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MLP-PG1, a major latex-like protein identified in *Cucurbita pepo*, confers resistance through the induction of pathogenesis-related genes

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Main Conclusion

MLP-PG1, identified in *Cucurbita pepo*, plays a crucial role in resistance against fungal pathogens through the induction of pathogenesis-related genes.

Abstract

MLP-PG1, a major latex-like protein (MLP) from zucchini (*Cucurbita pepo*), was identified as a transporting factor for hydrophobic organic pollutants. MLPs are members of the Bet v 1 family, similar to pathogenesis-related class 10 proteins (PR-10s). However, the biological functions of MLPs remain unclear. Herein, we show that MLP-PG1 induces the expression of pathogenesis-related (PR) genes and indirectly promotes resistance against pathogens. The activity of the *MLP-PG1* promoter in leaves of transgenic tobacco plants was significantly enhanced by inoculation with *Pseudomonas syringae* pv. *tabaci*. However, MLP-PG1 did not induce direct resistance through RNase activity. Therefore, we examined the possibility that MLP-PG1 is indirectly involved in resistance; indeed, we found that MLP-PG1 induced the expression of defense-related genes. Overexpression of *MLP-PG1* highly upregulated *PR-2* and *PR-5* and decreased the area of lesions caused by *Botrytis cinerea* in the leaves of transgenic tobacco plants. Our results demonstrate that MLP-PG1 is involved in indirect resistance against plant diseases, especially caused by fungal pathogens, through the induction of PR

genes. This study is the first report to show the induction of *PR* genes by the expression of *MLP* from the RNA sequencing analysis and the involvement of MLP-PG1 in the resistance.

Keywords

Major latex-like protein; Pathogen infection; Pathogenesis-related genes; Plant hormone; Resistance; RNA sequencing

Abbreviations

ACC, 1-aminocyclopropane-1-carboxylic acid; MeJA, methyl jasmonic acid; MLP, major latex-like protein; PR, pathogenesis-related protein; PR-10, pathogenesis-related class 10 protein; *Pst*, *Pseudomonas syringae* pv. *tabaci*; SA, salicylic acid

1. Introduction

Major latex-like proteins (MLPs) were first identified as laticifer-specific binding proteins in the latex of opium poppy (*Papaver somniferum*) (Nessler et al. 1985). To date, they have been identified mainly in dicots such as *Arabidopsis thaliana* (Wu et al. 2008), cotton (*Gossypium hirsutum*) (Yang et al. 2015), cucumber (*Cucumis sativus*) (Suyama et al. 1999), grapevine (*Vitis vinifera*) (Zhang et al. 2018), tobacco (*Nicotiana benthamiana*) (Song et al. 2020), and zucchini (*Cucurbita pepo*) (Inui et al. 2013). MLPs belong to the Bet v 1 family, similar to pathogenesis-related class 10 proteins (PR-10s), which represent one of the 17 families of PR proteins (Fernandes et al. 2013).

The most remarkable feature of MLP homologs is their internal hydrophobic cavity, which enables them to bind hydrophobic compounds. At1g24000.1, an MLP from *A. thaliana*, and LIPR-10 2.B from yellow lupine (*Lupinus luteus*) bind to progesterone and a synthetic cytokinin in their cavity, respectively (Fernandes et al. 2009; Lytle et al. 2009). Another feature of MLPs is their ability to respond to biotic stress. In particular, a glycine-rich loop in the secondary structure of MLP homologs plays a crucial role in pathogen resistance by interacting with RNA of pathogens (Chadha and Das 2006). *Gh-MLP* from *G. hirsutum* contains a *cis*-acting, elicitor-responsive regulatory element that is activated by a toxin from *Verticillium dahliae* (Chen and Dai 2010). The expression of *MLP* genes is regulated by plant hormones related to resistance against pathogens, such as ethylene (Aggelis et al. 1997) and jasmonic acid (JA) (Chen and Dai 2010). GhMLP29 from *G. hirsutum*, induced by ethylene, interacts with an ethylene-responsive factor and triggers resistance against *V. dahliae* (Yang et al. 2015). In addition, NbMLP28 from *N. benthamiana* and MuMLPL329 from mulberry (*Morus multicaulis*) confer resistance against *Potato virus Y* and phytoplasma, respectively, through the activation of the JA signaling pathway (Gai et al. 2018; Song et al. 2020). Therefore, the expression of *MLP* genes is thought to evoke resistance to pathogens through the activation of plant hormone signaling pathways.

MLPs identified in the Cucurbitaceae family are responsible for the transport of hydrophobic organic pollutants (Inui et al. 2013; Goto et al. 2019; Iwabuchi et al. 2020). MLPs bind to these compounds in root cells, and the resulting complexes are translocated into xylem vessels. Consequently, hydrophobic organic pollutants are transported to the fruit (Goto et al. 2019). Our recent studies demonstrated that the suppression of *MLP* genes leads to safer crop production via reduced accumulation of hydrophobic organic pollutants (Fujita et al. 2020; Inui et al. 2020). However, the biological functions of MLPs in members of the Cucurbitaceae family have not been extensively studied.

In this study, we elucidated the biological functions of MLP-PG1, identified in *C. pepo*, focusing on its role in resistance to pathogens. First, we evaluated the promoter activity of *MLP-PG1* by inoculation with *Pseudomonas syringae* pv. *tabaci* (*Pst*). We next evaluated the antimicrobial activity of MLP-PG1 harboring a glycine-rich loop and investigated the upregulation of genes by the overexpression of *MLP-PG1*. Finally, we tested whether overexpression of *MLP-PG1* enhanced resistance against *Botrytis cinerea* in transgenic tobacco plants.

2. Materials and methods

Plant materials

Seeds of *C. pepo* subspecies *ovifera* cultivar ‘Patty Green’ (PG) were purchased from Johnny’s Selected Seeds (Albion, ME, USA). After the seed coat was peeled off, seeds were incubated in tap water overnight at 4°C and sown in sterilized soil (Hyponex Japan Corp., Ltd., Osaka, Japan) in a glass jar. The seedlings were cultivated under a 16/8 h light/dark cycle at 26°C. Their organs (buds, flowers, leaves, stems, and roots) were ground in liquid nitrogen and stored at –80°C until use.

Seeds of sterilized transgenic tobacco (*Nicotiana tabacum*) plants were sown on Murashige and Skoog (MS) medium under a 16/8 h light/dark cycle at 24°C (Murashige and Skoog 1962). After 2 weeks, the seedlings were transferred to sterilized soil (Hyponex Japan Corp., Ltd.) in a plastic pot.

Plant hormone treatment

Seedlings of the PG cultivar were cultivated in tap water under a 16/8 h light/dark cycle at 26°C. After 2 weeks, they were transferred to a solution containing 0.1 mM methyl jasmonic acid (MeJA), 0.1 mM 1-aminocyclopropane-1-carboxylic acid (ACC), or 0.1 mM salicylic acid (SA). The roots were collected at 0, 1.5, and 3 h after treatment with plant hormones. After freezing in liquid nitrogen, the samples were ground and stored at –80°C until use.

Gene expression analysis

Total RNA extraction and reverse transcription quantitative PCR (qRT-PCR) were performed as described in our previous report (Inui et al. 2020). Briefly, total RNA was extracted from the organs of *C. pepo* and the leaves of transgenic tobacco plants using TRIzol (Thermo Fisher Scientific Inc., Waltham, MA, USA). After the addition of ReverTra Ace qPCR RT Master Mix with gDNA Remover (Toyobo Co., Ltd., Osaka, Japan) to remove contaminating genomic DNA, total RNA was treated with RT Master Mix according to the manufacturer's instructions to synthesize first-strand cDNA. qRT-PCR was performed using a Thunderbird SYBR qPCR Mix (Toyobo Co., Ltd.) and the primers listed in [Suppl. Table S1](#) on a Light Cycler 480 II (Roche Applied Science, Indianapolis, IN) under the following conditions: 1 min at 95°C; 40–60 cycles of 15 s at 95°C and 30 s at 60°C; 5 s at 95°C; and 1 min at 65°C. The relative expression levels of each gene were calculated using the $\Delta\Delta\text{CT}$ method, and the expression level of the *actin* gene was used as an internal control.

RNA sequencing

Total RNA was extracted using Plant Total RNA Extraction Miniprep System (Viogene- Biotek Corp, Taipei, Taiwan) from the leaves of six-week-old transgenic tobacco plants under a 16/8 h light/dark

cycle at 24°C. RNA sequencing (RNA-seq) analysis was performed by Macrogen Japan Corp. (Tokyo, Japan) as follows: the libraries were constructed with TruSeq Stranded mRNA LT Sample Prep Kit (Illumina, San Diego, CA) according to the manufacturer's instructions. They were sequenced with 100-bp paired-end reads on NovaSeq 6000 sequencer (Illumina). The quality of sequencing reads was evaluated using FASTQC software version 0.11.7. Trimmomatic version 0.38 was used to remove adapter sequences and bases with base quality lower than three from the ends. By using a sliding, reads with a length shorter than 36-bp are dropped to produce trimmed data. The filtered reads were mapped to the *N. tabacum* (common tobacco) reference genome annotated from Ntab-TN90 with HISAT2 version 2.1.0. StringTie version 1.3.4d was used for transcript assembly. The expression profile was calculated for each sample and transcript/gene as read count and Fragment Per Kilobase of transcript per Million mapped reads (FPKM). Differentially Expressed Genes (DEG) analysis was performed on 2 comparison pairs as requested using FPKM. The genes with fold change ≥ 2.00 were defined as DEGs.

Cloning of the promoter region

The promoter region of *MLP-PGI* was cloned by thermal asymmetric interlaced (TAIL) PCR (Liu et al. 1995), according to the method included in our previous report (Fujita et al. 2020). First, TAIL-PCR was performed with three arbitrary degenerate primers (AD1–AD3) and three specific primers (TAIL-specific1-as–TAIL-specific3-as). Nine additional specific antisense primers, TAIL-specific4-as–TAIL-specific12-as, were designed by referring to the cloned sequences to amplify further upstream regions. The sequences of these primers are listed in **Suppl.** Table S1. Genomic DNA extracted from *C. pepo* ssp. *ovifera* cv. PG was used as template, and the PCR reaction was performed using 2xQuick Taq HS DyeMix (Toyobo Co., Ltd.). The reaction conditions of TAIL-PCR followed

the PCR conditions described by Liu et al. (1995), with the exception that the annealing temperature of the arbitrary degenerate primers and specific primers was changed to 44°C and 65°C, respectively. A 1-month-old leaf of a PG seedling was sampled, and genomic DNA was extracted using an Isoplant kit (Nippon Gene Co., Tokyo, Japan). The DNA fragment that included the promoter region of the *MLP-PGI* gene was amplified from 100 ng of genomic DNA using a KOD FX Neo polymerase (Toyobo Co., Ltd.) and the primers PG-PG1-P-s1 and PG-PG-P-as under the following conditions: 5 min at 94°C; 32 cycles of 30 s at 94°C, 30 s at 56°C, and 2 min at 72°C; and 7 min at 72°C (Suppl. Table S1). The amplified fragment was purified using a Gel/PCR DNA Isolation System (Viogene-Biotek Corp). A 2075-bp fragment was finally isolated and cloned into the vector pBI221, after digestion with *Hind*III and *Xba*I, using an In-Fusion HD Cloning Kit (Takara Bio Inc., Shiga, Japan). After sequencing and digestion with *Hind*III and *Sac*I, the fragment containing the *MLP-PGI* gene promoter and a β -glucuronidase (*GUS*) gene was ligated with the plant expression vector pGWB402 Ω (provided by Dr. Tsuyoshi Nakagawa at Shimane University), digested using the same two restriction enzymes.

Production of transgenic tobacco plants

Transgenic tobacco plants overexpressing *MLP-PGI* under the control of the cauliflower mosaic virus 35S promoter (35S) were produced as described in our previous report (Stoykova and Inui 2021). The plasmid pTMLP-PG1-2 containing *MLP-PGI* (AB753855) (Inui et al. 2013) was used with the plant expression vector pGWB502 Ω (Nakagawa et al. 2007), resulting in the construction of pGWB-MLP-PG1.

Plant expression plasmids containing the constructs *MLP* gene *pro::GUS* and *35S::MLP-PGI* were introduced into *Rhizobium radiobacter* strain LBA4404, and the leaf disc method was employed to produce transgenic lines (Horsch et al. 1985).

Inoculation of transgenic tobacco plants with pathogens

Pst MAFF No. 301612 (National Agriculture and Food Research Organization, Ibaraki, Japan) was cultured in King's B liquid medium (1% [w/v] peptone, 0.15% [w/v] K₂HPO₄, 1.5% [w/v] glycerol, and 0.015% [w/v] MgSO₄) at 30°C overnight. After centrifugation, the pellet was diluted with 10 mM MgCl₂. Six-week-old transgenic tobacco plants were inoculated by the infiltration of 20 µL of the bacterial suspension (5×10⁶ cells/mL) onto the abaxial surfaces of the leaves with a needleless plastic syringe. *B. cinerea* MAFF No. 712108 (National Agriculture and Food Research Organization) was incubated on potato dextrose agar (0.4% [w/v] potato, 2% [w/v] glucose, and 1.5% [w/v] agarose) medium at 20°C for 5 days. Spores were formed under blacklight blue irradiation for 3 days. The inoculation was performed by spraying a spore suspension (2×10⁵ cells/mL) in sterilized water containing 1% peptone on the leaves of 6-week-old transgenic tobacco plants. These were then transferred to a tray, covered with a lid to maintain 100% humidity, and incubated at 23°C in the dark for 24 h. Next, the lid was removed, and inoculated plants were incubated under a 12/12 h light/dark cycle at 23°C until lesions were formed. Four days after inoculation, leaf and lesion areas were calculated using ImageJ (Schneider et al. 2012).

RNase activity assay

Roots from 3-week-old *C. pepo* plants were washed with tap water and ground in liquid nitrogen. Total RNA was isolated from root samples as described above. A reaction mixture containing 9.5 µg of total RNA and 10 µg of recombinant MLP-PG1 in Tris-HCl (pH 7.0; total volume, 50 µL) was incubated for 0.5, 1, and 2 h at 25°C. Boiled recombinant MLP-PG1 was used as the negative control. After isolation of total RNA from the reaction mixture, this was precipitated by ethanol precipitation and separated by electrophoresis on a 1% agarose gel.

GUS assay

Leaf disks at the infiltration point were sampled at 0, 12, 24, and 48 h after inoculation with *Pst*. Leaf disks were frozen in liquid nitrogen and homogenized with a protein extraction buffer (50 mM sodium phosphate buffer [pH 7.0], 10 mM EDTA [pH 8.0], 0.1% [v/v] Triton X-100, 0.5% [w/v] *N*-lauroylsarcosine sodium salt, and 0.072% [v/v] 2-mercaptoethanol). After centrifugation at 4°C and 20,700 ×g for 5 min, the supernatants were subjected to GUS assay, as described in our previous report (Fujita et al. 2020).

Sequence analysis

Multiple sequence alignment was performed using the MUSCLE tool (<https://www.ebi.ac.uk/Tools/msa/muscle/>), and conserved residues and secondary structures were identified using ESPrnt 3.0 (Robert and Gouet 2014). The 3D structure of MLP-PG1 was constructed using Kiwi allergen Act d 11 (PDB: 4IHR) as a template in SWISS-MODEL (Arnold et al. 2006). The cloned 2075-bp promoter region of *MLP-PG1* was analyzed on the Plant *cis*-acting regulatory DNA elements (PLACE) database (Higo et al. 1999).

Statistical analysis

Dunnett's multiple comparison test was used to determine significant differences among treatments using Rstudio software version 1.3.1073 (<http://www.rstudio.com>).

3. Results

Sequence alignment of MLP-PG1 with MLP orthologs

The sequence of MLP-PG1 was similar to that of the examined MLP orthologs (Fig. 1a). MLP-PG1 and its orthologs contained a glycine-rich loop between β 2 and β 3 in form of a GXXXXXG motif (Fig. 1a). The predicted 3D structure of MLP-PG1 showed a typical secondary structure formed by three α -helices and seven β -sheets (Fig. 1b).

Expression profile of *MLP-PG1*

The expression of *MLP-PG1* in the aerial parts (buds, flowers, leaves, and stems) of *C. pepo* cv. PG seedlings was very low (Fig. 2a). However, *MLP-PG1* expression was higher in the roots (Fig. 2a). Next, the expression level of *MLP-PG1* in the roots of *C. pepo* treated with MeJA, ACC (a precursor of ethylene), and SA was determined to investigate the regulation of *MLP-PG1* expression by defense-related plant hormones. MeJA treatment tended to induce the expression of *MLP-PG1* (Fig. 2b). In contrast, ACC and SA treatments tended to suppress and did not alter the expression of *MLP-PG1*, respectively (Fig. 2b).

Induction of the promoter activity of *MLP-PG1*

The *MLP-PG1* promoter was found to include several *cis*-acting regulatory elements related to biotic stress response, such as a GT-1 motif, a WRKY binding site, and an ELRE motif (Table 1). The transcriptional activity of *MLP-PG1* was investigated in transgenic tobacco plants inoculated with *Pst*. Inoculation did not increase GUS activity in transgenic tobacco plants expressing the empty vector (VC) (Fig. 3a). In contrast, GUS activity at 48 h after inoculation was significantly increased in transgenic tobacco plants expressing *MLP-PG1 pro::GUS* (Fig. 3b). Mock treatments for both types of transgenic plants did not induce GUS activity (Fig. 3a, b).

Differentially expressed genes in transgenic tobacco plants overexpressing *MLP-PG1*

Recombinant MLP-PG1 was purified from *Escherichia coli*, and its RNase activity was examined using total RNA from the roots of *C. pepo* as a substrate. Migration of total RNA was not distinct by gel electrophoresis after treatment with either MLP-PG1 or boiled MLP-PG1, indicating that MLP-PG1 does not possess RNase activity (Suppl. Fig. S1). Next, RNA-seq analysis of transgenic tobacco plants overexpressing *MLP-PG1* was performed to assess the involvement of MLP-PG1 in indirect resistance caused by the induction of defense-related genes. The top 10 upregulated genes in transgenic tobacco plants overexpressing *MLP-PG1* compared with VC plants are shown in Table 2. Two *glucan endo-1,3-β-glucosidase* genes (LOC107823411 and LOC107801151) were the most and second most upregulated transcripts in transgenic tobacco plants overexpressing *MLP-PG1* (Table 2), with a 85.6- and 82.1-fold upregulation, respectively. *Osmotin* and *osmotin-like* genes (LOC107794478, LOC107794479, and LOC107787819) were also included among the top 10 upregulated genes (Table 2). These genes were upregulated by 56.9-, 43.4-, and 36.5-fold, respectively. The expression of *PR-2* and *PR-5*, encoding a glucan endo-1,3-β-glucosidase and osmotin, respectively, was further analyzed by qRT-PCR to validate the RNA-seq results. We observed that *PR-2* and *PR-5* were significantly induced in transgenic tobacco plants overexpressing *MLP-PG1* by 165- and 87.1-fold, respectively (Fig. 4).

Decreased reaction by *B. cinerea* in transgenic tobacco plants overexpressing *MLP-PG1*

Because of technical difficulties in the transformation of *C. pepo*, transgenic tobacco plants overexpressing *MLP-PG1* were used. Wild-type (WT) tobacco plants, transgenic plants expressing the empty vector (VC), and transgenic plants overexpressing *MLP-PG1* (lines #13 and #28) were inoculated with *B. cinerea* because this pathogen is known to induce *PR-2* and *PR-5* (Hatmi et al. 2014). Four days after inoculation, many necrotic lesions were observed in the leaves of WT and VC plants (Fig. 5a). However, there were few lesions in the leaves of both lines of transgenic tobacco

plants overexpressing *MLP-PGI* (Fig. 5a). Nevertheless, VC plants and both lines of transgenic tobacco plants overexpressing *MLP-PGI* showed no necrotic lesions after treatment of the leaves with sterilized water containing peptone (Suppl. Fig. S2). The lesion areas of both lines of transgenic tobacco plants overexpressing *MLP-PGI* were significantly decreased compared with those of WT and VC plants (Fig. 5b). Conversely, WT and VC plants showed no significant difference in lesion area (Fig. 5b).

4. Discussion

The purpose of the present study was to elucidate the biological functions of MLP-PG1 in relation to biotic stress. However, the biological functions of MLP-PG1 have not yet been clarified. Among the organs of *C. pepo* examined, *MLP-PGI* showed the highest expression levels in the roots (Fig. 2a). Several *MLP* genes are highly expressed in the roots (Yang et al. 2015; Song et al. 2020), but *MLP-PGI* showed remarkably higher expression in the roots compared to that of *MLP* genes of other plants. *Cis*-elements in the promoter region of *MLP-PGI* included elements induced by pathogen infection (Table 1), and the promoter activity of *MLP-PGI* was enhanced by *Pst* inoculation (Fig. 3). Previous reports have shown that MLPs confer resistance to soil-borne pathogens (Yang et al. 2015; Holmquist et al. 2020). This suggests that MLP-PG1 is specialized in resistance against soil-borne pathogens such as *Didymella bryoniae*.

MLP-PGI expression tended to be induced by MeJA treatment but suppressed by ACC treatment (Fig. 2b). Several *MLP* genes are induced by JA treatment, which activates the necrotrophic pathogen resistance pathway. SA treatment did not influence on the expression of *MLP-PGI* (Fig. 2b), and RNA-seq analysis showed that SA-responsive genes were not induced and suppressed in the transgenic tobacco plants overexpressing *MLP-PGI* (Suppl. Table S2). In contrast, *PR-10* genes are located downstream of the SA signaling pathway and are induced by SA treatment, which activates the

biotrophic pathogen resistance pathway. This suggests that transgenic tobacco plants overexpressing *MLP-PG1* may show resistance against necrotrophic pathogens, such as *B. cinerea* (Williamson et al. 2007). Several plants carry both *MLP* and *PR-10* genes (Pühringer et al. 2000; Lebel et al. 2010; Zhang et al. 2018; Yuan et al. 2020), which play a crucial role in the defense against necrotrophic and biotrophic pathogens, respectively. However, *PR-10* genes have not been identified in *C. pepo*. Therefore, it is possible that MLPs play a crucial role in the defense against both types of pathogens in this plant species.

PR-10s exert RNase activity towards bacteria and fungi through their glycine-rich loop (Flores et al. 2002; Chadha and Das 2006). In the present study, *MLP-PG1* did not show RNase activity, despite also carrying a glycine-rich loop (Fig. 1a and Suppl. Fig. S1). Thus, we investigated the involvement of *MLP-PG1* in indirect resistance caused by the induction of *disease resistance* genes. RNA-seq analysis showed that *PR-2* and *PR-5* were included among the top 10 upregulated genes in transgenic tobacco plants overexpressing *MLP-PG1*. *PR-2* encodes β -1,3-glucanase and *PR-5* encodes osmotin, thaumatin, and zeamatin (Nawrath and Métraux 1999; Liu et al. 2016; Zhang et al. 2019). These proteins are basic and show antimicrobial activity, and basic *PR* genes are induced by JA (Niki et al. 1998). Our results suggest that *PR-2* and *PR-5* expression led to a significant decrease in the area of lesions caused by *B. cinerea* in transgenic tobacco plants overexpressing *MLP-PG1* (Fig. 5). *MLP* and *PR-5* are expressed in the ripening fruits of *Malus $\times$ domestica* (Shi et al. 2014) and *V. vinifera* (Davies and Robinson 2000), as well as in the roots of sugar beet (*Beta vulgaris*) (Kloos et al. 2002). In addition, *MLP*, *PR-2*, and *PR-5* are induced in *N. tabacum* during flower bud formation (Neale et al. 1990). Furthermore, GhMLP28 interacts with ethylene-responsive factor 6 (ERF6) and induces *PR-2* and *PR-5* by increasing the binding ability of ERF6 to the promoter region of *PR-5* (Yang et al. 2015). Several *ERF* genes are induced by the transgenic tobacco plants overexpressing *MLP-PG1* (Suppl. Table S2). It is thought that MLPs enhance the resistance through the induction of their interacting proteins. Our

results, together with previous observations, suggest that MLPs induce *PR-2* and *PR-5* during reproductive growth and pathogen infection in *C. pepo*.

The most remarkable feature of MLP-PG1 is its ability to effectuate long transport from the roots to the leaves via xylem vessels (Goto et al. 2019). Therefore, MLP-PG1 may be involved in systemic acquired resistance (SAR): after induction of *MLP-PG1* by pathogen infection, MLP-PG1 may be transported from the roots to the aerial parts of the plant and induce *PR-2* and *PR-5* in the leaves. *MLP* genes in phloem sap are induced by pathogen infection (Carella et al. 2016; Gai et al. 2018). In addition, proteins of the Bet v 1 family have an internal hydrophobic cavity, and hydrophobic organic pollutants are thought to bind to MLP-PG1 in its cavity (Fernandes et al. 2013; Goto et al. 2019). This suggests that MLP-PG1 transports hydrophobic SAR signal molecules, such as dehydroabietinal, to the leaves to induce SAR (Chaturvedi et al. 2012). Therefore, the long transport ability of MLP-PG1 may contribute to the induction of *PR* genes in the leaves of *C. pepo* through the transport of SAR signal molecules. However, the SAR pathway is activated by the SA signaling pathway (Choudhary et al. 2007), whereas MLP-PG1 is induced by MeJA (Fig. 2b). Thus, it is possible that MLP-PG1 is involved in induced systemic resistance (ISR) activated by rhizospheric microbes through the JA signaling pathway (Romera et al. 2019). Basic *PR* genes are induced by JA (Niki et al. 1998), and ISR is thought to induce basic *PR* genes. RNA-seq analysis showed that MLP-PG1 induced *PR-2* encoding β -1,3-glucanase and *PR-5* encoding osmotin as basic proteins (Niki et al. 1998) (Table 2). MLP-PG1 was found to be highly expressed in the roots (Fig. 2a) and is transported through xylem vessels (Goto et al. 2019); therefore, MLP-PG1 is more likely to play a central role in ISR rather than SAR.

