Artificial Shading Can Adversely Affect Heat-tolerant Lettuce Growth and Taste, with Concomitant Changes in Gene Expression

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ABSTRACT. Shading has been used to produce high-quality lettuce (*Lactuca sativa*) in locations where production conditions are not optimal for this cool-season crop. To learn what additional benefits shading provides if heat-tolerant cultivars are used and to understand the effects of shading on growth, sensory quality, chemical content, and transcriptome profile on heat-tolerant lettuce, we grew two romaine lettuce cultivars with and without shading using 50% black shade cloth in 2018 and 2019. Shading reduced plant leaf temperatures, lettuce head fresh weights, glucose and total sugars content, and sweetness, but not bitterness, whereas it increased lettuce chlorophyll b content compared with unshaded controls. Transcriptome analyses identified genes predominantly involved in chlorophyll biosynthesis, photosynthesis, and carbohydrate metabolism as upregulated in unshaded controls compared with shaded treatments. For the tested cultivars, which were bred to withstand high growing temperatures, it may be preferable to grow them under unshaded conditions to avoid increased infrastructure costs and obtain lettuce deemed sweeter than if shaded.

Lettuce (*Lactuca sativa*) is an important cool-season vegetable crop species, with more than 2 million tonnes produced in the United States in 2019 [U.S. Department of Agriculture (USDA), National Agricultural Statistics Service, 2020]. The ideal average daily temperature for field-grown lettuce is 18.5 °C, and high temperatures may negatively affect lettuce growth and development leading to tipburn, undesirable bitterness, and early bolting due to a reduced growing period (Waycott and Ryder, 1993). Bitterness, an important taste characteristic of lettuce usually associated with consumer rejection (Drewnowski and Gomez-Carneros, 2000), has been found to increase with higher growing season temperatures (Simonne et al., 2002).

Bunning et al. (2010) found that genotypic differences had a greater effect than environmental conditions on sensory and phenolic content of lettuces. Sensory analyses of lettuce have demonstrated genotypic differences (Simonne et al., 2002; Zhao and

Carey, 2009), especially in bitterness, which may be attributed to differing quantities of bitter components, including sesquiterpene lactones, lactucin, and lactucopicrin (Price et al., 1990). Bitterness perception may be counteracted by sweetness, with the ratio of bitter-to-sweet compounds determining bitterness perception and liking (Chadwick et al., 2016). Breeding efforts may lead to new cultivars that are more heat tolerant and less bitter, but the development of new cultivars can be expensive and time-consuming (Driedonks et al., 2016).

In addition to the development of heat-tolerant cultivars, technologies that alter light intensity and temperature can be used to improve growth and productivity of crops under high temperature conditions. Several research groups have studied the effects of shading on lettuce growth, yield, bitterness, and chemical composition. The use of 39% white shade cloth over high tunnels reduced lettuce leaf surface temperature by 1.5 to 2.5 °C, as well as head weights of loose-leaf and butterhead, but not romaine, lettuces compared with lettuce grown in the open field (Zhao and Carey, 2009). In contrast, lettuce grown in the field under 50% black shade had greater marketable head weight and diameter, and chlorophyll and carotene content, than unshaded controls (Ilić and Fallik, 2017; Ilić et al., 2017). Mastilović et al. (2019) observed that shaded lettuce had lower soluble solids content, which is linked to sweetness, than those grown in the open field. Because consumers have a preference for sweeter lettuce (Chadwick et al., 2016), open field-grown lettuce may be preferable to shaded lettuce.

To produce lettuce under high temperatures, the use of both well-adapted cultivars and suitable production technologies are needed to provide effective solutions to these problems. Growers may first choose to raise heat-adapted cultivars before adopting

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shading technology, due to the increased costs and labor in using shade technology. The objective of this study was to evaluate whether shading technology would improve production and consumer appeal of heat-tolerant lettuce cultivars under high temperature growing conditions. In this study we evaluated lettuce growth, sensory properties, chemical content, and transcriptomic differences of heat-tolerant lettuces grown under 50% black shade cloth or unshaded field conditions.

Methods

PLANT MATERIALS AND GROWING CONDITIONS. ‘Salvius’ and ‘Sparx’ romaine lettuce were grown from seed (Johnny’s Selected Seeds, Winslow, ME). These cultivars have been reported to be heat-tolerant (Holmes et al., 2019) and were chosen at the recommendation of Minnesota growers. Seeds were sown in organic growing media. In 2018, the growing media that was used was Sunshine (Sun Gro Horticulture, Agawam, MA) or Seed Starter Mix (Purple Cow Organics, Middleton, WI). In 2019, the growing media consisted of Pro-Mix Mycorrhizae Organik (Premier Horticulture, Victor, NY) mixed with 7N-2.2P-8.3K organic fertilizer (BioWorks Verdanta EcoVita; BFG Supply Co., St. Paul, MN). All seedlings were grown in a greenhouse set at 21 °C day/night on a mist bench for 4 to 6 weeks, and then hardened off in an outdoor coldframe until transplanted in the field.

FIELD EXPERIMENTAL DESIGN AND TREATMENTS. Experiments were replicated over 2 years at two locations (both USDA Plant Hardiness Zone 4b) on the St. Paul campus of the University of Minnesota (lat. 44.9740°N, long. 93.2277°W; Waukegan silt loam) and at the Southern Research and Outreach Center (SROC) in Waseca, MN (lat. 44.0707°N, long. 93.5264°W; Webster clay loam). Both field locations fall within Koppen climate zone Dfa (hot-summer humid continental).

Fertilizer was applied at rates based on soil test results and previous crop histories. In St. Paul, urea was applied to plots in 2018, but 8N-0.9P-3.3K organic fertilizer (Sustane Natural Fertilizer, Cannon Falls, MN) was used in 2019. At the SROC, lettuce plots received 5N-1.3P-2.1K and 3N-3.1P-3.3K organic fertilizers [Chickity Doo (Pearl Valley Organix, Pearl City, IL) and Sustane Natural Fertilizer, respectively] in 2018. In 2019, the fertilizer used at the SROC was 5N-1.3P-2.1K organic fertilizer (Sustane Natural Fertilizer) with the addition of 0N-20.1P-0K triple superphosphate (Ag Partners, Morristown, MN), 0N-0N-49.8K potassium chloride, 44N-0P-0K slow-release urea (Jordan Seeds, Woodbury, MN), and 46N-0N-0N urea (Ag Partners). Raised beds (0.1 m high at the SROC or 0.3 m high in St. Paul × 1 to 1.5 m wide) were made and covered with white on black embossed plastic mulch (Ag Resource, Detroit Lakes, MN) and equipped with 0.38-mm low flow drip irrigation (Aqua-Traxx; DripWorks, Willits, CA), used as needed based on weather conditions. Transplants were planted 30 cm apart in single rows.

A split-plot design was used for field experiments in 2018 and 2019. Blocks (15.24 m long × 1.5 m wide) were split into shaded or unshaded (control) plots (6 m long × 1.5 m wide). Cultivars were randomized into one of two subplots within each shade treatment. There were four replicate blocks at each location per year, with two whole plots (shade or no shade) per block and two subplots (‘Salvius’ or ‘Sparx’) per whole plot. Treatments consisted of shading with netting that was designed to

reduce photosynthetically active radiation by 50% (50% Pull and Cut Sunblocker; FarmTek, Dyersville, IA) attached to 1.5-m-tall hoops made from bent electrical conduit, and unshaded control treatments not covered by hoops or shading.

Lettuce plants were transplanted in four randomized blocks in each location on 1 June 2018 and 30 May 2019 at the SROC and 12 June 2018 and 26 May 2019 in St. Paul under each treatment. This was done to ensure that lettuce was grown under high temperatures. There were 19 plants staggered within each subplot. Lettuce was harvested at the SROC on 11 July 2018 and 15 July 2019 and in St. Paul on 16 July 2018 and 15 July 2019. All lettuce was harvested before bolting.

FIELD MEASUREMENTS. Weather stations at both locations recorded daily temperature and precipitation data. In 2018, plant leaf temperatures were measured using handheld infrared (IR) thermometers pointed at leaf surfaces. In 2019, microtemperature sensors were clipped onto adaxial leaf surfaces (unshaded by other leaves) about halfway between the core and outer leaves on a leaf of one plant per treatment per row, and data were recorded with data loggers (WatchDog; Spectrum Technologies, Aurora, IL). There were no differences between temperature measurements made using the handheld IR thermometer (mean of five measurements = 24.9 ± 1.3 °C) and the micro sensor (23.2 ± 1.7 °C). Photon flux density measurements were made at solar noon on 19 July 2021 using a field spectroradiometer (SS-110; Apogee Instruments, Logan, UT) equipped with a 180° field of view head placed 0.5 m aboveground surface. Three measurements were made for each treatment—under the shade cloth and without the shade cloth.

SENSORY EVALUATIONS. The University of Minnesota Institutional Review Board approved all recruiting and experimental procedures of all sensory tests. All tasters were 6-n-propylthiouracil tasters or supertasters, so have the ability to taste bitterness (supertasters are particularly sensitive) and were compensated for the testing session.

Sensory evaluations of lettuce were performed by 12 trained panelists in 2019 at the Sensory Center at the University of Minnesota. Two different sensory studies were done. The objective of the first study was to measure the intensity differences in sweetness and bitterness across two lettuce cultivars (Salvius and Sparx), under two shading treatments (shaded and unshaded), at two locations (St. Paul and the SROC). Three lettuce heads of each cultivar and treatment were harvested from each block at the two test locations the day before testing and stored at 0 °C until transported the next day to the Sensory Center. Outer leaves of each head of lettuce were removed at the time of harvest. All lettuce was harvested before bolting.

All samples used for sensory evaluations were prepared from the middle leaves. On the day of testing, 12 to 13 leaves were removed from each head of lettuce and washed thoroughly with cold tap water. The leaves were laid out on absorbent mats (up&up™, Target Corp., Minneapolis, MN) labeled with each sample’s three-digit blinding code. Lettuces were examined for damage caused by insects or bacteria and patted dry with cloth dish towels. Leaves with no visible damage were portioned into 6-cm sections from the middle of the leaf and cut in half lengthwise to include both rib and leafy material. Lettuces with pest or abiotic damage were portioned to avoid the damaged section. If unable to get 12 portions from 12 separate leaves, two portions were taken from one larger undamaged leaf. Lettuce samples were presented to participants in sets of eight, with each set

including one replicate of the two shadings by two cultivars by two locations in snack size zip-top bags (up&up™) coded with a random three-digit number. These bagged leaves were refrigerated until 30 min before serving, then allowed to equilibrate to room temperature.

Sixteen samples, replicates 1 and 2, were served on the first day (16 July 2019), and 16 samples, replicates 3 and 4, were served on the second day (17 July 2019). Panelists always tested replicate 1 before replicate 2, and replicate 3 before replicate 4. This was done to ensure that the same samples were not randomly served multiple times in a row and to expose panelists to the entire range of samples as early as possible. Samples within each replicate were served balanced for order and carryover effects using Williams Latin square designs. For the entirety of testing, panelists were instructed to use nose clips to ensure evaluation of basic tastes only. Panelists started each testing session with a set of two citric acid calibration solutions with immediate feedback. Panelists were instructed to use the citric acid scale intensity reference samples (Karalus et al., 2010) provided as needed. During the testing session, each panelist rated each sample for the intensity of sweetness and the intensity of bitterness. Panelists were instructed to “remove the entire piece of lettuce from your bag. Roll the lettuce and put the whole piece into your mouth at once. Chew the sample thoroughly and swallow before making your evaluations.” These attribute ratings were made on a 20-point line scale labeled *none* at the left end and *intense* at the right end. Panelists were provided with room-temperature filtered water to rinse their mouths between samples.

WEIGHT AND CHEMICAL MEASUREMENTS. Six heads of lettuce were sampled from each subplot within a block, and fresh weights were measured in the field immediately after harvest in both 2018 and 2019. All lettuce was harvested before bolting.

Lettuce leaf soluble sugars, chlorophyll, and carotenoid levels were measured only in 2019. Middle leaves from one head of each cultivar and treatment from each of four blocks of both growing locations were assayed. For soluble sugar analyses, ≈0.5 mg of finely sliced fresh leaf material was placed into 2-mL screwcap tubes with 1 mL of 80% (v/v) ethanol and incubated in a water bath at 80 °C for 4 h. After this time, supernatants were transferred to new 2-mL screwcap tubes. The plant material was washed with 0.5 mL 80% (v/v) ethanol and the supernatants were combined, and then completely dried using a concentrator (Savant SpeedVac model SVC-100H; Thermo Fisher Scientific, Waltham, MA) connected to a refrigerated vapor trap (Savant model RVT400, Thermo Fisher Scientific). The dried materials were dissolved in 100 µL of deionized water. Sucrose, fructose and glucose contents were determined enzymatically using a sugar analysis kit (K-SUFRG; Megazyme, Wicklow, Ireland) according to manufacturer instructions.

Chlorophyll levels were determined according to Han et al. (2016). Approximately 0.5 g of fresh leaf tissue was finely sliced and transferred into 50-mL tubes to which 10 mL of 95% (v/v) ethanol was added. Tubes were covered with aluminum foil, and chlorophyll was extracted at room temperature for 24 h. Aliquots (210 µL) were measured at 649 nm (A_{649}), 664 nm (A_{664}), and 470 nm (A_{470}) using a spectrophotometer (SpectraMax 190; Molecular Devices, San Jose, CA) equipped with data analysis software (SoftMaxPro 5.2, Molecular Devices). Chlorophyll a, chlorophyll b, and carotenoid concentrations were calculated using the following equations (Sumanta et al., 2014):

$$\text{Chlorophyll a} = 13.36 A_{664} - 5.19 A_{649}$$

$$\text{Chlorophyll b} = 27.43 A_{649} - 8.12 A_{664}$$

$$\text{Carotenoids} = (1000 A_{470} - 2.13 \text{ Chlorophyll a} - 97.63 \text{ Chlorophyll b})/209$$

RNA EXTRACTION AND SEQUENCING. One leaf was collected from each of four heads of ‘Sparx’ lettuce per treatment after sensory evaluation sampling in 2019 and pooled together for RNA analyses. Two biological replicates (biologically distinct samples) from each treatment (unshaded and shaded) were subjected to sequencing. RNA extraction was performed using an RNA extraction kit (RNeasy mini kit; Qiagen, Valencia, CA). RNA concentration was measured with a spectrophotometer (NanoDrop, Thermo Fisher Scientific) and tested for integrity using electrophoretic separation (RNA ScreenTape System, Agilent Technologies, Santa Clara, CA). RNAs with RNA Integrity Number ≥7.0 were selected for library preparation. cDNA libraries were constructed by the University of Minnesota Genomics Center using the Illumina TruSeq RNA sample preparation protocol stranded with ribosomal reduction. The libraries were sequenced on a sequencing system (Illumina HiSeq 2500 using the NextSeq Mid-Output platform; Illumina, San Diego, CA) to generate 150-bp paired-end sequence reads. Quality control of the sequence reads was performed using FastQC version 0.11.9 software (Andrews, 2010). Low-quality reads (Phred score < 30) and adapter contamination were removed using the Trimmomatic software tool (Bolger et al., 2014). The trimmed reads were mapped to the *L. sativa* cv. Salinas reference genome (Reyes-Chin-Wo et al., 2017) using HISAT2 software (Kim et al., 2019) with default settings. The number of reads aligned to each gene was counted using the featureCounts program from the Subread package (Liao et al., 2019).

TRANSCRIPTOME ANALYSES. Differentially expressed genes (DEGs) between unshaded control and shaded lettuce were identified using the Bioconductor edgeR software package (Robinson et al., 2010). False discovery rate (FDR) <0.05 and $|\text{Log}_2(\text{fold-change})| > 2.0$ were set as the thresholds for differential expression. Analyses to describe DEGs according to Gene Ontology project (GO) descriptors were performed using the Bioconductor goseq R software package (Young et al., 2010), and Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway analyses were conducted using the enrichKEGG function of the ClusterProfiler R package (Yu et al., 2012). Enriched GO terms and KEGG pathways were determined at FDR <0.05. Gene annotations were obtained from the National Center for Biotechnology Information database.

Quantitative reverse transcriptase polymerase chain reaction (qRT-PCR) methodology was used to validate transcriptome analyses (i.e., confirm RNA sequencing results) because only two biological replicates had been used for RNA sequencing (RNAseq). qRT-PCR was done using a SYBR green reagent system (CFX96 Touch Real-Time PCR Detection System; Bio-Rad, Hercules, CA). First strand cDNA was synthesized with a reverse transcriptase kit (GoScript; Promega Corp., Madison, WI) in two steps. The first step consisted of adding 4.0 µL of RNA (1200 ng), 0.7 µL of oligo dt₁₅ primer and 0.3 µL random primers. The mixture was heated to 70 °C for 5 min and then immediately chilled on ice for at least 5 min. Five microliters of the reaction mixture were added to 4.0 µL 5× reaction buffer, 2.0 µL MgCl₂, 1.0 µL PCR nucleotide mix, 0.5 µL recombinant ribonuclease inhibitor, 1.0 µL reverse transcriptase, and 6.5 µL nuclease free water, in a final volume of 20 µL, incubated for 5 min at 25 °C, followed by 1 h at 42 °C, and finally inactivated

for 15 min at 70 °C. cDNA was diluted 10× to be used for qRT-PCR reactions. qRT-PCR was performed for 26 DEG genes, including 15 downregulated, 11 upregulated, and four house-keeping genes (Supplemental Table 1). Primer pairs were designed using Primer-BLAST software (Ye et al., 2012). Each 10-μL qRT-PCR reaction contained a mixture of 2.0 μL cDNA, 5.0 μL cyanine dye (SYBR Green, Bio-Rad) and 0.2-μL pairs of primers (400 nM each). The thermal cycling conditions were initial denaturation for 5 min at 95 °C, 40 cycles at 95 °C for 20 s, 60 °C for 30 s, and 72 °C for 30 s. Melting curve analyses were performed at the end of qRT-PCR amplifications over the range of 65 to 95 °C, increasing temperature stepwise by 0.5 °C every 5 s. Gene expressions were normalized using tubulin beta-2 chain-like as a reference gene. Relative gene expression was calculated using the $2^{-\Delta\Delta CT}$ method (Livak and Schmittgen, 2001). Four biological replicates and two technical replicates (repeated measurements of each biological sample) were performed for each treatment.

STATISTICAL ANALYSES. Linear mixed effects models were performed using the lme4::nlme package (Bates et al., 2015) for R software (version 1.2.1335 or 4.1.1; RStudio, Boston, MA) to model treatment effects on lettuce fresh weight (measured in 2018 and 2019) and carotenoid, chlorophylls, fructose, glucose, sucrose, and total sugar content (measured in 2019). Dependent variable transformations were carried out as needed to meet analysis of variance (ANOVA) assumptions. Fresh weights and total sugars were square root transformed, and glucose and sucrose contents were log-transformed. Treatment, cultivar, and their interaction were included as fixed effects, while blocking [blocks, location, and year (fresh weight data)] and whole plot effects (year by location by block by treatment) were included as random effects.

To determine if sweetness or bitterness intensities differed by treatment, cultivar, location, or their interactions, ANOVA [PROC GLM (SAS version 9.4; SAS Institute, Cary, NC)] were used for sensory evaluations. Sweetness and bitterness were the dependent variables; treatment, cultivar, location, and replicate were fixed predictors; participant was a random predictor. All main effects, two-way interactions, and three-way interactions of treatment, cultivar, and location were present in the model.

