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Comparison of green and albino individuals of the partially mycoheterotrophic orchid *Epipactis helleborine* on molecular identities of mycorrhizal fungi, nutritional modes, and gene expression in mycorrhizal roots

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Runing title: Comparison of green and albino *Epipactis*

Abstract

Some green orchids obtain carbon from their mycorrhizal fungi, as well as from photosynthesis. These partially mycoheterotrophic orchids sometimes produce fully achlorophyllous, leaf-bearing (albino) variants. Comparing green and albino individuals of these orchids will help to uncover the molecular mechanisms associated with mycoheterotrophy. We compared green and albino *Epipactis helleborine* by molecular barcoding of mycorrhizal fungi, nutrient sources based on ^{15}N and ^{13}C abundances, and gene expression in their mycorrhizae by RNA-seq and cDNA *de novo* assembly. Molecular identification of mycorrhizal fungi showed that green and albino *E. helleborine* harbored similar mycobionts, mainly *Wilcoxina*. Stable isotope analyses indicated that albino *E. helleborine* plants were fully mycoheterotrophic, whereas green individuals were partially mycoheterotrophic. Gene expression analyses showed that genes involved in antioxidant metabolism were up-regulated in the albino variants, which indicates that these plants experience greater oxidative stress than the green variants, possibly due to a more frequent lysis of intracellular pelotons. It was also found that some genes involved in the transport of some metabolites, including carbon sources from plant to fungus, is higher in albino than in green variants. This result may indicate a bidirectional carbon flow even in the mycoheterotrophic symbiosis. The genes related to mycorrhizal symbiosis in autotrophic orchids and arbuscular mycorrhizal plants were also up-regulated in the albino variants, indicating the existence of common molecular mechanisms among the different mycorrhizal types.

Key words: *Epipactis*, mixotrophy, mycoheterotrophy, mycorrhizae, partial mycoheterotrophy, RNA sequencing, stable isotope, transcriptome analysis

Introduction

The largest family in the plant kingdom, the Orchidaceae, comprises approximately 25,000 species (Chase *et al.* 2015). One of the distinctive features of this family is the production of numerous minute seeds that depend on their associations with mycorrhizal fungi for the supply of carbohydrates and other nutrients until they develop into photosynthetic seedlings (Leake 1994).

The mycoheterotrophic nature of orchid protocorms makes them particularly predisposed to the evolution of life-long mycoheterotrophy, retaining their achlorophyllous status throughout their entire lifecycle (Leake 1994). Indeed, full mycoheterotrophy is surprisingly common among orchids, with more than 1% of all species having completely lost the ability to photosynthesize (Bidartondo 2005). This strategy probably allows them to colonize the dark forest understory and to occupy niches less accessible by photosynthetic plants (Bidartondo *et al.* 2004). Though the vast majority of orchids develop photosynthetic pigmentation with putative full autotrophy at adulthood (Cameron *et al.* 2006), several linages of orchids appear to adopt a partially mycoheterotrophic strategy that allows them to obtain carbon from their mycorrhizal fungi, as well as from their own photosynthesis (Gebauer & Meyer 2003). The trophic status of a plant appears to be an important factor determining the type of mycorrhizae they harbor. The majority of putatively autotrophic orchids form associations with fungi belonging to the anamorphic-form genus *Rhizoctonia* in the Basidiomycota (Roberts 1999). This is in contrast to most fully mycoheterotrophic and partially mycoheterotrophic species, which interact mainly with ectomycorrhiza-forming fungi, such as the Sebacinales, Russulaceae, and Thelephoraceae, suggesting that their ultimate source of carbon is the photosynthate produced by nearby trees (Selosse & Roy 2009 but also see Ogura-Tsujita *et al.* 2009; Lee *et al.* 2015; Gebauer *et al.* 2016).

The partially mycoheterotrophic state is often considered to be an intermediate evolutionary step toward full mycoheterotrophy because phylogenetic analyses have shown that full mycoheterotrophy evolves after the establishment of partial mycoheterotrophy, rather than through a direct shift from autotrophy to mycoheterotrophy (Selosse & Roy 2009; Motomura *et al.* 2010). Some partially mycoheterotrophic orchids, such as *Epipactis* and *Cephalanthera* species, produce fully achlorophyllous leaf-bearing variants that can reach almost the same size as their green counterparts (Selosse & Roy 2009). The genetic basis for this albinism remains unknown, but such albinism could result from permanent mutations, as suggested by the stability of this phenotype over a period of years (Tranchida-Lombardo *et al.* 2010; Roy *et al.* 2013). Notably, these albinos exhibit a physiological ecology distinct from that of their green counterparts but the same as that of fully mycoheterotrophic plants, having a highly elevated ^{13}C: ^{12}C ratio (Abadie *et al.* 2004; Julou *et al.* 2005; Stöckel *et al.* 2011).

Therefore, examining mixed populations of green and albino variants in species that usually adopt a partially mycoheterotrophic lifestyle provides a unique opportunity to investigate the physiological differences between partial mycoheterotrophy and full mycoheterotrophy (Roy *et al.* 2013). Evolutionary shifts from autotrophy to mycoheterotrophy are usually accompanied by the coevolution of a broad range of other phenotypes, including a reduction of vegetative structures, degeneration of the stomata, changes in the pattern of dormancy, and the development of novel defenses against herbivores (reviewed by Imhof *et al.* 2013; Hynson *et al.* 2013; Waterman *et al.* 2013). However, albino mutants of partially mycoheterotrophic orchids do not possess some of the characteristics associated with the usual mycoheterotrophic evolution because some traits are inherited intact from photosynthetic individuals. This indicates that the transition to full mycoheterotrophy requires the progressive coevolution of these additional traits, while the sudden loss of photosynthesis (i.e., albinism) leads to the production of unfit plants, even though they can parasitize their fungal partners throughout their entire lifecycle (Roy *et al.* 2013).

Albino variants of partially mycoheterotrophic species undoubtedly show increased dependence on their mycorrhizal fungi as a source of carbon. Therefore, green and albino variants of partially mycoheterotrophic orchids provide a fascinating model for comparing the physiological changes that occur in the mycorrhizae of partially mycoheterotrophic and mycoheterotrophic orchids that share similar genetic backgrounds (Selosse & Roy 2009). Although some studies have investigated the spectrum of green and albino variants of mycorrhizal fungi using molecular identification (Selosse & Roy 2009), no previous studies have conducted a detailed assessment of the molecular physiology of the two variants. Indeed, the molecular mechanisms underlying orchid mycorrhizal symbiosis remain poorly understood (Selosse 2014; Zhao *et al.* 2014). Since previous studies have only focused on putative autotrophic orchids that form associations with fungi belonging to *Rhizoctonia* (Perotto *et al.* 2014; Valadares 2014; Zhao *et al.* 2014), further investigations are needed.

In the current study, we focused on the coastal orchid *Epipactis helleborine* var. *sayekiana*. *E. helleborine* is one of the most widespread orchid species in Eurasia and North Africa having associations with ectomycorrhizal fungi (Bidartondo *et al.* 2004). Japanese *E. helleborine* is commonly found in cool mountainous areas, while the coastal populations occur in the Japanese black pine (*Pinus thunbergii)* forest (Makino 1918).

Coastal Japanese *E. helleborine* is often separated at the variety level as *E. helleborine* var. *sayekiana*, whereas inland populations are recognized as *E. helleborine* var. *papillosa* (Suetsugu 2013).

We identify the mycorrhizal fungi of green and albino variants to confirm that green and albino *E. helleborine var. sayekiana* harbored similar mycobionts, and we characterize the nutritional modes by assessing the natural abundance of ^{13}C and ^{15}N in the two variants as well as the surrounding autotrophic plants. After confirming the partially mycoheterotrophic and mycoheterotrophic status of green and albino variants, we aimed to characterize the molecular physiology of the green and albino variants of this species by analyzing gene expression in orchid mycorrhizae of the two variants by RNA-seq and cDNA *de novo* assembly. To the best of our knowledge, this study represents the first genome-wide gene expression profile of orchid mycorrhizal roots collected from a natural habitat.

Materials and Methods

Study species and site

A field study was conducted in a plantation of *Pinus thunbergii* in Fujisawa City, Kanawagawa Prefecture, which is situated in a warm, temperate area of Eastern Japan. The investigated population of *E. helleborine* var. *sayekiana* (hereafter *E. helleborine*) encompasses both green and albino individuals (Fig. 1). Salmia (1986) reported albino as well as variegated individuals in a Finnish *E. helleborine* population. Salmia (1989) also noted that albinos sometimes undergo greening (and vice versa), suggesting some plasticity in the albino phenotype. However, the investigated population harbors phenotypically stable albinos, for at least nine years, and no variegated individuals have been found.

Molecular identification of mycobionts

Root systems were harvested from four green (G1 to G4) and four albino (A1to A4) *E. helleborine* individuals on 4 June, 2014. Since our preliminary microscopic observation revealed that most of the cortical cells are filled with pelotons in fresh brownish root tissues, three root sections of such brownish tissues were collected per individual without disturbing the rhizome and other roots. The root samples were preserved in 100% ethanol before DNA extraction.

DNA was extracted from approximately 50 mg of mycorrhizal roots from each of the four green and four albino individuals of *E. helleborine*, using a DNeasy Plant Mini Kit (Qiagen). A primer pair ITS1F/ITS4 (Gardes & Bruns 1993) was used to amplify the internal transcribed spacer (ITS) region of the nuclear ribosomal RNA gene (rDNA). The PCR mixture contained 1 µl of the extracted DNA solution, 0.5 units of Taq polymerase, 0.25 µM of each primer, 200 µM of each deoxynucleotide triphosphate, and 2 µl of the supplied PCR buffer in a total volume of 20 µl. The PCR program, which was performed on a Thermal Cycler GeneAtlas G02 (Astec, Fukuoka, Japan), was as follows: initial denaturation at 94°C for 2 min, followed by 30 cycles at 94°C for 20 s, 55°C for 30 s, and 72°C for 1 min, and a final elongation step at 72°C for 10 min. All PCR products were cloned using the pGEM-T Easy Vector System I (Promega), and 16 or 24 colonies with DNA inserts were arbitrarily selected from each sample for sequencing. The DNA inserts were sequenced using the dideoxysequencing method with a BigDye Terminator v3.1 Cycle Sequencing Kit (Applied Biosystems, Tokyo, Japan) in a 3130 Genetic Analyzer

(Applied Biosystems). Multiple sequence alignments and neighbor-joining analysis (Saitou & Nei 1987) with a Kimura two-parameter model (Kimura 1980) were carried out using MEGA version 6 (Tamura *et al.* 2013) with a bootstrap analysis of 1000 replications (Felsenstein 1985). After division of all fungal ITS sequences into phylotypes, representative sequences were selected from each type. BLAST searches (Altschul *et al.* 1997) against the GenBank database were performed for the selected sequences, and some related sequences were downloaded as well. A second neighbor-joining analysis was performed for the selected and downloaded sequences in the same manner. The phylogenetic tree obtained in the second analysis was constructed using Treeview (Page 1996).

Relative quantification of fungal DNA

Root and shoot DNA samples were extracted from the four green and four albino individuals of *E. helleborine* as described above. Independent samples of 6 ng of total DNA were amplified with two primer pairs: ITS1F/ITS4 as described above, and EhUBQF (5′-CGA GAT ATC AGC AAC GGT AAC A-3′)/EhUBQR (5′-GCA GAG GAA TAC GCA AAC CC-3′). The EhUBQF/EhUBQR primer pair was designed based on the sequence of contig TR46759, which shares substantial sequence similarity with the *Cymbidium faberi* ubiquitin mRNA, *UBQ1*, as an internal control for *E. helleborine*. Real-time quantitative PCR was performed on a LightCycler 480 (Roche Diagnostics, Mannheim, Germany). The PCR program was as follows: initial denaturation at 94°C for 2 min, followed by 30 cycles at 94°C for 20 s, 55°C for 30 s, 72°C for 1 min, and a final elongation step at 72°C for 10 min. Individual Ct values of ITS were normalized to that of the internal control gene.

Stable isotope analysis

All samples were collected on 25 June, 2014. The collection of leaves from *Epipactis* and the reference autotrophic plants was limited to an area of 1 m^2 from an individual of the target species, and autotrophic reference plants were only sampled from understory saplings. This strategy was used to limit the variability of environmental factors, such as atmospheric CO_2 concentrations, isotope signatures (which could affect plant C isotope values), and soil type (which could affect N isotope values (Gebauer and Schulze, 1991)). Each collection site contained one green and/or albino *Epipactis helleborine*, plus an individual of at least two species that could be used as a reference plant representing the autotrophic understory. In total, six and three samples of green and albino *E. helleborine* were collected as well as 19 samples of autotrophic plants from eight collection sites (Table S1).

The collected leaves were dried at 60°C for four days and then cut into fine pieces in a small glass bottle using small scissors. The abundances of stable C and N isotopes were measured using a Delta V Advantage mass spectrometer (Thermo Fisher Scientific, Bremen, Germany) coupled with a Flash EA 1112 elemental analyzer (Thermo Fisher Scientific), in which phenylalanine was used as a standard for C and N. The relative abundances of stable isotopes are presented as $\delta^{13}C$ and $\delta^{15}N$ according to the equation $\delta^{15}N$ or $\delta^{13}C = (R_{sample} / R_{standard} - 1) \times 1000$ [‰], where R is the molar ratio of the stable isotopes, $^{13}C/^{12}C$ or $^{15}N/^{14}N$. One-way ANOVA was applied to evaluate the differences in $\delta^{13}C$ or $\delta^{15}N$ among green *E. helleborine*, albino *E. helleborine*, and the collected autotrophic plant species. The means were compared by Tukey-Kramer tests. The relative contribution of fungal association for the C gain in green (photosynthetic) *E. helleborine*

(%Egdf) was calculated using the equation %Egdf = (($\delta C_{Eg} - \delta C_R$) / ($\delta C_{Ea} - \delta C_R$)) x 100 [%], as described in Gebauer and Meyer (2003), with slight modifications, where δC_{Eg} is the values of $\delta^{13}C$ in green individuals of *E. helleborine*, and δC_{Ea}, and δC_R are the means of albino *E. helleborine*, and the surrounding autotrophic plant species (reference plants). For the values of $\delta^{13}C$ and $\delta^{15}N$ in green or albino *E. hellevorine*, enrichment factors (εC_E) were calcurated according to $\varepsilon C_E = \delta C_E - \delta C_R$, where δC_E is the values of $\delta^{13}C$ or $\delta^{15}N$ in green or albino individuals of *E. helleborine*, and δC_R is the means of $\delta^{13}C$ or $\delta^{15}N$ in autotrophic reference plants.

RNA extraction

Root systems were harvested from each of three green and three albino *E. helleborine* individuals on 4 June, 2014. Mycorrhizal root tissues were preserved in a RNAlater storage solution (Sigma-Aldrich, Saint Louis, MO, USA). The root samples were stored at 4°C until they were used for RNA extraction.

Total RNA was extracted from 50 mg of *E. helleborine* roots using an RNeasy Plant Kit (QIAGEN) in accordance with the manufacturer's protocol. The RNA was treated with RNase-free DNase I to remove residual genomic DNA and cleaned using an RNeasy Mini Kit (QIAGEN) according to the manufacturer's protocol. The quality and quantity of the purified RNA were confirmed by measuring the absorbance at 260 nm and 280 nm (A260/A280) using a Nano-drop ND-1000 spectrophotometer (LMS Co. Ltd.) and by electrophoresis using an Agilent 2100 Bioanalyzer (Agilent Technologies).

Library preparation and transcriptome sequencing

RNA sequencing libraries were constructed from 1.0 μg total RNA using a TruSeq RNA

Sample Prep Kit v2 and a TruSeq Stranded mRNA LT Sample Prep Kit (Illumina) following the manufacturer's instructions. Following purification, the mRNA was fragmented using Elute, Prime, and Fragment Mix (Illumina) at 94°C. A first-strand cDNA synthesis was then carried out using SuperScript II Reverse Transcriptase (Invitrogen Corp.) and random primers, followed by second-strand cDNA synthesis. The products were purified and enriched by PCR to create the final cDNA library. The quality and quantity of the cDNA library were confirmed by electrophoresis with Agilent 2100 Bioanalyzer (Agilent Technologies) and real-time PCR with ABI 7500 Real Time PCR system (Applied Biosystems). Multiplex sequencing of paired-end reads was performed on an Illumina HiSeq 1500 instrument at NIBB Core Research Facilities, followed by raw data processing, base-calling, and quality-control with the manufacturer's standard pipeline using RTA, OLB, and CASAVA.

Construction and *de novo* assembly

Prior to assembly, the reads were trimmed to remove low-quality ends (<QV30), and adapter sequences (parameter: –o 7) using the cutadapt program (http://code.google.com/p/cutadapt). Reads shorter than 50 bp were removed. *De novo* assembly of the trimmed reads derived from both green and albino was conducted using Trinity (ver. 2.0.6) (Grabherr *et al.* 2011) with default settings.

To predict the origins of the contigs, i.e., whether they derived from plants or fungi, BLASTX searches of the *de novo* assembly data were performed against the NCBI non-redundant protein (nr) database. The coding sequences within putative plant or fungal transcript sequences were predicted using TransDecoder with default settings (Hass *et al.* 2013). To reduce the sequence redundancy of the assembled transcript sequences, similar contigs were grouped using CD-HIT (parameter: -c sequence identity threshold = 0.98) (Li & Godzik 2006), which was then used as a reference model for the following analysis.

Differential expression analysis

Data from three biological replicates was used in this analysis. The paired-end reads were mapped to each plant and fungal reference genome assembly using Bowtie2 in the end-to-end mode (Langmead & Salzberg 2012). Transcript abundance was then estimated using eXpress (ver. 1.5.1) (Roberts & Pachter 2013). Differences in library size were corrected through Trimmed Mean of M-values normalization, and edgeR (Robinson *et al.* 2010) was used to identify differential expression genes (DEGs) between green and albino at FDR < 0.05.

Gene annotation and Gene ontology analysis

DEGs were annotated using BLAST searches against the the NR database for plant and fungal sequences using Blast2GO tool (Conesa *et al.* 2005). Gene ontology (GO) terms associated to blast hits were also obtained by the Blast2GO annotation procedure. GO enrhichment analysis of plant and fungal DEGs was performed using Blast2GO with one-sided Fisher's exact test (FDR < 0.05). The enrichment of plant and fungal DEGs was calculated by comparing the assembled reference genome for plant and fungi, respectively.

Results

Molecular identification of mycobionts

To identify the mycobionts, we examined the ITS sequences amplified from the total

DNA from root samples. In total, we obtained 128 fungal ITS rDNA sequences from four green and four albino individuals (Table 1). Among these, 98.2% (55/56) of the sequences from green individuals and 90.3% (65/72) of the sequences from albino individuals were identified as belonging to the Ascomycota genus *Wilcoxina* (Table 1). These sequences were divided into three groups, *Wilcoxina* 1 (73 sequences), *Wilcoxina* 2 (43 sequences), and *Wilcoxina* 3 (four sequences), and the fungi in all three groups were detected in both green and albino individuals (Table 1). Their phylogenetic relationship is shown by representative sequences (LC142800-LC142816), in which two sequences of the mycobionts of *E. helleborine* (AB428785 and AB428784) previously recognized by Ogura-Tsujita and Yukawa (2008) were nested within *Wilcoxina* 1 and 2 (Fig. 2). Other minor fungi, three *Exophiala*, two *Clavulina*, one *Astraeus*, and a few other fungi (LC143816-143823), were also detected in the roots (Table S2).

We also quantified the total amounts of fungal DNA with real-time quantitative PCR, comparing the levels of ITS to the plant's *UBQ* gene. Fungal DNA was detected in the roots of both green and albino plants. The amount of fungal DNA was significantly lower (approximately half) in albino *E. helleborine* than in green *E. helleborine* (Fig. 3). Small amount of the fungal DNA, which was eighteen percent of the roots of albino *E. helleborine*, was also found in the shoot, implying the existence of endophytic fungi associated with shoots. The amount of fungal DNA in the roots of albino can be distinguished from that in the shoots because the *p*-value is relatively low (0.06).

Stable isotope analysis

To examine the trophic status of *E. helleborine*, we measured the $^{13}C/^{12}C$ and $^{15}N/^{14}N$ ratios of green and albino plants. Because ectomycorrhizal fungi have higher levels of the heavier isotopes of these elements (Gebauer & Meyer 2003), higher $^{13}C/^{12}C$ and $^{15}N/^{14}N$ ratios, measured as high $\delta^{13}C$ and $\delta^{15}N$, would indicate that the plants derive some of their C and N from the fungal association. Six and three individuals of green and albino *E. helleborine* individuals were applied for stable isotope analysis as well as two to six individuals of surrounding autotrophic plant species, including *Oplismenus undulatifolius*, *Oxalis corniculata*, *Paederia scandens*, *Commelina communis*, and *Vitis ficifolia* var. *lobata* (Table 2). Since only two samples were obtained for *Oxalis corniculata*, this plant was excluded from the comparisons of $\delta^{13}C$ and $\delta^{15}N$ means. $\delta^{13}C$ of green *E. helleborine* was significantly more depleted than that of albino *E. helleborine* and significantly more enriched than the three autotrophic plant species *P. scandens*, *C. communis*, and *V. ficifolia* var. *lobata* ($p<0.01$), suggesting its partial mycoheterotrophic nutritional mode (enrichment factor for ^{13}C of green and albino *E. helleborine* shown as Means ± SD: 3.0 ± 0.7 ‰ and 7.2 ± 0.6 ‰, respectively). The contribution of fungal association for the C gain in green *E. helleborine* was calculated to be 41.7 ± 9.4%.

No significant differences were observed for $\delta^{15}N$ values between green and albino *E. helleborine*, yet they were significantly higher than the four reference autotrophic plant species (enrichment factor for ^{15}N of green and albino *E. helleborine*: 12.7 ± 2.2‰ and 14.8± 1.3‰, respectively).

Differential gene expression between green and albino variants

To identify genes involved in the interaction between mycoheterotrophic plants and ectomycorrhizal fungi, we compared the transcriptomes of green and albino *E. helleborine* individuals. We obtained 368 million (156 Mb) reads and assembled them into contigs using the *de novo* assembler Trinity to build reference gene models. We classified the contigs into sequences of plant, fungal, and unknown origin (61,007, 47,779, and 5,132 contigs, respectively) (Table S3). We predicted 28,557 and 27,123 non-redundant open reading frames from the plant and fungal categories, respectively (Table S3). Because the gene models in the plant category likely represent the gene set of the host plant *E. helleborine*, whereas those of the fungal category likely represent the gene set of the symbiont fungi *Wilcoxina*, we conducted DEG analyses separately.

In the genes of plant origin, we identified 493 DEGs, including 211 that were up-regulated and 282 that were down-regulated in albino *E. helleborine* (Table 3). To characterize the DEGs, we identified over-represented GO terms among plant DEGs. In the plant reference genome, a total of 427 genes were assigned to GO classes with 36 functional terms in up-regulated genes of albino plants ($FDR < 0.05$; Table 4). On the other hand, there were no significantly GO terms enriched in the DEGs of green plants. Many GO terms involved in membrane activity on Cellular Component and transport activity on Molecular Function or Biological Process were significantly over-represented in up-regulated genes of albino *E. helleborine* (Table 4). Indeed, several transporter genes showed specific expression patterns (Table S4): 18 genes, including two isoforms, were up-regulated, and seven genes were down-regulated in albino *E. helleborine*. The GO term 'regulation of phytohormone levels (GO:0010817)' was also over-represented in up-regulated genes of albino plant (Table 4). In fact, genes related to auxin response or signaling (TR31542, TR36150, TR39484, TR40989, TR44008, TR66633, and TR101941), gibberellin biosynthesis or response (TR24202, TR33838, and TR40127) and cytokinin (TR64539), and response to ethylene (TR1508) were significantly expressed at higher levels in albino plants (Table S4). Additionally, we found some genes categorized into secondary metabolism. For example, a caleosin-related gene (TR8579) encoding a membrane protein of oil bodies where phytoalexins are synthesized and a flavonoid biosynthetic enzyme were down-regulated in albino *E. helleborine*, but on the other hand, a chalcone synthase (TR55196) and caffeoyl-CoA methyltransferase (TR99894) were up-regulated in albino *E. helleborine* (Table S4). Genes encoding an antioxidant function, such as peroxidase precursor (TR933), dehydrogenase (TR14662), and ferredoxin (TR17474) were also up-regulated in albino *E. helleborine* (Table S4). We also identified homologous genes involved in arbuscular mycorrhizal (AM) symbiosis or rhizobium-legume symbiosis; e.g., subtillisin (TR46306 and TR75866), glycerol-3-phospate acyltransferase (GPAT; TR26368 and TR54777) which possibly function as REDUCED ARBUSCULAR MYCORRHIZA2 (RAM2), and nodulin family protein (TR5976, TR47495, TR88200, and TR48905) (Table S4). These genes were up-regulated in albino *E. helleborine*, except for one nodulin MtN3 family protein gene (TR48905).

In the genes of fungal origin, we identified 990 DEGs, including 986 that were up-regulated and four that were down-regulated in the symbionts of albino *E. helleborine*. We also identified over-represented GO terms among fungal DEGs. We assigned a total of 18,345 genes in the fungal reference genome and categorized into GO classes with 244 functional terms in up-regulated genes in albino plants (Table 5). Several GO terms of fungal DEGs potentially involved in transport (e.g., GO:1901677, GO:0000295, GO:0005337, GO:0015216) were over-represented in the symbionts of albino *E. helleborine*, as well as in the albino plants themselves. In fact, the expression levels of genes encoding three major facilitator superfamily transporters (TR38662, 47233, and TR49557), a nucleoside transporter, a NupC family nucleoside transporter (TR45156) and nuclear transport factor 2 (TR37712), and a phosphate transporter, were drastically altered in the albino symbiont (logFC > 10; Table S5). Moreover, fungal GO terms involved in cell redox regulation, e.g., 'oxidoreductase activity (GO:0016491, GO:0016616, and GO:0016667)', 'catalytic complex (GO:1902494)', and 'oxidation-reduction process (GO:0055114),' were also strongly associated with the symbionts of albino *E. helleborine* (Table 5). The expression levels of many genes that lead to change in cellular process, which were categorized into the GO term involved in mycelium development (GO:0043581) were also over-represented (Table 5). Of the four genes down-regulated in the symbionts of albino *E. helleborine*, two were annotated as alcohol dehydrogenase, whereas the others were not annotated (Table S5).

Discussion

Photosynthesis is often considered to be a defining feature of the plant kingdom; therefore, examination of the evolution of fully mycoheterotrophic plants that have lost their photosynthetic capacity remains one of the most interesting and challenging topics in plant biology. Although the process leading to the acquisition of plastids has been well-studied (Keeling 2010; Okamoto & Inouye 2005), the factors leading to the loss of photosynthesis and the transition to full mycoheterotrophy are less well-known. The discovery of partially mycoheterotrophic orchids that produce fully achlorophyllous, leaf-bearing variants has provided an ideal model for investigating the evolution of mycoheterotrophy within similar genetic backgrounds (Selosse & Roy 2009; Roy *et al.* 2013). In the current study, we investigated the molecular and physiological ecology of the green and albino variants of *E. helleborine*. In addition to using a combination of stable isotope analysis to determine the nutritional modes of the plants and molecular analysis to identify specific fungal partners, which are the most frequently used tools to characterize the mycoheterotrophic lifestyle, we also performed genome-wide gene expression profiling, a technique that has not previously been used to study mycoheterotrophic plants.

Nutritional mode and mycorrhizal associations of green and albino variants

Our data showed that both the green and albino variants of *E. helleborine* in the investigated population (i.e. *E. helleborine* var. *sayekiana*) were significantly more enriched in ^{13}C than the autotrophic plants growing in close proximity. Furthermore, the ^{13}C enrichment of the *E. helleborine* albinos (7.2 ± 0.6‰) fell within the range reported for mycoheterotrophic plants from temperate regions (7.2 ± 1.6‰; Preiss and Gebauer 2008). The *E. helleborine* albinos also had δ^{15}N levels higher than those of the surrounding autotrophic plants (14.8 ± 1.3‰), with values slightly higher than those reported for other temperate mycoheterotrophs (12.0 ± 1.7‰; Preiss and Gebauer 2008). These results confirmed the partially mycoheterotrophic and mycoheterotrophic status of green and albino *E. helleborine* revealed in Gonneau et al. (2014). Comparison of their δ^{13}C values with a linear mixing model based on an albino as 100% carbon gain from fungi and autotrophic plants as 0% baseline (Gebauer & Meyer 2003) revealed that the green *E. helleborine* obtained approximately 41.7 ± 9.4% of their total C from the mycobionts. These values fall well within the range reported for other partially mycoheterotrophic orchids, including *E. helleborine*, which can display a highly variable degree of dependence on their fungal partners depending on the species, light intensity, and growth status (Gebauer & Meyer 2003; Bidartondo *et al.* 2004; Abadie *et al.* 2006; Liebel *et al.* 2010; Preiss *et al.* 2010; Stöckel *et al.* 2014; Gonneau *et al.* 2014).

Our molecular analysis of mycorrhizal fungi revealed that both the green and albino variants of *E. helleborine* formed associations almost exclusively with the genus *Wilcoxina*. Since ectendomycorrhizal associations have been reported between *Pinus* trees and *Wilcoxina* species (Yu *et al.* 2001), the mycorrhizae formed on *Pinus thunbergii* by the *Wilcoxina* fungi in the study site may not be ectomycorrhizae but ectendomycorrhizae, and the C source of the *E. helleborine* is suggested to be photosynthate from the *Pinus thunbergii.* Over 90% of the mycobionts were identified as *Wilcoxina* in both green and albino *E. helleborine* in this study, which were divided into three phylogenetic groups, and the mycobionts in all three groups were found in both green and albino *E. helleborine*,. Though entire fungal community in roots of *E. helleborine* is not revealed because of the limited sampling and sequencing, these results indicate that the green and albino *E. helleborine* in this habitat have similar mycobionts with dominance of *Wilcoxina* fungi. Ogura-Tsujita and Yukawa (2008) also found that *E. helleborine* on Japanese coastal dunes mainly associated with *Wilcoxina* fungi. Since one of the coastal dunes used in their analysis (C5 in Ogura-Tsujita & Yukawa 2008) is the same as the sampling site of the current study, our results confirm their results (Ogura-Tsuita & Yukawa 2008). However, previous studies have also suggested that *E. helleborine* in other populations forms associations with a wide range of taxa among ectomycorrhizal fungi, including the genera *Wilcoxina, Tuber*, *Sebacina*, *Tomentella, Genea, Hymenogaster*, and *Hydnotrya* (Bidartondo *et al.* 2004: Ogura-Tsuita & Yukawa 2008; Liebel et al. 2010; Tesitelova *et al.* 2012; Stöckel *et al.* 2014). In general, autotrophic orchids interact with a diverse range of saprotrophic rhizoctonia-forming fungi, whereas fully mycoheterotrophic orchids tend to be highly specialized to a phylogenetically narrow range of ectomycorrhizal fungi (Selosse & Roy 2009). Mycorrhizal associations of partially mycoheterotrophic orchids may represent a transitional stage as suggested in *Cymbidium* species by Ogura-Tsujita et al. (2012). The shift in mycorrhizal association from soil-inhabiting rhizoctonia to ectomycorrhizal fungi is thought to have been driven by better access to C supplies provided by the latter (Selosse & Roy 2009). Our finding that both the green and albino variants of *E. helleborine* in the investigated population were almost exclusively associated with the *Wilcoxina* species group suggests that the study population might have taken a step toward fungal specificity. However, it is also probable that mycorrhizal associations may simply reflect the poor diversity of fungal communities in the investigated population.

The evolutionary processes that determine fungal specificity are still unclear, although two possible mechanisms have been suggested: (i) Partner filtering (selection of the most beneficial mutualist from a community of potential symbionts) on behalf of the plant, in which the best partner to meet its nutrient demands is chosen from the existing fungal community; and (ii) partner filtering on behalf of the fungi, whereby the parasitic-like interaction is rejected by most members of the fungal community until a susceptible fungus is "tricked" into forming an association with the plant (Bruns *et al.* 2002; Egger & Hibbett 2004; Hynson & Bruns 2009). In either case, it has been argued that once an appropriate fungal partner has been found, the plant fine-tunes its physiology to adapt to that particular fungus (Bidartondo & Bruns 2002; Hynson & Bruns 2009). It is therefore possible that the high degree of specialization toward certain mycorrhizal fungi found in *E. helleborine* could have facilitated the carbon requirement of the albino mutants (but also see Abadie *et al.* 2004; Julou *et al.* 2005; Zimmer e*t al.* 2008).

Differential gene expression between green and albino variants

High-throughput RNA sequencing and *de novo* read assembly are powerful, cost-efficient tools for analyzing global transcriptome changes, especially in species without reference genomes, and the application of these techniques can provide critical insight into the evolution and mechanistic basis of plants with unusual modes of nutrition. In the present study, we compared the transcriptomes of green and albino variants of the same species and with similar genetic backgrounds, which provided a unique opportunity to investigate the molecular mechanisms associated with mycoheterotrophy. Based on the notion that albino variants of otherwise partially mycoheterotrophic orchids should exhibit increased dependence on mycorrhizal fungi (Selosse & Roy 2009), we expected that symbiosis-related genes would be more highly expressed in the albino variants than in the green ones and, accordingly, investigated the functions of genes that were upregulated in the mycorrhizal roots of albino plants, in order to elucidate the molecular mechanisms underlying mycoheterotrophic symbiosis.

Both the albino variants and their associated fungi exhibited increased expression of genes involved in antioxidant function such as genes encoding thioredoxin, glutathione peroxidase, and catalase-peroxidase thioredoxin (Tables S4 and S5), indicating that both organisms were exposed to greater oxidative stress than their green counterparts. Since the digestion of pelotons has been reported to coincide with the peak activity of antioxidant enzymes in the mycorrhizal protocorms of some autotrophic orchids (Blakeman *et al.* 1976), it is possible that the upregulation of antioxidant enzymes in the albino variants indicated augmented peloton digestion. Indeed, although the expression level of many genes categorized into mycelium development (GO: 0043581) was higher in albino plants, the lower level of fungal DNA in the mycorrhizal tissues of albino plants also suggest albino plants exhibit more frequent peloton digestion, possibly in order to increase the fungi-to-plant carbon flux (Fig. 3). These findings also provide indirect support for the common notion that peloton digestion occurs in a process akin to phagocytosis (e.g., Johnson & Nylund 1979; Peterson & Currah 1990; Peterson *et al.* 1998; Bougoure *et al.* 2014), while our results do not exclude the possibility that live fungal pelotons also contribute to the transfer of carbon and nitrogen in the mycorrhizal symbiosis of *E. helleborine*. It is important to note that Bougoure *et al.* (2014) described two other potential pathways for the transfer of nutrients between the orchid and its mycorrhizal fungi: (1) biotrophic: the uni- or bi-directional transfer of nutrients across an active interface formed between the plant and fungus and (2) some combination of biotrophic transfer and necrotrophic transfer. Indeed, Kuga *et al.* (2014) reported that carbon and nitrogen are transferred from both live and degenerating pelotons to the symbiotic protocorms of the photosynthetic orchid *Spiranthes sinensis*. Further study is needed to integrate information from different perspectives such as direct observation of the fungal conditions forming pelotons within roots.

