059074 -0.62192 0.971985 0.022064 0.70105 0.40735 LOC_0511g11100 DLPF0183 protein, putative, -0.29968 0.366779 0.970571 -0.24061 -0.008 0.0924 LOC_0504g41460 transporter family protein, putative, -0.13945 0.079014 0.968329 0.316185 0.820313 0.10985 LOC_0504g51750 neclear prelamin A recognition 0.219473 0.050967 0.967272 0.326895 0.629775 -0.00635 LOC_0504g01080 zine finger, C3HC4 type domain -0.59401 0.153401 0.965815 0.039396 0.066125 0.34315 LOC_0506g13910 gutathione S-transferase, putative, -0.38116 -0.25495 0.960934 0.027744 1.319625		LOC_0s12g38850	DUF1336 domain containing	0.044845	0.126746	0.984692	0.106978	-1 15936	-0.4629	
IDCC_0s03g1869 26S protein sequences regulatory submit 4, 0.5S857 0.060749 0.983933 -0.01071 -0.14275 -0.3428 IDCC_0s06g49990 UPF0183 protein, putative, expressed -0.55074 -0.62192 0.971985 0.022064 0.70105 0.40735 LOC_0s11g1110 bZIP transcription factor domain -0.20968 0.366779 0.970571 -0.24061 -0.008 0.0924 LOC_0s04g41460 transporter family protein, putative, evpressed -0.13945 0.059067 0.970722 0.316185 0.820313 0.10985 LOC_0s04g51750 nuclear prelamin A recognition 0.219473 0.059067 0.967272 0.326895 0.629775 -0.00635 LOC_0s04g51750 nuclear prelamin A recognition 0.219473 0.059067 0.97722 0.326895 0.629775 -0.00635 LOC_0s04g10680 zine finger, C3HC4 type domain -0.25495 0.96934 0.027744 1.319625 0.1414 peroxisonal, putative, expressed -0.179 -4.60589 - expressed - LOC_0s05g3380 cysteine proteinase inhibitor		LOC_0312g38850	protein expressed	0.044045	0.120740	0.904092	0.100770	-1.15750	-0.4029	
LOC_0505g1000 LOS protects regulation y studint v, repressed 0.000/19 0.000/19 0.000/11 0.01011 0.01021 0.01021 LOC_0506g49990 UPF0183 protein, patative, expressed -0.20968 0.366779 0.970571 -0.24061 -0.008 0.0924 LOC_0504g41460 transcription factor domain -0.20968 0.366779 0.970571 -0.24061 -0.008 0.0924 LOC_0504g41460 transcription factor domain -0.20968 0.366779 0.970571 -0.24061 -0.008 0.0924 LOC_0504g41460 transcription factor domain -0.219473 0.050967 0.967272 0.326895 0.629775 -0.00635 factor, putative, expressed - - - - - - - - - - - - - 0.066125 0.34315 -		LOC 0s03g18690	268 protesse regulatory subunit 4	0 58587	0.060749	0.083033	0.01071	0 14275	0.3428	
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LOC_Os10g38710 glutathione S-transferase, putative, -0.47756 -0.71346 0.958159 -0.179 -4.60589 LOC_Os05g33880 cysteine proteinase inhibitor 0.038099 -0.32454 0.957805 -0.06224 0.178875 0.0182 precursor protein, putative, expressed -		LOC_Os06g01390	acyl-coenzyme A oxidase 1.2,	-0.38116	-0.25495	0.960934	0.027744	1.319625	0.1414	
LOC_Os10g38710 glutathione S-transferase, putative, -0.47756 -0.71346 0.958159 -0.179 -4.60589 LOC_Os05g33880 cysteine proteinase inhibitor 0.038099 -0.32454 0.957805 -0.06224 0.178875 0.0182 precursor protein, putative, expressed -0.57558 0.447174 0.956571 1.061583 0.790338 0.8929 LOC_Os03g32580 BRASSINOSTEROID -0.57558 0.447174 0.956571 1.061583 0.790338 0.8929 INSENSITIVE 1-associated receptor kinase 1 precursor, putative, expressed -0.00893 -0.26621 0.954226 -0.03531 -0.03531 LOC_Os04g34230 RING-H2 finger protein, putative, 0.636271 -0.25669 0.953731 -0.50699 -0.03531 expressed - - - - - - - LOC_Os04g34230 RING-H2 finger protein, putative, 0.636271 -0.25669 0.953731 -0.50699 -0.03531 expressed - - - - - - - LOC_Os010g26620 dof zinc finger domain containing 0.075263			peroxisomal, putative, expressed							
expressed LOC_Os05g3380 cysteine proteinase inhibitor 0.038099 -0.32454 0.957805 -0.06224 0.178875 0.0182 precursor protein, putative, expressed expressed 0.057558 0.447174 0.956571 1.061583 0.790338 0.8929 LOC_Os03g32580 BRASSINOSTEROID -0.57558 0.447174 0.956571 1.061583 0.790338 0.8929 INSENSITIVE 1-associated receptor kinase 1 precursor, putative, expressed 0.00893 -0.26621 0.954226 LOC_Os01g14630 polyprenyl synthetase, putative, -0.00893 -0.25669 0.953731 -0.50699 -0.03531 LOC_Os10g26620 dof zinc finger protein, putative, 0.075263 -0.40047 0.953127 -0.62638 0.328488 0.3899		LOC_Os10g38710	glutathione S-transferase, putative,	-0.47756	-0.71346	0.958159	-0.179	-4.60589		
LOC_Os05g33880 cysteine proteinase inhibitor 0.038099 -0.32454 0.957805 -0.06224 0.178875 0.0182 precursor protein, putative, expressed LOC_Os03g32580 BRASSINOSTEROID -0.57558 0.447174 0.956571 1.061583 0.790338 0.8929 INSENSITIVE 1-associated receptor kinase 1 precursor, putative, expressed 0.00893 -0.26621 0.954226 LOC_Os01g14630 polyprenyl synthetase, putative, -0.00893 -0.25669 0.953731 -0.50699 -0.03531 LOC_Os10g26620 dof zinc finger protein, putative, 0.636271 -0.25669 0.953127 -0.62638 0.328488 0.3899			expressed							
precursor protein, putative, expressed LOC_Os03g32580 BRASSINOSTEROID -0.57558 0.447174 0.956571 1.061583 0.790338 0.8929 INSENSITIVE 1-associated receptor kinase 1 precursor, 1 1.061583 0.790338 0.8929 LOC_Os01g14630 polyprenyl synthetase, putative, -0.00893 -0.26621 0.954226 1.050699 -0.03531 LOC_Os04g34230 RING-H2 finger protein, putative, 0.636271 -0.25669 0.953731 -0.50699 -0.03531 LOC_Os10g26620 dof zinc finger domain containing 0.075263 -0.40047 0.953127 -0.62638 0.328488 0.3899		LOC_Os05g33880	cysteine proteinase inhibitor	0.038099	-0.32454	0.957805	-0.06224	0.178875	0.0182	
expressed LOC_Os03g32580 BRASSINOSTEROID -0.57558 0.447174 0.956571 1.061583 0.790338 0.8929 INSENSITIVE 1-associated receptor kinase 1 precursor, - <td< td=""><td></td><td></td><td>precursor protein, putative,</td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></td<>			precursor protein, putative,							
LOC_Os03g32580 BRASSINOSTEROID -0.57558 0.447174 0.956571 1.061583 0.790338 0.8929 INSENSITIVE 1-associated receptor kinase 1 precursor, putative, expressed - - - - - - - - - - 0.790338 0.8929 0.8929 LOC_Os01g14630 polyprenyl synthetase, putative, -0.00893 -0.26621 0.954226 -			expressed							
INSENSITIVE 1-associated receptor kinase 1 precursor, putative, expressed LOC_Os01g14630 polyprenyl synthetase, putative, -0.00893 -0.26621 0.954226 expressed LOC_Os04g34230 RING-H2 finger protein, putative, 0.636271 -0.25669 0.953731 -0.50699 -0.03531 expressed LOC_Os10g26620 dof zinc finger domain containing 0.075263 -0.40047 0.953127 -0.62638 0.328488 0.3899 protein, putative, expressed		LOC_Os03g32580	BRASSINOSTEROID	-0.57558	0.447174	0.956571	1.061583	0.790338	0.8929	
receptor kinase 1 precursor, putative, expressed LOC_Os01g14630 polyprenyl synthetase, putative, -0.00893 -0.26621 0.954226 expressed - - - - LOC_Os04g34230 RING-H2 finger protein, putative, 0.636271 -0.25669 0.953731 -0.50699 -0.03531 expressed - - - - - - LOC_Os10g26620 dof zinc finger domain containing 0.075263 -0.40047 0.953127 -0.62638 0.328488 0.3899 protein, putative, expressed - - - - - -			INSENSITIVE 1-associated							
putative, expressed 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 0.075263 -0.40047 0.953127 -0.62638 0.328488 0.3899 protein, putative, expressed			receptor kinase 1 precursor,							
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 0.075263 -0.40047 0.953127 -0.62638 0.328488 0.3899 protein, putative, expressed - 0.953127 - 0.62638 0.328488 0.3899 -			putative, expressed							
expressed LOC_Os04g34230 RING-H2 finger protein, putative, 0.636271 -0.25669 0.953731 -0.50699 -0.03531 expressed - - - - - - - - - 0.03531 - 0.03531 - 0.03531 - - 0.03531 - 0.0328488 0.038		LOC_Os01g14630	polyprenyl synthetase, putative,	-0.00893	-0.26621	0.954226				
LOC_Os04g34230 RING-H2 finger protein, putative, 0.636271 -0.25669 0.953731 -0.50699 -0.03531 expressed expressed 0.075263 -0.40047 0.953127 -0.62638 0.328488 0.3899 protein, putative, expressed 0.075263 -0.40047 0.953127 -0.62638 0.328488 0.3899			expressed							
expressed LOC_Os10g26620 dof zinc finger domain containing 0.075263 -0.40047 0.953127 -0.62638 0.328488 0.3899 protein, putative, expressed		LOC_Os04g34230	RING-H2 finger protein, putative,	0.636271	-0.25669	0.953731	-0.50699	-0.03531		
LOC_Os10g26620 dof zinc finger domain containing 0.075263 -0.40047 0.953127 -0.62638 0.328488 0.3899 protein, putative, expressed			expressed							
protein, putative, expressed		LOC_Os10g26620	dof zinc finger domain containing	0.075263	-0.40047	0.953127	-0.62638	0.328488	0.3899	
	_		protein, putative, expressed							