To identify DEGs in lettuce grown with and without shade, the Bioconductor edgeR package (Robinson et al., 2010) was used. To designate changes in gene expression, FDR < 0.05 and $|\log_2 FC| > 2.0$ were set as the thresholds for differential expression. Correlations between results of qRT-PCR and RNAseq were analyzed using the Spearman coefficient.

Results

FIELD MEASUREMENTS. In 2018 and 2019, the St. Paul and the SROC sites experienced temperatures for lettuce production that were above the optimal (18.5 °C) listed by Zhao and Carey (2009). For the period of lettuce production, average maximum temperatures in St. Paul were 29.1 and 24.4 °C in 2018 and 2019, respectively, whereas they were 27.3 and 25.8 °C at the SROC in 2018 and 2019, respectively.

Lettuce leaf temperatures were unaffected by shading treatments in 2018 (data not shown), but temperatures were only measured at noon by handheld thermometers. In 2019, when thermistors connected to recorders were used to record leaf temperatures, the 50% shade cloth lowered plant maximum, but not minimum, temperatures (Fig. 1A and B). The maximum leaf

Fig. 1. Daily (month/day) surface leaf temperatures measured in 2019 using microtemperature sensors clipped onto adaxial leaf surfaces (unshaded by other leaves) about halfway between the core and outer leaves on a leaf of one plant per treatment per row of (A) lettuce under 50% shade cloth (shaded) and control (unshaded) at St. Paul, MN, and (B) lettuce under 50% shade cloth (shaded) and control (unshaded) at the Southern Research and Outreach Center in Waseca, MN. (C) Light spectra recorded with a field spectroradiometer on 19 July 2021 at solar noon without or with the shade cloth.

temperature reduction caused by shade cloth at St. Paul was observed when the leaf temperature was reduced from 38.8 to 27.2 °C (Fig. 1A). At the SROC, the maximum leaf temperature reduction due to shade cloth was from 40.2 to 28.7 °C (Fig. 1B).

Fig. 2. Quality of 'Salvius' and 'Sparx' (pooled for location) lettuce produced under unshaded (control) or 50% black shade cloth conditions. (A) Head fresh weights pooled for 2018 and 2019, showing median and interquartile range, and distribution of raw data for each cultivar ($n = 8$ per cultivar). (B and C) Marginal mean $\pm$ 95% confidence interval (CI) of fructose, glucose, sucrose, and total sugars in 2019. (D) Bootstrapped ($n = 100,000$) mean sweetness ratings $\pm$ 95% CI of lettuce harvested in 2019. Sweetness ratings were made on a 20-point line scale, with 0 = no sweetness and 20 = intense sweetness, but all ratings were < 5 , so the graphed y-axis maximum = 4. (E–G) Chlorophyll a and b and chlorophyll a-to-b ratio of 2019 lettuce (marginal means $\pm$ 95% confidence interval). CI bars that are not visible are obscured by the mean ($N = 16$ for means shown in B–G).

Average leaf temperature decreases for shaded lettuce compared with unshaded controls were 4.4 and 6.0 °C in St. Paul and the SROC, respectively.

The photosynthetic photon flux density under the shade cloth ranged from 572 to 595 $\mu\text{mol}\cdot\text{m}^{-2}\cdot\text{s}^{-1}\cdot\text{nm}^{-1}$, $\approx 35\%$ of that of full sunlight, which ranged from 1591 to 1880 $\mu\text{mol}\cdot\text{m}^{-2}\cdot\text{s}^{-1}\cdot\text{nm}^{-1}$. The spectral pattern was not changed by the shade cloth (Fig. 1C).

LETTUCE QUALITY. Cultivar and location effects were not significant for lettuce fresh weight, sweetness, or sugar content. Fresh weight was the same in both 2018 and 2019. Shading reduced lettuce fresh weights of 'Salvius' and 'Sparx' ($P < 0.001$) heads in both 2018 and 2019 (results shown in Fig. 2A aggregated across years and locations). The most abundant sugar found in lettuce was fructose (Fig. 2B). Total sugar and glucose content ($P = 0.04$ and 0.02 , respectively), but not fructose ($P = 0.06$) or sucrose ($P = 0.07$) contents, differed between unshaded and shaded lettuce. Mean total sugar and glucose contents were 128.7 and 15.3 $\mu\text{g}\cdot\text{mL}^{-1}$, respectively, for unshaded control lettuce, and 79.4 and 8.1 $\mu\text{g}\cdot\text{mL}^{-1}$ respectively, for shaded lettuce. Treatment ($P < 0.001$), cultivar ($P = 0.02$), and location ($P < 0.001$) had significant effects, but none of the interactions of these factors significantly affected sweetness ratings of lettuce in 2019. Sensory evaluation participants rated unshaded lettuce as slightly sweeter (mean sweetness intensity of 2.9) than shaded

Fig. 3. Heatmap showing how many of the 313 genes identified from the RNA sequencing experiment as differentially expressed between unshaded control and shaded lettuce were upregulated (red) or downregulated (green) relative to the other treatment; 1 and 2 refer to the two biological replicates that were sequenced for the unshaded control or shaded treatments.

(mean sweetness intensity of 2.3) lettuce (Fig. 2D) and did not discern differences in bitterness based on shading treatment (data not shown). 'Sparx' was rated sweeter than 'Salvius', and lettuce grown at the SROC was rated sweeter than those grown in St. Paul (data not shown).

In 2019, shaded lettuce in our study had higher chlorophyll b [$P = 0.02$ (Fig. 2F)], but not total chlorophyll ($P = 0.11$), chlorophyll a [$P = 0.20$ (Fig. 2E)], or carotenoid ($P = 0.34$) content. The ratio of chlorophyll a to chlorophyll b was greater in unshaded control lettuce ($2.31 \pm 0.08 \mu\text{g}\cdot\text{mL}^{-1}$) than in shaded lettuce ($2.18 \pm 0.08 \mu\text{g}\cdot\text{mL}^{-1}$), with $P = 0.01$ (Fig. 2G). Interactions of location or cultivar with treatment were not significant for chlorophyll b content or chlorophyll a-to-b ratio.

TRANSCRIPTOME ANALYSES. RNA sequencing generated 111 million paired-end 150-bp reads, where 16.4% of the raw reads were removed after adaptor trimming and quality filtering, resulting in an average of 25 million reads per sample. The clean reads ratio was higher than 83.6%. Genome mapping by HISAT2 successfully aligned 20.5 to 28.7 million reads to the lettuce genome. Using $\log_2$ -fold change ≥ 2 and FDR < 0.05 as cutoff values, 313 DEGs between unshaded and shaded lettuces were identified. Among the DEGs, 254 and 59 were upregulated in unshaded and shaded lettuce, respectively, and clustered by treatment (Fig. 3). There was a 0.86 Spearman coefficient ($P < 0.001$) between RNAseq and qRT-PCR data, indicating that the qRT-PCR data validated the RNAseq results, despite using only two biological replicates per treatment.

Analyses of identified DEGs using GO terms sorted their putative gene products into 10 biological process, three cellular component, and three molecular function categories (Supplemental Table 2). The greatest numbers of DEGs were involved in processes such as plasma membrane function, extracellular region metabolism (gene products not attached to the cell surface),

Fig. 4. Functions of differentially expressed genes (DEGs) between unshaded control and shaded lettuce identified from RNA sequencing and based on (A) Gene Ontology project (GO) and (B) Kyoto Encyclopedia of Genes and Genomes analyses. DEGs in the GO analyses were categorized as biological processes, cellular components, and molecular functions.

transmembrane transport, calcium ion binding, response to salt stress, and response to water deprivation (Fig. 4A). These DEGs under the enriched GO terms were mostly upregulated in unshaded controls compared with shaded lettuce. An insignificant number of genes were upregulated in shaded compared with unshaded lettuce.

KEGG enrichment analysis distributed DEGs into five categories, in which all DEGs were upregulated in unshaded compared with shaded lettuce (Fig. 4B). The categories included phenylpropanoid biosynthesis, plant-pathogen interaction, α -linoleic acid metabolism, aromatic amino acid metabolism, and flavonoid biosynthesis.

Examination of genes related to photosynthesis and carbohydrate metabolism showed that a few genes were upregulated in

unshaded compared with shaded lettuce (Table 1), including those coding for early light-induced proteins and the RuBisCO small and large subunits. Only 19% of differentially expressed genes were upregulated in shaded compared with unshaded control lettuce (Supplemental Table 3). Genes related to phenylpropanoid and flavonoid biosynthesis were upregulated in unshaded compared with shaded lettuce. No genes related to bitterness, such as squalene synthase (Testone et al., 2019) or sesquiterpene synthase (Bennett et al., 2002), were differentially expressed between unshaded and shaded lettuce.

Discussion

Shading decreased average temperatures of lettuce compared with unshaded controls (Fig. 1A and B) and was most effective in reducing temperature when leaf temperatures were above 35 °C. The heat-tolerant lettuce cultivars, Sparx and Salvius, grew well in unshaded conditions in both locations and years. However, shade reduced lettuce fresh weights of both tested cultivars (Fig. 2A). These results agree with those described by Zhao and Carey (2009) for romaine lettuce grown under high tunnels shaded with 39% white shade cloth, which had lesser head fresh weights compared to those grown in the open field; the white shade cloth decreased leaf surface temperature. However, our results contrast with those observed for butterhead lettuce shaded with 50% black netting (Ilić et al., 2017), and green- and red-leaf lettuce shaded with 50% black netting (Li et al., 2017), in which head fresh weights were greater than those grown in the open field. Li et al. (2017) reported that lettuce head dry weights did not differ among treatments, suggesting that differences among treatments in their study may have been due to differences in water content.

Unshaded ‘Sparx’ and ‘Salvius’ lettuces were rated by sensory evaluation participants as sweeter than shaded counterparts (Fig. 2D). These evaluations were positively correlated with the higher total sugars contents of unshaded compared with shaded lettuce (Fig. 2C) and the upregulation of genes related to glucose metabolism (Table 1). Our data were similar to results reported for soluble sugars by Mastilović et al. (2019). Unshaded lettuce has previously been shown to be more bitter than shaded lettuce (Zhao and Carey, 2009), but no difference in bitterness was discerned between the shaded and unshaded lettuce cultivars used in this study.

The higher content of sugars in the unshaded lettuce may be attributed to higher photosynthetic rates compared with shaded lettuce, although we did not measure lettuce photosynthetic rates.

Table 1. Differentially expressed genes with Gene Ontology project (GO) functions associated with chlorophyll biosynthesis, photosynthesis, and carbohydrate metabolism. GO analyses were performed on data from RNA sequencing results using the goseq R Bioconductor software package (Young et al., 2010). A positive Log_2 value indicates that the gene was upregulated in unshaded lettuce.

GO identifier	$\text{Log}_2(\text{fold-change})$	GO term	Gene annotation
Chlorophyll biosynthesis			
LOC111915584	2.63	Chlorophyll biosynthetic process	1-deoxy-D-xylulose-5-phosphate synthase
LOC111881935	2.29	Regulation of chlorophyll biosynthetic process	Early light-induced protein
LOC111881937	2.44	Regulation of chlorophyll biosynthetic process	Early light-induced protein
Photosynthesis			
LOC111908115	2.55	Photosynthetic electron transport in photosystem I	Protein proton gradient regulation
Carbohydrate metabolism			
LOC111900246	4.41	Carbon fixation	RuBisCO small subunit
LOC111908252	2.13	Carbon fixation	RuBisCO small subunit
LOC111898611	2.87	Carbon fixation	RuBisCO large subunit

These results suggest that greater photosynthesis in the unshaded lettuce, and consequently higher accumulation of sugars, may have resulted in sweeter unshaded than shaded lettuce. Shading treatments affected lettuce chlorophyll b content (Fig. 2F), but not total chlorophyll or chlorophyll a (Fig. 2E) content, in our study. Shaded lettuce had higher mean chlorophyll b content than unshaded lettuce, but the difference between treatments was small (means of $1.04 \mu\text{g}\cdot\text{mL}^{-1}$ for the unshaded vs. $1.18 \mu\text{g}\cdot\text{mL}^{-1}$ for the shaded lettuce). These data are different from those reported by Ilić and Fallik (2017) and Ilić et al. (2017) for butterhead lettuce, in which shading with black netting increased chlorophyll a, chlorophyll b, and carotenoid contents on a fresh weight basis compared with unshaded lettuce. Shade-tolerant species have been shown to have higher proportions of chlorophyll b relative to chlorophyll a (Boardman, 1977). It may be that the lettuce cultivars used in this study are more shade tolerant than the butterhead lettuce studied by Ilić et al. (2017). Also, genes associated with rubisco subunits were upregulated in unshaded lettuce (Table 1), which may have led to greater plant growth and soluble sugar accumulation under high light and high temperature in unshaded conditions. The higher fresh weights and sweetness of the cultivars grown in unshaded compared with shaded conditions in our study may be attributed to many different mechanisms, including carbohydrate metabolic processes, two of which were also upregulated in unshaded compared with shaded lettuce (Table 1). The extent to which RNAs were translated into active proteins could be studied in future work.

The differing results among the literature and our results highlight variability among genotypes in interactions with the environment. While greater fresh weight under shading conditions were observed for the cultivars Tizian (Ilić et al., 2017), Two Star (green-leaf) and New Red Fire [red leaf (Li et al., 2017)], opposite results were observed for the cultivars used in this study. Lafta et al. (2021) found significant genotype $\times$ environment differences in head weight, core length, and head diameter, among other traits in crisphead lettuce. The ability of the cultivars used in this study to tolerate heat may be related to modifications in many pathways that are involved in photosynthesis and secondary metabolism (Fig. 3, Table 1). As temperatures increase, lettuce growers will need to adapt by using as many tools as possible, including growing heat-tolerant cultivars. It could be possible that heat-tolerance limits of lettuce may be extended by growing them under shade.

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Supplemental Table 1. (Continued)

Downregulated						
Name	Sequence (5'→3')	Template strand	Start	Stop	Tm (°C)	Product size
Upregulated						
Delta9acyl_F	AGAGTGGCTGTTGCTCTGGG	Plus	435	454	59.89	133
Delta9acyl_R	AGGCGTGAGCACCAACAATAA	Minus	567	548	59.96	133
Un_914527_F	TAGCCGTTTGACGTGCATGA	Plus	412	431	60.32	103
Un_914527_R	GATCCCAGCGTGAACCTCA	Minus	514	495	60.04	103
ncRNA_884283_F	TGATCCCTTCGTCGCACTTC	Plus	99	118	60.11	102
ncRNA_884283_R	GGTGGTTGAAGGCAATGTGG	Minus	200	181	59.68	102
MKS1_F	ACACCGTCTCCCCAAAGGTA	Plus	326	345	60.47	124
MKS1_R	CCGTCACTGGTGAAAGCAGA	Minus	449	430	60.32	124
ncRNA_893409_F	GGATCGTCAACGCTTTCGGA	Plus	233	252	60.73	137
ncRNA_893409_R	CCACCGTAAACACAAGAAACCC	Minus	369	348	59.97	137
NCL1_F	ATTGACCCCTACAAACACCCG	Plus	1669	1688	59.67	105
NCL1_R	ACAGCTTTTGTCATCCCA	Minus	1773	1754	59.52	105
MYB98_F	TGCCGATGGCTATCACTGAC	Plus	4130	4149	59.9	114
MYB98_R	CCACTCCCAAGCAACTTGTGA	Minus	4243	4224	60.18	114
Un_900135_F	ACCGTCGCTTCCATCTACAC	Plus	328	347	59.83	143
Un_900135_R	GCCACTTCGCCGATTATGTC	Minus	470	451	59.42	143
Housekeeping						
SerThre_HK_F	AGACTTGGCGGAGGAGTTTGG	Plus	1572	1591	59.96	143
SerThre_HK_R	AACGGCGCTAAGAATGGTCA	Minus	1685	1666	60.04	143
TauESafe_HK_F	AGGGAGATTCCGACACCAAC	Plus	1267	1286	59.39	116
TauESafe_HK_R	GCCCATGATAAAACCCGCCAC	Minus	1382	1363	59.9	116
TUB_2_HK_F	TTGGTGTGCGAGTATCAGCAG	Plus	1324	1344	59.8	100
TUB_2_HK_R	ATACAACAGACTACGCCTCCTC	Minus	1423	1402	59.31	100
18S_HK_F	TGCTATGCGTGTGGATTTC	Plus	510	529	59.27	110
Predicted description						
						Delta-9 acyl-lipid desaturase 1-like (LOC111917517), mRNA
						Delta-9 acyl-lipid desaturase 1-like (LOC111917517), mRNA
						Uncharacterized LOC111914527 (LOC111914527), mRNA
						Uncharacterized LOC111914527 (LOC111914527), mRNA
						Uncharacterized LOC111884283 (LOC111884283), ncRNA
						Uncharacterized LOC111884283 (LOC111884283), ncRNA
						Protein MKS1-like (LOC111876100), mRNA
						Protein MKS1-like (LOC111876100), mRNA
						Uncharacterized LOC111893409 (LOC111893409), ncRNA
						Uncharacterized LOC111893409 (LOC111893409), ncRNA
						Sodium/calcium exchanger NCL1-like (LOC111913551), mRNA
						Sodium/calcium exchanger NCL1-like (LOC111913551), mRNA
						Transcription factor MYB98-like (LOC111913550), mRNA
						Transcription factor MYB98-like (LOC111913550), mRNA
						Uncharacterized LOC111900135 (LOC111900135), mRNA
						Uncharacterized LOC111900135 (LOC111900135), mRNA
						Serine/threonine-protein phosphatase 2A 65-kDa regulatory subunit A beta
						Serine/threonine-protein phosphatase 2A 65-kDa regulatory subunit A beta
						Sulfite exporter TauE/Safe family protein 3-like (LOC111885856), mRNA
						Sulfite exporter TauE/Safe family protein 3-like (LOC111885856), mRNA
						Rubulin beta-2 chain-like (LOC111907503), mRNA
						Tubulin beta-2 chain-like (LOC111907503), mRNA
						18S rRNA (guanine-N(7))-

Supplemental Table 2. List of Gene Ontology project (GO) unique identifiers, names (ID), and term names of all genes determined by RNA sequencing analyses to be differentially expressed between unshaded control and shaded lettuce. Differentially expressed genes were identified using the Bioconductor edgeR software package (Robinson et al., 2010). Enriched GO terms were determined using a false discovery rate <0.05 and generated using the Bioconductor goseq R software package (Young et al., 2010).

