UILIAN STEFANELLO DE MELLO

AN OVERVIEW OF THE TRANSCRIPTIONAL RESPONSES OF TOLERANT AND SUSCEPTIBLE SUGARCANE VARIETIES TO BORER (*Diatraea saccharalis*) INFESTATION

Dissertação apresentada à Universidade Federal de Viçosa, como parte das exigências do Programa de Pós-Graduação em Fitotecnia, para obtenção do título de *Magister Scientiae*.

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APROVADA: 22 de fevereiro de 2019.

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ABSTRACT

MELLO, Uilian Stefanello de, M.Sc., Universidade Federal de Viçosa, February, 2019. **An overview of the transcriptional responses of tolerant and susceptible sugarcane varieties to borer (*Diatraea saccharalis*) infestation.** Adviser: Márcio Henrique Pereira Barbosa. Co-adviser: Pedro Marcus Pereira Vidigal.

Diatraea saccharalis is a threat to the sugarcane productivity. Obtaining borer tolerant varieties is an alternative method of control. Although there are studies about the relationship between the interaction of *D. saccharalis* with sugarcane, little is known about the molecular mechanisms that confer tolerance to sugarcane varieties. The objective of this work was to characterize the transcriptional profile of sugarcane genotypes in response to borer attack and to identify differentially expressed transcripts and genes. For that, two sugarcane varieties were analysed, RB867515 and SP80-3280, considered tolerant and sensitive to the attack of the sugarcane borer, respectively. The experiment was conducted in DIC, with three replications, in a greenhouse. Individual 2-month-old plants were infested with 20 larvae (3^{rd} – 4^{th} instar). The plant material was collected after 12 hours of borer infestation to extract the total RNA, which was sent for sequencing using the *Illumina HighSeq 2500* system. The differential expression was analyzed using the abundance of reads per transcript/gene between the infested plants and the control group using the software KALLISTO version 0.43.1 and STAR version 2.7.0a, utilizing the transcripts of the SUGIT (*Sugarcane Iso-Seq Transcriptome*) and genes from STP (*Single Tiling Path*) databases as mapping references. The data were submitted to differential expression analysis using the DESeq2 1.6.3 package, implemented in R version 3.5.1 software. The differentially expressed transcripts and genes were termed to as DETs and DEGs, respectively. A total of 927 DETs and 516 DEGs were identified (FDR≤0.01) and both were annotated using similarity search. The DETs and DEGs identified are mainly related to the biosynthetic pathways of jasmonic acid (JA), ethylene (ET), defense proteins, photosynthesis and sugar/carbon metabolism. In general, RB867515 demonstrated a higher regulation of JA, ET, and defense protein genes, as well as a more expressive down-regulation of pathways involved in photosynthesis and sugar/carbon metabolism. The results will allow the study of the resistance mechanisms of sugarcane against *D. saccharalis* and the selection of new targets for breeding to obtain resistant cultivars.

RESUMO

MELLO, Uilian Stefanello de, M.Sc., Universidade Federal de Viçosa, fevereiro de 2019. **Uma visão das respostas transcricionais de variedades tolerantes e suscetíveis de cana-de-açúcar a infestação com a broca-da-cana (*Diatraea saccharalis*).** Orientador: Márcio Henrique Pereira Barbosa. Coorientador: Pedro Marcus Pereira Vidigal.

A broca-da-cana (*Diatraea saccharalis*) é uma ameaça a produtividade da cana-de-açúcar. A obtenção de variedades tolerantes a *D. saccharalis* é uma alternativa ao controle da praga. Embora existam estudos sobre a relação entre a interação da broca com a cana-de-açúcar, pouco se conhece sobre os mecanismos moleculares que conferem tolerância às variedades de cana contra a broca. O objetivo deste trabalho foi caracterizar o perfil transcricional de genótipos de cana-de-açúcar em resposta à infestação com a broca e identificar transcritos e genes diferencialmente expressos. Para isso, foram analisadas duas variedades de cana-de-açúcar, RB867515 e SP80-3280, consideradas tolerantes e sensíveis ao ataque da broca, respectivamente. O experimento foi conduzido em DIC, com três repetições, em casa-de-vegetação. Plantas individuais com 2 meses de cultivo foram infestadas com 20 larvas (3° - 4° ínstar). O material vegetal foi coletado após 12 horas da infestação com a broca para a extração do RNA total, que foi encaminhado para o sequenciamento usando o *Illumina HighSeq 2500*. A expressão diferencial foi analisada através da abundância de *reads* por transcrito/gene entre as plantas infestadas e o grupo controle usando os softwares KALLISTO versão 0.43.1 e STAR version 2.7.0a, tendo como referência para o alinhamento os transcritos do SUGIT (*Sugarcane Iso-Seq Transcriptome*) e genes do STP (*Single Tiling Path*). Os dados de abundância foram submetidos a análise de expressão diferencial usando o pacote DESeq2 1.6.3, implementado no software R versão 3.5.1. Os transcritos e genes diferencialmente expressos foram denominados de DETs (*Differentially expressed transcripts*) e DEGs (*Differentially expressed genes*), respectivamente. Foram identificados (FDR≤0.01) 927 DETs e 516 DEGs e ambos foram anotados usando pesquisas de similaridade. Os DETs e DEGs estão principalmente relacionados a vias do ácido jasmônico (JA), etileno (ET), proteínas de defesa, fotossíntese e metabolismo de açúcares/carbono. De forma geral, observou-se na variedade RB867515 uma maior regulação de vias do JA, ET e proteínas de defesa, assim como uma maior "*down*" regulação de vias fotossintéticas e do metabolismo de açúcares/carbono. Os resultados permitirão o estudo de mecanismos de resistência da cana-de-açúcar contra a broca e a seleção de novos alvos para o melhoramento e obtenção de cultivares resistentes.

1 INTRODUCTION

Sugarcane (*Saccharum* sp.) is an indigenous crop, derived from New Guine, southeast Asia. The crop provides raw material for sugar and energy production, which makes this crop an important component of many countries' economy. The worldwide sugarcane production area corresponded to more than 26 million hectares distributed in approximately 112 countries (FAOSTAT, 2016). Brazil accounts for most of the world's sugarcane production with a planting area of nearly 8.74 million hectares with a production outcome of 633.26 million tons, according to the 2017/2018 national harvest data (CONAB, 2018).

The *Saccharum* genus includes cultivated and wild species from which the modern varieties of sugarcane were bred through hybridization process. Typically, the modern sugarcane cultivars are interspecific hybrids derived from backcrosses between the cultivated *S. officinarum* (2n=10x=80) and the wild relative *S. spontaneum* (2n=8x=40-128) species. The genomes of these hybrids are composed basically of 80-85% from chromosomes derived of *S. officinarum*, 10-15% from *S. spontaneum*, and 5-10% from recombinant chromosomes between both species (D'HONT et al., 1996). As a consequence, sugarcane hybrids possess polyploid and aneuploid genomes, which hinders the understanding of the molecular and genetic traits of this crop. (HOTTA et al., 2010).

A drawback for the molecular and genetic advances in sugarcane was the absence of a reference genome. Its highly polyploid, aneuploid, heterozygous, and interspecific genome have been a major challenge for producing a reference genome sequence. For years, the genome of the diploid specie *Sorghum bicolor* had been used for this purpose. However, because of the complex polyploid genome, the transcriptome analysis of sugarcane varieties had been limited by the allelic variation and the presence of a variety of transcript isoforms, which it is difficult to identify using diploid genome models. Only recently, a sugarcane transcriptome reference named SUGIT (Sugarcane Iso-Seq transcriptome database) became available (HOANG et al., 2017). SUGIT database contains 107,598 unique transcript sequences derived from an RNA pool of 22 commercial and introgressed sugarcane varieties. The RNA was extracted at different development stages (young and adult plants) and different tissues (leaf, internode and root). SUGIT transcript database is thought to account for approximately 71% of the total predicted genes in the sugarcane genome. Despite not being annotated, SUGIT provides a good coverage of the sugarcane transcriptome and represents the first

reference for complete transcript sequences (*full-length*), contributing significantly for sugarcane gene expression and characterization analysis. More recently, a monoploid genome reference sequence for sugarcane, using the modern sugarcane variety R570, became available under the name STP (*Single Tiling Path*), (GARSMEUR et al., 2018). Encompassing a single genome copy, STP contains 25,316 predicted protein-coding genes and 83% of these sequences display gene collinearity with their sorghum orthologs.

STP and SUGIT databases are, respectively, a well-suited and novel genome and transcriptome reference for sugarcane genetic and molecular studies. They constitute a good source for gene similarity search and gene mapping analysis in sugarcane. Besides, these references become a helpful tool for studies focused on unraveling molecular-triggered responses at different environment conditions that pose a negative impact on sugarcane productivity, such as insect herbivory.

A threat to sugarcane productivity is the presence of pests that cause economic losses. The sugarcane borer (*Diatraea saccharalis*) is the main pest in sugarcane Brazilian growing areas. Estimates indicate that each 1% internode infested with sugarcane borer results in 144 kg of sugar loss (VARGAS; GÓMEZ; MICHAUD, 2015) and 1.5% stem loss (ARRIGONI, 2002). The selection and development of tolerant varieties through conventional breeding methods has assisted in the control of this pest. However, studies have been focusing on the phenotypic tolerance characterization of sugarcane (DEMETRIO; ZONETTI; MUNHOZ, 2008; DINARDO-MIRANDA et al., 2012; TOMAZ et al., 2017) and until now little is known about genes that confer resistance to this pest in sugarcane.

In general, the plant's defense mechanisms against insect-feeding involves the recognition of insect elicitors which induces a cascade of signal transduction pathways, leading to transcriptional changes of defense-related genes and consequently triggering the biosynthesis of defense metabolites. Throughout evolution, plants have been acquiring induced defense mechanisms for protection against insects. Usually, the first steps upon herbivory recognition is the activation of kinase networks and biosynthesis of phytohormones (MAFFEI; ARIMURA; MITHÖFER, 2012). Consequently, defense mechanisms are triggered and tend to involve direct interference with insect growth and development, mainly via the activation of toxic proteins and metabolites, such as proteinase inhibitors and peroxidases (GOVIND et al., 2010). It has been proposed that the main defense mechanisms against insect attack in sugarcane is regulated by genes involved in the jasmonic acid (JA) and ethylene (ET) biosynthetic pathways (FALCO et

al., 2001). JA- and ET-induced responses appear to be responsible for a large portion of the differential regulation of defense genes and regulatory elements, which can prime plants against biotic and abiotic stresses, improving tolerance.

The analysis of sugarcane transcriptome to identify differentially expressed genes (DEGs) related to hormone biosynthesis and insect defense-related genes is a powerful approach to unravel the molecular responses of sugarcane under insect herbivory. Among available methods, RNA sequencing (*RNA-seq*) is a tool which allows the analysis of transcriptional profiles of any species of interest that present contrasting characteristics, by quantifying the expression of genes activated or inactivated under certain conditions (LI et al., 2012). Despite the importance of sugarcane borer and the improvements in breeding programs related to borer tolerance, little is known about the molecular mechanisms related to resistance triggered upon *Diatraea saccharalis* infestation in sugarcane.

Here, we analyzed the changes in transcriptional profiles of two brazilian sugarcane varieties (RB867515 and SP80-3280) in response to *D. saccharalis* infestation. These varieties were chosen based on their susceptibility to the pest attack. In preliminary tests, both varieties presented different behaviors regarding culm injury and young larvae survival on leaves (TOMAZ et al., 2017). In general terms, RB867515 is characterized by relatively low survival of early-stage larvae feeding on leaves and is known to be more resistant in field conditions. Conversely, SP80-3280 is considered to be more susceptible in the field, and is characterized by lower mortality of early-stage larvae feeding on leaves, allowing then more larvae to penetrate into the stalks. Thus, under the presumption of that those varieties have contrasting phenotypes to borer infestation, we focused on characterizing the transcriptional changes and on identifying differences related to defense mechanisms possibly involved in the sugarcane tolerance to *D. saccharalis*.

2 MATERIAL AND METHODS

2.1 Sugarcane variety selection, cultivation and infestation

The sugarcane varieties (RB867515 and SP80-3280) used in this work were obtained from RIDESA (Inter-University Network for the Development of Sugarcane Industry) (BARBOSA et al., 2012). Culms from the varieties were planted in 30 L pots filled with a mixture of 28 kg soil/manure (2:1 v/v) and grown in greenhouse (average

temperature 28.5 °C and natural light conditions) with soil humidity kept at soil water capacity. *D. saccharalis* larvae were obtained from a reserve colony grown in artificial diet (HENSLEY; HAMMOND., 1968) with modifications (ARAÚJO; BOTELHO; ARAÚJO, S. M. S. S. ALMEIDA, L. C. DEGASPARI, 1985). The colony originated from a set of larvae collected in the field and grown in laboratory (GIRÓN-PÉREZ et al., 2014). The leaves of individual plants were infested with 20 *D. saccharalis* larvae (3^{rd} – 4^{th} instar) after two months from the planting date, period in which plants were approximately 1 m high (Figure 1B).

The experiment was conducted with a complete randomized factorial design containing 2 varieties (RB867515 and SP80-3280) x 2 conditions (control and infested) x 3 biological replicates (Figure 1A). The harvested vegetal material consisted of leaves +1, following the Kuijper system (DILLEWIJN, 1952), and were collected after 12 h from the infestation.

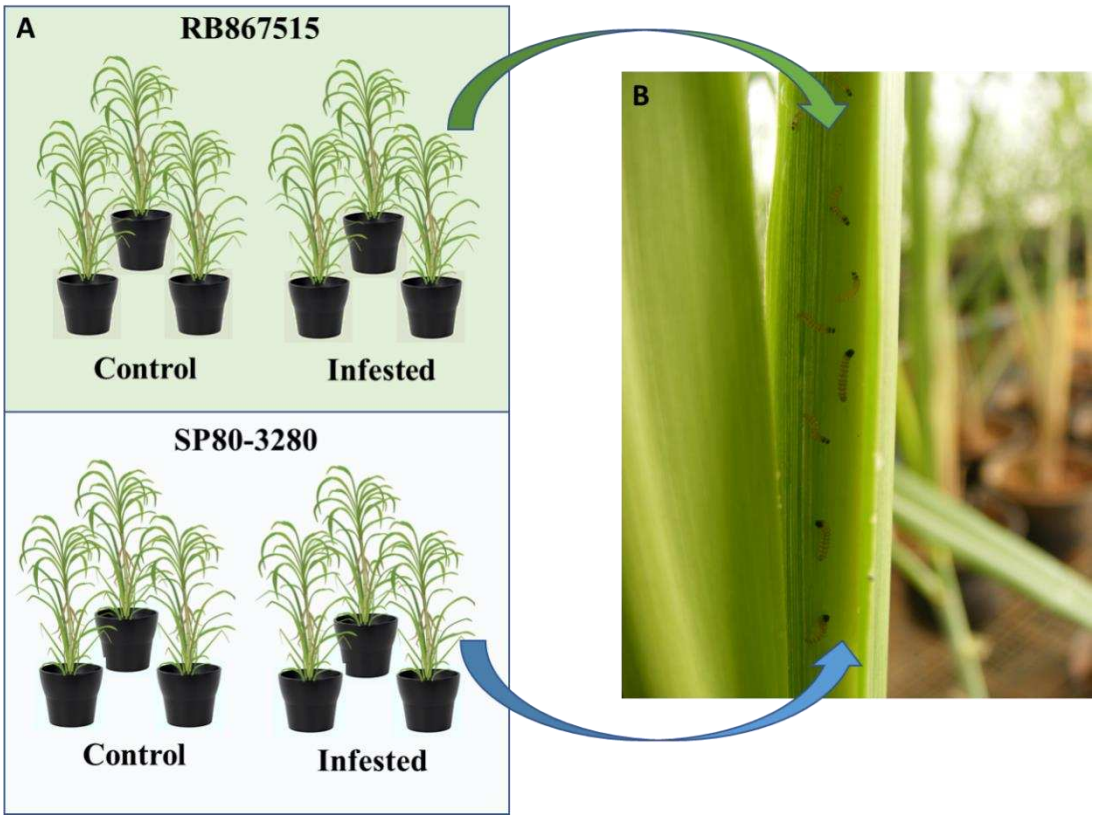

Figure 1. Schematic representation of the experiment design. (A) Sugarcane varieties RB867515 and SP80-3280 and their respectively three-replicate treatments (control and infested); (B) Infested leaf with *D. saccharalis* larvae.

2.2 RNA extraction, RNA-seq library construction, sequencing and bioinformatic analysis

Leaf samples were ground to fine powder under liquid nitrogen using stainless steel grind jars in the TissueLyser II (Qiagen) bead mill, and RNA was extracted using the PureLink® Plant RNA Reagent (Thermo Fisher) as described by the manufacturer. The quantification of total extracted RNA was accessed using a Qubit® 2.0 Fluorometer kit (Life technologies). The RNA integrity number (RIN) of the total RNA was analyzed using a 2100 Bioanalyzer 6000 Kit (Agilent Technologies, USA). A minimum of 10 μg of purified total RNA per sample with a RIN > 7.0 was sent out to GenOne Biotechnologies (Brazil) for constructing mRNA-seq libraries using paired-end mode (2x150bp) in the Illumina HiSeq 2500 sequencer (Illumina).

The libraries underwent filtering steps to obtain clean reads, which included: (1) raw reads quality assessment using FASTQC version 0.11.8 (https://github.com/s-andrews/FastQC), and (2) trimming and removal of low-quality reads using AfterQC version 0.97 (CHEN et al., 2017) and Trimmomatic version 0.38 (BOLGER; LOHSE; USADEL, 2014). After trimming and filtering, clean reads were mapped to the sugarcane monoploid genome database (STP) (GARSMEUR et al., 2018) using STAR version 2.7.0a (DOBIN et al., 2013). For complementary results, we also used the SUGIT transcriptome reference source (HOANG et al., 2017) to broaden the spectrum of read mapping using Kallisto version 0.45.0 (BRAY et al., 2016). It is worth mentioning that SUGIT database were constructed using a pool of RNA from different sugarcane genotypes under different stresses and from different tissues, which enhances the probability of catching a broader transcriptional-triggered response profiles in sugarcane. Before mapping, SUGIT database underwent a pre-processing step involving sequence complexity reduction, which creates a unified reference containing canonical sequences representatives of the transcriptome. For that purpose, CD-hit version 4.6.8 (LI; GODZIK, 2006) was used to cluster transcript sequences which share 80% of identity.

In this study, diferential expression analysis was conducted using the SUGIT and STP databases. For terminology purposes, we referred to diferentially expressed transcripts as DETs, and diferentially expressed genes as DEGs according to the respective database adopted. The integrative analysis of DEGs and DETs concomitantly broadens the spectrum of the transcriptional profile of sugarcane and gives a better grasp of the biological processes triggered upon infestation, which enhances the

exploitation of resistance traits in future studies and maximizes the understanding of how sugarcane responds to *D. saccharalis* infestation. A schematic overview of the analysis conducted in this study is shown in Figure 2.

DETs and DEGs were identified using the DESeq2 package version 1.6.3 (LOVE; HUBER; ANDERS, 2014) implemented in R version 3.5.1 (R DEVELOPMENT CORETEAM (2018), 2018). DETs and DEGs analysis were conducted using the read mapping information generated by Kallisto and STAR, respectively. A False Discovery Rate (FDR) ≤ 0.01 was used to select the significant DEGs and DETs. In addition, Pearson´s Correlation Coefficient analysis was performed to compare the read abundances from the mapping outputs obtained by STAR and Kallisto softwares. The read abundances were normalized as *transcripts per million* (TPM) and then transformed to $\log_2$. This analysis included pairwise comparisons of the $\log_2$ transformation of normalized read abundances relative to all biological replicates in control and infested plants (See Figure S1 and S2).

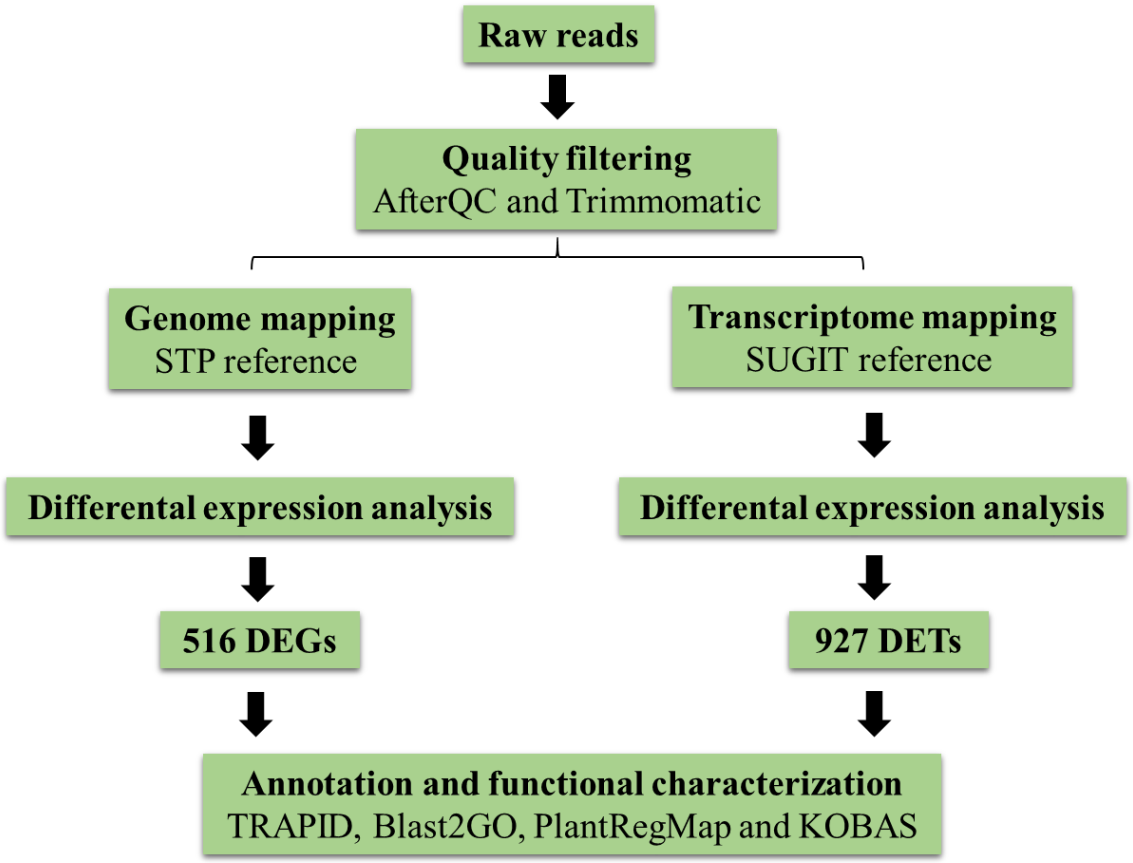

Figure 2. Pipeline of procedure analysis. Raw reads obtained from RNA-seq libraries of control and *D. saccharalis* treated sugarcane plants. First, quality filter was applied to all raw reads. Next, clean reads were mapped against SUGIT and STP databases. Last, differential expression analysis was conducted and DEGs and DETs were functionally annotated using TRAPID, Blast2GO, PlantRegMap and KOBAS.

2.3 Characterization and Functional annotation of DETs and DEGs

DETs and DEGs were functionally annotated using Blast2GO version 5.2.5 (CONESA; GÖTZ, 2008) through similarity searches using BLAST (MCGINNIS; MADDEN, 2004). The performed search parameters included: "Blast program: Blastx-fast"; "Blast database: nr"; "Taxonomy filter: monocots (taxa: 4447, Liliopsida)"; "Blast Expectation Value (E-Value): 1.0 e^{-5}"; and "Number of Blast Hits: 5". Conserved domains were assigned to the proteins encoded by DEGs and DETs using the online platform TRAPID: Rapid Analysis of Transcriptome Data (VAN BEL et al., 2013), which uses the PLAZA 2.5 database (https://bioinformatics.psb.ugent.be/plaza/) to assign functional annotations based on sequence similarity. The parameters of performed searches included the monocots database and an e-value of $1.0e^{-5}$. Gene ontology (GO) terms were assigned to DETs and DEGs using the online platform PlantRegMap (Plant Transcriptional Regulatory Map) (JIN et al., 2017), which adopt the topGo package and Fisher's exact tests to find significantly over-represented GO terms (p-value≤0.01). GO enrichment analysis was done using the *Sorghum bicolor* database as reference. We also used KOBAS (KEGG Orthology Based Annotation System) version 3.0 to identify enriched metabolic pathways among DETs and DEGs (XIE et al., 2011). Enriched KEGG pathways were determined by using Fisher's exact tests followed by Benjamini-Hochberg FDR correction method (FDR≤0.01).

3 RESULTS AND DISCUSSION

3.1 RNA quality assessment and sequencing analysis

RNA concentration varied between 631 and 828 ng/µl (741 ng/µl average) in all samples. RNA integrity number (RIN) ranged between 7.4 and 9.0 (8.1 average) (Figure 3A). In summary, the samples obtained in this study consisted of good quality RNAs. In terms of quality, RIN values range from 1 (degraded RNA) to 10 (intact RNA) (Figure 3B). Basically, RIN is calculated by taking the ratio of the area under the 18S and 28S rRNA peaks to the total area under the graph, and its error is mentioned to be forty times lower compared to conventional 28S/18S approach (SCHROEDER et al., 2006), which makes this method more reliable to measure RNA quality.

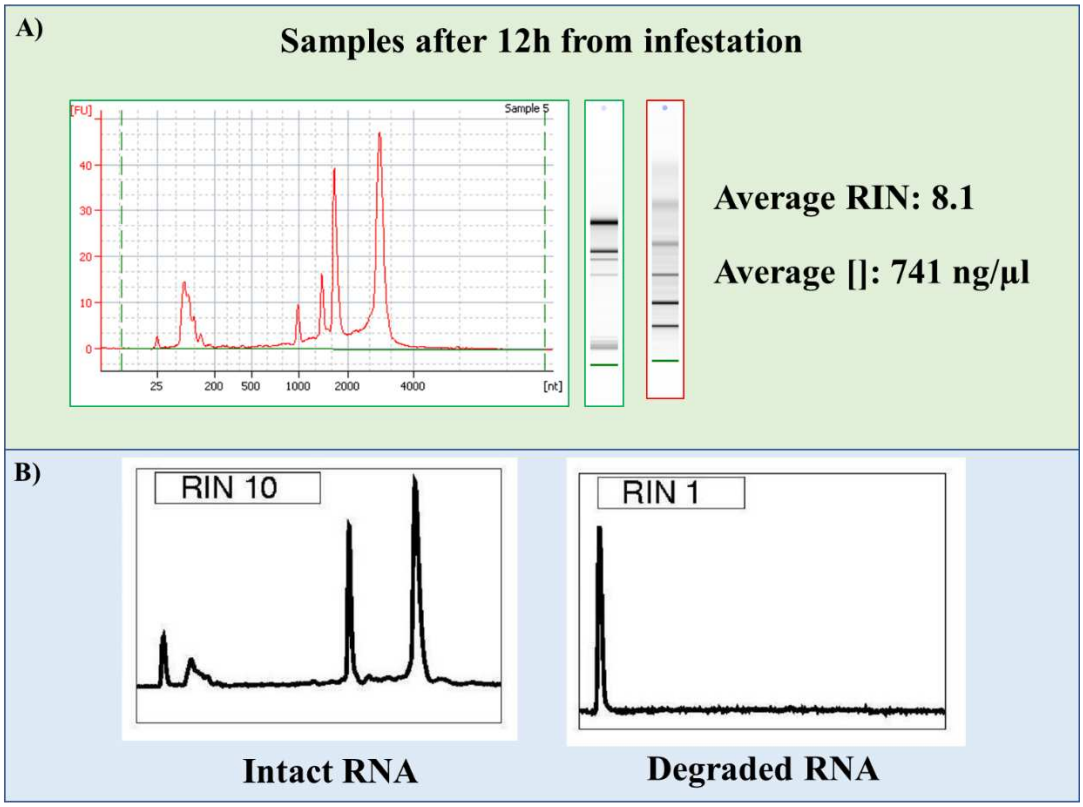

Figure 3. Schematic representation of RNA quality and concentration. (A) RIN quality graph built with a sample exposed to *D. saccharalis* after 12h from infestation, and representation of the experimental average quality (8.1) and concentration (741 ng/µl); (B) Graph representations of intact RNA with RIN 10 (left) and degraded RNA with RIN 1 (right), images adapted from SCHROEDER et al., 2006.

The sequencing raw data from the 12 libraries were trimmed to remove low-quality regions (Q<20), ambiguous nucleotides and adapters from reads. We removed approximately 4% of low-quality reads from all RNA libraries. The number of raw, filtered and mapped reads are listed in Table 1. In general, more reads were mapped to SUGIT database (69.5% average) than to STP´s (58.6% average) probably because of those differences in number of sequences included in each reference database. Despite having an overall low percentage of mapped reads to its genes, the correlation analysis showed R values between 0.98 and 0.99 in all pairwise comparisons among the output of read mapping generated by STAR software (See supplementary Figure S1). Likewise, R values between 0.97 and 0.99 were observed when Pearson´s Correlation Coefficient was employed to the normalized read abundances generated from Kallisto software (See supplementary Figure S2). The correlation results indicate that biological replicates have good reproducibility.

SUGIT database was diminished in 64.46% after sequence complexity reduction using CDhit, obtaining a reference containing 38,240 canonical sequences representatives of the transcriptome. Even with the complexity reduction, the number of

SUGIT transcripts was superior to STP´s (25,316 genes), which could represent isoform variants of genes, non-coding regions or translated regions still not annotated in sugarcane reference genome.

Table 1. Summary of sequencing, trimming and mapping data in varieties RB867515 and SP80-3280. Notes: [a] Total number of reads obtained after Illumina sequencing; [b] Total number of clean reads obtained after quality filter using AfterQC and Trimmomatic; [c] Number of clean reads mapped to the transcripts of SUGIT database; [d] Number of clean reads mapped to the genes of STP database.

Description	RB867515					
	Control			Infested		
	Replicate 1	Replicate 2	Replicate 3	Replicate 1	Replicate 2	Replicate 3
Total raw reads[a]	32,179,594	45,547,120	39,423,487	40,256,223	46,600,812	35,461,099
AfterQC filter[b]	31,817,945	44,961,584	38,986,933	39,871,276	46,245,737	35,217,036
Trimmomatic filter[b]	30,608,944	44,041,424	38,073,265	38,562,348	45,075,080	33,928,406
Trimming %	95.12	96.69	96.58	95.79	96.73	95.68
SUGIT mapped reads[c]	22,273,953	32,429,100	27,746,216	27,735,668	32,605,649	23,948,700
SUGIT mapping %	69.22	71.20	70.8	68.90	69.97	67.54
STP mapped reads[d]	19,038,128	26,251,435	22,790,464	23,027,575	26,282,287	20,445,196
STP mapping %	62.20	59.61	59.86	59.72	58.31	60.26
Description	**SP80-3280**					
	Control			Infested		
	Replicate 1	Replicate 2	Replicate 3	Replicate 1	Replicate 2	Replicate 3
Total raw reads[a]	41,806,059	41,688,084	35,308,871	41,755,181	36,111,508	40,123,108
AfterQC filter[b]	41,367,001	41,238,701	35,029,655	41,317,273	35,678,615	39,832,180
Trimmomatic filter[b]	40,344,164	40,172,061	33,904,678	40,285,528	34,894,543	38,556,759
Trimming %	96.50	96.36	96.02	96.48	96.63	96.10
SUGIT mapped reads[c]	28,932,001	29,347,004	24,879,637	29,048,250	25,305,804	27,526,909
SUGIT mapping %	69.21	70.40	70.46	69.57	70.08	68.61
STP mapped reads[d]	24,229,774	22,002,610	20,190,748	23,619,686	20,599,366	23,108,662
STP mapping %	60.06	54.77	59.55	58.63	59.03	59.93

3.2 Differential expression analysis

We calculated the $\log_2$ fold changes ($\log_2$ FCs) between control and infested libraries to obtain the differential expression of transcripts (DETs) and genes (DEGs). To screen DEGs/DETs, a false discovery rate (FDR) ≤ 0.01 was employed. Using the normalized read abundances calculated by Kallisto, a total of 727 DETs were identified for RB867515 (405 up-regulated and 322 down-regulated) and 303 DETs for SP80-3280 (258 up-regulated and 45 down-regulated) (Figure 4A). A total of 98 and 5 DETs were commonly up- and down-regulated between the varieties, respectively (Figure

4C). As for STP database, a total of 377 DEGs were identified for RB867515 (261 up-regulated and 116 down-regulated) and 221 DEGs for SP80-3280 (189 up-regulated and 32 down-regulated) (Figure 4B). A total of 79 and 3 DEGs were commonly up- and down-regulated between the varieties, respectively (Figure 4D). Venn Diagrams were built to demonstrate the cross-talking between overlapping and unique DETs/DEGs to each variety (Figure 4C and 4D). The complete list of overlapping and unique DETs and DEGs with the respective annotation and $\log_2$ FCs is shown in supplementary Tables S1 and S2, respectively.

Differential expression analysis was more abundant in terms of gene regulation for RB867515 regardless of the mapping source adopted (Figure 4C and 4D). Considering the time at which the samples were collected, this result suggests that RB867515 is more transcriptionally activated upon herbivory, which could imply in quicker responses by probably triggering more defense-related genes and mediating metabolic pathways to cope with *D. saccharalis* attack.

To verify gene similarity among these databases, DETs were aligned against the coding DNA sequences (CDS) of DEGs. The alignment was conducted using the BLAST tool of Blast2GO (e-value:1.0e-3), having the DETs as a local database. As a result, 293 DEGs were aligned against 369 DETs (Figure 4E). The difference in matching alignments is probably because of the presence of isoforms or allelic variations in the SUGIT database that aligned to a similar DEG. These aligned sequences provide an auxiliary tool for designing confidently specific primers in genes of interest, which could be used in gene expression analysis. Surprisingly, 558 DETs and 223 DEGs had no identity similarity, meaning that sequencing and annotation gaps or different genic regions might exist among these databases, which could be assigned not only to base-to-base identity dissimilarity but also to alternative gene splicing to still be discovered in sugarcane reference genome. The complete list of the blast results is shown in supplementary Table S3.

3.2.1 Comparison of differential expression analysis between varieties

Based on known herbivory responses and stress-related defense mechanisms, we selected and compared common and unique up- and down-regulated DETs and DEGs between the varieties as for the relative $\log_2$ FC (Table 2). Conserved protein domains (PDs) were assigned to DETs and DEGs when available. These comparisons give insight into gene specific regulation in each genotype in response to *D. saccharalis*

infestation. Also, to better understand the regulation pattern, we conducted differential expression analysis among control samples of SP80-3280 in relation to RB867515 (Table 3). We verified that differences in $\log_2$ FC of common DETs and DEGs to each variety (listed in Table 2) are not attributed to different basal levels of transcript expression in control samples, which supports the ideia that RB867515 is more transcriptionally active upon herbivory.

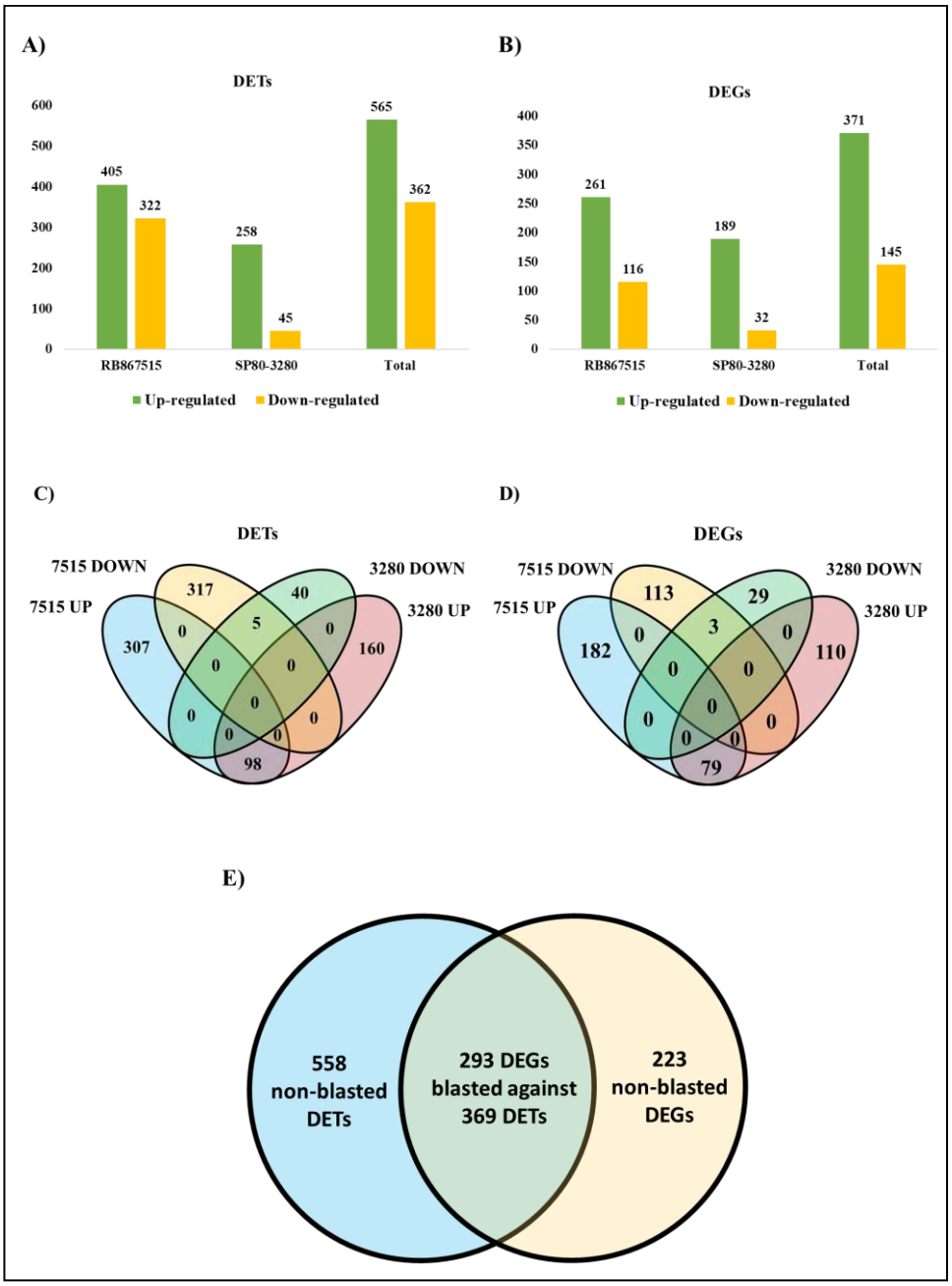

Figure 4. Number of differentially expressed transcripts (DETs) and genes (DEGs) identified in sugarcane in response to *D. saccharalis* after 12 h from infestation using SUGIT and STP databases as mapping references. (A and B) Number of up- and down-regulated DETs and DEGs, respectively, found (FDR≤0.01) in RB867515 and SP80-3280, and total number of DETs and DEGs identified in the experiment; (C and D) Venn diagram of unique and common up- and down-regulated DETs and DEGs found in the varieties RB867515 and SP80-3280; (E) Number of blasted (shared) and non-blasted (exclusive) DETs/DEGs.

Table 2. Log_2 FC comparison of common and unique DETs/DEGs to RB867515 and SP80-3280. Similar regulation pattern observed in both mapping references for common DETs/DEGs in each variety. Notes: * DETs with identity similarity to DEGs according to the blasting approach; ** DETs with no identity similarity to DEGs.

SUGIT ID	Log_2 FC (RB867515)	Log_2 FC (SP80-3280)	Protein domain
GFHJ01047708.1*	2,481235556	1,222585718	Lipoxygenase, plant
GFHJ01024452.1*	4,488776986	2,323548485	DNA-binding WRKY
GFHJ01053310.1*	3,728606534	1,672803522	Protein kinase, catalytic domain
GFHJ01060610.1*	5,106730053	3,877041972	Plant peroxidase
GFHJ01058630.1*	4,646091904	2,407987732	Oxoglutarate/iron-dependent oxygenase
GFHJ01079377.1*	5,694507527	----------	Terpene synthase-like
GFHJ01064943.1*	----------	1,506000369	Glycoside hydrolase, family 19
GFHJ01067101.1*	----------	4,721071185	NAD-dependent epimerase/dehydratase
GFHJ01021685.1*	-1,143169041	----------	Cellulose synthase
GFHJ01096227.1**	-1,769754825	----------	Chlorophyll A-B binding protein
GFHJ01020726.1**	-1,518240712	----------	UDP-glucose 4-epimerase
GFHJ01028757.1**	0,644140344	----------	Squalene cyclase
STP ID	**Log_2 FC (RB867515)**	**Log_2 FC (SP80-3280)**	**Protein domain**
Sh01_g010080*	2,480729053	1,257895322	Lipoxygenase, plant
Sh03_g015550*	4,497950169	2,316476743	DNA-binding WRKY
Sh09_g017390*	4,838364907	1,886451567	Protein kinase, catalytic domain
Sh01_g036120*	5,204327005	3,881502814	Plant peroxidase
Sh09_g004190*	3,911033490	1,933901408	Oxoglutarate/iron-dependent oxygenase
Sh07_g005540*	5,681245474	----------	Terpene synthase-like
Sh09_g010120*	----------	1,497754937	Glycoside hydrolase, family 19
Sh04_g026050*	----------	4,084322165	NAD-dependent epimerase/dehydratase
Sh02_g015820*	-1.203949150	----------	Cellulose synthase
Sh01_g040760**	----------	8.142033359	3-ketoacyl-CoA synthase
Sh01_g042260**	-6.733053083	----------	3-ketoacyl-CoA synthase
Sh10_g010920**	-1.773026942	----------	3Fe-4S ferredoxin

We observed a significant regulation in expression when comparing DETs and DEGs from control samples of SP80-3280 against RB867515´s (Table 3). These results demonstrate the innate expression of those genes in each variety at an unstressed state. Except for "squalene cyclase", the selected genes (listed in table 3) were down-regulated, meaning that their expression levels in control samples are significantly higher in RB867515. For example, RB867515 has shown a higher expresison of DETs and DEGs in untreated samples with the following PDs: "cellulose synthase", "NAD-dependent epimerase/dehydratase", "3-ketoacyl-CoA synthase", " Chlorophyll A-B binding protein", and "3Fe-4S ferredoxin" (Table 3). Genes with these PDs are involved

in cellulose, lignin, cuticular wax/suberin biosynthesis, photosynthesis and electron transport, respectively.

Upon *D. saccharalis* infestation, the expression of the above-mentioned genes remained unalterned or increased significantly in SP80-3280, whereas for RB867515 the regulation remained unaltered or decreased significantly (Table 2). This decrease in regulation could be associated with energy reallocation in favor of defense metabolites. "Squalene cyclase (SC)" PD is involved in the triterpenoid metabolism and was up-regulated in treated RB867515 (Figure 2), meaning that its expression tend to augment when treated with *D. saccharalis*. When comparing controls, SP80-3280 demonstrated a higher expression of SC but did not alter regulation upon infestation (Table 2). In overall, this regulation interplay demonstrates that both genotypes have different basal expression levels for the considered genes and respond differently by augmenting or diminishing gene expression after *D. saccharalis* infestation.

Table 3. Log_2 FC comparison of DETs/DEGs generated from SP80-3280 against RB867515 control samples. For the considered genes, expression levels were more expressive in RB867515 untreated samples than in SP80-3280 untreated samples.

SUGIT ID	Log_2 FC	Protein Domain
GFHJ01067101.1	-3,46746138	NAD-dependent epimerase/dehydratase
GFHJ01021685.1	-0,87964499	Cellulose synthase
GFHJ01096227.1	-2,48022436	Chlorophyll A-B binding protein
GFHJ01028757.1	0,96092873	Squalene cyclase
STP ID	**Log_2 FC**	**Protein Domain**
Sh02_g015820	-1,31966354	Cellulose synthase
Sh01_g040760	-11,3013379	3-ketoacyl-CoA synthase
Sh01_g042260	-6,68155678	3-ketoacyl-CoA synthase
Sh10_g010920	-1,00354319	3Fe-4S ferredoxin

3.3 Functional annotation

Differential expressed transcripts and genes were annotated by Blast2GO software (version 5.2.5) using the "nr" database. In total, 882 DETs (95.1%) and 497 DEGs (96.3%) were annotated (See supplementary Tables S1 and S2, respectively). With the parameters adopted, exactly 45 DETs and 19 DEGs could not be annotated, probably because these SUGIT transcript sequences represent non-coding RNA sequences and cytoplasmic RNA found in mitochondria and chloroplasts. The non-assigned STP sequences (CDS) could represent transcripts still not functionally annotated in other monocot species.

The online TRAPID tool was used to assign conserved protein domains (PDs) to DETs and DEGs (See supplementary Tables S4 and S5, respectively). To characterize transcriptional data, this platform utilizes *InterPro*, a database containing functionally annotated protein families, domains, and functional sites (HUNTER et al., 2009). TRAPID found 800 domains in 753 transcripts (81.2% of DETs) and 593 domains in 437 CDS sequences (84.7% of DEGs). A summary of the TRAPID statistical analysis is shown in Table 4. The top 5 most frequently occurred PDs in each up- and down-regulated samples from both mapping references are shown in Table 5 and Table 6, respectively. The data demonstrated that mapping references had consisted results as for the PDs most altered in up- and down-regulated samples.

Table 4. Summary of TRAPID statistics for DETs and DEGs. Statistics displaying high gene similarity with *Sorghum bicolor* and revealing Oxoglutarate and Peroxidase as the most representative gene families (GFs) among DEGs and DETs, respectively.

Description	**DEGs**	**DETs**
Information	**Number**	**Number**
Total number	516	927
Average length (bp)	1064.3	1700
Similarity search information		
Sorghum bicolor	394 (79.3%)	627 (71.1%)
Zea mays	72 (14.5%)	186 (21.1%)
Brachypodium distachyon	11 (2.2%)	22 (2.5%)
Oryza sativa ssp. *indica*	10 (2%)	24 (2.7%)
Oryza sativa ssp. *japonica*	10 (2%)	23 (2.6%)
Total	497	882
Gene family (GF) information		
Gene families	339	508
Transcriptis with GF	497 (96.3%)	882 (95.1%)
Largest GF	Oxoglutarate/iron-dependent oxygenase (10 genes)	Plant peroxidase (17 transcripts)
InterPro		
InterPro domains	593	800
Genes/Transcripts with PD	437 (84.7%)	753 (81.2%)

Among the up-regulated samples are DEGs and DETs with PDs involved in oxylipin metabolism, a pathway in which JA is synthesized; as well as possessing a kinase, peroxidase, membrane transport, oxidation-reduction, lipase and transcriptional factor activity. Most of them have already been reported to be involved in defense mechanisms against biotic stresses and plant-insect interaction (LA CAMERA et al., 2004; ZEBELO; MAFFEI, 2015). Alternatively, most of the PDs in down-regulated

samples were associated with carbon and sugar metabolism, pigment synthesis, electron transport, and kinase activity. Despite these response patterns were similar in both varieties, RB867515 demonstarted a higher number of up- and down-regulated DEGs and DETs containg these PDs as compared to SP80-3280 (Tables 5 and 6, respectively).

Table 5. Top 5 most frequent PDs in up-regulated DETs and DEGs from each variety.

InterPro ID	Description	Number
Common up-regulated DETs		
IPR005123	Oxoglutarate/iron-dependent oxygenase	7
IPR001024	Lipoxygenase, LH2	5
IPR001128	Cytochrome P450	5
IPR002283	Isopenicillin N synthase	5
IPR002641	Patatin	5
Common up-regulated DEGs		
IPR001128	Cytochrome P450	5
IPR005123	Oxoglutarate/iron-dependent oxygenase	5
IPR000864	Proteinase inhibitor I13, potato inhibitor I	4
IPR002401	Cytochrome P450, E-class, group I	4
IPR003657	DNA-binding WRKY	4
RB867515 up-regulated DETs		
IPR000719	Protein kinase, catalytic domain	18
IPR001092	Helix-loop-helix DNA-binding domain	13
IPR002290	Serine/threonine-protein kinase domain	13
IPR003593	ATPase, AAA+ type, core	12
IPR020635	Tyrosine-protein kinase, catalytic domain	12
RB867515 up-regulated DEGs		
IPR000719	Protein kinase, catalytic domain	7
IPR001092	Helix-loop-helix DNA-binding domain	7
IPR001611	Leucine-rich repeat	5
IPR002213	UDP-glucuronosyl/UDP-glucosyltransferase	5
IPR012287	Homeodomain-related	5
SP80-3280 up-regulated DETs		
IPR016196	Major facilitator superfamily, general substrate transporter	9
IPR016040	NAD(P)-binding domain	7
IPR000719	Protein kinase, catalytic domain	5
IPR000726	Glycoside hydrolase, family 19, catalytic	5
IPR001906	Terpene synthase-like	5
SP80-3280 up-regulated DEGs		
IPR000719	Protein kinase, catalytic domain	5
IPR001509	NAD-dependent epimerase/dehydratase	5
IPR016196	Major facilitator superfamily, general substrate transporter	4
IPR017442	Serine/threonine-protein kinase-like domain	4
IPR000726	Glycoside hydrolase, family 19, catalytic	3

Table 6. Top 5 most frequent PDs in down-regulated DETs and DEGs from each variety.

.

InterPro ID	Description	Number
Common down-regulated DETs		
IPR000146	Fructose-1,6-bisphosphatase	1
IPR013216	Methyltransferase type 11	1
IPR014778	Myb, DNA-binding	1
Common down-regulated DEGs		
IPR000767	Disease resistance protein	1
IPR002182	NB-ARC	1
RB867515 down-regulated DETs		
IPR000719	Protein kinase, catalytic domain	17
IPR008271	Serine/threonine-protein kinase, active site	12
IPR001344	Chlorophyll A-B binding protein	9
IPR012336	Thioredoxin-like fold	7
IPR001509	NAD-dependent epimerase/dehydratase	6
RB867515 down-regulated DEGs		
IPR001471	Pathogenesis-related transcriptional factor/ERF, DNA-binding	4
IPR012335	Thioredoxin fold	4
IPR015609	Molecular chaperone, heat shock protein, Hsp40, DnaJ	4
IPR016177	DNA-binding, integrase-type	4
IPR001623	Heat shock protein DnaJ, N-terminal	3
SP80-3280 down-regulated DETs		
IPR016040	NAD(P)-binding domain	5
IPR001433	Oxidoreductase FAD/NAD(P)-binding	2
IPR001509	NAD-dependent epimerase/dehydratase	2
IPR002213	UDP-glucuronosyl/UDP-glucosyltransferase	2
IPR008333	Oxidoreductase, FAD-binding domain	2
SP80-3280 down-regulated DEGs		
IPR002213	UDP-glucuronosyl/UDP-glucosyltransferase	2
IPR001128	Cytochrome P450	1
IPR016040	NAD(P)-binding domain	1
IPR001646	Pentapeptide repeat	1
IPR002130	Peptidyl-prolyl cis-trans isomerase, cyclophilin-type	1

Regarding the similarity search conducted by TRAPID, most of the assigned transcripts and CDS (71.7 and 79.3%, respectively) had significantly matches with annotated genes from *Sorghum bicolor* (Table 4). Sorghum is the closest-related diploid crop to sugarcane and both have high sequence identity similarity in the genic regions (BUNDOCK; CASU; HENRY, 2012). Other species with gene identity similarity in the search included: *Zea mays*, *Oryza sativa* ssp. *indica*, *Oryza sativa* ssp. *japonica*, and *Brachypodium distachyon* (Table 4). Also, TRAPID identified 508 and 339 different gene families among the annotated DEGs and DETs, having the "Plant peroxidase" (17

transcripts) and “Oxoglutarate family” (10 CDS) as the most abundant GFs, respectively. In general terms, peroxidases have been implicated in physiological processes that involve scavenging of reactive oxygen species (ROS) and synthesis of lignin and phytoalexins, important biological processes against biotic stresses (COSIO; DUNAND, 2009). Enzymes belonging to the oxoglutarate family participate in a variety of plant metabolic pathways, including the synthesis of hormones, signaling molecules and a variety of secondary metabolites (CHENG et al., 2014).

3.4 KEGG pathway and GO enrichment analysis of identified DETs and DEGs during infestation by *D. saccharalis*

The mapping of metabolic pathways available by the Kyoto Encyclopedia of Genes and Genomes (KEGG) provides systematic classifications of gene functions. The KEGG enrichment analysis was conducted using the online software KOBAS 3.0 (WU et al., 2006). The enrichment was performed using the group of DETs and DEGs that were common and unique to each variety (See supplementary Tables S6 and S7, respectively).

Pathways associated with hormone biosynthesis and signaling, such as the “linoleic acid metabolism”, “alpha-linoleic acid metabolism”, “cysteine and methionine metabolism”, and “plant hormone signal transduction” are metabolic pathways known to be involved in hormone biosynthesis and signaling and to be up-regulated by herbivory. Some genes from these pathways were significantly enriched in up-regulated samples of DETs and DEGs (Figures 5A and 5B, respectively). Other pathways normally known to be down-regulated by herbivory are: “Photosynthesis – antenna proteins”; “Carbon fixation in photosynthetic organisms”; “Pyruvate metabolism”; and “Glycolisis/Gluconeogenesis”. The down-regulation of genes involved in these pathways were enriched mainly in DETs (Figure 6).

The overall pathway regulation suggests that biosynthesis of hormones and their regulators, as well as photosynthetic and sugar enzymes, are strongly mediated after *D. saccharalis* herbivory in sugarcane. The result also demonstrated that RB867515 has a more expressive transcriptional potential in comparison to SP80-3280 regarding the down-regulation of metabolic pathways involved in photosynthesis and sugar/carbon metabolism, suggesting that this variety might have an immediate energy switch by probably allocating more resources to defense mechanisms in order to cope with the pest attack (Figure 6).

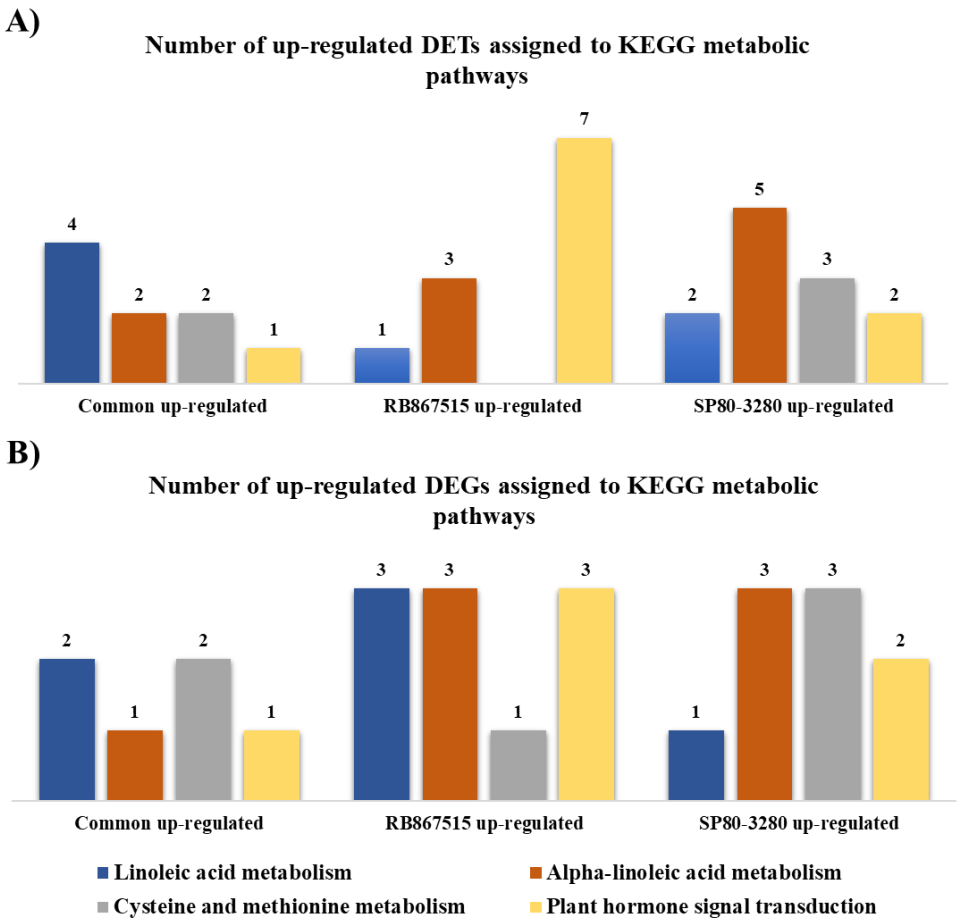

Figure 5. Histogram representation of KEGG metabolic pathways enriched to up-regulated DETs and DEGs of sugarcane infested wtih *D. saccharalis*. The y-axis indicates the number of DETs/DEGs assigned to a specific pathway, the x-axis indicates the KEGG pathway enriched in each regulation sample. (A) KEGG metabolic pathways enriched among DETs; (B) KEGG metabolic pathways enriched among DEGs.

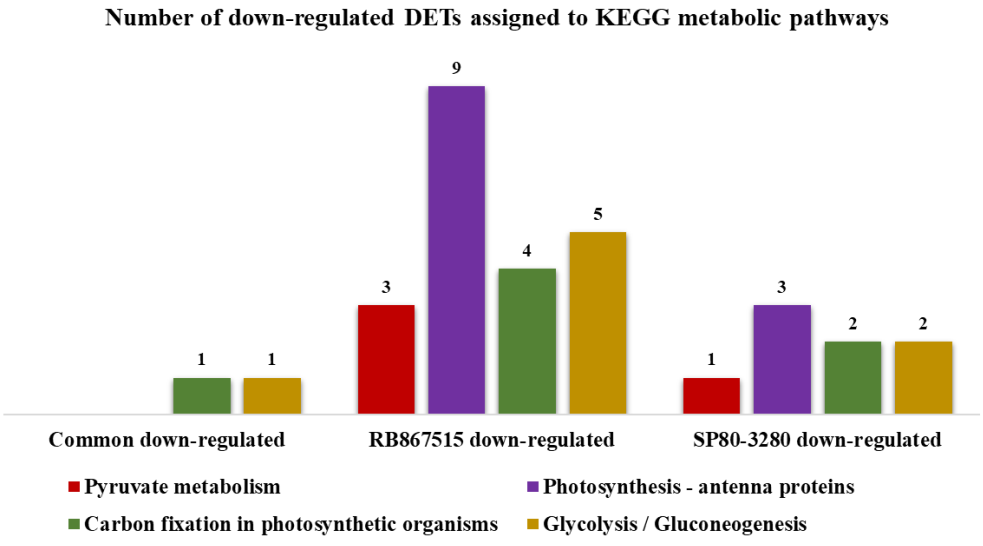

Figure 6. Histogram representation of KEGG metabolic pathways enriched to down-regulated DETs of sugarcane infested wtih *D. saccharalis*. The y-axis indicates the number of DETs assigned to a specific pathway, the x-axis indicates the KEGG pathway enriched in each regulation sample. In general, RB867515 demonstrated more DETs assigned to the considered pathways.

To better understand the regulation of the metabolic pathways, we illustrated the 10 most enriched pathways in up- and down-regulated DETs and DEGs in each variety (Figures 7 and 8, respectively), except for SP80-3280 down-regulated DEGs, which had only 5 enriched metabolic pathways (Figure 8B). The most distributed KEGG pathways among DETs in up-regulated samples from both varieties are involved in stress-related processes, including the biosynthesis of secondary metabolites and lignin ("phenylpropanoid biosynthesis"); hormone regulation and biosynthesis ("alpha-linoleic and linoleic acid metabolism"; "Plant hormone signal transduction"; "cysteine and methionine metabolism"); and amino acid metabolism ("biosynthesis of amino acids"; "phenylalanine, tyrosine and tryptophan biosynthesis"). In contrast, KEEG pathways in down-regulated DETs in both varieties showed regulation of general carbon metabolism processes ("carbon fixation in photosynthetic organisms"; pentose phosphate pathway, fructose and mannose pathway'; "photosynthesis"; "glycolysis and gluconeogenesis") (Figures 7A and 7B). Similar regulation patterns were observed in DEGs enrichment despite having fewer genes assigned per KEGG pathway (Figures 8A and 8B).

Other transcriptomal studies have demosntrated similar regulation patterns in enriched metabolic pathways in sugarcane submitted to other biotic and abiotic stresses, such as bacteria infection (SANTA BRIGIDA et al., 2016) and drought condition (BELESINI et al., 2017; PEREIRA-SANTANA et al., 2017; VITAL et al., 2017). Thus, apparently the regulation of these pathways is a common stress response in sugarcane and a network of specific gene regulations might appear to play a significant difference in conferring tolerance in genotypes alone.

Other general KEGG pathways, such as "metabolic pathways" and "biosynthesis of secondary metabolites" were both up- and down-regulated by RB867515 and SP80-3280 (Figures 7 and 8). These patterns were more expressive in RB867515 in terms of enrichment of DETs and DEGs, demonstrating that this variety might have a broader transcriptional capacity by probably augmenting and/or lowering expression of specific genes belonging to the above-mentioned pathways in favor of defense responses to cope with *D. saccharalis* herbivory.