In this study, we shed light on the biological functions of MLP-PG1, which is responsible for transporting hydrophobic organic pollutants in members of the Cucurbitaceae family. We showed by RNA-seq analysis that *PR-2* and *PR-5* were highly upregulated upon overexpression of *MLP-PG1*. Moreover, the areas of the lesions caused by *B. cinerea* were significantly decreased in lines of

transgenic tobacco plants overexpressing *MLP-PG1*. These results suggest that MLP-PG1 induces *PR* genes and enhances disease resistance against fungal pathogens in *C. pepo*. However, the mechanisms underlying the induction of these genes by MLP-PG1 are still unknown and should be addressed in future studies.

Declarations

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Competing interests

The authors have no conflicts of interest to declare that are relevant to the content of this article.

Data availability

The datasets generated during and/or analyzed during the current study are available from the corresponding author on reasonable request.

Authors' contributions

KF designed research; KF, SA, EI, RY, and HI performed experiments; HI and YU provided materials; KF and SA analyzed data; KF and HI wrote the manuscript, which was approved by all authors.

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486

Figure legends

Fig. 1 Alignment of major latex-like proteins identified in various plant species.

a Sequences of MLP-PG1 (AB753855), AtMLP28 (AT1G70830), NbMLP28 (MK780769), GhMLP28 (DQ123838.1), and MuMLPL329 (MG871460). Residues conserved in all proteins and some proteins are represented by white and red letters, respectively. η and TT represent 3_{10} -helices and β -turns, respectively. **b** 3D structure of MLP-PG1. This was constructed using Kiwi allergen Act d 11 (4IHR) as a template in SWISS-MODEL (Arnold et al. 2006) and visualized using PyMOL (Delano 2005)

Fig. 2 Expression profile of *MLP-PG1*.

a Expression levels of *MLP-PG1* in various organs of zucchini (*Cucurbita pepo*). *C. pepo* subspecies *ovifera* cultivar 'Patty Green' (PG) plants were cultivated under a 16/8 h light/dark cycle at 26°C. Leaves, stems, and roots were collected from 2 week-old *C. pepo* plants. Buds and flowers were collected after their formation. Total RNA was extracted and used for qRT-PCR. Primer sequences are listed in **Suppl.** Table S1. **b** Expression level of *MLP-PG1* in roots of *C. pepo* treated with methyl jasmonic acid (MeJA), 1-aminocyclopropane-1-carboxylic acid (ACC), or salicylic acid (SA). *C. pepo* ssp. *ovifera* cv. PG plants were hydroponically cultivated under a 16/8 h light/dark cycle at 26°C. After 2 weeks, the seedlings were transferred to tap water supplemented with 0.1 mM MeJA, 0.1 mM ACC, or 0.1 mM SA. The roots were collected at 0, 1.5, and 3 h after treatment. Total RNA was extracted and used for qRT-PCR. The expression level for each treatment was calculated in relation to that at 0 h. Primer sequences are listed in **Suppl.** Table S1

Fig. 3 Induced expression of a reporter gene in the leaves of transgenic tobacco plants inoculated with *Pseudomonas syringae*.

Seven-week-old transgenic tobacco plants expressing the empty vector (**a**) or the β -glucuronidase (*GUS*) gene downstream of the *MLP-PGI* promoter (**b**) were inoculated with *P. syringae* pv. *tabaci* (*Pst*; 5×10^6 cells/mL) under a 16/8 h light/dark cycle at 24°C. Proteins were extracted from the leaves of each plant and a GUS assay was performed. Error bars indicate the standard deviation ($n = 3-4$). Control plants were infiltrated with 10 mM $MgCl_2$. Asterisks indicate significant differences compared to GUS activity in transgenic tobacco plants expressing *MLP-PGI pro::GUS* before inoculation with *Pst* (0 h; *, $p < 0.05$). hpi, h post-inoculation

Fig. 4 Analysis of *PR* gene expression in the leaves of transgenic tobacco plants overexpressing *MLP-PGI* for the validation of RNA sequencing results.

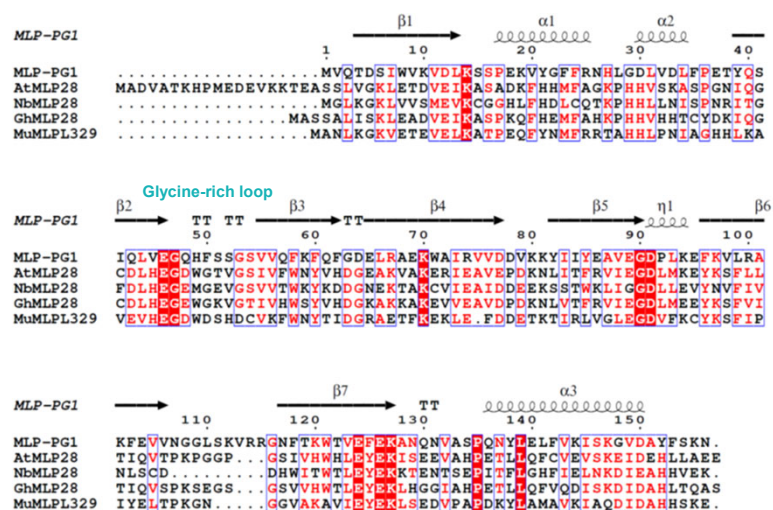
Transgenic tobacco plants overexpressing *MLP-PGI* were cultivated under a 16/8 h light/dark cycle at 24°C. After 6 weeks, the leaves were collected. Total RNA was extracted and used for qRT-PCR analysis. Primer sequences are listed in **Suppl.** Table S1. Error bars indicate the standard deviation ($n = 3-4$). Asterisks indicate significant differences compared to the relative expression levels in the leaves of transgenic tobacco plants expressing the empty vector (**, $p < 0.01$; ***, $p < 0.001$). VC, transgenic tobacco plants expressing the empty vector; 35S::*MLP-PGI*, transgenic tobacco plants overexpressing *MLP-PGI*

Fig. 5 Resistance against *Botrytis cinerea* in transgenic tobacco plants overexpressing *MLP-PGI*.

Transgenic tobacco plants overexpressing *MLP-PGI* were cultivated under a 16/8 h light/dark cycle at 24°C. After 6 weeks, these plants were inoculated with *B. cinerea* by spraying a spore suspension (2×10^5 cells/mL) on the leaves. After 4 days, the leaves were collected. Representative leaves are shown (**a**), and the lesion areas of the leaves were measured using ImageJ (Schneider et al. 2012) **b**. Different color intensities in the plot indicate different experiments. Asterisks indicate significant

535 differences compared to the lesion areas in the leaves of wild-type plants and transgenic tobacco plants
536 expressing the empty vector (**, $p < 0.01$; ***, $p < 0.001$, ****, $p < 0.0001$). WT, wild-type plants; VC,
537 transgenic tobacco plants expressing the empty vector; *35S::MLP-PGI*, transgenic tobacco plants
538 overexpressing *MLP-PGI*

a



b



Figure 1

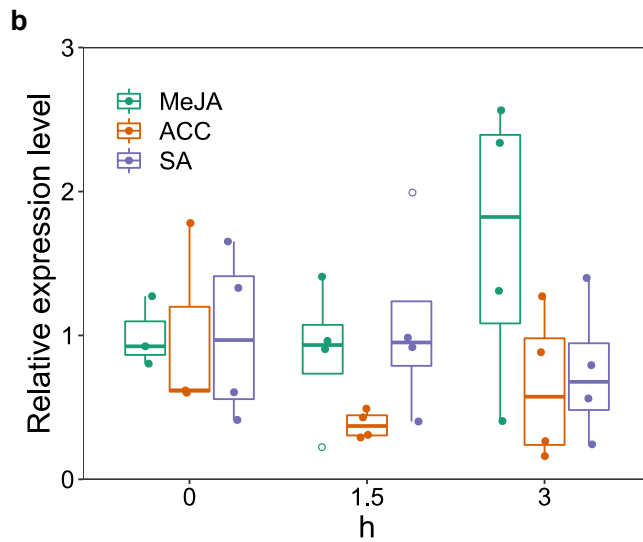
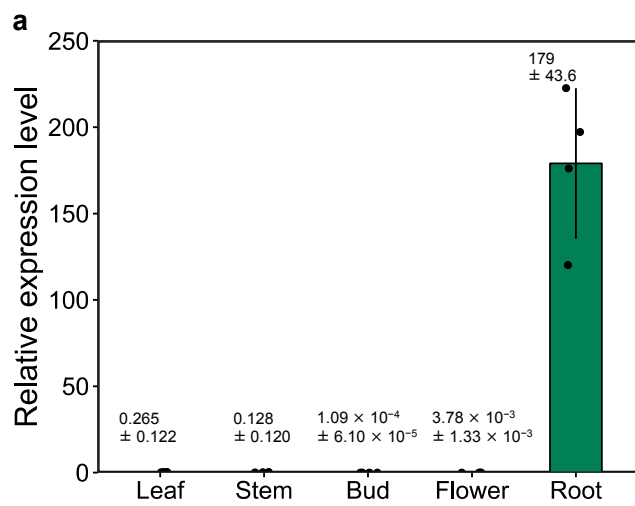


Figure 2

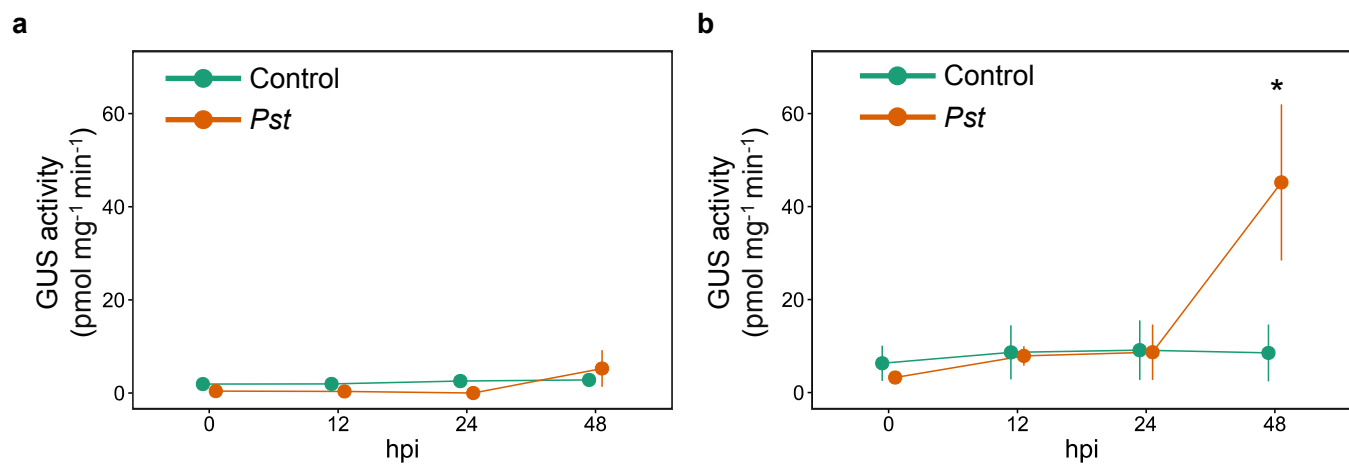


Figure 3

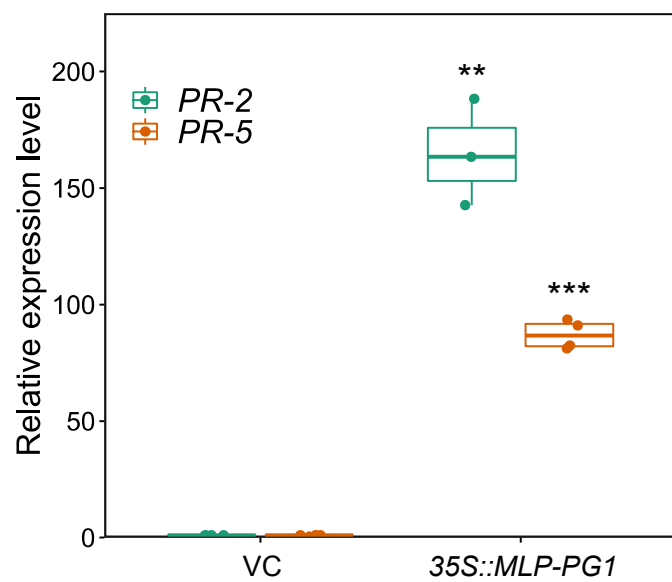


Figure 4

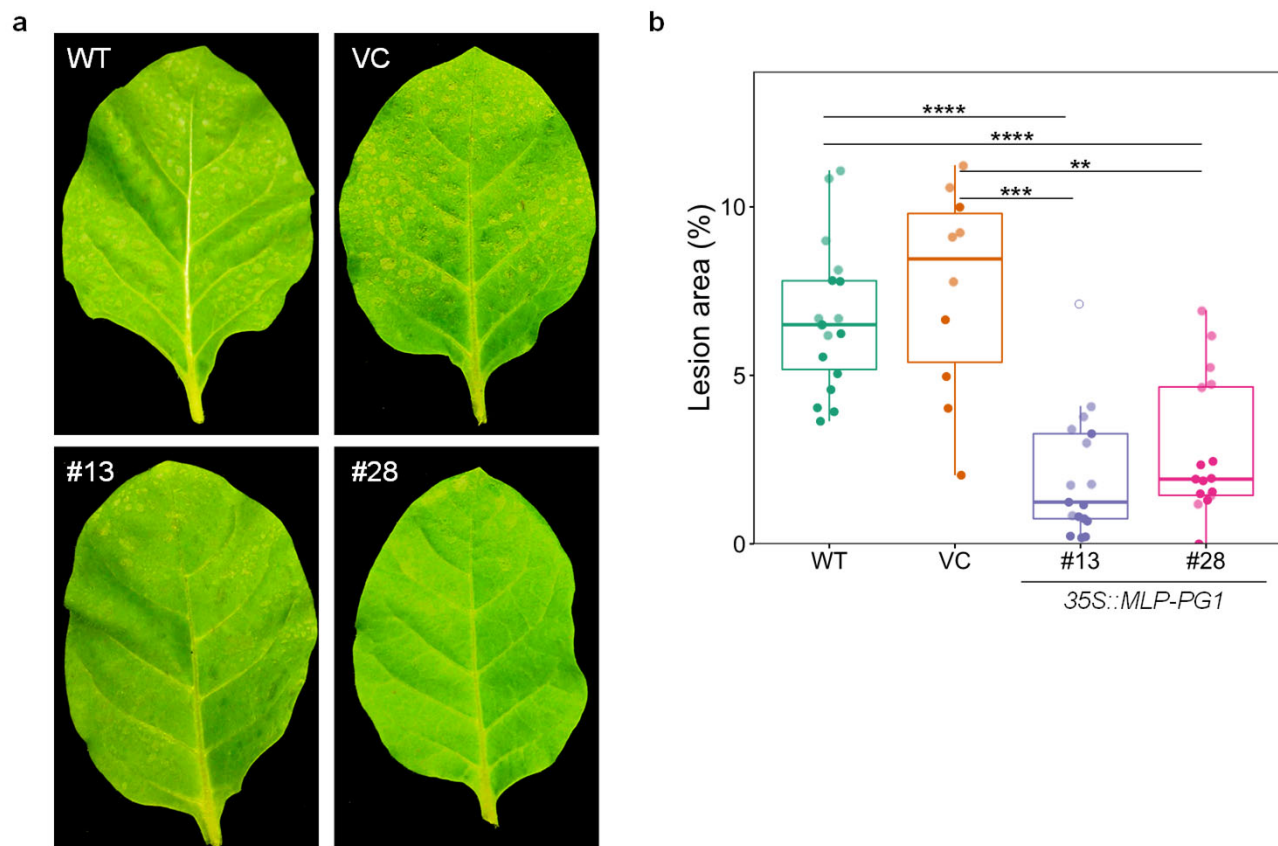


Figure 5

1 **Table 1** *Cis*-acting regulatory elements involved in stress response in the promoter region of *MLP*-
2 *PGI*.
3 The promoter region of *MLP-PGI* was cloned and analyzed on the Plant *cis*-acting regulatory DNA
4 elements (PLACE) database

Site	Amount	Sequence	Function
GT-1	16	GAAAAA	Response to light, pathogens, and salt
ARR1	15	NGATT	Response to cytokinin
WRKY binding site	12	TGAC	Response to pathogens
MYB binding site	4	CNGTTR	Response to water stress
ACGT	3	ACGT	Response to dehydration
BBF binding site	3	ACTTTA	Response to auxin
Inr	2	YTCANTYY	Response to light
MYC binding site	2	CANNTG	Response to dehydration
MYB binding site	2	YAACKG	Response to dehydration
ELRE	2	TTGACC	Elicitor Responsive Element
LTRE	1	CCGAC	Low temperature-responsive element
SURE	1	GAGAC	Response to auxin
GARE	1	TAACAGA	Gibberellin-responsive element

5

1 **Table 2** Top 10 upregulated genes in the leaves of transgenic tobacco plants overexpressing *MLP-PGI*.
2 Transgenic tobacco plants overexpressing *MLP-PGI* were cultivated under a 16/8 h light/dark cycle
3 at 24°C. After 6 weeks, total RNA was isolated from the leaves, and RNA sequencing analysis was
4 performed. The top 10 upregulated genes in transgenic tobacco plants overexpressing *MLP-PGI* are
5 listed. VC, transgenic tobacco plants expressing the empty vector; *35S::MLP-PGI*, transgenic tobacco
6 plants overexpressing *MLP-PGI*

Gene symbol	Fold change (<i>35S::MLP-PGI</i> /VC)	Transcript
LOC107823411	85.9	<i>glucan endo-1,3-β-glucosidase, basic vacuolar</i>
LOC107801151	82.4	<i>glucan endo-1,3-β-glucosidase, basic vacuolar</i>
LOC107773727	74.0	<i>auxin-binding protein ABP19a-like</i>
LOC107794478	57.0	<i>osmotin-like protein</i>
LOC107815767	50.6	<i>14 kDa proline-rich protein DC2.15-like</i>
LOC107806690	49.8	<i>auxin-binding protein ABP19a-like</i>
LOC107794479	43.4	<i>osmotin-like</i>
LOC107787819	36.6	<i>osmotin</i>
LOC107794480	36.5	<i>proteinase inhibitor I-B</i>

7

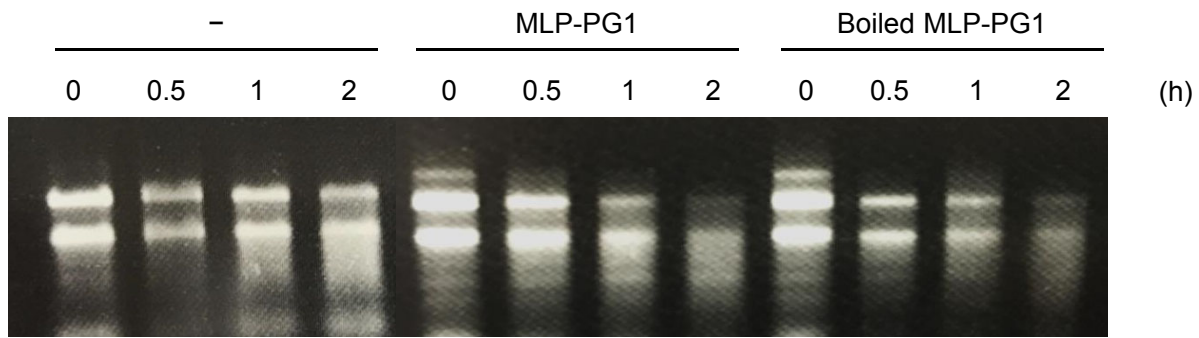


Fig. S1 RNase activity of MLP-PG1.

Ten micrograms of recombinant MLP-PG1 was incubated with total RNA from the roots of 3-week-old *Cucurbita pepo* plants for 0.5, 1, and 2 h at 25°C. After isolation and purification of total RNA from the reaction mixture, electrophoresis was performed on a 1% agarose gel. (-) represents total RNA incubated in Tris-HCl buffer in absence of recombinant MLP-PG1. Recombinant MLP-PG1 boiled for 10 min at 100°C was used as a negative control



Fig. S2 Phenotype of leaves treated with water containing peptone.

Transgenic tobacco plants overexpressing **MLP-PG1** were cultivated under a 16/8 h light/dark cycle at 24°C. After 6 weeks, the leaves were treated with water containing peptone. After 4 days, the leaves were collected. Representative leaves are shown.

1 **Table S1** Sequences of the primers used in this study

Primer	Sequence
NtActin/qPCR-s	5'-ATTACCATCGGTGCTGAACG-3'
NtActin/qPCR-as	5'-CCAATCATTGAAGGTTGGAAA-3'
NtPR-2/qPCR-s	5'-GACATGACCTTGATTGGAAACTC-3'
NtPR-2/qPCR-as	5'-AAACCACCTAGCATCGTTCC-3'
NtPR-5/qPCR-s	5'-TGGTGGAGTCCTACAATGCAC-3'
NtPR-5/qPCR-as	5'-AATGCGTATTTCGGCCAAG-3'
CpActin/qPCR-s	5'-TCCAGGCCGTTTTATCTC-3'
CpActin/qPCR-as	5'-CAGAATCCAACACAATACCTGT-3'
MLP-PG1/qPCR-s	5'-ATTCAAAGTGCTAAGAGCAAAAT-3'
MLP-PG1/qPCR-as	5'-CCTTTTCAAACCTCAACAGTCCA-3'
TAIL-specific1-as	5'-GGTCAACCTTTACCCAAATGCTATC-3'
TAIL-specific2-as	5'-CTCCCAAATGGTTCCTGAAGAACCC-3'
TAIL-specific3-as	5'-CAGGAAACAAGTCCACCAAATCTCCC-3'
TAIL-specific4-as	5'-GTTGCGAGGGTTTGTGTCCAAACTAG-3'
TAIL-specific5-as	5'-GCATAAATGTGAGATCGCATATCGATTGG-3'
TAIL-specific6-as	5'-CGATTGGAGAGGGAAATGAAATGTTCC-3'
TAIL-specific7-as	5'-TCGAGCCCCGAAAATTCTCCACGGTA-3'
TAIL-specific8-as	5'-GGTGGTGGGATGGAGGAAGACATCTC-3'
TAIL-specific9-as	5'-CGAGTATTAGAAGATAGCATAGAAGG-3'
TAIL-specific10-as	5'-GGCTAACAGCTTCCATCAATAATCCC-3'
TAIL-specific11-as	5'-CCCTTTATTGCACTAAATTAAGCATAC-3'
TAIL-specific12-as	5'-CTAATGTCATCTTACAGGTTGGGTAGG-3'
AD1	5'-NGTCGASWGANAWGAA-3'
AD2	5'-GTNCGASWCANAWGTT-3'
AD3	5'-WGTGNAGWANCANAGA-3'
PG-PG1-P-s1	5'-TGATTACGCCAAGCTTAACATTACTTTACACATCTT-3'
PG-PG1-P-as	5'-CCGGGGATCCTCTAGTTTCTTTGATGTGATGCAA-3'

2

Table S2. Differentially expressed genes in the leaves of transgenic tobacco plants overexpressing *MLP-PG1*. Transgenic tobacco plants overexpressing *MLP-PG1* were cultivated under a 16/8 h light/dark cycle at 24°C. After 6 weeks, total RNA was isolated from the leaves, and RNA sequencing analysis was performed. VC, transgenic tobacco plants expressing the empty vector; 35S::*MLP-PG1*, transgenic tobacco plants overexpressing *MLP-PG1*.