Surprisingly, we found that most of the fungal DEGs were upregulated in the albino *E. helleborine* variants, and among these genes, GO terms for membrane function, translation, and cytoplasmic component were highly represented. These results suggest that dynamic changes could occur in the cell states of fungal symbionts, depending on the nutritional mode of their host plants. In particular, a gene encoding a G protein-coupled receptor (Gpr) protein, *gpr-1* like plasma membrane protein (TR39115), was upregulated in the symbionts of albino *E. helleborine*. In *Saccharomyces cerevisiae*, Gpr homologs (e.g., Gpr1p) function as nutrient sensors, being transcriptionally induced by nitrogen starvation as well as the presence of fermentable sugars (Lorenz *et al.* 2000). Meanwhile, *ace1*, which encodes a putative zinc finger transcription factor and functions as an activator of cellulase expression (Saloheimo *et al.* 2000), was also upregulated in the symbionts of albino *E. helleborine*. Thus, the symbionts probably seem capable of recognizing the nutrient status of albino *E. helleborine.*

In addition, GO analysis also revealed the enrichment of transport-related genes in both the albino *E. helleborine* variants and their associated fungi may indicate the importance of active metabolite transport in mycoheterotrophic interactions. For example, the expression of a gene that encodes a putative bidirectional sugar transporter (SWEET), from the nodulin MtN3 protein family, was upregulated in the albino plants. SWEET proteins are also activated in the protocorms of *Serapias*, a genus of autotrophic orchids, in response to inoculation with orchid mycorrhizal fungi (Perotto *et al.* 2014), and their activation is also important during colonization by biotrophic pathogens, since they facilitate the extraction of sugars from their hosts (Chen *et al.* 2010). We also found that fungal genes that encode major facilitator superfamily (MFS) transporters were significantly upregulated in the albino variants. MFS transporters are involved in the uptake of various nutrients, including sugars, nitrate, phosphate, and nucleosides (Pao *et al.* 1998). For example, the MFS transporter monosaccharide transporter 2 (MST2) of the AM fungus *Glomus* sp. appears to play an important role in the uptake of sugar from plants (Helber *et al.* 2011).

Taken together, these results suggest that the transport of certain metabolites from plants to fungi may behigher in albino variants of *E. helleborine* than in green variants, even though mycoheterotrophic interactions are generally thought to involve the unidirectional flow of nutrients from fungi to plants (Leake 1994; Bidartondo 2005). Similarly, several other studies have also suggested that bidirectional carbon flow occurs in mutualistic mycorrhizal interactions (Abuzinadah & Read 1989; Cameron *et al.* 2008), even though such interactions are generally considered to involve the unidirectional flow of carbon from plants to fungi (Johnson *et al.* 2002). Therefore, bidirectional carbon flux may be important in the maintenance of mycorrhizal symbiosis, regardless of whether the relationship is mutualistic or parasitic.

The results of the present study also provide insight into the molecular mechanisms associated with life-long mycoheterotrophy. Our results indicated that orthologous genes encoding GPAT (*RAM2*) and subtilisin, which are required for AM colonization (Takeda *et al.* 2009; Gobbato *et al.* 2012), were upregulated in the albino variants and that a gene related to gibberellin biosynthesis (*gibberellin 20 oxidase*), which reduces hyphal colonization and arbuscule formation during AM symbioses (Takeda *et al.* 2015), were downregulated. We also found that a gene related to cytokinin degradation, a cytokinin dehydrogenase precursor gene, was downregulated in the albino variants, which is notable because cytokinin accumulates in AM-colonized roots (Hause *et al.* 2007). Furthermore, genes encoding auxin efflux carrier components were upregulated in the albino variants, which is important because auxin positively influences AM colonization, and the auxin efflux facilitator gene *PIN1* can also be activated during the symbioses of autotrophic orchids and AM plants (Gutjahr 2014; Zhao *et al.* 2014).

Our results indicate that a common mechanism at least partially underlies the mycorrhizal symbioses of (partial) mycoheterotrophs, autotrophic orchids, and AM-forming plants because recent studies have reported that genes related to AM symbiosis, such as *RAM1*, nodulin-like genes, and the auxin efflux facilitator gene *PIN1*, can be activated by symbioses in autotrophic orchids, even at the protocorm stage (Perotto *et al.* 2014; Zhao *et al.* 2013; Zhao *et al.* 2014). No GO terms associated with defense responses in *E. helleborine* may also support the conclusion that the relationship between *E. helleborine* and their associated fungi is suggesting a ‘friendly plant–fungus relationship’ (*dixit* Perotto et al., 2014), at least on the plant side. The activation of symbiosis-related genes in albino plants likely represents an adaptation to promote fungal colonization, in order to compensate for their lack of photosynthates.

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Data Accessibility

Raw sequencing reads were deposited in DDBJ sequence read archive under the accession number DRA004437. The assembly of *E. helleborine* and the mycorrhizal symbionts is available in DDBJ transcriptome shotgun assembly database under the accession numbers FX983745-FX984237 and FX984238-FX985227, respectively.

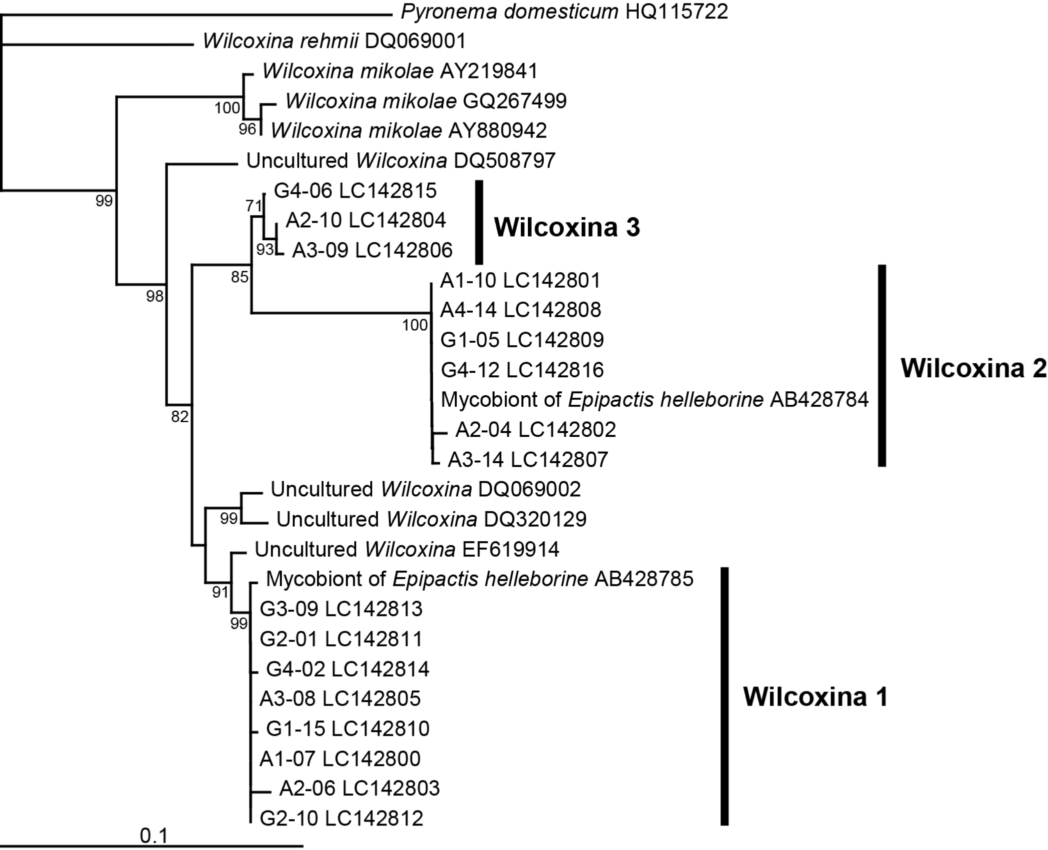
Figure Legends

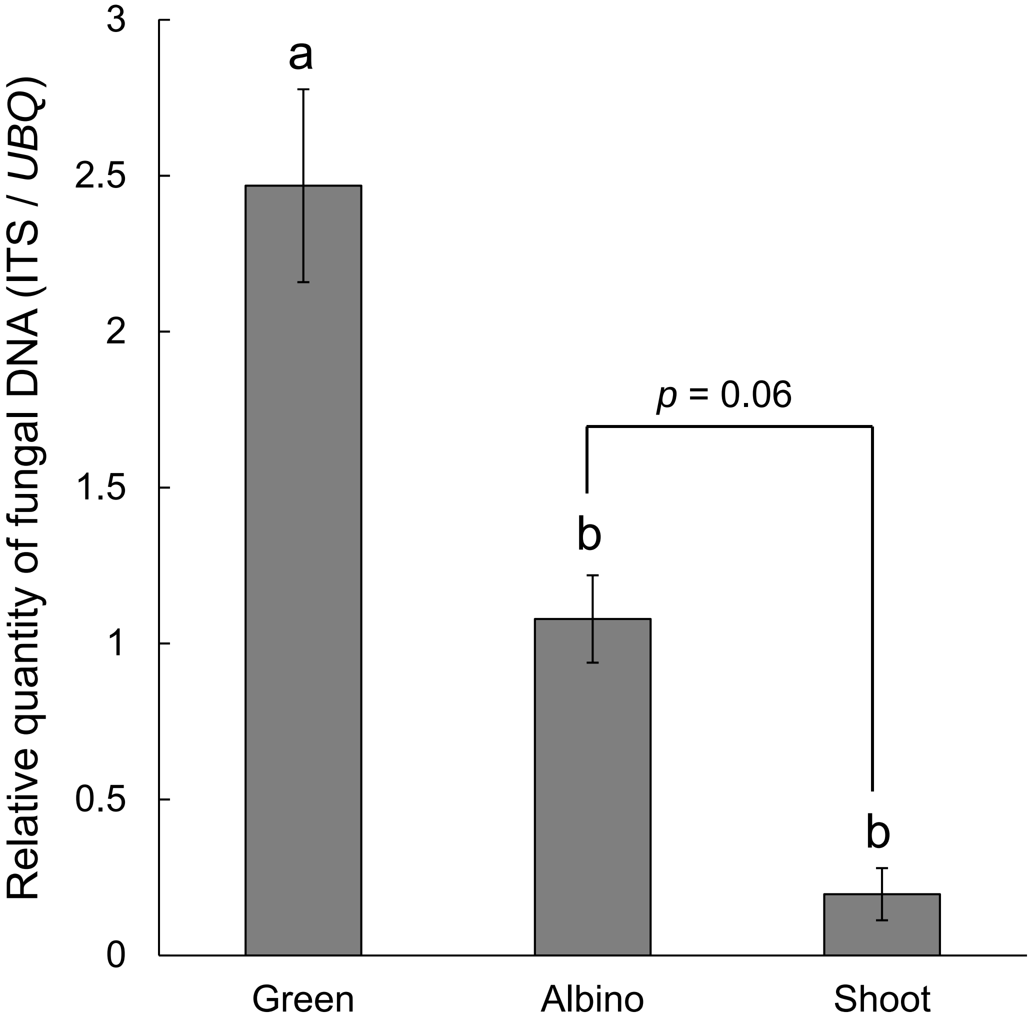
Fig. 1 (a) Albino and (b) green individuals of *Epipactis helleborine* from the investigated population.

Fig. 2 Neighbor-joining phylogenetic tree based on partial sequences (472–482 bps) of the internal transcribed spacer region of the nuclear ribosomal RNA gene (ITS rDNA) of *Wilcoxina* fungi obtained from roots of *Epipactis helleborine*. Each code corresponds to the plant and clone numbers. Phylotypes of the detected fungi (Wilcoxina 1, 2, and 3) are shown. GenBank accession numbers are given for all sequences. The tree is rooted to *Pyronema domesticum* (HQ115722). Bootstrap values with 1000 replications are shown where they exceed 70%. The scale bar shows the number of substitutions per site.

Fig. 3 Relative quantification of fungal DNA in *E. helleborine*. Each bar shows the amount of fungal DNA derived from the roots of green (Green) or albino (Albino) *E. helleborine* or the shoots of albino *E. helleborine* (Shoot). Data represent mean ± SE ($n = 3$ to 4). Different superscripts indicate significant differences between groups ($p < 0.05$, Tukey-Kramer test).


a
b


Pyronema domesticum HQ115722
Wilcoxina rehmii DQ069001
Wilcoxina mikolae AY219841
Wilcoxina mikolae GQ267499
Wilcoxina mikolae AY880942
100
96
Uncultured *Wilcoxina* DQ508797
99
G4-06 LC142815
71
A2-10 LC142804
93
A3-09 LC142806
Wilcoxina 3
85
98
A1-10 LC142801
A4-14 LC142808
100
G1-05 LC142809
G4-12 LC142816
Mycobiont of *Epipactis helleborine* AB428784
A2-04 LC142802
A3-14 LC142807
Wilcoxina 2
82
Uncultured *Wilcoxina* DQ069002
99
Uncultured *Wilcoxina* DQ320129
Uncultured *Wilcoxina* EF619914
Mycobiont of *Epipactis helleborine* AB428785
91
G3-09 LC142813
99
G2-01 LC142811
G4-02 LC142814
A3-08 LC142805
G1-15 LC142810
A1-07 LC142800
A2-06 LC142803
G2-10 LC142812
Wilcoxina 1
0.1



Relative quantity of fungal DNA (ITS / *UBQ*)
3
2.5
2
1.5
1
0.5
0
a
b
b
p = 0.06
Green
Albino
Shoot

Table 1 Numbers of ITS rDNA sequences in the fungal groups (*Wilcoxina* groups and others) obtained from green (G1-G4) and albino (A1-A4) individuals of *Epipactis helleborine*

Plant No.	Fungal groups				Ratio of *Wicoxina* fungi (%)
	Wilcoxina 1	*Wilcoxina* 2	*Wilcoxina* 3	Others	
G1	8	4	1	1	92.9
G2	16	0	0	0	100.0
G3	11	1	0	0	100.0
G4	11	2	1	0	100.0
Total in green plants	46	7	2	1	98.2
A1	19	3	0	1	95.7
A2	2	12	1	5	75.0
A3	6	5	1	1	92.3
A4	0	16	0	0	100.0
Total in albino plants	27	36	2	7	90.3

Table 2 Mean values of δ^{13}C and δ^{15}N in leaves of *Epipactis helleborine* and surrounding autotrophic plant species.

Plant species	n	δ^{13}C (‰)	δ^{15}N (‰)
Epipactis helleborine (green)	6	-29.2 ± 0.7^{b}	10.4 ± 2.2^{a}
Epipactis helleborine (albino)	3	-25.0 ± 0.6^{a}	12.5 ± 1.3^{a}
Oplismenus undulatifolius	3	-30.2 ± 2.1^{bc}	-3.5 ± 0.1^{b}
Oxalis corniculata	2	-32.0 ± 0.0	-2.4 ± 0.3
Paederia scandens	6	-32.5 ± 0.9^{c}	-2.2 ± 1.2^{b}
Commelina communis	5	-32.9 ± 0.3^{c}	-1.2 ± 1.5^{b}
Vitis ficifolia var. *lobata*	3	-33.0 ± 0.7^{c}	-2.9 ± 0.4^{b}

Number of samples (n) for each plants is indicated. Each data is shown as mean±SD. Different letters indicate significant diffferences between the plants by Tukey-Kramer test ($p < 0.01$).

Table 3 Summary of the differential expression analysis

	No. of albino *E. helleborine* genes that are significantly altered in expression	
Level of gene expression relative to green plants	Plant	Fungi
Up	211	986
Down	282	4

Table 4 GO enrichment of albino *E. helleborine*

Code	Term	FDR	DEGs count	Reference count
Cellular Component				
GO:0044459	plasma membrane part	1.14E-04	14	235
GO:0031226	intrinsic component of plasma membrane	1.14E-04	12	168
GO:0071944	cell periphery	2.54E-04	32	1376
GO:0005886	plasma membrane	4.45E-04	28	1136
GO:0005887	integral component of plasma membrane	2.02E-03	9	138
Molecular Function				
GO:0008271	secondary active sulfate transmembrane transporter activity	4.62E-04	5	14
GO:0015116	sulfate transmembrane transporter activity	4.62E-04	5	15
GO:1901682	sulfur compound transmembrane transporter activity	4.82E-04	5	16
GO:0022857	transmembrane transporter activity	4.47E-03	23	993
GO:0022891	substrate-specific transmembrane transporter activity	4.51E-03	19	717
GO:0005215	transporter activity	4.71E-03	26	1230
GO:0030570	pectate lyase activity	1.75E-02	3	6
GO:0016837	carbon-oxygen lyase activity, acting on polysaccharides	1.75E-02	3	6
GO:0022892	substrate-specific transporter activity	1.96E-02	19	819
GO:0015103	inorganic anion transmembrane transporter activity	3.18E-02	5	54
Biological Process				
GO:0055085	transmembrane transport	4.62E-04	28	1155
GO:1902358	sulfate transmembrane transport	4.62E-04	5	15
GO:0008272	sulfate transport	4.82E-04	5	16
GO:0072348	sulfur compound transport	7.15E-04	5	18
GO:0098661	inorganic anion transmembrane transport	1.85E-03	5	23
GO:0015698	inorganic anion transport	3.78E-03	8	113
GO:0009813	flavonoid biosynthetic process	1.77E-02	6	73
GO:0046475	glycerophospholipid catabolic process	1.96E-02	2	0
GO:0030643	cellular phosphate ion homeostasis	1.96E-02	2	0
GO:0030002	cellular anion homeostasis	1.96E-02	2	0
GO:0046503	glycerolipid catabolic process	1.96E-02	2	0
GO:0072502	cellular trivalent inorganic anion homeostasis	1.96E-02	2	0
GO:1902578	single-organism localization	2.15E-02	23	1143
GO:0048878	chemical homeostasis	2.40E-02	9	212
GO:0051234	establishment of localization	3.19E-02	40	2687
GO:0006810	transport	3.54E-02	39	2609
GO:0044765	single-organism transport	3.62E-02	22	1118
GO:0009395	phospholipid catabolic process	4.34E-02	2	1
GO:0055062	phosphate ion homeostasis	4.34E-02	2	1
GO:0072506	trivalent inorganic anion homeostasis	4.34E-02	2	1
GO:0010817	regulation of hormone levels	4.72E-02	8	189

Table 5 GO enrichment of fungi in albino plant

Code	Term	FDR	DEGs count	Reference count
Cellular component				
GO:0005737	cytoplasm	8.83E-20	440	6145
GO:0044444	cytoplasmic part	1.56E-16	389	5398
GO:0005829	cytosol	1.37E-10	205	2530
GO:0005739	mitochondrion	3.97E-10	127	1315
GO:0044429	mitochondrial part	2.44E-07	76	702
GO:0044424	intracellular part	3.85E-06	481	8259
GO:0044445	cytosolic part	3.99E-06	54	458
GO:0005740	mitochondrial envelope	5.67E-06	56	491
GO:0000502	proteasome complex	5.77E-06	22	97
GO:1905369	endopeptidase complex	5.77E-06	22	97
GO:0034515	proteasome storage granule	7.89E-06	14	36
GO:0031597	cytosolic proteasome complex	7.89E-06	15	43
GO:1905368	peptidase complex	1.26E-05	24	125
GO:0005622	intracellular	1.79E-05	485	8475
GO:0005623	cell	2.72E-05	499	8796
GO:0044464	cell part	5.71E-05	495	8758
GO:0005839	proteasome core complex	9.54E-05	11	28
GO:0005840	ribosome	1.63E-04	79	916
GO:0043226	organelle	2.48E-04	383	6546
GO:0043229	intracellular organelle	2.48E-04	383	6546
GO:0005743	mitochondrial inner membrane	3.80E-04	36	309
GO:0031966	mitochondrial membrane	5.02E-04	44	423
GO:0019866	organelle inner membrane	5.40E-04	36	315
GO:0005758	mitochondrial intermembrane space	6.37E-04	15	71
GO:0031967	organelle envelope	9.98E-04	67	783
GO:0031975	envelope	1.11E-03	67	786
GO:0031970	organelle envelope lumen	1.18E-03	15	76
GO:0044391	ribosomal subunit	1.18E-03	42	413
GO:0098798	mitochondrial protein complex	2.87E-03	27	225
GO:0019774	proteasome core complex, beta-subunit complex	3.16E-03	6	10
GO:1902494	catalytic complex	3.96E-03	56	652
GO:0015934	large ribosomal subunit	4.24E-03	28	245
GO:0022625	cytosolic large ribosomal subunit	6.82E-03	22	175
GO:0022626	cytosolic ribosome	9.03E-03	32	315
GO:0042645	mitochondrial nucleoid	1.33E-02	11	57
GO:0009295	nucleoid	1.33E-02	11	57
GO:0005759	mitochondrial matrix	2.21E-02	25	237
GO:0043232	intracellular non-membrane-bounded organelle	2.21E-02	137	2126
GO:0043228	non-membrane-bounded organelle	2.21E-02	137	2126
GO:0043231	intracellular membrane-bounded organelle	2.44E-02	309	5430
GO:0031090	organelle membrane	2.44E-02	62	815
GO:0043227	membrane-bounded organelle	2.44E-02	309	5431
GO:0008540	proteasome regulatory particle, base subcomplex	2.53E-02	6	18
GO:0030529	intracellular ribonucleoprotein complex	2.78E-02	95	1387
GO:1990904	ribonucleoprotein complex	2.78E-02	95	1387
GO:0019773	proteasome core complex, alpha-subunit complex	3.13E-02	5	12
GO:0022624	proteasome accessory complex	3.49E-02	8	37
GO:0005838	proteasome regulatory particle	3.49E-02	8	37
GO:0044455	mitochondrial membrane part	4.10E-02	24	238
GO:0044446	intracellular organelle part	4.27E-02	205	3455
GO:0044422	organelle part	4.63E-02	205	3462
Molecular Function				
GO:0016491	oxidoreductase activity	1.09E-06	150	1881
GO:0004298	threonine-type endopeptidase activity	9.54E-05	11	28
GO:0070003	threonine-type peptidase activity	9.54E-05	11	28
GO:0016616	oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor	3.99E-04	30	233
GO:0003746	translation elongation factor activity	9.98E-04	22	149
GO:0003735	structural constituent of ribosome	1.28E-03	64	744
GO:0005488	binding	1.73E-03	390	6829
GO:0048037	cofactor binding	4.94E-03	56	659
GO:0004175	endopeptidase activity	7.88E-03	19	140
GO:0016614	oxidoreductase activity, acting on CH-OH group of donors	8.02E-03	32	312
GO:0005198	structural molecule activity	1.21E-02	73	966
GO:0005515	protein binding	1.21E-02	68	883
GO:0008135	translation factor activity, RNA binding	1.33E-02	34	353
GO:1901677	phosphate transmembrane transporter activity	1.63E-02	11	59
GO:0000295	adenine nucleotide transmembrane transporter activity	1.90E-02	5	10
GO:0016887	ATPase activity	2.44E-02	49	603
GO:0016667	oxidoreductase activity, acting on a sulfur group of donors	2.86E-02	15	111

GO:0003723	RNA binding	3.72E-02	71	987
GO:0005337	nucleoside transmembrane transporter activity	4.70E-02	5	14
GO:0015216	purine nucleotide transmembrane transporter activity	4.70E-02	5	14
Biological Process				
GO:0043581	mycelium development	1.37E-16	46	151
GO:0044707	single-multicellular organism process	2.28E-15	47	178
GO:0032501	multicellular organismal process	2.28E-15	47	178
GO:0007275	multicellular organism development	2.28E-15	47	178
GO:0044699	single-organism process	4.32E-15	440	6529
GO:0048856	anatomical structure development	4.13E-12	60	357
GO:0044767	single-organism developmental process	6.57E-12	66	429
GO:0032502	developmental process	7.20E-12	66	431
GO:0055114	oxidation-reduction process	1.09E-10	167	1900
GO:1901564	organonitrogen compound metabolic process	2.63E-10	220	2805
GO:0044710	single-organism metabolic process	3.74E-09	285	4051
GO:1901566	organonitrogen compound biosynthetic process	2.38E-08	177	2213
GO:0043161	proteasome-mediated ubiquitin-dependent protein catabolic process	9.11E-07	28	136
GO:1901576	organic substance biosynthetic process	1.04E-06	267	3942
GO:0010498	proteasomal protein catabolic process	1.37E-06	28	140
GO:0044267	cellular protein metabolic process	3.13E-06	185	2514
GO:0009058	biosynthetic process	3.85E-06	271	4081
GO:1902101	positive regulation of metaphase/anaphase transition of cell cycle	3.85E-06	20	76
GO:1901970	positive regulation of mitotic sister chromatid separation	3.85E-06	20	76
GO:0045842	positive regulation of mitotic metaphase/anaphase transition	3.85E-06	20	76
GO:0019941	modification-dependent protein catabolic process	3.99E-06	35	225
GO:0071704	organic substance metabolic process	5.44E-06	432	7265
GO:0044237	cellular metabolic process	5.67E-06	419	7005
GO:0006511	ubiquitin-dependent protein catabolic process	7.89E-06	34	223
GO:0043632	modification-dependent macromolecule catabolic process	7.89E-06	36	247
GO:1901989	positive regulation of cell cycle phase transition	7.89E-06	22	100
GO:1901992	positive regulation of mitotic cell cycle phase transition	7.89E-06	22	100
GO:0044281	small molecule metabolic process	7.92E-06	155	2050
GO:0051984	positive regulation of chromosome segregation	8.54E-06	20	83
GO:0006412	translation	8.76E-06	108	1278
GO:0044763	single-organism cellular process	1.09E-05	293	4572
GO:2001252	positive regulation of chromosome organization	1.09E-05	20	85
GO:0045840	positive regulation of mitotic nuclear division	1.09E-05	20	85
GO:0033045	regulation of sister chromatid segregation	1.15E-05	24	123
GO:0033047	regulation of mitotic sister chromatid segregation	1.15E-05	24	123
GO:0006518	peptide metabolic process	1.15E-05	112	1353
GO:0051785	positive regulation of nuclear division	1.18E-05	20	86
GO:0044249	cellular biosynthetic process	1.18E-05	257	3902
GO:0043043	peptide biosynthetic process	1.22E-05	109	1308
GO:0019538	protein metabolic process	1.23E-05	192	2720
GO:0043603	cellular amide metabolic process	1.26E-05	116	1425
GO:0051983	regulation of chromosome segregation	1.26E-05	24	125
GO:0007091	metaphase/anaphase transition of mitotic cell cycle	1.26E-05	22	106
GO:1902099	regulation of metaphase/anaphase transition of cell cycle	1.26E-05	22	106
GO:0030071	regulation of mitotic metaphase/anaphase transition	1.26E-05	22	106
GO:0044784	metaphase/anaphase transition of cell cycle	1.26E-05	22	106
GO:0010965	regulation of mitotic sister chromatid separation	1.26E-05	22	106
GO:0010499	proteasomal ubiquitin-independent protein catabolic process	1.32E-05	11	21
GO:0051603	proteolysis involved in cellular protein catabolic process	1.32E-05	37	270
GO:0043604	amide biosynthetic process	1.41E-05	111	1350
GO:0051130	positive regulation of cellular component organization	1.55E-05	33	225
GO:0051306	mitotic sister chromatid separation	1.55E-05	22	108
GO:0044257	cellular protein catabolic process	1.59E-05	37	273
GO:0008152	metabolic process	1.71E-05	561	10108
GO:0009987	cellular process	2.10E-05	496	8717
GO:0033044	regulation of chromosome organization	3.00E-05	25	144
GO:0051304	chromosome separation	3.61E-05	22	115
GO:0030163	protein catabolic process	4.40E-05	37	287
GO:0043241	protein complex disassembly	4.82E-05	16	62
GO:0051128	regulation of cellular component organization	5.27E-05	49	447
GO:0007088	regulation of mitotic nuclear division	6.06E-05	25	151
GO:0051783	regulation of nuclear division	6.73E-05	26	163
GO:0010638	positive regulation of organelle organization	8.16E-05	25	154
GO:0032984	macromolecular complex disassembly	9.38E-05	17	75
GO:0045931	positive regulation of mitotic cell cycle	1.35E-04	22	127
GO:0022411	cellular component disassembly	1.41E-04	19	97
GO:0044711	single-organism biosynthetic process	2.15E-04	108	1393
GO:0006979	response to oxidative stress	2.23E-04	27	188
GO:0090068	positive regulation of cell cycle process	2.23E-04	22	132
GO:0044238	primary metabolic process	2.23E-04	393	6739

GO:0034599	cellular response to oxidative stress	2.23E-04	23	143
GO:0019752	carboxylic acid metabolic process	2.48E-04	85	1024
GO:0044271	cellular nitrogen compound biosynthetic process	2.57E-04	191	2855
GO:0009056	catabolic process	3.10E-04	79	936
GO:0044772	mitotic cell cycle phase transition	3.40E-04	29	218
GO:0045787	positive regulation of cell cycle	3.48E-04	22	137
GO:0044770	cell cycle phase transition	3.61E-04	29	219
GO:1901575	organic substance catabolic process	3.76E-04	76	895
GO:0043436	oxoacid metabolic process	4.62E-04	85	1045
GO:0044248	cellular catabolic process	6.17E-04	65	738
GO:0033043	regulation of organelle organization	6.76E-04	36	319
GO:0006839	mitochondrial transport	7.62E-04	16	82
GO:0048522	positive regulation of cellular process	8.03E-04	51	534
GO:0000070	mitotic sister chromatid segregation	8.25E-04	25	182
GO:0006082	organic acid metabolic process	1.18E-03	94	1226
GO:0048518	positive regulation of biological process	1.19E-03	52	559
GO:0015718	monocarboxylic acid transport	1.34E-03	7	13
GO:0042221	response to chemical	1.46E-03	47	490
GO:0044265	cellular macromolecule catabolic process	1.50E-03	40	390
GO:0000819	sister chromatid segregation	1.68E-03	25	192
GO:1901990	regulation of mitotic cell cycle phase transition	2.43E-03	25	197
GO:1901987	regulation of cell cycle phase transition	2.60E-03	25	198
GO:0006508	proteolysis	3.00E-03	48	522
GO:0006414	translational elongation	3.00E-03	26	213
GO:0046942	carboxylic acid transport	3.43E-03	10	38
GO:0007346	regulation of mitotic cell cycle	3.46E-03	30	268
GO:0009057	macromolecule catabolic process	4.00E-03	43	455
GO:0000278	mitotic cell cycle	4.22E-03	45	486
GO:0098813	nuclear chromosome segregation	4.26E-03	25	206
GO:1903047	mitotic cell cycle process	4.26E-03	43	457
GO:0015980	energy derivation by oxidation of organic compounds	5.45E-03	33	318
GO:0007067	mitotic nuclear division	5.74E-03	27	237
GO:0010564	regulation of cell cycle process	5.87E-03	30	278
GO:0043624	cellular protein complex disassembly	6.37E-03	11	51
GO:1990542	mitochondrial transmembrane transport	7.66E-03	12	62
GO:0015711	organic anion transport	8.63E-03	10	44
GO:1901607	alpha-amino acid biosynthetic process	8.71E-03	32	314
GO:0006950	response to stress	8.71E-03	71	920
GO:0010604	positive regulation of macromolecule metabolic process	8.71E-03	30	286
GO:0006091	generation of precursor metabolites and energy	8.77E-03	38	401
GO:0006996	organelle organization	1.05E-02	93	1299
GO:0051726	regulation of cell cycle	1.08E-02	35	362
GO:0007059	chromosome segregation	1.16E-02	25	223
GO:0044283	small molecule biosynthetic process	1.28E-02	59	738
GO:0015908	fatty acid transport	1.33E-02	4	4
GO:0015909	long-chain fatty acid transport	1.33E-02	4	4
GO:0006820	anion transport	1.33E-02	19	148
GO:0045454	cell redox homeostasis	1.33E-02	13	78
GO:0010628	positive regulation of gene expression	1.34E-02	24	213
GO:0070887	cellular response to chemical stimulus	1.48E-02	33	341
GO:0031325	positive regulation of cellular metabolic process	1.48E-02	30	298
GO:0009893	positive regulation of metabolic process	1.71E-02	30	301
GO:1902589	single-organism organelle organization	1.72E-02	49	589
GO:0015858	nucleoside transport	1.74E-02	6	16
GO:0048285	organelle fission	1.77E-02	30	302
GO:0072521	purine-containing compound metabolic process	1.89E-02	40	452
GO:0010557	positive regulation of macromolecule biosynthetic process	1.89E-02	23	206
GO:0072593	reactive oxygen species metabolic process	1.89E-02	12	71
GO:0000280	nuclear division	2.04E-02	29	291
GO:1901605	alpha-amino acid metabolic process	2.07E-02	40	455
GO:1901617	organic hydroxy compound biosynthetic process	2.07E-02	12	72
GO:0042278	purine nucleoside metabolic process	2.12E-02	35	380
GO:0045333	cellular respiration	2.15E-02	27	264
GO:0006415	translational termination	2.16E-02	8	33
GO:0034645	cellular macromolecule biosynthetic process	2.16E-02	163	2603
GO:0009059	macromolecule biosynthetic process	2.44E-02	164	2631
GO:0006807	nitrogen compound metabolic process	2.44E-02	284	4935
GO:0045727	positive regulation of translation	2.44E-02	8	34
GO:0015868	purine ribonucleotide transport	2.44E-02	5	11
GO:0051503	adenine nucleotide transport	2.44E-02	5	11
GO:0010035	response to inorganic substance	2.45E-02	16	121
GO:0043244	regulation of protein complex disassembly	2.62E-02	7	26
GO:0046128	purine ribonucleoside metabolic process	2.91E-02	34	375
GO:0030433	ER-associated ubiquitin-dependent protein catabolic process	2.96E-02	9	45

GO:0031328	positive regulation of cellular biosynthetic process	3.28E-02	23	218
GO:0009891	positive regulation of biosynthetic process	3.44E-02	23	219
GO:0051173	positive regulation of nitrogen compound metabolic process	3.44E-02	24	233
GO:0009161	ribonucleoside monophosphate metabolic process	3.49E-02	34	380
GO:0098869	cellular oxidant detoxification	3.49E-02	14	102
GO:0071450	cellular response to oxygen radical	3.49E-02	8	37
GO:0019430	removal of superoxide radicals	3.49E-02	8	37
GO:0000303	response to superoxide	3.49E-02	8	37
GO:0000305	response to oxygen radical	3.49E-02	8	37
GO:0071451	cellular response to superoxide	3.49E-02	8	37
GO:0008652	cellular amino acid biosynthetic process	3.57E-02	28	292
GO:0009123	nucleoside monophosphate metabolic process	3.62E-02	34	382
GO:0051247	positive regulation of protein metabolic process	3.62E-02	15	115
GO:0032270	positive regulation of cellular protein metabolic process	3.62E-02	15	115
GO:0050821	protein stabilization	3.84E-02	5	13
GO:0034250	positive regulation of cellular amide metabolic process	3.93E-02	8	38
GO:1990748	cellular detoxification	3.93E-02	14	104
GO:0001300	chronological cell aging	3.99E-02	7	29
GO:0009119	ribonucleoside metabolic process	4.06E-02	35	401
GO:0036503	ERAD pathway	4.46E-02	9	49
GO:0006753	nucleoside phosphate metabolic process	4.63E-02	45	563
GO:0009205	purine ribonucleoside triphosphate metabolic process	4.63E-02	28	299
GO:0019693	ribose phosphate metabolic process	4.66E-02	38	452
GO:0006103	2-oxoglutarate metabolic process	4.70E-02	5	14
GO:1901642	nucleoside transmembrane transport	4.70E-02	5	14
GO:0009141	nucleoside triphosphate metabolic process	4.95E-02	29	316
GO:0034976	response to endoplasmic reticulum stress	4.95E-02	11	72
GO:0006072	glycerol-3-phosphate metabolic process	4.95E-02	6	22
GO:0052646	alditol phosphate metabolic process	4.95E-02	6	22

Supplementary table 1 Values of $\delta^{13}C$ and $\delta^{15}N$ in each sample of *Epipactis helleborine* and surrounding autotrophic plant species obtained from each collection site

Collection site	Plant species	$\delta^{13}C$ (‰)	$\delta^{15}N$ (‰)
1	*Epipactis helleborine* (green)	-29.2	10.5
	Oxalis corniculata	-32.0	-2.6
	Paederia scandens	-31.4	-3.2
	Vitis ficifolia var *lobata*	-33.2	-3.2
2	*Epipactis helleborine* (green)	-29.5	6.9
	Epipactis helleborine (albino)	-25.4	11.7
	Oplismenus undulatifolius	-27.9	-3.5
3	*Epipactis helleborine* (albino)	-24.3	14.0
	Oplismenus undulatifolius	-31.7	-3.7
	Commelina communis	-32.9	-3.7
	Vitis ficifolia var *lobata*	-33.6	-3.1
4	*Epipactis helleborine* (green)	-29.6	9.4
	Oxalis corniculata	-31.9	-2.1
	Paederia scandens	-31.6	-3.3
	Commelina communis	-32.7	-0.3
	Vitis ficifolia var *lobata*	-32.2	-2.5
5	*Epipactis helleborine* (albino)	-25.4	11.9
	Oplismenus undulatifolius	-31.1	-3.5
	Paederia scandens	-32.3	-1.8
6	*Epipactis helleborine* (green)	-30.2	10.4
	Paederia scandens	-32.8	-1.0
	Commelina communis	-33.2	-0.4
7	*Epipactis helleborine* (green)	-28.4	12.8
	Paederia scandens	-32.9	-0.5
	Commelina communis	-32.4	-0.4
8	*Epipactis helleborine* (green)	-28.6	12.6
	Paederia scandens	-33.9	-3.4
	Commelina communis	-33.2	-1.1

Supplementary table 2 Non *Wilcoxina* fungi detected from roots of *Epipactis helleborine*

Plant No.	Accession No.	Putative fungal taxa	Closest matching sequences in GenBank		
			Fungal taxa	Accession No.	Ident (%)
A1	LC143816	*Clavulina*	Uncultured ECM fungus	AB636466	99
A2	LC143817	*Exophiala*	Ascomycota sp.	GU566289	99
A2	LC143818	*Exophiala*	Ascomycota sp.	GU566289	99
A2	LC143819	*Astraeus*	*Astraeus hygrometricus*	LC001788	100
A2	LC143820	Diaporthales	Uncultured Ascomycota	HM358998	98
A2	LC143821	*Exophiala*	Ascomycota sp.	GU566289	99
A3	LC143822	*Clavulina*	Uncultured ECM fungus	AB636466	99
G1	LC143823	Capnodiales	*Ramicholoridium brasilianum*	EU041797	91

Supplementary table 3 Summary of the *de novo* assembly of the sequence data

	Total	Plant	Fungi	Others	No BLAST hit
De novo assembled contigs	227966	61007	47779	5132	114048
after searching the ORF		41835	41434		
after removing redundant contigs		28557	27123		
average percentage of mapped reads from green plants (%)		46.2	10.06		
average percentage of mapped reads from albino plants (%)		51.4	7.56		

Each value represents the number of contigs.