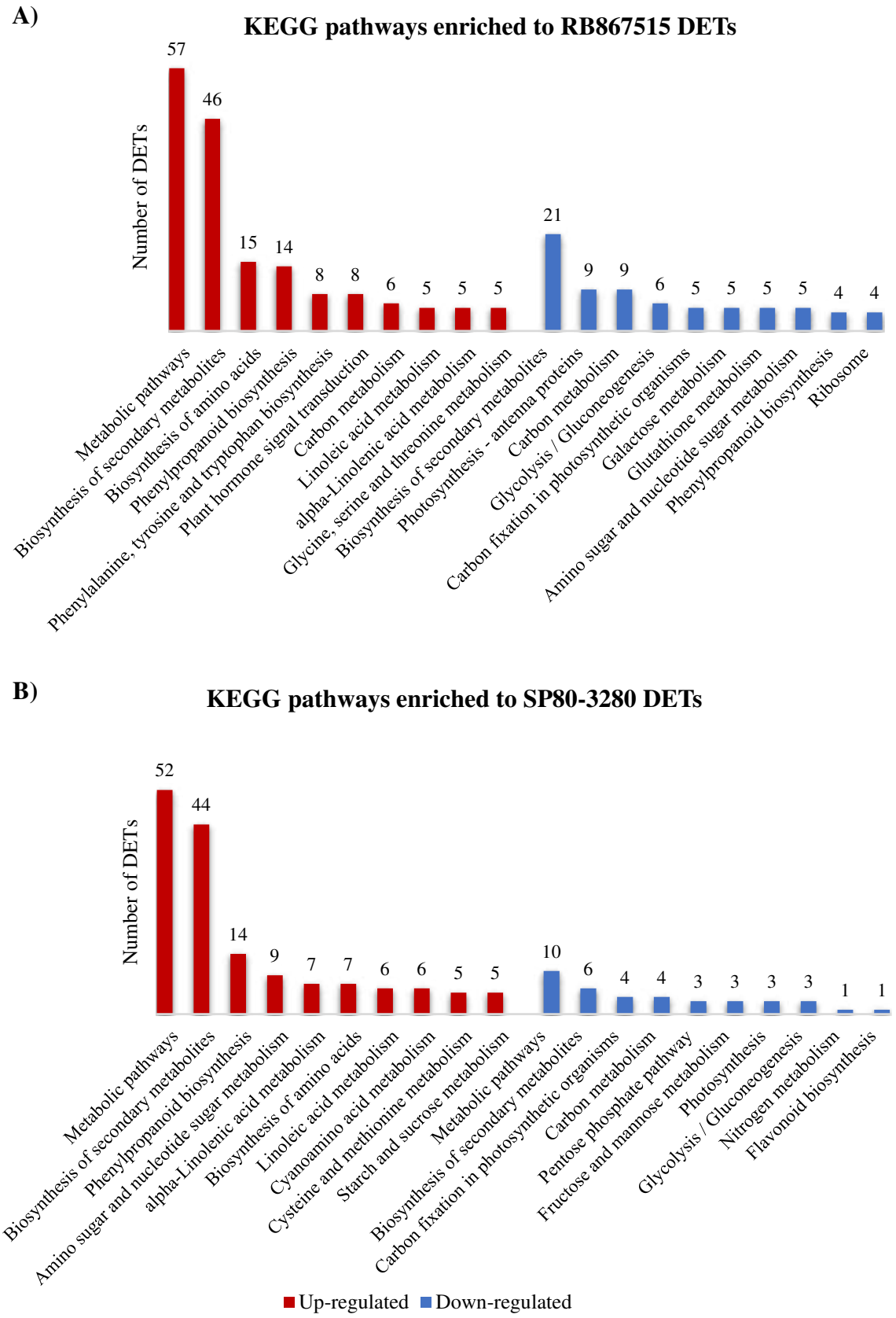

Figure 7. Top ten most significantly enriched KEGG pathways in two sugarcane varieties, RB867515 and SP80-3280, infested with *D. saccharalis*. Distribution of enriched KEGG pathways to up-regulated (red) and down-regulated (blue) DETs found in RB867515 (A) and SP80-3280 (B).

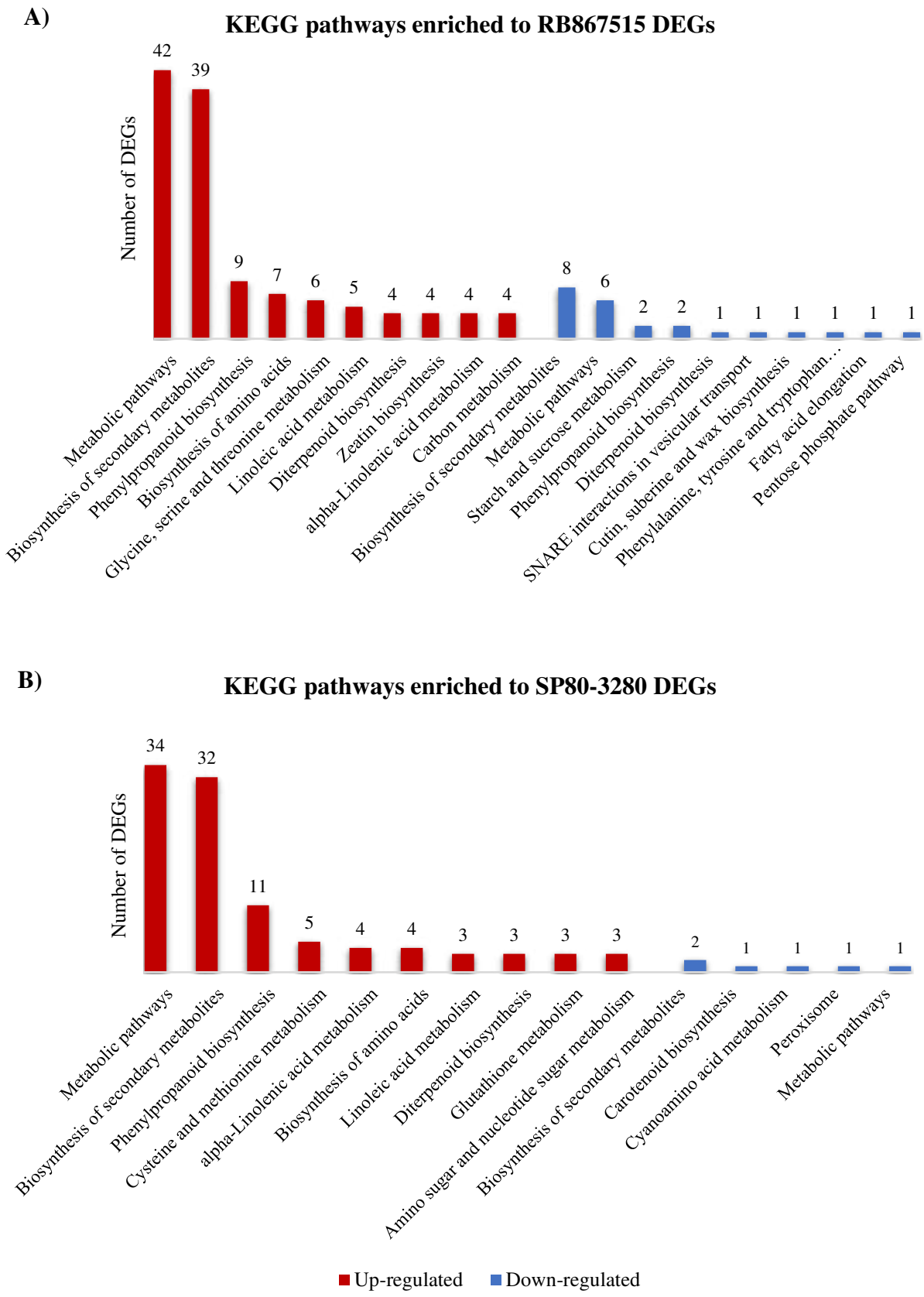

Figure 8. Top ten most significantly enriched KEGG pathways in two sugarcane varieties, RB867515 and SP80-3280, infested with *D. saccharalis*. Distribution of enriched KEGG pathways to up-regulated (red) and down-regulated (blue) DEGs found in RB867515 (A) and SP80-3280 (B).

Gene functions were classified using Gene Ontology (GO). DETs and DEGs were functionally attributed to three GO categories: biological process, molecular function and cellular component (See supplementary tables S8 and S9). In general, within the biological process category, we focused on GO terms reported to be involved in plant defense against herbivory, among them included: “response to wounding (GO:0009611)”, “response to jasmonic acid (GO:0009753)”, “jasmonic acid mediated signaling pathway (GO:0009867)”, and “oxylipin biosynthetic process (GO:0031408)”, which were found to be up-regulated (Figure 9A); and “photosynthesis (GO:0015979)”; “cellular glucan metabolic process”; “starch metabolic process”, and “generation of precursor metabolites and energy (GO:0006091)”, which were found to be down-regulated (Figure 9B). These GO terms were mainly distributed in DETs (Figure 9).

Compared to RB867515, fewer GO terms related to sugar/carbon metabolism were observed in SP80-3280 down-regulated DETs and DEGs (Figures 10B-D and 11B-D, respectively; and 9B). On the other hand, enrichment of SP80-3280 up-regulated DETs and DEGs has shown a more expressive regulation of sugar/carbon-related GO terms (Figures 10C and 11C, respectively), which demonstrates that this variety either does not alter energy metabolism in favor of defense metabolites or does not have an immediate energy switch to balance carbon allocation as verified in RB867515.

It has been demonstrated that carbon allocation and photosynthesis turnoff might be an advantageous strategy in response to herbivory. In plants, the photosynthetic and carbon metabolism might be compromised upon herbivory as a trade-off for the synthesis of defensive metabolites (ZHOU et al., 2015). Also, extensive review has suggested that transcriptional responses related to universal downregulation of photosynthesis-related gene expression is an adaptive response to biotic attack, which slow turnover of many photosynthetic proteins allows plants to invest resources in immediate defense needs without debilitating near term losses in photosynthetic capacity (BILGIN et al., 2010). Thus, according to KEGG and GO enrichment results, we hypothesize that RB867515 invest more resources in immediate defense mechanisms during *D. saccharalis* infestation, resulting in diminished expression of photosynthetic and sugar/carbon metabolism genes.

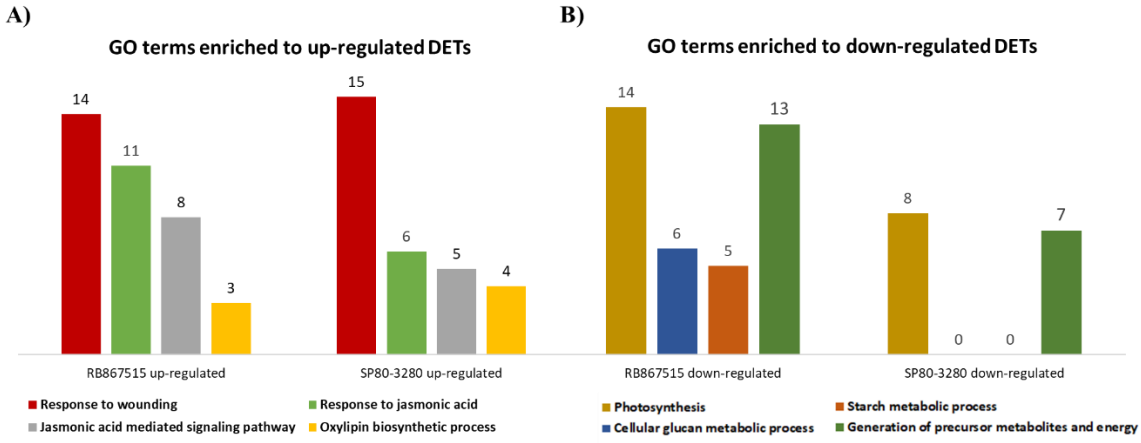

Figure 9. GO terms enriched to sugarcane down- and up-regulated DETs in two sugarcane varieties, RB867515 and SP80-3280. (A) Distribution of enriched GO terms enriched to RB867515 and SP80-3280 up-regulated DETs; (B) Distribution of enriched GO terms enriched to RB867515 and SP80-3280 down-regulated DETs.

3.4.1 DETs: KEGG pathways and GO terms profiles

A total of 211 DEGs were associated with 81 predicted KEGG metabolic pathways. There was a significant enrichment of 25 KEGG metabolic pathways among the common up-regulated DETs; 54 pathways unique to RB867515 up-regulated group; 44 pathways in the SP80-3280 up-regulated group; 41 pathways in the RB867515 down-regulated group; 16 pathways in the SP80-3280 down-regulated group and 7 pathways among the common down-regulated DETs (See supplementary Table S6). Considering the total number of DETs found for RB867515, 451 DETs were assigned to GO terms, and 214 GO terms were enriched, while 218 DETs were enriched to 150 GO terms in SP80-3280 (See supplementary Table S8). The most enriched DETs assigned to GO terms in each variety is shown in Figure 10.

3.4.1 DEGs: KEGG pathways and GO terms profiles

A total of 90 DEGs were associated with 66 predicted KEGG metabolic pathways. There was a significant enrichment of 30 KEGG metabolic pathways among the common up-regulated DEGs; 47 pathways in the RB86-7515 up-regulated group; 29 pathways in the SP80-3280 up-regulated group; 22 pathways in the RB86-7515 down-regulated group and 5 pathways in the SP80-3280 down-regulated group (See supplementary Table S7). None pathway was assigned to common down-regulated DEGs. GO enrichment analysis identified 127 enriched GO terms assigned to 288

DEGs for RB867515, and 129 GO terms enriched to 174 DEGs for SP80-3280 (See supplementary Table S9). The most enriched DEGs assigned to GO terms in each variety is shown in Figure 11.

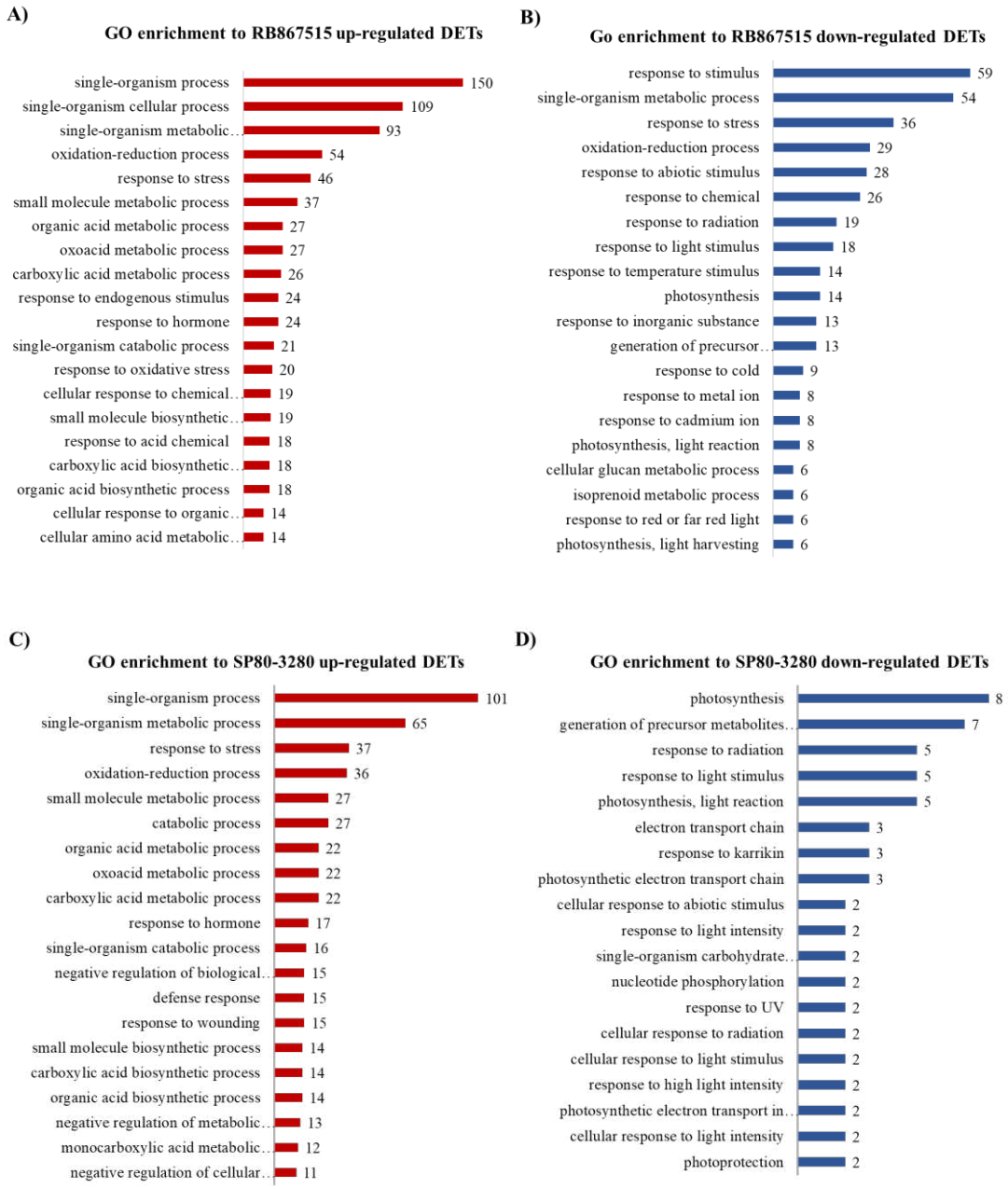

Figure 10. Most significantly enriched GO terms to DETs of sugarcane infested with *D. saccharalis*. (A) Distribution of enriched GO terms assigned to RB867515 up-regulated DETs; (B) Distribution of enriched GO terms assigned to RB867515 down-regulated DETs; (C) Distribution of enriched GO terms assigned to SP80-3280 up-regulated DETs; (D) Distribution of enriched GO terms assigned to SP80-3280 down-regulated DETs.

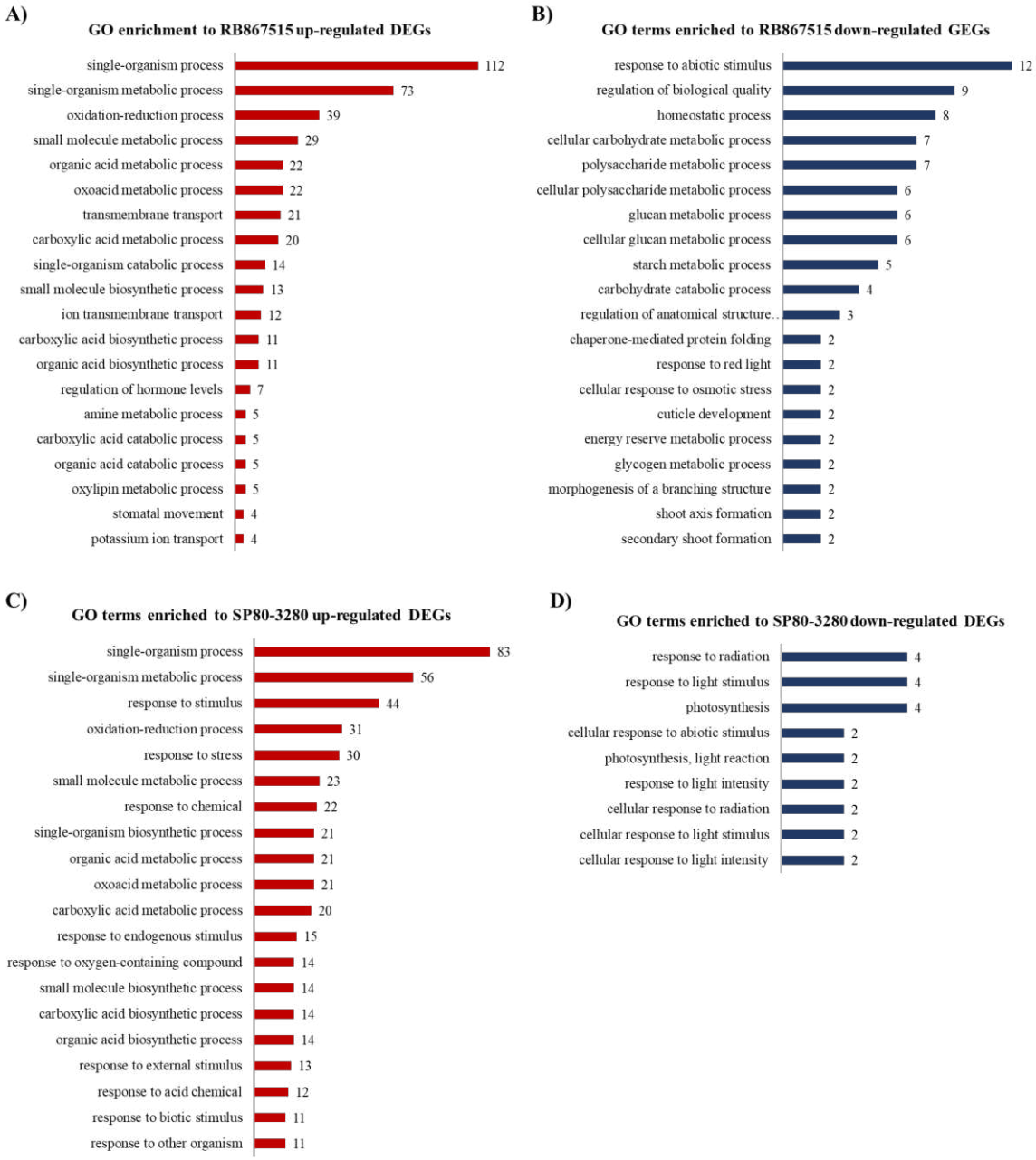

Figure 11. Most significantly enriched GO terms to DEGs of sugarcane infested with *D. saccharalis*. (A) Distribution of enriched GO terms assigned to RB867515 up-regulated DEGs; (B) Distribution of enriched GO terms assigned to RB867515 down-regulated DEGs; (C) Distribution of enriched GO terms assigned to SP80-3280 up-regulated DEGs; (D) Distribution of enriched GO terms assigned to SP80-3280 down-regulated DEGs.

3.5 Regulation of genes involved in the biosynthetic and signaling pathways of ET and JA after *D. saccharalis* infestation

Phytohormones are usually implicated in defense mechanisms against pests. Basically, hormones participate in signal transduction pathways, promoting cellular crosstalk communication and coordination of transcriptome changes. Analysis of differentially expressed transcripts and genes in this study revealed that the signaling

and biosynthetic pathways of ET and JA were upregulated in both varieties, suggesting the involvement of these molecules in the defense responses during infestation with *D. saccharalis* in sugarcane (See supplementary Table S10).

In infested treatments, key enzymes of the ET biosynthetic pathway, such as 1-aminocyclopropane-1-carboxylate synthase (ACS) and 1-aminocyclopropane-1-carboxylate oxidase (ACO), were upregulated (Figure 12). These enzymes belong to the "cysteine and methionine metabolism", an enriched KEGG metabolic pathway upon *D. saccharalis* infestation in this study. ACS is an enzyme that catalysis the synthesis of 1-aminocyclopropane-1-carboxylic acid from S-adenosyl methionine (SAM), and ACO catalyzes the last step of the ET biosynthetic pathway by converting 1-aminocyclopropane-1-carboxylic acid to ethylene (BOOKER; DELONG, 2015).

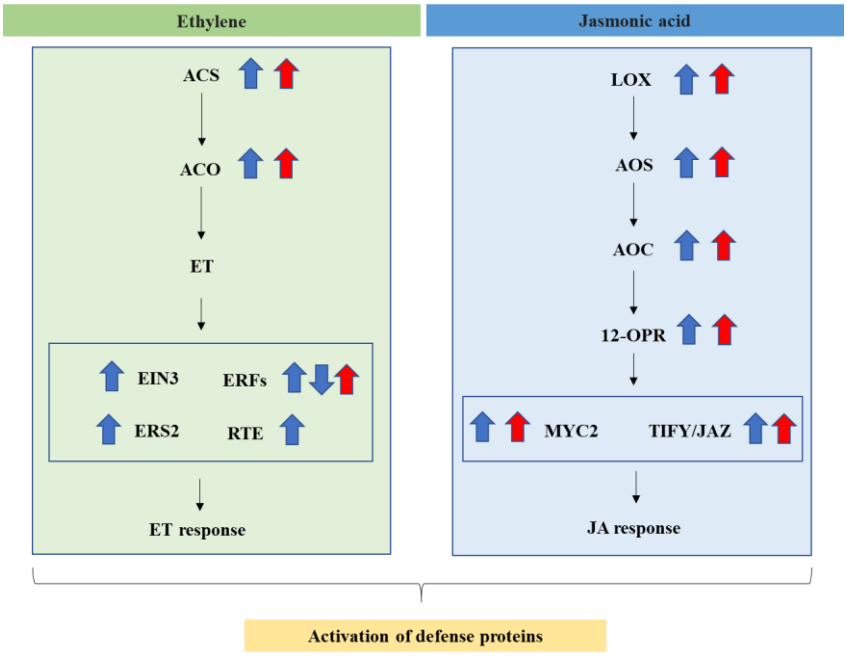

Figure 12. General hormonal responses implicated in sugarcane by *D. saccharalis* infestation. Genes related to the biosynthetic pathways of ET (left) and JA (right). Up- and down-pointed arrows correspond to up- and down regulation, respectively. Blue and red arrows correstond to regulation in RB867515 and SP80-3280, respectively.

ET signaling genes were also up-regulated, and among the annotated DETs and DEGs are included: ethylene-responsive factor (ERF), reversion-to-ethylene sensitivity (RTE), ethylene response sensor 2 (ERS2) and ethylene insensitive protein 3 (EIN3). These genes were more predominantly triggered in RB867515 after *D. saccharalis* infestation (See supplementary table S10). In overall, ERS2 belongs to a family of membrane-associated receptors responsible for recognizing ET (HUA; MEYEROWITZ, 1998); RTE is involved in the regulation of ET receptors and is described as a negative regulator of ET responses (RESNICK; RIVAROLA; CHANG,

2008); EIN3 and ERF transcription factors are involved in positively regulating ethylene responses (CHEN; ETHERIDGE; SCHALLER, 2005). These genes are reviewed to be responsible for triggering defenses against abiotic and insect herbivory (NGUYEN et al., 2016), but little is known about their interplay in sugarcane defense mechanisms against insect herbivory.

The JA and its derivatives have been recognized as key regulators in plant defense responses. The first steps in JA biosynthesis involve enzymes that participate in the "linoleic and alpha-linoleic acid metabolism", an enriched KEGG metabolic pathway in this study. During infestation with *D. saccharalis*, several DETs and DEGs belonging to the JA biosynthetic genes were annotated, such as lipoxygenase (LOX), allene oxide synthase (AOS), allene oxide cyclase (AOC), and 12-oxophytodienoate reductase (12-OPR). These enzymes participate in the oxylipin biosynthetic process, and more precisely they mediate the biosynthesis of JA and its derivatives from α-linoleic acid precursor via the octadecanoid pathway. The octadecanoid pathway has been reported to be involved in defense line mechanisms against biotic stresses (SANTINO et al., 2013). Here, LOX, AOS, AOC, and 12-OPR genes were up-regulated in both varieties (Figure 12). However, according to the RNA-seq data, these genes were more regulated in RB867515 in terms of expression level and number, an indication that the JA pathway is more activated in this variety upon herbivory (See supplementary Table S10).

Genes involved in JA signaling transduction pathway, such as jasmonate ZIM domain-containing protein (TIFY/JAZ) and MYC2 transcription factor, were found to be up-regulated in this study. Belonging to the "basic-helix-loop-helix (bHLH) related transcription factor" protein domain, MYC2 acts on the first line of signaling transduction after JA perception, positively modulating JA-dependent responses. Conversely, JAZ proteins are known to function as a repressor of MYC2 activity, posing a negative effect on the JA signaling pathway (PAUWELS et al., 2010). Considering DETs and DEGs, more TIFY/JAZ genes were assigned to SP80-3280, whereas more MYC2 genes were assigned to RB867515 (See supplementary Table S10). This indicates that RB867515 might have a better control of the interplay between JA repressors and promoters.

This hormonal regulation pattern indicates that larval herbivory by *D. saccharalis* triggers similar JA and ET genes in tolerant and susceptible varieties used in this study (Figure 12). However, some differences in number and regulation of DETs and DEGs annotated to these pathways were observed in both varieties, which could

represent different transcript isoforms of these genes and specific gene regulation that might be associated with defense mechanisms (See supplementary Table S10).

Other reports highlight the transcriptional changes of JA and ET related to the plant's defense responses under caterpillar infestation. For instance, using transcriptome sequencing and analysis, similar hormonal regulation results were identified in sugarcane submitted to infection with the bacterium *Acidovorax avena*e subsp. *avenae* (SANTA BRIGIDA et al., 2016), in corn infested with the borer *Ostrinia furcanalis* (WANG et al., 2017; YANG et al., 2015), and in cotton submitted to *Hellicoverpa armigera* larvae infestation (HUANG et al., 2015). Also, it has been demonstrated that particular LOX isoforms can play different signaling role in the regulation of plant growth and activation of stress-induced defense responses (CHEN et al., 2004) and confer tolerance against wounding and insect attack (WANG et al., 2008). Thus, it is speculated whether different genes of LOX identified in this study, or possible isoforms, could regulate defense-related genes and impair different levels of tolerance in sugarcane.

These findings collaborate to the importance and involvement of JA and ET in the responsive mechanisms and regulation of signaling networks against biotic stresses. However, because of the polyploidy characteristic of sugarcane and the array of identified DETs and DEGs assigned to these pathways, further molecular investigation on single transcripts and genes could elucidate associations with specific phenotypic responses of sugarcane to *D. saccharalis* herbivory.

3.6 Regulation of defense-related genes

3.6.1 Proteinase/Peptidase inhibitors

Generally, the recognition of insect elicitors by the plant´s receptors triggers signaling transduction pathways that leads to the synthesis and accumulation of defense-associated proteins. Plant proteinases or peptidases are an example of plant-defense proteins produced upon herbivory. These proteins have an antidigestive activity, acting on digestive enzymes synthesized by insects upon feeding, and thereby impairing the insect digestion, which consequently affects insect growth and development (JADHAV et al., 2016).

In this study, we identified a wide array of DETs and DEGs with a peptidase annotation. In summary, annotations included: "Bowman-Birk type bran trypsin

inhibitor and Bowman-Birk type trypsin inhibitor (BBTI)", "Bowman-Birk type wound-induced proteinase inhibitor WIP1 (BBWIP1)", "Subtilisin Chymotrypisin inhibitor-2B (SCI-2B)", "Subtilisin Chymotrypisin inhibitor-2A (SCI-2A)", "maize proteinase inhibitor (MPI)", "Serine carboxypeptidase II-3", "Serine carboxypeptidase like-2", "Serine carboxypeptidase 2", "Cysteine proteinase 1", "Cysteine proteinase 2", and "Metalloendoproteinase 2MMP (MP)". Interesting, DETs and DEGs assigned to BBTI, BBWIP1, SCI-2B were up-regulated in both varieties, and DEGs assigned to SCI-2A were only up-regulated in SP80-3280, suggesting that these genes play a role in the defense against *D. saccharalis* attack. MPI and MP were only up-regulated by RB867515. On the other hand, serine carboxypeptidase like-2 were only down-regulated in RB867515, whereas serine carboxypeptidase II-3 and 2 were up-regulated by both varieties. Cysteine inhibitor was only down-regulated in RB867515. Regulation of proteinase inhibitors with respective log_2 fold changes is shown in supplementary Table S11.

Similar regulation patterns for these proteinase inhibitors have been reported for sugarcane under *D. saccharalis* artificial attack using the same hybrid cultivar SP80-3280 (MEDEIROS et al., 2016). In addition to the regulation pattern, the authors verified that Bowman-Birk inhibitor genes have different levels of expression when submitted to *D. saccharalis* attack and to wounding, suggesting that these proteins have a specific-triggering line of defense, which might be involved in the recognition of insect-specific elicitors. Up-regulation and accumulation of proteinase inhibitors have also been reported in maize infested with the leaf-eater *Spodoptera frugiperda* (ANKALA et al., 2013), maize infested with the stem-borer *Ostrinia furcanalis* (YANG et al., 2015), and also in sugarcane after *D. saccharalis* infestation (MEDEIROS et al., 2012). It has been demonstrated that JA is involved in the synthesis of secondary metabolites including plant-defense proteins in certain species. For example, exogenous JA treatment induced the expression of pathogenesis related genes (PRs) in rice (YANG; YANG; HE, 2013). In sugarcane, JA-treated plants demonstrated certain resistance to *D. saccharalis* (SANCHES et al., 2017), which could be associated with regulation of defense proteins.

3.6.2 Chitinases

Chitinases are glycosyl hydrolases found in a wide range of organisms to serve specific functions. Here, we identified that most of the DETs and DEGs with a

"Glycoside hydrolase" protein domain was up-regulated in both varieties. Besides, most of the up-regulated chitinase-related DETs and DEGs was mediated by SP80-3280 variety (See supplementary Table S11).

It has been demonstrated that chitinases have an antifungal activity in plants, playing important role in defense mechanisms, inclusive in sugarcane (TARIQ et al., 2018). Despite mostly studied for its antifungal properties, chitinases are also a protective agent against insects, attacking on chitin molecules that compose the insect's skeleton. For long it has been verified an augment of chitinase expression under biotic stress, including insect attack, and this pattern has caught the attention to be involved in defense mechanisms. The defensive effects of chitinase genes have been reported in some species, including resistance of tomato against Colorado potato beetle (LAWRENCE; NOVAK, 2006) and transgenic corn, expressing a chitinase gene, against *Spodoptera littoralis* (OSMAN et al., 2015). However, the role of the sugarcane chitinase family genes remains unclear due to the highly heterozygous and aneuploidy chromosome genetic background of sugarcane (SU et al., 2015).

3.6.3 Patatin-like proteins

Patatins are reported to have a phospholipase activity, hydrolyzing membrane lipids to produce free polyunsaturated fatty acids, such as linolenic acid, that serves as a substrate for the synthesis of JA in response to stress (YANG et al., 2012). In this study, we found 6 DETs with a "Patatin" domain and all were annotated as "Patatin-like proteins 1 (PLP1)". Most of the DETs were commonly up-regulated by both varieties, none Patatin annotation was down-regulated, and one Patatin DET was unique to SP80-3280. None DEG with a patatin annotation was found to be differentially expressed in both varieties (See supplementary Table S11).

So far, most of the studies with patatin-like protein (PLPs) have been conducted in *Arabidopsis thaliana* regarding pathogen resistance. One such work proposed that the acyl hydrolyzing activity of PLP in *A. thaliana* is involved in maintaining the homeostatic pool of basal free fatty acids and JA, which in turn plays a positive role in defense responses against the fungus *Botrytis cinerea* (YANG et al., 2007). Also, a patatin isoform demonstrated inhibition of *Diabrotica* larval growth in corn, possibly having a mode of action involving lipid metabolism (STRICKLAND; WALSH, 1995). In *Nicotiana attenuata*, however, a PLP gene negatively affected plant resistance to the fungus *Alternaria alternata* likely by suppressing JA and ethylene biosynthetic gene

expression (CHENG; SONG; WU, 2018). Thus, PLPs seem to respond differently according to species and biotic stress exposed, and it is speculated whether these proteins might have different mode of actions due to presence of isoforms or polymorphisms among the different DETs observed in sugarcane.

3.6.4 Peroxidases

Peroxidases (PODs) are antioxidative enzymes mainly known for scavenging reactive oxygen species (ROS). Plant peroxidases have many forms, which are encoded by multi gene families. Besides ROS-scavenging activity, several utilities of peroxidases have been reported in plants, including defense against insect herbivory and many other stress related stimuli, acting as an important component of the immediate response of plants to insect damage. (RANI; JYOTHSNA, 2010).

Peroxidase was among the most regulated GF in this study. There were 17 DETs and 8 DEGs assigned to the "Plant Peroxidase" protein domain (See supplementary Table S11). Among them, 6 DETs were commonly up-regulated between the varieties, 5 DETs were uniquely up-regulated in RB867515, 5 DETs uniquely down-regulated in RB867515, and 2 DETs were up-regulated in SP80-3280. The same regulation pattern was observed in DEGs: 3 of them commonly up-regulated in both varieties, 1 unique to RB867515 up-regulated sample, 2 unique to SP80-3280 up-regulated sample, and 2 unique to RB867515 down-regulated sample. This POD regulation pattern and its annotation diversity suggest that different peroxidase genes, and probably different isoforms, are mediated for defense mechanisms in sugarcane upon herbivory.

It has been demonstrated that a peroxisomal catalase, another ROS scavenger enzyme, which also belongs to a multi-gene family, is responsive to biotic stresses and is suggested to be involved in the protection of sugarcane against oxidant-related environment stimuli (SU et al., 2014). Also, it has been shown that ROS burst can activate lipoxygenases to initiate the biosynthesis of oxylipins such as JA (PORTA; ROCHA-SOSA, 2002), process that could be associated with an increase of POD synthesis to counter-balance the negative effects of ROSs. The large number of POD genes in sugarcane together with the diversity of processes catalyzed by peroxidases suggests possible functional specialization of each isoform, but assigning a precise role for each individual peroxidase gene has continued to be a major bottleneck (CESARINO et al., 2012). Since *D. saccharalis* infestation resulted in differential

expression of PODs, a closer-detailed investigation could reveal new insights into function and specificity of peroxidase-related DETs and DEGs found in this work.

3.6.5 Lignin biosynthesis

Besides providing structural support for land plants, lignin also confers plants with resistance mechanisms to support biotic and abiotic stresses. Lignin accumulation plays an important role in the process of plant resistance to insect and can be used as a barrier directly or through the associated hormone signal pathway to increase insect resistance of plants (LIU; LUO; ZHENG, 2018). In general, lignin is a product of the phenylpropanoid pathway and a heteropolymer built from hydroxycinnamyl alcohol monolignols: p-coumaryl alcohol, coniferyl alcohol, and sinapyl alcohol (VANHOLME et al., 2010).

Genes involved in the biosynthetic pathway of lignin were regulated in this study. Cinnamoyl-CoA reductase (CCR), 4-coumarate:CoA ligase (4CL), and hydroxycinnamoyltransferase (HCT) are enzymes that participate in monolignol biosynthesis and were regulated after *D. saccharalis* infestation (See supplementary Table S11). In overall, most of the DEGs and DETs annotated to CCR, HCT and 4CL were up-regulated by SP80-3280, indicating that this variety transcriptionally tend to reinforce its structures upon *D. saccharalis* infestation.

The complex enzymatic machinery named “Cellulose synthase (CS)”, responsible for cellulose biosynthesis and indirectly involved in lignin biosynthesis, was significantly regulated in this study. It has been shown that reduced levels of cellulose synthesis can lead to lignin accumulation mediated in part by JA and ethylene, leading to defense responses in *Arabidopsis thaliana*. (PEN et al., 2003). Besides regulating common biosynthetic genes of lignin, RB867515 also showed a down- and up-regulation of CS, demonstrating its transcriptional versatility to mediate lignin biosynthesis upon biotic stress (See supplementary Table S11).

4 CONCLUSION

This study provides an overview of the transcriptomic changes of sugarcane in response to *D. saccharalis* infestation. A set of 12 RNA libraries were generated from 2 varieties that possess different behavior facing the pest attack. The differential expression analysis results, along with GO and KEGG enrichment, showed that *D. saccharalis* infestation triggers a wide array of stress/defense-related genes. Among them are genes involved in the ET/JA biosynthetic and signaling pathways and in the synthesis of defense proteins. These genes were highly regulated in this study, specially in RB867515. Compared to SP80-3280, RB867515 also demonstrated an expressive down-regulation of photosynthesis and sugar/carbon metabolism pathways, a process that might be advantageous for allocating energy resources for defense mechanisms after *D. saccharalis* insfestation.

We suggest that JA and ET genes are involved in the regulation of defense-related proteins found in this study and down-regulation of photosynthesis and sugar/carbon metabolism pathways might act as a tolerance mechanism to boost defense responses. Some differences regarding the regulation levels of common genes between the studied varieties and the presence of unique DETs and DEGs in these pathways deserve further investigation. Thus, a more detailed investigation of nucleotide polymorphisms among DETs and DEGs could give insight into how gene regulation is mediated between the two varieties after infestation with *D. saccharalis.* Furthermore, future analysis of phenotypic association with regulated genes identified in this work could open the opportunity for the development of molecular markers related to tolerance against *D. saccharalis* in sugarcane.

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6 SUPPLEMENTARY MATERIAL

Table S1. Annotation of up- and down-regulated DETs with the respective log_2 fold change (log_2 FC) of two sugarcane varieties (RB867515 and SP80-3280) after *Diatraea saccharalis* infestation.

SUGIT ID	Log_2 FC (RB867515)	Log_2 FC (SP80-3280)	Blast2GO Description
			Common up-regulated DETs
GFHJ01095263.1	8.24586184	3.367788436	aromatic-L-amino-acid decarboxylase-like
GFHJ01050454.1	6.535704064	6.32374012	O-methyltransferase ZRP4
GFHJ01062052.1	6.171868429	6.239688311	O-methyltransferase ZRP4
GFHJ01008843.1	6.092539205	3.922552621	Patatin-like protein 1
GFHJ01085645.1	6.050779233	2.085071736	chemocyanin precursor
GFHJ01031806.1	6.045340337	4.970105645	patatin-like protein 1
GFHJ01008846.1	5.849621829	5.189733003	Patatin-like protein 1
GFHJ01064634.1	5.762701153	4.806771715	patatin-like protein 1
GFHJ01063132.1	5.3927389	6.81231589	gibberellin 2-beta-dioxygenase
GFHJ01035233.1	5.150404783	3.280488328	indole-2-monooxygenase
GFHJ01060610.1	5.106730053	3.877041972	Peroxidase N
GFHJ01020952.1	5.023919636	3.878285425	Peroxidase 59
GFHJ01040277.1	4.944119514	3.814476291	benzoate carboxyl methyltransferase
GFHJ01020944.1	4.905457839	5.285110088	Peroxidase 59
GFHJ01086482.1	4.822191342	2.890047395	beta-sesquiphellandrene synthase-like isoform X1
GFHJ01009337.1	4.674901908	4.687749395	patatin-like protein 1
GFHJ01058630.1	4.646091905	2.407987733	1-aminocyclopropane-1-carboxylate oxidase
GFHJ01024452.1	4.488776986	2.323548485	putative WRKY transcription factor 71
GFHJ01061489.1	4.381209074	2.000717775	gibberellin 2-beta-dioxygenase 3-like
GFHJ01008499.1	4.047196372	1.404780891	amino acid transporter ANTL1-like
GFHJ01066042.1	3.943806283	4.150489112	Protein P21
GFHJ01083093.1	3.888303792	4.232093953	Inactive TPR repeat-containing thioredoxin TTL3
GFHJ01085227.1	3.786906625	2.88766325	Bowman-Birk type bran trypsin inhibitor
GFHJ01104898.1	3.786236118	1.982029181	cytochrome P450 94C1
GFHJ01097366.1	3.758038036	2.450412519	subtilisin-chymotrypsin inhibitor-2B
GFHJ01033164.1	3.730211554	2.893511884	acyl transferase 15
GFHJ01053310.1	3.728606534	1.672803522	mitogen-activated protein kinase kinase kinase 17
GFHJ01035099.1	3.717438422	1.938327013	Type IV inositol polyphosphate 5-phosphatase 9
GFHJ01095424.1	3.669615635	4.080929249	protein TIFY 5
GFHJ01107262.1	3.614275706	1.613953693	Protein kinase superfamily protein
GFHJ01041106.1	3.595736518	1.478033753	1-aminocyclopropane-1-carboxylate synthase
GFHJ01058226.1	3.494379887	1.575196242	protein TIFY 11e
GFHJ01023677.1	3.255385691	3.448981296	xylanase inhibitor protein 1
GFHJ01093561.1	3.157094326	3.471773307	---NA---
GFHJ01067577.1	3.152882391	1.486099326	Secoisolariciresinol dehydrogenase
GFHJ01030575.1	3.10119378	2.010984708	formate dehydrogenase 2, mitochondrial

GFHJ01100258.1	2.959839992	1.389363142	ZIM motif family protein
GFHJ01053958.1	2.955155897	1.401707736	cytochrome P450 94C1
GFHJ01029350.1	2.948520748	2.783777619	cytochrome P450 714C3
GFHJ01065012.1	2.883915314	1.278180898	---NA---
GFHJ01064115.1	2.723896592	2.644704676	putative transcription factor bHLH041
GFHJ01073695.1	2.700989813	1.443472132	putative 2-oxoglutarate-dependent dioxygenase
GFHJ01047957.1	2.642816374	1.173227276	Linoleate 9S-lipoxygenase 2
GFHJ01103467.1	2.531715572	3.223057918	phytosulfokines 2
GFHJ01048883.1	2.500410939	1.856504802	probable 2-oxoglutarate-dependent dioxygenase At5g05600
GFHJ01047708.1	2.481235556	1.222585718	putative linoleate 9S-lipoxygenase 3
GFHJ01079850.1	2.477794928	2.213678304	uncharacterized protein LOC8083096
GFHJ01065386.1	2.451637893	3.489893542	chitinase
GFHJ01066378.1	2.440978215	1.028792796	cytokinin dehydrogenase 5
GFHJ01033111.1	2.41364288	0.984380094	disease resistance protein RPS2
GFHJ01017539.1	2.400336856	1.294895509	probable linoleate 9S-lipoxygenase 4
GFHJ01098986.1	2.354475928	1.833621533	negatively light-regulated protein
GFHJ01027133.1	2.351624964	1.886343801	probable 2-oxoglutarate-dependent dioxygenase At3g111800
GFHJ01015592.1	2.263752245	1.294329286	linoleate 9S-lipoxygenase5
GFHJ01062542.1	2.223214505	2.650601216	uncharacterized protein LOC112902147
GFHJ01040677.1	2.191922161	1.074818051	Auxin response factor 7
GFHJ01023235.1	2.17855807	1.584188059	hypothetical protein SORBI_3007G042150
GFHJ01063084.1	2.078130204	1.183280533	hypothetical protein PAHAL_1G065700
GFHJ01080409.1	2.068759104	1.567298777	transcription factor DIVARICATA
GFHJ01070230.1	2.066266848	1.753380052	RHOMBOID-like protein 2
GFHJ01079768.1	2.040542137	2.611791578	uncharacterized protein LOC8083096
GFHJ01018680.1	2.04031549	1.321285685	allene oxide synthase 2
GFHJ01091797.1	1.933692288	1.271633756	S-norcoclaurine synthase 1 isoform X2
GFHJ01094296.1	1.928731959	2.285206369	B12D protein
GFHJ01105622.1	1.92060734	2.124187345	TPA_exp: putative phytosulfokine peptide precursor
GFHJ01080410.1	1.812613705	1.378199028	peroxidase 47
GFHJ01066585.1	1.790795501	1.600826844	soluble inorganic pyrophosphatase
GFHJ01081877.1	1.774674999	0.918644267	transcription factor bHLH168
GFHJ01025477.1	1.758603551	1.603987227	cytokinin oxidase 3
GFHJ01047146.1	1.726529044	2.133069103	C4-specific pyruvate orthophosphate dikinase
GFHJ01010968.1	1.709808719	0.818973439	cell wall invertase
GFHJ01038917.1	1.681170427	0.540549518	putative polygalacturonase
GFHJ01028527.1	1.660299497	1.582735499	L-aspartate oxidase chloroplastic
GFHJ01101439.1	1.613658846	1.509134288	putative lipid-transfer protein DIR1
GFHJ01031231.1	1.594080009	1.140695347	cationic peroxidase 1
GFHJ01063438.1	1.543279961	0.883564713	myb-related protein P
GFHJ01049628.1	1.440221053	1.052102457	probable polygalacturonase At1g80170
GFHJ01022916.1	1.438929197	0.843794141	probable disease resistance protein RF9 isoform X1
GFHJ01037736.1	1.412873614	0.830931282	potassium channel AKT2
GFHJ01039690.1	1.400792585	0.863660427	putative UPF0481 protein At3g02645
GFHJ01050005.1	1.383993415	1.119398703	probable sarcosine oxidase

GFHJ01029121.1	1.355913085	1.48152826	NAC domain-containing protein 79
GFHJ01096902.1	1.352483427	3.068463102	subtilisin-chymotrypsin inhibitor-2B
GFHJ01060415.1	1.27704898	0.615532554	bidirectional sugar transporter SWEET2b
GFHJ01077565.1	1.256741087	1.063440731	thioredoxin M2, chloroplastic
GFHJ01016962.1	1.246491722	0.726209228	sulfite exporter TauE/SafE family protein 4
GFHJ01090167.1	1.244883548	1.067345605	uncharacterized protein LOC100277551
GFHJ01038506.1	1.229198479	0.619264251	peroxidase 5
GFHJ01039929.1	1.228077861	0.55133984	Tryptophan synthase beta chain 2
GFHJ01075912.1	1.205391751	1.168948313	PLAT/LH2 domain
GFHJ01022012.1	1.140815469	1.046612684	serine carboxypeptidase II-3
GFHJ01012804.1	1.109459131	0.553943221	anthranilate synthase alpha subunit 2, chloroplastic
GFHJ01061966.1	1.022215255	1.267132002	probable glycerol-3-phosphate acyltransferase 3
GFHJ01092362.1	0.99294942	0.622674171	Methyltransferase-related protein
GFHJ01057103.1	0.970233376	0.568119017	epoxide hydrolase 2
GFHJ01020748.1	0.964247169	0.556932002	4-coumarate--CoA ligase-like 4
GFHJ01034905.1	0.894083048	0.79607905	transcription factor BIM1
GFHJ01022680.1	0.672615006	0.732300084	Retinol dehydrogenase 14
			RB867517 up-regulated DETs
GFHJ01105200.1	7.301690337	----------	hypothetical protein SORBI_3009G076500
GFHJ01049966.1	6.495539746	----------	polygalacturonase inhibitor
GFHJ01044440.1	6.425615496	----------	xanthine dehydrogenase
GFHJ01001666.1	6.024686786	----------	---NA---
GFHJ01079377.1	5.694507527	----------	beta-sesquiphellandrene synthase-like
GFHJ01082474.1	5.461928623	----------	myb-related protein Myb4
GFHJ01086498.1	5.276588462	----------	inactive TPR repeat-containing thioredoxin TTL3
GFHJ01043455.1	5.246734623	----------	beta-sesquiphellandrene synthase-like
GFHJ01101716.1	5.134108531	----------	VQ motif
GFHJ01080600.1	4.874456381	----------	xylanase inhibitor protein 1
GFHJ01080434.1	4.772891164	----------	probable 2-oxoglutarate-dependent dioxygenase At3g111800
GFHJ01006695.1	4.724092362	----------	cytochrome P450
GFHJ01098465.1	4.649285322	----------	uncharacterized protein LOC8060516
GFHJ01091956.1	4.496841876	----------	hypothetical protein GQ55_5G004900
GFHJ01002520.1	4.451005559	----------	uncharacterized protein LOC112898057
GFHJ01074758.1	4.296915192	----------	---NA---
GFHJ01099402.1	4.115339846	----------	Bowman-Birk type wound-induced proteinase inhibitor WIP1
GFHJ01106068.1	4.070889551	----------	hypothetical protein ZEAMMB73_Zm00001d003485
GFHJ01091853.1	3.96971042	----------	Fructose-bisphosphate aldolase cytoplasmic isozyme
GFHJ01086879.1	3.731072297	----------	transcription factor bHLH13-like
GFHJ01100468.1	3.644291044	----------	uncharacterized protein LOC8055401
GFHJ01011951.1	3.498310374	----------	G-type lectin S-receptor-like serine/threonine-protein kinase At2g19130
GFHJ01086966.1	3.472950261	----------	flowering-promoting factor 1-like protein 1
GFHJ01041963.1	3.462490802	----------	cytochrome P450 72A11
GFHJ01011746.1	3.46204653	----------	AAA-ATPase At3g28580
GFHJ01096735.1	3.460293443	----------	putative methyltransferase DDB_G0268948
GFHJ01099985.1	3.35143009	----------	uncharacterized protein CG5098

GFHJ01107030.1	3.333639438	----------	aspartic proteinase isoform X4
GFHJ01019663.1	3.33232623	----------	putative disease resistance RPP13-like protein 1
GFHJ01096383.1	3.298169128	----------	hypothetical protein Zm00014a_028659
GFHJ01052559.1	3.262368585	----------	hypothetical protein SORBI_3005G217700
GFHJ01065666.1	3.186804642	----------	protein DMR6-LIKE OXYGENASE 2
GFHJ01031600.1	3.177794255	----------	nodulation-signaling pathway 2 protein
GFHJ01102192.1	3.17499236	----------	rho guanine nucleotide exchange factor 18
GFHJ01095719.1	3.152368015	----------	subtilisin-chymotrypsin inhibitor-2B
GFHJ01100704.1	3.128100004	----------	pyruvate decarboxylase
GFHJ01058695.1	3.104200146	----------	uncharacterized protein LOC112894808
GFHJ01003682.1	3.060855287	----------	hypothetical protein SORBI_3008G075400
GFHJ01088340.1	3.048259562	----------	ethylene-responsive transcription factor ERF109
GFHJ01007560.1	2.982023771	----------	disease resistance protein RPS2 isoform X1
GFHJ01074010.1	2.944229478	----------	transcription factor bHLH35
GFHJ01056527.1	2.902115715	----------	bifunctional protein FolD 2
GFHJ01000238.1	2.888790709	----------	---NA---
GFHJ01055933.1	2.888748415	----------	transcription factor JAMYB
GFHJ01086631.1	2.876323325	----------	putative WRKY transcription factor 50
GFHJ01092670.1	2.7868084	----------	nuclear protein
GFHJ01062343.1	2.736857769	----------	transcription factor bHLH129 isoform X2
GFHJ01065621.1	2.698223827	----------	helix-loop-helix DNA-binding domain containing protein
GFHJ01098099.1	2.689796902	----------	maize proteinase inhibitor
GFHJ01078900.1	2.662721474	----------	uncharacterized protein LOC8058985
GFHJ01081036.1	2.662175086	----------	probable WRKY transcription factor 57
GFHJ01015468.1	2.613986249	----------	receptor-like protein kinase RK20-1 precursor
GFHJ01024721.1	2.584986917	----------	protein trichome birefringence-like 21
GFHJ01104477.1	2.537603724	----------	Spc97 / Spc98 family of spindle pole body (SBP) component
GFHJ01067301.1	2.474665029	----------	late embryogenesis abundant protein-related / LEA protein-related
GFHJ01102517.1	2.47051931	----------	uncharacterized protein LOC8083979
GFHJ01077005.1	2.431458199	----------	Arogenate dehydratase/prephenate dehydratase 6, chloroplastic
GFHJ01054110.1	2.400809511	----------	probable cytokinin riboside 5'-monophosphate phosphoribohydrolase LOGL1
GFHJ01011303.1	2.356319335	----------	putative ABC transporter C family member 15 isoform X1
GFHJ01047960.1	2.319264371	----------	Linoleate 9S-lipoxygenase 2
GFHJ01022330.1	2.314466555	----------	solute carrier family 35 member F1
GFHJ01096342.1	2.305255209	----------	WRKY transcription factor
GFHJ01099021.1	2.264008129	----------	hypothetical protein BAE44_0016826
GFHJ01028958.1	2.255411629	----------	wall-associated receptor kinase 2
GFHJ01100957.1	2.234081873	----------	hypothetical protein
GFHJ01105595.1	2.184640572	----------	uncharacterized protein LOC103629542
GFHJ01032322.1	2.156374418	----------	peroxidase P7
GFHJ01096374.1	2.149042912	----------	transcription factor bHLH35
GFHJ01086616.1	2.102833534	----------	bidirectional sugar transporter SWEET11
GFHJ01002484.1	2.097988399	----------	---NA---
GFHJ01047486.1	2.09312022	----------	putative glucosyl transferase
GFHJ01028182.1	2.083044085	----------	salutaridine reductase

GFHJ01099274.1	2.078421594	----------	negatively light-regulated protein
GFHJ01070132.1	1.999752142	----------	Peroxidase 12
GFHJ01104501.1	1.980277801	----------	protein app1
GFHJ01077665.1	1.970623013	----------	WRKY transcription factor
GFHJ01055347.1	1.956232886	----------	WAT1-related protein
GFHJ01098283.1	1.939943533	----------	uncharacterized protein LOC8075191
GFHJ01098790.1	1.918208559	----------	cytochrome P450 94C1-like
GFHJ01093177.1	1.898284189	----------	basic blue protein
GFHJ01100715.1	1.88634676	----------	uncharacterized LOC103627704
GFHJ01005838.1	1.866107911	----------	arogenate dehydratase/prephenate dehydratase 6, chloroplastic
GFHJ01101410.1	1.850133971	----------	GDSL esterase/lipase
GFHJ01086593.1	1.845267331	----------	putative polygalacturonase
GFHJ01045724.1	1.819958489	----------	putative pectinesterase/pectinesterase inhibitor 7
GFHJ01025646.1	1.814214096	----------	B3 domain-containing protein Os03g0120900 isoform X1
GFHJ01020662.1	1.788148562	----------	cytochrome P450 71A1
GFHJ01107207.1	1.763328466	----------	40S ribosomal protein S4-3
GFHJ01058474.1	1.756942245	----------	L-gulonolactone oxidase 2-like
GFHJ01056273.1	1.748062331	----------	hypothetical protein Shy3280Sca034_059
GFHJ01068348.1	1.7448955	----------	hevamine-A precursor
GFHJ01057794.1	1.741296609	----------	expansin 92
GFHJ01009411.1	1.720359491	----------	SPX domain-containing membrane protein
GFHJ01036694.1	1.694760757	----------	amino acid permease 3
GFHJ01100741.1	1.674292509	----------	Sex determination protein tasselseed-2
GFHJ01043266.1	1.660821929	----------	F-box/kelch-repeat protein At1g74510-like
GFHJ01026590.1	1.631544675	----------	acyl transferase 9
GFHJ01102346.1	1.619686475	----------	transcription factor MYB2
GFHJ01054187.1	1.619410301	----------	transcription factor bHLH35
GFHJ01031964.1	1.614475417	----------	magnesium/proton exchanger 1
GFHJ01050020.1	1.607911818	----------	berberine bridge enzyme-like 8
GFHJ01088940.1	1.607628447	----------	cytokinin dehydrogenase 4
GFHJ01023603.1	1.601372704	----------	hypersensitive-induced response protein-like protein 2
GFHJ01056112.1	1.577711105	----------	synaptotagmin-3 isoform X3
GFHJ01095343.1	1.559785139	----------	uncharacterized protein LOC8059815
GFHJ01030835.1	1.542505876	----------	basic helix-loop-helix (bHLH) DNA-binding superfamily protein
GFHJ01025648.1	1.537876658	----------	putative ABC transporter B family member 8
GFHJ01065730.1	1.530098169	----------	gibberellin 2-beta-dioxygenase
GFHJ01039456.1	1.508207325	----------	multidrug resistance protein associated1
GFHJ01076443.1	1.50387288	----------	E3 ubiquitin-protein ligase RZFP34-like isoform X1
GFHJ01083310.1	1.499350078	----------	probable glutathione S-transferase GSTU6
GFHJ01079503.1	1.49033521	----------	DNA binding protein
GFHJ01099159.1	1.486822986	----------	uncharacterized LOC100284300
GFHJ01034903.1	1.481696935	----------	transcription factor BIM1
GFHJ01071337.1	1.47638068	----------	uncharacterized protein LOC8070769
GFHJ01099823.1	1.453962564	----------	putative ABC transporter B family member 8
GFHJ01010817.1	1.447338579	----------	Disease resistance protein RPM1

GFHJ01062836.1	1.43910198	----------	putative laccase-17
GFHJ01055953.1	1.435627329	----------	cation transport protein chaC
GFHJ01068021.1	1.432312745	----------	hypothetical protein SETIT_8G042300v2
GFHJ01079979.1	1.431541139	----------	gamma-glutamyl peptidase 3
GFHJ01101185.1	1.426744777	----------	uncharacterized protein LOC8085386
GFHJ01099284.1	1.410334107	----------	uncharacterized protein LOC8079293
GFHJ01073517.1	1.409840947	----------	nodulin protein
GFHJ01009875.1	1.407187472	----------	cis-zeatin O-glucosyltransferase 1
GFHJ01029600.1	1.406565763	----------	acetolactate synthase/ amino acid binding protein
GFHJ01100685.1	1.380349742	----------	protein FATTY ACID EXPORT 4, chloroplastic
GFHJ01104167.1	1.376817254	----------	auxin-responsive protein IAA16
GFHJ01016930.1	1.376412366	----------	CBL-interacting serine/threonine-protein kinase 15
GFHJ01057648.1	1.364901755	----------	phosphoenolpyruvate/phosphate translocator 3, chloroplastic
GFHJ01056479.1	1.359927671	----------	O-methyltransferase ZRP4
GFHJ01084511.1	1.355980462	----------	14 kDa proline-rich protein DC2.15
GFHJ01047738.1	1.353230014	----------	trans-cinnamate 4-monooxygenase
GFHJ01034732.1	1.352626889	----------	ABC transporter C family member 10
GFHJ01080352.1	1.350455205	----------	ferritin-1, chloroplastic-like
GFHJ01058620.1	1.348761089	----------	E3 ubiquitin-protein ligase RZFP34
GFHJ01077120.1	1.345895295	----------	transcription factor bHLH128
GFHJ01026592.1	1.345746122	----------	acyl transferase 9
GFHJ01061110.1	1.336881398	----------	thaumatin-like protein 1b
GFHJ01092711.1	1.328308563	----------	uncharacterized protein LOC8058984
GFHJ01018364.1	1.324097998	----------	predicted protein
GFHJ01054358.1	1.311547368	----------	GEM-like protein 4
GFHJ01047488.1	1.307776357	----------	UDP-glycosyltransferase 83A1
GFHJ01049786.1	1.302269086	----------	probable protein phosphatase 2C 48
GFHJ01104025.1	1.291949949	----------	uncharacterized protein LOC8055740
GFHJ01021634.1	1.291388035	----------	putative cellulose synthase A catalytic subunit 6 [UDP-forming]
GFHJ01006030.1	1.291188583	----------	allene oxide synthase 1, chloroplastic
GFHJ01062563.1	1.290238704	----------	Thiamine pyrophosphokinase 1
GFHJ01053148.1	1.280221281	----------	haloacid dehalogenase-like hydrolase domain-containing protein Sgpp isoform X1
GFHJ01079523.1	1.279504211	----------	expansin-like A3
GFHJ01049084.1	1.27633125	----------	indole-3-glycerol phosphate synthase, chloroplastic
GFHJ01008907.1	1.27625702	----------	inosine-5'-monophosphate dehydrogenase
GFHJ01092524.1	1.271154693	----------	uncharacterized protein LOC110429809
GFHJ01052770.1	1.253923825	----------	amino acid permease 3
GFHJ01019894.1	1.252690135	----------	serine/threonine-protein kinase RIPK
GFHJ01030827.1	1.248330704	----------	transcription factor bHLH157
GFHJ01003895.1	1.24486228	----------	---NA---
GFHJ01025647.1	1.244527022	----------	putative ABC transporter B family member 8
GFHJ01033779.1	1.243260308	----------	potassium transporter 1
GFHJ01020674.1	1.237030389	----------	rhomboid-like protein 19
GFHJ01088882.1	1.233618396	----------	putative gamma-glutamylcyclotransferase At3g02910
GFHJ01032944.1	1.217158423	----------	CMP-sialic acid transporter 4