Unique identifier	ID	GO term
LOC111876247	GO:0046872	Metal ion binding
LOC111876394	GO:0010088	Phloem development
LOC111876394	GO:0016021	Integral component of membrane
LOC111876517	GO:0055085	Transmembrane transport
LOC111876517	GO:0005886	Plasma membrane
LOC111876517	GO:0008308	Voltage-gated anion channel activity
LOC111876517	GO:0016021	Integral component of membrane
LOC111876517	GO:0006873	Cellular ion homeostasis
LOC111876517	GO:0015698	Inorganic anion transport
LOC111876728	GO:0003887	DNA-directed DNA polymerase activity
LOC111876728	GO:0071897	DNA biosynthetic process
LOC111876728	GO:0005634	Nucleus
LOC111876728	GO:0006260	DNA replication
LOC111876728	GO:0051539	4 iron, 4 sulfur cluster binding
LOC111876728	GO:0022616	DNA strand elongation
LOC111876728	GO:0019103	Pyrimidine nucleotide binding
LOC111876728	GO:0000428	DNA-directed RNA polymerase complex
LOC111876728	GO:0003677	DNA binding
LOC111876728	GO:0003896	DNA primase activity
LOC111876728	GO:0030894	Replisome
LOC111876728	GO:0042575	DNA polymerase complex
LOC111876728	GO:0046872	Metal ion binding
LOC111876728	GO:0003682	Chromatin binding
LOC111876728	GO:0070013	Intracellular organelle lumen
LOC111876728	GO:0043233	Organelle lumen
LOC111876728	GO:0009965	Leaf morphogenesis
LOC111876728	GO:1903047	Mitotic cell cycle process
LOC111876728	GO:0017076	Purine nucleotide binding
LOC111876728	GO:0032774	RNA biosynthetic process
LOC111876787	GO:0016881	Acid-amino acid ligase activity
LOC111876787	GO:0005737	Cytoplasm
LOC111876787	GO:0102057	Jasmonoyl-valine synthetase activity
LOC111876787	GO:0102053	(-)-jasmonoyl-isoleucine synthetase activity
LOC111876787	GO:0102058	Jasmonoyl-leucine synthetase activity
LOC111877039	GO:0031012	Extracellular matrix
LOC111877039	GO:0030574	Collagen catabolic process
LOC111877039	GO:0004222	Metalloendopeptidase activity
LOC111877039	GO:0030198	Extracellular matrix organization
LOC111877039	GO:0008270	Zinc ion binding
LOC111877039	GO:0006508	Proteolysis
LOC111877141	GO:0016787	Hydrolase activity
LOC111877485	GO:0005507	Copper ion binding
LOC111877485	GO:0030001	Metal ion transport
LOC111877485	GO:0016021	Integral component of membrane
LOC111877485	GO:0019829	ATPase-coupled cation transmembrane transporter activity
LOC111877485	GO:0035434	Copper ion transmembrane transport
LOC111877485	GO:0043682	Copper transmembrane transporter activity, phosphorylative mechanism
LOC111877485	GO:0072511	Divalent inorganic cation transport
LOC111877485	GO:0005524	ATP binding
LOC111877830	GO:0016787	Hydrolase activity
LOC111877830	GO:0043531	ADP binding
LOC111879316	GO:0009506	Plasmodesma
LOC111879316	GO:0046777	Protein autophosphorylation
LOC111879316	GO:0004672	Protein kinase activity

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Supplemental Table 2. (Continued)

Unique identifier	ID	GO term
LOC111879316	GO:0005886	Plasma membrane
LOC111879316	GO:0005524	ATP binding
LOC111879316	GO:0016021	Integral component of membrane
LOC111879316	GO:0005509	Calcium ion binding
LOC111879403	GO:0005737	Cytoplasm
LOC111879403	GO:0009651	Response to salt stress
LOC111879403	GO:0003968	RNA-directed 5'-3' RNA polymerase activity
LOC111879403	GO:0009414	Response to water deprivation
LOC111879403	GO:0009409	Response to cold
LOC111879403	GO:0042651	Thylakoid membrane
LOC111879403	GO:0001172	Transcription, RNA-templated
LOC111879403	GO:0039694	Viral RNA genome replication
LOC111879403	GO:0098588	Bounding membrane of organelle
LOC111879403	GO:0031984	Organelle subcompartment
LOC111879403	GO:0012505	Endomembrane system
LOC111879403	GO:0016021	Integral component of membrane
LOC111879403	GO:0043231	Intracellular membrane-bounded organelle
LOC111879403	GO:0005886	Plasma membrane
LOC111880353	GO:0016787	Hydrolase activity
LOC111880353	GO:0016021	Integral component of membrane
LOC111880881	GO:0010091	Trichome branching
LOC111880979	GO:0046983	Protein dimerization activity
LOC111880979	GO:0005634	Nucleus
LOC111880979	GO:0003723	RNA binding
LOC111880979	GO:0016021	Integral component of membrane
LOC111881022	GO:0106311	NA
LOC111881022	GO:0006468	Protein phosphorylation
LOC111881022	GO:0005886	Plasma membrane
LOC111881022	GO:0106310	NA
LOC111881022	GO:0030246	Carbohydrate binding
LOC111881022	GO:0016021	Integral component of membrane
LOC111881022	GO:0005524	ATP binding
LOC111881482	GO:0006629	Lipid metabolic process
LOC111881482	GO:0005634	Nucleus
LOC111881482	GO:0016787	Hydrolase activity
LOC111881492	GO:0006629	Lipid metabolic process
LOC111881492	GO:0005634	Nucleus
LOC111881492	GO:0080030	Methyl indole-3-acetate esterase activity
LOC111881492	GO:0009820	Alkaloid metabolic process
LOC111881492	GO:0016021	Integral component of membrane
LOC111881554	GO:0004672	Protein kinase activity
LOC111881554	GO:0006468	Protein phosphorylation
LOC111881554	GO:0016021	Integral component of membrane
LOC111881554	GO:0005886	Plasma membrane
LOC111881554	GO:0005524	ATP binding
LOC111881554	GO:0005525	GTP binding
LOC111881554	GO:0003676	Nucleic acid binding
LOC111881702	GO:0016021	Integral component of membrane
LOC111881702	GO:0003735	Structural constituent of ribosome
LOC111881702	GO:0006412	Translation
LOC111881702	GO:0005840	Ribosome
LOC111881935	GO:0009507	Chloroplast
LOC111881935	GO:0015979	Photosynthesis
LOC111881935	GO:0046872	Metal ion binding
LOC111881935	GO:0071491	Cellular response to red light
LOC111881935	GO:0009579	Thylakoid
LOC111881935	GO:0071490	Cellular response to far red light

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Supplemental Table 2. (Continued)

Unique identifier	ID	GO term
LOC111881935	GO:0010117	Photoprotection
LOC111881935	GO:0071486	Cellular response to high light intensity
LOC111881935	GO:0010030	Positive regulation of seed germination
LOC111881935	GO:0071492	Cellular response to ultraviolet A
LOC111881935	GO:0031984	Organelle subcompartment
LOC111881935	GO:0098796	Membrane protein complex
LOC111881935	GO:0071483	Cellular response to blue light
LOC111881935	GO:0010380	Regulation of chlorophyll biosynthetic process
LOC111881935	GO:0016021	Integral component of membrane
LOC111881935	GO:0080167	Response to karrikin
LOC111881935	GO:0034605	Cellular response to heat
LOC111881935	GO:0009409	Response to cold
LOC111881935	GO:0010224	Response to ultraviolet B
LOC111881937	GO:0009507	Chloroplast
LOC111881937	GO:0015979	Photosynthesis
LOC111881937	GO:0046872	Metal ion binding
LOC111881937	GO:0071491	Cellular response to red light
LOC111881937	GO:0009579	Thylakoid
LOC111881937	GO:0071490	Cellular response to far red light
LOC111881937	GO:0010117	Photoprotection
LOC111881937	GO:0071486	Cellular response to high light intensity
LOC111881937	GO:0010030	Positive regulation of seed germination
LOC111881937	GO:0071492	Cellular response to ultraviolet A
LOC111881937	GO:0031984	Organelle subcompartment
LOC111881937	GO:0098796	Membrane protein complex
LOC111881937	GO:0071483	Cellular response to blue light
LOC111881937	GO:0010380	Regulation of chlorophyll biosynthetic process
LOC111881937	GO:0016021	Integral component of membrane
LOC111881937	GO:0080167	Response to karrikin
LOC111881937	GO:0034605	Cellular response to heat
LOC111881937	GO:0009409	Response to cold
LOC111881937	GO:0010224	Response to ultraviolet B
LOC111882123	GO:0006817	Phosphate ion transport
LOC111882123	GO:0022857	Transmembrane transporter activity
LOC111882123	GO:0016021	Integral component of membrane
LOC111882123	GO:0055085	Transmembrane transport
LOC111882377	GO:0019953	Sexual reproduction
LOC111882377	GO:0005576	Extracellular region
LOC111882479	GO:0005524	ATP binding
LOC111882484	GO:0003700	DNA-binding transcription factor activity
LOC111882484	GO:0005634	Nucleus
LOC111882484	GO:0006355	Regulation of transcription, DNA-templated
LOC111882484	GO:0003677	DNA binding
LOC111882484	GO:0005515	Protein binding
LOC111882484	GO:0006952	Defense response
LOC111882484	GO:0009873	Ethylene-activated signaling pathway
LOC111882588	GO:0004707	MAP kinase activity
LOC111882588	GO:0000165	MAPK cascade
LOC111882588	GO:0005938	Cell cortex
LOC111882588	GO:0006468	Protein phosphorylation
LOC111882588	GO:0005634	Nucleus
LOC111882588	GO:0005524	ATP binding
LOC111882588	GO:0016021	Integral component of membrane
LOC111882588	GO:0080136	Priming of cellular response to stress
LOC111882588	GO:0052317	Camalexin metabolic process
LOC111882588	GO:0009700	Indole phytoalexin biosynthetic process
LOC111882588	GO:1902065	Response to L-glutamate

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Supplemental Table 2. (Continued)

Unique identifier	ID	GO term
LOC111882588	GO:0005515	Protein binding
LOC111882588	GO:1901002	Positive regulation of response to salt stress
LOC111882588	GO:0022857	Transmembrane transporter activity
LOC111882588	GO:0010229	Inflorescence development
LOC111882588	GO:0050826	Response to freezing
LOC111882588	GO:0048481	Plant ovule development
LOC111882588	GO:0010183	Pollen tube guidance
LOC111882588	GO:0010200	Response to chitin
LOC111882588	GO:0010224	Response to ultraviolet B
LOC111882588	GO:0009555	Pollen development
LOC111882588	GO:0009414	Response to water deprivation
LOC111882588	GO:0050832	Defense response to fungus
LOC111882588	GO:0006970	Response to osmotic stress
LOC111882588	GO:0009611	Response to wounding
LOC111882588	GO:0009617	Response to bacterium
LOC111882588	GO:0006979	Response to oxidative stress
LOC111882588	GO:0044272	Sulfur compound biosynthetic process
LOC111882588	GO:0010468	Regulation of gene expression
LOC111882588	GO:0009626	Plant-type hypersensitive response
LOC111882588	GO:0009738	Abscisic acid-activated signaling pathway
LOC111882588	GO:0006857	Oligopeptide transport
LOC111882588	GO:0055085	Transmembrane transport
LOC111882695	GO:0016787	Hydrolase activity
LOC111882721	GO:0005886	Plasma membrane
LOC111882721	GO:0034154	Toll-like receptor 7 signaling pathway
LOC111882721	GO:0003727	Single-stranded RNA binding
LOC111882721	GO:0002755	MyD88-dependent toll-like receptor signaling pathway
LOC111882721	GO:0004888	Transmembrane signaling receptor activity
LOC111882721	GO:0016021	Integral component of membrane
LOC111882721	GO:0051607	Defense response to virus
LOC111882721	GO:0006955	Immune response
LOC111882970	GO:0050290	Sphingomyelin phosphodiesterase D activity
LOC111882970	GO:0016021	Integral component of membrane
LOC111882972	GO:0015267	Channel activity
LOC111882972	GO:0006833	Water transport
LOC111882972	GO:0016021	Integral component of membrane
LOC111882972	GO:0055085	Transmembrane transport
LOC111882972	GO:0005372	Water transmembrane transporter activity
LOC111882972	GO:0005774	Vacuolar membrane
LOC111883018	GO:0042626	ATPase-coupled transmembrane transporter activity
LOC111883018	GO:0055085	Transmembrane transport
LOC111883018	GO:0016021	Integral component of membrane
LOC111883018	GO:0005524	ATP binding
LOC111883438	GO:0005975	Carbohydrate metabolic process
LOC111883612	GO:0006857	Oligopeptide transport
LOC111883612	GO:0022857	Transmembrane transporter activity
LOC111883612	GO:0016021	Integral component of membrane
LOC111883612	GO:0006817	Phosphate ion transport
LOC111883612	GO:0055085	Transmembrane transport
LOC111883728	GO:0046872	Metal ion binding
LOC111883728	GO:0005774	Vacuolar membrane
LOC111883728	GO:0009507	Chloroplast
LOC111883728	GO:0005886	Plasma membrane
LOC111883899	GO:0003700	DNA-binding transcription factor activity
LOC111883899	GO:0005634	Nucleus
LOC111883899	GO:0006355	Regulation of transcription, DNA-templated
LOC111883899	GO:0003677	DNA binding

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Supplemental Table 2. (Continued)

Unique identifier	ID	GO term
LOC111883899	GO:0006952	Defense response
LOC111883899	GO:0009873	Ethylene-activated signaling pathway
LOC111883899	GO:0009834	Plant-type secondary cell wall biogenesis
LOC111883899	GO:0009793	Embryo development ending in seed dormancy
LOC111884088	GO:0033834	Kaempferol 3-O-galactosyltransferase activity
LOC111884088	GO:0102479	Quercetin 3-O-beta;-D-galactosyltransferase activity
LOC111884088	GO:0008194	UDP-glycosyltransferase activity
LOC111884614	GO:0048544	Recognition of pollen
LOC111884614	GO:0106311	NA
LOC111884614	GO:0016021	Integral component of membrane
LOC111884614	GO:0106310	NA
LOC111884614	GO:0005886	Plasma membrane
LOC111884614	GO:0005524	ATP binding
LOC111884614	GO:0006468	Protein phosphorylation
LOC111884614	GO:0030246	carbohydrate binding
LOC111884614	GO:0008270	Zinc ion binding
LOC111884614	GO:0016818	Hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides
LOC111884614	GO:0003676	Nucleic acid binding
LOC111885053	GO:0008017	microtubule binding
LOC111885053	GO:0005874	Microtubule
LOC111885053	GO:0010499	Proteasomal ubiquitin-independent protein catabolic process
LOC111885053	GO:0010952	Positive regulation of peptidase activity
LOC111885053	GO:0070577	Lysine-acetylated histone binding
LOC111885053	GO:0016504	Peptidase activator activity
LOC111885053	GO:0070628	Proteasome binding
LOC111885053	GO:0005829	Cytosol
LOC111885053	GO:0005634	Nucleus
LOC111885053	GO:0016021	Integral component of membrane
LOC111885299	GO:0004674	Protein serine/threonine kinase activity
LOC111885299	GO:0016310	Phosphorylation
LOC111885299	GO:0016021	Integral component of membrane
LOC111885299	GO:0006464	Cellular protein modification process
LOC111885299	GO:0005524	ATP binding
LOC111885713	GO:0042409	Caffeoyl-CoA O-methyltransferase activity
LOC111885713	GO:0009809	Lignin biosynthetic process
LOC111885713	GO:0005829	Cytosol
LOC111885713	GO:0005840	Ribosome
LOC111885713	GO:0032259	Methylation
LOC111885713	GO:0080076	Caffeoyl CoA:S-adenosyl-L-methionine O-methyltransferase activity
LOC111885713	GO:0046872	Metal ion binding
LOC111885713	GO:0016779	Nucleotidyltransferase activity
LOC111885713	GO:0003735	Structural constituent of ribosome
LOC111885713	GO:0003723	RNA binding
LOC111885713	GO:0007623	Circadian rhythm
LOC111885713	GO:0010467	Gene expression
LOC111885713	GO:0016070	RNA metabolic process
LOC111885713	GO:0043043	Peptide biosynthetic process
LOC111885713	GO:0034645	Cellular macromolecule biosynthetic process
LOC111885713	GO:0044267	Cellular protein metabolic process
LOC111885749	GO:0003824	Catalytic activity
LOC111886218	GO:0061630	Ubiquitin protein ligase activity
LOC111886218	GO:0006511	Ubiquitin-dependent protein catabolic process
LOC111886218	GO:0016567	Protein ubiquitination
LOC111886240	GO:0003723	RNA binding
LOC111886240	GO:0016021	Integral component of membrane
LOC111886240	GO:0003824	Catalytic activity
LOC111886521	GO:0008233	Peptidase activity

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Supplemental Table 2. (Continued)

Unique identifier	ID	GO term
LOC111886521	GO:0006508	Proteolysis
LOC111886521	GO:0016887	ATPase activity
LOC111886521	GO:0005524	ATP binding
LOC111886524	GO:0008270	Zinc ion binding
LOC111886524	GO:0016567	Protein ubiquitination
LOC111886524	GO:0005829	Cytosol
LOC111886524	GO:0004842	Ubiquitin-protein transferase activity
LOC111886524	GO:0016874	Ligase activity
LOC111886530	GO:0043565	Sequence-specific DNA binding
LOC111886530	GO:0005634	Nucleus
LOC111886530	GO:0006355	Regulation of transcription, DNA-templated
LOC111886530	GO:0003700	DNA-binding transcription factor activity
LOC111886530	GO:0001067	Regulatory region nucleic acid binding
LOC111886530	GO:0003690	Double-stranded DNA binding
LOC111886670	GO:0003735	Structural constituent of ribosome
LOC111886670	GO:0005840	Ribosome
LOC111886670	GO:0006412	Translation
LOC111886670	GO:0005829	Cytosol
LOC111886670	GO:0000027	Ribosomal large subunit assembly
LOC111886670	GO:1990904	Ribonucleoprotein complex
LOC111886670	GO:0016021	Integral component of membrane
LOC111886856	GO:0016788	Hydrolase activity, acting on ester bonds
LOC111886948	GO:0043565	Sequence-specific DNA binding
LOC111886948	GO:0005634	Nucleus
LOC111886948	GO:0006355	Regulation of transcription, DNA-templated
LOC111886948	GO:0003700	DNA-binding transcription factor activity
LOC111886948	GO:0001067	Regulatory region nucleic acid binding
LOC111886948	GO:0016740	Transferase activity
LOC111886948	GO:0003690	Double-stranded DNA binding
LOC111886948	GO:0009651	Response to salt stress
LOC111886948	GO:0009414	Response to water deprivation
LOC111887204	GO:0006979	Response to oxidative stress
LOC111887204	GO:0004601	Peroxidase activity
LOC111887204	GO:0098869	Cellular oxidant detoxification
LOC111887204	GO:0020037	Heme binding
LOC111887204	GO:0046872	Metal ion binding
LOC111887525	GO:0016887	ATPase activity
LOC111887525	GO:0016021	Integral component of membrane
LOC111887525	GO:0005524	ATP binding
LOC111887623	GO:0004190	Aspartic-type endopeptidase activity
LOC111887623	GO:0006508	Proteolysis
LOC111887623	GO:0005576	Extracellular region
LOC111887623	GO:0016021	Integral component of membrane
LOC111887689	GO:0016747	Transferase activity, transferring acyl groups other than amino-acyl groups
LOC111887815	GO:0016042	Lipid catabolic process
LOC111887815	GO:0045735	Nutrient reservoir activity
LOC111887815	GO:0005773	Vacuole
LOC111887815	GO:0016787	Hydrolase activity
LOC111887815	GO:0016740	Transferase activity
LOC111887815	GO:0016021	Integral component of membrane
LOC111887879	GO:0048046	Apoplast
LOC111887879	GO:0042973	Glucan endo-1,3-beta-D-glucosidase activity
LOC111887879	GO:0005975	Carbohydrate metabolic process
LOC111887879	GO:0016021	Integral component of membrane
LOC111887879	GO:0016874	Ligase activity
LOC111887884	GO:0048046	Apoplast
LOC111887884	GO:0042973	Glucan endo-1,3-beta-D-glucosidase activity

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Supplemental Table 2. (Continued)