Supplementary table 4 Differentially expressed genes of *E. helleborine*

Sequence ID	Description (BLASTX search against the nr database)	logFC[a]	*p* -value	FDR
TR319|c0_g1_i1|m.163	OTU domain-containing DDB_G0284757-like	-1.23	4.26E-04	3.07E-02
TR532|c0_g1_i1|m.365	myosin-binding 2 [Glycine max]	-1.63	6.33E-05	8.49E-03
TR933|c0_g1_i1|m.543	peroxidase 5-like	5.46	2.82E-04	2.32E-02
TR1508|c0_g1_i1|m.747	ethylene-responsive transcription factor RAP2-4-like	2.04	6.82E-04	4.31E-02
TR2324|c0_g1_i1|m.981	aspartic ase CDR1-like	4.63	1.89E-04	1.76E-02
TR2557|c0_g1_i1|m.1167	NAC transcription factor 29-like	-3.75	2.72E-08	1.99E-05
TR2598|c0_g1_i1|m.1200	transcription factor bHLH155-like isoform X1	1.97	5.88E-04	3.94E-02
TR2867|c0_g1_i1|m.1263	myb-related P-like	2.99	2.72E-07	1.41E-04
TR2987|c0_g1_i1|m.1292	Os03g0114400 [Oryza sativa Japonica Group]	-2.14	7.02E-04	4.37E-02
TR3003|c0_g1_i1|m.1300	BURP domain-containing 12-like	1.89	1.16E-05	2.27E-03
TR3076|c0_g1_i1|m.1330	histone H2B-like	-1.42	7.31E-06	1.66E-03
TR3228|c0_g1_i1|m.1367	deoxyribodipyrimidine photo-lyase	2.04	3.54E-05	5.34E-03
TR3346|c0_g1_i1|m.1408	Os10g0501500 [Oryza sativa Japonica Group]	-3.59	1.76E-04	1.72E-02
TR4128|c0_g2_i1|m.1626	zinc finger AN1 domain-containing stress-associated 12	-1.94	7.89E-05	9.69E-03
TR4128|c0_g1_i1|m.1624	zinc finger AN1 domain-containing stress-associated 12	-2.09	2.11E-04	1.88E-02
TR5196|c0_g2_i1|m.1847	CSC1 ERD4	2.04	2.13E-06	6.55E-04
TR5279|c0_g1_i1|m.1883	probable membrane-associated kinase regulator 6	2.06	7.90E-04	4.74E-02
TR5705|c0_g2_i1|m.2012	syntaxin-22-like	-1.38	1.30E-04	1.38E-02
TR5927|c0_g1_i1|m.2303	Os01g0825800 [Oryza sativa Japonica Group]	1.45	1.33E-04	1.40E-02
TR5927|c0_g1_i1|m.2304	Transmembrane amino acid transporter family isoform 1 [Theobroma cacao]	1.58	2.97E-04	2.39E-02
TR5976|c0_g1_i1|m.2352	bidirectional sugar transporter SWEET14-like	1.61	4.66E-04	3.33E-02
TR6107|c0_g1_i1|m.2479	BAHD acyltransferase DCR	2.46	3.11E-04	2.44E-02
TR6402|c0_g1_i1|m.2597	PREDICTED: uncharacterized protein LOC103713491	2.01	2.79E-04	2.32E-02
TR6521|c0_g1_i1|m.2643	serine threonine- kinase At1g28390	-2.06	3.41E-06	9.19E-04
TR6872|c0_g1_i1|m.2814	proteoglycan 4-like	2.67	4.85E-04	3.41E-02
TR8094|c0_g2_i1|m.3180	ribonuclease H At1g65750	-1.95	5.40E-04	3.67E-02
TR8579|c0_g1_i1|m.3280	probable peroxygenase 4	-2.68	3.93E-07	1.90E-04
TR8630|c0_g1_i1|m.3291	transcription factor FER-LIKE IRON DEFICIENCY-INDUCED TRANSCRIPTION FACTOR-like	1.93	1.09E-05	2.17E-03
TR8630|c0_g2_i1|m.3292	transcription factor FER-LIKE IRON DEFICIENCY-INDUCED TRANSCRIPTION FACTOR-like	2.16	3.15E-04	2.46E-02
TR9258|c0_g1_i1|m.3417	UDP-glycosyltransferase 73C6-like	-1.58	5.15E-04	3.58E-02
TR10854|c0_g1_i1|m.3757	phytohormone-binding -like	1.63	8.59E-05	1.04E-02
TR11047|c0_g2_i1|m.3867	callose synthase 3-like	2.23	1.73E-04	1.70E-02
TR11596|c0_g2_i1|m.4340	probable trehalose-phosphate phosphatase 6	-2.26	1.38E-04	1.44E-02
TR11797|c0_g1_i1|m.4554	prostamide prostaglandin F synthase isoform X1 [Musa acuminata malaccensis]	1.32	2.42E-04	2.09E-02
TR11863|c1_g1_i1|m.4611	G-type lectin S-receptor-like serine threonine- kinase B120	-3.75	1.04E-05	2.14E-03
TR13870|c0_g2_i1|m.5116	probable aldo-keto reductase 2	-10.74	1.22E-40	1.75E-36
TR14218|c0_g1_i1|m.5186	TBC1 domain family member 8B-like isoform X2	-2.06	6.79E-04	4.31E-02
TR14662|c0_g2_i1|m.5295	quinone-oxidoreductase homolog, chloroplastic	11.30	8.75E-19	4.17E-15
TR14662|c0_g2_i1|m.5297	quinone-oxidoreductase homolog, chloroplastic	7.24	9.04E-07	3.49E-04
TR14828|c0_g1_i1|m.5331	organic cation carnitine transporter 3-like	1.96	2.07E-08	1.64E-05
TR14868|c0_g2_i1|m.5347	prostatic spermine-binding -like isoform X1 [Elaeis guineensis]	-3.96	2.19E-04	1.94E-02
TR15941|c0_g1_i1|m.5578	PREDICTED: uncharacterized protein LOC105036106	-4.29	3.22E-07	1.61E-04
TR16229|c0_g1_i1|m.5901	Uncharacterized protein TCM_021519 [Theobroma cacao]	-4.23	8.62E-04	4.99E-02
TR16250|c0_g1_i1|m.5918	Os03g0266700 [Oryza sativa Japonica Group]	-1.94	2.34E-06	6.82E-04
TR16389|c0_g1_i1|m.6064	heme oxygenase 1, chloroplastic-like	-2.93	1.17E-07	6.57E-05
TR16643|c0_g1_i1|m.6242	MATE efflux family DTX1-like	2.49	2.57E-04	2.18E-02
TR16711|c0_g1_i1|m.6288	beta-glucosidase 12-like	-2.62	5.60E-09	5.16E-06
TR16749|c0_g1_i1|m.6318	zinc finger ZAT9-like	-2.42	8.18E-04	4.85E-02
TR17381|c0_g1_i1|m.6628	PREDICTED: uncharacterized protein LOC103996876	-2.72	2.43E-10	3.47E-07
TR17474|c0_g2_i1|m.6721	ferredoxin--nitrite reductase, chloroplastic	4.31	5.72E-07	2.40E-04
TR17534|c0_g2_i1|m.6774	cinnamoyl- reductase	1.43	1.79E-04	1.73E-02
TR17639|c0_g1_i1|m.6860	NAC domain-containing 94	-3.70	1.37E-05	2.52E-03
TR17688|c0_g1_i1|m.6882	phospholipase A1-Ibeta2, chloroplastic-like	-1.36	7.12E-04	4.40E-02
TR17730|c0_g2_i1|m.6902	Os03g0123800 [Oryza sativa Japonica Group]	-1.67	4.13E-04	3.00E-02
TR18052|c0_g2_i1|m.7032	probable membrane-associated kinase regulator 6	-2.51	8.35E-04	4.93E-02
TR18138|c0_g1_i1|m.7062	adenine nucleotide alpha hydrolase superfamily [Medicago truncatula]	-3.85	1.60E-05	2.86E-03
TR19942|c0_g1_i1|m.7418	zinc-finger homeodomain 4 [Tarenaya hassleriana]	2.72	4.19E-07	1.96E-04
TR20257|c0_g1_i1|m.7515	NRT1 PTR FAMILY -like	1.96	2.89E-05	4.55E-03
TR20894|c0_g2_i1|m.7697	probable receptor kinase At5g24010	1.73	1.12E-04	1.22E-02
TR20937|c0_g1_i1|m.7705	ethylene-responsive transcription factor 1B-like	-1.66	1.78E-04	1.73E-02
TR22109|c0_g1_i1|m.8191	gibberellin 20 oxidase 2-like	-5.46	3.02E-09	3.08E-06
TR22278|c0_g1_i1|m.8266	pentatricopeptide repeat-containing At3g04760, chloroplastic	2.05	7.06E-05	8.96E-03
TR22333|c0_g1_i2|m.8290	probable BOI-related E3 ubiquitin- ligase 3	2.05	5.39E-04	3.67E-02
TR22424|c0_g1_i1|m.8328	probable receptor kinase At1g33260	1.49	4.96E-05	6.88E-03
TR22738|c1_g1_i1|m.8518	2-deoxyglucose-6-phosphate phosphatase, [Ricinus communis]	-1.58	1.30E-04	1.38E-02
TR22878|c0_g2_i1|m.8611	PREDICTED: uncharacterized protein LOC103714814 isoform X3	-1.64	1.19E-06	4.15E-04
TR22895|c0_g1_i1|m.8630	probable polyamine oxidase 5	1.59	8.15E-04	4.85E-02
TR22911|c0_g2_i1|m.8647	transcription factor bHLH62-like	1.54	1.57E-04	1.58E-02
TR22994|c0_g1_i2|m.8722	ABC transporter G family member 11-like	-1.80	4.07E-04	2.98E-02
TR22994|c0_g1_i1|m.8720	ABC transporter G family member 11-like	-1.76	7.39E-04	4.51E-02
TR23021|c0_g2_i1|m.8745	Os06g0236300 [Oryza sativa Japonica Group]	-4.15	1.28E-06	4.26E-04
TR23201|c0_g1_i1|m.8959	Os05g0171900 [Oryza sativa Japonica Group]	-4.29	1.42E-06	4.62E-04
TR23638|c0_g1_i1|m.9371	endoglucanase 6	3.39	1.09E-05	2.17E-03
TR23924|c0_g2_i1|m.9561	root phototropism 3 [Musa acuminata malaccensis]	1.26	6.28E-04	4.12E-02
TR23988|c0_g2_i1|m.9616	non-specific phospholipase C4-like	-3.55	4.75E-07	2.05E-04
TR24093|c0_g2_i1|m.9690	nudix hydrolase 17, mitochondrial-like	-3.57	3.36E-04	2.58E-02
TR24202|c0_g2_i1|m.9790	gibberellin 2-beta-dioxygenase 1-like	2.97	1.05E-05	2.14E-03
TR24202|c0_g3_i1|m.9792	gibberellin 2-beta-dioxygenase 1-like	3.03	2.73E-05	4.36E-03
TR24202|c0_g1_i1|m.9786	gibberellin 2-beta-dioxygenase 1-like	2.82	6.72E-05	8.77E-03
TR24498|c0_g1_i1|m.9998	dof zinc finger -like	2.03	2.59E-04	2.19E-02
TR24563|c0_g1_i2|m.10057	ubiquitin-conjugating enzyme E2 20-like	-3.64	1.70E-10	2.69E-07
TR24857|c2_g1_i1|m.10282	probable choline kinase 2	-2.52	9.95E-05	1.12E-02
TR24870|c0_g2_i1|m.10305	cysteine ase 15A	-2.27	6.28E-07	2.56E-04
TR25178|c0_g1_i1|m.10485	probable GPI-anchored adhesin PGA55 isoform X2 [Prunus mume]	1.45	2.61E-05	4.18E-03

TR25625|c0_g1_i1|m.10764	allantoate deiminase	-1.57	2.26E-05	3.82E-03
TR26152|c0_g3_i1|m.11283	probable purine permease 11 [Phoenix dactylifera]	1.28	8.14E-04	4.85E-02
TR26339|c0_g1_i1|m.11484	flavonoid 3 -hydroxylase	5.43	5.17E-06	1.31E-03
TR26368|c0_g1_i1|m.11522	glycerol-3-phosphate 2-O-acyltransferase 6	2.36	2.42E-04	2.09E-02
TR26383|c0_g2_i1|m.11538	-No hit found-	1.77	6.70E-04	4.30E-02
TR26443|c0_g1_i1|m.11586	LRR receptor-like serine threonine- kinase GSO1	1.99	2.30E-04	2.02E-02
TR26615|c0_g1_i1|m.11716	seed biotin-containing SBP65-like isoform X2	3.65	3.61E-05	5.38E-03
TR26642|c0_g1_i1|m.11731	cytochrome P450 90B1-like	1.52	1.93E-04	1.78E-02
TR26750|c0_g1_i1|m.11813	ELF4-LIKE 3-like [Glycine max]	-1.66	3.48E-04	2.64E-02
TR26906|c0_g1_i2|m.11924	phosphatidylinositol:ceramide inositolphosphotransferase-like isoform X2 [Elaeis guineensis]	-1.50	1.46E-04	1.50E-02
TR27043|c0_g1_i1|m.12052	PREDICTED: uncharacterized protein LOC103972565	-2.12	1.26E-06	4.26E-04
TR27043|c0_g1_i2|m.12054	PREDICTED: uncharacterized protein LOC103972565	-2.04	9.80E-06	2.07E-03
TR27088|c0_g1_i1|m.12073	CMP-N-acetylneuraminate-beta-galactosamide-alpha-2,3-sialyltransferase 1-like	-3.61	7.39E-05	9.25E-03
TR27546|c0_g3_i1|m.12496	ethylene-responsive transcription factor ERF113-like	-2.53	4.97E-04	3.48E-02
TR27814|c0_g1_i1|m.12657	probable phosphatase 2C 33	2.46	8.91E-06	1.93E-03
TR27814|c0_g2_i1|m.12660	probable phosphatase 2C 33	2.76	1.03E-05	2.14E-03
TR28036|c0_g2_i2|m.12930	probable peroxidase 26	-2.11	8.01E-04	4.78E-02
TR28107|c0_g1_i1|m.12988	probable phosphatase 2C 12	2.32	2.75E-04	2.30E-02
TR28188|c0_g1_i1|m.13073	Mediator of RNA polymerase II transcription subunit 26, [Theobroma cacao]	2.59	1.72E-07	9.29E-05
TR28322|c1_g1_i1|m.13284	24-methylenesterol C-methyltransferase 2-like	1.39	6.80E-04	4.31E-02
TR28396|c0_g1_i1|m.13441	pentatricopeptide repeat-containing At3g09650, chloroplastic	1.31	6.38E-04	4.16E-02
TR28436|c0_g2_i1|m.13482	F-box LRR-repeat At3g48880-like	-4.29	5.80E-10	6.90E-07
TR28446|c0_g2_i1|m.13493	cysteine-rich receptor kinase 2	-1.45	3.10E-04	2.44E-02
TR28446|c0_g3_i1|m.13495	cysteine-rich receptor kinase 2 isoform X1	-1.45	4.38E-04	3.15E-02
TR28554|c0_g3_i1|m.13643	myb-related 306-like	2.56	1.54E-05	2.80E-03
TR28866|c0_g1_i1|m.13863	NAC domain-containing 94	-1.87	2.21E-04	1.96E-02
TR28926|c1_g1_i1|m.13884	probable phosphatase 2C 63	-1.82	9.29E-05	1.08E-02
TR28976|c0_g1_i1|m.13946	probable sulfate transporter	2.12	1.06E-04	1.19E-02
TR29094|c1_g1_i1|m.14033	transmembrane 64 [Pyrus x bretschneideri]	-1.63	2.57E-06	7.41E-04
TR29247|c0_g1_i1|m.14131	Os08g0439600 [Oryza sativa Japonica Group]	-2.95	4.92E-05	6.85E-03
TR29364|c0_g2_i1|m.14258	probable S-acyltransferase 14	-1.45	1.58E-05	2.86E-03
TR29365|c1_g1_i1|m.14264	crocetin glucosyltransferase, chloroplastic-like	1.26	2.65E-04	2.23E-02
TR29822|c0_g2_i1|m.14646	phenylalanine ammonia-lyase	-4.19	2.48E-18	8.84E-15
TR29830|c0_g1_i1|m.14648	S-adenosyl-L-methionine-dependent methyltransferases superfamily isoform 1 [Theobroma cacao]	1.80	1.90E-05	3.33E-03
TR29909|c1_g1_i1|m.14716	UDP-galactose transporter 2-like	-1.46	1.53E-04	1.56E-02
TR30144|c0_g1_i1|m.14905	NADPH:quinone oxidoreductase-like	2.86	1.53E-07	8.38E-05
TR30161|c0_g2_i1|m.14914	phenylalanine ammonia-lyase	-1.74	7.36E-05	9.25E-03
TR30267|c0_g1_i1|m.14974	Os11g0703900 [Oryza sativa Japonica Group]	-1.52	4.45E-05	6.28E-03
TR30344|c0_g1_i1|m.15050	heat shock 70 [Populus trichocarpa]	-2.50	7.61E-05	9.45E-03
TR30470|c0_g1_i1|m.15142	tropinone reductase homolog At1g07440-like	-3.29	1.99E-10	3.00E-07
TR30791|c0_g2_i1|m.15395	Os03g0299800 [Oryza sativa Japonica Group]	-2.23	4.69E-04	3.34E-02
TR30975|c0_g1_i2|m.15578	1-aminocyclopropane-1-carboxylate synthase [Musa acuminata AAA Group]	-2.58	1.91E-04	1.76E-02
TR31045|c0_g1_i1|m.15608	transcription factor MYB39-like	3.02	4.77E-06	1.23E-03
TR31045|c0_g1_i2|m.15609	transcription factor MYB39-like	2.48	2.16E-05	3.70E-03
TR31214|c0_g1_i1|m.15723	ethylene-responsive transcription factor ERF113-like	-1.44	1.13E-04	1.24E-02
TR31496|c0_g3_i1|m.16153	Os04g0563000, partial	-1.75	7.48E-06	1.68E-03
TR31496|c0_g2_i1|m.16150	Os04g0563000, partial	-1.36	7.35E-04	4.50E-02
TR31542|c0_g1_i1|m.16234	WAT1-related At5g64700-like	2.38	7.28E-06	1.66E-03
TR31556|c0_g2_i1|m.16242	cytokinin dehydrogenase 3-like	-2.45	5.32E-04	3.65E-02
TR31664|c0_g1_i1|m.16434	transcription repressor OFP1-like	2.56	1.63E-04	1.62E-02
TR31896|c0_g2_i1|m.16852	butyrate-- ligase AAE11, peroxisomal-like	-2.17	2.34E-04	2.04E-02
TR32037|c0_g1_i1|m.17146	zinc finger 7-like	2.04	3.32E-04	2.55E-02
TR32048|c0_g1_i1|m.17178	equilibrative nucleotide transporter 1	-10.46	7.20E-37	6.85E-33
TR32181|c0_g1_i1|m.17377	ABC transporter G family member 14	1.38	1.96E-04	1.79E-02
TR32239|c0_g1_i2|m.17496	low affinity sulfate transporter 3-like	1.36	2.05E-04	1.84E-02
TR32315|c0_g1_i1|m.17658	kDa class I heat shock -like	-1.82	6.60E-05	8.68E-03
TR32315|c0_g1_i2|m.17659	kDa class I heat shock -like	-1.60	3.30E-04	2.55E-02
TR32317|c1_g2_i1|m.17673	ferritin-3, chloroplastic-like	1.48	2.90E-04	2.35E-02
TR32385|c0_g1_i2|m.17851	homeobox-leucine zipper HOX3-like	-1.96	4.12E-04	3.00E-02
TR32385|c0_g1_i1|m.17848	homeobox-leucine zipper HOX3-like	-2.21	6.57E-04	4.24E-02
TR32404|c1_g1_i1|m.17899	probable N-acetyltransferase HLS1	-4.36	9.15E-09	7.46E-06
TR32466|c0_g1_i1|m.18001	probable BOI-related E3 ubiquitin- ligase 2	-4.15	2.68E-09	2.86E-06
TR32504|c0_g2_i1|m.18050	amino acid permease 6-like	1.74	4.70E-04	3.34E-02
TR32919|c0_g1_i1|m.18397	ethylene-responsive transcription factor ERF026-like	4.21	8.47E-06	1.86E-03
TR33257|c0_g1_i1|m.18807	amino acid permease 4-like	3.18	1.11E-05	2.18E-03
TR33289|c0_g1_i1|m.18846	CBL-interacting kinase 23	-1.71	3.50E-07	1.72E-04
TR33289|c0_g2_i1|m.18848	CBL-interacting kinase 23	-1.64	4.48E-07	2.03E-04
TR33837|c0_g2_i1|m.19352	-No hit found-	2.97	2.98E-06	8.25E-04
TR33838|c0_g1_i1|m.19354	probable carboxylesterase 17	5.23	8.21E-07	3.26E-04
TR33915|c0_g1_i3|m.19405	probable receptor kinase At1g80640	2.98	4.45E-07	2.03E-04
TR34229|c0_g1_i1|m.19831	monoacylglycerol lipase ABHD6-like	2.43	6.48E-04	4.20E-02
TR34234|c0_g2_i1|m.19858	tubby-like F-box 1	-1.72	5.72E-04	3.85E-02
TR34319|c0_g1_i1|m.19988	phosphatidylinositol 4-kinase gamma 4-like	-3.12	7.10E-06	1.65E-03
TR34367|c0_g3_i2|m.20112	nuclear transcription factor Y subunit A-7-like [Gossypium raimondii]	1.42	4.04E-04	2.98E-02
TR34416|c0_g3_i1|m.20207	HVA22 g [Populus euphratica]	-1.67	3.12E-06	8.57E-04
TR34416|c0_g2_i1|m.20205	HVA22 g	-1.56	9.13E-05	1.07E-02
TR34493|c1_g1_i1|m.20377	calmodulin-binding family [Populus trichocarpa]	-1.60	8.58E-06	1.87E-03
TR34688|c1_g1_i1|m.20685	chaperone 1	-2.67	2.57E-05	4.16E-03
TR34743|c0_g2_i3|m.20764	squamosa promoter-binding 14	-1.25	1.90E-04	1.76E-02
TR34743|c0_g2_i1|m.20762	squamosa promoter-binding 14	-1.24	6.05E-04	4.01E-02
TR35007|c0_g1_i1|m.21018	Signal transducer and transcription activator isoform 1 [Theobroma cacao]	-1.52	2.82E-04	2.32E-02
TR35165|c0_g1_i1|m.21227	Os01g0825900 [Oryza sativa Japonica Group]	-1.79	6.03E-04	4.01E-02
TR35202|c0_g2_i1|m.21315	cyclic nucleotide-gated ion channel 18	-2.43	3.40E-04	2.59E-02
TR35428|c0_g1_i2|m.21612	C2 domain-containing At1g53590-like isoform X2	-1.14	6.02E-04	4.01E-02
TR35484|c0_g1_i1|m.21690	BTB POZ domain-containing At3g50780-like [Musa acuminata malaccensis]	1.55	1.75E-04	1.71E-02
TR35487|c0_g1_i3|m.21698	anthocyanidin reductase-like	2.11	9.51E-05	1.09E-02

TR35598|c0_g3_i2|m.21885	cryptochrome DASH, chloroplastic mitochondrial	1.32	6.46E-04	4.19E-02
TR35617|c0_g2_i1|m.21910	transcription factor bHLH87-like	-2.19	1.28E-06	4.26E-04
TR35680|c0_g1_i2|m.22012	AC025782_3Ty1 copia-element poly	5.56	6.27E-04	4.12E-02
TR35726|c0_g2_i1|m.22087	Extra-large GTP-binding 3 [Theobroma cacao]	-2.72	1.49E-05	2.73E-03
TR35746|c0_g1_i2|m.22119	probable WRKY transcription factor 41	-2.36	7.30E-04	4.48E-02
TR35950|c2_g1_i1|m.22478	patatin 2	-1.34	6.37E-04	4.16E-02
TR36150|c0_g2_i1|m.22852	PIN , partial	2.22	3.40E-05	5.20E-03
TR36229|c0_g1_i2|m.23050	nascent polypeptide-associated complex subunit alpha, muscle-specific form-like	-2.99	2.04E-04	1.84E-02
TR36237|c1_g2_i1|m.23073	beta-1,4-mannosyl-glyco 4-beta-N-acetylglucosaminyltransferase-like isoform X2	-1.60	2.87E-04	2.34E-02
TR36252|c1_g1_i2|m.23112	Os06g0256300 [Oryza sativa Japonica Group]	-1.76	3.25E-05	5.01E-03
TR36252|c1_g1_i5|m.23124	Os06g0256300 [Oryza sativa Japonica Group]	-1.74	1.91E-04	1.76E-02
TR36397|c0_g1_i1|m.23388	-No hit found-	-3.19	2.31E-05	3.86E-03
TR36489|c0_g1_i1|m.23629	probable receptor-like serine threonine- kinase At5g57670	-3.34	9.56E-07	3.59E-04
TR36489|c0_g1_i1|m.23628	probable receptor-like serine threonine- kinase At5g57670	-2.31	3.59E-05	5.36E-03
TR36585|c0_g1_i5|m.23813	trans-cinnamate 4-monooxygenase	2.03	5.25E-04	3.62E-02
TR36820|c0_g1_i1|m.24289	pentatricopeptide repeat-containing At5g59200, chloroplastic isoform X1 [Gossypium raimondii]	2.42	1.27E-06	4.26E-04
TR36910|c0_g1_i1|m.24467	PREDICTED: uncharacterized protein LOC105037495	1.63	6.78E-04	4.31E-02
TR36945|c0_g2_i1|m.24543	probable aquaporin PIP1-2	1.56	2.72E-04	2.28E-02
TR37001|c2_g1_i2|m.24622	transcription factor HY5	1.91	3.62E-04	2.72E-02
TR37118|c0_g1_i1|m.24855	HHL1, chloroplastic	2.23	7.01E-09	6.26E-06
TR37125|c1_g2_i1|m.24870	blue copper -like	1.87	6.95E-04	4.36E-02
TR37134|c0_g2_i1|m.24918	Os02g0159200 [Oryza sativa Japonica Group]	-2.75	3.02E-04	2.40E-02
TR37204|c0_g1_i1|m.25042	programmed cell death 4 [Fragaria vesca vesca]	-2.32	1.56E-04	1.58E-02
TR37279|c1_g1_i1|m.25148	calcium-dependent kinase 8-like	-1.42	6.53E-05	8.63E-03
TR37287|c0_g1_i1|m.25156	pectate lyase-like	5.27	6.02E-04	4.01E-02
TR37493|c0_g1_i3|m.25520	Os09g0468900 [Oryza sativa Japonica Group]	-1.91	1.08E-04	1.20E-02
TR37515|c1_g3_i1|m.25534	dentin sialophospho -like	-1.64	9.87E-06	2.07E-03
TR37660|c0_g1_i1|m.25770	PREDICTED: uncharacterized protein LOC102583496	2.13	7.46E-04	4.52E-02
TR37695|c0_g1_i1|m.25816	-No hit found-	3.53	5.29E-10	6.57E-07
TR37695|c0_g1_i2|m.25820	-No hit found-	-4.35	4.80E-17	1.52E-13
TR37762|c1_g1_i3|m.25984	probable inorganic phosphate transporter 1-8	1.44	2.64E-04	2.23E-02
TR37762|c1_g1_i1|m.25980	probable inorganic phosphate transporter 1-8	1.33	4.84E-04	3.41E-02
TR37793|c1_g1_i1|m.26044	cucumber peeling cupredoxin-like	-1.68	3.72E-04	2.79E-02
TR37794|c0_g1_i1|m.26045	Os03g0295600 [Oryza sativa Japonica Group]	2.95	1.27E-04	1.36E-02
TR37948|c0_g1_i1|m.26346	metal-nicotianamine transporter YSL3-like [Nelumbo nucifera]	1.63	6.17E-05	8.35E-03
TR37948|c0_g1_i4|m.26357	metal-nicotianamine transporter YSL3-like [Nelumbo nucifera]	1.48	1.21E-04	1.30E-02
TR37948|c0_g1_i5|m.26361	probable metal-nicotianamine transporter YSL9 isoform X2 [Brachypodium distachyon]	1.64	3.03E-04	2.40E-02
TR37948|c0_g1_i1|m.26347	metal-nicotianamine transporter YSL3-like [Nelumbo nucifera]	1.71	3.16E-04	2.47E-02
TR37981|c0_g2_i1|m.26424	SNAP25 homologous SNAP33-like	-2.26	2.50E-05	4.08E-03
TR38113|c0_g1_i1|m.26646	Adenine guanine permease AZG2	3.11	5.85E-05	7.95E-03
TR38271|c0_g1_i1|m.27058	transposon CACTA, En Spm sub-class [Zea mays]	-1.46	1.08E-04	1.20E-02
TR38271|c0_g1_i2|m.27060	DNA-directed RNA polymerase II subunit RPB1-like	-1.23	7.54E-04	4.56E-02
TR38296|c0_g1_i1|m.27095	cytokinin dehydrogenase 9-like	-4.62	1.48E-18	6.03E-15
TR38347|c0_g3_i1|m.27196	apetala1 squamosa	6.32	7.22E-04	4.44E-02
TR38372|c0_g2_i1|m.27245	Os08g0476100, partial [Oryza sativa Japonica Group]	1.31	1.84E-04	1.75E-02
TR38372|c0_g1_i1|m.27238	Os09g0463300 [Oryza sativa Japonica Group]	1.30	5.25E-04	3.62E-02
TR38372|c0_g1_i2|m.27240	Os09g0463300 [Oryza sativa Japonica Group]	1.22	8.42E-04	4.94E-02
TR38374|c0_g2_i1|m.27249	ALA-interacting subunit 3-like	-2.29	2.20E-05	3.73E-03
TR38374|c0_g2_i3|m.27254	ALA-interacting subunit 5-like	-3.40	4.27E-05	6.12E-03
TR38403|c0_g1_i3|m.27365	phospholipid-transporting ATPase 9	-1.54	1.57E-04	1.58E-02
TR38403|c0_g1_i2|m.27362	phospholipid-transporting ATPase 9	-1.49	1.59E-04	1.60E-02
TR38413|c0_g1_i1|m.27404	serine threonine- kinase HT1-like	-1.86	9.20E-08	5.47E-05
TR38413|c0_g1_i1|m.27403	serine threonine- kinase HT1-like	-1.50	1.64E-04	1.63E-02
TR38456|c0_g1_i1|m.27513	MATE efflux family 5 [Vitis vinifera]	2.49	4.29E-05	6.12E-03
TR38507|c0_g1_i2|m.27610	transcription factor bHLH18-like	2.03	8.74E-07	3.42E-04
TR38736|c0_g1_i1|m.27991	Peptide transporter family 1	2.35	2.70E-09	2.86E-06
TR38747|c0_g1_i3|m.28055	galacturonosyltransferase 8	1.24	8.44E-04	4.94E-02
TR38902|c0_g1_i1|m.28365	transmembrane , [Medicago truncatula]	2.01	7.39E-04	4.51E-02
TR38921|c0_g1_i1|m.28421	chalcone synthase, partial	3.92	4.37E-06	1.16E-03
TR38987|c2_g2_i1|m.28520	MATE efflux family 5-like	-1.89	1.17E-05	2.27E-03
TR39004|c0_g1_i2|m.28536	PREDICTED: uncharacterized protein LOC105059154 isoform X2	1.15	7.14E-04	4.40E-02
TR39136|c0_g1_i2|m.28805	probable trehalose-phosphate phosphatase 6	3.02	6.65E-04	4.27E-02
TR39282|c0_g1_i1|m.29150	Os02g0732200 [Oryza sativa Japonica Group]	-2.86	2.67E-06	7.56E-04
TR39289|c0_g1_i1|m.29169	receptor kinase HSL1	1.86	3.65E-05	5.41E-03
TR39318|c2_g1_i1|m.29265	GTPase-activating GYP7-like isoform X2	-1.46	8.57E-04	4.99E-02
TR39346|c0_g2_i14|m.29357	type I inositol 1,4,5-trisphosphate 5-phosphatase 1 isoform X3 [Vitis vinifera]	-1.49	8.66E-05	1.04E-02
TR39346|c0_g2_i2|m.29338	type I inositol 1,4,5-trisphosphate 5-phosphatase 1-like isoform X3	-1.48	2.55E-04	2.18E-02
TR39459|c2_g1_i1|m.29727	calcium-dependent kinase 8-like	-1.58	3.56E-05	5.35E-03
TR39484|c0_g1_i1|m.29762	PIN , partial	1.74	8.78E-05	1.05E-02
TR39572|c0_g1_i3|m.29931	gibberellin 2-beta-dioxygenase 8-like	-1.94	1.22E-04	1.31E-02
TR39594|c0_g1_i1|m.29977	endoglucanase 6	4.43	3.01E-11	5.06E-08
TR39730|c0_g1_i7|m.30520	UPSTREAM OF FLC [Nelumbo nucifera]	1.63	5.22E-04	3.62E-02
TR39795|c0_g1_i4|m.30615	ATP-dependent 6-phosphofructokinase 3-like	-1.62	1.86E-04	1.76E-02
TR39932|c0_g2_i2|m.30812	growth-regulating factor 4-like	-2.10	7.79E-04	4.69E-02
TR40026|c0_g1_i2|m.31025	magnesium-chelatase subunit , chloroplastic	1.65	4.36E-05	6.19E-03
TR40122|c0_g1_i1|m.31381	probable polygalacturonase isoform X1	2.41	3.10E-08	2.21E-05
TR40127|c1_g1_i1|m.31390	gibberellin 3-beta-dioxygenase 1-like	2.11	1.36E-05	2.52E-03
TR40170|c1_g1_i1|m.31462	NAC transcription factor 29-like	-2.56	2.86E-04	2.34E-02
TR40172|c0_g1_i1|m.31463	pentatricopeptide repeat-containing At1g09190	1.79	2.85E-04	2.34E-02
TR40385|c4_g1_i1|m.31899	receptor kinase HSL1	1.84	7.07E-04	4.39E-02
TR40390|c0_g1_i1|m.31915	phytochrome A-associated F-box	1.81	2.33E-04	2.04E-02
TR40427|c0_g1_i1|m.31998	microtubule-associated TORTIFOLIA1-like	1.35	7.02E-05	8.95E-03
TR40434|c0_g1_i1|m.32026	beta-carotene hydroxylase	1.70	1.63E-04	1.62E-02
TR40467|c2_g1_i3|m.32087	sugar transporter ERD6-like 16	-1.39	2.69E-04	2.26E-02
TR40524|c0_g3_i11|m.32191	probable glucan 1,3-beta-glucosidase A [Populus euphratica]	-2.07	6.46E-05	8.60E-03
TR40563|c1_g1_i2|m.32284	4-coumarate-- ligase-like 7 isoform X2	2.20	5.84E-04	3.92E-02