Gene symbol	Fold change (35S:: <i>MLP-PG1</i> /VC)	Transcript
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LOC107794478	57.0	<i>osmotin-like protein</i>
LOC107815767	50.6	<i>14 kDa proline-rich protein DC2.15-like</i>
LOC107806690	49.8	<i>auxin-binding protein ABP19a-like</i>
LOC107794479	43.4	<i>osmotin-like</i>
LOC107787819	36.6	<i>osmotin</i>
LOC107794480	36.5	<i>proteinase inhibitor I-B</i>
LOC107768773	28.8	<i>carbonic anhydrase, chloroplastic</i>
LOC107802774	27.4	<i>U1 small nuclear ribonucleoprotein C-2-like</i>
LOC107776602	26.8	<i>uncharacterized LOC107776602</i>
LOC107806312	25.9	<i>expansin-A1-like</i>
LOC107828285	24.8	<i>β-galactosidase 3-like</i>
LOC107815747	23.8	<i>uncharacterized LOC107815747</i>
LOC107826794	22.9	<i>endochitinase B</i>
LOC107786959	22.0	<i>14 kDa proline-rich protein DC2.15-like</i>
LOC107784278	21.9	<i>auxin-binding protein ABP19a-like</i>
LOC107807939	20.4	<i>14 kDa proline-rich protein DC2.15-like</i>
LOC107802876	18.6	.
LOC107810528	18.6	<i>chlorophyll a-b binding protein 21, chloroplastic-like</i>
LOC107822445	18.4	<i>β-galactosidase 3-like</i>
LOC107770844	17.8	<i>chlorophyll a-b binding protein 50, chloroplastic-like</i>
LOC107788934	17.1	<i>14 kDa proline-rich protein DC2.15-like</i>
LOC107775280	17.0	<i>aquaporin TIP1-1-like</i>
LOC107772133	16.7	<i>wound-induced protein WIN1-like</i>
LOC107804928	16.5	<i>protochlorophyllide reductase-like</i>
LOC107788809	16.3	<i>repetitive proline-rich cell wall protein 1-like</i>
LOC107820187	15.9	<i>repetitive proline-rich cell wall protein 1-like</i>
LOC107819631	15.8	<i>probable xyloglucan endotransglucosylase/hydrolase protein 7</i>
LOC107802501	15.0	<i>aquaporin TIP2-1-like</i>
LOC107778264	15.0	<i>chlorophyll a-b binding protein 37, chloroplastic-like</i>
LOC107790002	14.8	<i>chlorophyll a-b binding protein 36, chloroplastic-like</i>
LOC107772871	14.8	<i>chlorophyll a-b binding protein 16, chloroplastic-like</i>
LOC107794263	14.2	<i>wound-induced protein WIN1-like</i>
LOC107788163	14.0	<i>monothiol glutaredoxin-S2-like</i>
LOC107814072	14.0	<i>uncharacterized LOC107814072</i>
LOC107790956	13.9	<i>chlorophyll a-b binding protein 36, chloroplastic-like</i>
LOC107808676	13.8	<i>expansin-A1-like</i>
LOC107806780	13.6	<i>chlorophyll a-b binding protein 40, chloroplastic-like</i>
LOC107773590	13.5	<i>stem-specific protein TSJT1-like</i>
LOC107822687	13.3	<i>carbonic anhydrase, chloroplastic-like</i>
LOC107825583	13.2	<i>uncharacterized LOC107825583</i>
LOC107780379	12.6	<i>chlorophyll a-b binding protein 50, chloroplastic</i>

LOC107830508	12.3	<i>chlorophyll a-b binding protein CP24 10A, chloroplastic-like</i>
LOC107798146	12.1	<i>LOB domain-containing protein 37-like</i>
LOC107820326	11.5	<i>protochlorophyllide reductase-like</i>
LOC107772544	11.3	<i>epidermis-specific secreted glycoprotein EP1-like</i>
LOC107793976	11.1	<i>protochlorophyllide reductase-like</i>
LOC107816645	10.9	<i>epidermis-specific secreted glycoprotein EP1-like</i>
LOC107773002	10.9	<i>chlorophyll a-b binding protein 1D</i>
LOC107775016	10.8	<i>chlorophyll a-b binding protein 21, chloroplastic</i>
LOC107781236	10.7	.
LOC107787884	10.7	<i>monothiol glutaredoxin-S2-like</i>
LOC107815182	10.7	<i>aquaporin PIP2-7-like</i>
LOC107794176	10.6	<i>probable xyloglucan endotransglucosylase/hydrolase protein 7</i>
LOC107784140	10.5	<i>nudix hydrolase 8-like</i>
LOC107809994	10.3	<i>epidermis-specific secreted glycoprotein EP1-like</i>
LOC107787802	10.2	<i>osmotin-like protein</i>
LOC107787825	10.0	<i>proteinase inhibitor I-A</i>
LOC107766368	9.8	<i>TBC1 domain family member 5 homolog A-like</i>
LOC107764358	9.7	<i>chlorophyll a-b binding protein 16, chloroplastic</i>
LOC107790089	9.6	<i>chlorophyll a-b binding protein 13, chloroplastic</i>
LOC107781812	9.3	<i>14 kDa proline-rich protein DC2.15-like</i>
LOC107785215	9.0	<i>ribulose biphosphate carboxylase small chain S41, chloroplastic-like</i>
LOC107800666	8.9	<i>protein RADIALIS-like 3</i>
LOC107773466	8.9	<i>chlorophyll a-b binding protein 50, chloroplastic-like</i>
LOC107809147	8.7	<i>phylloplanin</i>
LOC107825008	8.7	<i>probable xyloglucan endotransglucosylase/hydrolase protein 7</i>
LOC107789972	8.5	<i>aquaporin PIP2-7</i>
LOC107784221	8.3	<i>rapid alkalization factor-like</i>
LOC107807891	8.2	<i>chlorophyll a-b binding protein 21, chloroplastic-like</i>
LOC107765079	8.1	<i>chlorophyll a-b binding protein 13, chloroplastic-like</i>
LOC107831306	8.1	<i>uncharacterized LOC107831306</i>
LOC107760717	8.1	<i>uncharacterized LOC107760717</i>
LOC107798774	7.7	<i>uncharacterized LOC107798774</i>
LOC107812102	7.7	<i>DNA-damage-repair/tolerance protein DRT100-like</i>
LOC107798325	7.6	<i>LOB domain-containing protein 37-like</i>
LOC107830507	7.6	<i>chlorophyll a-b binding protein CP24 10A, chloroplastic</i>
LOC107792932	7.5	<i>protein RADIALIS-like 4</i>
LOC107767724	7.5	<i>uncharacterized LOC107767724</i>
LOC107767414	7.4	<i>subtilisin-like protease SBT1.9</i>
LOC107787712	7.3	<i>oxygen-evolving enhancer protein 1, chloroplastic-like</i>
LOC107772627	7.2	.
LOC107765860	7.2	<i>peptidyl-prolyl cis-trans isomerase CYP37, chloroplastic-like</i>
LOC107773810	7.2	<i>chlorophyll a-b binding protein 40, chloroplastic-like</i>
LOC107791896	7.1	<i>chlorophyll a-b binding protein 7, chloroplastic</i>
LOC107830543	7.1	<i>chlorophyll a-b binding protein 4, chloroplastic-like</i>
LOC107807254	7.1	<i>chlorophyll a-b binding protein 7, chloroplastic</i>
LOC107798610	7.1	<i>LOB domain-containing protein 37-like</i>
LOC107793233	6.9	<i>peptidyl-prolyl cis-trans isomerase CYP26-2, chloroplastic-like</i>
LOC107798595	6.8	<i>uncharacterized LOC107798595</i>
LOC107811419	6.8	<i>chlorophyll a-b binding protein P4, chloroplastic</i>
LOC107787316	6.8	<i>protochlorophyllide reductase, chloroplastic-like</i>

LOC107804389	6.8	<i>lamin-like protein</i>
LOC107779034	6.7	<i>uncharacterized LOC107779034</i>
LOC107828063	6.6	<i>F-box protein PP2-A13-like</i>
LOC107792047	6.5	<i>chlorophyll a-b binding protein CP24 10A, chloroplastic-like</i>
LOC107821598	6.5	<i>subtilisin-like protease SBT1.8</i>
LOC107773487	6.5	<i>chlorophyll a-b binding protein 16, chloroplastic-like</i>
LOC107766787	6.5	<i>transcription factor bHLH63-like</i>
LOC107772117	6.5	<i>uncharacterized LOC107772117</i>
LOC107776510	6.5	<i>thiosulfate sulfurtransferase 16, chloroplastic-like</i>
LOC107798057	6.4	<i>CASP-like protein 4D2</i>
LOC107812631	6.4	<i>14 kDa proline-rich protein DC2.15-like</i>
LOC107780755	6.4	<i>subtilisin-like protease SBT1.9</i>
LOC107810540	6.4	<i>defensin-like protein P322</i>
LOC107799234	6.3	<i>fasciclin-like arabinogalactan protein 8</i>
LOC107800172	6.2	<i>auxin-induced protein 15A-like</i>
LOC107802909	6.2	<i>dihydrodipicolinate reductase-like protein CRR1, chloroplastic</i>
LOC107830956	6.2	<i>monothiol glutaredoxin-S10-like</i>
LOC107812076	6.2	<i>ycf54-like protein</i>
LOC107764924	6.1	<i>glycine-rich protein-like</i>
LOC107821470	6.1	<i>thylakoid lumenal 29 kDa protein, chloroplastic-like</i>
LOC107812074	6.1	<i>chitotriosidase-1-like</i>
LOC107781399	6.1	<i>auxin-binding protein ABP19a-like</i>
LOC107779946	6.1	<i>aspartyl protease AED3-like</i>
LOC107759301	6.0	<i>uncharacterized LOC107759301</i>
LOC107759587	6.0	<i>chaperone protein dnaJ 11, chloroplastic-like</i>
LOC107784637	6.0	<i>expansin-A11-like</i>
LOC107773233	5.9	<i>GATA zinc finger domain-containing protein 14-like</i>
LOC107805401	5.9	<i>F-box protein PP2-A13-like</i>
LOC107773838	5.9	.
LOC107817323	5.9	<i>chlorophyll a-b binding protein 8, chloroplastic-like</i>
LOC107831173	5.8	<i>uncharacterized LOC107831173</i>
LOC107820834	5.8	<i>photosystem I reaction center subunit VI-2, chloroplastic-like</i>
LOC107814258	5.8	<i>protein NDH-DEPENDENT CYCLIC ELECTRON FLOW 5-like</i>
LOC107800537	5.8	<i>lysine-rich arabinogalactan protein 19-like</i>
LOC107812088	5.7	<i>uncharacterized LOC107812088</i>
LOC107781417	5.7	<i>uncharacterized LOC107781417</i>
LOC107831975	5.7	<i>uncharacterized LOC107831975</i>
LOC107822178	5.6	<i>leucine-rich repeat extensin-like protein 4</i>
LOC107821835	5.6	<i>photosystem I subunit O-like</i>
LOC107830195	5.6	<i>chlorophyll a-b binding protein 13, chloroplastic-like</i>
LOC107830468	5.6	<i>lipxygenase homology domain-containing protein 1-like</i>
LOC107814646	5.6	<i>protein IQ-DOMAIN 1-like</i>
LOC107801382	5.5	<i>uncharacterized LOC107801382</i>
LOC107768034	5.5	<i>NAD(P)H-quinone oxidoreductase subunit U, chloroplastic-like</i>
LOC107809429	5.5	<i>auxin-responsive protein IAA16-like</i>
LOC107797524	5.5	<i>uncharacterized LOC107797524</i>
LOC107772254	5.5	<i>probable protein phosphatase 2C 5</i>
LOC107775721	5.5	<i>uncharacterized LOC107775721</i>
LOC107819904	5.4	<i>14 kDa proline-rich protein DC2.15-like</i>
LOC107816431	5.4	<i>transcription factor bHLH77-like</i>

LOC107764174	5.4	<i>nudix hydrolase 8-like</i>
LOC107788814	5.4	<i>bifunctional L-3-cyanoalanine synthase/cysteine synthase 2, mitochondrial</i>
LOC107778191	5.4	<i>β-galactosidase-like</i>
LOC107780887	5.4	<i>photosystem II 5 kDa protein, chloroplastic</i>
LOC107784037	5.4	<i>fasciclin-like arabinogalactan protein 9</i>
LOC107802970	5.3	<i>3-ketoacyl-CoA synthase 20-like</i>
LOC107771822	5.3	<i>protein LOL1</i>
LOC107786708	5.3	<i>uncharacterized LOC107786708</i>
LOC107794264	5.2	<i>auxin-responsive protein IAA16-like</i>
LOC107762230	5.2	<i>putative S-adenosyl-L-methionine-dependent methyltransferase Mb0746c</i>
LOC107794227	5.2	<i>probable xyloglucan endotransglucosylase/hydrolase protein 23</i>
LOC107760508	5.2	<i>probable galacturonosyltransferase-like 3</i>
LOC107779390	5.2	<i>fasciclin-like arabinogalactan protein 2</i>
LOC107799261	5.2	<i>auxin-binding protein ABP19a-like</i>
LOC107781760	5.2	<i>classical arabinogalactan protein 25-like</i>
LOC107773465	5.1	<i>chlorophyll a-b binding protein 40, chloroplastic-like</i>
LOC107772798	5.1	<i>PLASMODESMATA CALLOSE-BINDING PROTEIN 3-like</i>
LOC107807889	5.1	<i>chlorophyll a-b binding protein 21, chloroplastic-like</i>
LOC107792369	5.1	<i>aspartyl protease AED3-like</i>
LOC107770076	5.1	<i>uncharacterized LOC107770076</i>
LOC107774933	5.1	<i>chlorophyll a-b binding protein P4, chloroplastic-like</i>
LOC107832242	5.1	<i>plasma membrane-associated cation-binding protein 1-like</i>
LOC107769403	5.0	<i>GDSL esterase/lipase APG-like</i>
LOC107820174	5.0	<i>polygalacturonase-1 non-catalytic subunit β-like</i>
LOC107810527	5.0	<i>chlorophyll a-b binding protein 21, chloroplastic-like</i>
LOC107764661	5.0	<i>protein SENESENCE-ASSOCIATED GENE 21, mitochondrial-like</i>
LOC107784379	5.0	<i>protein NRT1/ PTR FAMILY 6.2-like</i>
LOC107794160	5.0	<i>photosystem I reaction center subunit V, chloroplastic-like</i>
LOC107768914	4.9	<i>photosystem I reaction center subunit psaK, chloroplastic-like</i>
LOC107795435	4.9	<i>uncharacterized LOC107795435</i>
LOC107814785	4.8	<i>aquaporin TIP2-1-like</i>
LOC107774398	4.8	<i>ribulose biphosphate carboxylase small chain S41, chloroplastic-like</i>
LOC107762980	4.8	<i>β-galactosidase-like</i>
LOC107815759	4.7	<i>chlorophyll a-b binding protein 6A, chloroplastic-like</i>
LOC107760174	4.7	<i>transcription factor bHLH63-like</i>
LOC107764264	4.7	<i>photosystem I subunit O-like</i>
LOC107827536	4.7	<i>glycine-rich protein 3-like</i>
LOC107768731	4.7	<i>transcription factor HBI1-like</i>
LOC107766707	4.7	<i>1,4-dihydroxy-2-naphthoyl-CoA synthase, peroxisomal-like</i>
LOC107794830	4.7	<i>peroxidase 21-like</i>
LOC107814800	4.7	<i>non-specific lipid-transfer protein 2</i>
LOC107775402	4.6	<i>SNF1-related protein kinase regulatory subunit β-1-like</i>
LOC107785040	4.6	<i>ribulose biphosphate carboxylase small chain S41, chloroplastic-like</i>
LOC107793205	4.6	<i>chlorophyll a-b binding protein 13, chloroplastic</i>
LOC107828311	4.6	<i>14 kDa proline-rich protein DC2.15-like</i>
LOC107787172	4.6	<i>aldose 1-epimerase-like</i>
LOC107793459	4.6	<i>uncharacterized LOC107793459</i>
LOC107780223	4.6	<i>cyclin-D4-1-like</i>
LOC107825155	4.6	<i>annexin D1-like</i>
LOC107829137	4.6	<i>DNA-binding protein DDB_G0278111-like</i>

LOC107814932	4.5	<i>uncharacterized LOC107814932</i>
LOC107773808	4.5	<i>chlorophyll a-b binding protein 40, chloroplastic-like</i>
LOC107770478	4.5	<i>auxin-binding protein ABP19a-like</i>
LOC107772663	4.5	<i>chlorophyll a-b binding protein 40, chloroplastic</i>
LOC107809852	4.5	<i>chlorophyll a-b binding protein 36, chloroplastic-like</i>
LOC107765738	4.4	<i>uncharacterized LOC107765738</i>
LOC107802461	4.4	<i>CBL-interacting serine/threonine-protein kinase 1-like</i>
LOC107797365	4.4	<i>dihydrodipicolinate reductase-like protein CRR1, chloroplastic</i>
LOC107825947	4.4	.
LOC107789641	4.4	<i>omega-hydroxypalmitate O-feruloyl transferase-like</i>
LOC107769475	4.4	<i>oxygen-evolving enhancer protein 2-1, chloroplastic-like</i>
LOC107806416	4.4	<i>fasciclin-like arabinogalactan protein 8</i>
LOC107786553	4.4	<i>uncharacterized LOC107786553</i>
LOC107807890	4.3	<i>chlorophyll a-b binding protein 21, chloroplastic-like</i>
LOC107779301	4.3	<i>lysine-rich arabinogalactan protein 18-like</i>
LOC107807584	4.3	<i>uncharacterized LOC107807584</i>
LOC107796224	4.3	<i>uncharacterized LOC107796224</i>
LOC107759893	4.3	<i>heavy metal-associated isoprenylated plant protein 3-like</i>
LOC107773232	4.3	<i>chlorophyll a-b binding protein 40, chloroplastic</i>
LOC107829059	4.3	<i>21 kDa protein-like</i>
LOC107800806	4.3	<i>lysine-rich arabinogalactan protein 18-like</i>
LOC107778084	4.3	<i>probable pectate lyase 13</i>
LOC107773547	4.2	<i>glutamate synthase [NADH], amyloplastic-like</i>
LOC107815983	4.2	<i>leucine-rich repeat extensin-like protein 3</i>
LOC107825649	4.2	<i>GDSL esterase/lipase At5g45670-like</i>
LOC107768328	4.2	<i>rho GDP-dissociation inhibitor 1-like</i>
LOC107777466	4.2	<i>photosystem II 5 kDa protein, chloroplastic-like</i>
LOC107773042	4.2	<i>peroxidase N1</i>
LOC107771462	4.2	<i>uncharacterized LOC107771462</i>
LOC107830695	4.1	<i>uncharacterized LOC107830695</i>
LOC107790143	4.1	<i>chloride channel protein CLC-c-like</i>
LOC107808809	4.1	<i>glycine-rich cell wall structural protein-like</i>
LOC107827010	4.1	<i>uncharacterized LOC107827010</i>
LOC107823062	4.1	<i>keratinocyte proline-rich protein-like</i>
LOC107767898	4.1	<i>L-ascorbate oxidase homolog</i>
LOC107779687	4.1	<i>transcription factor EMB1444-like</i>
LOC107760712	4.1	<i>NAD(P)H-quinone oxidoreductase subunit T, chloroplastic-like</i>
LOC107803004	4.0	<i>LOB domain-containing protein 37-like</i>
LOC107766003	4.0	<i>heavy metal-associated isoprenylated plant protein 3-like</i>
LOC107788953	4.0	<i>pectinesterase/pectinesterase inhibitor U1</i>
LOC107774399	4.0	<i>ribulose biphosphate carboxylase small chain S41, chloroplastic</i>
LOC107790938	4.0	<i>RING-H2 finger protein ATL78-like</i>
LOC107778234	4.0	<i>xyloglucan endotransglucosylase/hydrolase 2-like</i>
LOC107762154	4.0	<i>purine permease 3-like</i>
LOC107786743	4.0	<i>aquaporin PIP2-7-like</i>
LOC107820719	3.9	<i>psbP domain-containing protein 6, chloroplastic-like</i>
LOC107789143	3.9	<i>cyclin-U4-1-like</i>
LOC107775375	3.9	<i>photosystem I chlorophyll a/b-binding protein 5, chloroplastic-like</i>
LOC107767222	3.9	<i>uncharacterized LOC107767222</i>
LOC107815525	3.9	<i>oryzain β chain-like</i>

LOC107826669	3.9	<i>metallocarboxypeptidase inhibitor-like</i>
LOC107784434	3.9	<i>endochitinase 3</i>
LOC107806715	3.8	<i>uncharacterized LOC107806715</i>
LOC107828255	3.8	<i>uncharacterized transporter YBR287W-like</i>
LOC107811379	3.8	<i>uncharacterized LOC107811379</i>
LOC107804241	3.8	<i>protein STAY-GREEN LIKE, chloroplastic-like</i>
LOC107800085	3.8	<i>putative protein TPRXL</i>
LOC107823127	3.8	<i>uncharacterized protein At5g01610-like</i>
LOC107800495	3.8	<i>photosystem I reaction center subunit VI-1, chloroplastic-like</i>
LOC107810681	3.8	<i>xyloglucan endotransglucosylase/hydrolase protein 24-like</i>
LOC107786610	3.8	<i>zinc finger protein CONSTANS-LIKE 16-like</i>
LOC107798790	3.8	<i>probable LRR receptor-like serine/threonine-protein kinase At4g30520</i>
LOC107782832	3.8	<i>mechanosensitive ion channel protein 2, chloroplastic-like</i>
LOC107797149	3.7	<i>ethylene-responsive transcription factor ERF011-like</i>
LOC107794540	3.7	<i>glycine-rich cell wall structural protein 1-like</i>
LOC107793736	3.7	<i>transcription factor HBI1-like</i>
LOC107786526	3.7	<i>omega-3 fatty acid desaturase, endoplasmic reticulum-like</i>
LOC107787097	3.7	<i>bifunctional L-3-cyanoalanine synthase/cysteine synthase 2, mitochondrial-like</i>
LOC107768438	3.7	<i>serine hydroxymethyltransferase, mitochondrial-like</i>
LOC107824549	3.7	<i>2-phytyl-1,4-β-naphthoquinone methyltransferase, chloroplastic-like</i>
LOC107763187	3.7	<i>protein plastid transcriptionally active 16, chloroplastic-like</i>
LOC107821676	3.7	<i>photosystem I reaction center subunit VI-1, chloroplastic-like</i>
LOC107772048	3.7	<i>uncharacterized LOC107772048</i>
LOC107796846	3.7	<i>fatty-acid-binding protein 3, chloroplastic-like</i>
LOC107811031	3.7	<i>thylakoid lumenal 16.5 kDa protein, chloroplastic-like</i>
LOC107784622	3.7	<i>chlorophyll a-b binding protein 8, chloroplastic-like</i>
LOC107784169	3.7	<i>bidirectional sugar transporter SWEET1-like</i>
LOC107807593	3.7	<i>glycine-rich protein</i>
LOC107765795	3.7	<i>ribulose biphosphate carboxylase small chain S41, chloroplastic-like</i>
LOC107800284	3.7	<i>phosphoethanolamine N-methyltransferase-like</i>
LOC107820753	3.6	<i>uncharacterized LOC107820753</i>
LOC107765793	3.6	<i>ribulose biphosphate carboxylase/oxygenase activase 1, chloroplastic-like</i>
LOC107762601	3.6	<i>uncharacterized LOC107762601</i>
LOC107830259	3.6	<i>protein RADIALIS-like 1</i>
LOC107806511	3.6	<i>photosystem I reaction center subunit psaK, chloroplastic-like</i>
LOC107762483	3.6	<i>serine carboxypeptidase-like 40</i>
LOC107793316	3.6	<i>uncharacterized LOC107793316</i>
LOC107769471	3.6	<i>uncharacterized LOC107769471</i>
LOC107810842	3.6	<i>photosynthetic NDH subunit of subcomplex B 5, chloroplastic-like</i>
LOC107810184	3.6	<i>AT-hook motif nuclear-localized protein 9-like</i>
LOC107813817	3.6	<i>photosystem I reaction center subunit psaK, chloroplastic-like</i>
LOC107821072	3.6	<i>dirigent protein 22-like</i>
LOC107773083	3.6	<i>phylloplanin-like</i>
LOC107759521	3.6	<i>homeobox-leucine zipper protein HAT4-like</i>
LOC107818832	3.6	<i>β-D-xylosidase 1-like</i>
LOC107798909	3.6	<i>fimbrin-2-like</i>
LOC107828640	3.6	<i>chlorophyll a-b binding protein 6A, chloroplastic-like</i>
LOC107829478	3.6	<i>inositol 2-dehydrogenase 2-like</i>
LOC107767514	3.6	<i>chloride channel protein CLC-b-like</i>
LOC107793530	3.6	<i>uncharacterized LOC107793530</i>