Unique identifier	ID	GO term
LOC111887884	GO:0005975	Carbohydrate metabolic process
LOC111887884	GO:0016021	Integral component of membrane
LOC111887884	GO:0016874	Ligase activity
LOC111888402	GO:0006749	Glutathione metabolic process
LOC111888402	GO:0004364	Glutathione transferase activity
LOC111888402	GO:0005737	Cytoplasm
LOC111888833	GO:0004553	Hydrolase activity, hydrolyzing O-glycosyl compounds
LOC111888833	GO:0005975	Carbohydrate metabolic process
LOC111888833	GO:0005576	Extracellular region
LOC111888833	GO:0009501	Amyloplast
LOC111888833	GO:0042631	Cellular response to water deprivation
LOC111888833	GO:0005618	Cell wall
LOC111888833	GO:0006032	Chitin catabolic process
LOC111888833	GO:0016021	Integral component of membrane
LOC111888833	GO:0009642	Response to light intensity
LOC111888833	GO:0061783	Peptidoglycan muralytic activity
LOC111888833	GO:0004315	3-oxoacyl-[acyl-carrier-protein] synthase activity
LOC111888833	GO:0005509	Calcium ion binding
LOC111888833	GO:0009651	Response to salt stress
LOC111888833	GO:0004672	Protein kinase activity
LOC111888833	GO:0005524	ATP binding
LOC111888833	GO:0002221	Pattern recognition receptor signaling pathway
LOC111888833	GO:0009409	Response to cold
LOC111888833	GO:0009611	Response to wounding
LOC111888833	GO:0009845	Seed germination
LOC111888833	GO:0006633	Fatty acid biosynthetic process
LOC111888833	GO:0006468	Protein phosphorylation
LOC111889457	GO:0004864	Protein phosphatase inhibitor activity
LOC111889457	GO:0032515	Negative regulation of phosphoprotein phosphatase activity
LOC111889457	GO:0005737	Cytoplasm
LOC111889457	GO:0005886	Plasma membrane
LOC111889537	GO:0003824	Catalytic activity
LOC111889614	GO:0009651	Response to salt stress
LOC111889614	GO:0005802	Trans-Golgi network
LOC111889614	GO:0003729	mRNA binding
LOC111889614	GO:0005768	Endosome
LOC111889614	GO:0016021	Integral component of membrane
LOC111889708	GO:0019953	Sexual reproduction
LOC111889708	GO:0005576	Extracellular region
LOC111889708	GO:0003676	Nucleic acid binding
LOC111889708	GO:0009505	Plant-type cell wall
LOC111889708	GO:0009506	Plasmodesma
LOC111889708	GO:0015074	DNA integration
LOC111889708	GO:0005794	Golgi apparatus
LOC111889708	GO:0016021	Integral component of membrane
LOC111890174	GO:0000786	Nucleosome
LOC111890174	GO:0046982	Protein heterodimerization activity
LOC111890174	GO:0010274	Hydrotropism
LOC111890174	GO:0003677	DNA binding
LOC111890174	GO:0032259	Methylation
LOC111890174	GO:0016310	Phosphorylation
LOC111890174	GO:0005634	Nucleus
LOC111890174	GO:0016301	Kinase activity
LOC111890174	GO:0008168	Methyltransferase activity
LOC111890174	GO:0010369	Chromocenter
LOC111890174	GO:0016021	Integral component of membrane
LOC111890186	GO:0031408	Oxylipin biosynthetic process

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Supplemental Table 2. (Continued)

Unique identifier	ID	GO term
LOC111890186	GO:0046872	Metal ion binding
LOC111890404	GO:0006869	Lipid transport
LOC111890404	GO:0008289	Lipid binding
LOC111890404	GO:0016021	Integral component of membrane
LOC111890855	GO:0000325	Plant-type vacuole
LOC111890855	GO:0042626	ATPase-coupled transmembrane transporter activity
LOC111890855	GO:0055085	Transmembrane transport
LOC111890855	GO:0005774	Vacuolar membrane
LOC111890855	GO:0005524	ATP binding
LOC111890855	GO:0016021	Integral component of membrane
LOC111890880	GO:0042555	MCM complex
LOC111890880	GO:0006270	DNA replication initiation
LOC111890880	GO:0003678	DNA helicase activity
LOC111890880	GO:0005634	Nucleus
LOC111890880	GO:0032508	DNA duplex unwinding
LOC111890880	GO:0003677	DNA binding
LOC111890880	GO:0005524	ATP binding
LOC111890880	GO:0016021	Integral component of membrane
LOC111890880	GO:1902299	Pre-replicative complex assembly involved in cell cycle DNA replication
LOC111890880	GO:0000727	Double-strand break repair via break-induced replication
LOC111890880	GO:1902969	Mitotic DNA replication
LOC111890880	GO:0006271	DNA strand elongation involved in DNA replication
LOC111890880	GO:0004315	3-oxoacyl-[acyl-carrier-protein] synthase activity
LOC111890880	GO:0006633	Fatty acid biosynthetic process
LOC111890944	GO:0005524	ATP binding
LOC111890944	GO:0005829	Cytosol
LOC111890944	GO:0005634	Nucleus
LOC111890944	GO:0005788	Endoplasmic reticulum lumen
LOC111890944	GO:0016021	Integral component of membrane
LOC111890944	GO:0008270	Zinc ion binding
LOC111890944	GO:0003723	RNA binding
LOC111891003	GO:0016021	Integral component of membrane
LOC111891021	GO:0030246	Carbohydrate binding
LOC111891175	GO:0033897	Ribonuclease T2 activity
LOC111891175	GO:0090502	RNA phosphodiester bond hydrolysis, endonucleolytic
LOC111891175	GO:0005576	Extracellular region
LOC111891175	GO:0071944	Cell periphery
LOC111891175	GO:0016020	Membrane
LOC111891175	GO:0016829	Lyase activity
LOC111891175	GO:0006401	RNA catabolic process
LOC111891175	GO:0003723	RNA binding
LOC111891175	GO:0009718	Anthocyanin-containing compound biosynthetic process
LOC111891175	GO:0016036	Cellular response to phosphate starvation
LOC111891175	GO:0009611	Response to wounding
LOC111891175	GO:0009867	Jasmonic acid mediated signaling pathway
LOC111891273	GO:0006817	Phosphate ion transport
LOC111891273	GO:0022857	Transmembrane transporter activity
LOC111891273	GO:0005886	Plasma membrane
LOC111891273	GO:0016021	Integral component of membrane
LOC111891273	GO:0055085	Transmembrane transport
LOC111891273	GO:0006857	Oligopeptide transport
LOC111891273	GO:0015706	Nitrate transport
LOC111891273	GO:0010167	Response to nitrate
LOC111891616	GO:0015267	Channel activity
LOC111891616	GO:0006833	Water transport
LOC111891616	GO:0016021	Integral component of membrane
LOC111891616	GO:0055085	Transmembrane transport

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Supplemental Table 2. (Continued)

Unique identifier	ID	GO term
LOC111891616	GO:0005372	Water transmembrane transporter activity
LOC111891616	GO:0005774	Vacuolar membrane
LOC111891616	GO:0000326	Protein storage vacuole
LOC111891669	GO:0004672	Protein kinase activity
LOC111891669	GO:0006468	Protein phosphorylation
LOC111891669	GO:0005737	Cytoplasm
LOC111891669	GO:0005524	ATP binding
LOC111891669	GO:0007165	Signal transduction
LOC111891669	GO:0000186	Activation of MAPKK activity
LOC111892091	GO:0004185	Serine-type carboxypeptidase activity
LOC111892091	GO:0006508	Proteolysis
LOC111892091	GO:0016021	Integral component of membrane
LOC111892091	GO:0019748	Secondary metabolic process
LOC111892091	GO:0016747	Transferase activity, transferring acyl groups other than amino-acyl groups
LOC111892643	GO:0016301	Kinase activity
LOC111892643	GO:0006468	Protein phosphorylation
LOC111892643	GO:0005886	Plasma membrane
LOC111892643	GO:0016773	Phosphotransferase activity, alcohol group as acceptor
LOC111892643	GO:0140096	Catalytic activity, acting on a protein
LOC111892643	GO:0005524	ATP binding
LOC111892643	GO:0042742	Defense response to bacterium
LOC111892643	GO:0005515	Protein binding
LOC111893008	GO:0004478	Methionine adenosyltransferase activity
LOC111893008	GO:0006556	S-adenosylmethionine biosynthetic process
LOC111893008	GO:0005737	Cytoplasm
LOC111893008	GO:0006730	One-carbon metabolic process
LOC111893008	GO:0005524	ATP binding
LOC111893008	GO:0009506	Plasmodesma
LOC111893008	GO:0005634	Nucleus
LOC111893008	GO:0046872	Metal ion binding
LOC111893008	GO:0005886	Plasma membrane
LOC111893008	GO:0009860	Pollen tube growth
LOC111893008	GO:0012505	Endomembrane system
LOC111893008	GO:0016021	Integral component of membrane
LOC111893008	GO:0005515	Protein binding
LOC111893008	GO:0009809	Lignin biosynthetic process
LOC111893041	GO:0015267	Channel activity
LOC111893041	GO:0055085	Transmembrane transport
LOC111893041	GO:0016021	Integral component of membrane
LOC111893041	GO:0006833	Water transport
LOC111893041	GO:0005372	Water transmembrane transporter activity
LOC111893041	GO:0045490	Pectin catabolic process
LOC111893041	GO:0030599	Pectinesterase activity
LOC111893156	GO:0004435	Phosphatidylinositol phospholipase C activity
LOC111893156	GO:0016042	Lipid catabolic process
LOC111893156	GO:0005886	Plasma membrane
LOC111893156	GO:0035556	Intracellular signal transduction
LOC111893156	GO:0005509	Calcium ion binding
LOC111893156	GO:0003677	DNA binding
LOC111893156	GO:0042823	Pyridoxal phosphate biosynthetic process
LOC111893157	GO:0004435	Phosphatidylinositol phospholipase C activity
LOC111893157	GO:0016042	Lipid catabolic process
LOC111893157	GO:0005886	Plasma membrane
LOC111893157	GO:0035556	Intracellular signal transduction
LOC111893157	GO:0005509	Calcium ion binding
LOC111893157	GO:0005525	GTP binding
LOC111893157	GO:0042254	Ribosome biogenesis

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Supplemental Table 2. (Continued)

Unique identifier	ID	GO term
LOC111893573	GO:0016021	Integral component of membrane
LOC111893604	GO:0003700	DNA-binding transcription factor activity
LOC111893604	GO:0006355	Regulation of transcription, DNA-templated
LOC111893604	GO:0005634	Nucleus
LOC111893604	GO:0000976	Transcription regulatory region sequence-specific DNA binding
LOC111893604	GO:0016021	Integral component of membrane
LOC111893604	GO:0046982	Protein heterodimerization activity
LOC111893604	GO:0004707	MAP kinase activity
LOC111893604	GO:1903508	Positive regulation of nucleic acid-templated transcription
LOC111893604	GO:0000165	MAPK cascade
LOC111893677	GO:0043531	ADP binding
LOC111893677	GO:0006952	Defense response
LOC111893677	GO:0016021	Integral component of membrane
LOC111893677	GO:0006508	proteolysis
LOC111893677	GO:0008234	Cysteine-type peptidase activity
LOC111893677	GO:0005524	ATP binding
LOC111893962	GO:0008643	Carbohydrate transport
LOC111893962	GO:0051119	Sugar transmembrane transporter activity
LOC111893962	GO:0005886	Plasma membrane
LOC111893962	GO:0016021	Integral component of membrane
LOC111893962	GO:0008515	Sucrose transmembrane transporter activity
LOC111893962	GO:0098656	Anion transmembrane transport
LOC111894107	GO:0045548	Phenylalanine ammonia-lyase activity
LOC111894107	GO:0009800	Cinnamic acid biosynthetic process
LOC111894107	GO:0005737	Cytoplasm
LOC111894107	GO:0032991	Protein-containing complex
LOC111894107	GO:0016597	Amino acid binding
LOC111894107	GO:1902222	Erythrose 4-phosphate/phosphoenolpyruvate family amino acid catabolic process
LOC111894107	GO:0006558	L-phenylalanine metabolic process
LOC111894107	GO:0009074	Aromatic amino acid family catabolic process
LOC111894107	GO:0009063	Cellular amino acid catabolic process
LOC111894107	GO:0009820	Alkaloid metabolic process
LOC111894162	GO:0008194	UDP-glycosyltransferase activity
LOC111894162	GO:0016114	Terpenoid biosynthetic process
LOC111894162	GO:0048046	Apoplast
LOC111894162	GO:0022625	Cytosolic large ribosomal subunit
LOC111894162	GO:0005618	Cell wall
LOC111894162	GO:0004142	Diacylglycerol cholinephosphotransferase activity
LOC111894162	GO:0046527	Glucosyltransferase activity
LOC111894162	GO:0009718	Anthocyanin-containing compound biosynthetic process
LOC111894162	GO:0006657	CDP-choline pathway
LOC111894162	GO:0003735	Structural constituent of ribosome
LOC111894162	GO:0016021	Integral component of membrane
LOC111894162	GO:0043231	Intracellular membrane-bounded organelle
LOC111894162	GO:0002182	Cytoplasmic translational elongation
LOC111894162	GO:0006073	Cellular glucan metabolic process
LOC111894285	GO:0003978	UDP-glucose 4-epimerase activity
LOC111894285	GO:0006012	Galactose metabolic process
LOC111894375	GO:0005634	Nucleus
LOC111894375	GO:0043565	Sequence-specific DNA binding
LOC111894375	GO:0006355	Regulation of transcription, DNA templated
LOC111894375	GO:0003700	DNA-binding transcription factor activity
LOC111894375	GO:0003824	Catalytic activity
LOC111894375	GO:0010373	Negative regulation of gibberellin biosynthetic process
LOC111894375	GO:0009686	Gibberellin biosynthetic process
LOC111894375	GO:0010015	Root morphogenesis
LOC111894375	GO:0009740	Gibberellic acid mediated signaling pathway

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Supplemental Table 2. (Continued)

Unique identifier	ID	GO term
LOC111894375	GO:0016036	Cellular response to phosphate starvation
LOC111894375	GO:0072506	Trivalent inorganic anion homeostasis
LOC111894375	GO:1903507	Negative regulation of nucleic acid-templated transcription
LOC111894375	GO:2000113	Negative regulation of cellular macromolecule biosynthetic process
LOC111894539	GO:0016757	Transferase activity, transferring glycosyl groups
LOC111894539	GO:0016020	Membrane
LOC111894539	GO:0042546	Cell wall biogenesis
LOC111894539	GO:0005773	Vacuole
LOC111894781	GO:0008194	UDP-glycosyltransferase activity
LOC111894781	GO:0009718	Anthocyanin-containing compound biosynthetic process
LOC111894781	GO:0016021	Integral component of membrane
LOC111894781	GO:0046527	Glucosyltransferase activity
LOC111894781	GO:0016114	Terpenoid biosynthetic process
LOC111895349	GO:0008643	Carbohydrate transport
LOC111895349	GO:0051119	Sugar transmembrane transporter activity
LOC111895349	GO:0005886	Plasma membrane
LOC111895349	GO:0016021	Integral component of membrane
LOC111895349	GO:0098656	Anion transmembrane transport
LOC111895776	GO:0031408	Oxylipin biosynthetic process
LOC111895776	GO:0046872	Metal ion binding
LOC111895825	GO:0004672	Protein kinase activity
LOC111895825	GO:0006468	Protein phosphorylation
LOC111895825	GO:0005886	Plasma membrane
LOC111895825	GO:0016021	Integral component of membrane
LOC111895825	GO:0005524	ATP binding
LOC111895825	GO:0005634	Nucleus
LOC111895825	GO:0009755	Hormone-mediated signaling pathway
LOC111895825	GO:0033612	Receptor serine/threonine kinase binding
LOC111895825	GO:0008168	Methyltransferase activity
LOC111895825	GO:0046873	Metal ion transmembrane transporter activity
LOC111895825	GO:0006397	mRNA processing
LOC111895825	GO:0032259	Methylation
LOC111895825	GO:0030001	Metal ion transport
LOC111895937	GO:0005576	Extracellular region
LOC111895937	GO:0019953	Sexual reproduction
LOC111895937	GO:0016021	Integral component of membrane
LOC111896412	GO:0006979	Response to oxidative stress
LOC111896412	GO:0020037	Heme binding
LOC111896412	GO:0004601	Peroxidase activity
LOC111896412	GO:0098869	Cellular oxidant detoxification
LOC111896412	GO:0046872	Metal ion binding
LOC111896417	GO:0005634	Nucleus
LOC111896417	GO:0010119	Regulation of stomatal movement
LOC111896417	GO:0016021	Integral component of membrane
LOC111896675	GO:0006629	Lipid metabolic process
LOC111897180	GO:0031012	Extracellular matrix
LOC111897180	GO:0030574	Collagen catabolic process
LOC111897180	GO:0004222	Metalloendopeptidase activity
LOC111897180	GO:0030198	Extracellular matrix organization
LOC111897180	GO:0008270	Zinc ion binding
LOC111897180	GO:0006508	Proteolysis
LOC111897395	GO:0004672	Protein kinase activity
LOC111897395	GO:0006468	Protein phosphorylation
LOC111897395	GO:0016021	Integral component of membrane
LOC111897395	GO:0005886	Plasma membrane
LOC111897395	GO:0005524	ATP binding
LOC111897395	GO:0006004	Fucose metabolic process

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Supplemental Table 2. (Continued)

Unique identifier	ID	GO term
LOC111897395	GO:0005515	Protein binding
LOC111898199	GO:0043565	Sequence-specific DNA binding
LOC111898199	GO:0005634	Nucleus
LOC111898199	GO:0006355	Regulation of transcription, DNA-templated
LOC111898199	GO:0003700	DNA-binding transcription factor activity
LOC111898199	GO:0016021	Integral component of membrane
LOC111898199	GO:0001067	Regulatory region nucleic acid binding
LOC111898199	GO:0003690	Double-stranded DNA binding
LOC111898200	GO:0043565	Sequence-specific DNA binding
LOC111898200	GO:0005634	Nucleus
LOC111898200	GO:0006355	Regulation of transcription, DNA-templated
LOC111898200	GO:0003700	DNA-binding transcription factor activity
LOC111898200	GO:0001067	Regulatory region nucleic acid binding
LOC111898200	GO:0003690	Double-stranded DNA binding
LOC111898200	GO:0043531	ADP binding
LOC111898200	GO:0005515	Protein binding
LOC111898200	GO:0080151	Positive regulation of salicylic acid-mediated signaling pathway
LOC111898200	GO:0080187	Floral organ senescence
LOC111898200	GO:1900056	Negative regulation of leaf senescence
LOC111898200	GO:0009862	Systemic acquired resistance, salicylic acid mediated signaling pathway
LOC111898200	GO:0009625	Response to insect
LOC111898200	GO:0010104	Regulation of ethylene-activated signaling pathway
LOC111898200	GO:0009864	Induced systemic resistance, jasmonic acid-mediated signaling pathway
LOC111898200	GO:1900457	Regulation of brassinosteroid-mediated signaling pathway
LOC111898200	GO:0090333	Regulation of stomatal closure
LOC111898200	GO:2000070	Regulation of response to water deprivation
LOC111898200	GO:0010200	Response to chitin
LOC111898200	GO:2000022	Regulation of jasmonic acid-mediated Signaling pathway
LOC111898200	GO:0010150	Leaf senescence
LOC111898200	GO:0047484	Regulation of response to osmotic stress
LOC111898200	GO:0002229	Defense response to oomycetes
LOC111898200	GO:0050832	Defense response to fungus
LOC111898200	GO:0006970	Response to osmotic stress
LOC111898200	GO:0000302	Response to reactive oxygen species
LOC111898200	GO:1903507	Negative regulation of nucleic acid-templated transcription
LOC111898200	GO:2000113	Negative regulation of cellular macromolecule biosynthetic process
LOC111898200	GO:0009742	Brassinosteroid-mediated signaling pathway
LOC111898200	GO:0009873	Ethylene-activated signaling pathway
LOC111898200	GO:0071456	Cellular response to hypoxia
LOC111898297	GO:0047325	Inositol tetrakisphosphate 1-kinase activity
LOC111898297	GO:0032957	Inositol trisphosphate metabolic process
LOC111898297	GO:0005829	Cytosol
LOC111898297	GO:0052726	Inositol-1,3,4-trisphosphate 5-kinase activity
LOC111898297	GO:0052725	Inositol-1,3,4-trisphosphate 6-kinase activity
LOC111898297	GO:0005840	Ribosome
LOC111898297	GO:0000287	Magnesium ion binding
LOC111898297	GO:0052746	Inositol phosphorylation
LOC111898297	GO:0005524	ATP binding
LOC111898297	GO:0010264	Myo-inositol hexakisphosphate biosynthetic process
LOC111898297	GO:0003735	Structural constituent of ribosome
LOC111898297	GO:0006412	Translation
LOC111898348	GO:0031490	Chromatin DNA binding
LOC111898348	GO:0045893	Positive regulation of transcription, DNA-templated
LOC111898348	GO:0005634	Nucleus
LOC111898348	GO:0003713	Transcription coactivator activity
LOC111898411	GO:0009734	Auxin-activated signaling pathway
LOC111898411	GO:0005634	Nucleus