LOC_Os03g10500	adenylyl-sulfate kinase, putative,	-0.04053	0.195067	0.953105				
LOC_Os08g28670	pathogenesis-related Bet v I family	0.508105	-0.49746	0.953034	-0.94187	-1.13256	-0.2104	
LOC_Os07g08710	AT hook-containing DNA-binding	-0.12135	0.145286	0.95296	-0.13783	-0.882	-0.08055	
LOC_Os02g02980	protein, putative, expressed MATE domain containing protein,	-0.27363	-0.32832	0.952817	-0.01301	0.500888		
LOC_Os06g10520	expressed pantothenate kinase, putative,	-0.39789	-0.02842	0.952438	1.122785	2.181963	0.7178	
LOC_Os01g33784	expressed lipase family protein, putative,	-0.26582	0.129191	0.951342	-0.1599	0.195988	0.56145	
LOC_Os07g47510	expressed stress-related protein, putative,	-0.19998	-0.31335	0.950471	-0.30777	-0.67575	-0.72635	
LOC Os08g32870	expressed aldehvde dehvdrogenase, putative,	-0.34967	-0.44655	0.949209	-0.13667	0.45675	-0.0291	
	expressed	0.507(7	0.520276	0.04126	0.041076	0.00175	0.2642	
LOC_0s05g51480	cleavage and polyadenylation specificity factor, putative,	-0.50767	0.538376	0.94136	0.041876	-0.00175	-0.2642	
LOC_Os10g28360	1,2-dihydroxy-3-keto-5-methylthiop entene dioxygenase protein,	-0.23444	-0.42388	0.940983	-0.83293	-0.42488	0.48755	
LOC_Os03g31170	putative, expressed inosine-uridine preferring nucleoside hydrolase family protein,	-0.41041	-0.6169	0.936446	-0.10343	-0.06238	0.06215	
LOC_Os03g37470	putative, expressed MATE efflux family protein, putative, expressed	-0.42537	0.047182	0.935713	-0.47235	-0.70395	-0.31705	
LOC_Os03g40100	ACT domain containing protein,	-0.04836	0.597238	0.93264	0.697239	-0.64331	-0.0025	
LOC_Os03g15000	Zinc finger, C3HC4 type domain	-0.16019	-0.10785	0.931465	0.067046	0.3025	0.3585	
LOC_Os06g11310	plastocyanin-like domain containing	0.181089	0.125639	0.930544	-1.48508	-1.31138	0.2308	
LOC_Os02g11640	protein, putative, expressed UDP-glucoronosyl and UDP-glucosyl transferase, putative,	0.105678	0.017209	0.926131	-0.42564	-0.42626		
LOC_Os06g05130	expressed myristoyl-acyl carrier protein thioesterase, chloroplast precursor,	-0.23713	0.463926	0.925612	0.039041	0.2511	2.42285	
LOC_Os08g09690	putative, expressed nuclear transcription factor Y	-0.05626	0.099756	0.924744	-0.61638	-0.56145	-0.2188	
LOC_Os04g56160	subunit, putative, expressed plasma membrane ATPase,	-0.45533	-0.03629	0.924593	0.047113	0.173875	0.2996	
LOC_Os01g66720	putative, expressed NADP-dependent oxidoreductase,	-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	0.264048	-0.51953	0.921864	0.335769	0.42325	0.1149	
200_0001800000	Aux/IAA gene family member	0.201040	0.01700	5.721004	5.555707	0.12020	0.1117	
	expressed							
LOC Os04g39190	cell division protease ftsH homolog	-0.48118	-0.49971	0.919882	-0.05561	0.026188		
	4, putative, expressed							
LOC_Os07g36190	hydrolase, NUDIX family, domain	0.347625	0.250483	0.917119	-0.24771	-1.88038	-0.3294	
	containing protein, expressed							
LOC_Os06g22060	pyrophosphatefructose	-0.05982	-0.23702	0.916024	-0.07601	-1.28843	-0.66225	
	6-phosphate 1-phosphotransferase							
	subunit alpha, putative, expressed							