GFHJ01063311.1	1.215889726	----------	D-3-phosphoglycerate dehydrogenase 2, chloroplastic
GFHJ01097835.1	1.215646155	----------	soluble acid invertase
GFHJ01006204.1	1.214606998	----------	ATP binding protein
GFHJ01107170.1	1.211681801	----------	40S ribosomal protein S4-3
GFHJ01017291.1	1.206664105	----------	threonine dehydratase biosynthetic, chloroplastic
GFHJ01032945.1	1.197721134	----------	CMP-sialic acid transporter 4
GFHJ01088501.1	1.194858282	----------	gamma-glutamyl peptidase 3
GFHJ01058998.1	1.194503665	----------	protein REVERSION-TO-ETHYLENE SENSITIVITY1-like
GFHJ01101068.1	1.188672455	----------	polygalacturonase At1g48100-like
GFHJ01053520.1	1.178571019	----------	Magnesium-chelatase subunit ChlH chloroplastic
GFHJ01006163.1	1.169263972	----------	chaperone protein
GFHJ01095350.1	1.167260246	----------	cyclin-T1-1 isoform X2
GFHJ01018852.1	1.159765136	----------	uncharacterized protein At4g15970
GFHJ01037378.1	1.150080633	----------	probable protein phosphatase 2C 48
GFHJ01030758.1	1.147107474	----------	cytochrome P450 CYP73A100
GFHJ01054214.1	1.141372509	----------	cytochrome P450 72A14
GFHJ01107352.1	1.137303262	----------	40S ribosomal protein S4-3
GFHJ01046275.1	1.134488315	----------	potassium channel protein ZMK2
GFHJ01020273.1	1.126820021	----------	pheophorbide a oxygenase, chloroplastic
GFHJ01101150.1	1.125425329	----------	hypothetical protein SETIT_5G371700v2
GFHJ01095331.1	1.12482256	----------	cortical cell-delineating protein
GFHJ01022453.1	1.119676165	----------	Potassium transporter 18
GFHJ01073427.1	1.113888742	----------	uncharacterized protein LOC8057839
GFHJ01080807.1	1.113855845	----------	cationic peroxidase SPC4-like
GFHJ01013004.1	1.111146904	----------	putative fructokinase 1
GFHJ01029953.1	1.096670329	----------	putative pectin methyltransferase QUA2
GFHJ01091662.1	1.085150408	----------	protein YLS3-like
GFHJ01079712.1	1.082156892	----------	fructose-bisphosphate aldolase 3, chloroplastic
GFHJ01107158.1	1.081494832	----------	40S ribosomal protein S4-3
GFHJ01065023.1	1.081411111	----------	allene oxide cyclase, chloroplastic
GFHJ01016511.1	1.079072936	----------	epoxide hydrolase 2
GFHJ01026724.1	1.066563509	----------	UDP-glycosyltransferase 73C3
GFHJ01050752.1	1.065459372	----------	Lecithin-cholesterol acyltransferase-like 1
GFHJ01002462.1	1.064375795	----------	---NA---
GFHJ01096899.1	1.064123519	----------	ubiquitin
GFHJ01045627.1	1.060657422	----------	putative peptide/nitrate transporter
GFHJ01094117.1	1.053849466	----------	uncharacterized protein LOC8058547
GFHJ01065981.1	1.050878683	----------	OSJNBb0045P24.5-like protein
GFHJ01001480.1	1.046197378	----------	---NA---
GFHJ01024529.1	1.044571563	----------	amino acid permease 3
GFHJ01081853.1	1.043910777	----------	---NA---
GFHJ01107261.1	1.036141223	----------	40S ribosomal protein S4-3
GFHJ01096431.1	1.034563724	----------	glucan endo-1,3-beta-glucosidase 8
GFHJ01086005.1	1.027968444	----------	ATP sulfurylase 2
GFHJ01012460.1	1.015572262	----------	aquaporin NIP2-2

GFHJ01055571.1	1.012212249	----------	phosphoinositide phosphatase SAC2
GFHJ01094871.1	1.009853034	----------	transcription factor bHLH112
GFHJ01060404.1	1.003857588	----------	protein NRT1/ PTR FAMILY 5.10
GFHJ01094138.1	1.000309748	----------	receptor-like protein kinase HAIKU2
GFHJ01033642.1	0.986752102	----------	calcium-dependent protein kinase 13
GFHJ01013640.1	0.985599615	----------	catalytic/ hydrolase isoform X1
GFHJ01006127.1	0.982365898	----------	ABC transporter C family member 3
GFHJ01038441.1	0.97844071	----------	probable ethylene response sensor 2
GFHJ01021401.1	0.969615404	----------	Phospholipid-transporting ATPase 1
GFHJ01022452.1	0.968898707	----------	Potassium transporter 10
GFHJ01058890.1	0.965437157	----------	Protein ULTRAPETALA 1
GFHJ01060941.1	0.965025798	----------	rac-like GTP-binding protein 3
GFHJ01099936.1	0.961272643	----------	Bowman-Birk type trypsin inhibitor
GFHJ01106271.1	0.959039178	----------	hypothetical protein ZEAMMB73_Zm00001d026339, partial
GFHJ01056016.1	0.952551048	----------	NAD(P)-binding Rossmann-fold superfamily protein
GFHJ01028868.1	0.9453884	----------	auxin response factor 7
GFHJ01030139.1	0.941955222	----------	histidine kinase1
GFHJ01017479.1	0.93776584	----------	uncharacterized protein LOC8063402
GFHJ01107548.1	0.93644545	----------	cytosolic invertase 1
GFHJ01082110.1	0.936223937	----------	thioredoxin M3, chloroplastic
GFHJ01011391.1	0.934390868	----------	CBL-interacting protein kinase 23
GFHJ01035485.1	0.927501272	----------	glycosyltransferase family 92 protein Os08g0121900
GFHJ01023629.1	0.927000382	----------	cysteine-rich receptor-like protein kinase 6
GFHJ01023170.1	0.926069109	----------	hypothetical protein SORBI_3002G026100, partial
GFHJ01060409.1	0.922617188	----------	type IV inositol polyphosphate 5-phosphatase 7
GFHJ01097097.1	0.913923526	----------	auxin-responsive protein SAUR36
GFHJ01003852.1	0.908602598	----------	---NA---
GFHJ01098274.1	0.904083414	----------	nonspecific lipid-transfer protein AKCS9 precursor
GFHJ01024443.1	0.897234453	----------	Fructose-bisphosphate aldolase 3, chloroplastic
GFHJ01095558.1	0.886108901	----------	non-specific lipid-transfer protein-like protein At2g13820
GFHJ01013307.1	0.88028726	----------	purple acid phosphatase precursor
GFHJ01093788.1	0.875860867	----------	---NA---
GFHJ01019807.1	0.873430036	----------	probable methyltransferase PMT18
GFHJ01070084.1	0.869281902	----------	cell number regulator 13
GFHJ01042717.1	0.868914051	----------	putative 12-oxophytodienoate reductase 11
GFHJ01021896.1	0.862746935	----------	probable WRKY transcription factor 2
GFHJ01023928.1	0.861806059	----------	protein TIFY 6b
GFHJ01055544.1	0.859316613	----------	putative WRKY transcription factor 34
GFHJ01093659.1	0.855869895	----------	mini zinc finger protein 1
GFHJ01013955.1	0.855065081	----------	Bifunctional aspartate aminotransferase and glutamate/aspartate-prephenate aminotransferase
GFHJ01065695.1	0.853013515	----------	transcription factor MYB74
GFHJ01024559.1	0.847557567	----------	abhydrolase domain-containing protein C22H12.03
GFHJ01053160.1	0.841719949	----------	neutral/alkaline invertase
GFHJ01072822.1	0.827156901	----------	remorin 4.1
GFHJ01040802.1	0.818978196	----------	peroxidase 4

GFHJ01101737.1	0.815452791	----------	probable receptor-like protein kinase At4g10390
GFHJ01073065.1	0.815242438	----------	Protein TIFY 10a
GFHJ01103099.1	0.814776987	----------	uncharacterized LOC100304006 precursor
GFHJ01040547.1	0.814107162	----------	Phosphatidylinositol 4-kinase gamma 7
GFHJ01053198.1	0.80898752	----------	probable polyamine oxidase 2
GFHJ01086333.1	0.807563406	----------	Zn-dependent exopeptidase superfamily protein
GFHJ01073294.1	0.805750335	----------	transcription factor bHLH112
GFHJ01043445.1	0.801702817	----------	BEL1-like homeodomain protein 7
GFHJ01052774.1	0.79895989	----------	sulfite exporter TauE/SafE family protein 4
GFHJ01041176.1	0.791692801	----------	5-enolpyruvylshikimate-3-phosphate synthase (plastid)
GFHJ01004876.1	0.78598789	----------	---NA---
GFHJ01095823.1	0.783616368	----------	hypothetical protein SORBI_3007G032300
GFHJ01009649.1	0.782866848	----------	probable low-specificity L-threonine aldolase 2
GFHJ01095596.1	0.776952624	----------	hypoxia induced protein conserved region containing protein
GFHJ01088438.1	0.762777415	----------	D-3-phosphoglycerate dehydrogenase 3, chloroplastic
GFHJ01045097.1	0.762501864	----------	Chloride channel protein CLC-c
GFHJ01040602.1	0.751524337	----------	mitogen-activated protein kinase 4
GFHJ01020758.1	0.749101042	----------	protein NLP1
GFHJ01043393.1	0.737527702	----------	probable leucine-rich repeat receptor-like protein kinase At5g49770
GFHJ01035116.1	0.734438294	----------	putative 1-phosphatidylinositol-3-phosphate 5-kinase FAB1C
GFHJ01059381.1	0.728265055	----------	aquaporin NIP2-2
GFHJ01077519.1	0.716731829	----------	probable C-terminal domain small phosphatase
GFHJ01034880.1	0.711838928	----------	NADPH--cytochrome P450 reductase
GFHJ01050268.1	0.710040817	----------	peroxidase 42
GFHJ01017832.1	0.703655574	----------	Haloacid dehalogenase-like hydrolase (HAD) superfamily protein
GFHJ01095827.1	0.700172718	----------	maternal effect embryo arrest 59
GFHJ01025467.1	0.697927508	----------	probable glycerol-3-phosphate dehydrogenase [NAD(+)] 1, cytosolic
GFHJ01020586.1	0.695555607	----------	putative LRR receptor-like serine/threonine-protein kinase
GFHJ01021939.1	0.690545278	----------	ETHYLENE INSENSITIVE 3-like 3 protein
GFHJ01039778.1	0.689717956	----------	protein argonaute PNH1
GFHJ01061978.1	0.688733309	----------	MADS-box transcription factor 4
GFHJ01001460.1	0.680860737	----------	cullin-1 isoform X1
GFHJ01029986.1	0.668824153	----------	NHL domain-containing protein
GFHJ01007499.1	0.661891934	----------	sodium/hydrogen exchanger 2
GFHJ01077821.1	0.658298014	----------	thioredoxin-like 3-3
GFHJ01039988.1	0.656048957	----------	uncharacterized protein LOC8077349
GFHJ01053228.1	0.654855877	----------	ATP sulfurylase 2
GFHJ01028757.1	0.644140344	----------	Cycloartenol synthase
GFHJ01006559.1	0.643107631	----------	TBC1 domain family member 5 homolog B-like
GFHJ01079710.1	0.639876287	----------	septum-promoting GTP-binding protein 1
GFHJ01092994.1	0.628759746	----------	Phospho-2-dehydro-3-deoxyheptonate aldolase 2 chloroplastic
GFHJ01060526.1	0.628666775	----------	putative methyltransferase
GFHJ01038518.1	0.590119497	----------	receptor-like protein kinase HERK 1
GFHJ01017319.1	0.587552449	----------	probable glucan 1,3-beta-glucosidase A
GFHJ01062789.1	0.583422083	----------	bidirectional sugar transporter SWEET2a

GFHJ01068924.1	0.573782257	----------	homeobox-leucine zipper protein HOX15
GFHJ01052731.1	0.559398001	----------	Lipase
GFHJ01031243.1	0.547474888	----------	probable serine/threonine-protein kinase PBL8
GFHJ01037316.1	0.52993822	----------	P-loop containing nucleoside triphosphate hydrolase superfamily protein
GFHJ01047726.1	0.522757989	----------	AC090485_10Putative retroelement
GFHJ01041178.1	0.511595556	----------	Actin-1
GFHJ01045557.1	0.496818578	----------	wall-associated receptor kinase 2
GFHJ01079792.1	0.486632098	----------	protein SRC2 homolog
GFHJ01045135.1	0.479878751	----------	OSJNBa0089E12.13-like protein
			SP80-3280 up-regulated DETs
GFHJ01024502.1	----------	8.597527291	dihydroflavonol 4-reductase
GFHJ01054996.1	----------	6.461669489	tyrosine N-monooxygenase-like
GFHJ01082897.1	----------	5.744724523	thaumatin-like pathogenesis-related protein 4
GFHJ01073642.1	----------	5.601083081	hypothetical protein SORBI_3003G405200
GFHJ01094860.1	----------	5.3368513	stress-response A/B barrel domain-containing protein At5g22580
GFHJ01027635.1	----------	5.173648043	(S)-beta-bisabolene synthase
GFHJ01067327.1	----------	4.982467815	acetylserotonin O-methyltransferase 3-like isoform X1
GFHJ01022108.1	----------	4.923876818	protein PIN-LIKES 3 isoform X1
GFHJ01086460.1	----------	4.77016545	Hevein-like preproprotein
GFHJ01067101.1	----------	4.721071186	Cinnamoyl-CoA reductase 1
GFHJ01049444.1	----------	4.564984837	beta-sesquiphellandrene synthase-like
GFHJ01025729.1	----------	4.226881131	putative pectinesterase/pectinesterase inhibitor 41
GFHJ01080813.1	----------	4.120982926	acidic endochitinase
GFHJ01075831.1	----------	4.021259336	salicylate carboxymethyltransferase
GFHJ01057202.1	----------	3.997603017	cinnamoyl-CoA reductase 1
GFHJ01097420.1	----------	3.940565458	rRNA intron-encoded homing endonuclease
GFHJ01097445.1	----------	3.837191556	dirigent protein 11-like
GFHJ01086877.1	----------	3.662832366	EG45-like domain containing protein
GFHJ01081719.1	----------	3.485421527	zeamatin-like protein
GFHJ01106503.1	----------	3.010935707	---NA---
GFHJ01094901.1	----------	2.969560887	---NA---
GFHJ01097912.1	----------	2.908286947	subtilisin-chymotrypsin inhibitor-2B
GFHJ01062466.1	----------	2.745359037	basic 7S globulin
GFHJ01090340.1	----------	2.725431386	pathogenesis-related protein 5
GFHJ01021532.1	----------	2.725055039	alpha-amylase isozyme 3C
GFHJ01107271.1	----------	2.686777146	---NA---
GFHJ01077203.1	----------	2.602611227	pathogenesis-related protein 5
GFHJ01048138.1	----------	2.544476136	beta-sesquiphellandrene synthase
GFHJ01018851.1	----------	2.536043983	cyanohydrin beta-glucosyltransferase
GFHJ01083194.1	----------	2.519058354	tonoplast dicarboxylate transporter
GFHJ01103113.1	----------	2.485540636	hydroxycinnamoyltransferase 4
GFHJ01096061.1	----------	2.481171019	Bowman-Birk type wound-induced proteinase inhibitor WIP1
GFHJ01096577.1	----------	2.469474274	subtilisin-chymotrypsin inhibitor-2B
GFHJ01084293.1	----------	2.459628252	endochitinase A
GFHJ01059363.1	----------	2.387268855	salicylate carboxymethyltransferase

GFHJ01031815.1	----------	2.343721126	P-(S)-hydroxymandelonitrile lyase-like isoform X1
GFHJ01043086.1	----------	2.324246512	putative 4-coumarate--CoA ligase 3
GFHJ01046286.1	----------	2.313952979	triacylglycerol lipase-like 1
GFHJ01083759.1	----------	2.266576521	triacylglycerol lipase-like 1
GFHJ01031813.1	----------	2.208055975	P-(S)-hydroxymandelonitrile lyase-like isoform X1
GFHJ01087603.1	----------	2.159443217	RHOMBOID-like protein 2
GFHJ01059406.1	----------	2.112514096	9-cis-epoxycarotenoid dioxygenase 1, chloroplastic
GFHJ01084013.1	----------	2.062607117	protein TIFY 9
GFHJ01059808.1	----------	2.053918911	acetolactate synthase/ amino acid binding protein
GFHJ01011348.1	----------	2.028056457	carbohydrate transporter/ sugar porter/ transporter
GFHJ01022738.1	----------	2.02371374	GDSL esterase/lipase EXL3
GFHJ01053885.1	----------	1.996330566	starch binding domain containing protein
GFHJ01091681.1	----------	1.958790569	putative lipid-transfer protein DIR1
GFHJ01092359.1	----------	1.931586552	E3 ubiquitin-protein ligase EL5
GFHJ01031254.1	----------	1.915238307	probable apyrase 3
GFHJ01025128.1	----------	1.862360202	Carbohydrate transporter/ sugar porter/ transporter
GFHJ01084254.1	----------	1.85347392	hypothetical protein GQ55_5G013300
GFHJ01023951.1	----------	1.825858655	carbohydrate transporter/ sugar porter/ transporter
GFHJ01096130.1	----------	1.823298773	copper transport protein CCH
GFHJ01057403.1	----------	1.787336395	flavonoid O-methyltransferase-like protein Os11g0303600
GFHJ01024041.1	----------	1.785913584	uncharacterized protein LOC8055685
GFHJ01018660.1	----------	1.749534358	allene oxide synthase 2
GFHJ01063107.1	----------	1.746373818	chitinase 8
GFHJ01106208.1	----------	1.730419843	uncharacterized protein LOC8064712
GFHJ01014227.1	----------	1.727765323	oxysterol-binding protein-related protein 1B
GFHJ01091541.1	----------	1.725095255	uncharacterized protein LOC8066974
GFHJ01021927.1	----------	1.717757715	tonoplast dicarboxylate transporter
GFHJ01069446.1	----------	1.714246018	xylanase inhibitor protein 1
GFHJ01078083.1	----------	1.705647548	alpha-humulene synthase isoform X1
GFHJ01038040.1	----------	1.661767276	pyruvate decarboxylase 1
GFHJ01097974.1	----------	1.645401091	Bowman-Birk type trypsin inhibitor
GFHJ01055926.1	----------	1.629059673	NAC domain-containing protein 68
GFHJ01102776.1	----------	1.622994912	VQ motif family protein
GFHJ01073898.1	----------	1.622303506	esterase precursor
GFHJ01044133.1	----------	1.571738244	auxin Efflux Carrier family protein isoform X1
GFHJ01090827.1	----------	1.566384522	chaperone protein dnaJ
GFHJ01015521.1	----------	1.548071997	Phospholipase A1-Ibeta2, chloroplastic
GFHJ01088748.1	----------	1.52688772	hypothetical protein BAE44_0000149
GFHJ01098145.1	----------	1.526795089	subtilisin-chymotrypsin inhibitor-2B
GFHJ01096495.1	----------	1.51928336	zinc finger protein 1
GFHJ01094034.1	----------	1.513117616	copper transporter 5.1
GFHJ01064943.1	----------	1.506000369	chitinase 2
GFHJ01093164.1	----------	1.464285377	uncharacterized protein LOC8070745
GFHJ01101640.1	----------	1.463684637	unknow protein
GFHJ01018676.1	----------	1.447861768	allene oxide synthase 2

GFHJ01093930.1	----------	1.439321661	PLAT domain-containing protein 3
GFHJ01093329.1	----------	1.396350068	unknow protein
GFHJ01025132.1	----------	1.384335102	Carbohydrate transporter/ sugar porter/ transporter
GFHJ01094711.1	----------	1.367632531	linoleate 9S-lipoxygenase 2
GFHJ01076652.1	----------	1.318957189	Protein TIFY 11c
GFHJ01023623.1	----------	1.283777888	Cysteine-rich receptor-like protein kinase 25
GFHJ01081835.1	----------	1.274887402	putative serine acetyltransferase 1
GFHJ01020013.1	----------	1.273740156	leucine-rich repeat extensin-like protein 6
GFHJ01010892.1	----------	1.273218671	NAC domain-containing protein 68
GFHJ01056038.1	----------	1.264173276	peroxidase 47
GFHJ01035611.1	----------	1.241774959	External alternative NAD(P)H-ubiquinone oxidoreductase B4 mitochondrial
GFHJ01055904.1	----------	1.238057962	psbP domain-containing protein 7, chloroplastic
GFHJ01065581.1	----------	1.233584622	beta-carotene 3-hydroxylase, chloroplastic
GFHJ01058655.1	----------	1.221430582	alpha carbonic anhydrase 7
GFHJ01032203.1	----------	1.219221234	ABC transporter B family member 19
GFHJ01020226.1	----------	1.203393473	FAD/NAD(P)-binding oxidoreductase family protein
GFHJ01089295.1	----------	1.166654678	zinc finger protein 1-like
GFHJ01075569.1	----------	1.16547026	beta-sesquiphellandrene synthase
GFHJ01068839.1	----------	1.158612776	probable glutathione S-transferase GSTU6 isoform X1
GFHJ01066245.1	----------	1.150466511	WRKY transcription factor WRKY24
GFHJ01084771.1	----------	1.144346607	AP2/ERF and B3 domain-containing protein Os05g0549800
GFHJ01043591.1	----------	1.138776321	GDSL esterase/lipase At5g45910-like
GFHJ01044700.1	----------	1.133544617	sugar transport protein MST4
GFHJ01100243.1	----------	1.130346674	TPA_exp: putative phytosulfokine peptide precursor
GFHJ01037104.1	----------	1.121308657	putative receptor protein kinase ZmPK1
GFHJ01096817.1	----------	1.120548275	subtilisin-chymotrypsin inhibitor-2B
GFHJ01070808.1	----------	1.120157689	chitinase
GFHJ01028750.1	----------	1.11618344	benzoate O-methyltransferase
GFHJ01063249.1	----------	1.115508508	NAC1
GFHJ01048669.1	----------	1.102411684	DIBOA-glucoside dioxygenase BX6
GFHJ01047959.1	----------	1.093556284	Linoleate 9S-lipoxygenase 2
GFHJ01014022.1	----------	1.041039738	asparagine synthetase
GFHJ01065519.1	----------	1.038646977	Tropinone reductase-like protein
GFHJ01023723.1	----------	1.028058824	enolase 1, chloroplastic
GFHJ01086813.1	----------	1.018765585	AAA-ATPase ASD, mitochondrial
GFHJ01010899.1	----------	1.007932857	NAC protein
GFHJ01024366.1	----------	1.003939601	cytosolic sulfotransferase 5
GFHJ01059284.1	----------	1.001367923	ribonuclease 1
GFHJ01040678.1	----------	0.99004636	Auxin response factor 7
GFHJ01031863.1	----------	0.981371464	glycine-rich domain-containing protein 1
GFHJ01014829.1	----------	0.963947233	receptor-like protein kinase RK20-1
GFHJ01048793.1	----------	0.963689923	amino acid transporter AVT6C isoform X1
GFHJ01048585.1	----------	0.947344538	crocetin glucosyltransferase 2
GFHJ01014659.1	----------	0.941487103	cysteine synthase
GFHJ01022146.1	----------	0.933064	UDP-glucuronate 4-epimerase 6

GFHJ01046606.1	----------	0.880702245	isoamylase 1, chloroplastic
GFHJ01031810.1	----------	0.876599572	patatin-like protein 1
GFHJ01074552.1	----------	0.843497146	probable glutathione S-transferase GSTU6
GFHJ01069555.1	----------	0.840161588	Short-chain dehydrogenase TIC 32 chloroplastic
GFHJ01098566.1	----------	0.83023152	probable metal-nicotianamine transporter YSL16
GFHJ01018649.1	----------	0.816032625	Protein NRT1/ PTR FAMILY 6.3
GFHJ01009285.1	----------	0.815480861	Putative homeodomain-like transcription factor superfamily protein
GFHJ01085167.1	----------	0.80917088	mitogen-activated protein kinase kinase kinase A-like
GFHJ01023158.1	----------	0.781281014	serine carboxypeptidase 2
GFHJ01080871.1	----------	0.781071328	replication factor A protein 1 isoform X4
GFHJ01090857.1	----------	0.780006141	hypothetical protein SORBI_3002G401000
GFHJ01019514.1	----------	0.761723836	protein NRT1/ PTR FAMILY 5.6
GFHJ01066991.1	----------	0.716556167	glutathione S-transferase 3
GFHJ01019681.1	----------	0.713925602	interferon-related developmental regulator 2
GFHJ01033685.1	----------	0.687724773	protein NUCLEAR FUSION DEFECTIVE 4
GFHJ01037209.1	----------	0.679078444	sugar transporter ERD6-like 4
GFHJ01035515.1	----------	0.676219207	structural maintenance of chromosomes protein 1
GFHJ01018844.1	----------	0.675164443	aspartokinase 1, chloroplastic-like
GFHJ01077806.1	----------	0.670276534	alpha-expansin 1
GFHJ01010616.1	----------	0.664299076	Proton pump-interactor 1
GFHJ01052754.1	----------	0.632514585	sulfite exporter TauE/SafE family protein 3
GFHJ01026538.1	----------	0.60488112	NADP-dependent malic enzyme, chloroplastic isoform X1
GFHJ01050508.1	----------	0.599982493	Peroxidase 1
GFHJ01063459.1	----------	0.594967696	hypothetical protein BRADI_4g21980v3
GFHJ01037850.1	----------	0.581196102	Protein ROS1
GFHJ01057651.1	----------	0.566886505	exoglucanase 1 precursor
GFHJ01045980.1	----------	0.548916553	uncharacterized protein LOC103635119 isoform X2
GFHJ01028878.1	----------	0.54067208	chloride channel protein CLC-c
GFHJ01044983.1	----------	0.529571548	myosin-12 isoform X1
GFHJ01046914.1	----------	0.507279458	12-oxophytodienoate reductase 7
GFHJ01019713.1	----------	0.501180574	phosphoinositide phosphatase SAC2
GFHJ01044389.1	----------	0.458426675	UDP-glucose:glycoprotein glucosyltransferase
GFHJ01029403.1	----------	0.455740612	Zn-dependent hydrolases, including glyoxylases
GFHJ01043982.1	----------	0.430095018	Phospholipid-transporting ATPase 2
			Common down-regulated DETs
GFHJ01066158.1	-0.63899901	-0.451443267	hypothetical protein GQ55_5G457000
GFHJ01069775.1	-0.785067367	-0.452578214	S-adenosyl-L-methionine-dependent methyltransferase superfamily protein
GFHJ01059881.1	-0.96108738	-0.539636588	fructose-1,6-bisphosphatase, cytosolic
GFHJ01093985.1	-1.225113603	-0.902242824	protein RADIALIS-like 3
GFHJ01099416.1	-1.62785192	-1.270411238	uncharacterized protein LOC8060547
			RB867517 down-regulated DETs
GFHJ01041033.1	-0.420236528	----------	enolase 1
GFHJ01020415.1	-0.457419947	----------	malate dehydrogenase, cytoplasmic
GFHJ01070911.1	-0.492427913	----------	lysine-specific demethylase JMJ30 isoform X2
GFHJ01041375.1	-0.50910723	----------	LINE-1 retrotransposable element ORF2 protein

GFHJ01082566.1	-0.521136133	----------	hypothetical protein SORBI_3002G072100
GFHJ01092425.1	-0.528512189	----------	histone H2A
GFHJ01025332.1	-0.543865329	----------	probable anion transporter 1, chloroplastic
GFHJ01000277.1	-0.585806337	----------	---NA---
GFHJ01096026.1	-0.599679728	----------	uncharacterized protein LOC8065126
GFHJ01015758.1	-0.600661875	----------	serine carboxypeptidase-like 2
GFHJ01042652.1	-0.60323326	----------	Trypsin family protein
GFHJ01059486.1	-0.605286293	----------	15-cis-phytoene desaturase chloroplastic/chromoplastic
GFHJ01000260.1	-0.605606717	----------	---NA---
GFHJ01015244.1	-0.606220624	----------	zeaxanthin epoxidase
GFHJ01078925.1	-0.613110289	----------	Cysteine proteinase 1
GFHJ01102285.1	-0.616468152	----------	Zinc finger CCCH domain-containing protein 58
GFHJ01088570.1	-0.617727884	----------	---NA---
GFHJ01032288.1	-0.619958304	----------	ferric reduction oxidase 7, chloroplastic
GFHJ01083109.1	-0.622141695	----------	probable solanesyl-diphosphate synthase 3, chloroplastic
GFHJ01086821.1	-0.626523375	----------	protein LSD1
GFHJ01076524.1	-0.629599056	----------	---NA---
GFHJ01079189.1	-0.637999432	----------	serine carboxypeptidase-like 2
GFHJ01070276.1	-0.6399766	----------	15-cis-phytoene desaturase chloroplastic/chromoplastic
GFHJ01001180.1	-0.641579965	----------	hypothetical protein SORBI_3003G145050
GFHJ01061626.1	-0.644625337	----------	ATP-dependent zinc metalloprotease FTSH 1, chloroplastic
GFHJ01040885.1	-0.645870662	----------	O-methyltransferase ZRP4
GFHJ01034376.1	-0.646975136	----------	RNA polymerase sigma factor sigA
GFHJ01094731.1	-0.648458958	----------	ferredoxin-thioredoxin reductase catalytic chain, chloroplastic
GFHJ01037184.1	-0.652207066	----------	16S rRNA processing protein RimM family
GFHJ01009116.1	-0.666184429	----------	ferrochelatase-2, chloroplastic
GFHJ01033056.1	-0.668731657	----------	pyruvate dehydrogenase E1 component subunit alpha-3, chloroplastic
GFHJ01028189.1	-0.676504695	----------	presequence protease 1, chloroplastic/mitochondrial
GFHJ01036357.1	-0.679386516	----------	phosphoglucan phosphatase LSF2, chloroplastic
GFHJ01036976.1	-0.694566169	----------	putative serine/threonine kinase protein
GFHJ01066988.1	-0.694918004	----------	---NA---
GFHJ01043408.1	-0.699720686	----------	chaperone protein ClpC2, chloroplastic
GFHJ01055385.1	-0.703506209	----------	probable 6-phosphogluconolactonase 1
GFHJ01103623.1	-0.707683161	----------	uncharacterized LOC100280925 isoform 1
GFHJ01078999.1	-0.712466609	----------	L-ascorbate peroxidase 2, cytosolic
GFHJ01087195.1	-0.717029887	----------	1,4-alpha-glucan-branching enzyme 2, chloroplastic/amyloplastic
GFHJ01036360.1	-0.720940746	----------	phosphoglucan phosphatase LSF2, chloroplastic
GFHJ01058580.1	-0.725190543	----------	serotonin N-acetyltransferase 1, chloroplastic
GFHJ01107392.1	-0.728574256	----------	---NA---
GFHJ01043412.1	-0.729911096	----------	chaperone protein ClpC2, chloroplastic
GFHJ01050973.1	-0.736131734	----------	---NA---
GFHJ01103044.1	-0.738028933	----------	thioredoxin H2-2
GFHJ01091798.1	-0.739298024	----------	tubby-like F-box protein 7
GFHJ01064127.1	-0.742878979	----------	zinc finger protein CONSTANS-LIKE 9
GFHJ01106488.1	-0.745037794	----------	hypothetical protein SORBI_3001G311601

GFHJ01100790.1	-0.746091941	----------	protein CURVATURE THYLAKOID 1A, chloroplastic
GFHJ01032238.1	-0.747920968	----------	LRR binding protein
GFHJ01052107.1	-0.769428975	----------	Starch synthase I
GFHJ01046349.1	-0.770862581	----------	sister chromatid cohesion protein PDS5 homolog B
GFHJ01033622.1	-0.772623823	----------	rho GTPase-activating protein 5 isoform X1
GFHJ01084366.1	-0.774227344	----------	histone H3.2
GFHJ01091888.1	-0.77526099	----------	---NA---
GFHJ01011780.1	-0.776277416	----------	receptor kinase-like protein Xa21
GFHJ01094515.1	-0.778311612	----------	CBS domain containing protein
GFHJ01075013.1	-0.778983975	----------	uncharacterized protein LOC8067653
GFHJ01101178.1	-0.780613579	----------	chlorophyll a-b binding protein
GFHJ01067736.1	-0.784609897	----------	chlorophyll a-b binding protein 5, chloroplastic
GFHJ01092227.1	-0.788824008	----------	50S ribosomal protein L31, chloroplastic
GFHJ01071762.1	-0.791559068	----------	maf-like protein DDB_G0281937
GFHJ01086519.1	-0.795439659	----------	ethylene-responsive transcription factor-like protein At4g13040 isoform X4
GFHJ01094286.1	-0.803316089	----------	Histone H2B.4
GFHJ01033345.1	-0.805612667	----------	uncharacterized protein LOC8085736 isoform X1
GFHJ01091671.1	-0.806191832	----------	RALFL33 precursor
GFHJ01090992.1	-0.812233138	----------	chlorophyll a-b binding protein 1B-21, chloroplastic
GFHJ01020704.1	-0.815693445	----------	sanguinarine reductase
GFHJ01095682.1	-0.817395265	----------	ethylene-responsive transcription factor 1
GFHJ01096126.1	-0.826636765	----------	Hypoxia-responsive family protein
GFHJ01078696.1	-0.828511959	----------	probable cytokinin riboside 5'-monophosphate phosphoribohydrolase LOGL10
GFHJ01072287.1	-0.828593509	----------	calmodulin-like protein 1
GFHJ01095716.1	-0.830331909	----------	chloroplast 30S ribosomal protein S10
GFHJ01102843.1	-0.830769553	----------	uncharacterized protein LOC8063818
GFHJ01096610.1	-0.833463361	----------	AF466200_10TNP2-like protein
GFHJ01080212.1	-0.838277575	----------	chlorophyll a-b binding protein 5, chloroplastic
GFHJ01082195.1	-0.843941028	----------	RNA-binding protein CP31B chloroplastic
GFHJ01014122.1	-0.844346583	----------	ABC transporter F family member 5
GFHJ01100852.1	-0.84509945	----------	auxin-repressed 12.5 kDa protein
GFHJ01091722.1	-0.84540059	----------	granule-bound starch synthase 1b, chloroplastic/amyloplastic
GFHJ01089337.1	-0.845995845	----------	peptidyl-prolyl cis-trans isomerase FKBP16-4, chloroplastic
GFHJ01064172.1	-0.847608255	----------	Trypsin family protein
GFHJ01097057.1	-0.855118454	----------	transcription factor UNE10 isoform X5
GFHJ01070513.1	-0.85541918	----------	uncharacterized protein LOC100278102
GFHJ01097620.1	-0.861552272	----------	calvin cycle protein CP12-1, chloroplastic
GFHJ01055014.1	-0.861992991	----------	---NA---
GFHJ01103585.1	-0.863873012	----------	stromal 70 kDa heat shock-related protein, chloroplastic
GFHJ01004661.1	-0.864791865	----------	---NA---
GFHJ01095644.1	-0.86568425	----------	uncharacterized protein LOC8079483
GFHJ01068635.1	-0.866159472	----------	SOUL heme-binding protein
GFHJ01077049.1	-0.868996291	----------	CCG-binding protein 1
GFHJ01073772.1	-0.870255785	----------	30S ribosomal protein S13
GFHJ01005086.1	-0.871794066	----------	---NA---

GFHJ01098644.1	-0.874732191	----------	uncharacterized protein LOC8076621
GFHJ01033759.1	-0.875313758	----------	protein SRG1
GFHJ01069025.1	-0.880251631	----------	chlorophyll a-b binding protein 1B-21, chloroplastic
GFHJ01004902.1	-0.881597714	----------	uncharacterized protein LOC110434417
GFHJ01079207.1	-0.883644516	----------	heme-binding protein 2
GFHJ01092818.1	-0.885424516	----------	histone H2A
GFHJ01005549.1	-0.887618143	----------	---NA---
GFHJ01004729.1	-0.893422983	----------	hypothetical protein PAHAL_9G046900
GFHJ01103676.1	-0.894907585	----------	Tetratricopeptide repeat (TPR)-like superfamily protein
GFHJ01074615.1	-0.898327123	----------	serine carboxypeptidase-like 2
GFHJ01071674.1	-0.899279113	----------	CCG-binding protein 1
GFHJ01096634.1	-0.903682136	----------	chaperone protein dnaJ 11
GFHJ01040392.1	-0.904602466	----------	potassium channel KOR1 isoform X2
GFHJ01050058.1	-0.905320753	----------	G-type lectin S-receptor-like serine/threonine-protein kinase At1g11410
GFHJ01071714.1	-0.91415292	----------	extra-large guanine nucleotide-binding protein 1
GFHJ01068212.1	-0.925993303	----------	Protein ECERIFERUM 3
GFHJ01099357.1	-0.930545799	----------	chaperonin-like RBCX protein 1, chloroplastic
GFHJ01069442.1	-0.933664158	----------	peroxisomal membrane protein 11-1
GFHJ01096704.1	-0.934307206	----------	dormancy-associated protein 1
GFHJ01066943.1	-0.934414117	----------	uncharacterized protein LOC110431858
GFHJ01105209.1	-0.935562257	----------	---NA---
GFHJ01066862.1	-0.9377545	----------	chloroplast post-illumination chlorophyll fluorescence increase protein
GFHJ01063405.1	-0.941431753	----------	---NA---
GFHJ01101501.1	-0.946628056	----------	hypothetical protein PAHAL_2G037300
GFHJ01040886.1	-0.950227742	----------	O-methyltransferase ZRP4
GFHJ01046806.1	-0.950674338	----------	C4-specific pyruvate orthophosphate dikinase
GFHJ01011497.1	-0.957850019	----------	glyceraldehyde-3-phosphate dehydrogenase B, chloroplastic
GFHJ01095070.1	-0.959802721	----------	uncharacterized protein LOC8081846
GFHJ01080205.1	-0.959884256	----------	Chloroplast post-illumination chlorophyll fluorescence increase protein
GFHJ01077010.1	-0.962035807	----------	glutathione transferase GST 23
GFHJ01093069.1	-0.962449663	----------	putative LRR receptor-like serine/threonine-protein kinase
GFHJ01024329.1	-0.963481791	----------	cysteine proteinase 2
GFHJ01098613.1	-0.964986521	----------	chlorophyll a-b binding protein 8
GFHJ01096370.1	-0.965028581	----------	dormancy-associated protein 1
GFHJ01092941.1	-0.966339668	----------	Hypoxia-responsive family protein
GFHJ01099629.1	-0.967136657	----------	dormancy-associated protein 1
GFHJ01005826.1	-0.968158284	----------	replication protein
GFHJ01020069.1	-0.968456463	----------	alpha-galactosidase precursor
GFHJ01101958.1	-0.974519729	----------	dehydrin1 DHN1
GFHJ01085383.1	-0.979920029	----------	OSJNBa0088A01.13-like protein
GFHJ01059827.1	-0.980609	----------	E3 ubiquitin-protein ligase AIRP2-like isoform X2
GFHJ01102111.1	-0.983632099	----------	dormancy-associated protein 1
GFHJ01106984.1	-0.992083559	----------	metallothionein type 1
GFHJ01062002.1	-0.996728728	----------	NAC domain-containing protein 21/22
GFHJ01092635.1	-0.999054978	----------	Zinc finger CCCH domain-containing protein 22

GFHJ01074611.1	-1.004520062	----------	MT10, partial
GFHJ01098428.1	-1.011379835	----------	calvin cycle protein CP12-1, chloroplastic
GFHJ01083597.1	-1.012482996	----------	---NA---
GFHJ01095985.1	-1.017692966	----------	Hypoxia-responsive family protein
GFHJ01079569.1	-1.030303415	----------	multiple organellar RNA editing factor 2, chloroplastic-like
GFHJ01005336.1	-1.042128088	----------	DNA-binding protein SMUBP-2 isoform X3
GFHJ01066266.1	-1.043320112	----------	B-box zinc finger protein 24
GFHJ01088768.1	-1.044488348	----------	protein LSD1
GFHJ01079680.1	-1.047153328	----------	gamma-tocopherol methyltransferase
GFHJ01076564.1	-1.047852662	----------	cytochrome b6-f complex iron-sulfur subunit
GFHJ01101560.1	-1.05394933	----------	Hypoxia-responsive family protein
GFHJ01050226.1	-1.056077849	----------	putative receptor-like protein kinase 4
GFHJ01102985.1	-1.062943572	----------	Wound-responsive family protein
GFHJ01064858.1	-1.065734506	----------	translation elongation factor G
GFHJ01102971.1	-1.067984447	----------	dormancy-associated protein 1
GFHJ01071488.1	-1.074023878	----------	tropinone reductase homolog At1g07440-like isoform X1
GFHJ01084279.1	-1.083387953	----------	probable isoaspartyl peptidase/L-asparaginase 2
GFHJ01082469.1	-1.084483168	----------	---NA---
GFHJ01099736.1	-1.089733422	----------	transcription factor MYB48
GFHJ01074636.1	-1.091825697	----------	receptor kinase-like protein Xa21
GFHJ01065076.1	-1.095166354	----------	probable glutathione S-transferase GSTU1
GFHJ01092870.1	-1.097875109	----------	uncharacterized protein LOC8068774
GFHJ01087713.1	-1.099052365	----------	---NA---
GFHJ01093674.1	-1.101212793	----------	Glutathione transferase GST 23
GFHJ01068410.1	-1.104919883	----------	maf-like protein DDB_G0281937
GFHJ01091011.1	-1.105752058	----------	early nodulin-93
GFHJ01090018.1	-1.108498898	----------	uncharacterized protein LOC110434417
GFHJ01087585.1	-1.108650301	----------	alcohol dehydrogenase class 3
GFHJ01094032.1	-1.113400461	----------	---NA---
GFHJ01100340.1	-1.114838149	----------	alpha/beta-Hydrolases superfamily protein
GFHJ01093518.1	-1.115954709	----------	uncharacterized protein LOC8068774
GFHJ01033616.1	-1.116035761	----------	violaxanthin de-epoxidase, chloroplastic
GFHJ01077828.1	-1.12139113	----------	protein ECERIFERUM 1
GFHJ01018987.1	-1.121872564	----------	ent-cassadiene C2-hydroxylase
GFHJ01101707.1	-1.124519594	----------	Hypoxia-responsive family protein
GFHJ01063697.1	-1.124756549	----------	Trypsin family protein
GFHJ01031217.1	-1.125270979	----------	alpha-humulene synthase isoform X2
GFHJ01078027.1	-1.126987435	----------	octicosapeptide/Phox/Bem1p (PB1) domain-containing protein
GFHJ01021685.1	-1.143169042	----------	cellulose synthase-like protein E6
GFHJ01005544.1	-1.147403838	----------	uncharacterized protein LOC110434417
GFHJ01094439.1	-1.14744304	----------	OSJNBa0088A01.13-like protein
GFHJ01087833.1	-1.150660089	----------	UDP-glucose 4-epimerase 1
GFHJ01052678.1	-1.151121461	----------	UDP-glucose 4-epimerase 3
GFHJ01107253.1	-1.153665878	----------	sequence-specific DNA binding transcription factor
GFHJ01074730.1	-1.157465164	----------	Thiazole biosynthetic enzyme Thi4 family

GFHJ01007459.1	-1.158937553	----------	Leucine-rich repeat protein kinase family protein
GFHJ01043092.1	-1.160593634	----------	Transcription factor bHLH82
GFHJ01099249.1	-1.160674158	----------	SNF7 family protein
GFHJ01093345.1	-1.164990279	----------	putative disease resistance RPP13-like protein 3
GFHJ01098776.1	-1.165588984	----------	uncharacterized protein LOC107546779
GFHJ01103251.1	-1.170202116	----------	Protein MARD1
GFHJ01075437.1	-1.176366317	----------	tetraketide alpha-pyrone reductase 1
GFHJ01098624.1	-1.177735072	----------	Protein MARD1
GFHJ01056588.1	-1.18283794	----------	auxin response factor 5
GFHJ01085136.1	-1.187722937	----------	transcription factor MYB21
GFHJ01032317.1	-1.195038529	----------	probable isoaspartyl peptidase/L-asparaginase 2
GFHJ01096919.1	-1.203622919	----------	ABC transporter F family member 4-like
GFHJ01098877.1	-1.203662436	----------	uncharacterized protein LOC8056152
GFHJ01098783.1	-1.206693789	----------	seed specific protein Bn15D17A
GFHJ01100223.1	-1.211121539	----------	salT gene product
GFHJ01084124.1	-1.212530533	----------	MYB31 transcription factor31
GFHJ01041087.1	-1.219104214	----------	wall-associated receptor kinase 1
GFHJ01067153.1	-1.222167595	----------	nucleolin 1-like
GFHJ01070966.1	-1.224860257	----------	high mobility group B protein 7
GFHJ01098695.1	-1.228488842	----------	light-regulated protein
GFHJ01105730.1	-1.232001706	----------	hypothetical protein SORBI_3001G291200
GFHJ01102980.1	-1.232521392	----------	uncharacterized protein LOC110430516
GFHJ01052465.1	-1.238036511	----------	momilactone A synthase
GFHJ01102767.1	-1.242884154	----------	Hypoxia-responsive family protein
GFHJ01099172.1	-1.249616397	----------	H0303A11-B0406H05.7
GFHJ01073199.1	-1.253694479	----------	glutathione S-transferase GSTU6
GFHJ01067387.1	-1.253809691	----------	stress responsive protein
GFHJ01097755.1	-1.25934109	----------	Peptide chain release factor APG3, chloroplastic
GFHJ01061783.1	-1.263549715	----------	glyceraldehyde-3-phosphate dehydrogenase 1, cytosolic-like
GFHJ01053516.1	-1.266666611	----------	chlorophyll a-b binding protein 1, chloroplastic
GFHJ01083343.1	-1.276462906	----------	probable isoaspartyl peptidase/L-asparaginase 2
GFHJ01099884.1	-1.280351821	----------	uncharacterized protein LOC8056152
GFHJ01091931.1	-1.28602418	----------	uncharacterized protein LOC101764334
GFHJ01020730.1	-1.289676599	----------	UDP-glucose 4-epimerase 1
GFHJ01077987.1	-1.291960087	----------	DUF581 family protein
GFHJ01051523.1	-1.292478332	----------	Cyclin-dependent kinase B2-1
GFHJ01031705.1	-1.30846879	----------	putative receptor-like protein kinase 4
GFHJ01083506.1	-1.310791581	----------	E3 ubiquitin-protein ligase AIRP2-like isoform X2
GFHJ01021380.1	-1.317006966	----------	probable leucine-rich repeat receptor-like protein kinase At5g49770
GFHJ01083078.1	-1.319129621	----------	Auxin-responsive protein IAA12
GFHJ01101899.1	-1.320896393	----------	DNA topoisomerase 2
GFHJ01035477.1	-1.327255088	----------	uncharacterized protein LOC8074041
GFHJ01054086.1	-1.328299116	----------	hypothetical protein SORBI_3010G271800
GFHJ01071855.1	-1.330061479	----------	chaperonin-like RBCX protein 1, chloroplastic
GFHJ01057238.1	-1.332422965	----------	esterase precursor

GFHJ01101440.1	-1.334528862	----------	histone H1
GFHJ01061222.1	-1.335203812	----------	soluble inorganic pyrophosphatase-like
GFHJ01063452.1	-1.335841428	----------	MLO-like protein 1
GFHJ01085058.1	-1.351672997	----------	putative cytochrome P450 superfamily protein
GFHJ01035072.1	-1.357815981	----------	uncharacterized protein LOC112896424
GFHJ01025754.1	-1.361928936	----------	chaperone protein dnaJ C76, chloroplastic
GFHJ01055882.1	-1.363034388	----------	L-type lectin-domain containing receptor kinase IX.1-like isoform X1
GFHJ01073459.1	-1.366019157	----------	Protein RIK
GFHJ01069729.1	-1.369053296	----------	uncharacterized protein LOC110431858
GFHJ01027940.1	-1.37743604	----------	cytochrome P450 89A2-like
GFHJ01093178.1	-1.380812641	----------	Basic leucine zipper 25
GFHJ01096440.1	-1.386892451	----------	LOW QUALITY PROTEIN: hypothetical protein SETIT_4G038600v2
GFHJ01007708.1	-1.399063131	----------	7-deoxyloganetin glucosyltransferase
GFHJ01098817.1	-1.411517004	----------	dehydration-responsive element-binding protein 1A
GFHJ01097801.1	-1.43728344	----------	uncharacterized protein LOC8058901
GFHJ01063999.1	-1.469550852	----------	alpha-expansin 1
GFHJ01094429.1	-1.471571201	----------	Histone H4
GFHJ01090399.1	-1.476319891	----------	hypothetical protein BAE44_0009449
GFHJ01096561.1	-1.502395974	----------	uncharacterized protein LOC8061776
GFHJ01056140.1	-1.507213021	----------	L-type lectin-domain containing receptor kinase IX.1
GFHJ01086277.1	-1.50763215	----------	octicosapeptide/Phox/Bem1p (PB1) domain-containing protein
GFHJ01103699.1	-1.516982037	----------	Protein MARD1
GFHJ01020726.1	-1.518240712	----------	UDP-glucose 4-epimerase 1
GFHJ01103747.1	-1.518935172	----------	uncharacterized protein LOC110434000
GFHJ01068795.1	-1.526540156	----------	LOB domain-containing protein 41
GFHJ01033919.1	-1.532795238	----------	catalytic/ hydrolase
GFHJ01090008.1	-1.537810244	----------	uncharacterized LOC100276059
GFHJ01022846.1	-1.540784632	----------	probable flavin-containing monooxygenase 1
GFHJ01066600.1	-1.552832009	----------	uncharacterized protein LOC101766871
GFHJ01099775.1	-1.560786101	----------	transcription factor MYB21
GFHJ01083732.1	-1.578543784	----------	bundle sheath cell specific protein 1
GFHJ01057612.1	-1.580825848	----------	chlorophyll a-b binding protein 2
GFHJ01083082.1	-1.611184614	----------	dnaJ-like protein
GFHJ01086468.1	-1.613651965	----------	NAD(P)-binding Rossmann-fold superfamily protein
GFHJ01083818.1	-1.637775027	----------	seed specific protein Bn15D17A
GFHJ01077623.1	-1.638922955	----------	prostamide/prostaglandin F synthase
GFHJ01100077.1	-1.641897025	----------	Hypoxia-responsive family protein
GFHJ01003828.1	-1.647073962	----------	---NA---
GFHJ01100756.1	-1.647454478	----------	dehydration-responsive element-binding protein 1A
GFHJ01026633.1	-1.659256338	----------	cyclin IaZm
GFHJ01074850.1	-1.66049717	----------	Leucine-rich repeat protein kinase family protein
GFHJ01084290.1	-1.676008492	----------	bundle sheath cell specific protein 1
GFHJ01094391.1	-1.687342193	----------	transcription factor MYB59
GFHJ01101520.1	-1.687393296	----------	seed specific protein Bn15D17A
GFHJ01098950.1	-1.700384085	----------	Peroxidase P7

GFHJ01033654.1	-1.70507545	----------	probable purine permease 11
GFHJ01099579.1	-1.708881198	----------	hypothetical protein
GFHJ01098376.1	-1.732387223	----------	F-box/kelch-repeat protein At1g80440-like
GFHJ01057253.1	-1.74334219	----------	Cysteine proteinase 2
GFHJ01089427.1	-1.755984781	----------	uncharacterized protein LOC8067364
GFHJ01096227.1	-1.769754825	----------	photosystem II subunit29
GFHJ01103288.1	-1.795845871	----------	uncharacterized protein LOC112900216
GFHJ01107459.1	-1.828312777	----------	hypothetical protein SORBI_3005G128550
GFHJ01091650.1	-1.841453594	----------	L-type lectin-domain containing receptor kinase IX.1
GFHJ01060091.1	-1.849572597	----------	gibberellin 2-beta-dioxygenase 8
GFHJ01098081.1	-1.871489412	----------	hypothetical protein PAHAL_7G305300
GFHJ01049319.1	-1.891558869	----------	chaperone protein dnaJ C76, chloroplastic isoform X2
GFHJ01021670.1	-1.912821653	----------	peroxidase 17
GFHJ01101650.1	-1.93091833	----------	uncharacterized protein LOC8056152
GFHJ01038937.1	-1.940240053	----------	phosphate transporter PHO1-3
GFHJ01106470.1	-1.970008515	----------	hypothetical protein SORBI_3002G124832
GFHJ01065578.1	-2.006486362	----------	chaperone protein dnaJ C76, chloroplastic isoform X2
GFHJ01097335.1	-2.073044522	----------	uncharacterized protein LOC112900216
GFHJ01104819.1	-2.075415881	----------	zinc finger protein ZAT5-like
GFHJ01097047.1	-2.108080213	----------	cortical cell-delineating protein
GFHJ01094961.1	-2.147499258	----------	dehydration-responsive element-binding protein 1A
GFHJ01098819.1	-2.164739377	----------	octicosapeptide/Phox/Bem1p (PB1) domain-containing protein
GFHJ01053899.1	-2.168490609	----------	chaperone protein dnaJ C76, chloroplastic
GFHJ01103858.1	-2.182437719	----------	hypothetical protein BAE44_0018849
GFHJ01081319.1	-2.186777697	----------	Auxin-responsive protein SAUR36
GFHJ01050057.1	-2.205504016	----------	Acetylserotonin O-methyltransferase 3
GFHJ01105755.1	-2.233500591	----------	protein app1
GFHJ01033840.1	-2.310986593	----------	putative nucleoredoxin 3
GFHJ01003890.1	-2.566778159	----------	---NA---
GFHJ01034939.1	-2.600029498	----------	indole-2-monooxygenase
GFHJ01100144.1	-2.788514382	----------	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein
GFHJ01079817.1	-2.938414894	----------	Protein G1-like5
GFHJ01100031.1	-3.115420495	----------	uncharacterized protein LOC110436182 isoform X1
GFHJ01043991.1	-3.205628326	----------	PDR12 (PLEIOTROPIC DRUG RESISTANCE 12)
GFHJ01073037.1	-3.22136068	----------	Peroxidase 17
GFHJ01102244.1	-3.383843404	----------	Chitinase 11
GFHJ01106234.1	-3.468044139	----------	peroxidase P7
GFHJ01095589.1	-4.341596132	----------	hypothetical protein SORBI_3006G026700
GFHJ01094742.1	-4.959576341	----------	putative receptor-like protein kinase At4g00960
GFHJ01106113.1	-5.600398324	----------	metallothionein
GFHJ01101303.1	-5.853581031	----------	predicted protein
GFHJ01040685.1	-6.629670381	----------	probable histone acetyltransferase HAC-like 1 isoform X2
GFHJ01093438.1	-7.442700587	----------	Seed maturation protein
			SP80-3280 down-regulated DETs
GFHJ01064564.1	----------	-0.410744392	PGR5-like protein 1A, chloroplastic

GFHJ01013686.1	----------	-0.51035214	uncharacterized protein LOC100276100 isoform X1
GFHJ01041053.1	----------	-0.529120022	fructose-1,6-bisphosphatase, cytosolic
GFHJ01049433.1	----------	-0.533719372	uncharacterized protein LOC8061566
GFHJ01025664.1	----------	-0.543592185	ferredoxin--NADP reductase, leaf isozyme, chloroplastic
GFHJ01069375.1	----------	-0.546928768	GDSL esterase/lipase At5g55050
GFHJ01063325.1	----------	-0.547282302	transmembrane protein 45A
GFHJ01087360.1	----------	-0.586748331	Protein CURVATURE THYLAKOID 1B, chloroplastic
GFHJ01021607.1	----------	-0.591903215	uncharacterized protein LOC8061566
GFHJ01080622.1	----------	-0.600183208	cinnamoyl-CoA reductase 1
GFHJ01055109.1	----------	-0.600211593	OSJNBa0072F16.18-like protein
GFHJ01025662.1	----------	-0.610293439	ferredoxin--NADP reductase, leaf isozyme, chloroplastic
GFHJ01049738.1	----------	-0.61244866	dihydrodipicolinate reductase
GFHJ01035667.1	----------	-0.62858733	NAD(P)-binding Rossmann-fold superfamily protein
GFHJ01097842.1	----------	-0.636523597	---NA---
GFHJ01107302.1	----------	-0.646603096	uncharacterized protein LOC8056436
GFHJ01092078.1	----------	-0.649284928	uncharacterized LOC103649536
GFHJ01004520.1	----------	-0.649302574	---NA---
GFHJ01069265.1	----------	-0.652186131	uncharacterized protein LOC8058953
GFHJ01072505.1	----------	-0.652228412	carbonic anhydrase3
GFHJ01077427.1	----------	-0.65731742	probable glutathione S-transferase GSTU1
GFHJ01102603.1	----------	-0.666392745	UDP-glycosyltransferase 91C1
GFHJ01050975.1	----------	-0.688460527	protein MET1, chloroplastic
GFHJ01069084.1	----------	-0.694883166	photosystem II subunit PsbS1
GFHJ01036763.1	----------	-0.707149575	amino acid permease 6
GFHJ01019552.1	----------	-0.713051931	cinnamoyl-CoA reductase 1
GFHJ01087156.1	----------	-0.721962809	chalcone--flavonone isomerase
GFHJ01032183.1	----------	-0.723797427	uncharacterized protein LOC112899230
GFHJ01096089.1	----------	-0.72960301	early light-induced protein
GFHJ01069132.1	----------	-0.730717836	adenylate kinase, chloroplastic
GFHJ01082292.1	----------	-0.744685313	Protein PROTON GRADIENT REGULATION 5, chloroplastic
GFHJ01097979.1	----------	-0.753183801	Protein CHLORORESPIRATORY REDUCTION 7, chloroplastic
GFHJ01010603.1	----------	-0.76652569	probable cinnamyl alcohol dehydrogenase 1
GFHJ01066017.1	----------	-0.788596599	psbP domain-containing protein 2, chloroplastic
GFHJ01083566.1	----------	-0.807576145	---NA---
GFHJ01083179.1	----------	-0.886714134	uncharacterized protein LOC101758396
GFHJ01082151.1	----------	-0.938558048	Fructose-bisphosphate aldolase 5, cytosolic
GFHJ01104111.1	----------	-1.192275662	UDP-glycosyltransferase 91A1
GFHJ01028928.1	----------	-1.538131799	pyrophosphate-energized vacuolar membrane proton pump
GFHJ01047830.1	----------	-5.558132758	putative C4 phosphoenolpyruvate carboxylase

Table S2. Annotation of up- and down-regulated DEGs with the respective log_2 fold change (Log_2 FC) of two sugarcane varieties (RB867515 and SP80-3280) after *Diatraea saccharalis* infestation.