LOC107774864	3.5	<i>oxygen-evolving enhancer protein 1, chloroplastic-like</i>
LOC107825347	3.5	<i>zinc finger protein CONSTANS-LIKE 16-like</i>
LOC107798001	3.5	<i>uncharacterized LOC107798001</i>
LOC107821820	3.5	<i>uncharacterized LOC107821820</i>
LOC107797166	3.5	<i>ABC transporter A family member 7-like</i>
LOC107782055	3.5	<i>protein EXORDIUM-like 5</i>
LOC107823557	3.4	<i>photosystem I reaction center subunit II, chloroplastic-like</i>
LOC107771896	3.4	<i>thylakoid lumenal 16.5 kDa protein, chloroplastic-like</i>
LOC107768592	3.4	<i>uncharacterized LOC107768592</i>
LOC107824971	3.4	<i>β-hexosaminidase 3-like</i>
LOC107762020	3.4	<i>SNF1-related protein kinase regulatory subunit β-1-like</i>
LOC107774710	3.4	<i>transcription factor PRE6-like</i>
LOC107805093	3.4	<i>uncharacterized protein At5g48480-like</i>
LOC107767231	3.4	<i>uncharacterized LOC107767231</i>
LOC107803841	3.4	<i>peroxidase N1-like</i>
LOC107819218	3.4	<i>ribosome-binding factor PSRP1, chloroplastic-like</i>
LOC107802951	3.4	<i>subtilisin-like protease SBT1.9</i>
LOC107826490	3.4	<i>peroxidase 21-like</i>
LOC107811300	3.4	<i>xylulose kinase-like</i>
LOC107765730	3.4	<i>21 kDa protein-like</i>
LOC107763283	3.4	<i>glutamyl-tRNA reductase 1, chloroplastic-like</i>
LOC107772557	3.4	<i>protein RADIALIS-like 1</i>
LOC107814858	3.4	<i>trehalose-phosphate phosphatase A-like</i>
LOC107767419	3.4	<i>photosystem I subunit O-like</i>
LOC107763147	3.4	<i>sugar transport protein 8-like</i>
LOC107807510	3.4	<i>cysteine proteinase inhibitor 1-like</i>
LOC107791351	3.4	<i>mitogen-activated protein kinase kinase kinase 1-like</i>
LOC107818720	3.3	<i>classical arabinogalactan protein 9-like</i>
LOC107830751	3.3	<i>photosystem II reaction center W protein, chloroplastic-like</i>
LOC107769321	3.3	<i>polygalacturonase-1 non-catalytic subunit β-like</i>
LOC107768737	3.3	<i>uncharacterized LOC107768737</i>
LOC107816302	3.3	<i>fasciclin-like arabinogalactan protein 1</i>
LOC107830487	3.3	<i>lignin-forming anionic peroxidase</i>
LOC107800132	3.3	<i>uncharacterized LOC107800132</i>
LOC107808758	3.3	<i>peroxidase 12-like</i>
LOC107774577	3.3	<i>β-glucosidase BoGH3B-like</i>
LOC107767928	3.3	<i>oxygen-evolving enhancer protein 3-2, chloroplastic-like</i>
LOC107794164	3.3	<i>uncharacterized LOC107794164</i>
LOC107797281	3.3	<i>F-box/kelch-repeat protein At1g15670-like</i>
LOC107801592	3.3	<i>auxin-responsive protein SAUR32-like</i>
LOC107829515	3.3	<i>GDSL esterase/lipase APG-like</i>
LOC107827635	3.3	<i>elongation factor P-like</i>
LOC107775135	3.3	<i>photosystem I reaction center subunit VI-2, chloroplastic-like</i>
LOC107813984	3.3	<i>terpene synthase 10-like</i>
LOC107784985	3.3	<i>photosystem I subunit O-like</i>
LOC107766553	3.3	<i>WD repeat-containing protein 44-like</i>
LOC107765621	3.3	<i>probable glutathione S-transferase</i>
LOC107807258	3.3	<i>RING-H2 finger protein ATL8-like</i>
LOC107822594	3.3	<i>GDSL esterase/lipase At5g03980-like</i>
LOC107810245	3.2	<i>gibberellin-regulated protein 9-like</i>

LOC107778240	3.2	<i>ethylene-responsive transcription factor ERF118-like</i>
LOC107821135	3.2	<i>cysteine proteinase inhibitor B-like</i>
LOC107819052	3.2	<i>psbP domain-containing protein 6, chloroplastic-like</i>
LOC107799559	3.2	<i>nematode resistance protein-like HSPRO2</i>
LOC107802017	3.2	<i>expansin-A10-like</i>
LOC107791852	3.2	<i>magnesium-chelatase subunit ChlH, chloroplastic-like</i>
LOC107830566	3.2	<i>probable carboxylesterase 2</i>
LOC107824245	3.2	<i>BURP domain-containing protein 5-like</i>
LOC107820648	3.2	<i>protein RADIALIS-like 5</i>
LOC107797008	3.2	<i>uncharacterized LOC107797008</i>
LOC107814256	3.2	<i>photosynthetic NDH subunit of subcomplex B 2, chloroplastic-like</i>
LOC107792159	3.2	<i>expansin-A4-like</i>
LOC107804965	3.2	<i>protein RADIALIS-like 5</i>
LOC107795195	3.2	<i>thylakoid lumenal 29 kDa protein, chloroplastic</i>
LOC107760477	3.1	<i>uncharacterized LOC107760477</i>
LOC107796964	3.1	<i>chlorophyll a-b binding protein, chloroplastic-like</i>
LOC107778231	3.1	<i>zinc finger protein CONSTANS-LIKE 16-like</i>
LOC107819642	3.1	<i>uncharacterized LOC107819642</i>
LOC107822486	3.1	<i>low-temperature-induced cysteine proteinase-like</i>
LOC107799880	3.1	<i>BTB/POZ and TAZ domain-containing protein 1-like</i>
LOC107796443	3.1	<i>30S ribosomal protein S31, chloroplastic-like</i>
LOC107776048	3.1	<i>plasma membrane-associated cation-binding protein 1-like</i>
LOC107784032	3.1	<i>uncharacterized LOC107784032</i>
LOC107763485	3.1	<i>uncharacterized LOC107763485</i>
LOC107761752	3.1	<i>probable methyltransferase PMT15</i>
LOC107816043	3.1	<i>MAR-binding filament-like protein 1-1</i>
LOC107788532	3.1	<i>vegetative cell wall protein gp1-like</i>
LOC107785376	3.1	<i>photosystem I chlorophyll a/b-binding protein 6, chloroplastic-like</i>
LOC107767943	3.1	<i>glutamate synthase [NADH], amyloplastic-like</i>
LOC107763119	3.1	<i>thylakoid lumenal 19 kDa protein, chloroplastic-like</i>
LOC107795354	3.1	<i>PCTP-like protein</i>
LOC107831953	3.1	<i>chlorophyll a-b binding protein, chloroplastic</i>
LOC107762899	3.1	<i>gibberellin-regulated protein 9-like</i>
LOC107827354	3.1	<i>SNF1-related protein kinase regulatory subunit β-1-like</i>
LOC107829247	3.1	<i>cyclin-D4-2-like</i>
LOC107800570	3.0	<i>F-box protein PP2-A13-like</i>
LOC107791565	3.0	<i>probable β-D-xylosidase 7</i>
LOC107798218	3.0	<i>uncharacterized LOC107798218</i>
LOC107795891	3.0	<i>protochlorophyllide reductase, chloroplastic-like</i>
LOC107815873	3.0	<i>uncharacterized LOC107815873</i>
LOC107778472	3.0	.
LOC107771123	3.0	<i>3-ketoacyl-CoA synthase 20-like</i>
LOC107792758	3.0	<i>plastocyanin</i>
LOC107817810	3.0	<i>uncharacterized LOC107817810</i>
LOC107820290	3.0	<i>protein EXORDIUM-like 5</i>
LOC107789070	3.0	<i>glutamine synthetase cytosolic isozyme 1-1</i>
LOC107820749	3.0	<i>uncharacterized protein At5g01610-like</i>
LOC107815134	3.0	<i>UDP-glycosyltransferase 83A1-like</i>
LOC107774142	3.0	<i>protein NRT1/ PTR FAMILY 4.5-like</i>
LOC107794010	3.0	<i>abscisic acid receptor PYL4-like</i>

LOC107782430	3.0	<i>chlorophyll a-b binding protein CP26, chloroplastic</i>
LOC107816469	3.0	<i>oxygen-evolving enhancer protein 3-2, chloroplastic-like</i>
LOC107794556	3.0	<i>protein NUCLEAR FUSION DEFECTIVE 4-like</i>
LOC107810464	3.0	<i>very-long-chain enoyl-CoA reductase-like</i>
LOC107802816	3.0	<i>protein TIC 20-I, chloroplastic</i>
LOC107787887	3.0	<i>protein CHLORORESPIRATORY REDUCTION 7, chloroplastic-like</i>
LOC107779266	2.9	<i>β-galactosidase-like</i>
LOC107784162	2.9	<i>protein RADIALIS-like 3</i>
LOC107787953	2.9	<i>internal alternative NAD(P)H-ubiquinone oxidoreductase A1, mitochondrial</i>
LOC107806733	2.9	<i>probable trehalose-phosphate phosphatase H</i>
LOC107793268	2.9	<i>uncharacterized LOC107793268</i>
LOC107799631	2.9	<i>root phototropism protein 2-like</i>
LOC107817303	2.9	<i>uncharacterized LOC107817303</i>
LOC107788852	2.9	<i>hydroxyproline-rich systemin B</i>
LOC107773374	2.9	<i>auxin transporter-like protein 4</i>
LOC107828666	2.9	<i>annexin D1-like</i>
LOC107823449	2.9	<i>uncharacterized LOC107823449</i>
LOC107760383	2.9	<i>MOB kinase activator-like 1A</i>
LOC107829257	2.9	<i>fasciclin-like arabinogalactan protein 1</i>
LOC107765752	2.9	<i>xanthoxin dehydrogenase-like</i>
LOC107780908	2.9	<i>photosynthetic NDH subunit of subcomplex B 1, chloroplastic-like</i>
LOC107804245	2.9	<i>miraculin-like</i>
LOC107777715	2.9	<i>major latex allergen Hev b 5-like</i>
LOC107816203	2.9	<i>phospholipase A1-IIdelta-like</i>
LOC107798677	2.9	<i>chlorophyll a-b binding protein CP29.2, chloroplastic</i>
LOC107831948	2.9	<i>glycine-rich cell wall structural protein 1-like</i>
LOC107815259	2.9	<i>pectinesterase/pectinesterase inhibitor U1-like</i>
LOC107780631	2.9	<i>subtilisin-like protease SBT1.9</i>
LOC107773938	2.9	<i>cysteine-rich repeat secretory protein 3-like</i>
LOC107818087	2.9	<i>chlorophyll a-b binding protein CP26, chloroplastic-like</i>
LOC107811037	2.9	<i>strigolactone esterase D14-like</i>
LOC107819250	2.9	<i>LIM domain-containing protein WLIM2b-like</i>
LOC107811439	2.8	<i>plastocyanin A/A"-like</i>
LOC107787239	2.8	<i>GDSL esterase/lipase At5g45670-like</i>
LOC107761096	2.8	<i>cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG3-like</i>
LOC107828979	2.8	<i>trehalose-phosphate phosphatase A-like</i>
LOC107816657	2.8	<i>homeobox-leucine zipper protein HAT4-like</i>
LOC107778185	2.8	<i>LIM domain-containing protein WLIM1-like</i>
LOC107764717	2.8	<i>nudix hydrolase 8-like</i>
LOC107815787	2.8	<i>E3 ubiquitin-protein ligase MIEL1-like</i>
LOC107788269	2.8	<i>β-carotene isomerase D27, chloroplastic-like</i>
LOC107761020	2.8	<i>uncharacterized LOC107761020</i>
LOC107799177	2.8	<i>ycf54-like protein</i>
LOC107768941	2.8	<i>uncharacterized LOC107768941</i>
LOC107803807	2.8	<i>probable pectinesterase/pectinesterase inhibitor 34</i>
LOC107790411	2.8	<i>probable protein phosphatase 2C 34</i>
LOC107786892	2.8	<i>peptide-N4-(N-acetyl-β-glucosaminy)asparagine amidase A-like</i>
LOC107805477	2.8	<i>peroxiredoxin Q, chloroplastic-like</i>
LOC107778553	2.8	<i>uncharacterized LOC107778553</i>
LOC107768560	2.8	<i>uncharacterized LOC107768560</i>

LOC107787511	2.8	<i>uncharacterized LOC107787511</i>
LOC107817033	2.8	<i>protein NRT1/ PTR FAMILY 4.5-like</i>
LOC107803370	2.8	<i>protein PMR5-like</i>
LOC107805832	2.8	<i>uncharacterized LOC107805832</i>
LOC107786718	2.8	<i>uncharacterized LOC107786718</i>
LOC107800300	2.8	<i>uncharacterized LOC107800300</i>
LOC107791167	2.8	<i>protein plastid transcriptionally active 16, chloroplastic-like</i>
LOC107824481	2.8	<i>L-galactose dehydrogenase-like</i>
LOC107774056	2.7	<i>uncharacterized LOC107774056</i>
LOC107766445	2.7	<i>uncharacterized LOC107766445</i>
LOC107821528	2.7	<i>protein SENESENCE-ASSOCIATED GENE 21, mitochondrial-like</i>
LOC107762834	2.7	<i>lamin-like protein</i>
LOC107774787	2.7	<i>uncharacterized LOC107774787</i>
LOC107818395	2.7	<i>glycine-rich cell wall structural protein-like</i>
LOC107770344	2.7	<i>uncharacterized LOC107770344</i>
LOC107773657	2.7	<i>photosynthetic NDH subunit of lumenal location 2, chloroplastic-like</i>
LOC107794948	2.7	<i>indole-3-glycerol phosphate synthase, chloroplastic-like</i>
LOC107775293	2.7	<i>F-box/kelch-repeat protein At1g15670-like</i>
LOC107782436	2.7	<i>uncharacterized LOC107782436</i>
LOC107786828	2.7	<i>magnesium-protoporphyrin IX monomethyl ester [oxidative] cyclase, chloroplastic-like</i>
LOC107772591	2.7	<i>proteinase inhibitor PSI-1.2-like</i>
LOC107785785	2.7	<i>oxygen-evolving enhancer protein 2-1, chloroplastic</i>
LOC107788470	2.7	<i>ylmG homolog protein 2, chloroplastic-like</i>
LOC107796663	2.7	<i>lamin-like protein</i>
LOC107769274	2.7	<i>mannan endo-1,4-β-mannosidase 7-like</i>
LOC107802966	2.7	<i>cysteine proteinase inhibitor B-like</i>
LOC107802626	2.7	<i>uncharacterized LOC107802626</i>
LOC107765903	2.7	<i>probable protein phosphatase 2C 5</i>
LOC107793983	2.7	<i>thylakoid lumenal 17.4 kDa protein, chloroplastic-like</i>
LOC107789973	2.7	<i>heparan-α-glucosaminide N-acetyltransferase-like</i>
atpA	2.7	.
LOC107812085	2.7	<i>uncharacterized LOC107812085</i>
LOC107779114	2.7	<i>NADPH--cytochrome P450 reductase-like</i>
LOC107828990	2.7	<i>uncharacterized LOC107828990</i>
LOC107763781	2.7	<i>protein STAY-GREEN LIKE, chloroplastic-like</i>
LOC107805800	2.7	<i>peroxiredoxin Q, chloroplastic-like</i>
LOC107800268	2.7	<i>probable xyloglucan endotransglucosylase/hydrolase protein 6</i>
LOC107788662	2.7	<i>probable plastid-lipid-associated protein 12, chloroplastic</i>
LOC107830567	2.6	<i>probable carboxylesterase 5</i>
LOC107790478	2.6	<i>uncharacterized LOC107790478</i>
LOC107811505	2.6	<i>photosystem II 5 kDa protein, chloroplastic-like</i>
LOC107781811	2.6	<i>ATP synthase subunit b', chloroplastic-like</i>
LOC107793272	2.6	<i>glucan endo-1,3-β-D-glucosidase-like</i>
LOC107776485	2.6	<i>protein THYLAKOID FORMATION1, chloroplastic</i>
LOC107774251	2.6	<i>chlorophyll a-b binding protein CP29.1, chloroplastic-like</i>
LOC107810529	2.6	<i>chlorophyll a-b binding protein 21, chloroplastic-like</i>
LOC107817095	2.6	<i>isoamylase 3, chloroplastic-like</i>
LOC107791485	2.6	<i>2-succinylbenzoate--CoA ligase, chloroplastic/peroxisomal-like</i>
LOC107819832	2.6	<i>probable strigolactone esterase DAD2</i>
LOC107797030	2.6	<i>photosystem II reaction center Psb28 protein-like</i>

LOC107791294	2.6	<i>glycine-rich protein-like</i>
LOC107796678	2.6	<i>glyceraldehyde-3-phosphate dehydrogenase B, chloroplastic</i>
LOC107831183	2.6	<i>heavy metal-associated isoprenylated plant protein 22-like</i>
LOC107829453	2.6	<i>probable plastid-lipid-associated protein 13, chloroplastic</i>
LOC107809441	2.6	<i>enoyl-[acyl-carrier-protein] reductase [NADH], chloroplastic-like</i>
LOC107788622	2.6	<i>abscisic acid receptor PYL4-like</i>
LOC107772132	2.6	<i>uncharacterized LOC107772132</i>
LOC107790339	2.6	<i>18.2 kDa class I heat shock protein-like</i>
LOC107762067	2.6	<i>plastidic glucose transporter 4-like</i>
LOC107798633	2.6	<i>acyl-lipid (9-3)-desaturase-like</i>
LOC107829490	2.6	<i>photosystem II reaction center W protein, chloroplastic-like</i>
LOC107770944	2.6	<i>non-specific lipid-transfer protein 2-like</i>
LOC107795174	2.6	<i>malate dehydrogenase, mitochondrial-like</i>
LOC107759169	2.6	<i>umecyanin-like</i>
LOC107817220	2.6	<i>peptidyl-prolyl cis-trans isomerase FKBP16-3, chloroplastic-like</i>
LOC107803843	2.6	<i>BAHD acyltransferase DCR</i>
LOC107820526	2.6	<i>long-chain-alcohol oxidase FAO2-like</i>
LOC107784187	2.6	<i>uncharacterized LOC107784187</i>
LOC107786260	2.6	<i>root phototropism protein 2-like</i>
LOC107761533	2.6	<i>uncharacterized LOC107761533</i>
LOC107768014	2.6	<i>photosystem II reaction center Psb28 protein-like</i>
LOC107764291	2.6	<i>acetylajmalan esterase-like</i>
LOC107817913	2.6	<i>thylakoid lumenal 19 kDa protein, chloroplastic-like</i>
LOC107824587	2.6	<i>probable WRKY transcription factor 40</i>
LOC107790752	2.6	<i>probable DEAD-box ATP-dependent RNA helicase 48</i>
LOC107780377	2.6	<i>photosynthetic NDH subunit of lumenal location 3, chloroplastic-like</i>
LOC107758987	2.6	<i>chlorophyll a-b binding protein, chloroplastic-like</i>
LOC107789632	2.6	<i>cytochrome P450 78A6-like</i>
LOC107790513	2.6	<i>loricrin-like</i>
LOC107804058	2.6	<i>VIN3-like protein 1</i>
LOC107801037	2.6	<i>aspartate aminotransferase, mitochondrial-like</i>
LOC107783687	2.6	<i>transcription factor bHLH130-like</i>
LOC107765667	2.6	<i>phyloplanin-like</i>
LOC107761637	2.6	<i>F-box protein At4g18380-like</i>
LOC107783393	2.6	<i>ribosome-binding factor PSRP1, chloroplastic-like</i>
LOC107818209	2.6	<i>chlorophyll a-b binding protein 6A, chloroplastic</i>
LOC107788710	2.6	<i>biotin carboxyl carrier protein of acetyl-CoA carboxylase 1, chloroplastic-like</i>
LOC107823034	2.6	<i>NAD(P)H-quinone oxidoreductase subunit O, chloroplastic-like</i>
LOC107769959	2.6	<i>transcription factor TCP7-like</i>
LOC107774945	2.6	<i>photosystem I chlorophyll a/b-binding protein 5, chloroplastic-like</i>
LOC107797274	2.6	<i>uncharacterized LOC107797274</i>
LOC107816963	2.5	<i>uncharacterized LOC107816963</i>
LOC107784542	2.5	<i>tubulin β-2 chain-like</i>
LOC107778373	2.5	<i>subtilisin-like protease SBT1.8</i>
LOC107759483	2.5	<i>omega-6 fatty acid desaturase, chloroplastic-like</i>
LOC107774922	2.5	<i>kirola-like</i>
LOC107827858	2.5	<i>uncharacterized LOC107827858</i>
LOC107769385	2.5	<i>uncharacterized LOC107769385</i>
LOC107793769	2.5	<i>uncharacterized LOC107793769</i>
LOC107830418	2.5	<i>CBL-interacting serine/threonine-protein kinase 1-like</i>

LOC107813997	2.5	<i>uncharacterized protein At5g48480-like</i>
LOC107805556	2.5	<i>calvin cycle protein CP12-2, chloroplastic-like</i>
LOC107780180	2.5	<i>protein EARLY FLOWERING 4-like</i>
LOC107785853	2.5	<i>28 kDa ribonucleoprotein, chloroplastic-like</i>
LOC107777321	2.5	<i>chloride channel protein CLC-b-like</i>
LOC107793358	2.5	<i>heavy metal-associated isoprenylated plant protein 3-like</i>
LOC107761248	2.5	<i>lysM domain-containing GPI-anchored protein 1-like</i>
LOC107800278	2.5	<i>MOB kinase activator-like 1A</i>
LOC107794327	2.5	<i>photosynthetic NDH subunit of lumenal location 5, chloroplastic-like</i>
LOC107815514	2.5	<i>protein NUCLEAR FUSION DEFECTIVE 4-like</i>
LOC107764102	2.5	<i>pollen-specific protein C13-like</i>
LOC107790700	2.5	<i>uncharacterized LOC107790700</i>
LOC107828196	2.5	<i>lactoylglutathione lyase-like</i>
LOC107823842	2.5	<i>fasciclin-like arabinogalactan protein 17</i>
LOC107806384	2.5	<i>LIM domain-containing protein WLIM1-like</i>
LOC107778915	2.5	<i>AT-hook motif nuclear-localized protein 9-like</i>
LOC107809539	2.5	<i>interactor of constitutive active ROPs 3-like</i>
LOC107818347	2.5	<i>LIM domain-containing protein WLIM2b-like</i>
LOC107788585	2.5	<i>probable galacturonosyltransferase-like 3</i>
LOC107827796	2.5	<i>caffeoylshikimate esterase-like</i>
LOC107813440	2.5	<i>uncharacterized protein At5g65660-like</i>
LOC107817732	2.5	<i>keratin, type II cytoskeletal 1-like</i>
LOC107779056	2.5	<i>50S ribosomal protein L12, chloroplastic-like</i>
ycf3	2.5	.
LOC107818796	2.5	<i>probable 1-deoxy-D-xylulose-5-phosphate synthase, chloroplastic</i>
LOC107796760	2.5	<i>tetrapyrrole-binding protein, chloroplastic-like</i>
LOC107818269	2.5	<i>tubulin β-2 chain-like</i>
LOC107786882	2.5	<i>probable xyloglucan endotransglucosylase/hydrolase protein 23</i>
LOC107826704	2.5	<i>linoleate 13S-lipoxygenase 2-1, chloroplastic-like</i>
LOC107811943	2.5	<i>zerumbone synthase-like</i>
LOC107766898	2.5	<i>aspartic proteinase A1-like</i>
LOC107802704	2.5	<i>probable glutathione S-transferase</i>
LOC107807641	2.5	<i>uncharacterized LOC107807641</i>
LOC107778620	2.5	<i>fructose-bisphosphate aldolase, cytoplasmic isozyme 1</i>
LOC107777349	2.5	<i>thioredoxin-like 1-2, chloroplastic</i>
LOC107766449	2.5	<i>protein SPA, chloroplastic</i>
LOC107819889	2.5	<i>putative zinc finger protein At1g68190</i>
LOC107790514	2.5	<i>probable serine/threonine-protein kinase At1g01540</i>
LOC107815070	2.5	<i>D-glycerate 3-kinase, chloroplastic-like</i>
LOC107784214	2.5	<i>fructose-bisphosphate aldolase, cytoplasmic isozyme 1-like</i>
LOC107797063	2.5	<i>IAA-amino acid hydrolase ILR1-like 6</i>
LOC107802235	2.5	<i>probable esterase KAI2</i>
LOC107763926	2.5	<i>uncharacterized LOC107763926</i>
LOC107794349	2.5	.
LOC107805493	2.5	<i>uncharacterized LOC107805493</i>
LOC107775821	2.5	<i>fatty-acid-binding protein 3, chloroplastic-like</i>
LOC107832630	2.5	<i>uncharacterized LOC107832630</i>
LOC107816541	2.5	<i>glucose-1-phosphate adenylyltransferase large subunit 3, chloroplastic/amyloplast</i>
LOC107820579	2.5	<i>abscisic stress-ripening protein 2-like</i>
LOC107786803	2.5	<i>stomatal closure-related actin-binding protein 3-like</i>