TR40772|c0_g1_i4|m.32740	E2F DP family winged-helix DNA-binding domain isoform 1 [Theobroma cacao]	-2.11	2.82E-05	4.48E-03
TR40851|c1_g3_i3|m.32949	G-type lectin S-receptor-like serine threonine- kinase B120	-1.22	5.52E-04	3.75E-02
TR40874|c1_g1_i1|m.33031	Caffeic acid 3-O-methyltransferase	1.40	1.35E-05	2.52E-03
TR40885|c0_g1_i1|m.33063	potassium transporter 8-like isoform X1 [Nelumbo nucifera]	1.76	9.46E-07	3.59E-04
TR40886|c3_g1_i1|m.33071	PREDICTED: uncharacterized protein LOC103994823	-3.00	8.38E-04	4.94E-02
TR40902|c0_g4_i1|m.33130	agamous-like MADS-box AGL80	-2.32	3.81E-04	2.85E-02
TR40939|c0_g1_i1|m.33264	probable RNA helicase SDE3	1.66	5.05E-04	3.53E-02
TR40989|c0_g1_i1|m.33400	auxin-induced 6B-like	-3.72	2.31E-05	3.86E-03
TR41005|c0_g1_i1|m.33438	[Hordeum vulgare vulgare]	1.72	4.84E-04	3.41E-02
TR41061|c0_g1_i1|m.33585	orf169 (mitochondrion) [Batis maritima]	-1.74	1.64E-05	2.91E-03
TR41094|c5_g1_i1|m.33745	-No hit found-	-1.93	2.07E-04	1.86E-02
TR41094|c1_g1_i1|m.33733	probable WRKY transcription factor 41	-1.59	6.29E-04	4.12E-02
TR41280|c1_g1_i2|m.34222	isoflavone 2 -hydroxylase-like	-1.87	3.59E-04	2.71E-02
TR41308|c0_g1_i1|m.34285	ethylene-responsive transcription factor 1B-like	-3.72	4.14E-09	4.08E-06
TR41513|c1_g1_i1|m.34802	probable inactive receptor kinase At5g58300 [Nelumbo nucifera]	-2.21	1.50E-06	4.80E-04
TR41551|c1_g3_i1|m.34865	probable phosphatase 2C 78	-1.72	2.07E-04	1.86E-02
TR41557|c0_g1_i1|m.34888	TOM1 2	-1.45	3.40E-04	2.59E-02
TR41557|c0_g1_i2|m.34890	TOM1 2	-1.41	4.21E-04	3.05E-02
TR41575|c2_g1_i1|m.34939	cysteine-rich receptor kinase 2	-1.47	7.80E-06	1.74E-03
TR41575|c2_g2_i1|m.34941	cysteine-rich receptor kinase 2	-1.60	2.49E-05	4.08E-03
TR41667|c0_g1_i1|m.35198	PREDICTED: uncharacterized protein LOC103715017	1.91	1.80E-04	1.74E-02
TR41744|c0_g2_i5|m.35412	guanylate kinase 1-like isoform X1 [Elaeis guineensis]	-1.77	3.27E-05	5.02E-03
TR41744|c0_g2_i2|m.35410	guanylate kinase 1-like isoform X1 [Elaeis guineensis]	-1.60	1.09E-04	1.20E-02
TR41868|c1_g1_i1|m.35746	hypothetical protein EUGRSUZ_B02857	-1.68	3.97E-05	5.76E-03
TR41868|c1_g1_i2|m.35748	-No hit found-	-1.95	6.85E-05	8.82E-03
TR42060|c0_g1_i3|m.36131	AF439853_1pathogen-induced calmodulin-binding	-1.52	6.76E-06	1.60E-03
TR42090|c1_g2_i2|m.36204	cyclin-D3-1-like	2.63	9.22E-06	1.98E-03
TR42110|c0_g1_i12|m.36257	serine threonine- kinase HT1-like	-1.94	7.15E-06	1.65E-03
TR42110|c0_g1_i11|m.36256	serine threonine- kinase HT1-like	-2.02	1.10E-05	2.17E-03
TR42110|c0_g1_i10|m.36255	serine threonine- kinase HT1-like	-1.77	9.53E-05	1.09E-02
TR42167|c0_g1_i1|m.36415	probable pectate lyase 5 [Brachypodium distachyon]	3.00	8.46E-09	7.10E-06
TR42167|c0_g1_i2|m.36418	probable pectate lyase 5 [Brachypodium distachyon]	2.72	1.12E-06	4.00E-04
TR42167|c2_g1_i1|m.36424	probable pectate lyase 8	-2.59	1.81E-04	1.74E-02
TR42253|c0_g3_i1|m.36705	malate synthase, glyoxysomal	-3.53	5.16E-14	1.47E-10
TR42268|c0_g1_i3|m.36734	PREDICTED: uncharacterized protein LOC104595815	-2.47	1.01E-04	1.14E-02
TR42275|c0_g1_i1|m.36783	UDP-glycosyltransferase 73C6-like	-2.12	6.53E-06	1.55E-03
TR42297|c0_g1_i1|m.36824	E3 ubiquitin- ligase ATL41-like	-2.73	9.97E-07	3.70E-04
TR42325|c1_g1_i3|m.36876	NAC domain-containing 94	-4.08	1.17E-04	1.27E-02
TR42325|c1_g1_i1|m.36874	NAC domain-containing 94	-3.56	2.78E-04	2.31E-02
TR42420|c0_g1_i1|m.37211	hsp70 nucleotide exchange factor FES1 isoform X2	-10.19	7.72E-34	5.51E-30
TR42548|c0_g1_i2|m.37663	receptor-like serine threonine- kinase SD1-8	-1.50	4.65E-04	3.33E-02
TR42625|c0_g1_i1|m.37903	vacuolar iron transporter [Tulipa gesneriana]	1.97	7.49E-05	9.34E-03
TR42949|c2_g1_i2|m.38975	equilibrative nucleotide transporter 3-like [Nelumbo nucifera]	-1.50	6.47E-05	8.60E-03
TR43326|c0_g1_i1|m.40068	IQ-DOMAIN 14-like	-3.14	4.48E-05	6.30E-03
TR43326|c0_g1_i1|m.40069	IQ-DOMAIN 14-like	-2.90	1.89E-04	1.76E-02
TR43331|c0_g1_i1|m.40072	probable trehalose-phosphate phosphatase F [Nelumbo nucifera]	-2.10	7.42E-04	4.51E-02
TR43497|c1_g1_i1|m.40500	-No hit found-	-2.41	3.60E-06	9.61E-04
TR43801|c0_g1_i1|m.41338	BURP domain-containing 12-like	1.99	1.14E-07	6.49E-05
TR43821|c2_g2_i1|m.41471	methylesterase 11, chloroplastic	-2.11	7.18E-06	1.65E-03
TR43858|c0_g1_i1|m.41579	transcription factor EMB1444-like isoform X1	2.86	1.31E-04	1.38E-02
TR44008|c1_g1_i1|m.42130	auxin-induced 6B-like	-4.07	2.66E-06	7.56E-04
TR44022|c0_g1_i1|m.42169	ZCF37, [Theobroma cacao]	-4.24	3.01E-04	2.40E-02
TR44058|c0_g1_i4|m.42263	catalytic hydrolase [Zea mays]	2.22	1.05E-05	2.14E-03
TR44146|c11_g1_i1|m.42691	PREDICTED: uncharacterized protein LOC103714925 [Phoenix dactylifera]	-2.04	1.19E-06	4.15E-04
TR44242|c0_g1_i1|m.43064	PREDICTED: uncharacterized protein LOC105047454	-3.70	3.71E-05	5.43E-03
TR44319|c6_g1_i1|m.43407	zinc finger NUTCRACKER-like [Elaeis guineensis]	1.84	6.05E-04	4.01E-02
TR44379|c0_g1_i8|m.43666	-No hit found-	-2.80	3.83E-04	2.85E-02
TR44794|c0_g1_i23|m.45055	alpha-xylosidase 2	-1.37	3.08E-04	2.44E-02
TR44909|c3_g3_i2|m.45334	NEP1-interacting 1	-1.96	6.17E-06	1.51E-03
TR45000|c0_g1_i1|m.45617	homeobox-leucine zipper HAT22-like	2.01	3.28E-04	2.54E-02
TR45148|c0_g1_i1|m.46044	PREDICTED: uncharacterized protein LOC103701651 [Phoenix dactylifera]	-1.13	3.91E-04	2.90E-02
TR45260|c0_g1_i1|m.46458	sulfate transporter -like	3.01	2.94E-06	8.23E-04
TR45313|c1_g5_i2|m.46576	probable inactive receptor kinase At5g10020	1.65	4.21E-04	3.05E-02
TR45362|c0_g1_i3|m.46779	heptahelical transmembrane 4-like	-1.93	3.53E-04	2.66E-02
TR45363|c0_g6_i1|m.46792	G-type lectin S-receptor-like serine threonine- kinase SD2-5	2.23	9.05E-05	1.07E-02
TR45437|c0_g1_i1|m.47140	scopoletin glucosyltransferase-like	2.42	2.97E-04	2.39E-02
TR45588|c1_g1_i1|m.47570	myb-related Hv1-like	-1.35	1.95E-04	1.79E-02
TR45608|c0_g2_i1|m.47694	premnaspirodiene oxygenase-like	-1.64	9.23E-05	1.08E-02
TR45608|c0_g2_i2|m.47695	premnaspirodiene oxygenase-like	-1.60	9.42E-05	1.09E-02
TR45661|c2_g1_i3|m.47873	cytochrome P450 CYP72A219-like	-2.11	5.76E-06	1.42E-03
TR45661|c2_g1_i2|m.47870	cytochrome P450 CYP72A219-like	-2.58	2.39E-05	3.96E-03
TR45895|c0_g2_i2|m.48604	histone 3	5.23	1.41E-11	2.51E-08
TR45921|c0_g1_i1|m.48681	tricetin 3 ,4 ,5 -O-trimethyltransferase-like	3.77	7.63E-08	4.69E-05
TR45981|c0_g1_i7|m.48883	soluble inorganic pyrophosphatase-like	-2.16	6.26E-08	4.15E-05
TR45981|c0_g1_i3|m.48879	soluble inorganic pyrophosphatase-like	-2.50	2.38E-07	1.26E-04
TR46101|c1_g1_i6|m.49141	PREDICTED: uncharacterized protein LOC103720282 [Phoenix dactylifera]	2.61	1.76E-06	5.51E-04
TR46101|c1_g1_i2|m.49135	PREDICTED: uncharacterized protein LOC103720282 [Phoenix dactylifera]	-2.97	1.03E-06	3.79E-04
TR46101|c1_g1_i4|m.49138	Os06g0711100 [Oryza sativa Japonica Group]	-2.06	4.26E-05	6.12E-03
TR46101|c1_g1_i1|m.49133	Os06g0711100 [Oryza sativa Japonica Group]	-1.91	1.88E-04	1.76E-02
TR46306|c2_g1_i1|m.49798	subtilisin-like protease SDD1	3.10	1.29E-05	2.44E-03
TR46306|c2_g1_i2|m.49800	subtilisin-like protease	3.15	5.06E-05	6.97E-03
TR46309|c0_g1_i2|m.49815	bZIP transcription factor bZIP100	1.66	3.00E-05	4.68E-03
TR46334|c0_g2_i1|m.49987	high affinity nitrate transporter -like	1.54	1.49E-04	1.52E-02
TR46434|c3_g1_i6|m.50370	calmodulin-binding family [Populus trichocarpa]	-6.67	3.22E-13	7.66E-10
TR46434|c3_g1_i5|m.50369	calmodulin-binding family [Populus trichocarpa]	-5.15	4.47E-10	5.80E-07
TR47001|c0_g1_i1|m.51909	calcium-binding CML19	-3.99	1.43E-04	1.47E-02

TR47001|c0_g1_i2|m.51911	calcium-binding CML19	-3.57	2.05E-04	1.84E-02
TR47151|c1_g2_i3|m.52454	respiratory burst oxidase homolog H	2.92	1.70E-04	1.68E-02
TR47151|c0_g1_i1|m.52441	respiratory burst oxidase homolog H	1.64	6.42E-04	4.18E-02
TR47291|c0_g3_i2|m.52795	probable WRKY transcription factor 70	-2.24	5.39E-05	7.37E-03
TR47330|c1_g2_i1|m.52912	cytosolic class I small heat shock 3B, partial [Nicotiana tabacum]	-2.34	1.10E-05	2.17E-03
TR47395|c0_g1_i1|m.53050	photosystem II D1 (chloroplast) [Triticum turgidum]	-3.09	1.26E-05	2.41E-03
TR47495|c4_g1_i1|m.53287	WAT1-related At4g30420-like	2.22	7.73E-08	4.69E-05
TR47753|c0_g1_i1|m.53958	ribonuclease H2 subunit B isoform X1 [Elaeis guineensis]	2.85	5.19E-07	2.21E-04
TR47753|c0_g1_i3|m.53962	ribonuclease H2 subunit B isoform X1 [Elaeis guineensis]	3.60	1.85E-04	1.76E-02
TR48005|c6_g7_i14|m.54765	hypothetical protein CICLE_v10033129mg [Citrus clementina]	1.65	1.09E-06	3.96E-04
TR48023|c2_g1_i9|m.54838	pleiotropic drug resistance 7	-1.79	8.24E-05	1.00E-02
TR48102|c0_g1_i3|m.55085	Os11g0594700 [Oryza sativa Japonica Group]	-1.87	1.87E-06	5.81E-04
TR48102|c0_g1_i1|m.55082	Os11g0594700 [Oryza sativa Japonica Group]	-1.86	2.31E-06	6.79E-04
TR48102|c0_g1_i2|m.55084	Os11g0594700 [Oryza sativa Japonica Group]	-1.78	6.44E-06	1.55E-03
TR48205|c0_g1_i1|m.55438	BAG family molecular chaperone regulator 5 [Morus notabilis]	-2.10	3.69E-05	5.42E-03
TR48205|c0_g1_i4|m.55444	BAG family molecular chaperone regulator 5 [Morus notabilis]	-1.87	3.33E-04	2.55E-02
TR48274|c3_g13_i1|m.55617	Os05g0474900 [Oryza sativa Japonica Group]	-1.33	8.59E-04	4.99E-02
TR48359|c0_g1_i1|m.55785	glycosyltransferase family 64 C4	-1.91	3.84E-04	2.86E-02
TR48361|c2_g2_i1|m.55799	oligopeptide transporter 1-like	-2.49	7.92E-04	4.74E-02
TR48498|c0_g1_i2|m.55978	cytochrome P450 71A1-like	1.58	1.81E-04	1.74E-02
TR48498|c0_g1_i1|m.55973	cytochrome P450 71A1-like	1.62	5.35E-04	3.65E-02
TR48501|c0_g1_i1|m.55980	probable mitochondrial chaperone BCS1-B	-1.60	3.93E-04	2.91E-02
TR48541|c3_g1_i4|m.56034	bifunctional 1, mitochondrial isoform X1 [Vitis vinifera]	2.02	3.23E-06	8.77E-04
TR48748|c0_g1_i3|m.56279	probable sulfate transporter	3.25	2.67E-10	3.63E-07
TR48791|c2_g2_i1|m.56431	-No hit found-	-1.91	1.18E-04	1.28E-02
TR48849|c3_g1_i3|m.56521	CHUP1, chloroplastic-like isoform X1	-1.68	6.43E-06	1.55E-03
TR48849|c3_g1_i2|m.56519	CHUP1, chloroplastic-like isoform X2	-1.91	6.81E-05	8.82E-03
TR48849|c3_g1_i1|m.56518	CHUP1, chloroplastic-like	-1.82	1.39E-04	1.44E-02
TR48905|c2_g3_i13|m.56641	bidirectional sugar transporter SWEET4-like	-3.96	2.58E-05	4.17E-03
TR48905|c2_g3_i8|m.56634	bidirectional sugar transporter SWEET4-like	-4.04	1.06E-04	1.19E-02
TR49099|c4_g1_i15|m.56954	probable galactinol--sucrose galactosyltransferase 6	1.60	3.81E-05	5.55E-03
TR49099|c4_g2_i3|m.56971	probable galactinol--sucrose galactosyltransferase 6	1.77	7.81E-05	9.66E-03
TR49099|c4_g1_i8|m.56937	probable galactinol--sucrose galactosyltransferase 6	1.56	9.46E-05	1.09E-02
TR49343|c2_g2_i7|m.57797	BPS1, chloroplastic-like	-2.85	6.97E-04	4.36E-02
TR49343|c2_g2_i6|m.57795	BPS1, chloroplastic-like	-3.50	7.71E-04	4.65E-02
TR49343|c2_g2_i4|m.57791	BPS1, chloroplastic-like	-2.92	8.50E-04	4.96E-02
TR49551|c3_g2_i11|m.58151	Uncharacterized protein TCM_016762 [Theobroma cacao]	-3.14	3.27E-04	2.54E-02
TR50279|c1_g1_i5|m.59576	BED zinc finger,hAT family dimerization domain, isoform 1 [Theobroma cacao]	1.43	6.96E-04	4.36E-02
TR50331|c2_g2_i5|m.59707	S-type anion channel SLAH2-like isoform X1 [Phoenix dactylifera]	-3.57	9.68E-05	1.10E-02
TR50337|c8_g2_i1|m.59729	PREDICTED: uncharacterized protein LOC103628351	4.50	2.39E-04	2.07E-02
TR50341|c2_g1_i1|m.59757	Sec14p-like phosphatidylinositol transfer family isoform 1 [Theobroma cacao]	-2.03	9.33E-06	1.99E-03
TR50409|c0_g1_i2|m.59867	histone-lysine N-methyltransferase SUVR2	1.19	6.21E-04	4.10E-02
TR50510|c1_g2_i5|m.60014	S-norcoclaurine synthase 1-like	-2.22	3.06E-05	4.75E-03
TR50510|c1_g2_i13|m.60025	S-norcoclaurine synthase 1-like	-2.47	9.59E-05	1.09E-02
TR50772|c1_g2_i10|m.60505	[Physcomitrella patens]	-3.08	2.74E-13	7.10E-10
TR50772|c1_g2_i1|m.60498	[Physcomitrella patens]	-2.54	3.15E-12	6.91E-09
TR50772|c1_g2_i8|m.60504	[Arabidopsis lyrata lyrata]	-3.35	1.16E-11	2.36E-08
TR51129|c1_g3_i1|m.61033	leucine-rich repeat receptor-like serine threonine- kinase BAM1	3.28	5.46E-06	1.36E-03
TR51129|c3_g1_i1|m.61038	leucine-rich repeat receptor-like serine threonine- kinase BAM1	3.07	1.37E-04	1.43E-02
TR51129|c1_g2_i1|m.61030	leucine-rich repeat receptor-like serine threonine- kinase BAM1	2.35	1.82E-04	1.74E-02
TR51258|c5_g4_i12|m.61164	exocyst complex component SEC3B-like, partial [Vigna radiata radiata]	-2.28	2.29E-06	6.79E-04
TR51258|c5_g4_i1|m.61149	-No hit found-	-2.26	6.72E-05	8.77E-03
TR52411|c0_g3_i1|m.62579	pectinesterase pectinesterase inhibitor U1	2.26	2.12E-08	1.64E-05
TR52426|c3_g2_i1|m.62615	S-locus lectin kinase family , [Theobroma cacao]	-2.36	5.24E-04	3.62E-02
TR52426|c2_g1_i2|m.62605	PREDICTED: uncharacterized protein LOC103328423	-1.80	8.44E-04	4.94E-02
TR52667|c1_g2_i5|m.62815	transposon Tf2-1 poly isoform X1	-3.84	8.21E-04	4.87E-02
TR52721|c0_g2_i2|m.62935	premnaspirodiene oxygenase-like	1.90	2.29E-04	2.02E-02
TR52721|c0_g2_i1|m.62934	premnaspirodiene oxygenase-like	1.30	5.00E-04	3.50E-02
TR52795|c3_g1_i1|m.62999	gag-pol poly	-3.85	6.17E-07	2.55E-04
TR52795|c3_g1_i1|m.63000	hypothetical protein CICLE_v10024522mg, partial [Citrus clementina]	-3.23	2.40E-05	3.96E-03
TR52896|c2_g3_i1|m.63334	heat stress transcription factor B-1-like	-2.04	6.92E-04	4.36E-02
TR52967|c2_g1_i1|m.63442	integrase core domain	-3.00	4.47E-04	3.21E-02
TR53035|c1_g4_i7|m.63530	integrase core domain	-6.63	6.40E-08	4.15E-05
TR53212|c4_g1_i1|m.64161	Oxidative stress 3, isoform 2 [Theobroma cacao]	-2.39	2.08E-05	3.63E-03
TR53232|c0_g1_i1|m.64327	-No hit found-	-1.56	7.91E-05	9.69E-03
TR53358|c0_g1_i1|m.64652	receptor kinase HSL1	1.38	6.79E-04	4.31E-02
TR53427|c0_g1_i1|m.64746	kDa proline-rich -like	3.70	2.27E-06	6.79E-04
TR53449|c0_g1_i1|m.64769	NRT1 PTR FAMILY -like	1.70	2.00E-04	1.82E-02
TR53486|c0_g1_i1|m.64803	-No hit found-	-2.29	2.72E-08	1.99E-05
TR53541|c0_g1_i1|m.64858	xyloglucan endotransglucosylase hydrolase 2-like	2.06	1.87E-04	1.76E-02
TR53914|c0_g1_i1|m.65152	Subtilisin inhibitor 1, [Theobroma cacao]	-1.69	5.36E-06	1.34E-03
TR54163|c0_g1_i1|m.65297	zinc finger 4-like [Elaeis guineensis]	1.29	2.15E-04	1.91E-02
TR54777|c0_g1_i1|m.65513	glycerol-3-phosphate 2-O-acyltransferase 6-like	2.22	2.24E-06	6.79E-04
TR55196|c0_g1_i1|m.65624	chalcone synthase, partial	8.51	1.40E-50	3.99E-46
TR55408|c0_g1_i1|m.65674	PREDICTED: uncharacterized protein LOC105048063	1.53	4.80E-04	3.40E-02
TR56545|c0_g1_i1|m.65808	MKS1-like [Setaria italica]	-1.43	5.35E-05	7.34E-03
TR56672|c0_g1_i1|m.65821	calcium-binding CML19	-2.37	6.31E-05	8.49E-03
TR64441|c0_g1_i1|m.66169	heat shock 83	-2.13	1.27E-05	2.42E-03
TR64453|c0_g1_i1|m.66185	glutamine synthetase nodule isozyme	-2.12	4.08E-04	2.98E-02
TR64489|c0_g1_i1|m.66221	E3 ubiquitin- ligase ATL41-like	-3.37	2.14E-05	3.67E-03
TR64515|c0_g1_i1|m.66270	heat shock 70 [Populus trichocarpa]	-1.61	1.36E-04	1.42E-02
TR64539|c0_g1_i1|m.66295	7-deoxyloganetin glucosyltransferase-like	1.64	4.65E-05	6.51E-03
TR64600|c0_g1_i1|m.66394	dnaJ homolog subfamily B member 13-like	-1.44	7.10E-04	4.40E-02
TR64807|c0_g1_i1|m.66568	VQ motif [Medicago truncatula]	-3.42	3.79E-08	2.64E-05
TR64909|c0_g1_i1|m.66658	probable phosphatase 2C 74	-2.72	2.98E-07	1.52E-04
TR65094|c0_g1_i1|m.66765	ferredoxin, leaf L-A-like [Brassica napus]	1.20	8.61E-04	4.99E-02

TR65496|c0_g1_i1|m.66973	serine threonine- kinase WNK4-like	-2.51	5.55E-09	5.16E-06
TR65848|c0_g1_i1|m.67109	-No hit found-	2.06	6.29E-04	4.12E-02
TR65931|c0_g1_i1|m.67144	Mediator of RNA polymerase II transcription subunit 8 [Theobroma cacao]	1.41	3.98E-04	2.93E-02
TR66383|c0_g1_i1|m.67267	chaperone dnaJ 20, chloroplastic-like	-1.66	8.19E-05	9.99E-03
TR66507|c0_g1_i1|m.67283	ULTRAPETALA 1-like	-2.40	4.02E-08	2.73E-05
TR66507|c0_g1_i1|m.67284	ULTRAPETALA 1-like [Phoenix dactylifera]	-2.22	4.20E-07	1.96E-04
TR66633|c0_g1_i1|m.67303	auxin-induced 6B-like	-3.67	2.88E-04	2.35E-02
TR68369|c0_g1_i1|m.67510	RING-H2 finger ATL3-like	-4.09	8.54E-05	1.03E-02
TR75610|c0_g1_i1|m.67834	YLS9-like	-1.61	8.42E-04	4.94E-02
TR75733|c0_g1_i1|m.67951	CBS domain-containing CBSX5-like	1.66	1.36E-04	1.42E-02
TR75801|c0_g1_i1|m.68035	COBRA 1	1.42	2.31E-04	2.02E-02
TR75866|c0_g1_i1|m.68097	subtilisin-like protease	1.23	5.71E-04	3.85E-02
TR75896|c0_g1_i1|m.68125	pleiotropic drug resistance 7	-2.93	7.07E-04	4.39E-02
TR75982|c0_g1_i1|m.68193	suppressor SRP40-like	1.79	1.52E-06	4.84E-04
TR76125|c0_g1_i1|m.68286	transcription factor bHLH18-like	1.73	6.52E-04	4.21E-02
TR76207|c0_g1_i1|m.68334	oxygen-evolving enhancer 3-1, chloroplastic-like	1.57	7.89E-04	4.74E-02
TR76556|c0_g1_i1|m.68508	chloroplast-targeted copper chaperone, [Ricinus communis]	2.36	1.59E-05	2.86E-03
TR76748|c0_g1_i1|m.68576	Os07g0499800 [Oryza sativa Japonica Group]	-2.92	6.85E-05	8.82E-03
TR76949|c0_g5_i1|m.68655	[Hordeum vulgare vulgare]	-2.08	4.70E-07	2.05E-04
TR77009|c0_g1_i1|m.68667	PREDICTED: uncharacterized protein LOC103715832	1.64	2.11E-05	3.65E-03
TR77069|c0_g1_i1|m.68690	ASPARTIC PROTEASE IN GUARD CELL 1-like	2.31	1.31E-05	2.46E-03
TR77297|c0_g1_i1|m.68749	copper transporter 6-like	3.40	2.44E-04	2.10E-02
TR86691|c2_g3_i1|m.69277	PREDICTED: uncharacterized protein LOC105056005	1.78	2.03E-04	1.84E-02
TR86852|c0_g1_i1|m.69459	glutathione S-transferase U17-like	-1.90	9.15E-05	1.07E-02
TR87238|c0_g1_i1|m.69779	isoflavone 2 -hydroxylase-like	-2.07	4.86E-06	1.24E-03
TR87358|c0_g1_i1|m.69855	isocitrate lyase	3.55	2.99E-04	2.39E-02
TR87520|c0_g1_i1|m.69943	Soluble secretory phospholipase A2 receptor [Theobroma cacao]	-2.53	6.90E-05	8.84E-03
TR87569|c0_g1_i1|m.69977	alpha beta hydrolase domain-containing 17C-like	-1.22	3.28E-04	2.54E-02
TR87610|c0_g1_i1|m.69993	calcium-binding PBP1-like	-4.68	7.12E-08	4.52E-05
TR87910|c0_g1_i1|m.70122	patatin 3	2.13	5.26E-04	3.62E-02
TR88200|c0_g1_i1|m.70206	bidirectional sugar transporter SWEET14-like	2.42	7.36E-09	6.37E-06
TR88204|c0_g1_i1|m.70211	ethylene-responsive transcription factor ERF105-like	-2.09	4.54E-06	1.18E-03
TR88485|c0_g1_i1|m.70292	UDP-glycosyltransferase 73C6-like	-2.06	2.52E-04	2.15E-02
TR88485|c0_g1_i1|m.70293	UDP-glycosyltransferase 73C6-like	-1.63	2.97E-04	2.39E-02
TR88572|c0_g1_i1|m.70313	[Arabidopsis lyrata lyrata]	-2.78	5.35E-04	3.65E-02
TR88754|c0_g1_i1|m.70352	PREDICTED: uncharacterized protein LOC103718746	-2.30	3.49E-05	5.29E-03
TR88838|c0_g1_i1|m.70361	Os04g0136700 [Oryza sativa Japonica Group]	1.73	1.25E-05	2.41E-03
TR88916|c0_g1_i1|m.70370	UDP-glycosyltransferase 88A1-like	1.60	6.99E-04	4.37E-02
TR89872|c0_g1_i1|m.70510	basic leucine zipper 43	3.65	3.09E-04	2.44E-02
TR90480|c0_g1_i1|m.70557	chaperone dnaJ 8, chloroplastic-like	-2.17	8.02E-06	1.78E-03
TR91749|c0_g1_i1|m.70635	Uveal autoantigen with coiled-coil domains and ankyrin repeats isoform 2 [Theobroma cacao]	-2.74	3.52E-04	2.66E-02
TR92595|c0_g1_i1|m.70669	bifunctional UDP-glucose 4-epimerase and UDP-xylose 4-epimerase 1-like	-4.54	1.31E-06	4.30E-04
TR98242|c0_g1_i1|m.70801	[Oryza sativa Indica Group]	-1.71	3.00E-05	4.68E-03
TR98242|c0_g4_i1|m.70807	[Oryza sativa Indica Group]	-1.51	6.75E-04	4.31E-02
TR98425|c0_g1_i1|m.71017	-No hit found-	-3.91	2.27E-09	2.60E-06
TR99161|c0_g1_i1|m.71535	kDa class II heat shock -like	-1.80	7.41E-04	4.51E-02
TR99651|c0_g1_i1|m.71703	PREDICTED: uncharacterized protein LOC105061488	4.17	4.55E-06	1.18E-03
TR99800|c0_g1_i1|m.71752	serine threonine- kinase WAG1-like	1.55	2.52E-04	2.15E-02
TR99894|c0_g1_i1|m.71775	caffeoyl- O-methyltransferase	1.59	1.09E-04	1.20E-02
TR99930|c0_g1_i1|m.71785	hypothetical protein PHAVU_003G272000g [Phaseolus vulgaris]	-3.83	1.31E-11	2.50E-08
TR100616|c0_g1_i1|m.71903	Os02g0134200 [Oryza sativa Japonica Group]	-1.75	6.74E-04	4.31E-02
TR101099|c0_g1_i1|m.71966	DNA-damage-repair toleration DRT100-like	2.98	6.72E-07	2.70E-04
TR101222|c0_g1_i1|m.71976	heat shock 22 kDa , mitochondrial	-2.13	1.08E-07	6.29E-05
TR101941|c0_g1_i1|m.72043	auxin-induced 6B-like	-2.71	4.56E-07	2.03E-04
TR102342|c0_g1_i1|m.72065	ferredoxin, root R-B1-like [Elaeis guineensis]	10.11	2.35E-29	1.34E-25
TR109431|c0_g1_i1|m.72343	-No hit found-	-2.02	1.81E-05	3.19E-03
TR109620|c0_g1_i1|m.72562	thaumatin 1b	1.53	9.02E-05	1.07E-02
TR110169|c0_g1_i1|m.73014	transmembrane , [Medicago truncatula]	-1.55	7.28E-05	9.19E-03
TR110258|c0_g1_i1|m.73061	glycerophosphodiester phosphodiesterase GDE1-like	3.00	9.27E-05	1.08E-02
TR110476|c0_g1_i1|m.73148	BURP domain-containing 12-like	2.00	4.07E-04	2.98E-02
TR110753|c0_g1_i1|m.73247	lipid phosphate phosphatase 2-like [Musa acuminata malaccensis]	-2.00	1.61E-04	1.61E-02
TR111510|c0_g1_i1|m.73410	R2R3-MYB transcription factor [Quercus suber]	2.39	5.67E-04	3.84E-02
TR111561|c0_g1_i1|m.73419	mavicyanin-like	1.30	1.71E-04	1.69E-02
TR112951|c0_g1_i1|m.73594	glycerophosphodiester phosphodiesterase GDPD1, chloroplastic-like	2.05	2.91E-04	2.35E-02
TR113773|c0_g1_i1|m.73644	Sulfate transporter 1,3 isoform 1 [Theobroma cacao]	5.94	2.82E-04	2.32E-02

[a]logFC represents log2 of albino versus green plants based on transcriptome analysis.