STP ID	Log_2 FC (RB867515)	Log_2 FC (SP80-3280)	STP description	Blast2GO description
			Common up-regulated DEGs	
Sh02_g009130	8.421444032	6.41054098	similar to Chromosome chr7 scaffold_31, whole genome shotgun sequence	chlorophyllase-2, chloroplastic
Sh07_g003030	7.072154833	3.314321934	Aromatic-L-amino-acid decarboxylase	aromatic-L-amino-acid decarboxylase
Sh09_g014970	6.971496553	3.228033004	Tyrosine/DOPA decarboxylase 2	tyrosine/DOPA decarboxylase 1
Sh01_g000220	6.843092829	4.780668359	Ethylene-responsive transcription factor 1B	ethylene-responsive transcription factor 1B
Sh01_g028240	6.610677604	2.153989536	similar to Terpene synthase family, metal binding domain containing protein, expressed	alpha-humulene synthase
Sh01_g015030	6.436943541	8.044393949	Tyrosine N-monooxygenase	tyrosine N-monooxygenase-like
Sh09_g015440	5.969914949	5.957316066	O-methyltransferase ZRP4	O-methyltransferase ZRP4
Sh01_g009380	5.87645256	2.059106414	Chemocyanin	chemocyanin precursor
Sh09_g004160	5.360704274	3.07707371	1-aminocyclopropane-1-carboxylate oxidase	1-aminocyclopropane-1-carboxylate oxidase
Sh01_g036120	5.204327005	3.881502814	Peroxidase	peroxidase N
Sh10_g014690	5.089197794	3.268048592	WRKY transcription factor WRKY28	WRKY transcription factor WRKY28
Sh03_g021370	4.979605238	4.518844963	Gibberellin 2-beta-dioxygenase	gibberellin 2-beta-dioxygenase
Sh04_g013230	4.932410519	6.880108928	Nitrate reductase [NADH] 3	nitrate reductase [NADH] 3
Sh09_g017390	4.838364907	1.886451567	Mitogen-activated protein kinase kinase kinase 17	mitogen-activated protein kinase kinase kinase 17
Sh09_g006390	4.837953384	2.271021134	Gibberellin 2-beta-dioxygenase	gibberellin 2-beta-dioxygenase 3-like
Sh01_g018600	4.736834378	4.156135571	Peroxidase	Peroxidase 59
Sh10_g014670	4.602956479	2.72037358	WRKY transcription factor WRKY28	WRKY transcription factor WRKY28
Sh03_g015550	4.497950169	2.316476743	similar to DNA-binding protein WRKY2-like	putative WRKY transcription factor 71
Sh04_g016240	4.458924817	3.943370404	TPR repeat-containing thioredoxin TTL4	TPR repeat-containing thioredoxin TTL4
Sh10_g013800	4.282089211	2.265070152	p10Sh249C12	protein GLUTAMINE DUMPER 5
Sh01_g028430	4.179937824	4.130280013	Cytochrome P450 71A1	cytochrome P450 71A1-like
Sh07_g009490	3.953152816	2.038185314	Type IV inositol polyphosphate 5-phosphatase 9	type IV inositol polyphosphate 5-phosphatase 9-like
Sh09_g004190	3.911033491	1.933901409	Acc oxidase	1-aminocyclopropane-1-carboxylate oxidase
Sh09_g001130	3.80097038	2.445826936	Subtilisin-chymotrypsin inhibitor-2B (Fragment)	Subtilisin-chymotrypsin inhibitor-2A
Sh06_g007560	3.755822476	2.892064342	Bowman-Birk type bran trypsin inhibitor	Bowman-Birk type bran trypsin inhibitor
Sh09_g001140	3.498118986	3.486357068	Subtilisin-chymotrypsin inhibitor-2B (Fragment)	maize proteinase inhibitor
Sh02_g002470	3.490161191	3.187305712	Protein TIFY 5	Protein TIFY 5A
Sh10_g004030	3.436691261	3.255778646	weakly similar to Transcription factor WRKY35	probable WRKY transcription factor 53
Sh09_g019880	3.349737506	3.561213013	S-type anion channel SLAH2	S-type anion channel SLAH2
Sh09_g001060	3.155764824	2.378797789	Subtilisin-chymotrypsin inhibitor-2B (Fragment)	MPI
Sh04_g019170	3.080747142	1.945141386	Formate dehydrogenase, mitochondrial	formate dehydrogenase 2, mitochondrial
Sh01_g010060	2.958690729	2.311116954	Conserved hypothetical protein	---NA---
Sh_254A06_g000020	2.890868952	2.258498884	ABC transporter G family member 11	ABC transporter G family member 11
Sh01_g003650	2.878010564	1.410005193	similar to Indole-3-glycerol phosphate lyase	indole-3-glycerol phosphate lyase, chloroplastic
Sh10_g010440	2.765519616	1.141230524	Conserved hypothetical protein	---NA---
Sh09_g001120	2.705942797	0.842835781	Subtilisin-chymotrypsin inhibitor-2B (Fragment)	subtilisin-chymotrypsin inhibitor-2B
Sh01_g032670	2.611950283	2.009761619	similar to Oxidoreductase, 2OG-Fe oxygenase family protein, expressed	---NA---

Sh09_g015890	2.608350092	1.580835534	Protein IQ-DOMAIN 14	protein IQ-DOMAIN 14 isoform X3
Sh04_g012170	2.550582104	2.170695351	E3 ubiquitin-protein ligase EL5	E3 ubiquitin-protein ligase EL5
Sh01_g010080	2.480729053	1.257895322	Linoleate 9S-lipoxygenase 1	putative linoleate 9S-lipoxygenase 3
Sh06_g003700	2.468859587	2.853648281	Beta-fructofuranosidase, insoluble isoenzyme 2	beta-fructofuranosidase, insoluble isoenzyme 2
Sh09_g013600	2.421615805	2.544634123	Pyruvate decarboxylase 1	pyruvate decarboxylase 1
Sh03_g022570	2.415733577	1.066838983	Cytokinin dehydrogenase 5	cytokinin dehydrogenase 5
Sh04_g011610	2.385703942	1.609283398	U-box domain-containing protein 29	U-box domain-containing protein 27
Sh02_g031530	2.357770802	1.893782657	Negatively light-regulated protein	negatively light-regulated protein
Sh01_g010070	2.277251983	1.344382701	Lipoxygenase	probable linoleate 9S-lipoxygenase 4
Sh02_g006970	2.120192361	2.007078273	Non-specific lipid-transfer protein	putative lipid-transfer protein DIR1
Sh01_g039440	2.112296054	1.75894589	Protein MARD1	Protein MARD1
Sh09_g014360	2.077242441	1.425160817	Glycerol-3-phosphate dehydrogenase [NAD(+)]	probable glycerol-3-phosphate dehydrogenase [NAD(+)] 3, cytosolic
Sh_251K17_contig-3_g000010	2.015096614	1.897490164	Cytokinin oxidase 2	cytokinin dehydrogenase 4
Sh09_g015870	1.976436166	1.225189209	similar to Os05g0521900 protein	protein IQ-DOMAIN 14 isoform X3
Sh02_g014540	1.904598098	1.046134226	similar to Basic helix-loop-helix (BHLH)-like protein	DNA binding protein
Sh_212O05_g000080	1.862686088	0.756192048	Glycoside hydrolase, family 28	putative polygalacturonase
Sh10_g005670	1.820262368	0.928771354	similar to Pentatricopeptide (PPR) repeat-containing protein-like	putative UPF0481 protein At3g02645
Sh07_g018230	1.803587306	0.717858015	Uclacyanin 1	blue copper protein precursor
Sh02_g013500	1.731142514	1.08219646	similar to AAA ATPase, central region (50.1 kD)-like protein	AAA-ATPase At4g25835
Sh08_g002730	1.692298856	1.797512039	similar to Putative phytosulfokine peptide	phytosulfokines 2
Sh08_g008510	1.690466178	0.574105146	GDSL esterase/lipase	GDSL esterase/lipase
Sh04_g002160	1.673046332	1.715681976	L-aspartate oxidase	L-aspartate oxidase chloroplastic
Sh04_g024240	1.63926559	1.55072748	similar to Heat shock-like protein	Chaperone protein DnaJ
Sh02_g012240	1.607633802	1.168536217	Protein CCC1	vacuolar iron transporter 1.2
Sh02_g006950	1.574870369	1.523640335	PVR3-like protein	putative lipid-transfer protein DIR1
Sh02_g010820	1.537112149	0.640116758	similar to Membrane protein-like	Sulfite exporter TauE/SafE family protein 3
Sh03_g010280	1.522603762	0.878119534	Myb-related protein P	myb-related protein P
Sh04_g011010	1.461641601	0.774584598	Chaperone protein ClpD1, chloroplastic	chaperone protein
Sh10_g013560	1.443949136	1.819589892	Putative Cinnamoyl-CoA reductase 1	NAD(P)-binding Rossmann-fold superfamily protein
Sh02_g008510	1.417974624	0.78336866	Trans-cinnamate 4-monooxygenase	trans-cinnamate 4-monooxygenase
Sh04_g016280	1.409966951	1.196248313	PLAT domain-containing protein 1	PLAT/LH2 domain
Sh02_g016750	1.382209784	1.111696765	Squalene monooxygenase 1,1	probable sarcosine oxidase
Sh04_g012870	1.381535406	1.537552872	NAC domain-containing protein 92	NAC domain-containing protein 79
Sh09_g011520	1.367497614	0.898323944	Potassium channel AKT2	potassium channel AKT2
Sh01_g005370	1.286047435	0.700199396	Cytochrome P450	allene oxide synthase 1, chloroplastic
Sh09_g004840	1.24909075	0.635611343	Peroxidase	peroxidase 5
Sh05_g001320	1.23956433	0.536567535	Carbohydrate transporter/ sugar porter/ transporter	carbohydrate transporter/ sugar porter/ transporter
Sh04_g018400	1.232370039	0.610411744	Bidirectional sugar transporter SWEET	bidirectional sugar transporter SWEET2b
Sh03_g015730	1.166139682	0.614286699	Cytochrome P450 72A14	cytochrome P450 72A14
Sh10_g012240	1.135476363	0.749891771	ATP binding protein	ATP binding protein
Sh01_g034360	1.08538603	0.577528713	Anthranilate synthase alpha subunit 2, chloroplastic	anthranilate synthase alpha subunit 2, chloroplastic
Sh01_g001720	0.952004199	0.578729251	Epoxide hydrolase 2	soluble epoxide hydrolase
			RB867515 up-regulated DEGs	
Sh10_g013780	6.813825288	----------	p10Sh249C12	protein GLUTAMINE DUMPER 5

Sh01_g025350	6.42116217	----------	similar to Leucine rich repeat containing protein	polygalacturonase inhibitor
Sh01_g028230	5.812734247	----------	Zingiberene synthase	alpha-humulene synthase
Sh07_g005540	5.681245474	----------	(E)-beta-caryophyllene synthase	(E)-beta-caryophyllene synthase
Sh02_g005480	5.135916929	----------	Gibberellin 2-beta-dioxygenase 1	gibberellin 2-beta-dioxygenase
Sh07_g003020	5.130774283	----------	Terpene synthase 6	(E)-beta-farnesene synthase
Sh04_g016230	4.985624513	----------	VQ motif-containing protein 22	VQ motif
Sh10_g014280	4.824901722	----------	similar to Crocetin dialdehyde-like	carotenoid 9,10(9',10')-cleavage dioxygenase 1-like
Sh04_g011550	4.80397397	----------	E3 ubiquitin-protein ligase PUB23	E3 ubiquitin-protein ligase PUB23
Sh04_g012210	4.665783707	----------	Protein CROWDED NUCLEI 2	protein AUXIN-REGULATED GENE INVOLVED IN ORGAN SIZE
Sh09_g001050	4.170178131	----------	Conserved hypothetical protein	uncharacterized protein LOC101762386
Sh03_g010070	3.804496086	----------	Transcription factor JAMYB	transcription factor JAMYB
Sh01_g011070	3.742503811	----------	VQ motif-containing protein 29	uncharacterized protein LOC8054180
Sh06_g011550	3.711796097	----------	Oleosin Zm-I	Oleosin Zm-I
Sh01_g024450	3.705886697	----------	similar to Expressed protein	peptidoglycan-binding LysM domain-containing protein
Sh04_g012790	3.608927918	----------	similar to YGL010w-like protein	uncharacterized protein LOC8055401
Sh07_g011720	3.547614992	----------	Ethylene-responsive transcription factor ERF109	ethylene-responsive transcription factor ERF109
Sh03_g030540	3.477855735	----------	Cold-regulated 413 plasma membrane protein 4	hypothetical protein SORBI_3003G407001
Sh01_g036340	3.357072171	----------	Thaumatin-like protein 1	thaumatin-like protein 1b
Sh03_g008000	3.320038401	----------	Flowering-promoting factor 1-like protein 1	flowering-promoting factor 1-like protein 1
Sh05_g002670	3.239546291	----------	Putative Scarecrow-like protein 23	nodulation-signaling pathway 2 protein
Sh04_g026080	3.21258053	----------	Cinnamoyl-CoA reductase 1	cinnamoyl-CoA reductase 1
Sh09_g010890	3.062869359	----------	Conserved hypothetical protein	---NA---
Sh02_g002520	2.980277029	----------	Viviparous-14	9-cis-epoxycarotenoid dioxygenase 1, chloroplastic
Sh01_g028420	2.964340638	----------	Flavonoid 3'-monooxygenase	putative elicitor-inducible cytochrome P450
Sh03_g015570	2.873794122	----------	similar to Cytochrome P450	cytochrome P450 72A11
Sh04_g012160	2.821122871	----------	E3 ubiquitin-protein ligase EL5	E3 ubiquitin-protein ligase EL5-like
Sh03_g001570	2.79514143	----------	Gibberellin 2-beta-dioxygenase 1	Gibberellin 2-beta-dioxygenase 1
Sh04_g003140	2.734704675	----------	Os02g0153300 protein	Tyrosine-sulfated glycopeptide receptor 1
Sh01_g007270	2.733896154	----------	Transcription factor BHLH148	helix-loop-helix DNA-binding domain containing protein
Sh10_g010680	2.731173812	----------	ABC transporter G family member 11	ABC transporter G family member 11
Sh06_g009530	2.683888331	----------	Disease resistance protein RPS2	disease resistance protein RPS2
Sh03_g019730	2.623413159	----------	B3 domain-containing protein Os03g0120900	B3 domain-containing protein Os03g0120900 isoform X1
Sh04_g025970	2.613239345	----------	similar to Os02g0111600 protein	wall-associated receptor kinase 2
Sh05_g011820	2.446520435	----------	Linoleate 9S-lipoxygenase 2	Linoleate 9S-lipoxygenase 2
Sh05_g001970	2.374922264	----------	Phytosulfokines 5	TPA_exp: putative phytosulfokine peptide precursor
Sh03_g028360	2.373301236	----------	Linoleate 9S-lipoxygenase 2	Linoleate 9S-lipoxygenase 1
Sh02_g017700	2.247521934	----------	Solute carrier family 35, member F1	solute carrier family 35 member F1
Sh03_g002690	2.224299798	----------	similar to WRKY transcription factor 6-like	probable WRKY transcription factor 72
Sh06_g015050	2.208036423	----------	Acyclic sesquiterpene synthase	acyclic sesquiterpene synthase
Sh01_g005990	2.191298063	----------	Putative UDP-glycosyltransferase 83A1	putative glucosyl transferase
Sh06_g019250	2.189963386	----------	Conserved hypothetical protein	uncharacterized protein LOC8083096
Sh04_g022690	2.186131866	----------	Salutaridine reductase	salutaridine reductase
Sh10_g003560	2.178202577	----------	Transferase	transferase isoform X1
Sh08_g003170	2.166438157	----------	Transcription factor TGAL4	transcription factor TGAL4 isoform X1
Sh09_g019820	2.13522851	----------	WRKY transcription factor 22	WRKY transcription factor 22

Sh06_g009870	2.128586422	----------	Cytokinin dehydrogenase	cytokinin dehydrogenase 8
Sh03_g031950	2.094420173	----------	Cytokinin dehydrogenase 4	cytokinin dehydrogenase 4
Sh06_g017710	2.083016884	----------	UDP-glycosyltransferase 89B1	UDP-glycosyltransferase 89B1
Sh06_g015810	2.039283307	----------	LRR receptor-like serine/threonine-protein kinase FLS2	LRR receptor-like serine/threonine-protein kinase FLS2
Sh03_g002680	2.020955918	----------	WRKY transcription factor	WRKY transcription factor
Sh06_g004810	2.008751497	----------	Transcription factor bHLH18	transcription factor bHLH18
Sh09_g007690	1.996033148	----------	Transcription factor MYB44	transcription factor MYB44
Sh10_g007860	1.983000264	----------	weakly similar to Os04g0451700 protein	hypothetical protein SETIT_4G091100v2
Sh01_g018040	1.975955839	----------	Beta-amylase 1, chloroplastic	beta-amylase 1, chloroplastic
Sh10_g007330	1.972422187	----------	WAT1-related protein At4g08300	nodulin protein
Sh04_g002150	1.96591875	----------	Conserved hypothetical protein	uncharacterized protein LOC8057525
Sh09_g008170	1.939429599	----------	Pectinesterase	putative pectinesterase/pectinesterase inhibitor 7
Sh02_g029550	1.937023862	----------	Hexosyltransferase	probable galacturonosyltransferase-like 4
Sh01_g009390	1.924655916	----------	Basic blue protein	basic blue protein
Sh09_g001420	1.904940951	----------	Cysteine-rich repeat secretory protein 55	cysteine-rich repeat secretory protein 55
Sh06_g000290	1.883283466	----------	Glyoxylate/hydroxypyruvate reductase HPR3	glyoxylate/hydroxypyruvate reductase HPR3
Sh10_g007340	1.876487885	----------	WAT1-related protein At1g21890	WAT1-related protein
Sh04_g017170	1.866142912	----------	Conserved hypothetical protein	protein RNA-directed DNA methylation 3-like
Sh04_g023020	1.857451105	----------	Conserved hypothetical protein	hypothetical protein BAE44_0006983, partial
Sh03_g010030	1.839581464	----------	Polygalacturonase At1g48100	polygalacturonase At1g48100
Sh06_g005090	1.839439964	----------	12-oxo-phytodienoic acid reductase	putative 12-oxophytodienoate reductase 11
Sh04_g018550	1.836400783	----------	Phosphoenolpyruvate carboxylase	hypothetical protein SHCRBa_257_A20_F_30
Sh09_g017400	1.830265992	----------	similar to Os01g0699500 protein	mitogen-activated protein kinase kinase kinase 17
Sh02_g005570	1.82570814	----------	similar to Os03g0824600 protein	DIMBOA UDP-glucosyltransferase BX9
Sh03_g033200	1.819913909	----------	Protein NRT1/ PTR FAMILY 2.3	protein NRT1/ PTR FAMILY 2.7-like
Sh03_g000850	1.797061714	----------	Mitochondrial arginine transporter BAC2	mitochondrial arginine transporter BAC2
Sh10_g014750	1.789518268	----------	Conserved hypothetical protein	chaperone protein dnaJ 8, chloroplastic
Sh10_g008750	1.789355804	----------	Metalloendoproteinase 2-MMP	Metalloendoproteinase 2-MMP
Sh04_g020990	1.775580368	----------	Conserved hypothetical protein	uncharacterized protein LOC8073915
Sh01_g040190	1.710180541	----------	Cysteine-rich and transmembrane domain-containing protein PCC1	uncharacterized protein LOC8059815
Sh04_g016270	1.704310182	----------	similar to Os02g0753400 protein	hypothetical protein Shy3280Sca034_059
Sh01_g005830	1.681246177	----------	Conserved hypothetical protein	transcription factor bHLH110-like
Sh02_g014880	1.674470906	----------	Putative Tuliposide A-converting enzyme 1, chloroplastic	Tuliposide A-converting enzyme b1, amyloplastic
Sh02_g006520	1.673648594	----------	Glycosyltransferase	UDP-glycosyltransferase 91C1
Sh10_g000410	1.664382504	----------	Glycoside hydrolase, family 28	putative polygalacturonase
Sh02_g016760	1.658358329	----------	Sarcosine oxidase	putative sarcosine oxidase
Sh03_g027110	1.650007052	----------	Acidic endochitinase	hevamine-A precursor
Sh10_g002110	1.624099898	----------	Protein SOMBRERO	NAC domain-containing protein 43
Sh01_g019120	1.612217677	----------	Protein trichome birefringence-like 20	Protein trichome birefringence-like 19
Sh06_g012090	1.607390703	----------	Cis-zeatin O-glucosyltransferase 1	putative cis-zeatin O-glucosyltransferase
Sh05_g010930	1.600536049	----------	Magnesium/proton exchanger 1	magnesium/proton exchanger 1
Sh03_g019720	1.599352354	----------	Ribose-phosphate pyrophosphokinase 3, chloroplastic	ribose-phosphate pyrophosphokinase 3, chloroplastic
Sh02_g016780	1.575213635	----------	Squalene monooxygenase	putative sarcosine oxidase
Sh05_g003050	1.552269388	----------	LAX3	auxin transporter-like protein 3
Sh05_g004570	1.534127902	----------	Argos-like protein	protein AUXIN-REGULATED GENE INVOLVED IN ORGAN SIZE

Sh07_g010500	1.532399541	----------	Anthranilate N-benzoyltransferase protein 1	putrescine hydroxycinnamoyltransferase 1
Sh03_g017800	1.517344968	----------	Transcription factor RAX1	O-acyltransferase WSD1
Sh05_g010060	1.493046626	----------	Conserved hypothetical protein	---NA---
Sh04_g016830	1.480166982	----------	Hexosyltransferase	probable galacturonosyltransferase 9
Sh09_g011530	1.474756978	----------	Potassium channel AKT2	potassium channel AKT2
Sh04_g016720	1.468485156	----------	similar to Kelch repeat-containing F-box-like	F-box/kelch-repeat protein At1g74510-like
Sh06_g009610	1.46668215	----------	similar to OSIGBa0145M07.1 protein	putative low-specificity L-threonine aldolase 1
Sh_250P04_g000030	1.444405741	----------	Pheophorbide a oxygenase, chloroplastic	pheophorbide a oxygenase, chloroplastic
Sh10_g007530	1.434243546	----------	RING-H2 finger protein ATL34	uncharacterized protein LOC8070769
Sh01_g036370	1.42262438	----------	Cytochrome P450 90B2	brassinosteroid synthesis1
Sh05_g010020	1.406503181	----------	ELF3-like protein 2	uncharacterized protein LOC110435610
Sh05_g004390	1.399282094	----------	similar to At1g18480/F15H18_1	shewanella-like protein phosphatase 2
Sh04_g010070	1.369444495	----------	Gamma-glutamylcyclotransferase	cation transport protein chaC
Sh06_g005430	1.361869577	----------	Lipoxygenase	putative lipoxygenase 5
Sh06_g003200	1.332242623	----------	Potassium transporter	potassium transporter 1
Sh04_g020950	1.329091942	----------	Transcription factor LHW	transcription factor bHLH157
Sh03_g022940	1.316731909	----------	Protein PAM71-homolog, chloroplastic	uncharacterized protein LOC101755031
Sh04_g000530	1.31385377	----------	Glycerol-3-phosphate acyltransferase	glycerol-3-phosphate 2-O-acyltransferase 6
Sh04_g020600	1.298226335	----------	E3 ubiquitin-protein ligase RHA2B	E3 ubiquitin-protein ligase RHA1B
Sh03_g003850	1.280682567	----------	Lactoylglutathione lyase	lactoylglutathione lyase
Sh08_g008730	1.271426297	----------	ATPase 3, plasma membrane-type	uncharacterized protein LOC110429809
Sh01_g041500	1.259332574	----------	similar to CHY zinc finger family protein, expressed	E3 ubiquitin-protein ligase RZFP34
Sh09_g001630	1.250474028	----------	Conserved hypothetical protein	uncharacterized protein LOC8068694
Sh01_g004680	1.24744097	----------	Inosine-5'-monophosphate dehydrogenase	inosine-5'-monophosphate dehydrogenase
Sh10_g000700	1.240124415	----------	Haloacid dehalogenase-like hydrolase domain-containing protein Sgpp	haloacid dehalogenase-like hydrolase domain-containing protein Sgpp isoform X1
Sh03_g031270	1.239464988	----------	Thiamine pyrophosphokinase 1	thiamine pyrophosphokinase 1
Sh01_g003070	1.237219915	----------	Transcription factor bHLH106	transcription factor bHLH106
Sh02_g013280	1.231152419	----------	Gamma-glutamyl peptidase 3	---NA---
Sh03_g019740	1.225330386	----------	similar to P-glycoprotein homologue	putative ABC transporter B family member 8
Sh01_g028460	1.219291772	----------	Rhomboid-like protein 19	rhomboid-like protein 19
Sh06_g008140	1.218157693	----------	CMP-sialic acid transporter 4	CMP-sialic acid transporter 4
Sh01_g009020	1.203153058	----------	Threonine dehydratase biosynthetic, chloroplastic	threonine dehydratase biosynthetic, chloroplastic
Sh10_g000450	1.198368206	----------	WAT1-related protein At4g01440	WAT1-related protein At3g30340
Sh06_g006180	1.177957801	----------	weakly similar to H0523F07.3 protein	OSJNBa0006M15.15-like protein
Sh02_g008530	1.142700277	----------	Cinnamic acid 4-hydroxylase	trans-cinnamate 4-monooxygenase
Sh09_g006100	1.13244073	----------	Auxin-responsive protein IAA16	IAA16-auxin-responsive Aux/IAA family member
Sh09_g004400	1.123421391	----------	similar to Os05g0155200 protein	probable ethylene response sensor 2
Sh03_g005760	1.113130724	----------	Multicopper oxidase LPR1 homolog 1	multicopper oxidase LPR1 homolog 1
Sh01_g017360	1.109947797	----------	Homeobox-leucine zipper protein HOX10	homeobox-leucine zipper protein HOX9 isoform X1
Sh09_g017120	1.081214933	----------	Conserved hypothetical protein	alpha/beta-Hydrolases superfamily protein
Sh06_g010180	1.066201754	----------	GEM-like protein 4	putative GEM-like protein 8
Sh07_g013690	1.064445525	----------	Conserved hypothetical protein	uncharacterized protein LOC8057839
Sh04_g013480	1.041534301	----------	Hypoxia induced protein conserved region containing protein	hypoxia induced protein conserved region containing protein
Sh03_g003830	1.037879129	----------	ABC transporter C family member 3	ABC transporter C family member 3

Sh06_g004950	1.019571232	----------	Chloride channel protein CLC-c	Chloride channel protein CLC-c
Sh06_g016500	1.017069172	----------	similar to H0105C05.9 protein	transcription factor bHLH112
Sh03_g019240	1.004662651	----------	S-adenosylmethionine-dependent methyltransferase	putative methyltransferase
Sh04_g017090	1.004615423	----------	similar to Rop1 small GTP binding protein	rac-like GTP-binding protein 3 isoform X2
Sh03_g033490	0.999237121	----------	Cationic peroxidase SPC4	cationic peroxidase SPC4-like
Sh02_g013070	0.97971435	----------	Orphans transcription factor (Fragment)	---NA---
Sh06_g009600	0.970979525	----------	similar to OSIGBa0145M07.1 protein	putative low-specificity L-threonine aldolase 1
Sh04_g017420	0.9707999	----------	similar to Histidine kinase	probable histidine kinase 6 isoform X1
Sh02_g002360	0.951109054	----------	CBL-interacting protein kinase 23	CBL-interacting protein kinase 23
Sh_227A23_contig-1_g000020	0.94851194	----------	12-oxo-phytodienoic acid reductase	putative 12-oxophytodienoate reductase 11
Sh07_g002780	0.926913091	----------	Conserved hypothetical protein	uncharacterized protein LOC8076535
Sh03_g026240	0.910210595	----------	Bowman-Birk type trypsin inhibitor	Bowman-Birk type trypsin inhibitor
Sh04_g018720	0.909286608	----------	Putative Outer envelope membrane protein 7	outer envelope membrane protein 7
Sh03_g006380	0.908440629	----------	Fructose-bisphosphate aldolase	Fructose-bisphosphate aldolase 3, chloroplastic
Sh04_g002850	0.90767384	----------	Cytosolic invertase 1	cytosolic invertase 1
Sh02_g003290	0.875028126	----------	Glucan endo-1,3-beta-glucosidase 8	glucan endo-1,3-beta-glucosidase 8
Sh04_g006090	0.865776927	----------	Conserved hypothetical protein	uncharacterized LOC100383953 isoform X2
Sh01_g011550	0.859462879	----------	Type IV inositol polyphosphate 5-phosphatase 7	type IV inositol polyphosphate 5-phosphatase 7
Sh05_g001030	0.857691578	----------	similar to ZF-HD protein dimerisation region containing protein, expressed	mini zinc finger protein 1
Sh10_g008260	0.852775474	----------	Aquaporin NIP2-2	aquaporin NIP2-2
Sh03_g019070	0.847341761	----------	similar to Hydrolase-like protein	abhydrolase domain-containing protein C22H12.03
Sh04_g018310	0.842921122	----------	Cellulose synthase-like protein E2	cellulose synthase-like protein E2
Sh10_g017770	0.831656427	----------	Two-component response regulator ARR2	---NA---
Sh02_g016260	0.826540388	----------	similar to Os09g0481700 protein	probable WRKY transcription factor 2
Sh02_g030770	0.824310005	----------	Hypoxia induced protein conserved region containing protein	hypoxia induced protein conserved region containing protein
Sh07_g016480	0.788976534	----------	3-hydroxy-3-methylglutaryl-coenzyme A reductase 3	3-hydroxy-3-methylglutaryl-coenzyme A reductase 3
Sh03_g025360	0.786252396	----------	Conserved hypothetical protein	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
Sh10_g009860	0.780004176	----------	Phosphatidylinositol 4-kinase gamma 7	Phosphatidylinositol 4-kinase gamma 7
Sh10_g007440	0.773481894	----------	similar to Lipase class 3-like	triacylglycerol lipase-like 1
Sh03_g013570	0.763793495	----------	Cytosolic aldehyde dehydrogenase RF2D	aldehyde dehydrogenase family 2 member C4
Sh09_g012390	0.733038496	----------	similar to Expressed protein	uncharacterized protein LOC8072519
Sh07_g009680	0.730171665	----------	similar to FYVE finger-containing phosphoinositide kinase-like	putative 1-phosphatidylinositol-3-phosphate 5-kinase FAB1C
Sh10_g002260	0.720337759	----------	3-phosphoshikimate 1-carboxyvinyltransferase	5-enolpyruvylshikimate-3-phosphate synthase (plastid)
Sh06_g000270	0.704013657	----------	Arginase 1, mitochondrial	Arginase 1 mitochondrial
Sh07_g013970	0.699069838	----------	60S ribosomal protein L2, mitochondrial	ribosomal protein L2
Sh07_g017180	0.698163052	----------	Glycerophosphodiester phosphodiesterase GDPDL4	glycerophosphodiester phosphodiesterase GDPDL4 isoform X1
Sh01_g033810	0.69128173	----------	Catalytic/ hydrolase	---NA---
Sh10_g012490	0.675620783	----------	similar to ZLL/PNH homologous protein	protein argonaute PNH1
Sh01_g005080	0.66314796	----------	similar to Wound and phytochrome signaling involved receptor like kinase	wound and phytochrome signaling involved receptor like kinase
Sh05_g010380	0.65994315	----------	Glutathione synthetase, chloroplastic	glutathione synthetase, chloroplastic
Sh01_g021230	0.6527292	----------	weakly similar to Homeobox-leucine zipper protein HAT22	homeobox-leucine zipper protein HOX15
Sh02_g015420	0.649882476	----------	Dicarboxylate transporter 2.1, chloroplastic	2-oxoglutarate/malate translocator, chloroplastic
Sh07_g005650	0.646687306	----------	Glucose-6-phosphate/phosphate translocator 2	putative glucose-6-phosphate translocator

Sh07_g016180	0.613144041	----------	Conserved hypothetical protein	TBC1 domain family member 5 homolog B-like
Sh03_g001850	0.569747505	----------	MADS-box transcription factor 3	MADS-box transcription factor 3 isoform X2
Sh02_g020090	0.55516886	----------	Conserved hypothetical protein	---NA---
Sh03_g012130	0.539606302	----------	Bidirectional sugar transporter SWEET2a	bidirectional sugar transporter SWEET2a
			SP80-3280 up-regulated DEGs	
Sh01_g040760	----------	8.142033359	3-ketoacyl-CoA synthase	3-ketoacyl-CoA synthase 2
Sh04_g026060	----------	6.880240679	Cinnamoyl-CoA reductase 1	cinnamoyl-CoA reductase 1
Sh07_g004930	----------	6.015389613	Inactive 7-epi-sesquithujene synthase	sesquithujene synthase A
Sh05_g011500	----------	5.724500401	Bowman-Birk type trypsin inhibitor	Bowman-Birk type trypsin inhibitor
Sh01_g032750	----------	5.655351911	LOB domain-containing protein 1	---NA---
Sh03_g005580	----------	5.651886598	Bowman-Birk type wound-induced proteinase inhibitor WIP1	Bowman-Birk type wound-induced proteinase inhibitor WIP1
Sh09_g000100	----------	5.384760756	Putative Separase	salicylate carboxymethyltransferase
Sh08_g002840	----------	5.319534927	similar to Expressed protein	stress-response A/B barrel domain-containing protein At5g22580-like isoform X2
Sh02_g008750	----------	5.007651253	5-pentadecatrienyl resorcinol O-methyltransferase	5-pentadecatrienyl resorcinol O-methyltransferase
Sh04_g026070	----------	4.977100571	Cinnamoyl-CoA reductase 1	Cinnamoyl-CoA reductase 1
Sh07_g005550	----------	4.759869455	Delta-guaiene synthase 1	(E)-beta-caryophyllene synthase
Sh05_g008620	----------	4.433902993	Pathogenesis-related protein	pathogenesis-related protein
Sh04_g027090	----------	4.386450832	Xyloglucan endotransglucosylase/hydrolase protein 31	putative xyloglucan endotransglucosylase/hydrolase protein 32
Sh03_g010470	----------	4.215325899	Pectinesterase	putative pectinesterase/pectinesterase inhibitor 41
Sh04_g026050	----------	4.084322166	Cinnamoyl-CoA reductase-like protein 3	cinnamoyl-CoA reductase 1
Sh07_g004880	----------	3.99018035	similar to Terpene synthase 10	terpene synthase 10
Sh10_g008980	----------	3.745551734	Putative Defensin-like protein 259	hypothetical protein ZEAMMB73_Zm00001d037281
Sh07_g011490	----------	3.421602159	Bifunctional monodehydroascorbate reductase and carbonic anhydrase nectarin-3	alpha carbonic anhydrase 7
Sh01_g003660	----------	3.396691571	Indole-3-glycerol phosphate lyase, chloroplastic	indole-3-glycerol phosphate lyase, chloroplastic
Sh03_g020000	----------	3.293465092	GDSL esterase/lipase At5g45670	GDSL esterase/lipase
Sh09_g001150	----------	3.287380189	Subtilisin-chymotrypsin inhibitor-2A	hypothetical protein SORBI_3009G009700
Sh09_g011200	----------	3.11987184	Gibberellin 20 oxidase 2	Gibberellin 20 oxidase 2
Sh03_g010670	----------	3.031655786	Polycomb group protein VERNALIZATION 2	---NA---
Sh06_g008450	----------	3.008957752	similar to Endochitinase A precursor	endochitinase A
Sh07_g005060	----------	2.856653249	Transferase family protein	Phenolic glucoside malonyltransferase 2
Sh04_g026040	----------	2.791723444	Cinnamoyl-CoA reductase-like protein 3	cinnamoyl-CoA reductase 1
Sh04_g017430	----------	2.74806043	Immediate-early fungal elicitor protein CMPG1	U-box domain-containing protein 21
Sh04_g019970	----------	2.702751828	4-coumarate:coenzyme A ligase 2	probable 4-coumarate--CoA ligase 2
Sh06_g010040	----------	2.665832643	UDP-glycosyltransferase 82A1	UDP-glycosyltransferase 82A1
Sh03_g032820	----------	2.593549722	Putative similar to Expressed protein	uncharacterized protein LOC8077368
Sh02_g006640	----------	2.455640066	GTP-binding protein YPTM1	B12D protein
Sh06_g002930	----------	2.387759636	Protein TIFY 9	protein TIFY 9
Sh07_g001350	----------	2.356268656	L-gulonolactone oxidase 2	L-gulonolactone oxidase 2
Sh02_g005470	----------	2.339879737	Gibberellin 2-beta-dioxygenase 1	Gibberellin 2-beta-dioxygenase 1
Sh09_g004240	----------	2.297871305	similar to Lipase class 3-like	triacylglycerol lipase-like 1
Sh03_g030410	----------	2.272312619	similar to Putative regulatory protein	hypothetical protein SORBI_3003G405200
Sh02_g018640	----------	2.270542433	NAC domain-containing protein 18	uncharacterized LOC100277053
Sh09_g004230	----------	2.260540317	DNA-directed RNA polymerase subunit beta'	triacylglycerol lipase-like 1

Sh03_g007190	----------	2.222240984	Putative similar to Symbiosis-related protein-like protein	Glycosyltransferase family 61 protein
Sh04_g013840	----------	2.214437013	Protein binding protein	Protein binding protein
Sh02_g016470	----------	2.166239438	similar to Os09g0484900 protein	tonoplast dicarboxylate transporter
Sh01_g022080	----------	2.112632258	Protein WIR1A	protein WIR1A-like
Sh02_g019540	----------	2.059338533	GDSL esterase/lipase EXL3	GDSL esterase/lipase EXL3
Sh01_g043890	----------	1.993856278	RHOMBOID-like protein 3	RHOMBOID-like protein 2
Sh10_g014900	----------	1.992553154	Heptahelical transmembrane protein 2	heptahelical transmembrane protein ADIPOR2
Sh06_g002900	----------	1.989942594	Protein TIFY 9	protein TIFY 9
Sh03_g026740	----------	1.967818418	Starch binding domain containing protein	starch binding domain containing protein
Sh03_g010330	----------	1.945431682	Embryonic abundant protein-like	putative methyltransferase DDB_G0268948
Sh08_g003180	----------	1.795391013	similar to Os11g0153000 protein	uncharacterized protein LOC8066974
Sh01_g022420	----------	1.77285502	similar to Cyclin-P4-1	cyclin-P4-1-like
Sh02_g025560	----------	1.761146932	similar to OSJNBa0031O09.02	uncharacterized protein LOC8055685
Sh09_g001000	----------	1.756997747	NAC domain-containing protein 68	NAC domain-containing protein 68
Sh01_g012390	----------	1.690812112	9-cis-epoxycarotenoid dioxygenase 1, chloroplastic	9-cis-epoxycarotenoid dioxygenase 1, chloroplastic
Sh06_g013830	----------	1.6029603	Receptor-like protein kinase FERONIA	receptor-like protein kinase FERONIA
Sh05_g011490	----------	1.602164961	Bowman-Birk type trypsin inhibitor	Bowman-Birk type trypsin inhibitor
Sh03_g018900	----------	1.581486437	Transcription factor bHLH87	transcription factor bHLH84
Sh02_g028030	----------	1.50717085	Calmodulin binding protein	uncharacterized protein LOC8079201
Sh04_g020790	----------	1.498570124	Protein DETOXIFICATION	protein DETOXIFICATION 49
Sh09_g010120	----------	1.497754937	Basic endochitinase A	chitinase 2
Sh03_g032870	----------	1.484478125	NAD(P)H:quinone oxidoreductase	probable NADPH:quinone oxidoreductase 2
Sh03_g021960	----------	1.470329733	BHLH transcription factor (Fragment)	DNA binding protein
Sh04_g023370	----------	1.462831542	similar to AP2 domain-containing transcription factor-like	ethylene-responsive transcription factor ERF014
Sh09_g001230	----------	1.435295311	Subtilisin-chymotrypsin inhibitor-2A	Subtilisin-chymotrypsin inhibitor-2A
Sh01_g031180	----------	1.41838847	similar to Myb-like DNA-binding domain containing protein, expressed	transcription factor MYB2
Sh07_g001070	----------	1.330792431	Peroxidase	peroxidase 47
Sh03_g019470	----------	1.313292538	Serine acetyltransferase 3	probable serine acetyltransferase 1
Sh08_g007000	----------	1.304319237	Putative LRR receptor-like serine/threonine-protein kinase At3g47570	receptor kinase-like protein Xa21 isoform X2
Sh07_g003070	----------	1.284307504	External alternative NAD(P)H-ubiquinone oxidoreductase B2, mitochondrial	External alternative NAD(P)H-ubiquinone oxidoreductase B4 mitochondrial
Sh09_g010250	----------	1.22802584	Glycosyltransferase	indole-3-acetate beta-glucosyltransferase
Sh04_g018560	----------	1.200548989	similar to Os02g0717600 protein	hypothetical protein SHCRBa_257_A20_F_30
Sh01_g010050	----------	1.186374714	Lipoxygenase	probable linoleate 9S-lipoxygenase 4
Sh01_g040910	----------	1.178037754	similar to FAD binding domain containing protein, expressed	FAD/NAD(P)-binding oxidoreductase family protein
Sh05_g001960	----------	1.115255509	Myosin-15	---NA---
Sh01_g037130	----------	1.088111251	Os03g0218400 protein	---NA---
Sh10_g006890	----------	1.072282719	Auxin response factor	auxin response factor 16 isoform X1
Sh02_g017080	----------	1.060387683	Protein capI	UDP-glucuronate 4-epimerase 6
Sh06_g017080	----------	1.047092789	ABC transporter B family member 19	ABC transporter B family member 19
Sh06_g001230	----------	1.024715324	Cysteine synthase	cysteine synthase
Sh03_g025130	----------	1.024396583	Amino acid transporter AVT6C	probable sodium-coupled neutral amino acid transporter 6 isoform X2
Sh07_g010230	----------	1.015433427	Ribonuclease 3	ribonuclease 1
Sh05_g009980	----------	0.986831148	Glycine-rich domain-containing protein 2	glycine-rich domain-containing protein 1
Sh01_g002980	----------	0.981270953	NAC12	stress-induced NAc protein 1 SNAC1

Sh02_g019010	----------	0.932216321	Phosphatase DCR2	Phosphatase DCR2
Sh01_g024140	----------	0.845357153	similar to Glutathione S-transferase GST 25	glutathione transferase25
Sh04_g018650	----------	0.806141499	Proton-dependent oligopeptide transporter family	protein NRT1/ PTR FAMILY 7.3
Sh_217A12_contig-1_g000010	----------	0.801603115	Phosphatase DCR2	Phosphatase DCR2
Sh_020J14_contig-3_g000010	----------	0.765879841	Glutathione S-transferase U17	glutathione transferase30
Sh06_g011210	----------	0.76556323	similar to Iron transport protein 2	probable metal-nicotianamine transporter YSL16
Sh01_g027080	----------	0.763306655	Copper transporter 5.1	copper transporter 5.1
Sh01_g000860	----------	0.763022905	Monofunctional aspartate kinase 1	aspartokinase 1, chloroplastic
Sh09_g018510	----------	0.738124518	Solute carrier family 2, facilitated glucose transporter member 8	sugar transporter ERD6-like 4
Sh01_g025140	----------	0.732923684	Interferon-related developmental regulator 2	interferon-related developmental regulator 2
Sh10_g003070	----------	0.712774801	Sulfate transporter 3.1	probable sulfate transporter 3.4
Sh08_g008690	----------	0.70634818	similar to Thaumatin family protein, expressed	osmotin-like protein
Sh03_g031420	----------	0.701527018	similar to Glutathione S-transferase 3	glutathione S-transferase 3
Sh02_g016570	----------	0.677394643	Conserved hypothetical protein	Proton pump-interactor 1
Sh06_g002720	----------	0.667459549	similar to OSIGBa0096P03.3 protein	protein NUCLEAR FUSION DEFECTIVE 4
Sh_201L24_g000030	----------	0.662018191	Coatomer subunit beta'-2	hypothetical protein BRADI_4g21980v3
Sh03_g028470	----------	0.654485402	Calreticulin-3	calreticulin-3 precursor
Sh04_g002020	----------	0.585617479	Cyclin-T1-2	cyclin-T1-1 isoform X2
Sh10_g002700	----------	0.572337003	U-box domain-containing protein 35	U-box domain-containing protein 35 isoform X1
Sh04_g012030	----------	0.567864096	Chloride channel protein	chloride channel protein CLC-c
Sh03_g010780	----------	0.563126849	Peroxidase 1	Peroxidase 64
Sh04_g027510	----------	0.558584485	U-box domain-containing protein 62	U-box domain-containing protein 62
Sh01_g006730	----------	0.537566689	similar to Myosin heavy chain class XI E1 protein	myosin-12 isoform X1
Sh_227O13_g000010	----------	0.521625972	Putative Coilin	---NA---
Sh_250B17_g000100	----------	0.520261932	similar to Zinc-finger protein	protein binding protein
Sh07_g011190	----------	0.511775554	12-oxo-phytodienoic acid reductase	12-oxophytodienoate reductase 7
Sh01_g025260	----------	0.506346769	Allene oxide cyclase	Allene oxide cyclase, chloroplastic
Sh02_g031050	----------	0.485284992	similar to Ribosomal protein S6 kinase	ribosomal protein S6 kinase
			Common down-regulated DEGs	
Sh03_g006150	-0.672889998	-0.460752466	Conserved hypothetical protein	uncharacterized protein LOC112891657
Sh06_g000940	-1.108108821	-0.757829787	weakly similar to H0716A07.5 protein	uncharacterized protein LOC8080276
Sh01_g008250	-1.753396315	-1.243432177	Putative protein	uncharacterized protein LOC8060547
			RB867515 down-regulated DEGs	
Sh01_g009060	-0.478271068	----------	Phosphoglucomutase, cytoplasmic 2	phosphoglucomutase, cytoplasmic 2
Sh04_g001220	-0.498202457	----------	NADP-dependent D-sorbitol-6-phosphate dehydrogenase	NADP-dependent D-sorbitol-6-phosphate dehydrogenase
Sh01_g023880	-0.499679078	----------	Histone H4	histone H4
Sh04_g008870	-0.510961693	----------	Phosphoglucan, water dikinase, chloroplastic	Phosphoglucan water dikinase chloroplastic
Sh07_g016800	-0.517945676	----------	Lysine-specific demethylase JMJ30	lysine-specific demethylase JMJ30 isoform X2
Sh03_g009410	-0.545538257	----------	Sodium-dependent phosphate transport protein 1, chloroplastic	probable anion transporter 1, chloroplastic
Sh09_g016870	-0.558241244	----------	ADP,ATP carrier protein	probable ADP,ATP carrier protein At5g56450
Sh04_g010380	-0.581160643	----------	Ethylene-responsive transcription factor-like protein At4g13040	ethylene-responsive transcription factor-like protein At4g13040 isoform X4
Sh03_g015130	-0.581471801	----------	Auxin-induced protein PCNT115	probable aldo-keto reductase 1

Sh02_g004650	-0.591425049	----------	weakly similar to Expressed protein	hypothetical protein SORBI_3002G072100
Sh09_g016270	-0.606141442	----------	Conserved hypothetical protein	uncharacterized protein LOC110430331
Sh06_g005670	-0.614436791	----------	Zeaxanthin epoxidase, chloroplastic	zeaxanthin epoxidase, chloroplastic isoform X2
Sh01_g002120	-0.618614767	----------	similar to Anthranilate synthase alpha 1 subunit	anthranilate synthase alpha subunit 1, chloroplastic
Sh06_g003460	-0.637567736	----------	1,4-alpha-glucan-branching enzyme 2, chloroplastic/amyloplastic	Starch branching enzyme IIa
Sh01_g019640	-0.644990305	----------	Acylamino-acid-releasing enzyme 1	Acylamino-acid-releasing enzyme
Sh03_g019140	-0.647181706	----------	Alpha-amylase 3, chloroplastic	alpha-amylase 3, chloroplastic
Sh10_g006950	-0.663112144	----------	Putative Pentatricopeptide repeat-containing protein At4g04370	pentatricopeptide repeat-containing protein At3g53360, mitochondrial-like
Sh01_g026050	-0.666678041	----------	Conserved hypothetical protein	uncharacterized protein LOC8080422
Sh01_g000850	-0.671531629	----------	Integral membrane protein	uncharacterized protein LOC110431735
Sh09_g005060	-0.706893701	----------	6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase	fructose-6-phosphate 2-kinase/fructose-2,6-bisphosphatase
Sh01_g005600	-0.720559255	----------	Conserved hypothetical protein	---NA---
Sh03_g031630	-0.735281475	----------	Conserved hypothetical protein	Spermatogenesis-associated protein 20
Sh01_g026060	-0.755391692	----------	Conserved hypothetical protein	uncharacterized protein LOC8080422
Sh08_g002650	-0.758207887	----------	Dual-specificity protein-like phosphatase 3	phosphoglucan phosphatase LSF2, chloroplastic
Sh01_g005440	-0.802208963	----------	Putative CCG-binding protein 1	CCG-binding protein 1
Sh02_g026330	-0.81194823	----------	Threonine--tRNA ligase, chloroplastic/mitochondrial 2	threonine--tRNA ligase, chloroplastic/mitochondrial 2
Sh06_g015390	-0.8138634	----------	similar to OSIGBa0126B18.9 protein	uncharacterized protein LOC8063969 isoform X1
Sh01_g032350	-0.834539155	----------	Gamma-interferon-inducible lysosomal thiol reductase	gamma-interferon-inducible lysosomal thiol reductase-like isoform X1
Sh07_g012920	-0.83626774	----------	Putative Elongation factor 1-gamma 3	Thioredoxin family protein
Sh03_g009430	-0.845873193	----------	Ascorbate transporter, chloroplastic	predicted protein
Sh01_g005430	-0.848336941	----------	CCG-binding protein 1	CCG-binding protein 1
Sh01_g034840	-0.861500008	----------	similar to Expressed protein	Regulator of Vps4 activity in the MVB pathway protein
Sh03_g018800	-0.86284684	----------	Putative F-box/kelch-repeat protein At1g23390	F-box/kelch-repeat protein At1g23390
Sh04_g017900	-0.866605674	----------	Organelle RRM domain-containing protein 1, chloroplastic	organelle RRM protein1
Sh07_g017900	-0.875672318	----------	Histone H2B.3	Histone H2B.4
Sh02_g004030	-0.877710505	----------	Peptidyl-prolyl cis-trans isomerase FKBP16-4, chloroplastic	Peptidyl-prolyl cis-trans isomerase FKBP16-4, chloroplastic
Sh10_g010930	-0.891510163	----------	Alpha-glucan water dikinase, chloroplastic	Alpha-glucan water dikinase 1 chloroplastic
Sh04_g011250	-0.904098638	----------	Heme-binding-like protein At3g10130, chloroplastic	SOUL heme-binding protein
Sh01_g018460	-0.941443324	----------	similar to H0801D08.18 protein	E3 ubiquitin-protein ligase AIRP2-like isoform X2
Sh02_g017090	-0.942203486	----------	ABC transporter G family member 50	hypothetical protein PAHAL_9G046900
Sh02_g014660	-0.98950067	----------	Polcalcin Jun o 2	calmodulin-like protein 1
Sh01_g030770	-1.002453221	----------	DnaJ protein homolog 2	chaperone protein dnaJ 20, chloroplastic
Sh01_g028190	-1.010476117	----------	similar to Universal stress protein family protein, expressed	universal stress protein PHOS34
Sh03_g023420	-1.023837426	----------	similar to Membrane protein-like	sulfite exporter TauE/SafE family protein 5
Sh04_g016360	-1.028594612	----------	Beta-D-xylosidase 4	putative beta-D-xylosidase 7
Sh10_g004390	-1.032245568	----------	Cysteine-rich receptor-like protein kinase 42	---NA---
Sh07_g009450	-1.034415691	----------	Chaperonin-like RBCX protein 1, chloroplastic	chaperonin-like RBCX protein 1, chloroplastic
Sh09_g010950	-1.04459797	----------	MLO-like protein 1	MLO-like protein 1
Sh05_g000580	-1.072144197	----------	Non-specific lipid-transfer protein 2	phospholipid transfer protein 1
Sh10_g009000	-1.080322251	----------	Potassium channel KOR1	potassium channel KOR1 isoform X2
Sh07_g006160	-1.093233259	----------	NAC domain-containing protein 21/22	NAC domain-containing protein 21/22
Sh07_g010780	-1.119524197	----------	Protein MARD1	Protein MARD1
Sh09_g001590	-1.151476459	----------	Myb-related protein MYBAS1	Putative MYB DNA-binding domain superfamily protein

Sh01_g019030	-1.152693073	----------	U-box domain-containing protein 34	hypothetical protein SHCRBa_260_G18_F_60
Sh03_g024960	-1.159256858	----------	Alpha-expansin 1	alpha-expansin 1
Sh08_g004490	-1.171254799	----------	Trans-resveratrol di-O-methyltransferase	trans-resveratrol di-O-methyltransferase
Sh02_g002300	-1.183442264	----------	Photosystem I reaction center subunit psaK, chloroplastic	photosystem I reaction center subunit psaK
Sh04_g008180	-1.194834336	----------	RING-H2 finger protein ATL7	RING-H2 finger protein ATL5H
Sh02_g015820	-1.20394915	----------	Cellulose synthase-like protein E6	cellulose synthase-like protein E6
Sh04_g012260	-1.215973482	----------	Transcription factor bHLH82	Transcription factor bHLH82
Sh01_g044060	-1.228515131	----------	Conserved hypothetical protein	hypothetical protein Zm00014a_021413
Sh01_g030230	-1.236481204	----------	similar to Protein kinase domain containing protein, expressed	probable leucine-rich repeat receptor-like protein kinase At5g49770
Sh03_g027550	-1.261197586	----------	Peptide/nitrate transporter	peptide/nitrate transporter
Sh08_g004450	-1.280093818	----------	Trans-resveratrol di-O-methyltransferase	trans-resveratrol di-O-methyltransferase
Sh01_g007620	-1.303988285	----------	Oryza sativa protein similar to cytokinesis-specific syntaxin-related protein AAP03411	syntaxin-related protein KNOLLE
Sh02_g018320	-1.309818953	----------	Dehydration-responsive element-binding protein 1A	dehydration-responsive element-binding protein 1A
Sh01_g022040	-1.31476052	----------	Conserved hypothetical protein	hypothetical protein SORBI_3001G291200
Sh03_g015980	-1.330650604	----------	DNA binding protein	protein RADIALIS-like 3
Sh07_g016510	-1.339898656	----------	Cyclin-dependent kinase B2-1	Cyclin-dependent kinase B2-1
Sh09_g000590	-1.343187009	----------	Conserved hypothetical protein	hypothetical protein SORBI_3005G128550
Sh07_g000020	-1.348854524	----------	High mobility group B protein 7	high mobility group B protein 7
Sh01_g033430	-1.362745589	----------	Histone H2A	histone H2A
Sh01_g017790	-1.368209798	----------	Protein ECERIFERUM 1	protein ECERIFERUM 1
Sh06_g017550	-1.370556943	----------	weakly similar to OSJNBb0059K02.4 protein	DNA topoisomerase 2
Sh01_g033110	-1.38057241	----------	ATPase, coupled to transmembrane movement of substances	ATPase, coupled to transmembrane movement of substances
Sh01_g013040	-1.380777089	----------	Auxin-responsive protein IAA12	Auxin-responsive protein IAA12
Sh06_g001090	-1.400241932	----------	similar to OSIGBa0147B06.5 protein	OSIGBa0147B06.5 protein
Sh09_g012990	-1.413454912	----------	Soluble starch synthase 3, chloroplastic/amyloplastic	uncharacterized protein LOC8061776
Sh07_g008990	-1.414521506	----------	Conserved hypothetical protein	uncharacterized protein LOC112896424
Sh03_g009000	-1.436856889	----------	Ubiquitin-conjugating enzyme E2 19	ubiquitin-conjugating enzyme X
Sh09_g008020	-1.463462772	----------	Putative lipoxygenase 6	NADP-dependent malic enzyme 3
Sh03_g020120	-1.464763508	----------	Conserved hypothetical protein	chaperone protein dnaJ C76, chloroplastic
Sh03_g027370	-1.514556678	----------	Soluble inorganic pyrophosphatase	soluble inorganic pyrophosphatase-like
Sh03_g028560	-1.551558346	----------	similar to P0696G06.26 protein	uncharacterized protein LOC8078672
Sh04_g007800	-1.558850201	----------	Peroxidase	Peroxidase P7
Sh07_g001950	-1.609943076	----------	Putative protein	uncharacterized protein LOC8074041
Sh03_g033550	-1.616994754	----------	Abscisic stress ripening protein	bundle sheath cell specific protein 1
Sh06_g008670	-1.669777263	----------	similar to P0696G06.26 protein	uncharacterized protein LOC8060199
Sh02_g018310	-1.684162713	----------	Dehydration-responsive element-binding protein 1A	dehydration-responsive element-binding protein 1A
Sh_218C24_contig-3_g000020	-1.753486974	----------	Cyclin-A3-1	cyclin superfamily protein, putative
Sh06_g013900	-1.769837742	----------	similar to OSJNBb0016D16.7 protein	probable purine permease 11
Sh10_g010920	-1.773026942	----------	3Fe-4S ferredoxin	chaperone protein dnaJ C76, chloroplastic isoform X2
Sh02_g000180	-1.775308284	----------	Gibberellin 2-beta-dioxygenase 8	gibberellin 2-beta-dioxygenase 8
Sh01_g001800	-1.879562441	----------	similar to Os03g0833100 protein	short-chain dehydrogenase reductase 3b
Sh07_g000320	-1.89683746	----------	3-hydroxyindolin-2-one monooxygenase	indole-2-monooxygenase isoform X1
Sh02_g015490	-1.957502047	----------	Peroxidase	peroxidase 17

Sh04_g019630	-1.987449826	----------	Growth-regulating factor 4	growth-regulating factor 4
Sh07_g001220	-2.017387701	----------	similar to Os03g0126900 protein	hypothetical protein BAE44_0018849
Sh06_g003630	-2.02410473	----------	similar to OSIGBa0134P10.4 protein	Glutaredoxin family protein
Sh10_g010830	-2.029043573	----------	Phosphate transporter PHO1-3	phosphate transporter PHO1-3
Sh02_g019380	-2.308373442	----------	Protein POLLENLESS 3-LIKE 2	Protein POLLENLESS 3-LIKE 2
Sh02_g018300	-2.421547547	----------	Dehydration-responsive element-binding protein 1A	dehydration-responsive element-binding protein 1A
Sh06_g011090	-2.443636625	----------	similar to Chromosome chr4 scaffold_6, whole genome shotgun sequence	putative nucleoredoxin 3
Sh01_g026070	-2.456164581	----------	Nodulation-signaling pathway 1 protein	nodulation-signaling pathway 1 protein
Sh01_g014390	-2.504249696	----------	Conserved hypothetical protein	hypothetical protein SORBI_3002G124832
Sh03_g023060	-2.671310012	----------	BTB/POZ domain-containing protein At5g03250	BTB/POZ domain-containing protein
Sh_236C09_g000010	-2.70347999	----------	Cytochrome P450 87A3	cytochrome P450 87A3
Sh01_g005650	-3.062024234	----------	Gibberellin-regulated protein 8	gibberellin-regulated protein 2 precursor
Sh02_g029430	-3.282037881	----------	Putative carboxylesterase 18	putative carboxylesterase 18
Sh04_g010640	-3.494595575	----------	Bidirectional sugar transporter SWEET15	bidirectional sugar transporter SWEET15-like
Sh10_g014930	-4.020594918	----------	Gl1 protein	protein ECERIFERUM 3
Sh02_g018060	-4.15089003	----------	weakly similar to Phaseolin G-box binding protein PG1-like	transcription factor MYC2
Sh01_g042260	-6.733053083	----------	3-ketoacyl-CoA synthase 6	3-ketoacyl-CoA synthase 5
			SP80-3280 down-regulated DEGs	
Sh01_g019240	----------	-0.444168463	Heat stress transcription factor A-2c	heat stress transcription factor A-2c
Sh01_g043820	----------	-0.48296377	Peroxisomal membrane protein 11-1	peroxisomal membrane protein 11-1
Sh04_g023200	----------	-0.485009478	similar to Protein DCL, chloroplast precursor	protein DCL, chloroplastic
Sh03_g021350	----------	-0.491398858	similar to OSIGBa0159F11.1 protein	uncharacterized protein LOC100276100 isoform X1
Sh08_g000700	----------	-0.496348343	Conserved hypothetical protein	transmembrane protein 45A
Sh04_g020290	----------	-0.505618837	Structural constituent of ribosome	structural constituent of ribosome
Sh10_g017330	----------	-0.521235515	Putative Long-chain-alcohol oxidase FAO3	uncharacterized protein LOC8064951
Sh03_g021710	----------	-0.528644504	Protein CHLORORESPIRATORY REDUCTION 7, chloroplastic	Protein CHLORORESPIRATORY REDUCTION 7, chloroplastic
Sh06_g006520	----------	-0.540887696	Conserved hypothetical protein	hypothetical protein SHCRBa_121_P14_R_150
Sh03_g000350	----------	-0.550459307	GDSL esterase/lipase At5g08460	uncharacterized LOC103649536
Sh02_g028380	----------	-0.553146298	similar to Expressed protein	uncharacterized protein LOC8061566
Sh01_g022870	----------	-0.561487624	Holliday junction resolvase	holliday junction resolvase
Sh04_g009410	----------	-0.573659766	similar to Os05g0401200 protein	uncharacterized protein LOC101759227
Sh04_g026510	----------	-0.581216602	Protein LUTEIN DEFICIENT 5, chloroplastic	protein LUTEIN DEFICIENT 5, chloroplastic
Sh04_g001770	----------	-0.588234203	Conserved hypothetical protein	uncharacterized LOC100382661
Sh07_g013570	----------	-0.604608488	Putative Divinyl chlorophyllide a 8-vinyl-reductase, chloroplastic	NAD(P)-binding Rossmann-fold superfamily protein
Sh02_g007090	----------	-0.608352512	Cyanohydrin beta-glucosyltransferase	cytokinin-O-glucosyltransferase 2
Sh07_g001230	----------	-0.623395306	Plasma membrane ATPase	beta-carotene isomerase D27, chloroplastic
Sh07_g012550	----------	-0.649429473	Superoxide dismutase [Cu-Zn], chloroplastic	superoxide dismutase
Sh07_g012140	----------	-0.695461384	Protein PROTON GRADIENT REGULATION 5, chloroplastic	protein PROTON GRADIENT REGULATION 5, chloroplastic
Sh_079H19_g000030	----------	-0.708780458	Protein MET1, chloroplastic	protein MET1, chloroplastic
Sh06_g016900	----------	-0.720936937	similar to OSJNBb0003B01.9 protein	uncharacterized protein LOC112899230
Sh08_g003520	----------	-0.742664685	BnaCnng78320D protein	---NA---
Sh04_g022430	----------	-0.755942572	Thylakoid lumenal protein TL20.3, chloroplastic	Thylakoid lumenal protein TL20.3, chloroplastic
Sh06_g004520	----------	-0.773860791	similar to OSIGBa0102D10.5 protein	psbP domain-containing protein 2, chloroplastic
Sh03_g000360	----------	-0.785409756	50S ribosomal protein L23, chloroplastic	---NA---
Sh03_g006590	----------	-0.853221907	Peptidyl-prolyl cis-trans isomerase	Peptidyl-prolyl cis-trans isomerase CYP26-2, chloroplastic

Sh08_g005070	----------	-0.860488794	Zinc-finger homeodomain protein 3	zinc-finger homeodomain protein 3-like
Sh08_g007630	----------	-1.258899198	Os09g0119600 protein	predicted protein

Table S3. Blast results of DEGs against DETs.