LOC107781227	2.5	<i>phytoene dehydrogenase, chloroplastic/chromoplastic-like</i>
LOC107781290	2.5	<i>serine carboxypeptidase-like 25</i>
LOC107802637	2.5	<i>heat shock cognate 70 kDa protein 2-like</i>
LOC107830251	2.5	<i>protein TIC 62, chloroplastic-like</i>
LOC107806837	2.5	<i>peroxiredoxin-2E-2, chloroplastic-like</i>
LOC107789149	2.5	<i>DNA-damage-repair/toleration protein DRT100-like</i>
LOC107772768	2.5	<i>uncharacterized LOC107772768</i>
LOC107759735	2.5	<i>photosystem I reaction center subunit N, chloroplastic-like</i>
LOC107783263	2.5	<i>ylmG homolog protein 2, chloroplastic</i>
LOC107769242	2.5	<i>transcription factor LUX-like</i>
LOC107760084	2.5	<i>thylakoid lumenal 17.4 kDa protein, chloroplastic-like</i>
LOC107812849	2.5	<i>heavy metal-associated isoprenylated plant protein 3-like</i>
LOC107765654	2.5	<i>lysosomal Pro-X carboxypeptidase-like</i>
LOC107781754	2.5	<i>heavy metal-associated isoprenylated plant protein 21-like</i>
LOC107811985	2.5	<i>uncharacterized LOC107811985</i>
LOC107810830	2.4	<i>photosystem I reaction center subunit XI, chloroplastic-like</i>
LOC107766400	2.4	<i>fasciclin-like arabinogalactan protein 17</i>
LOC107818396	2.4	<i>glycine-rich protein-like</i>
LOC107763687	2.4	<i>D-glycerate 3-kinase, chloroplastic-like</i>
LOC107805047	2.4	<i>uncharacterized LOC107805047</i>
LOC107794130	2.4	<i>probable serine/threonine-protein kinase At1g01540</i>
LOC107788887	2.4	<i>30S ribosomal protein S9, chloroplastic-like</i>
LOC107793176	2.4	<i>subtilisin-like protease SBT1.9</i>
LOC107775857	2.4	<i>protein IQ-DOMAIN 1-like</i>
LOC107771513	2.4	<i>photosynthetic NDH subunit of lumenal location 4, chloroplastic-like</i>
LOC107816558	2.4	<i>β-glucosidase 40-like</i>
LOC107787089	2.4	<i>glycerol-3-phosphate 2-O-acyltransferase 4-like</i>
LOC107759503	2.4	<i>protein PLANT CADMIUM RESISTANCE 8-like</i>
LOC107831039	2.4	<i>photosynthetic NDH subunit of lumenal location 2, chloroplastic-like</i>
LOC107768293	2.4	<i>signal recognition particle 43 kDa protein, chloroplastic-like</i>
LOC107819449	2.4	<i>chlorophyll a-b binding protein, chloroplastic-like</i>
LOC107776078	2.4	<i>F-box/LRR-repeat protein 14-like</i>
LOC107761116	2.4	<i>probable receptor-like protein kinase At2g42960</i>
LOC107785178	2.4	<i>uncharacterized LOC107785178</i>
LOC107773320	2.4	<i>uncharacterized protein At4g00950-like</i>
LOC107774695	2.4	<i>uncharacterized LOC107774695</i>
LOC107759486	2.4	<i>ACT domain-containing protein DS12, chloroplastic-like</i>
LOC107770242	2.4	<i>protein PLANT CADMIUM RESISTANCE 8-like</i>
LOC107761048	2.4	<i>uncharacterized protein At5g02240-like</i>
LOC107790670	2.4	<i>protein PMR5-like</i>
LOC107761273	2.4	<i>rapid alkalization factor-like</i>
LOC107798023	2.4	<i>β-glucosidase 40-like</i>
LOC107777980	2.4	<i>magnesium-protoporphyrin IX monomethyl ester [oxidative] cyclase, chloroplastic</i>
LOC107802214	2.4	<i>tubulin β-2 chain-like</i>
LOC107762882	2.4	<i>uncharacterized LOC107762882</i>
LOC107832423	2.4	<i>fatty-acid-binding protein 1-like</i>
LOC107759661	2.4	<i>uncharacterized LOC107759661</i>
LOC107762234	2.4	<i>glycine-rich protein DOT1-like</i>
LOC107826514	2.4	<i>heparan-α-glucosaminide N-acetyltransferase-like</i>
LOC107795717	2.4	<i>protein SENESCENCE-ASSOCIATED GENE 21, mitochondrial-like</i>

LOC107761143	2.4	<i>cytochrome P450 77A1-like</i>
LOC107776721	2.4	<i>trans-resveratrol di-O-methyltransferase-like</i>
LOC107819460	2.4	<i>uncharacterized LOC107819460</i>
LOC107776344	2.4	<i>late embryogenesis abundant protein-like</i>
rps14	2.4	.
LOC107828672	2.4	<i>70 kDa peptidyl-prolyl isomerase-like</i>
LOC107791305	2.4	<i>uncharacterized LOC107791305</i>
LOC107828094	2.4	.
LOC107760335	2.4	<i>leucine-rich repeat receptor-like serine/threonine-protein kinase BAM1</i>
LOC107832034	2.4	<i>uncharacterized LOC107832034</i>
LOC107775828	2.4	<i>uncharacterized LOC107775828</i>
LOC107821791	2.4	<i>uncharacterized protein At4g14100-like</i>
LOC107778186	2.4	<i>peroxiredoxin Q, chloroplastic-like</i>
LOC107761800	2.4	<i>uncharacterized LOC107761800</i>
LOC107770398	2.4	<i>photosystem I reaction center subunit psaK, chloroplastic</i>
LOC107783228	2.4	<i>uncharacterized LOC107783228</i>
LOC107811993	2.4	<i>uncharacterized GPI-anchored protein At4g28100-like</i>
LOC107760646	2.4	<i>chitinase 6-like</i>
LOC107818244	2.4	<i>uncharacterized LOC107818244</i>
LOC107763446	2.4	<i>omega-3 fatty acid desaturase, endoplasmic reticulum</i>
LOC107832794	2.4	<i>photosystem II repair protein PSB27-H1, chloroplastic-like</i>
LOC107832752	2.4	<i>uncharacterized LOC107832752</i>
LOC107774794	2.3	<i>uncharacterized LOC107774794</i>
LOC107792822	2.3	<i>uncharacterized LOC107792822</i>
LOC107792514	2.3	<i>uncharacterized LOC107792514</i>
LOC107825870	2.3	<i>plastidic glucose transporter 4-like</i>
LOC107825900	2.3	<i>ferredoxin-thioredoxin reductase, variable chain-like</i>
LOC107763963	2.3	<i>uncharacterized LOC107763963</i>
LOC107768840	2.3	<i>GDSL esterase/lipase At1g28590-like</i>
LOC107819200	2.3	<i>uncharacterized LOC107819200</i>
LOC107802920	2.3	<i>bidirectional sugar transporter SWEET1-like</i>
LOC107800421	2.3	<i>probable methyltransferase PMT20</i>
LOC107782283	2.3	<i>dihydrolipoyl dehydrogenase 2, chloroplastic-like</i>
LOC107765837	2.3	<i>photosystem I reaction center subunit III, chloroplastic-like</i>
LOC107802298	2.3	<i>ethylene-responsive transcription factor ERF106-like</i>
LOC107803206	2.3	<i>uncharacterized LOC107803206</i>
LOC107774097	2.3	<i>putative S-adenosyl-L-methionine-dependent methyltransferase Mb0746c</i>
LOC107777133	2.3	<i>peroxiredoxin Q, chloroplastic-like</i>
LOC107831462	2.3	<i>dicarboxylate transporter 2.1, chloroplastic-like</i>
LOC107777488	2.3	<i>E3 ubiquitin-protein ligase MIEL1-like</i>
psbL	2.3	.
LOC107783419	2.3	<i>glyoxylate/succinic semialdehyde reductase 2, chloroplastic-like</i>
LOC107772038	2.3	<i>thioredoxin-like 1-1, chloroplastic</i>
LOC107803361	2.3	<i>thioredoxin-like 1-1, chloroplastic</i>
LOC107813684	2.3	<i>uroporphyrinogen decarboxylase, chloroplastic</i>
LOC107826812	2.3	<i>probable pectinesterase/pectinesterase inhibitor 61</i>
LOC107822298	2.3	<i>uncharacterized LOC107822298</i>
LOC107804815	2.3	<i>uncharacterized LOC107804815</i>
LOC107813410	2.3	<i>uncharacterized LOC107813410</i>
LOC107829571	2.3	<i>peptidyl-prolyl cis-trans isomerase FKBP19, chloroplastic-like</i>

LOC107801920	2.3	<i>protein HHL1, chloroplastic-like</i>
LOC107808272	2.3	<i>uncharacterized LOC107808272</i>
LOC107801762	2.3	<i>elongation factor P-like</i>
LOC107805390	2.3	<i>uncharacterized LOC107805390</i>
LOC107761484	2.3	<i>uncharacterized LOC107761484</i>
LOC107800087	2.3	<i>probable polyamine oxidase 4</i>
LOC107812610	2.3	<i>β-galactosidase-like</i>
LOC107826801	2.3	<i>secoisolariciresinol dehydrogenase-like</i>
LOC107773523	2.3	<i>protein FLUORESCENT IN BLUE LIGHT, chloroplastic-like</i>
LOC107765731	2.3	<i>21 kDa protein-like</i>
LOC107784408	2.3	<i>uncharacterized LOC107784408</i>
LOC107814069	2.3	<i>uncharacterized LOC107814069</i>
LOC107774509	2.3	<i>ethylene-responsive transcription factor 5-like</i>
LOC107798138	2.3	<i>uncharacterized LOC107798138</i>
LOC107783575	2.3	<i>nicotinamidase 2-like</i>
LOC107829118	2.3	<i>uroporphyrinogen decarboxylase, chloroplastic-like</i>
LOC107802154	2.3	<i>photosynthetic NDH subunit of lumenal location 5, chloroplastic-like</i>
LOC107812388	2.3	<i>uncharacterized LOC107812388</i>
LOC107815772	2.3	<i>uncharacterized LOC107815772</i>
LOC107778342	2.3	<i>epsin-like</i>
LOC107772739	2.3	<i>glycine cleavage system H protein, mitochondrial</i>
LOC107809769	2.3	<i>omega-6 fatty acid desaturase, chloroplastic-like</i>
LOC107816420	2.3	<i>uncharacterized LOC107816420</i>
LOC107810718	2.3	<i>uncharacterized LOC107810718</i>
LOC107781838	2.3	<i>rust resistance kinase Lr10-like</i>
LOC107830197	2.3	.
LOC107775757	2.3	<i>3-oxoacyl-[acyl-carrier-protein] synthase I, chloroplastic-like</i>
LOC107777352	2.3	<i>hydroxymethylglutaryl-CoA synthase-like</i>
LOC107772738	2.3	<i>cytochrome P450 71A4-like</i>
LOC107773564	2.3	<i>UDP-glucuronate 4-epimerase 1-like</i>
LOC107781891	2.3	<i>bifunctional UDP-glucose 4-epimerase and UDP-xylose 4-epimerase 1-like</i>
LOC107786804	2.3	<i>peptidyl-prolyl cis-trans isomerase CYP38, chloroplastic</i>
LOC107803192	2.3	<i>3-oxoacyl-[acyl-carrier-protein] synthase I, chloroplastic-like</i>
LOC107794418	2.3	<i>protein SPA, chloroplastic-like</i>
LOC107776229	2.2	<i>chlorophyll a-b binding protein 21, chloroplastic</i>
LOC107821994	2.2	<i>hevamine-A-like</i>
LOC107773365	2.2	<i>2-methyl-6-phytyl-1,4-hydroquinone methyltransferase, chloroplastic-like</i>
LOC107789964	2.2	<i>microtubule-associated protein TORTIFOLIA1-like</i>
LOC107760041	2.2	<i>50S ribosomal protein L6, chloroplastic-like</i>
LOC107826042	2.2	<i>acetyl-coenzyme A carboxylase carboxyl transferase subunit α, chloroplastic-like</i>
LOC107830733	2.2	<i>photosystem II stability/assembly factor HCF136, chloroplastic-like</i>
LOC107779625	2.2	<i>enoyl-[acyl-carrier-protein] reductase [NADH], chloroplastic-like</i>
LOC107783673	2.2	<i>uncharacterized LOC107783673</i>
LOC107800299	2.2	<i>uncharacterized LOC107800299</i>
LOC107797922	2.2	<i>protein LONGIFOLIA 2-like</i>
LOC107819763	2.2	<i>probable serine/threonine-protein kinase At1g01540</i>
LOC107794025	2.2	<i>E3 ubiquitin-protein ligase MIEL1-like</i>
LOC107780285	2.2	<i>translocon-associated protein subunit α-like</i>
LOC107800584	2.2	<i>uncharacterized LOC107800584</i>
LOC107799363	2.2	<i>uncharacterized LOC107799363</i>

LOC107797441	2.2	<i>uncharacterized LOC107797441</i>
LOC107807036	2.2	<i>subtilisin-like protease SBT2.5</i>
LOC107826653	2.2	<i>uncharacterized protein ycf39-like</i>
LOC107761885	2.2	<i>uncharacterized LOC107761885</i>
LOC107770365	2.2	<i>uncharacterized LOC107770365</i>
LOC107796776	2.2	<i>3-ketoacyl-CoA synthase 6-like</i>
LOC107769537	2.2	<i>upstream activation factor subunit spp27-like</i>
LOC107788629	2.2	<i>ninja-family protein AFP3-like</i>
LOC107763426	2.2	<i>tetrapyrrole-binding protein, chloroplastic-like</i>
LOC107798564	2.2	<i>delta-aminolevulinic acid dehydratase, chloroplastic-like</i>
LOC107796328	2.2	<i>putative E3 ubiquitin-protein ligase LIN</i>
LOC107806069	2.2	<i>sphingolipid delta(4)-desaturase DES1-like</i>
LOC107811877	2.2	<i>protein IQ-DOMAIN 1-like</i>
LOC107829548	2.2	<i>uncharacterized LOC107829548</i>
LOC107793161	2.2	<i>ethylene-responsive transcription factor ERF061-like</i>
LOC107796017	2.2	<i>lysosomal Pro-X carboxypeptidase-like</i>
LOC107774960	2.2	<i>uncharacterized LOC107774960</i>
LOC107798332	2.2	.
LOC107830918	2.2	<i>lycopene epsilon cyclase, chloroplastic-like</i>
LOC107762170	2.2	<i>AP2/ERF and B3 domain-containing transcription factor RAV1-like</i>
LOC107795962	2.2	<i>probable polygalacturonase</i>
LOC107816296	2.2	<i>uncharacterized LOC107816296</i>
LOC107827350	2.2	<i>2-phytyl-1,4-β-naphthoquinone methyltransferase, chloroplastic-like</i>
LOC107785549	2.2	.
LOC107798622	2.2	<i>probable WRKY transcription factor 40</i>
LOC107827673	2.2	<i>glycine-rich protein-like</i>
LOC107773728	2.2	<i>transcription factor TCP5-like</i>
LOC107766783	2.2	<i>BAG family molecular chaperone regulator 3-like</i>
LOC107767666	2.2	<i>lamin-like protein</i>
LOC107816458	2.2	<i>uncharacterized LOC107816458</i>
LOC107815824	2.2	<i>pyrophosphate-energized vacuolar membrane proton pump-like</i>
LOC107801536	2.2	<i>preprotein translocase subunit SECE1-like</i>
LOC107798211	2.2	<i>tRNA uridine 5-carboxymethylaminomethyl modification enzyme MnmG-like</i>
LOC107774426	2.2	<i>early nodulin-like protein 2</i>
LOC107830818	2.2	<i>50S ribosomal protein L18, chloroplastic-like</i>
LOC107761153	2.2	<i>transcription factor DIVARICATA-like</i>
LOC107806591	2.2	<i>uncharacterized LOC107806591</i>
LOC107799246	2.2	<i>membrane protein of ER body-like protein</i>
LOC107814761	2.2	<i>pollen-specific protein C13-like</i>
LOC107816664	2.2	<i>abscisic acid receptor PYL4-like</i>
LOC107809788	2.2	<i>probable xyloglucan endotransglucosylase/hydrolase protein 28</i>
LOC107791402	2.2	<i>abscisic acid 8'-hydroxylase 1-like</i>
LOC107802809	2.2	<i>putative late blight resistance protein homolog R1A-4</i>
LOC107804926	2.2	<i>internal alternative NAD(P)H-ubiquinone oxidoreductase A1, mitochondrial-like</i>
LOC107795406	2.2	<i>uncharacterized LOC107795406</i>
LOC107826831	2.2	<i>RING-H2 finger protein ATL38-like</i>
LOC107809027	2.2	<i>NAD(P)H-quinone oxidoreductase subunit M, chloroplastic-like</i>
LOC107771278	2.2	<i>50S ribosomal protein L18, chloroplastic</i>
LOC107808853	2.2	<i>photosynthetic NDH subunit of lumenal location 4, chloroplastic-like</i>
LOC107770736	2.2	<i>protein PMR5-like</i>

LOC107824317	2.2	<i>uncharacterized LOC107824317</i>
LOC107762739	2.2	<i>probable pectate lyase 13</i>
LOC107797915	2.2	<i>protein FANTASTIC FOUR 1-like</i>
LOC107811550	2.2	<i>uncharacterized LOC107811550</i>
psbl	2.2	.
LOC107829409	2.2	<i>protein RADIALIS-like 1</i>
LOC107763650	2.2	<i>protein CURVATURE THYLAKOID 1B, chloroplastic-like</i>
LOC107793435	2.2	<i>ribulose biphosphate carboxylase/oxygenase activase 1, chloroplastic-like</i>
LOC107812824	2.2	<i>protein CHLORORESPIRATORY REDUCTION 7, chloroplastic-like</i>
LOC107764627	2.2	<i>uncharacterized LOC107764627</i>
LOC107794468	2.2	<i>thiosulfate sulfurtransferase 16, chloroplastic-like</i>
LOC107797701	2.2	<i>probable receptor-like protein kinase At5g56460</i>
LOC107824524	2.2	<i>transcription factor DIVARICATA-like</i>
LOC107788958	2.2	<i>uncharacterized LOC107788958</i>
LOC107821710	2.2	<i>maf-like protein DDB_G0281937</i>
LOC107792593	2.2	<i>uncharacterized LOC107792593</i>
LOC107776709	2.2	<i>rubredoxin-like</i>
LOC107761249	2.2	<i>zinc finger protein CONSTANS-LIKE 16-like</i>
LOC107829496	2.2	<i>nucleoside diphosphate kinase 2, chloroplastic-like</i>
LOC107815881	2.2	<i>uncharacterized LOC107815881</i>
LOC107818393	2.2	<i>glycine-rich RNA-binding protein 8-like</i>
LOC107760716	2.2	<i>uncharacterized LOC107760716</i>
LOC107802603	2.2	<i>porphobilinogen deaminase, chloroplastic-like</i>
LOC107815755	2.2	<i>probable adenylate kinase 7, mitochondrial</i>
LOC107799535	2.2	<i>uncharacterized LOC107799535</i>
LOC107774749	2.2	<i>probable LRR receptor-like serine/threonine-protein kinase At1g67720</i>
LOC107818331	2.2	<i>LRR receptor-like serine/threonine-protein kinase GSO1</i>
LOC107832820	2.2	<i>phospholipase A1-II 1-like</i>
LOC107822960	2.2	<i>β-D-xylosidase 1-like</i>
LOC107802356	2.2	<i>protein GrpE-like</i>
LOC107792268	2.2	<i>uncharacterized zinc finger CCHC domain-containing protein At4g19190</i>
LOC107787836	2.1	<i>dihydroxy-acid dehydratase, chloroplastic-like</i>
LOC107786262	2.1	<i>B-box zinc finger protein 21-like</i>
LOC107778570	2.1	<i>protein IQ-DOMAIN 1-like</i>
LOC107830749	2.1	<i>auxin-induced protein 22D-like</i>
LOC107818231	2.1	<i>release factor glutamine methyltransferase-like</i>
LOC107784902	2.1	<i>protein TIC 62, chloroplastic-like</i>
LOC107760472	2.1	<i>S-norococlaurine synthase 1-like</i>
LOC107816377	2.1	<i>protein PMR5-like</i>
LOC107820813	2.1	<i>peptidyl-prolyl cis-trans isomerase FKBP18, chloroplastic-like</i>
LOC107810808	2.1	<i>uncharacterized LOC107810808</i>
LOC107794696	2.1	<i>subtilisin-like protease SBT2.5</i>
LOC107826360	2.1	<i>catalase isozyme 1-like</i>
LOC107782072	2.1	<i>uncharacterized LOC107782072</i>
LOC107766389	2.1	<i>maf-like protein DDB_G0281937</i>
LOC107815524	2.1	<i>oxygen-dependent coproporphyrinogen-III oxidase, chloroplastic</i>
LOC107765998	2.1	<i>peptidyl-prolyl cis-trans isomerase FKBP16-3, chloroplastic-like</i>
LOC107818655	2.1	<i>ethylene-responsive transcription factor ERF106-like</i>
LOC107825540	2.1	<i>protochlorophyllide reductase, chloroplastic-like</i>
LOC107772839	2.1	<i>uncharacterized LOC107772839</i>

LOC107803095	2.1	<i>auxilin-like protein 1</i>
LOC107796488	2.1	<i>30S ribosomal protein 3, chloroplastic-like</i>
LOC107767963	2.1	<i>arginine decarboxylase</i>
LOC107830424	2.1	<i>NAD(P)H:quinone oxidoreductase-like</i>
LOC107766169	2.1	<i>uncharacterized LOC107766169</i>
LOC107822890	2.1	<i>RNA-binding protein 24-like</i>
LOC107820884	2.1	<i>probable carbohydrate esterase At4g34215</i>
LOC107825362	2.1	<i>photosystem II reaction center W protein, chloroplastic-like</i>
LOC107792681	2.1	<i>3-hydroxyisobutyryl-CoA hydrolase-like protein 1, mitochondrial</i>
LOC107830453	2.1	<i>geranylgeranyl diphosphate reductase, chloroplastic-like</i>
LOC107782580	2.1	.
LOC107775512	2.1	<i>thioredoxin-like protein CITRX1, chloroplastic</i>
LOC107775352	2.1	<i>thylakoid lumenal 17.9 kDa protein, chloroplastic-like</i>
LOC107803670	2.1	<i>cellulose synthase-like protein E1</i>
LOC107809578	2.1	<i>α-L-arabinofuranosidase 1-like</i>
LOC107820363	2.1	<i>protein CURVATURE THYLAKOID 1A, chloroplastic-like</i>
LOC107783257	2.1	<i>geranylgeranyl diphosphate reductase, chloroplastic</i>
LOC107823267	2.1	<i>tubulin α-3 chain</i>
LOC107828876	2.1	<i>protein EXORDIUM-like</i>
LOC107798300	2.1	<i>uncharacterized LOC107798300</i>
LOC107815456	2.1	<i>inositol polyphosphate multikinase α-like</i>
LOC107820555	2.1	<i>endoglucanase 25-like</i>
LOC107802456	2.1	<i>cysteine-rich receptor-like protein kinase 3</i>
LOC107829909	2.1	<i>3-hydroxyacyl-[acyl-carrier-protein] dehydratase FabZ-like</i>
LOC107784643	2.1	<i>3-ketoacyl-CoA synthase 6-like</i>
LOC107767592	2.1	<i>uncharacterized LOC107767592</i>
LOC107767835	2.1	<i>transcription factor MYB44-like</i>
LOC107829353	2.1	<i>uncharacterized LOC107829353</i>
LOC107830873	2.1	<i>ethylene-responsive transcription factor 4-like</i>
LOC107799054	2.1	<i>RING-H2 finger protein ATL72-like</i>
psaB	2.1	.
LOC107777304	2.1	<i>thioredoxin-like 3-1, chloroplastic</i>
LOC107799644	2.1	<i>zinc finger protein CONSTANS-LIKE 6-like</i>
LOC107799338	2.1	<i>uncharacterized LOC107799338</i>
LOC107775004	2.1	<i>light-inducible protein CPRF2-like</i>
LOC107759209	2.1	<i>bifunctional epoxide hydrolase 2-like</i>
LOC107814768	2.1	<i>2-Cys peroxiredoxin BAS1, chloroplastic-like</i>
LOC107779630	2.1	<i>protein LOW PSII ACCUMULATION 1, chloroplastic-like</i>
LOC107770826	2.1	<i>photosynthetic NDH subunit of lumenal location 3, chloroplastic-like</i>
LOC107766361	2.1	<i>probable ribosome-binding factor A, chloroplastic</i>
LOC107809011	2.1	<i>uncharacterized LOC107809011</i>
LOC107771063	2.1	<i>putative RING-H2 finger protein ATL37</i>
LOC107779615	2.1	<i>cytochrome P450 90B1-like</i>
LOC107772965	2.1	<i>uncharacterized LOC107772965</i>
LOC107766654	2.1	<i>uncharacterized LOC107766654</i>
LOC107770182	2.1	<i>uncharacterized LOC107770182</i>
LOC107761514	2.1	<i>uncharacterized membrane protein YjcL-like</i>
LOC107778043	2.1	<i>zinc finger CCCH domain-containing protein 2-like</i>
LOC107814068	2.1	<i>α-mannosidase-like</i>
LOC107772032	2.1	<i>GATA transcription factor 4-like</i>

LOC107766981	2.1	<i>BURP domain protein USPL1-like</i>
LOC107802475	2.1	<i>uncharacterized LOC107802475</i>
LOC107776099	2.1	<i>protein RADIALIS-like 1</i>
LOC107806638	2.1	<i>auxin response factor 9-like</i>
LOC107816590	2.1	<i>auxin-induced protein 22D-like</i>
LOC107812828	2.1	<i>DCN1-like protein 4</i>
LOC107778980	2.1	<i>alkaline/neutral invertase A, mitochondrial-like</i>
LOC107769373	2.1	<i>F-actin-capping protein subunit α-like</i>
LOC107768964	2.1	<i>30S ribosomal protein S6 α, chloroplastic-like</i>
LOC107761018	2.1	<i>50S ribosomal protein L3-2, chloroplastic-like</i>
LOC107793798	2.1	<i>(+)-neomenthol dehydrogenase-like</i>
LOC107770791	2.1	<i>aquaporin NIP1-1-like</i>
LOC107823255	2.1	<i>inactive protein kinase SELMODRAFT_444075-like</i>
LOC107761626	2.1	<i>uncharacterized LOC107761626</i>
LOC107802618	2.1	<i>WUSCHEL-related homeobox 8-like</i>
LOC107806267	2.1	<i>uncharacterized LOC107806267</i>
LOC107766330	2.1	<i>protein MID1-COMPLEMENTING ACTIVITY 1-like</i>
LOC107772775	2.1	<i>syntaxin-71-like</i>
LOC107814192	2.1	<i>acetolactate synthase 1, chloroplastic-like</i>
LOC107790852	2.1	<i>serine/threonine-protein kinase STY46-like</i>
LOC107820645	2.1	<i>uncharacterized LOC107820645</i>
LOC107777797	2.1	<i>uncharacterized LOC107777797</i>
LOC107807794	2.1	<i>transcription factor bHLH93-like</i>
LOC107807409	2.1	<i>methylecgonone reductase-like</i>
LOC107764062	2.1	<i>50S ribosomal protein 6, chloroplastic</i>
LOC107816863	2.1	<i>uncharacterized LOC107816863</i>
LOC107808435	2.1	<i>protein CURVATURE THYLAKOID 1A, chloroplastic-like</i>
LOC107797242	2.1	<i>peptidyl-prolyl cis-trans isomerase FKBP19, chloroplastic-like</i>
LOC107818698	2.1	.
LOC107795678	2.1	<i>PLASMODESMATA CALLOSE-BINDING PROTEIN 3-like</i>
LOC107800100	2.1	<i>24-methylenesterol C-methyltransferase 2-like</i>
LOC107787072	2.1	<i>rhodanese-like domain-containing protein 11, chloroplastic</i>
LOC107824830	2.1	<i>rubredoxin-like</i>
LOC107811518	2.1	<i>protein IQ-DOMAIN 1-like</i>
LOC107813548	2.1	<i>uncharacterized LOC107813548</i>
LOC107791770	2.1	<i>ribulose biphosphate carboxylase small chain S41, chloroplastic-like</i>
psbK	2.1	.
LOC107806705	2.0	<i>uncharacterized LOC107806705</i>
LOC107784674	2.0	<i>uncharacterized LOC107784674</i>
LOC107827610	2.0	<i>putative rRNA methylase YtqB</i>
LOC107795290	2.0	<i>uncharacterized LOC107795290</i>
LOC107819116	2.0	<i>uncharacterized LOC107819116</i>
LOC107768418	2.0	<i>acyl-lipid (9-3)-desaturase-like</i>
LOC107825140	2.0	<i>ribosome-recycling factor, chloroplastic-like</i>
LOC107803758	2.0	<i>uncharacterized LOC107803758</i>
LOC107802823	2.0	<i>porphobilinogen deaminase, chloroplastic-like</i>
LOC107816446	2.0	<i>uncharacterized LOC107816446</i>
LOC107774635	2.0	<i>stearoyl-[acyl-carrier-protein] 9-desaturase, chloroplastic</i>
LOC107773926	2.0	<i>probable inactive receptor kinase At2g26730</i>
LOC107782003	2.0	<i>protein GLUTAMINE DUMPER 2-like</i>