Supplementary table 5 Differentially expressed genes of fungi

Sequence ID	Description (BLASTX search against the nr database)	logFC^{a}	*p* -value	FDR
TR28|c0_g1_i1|m.16	peroxisomal carrier [Colletotrichum gloeosporioides Nara gc5]	7.45	8.15E-04	2.97E-02
TR197|c0_g1_i1|m.45	glycerol-3-phosphate dehydrogenase [Exophiala aquamarina CBS 119918]	7.64	2.13E-04	1.34E-02
TR301|c0_g1_i1|m.72	integral membrane	9.12	2.06E-04	1.32E-02
TR378|c0_g1_i1|m.91	integral membrane [Verticillium alfalfae]	9.95	6.69E-04	2.65E-02
TR461|c0_g1_i1|m.116	hypothetical protein PFICI_07893 [Pestalotiopsis fici W106-1]	8.30	1.68E-06	1.18E-03
TR534|c0_g2_i1|m.125	glutathione-dependent formaldehyde-activating [Neofusicoccum parvum UCRNP2]	11.90	7.40E-06	2.26E-03
TR699|c0_g1_i1|m.155	hypothetical protein VP1G_04068	10.48	1.77E-05	3.30E-03
TR1002|c0_g1_i1|m.209	related to rasp f 7 allergen [Neurospora crassa]	11.16	9.11E-08	3.06E-04
TR1010|c0_g1_i1|m.211	CMGC SRPK kinase [Fusarium oxysporum FOSC 3-a]	9.08	8.14E-04	2.97E-02
TR1257|c0_g1_i1|m.270	quercetin 2,3-dioxygenase	6.91	4.58E-04	2.08E-02
TR1411|c0_g1_i1|m.294	hexokinase family [Phaeoacremonium minimum UCRPA7]	6.83	6.20E-04	2.51E-02
TR1672|c0_g1_i1|m.336	Cytochrome P450 61	6.41	1.54E-03	4.56E-02
TR1893|c0_g1_i1|m.397	serine threonine- phosphatase 2B catalytic subunit	9.22	8.06E-04	2.96E-02
TR1931|c0_g1_i1|m.405	A49-like RNA polymerase I associated factor	7.98	1.04E-03	3.45E-02
TR2145|c0_g1_i1|m.462	Cerato-platanin [Dichomitus squalens LYAD-421 SS1]	-3.70	1.81E-03	4.98E-02
TR2217|c0_g1_i1|m.485	arg-6 [Verticillium dahliae]	9.72	2.46E-04	1.46E-02
TR2334|c0_g1_i1|m.512	dicarboxylic amino acid permease	8.32	1.44E-05	2.91E-03
TR2346|c0_g1_i1|m.515	serine hydroxymethyltransferase	9.41	8.63E-04	3.06E-02
TR2463|c0_g1_i1|m.556	[Trichoderma reesei QM6a]	7.27	1.10E-03	3.60E-02
TR2470|c0_g1_i1|m.566	ochre suppressor tyr-tRNA [Fusarium fujikuroi]	8.02	6.87E-04	2.68E-02
TR2550|c0_g1_i1|m.586	alkaline phosphatase	9.34	9.09E-05	8.50E-03
TR2685|c0_g1_i1|m.635	homoserine dehydrogenase	6.84	1.67E-03	4.80E-02
TR2848|c0_g1_i1|m.658	FAD monooxygenase [Exophiala dermatitidis NIH UT8656]	8.44	1.77E-03	4.94E-02
TR2956|c1_g1_i1|m.694	Polyadenylate-binding , cytoplasmic and nuclear	8.80	1.62E-03	4.69E-02
TR3055|c0_g1_i1|m.715	AVT6-involved in amino acid efflux from the vacuole [Fusarium fujikuroi]	9.22	7.03E-04	2.72E-02
TR3119|c0_g1_i1|m.745	maleylacetoacetate isomerase	7.91	5.36E-04	2.28E-02
TR3251|c0_g1_i1|m.770	protoplast regeneration and killer toxin resistance [Magnaporthe oryzae 70-15]	8.93	3.84E-06	1.58E-03
TR3364|c0_g1_i1|m.802	Tetratricopeptide-like helical	11.03	9.87E-06	2.51E-03
TR3988|c0_g1_i1|m.925	alcohol dehydrogenase [Exophiala dermatitidis NIH UT8656]	10.03	1.33E-03	4.12E-02
TR4223|c0_g1_i1|m.963	hsp90 [Magnaporthe oryzae 70-15]	9.72	2.46E-04	1.46E-02
TR4457|c0_g2_i1|m.1016	Short-chain dehydrogenase reductase SDR	8.65	2.66E-05	4.17E-03
TR4811|c0_g2_i1|m.1119	thiamine biosynthetic bifunctional enzyme [Eutypa lata UCREL1]	7.34	1.68E-03	4.80E-02
TR5306|c0_g2_i1|m.1238	DNA-binding creA	7.14	1.21E-03	3.87E-02
TR5322|c0_g1_i2|m.1245	hsp70 nucleotide exchange factor fes1 [Phaeoacremonium minimum UCRPA7]	10.60	5.51E-05	6.64E-03
TR5322|c0_g1_i1|m.1243	hsp70 nucleotide exchange factor fes1 [Phaeoacremonium minimum UCRPA7]	9.99	3.17E-04	1.71E-02
TR5349|c0_g1_i1|m.1254	cytochrome p450	9.47	1.97E-04	1.29E-02
TR5750|c0_g1_i1|m.1328	feruloyl esterase B precursor [Fusarium fujikuroi]	8.75	1.10E-03	3.59E-02
TR6060|c0_g1_i1|m.1425	blue-light-inducible Bli-3	11.12	3.55E-04	1.80E-02
TR6330|c1_g1_i1|m.1516	arsenite efflux transporter	10.18	8.25E-05	8.22E-03
TR6885|c0_g1_i1|m.1640	Peroxisomal targeting signal receptor	8.85	8.58E-04	3.05E-02
TR7106|c0_g1_i1|m.1673	alcohol dehydrogenase	11.29	7.90E-05	8.20E-03
TR7152|c0_g1_i1|m.1682	NADH-ubiquinone oxidoreductase kDa subunit, mitochondrial	9.40	1.69E-03	4.81E-02
TR7229|c0_g1_i1|m.1700	pirin domain-containing , partial [Colletotrichum gloeosporioides Nara gc5]	9.63	1.19E-04	9.70E-03
TR7232|c0_g1_i1|m.1706	orotidine-5 -phosphate decarboxylase	9.28	1.07E-03	3.53E-02
TR7360|c0_g1_i1|m.1716	NAD(P)-binding Rossmann-fold containing [Glarea lozoyensis ATCC 20868]	9.55	6.06E-04	2.47E-02
TR7404|c0_g2_i1|m.1726	Peroxisomal membrane PER10	7.15	7.00E-04	2.72E-02
TR7430|c0_g1_i1|m.1736	Sorting nexin-41	7.71	1.31E-04	1.02E-02
TR8211|c0_g2_i1|m.1876	mitochondria fission 1 [Magnaporthe oryzae 70-15]	7.44	8.47E-04	3.03E-02
TR8284|c0_g1_i1|m.1887	serine-threonine rich [Phaeoacremonium minimum UCRPA7]	9.56	3.95E-04	1.91E-02
TR9403|c1_g1_i1|m.2111	branched-chain amino acid aminotransferase	7.70	9.59E-04	3.29E-02
TR10025|c0_g1_i1|m.2233	2-nitropropane dioxygenase	8.97	5.10E-04	2.22E-02
TR10682|c0_g1_i1|m.2356	hypothetical protein A1O5_12104 [Cladophialophora psammophila CBS 110553]	7.78	6.34E-04	2.55E-02
TR10904|c0_g2_i1|m.2419	hypothetical protein [Podospora anserina S mat+]	9.61	2.79E-04	1.57E-02
TR11063|c0_g1_i1|m.2446	alpha-l-rhamnosidase c [Phaeoacremonium minimum UCRPA7]	8.81	1.12E-05	2.63E-03
TR11267|c0_g1_i1|m.2499	Mitochondrial phosphate carrier 3, mitochondrial	8.67	8.68E-05	8.26E-03
TR11273|c0_g1_i1|m.2503	[Aspergillus terreus NIH2624]	10.04	5.34E-05	6.55E-03
TR11440|c0_g2_i1|m.2553	Argininosuccinate synthase	9.68	3.89E-04	1.90E-02
TR11603|c0_g1_i1|m.2584	Mitogen activated kinase kinase	7.68	3.17E-05	4.62E-03
TR11898|c0_g1_i1|m.2643	[Trichoderma reesei QM6a]	9.14	8.90E-04	3.11E-02
TR12709|c0_g1_i1|m.2883	translation elongation factor EF1-alpha, partial	10.15	1.03E-03	3.45E-02
TR12928|c0_g1_i1|m.2935	ABC-2 type transporter	8.00	1.19E-05	2.67E-03
TR13129|c0_g1_i1|m.2982	NAD dependent epimerase dehydratase	7.07	4.90E-04	2.15E-02
TR13192|c0_g1_i1|m.3007	dienelactone hydrolase	9.05	1.81E-03	4.98E-02
TR13378|c0_g1_i1|m.3042	bifunctional P-450:NADPH-P450 reductase	11.01	1.14E-07	3.06E-04
TR13561|c0_g1_i1|m.3090	1,4-alpha-glucan-branching enzyme	7.35	1.26E-03	3.97E-02
TR13994|c0_g1_i1|m.3172	MYG1 [Verticillium alfalfae]	8.37	1.96E-04	1.28E-02
TR14289|c0_g1_i1|m.3226	NADPH-dependent beta-ketoacyl reductase (rhlG) [Fusarium fujikuroi]	10.90	3.59E-06	1.52E-03
TR14386|c1_g1_i1|m.3246	glycosyl hydrolase family 76	7.48	1.21E-03	3.87E-02
TR14503|c0_g1_i1|m.3287	universal stress family	7.08	1.73E-03	4.89E-02
TR14676|c0_g1_i1|m.3313	scytalone dehydratase	10.55	6.42E-04	2.58E-02
TR14949|c0_g2_i1|m.3389	myb-like DNA-binding	9.25	3.81E-04	1.89E-02
TR15965|c0_g1_i1|m.3619	cystathionine beta-synthase	10.17	8.39E-05	8.22E-03
TR16060|c0_g1_i1|m.3637	glutaredoxin, [Neosartorya fischeri NRRL 181]	10.66	8.82E-06	2.42E-03
TR16166|c0_g2_i1|m.3655	fatty acid-binding	10.18	2.40E-05	4.04E-03
TR16175|c0_g1_i1|m.3662	hypothetical protein UCRPA7_7621 [Phaeoacremonium minimum UCRPA7]	10.21	9.78E-05	8.84E-03
TR16335|c0_g1_i1|m.3700	bZIP transcription factor	6.61	8.94E-05	8.48E-03
TR16519|c0_g1_i1|m.3728	fungal specific transcription factor domain-containing [Phaeoacremonium minimum UCRPA7]	7.29	9.99E-04	3.41E-02
TR16660|c0_g1_i1|m.3772	lactobacillus shifted	9.70	7.30E-04	2.78E-02
TR16802|c0_g1_i1|m.3816	amidophosphoribosyltransferase [Talaromyces marneffei ATCC 18224]	7.71	7.16E-04	2.76E-02
TR16831|c0_g1_i1|m.3824	MSF1 domain-containing [Gaeumannomyces graminis tritici R3-111a-1]	7.21	1.37E-03	4.20E-02
TR16977|c0_g2_i1|m.3871	glycosyltransferase family 17	9.68	1.88E-04	1.25E-02
TR17006|c0_g1_i1|m.3877	gtp-binding sar1	8.64	1.29E-03	4.03E-02
TR17097|c0_g1_i1|m.3897	[Glarea lozoyensis ATCC 20868]	11.14	7.18E-04	2.76E-02

TR17103|c0_g1_i1|m.3898	hypothetical protein UCDDA912_g01537	8.62	1.57E-03	4.59E-02
TR17408|c0_g1_i1|m.3977	delta-aminolevulinic acid dehydratase	10.68	4.93E-06	1.81E-03
TR17426|c0_g1_i1|m.3990	1,3-beta-glucan synthase component [Colletotrichum gloeosporioides Nara gc5]	6.18	1.08E-03	3.56E-02
TR17575|c0_g1_i1|m.4007	glycerol-3-phosphate dehydrogenase [NAD+] [Exophiala aquamarina CBS 119918]	7.18	3.92E-04	1.90E-02
TR17596|c0_g1_i1|m.4020	hypothetical protein NEUTE2DRAFT_55305	8.11	8.43E-05	8.23E-03
TR17661|c0_g1_i1|m.4044	nadh-ubiquinone oxidoreductase 23 kda mitochondrial	8.02	3.33E-04	1.74E-02
TR18150|c0_g1_i1|m.4181	metal homeostatis bsd2	7.93	1.44E-04	1.07E-02
TR18175|c0_g1_i1|m.4183	Peroxisomal membrane PMP47A	8.00	9.05E-05	8.50E-03
TR18536|c0_g1_i1|m.4229	HAL kinase	8.00	1.51E-04	1.10E-02
TR18549|c0_g1_i1|m.4237	endoplasmic reticulum [Colletotrichum graminicola]	8.93	7.16E-04	2.76E-02
TR19004|c0_g1_i1|m.4321	conserved domain typically associated with flavo oxygenase, DIM6 NTAB family [Fusarium fujikuroi]	12.00	6.67E-07	6.96E-04
TR19042|c0_g1_i1|m.4335	Respiratory supercomplex factor 2, mitochondrial	7.56	1.22E-03	3.87E-02
TR19374|c0_g1_i1|m.4394	methyltransferase domain-containing [Colletotrichum fioriniae PJ7]	9.07	1.17E-03	3.77E-02
TR19531|c0_g1_i1|m.4426	nitrilase 2	6.30	1.77E-03	4.94E-02
TR20083|c0_g2_i1|m.4519	short chain dehydrogenase ( ), [Aspergillus clavatus NRRL 1]	11.31	1.32E-05	2.76E-03
TR20400|c0_g1_i1|m.4583	phosphoglucomutase	6.10	9.54E-04	3.29E-02
TR20579|c0_g1_i1|m.4617	o-methyltransferase family	7.02	1.28E-03	4.03E-02
TR20704|c0_g1_i1|m.4637	Sulfate adenylyltransferase	8.06	7.89E-04	2.91E-02
TR20817|c0_g1_i1|m.4650	MFS transporter, DHA1 family, multidrug resistance [Exophiala dermatitidis NIH UT8656]	5.62	5.20E-04	2.23E-02
TR21171|c0_g1_i1|m.4722	epimerase hydratase [Myceliophthora thermophila ATCC 42464]	9.42	6.84E-04	2.68E-02
TR21302|c0_g2_i1|m.4769	spo7 [Phaeoacremonium minimum UCRPA7]	8.13	1.13E-04	9.41E-03
TR21348|c0_g1_i1|m.4777	peroxisomal long-chain fatty acid import [Phaeoacremonium minimum UCRPA7]	8.09	1.24E-04	9.91E-03
TR21374|c0_g1_i1|m.4789	Vacuolar calcium ion transporter	9.99	8.39E-05	8.22E-03
TR21634|c0_g1_i1|m.4847	Cytochrome B-561 [Fusarium fujikuroi]	9.55	4.19E-04	1.98E-02
TR21712|c0_g1_i1|m.4878	multi -bridging factor 1	7.76	8.64E-06	2.42E-03
TR21887|c0_g1_i1|m.4927	succinyl- ligase subunit alpha [Verticillium dahliae]	9.91	2.19E-04	1.36E-02
TR21905|c0_g1_i1|m.4943	hypothetical protein UCRPA7_6909 [Phaeoacremonium minimum UCRPA7]	7.71	1.15E-04	9.48E-03
TR21934|c0_g1_i1|m.4953	oxidoreductase [Neurospora crassa OR74A]	9.20	1.81E-03	4.98E-02
TR22146|c0_g1_i1|m.5001	oxidoreductase [Colletotrichum graminicola]	7.52	5.96E-04	2.45E-02
TR22184|c0_g1_i1|m.5017	deubiquitination-protection dph1	7.11	1.29E-03	4.05E-02
TR22337|c0_g3_i1|m.5082	elongation factor 3 [Exophiala aquamarina CBS 119918]	6.29	8.83E-04	3.10E-02
TR22394|c0_g2_i1|m.5117	60s ribosomal l31	9.42	8.38E-04	3.02E-02
TR22481|c0_g1_i1|m.5144	TBC1 domain family member 14 [Gaeumannomyces graminis tritici R3-111a-1]	9.01	7.22E-04	2.76E-02
TR22759|c0_g1_i1|m.5222	transport sec13	9.59	1.02E-03	3.43E-02
TR23053|c0_g1_i1|m.5289	BAG domain	8.14	7.92E-05	8.20E-03
TR23088|c0_g1_i1|m.5299	het-c [Cordyceps militaris CM01]	9.91	2.35E-04	1.43E-02
TR23217|c0_g1_i2|m.5331	transcription factor pap1 [Phaeoacremonium minimum UCRPA7]	9.23	1.17E-06	8.85E-04
TR23370|c0_g1_i1|m.5383	RNQ1-prion, epigenetic modifier of function [Fusarium fujikuroi]	7.62	2.80E-04	1.57E-02
TR23736|c0_g2_i1|m.5458	acyl- desaturase	6.57	5.45E-04	2.30E-02
TR23922|c0_g1_i1|m.5519	eukaryotic initiation factor 4f subunit p130 [Phaeoacremonium minimum UCRPA7]	6.92	1.38E-03	4.21E-02
TR24028|c0_g1_i1|m.5547	upf0041 domain-containing [Phaeoacremonium minimum UCRPA7]	9.59	1.81E-03	4.98E-02
TR24047|c0_g1_i1|m.5553	AChain A, The Aspergillus Fumigatus Sialidase Is A Kdnase: Structural And Mechanistic Insights	11.36	1.35E-05	2.79E-03
TR24054|c0_g2_i1|m.5556	hypothetical protein UCDDA912_g08545	8.29	6.67E-05	7.47E-03
TR24170|c0_g1_i1|m.5589	[Trichoderma reesei QM6a]	10.73	1.15E-05	2.64E-03
TR24451|c0_g1_i1|m.5693	hypothetical protein MYCTH_2302928 [Myceliophthora thermophila ATCC 42464]	9.56	1.05E-04	9.16E-03
TR24584|c0_g1_i1|m.5738	pho85 cyclin-1	9.31	1.13E-06	8.72E-04
TR24716|c0_g2_i1|m.5778	Fatty acid synthase subunit alpha	9.35	8.43E-04	3.03E-02
TR24760|c1_g1_i1|m.5794	fungal specific transcription factor domain	9.05	4.42E-04	2.04E-02
TR25057|c0_g1_i1|m.5879	aspartic-type endopeptidase opsB	9.27	1.42E-04	1.06E-02
TR25090|c0_g1_i1|m.5896	proteasome component PRE2	8.23	7.69E-04	2.86E-02
TR25313|c0_g1_i1|m.5956	alkaline phosphatase [Exophiala dermatitidis NIH UT8656]	8.03	1.67E-04	1.17E-02
TR25423|c0_g1_i1|m.5992	Carbamoyl-phosphate synthase arginine-specific small chain	7.18	1.58E-03	4.59E-02
TR25466|c0_g2_i1|m.6009	alternative NADH-dehydrogenase, partial [Metarhizium brunneum ARSEF 3297]	6.86	1.00E-03	3.41E-02
TR25523|c0_g1_i1|m.6011	hyphal anastamosis-8 [Neurospora crassa OR74A]	7.65	2.45E-04	1.46E-02
TR25609|c0_g1_i1|m.6040	suppressor of mrs2-1 mutation [Fusarium fujikuroi]	8.15	2.96E-04	1.64E-02
TR25629|c0_g1_i1|m.6044	[Verticillium alfalfae]	10.98	1.21E-05	2.69E-03
TR25737|c0_g2_i1|m.6073	Delta(12) fatty acid desaturase	8.92	8.48E-04	3.03E-02
TR25857|c0_g2_i1|m.6128	glycoside hydrolase	10.69	8.53E-06	2.42E-03
TR25985|c0_g1_i1|m.6155	external nadh-ubiquinone oxidoreductase mitochondrial precursor [Phaeoacremonium minimum UCRPA7]	8.42	1.15E-04	9.48E-03
TR26030|c0_g1_i1|m.6166	IMP-specific 5 -nucleotidase 1	10.76	9.21E-06	2.45E-03
TR26183|c0_g1_i1|m.6241	pyruvate dehydrogenase E1 component alpha subunit [Metarhizium acridum CQMa 102]	9.75	6.70E-04	2.65E-02
TR26214|c0_g1_i1|m.6256	Extracellular membrane , CFEM domain [Metarhizium robertsii ARSEF 23]	9.02	5.93E-04	2.45E-02
TR26251|c0_g1_i1|m.6269	AMP-binding enzyme	9.17	9.56E-05	8.79E-03
TR26251|c0_g2_i1|m.6272	AMP-binding enzyme	8.94	1.47E-04	1.08E-02
TR26296|c0_g2_i1|m.6286	thioredoxin [Colletotrichum graminicola]	13.42	1.79E-08	2.43E-04
TR26360|c0_g1_i1|m.6314	synaptobrevin [Colletotrichum fioriniae PJ7]	9.14	1.02E-03	3.43E-02
TR26491|c1_g1_i1|m.6340	succinate dehydrogenase (ubiquinone) membrane anchor subunit	9.27	1.64E-03	4.73E-02
TR26500|c0_g1_i1|m.6343	mitochondrial DNA replication YHM2	9.83	1.70E-04	1.18E-02
TR26534|c0_g1_i1|m.6348	GTP-binding SAR1 [Fusarium fujikuroi]	7.82	1.04E-03	3.46E-02
TR26544|c1_g1_i1|m.6357	plasma membrane snare [Colletotrichum gloeosporioides Nara gc5]	9.39	3.12E-04	1.69E-02
TR26797|c0_g2_i1|m.6426	chitin synthase	9.50	3.90E-04	1.90E-02
TR26857|c0_g1_i1|m.6452	bZIP transcription factor	6.75	8.81E-04	3.10E-02
TR26893|c0_g1_i1|m.6463	Sterol 24-C-methyltransferase	8.37	2.17E-04	1.36E-02
TR26980|c0_g1_i1|m.6480	Mitochondrial intermembrane space cysteine motif-containing MIX17	8.29	2.69E-04	1.52E-02
TR27163|c0_g1_i1|m.6535	mechanosensitive ion channel	9.01	6.67E-04	2.65E-02
TR27184|c0_g2_i1|m.6550	upf0187 domain membrane [Phaeoacremonium minimum UCRPA7]	10.67	1.40E-05	2.86E-03
TR27197|c0_g1_i1|m.6555	dead box rna helicase [Phaeoacremonium minimum UCRPA7]	7.50	9.59E-04	3.29E-02
TR27221|c0_g1_i1|m.6561	F-box and leucine-rich repeat GRR1 [Fusarium verticillioides 7600]	11.12	4.72E-06	1.81E-03
TR27379|c0_g1_i1|m.6627	transcriptional regulator ARG82 [Fusarium fujikuroi]	7.55	1.88E-04	1.25E-02
TR27388|c1_g1_i1|m.6636	-like family domain-containing 1	9.06	1.65E-03	4.75E-02
TR27833|c0_g2_i1|m.6797	Isocitrate dehydrogenase [NAD] subunit 1, mitochondrial	7.83	1.14E-03	3.68E-02
TR27874|c0_g1_i1|m.6813	translation initiation factor 5	6.57	6.53E-04	2.62E-02
TR28086|c0_g2_i1|m.6918	anchored cell wall 4 [Neurospora crassa OR74A]	10.19	2.40E-04	1.45E-02
TR28137|c0_g1_i1|m.6931	endo alpha-1,4 polygalactosaminidase precursor [Fusarium fujikuroi]	9.31	4.77E-04	2.14E-02
TR28240|c0_g1_i1|m.6954	glycosyltransferase family 20	9.84	1.07E-04	9.19E-03
TR28244|c0_g1_i1|m.6957	glutaredoxin 3 [Fusarium oxysporum pisi HDV247]	10.58	1.28E-04	1.01E-02

TR28620|c1_g1_i1|m.7041	tRNA synthetase class II core domain-containing	7.42	1.51E-03	4.49E-02
TR28726|c0_g1_i1|m.7066	translation initiation factor 3 subunit A [Fusarium oxysporum pisi HDV247]	7.14	1.13E-03	3.67E-02
TR28789|c0_g1_i1|m.7083	arp2 3 complex 20 kda subunit	9.95	4.12E-04	1.96E-02
TR28880|c0_g1_i1|m.7115	ZZ type zinc finger domain-containing [Gaeumannomyces graminis tritici R3-111a-1]	8.90	1.69E-03	4.81E-02
TR28948|c0_g1_i1|m.7145	H ACA ribonucleo complex subunit 1	7.73	1.66E-03	4.79E-02
TR28953|c0_g1_i1|m.7147	duf1348 domain containing [Colletotrichum gloeosporioides Nara gc5]	8.42	1.68E-03	4.80E-02
TR29209|c0_g1_i1|m.7220	Carbonic anhydrase	9.69	1.45E-04	1.07E-02
TR29254|c0_g1_i1|m.7233	2-nitropropane dioxygenase	6.81	1.79E-04	1.21E-02
TR29259|c1_g1_i1|m.7239	Reticulocyte-binding 2 a	6.91	1.64E-03	4.73E-02
TR29407|c1_g1_i1|m.7293	calcium calmodulin-dependent kinase	7.03	1.25E-03	3.94E-02
TR29682|c0_g1_i1|m.7364	mitochondrial import inner membrane translocase subunit tim10	9.76	5.32E-04	2.27E-02
TR29774|c0_g1_i1|m.7400	major facilitator superfamily transporter	9.41	1.00E-03	3.41E-02
TR29779|c0_g2_i1|m.7405	[Nectria haematococca mpVI 77-13-4]	9.15	8.45E-04	3.03E-02
TR29870|c0_g1_i1|m.7436	hypothetical protein FAVG1_07552	7.98	1.72E-04	1.18E-02
TR29939|c0_g1_i1|m.7451	Desumoylating isopeptidase 1	8.15	4.91E-04	2.15E-02
TR30202|c0_g2_i1|m.7525	Ctr copper transporter, partial [Metarhizium brunneum ARSEF 3297]	11.18	9.15E-06	2.45E-03
TR30203|c0_g1_i1|m.7527	[Trichoderma reesei QM6a]	10.53	9.48E-05	8.74E-03
TR30234|c0_g1_i1|m.7530	cell division CDC50 [Fusarium fujikuroi]	9.22	8.19E-04	2.98E-02
TR30346|c0_g2_i1|m.7548	conserved glutamic acid rich	7.00	9.61E-05	8.81E-03
TR30435|c0_g1_i1|m.7583	platelet-activating factor acetylhydrolase	9.38	1.05E-06	8.52E-04
TR30677|c0_g2_i1|m.7658	s-adenosylmethionine synthase	7.94	6.01E-04	2.47E-02
TR30692|c0_g1_i1|m.7660	hypothetical protein A1O9_12690 [Exophiala aquamarina CBS 119918]	5.73	1.54E-03	4.56E-02
TR30830|c0_g1_i1|m.7709	na(+) h(+) antiporter 2	7.84	1.73E-04	1.18E-02
TR30864|c1_g1_i1|m.7719	hypothetical protein UCRPA7_3754 [Phaeoacremonium minimum UCRPA7]	7.34	4.46E-04	2.06E-02
TR30985|c0_g2_i1|m.7742	mitochondrial chaperone BCS1	8.93	1.64E-05	3.24E-03
TR31066|c0_g2_i1|m.7766	hypothetical protein VM1G_05042	10.30	1.24E-04	9.91E-03
TR31072|c0_g1_i1|m.7767	integral membrane [Marssonina brunnea multigermtubi MB_m1]	10.25	7.33E-05	7.83E-03
TR31203|c0_g1_i1|m.7791	NAPE-hydrolyzing phospholipase D	10.12	2.30E-05	3.92E-03
TR31352|c0_g1_i1|m.7839	rRNA methyltransferase NOP1	7.20	1.20E-03	3.84E-02
TR31380|c0_g2_i1|m.7865	7alpha-cephem-methoxylase p8 chain related [Phaeoacremonium minimum UCRPA7]	10.78	3.10E-05	4.57E-03
TR31411|c0_g1_i2|m.7877	hydroxyacylglutathione hydrolase	10.46	3.54E-05	4.92E-03
TR31412|c0_g1_i1|m.7879	hypothetical protein O988_08481	10.08	2.91E-04	1.62E-02
TR31423|c0_g2_i1|m.7881	Mitochondrial folate carrier	7.58	6.69E-04	2.65E-02
TR31446|c0_g1_i1|m.7899	electron transfer flavo subunit alpha [Eutypa lata UCREL1]	7.65	1.91E-04	1.27E-02
TR31511|c0_g1_i1|m.7910	family c-likeg- -coupled receptor [Phaeoacremonium minimum UCRPA7]	7.91	1.25E-04	9.91E-03
TR31572|c0_g1_i1|m.7922	proteasome subunit alpha type-1 [Magnaporthe oryzae 70-15]	7.94	8.90E-04	3.11E-02
TR31580|c0_g1_i1|m.7924	ABC transporter ATP-binding ARB1	8.80	1.57E-03	4.59E-02
TR31594|c0_g1_i1|m.7926	hypothetical protein BN1708_007124	9.22	1.09E-03	3.58E-02
TR31612|c0_g1_i1|m.7936	glucose-6-phosphate 1-dehydrogenase	8.31	1.17E-04	9.58E-03
TR31654|c0_g1_i1|m.7955	zz type zinc finger domain-containing	6.28	1.38E-03	4.21E-02
TR31661|c0_g1_i2|m.7960	hypothetical protein Z518_01005 [Rhinocladiella mackenziei CBS 650.93]	9.87	2.02E-04	1.30E-02
TR31662|c0_g1_i1|m.7961	benzoquinone reductase	9.53	1.76E-03	4.93E-02
TR31682|c0_g2_i2|m.7969	dnase1 [Fusarium fujikuroi]	10.34	3.45E-05	4.85E-03
TR31686|c0_g1_i1|m.7973	calcium-transporting ATPase [Trichoderma atroviride IMI 206040]	7.16	9.71E-05	8.84E-03
TR31736|c0_g1_i1|m.7998	Uridylate kinase	7.01	1.42E-04	1.06E-02
TR31744|c0_g1_i1|m.8000	isocitrate dehydrogenase subunit 2	7.46	5.17E-04	2.23E-02
TR31846|c0_g1_i1|m.8036	tata-box-binding [Eutypa lata UCREL1]	6.67	1.10E-03	3.60E-02
TR31871|c0_g2_i1|m.8051	Acetyl- acetyltransferase	8.34	4.30E-04	2.01E-02
TR31924|c0_g1_i1|m.8072	aquaglyceroporin like , other eukaryote [Cladophialophora yegresii CBS 114405]	9.11	1.07E-04	9.19E-03
TR31976|c1_g2_i1|m.8088	chaperone [Colletotrichum graminicola]	9.99	4.36E-04	2.02E-02
TR32124|c0_g1_i1|m.8169	inosine-5 -monophosphate dehydrogenase imd2	6.84	3.52E-04	1.80E-02
TR32140|c0_g1_i1|m.8170	L-aminoadipate-semialdehyde dehydrogenase	8.21	1.05E-04	9.16E-03
TR32277|c0_g1_i1|m.8244	branched-chain-amino-acid aminotransferase 1	10.12	4.83E-04	2.15E-02
TR32367|c0_g1_i1|m.8263	Zinc finger ZPR1	7.71	2.62E-04	1.51E-02
TR32422|c0_g1_i1|m.8276	alpha beta [Phaeoacremonium minimum UCRPA7]	9.08	1.84E-06	1.19E-03
TR32551|c0_g1_i1|m.8305	glycosyltransferase family 8	9.05	1.38E-03	4.21E-02
TR32553|c1_g1_i1|m.8310	glycerol kinase	10.08	5.65E-04	2.37E-02
TR32553|c0_g1_i1|m.8309	glycerol kinase	8.73	6.58E-04	2.63E-02
TR32615|c0_g1_i1|m.8348	thioredoxin, [Neosartorya fischeri NRRL 181]	9.40	1.69E-03	4.81E-02
TR32646|c0_g1_i1|m.8356	Mitochondrial import inner membrane translocase subunit TIM9	8.80	1.41E-03	4.24E-02
TR32648|c0_g1_i2|m.8362	thioredoxin reductase	7.43	7.89E-04	2.91E-02
TR32665|c0_g2_i1|m.8372	short chain dehydrogenase [Colletotrichum graminicola]	11.20	1.23E-05	2.69E-03
TR32676|c0_g1_i1|m.8378	ubiquitin [Pyrenophora tritici-repentis Pt-1C-BFP]	9.17	9.19E-07	8.04E-04
TR32688|c0_g1_i1|m.8388	serine threonine- kinase hal4 [Neurospora crassa OR74A]	7.84	1.28E-04	1.01E-02
TR32709|c0_g1_i1|m.8401	Ish1 domain	10.96	2.92E-04	1.63E-02
TR32729|c0_g2_i1|m.8414	succinyl- ligase [GDP-forming] subunit beta, mitochondrial [Fusarium oxysporum Fo47]	7.21	2.51E-04	1.48E-02
TR32730|c0_g1_i1|m.8418	putative magnesium transporter alr2 protein [Togninia minima UCRPA7]	9.07	1.03E-03	3.44E-02
TR32755|c1_g1_i1|m.8430	[Nematostella vectensis]	9.58	1.66E-04	1.17E-02
TR32784|c0_g1_i1|m.8434	[Trichoderma reesei QM6a]	9.05	1.55E-03	4.58E-02
TR32816|c1_g2_i1|m.8455	phosphatase 2C	9.88	1.25E-04	9.92E-03
TR32816|c0_g1_i1|m.8449	phosphatase 2C	9.01	7.62E-04	2.84E-02
TR32876|c0_g1_i1|m.8470	[Trichoderma reesei QM6a]	9.14	1.67E-04	1.17E-02
TR32969|c0_g1_i1|m.8507	[Uncinocarpus reesii 1704]	10.40	3.49E-05	4.89E-03
TR33038|c0_g1_i1|m.8515	peptide alpha-N-acetyltransferase Nat2	7.66	4.80E-04	2.14E-02
TR33059|c0_g1_i1|m.8528	mitochondrial carrier [Fusarium fujikuroi]	9.20	1.41E-03	4.25E-02
TR33154|c0_g1_i2|m.8563	-like family [Eutypa lata UCREL1]	10.23	8.59E-05	8.24E-03
TR33208|c0_g1_i1|m.8589	ring-like domain-containing [Phaeoacremonium minimum UCRPA7]	7.40	5.05E-04	2.20E-02
TR33271|c0_g3_i1|m.8613	Xanthine dehydrogenase	9.53	1.70E-03	4.82E-02
TR33294|c1_g1_i1|m.8626	Cell division control 3	7.57	1.53E-03	4.56E-02
TR33324|c0_g1_i1|m.8654	myo-inositol transporter 1 [Phaeoacremonium minimum UCRPA7]	9.28	8.59E-04	3.05E-02
TR33361|c0_g2_i1|m.8656	zinc-binding oxidoreductase [Fusarium fujikuroi]	6.84	1.55E-03	4.58E-02
TR33363|c0_g1_i1|m.8661	hypothetical protein UCRPA7_274 [Phaeoacremonium minimum UCRPA7]	9.30	6.74E-04	2.66E-02
TR33529|c0_g2_i1|m.8746	aldehyde dehydrogenase	8.18	9.97E-05	8.95E-03
TR33529|c0_g1_i1|m.8743	aldehyde dehydrogenase	9.23	1.23E-03	3.91E-02
TR33554|c0_g1_i1|m.8754	cell wall biogenesis Mhp1	7.97	2.12E-04	1.34E-02
TR33680|c0_g1_i1|m.8788	phosphate permease [Punctularia strigosozonata HHB-11173 SS5]	11.16	7.06E-04	2.73E-02