SUGIT ID	Blast2GO Description	STP ID	STP Description
GFHJ01074552.1	probable glutathione S-transferase GSTU6	Sh_020J14_contig-3_g000010	Glutathione S-transferase U17
GFHJ01083310.1	probable glutathione S-transferase GSTU6	Sh_020J14_contig-3_g000010	Glutathione S-transferase U17
GFHJ01050975.1	protein MET1, chloroplastic	Sh_079H19_g000030	Protein MET1, chloroplastic
GFHJ01063459.1	hypothetical protein BRADI_4g21980v3	Sh_201L24_g000030	Coatomer subunit beta'-2
GFHJ01038917.1	putative polygalacturonase	Sh_212O05_g000080	Glycoside hydrolase, family 28
GFHJ01086593.1	putative polygalacturonase	Sh_212O05_g000080	Glycoside hydrolase, family 28
GFHJ01009082.1	probable inactive purple acid phosphatase 29	Sh_217A12_contig-1_g000010	Phosphatase DCR2
GFHJ01042717.1	putative 12-oxophytodienoate reductase 11	Sh_227A23_contig-1_g000020	12-oxo-phytodienoic acid reductase
GFHJ01020273.1	pheophorbide a oxygenase, chloroplastic	Sh_250P04_g000030	Pheophorbide a oxygenase, chloroplastic
GFHJ01025477.1	cytokinin oxidase 3	Sh_251K17_contig-3_g000010	Cytokinin oxidase 2
GFHJ01088940.1	cytokinin dehydrogenase 4	Sh_251K17_contig-3_g000010	Cytokinin oxidase 2
GFHJ01018844.1	aspartokinase 1, chloroplastic-like	Sh01_g000860	Monofunctional aspartate kinase 1
GFHJ01016511.1	epoxide hydrolase 2	Sh01_g001720	Epoxide hydrolase 2
GFHJ01057103.1	epoxide hydrolase 2	Sh01_g001720	NAC12
GFHJ01010899.1	NAC protein	Sh01_g002980	Inosine-5'-monophosphate dehydrogenase
GFHJ01063249.1	NAC1	Sh01_g002980	similar to Wound and phytochrome signaling involved receptor like kinase
GFHJ01008907.1	inosine-5'-monophosphate dehydrogenase	Sh01_g004680	similar to Wound and phytochrome signaling involved receptor like kinase
GFHJ01020586.1	putative LRR receptor-like serine/threonine-protein kinase	Sh01_g005080	similar to Wound and phytochrome signaling involved receptor like kinase
GFHJ01006030.1	allene oxide synthase 1, chloroplastic	Sh01_g005370	Cytochrome P450
GFHJ01071674.1	CCG-binding protein 1	Sh01_g005430	CCG-binding protein 1
GFHJ01077049.1	CCG-binding protein 1	Sh01_g005440	Putative CCG-binding protein 1
GFHJ01106488.1	hypothetical protein SORBI_3001G311601	Sh01_g005600	Conserved hypothetical protein
GFHJ01047486.1	putative glucosyl transferase	Sh01_g005990	Putative UDP-glycosyltransferase 83A1
GFHJ01044983.1	myosin-12 isoform X1	Sh01_g006730	similar to Myosin heavy chain class XI E1 protein
GFHJ01065621.1	helix-loop-helix DNA-binding domain containing protein	Sh01_g007270	Transcription factor BHLH148
GFHJ01099416.1	uncharacterized protein LOC8060547	Sh01_g008250	Putative protein
GFHJ01017291.1	threonine dehydratase biosynthetic, chloroplastic	Sh01_g009020	Threonine dehydratase biosynthetic, chloroplastic
GFHJ01085645.1	chemocyanin precursor	Sh01_g009380	Chemocyanin
GFHJ01093177.1	basic blue protein	Sh01_g009390	Basic blue protein
GFHJ01015592.1	linoleate 9S-lipoxygenase5	Sh01_g010070	Lipoxygenase
GFHJ01017539.1	probable linoleate 9S-lipoxygenase 4	Sh01_g010070	Lipoxygenase
GFHJ01047708.1	putative linoleate 9S-lipoxygenase 3	Sh01_g010080	Linoleate 9S-lipoxygenase 1
GFHJ01102776.1	VQ motif family protein	Sh01_g011070	VQ motif-containing protein 29
GFHJ01060409.1	type IV inositol polyphosphate 5-phosphatase 7	Sh01_g011550	Type IV inositol polyphosphate 5-phosphatase 7
GFHJ01083078.1	Auxin-responsive protein IAA12	Sh01_g013040	Auxin-responsive protein IAA12

GFHJ01106470.1	hypothetical protein SORBI_3002G124832
GFHJ01054996.1	tyrosine N-monooxygenase-like
GFHJ01059827.1	E3 ubiquitin-protein ligase AIRP2-like isoform X2
GFHJ01083506.1	E3 ubiquitin-protein ligase AIRP2-like isoform X2
GFHJ01020944.1	Peroxidase 59
GFHJ01020952.1	Peroxidase 59
GFHJ01047146.1	C4-specific pyruvate orthophosphate dikinase
GFHJ01089427.1	uncharacterized protein LOC8067364
GFHJ01068924.1	homeobox-leucine zipper protein HOX15
GFHJ01105730.1	hypothetical protein SORBI_3001G291200
GFHJ01094429.1	Histone H4
GFHJ01019681.1	interferon-related developmental regulator 2
GFHJ01065023.1	allene oxide cyclase, chloroplastic
GFHJ01049966.1	polygalacturonase inhibitor
GFHJ01094034.1	copper transporter 5.1
GFHJ01020662.1	cytochrome P450 71A1
GFHJ01020674.1	rhomboid-like protein 19
GFHJ01007459.1	Leucine-rich repeat protein kinase family protein
GFHJ01021380.1	probable leucine-rich repeat receptor-like protein kinase At5g49770
GFHJ01043393.1	probable leucine-rich repeat receptor-like protein kinase At5g49770
GFHJ01074850.1	Leucine-rich repeat protein kinase family protein
GFHJ01102346.1	transcription factor MYB2
GFHJ01027133.1	probable 2-oxoglutarate-dependent dioxygenase At3g111800
GFHJ01048883.1	probable 2-oxoglutarate-dependent dioxygenase At5g05600
GFHJ01073695.1	putative 2-oxoglutarate-dependent dioxygenase
GFHJ01080434.1	probable 2-oxoglutarate-dependent dioxygenase At3g111800
GFHJ01092425.1	histone H2A
GFHJ01092818.1	histone H2A
GFHJ01017832.1	Haloacid dehalogenase-like hydrolase (HAD) superfamily protein
GFHJ01012804.1	anthranilate synthase alpha subunit 2, chloroplastic
GFHJ01050268.1	peroxidase 42
GFHJ01060610.1	Peroxidase N
GFHJ01061110.1	thaumatin-like protein 1b
GFHJ01018364.1	predicted protein
GFHJ01044700.1	sugar transport protein MST4
GFHJ01023235.1	hypothetical protein SORBI_3007G042150
GFHJ01095343.1	uncharacterized protein LOC8059815
GFHJ01020226.1	FAD/NAD(P)-binding oxidoreductase family protein
GFHJ01058620.1	E3 ubiquitin-protein ligase RZFP34
GFHJ01076443.1	E3 ubiquitin-protein ligase RZFP34-like isoform X1
GFHJ01069442.1	peroxisomal membrane protein 11-1
GFHJ01070230.1	RHOMBOID-like protein 2
GFHJ01087603.1	RHOMBOID-like protein 2
GFHJ01060091.1	gibberellin 2-beta-dioxygenase 8
GFHJ01093561.1	---NA---

Sh01_g014390	Conserved hypothetical protein
Sh01_g015030	Tyrosine N-monooxygenase
Sh01_g018460	similar to H0801D08.18 protein
Sh01_g018460	similar to H0801D08.18 protein
Sh01_g018600	Peroxidase
Sh01_g018600	Peroxidase
Sh01_g018600	Peroxidase
Sh01_g019030	U-box domain-containing protein 34
Sh01_g021230	weakly similar to Homeobox-leucine zipper protein HAT22
Sh01_g022040	Conserved hypothetical protein
Sh01_g023880	Histone H4
Sh01_g025140	Interferon-related developmental regulator 2
Sh01_g025260	Allene oxide cyclase
Sh01_g025350	similar to Leucine rich repeat containing protein
Sh01_g027080	Copper transporter 5.1
Sh01_g028420	Flavonoid 3'-monooxygenase
Sh01_g028460	Rhomboid-like protein 19
Sh01_g030230	similar to Protein kinase domain containing protein, expressed
Sh01_g030230	similar to Protein kinase domain containing protein, expressed
Sh01_g030230	similar to Protein kinase domain containing protein, expressed
Sh01_g030230	similar to Protein kinase domain containing protein, expressed
Sh01_g031180	similar to Myb-like DNA-binding domain containing protein, expressed
Sh01_g032670	similar to Oxidoreductase, 2OG-Fe oxygenase family protein, expressed
Sh01_g032670	similar to Oxidoreductase, 2OG-Fe oxygenase family protein, expressed
Sh01_g032670	similar to Oxidoreductase, 2OG-Fe oxygenase family protein, expressed
Sh01_g032670	similar to Oxidoreductase, 2OG-Fe oxygenase family protein, expressed
Sh01_g033430	Histone H2A
Sh01_g033430	Histone H2A
Sh01_g033810	Catalytic/ hydrolase
Sh01_g034360	Anthranilate synthase alpha subunit 2, chloroplastic
Sh01_g036120	Peroxidase
Sh01_g036120	Peroxidase
Sh01_g036340	Thaumatin-like protein 1
Sh01_g036370	Cytochrome P450 90B2
Sh01_g037130	Os03g0218400 protein
Sh01_g039440	Protein MARD1
Sh01_g040190	Cysteine-rich and transmembrane domain-containing protein PCC1
Sh01_g040910	similar to FAD binding domain containing protein, expressed
Sh01_g041500	similar to CHY zinc finger family protein, expressed
Sh01_g041500	similar to CHY zinc finger family protein, expressed
Sh01_g043820	Peroxisomal membrane protein 11-1
Sh01_g043890	RHOMBOID-like protein 3
Sh01_g043890	RHOMBOID-like protein 3
Sh02_g000180	Gibberellin 2-beta-dioxygenase 8
Sh02_g002470	Protein TIFY 5

GFHJ01095424.1	protein TIFY 5
GFHJ01059406.1	9-cis-epoxycarotenoid dioxygenase 1, chloroplastic
GFHJ01096431.1	glucan endo-1,3-beta-glucosidase 8
GFHJ01089337.1	peptidyl-prolyl cis-trans isomerase FKBP16-4, chloroplastic
GFHJ01082566.1	hypothetical protein SORBI_3002G072100
GFHJ01104111.1	UDP-glycosyltransferase 91A1
GFHJ01094296.1	B12D protein
GFHJ01101439.1	putative lipid-transfer protein DIR1
GFHJ01091681.1	putative lipid-transfer protein DIR1
GFHJ01047738.1	trans-cinnamate 4-monooxygenase
GFHJ01030758.1	cytochrome P450 CYP73A100
GFHJ01067327.1	acetylserotonin O-methyltransferase 3-like isoform X1
GFHJ01052754.1	sulfite exporter TauE/SafE family protein 3
GFHJ01088501.1	gamma-glutamyl peptidase 3
GFHJ01086813.1	AAA-ATPase ASD, mitochondrial
GFHJ01079503.1	DNA binding protein
GFHJ01072287.1	calmodulin-like protein 1
GFHJ01047726.1	AC090485_10Putative retroelement
GFHJ01021670.1	peroxidase 17
GFHJ01073037.1	Peroxidase 17
GFHJ01021685.1	cellulose synthase-like protein E6
GFHJ01021896.1	probable WRKY transcription factor 2
GFHJ01055544.1	putative WRKY transcription factor 34
GFHJ01021927.1	tonoplast dicarboxylate transporter
GFHJ01083194.1	tonoplast dicarboxylate transporter
GFHJ01010616.1	Proton pump-interactor 1
GFHJ01050005.1	probable sarcosine oxidase
GFHJ01022146.1	UDP-glucuronate 4-epimerase 6
GFHJ01004729.1	hypothetical protein PAHAL_9G046900
GFHJ01022330.1	solute carrier family 35 member F1
GFHJ01094961.1	dehydration-responsive element-binding protein 1A
GFHJ01100756.1	dehydration-responsive element-binding protein 1A
GFHJ01098817.1	dehydration-responsive element-binding protein 1A
GFHJ01022738.1	GDSL esterase/lipase EXL3
GFHJ01024041.1	uncharacterized protein LOC8055685
GFHJ01088748.1	hypothetical protein BAE44_0000149
GFHJ01021607.1	uncharacterized protein LOC8061566
GFHJ01049433.1	uncharacterized protein LOC8061566
GFHJ01095596.1	hypoxia induced protein conserved region containing protein
GFHJ01098986.1	negatively light-regulated protein
GFHJ01099274.1	negatively light-regulated protein
GFHJ01092078.1	uncharacterized LOC103649536
GFHJ01061978.1	MADS-box transcription factor 4
GFHJ01077665.1	WRKY transcription factor
GFHJ01096342.1	WRKY transcription factor

Sh02_g002470	Protein TIFY 5
Sh02_g002520	Viviparous-14
Sh02_g003290	Glucan endo-1,3-beta-glucosidase 8
Sh02_g004030	Peptidyl-prolyl cis-trans isomerase FKBP16-4, chloroplastic
Sh02_g004650	weakly similar to Expressed protein
Sh02_g006520	Glycosyltransferase
Sh02_g006640	GTP-binding protein YPTM1
Sh02_g006950	PVR3-like protein
Sh02_g006970	Non-specific lipid-transfer protein
Sh02_g008510	Trans-cinnamate 4-monooxygenase
Sh02_g008530	Cinnamic acid 4-hydroxylase
Sh02_g008750	5-pentadecatrienyl resorcinol O-methyltransferase
Sh02_g010820	similar to Membrane protein-like
Sh02_g013280	Gamma-glutamyl peptidase 3
Sh02_g013500	similar to AAA ATPase, central region (50.1 kD)-like protein
Sh02_g014540	similar to Basic helix-loop-helix (BHLH)-like protein
Sh02_g014660	Polcalcin Jun o 2
Sh02_g015420	Dicarboxylate transporter 2.1, chloroplastic
Sh02_g015490	Peroxidase
Sh02_g015490	Peroxidase
Sh02_g015820	Cellulose synthase-like protein E6
Sh02_g016260	similar to Os09g0481700 protein
Sh02_g016260	similar to Os09g0481700 protein
Sh02_g016470	similar to Os09g0484900 protein
Sh02_g016470	similar to Os09g0484900 protein
Sh02_g016570	Conserved hypothetical protein
Sh02_g016750	Squalene monooxygenase 1,1
Sh02_g017080	Protein capI
Sh02_g017090	ABC transporter G family member 50
Sh02_g017700	Solute carrier family 35, member F1
Sh02_g018300	Dehydration-responsive element-binding protein 1A
Sh02_g018310	Dehydration-responsive element-binding protein 1A
Sh02_g018320	Dehydration-responsive element-binding protein 1A
Sh02_g019540	GDSL esterase/lipase EXL3
Sh02_g025560	similar to OSJNBa0031O09.02
Sh02_g028030	Calmodulin binding protein
Sh02_g028380	similar to Expressed protein
Sh02_g028380	similar to Expressed protein
Sh02_g030770	Hypoxia induced protein conserved region containing protein
Sh02_g031530	Negatively light-regulated protein
Sh02_g031530	Negatively light-regulated protein
Sh03_g000350	GDSL esterase/lipase At5g08460
Sh03_g001850	MADS-box transcription factor 3
Sh03_g002680	WRKY transcription factor
Sh03_g002680	WRKY transcription factor

GFHJ01006127.1	ABC transporter C family member 3
GFHJ01096061.1	Bowman-Birk type wound-induced proteinase inhibitor WIP1
GFHJ01066158.1	hypothetical protein GQ55_5G457000
GFHJ01024443.1	Fructose-bisphosphate aldolase 3, chloroplastic
GFHJ01079712.1	fructose-bisphosphate aldolase 3, chloroplastic
GFHJ01084254.1	hypothetical protein GQ55_5G013300
GFHJ01086966.1	flowering-promoting factor 1-like protein 1
GFHJ01025332.1	probable anion transporter 1, chloroplastic
GFHJ01049628.1	probable polygalacturonase At1g80170
GFHJ01101068.1	polygalacturonase At1g48100-like
GFHJ01055933.1	transcription factor JAMYB
GFHJ01063438.1	myb-related protein P
GFHJ01096735.1	putative methyltransferase DDB_G0268948
GFHJ01025729.1	putative pectinesterase/pectinesterase inhibitor 41
GFHJ01106503.1	---NA---
GFHJ01050508.1	Peroxidase 1
GFHJ01062789.1	bidirectional sugar transporter SWEET2a
GFHJ01024452.1	putative WRKY transcription factor 71
GFHJ01074758.1	---NA---
GFHJ01041963.1	cytochrome P450 72A11
GFHJ01054214.1	cytochrome P450 72A14
GFHJ01093985.1	protein RADIALIS-like 3
GFHJ01024559.1	abhydrolase domain-containing protein C22H12.03
GFHJ01060526.1	putative methyltransferase
GFHJ01081835.1	putative serine acetyltransferase 1
GFHJ01025646.1	B3 domain-containing protein Os03g0120900 isoform X1
GFHJ01025647.1	putative ABC transporter B family member 8
GFHJ01025648.1	putative ABC transporter B family member 8
GFHJ01099823.1	putative ABC transporter B family member 8
GFHJ01025754.1	chaperone protein dnaJ C76, chloroplastic
GFHJ01053899.1	chaperone protein dnaJ C76, chloroplastic
GFHJ01013686.1	uncharacterized protein LOC100276100 isoform X1
GFHJ01063132.1	gibberellin 2-beta-dioxygenase
GFHJ01065730.1	gibberellin 2-beta-dioxygenase
GFHJ01097979.1	Protein CHLORORESPIRATORY REDUCTION 7, chloroplastic
GFHJ01086879.1	transcription factor bHLH13-like
GFHJ01066378.1	cytokinin dehydrogenase 5
GFHJ01099284.1	uncharacterized protein LOC8079293
GFHJ01063999.1	alpha-expansin 1
GFHJ01077806.1	alpha-expansin 1
GFHJ01048793.1	amino acid transporter AVT6C isoform X1
GFHJ01099936.1	Bowman-Birk type trypsin inhibitor
GFHJ01053885.1	starch binding domain containing protein
GFHJ01068348.1	hevamine-A precursor
GFHJ01061222.1	soluble inorganic pyrophosphatase-like

Sh03_g003830	ABC transporter C family member 3
Sh03_g005580	Bowman-Birk type wound-induced proteinase inhibitor WIP1
Sh03_g006150	Conserved hypothetical protein
Sh03_g006380	Fructose-bisphosphate aldolase
Sh03_g006380	Fructose-bisphosphate aldolase
Sh03_g007190	Putative similar to Symbiosis-related protein-like protein
Sh03_g008000	Flowering-promoting factor 1-like protein 1
Sh03_g009410	Sodium-dependent phosphate transport protein 1, chloroplastic
Sh03_g010030	Polygalacturonase At1g48100
Sh03_g010030	Polygalacturonase At1g48100
Sh03_g010070	Transcription factor JAMYB
Sh03_g010280	Myb-related protein P
Sh03_g010330	Embryonic abundant protein-like
Sh03_g010470	Pectinesterase
Sh03_g010670	Polycomb group protein VERNALIZATION 2
Sh03_g010780	Peroxidase 1
Sh03_g012130	Bidirectional sugar transporter SWEET2a
Sh03_g015550	similar to DNA-binding protein WRKY2-like
Sh03_g015550	similar to DNA-binding protein WRKY2-like
Sh03_g015570	similar to Cytochrome P450
Sh03_g015730	Cytochrome P450 72A14
Sh03_g015980	DNA binding protein
Sh03_g019070	similar to Hydrolase-like protein
Sh03_g019240	S-adenosylmethionine-dependent methyltransferase
Sh03_g019470	Serine acetyltransferase 3
Sh03_g019730	B3 domain-containing protein Os03g0120900
Sh03_g019740	similar to P-glycoprotein homologue
Sh03_g019740	similar to P-glycoprotein homologue
Sh03_g019740	similar to P-glycoprotein homologue
Sh03_g020120	Conserved hypothetical protein
Sh03_g020120	Conserved hypothetical protein
Sh03_g021350	similar to OSIGBa0159F11.1 protein
Sh03_g021370	Gibberellin 2-beta-dioxygenase
Sh03_g021370	Gibberellin 2-beta-dioxygenase
Sh03_g021710	Protein CHLORORESPIRATORY REDUCTION 7, chloroplastic
Sh03_g021960	BHLH transcription factor (Fragment)
Sh03_g022570	Cytokinin dehydrogenase 5
Sh03_g022940	Protein PAM71-homolog, chloroplastic
Sh03_g024960	Alpha-expansin 1
Sh03_g024960	Alpha-expansin 1
Sh03_g025130	Amino acid transporter AVT6C
Sh03_g026240	Bowman-Birk type trypsin inhibitor
Sh03_g026740	Starch binding domain containing protein
Sh03_g027110	Acidic endochitinase
Sh03_g027370	Soluble inorganic pyrophosphatase

GFHJ01066585.1	soluble inorganic pyrophosphatase
GFHJ01018649.1	Protein NRT1/ PTR FAMILY 6.3
GFHJ01060404.1	protein NRT1/ PTR FAMILY 5.10
GFHJ01094711.1	linoleate 9S-lipoxygenase 2
GFHJ01073642.1	hypothetical protein SORBI_3003G405200
GFHJ01062563.1	Thiamine pyrophosphokinase 1
GFHJ01066991.1	glutathione S-transferase 3
GFHJ01080807.1	cationic peroxidase SPC4-like
GFHJ01083732.1	bundle sheath cell specific protein 1
GFHJ01084290.1	bundle sheath cell specific protein 1
GFHJ01028527.1	L-aspartate oxidase chloroplastic
GFHJ01107548.1	cytosolic invertase 1
GFHJ01040802.1	peroxidase 4
GFHJ01098950.1	Peroxidase P7
GFHJ01106234.1	peroxidase P7
GFHJ01055953.1	cation transport protein chaC
GFHJ01086519.1	ethylene-responsive transcription factor-like protein At4g13040 isoform X4
GFHJ01006163.1	chaperone protein
GFHJ01068635.1	SOUL heme-binding protein
GFHJ01028878.1	chloride channel protein CLC-c
GFHJ01045097.1	Chloride channel protein CLC-c
GFHJ01092359.1	E3 ubiquitin-protein ligase EL5
GFHJ01043092.1	Transcription factor bHLH82
GFHJ01100468.1	uncharacterized protein LOC8055401
GFHJ01029121.1	NAC domain-containing protein 79
GFHJ01101716.1	VQ motif
GFHJ01083093.1	Inactive TPR repeat-containing thioredoxin TTL3
GFHJ01086498.1	inactive TPR repeat-containing thioredoxin TTL3
GFHJ01056273.1	hypothetical protein Shy3280Sca034_059
GFHJ01075912.1	PLAT/LH2 domain
GFHJ01093930.1	PLAT domain-containing protein 3
GFHJ01043266.1	F-box/kelch-repeat protein At1g74510-like
GFHJ01060941.1	rac-like GTP-binding protein 3
GFHJ01100715.1	uncharacterized LOC103627704
GFHJ01030139.1	histidine kinase1
GFHJ01060415.1	bidirectional sugar transporter SWEET2b
GFHJ01030575.1	formate dehydrogenase 2, mitochondrial
GFHJ01043086.1	putative 4-coumarate--CoA ligase 3
GFHJ01030827.1	transcription factor bHLH157
GFHJ01030835.1	basic helix-loop-helix (bHLH) DNA-binding superfamily protein
GFHJ01028182.1	salutaridine reductase
GFHJ01098283.1	uncharacterized protein LOC8075191
GFHJ01090827.1	chaperone protein dnaJ
GFHJ01028958.1	wall-associated receptor kinase 2
GFHJ01067101.1	Cinnamoyl-CoA reductase 1

Sh03_g027370	Soluble inorganic pyrophosphatase
Sh03_g027550	Peptide/nitrate transporter
Sh03_g027550	Peptide/nitrate transporter
Sh03_g028360	Linoleate 9S-lipoxygenase 2
Sh03_g030410	similar to Putative regulatory protein
Sh03_g031270	Thiamine pyrophosphokinase 1
Sh03_g031420	similar to Glutathione S-transferase 3
Sh03_g033490	Cationic peroxidase SPC4
Sh03_g033550	Abscisic stress ripening protein
Sh03_g033550	Abscisic stress ripening protein
Sh04_g002160	L-aspartate oxidase
Sh04_g002850	Cytosolic invertase 1
Sh04_g007800	Peroxidase
Sh04_g007800	Peroxidase
Sh04_g007800	Peroxidase
Sh04_g010070	Gamma-glutamylcyclotransferase
Sh04_g010380	Ethylene-responsive transcription factor-like protein At4g13040
Sh04_g011010	Chaperone protein ClpD1, chloroplastic
Sh04_g011250	Heme-binding-like protein At3g10130, chloroplastic
Sh04_g012030	Chloride channel protein
Sh04_g012030	Chloride channel protein
Sh04_g012170	E3 ubiquitin-protein ligase EL5
Sh04_g012260	Transcription factor bHLH82
Sh04_g012790	similar to YGL010w-like protein
Sh04_g012870	NAC domain-containing protein 92
Sh04_g016230	VQ motif-containing protein 22
Sh04_g016240	TPR repeat-containing thioredoxin TTL4
Sh04_g016240	TPR repeat-containing thioredoxin TTL4
Sh04_g016270	similar to Os02g0753400 protein
Sh04_g016280	PLAT domain-containing protein 1
Sh04_g016280	PLAT domain-containing protein 1
Sh04_g016720	similar to Kelch repeat-containing F-box-like
Sh04_g017090	similar to Rop1 small GTP binding protein
Sh04_g017170	Conserved hypothetical protein
Sh04_g017420	similar to Histidine kinase
Sh04_g018400	Bidirectional sugar transporter SWEET
Sh04_g019170	Formate dehydrogenase, mitochondrial
Sh04_g019970	4-coumarate:coenzyme A ligase 2
Sh04_g020950	Transcription factor LHW
Sh04_g020990	Conserved hypothetical protein
Sh04_g022690	Salutaridine reductase
Sh04_g023020	Conserved hypothetical protein
Sh04_g024240	similar to Heat shock-like protein
Sh04_g025970	similar to Os02g0111600 protein
Sh04_g026050	Cinnamoyl-CoA reductase-like protein 3

GFHJ01057202.1	cinnamoyl-CoA reductase 1
GFHJ01029403.1	Zn-dependent hydrolases, including glyoxylases
GFHJ01093659.1	mini zinc finger protein 1
GFHJ01045627.1	putative peptide/nitrate transporter
GFHJ01100243.1	TPA_exp: putative phytosulfokine peptide precursor
GFHJ01105622.1	TPA_exp: putative phytosulfokine peptide precursor
GFHJ01031600.1	nodulation-signaling pathway 2 protein
GFHJ01099159.1	uncharacterized LOC100284300
GFHJ01086460.1	Hevein-like preproprotein
GFHJ01031863.1	glycine-rich domain-containing protein 1
GFHJ01031964.1	magnesium/proton exchanger 1
GFHJ01097974.1	Bowman-Birk type trypsin inhibitor
GFHJ01047957.1	Linoleate 9S-lipoxygenase 2
GFHJ01047959.1	Linoleate 9S-lipoxygenase 2
GFHJ01047960.1	Linoleate 9S-lipoxygenase 2
GFHJ01014659.1	cysteine synthase
GFHJ01033685.1	protein NUCLEAR FUSION DEFECTIVE 4
GFHJ01084013.1	protein TIFY 9
GFHJ01033779.1	potassium transporter 1
GFHJ01087195.1	1,4-alpha-glucan-branching enzyme 2, chloroplastic/amyloplastic
GFHJ01010968.1	cell wall invertase
GFHJ01097835.1	soluble acid invertase
GFHJ01066017.1	psbP domain-containing protein 2, chloroplastic
GFHJ01015244.1	zeaxanthin epoxidase
GFHJ01055109.1	OSJNBa0072F16.18-like protein
GFHJ01085227.1	Bowman-Birk type bran trypsin inhibitor
GFHJ01032944.1	CMP-sialic acid transporter 4
GFHJ01032945.1	CMP-sialic acid transporter 4
GFHJ01084293.1	endochitinase A
GFHJ01033111.1	disease resistance protein RPS2
GFHJ01009649.1	probable low-specificity L-threonine aldolase 2
GFHJ01054358.1	GEM-like protein 4
GFHJ01033840.1	putative nucleoredoxin 3
GFHJ01098566.1	probable metal-nicotianamine transporter YSL16
GFHJ01009875.1	cis-zeatin O-glucosyltransferase 1
GFHJ01033654.1	probable purine permease 11
GFHJ01042652.1	Trypsin family protein
GFHJ01063697.1	Trypsin family protein
GFHJ01064172.1	Trypsin family protein
GFHJ01073294.1	transcription factor bHLH112
GFHJ01094871.1	transcription factor bHLH112
GFHJ01032183.1	uncharacterized protein LOC112899230
GFHJ01032203.1	ABC transporter B family member 19
GFHJ01101899.1	DNA topoisomerase 2
GFHJ01079768.1	uncharacterized protein LOC8083096

Sh04_g026070	Cinnamoyl-CoA reductase 1
Sh04_g027510	U-box domain-containing protein 62
Sh05_g001030	similar to ZF-HD protein dimerisation region containing protein, expressed
Sh05_g001320	Carbohydrate transporter/ sugar porter/ transporter
Sh05_g001970	Phytosulfokines 5
Sh05_g001970	Phytosulfokines 5
Sh05_g002670	Putative Scarecrow-like protein 23
Sh05_g004570	Argos-like protein
Sh05_g008620	Pathogenesis-related protein
Sh05_g009980	Glycine-rich domain-containing protein 2
Sh05_g010930	Magnesium/proton exchanger 1
Sh05_g011500	Bowman-Birk type trypsin inhibitor
Sh05_g011820	Linoleate 9S-lipoxygenase 2
Sh05_g011820	Linoleate 9S-lipoxygenase 2
Sh05_g011820	Linoleate 9S-lipoxygenase 2
Sh06_g001230	Cysteine synthase
Sh06_g002720	similar to OSIGBa0096P03.3 protein
Sh06_g002900	Protein TIFY 9
Sh06_g003200	Potassium transporter
Sh06_g003460	1,4-alpha-glucan-branching enzyme 2, chloroplastic/amyloplastic
Sh06_g003700	Beta-fructofuranosidase, insoluble isoenzyme 2
Sh06_g003700	Beta-fructofuranosidase, insoluble isoenzyme 2
Sh06_g004520	similar to OSIGBa0102D10.5 protein
Sh06_g005670	Zeaxanthin epoxidase, chloroplastic
Sh06_g006520	Conserved hypothetical protein
Sh06_g007560	Bowman-Birk type bran trypsin inhibitor
Sh06_g008140	CMP-sialic acid transporter 4
Sh06_g008140	CMP-sialic acid transporter 4
Sh06_g008450	similar to Endochitinase A precursor
Sh06_g009530	Disease resistance protein RPS2
Sh06_g009610	similar to OSIGBa0145M07.1 protein
Sh06_g010180	GEM-like protein 4
Sh06_g011090	similar to Chromosome chr4 scaffold_6, whole genome shotgun sequence
Sh06_g011210	similar to Iron transport protein 2
Sh06_g012090	Cis-zeatin O-glucosyltransferase 1
Sh06_g013900	similar to OSJNBb0016D16.7 protein
Sh06_g015390	similar to OSIGBa0126B18.9 protein
Sh06_g015390	similar to OSIGBa0126B18.9 protein
Sh06_g015390	similar to OSIGBa0126B18.9 protein
Sh06_g016500	similar to H0105C05.9 protein
Sh06_g016500	similar to H0105C05.9 protein
Sh06_g016900	similar to OSJNBb0003B01.9 protein
Sh06_g017080	ABC transporter B family member 19
Sh06_g017550	weakly similar to OSJNBb0059K02.4 protein
Sh06_g019250	Conserved hypothetical protein

GFHJ01079850.1	uncharacterized protein LOC8083096
GFHJ01070966.1	high mobility group B protein 7
GFHJ01034939.1	indole-2-monooxygenase
GFHJ01056038.1	peroxidase 47
GFHJ01080410.1	peroxidase 47
GFHJ01103858.1	hypothetical protein BAE44_0018849
GFHJ01058474.1	L-gulonolactone oxidase 2-like
GFHJ01035477.1	uncharacterized protein LOC8074041
GFHJ01095823.1	hypothetical protein SORBI_3007G032300
GFHJ01095263.1	aromatic-L-amino-acid decarboxylase-like
GFHJ01035611.1	External alternative NAD(P)H-ubiquinone oxidoreductase B4 mitochondrial
GFHJ01048138.1	beta-sesquiphellandrene synthase
GFHJ01075569.1	beta-sesquiphellandrene synthase
GFHJ01079377.1	beta-sesquiphellandrene synthase-like
GFHJ01062002.1	NAC domain-containing protein 21/22
GFHJ01035072.1	uncharacterized protein LOC112896424
GFHJ01071855.1	chaperonin-like RBCX protein 1, chloroplastic
GFHJ01099357.1	chaperonin-like RBCX protein 1, chloroplastic
GFHJ01035099.1	Type IV inositol polyphosphate 5-phosphatase 9
GFHJ01035116.1	putative 1-phosphatidylinositol-3-phosphate 5-kinase FAB1C
GFHJ01059284.1	ribonuclease 1
GFHJ01077987.1	DUF581 family protein
GFHJ01098624.1	Protein MARD1
GFHJ01103251.1	Protein MARD1
GFHJ01103699.1	Protein MARD1
GFHJ01046914.1	12-oxophytodienoate reductase 7
GFHJ01058655.1	alpha carbonic anhydrase 7
GFHJ01088340.1	ethylene-responsive transcription factor ERF109
GFHJ01082292.1	Protein PROTON GRADIENT REGULATION 5, chloroplastic
GFHJ01035667.1	NAD(P)-binding Rossmann-fold superfamily protein
GFHJ01073427.1	uncharacterized protein LOC8057839
GFHJ01006559.1	TBC1 domain family member 5 homolog B-like
GFHJ01051523.1	Cyclin-dependent kinase B2-1
GFHJ01070911.1	lysine-specific demethylase JMJ30 isoform X2
GFHJ01094286.1	Histone H2B.4
GFHJ01063325.1	transmembrane protein 45A
GFHJ01036357.1	phosphoglucan phosphatase LSF2, chloroplastic
GFHJ01036360.1	phosphoglucan phosphatase LSF2, chloroplastic
GFHJ01103467.1	phytosulfokines 2
GFHJ01094860.1	stress-response A/B barrel domain-containing protein At5g22580
GFHJ01091541.1	uncharacterized protein LOC8066974
GFHJ01094117.1	uncharacterized protein LOC8058547
GFHJ01097842.1	---NA---
GFHJ01083566.1	---NA---
GFHJ01101410.1	GDSL esterase/lipase

Sh06_g019250	Conserved hypothetical protein
Sh07_g000020	High mobility group B protein 7
Sh07_g000320	3-hydroxyindolin-2-one monooxygenase
Sh07_g001070	Peroxidase
Sh07_g001070	Peroxidase
Sh07_g001220	similar to Os03g0126900 protein
Sh07_g001350	L-gulonolactone oxidase 2
Sh07_g001950	Putative protein
Sh07_g002780	Conserved hypothetical protein
Sh07_g003030	Aromatic-L-amino-acid decarboxylase
Sh07_g003070	External alternative NAD(P)H-ubiquinone oxidoreductase B2, mitochondrial
Sh07_g004880	similar to Terpene synthase 10
Sh07_g004880	similar to Terpene synthase 10
Sh07_g005540	(E)-beta-caryophyllene synthase
Sh07_g006160	NAC domain-containing protein 21/22
Sh07_g008990	Conserved hypothetical protein
Sh07_g009450	Chaperonin-like RBCX protein 1, chloroplastic
Sh07_g009450	Chaperonin-like RBCX protein 1, chloroplastic
Sh07_g009490	Type IV inositol polyphosphate 5-phosphatase 9
Sh07_g009680	similar to FYVE finger-containing phosphoinositide kinase-like
Sh07_g010230	Ribonuclease 3
Sh07_g010780	Protein MARD1
Sh07_g010780	Protein MARD1
Sh07_g010780	Protein MARD1
Sh07_g010780	Protein MARD1
Sh07_g011190	12-oxo-phytodienoic acid reductase
Sh07_g011490	Bifunctional monodehydroascorbate reductase and carbonic anhydrase nectarin-3
Sh07_g011720	Ethylene-responsive transcription factor ERF109
Sh07_g012140	Protein PROTON GRADIENT REGULATION 5, chloroplastic
Sh07_g013570	Putative Divinyl chlorophyllide a 8-vinyl-reductase, chloroplastic
Sh07_g013690	Conserved hypothetical protein
Sh07_g016180	Conserved hypothetical protein
Sh07_g016510	Cyclin-dependent kinase B2-1
Sh07_g016800	Lysine-specific demethylase JMJ30
Sh07_g017900	Histone H2B.3
Sh08_g000700	Conserved hypothetical protein
Sh08_g002650	Dual-specificity protein-like phosphatase 3
Sh08_g002650	Dual-specificity protein-like phosphatase 3
Sh08_g002730	similar to Putative phytosulfokine peptide
Sh08_g002840	similar to Expressed protein
Sh08_g003180	similar to Os11g0153000 protein
Sh08_g003180	similar to Os11g0153000 protein
Sh08_g003520	BnaCnng78320D protein
Sh08_g005070	Zinc-finger homeodomain protein 3
Sh08_g008510	GDSL esterase/lipase

GFHJ01092524.1	uncharacterized protein LOC110429809
GFHJ01059363.1	salicylate carboxymethyltransferase
GFHJ01075831.1	salicylate carboxymethyltransferase
GFHJ01102980.1	uncharacterized protein LOC110430516
GFHJ01010892.1	NAC domain-containing protein 68
GFHJ01055926.1	NAC domain-containing protein 68
GFHJ01095719.1	subtilisin-chymotrypsin inhibitor-2B
GFHJ01096577.1	subtilisin-chymotrypsin inhibitor-2B
GFHJ01097366.1	subtilisin-chymotrypsin inhibitor-2B
GFHJ01098099.1	maize proteinase inhibitor
GFHJ01098145.1	subtilisin-chymotrypsin inhibitor-2B
GFHJ01096817.1	subtilisin-chymotrypsin inhibitor-2B
GFHJ01096902.1	subtilisin-chymotrypsin inhibitor-2B
GFHJ01097912.1	subtilisin-chymotrypsin inhibitor-2B
GFHJ01085136.1	transcription factor MYB21
GFHJ01094391.1	transcription factor MYB59
GFHJ01099736.1	transcription factor MYB48
GFHJ01099775.1	transcription factor MYB21
GFHJ01058630.1	1-aminocyclopropane-1-carboxylate oxidase
GFHJ01046286.1	triacylglycerol lipase-like 1
GFHJ01083759.1	triacylglycerol lipase-like 1
GFHJ01038441.1	probable ethylene response sensor 2
GFHJ01038506.1	peroxidase 5
GFHJ01104167.1	auxin-responsive protein IAA16
GFHJ01061489.1	gibberellin 2-beta-dioxygenase 3-like
GFHJ01045724.1	putative pectinesterase/pectinesterase inhibitor 7
GFHJ01064943.1	chitinase 2
GFHJ01048585.1	crocetin glucosyltransferase 2
GFHJ01000238.1	---NA---
GFHJ01063452.1	MLO-like protein 1
GFHJ01037736.1	potassium channel AKT2
GFHJ01046275.1	potassium channel protein ZMK2
GFHJ01095827.1	maternal effect embryo arrest 59
GFHJ01096561.1	uncharacterized protein LOC8061776
GFHJ01038040.1	pyruvate decarboxylase 1
GFHJ01100704.1	pyruvate decarboxylase
GFHJ01025467.1	probable glycerol-3-phosphate dehydrogenase [NAD(+)] 1, cytosolic
GFHJ01050454.1	O-methyltransferase ZRP4
GFHJ01062052.1	O-methyltransferase ZRP4
GFHJ01013640.1	catalytic/ hydrolase isoform X1
GFHJ01053310.1	mitogen-activated protein kinase kinase kinase 17
GFHJ01085167.1	mitogen-activated protein kinase kinase kinase A-like
GFHJ01037209.1	sugar transporter ERD6-like 4
GFHJ01053148.1	haloacid dehalogenase-like hydrolase domain-containing protein Sgpp isoform X1
GFHJ01041176.1	5-enolpyruvylshikimate-3-phosphate synthase (plastid)
Sh08_g008730	ATPase 3, plasma membrane-type
Sh09_g000100	Putative Separase
Sh09_g000100	Putative Separase
Sh09_g000590	Conserved hypothetical protein
Sh09_g001000	NAC domain-containing protein 68
Sh09_g001000	NAC domain-containing protein 68
Sh09_g001060	Subtilisin-chymotrypsin inhibitor-2B (Fragment)
Sh09_g001060	Subtilisin-chymotrypsin inhibitor-2B (Fragment)
Sh09_g001060	Subtilisin-chymotrypsin inhibitor-2B (Fragment)
Sh09_g001060	Subtilisin-chymotrypsin inhibitor-2B (Fragment)
Sh09_g001060	Subtilisin-chymotrypsin inhibitor-2B (Fragment)
Sh09_g001120	Subtilisin-chymotrypsin inhibitor-2B (Fragment)
Sh09_g001120	Subtilisin-chymotrypsin inhibitor-2B (Fragment)
Sh09_g001140	Subtilisin-chymotrypsin inhibitor-2B (Fragment)
Sh09_g001590	Myb-related protein MYBAS1
Sh09_g001590	Myb-related protein MYBAS1
Sh09_g001590	Myb-related protein MYBAS1
Sh09_g001590	Myb-related protein MYBAS1
Sh09_g004190	Acc oxidase
Sh09_g004240	similar to Lipase class 3-like
Sh09_g004240	similar to Lipase class 3-like
Sh09_g004400	similar to Os05g0155200 protein
Sh09_g004840	Peroxidase
Sh09_g006100	Auxin-responsive protein IAA16
Sh09_g006390	Gibberellin 2-beta-dioxygenase
Sh09_g008170	Pectinesterase
Sh09_g010120	Basic endochitinase A
Sh09_g010250	Glycosyltransferase
Sh09_g010890	Conserved hypothetical protein
Sh09_g010950	MLO-like protein 1
Sh09_g011520	Potassium channel AKT2
Sh09_g011520	Potassium channel AKT2
Sh09_g012390	similar to Expressed protein
Sh09_g012990	Soluble starch synthase 3, chloroplastic/amyloplastic
Sh09_g013600	Pyruvate decarboxylase 1
Sh09_g013600	Pyruvate decarboxylase 1
Sh09_g014360	Glycerol-3-phosphate dehydrogenase [NAD(+)]
Sh09_g015440	O-methyltransferase ZRP4
Sh09_g015440	O-methyltransferase ZRP4
Sh09_g017120	Conserved hypothetical protein
Sh09_g017390	Mitogen-activated protein kinase kinase kinase 17
Sh09_g017400	similar to Os01g0699500 protein
Sh09_g018510	Solute carrier family 2, facilitated glucose transporter member 8
Sh10_g000700	Haloacid dehalogenase-like hydrolase domain-containing protein Sgpp
Sh10_g002260	3-phosphoshikimate 1-carboxyvinyltransferase

GFHJ01052107.1	Starch synthase I	Sh10_g004390	Cysteine-rich receptor-like protein kinase 42
GFHJ01039690.1	putative UPF0481 protein At3g02645	Sh10_g005670	similar to Pentatricopeptide (PPR) repeat-containing protein-like
GFHJ01055347.1	WAT1-related protein	Sh10_g007330	WAT1-related protein At4g08300
GFHJ01073517.1	nodulin protein	Sh10_g007330	WAT1-related protein At4g08300
GFHJ01039988.1	uncharacterized protein LOC8077349	Sh10_g007440	similar to Lipase class 3-like
GFHJ01071337.1	uncharacterized protein LOC8070769	Sh10_g007530	RING-H2 finger protein ATL34
GFHJ01012460.1	aquaporin NIP2-2	Sh10_g008260	Aquaporin NIP2-2
GFHJ01059381.1	aquaporin NIP2-2	Sh10_g008260	Aquaporin NIP2-2
GFHJ01040392.1	potassium channel KOR1 isoform X2	Sh10_g009000	Potassium channel KOR1
GFHJ01040547.1	Phosphatidylinositol 4-kinase gamma 7	Sh10_g009860	Phosphatidylinositol 4-kinase gamma 7
GFHJ01065012.1	---NA---	Sh10_g010440	Conserved hypothetical protein
GFHJ01038937.1	phosphate transporter PHO1-3	Sh10_g010830	Phosphate transporter PHO1-3
GFHJ01049319.1	chaperone protein dnaJ C76, chloroplastic isoform X2	Sh10_g010920	3Fe-4S ferredoxin
GFHJ01065578.1	chaperone protein dnaJ C76, chloroplastic isoform X2	Sh10_g010920	3Fe-4S ferredoxin
GFHJ01006204.1	ATP binding protein	Sh10_g012240	ATP binding protein
GFHJ01039778.1	protein argonaute PNH1	Sh10_g012490	similar to ZLL/PNH homologous protein
GFHJ01056016.1	NAD(P)-binding Rossmann-fold superfamily protein	Sh10_g013560	Putative Cinnamoyl-CoA reductase 1
GFHJ01068212.1	Protein ECERIFERUM 3	Sh10_g014930	Gl1 protein
GFHJ01003852.1	---NA---	Sh10_g017770	Two-component response regulator ARR2

Table S4. List of up- and down-regulated DETs enriched to protein domains.

InterPro	Description	Number
Common up-regulated DETs		
IPR005123	Oxoglutarate/iron-dependent oxygenase	7
IPR000823	Plant peroxidase	6
IPR002016	Haem peroxidase, plant/fungal/bacterial	6
IPR010255	Haem peroxidase	6
IPR019793	Peroxidases heam-ligand binding site	6
IPR019794	Peroxidase, active site	6
IPR001024	Lipoxygenase, LH2	5
IPR001128	Cytochrome P450	5
IPR002283	Isopenicillin N synthase	5
IPR002641	Patatin	5
IPR008976	Lipase/lipooxygenase, PLAT/LH2	5
IPR016035	Acyl transferase/acyl hydrolase/lysophospholipase	5
IPR000907	Lipoxygenase	4
IPR001246	Lipoxygenase, plant	4
IPR002401	Cytochrome P450, E-class, group I	4
IPR013819	Lipoxygenase, C-terminal	4
IPR017973	Cytochrome P450, C-terminal	4

IPR001092	Helix-loop-helix DNA-binding domain	3
IPR010399	Tify	3
IPR011598	Helix-loop-helix DNA-binding	3
IPR016040	NAD(P)-binding domain	3
IPR018467	CCT domain-like	3
IPR000743	Glycoside hydrolase, family 28	2
IPR000767	Disease resistance protein	2
IPR000864	Proteinase inhibitor I13, potato inhibitor I	2
IPR001005	SANT, DNA-binding	2
IPR001077	O-methyltransferase, family 2	2
IPR002182	NB-ARC	2
IPR002198	Short-chain dehydrogenase/reductase SDR	2
IPR002347	Glucose/ribitol dehydrogenase	2
IPR006093	Oxygen oxidoreductase covalent FAD-binding site	2
IPR006094	FAD linked oxidase, N-terminal	2
IPR006626	Parallel beta-helix repeat	2
IPR009057	Homeodomain-like	2
IPR009438	Phytosulfokine	2
IPR011050	Pectin lyase fold/virulence factor	2
IPR011991	Winged helix-turn-helix transcription repressor DNA-binding	2
IPR012334	Pectin lyase fold	2
IPR012967	Plant methyltransferase dimerisation	2
IPR014778	Myb, DNA-binding	2
IPR015345	Cytokinin dehydrogenase 1, FAD/cytokinin binding domain	2
IPR015421	Pyridoxal phosphate-dependent transferase, major region, subdomain 1	2
IPR015422	Pyridoxal phosphate-dependent transferase, major region, subdomain 2	2
IPR015424	Pyridoxal phosphate-dependent transferase, major domain	2
IPR016164	FAD-linked oxidase-like, C-terminal	2
IPR016166	FAD-binding, type 2	2
IPR016461	O-methyltransferase, COMT, eukaryota	2
IPR017930	HTH transcriptional regulator, Myb-type, DNA-binding	2
IPR017972	Cytochrome P450, conserved site	2
IPR000073	Alpha/beta hydrolase fold-1	1
IPR000121	PEP-utilising enzyme	1
IPR000300	Inositol polyphosphate related phosphatase	1
IPR000477	RNA-directed DNA polymerase (reverse transcriptase)	1
IPR000595	Cyclic nucleotide-binding	1
IPR000639	Epoxide hydrolase-like	1
IPR000719	Protein kinase, catalytic domain	1
IPR000726	Glycoside hydrolase, family 19, catalytic	1
IPR000873	AMP-dependent synthetase/ligase	1
IPR000877	Proteinase inhibitor I12, Bowman-Birk	1
IPR000923	Blue (type 1) copper domain	1
IPR001002	Chitin-binding, type 1	1
IPR001176	1-aminocyclopropane-1-carboxylate synthase	1

IPR001223	Glycoside hydrolase, family 18, catalytic domain	1
IPR001362	Glycoside hydrolase, family 32	1
IPR001440	Tetratricopeptide TPR-1	1
IPR001563	Peptidase S10, serine carboxypeptidase	1
IPR001611	Leucine-rich repeat	1
IPR001878	Zinc finger, CCHC-type	1
IPR001906	Terpene synthase-like	1
IPR001926	Pyridoxal phosphate-dependent enzyme, beta subunit	1
IPR001938	Thaumatin, pathogenesis-related	1
IPR002110	Ankyrin repeat	1
IPR002123	Phospholipid/glycerol acyltransferase	1
IPR002129	Pyridoxal phosphate-dependent decarboxylase	1
IPR002192	Pyruvate phosphate dikinase, PEP/pyruvate-binding	1
IPR002290	Serine/threonine-protein kinase domain	1
IPR002403	Cytochrome P450, E-class, group IV	1
IPR002610	Peptidase S54, rhomboid	1
IPR002781	Protein of unknown function DUF81	1
IPR003245	Plastocyanin-like	1
IPR003340	Transcriptional factor B3	1
IPR003441	No apical meristem (NAM) protein	1
IPR003480	Transferase	1
IPR003612	Plant lipid transfer protein/seed storage/trypsin-alpha amylase inhibitor	1
IPR003657	DNA-binding WRKY	1
IPR003938	Potassium channel, voltage-dependent, EAG/ELK/ERG	1
IPR003953	Fumarate reductase/succinate dehydrogenase flavoprotein, N-terminal	1
IPR004112	Fumarate reductase/succinate dehydrogenase flavoprotein, C-terminal	1
IPR004158	Protein of unknown function DUF247, plant	1
IPR004316	RAG1-activating protein-1-related	1
IPR004838	Aminotransferases, class-I, pyridoxal-phosphate-binding site	1
IPR004839	Aminotransferase, class I/II	1
IPR005135	Endonuclease/exonuclease/phosphatase	1
IPR005256	Anthranilate synthase component I	1
IPR005288	L-aspartate oxidase	1
IPR005299	SAM dependent carboxyl methyltransferase	1
IPR005630	Terpene synthase, metal-binding domain	1
IPR005746	Thioredoxin	1
IPR005801	ADC synthase	1
IPR005821	Ion transport	1
IPR005830	Aerolysin/haemolysin/leukocidin toxin	1
IPR006076	FAD dependent oxidoreductase	1
IPR006139	D-isomer specific 2-hydroxyacid dehydrogenase, catalytic domain	1
IPR006140	D-isomer specific 2-hydroxyacid dehydrogenase, NAD-binding	1
IPR006316	Tryptophan synthase, beta chain-like	1
IPR006447	Myb-like DNA-binding domain, SHAQKYF class	1
IPR006662	Thioredoxin-like subdomain	1

IPR006805	Anthranilate synthase component I, N-terminal	1
IPR007650	Protein of unknown function DUF581	1
IPR008162	Inorganic pyrophosphatase	1
IPR008271	Serine/threonine-protein kinase, active site	1
IPR008279	PEP-utilising enzyme, mobile domain	1
IPR008930	Terpenoid cylases/protein prenyltransferase alpha-alpha toroid	1
IPR008949	Terpenoid synthase	1
IPR008972	Cupredoxin	1
IPR008985	Concanavalin A-like lectin/glucanase	1
IPR008998	Agglutinin	1
IPR010121	Pyruvate, phosphate dikinase	1
IPR010417	Embryo-specific 3	1
IPR010525	Auxin response factor	1
IPR010530	B12D	1
IPR010977	Aromatic-L-amino-acid decarboxylase	1
IPR011009	Protein kinase-like domain	1
IPR011525	Aux/IAA-ARF-dimerisation	1
IPR011990	Tetratricopeptide-like helical	1
IPR012287	Homeodomain-related	1
IPR012335	Thioredoxin fold	1
IPR012336	Thioredoxin-like fold	1
IPR013026	Tetratricopeptide repeat-containing	1
IPR013057	Amino acid transporter, transmembrane	1
IPR013148	Glycosyl hydrolases family 32, N-terminal	1
IPR013189	Glycosyl hydrolase family 32, C-terminal	1
IPR013766	Thioredoxin domain	1
IPR013781	Glycoside hydrolase, subgroup, catalytic core	1
IPR013815	ATP-grasp fold, subdomain 1	1
IPR013816	ATP-grasp fold, subdomain 2	1
IPR014710	RmlC-like jelly roll fold	1
IPR015467	Thioredoxin, core	1
IPR015495	Myb transcription factor	1
IPR015609	Molecular chaperone, heat shock protein, Hsp40, DnaJ	1
IPR015706	RNA-directed DNA polymerase (reverse transcriptase), related	1
IPR015813	Pyruvate/Phosphoenolpyruvate kinase, catalytic core	1
IPR015890	Chorismate binding, C-terminal	1
IPR015939	Fumarate reductase/succinate dehydrogenase flavoprotein-like, C-terminal	1
IPR016140	Bifunctional inhibitor/plant lipid transfer protein/seed storage	1
IPR016283	Glycoside hydrolase, family 19	1
IPR017442	Serine/threonine-protein kinase-like domain	1
IPR017853	Glycoside hydrolase, catalytic core	1
IPR017877	MYB-like	1
IPR017936	Thioredoxin-like	1
IPR017937	Thioredoxin, conserved site	1
IPR017949	Thaumatin, conserved site	1

IPR018169	MtN3/saliva-related transmembrane protein, conserved region	1
IPR018179	RAG1-activating protein 1 homologue	1
IPR018202	Peptidase S10, serine carboxypeptidase, active site	1
IPR018490	Cyclic nucleotide-binding-like	1
IPR019734	Tetratricopeptide repeat	1
IPR019999	Anthranilate synthase component I, C-terminal	1
IPR020635	Tyrosine-protein kinase, catalytic domain	1
IPR020683	Ankyrin repeat-containing domain	1
IPR020845	AMP-binding, conserved site	1
IPR021115	Pyridoxal-phosphate binding site	1
IPR021789	Protein of unknown function DUF3354	1
Common down-regulated DETs		
IPR000146	Fructose-1,6-bisphosphatase	1
IPR001005	SANT, DNA-binding	1
IPR006447	Myb-like DNA-binding domain, SHAQKYF class	1
IPR009057	Homeodomain-like	1
IPR013216	Methyltransferase type 11	1
IPR014778	Myb, DNA-binding	1
IPR015609	Molecular chaperone, heat shock protein, Hsp40, DnaJ	1
IPR017930	HTH transcriptional regulator, Myb-type, DNA-binding	1
IPR020548	Fructose-1,6-bisphosphatase, active site	1
RB867515 up-regulated DETs		
IPR000719	Protein kinase, catalytic domain	18
IPR011009	Protein kinase-like domain	18
IPR001092	Helix-loop-helix DNA-binding domain	13
IPR002290	Serine/threonine-protein kinase domain	13
IPR003593	ATPase, AAA+ type, core	12
IPR008271	Serine/threonine-protein kinase, active site	12
IPR011598	Helix-loop-helix DNA-binding	12
IPR020635	Tyrosine-protein kinase, catalytic domain	12
IPR017441	Protein kinase, ATP binding site	11
IPR017442	Serine/threonine-protein kinase-like domain	11
IPR001128	Cytochrome P450	9
IPR001245	Serine/threonine/tyrosine-protein kinase	9
IPR001140	ABC transporter, transmembrane domain	8
IPR002401	Cytochrome P450, E-class, group I	8
IPR003439	ABC transporter-like	8
IPR011527	ABC transporter, transmembrane domain, type 1	8
IPR017940	ABC transporter integral membrane type 1	8
IPR017973	Cytochrome P450, C-terminal	8
IPR012287	Homeodomain-related	7
IPR016040	NAD(P)-binding domain	7
IPR003657	DNA-binding WRKY	6
IPR009057	Homeodomain-like	6
IPR000823	Plant peroxidase	5

IPR002016	Haem peroxidase, plant/fungal/bacterial	5
IPR010255	Haem peroxidase	5
IPR013785	Aldolase-type TIM barrel	5
IPR017972	Cytochrome P450, conserved site	5
IPR000620	Protein of unknown function DUF6, transmembrane	4
IPR001005	SANT, DNA-binding	4
IPR001611	Leucine-rich repeat	4
IPR002213	UDP-glucuronosyl/UDP-glucosyltransferase	4
IPR012335	Thioredoxin fold	4
IPR012336	Thioredoxin-like fold	4
IPR013781	Glycoside hydrolase, subgroup, catalytic core	4
IPR014778	Myb, DNA-binding	4
IPR015495	Myb transcription factor	4
IPR016166	FAD-binding, type 2	4
IPR017853	Glycoside hydrolase, catalytic core	4
IPR017930	HTH transcriptional regulator, Myb-type, DNA-binding	4
IPR019793	Peroxidases heam-ligand binding site	4
IPR019794	Peroxidase, active site	4
IPR001841	Zinc finger, RING-type	3
IPR002182	NB-ARC	3
IPR002912	Amino acid-binding ACT	3
IPR003612	Plant lipid transfer protein/seed storage/trypsin-alpha amylase inhibitor	3
IPR003855	K+ potassium transporter	3
IPR003959	ATPase, AAA-type, core	3
IPR005123	Oxoglutarate/iron-dependent oxygenase	3
IPR005834	Haloacid dehalogenase-like hydrolase	3
IPR006094	FAD linked oxidase, N-terminal	3
IPR006662	Thioredoxin-like subdomain	3
IPR007658	Protein of unknown function DUF594	3
IPR008930	Terpenoid cylases/protein prenyltransferase alpha-alpha toroid	3
IPR009646	Root cap	3
IPR011050	Pectin lyase fold/virulence factor	3
IPR012334	Pectin lyase fold	3
IPR013057	Amino acid transporter, transmembrane	3
IPR013766	Thioredoxin domain	3
IPR013770	Plant lipid transfer protein/hydrophobic protein, helical domain	3
IPR015467	Thioredoxin, core	3
IPR016140	Bifunctional inhibitor/plant lipid transfer protein/seed storage	3
IPR016196	Major facilitator superfamily, general substrate transporter	3
IPR017871	ABC transporter, conserved site	3
IPR017936	Thioredoxin-like	3
IPR018519	Potassium uptake protein, kup	3
IPR020636	Calcium/calmodulin-dependent protein kinase-like	3
IPR000008	C2 calcium-dependent membrane targeting	2
IPR000073	Alpha/beta hydrolase fold-1	2

IPR000425	Major intrinsic protein	2
IPR000644	Cystathionine beta-synthase, core	2
IPR000741	Fructose-bisphosphate aldolase, class-I	2
IPR000743	Glycoside hydrolase, family 28	2
IPR000767	Disease resistance protein	2
IPR000864	Proteinase inhibitor I13, potato inhibitor I	2
IPR000991	Glutamine amidotransferase class-I, C-terminal	2
IPR001086	Prephenate dehydratase	2
IPR001223	Glycoside hydrolase, family 18, catalytic domain	2
IPR001356	Homeobox	2
IPR001789	Signal transduction response regulator, receiver domain	2
IPR001806	Ras GTPase	2
IPR001906	Terpene synthase-like	2
IPR001932	Protein phosphatase 2C-related	2
IPR002198	Short-chain dehydrogenase/reductase SDR	2
IPR002283	Isopenicillin N synthase	2
IPR002347	Glucose/ribitol dehydrogenase	2
IPR002403	Cytochrome P450, E-class, group IV	2
IPR002650	Sulphate adenylyltransferase	2
IPR002902	Protein of unknown function DUF26	2
IPR002963	Expansin	2
IPR003480	Transferase	2
IPR003579	Ras small GTPase, Rab type	2
IPR003594	ATPase-like, ATP-binding domain	2
IPR003661	Signal transduction histidine kinase, subgroup 1, dimerisation/phosphoacceptor domain	2
IPR004041	NAF domain	2
IPR004159	Protein of unknown function DUF248, methyltransferase putative	2
IPR004316	RAG1-activating protein-1-related	2
IPR004358	Signal transduction histidine kinase-related protein, C-terminal	2
IPR005132	Rare lipoprotein A	2
IPR005225	Small GTP-binding protein	2
IPR005467	Signal transduction histidine kinase, core	2
IPR005630	Terpene synthase, metal-binding domain	2
IPR006139	D-isomer specific 2-hydroxyacid dehydrogenase, catalytic domain	2
IPR006140	D-isomer specific 2-hydroxyacid dehydrogenase, NAD-binding	2
IPR006210	EGF-like	2
IPR006236	D-3-phosphoglycerate dehydrogenase	2
IPR006402	HAD-superfamily hydrolase, subfamily IA, variant 3	2
IPR006626	Parallel beta-helix repeat	2
IPR006937	Plant neutral invertase	2
IPR007112	Expansin 45, endoglucanase-like	2
IPR007117	Pollen allergen/expansin, C-terminal	2
IPR007118	Expansin/Lol pI	2
IPR007271	Nucleotide-sugar transporter	2
IPR008913	Zinc finger, CHY-type	2

IPR008928	Six-hairpin glycosidase-like	2
IPR008949	Terpenoid synthase	2
IPR008972	Cupredoxin	2
IPR008973	C2 calcium/lipid-binding domain, CaLB	2
IPR009009	Barwin-related endoglucanase	2
IPR009082	Signal transduction histidine kinase, homodimeric	2
IPR010399	Tify	2
IPR011006	CheY-like	2
IPR011525	Aux/IAA-ARF-dimerisation	2
IPR011701	Major facilitator superfamily MFS-1	2
IPR011991	Winged helix-turn-helix transcription repressor DNA-binding	2
IPR012269	Aquaporin	2
IPR013210	Leucine-rich repeat-containing N-terminal domain, type 2	2
IPR013216	Methyltransferase type 11	2
IPR013753	Ras	2
IPR014045	Protein phosphatase 2C, N-terminal	2
IPR014729	Rossmann-like alpha/beta/alpha sandwich fold	2
IPR014734	Pollen allergen, N-terminal	2
IPR015421	Pyridoxal phosphate-dependent transferase, major region, subdomain 1	2
IPR015422	Pyridoxal phosphate-dependent transferase, major region, subdomain 2	2
IPR015424	Pyridoxal phosphate-dependent transferase, major domain	2
IPR015508	D-3-phosphogylcerate Dehydrogenase	2
IPR015609	Molecular chaperone, heat shock protein, Hsp40, DnaJ	2
IPR015655	Protein phosphatase 2C	2
IPR015947	Pseudouridine synthase/archaeosine transglycosylase-like	2
IPR017921	Zinc finger, CTCHY-type	2
IPR017926	Glutamine amidotransferase type 1	2
IPR018029	C2 membrane targeting protein	2
IPR018169	MtN3/saliva-related transmembrane protein, conserved region	2
IPR018179	RAG1-activating protein 1 homologue	2
IPR018451	NAF/FISL domain	2
IPR018467	CCT domain-like	2
IPR018528	Prephenate dehydratase, conserved site	2
IPR018957	Zinc finger, C3HC4 RING-type	2
IPR020660	CBL-interacting protein kinase	2
IPR020851	Small GTPase	2
IPR021189	UDP/CMP-sugar transporter	2
IPR000047	Helix-turn-helix motif, lambda-like repressor	1
IPR000070	Pectinesterase, catalytic	1
IPR000109	Oligopeptide transporter	1
IPR000152	EGF-type aspartate/asparagine hydroxylation site	1
IPR000172	Glucose-methanol-choline oxidoreductase, N-terminal	1
IPR000195	RabGAP/TBC	1
IPR000270	Octicosapeptide/Phox/Bem1p	1
IPR000300	Inositol polyphosphate related phosphatase	1

IPR000403	Phosphatidylinositol 3-/4-kinase, catalytic	1
IPR000490	Glycoside hydrolase, family 17	1
IPR000528	Plant lipid transfer protein/Par allergen	1
IPR000595	Cyclic nucleotide-binding	1
IPR000626	Ubiquitin	1
IPR000634	Serine/threonine dehydratase, pyridoxal-phosphate-binding site	1
IPR000639	Epoxide hydrolase-like	1
IPR000672	Tetrahydrofolate dehydrogenase/cyclohydrolase	1
IPR000674	Aldehyde oxidase/xanthine dehydrogenase, a/b hammerhead	1
IPR000742	EGF-like, type 3	1
IPR000858	S-locus glycoprotein	1
IPR000877	Proteinase inhibitor I12, Bowman-Birk	1
IPR000907	Lipoxygenase	1
IPR000923	Blue (type 1) copper domain	1
IPR001024	Lipoxygenase, LH2	1
IPR001031	Thioesterase	1
IPR001041	Ferredoxin	1
IPR001063	Ribosomal protein L22/L17	1
IPR001077	O-methyltransferase, family 2	1
IPR001087	Lipase, GDSL	1
IPR001093	IMP dehydrogenase/GMP reductase	1
IPR001094	Flavodoxin-like	1
IPR001107	Band 7 protein	1
IPR001117	Multicopper oxidase, type 1	1
IPR001155	NADH:flavin oxidoreductase/NADH oxidase, N-terminal	1
IPR001176	1-aminocyclopropane-1-carboxylate synthase	1
IPR001246	Lipoxygenase, plant	1
IPR001258	NHL repeat	1
IPR001270	Chaperonin clpA/B	1
IPR001330	Prenyltransferase/squalene oxidase	1
IPR001362	Glycoside hydrolase, family 32	1
IPR001373	Cullin, N-terminal	1
IPR001433	Oxidoreductase FAD/NAD(P)-binding	1
IPR001440	Tetratricopeptide TPR-1	1
IPR001468	Indole-3-glycerol phosphate synthase, conserved site	1
IPR001471	Pathogenesis-related transcriptional factor/ERF, DNA-binding	1
IPR001480	Curculin-like (mannose-binding) lectin	1
IPR001509	NAD-dependent epimerase/dehydratase	1
IPR001519	Ferritin, N-terminal	1
IPR001547	Glycoside hydrolase, family 5	1
IPR001574	Ribosome-inactivating protein	1
IPR001597	Aromatic amino acid beta-eliminating lyase/threonine aldolase	1
IPR001613	Flavin-containing amine oxidase	1
IPR001623	Heat shock protein DnaJ, N-terminal	1
IPR001709	Flavoprotein pyridine nucleotide cytochrome reductase	1