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Supplemental Table 2. (Continued)

Unique identifier	ID	GO term
LOC111898411	GO:0003830	Beta-1,4-mannosylglycoprotein 4-beta-N-acetylglucosaminyltransferase activity
LOC111898411	GO:0016020	Membrane
LOC111898411	GO:0006355	Regulation of transcription, DNA-templated
LOC111898411	GO:0010218	Response to far red light
LOC111898411	GO:0010114	Response to red light
LOC111898411	GO:0006487	Protein N-linked glycosylation
LOC111898411	GO:0009736	Cytokinin-activated signaling pathway
LOC111898411	GO:0018215	Protein phosphopantetheinylation
LOC111898411	GO:0000160	Phosphorelay signal transduction system
LOC111898508	GO:0008194	UDP-glycosyltransferase activity
LOC111898611	GO:0042026	Protein refolding
LOC111898611	GO:0005524	ATP binding
LOC111898611	GO:0009570	Chloroplast stroma
LOC111898611	GO:0051085	Chaperone cofactor-dependent protein refolding
LOC111898611	GO:0022626	Cytosolic ribosome
LOC111898626	GO:0008194	UDP-glycosyltransferase activity
LOC111898626	GO:0009718	Anthocyanin-containing compound biosynthetic process
LOC111898626	GO:0046527	Glucosyltransferase activity
LOC111898626	GO:0019761	Glucosinolate biosynthetic process
LOC111898626	GO:0052544	Defense response by callose deposition in cell wall
LOC111898626	GO:0042742	Defense response to bacterium
LOC111898732	GO:0046872	Metal ion binding
LOC111898732	GO:0016567	Protein ubiquitination
LOC111898732	GO:0005634	Nucleus
LOC111898732	GO:0005516	Calmodulin binding
LOC111898732	GO:0005737	Cytoplasm
LOC111898732	GO:0009751	Response to salicylic acid
LOC111898732	GO:0009553	ERmbryo sac development
LOC111898732	GO:0009555	Pollen development
LOC111898732	GO:0042542	Response to hydrogen peroxide
LOC111898732	GO:0009733	Response to auxin
LOC111898732	GO:0006355	Regulation of transcription, DNA-templated
LOC111899032	GO:0004197	Cysteine-type endopeptidase activity
LOC111899032	GO:0006508	Proteolysis
LOC111899252	GO:0010333	Terpene synthase activity
LOC111899252	GO:0006720	Isoprenoid metabolic process
LOC111899252	GO:0005737	Cytoplasm
LOC111899252	GO:0000287	Magnesium ion binding
LOC111899252	GO:0008610	Lipid biosynthetic process
LOC111899252	GO:0102698	5-epi-aristolochene synthase activity
LOC111899252	GO:0120252	Hydrocarbon metabolic process
LOC111899252	GO:0006952	Defense response
LOC111899252	GO:0009975	Cyclase activity
LOC111899252	GO:0044249	Cellular biosynthetic process
LOC111899252	GO:0052682	Epi-cedrol synthase activity
LOC111899252	GO:0009739	Response to gibberellin
LOC111899252	GO:0000302	Response to reactive oxygen species
LOC111899324	GO:0004805	Trehalose-phosphatase activity
LOC111899324	GO:0005992	Trehalose biosynthetic process
LOC111899324	GO:0016021	Integral component of membrane
LOC111899324	GO:0005829	Cytosol
LOC111899324	GO:0009507	Chloroplast
LOC111899324	GO:0016311	Dephosphorylation
LOC111899324	GO:0015927	Trehalase activity
LOC111899324	GO:0005634	Nucleus
LOC111899324	GO:0009651	Response to salt stress
LOC111899324	GO:0006979	Response to oxidative stress

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Supplemental Table 2. (Continued)

Unique identifier	ID	GO term
LOC111899382	GO:0042973	Glucan endo-1,3-beta-D-glucosidase activity
LOC111899382	GO:0006952	Defense response
LOC111899382	GO:0046658	Anchored component of plasma membrane
LOC111899382	GO:0005975	Carbohydrate metabolic process
LOC111899806	GO:0090376	Seed trichome differentiation
LOC111899806	GO:0016021	Integral component of membrane
LOC111899806	GO:0009735	Response to cytokinin
LOC111899806	GO:0005576	Extracellular region
LOC111899806	GO:0009739	Response to gibberellin
LOC111899806	GO:0009651	Response to salt stress
LOC111899806	GO:0009737	Response to abscisic acid
LOC111899806	GO:0009733	Response to auxin
LOC111899806	GO:0007155	Cell adhesion
LOC111900059	GO:0016787	Hydrolase activity
LOC111900135	GO:0005524	ATP binding
LOC111900135	GO:0016021	Integral component of membrane
LOC111900177	GO:0016042	Lipid catabolic process
LOC111900177	GO:0045735	Nutrient reservoir activity
LOC111900177	GO:0005773	Vacuole
LOC111900177	GO:0016787	Hydrolase activity
LOC111900177	GO:0016740	Transferase activity
LOC111900177	GO:0016021	Integral component of membrane
LOC111900246	GO:0016984	Ribulose-bisphosphate carboxylase activity
LOC111900246	GO:0009853	Photorespiration
LOC111900246	GO:0015979	Photosynthesis
LOC111900275	GO:0030001	Metal ion transport
LOC111900275	GO:0046872	Metal ion binding
LOC111900275	GO:0016020	Membrane
LOC111900275	GO:0055073	Cadmium ion homeostasis
LOC111900275	GO:0071585	Detoxification of cadmium ion
LOC111900788	GO:0031225	Anchored component of membrane
LOC111900788	GO:0016021	Integral component of membrane
LOC111900976	GO:0004185	Serine-type carboxypeptidase activity
LOC111900976	GO:0019748	Secondary metabolic process
LOC111900976	GO:0005576	Extracellular region
LOC111900976	GO:0006508	Proteolysis
LOC111900976	GO:0016021	Integral component of membrane
LOC111900976	GO:0016747	Transferase activity, transferring acyl groups other than amino-acyl groups
LOC111901004	GO:0010333	Terpene synthase activity
LOC111901004	GO:0016102	Diterpenoid biosynthetic process
LOC111901004	GO:0009536	Plastid
LOC111901004	GO:0000287	Magnesium ion binding
LOC111901004	GO:0016021	Integral component of membrane
LOC111901004	GO:0080027	Response to herbivore
LOC111901004	GO:0000304	Response to singlet oxygen
LOC111901004	GO:0080013	(E,E)-geranylinalool synthase activity
LOC111901004	GO:0009753	Response to jasmonic acid
LOC111901004	GO:0050554	Abietadiene synthase activity
LOC111901004	GO:0009611	Response to wounding
LOC111901004	GO:0009617	Response to bacterium
LOC111901011	GO:0005634	Nucleus
LOC111901011	GO:0043565	Sequence-specific DNA binding
LOC111901011	GO:0006355	Regulation of transcription, DNA-templated
LOC111901011	GO:0003700	DNA-binding transcription factor activity
LOC111901019	GO:0005509	Calcium ion binding
LOC111901426	GO:0047769	Arogenate dehydratase activity
LOC111901426	GO:0009570	Chloroplast stroma

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Supplemental Table 2. (Continued)

Unique identifier	ID	GO term
LOC111901426	GO:1902223	Erythrose 4-phosphate/phosphoenolpyruvate family amino acid biosynthetic process
LOC111901426	GO:0004664	Prephenate dehydratase activity
LOC111901426	GO:0009095	Aromatic amino acid family biosynthetic process, prephenate pathway
LOC111901426	GO:0006558	L-phenylalanine metabolic process
LOC111901426	GO:0004106	Chorismate mutase activity
LOC111901426	GO:0008652	Cellular amino acid biosynthetic process
LOC111901426	GO:0016021	Integral component of membrane
LOC111901426	GO:0007623	Circadian rhythm
LOC111901838	GO:0005634	Nucleus
LOC111901838	GO:0006355	Regulation of transcription, DNA-templated
LOC111901838	GO:0005737	Cytoplasm
LOC111901841	GO:0046423	Allene-oxide cyclase activity
LOC111901841	GO:0009695	Jasmonic acid biosynthetic process
LOC111901841	GO:0009507	Chloroplast
LOC111901841	GO:0046872	Metal ion binding
LOC111901841	GO:0005634	Nucleus
LOC111901841	GO:0016021	Integral component of membrane
LOC111901841	GO:0033274	Response to vitamin B ₂
LOC111901841	GO:1900367	Positive regulation of defense response to insect
LOC111901841	GO:0080186	Developmental vegetative growth
LOC111901841	GO:0009625	Response to insect
LOC111901841	GO:0009864	Induced systemic resistance, jasmonic acid-mediated signaling pathway
LOC111901841	GO:0010218	Response to far red light
LOC111901841	GO:0009646	Response to absence of light
LOC111901841	GO:0010114	Response to red light
LOC111901841	GO:0048573	Photoperiodism, flowering
LOC111901841	GO:0009751	Response to salicylic acid
LOC111901841	GO:0009723	Response to ethylene
LOC111901841	GO:0042542	Response to hydrogen peroxide
LOC111901841	GO:0009651	Response to salt stress
LOC111901841	GO:0009908	Flower development
LOC111901841	GO:0050832	Defense response to fungus
LOC111901841	GO:0009637	Response to blue light
LOC111901841	GO:0009737	Response to abscisic acid
LOC111901841	GO:0007623	Circadian rhythm
LOC111901841	GO:0009734	Auxin-activated signaling pathway
LOC111901841	GO:0009611	Response to wounding
LOC111901841	GO:0010038	Response to metal ion
LOC111902058	GO:0004553	Hydrolase activity, hydrolyzing O-glycosyl compounds
LOC111902058	GO:0005576	Extracellular region
LOC111902058	GO:0031222	Arabinan catabolic process
LOC111902058	GO:0009505	Plant-type cell wall
LOC111902058	GO:0045493	Xylan catabolic process
LOC111902058	GO:0016021	Integral component of membrane
LOC111902216	GO:0009664	Plant-type cell wall organization
LOC111902216	GO:0005618	Cell wall
LOC111902216	GO:0005576	Extracellular region
LOC111902216	GO:0016020	Membrane
LOC111902216	GO:0006949	Syncytium formation
LOC111902319	GO:0016874	Ligase activity
LOC111903004	GO:0008171	O-methyltransferase activity
LOC111903004	GO:0032259	Methylation
LOC111903004	GO:0016021	Integral component of membrane
LOC111903004	GO:0019438	Aromatic compound biosynthetic process
LOC111903004	GO:0046983	Protein dimerization activity
LOC111903004	GO:0008757	S-adenosylmethionine-dependent methyltransferase activity
LOC111903226	GO:0042910	Xenobiotic transmembrane transporter activity

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Supplemental Table 2. (Continued)

Unique identifier	ID	GO term
LOC111903226	GO:0042908	Xenobiotic transport
LOC111903226	GO:0016021	Integral component of membrane
LOC111903226	GO:0015297	Antiporter activity
LOC111903226	GO:0055085	Transmembrane transport
LOC111903232	GO:0003700	DNA-binding transcription factor activity
LOC111903232	GO:0005634	Nucleus
LOC111903232	GO:0006355	Regulation of transcription, DNA-templated
LOC111903232	GO:0003677	DNA binding
LOC111903232	GO:0001067	Regulatory region nucleic acid binding
LOC111903232	GO:0009873	Ethylene-activated signaling pathway
LOC111903232	GO:0006952	Defense response
LOC111903232	GO:0019757	glycosinolate metabolic process
LOC111903232	GO:0016143	S-glycoside metabolic process
LOC111903232	GO:0009620	Response to fungus
LOC111903232	GO:1901564	Organonitrogen compound metabolic process
LOC111903507	GO:0016787	Hydrolase activity
LOC111903507	GO:0070646	Protein modification by small protein removal
LOC111903507	GO:0005634	Nucleus
LOC111903507	GO:0005737	Cytoplasm
LOC111903572	GO:0010333	Terpene synthase activity
LOC111903572	GO:0033383	Geranyl diphosphate metabolic process
LOC111903572	GO:0009536	plastid
LOC111903572	GO:0016114	Terpenoid biosynthetic process
LOC111903572	GO:0000287	Magnesium ion binding
LOC111903572	GO:0009611	Response to wounding
LOC111903572	GO:0034008	R-linalool synthase activity
LOC111903572	GO:1901941	(+)-epi-alpha-bisabolol metabolic process
LOC111903572	GO:0045339	Farnesyl diphosphate catabolic process
LOC111903849	GO:0003700	DNA-binding transcription factor activity
LOC111903849	GO:0005634	Nucleus
LOC111903849	GO:0006355	Regulation of transcription, DNA-templated
LOC111903849	GO:0003677	DNA binding
LOC111903849	GO:0006952	Defense response
LOC111903849	GO:0010492	Maintenance of shoot apical meristem identity
LOC111903849	GO:0019757	Glycosinolate metabolic process
LOC111903849	GO:0016143	S-glycoside metabolic process
LOC111903849	GO:0009908	Flower development
LOC111903849	GO:0042127	Regulation of cell population proliferation
LOC111903849	GO:0030154	Cell differentiation
LOC111903849	GO:1901564	Organonitrogen compound metabolic process
LOC111903871	GO:0004672	Protein kinase activity
LOC111903871	GO:0006468	Protein phosphorylation
LOC111903871	GO:0005829	Cytosol
LOC111903871	GO:0005524	ATP binding
LOC111903871	GO:0071456	Cellular response to hypoxia
LOC111903871	GO:0009658	Chloroplast organization
LOC111903871	GO:0009737	Response to abscisic acid
LOC111904177	GO:0005773	Vacuole
LOC111904177	GO:0015031	Protein transport
LOC111904177	GO:0061630	Ubiquitin protein ligase activity
LOC111904177	GO:0016021	Integral component of membrane
LOC111904177	GO:0030170	Pyridoxal phosphate binding
LOC111904177	GO:0005515	Protein binding
LOC111904177	GO:0022857	Transmembrane transporter activity
LOC111904177	GO:0006511	Ubiquitin-dependent protein catabolic process
LOC111904177	GO:0046872	Metal ion binding
LOC111904177	GO:0016567	Protein ubiquitination

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Supplemental Table 2. (Continued)

Unique identifier	ID	GO term
LOC111904177	GO:0000139	Golgi membrane
LOC111904177	GO:0019346	Transsulfuration
LOC111904177	GO:0006817	Phosphate ion transport
LOC111904177	GO:0055085	Transmembrane transport
LOC111904236	GO:0004185	Serine-type carboxypeptidase activity
LOC111904236	GO:0006508	Proteolysis
LOC111904561	GO:0016757	Transferase activity, transferring glycosyl groups
LOC111904561	GO:0005794	Golgi apparatus
LOC111904561	GO:0090406	Pollen tube
LOC111904561	GO:0016021	Integral component of membrane
LOC111905143	GO:0008194	UDP-glycosyltransferase activity
LOC111905143	GO:0009718	Anthocyanin-containing compound biosynthetic process
LOC111905143	GO:0016021	Integral component of membrane
LOC111905143	GO:0046527	Glucosyltransferase activity
LOC111905143	GO:0016114	Terpenoid biosynthetic process
LOC111905143	GO:0004672	Protein kinase activity
LOC111905143	GO:0005524	ATP binding
LOC111905143	GO:0006468	Protein phosphorylation
LOC111905147	GO:0004013	Adenosylhomocysteinase activity
LOC111905147	GO:0006730	One-carbon metabolic process
LOC111905147	GO:0005829	Cytosol
LOC111905147	GO:0033353	S-adenosylmethionine cycle
LOC111905147	GO:0005773	Vacuole
LOC111905147	GO:0009506	Plasmodesma
LOC111905147	GO:0003729	mRNA binding
LOC111905147	GO:0006346	DNA methylation-dependent heterochromatin assembly
LOC111905147	GO:0005507	Copper ion binding
LOC111905147	GO:0005515	Protein binding
LOC111876248	GO:0046873	Metal ion binding
LOC111876395	GO:0010089	Phloem development
LOC111876395	GO:0016022	Integral component of membrane
LOC111876518	GO:0055086	Transmembrane transport
LOC111876518	GO:0005887	Plasma membrane
LOC111876518	GO:0008309	Voltage-gated anion channel activity
LOC111876518	GO:0016022	Integral component of membrane
LOC111876518	GO:0006874	Cellular ion homeostasis
LOC111876518	GO:0015699	Inorganic anion transport
LOC111876729	GO:0003888	DNA-directed DNA polymerase activity
LOC111876729	GO:0071898	DNA biosynthetic process
LOC111876729	GO:0005635	Nucleus
LOC111876729	GO:0006261	DNA replication
LOC111876729	GO:0051540	5 iron, 4 sulfur cluster binding
LOC111876729	GO:0022617	DNA strand elongation
LOC111876729	GO:0019104	Pyrimidine nucleotide binding
LOC111876729	GO:0000429	DNA-directed RNA polymerase complex
LOC111876729	GO:0003678	DNA binding
LOC111876729	GO:0003897	DNA primase activity
LOC111876729	GO:0030895	Replisome
LOC111876729	GO:0042576	DNA polymerase complex
LOC111876729	GO:0046873	Metal ion binding
LOC111876729	GO:0003683	Chromatin binding
LOC111876729	GO:0070014	Intracellular organelle lumen
LOC111876729	GO:0043234	Organelle lumen
LOC111876729	GO:0009966	Leaf morphogenesis
LOC111876729	GO:1903048	Mitotic cell cycle process
LOC111876729	GO:0017077	Purine nucleotide binding
LOC111876729	GO:0032775	RNA biosynthetic process

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Supplemental Table 2. (Continued)