LOC107775041	2.0	<i>bifunctional UDP-glucose 4-epimerase and UDP-xylose 4-epimerase 1-like</i>
LOC107802206	2.0	<i>uncharacterized LOC107802206</i>
LOC107824248	2.0	<i>50S ribosomal protein L13, chloroplastic-like</i>
LOC107832570	2.0	<i>probable NAD(P)H dehydrogenase subunit CRR3, chloroplastic</i>
LOC107813196	2.0	<i>phosphoenolpyruvate carboxylase kinase 1-like</i>
LOC107818307	2.0	<i>probable receptor-like protein kinase At1g80640</i>
LOC107789905	2.0	<i>protein TIC 100-like</i>
LOC107825184	2.0	<i>alkane hydroxylase MAH1-like</i>
LOC107770672	2.0	<i>photosystem I reaction center subunit III, chloroplastic-like</i>
LOC107816776	2.0	<i>UDP-glucuronate 4-epimerase 6-like</i>
LOC107767301	2.0	<i>glyceraldehyde-3-phosphate dehydrogenase B, chloroplastic-like</i>
LOC107800803	2.0	<i>α-xylosidase 1-like</i>
LOC107826869	2.0	<i>RING-H2 finger protein ATL34-like</i>
LOC107811668	2.0	<i>uncharacterized LOC107811668</i>
LOC107777044	2.0	<i>uncharacterized LOC107777044</i>
LOC107800173	2.0	<i>uncharacterized LOC107800173</i>
LOC107765219	2.0	<i>3-hydroxy-3-methylglutaryl-coenzyme A reductase 1-like</i>
LOC107803895	2.0	<i>non-specific lipid-transfer protein-like protein At2g13820</i>
LOC107808171	2.0	<i>putative G3BP-like protein</i>
LOC107773771	2.0	<i>aspartate aminotransferase, cytoplasmic</i>
LOC107813278	2.0	<i>phosphoglycolate phosphatase-like</i>
LOC107803761	2.0	<i>probable methyltransferase PMT21</i>
LOC107815412	2.0	<i>photosystem I reaction center subunit IV B, chloroplastic</i>
LOC107810928	2.0	.
LOC107784558	2.0	<i>RING-H2 finger protein ATL8-like</i>
LOC107808989	2.0	<i>probable pectinesterase/pectinesterase inhibitor 61</i>
LOC107828980	2.0	<i>BAG family molecular chaperone regulator 7-like</i>
LOC107818052	2.0	<i>transcription factor bHLH79-like</i>
LOC107780929	2.0	<i>uncharacterized LOC107780929</i>
LOC107805982	2.0	<i>uncharacterized LOC107805982</i>
LOC107806770	2.0	<i>uncharacterized LOC107806770</i>
LOC107775253	2.0	<i>psbQ-like protein 3, chloroplastic</i>
LOC107766963	2.0	<i>putative glycine-rich cell wall structural protein 1</i>
LOC107779933	2.0	<i>photosystem I reaction center subunit II, chloroplastic-like</i>
LOC107774123	2.0	<i>50S ribosomal protein L27, chloroplastic</i>
LOC107775975	2.0	<i>ethylene-responsive transcription factor ERF118-like</i>
LOC107761768	2.0	<i>signal recognition particle 43 kDa protein, chloroplastic-like</i>
LOC107826614	2.0	<i>zinc finger protein CONSTANS-LIKE 4-like</i>
LOC107803119	2.0	<i>uncharacterized LOC107803119</i>
LOC107763149	2.0	<i>photosystem I reaction center subunit II, chloroplastic-like</i>
LOC107771799	2.0	<i>50S ribosomal protein L24, chloroplastic-like</i>
LOC107774008	2.0	<i>60S ribosomal protein L23</i>
LOC107798154	2.0	<i>acyl carrier protein 1, chloroplastic-like</i>
LOC107784969	2.0	<i>uncharacterized LOC107784969</i>
LOC107810840	2.0	<i>kirola-like</i>
LOC107820742	2.0	<i>phosphatidylinositol 4-kinase α 2-like</i>
LOC107802178	2.0	<i>probable LRR receptor-like serine/threonine-protein kinase MRH1</i>
LOC107777780	2.0	<i>protein NDH-DEPENDENT CYCLIC ELECTRON FLOW 5-like</i>
LOC107797489	2.0	<i>dihydrolipoyllysine-residue acetyltransferase component 5 of pyruvate dehydrogen</i>
LOC107810096	2.0	<i>uncharacterized LOC107810096</i>

LOC107794159	2.0	<i>photosystem I reaction center subunit V, chloroplastic-like</i>
LOC107788273	-2.0	<i>uncharacterized LOC107788273</i>
LOC107764844	-2.0	<i>protein MEI2-like 2</i>
LOC107767738	-2.0	<i>reticulon-like protein B5</i>
LOC107759306	-2.0	<i>uncharacterized LOC107759306</i>
LOC107766034	-2.0	<i>E3 ubiquitin-protein ligase RHA1B-like</i>
LOC107782785	-2.0	<i>jacalin-related lectin 3-like</i>
LOC107802777	-2.0	<i>putative SERF-like protein</i>
LOC107782555	-2.0	<i>uncharacterized LOC107782555</i>
LOC107813765	-2.0	<i>putative NAC domain-containing protein 94</i>
LOC107820210	-2.0	<i>short-chain dehydrogenase TIC 32, chloroplastic-like</i>
LOC107816692	-2.0	<i>probable receptor-like protein kinase At5g47070</i>
LOC107780851	-2.0	<i>L-ascorbate oxidase-like</i>
LOC107766292	-2.0	<i>probable calcium-binding protein CML35</i>
LOC107812832	-2.0	<i>GDP-L-galactose phosphorylase 1-like</i>
LOC107785346	-2.0	<i>1-aminocyclopropane-1-carboxylate oxidase</i>
LOC107810298	-2.0	<i>serine/threonine-protein kinase HT1-like</i>
LOC107799583	-2.0	<i>catalase isozyme 1</i>
LOC107829293	-2.0	<i>kynurenine formamidase-like</i>
LOC107785545	-2.0	<i>aquaporin PIP2-1-like</i>
LOC107807136	-2.0	<i>ubiquitin-conjugating enzyme E2 2</i>
LOC107777753	-2.0	<i>U-box domain-containing protein 2</i>
LOC107808402	-2.0	<i>mitochondrial phosphate carrier protein 3, mitochondrial-like</i>
LOC107786634	-2.0	<i>digalactosyldiacylglycerol synthase 1, chloroplastic-like</i>
LOC107821365	-2.0	<i>actin-depolymerizing factor 2-like</i>
LOC107765182	-2.0	<i>clathrin light chain 2-like</i>
LOC107775371	-2.0	<i>glycine cleavage system H protein 2, mitochondrial-like</i>
LOC107805240	-2.0	<i>peroxisomal (S)-2-hydroxy-acid oxidase GLO4-like</i>
LOC107770606	-2.0	<i>uncharacterized protein ycf45-like</i>
LOC107802472	-2.0	<i>homeobox-leucine zipper protein HAT5-like</i>
LOC107778181	-2.0	<i>uncharacterized LOC107778181</i>
LOC107790218	-2.0	<i>uncharacterized LOC107790218</i>
LOC107772225	-2.0	<i>uncharacterized LOC107772225</i>
LOC107831596	-2.0	<i>homocysteine S-methyltransferase 2-like</i>
LOC107780344	-2.0	<i>nudix hydrolase 15, mitochondrial-like</i>
LOC107773570	-2.0	<i>tetraspanin-8-like</i>
LOC107826982	-2.0	<i>scopoletin glucosyltransferase</i>
LOC107798176	-2.0	<i>BTB/POZ and MATH domain-containing protein 2-like</i>
LOC107775713	-2.0	<i>non-specific phospholipase C2</i>
LOC107788319	-2.0	<i>probable terpene synthase 3</i>
LOC107816898	-2.0	<i>uncharacterized LOC107816898</i>
LOC107772321	-2.0	<i>protein phosphatase 2C 16-like</i>
LOC107809051	-2.0	<i>calreticulin-3-like</i>
LOC107787302	-2.0	<i>probable WRKY transcription factor 41</i>
LOC107794162	-2.0	<i>uncharacterized WD repeat-containing protein C2A9.03-like</i>
LOC107809445	-2.0	<i>uncharacterized LOC107809445</i>
LOC107785806	-2.0	<i>F-box protein At2g16365-like</i>
LOC107817239	-2.0	<i>xyloglucan endotransglucosylase/hydrolase protein 31-like</i>
LOC107763851	-2.0	<i>protein TIFY 10c-like</i>
LOC107775662	-2.0	<i>uncharacterized LOC107775662</i>

LOC107830849	-2.0	<i>cysteine-rich receptor-like protein kinase 10</i>
LOC107775919	-2.0	<i>defensin-like protein P322</i>
LOC107781040	-2.0	<i>outer envelope pore protein 16, chloroplastic-like</i>
LOC107820014	-2.0	<i>exocyst complex component EXO70A1-like</i>
LOC107811585	-2.0	<i>glutathione S-transferase zeta class-like</i>
LOC107800679	-2.0	<i>glycine-rich RNA-binding protein-like</i>
LOC107787860	-2.0	<i>probable pectate lyase 4</i>
LOC107832451	-2.0	<i>CBS domain-containing protein CBSCBSPB1-like</i>
LOC107813188	-2.0	<i>homeobox-leucine zipper protein ATHB-6-like</i>
LOC107783258	-2.0	<i>malate dehydrogenase, chloroplastic-like</i>
LOC107818598	-2.0	<i>aspartic proteinase-like</i>
LOC107802840	-2.0	<i>SNF1-related protein kinase catalytic subunit α KIN10-like</i>
LOC107830770	-2.0	<i>nuclear transcription factor Y subunit A-9-like</i>
LOC107781926	-2.0	<i>probable aquaporin PIP1-2</i>
LOC107790947	-2.0	<i>calmodulin-binding protein 60 A-like</i>
LOC107827614	-2.0	<i>metal tolerance protein 9-like</i>
LOC107777896	-2.0	<i>protein DETOXIFICATION 40-like</i>
LOC107811351	-2.0	<i>CASP-like protein ARALYDRAFT_485429</i>
LOC107785811	-2.0	<i>receptor-like protein 12</i>
LOC107795609	-2.0	<i>methylsterol monooxygenase 2-2-like</i>
LOC107831869	-2.0	<i>uncharacterized oxidoreductase At4g09670-like</i>
LOC107800630	-2.0	<i>myosin-11-like</i>
LOC107780707	-2.0	<i>uncharacterized LOC107780707</i>
LOC107785406	-2.1	<i>tuberculostearic acid methyltransferase UfaA1-like</i>
LOC107810817	-2.1	<i>receptor-like protein kinase HAIKU2</i>
LOC107764653	-2.1	<i>uncharacterized LOC107764653</i>
LOC107787785	-2.1	<i>zinc finger CCCH domain-containing protein 30-like</i>
LOC107773033	-2.1	<i>uncharacterized LOC107773033</i>
LOC107809310	-2.1	<i>protein ECERIFERUM 1-like</i>
LOC107795995	-2.1	<i>protein CHAPERONE-LIKE PROTEIN OF POR1, chloroplastic-like</i>
LOC107789602	-2.1	<i>uncharacterized LOC107789602</i>
LOC107816628	-2.1	<i>cinnamoyl-CoA reductase 1-like</i>
LOC107778716	-2.1	<i>uncharacterized LOC107778716</i>
LOC107832748	-2.1	<i>glutathione synthetase, chloroplastic</i>
LOC107786400	-2.1	<i>peroxisomal fatty acid β-oxidation multifunctional protein AIM1-like</i>
LOC107777855	-2.1	<i>somatic embryogenesis receptor kinase 2-like</i>
LOC107800412	-2.1	<i>probable aspartyl aminopeptidase</i>
LOC107814420	-2.1	<i>G-type lectin S-receptor-like serine/threonine-protein kinase At2g19130</i>
LOC107832525	-2.1	<i>proteinase inhibitor PSI-1.2-like</i>
LOC107814830	-2.1	<i>uncharacterized protein At1g76660-like</i>
LOC107761179	-2.1	<i>dehydrin HIRD11-like</i>
LOC107797035	-2.1	<i>4-coumarate--CoA ligase-like 7</i>
LOC107792921	-2.1	<i>plastidic ATP/ADP-transporter-like</i>
LOC107800341	-2.1	<i>zinc finger A20 and AN1 domain-containing stress-associated protein 8-like</i>
LOC107803496	-2.1	<i>CBS domain-containing protein CBSX1, chloroplastic-like</i>
LOC107760324	-2.1	<i>abscisic acid receptor PYL9-like</i>
LOC107817286	-2.1	<i>probable WRKY transcription factor 7</i>
LOC107779747	-2.1	<i>uncharacterized LOC107779747</i>
LOC107823695	-2.1	<i>expansin-like B1</i>
LOC107780466	-2.1	<i>7-deoxyloganetic acid glucosyltransferase-like</i>

LOC107767041	-2.1	<i>plant intracellular Ras-group-related LRR protein 5-like</i>
LOC107785690	-2.1	<i>NADP-dependent glyceraldehyde-3-phosphate dehydrogenase</i>
LOC107787118	-2.1	<i>aspartic proteinase-like</i>
LOC107804363	-2.1	<i>serine acetyltransferase 2-like</i>
LOC107782898	-2.1	<i>protein argonaute 10-like</i>
LOC107815995	-2.1	<i>abscisic acid receptor PYL2-like</i>
LOC107785179	-2.1	<i>homeobox-leucine zipper protein HAT5-like</i>
LOC107778557	-2.1	.
LOC107763415	-2.1	<i>uncharacterized LOC107763415</i>
LOC107762702	-2.1	<i>regulatory protein NPR3-like</i>
LOC107781193	-2.1	<i>amino acid transporter ANTL1-like</i>
LOC107824520	-2.1	<i>photosynthetic NDH subunit of subcomplex B 3, chloroplastic-like</i>
LOC107800751	-2.1	<i>uncharacterized LOC107800751</i>
LOC107771709	-2.1	<i>uncharacterized LOC107771709</i>
LOC107782875	-2.1	<i>abscisic stress-ripening protein 2-like</i>
LOC107777347	-2.1	<i>protein LURP-one-related 10-like</i>
LOC107760261	-2.1	<i>uncharacterized LOC107760261</i>
LOC107766078	-2.1	<i>putative UPF0481 protein At3g02645</i>
LOC107821924	-2.1	<i>WAT1-related protein At1g09380-like</i>
LOC107807552	-2.1	<i>dirigent protein 22-like</i>
LOC107814972	-2.1	<i>uncharacterized LOC107814972</i>
LOC107803582	-2.1	<i>uncharacterized LOC107803582</i>
LOC107824109	-2.1	<i>thioredoxin H2-like</i>
LOC107767998	-2.1	<i>HMG1/2-like protein</i>
LOC107780280	-2.1	<i>leucine-rich repeat receptor-like tyrosine-protein kinase PXC3</i>
LOC107801191	-2.1	<i>cytochrome P450 78A5-like</i>
LOC107827983	-2.1	<i>phosphoenolpyruvate carboxylase kinase 1-like</i>
LOC107760100	-2.1	<i>zinc finger A20 and AN1 domain-containing stress-associated protein 4-like</i>
LOC107799015	-2.1	<i>gibberellin receptor GID1B-like</i>
LOC107820614	-2.1	<i>uncharacterized LOC107820614</i>
LOC107783010	-2.1	<i>glycine dehydrogenase (decarboxylating), mitochondrial-like</i>
LOC107794535	-2.1	<i>plastidial pyruvate kinase 4, chloroplastic-like</i>
LOC107759381	-2.1	<i>uncharacterized LOC107759381</i>
LOC107788857	-2.1	<i>AAA-ATPase At2g46620-like</i>
LOC107760145	-2.1	<i>uncharacterized LOC107760145</i>
LOC107830911	-2.1	<i>2-alkenal reductase (NADP(+)-dependent)-like</i>
LOC107778375	-2.1	<i>translationally-controlled tumor protein homolog</i>
LOC107818808	-2.1	<i>homeobox-leucine zipper protein ATHB-12-like</i>
LOC107822042	-2.1	<i>probable E3 ubiquitin-protein ligase XERICO</i>
LOC107789753	-2.1	<i>5'-adenylylsulfate reductase 3, chloroplastic-like</i>
LOC107813897	-2.1	<i>PLASMODESMATA CALLOSE-BINDING PROTEIN 3-like</i>
LOC107799451	-2.1	<i>BEL1-like homeodomain protein 1</i>
LOC107825570	-2.1	<i>uncharacterized LOC107825570</i>
LOC107830910	-2.1	<i>2-alkenal reductase (NADP(+)-dependent)</i>
LOC107795323	-2.1	<i>thioredoxin H-type 2-like</i>
LOC107772695	-2.1	<i>probably inactive leucine-rich repeat receptor-like protein kinase At5g48380</i>
LOC107818112	-2.1	<i>receptor-like protein kinase 5</i>
LOC107789430	-2.1	<i>uncharacterized LOC107789430</i>
LOC107795473	-2.1	<i>FACT complex subunit SPT16-like</i>
LOC107807620	-2.1	<i>E3 ubiquitin-protein ligase At3g02290-like</i>

LOC107806197	-2.1	<i>uncharacterized LOC107806197</i>
LOC107795333	-2.1	<i>uncharacterized LOC107795333</i>
LOC107775061	-2.1	<i>plasma membrane ATPase 3</i>
LOC107809266	-2.1	<i>probable sodium/metabolite cotransporter BASS3, chloroplastic</i>
LOC107787957	-2.1	<i>xyloglucan endotransglucosylase/hydrolase protein 9-like</i>
LOC107772220	-2.1	<i>scopoletin glucosyltransferase-like</i>
LOC107809659	-2.1	<i>UDP-glycosyltransferase 74E2-like</i>
LOC107789547	-2.1	<i>ubiquitin-conjugating enzyme E2 5B-like</i>
LOC107806751	-2.1	<i>uncharacterized LOC107806751</i>
LOC107825128	-2.1	<i>uncharacterized LOC107825128</i>
LOC107821946	-2.1	<i>E3 ubiquitin ligase BIG BROTHER-like</i>
LOC107778391	-2.1	<i>SPX domain-containing protein 1-like</i>
LOC107791229	-2.1	<i>acetate/butyrate--CoA ligase AAE7, peroxisomal-like</i>
LOC107774785	-2.1	<i>CBL-interacting serine/threonine-protein kinase 23-like</i>
LOC107785570	-2.1	<i>probable acyl-activating enzyme 17, peroxisomal</i>
LOC107809316	-2.1	<i>uncharacterized LOC107809316</i>
LOC107811873	-2.1	<i>BEL1-like homeodomain protein 1</i>
LOC107781740	-2.1	<i>VAN3-binding protein-like</i>
LOC107795522	-2.1	<i>plastidic ATP/ADP-transporter-like</i>
LOC107770720	-2.2	<i>homogentisate 1,2-dioxygenase-like</i>
LOC107781010	-2.2	<i>glycine dehydrogenase (decarboxylating), mitochondrial</i>
LOC107771831	-2.2	<i>probable sodium-coupled neutral amino acid transporter 6</i>
LOC107773293	-2.2	<i>inositol oxygenase 2-like</i>
LOC107782584	-2.2	<i>L-type lectin-domain containing receptor kinase VIII.1-like</i>
LOC107775774	-2.2	<i>α-glucan water dikinase, chloroplastic</i>
LOC107778719	-2.2	<i>protein yippee-like At5g53940</i>
LOC107794645	-2.2	<i>protein NRT1/ PTR FAMILY 2.13-like</i>
LOC107815999	-2.2	<i>1-aminocyclopropane-1-carboxylate oxidase 1</i>
LOC107805064	-2.2	<i>NAC transcription factor 56-like</i>
LOC107790940	-2.2	<i>uncharacterized LOC107790940</i>
LOC107801114	-2.2	<i>ACT domain-containing protein ACR10-like</i>
LOC107801815	-2.2	<i>α-glucosidase 2-like</i>
LOC107792392	-2.2	<i>protein ECERIFERUM 3-like</i>
LOC107790120	-2.2	<i>uncharacterized LOC107790120</i>
LOC107784657	-2.2	<i>uncharacterized LOC107784657</i>
LOC107794698	-2.2	<i>probable aquaporin PIP1-5</i>
LOC107768664	-2.2	<i>potassium transporter 11-like</i>
LOC107794509	-2.2	<i>CASP-like protein 1</i>
LOC107763145	-2.2	<i>jacalin-related lectin 19-like</i>
LOC107807809	-2.2	<i>auxin-responsive protein IAA26-like</i>
LOC107776271	-2.2	<i>acyl-protein thioesterase 1 homolog 1-like</i>
LOC107787033	-2.2	<i>ankycorbin-like</i>
LOC107775626	-2.2	<i>protein C2-DOMAIN ABA-RELATED 4-like</i>
LOC107821406	-2.2	<i>uncharacterized protein sll0005</i>
LOC107820904	-2.2	<i>uncharacterized LOC107820904</i>
LOC107797778	-2.2	<i>RING-H2 zinc finger protein RHA4a-like</i>
LOC107773674	-2.2	<i>G-box-binding factor 4-like</i>
LOC107832331	-2.2	<i>putative nuclease HARBI1</i>
LOC107775814	-2.2	<i>mitogen-activated protein kinase 19-like</i>
LOC107797101	-2.2	<i>myosin heavy chain kinase C-like</i>

LOC107829502	-2.2	cytochrome P450 82A4-like
LOC107812620	-2.2	uncharacterized LOC107812620
LOC107803391	-2.2	glutamate receptor 3.4-like
LOC107812305	-2.2	WAS/WASL-interacting protein family member 3-like
LOC107826177	-2.2	probable adenylate kinase 6, chloroplastic
LOC107793424	-2.2	dnaJ protein homolog
LOC107766900	-2.2	LRR receptor-like serine/threonine-protein kinase FLS2
LOC107820447	-2.2	metacaspase-3-like
LOC107788618	-2.2	amino acid permease 3-like
LOC107810442	-2.2	protein DETOXIFICATION 40-like
LOC107817549	-2.2	β -glucosidase BoGH3B-like
LOC107783342	-2.2	purple acid phosphatase 2-like
LOC107777454	-2.2	uncharacterized protein At4g00950-like
LOC107778022	-2.2	glycine-rich protein-like
LOC107761957	-2.2	potassium channel AKT2/3-like
LOC107783772	-2.2	uncharacterized LOC107783772
LOC107782783	-2.2	cytochrome P450 CYP736A12-like
LOC107819141	-2.2	uncharacterized LOC107819141
LOC107767887	-2.2	putative lactoylglutathione lyase
LOC107780320	-2.2	ornithine aminotransferase, mitochondrial-like
LOC107773632	-2.2	LEAF RUST 10 DISEASE-RESISTANCE LOCUS RECEPTOR-LIKE PROTEIN KI
LOC107780574	-2.2	uncharacterized LOC107780574
LOC107818184	-2.2	probable calcium-binding protein CML36
LOC107779761	-2.2	bifunctional riboflavin kinase/FMN phosphatase-like
LOC107827582	-2.2	REF/SRPP-like protein At3g05500
LOC107761993	-2.2	glycosyltransferase family protein 64 protein C5-like
LOC107808920	-2.2	probable peroxygenase 5
LOC107819908	-2.2	phosphoprotein ECPP44-like
LOC107818467	-2.2	sugar phosphatase YfbT-like
LOC107761466	-2.2	uncharacterized LOC107761466
LOC107787163	-2.2	protein LURP-one-related 17-like
LOC107820815	-2.2	protein DETOXIFICATION 27-like
LOC107763626	-2.2	uncharacterized LOC107763626
LOC107763202	-2.2	uncharacterized LOC107763202
LOC107780983	-2.2	serine/threonine-protein kinase SAPK3-like
LOC107767543	-2.2	protein UPSTREAM OF FLC-like
LOC107794399	-2.2	sphingosine-1-phosphate lyase
LOC107826672	-2.2	protein SRC2-like
LOC107793060	-2.2	autophagy-related protein 18f-like
LOC107760731	-2.2	uncharacterized LOC107760731
LOC107829052	-2.2	vacuolar-sorting receptor 1-like
LOC107780873	-2.2	protein-tyrosine-phosphatase MKP1-like
LOC107795874	-2.2	U-box domain-containing protein 4-like
LOC107771984	-2.2	uncharacterized protein At4g00950-like
LOC107761819	-2.3	probable protein phosphatase 2C 50
LOC107810092	-2.3	remorin-like
LOC107777191	-2.3	geraniol 8-hydroxylase-like
LOC107805164	-2.3	putative lactoylglutathione lyase
LOC107760898	-2.3	tuberculostearic acid methyltransferase UfaA1-like
LOC107798347	-2.3	ATP-dependent Clp protease ATP-binding subunit ClpA homolog CD4B, chloropla