IPR001721	Threonine dehydratase, C-terminal	1
IPR001757	ATPase, P-type, K/Mg/Cd/Cu/Zn/Na/Ca/Na/H-transporter	1
IPR001807	Chloride channel, voltage gated	1
IPR001881	EGF-like calcium-binding	1
IPR001898	Sodium/sulphate symporter	1
IPR001926	Pyridoxal phosphate-dependent enzyme, beta subunit	1
IPR001938	Thaumatin, pathogenesis-related	1
IPR001986	3-phosphoshikimate 1-carboxyvinyltransferase, core	1
IPR002013	Synaptojanin, N-terminal	1
IPR002048	Calcium-binding EF-hand	1
IPR002100	Transcription factor, MADS-box	1
IPR002110	Ankyrin repeat	1
IPR002139	Ribokinase	1
IPR002251	Chloride channel plant CLC	1
IPR002346	Molybdopterin dehydrogenase, FAD-binding	1
IPR002355	Multicopper oxidase, copper-binding site	1
IPR002423	Chaperonin Cpn60/TCP-1	1
IPR002480	DAHP synthetase, class II	1
IPR002487	Transcription factor, K-box	1
IPR002498	Phosphatidylinositol-4-phosphate 5-kinase, core	1
IPR002781	Protein of unknown function DUF81	1
IPR002888	[2Fe-2S]-binding	1
IPR002921	Lipase, class 3	1
IPR002937	Amine oxidase	1
IPR003018	GAF	1
IPR003035	Plant regulator RWP-RK	1
IPR003097	FAD-binding, type 1	1
IPR003100	Argonaute/Dicer protein, PAZ	1
IPR003106	Leucine zipper, homeobox-associated	1
IPR003165	Stem cell self-renewal protein Piwi	1
IPR003245	Plastocyanin-like	1
IPR003340	Transcriptional factor B3	1
IPR003347	Transcription factor jumonji/aspartyl beta-hydroxylase	1
IPR003386	Lecithin:cholesterol acyltransferase	1
IPR003527	MAP kinase, conserved site	1
IPR003577	Ras small GTPase, Ras type	1
IPR003578	Small GTPase, Rho type	1
IPR003591	Leucine-rich repeat, typical subtype	1
IPR003609	Apple-like	1
IPR003672	CobN/magnesium chelatase	1
IPR003676	Auxin responsive SAUR protein	1
IPR003938	Potassium channel, voltage-dependent, EAG/ELK/ERG	1
IPR004000	Actin/actin-like	1
IPR004001	Actin, conserved site	1
IPR004045	Glutathione S-transferase, N-terminal	1

IPR004046	Glutathione S-transferase, C-terminal	1
IPR004176	Clp, N-terminal	1
IPR004182	GRAM	1
IPR004253	Protein of unknown function DUF231, plant	1
IPR004274	NLI interacting factor	1
IPR004314	Protein of unknown function DUF239, plant	1
IPR004320	Protein of unknown function DUF241, plant	1
IPR004331	SPX, N-terminal	1
IPR004696	Tpt phosphate/phosphoenolpyruvate translocator	1
IPR004709	Na+/H+ exchanger, subfamily	1
IPR004789	Acetolactate synthase, small subunit	1
IPR004837	Sodium/calcium exchanger membrane region	1
IPR004838	Aminotransferases, class-I, pyridoxal-phosphate-binding site	1
IPR004839	Aminotransferase, class I/II	1
IPR004843	Metallophosphoesterase	1
IPR004853	Protein of unknown function DUF250	1
IPR005107	CO dehydrogenase flavoprotein, C-terminal	1
IPR005135	Endonuclease/exonuclease/phosphatase	1
IPR005202	Transcription factor GRAS	1
IPR005269	Conserved hypothetical protein CHP00730	1
IPR005349	Uncharacterised protein family UPF0136, Transmembrane	1
IPR005516	Remorin, C-terminal	1
IPR005721	Ribosomal protein L22/L17, eukaryotic/archaeal	1
IPR005746	Thioredoxin	1
IPR005787	Threonine dehydratase I	1
IPR005795	Major pollen allergen Lol pI	1
IPR005821	Ion transport	1
IPR005990	IMP dehydrogenase	1
IPR006069	ATPase, P-type cation exchange, alpha subunit	1
IPR006093	Oxygen oxidoreductase covalent FAD-binding site	1
IPR006109	NAD-dependent glycerol-3-phosphate dehydrogenase, C-terminal	1
IPR006153	Cation/H+ exchanger	1
IPR006168	NAD-dependent glycerol-3-phosphate dehydrogenase	1
IPR006189	CHASE	1
IPR006264	3-phosphoshikimate 1-carboxyvinyltransferase, subgroup	1
IPR006282	Thiamin pyrophosphokinase	1
IPR006455	Homeobox domain, ZF-HD class	1
IPR006456	ZF-HD homeobox protein, Cys/His-rich dimerisation domain	1
IPR006501	Pectinesterase inhibitor	1
IPR006539	ATPase, P-type, phospholipid-translocating, flippase	1
IPR006563	POX	1
IPR006652	Kelch repeat type 1	1
IPR006670	Cyclin	1
IPR006671	Cyclin, N-terminal	1
IPR006840	ChaC-like protein	1

IPR006957	Ethylene insensitive 3	1
IPR007173	D-arabinono-1,4-lactone oxidase	1
IPR007259	Spc97/Spc98	1
IPR007371	Thiamin pyrophosphokinase, catalytic domain	1
IPR007373	Thiamin pyrophosphokinase, vitamin B1-binding domain	1
IPR007484	Peptidase M28	1
IPR007608	Protein of unknown function DUF584	1
IPR007650	Protein of unknown function DUF581	1
IPR007867	Glucose-methanol-choline oxidoreductase, C-terminal	1
IPR008166	Protein of unknown function DUF23	1
IPR008250	ATPase, P-type, ATPase-associated domain	1
IPR008254	Flavodoxin/nitric oxide synthase	1
IPR008265	Lipase, GDSL, active site	1
IPR008274	Aldehyde oxidase/xanthine dehydrogenase, molybdopterin binding	1
IPR008331	Ferritin/Dps protein	1
IPR008496	Protein of unknown function DUF778	1
IPR008824	DNA helicase, Holliday junction RuvB type, N-terminal	1
IPR008889	VQ	1
IPR008927	6-phosphogluconate dehydrogenase, C-terminal-like	1
IPR008963	Purple acid phosphatase-like, N-terminal	1
IPR008976	Lipase/lipooxygenase, PLAT/LH2	1
IPR008985	Concanavalin A-like lectin/glucanase	1
IPR008999	Actin cross-linking	1
IPR009040	Ferritin-like	1
IPR009078	Ferritin/ribonucleotide reductase-like	1
IPR009262	Protein of unknown function DUF914, eukaryotic	1
IPR009288	AIG2-like	1
IPR009410	Allene oxide cyclase	1
IPR010030	Plant-specific FAD-dependent oxidoreductase	1
IPR010237	Pyrimidine 5-nucleotidase	1
IPR010525	Auxin response factor	1
IPR010987	Glutathione S-transferase, C-terminal-like	1
IPR011028	Cyclin-like	1
IPR011042	Six-bladed beta-propeller, TolB-like	1
IPR011043	Galactose oxidase/kelch, beta-propeller	1
IPR011060	Ribulose-phosphate binding barrel	1
IPR011128	NAD-dependent glycerol-3-phosphate dehydrogenase, N-terminal	1
IPR011611	Carbohydrate/purine kinase	1
IPR011706	Multicopper oxidase, type 2	1
IPR011707	Multicopper oxidase, type 3	1
IPR011766	Thiamine pyrophosphate enzyme, C-terminal TPP-binding	1
IPR011771	Magnesium-chelatase, subunit H	1
IPR011990	Tetratricopeptide-like helical	1
IPR011992	EF-hand-like domain	1
IPR012000	Thiamine pyrophosphate enzyme, central domain	1

IPR012001	Thiamine pyrophosphate enzyme, N-terminal TPP-binding domain	1
IPR012110	Pyruvate decarboxylase/indolepyruvate decarboxylase	1
IPR012132	Glucose-methanol-choline oxidoreductase	1
IPR012337	Polynucleotidyl transferase, ribonuclease H fold	1
IPR012340	Nucleic acid-binding, OB-fold	1
IPR012347	Ferritin-related	1
IPR012442	Protein of unknown function DUF1645	1
IPR012675	Beta-grasp fold, ferredoxin-type	1
IPR012946	X8	1
IPR012951	Berberine/berberine-like	1
IPR012967	Plant methyltransferase dimerisation	1
IPR013024	Butirosin biosynthesis, BtrG-like	1
IPR013026	Tetratricopeptide repeat-containing	1
IPR013089	Kelch related	1
IPR013091	EGF calcium-binding	1
IPR013093	ATPase, AAA-2	1
IPR013148	Glycosyl hydrolases family 32, N-terminal	1
IPR013189	Glycosyl hydrolase family 32, C-terminal	1
IPR013227	PAN-2 domain	1
IPR013328	Dehydrogenase, multihelical	1
IPR013626	Pheophorbide a oxygenase	1
IPR013684	MIRO-like	1
IPR013763	Cyclin-related	1
IPR013792	RNA 3'-terminal phosphate cyclase/enolpyruvate transferase, alpha/beta	1
IPR013798	Indole-3-glycerol phosphate synthase	1
IPR013819	Lipoxygenase, C-terminal	1
IPR013861	Protein of unknown function DUF1751, integral membrane, eukaryotic	1
IPR014710	RmlC-like jelly roll fold	1
IPR014743	Chloride channel, core	1
IPR014811	Domain of unknown function DUF1785	1
IPR015345	Cytokinin dehydrogenase 1, FAD/cytokinin binding domain	1
IPR015429	Transcription regulator cyclin	1
IPR015702	NADPH Cytochrome P450 Reductase	1
IPR015766	Leucine-rich repeat-containing protein	1
IPR015875	IMP dehydrogenase / GMP reductase, conserved site	1
IPR015914	Purple acid phosphatase, N-terminal	1
IPR015915	Kelch-type beta propeller	1
IPR016027	Nucleic acid-binding, OB-fold-like	1
IPR016034	Phosphatidylinositol-4-phosphate 5-kinase, core, subgroup	1
IPR016138	Ribosome-inactivating protein, subdomain 1	1
IPR016157	Cullin, conserved site	1
IPR016158	Cullin homology	1
IPR016159	Cullin repeat-like-containing domain	1
IPR016164	FAD-linked oxidase-like, C-terminal	1
IPR016167	FAD-binding, type 2, subdomain 1	1

IPR016169	CO dehydrogenase flavoprotein-like, FAD-binding, subdomain 2	1
IPR016177	DNA-binding, integrase-type	1
IPR016208	Aldehyde oxidase/xanthine dehydrogenase	1
IPR016228	3-phosphoshikimate 1-carboxyvinyltransferase	1
IPR016461	O-methyltransferase, COMT, eukaryota	1
IPR016966	Thiamin pyrophosphokinase, eukaryotic	1
IPR017231	GTPase, Tem1	1
IPR017761	Laccase	1
IPR017877	MYB-like	1
IPR017909	Twin arginine translocation signal, Tat	1
IPR017927	Ferredoxin reductase-type FAD-binding domain	1
IPR017933	Glutathione S-transferase/chloride channel, C-terminal	1
IPR017937	Thioredoxin, conserved site	1
IPR017938	Riboflavin synthase-like beta-barrel	1
IPR017941	Rieske [2Fe-2S] iron-sulphur domain	1
IPR017970	Homeobox, conserved site	1
IPR018040	Pectinesterase, active site	1
IPR018087	Glycoside hydrolase, family 5, conserved site	1
IPR018097	EGF-like calcium-binding, conserved site	1
IPR018247	EF-Hand 1, calcium-binding site	1
IPR018248	EF-Hand, Calmodulin	1
IPR018249	EF-HAND 2	1
IPR018333	Squalene cyclase	1
IPR018406	Na+/H+ exchanger, conserved region	1
IPR018407	Na+/H+ exchanger, isoforms 1-4, conserved region	1
IPR018422	Cation/H+ exchanger, conserved region	1
IPR018456	PTR2 family proton/oligopeptide symporter, conserved site	1
IPR018490	Cyclic nucleotide-binding-like	1
IPR018529	IMP dehydrogenase related	1
IPR019455	Acetolactate synthase, small subunit, C-terminal	1
IPR019489	Clp ATPase, C-terminal	1
IPR019559	Cullin protein, neddylation domain	1
IPR019734	Tetratricopeptide repeat	1
IPR019955	Ubiquitin supergroup	1
IPR019956	Ubiquitin subgroup	1
IPR020477	C2 region	1
IPR020533	Developmental regulator, ULTRAPETALA	1
IPR020630	Tetrahydrofolate dehydrogenase/cyclohydrolase, catalytic domain	1
IPR020631	Tetrahydrofolate dehydrogenase/cyclohydrolase, NAD(P)-binding domain	1
IPR020642	Calcium-dependent protein kinase	1
IPR020683	Ankyrin repeat-containing domain	1
IPR020902	Actin/actin-like conserved site	1
IPR021720	Di-glucose binding within endoplasmic reticulum	1
IPR021789	Protein of unknown function DUF3354	1
RB867515 down-regulated DETs		

IPR000719	Protein kinase, catalytic domain	17
IPR011009	Protein kinase-like domain	17
IPR016040	NAD(P)-binding domain	14
IPR017441	Protein kinase, ATP binding site	13
IPR008271	Serine/threonine-protein kinase, active site	12
IPR017442	Serine/threonine-protein kinase-like domain	12
IPR001344	Chlorophyll A-B binding protein	9
IPR001245	Serine/threonine/tyrosine-protein kinase	7
IPR012336	Thioredoxin-like fold	7
IPR001509	NAD-dependent epimerase/dehydratase	6
IPR001623	Heat shock protein DnaJ, N-terminal	6
IPR002290	Serine/threonine-protein kinase domain	6
IPR003593	ATPase, AAA+ type, core	6
IPR008406	Dormancyauxin associated	6
IPR012335	Thioredoxin fold	6
IPR015609	Molecular chaperone, heat shock protein, Hsp40, DnaJ	6
IPR020635	Tyrosine-protein kinase, catalytic domain	6
IPR001005	SANT, DNA-binding	5
IPR001471	Pathogenesis-related transcriptional factor/ERF, DNA-binding	5
IPR001611	Leucine-rich repeat	5
IPR002016	Haem peroxidase, plant/fungal/bacterial	5
IPR003095	Heat shock protein DnaJ	5
IPR004883	Lateral organ boundaries, LOB	5
IPR007125	Histone core	5
IPR007650	Protein of unknown function DUF581	5
IPR009057	Homeodomain-like	5
IPR009072	Histone-fold	5
IPR010255	Haem peroxidase	5
IPR011991	Winged helix-turn-helix transcription repressor DNA-binding	5
IPR012287	Homeodomain-related	5
IPR014778	Myb, DNA-binding	5
IPR015495	Myb transcription factor	5
IPR016177	DNA-binding, integrase-type	5
IPR017930	HTH transcriptional regulator, Myb-type, DNA-binding	5
IPR019793	Peroxidases heam-ligand binding site	5
IPR019794	Peroxidase, active site	5
IPR022251	Protein of unknown function wound-induced	5
IPR000823	Plant peroxidase	4
IPR001128	Cytochrome P450	4
IPR002401	Cytochrome P450, E-class, group I	4
IPR002902	Protein of unknown function DUF26	4
IPR004045	Glutathione S-transferase, N-terminal	4
IPR004046	Glutathione S-transferase, C-terminal	4
IPR005886	UDP-glucose 4-epimerase	4
IPR010987	Glutathione S-transferase, C-terminal-like	4

IPR013210	Leucine-rich repeat-containing N-terminal domain, type 2	4
IPR017896	4Fe-4S ferredoxin, iron-sulpur binding domain	4
IPR017933	Glutathione S-transferase/chloride channel, C-terminal	4
IPR017972	Cytochrome P450, conserved site	4
IPR017973	Cytochrome P450, C-terminal	4
IPR000169	Peptidase, cysteine peptidase active site	3
IPR000246	Peptidase T2, asparaginase 2	3
IPR000270	Octicosapeptide/Phox/Bem1p	3
IPR000668	Peptidase C1A, papain C-terminal	3
IPR001077	O-methyltransferase, family 2	3
IPR001220	Legume lectin, beta chain	3
IPR001563	Peptidase S10, serine carboxypeptidase	3
IPR003496	ABA/WDS induced protein	3
IPR003823	Protein of unknown function CP12	3
IPR003959	ATPase, AAA-type, core	3
IPR005123	Oxoglutarate/iron-dependent oxygenase	3
IPR008985	Concanavalin A-like lectin/glucanase	3
IPR009003	Serine/cysteine peptidase, trypsin-like	3
IPR012967	Plant methyltransferase dimerisation	3
IPR013128	Peptidase C1A, papain	3
IPR013201	Proteinase inhibitor I29, cathepsin propeptide	3
IPR013320	Concanavalin A-like lectin/glucanase, subgroup	3
IPR016461	O-methyltransferase, COMT, eukaryota	3
IPR019825	Legume lectin, beta chain, Mn/Ca-binding site	3
IPR020474	Toll-like receptor, leucine rich repeat-containing	3
IPR000173	Glyceraldehyde 3-phosphate dehydrogenase subfamily	2
IPR000315	Zinc finger, B-box	2
IPR000340	Dual specificity phosphatase, catalytic domain	2
IPR000347	Plant metallothionein, family 15	2
IPR000387	Dual-specific/protein-tyrosine phosphatase, conserved region	2
IPR000866	Alkyl hydroperoxide reductase/ Thiol specific antioxidant/ Mal allergen	2
IPR000985	Legume lectin, alpha chain, conserved site	2
IPR001270	Chaperonin clpA/B	2
IPR001296	Glycosyl transferase, group 1	2
IPR001765	Carbonic anhydrase	2
IPR001810	Cyclin-like F-box	2
IPR001841	Zinc finger, RING-type	2
IPR001943	UvrB/UvrC protein	2
IPR002119	Histone H2A	2
IPR002198	Short-chain dehydrogenase/reductase SDR	2
IPR002347	Glucose/ribitol dehydrogenase	2
IPR003435	Chaperonin-like RbcX	2
IPR003439	ABC transporter-like	2
IPR003591	Leucine-rich repeat, typical subtype	2
IPR003612	Plant lipid transfer protein/seed storage/trypsin-alpha amylase inhibitor	2

IPR003697	Maf-like protein	2
IPR004176	Clp, N-terminal	2
IPR004326	Mlo-related protein	2
IPR005024	Snf7	2
IPR005735	Zinc finger, LSD1-type	2
IPR006424	Glyceraldehyde-3-phosphate dehydrogenase, type I	2
IPR006694	Fatty acid hydroxylase	2
IPR006917	SOUL haem-binding protein	2
IPR008949	Terpenoid synthase	2
IPR011011	Zinc finger, FYVE/PHD-type	2
IPR011525	Aux/IAA-ARF-dimerisation	2
IPR011835	Glycogen/starch synthases, ADP-glucose type	2
IPR013093	ATPase, AAA-2	2
IPR013534	Starch synthase, catalytic domain	2
IPR013770	Plant lipid transfer protein/hydrophobic protein, helical domain	2
IPR016140	Bifunctional inhibitor/plant lipid transfer protein/seed storage	2
IPR017853	Glycoside hydrolase, catalytic core	2
IPR017936	Thioredoxin-like	2
IPR019489	Clp ATPase, C-terminal	2
IPR020422	Dual specificity phosphatase, subgroup, catalytic domain	2
IPR020828	Glyceraldehyde 3-phosphate dehydrogenase, NAD(P) binding domain	2
IPR020829	Glyceraldehyde 3-phosphate dehydrogenase, catalytic domain	2
IPR020830	Glyceraldehyde 3-phosphate dehydrogenase, active site	2
IPR020832	Glyceraldehyde 3-phosphate dehydrogenase, catalytic domain, subgroup	2
IPR021940	Uncharacterised protein, Wax2 C-terminal	2
IPR000007	Tubby, C-terminal	1
IPR000073	Alpha/beta hydrolase fold-1	1
IPR000092	Polyprenyl synthetase	1
IPR000095	PAK-box/P21-Rho-binding	1
IPR000111	Glycoside hydrolase, clan GH-D	1
IPR000121	PEP-utilising enzyme	1
IPR000152	EGF-type aspartate/asparagine hydroxylation site	1
IPR000164	Histone H3	1
IPR000167	Dehydrin	1
IPR000182	GCN5-related N-acetyltransferase	1
IPR000197	Zinc finger, TAZ-type	1
IPR000198	RhoGAP	1
IPR000253	Forkhead-associated	1
IPR000352	Class I peptide chain release factor	1
IPR000433	Zinc finger, ZZ-type	1
IPR000477	RNA-directed DNA polymerase (reverse transcriptase)	1
IPR000504	RNA recognition motif, RNP-1	1
IPR000535	Major sperm protein	1
IPR000558	Histone H2B	1
IPR000571	Zinc finger, CCCH-type	1

IPR000595	Cyclic nucleotide-binding	1
IPR000640	Translation elongation factor EFG/EF2, C-terminal	1
IPR000642	Peptidase M41	1
IPR000644	Cystathionine beta-synthase, core	1
IPR000726	Glycoside hydrolase, family 19, catalytic	1
IPR000742	EGF-like, type 3	1
IPR000767	Disease resistance protein	1
IPR000795	Protein synthesis factor, GTP-binding	1
IPR000910	High mobility group, HMG1/HMG2	1
IPR000941	Enolase	1
IPR000943	RNA polymerase sigma-70 factor	1
IPR001015	Ferrochelatase	1
IPR001017	Dehydrogenase, E1 component	1
IPR001019	Guanine nucleotide binding protein (G-protein), alpha subunit	1
IPR001023	Heat shock protein Hsp70	1
IPR001087	Lipase, GDSL	1
IPR001092	Helix-loop-helix DNA-binding domain	1
IPR001179	Peptidyl-prolyl cis-trans isomerase, FKBP-type	1
IPR001229	Mannose-binding lectin	1
IPR001236	Lactate/malate dehydrogenase	1
IPR001252	Malate dehydrogenase, active site	1
IPR001515	Ribosomal protein L32e	1
IPR001557	L-lactate/malate dehydrogenase	1
IPR001848	Ribosomal protein S10	1
IPR001881	EGF-like calcium-binding	1
IPR001892	Ribosomal protein S13	1
IPR001906	Terpene synthase-like	1
IPR001951	Histone H4	1
IPR002048	Calcium-binding EF-hand	1
IPR002085	Alcohol dehydrogenase superfamily, zinc-containing	1
IPR002110	Ankyrin repeat	1
IPR002150	Ribosomal protein L31	1
IPR002182	NB-ARC	1
IPR002192	Pyruvate phosphate dikinase, PEP/pyruvate-binding	1
IPR002207	Plant ascorbate peroxidase	1
IPR002213	UDP-glucuronosyl/UDP-glucosyltransferase	1
IPR002241	Glycoside hydrolase, family 27	1
IPR002283	Isopenicillin N synthase	1
IPR002328	Alcohol dehydrogenase, zinc-containing, conserved site	1
IPR002618	UTP--glucose-1-phosphate uridylyltransferase	1
IPR002676	RimM protein	1
IPR002922	Thiamine biosynthesis Thi4 protein	1
IPR002937	Amine oxidase	1
IPR002938	Monooxygenase, FAD-binding	1
IPR002963	Expansin	1

IPR003042	Aromatic-ring hydroxylase-like	1
IPR003340	Transcriptional factor B3	1
IPR003347	Transcription factor jumonji/aspartyl beta-hydroxylase	1
IPR003388	Reticulon	1
IPR003441	No apical meristem (NAM) protein	1
IPR003676	Auxin responsive SAUR protein	1
IPR003938	Potassium channel, voltage-dependent, EAG/ELK/ERG	1
IPR004140	Exo70 exocyst complex subunit	1
IPR004161	Translation elongation factor EFTu/EF1A, domain 2	1
IPR004193	Glycoside hydrolase, family 13, N-terminal	1
IPR004209	Ferredoxin thioredoxin reductase, beta subunit	1
IPR004242	Transposon, En/Spm-like	1
IPR004265	Plant disease resistance response protein	1
IPR004331	SPX, N-terminal	1
IPR004342	EXS, C-terminal	1
IPR004365	Nucleic acid binding, OB-fold, tRNA/helicase-type	1
IPR004367	Cyclin, C-terminal	1
IPR004373	Peptide chain release factor 1	1
IPR004483	DNA helicase, putative	1
IPR004540	Translation elongation factor EFG/EF2	1
IPR004591	Replication factor-a protein 1 Rpa1	1
IPR004827	Basic-leucine zipper (bZIP) transcription factor	1
IPR004853	Protein of unknown function DUF250	1
IPR004926	Late embryogenesis abundant protein 3	1
IPR005050	Early nodulin 93 ENOD93 protein	1
IPR005132	Rare lipoprotein A	1
IPR005135	Endonuclease/exonuclease/phosphatase	1
IPR005139	Peptide chain release factor	1
IPR005225	Small GTP-binding protein	1
IPR005269	Conserved hypothetical protein CHP00730	1
IPR005474	Transketolase, N-terminal	1
IPR005517	Translation elongation factor EFG/EF2, domain IV	1
IPR005630	Terpene synthase, metal-binding domain	1
IPR005731	Ribosomal protein S10 subgroup	1
IPR005805	Rieske iron-sulphur protein, C-terminal	1
IPR005818	Histone H1/H5	1
IPR005819	Histone H5	1
IPR005821	Ion transport	1
IPR005900	6-phosphogluconolactonase	1
IPR005936	Peptidase M41, FtsH	1
IPR006015	Universal stress protein A	1
IPR006016	UspA	1
IPR006047	Glycosyl hydrolase, family 13, catalytic domain	1
IPR006048	Alpha-amylase, C-terminal all beta	1
IPR006476	Conserved hypothetical protein CHP01589, plant	1

IPR006652	Kelch repeat type 1	1
IPR006662	Thioredoxin-like subdomain	1
IPR006670	Cyclin	1
IPR006671	Cyclin, N-terminal	1
IPR006935	Restriction endonuclease, type I, R subunit/Type III, Res subunit	1
IPR006936	Protein of unknown function DUF640	1
IPR007087	Zinc finger, C2H2-type	1
IPR007110	Immunoglobulin-like	1
IPR007112	Expansin 45, endoglucanase-like	1
IPR007117	Pollen allergen/expansin, C-terminal	1
IPR007118	Expansin/Lol pI	1
IPR007199	Replication factor-A protein 1, N-terminal	1
IPR007321	Transposase (putative), gypsy type	1
IPR007493	Protein of unknown function DUF538	1
IPR007624	RNA polymerase sigma-70 region 3	1
IPR007627	RNA polymerase sigma-70 region 2	1
IPR007630	RNA polymerase sigma-70 region 4	1
IPR007658	Protein of unknown function DUF594	1
IPR007863	Peptidase M16, C-terminal	1
IPR007903	PRC-barrel	1
IPR008162	Inorganic pyrophosphatase	1
IPR008279	PEP-utilising enzyme, mobile domain	1
IPR008733	Peroxisomal biogenesis factor 11	1
IPR008801	Rapid ALkalinization Factor	1
IPR008930	Terpenoid cylases/protein prenyltransferase alpha-alpha toroid	1
IPR008936	Rho GTPase activation protein	1
IPR008962	PapD-like	1
IPR008984	SMAD/FHA domain	1
IPR008997	Ricin B-related lectin	1
IPR009000	Translation elongation/initiation factor/Ribosomal, beta-barrel	1
IPR009009	Barwin-related endoglucanase	1
IPR009022	Elongation factor G/III/V	1
IPR009071	High mobility group, superfamily	1
IPR009856	Light regulated Lir1	1
IPR010121	Pyruvate, phosphate dikinase	1
IPR010402	CCT domain	1
IPR010525	Auxin response factor	1
IPR010683	Protein of unknown function DUF1262	1
IPR010788	Violaxanthin de-epoxidase	1
IPR010945	Malate dehydrogenase, NAD/NADP	1
IPR010979	Ribosomal protein S13-like, H2TH	1
IPR011025	G protein alpha subunit, helical insertion	1
IPR011028	Cyclin-like	1
IPR011032	GroES-like	1
IPR011038	Calycin-like	1

IPR011043	Galactose oxidase/kelch, beta-propeller	1
IPR011237	Peptidase M16, core	1
IPR011249	Metalloenzyme, LuxS/M16 peptidase-like, metal-binding	1
IPR011274	Malate dehydrogenase, NAD-dependent, cytosolic	1
IPR011424	C1-like	1
IPR011598	Helix-loop-helix DNA-binding	1
IPR011616	bZIP transcription factor, bZIP-1	1
IPR011701	Major facilitator superfamily MFS-1	1
IPR011765	Peptidase M16, N-terminal	1
IPR011766	Thiamine pyrophosphate enzyme, C-terminal TPP-binding	1
IPR011961	16S rRNA processing protein RimM	1
IPR011990	Tetratricopeptide-like helical	1
IPR011992	EF-hand-like domain	1
IPR012143	Dimethylaniline monooxygenase, N-oxide-forming	1
IPR012340	Nucleic acid-binding, OB-fold	1
IPR012674	Calycin	1
IPR012677	Nucleotide-binding, alpha-beta plait	1
IPR012725	Chaperone DnaK	1
IPR012876	Protein of unknown function DUF1677, plant	1
IPR013026	Tetratricopeptide repeat-containing	1
IPR013089	Kelch related	1
IPR013091	EGF calcium-binding	1
IPR013112	FAD-binding 8	1
IPR013121	Ferric reductase, NAD binding	1
IPR013126	Heat shock protein 70	1
IPR013130	Ferric reductase-like transmembrane component, N-terminal	1
IPR013149	Alcohol dehydrogenase, zinc-binding	1
IPR013154	Alcohol dehydrogenase GroES-like	1
IPR013181	Protein of unknown function DUF1719, Oryza sativa	1
IPR013216	Methyltransferase type 11	1
IPR013324	RNA polymerase sigma factor, region 3/4	1
IPR013325	RNA polymerase sigma factor, region 2	1
IPR013525	ABC-2 type transporter	1
IPR013578	Peptidase M16C associated	1
IPR013581	Plant PDR ABC transporter associated	1
IPR013763	Cyclin-related	1
IPR013766	Thioredoxin domain	1
IPR013780	Glycosyl hydrolase, family 13, all-beta	1
IPR013781	Glycoside hydrolase, subgroup, catalytic core	1
IPR013783	Immunoglobulin-like fold	1
IPR013785	Aldolase-type TIM barrel	1
IPR013815	ATP-grasp fold, subdomain 1	1
IPR013816	ATP-grasp fold, subdomain 2	1
IPR013955	Replication factor A, C-terminal	1
IPR014001	DEAD-like helicase, N-terminal	1

IPR014102	Phytoene desaturase	1
IPR014120	Solanesyl diphosphate synthase	1
IPR014183	Alcohol dehydrogenase class III/S-(hydroxymethyl)glutathione dehydrogenase	1
IPR014284	RNA polymerase sigma-70	1
IPR014349	Rieske iron-sulphur protein	1
IPR014400	Cyclin, A/B/D/E	1
IPR014710	RmlC-like jelly roll fold	1
IPR014721	Ribosomal protein S5 domain 2-type fold, subgroup	1
IPR014729	Rossmann-like alpha/beta/alpha sandwich fold	1
IPR014734	Pollen allergen, N-terminal	1
IPR014756	Immunoglobulin E-set	1
IPR014909	Cytochrome b6-f complex Fe-S subunit	1
IPR015467	Thioredoxin, core	1
IPR015706	RNA-directed DNA polymerase (reverse transcriptase), related	1
IPR015813	Pyruvate/Phosphoenolpyruvate kinase, catalytic core	1
IPR015880	Zinc finger, C2H2-like	1
IPR015915	Kelch-type beta propeller	1
IPR015955	Lactate dehydrogenase/glycoside hydrolase, family 4, C-terminal	1
IPR016024	Armadillo-type fold	1
IPR016027	Nucleic acid-binding, OB-fold-like	1
IPR016181	Acyl-CoA N-acyltransferase	1
IPR016196	Major facilitator superfamily, general substrate transporter	1
IPR016283	Glycoside hydrolase, family 19	1
IPR017079	Zeaxanthin epoxidase	1
IPR017446	Polyprenyl synthetase-related	1
IPR017597	Pyruvate dehydrogenase (acetyl-transferring) E1 component, alpha subunit, subgroup y	1
IPR017871	ABC transporter, conserved site	1
IPR017927	Ferredoxin reductase-type FAD-binding domain	1
IPR017938	Riboflavin synthase-like beta-barrel	1
IPR017941	Rieske [2Fe-2S] iron-sulphur domain	1
IPR017956	AT hook, DNA-binding motif	1
IPR018097	EGF-like calcium-binding, conserved site	1
IPR018247	EF-Hand 1, calcium-binding site	1
IPR018248	EF-Hand, Calmodulin	1
IPR018249	EF-HAND 2	1
IPR018253	Heat shock protein DnaJ, conserved site	1
IPR018268	Ribosomal protein S10, conserved site	1
IPR018368	Chaperonin ClpA/B, conserved site	1
IPR018490	Cyclic nucleotide-binding-like	1
IPR019734	Tetratricopeptide repeat	1
IPR019980	Ribosomal protein S13, bacterial-type	1
IPR020568	Ribosomal protein S5 domain 2-type fold	1
IPR020636	Calcium/calmodulin-dependent protein kinase-like	1
IPR020683	Ankyrin repeat-containing domain	1
IPR020810	Enolase, C-terminal	1

IPR020811	Enolase, N-terminal	1
IPR020831	Glyceraldehyde 3-phosphate dehydrogenase family	1
IPR020904	Short-chain dehydrogenase/reductase, conserved site	1
IPR020946	Flavin-containing monooxygenase-like	1
IPR020983	Basic leucine-zipper, C-terminal	1
IPR021789	Protein of unknown function DUF3354	1
SP80-3280 up-regulated DETs		
IPR016196	Major facilitator superfamily, general substrate transporter	9
IPR016040	NAD(P)-binding domain	7
IPR000719	Protein kinase, catalytic domain	5
IPR000726	Glycoside hydrolase, family 19, catalytic	5
IPR001906	Terpene synthase-like	5
IPR005630	Terpene synthase, metal-binding domain	5
IPR008930	Terpenoid cylases/protein prenyltransferase alpha-alpha toroid	5
IPR008949	Terpenoid synthase	5
IPR011009	Protein kinase-like domain	5
IPR017853	Glycoside hydrolase, catalytic core	5
IPR000864	Proteinase inhibitor I13, potato inhibitor I	4
IPR001509	NAD-dependent epimerase/dehydratase	4
IPR001938	Thaumatin, pathogenesis-related	4
IPR003441	No apical meristem (NAM) protein	4
IPR011701	Major facilitator superfamily MFS-1	4
IPR013781	Glycoside hydrolase, subgroup, catalytic core	4
IPR016283	Glycoside hydrolase, family 19	4
IPR017442	Serine/threonine-protein kinase-like domain	4
IPR001002	Chitin-binding, type 1	3
IPR001024	Lipoxygenase, LH2	3
IPR001087	Lipase, GDSL	3
IPR001128	Cytochrome P450	3
IPR001563	Peptidase S10, serine carboxypeptidase	3
IPR002290	Serine/threonine-protein kinase domain	3
IPR002921	Lipase, class 3	3
IPR004045	Glutathione S-transferase, N-terminal	3
IPR004046	Glutathione S-transferase, C-terminal	3
IPR005299	SAM dependent carboxyl methyltransferase	3
IPR008976	Lipase/lipooxygenase, PLAT/LH2	3
IPR009009	Barwin-related endoglucanase	3
IPR010987	Glutathione S-transferase, C-terminal-like	3
IPR012335	Thioredoxin fold	3
IPR012336	Thioredoxin-like fold	3
IPR017933	Glutathione S-transferase/chloride channel, C-terminal	3
IPR017949	Thaumatin, conserved site	3
IPR018202	Peptidase S10, serine carboxypeptidase, active site	3
IPR020635	Tyrosine-protein kinase, catalytic domain	3
IPR000109	Oligopeptide transporter	2

IPR000620	Protein of unknown function DUF6, transmembrane	2
IPR000823	Plant peroxidase	2
IPR000877	Proteinase inhibitor I12, Bowman-Birk	2
IPR000907	Lipoxygenase	2
IPR001077	O-methyltransferase, family 2	2
IPR001223	Glycoside hydrolase, family 18, catalytic domain	2
IPR001246	Lipoxygenase, plant	2
IPR001898	Sodium/sulphate symporter	2
IPR002016	Haem peroxidase, plant/fungal/bacterial	2
IPR002198	Short-chain dehydrogenase/reductase SDR	2
IPR002213	UDP-glucuronosyl/UDP-glucosyltransferase	2
IPR002347	Glucose/ribitol dehydrogenase	2
IPR002403	Cytochrome P450, E-class, group IV	2
IPR002902	Protein of unknown function DUF26	2
IPR002912	Amino acid-binding ACT	2
IPR003340	Transcriptional factor B3	2
IPR003593	ATPase, AAA+ type, core	2
IPR003663	Sugar/inositol transporter	2
IPR004776	Auxin efflux carrier	2
IPR005132	Rare lipoprotein A	2
IPR005829	Sugar transporter, conserved site	2
IPR006047	Glycosyl hydrolase, family 13, catalytic domain	2
IPR007087	Zinc finger, C2H2-type	2
IPR007112	Expansin 45, endoglucanase-like	2
IPR008271	Serine/threonine-protein kinase, active site	2
IPR010255	Haem peroxidase	2
IPR010399	Tify	2
IPR011991	Winged helix-turn-helix transcription repressor DNA-binding	2
IPR012967	Plant methyltransferase dimerisation	2
IPR013783	Immunoglobulin-like fold	2
IPR013819	Lipoxygenase, C-terminal	2
IPR014734	Pollen allergen, N-terminal	2
IPR015880	Zinc finger, C2H2-like	2
IPR016461	O-methyltransferase, COMT, eukaryota	2
IPR017441	Protein kinase, ATP binding site	2
IPR018371	Chitin-binding, type 1, conserved site	2
IPR018467	CCT domain-like	2
IPR019793	Peroxidases heam-ligand binding site	2
IPR019794	Peroxidase, active site	2
IPR000048	IQ calmodulin-binding region	1
IPR000070	Pectinesterase, catalytic	1
IPR000407	Nucleoside phosphatase GDA1/CD39	1
IPR000535	Major sperm protein	1
IPR000644	Cystathionine beta-synthase, core	1
IPR000648	Oxysterol-binding protein	1

IPR000742	EGF-like, type 3	1
IPR000858	S-locus glycoprotein	1
IPR000863	Sulfotransferase domain	1
IPR000873	AMP-dependent synthetase/ligase	1
IPR000941	Enolase	1
IPR001048	Aspartate/glutamate/uridylate kinase	1
IPR001140	ABC transporter, transmembrane domain	1
IPR001148	Carbonic anhydrase, alpha-class, catalytic domain	1
IPR001153	Barwin	1
IPR001155	NADH:flavin oxidoreductase/NADH oxidase, N-terminal	1
IPR001216	Cysteine synthase/cystathionine beta-synthase P-phosphate-binding site	1
IPR001229	Mannose-binding lectin	1
IPR001245	Serine/threonine/tyrosine-protein kinase	1
IPR001279	Beta-lactamase-like	1
IPR001327	Pyridine nucleotide-disulphide oxidoreductase, NAD-binding region	1
IPR001341	Aspartate kinase domain	1
IPR001356	Homeobox	1
IPR001461	Peptidase A1	1
IPR001471	Pathogenesis-related transcriptional factor/ERF, DNA-binding	1
IPR001480	Curculin-like (mannose-binding) lectin	1
IPR001568	Ribonuclease T2	1
IPR001579	Glycoside hydrolase, chitinase active site	1
IPR001609	Myosin head, motor domain	1
IPR001611	Leucine-rich repeat	1
IPR001623	Heat shock protein DnaJ, N-terminal	1
IPR001680	WD40 repeat	1
IPR001757	ATPase, P-type, K/Mg/Cd/Cu/Zn/Na/Ca/Na/H-transporter	1
IPR001764	Glycoside hydrolase, family 3, N-terminal	1
IPR001807	Chloride channel, voltage gated	1
IPR001841	Zinc finger, RING-type	1
IPR001849	Pleckstrin homology	1
IPR001891	Malic oxidoreductase	1
IPR001926	Pyridoxal phosphate-dependent enzyme, beta subunit	1
IPR001962	Asparagine synthase	1
IPR002013	Synaptojanin, N-terminal	1
IPR002044	Glycoside hydrolase, carbohydrate-binding	1
IPR002048	Calcium-binding EF-hand	1
IPR002251	Chloride channel plant CLC	1
IPR002401	Cytochrome P450, E-class, group I	1
IPR002610	Peptidase S54, rhomboid	1
IPR002641	Patatin	1
IPR002683	Photosystem II oxygen evolving complex protein PsbP	1
IPR002710	Dilute	1
IPR002772	Glycoside hydrolase, family 3, C-terminal	1
IPR002781	Protein of unknown function DUF81	1

IPR002938	Monooxygenase, FAD-binding	1
IPR002963	Expansin	1
IPR003042	Aromatic-ring hydroxylase-like	1
IPR003265	HhH-GPD domain	1
IPR003395	RecF/RecN/SMC protein, N-terminal	1
IPR003439	ABC transporter-like	1
IPR003480	Transferase	1
IPR003609	Apple-like	1
IPR003612	Plant lipid transfer protein/seed storage/trypsin-alpha amylase inhibitor	1
IPR003651	Endonuclease III-like, iron-sulphur cluster loop motif	1
IPR003657	DNA-binding WRKY	1
IPR003959	ATPase, AAA-type, core	1
IPR003960	ATPase, AAA-type, conserved site	1
IPR004022	DDT domain	1
IPR004193	Glycoside hydrolase, family 13, N-terminal	1
IPR004265	Plant disease resistance response protein	1
IPR004294	Carotenoid oxygenase	1
IPR004789	Acetolactate synthase, small subunit	1
IPR004813	Oligopeptide transporter OPT superfamily	1
IPR004843	Metallophosphoesterase	1
IPR005123	Oxoglutarate/iron-dependent oxygenase	1
IPR005134	Uncharacterised protein family UPF0114, prokaryotic	1
IPR005834	Haloacid dehalogenase-like hydrolase	1
IPR005856	Cysteine synthase K/M	1
IPR005859	Cysteine synthase A	1
IPR005881	Serine O-acetyltransferase	1
IPR006046	Glycoside hydrolase family 13	1
IPR006121	Heavy metal transport/detoxification protein	1
IPR006210	EGF-like	1
IPR006311	Twin-arginine translocation pathway, signal sequence	1
IPR006426	Asparagine synthase, glutamine-hydrolyzing	1
IPR006501	Pectinesterase inhibitor	1
IPR006539	ATPase, P-type, phospholipid-translocating, flippase	1
IPR006589	Glycosyl hydrolase, family 13, subfamily, catalytic domain	1
IPR006694	Fatty acid hydroxylase	1
IPR007117	Pollen allergen/expansin, C-terminal	1
IPR007118	Expansin/Lol pI	1
IPR007274	Ctr copper transporter	1
IPR007657	Glycosyltransferase AER61, uncharacterised	1
IPR007701	Interferon-related developmental regulator, N-terminal	1
IPR008089	Nucleotide sugar epimerase	1
IPR008250	ATPase, P-type, ATPase-associated domain	1
IPR008265	Lipase, GDSL, active site	1
IPR008889	VQ	1
IPR008962	PapD-like	1

IPR009007	Peptidase aspartic, catalytic	1
IPR009057	Homeodomain-like	1
IPR009438	Phytosulfokine	1
IPR009448	UDP-glucose:Glycoprotein Glucosyltransferase	1
IPR009836	Protein of unknown function DUF1399	1
IPR010417	Embryo-specific 3	1
IPR010525	Auxin response factor	1
IPR010935	SMCs flexible hinge	1
IPR011004	Trimeric LpxA-like	1
IPR011008	Dimeric alpha-beta barrel	1
IPR011046	WD40 repeat-like-containing domain	1
IPR011050	Pectin lyase fold/virulence factor	1
IPR011230	Phosphoesterase At2g46880	1
IPR011257	DNA glycosylase	1
IPR011525	Aux/IAA-ARF-dimerisation	1
IPR011527	ABC transporter, transmembrane domain, type 1	1
IPR011766	Thiamine pyrophosphate enzyme, C-terminal TPP-binding	1
IPR011993	Pleckstrin homology-type	1
IPR012000	Thiamine pyrophosphate enzyme, central domain	1
IPR012001	Thiamine pyrophosphate enzyme, N-terminal TPP-binding domain	1
IPR012110	Pyruvate decarboxylase/indolepyruvate decarboxylase	1
IPR012287	Homeodomain-related	1
IPR012301	Malic enzyme, N-terminal	1
IPR012302	Malic enzyme, NAD-binding	1
IPR012334	Pectin lyase fold	1
IPR012340	Nucleic acid-binding, OB-fold	1
IPR012442	Protein of unknown function DUF1645	1
IPR012850	Alpha-amylase, C-terminal beta-sheet	1
IPR013027	FAD-dependent pyridine nucleotide-disulphide oxidoreductase	1
IPR013057	Amino acid transporter, transmembrane	1
IPR013097	Stress responsive alpha-beta barrel	1
IPR013210	Leucine-rich repeat-containing N-terminal domain, type 2	1
IPR013227	PAN-2 domain	1
IPR013775	Alpha-amylase, plant	1
IPR013780	Glycosyl hydrolase, family 13, all-beta	1
IPR013784	Carbohydrate-binding-like fold	1
IPR013785	Aldolase-type TIM barrel	1
IPR013830	Esterase, SGNH hydrolase-type	1
IPR013955	Replication factor A, C-terminal	1
IPR014729	Rossmann-like alpha/beta/alpha sandwich fold	1
IPR014733	Barwin-like endoglucanase	1
IPR014743	Chloride channel, core	1
IPR014756	Immunoglobulin E-set	1
IPR015609	Molecular chaperone, heat shock protein, Hsp40, DnaJ	1
IPR015884	Malic enzyme, conserved site	1

IPR015943	WD40/YVTN repeat-like-containing domain	1
IPR016027	Nucleic acid-binding, OB-fold-like	1
IPR016035	Acyl transferase/acyl hydrolase/lysophospholipase	1
IPR016123	Mog1/PsbP, alpha/beta/alpha sandwich	1
IPR016124	Mog1/PsbP/DUF1795, alpha/beta/alpha sandwich	1
IPR016140	Bifunctional inhibitor/plant lipid transfer protein/seed storage	1
IPR016177	DNA-binding, integrase-type	1
IPR017871	ABC transporter, conserved site	1
IPR017932	Glutamine amidotransferase, type II	1
IPR017940	ABC transporter integral membrane type 1	1
IPR017972	Cytochrome P450, conserved site	1
IPR017973	Cytochrome P450, C-terminal	1
IPR017986	WD40-repeat-containing domain	1
IPR018040	Pectinesterase, active site	1
IPR018042	Aspartate kinase, conserved site	1
IPR018188	Ribonuclease T2, active site	1
IPR018249	EF-HAND 2	1
IPR018253	Heat shock protein DnaJ, conserved site	1
IPR018303	ATPase, P-type phosphorylation site	1
IPR018338	Carbonic anhydrase, alpha-class, conserved site	1
IPR018340	Carbonic anhydrase, CAH1-like	1
IPR018357	Hexapeptide transferase, conserved site	1
IPR018444	Dil domain	1
IPR018456	PTR2 family proton/oligopeptide symporter, conserved site	1
IPR018500	DDT domain, subgroup	1
IPR018501	DDT domain superfamily	1
IPR018957	Zinc finger, C3HC4 RING-type	1
IPR019455	Acetolactate synthase, small subunit, C-terminal	1
IPR019781	WD40 repeat, subgroup	1
IPR019782	WD40 repeat 2	1
IPR020472	G-protein beta WD-40 repeat, region	1
IPR020809	Enolase, conserved site	1
IPR020810	Enolase, C-terminal	1
IPR020811	Enolase, N-terminal	1
IPR020833	Lipoxygenase, iron binding site	1
IPR020834	Lipoxygenase, conserved site	1
IPR020845	AMP-binding, conserved site	1
IPR020904	Short-chain dehydrogenase/reductase, conserved site	1
IPR021109	Peptidase aspartic	1
IPR021260	Protein of unknown function DUF2837	1
SP80-3280 down-regulated DETs		
IPR016040	NAD(P)-binding domain	5
IPR001433	Oxidoreductase FAD/NAD(P)-binding	2
IPR001509	NAD-dependent epimerase/dehydratase	2
IPR001709	Flavoprotein pyridine nucleotide cytochrome reductase	2

IPR002213	UDP-glucuronosyl/UDP-glucosyltransferase	2
IPR008333	Oxidoreductase, FAD-binding domain	2
IPR012146	Ferredoxin--NADP reductase	2
IPR015701	Ferredoxin Reductase	2
IPR017927	Ferredoxin reductase-type FAD-binding domain	2
IPR017938	Riboflavin synthase-like beta-barrel	2
IPR000146	Fructose-1,6-bisphosphatase	1
IPR000741	Fructose-bisphosphate aldolase, class-I	1
IPR000846	Dihydrodipicolinate reductase	1
IPR000850	Adenylate kinase	1
IPR001087	Lipase, GDSL	1
IPR001449	Phosphoenolpyruvate carboxylase	1
IPR001478	PDZ/DHR/GLGF	1
IPR001765	Carbonic anhydrase	1
IPR002085	Alcohol dehydrogenase superfamily, zinc-containing	1
IPR002683	Photosystem II oxygen evolving complex protein PsbP	1
IPR003466	Chalcone isomerase, subgroup	1
IPR004045	Glutathione S-transferase, N-terminal	1
IPR004046	Glutathione S-transferase, C-terminal	1
IPR004131	Inorganic H+ pyrophosphatase	1
IPR005336	Uncharacterised protein family UPF0041	1
IPR006259	Adenylate kinase, subfamily	1
IPR006904	Protein of unknown function DUF716	1
IPR006946	Protein of unknown function DUF642	1
IPR007862	Adenylate kinase, active site lid domain	1
IPR008979	Galactose-binding domain-like	1
IPR009500	Protein of unknown function DUF1118	1
IPR010987	Glutathione S-transferase, C-terminal-like	1
IPR011032	GroES-like	1
IPR011770	Dihydrodipicolinate reductase, bacterial/plant	1
IPR011990	Tetratricopeptide-like helical	1
IPR012335	Thioredoxin fold	1
IPR012336	Thioredoxin-like fold	1
IPR013026	Tetratricopeptide repeat-containing	1
IPR013057	Amino acid transporter, transmembrane	1
IPR013149	Alcohol dehydrogenase, zinc-binding	1
IPR013154	Alcohol dehydrogenase GroES-like	1
IPR013785	Aldolase-type TIM barrel	1
IPR015813	Pyruvate/Phosphoenolpyruvate kinase, catalytic core	1
IPR016087	Chalcone isomerase	1
IPR016088	Chalcone isomerase, 3-layer sandwich	1
IPR016123	Mog1/PsbP, alpha/beta/alpha sandwich	1
IPR016124	Mog1/PsbP/DUF1795, alpha/beta/alpha sandwich	1
IPR017933	Glutathione S-transferase/chloride channel, C-terminal	1
IPR018129	Phosphoenolpyruvate carboxylase, active site	1

IPR019734	Tetratricopeptide repeat	1
IPR020548	Fructose-1,6-bisphosphatase, active site	1
IPR020843	Polyketide synthase, enoylreductase	1
IPR021135	Phosphoenolpyruvate carboxylase, C-terminal region	1
IPR021954	Protein of unknown function DUF3571	1

Table S5. List of up- and down-regulated DEGs enriched to protein domains.

InterPro	Description	Number
Common up-regulated DETs		
IPR001128	Cytochrome P450	5
IPR005123	Oxoglutarate/iron-dependent oxygenase	5
IPR000864	Proteinase inhibitor I13, potato inhibitor I	4
IPR002401	Cytochrome P450, E-class, group I	4
IPR003657	DNA-binding WRKY	4
IPR017972	Cytochrome P450, conserved site	4
IPR017973	Cytochrome P450, C-terminal	4
IPR000823	Plant peroxidase	3
IPR001024	Lipoxygenase, LH2	3
IPR002016	Haem peroxidase, plant/fungal/bacterial	3
IPR002283	Isopenicillin N synthase	3
IPR003593	ATPase, AAA+ type, core	3
IPR008976	Lipase/lipooxygenase, PLAT/LH2	3
IPR010255	Haem peroxidase	3
IPR016040	NAD(P)-binding domain	3
IPR019793	Peroxidases heam-ligand binding site	3
IPR019794	Peroxidase, active site	3
IPR000048	IQ calmodulin-binding region	2
IPR000719	Protein kinase, catalytic domain	2
IPR000907	Lipoxygenase	2
IPR001246	Lipoxygenase, plant	2
IPR002129	Pyridoxal phosphate-dependent decarboxylase	2
IPR002290	Serine/threonine-protein kinase domain	2
IPR003245	Plastocyanin-like	2
IPR003612	Plant lipid transfer protein/seed storage/trypsin-alpha amylase inhibitor	2
IPR003959	ATPase, AAA-type, core	2
IPR006093	Oxygen oxidoreductase covalent FAD-binding site	2
IPR006094	FAD linked oxidase, N-terminal	2
IPR007650	Protein of unknown function DUF581	2
IPR008972	Cupredoxin	2
IPR010977	Aromatic-L-amino-acid decarboxylase	2
IPR011009	Protein kinase-like domain	2

IPR013819	Lipoxygenase, C-terminal	2
IPR015345	Cytokinin dehydrogenase 1, FAD/cytokinin binding domain	2
IPR015421	Pyridoxal phosphate-dependent transferase, major region, subdomain 1	2
IPR015422	Pyridoxal phosphate-dependent transferase, major region, subdomain 2	2
IPR015424	Pyridoxal phosphate-dependent transferase, major domain	2
IPR015609	Molecular chaperone, heat shock protein, Hsp40, DnaJ	2
IPR016140	Bifunctional inhibitor/plant lipid transfer protein/seed storage	2
IPR016164	FAD-linked oxidase-like, C-terminal	2
IPR016166	FAD-binding, type 2	2
IPR020635	Tyrosine-protein kinase, catalytic domain	2
IPR021115	Pyridoxal-phosphate binding site	2
IPR000073	Alpha/beta hydrolase fold-1	1
IPR000225	Armadillo	1
IPR000300	Inositol polyphosphate related phosphatase	1
IPR000572	Oxidoreductase, molybdopterin binding	1
IPR000595	Cyclic nucleotide-binding	1
IPR000639	Epoxide hydrolase-like	1
IPR000743	Glycoside hydrolase, family 28	1
IPR000877	Proteinase inhibitor I12, Bowman-Birk	1
IPR000923	Blue (type 1) copper domain	1
IPR001005	SANT, DNA-binding	1
IPR001077	O-methyltransferase, family 2	1
IPR001087	Lipase, GDSL	1
IPR001092	Helix-loop-helix DNA-binding domain	1
IPR001199	Cytochrome b5	1
IPR001245	Serine/threonine/tyrosine-protein kinase	1
IPR001270	Chaperonin clpA/B	1
IPR001362	Glycoside hydrolase, family 32	1
IPR001433	Oxidoreductase FAD/NAD(P)-binding	1
IPR001440	Tetratricopeptide TPR-1	1
IPR001471	Pathogenesis-related transcriptional factor/ERF, DNA-binding	1
IPR001509	NAD-dependent epimerase/dehydratase	1
IPR001611	Leucine-rich repeat	1
IPR001623	Heat shock protein DnaJ, N-terminal	1
IPR001709	Flavoprotein pyridine nucleotide cytochrome reductase	1
IPR001834	NADH:cytochrome b5 reductase (CBR)	1
IPR001841	Zinc finger, RING-type	1
IPR001906	Terpene synthase-like	1
IPR002028	Tryptophan synthase, alpha chain	1
IPR002110	Ankyrin repeat	1
IPR002403	Cytochrome P450, E-class, group IV	1
IPR002781	Protein of unknown function DUF81	1
IPR003439	ABC transporter-like	1
IPR003441	No apical meristem (NAM) protein	1
IPR003613	U box domain	1

IPR003938	Potassium channel, voltage-dependent, EAG/ELK/ERG	1
IPR003953	Fumarate reductase/succinate dehydrogenase flavoprotein, N-terminal	1
IPR004112	Fumarate reductase/succinate dehydrogenase flavoprotein, C-terminal	1
IPR004158	Protein of unknown function DUF247, plant	1
IPR004176	Clp, N-terminal	1
IPR004316	RAG1-activating protein-1-related	1
IPR004695	C4-dicarboxylate transporter/malic acid transport protein	1
IPR005066	Moybdenum cofactor oxidoreductase, dimerisation	1
IPR005135	Endonuclease/exonuclease/phosphatase	1
IPR005256	Anthranilate synthase component I	1
IPR005288	L-aspartate oxidase	1
IPR005630	Terpene synthase, metal-binding domain	1
IPR005801	ADC synthase	1
IPR005821	Ion transport	1
IPR006076	FAD dependent oxidoreductase	1
IPR006109	NAD-dependent glycerol-3-phosphate dehydrogenase, C-terminal	1
IPR006139	D-isomer specific 2-hydroxyacid dehydrogenase, catalytic domain	1
IPR006140	D-isomer specific 2-hydroxyacid dehydrogenase, NAD-binding	1
IPR006168	NAD-dependent glycerol-3-phosphate dehydrogenase	1
IPR006626	Parallel beta-helix repeat	1
IPR006805	Anthranilate synthase component I, N-terminal	1
IPR008217	Protein of unknown function DUF125, transmembrane	1
IPR008265	Lipase, GDSL, active site	1
IPR008271	Serine/threonine-protein kinase, active site	1
IPR008333	Oxidoreductase, FAD-binding domain	1
IPR008335	Eukaryotic molybdopterin oxidoreductase	1
IPR008927	6-phosphogluconate dehydrogenase, C-terminal-like	1
IPR008930	Terpenoid cylases/protein prenyltransferase alpha-alpha toroid	1
IPR008949	Terpenoid synthase	1
IPR008985	Concanavalin A-like lectin/glucanase	1
IPR009057	Homeodomain-like	1
IPR010399	Tify	1
IPR010417	Embryo-specific 3	1
IPR010821	Chlorophyllase-like	1
IPR011050	Pectin lyase fold/virulence factor	1
IPR011060	Ribulose-phosphate binding barrel	1
IPR011128	NAD-dependent glycerol-3-phosphate dehydrogenase, N-terminal	1
IPR011598	Helix-loop-helix DNA-binding	1
IPR011701	Major facilitator superfamily MFS-1	1
IPR011766	Thiamine pyrophosphate enzyme, C-terminal TPP-binding	1
IPR011989	Armadillo-like helical	1
IPR011990	Tetratricopeptide-like helical	1
IPR011991	Winged helix-turn-helix transcription repressor DNA-binding	1
IPR012000	Thiamine pyrophosphate enzyme, central domain	1
IPR012001	Thiamine pyrophosphate enzyme, N-terminal TPP-binding domain	1

IPR012110	Pyruvate decarboxylase/indolepyruvate decarboxylase	1
IPR012137	Nitrate reductase NADH dependent	1
IPR012287	Homeodomain-related	1
IPR012334	Pectin lyase fold	1
IPR012967	Plant methyltransferase dimerisation	1
IPR013026	Tetratricopeptide repeat-containing	1
IPR013093	ATPase, AAA-2	1
IPR013148	Glycosyl hydrolases family 32, N-terminal	1
IPR013189	Glycosyl hydrolase family 32, C-terminal	1
IPR013328	Dehydrogenase, multihelical	1
IPR013525	ABC-2 type transporter	1
IPR013785	Aldolase-type TIM barrel	1
IPR014710	RmlC-like jelly roll fold	1
IPR014756	Immunoglobulin E-set	1
IPR014778	Myb, DNA-binding	1
IPR015495	Myb transcription factor	1
IPR015890	Chorismate binding, C-terminal	1
IPR015939	Fumarate reductase/succinate dehydrogenase flavoprotein-like, C-terminal	1
IPR016024	Armadillo-type fold	1
IPR016177	DNA-binding, integrase-type	1
IPR016196	Major facilitator superfamily, general substrate transporter	1
IPR016461	O-methyltransferase, COMT, eukaryota	1
IPR017442	Serine/threonine-protein kinase-like domain	1
IPR017871	ABC transporter, conserved site	1
IPR017927	Ferredoxin reductase-type FAD-binding domain	1
IPR017930	HTH transcriptional regulator, Myb-type, DNA-binding	1
IPR017938	Riboflavin synthase-like beta-barrel	1
IPR018169	MtN3/saliva-related transmembrane protein, conserved region	1
IPR018179	RAG1-activating protein 1 homologue	1
IPR018204	Tryptophan synthase, alpha chain, active site	1
IPR018253	Heat shock protein DnaJ, conserved site	1
IPR018368	Chaperonin ClpA/B, conserved site	1
IPR018467	CCT domain-like	1
IPR018490	Cyclic nucleotide-binding-like	1
IPR018506	Cytochrome b5, heme-binding site	1
IPR018957	Zinc finger, C3HC4 RING-type	1
IPR019489	Clp ATPase, C-terminal	1
IPR019734	Tetratricopeptide repeat	1
IPR019999	Anthranilate synthase component I, C-terminal	1
IPR020683	Ankyrin repeat-containing domain	1
IPR020833	Lipoxygenase, iron binding site	1
IPR020834	Lipoxygenase, conserved site	1
IPR021789	Protein of unknown function DUF3354	1
Common down-regulated DEGs		
IPR000767	Disease resistance protein	1

IPR002182	NB-ARC	1
RB867515 up-regulated DEGs		
IPR000719	Protein kinase, catalytic domain	7
IPR001092	Helix-loop-helix DNA-binding domain	7
IPR011009	Protein kinase-like domain	7
IPR011598	Helix-loop-helix DNA-binding	6
IPR001611	Leucine-rich repeat	5
IPR002213	UDP-glucuronosyl/UDP-glucosyltransferase	5
IPR012287	Homeodomain-related	5
IPR000620	Protein of unknown function DUF6, transmembrane	4
IPR001128	Cytochrome P450	4
IPR001906	Terpene synthase-like	4
IPR002290	Serine/threonine-protein kinase domain	4
IPR002401	Cytochrome P450, E-class, group I	4
IPR003657	DNA-binding WRKY	4
IPR005630	Terpene synthase, metal-binding domain	4
IPR008930	Terpenoid cylases/protein prenyltransferase alpha-alpha toroid	4
IPR008949	Terpenoid synthase	4
IPR009057	Homeodomain-like	4
IPR011050	Pectin lyase fold/virulence factor	4
IPR012334	Pectin lyase fold	4
IPR013785	Aldolase-type TIM barrel	4
IPR017442	Serine/threonine-protein kinase-like domain	4
IPR017973	Cytochrome P450, C-terminal	4
IPR020635	Tyrosine-protein kinase, catalytic domain	4
IPR000907	Lipoxygenase	3
IPR001024	Lipoxygenase, LH2	3
IPR001246	Lipoxygenase, plant	3
IPR001841	Zinc finger, RING-type	3
IPR003439	ABC transporter-like	3
IPR003593	ATPase, AAA+ type, core	3
IPR008271	Serine/threonine-protein kinase, active site	3
IPR008976	Lipase/lipooxygenase, PLAT/LH2	3
IPR013210	Leucine-rich repeat-containing N-terminal domain, type 2	3
IPR013781	Glycoside hydrolase, subgroup, catalytic core	3
IPR013819	Lipoxygenase, C-terminal	3
IPR016040	NAD(P)-binding domain	3
IPR017853	Glycoside hydrolase, catalytic core	3
IPR017972	Cytochrome P450, conserved site	3
IPR018957	Zinc finger, C3HC4 RING-type	3
IPR000070	Pectinesterase, catalytic	2
IPR000644	Cystathionine beta-synthase, core	2
IPR000743	Glycoside hydrolase, family 28	2
IPR001005	SANT, DNA-binding	2
IPR001140	ABC transporter, transmembrane domain	2