Unique identifier	ID	GO term
LOC111876788	GO:0016882	Acid-amino acid ligase activity
LOC111876788	GO:0005738	Cytoplasm
LOC111876788	GO:0102058	Jasmonoyl-valine synthetase activity
LOC111876788	GO:0102054	(-)-jasmonoyl-isoleucine synthetase activity
LOC111876788	GO:0102059	Jasmonoyl-leucine synthetase activity
LOC111877040	GO:0031013	Extracellular matrix
LOC111877040	GO:0030575	Collagen catabolic process
LOC111877040	GO:0004223	Metalloendopeptidase activity
LOC111877040	GO:0030199	Extracellular matrix organization
LOC111877040	GO:0008271	Zinc ion binding
LOC111877040	GO:0006509	Proteolysis
LOC111877142	GO:0016788	Hydrolase activity
LOC111877486	GO:0005508	Copper ion binding
LOC111877486	GO:0030002	Metal ion transport
LOC111877486	GO:0016022	Integral component of membrane
LOC111877486	GO:0019830	ATPase-coupled cation transmembrane transporter activity
LOC111877486	GO:0035435	Copper ion transmembrane transport
LOC111877486	GO:0043683	Copper transmembrane transporter activity, phosphorylative mechanism
LOC111877486	GO:0072512	Divalent inorganic cation transport
LOC111877486	GO:0005525	ATP binding
LOC111877831	GO:0016788	Hydrolase activity
LOC111877831	GO:0043532	ADP binding
LOC111879317	GO:0009507	Plasmodesma
LOC111879317	GO:0046778	Protein autophosphorylation
LOC111879317	GO:0004673	Protein kinase activity
LOC111879317	GO:0005887	Plasma membrane
LOC111879317	GO:0005525	ATP binding
LOC111879317	GO:0016022	Integral component of membrane
LOC111879317	GO:0005510	Calcium ion binding
LOC111879404	GO:0005738	Cytoplasm
LOC111879404	GO:0009652	Response to salt stress
LOC111879404	GO:0003969	RNA-directed 5'-3' RNA polymerase activity
LOC111879404	GO:0009415	Response to water deprivation
LOC111879404	GO:0009410	Response to cold
LOC111879404	GO:0042652	Thylakoid membrane
LOC111879404	GO:0001173	Transcription, RNA-templated
LOC111879404	GO:0039695	Viral RNA genome replication
LOC111879404	GO:0098589	Bounding membrane of organelle
LOC111879404	GO:0031985	Organelle subcompartment
LOC111879404	GO:0012506	Endomembrane system
LOC111879404	GO:0016022	Integral component of membrane
LOC111879404	GO:0043232	Intracellular membrane-bounded organelle
LOC111879404	GO:0005887	Plasma membrane
LOC111880354	GO:0016788	Hydrolase activity
LOC111880354	GO:0016022	Integral component of membrane
LOC111880882	GO:0010092	Trichome branching
LOC111880980	GO:0046984	Protein dimerization activity
LOC111880980	GO:0005635	Nucleus
LOC111880980	GO:0003724	RNA binding
LOC111880980	GO:0016022	Integral component of membrane
LOC111881023	GO:0106312	NA
LOC111881023	GO:0006469	Protein phosphorylation
LOC111881023	GO:0005887	Plasma membrane
LOC111881023	GO:0106311	NA
LOC111881023	GO:0030247	Carbohydrate binding
LOC111881023	GO:0016022	Integral component of membrane
LOC111881023	GO:0005525	ATP binding

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Supplemental Table 2. (Continued)

Unique identifier	ID	GO term
LOC111881483	GO:0006630	Lipid metabolic process
LOC111881483	GO:0005635	Nucleus
LOC111881483	GO:0016788	Hydrolase activity
LOC111881493	GO:0006630	Lipid metabolic process
LOC111881493	GO:0005635	Nucleus
LOC111881493	GO:0080031	Methyl indole-3-acetate esterase activity
LOC111881493	GO:0009821	Alkaloid metabolic process
LOC111881493	GO:0016022	Integral component of membrane
LOC111881555	GO:0004673	Protein kinase activity
LOC111881555	GO:0006469	Protein phosphorylation
LOC111881555	GO:0016022	Integral component of membrane
LOC111881555	GO:0005887	Plasma membrane
LOC111881555	GO:0005525	ATP binding
LOC111881555	GO:0005526	GTP binding
LOC111881555	GO:0003677	Nucleic acid binding
LOC111881703	GO:0016022	Integral component of membrane
LOC111881703	GO:0003736	Structural constituent of ribosome
LOC111881703	GO:0006413	Translation
LOC111881703	GO:0005841	Ribosome
LOC111881936	GO:0009508	Chloroplast
LOC111881936	GO:0015980	Photosynthesis
LOC111881936	GO:0046873	Metal ion binding
LOC111881936	GO:0071492	Cellular response to red light
LOC111881936	GO:0009580	Thylakoid
LOC111881936	GO:0071491	Cellular response to far red light
LOC111881936	GO:0010118	Photoprotection
LOC111881936	GO:0071487	Cellular response to high light intensity
LOC111881936	GO:0010031	Positive regulation of seed germination
LOC111881936	GO:0071493	Cellular response to ultraviolet-A
LOC111881936	GO:0031985	Organelle subcompartment
LOC111881936	GO:0098797	Membrane protein complex
LOC111881936	GO:0071484	Cellular response to blue light
LOC111881936	GO:0010381	Regulation of chlorophyll biosynthetic process
LOC111881936	GO:0016022	Integral component of membrane
LOC111881936	GO:0080168	Response to karrikin
LOC111881936	GO:0034606	Cellular response to heat
LOC111881936	GO:0009410	Response to cold
LOC111881936	GO:0010225	Response to ultraviolet-B
LOC111881938	GO:0009508	Chloroplast
LOC111881938	GO:0015980	Photosynthesis
LOC111881938	GO:0046873	Metal ion binding
LOC111881938	GO:0071492	Cellular response to red light
LOC111881938	GO:0009580	Thylakoid
LOC111881938	GO:0071491	Cellular response to far red light
LOC111881938	GO:0010118	Photoprotection
LOC111881938	GO:0071487	Cellular response to high light intensity
LOC111881938	GO:0010031	Positive regulation of seed germination
LOC111881938	GO:0071493	Cellular response to ultraviolet-A
LOC111881938	GO:0031985	Organelle subcompartment
LOC111881938	GO:0098797	Membrane protein complex
LOC111881938	GO:0071484	Cellular response to blue light
LOC111881938	GO:0010381	Regulation of chlorophyll biosynthetic process
LOC111881938	GO:0016022	Integral component of membrane
LOC111881938	GO:0080168	Response to karrikin
LOC111881938	GO:0034606	Cellular response to heat
LOC111881938	GO:0009410	Response to cold
LOC111881938	GO:0010225	Response to ultraviolet B

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Supplemental Table 2. (Continued)

Unique identifier	ID	GO term
LOC111882124	GO:0006818	Phosphate ion transport
LOC111882124	GO:0022858	Transmembrane transporter activity
LOC111882124	GO:0016022	Integral component of membrane
LOC111882124	GO:0055086	Transmembrane transport
LOC111882378	GO:0019954	Sexual reproduction
LOC111882378	GO:0005577	Extracellular region
LOC111882480	GO:0005525	ATP binding
LOC111882485	GO:0003701	DNA-binding transcription factor activity
LOC111882485	GO:0005635	Nucleus
LOC111882485	GO:0006356	Regulation of transcription, DNA-templated
LOC111882485	GO:0003678	DNA binding
LOC111882485	GO:0005516	Protein binding
LOC111882485	GO:0006953	Defense response
LOC111882485	GO:0009874	Ethylene-activated signaling pathway
LOC111882589	GO:0004708	MAP kinase activity
LOC111882589	GO:0000166	MAPK cascade
LOC111882589	GO:0005939	Cell cortex
LOC111882589	GO:0006469	Protein phosphorylation
LOC111882589	GO:0005635	Nucleus
LOC111882589	GO:0005525	ATP binding
LOC111882589	GO:0016022	Integral component of membrane
LOC111882589	GO:0080137	Priming of cellular response to stress
LOC111882589	GO:0052318	Camalexin metabolic process
LOC111882589	GO:0009701	Indole phytoalexin biosynthetic process
LOC111882589	GO:1902066	Response to L-glutamate
LOC111882589	GO:0005516	Protein binding
LOC111882589	GO:1901003	Positive regulation of response to salt stress
LOC111882589	GO:0022858	Transmembrane transporter activity
LOC111882589	GO:0010230	Inflorescence development
LOC111882589	GO:0050827	Response to freezing
LOC111882589	GO:0048482	Plant ovule development
LOC111882589	GO:0010184	Pollen tube guidance
LOC111882589	GO:0010201	Response to chitin
LOC111882589	GO:0010225	Response to ultraviolet B
LOC111882589	GO:0009556	Pollen development
LOC111882589	GO:0009415	Response to water deprivation
LOC111882589	GO:0050833	Defense response to fungus
LOC111882589	GO:0006971	Response to osmotic stress
LOC111882589	GO:0009612	Response to wounding
LOC111882589	GO:0009618	Response to bacterium
LOC111882589	GO:0006980	Response to oxidative stress
LOC111882589	GO:0044273	Sulfur compound biosynthetic process
LOC111882589	GO:0010469	Regulation of gene expression
LOC111882589	GO:0009627	Plant-type hypersensitive response
LOC111882589	GO:0009739	Absciscic acid-activated signaling pathway
LOC111882589	GO:0006858	Oligopeptide transport
LOC111882589	GO:0055086	Transmembrane transport
LOC111882696	GO:0016788	Hydrolase activity
LOC111882722	GO:0005887	Plasma membrane
LOC111882722	GO:0034155	Toll-like receptor 7 signaling pathway
LOC111882722	GO:0003728	Single-stranded RNA binding
LOC111882722	GO:0002756	MyD88-dependent toll-like receptor signaling pathway
LOC111882722	GO:0004889	Transmembrane signaling receptor activity
LOC111882722	GO:0016022	Integral component of membrane
LOC111882722	GO:0051608	Defense response to virus
LOC111882722	GO:0006956	Immune response
LOC111882971	GO:0050291	Sphingomyelin phosphodiesterase D activity

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Supplemental Table 2. (Continued)

Unique identifier	ID	GO term
LOC111882971	GO:0016022	Integral component of membrane
LOC111882973	GO:0015268	Channel activity
LOC111882973	GO:0006834	Water transport
LOC111882973	GO:0016022	Integral component of membrane
LOC111882973	GO:0055086	Transmembrane transport
LOC111882973	GO:0005373	Water transmembrane transporter activity
LOC111882973	GO:0005775	Vacuolar membrane
LOC111883019	GO:0042627	ATPase-coupled transmembrane transporter activity
LOC111883019	GO:0055086	Transmembrane transport
LOC111883019	GO:0016022	Integral component of membrane
LOC111883019	GO:0005525	ATP binding
LOC111883439	GO:0005976	Carbohydrate metabolic process
LOC111883613	GO:0006858	Oligopeptide transport
LOC111883613	GO:0022858	Transmembrane transporter activity
LOC111883613	GO:0016022	Integral component of membrane
LOC111883613	GO:0006818	Phosphate ion transport
LOC111883613	GO:0055086	Transmembrane transport
LOC111883729	GO:0046873	Metal ion binding
LOC111883729	GO:0005775	Vacuolar membrane
LOC111883729	GO:0009508	Chloroplast
LOC111883729	GO:0005887	Plasma membrane
LOC111883900	GO:0003701	DNA-binding transcription factor activity
LOC111883900	GO:0005635	Nucleus
LOC111883900	GO:0006356	Regulation of transcription, DNA-templated
LOC111883900	GO:0003678	DNA binding
LOC111883900	GO:0006953	Defense response
LOC111883900	GO:0009874	Ethylene-activated signaling pathway
LOC111883900	GO:0009835	Plant-type secondary cell wall biogenesis
LOC111883900	GO:0009794	Embryo development ending in seed dormancy
LOC111884089	GO:0033835	Kaempferol 3-O-galactosyltransferase activity
LOC111884089	GO:0102480	Quercetin 3-O-beta:-D-galactosyltransferase activity
LOC111884089	GO:0008195	UDP-glycosyltransferase activity
LOC111884615	GO:0048545	Recognition of pollen
LOC111884615	GO:0106312	NA
LOC111884615	GO:0016022	Integral component of membrane
LOC111884615	GO:0106311	NA
LOC111884615	GO:0005887	Plasma membrane
LOC111884615	GO:0005525	ATP binding
LOC111884615	GO:0006469	Protein phosphorylation
LOC111884615	GO:0030247	Carbohydrate binding
LOC111884615	GO:0008271	Zinc ion binding
LOC111884615	GO:0016819	Hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides
LOC111884615	GO:0003677	Nucleic acid binding
LOC111885054	GO:0008018	Microtubule binding
LOC111885054	GO:0005875	Microtubule
LOC111885054	GO:0010500	Proteasomal ubiquitin-independent protein catabolic process
LOC111885054	GO:0010953	Positive regulation of peptidase activity
LOC111885054	GO:0070578	Lysine-acetylated histone binding
LOC111885054	GO:0016505	Peptidase activator activity
LOC111885054	GO:0070629	Proteasome binding
LOC111885054	GO:0005830	Cytosol
LOC111885054	GO:0005635	Nucleus
LOC111885054	GO:0016022	Integral component of membrane
LOC111885300	GO:0004675	Protein serine/threonine kinase activity
LOC111885300	GO:0016311	Phosphorylation
LOC111885300	GO:0016022	Integral component of membrane
LOC111885300	GO:0006465	Cellular protein modification process

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Supplemental Table 2. (Continued)

Unique identifier	ID	GO term
LOC111885300	GO:0005525	ATP binding
LOC111885714	GO:0042410	Caffeoyl-CoA O-methyltransferase activity
LOC111885714	GO:0009810	Lignin biosynthetic process
LOC111885714	GO:0005830	Cytosol
LOC111885714	GO:0005841	Ribosome
LOC111885714	GO:0032260	Methylation
LOC111885714	GO:0080077	Caffeoyl CoA:S-adenosyl-L-methionine O-methyltransferase activity
LOC111885714	GO:0046873	Metal ion binding
LOC111885714	GO:0016780	Nucleotidyltransferase activity
LOC111885714	GO:0003736	Structural constituent of ribosome
LOC111885714	GO:0003724	RNA binding
LOC111885714	GO:0007624	Circadian rhythm
LOC111885714	GO:0010468	Gene expression
LOC111885714	GO:0016071	RNA metabolic process
LOC111885714	GO:0043044	Peptide biosynthetic process
LOC111885714	GO:0034646	Cellular macromolecule biosynthetic process
LOC111885714	GO:0044268	Cellular protein metabolic process
LOC111885750	GO:0003825	Catalytic activity
LOC111886219	GO:0061631	Ubiquitin protein ligase activity
LOC111886219	GO:0006512	Ubiquitin-dependent protein catabolic process
LOC111886219	GO:0016568	Protein ubiquitination
LOC111886241	GO:0003724	RNA binding
LOC111886241	GO:0016022	Integral component of membrane
LOC111886241	GO:0003825	Catalytic activity
LOC111886522	GO:0008234	Peptidase activity
LOC111886522	GO:0006509	Proteolysis
LOC111886522	GO:0016888	ATPase activity
LOC111886522	GO:0005525	ATP binding
LOC111886525	GO:0008271	Zinc ion binding
LOC111886525	GO:0016568	Protein ubiquitination
LOC111886525	GO:0005830	Cytosol
LOC111886525	GO:0004843	Ubiquitin-protein transferase activity
LOC111886525	GO:0016875	Ligase activity
LOC111886531	GO:0043566	Sequence-specific DNA binding
LOC111886531	GO:0005635	Nucleus
LOC111886531	GO:0006356	Regulation of transcription, DNA-templated
LOC111886531	GO:0003701	DNA-binding transcription factor activity
LOC111886531	GO:0001068	Regulatory region nucleic acid binding
LOC111886531	GO:0003691	Double-stranded DNA binding
LOC111886671	GO:0003736	Structural constituent of ribosome
LOC111886671	GO:0005841	Ribosome
LOC111886671	GO:0006413	Translation
LOC111886671	GO:0005830	Cytosol
LOC111886671	GO:0000028	Ribosomal large subunit assembly
LOC111886671	GO:1990905	Ribonucleoprotein complex
LOC111886671	GO:0016022	Integral component of membrane
LOC111886857	GO:0016789	Hydrolase activity, acting on ester bonds
LOC111886949	GO:0043566	Sequence-specific DNA binding
LOC111886949	GO:0005635	Nucleus
LOC111886949	GO:0006356	Regulation of transcription, DNA-templated
LOC111886949	GO:0003701	DNA-binding transcription factor activity
LOC111886949	GO:0001068	Regulatory region nucleic acid binding
LOC111886949	GO:0016741	Transferase activity
LOC111886949	GO:0003691	Double-stranded DNA binding
LOC111886949	GO:0009652	Response to salt stress
LOC111886949	GO:0009415	Response to water deprivation
LOC111887205	GO:0006980	Response to oxidative stress

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Supplemental Table 2. (Continued)

Unique identifier	ID	GO term
LOC111887205	GO:0004602	Peroxidase activity
LOC111887205	GO:0098870	Cellular oxidant detoxification
LOC111887205	GO:0020038	Heme binding
LOC111887205	GO:0046873	Metal ion binding
LOC111887526	GO:0016888	ATPase activity
LOC111887526	GO:0016022	Integral component of membrane
LOC111887526	GO:0005525	ATP binding
LOC111887624	GO:0004191	Aspartic-type endopeptidase activity
LOC111887624	GO:0006509	Proteolysis
LOC111887624	GO:0005577	Extracellular region
LOC111887624	GO:0016022	Integral component of membrane
LOC111887690	GO:0016748	Transferase activity, transferring acyl groups other than amino-acyl groups
LOC111887816	GO:0016043	Lipid catabolic process
LOC111887816	GO:0045736	Nutrient reservoir activity
LOC111887816	GO:0005774	Vacuole
LOC111887816	GO:0016788	Hydrolase activity
LOC111887816	GO:0016741	Transferase activity
LOC111887816	GO:0016022	Integral component of membrane
LOC111887880	GO:0048047	Apoplast
LOC111887880	GO:0042974	Glucan endo-1,3-beta-D-glucosidase activity
LOC111887880	GO:0005976	Carbohydrate metabolic process
LOC111887880	GO:0016022	Integral component of membrane
LOC111887880	GO:0016875	Ligase activity
LOC111887885	GO:0048047	Apoplast
LOC111887885	GO:0042974	Glucan endo-1,3-beta-D-glucosidase activity
LOC111887885	GO:0005976	Carbohydrate metabolic process
LOC111887885	GO:0016022	Integral component of membrane
LOC111887885	GO:0016875	Ligase activity
LOC111888403	GO:0006750	Glutathione metabolic process
LOC111888403	GO:0004365	Glutathione transferase activity
LOC111888403	GO:0005738	Cytoplasm
LOC111888834	GO:0004554	Hydrolase activity, hydrolyzing O-glycosyl compounds
LOC111888834	GO:0005976	Carbohydrate metabolic process
LOC111888834	GO:0005577	Extracellular region
LOC111888834	GO:0009502	Amyloplast
LOC111888834	GO:0042632	Cellular response to water deprivation
LOC111888834	GO:0005619	Cell wall
LOC111888834	GO:0006033	Chitin catabolic process
LOC111888834	GO:0016022	Integral component of membrane
LOC111888834	GO:0009643	Response to light intensity
LOC111888834	GO:0061784	Peptidoglycan muralytic activity
LOC111888834	GO:0004316	4-oxoacyl-[acyl-carrier-protein] synthase activity
LOC111888834	GO:0005510	Calcium ion binding
LOC111888834	GO:0009652	Response to salt stress
LOC111888834	GO:0004673	Protein kinase activity
LOC111888834	GO:0005525	ATP binding
LOC111888834	GO:0002222	Pattern recognition receptor signaling pathway
LOC111888834	GO:0009410	Response to cold
LOC111888834	GO:0009612	Response to wounding
LOC111888834	GO:0009846	Seed germination
LOC111888834	GO:0006634	Fatty acid biosynthetic process
LOC111888834	GO:0006469	Protein phosphorylation
LOC111889458	GO:0004865	Protein phosphatase inhibitor activity
LOC111889458	GO:0032516	Negative regulation of phosphoprotein phosphatase activity
LOC111889458	GO:0005738	Cytoplasm
LOC111889458	GO:0005887	Plasma membrane
LOC111889538	GO:0003825	Catalytic activity