TR33682|c0_g1_i1|m.8792	methionine-r-sulfoxide reductase	7.70	7.54E-06	2.27E-03
TR33786|c0_g1_i2|m.8828	adenylosuccinate synthetase	9.90	2.98E-04	1.64E-02
TR33818|c0_g1_i1|m.8841	DUF221 domain	8.89	1.38E-03	4.21E-02
TR33832|c0_g1_i1|m.8849	isochorismatase family	8.73	9.44E-05	8.74E-03
TR33936|c0_g1_i1|m.8876	RNA polymerase Rpb1 repeat domain [Metarhizium acridum CQMa 102]	7.64	1.08E-04	9.20E-03
TR33946|c0_g1_i2|m.8881	heavy-metal-associated domain-containing [Colletotrichum graminicola]	7.28	1.65E-03	4.76E-02
TR33956|c0_g1_i1|m.8887	trafficking pga2	9.77	2.65E-04	1.51E-02
TR34039|c0_g1_i1|m.8907	ribosomal subunit l37 [Colletotrichum gloeosporioides Nara gc5]	7.77	9.69E-04	3.32E-02
TR34088|c0_g2_i1|m.8921	hypothetical protein CTHT_0032400 [Chaetomium thermophilum var. thermophilum DSM 1495]	9.26	1.60E-04	1.14E-02
TR34098|c1_g1_i1|m.8935	mitochondrial inner membrane translocase subunit TIM44	7.34	1.46E-03	4.38E-02
TR34183|c0_g1_i1|m.8953	NAD-specific glutamate dehydrogenase [Exophiala aquamarina CBS 119918]	8.91	2.23E-05	3.88E-03
TR34194|c0_g1_i1|m.8967	mitochondrial carrier family [Fusarium fujikuroi]	6.93	1.00E-03	3.41E-02
TR34237|c0_g1_i1|m.8972	bar domain	7.36	8.74E-04	3.08E-02
TR34293|c0_g1_i1|m.8986	glutathione-dependent formaldehyde-activating enzyme	7.22	7.04E-04	2.72E-02
TR34350|c0_g1_i1|m.8998	-No hit found-	10.84	3.22E-04	1.72E-02
TR34388|c0_g1_i1|m.9044	CMGC MAPK P38 kinase [Fusarium verticillioides 7600]	8.57	7.40E-05	7.87E-03
TR34397|c0_g1_i1|m.9050	SIX gene expression 1, partial [Fusarium oxysporum]	9.47	1.82E-03	4.99E-02
TR34475|c0_g1_i1|m.9092	phospholipase [Verticillium dahliae]	6.30	3.30E-04	1.74E-02
TR34488|c0_g1_i1|m.9099	valyl-tRNA synthetase	9.43	5.13E-04	2.22E-02
TR34514|c0_g1_i1|m.9108	NADH-ubiquinone oxidoreductase 40 kDa subunit	7.46	5.25E-04	2.25E-02
TR34537|c0_g2_i1|m.9111	-like family [Colletotrichum gloeosporioides Nara gc5]	10.18	3.51E-04	1.80E-02
TR34537|c0_g1_i1|m.9110	-like family [Colletotrichum gloeosporioides Nara gc5]	9.54	6.43E-04	2.58E-02
TR34591|c0_g2_i1|m.9136	nascent polypeptide-associated complex subunit beta	7.35	7.33E-04	2.79E-02
TR34591|c0_g1_i1|m.9135	nascent polypeptide-associated complex subunit beta	9.21	1.20E-03	3.83E-02
TR34604|c0_g1_i1|m.9137	mitochondrial co-chaperone [Colletotrichum gloeosporioides Nara gc5]	9.47	1.55E-03	4.58E-02
TR34675|c0_g3_i1|m.9153	26S proteasome regulatory subunit rpn-1	7.91	3.95E-04	1.91E-02
TR34696|c0_g2_i1|m.9162	cytochrome c oxidase polypeptide vi [Phaeoacremonium minimum UCRPA7]	10.15	2.42E-04	1.45E-02
TR34707|c0_g1_i1|m.9167	related to mismatch base pair and cruciform DNA recognition Hmp1	14.02	9.96E-05	8.95E-03
TR34708|c0_g1_i1|m.9168	acyl- dehydrogenase family member 11 [Phaeoacremonium minimum UCRPA7]	7.16	7.60E-04	2.84E-02
TR34717|c0_g2_i1|m.9175	Sulfate adenylyltransferase	9.76	4.84E-04	2.15E-02
TR34804|c0_g2_i1|m.9197	[Botrytis cinerea]	7.48	4.86E-04	2.15E-02
TR34843|c0_g1_i1|m.9212	cytochrome c oxidase subunit Vb [Colletotrichum graminicola]	7.37	5.96E-04	2.45E-02
TR34932|c0_g1_i1|m.9241	integral membrane	6.64	1.57E-03	4.59E-02
TR34973|c0_g1_i1|m.9252	hypothetical protein A1O1_04515 [Capronia coronata CBS 617.96]	6.74	7.84E-04	2.90E-02
TR34973|c1_g1_i1|m.9254	hypothetical protein A1O1_04515 [Capronia coronata CBS 617.96]	5.76	1.29E-03	4.04E-02
TR35019|c0_g1_i1|m.9270	ATP synthase subunit D	8.69	5.93E-05	6.98E-03
TR35083|c0_g1_i1|m.9288	amino acid permease	9.84	2.33E-06	1.27E-03
TR35108|c0_g1_i1|m.9291	dna-directed rna polymerase iii 130 kda polypeptide [Phaeoacremonium minimum UCRPA7]	8.26	1.18E-04	9.62E-03
TR35381|c0_g1_i1|m.9361	eukaryotic aspartyl protease	10.46	1.15E-05	2.64E-03
TR35424|c0_g1_i1|m.9369	calmodulin, partial [Fusarium temperatum]	7.13	1.72E-03	4.86E-02
TR35480|c1_g1_i1|m.9384	transcription initiation factor iie subunit alpha	7.19	1.19E-03	3.83E-02
TR35517|c0_g1_i1|m.9395	annexin [Phaeoacremonium minimum UCRPA7]	12.81	1.66E-08	2.43E-04
TR35549|c0_g1_i1|m.9400	Sec14 cytosolic factor	7.71	5.31E-04	2.27E-02
TR35674|c0_g1_i2|m.9426	ribosomal S2	9.70	5.51E-04	2.32E-02
TR35724|c0_g1_i1|m.9433	RNase III domain-containing	10.00	2.09E-04	1.33E-02
TR35740|c0_g1_i1|m.9440	Eukaryotic translation initiation factor 2 subunit gamma	9.71	3.39E-04	1.76E-02
TR35802|c0_g1_i1|m.9461	T-complex 1 subunit gamma	7.14	1.19E-03	3.83E-02
TR35825|c0_g1_i1|m.9475	fatty acid desaturase	8.90	1.45E-03	4.35E-02
TR35828|c0_g1_i1|m.9486	Alkali-sensitive linkage	10.08	1.82E-04	1.23E-02
TR35833|c0_g1_i1|m.9488	-No hit found-	8.81	1.37E-03	4.20E-02
TR35875|c0_g2_i1|m.9510	AGC AKT kinase	7.35	2.93E-04	1.63E-02
TR35912|c0_g1_i1|m.9529	2-dehydropantoate 2-reductase	7.78	5.44E-04	2.30E-02
TR35927|c0_g1_i1|m.9533	Tyrosine--tRNA ligase, cytoplasmic	10.49	4.28E-04	2.00E-02
TR35948|c2_g1_i1|m.9547	N-acetyl-gamma-glutamyl-phosphate reductase	7.77	8.54E-04	3.05E-02
TR36038|c0_g1_i2|m.9596	glutathione peroxidase	9.37	2.54E-06	1.29E-03
TR36041|c0_g1_i1|m.9598	related to mismatch base pair and cruciform DNA recognition Hmp1	11.97	2.30E-04	1.41E-02
TR36049|c0_g2_i1|m.9602	lipopolysaccharide-induced transcription factor regulating tumor necrosis factor [Neofusicoccum parvum UCRNP2]	9.48	6.93E-04	2.70E-02
TR36055|c0_g2_i1|m.9607	Eukaryotic peptide chain release factor subunit 1	6.75	7.59E-04	2.84E-02
TR36086|c0_g1_i1|m.9617	NADP-dependent oxidoreductase	9.58	2.60E-07	4.15E-04
TR36131|c0_g1_i1|m.9634	isocitrate dehydrogenase	6.27	1.71E-03	4.85E-02
TR36134|c0_g1_i1|m.9636	Cytochrome c peroxidase, mitochondrial	7.55	1.11E-04	9.32E-03
TR36136|c0_g1_i1|m.9639	MICOS complex subunit MIC60	7.71	2.06E-04	1.32E-02
TR36139|c0_g2_i1|m.9645	60S ribosomal L18	10.26	5.17E-04	2.23E-02
TR36139|c0_g1_i2|m.9644	60s ribosomal l18	8.90	1.32E-03	4.09E-02
TR36179|c0_g1_i1|m.9651	serine protease p2 [Neurospora crassa OR74A]	6.14	3.33E-04	1.74E-02
TR36228|c0_g1_i1|m.9674	Glycogen phosphorylase	10.18	6.98E-05	7.67E-03
TR36263|c0_g1_i1|m.9687	hypothetical protein BOTBODRAFT_170215	9.21	1.56E-03	4.58E-02
TR36269|c0_g1_i1|m.9690	malate dehydrogenase	9.22	7.85E-04	2.90E-02
TR36294|c0_g1_i1|m.9697	acyl binding	7.60	3.32E-04	1.74E-02
TR36330|c0_g1_i1|m.9705	heat shock 78 [Phaeoacremonium minimum UCRPA7]	7.28	1.30E-03	4.06E-02
TR36332|c0_g1_i2|m.9714	40S ribosomal S19	9.20	1.81E-03	4.98E-02
TR36336|c1_g1_i1|m.9719	UV excision repair Rad23	9.71	4.82E-04	2.15E-02
TR36342|c0_g1_i1|m.9722	S-adenosyl-L-methionine-dependent methyltransferase	7.54	2.63E-04	1.51E-02
TR36415|c0_g1_i1|m.9760	Small glutamine-rich tetratricopeptide repeat-containing 2	8.26	4.89E-04	2.15E-02
TR36443|c0_g1_i1|m.9765	cytochrome b-c1 complex subunit Rieske	6.31	1.77E-03	4.94E-02
TR36454|c0_g2_i1|m.9773	acyl- dehydrogenase	7.66	2.86E-06	1.34E-03
TR36518|c0_g1_i1|m.9781	heat-shock hsp60 [Fusarium fujikuroi]	7.32	1.96E-04	1.28E-02
TR36531|c0_g1_i1|m.9789	G- coupled receptor [Metarhizium robertsii ARSEF 23]	7.19	2.40E-04	1.45E-02
TR36557|c0_g2_i1|m.9808	plac8 family	7.64	1.02E-03	3.43E-02
TR36671|c0_g1_i1|m.9849	MFS transporter, SP family, general alpha glucoside:H+ symporter	10.69	5.92E-06	2.00E-03
TR36699|c0_g1_i1|m.9858	eukaryotic translation initiation factor 3 subunit I	7.70	4.80E-04	2.14E-02
TR36739|c0_g1_i1|m.9891	[Nectria haematococca mpVI 77-13-4]	6.04	1.37E-03	4.20E-02
TR36742|c0_g1_i1|m.9893	serine hydroxymethyltransferase	7.83	8.87E-04	3.11E-02
TR36742|c1_g1_i1|m.9897	Serine hydroxymethyltransferase, cytosolic	8.88	1.76E-03	4.93E-02
TR36775|c0_g1_i1|m.9900	hypothetical protein FOMMEDRAFT_166964 [Fomitiporia mediterranea MF3/22]	10.69	1.04E-03	3.46E-02
TR36794|c0_g1_i1|m.9906	copper resistance-associated p-type atpase [Phaeoacremonium minimum UCRPA7]	9.64	8.29E-05	8.22E-03

TR36818|c0_g1_i1|m.9912	[Glarea lozoyensis ATCC 20868]	9.66	5.86E-07	6.91E-04
TR36848|c0_g1_i1|m.9924	family , partial [Metarhizium majus ARSEF 297]	9.71	3.56E-04	1.80E-02
TR36901|c0_g1_i1|m.9937	g1 s-specific cyclin pcl5 [Phaeoacremonium minimum UCRPA7]	7.99	2.46E-05	4.07E-03
TR36977|c0_g2_i1|m.9966	YKT6-SNARE for Endoplasmic Reticulum-Golgi transport [Fusarium fujikuroi]	8.70	8.25E-05	8.22E-03
TR37079|c0_g1_i1|m.10003	26s proteasome regulatory subunit n3	8.94	6.30E-05	7.24E-03
TR37088|c0_g1_i1|m.10007	Plectin S10 [Metarhizium robertsii ARSEF 23]	8.42	1.24E-04	9.91E-03
TR37088|c0_g1_i2|m.10009	Plectin S10 [Metarhizium robertsii ARSEF 23]	8.05	4.70E-04	2.13E-02
TR37095|c0_g1_i1|m.10014	2 [Metarhizium robertsii ARSEF 23]	9.54	1.51E-03	4.50E-02
TR37121|c0_g1_i1|m.10017	[Trichoderma reesei QM6a]	7.70	4.36E-04	2.02E-02
TR37159|c0_g2_i1|m.10030	glycosyl hydrolase family 18	6.86	4.92E-05	6.33E-03
TR37267|c0_g1_i1|m.10087	POT1-acetyl- C-acyltransferase, peroxisomal [Fusarium fujikuroi]	7.97	2.64E-05	4.17E-03
TR37358|c0_g1_i1|m.10127	nadh dehydrogenase 1 alpha beta subcomplex 1	9.75	1.10E-03	3.59E-02
TR37382|c2_g1_i1|m.10148	fumarate hydratase	7.08	8.65E-04	3.06E-02
TR37415|c0_g1_i1|m.10167	Glycosyl hydrolase family 16	8.20	8.26E-05	8.22E-03
TR37469|c0_g1_i1|m.10191	dihydrolipoyllysine-residue succinyltransferase [Gaeumannomyces graminis tritici R3-111a-1]	7.62	2.64E-04	1.51E-02
TR37473|c0_g2_i1|m.10194	GPI anchored serine-threonine rich [Colletotrichum fioriniae PJ7]	9.70	8.70E-04	3.07E-02
TR37507|c0_g1_i2|m.10201	WLM domain-containing	7.66	4.21E-04	1.98E-02
TR37517|c0_g1_i1|m.10206	carboxylic acid transporter	7.43	1.81E-03	4.98E-02
TR37555|c0_g1_i1|m.10229	methionine-R-sulfoxide reductase	7.34	7.06E-05	7.69E-03
TR37588|c0_g1_i1|m.10243	SOM1 [Colletotrichum fioriniae PJ7]	8.33	1.56E-03	4.58E-02
TR37613|c0_g1_i1|m.10271	arsenite methyltransferase	11.87	2.69E-08	2.43E-04
TR37613|c0_g1_i2|m.10276	arsenite S-adenosylmethyltransferase [Neurospora crassa OR74A]	10.48	1.73E-05	3.25E-03
TR37625|c0_g1_i1|m.10281	ketol-acid reductoisomerase	7.87	1.73E-04	1.18E-02
TR37638|c0_g1_i1|m.10284	RNA recognition domain-containing	7.99	8.10E-04	2.96E-02
TR37639|c0_g2_i1|m.10296	calreticulin [Metarhizium acridum CQMa 102]	7.63	4.09E-04	1.95E-02
TR37680|c1_g1_i1|m.10320	conserved hypothetical protein	9.59	1.02E-03	3.43E-02
TR37712|c0_g1_i2|m.10333	Nuclear transport factor 2	10.16	1.76E-04	1.19E-02
TR37724|c0_g1_i1|m.10335	rna recognition domain-containing [Phaeoacremonium minimum UCRPA7]	8.53	4.03E-04	1.94E-02
TR37735|c0_g2_i2|m.10354	murein transglycosylase [Exophiala aquamarina CBS 119918]	7.71	5.89E-04	2.45E-02
TR37746|c0_g1_i2|m.10365	GPI anchored serine-rich [Colletotrichum graminicola]	7.58	8.90E-04	3.11E-02
TR37761|c0_g1_i1|m.10373	alpha-galactosidase, partial [Metarhizium majus ARSEF 297]	10.94	1.29E-05	2.74E-03
TR37784|c0_g2_i1|m.10391	Vacuolar ATP synthase subunit B	8.41	3.10E-04	1.69E-02
TR37790|c0_g1_i2|m.10394	C2 domain-containing	5.85	2.18E-04	1.36E-02
TR37802|c1_g1_i1|m.10414	Histone chaperone ASF1	9.59	1.02E-03	3.43E-02
TR37808|c0_g1_i1|m.10428	bzip transcription factor [Phaeoacremonium minimum UCRPA7]	8.00	1.09E-03	3.59E-02
TR37816|c0_g1_i1|m.10438	arsenical-resistance [Pseudogymnoascus destructans 20631-21]	10.18	9.71E-05	8.84E-03
TR37820|c0_g1_i2|m.10442	cell wall	5.93	1.30E-03	4.06E-02
TR37890|c1_g1_i1|m.10461	C4-dicarboxylate transporter malic acid transporter	9.44	1.10E-03	3.59E-02
TR37930|c0_g1_i1|m.10487	Phosphopantothenate--cysteine ligase CAB2	6.19	5.79E-04	2.41E-02
TR37947|c0_g1_i1|m.10512	stf2 [Colletotrichum gloeosporioides Nara gc5]	9.59	1.56E-03	4.58E-02
TR38033|c0_g1_i1|m.10529	Nucleotide-binding, alpha-beta plait	9.98	4.88E-04	2.15E-02
TR38092|c0_g1_i1|m.10558	60S ribosomal L10a	8.64	1.06E-04	9.19E-03
TR38287|c0_g1_i1|m.10658	[Pyrenophora tritici-repentis Pt-1C-BFP]	9.47	6.94E-05	7.67E-03
TR38290|c0_g1_i1|m.10665	Allergen Asp f 15	9.41	1.32E-03	4.09E-02
TR38301|c0_g1_i1|m.10670	ribosomal L23a, cytosolic [Fusarium fujikuroi]	10.17	1.12E-04	9.34E-03
TR38349|c0_g1_i1|m.10693	DUF1713 domain	7.39	1.08E-03	3.55E-02
TR38356|c0_g1_i1|m.10695	hypothetical protein GGTG_03137 [Gaeumannomyces graminis var. tritici R3-111a-1]	10.88	8.53E-06	2.42E-03
TR38380|c1_g1_i1|m.10702	DEAD DEAH box helicase	9.34	1.45E-03	4.34E-02
TR38454|c0_g1_i1|m.10729	predicted protein	7.54	4.56E-04	2.08E-02
TR38461|c0_g1_i1|m.10733	extracellular proline-serine rich	7.52	1.19E-03	3.83E-02
TR38496|c0_g1_i1|m.10744	serine threonine phosphatase type 1 [Beauveria bassiana ARSEF 2860]	9.61	3.69E-04	1.84E-02
TR38512|c0_g2_i1|m.10756	PH domain-containing	8.69	4.91E-04	2.15E-02
TR38588|c0_g1_i1|m.10796	dsba oxidoreductase	10.39	5.20E-05	6.50E-03
TR38593|c0_g1_i1|m.10797	uricase [Phaeoacremonium minimum UCRPA7]	9.59	2.17E-06	1.23E-03
TR38624|c1_g2_i1|m.10803	fungal specific transcription factor domain-containing	9.42	2.60E-04	1.50E-02
TR38624|c0_g1_i1|m.10800	Transcription factor, fungi, partial [Metarhizium brunneum ARSEF 3297]	8.83	9.96E-04	3.41E-02
TR38662|c0_g1_i1|m.10814	major facilitator superfamily transporter	12.88	7.23E-08	3.06E-04
TR38674|c0_g1_i1|m.10819	Methyltransferase type 11 [Metarhizium robertsii ARSEF 23]	9.20	1.81E-03	4.98E-02
TR38688|c0_g1_i1|m.10839	atp synthase gamma chain	7.41	3.29E-04	1.74E-02
TR38784|c0_g1_i1|m.10884	hypothetical protein CHGG_00100 [Chaetomium globosum CBS 148.51]	7.72	8.01E-05	8.22E-03
TR38789|c0_g2_i1|m.10886	uracil phosphoribosyltransferase	11.09	1.10E-05	2.63E-03
TR38870|c0_g1_i1|m.10946	NADH-ubiquinone oxidoreductase kDa subunit	7.08	1.81E-03	4.98E-02
TR38874|c2_g1_i1|m.10957	zinc finger sfp1 [Phaeoacremonium minimum UCRPA7]	6.91	1.75E-03	4.93E-02
TR38900|c0_g2_i1|m.10966	serine palmitoyltransferase 1 [Phaeoacremonium minimum UCRPA7]	7.29	8.97E-04	3.13E-02
TR38951|c0_g1_i1|m.10985	pirin [Verticillium alfalfae]	6.56	5.18E-04	2.23E-02
TR38960|c0_g1_i1|m.10997	[Trichoderma reesei QM6a]	7.11	1.48E-04	1.08E-02
TR39097|c0_g1_i1|m.11066	Homeobox domain-containing	8.47	9.66E-06	2.51E-03
TR39099|c0_g2_i1|m.11075	p-type calcium atpase [Neofusicoccum parvum UCRNP2]	9.32	3.37E-04	1.75E-02
TR39099|c1_g1_i1|m.11076	calcium-translocating P-type ATPase	6.01	7.57E-04	2.84E-02
TR39115|c0_g2_i1|m.11091	GPR1 FUN34 -class plasma membrane	11.56	7.32E-05	7.83E-03
TR39123|c0_g1_i2|m.11095	flavohemoglobin [Gaeumannomyces graminis tritici R3-111a-1]	6.49	6.56E-04	2.63E-02
TR39130|c0_g1_i1|m.11099	profilin [Eutypa lata UCREL1]	9.48	8.27E-04	3.00E-02
TR39149|c0_g1_i1|m.11105	eukaryotic translation initiation factor 2 subunit beta	7.09	1.39E-03	4.21E-02
TR39156|c0_g1_i1|m.11125	UMTA methyltransferase family	9.87	3.14E-04	1.70E-02
TR39184|c0_g1_i1|m.11147	adenosylhomocysteinase, partial [Metarhizium majus ARSEF 297]	7.27	7.18E-04	2.76E-02
TR39234|c0_g2_i1|m.11164	NADH-cytochrome b5 reductase 1	8.15	2.21E-04	1.37E-02
TR39308|c0_g2_i2|m.11215	iron transport multicopper oxidase FET3	10.29	3.87E-04	1.90E-02
TR39313|c0_g1_i1|m.11220	NADP-dependent malic enzyme	10.15	2.08E-04	1.32E-02
TR39321|c0_g1_i1|m.11227	prohibitin PHB2 [Fusarium fujikuroi]	8.01	2.07E-04	1.32E-02
TR39412|c0_g1_i1|m.11266	2-methylcitrate dehydratase	6.14	1.14E-03	3.68E-02
TR39416|c1_g2_i1|m.11271	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	8.75	1.05E-05	2.60E-03
TR39446|c0_g2_i1|m.11291	guanine deaminase	7.56	2.46E-04	1.46E-02
TR39449|c0_g1_i1|m.11292	inosine-uridine preferring nucleoside hydrolase	8.24	1.35E-04	1.04E-02
TR39478|c1_g5_i1|m.11314	60s ribosomal l10a	6.85	1.33E-03	4.11E-02
TR39518|c0_g1_i2|m.11335	conserved hypothetical protein [Verticillium alfalfae VaMs.102]	7.29	1.24E-03	3.93E-02
TR39534|c0_g1_i2|m.11345	Adenine phosphoribosyltransferase	9.23	6.86E-04	2.68E-02

TR39563|c0_g1_i1|m.11358	60S ribosomal L7 [Punctularia strigosozonata HHB-11173 SS5]	10.33	1.57E-03	4.59E-02
TR39634|c2_g1_i1|m.11401	Pyruvate carboxylase	6.47	1.91E-04	1.27E-02
TR39663|c0_g1_i1|m.11413	ca2+:h+ antiporter	6.60	2.57E-04	1.50E-02
TR39678|c0_g2_i1|m.11424	Pyridoxamine 5 -phosphate oxidase	9.04	1.16E-05	2.64E-03
TR39701|c0_g1_i1|m.11445	extracellular matrix [Phaeoacremonium minimum UCRPA7]	11.23	3.12E-06	1.38E-03
TR39709|c0_g1_i1|m.11447	ribose 5-phosphate isomerase A	8.52	3.33E-04	1.74E-02
TR39731|c0_g1_i1|m.11464	-tyrosine phosphatase [Colletotrichum graminicola]	7.73	2.10E-05	3.74E-03
TR39744|c0_g1_i1|m.11473	myo-inositol-1-phosphate synthase	9.22	1.09E-03	3.58E-02
TR39778|c0_g1_i1|m.11487	dynein light chain	9.53	1.43E-03	4.31E-02
TR39797|c0_g1_i1|m.11500	carbohydrate-binding module family 21 [Thielavia terrestris NRRL 8126]	10.05	1.25E-04	9.92E-03
TR39797|c1_g1_i1|m.11501	GIP2 Glc7p-interacting	9.23	6.86E-04	2.68E-02
TR39818|c0_g1_i1|m.11510	pyruvate dehydrogenase E2 component (dihydrolipoamide acetyltransferase)	11.23	2.09E-05	3.74E-03
TR39840|c0_g1_i1|m.11527	40S ribosomal S18-coprinopsis cinerea ,	10.46	1.37E-03	4.20E-02
TR39877|c0_g1_i1|m.11553	Cytochrome b-c1 complex subunit 2, mitochondrial	7.64	1.73E-04	1.18E-02
TR39883|c0_g1_i1|m.11554	chloroperoxidase [Colletotrichum gloeosporioides Nara gc5]	9.46	7.41E-07	7.18E-04
TR39892|c0_g1_i1|m.11562	40s ribosomal s20	7.81	6.53E-04	2.62E-02
TR39903|c0_g1_i2|m.11573	60S ribosomal L39 [Trichophyton rubrum CBS]	8.22	4.04E-04	1.94E-02
TR39913|c0_g1_i1|m.11575	40 kDa peptidyl-prolyl cis-trans isomerase [Neurospora tetrasperma FGSC 2508]	8.28	7.55E-04	2.84E-02
TR39941|c0_g1_i1|m.11607	Fatty acid synthase subunit beta	7.57	1.31E-03	4.09E-02
TR39941|c1_g1_i1|m.11610	fatty acid synthase subunit beta, fungi type	7.26	1.49E-03	4.43E-02
TR39969|c0_g1_i1|m.11628	26S proteasome regulatory subunit rpn11	8.22	7.56E-04	2.84E-02
TR39972|c0_g1_i2|m.11634	-No hit found-	8.98	3.21E-06	1.38E-03
TR39972|c0_g1_i1|m.11630	-No hit found-	7.67	3.35E-04	1.74E-02
TR39974|c1_g1_i1|m.11642	NAD-specific glutamate dehydrogenase	7.88	2.29E-04	1.41E-02
TR39974|c0_g1_i1|m.11639	NAD-specific glutamate dehydrogenase	7.82	3.56E-04	1.80E-02
TR39992|c0_g1_i1|m.11666	amid-like mitochondrial oxidoreductase [Phaeoacremonium minimum UCRPA7]	8.46	1.48E-05	2.97E-03
TR39996|c0_g1_i1|m.11675	Ubiquitin-activating enzyme E1 1	7.85	2.67E-04	1.52E-02
TR40002|c0_g1_i1|m.11682	sucrose utilization SUC1	9.39	2.56E-06	1.29E-03
TR40029|c0_g1_i1|m.11687	Ras [Fusarium verticillioides 7600]	7.36	9.90E-04	3.39E-02
TR40036|c0_g1_i1|m.11688	SUR7 [Colletotrichum fioriniae PJ7]	7.49	1.29E-04	1.01E-02
TR40074|c1_g1_i1|m.11705	MEAB [Verticillium dahliae]	7.09	1.40E-03	4.23E-02
TR40091|c0_g1_i1|m.11718	ran binding in the microtubule-organising centre	8.08	1.33E-03	4.12E-02
TR40102|c0_g1_i2|m.11725	argininosuccinate lyase	9.38	6.65E-05	7.47E-03
TR40133|c1_g1_i1|m.11742	RPT4-26S proteasome regulatory subunit [Fusarium fujikuroi]	10.19	2.69E-04	1.52E-02
TR40147|c0_g1_i1|m.11746	spi1-GTP-binding [Fusarium fujikuroi]	10.59	7.19E-05	7.80E-03
TR40147|c0_g1_i2|m.11748	spi1-GTP-binding [Fusarium fujikuroi]	9.47	1.55E-03	4.58E-02
TR40249|c0_g1_i1|m.11808	gamma hydroxybutyrate dehydrogenase [Fusarium fujikuroi]	11.55	6.44E-05	7.31E-03
TR40284|c0_g1_i1|m.11816	Transcription factor steA	9.67	1.07E-05	2.62E-03
TR40287|c0_g1_i1|m.11822	SUR7 [Colletotrichum fioriniae PJ7]	7.87	2.59E-05	4.16E-03
TR40311|c0_g1_i1|m.11837	3-ketoacyl- thiolase, peroxisomal	7.61	5.45E-06	1.89E-03
TR40311|c0_g1_i1|m.11838	3-ketoacyl- thiolase, peroxisomal	9.47	9.19E-05	8.57E-03
TR40316|c0_g1_i1|m.11840	26S proteasome regulatory subunit rpn-1	9.86	2.58E-04	1.50E-02
TR40334|c0_g1_i1|m.11848	WD repeat containing 44 [Metarhizium robertsii ARSEF 23]	10.37	1.00E-04	8.95E-03
TR40407|c0_g1_i1|m.11897	[Fibroporia radiculosa]	11.12	2.03E-04	1.31E-02
TR40410|c1_g3_i1|m.11914	plasma-membrane proton-efflux P-type ATPase	5.69	8.00E-04	2.94E-02
TR40454|c0_g2_i1|m.11943	60S ribosomal L36	7.28	3.86E-04	1.90E-02
TR40584|c0_g1_i1|m.11993	ribosomal s17 [Neofusicoccum parvum UCRNP2]	9.12	4.55E-04	2.08E-02
TR40617|c0_g1_i1|m.12009	nadph-cytochrome p450 reductase	9.48	6.89E-04	2.69E-02
TR40633|c0_g1_i1|m.12028	glycoside hydrolase family 17 [Myceliophthora thermophila ATCC 42464]	7.69	3.38E-05	4.80E-03
TR40694|c0_g3_i1|m.12072	Mitochondrial import inner membrane translocase subunit tim23	8.47	1.17E-04	9.58E-03
TR40704|c0_g1_i2|m.12083	60s ribosomal l17	6.98	6.13E-04	2.49E-02
TR40716|c0_g1_i1|m.12089	nitroreductase family	10.99	2.28E-07	3.86E-04
TR40727|c0_g1_i1|m.12094	duf221 domain-containing [Colletotrichum gloeosporioides Nara gc5]	7.28	4.08E-06	1.60E-03
TR40735|c0_g1_i1|m.12107	Amino-acid permease inda1	10.31	7.19E-08	3.06E-04
TR40736|c0_g1_i1|m.12111	RPL33B-ribosomal [Fusarium fujikuroi]	9.48	8.26E-04	3.00E-02
TR40741|c0_g1_i1|m.12112	ATP-citrate synthase subunit 1	9.05	1.39E-03	4.21E-02
TR40757|c0_g1_i1|m.12123	ATP synthase subunit alpha	7.52	1.30E-04	1.01E-02
TR40771|c0_g1_i1|m.12132	60S ribosomal L12	8.19	2.09E-04	1.33E-02
TR40808|c0_g1_i1|m.12150	cofilin [Fusarium oxysporum FOSC 3-a]	10.03	3.33E-04	1.74E-02
TR40809|c0_g1_i1|m.12153	threonine synthase	8.29	6.92E-05	7.67E-03
TR40817|c0_g1_i2|m.12164	Sucrase-isomaltase, intestinal	10.38	7.28E-05	7.83E-03
TR40840|c0_g2_i1|m.12166	short chain dehydrogenase [Colletotrichum fioriniae PJ7]	6.91	2.28E-05	3.92E-03
TR40841|c0_g1_i1|m.12170	BTB POZ fold domain containing , partial [Metarhizium brunneum ARSEF 3297]	8.11	6.43E-05	7.31E-03
TR40848|c0_g1_i2|m.12177	calcium calmodulin-dependent [Colletotrichum gloeosporioides Nara gc5]	7.17	3.89E-04	1.90E-02
TR40854|c0_g1_i2|m.12180	60S ribosomal L30	7.66	5.12E-04	2.22E-02
TR40929|c0_g1_i1|m.12199	Cytochrome c oxidase polypeptide 5, mitochondrial	9.29	8.52E-04	3.04E-02
TR40942|c0_g1_i1|m.12211	mRNA binding post-transcriptional regulator	6.57	3.88E-04	1.90E-02
TR40966|c0_g1_i1|m.12217	small nuclear ribonucleo B and B [Fusarium oxysporum Fo47]	8.10	4.25E-04	1.99E-02
TR40974|c0_g2_i1|m.12220	[Trichoderma reesei QM6a]	6.91	8.06E-05	8.22E-03
TR40998|c0_g1_i1|m.12246	Growth hormone-inducible transmembrane	8.22	9.06E-05	8.50E-03
TR41024|c0_g1_i1|m.12261	hypothetical protein UCRPA7_8004 [Phaeoacremonium minimum UCRPA7]	10.35	1.87E-05	3.43E-03
TR41059|c0_g1_i1|m.12327	cytochrome c oxidase subunit 6A, mitochondrial	6.92	1.28E-03	4.02E-02
TR41097|c0_g1_i1|m.12370	atp synthase subunit 9 [Eutypa lata UCREL1]	9.28	1.69E-05	3.24E-03
TR41103|c0_g2_i1|m.12372	Translationally-controlled tumor	9.41	7.08E-06	2.18E-03
TR41132|c0_g1_i1|m.12393	gtp-binding [Phaeoacremonium minimum UCRPA7]	7.21	3.64E-04	1.83E-02
TR41139|c0_g1_i1|m.12395	-like family [Colletotrichum gloeosporioides Nara gc5]	7.31	4.30E-04	2.01E-02
TR41140|c0_g1_i1|m.12398	mitochondrial carrier LEU5	5.85	1.69E-03	4.81E-02
TR41148|c0_g1_i1|m.12404	zinc finger [Phaeoacremonium minimum UCRPA7]	9.13	1.56E-03	4.58E-02
TR41158|c0_g1_i1|m.12408	E3 ubiquitin- ligase RBX1	9.59	1.02E-03	3.43E-02
TR41184|c0_g1_i2|m.12417	cytochrome b5	8.29	8.61E-05	8.24E-03
TR41185|c0_g1_i2|m.12419	aspartate aminotransferase	9.36	5.40E-04	2.29E-02
TR41185|c0_g2_i1|m.12420	aspartate aminotransferase	9.22	8.10E-04	2.96E-02
TR41188|c0_g1_i1|m.12424	carnitine acyl carnitine carrier [Magnaporthe oryzae 70-15]	5.47	8.67E-04	3.06E-02
TR41204|c0_g1_i1|m.12440	family transcriptional regulator [Colletotrichum gloeosporioides Nara gc5]	10.52	7.53E-04	2.84E-02
TR41219|c0_g1_i1|m.12446	[Trichoderma reesei QM6a]	9.61	1.79E-06	1.19E-03
TR41269|c0_g1_i1|m.12486	pyrroline-5-carboxylate reductase	6.36	1.40E-03	4.23E-02