LOC107790659	-2.3	<i>receptor like protein kinase S.2-like</i>
LOC107790585	-2.3	<i>zinc finger A20 and AN1 domain-containing stress-associated protein 8-like</i>
LOC107760413	-2.3	<i>ferric reduction oxidase 6-like</i>
LOC107798576	-2.3	<i>gamma-glutamyltranspeptidase 3-like</i>
LOC107831641	-2.3	<i>β-1,3-galactosyltransferase 7-like</i>
LOC107780317	-2.3	<i>uncharacterized LOC107780317</i>
LOC107805002	-2.3	<i>pheophorbide a oxygenase, chloroplastic-like</i>
LOC107776003	-2.3	<i>uncharacterized LOC107776003</i>
LOC107776262	-2.3	<i>uncharacterized LOC107776262</i>
LOC107799395	-2.3	<i>EID1-like F-box protein 3</i>
LOC107813538	-2.3	<i>metallothionein-like protein type 2</i>
LOC107829289	-2.3	.
LOC107783027	-2.3	<i>protein CHAPERONE-LIKE PROTEIN OF POR1, chloroplastic-like</i>
LOC107764465	-2.3	<i>plasma membrane-associated cation-binding protein 1-like</i>
LOC107786327	-2.3	<i>uncharacterized LOC107786327</i>
LOC107777843	-2.3	<i>fumarylacetoacetase-like</i>
LOC107760741	-2.3	<i>β-glucosidase-like SFR2, chloroplastic</i>
LOC107763337	-2.3	<i>putative lysine-specific demethylase JMJD5</i>
LOC107815635	-2.3	<i>U-box domain-containing protein 44-like</i>
LOC107779707	-2.3	<i>probable glutathione S-transferase</i>
LOC107820122	-2.3	<i>UDP-glucuronic acid decarboxylase 5-like</i>
LOC107787998	-2.3	<i>ureide permease 1-like</i>
LOC107761818	-2.3	<i>uncharacterized LOC107761818</i>
LOC107828070	-2.3	<i>calcium-dependent protein kinase 8-like</i>
LOC107782185	-2.3	<i>ABSCISIC ACID-INSENSITIVE 5-like protein 7</i>
LOC107823693	-2.3	<i>haloacid dehalogenase-like hydrolase domain-containing protein Sgpp</i>
LOC107821014	-2.3	<i>uncharacterized LOC107821014</i>
LOC107790390	-2.3	<i>uncharacterized LOC107790390</i>
LOC107827734	-2.3	<i>TGACG-sequence-specific DNA-binding protein TGA-1A-like</i>
LOC107771859	-2.3	<i>ATP-dependent Clp protease proteolytic subunit 5, chloroplastic-like</i>
LOC107827895	-2.3	<i>sulfate transporter 1.3-like</i>
LOC107792342	-2.3	<i>uncharacterized LOC107792342</i>
LOC107778898	-2.3	<i>bidirectional sugar transporter SWEET3-like</i>
LOC107767317	-2.3	<i>zinc transporter 8-like</i>
LOC107774103	-2.3	<i>transmembrane protein 230-like</i>
LOC107824084	-2.3	<i>glycine-rich protein A3-like</i>
LOC107796058	-2.3	<i>glutathione S-transferase T1-like</i>
LOC107809891	-2.3	<i>ACT domain-containing protein ACR6-like</i>
LOC107798611	-2.3	<i>zinc finger protein ZAT10-like</i>
LOC107806346	-2.3	<i>protein SRC2-like</i>
LOC107775583	-2.3	<i>non-specific lipid-transfer protein 1-like</i>
LOC107811368	-2.3	<i>E3 ubiquitin-protein ligase RNF5-like</i>
LOC107830771	-2.3	<i>probable protein phosphatase 2C 58</i>
LOC107783040	-2.3	<i>methyl-CpG-binding domain-containing protein 11-like</i>
LOC107769289	-2.3	<i>BOI-related E3 ubiquitin-protein ligase 1-like</i>
LOC107797488	-2.3	<i>leucine-rich repeat receptor-like tyrosine-protein kinase PXC3</i>
LOC107786583	-2.3	<i>B2 protein-like</i>
LOC107810498	-2.3	<i>phosphomethylpyrimidine synthase, chloroplastic</i>
LOC107771784	-2.3	<i>U-box domain-containing protein 52-like</i>
LOC107827490	-2.3	<i>transcription factor bHLH144-like</i>

LOC107795472	-2.3	<i>probable acyl-activating enzyme 6</i>
LOC107827940	-2.3	<i>nicotinamidase 1-like</i>
LOC107818093	-2.3	<i>cyprosin-like</i>
LOC107792477	-2.3	<i>ABC transporter G family member 22-like</i>
LOC107823371	-2.3	<i>NAC domain-containing protein 2-like</i>
LOC107772422	-2.3	<i>uncharacterized LOC107772422</i>
LOC107776034	-2.3	<i>CDP-diacylglycerol--serine O-phosphatidyltransferase 1-like</i>
LOC107802038	-2.3	<i>peroxidase 17-like</i>
LOC107824296	-2.3	<i>uncharacterized LOC107824296</i>
LOC107778731	-2.3	<i>chaperone protein ClpD, chloroplastic-like</i>
LOC107764913	-2.3	<i>serine/threonine-protein kinase HT1-like</i>
LOC107785428	-2.3	<i>ubiquitin-conjugating enzyme E2-17 kDa</i>
LOC107770509	-2.3	<i>glutathione S-transferase L3-like</i>
LOC107806665	-2.3	<i>patellin-3-like</i>
LOC107786841	-2.3	<i>CASP-like protein 5C1</i>
LOC107780184	-2.3	<i>probable isoaspartyl peptidase/L-asparaginase 2</i>
LOC107769367	-2.3	<i>aquaporin TIP4-1-like</i>
LOC107829355	-2.3	<i>uncharacterized LOC107829355</i>
LOC107821173	-2.3	<i>gamma aminobutyrate transaminase 3, chloroplastic</i>
LOC107808833	-2.3	<i>uncharacterized LOC107808833</i>
LOC107815447	-2.3	<i>probable protein phosphatase 2C 25</i>
LOC107810124	-2.4	<i>probable tyrosine-protein phosphatase At1g05000</i>
LOC107768764	-2.4	<i>glutamate dehydrogenase A</i>
LOC107808635	-2.4	<i>isopentenyl-diphosphate Delta-isomerase I-like</i>
LOC107780062	-2.4	<i>phosphoinositide phospholipase C 6-like</i>
LOC107765037	-2.4	<i>protein TIFY 6B-like</i>
LOC107821516	-2.4	<i>receptor-like protein kinase HAIKU2</i>
LOC107832044	-2.4	<i>histone H1-like</i>
LOC107818897	-2.4	<i>scarecrow-like protein 3</i>
LOC107789616	-2.4	<i>annexin D5-like</i>
LOC107774229	-2.4	<i>NAC domain-containing protein 74-like</i>
LOC107775428	-2.4	<i>polyol transporter 5-like</i>
LOC107823947	-2.4	<i>uncharacterized LOC107823947</i>
LOC107776835	-2.4	<i>gibberellin receptor GID1C-like</i>
LOC107768954	-2.4	<i>probable 6-phosphogluconolactonase 1</i>
LOC107767480	-2.4	<i>uncharacterized LOC107767480</i>
LOC107822791	-2.4	<i>UV-B-induced protein At3g17800, chloroplastic-like</i>
LOC107816753	-2.4	<i>protein TSS</i>
LOC107832203	-2.4	<i>β-galactosidase 8-like</i>
LOC107807419	-2.4	<i>MFP1 attachment factor 1-like</i>
LOC107803077	-2.4	<i>plastidial pyruvate kinase 4, chloroplastic-like</i>
LOC107782418	-2.4	<i>zinc transporter 8-like</i>
LOC107829655	-2.4	<i>uncharacterized LOC107829655</i>
LOC107795025	-2.4	<i>heptahelical transmembrane protein 4-like</i>
LOC107816973	-2.4	<i>glycosyltransferase family 92 protein RCOM_0530710-like</i>
LOC107773641	-2.4	<i>uncharacterized LOC107773641</i>
LOC107768181	-2.4	<i>uncharacterized LOC107768181</i>
LOC107765542	-2.4	<i>glutamate dehydrogenase A-like</i>
LOC107795825	-2.4	<i>protein DETOXIFICATION 27-like</i>
LOC107770659	-2.4	<i>heat shock cognate protein 80-like</i>

LOC107773745	-2.4	<i>probable protein phosphatase 2C 2</i>
LOC107801023	-2.4	<i>GTP-binding protein YPTM2-like</i>
LOC107778150	-2.4	<i>uncharacterized LOC107778150</i>
LOC107784267	-2.4	<i>uncharacterized LOC107784267</i>
LOC107820913	-2.4	<i>monothiol glutaredoxin-S11-like</i>
LOC107820216	-2.4	<i>probable protein phosphatase 2C 9</i>
LOC107767245	-2.4	<i>ferredoxin, root R-B1-like</i>
LOC107794003	-2.4	<i>1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase 1-like</i>
LOC107816353	-2.4	<i>probable glutathione S-transferase</i>
LOC107799279	-2.4	<i>2-oxoisovalerate dehydrogenase subunit β 1, mitochondrial-like</i>
LOC107810674	-2.4	.
LOC107797779	-2.4	<i>cellulose synthase-like protein G3</i>
LOC107783528	-2.4	<i>S-adenosylmethionine decarboxylase proenzyme-like</i>
LOC107808821	-2.4	<i>histone H1-like</i>
LOC107796971	-2.4	<i>aldehyde dehydrogenase family 7 member B4-like</i>
LOC107780623	-2.4	<i>GTP-binding protein At2g22870-like</i>
LOC107773764	-2.4	.
LOC107778647	-2.4	<i>serine/threonine-protein kinase Nek7-like</i>
LOC107771910	-2.4	<i>zinc finger CCCH domain-containing protein 20-like</i>
LOC107767330	-2.4	<i>altered inheritance of mitochondria protein 32-like</i>
LOC107760263	-2.4	<i>sodium/hydrogen exchanger 1-like</i>
LOC107766769	-2.4	<i>probable LRR receptor-like serine/threonine-protein kinase At2g16250</i>
LOC107794992	-2.4	<i>double-stranded RNA-binding protein 1-like</i>
LOC107798406	-2.4	<i>protein N-lysine methyltransferase METTL21A-like</i>
LOC107768720	-2.4	<i>5'-adenylylsulfate reductase 3, chloroplastic-like</i>
LOC107800203	-2.4	<i>malonate--CoA ligase-like</i>
LOC107800083	-2.4	<i>zinc finger A20 and AN1 domain-containing stress-associated protein 9-like</i>
LOC107829640	-2.4	<i>dnaJ protein homolog</i>
LOC107803154	-2.4	<i>uncharacterized LOC107803154</i>
LOC107804811	-2.4	<i>polyadenylate-binding protein RBP47</i>
LOC107765375	-2.4	<i>protein DETOXIFICATION 40-like</i>
LOC107791959	-2.4	<i>uncharacterized LOC107791959</i>
LOC107800715	-2.4	<i>putative GATA transcription factor 22</i>
LOC107783391	-2.4	<i>probable protein phosphatase 2C 63</i>
LOC107793843	-2.4	<i>phosphoprotein ECPP44-like</i>
LOC107823966	-2.5	<i>sugar phosphatase YfbT-like</i>
LOC107777821	-2.5	<i>21.7 kDa class VI heat shock protein-like</i>
LOC107818807	-2.5	<i>methionine gamma-lyase-like</i>
LOC107804215	-2.5	<i>lanC-like protein GCL1</i>
LOC107794078	-2.5	<i>protein LYK5-like</i>
LOC107814784	-2.5	<i>ethylene-responsive transcription factor RAP2-7-like</i>
LOC107806807	-2.5	<i>acetate/butyrate--CoA ligase AAE7, peroxisomal-like</i>
LOC107767113	-2.5	<i>uncharacterized LOC107767113</i>
LOC107813435	-2.5	<i>gibberellin receptor GID1C-like</i>
LOC107830058	-2.5	<i>probable plastidic glucose transporter 2</i>
LOC107811568	-2.5	<i>protein PHLOEM PROTEIN 2-LIKE A9-like</i>
LOC107823826	-2.5	<i>uncharacterized LOC107823826</i>
LOC107797615	-2.5	<i>uncharacterized LOC107797615</i>
LOC107779100	-2.5	<i>putative methyltransferase DDB_G0268948</i>
LOC107778753	-2.5	<i>C2 domain-containing protein At1g53590-like</i>

LOC107770814	-2.5	<i>galactan β-1,4-galactosyltransferase GALS3-like</i>
LOC107761377	-2.5	<i>uncharacterized LOC107761377</i>
LOC107821077	-2.5	<i>histidine-containing phosphotransfer protein 4-like</i>
LOC107827030	-2.5	<i>putative NAC domain-containing protein 94</i>
LOC107817589	-2.5	<i>chitin-binding lectin 1-like</i>
LOC107818543	-2.5	<i>zinc transporter 11-like</i>
LOC107763554	-2.5	<i>uncharacterized LOC107763554</i>
LOC107819330	-2.5	<i>probable terpene synthase 3</i>
LOC107768467	-2.5	<i>protein NRT1/ PTR FAMILY 7.3-like</i>
LOC107800958	-2.5	<i>uncharacterized LOC107800958</i>
LOC107795199	-2.5	<i>histone H3.3</i>
LOC107817827	-2.5	<i>serine/threonine-protein kinase SRK2A-like</i>
LOC107761131	-2.5	<i>squalene epoxidase 3-like</i>
LOC107804297	-2.5	<i>UPF0695 membrane protein C977.11/PB8B6.06c-like</i>
LOC107831070	-2.5	<i>uncharacterized LOC107831070</i>
LOC107769460	-2.5	<i>uncharacterized LOC107769460</i>
LOC107827795	-2.5	<i>cytochrome P450 89A2-like</i>
LOC107827981	-2.5	<i>RNA-dependent RNA polymerase 1-like</i>
LOC107769628	-2.5	<i>uncharacterized LOC107769628</i>
LOC107760735	-2.5	<i>mitochondrial uncoupling protein 5-like</i>
LOC107827662	-2.5	<i>translationally-controlled tumor protein homolog</i>
LOC107798706	-2.5	<i>WAT1-related protein At4g08300-like</i>
LOC107778346	-2.5	<i>granule-bound starch synthase 2, chloroplastic/amyloplastic</i>
LOC107809120	-2.5	<i>serine/arginine-rich splicing factor RSZ21A-like</i>
LOC107772446	-2.5	<i>uncharacterized LOC107772446</i>
LOC107831113	-2.5	<i>serine carboxypeptidase II-2-like</i>
LOC107779794	-2.5	<i>calreticulin-3-like</i>
LOC107804539	-2.5	<i>probable inactive purple acid phosphatase 1</i>
LOC107777148	-2.5	<i>serine acetyltransferase 2-like</i>
LOC107769442	-2.5	<i>CBL-interacting serine/threonine-protein kinase 6-like</i>
LOC107759116	-2.5	<i>β-glucosidase BoGH3B-like</i>
LOC107781650	-2.5	<i>patellin-3-like</i>
LOC107817936	-2.5	<i>glycine-rich protein A3-like</i>
LOC107766920	-2.5	<i>12-oxophytodienoate reductase 1-like</i>
LOC107804076	-2.6	<i>UDP-glycosyltransferase 89B2-like</i>
LOC107790949	-2.6	<i>tetraspanin-3-like</i>
LOC107762275	-2.6	<i>lipase-like PAD4</i>
LOC107759650	-2.6	<i>myricetin O-methyltransferase-like</i>
LOC107759349	-2.6	<i>actin-101</i>
LOC107818866	-2.6	<i>WAT1-related protein At1g70260-like</i>
LOC107815175	-2.6	<i>BTB/POZ and TAZ domain-containing protein 1-like</i>
LOC107763440	-2.6	<i>aspartyl protease family protein At5g10770-like</i>
LOC107792651	-2.6	<i>UDP-N-acetylglucosamine transferase subunit ALG13 homolog</i>
LOC107781091	-2.6	<i>gibberellin 2-β-dioxygenase 8-like</i>
LOC107817665	-2.6	<i>uncharacterized LOC107817665</i>
LOC107806565	-2.6	<i>putative UDP-rhamnose:rhamnosyltransferase 1</i>
LOC107786744	-2.6	<i>polyadenylate-binding protein RBP47-like</i>
LOC107781188	-2.6	<i>HMG1/2-like protein</i>
LOC107777197	-2.6	<i>serine/threonine-protein kinase SAPK3-like</i>
LOC107818699	-2.6	<i>uncharacterized LOC107818699</i>

LOC107780988	-2.6	<i>probable acyl-activating enzyme 6</i>
LOC107813586	-2.6	<i>probable purine permease 9</i>
LOC107803188	-2.6	<i>snakin-2</i>
LOC107804268	-2.6	<i>REF/SRPP-like protein At1g67360</i>
LOC107799405	-2.6	<i>B2 protein-like</i>
LOC107825214	-2.6	<i>plasma membrane ATPase 3-like</i>
LOC107782237	-2.6	<i>phosphomethylpyrimidine synthase, chloroplastic-like</i>
LOC107821927	-2.6	<i>21 kDa protein-like</i>
LOC107792156	-2.6	<i>1,4-α-glucan-branching enzyme-like</i>
LOC107788038	-2.6	<i>caffeic acid 3-O-methyltransferase</i>
LOC107819245	-2.6	<i>cytochrome P450 704C1-like</i>
LOC107759348	-2.6	<i>L-ascorbate peroxidase 1, cytosolic</i>
LOC107828005	-2.6	<i>CASP-like protein 2D1</i>
LOC107805587	-2.6	<i>polyol transporter 5-like</i>
LOC107769273	-2.6	<i>uncharacterized LOC107769273</i>
LOC107815706	-2.6	<i>protein PLANT CADMIUM RESISTANCE 2-like</i>
LOC107810147	-2.6	<i>transcription factor bHLH112-like</i>
LOC107791272	-2.6	<i>dynein light chain LC6, flagellar outer arm-like</i>
LOC107823460	-2.6	<i>zinc transporter 11-like</i>
LOC107805241	-2.6	<i>NAC domain-containing protein 2-like</i>
LOC107768730	-2.6	<i>lipase-like PAD4</i>
LOC107815150	-2.6	<i>uncharacterized LOC107815150</i>
LOC107761694	-2.6	<i>nectarin-1-like</i>
LOC107831992	-2.6	<i>uncharacterized protein At3g27210-like</i>
LOC107826405	-2.6	<i>uncharacterized LOC107826405</i>
LOC107783650	-2.6	<i>homeobox-leucine zipper protein ATHB-6-like</i>
LOC107820342	-2.6	<i>phosphoglycerate mutase-like protein AT74H</i>
LOC107784687	-2.6	<i>aldo-keto reductase family 4 member C10-like</i>
LOC107774196	-2.7	<i>uncharacterized LOC107774196</i>
LOC107823208	-2.7	<i>cysteine proteinase 3-like</i>
LOC107829632	-2.7	<i>protein NRT1/ PTR FAMILY 3.1-like</i>
LOC107776597	-2.7	<i>U-box domain-containing protein 52-like</i>
LOC107829356	-2.7	<i>uncharacterized LOC107829356</i>
LOC107829967	-2.7	<i>HMG1/2-like protein</i>
LOC107828153	-2.7	<i>uncharacterized LOC107828153</i>
LOC107763550	-2.7	<i>uncharacterized LOC107763550</i>
LOC107784433	-2.7	<i>expansin-like A2</i>
LOC107795731	-2.7	<i>uncharacterized LOC107795731</i>
LOC107831574	-2.7	<i>uncharacterized LOC107831574</i>
LOC107827281	-2.7	<i>α-aminoadipic semialdehyde synthase-like</i>
LOC107781534	-2.7	<i>ATP sulfurylase 1, chloroplastic-like</i>
LOC107818763	-2.7	<i>ATP-dependent Clp protease proteolytic subunit 5, chloroplastic-like</i>
LOC107773712	-2.7	<i>malonate--CoA ligase-like</i>
LOC107767696	-2.7	<i>uncharacterized LOC107767696</i>
LOC107821397	-2.7	<i>cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG1-like</i>
LOC107812031	-2.7	<i>protein DA1-related 1-like</i>
LOC107788900	-2.7	<i>probable RNA-dependent RNA polymerase 1</i>
LOC107806231	-2.7	<i>premnaspirodien oxygenase-like</i>
LOC107817745	-2.7	<i>HD domain-containing protein 2-like</i>
LOC107767001	-2.7	<i>O-acyltransferase WSD1-like</i>

LOC107815273	-2.7	<i>cinnamoyl-CoA reductase 2-like</i>
LOC107778300	-2.7	<i>histone H2B-like</i>
LOC107785077	-2.7	<i>trans-resveratrol di-O-methyltransferase-like</i>
LOC107823556	-2.7	<i>uncharacterized LOC107823556</i>
LOC107820576	-2.7	<i>transcription factor MYB44-like</i>
LOC107770846	-2.7	<i>uncharacterized WD repeat-containing protein C2A9.03-like</i>
LOC107812546	-2.7	<i>probable aquaporin NIP5-1</i>
LOC107782343	-2.7	<i>DNA-binding protein S1FA-like</i>
LOC107768503	-2.7	<i>light-induced protein, chloroplastic-like</i>
LOC107769747	-2.7	<i>jasmonic acid-amido synthetase JAR1-like</i>
LOC107774583	-2.7	<i>dihydroflavonol-4-reductase-like</i>
LOC107804205	-2.8	<i>binding partner of ACD11 1-like</i>
LOC107762264	-2.8	<i>uncharacterized LOC107762264</i>
LOC107813540	-2.8	<i>metallothionein-like protein type 2</i>
LOC107804911	-2.8	<i>bifunctional epoxide hydrolase 2-like</i>
LOC107766591	-2.8	<i>transcription factor LHW-like</i>
LOC107824132	-2.8	<i>WAT1-related protein At5g40240-like</i>
LOC107801230	-2.8	<i>5'-adenylylsulfate reductase 1, chloroplastic-like</i>
LOC107807751	-2.8	<i>probable 6-phosphogluconolactonase 1</i>
LOC107770293	-2.8	<i>cold-regulated 413 inner membrane protein 1, chloroplastic-like</i>
LOC107797481	-2.8	<i>trans-resveratrol di-O-methyltransferase-like</i>
LOC107809364	-2.8	<i>protein DETOXIFICATION 40-like</i>
LOC107766895	-2.8	<i>protein SENESCENCE-ASSOCIATED GENE 21, mitochondrial-like</i>
LOC107769193	-2.8	<i>uncharacterized LOC107769193</i>
LOC107810943	-2.8	<i>U-box domain-containing protein 2-like</i>
LOC107768362	-2.8	<i>shikimate O-hydroxycinnamoyltransferase-like</i>
LOC107796119	-2.8	<i>uncharacterized LOC107796119</i>
LOC107796190	-2.8	<i>uncharacterized LOC107796190</i>
LOC107764464	-2.8	<i>AIG2-like protein</i>
LOC107801354	-2.8	<i>low affinity sulfate transporter 3-like</i>
LOC107818917	-2.8	<i>protein LYK5-like</i>
LOC107805030	-2.8	<i>SPX domain-containing membrane protein At4g22990-like</i>
LOC107770535	-2.8	<i>protein MEI2-like 2</i>
LOC107793857	-2.8	<i>ubiquitin-activating enzyme E1 1-like</i>
LOC107785971	-2.8	<i>sugar transporter ERD6-like 5</i>
LOC107824093	-2.8	<i>IAA-amino acid hydrolase ILR1-like 6</i>
LOC107766259	-2.8	<i>uncharacterized LOC107766259</i>
LOC107816273	-2.8	<i>aldehyde dehydrogenase family 7 member B4-like</i>
LOC107829885	-2.8	<i>5'-adenylylsulfate reductase 2, chloroplastic-like</i>
LOC107766937	-2.9	<i>protein C2-DOMAIN ABA-RELATED 7-like</i>
LOC107795694	-2.9	<i>UDP-galactose/UDP-glucose transporter 4-like</i>
LOC107760226	-2.9	<i>cysteine proteinase 15A-like</i>
LOC107811757	-2.9	<i>NAC transcription factor 29-like</i>
LOC107824708	-2.9	<i>purple acid phosphatase 8-like</i>
LOC107783527	-2.9	<i>proline dehydrogenase 2, mitochondrial-like</i>
LOC107817177	-2.9	<i>probable aquaporin PIP1-2</i>
LOC107777238	-2.9	<i>NAC domain-containing protein 19-like</i>
LOC107827936	-2.9	<i>protein DETOXIFICATION 40-like</i>
LOC107828497	-2.9	<i>early nodulin-like protein 2</i>
LOC107810159	-2.9	<i>zingipain-2-like</i>