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Supplemental Table 2. (Continued)

Unique identifier	ID	GO term
LOC111889615	GO:0009652	Response to salt stress
LOC111889615	GO:0005803	Trans-Golgi network
LOC111889615	GO:0003730	mRNA binding
LOC111889615	GO:0005769	Endosome
LOC111889615	GO:0016022	Integral component of membrane
LOC111889709	GO:0019954	Sexual reproduction
LOC111889709	GO:0005577	Extracellular region
LOC111889709	GO:0003677	Nucleic acid binding
LOC111889709	GO:0009506	Plant-type cell wall
LOC111889709	GO:0009507	Plasmodesma
LOC111889709	GO:0015075	DNA integration
LOC111889709	GO:0005795	Golgi apparatus
LOC111889709	GO:0016022	Integral component of membrane
LOC111890175	GO:0000787	Nucleosome
LOC111890175	GO:0046983	Protein heterodimerization activity
LOC111890175	GO:0010275	Hydrotropism
LOC111890175	GO:0003678	DNA binding
LOC111890175	GO:0032260	Methylation
LOC111890175	GO:0016311	Phosphorylation
LOC111890175	GO:0005635	Nucleus
LOC111890175	GO:0016302	Kinase activity
LOC111890175	GO:0008169	Methyltransferase activity
LOC111890175	GO:0010370	Chromocenter
LOC111890175	GO:0016022	Integral component of membrane
LOC111890187	GO:0031409	Oxylipin biosynthetic process
LOC111890187	GO:0046873	Metal ion binding
LOC111890405	GO:0006870	Lipid transport
LOC111890405	GO:0008290	Lipid binding
LOC111890405	GO:0016022	Integral component of membrane
LOC111890856	GO:0000326	Plant-type vacuole
LOC111890856	GO:0042627	ATPase-coupled transmembrane transporter activity
LOC111890856	GO:0055086	Transmembrane transport
LOC111890856	GO:0005775	Vacuolar membrane
LOC111890856	GO:0005525	ATP binding
LOC111890856	GO:0016022	Integral component of membrane
LOC111890881	GO:0042556	MCM complex
LOC111890881	GO:0006271	DNA replication initiation
LOC111890881	GO:0003679	DNA helicase activity
LOC111890881	GO:0005635	Nucleus
LOC111890881	GO:0032509	DNA duplex unwinding
LOC111890881	GO:0003678	DNA binding
LOC111890881	GO:0005525	ATP binding
LOC111890881	GO:0016022	Integral component of membrane
LOC111890881	GO:1902300	Prereplicative complex assembly involved in cell cycle DNA replication
LOC111890881	GO:0000728	Double-strand break repair via break-induced replication
LOC111890881	GO:1902970	Mitotic DNA replication
LOC111890881	GO:0006272	DNA strand elongation involved in DNA replication
LOC111890881	GO:0004316	4-oxoacyl-[acyl-carrier-protein] synthase activity
LOC111890881	GO:0006634	Fatty acid biosynthetic process
LOC111890945	GO:0005525	ATP binding
LOC111890945	GO:0005830	Cytosol
LOC111890945	GO:0005635	Nucleus
LOC111890945	GO:0005789	Endoplasmic reticulum lumen
LOC111890945	GO:0016022	Integral component of membrane
LOC111890945	GO:0008271	Zinc ion binding
LOC111890945	GO:0003724	RNA binding
LOC111891004	GO:0016022	Integral component of membrane

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Supplemental Table 2. (Continued)

Unique identifier	ID	GO term
LOC111891022	GO:0030247	Carbohydrate binding
LOC111891176	GO:0033898	Ribonuclease T2 activity
LOC111891176	GO:0090503	RNA phosphodiester bond hydrolysis, endonucleolytic
LOC111891176	GO:0005577	Extracellular region
LOC111891176	GO:0071945	Cell periphery
LOC111891176	GO:0016021	Membrane
LOC111891176	GO:0016830	Lyase activity
LOC111891176	GO:0006402	RNA catabolic process
LOC111891176	GO:0003724	RNA binding
LOC111891176	GO:0009719	Anthocyanin-containing compound biosynthetic process
LOC111891176	GO:0016037	Cellular response to phosphate starvation
LOC111891176	GO:0009612	Response to wounding
LOC111891176	GO:0009868	Jasmonic acid-mediated signaling pathway
LOC111891274	GO:0006818	Phosphate ion transport
LOC111891274	GO:0022858	Transmembrane transporter activity
LOC111891274	GO:0005887	Plasma membrane
LOC111891274	GO:0016022	Integral component of membrane
LOC111891274	GO:0055086	Transmembrane transport
LOC111891274	GO:0006858	Oligopeptide transport
LOC111891274	GO:0015707	Nitrate transport
LOC111891274	GO:0010168	Response to nitrate
LOC111891617	GO:0015268	Channel activity
LOC111891617	GO:0006834	Water transport
LOC111891617	GO:0016022	Integral component of membrane
LOC111891617	GO:0055086	Transmembrane transport
LOC111891617	GO:0005373	Water transmembrane transporter activity
LOC111891617	GO:0005775	Vacuolar membrane
LOC111891617	GO:0000327	Protein storage vacuole
LOC111891670	GO:0004673	Protein kinase activity
LOC111891670	GO:0006469	Protein phosphorylation
LOC111891670	GO:0005738	Cytoplasm
LOC111891670	GO:0005525	ATP binding
LOC111891670	GO:0007166	Signal transduction
LOC111891670	GO:0000187	Activation of MAPKK activity
LOC111892092	GO:0004186	Serine-type carboxypeptidase activity
LOC111892092	GO:0006509	Proteolysis
LOC111892092	GO:0016022	Integral component of membrane
LOC111892092	GO:0019749	Secondary metabolic process
LOC111892092	GO:0016748	Transferase activity, transferring acyl groups other than amino-acyl groups
LOC111892644	GO:0016302	Kinase activity
LOC111892644	GO:0006469	Protein phosphorylation
LOC111892644	GO:0005887	Plasma membrane
LOC111892644	GO:0016774	Phosphotransferase activity, alcohol group as acceptor
LOC111892644	GO:0140097	Catalytic activity, acting on a protein
LOC111892644	GO:0005525	ATP binding
LOC111892644	GO:0042743	Defense response to bacterium
LOC111892644	GO:0005516	Protein binding
LOC111893009	GO:0004479	Methionine adenosyltransferase activity
LOC111893009	GO:0006557	S-adenosylmethionine biosynthetic process
LOC111893009	GO:0005738	Cytoplasm
LOC111893009	GO:0006731	One-carbon metabolic process
LOC111893009	GO:0005525	ATP binding
LOC111893009	GO:0009507	Plasmodesma
LOC111893009	GO:0005635	Nucleus
LOC111893009	GO:0046873	Metal ion binding

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Supplemental Table 2. (Continued)

Unique identifier	ID	GO term
LOC111893009	GO:0005887	Plasma membrane
LOC111893009	GO:0009861	Pollen tube growth
LOC111893009	GO:0012506	Endomembrane system
LOC111893009	GO:0016022	Integral component of membrane
LOC111893009	GO:0005516	Protein binding
LOC111893009	GO:0009810	Lignin biosynthetic process
LOC111893042	GO:0015268	Channel activity
LOC111893042	GO:0055086	Transmembrane transport
LOC111893042	GO:0016022	Integral component of membrane
LOC111893042	GO:0006834	Water transport
LOC111893042	GO:0005373	Water transmembrane transporter activity
LOC111893042	GO:0045491	Pectin catabolic process
LOC111893042	GO:0030600	Pectinesterase activity
LOC111893157	GO:0004436	Phosphatidylinositol phospholipase C activity
LOC111893157	GO:0016043	Lipid catabolic process
LOC111893157	GO:0005887	Plasma membrane
LOC111893157	GO:0035557	Intracellular signal transduction
LOC111893157	GO:0005510	Calcium ion binding
LOC111893157	GO:0003678	DNA binding
LOC111893157	GO:0042824	Pyridoxal phosphate biosynthetic process
LOC111893158	GO:0004436	Phosphatidylinositol phospholipase C activity
LOC111893158	GO:0016043	Lipid catabolic process
LOC111893158	GO:0005887	Plasma membrane
LOC111893158	GO:0035557	Intracellular signal transduction
LOC111893158	GO:0005510	Calcium ion binding
LOC111893158	GO:0005526	GTP binding
LOC111893158	GO:0042255	Ribosome biogenesis
LOC111893574	GO:0016022	Integral component of membrane
LOC111893605	GO:0003701	DNA-binding transcription factor activity
LOC111893605	GO:0006356	Regulation of transcription, DNA-templated
LOC111893605	GO:0005635	Nucleus
LOC111893605	GO:0000977	Transcription regulatory region sequence-specific DNA binding
LOC111893605	GO:0016022	Integral component of membrane
LOC111893605	GO:0046983	Protein heterodimerization activity
LOC111893605	GO:0004708	MAP kinase activity
LOC111893605	GO:1903509	Positive regulation of nucleic acid-templated transcription
LOC111893605	GO:0000166	MAPK cascade
LOC111893678	GO:0043532	ADP binding
LOC111893678	GO:0006953	Defense response
LOC111893678	GO:0016022	Integral component of membrane
LOC111893678	GO:0006509	Proteolysis
LOC111893678	GO:0008235	Cysteine-type peptidase activity
LOC111893678	GO:0005525	ATP binding
LOC111893963	GO:0008644	Carbohydrate transport
LOC111893963	GO:0051120	Sugar transmembrane transporter activity
LOC111893963	GO:0005887	Plasma membrane
LOC111893963	GO:0016022	Integral component of membrane
LOC111893963	GO:0008516	Sucrose transmembrane transporter activity
LOC111893963	GO:0098657	Anion transmembrane transport
LOC111894108	GO:0045549	Phenylalanine ammonia-lyase activity
LOC111894108	GO:0009801	Cinnamic acid biosynthetic process
LOC111894108	GO:0005738	Cytoplasm
LOC111894108	GO:0032992	Protein-containing complex
LOC111894108	GO:0016598	Amino acid binding
LOC111894108	GO:1902223	Erythrose 4-phosphate/phosphoenolpyruvate family amino acid catabolic process
LOC111894108	GO:0006559	L-phenylalanine metabolic process

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Supplemental Table 2. (Continued)

Unique identifier	ID	GO term
LOC111894108	GO:0009075	Aromatic amino acid family catabolic process
LOC111894108	GO:0009064	Cellular amino acid catabolic process
LOC111894108	GO:0009821	Alkaloid metabolic process
LOC111894163	GO:0008195	UDP-glycosyltransferase activity
LOC111894163	GO:0016115	Terpenoid biosynthetic process
LOC111894163	GO:0048047	Apoplast
LOC111894163	GO:0022626	Cytosolic large ribosomal subunit
LOC111894163	GO:0005619	Cell wall
LOC111894163	GO:0004143	Diacylglycerol cholinephosphotransferase activity
LOC111894163	GO:0046528	Glucosyltransferase activity
LOC111894163	GO:0009719	Anthocyanin-containing compound biosynthetic process
LOC111894163	GO:0006658	CDP-choline pathway
LOC111894163	GO:0003736	Structural constituent of ribosome
LOC111894163	GO:0016022	Integral component of membrane
LOC111894163	GO:0043232	Intracellular membrane-bounded organelle
LOC111894163	GO:0002183	Cytoplasmic translational elongation
LOC111894163	GO:0006074	Cellular glucan metabolic process
LOC111894286	GO:0003979	UDP-glucose 4-epimerase activity
LOC111894286	GO:0006013	Galactose metabolic process
LOC111894376	GO:0005635	Nucleus
LOC111894376	GO:0043566	Sequence-specific DNA binding
LOC111894376	GO:0006356	Regulation of transcription, DNA-templated
LOC111894376	GO:0003701	DNA-binding transcription factor activity
LOC111894376	GO:0003825	Catalytic activity
LOC111894376	GO:0010374	Negative regulation of gibberellin biosynthetic process
LOC111894376	GO:0009687	Gibberellin biosynthetic process
LOC111894376	GO:0010016	Root morphogenesis
LOC111894376	GO:0009741	Gibberellic acid mediated signaling pathway
LOC111894376	GO:0016037	Cellular response to phosphate starvation
LOC111894376	GO:0072507	Trivalent inorganic anion homeostasis
LOC111894376	GO:1903508	Negative regulation of nucleic acid-templated transcription
LOC111894376	GO:2000114	Negative regulation of cellular macromolecule biosynthetic process
LOC111894540	GO:0016758	Transferase activity, transferring glycosyl groups
LOC111894540	GO:0016021	Membrane
LOC111894540	GO:0042547	Cell wall biogenesis
LOC111894540	GO:0005774	Vacuole
LOC111894782	GO:0008195	UDP-glycosyltransferase activity
LOC111894782	GO:0009719	Anthocyanin-containing compound biosynthetic process
LOC111894782	GO:0016022	Integral component of membrane
LOC111894782	GO:0046528	Glucosyltransferase activity
LOC111894782	GO:0016115	Terpenoid biosynthetic process
LOC111895350	GO:0008644	Carbohydrate transport
LOC111895350	GO:0051120	Sugar transmembrane transporter activity
LOC111895350	GO:0005887	Plasma membrane
LOC111895350	GO:0016022	Integral component of membrane
LOC111895350	GO:0098657	Anion transmembrane transport
LOC111895777	GO:0031409	Oxylipin biosynthetic process
LOC111895777	GO:0046873	Metal ion binding
LOC111895826	GO:0004673	Protein kinase activity
LOC111895826	GO:0006469	Protein phosphorylation
LOC111895826	GO:0005887	Plasma membrane
LOC111895826	GO:0016022	Integral component of membrane
LOC111895826	GO:0005525	ATP binding
LOC111895826	GO:0005635	Nucleus
LOC111895826	GO:0009756	Hormone-mediated signaling pathway
LOC111895826	GO:0033613	Receptor serine/threonine kinase binding
LOC111895826	GO:0008169	Methyltransferase activity

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Supplemental Table 2. (Continued)

Unique identifier	ID	GO term
LOC111895826	GO:0046874	Metal ion transmembrane transporter activity
LOC111895826	GO:0006398	mRNA processing
LOC111895826	GO:0032260	Methylation
LOC111895826	GO:0030002	Metal ion transport
LOC111895938	GO:0005577	Extracellular region
LOC111895938	GO:0019954	Sexual reproduction
LOC111895938	GO:0016022	Integral component of membrane
LOC111896413	GO:0006980	Response to oxidative stress

Supplemental Table 3. List of genes determined to be differentially expressed from RNA sequencing analyses between lettuce grown unshaded (control) or shaded and their putative functions as annotated in the National Center for Biotechnology Information database.

Log₂FC = log-fold change >2 of unshaded control lettuce relative to the shaded lettuce; genes with positive Log₂FC were expressed to a greater degree in control than shaded lettuce. All gene functions were identified for *Lactuca sativa*.

Unique identifier	Log ₂ FC	Function
LOC111876243	2.06136	Allene oxide synthase
LOC111876247	4.1364	Protein DA1-like
LOC111876394	3.945	Protein sieve element occlusion B-like
LOC111876517	2.65633	S-type anion channel SLAH2-like
LOC111876728	2.59556	DNA polymerase alpha catalytic subunit
LOC111876787	2.59965	Jasmonic acid-amidosynthetase JAR1-like isoform X1
LOC111877021	2.11832	Alcohol dehydrogenase-like 6
LOC111877039	4.98541	Metalloendoproteinase 1-like
LOC111877094	-2.41292	NA
LOC111877141	2.92282	Acyl-protein thioesterase 2-like
LOC111877485	-2.21536	Copper-transporting ATPase HMA4-like
LOC111877830	2.4533	Probable carboxylesterase 12
LOC111877880	-2.1754	NA
LOC111877933	2.46812	NA
LOC111878550	-2.09136	NA
LOC111878863	-2.07719	Uncharacterized protein LOC111878863 isoform X1
LOC111879316	2.34726	Probable carboxylesterase 12
LOC111879403	2.38039	PLAT domain-containing protein 3-like
LOC111880353	2.07473	Uncharacterized protein C24B11.05-like
LOC111880881	-2.32772	Protein branchless trichome-like
LOC111880979	-2.88539	Transcription factor PIF1 isoform X1
LOC111881022	-2.04798	L-type lectin-domain containing receptor kinase IX1-like
LOC111881332	2.16011	Protein downy mildew resistance 6-like
LOC111881482	2.00605	Protein EDS1-like
LOC111881492	2.94923	Protein EDS1-like
LOC111881554	3.5532	Cysteine-rich receptor-like protein kinase 2
LOC111881702	2.45879	Protein SRC2 homolog
LOC111881935	2.27995	Early light-induced protein 1, chloroplastic-like
LOC111881937	2.40866	Early light-induced protein 1, chloroplastic-like
LOC111881993	-2.22421	Uncharacterized protein
LOC111882123	2.3901	Protein NRT1/PTR family 2.10-like isoform X1
LOC111882377	2.35961	Expansin-B3-like
LOC111882479	2.38806	Ribonucleoside-diphosphate reductase large subunit
LOC111882484	3.73582	Ethylene-responsive transcription factor ERF110-like
LOC111882588	2.17476	Mitogen-activated protein kinase 3-like
LOC111882695	2.37048	Uncharacterized protein
LOC111882721	3.13039	Probable leucine-rich repeat receptor-like protein kinase At1g35710
LOC111882970	2.07176	Uncharacterized protein
LOC111882972	2.14772	Probable aquaporin TIP-type RB7-5A
LOC111883018	2.73285	ABC transporter G family member 14-like

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Supplemental Table 3. (Continued)