LOC_Os08g27010	APE1, putative, expressed	-0.55259	-0.5823	0.91329	-0.17276	-2.31463	0.17095	
LOC_Os05g38550	ubiquitin-conjugating enzyme,	-0.45461	-0.20611	0.912858	0.011173	-0.21763		
	putative, expressed							
LOC_Os06g02420	ATOZI1, putative, expressed	0.168433	-0.42336	0.910915	-0.40661	-1.8432	-0.81195	
LOC_Os09g38130	auxin efflux carrier component,	0.402758	0.51029	0.909661	0.318828	1.52	0.1604	
	putative, expressed							
LOC_Os04g56620	molybdopterin biosynthesis protein	-0.35423	0.02123	0.909087				
	CNX1, putative, expressed							
LOC_Os03g27010	expressed protein	-0.05657	0.280987	0.908628	-0.0967	1.071625	-0.22905	
LOC_Os08g09200	aconitate hydratase protein,	-0.45228	0.279104	0.908333	-0.06238	2.100625	0.15155	
	putative, expressed							
LOC_Os11g37730	glutathione S-transferase,	-0.35628	-0.344	0.906745	0.272657	1.43675	0.9467	
	N-terminal domain containing							
	protein, expressed							
LOC_Os06g39690	SOUL heme-binding protein,	-0.32928	-0.27064	0.90282	-0.17921	-0.73008	-0.63805	
	putative, expressed							
LOC_Os08g16930	expressed protein	-0.39588	-0.51175	0.902631	0.044066	0.327	0.78295	
LOC_Os06g23530	pre-mRNA-splicing factor	-0.52396	-0.32974	0.901173	-0.12048	-0.1842	0.00525	
	ATP-dependent RNA helicase,							
	putative, expressed							
LOC_Os03g20900	Myb transcription factor, putative,	-0.18326	-0.03901	0.896889	-0.4615	-0.0525	-0.1282	
	expressed						4.005.04	
LOC_Os07g43700	lactate/malate dehydrogenase,	0.085509	-0.20581	0.892387	-1.01888	-2.05089	1.00E-04	
	putative, expressed	0.01004	0.11004	0.000000	0.101022	0.04005	0.0051	
LOC_Os10g35250	vacuolar protein-sorting protein	0.21204	-0.11224	0.890238	0.101033	0.34025	0.2251	
100 0 02 02840	bro1, putative, expressed	0.157645	0.057190	0.007044	0.00405	0.000075	0.00((
LOC_Os02g03840	expressed protein	0.157645	0.05/189	0.88/944	-0.08485	0.228375	0.0078	
LOC_0503g02000	unalassified expressed	-0.45552	0.038827	0.880757	-0.00003	0.17303	-0.0078	
LOC 0s07g10150	costomer subunit gamma-2	-0.49127	0 254893	0.886018	0.034845	0 72725	0 28335	
LOC_050/g10150	putative expressed	-0.49127	0.254895	0.880018	0.054845	0.72725	0.28555	
LOC 0s09g26670	expressed protein	-0.09807	-0 39363	0.885966	-2 61947	-1 84009	0.169	
LOC_0s02g18450	GTP-binding protein typA/binA	-0.35267	0.078962	0.885346	-0 24902	-2 55079	-0 5319	
200_0002610100	putative expressed	0.00207	0.070902	0.000010	0.21702	2.00017	0.0017	
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	0.036931	0.065427	0.881167	-0.00263	-0.93379	-0.0278	
_ 0	protein, expressed							
LOC_Os04g45070	remorin, putative, expressed	-0.31149	-0.48699	0.878158	-0.14335	-1.08863	-0.37375	
LOC_Os07g10460	5-nucleotidase surE, putative,	-0.35841	-0.02737	0.877157	-0.10429	0.611063	0.12145	
	expressed							
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,	-0.22079	0.173247	0.874567	3.276763	-1.99279	2.9547	
	putative, expressed							
LOC_Os03g19580	expressed protein	-0.16672	0.299404	0.873189	0.487985	1.694875	1.13015	
LOC_Os04g40040	copper methylamine oxidase	0.08753	-0.39684	0.867393	0.475336	0.277	-1.19655	
	precursor, putative, expressed							
LOC_Os01g71240	calcium-transporting ATPase,	-0.32338	-0.18442	0.867241	0.07072	-0.0215	0.70065	
	plasma membrane-type, putative,							
	expressed							
LOC_Os05g01760	lysine ketoglutarate reductase	0.11533	-0.32697	0.866619	-0.43484	0.829	0.37055	
	trans-splicing related 1, putative,							
	expressed							
LOC_Os07g44610	pyrrolidone-carboxylate peptidase,	-0.09326	-0.26084	0.864527	0.066857	0.86925	-0.31845	
	putative, expressed							