TR41276|c0_g1_i1|m.12500	DOPA 4,5-dioxygenase	9.14	1.01E-03	3.43E-02
TR41314|c0_g1_i1|m.12520	proteasome component pre6	10.79	1.60E-04	1.14E-02
TR41333|c0_g1_i1|m.12531	myo-inositol-1-phosphate synthase	10.38	1.09E-04	9.25E-03
TR41401|c0_g1_i1|m.12555	nascent polypeptide-associated complex subunit alpha	6.83	1.43E-03	4.30E-02
TR41404|c0_g1_i1|m.12557	60s ribosomal l44 [Eutypa lata UCREL1]	8.43	3.16E-04	1.71E-02
TR41424|c1_g1_i1|m.12565	Mitochondrial peroxiredoxin PRX1	7.94	1.06E-03	3.50E-02
TR41467|c1_g1_i1|m.12601	26S protease regulatory subunit 4	8.91	2.26E-04	1.39E-02
TR41505|c0_g1_i2|m.12627	translation elongation factor 1-alpha, partial	5.85	5.42E-04	2.29E-02
TR41521|c0_g4_i1|m.12646	Major facilitator superfamily domain, general substrate transporter, partial [Metarhizium brunneum ARSEF 3297]	7.44	9.24E-05	8.58E-03
TR41542|c0_g1_i2|m.12677	Cysteine--tRNA ligase	11.25	3.20E-04	1.72E-02
TR41542|c0_g1_i1|m.12676	Cysteine--tRNA ligase	10.39	1.46E-03	4.37E-02
TR41542|c0_g1_i2|m.12678	hypothetical protein MAPG_04201	9.53	1.76E-03	4.93E-02
TR41556|c0_g1_i1|m.12687	bzip transcription factor	5.65	1.00E-03	3.41E-02
TR41568|c0_g1_i1|m.12689	nmra-like family [Eutypa lata UCREL1]	9.70	3.06E-06	1.38E-03
TR41627|c0_g1_i1|m.12737	ATP synthase subunit g	7.73	3.17E-04	1.71E-02
TR41629|c0_g1_i1|m.12739	translation initiation factor 3 subunit B	8.50	2.24E-04	1.39E-02
TR41659|c0_g1_i1|m.12782	FKBP-type peptidyl-prolyl cis-trans isomerase	7.57	3.46E-04	1.78E-02
TR41659|c0_g1_i2|m.12786	FK506-binding 4	9.82	4.22E-04	1.98E-02
TR41666|c0_g1_i1|m.12798	glycoside hydrolase family 16	8.03	1.34E-04	1.03E-02
TR41687|c0_g1_i1|m.12824	glycolipid anchored surface	7.04	3.57E-04	1.80E-02
TR41715|c2_g1_i2|m.12857	60S ribosomal L15	8.23	3.10E-04	1.69E-02
TR41718|c0_g1_i1|m.12862	FKBP-type peptidyl-prolyl cis-trans isomerase	9.90	7.61E-04	2.84E-02
TR41735|c0_g1_i1|m.12877	proteasome component C5	10.30	4.52E-04	2.07E-02
TR41748|c0_g1_i1|m.12889	cutinase negative acting	10.00	1.64E-04	1.16E-02
TR41748|c0_g1_i1|m.12890	cutinase negative acting	8.80	1.76E-03	4.93E-02
TR41753|c1_g1_i1|m.12892	T-complex 11	7.08	6.03E-04	2.47E-02
TR41774|c0_g1_i1|m.12914	Elongation factor 2	8.75	1.34E-04	1.03E-02
TR41781|c0_g1_i1|m.12928	regulator of g- signaling	9.64	2.73E-06	1.30E-03
TR41781|c0_g1_i1|m.12929	a-agglutinin core AGA1 of Neurospora crassa [Podospora anserina S mat+]	7.68	4.69E-04	2.13E-02
TR41792|c0_g1_i1|m.12932	hypothetical protein MBM_03450 [Marssonina brunnea f. sp. 'multigermtubi' MB_m1]	10.07	1.28E-03	4.02E-02
TR41854|c0_g1_i1|m.12985	Alcohol dehydrogenase, iron-type	8.97	1.76E-03	4.93E-02
TR41861|c0_g1_i2|m.12993	adenylyl-sulfate kinase [Neurospora crassa OR74A]	8.24	3.01E-04	1.65E-02
TR41906|c0_g1_i1|m.13015	solute carrier family 35 member E3	8.92	1.11E-05	2.63E-03
TR41912|c0_g1_i1|m.13024	NADP-specific glutamate dehydrogenase	6.50	1.53E-04	1.11E-02
TR41934|c1_g1_i1|m.13044	Heat shock Hsp88	8.35	5.80E-05	6.90E-03
TR42003|c0_g1_i2|m.13091	60s ribosomal l20	6.56	4.20E-04	1.98E-02
TR42004|c0_g1_i2|m.13095	ribosomal L28e	7.95	3.69E-04	1.84E-02
TR42015|c0_g2_i1|m.13103	[Glarea lozoyensis ATCC 20868]	9.35	5.96E-04	2.45E-02
TR42050|c0_g1_i1|m.13139	Fatty acid synthase subunit alpha	7.97	1.73E-04	1.18E-02
TR42071|c0_g2_i2|m.13164	hypothetical protein TRIVIDRAFT_27827 [Trichoderma virens Gv29-8]	9.90	1.02E-03	3.43E-02
TR42081|c0_g1_i1|m.13169	Cross-pathway control 1	8.50	2.85E-05	4.33E-03
TR42081|c0_g1_i2|m.13171	Cross-pathway control 1	7.64	1.38E-04	1.05E-02
TR42092|c0_g1_i1|m.13188	mitochondrial intermembrane space mia40 [Colletotrichum gloeosporioides Nara gc5]	8.70	1.70E-04	1.18E-02
TR42099|c0_g2_i1|m.13191	related to a-agglutinin core AGA1 [Neurospora crassa]	6.65	1.44E-03	4.34E-02
TR42140|c0_g1_i1|m.13232	GTP-binding ypt1	8.32	3.23E-04	1.72E-02
TR42145|c0_g3_i1|m.13235	methyltransferase domain-containing [Colletotrichum gloeosporioides Nara gc5]	9.53	9.44E-04	3.27E-02
TR42205|c0_g1_i1|m.13265	ceramide glucosyltransferase	9.10	2.87E-05	4.33E-03
TR42246|c0_g2_i1|m.13297	fructose-bisphosphate aldolase	6.77	4.05E-04	1.94E-02
TR42266|c0_g1_i1|m.13325	efflux pump antibiotic resistance [Phaeoacremonium minimum UCRPA7]	7.65	3.38E-05	4.80E-03
TR42276|c0_g1_i1|m.13334	heat shock 9	12.98	1.42E-04	1.06E-02
TR42292|c1_g2_i2|m.13352	mhyt domain signaling	8.99	4.54E-05	5.92E-03
TR42292|c0_g1_i1|m.13348	mhyt domain signaling [Colletotrichum gloeosporioides Nara gc5]	8.39	2.63E-04	1.51E-02
TR42300|c0_g2_i1|m.13369	glycogenin [Phaeoacremonium minimum UCRPA7]	9.06	4.06E-06	1.60E-03
TR42308|c0_g1_i1|m.13380	GTP-binding rhb1 [Pseudogymnoascus destructans 20631-21]	9.14	1.02E-03	3.43E-02
TR42346|c0_g1_i1|m.13418	alcohol dehydrogenase 1 [Exophiala aquamarina CBS 119918]	8.74	1.40E-04	1.06E-02
TR42453|c0_g2_i1|m.13540	regulatory suaprga1 [Eutypa lata UCREL1]	7.48	1.13E-03	3.66E-02
TR42480|c0_g1_i1|m.13562	glycerol-3-phosphate dehydrogenase	9.81	1.00E-07	3.06E-04
TR42480|c0_g2_i1|m.13564	Glycerol-3-phosphate dehydrogenase [NAD+]	8.77	2.69E-06	1.30E-03
TR42482|c0_g1_i1|m.13568	Minor allergen Alt a 7	8.63	6.94E-06	2.16E-03
TR42510|c0_g1_i1|m.13589	PH domain-containing	8.85	6.75E-06	2.13E-03
TR42523|c0_g2_i1|m.13599	eukaryotic translation initiation factor 5a-2	7.97	5.00E-05	6.40E-03
TR42523|c0_g1_i1|m.13598	eukaryotic translation initiation factor 5a-2	8.54	1.94E-04	1.28E-02
TR42533|c0_g1_i1|m.13601	L-threonine 3-dehydrogenase	8.85	2.77E-05	4.27E-03
TR42559|c0_g1_i1|m.13621	Hsp90 associated co-chaperone [Beauveria bassiana ARSEF 2860]	8.32	3.22E-04	1.72E-02
TR42559|c0_g1_i2|m.13623	Hsp90 associated co-chaperone [Beauveria bassiana ARSEF 2860]	7.83	5.95E-04	2.45E-02
TR42594|c0_g1_i1|m.13685	ATP-dependent RNA helicase SUB2	9.16	4.25E-05	5.64E-03
TR42596|c0_g1_i1|m.13691	seryl-tRNA synthetase	7.15	8.64E-04	3.06E-02
TR42601|c0_g1_i1|m.13695	26s protease regulatory subunit 6a	8.98	5.78E-04	2.41E-02
TR42617|c0_g1_i1|m.13698	rab gdp-dissociation inhibitor	7.79	2.34E-04	1.42E-02
TR42688|c1_g2_i1|m.13745	Heat shock hsp98	8.98	3.44E-05	4.85E-03
TR42688|c1_g1_i1|m.13743	heat shock 78, mitochondrial	10.58	6.10E-04	2.48E-02
TR42692|c0_g1_i1|m.13757	50S ribosomal L22e	7.25	7.78E-04	2.88E-02
TR42698|c0_g1_i1|m.13762	D-arabinitol 2-dehydrogenase [Fusarium fujikuroi]	10.00	2.98E-05	4.44E-03
TR42780|c0_g1_i1|m.13877	40s ribosomal s2	8.70	1.70E-04	1.18E-02
TR42826|c0_g1_i3|m.13932	heat shock 16	8.61	2.49E-06	1.29E-03
TR42826|c0_g1_i2|m.13928	hsp20 [Phaeoacremonium minimum UCRPA7]	6.45	1.42E-03	4.28E-02
TR42902|c0_g1_i1|m.13998	Mitosis inhibitor kinase SWE1	6.20	3.32E-04	1.74E-02
TR42902|c0_g1_i2|m.14000	Mitosis inhibitor kinase SWE1	6.43	3.96E-04	1.91E-02
TR42911|c0_g1_i1|m.14002	40S ribosomal S18	8.30	6.17E-05	7.15E-03
TR42934|c0_g2_i1|m.14027	[Neurospora crassa]	8.80	1.85E-05	3.41E-03
TR42947|c0_g1_i1|m.14032	alanine-glyoxylate aminotransferase	9.99	6.75E-04	2.66E-02
TR42966|c0_g1_i3|m.14057	[Chaetomium globosum CBS]	8.38	2.26E-04	1.39E-02
TR42974|c0_g1_i2|m.14063	Disulfide-bond oxidoreductase	9.63	3.73E-06	1.55E-03
TR42974|c0_g1_i1|m.14062	Disulfide-bond oxidoreductase	11.27	3.66E-04	1.84E-02
TR42975|c0_g1_i1|m.14064	s- glutathione dehydrogenase [Phaeoacremonium minimum UCRPA7]	8.01	1.93E-04	1.28E-02
TR43006|c0_g1_i1|m.14089	beta-tubulin [Blumeria graminis tritici]	9.60	1.54E-04	1.11E-02

TR43009|c0_g1_i1|m.14091	glycosidase crf1	8.95	8.73E-04	3.08E-02
TR43031|c0_g1_i1|m.14116	hnrnp arginine n-methyltransferase	7.83	1.10E-04	9.29E-03
TR43032|c0_g2_i1|m.14118	cdp-alcohol phosphatidyltransferase [Eutypa lata UCREL1]	10.56	7.70E-05	8.03E-03
TR43056|c0_g2_i1|m.14180	Elongation factor Tu	8.20	3.03E-04	1.66E-02
TR43057|c0_g1_i1|m.14182	pyruvate dehydrogenase E1 component subunit beta	7.43	1.57E-04	1.13E-02
TR43079|c0_g1_i1|m.14202	proteasome subunit alpha type-2	8.20	7.70E-04	2.86E-02
TR43097|c0_g1_i1|m.14210	GTP-binding rho2	6.22	1.82E-03	4.99E-02
TR43099|c0_g1_i1|m.14213	rrna-processing fcf2 [Eutypa lata UCREL1]	9.99	2.58E-04	1.50E-02
TR43101|c0_g1_i1|m.14216	aldehyde reductase 2	10.73	3.25E-05	4.66E-03
TR43101|c0_g1_i2|m.14218	aldehyde reductase 2	11.12	7.27E-04	2.77E-02
TR43141|c0_g1_i1|m.14305	60S ribosomal L19 [Neurospora crassa OR74A]	10.75	5.41E-05	6.57E-03
TR43141|c0_g1_i1|m.14304	60S ribosomal L19	7.11	3.39E-04	1.76E-02
TR43155|c0_g1_i1|m.14314	40S ribosomal S13	7.02	6.99E-04	2.72E-02
TR43229|c0_g1_i1|m.14358	Elongation factor 1-beta	8.26	7.24E-04	2.77E-02
TR43239|c0_g1_i1|m.14370	[Trichoderma reesei QM6a]	9.41	1.12E-03	3.65E-02
TR43265|c0_g1_i1|m.14397	proteasome subunit beta type 7 precursor	10.26	5.42E-04	2.29E-02
TR43280|c0_g1_i1|m.14411	14-3-3 [Eutypa lata UCREL1]	8.57	7.06E-05	7.69E-03
TR43308|c0_g1_i2|m.14444	siderophore biosynthesis enzyme, [Glarea lozoyensis ATCC 20868]	10.16	1.67E-04	1.17E-02
TR43317|c0_g1_i1|m.14454	PAP2 superfamily	10.52	5.03E-05	6.40E-03
TR43340|c0_g1_i1|m.14499	hypothetical protein Z518_01280 [Rhinocladiella mackenziei CBS 650.93]	8.89	1.68E-03	4.80E-02
TR43353|c0_g2_i1|m.14510	[Nectria haematococca mpVI 77-13-4]	9.01	6.99E-07	7.02E-04
TR43381|c1_g1_i1|m.14541	60S acidic ribosomal P0	7.44	1.21E-04	9.83E-03
TR43390|c0_g1_i1|m.14554	proteasome component PUP3	8.11	1.47E-04	1.08E-02
TR43411|c0_g1_i1|m.14581	ribose-phosphate pyrophosphokinase ii	7.61	9.47E-04	3.28E-02
TR43442|c0_g1_i1|m.14610	Succinate fumarate mitochondrial transporter	6.23	6.33E-04	2.55E-02
TR43487|c0_g2_i1|m.14699	glutamate-cysteine ligase modifier subunit	7.24	1.71E-03	4.85E-02
TR43580|c0_g1_i1|m.14784	[Nectria haematococca mpVI 77-13-4]	7.27	8.27E-04	3.00E-02
TR43593|c0_g1_i2|m.14798	proteasome component PUP2	10.23	2.62E-04	1.51E-02
TR43594|c0_g1_i1|m.14799	MFS general substrate transporter [Glarea lozoyensis ATCC 20868]	9.43	1.01E-06	8.52E-04
TR43631|c0_g1_i1|m.14843	proteasome subunit beta type-2	10.44	1.09E-04	9.25E-03
TR43645|c0_g2_i1|m.14891	extracellular conserved serine-rich [Talaromyces stipitatus ATCC 10500]	11.56	1.00E-05	2.51E-03
TR43677|c0_g1_i2|m.14944	[Trichoderma reesei QM6a]	6.80	5.51E-05	6.64E-03
TR43684|c0_g1_i3|m.14955	ubiquitin-like modifier	7.57	1.06E-03	3.51E-02
TR43696|c0_g1_i1|m.14970	Cholesterol oxidase	8.35	5.74E-06	1.97E-03
TR43732|c0_g1_i1|m.15003	60s ribosomal l13	6.88	4.17E-04	1.97E-02
TR43733|c0_g1_i2|m.15009	hypothetical protein VDAG_05968 [Verticillium dahliae VdLs.17]	8.72	1.47E-03	4.39E-02
TR43738|c0_g1_i1|m.15017	1-acyldihydroxyacetone-phosphate reductase	10.86	4.20E-05	5.61E-03
TR43761|c0_g1_i2|m.15129	Superoxide dismutase	7.40	5.61E-05	6.74E-03
TR43761|c0_g1_i1|m.15127	Superoxide dismutase	7.57	6.67E-04	2.65E-02
TR43768|c0_g1_i1|m.15136	[Trichoderma reesei QM6a]	9.23	2.73E-06	1.30E-03
TR43780|c0_g1_i1|m.15163	Hydroxymethylglutaryl- synthase	8.40	1.31E-04	1.02E-02
TR43793|c0_g2_i3|m.15182	-No hit found-	8.80	9.70E-06	2.51E-03
TR43795|c0_g1_i1|m.15188	peptide methionine sulfoxide reductase [Zymoseptoria tritici IPO323]	10.04	4.56E-07	6.18E-04
TR43869|c0_g1_i1|m.15287	isopentenyl-diphosphate delta-isomerase	9.85	8.83E-04	3.10E-02
TR43874|c0_g1_i1|m.15293	60S ribosomal L27a	7.78	4.33E-04	2.01E-02
TR43895|c0_g1_i1|m.15305	fimbrin	6.50	2.00E-04	1.30E-02
TR43926|c0_g1_i2|m.15336	60S ribosomal L34-B	9.21	1.38E-03	4.21E-02
TR43953|c0_g1_i2|m.15370	Mitochondrial outer membrane porin	8.10	1.42E-04	1.06E-02
TR43969|c0_g1_i1|m.15426	Ubiquitin [Glarea lozoyensis ATCC 20868]	10.00	2.07E-04	1.32E-02
TR43971|c0_g2_i1|m.15431	C6 transcription factor [Colletotrichum gloeosporioides Nara gc5]	9.07	1.13E-05	2.64E-03
TR44011|c0_g1_i1|m.15505	FMN-binding split barrel	9.04	7.33E-04	2.79E-02
TR44031|c0_g1_i2|m.15510	ATP synthase subunit 5	7.28	9.53E-04	3.29E-02
TR44033|c0_g1_i1|m.15513	60s acidic ribosomal p0 [Moniliophthora roreri MCA 2997]	10.69	1.04E-03	3.46E-02
TR44034|c0_g2_i1|m.15517	methionine aminopeptidase [Verticillium alfalfae]	7.73	2.60E-04	1.50E-02
TR44133|c0_g1_i1|m.15665	[Laccaria bicolor S238N-H82]	11.59	2.52E-04	1.48E-02
TR44159|c0_g1_i1|m.15699	thioredoxin [Colletotrichum fioriniae PJ7]	11.14	5.97E-06	2.00E-03
TR44180|c0_g1_i1|m.15742	CK1 CK1 CK1-D kinase [Fusarium oxysporum FOSC 3-a]	5.85	1.75E-03	4.93E-02
TR44183|c1_g1_i1|m.15749	delta-9 fatty acid desaturase	8.00	3.76E-05	5.12E-03
TR44214|c0_g1_i1|m.15799	60S ribosomal L24	7.88	3.31E-04	1.74E-02
TR44247|c1_g1_i1|m.15822	Histone H2B	8.90	2.08E-05	3.74E-03
TR44314|c0_g2_i2|m.15892	40s ribosomal s5	7.66	8.50E-05	8.24E-03
TR44342|c0_g1_i1|m.15951	aflatoxin B1 aldehyde reductase member 3	10.51	5.33E-05	6.55E-03
TR44342|c0_g1_i2|m.15953	aflatoxin B1 aldehyde reductase member 3	8.97	1.57E-03	4.59E-02
TR44349|c1_g1_i2|m.15968	caspase domain-containing	10.39	5.16E-06	1.84E-03
TR44349|c1_g1_i1|m.15966	caspase domain-containing	7.20	1.34E-03	4.12E-02
TR44356|c0_g1_i1|m.15980	nadph dehydrogenase	8.60	8.08E-06	2.38E-03
TR44356|c0_g1_i1|m.15982	hypothetical protein BN1723_014332	9.97	1.22E-04	9.85E-03
TR44401|c0_g2_i1|m.16054	40s ribosomal s12	8.68	3.81E-04	1.89E-02
TR44422|c0_g1_i1|m.16092	ATP synthase subunit delta [Gaeumannomyces graminis tritici R3-111a-1]	8.36	6.34E-05	7.26E-03
TR44425|c1_g1_i1|m.16097	60s acidic ribosomal p2	9.53	1.11E-03	3.63E-02
TR44426|c0_g1_i2|m.16101	mitochondrial 2-oxodicarboxylate carrier [Colletotrichum gloeosporioides Nara gc5]	8.49	2.48E-05	4.08E-03
TR44475|c0_g1_i3|m.16187	hypothetical protein VDAG_04935 [Verticillium dahliae VdLs.17]	8.78	1.70E-06	1.18E-03
TR44488|c0_g2_i1|m.16211	26S proteasome regulatory subunit N4 [Cladophialophora psammophila CBS 110553]	7.37	4.85E-04	2.15E-02
TR44488|c0_g2_i2|m.16212	26S proteasome regulatory subunit N4 [Cladophialophora psammophila CBS 110553]	6.65	7.54E-04	2.84E-02
TR44542|c0_g1_i1|m.16289	stress-induced-phospho 1	11.15	2.54E-05	4.12E-03
TR44554|c0_g1_i1|m.16305	40s ribosomal s9	7.96	2.48E-04	1.47E-02
TR44585|c0_g1_i1|m.16362	aldehyde dehydrogenase	9.52	5.04E-07	6.34E-04
TR44592|c3_g1_i1|m.16381	hsp70 [Phaeoacremonium minimum UCRPA7]	9.16	5.00E-06	1.81E-03
TR44592|c3_g1_i2|m.16383	hsp70 [Phaeoacremonium minimum UCRPA7]	7.70	1.84E-05	3.41E-03
TR44592|c2_g3_i1|m.16379	glucose-regulated 78 of hsp70 family [Fusarium fujikuroi]	7.73	8.54E-04	3.05E-02
TR44622|c0_g1_i1|m.16408	hypothetical protein GALMADRAFT_147259	11.79	2.61E-05	4.17E-03
TR44629|c0_g1_i1|m.16424	eukaryotic translation initiation factor eIF-1A subunit, [Talaromyces stipitatus ATCC 10500]	8.38	3.23E-04	1.72E-02
TR44632|c0_g1_i2|m.16432	hypothetical protein MBR_06041, partial [Metarhizium brunneum ARSEF 3297]	7.40	6.10E-05	7.10E-03
TR44637|c0_g1_i1|m.16454	short chain dehydrogenase [Colletotrichum gloeosporioides Nara gc5]	10.75	5.40E-05	6.57E-03
TR44637|c0_g1_i2|m.16456	short chain dehydrogenase [Colletotrichum graminicola]	9.41	1.33E-03	4.11E-02
TR44638|c0_g1_i1|m.16458	Protein ECM13	10.58	2.80E-05	4.30E-03

TR44659|c0_g1_i1|m.16487	gpi-anchored cell wall organization ecm33 [Eutypa lata UCREL1]	9.06	8.85E-06	2.42E-03
TR44676|c1_g1_i2|m.16522	Heat shock 70 kDa	6.22	1.72E-03	4.86E-02
TR44720|c0_g1_i1|m.16580	60s Acidic ribosomal	7.65	6.10E-04	2.48E-02
TR44753|c0_g1_i1|m.16639	C2H2 type zinc finger domain-containing [Colletotrichum gloeosporioides Nara gc5]	8.83	4.67E-05	6.05E-03
TR44754|c0_g2_i2|m.16642	[Nectria haematococca mpVI 77-13-4]	10.38	6.63E-07	6.96E-04
TR44754|c0_g2_i1|m.16641	peptidyl-prolyl cis-trans isomerase, mitochondrial [Fusarium oxysporum cubense tropical race 4 54006]	7.00	3.41E-04	1.76E-02
TR44761|c0_g1_i1|m.16647	40s ribosomal s3	10.72	6.27E-05	7.24E-03
TR44778|c0_g1_i1|m.16664	eliciting plant response	9.54	1.12E-05	2.63E-03
TR44780|c0_g3_i1|m.16665	transcription factor TFIIB	8.91	2.64E-05	4.17E-03
TR44784|c0_g1_i2|m.16679	Alcohol dehydrogenase 1	10.99	1.84E-07	3.33E-04
TR44784|c0_g1_i1|m.16676	Alcohol dehydrogenase 1	9.54	2.70E-05	4.21E-03
TR44830|c0_g1_i2|m.16743	hypothetical protein CMQ_2256	9.48	1.64E-03	4.73E-02
TR44836|c0_g1_i1|m.16747	non-histone chromosomal 6	8.88	1.32E-04	1.02E-02
TR44841|c0_g1_i1|m.16751	glutathione reductase	7.37	1.71E-05	3.24E-03
TR44922|c0_g2_i1|m.16852	40S ribosomal S4	6.91	3.00E-04	1.65E-02
TR44922|c0_g2_i3|m.16859	40S ribosomal S4	7.75	3.67E-04	1.84E-02
TR44964|c0_g1_i1|m.16927	ferrous iron binding [Chaetomium thermophilum thermophilum DSM 1495]	9.17	2.46E-05	4.07E-03
TR44982|c3_g1_i3|m.16984	60s ribosomal l10 [Phaeoacremonium minimum UCRPA7]	7.88	1.70E-05	3.24E-03
TR44982|c3_g1_i2|m.16983	60s ribosomal l10 [Phaeoacremonium minimum UCRPA7]	9.67	1.23E-04	9.86E-03
TR44988|c0_g1_i2|m.16998	[Nectria haematococca mpVI 77-13-4]	7.73	1.98E-04	1.29E-02
TR45005|c1_g1_i1|m.17013	gtp-binding rhoa	6.36	2.48E-04	1.47E-02
TR45039|c0_g1_i1|m.17050	60S ribosomal L7	8.68	1.40E-05	2.86E-03
TR45042|c0_g2_i1|m.17055	nmra-like family [Colletotrichum gloeosporioides Nara gc5]	9.82	3.69E-04	1.84E-02
TR45067|c0_g1_i2|m.17111	transcription factor bZIP	10.22	5.97E-05	6.98E-03
TR45067|c0_g1_i1|m.17109	transcription factor bZIP	9.85	5.20E-04	2.23E-02
TR45115|c1_g1_i1|m.17213	50S ribosomal L6e [Fusarium oxysporum FOSC 3-a]	7.32	5.00E-04	2.18E-02
TR45116|c0_g1_i1|m.17215	triosephosphate isomerase	10.45	8.57E-05	8.24E-03
TR45126|c0_g1_i1|m.17223	endo alpha-1,4 polygalactosaminidase precursor [Fusarium fujikuroi]	8.35	3.10E-05	4.57E-03
TR45126|c0_g1_i2|m.17226	endo alpha- polygalactosaminidase precursor [Eutypa lata UCREL1]	9.28	1.39E-03	4.21E-02
TR45156|c0_g1_i1|m.17250	CNT family concentrative nucleoside transporter	11.56	5.14E-07	6.34E-04
TR45165|c0_g1_i2|m.17272	Mitochondrial phosphate carrier	7.70	1.40E-04	1.06E-02
TR45174|c0_g1_i1|m.17281	60s ribosomal l8	8.03	1.02E-04	9.04E-03
TR45174|c0_g1_i2|m.17283	60s ribosomal l8 [Colletotrichum gloeosporioides Nara gc5]	6.80	4.98E-04	2.18E-02
TR45175|c2_g2_i1|m.17290	Nucleoside diphosphate kinase	8.28	1.04E-04	9.16E-03
TR45197|c0_g1_i1|m.17339	60S ribosomal L32	7.40	4.82E-04	2.15E-02
TR45218|c0_g3_i1|m.17397	Acriflavine sensitivity control acr-2	9.43	4.82E-06	1.81E-03
TR45218|c0_g1_i2|m.17394	acriflavine sensitivity control ACR-2 [Fusarium fujikuroi]	8.06	8.40E-05	8.22E-03
TR45218|c0_g1_i1|m.17390	fungal transcriptional regulatory [Colletotrichum gloeosporioides Nara gc5]	7.84	3.68E-04	1.84E-02
TR45252|c0_g2_i1|m.17464	-No hit found-	9.38	2.27E-06	1.26E-03
TR45281|c0_g1_i1|m.17528	60s ribosomal l9 [Phaeoacremonium minimum UCRPA7]	10.32	6.98E-05	7.67E-03
TR45281|c0_g1_i1|m.17529	60s ribosomal l9	7.50	1.19E-03	3.83E-02
TR45299|c0_g1_i2|m.17563	heterokaryon incompatibility Het-C	7.07	2.86E-05	4.33E-03
TR45337|c0_g1_i1|m.17640	60s ribosomal l11	10.05	1.03E-04	9.12E-03
TR45361|c0_g1_i1|m.17683	40S ribosomal S11	7.24	6.63E-04	2.64E-02
TR45366|c0_g1_i1|m.17685	proteasome component PRE3	9.94	6.21E-04	2.51E-02
TR45378|c0_g1_i6|m.17699	40S ribosomal S23	6.09	4.24E-04	1.99E-02
TR45404|c0_g1_i1|m.17732	G alpha chain [Fusarium fujikuroi]	8.20	1.29E-05	2.74E-03
TR45411|c0_g1_i1|m.17737	E3 ubiquitin ligase complex SCF subunit scon-3 [Fusarium verticillioides 7600]	7.57	3.89E-04	1.90E-02
TR45426|c0_g1_i1|m.17750	atp synthase subunit 4	7.83	1.70E-04	1.18E-02
TR45465|c0_g1_i4|m.17835	Woronin body major	12.38	1.58E-07	3.06E-04
TR45465|c0_g1_i3|m.17830	Woronin body major	12.63	1.56E-07	3.06E-04
TR45465|c0_g1_i1|m.17824	-No hit found-	9.26	2.98E-06	1.37E-03
TR45465|c0_g1_i3|m.17832	Woronin body major	9.17	1.54E-05	3.07E-03
TR45473|c1_g1_i1|m.17859	translation elongation factor 1 alpha, partial [Beauveria bassiana]	6.48	8.63E-05	8.24E-03
TR45473|c1_g1_i5|m.17867	translation elongation factor 1 alpha, partial	6.48	1.15E-04	9.48E-03
TR45473|c1_g1_i2|m.17862	Elongation factor 1-alpha	6.59	1.40E-04	1.06E-02
TR45473|c1_g1_i7|m.17868	translation elongation factor 1 alpha	6.62	3.96E-04	1.91E-02
TR45490|c0_g1_i2|m.17921	6-phosphogluconate dehydrogenase	8.64	4.95E-06	1.81E-03
TR45502|c1_g1_i1|m.17946	heat shock SSB	7.34	4.71E-04	2.13E-02
TR45502|c0_g1_i1|m.17941	heat shock SSB1	8.05	5.81E-04	2.42E-02
TR45510|c1_g1_i1|m.17968	60s ribosomal l27-a	7.78	1.22E-03	3.87E-02
TR45546|c0_g1_i1|m.18027	D-3-phosphoglycerate dehydrogenase 2	8.15	7.47E-05	7.91E-03
TR45554|c0_g1_i1|m.18037	glycine-rich [Phaeoacremonium minimum UCRPA7]	8.29	5.95E-05	6.98E-03
TR45635|c0_g2_i1|m.18206	glycosyl transferase, [Metarhizium acridum CQMa 102]	7.17	3.88E-05	5.23E-03
TR45639|c0_g2_i2|m.18225	40S ribosomal S1	7.65	2.21E-04	1.37E-02
TR45651|c0_g1_i1|m.18249	nucleosome assembly	7.86	3.72E-05	5.10E-03
TR45657|c0_g1_i2|m.18255	Histone H2A	8.17	1.40E-04	1.06E-02
TR45667|c0_g1_i1|m.18260	ubiquitin carboxyl-terminal hydrolase L3	6.71	4.53E-04	2.07E-02
TR45673|c0_g1_i1|m.18268	mitochondrial-processing peptidase subunit beta	7.82	1.45E-04	1.07E-02
TR45683|c0_g3_i1|m.18301	ATP synthase subunit alpha, mitochondrial	9.31	6.67E-06	2.13E-03
TR45743|c0_g1_i1|m.18431	WSC domain containing	10.70	1.23E-05	2.69E-03
TR45783|c0_g1_i2|m.18537	GTP cyclohydrolase II	10.60	2.72E-05	4.22E-03
TR45797|c0_g2_i1|m.18571	carnitine O-acetyltransferase	6.25	7.58E-05	7.96E-03
TR45821|c1_g1_i1|m.18597	disulfide isomerase [Phaeoacremonium minimum UCRPA7]	6.78	3.98E-04	1.92E-02
TR45824|c0_g1_i2|m.18618	glutamine synthetase	8.77	1.87E-04	1.25E-02
TR45824|c0_g1_i1|m.18615	glutamine synthetase	8.20	2.15E-04	1.35E-02
TR45879|c0_g1_i1|m.18740	elicitor [Phaeoacremonium minimum UCRPA7]	7.76	3.78E-04	1.88E-02
TR45881|c2_g1_i1|m.18749	14-3-3 family	7.15	6.95E-05	7.67E-03
TR45886|c2_g2_i2|m.18767	glyceraldehyde-3-phosphate dehydrogenase	7.93	3.84E-05	5.21E-03
TR45899|c0_g1_i3|m.18815	NmrA-like family protein [Colletotrichum gloeosporioides Cg-14]	10.26	1.53E-07	3.06E-04
TR45899|c0_g1_i2|m.18813	NmrA-like family protein [Colletotrichum gloeosporioides Cg-14]	6.83	3.53E-04	1.80E-02
TR45913|c0_g1_i1|m.18852	60s ribosomal l21-a	8.09	1.01E-04	8.97E-03
TR45923|c0_g1_i1|m.18872	NAD dependent epimerase dehydratase	7.92	1.76E-04	1.19E-02
TR45941|c0_g4_i3|m.18913	40S RIBOSOMAL PROTEIN S24 [Fusarium fujikuroi]	7.38	5.50E-04	2.32E-02
TR45972|c0_g1_i1|m.18958	thioredoxin reductase	9.40	6.41E-06	2.07E-03
TR45972|c0_g1_i3|m.18965	thioredoxin reductase	7.90	1.79E-03	4.96E-02