Unique identifier	Log ₂ FC	Function
LOC111883438	2.53294	IanC-like protein GCL1 isoform X1
LOC111883612	-2.36808	Protein NRT1/ PTR FAMILY 5.4
LOC111883689	-2.20867	WAT1-related protein At4g30420-like
LOC111883728	2.23753	Protein ALP1-like
LOC111883899	2.41745	Ethylene-responsive transcription factor TINY-like
LOC111884088	3.60776	Kaempferol 3-O-beta-D-galactosyltransferase-like
LOC111884104	-2.36114	NA
LOC111884283	-2.53107	NA
LOC111884410	2.7522	Probable polyamine oxidase 2 isoform X1
LOC111884614	-2.06201	G-type lectin S-receptor-like serine/threonine-protein kinase At2g19130
LOC111885053	2.28411	TORTIFOLIA1-like protein 2
LOC111885299	-2.13277	Probable serine/threonine-protein kinase PIX7
LOC111885626	2.88604	Uncharacterized protein
LOC111885713	3.43415	Caffeoyl-CoA O-methyltransferase-like
LOC111885749	2.29546	Cinnamoyl-CoA reductase-like SNL6
LOC111886218	2.07358	E3 ubiquitin-protein ligase RNF165-like
LOC111886240	4.00899	Uncharacterized protein
LOC111886268	-2.91247	NA
LOC111886521	-2.15879	Putative cell division cycle ATPase
LOC111886524	2.61458	Probable E3 ubiquitin-protein ligase RHB1A
LOC111886530	3.38101	Probable WRKY transcription factor 29
LOC111886666	2.19204	Trans-cinnamate 4-monooxygenase-like
LOC111886670	3.00294	60S ribosomal protein L10
LOC111886856	2.66041	GDSL esterase/lipase At1g29670-like
LOC111886948	2.63954	Probable WRKY transcription factor 48
LOC111887204	2.52458	Peroxidase 25
LOC111887525	3.10972	AAA-ATPase ASD, mitochondrial-like
LOC111887623	2.05109	Aspartyl protease family protein 2-like
LOC111887689	2.73158	Putrescine hydroxycinnamoyltransferase 1-like
LOC111887815	3.59888	Patatin-like protein 6
LOC111887879	2.13264	Dirigent protein 22-like
LOC111887884	3.23106	Dirigent protein 22-like
LOC111888402	2.65769	Glutathione S-transferase U17-like
LOC111888833	2.20048	Acidic endochitinase SE2-like
LOC111889457	2.03602	Uncharacterized protein
LOC111889537	2.19423	Cinnamoyl-CoA reductase 2-like
LOC111889614	-2.68813	BURP domain protein RD22-like
LOC111889708	2.21254	Expansin-like A1
LOC111890174	3.41477	Histone H3.2
LOC111890186	2.46636	Linoleate 13S-lipoxygenase 2-1, chloroplastic-like
LOC111890404	2.64078	Nonspecific lipid-transfer protein 2-like
LOC111890529	4.46035	Protein DMR6-like oxygenase 1-like
LOC111890608	2.07046	WAT1-related protein At1g43650-like
LOC111890855	2.11449	A xBC transporter C family member 10-like
LOC111890880	2.44881	DNA replication licensing factor MCM3
LOC111890944	2.31882	Heat shock 70 kDa protein 16-like
LOC111891003	2.89468	Protein Restricted TEV movement 2-like
LOC111891021	2.48021	Mannose/glucose-specific lectin-like
LOC111891175	2.59822	Extracellular ribonuclease LE-like
LOC111891273	2.3025	Protein NRT1/PTR family 1.2-like
LOC111891593	-2.26827	Uncharacterized protein LOC111891593 isoform X1
LOC111891616	3.66593	Probable aquaporin TIP-type RB7-5A
LOC111891669	-2.00956	Serine/threonine-protein kinase HT1-like
LOC111891797	2.2117	Elicitor-responsive protein 3-like
LOC111892091	3.21446	Serine carboxypeptidase-like 3
LOC111892191	3.09242	Putative UPF0481 protein At3g02645

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Supplemental Table 3. (Continued)

Unique identifier	Log ₂ FC	Function
LOC111892407	2.22091	F-box protein SKIP27-like
LOC111892511	2.13289	Artemisinic aldehyde Delta(11(13)) reductase
LOC111892643	2.47764	Serine/threonine-protein kinase RIPK-like
LOC111893008	2.5538	S-adenosylmethionine synthase 2-like
LOC111893041	-3.82352	Aquaporin TIP1-1-like
LOC111893156	2.656	Phosphoinositide phospholipase C 4-like
LOC111893157	2.89318	Phosphoinositide phospholipase C 2-like
LOC111893409	-2.28432	NA
LOC111893573	-2.65074	F-box protein At2g27310-like
LOC111893604	2.01957	bZIP transcription factor 11-like
LOC111893677	2.5044	Putative disease resistance RPP12-like protein 2
LOC111893685	2.24254	Uncharacterized protein LOC111893685 isoform X1
LOC111893884	-2.10778	NA
LOC111893962	2.06514	Bidirectional sugar transporter SWEET14-like
LOC111894107	2.12791	Phenylalanine ammonia-lyase-like
LOC111894162	-3.00172	UDP-glycosyltransferase 73C3-like
LOC111894285	2.01909	UDP-glucose 4-epimerase GEPI48-like
LOC111894375	-2.18355	Transcription factor MYB62-like
LOC111894539	2.3947	Galactan beta-1,4-galactosyltransferase GAL53-like
LOC111894781	2.83561	Kaempferol 3-O-beta-D-galactosyltransferase-like
LOC111895349	2.49039	Bidirectional sugar transporter SWEET14-like
LOC111895541	-2.01298	NA
LOC111895744	2.16822	Organ-specific protein S2-like
LOC111895776	2.6741	Probable linoleate 9S-lipoxygenase
LOC111895825	2.45401	Probable leucine-rich repeat receptor-like protein kinase At1g35710
LOC111895937	-2.01183	Expansin-like B1
LOC111896412	2.88668	Peroxidase N1-like
LOC111896417	2.45955	Transcription factor MYB61-like
LOC111896675	2.85416	Uncharacterized protein
LOC111897139	2.38531	Uncharacterized protein
LOC111897180	2.78593	Metalloendoproteinase 2-MMP-like
LOC111897395	2.76588	Protein strubbelig-receptor family 8-like isoform X1
LOC111897605	2.09868	Extradiol ring-cleavage dioxygenase
LOC111897843	2.17395	Delta-9 acyl-lipid desaturase 1-like
LOC111898199	2.59945	Probable WRKY transcription factor 38
LOC111898200	2.38321	Probable WRKY transcription factor 70
LOC111898223	2.58181	Protein LURP-one-related 10-like
LOC111898297	2.19462	Inositol-tetrakisphosphate 1-kinase 5-like
LOC111898348	2.51157	Uncharacterized protein
LOC111898411	-2.88755	Auxin-responsive protein IAA29-like
LOC111898507	2.59846	Isoflavone reductase homolog
LOC111898508	2.19367	UDP-glucosyl transferase 73B2-like
LOC111898605	2.02453	NA
LOC111898611	2.84834	ruBisCO large subunit-binding protein subunit beta, chloroplastic-like
LOC111898626	3.4482	UDP-glycosyltransferase 74G1-like
LOC111898732	2.87366	BTB/POZ and TAZ domain-containing protein 1-like
LOC111899032	2.46596	Metacaspase-1-like
LOC111899252	2.56638	Beta-caryophyllene synthase-like
LOC111899324	2.45384	Probable trehalose-phosphatase D
LOC111899382	2.21906	Glucan endo-1,3-beta-glucosidase, acidic-like
LOC111899637	2.26143	Uncharacterized protein
LOC111899806	2.11987	Fasciclin-like arabinogalactan protein 17
LOC111900009	-2.11973	Monothiol glutaredoxin-S4-like
LOC111900059	2.49352	Probable carboxylesterase 17
LOC111900135	-2.0976	Uncharacterized protein
LOC111900177	2.12291	Patatin-like protein 7

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Supplemental Table 3. (Continued)

Unique identifier	Log ₂ FC	Function
LOC111900246	4.43221	Ribulose biphosphate carboxylase small chain 4, chloroplastic-like
LOC111900275	2.35518	Heavy metal-associated isoprenylated plant protein 21-like isoform X1
LOC111900788	2.98652	Arabinogalactan peptide 13-like
LOC111900911	2.24482	Bifunctional 3-dehydroquinate dehydratase/shikimate dehydrogenase, chloroplastic-like
LOC111900976	2.55533	Serine carboxypeptidase-like
LOC111901004	2.18256	S-linalool synthase
LOC111901011	2.75193	Chitin-inducible gibberellin-responsive protein 1-like
LOC111901019	2.3001	Calcium-binding protein PBP1-like
LOC111901270	2.94566	Probable 2-oxoglutarate-dependent dioxygenase At5g05600
LOC111901413	-2.39575	NA
LOC111901426	2.26332	Arogenate dehydratase/prephenate dehydratase 6, chloroplastic-like
LOC111901609	2.20249	Uncharacterized protein
LOC111901674	-2.22187	NA
LOC111901838	2.35442	Uncharacterized protein
LOC111901841	2.00742	Allene oxide cyclase, chloroplastic-like
LOC111902058	-2.66427	Probable beta-D-xylosidase 2 isoform X1
LOC111902216	2.21109	Expansin-A4-like
LOC111902319	2.41221	Butyrate-CoA ligase AAE11, peroxisomal-like
LOC111902855	4.18664	Glycine-rich protein DC7.1-like
LOC111903004	2.7961	Caffeic acid 3-O-methyltransferase-like
LOC111903226	2.61053	Protein detoxification 49-like
LOC111903232	2.54125	Ethylene-responsive transcription factor ERF027-like
LOC111903507	2.42471	Desumoylating isopeptidase 1-like
LOC111903572	2.24376	R-linalool synthase QH1, chloroplastic-like
LOC111903849	2.06014	AP2-like ethylene-responsive transcription factor AIL 1
LOC111903871	-2.00381	Serine/threonine-protein kinase STY46-like
LOC111904177	-2.1879	Receptor homology region, transmembrane domain- and RING domain-containing protein 2-like
LOC111904236	3.36666	Serine carboxypeptidase-like 13
LOC111904561	2.179	Probable galacturonosyltransferase-like 3
LOC111904670	2.35439	Clavamate synthase-like protein At3g21360
LOC111905143	2.11671	Crocetin glucosyltransferase, chloroplastic-like 3
LOC111905147	2.49817	Adenosylhomocysteinase 1-like
LOC111905180	-2.46176	Formin-like protein 3
LOC111905312	2.85524	Dirigent protein 22-like
LOC111905362	2.36382	Ricin B-like lectin EULS3
LOC111905399	4.22205	Cytochrome P450 94C1
LOC111905890	3.29579	Auxin response factor 16-like
LOC111906005	2.44252	Benzoate carboxyl methyltransferase-like
LOC111906255	2.12874	probable aquaporin PIP2-5
LOC111906468	2.40144	Mitochondrial phosphate carrier protein 3, mitochondrial-like
LOC111906534	2.68468	Probable glutathione S-transferase parA
LOC111906761	3.13159	Probable anion transporter 3, chloroplastic
LOC111906858	2.37683	Inorganic pyrophosphatase 2-like
LOC111906884	-2.43753	NA
LOC111907185	2.77558	Late embryogenesis abundant protein -like
LOC111907568	2.23141	Amino-acid permease BAT1 homolog isoform X1
LOC111907636	2.40167	Peptidyl-prolyl cis-trans isomerase FKBP62-like
LOC111907716	3.99943	Steroid 5-alpha-reductase DET2-like
LOC111907787	-2.30506	Auxin-responsive protein SAUR71-like
LOC111907847	3.10352	Protein detoxification 40-like
LOC111907858	2.05972	5'-adenylylsulfate reductase 3, chloroplastic-like
LOC111907932	2.74001	ABC transporter G family member 29-like
LOC111907938	-2.19636	FK506-binding protein 5-like
LOC111908023	2.9191	Probable boron transporter 6
LOC111908115	2.55272	Protein proton gradient regulation 5, chloroplastic-like

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Supplemental Table 3. (Continued)

Unique identifier	Log ₂ FC	Function
LOC111908252	-2.1345	Ribulose biphosphate carboxylase small chain, chloroplastic-like
LOC111908579	2.1753	Mannose/glucose-specific lectin-like isoform X1
LOC111908651	-2.57869	RING-H2 finger protein ATL3-like
LOC111909087	3.20288	ATP-dependent Clp protease adapter protein CLPS1, chloroplastic-like
LOC111909313	2.93982	Protein EXORDIUM-like
LOC111909436	2.47116	Heat shock cognate 70 kDa protein 2-like
LOC111909468	3.15559	Uncharacterized protein At1g24485-like
LOC111909471	2.54267	Caffeoylshikimate esterase-like
LOC111909531	2.2964	Protein SRG1-like
LOC111909574	-2.23955	Probably inactive leucine-rich repeat receptor-like protein kinase IMK2
LOC111909618	3.23389	Probable xyloglucan endotransglucosylase/hydrolase protein 23
LOC111909622	3.42536	Probable xyloglucan endotransglucosylase/hydrolase protein 23
LOC111909624	4.26806	Probable xyloglucan endotransglucosylase/hydrolase protein 23
LOC111909659	-2.60432	Palmitoyl-monogalactosyldiacylglycerol delta-7 desaturase, chloroplastic-like
LOC111909664	-3.40969	Palmitoyl-monogalactosyldiacylglycerol delta-7 desaturase, chloroplastic-like isoform X1
LOC111909702	2.34432	Glycine cleavage system H protein 2, mitochondrial
LOC111909907	2.62365	Pectate lyase
LOC111910354	2.83868	Protein TIFY 10A-like
LOC111910453	2.82468	Protein ECERIFERUM 3-like
LOC111910620	-2.79191	F-box/kelch-repeat protein At3g23880-like
LOC111910646	2.15115	Probable BOI-related E3 ubiquitin-protein ligase 2
LOC111910767	2.75308	Uncharacterized protein
LOC111910872	2.18251	O-fucosyltransferase 34-like isoform X1
LOC111911281	2.20192	ABC transporter B family member 25-like
LOC111911287	2.45941	berberine bridge enzyme-like 21
LOC111911307	2.11547	Malonyl-coenzyme A:anthocyanin 3-O-glucoside-6"-O-malonyltransferase-like, partial
LOC111911466	2.55287	Transcription factor bHLH18-like
LOC111911571	2.29104	Probable aspartyl protease At4g16563
LOC111912126	2.30542	Phospho-2-dehydro-3-deoxyheptonate aldolase 1, chloroplastic-like
LOC111912165	-2.09204	Transcription repressor OFP15-like
LOC111912265	2.86329	Heat shock cognate 70 kDa protein 2-like
LOC111912278	-2.02333	Uncharacterized protein
LOC111912330	2.69766	Protein TIFY 9
LOC111912456	2.07431	Polyphenol oxidase I, chloroplastic-like
LOC111912461	3.62611	9-cis-epoxycarotenoid dioxygenase NCED3, chloroplastic-like
LOC111912542	-2.29895	NA
LOC111912595	2.72168	Calcium-binding allergen Ole e 8-like
LOC111913194	2.23945	Kunitz trypsin inhibitor 2-like
LOC111913243	2.59058	Ethylene-responsive transcription factor ERF026-like isoform X1
LOC111913550	-2.18355	Transcription factor MYB98-like
LOC111913551	-2.14973	Sodium/calcium exchanger NCL1-like
LOC111913698	2.17375	U-box domain-containing protein 19-like
LOC111914035	2.38657	Trifunctional UDP-glucose 4,6-dehydratase/UDP-4-keto-6-deoxy-D-glucose 3,5-epimerase/UDP-4-keto-L-rhamnose-reductase RHM1
LOC111914172	3.38596	Calmodulin-like
LOC111914173	3.20703	Calmodulin-like
LOC111914174	2.45295	Gibberellin 2-beta-dioxygenase 1-like
LOC111914319	3.49066	L-ascorbate oxidase homolog
LOC111914339	2.69766	DNA replication licensing factor MCM7
LOC111914394	3.83192	Transcription factor bHLH35
LOC111914527	-3.50741	Uncharacterized protein
LOC111914848	2.70491	4-coumarate-CoA ligase 1-like
LOC111914968	3.2706	L-ascorbate oxidase homolog
LOC111915059	2.53798	GATA transcription factor 8-like
LOC111915345	2.04442	Uncharacterized protein
LOC111915373	2.10145	COBRA-like protein

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Supplemental Table 3. (Continued)

Unique identifier	Log ₂ FC	Function
LOC111915479	2.90372	Receptor-like protein kinase feronia
LOC111915584	2.60677	Probable 1-deoxy-D-xylulose-5-phosphate synthase 2, chloroplastic
LOC111915607	2.1966	Dirigent protein 22-like
LOC111915618	2.39941	UDP-glycosyltransferase 89B1-like
LOC111915766	3.06365	Jasmonate O-methyltransferase isoform X1
LOC111915837	2.04625	Probable peroxxygenase 4
LOC111915905	4.59722	Alkaline ceramidase-like
LOC111916006	2.61926	Protein PIN-LIKES 3-like
LOC111916009	3.63189	Protein PIN-LIKES 3-like
LOC111916010	2.47871	Protein SRC2-like
LOC111916178	-2.54585	Uncharacterized protein
LOC111916311	2.21427	Fasciclin-like arabinogalactan protein 15
LOC111916339	2.84009	Glycerol-3-phosphate acyltransferase 1
LOC111916376	2.54931	Phenylalanine ammonia-lyase-like
LOC111916390	2.44656	Aquaporin PIP2-4-like
LOC111916602	2.67129	Protein QUIRKY
LOC111916769	2.95094	Cytochrome P450 71A4-like
LOC111916886	3.49122	Sodium/calcium exchanger NCL2-like
LOC111917061	-2.10623	Uncharacterized protein LOC111917061 isoform X1
LOC111917129	2.05094	Uncharacterized protein
LOC111917191	2.10239	WRKY transcription factor 18-like
LOC111917379	2.1246	UDP-glycosyltransferase 85C1-like
LOC111917517	-3.60641	Delta-9 acyl-lipid desaturase 1-like
LOC111917742	2.4799	Uncharacterized protein LOC111917742 isoform X1
LOC111918093	2.71436	Uncharacterized protein
LOC111918157	2.43292	Flavonoid 3'-monooxygenase-like
LOC111918237	2.06285	Isoflavone reductase homolog PCBER-like
LOC111918253	2.00479	Chaperone protein dnaJ 10-like isoform X1
LOC111918309	2.4395	D-galacturonate reductase-like
LOC111918331	2.85392	Transcription factor MYB14-like
LOC111918349	2.81867	Small heat shock protein, chloroplastic-like
LOC111918783	2.282	Hydroquinone glucosyltransferase-like
LOC111918791	2.13661	Endoglucanase 6-like
LOC111918869	-2.06287	NA
LOC111918933	3.69079	Cellulose synthase-like protein D3
LOC111919005	2.49331	Dehydrodolichyl disphosphate synthase 6-like
LOC111919520	2.41184	ethylene-responsive transcription factor ABR1-like isoform X1
LOC111919665	2.18169	Uncharacterized protein
LOC111919702	2.20474	Omega-3 fatty acid desaturase, chloroplastic
LOC111919969	-2.27404	Probable aminotransferase TAT2
LOC111919987	2.79172	Sodium/calcium exchanger NCL-like
LOC111920239	2.20081	Uncharacterized protein LOC111920239 isoform X1
LOC111920356	-2.04893	Uncharacterized protein
LOC111920377	2.71295	Galactinol synthase 2-like
LOC111920798	3.16875	RHOMBOID-like protein 2
LOC111921165	3.04456	NA
LOC111921267	2.02166	TPR repeat-containing thioredoxin TTL1-like
LOC111921280	2.14829	Probable glucan 1,3-beta-glucosidase A
LOC111921603	-2.4112	Protein FEZ-like
LOC111921651	-2.61606	Uncharacterized protein LOC111921651 isoform X1
LOC111921786	3.69538	Extensin-2-like