LOC_Os08g07960	mitotic checkpoint protein, putative,	-0.1899	-0.15662	0.862359	0.098055	0.35525	-0.1822
	expressed	0.4001	0.00051	0.000502	0.0250/2	0.645	
LOC_Os05g34210	expressed protein	-0.4021	-0.23351	0.860503	0.035063	0.645	0.17055
LOC_0s08g40620	rabGAP/1BC domain-containing	-0.53594	0.059602	0.859402	0.128107	0.758	0.17955
1.00 0-01-04020	protein, putative, expressed	0 12075	0.040421	0.959395	0.08226	0.21200	0.11055
LOC_0501g64930	expressed protein	-0.12075	0.040451	0.858285	-0.08230	-0.31309	-0.11055
LOC_0s04g52400	oxidoreductase, snort chain	-0.2/208	0.036475	0.857444	0.0/2639	-0.02725	-0.13495
	protain putative expressed						
LOC 0s10g35490	hydrolase alpha/beta fold family	0.054089	-0 76912	0.855528	-0.92646	-0.08981	-0.4031
200_0310g55470	domain containing protein	0.054087	-0.70712	0.055520	-0.72040	-0.00701	-0.4051
	expressed						
LOC Os02908440	WRKY71 expressed	-0 47413	0 007454	0.854112	2.052449	0 973375	1 6468
LOC_0s09g32690	zinc finger C3HC4 type domain	-0.5495	-0.27768	0.854035	-0.31063	0.089263	-0 13275
	containing protein, expressed						
LOC Os12g02700	harpin-induced protein 1 domain	-0.28076	0.004513	0.852895	-0.07453	1.044563	0.29895
	containing protein, expressed						
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	mps one binder kinase activator-like	-0.18298	-0.01507	0.848658	-0.14961	-0.23475	-0.36265
_ 0	1A, putative, expressed						
LOC_Os01g43420	expressed protein	-0.21818	0.288031	0.848465	0.077794	-0.016	0.1221
LOC_Os08g04840	MYB family transcription factor,	0.011449	0.106286	0.847558	-0.14165	-0.74614	0.1596
	putative, expressed						
LOC_Os01g64650	VAMP-like protein YKT62,	-0.31844	-0.50098	0.845032	-0.04264	0.3475	0.45925
	putative, expressed						
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,	-0.3156	-0.01438	0.842149	-0.07643	0.335875	-0.12655
	expressed						
LOC_Os03g59090	retrotransposon protein, putative,	-0.17188	-0.20476	0.841384	-0.31224	-2.00045	
	unclassified, expressed						
LOC_Os03g17590	cat eye syndrome critical region	0.030441	-0.19414	0.84115	-0.13114	-0.73764	-0.0591
	protein 5 precursor, putative,						
	expressed						
LOC_Os04g39290	heavy metal transport/detoxification	-0.00431	0.263241	0.840143			
	protein, putative, expressed						
LOC_Os06g35160	CAMK_KIN1/SNF1/Nim1_like.26	-0.32916	-0.09363	0.840086	-0.49926	-1.94425	-0.557
	- CAMK includes						
	calcium/calmodulin depedent						
	protein kinases, expressed						
LOC_Os02g47000	expressed protein	-0.43421	-0.18495	0.837074	-0.32926	-0.27038	
LOC_Os03g01880	possible lysine decarboxylase	0.152933	-0.44603	0.830364	-0.06343	1.963125	-1.24905
	domain containing protein,						
	expressed						
LOC_Os08g06140	no apical meristem protein, putative,	-0.43648	-0.21526	0.827665	0.229323	0.58575	0.52855
	expressed	0.06075	0.16050	0.02(072	0.001/0	0.040	0.15645
LOC_Os0/g23550	expressed protein	-0.26275	-0.16058	0.826972	-0.09168	-0.248	0.15645
LOC_0501g70550	N gastaltanafanan mutating	0.021875	-0.22130	0.820037	-0.03771	-1./030	-0.47855
	iv-acetyliransierase, putative,						
LOC 0s07g21240	regulator of nonsense transprints 1	-0 24961	-0.15508	0 82605	-0.00124	-0 10788	
LOC_030/g51540	nutative expressed	-0.24901	-0.15508	0.62005	-0.00124	-0.10/00	
LOC 0s01056180	expressed protein	0 145358	-0 29868	0 825376	-0 19569	0 951225	0 64425
LOC Os02932730	neutral/alkaline invertase putative	-0.57031	-0 0594	0.822657	0.202511	-0 30475	0.01120
	expressed						