IPR001155	NADH:flavin oxidoreductase/NADH oxidase, N-terminal	2
IPR001245	Serine/threonine/tyrosine-protein kinase	2
IPR001356	Homeobox	2
IPR001597	Aromatic amino acid beta-eliminating lyase/threonine aldolase	2
IPR001789	Signal transduction response regulator, receiver domain	2
IPR002495	Glycosyl transferase, family 8	2
IPR003480	Transferase	2
IPR003591	Leucine-rich repeat, typical subtype	2
IPR003594	ATPase-like, ATP-binding domain	2
IPR003661	Signal transduction histidine kinase, subgroup 1, dimerisation/phosphoacceptor domain	2
IPR004294	Carotenoid oxygenase	2
IPR004358	Signal transduction histidine kinase-related protein, C-terminal	2
IPR005123	Oxoglutarate/iron-dependent oxygenase	2
IPR005467	Signal transduction histidine kinase, core	2
IPR005834	Haloacid dehalogenase-like hydrolase	2
IPR006076	FAD dependent oxidoreductase	2
IPR006094	FAD linked oxidase, N-terminal	2
IPR006402	HAD-superfamily hydrolase, subfamily IA, variant 3	2
IPR006626	Parallel beta-helix repeat	2
IPR008889	VQ	2
IPR008972	Cupredoxin	2
IPR009082	Signal transduction histidine kinase, homodimeric	2
IPR011006	CheY-like	2
IPR011527	ABC transporter, transmembrane domain, type 1	2
IPR012442	Protein of unknown function DUF1645	2
IPR014778	Myb, DNA-binding	2
IPR015345	Cytokinin dehydrogenase 1, FAD/cytokinin binding domain	2
IPR015421	Pyridoxal phosphate-dependent transferase, major region, subdomain 1	2
IPR015422	Pyridoxal phosphate-dependent transferase, major region, subdomain 2	2
IPR015424	Pyridoxal phosphate-dependent transferase, major domain	2
IPR015495	Myb transcription factor	2
IPR016164	FAD-linked oxidase-like, C-terminal	2
IPR016166	FAD-binding, type 2	2
IPR017441	Protein kinase, ATP binding site	2
IPR017930	HTH transcriptional regulator, Myb-type, DNA-binding	2
IPR017940	ABC transporter integral membrane type 1	2
IPR020474	Toll-like receptor, leucine rich repeat-containing	2
IPR020833	Lipoxygenase, iron binding site	2
IPR020834	Lipoxygenase, conserved site	2
IPR000047	Helix-turn-helix motif, lambda-like repressor	1
IPR000073	Alpha/beta hydrolase fold-1	1
IPR000109	Oligopeptide transporter	1
IPR000136	Oleosin	1
IPR000152	EGF-type aspartate/asparagine hydroxylation site	1
IPR000195	RabGAP/TBC	1

IPR000196	Ribosomal protein L19/L19e	1
IPR000210	BTB/POZ-like	1
IPR000225	Armadillo	1
IPR000300	Inositol polyphosphate related phosphatase	1
IPR000403	Phosphatidylinositol 3-/4-kinase, catalytic	1
IPR000425	Major intrinsic protein	1
IPR000490	Glycoside hydrolase, family 17	1
IPR000504	RNA recognition motif, RNP-1	1
IPR000595	Cyclic nucleotide-binding	1
IPR000634	Serine/threonine dehydratase, pyridoxal-phosphate-binding site	1
IPR000741	Fructose-bisphosphate aldolase, class-I	1
IPR000767	Disease resistance protein	1
IPR000823	Plant peroxidase	1
IPR000836	Phosphoribosyltransferase	1
IPR000877	Proteinase inhibitor I12, Bowman-Birk	1
IPR000923	Blue (type 1) copper domain	1
IPR000991	Glutamine amidotransferase class-I, C-terminal	1
IPR001031	Thioesterase	1
IPR001093	IMP dehydrogenase/GMP reductase	1
IPR001117	Multicopper oxidase, type 1	1
IPR001223	Glycoside hydrolase, family 18, catalytic domain	1
IPR001371	Glycoside hydrolase, family 14B, plant	1
IPR001471	Pathogenesis-related transcriptional factor/ERF, DNA-binding	1
IPR001509	NAD-dependent epimerase/dehydratase	1
IPR001554	Glycoside hydrolase, family 14	1
IPR001579	Glycoside hydrolase, chitinase active site	1
IPR001623	Heat shock protein DnaJ, N-terminal	1
IPR001721	Threonine dehydratase, C-terminal	1
IPR001806	Ras GTPase	1
IPR001807	Chloride channel, voltage gated	1
IPR001818	Peptidase M10, metallopeptidase	1
IPR001898	Sodium/sulphate symporter	1
IPR001926	Pyridoxal phosphate-dependent enzyme, beta subunit	1
IPR001938	Thaumatin, pathogenesis-related	1
IPR001986	3-phosphoshikimate 1-carboxyvinyltransferase, core	1
IPR001993	Mitochondrial substrate carrier	1
IPR001995	Peptidase A2A, retrovirus, catalytic	1
IPR002016	Haem peroxidase, plant/fungal/bacterial	1
IPR002067	Mitochondrial carrier protein	1
IPR002100	Transcription factor, MADS-box	1
IPR002110	Ankyrin repeat	1
IPR002123	Phospholipid/glycerol acyltransferase	1
IPR002171	Ribosomal protein L2	1
IPR002182	NB-ARC	1
IPR002198	Short-chain dehydrogenase/reductase SDR	1

IPR002202	Hydroxymethylglutaryl-CoA reductase, class I/II, catalytic	1
IPR002251	Chloride channel plant CLC	1
IPR002283	Isopenicillin N synthase	1
IPR002347	Glucose/ribitol dehydrogenase	1
IPR002355	Multicopper oxidase, copper-binding site	1
IPR002423	Chaperonin Cpn60/TCP-1	1
IPR002477	Peptidoglycan binding-like	1
IPR002487	Transcription factor, K-box	1
IPR002498	Phosphatidylinositol-4-phosphate 5-kinase, core	1
IPR002902	Protein of unknown function DUF26	1
IPR002913	Lipid-binding START	1
IPR002921	Lipase, class 3	1
IPR003018	GAF	1
IPR003095	Heat shock protein DnaJ	1
IPR003100	Argonaute/Dicer protein, PAZ	1
IPR003106	Leucine zipper, homeobox-associated	1
IPR003165	Stem cell self-renewal protein Piwi	1
IPR003245	Plastocyanin-like	1
IPR003340	Transcriptional factor B3	1
IPR003441	No apical meristem (NAM) protein	1
IPR003577	Ras small GTPase, Ras type	1
IPR003578	Small GTPase, Rho type	1
IPR003579	Ras small GTPase, Rab type	1
IPR003613	U box domain	1
IPR003855	K+ potassium transporter	1
IPR003938	Potassium channel, voltage-dependent, EAG/ELK/ERG	1
IPR004041	NAF domain	1
IPR004129	Glycerophosphoryl diester phosphodiesterase	1
IPR004182	GRAM	1
IPR004249	NPH3	1
IPR004253	Protein of unknown function DUF231, plant	1
IPR004255	Uncharacterised protein family UPF0089	1
IPR004316	RAG1-activating protein-1-related	1
IPR004320	Protein of unknown function DUF241, plant	1
IPR004360	Glyoxalase/bleomycin resistance protein/dioxygenase	1
IPR004554	Hydroxymethylglutaryl-CoA reductase, class I, catalytic	1
IPR004696	Tpt phosphate/phosphoenolpyruvate translocator	1
IPR004827	Basic-leucine zipper (bZIP) transcription factor	1
IPR004837	Sodium/calcium exchanger membrane region	1
IPR004843	Metallophosphoesterase	1
IPR004853	Protein of unknown function DUF250	1
IPR004887	Glutathione synthase, substrate-binding, eukaryotic	1
IPR005135	Endonuclease/exonuclease/phosphatase	1
IPR005202	Transcription factor GRAS	1
IPR005225	Small GTP-binding protein	1

IPR005615	Glutathione synthase, eukaryotic	1
IPR005787	Threonine dehydratase I	1
IPR005821	Ion transport	1
IPR005880	Ribosomal protein L2, bacterial-type	1
IPR005946	Phosphoribosyl pyrophosphokinase	1
IPR005990	IMP dehydrogenase	1
IPR006026	Peptidase, metallopeptidase	1
IPR006035	Ureohydrolase	1
IPR006093	Oxygen oxidoreductase covalent FAD-binding site	1
IPR006139	D-isomer specific 2-hydroxyacid dehydrogenase, catalytic domain	1
IPR006140	D-isomer specific 2-hydroxyacid dehydrogenase, NAD-binding	1
IPR006189	CHASE	1
IPR006210	EGF-like	1
IPR006264	3-phosphoshikimate 1-carboxyvinyltransferase, subgroup	1
IPR006282	Thiamin pyrophosphokinase	1
IPR006455	Homeobox domain, ZF-HD class	1
IPR006456	ZF-HD homeobox protein, Cys/His-rich dimerisation domain	1
IPR006501	Pectinesterase inhibitor	1
IPR006652	Kelch repeat type 1	1
IPR006840	ChaC-like protein	1
IPR006937	Plant neutral invertase	1
IPR007271	Nucleotide-sugar transporter	1
IPR007371	Thiamin pyrophosphokinase, catalytic domain	1
IPR007373	Thiamin pyrophosphokinase, vitamin B1-binding domain	1
IPR007650	Protein of unknown function DUF581	1
IPR007700	Protein of unknown function DUF668	1
IPR008913	Zinc finger, CHY-type	1
IPR008928	Six-hairpin glycosidase-like	1
IPR008991	Translation protein SH3-like	1
IPR009023	Hydroxymethylglutaryl-CoA reductase, class I/II, NAD/NADP-binding	1
IPR009029	Hydroxymethylglutaryl-CoA reductase, class I/II, substrate-binding	1
IPR009262	Protein of unknown function DUF914, eukaryotic	1
IPR009438	Phytosulfokine	1
IPR010237	Pyrimidine 5-nucleotidase	1
IPR010255	Haem peroxidase	1
IPR011043	Galactose oxidase/kelch, beta-propeller	1
IPR011333	BTB/POZ fold	1
IPR011525	Aux/IAA-ARF-dimerisation	1
IPR011616	bZIP transcription factor, bZIP-1	1
IPR011706	Multicopper oxidase, type 2	1
IPR011707	Multicopper oxidase, type 3	1
IPR011989	Armadillo-like helical	1
IPR012269	Aquaporin	1
IPR012337	Polynucleotidyl transferase, ribonuclease H fold	1
IPR012340	Nucleic acid-binding, OB-fold	1

IPR012677	Nucleotide-binding, alpha-beta plait	1
IPR012862	Protein of unknown function DUF1635	1
IPR012946	X8	1
IPR013057	Amino acid transporter, transmembrane	1
IPR013069	BTB/POZ	1
IPR013089	Kelch related	1
IPR013216	Methyltransferase type 11	1
IPR013525	ABC-2 type transporter	1
IPR013626	Pheophorbide a oxygenase	1
IPR013753	Ras	1
IPR013792	RNA 3'-terminal phosphate cyclase/enolpyruvate transferase, alpha/beta	1
IPR013816	ATP-grasp fold, subdomain 2	1
IPR013861	Protein of unknown function DUF1751, integral membrane, eukaryotic	1
IPR013978	MEKHLA	1
IPR014042	Glutathione synthase, alpha-helical, eukaryotic	1
IPR014710	RmlC-like jelly roll fold	1
IPR014722	Translation protein SH3-like, subgroup	1
IPR014743	Chloride channel, core	1
IPR014811	Domain of unknown function DUF1785	1
IPR015590	Aldehyde dehydrogenase	1
IPR015609	Molecular chaperone, heat shock protein, Hsp40, DnaJ	1
IPR015875	IMP dehydrogenase / GMP reductase, conserved site	1
IPR015915	Kelch-type beta propeller	1
IPR015972	Ribosomal protein L19/L19e, domain 1	1
IPR015974	Ribosomal protein L19/L19e, domain 3	1
IPR016024	Armadillo-type fold	1
IPR016027	Nucleic acid-binding, OB-fold-like	1
IPR016034	Phosphatidylinositol-4-phosphate 5-kinase, core, subgroup	1
IPR016160	Aldehyde dehydrogenase, conserved site	1
IPR016161	Aldehyde/histidinol dehydrogenase	1
IPR016162	Aldehyde dehydrogenase, N-terminal	1
IPR016177	DNA-binding, integrase-type	1
IPR016185	PreATP-grasp-like fold	1
IPR016196	Major facilitator superfamily, general substrate transporter	1
IPR016228	3-phosphoshikimate 1-carboxyvinyltransferase	1
IPR016966	Thiamin pyrophosphokinase, eukaryotic	1
IPR017871	ABC transporter, conserved site	1
IPR017921	Zinc finger, CTCHY-type	1
IPR017926	Glutamine amidotransferase type 1	1
IPR017941	Rieske [2Fe-2S] iron-sulphur domain	1
IPR017946	PLC-like phosphodiesterase, TIM beta/alpha-barrel domain	1
IPR017970	Homeobox, conserved site	1
IPR018040	Pectinesterase, active site	1
IPR018097	EGF-like calcium-binding, conserved site	1
IPR018108	Mitochondrial substrate/solute carrier	1

IPR018169	MtN3/saliva-related transmembrane protein, conserved region	1
IPR018179	RAG1-activating protein 1 homologue	1
IPR018238	Glycoside hydrolase, family 14, conserved site	1
IPR018392	Peptidoglycan-binding lysin domain	1
IPR018451	NAF/FISL domain	1
IPR018490	Cyclic nucleotide-binding-like	1
IPR018519	Potassium uptake protein, kup	1
IPR018529	IMP dehydrogenase related	1
IPR019793	Peroxidases heam-ligand binding site	1
IPR019794	Peroxidase, active site	1
IPR020636	Calcium/calmodulin-dependent protein kinase-like	1
IPR020660	CBL-interacting protein kinase	1
IPR020683	Ankyrin repeat-containing domain	1
IPR020851	Small GTPase	1
IPR020855	Ureohydrolase, manganese-binding site	1
IPR021189	UDP/CMP-sugar transporter	1
IPR021190	Peptidase M10A, matrix metallopeptidase, conserved region	1
IPR021775	Protein of unknown function DUF3339	1
IPR021789	Protein of unknown function DUF3354	1
IPR021864	Protein of unknown function DUF3475	1
RB867515 down-regulated DEGs		
IPR001471	Pathogenesis-related transcriptional factor/ERF, DNA-binding	4
IPR012335	Thioredoxin fold	4
IPR012336	Thioredoxin-like fold	4
IPR015609	Molecular chaperone, heat shock protein, Hsp40, DnaJ	4
IPR016177	DNA-binding, integrase-type	4
IPR001623	Heat shock protein DnaJ, N-terminal	3
IPR003095	Heat shock protein DnaJ	3
IPR007125	Histone core	3
IPR009072	Histone-fold	3
IPR016196	Major facilitator superfamily, general substrate transporter	3
IPR017853	Glycoside hydrolase, catalytic core	3
IPR000719	Protein kinase, catalytic domain	2
IPR000823	Plant peroxidase	2
IPR001005	SANT, DNA-binding	2
IPR001077	O-methyltransferase, family 2	2
IPR001128	Cytochrome P450	2
IPR001395	Aldo/keto reductase	2
IPR001841	Zinc finger, RING-type	2
IPR002016	Haem peroxidase, plant/fungal/bacterial	2
IPR002044	Glycoside hydrolase, carbohydrate-binding	2
IPR002109	Glutaredoxin	2
IPR002192	Pyruvate phosphate dikinase, PEP/pyruvate-binding	2
IPR002290	Serine/threonine-protein kinase domain	2
IPR002401	Cytochrome P450, E-class, group I	2

IPR003111	Peptidase S16, lon N-terminal	2
IPR004326	Mlo-related protein	2
IPR006015	Universal stress protein A	2
IPR006016	UspA	2
IPR006047	Glycosyl hydrolase, family 13, catalytic domain	2
IPR006694	Fatty acid hydroxylase	2
IPR007650	Protein of unknown function DUF581	2
IPR009057	Homeodomain-like	2
IPR010255	Haem peroxidase	2
IPR011009	Protein kinase-like domain	2
IPR011701	Major facilitator superfamily MFS-1	2
IPR011991	Winged helix-turn-helix transcription repressor DNA-binding	2
IPR012967	Plant methyltransferase dimerisation	2
IPR013780	Glycosyl hydrolase, family 13, all-beta	2
IPR013781	Glycoside hydrolase, subgroup, catalytic core	2
IPR013783	Immunoglobulin-like fold	2
IPR013784	Carbohydrate-binding-like fold	2
IPR014729	Rossmann-like alpha/beta/alpha sandwich fold	2
IPR014778	Myb, DNA-binding	2
IPR016040	NAD(P)-binding domain	2
IPR016461	O-methyltransferase, COMT, eukaryota	2
IPR017442	Serine/threonine-protein kinase-like domain	2
IPR017896	4Fe-4S ferredoxin, iron-sulpur binding domain	2
IPR017930	HTH transcriptional regulator, Myb-type, DNA-binding	2
IPR017972	Cytochrome P450, conserved site	2
IPR017973	Cytochrome P450, C-terminal	2
IPR019793	Peroxidases heam-ligand binding site	2
IPR019794	Peroxidase, active site	2
IPR020635	Tyrosine-protein kinase, catalytic domain	2
IPR021940	Uncharacterised protein, Wax2 C-terminal	2
IPR000109	Oligopeptide transporter	1
IPR000210	BTB/POZ-like	1
IPR000253	Forkhead-associated	1
IPR000340	Dual specificity phosphatase, catalytic domain	1
IPR000387	Dual-specific/protein-tyrosine phosphatase, conserved region	1
IPR000504	RNA recognition motif, RNP-1	1
IPR000528	Plant lipid transfer protein/Par allergen	1
IPR000549	Photosystem I PsaG/PsaK protein	1
IPR000558	Histone H2B	1
IPR000595	Cyclic nucleotide-binding	1
IPR000608	Ubiquitin-conjugating enzyme, E2	1
IPR000644	Cystathionine beta-synthase, core	1
IPR000727	Target SNARE coiled-coil domain	1
IPR000866	Alkyl hydroperoxide reductase/ Thiol specific antioxidant/ Mal allergen	1
IPR000910	High mobility group, HMG1/HMG2	1

IPR001092	Helix-loop-helix DNA-binding domain	1
IPR001179	Peptidyl-prolyl cis-trans isomerase, FKBP-type	1
IPR001245	Serine/threonine/tyrosine-protein kinase	1
IPR001345	Phosphoglycerate/bisphosphoglycerate mutase, active site	1
IPR001440	Tetratricopeptide TPR-1	1
IPR001764	Glycoside hydrolase, family 3, N-terminal	1
IPR001765	Carbonic anhydrase	1
IPR001951	Histone H4	1
IPR001993	Mitochondrial substrate carrier	1
IPR002048	Calcium-binding EF-hand	1
IPR002067	Mitochondrial carrier protein	1
IPR002110	Ankyrin repeat	1
IPR002113	Adenine nucleotide translocator 1	1
IPR002119	Histone H2A	1
IPR002198	Short-chain dehydrogenase/reductase SDR	1
IPR002283	Isopenicillin N synthase	1
IPR002314	Aminoacyl-tRNA synthetase, class II (G/ H/ P/ S), conserved domain	1
IPR002320	Threonyl-tRNA synthetase, class IIa	1
IPR002347	Glucose/ribitol dehydrogenase	1
IPR002772	Glycoside hydrolase, family 3, C-terminal	1
IPR002781	Protein of unknown function DUF81	1
IPR002938	Monooxygenase, FAD-binding	1
IPR002963	Expansin	1
IPR003042	Aromatic-ring hydroxylase-like	1
IPR003094	Fructose-2,6-bisphosphatase	1
IPR003347	Transcription factor jumonji/aspartyl beta-hydroxylase	1
IPR003435	Chaperonin-like RbcX	1
IPR003439	ABC transporter-like	1
IPR003441	No apical meristem (NAM) protein	1
IPR003496	ABA/WDS induced protein	1
IPR003593	ATPase, AAA+ type, core	1
IPR003612	Plant lipid transfer protein/seed storage/trypsin-alpha amylase inhibitor	1
IPR003854	Gibberellin regulated protein	1
IPR003938	Potassium channel, voltage-dependent, EAG/ELK/ERG	1
IPR004045	Glutathione S-transferase, N-terminal	1
IPR004154	Anticodon-binding	1
IPR004193	Glycoside hydrolase, family 13, N-terminal	1
IPR004249	NPH3	1
IPR004316	RAG1-activating protein-1-related	1
IPR004331	SPX, N-terminal	1
IPR004342	EXS, C-terminal	1
IPR004367	Cyclin, C-terminal	1
IPR004853	Protein of unknown function DUF250	1
IPR004911	Gamma interferon inducible lysosomal thiol reductase GILT	1
IPR005061	Protein of unknown function DUF292, eukaryotic	1

IPR005123	Oxoglutarate/iron-dependent oxygenase	1
IPR005132	Rare lipoprotein A	1
IPR005202	Transcription factor GRAS	1
IPR005256	Anthranilate synthase component I	1
IPR005801	ADC synthase	1
IPR005821	Ion transport	1
IPR005841	Alpha-D-phosphohexomutase, N-terminal	1
IPR005843	Alpha-D-phosphohexomutase, C-terminal	1
IPR005844	Alpha-D-phosphohexomutase, alpha/beta/alpha domain I	1
IPR005845	Alpha-D-phosphohexomutase, alpha/beta/alpha domain II	1
IPR005846	Alpha-D-phosphohexomutase, alpha/beta/alpha domain III	1
IPR006011	Syntaxin, N-terminal	1
IPR006012	Syntaxin/epimorphin, conserved site	1
IPR006046	Glycoside hydrolase family 13	1
IPR006048	Alpha-amylase, C-terminal all beta	1
IPR006195	Aminoacyl-tRNA synthetase, class II, conserved domain	1
IPR006447	Myb-like DNA-binding domain, SHAQKYF class	1
IPR006476	Conserved hypothetical protein CHP01589, plant	1
IPR006589	Glycosyl hydrolase, family 13, subfamily, catalytic domain	1
IPR006670	Cyclin	1
IPR006671	Cyclin, N-terminal	1
IPR006805	Anthranilate synthase component I, N-terminal	1
IPR006917	SOUL haem-binding protein	1
IPR007110	Immunoglobulin-like	1
IPR007112	Expansin 45, endoglucanase-like	1
IPR007117	Pollen allergen/expansin, C-terminal	1
IPR007118	Expansin/Lol pI	1
IPR008162	Inorganic pyrophosphatase	1
IPR008271	Serine/threonine-protein kinase, active site	1
IPR008928	Six-hairpin glycosidase-like	1
IPR008984	SMAD/FHA domain	1
IPR009003	Serine/cysteine peptidase, trypsin-like	1
IPR009009	Barwin-related endoglucanase	1
IPR009071	High mobility group, superfamily	1
IPR010683	Protein of unknown function DUF1262	1
IPR010989	t-SNARE	1
IPR011028	Cyclin-like	1
IPR011333	BTB/POZ fold	1
IPR011424	C1-like	1
IPR011525	Aux/IAA-ARF-dimerisation	1
IPR011598	Helix-loop-helix DNA-binding	1
IPR011659	WD40-like Beta Propeller	1
IPR011767	Glutaredoxin active site	1
IPR011990	Tetratricopeptide-like helical	1
IPR011992	EF-hand-like domain	1

IPR012287	Homeodomain-related	1
IPR012392	Very-long-chain 3-ketoacyl-CoA synthase	1
IPR012677	Nucleotide-binding, alpha-beta plait	1
IPR012850	Alpha-amylase, C-terminal beta-sheet	1
IPR012947	Threonyl/alanyl tRNA synthetase, SAD	1
IPR013026	Tetratricopeptide repeat-containing	1
IPR013069	BTB/POZ	1
IPR013078	Histidine phosphatase superfamily, clade-1	1
IPR013079	6-phosphofructo-2-kinase	1
IPR013181	Protein of unknown function DUF1719, Oryza sativa	1
IPR013525	ABC-2 type transporter	1
IPR013601	FAE1/Type III polyketide synthase-like protein	1
IPR013747	3-Oxoacyl-[acyl-carrier-protein (ACP)] synthase III C-terminal	1
IPR013763	Cyclin-related	1
IPR013770	Plant lipid transfer protein/hydrophobic protein, helical domain	1
IPR013785	Aldolase-type TIM barrel	1
IPR013815	ATP-grasp fold, subdomain 1	1
IPR014400	Cyclin, A/B/D/E	1
IPR014710	RmlC-like jelly roll fold	1
IPR014734	Pollen allergen, N-terminal	1
IPR014756	Immunoglobulin E-set	1
IPR014977	WRC	1
IPR014978	Glutamine-Leucine-Glutamine, QLQ	1
IPR015453	G2/mitotic-specific cyclin A	1
IPR015495	Myb transcription factor	1
IPR015582	Ubiquitin-conjugating enzyme E2 H10	1
IPR015890	Chorismate binding, C-terminal	1
IPR016038	Thiolase-like, subgroup	1
IPR016039	Thiolase-like	1
IPR016055	Alpha-D-phosphohexomutase, alpha/beta/alpha I/II/III	1
IPR016066	Alpha-D-phosphohexomutase, conserved site	1
IPR016135	Ubiquitin-conjugating enzyme/RWD-like	1
IPR016140	Bifunctional inhibitor/plant lipid transfer protein/seed storage	1
IPR016260	Bifunctional 6-phosphofructo-2-kinase/fructose-2, 6-bisphosphate 2-phosphatase	1
IPR016370	Photosystem I reaction centre, PsaG/PsaK, plant	1
IPR017079	Zeaxanthin epoxidase	1
IPR017441	Protein kinase, ATP binding site	1
IPR017493	Photosystem I reaction centre, PsaK, plant	1
IPR017884	SANT, eukarya	1
IPR017936	Thioredoxin-like	1
IPR018108	Mitochondrial substrate/solute carrier	1
IPR018158	Threonyl-tRNA synthetase, class IIa, conserved region	1
IPR018163	Threonyl/alanyl tRNA synthetase, class II-like, putative editing domain	1
IPR018169	MtN3/saliva-related transmembrane protein, conserved region	1
IPR018179	RAG1-activating protein 1 homologue	1

IPR018247	EF-Hand 1, calcium-binding site	1
IPR018248	EF-Hand, Calmodulin	1
IPR018249	EF-HAND 2	1
IPR018490	Cyclic nucleotide-binding-like	1
IPR018957	Zinc finger, C3HC4 RING-type	1
IPR019275	Protein of unknown function DUF2301, transmembrane	1
IPR019734	Tetratricopeptide repeat	1
IPR019999	Anthranilate synthase component I, C-terminal	1
IPR020422	Dual specificity phosphatase, subgroup, catalytic domain	1
IPR020471	Aldo/keto reductase subgroup	1
IPR020636	Calcium/calmodulin-dependent protein kinase-like	1
IPR020683	Ankyrin repeat-containing domain	1
IPR020842	Polyketide synthase/Fatty acid synthase, KR	1
IPR021789	Protein of unknown function DUF3354	1
SP80-3280 up-regulated DEGs		
IPR000719	Protein kinase, catalytic domain	5
IPR001509	NAD-dependent epimerase/dehydratase	5
IPR011009	Protein kinase-like domain	5
IPR016040	NAD(P)-binding domain	5
IPR016196	Major facilitator superfamily, general substrate transporter	4
IPR017442	Serine/threonine-protein kinase-like domain	4
IPR000726	Glycoside hydrolase, family 19, catalytic	3
IPR000877	Proteinase inhibitor I12, Bowman-Birk	3
IPR001906	Terpene synthase-like	3
IPR002290	Serine/threonine-protein kinase domain	3
IPR004045	Glutathione S-transferase, N-terminal	3
IPR004046	Glutathione S-transferase, C-terminal	3
IPR005630	Terpene synthase, metal-binding domain	3
IPR008271	Serine/threonine-protein kinase, active site	3
IPR008930	Terpenoid cylases/protein prenyltransferase alpha-alpha toroid	3
IPR008949	Terpenoid synthase	3
IPR010987	Glutathione S-transferase, C-terminal-like	3
IPR012335	Thioredoxin fold	3
IPR012336	Thioredoxin-like fold	3
IPR017441	Protein kinase, ATP binding site	3
IPR017933	Glutathione S-transferase/chloride channel, C-terminal	3
IPR020635	Tyrosine-protein kinase, catalytic domain	3
IPR000823	Plant peroxidase	2
IPR000864	Proteinase inhibitor I13, potato inhibitor I	2
IPR001002	Chitin-binding, type 1	2
IPR001087	Lipase, GDSL	2
IPR001092	Helix-loop-helix DNA-binding domain	2
IPR002016	Haem peroxidase, plant/fungal/bacterial	2
IPR002213	UDP-glucuronosyl/UDP-glucosyltransferase	2
IPR002921	Lipase, class 3	2

IPR003441	No apical meristem (NAM) protein	2
IPR003613	U box domain	2
IPR003663	Sugar/inositol transporter	2
IPR004843	Metallophosphoesterase	2
IPR005123	Oxoglutarate/iron-dependent oxygenase	2
IPR005829	Sugar transporter, conserved site	2
IPR008985	Concanavalin A-like lectin/glucanase	2
IPR010255	Haem peroxidase	2
IPR010399	Tify	2
IPR011028	Cyclin-like	2
IPR011230	Phosphoesterase At2g46880	2
IPR011598	Helix-loop-helix DNA-binding	2
IPR013320	Concanavalin A-like lectin/glucanase, subgroup	2
IPR013785	Aldolase-type TIM barrel	2
IPR016283	Glycoside hydrolase, family 19	2
IPR018371	Chitin-binding, type 1, conserved site	2
IPR018467	CCT domain-like	2
IPR019793	Peroxidases heam-ligand binding site	2
IPR019794	Peroxidase, active site	2
IPR000048	IQ calmodulin-binding region	1
IPR000070	Pectinesterase, catalytic	1
IPR000109	Oligopeptide transporter	1
IPR000197	Zinc finger, TAZ-type	1
IPR000210	BTB/POZ-like	1
IPR000225	Armadillo	1
IPR000535	Major sperm protein	1
IPR000644	Cystathionine beta-synthase, core	1
IPR000757	Glycoside hydrolase, family 16	1
IPR000873	AMP-dependent synthetase/ligase	1
IPR000907	Lipoxygenase	1
IPR000961	AGC-kinase, C-terminal	1
IPR001005	SANT, DNA-binding	1
IPR001024	Lipoxygenase, LH2	1
IPR001048	Aspartate/glutamate/uridylate kinase	1
IPR001077	O-methyltransferase, family 2	1
IPR001140	ABC transporter, transmembrane domain	1
IPR001148	Carbonic anhydrase, alpha-class, catalytic domain	1
IPR001153	Barwin	1
IPR001155	NADH:flavin oxidoreductase/NADH oxidase, N-terminal	1
IPR001216	Cysteine synthase/cystathionine beta-synthase P-phosphate-binding site	1
IPR001245	Serine/threonine/tyrosine-protein kinase	1
IPR001246	Lipoxygenase, plant	1
IPR001279	Beta-lactamase-like	1
IPR001327	Pyridine nucleotide-disulphide oxidoreductase, NAD-binding region	1
IPR001341	Aspartate kinase domain	1

IPR001471	Pathogenesis-related transcriptional factor/ERF, DNA-binding	1
IPR001568	Ribonuclease T2	1
IPR001580	Calreticulin/calnexin	1
IPR001609	Myosin head, motor domain	1
IPR001611	Leucine-rich repeat	1
IPR001680	WD40 repeat	1
IPR001807	Chloride channel, voltage gated	1
IPR001841	Zinc finger, RING-type	1
IPR001898	Sodium/sulphate symporter	1
IPR001902	Sulphate anion transporter	1
IPR001926	Pyridoxal phosphate-dependent enzyme, beta subunit	1
IPR001938	Thaumatin, pathogenesis-related	1
IPR002028	Tryptophan synthase, alpha chain	1
IPR002044	Glycoside hydrolase, carbohydrate-binding	1
IPR002251	Chloride channel plant CLC	1
IPR002283	Isopenicillin N synthase	1
IPR002528	Multi antimicrobial extrusion protein MatE	1
IPR002610	Peptidase S54, rhomboid	1
IPR002645	Sulphate transporter/antisigma-factor antagonist STAS	1
IPR002710	Dilute	1
IPR002912	Amino acid-binding ACT	1
IPR002938	Monooxygenase, FAD-binding	1
IPR003042	Aromatic-ring hydroxylase-like	1
IPR003340	Transcriptional factor B3	1
IPR003439	ABC transporter-like	1
IPR003480	Transferase	1
IPR003593	ATPase, AAA+ type, core	1
IPR004009	Myosin, N-terminal, SH3-like	1
IPR004254	Hly-III related	1
IPR004294	Carotenoid oxygenase	1
IPR004813	Oligopeptide transporter OPT superfamily	1
IPR004883	Lateral organ boundaries, LOB	1
IPR005025	NADPH-dependent FMN reductase	1
IPR005299	SAM dependent carboxyl methyltransferase	1
IPR005856	Cysteine synthase K/M	1
IPR005859	Cysteine synthase A	1
IPR005881	Serine O-acetyltransferase	1
IPR006016	UspA	1
IPR006094	FAD linked oxidase, N-terminal	1
IPR006501	Pectinesterase inhibitor	1
IPR006670	Cyclin	1
IPR006671	Cyclin, N-terminal	1
IPR007173	D-arabinono-1,4-lactone oxidase	1
IPR007274	Ctr copper transporter	1
IPR007657	Glycosyltransferase AER61, uncharacterised	1

IPR007701	Interferon-related developmental regulator, N-terminal	1
IPR008089	Nucleotide sugar epimerase	1
IPR008265	Lipase, GDSL, active site	1
IPR008962	PapD-like	1
IPR008976	Lipase/lipooxygenase, PLAT/LH2	1
IPR009009	Barwin-related endoglucanase	1
IPR009033	Calreticulin/calnexin, P	1
IPR009057	Homeodomain-like	1
IPR009169	Calreticulin	1
IPR009410	Allene oxide cyclase	1
IPR009836	Protein of unknown function DUF1399	1
IPR010030	Plant-specific FAD-dependent oxidoreductase	1
IPR010525	Auxin response factor	1
IPR010530	B12D	1
IPR010713	Xyloglucan endo-transglycosylase, C-terminal	1
IPR011004	Trimeric LpxA-like	1
IPR011008	Dimeric alpha-beta barrel	1
IPR011046	WD40 repeat-like-containing domain	1
IPR011050	Pectin lyase fold/virulence factor	1
IPR011060	Ribulose-phosphate binding barrel	1
IPR011333	BTB/POZ fold	1
IPR011525	Aux/IAA-ARF-dimerisation	1
IPR011527	ABC transporter, transmembrane domain, type 1	1
IPR011547	Sulphate transporter	1
IPR011989	Armadillo-like helical	1
IPR011991	Winged helix-turn-helix transcription repressor DNA-binding	1
IPR012287	Homeodomain-related	1
IPR012334	Pectin lyase fold	1
IPR012389	Negative regulatory factor PREG	1
IPR012392	Very-long-chain 3-ketoacyl-CoA synthase	1
IPR012442	Protein of unknown function DUF1645	1
IPR012967	Plant methyltransferase dimerisation	1
IPR013027	FAD-dependent pyridine nucleotide-disulphide oxidoreductase	1
IPR013057	Amino acid transporter, transmembrane	1
IPR013069	BTB/POZ	1
IPR013089	Kelch related	1
IPR013097	Stress responsive alpha-beta barrel	1
IPR013210	Leucine-rich repeat-containing N-terminal domain, type 2	1
IPR013216	Methyltransferase type 11	1
IPR013601	FAE1/Type III polyketide synthase-like protein	1
IPR013747	3-Oxoacyl-[acyl-carrier-protein (ACP)] synthase III C-terminal	1
IPR013763	Cyclin-related	1
IPR013783	Immunoglobulin-like fold	1
IPR013784	Carbohydrate-binding-like fold	1
IPR013819	Lipoxygenase, C-terminal	1

IPR013830	Esterase, SGNH hydrolase-type	1
IPR013922	Cyclin-related 2	1
IPR014729	Rossmann-like alpha/beta/alpha sandwich fold	1
IPR014733	Barwin-like endoglucanase	1
IPR014743	Chloride channel, core	1
IPR014778	Myb, DNA-binding	1
IPR015429	Transcription regulator cyclin	1
IPR015495	Myb transcription factor	1
IPR015943	WD40/YVTN repeat-like-containing domain	1
IPR016024	Armadillo-type fold	1
IPR016038	Thiolase-like, subgroup	1
IPR016039	Thiolase-like	1
IPR016166	FAD-binding, type 2	1
IPR016177	DNA-binding, integrase-type	1
IPR016455	Xyloglucan endotransglucosylase/hydrolase	1
IPR016461	O-methyltransferase, COMT, eukaryota	1
IPR017871	ABC transporter, conserved site	1
IPR017892	Protein kinase, C-terminal	1
IPR017930	HTH transcriptional regulator, Myb-type, DNA-binding	1
IPR017940	ABC transporter integral membrane type 1	1
IPR017986	WD40-repeat-containing domain	1
IPR018040	Pectinesterase, active site	1
IPR018042	Aspartate kinase, conserved site	1
IPR018045	Sulphate anion transporter, conserved site	1
IPR018124	Calreticulin/calnexin, conserved site	1
IPR018188	Ribonuclease T2, active site	1
IPR018204	Tryptophan synthase, alpha chain, active site	1
IPR018247	EF-Hand 1, calcium-binding site	1
IPR018249	EF-HAND 2	1
IPR018338	Carbonic anhydrase, alpha-class, conserved site	1
IPR018340	Carbonic anhydrase, CAH1-like	1
IPR018357	Hexapeptide transferase, conserved site	1
IPR018444	Dil domain	1
IPR018957	Zinc finger, C3HC4 RING-type	1
IPR019781	WD40 repeat, subgroup	1
IPR019782	WD40 repeat 2	1
IPR020472	G-protein beta WD-40 repeat, region	1
IPR020636	Calcium/calmodulin-dependent protein kinase-like	1
IPR020845	AMP-binding, conserved site	1
IPR021720	Di-glucose binding within endoplasmic reticulum	1
SP80-3280 down-regulated DEGs		
IPR000232	Heat shock factor (HSF)-type, DNA-binding	1
IPR001128	Cytochrome P450	1
IPR001478	PDZ/DHR/GLGF	1
IPR001646	Pentapeptide repeat	1

IPR002130	Peptidyl-prolyl cis-trans isomerase, cyclophilin-type	1
IPR002213	UDP-glucuronosyl/UDP-glucosyltransferase	2
IPR002401	Cytochrome P450, E-class, group I	1
IPR002683	Photosystem II oxygen evolving complex protein PsbP	1
IPR005227	Resolvase, holliday junction-type, YqgF-like	1
IPR006455	Homeobox domain, ZF-HD class	1
IPR006456	ZF-HD homeobox protein, Cys/His-rich dimerisation domain	1
IPR006641	Resolvase, RNase H-like fold	1
IPR006904	Protein of unknown function DUF716	1
IPR006946	Protein of unknown function DUF642	1
IPR008733	Peroxisomal biogenesis factor 11	1
IPR011990	Tetratricopeptide-like helical	1
IPR011991	Winged helix-turn-helix transcription repressor DNA-binding	1
IPR012287	Homeodomain-related	1
IPR012337	Polynucleotidyl transferase, ribonuclease H fold	1
IPR012474	Frigida-like	1
IPR013026	Tetratricopeptide repeat-containing	1
IPR015891	Cyclophilin-like	1
IPR016040	NAD(P)-binding domain	1
IPR016123	Mog1/PsbP, alpha/beta/alpha sandwich	1
IPR016124	Mog1/PsbP/DUF1795, alpha/beta/alpha sandwich	1
IPR017973	Cytochrome P450, C-terminal	1
IPR021467	Protein of unknown function DUF3119	1
IPR021602	Protein of unknown function DUF3223	1
IPR021954	Protein of unknown function DUF3571	1

Table S6. List of KEGG metabolic pathways significantly enriched to common and unique up- and down-regulated DETs generated in two sugarcane varieties (RB867515 and SP80-3280) infested with *Diatraea saccharalis.*

Term	Database	Sorghum orthologous ID	Number of enriched DETs
Metabolic pathways significantly enriched to both up-regulated DETs from RB867515 and SP80-3280			
Metabolic pathways	KEGG PATHWAY	sbi01100	21
Biosynthesis of secondary metabolites	KEGG PATHWAY	sbi01110	17
Phenylpropanoid biosynthesis	KEGG PATHWAY	sbi00940	7
Linoleic acid metabolism	KEGG PATHWAY	sbi00591	4
Diterpenoid biosynthesis	KEGG PATHWAY	sbi00904	2
Zeatin biosynthesis	KEGG PATHWAY	sbi00908	2
alpha-Linolenic acid metabolism	KEGG PATHWAY	sbi00592	2
Phenylalanine, tyrosine and tryptophan biosynthesis	KEGG PATHWAY	sbi00400	2
Cysteine and methionine metabolism	KEGG PATHWAY	sbi00270	2
Amino sugar and nucleotide sugar metabolism	KEGG PATHWAY	sbi00520	2

Biosynthesis of amino acids	KEGG PATHWAY	sbi01230	2
Nicotinate and nicotinamide metabolism	KEGG PATHWAY	sbi00760	1
Isoquinoline alkaloid biosynthesis	KEGG PATHWAY	sbi00950	1
Alanine, aspartate and glutamate metabolism	KEGG PATHWAY	sbi00250	1
Tyrosine metabolism	KEGG PATHWAY	sbi00350	1
Glyoxylate and dicarboxylate metabolism	KEGG PATHWAY	sbi00630	1
Glycine, serine and threonine metabolism	KEGG PATHWAY	sbi00260	1
Glycerolipid metabolism	KEGG PATHWAY	sbi00561	1
Galactose metabolism	KEGG PATHWAY	sbi00052	1
Glycerophospholipid metabolism	KEGG PATHWAY	sbi00564	1
Oxidative phosphorylation	KEGG PATHWAY	sbi00190	1
Plant-pathogen interaction	KEGG PATHWAY	sbi04626	1
Starch and sucrose metabolism	KEGG PATHWAY	sbi00500	1
Carbon metabolism	KEGG PATHWAY	sbi01200	1
Plant hormone signal transduction	KEGG PATHWAY	sbi04075	1
Metabolic pathways significantly enriched to up-regulated RB867515 DETs			
Metabolic pathways	KEGG PATHWAY	sbi01100	36
Biosynthesis of secondary metabolites	KEGG PATHWAY	sbi01110	29
Biosynthesis of amino acids	KEGG PATHWAY	sbi01230	13
Plant hormone signal transduction	KEGG PATHWAY	sbi04075	7
Phenylpropanoid biosynthesis	KEGG PATHWAY	sbi00940	7
Phenylalanine, tyrosine and tryptophan biosynthesis	KEGG PATHWAY	sbi00400	6
Carbon metabolism	KEGG PATHWAY	sbi01200	5
Glycine, serine and threonine metabolism	KEGG PATHWAY	sbi00260	4
ABC transporters	KEGG PATHWAY	sbi02010	3
alpha-Linolenic acid metabolism	KEGG PATHWAY	sbi00592	3
Phenylalanine metabolism	KEGG PATHWAY	sbi00360	3
Fructose and mannose metabolism	KEGG PATHWAY	sbi00051	3
Glycolysis / Gluconeogenesis	KEGG PATHWAY	sbi00010	3
Ubiquitin mediated proteolysis	KEGG PATHWAY	sbi04120	3
Amino sugar and nucleotide sugar metabolism	KEGG PATHWAY	sbi00520	3
Plant-pathogen interaction	KEGG PATHWAY	sbi04626	3
Purine metabolism	KEGG PATHWAY	sbi00230	3
Starch and sucrose metabolism	KEGG PATHWAY	sbi00500	3
Monobactam biosynthesis	KEGG PATHWAY	sbi00261	2
Valine, leucine and isoleucine biosynthesis	KEGG PATHWAY	sbi00290	2
Selenocompound metabolism	KEGG PATHWAY	sbi00450	2
Stilbenoid, diarylheptanoid and gingerol biosynthesis	KEGG PATHWAY	sbi00945	2
Zeatin biosynthesis	KEGG PATHWAY	sbi00908	2
Sulfur metabolism	KEGG PATHWAY	sbi00920	2
Ubiquinone and other terpenoid-quinone biosynthesis	KEGG PATHWAY	sbi00130	2
Porphyrin and chlorophyll metabolism	KEGG PATHWAY	sbi00860	2
Pentose phosphate pathway	KEGG PATHWAY	sbi00030	2
Carbon fixation in photosynthetic organisms	KEGG PATHWAY	sbi00710	2
Flavonoid biosynthesis	KEGG PATHWAY	sbi00941	2

Phagosome	KEGG PATHWAY	sbi04145	2
Glycerophospholipid metabolism	KEGG PATHWAY	sbi00564	2
C5-Branched dibasic acid metabolism	KEGG PATHWAY	sbi00660	1
AGE-RAGE signaling pathway in diabetic complications	KEGG PATHWAY	sbi04933	1
Linoleic acid metabolism	KEGG PATHWAY	sbi00591	1
Brassinosteroid biosynthesis	KEGG PATHWAY	sbi00905	1
Thiamine metabolism	KEGG PATHWAY	sbi00730	1
Butanoate metabolism	KEGG PATHWAY	sbi00650	1
Diterpenoid biosynthesis	KEGG PATHWAY	sbi00904	1
Tropane, piperidine and pyridine alkaloid biosynthesis	KEGG PATHWAY	sbi00960	1
Pantothenate and CoA biosynthesis	KEGG PATHWAY	sbi00770	1
Isoquinoline alkaloid biosynthesis	KEGG PATHWAY	sbi00950	1
beta-Alanine metabolism	KEGG PATHWAY	sbi00410	1
2-Oxocarboxylic acid metabolism	KEGG PATHWAY	sbi01210	1
Tryptophan metabolism	KEGG PATHWAY	sbi00380	1
Arginine and proline metabolism	KEGG PATHWAY	sbi00330	1
Inositol phosphate metabolism	KEGG PATHWAY	sbi00562	1
Tyrosine metabolism	KEGG PATHWAY	sbi00350	1
Pentose and glucuronate interconversions	KEGG PATHWAY	sbi00040	1
Steroid biosynthesis	KEGG PATHWAY	sbi00100	1
Phosphatidylinositol signaling system	KEGG PATHWAY	sbi04070	1
Galactose metabolism	KEGG PATHWAY	sbi00052	1
Glutathione metabolism	KEGG PATHWAY	sbi00480	1
Protein processing in endoplasmic reticulum	KEGG PATHWAY	sbi04141	1
Ribosome	KEGG PATHWAY	sbi03010	1
Metabolic pathways significantly enriched to up-regulated RB80-3280 DETs			
Metabolic pathways	KEGG PATHWAY	sbi01100	31
Biosynthesis of secondary metabolites	KEGG PATHWAY	sbi01110	27
Amino sugar and nucleotide sugar metabolism	KEGG PATHWAY	sbi00520	7
Phenylpropanoid biosynthesis	KEGG PATHWAY	sbi00940	7
Cyanoamino acid metabolism	KEGG PATHWAY	sbi00460	6
alpha-Linolenic acid metabolism	KEGG PATHWAY	sbi00592	5
Biosynthesis of amino acids	KEGG PATHWAY	sbi01230	5
Starch and sucrose metabolism	KEGG PATHWAY	sbi00500	4
Carbon metabolism	KEGG PATHWAY	sbi01200	4
2-Oxocarboxylic acid metabolism	KEGG PATHWAY	sbi01210	3
Cysteine and methionine metabolism	KEGG PATHWAY	sbi00270	3
Glutathione metabolism	KEGG PATHWAY	sbi00480	3
Linoleic acid metabolism	KEGG PATHWAY	sbi00591	2
Carotenoid biosynthesis	KEGG PATHWAY	sbi00906	2
Sulfur metabolism	KEGG PATHWAY	sbi00920	2
Flavonoid biosynthesis	KEGG PATHWAY	sbi00941	2
Glycolysis / Gluconeogenesis	KEGG PATHWAY	sbi00010	2
Plant hormone signal transduction	KEGG PATHWAY	sbi04075	2
C5-Branched dibasic acid metabolism	KEGG PATHWAY	sbi00660	1

Glucosinolate biosynthesis	KEGG PATHWAY	sbi00966	1
Monobactam biosynthesis	KEGG PATHWAY	sbi00261	1
Valine, leucine and isoleucine biosynthesis	KEGG PATHWAY	sbi00290	1
Lysine biosynthesis	KEGG PATHWAY	sbi00300	1
Butanoate metabolism	KEGG PATHWAY	sbi00650	1
Tropane, piperidine and pyridine alkaloid biosynthesis	KEGG PATHWAY	sbi00960	1
Pantothenate and CoA biosynthesis	KEGG PATHWAY	sbi00770	1
ABC transporters	KEGG PATHWAY	sbi02010	1
Stilbenoid, diarylheptanoid and gingerol biosynthesis	KEGG PATHWAY	sbi00945	1
Nitrogen metabolism	KEGG PATHWAY	sbi00910	1
Alanine, aspartate and glutamate metabolism	KEGG PATHWAY	sbi00250	1
Ubiquinone and other terpenoid-quinone biosynthesis	KEGG PATHWAY	sbi00130	1
Phenylalanine metabolism	KEGG PATHWAY	sbi00360	1
Carbon fixation in photosynthetic organisms	KEGG PATHWAY	sbi00710	1
Pentose and glucuronate interconversions	KEGG PATHWAY	sbi00040	1
Mismatch repair	KEGG PATHWAY	sbi03430	1
Glycine, serine and threonine metabolism	KEGG PATHWAY	sbi00260	1
Homologous recombination	KEGG PATHWAY	sbi03440	1
Pyruvate metabolism	KEGG PATHWAY	sbi00620	1
DNA replication	KEGG PATHWAY	sbi03030	1
Nucleotide excision repair	KEGG PATHWAY	sbi03420	1
RNA degradation	KEGG PATHWAY	sbi03018	1
Pyrimidine metabolism	KEGG PATHWAY	sbi00240	1
Purine metabolism	KEGG PATHWAY	sbi00230	1
Protein processing in endoplasmic reticulum	KEGG PATHWAY	sbi04141	1
Metabolic pathways significantly enriched to down-regulated RB867515 DETs			
Metabolic pathways	KEGG PATHWAY	sbi01100	32
Biosynthesis of secondary metabolites	KEGG PATHWAY	sbi01110	20
Photosynthesis - antenna proteins	KEGG PATHWAY	sbi00196	9
Carbon metabolism	KEGG PATHWAY	sbi01200	8
Galactose metabolism	KEGG PATHWAY	sbi00052	5
Glycolysis / Gluconeogenesis	KEGG PATHWAY	sbi00010	5
Glutathione metabolism	KEGG PATHWAY	sbi00480	5
Amino sugar and nucleotide sugar metabolism	KEGG PATHWAY	sbi00520	5
Carbon fixation in photosynthetic organisms	KEGG PATHWAY	sbi00710	4
Phenylpropanoid biosynthesis	KEGG PATHWAY	sbi00940	4
Ribosome	KEGG PATHWAY	sbi03010	4
Pyruvate metabolism	KEGG PATHWAY	sbi00620	3
Biosynthesis of amino acids	KEGG PATHWAY	sbi01230	3
Citrate cycle (TCA cycle)	KEGG PATHWAY	sbi00020	2
Starch and sucrose metabolism	KEGG PATHWAY	sbi00500	2
Glycosphingolipid biosynthesis - globo series	KEGG PATHWAY	sbi00603	1
Thiamine metabolism	KEGG PATHWAY	sbi00730	1
Diterpenoid biosynthesis	KEGG PATHWAY	sbi00904	1
Tropane, piperidine and pyridine alkaloid biosynthesis	KEGG PATHWAY	sbi00960	1

Carotenoid biosynthesis	KEGG PATHWAY	sbi00906	1
Ascorbate and aldarate metabolism	KEGG PATHWAY	sbi00053	1
Fatty acid degradation	KEGG PATHWAY	sbi00071	1
Cutin, suberine and wax biosynthesis	KEGG PATHWAY	sbi00073	1
Sphingolipid metabolism	KEGG PATHWAY	sbi00600	1
Ubiquinone and other terpenoid-quinone biosynthesis	KEGG PATHWAY	sbi00130	1
Porphyrin and chlorophyll metabolism	KEGG PATHWAY	sbi00860	1
Pentose phosphate pathway	KEGG PATHWAY	sbi00030	1
Terpenoid backbone biosynthesis	KEGG PATHWAY	sbi00900	1
Tyrosine metabolism	KEGG PATHWAY	sbi00350	1
Glyoxylate and dicarboxylate metabolism	KEGG PATHWAY	sbi00630	1
Mismatch repair	KEGG PATHWAY	sbi03430	1
Homologous recombination	KEGG PATHWAY	sbi03440	1
Glycerolipid metabolism	KEGG PATHWAY	sbi00561	1
DNA replication	KEGG PATHWAY	sbi03030	1
Cysteine and methionine metabolism	KEGG PATHWAY	sbi00270	1
Nucleotide excision repair	KEGG PATHWAY	sbi03420	1
Photosynthesis	KEGG PATHWAY	sbi00195	1
RNA degradation	KEGG PATHWAY	sbi03018	1
Oxidative phosphorylation	KEGG PATHWAY	sbi00190	1
Plant-pathogen interaction	KEGG PATHWAY	sbi04626	1
Plant hormone signal transduction	KEGG PATHWAY	sbi04075	1
Metabolic pathways significantly enriched to down-regulated RB80-3280 DETs			
Metabolic pathways	KEGG PATHWAY	sbi01100	9
Biosynthesis of secondary metabolites	KEGG PATHWAY	sbi01110	5
Carbon fixation in photosynthetic organisms	KEGG PATHWAY	sbi00710	3
Photosynthesis	KEGG PATHWAY	sbi00195	3
Carbon metabolism	KEGG PATHWAY	sbi01200	3
Pentose phosphate pathway	KEGG PATHWAY	sbi00030	2
Fructose and mannose metabolism	KEGG PATHWAY	sbi00051	2
Glycolysis / Gluconeogenesis	KEGG PATHWAY	sbi00010	2
Nitrogen metabolism	KEGG PATHWAY	sbi00910	1
Flavonoid biosynthesis	KEGG PATHWAY	sbi00941	1
Pyruvate metabolism	KEGG PATHWAY	sbi00620	1
Glutathione metabolism	KEGG PATHWAY	sbi00480	1
Oxidative phosphorylation	KEGG PATHWAY	sbi00190	1
Purine metabolism	KEGG PATHWAY	sbi00230	1
Biosynthesis of amino acids	KEGG PATHWAY	sbi01230	1
Phenylpropanoid biosynthesis	KEGG PATHWAY	sbi00940	1
Metabolic pathways significantly enriched to both down-regulated DETs from RB867515 and SP80-3280			
Pentose phosphate pathway	KEGG PATHWAY	sbi00030	1
Carbon fixation in photosynthetic organisms	KEGG PATHWAY	sbi00710	1
Fructose and mannose metabolism	KEGG PATHWAY	sbi00051	1
Glycolysis / Gluconeogenesis	KEGG PATHWAY	sbi00010	1
Carbon metabolism	KEGG PATHWAY	sbi01200	1

Biosynthesis of secondary metabolites	KEGG PATHWAY	sbi01110	1
Metabolic pathways	KEGG PATHWAY	sbi01100	1

Table S7. List of KEGG metabolic pathways significantly enriched to common and unique up- and down-regulated DEGs generated in two sugarcane varieties (RB867515 and SP80-3280) infested with *Diatraea saccharalis*.

Term	Database	Sorghum orthologous ID	Number of enriched DEGs
Metabolic pathways significantly enriched to both up-regulated DEGs from RB867515 and SP80-3280			
Biosynthesis of secondary metabolites	KEGG PATHWAY	sbi01110	16
Metabolic pathways	KEGG PATHWAY	sbi01100	16
Linoleic acid metabolism	KEGG PATHWAY	sbi00591	2
Diterpenoid biosynthesis	KEGG PATHWAY	sbi00904	2
Zeatin biosynthesis	KEGG PATHWAY	sbi00908	2
Isoquinoline alkaloid biosynthesis	KEGG PATHWAY	sbi00950	2
Phenylpropanoid biosynthesis	KEGG PATHWAY	sbi00940	4
Tyrosine metabolism	KEGG PATHWAY	sbi00350	2
Cysteine and methionine metabolism	KEGG PATHWAY	sbi00270	2
Glucosinolate biosynthesis	KEGG PATHWAY	sbi00966	1
Nicotinate and nicotinamide metabolism	KEGG PATHWAY	sbi00760	1
Stilbenoid, diarylheptanoid and gingerol biosynthesis	KEGG PATHWAY	sbi00945	1
Nitrogen metabolism	KEGG PATHWAY	sbi00910	1
Alanine, aspartate and glutamate metabolism	KEGG PATHWAY	sbi00250	1
alpha-Linolenic acid metabolism	KEGG PATHWAY	sbi00592	1
2-Oxocarboxylic acid metabolism	KEGG PATHWAY	sbi01210	1
Phenylalanine, tyrosine and tryptophan biosynthesis	KEGG PATHWAY	sbi00400	1
Ubiquinone and other terpenoid-quinone biosynthesis	KEGG PATHWAY	sbi00130	1
Porphyrin and chlorophyll metabolism	KEGG PATHWAY	sbi00860	1
Phenylalanine metabolism	KEGG PATHWAY	sbi00360	1
Glyoxylate and dicarboxylate metabolism	KEGG PATHWAY	sbi00630	1
Cyanoamino acid metabolism	KEGG PATHWAY	sbi00460	1
Flavonoid biosynthesis	KEGG PATHWAY	sbi00941	1
Galactose metabolism	KEGG PATHWAY	sbi00052	1
Glycerophospholipid metabolism	KEGG PATHWAY	sbi00564	1
Glycolysis / Gluconeogenesis	KEGG PATHWAY	sbi00010	1
Biosynthesis of amino acids	KEGG PATHWAY	sbi01230	1
Starch and sucrose metabolism	KEGG PATHWAY	sbi00500	1
Carbon metabolism	KEGG PATHWAY	sbi01200	1
Plant hormone signal transduction	KEGG PATHWAY	sbi04075	1
Metabolic pathways significantly enriched to up-regulated RB867515 DEGs			
Metabolic pathways	KEGG PATHWAY	sbi01100	26
Biosynthesis of secondary metabolites	KEGG PATHWAY	sbi01110	23

Glycine, serine and threonine metabolism	KEGG PATHWAY	sbi00260	6
Biosynthesis of amino acids	KEGG PATHWAY	sbi01230	6
Phenylpropanoid biosynthesis	KEGG PATHWAY	sbi00940	5
Linoleic acid metabolism	KEGG PATHWAY	sbi00591	3
alpha-Linolenic acid metabolism	KEGG PATHWAY	sbi00592	3
Plant-pathogen interaction	KEGG PATHWAY	sbi04626	3
Carbon metabolism	KEGG PATHWAY	sbi01200	3
Plant hormone signal transduction	KEGG PATHWAY	sbi04075	3
Diterpenoid biosynthesis	KEGG PATHWAY	sbi00904	2
Zeatin biosynthesis	KEGG PATHWAY	sbi00908	2
Stilbenoid, diarylheptanoid and gingerol biosynthesis	KEGG PATHWAY	sbi00945	2
Lysine degradation	KEGG PATHWAY	sbi00310	2
Terpenoid backbone biosynthesis	KEGG PATHWAY	sbi00900	2
Flavonoid biosynthesis	KEGG PATHWAY	sbi00941	2
Phagosome	KEGG PATHWAY	sbi04145	2
Peroxisome	KEGG PATHWAY	sbi04146	2
Starch and sucrose metabolism	KEGG PATHWAY	sbi00500	2
Sesquiterpenoid and triterpenoid biosynthesis	KEGG PATHWAY	sbi00909	1
AGE-RAGE signaling pathway in diabetic complications	KEGG PATHWAY	sbi04933	1
Brassinosteroid biosynthesis	KEGG PATHWAY	sbi00905	1
Thiamine metabolism	KEGG PATHWAY	sbi00730	1
Valine, leucine and isoleucine biosynthesis	KEGG PATHWAY	sbi00290	1
Arginine biosynthesis	KEGG PATHWAY	sbi00220	1
Carotenoid biosynthesis	KEGG PATHWAY	sbi00906	1
ABC transporters	KEGG PATHWAY	sbi02010	1
Phenylalanine, tyrosine and tryptophan biosynthesis	KEGG PATHWAY	sbi00400	1
Ubiquinone and other terpenoid-quinone biosynthesis	KEGG PATHWAY	sbi00130	1
Porphyrin and chlorophyll metabolism	KEGG PATHWAY	sbi00860	1
Arginine and proline metabolism	KEGG PATHWAY	sbi00330	1
Pentose phosphate pathway	KEGG PATHWAY	sbi00030	1
Inositol phosphate metabolism	KEGG PATHWAY	sbi00562	1
Phenylalanine metabolism	KEGG PATHWAY	sbi00360	1
Carbon fixation in photosynthetic organisms	KEGG PATHWAY	sbi00710	1
Pentose and glucuronate interconversions	KEGG PATHWAY	sbi00040	1
Glyoxylate and dicarboxylate metabolism	KEGG PATHWAY	sbi00630	1
Fructose and mannose metabolism	KEGG PATHWAY	sbi00051	1
Phosphatidylinositol signaling system	KEGG PATHWAY	sbi04070	1
Glycerolipid metabolism	KEGG PATHWAY	sbi00561	1
Cysteine and methionine metabolism	KEGG PATHWAY	sbi00270	1
Glycerophospholipid metabolism	KEGG PATHWAY	sbi00564	1
Glycolysis / Gluconeogenesis	KEGG PATHWAY	sbi00010	1
Glutathione metabolism	KEGG PATHWAY	sbi00480	1
Ubiquitin mediated proteolysis	KEGG PATHWAY	sbi04120	1
Amino sugar and nucleotide sugar metabolism	KEGG PATHWAY	sbi00520	1
Purine metabolism	KEGG PATHWAY	sbi00230	1

Metabolic pathways significantly enriched to up-regulated RB80-3280 DEGs			
Metabolic pathways	KEGG PATHWAY	sbi01100	18
Biosynthesis of secondary metabolites	KEGG PATHWAY	sbi01110	16
Phenylpropanoid biosynthesis	KEGG PATHWAY	sbi00940	7
alpha-Linolenic acid metabolism	KEGG PATHWAY	sbi00592	3
Cysteine and methionine metabolism	KEGG PATHWAY	sbi00270	3
Glutathione metabolism	KEGG PATHWAY	sbi00480	3
Amino sugar and nucleotide sugar metabolism	KEGG PATHWAY	sbi00520	3
Biosynthesis of amino acids	KEGG PATHWAY	sbi01230	3
Sulfur metabolism	KEGG PATHWAY	sbi00920	2
Starch and sucrose metabolism	KEGG PATHWAY	sbi00500	2
Carbon metabolism	KEGG PATHWAY	sbi01200	2
Plant hormone signal transduction	KEGG PATHWAY	sbi04075	2
Sesquiterpenoid and triterpenoid biosynthesis	KEGG PATHWAY	sbi00909	1
Monobactam biosynthesis	KEGG PATHWAY	sbi00261	1
Linoleic acid metabolism	KEGG PATHWAY	sbi00591	1
Lysine biosynthesis	KEGG PATHWAY	sbi00300	1
Diterpenoid biosynthesis	KEGG PATHWAY	sbi00904	1
Carotenoid biosynthesis	KEGG PATHWAY	sbi00906	1
ABC transporters	KEGG PATHWAY	sbi02010	1
Nitrogen metabolism	KEGG PATHWAY	sbi00910	1
2-Oxocarboxylic acid metabolism	KEGG PATHWAY	sbi01210	1
Ubiquinone and other terpenoid-quinone biosynthesis	KEGG PATHWAY	sbi00130	1
Fatty acid elongation	KEGG PATHWAY	sbi00062	1
Phenylalanine metabolism	KEGG PATHWAY	sbi00360	1
Pentose and glucuronate interconversions	KEGG PATHWAY	sbi00040	1
Glycine, serine and threonine metabolism	KEGG PATHWAY	sbi00260	1
Cyanoamino acid metabolism	KEGG PATHWAY	sbi00460	1
Phagosome	KEGG PATHWAY	sbi04145	1
Protein processing in endoplasmic reticulum	KEGG PATHWAY	sbi04141	1
Metabolic pathways significantly enriched to down-regulated RB867515 DEGs			
Biosynthesis of secondary metabolites	KEGG PATHWAY	sbi01110	8
Metabolic pathways	KEGG PATHWAY	sbi01100	6
Starch and sucrose metabolism	KEGG PATHWAY	sbi00500	2
Phenylpropanoid biosynthesis	KEGG PATHWAY	sbi00940	2
Diterpenoid biosynthesis	KEGG PATHWAY	sbi00904	1
SNARE interactions in vesicular transport	KEGG PATHWAY	sbi04130	1
Cutin, suberine and wax biosynthesis	KEGG PATHWAY	sbi00073	1
Phenylalanine, tyrosine and tryptophan biosynthesis	KEGG PATHWAY	sbi00400	1
Fatty acid elongation	KEGG PATHWAY	sbi00062	1
Pentose phosphate pathway	KEGG PATHWAY	sbi00030	1
Fructose and mannose metabolism	KEGG PATHWAY	sbi00051	1
Galactose metabolism	KEGG PATHWAY	sbi00052	1
Photosynthesis	KEGG PATHWAY	sbi00195	1
Glycolysis / Gluconeogenesis	KEGG PATHWAY	sbi00010	1

Aminoacyl-tRNA biosynthesis	KEGG PATHWAY	sbi00970	1
Ubiquitin mediated proteolysis	KEGG PATHWAY	sbi04120	1
Amino sugar and nucleotide sugar metabolism	KEGG PATHWAY	sbi00520	1
Oxidative phosphorylation	KEGG PATHWAY	sbi00190	1
Plant-pathogen interaction	KEGG PATHWAY	sbi04626	1
Purine metabolism	KEGG PATHWAY	sbi00230	1
Biosynthesis of amino acids	KEGG PATHWAY	sbi01230	1
Plant hormone signal transduction	KEGG PATHWAY	sbi04075	1
Metabolic pathways significantly enriched to down-regulated RB80-3280 DEGs			
Biosynthesis of secondary metabolites	KEGG PATHWAY	sbi01110	2
Carotenoid biosynthesis	KEGG PATHWAY	sbi00906	1
Cyanoamino acid metabolism	KEGG PATHWAY	sbi00460	1
Peroxisome	KEGG PATHWAY	sbi04146	1
Metabolic pathways	KEGG PATHWAY	sbi01100	1

Table S8. List of GO terms significantly enriched to common and unique up- and down-regulated DETs generated in two sugarcane varieties (RB867515 and SP80-3280) infested with *Diatraea saccharalis*.