LOC107816559	-2.9	<i>uncharacterized WD repeat-containing protein C2A9.03-like</i>
LOC107779843	-2.9	<i>vacuolar-processing enzyme-like</i>
LOC107811392	-2.9	<i>βine aldehyde dehydrogenase, chloroplastic-like</i>
LOC107827814	-2.9	<i>glycine-rich protein 3 short isoform-like</i>
LOC107812522	-2.9	<i>β-glucosidase-like SFR2, chloroplastic</i>
LOC107759604	-2.9	<i>thioredoxin H2-like</i>
LOC107824735	-2.9	<i>gibberellin 3-β-dioxygenase 1-like</i>
LOC107794578	-2.9	<i>UDP-glycosyltransferase 74E2-like</i>
LOC107832742	-2.9	<i>gamma aminobutyrate transaminase 3, chloroplastic-like</i>
LOC107822315	-2.9	<i>clathrin light chain 2-like</i>
LOC107828044	-2.9	<i>cytochrome P450 CYP736A12-like</i>
LOC107785001	-2.9	<i>ureide permease 1-like</i>
LOC107764778	-2.9	<i>mechanosensitive ion channel protein 6-like</i>
LOC107809174	-2.9	<i>syntaxin-22-like</i>
LOC107809709	-2.9	<i>acetyl-CoA acetyltransferase, cytosolic 1-like</i>
LOC107769229	-2.9	<i>(+)-neomenthol dehydrogenase-like</i>
LOC107763344	-2.9	<i>probable protein phosphatase 2C 50</i>
LOC107784796	-2.9	<i>sugar transport protein 13-like</i>
LOC107764947	-2.9	<i>geraniol 8-hydroxylase-like</i>
LOC107802334	-2.9	<i>plasma membrane ATPase 3-like</i>
LOC107775674	-2.9	<i>protein NRT1/ PTR FAMILY 2.13-like</i>
LOC107766460	-2.9	<i>uncharacterized LOC107766460</i>
LOC107817296	-2.9	<i>pheophorbide a oxygenase, chloroplastic-like</i>
LOC107796775	-3.0	<i>probable metal-nicotianamine transporter YSL7</i>
LOC107797085	-3.0	<i>18.1 kDa class I heat shock protein-like</i>
LOC107806832	-3.0	<i>heat stress transcription factor A-6b-like</i>
LOC107802395	-3.0	<i>uncharacterized LOC107802395</i>
LOC107823280	-3.0	<i>GTP-binding protein YPTM2</i>
LOC107777659	-3.0	<i>peroxisomal (S)-2-hydroxy-acid oxidase-like</i>
LOC107783799	-3.0	<i>uncharacterized LOC107783799</i>
LOC107786749	-3.0	<i>vicianin hydrolase-like</i>
LOC107775508	-3.0	<i>uncharacterized LOC107775508</i>
LOC107775518	-3.0	<i>auxin-responsive protein SAUR32-like</i>
LOC107790216	-3.0	<i>S-adenosylmethionine decarboxylase proenzyme-like</i>
LOC107828525	-3.0	<i>protein ROOT HAIR DEFECTIVE 3 homolog 2-like</i>
LOC107793046	-3.0	<i>WAT1-related protein At3g28050-like</i>
LOC107779849	-3.0	<i>protein DETOXIFICATION 31-like</i>
LOC107785348	-3.0	<i>ornithine aminotransferase, mitochondrial-like</i>
LOC107760776	-3.0	<i>pectin acetylesterase 8-like</i>
LOC107795657	-3.0	<i>altered inheritance of mitochondria protein 32-like</i>
LOC107782595	-3.0	<i>E3 ubiquitin-protein ligase At3g02290-like</i>
LOC107786771	-3.0	<i>UDP-glycosyltransferase 90A1-like</i>
LOC107788067	-3.0	<i>remorin-like</i>
LOC107777621	-3.1	<i>glutathione transferase GST 23-like</i>
LOC107791015	-3.1	<i>MLO-like protein 6</i>
LOC107762043	-3.1	<i>uncharacterized LOC107762043</i>
LOC107765352	-3.1	<i>receptor-like protein kinase HAIKU2</i>
LOC107771009	-3.1	<i>NAC domain-containing protein 72-like</i>
LOC107776863	-3.1	<i>peroxidase 15-like</i>
LOC107797318	-3.1	<i>uncharacterized LOC107797318</i>

LOC107823662	-3.1	<i>scarecrow-like protein 3</i>
LOC107763397	-3.1	<i>probable xyloglucan endotransglucosylase/hydrolase protein 30</i>
LOC107760873	-3.1	<i>zinc-regulated protein 8-like</i>
LOC107768790	-3.1	<i>nuclear transcription factor Y subunit A-1-like</i>
LOC107762339	-3.1	<i>1-aminocyclopropane-1-carboxylate oxidase homolog</i>
LOC107825809	-3.1	<i>uncharacterized LOC107825809</i>
LOC107795732	-3.1	<i>putative phytosulfokines 6</i>
LOC107766503	-3.1	<i>uncharacterized LOC107766503</i>
LOC107763186	-3.1	<i>cyprosin-like</i>
LOC107777640	-3.1	<i>ACT domain-containing protein ACR10-like</i>
LOC107784768	-3.2	<i>cysteine proteinase 3</i>
LOC107796177	-3.2	<i>actin-53-like</i>
LOC107761689	-3.2	<i>protein ZINC INDUCED FACILITATOR-LIKE 1-like</i>
LOC107800538	-3.2	<i>protein LYK5-like</i>
LOC107813464	-3.2	<i>WAT1-related protein At4g15540-like</i>
LOC107827644	-3.2	<i>9-cis-epoxycarotenoid dioxygenase NCED1, chloroplastic-like</i>
LOC107763645	-3.2	<i>low affinity sulfate transporter 3-like</i>
LOC107787913	-3.2	<i>acid phosphatase 1-like</i>
LOC107776980	-3.2	<i>uncharacterized LOC107776980</i>
LOC107824465	-3.2	<i>vacuolar-processing enzyme-like</i>
LOC107817360	-3.2	<i>uncharacterized LOC107817360</i>
LOC107763065	-3.2	<i>18.1 kDa class I heat shock protein-like</i>
LOC107793211	-3.2	<i>probable amino-acid racemase</i>
LOC107831286	-3.2	<i>uncharacterized LOC107831286</i>
LOC107793550	-3.2	<i>uncharacterized LOC107793550</i>
LOC107799270	-3.3	<i>uncharacterized LOC107799270</i>
LOC107774040	-3.3	<i>uncharacterized LOC107774040</i>
LOC107805169	-3.3	<i>cold-regulated 413 inner membrane protein 1, chloroplastic-like</i>
LOC107760143	-3.3	<i>probable glutathione S-transferase parA</i>
LOC107829449	-3.3	<i>blue copper protein-like</i>
LOC107801748	-3.3	<i>WAT1-related protein At3g30340-like</i>
LOC107789349	-3.3	<i>pheophytinase, chloroplastic-like</i>
LOC107771931	-3.3	<i>thioredoxin H-type 2</i>
LOC107771614	-3.3	<i>ureide permease 1-like</i>
LOC107765167	-3.3	<i>REF/SRPP-like protein At1g67360</i>
LOC107784013	-3.3	<i>NAC domain-containing protein 21/22-like</i>
LOC107810190	-3.3	<i>uncharacterized LOC107810190</i>
LOC107783297	-3.3	<i>cathepsin B-like</i>
LOC107788463	-3.3	<i>uncharacterized LOC107788463</i>
LOC107799367	-3.3	<i>probable E3 ubiquitin-protein ligase XERICO</i>
LOC107810794	-3.3	<i>probable glutathione S-transferase</i>
LOC107817157	-3.3	<i>glutaredoxin-C13-like</i>
LOC107759703	-3.3	<i>L-ascorbate peroxidase 2, cytosolic-like</i>
LOC107764254	-3.4	<i>uncharacterized LOC107764254</i>
LOC107819006	-3.4	<i>cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG1-like</i>
LOC107810300	-3.4	<i>polyubiquitin</i>
LOC107799511	-3.4	<i>9-cis-epoxycarotenoid dioxygenase NCED1, chloroplastic-like</i>
LOC107792780	-3.4	<i>solute carrier family 35 member F1-like</i>
LOC107830673	-3.4	<i>aspartic proteinase-like</i>
LOC107802851	-3.4	<i>ATP sulfurylase 1, chloroplastic-like</i>

LOC107815271	-3.4	<i>uncharacterized LOC107815271</i>
LOC107808322	-3.4	<i>cell wall / vacuolar inhibitor of fructosidase 1-like</i>
LOC107767352	-3.4	<i>ABSCISIC ACID-INSENSITIVE 5-like protein 7</i>
LOC107772279	-3.4	<i>AAA-ATPase At3g28510-like</i>
LOC107798789	-3.4	<i>uncharacterized LOC107798789</i>
LOC107793029	-3.4	<i>oxalate--CoA ligase-like</i>
LOC107805342	-3.4	<i>(+)-neomenthol dehydrogenase-like</i>
LOC107767570	-3.4	<i>chlorophyllase-2, chloroplastic-like</i>
LOC107815425	-3.4	<i>probable WRKY transcription factor 53</i>
LOC107793612	-3.5	<i>amino acid permease 3-like</i>
LOC107806520	-3.5	<i>jasmonic acid-amido synthetase JAR1-like</i>
LOC107806757	-3.5	<i>mitochondrial pyruvate carrier 1-like</i>
LOC107829373	-3.5	<i>polyubiquitin-like</i>
LOC107803654	-3.5	<i>random slug protein 5-like</i>
LOC107789800	-3.5	<i>ferritin-1, chloroplastic</i>
LOC107795859	-3.5	<i>zinc finger protein CONSTANS-LIKE 1-like</i>
LOC107776681	-3.5	<i>allantoinase-like</i>
LOC107759714	-3.5	<i>glutamine synthetase-like</i>
LOC107824997	-3.5	<i>zingipain-1-like</i>
LOC107797772	-3.5	<i>uncharacterized LOC107797772</i>
LOC107775179	-3.5	<i>transmembrane protein 184C-like</i>
LOC107794361	-3.6	<i>gibberellin 2-β-dioxygenase-like</i>
LOC107813698	-3.6	<i>protein DETOXIFICATION 46, chloroplastic-like</i>
LOC107795681	-3.6	<i>BAG family molecular chaperone regulator 6-like</i>
LOC107818616	-3.6	<i>protein STAY-GREEN, chloroplastic-like</i>
LOC107778269	-3.6	<i>uncharacterized LOC107778269</i>
LOC107786009	-3.6	<i>2-oxoisovalerate dehydrogenase subunit α 1, mitochondrial-like</i>
LOC107787047	-3.6	<i>cysteine proteinase 15A-like</i>
LOC107771200	-3.6	<i>acidic endochitinase P</i>
LOC107770959	-3.6	<i>uncharacterized LOC107770959</i>
LOC107823732	-3.7	<i>nitrate reductase [NADH] 1</i>
LOC107823813	-3.7	<i>heavy metal-associated isoprenylated plant protein 3-like</i>
LOC107804321	-3.7	<i>remorin-like</i>
LOC107821969	-3.7	<i>oleosin 18.2 kDa-like</i>
LOC107780033	-3.7	<i>gibberellin 2-β-dioxygenase 1-like</i>
LOC107795650	-3.7	<i>low-temperature-induced cysteine proteinase-like</i>
LOC107807774	-3.7	<i>ACT domain-containing protein ACR6-like</i>
LOC107788083	-3.7	<i>1-aminocyclopropane-1-carboxylate oxidase 3-like</i>
LOC107821463	-3.7	<i>malate dehydrogenase, chloroplastic-like</i>
LOC107763850	-3.7	<i>probable boron transporter 2</i>
LOC107764356	-3.7	<i>copper transport protein CCH-like</i>
LOC107818394	-3.7	<i>cytochrome P450 83B1-like</i>
LOC107767094	-3.7	<i>peptidyl-prolyl cis-trans isomerase CYP20-1-like</i>
LOC107800135	-3.7	<i>probable trehalase</i>
LOC107773719	-3.8	<i>SNF1-related protein kinase regulatory subunit β-2-like</i>
LOC107772942	-3.8	<i>shikimate O-hydroxycinnamoyltransferase-like</i>
LOC107815880	-3.8	<i>heavy metal-associated isoprenylated plant protein 20-like</i>
LOC107783935	-3.8	<i>uncharacterized LOC107783935</i>
LOC107793596	-3.8	<i>uncharacterized oxidoreductase At4g09670-like</i>
LOC107768611	-3.8	<i>uncharacterized LOC107768611</i>

LOC107827398	-3.8	glutamine synthetase-like
LOC107793405	-3.8	glutamine synthetase-like
LOC107763384	-3.8	protein DETOXIFICATION 21-like
LOC107781761	-3.8	ubiquinol oxidase 2, mitochondrial
LOC107780562	-3.8	stem-specific protein TSJT1-like
LOC107777317	-3.8	bZIP transcription factor 53-like
LOC107788511	-3.8	chaperone protein ClpB4, mitochondrial-like
LOC107759987	-3.9	glutathione S-transferase L3-like
LOC107784440	-3.9	stem-specific protein TSJT1-like
LOC107769012	-3.9	protein C2-DOMAIN ABA-RELATED 7-like
LOC107785558	-3.9	protein UPSTREAM OF FLC-like
LOC107760209	-3.9	CBL-interacting serine/threonine-protein kinase 7-like
LOC107768268	-3.9	blue copper protein-like
LOC107814610	-3.9	carboxyl-terminal-processing peptidase 3, chloroplastic-like
LOC107771814	-4.0	vignain-like
LOC107820357	-4.0	uncharacterized LOC107820357
LOC107790219	-4.0	proline dehydrogenase 2, mitochondrial-like
LOC107805963	-4.0	uncharacterized LOC107805963
LOC107797791	-4.0	transcription factor TGA1-like
LOC107759522	-4.1	granule-bound starch synthase 1, chloroplastic/amyloplastic
LOC107759912	-4.1	1-aminocyclopropane-1-carboxylate oxidase-like
LOC107828324	-4.1	remorin-like
LOC107825213	-4.1	protein NRT1/ PTR FAMILY 2.11-like
LOC107824158	-4.1	pheophytinase, chloroplastic-like
LOC107822411	-4.1	methanol O-anthraniloyltransferase-like
LOC107829604	-4.2	zinc finger protein CONSTANS-LIKE 9-like
LOC107792716	-4.2	suppressor of disruption of TFIIIS-like
LOC107775062	-4.2	protein NRT1/ PTR FAMILY 2.11-like
LOC107826565	-4.2	glucose-1-phosphate adenylyltransferase large subunit 1-like
LOC107830184	-4.2	uncharacterized LOC107830184
LOC107805669	-4.2	2-oxoisovalerate dehydrogenase subunit α 1, mitochondrial-like
LOC107759315	-4.2	uncharacterized LOC107759315
LOC107813292	-4.3	AAA-ATPase At3g28580-like
LOC107772524	-4.3	probable glutathione S-transferase parA
LOC107826987	-4.3	metallothionein-like protein type 3
LOC107764067	-4.3	glutathione transferase GST 23-like
LOC107768051	-4.4	hydrophobic protein RCI2B-like
LOC107795252	-4.4	protein NRT1/ PTR FAMILY 1.2-like
LOC107763496	-4.4	glucose-6-phosphate/phosphate translocator 2, chloroplastic-like
LOC107815477	-4.4	vignain-like
LOC107816141	-4.5	constitutive photomorphogenesis protein 10
LOC107798787	-4.5	cytochrome P450 CYP72A219-like
LOC107820490	-4.5	probable WRKY transcription factor 70
LOC107796811	-4.5	UDP-glycosyltransferase 71K1-like
LOC107770851	-4.5	1-aminocyclopropane-1-carboxylate oxidase homolog
LOC107762763	-4.5	NAC domain-containing protein 21/22-like
LOC107795866	-4.6	inositol-3-phosphate synthase-like
LOC107823250	-4.6	early light-induced protein 1, chloroplastic-like
LOC107807051	-4.6	glutamine synthetase
LOC107763364	-4.6	ubiquinol oxidase 1, mitochondrial

LOC107803257	-4.6	<i>mechanosensitive ion channel protein 6-like</i>
LOC107794792	-4.7	<i>gamma-glutamyltranspeptidase 3-like</i>
LOC107765259	-4.7	<i>uncharacterized LOC107765259</i>
LOC107817409	-4.7	<i>putative phytosulfokines 6</i>
LOC107767686	-4.7	<i>NAC domain-containing protein 86-like</i>
LOC107808257	-4.7	<i>1-aminocyclopropane-1-carboxylate oxidase 1-like</i>
LOC107778784	-4.7	<i>putative F-box protein PP2-B12</i>
LOC107793668	-4.7	<i>bifunctional epoxide hydrolase 2-like</i>
LOC107804586	-4.7	<i>lipid transfer-like protein VAS</i>
LOC107802452	-4.7	<i>ammonium transporter 1 member 2</i>
LOC107817132	-4.7	<i>inorganic pyrophosphatase 1-like</i>
LOC107787638	-4.8	<i>ABC transporter C family member 14-like</i>
LOC107821493	-4.8	<i>probable nucleoredoxin 1</i>
LOC107803133	-4.8	<i>stress enhanced protein 2, chloroplastic</i>
LOC107764843	-4.8	<i>probable carboxylesterase 15</i>
LOC107829009	-4.8	<i>granule-bound starch synthase 1, chloroplastic/amyloplastic-like</i>
LOC107786099	-4.8	<i>mulatexin-like</i>
LOC107801146	-4.9	<i>ferritin-1, chloroplastic-like</i>
LOC107826264	-4.9	<i>uncharacterized LOC107826264</i>
LOC107766873	-4.9	<i>uncharacterized LOC107766873</i>
LOC107765289	-4.9	<i>L-ascorbate peroxidase 2, cytosolic</i>
LOC107776231	-5.0	<i>pyruvate, phosphate dikinase, chloroplastic</i>
LOC107802787	-5.0	<i>E3 ubiquitin-protein ligase MIEL1-like</i>
LOC107782531	-5.1	<i>allantoinase-like</i>
LOC107825777	-5.1	<i>protein SENESCENCE-ASSOCIATED GENE 21, mitochondrial-like</i>
LOC107779831	-5.1	<i>protein NRT1/ PTR FAMILY 1.2-like</i>
LOC107807601	-5.1	<i>basic endochitinase</i>
LOC107777858	-5.1	<i>glutamine synthetase-like</i>
LOC107805948	-5.3	<i>induced stolen tip protein TUB8-like</i>
LOC107812784	-5.3	<i>probable nucleoredoxin 2</i>
LOC107804413	-5.4	<i>heavy metal-associated isoprenylated plant protein 3-like</i>
LOC107801270	-5.4	<i>inorganic pyrophosphatase 1-like</i>
LOC107795867	-5.4	<i>pectin acetylesterase 12-like</i>
LOC107765251	-5.4	<i>BTB/POZ domain-containing protein At1g55760-like</i>
LOC107765920	-5.5	<i>homeobox-leucine zipper protein ATHB-12-like</i>
LOC107770443	-5.6	<i>inositol-tetrakisphosphate 1-kinase 1-like</i>
LOC107791784	-5.6	<i>uncharacterized LOC107791784</i>
LOC107824547	-5.6	<i>uncharacterized LOC107824547</i>
LOC107769013	-5.7	<i>carboxyl-terminal-processing peptidase 3, chloroplastic-like</i>
LOC107761364	-5.7	<i>serine/arginine-rich splicing factor SR30-like</i>
LOC107798226	-5.8	<i>protein RALF-like 27</i>
LOC107769850	-5.9	<i>glutaredoxin-C6-like</i>
LOC107832324	-5.9	.
LOC107781969	-5.9	<i>protein LURP-one-related 11-like</i>
LOC107796039	-6.0	<i>cellulose synthase-like protein H1</i>
LOC107781604	-6.1	<i>low-temperature-induced cysteine proteinase-like</i>
LOC107824323	-6.1	<i>protein STAY-GREEN, chloroplastic-like</i>
LOC107770733	-6.2	<i>basic endochitinase</i>
LOC107792684	-6.2	<i>uncharacterized LOC107792684</i>
LOC107780718	-6.2	<i>pyruvate, phosphate dikinase, chloroplastic-like</i>

LOC107763494	-6.3	<i>glutaredoxin-C6-like</i>
LOC107831572	-6.3	<i>probable purine permease 9</i>
LOC107762610	-6.4	<i>probable WRKY transcription factor 70</i>
LOC107814060	-6.4	<i>tuberculostearic acid methyltransferase UfaA1-like</i>
LOC107831012	-6.5	<i>cinnamate β-D-glucosyltransferase-like</i>
LOC107775283	-6.6	<i>probable purine permease 10</i>
LOC107784308	-6.6	<i>cytochrome P450 CYP749A22-like</i>
LOC107809847	-6.6	<i>vacuolar-processing enzyme-like</i>
LOC107783543	-6.6	<i>oxalate--CoA ligase-like</i>
LOC107758920	-6.7	<i>transcription factor MYB1R1-like</i>
LOC107794052	-6.7	<i>pleckstrin homology domain-containing protein 1-like</i>
LOC107790227	-6.8	<i>classical arabinogalactan protein 4-like</i>
LOC107828779	-6.8	<i>inorganic phosphate transporter 1-4-like</i>
LOC107827891	-7.3	<i>proteinase inhibitor I-B-like</i>
LOC107811349	-7.4	<i>uncharacterized LOC107811349</i>
LOC107774220	-7.4	<i>zinc-regulated protein 8-like</i>
LOC107819606	-7.6	<i>uncharacterized LOC107819606</i>
LOC107806033	-7.7	<i>protein trichome birefringence-like 37</i>
LOC107765376	-7.8	<i>uncharacterized LOC107765376</i>
LOC107797935	-8.1	<i>uncharacterized LOC107797935</i>
LOC107810714	-8.1	<i>metallocarboxypeptidase inhibitor-like</i>
LOC107824732	-8.2	<i>ammonium transporter 1 member 1</i>
LOC107777338	-8.3	<i>proline dehydrogenase 2, mitochondrial-like</i>
LOC107796351	-8.5	<i>proteinase inhibitor I-B-like</i>
LOC107817198	-8.6	<i>high-affinity nitrate transporter 3.1-like</i>
LOC107776942	-8.6	<i>ammonium transporter 1 member 1-like</i>
LOC107783309	-8.9	<i>oxalate--CoA ligase-like</i>
LOC107759913	-9.1	<i>1-aminocyclopropane-1-carboxylate oxidase-like</i>
LOC107782665	-9.3	<i>uncharacterized LOC107782665</i>
LOC107814975	-9.6	<i>glycine-rich protein-like</i>
LOC107813543	-10.1	<i>uncharacterized LOC107813543</i>
LOC107781126	-10.2	<i>1-aminocyclopropane-1-carboxylate oxidase</i>
LOC107828624	-10.2	<i>urea-proton symporter DUR3</i>
LOC107772445	-10.6	<i>uncharacterized LOC107772445</i>
LOC107813808	-11.0	<i>basic endochitinase-like</i>
LOC107780204	-11.2	<i>probable α-amylase 2</i>
LOC107764910	-11.4	<i>primary amine oxidase</i>
LOC107781493	-11.6	<i>probable galactinol--sucrose galactosyltransferase 2</i>
LOC107790557	-12.4	<i>proteinase inhibitor I-B-like</i>
LOC107772757	-13.0	<i>vacuolar-processing enzyme gamma-isozyme-like</i>
LOC107804914	-13.3	<i>dCTP pyrophosphatase 1-like</i>
LOC107782140	-13.8	<i>probable α-amylase 2</i>
LOC107784001	-14.0	<i>uncharacterized LOC107784001</i>
LOC107816051	-14.4	<i>miraculin-like</i>
LOC107821651	-15.0	<i>gibberellin 3-β-dioxygenase 1-like</i>
LOC107807349	-15.0	<i>vacuolar-processing enzyme-like</i>
LOC107761493	-15.1	<i>proteinase inhibitor I-B-like</i>
LOC107766502	-15.7	<i>inositol-3-phosphate synthase</i>
LOC107810534	-16.0	<i>18.1 kDa class I heat shock protein-like</i>
LOC107759078	-16.7	<i>primary amine oxidase-like</i>

LOC107801320	-17.9	<i>glutaredoxin-C13-like</i>
LOC107791801	-18.0	.
LOC107811291	-22.1	<i>uncharacterized LOC107811291</i>
LOC107811787	-25.3	<i>uncharacterized LOC107811787</i>
LOC107824656	-25.7	<i>glutaredoxin-C13-like</i>
LOC107791110	-28.7	<i>primary amine oxidase-like</i>
LOC107774651	-29.0	<i>zingipain-2-like</i>