LOC_Os03g52010	lecithin cholesterol acyltransferase,	0.398442	0.338636	0.819373	3.75E-04	-0.94103	-0.33725	
	putative, expressed							
LOC_Os01g04930	MYB family transcription factor,	-0.01295	0.055304	0.819314	-0.22055	0.140738	-0.2583	
LOC Os01g04350	hsp20/alpha crystallin family	-0 24291	0 223939	0.816001	-0.1836	-0 29675	1.58775	
200_0001g01000	protein, putative, expressed	0.212/1	0.220707	0.010001	0.1050	0.27070	1.00770	
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	-0.21578	-0.0268	0.812853	-0.13265	-0.23963	-0.48655	
	containing protein, expressed							
LOC_Os06g49030	activator of 90 kDa heat shock	-0.18459	-0.07275	0.809719	-0.14561	0.85225	-0.0357	
	protein ATPase homolog, putative,							
	expressed							
LOC_Os03g50540	2Fe-2S iron-sulfur cluster binding	-0.4094	0.023369	0.809633	-0.18206	0.28075	-0.34695	
	domain containing protein,							
	expressed							
LOC_Os02g56900	thioredoxin family protein, putative,	-0.07804	0.198618	0.808507	0.47091	1.566088	0.61405	
	expressed							
LOC_Os02g38020	inorganic phosphate transporter 2-1,	-0.56644	-1.41308	0.807135	0.136627	-2.89613	-0.35445	
	chloroplast precursor, putative,							
	expressed							
LOC_Os08g41250	signal recognition particle receptor	-0.35516	0.39582	0.806449	0.139672	0.804288	0.13225	
	subunit beta, putative, expressed							
LOC_Os02g34950	ATP binding protein, putative,	-0.22906	0.012093	0.805621	-0.11701	-0.22088	-0.16445	
100 0-02-27280	CAMIC CAMIC File 10 CAMIC	0.1622	0.20010	0.903996	1 100100	0.266975	0.9224	
LOC_0s03g2/280	includes caloium/colmodulin	-0.1625	-0.30819	0.803880	1.188188	0.2008/3	0.8234	
	depedent protein kinases, expressed							
LOC Os03950160	plastocyanin-like domain containing	0 169646	0 400857	0 792071	-0 10237	-1 30999	-0.031	
200_0305g50100	protein putative expressed	0.109040	0.400057	0.772071	-0.10257	-1.50777	-0.051	
LOC Os01g28500	SCP-like extracellular protein.	-1.27654	0.156779	0.510968	0.319973	3.092325		
	expressed							
LOC Os01g01280	expressed protein	-0.92657	-0.76745	0.565966	0.107372	-1.52293		
LOC_Os08g44850	C2 domain containing protein,	-1.10551	-0.42785	0.561437	0.208983	-0.12338	1.02175	
	putative, expressed							
LOC_Os04g49450	MYB family transcription factor,	-1.20391	-1.44493	0.546397	1.502378	-0.90873	0.78825	
	putative, expressed							
LOC_Os11g42970	membrane associated DUF588	-0.94065	-0.40201	0.537829	0.430146	-0.32045	0.16165	
	domain containing protein, putative,							
	expressed							
LOC_Os01g04950	peptide transporter PTR2, putative,	-0.8949	-0.26131	0.508428	0.084373	-0.85049	-0.0532	
	expressed							
LOC_Os08g09840	WRKY117, expressed	-1.17757	0.446533	0.486271				
LOC_Os01g26240	retrotransposon protein, putative,	-0.9164	0.283896	0.485366				
	Ty1-copia subclass, expressed		4 4 9 4 9 9					
LOC_Os04g32110	ACT domain containing protein,	-0.9244	-1.19439	0.484351	1.49141	0.968438		
100 0-02-25500	expressed	0.97006	0.02776	0 474255	0.02421	0.021075	1 42295	
LOC_0s03g25500	expressed	-0.8/990	-0.02776	0.474355	-0.03431	0.021075	1.43283	
LOC 0s05048300	ubiquitin conjugating enzyme	-0 8038	0.022004	0 470622	-0 12302	0 313725		
200_0303540390	protein putative expressed	0.0750	0.022004	0.170022	0.12372	0.513723		
LOC Os01g51410	glycine dehydrogenase. putative	-1.17287	-0.1527	0.463928	-0.07181	-2.65488	-0.46645	
	expressed		/					
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,	-0.91644	-0.16499	0.438785				
LOC Os04g42480	receptor-like protein kinase	-0 95343	0.165115	0 434655	0.549117	0 2085	1 0897	
	At3g46290 precursor, putative,							
	expressed							
LOC Os10g03570	RGH1A, putative, expressed	-0.85295	-0.12991	0.433056				
LOC_Os09g18594	protein kinase domain containing	-1.22572	0.38545	0.393538	0.771443	-0.51548	-0.0381	
_ 0	protein, expressed							
LOC Os10g22560	peptide transporter PTR2, putative,	-0.8836	-0.18276	0.345746	0.105738	-0.06888	-0.29805	
	expressed							
LOC_Os04g41960	NADP-dependent oxidoreductase,	-1.19039	-0.15611	0.344807	1.916629	0.384375	1.30305	
	putative, expressed							
LOC_Os09g25760	tetraspanin family protein, putative,	-0.80015	-0.21851	0.337457	0.601217	0.148125		
	expressed							
LOC_Os07g12890	metal cation transporter, putative,	-0.99955	0.583405	0.327977	1.680573	-1.00849		
	expressed							
LOC_Os11g07020	fructose-bisphospate aldolase	-1.00126	-0.39168	0.323839	-0.45039	-2.11388	-0.22875	
	isozyme, putative, expressed							
LOC_Os06g40640	fructose-bisphospate aldolase	-1.3972	-1.39504	0.318024	0.156639	-2.673	0.2687	
	isozyme, putative, expressed							
LOC_Os07g47290	xylose isomerase, putative,	-0.8127	0.024919	0.284689	0.051438	-0.41068	-0.17735	
	expressed							
LOC_Os10g41550	beta-amylase, putative, expressed	-1.14388	-1.25697	0.282577	0.85704	0.667575		
LOC_Os12g13350	retrotransposon protein, putative,	-0.83569	-0.74303	0.280265				
	Tyl-copia subclass, expressed	1 (1020	1 200 44	0.074105	0.571100	0.04504		
LOC_0s06g19444	CC I/B-box zinc finger protein,	-1.61839	-1.28844	0.2/4135	0.5/1109	-0.24/34		
LOC Oc03a28940	ZIM domain containing protein	0.05214	0.65904	0 26272	1 480121	2 040875	0.3204	
LOC_0303g28940	putative expressed	-0.93214	-0.03904	0.20272	1.480151	2.049875	0.5204	
LOC Os01905530	expressed protein	-0.91885	-0 19477	0.25055	-0 16191	-0.06725	-0.337	
LOC Os01g66820	inactive receptor kinase At1g27190	-0.82449	0.217705	0.248969	0.112999	-0.24355		
	precursor, putative, expressed							
LOC_Os04g54840	DNA-directed RNA polymerase	-0.83773	-0.17416	0.248168	-0.15713	-0.024	-0.7632	
	subunit, putative, expressed							
LOC_Os01g36350	cytochrome P450, putative,	-0.80902	-0.7103	0.242662	0.088498	-0.03906	1.0506	
	expressed							
LOC_Os09g36680	ribonuclease T2 family domain	-1.02395	-1.30235	0.225962	-0.66071	-0.5	-0.12115	
	containing protein, expressed							
LOC_Os08g17390	expressed protein	-0.99865	-1.02892	0.223714	0.119238	-4.44279	0.1205	
LOC_Os02g43370	transposon protein, putative,	-1.00615	-0.05865	0.221107	-0.08313	-0.04174		
	unclassified, expressed							
LOC_Os01g56200	BTBA2 - Bric-a-Brac, Tramtrack,	-0.89483	0.112626	0.214182	0.603712	0.08725	0.59835	
	Broad Complex BTB domain with							
	Ankyrin repeat region, expressed							
LOC_Os11g39190	NB-ARC domain containing	-0.90255	-0.82414	0.198438	0.041085	-1.09833	-0.575	
100.010.0000	protein, putative, expressed	0.0(704	0.40054	0.105((2)			0.10515	
LOC_Os10g38292	hypothetical protein	-0.86/94	-0.48054	0.197663	0.204010	0.05775	0.18515	
LOC_0s01g41/80	expressed protein	-0.88313	0.00626	0.190092	0.204918	-0.05775	0.5412	
LUC_USU1g15490	phosphoauchosine phosphosultate,	-0.804/2	-0.30230	0.18381	0.204022	-0.4/323	0.3415	
LOC Oc01g67054	calreticulin precursor protein	-1 02093	0 152575	0 176661	0 359649	0.6315	0.80815	
100_0501g0/054	nutative expressed	-1.02093	0.1323/3	0.1/0001	0.337047	0.0313	0.00015	
LOC Os06939730	hypothetical protein	-1.10294	-0 74241	0.175028				
LOC Os01g58020	ribulose bisphosphate carboxylase	-1.13135	-1.61236	0.16403				
	large chain precursor, putative,							
	expressed							