RB867515 up-regulated DETs		
Biological process		
GO.ID	**Term**	**Count**
GO:0044699	single-organism process	150
GO:0044763	single-organism cellular process	109
GO:0044710	single-organism metabolic process	93
GO:0055114	oxidation-reduction process	54
GO:0006950	response to stress	46
GO:0044281	small molecule metabolic process	37
GO:0043436	oxoacid metabolic process	27
GO:0006082	organic acid metabolic process	27
GO:0019752	carboxylic acid metabolic process	26
GO:0009725	response to hormone	24
GO:0009719	response to endogenous stimulus	24
GO:0044712	single-organism catabolic process	21
GO:0006979	response to oxidative stress	20
GO:0044283	small molecule biosynthetic process	19
GO:0070887	cellular response to chemical stimulus	19
GO:0016053	organic acid biosynthetic process	18
GO:0046394	carboxylic acid biosynthetic process	18
GO:0001101	response to acid chemical	18
GO:0009611	response to wounding	14
GO:0009755	hormone-mediated signaling pathway	14

GO:0032870	cellular response to hormone stimulus	14
GO:0071495	cellular response to endogenous stimulus	14
GO:0006520	cellular amino acid metabolic process	14
GO:0071310	cellular response to organic substance	14
GO:0008652	cellular amino acid biosynthetic process	12
GO:0031324	negative regulation of cellular metabolic process	12
GO:0009753	response to jasmonic acid	11
GO:0072593	reactive oxygen species metabolic process	11
GO:0042744	hydrogen peroxide catabolic process	10
GO:0042743	hydrogen peroxide metabolic process	10
GO:0071229	cellular response to acid chemical	10
GO:1901607	alpha-amino acid biosynthetic process	9
GO:0010646	regulation of cell communication	9
GO:1901605	alpha-amino acid metabolic process	9
GO:0009867	jasmonic acid mediated signaling pathway	8
GO:0071395	cellular response to jasmonic acid stimulus	8
GO:0031347	regulation of defense response	8
GO:0009966	regulation of signal transduction	8
GO:0023051	regulation of signaling	8
GO:0080134	regulation of response to stress	8
GO:0009073	aromatic amino acid family biosynthetic process	7
GO:0009072	aromatic amino acid family metabolic process	7
GO:2000022	regulation of jasmonic acid mediated signaling pathway	6
GO:0009308	amine metabolic process	6
GO:0071804	cellular potassium ion transport	5
GO:0071805	potassium ion transmembrane transport	5
GO:0006813	potassium ion transport	5
GO:0010118	stomatal movement	5
GO:0042445	hormone metabolic process	5
GO:0045944	positive regulation of transcription from RNA polymerase II promoter	5
GO:0031407	oxylipin metabolic process	4
GO:0042435	indole-containing compound biosynthetic process	4
GO:0000103	sulfate assimilation	4
GO:0034754	cellular hormone metabolic process	4
GO:0042430	indole-containing compound metabolic process	4
GO:0031408	oxylipin biosynthetic process	3
GO:0009695	jasmonic acid biosynthetic process	3
GO:0090332	stomatal closure	3
GO:0000162	tryptophan biosynthetic process	3
GO:0046219	indolalkylamine biosynthetic process	3
GO:0009694	jasmonic acid metabolic process	3
GO:0006568	tryptophan metabolic process	3
GO:0006586	indolalkylamine metabolic process	3
GO:0010039	response to iron ion	3
GO:0010107	potassium ion import	2

GO:2000068	regulation of defense response to insect	2
GO:0006564	L-serine biosynthetic process	2
GO:0006549	isoleucine metabolic process	2
GO:0009097	isoleucine biosynthetic process	2
GO:0090333	regulation of stomatal closure	2
GO:0007584	response to nutrient	2
GO:0006662	glycerol ether metabolic process	2
GO:0008300	isoprenoid catabolic process	2
GO:0009095	aromatic amino acid family biosynthetic process, prephenate pathway	2
GO:0016115	terpenoid catabolic process	2
GO:0018904	ether metabolic process	2
Cellular component		
GO:0005576	extracellular region	24
GO:0005773	vacuole	16
GO:0005774	vacuolar membrane	15
GO:0044437	vacuolar part	15
GO:0098805	whole membrane	15
Molecular function		
GO:0003824	catalytic activity	158
GO:0016491	oxidoreductase activity	54
GO:0020037	heme binding	22
GO:0046906	tetrapyrrole binding	22
GO:0005506	iron ion binding	18
GO:0048037	cofactor binding	18
GO:0046983	protein dimerization activity	18
GO:0016829	lyase activity	13
GO:0050662	coenzyme binding	13
GO:0016705	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen	13
GO:0004601	peroxidase activity	10
GO:0016684	oxidoreductase activity, acting on peroxide as acceptor	10
GO:0016614	oxidoreductase activity, acting on CH-OH group of donors	10
GO:0016209	antioxidant activity	10
GO:0008757	S-adenosylmethionine-dependent methyltransferase activity	9
GO:0051213	dioxygenase activity	8
GO:0003714	transcription corepressor activity	6
GO:0003712	transcription cofactor activity	6
GO:0000989	transcription factor activity, transcription factor binding	6
GO:0000988	transcription factor activity, protein binding	6
GO:0015079	potassium ion transmembrane transporter activity	5
GO:0000976	transcription regulatory region sequence-specific DNA binding	5
GO:0030170	pyridoxal phosphate binding	5
GO:0001046	core promoter sequence-specific DNA binding	4
GO:0001047	core promoter binding	4
GO:0016597	amino acid binding	4
GO:0016701	oxidoreductase activity, acting on single donors with incorporation of molecular oxygen	4

GO:0001228	transcriptional activator activity, RNA polymerase II transcription regulatory region sequence-specific binding	4
GO:0005057	receptor signaling protein activity	4
GO:0016645	oxidoreductase activity, acting on the CH-NH group of donors	3
GO:0022821	potassium ion antiporter activity	2
GO:0004564	beta-fructofuranosidase activity	2
GO:0004575	sucrose alpha-glucosidase activity	2
GO:0004617	phosphoglycerate dehydrogenase activity	2
GO:0090599	alpha-glucosidase activity	2
GO:0033926	glycopeptide alpha-N-acetylgalactosaminidase activity	2
GO:0019139	cytokinin dehydrogenase activity	2

RB867515 down-regulated DETs

Biological process

GO.ID	Term	Count
GO:0050896	response to stimulus	59
GO:0044710	single-organism metabolic process	54
GO:0006950	response to stress	36
GO:0055114	oxidation-reduction process	29
GO:0009628	response to abiotic stimulus	28
GO:0042221	response to chemical	26
GO:0009314	response to radiation	19
GO:0009416	response to light stimulus	18
GO:0015979	photosynthesis	14
GO:0009266	response to temperature stimulus	14
GO:0006091	generation of precursor metabolites and energy	13
GO:0010035	response to inorganic substance	13
GO:0009409	response to cold	9
GO:0019684	photosynthesis, light reaction	8
GO:0046686	response to cadmium ion	8
GO:0010038	response to metal ion	8
GO:0009768	photosynthesis, light harvesting in photosystem I	6
GO:0009765	photosynthesis, light harvesting	6
GO:0009639	response to red or far red light	6
GO:0006720	isoprenoid metabolic process	6
GO:0006073	cellular glucan metabolic process	6
GO:0010114	response to red light	5
GO:0005982	starch metabolic process	5
GO:0019318	hexose metabolic process	5
GO:0009408	response to heat	5
GO:0018298	protein-chromophore linkage	4
GO:0009644	response to high light intensity	4
GO:0009743	response to carbohydrate	4
GO:0006721	terpenoid metabolic process	4
GO:0015980	energy derivation by oxidation of organic compounds	4
GO:0008299	isoprenoid biosynthetic process	4
GO:0009642	response to light intensity	4

GO:0009750	response to fructose	3
GO:0009645	response to low light intensity stimulus	3
GO:0016108	tetraterpenoid metabolic process	3
GO:0016116	carotenoid metabolic process	3
GO:0010218	response to far red light	3
GO:0009746	response to hexose	3
GO:0034284	response to monosaccharide	3
GO:0009744	response to sucrose	3
GO:0034285	response to disaccharide	3
GO:0009637	response to blue light	3
GO:0006334	nucleosome assembly	3
GO:0016122	xanthophyll metabolic process	2
GO:0005983	starch catabolic process	2
GO:0006012	galactose metabolic process	2
Cellular component		
GO:0044424	intracellular part	104
GO:0005622	intracellular	104
GO:0043229	intracellular organelle	89
GO:0043226	organelle	89
GO:0043231	intracellular membrane-bounded organelle	88
GO:0043227	membrane-bounded organelle	88
GO:0005737	cytoplasm	81
GO:0044444	cytoplasmic part	71
GO:0009536	plastid	51
GO:0009507	chloroplast	50
GO:0044446	intracellular organelle part	48
GO:0044422	organelle part	48
GO:0044434	chloroplast part	33
GO:0044435	plastid part	33
GO:0009570	chloroplast stroma	23
GO:0009532	plastid stroma	23
GO:0009579	thylakoid	19
GO:0031967	organelle envelope	19
GO:0031975	envelope	19
GO:0031984	organelle subcompartment	17
GO:0044436	thylakoid part	16
GO:0009534	chloroplast thylakoid	16
GO:0031976	plastid thylakoid	16
GO:0009941	chloroplast envelope	16
GO:0009526	plastid envelope	16
GO:0034357	photosynthetic membrane	15
GO:0009535	chloroplast thylakoid membrane	14
GO:0055035	plastid thylakoid membrane	14
GO:0042651	thylakoid membrane	14
GO:0005576	extracellular region	13

GO:0048046	apoplast	8
GO:0010287	plastoglobule	7
GO:0032993	protein-DNA complex	7
GO:0044427	chromosomal part	7
GO:0000786	nucleosome	6
GO:0044815	DNA packaging complex	6
GO:0000785	chromatin	6
GO:0009523	photosystem II	5
GO:0009521	photosystem	5
GO:0009522	photosystem I	4
GO:0009501	amyloplast	2
Molecular function		
GO:0016491	oxidoreductase activity	24
GO:0046906	tetrapyrrole binding	11
GO:0046983	protein dimerization activity	10
GO:0046982	protein heterodimerization activity	5
GO:0031409	pigment binding	4
GO:0016168	chlorophyll binding	4
GO:0003978	UDP-glucose 4-epimerase activity	2
GO:0004373	glycogen (starch) synthase activity	2
GO:0050308	sugar-phosphatase activity	2

SP80-3280 up-regulated DETs

Biological process		
GO.ID	**Term**	**Count**
GO:0044699	single-organism process	101
GO:0044710	single-organism metabolic process	65
GO:0006950	response to stress	37
GO:0055114	oxidation-reduction process	36
GO:0009056	catabolic process	27
GO:0044281	small molecule metabolic process	27
GO:0019752	carboxylic acid metabolic process	22
GO:0043436	oxoacid metabolic process	22
GO:0006082	organic acid metabolic process	22
GO:0009725	response to hormone	17
GO:0044712	single-organism catabolic process	16
GO:0009611	response to wounding	15
GO:0006952	defense response	15
GO:0048519	negative regulation of biological process	15
GO:0016053	organic acid biosynthetic process	14
GO:0046394	carboxylic acid biosynthetic process	14
GO:0044283	small molecule biosynthetic process	14
GO:0009892	negative regulation of metabolic process	13
GO:0032787	monocarboxylic acid metabolic process	12
GO:0031324	negative regulation of cellular metabolic process	11
GO:0010605	negative regulation of macromolecule metabolic process	11

GO:0048523	negative regulation of cellular process	11
GO:0006979	response to oxidative stress	10
GO:0048583	regulation of response to stimulus	9
GO:0031347	regulation of defense response	8
GO:0009620	response to fungus	8
GO:0080134	regulation of response to stress	8
GO:0006026	aminoglycan catabolic process	7
GO:0006030	chitin metabolic process	7
GO:0006032	chitin catabolic process	7
GO:0046348	amino sugar catabolic process	7
GO:1901072	glucosamine-containing compound catabolic process	7
GO:1901071	glucosamine-containing compound metabolic process	7
GO:0006022	aminoglycan metabolic process	7
GO:0006040	amino sugar metabolic process	7
GO:1901136	carbohydrate derivative catabolic process	7
GO:1901565	organonitrogen compound catabolic process	7
GO:1902679	negative regulation of RNA biosynthetic process	7
GO:1903507	negative regulation of nucleic acid-templated transcription	7
GO:0051253	negative regulation of RNA metabolic process	7
GO:0008652	cellular amino acid biosynthetic process	7
GO:0045934	negative regulation of nucleobase-containing compound metabolic process	7
GO:0072330	monocarboxylic acid biosynthetic process	7
GO:0010558	negative regulation of macromolecule biosynthetic process	7
GO:0031327	negative regulation of cellular biosynthetic process	7
GO:0009890	negative regulation of biosynthetic process	7
GO:0051172	negative regulation of nitrogen compound metabolic process	7
GO:0009753	response to jasmonic acid	6
GO:0042744	hydrogen peroxide catabolic process	6
GO:0050832	defense response to fungus	6
GO:0042743	hydrogen peroxide metabolic process	6
GO:0009966	regulation of signal transduction	6
GO:0023051	regulation of signaling	6
GO:1901607	alpha-amino acid biosynthetic process	6
GO:0010646	regulation of cell communication	6
GO:0006955	immune response	6
GO:2000022	regulation of jasmonic acid mediated signaling pathway	5
GO:0009867	jasmonic acid mediated signaling pathway	5
GO:0071395	cellular response to jasmonic acid stimulus	5
GO:0031408	oxylipin biosynthetic process	4
GO:0031407	oxylipin metabolic process	4
GO:0016998	cell wall macromolecule catabolic process	4
GO:0010466	negative regulation of peptidase activity	4
GO:0010951	negative regulation of endopeptidase activity	4
GO:0052547	regulation of peptidase activity	4
GO:0052548	regulation of endopeptidase activity	4

GO:0006721	terpenoid metabolic process	4
GO:0042435	indole-containing compound biosynthetic process	3
GO:0034754	cellular hormone metabolic process	3
GO:0042430	indole-containing compound metabolic process	3
GO:0008300	isoprenoid catabolic process	2
GO:0016115	terpenoid catabolic process	2
GO:0043901	negative regulation of multi-organism process	2
GO:0006535	cysteine biosynthetic process from serine	2
Cellular component		
GO:0005576	extracellular region	19
GO:0009505	plant-type cell wall	6
Molecular function		
GO:0003824	catalytic activity	118
GO:0016491	oxidoreductase activity	35
GO:0048037	cofactor binding	14
GO:0004553	hydrolase activity, hydrolyzing O-glycosyl compounds	13
GO:0016798	hydrolase activity, acting on glycosyl bonds	13
GO:0016829	lyase activity	12
GO:0050662	coenzyme binding	10
GO:0051213	dioxygenase activity	9
GO:0000287	magnesium ion binding	8
GO:0016835	carbon-oxygen lyase activity	8
GO:0004568	chitinase activity	7
GO:0004857	enzyme inhibitor activity	7
GO:0008061	chitin binding	6
GO:0004601	peroxidase activity	6
GO:0016684	oxidoreductase activity, acting on peroxide as acceptor	6
GO:0003714	transcription corepressor activity	5
GO:0004867	serine-type endopeptidase inhibitor activity	5
GO:0003712	transcription cofactor activity	5
GO:0000989	transcription factor activity, transcription factor binding	5
GO:0004866	endopeptidase inhibitor activity	5
GO:0061135	endopeptidase regulator activity	5
GO:0030414	peptidase inhibitor activity	5
GO:0061134	peptidase regulator activity	5
GO:0000988	transcription factor activity, protein binding	5
GO:0016702	oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen	4
GO:0010333	terpene synthase activity	4
GO:0016838	carbon-oxygen lyase activity, acting on phosphates	4
GO:0016701	oxidoreductase activity, acting on single donors with incorporation of molecular oxygen	4
GO:0008083	growth factor activity	2
GO:0019139	cytokinin dehydrogenase activity	2
	SP80-3280 down-regulated DETs	
Biological process		
GO.ID	**Term**	**Count**

GO:0015979	photosynthesis	8
GO:0006091	generation of precursor metabolites and energy	7
GO:0019684	photosynthesis, light reaction	5
GO:0009416	response to light stimulus	5
GO:0009314	response to radiation	5
GO:0009767	photosynthetic electron transport chain	3
GO:0080167	response to karrikin	3
GO:0022900	electron transport chain	3
GO:0010117	photoprotection	2
GO:0071484	cellular response to light intensity	2
GO:0009773	photosynthetic electron transport in photosystem I	2
GO:0009644	response to high light intensity	2
GO:0071482	cellular response to light stimulus	2
GO:0071478	cellular response to radiation	2
GO:0009411	response to UV	2
GO:0046939	nucleotide phosphorylation	2
GO:0044724	single-organism carbohydrate catabolic process	2
GO:0009642	response to light intensity	2
GO:0071214	cellular response to abiotic stimulus	2
Cellular component		
GO:0005737	cytoplasm	25
GO:0044444	cytoplasmic part	24
GO:0043231	intracellular membrane-bounded organelle	23
GO:0043227	membrane-bounded organelle	23
GO:0043229	intracellular organelle	23
GO:0043226	organelle	23
GO:0009507	chloroplast	21
GO:0009536	plastid	21
GO:0044446	intracellular organelle part	18
GO:0044422	organelle part	18
GO:0044434	chloroplast part	17
GO:0044435	plastid part	17
GO:0009579	thylakoid	13
GO:0009534	chloroplast thylakoid	12
GO:0031976	plastid thylakoid	12
GO:0031984	organelle subcompartment	12
GO:0042651	thylakoid membrane	11
GO:0034357	photosynthetic membrane	11
GO:0044436	thylakoid part	11
GO:0009535	chloroplast thylakoid membrane	10
GO:0055035	plastid thylakoid membrane	10
GO:0009570	chloroplast stroma	7
GO:0009532	plastid stroma	7
GO:0019898	extrinsic component of membrane	2
Molecular function		

GO:0016829	lyase activity	3

Table S9. List of GO terms significantly enriched to common and unique up- and down-regulated DEGs generated in two sugarcane varieties (RB867515 and SP80-3280) infested with *Diatraea saccharalis*.

RB867515 up-regulated DEGs		
Biological process		
GO.ID	**Term**	**Count**
GO:0044699	single-organism process	112
GO:0044710	single-organism metabolic process	73
GO:0055114	oxidation-reduction process	39
GO:0044281	small molecule metabolic process	29
GO:0043436	oxoacid metabolic process	22
GO:0006082	organic acid metabolic process	22
GO:0055085	transmembrane transport	21
GO:0019752	carboxylic acid metabolic process	20
GO:0044712	single-organism catabolic process	14
GO:0044283	small molecule biosynthetic process	13
GO:0034220	ion transmembrane transport	12
GO:0016053	organic acid biosynthetic process	11
GO:0046394	carboxylic acid biosynthetic process	11
GO:0010817	regulation of hormone levels	7
GO:0031407	oxylipin metabolic process	5
GO:0016054	organic acid catabolic process	5
GO:0046395	carboxylic acid catabolic process	5
GO:0009308	amine metabolic process	5
GO:0031408	oxylipin biosynthetic process	4
GO:0023014	signal transduction by protein phosphorylation	4
GO:0071804	cellular potassium ion transport	4
GO:0071805	potassium ion transmembrane transport	4
GO:0080167	response to karrikin	4
GO:0006813	potassium ion transport	4
GO:0010118	stomatal movement	4
GO:0010311	lateral root formation	3
GO:0009690	cytokinin metabolic process	3
GO:0010102	lateral root morphogenesis	3
GO:0010101	post-embryonic root morphogenesis	3
GO:0034754	cellular hormone metabolic process	3
GO:0010540	basipetal auxin transport	2
GO:0016103	diterpenoid catabolic process	2
GO:0045487	gibberellin catabolic process	2

GO:0043090	amino acid import	2
GO:0008300	isoprenoid catabolic process	2
GO:0016115	terpenoid catabolic process	2
GO:0033617	mitochondrial respiratory chain complex IV assembly	2
GO:0097034	mitochondrial respiratory chain complex IV biogenesis	2
GO:0008535	respiratory chain complex IV assembly	2
Cellular component		
GO:0097249	mitochondrial respiratory chain supercomplex	2
GO:0031012	extracellular matrix	2
GO:0031305	integral component of mitochondrial inner membrane	2
Molecular function		
GO:0003824	catalytic activity	111
GO:0016491	oxidoreductase activity	39
GO:0022857	transmembrane transporter activity	19
GO:0048037	cofactor binding	16
GO:0022891	substrate-specific transmembrane transporter activity	16
GO:0022892	substrate-specific transporter activity	16
GO:0003700	transcription factor activity, sequence-specific DNA binding	15
GO:0001071	nucleic acid binding transcription factor activity	15
GO:0016829	lyase activity	13
GO:0015075	ion transmembrane transporter activity	13
GO:0050662	coenzyme binding	12
GO:0020037	heme binding	12
GO:0043565	sequence-specific DNA binding	12
GO:0046906	tetrapyrrole binding	12
GO:0051213	dioxygenase activity	11
GO:0005506	iron ion binding	11
GO:0016614	oxidoreductase activity, acting on CH-OH group of donors	8
GO:0016701	oxidoreductase activity, acting on single donors with incorporation of molecular oxygen	7
GO:0016702	oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen	6
GO:0016830	carbon-carbon lyase activity	6
GO:0016835	carbon-oxygen lyase activity	6
GO:0016616	oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor	5
GO:0046943	carboxylic acid transmembrane transporter activity	5
GO:0005342	organic acid transmembrane transporter activity	5
GO:0016645	oxidoreductase activity, acting on the CH-NH group of donors	4
GO:0010333	terpene synthase activity	4
GO:0016838	carbon-oxygen lyase activity, acting on phosphates	4
GO:0005057	receptor signaling protein activity	4
GO:0015079	potassium ion transmembrane transporter activity	4
GO:0019139	cytokinin dehydrogenase activity	3
GO:0001046	core promoter sequence-specific DNA binding	3
GO:0001047	core promoter binding	3
GO:0005244	voltage-gated ion channel activity	3
GO:0022832	voltage-gated channel activity	3

GO:0052634	C-19 gibberellin 2-beta-dioxygenase activity	2
GO:0045543	gibberellin 2-beta-dioxygenase activity	2
GO:0016832	aldehyde-lyase activity	2

RB867515 down-regulated DEGs

Biological process		
GO.ID	**Term**	**Count**
GO:0009628	response to abiotic stimulus	12
GO:0065008	regulation of biological quality	9
GO:0042592	homeostatic process	8
GO:0005976	polysaccharide metabolic process	7
GO:0044262	cellular carbohydrate metabolic process	7
GO:0006073	cellular glucan metabolic process	6
GO:0044042	glucan metabolic process	6
GO:0044264	cellular polysaccharide metabolic process	6
GO:0005982	starch metabolic process	5
GO:0016052	carbohydrate catabolic process	4
GO:0022603	regulation of anatomical structure morphogenesis	3
GO:0060688	regulation of morphogenesis of a branching structure	2
GO:2000032	regulation of secondary shoot formation	2
GO:0043446	cellular alkane metabolic process	2
GO:0043447	alkane biosynthetic process	2
GO:1900618	regulation of shoot system morphogenesis	2
GO:0055075	potassium ion homeostasis	2
GO:0005978	glycogen biosynthetic process	2
GO:0005983	starch catabolic process	2
GO:0010025	wax biosynthetic process	2
GO:0010166	wax metabolic process	2
GO:0010223	secondary shoot formation	2
GO:0010346	shoot axis formation	2
GO:0001763	morphogenesis of a branching structure	2
GO:0005977	glycogen metabolic process	2
GO:0006112	energy reserve metabolic process	2
GO:0042335	cuticle development	2
GO:0071470	cellular response to osmotic stress	2
GO:0010114	response to red light	2
GO:0061077	chaperone-mediated protein folding	2
Cellular component		
GO:0009507	chloroplast	21
GO:0009536	plastid	21
GO:0044434	chloroplast part	13
GO:0044435	plastid part	13
GO:0009570	chloroplast stroma	7
GO:0009532	plastid stroma	7
GO:0009534	chloroplast thylakoid	6
GO:0031976	plastid thylakoid	6

GO:0009535	chloroplast thylakoid membrane	5
GO:0055035	plastid thylakoid membrane	5
GO:0000786	nucleosome	3
GO:0044815	DNA packaging complex	3
Molecular function		
GO:0005506	iron ion binding	6
GO:2001070	starch binding	3
GO:0016781	phosphotransferase activity, paired acceptors	2
GO:0050308	sugar-phosphatase activity	2
GO:0019203	carbohydrate phosphatase activity	2
GO:0019200	carbohydrate kinase activity	2

SP80-3280 up-regulated DEGs

Biological process		
GO.ID	**Term**	**Count**
GO:0044699	single-organism process	83
GO:0044710	single-organism metabolic process	56
GO:0050896	response to stimulus	44
GO:0055114	oxidation-reduction process	31
GO:0006950	response to stress	30
GO:0044281	small molecule metabolic process	23
GO:0042221	response to chemical	22
GO:0043436	oxoacid metabolic process	21
GO:0006082	organic acid metabolic process	21
GO:0044711	single-organism biosynthetic process	21
GO:0019752	carboxylic acid metabolic process	20
GO:0009719	response to endogenous stimulus	15
GO:0016053	organic acid biosynthetic process	14
GO:0046394	carboxylic acid biosynthetic process	14
GO:0044283	small molecule biosynthetic process	14
GO:1901700	response to oxygen-containing compound	14
GO:0009605	response to external stimulus	13
GO:0001101	response to acid chemical	12
GO:0043207	response to external biotic stimulus	11
GO:0051707	response to other organism	11
GO:0009607	response to biotic stimulus	11
GO:0009611	response to wounding	10
GO:0098542	defense response to other organism	9
GO:0009620	response to fungus	8
GO:0072330	monocarboxylic acid biosynthetic process	7
GO:0050832	defense response to fungus	6
GO:0008652	cellular amino acid biosynthetic process	6
GO:0072593	reactive oxygen species metabolic process	6
GO:0043086	negative regulation of catalytic activity	6
GO:0010466	negative regulation of peptidase activity	5
GO:0010951	negative regulation of endopeptidase activity	5

GO:0052547	regulation of peptidase activity	5
GO:0052548	regulation of endopeptidase activity	5
GO:0051346	negative regulation of hydrolase activity	5
GO:0045861	negative regulation of proteolysis	5
GO:0009308	amine metabolic process	5
GO:0009753	response to jasmonic acid	5
GO:0030162	regulation of proteolysis	5
GO:0042744	hydrogen peroxide catabolic process	5
GO:0031347	regulation of defense response	5
GO:0042743	hydrogen peroxide metabolic process	5
GO:1901607	alpha-amino acid biosynthetic process	5
GO:0032269	negative regulation of cellular protein metabolic process	5
GO:0051248	negative regulation of protein metabolic process	5
GO:0031407	oxylipin metabolic process	4
GO:0031408	oxylipin biosynthetic process	3
GO:0009695	jasmonic acid biosynthetic process	3
GO:0000162	tryptophan biosynthetic process	3
GO:0046219	indolalkylamine biosynthetic process	3
GO:0009694	jasmonic acid metabolic process	3
GO:0006568	tryptophan metabolic process	3
GO:0006586	indolalkylamine metabolic process	3
GO:0016998	cell wall macromolecule catabolic process	3
GO:0042435	indole-containing compound biosynthetic process	3
GO:0009309	amine biosynthetic process	3
GO:0042401	cellular biogenic amine biosynthetic process	3
GO:0009073	aromatic amino acid family biosynthetic process	3
GO:0042430	indole-containing compound metabolic process	3
GO:0002831	regulation of response to biotic stimulus	3
GO:0032101	regulation of response to external stimulus	3
GO:2000068	regulation of defense response to insect	2
GO:0002213	defense response to insect	2
GO:0006535	cysteine biosynthetic process from serine	2
GO:0034605	cellular response to heat	2
GO:0009625	response to insect	2
GO:0019344	cysteine biosynthetic process	2
Cellular component		
GO:0005576	extracellular region	12
GO:0005773	vacuole	10
GO:0005774	vacuolar membrane	7
GO:0044437	vacuolar part	7
Molecular function		
GO:0003824	catalytic activity	86
GO:0016491	oxidoreductase activity	31
GO:0048037	cofactor binding	17
GO:0016829	lyase activity	13

GO:0050662	coenzyme binding	12
GO:0020037	heme binding	11
GO:0046906	tetrapyrrole binding	11
GO:0016835	carbon-oxygen lyase activity	9
GO:0051213	dioxygenase activity	8
GO:0004857	enzyme inhibitor activity	6
GO:0004867	serine-type endopeptidase inhibitor activity	5
GO:0030170	pyridoxal phosphate binding	5
GO:0004866	endopeptidase inhibitor activity	5
GO:0061135	endopeptidase regulator activity	5
GO:0030414	peptidase inhibitor activity	5
GO:0061134	peptidase regulator activity	5
GO:0000287	magnesium ion binding	5
GO:0050660	flavin adenine dinucleotide binding	5
GO:0016702	oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen	4
GO:0010333	terpene synthase activity	4
GO:0016838	carbon-oxygen lyase activity, acting on phosphates	4
GO:0016701	oxidoreductase activity, acting on single donors with incorporation of molecular oxygen	4
GO:0016836	hydro-lyase activity	4
GO:0015103	inorganic anion transmembrane transporter activity	3
GO:0004834	tryptophan synthase activity	2
GO:0019139	cytokinin dehydrogenase activity	2

SP80-3280 down-regulated DEGs

Biological process		
GO.ID	**Term**	**Count**
GO:0015979	photosynthesis	4
GO:0009416	response to light stimulus	4
GO:0009314	response to radiation	4
GO:0071484	cellular response to light intensity	2
GO:0071482	cellular response to light stimulus	2
GO:0071478	cellular response to radiation	2
GO:0009642	response to light intensity	2
GO:0019684	photosynthesis, light reaction	2
GO:0071214	cellular response to abiotic stimulus	2
Cellular component		
GO:0043229	intracellular organelle	18
GO:0043226	organelle	18
GO:0044444	cytoplasmic part	17
GO:0005737	cytoplasm	17
GO:0043231	intracellular membrane-bounded organelle	17
GO:0043227	membrane-bounded organelle	17
GO:0009507	chloroplast	15
GO:0009536	plastid	15
GO:0044446	intracellular organelle part	12
GO:0044422	organelle part	12

GO:0044434	chloroplast part	11
GO:0044435	plastid part	11
GO:0009579	thylakoid	9
GO:0009534	chloroplast thylakoid	7
GO:0031976	plastid thylakoid	7
GO:0031984	organelle subcompartment	7
GO:0042651	thylakoid membrane	5
GO:0034357	photosynthetic membrane	5
GO:0044436	thylakoid part	5
GO:0009535	chloroplast thylakoid membrane	4
GO:0055035	plastid thylakoid membrane	4
GO:0009941	chloroplast envelope	4
GO:0009526	plastid envelope	4
Molecular function		
GO:0042802	identical protein binding	2

Table S10. List of differentially expressed transcripts (DETs) and genes (DEGs) coding for JA and ET biosynthetic and signaling pathways in two sugarcane varieties (RB867515 and SP80-3280) infested with *Diatraea saccharalis*.

DETs				
ID SUGIT	**Blast2GO Description**	**TRAPID Protein Domain**	**Log_2 FC**	
ET biosynthesis			**RB867515**	**SP80-3280**
GFHJ01041106.1	1-aminocyclopropane-1-carboxylate synthase 1	1-aminocyclopropane-1-carboxylate synthase	3.595736518	1.478033753
GFHJ01058630.1	1-aminocyclopropane-1-carboxylate oxidase	Oxoglutarate/iron-dependent oxygenase	4.646091905	2.407987733
GFHJ01080434.1	1-aminocyclopropane-1-carboxylate oxidase 1	Oxoglutarate/iron-dependent oxygenase	4.772891164	----------
ET signaling				
GFHJ01088340.1	ethylene-responsive transcription factor ERF109	Pathogenesis-related transcriptional factor/ERF, DNA-binding	3.048259562	----------
GFHJ01086519.1	ethylene-responsive transcription factor-like protein At4g13040 isoform X4	Pathogenesis-related transcriptional factor/ERF, DNA-binding	-0.795439659	----------
GFHJ01095682.1	ethylene-responsive transcription factor 1	Pathogenesis-related transcriptional factor/ERF, DNA-binding	-0.817395265	----------
GFHJ01058998.1	protein REVERSION-TO-ETHYLENE SENSITIVITY1-like	Protein of unknown function DUF778	1.194503665	----------
GFHJ01038441.1	probable ethylene response sensor 2	Signal transduction response regulator, receiver domain	0.97844071	----------
GFHJ01021939.1	ETHYLENE INSENSITIVE 3-like 3 protein	Ethylene insensitive 3	0.690545278	----------
JA biosynthesis				
GFHJ01015592.1	Probable linoleate 9S-lipoxygenase 4	Plant lipoxygenase	2.263752245	1.294329286
GFHJ01017539.1	Probable linoleate 9S-lipoxygenase 4	Plant lipoxygenase	2.400336856	1.294895509
GFHJ01047708.1	Putative linoleate 9S-lipoxygenase 3	Plant lipoxygenase	2.481235556	1.222585718
GFHJ01047957.1	Linoleate 9S-lipoxygenase 2	Plant lipoxygenase	2.642816374	1.173227276
GFHJ01047960.1	Linoleate 9S-lipoxygenase 2	Plant lipoxygenase	2.319264371	----------
GFHJ01047959.1	Linoleate 9S-lipoxygenase 2	Plant lipoxygenase	----------	1.093556284
GFHJ01094711.1	Linoleate 9S-lipoxygenase 2	Lipoxygenase, LH2	----------	1.367632531
GFHJ01042717.1	putative 12-oxophytodienoate reductase 11	NADH:flavin oxidoreductase/NADH oxidase, N-terminal	0.868914051	----------

GFHJ01046914.1	12-oxophytodienoate reductase 7	NADH:flavin oxidoreductase/NADH oxidase, N-terminal	----------	0.507279458
GFHJ01018680.1	Allene oxide synthase 2	Cytochrome P450	2.04031549	1.321285685
GFHJ01006030.1	Allene oxide synthase 1	Cytochrome P450	1.291188583	----------
GFHJ01018660.1	Allene oxide synthase 2	Cytochrome P450	----------	1.749534358
GFHJ01018676.1	Allene oxide synthase 2	Cytochrome P450	----------	1.447861768
GFHJ01065023.1	Allene oxide cyclase	Allene Oxide Cyclase	1.081411111	----------
JA signaling				
GFHJ01063084.1	Protein TIFY 11c	RNA-directed DNA polymerase (reverse transcriptase)	2.078130204	1.183280533
GFHJ01095424.1	protein TIFY 5	Tify	3.669615635	4.080929249
GFHJ01100258.1	ZIM motif family protein	Tify	2.959839992	1.389363142
GFHJ01023928.1	protein TIFY 6b	Tify	0.861806059	----------
GFHJ01076652.1	Protein TIFY 11c	Tify	----------	1.318957189
GFHJ01084013.1	protein TIFY 9	Tify	----------	2.062607117
GFHJ01064115.1	putative transcription factor bHLH041	Helix-loop-helix DNA-binding domain	2.723896592	2.644704676
GFHJ01086879.1	transcription factor bHLH13-like	Helix-loop-helix DNA-binding domain	3.731072297	----------

DEGs

ID SUGIT	STP Description	TRAPID Protein Domain	Log_2 FC	
ET biosynthesis			**RB867515**	**SP80-3280**
Sh09_g004160	1-aminocyclopropane-1-carboxylate oxidase	Oxoglutarate/iron-dependent oxygenase	5.360704274	3.07707371
Sh09_g004190	Acc oxidase	Oxoglutarate/iron-dependent oxygenase	3.911033491	1.933901409
ET signaling				
Sh01_g000220	Ethylene-responsive transcription factor 1B	Pathogenesis-related transcriptional factor/ERF, DNA-binding	6.843092829	4.780668359
Sh07_g011720	Ethylene-responsive transcription factor ERF109	Pathogenesis-related transcriptional factor/ERF, DNA-binding	3.547614992	----------
Sh04_g010380	Ethylene-responsive transcription factor-like protein At4g13040	Pathogenesis-related transcriptional factor/ERF, DNA-binding	-0.581160643	----------
Sh04_g023370	similar to AP2 domain-containing transcription factor-like	Pathogenesis-related transcriptional factor/ERF, DNA-binding	----------	1.462831542
JA biosynthesis				
Sh01_g010080	Linoleate 9S-lipoxygenase 1	Lipoxygenase, plant	2.480729053	1.257895322
Sh01_g010070	Lipoxygenase	Lipoxygenase, plant	2.277251983	1.344382701
Sh05_g011820	Linoleate 9S-lipoxygenase 2	Lipoxygenase, plant	2.446520435	----------
Sh03_g028360	Linoleate 9S-lipoxygenase 2	Lipoxygenase, plant	2.373301236	----------
Sh06_g005430	Lipoxygenase	Lipoxygenase, plant	1.361869577	----------
Sh01_g010050	Lipoxygenase	Lipoxygenase, plant	----------	1.186374714
Sh09_g008020	Putative lipoxygenase 6	----------	-1.463462772	----------
Sh06_g005090	12-oxo-phytodienoic acid reductase	NADH:flavin oxidoreductase/NADH oxidase, N-terminal	1.839439964	----------
Sh_227A23_contig-1_g000020	12-oxo-phytodienoic acid reductase	NADH:flavin oxidoreductase/NADH oxidase, N-terminal	0.94851194	----------
Sh07_g011190	12-oxo-phytodienoic acid reductase	NADH:flavin oxidoreductase/NADH oxidase, N-terminal	----------	0.511775554
Sh01_g025260	Allene oxide cyclase	Allene oxide cyclase	----------	0.506346769
JA signaling				
Sh02_g002470	Protein TIFY 5	Tify	3.490161191	3.187305712
Sh06_g002930	Protein TIFY 9	Tify	----------	2.387759636
Sh06_g002900	Protein TIFY 9	Tify	----------	1.989942594

Table 11. List of differentially expressed transcripts (DETs) and genes (DEGs) coding for defense-related proteins in two sugarcane varieties (RB867515 and SP80-3280) infested with *Diatraea saccharalis*.

DETs				
ID SUGIT	**Blast2GO Description**	**TRAPID Protein Domain**	**Log_2 FC**	
Proteinase inhibitors			**RB867515**	**SP80-3280**
GFHJ01085227.1	Bowman-Birk type bran trypsin inhibitor	Proteinase inhibitor I12, Bowman-Birk	3.786906625	2.88766325
GFHJ01099402.1	Bowman-Birk type wound-induced proteinase inhibitor WIP1	----------	4.115339846	----------
GFHJ01099936.1	Bowman-Birk type trypsin inhibitor	Proteinase inhibitor I12, Bowman-Birk	0.961272643	----------
GFHJ01096061.1	Bowman-Birk type wound-induced proteinase inhibitor WIP1	Proteinase inhibitor I12, Bowman-Birk	----------	2.481171019
GFHJ01097974.1	Bowman-Birk type trypsin inhibitor	Proteinase inhibitor I12, Bowman-Birk	----------	1.645401091
GFHJ01097366.1	subtilisin-chymotrypsin inhibitor-2B	Proteinase inhibitor I13, potato inhibitor I	3.758038036	2.450412519
GFHJ01096902.1	subtilisin-chymotrypsin inhibitor-2B	Proteinase inhibitor I13, potato inhibitor I	1.352483427	3.068463102
GFHJ01095719.1	subtilisin-chymotrypsin inhibitor-2B	Proteinase inhibitor I13, potato inhibitor I	3.152368015	----------
GFHJ01095719.1	subtilisin-chymotrypsin inhibitor-2B	Proteinase inhibitor I13, potato inhibitor I	3.152368015	----------
GFHJ01096817.1	subtilisin-chymotrypsin inhibitor-2B	Proteinase inhibitor I13, potato inhibitor I	----------	1.120548275
GFHJ01097912.1	subtilisin-chymotrypsin inhibitor-2B	Proteinase inhibitor I13, potato inhibitor I	----------	2.908286947
GFHJ01098145.1	subtilisin-chymotrypsin inhibitor-2B	Proteinase inhibitor I13, potato inhibitor I	----------	1.526795089
GFHJ01022012.1	serine carboxypeptidase II-3	Peptidase S10, serine carboxypeptidase	1.140815469	1.046612684
GFHJ01023158.1	serine carboxypeptidase 2	Peptidase S10, serine carboxypeptidase	----------	0.781281014
GFHJ01015758.1	serine carboxypeptidase-like 2	Peptidase S10, serine carboxypeptidase	-0.600661875	----------
GFHJ01074615.1	serine carboxypeptidase-like 2	Peptidase S10, serine carboxypeptidase	-0.898327123	----------
GFHJ01079189.1	serine carboxypeptidase-like 2	Peptidase S10, serine carboxypeptidase	-0.637999432	----------
GFHJ01098099.1	maize proteinase inhibitor	Proteinase inhibitor I13, potato inhibitor I	2.689796902	----------
GFHJ01024329.1	cysteine proteinase 2	Peptidase, cysteine peptidase active site	-0.963481791	----------
GFHJ01057253.1	Cysteine proteinase 2	Peptidase, cysteine peptidase active site	-1.74334219	----------
GFHJ01078925.1	Cysteine proteinase 1	Peptidase, cysteine peptidase active site	-0.613110289	----------
Chitinases			**RB867515**	**SP80-3280**
GFHJ01065386.1	chitinase	Glycoside hydrolase, family 19, catalytic	2.451637893	3.489893542
GFHJ01063107.1	chitinase 8	Glycoside hydrolase, family 19, catalytic	----------	1.746373818
GFHJ01064943.1	chitinase 2	Glycoside hydrolase, family 19, catalytic	----------	1.506000369
GFHJ01070808.1	chitinase	Glycoside hydrolase, family 19, catalytic	----------	1.120157689
GFHJ01080813.1	acidic endochitinase	Glycoside hydrolase, chitinase active site	----------	4.120982926
GFHJ01084293.1	endochitinase A	Glycoside hydrolase, family 19, catalytic	----------	2.459628252
GFHJ01102244.1	Chitinase 11	Glycoside hydrolase, family 19, catalytic	-3.383843404	----------
Patatin-like proteins			**RB867515**	**SP80-3280**
GFHJ01008843.1	Patatin-like protein 1	Patatin	6.092539205	3.922552621
GFHJ01031806.1	patatin-like protein 1	Patatin	6.045340337	4.970105645
GFHJ01008846.1	Patatin-like protein 1	Patatin	5.849621829	5.189733003
GFHJ01064634.1	patatin-like protein 1	Patatin	5.762701153	4.806771715
GFHJ01009337.1	patatin-like protein 1	Patatin	4.674901908	4.687749395
GFHJ01031810.1	patatin-like protein 1	Patatin	----------	0.876599572
Peroxidases			**RB867515**	**SP80-3280**
GFHJ01060610.1	Peroxidase N	Plant peroxidase	5.106730053	3.877041972

GFHJ01020952.1	Peroxidase 59	Plant peroxidase	5.023919636	3.878285425
GFHJ01020944.1	Peroxidase 59	Plant peroxidase	4.905457839	5.285110088
GFHJ01080410.1	peroxidase 47	Plant peroxidase	1.812613705	1.378199028
GFHJ01031231.1	cationic peroxidase 1	Plant peroxidase	1.594080009	1.140695347
GFHJ01038506.1	peroxidase 5	Plant peroxidase	1.229198479	0.619264251
GFHJ01032322.1	peroxidase P7	Plant peroxidase	2.156374418	----------
GFHJ01070132.1	Peroxidase 12	Plant peroxidase	1.999752142	----------
GFHJ01080807.1	cationic peroxidase SPC4-like	Plant peroxidase	1.113855845	----------
GFHJ01040802.1	peroxidase 4	Plant peroxidase	0.818978196	----------
GFHJ01050268.1	peroxidase 42	Plant peroxidase	0.710040817	----------
GFHJ01050508.1	Peroxidase 1	Plant peroxidase	----------	0.599982493
GFHJ01056038.1	peroxidase 47	Plant peroxidase	----------	1.264173276
GFHJ01021670.1	peroxidase 17	Plant peroxidase	-1.912821653	----------
GFHJ01073037.1	Peroxidase 17	Plant peroxidase	-3.22136068	----------
GFHJ01078999.1	L-ascorbate peroxidase 2, cytosolic	Haem peroxidase	-0.712466609	----------
GFHJ01098950.1	Peroxidase P7	Plant peroxidase	-1.700384085	----------
GFHJ01106234.1	peroxidase P7	Plant peroxidase	-3.468044139	----------
Lignin biosynthesis			**RB867515**	**SP80-3280**
GFHJ01057202.1	cinnamoyl-CoA reductase 1	NAD-dependent epimerase/dehydratase	----------	3.997603017
GFHJ01067101.1	Cinnamoyl-CoA reductase 1	NAD-dependent epimerase/dehydratase	----------	4.721071186
GFHJ01080622.1	cinnamoyl-CoA reductase 1	NAD-dependent epimerase/dehydratase	----------	-0.600183208
GFHJ01019552.1	cinnamoyl-CoA reductase 1	NAD-dependent epimerase/dehydratase	----------	-0.713051931
GFHJ01103113.1	hydroxycinnamoyltransferase 4	Transferase	----------	2.485540636
GFHJ01020748.1	4-coumarate--CoA ligase-like 4	AMP-dependent synthetase/ligase	0.964247169	0.556932002
GFHJ01043086.1	putative 4-coumarate--CoA ligase 3	AMP-dependent synthetase/ligase	----------	2.324246512
GFHJ01021634.1	putative cellulose synthase A catalytic subunit 6 [UDP-forming]	Zinc finger, RING-type	1.291388035	----------
GFHJ01021685.1	cellulose synthase-like protein E6	----------	-1.143169042	----------

DEGs

ID STP	Description	TRAPID Protein Domain	Log_2 FC	
Proteinase inhibitors			**RB867515**	**SP80-3280**
Sh06_g007560	Bowman-Birk type bran trypsin inhibitor	Proteinase inhibitor I12, Bowman-Birk	3.755822476	2.892064342
Sh03_g026240	Bowman-Birk type trypsin inhibitor	Proteinase inhibitor I12, Bowman-Birk	0.910210595	----------
Sh05_g011500	Bowman-Birk type trypsin inhibitor	Proteinase inhibitor I12, Bowman-Birk	----------	5.724500401
Sh03_g005580	Bowman-Birk type wound-induced proteinase inhibitor WIP1	Proteinase inhibitor I12, Bowman-Birk	----------	5.651886598
Sh05_g011490	Bowman-Birk type trypsin inhibitor	Proteinase inhibitor I12, Bowman-Birk	----------	1.602164961
Sh09_g001130	Subtilisin-chymotrypsin inhibitor-2B (Fragment)	Proteinase inhibitor I13, potato inhibitor I	3.80097038	2.445826936
Sh09_g001140	Subtilisin-chymotrypsin inhibitor-2B (Fragment)	Proteinase inhibitor I13, potato inhibitor I	3.498118986	3.486357068
Sh09_g001060	Subtilisin-chymotrypsin inhibitor-2B (Fragment)	Proteinase inhibitor I13, potato inhibitor I	3.155764824	2.378797789
Sh09_g001120	Subtilisin-chymotrypsin inhibitor-2B (Fragment)	Proteinase inhibitor I13, potato inhibitor I	2.705942797	0.842835781
Sh09_g001150	Subtilisin-chymotrypsin inhibitor-2A	Proteinase inhibitor I13, potato inhibitor I	----------	3.287380189
Sh09_g001230	Subtilisin-chymotrypsin inhibitor-2A	Proteinase inhibitor I13, potato inhibitor I	----------	1.435295311
Sh10_g008750	Metalloendoproteinase 2-MMP	Peptidase M10, metallopeptidase	1.789355804	----------
Chitinases			**RB867515**	**SP80-3280**
Sh03_g027110	Acidic endochitinase	Glycoside hydrolase, chitinase active site	1.650007052	----------
Sh06_g008450	similar to Endochitinase A precursor	Glycoside hydrolase, family 19, catalytic	----------	3.008957752

Sh09_g010120	Basic endochitinase A	Glycoside hydrolase, family 19, catalytic	----------	1.497754937
Peroxidases			**RB867515**	**SP80-3280**
Sh01_g036120	Peroxidase	Plant peroxidase	5.204327005	3.881502814
Sh01_g018600	Peroxidase	Plant peroxidase	4.736834378	4.156135571
Sh09_g004840	Peroxidase	Plant peroxidase	1.24909075	0.635611343
Sh03_g033490	Cationic peroxidase SPC4	Plant peroxidase	0.999237121	----------
Sh07_g001070	Peroxidase	Plant peroxidase	----------	1.330792431
Sh03_g010780	Peroxidase 1	Plant peroxidase	----------	0.563126849
Sh04_g007800	Peroxidase	Plant peroxidase	-1.558850201	----------
Sh02_g015490	Peroxidase	Plant peroxidase	-1.957502047	----------
Lignin biosynthesis			**RB867515**	**SP80-3280**
Sh10_g013560	Putative Cinnamoyl-CoA reductase 1	NAD-dependent epimerase/dehydratase	1.443949136	1.819589892
Sh04_g026080	Cinnamoyl-CoA reductase 1	NAD-dependent epimerase/dehydratase	3.21258053	----------
Sh04_g026060	Cinnamoyl-CoA reductase 1	NAD-dependent epimerase/dehydratase	----------	6.880240679
Sh04_g026070	Cinnamoyl-CoA reductase 1	NAD-dependent epimerase/dehydratase	----------	4.977100571
Sh04_g026050	Cinnamoyl-CoA reductase-like protein 3	NAD-dependent epimerase/dehydratase	----------	4.084322166
Sh04_g026040	Cinnamoyl-CoA reductase-like protein 3	NAD-dependent epimerase/dehydratase	----------	2.791723444
Sh04_g019970	4-coumarate:coenzyme A ligase 2	AMP-dependent synthetase/ligase	----------	2.702751828
Sh04_g018310	Cellulose synthase-like protein E2	----------	0.842921122	----------
Sh02_g015820	Cellulose synthase-like protein E6	----------	-1.20394915	----------

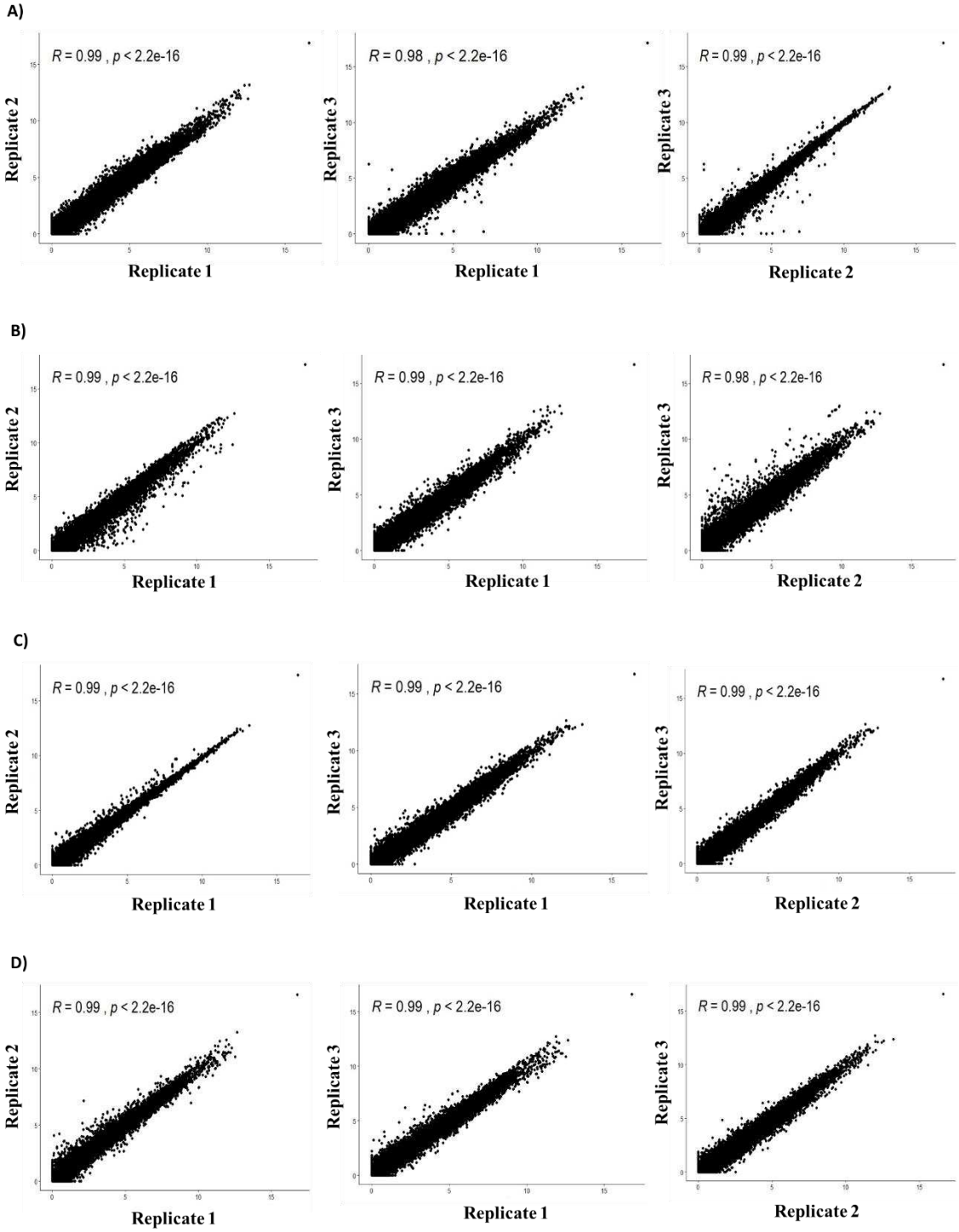

Figure S1. Pairwise comparison of Pearson´s Correlation Coefficients of log_2-transformed TPM values among biological replicates of sugarcane infested with *D. saccharalis* using STP genome as a reference source for read mapping. (A) R values among replicates of RB867515 control treatment; (B) R values among replicates of RB867515 infested treatment; (C) R values among replicates of SP80-3280 control treatment; (D) R values among replicates of SP80-3280 infested treatment.

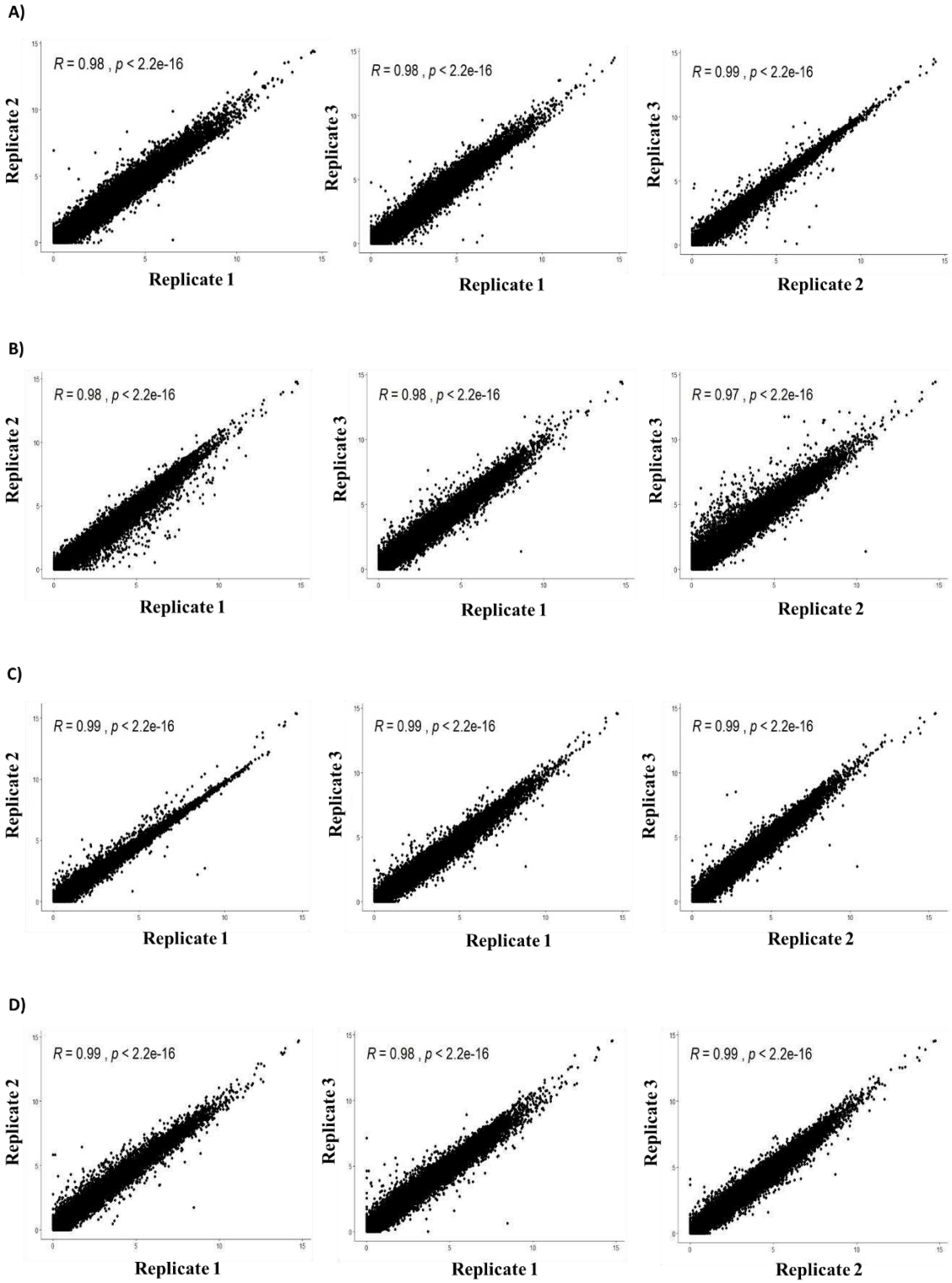

Figure S2. *Pairwise comparison of Pearson´s Correlation Coefficients of log_2-transformed TPM values among replicates of sugarcane infested with D. saccharalis using SUGIT transcriptome as a source reference for read mapping.* (*A) R* values among replicates of RB867515 control treatment; (B) R values among replicates of RB867515 infested treatment; (C) R values among replicates of SP80-3280 control treatment; (D) R values among replicates of SP80-3280 infested treatment.