TR45983|c0_g1_i2|m.18978	60S ribosomal L3	8.21	1.07E-04	9.19E-03
TR46109|c0_g1_i2|m.19322	inorganic pyrophosphatase	9.16	5.83E-05	6.90E-03
TR46115|c0_g1_i1|m.19347	40s ribosomal s8	9.38	7.29E-05	7.83E-03
TR46234|c0_g1_i2|m.19618	dihydrolipoyl dehydrogenase	7.10	3.18E-04	1.71E-02
TR46238|c0_g1_i1|m.19632	aminotransferase class I and II	10.02	1.07E-06	8.52E-04
TR46320|c0_g1_i1|m.19862	ubiquitin conjugating enzyme ( ), [Talaromyces stipitatus ATCC 10500]	7.05	3.33E-04	1.74E-02
TR46350|c1_g1_i2|m.19942	40S ribosomal S7	7.49	7.19E-04	2.76E-02
TR46361|c0_g1_i2|m.19986	mpv17 pmp22 family [Phaeoacremonium minimum UCRPA7]	10.69	1.95E-05	3.55E-03
TR46367|c0_g1_i4|m.20005	cytochrome c	8.91	1.69E-05	3.24E-03
TR46367|c0_g1_i2|m.20002	Cytochrome c	9.44	3.70E-04	1.84E-02
TR46483|c0_g1_i1|m.20261	SEC14 cytosolic factor	8.76	9.90E-06	2.51E-03
TR46564|c0_g1_i1|m.20616	aconitate hydratase	6.31	1.96E-04	1.28E-02
TR46616|c0_g2_i2|m.20765	ribosomal L14	6.19	9.04E-04	3.15E-02
TR46625|c0_g1_i2|m.20802	short chain dehydrogenase reductase [Phaeoacremonium minimum UCRPA7]	11.51	8.54E-05	8.24E-03
TR46625|c0_g1_i1|m.20801	short-chain dehydrogenase [Colletotrichum fioriniae PJ7]	11.02	7.68E-04	2.86E-02
TR46637|c0_g1_i2|m.20828	ATP-dependent RNA helicase eIF4A	7.47	8.00E-05	8.22E-03
TR46652|c1_g1_i1|m.20861	-No hit found-	6.98	3.68E-05	5.08E-03
TR46654|c0_g1_i2|m.20872	nucleoside-diphosphate-sugar epimerase family [Talaromyces marneffei ATCC 18224]	10.50	5.30E-05	6.55E-03
TR46654|c0_g1_i1|m.20869	hypothetical protein W97_07538 [Coniosporium apollinis CBS 100218]	9.80	1.14E-03	3.67E-02
TR46655|c0_g1_i1|m.20880	von willebrand factor	6.84	1.86E-04	1.25E-02
TR46682|c3_g2_i6|m.20959	ADP,ATP carrier	7.01	4.20E-05	5.61E-03
TR46682|c3_g2_i1|m.20953	ADP,ATP carrier	6.62	3.07E-04	1.67E-02
TR46696|c0_g2_i1|m.21012	pot family proton-dependent oligopeptide transporter	7.82	1.98E-06	1.22E-03
TR46709|c0_g1_i1|m.21035	lustrin A	11.57	3.17E-07	4.78E-04
TR46709|c0_g1_i1|m.21036	-No hit found-	8.51	8.78E-06	2.42E-03
TR46711|c0_g1_i3|m.21042	3,4-dihydroxy-2-butanone 4-phosphate synthase	10.22	1.19E-05	2.67E-03
TR46711|c0_g1_i2|m.21040	3,4-dihydroxy-2-butanone 4-phosphate synthase	10.36	1.70E-05	3.24E-03
TR46716|c0_g1_i1|m.21046	mitochondrial hypoxia responsive domain [Fusarium fujikuroi]	7.95	5.10E-05	6.44E-03
TR46760|c0_g4_i1|m.21203	transaldolase	6.19	8.30E-04	3.00E-02
TR46845|c0_g1_i1|m.21443	c6 transcription factor [Eutypa lata UCREL1]	8.02	3.17E-05	4.62E-03
TR46890|c0_g2_i2|m.21613	2,3-bisphosphoglycerate-independent phosphoglycerate mutase	10.08	1.58E-04	1.13E-02
TR47011|c2_g2_i1|m.21856	60s ribosomal l2	8.59	4.36E-05	5.73E-03
TR47049|c0_g1_i1|m.21998	alpha-tubulin B [Fusarium fujikuroi]	7.15	4.48E-04	2.06E-02
TR47090|c0_g1_i3|m.22142	Enolase	8.73	6.67E-05	7.47E-03
TR47094|c0_g1_i1|m.22154	Chitin synthase 1	7.71	1.00E-05	2.51E-03
TR47108|c0_g1_i1|m.22197	40s ribosomal s17	8.18	1.58E-04	1.13E-02
TR47162|c0_g1_i1|m.22351	gpi anchored serine-threonine rich [Colletotrichum gloeosporioides Nara gc5]	11.43	1.75E-06	1.19E-03
TR47177|c0_g1_i1|m.22393	heat shock 30 [Fusarium fujikuroi]	8.53	5.14E-05	6.45E-03
TR47186|c0_g1_i2|m.22432	adp-ribosylation factor [Eutypa lata UCREL1]	7.68	5.08E-05	6.44E-03
TR47195|c0_g1_i1|m.22445	alcohol dehydrogenase -like domain-containing	11.12	5.39E-06	1.89E-03
TR47195|c0_g1_i2|m.22447	alcohol dehydrogenase -like domain-containing	8.94	8.41E-04	3.03E-02
TR47217|c0_g1_i1|m.22520	c2h2 transcription factor [Phaeoacremonium minimum UCRPA7]	10.69	8.97E-06	2.43E-03
TR47217|c0_g1_i1|m.22519	C2H2 transcription factor [Colletotrichum gloeosporioides Nara gc5]	7.90	1.01E-05	2.51E-03
TR47233|c0_g1_i1|m.22568	major facilitator superfamily transporter	11.46	2.15E-06	1.23E-03
TR47278|c0_g2_i1|m.22725	chaperone dnaj 2 [Phaeoacremonium minimum UCRPA7]	7.73	1.07E-04	9.19E-03
TR47511|c0_g1_i1|m.23437	60s ribosomal l16	10.16	1.20E-04	9.75E-03
TR47590|c2_g1_i3|m.23722	WD40 repeat	10.65	3.18E-06	1.38E-03
TR47590|c2_g1_i5|m.23724	hypothetical protein TRIVIDRAFT_134520, partial [Trichoderma virens Gv29-8]	9.44	1.48E-04	1.08E-02
TR47590|c2_g4_i1|m.23729	ankyrin repeat [Colletotrichum gloeosporioides Nara gc5]	9.04	4.76E-04	2.14E-02
TR47624|c0_g1_i2|m.23893	Cys Met metabolism PLP-dependent enzyme [Colletotrichum fioriniae PJ7]	12.50	6.48E-07	6.96E-04
TR47635|c0_g1_i2|m.23929	family [Phaeoacremonium minimum UCRPA7]	10.13	1.24E-05	2.69E-03
TR47635|c0_g1_i4|m.23931	family [Phaeoacremonium minimum UCRPA7]	9.38	1.59E-03	4.62E-02
TR47692|c0_g1_i1|m.24130	60s ribosomal l4-a	7.96	2.69E-04	1.52E-02
TR47738|c1_g1_i1|m.24274	Elongation factor 3	7.79	2.42E-05	4.05E-03
TR47738|c2_g2_i10|m.24304	elongation factor 3 [Exophiala aquamarina CBS 119918]	6.82	1.68E-04	1.18E-02
TR47738|c2_g1_i2|m.24279	elongation factor 3 [Exophiala aquamarina CBS 119918]	5.98	2.31E-04	1.41E-02
TR47738|c2_g2_i3|m.24287	Elongation factor 3	6.14	2.66E-04	1.52E-02
TR47738|c2_g2_i7|m.24297	elongation factor 3	6.55	7.73E-04	2.87E-02
TR47738|c2_g1_i1|m.24277	elongation factor 3 [Exophiala aquamarina CBS 119918]	5.26	1.24E-03	3.92E-02
TR47764|c0_g1_i2|m.24403	alcohol dehydrogenase	10.66	8.22E-07	7.69E-04
TR47764|c0_g1_i1|m.24399	alcohol dehydrogenase	11.10	3.56E-04	1.80E-02
TR47766|c1_g1_i1|m.24409	glucosamine-fructose-6-phosphate aminotransferase	8.95	8.55E-07	7.73E-04
TR47786|c0_g1_i1|m.24454	hsp70 [Phaeoacremonium minimum UCRPA7]	10.04	2.09E-06	1.23E-03
TR47884|c0_g1_i2|m.24844	vacuolar protease a	7.78	4.68E-05	6.05E-03
TR47978|c0_g2_i3|m.25223	formate dehydrogenase	7.40	1.08E-04	9.19E-03
TR47978|c0_g2_i2|m.25220	formate dehydrogenase	7.26	1.30E-03	4.06E-02
TR48014|c0_g3_i1|m.25326	hypothetical protein CGLO_03011	6.92	8.39E-05	8.22E-03
TR48014|c0_g3_i1|m.25329	-No hit found-	6.61	3.04E-04	1.66E-02
TR48026|c1_g2_i1|m.25363	atp synthase subunit beta [Phaeoacremonium minimum UCRPA7]	8.77	1.71E-05	3.24E-03
TR48026|c1_g4_i1|m.25375	atp synthase subunit beta [Phaeoacremonium minimum UCRPA7]	9.83	1.36E-04	1.04E-02
TR48080|c0_g1_i1|m.25587	[Pyrenophora tritici-repentis Pt-1C-BFP]	8.17	1.05E-04	9.16E-03
TR48080|c0_g1_i2|m.25588	[Pyrenophora tritici-repentis Pt-1C-BFP]	9.23	3.48E-04	1.78E-02
TR48091|c0_g1_i1|m.25650	Cell division control 48	9.43	6.25E-06	2.04E-03
TR48091|c0_g3_i1|m.25655	Cell division control 48	9.82	1.87E-04	1.25E-02
TR48093|c0_g3_i2|m.25665	glutathione S-transferase	10.56	8.28E-05	8.22E-03
TR48093|c0_g3_i3|m.25666	glutathione S-transferase	8.33	2.10E-04	1.33E-02
TR48093|c0_g2_i1|m.25663	glutathione s-transferase GST3	7.01	1.23E-03	3.90E-02
TR48284|c0_g1_i3|m.26454	Versicolorin reductase	10.61	6.68E-04	2.65E-02
TR48284|c0_g1_i2|m.26451	Versicolorin reductase	11.12	7.27E-04	2.77E-02
TR48327|c0_g2_i1|m.26675	aldehyde dehydrogenase	8.43	2.59E-05	4.16E-03
TR48327|c0_g2_i2|m.26677	aldehyde dehydrogenase	9.28	6.81E-04	2.68E-02
TR48412|c0_g2_i1|m.27092	Malate synthase	7.32	3.69E-05	5.08E-03
TR48491|c1_g1_i2|m.27511	transketolase [Trichoderma atroviride IMI 206040]	6.54	1.01E-03	3.41E-02
TR48514|c0_g1_i1|m.27605	dna damage-inducible 1	9.63	2.23E-05	3.88E-03
TR48674|c0_g1_i1|m.28479	ABC-2 type transporter	9.51	1.16E-07	3.06E-04
TR48681|c1_g2_i1|m.28515	utp-glucose-1-phosphate uridylyltransferase	6.73	6.98E-04	2.72E-02

TR48711|c0_g1_i2|m.28684	non-anchored cell wall 1 [Neurospora crassa OR74A]	11.13	1.97E-06	1.22E-03
TR48711|c0_g1_i3|m.28689	non-anchored cell wall 1 [Neurospora crassa OR74A]	9.02	2.12E-06	1.23E-03
TR48711|c0_g1_i2|m.28683	non-anchored cell wall 1 [Neurospora crassa OR74A]	8.47	4.99E-06	1.81E-03
TR48812|c0_g1_i1|m.29274	Elongation factor 1-gamma 1	7.98	7.51E-04	2.84E-02
TR48871|c0_g1_i2|m.29577	alcohol dehydrogenase 1	-5.52	8.21E-05	8.22E-03
TR48871|c0_g1_i2|m.29578	alcohol dehydrogenase 1	-4.48	1.79E-03	4.96E-02
TR48914|c0_g3_i1|m.29748	glycogen synthase	6.53	3.40E-04	1.76E-02
TR48914|c0_g4_i3|m.29754	glycogen synthase	7.84	3.46E-04	1.78E-02
TR48947|c0_g2_i2|m.29906	Phosphoenolpyruvate carboxykinase	6.52	9.56E-04	3.29E-02
TR48991|c0_g1_i2|m.30191	ribosome biogenesis sqt1 [Phaeoacremonium minimum UCRPA7]	12.11	4.04E-06	1.60E-03
TR49112|c5_g1_i2|m.30871	Plasma membrane ATPase	7.77	1.28E-04	1.01E-02
TR49112|c2_g1_i1|m.30860	Plasma membrane ATPase	6.51	4.49E-04	2.06E-02
TR49120|c0_g1_i2|m.30895	C2H2 transcription factor [Colletotrichum gloeosporioides Nara gc5]	8.13	2.13E-05	3.78E-03
TR49191|c4_g1_i2|m.31344	Citrate synthase, mitochondrial	8.33	2.98E-05	4.44E-03
TR49289|c0_g1_i1|m.31862	zinc finger MSN2 4	8.97	3.40E-07	4.85E-04
TR49347|c1_g3_i1|m.32247	40S ribosomal S6-B	9.06	2.28E-04	1.40E-02
TR49456|c0_g2_i1|m.32960	vegetative cell wall gp1	10.89	2.54E-06	1.29E-03
TR49456|c0_g2_i2|m.32965	vegetative cell wall gp1	8.39	2.32E-05	3.94E-03
TR49557|c0_g2_i1|m.33578	major facilitator superfamily transporter [Phaeoacremonium minimum UCRPA7]	9.54	1.35E-07	3.06E-04
TR49557|c0_g2_i2|m.33580	major facilitator superfamily transporter [Phaeoacremonium minimum UCRPA7]	12.04	1.47E-06	1.08E-03
TR49605|c1_g1_i2|m.33892	Heat shock 70 kDa	8.00	1.26E-05	2.71E-03
TR49623|c1_g4_i2|m.33978	phosphate transporter	10.10	6.10E-06	2.02E-03
TR49623|c1_g1_i1|m.33968	Phosphate transporter	8.31	1.11E-04	9.32E-03
TR49623|c1_g2_i2|m.33976	phosphate transporter	9.82	2.54E-04	1.49E-02
TR49623|c1_g4_i3|m.33982	phosphate transporter	9.65	6.07E-04	2.47E-02
TR49669|c1_g2_i2|m.34338	heat shock 90	8.64	2.51E-05	4.10E-03
TR49669|c1_g2_i1|m.34336	Heat shock 90	8.05	5.79E-05	6.90E-03
TR49669|c1_g2_i3|m.34340	heat shock 90	7.09	1.34E-03	4.13E-02
TR49779|c0_g1_i2|m.35090	ABC transporter	3.45	1.20E-03	3.83E-02
TR49897|c2_g2_i1|m.35786	actin beta gamma 1 [Fusarium oxysporum FOSC 3-a]	7.24	4.42E-05	5.79E-03
TR49939|c0_g1_i4|m.36112	malate dehydrogenase	7.05	4.88E-04	2.15E-02
TR50048|c0_g2_i4|m.36756	-No hit found-	9.75	9.76E-05	8.84E-03
TR50048|c0_g2_i2|m.36754	-No hit found-	8.81	4.17E-04	1.97E-02
TR50048|c0_g2_i3|m.36755	-No hit found-	10.15	5.52E-04	2.32E-02
TR50477|c0_g1_i5|m.39623	isocitrate lyase	7.34	1.68E-03	4.80E-02
TR50477|c0_g1_i2|m.39619	isocitrate lyase	5.57	1.79E-03	4.96E-02
TR50587|c0_g1_i2|m.40423	mitochondrial carnitine O-acetyltransferase	8.51	2.21E-05	3.88E-03
TR51670|c1_g1_i2|m.49345	acetyl-coenzyme a synthetase	9.68	2.01E-04	1.30E-02
TR51670|c1_g2_i1|m.49346	Acetyl-coenzyme A synthetase	6.79	7.50E-04	2.84E-02
TR51979|c1_g1_i1|m.52252	glycoside hydrolase [Trichoderma reesei QM6a]	11.70	5.92E-08	3.06E-04
TR52296|c0_g1_i1|m.55491	Helicase, C-terminal [Penicillium expansum]	6.73	1.58E-03	4.59E-02
TR53479|c0_g1_i1|m.66917	copper resistance-associated p-type atpase [Phaeoacremonium minimum UCRPA7]	8.12	8.26E-05	8.22E-03
TR53485|c0_g1_i1|m.66923	pci domain-containing	10.40	3.23E-05	4.66E-03
TR53600|c0_g2_i1|m.66941	integral membrane	9.16	5.94E-04	2.45E-02
TR53777|c0_g1_i1|m.66971	ubiquitin conjugation factor E4 B	9.65	4.41E-04	2.04E-02
TR54183|c0_g2_i1|m.67038	casein kinase i [Colletotrichum gloeosporioides Nara gc5]	9.69	1.66E-04	1.17E-02
TR54473|c0_g1_i1|m.67067	Homocitrate synthase	8.82	8.21E-05	8.22E-03
TR54544|c0_g1_i1|m.67081	[Trichoderma reesei QM6a]	9.49	5.33E-04	2.27E-02
TR54926|c0_g1_i1|m.67129	NAD(P)-binding [Auricularia subglabra TFB-10046 SS5]	9.70	1.56E-03	4.58E-02
TR55177|c0_g1_i1|m.67175	2-oxoglutarate dehydrogenase, mitochondrial	7.15	1.34E-03	4.13E-02
TR55361|c0_g1_i1|m.67219	beta-tubulin [Scytalidium thermophilum]	7.50	9.58E-04	3.29E-02
TR55572|c0_g1_i1|m.67250	3-isopropylmalate dehydratase	8.49	1.67E-03	4.80E-02
TR56250|c0_g1_i1|m.67368	COPI-coated vesicle	8.98	1.72E-03	4.86E-02
TR58105|c0_g1_i1|m.67622	DUF1682 domain-containing [Neurospora crassa OR74A]	9.41	1.02E-03	3.43E-02
TR64772|c0_g1_i1|m.68341	[Laccaria bicolor S238N-H82]	13.57	7.80E-06	2.33E-03
TR64931|c0_g1_i1|m.68367	haloacid dehalogenase-like hydrolase [Phaeoacremonium minimum UCRPA7]	6.83	1.77E-03	4.93E-02
TR64949|c0_g1_i1|m.68378	hypothetical protein A1O9_02901 [Exophiala aquamarina CBS 119918]	8.28	4.10E-04	1.95E-02
TR65250|c0_g1_i1|m.68430	ubiquitin domain containing [Pseudozyma antarctica]	7.04	8.52E-06	2.42E-03
TR65336|c0_g1_i1|m.68438	dihydroflavonol-4-reductase	8.71	1.62E-03	4.71E-02
TR66142|c0_g1_i1|m.68605	duf221 domain [Phaeoacremonium minimum UCRPA7]	9.23	6.04E-04	2.47E-02
TR66884|c0_g1_i1|m.68736	Mitochondrial fission process	7.66	4.75E-04	2.14E-02
TR66978|c0_g1_i1|m.68746	E3 ubiquitin ligase [Fusarium fujikuroi]	7.51	7.61E-04	2.84E-02
TR67281|c0_g1_i1|m.68787	predicted protein	10.00	1.75E-04	1.19E-02
TR68911|c0_g1_i1|m.69020	mitochondrial import inner membrane translocase subunit tim-17	7.53	8.31E-04	3.00E-02
TR69476|c0_g1_i1|m.69093	fumarylacetoacetate hydrolase family [Eutypa lata UCREL1]	8.61	7.60E-05	7.96E-03
TR70373|c0_g1_i1|m.69222	Pyruvate dehydrogenase complex X component, mitochondrial	9.94	6.22E-04	2.51E-02
TR75693|c0_g1_i1|m.69764	hypothetical protein THITE_2169894 [Thielavia terrestris NRRL 8126]	8.98	1.10E-03	3.59E-02
TR75710|c0_g1_i1|m.69770	Nuclear polyadenylated RNA-binding NAB2	9.30	5.69E-04	2.38E-02
TR76541|c0_g1_i1|m.69895	elongation factor 3 [Moniliophthora roreri MCA 2997]	9.85	1.47E-03	4.38E-02
TR76565|c0_g1_i1|m.69906	zinc finger , partial [Metarhizium majus ARSEF 297]	8.69	8.13E-04	2.97E-02
TR76710|c0_g1_i1|m.69928	Syntaxin pep12	9.15	8.45E-04	3.03E-02
TR76819|c0_g1_i1|m.69946	aryl-alcohol dehydrogenase AAD14	9.86	7.58E-05	7.96E-03
TR76830|c0_g1_i1|m.69953	ribosomal biogenesis Gar2 [Verticillium dahliae]	9.27	1.26E-03	3.98E-02
TR77445|c0_g1_i1|m.70038	thioredoxin	10.43	4.60E-04	2.09E-02
TR77495|c0_g1_i1|m.70056	zinc-binding dehydrogenase	8.37	1.23E-03	3.91E-02
TR77836|c0_g1_i1|m.70130	diacylglycerol acyltransferase [Colletotrichum graminicola]	7.84	2.38E-04	1.44E-02
TR78584|c0_g1_i1|m.70278	CDF family cation efflux system [Exophiala aquamarina CBS 119918]	9.41	1.79E-03	4.96E-02
TR78890|c0_g1_i1|m.70330	endoglucanase [Colletotrichum fioriniae PJ7]	8.52	1.67E-03	4.80E-02
TR79008|c0_g1_i1|m.70350	Nuclear movement nudC	10.11	4.99E-04	2.18E-02
TR80477|c0_g1_i1|m.70568	[Trichoderma reesei QM6a]	8.73	2.35E-04	1.43E-02
TR86810|c0_g1_i1|m.71278	Indoleamine 2,3-dioxygenase	7.80	2.40E-04	1.45E-02
TR86947|c0_g1_i1|m.71297	ran1 kinase [Colletotrichum gloeosporioides Nara gc5]	10.63	3.20E-05	4.64E-03
TR87191|c0_g1_i1|m.71322	integral membrane	6.71	2.91E-04	1.62E-02
TR87925|c0_g1_i1|m.71445	3,4-dihydroxy-2-butanone-4-phosphate synthase	6.98	1.73E-03	4.89E-02
TR87951|c0_g1_i1|m.71450	C2 domain-containing	9.19	1.77E-04	1.20E-02
TR88030|c0_g1_i1|m.71486	infection structure specific [Colletotrichum gloeosporioides Nara gc5]	10.02	1.01E-04	8.97E-03

TR88111|c0_g1_i1|m.71501	zinc finger 2 [Grosmannia clavigera kw1407]	8.49	1.30E-05	2.74E-03
TR88384|c0_g1_i1|m.71555	ABC-2 type transporter	9.17	5.17E-04	2.23E-02
TR88529|c0_g1_i1|m.71575	F-box domain [Aspergillus fumigatus Af293]	7.67	4.13E-04	1.96E-02
TR88852|c0_g1_i1|m.71651	phospho-2-dehydro-3-deoxyheptonate aldolase	9.36	5.80E-04	2.42E-02
TR88965|c0_g1_i1|m.71666	Ribosome biogenesis BRX1	9.38	3.84E-04	1.89E-02
TR89501|c0_g2_i1|m.71760	Zinc finger transcription factor ace1	10.23	2.28E-05	3.92E-03
TR89516|c0_g1_i1|m.71763	MFS transporter, DHA1 family, multidrug resistance [Exophiala dermatitidis NIH UT8656]	7.65	4.48E-04	2.06E-02
TR89698|c0_g1_i1|m.71784	NADPH-dependent 1-acyldihydroxyacetone phosphate reductase	9.95	2.79E-04	1.57E-02
TR90066|c0_g1_i1|m.71854	major facilitator superfamily transporter	7.78	4.76E-04	2.14E-02
TR90096|c0_g1_i1|m.71861	u3 small nucleolar rna-associated 6	8.86	6.85E-04	2.68E-02
TR90402|c0_g1_i1|m.71913	major facilitator superfamily transporter [Phaeoacremonium minimum UCRPA7]	9.94	9.02E-05	8.50E-03
TR90602|c0_g1_i1|m.71946	dienelactone hydrolase family	6.38	7.94E-04	2.92E-02
TR90874|c0_g1_i1|m.71989	succinate dehydrogenase flavo subunit	9.23	5.96E-04	2.45E-02
TR91009|c0_g1_i1|m.72018	pre-mRNA splicing factor cwc24	7.08	1.38E-03	4.21E-02
TR91957|c0_g1_i1|m.72135	Vacuolar -sorting-associated 46	8.71	1.79E-03	4.96E-02
TR98454|c0_g1_i1|m.72833	glutamine synthetase	7.67	1.24E-03	3.93E-02
TR98731|c0_g1_i1|m.72870	Catalase-peroxidase [Endocarpon pusillum Z07020]	10.66	5.25E-05	6.54E-03
TR98731|c1_g1_i1|m.72872	bifunctional catalase-peroxidase cat2 [Phaeoacremonium minimum UCRPA7]	9.29	1.04E-03	3.45E-02
TR98751|c0_g1_i1|m.72875	[Trichoderma reesei QM6a]	7.74	2.85E-04	1.59E-02
TR99555|c0_g1_i1|m.72995	acyl- dehydrogenase	7.50	4.35E-05	5.73E-03
TR99586|c0_g1_i1|m.73003	von Willebrand factor type A domain-containing	10.40	2.79E-04	1.57E-02
TR99644|c0_g1_i1|m.73020	Pre-mRNA-splicing factor cwf14	9.05	1.55E-03	4.58E-02
TR100118|c0_g1_i1|m.73094	Regulator of phospholipase D SRF1	7.65	2.55E-04	1.49E-02
TR100371|c0_g1_i1|m.73142	indole-diterpene biosynthesis , [Metarhizium acridum CQMa 102]	9.54	1.55E-04	1.12E-02
TR100763|c0_g2_i1|m.73203	proteasome subunit alpha type 6	8.17	1.76E-03	4.93E-02
TR100941|c0_g1_i1|m.73242	NAD dependent epimerase dehydratase	10.47	1.05E-04	9.16E-03
TR101324|c0_g1_i1|m.73317	glycosyl hydrolases family 32 superfamily [Colletotrichum gloeosporioides Nara gc5]	9.10	5.39E-04	2.29E-02
TR101530|c0_g1_i1|m.73351	adenosine deaminase	9.14	9.24E-04	3.21E-02
TR103485|c0_g1_i1|m.73636	-No hit found-	-9.23	1.35E-03	4.14E-02
TR103593|c0_g1_i1|m.73658	peroxisomal dehydratase	9.08	8.10E-04	2.96E-02
TR103966|c0_g1_i1|m.73710	Delta(14)-sterol reductase	8.99	9.43E-04	3.27E-02
TR104216|c0_g1_i1|m.73732	bar domain-containing [Phaeoacremonium minimum UCRPA7]	9.26	3.84E-04	1.89E-02
TR109408|c0_g1_i1|m.74260	glutamate decarboxylase	7.00	1.68E-03	4.80E-02
TR109715|c0_g1_i1|m.74294	Nuc-1 negative regulatory preg	7.51	2.54E-04	1.49E-02
TR109941|c0_g1_i1|m.74329	Ribonucleoside-diphosphate reductase small chain	6.94	1.82E-03	4.99E-02
TR110194|c0_g1_i1|m.74362	f-box domain containing	8.85	7.42E-04	2.82E-02
TR110397|c0_g1_i1|m.74407	MIT family metal ion transporter [Exophiala dermatitidis NIH UT8656]	6.27	1.04E-03	3.45E-02
TR110427|c0_g1_i1|m.74410	PX domain-containing	9.82	2.54E-04	1.49E-02
TR110603|c0_g1_i1|m.74452	54s ribosomal l10 [Phaeoacremonium minimum UCRPA7]	9.47	1.03E-03	3.44E-02
TR110633|c0_g1_i1|m.74457	hypothetical protein CH063_14175	9.88	1.47E-04	1.08E-02
TR110726|c0_g1_i1|m.74470	Interferon-induced GTP-binding Mx	5.89	2.97E-04	1.64E-02
TR110792|c0_g1_i1|m.74486	arrestin domain-containing [Colletotrichum graminicola]	6.36	1.61E-03	4.67E-02
TR111385|c0_g1_i1|m.74595	retinol dehydrogenase 12	8.76	1.05E-03	3.49E-02
TR111819|c0_g1_i1|m.74655	Epoxide hydrolase 2	7.04	9.43E-04	3.27E-02
TR112367|c0_g1_i1|m.74727	[Neurospora crassa]	9.55	4.06E-04	1.94E-02
TR113997|c0_g1_i1|m.74996	glyceraldehyde-3-phosphate dehydrogenase [Auricularia auricula-judae]	9.94	1.31E-03	4.09E-02
TR115636|c0_g1_i1|m.75200	RNA binding	9.55	4.79E-04	2.14E-02

[a] logFC represents log2 of albino versus green plants based on transcriptome analysis.