LOC_Os11g05260	phosphoglycerate mutase, putative,	-0.91507	-0.50071	0.138497	-0.2328	-1.23975	0.36745	
	expressed	-1 0/919	0 560898	0 115682	-0.01628	0.023088		
LOC_0301g05020	putative, expressed	-1.04919	0.500878	0.115082	-0.01020	0.025000		
LOC Os01g22980	OsSCP3 - Putative Serine	-0.86341	-0.61157	0.022632	-0.27986	-0.58364	-0.0994	
_ 0	Carboxypeptidase homologue,							
	expressed							
LOC_Os01g02570	protein kinase domain containing	-0.88617	0.100562	0.014902	0.663198	-0.07761		
	protein, expressed							
LOC_Os02g49800	eukaryotic aspartyl protease domain	-0.93869	0.344194	-0.0015	0.372282	0.141625	0.1934	
	containing protein, expressed							
LOC_Os12g36110	calmodulin binding protein,	-0.96476	0.497316	-0.00529	1.124285	-0.02036	1.90655	
	putative, expressed							
LOC_Os08g15460	preprotein translocase subunit secY,	-0.80462	-0.33823	-0.00607	-0.11058	-2.64404	-0.74025	
	putative, expressed							
LOC_Os02g49780	expressed protein	-0.89868	0.276333	-0.01359	-0.14391	-0.29863		
LOC_Os03g46440	BTBA4 - Bric-a-Brac, Tramtrack,	-1.03721	0.594456	-0.02212	1.756894	-0.02814		
	Broad Complex BTB domain with							
	Ankyrin repeat region, expressed							
LOC_Os05g34630	hydrolase, alpha/beta fold family	-0.79664	-0.47977	-0.0314	0.102746	-1.75278	-0.3509	
	domain containing protein,							
	expressed							
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	-0.90915	-0.01035	-0.06937				
100 0.0(20450	protein, putative, expressed	0.00007	0.140469	0.1464	0.020005	1 (049	0.65525	
LUC_0s06g38450	vignain precursor, putative,	-0.99007	0.140468	-0.1464	0.829805	-1.6048	-0.65525	
100 0-12-20420	expressed	0.05522	0.05572	0 1547	0.210221	0.270	0.020	
LOC_0\$12g39420	nucleobase-ascoloate transporter,	-0.95555	-0.03373	-0.1347	0.219221	-0.379	0.029	
LOC Os09919380	receptor-like protein kinase	-1 39523	-0 19256	-0 17787				
100_0307917500	precursor putative expressed	1.57525	0.17250	0.17707				
LOC Os10g42410	zinc-binding protein, putative.	-0.82606	-0.3669	-0.2089	1.112846	0.637375		
	expressed							
LOC Os02g14250	transposon protein, putative,	-1.23327	0.526342	-0.21481				
_ 0 /0	unclassified, expressed			-				
LOC_Os01g09540	HAD superfamily phosphatase,	-0.90027	-0.94828	-0.21719	0.274522	-2.80386	0.0606	
_ •	putative, expressed							
LOC_Os01g18630	aspartic proteinase oryzasin-1	-1.14608	0.113063	-0.21789	-0.20188	0.015875	-0.4473	
	precursor, putative, expressed							
LOC_Os09g19500	senescence-induced receptor-like	-1.13816	-0.9396	-0.23492	-0.029	-0.18153	-0.1472	
	serine/threonine-protein kinase							
	precursor, putative, expressed							
LOC_Os09g19390	senescence-induced receptor-like	-1.37248	0.38207	-0.28151				
	serine/threonine-protein kinase							
	precursor, putative, expressed							
LOC_Os01g48300	ATP synthase protein I related,	-0.91854	-0.45885	-0.33156	-0.28296	-0.16436	-0.24695	
	putative, expressed							
LOC_Os07g18230	lectin-like receptor kinase, putative,	-0.84463	0.413007	-0.34929				
	expressed							
LOC_Os06g07932	flavonol synthase/flavanone	-0.80454	-0.38232	-0.37278	0.95579	0.52		
	3-hydroxylase, putative, expressed							
LOC_Os02g20360	tyrosine aminotransferase, putative,	-2.07831	0.31498	-0.37521				
	expressed							

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

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

GO ID	GO Name	GO	Ref	Ref	Query	Query	Query	Hyper p	GO enrichment
		Level	Total	Number	Total	Number	Exp	value	value
GO:00096 07	response to biotic stimulus	3	39571	19	333	4	0.2	0	25
GO:00060 32	chitin catabolic process	8	39571	37	333	4	0.3	0.0002	12.8
GO:00068 08	regulation of nitrogen utilization	3, 4	39571	30	333	3	0.3	0.0019	11.9
GO:00060 99	tricarboxylic acid cycle	7, 8	39571	33	333	3	0.3	0.0025	10.8
GO:00086 10	lipid biosynthetic process	4	39571	50	333	3	0.4	0.0078	7.1
GO:00066 94	steroid biosynthetic process	6	39571	69	333	4	0.6	0.0025	6.9
GO:00442 37	cellular metabolic process	3	39571	133	333	7	1.1	0.0001	6.3
GO:00060 96	glycolysis	5	39571	124	333	5	1	0.0034	4.8
GO:00081 52	metabolic process	2	39571	1968	333	41	16.6	0	2.5
GO:00068 10	transport	3, 4	39571	978	333	19	8.2	0.0004	2.3
GO:00069 52	defense response	4	39571	626	333	12	5.3	0.0045	2.3

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

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

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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	lipoxygenase 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

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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

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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-epoxycarote noid dioxygenase 1	NRR, Xa21	-0.89	-0.71	0.944	-0.11	-1.44
LOC_Os04g49194	Hormone Metabolism: Ethylene	naringenin,2-oxo glutarate 3-dioxygenase	NRR, NH1	-0.84	0.663	0.398	0.941	0.89
LOC_Os04g49210	Hormone Metabolism: Ethylene	naringenin,2-oxo glutarate 3-dioxygenase	NH1, Xa21	-0.31	1.544	0.818	3.918	0.636
LOC_Os10g39140	Hormone Metabolism: Ethylene	flavonol synthase/flavanon e 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	lipozygenase 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	BRASSINOSTE ROID 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	BRASSINOSTE ROID 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-responsi ve 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-relat ed Bet v I	NH1, Xa21	0.66	1.05	1.11	0.43	-4.09
LOC_Os12g36830	Stress Biotic: PR protein	pathogenesis-relat ed Bet v I	NH1, Xa21	-0.33	1.62	1.67	1.65	1.48

LOC_Os12g36860	Stress Biotic: PR protein	pathogenesis-relat ed Bet v I	NH1, Xa21	-0.21	1.41	0.6	1.95	2.18
LOC_Os12g36880	Stress Biotic: PR protein	pathogenesis-relat ed 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	Mise: PR protein	glucan endo-1,3-beta-glu cosidase 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-xylulo se 5-phosphate reductoisomerase	NRR, Xa21	-0.733	-0.22	1.159		
LOC_Os02g39160	Secondary Metabolism	hydroxymethylbu tenyl 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	leucoanthocyanid in 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-processi ng 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	phosphatidylinosi tol 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
Os09g20350	TGCAGCTATAGATCTGTCAG	TGGATGTAGTGCATCTGGG
Os05g46020	AAGAAGTCCGTCAAGAACAG	GCGTAGTACACCGTGCTG
Os09g25060	ACGCTCGACCTCACCAAGAA	AACTTGGGGTCGCTGGTGAG
Os09g25070	TTCCGCTGCGCATTCGCG	TGCTGGCTCGTAGTGCAG
Os11g02530	GCCAACAGCTACAATGGC	TTCCGCAGCCTGCAGATC
Os11g02540	CATGCCGACAGATGATCGC	CAAGGAGCAAATCGTCCATC
Os12g02450	GCCAACAGCTACAATGGC	CGCAGCCTGCAGCTCGCT
Os12g02470	GACGACCACCTCTGGTTCT	CAAATGGGTGATGTTAGCGC
Os03g18850	GTCAGGCAGTTCAACTTCAC	CGGCTCCACCTTGATGTG
Os12g36830	CTGTCACCACCATGAAGCTC	GCCAAGCAAGAGCCGGCA
Os12g36860	CAATGCAGCACGCGTGCTA	GAAGTAGCCGTCGACCATC
Os12g36880	CGCCGCAAGTCATGTCCTA	ATAGTAGCCATCCACGATG
Os11g37950	GTCAGAAGTATGGCTGGAC	TGTCCCAGTCCAGGTCAAG
Os11g37960	GAAGTATGGATGGACCGCCT	AGCCTTGACCGTCGCTGT
Os12g43380	AGCATCTCGATCCTACCACA	ACCGGTTGGTGATGGTGAA
Os01g71350	CGTACAACCAGAAGCTTATC	TAATTTTGTAGGACGGCGAC
Os05g31140	TCTACAACCAGAACCTCATC	AGAAGCTGATGGGGTAGAC
Os07g35560	TATTGTCTACAAGCCTTCAC	CTTGGTGTCAGGGTCAAAGC
Os01g22490(OsUbi5)	GCACAAGCACAAGAAGGTGA	GCCTGCTGGTTGTAGACGTA
Os03g08010(OseEF1)	TCAAGTTTGCTGAGCTGGTG	TTTGCCTCATGTCCCGCAC

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

Locus_ID	Gene name	Abbreviatio n of gene name	Category of function	Description of gene function	References (DOI)
LOC_Os01g09800	NONEXPRESSO R OF PATHOGENESIS -RELATED GENES1	OsNPR1	Bacterial blight resistance	Enhanced bacterial blight resistance and herbivore susceptibility.	10.1111/j.1467- 7652.2007.0024 3.x
LOC_Os09g25070	OsWRKY62	OsWRKY62	Bacterial blight resistance	Resistance to Xanthomonas oryzae pv. oryzae.	10.1093/mp/ssn 024
LOC_Os02g08440	OsWRKY71	OsWRKY71	Bacterial blight resistance	Resistance to Xanthomonas oryzae pv. oryzae.	10.1016/j.jplph. 2006.07.006
LOC_Os09g25060	OsWRKY76	OsWRKY76	Bacterial blight resistance	Resistance to Xanthomonas oryzae pv. oryzae.	10.1007/s12284- 010-9039-6
LOC_Os10g41980	RALFL26	Rir1b	Blast resistance	Resistance to Magnaporthe grisea.	10.1023/A:1006 423232753
LOC_Os06g03580	zinc RING finger protein	osbbi1	Blast resistance	Resistance to Magnaporthe oryzae. Cell wall defense.	10.1038/cr.2011 .4
LOC_Os05g31140	beta-glucanase1	Gns1	Blast resistance	Resistance to Magnaporthe grisea. Lesion mimic.	10.1023/A:1020 714426540
LOC_Os03g51030	phytochromeA	phyA	Blast resistance	Resistance to Magnaporthe grisea.	10.1093/mp/ssr0 05
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 conten. 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:1025 001304994
LOC_Os02g09490	GOLDHULLAN DINTERNODE2	gh2	Culm leaf	Lignin content. Seed color. Internode color.	10.1104/pp.105. 073007
LOC_Os02g08100	4-Coumarate:coen zyme A ligase	Os4CL3	Dwarf	Lignin content. Dwarfism. Culm length. Anther development.	10.1104/pp.111. 178301
LOC_Os08g06480	Lissencephaly 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-met hionine 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/pch 082
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

LOC_Os05g33570	floury endosperm-4	flo4	Eating quality	Seed protein and lipid content.	10.1111/j.1365- 313X.2005.0242 3.x
LOC_Os09g29404	isoamylase3	isa3	Eating quality	Seed starch content.	10.1093/pcp/pcr 058
LOC_Os03g09250	rice myo -inositol 3-phosphate synthase 1	RINO1	Eating quality	Seed phytic acid content.	10.1093/pcp/pcp 071
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.2010.0415 8.x
LOC_Os09g06464	CONSTANS-LIK E 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- 3040.2009.0195 4.x
LOC_Os03g13970	26S proteasome non-ATPase regulatory subunit 4	RPN10	Other soil stress tolerance	Canavanine resistance.	10.5511/plantbi otechnology.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.2007.0314 9.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	ltn 1	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 starvationinduced transcription factor 1	OsPTF1	Other soil stress tolerance	Phosphate starvation tolerance.	10.1104/pp.105. 063115
LOC_Os06g40120	SYG/PHO81/XPR 1 domain1	OsSPX1	Other soil stress tolerance	Phosphate homeostasis.	10.1111/j.1365- 313X.2008.0373 4.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- 3054.2009.0129 0.x
LOC_Os08g03290	cytosolic GAPDH	OsGAPC3	Salinity tolerance	Salinity tolerance.	10.1007/s11240-

biosynthesis.

	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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